Uncovering the effects of early life cigarette smoke exposure on offspring lung function and DNA methylation patterns using a mouse model

by

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Abstract

Early life cigarette smoke (CS) exposure has been associated with the development of sex-specific, persistent health deficits in offspring, and changes in epigenetic marks such as DNA methylation (DNAm) potentially link early life CS to these health outcomes. There is also evidence that addition of a secondary CS exposure in adulthood further exacerbates these health alterations, a process known as priming. However, while past studies have identified DNAm patterns which are altered following early life CS, the impacts of prenatal and early postnatal CS have not been studied separately, most of the past research was conducted in blood with little evidence from the lungs and other more proximal tissues, and DNAm patterns underlying sex-specific health outcomes have not been investigated. In addition, the molecular mechanisms underlying priming upon combined early and later life CS have not been reported. Using a mouse model which we developed to separately study the effects of prenatal, early postnatal, or combined CS exposure on offspring lung function and DNAm, we uncovered differentially methylated sites and lung function phenotypes which are unique to each type of CS exposure, with minimal overlaps across groups, across tissues and between sexes. We also identify DNAm alterations which persist into adulthood following early life CS, identifying a period in adulthood where the effects of early life CS exposure are most pronounced. Our results also demonstrate for the first time, epigenetic priming in mice following repeated CS exposure, and we identify novel biomarkers specific to prenatal CS exposure and smoking in adulthood. Overall, this research offers deeper insights into the molecular mechanisms underlying early life CS-induced phenotypes, as this understanding is important to the development of intervention strategies to mitigate the effects of early life CS exposure on offspring health.

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Forward

This thesis is formatted in accordance with the requirements of the Department of Biochemistry and Medical Genetics and the Faculty of Graduate Studies of the University of Manitoba. It begins with a literature review chapter, followed by three manuscripts, and a concluding chapter. The first two manuscripts (Chapters 2 and 3) have been published in *Epigenetics* and *American Journal of Physiology – Lung Cellular and Molecular Physiology* respectively, while Chapter 4 will be submitted to peer-reviewed journals.

Chapter 1: Introduction

1.1 Smoking prevalence worldwide and in Canada

Tobacco use worldwide has gradually reduced over time, but is still significant, as around 8 million people worldwide die due to tobacco-related health complications[1]. Of these, 7 million deaths are due to personal smoking, while second-hand smoke exposure causes mortality in about 1.3 million individuals worldwide[1]. As of 2020, the World Health Organization reported the total worldwide prevalence of tobacco use in individuals above 15 years of age to be 22.3%, and the most tobacco use was reported amongst people living in upper-middle income countries[2]. In all cases, men consume more tobacco on average than women (1 billion males versus 231 million females worldwide), and age-specific reports also indicate that the rates of tobacco use peaks at ages 45-54 (46.9%) in males and later at ages 55-64 (10.8%) in females[2]. Tobacco is consumed in different ways, but cigarette smoking is the most common form of consumption. In Canada in 2022, the prevalence of current cigarette smokers aged 15 years and above was reported as 10.9% or 3.5 million[3]. Of these, 8.2% are daily smokers, while the remainder are occasional smokers, and more males (9.1%) smoked cigarettes daily than females (7.3%)[3]. Additionally, certain populations still report significant levels of smoking, including individuals with lower educational achievements, people who identify as Indigenous, and those living with disabilities[4]. The general consensus is thus that while cigarette smoking and tobacco use in general are declining over time, the levels remain high enough to constitute a significant burden on the health sector.

1.2 Health consequences of cigarette smoke

The efforts to reduce cigarette smoking levels even further are being intensified largely due to the numerous detrimental effects cigarette smoking has on an individual's health. Cigarette smoke is a complex mixture of more than 7000 components, including nicotine, carbon monoxide, tar, and heavy metals such as lead and mercury, and many of these components are known carcinogens[5,6]. These components are divided into 2 major phases: the tar/particulate phase and the gas phase, and both are rich in reactive oxygen and nitrogen species, via which cigarette smoke elicits most of its damage[7,8]. The particulate phase is composed of compounds such as heavy metals, nitrosamines and nicotine, as well as polyaromatic hydrocarbons[9,10]. These components can be absorbed by the lungs, mucous membranes, skin and by the gastrointestinal tract[9]. The gas phase consists of low molecular weight components like aldehydes and carbon monoxide which are easily absorbed into the pulmonary circulation[10,11].

Cigarette smoke affects virtually all body systems, and has been linked to the development of pulmonary and lung function deficits such as asthma, emphysema and chronic obstructive pulmonary disease (COPD), cardiovascular defects like hypertension and atherosclerosis, reproductive and gastrointestinal defects, neurological defects like multiple sclerosis and attention deficit hyperactivity disorder (ADHD), as well as many types of cancer. This summary goes into more details on some of the common health effects of cigarette smoke but it is not exhaustive, as they are numerous.

1.2.1 Pulmonary deficits: Cigarette smoke directly damages the respiratory tract, initiating and increasing the risk of developing COPD, characterized by mucus gland hyperplasia, impaired endothelial functioning, loss of airway cilia and worsening of inflammation leading to

lung injury[12–14]. The severity of lung abnormalities resulting due to COPD is directly related to the number of packs smoked per day and the duration of smoking[15–17]. Cigarette smoke has also been shown to exacerbate asthma by increasing airway hyperresponsiveness, altering mucociliary clearance in airways, increasing IgE production and allergic sensitization, and exacerbating chronic inflammation[18,19]. Cigarette smoke increases the risk of infection by tuberculosis, influenza and other infectious agents[18,20,21], and is a major cause of lung cancer, increasing risk by over ten-fold[22,23].

1.2.2 Cardiovascular deficits: Cigarette smoke is a major cause of and contributor to the development of cardiovascular defects. Smokers have a greater-than-five-fold likelihood to develop myocardial infarctions compared to nonsmokers[24,25]. In a similar vein, atherosclerosis progression is cumulative and directly related to the number of pack years of smoking[26,27]. While there is generally a positive relationship between cigarette smoke consumption and the risk of smoking-induced disease outcomes, the relationship is non-linear in the case of cardiovascular diseases, as people who smoke less have a higher than expected risk of developing cardiovascular defects[28].

1.2.3 Gastrointestinal deficits: Cigarette smoking is a risk factor for the development of gastrointestinal and digestive disorders such as peptic ulcers and inflammatory bowel disease. A large US-based cohort reported that the prevalence of peptic ulcer in current smokers (11.4%) is almost double that of nonsmokers (6%)[29], and the risk of developing ulcer increases with increasing doses of cigarette smoke[30,31]. Cigarette smoking alters cellular proliferation, reduces mucus synthesis and secretion, and reduces blood vessel

formation and blood flow in the mucosa of the gastrointestinal tract, ultimately favoring the development of inflammatory diseases[32,33].

1.2.4 Reproductive deficits: Cigarette smoking has detrimental consequences both on the smokers' reproductive system, and on the health of their offspring. In men, cigarette smoking has been associated with reduced male fertility, reduced sperm motility and increased sperm DNA fragmentation[34]. In women, smoking reduces fertility via mechanisms including delayed corpora lutea formation and gamete implantation, delayed postfertilization cleavage, shortened menstrual cycles and increased chances of anovulation[35]. Offspring health is also affected by smoking, as it increases the rates of stillbirth, pre-term deliveries, low birth weight, preeclampsia, preterm birth and sudden infant death syndrome[12,36].

1.3 Mechanisms underlying cigarette smoke-induced damages

While the mechanisms underlying the detrimental effects of cigarette smoke are not fully understood, some of them have been attributed to the action of reactive species, oxidative damage and DNA damage resulting from cigarette smoke[37–45]. Cigarette smoking induces DNA damage in bronchial epithelial cells by causing single strand breaks to the DNA, but this damage is not accompanied by increased apoptosis, thereby increasing the accumulation of oncogenic mutations in smokers[37].

A less well understood mechanism involves direct damage to alveolar epithelial cells by the reactive oxygen and nitrogen species found in cigarette smoke. One of these reactive oxygen species, hydrogen peroxide, induces alveolar and bronchial epithelial death by causing the activation of a complex cascade involving decrease in glutathione, and increase in ceramide production[39,40]. Cigarette smoking damages the tight junctions of the lung

epithelia, causing oversecretion of mucus and increase in infiltration of inflammatory immune cells into the damaged lung tissue[46–50].

Another mechanism by which cigarette smoking damages the lungs involves infiltration and accumulation of immune cells such as neutrophils, monocytes, macrophages, mast cells, natural killer cells and dendritic cells[46,51], contributing to inflammation. These cells are major components of the innate immunity, and cigarette smoking disrupts these defense mechanisms, making the individual more likely to develop infections[51,52]. Cigarette smoke exposure in humans and animals leads to drastic increase in the numbers of lung macrophages and dendritic cells, with this increase leading to the exacerbation of inflammation, release of cytokines, chemokines and reactive oxygen species[53–55]. Although cigarette smoking increases the number of macrophages in the lungs, these macrophages do not function properly, as alveolar macrophages from smokers have reduced ability to release pro-inflammatory cytokines[56–60], and cannot properly phagocytose bacterial and apoptotic cells[61–63]. Similarly, cigarette smoke exposure in mice causes accumulation of lipids in pulmonary macrophages, followed by increase in interleukin 1α, possibly to protect against this lipid accumulation, thereby resulting in increased inflammation[38]. Cigarette smoking is also associated with an increased number of eosinophils in tissues such as blood, lung lavage fluid, lungs and nasal epithelial cells[64–68]. In a large cohort of non-asthmatic and non-COPD patients, smoking led to an increase in eosinophils in the blood, and this increase was predictive of future development of obstructive lung diseases[69]. Therefore, counting eosinophils in the blood of smokers may help predict their predisposition to COPD and other obstructive diseases, and can be used as a means for early intervention. Similarly, neutrophil accumulation in smokers' lungs leads to the release of proteases and reactive oxygen

species, and these molecules play a crucial role in the development and progression of COPD[70].

Cigarette smoking also increases infiltration of adaptive immune cells into tissues, with an increase in the numbers of CD3+ and CD4+ T cells in peripheral blood[71], and CD8+, Th1 and Th17 cells in bronchoalveolar lavage of current smokers and in smokers with COPD[72–74]. Another important component of the adaptive immune system, B lymphocytes, are also affected by cigarette smoke, as B cell development and immunoglobulin production are impaired in current smokers[75] and in active smokers with COPD[76]. While IgG, IgA and IgM levels in smokers are decreased compared to nonsmokers, IgE levels are increased by cigarette smoking, and this increases the risk of developing atopy and asthma[77,78].

Altogether, cigarette smoke affects numerous signaling pathways, increasing immune cell infiltration and inflammation via complex mechanisms. These alterations contribute to the development of allergic diseases as shown by *in vitro* and *in vivo* studies. This section summarizes some of the mechanisms underlying cigarette smoke-mediated inflammation and injury, but is not an exhaustive review.

1.4 Methods used to measure lung function

There are many methods used to measure lung function, such as spirometry, plethysmography, forced oscillation techniques and bronchial challenge tests. These tests measure parameters such as airway resistance, elastance and responsiveness, either unchallenged, or in response to an inhaled stimulant, and this way, can be used to detect and monitor lung diseases. Cigarette smoking results in a decline in all lung function parameters and given its numerous detrimental consequences on the lungs, this section highlights three

of the common methods used to measure lung function in both smokers and nonsmokers, which are relevant to this research.

1.4.1 Spirometry: Spirometry is the most widely used pulmonary function test in humans. It assesses lung function by measuring specifically the volume and flow of air that can be inhaled and exhaled per time[79]. It provides measurements such as the forced vital capacity (FVC) which is the total volume of exhaled air, and forced expiratory volume in one second (FEV1) which is the volume of air that can be exhaled in one second, as well as their ratio FEV1/FVC[80]. These parameters can be used to diagnose and monitor obstructive and restrictive lung diseases such as asthma, COPD, and lung fibrosis, and can help improve the rates of smoking cessation[81]. Generally, the process involves the use of nose clips to prevent air escape, and a mouth sensor to provide a tight seal. The patient is then guided to inhale abruptly and with maximum effort, followed by maximal exhale[79]. Due to the effort involved on the part of the patient, this test needs to be repeated multiple times to ensure reproducibility, and it cannot be conducted on small children or in animals[79,82].

1.4.2 Bronchial challenge tests: Airway hyperresponsiveness is a marked characteristic of lung diseases such as asthma[83]. Bronchoprovocation tests are dose-response tests which measure the tendency to develop airway obstruction and/or hyperresponsiveness once the airways are challenged either by a direct-acting or an indirect-acting stimulus[84,85]. Direct acting agents induce bronchoconstriction by acting directly on airway smooth muscle receptors such as muscarinic receptors (acted on by the muscarinic agents methacholine and acetylcholine) and H1 receptors (acted on by histamine)[84]. Indirect-acting agents induce bronchoconstriction via intermediate pathways, such as release of inflammatory

cells/mediators, and they include physical stimuli such as cold air and exercise, and chemical stimuli such as bradykinin and adenosine monophosphate[84,85]. Methacholine is the most commonly used bronchial challenge test[86]. The challenge generally begins with aerosolizing methacholine using a nebulizer, and then administering different concentrations of the aerosols into the lungs[84,87]. The doses are administered in increments until there is a >20% fall in FEV1, after which bronchoconstriction is reversed by administration of an inhaled β2 agonist[84]. Methacholine tests can be conducted both in humans and mice, but in mice, they are usually used in combination with other lung function tests such as forced oscillation technique.

1.4.3 Forced Oscillation Technique (FOT): This is a noninvasive and versatile method of investigating lung function. It involves applying oscillating pressure airwaves or forced perturbations of different frequencies (3-30Hz) to the mouth while the subject continues to breathe normally/quietly[88–90]. The resultant pressure and flow changes at the mouth are analyzed and used to calculate metrics such as elastance, resistance (Rrs) and reactance[91]. Low frequencies penetrate deep into the lungs while higher frequencies are absorbed before getting to the smaller lung airways. Therefore, resistance taken after low frequency oscillations represent total airway resistance, those taken after high frequency oscillations represent central airway resistance, while the difference between the two represents small airway resistance[91]. FOT has been used to detect bronchoconstriction and in detecting the severity of airway obstruction in patients with asthma or COPD[92–94]. For example, elevated Rrs as determined by low frequency oscillations, is reflective of obstruction to the distal airways, which is a characteristic of asthma and COPD[89,95,96]. The advantage of FOT over other lung function techniques is that it is noninvasive and does not require co-operation from

the patient, since the forced oscillations are superimposed on the subject's normal breathing[88]. This means it can also be used to measure lung function in smaller organisms such as mice.

Although some of the major parameters measured by FOT differ slightly between humans and mice, the following sections briefly describe the parameters measured in mice:

1.4.3.1 Respiratory resistance (Rrs) and reactance (Xrs): These two measurements describe the state of air flow through the lungs[97]. Rrs measures the degree of obstruction in the major central airways, while smaller airways less than 2mm contribute to 10% of the measurement. In healthy individuals, Rrs measurements are usually independent of pressure applied. However, in cases of severe obstruction, Rrs increases drastically[97]. Xrs on the other hand, measures the elastic recoil potential of the lungs, and how effectively air reaches the peripheral/distal airways. Xrs values become abnormal in cases of alveolar gas trapping or peripheral airway obstruction[97,98].

1.4.3.2 Newtonian airway resistance (Rn): Rn estimates the resistance of the central conducting airways[99–101]. Diseases such as acute lung injury and acute respiratory distress syndrome have been associated with increase in Rn[102,103]. Similar to Rrs, bronchoconstriction also causes an increase in Rn values[104].

1.4.3.3 Tissue resistance or tissue damping (G): G is a measurement of the resistance at the smaller peripheral airways, and the amount of energy dissipated in the lung alveoli or lost to heat during ventilation[99,100]. In a mouse model of COPD, chronic cigarette smoke exposure led to an increase in G in females, but not in males.[105]. Similarly, loss of

elastic recoil of the lungs due to emphysema is associated with a decrease in G[106], while increase in tissue stiffness and elastic recoil in lung fibrosis is associated with an increase in G[106].

1.4.3.4 Airway elastance (H): This is a measure of alveolar stiffness, and represents energy storage in the tissues[100,101]. Chronic cigarette smoke exposure causes a decrease in H, and this has been linked to the development of COPD-like phenotypes[105]. Similar to G, induction of emphysema in mouse lungs using porcine pancreatic elastase decreases H values compared to controls[106,107], while induction of lung fibrosis using bleomycin increases H[106].

1.5 Epigenetic modifications

There is a growing body of evidence that suggests that epigenetic mechanisms may be the link between cigarette smoking and disease pathology. This is because epigenetic mechanisms are sensitive to, and reflective of past environments and therefore can be used to investigate disease patterns arising due to past environmental insults. The term 'Epigenetics' was coined in 1942 by Conrad Waddington, who initially used it to describe gene-environment interactions and how they contribute to a phenotype[108]. Over time, the definition has been refined numerous times, resulting in several slightly different versions. One common definition describes it as "mitotically and meiotically stable and heritable changes in gene expression and/or function which are not as a result of alterations in the underlying DNA sequence"[109]. However, based on current evidence, we can modify the definition of epigenetics to be "the study of how gene expression is regulated through potentially reversible modifications that do not alter the DNA sequence, encompassing both

heritable and non-heritable changes". The major epigenetic modifications: DNA methylation (DNAm), histone modifications, chromatin remodeling complexes and transcription factors, and non-coding RNAs (ncRNAs) function together in regulating gene expression, maintenance of chromosomal stability, silencing transposable elements, cellular and tissue differentiation, X chromosome inactivation and genomic imprinting, chromatin remodeling, stem cell maintenance and differentiation[110–117].

1.5.1 DNA methylation (DNAm) and transcription factors: DNAm is the addition of a methyl group to the C5 position of a cytosine residue in DNA to form 5-methylcytosine, catalyzed by a family of enzymes called DNA methyltransferases (DNMTs)[111,118,119]. In mammalian somatic cells, DNAm mostly occurs at regions where cytosine is followed by guanine, referred to as CpG sites[111,120], though up to a quarter of DNAm in embryonic stem cells occur in non-CpG contexts[119,121,122]. About 70% of all CpGs in the genome are constitutively methylated, but this highly methylated state comes at an evolutionary cost, since 5-methylcytosine is prone to frequent deamination to form thymine[123,124]. Therefore, CpG dinucleotides are grossly underrepresented in the mammalian genome[125,126] (CpGs occur at only 21% of the expected frequency in the human genome[127]). Frequent CpG to TpG mutations occurring in mammals have been shown to increase the rate of *de novo* mutations 18-fold[128,129]. Clusters of CpGs, called *CpG islands,* which make up about 15% of total CpGs, account for roughly 50% of the unmethylated CpGs[130]. CpG islands are found clustered around gene promoters and transcription start sites, and are usually unmethylated[131,132]. As a result of their very low methylation state, CpGs are 7-10 times more abundant in CpG islands, and CpG to TpG substitution rates are 7 times lower in CpG islands compared to the rest of the genome[133].

Enzymes which initiate, recognize and erase DNAm marks are broadly classified into three categories: writers, readers and erasers[111,118]. Writers are enzymes which catalyze the addition of methyl groups to DNA, and they are made up of DNMT1, DNMT3A, DNMT3B and the non-enzymatically active DNMT3L[111]. DNMT1 is referred to as the *maintenance* DNMT because it maintains the original DNAm patterns in a cell. It functions during DNA replication to copy DNAm patterns from the parent strand to the newly synthesized strand[134–136]. DNMT1 has also been shown to repair DNAm[137]. DNMT3A and DNMT3B are known as *de novo* DNMTs due to their ability to confer new DNAm marks on unmethylated DNA strands[138]. DNMT3L is not catalytically active, as it lacks the catalytic domains of the other DNMTs[139,140]. It is ubiquitously expressed across all mammalian tissues during early development, but is only expressed in thymus and germ cells in adult tissues[139,141]. Though lacking in a catalytic domain, it is found closely associated with the *de novo* DNMTs and aids their activity[140,142]. Readers are proteins with high affinity for 5-methylcytosine, as they can recognize existing DNAm marks. They are broadly classified into 3 protein groups: methyl-CpG-binding domain (MBD) proteins, ubiquitin-like, containing PHD and RING finger domain (UHRF) proteins and zinc finger proteins[111,118]. The five best characterized MBD proteins are MeCp2, MBD1, MBD2, MBD3 and MBD4, and most of them recognize methylated DNA and bind them to recruit repressive complexes via their transcriptional repression domains[111,143]. In addition to its repressive capability, MeCP2 also plays an important role in maintenance of DNAm due to its ability to bind DNMT1 via its transcriptional repression domain, facilitating its maintenance role[144]. UHRF proteins bind methylated DNA via SET- and RING-associated DNA-binding domains[145,146]. They operate by binding DNMT1 and targeting it to hemimethylated DNA to enable maintenance of DNAm[147–149]. The third group of DNAm readers, the zinc finger proteins, bind methylated DNA via their zinc finger domains. They are made up of Kaiso,

ZBTB38 and ZBTB4 and just like MBDs, they repress transcription of DNA[111]. DNAm erasers are enzymes which remove methyl groups from DNA. DNA demethylation can occur either passively during DNA replication or actively via the action of the ten-eleven translocation (TET) family of proteins comprising TET1, TET2 and TET3[111,118,150]. TET enzymes catalyze DNA demethylation by first oxidizing 5-methylcytosine to 5-hydroxylmethylcytosine (5hmC)[151,152]. Following this, 5-hmC can further be removed from DNA via two major mechanisms: it can be gradually diluted over cycles of DNA replication[153], or it can be further oxidized to 5-formyl and 5-carboxycytosine by TET, removed by the thymine-DNA glycosylase enzyme and shunted into the base excision repair pathway[151,154].

The role of DNAm in regulating gene expression largely depends on the genomic region being methylated. For example, DNAm in CpG islands and promoters usually results in transcriptional silencing, while DNAm within gene bodies of rapidly dividing cells results in upregulation of gene expression[155–158]. One theory about how DNAm regulates gene expression is that the methyl groups on CpGs in promoters and CpG islands block the binding of transcription factors to promoters, repressing initiation of gene expression[117,159]. This is not the only mechanism; however, as DNAm within promoters but outside transcription factor binding sites, also affects gene expression[160]. On the opposite end, there is also evidence that the reverse is also true: that is, that binding of transcription factors can repress DNAm, as they prevent DNMTs from accessing DNA[161,162]. Therefore, while one of the ways in which DNAm can influence gene expression involves blocking the binding of transcription factors, transcription factors themselves also influence DNAm patterns[159]. Another mechanism via which DNAm can influence transcription involves recruitment of methyl-CpG binding proteins. As outlined above, these proteins bind methylated DNA and recruit co-repressor complexes in order to repress gene expression[159]. There are a few

theories as to how DNAm within gene bodies upregulates transcription. The first suggests that DNAm in intragenic regions may repress transcription at the noncoding strand, and this may in turn affect expression of the gene on the coding/sense strand[163,164]. Another theory holds that DNAm within gene bodies improves the efficiency of transcription, as it represses cryptic promoters (promoters found at intragenic regions)[165].

Overall, DNAm is dynamic, reversible (proven by the presence of demethylase enzymes which catalyze the removal of methyl groups from DNA) and can be modulated by the environment[166–168], making it a potential biomarker for various pathological conditions and a potential target for therapeutic interventions.

1.5.2 Histone modifications: Histone modifications, another epigenetic mark, refer to covalent post-translational modifications to histone proteins, and they include acetylation, phosphorylation, methylation, sumoylation, ubiquitination, deamination and ADP ribosylation[112,169]. These modifications can alter chromatin structure either directly by modulating the interactions between nucleosomes, or indirectly by recruiting remodeling enzymes which utilize energy from ATP hydrolysis to alter the nucleosome structure[112]. The roles played by various histone modifications vary depending on the modification. For instance, histone acetylation is catalyzed by lysine acetyltransferases, which transfer an acetyl group from acetyl-CoA to the ε-amino groups of lysine residues on histones. By doing this, they neutralize lysine's positive charge and weaken the bond between histones and DNA, decondensing chromatin and opening it up for gene transcription to occur[170,171]. On the other hand, lysine methylation can lead to activation or repression of gene expression, depending on the context. Methylation of histone H3 at lysines 9 (H3K9) and 27 (H3K27) are transcriptionally repressive marks, for example, while methylation at lysines 4 (H3K4) and 36

(H3K36) are known as marks of transcriptional activation[172,173]. Histone modifications, just like DNAm, are also reversible and can be modulated by the environment, making them possible targets for disease tharapies[112,174–177].

1.5.3 Non-coding RNAs: About 90% of the eukaryotic genome is transcribed, but only 1-2% of the transcripts are translated to proteins[178]. The untranslated transcripts, called noncoding RNAs are therefore a group of RNA molecules which do not encode functional proteins, and they can broadly be classified into housekeeping/infrastructural RNAs (including ribosomal RNAs, transfer RNAs, small nuclear RNAs and small nucleolar RNAs) and regulatory RNAs[179,180]. Regulatory RNAs can further be divided into two groups, based on their lengths: short noncoding RNAs (miRNAs, piRNAs, and siRNAs) and long noncoding RNAs (lncRNAs)[180]. These different ncRNAs regulate gene expression using different mechanisms[181–185], and they can be modified by the environment just like the other two epigenetic mechanisms. As an example, the H19 gene encodes a lncRNA which is highly expressed at birth but switched off in most tissues later in life[186], and the maternal environment (specifically maternal undernutrition) modifies the expression of this gene in a sex-specific manner[187]. Therefore, the ability of ncRNAs to be affected by the environment means that studying how they change following environmental insults (such as from cigarette smoke) could be useful in understanding mechanisms underlying these exposures.

1.6 Methods used to measure DNA methylation

There are many methods currently used to investigate DNAm, but most of them are broadly classified into: bisulfite-based approaches, affinity-based approaches, restriction enzyme-based approaches, and direct-sequencing methods (nanopore sequencing).

1.6.1 Bisulfite-based approaches for measuring DNAm: These approaches rely on the ability of the reagent sodium bisulfite to convert unmethylated cytosines to uracil, leaving methylated cytosines unmodified[188], thereby creating a means by which methylated cytosines can be differentiated from unmethylated cytosines. Bisulfite-based methods are considered the gold standard for measuring DNAm as they can measure DNAm at single base resolution, can be applied to virtually all areas of the genome, and can be used to measure strand-specific DNAm[189]. However, treatment with sodium bisulfite results in DNA strand degradation and loss of sequence complexity, posing certain problems for downstream microarray and/or sequencing platforms[190]. To address this problem, researchers use specific methods for sequence alignment and statistical analysis. Another disadvantage of this method is that since it requires complete conversion of unmethylated cytosines to uracil, any partial or incomplete conversion would result in wrongly interpreted results[190]. Additionally, sodium bisulfite cannot distinguish between 5-methylcytosine and 5-hydroxymethylcytosine[191], raising the possibility that methylated sites measured via this method may have in fact been hydroxymethylated. A method called *oxidative bisulfite sequencing* has been developed to solve this problem[192]. This method involves initial oxidation of 5-hydroxymethylcytosine to 5-formylcytosine using potassium perruthenate, followed by bisulfite conversion where 5-formylcytosine is further modified to uracil, making it distinguishable from methylated cytosines[192].

Some methods commonly combined with bisulfite conversion to measure DNAm include: i) whole epigenome bisulfite sequencing, which provides single base-pair DNAm measurements across the entire genome[122,193]. While it is the most comprehensive method for DNAm measurement, it is more expensive than other methods and so, less widely employed[189,194]; ii) Reduced Representation Bisulfite Sequencing (RRBS), which uses

restriction enzymes to enrich for CpG-dense regions, reducing genome complexity and sequence redundancy[195,196]. One disadvantage of this method is that it cannot be used to measure DNAm at non-CpG dense areas[189]; iii) microarray-based technologies. The most common of these, the Illumina Infinium microarrays, involves bisulfite conversion of genomic DNA followed by PCR and then hybridization of converted DNA to the microarray chips[197]. These bead chips are pre-coated with oligonucleotide sequences, one corresponding to the methylated sequence and the other complementary to the unmethylated DNA sequence. Next, fluorescently labelled primers are introduced and result in signal production in cases of sequence complementarity between the converted DNA sequence and the probes on the array[189,194]. Microarrays offer advantages over enrichment methods like RRBS, because they can measure DNAm at a wide variety of CpGs, and they can also be custom-made to suit individual research needs[189].

1.6.2 Affinity-based approaches for measuring DNAm: These methods use affinity purification to enrich for and capture methylated DNA, and they are effective methods for measuring mean DNAm across large CpG regions[189]. The most commonly employed method under this category is methylated CpG immunoprecipitation assay (MeDIP). MeDIP begins with DNA fragmentation and denaturation to produce single stranded DNA which is then precipitated with at least one monoclonal anti-5-methylcytosine antibody[189,198]. Precipitated DNA is then amplified and taken for sequencing or applied to microarrays[198,199]. Some disadvantages of MeDIP are that it relies on the antibodies being of high quality and specificity, and that it requires DNA to be single-stranded, which can be difficult to achieve with CpG dense regions[189]. Another affinity-based method, MethylMiner, works by utilizing MBD proteins with high affinity for methylated CpGs[200,201]. The isolated methylated DNA can

then be used for downstream analyses like next-generation sequencing. Affinity-based methods are widely used because the reagents required are readily available and are easy to use. However, one disadvantage is that these methods require large DNA input[189].

1.6.3 Restriction enzyme-based approaches for measuring DNAm: These methods exploit the ability of methylation-dependent restriction enzymes to cleave methylated CpGs, and methylation-sensitive restriction enzymes to cleave unmethylated DNA, thus enriching for methylated or unmethylated CpGs[189]. One commonly used method is called *HpaII* tiny fragment enrichment by ligation-mediated PCR (HELP). HELP involves digestion of one aliquot of DNA with the methylation-sensitive enzyme *HpaII*, and concurrent digestion of another aliquot of DNA with the methylation-insensitive enzyme *Msp1*[189]. This way, fragments present in *Msp1* but not in *HpaII* libraries represent methylated sequences and vice versa[202]. HELP, along with other restriction enzyme-based methods can be combined with sequencing and/or microarray platforms[202,203].

1.6.4 Direct sequencing of modified bases: Advances in sequencing technologies now enable simultaneous analysis of epigenetic modifications such as DNAm, alongside determining DNA sequences, thus removing the need for bisulfite treatment. Oxford Nanopore Technologies (ONT) platforms utilize known electrical signal profiles of nucleotide bases, which can also reveal distinctions between methylated and unmethylated cytosines[204,205]. Though expensive, especially for large population studies, questions remain about the accuracy of DNAm quantification using these methods and how they compare to methylation microarrays for detecting differentially methylated sites in epidemiological research.

In summary, methods which measure DNAm are essential in understanding gene regulation at a mechanistic level. The data obtained from these techniques should be integrated with other epigenetic mechanisms to understand how epigenetic marks function together to regulate gene expression.

1.7 First-hand cigarette smoking and its effects on epigenetic marks

There is abundant evidence that first-hand cigarette smoke alters epigenetic marks at various tissues, but most of the research has been conducted on DNAm, due to its ease of measurement and accessibility. Studies which investigate links between epigenetic variations and biological traits are referred to as epigenome-wide association studies (EWAS)[206]. Numerous EWAS have identified altered DNAm patterns in the blood[207–216] and leucocyte subtypes[210], lymphoblasts and pulmonary macrophages[217], and epithelial oral cells[218] of adult smokers compared to nonsmokers. Some studies have gone further to identify differentially methylated CpGs in smokers which are biomarkers to predict smoking status[219], and certain disease conditions such as COPD[220] and lung cancer incidence[215]. While not as abundant as DNAm studies, there is also evidence that cigarette smoking alters histone modifications and chromatin state, leading to differential gene expression in smokers compared to nonsmokers. Cigarette smoking leads to reduced expression of histone deacetylases (HDACs)[221–224], and this downregulation has also been observed in the lungs of asthmatic smokers, severe asthmatics and COPD patients, suggesting the role of HDACs in the pathologies of these conditions[225–227]. Some of these reports have also shown that inactivation of HDACs in smokers leads to concurrent increase in H3 and H4 acetylation in lungs of current smokers and ex-smokers with COPD[228], in alveolar epithelial cells[223], and in rat lungs[222]. Other histone modifications are also affected, as alterations in the methylation marks H3K27me1 and me2,

H4K31me2, H3K9me3 and H4K20me3 have been identified in smokers[229,230]. Cigarette smoking causes dysregulation of several miRNAs and thus, smokers and nonsmokers possess different miRNA profiles. Most of these dysregulated miRNAs were associated with lung function and development disruption, altered differentiation of the airway epithelia, increased inflammation and cancer[231–233].

While these studies have shown that epigenetic mechanisms can provide effective biomarkers for smoking-related disease and thus be used to understand mechanisms underlying cigarette smoke-induced health conditions, there remain some challenges to achieve this goal. The major hurdles include different durations and/or cigarette smoke doses and different cell types being investigated, which lead to differing results. In human studies, this is further complicated by confounding variables such as age, race/ethnicity and sex. Thus, a lot of work remains to be done to fully understand how first-hand cigarette smoking affects DNAm, histone modifications and ncRNAs, the interplay between all 3 mechanisms and how they all contribute to disease.

1.8 Conservation and tissue-specificity of epigenetic mechanisms

Epigenetic modifications, and particularly DNAm, have been shown to be conserved to some extent across tissues, but also to be cell type and tissue-specific[234–237]. In an anlysis of DNAm across 17 somatic tissues of four autopsied humans using the Illumina Infinium HumanMethylation450 BeadChip which measures DNAm at >450,000 CpGs[236], 2% of the CpGs analyzed had very high DNAm levels that were shared across all tissues, and these CpGs were located mostly within gene bodies[236]. Similarly, about 15% of sites analyzed had very low DNAm levels which were similar across all tissues, and these CpGs were located proximal to transcription start sites[236]. This shows that some sites have similar DNAm levels

across multiple tissues. However, several tissue-specific differentially methylated regions have been identified[236,237], with speculations that these regions likely play a role in tissue differentiation since positions with very low DNAm levels per tissue are associated with functions specific to that tissue[236]. Similarly, DNAm measurement at approximately 1.9 million CpGs within CpG islands in human sperm and 11 somatic tissues, revealed that CpG island methylation is highly consistent across somatic tissues but distinct in sperm[238]. The data on DNAm conservation and/or tissue-specificity are not limited to humans; however, as there are reports of similar patterns across other species including mice[239,240] and rats[234,241,242].

The existence of tissue-specific DNAm patterns raises the possibility that exposure to environmental insults would lead to changes which are unique per tissue. As an example of how DNAm can differ across tissues upon cigarette smoke exposure, global DNAm in cord blood[243,244] and buccal cells[245] of babies exposed to prenatal cigarette smoke decreases, but increases in the placenta and whole blood[246,247]. Given these mixed patterns therefore, it is very important for epigenetic studies to investigate the effects of environmental exposures on DNAm at different tissues, as they can have varying epigenetic signatures.

1.9 Maternal smoking and its effects on offspring

The previous paragraphs have emphasized the dangers of first-hand cigarette smoking, and some mechanisms underlying the development of smoking-related diseases. In a similar vein, exposure to cigarette smoke early in life (such as during the *in utero* period and the early postnatal period) can be as detrimental to health as personal smoking. While smoking levels have declined in women over time, some studies have reported significant increase in smoking rates in pregnant women[248,249]. In 2021, a survey reported that about 9.5% of Canadian women of reproductive age (18 to 34 years old) were active smokers[250].

These numbers are concerning, since numerous components of cigarette smoke can cross the placental barrier to the developing fetus, affecting its development[251–253]. In some instances, the concentration of nicotine in the fetus can be up to 15 times higher than the concentration of maternal cotinine[254].

Prenatal and early life exposure to cigarette smoke has been associated with the development of numerous adverse health outcomes in offspring, including low birth weight and altered growth and development, respiratory abnormalities such as airway hyperresponsiveness, wheeze, asthma and COPD, neurodevelopmental and cognitive defects, amongst others[255–257]. This is because the early life environment is particularly susceptible to environmentally-induced insults, as during this stage, while cell and tissue differentiation is at its peak, the immune system, xenobiotic and antioxidant defense mechanisms against environmental toxicants are as yet underdeveloped[258–262].

The developmental origins of health and disease (DOHaD) hypothesis postulates that the prenatal and early postnatal periods in development are highly sensitive, such that environmental insults during these periods can reprogram the fetus via changes in cellular structure and function, and these reprogrammed features last till adulthood[263,264]. Therefore, the effects of early life cigarette smoke exposure on the offspring are not restricted to childhood, as in many cases, these alterations last well into adulthood, long after cigarette smoke exposure cessation, and independent of the offspring's smoking habits later in life[265–267]. The occurrence of persistent health outcomes suggests that the effects of early life cigarette smoke exposure are somehow embedded in the offspring, and epigenetic signatures are a potential mechanism by which this biological embedding can occur[267,268] (Figure 1.1).

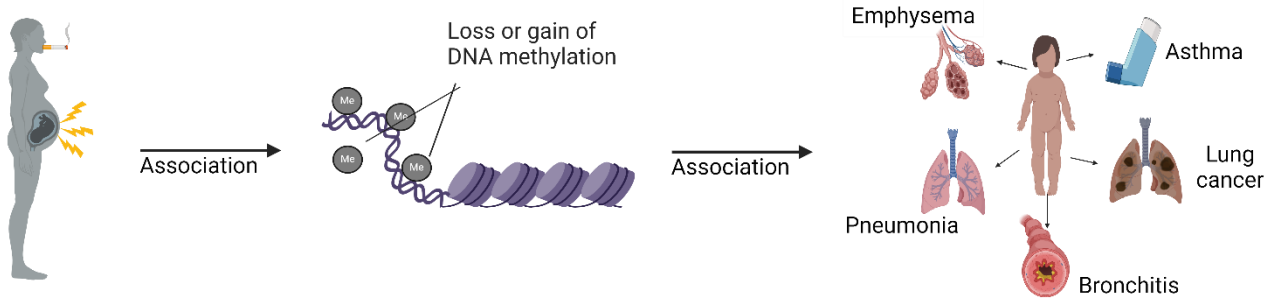

Figure 1. 1: Maternal smoking, DNA methylation and health outcomes.
Smoking during pregnancy has been associated with the development of lung function deficits in offspring, and DNAm alterations may be the link between smoking with these health outcomes.

Prenatal exposure to cigarette smoke has been associated with differential DNAm at numerous CpGs in offspring umbilical cord blood[269–273], placenta[274], buccal cells and peripheral blood[245,275–278]. Maternal smoking altered DNAm at 26 CpGs mapping to 10 genes in umbilical cord blood, with the most significantly affected gene being decreased DNAm in *AHRR* at cg05575921[269]. This particular CpG has been identified severally to be differentially methylated following prenatal cigarette smoke exposure[270,279,280], and to be involved in asthma development[281]. Other genes which commonly show altered DNAm patterns in newborn umbilical cord blood and adult peripheral blood following prenatal cigarette smoke exposure include *CYP1A1*, *GF1*, *MYO1G* and *CNTNAP2*[269–273,275,276,278]. These genes are involved in xenobiotic metabolism, obesity, cancer development, cell signaling and maintaining developmental processes[276]. These genes, along with thousands more, were confirmed to be differentially methylated in a large meta-analysis of 13 cohorts conducted to measure the effects of maternal smoking on DNAm in offspring umbilical cord blood and consisting of 6685 mother-child pairs. They measured DNAm at > 450,000 CpGs using the Illumina Infinium HumanMethylation450 BeadChip, and their results revealed that maternal smoking was associated with differential DNAm at over 6000 CpGs, over 2000 of which had never been associated with smoking in the past[270].

In the placenta, prenatal cigarette smoke exposure was found to cause increased expression of the *CYP1A1* gene and subsequent decreased DNAm at the *CYP1A1* promoter of smokers compared to nonsmokers[274]. Another group of researchers measured global and gene-specific DNAm in buccal cells of 348 children exposed to cigarette smoke *in utero*[245]. They found generally decreased DNAm at the repetitive elements AluYb8, and using the Illumina 27k microarray, identified differential DNAm at multiple CpGs mapping to 8 genes. To validate the microarray results, they later used pyrosequencing to measure DNAm at

these 8 genes, and reported that 2 genes, *ATP* and *PTPRO* had increased DNAm in buccal cells of smoke-exposed children, similar to the direction observed in the microarrays[245].

Conversely, the evidence for histone modifications being altered by prenatal cigarette smoke exposure is severely lacking, likely due to the ease of measuring DNAm compared to histone modifications. In an analysis consisting of six mother-child pairs (made up of three smoking and three non-smoking mothers and their offspring), one group of researchers measured the effects of prenatal cigarette smoke exposure on offspring histone marks (H3K4me1, H3K27ac, H3K9me3 and H3K27me3) using Chromatin Immunoprecipitation-sequencing (ChIP-seq), and reported a transition from repressive to active chromatin in the blood of children exposed to prenatal cigarette smoke, but not in controls[282]. They also measured DNAm across the whole epigenome of these offspring, and reported 1404 differentially methylated regions (DMRs) in the cord blood of babies exposed to cigarette smoke *in utero*[282]. Interestingly, these smoking-related DMRs were found close to the most significantly transitioned chromatin sites[282], demonstrating that DNAm and chromatin state due to maternal smoking are closely associated. This study emphasizes the need to investigate the effects of prenatal cigarette smoke exposure across all epigenetic mechanisms, and not in isolation, as they are all interconnected.

Compared to DNAm, much less work has been done to investigate the effects of prenatal cigarette smoke exposure on ncRNAs. Prenatal cigarette smoke exposure causes significant downregulation of miRs-16, 21 and 146a in offspring placentas[283], and all these miRNAs play important roles in growth and developmental processes[284].

1.10 Effects of timing of early life cigarette smoke exposure on offspring

While studying the effects of early life exposure to cigarette smoke, it is important to consider that women who smoke while pregnant are likely to be nicotine-dependent, less likely to quit immediately after pregnancy, and more likely to have a partner who smokes as well[285,286]. In addition, these offspring may also be exposed to second-hand smoke both *in utero* and immediately after birth. Therefore, it can be extremely difficult, especially in humans, to separate the effects of prenatal cigarette smoke exposure only from that of early postnatal cigarette smoke in offspring. This distinction is important as prenatal and early postnatal cigarette smoke exposure might have very distinct effects on the offspring[287–290], and other sources of smoke exposure such as second-hand smoke, can make this distinction even more difficult.

A meta-analysis of 15 European cohorts consisting of 27993 mother-child pairs reported that prenatal maternal smoking combined with postnatal passive smoke exposure increased the chance of the offspring developing wheeze before the age of 2[287]. Exposure of Sprague-Dawley rats to second-hand cigarette smoke either during the prenatal window only, during the postnatal window only, or during both the prenatal and postnatal windows revealed decreased lung function (decreased lung compliance and increased sensitivity to methacholine) in rats exposed to cigarette smoke during both windows, but not only prenatally or only postnatally[288]. The molecular mechanisms driving these similarities between prenatal and postnatal cigarette smoke exposure are not known and need to be investigated further. These studies all point out the importance of separating prenatal from postnatal cigarette smoke in future research, since they can elicit different responses.

1.11 The cumulative stress versus developmental mismatch hypotheses, and their relation to early life cigarette smoke exposure

There are 2 contradicting hypotheses which are commonly used to potentially predict the effect of environmental insults on an individual's health. The first is called the cumulative stress hypothesis, and it postulates that when an individual is exposed to adverse environmental stressors during development, they become more sensitive/vulnerable to these adverse stressors later in life[291]. This hypothesis is also referred to as the two-hit hypothesis[292,293], although the term can be misleading as it limits the number of hits to no more than two. Simply put, the effects of environmental insults on an individual are cumulative such that the higher the load, the greater the adverse health outcomes experienced[294]. In our case therefore, individuals exposed to cigarette smoke both prenatally and postnatally would experience greater health defects than those exposed to cigarette smoke only postnatally or only prenatally.

On the other hand, the developmental mismatch hypothesis states that traits which develop in one environment may be disadvantageous to an organism in a different environment[295–297]. If an individual experiences a mismatch in the prenatal and early postnatal environments, they are more likely to develop severe health consequences than those who had similar environments[291]. In our context, this would imply that individuals who are exposed to cigarette smoke during the prenatal period, but not postnatally, or vice versa, would experience more detrimental health outcomes than those who are exposed to cigarette smoke both pre- and post-natally. However, one controversial aspect of this hypothesis is the implication that if an organism is exposed to an insult in the prenatal and early postnatal environments, they would adapt better and may experience less detrimental health

consequences than organisms which are exposed to the insult in either environment, but not both.

Whether the cumulative stress or mismatch hypothesis is more correct as relates to environmental insults is still under debate, however, it is made more complicated by the fact that health outcomes are also subject to gene-environment interactions[298,299]. Therefore, individuals exposed to similar adverse conditions may exhibit different outcomes depending on their genetic predisposition. These are some reasons why using inbred animal models may be beneficial over human studies in examining the effects of prenatal and/or early postnatal cigarette smoke, as it excludes this great confounding variable of different genetic backgrounds.

1.12 The concept of epigenetic priming and its relation to disease

Epigenetic priming is the phenomenon whereby cells develop “memories” of past environmental stimuli/stressors, such that subsequent exposure to these stressors would result in heightened responses[300–302] (Figure 1.2).

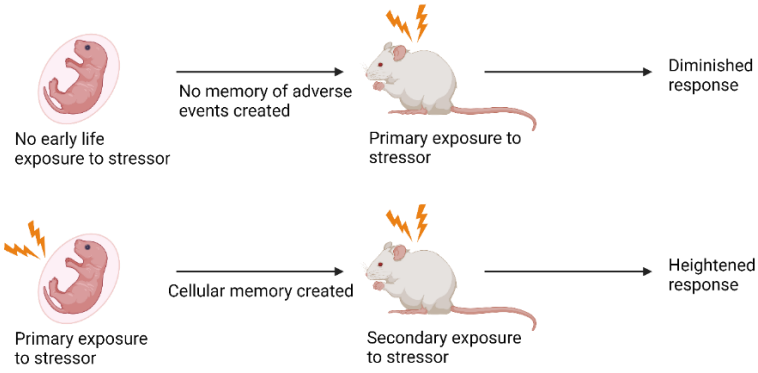

Figure 1. 2: Epigenetic priming.
Initial exposure to an environmental stressor leads to the creation of cellular memories, resulting in exacerbated responses upon secondary exposure.

This concept is not only observed following adverse environmental exposures but is a normal occurrence in maintaining important biological processes. For example, epigenetic priming plays an important role in mammalian germ layer specification and lineage commitment, as cells are primed epigenetically to differentiate into a default cell type[303]. Priming is not limited to stem cells; it has been proposed that differentiated cells also exhibit profound priming[304]. There is also evidence for intergenerational immune priming where parents transmit acquired resistance against pathogens to their offspring, improving their resistance/response to the same pathogens in their offspring[305]. In summary, epigenetic priming is important for a broad spectrum of biological processes, including cellular differentiation, disease development, stress responses and intergenerational inheritance.

This concept of priming in the context of early life cigarette smoke exposure has been investigated[306–309]. Early life secondhand cigarette smoke exposure did not affect offspring lung function until a postnatal allergen (*A. fumigatus* extract) was introduced[309]. Similarly, *in utero* exposure to secondhand smoke worsened allergic responses and lung function abnormalities when offspring were further exposed to ovalbumin at 23 weeks of age[306]. To my knowledge, only one study has investigated the effects of firsthand maternal smoking and later cigarette smoke exposure on offspring lung function[308]. This group exposed adult female mice to cigarette smoke beginning 3 weeks before mating, and stopped at birth of offspring. Cigarette smoke exposure was then continued in offspring from days 21 to 49 which corresponds to adolescence. They reported that postnatal cigarette smoke exposure only caused significant lung function alterations in mice also exposed to cigarette smoke prenatally[308]. While these results are a start, there have been no investgations on how epigenetic marks could contribute to the priming phenotypes reported in offspring exposed to cigarette smoke *in utero*, and this is essential as it could give insights into the underlying

mechanisms and suggest potential markers that could be targeted for therapeutic interventions in future.

1.13 Sex-specific effects of early life cigarette smoke exposure

There are sex-specific differences in development that exist in healthy individuals, and many sex differences exist in human and mouse lung development. Men are more prone than women to develop lung function deficiencies early in life[310], partly because crucial developmental processes, such as surfactant synthesis and mouth movement, begin later in males (20-23 weeks gestation) than in females (18 weeks gestation)[311,312]. This delay is possibly due to higher androgen levels in male fetuses[313], as administration of androgens to pregnant female rabbits delayed lung maturation in their fetuses, and administration of an anti-androgen increased surfactant synthesis in male fetuses to the level of the females[314]. Additionally, male children have larger but fewer lung airways, while females have smaller but more numerous airways which increases air flow in females[315]. Thus, prepubescent males are more susceptible to the effects of environmental toxicants, and they are more susceptible to asthma and lower respiratory tract infections than age-matched females[310]. Male lung function steadily improves over time and surpasses female lung function as puberty approaches, and while hormonal influences have been implicated in this phenomenon[315], the precise mechanisms remain unknown. It follows therefore that if there exist baseline differences between male and female lungs in healthy individuals, exposure to environmental stressors such as cigarette smoke in early life would result in sex-specific molecular and physiological differences.

In this light, there is abundant evidence of sex-specific differences in lung function of mouse[312] and human[316–320] offspring exposed to cigarette smoke *in utero,* with males

displaying worse lung function than females. However, the number of studies reporting sex-specific DNAm alterations following early life cigarette smoke exposure is limited. In an analysis of DNAm in whole blood of 608 children of smoking mothers, sex-based DNAm differences were reported as females showed increased DNAm at a CpG close to the *HLA-DPB2* gene, while males showed a decrease[321]. However, these results do not take into consideration the effects of postnatal cigarette smoke as well as other environmental influences because whole blood samples were taken from offspring at around 6 years of age. Simiilarly, measurement of DNAm in umbilical cord blood leukocytes of babies born to mothers who were active smokers or who quit smoking while pregnant[311] revealed that cigarette smoke-exposed babies had higher DNAm at the *IGF2* differentially methylated region, with this increase being more dramatic in male than female offspring[311]. To my knowledge, only one study to date has reported sex-specific DNAm differences in offspring lungs following maternal smoking. Here, DNAm was measured at > 450,000 CpGs in 78 human fetal lung tissues collected between days 57 and 122 of gestation. Their analyses revealed that 1233 genes showed sex-specific differences in DNAm in fetal lung tissues, with the most pronounced sex difference at cg03691818 in the *KRT77* gene[322]. Comparing the sex-specific DNAm loci in fetal lungs with those obtained from lung tissues of adult smokers, they identified overlapping positions, but noted that the most significantly altered gene in adult lungs was also cg03691818 in the *KRT77* gene. Their results suggest that lung-specific DNAm alterations at this gene due to cigarette smoke exposure may be long-lasting[322].

1.14 Timing of early life cigarette smoke exposure and identification of critical periods of exposure

One important question which remains under-investigated is regarding timing of *in utero* cigarette smoke exposure, and how it affects offspring biological or physiological outcomes. It has been reported that smoking in the third trimester has the greatest influence on birth weight, such that offspring born to mothers who quit before the third trimester weighed similar to those born to nonsmoking mothers[323]. This may imply that maternal smoking may produce the greatest effects later in pregnancy, but the evidence is sparse and needs further clarification. On a slightly different note, persistent maternal smoking throughout pregnancy has been shown to produce the most dramatic DNAm difference in offspring, while quitting early in pregnancy returns these DNAm patterns almost to the levels of the offspring of never-smokers[324]. In this study, the effects of maternal smoking on DNAm in offspring at birth was notably stronger when the mothers smoked past the first 18 weeks of pregnancy, than if she quit smoking earlier[324]. Further studies are needed to corroborate these results. It is important to determine periods in pregnancy where the developing fetus is the most sensitive to the effects of maternal smoking, as this can help evaluate the risks of developing cigarette smoke-mediated health outcomes. It would also be beneficial in planning of smoking cessation interventions, especially for women of childbearing age.

1.15 Longitudinal DNAm patterns of early life cigarette smoke exposure

Most of the previous research discussed so far has focused on investigating the effects of early life cigarette smoke exposure on offspring immediately after or close to birth, but fewer studies have measured these effects later on. The physiological outcomes of prenatal cigarette smoke exposure are indeed long-lasting, with reports of persistent lung

function alterations in humans until 12[319] and 21[317] years of age. Other than lung function, maternal smoking has also been shown to cause obesity, cardiovascular and behavioral/neurological defects which are long-lasting in offspring[325–330].

While there is abundant evidence that prenatal cigarette smoke exposure causes long-lasting physiological defects in offspring, the longevity of epigenetic signatures induced by cigarette smoke, and which may potentially modulate these physiological outcomes, remain underinvestigated. Prenatal cigarette smoke exposure leads to differential DNAm changes which last in whole blood till 5-12 years[331]. An extension to these findings show that prenatal cigarette smoke-induced DNAm alterations persist in peripheral blood till adolescence (17 years of age) and midlife (48 years of age)[272,273]. Interestingly, CpG sites identified in these studies were highly similar to those identified in newborns[269], confirming lasting effects of prenatal cigarette smoke on offspring DNAm. Given these findings however, more detailed research which measures DNAm at multiple timepoints following early life cigarette smoke exposure is still needed. One such research exists; a large cohort of 800 mother-child pairs which investigated effects of prenatal cigarette smoke on offspring DNAm at birth, 7 and 17 years of age[271]. At birth, they identified 15 CpGs mapping to 7 genes which were differentially methylated in the cord blood of offspring exposed to *in utero* cigarette smoke. Over time, the DNAm levels of some of the CpGs were reversed to levels similar to controls, while some others remained persistently altered until 17 years[271]. Furthermore, they explored the potential effects of postnatal smoke exposure on these DNAm patterns and found the prenatal period to be the critical window for the development of the observed DNAm alterations[271].

The relationships between prenatal cigarette smoke exposure and DNAm in the offspring during adolescence does not wane after controlling for either the parents' or the

offspring's own postnatal smoking[273,331]. However, the challenge with adjusting for mediators statistically in order to measure the effects of an exposure directly is that it may lead to the generation of false results[332,333]. Therefore, studies which can effectively measure long-term effects of exclusively prenatal cigarette smoke exposure and/or exclusively early postnatal cigarette smoke exposure would be advantageous and could potentially identify what the critical period is which influences offspring DNAm patterns later in life.

1.16 Knowledge gaps/rationale, thesis hypothesis and objectives

Given this background, several areas remain to be adequately investigated to understand how early life cigarette smoke exposure leads to disease outcomes in later life.

1. First, most of the past research investigating the effects of early life cigarette smoke exposure has been conducted in the blood, with very little evidence from the lungs. As highlighted earlier, DNAm is tissue-specific, and therefore, there is the need to investigate lung-specific DNAm patterns, as they may offer better insights into the mechanism of embedding of maternal cigarette smoke. My project contributes significantly to this field by investigating the effects of maternal smoking on offspring DNAm in the left lungs. I also measured DNAm in the blood to compare results across both tissues.
2. Next, the need to separate the effects of prenatal from early postnatal cigarette smoke is important, as studies reporting DNAm alterations in tissues taken after birth cannot fully separate these exposures. This becomes further complicated in human studies, as the complex nature of the human environment precludes the possibility of making this distinction. In this project, I established a mouse model which effectively separates prenatal from early postnatal cigarette smoke exposure, and measured physiological

outcomes, as well as DNAm and histone marks observed in mice exposed to only prenatal, only postnatal, or a combination of prenatal and postnatal cigarette smoke exposures. This approach is important, as it will identify more critical windows in disease susceptibility following early life cigarette smoke.

3. Next, there is a need for a comprehensive study outlining the effects of early life cigarette smoke on offspring at multiple timepoints throughout the lifespan. My project fills this gap, as the mouse model used investigates the outcomes of early life cigarette smoke exposure at multiple timepoints: immediately after birth, and then at 8, 16 and 63 weeks of age. Taking this approach could inform on the dynamic patterns set by early life cigarette smoke, and potentially identify periods where the effects of early life cigarette smoke may be the most pronounced.
4. Early life cigarette smoke exposure produces DNAm alterations which vary by sex. However, these sex-specific patterns have not been measured over time, and seldom in the lungs. In this project, I perform sex-disaggregated analyses to measure both physiological and DNAm patterns across the lifespan, and in the lungs.
5. Finally, there is limited information known about how the effects of early life cigarette smoke exposure are modulated by smoke exposure in adulthood. I address this by exposing some of the mice to cigarette smoke in adulthood and measuring lung function outcomes and DNAm.

The major objectives and hypotheses of my thesis are:

1. To identify DNAm changes associated with early life cigarette smoke exposure in male and female offspring lungs. *We hypothesize different types and durations of early life cigarette smoke exposure to produce sex-specific lung function and lung DNAm*

patterns. We expect these physiological and molecular alterations to be specific to the type of early life cigarette smoke exposure, with some shared characteristics across exposure types. Some of our identified DNAm differences would corroborate previous research, and reveal novel DNAm patterns.

2. To identify longitudinal effects of early life cigarette smoke exposure. *We hypothesize that some DNAm differences identified within the lungs will persist till 63 weeks of age, long into adulthood.*
3. To determine what effects secondary exposure to smoke in adulthood has on early life DNAm patterns. *We hypothesize that secondary exposure to cigarette smoke in addition to early life cigarette smoke exposure will result in more abundant and exacerbated differences in DNAm and lung function, indicating priming in mice following cigarette smoke exposure.*
4. To compare DNAm patterns between blood and lungs, following early life smoke exposure. *Our hypothesis is that DNAm patterns across blood and lungs following early life cigarette smoke exposure will mostly be distinct.*

We address these objectives by establishing an animal model to measure the effects of maternal smoking during the prenatal and/or early postnatal windows on offspring lung physiological and epigenetic (DNAm) outcomes. The complete details on the animal models and the smoking paradigm used are detailed in Figure 1.3 and in the research papers in subsequent chapters.

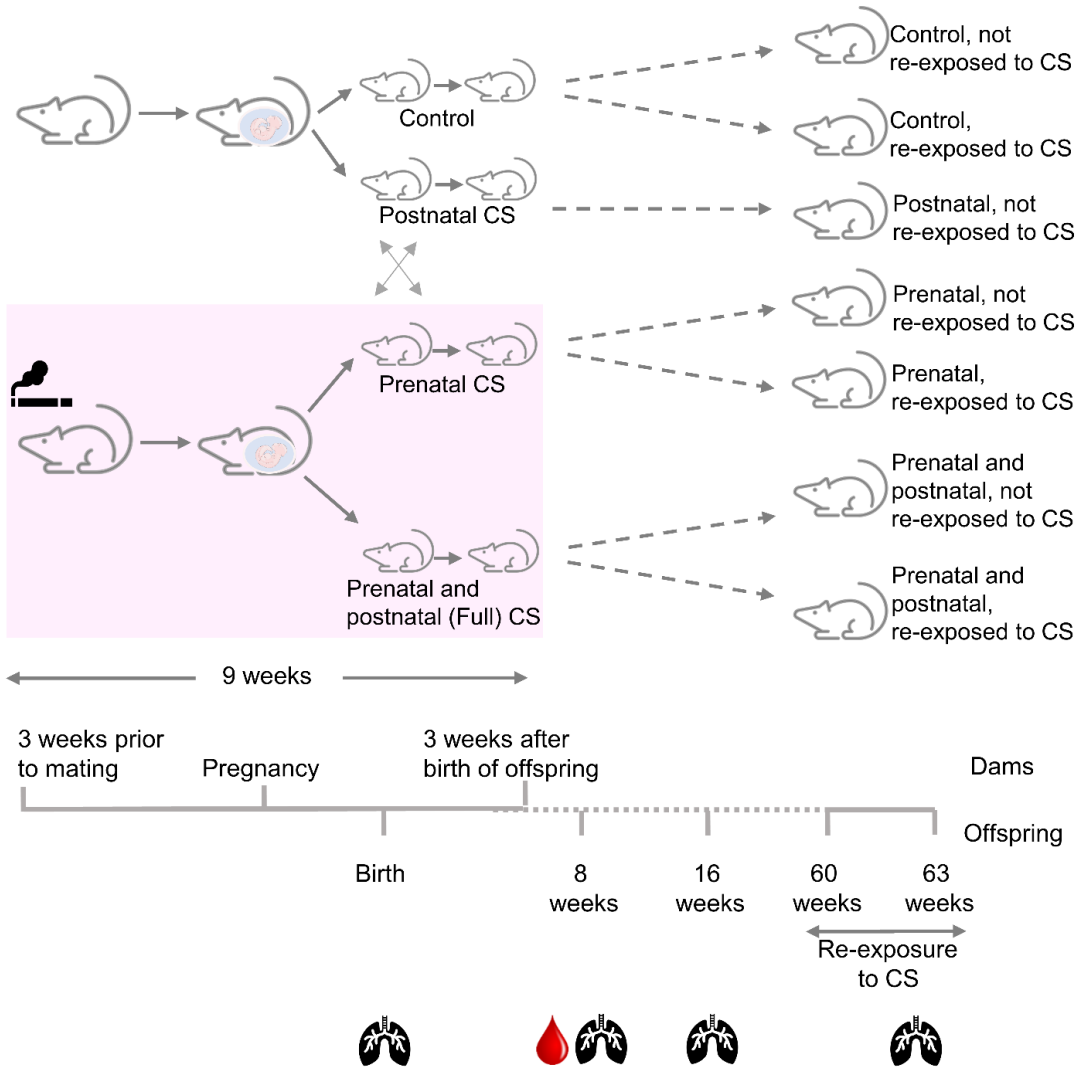

Figure 1. 3: Mouse model used to study the effects of early life cigarette smoke exposure on offspring lung function and DNAm.
Adult female mice were exposed to cigarette smoke for 9 weeks, beginning 3 weeks before mating and ending 3 weeks after birth of offspring. At birth, half of control offspring were cross-fostered with half of the cigarette smoke-exposed offspring to generate 4 groups of offspring: control with no cigarette smoke exposure, offspring exposed to prenatal cigarette smoke, offspring exposed to postnatal cigarette smoke, and offspring exposed to both prenatal and postnatal cigarette smoke. Lungs and blood were collected from dams and offspring at birth, at 8 weeks, and at 16 weeks of age after lung function measurement. At age 60 weeks, half of the remaining female offspring were re-exposed to cigarette smoke for 3 weeks, followed by lung function and tissue collection. The remaining half were not re-exposed to cigarette smoke and served as adult controls. Lung function and tissue collection were performed at 60 weeks immediately after cigarette smoke exposure.

Briefly, adult female mice were equally divided into control and cigarette smoke-exposed groups. Cigarette smoke mice were exposed to whole body cigarette smoke for a total period of 9 weeks, starting 3 weeks prior to mating, lasting throughout gestation and ending at weaning of pups (3 weeks after birth). Control mice were exposed to air during this timeframe. Immediately after birth of offspring, some from either group were sacrificed, while the rest were cross-fostered. Cross-fostering was achieved by exchanging half of the remaining control offspring with half of the offspring born to cigarette smoke-exposed dams, leading to the generation of four groups of offspring: offspring which received no cigarette smoke exposure (Control), offspring exposed to prenatal cigarette smoke only, offspring exposed to postnatal cigarette smoke only, and those exposed to both prenatal and postnatal cigarette smoke (Full cigarette smoke). Following cessation of cigarette smoke exposure to the dams, offspring were left to grow undisturbed, and at 63 weeks of age, half of the remaining offspring were exposed to acute doses of whole body cigarette smoke. Lungs and blood were collected from dams immediately after smoking and 13 weeks after cessation, and from offspring at multiple points over their lifespan: at birth, 8, 16 and 63 weeks of age. Physiological outcomes were assessed in form of lung function and lung immune cell infiltration. DNAm was measured first at a single candidate gene and then across thousands of CpGs in the mouse epigenome.

To explain the outcomes of these analyses, this document is divided into four chapters, consisting of three research papers and a concluding chapter as summarized below:

Chapter 2: In the first published paper, we investigate the effects of chronic first-hand smoking in adulthood on DNAm and lung function of adult mice[334]. The adult mice referred to in this paper are the pregnant dams which gave rise to the offspring investigated in subsequent papers. This paper reports novel and lung-specific DNAm alterations following

cigarette smoke exposure, some of which align with the results observed later in their offspring[334].

Chapter 3: In the second published paper, we report that offspring exposed to cigarette smoke prenatally, postnatally, or during both periods, display distinct lung DNAm patterns at a candidate gene previously reported to be responsive to cigarette smoke in human studies[335]. We also show that offspring exposed to cigarette smoke during either period produces similar DNAm patterns than offspring exposed to both prenatal and postnatal cigarette smoke. Finally, we confirm the occurrence of epigenetic priming in offspring lungs following early life cigarette smoke exposure, as reexposure to cigarette smoke in adulthood re-established otherwise transient early life DNAm patterns at the same candidate gene[335].

Chapter 4: In the third paper, we extend the candidate gene analysis of paper two by measuring DNAm in cigarette smoke-exposed offspring across the whole epigenome, using a mouse methylation microarray. We focus on how these DNAm patterns vary across the lifespan and how they differ by sex, and between blood and lungs. We discover sex-specific DNAm alterations in the lungs of cigarette smoke-exposed offspring, with males showing more susceptibility to developing long-lasting DNAm alterations than females. We also report the effects of re-exposure to cigarette smoke in adulthood on offspring lung DNAm, providing insights on molecular mechanisms underlying priming in mammals following cigarette smoke exposure.

Chapter 5: I conclude by summarizing all important findings, identifying limitations and gaps for future research.

Chapter 2: Novel DNA methylation changes in mouse lungs associated with chronic smoking

Authors

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Citation

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Disclosure statements

The authors report no conflicts of interest.

Data Availability

The data supporting the findings from this study are available from the corresponding author, M.J.J., upon request.

Supplemental information

All supplemental data can be accessed online at:

https://doi.org/10.6084/m9.figshare.24546013.v3.

AUTHOR CONTRIBUTIONS

M.J.J. conceived and designed research; C.D.O., S.L., S.B., J.C., Y.H., N.H., S.C. and M.S.F. performed experiments; C.D.O. and C.P. analyzed data; M.J.J. and C.D.O. interpreted results of experiments; C.D.O. prepared figures; C.D.O. prepared manuscript; M.J.J., C.P. and A.J.H. edited and revised manuscript; S.L., S.B., J.C., Y.H., N.H., S.C., M.S.F., A.J.H., C.P. and M.J.J. approved final version of manuscript.

2.1 Abstract

Smoking is a potent cause of asthma exacerbations, chronic obstructive pulmonary disease (COPD) and many other health defects, and changes in DNA methylation (DNAm) have been identified as a potential link between smoking and these health outcomes. However, most studies of smoking and DNAm have been done using blood and other easily accessible tissues in humans, while evidence from more directly affected tissues such as the lungs is lacking. Here, we identified DNAm patterns in the lungs that are altered by smoking. We used an established mouse model to measure the effects of chronic smoke exposure first on lung phenotype immediately after smoking and then after a period of smoking cessation. Next, we determined whether our mouse model recapitulates previous DNAm patterns observed in smoking humans, specifically measuring DNAm at a candidate gene responsive to cigarette smoke, *Cyp1a1.* Finally, we carried out epigenome-wide DNAm analyses using the newly released Illumina mouse methylation microarrays. Our results recapitulate some of the phenotypes and DNAm patterns observed in human studies but reveal 32 differentially methylated genes specific to the lungs which have not been previously associated with smoking. The affected genes are associated with nicotine dependency, tumorigenesis and metastasis, immune cell dysfunction, lung function decline, and COPD. This research emphasizes the need to study CS-mediated DNAm signatures in directly affected tissues like the lungs, to fully understand mechanisms underlying CS-mediated health outcomes.

Keywords: Chronic smoking, DNA methylation, lung function, epigenome-wide

2.2 Introduction

Smoking is one of the leading causes of preventable mortality worldwide, and poses a great burden on the healthcare system, as it has been linked to the development and poor clinical control of diseases like asthma, chronic obstructive pulmonary disease (COPD), bronchitis, obesity, and cancers[336–340]. Epigenetic mechanisms, particularly DNA methylation (DNAm), have been suggested as potential links between environmental exposures such as smoking and disease outcomes that might manifest later in life.

There is abundant evidence that smoking alters DNAm patterns in human peripheral blood[210,214,216,341] and leucocyte subtypes[210], lymphoblasts and pulmonary macrophages[217], and epithelial oral cells[218]. In fact, there are reports that methylation levels of certain CpGs are effective markers for predicting smoking status[219] and lung cancer incidence[215]. However, most of these past studies associating smoking with DNAm alterations were done in accessible tissues, such as blood or epithelia, where large scale sample collections are possible. Data from large human studies using accessible tissues is extremely helpful in identifying potential biomarkers of exposure or outcome, but evidence from more proximal tissues such as lungs which could develop our mechanistic understanding is severely lacking[211]. DNAm is cell type and tissue-specific, and so it is not clear whether findings from peripheral tissues like blood can be applied to the lungs[234,342–344]. One recent study measured epigenome-wide DNAm in current smokers and reported that only a third of the significantly altered CpGs which they originally identified in whole blood were also altered in the lungs of current compared to never-smokers[211]. Another study compared smoking-induced DNAm changes in blood versus buccal cells and reported that DNAm sites from buccal cells outperformed those identified in blood cells in discrimination of 14 of 15 epithelial cancer types[345]. The latter study showed that tissues directly exposed to cigarette smoke

(CS) such as lungs, buccal cells and saliva may demonstrate more similar effects of smoking on DNAm, but it is clear that for truly mechanistic understanding, it is essential to examine the main tissues of interest. It can be difficult to access these tissues in humans, so model organisms are often employed.

Studies using animal models to measure the effects of smoking on DNAm in the lungs are also limited[211,346,347]. One study measured the effect of four weeks of smoking on lung DNAm using capture based bisulfite sequencing and found altered DNAm patterns for numerous genes, most involved in inflammation and in inflammatory injury in COPD[347]. Another measured epigenome-wide DNAm in the blood of current and never-smokers and then measured the corresponding DNAm at the significant CpGs in the lungs via pyrosequencing[211]. Their results revealed that only 1/3 significant CpGs in the blood also showed changes in DNAm in the lungs, demonstrating the importance of assessing DNAm in the specific tissue of interest[211]. A third study measured the effects of whole-body CS, tobacco carcinogens and lipopolysaccharides in mouse lungs using reduced representation bisulfite sequencing (RRBS)[346]. They reported DNAm and hydroxymethylation differences across multiple differentially methylated regions[346]. These studies are few and thus indicate that there is a clear need for more research on the effects of smoking on DNAm patterns in lung tissues.

DNAm microarray is a high-throughput method for epigenome-wide DNAm measurements at a lower cost and is less labour intensive than bisulfite sequencing. Sequentially increasing scales of the Infinium microarrays have been developed for human samples, but no such solution was available for use on mouse samples until recently, with the release of the Illumina Infinium mouse microarrays[348]. In the current study, we used an animal model of chronic smoking to measure effects of smoking on lung function, as well as

gene expression and DNAm of a candidate gene, both immediately after smoking and 15 weeks after smoking cessation. We also employed the new mouse methylation array to measure epigenome-wide DNAm immediately after smoking. Our model successfully recapitulated some of the lung phenotypes and DNAm signatures observed in humans. It also reveals many novel sites in the lungs which are differentially methylated by smoking, involved in nicotine dependence, altered immune response and development of malignancies, lung function decline and COPD, cardiovascular defects and neurodegenerative disorders. This study is an essential step in understanding mechanisms underlying CS-induced health alterations, and therefore would help in developing therapies to mitigate the effects of smoking.

2.3 Methods

2.3.1 Animals and smoking model

This experiment was approved by the Animal Research Ethics and Compliance Committee of the University of Manitoba (protocol number 19-021 (AC11461)). Adult BALB/c mice (Charles River Laboratories, Massachusetts, United States) were given standard laboratory chow and clean water *ad libitum* and housed, four mice of a single sex per cage (except where noted), in individually ventilated cages in a 12-hour light/dark cycle throughout the duration of this experiment.

The full details of the smoke exposure paradigm have been published previously[335]. Briefly, 8-week-old adult female BALB/c mice were separated into 2 groups: 16 control mice and 16 smoke-exposed mice. Treatments were for a total period of 9 weeks, beginning 3 weeks prior to mating (at which point mice were singly housed), continuing throughout pregnancy and lasting until 3 weeks after birth of offspring. Control mice were moved to a

clean cage and exposed to room air, while CS mice were exposed to whole body 1R6F research cigarettes (University of Kentucky, Lexington, KY), twice daily using the SCIREQ InExpose smoking robot (SCIREQ, Montreal, QC, Canada). The results reported in this study are a part of a larger experiment to investigate the effects of maternal smoking on offspring[335]. Therefore, the 'dams' referred to from this point forward were all pregnant in line with that experiment. Dams were weighed weekly and 48 to 72 hours after the last smoke exposure (referred to hereafter as "immediately after smoking"), a subset of dams underwent lung function testing followed by tissue collection. The remaining dams underwent lung function testing and tissue collection 15 to 16 weeks after smoking cessation (referred to hereafter as "15 weeks after smoking cessation"), resulting in data from 2 timepoints: immediately after 9 weeks of smoking and 15 weeks after smoking cessation (Sample and group information can be found in Appendix 2.1). All supplemental information is available at: https://doi.org/10.6084/m9.figshare.24546013.v3.

2.3.2 Measurement of maternal cotinine

To verify delivery of CS, cotinine levels were measured in plasma immediately after smoking, and again 15 weeks later in a subset of dams. Cotinine was measured using a commercially available ELISA kit (CalBiotech, Spring Valley, CA), according to the manufacturer's instructions, and the concentration of cotinine in each sample was measured at 450 nm.

2.3.3 Lung function measurement and Bronchoalveolar lavage fluid collection

Mice were anesthetized with sodium pentobarbital and lung function measured using the SCREQ Flexivent small animal ventilator (SCIREQ Inc., Montreal, QC, Canada) as

described previously[349,350]. Four lung function metrics: Total airway resistance (Rrs), Newtonian resistance (Rn), tissue resistance (G) and elastance (H) were assessed, first at baseline after injection of nebulized saline into the lungs, and then after introduction of increasing concentrations of nebulized methacholine (3 to 50 mg/mL). Methacholine serves as a cholinergic agonist which acts on muscarinic receptors in airway smooth muscles, thereby inducing bronchoconstriction and decreasing lung function[87,351]. As a result, methacholine challenge tests are considered the gold standard for measuring airway hyperresponsiveness in mouse models[87,351].

Once lung function measurements were complete, mouse lungs were washed twice with 1 mL of phosphate buffer saline (PBS) per wash, introduced via tracheal cannulation. The bronchoalveolar lavage fluid (BALF) obtained was centrifuged at 4°C at 1500 x g for 10 min, and the supernatants were stored at -20°C to be used for future analysis. Cell pellets were resuspended in 1 mL of PBS for total cell counts using a hemocytometer. Differential cell counts of macrophages, eosinophils and lymphocytes were performed by first pipetting 100 uL of PBS-resuspended cell pellets onto glass slides using cytospin columns, staining with a modified Wright-Giemsa stain (Hema 3 Stat Pack), and then counting cells using a Carl Zeiss Axio Observer ZI microscope.

2.3.4 Tissue collection, DNA/RNA isolation

We collected whole blood from dams immediately after 9 weeks of CS exposure and 15 weeks after smoking cessation. Blood obtained from the severed abdominal aorta was immediately pipetted into EDTA-coated tubes and centrifuged at 4000 rpm for 15 min to obtain plasma. Following separation, blood cell pellets and plasma were snap-frozen in dry

ice and stored at -80°C. Next, left, middle, superior, inferior and postcaval lung lobes were collected into separate tubes and snap-frozen in dry ice.

To prepare for simultaneous DNA and RNA extraction using the Invitrogen DNA and RNA isolation kits, we homogenized whole lavaged left lungs in Qiagen RLT Plus buffer using the Qiagen Tissue Lyser II. We also extracted DNA from blood cell pellets using the Qiagen DNAeasy Blood and Tissue kit and quantified all extracted DNA and RNA using a NanoDrop spectrophotometer (NanoDrop Technologies, USA).

2.3.5 Selection of candidate genes to measure DNAm in mice

As our mouse model was novel, we needed to confirm that we could use it to recapitulate some of the DNAm signatures previously reported in humans exposed to CS. We decided to measure DNAm at candidate genes first on a small scale and then proceed to epigenome-wide DNAm measurements. Complete details of how we selected our 2 candidate genes have been published previously[335]. Briefly, we selected 2 CpGs which were the most responsive to *in utero* CS in newborn umbilical cord blood samples as reported in a meta-analysis conducted across human cohorts, and had also been associated with exposure to CS in adulthood[270]. The two chosen human CpGs were *AHRR* (cg05575921) and *CYP1A1* (cg22549041). We then aligned these sequences against the GRCm38/mm10 *Mus musculus* genome assembly using muscle[352] alignment on R studio version 3.6. This produced mouse CpGs which exactly aligned with or were closest in position to the human CpGs selected from the meta-analysis. The two mouse CpGs were at chr13:74260517 for *Ahrr* and chr9:57696231 for *Cyp1a1* (GRCm38/mm10). It is essential to note that this region of *Ahrr* is not conserved between humans and mice, and while we selected the closest mouse CpG, it may not be comparable to the human position.

2.3.6 Gene expression measurement

200 ng of lung mRNA was converted to cDNA using Maxima cDNA synthesis Kit (Thermo Fisher Scientific, Inc.) following manufacturer's protocol. We measured relative expression of *Ahrr* and *Cyp1a1* in dam lungs using quantitative real-time RT-PCR (qPCR) performed on the QuantStudio 3 Real-Time PCR System (Thermo Fisher Scientific, Waltham, MA). *Ahrr* and *Cyp1a1* expression was quantified using the $\Delta\Delta^{Cq}$ method[353,354] after normalizing against mean *β-actin* and *Eif2a* levels in the same sample. Samples were run in duplicates under cycling conditions that were recommended by the manufacturer, and the primer sequences used have been published previously[335].

2.3.7 Measurement of DNAm at the candidate genes, *Ahrr* and *Cyp1a1*

We measured DNAm at the two chosen mouse candidate genes, *Ahrr* and *Cyp1a1,* via pyrosequencing, as previously described[335]. Briefly, we performed bisulfite conversion (Zymo Research) on 500 ng of DNA isolated from the left lungs or blood to generate bisulfite-converted DNA (bcDNA), following the manufacturer's protocol. Converted DNA was amplified using primers and conditions published previously[335]. DNAm at candidate genes was measured in duplicates using the Qiagen Q48 pyrosequencer, alongside mouse control DNA of increasing methylation concentrations: 0%, 25%, 50%, 75%, and 100%.

2.3.8 Measurement of epigenome-wide DNAm in dam lung autosomes

We used the Illumina Infinium Mouse Methylation BeadChip (Illumina, San Diego, CA, USA) to measure DNAm across the whole mouse epigenome in accordance to the manufacturer's protocol. Briefly, 750 ng of genomic DNA was bisulfite converted as described

above. Next, bisulfite converted samples were randomized, amplified, fragmented, hybridized onto the array chip and scanned according to the standard protocol.

We exported IDAT files into R and performed preprocessing using the SeSAMe package[355]. Preprocessing steps included removal of 18,920 of 296,070 probes mapping to the X, Y and mitochondrial chromosomes, calculation of detection *p* values per probe using pOOBAH[355], background subtraction using noob[356], dye bias correction using the dyeBiasCorrTypeINorm function in the SeSAMe package and filtering out probes with detection $p > 0.05$. Next, signal intensities of the remaining 208,606 probes were quantified as β-values and used in downstream analyses.

2.3.9 Measurement of epigenome-wide DNAm in dam lung X and Y chromosomes

We measured the effect of smoking for 9 weeks on DNAm in Illumina mouse microarray probes mapping to the female X chromosomes separately. Similar to autosomal probes, preprocessing was conducted using the SeSAMe package in R[355]. We performed the preprocessing steps highlighted above on 15,117 of 296,070 probes mapping to the female X chromosome, and were left with 11,529 probes used in downstream analyses.

2.3.10 Statistical analyses

Statistical analyses were performed in RStudio (versions 3.6.1 and 4.2). To analyze candidate gene pyrosequencing data, we averaged DNAm at each CpG across duplicates and measured between-group differences using student t-tests. We used one-way ANOVA to analyze lung function and differential cell count data, followed by student t-tests for multiple comparisons between groups at each methacholine dose. We considered *P* values < 0.05 as significant.

To analyze epigenome-wide DNAm microarray data, we first performed chip, run, row and column batch correction on β values using ComBat[357], included in the SVA package[358]. Next, we used the SVA package to capture technical covariates to be included in our linear regression model, and included the recommended 1 surrogate variable in our model. Next, we used multivariable linear regression contained within the limma R package to measure differential DNAm on the β values. Since our study design has a very small sample size (N = 3 control, N = 3 CS) and our *p* values would therefore not accurately reflect very small differences[359] in DNAm, we considered CpGs as significant at $p < 10e\text{-}3$ and an effect size > 0.05. We produced figures in R using the *ggplot2* and *Gviz* packages.

2.3.11 Gene Ontology

To obtain biological significance from identified differentially methylated probes, we used the ClusterProfiler R package[360] (v3.16.1) for gene enrichment analysis. We considered pathways with FDR < 0.05 to be significantly enriched.

2.4 Results

The research presented here is one part of a larger animal experiment to investigate the effects of prenatal CS exposure on offspring. We exposed BALB/c dams (N = 16 controls and N = 16 CS-exposed) to whole-body CS for a total period of 9 weeks, starting 3 weeks before mating, and lasting throughout pregnancy until 3 weeks after the birth of their pups (Figure 2.1A). CS-exposed dams tolerated smoking, with no losses or adverse events during the course of the experiments. We performed lung function and collected tissues for further analyses at 2 timepoints: 48-72 hours after the last day of 9 weeks of smoking (referred to

hereafter as “immediately after smoking”), and 15-16 weeks after smoking cessation (referred to hereafter as “15 weeks after smoking cessation”) (Figure 2.1A, Appendix 2.1).

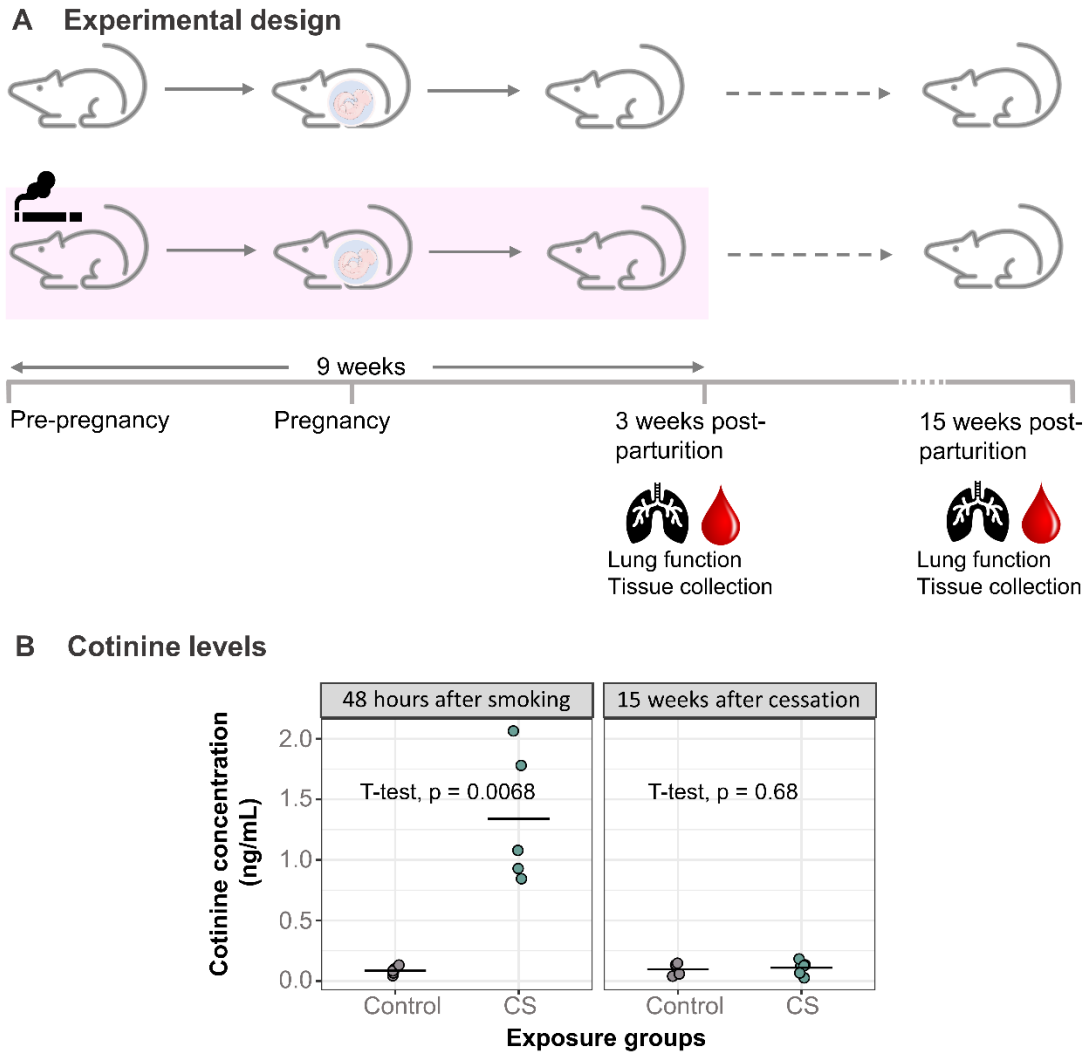

Figure 2. 1: Development of a mouse model to study the effects of heavy smoking. (A) Adult female mice (N = 16 control, N = 16 CS) were exposed to heavy doses of whole-body CS for 9 weeks, from a pre-pregnancy period of 3 weeks and ending 3 weeks after birth of offspring. Fifteen of these had their litters within one week of each other and were included in this study. Following lung function measurements, tissues were collected from dams 48 hours after the last day of 9 weeks of smoke exposure and then 15 weeks after smoking cessation. (B) Dam cotinine levels measured in plasma 48 hours and 15 weeks after smoking cessation. N = 5 per group. Differences in plasma cotinine were analyzed using student t-tests.

To verify absorption of CS components, we measured cotinine levels in plasma collected at these 2 different timepoints (Figure 2.1B). Dams which were exposed to CS had 15 times more elevated plasma cotinine levels (Mean = 1.34, SD = 0.55) immediately after smoking cessation compared to control dams (Mean = 0.09, SD = 0.03) (Figure 2.1B, p = 0.0068). The relatively low levels of cotinine observed overall in the smoke-exposed dams can be attributed to the collection of plasma from dams approximately 48 hours after smoking, with the reported half-life of cotinine being about 24 hours[361,362]. Cotinine levels measured 15 weeks after CS exposure showed no significant difference between control and smoking dams (Figure 2.1B).

2.4.1 Lung phenotype immediately after 9 weeks of smoking and 15 weeks after smoking cessation

Several studies have shown that personal smoking alters lung function and induces airway hyperresponsiveness[363–365]. Therefore, we assessed the effects of chronic smoking on the lung phenotype by measuring lung function and immune cell infiltration.

Smoking for 9 weeks caused a 4-fold and 8-fold increase in eosinophils and lymphocytes respectively immediately after smoking, compared to controls (Figure 2.2A-2.2D). The immune cell infiltration differences, however, did not persist until 15 weeks after smoking cessation (Figure 2.2A-2.2D).

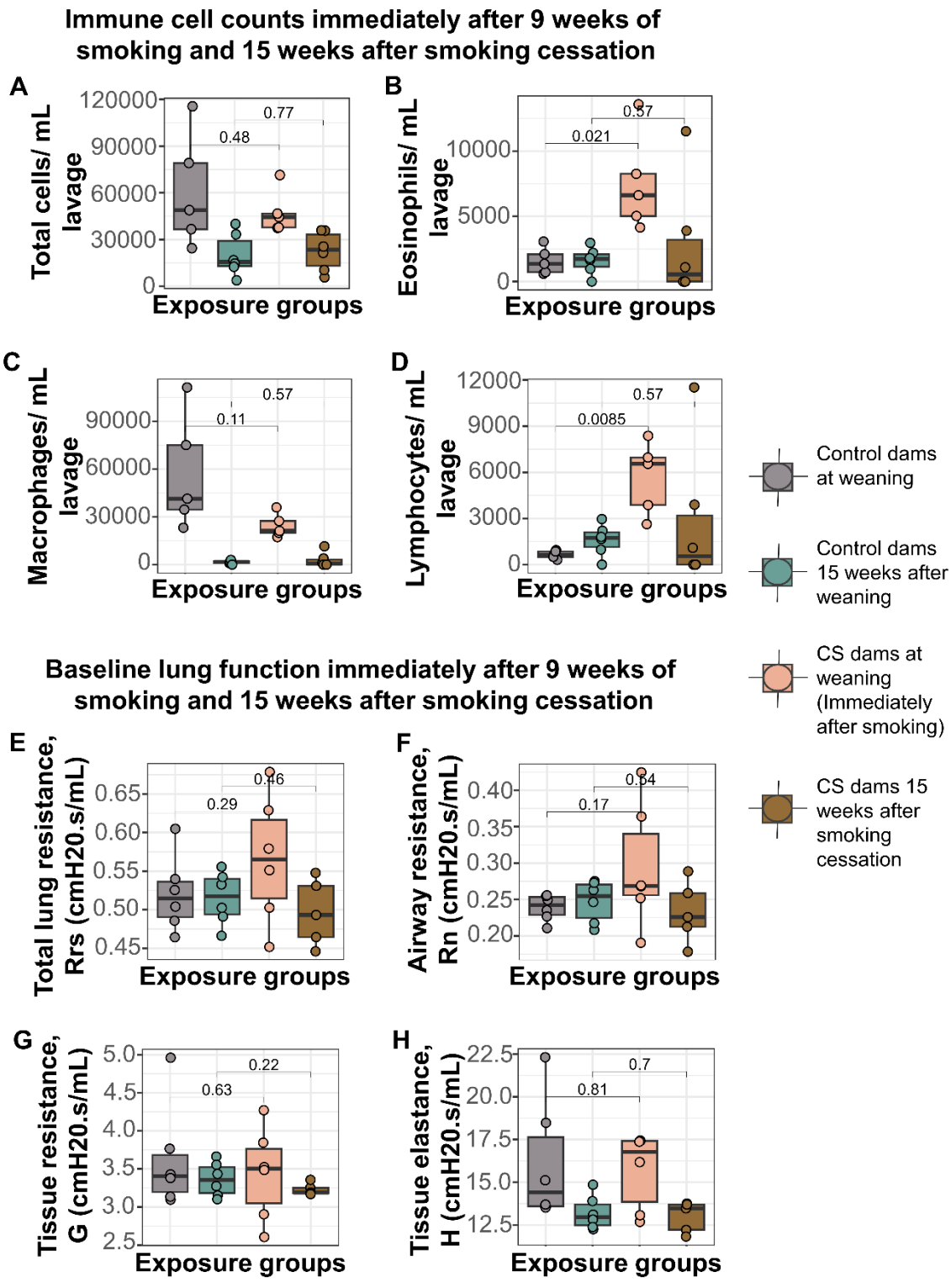

Figure 2. 2: Smoke exposure causes transient changes to immune cell infiltration into dam lungs, but does not alter dam baseline lung function over time.
(A) Total immune cells per mL lavage immediately after smoking and 15 weeks after smoking cessation. (B) Eosinophils per mL lavage in the CS-exposed dams (Mean = 7528, SD = 3736) was over 4 times more elevated than control dams (Mean = 1569, SD = 1029)

immediately after smoking, but normalized to controls 15 weeks after smoking cessation. (C) Macrophages per mL lavage immediately after smoking and 15 weeks after smoking cessation. (D) Lymphocytes per mL lavage in the CS-exposed dams (Mean = 5680, SD = 2357) was over 8 times elevated compared to control dams (Mean = 649, SD = 256) immediately after smoking, but normalized to controls 15 weeks after smoking cessation. (E) Total lung resistance at baseline. (F) Airway resistance at baseline. (G) Tissue resistance at baseline. (H) Alveolar elastance at baseline. N = 4-6 per group. Differential cell counts were normalized to lavage volume. Lung function values were measured using 90^{th} percentile values after injection of saline into the lungs. Two-group comparisons were conducted using a student t-test and $p < 0.05$ was considered significant.

Also of note is that total cell count and macrophage cell count were higher in both groups at the immediate post-smoking timepoint, when the dams were 3 weeks post-parturition and still lactating, than 15 weeks later (Figure 2.2A and 2.2C). We also found that direct CS exposure did not alter dam lung function either at baseline (Figure 2.2E-2.2H) or after methacholine challenge after 9 weeks of smoking (Figure 2.3A-2.3D), though tissue elastance was lower but not statistically significant in CS exposed than unexposed dams (Figure 2.3D). Thirteen weeks after smoking cessation, baseline lung function was also not altered (Figure 2.2E-2.2H), but we observed significant differences between CS exposed and unexposed animals in tissue elastance, tissue resistance and total lung resistance values (Figure 2.3E-2.3H).

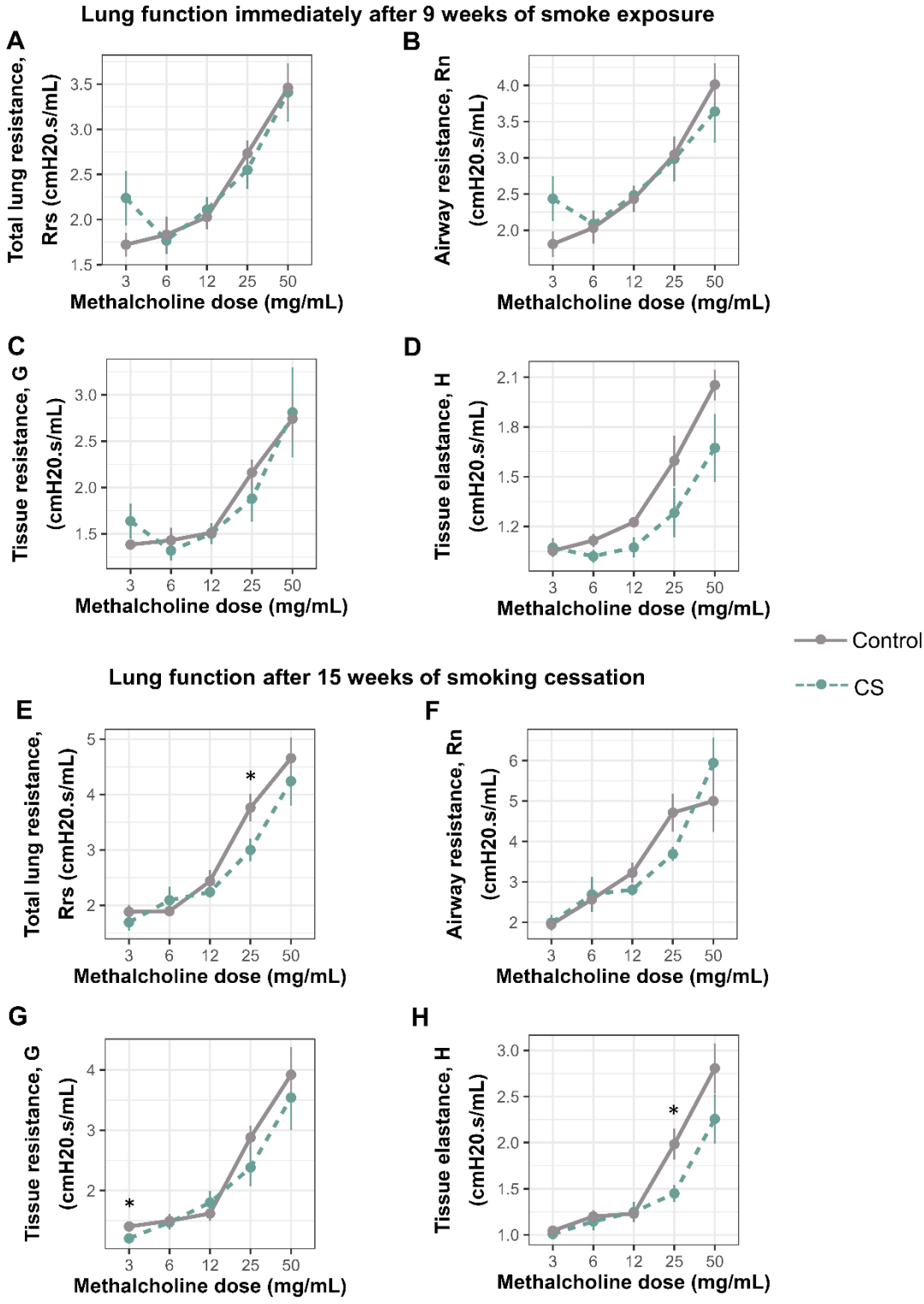

Figure 2. 3: Smoke exposure alters methacholine responsiveness in mouse lungs up to 15 weeks after smoking cessation.
(A) Total lung resistance immediately after smoking. (B) Airway resistance immediately after smoking. (C) Tissue resistance immediately after smoking. (D) Alveolar elastance immediately after smoking. (E) Total lung resistance after 15 weeks of smoking cessation. (F)

Airway resistance after 15 weeks of smoking cessation. (G) Tissue resistance after 15 weeks of smoking cessation. (H) Alveolar elastance after 15 weeks of smoking cessation. N = 5-6 per group. Lung function values were measured using 90^{th} percentile values upon administration of increasing doses of methacholine. Data were analyzed using one-way ANOVA, followed by multiple comparisons at each methacholine dose where significant. *p < 0.05 in control vs smoke-exposed group.

Together, these data show that smoking for 9 weeks alters lung phenotype by increasing immune cell infiltration into the lungs immediately after smoking, accompanied by persistent decline in lung function even after smoking cessation.

2.4.2 Candidate gene DNAm and expression immediately after 9 weeks of smoking and 15 weeks after smoking cessation

To determine whether CS-induced DNAm changes observed in humans are recapitulated in our mouse model, we identified candidate genes to assess initially via pyrosequencing. We first measured DNAm and expression at *Cyp1a1* immediately after smoking and 15 weeks after cessation. We found an increase in *Cyp1a1* DNAm in the blood of CS-exposed dams 15 weeks after smoking cessation compared to controls, though this increase was not statistically significant (Figure 2.4A). *Cyp1a1* expression in the lungs of CS-exposed dams was slightly but not significantly elevated 15 weeks after smoking cessation (Figure 2.4B). Chronic exposure to CS for 9 weeks led to a significant decrease in *Cyp1a1* DNAm in the left lungs of CS-exposed dams immediately after smoking (Figure 2.4C, Mean = 11.20, SD = 1.05), compared to controls (Figure 2.4C, Mean = 19.20, SD = 0.80). Interestingly, *Cyp1a1* DNAm remained significantly decreased in the lungs of smoking dams (Figure 2.4D, Mean = 15.00, SD = 1.07) compared to controls (Figure 2.4D, Mean = 17.60, SD = 0.58) till 15 weeks after smoking cessation, though the magnitude had reduced slightly.

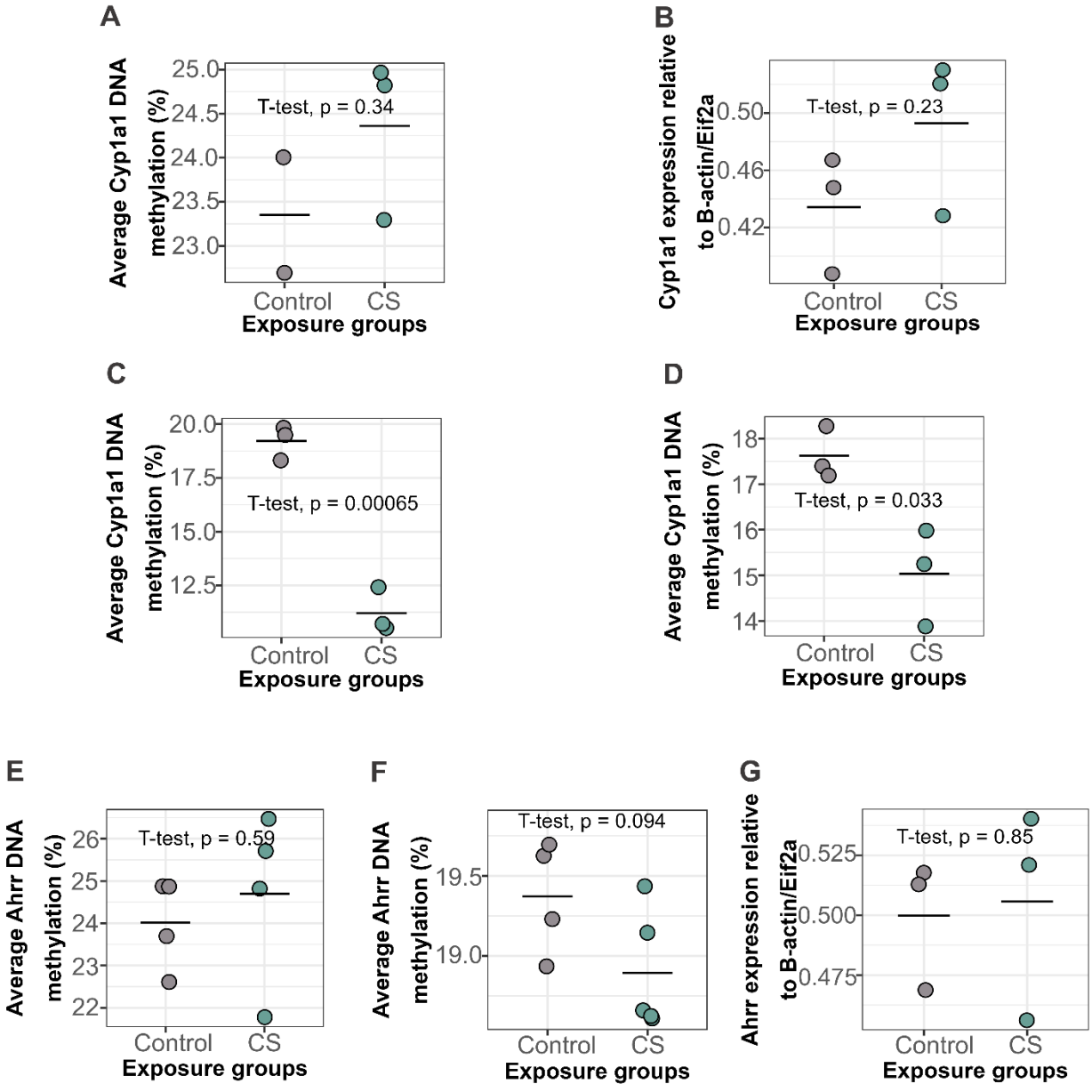

Figure 2. 4: *Cyp1a1* and *Ahrr* DNAm and expression levels in dam blood and lungs immediately after smoking and 15 weeks after smoking cessation.
(A) *Cyp1a1* DNAm in dam blood 15 weeks after smoking cessation. (B) *Cyp1a1* expression in dam lungs 15 weeks after smoking cessation. (C) *Cyp1a1* DNAm in dam lungs immediately after 9 weeks of smoking (D) *Cyp1a1* DNAm in dam lungs 15 weeks after smoking cessation. (E) *Ahrr* DNAm in dam blood after 15 weeks of smoking cessation. (F) *Ahrr* DNAm in dam lungs after 15 weeks of smoking cessation. (G) *Ahrr* expression in dam lungs after 15 weeks of smoking cessation. N = 2-5 per group. Differences in DNAm and expression were analyzed using student t-tests.

Conversely, we found no significant differences in *Ahrr* DNAm in dam blood 15 weeks after smoking cessation (Figure 2.4E). Similarly, *Ahrr* DNAm (Figure 2.4F) and *Ahrr* expression (Figure 2.4G) in dam lungs at this same timepoint were also not significantly different between groups. These results thus show that personal smoking for 9 weeks causes alterations in *Cyp1a1* DNAm in the lungs which persist for 15 weeks after smoking cessation.

2.4.3 Measurement of effects of smoking on mouse lungs across the whole mouse epigenome using the Illumina mouse methylation microarrays

Following candidate gene DNAm measurements at *Ahrr* and *Cyp1a1*, we evaluated the association between smoking and epigenome-wide DNAm in the lungs immediately after 9 weeks of smoking, using normalized β values from the Illumina mouse microarrays. Due to our small sample size (N = 2-6 per group), we used a combination of *p* value ($p < 1e-3$) and effect size (0.05) cutoffs to determine significance. After adjusting for the 1 surrogate variable recommended by SVA (Appendix 2.2A), we performed multivariable regression on beta values from the autosomal probes (Appendix 2.2B) and identified 40 significant CpGs differentially methylated in dams exposed to heavy doses of CS for 9 weeks (Table 2.1). Maternal smoking in pregnancy led to higher DNAm at 37.5% (15 CpGs) and lower DNAm at 62.5% (25 CpGs) of these significant CpGs (Table 2.1). While our candidate gene, *Cyp1a1*, was not among our list of significant genes, a closer look at each of the *Cyp1a1* probes on the mouse array reveal large differences in DNAm between controls and CS-exposed dams in 3 of 9 *Cyp1a1* probes that passed preprocessing (Appendix 2.3, positions E, F and G). The second candidate gene, *Ahrr,* was also not significant in our epigenome-wide analysis and showed small effect size differences overall (Appendix 2.4).

Table 2. 1: CpGs significantly altered immediately after exposure to CS for 9 weeks.

CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	CpG position	Feature
cg28865575_TC11	0.000636	0.052702	Increase	Tmcc3	chr10	+	94565729	tss_body
cg29251423_BC21	0.000807	-0.06824	Decrease	Ddc	chr11	-	11849043	tss_body
cg29406381_BC11	0.000487	0.057487	Increase	Slit3	chr11	+	35415800	tss_body
cg29805460_BC21	0.000956	0.054231	Increase	Lyrm9	chr11	+	78837975	tss_body
cg30483569_TC21	0.000306	-0.07163	Decrease	Sox11	chr12	-	27337170	tss_body
cg30755159_TC21	0.000786	-0.05114	Decrease	Atl1	chr12	+	69922712	tss_body
cg30957340_TC21	0.000692	-0.05017	Decrease	Tshr	chr12	+	91500661	tss_body
cg31222899_BC21	0.000181	-0.06422	Decrease	Akr1c19	chr13	+	4233410	tss_1500
cg31361083_BC21	0.000395	-0.06943	Decrease	Mrs2	chr13	-	25018568	tss_body
cg31429252_TC21	0.00099	-0.05489	Decrease	NA	chr13	+	35067277	tss_body
cg32309765_TC21	0.000418	-0.06221	Decrease	Wnt5a	chr14	+	28520202	tss_body
cg34791132_BC11	0.000909	-0.06719	Decrease	Fkbp5	chr17	-	28420600	tss_body
cg34837962_BC21	0.000606	0.051306	Increase	NA	chr17	-	31905760	NA
cg35952853_BC21	0.000398	0.060032	Increase	Katnal2	chr18	-	77019702	tss_body
cg36020879_TC21	0.000498	-0.07337	Decrease	NA	chr18	+	83381494	NA
cg37170929_TC21	0.000902	-0.05191	Decrease	Sp100	chr1	+	85694662	tss_body
cg37188755_TC21	0.000491	0.064006	Increase	Snorc	chr1	+	87475345	tss_body
cg37214886_TC11	0.000816	0.058147	Increase	Asb18	chr1	-	89993031	tss_body
cg38811965_BC21	0.000584	-0.07976	Decrease	Aven	chr2	+	112625271	tss_body
cg39112318_BC11	0.000604	0.057822	Increase	NA	chr2	-	151984366	NA
cg39272146_BC11	0.00085	0.053982	Increase	NA	chr2	-	166209426	tss_1500
cg39843142_BC21	0.000369	-0.08598	Decrease	NA	chr3	-	66031662	tss_200
cg40162834_BC21	0.000984	-0.06193	Decrease	Strip1	chr3	-	107616877	tss_body
cg40351477_TC11	0.000227	-0.06665	Decrease	Npnt	chr3	-	132882166	tss_body
cg41660449_TC21	0.000465	-0.07261	Decrease	Aadacl3	chr4	-	144458573	tss_body
cg41773149_BC21	0.000755	-0.0517	Decrease	Megf6	chr4	+	154225613	tss_body
cg41898551_BC21	0.000703	-0.05057	Decrease	Magi2	chr5	+	20228413	tss_body
cg42734289_BC21	0.000476	0.070828	Increase	Atxn2	chr5	+	121811603	tss_body
cg42831686_BC11	0.000298	0.061434	Increase	NA	chr5	-	129621191	NA

cg43672977_TC21	0.000115	-0.07605	Decrease	Eefsec	chr6	-	88299565	tss_body
cg43685030_TC21	0.000655	-0.05455	Decrease	Chchd6	chr6	-	89496798	tss_body
cg44396689_TC21	0.000662	-0.08133	Decrease	NA	chr7	+	30681712	NA
cg44775237_BC21	0.000229	-0.06595	Decrease	Furin	chr7	-	80405386	tss_body
cg44780944_TC11	0.000578	0.057629	Increase	NA	chr7	+	80880504	NA
cg44880684_BC21	0.000489	-0.06252	Decrease	Nars2	chr7	+	97034436	tss_body
cg45732545_BC11	0.000884	-0.06968	Decrease	Galntl6	chr8	-	57805818	tss_body
cg45830215_BC11	8.72E-05	0.08256	Increase	B3gnt3	chr8	-	71701592	tss_body
cg45830217_BC21	0.000449	0.062246	Increase	B3gnt3	chr8	-	71701624	tss_body
cg46292742_BC21	0.000316	0.056784	Increase	Fbxo31	chr8	-	121575825	tss_body
cg46811672_TC21	0.000653	-0.06822	Decrease	Hcn4	chr9	+	58833272	tss_body

Linear regression was computed using LIMMA, after adjusting for 1 surrogate variable recommended by SVA (see Figure S1). Results are sorted by CpG name. Direction: direction of change in DNAm compared to controls. Gene: gene names as annotated by UCSC Genome browser. Strand: direction of gene on the chromosomal strand ("+" = forward, "-" = reverse). Feature: gene region feature as annotated by UCSC Genome browser (tss_body = located within the gene body, tss_200 = located 0-200 bases upstream of transcriptional start site, tss_1500 = located 200-1500 bases upstream of transcriptional start site). N = 3 Control and N = 3 CS. CpG sites were considered significant at $p < 1e\text{-}3$ and effect size > 0.05.

We performed a similar analysis on probes from the X chromosome, and after adjusting for the 1 surrogate variable recommended by SVA, found no significantly altered CpGs in dam lungs immediately after smoking (Appendix 2.5).

2.4.4 Gene Ontology terms associated with smoking in the lungs

To gain insights into biological processes potentially affected by smoking in the lungs, we performed gene ontology analyses on genes mapping to the identified 40 significant CpGs. Gene ontology analysis revealed 54 biological processes which passed the FDR cutoff of 0.05 (Table 2.2).

Table 2. 2: **List of significantly enriched biological pathways/processes immediately after 9 weeks of smoking.**

ID	Description	P value	FDR	Gene ID	Gene count
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	4.90E-06	0.007594	Sox11/Wnt5a/Npnt/Magi2/Furin	5
GO:0060412	ventricular septum morphogenesis	1.64E-05	0.012732	Slit3/Sox11/Wnt5a	3
GO:0009653	anatomical structure morphogenesis	2.86E-05	0.012997	Slit3/Sox11/Atl1/Tshr/Wnt5a/Sp100/Strip1/Npnt/Atxn2/Furin/Fbxo31	11
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	3.36E-05	0.012997	Sox11/Wnt5a/Npnt/Magi2/Furin	5
GO:0031175	neuron projection development	6.38E-05	0.01459	Slit3/Atl1/Tshr/Wnt5a/Magi2/Atxn2/Fbxo31	7
GO:0060411	cardiac septum morphogenesis	6.79E-05	0.01459	Slit3/Sox11/Wnt5a	3
GO:0030182	neuron differentiation	6.97E-05	0.01459	Slit3/Sox11/Atl1/Tshr/Wnt5a/Magi2/Atxn2/Fbxo31	8
GO:0003281	ventricular septum development	7.54E-05	0.01459	Slit3/Sox11/Wnt5a	3
GO:0048699	generation of neurons	9.98E-05	0.017177	Slit3/Sox11/Atl1/Tshr/Wnt5a/Magi2/Atxn2/Fbxo31	8
GO:0048666	neuron development	0.000146	0.02261	Slit3/Atl1/Tshr/Wnt5a/Magi2/Atxn2/Fbxo31	7
GO:0071495	cellular response to endogenous stimulus	0.000173	0.024346	Sox11/Tshr/Wnt5a/Npnt/Magi2/Furin/Hcn4	7
GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	0.000194	0.024492	Sox11/Npnt/Furin	3
GO:0090287	regulation of cellular response to growth factor stimulus	0.000206	0.024492	Sox11/Wnt5a/Npnt/Furin	4
GO:0003279	cardiac septum development	0.000229	0.02522	Slit3/Sox11/Wnt5a	3
GO:0022008	neurogenesis	0.00025	0.02522	Slit3/Sox11/Atl1/Tshr/Wnt5a/Magi2/Atxn2/Fbxo31	8
GO:0040011	locomotion	0.00026	0.02522	Slit3/Tshr/Wnt5a/Sp100/Magi2/Furin/Fbxo31	7
GO:0062009	secondary palate development	0.00029	0.025719	Sox11/Wnt5a	2
GO:0090103	cochlea morphogenesis	0.000312	0.025719	Tshr/Wnt5a	2
GO:0071363	cellular response to growth factor stimulus	0.000328	0.025719	Sox11/Wnt5a/Npnt/Magi2/Furin	5
GO:0070848	response to growth factor	0.000361	0.025719	Sox11/Wnt5a/Npnt/Magi2/Furin	5
GO:0003206	cardiac chamber morphogenesis	0.000371	0.025719	Slit3/Sox11/Wnt5a	3
GO:0003231	cardiac ventricle development	0.000379	0.025719	Slit3/Sox11/Wnt5a	3
GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	0.000409	0.025719	Npnt/Furin	2
GO:1903846	positive regulation of cellular response to transforming growth factor beta stimulus	0.000409	0.025719	Npnt/Furin	2
GO:0009719	response to endogenous stimulus	0.000432	0.025719	Sox11/Tshr/Wnt5a/Npnt/Magi2/Furin/Hcn4	7
GO:0040012	regulation of locomotion	0.000434	0.025719	Tshr/Wnt5a/Sp100/Magi2/Furin/Fbxo31	6
GO:0048812	neuron projection morphogenesis	0.000466	0.025719	Slit3/Atl1/Wnt5a/Atxn2/Fbxo31	5

GO:0120039	plasma membrane bounded cell projection morphogenesis	0.000513	0.025719	Slit3/Atl1/Wnt5a/Atxn2/Fbxo31	5
GO:0010922	positive regulation of phosphatase activity	0.000518	0.025719	Npnt/Magi2	2
GO:0048858	cell projection morphogenesis	0.000529	0.025719	Slit3/Atl1/Wnt5a/Atxn2/Fbxo31	5
GO:0048846	axon extension involved in axon guidance	0.000547	0.025719	Slit3/Wnt5a	2
GO:1902284	neuron projection extension involved in neuron projection guidance	0.000547	0.025719	Slit3/Wnt5a	2
GO:0000902	cell morphogenesis	0.000548	0.025719	Slit3/Atl1/Wnt5a/Strip1/Atxn2/Fbxo31	6
GO:0032990	cell part morphogenesis	0.000608	0.027706	Slit3/Atl1/Wnt5a/Atxn2/Fbxo31	5
GO:0120036	plasma membrane bounded cell projection organization	0.000629	0.027857	Slit3/Atl1/Tshr/Wnt5a/Magi2/Atxn2/Fbxo31	7
GO:0030030	cell projection organization	0.000731	0.030942	Slit3/Atl1/Tshr/Wnt5a/Magi2/Atxn2/Fbxo31	7
GO:0050919	negative chemotaxis	0.000739	0.030942	Slit3/Wnt5a	2
GO:0003205	cardiac chamber development	0.000829	0.033589	Slit3/Sox11/Wnt5a	3
GO:0071542	dopaminergic neuron differentiation	0.000846	0.033589	Tshr/Wnt5a	2
GO:0090102	cochlea development	0.000999	0.038672	Tshr/Wnt5a	2
GO:0032989	cellular component morphogenesis	0.001078	0.040397	Slit3/Atl1/Wnt5a/Atxn2/Fbxo31	5
GO:0043392	negative regulation of DNA binding	0.001121	0.040397	Sox11/Sp100	2
GO:0046189	phenol-containing compound biosynthetic process	0.001121	0.040397	Ddc/Wnt5a	2
GO:0048546	digestive tract morphogenesis	0.001207	0.042496	Sox11/Wnt5a	2
GO:0051239	regulation of multicellular organismal process	0.001241	0.042728	Sox11/Tshr/Wnt5a/Sp100/Npnt/Atxn2/Furin/Fbxo31/Hcn4	9
GO:0030100	regulation of endocytosis	0.001355	0.045622	Wnt5a/Magi2/Atxn2	3
GO:0048468	cell development	0.001461	0.047429	Slit3/Sox11/Atl1/Tshr/Wnt5a/Magi2/Atxn2/Fbxo31	8
GO:0002011	morphogenesis of an epithelial sheet	0.001531	0.047429	Sox11/Wnt5a	2
GO:0034340	response to type I interferon	0.001531	0.047429	Wnt5a/Sp100	2
GO:0045778	positive regulation of ossification	0.001531	0.047429	Sox11/Wnt5a	2
GO:0007399	nervous system development	0.001566	0.047577	Slit3/Sox11/Atl1/Tshr/Wnt5a/Magi2/Atxn2/Fbxo31	8
GO:0051049	regulation of transport	0.00167	0.049132	Sox11/Wnt5a/Sp100/Magi2/Atxn2/Furin/Hcn4	7
GO:0035306	positive regulation of dephosphorylation	0.001681	0.049132	Npnt/Magi2	2
GO:2000648	positive regulation of stem cell proliferation	0.001733	0.049701	Sox11/Wnt5a	2

ID: gene ontology identification code. Description: description of the enriched process. Gene ID: genes contributing to enrichment of the biological process. Gene count: number of genes contributing to the biological process. Biological processes were considered significantly enriched at FDR < 0.05.

The top pathway findings were mostly driven by *Sox11, Wnt5a, Npnt, Slit3, Magi2* and *Furin*, all being involved in numerous processes. The most significantly implicated pathway with the smallest FDR (FDR = 0.007) was involved in regulation of transmembrane receptor protein serine/threonine kinase signaling pathways.

2.5 Discussion

Cigarette smoke is a complex mixture of over 7000 components[366–369], which affect virtually all body systems via mechanisms such as inflammation and DNA damage. While the processes linking smoking and adverse health outcomes are poorly understood, DNA methylation alterations have been identified as possible links due to their sensitivity to the environment and relative stability[370]. The association between smoking and changes in DNAm has been well documented, especially in human blood[210,214,216,341]. However, while there may be shared DNAm patterns between tissues[211,344], overall DNAm is highly variable across tissues[234,342,343], emphasizing the need to study smoke-induced DNAm alterations in more directly affected tissues such as the lungs. The major aim of this study therefore, was to identify DNAm changes in mouse lungs arising due to smoking, and determine how these patterns would change after a period of smoking cessation. To this effect, we adapted an effective smoking mouse model which we have also used to measure the effects of early life smoke exposure on offspring[335]. Using this model, we identified 40 lung-specific CpGs which were differentially methylated following chronic smoke exposure, 32 of which had never been linked to smoking in the past. We also showed that chronic smoking causes alterations in mouse lung function that can last into adulthood, even after a long period of smoking cessation. These results are important, as identification of lung-specific DNAm patterns may

provide more effective biomarkers for smoking, and may potentially be used to develop therapeutic interventions against the effects of chronic smoke exposure.

Prior to this study, much of what was known about smoking and DNAm was from studies conducted in blood in humans. Only a quarter of the sites we identified were associated with genes that had previously been connected to CS exposure in any tissue, and of those, there was existing evidence about DNAm differences specifically only at one gene, *Fkbp5*[371]. *O*ne study reported that smoking decreases *Fkbp5* DNAm in blood, which might be connected to dysregulation of the hypothalamic-pituitary-adrenal axis[371]. Our study replicated this finding, as we also observed a decrease in *Fkbp5* DNAm in mouse lungs our study, which might implicate the hypothalamic-pituitary-adrenal axis more broadly across tissues in the response to early life CS exposure.

Of the other genes with prior evidence of connection to CS exposure, the majority have genetic or transcriptomic connections. For example, one of our hits mapped to the Ataxin 2 (*Atxn2)* gene, expression of which has been linked to pancreatic cancer development in smokers[372]. The CpG we identified is located in an intragenic exon which is actively transcribed in mouse lungs, with high levels of H3K36me3[373–375]. Generally, the function of DNAm at exons varies depending on where the exon is located[376–378], but most studies have discovered positive correlations between DNAm in intragenic exons and expression levels[376,379]. As our significant CpG is located in an intragenic exon, increased DNAm in smoking dams could signal an increase in *Atxn2* expression linked with an increased risk of malignancy. This is the first study associating smoking with altered DNAm at *Atxn2.*

We also found for the first time that heavy smoking resulted in a significant decrease in lung DNAm at Dopa decarboxylase (*Ddc*), a gene encoding a protein which catalyzes the

final steps of dopamine and serotonin biosynthesis[380]. Genetic variants in *Ddc*, especially at the introns[381], have been associated with smoking behavior and nicotine dependency[381–383] in African-American and European-American populations. It therefore follows that alterations in DNAm at this gene as observed here could contribute to nicotine dependency in individuals who smoke. It is however important to note that genetic variants or genes alone do not determine susceptibility to addiction, and that the environment plays a major role[298,299]. In a Finnish twin study, it was discovered that the influence of genetics in adolescent smokers was decreased when the adolescents were highly monitored by their parents[384]. This emphasizes the need for more research to focus on understanding gene-environment interactions, as it could be crucial in deciphering the mechanism behind addiction.

The six other genes with prior evidence for association with smoking are summarized as follows: 1) Slit guidance ligand 3 (*Slit3*) whose expression has been associated with the development of nicotine preference in zebrafish, [385] and which is down-regulated in human lung adenocarcinoma cell lines and tissues[386]. Expression levels of *SLIT3* are also significantly correlated with smoking history, as non-smokers with high expression of *SLIT3* had better prognosis among lung adenocarcinoma patients[386]; 2) Wingless-type MMTV integration site family, member 5A (*Wnt5a*) which is upregulated by tobacco smoke condensate in lung cancer cells[387], and in mouse and human lung tissues[388], and has been associated with the development of lung carcinogenesis in bronchial epithelial cells of smokers[389]; 3) Ankyrin repeat and SOCS box-containing 18 (*Asb18*) which shows differential expression levels in smokers[390]; 4) Nephronectin (*Npnt*), whose variants were shown to be involved in COPD-mediated airflow obstruction both in heavy smokers and non-smokers in a UK-based cohort[391]; 5) Membrane associated guanylate kinase, WW and PDZ domain containing 2 (*Magi2*) which shows higher expression in bronchial biopsies of heavy smokers

with COPD[392]. *Magi2* polymorphisms may also influence nicotine dependence in smokers[393]; and 6) FK506 binding protein 5 (*Fkbp5*) which has been linked to DNAm changes in blood as discussed, but also modulates the effects of nicotine on the hypothalamic pituitary adrenal axis in female smokers[394].

Of the 32 novel sites identified in this study, two mapped to the promoter of *B3gnt3* (UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3) gene. Both CpGs, which are 32 bp apart, showed significantly higher DNAm in the lungs of dams exposed to CS compared to controls. This gene codes for a type II transmembrane protein which is involved in the biosynthesis of poly-N-acetyllactosamine chains, L-selectin ligand biosynthesis, lymphocyte homing and lymphocyte trafficking and recirculation[395,396]. One study reported increased *B3gnt3* expression levels corresponding to increased immune cell infiltration and correlated with poorer outcomes in patients with lung adenocarcinoma[397]. Other studies have also associated differential *B3gnt3* expression levels with development of many other types of cancers[398–402]. It therefore follows that increased DNAm in our two CpG sites, which are located in a weak promoter, could translate to decreased expression of the gene, consequently resulting in increased tolerance to and reduced sensitivity and response to foreign antigens by T cells. This is the first study associating smoking with altered DNAm at *B3gnt3.*

While there is a relative dearth of studies examining DNAm in the lungs, we found three other studies which directly measured effects of personal smoking on DNAm in the lungs. The first measured epigenome-wide DNAm in the blood of current and never-smokers. Next, using the identified significant CpGs from the epigenome-wide analysis, they measured DNAm in the lungs of current, ex- and never-smokers using pyrosequencing[211]. Out of 15 CpGs differentially methylated sites in the blood, only five replicated in the lungs, confirming

that while these tissues share some similarities, not all blood-based findings will replicate in the lung[211]. Two of their 5 CpGs mapped to *AHRR*, and one corresponded to the human position we used to identify our mouse candidate *Ahrr* position (cg05575921). We did not observe DNAm changes in the lungs at *Ahrr*, but its poor conservation with the human genome in this region may limit comparability. In the second study, the effects of a) whole-body CS, b) the tobacco carcinogen 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone, and c) the inflammatory agent lipopolysaccharide were measured in mouse lungs using RRBS[346]. They found DNAm and hydroxymethylation differences across multiple differentially methylated regions[346]. While there were no overlapping differentially methylated sites between their results and ours, they identified 10 hydroxymethylated sites which corresponded to, or whose isoforms corresponded to 10 of our differentially methylated sites: *Strip1, Slit3, Megf6, Magi2, Atxn2, Sox10/Sox18, Wnt5b, Fkbp3, Asb13* and *Fbxo41/Fbxo45*. The microarrays we used here cannot distinguish between methylcytosine and hydroxymethylcytosine, and so it is possible that some of our findings are due to similar hydroxymethylcytosine changes. A third study exposed mice to 2 hours of CS twice daily, for 4 weeks consecutively in order to analyze the effect of smoking on lung DNAm. Using liquid hybridization capture-based bisulfite sequencing, they found that smoking altered DNAm patterns at numerous genes, most of which were involved in inflammation and in inflammatory injury in COPD, but due to limits on data availability it was not possible to determine whether specific findings overlapped with ours[347].

Gene ontology analysis on our list of significant genes revealed enrichment in multiple biological processes, with the most significant being involved in regulation of transmembrane receptor protein serine/threonine kinase signaling pathways. Components of CS, such as nicotine and the CS-specific carcinogen 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone,

when bound to nicotinic-acetylcholine receptors, activate serine/threonine kinase Akt[403]. Activation of Akt resulted in increased phosphorylation of downstream molecules involved in controlling the cell cycle and protein translation, such as glycogen synthase kinase 3 (GSK-3)[403]. This in turn leads to cancer-like phenotypes such as loss of contact inhibition, desensitization to regulation by growth factors, decreased apoptosis, angiogenesis and increased cellular proliferation[403,404]. Since our current study identified an enrichment for genes involved in regulation of serine/threonine Akt pathways, it could support a predisposition to lung tumorigenesis in smoke-exposed mice.

Our candidate gene DNAm analysis also revealed interesting patterns. Our first candidate gene, *AHRR,* particularly locus cg05575921, has repeatedly shown decreased DNAm in human serum[208], whole and peripheral blood[216,405], saliva[406], monocytes[407] and alveolar macrophages[217] of current smokers compared to never-smokers. In the same vein, even offspring exposed to CS *in utero* have shown altered *AHRR* DNAm at the same locus compared to controls[269–271,273]. Compared to these studies however, our candidate gene analysis did not reveal significant differences in *Ahrr* DNAm or expression in blood or lungs at the corresponding mouse locus. This was interesting but not entirely surprising, since *Ahrr* is not well conserved between mouse and humans at this region. Therefore, further mapping of DNAm in the *Ahrr* gene in mouse lung may reveal deeper insights.

At *Cyp1a1*, we found that smoking for 9 weeks caused a significant decrease in DNAm immediately after smoking, and that this pattern remained significant until 15 weeks after smoking cessation. However, *Cyp1a1* expression in mouse lungs after smoking cessation, though increased, was not significant, indicating that DNAm changes may last after expression differences have subsided. *Cyp1a1* belongs to the cytochrome p450 enzyme subclass, and is involved in drug/xenobiotic metabolism[408–410]. Therefore, reduced DNAm of

Cyp1a1 in CS-exposed mice as observed in this study could indicate induction of the enzyme to aid detoxification of CS components. These results mimic reduced *Cyp1a1* DNAm and increased expression patterns observed in the lungs[411], adipose tissue[412], prostate cancer tissues[413], buccal cells[345] and blood[345] of humans exposed to CS in previous studies. Even though none of the *Cyp1a1* probes in the mouse methylation microarray was among our 40 significant CpGs, we showed that 3 of the 9 *Cyp1a1* probes have large differences in DNAm. Our inability to detect these positions (and likely some other CpGs) as significant is likely due to our small sample size. So, while these 3 probes met our strict effect size cutoff of 0.05, they did not meet the *p* value cutoff. Future studies with larger sample sizes would be helpful in generating more precise measurements.

In addition to molecular alterations, we also assessed the effects of chronic smoking on physiological outcomes in form of lung function. We observed that the changes in lung function immediately after smoking for 9 weeks were small and not significant. However, 15 weeks after smoking cessation, lung function in CS-exposed dams had significantly declined, as evidenced by increased airway responsiveness to methacholine. One reason why lung function worsens over time in our smoke-exposed mice may be due to aging. Past research indicates that lung function declines with age due to structural and immunological factors which impair gas exchange and increase susceptibility to infections[414–416]. Other studies report that smoking exacerbates this lung function decline, even in ex-smokers[417–420]. This trend of worsening/decline in lung function is a characteristic of COPD[421,422]. In line with our finding of declining lung function even with smoking cessation, in a large multi-ethnic pooled cohort study[420], smoking cessation slightly improved lung function, but these “improvements” still resulted in lung function similar to light/low-intensity current smokers. In fact, smoking cessation does not completely restore lung function to the levels of never-smokers[420]. This

pattern of lung function decline despite smoking cessation may be due to sustained dysregulation of epigenetic patterns[231,423,424], immune responses[425–427] and airway hyperresponsiveness[428].

This study represents an important contribution to our understanding of the impacts of CS on the lungs, but is not without limitations. The first limitation is our small sample size for the EWAS and hence, low statistical power in identifying small DNAm differences. We also could not distinguish between hydroxymethylcytosine and methylcytosine, meaning that some of our differential DNAm findings may be due to changes in hydroxymethylcytosine. It is also worth noting that whole lungs were used in this study, making it impossible to determine whether differences in cell composition are masking some of our findings. However, we took two approaches to mitigate this problem. First, we lavaged the lungs prior to analysis to remove immune cells which we know to be different between CS and control animals, making it unlikely that immune cells are responsible for our observed results. To further support this, we found that *Cyp1a1* DNAm in the blood of adult female control mice (Figure 3.4A) is higher than *Cyp1a1* DNAm in lungs of control mice (Figure 3.4D), therefore, infiltration of immune cells from blood to lungs is unlikely to cause the decrease in lung *Cyp1a1* DNAm in the present study. Second, we used surrogate variables to control for variance likely associated with cell type. This approach removes the effects of cell type such that further work will be required to determine which lung cell types exhibit the observed DNAm differences.

In summary, we have shown here that chronic smoking alters DNAm patterns in mouse lungs at multiple CpGs, some which have never been associated with smoking in the past. These CpGs map to genes implicated in tumorigenesis and metastasis, neurodegenerative disorders, nicotine dependency and immune cell responses. Moreover, lung function defects persist up to 15 weeks after smoking cessation. The fact that 75% of

the significant CpGs reported here have never been linked to CS in the past, even in studies which investigated effects of CS in the blood, emphasizes the need for more studies to be done on the lungs, as it clearly has different responses than other tissues. This research is one part of a much larger study to investigate the effects of early life CS exposure on offspring DNAm patterns. Therefore, the results presented here will hopefully also shed more light on some of the patterns we observe in offspring exposed to CS *in utero*.

Chapter 3: Early life exposure to cigarette smoke primes lung function and DNA methylation changes at *Cyp1a1* upon exposure later in life

RUNNING HEAD: Maternal smoking primes offspring lungs for later exposures

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AUTHOR CONTRIBUTIONS

M.J.J. conceived and designed research; C.D.O., S.L., S.B., J.C., Y.H., N.H., S.C., M.S.F., S.K. and B.X. performed experiments; C.D.O. and C.P. analyzed data; M.J.J. and C.D.O. interpreted results of experiments; C.D.O. prepared figures; C.D.O. prepared manuscript; M.J.J., C.P., A.J.H, and V.W.D. edited and revised manuscript; S.L., S.B., J.C., Y.H., N.H., S.C., M.S.F., S.K., B.X., A.J.H., V.W.D., C.P. and M.J.J. approved final version of manuscript.

3.1 Abstract

Prenatal and early life exposure to cigarette smoke (CS) have repeatedly been shown to induce stable, long-term changes in DNA methylation (DNAm) in offspring. It has been hypothesized that these changes might be functionally related to the known outcomes of prenatal and early life CS exposure, which include impaired lung development, altered lung function and increased risk of asthma and wheeze. However, to date, few studies have examined DNAm changes induced by prenatal CS in tissues of the lung, and even fewer have attempted to examine the specific influences of prenatal versus early postnatal exposures. Here, we have established a mouse model of CS exposure which isolates the effects of prenatal and early postnatal CS exposures in early life. We have used this model to measure the effects of prenatal and/or postnatal CS exposures on lung function and immune cell infiltration as well as DNAm and expression of *Cyp1a1*, a candidate gene previously observed to demonstrate DNAm differences upon CS exposure in humans. Our study revealed that exposure to CS prenatally and in the early postnatal period causes long-lasting differences in offspring lung function, gene expression and lung *Cyp1a1* DNAm, which wane over time but are reestablished upon re-exposure to CS in adulthood. This study creates a testable mouse model which can be used to investigate the effects of prenatal and early postnatal CS exposures and will contribute to the design of intervention strategies to mediate these detrimental effects.

3.2 New and Noteworthy

Here, we isolated effects of prenatal from early postnatal cigarette smoke, and showed that exposure to cigarette smoke early in life causes changes in offspring DNA methylation at *Cyp1a1* that last through early adulthood but not into late adulthood. We also showed that smoking in adulthood re-established these DNA methylation patterns at *Cyp1a1*, suggesting that a mechanism other than DNA methylation results in long-term memory associated with early life cigarette smoke exposures at this gene.

Keywords: Cigarette smoke; DNA methylation; lung function; priming

3.3 Introduction

The developmental origins of health and disease (DOHaD) hypothesis postulates that environmental insults in the intrauterine and early postnatal environment program the developing fetus through changes in cellular function and structure, and that these changes can last through adulthood[263,264]. Numerous studies have shown that factors such as maternal nutrition, infections, stress and environmental exposure to toxins such as cigarette smoke (CS) can in fact produce long-lasting health consequences in offspring[429,430]. CS is a common environmental toxin in humans with about 9.5% of women of reproductive age (18-34 years) reported as active tobacco smokers in Canada in 2021[250]. Worldwide statistics show that as at 2019, about 20.1% of men and 5% of women between the ages of 15 and 24 were active smokers[431,432]. Cigarette smoke is made up of thousands of components which have detrimental effects, some of which can also cross the placenta and affect offspring development[251–253,433,434].

Early life CS exposure alters offspring growth and development, lung function, and is associated with airway hyperresponsiveness, asthma and wheeze in children[255,257,435]. In some cases, these outcomes persist into adulthood, suggesting that early life CS 'leaves a mark' on the offspring, a process that has been called *biological embedding*[266,267,436]. Epigenetic modifications have been identified as potential mechanisms by which biological embedding takes place[267,268]. The three main components of the epigenome – DNA methylation (DNAm), histone modifications, and non-coding RNAs[437] - are dynamic and reflect past environmental exposures, meaning that environmental insults in early life can elicit changes in epigenetic marks which cells would propagate over time, and thus could translate to disease phenotypes in later life.

CS exposure *in utero* has been associated with differential DNAm across thousands of genes in exposed children, suggesting that DNAm changes might directly or indirectly link early life CS exposure with later life outcomes[269–271 271–273,275,278]. While most epigenome-wide association studies (EWAS) investigating association between maternal smoking and DNAm have been conducted in newborn umbilical cord blood[269–273,275,278], others have also reported differential DNAm in placenta[274], nasal epithelia[438], buccal cells and peripheral blood of adolescents or adults[245,272,277,439]. The largest EWAS to date which investigated effects of prenatal smoke exposure on umbilical cord blood DNAm was a meta-analysis across 13 cohorts (n = 6685) in the Pregnancy and Childhood Epigenetics Consortium (PACE)[270]. Results from the PACE study reported differential methylation at over 6000 CpGs, with some of the top sites being Aryl Hydrocarbon Receptor Repressor (*AHRR*), Cytochrome P450 1A1 (*CYP1A1*), Myosin 1G (*MYO1G*) and Growth Factor Independent 1 Transcriptional Repressor (*GFI1*). These genes have also been associated with maternal smoking in other similar EWAS studies[269,270,273,281]. They are important in detoxification, apoptosis and cell proliferation, and have been linked to the development of orofacial clefts, oncogenesis and asthma[269,270,281]. Existing studies including PACE have not been able to investigate the effects of prenatal smoking after birth, nor could they measure DNAm in tissues that might be more proximal to CS-mediated disease, such as the lungs. We have chosen to focus on *Cyp1a1* in particular, as while it is differentially methylated in placenta[274,440] , umbilical cord blood[269–273,275,278] and adult blood[278,439] of children exposed to CS *in utero*, it has not been replicated in an animal model with the ability to link it directly to a phenotype.

While there have been human studies outlining the long-term effects of prenatal CS exposure on offspring, one challenge of these studies is their inability to effectively account for the effects of the postnatal environment. One study which measured the long-term effects

of prenatal CS on offspring lung function found no significant association between second-hand smoke exposure while pregnant and long-term offspring lung function after controlling for postnatal smoke exposure[441]. It is difficult in human studies to completely rule out the effect of postnatal smoke exposure since prenatal and postnatal exposures are typically very similar[285,286]. Therefore, there is a need to investigate the differences between DNAm signatures and health outcomes observed due to prenatal versus postnatal CS exposure, especially since they have been shown to produce mixed/confounding effects[287–290]. Animal models provide a solution to these problems by allowing the study of the effects of prenatal versus postnatal CS exposure, and enable research into longitudinal, cross-tissue and sex-specific effects of early life CS exposure.

Here, we have created a mouse model to study the effects of prenatal, postnatal, and combined early life CS on offspring DNAm and lung phenotype. Our model successfully recapitulates some of the phenotypes identified in humans exposed to prenatal CS and provides further information on the dynamics of early life CS exposure. We show that early life CS exposure alters offspring DNAm at *Cyp1a1*, lung function, and gene expression in patterns specific to their early life exposure periods. Critically, we show that the early life period can create lasting molecular memories, and that exposure to CS in adulthood recapitulates patterns set by early life CS exposure.

3.4 Materials and Methods

3.4.1 Animals

This experiment was approved by the Animal Research Ethics and Compliance Committee of the University of Manitoba. Balb/C mice (Charles River Laboratories, Massachusetts, United States) were supplied with standard laboratory chow and clean water *ad libitum* except during exposures and housed, four mice of a single sex per cage unless otherwise noted, in individually ventilated cages in a 12-hour light/dark cycle throughout the experiment.

3.4.2 Development of murine model of early life CS exposure

Standard 1R6F research cigarettes (University of Kentucky, Lexington, KY) were used for this experiment. CS was delivered via the SCIREQ InExpose smoking robot (SCIREQ, Montreal, QC, Canada). Female mice were left to acclimate for 1 week, then divided into 2 groups: 16 control and 16 CS-exposed mice. Beginning at 8 weeks, control mice were exposed to room air in a foreign cage, and CS mice exposed to whole body CS twice daily. Total estimated particulate matter per certificate of analysis from the cigarette manufacturer was 46.8 mg/cigarette, administered with a flow rate of 2L/min and one puff per minute, with 6 puffs per cigarette. CS mice were exposed for 9 weeks, beginning with a pre-pregnancy period of 3 weeks, after which they were mated (2 females to 1 male) with male mice. Once a vaginal plug was achieved, we separated female mice into individual cages for the rest of the experiment. We continued all smoke and room air exposures on CS and control mice respectively, throughout mating, pregnancy, birth, and stopped at weaning (3 weeks post-birth). At birth, we culled offspring to 6 offspring per litter, and cross-fostered half of CS offspring with half of control offspring, matching offspring by birth date to reduce potential of

rejection. Pups were marked with toe tattoos to identify birth group. Using our cross-fostering strategy, we generated 4 distinct offspring groups: control with no CS exposure ("Con"), offspring exposed to prenatal CS only ("Pre"), offspring exposed to postnatal CS only ("Post"), and offspring that received both prenatal and postnatal CS ("Full"). Throughout the experiment, offspring were never directly exposed to CS, but were indirectly exposed *in utero*, or via breastmilk or fur from dams. We sacrificed and collected tissues from offspring not cross-fostered at birth. Dams and offspring were weighed weekly. Three weeks after birth, offspring were weaned, CS exposures stopped, and dams underwent lung function testing followed by tissue collection. Pups were housed by sex, 4-6 to a cage. While original plans were to assess phenotype at 8 weeks of age, due to SARS-CoV2-related lab lockdowns animals were maintained until 16-20 weeks of age, after which lung function and tissue collection were conducted.

3.4.3 CS re-exposure experiment

Female offspring which were not euthanized at 16-20 weeks were left undisturbed until 60 weeks of age. Half of them were re-exposed for 2 hours to full body CS for 5 consecutive days per week, for 21 days in total. The other half which was not re-exposed to CS served as the adult controls. Lung function, lavage and tissue collection were performed as described.

2.4.4 Lung function measurement

As previously described[349,350], mice were anesthetized with sodium pentobarbital and lung function measured using the SCREQ Flexivent small animal ventilator (SCIREQ Inc., Montreal, QC, Canada). Total airway resistance (Rrs), Newtonian resistance (Rn), tissue resistance (G) and elastance (H) were measured at baseline in response to nebulized saline,

and changes in these parameters were also measured in response to increasing concentrations of nebulized methacholine (3 to 50 mg/ml). Using a three-parameter logistic regression, we fitted a dose-response curve and then calculated the slope of the curve in order to assess overall methacholine sensitivity[442] in the lungs after CS exposure.

3.4.5 Bronchoalveolar lavage

Following lung function measurement, mouse lungs were washed twice through a tracheal cannula with 1 ml of phosphate buffer saline (PBS) each wash. Bronchoalveolar lavage fluid (BALF) was then centrifuged at 4°C at 1200 rpm for 10 minutes to obtain cell-free supernatants which were stored at -20°C for later cytokine analysis. Cell pellets were resuspended in 1 ml of PBS and total cell counts were performed using a hemocytometer. Differential cell counts were performed by placing 100ul of resuspended pellets on glass slides using cytospin columns, and staining cells using a modified Wright-Giemsa stain (Hema 3 Stat Pack). Cell differentials were counted using a Carl Zeiss Axio Observer ZI microscope.

3.4.6 Blood and tissue collection and preparation

Whole blood was collected from dams at pup weaning and from offspring at 16 and 63 weeks. Blood was collected by severing the abdominal aorta, into EDTA-coated tubes, centrifuged at 4000 rpm for 15 minutes to obtain plasma. Blood cell pellets and plasma were snap-frozen in dry ice and stored at -80°C for future measurements. Left, inferior, postcaval and middle and superior lung lobes were collected separately and snap-frozen in dry ice for DNAm and gene expression analyses.

3.4.7 DNA/RNA isolation from lungs and blood

DNA and RNA were extracted from mouse tissues using the Invitrogen DNA and RNA isolation kits respectively. Left lungs were homogenized using the Qiagen Tissue Lyser II, followed by simultaneous DNA and RNA isolation using same Invitrogen DNA and RNA isolation kits. DNA and RNA were quantified using a NanoDrop spectrophotometer (NanoDrop Technologies, USA).

3.4.8 Selection of mouse candidate genes to measure DNAm

To obtain candidate genes at which to measure DNAm, we selected 2 of the top differentially methylated CpGs from the meta-analysis conducted in human cohorts[270]. The 2 chosen human CpGs with some of the largest effect sizes were selected from genome build GRCh37/hg19: *AHRR* at position chr5:373378 (cg05575921) and *CYP1A1* at position chr15:75019251 (cg22549041). We then blasted the resulting human sequence against the *Mus musculus* genome assembly on NCBI. Using R studio version 3.6, we performed a muscle[352] alignment between human and resulting mouse sequences to detect mouse CpGs which exactly aligned with or were closest in position to the human CpGs. The 2 mouse CpGs were selected from genome build GRCm38/mm10 based on results of the alignment: position chr13:74260517 for *Ahrr* and position chr9:57696231 for *Cyp1a1.* Importantly, the *Ahrr* gene is not conserved between human and mice, and while we selected the closest mouse CpG, it may not be comparable to the human position. To select a CpG position for the mouse control gene, we selected a human CpG position which was not differentially methylated in newborn cord blood (human genome GRCh38/hg38, *PRKAA1* cg13345558, position chr5:40796738), as reported in the PACE study. We then identified a corresponding mouse CpG (genome build GRCm39/mm39 position chr15:5174566) as described above.

3.4.9 Measurement of candidate gene DNAm

500 ng of DNA isolated from the left lungs or right liver lobe was treated with sodium bisulfite (Zymo Research) to generate bisulfite-converted DNA (bcDNA), following the manufacturer's protocol. Following conversion, bcDNA was then amplified by PCR using the following conditions: 95°C for 15 min, followed by 45 cycles of 95°C for 30 secs, 58°C for 30 secs, 72°C for 30 secs, and then followed by 72°C for 5 min. Mouse *Ahrr* and *Cyp1a1* primers were generated using the PyroMark Assay Design software version 2.0 (Qiagen). Primer sequences can be found in Appendix 3.1 (All Supplemental material is available at https://doi.org/10.6084/m9.figshare.24002385.v2). DNAm at candidate genes was measured using the Qiagen Q48 pyrosequencer. Prior to DNAm measurement in samples, CpG assays were validated in duplicates using mixtures of completely methylated and completely unmethylated control DNA (0%, 25%, 50%, 75%, and 100% methylated). After validation, sample DNAm was then measured using the optimized assay conditions.

3.4.10 Measurement of epigenome-wide DNAm

We measured epigenome-wide DNAm in mouse lungs using the Illumina Infinium Mouse Methylation BeadChip (Illumina, San Diego, CA, USA) following the manufacturer's protocol. 750 ng of genomic DNA was bisulfite converted as described earlier, followed by amplification, fragmentation and hybridization onto the array chips. Chips were stained, washed and scanned on the Illumina iScan. Samples were randomized prior to hybridization to the beadchip, using Omixer[443]. After scanning, IDAT files were exported and read into R and preprocessed using the SeSAMe package[355]. Detection p-values were calculated for each probe using pOOBAH[355], followed by background subtraction using noob[356], dye bias

correction using the dyeBiasCorrTypeINorm function in the SeSAMe package and masking and removal of probes with detection $p > 0.05$, leaving a total of 217,907 of 296,070 probes. Next, 8,269 probes mapping to sex chromosomes and those with detection $p > 0.05$ were masked and removed, leaving a total of 209,638 probes for analyses. We corrected for chip, row and column batch effects on β values using ComBat[357], included in the SVA package[358], which uses an empirical Bayes method for batch correction and is robust for use on small sample sizes[444]. Signal intensities were quantified as β-values and used for downstream analyses. Probes mapping to *Ahrr* and *Cyp1a1* were identified using the Illumina default manifest.

3.4.11 Gene expression measurement

200ng of lung or liver mRNA was treated with ezDNase (Thermo Fisher Scientific, Inc.) and then converted to cDNA using Maxima cDNA synthesis Kit (Thermo Fisher Scientific, Inc.) according to the manufacturer's protocol. Quantitative real-time RT-PCR (qPCR) was performed on the QuantStudio 3 Real-Time PCR System (Thermo Fisher Scientific, Waltham, MA), using the SYBR-Green Master Mix (Applied Biosystems; Thermo Fisher Scientific, Inc.) to determine the relative expression levels of *Ahrr* and *Cyp1a1*. *β-actin* and *Eif2a* were used as reference and normalization controls. Samples were run in duplicates under the following cycling conditions: Holding stage, 1 cycle of 50°C for 2 min and 95°C for 2 min; cycling stage, 40 cycles of 95°C for 15 sec, 57°C for 15 sec and 72°C for 1 min; and melt curve stage, 95°C for 15 sec, 60°C for 1 min and 95°C for 15. The primer sequences used can be found in Appendix 3.2. *Ahrr* and *Cyp1a1* mRNA levels were quantified using the $\Delta\Delta^{Cq}$ method[353,354] and normalized against mean *β-actin* and *Eif2a* levels in the same sample.

3.4.12 Measurement of the effects of cross-fostering

Since we cross-fostered offspring at birth to create our model for early life CS exposure, we needed to rule out any potential effects of the cross-fostering process on offspring. 4 female and 2 male Balb/C mice were purchased at 6 weeks of age, separate from the mice used for the major experiment. They were left to acclimate for 2 weeks, fed and housed as described above. At 8 weeks of age, mice were placed together (2 females to 1 male) and mated for 3 days. At birth, we culled offspring to 6 offspring per litter, and cross-fostered half of resulting offspring, matching offspring by birth date to reduce potential of rejection. Pups were marked with a toe tattoo to identify birth group. Cross-fostering led to the generation of 2 groups of offspring: non cross-fostered and cross-fostered groups. We performed lung lavage, sacrificed and collected tissues from all offspring at 8 weeks of age.

3.4.13 Transthoracic echocardiography

As described previously[445], serial echocardiography was performed using a Vevo 2100 ultrasound (Fujifilm-Visual Sonics, ON Canada) equipped with a 30 MHz transducer to assess cardiac morphology and function in 12-14 week-old mice. Imaging by a blinded and experienced sonographer was performed under mild anesthesia (induced with 3% isoflurane and 1.0L/min oxygen and maintained at 1 – 1.5% isoflurane and 1.0 L/min oxygen) during echocardiography. Pulse Wave Doppler Mode was used to measure the velocity time integral of blood flow passing through the right ventricular outflow tract (RVOT). Vevo software was used to determine pulmonary acceleration times (PAT), pulmonary ejection times (PET), and ventricle thickness from the RVOT for each subject. Measurements of PAT and PET were taken from three different doppler waves for each subject and ventricle thickness was

measured from three image stills. The average of these three measurements was then recorded.

3.4.14 Statistical analyses

Statistical analysis was done using R (version 3.6.1). All statistical analyses were conducted blinded. Percent DNAm at each CpG was averaged across duplicates and between-group differences were analyzed using a one-way ANOVA. Lung function and differential cell count data were analyzed using two-way ANOVA, and multiple comparison was performed between groups at each methacholine dose. *P* values < 0.05 were considered significant. Adjustment for litter size effects was conducted on significant values using simple linear regression.

Data for sites in *Ahrr* and *Cyp1a1* isolated from microarray data was analyzed using ANOVA, followed by post-hoc t-tests on β values to determine significance. We considered sites to be significant if they had a *p* value < 0.05. Figures were produced in R, using the *ggplot2* and *Gviz* packages.

3.5 Results

3.5.1 Development of a protocol to study the effects of early life CS exposures

We created a mouse model to study the effects of early life CS exposure on offspring, and specifically, to isolate prenatal and postnatal CS exposures. Exposure of Balb/C dams to whole-body CS was carried out for 9 weeks, beginning 3 weeks before mating and pregnancy, and lasting until 3 weeks after birth (Figure 3.1A). To isolate the effects of prenatal and postnatal-only smoke exposures, we cross-fostered half of the offspring born to control and smoke-exposed dams at birth, with toe tattoos to identify cross fostered offspring

(Figure 3.1A). All cross-fostering was carried out no more than 24 hours after birth of matched control and CS-exposed litters. Only one litter, including both cross fostered and not cross fostered offspring, was lost. All smoke-exposed dams tolerated smoke exposures well, and our exposure paradigm did not result in loss of any dams. Since mating resulted in variable plug/conception dates, we ensured that all analyses reported here were carried out on offspring born no more than 48 hours apart.

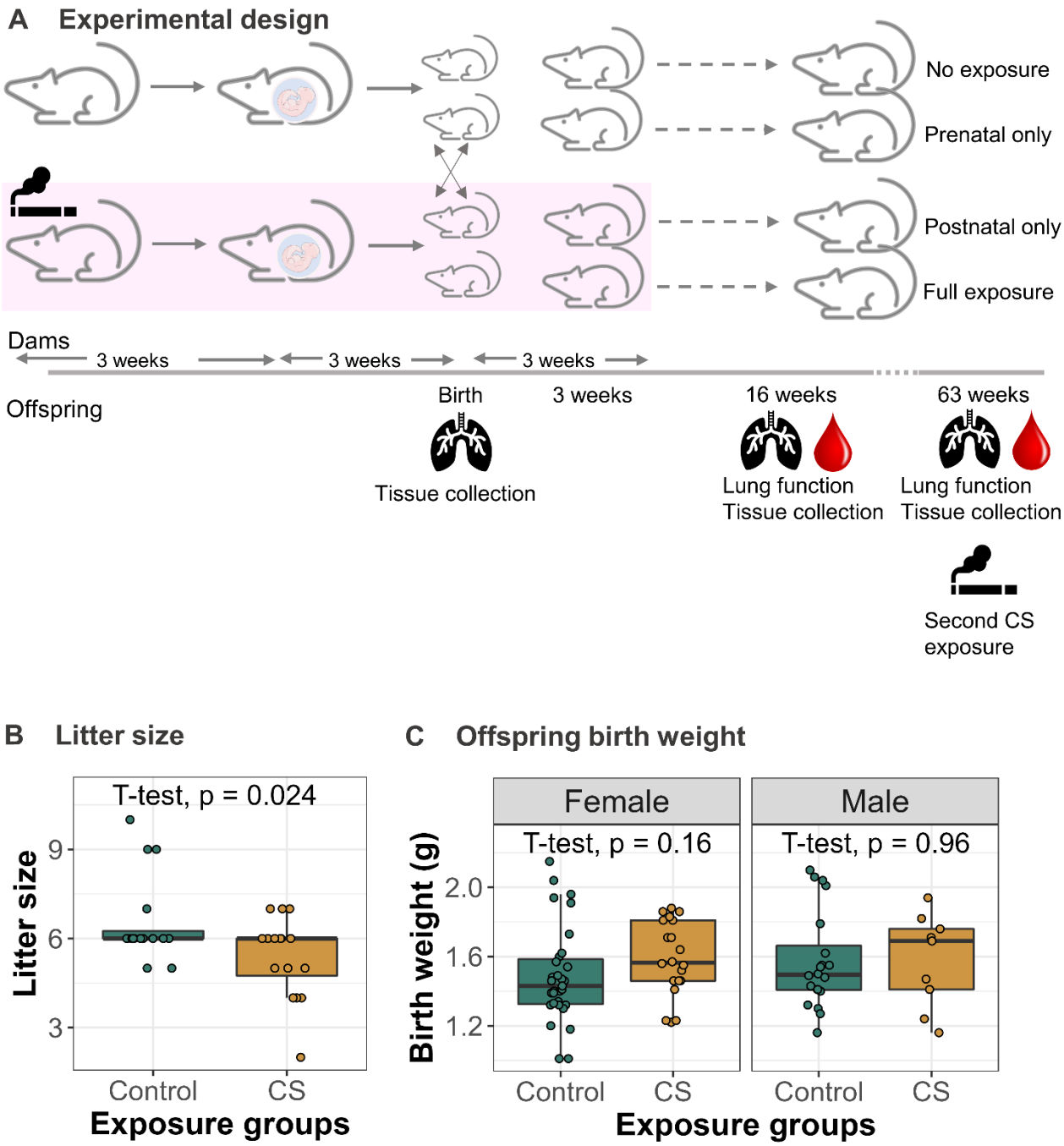

Figure 3. 1: Development of a mouse model to study the effects of early life CS exposure.

(A) Experimental design: Adult female mice were exposed to CS for 9 weeks, starting 3 weeks prior to mating and ending 3 weeks after birth. Half of control offspring were cross-fostered at birth with half of the CS-exposed offspring to generate 4 groups of offspring: control (N = 43), prenatal CS-exposed (N = 42), postnatal CS-exposed (N = 42) and combined prenatal and postnatal CS-exposed (N = 36) groups. Lungs, blood and other tissues were collected from dams (N = 16 control, N = 16 CS) and offspring at birth (N = 19 control, N = 13 CS-exposed) and at 16 weeks of age (N = 136), after lung function measurement. At age 60 weeks, half of the remaining female offspring were re-exposed (N =

13) to CS for 3 weeks, followed by lung function and tissue collection. The remaining half (N = 14) were not re-exposed to CS and served as adult controls (B) Litter size of control and smoke-exposed dams. Student t-test was used to measure differences in litter size between control and smoke-exposed dams. (C) Weight of control and CS-exposed male (N = 23 control, N = 16 CS) and female (N = 44 control, N = 30 CS) offspring at birth. Differences in birth weight were analyzed using student t-tests within sexes.

Maternal smoking can reduce litter size[446,447] and pup birth weight in mice, which might have indirect effects on pup development[447,448]. To ensure that our DNAm and phenotypic analyses are not confounded by such effects, we tested the effects of our smoking model on offspring birth weight and litter size. We found a slightly larger litter size in control dams (Mean = 6.56, SD = 1.46) than smoke-exposed ones (Mean = 5.38, SD = 1.36) (Figure 3.1B, T-test p = 0.024). Birthweight in male and female animals was slightly but not significantly larger in CS than control pups, perhaps due to the smaller litter size (Figure 3.1C). We performed sensitivity tests in downstream analyses to identify the potential effects of litter size.

3.5.2 Offspring lung phenotype at 16 weeks of age, 13 weeks after cessation of smoke exposure

At 16 weeks of age, in the absence of a methacholine challenge, male offspring with prenatal CS exposure had increased tissue elastance (Figure 3.2D, p = 0.029) and female offspring with prenatal CS exposure had increased airway resistance (Figure 3.2B, p = 0.018), compared to control offspring. When methacholine was introduced, male offspring in the postnatal CS group showed significant decrease in responsiveness for total lung resistance, airway resistance and tissue elastance (Figures 3.2E, 3.2F and 3.2H), while fully exposed male offspring showed increased methacholine sensitivity for total lung resistance (Figure 3.2E). Similarly, prenatal only and full CS exposures induced decreased methacholine responsiveness for airway resistance in female offspring (Figure 3.2F). While these data show increased responsiveness to specific methacholine doses in CS-exposed offspring, dose response slope analysis showed that overall, there were no significant differences in offspring sensitivity to methacholine (Appendix 3.3). In association with the

altered lung resistance and tissue elastance, right ventricle wall thickness was increased in male and female offspring with full CS exposure (Appendix 3.4). However, female right ventricular function and hemodynamic parameters were more sensitive to the effects of CS than males (Appendix 3.5).

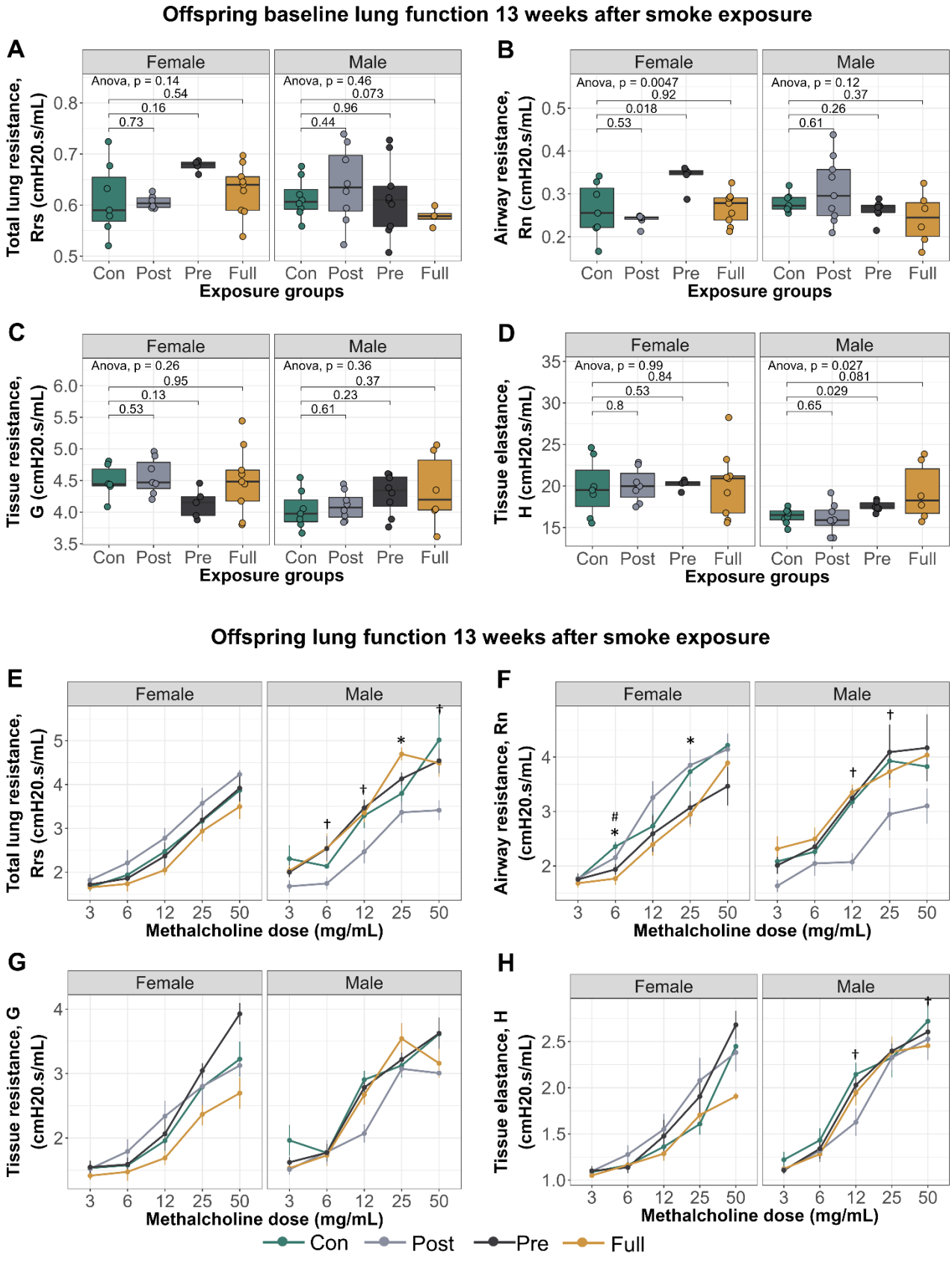
Offspring baseline lung function 13 weeks after smoke exposure
A
Female
Male
Anova, p = 0.14
0.54
0.16
0.73
Anova, p = 0.46
0.073
0.96
0.44
Total lung resistance, Rrs (cmH20.s/mL)
0.8
0.7
0.6
0.5
Con Post Pre Full
Exposure groups
B
Female
Male
Anova, p = 0.0047
0.92
0.018
0.53
Anova, p = 0.12
0.37
0.26
0.61
Airway resistance, Rn (cmH20.s/mL)
0.5
0.4
0.3
0.2
Con Post Pre Full
Exposure groups
C
Female
Male
Anova, p = 0.26
0.95
0.13
0.53
Anova, p = 0.36
0.37
0.23
0.61
Tissue resistance, G (cmH20.s/mL)
6.0
5.5
5.0
4.5
4.0
3.5
Con Post Pre Full
Exposure groups
D
Female
Male
Anova, p = 0.99
0.84
0.53
0.8
Anova, p = 0.027
0.081
0.029
0.65
Tissue elastance, H (cmH20.s/mL)
35
30
25
20
15
Con Post Pre Full
Exposure groups
Offspring lung function 13 weeks after smoke exposure
E
Female
Male
Total lung resistance, Rrs (cmH20.s/mL)
5
4
3
2
3 6 12 25 50
Methalcholine dose (mg/mL)
F
Female
Male
Airway resistance, Rn (cmH20.s/mL)
4
3
2
3 6 12 25 50
Methalcholine dose (mg/mL)
G
Female
Male
Tissue resistance, G (cmH20.s/mL)
4
3
2
3 6 12 25 50
Methalcholine dose (mg/mL)
H
Female
Male
Tissue elastance, H (cmH20.s/mL)
2.5
2.0
1.5
1.0
3 6 12 25 50
Methalcholine dose (mg/mL)
Con
Post
Pre
Full

Figure 3. 2: Early life exposure to CS alters sensitivity to methacholine up to 13 weeks after cessation of smoke exposure.
Lung function parameters (A) Total lung resistance at baseline. (B) Airway resistance at baseline. Female offspring exposed to prenatal CS had significantly higher Rn (Mean = 0.34, SD = 0.03) compared to female controls (Mean = 0.26, SD = 0.06). (C) Tissue resistance at baseline. (D) Alveolar elastance at baseline. Male offspring exposed to prenatal CS had significantly higher H (Mean = 17.50, SD = 0.63) compared to male controls (Mean = 16.40, SD = 0.91). (E) Total lung resistance with methacholine. (F) Airway resistance with methacholine. (G) Tissue resistance with methacholine. (H) Alveolar elastance with methacholine. Lung function with methacholine (*E*–*H*): **P* < 0.05, control vs. full CS; †*P* < 0.05 control vs postnatal CS; #*P* < 0.05 control vs prenatal CS groups. Group numbers: Control females = 6, Postnatal females = 7, Prenatal females = 5, Full females = 9, Control males = 7, Postnatal males = 8, Prenatal males = 9, Full males = 6. Lung function was assessed by taking 90^{th} percentile values in response to injection of saline into the lungs (baseline) and in response to increasing doses of methacholine. Lung function data was analyzed in a sex-disaggregated manner using a two-way ANOVA, followed by multiple comparisons between groups at each methacholine dose where significant.

When examining immune cell infiltration in the lung, female offspring exposed to postnatal only CS had significantly elevated eosinophils (Mean = 1691, SD = 1647) compared to control females (Mean = 475, SD = 800) (Figure 3.3B, $p = 0.0046$), while male offspring with full CS exposure had significantly elevated lymphocytes (Mean = 3479, SD = 3064) compared to control males (Mean = 601, SD = 659) (Figure 3.3D, $p = 0.029$).

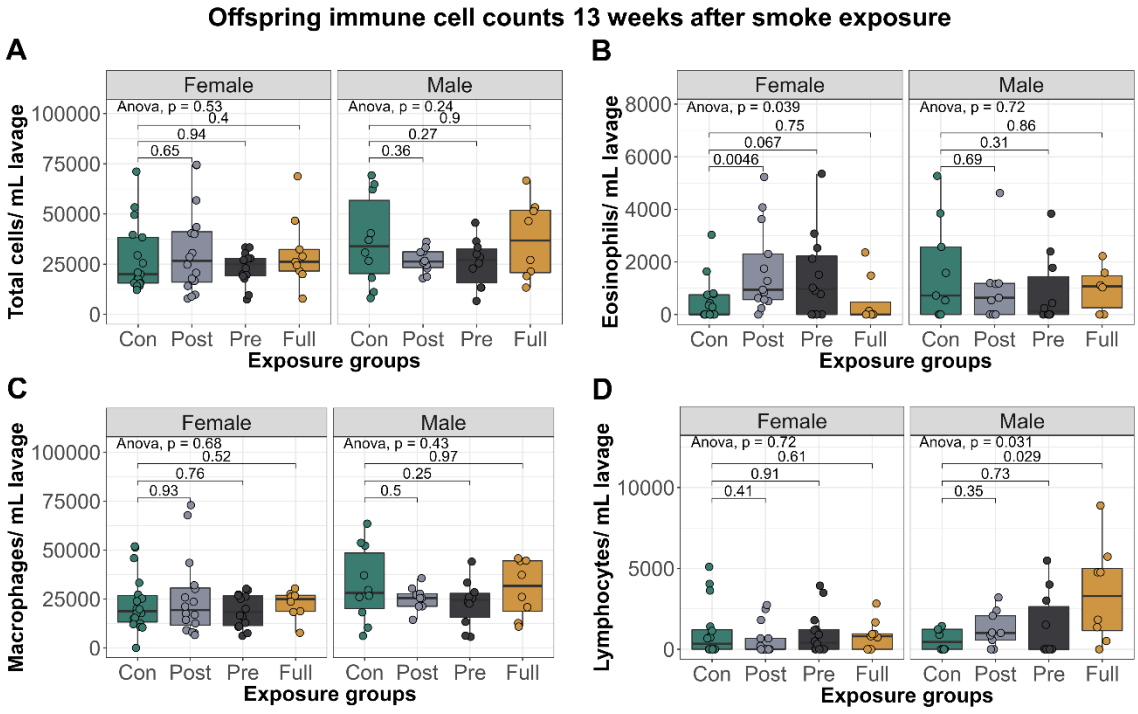

Figure 3. 3: **Early life exposure to CS increases immune cell infiltration into offspring lungs, up to 13 weeks after smoke exposure.**
(A) Total immune cells per mL lavage. (B) Eosinophils per mL lavage. (C) Macrophages per mL lavage. (D) Lymphocytes per mL lavage. Group numbers: Control females = 17, Postnatal females = 14, Prenatal females = 13, Full females = 8, Control males = 10, Postnatal males = 10, Prenatal males = 10, Full males = 7. Differential cell counts were normalized to lavage volume. Pairwise comparisons were conducted using t-tests.

Together, our data suggested a mild lung phenotype induced by early life smoke exposure in indirectly exposed offspring that persists to 16 weeks of age, as observed by persistent decline in lung function and increased infiltration of immune cells into the lungs.

3.5.3 DNAm and gene expression at birth and 16 weeks of age in candidate genes

Results from human studies have shown that maternal smoking causes decreased and increased DNAm of *AHRR* and *CYP1A1* respectively, in newborn umbilical cord blood[269–271,273,439], and that these differential methylation patterns persist in adult blood at midlife[272,278]. The effects of smoking on the human respiratory system is less well documented, as only one study to our knowledge has reported increased *AHRR* and *CYP1A1* DNAm in nasal epithelia of adult smokers[438]. Therefore, as DNAm is species and tissue-specific, and studies investigating effects of prenatal CS exposure on the lungs is lacking, we measured *Ahrr* and *Cyp1a1* DNAm and gene expression in the lungs and blood of offspring at birth immediately after CS exposure and at 16 weeks of age (13 weeks after cessation of smoke exposure).

At birth, *Ahrr* and *Cyp1a1* DNAm in the lung and blood were not significantly different between control and smoke-exposed offspring (Figure 3.4A and 3.4C). However, both male and female offspring born to CS-exposed dams showed lung *Cyp1a1* expression levels which were over 20 times higher than controls (Figure 3.4B).

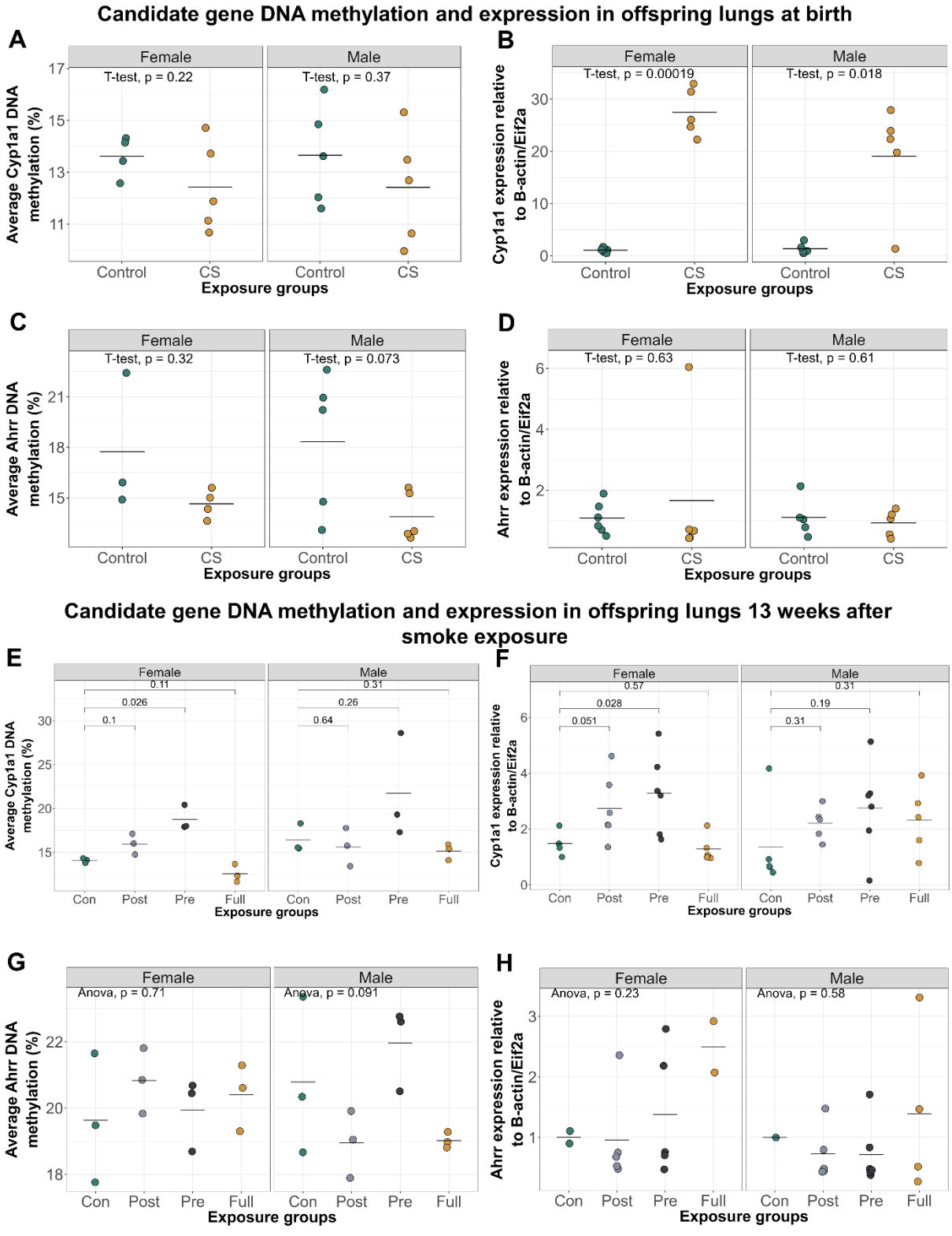

Figure 3. 4: Early life exposure to CS significantly alters lung *Cyp1a1* expression at birth and *Cyp1a1* DNAm 13 weeks after smoke cessation.

(A) *Cyp1a1* DNAm in offspring lungs at birth (N = 10 control, N = 10 CS). (B) *Cyp1a1* expression in offspring lungs at birth was significantly increased in CS-exposed males (N = 5,

Mean = 19.00, SD = 10.30) and females (N = 5, Mean = 27.50, SD = 4.54) offspring, compared to control males (N = 5, Mean = 1.36, SD = 0.93) and control females (N = 5, Mean = 1.47, SD = 0.43). (C) *Ahrr* DNAm in offspring lungs at birth (N = 8 control, N = 10 CS). (D) *Ahrr* expression in offspring lungs at birth (N = 10 control, N = 10 CS). (E) *Cyp1a1* DNAm in offspring lungs at 16 weeks of age. Prenatal and postnatal CS exposure caused an increase in female lung *Cyp1a1* DNAm, while fully exposed offspring showed a decrease. Only prenatally exposed female offspring had significantly elevated *Cyp1a1* DNAm (Mean = 18.80, SD = 1.42) compared to control females (Mean = 14.10, SD = 0.26). N = 3 per group (F) *Cyp1a1* expression in offspring lungs at 16 weeks of age. Prenatally exposed female offspring had significantly elevated lung *Cyp1a1* expression levels (Mean = 3.28, SD = 1.44) compared to control females (Mean = 1.48, SD = 0.47). N = 3-6 per group (G) *Ahrr* DNAm in offspring lungs at 16 weeks of age. N = 3 per group (H) *Ahrr* expression in offspring lungs at 16 weeks of age. N = 3-6 per group One-way ANOVA was used to compare DNAm values between groups ($p<0.05$ was significant), followed by two-group comparisons where significant.

We next measured *Ahrr* and *Cyp1a1* DNAm levels in lungs and blood of offspring at 16 weeks of age to determine longitudinal effects of early life smoke exposure on offspring (Figure 3.4E – 3.4H). There were no significant differences in *Ahrr* DNAm between control and CS-exposed groups in offspring blood 13 weeks after cessation of smoke exposure (Appendix 3.6). In the lung in male offspring only, *Ahrr* DNAm in prenatally exposed offspring was significantly higher than offspring exposed only postnatally (Figure 3.4G, $p = 0.03221$), but none of the CS-exposed offspring showed significantly altered *Ahrr* DNAm compared to control offspring. In female offspring at 16 weeks, those exposed to prenatal or postnatal CS had higher *Cyp1a1* DNAm in the lung compared to controls (Figure 3.4E), while offspring with full CS exposure showed significantly decreased *Cyp1a1* methylation compared to either postnatal (Figure 3.4E, $p = 0.02$) or prenatal groups (Figure 3.4E, $p = 0.0049$). These differences remained significant even after adjusting for possible effects of litter size on DNAm ($p = 0.01$).

We observed the same trend when we measured offspring lung *Cyp1a1* expression: increased expression levels of *Cyp1a1* in the postnatal only and prenatal only CS groups but decreased expression in the lungs of offspring exposed to both prenatal and postnatal CS, compared to controls, though these differences were not statistically significant (Figure 3.4F).

To show that the differences in candidate gene DNAm observed in offspring was not because of changes in global DNAm, we measured DNAm at a control gene, *Prkaa1*, which has not been associated with smoking. As expected, *Prkaa1* methylation in lungs of offspring exposed to both prenatal and postnatal CS was not significantly different from *Prkaa1* methylation in control offspring (Appendix 3.7). To rule out the potential effects of cross-fostering on DNAm, we cross fostered litters without any exposures and measured *Cyp1a1*

DNAm in lungs. We found no differences in *Cyp1a1* DNAm between cross-fostered and non-cross fostered offspring (Appendix 3.8).

This data suggested that early-life exposure to CS creates mild but long-lasting lung DNAm and gene expression changes at one of our two candidate genes.

3.5.4 Acute re-exposure to CS at 60 weeks alters lung function and re-establishes DNAm patterns

There has been some evidence in humans that maternal smoking in pregnancy induces persistent DNAm changes until midlife, regardless of smoking habits later in life[272,278]. We thus sought to test what effects re-exposure to CS in adulthood would have on the lung phenotype and DNAm patterns set by early life CS exposure. To achieve this, at 60 weeks of age, we re-exposed half of the offspring remaining to CS for 3 weeks, followed by lung function, differential immune cell analyses and DNAm measurement. At the time of re-exposure, we had a limited number of male offspring remaining, and so the following experiments were conducted solely on female offspring. We also had a low number of animals in the exclusively postnatal CS group, so they contribute to the baseline data only at 60 weeks of age.

Offspring that received full CS exposure in early life, followed by re-exposure to CS at 60 weeks, had significantly increased tissue resistance (Figure 3.5C) and total lung resistance (Figure 3.5A) levels at baseline, while re-exposed prenatal CS offspring had increased tissue resistance compared to offspring who had no early life CS exposure (controls), but were exposed to CS at 60 weeks (Figure 3.5). Immune cell infiltration specifically by macrophages was increased only in animals with full early life CS exposure

who were also re-exposed later in life, but this increase was not statistically significant (p = 0.1223) (Figure 3.5E - 3.5H).

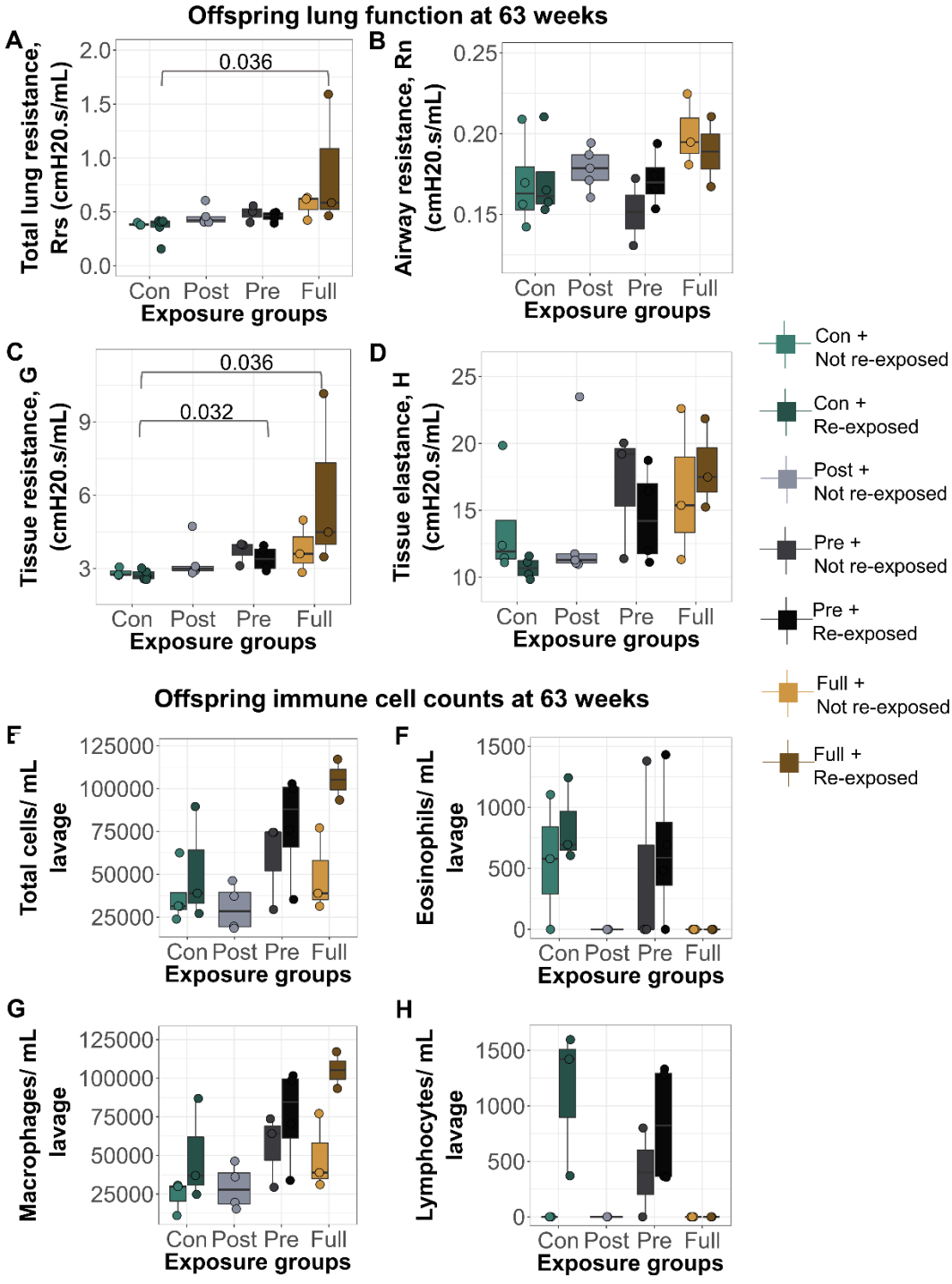

Figure 3. 5: Acute re-exposure to CS at 60 weeks induced significant alterations in baseline lung function compared to early life control offspring which were exposed to CS in adulthood.

Lung function parameters at baseline (A) total lung resistance. Offspring with full early life CS exposure and re-exposed to CS at 63 weeks (N = 3) had higher Rrs (Mean = 0.88, SD = 0.62) compared to early life control offspring exposed to CS at 63 weeks only (N = 4, Mean = 0.35, SD = 0.11). (B) airway resistance. (C) tissue resistance. Offspring with full early life CS exposure and re-exposed to CS at 63 weeks (N = 3) had higher G (Mean = 6.04, SD = 3.60) compared to early life control offspring exposed to CS at 63 weeks only (N = 4, Mean = 2.74,

SD = 0.20). Offspring exposed to prenatal CS early in life and re-exposed to CS at 63 weeks (N = 3) had higher G (Mean = 3.40, SD = 0.51) compared to early life control offspring exposed to CS at 63 weeks only. (D) alveolar elastance. (E) Total immune cells per mL lavage. (F) Eosinophils per mL lavage. (G) Macrophages per mL lavage. (H) Lymphocytes per mL lavage. For lung function, 90^{th} percentile values were calculated in response to saline administered into the lungs. Differential cell counts were normalized to lavage volume.

DNAm and gene expression at *Cyp1a1* showed a similar pattern, they were altered only in offspring with full CS exposure in early life who were also re-exposed to CS (Figure 3.6A, $p = 0.036$). This decrease in DNAm was not significant after adjusting for possible effects of litter size on DNAm using linear regression ($p = 0.13$), but it is unlikely that litter size continues to influence DNAm at 60 weeks of age. Interestingly, the *Cyp1a1* DNAm patterns established upon re-exposure to CS in adulthood were similar to those observed at 16 weeks.

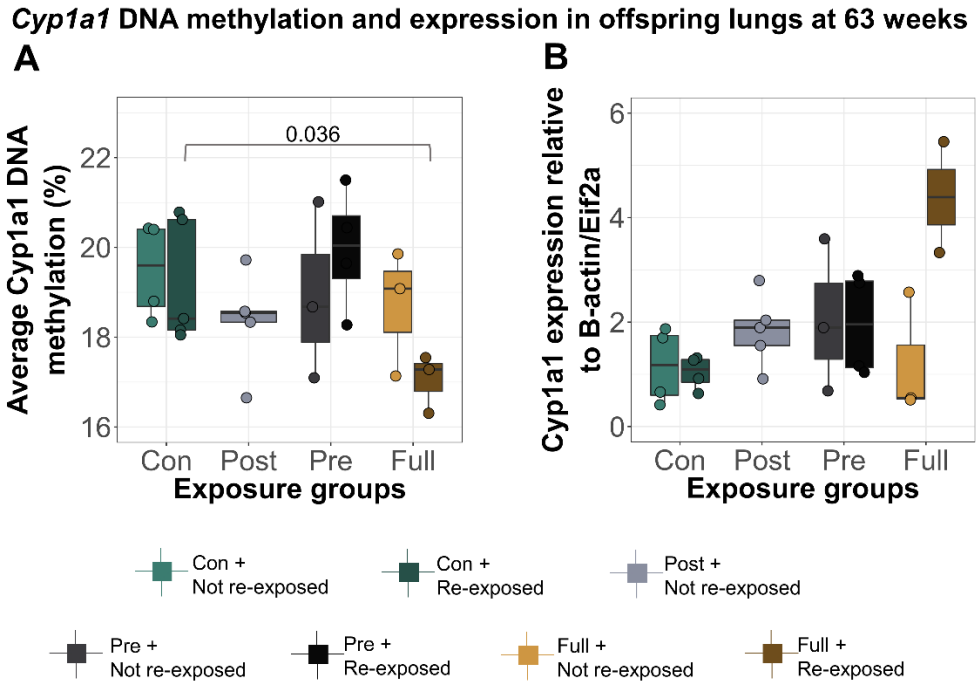

Figure 3. 6: Re-exposure of offspring to CS at 60 weeks induced changes in lung DNAm which were similar to those observed at 16 weeks.
(A) *Cyp1a1* DNAm in offspring lungs at 63 weeks. Offspring with full early life CS exposure and re-exposed to CS at 63 weeks (N = 3) had higher lung *Cyp1a1* DNAm (Mean = 17.00, SD = 0.65) compared to early life control offspring exposed to CS at 63 weeks only (N = 5, Mean = 19.20, SD = 1.37). (B) *Cyp1a1* expression in offspring lungs at 63 weeks (N = 27). Differences in DNAm and expression were calculated using a one-way ANOVA, followed by two-group comparisons.

Taken together, this data demonstrates that early life exposure to CS induces transient changes in lung phenotype and *Cyp1a1* DNAm, which become re-established upon personal smoking in adulthood.

3.5.5 Effects of early and later life CS exposures on offspring DNAm at *Ahrr* and *Cyp1a1* sites on the Illumina mouse microarray

Following our findings from our *Ahrr* and *Cyp1a1* candidate positions (74260517 and 57696231 respectively), we measured DNAm across the entire mouse epigenome using the newly released Illumina mouse microarrays. We isolated probes mapping to *Ahrr* and *Cyp1a1* to get a clearer understanding on how CS exposure in early life followed by late adulthood affects the genes as a whole. Of the 10 *Cyp1a1* sites on the mouse microarray, 9 of them passed quality control and preprocessing (Appendices 3.9 and 3.10). Chromatin states and genomic locations of these CpGs are shown in Figure 3.7I, in relation to the location of our candidate CpG. Our candidate CpG (highlighted in red) is located in a bivalent promoter region, with the closest site from the arrays to it (site C in Figure 3.7I) being 102bp away.

In site C, fully exposed female offspring had decreased *Cyp1a1* DNAm compared to controls at 16 weeks (Appendix 3.9C, $p = 0.07$), though this decrease was not significant at our p value cutoff of $p < 0.05$. Similar to what we observe with our candidate CpG, the decrease in DNAm in the fully exposed groups at 16 weeks normalizes to the same level as other groups by 63 weeks, but returns to earlier patterns though lower magnitude upon re-exposure to CS at 63 week (Appendix 3.9C). We observed a different pattern in male offspring, as based on effect size, CS exposure caused the most decrease in DNAm in the postnatal group (effect size = 0.055), followed by prenatal (effect size = 0.030), with the fully exposed group being the most similar to controls (Appendix 3.10C).

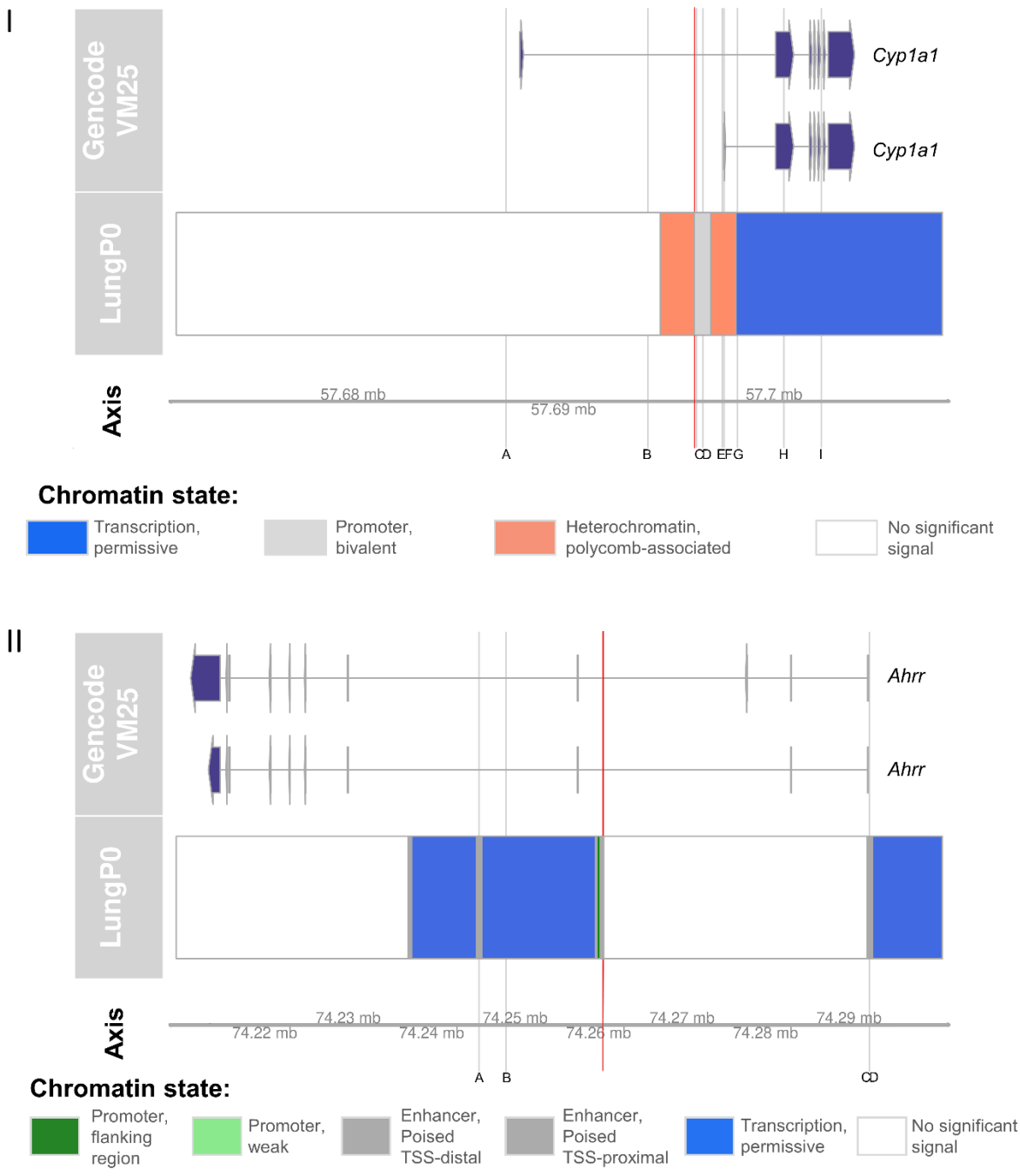

Figure 3. 7: **Chromatin state and genomic locations of 9 *Cyp1a1* and 4 *Ahrr* positions on the Illumina mouse methylation microarray.**
(I) *Cyp1a1* sites from the Illumina mouse array are highlighted in grey and labelled A-I, while the chosen candidate *Cyp1a1* position (not contained in the mouse array) is highlighted in red. The genomic locations of the 9 *Cyp1a1* array sites are as follows: A at position 57687270, B at position 57694012, C at position 57696335, D at position 57696629, E at position 57697560, F at position 57697641, G at position 57698266, H at position 57700489 and I at position 57702263. The genomic location of the candidate CpG is at position 57696231. (II) *Ahrr* sites from the Illumina mouse array are highlighted in grey and labelled A-D, while the chosen candidate *Ahrr* position (not contained in the mouse array) is highlighted

in red. The genomic locations of the 4 *Ahrr* array sites are as follows: A at position 74245665, B at position 74248917, C at position 74292502 and D at position 74292541. The genomic location of the candidate CpG is at position 74260517. Information on genomic locations and chromatin state was obtained from UCSC genome browser (mouse genome assembly GRCm38/mm10). Chromatin state displayed here is of mouse lungs at postnatal day 0, as this is the latest and most relevant period currently available.

Of the 8 *Ahrr* sites on the mouse microarray, 4 of them passed quality control and preprocessing (Appendices 3.11 and 3.12). Chromatin states and genomic locations of these CpGs are shown in Figure 3.7II, in relation to the location of our candidate CpG. Our candidate CpG (highlighted in red) is located in a poised enhancer region, while the 4 *Ahrr* sites on the mouse microarray are located >10,000 bp on either side. In positions A and D of Figure 3.7II, female offspring exposed to prenatal CS had significantly higher DNAm levels compared to control offspring (Appendix 3.11A and 3.11D, $p = 0.04$). In males however, prenatally exposed offspring were not significantly different from controls at this position, but offspring in the full and postnatal groups had significantly higher (Appendix 3.12A, $p = 0.04$) and lower (Appendix 3.12D, $p = 0.005$) *Ahrr* DNAm levels compared to controls, in same positions A and D.

3.5.6 Measurement of candidate *Cyp1a1* DNAm and expression in offspring livers

Finally, we examined DNAm and expression of our candidate *Cyp1a1* CpG (position 57696231) in the livers of mice in this experiment, to determine whether priming also occurs in the tissue with highest *Cyp1a1* gene expression and activity (Appendix 3.13). At birth, *Cyp1a1* DNAm and expression in the liver were not significantly altered by prenatal CS exposure, and this trend remained non-significant till 63 weeks of age, even upon re-exposure to CS. This is important, as it shows that the priming phenotype developed due to early life CS exposure is not universal across tissues.

3.6 Discussion

The global burden of smoking still remains significant, despite numerous campaigns against its use, and exposure to cigarette smoke in pregnancy predisposes offspring to

harmful health outcomes[449–451]. CS components have been known to pass through the placenta to the developing fetus, but it is not yet clear what specific mechanisms link CS exposure to offspring health[274,452–454]. Past studies have shown that prenatal exposure to CS induces differential DNAm in newborn umbilical cord blood, placenta, buccal and nasal epithelia, and adult peripheral blood granulocytes[245,270,273,438,453]. However, previous studies in humans have not been able to isolate the influence of postnatal exposure to smoke, as prenatal and postnatal exposures tend to be highly correlated in humans. In addition, while the effects of maternal smoking on peripheral tissues are well documented, less is known about the effects on the lungs, despite significant epidemiological evidence linking maternal smoking to long term lung health, including asthma and COPD[317,455–458]. Since we know that each tissue has a unique epigenetic signature[234,459–466], it is essential to measure the effects of early life smoke exposure in the lungs. Therefore, we created a mouse model to study the independent effects of prenatal and postnatal CS exposure that would also allow us to measure lung phenotype and DNAm in the lung. We used cross-fostering to isolate prenatal and postnatal exposures rather than altering exposure to CS in the dams to avoid the effects of nicotine withdrawal on the dams and pups[467–470]. Here, we showed that exposure to CS early in life alters offspring lung function, DNAm and gene expression profiles, priming the lungs such that secondary smoke exposure in adulthood re-establishes some of these outcomes. Appendix 3.14 depicts summaries of our findings.

Cigarette smoking has been shown to decrease offspring lung function[435,457,471–473], but many studies identified female lungs as less sensitive to the effects of environmental toxins such as from CS[306,307,312,474] due to earlier development of protective factors like surfactants in female lungs compared to males[313,475,476]. Our results largely agree with these past studies, as most of the differences in lung function we observed after methacholine exposure

were in males exposed to postnatal or full CS. Only prenatally or fully exposed females showed altered airway resistance upon sensitization with methacholine. In line with past human and animal studies also[312,319,457], the observed lung function defects in female offspring persisted until 16 weeks of age. For example, maternal smoking has been shown to decrease offspring lung function till 12[319] and 21 years of age[317]. It is worth noting that while offspring showed increased *responsiveness* to different doses of methacholine at 16 weeks, overall dose response analysis showed no significant differences in methacholine *sensitivity* between groups. This implies that early life smoke exposure alone may not modulate airway reactivity but may require a secondary stimulant. To further support this finding is the fact that in female offspring, the alterations in methacholine responsiveness disappeared by 60 weeks of age but reappeared upon re-exposure to CS, suggesting that early-life CS exposure alone may not be enough to induce life-long lung function alterations but may prime the lungs so that upon re-exposure to CS, lung function is altered. This idea of priming has been well documented[307–309], but few studies have extended exposures as long as this. One study showed that early-life secondhand smoke exposure did not alter lung function until the administration of a postnatal allergen (*A. fumigatus* extract)[309]. Another study found that *in utero* exposure to second-hand smoke exacerbated allergic response and lung function deficits in offspring when exposed to ovalbumin at 23 weeks of age[306].

In addition to phenotype, it is important to investigate the effects of CS on lung DNAm to gain insights into the molecular mechanisms of disease development. Cytochrome P450 (Cyp) enzymes are hemoproteins which are involved in drug/xenobiotic metabolism in the liver[477]. Its major substrates are polyaromatic hydrocarbons and nitrosamines (major carcinogenic components of CS[478]), and activation by these ligands usually occurs via an aryl hydrocarbon receptor (Ahr)-dependent pathway[479,480]. There are many subclasses of Cyp

enzymes, but CYP1A1 is extensively studied as it is expressed at basal levels in extra-hepatic tissues[481] and is highly inducible, leading to the speculation that it may be primarily responsible for xenobiotic metabolism in extra-hepatic tissues[482]. When activated by Ahr, CYP1A1 directly hydroxylates or oxidizes its bound ligand and detoxifies it[409,410,483]. CS is a potent inducer of the Ahr-Cyp pathway in humans and murine models[484–486], so it follows that measuring the effects of CS on DNAm in these genes would be informative on CS-induced phenotypes.

While many studies have shown that prenatal CS exposure alters *Cyp1a1* DNAm, the effects of prenatal versus postnatal CS have not been studied separately, especially as they relate to the lungs. Using our unique model, we found unexpected patterns in the dynamics of *Cyp1a1* DNAm and expression over the life course in CS-exposed lungs. First, we noted that maternal smoking did not alter offspring *Ahrr* or *Cyp1a1* DNAm in the lung at birth at our chosen CpGs but causes a 20-fold increase in expression of just *Cyp1a1*. At 16 weeks, offspring exposed to only prenatal CS or only postnatal CS showed a slight increase in *Cyp1a1* DNAm (and expression), while those exposed to both prenatal and postnatal CS showed decreased *Cyp1a1* DNAm and expression in their left lungs compared to control offspring. We tested the effects of cross-fostering independently and saw no difference in *Cyp1a1* DNAm, which implies these differences are not an effect of cross-fostering itself. These opposing results could possibly be explained by the *developmental mismatch hypothesis*, which surmises that traits that develop in an organism in one environment may be disadvantageous in a different environment[295–297]. In other words, the mismatch between prenatal and postnatal environments in the cross-fostered offspring would confer different characteristics from offspring with matched prenatal and postnatal environments. The fact that the *Cyp1a1* DNAm in the prenatal CS only group and postnatal CS only group changes

in the same direction emphasizes the need for future animal models to isolate and study them separately, as it is evident that they produce different effects from combined pre- and post-natal exposure, and can be difficult to differentiate in more long-term studies. The increase in *Cyp1a1* DNAm observed in the prenatal CS only group is in fact in line with many human studies which have measured prenatal CS-induced DNAm changes in newborn umbilical cord blood[270–273,275].

Finally, we observed that while early life CS-induced *Cyp1a1* DNAm changes do not persist to 60 weeks, acute exposure to CS in adulthood re-established DNAm patterns observed at 16 weeks and was associated with an immune cell infiltration phenotype that was dependent on both early life and later life CS exposure. The disappearance and re-establishment of the *Cyp1a1* DNAm patterns at 60 weeks proves that DNAm alone is unlikely to be the epigenetic mark responsible for long-term memory of early life CS at *Cyp1a1*. The next most likely candidate for a mechanism linking early life exposure with later life response is histone modifications. One study has in fact shown that early life smoke exposure in rats causes chromatin remodeling, marked by increased histone acetylation and altered transcription factor binding in the lungs[222]. The DNAm and lung phenotype changes observed at this timepoint are further evidence of priming. Some studies have suggested that disappearance of detrimental phenotypes over time is an adaptation mechanism in response to adversity[487,488], which allows affected individuals to function as close to optimal as possible. However, the underlying detrimental signatures are embedded until a secondary stimulant is introduced[487,488].

To determine whether our observed pattern was universal across tissues, we also measured DNAm at our candidate *Cyp1a1* position in offspring livers as primary site of *Cyp1a1* expression. It was interesting to find that none of the differences we observed in the

lungs were observed in the liver. This suggests that the priming effect due to early life CS we observe at 63 weeks following secondary CS exposure is lung-specific, or at least is not found in all tissues. This further emphasizes the need for future analyses of the effects of smoking to be conducted on the lungs.

While it appears that our candidate CpG is the most responsive to the effects of smoke exposure in female offspring, expanded analysis using the Illumina microarray identified a site at position 57696335 which exhibits similar patterns observed in the candidate position. That site also demonstrates the disappearance and reestablishment of differential DNAm associated with early life exposure, though it is less dramatic than the candidate CpG.

Taken together, our results represent a novel model for the DOHaD hypothesis, which surmises that the early life environment can shape offspring phenotype to produce long term consequences in an individual. While some hypotheses such as the thrifty phenotype[489] and adaptive response[490] have been used to explain the longevity of health conditions following early-life adversity, the underlying mechanisms are largely unknown[491]. Epigenetic mechanisms are suspected to play major roles in this phenomenon and there are many studies which have investigated the effects of early life environment on offspring DNAm. For example, early life smoke exposure and air pollution exposure in general has been shown to cause conditions like asthma and cancer in adulthood, and many studies have suggested DNAm as the underlying mechanism[270,281,492,493]. However, we have shown that in our model DNAm was not responsible for long-term CS-associated phenotype, and future work will investigate other epigenetic marks.

One limitation of this study is that we measured DNAm in whole mouse lungs and so, cannot say what specific lung cell type is responsible for the observed changes in DNAm. It is

unlikely that immune cell infiltration is the cause of the DNAm changes, as lungs were lavaged to remove most of the immune cells, and the relative number of immune cells residing in lung tissue is very small. A second limitation is that our model involves administration of heavy doses of CS and so we cannot extrapolate these results to analyze the effects of light or moderate smoking. Finally, we did not isolate the effects of periconceptional smoking on offspring, though there is evidence that environmental insults just prior to conception can impair offspring DNAm and physiological outcomes[494–497].

In conclusion, this study has created an effective model for DOHaD to investigate the effects of early life CS exposure, providing an essential foundation for future animal studies. Using this model, we have shown that the effects of early life smoke exposure are embedded into the offspring, producing phenotypes which are re-established by smoking in adulthood. Future studies are needed to investigate these effects across the mouse epigenome and measure the effects of early life CS on chromatin accessibility and specific histone marks or variants, to identify the specific mechanism responsible for the long-term memory due to early life CS exposure.

Chapter 4: Longitudinal effects of early life cigarette smoke exposure and impact of secondary smoking in adulthood on offspring lung DNA methylation

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AUTHOR CONTRIBUTIONS

M.J.J. conceived and designed research; C.D.O., O.S. and H.K. performed microarrays, C.D.O. performed all other experiments and analyzed data; M.J.J. and C.D.O. interpreted results of experiments; C.D.O. prepared figures; C.D.O. prepared manuscript; M.J.J. edited and revised manuscript, and all authors approved final version of manuscript.

4.1 Abstract

Exposure to cigarette smoke (CS) in early life can cause sex-specific alterations to offspring health by perturbing numerous biological processes, some of which last well into adulthood, years after the cessation of smoke exposure. Previous research suggests that subsequent exposure to CS in later life intensifies the lung function alterations induced by early life CS exposure, a phenomenon known as priming. However, molecular mechanisms underlying these sex-specific and lasting health outcomes following early life CS exposure are unknown. In addition, the evidence for priming in mammals following repeated CS exposure remains limited, particularly concerning the role of epigenetic mechanisms like DNA methylation (DNAm) in establishing priming. In this study, we investigated the longitudinal, sex and tissue-specific effects of early life CS exposure on offspring lung DNAm, and explore whether CS exposure in adulthood further alters DNAm patterns set by early life CS. We use an established mouse smoking model to measure the effects of CS exposure in the prenatal period only, in the early postnatal period, or throughout the prenatal and early postnatal periods combined, on offspring lung DNAm at multiple timepoints across the lifespan, measuring DNAm across >200,000 CpGs in the mouse epigenome. Next, we analyzed DNAm in the lungs of offspring of the same early life groups when re-exposed to CS later in life, to determine whether DNAm signatures are associated with priming. Our results reveal distinct and sex-specific DNAm patterns in the mouse lungs, with male offspring being more likely to demonstrate long-lasting DNAm alterations than females. Upon CS exposure in adulthood, our findings indicate substantially more differentially methylated sites in lungs of offspring who also had early life CS exposure, suggesting priming of DNAm patterns in mouse lungs following early life CS exposure. Furthermore, we identified distinct DNAm patterns in offspring exposed to different doses of early life CS and discovered novel DNAm

sites that could serve as biomarkers for prenatal CS exposure and smoking in late adulthood. This study establishes a framework for future research to investigate DNAm and other epigenetic mechanisms, as they offer valuable insights into the underlying mechanisms of health outcomes. It also highlights the need for sex-specific interventions against CS and underscores the importance of distinguishing between the timing and duration of early life exposures, especially in human studies where such differentiation can be challenging.

4.2 Introduction

Maternal smoking has remained a public health concern for decades, as it can have lasting effects on offspring health. A recent census conducted in 2018 reported that 1-7% of pregnant women worldwide smoked while pregnant[498]. Of these, 72.5% smoked daily, while 27.5% smoked occasionally[498]. These levels remain concerning, as *in utero* exposure to CS negatively affects almost all the body functions, leading to detrimental health outcomes such as neurodevelopmental deficits, low birth weight, cancers, and long-lasting lung function deficits like lower respiratory infections, asthma, wheeze and bronchitis[289,499–505]. In many cases, these impairments last well into adulthood, and are independent of the offspring's own smoking habits later in life[317,455,456,506]. This concept is supported by the Developmental Origins of Health and Disease hypothesis (DOHaD) which postulates that the origins of many non-communicable diseases stem from environmental insults which occur early in life[507]. This means that studying how the early life environment (factors such as maternal stress and nutrition, or exposure to environmental toxins such as those from CS) affects health outcomes in later life could provide insights as to how to combat adult diseases.

Epigenetic marks, including DNA methylation (DNAm), histone modifications and non-coding RNAs, are sensitive to the environment and are being investigated as potential links between early life environmental insults and disease outcomes. Early life CS exposure alters DNAm patterns in multiple tissues, especially in offspring umbilical cord blood[269–273], peripheral blood[245,276,277], placenta[274], and buccal cells[245,345]. These reported early life CS-induced DNAm alterations are sex-specific[311,321,508] and persist into adulthood[271–273,276,278,331,509,510]. However, most previous research was conducted in surrogate tissues such as blood, leaving tissues such as the lungs, which are more proximal to CS exposure, under-investigated. Since DNAm is highly tissue-specific[234–236], it is critical to explore these effects

in lung tissue. Our previous research demonstrated that early life CS exposure leads to sex-specific differences in DNAm at the *Cyp1a1* gene in offspring lungs, with females showing greater responsiveness than males[335]. Additionally, another study revealed that prenatal CS exposure resulted in sex-specific DNAm changes at 1233 genes in human fetal lung tissue[322]. Despite these findings, there is a paucity of studies focusing on lung-specific DNAm alterations, particularly those tracking changes over time. Understanding how early life CS exposure modifies DNAm in lung tissues over time can provide crucial insights into the mechanisms of CS-induced lung injury. This knowledge is essential for developing targeted interventions and improving outcomes for individuals exposed to CS early in life.

Studies investigating the effects of prenatal CS on offspring outcomes are important, but one area that remains under-investigated is the potential effects of early postnatal smoke (smoke exposure during breastfeeding). The distinction between prenatal and postnatal CS is important because prenatal and early postnatal CS exposure may have very distinct effects on offspring[287–290,335,511]. For example, prenatal CS exposure alone was associated with an increased risk of offspring developing asthma and chronic bronchitis, while postnatal CS exposure produced different effects as it increased risk of developing upper respiratory tract infections[511,512]. Given that the complexity of the human environment makes it challenging to separate prenatal from early postnatal CS exposures[285,286], smaller model organisms such as animal models, can be employed and may help identify critical periods in development which influence offspring health later in life.

Secondary exposure to CS can also lead to more severe outcomes later in life than exposure during one period alone[513–516]. This pattern is particularly evident in COPD, where early life CS exposure alone increases airflow limitation and COPD risk, but additional personal smoking in adulthood further exacerbates lung function decline, significantly

heightening the risk of COPD[513,514]. The importance of studying the combined effects of early and later life CS exposures lies in the fact that while smoking levels have reduced globally over the years, many adults today were inadvertently exposed to some CS early in life when smoking levels were much higher. As a result, many human studies today which report the effects of CS exposure in adulthood do not effectively account for possible early life CS exposures, underscoring the need for model organisms to understand these interactions for effective preventive strategies against COPD and other CS-associated deficits. In murine models, while there is abundant evidence for synergistic effects of maternal CS and other non-CS allergens in adulthood[307,309], effects of combined CS exposures in early and later life have only been investigated by one group to our knowledge[308]. This singular study reported the effects of a combination of prenatal firsthand smoke exposure and re-exposure to CS for four weeks in adolescence (days 21-49 in mice) on offspring lung function[308]. They found significant functional changes in lung function in offspring only when exposed to CS during both periods, concluding that CS exposure has a synergistic or additive effect on mouse lung function[308].

At a molecular level, an initial exposure resulting in a different response to a second exposure is known as *priming*. This concept surmises that environmental exposures induce changes within cells which are maintained over time, resulting in differential responses upon subsequent exposure[300–302]. Priming is a well-established, epigenetically driven process in plants[517–520], but is less well studied in mammals. A recent study showed that exposure of mouse epithelial stem cells to acute inflammation resulted in long-term chromatin modifications which led to faster response to tissue damage[521]. This study provided evidence that epigenetic marks can be involved in maintenance of environmentally-induced signals in mammals that are associated with differential responses in the future. While there are

numerous studies demonstrating the effects of early life CS exposure alone on offspring DNAm[245,269–274,276–278], the effects of a combination of early and later life CS exposures on DNAm is severely lacking, and this is an important question as it will provide insights into mechanisms underlying health outcomes due to these combined exposures. We have previously shown that early life CS exposure causes long-lasting alterations in DNAm patterns at the Cytochrome P450 1A1 (*Cyp1a1*) gene in offspring lungs, that these patterns disappear in late adulthood, and that they are re-established upon re-exposure of adult offspring to CS[335]. Epigenome-wide investigation into DNAm patterns underlying combined early and later life CS exposure would offer insights into the evidence of priming in mammals beyond our candidate gene.

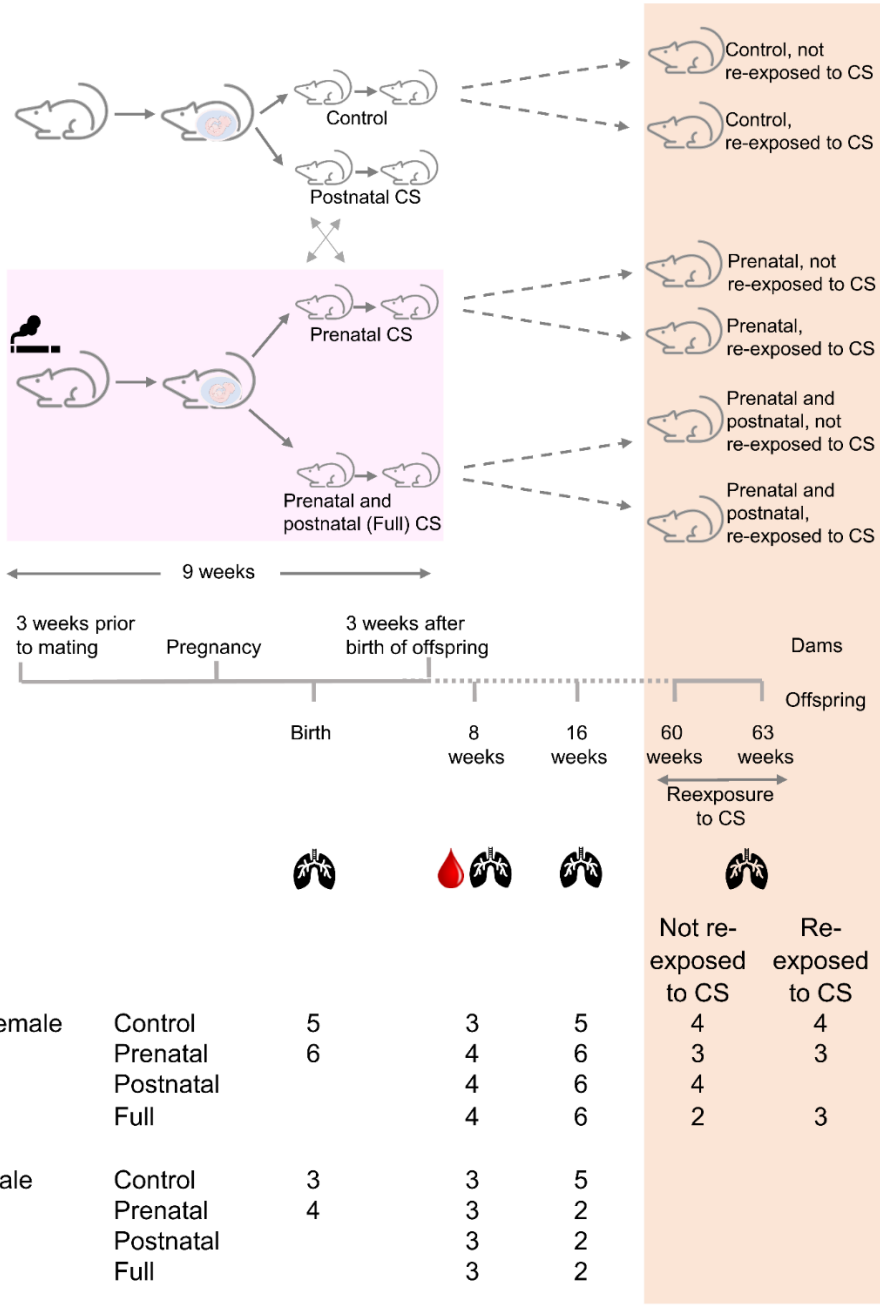
In this study, we measure DNAm in offspring lungs following early life CS exposure, both at individual timepoints and across the lifespan, and then, investigate how these DNAm patterns change upon secondary exposure to CS. We identified novel DNAm alterations following prenatal only, early postnatal only, or combined early life CS exposures, showing that males are likely to develop long-lasting DNAm alterations in the lungs following early life CS exposure alone. Upon addition of a secondary CS exposure, we determined that combined CS exposure in early life and adulthood have synergistic effects on lung DNAm, thus confirming the occurrence of priming in mice following CS exposure and suggesting that DNAm differences may be associated with the exacerbated lung alterations observed following repeated CS exposures. This research is important, as it is a step to understanding the epigenetic patterns underlying singular and combined CS-induced lung function outcomes, and could help drive interventions to mitigate the effects of CS exposure.

4.3 Methods

4.3.1 Mouse model to measure the effects of early life CS exposure alone and the effects of combined early and later life CS exposures

The complete details of this exposure paradigm have been published previously[335]. Briefly, 32 adult female BALB/C mice (N = 16 Control, N = 16 CS-exposed) were exposed to whole body CS for a total period of 9 weeks. CS exposure began 3 weeks prior to mating, and lasted throughout gestation (3 weeks), ending at weaning of pups (3 weeks after birth). Therefore, no offspring was directly exposed to CS: instead, they were exposed to CS *in utero*, or via bedding, milk or fur after birth. Whole body smoke was administered to dams by burning 1R6F standard research cigarettes (University of Kentucky, Lexington, KY), at one puff per minute for two hours twice daily using the SCIREQ InExpose smoking robot (SCIREQ, Montreal, QC, Canada). At birth, litters were culled to six offspring per litter, while the rest were cross-fostered and allowed to grow for tissue collection in future. To achieve cross-fostering, immediately after birth, half of the offspring born to control dams were cross-fostered with half of those born to CS-exposed dams, to generate four groups of offspring: No CS exposure (Control), Prenatal CS only (Pre), Postnatal CS only (Post), and offspring exposed to CS both prenatally and postnatally (Full). Three weeks after birth (at weaning of pups), all CS exposures stopped, and offspring of the same sex were housed 4-6 per cage in individually ventilated cages for the remaining duration of the experiment. Lung function, lavage and tissue collection were performed as described previously[335] at birth, at 8 weeks of age (5 weeks after weaning and therefore, cessation of smoke exposure) and at 16 weeks of age (13 weeks after weaning and cessation of smoke exposure). Female offspring which were not euthanized at the 16 week timepoint were left undisturbed until 60 weeks of age. At 60 weeks of age, half of the remaining female offspring in the control, prenatal and full

exposure groups were re-exposed to whole body CS for 2 hours a day, for 5 consecutive days per week, and for 21 days in total. The other half which was not re-exposed to CS served as the adult controls. Due to insufficient numbers, we did not re-expose the postnatal group of female offspring, nor any male animals to CS in adulthood, and so they are excluded from analyses here. Similar to the earlier timepoints, lung function and bronchoalveolar lavage were performed at the 63 week timepoint followed by tissue collection. Note that this entire experiment was repeated twice, with the first experiment being the source of some birth, all 16 and 63 week samples, and the second being the source of some birth and all 8 week samples. Details of experimental design are highlighted in Figure 4.1.



					Not re-exposed to CS	Re-exposed to CS
Female	Control	5	3	5	4	4
	Prenatal	6	4	6	3	3
	Postnatal		4	6	4	
	Full		4	6	2	3
Male	Control	3	3	5		
	Prenatal	4	3	2		
	Postnatal		3	2		
	Full		3	2		

Figure 4. 1: Experimental design to measure the longitudinal effects of early life CS exposure, and additional effects of secondary CS exposure in adulthood on DNAm
Adult female BALB/c mice (N = 16 control, N = 16 CS) were exposed to whole-body CS for 9 weeks, beginning 3 weeks before mating and conception and ending 3 weeks after birth of offspring. At birth, half of the offspring from control and smoke-exposed dams were cross-fostered to generate four early life offspring groups: Control, offspring exposed to Prenatal CS only, offspring exposed to Postnatal CS only, and offspring exposed to combined prenatal and early postnatal CS (Full). Offspring were allowed to grow till 60 weeks of age. At 60 weeks, half of the female offspring from the control, prenatal and fully exposed early life groups was re-exposed to CS for 3 weeks, while the other half were exposed to room air. Lungs were collected from offspring at birth, and then following lavage and lung function measurements, at 8, 16 and 63 weeks of age.

4.3.2 DNA extraction and processing from lungs and blood

We homogenized whole left lungs of offspring at all timepoints using the Qiagen Tissue Lyser II, and extracted DNA from the homogenate using the Invitrogen DNA extraction kit. We also extracted DNA from whole blood collected at the 8 week timepoint using the Qiagen DNAeasy Blood and Tissue kit, according to the manufacturer. We measured DNA concentration using the NanoDrop spectrophotometer (NanoDrop Technologies, USA). Next, we performed bisulfite conversion (kit from Zymo Research) on about 750 ng of blood or lung DNA, and used 100 -160 ng of the resulting bisulfite-converted DNA for the epigenome-wide DNAm analysis.

4.3.3 Measurement of epigenome-wide DNAm in offspring lung and blood autosomes at individual timepoints

We measured DNAm across the whole mouse epigenome using the Illumina Infinium Mouse Methylation BeadChip (Illumina, San Diego, CA, USA), according to the manufacturer's protocol. Briefly, following bisulfite conversion, we randomized samples using Omixer[443], amplified, fragmented and hybridized converted samples onto the Illumina beadchip and scanned using the Illumina iScan. Samples applied to the chip include blood samples collected at 8 weeks, and lung samples collected at all timepoints (birth, 8, 16 and 63 weeks). We performed preprocessing on the exported intensity files using the SeSAMe R package[355]. Briefly, preprocessing included removing 18,920 probes mapping to the X, Y and mitochondrial chromosomes, background subtraction using noob[356], dye bias correction and filtering out probes with detection $p > 0.05$[355]. The intensities of the remaining 208,606 of 296,070 probes were quantified as DNAm β-values and used in downstream analyses. Following preprocessing, we performed batch correction using ComBat[357] to correct for chip,

row, column and run effects. We accounted for remaining technical variation using SVA[358], and added the recommended surrogate variables to our regression models. We next measured differences in DNAm using linear regression using the limma package in R. We considered probes to be differentially methylated at $p < 1e\text{-}3$ and an effect size greater than 0.05. Probes were mapped to their corresponding genes (GRCm38/mm10 genome assembly) using the Illumina default manifest. All analyses were conducted in R version 4.3.1.

4.3.4 Measurement of DNAm at offspring lung and blood sex chromosomal probes

We separately measured the effects of early life CS exposure on DNAm in probes mapping to the X and Y chromosomes. The preprocessing and normalization steps were similar to those performed previously on the autosomal probes, except that each sex chromosome was processed differently, from start until the end of the analysis. After preprocessing and filtering, we were left with 11,529 of 15,117 probes on the X chromosome in female samples, 10,769 of 15,117 probes on the X chromosome in male samples, and 1,991 of 3,767 probes in the Y chromosome for use in downstream analyses. We next performed batch correction, SVA and limma as described above and set the same significance cutoffs.

4.3.5 Measurement of the longitudinal effects of early life CS exposure on DNAm in offspring lungs

Following our individual timepoint analyses, we investigated the long-term effects of early life CS exposure on offspring lung DNAm. We performed our longitudinal analyses

using two approaches. First, we sought to determine which of the significantly altered CpGs would wane or remain altered with aging. To determine this, we took the CpGs which were significantly differentially methylated CpGs by prenatal CS at birth and then examined their trajectories at the end timepoints for both sexes (63 weeks for females and 16 weeks for males). We also did the reverse: that is, we took CpGs which were significantly differentially methylated by prenatal CS in adulthood (63 weeks and 16 weeks in females and males respectively) and examined their trajectories at the birth timepoint. We only measured trajectories of DNAm on CpGs identified in the prenatal group, and not the postnatal or fully exposed CS groups, because we collected lung tissues at birth from only the control and prenatal groups, due to the study design. We performed these analyses using student-t-tests, which compares mean DNAm between control and prenatal CS-exposed offspring within all timepoints. We determined a CpG as altered longitudinally at $p < 0.05$.

In our second approach to longitudinal analyses, we investigated the trajectories of DNAm patterns set by early life CS over time using a more conventional analysis which involved determining persistence of DNAm across all autosomal and sex chromosome CpGs, and not just in the ones which had been identified as significant earlier. For this analysis, we used limma's linear regression and included the timepoint variable as a factor. We also included surrogate variables recommended by SVA to our regression models as mentioned above. CpGs in this analysis were determined as persistently altered at $p < 1e\text{-}3$ and effect size > 0.025.

4.3.6 Gene ontology

We performed gene ontology analysis on differentially methylated CpGs using the ClusterProfiler[360] package in R. Biological processes and pathways were considered significantly enriched at FDR < 0.05.

4.4 Results

4.4.1 Effects of early life smoke exposure on DNAm in offspring lungs at multiple individual timepoints across the lifespan

To assess the effects of early life CS exposure on offspring lung DNAm over time, we first measured DNAm at multiple timepoints: at birth (immediately after 3 weeks of *in utero* CS exposure), 8 (after 5 weeks of cessation of early life CS exposure), 16 (after 13 weeks of cessation of early life CS) and at 63 weeks of age (after 60 weeks of cessation of early life CS). A summary of the numbers of differentially methylated CpGs in both autosomes and sex chromosomes can be found in Table 4.1, and full details on the results for each stage and group are found in Appendices 4.1 - 4.8, 4.10 – 4.15, 4.18 – 4.20.

Table 4. 1: Summary of number of differentially methylated CpGs in the lungs of offspring exposed to early life CS, measured at individual timepoints

Autosomes					
Timepoint	**Sex**	**Direction of change**	**Prenatal CS**	**Postnatal CS**	**Full CS**
Birth	Female	Higher	5		
		Lower	9		
	Male	Higher	29		
		Lower	33		
8 weeks	Female	Higher	16	28	13
		Lower	7	21	11
	Male	Higher	9	15	12
		Lower	11	30	36
16 weeks	Female	Higher	21	39	21
		Lower	6	11	12
	Male	Higher	751	535	28
		Lower	1249	649	3
63 weeks	Female	Higher	51	9	147
		Lower	48	20	145
X chromosome					
Birth	Female	Higher	1		
		Lower	-		
	Male	Higher	-		
		Lower	-		
8 weeks	Female	Higher	3	2	3
		Lower	-	2	-
	Male	Higher	3	2	1
		Lower	4	3	1
16 weeks	Female	Higher	-	6	1
		Lower	-	2	1
	Male	Higher	20	8	3
		Lower	46	13	7
63 weeks	Female	Higher	3	5	8
		Lower	16	2	9
Y chromosome					
Birth	Male	Higher	-		
		Lower	-		
8 weeks	Male	Higher	3	1	-
		Lower	2	1	1
16 weeks	Male	Higher	4	1	2
		Lower	1	-	2

At birth, male lungs showed higher number of differentially methylated autosomal CpGs than female lungs, and there were no overlapping positions between sexes, highlighting the distinct effects of prenatal CS on males and females (Table 4.1, Figures 4.2 and 4.6, and Appendices 4.1 and 4.2). There were no differentially methylated CpGs on either the X or Y chromosome in males, but in female offspring exposed to CS *in utero,* 1

CpG (cg47855939_BC21 mapping to the *Yipf6* gene) was differentially methylated (Table 4.1, Figure 4.6 and Appendices 4.1 – 4.2).

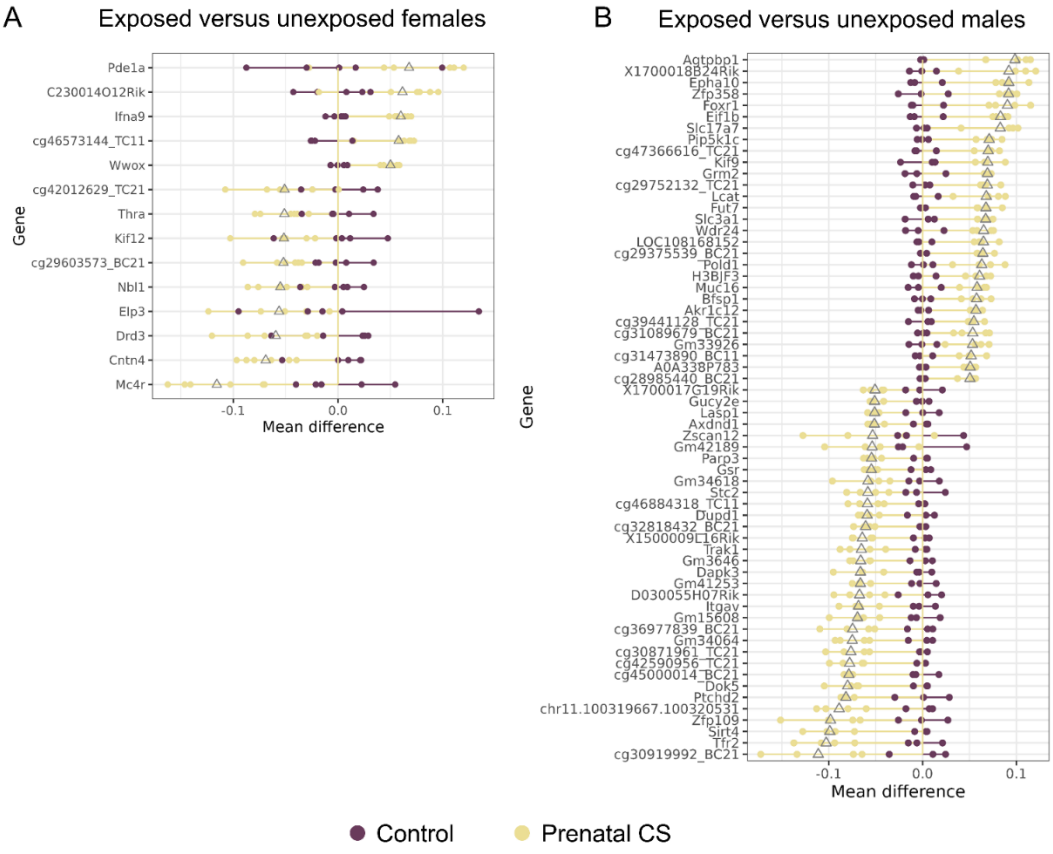


Figure 4. 2: DNA methylation differences on the autosomes due to prenatal CS exposure at birth.

(A) Fourteen CpGs (5 higher, 9 lower) are differentially methylated due to prenatal CS exposure in female offspring lung autosomes at birth (B) 62 CpGs (29 higher, 33 lower) are differentially methylated due to prenatal CS exposure in male offspring lung autosomes at birth. DNAm differences were analyzed using linear regression, and CpGs were considered differentially methylated at $p < 10e\text{-}3$ and effect size > 0.05. Mean of controls are shown at the midpoint (the 0.0 mark) on the x axis. Purple and yellow dots represent the difference between the means of the controls and the beta values of the individual samples in the control and prenatal CS groups respectively (mean difference). Grey triangles represent effect size differences (delta beta), which were calculated by subtracting mean beta values of exposed offspring from control mean betas. Plots are ordered from largest to smallest effect sizes for better visualization. N = 3-6 per group.

At the 8 week timepoint, the numbers of altered autosomal CpGs were more similar between males and females exposed to prenatal, postnatal or full CS, with some overlaps (Table 4.1, Figure 4.3, and Appendices 4.3 – 4.9). Two CpGs: cg29853438_TC21 (unannotated) and cg38499186_TC21 (mapping to the Ceramide synthase 6 or *Cers6* gene) were commonly differently methylated in lung autosomes across all female groups at 8 weeks, while one CpG (cg48190254 mapping to the *Ofd1* gene) on the X chromosome was commonly differentially methylated across all female exposure groups (Appendices 4.3 – 4.5). There were no overlapping CpGs identified across all male exposure groups at 8 weeks (Figure 4.6).

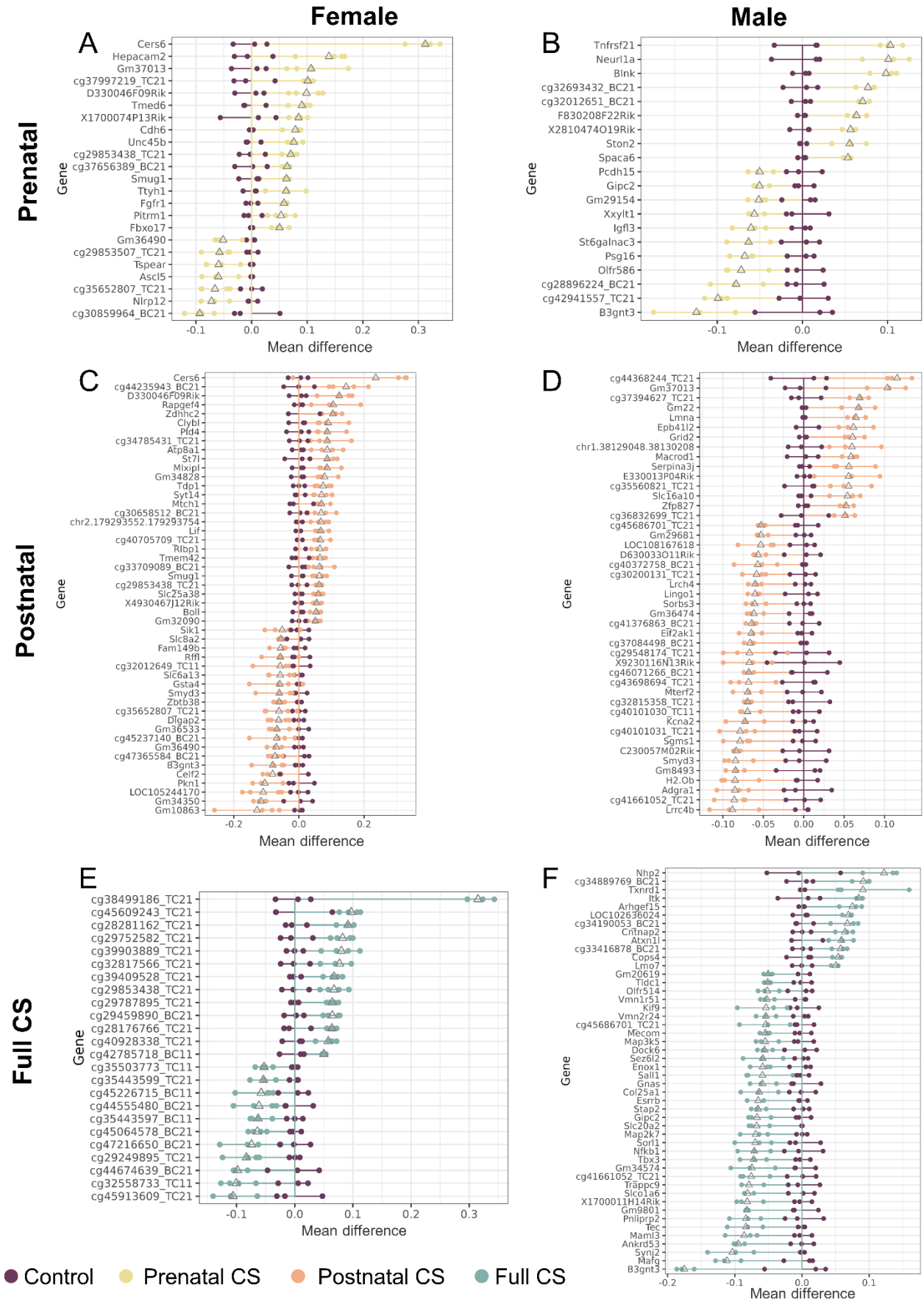

Female
Male
Prenatal
Postnatal
Full CS
A
B
C
D
E
F
Gene
Mean difference
Control
Prenatal CS
Postnatal CS
Full CS

Figure 4. 3: Significant CpGs due to CS exposure in female and male lung autosomes at 8 weeks of age.

At 8 weeks, prenatal CS exposure led to differential DNAm at (A) 23 CpGs (16 higher, 7 lower) in female offspring and (B) 20 CpGs (9 higher, 11 lower) in male offspring. Postnatal CS exposure led to differential DNAm at (C) 49 CpGs (28 higher, 21 lower) in female offspring and (D) 45 CpGs (15 higher, 30 lower) in male offspring. Full CS exposure led to differential DNAm at (E) 24 CpGs (13 higher, 11 lower) in female offspring and (F) 48 CpGs (12 higher, 36 lower) in male offspring. DNAm differences were analyzed using linear regression, and CpGs were considered differentially methylated at $p < 10e\text{-}3$ and effect size > 0.05. Mean of controls are shown at the midpoint (the 0.0 mark) on the x axis. Purple, yellow, orange and green dots represent the difference between the means of the controls and the beta values of the individual samples in the control, prenatal, postnatal and full CS groups respectively (mean difference). Grey triangles represent effect size differences (delta beta), which were calculated by subtracting mean beta values of exposed offspring from control mean betas. Plots are ordered from largest to smallest effect sizes for better visualization. N = 3-4 per group.

At 16 weeks, male offspring exposed to prenatal only or postnatal only CS showed a substantially greater number of altered CpGs compared to females in the same group (Table 4.1, Figure 4.4, and Appendices 4.10 – 4.16). The number of differentially methylated CpGs in fully exposed male offspring, on the other hand, remained comparable to fully exposed females (Figure 4.4). While there were no commonly altered CpGs across all female groups, male offspring exposed to prenatal, postnatal or full CS showed differential DNAm at cg43372777_BC21, mapping to the *Cntnap2* gene (Appendices 4.13 – 4.15). Given the substantially larger number of significant CpGs in males at 16 weeks compared to females (Table 4.1), we needed to make sure that our significant hits were truly different, and not because of the smaller sample size of males at 16 weeks (Figure 4.1). Therefore, we performed a sensitivity analysis where we subsampled the number of females at 16 weeks to mirror the male sample size (Figure 4.1), and repeated linear regression on the reduced female sample numbers. Results from our sensitivity analysis showed that prenatal, postnatal or full CS altered 20, 89 and 5 CpGs respectively in females at 16 weeks of age (Appendix 4.17). Compared to age-matched males, these numbers of altered positions in females are significantly lower despite the reduction in sample size, confirming that the much higher numbers of altered CpGs in males at 16 weeks is not as a result of sample size.

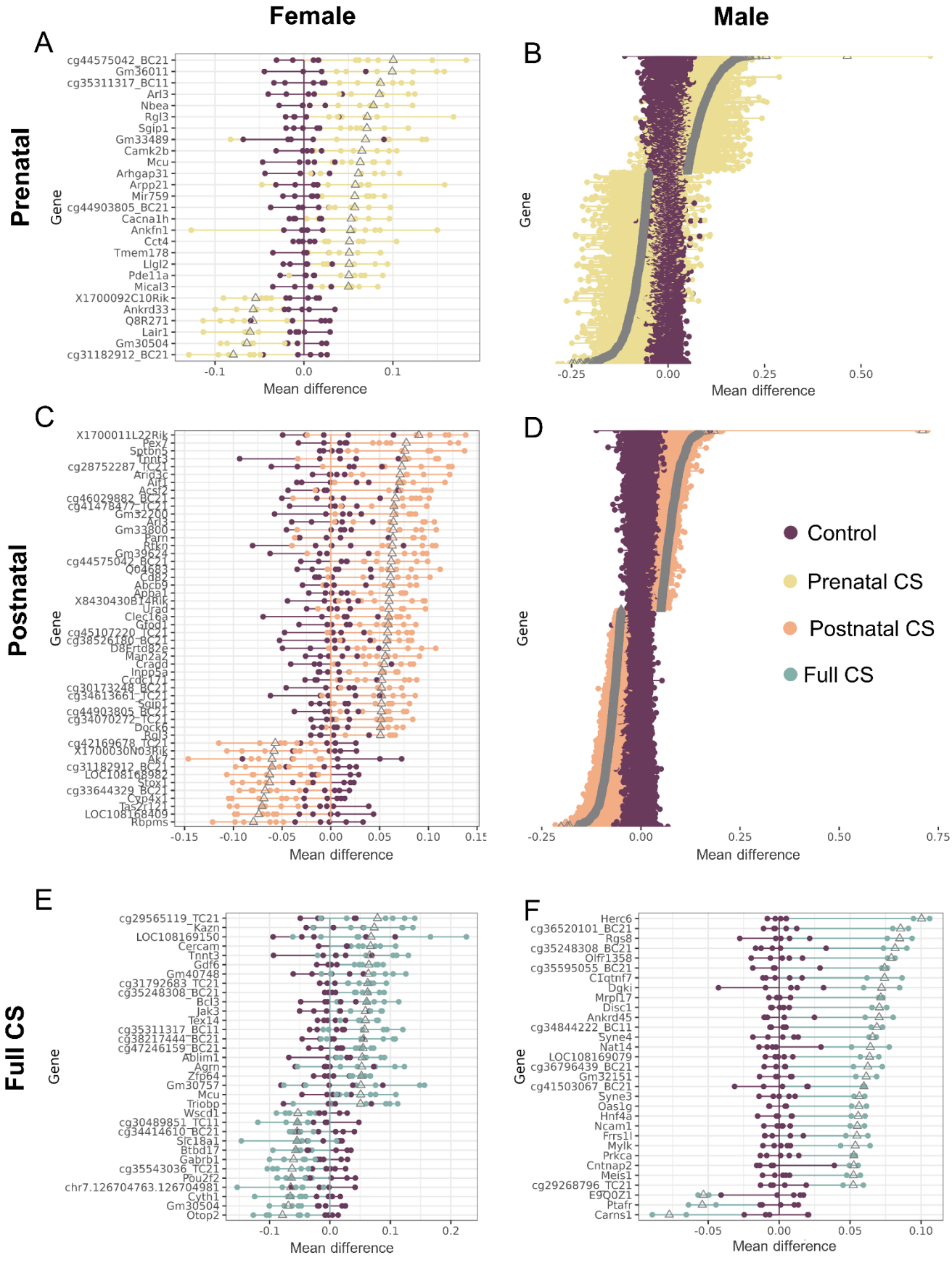

Female
Male
A
B
C
D
E
F
Prenatal
Postnatal
Full CS
Gene
Mean difference
Control
Prenatal CS
Postnatal CS
Full CS

Figure 4. 4: Significant CpGs due to CS exposure in female and male lung autosomes at 16 weeks of age.

At 16 weeks, prenatal CS exposure led to differential DNAm at (A) 27 CpGs (21 higher, 6 lower) in female offspring and (B) 2000 CpGs (751 higher, 1249 lower) in male offspring. Postnatal CS exposure led to differential DNAm at (C) 50 CpGs (39 higher, 11 lower) in female offspring and (D) 1184 CpGs (535 higher, 649 lower) in male offspring. Full CS exposure led to differential DNAm at (E) 33 CpGs (21 higher, 12 lower) in female offspring and (F) 31 CpGs (28 higher, 3 lower) in male offspring. DNAm differences were analyzed using linear regression, and CpGs were considered differentially methylated at $p < 10e\text{-}3$ and effect size > 0.05. Mean of controls are shown at the midpoint (the 0.0 mark) on the x axis. Purple, yellow, orange and green dots represent the difference between the means of the controls and the beta values of the individual samples in the control, prenatal, postnatal and full CS groups respectively (mean difference). Grey triangles represent effect size differences (delta beta), which were calculated by subtracting mean beta values of exposed offspring from control mean betas. Plots are ordered from largest to smallest effect sizes for better visualization. N = 2-6 per group.

At 63 weeks of age, female offspring exposed to full CS showed a substantially greater number of altered autosomal CpGs (292 CpGs) compared to prenatal CS-exposed (99 CpGs) or postnatal CS-exposed (29 CpGs) offspring, a pattern suggestive of the longevity of early life CS effects (Table 4.1, Figure 4.5, Appendices 4.18 – 4.21). We also found one autosomal CpG (cg46018659_TC21 mapping to the *Gnao1* gene) to be commonly differentially methylated across all three female exposure groups compared to controls (Table 4.1, Figure 4.5, Appendices 4.18 – 4.21), as early life CS exposure led to a decrease in DNAm at this CpG in all groups.

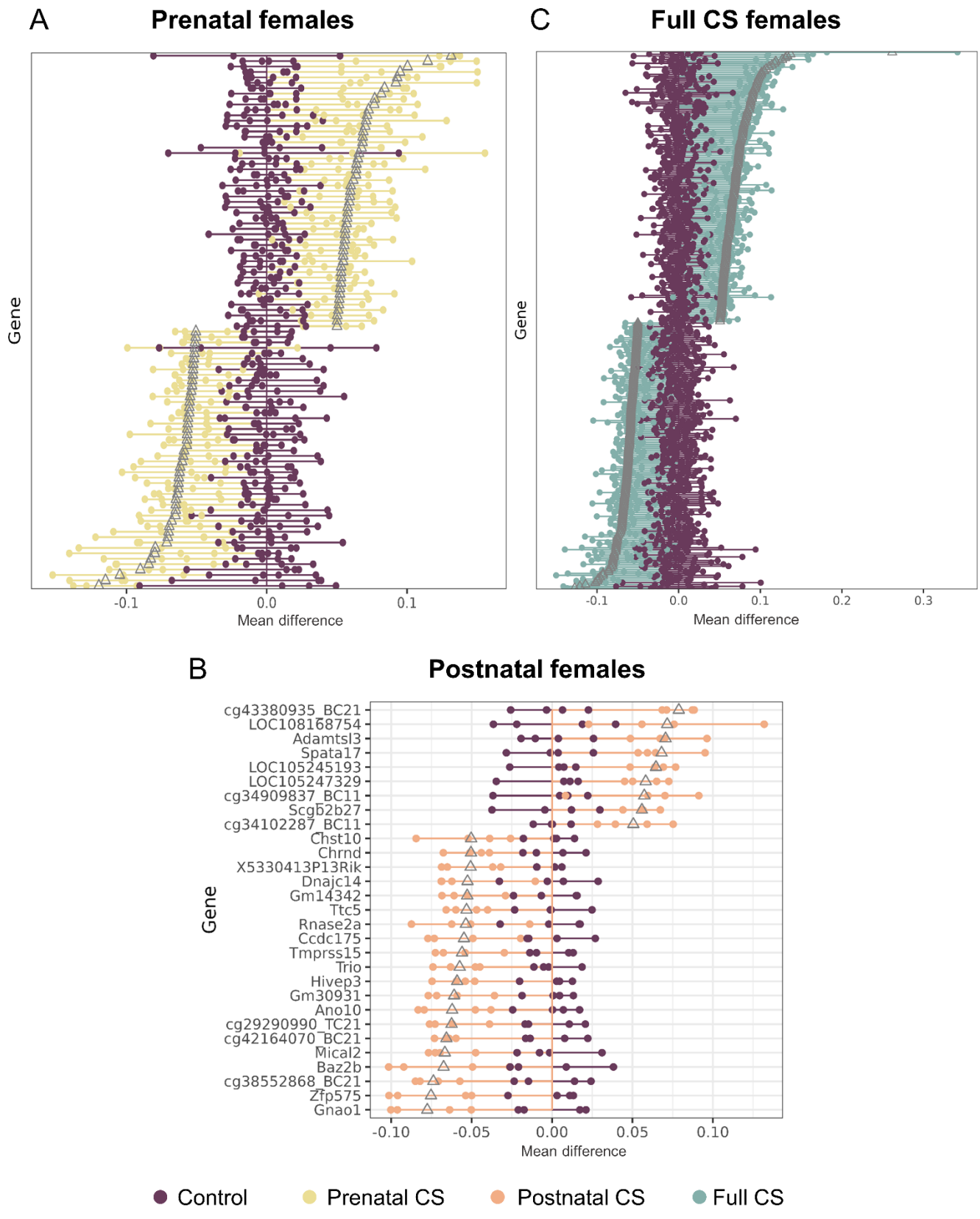
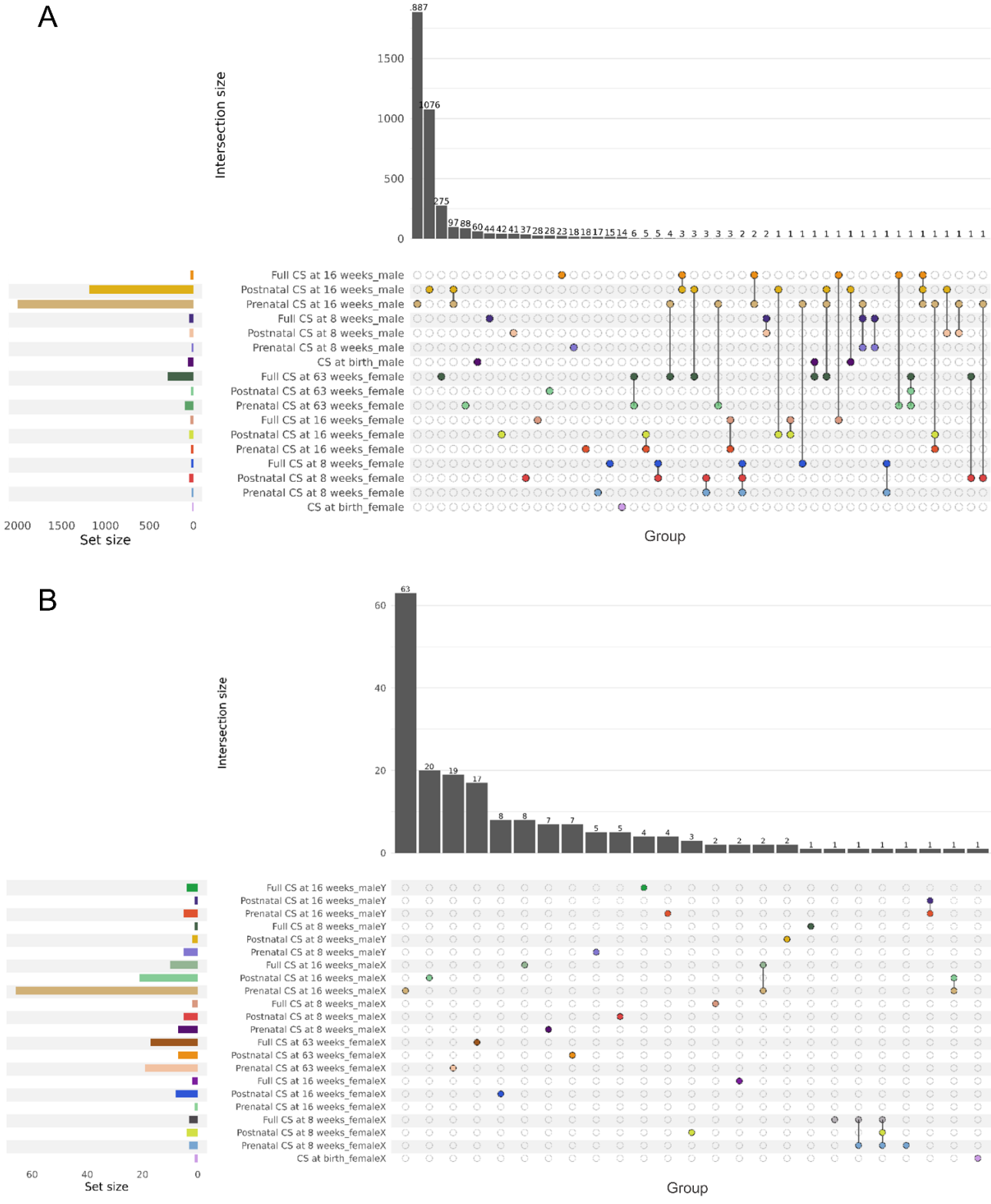


Figure 4. 5: Significant CpGs due to CS exposure in female lung autosomes at 63 weeks of age.

(A) 99 CpGs (51 higher, 48 lower) are differentially methylated due to prenatal CS exposure in female offspring lung autosomes at 63 weeks (B) 29 CpGs (9 higher, 20 lower) are differentially methylated due to postnatal CS exposure in female offspring lung autosomes at 63 weeks (C) 292 CpGs (147 higher, 145 lower) are differentially methylated due to full CS exposure in female offspring lung autosomes at 63 weeks. DNAm differences were analyzed using linear regression, and CpGs were considered differentially methylated at $p < 10e\text{-}3$ and effect size > 0.05. Mean of controls are shown at the midpoint (the 0.0 mark) on the x axis. Purple, yellow, orange and green dots represent the difference between the means of the controls and the beta values of the individual samples in the control, prenatal, postnatal and full CS groups respectively (mean difference). Grey triangles represent effect size differences (delta beta), which were calculated by subtracting mean beta values of exposed offspring from control mean betas. Plots are ordered from largest to smallest effect sizes for better visualization. N = 2-6 per group.


A
Intersection size
1887
1076
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1

Together, our results show novel CpGs differentially methylated in offspring lungs at four timepoints over the course of life. They also show that while different types of early life CS exposure do share common DNAm patterns in the lungs, they are mostly distinct. It also contributes to the knowledge that the effects of *in utero* smoke exposure causes sex-specific alterations in DNAm in offspring.

4.4.2 Effects of early life smoke exposure on DNAm in offspring blood at eight weeks of age

Given that most of what is currently known about the effects of early life smoke exposure is from human blood, we measured DNAm in offspring blood at 8 weeks to compare to the lungs. We chose to measure DNAm at 8 weeks only and not at other timepoints, as it is the closest timepoint to CS exposure that is feasible to obtain blood, as it is difficult to obtain sufficient blood from pups at birth. DNAm analysis was conducted using multivariable linear regression in exactly the same way as the lungs. Table 4.2 contains a summary of the number of differentially methylated CpGs in the blood of offspring exposed to early life CS.

Table 4. 2: Summary of number of differentially methylated CpGs in the blood of offspring exposed to early life CS, measured at 8 weeks of age

Autosomes					
Timepoint	**Sex**	**Direction of change**	**Prenatal CS**	**Postnatal CS**	**Full CS**
8 weeks	Female	Higher	14	3	21
		Lower	29	9	32
	Male	Higher	79	44	28
		Lower	106	34	82
X chromosome					
8 weeks	Female	Higher	13	1	19
		Lower	10	6	6
	Male	Higher	10	8	6
		Lower	21	9	7
Y chromosome					
8 weeks	Male	Higher	-	1	1
		Lower	1	1	2

Between sexes, none of the differentially methylated CpGs identified in the blood overlapped (Figure 4.8). In male offspring blood alone, two CpGs (cg38955541_TC21 mapping to *Stk35* and cg46577765_BC21 mapping to *Fli1*) were commonly differentially methylated across all male offspring groups at 8 weeks (Figure 4.7, Appendices 4.22 – 4.25).

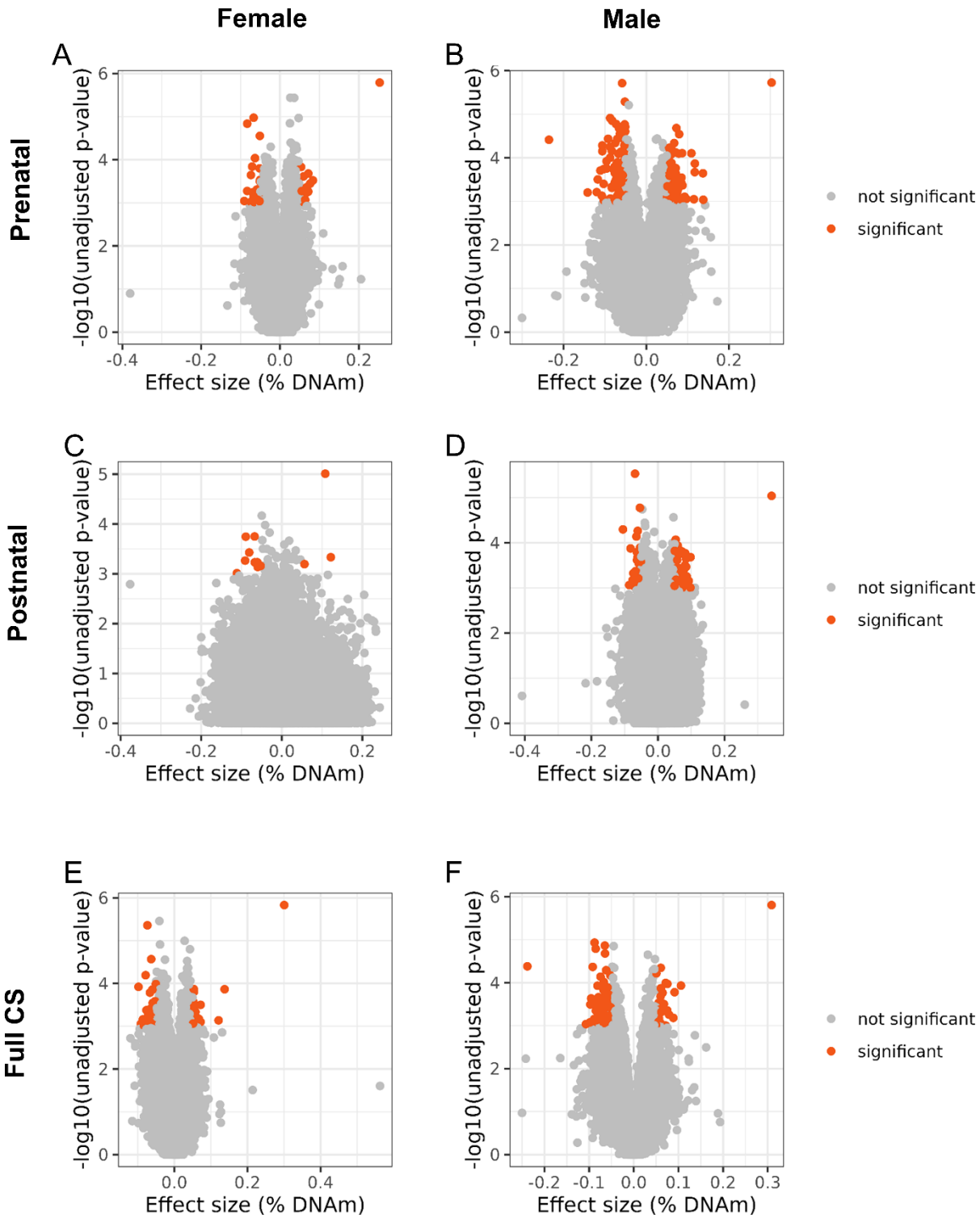

Figure 4. 7: Differentially methylated CpGs due to early life CS exposure in blood autosomes at 8 weeks.

(A) Forty-three CpGs (14 higher, 29 lower) are differentially methylated due to prenatal CS exposure in the female offspring blood autosomes at 8 weeks (B) 185 CpGs (79 higher, 106 lower) are differentially methylated due to prenatal CS exposure in the male offspring blood autosomes at 8 weeks (C) 12 CpGs (3 higher, 9 lower) are differentially methylated due to

postnatal CS exposure in the female offspring blood autosomes at 8 weeks (D) 78 CpGs (44 higher, 34 lower) are differentially methylated due to postnatal CS exposure in the male offspring blood autosomes at 8 weeks (E) 53 CpGs (21 higher, 32 lower) are differentially methylated due to full CS exposure in the female offspring blood autosomes at 8 weeks (F) 110 CpGs (28 higher, 82 lower) are differentially methylated due to full CS exposure in the male offspring blood autosomes at 8 weeks. DNAm differences were analyzed using linear regression, and CpGs were considered differentially methylated at $p < 10e-3$ and effect size > 0.05. Delta beta (effect size) was calculated by subtracting beta values of exposed offspring from control mean betas. N = 3-4 per group. Significant CpGs are highlighted in orange, while non-significant ones are highlighted in grey.

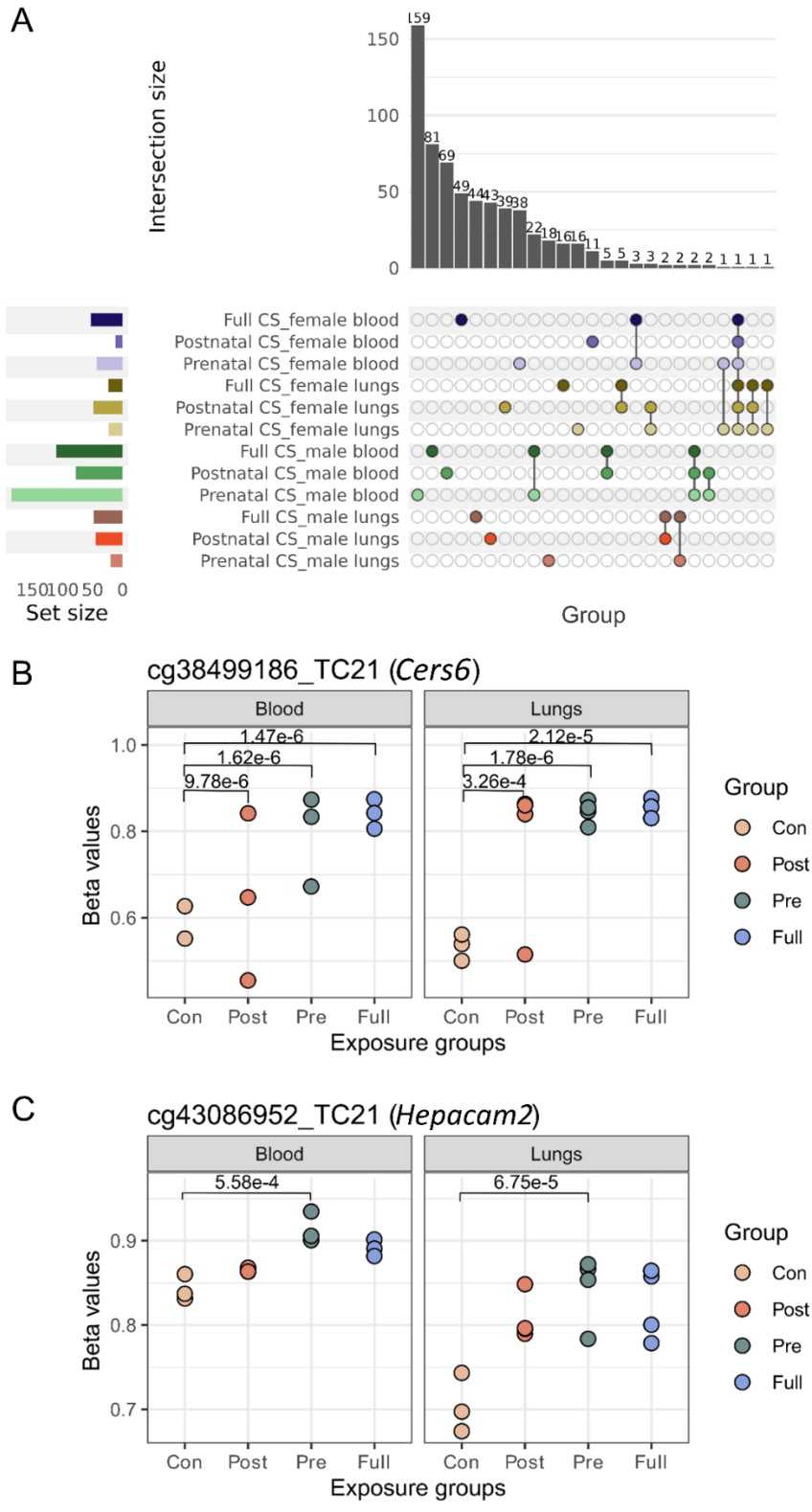

Figure 4. 8: Comparisons between the effects of early life CS on DNAm in the blood and lung autosomes, at 8 weeks of age (5 weeks after smoking cessation).

(A) Upset plot showing distinct and common CpGs differentially methylated in offspring blood and lungs (B) *Cers6* DNAm in female blood and lungs across time (C) *Hepacam2* DNAm in female blood and lungs across time.

In female offspring blood, *Cers6* was commonly altered across all CS exposure groups (Figure 4.8, Appendices 4.26 – 4.28), similar to the female offspring lungs at 8 weeks as highlighted in the previous section. An additional CpG (cg43086952_TC21), mapping to Hepacam family member 2 (*Hepacam2*), was commonly altered in blood and lungs of female offspring exposed to prenatal CS only (Figure 4.8, Appendices 4.26 – 4.28). In contrast, there were no shared CpG sites between male offspring blood and lungs across groups, and neither *Cers6* nor *Hepacam2* was differentially methylated in CS-exposed males compared to controls.

These results further emphasize the sex and tissue-specificity of DNAm alterations following early life CS exposure.

4.4.3 Persistence of prenatal CS-induced DNAm changes at sites identified at individual timepoints

Following our analyses at individual timepoints, we performed longitudinal analyses in two stages to determine persistence of DNAm alterations which arise due to early life CS. The first stage of the analysis involved two questions: (1) Among the CpGs which are most responsive to prenatal CS at birth, which ones remain altered until adulthood and which ones wane over time? and (2) Were the CpGs which are most responsive to prenatal CS in adulthood (63 weeks of age for females and 16 weeks of age for males) also differentially methylated significantly at earlier timepoints? Using the CpGs identified as differentially methylated at the earliest and latest timepoints (birth for both male and female compared to 16 weeks for males and 63 weeks for females) from our individual timepoint analyses, we

performed student t-tests within the other timepoints to see which sites remained altered over time.

In female offspring exposed to prenatal CS only, there were no birth CpGs which remained persistently altered until 63 weeks: instead, 71% of birth CpGs were not significant at any of the other timepoints, while the rest were significant at least one of the 8, 16 or 63 week timepoints, but not at all three (Figure 4.9A, Appendix 4.29). Similarly, none of the CpGs identified in prenatal CS-exposed females at 63 weeks of age were persistently altered at all earlier timepoints (Figure 4.9C, Appendix 4.29). Of the 62 significantly altered CpGs identified in prenatal CS-exposed males at birth, only cg46104911_BC21 (mapping to the Lecithin cholesterol acetyltransferase or *Lcat* gene) was persistently altered throughout all other timepoints (Figure 4.9B, Appendix 4.30), while no male CpG identified at 16 weeks was persistently altered at the birth and 8 week timepoints (Figure 4.9D, Appendix 4.30).

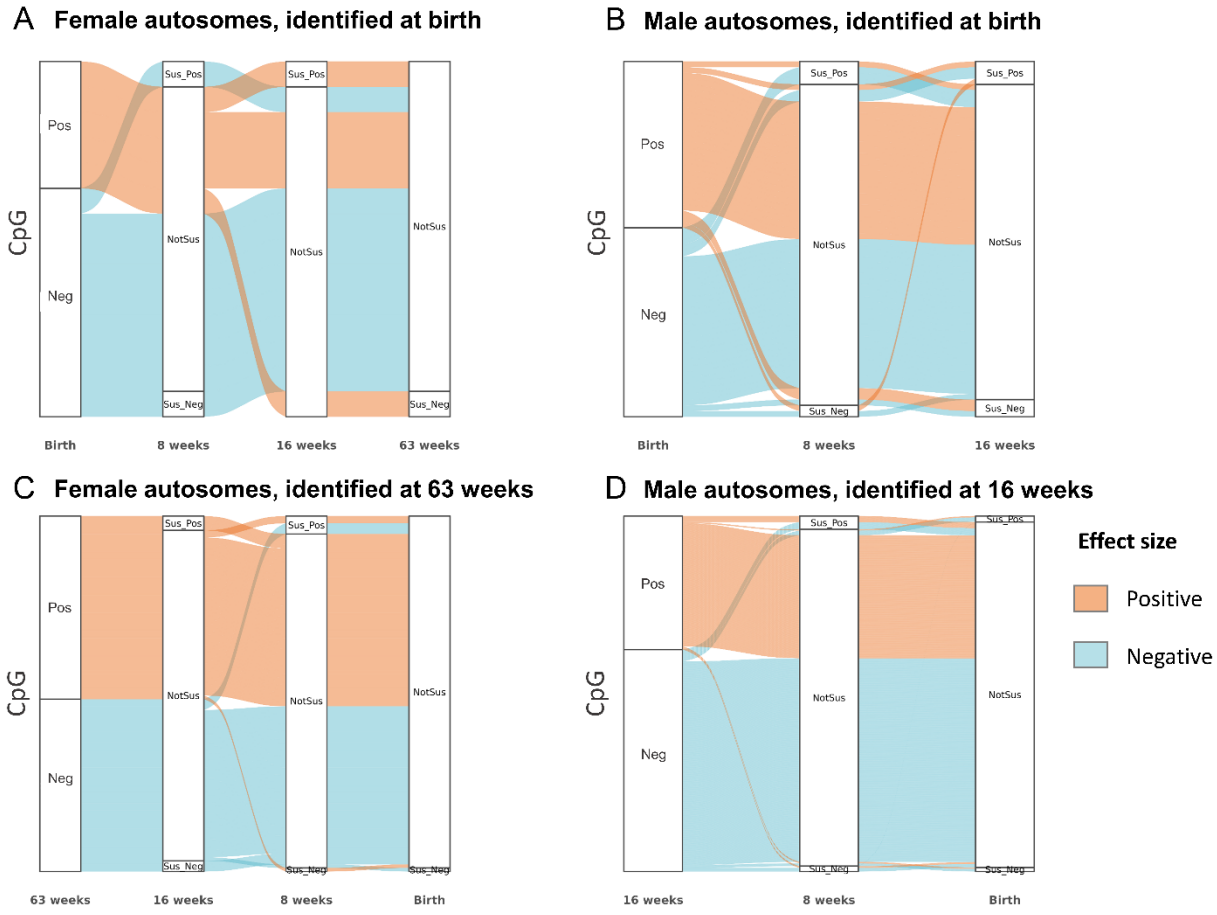

Figure 4. 9: Persistently altered CpGs among total list of significant CpGs identified at individual timepoints in offspring autosomes.

(A) None of the 14 significant CpGs identified in prenatal CS-exposed females at birth remained persistently altered at all other timepoints. Ten of 14 birth CpGs were not significant at any of the other timepoints (B) One of 62 CpGs which were differentially methylated in prenatal CS-exposed males at birth was also persistently altered till 16 weeks (C) None of the 99 significant CpGs identified in 63 week-old prenatal CS-exposed females remained persistently altered at all earlier timepoints. Ten of 14 birth CpGs were not significant at any of the other timepoints (D) None of the 2000 significant CpGs identified in 16 week-old prenatal CS-exposed males remained persistently altered at all earlier timepoints. DNAm differences were initially calculated by limma at each end timepoint (birth and 63 weeks in females and birth and 16 weeks in males), and significant CpGs were identified a $p < 1e\text{-}3$ and effect size > 0.05. Student t-test was used to determine whether CpGs which were significantly altered at birth or at the end timepoint (63 weeks for females and 16 weeks for males) were persistently altered within the other individual timepoints. Pos = Positive, Neg = Negative, Sus_Pos = Sustained/persistent with positive effect size compared to controls, Sus_Neg = Sustained/persistent with negative effect size compared to controls, NotSus = Not sustained/persistent. Persistently altered CpGs were identified at a cutoff of $p < 0.05$.

Similarly, sex chromosome analyses revealed that none of the CpGs identified in the X or Y chromosomes of males or females were persistently altered at all other timepoints. Rather, most of the significant CpGs were not sustained at timepoints other than where they were identified (Figure 4.10, Appendix 4.30).

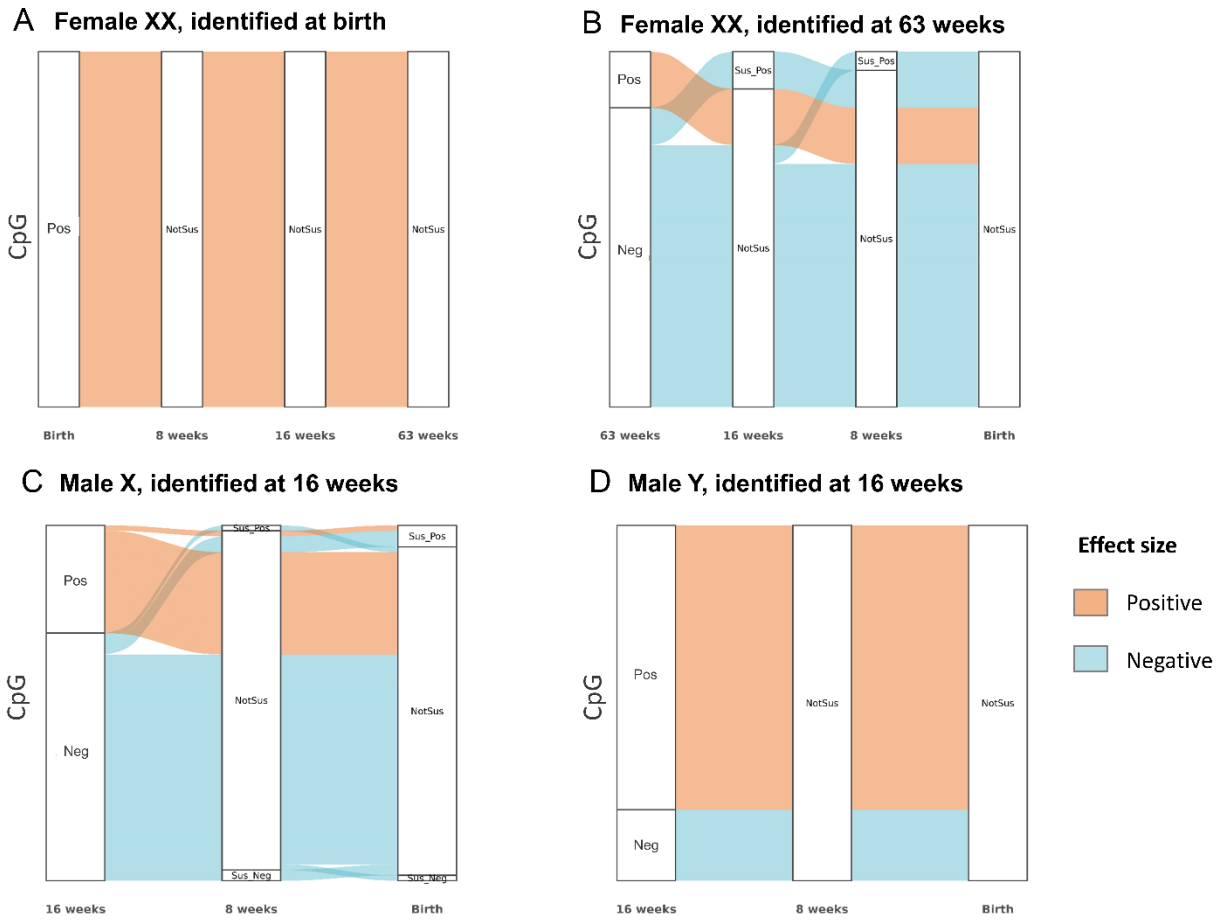

Figure 4. 10: Persistently altered CpGs among total list of significant CpGs identified at individual timepoints in offspring sex chromosomes.

(A) The only CpG which was differentially methylated on the X chromosome of prenatal CS-exposed females at birth was not persistently altered till 63 weeks (B) None of the 19 CpGs which were differentially methylated on the X chromosome of prenatal CS-exposed females at 63 weeks were also persistently altered at earlier timepoints (C) None of 66 CpGs which were differentially methylated on the X chromosome of prenatal CS-exposed males at 16 weeks were also persistently altered at earlier timepoints (D) None of the 5 CpGs which were differentially methylated on the Y chromosome of prenatal CS-exposed males at 16 weeks were also persistently altered at earlier timepoints. DNAm differences were initially calculated by limma at each end timepoint (birth and 63 weeks in females and birth and 16 weeks in males), and significant CpGs were identified a $p < 1e\text{-}3$ and effect size > 0.05. Student t-test was used to determine whether CpGs which were significantly altered at birth or at the end timepoint (63 weeks for females and 16 weeks for males) were persistently altered within the other individual timepoints. Pos = Positive, Neg = Negative, Sus_Pos = Sustained/persistent with positive effect size compared to controls, Sus_Neg = Sustained/persistent with negative effect size compared to controls, NotSus = Not sustained/persistent. Persistently altered CpGs were identified at a cutoff of $p < 0.05$.

Throughout our analyses, we observed that in most cases, if a CpG is identified as significant within one timepoint, it is unique to that timepoint and is not persistently altered across time. Additionally, the majority of the analyzed CpGs exhibited inconsistent DNAm patterns over time, fluctuating seemingly randomly between negative and positive effect sizes when compared to controls. Since we performed these longitudinal analyses on only significant CpGs, we cannot say whether these trends observed translate to other CpGs across the mouse epigenome.

These results show that DNAm sites identified at specific points in life following prenatal CS exposure are mostly unique to that timepoint and do not display predictable patterns with age.

4.4.4 Genome-wide longitudinal effects of early life CS exposure on DNAm in offspring lungs

As outlined above, the t-test method limits longitudinal analysis to DNAm sites which met statistical thresholds from analyses at the individual timepoints. Given our small sample size; however, it is likely that some CpGs which could not meet statistical cutoffs from our individual timepoint analyses could be persistently altered across time. Given the limitations with our t-test analyses, in the second step of our longitudinal analysis, we used linear regression to perform a more conventional analysis to determine which CpGs are consistently altered by early life CS in the total list of probes, and not just in the significantly altered DNAm sites from our individual timepoint analyses.

Of the 208,606 autosomal CpGs investigated, 98 were persistently altered across time in the lungs of females exposed to prenatal CS only (Figure 4.11A, Appendix 4.31), 53 were consistently altered in the lungs of females exposed to postnatal CS only (Figure 4.11B,

Appendix 4.32) and 58 CpGs were consistently altered in the lungs of females exposed to both prenatal and postnatal CS (Figure 4.11C, Appendix 4.33).

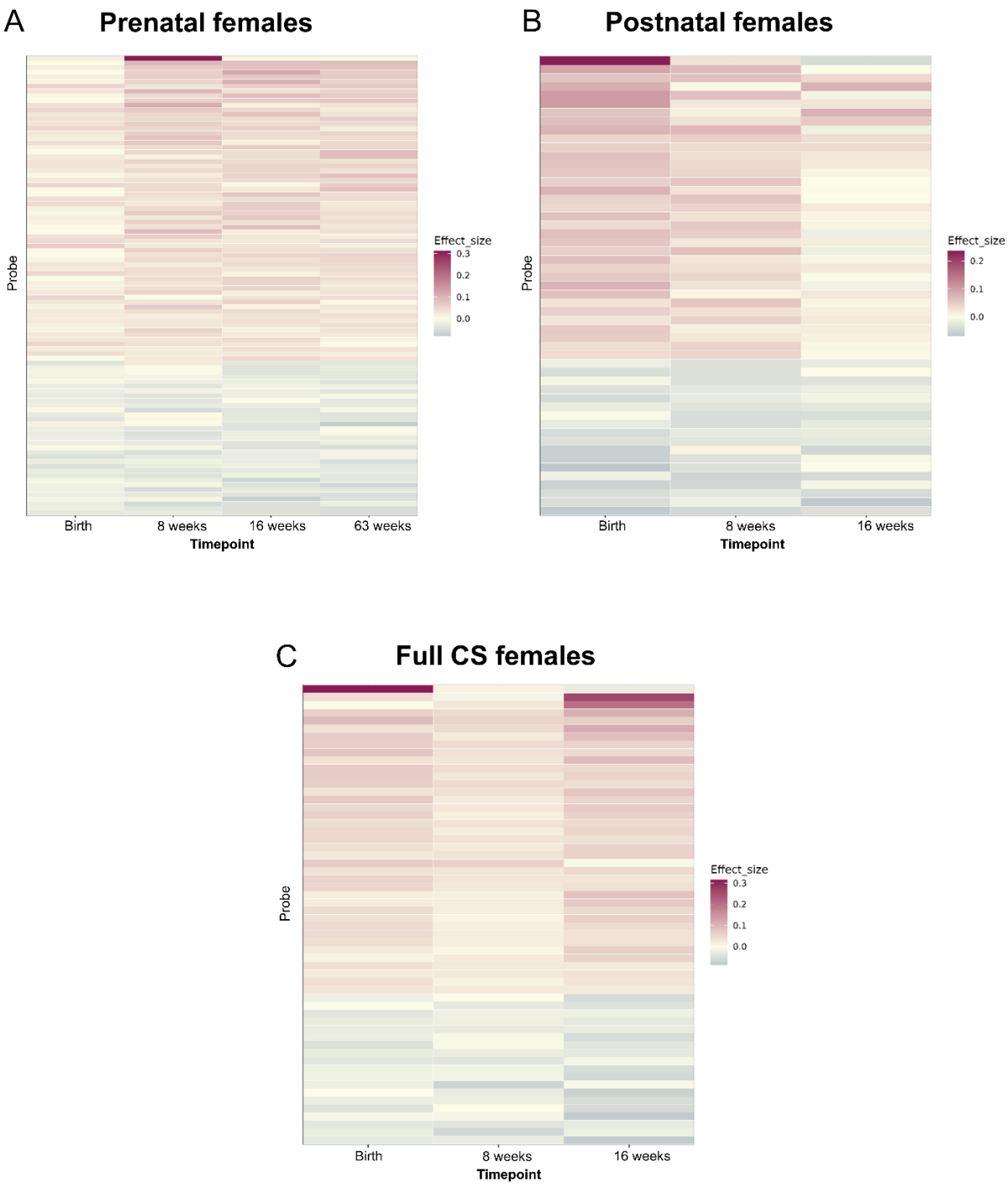

Figure 4. 11: Longitudinal DNAm changes over time in females amongst autosomal CpGs, identified by limma.

(A) 98 CpGs are persistently altered across time following prenatal CS exposure in female offspring lung autosomes (B) 53 CpGs are persistently altered across time following postnatal CS exposure in female offspring lung autosomes (C) 58 CpGs are persistently altered across time following full CS exposure in female offspring lung autosomes. Longitudinal DNAm changes were analyzed using linear regression, and controlling for the timepoint variable. CpGs were significantly altered across time at p < 1e-3 and effect size > 0.025.

In male offspring, 1492 (Figure 4.12A, Appendix 4.34), 1277 (Figure 4.12B, Appendix 4.35) and 59 (Figure 4.12C, Appendix 4.36) CpGs were consistently altered in the lungs of males exposed to prenatal, postnatal and full CS respectively. Interestingly, while in females, the DNAm differences between controls and CS-exposed groups showed no particular trends, we found a trend of increasing effect size magnitudes in males exposed to prenatal CS only or postnatal CS only, but not both (Figure 4.12), and these differences were the largest at 16 weeks of age.

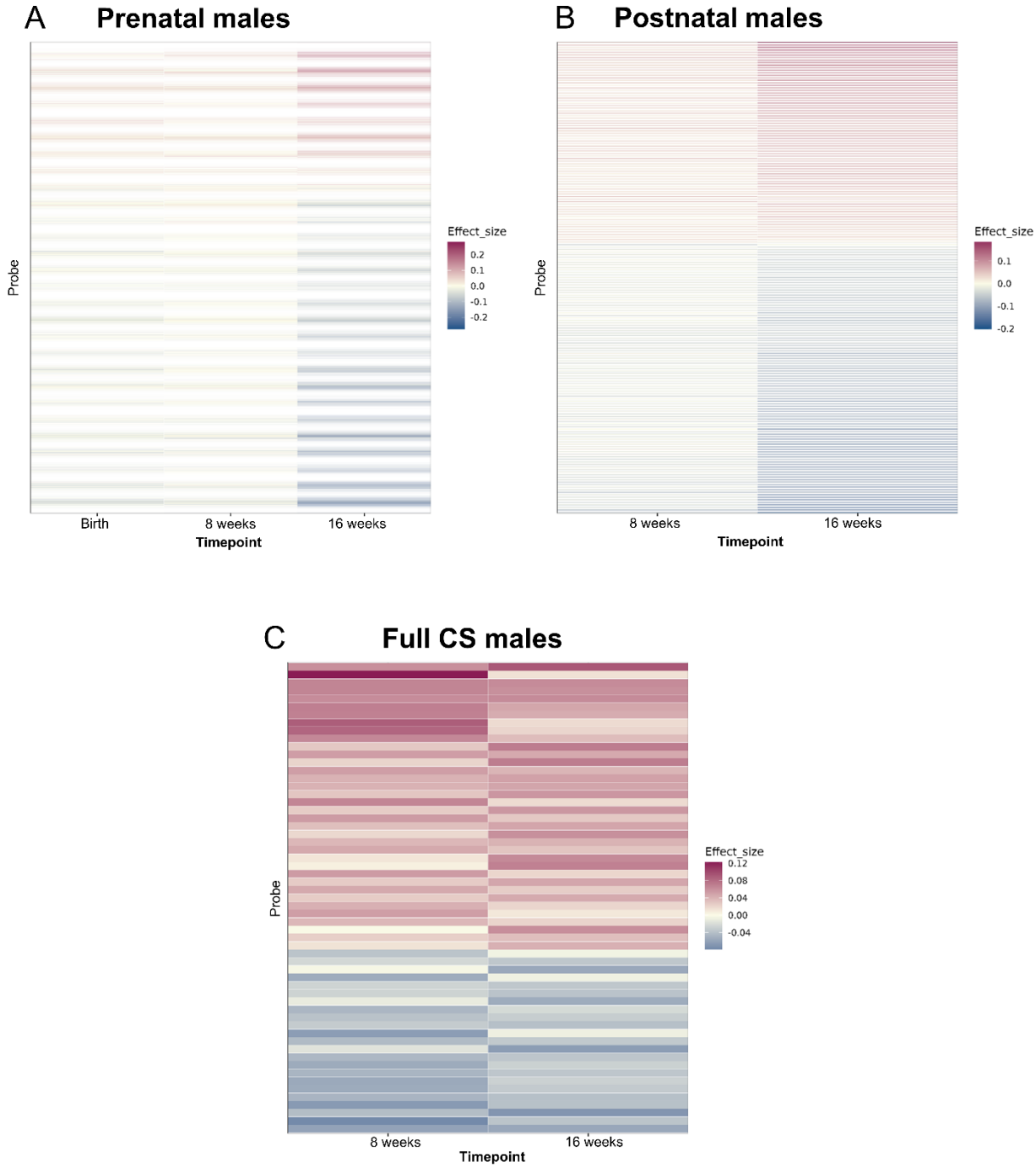

Figure 4. 12: Longitudinal DNAm changes over time in males amongst autosomal CpGs, identified by limma.

(A) 1492 CpGs are persistently altered across time following prenatal CS exposure in male offspring lung autosomes (B) 1277 CpGs are persistently altered across time following postnatal CS exposure in male offspring lung autosomes (C) 59 CpGs are persistently altered across time following full CS exposure in male offspring lung autosomes. Longitudinal DNAm changes were analyzed using Limma, and controlling for the timepoint variable. CpGs were significantly altered across time at $p < 1e\text{-}3$ and effect size > 0.025.

When we compared all significant persistently altered CpGs in males and female autosomes, we found that while there are some shared sites, different types of early life CS exposure persistently altered vastly different DNAm sites (Figure 4.13). Amongst these shared sites was cg38499186_TC21 mapping to the *Cers6* gene (Appendices 4.31 – 4.33), which was commonly persistently methylated across all female exposure groups (and was shown above to be differentially methylated across all female exposure groups in the blood at 8 weeks). Comparing males and females, we found one CpG (cg34890974_BC21) mapping to an unannotated gene to be commonly persistently methylated between male and female offspring exposed to prenatal CS only (Figure 4.13).

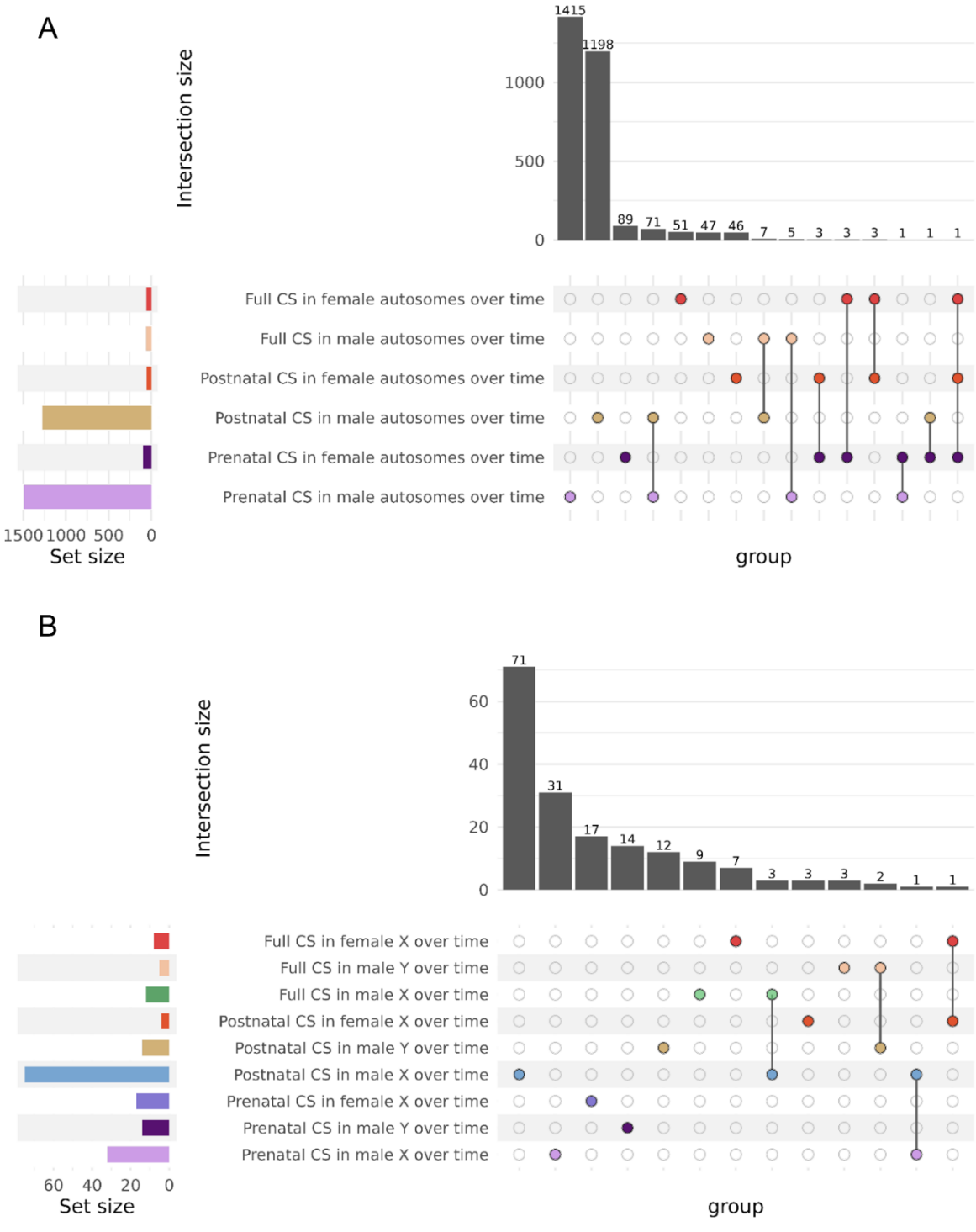

Figure 4. 13: Comparisons between CpGs differentially methylated across time (longitudinal analysis) following early life CS exposure.

(A) Upset plot showing distinct and common elements between CpGs persistently differentially methylated in autosomal probes (B) Upset plot showing distinct and common elements between CpGs persistently differentially methylated in sex chromosome probes

On the X chromosome in females, prenatal, postnatal or full CS exposure altered DNAm at 17 (Appendices 4.31 and 4.37), 4 (Appendices 4.32 and 4.37) and 8 (Appendices 4.33 and 4.37) CpGs respectively across time. Similar to the autosomes, males were more responsive to CS, as prenatal, postnatal or full CS exposure altered DNAm at 32 (Appendices 4.34 and 4.37), 75 (Appendices 4.35 and 4.37) and 12 (Appendices 4.36 and 4.37) CpGs on the X, and at 14 (Appendices 4.34 and 4.37), 14 (Appendices 4.35 and 4.37) and 5 (Appendices 4.36 and 4.37) CpGs on the Y chromosomes.

These analyses reveal novel sites in the lungs which are persistently altered by early life CS exposure. We also show that in males, the DNAm changes caused by prenatal CS exposure only or postnatal CS exposure only exhibit the greatest differences compared to controls at 16 weeks of age.

4.4.5. Effects of combined early and later life CS exposures on DNAm in offspring lungs

The results reported until now have been on the effects of early life CS exposure alone on DNAm in offspring blood and lungs. However, combined early and later life CS exposures lead to exacerbated health conditions when compared to CS exposure during one period alone. Therefore, the next step of our analyses was to measure the effects of combined early life and adulthood CS exposure on offspring DNAm, and compare the observed patterns to those we previously identified following early life CS exposure alone.

Given that only the control, prenatal and full early life CS groups were reexposed to CS in adulthood (and not the early postnatal CS group due to limited sample size), we sought to answer two questions: (1) Compared to CS exposure in adulthood alone, what are the effects of combined *prenatal* and adulthood CS on DNAm in offspring lungs?, and (2)

Compared to CS exposure in adulthood alone, what are the effects of a combination of early life *full* CS and adulthood CS on DNAm in offspring lungs?

We found that compared to offspring exposed to CS in adulthood alone, combined prenatal and adulthood CS exposure altered DNAm at 304 autosomal CpGs (204 lower and 100 higher) and at 5 X chromosome (1 lower and 4 higher) CpGs (Figures 4.14A and 4.14B, Appendix 4.38). To understand how combined prenatal and adulthood CS exposures may impact biological processes, we conducted gene ontology analyses on genes associated with the 304 significant autosomal CpGs. The analysis identified 20 biological processes that met the FDR cutoff of 0.05 (Appendix 4.39). Notably, the primarily affected pathways were related to the regulation of developmental processes.

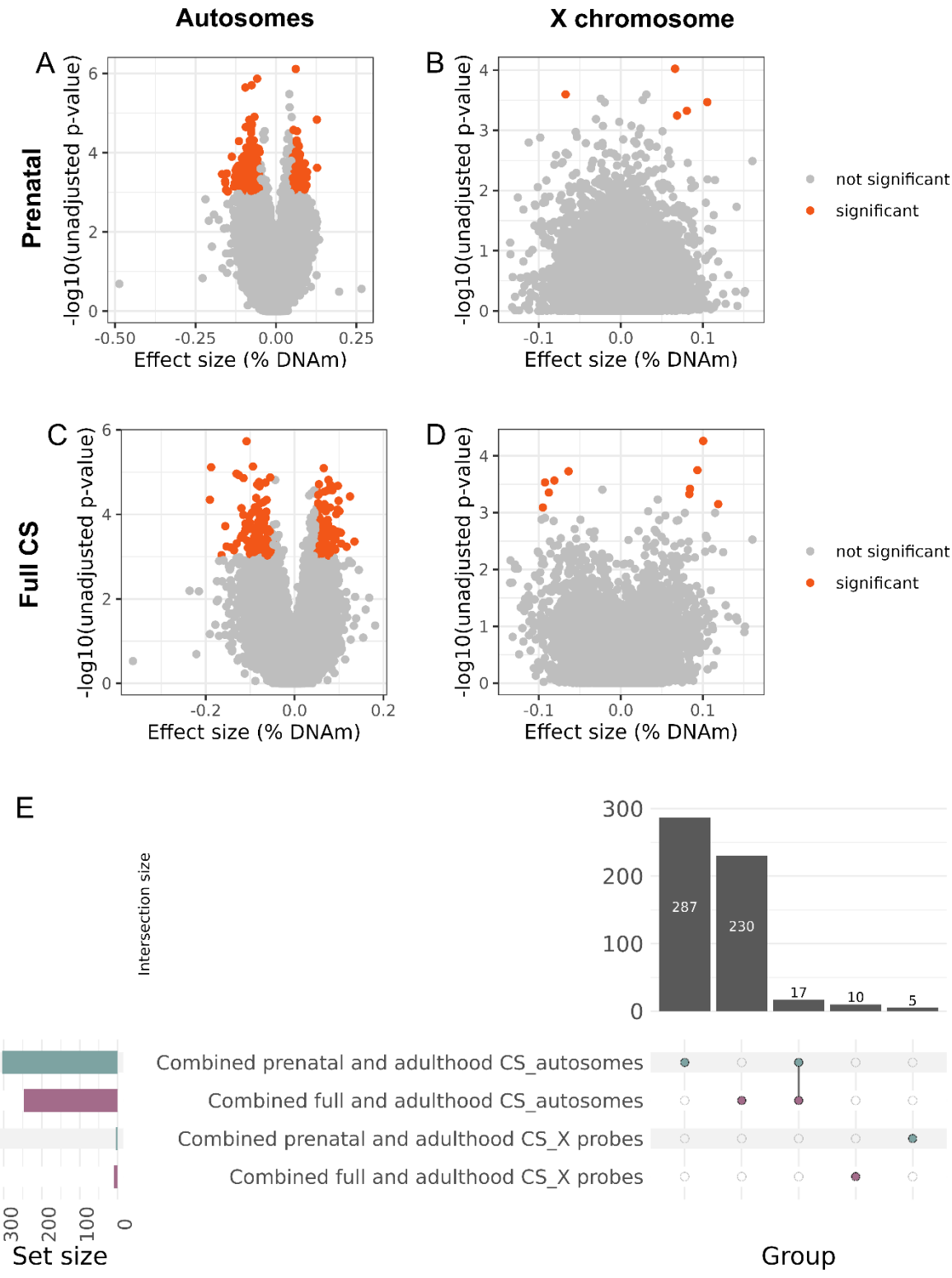

Figure 4. 14: Differentially methylated CpGs at 63 weeks in offspring exposed to combined early and later life CS, compared to singular CS exposure.

(A) 304 CpGs (100 higher, 204 lower) were differentially methylated in the lung autosomes of female offspring exposed to combined prenatal and adulthood CS (B) 5 CpGs (4 higher, 1 lower) were differentially methylated in the lung X chromosome probes of female offspring exposed to combined prenatal and adulthood CS (C) 247 CpGs (140 higher, 107 lower) were differentially methylated in the lung autosomes of female offspring exposed to combined full and adulthood CS (D) 10 CpGs (5 higher, 5 lower) were differentially methylated in the lung X chromosome probes of female offspring exposed to combined full and adulthood CS (E) Upset plot showing distinct and commonly differentially methylated CpGs across combined prenatal and adulthood versus combined full and adulthood comparisons. DNAm differences were determined using linear regression, and CpGs were considered differentially methylated at $p < 10e\text{-}3$ and effect size > 0.05. Effect size was calculated by finding the mean difference between beta values of re-exposed and non re-exposed offspring. N = 3-4 per group.

The number of differentially methylated autosomal sites in offspring exposed to a combination of full early life CS and adulthood CS was slightly lower than the number of altered sites in mice exposed to combined prenatal and adulthood CS, as 247 autosomal CpGs (140 of which were higher and 107 of which were lower) and 10 CpGs on the X chromosome (5 higher, 5 lower) were altered (Figures 4.14C and 4.14D, Appendix 4.40). Gene ontology analyses on the significant autosomal CpGs revealed 20 affected biological pathways, most of which were essential for cellular transport, communication and localization (Appendix 4.41).

When we compared the differentially methylated CpGs following combined prenatal and adulthood CS versus combined full and adulthood CS exposures to find common patterns, we found 17 commonly altered CpGs, while most were distinct to each group (Figure 4.14E). This is an unexpectedly small number of common CpGs given that offspring with combined prenatal and adulthood CS and those with combined full and adulthood CS were both exposed to prenatal CS and should have more similar patterns. These 17 common CpGs therefore represent CpGs which are specific to prenatal CS exposure.

Together, these results report differential DNAm patterns in lungs of offspring with combined prenatal and later life CS and in offspring with combined full and later life CS exposure. They also reveal that the number of differentially methylated sites in current smokers with prenatal CS exposure exceeds those of current smokers exposed to CS prenatally and in the early postnatal period.

4.4.6 Evidence of epigenetic priming in offspring lungs following combined early and later life CS exposures

The previous paragraph compared DNAm patterns in current smokers exposed to prenatal CS versus current smokers exposed to full early life CS. However, given the lack of research into DNAm patterns underlying priming in mammals, our next step was to determine whether epigenetic priming occurs in mice following CS exposure. To achieve this, we performed step-wise comparisons in the following order: 1) First, we identified CpGs which are differentially methylated following exposure to CS in adulthood alone, by comparing early life control offspring with no later life CS exposure to early life controls which were exposed to CS in adulthood; 2) Next, we compared offspring exposed to full early life CS alone to those exposed to combined full and adulthood CS exposures. This comparison gave us the CpGs which are differentially methylated following combined early and later life CS. To show epigenetic priming, we expect the number of differentially methylated CpGs in offspring exposed to CS in adulthood alone to be lower than the number of altered CpGs in offspring exposed to both early life and adulthood CS.

Our analyses revealed 40 autosomal CpGs (of which 20 had lower DNAm while 20 had higher DNAm) and 11 CpGs on the X chromosome (5 CpG sites with lower DNAm and 6 CpG sites with higher DNAm) were differentially methylated by CS exposure in adulthood alone (Figure 4.15, Appendix 4.42). Pathways which were involved in regulation and maintenance of transmembrane transporter complexes were the most affected by CS exposure in adulthood (Appendix 4.43).

In offspring with combined early and later life CS, we found that the number of differentially methylated CpGs was significantly higher than in adulthood CS exposure alone,

with 291 autosomal CpGs (179 lower, 112 higher) and 13 X chromosome CpGs (4 lower, 9 higher) differentially methylated (Figure 4.15, Appendix 4.44).

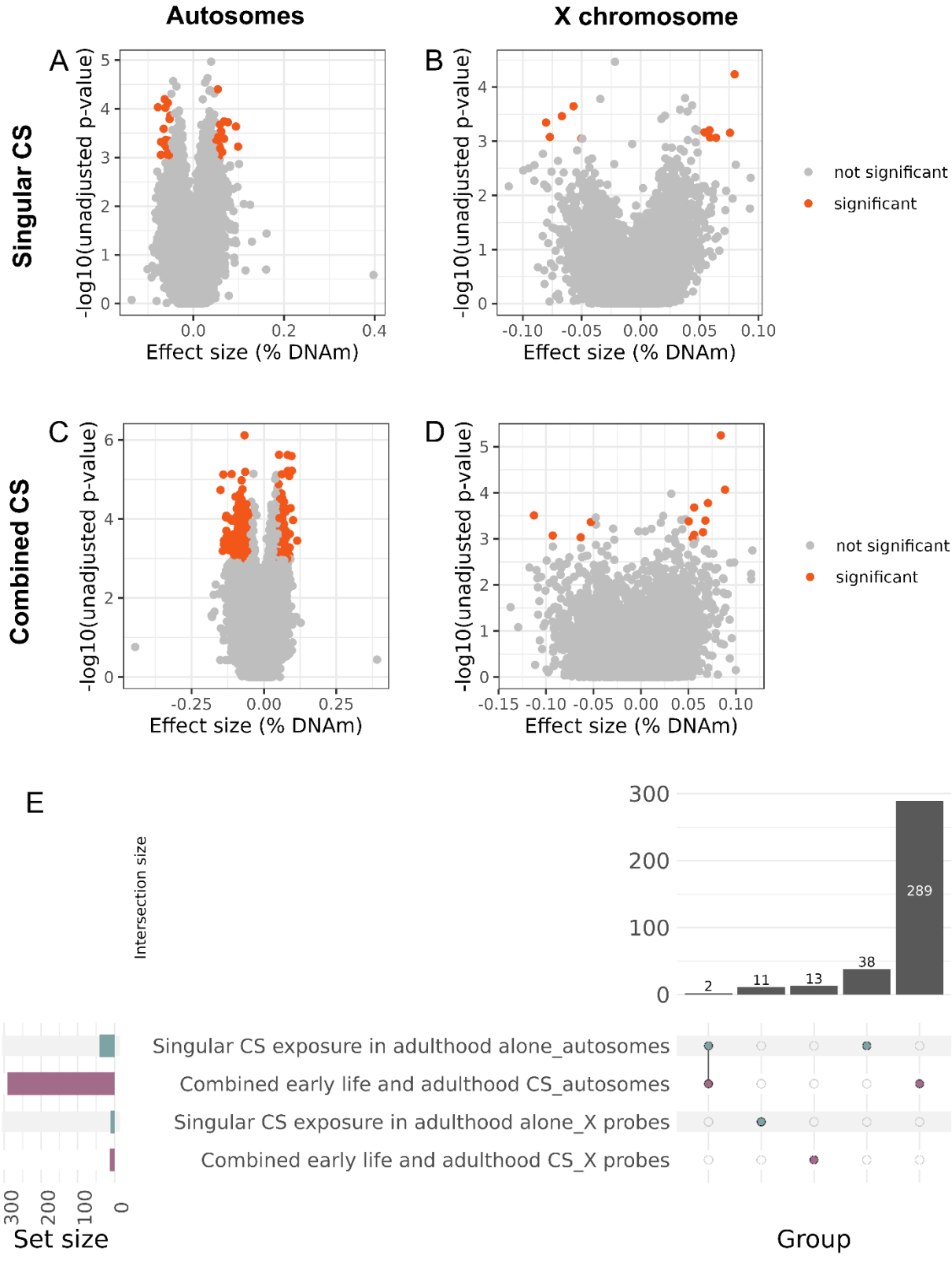

Figure 4. 15: Evidence of epigenetic priming in female offspring lungs following CS exposure.

CS exposure in adulthood alone led to differential DNAm at (A) 40 CpGs (20 higher, 20 lower) in the lung autosomes, and (B) 11 CpGs (6 higher, 5 lower) in the lung X chromosome probes. Combined early life and adulthood CS exposures led to differential DNAm at (C) 291 CpGs (112 higher, 179 lower) in the lung autosomes, and (D) 13 CpGs (9 higher, 4 lower) in the lung X chromosome probes (E) Upset plot showing distinct and commonly differentially methylated CpGs across adulthood vs combined CS comparisons. DNAm differences were determined using linear regression, and CpGs were considered differentially methylated at $p < 10e-3$ and effect size > 0.05. Effect size was calculated by finding the mean difference between beta values of re-exposed and non re-exposed offspring. N = 3-4 per group.

These results show that DNAm is associated with priming following CS exposure, as the number of differentially methylated CpGs after later life CS exposure was less that after combined early and later life CS. Additionally, these differentially methylated CpGs are mostly distinct to its corresponding early life group, with very minimal overlaps.

4.5 Discussion

Maternal smoking has been shown to negatively impact offspring lung function and lead to the development of restrictive and obstructive lung defects from birth until adulthood[506,522,523]. While some studies suggest sex-specific effects of early life CS exposure[311,508,510,524–527], these have mostly focused on non-lung tissues and could not completely isolate prenatal from early postnatal CS exposure, examining single timepoints rather than longitudinal effects. In addition, while maternal smoking alone is detrimental to offspring, there is evidence that additional CS exposure in adulthood may increase the likelihood of developing lung function deficits[308,514,516]. At the cellular level, these synergistic effects can be explained by priming, where initial contact with a stressor creates lasting memories which persist over time, such that subsequent exposures create different or exacerbated responses[300,528]. However, the molecular mechanisms underlying these exacerbated health outcomes following repeated CS exposure in mammals are unknown. To bridge these gaps, this study employs a well-established mouse model that distinguishes between prenatal and early postnatal CS exposure to identify DNAm sites in the lungs associated with early life CS exposure, and to track these DNAm changes across the lifespan. Furthermore, it seeks to determine whether DNAm is associated with priming in mice by examining how additional CS exposure in adulthood alters DNAm set by early life CS exposure. To our knowledge, this is the first study investigating the effects of both timing and

duration of early life CS exposure on lung DNAm patterns of offspring at multiple points throughout life, followed up to late adulthood (63 weeks of age). We are also the first to identify DNAm signatures underlying combined early and later life CS exposures in a murine model.

Previous research indicates that males, at birth, are at higher risk for airway diseases like asthma due to factors such as delayed surfactant production[311,312] and presence of larger but fewer airways [529,530] compared to females. As individuals age, these differences diminish, with female lung efficiency decreasing at puberty[315], but as midlife approaches, male lung function begins to decline more rapidly than females[531,532]. Given these inherent physiological distinctions, it follows that environmental factors may produce sex-specific effects. As epigenetic mechanisms like DNAm can provide insights into the molecular basis of sex-specific lung function differences, we analyzed DNAm in the lungs of early life CS-exposed offspring to uncover these molecular patterns.

Our results show sex-specific DNAm alterations following CS exposure with males being more sensitive to CS than females both at individual timepoints and across the lifespan. This corroborates previous reports[311,312,531,532] as well as our previous lung function findings which showed that males exposed to early life CS developed worse lung function outcomes overall than females[335]. This sex-specific trend also revealed interesting patterns: DNAm changes associated with prenatal CS exposure were more abundant and in males at birth, sex differences normalized at 8 weeks but at 16 weeks, reverted to earlier patterns indicated by more abundant and more pronounced DNAm differences. This normalization at 8 weeks (which corresponds to puberty in humans) may corroborate previous reports that male lung function normalizes and even surpasses females in adolescence, likely due to hormonal influence[315]. The trend also corroborates our lung function results which showed

that the effects of early life CS exposure on offspring lung function at 8 weeks was present but not significant (Appendix 4.45), while the most significant alterations in lung function occurred at 16 weeks of age in male offspring[335]. It was interesting to note that our previous reports of larger lung function differences in male lungs at 16 weeks[335] compared to the 8-week timepoint match the observed pattern of larger and more abundant DNAm differences in male lungs at 16 weeks in the present study. The developmental mismatch hypothesis can explain why males exposed to prenatal or postnatal CS, but not both, showed the greatest DNAm differences at 16 weeks[295,297]. As it relates to this study, the hypothesis suggests that offspring exposed to CS *in utero* and then raised in a smoke-free environment, or vice versa, develop different lung function and DNAm patterns compared to those consistently exposed to CS. These findings highlight sex-based differences in response to early life CS and imply that adult males may be more prone to developing altered phenotypes due to mismatches in their early life environment compared to females. The reason for this may stem from our focus on lung-specific DNAm patterns. As previously mentioned, there are pre-existing sex-specific differences in lung physiology, particularly during development, with male lungs being at a disadvantage. Consequently, environmental mismatches during this sensitive developmental period are likely to further accentuate these differences. Although the smaller sample size of males at 16 weeks compared to females might suggest that the greater number of altered DNAm sites in prenatal or postnatal CS males is due to sample size, this is unlikely. Our sensitivity analyses on a reduced number of female lung samples at 16 weeks showed a much smaller number of differentially methylated CpGs than age-matched males, supporting that the observed DNAm differences in males at 16 weeks are real, and are not simply inflated due to sample size.

Our analysis revealed distinct DNAm changes at each timepoint for offspring exposed to prenatal, postnatal, or full CS, with minimal overlap between tissues. Given that blood is a commonly used surrogate for other tissues due to its ease of accessibility, it is crucial to determine the extent to which DNAm alterations in lungs are reflected in the blood. We found 2 CpGs to be commonly altered between blood and lungs following early life CS. One, mapping to the *Cers6* gene, showed differential DNAm in all female CS groups in both tissues. Prior research has shown that following smoke exposure, ceramides are released from the lungs, contributing to respiratory dysfunction and metabolic disruption in smokers[533–535]. However, prior to this research, there was no prior evidence that maternal smoking affects offspring ceramide levels. The identification of a differentially methylated CpG within the *Cers6* gene in female offspring exposed to CS in early life therefore, could be a marker for respiratory and metabolic dysfunction and this gene can be investigated further as a marker for such dysfunctions in females exposed to CS in early life. The second shared CpG *Hepacam2*, differentially methylated in female offspring exposed to prenatal CS only, encodes an immunoglobulin-like protein which mediates cell-cell adhesion and is often silenced in some tumors[536,537]. While a past study reported increased *HEPACAM2* expression in peripheral leucocytes of former smokers[537], our study further identifies that *in utero* smoke exposure can also affect this gene, narrowing down the period of susceptibility to the prenatal period. The fact that only *Cers6* and *Hepacam2* were common between both tissues in this study, and observed in only females, speaks to the uniqueness of DNAm patterns following CS exposure. This finding is not entirely unexpected, given that DNAm is known to be tissue-specific[234–236]. However, it serves as a crucial reminder for researchers using blood as a surrogate tissue to exercise caution, as it may not accurately reflect the DNAm patterns in other tissues.

While singular exposure to CS is detrimental to health, combined early and later life CS exposures have synergistic health outcomes such that individuals with combined early and later life exposures experience worse outcomes than those exposed to environmental stressors during a singular period[300,528]. At the cellular level, these synergistic effects can be explained by priming[300,528]. While priming is a well-known mechanism in plants[517,518,538–540], evidence of priming in mammals is limited[306–309] and there has been no prior research exploring the molecular basis of priming in mammals. In our study, we found that early life exposure to CS alone results in DNAm changes at fewer CpGs compared to repeated exposures, suggesting that DNAm is linked to priming in mice after CS exposure, and that DNAm differences might be responsible for the heightened lung alterations we observed after repeated CS exposures in our previous study[335].

Having established that DNAm is associated with priming in mice following CS exposure, we sought to determine the effects of varying durations of early life CS on lung DNAm following secondary CS exposure: that is, what are the differences in DNAm patterns in individuals exposed to both prenatal and adulthood CS, versus those exposed to both full and adulthood CS?. While it was initially surprising that current smokers exposed to prenatal CS only had a greater number of differentially methylated CpGs than current smokers with full early life CS exposure, it extends our previously reported lung function results[335] that following early life CS exposure alone, lung function defects are greatest in prenatal CS followed by full CS females. The biological pathways altered by combined prenatal and adulthood CS compared to combined full and adulthood CS were also extremely different. Processes majorly affected in offspring exposed to combined prenatal and adulthood CS were related to development, aligning with previous findings that highlight the prenatal period as crucial for important developmental processes[258–261]. On the other hand, the majorly

affected pathways in offspring exposed to combined full and adulthood CS were related to cellular transport, communication and localization. The differences in affected pathways between these exposures can possibly be attributed to the developmental mismatch hypothesis as explained above. In our prior study, we demonstrated developmental mismatch by revealing contrasting DNAm changes in *Cyp1a1* between offspring exposed to prenatal versus full CS[335]. Our current findings extend these differences from DNAm to observable traits in form of altered biological processes. Another important observation is that the continual identification of developmental pathways in adult offspring initially exposed to CS in early life, underscores the persistence of DNAm patterns established by early-life CS exposure, as shown in the previous paragraphs. However, our study is the first to show that these enduring DNAm alterations set by early life CS persist even after a secondary exposure to CS in adulthood.

To further emphasize the uniqueness of DNAm patterns resulting from combined prenatal and adulthood CS exposure compared to combined full versus adulthood CS exposure, our analysis revealed only 17 differentially methylated CpGs shared between both groups. Despite the scarcity of common CpGs in this study, we remain confident in our findings because our results are consistent with previous reports indicating that CS exposure during different developmental periods produces varying effects[287–290,335,511]. Our 17 shared CpGs are important as they represent specific DNAm changes associated with prenatal CS exposure that last into adulthood. Interestingly, only 5 out of 17 of these CpGs have been previously linked to smoking. The five genes previously associated with CS exposure in the past are: 1) *Aire* (Autoimmune regulator) whose variants are known to increase the risk of rheumatoid arthritis among smokers[541], and whose DNAm and expression patterns can distinguish between low and high intensity smokers[542]; 2) *Sept9* (Septin 9) which is highly

methylated in smokers compared to nonsmokers[543]; 3) *Fbxl17* (F-box and leucine-rich repeat protein 17), whose SNPs may mediate the potential to quit smoking[544]; 4) *Cp* (Ceruloplasmin), which has been shown to increase the risk of developing atherosclerosis and cardiovascular disease in smokers[545,546]; 5) *Kazn* (kazrin, periplakin interacting protein), which is a reliable biomarker for frequent asthma exacerbation in smokers[547]. As mentioned earlier, these five genes have been associated with current smoking, but none of them have specifically been linked to long lasting effects of prenatal CS exposure. Our discovery that these genes are specific to prenatal CS exposure raises the question of whether individuals in previous studies where these genes were identified might have been exposed to prenatal CS, either directly or indirectly through secondhand smoke. This is an important consideration given that smoking rates were higher in the past when these adults were younger. Therefore, it is highly probable that many current smokers may have had some level of prenatal CS exposure, which could remain unreported due to challenges in accurately tracking environmental exposures in humans.

Unlike the five genes discussed in the previous paragraph, 12 of the 17 prenatal CS-specific genes which we identified in this study have never been previously associated with any form of smoking, and the nine which are annotated are: 1) *Lrrc16a* or *Carmil1* (capping protein regulator and myosin 1 linker 1), which plays critical roles in cellular development, differentiation, and disease, and in regulation of actin assembly, which is important to actin motility[548]. *Carmil1* is also involved in the development of atrial fibrilation and rheumatoid arthritis[549]; 2) *Tpbpb* (trophoblast specific protein beta), which is enriched in the junctional zone of the mouse placenta[550,551]; 3) *Cbx5* (Chromobox 5), which is involved in the development of lung fibrosis and lung cancer[552,553]; 4) *Amer3* (APC membrane recruitment 3), whose DNAm patterns mediate polyaromatic hydrocarbon-associated fasting plasma

glucose reduction in nonsmokers; 5) *Ralgps1* (Ral GEF with PH domain and SH3 binding motif 1) which mediates guanyl-nucleotide exchange factor activity and signal transduction[554]; 6) *Pglyrp4* (peptidoglycan recognition protein 4) whose polymorphisms have been associated with Parkinson's disease[555,556]; 7) *Rfc5* (replication factor C (activator 1) 5) which is a prognostic biomarker for lung cancer[557]. *RFC* complexes also function as checkpoints in DNA replication to mitigate DNA damage[558]; 8) *Auts2* (autism susceptibility candidate 2), a gene which has severally been implicated in the development and advancement of neurodegenerative disorders such as autism and schizophrenia[559,560]; and 9) *Tmem218* (transmembrane protein 218) which has been implicated in the development of syndromic ciliopathies like Joubert and Meckel syndromes[561,562]. The fact that 71% of these prenatal CS-specific CpGs have never been previously associated with smoking underscores the novelty of our study in elucidating molecular mechanisms underlying prenatal CS exposure. These findings hold promise for human applications, offering a way to distinguish prenatal CS exposure from other periods, which is challenging in human studies.

Our study also identified novel genes which are associated with smoking in adulthood. Our comparison between early life controls exposed to CS in adulthood to early life controls with no adulthood CS exposure revealed 40 differentially methylated CpGs, and to our knowledge, 70% of these CpGs have not been associated with smoking in the past. Of the genes mapping to our 40 differentially methylated CpGs in adult smokers, 10 were found in a previous study to be differentially expressed in the peripheral blood monocytes of smokers with COPD[563]. Out of 10,583 differentially expressed genes identified in the study, the 10 which corresponded to our differentially methylated sites are: *Gria1, Gprc5c, Hoxc9, Nfasc, Ntsr1, Slc44a5, Dpp6, Mical2, Tenm3,* and *Gnao1.* The high level of correlation between our study and theirs, despite the different species and tissues in both studies, may be due to the

fact that the age of smoke exposure is similar: they measured differential expression in human blood at an average of 50 years (midlife)[563,564], while we measured differential DNAm at about 63 weeks in mice, corresponding to midlife in humans. In addition to these 10 genes, two others from our study have been previously linked to smoking: *Rbfox3* which whose DNAm levels were lower in small airway epithelia of smokers compared to nonsmokers[565], and *Pik3cd*, whose differential DNAm and expression has been shown to increase susceptibility to COPD in smokers[566]. These 12 genes which have been previously associated with smoking, along with the other 28 which are novel, are important as they offer insights into mechanisms underlying detrimental health outcomes following smoking in midlife. We also compared these 40 CpGs with differentially methylated CpGs from our previous study which measured DNAm in female dams exposed to CS in adulthood[334]. These dams from the previous study are the dams which gave rise to the offspring being reported in the present study. However, none of the differentially methylated CpGs from the dams overlapped with CpGs from the offspring. This lack of overlap is likely due to the different ages and/or duration/intensities (pack years) of smoking. Dams were exposed to whole body CS for 9 weeks, ending at about 18 weeks of age[334], while early life control offspring were exposed to whole body CS for 3 weeks, ending at about 63 weeks of age. These results are interesting but not completely surprising, since there is evidence that different ages and pack years of smoking yield varying molecular and physiological outcomes[567–571].

A limitation to our study is our small sample size which makes it difficult to detect smaller DNAm differences. To mitigate this and increase our accuracy in identifying actual DNAm differences, we used a high effect size cutoff, but further studies with larger sample sizes are needed to compare to ours. In addition, we could not measure the effects of early postnatal CS exposure combined with CS exposure in adulthood, as we did not have

sufficient samples in the early life postnatal CS group. It is important for future studies to investigate this combination as it could reveal interesting patterns which can offer further insights into how timing of early life CS exposure can affect DNAm. Another possible limitation is our inability to extend the male timepoint to 63 weeks due to insufficient male offspring, making it impossible to determine DNAm patterns in late adulthood in males. Other studies comparing DNAm in males and females with combined CS exposures in late adulthood would provide insights into similarities and differences.

This study marks the first comprehensive analysis of early life CS exposure effects on offspring DNAm across multiple timepoints in the lungs. We identify numerous known and novel DNAm sites altered by early life CS at individual timepoints and across the lifespan, showcasing distinct sex-specific patterns with heightened male responsiveness. Our study also explores how additional CS exposure in adulthood modifies these DNAm patterns established in early life, revealing how these patterns vary with different durations of early life CS. We also show for the first time that DNAm may be associated with priming in mice following combined CS exposure and identify novel CpGs specific to prenatal CS and midlife smoking. These findings lay a crucial foundation for future studies investigating early life CS-induced health alterations, emphasizing the necessity of sex-tailored interventions, lung-specific studies, and differentiation of prenatal and postnatal CS exposures. Given the prevalence of repeated CS exposures in humans, further research, particularly into other epigenetic mechanisms like histone modifications, is warranted to validate and expand upon these findings.

Chapter 5: Discussion

5.1 Summary

In this research, we established a mouse model which we used to study the effects of early life cigarette smoke exposure on offspring phenotypic and molecular outcomes. We used this model to answer numerous questions which have not previously been addressed in literature. Foremost is the fact that most of the past research on the effects of early life cigarette smoke exposure on offspring outcomes does not account for potential effects of early postnatal and secondhand cigarette smoke exposure, which may impact results. These types of early life exposures are difficult to disentangle in human studies due to the complex nature of the human environment, emphasizing the need for a smaller model organism with controlled environment to examine the distinctions. Our mouse model was created to completely isolate prenatal cigarette smoke exposure from early postnatal cigarette smoke exposure (cigarette smoke exposure during lactation), and also study the effects of combined prenatal and early postnatal (full) cigarette smoke. Our results revealed distinct DNAm patterns established by cigarette smoke exposure during different developmental windows, and further revealed that the postnatal window is the most sensitive to the effects of cigarette smoke in male offspring, while female offspring are most sensitive to the effects of early life cigarette smoke during the prenatal window. Additionally, full cigarette smoke exposure was observed to confer tolerance to offspring, as it caused the least amount of lung function and DNAm alteration than other types of early life cigarette smoke. This result reveals distinct phenotypic outcomes following different durations and timing of early life cigarette smoke exposure and identifies critical periods in development where the effects of cigarette smoke exposure are greatest.

Next, we were interested in identifying DNAm signatures underlying the sex-specific outcomes which have been reported in previous studies following early life cigarette smoke exposure. Our analyses revealed that similar to previously reported lung function patterns, males are more sensitive than females to the effects of prenatal or postnatal cigarette smoke, but by adolescence their lung function and molecular patterns catch up and may surpass females, only to decline more rapidly than females in adulthood. These unique patterns across sexes emphasize the unique sex-specific DNAm and lung function changes which arise due to early life cigarette smoke exposure, indicating the need for sex-tailored interventions against the detrimental effects of cigarette smoke.

The next important objective was to uncover DNAm patterns underlying early life cigarette smoke exposure specifically in the lungs. This question is important, as most of the past research on early life cigarette smoke has been conducted in the blood and other readily available tissues and while they can be adequate surrogates, there is evidence that more closely impacted tissues (such as lungs and buccal cells in the case of smoking) may yield more targeted results[211,345]. When we compared DNAm between blood and lungs of offspring exposed to cigarette smoke in early life, we discovered that only 2 of hundreds of differentially methylated CpGs were common between blood and lungs, emphasizing the specificity of DNAm alterations between tissues. The differentially methylated CpGs which we identified therefore, provide potential lung-based biomarkers for early life cigarette smoke, and can be instrumental to the development of targeted interventions tailored to specific tissues.

Next, we determined how lung function and DNAm differences in offspring exposed to early life cigarette smoke compare with first-hand cigarette smoking in dams. This comparison is crucial as it has the potential to illuminate the underlying mechanisms that

account for the effects of cigarette smoke throughout the lifespan. Our results reveal that DNAm patterns of current smokers may not accurately reflect DNAm in individuals who were exposed to cigarette smoke early in life, as only 5% of our differentially methylated sites in current smoking dams were shared with offspring, and the direction of DNAm change were opposite in dams and offspring. These opposing patterns demonstrate how the route and length of cigarette smoke exposure influence DNAm and highlights the need for additional research to clarify the precise mechanisms responsible for the variances.

Finally, while singular early life exposure to cigarette smoke is detrimental to health, secondary exposure to cigarette smoke exacerbates detrimental health consequences, a concept known as *priming.* The concept of priming has been shown in COPD, as current smokers who were also exposed to cigarette smoke earlier in life show a higher susceptibility to developing COPD compared to nonsmoking individuals who were exposed to cigarette smoke early in life alone[513,514]. However, the molecular mechanisms underlying/driving priming are not well established in mammals, and this is important as it can provide candidates/targets which can be used to develop therapeutic interventions. Our finding that there were more differentially methylated sites following combined early and later life cigarette smoke exposures compared with later life cigarette smoke exposure alone demonstrated that priming extends to the molecular level in mice, and the increased number of differentially methylated sites corresponded to the exacerbated lung function decline in offspring with combined compared to singular cigarette smoke exposure. These findings are especially significant because a considerable number of adults today were exposed to cigarette smoke during their childhood, given the higher prevalence of cigarette smoking in previous decades. Consequently, our study potentially provides a more precise portrayal of the molecular makeup in these individuals.

Together, this research uncovers molecular mechanisms underlying cigarette smoke exposure during different periods in early life and matches them with lung function outcomes. We identified which periods are most sensitive to the development of health deficits following early life cigarette smoke exposure and revealed molecular signatures underlying the sex and tissue-specific patterns observed following early life cigarette smoke. We also identified for the first time that mouse lungs are subject to epigenetic priming following combined early and later life cigarette smoke exposure and revealed the DNAm patterns which may underlie the exacerbated phenotypes observed following these combined cigarette smoke exposures.

5.2 Prenatal versus early postnatal versus combined cigarette smoke: which window is most sensitive?

Before comparing the three types of early life cigarette smoke exposure investigated in this research, it is essential to consider their distinct characteristics. Offspring in the prenatal cigarette smoke group were indirectly exposed to cigarette smoke and its components/metabolites via the placenta. In contrast, postnatal cigarette smoke-exposed offspring encountered third-hand smoke through bedding, fur, and/or breastmilk from the cigarette smoke-exposed dams. These distinct exposure pathways may explain some of the variations in lung function and DNAm patterns observed in this study.

It is well known that prenatal cigarette smoke exposure is detrimental to offspring health, with these health complications lasting until adulthood[572,573]. Cigarette smoke exposure during early postnatal development (during lactation and breastfeeding) is also detrimental, as components of cigarette smoke like nicotine are readily available in breastmilk[330,574]. The effects of prenatal and postnatal cigarette smoke exposure on offspring health, however, are very different[287–289,335,511]: in general, literature suggests that prenatal

cigarette smoke exposure alone is associated with an increased risk of offspring developing asthma and chronic bronchitis[512], while postnatal cigarette smoke exposure is more strongly associated with development of allergies and upper respiratory infections[511,512]. Additionally, though maternal smoking during pregnancy significantly contributes to adverse postnatal outcomes, its negative impact can be compounded when combined with smoking during lactation[288,330].

While these patterns are interesting, the question of whether the prenatal or early postnatal window is more sensitive to the effects of cigarette smoke remains unanswered. This is largely because there are very few studies which directly compare both types of exposure, since human studies cannot completely separate them. In this project, we can infer what window is most sensitive to cigarette smoke by examining the magnitude of lung function differences and the number of differentially methylated CpGs compared to controls. Our lung function results (measured 13 weeks after smoking cessation) indicate that males exposed solely to postnatal cigarette smoke exhibited the highest sensitivity to methacholine (and hence the greatest airway hyperresponsiveness), followed by those exposed to full cigarette smoke and then prenatal cigarette smoke. Conversely, in females, prenatal cigarette smoke exposure produced the greatest response to methacholine, followed by full cigarette smoke, and then postnatal cigarette smoke exposure. These sex-specific lung function differences following early life cigarette smoke exposure may be attributed to the inherent differences in lung development between sexes. It can be inferred that since male lung development progresses more slowly during development compared to females[575,576], a greater proportion of these developmental processes in the lungs occurs during the early postnatal period for males, heightening the vulnerability of males in the postnatal cigarette smoke group to worse lung function compared to males in the prenatal cigarette smoke

group. Conversely, it makes sense that prenatal females exhibit worse lung function than males, given that female lungs develop more rapidly during the prenatal window than male lungs. Our longitudinal DNAm analyses also supported the lung function results by showing that female offspring exposed to prenatal cigarette smoke had the greatest number of differentially methylated sites which persisted across the lifespan compared to other cigarette smoke groups. Our results corroborate results from a similar cross-fostering model to ours involving early life cigarette smoke exposure in rats, as they showed that females exposed to prenatal nicotine had the worst developmental and cognitive impairments compared to either postnatal only or full nicotine exposure, and compared to male offspring[577].

In both sexes, offspring with full cigarette smoke exposure had better lung function than postnatal males and prenatal females. In addition, longitudinal DNAm analysis revealed much smaller numbers of differentially methylated CpGs in fully exposed male and female offspring than offspring with either prenatal or postnatal cigarette smoke exposure. These findings indicate that contrary to previous literature, combined prenatal and early postnatal cigarette smoke exposure may confer some sort of adaptation on offspring lung function compared to cigarette smoke exposure during either window. This pattern is suggestive of a theory called the *thrifty phenotype* hypothesis, which surmises that offspring exposed to adversities early in development develop characteristics which help them adapt better to limited resources in their postnatal environments[489,490]. In relation to our study, it may be inferred that offspring exposed to full cigarette smoke would optimize their lung function to better adapt to their postnatal environment as opposed to offspring with shorter durations of cigarette smoke exposure. The thrifty phenotype hypothesis emerged as an explanation for the link between poor fetal and infant growth and the increased likelihood of developing

impaired glucose tolerance and metabolic syndrome later in adulthood[489]. However, our study is the first to associate it with early life cigarette smoke exposure.

5.3 Sex-specificity of results

Males have a higher likelihood of developing asthma and lung function impairments in early life compared to females of the same age. The most common explanation for this phenomenon revolves around differences in crucial lung developmental processes, such as surfactant synthesis which begins later in development in males[311,312] and presence of larger but fewer airways in males [529,530]. Consequently, female lungs may exhibit a heightened resilience to early-life environmental insults in contrast to age-matched males. As puberty ensues, male lung function gradually surpasses that of females, likely due to hormonal changes[315], but as midlife approaches, male lung function begins to decline more rapidly than females, and this decline is potentiated by smoking[531,532]. In this research, lung function was measured at 8 and 16 weeks (corresponding to adolescence and early adulthood respectively in mice) and so, it is impossible to tell what earlier patterns looked like. However, our observed lung function decline at 16 weeks compared to lung function at 8 weeks, especially in males, suggests that earlier life patterns may reappear in the lungs of male mice and supports previous reports that male lung function declines faster than females.

These sex-specific differences in lung function may be attributed to sex-specific molecular effects of early life cigarette smoke exposure on offspring lungs. To this end, our DNAm analyses provide perhaps one of the most compelling pieces of evidence for sex-specific DNAm differences following early life cigarette smoke. At *Cyp1a1*, while DNAm in the lungs of male offspring exposed to any type of early life cigarette smoke in early life remained similar to controls, DNAm was higher in cross-fostered females, and lower in fully exposed

females compared to controls. Epigenome-wide DNAm analyses also revealed sex-related differences, as at birth, males had a higher number of differentially methylated CpGs than females. The number of altered CpGs across both sexes evened out at 8 weeks of age (just past adolescence in mice), but by early adulthood (16 weeks of age), this number rose significantly once more in males, corroborating our lung function patterns at 16 weeks. Together, these results suggest that while male lungs are more sensitive than females to early life cigarette smoke at birth, they catch up to females in adolescence but decline in early adulthood, much like the lung function patterns discussed earlier[311,312,529,530]. In addition, similar to previous research, our study indicates a more rapid decline in male lung function during adulthood compared to females, albeit with an earlier onset (early adulthood) than previously reported (midlife)[531,532]. The earlier onset of lung function decline could potentially be a phenotype unique to mice, since we identified only one other mouse study that reported cigarette smoke exposure effects on lung function lasting until 15 weeks of age, although this study specifically involved *in utero* smoke exposure[312]. Interestingly, this study also highlighted that male offspring exposed *in utero* to secondhand smoke were more susceptible to developing lung function deficits, aligning with our observation of decreased lung function in adult males. This similarity between our findings and the previous study[312] despite differences in the type of cigarette smoke exposure, underscores the robustness of our results regarding rapid male lung function decline long before midlife compared to females. Therefore, this research reveals DNAm differences which may underlie lung function decline following early life cigarette smoke exposure, and reports for the first time, that lung function in male early adults is worse than females of the same age.

5.4 Tissue specificity of DNAm patterns following early life cigarette smoke

Epigenetic mechanisms, especially DNAm, demonstrate a small degree of uniformity across tissues while also displaying distinct patterns specific to cell types and tissues[234–236]. This phenomenon is not exclusive to humans, with similar patterns observed in mice[239,240] and rats[234,241,242]. Tissue-specific DNAm patterns suggest that exposure to environmental stressors may induce unique changes in each tissue. For instance, exposure to cigarette smoke during pregnancy decreases cord blood[243,244] and buccal cells[245] DNAm but increases placental and whole blood[246,247] DNAm in offspring. Considering these variations, it is crucial for DNAm studies to explore the impact of cigarette smoke exposures on DNAm in different tissues. As most of the past studies investigating the effects of early life cigarette smoke exposure have been conducted on tissues other than the lungs, we compared DNAm in the blood and lungs of offspring exposed to early life cigarette smoke at 8 weeks of age (5 weeks after the cessation of cigarette smoke exposure).

In our analyses, only 2 CpGs, mapping to *Cers6* and *Hepacam2* were commonly differentially methylated between both tissues. *Cers6* was altered in all 3 female early life cigarette smoke groups across both tissues. Following first-hand cigarette smoke exposure, ceramides are released from the lungs, contributing to respiratory dysfunction and metabolic disruption in smokers[533–535]. However, prior to this research, there was no evidence that maternal smoking affects offspring ceramide levels. The identification of a differentially methylated CpG within the *Cers6* gene in female offspring exposed to cigarette smoke in early life therefore, could be a marker for respiratory and metabolic dysfunction and this gene can be investigated further as a marker for such dysfunctions in females exposed to cigarette smoke in early life. The fact that *Cers6* was not commonly differentially methylated in male

offspring blood or lungs further emphasizes the fact that early life cigarette smoke exposure causes sex-specific DNAm alterations in offspring.

Hepacam2 on the other hand, was differentially methylated in the blood and lungs of female offspring exposed to prenatal cigarette smoke only, but not in other cigarette smoke groups. This gene encodes a protein that facilitates cell-cell adhesion and is frequently suppressed in certain tumors[536,537]. *HEPACAM2* expression has been shown to increase in human peripheral leukocytes of former smokers[537]. Our research extends this knowledge, revealing that prenatal cigarette smoke exposure also influences expression of this gene in females, pinpointing the susceptibility period to the prenatal window. Since this CpG within the *Hepacam2* gene is located within the gene body, the increase in *Hepacam2* DNAm in blood and lungs of prenatal cigarette smoke female offspring could therefore indicate increase in expression of the gene and in effect, tumor initiation/progression.

The fact that only these 2 genes out of hundreds of differentially methylated genes were common between both blood and lungs, and observed in only females, speaks to the uniqueness of DNAm patterns following cigarette smoke exposure. Since they are commonly differentially methylated between blood and lungs, these two genes could serve as diagnostic biomarkers for prenatal cigarette smoke exposure, particularly in human blood due to its accessibility. An epigenome-wide DNAm analysis in current smokers found that only about a third of the CpGs significantly altered in whole blood were also altered in the lungs of current smokers compared to never-smokers[211]. Cigarette smoke-induced DNAm changes in blood and buccal cells also revealed that DNAm sites in buccal cells were more effective in distinguishing 14 out of 15 epithelial cancer types[345]. On a similar note, comparisons of *AHRR* DNAm in the cord blood, placenta and buccal epithelia of offspring exposed to prenatal cigarette smoke[462] have revealed that though prenatal cigarette smoke decreases

AHRR DNAm in cord blood, corresponding *AHRR* DNAm in the placenta and buccal epithelia remain unchanged compared to control offspring[462]. These findings support our results showing a dearth of commonly altered DNAm patterns across tissues, and underscore the importance of considering tissue-specific differences in DNAm patterns following cigarette smoke exposure, as tissues directly exposed to cigarette smoke, such as lungs, buccal cells, and saliva, may exhibit more consistent effects of cigarette smoking on DNAm. Understanding these tissue-specific DNAm patterns not only enhances our ability to accurately assess the effects of environmental exposures, such as smoking, but also contributes to the development of targeted interventions and personalized medicine approaches tailored to specific tissues and cell types.

5.5 Comparison of lung DNAm patterns following personal smoking in adulthood and early life cigarette smoke exposure

When comparing personal smoking to early life cigarette smoke exposure, it is essential to recognize that the distinct routes of delivery inherent in both types of exposure may produce different impacts on the exposed individual. Cigarette smoke is composed of over 7000 components and measuring the effects of personal smoking on DNAm or other biological metrics would imply measuring the combined effects of all these components. However, not all these components have been proven to cross the placenta to the fetus. Therefore, in offspring exposed to cigarette smoke *in utero,* some of the components of cigarette smoke may not be present, making it plausible that comparisons between personal and maternal smoking would yield unique results.

To emphasize the distinctiveness of personal smoking and early life cigarette smoke exposure, only 2 CpGs were commonly differentially methylated between dams exposed to

direct cigarette smoke and all offspring groups, male and female. In total, only 5% (2 out of 40 CpGs) which were differentially methylated in dam lungs were also observed in lungs of offspring exposed to cigarette smoke in early life. The first was cg45830215_BC11 (mapping to *B3gnt3* and located within the gene body), which was increased in dam lungs, but decreased in lungs of male offspring exposed to prenatal only or full cigarette smoke at the 8 week timepoint. This gene codes for a protein that is involved in lymphocyte homing, trafficking and recirculation, the biosynthesis of L-selectin ligands and poly-N-acetyllactosamine chains[395,396]. In patients with lung adenocarcinoma, higher *B3gnt3* expression is correlated with increased immune cell infiltration and worse outcomes[397]; differential *B3gnt3* expression has also been linked to the development of multiple other cancer types[398–402]. The second, cg37214886_TC11 (mapping to *Asb18*), was also increased in dam lungs but decreased in the lungs of female offspring exposed to prenatal cigarette smoke at 63 weeks. *Asb18* has been associated with personal smoking, as differential expression at this gene may be involved in development of lung adenocarcinoma in smokers[390]. Therefore, differential DNAm in the dams and offspring in this study may indicate tumor initiation/development.

Therefore, increased *B3gnt3* and *Asb18* DNAm in the dams could indicate increased expression of the genes (since they are located within the gene body), resulting in outcomes such as increased immune cell infiltration into dam lungs, worse lung function and increased likelihood of tumor development. This aligns with ours and previous studies which have shown that personal smoking increases infiltration of immune cells into the lungs, alters lung function significantly and causes tumor initiation and progression[334,506,578–580]. Conversely, the decrease in *B3gnt3* and *Asb18* DNAm in lungs of offspring exposed to prenatal cigarette smoke or full early life cigarette smoke may be indicative of the opposite: increased tolerance

to and reduced sensitivity and response to foreign antigens by T cells. This result may indicate that offspring in these groups may develop adaptation to cigarette smoke exposure at these genes, and this is supported by the thrifty phenotype hypothesis[489,490], as explained in the previous section. Therefore, since developmental processes occur alongside cigarette smoke exposure, basic defense mechanisms may be adapted to these exposures, conferring tolerance to affected offspring which lasts till later in life. However, while the concept of adaptation is well established in studies investigating the link between poor fetal growth and the development of impaired glucose tolerance[489,490], this is the first study showing that early life cigarette smoke exposure can also confer adaptation to the exposed offspring.

The opposing direction of DNAm change in dams and offspring shown in previous paragraphs is interesting, as it may be an indicator as to different adaptation mechanisms employed to combat or adapt to cigarette smoke exposure at different points in development. Further research is needed to study other under-investigated cigarette smoke components, to determine which cross the placenta and which do not, as this will help determine which components are responsible for the vast DNAm differences following personal and maternal smoke exposures.

Similar to our results, a previous human study measured DNAm at over 450,000 CpGs in the blood of current smokers and individuals exposed to prenatal cigarette smoke[581]. This study revealed that while each exposure produced unique DNAm differences, approximately 30% of the significant CpGs in newborn blood (1709 of 5547 CpGs) were also observed in adults with a history of personal smoking[581]. This number (30%) is much higher than the number of shared sites in the present research (5%), likely due to the different reasons. First, they measured DNAm immediately after prenatal cigarette smoke or current smoking, while our shared sites between dams and pups were measured immediately after smoking in

dams, but after a period of smoking cessation in the offspring. Additionally, the tissues under investigation in our study and theirs are different: they compared DNAm in blood of current smokers and in fetal blood, both of which are indirectly affected by smoking. In our case however, we likely see less overlaps because we compared DNAm between lungs of current smokers which are directly exposed to cigarette smoke, and offspring lungs, which are exposed to cigarette smoke indirectly. However, as DNAm is tissue-specific, this result further emphasizes the need for future DNAm analyses to be conducted in the lungs. It is worth noting that one of the CpGs in their study which was commonly differentiated in blood of current smokers and prenatal cigarette smoke-exposed offspring, *B3GNT1L*[581]*,* is an isoform of one of our common CpGs *B3gnt3,* and this further corroborates the accuracy of our findings.

The absence of shared DNAm sites between postnatal cigarette smoke exposure and personal smoking, alongside the presence of shared sites between prenatal/full cigarette smoke exposure and personal smoking, can be attributed to the fact that offspring exposed to cigarette smoke *in utero* are separated from dam circulation by a placenta, and therefore in closer proximity to components of cigarette smoke for a longer duration, making them more likely to exhibit more similar DNAm patterns to the dams than offspring solely exposed to cigarette smoke via breastmilk. There are also marked differences in the chemical composition of postnatal third-hand smoke compared to firsthand smoke which could account for the lack of shared altered CpGs between smoke-exposed dms and postnatal cigarette smoke-exposed offspring[368,582]. This distinction underscores the significance of type, route and duration of exposure in shaping epigenetic responses and highlights the need for further research to elucidate the specific mechanisms underlying these differences.

An important consideration while making these comparisons is that all our research on personal smoking was conducted in pregnant females, therefore, caution should be taken in extending/comparing our findings to male or non-pregnant female smokers.

5.6 Evidence of priming in mice following combined early and later life cigarette smoke exposure

While early life exposure to cigarette smoke is detrimental to health, combined early and later life cigarette smoke exposures have synergistic health outcomes such that individuals with combined early and later life exposures experience worse outcomes than those exposed to environmental stressors during one period. This concept is illustrated in COPD, as current smokers who were also initially exposed to cigarette smoke earlier in life are more susceptible to developing COPD than non-smokers exposed to cigarette smoke in early life alone[513,514]. This phenomenon is explained by the concept of priming which suggests that environmental stressors create lasting "memories" in cells, leading to heightened reactions when exposed to the same stressors subsequently[300–302]. Priming is a well-established mechanism of defense in plants, as it aids in facilitating responses to biotic and abiotic stress[517,518,538–540]. Plants which have been primed by environmental stressors therefore produce stronger and quicker responses than unprimed plants. However, the evidence for priming in mammals is not as common[306–309], and no previous research has been conducted to determine molecular mechanisms underlying priming in mammals. Our finding that cigarette smoke exposure in adulthood alone causes differential DNAm at fewer CpGs than repeated cigarette smoke exposure is evidence that DNAm marks are subject to epigenetic priming in mice following cigarette smoke exposure, and that DNAm differences may underlie the exacerbated lung alterations we also observed following repeated cigarette

smoke exposures. Therefore, further exploration of these differentially methylated CpGs can enhance efforts in developing intervention strategies or therapies to alleviate the effects of early life cigarette smoke exposure or combined early and later life cigarette smoke.

As a follow-up of these findings, we also sought to determine the effects of varying durations of early life cigarette smoke on lung DNAm. We performed this analysis because most of the previous human studies which have reported on effects of early life cigarette smoke exposure have in fact not been able to completely exclude postnatal and/or secondhand cigarette smoke exposure and therefore, may inadvertently have reported some effects of early postnatal cigarette smoke. While it was initially surprising in our study that current smokers exposed to prenatal cigarette smoke had a greater number of differentially methylated CpGs than those with full cigarette smoke exposure in early life, it extends our previously reported lung function results that following early life cigarette smoke exposure alone, lung function defects are greatest in prenatal cigarette smoke followed by full cigarette smoke females. This phenomenon can be attributed to and further confirms the development of tolerance to cigarette smoke in fully exposed offspring due to prolonged cigarette smoke exposure. This concept of tolerance after extended early life cigarette smoke exposure contradicts earlier findings that linked increased maternal smoking intensity/duration to more severe neonatal growth restrictions (reduced birth weight, height, and head circumference)[583,584]. The difference between these prior studies and ours is not entirely surprising, given that the comparisons in those studies focused solely on varying durations of cigarette smoke exposure during the prenatal period, without including the early postnatal phase, as we did in our research. The biological pathways altered by both types of combined cigarette smoke exposures were also extremely different. Combined prenatal and adulthood cigarette smoke affected mostly developmental processes, with the top contributory genes

being *Esr1* and *Aire*. *Esr1* (Estrogen receptor 1) encodes estrogen receptor alpha, and differential expression and genetic polymorphisms at this gene have been linked severally to the development of various human epithelial cancers[585,586]. Differential DNAm at this gene in our research could therefore indicate cancer development in prenatal females re-exposed to cigarette smoke in adulthood. *Aire* (Autoimmune regulator) is a gene whose variants have been shown to increase the risk of smokers developing rheumatoid arthritis[541]. Differential DNAm and expression in *Aire* has also been shown to be able to distinguish between low and high intensity smokers[542]. Since this gene was identified as differentially methylated in our comparison of prenatal only (shorter duration of cigarette smoke exposure) versus combined prenatal and adulthood cigarette smoke (longer duration), it corroborates the finding that *Aire* can distinguish low versus higher intensity smoking, and offers up possibilities for future use of this gene to make this distinction in humans.

On the other hand, combined full and adulthood cigarette smoke altered pathways associated with cellular transport and localization. *Plagl1* and *Pla2g12b* were two of the greatest contributors to this enriched process. *Plagl1* (Pleomorphic Adenoma gene-like zinc finger 1) is a paternally imprinted gene which encodes a zinc finger transcription factor which triggers cell-cycle arrest and apoptosis[587,588], and has been associated with the development of intrauterine growth restriction in babies with transient neonatal diabetes mellitus[587,589]. While there was no evidence for intrauterine growth restriction in our results, aberrant epigenetic profiles at this gene following combined full and adulthood cigarette smoke exposure could be transferred to subsequent generations since it is imprinted[590]. Differential expression of *Pla2g12b* (Phospholipase A2 Group XIIB) is a known biomarker for cholangiocarcinoma, and its differential DNAm in our study further strengthens the

speculation that the offspring with combined full and adulthood cigarette smoke are more prone to tumorigenesis[591].

The previous paragraph highlights the distinctiveness of different types of early life cigarette smoke combined with adulthood cigarette smoke exposure. While the majority of the differentially methylated DNAm sites are indeed different, we also identified 17 CpGs which were commonly differentially methylated between re-exposed prenatal and re-exposed full offspring. In essence, these CpGs are unique to prenatal cigarette smoke exposure alone and are important because they could potentially be investigated as biomarkers of prenatal cigarette smoke exposure or as potential therapeutic targets in current smokers exposed to cigarette smoke during the prenatal period. While not yet implemented in healthcare, some differentially methylated sites in blood have been identified as potential biomarkers for prenatal cigarette smoke exposure[275,321,592,593]. The fact that these previously identified biomarkers were blood-derived while ours are derived from the lungs may explain why none of our identified 17 prenatal cigarette smoke-specific CpGs overlap with any of the previously reported biomarkers. However, even though blood is an adequate surrogate when studying exposures/disease that affect other tissues, measuring DNAm in more proximal tissues (like the lungs in case of smoking) may yield more accurate results[345]. Thus, these lung-derived prenatal cigarette smoke-specific genes show potential for practical use in human research, providing a method to differentiate prenatal cigarette smoke exposure from exposures during other periods, a task that proves difficult in human research.

The findings presented here are especially important due to the fact that many adults today were exposed to some level of cigarette smoke during development, as smoking levels were much higher in the past. Therefore, our study may be a more accurate representation of the molecular constitution in these individuals.

5.7 Limitations and future directions

Though novel, this research is not without limitations. Perhaps the greatest one is the small sample size for the epigenome-wide DNAm and some of the lung function analyses. The limited sample sizes in the epigenome-wide DNAm analyses made it difficult to identify CpGs with small DNAm differences between controls and cigarette smoke-exposed groups. To mitigate this, we used a strict effect size cutoff for identification of differentially methylated sites. However, it is worth noting that despite the stricter effect size cutoff, the absence of FDR correction for p-values suggests that some of the observed DNAm differences could potentially be false positives. Plans are being made to extend the current research using larger sample sizes, to corroborate results presented here and possibly identify CpGs with smaller DNAm differences. Additionally, we used DNAm microarrays to measure epigenome-wide DNAm and while these are useful, they do not encompass the entire mouse epigenome and may be missing some important loci. The CpG location information provided by the Illumina mouse microarray manifest is broad, and do not specifically state where each CpG is located (for example, intergenic regions, transcription start sites, exon-intron boundaries, and so on). Next is the use of whole left lungs in our analyses. While our research provides a full picture of how cigarette smoke exposure alters physiological and molecular outcomes, it does not offer insights into what particular cell types within the lungs are affected since the mouse lung is composed of numerous cell types. It is important to identify which cells in particular are responsible for the observed DNAm patterns in order to guide targeted therapies following early life cigarette smoke exposure. We minimized the possibility of immune cells being responsible for DNAm differences in this study by lavaging the lungs prior to all analyses, but the role of immune cells resident within the lungs and of lung structural

cells remains unknown. Currently, my lab has an established protocol for lung structural cell isolation, and plans are underway to apply this to the next cycle of cigarette smoke exposures. Our study gives insights into the DNAm landscape underlying early life cigarette smoke exposure, but it is impossible to deduce the contribution of other epigenetic mechanisms to our observed phenotype since they all function together to regulate gene expression. To expand on this study therefore, we have performed ATAC-seq experiments on samples from this study to determine differences in chromatin conformation following cigarette smoke exposure. Future research on histone modifications are also necessary to understand how all these epigenetic modifications synergize to produce the phenotype observed following early life cigarette smoke exposure. Next, the experiments described in this document were conducted on BALB/c mice and therefore, may not be representative of other mouse strains. Future similar studies conducted on other strains are needed to determine the extent to which we can extend these results. Finally, since this study provides some insights into biological mechanisms underlying early life cigarette smoke-mediated effects, it provides a foundation for investigating similar mechanisms upon exposure to cannabis, e-cigarettes, and other combustible products. This can lead to identifying common pathways of damage or unique effects specific to each substance, eventually shaping regulatory standards and public health policies.

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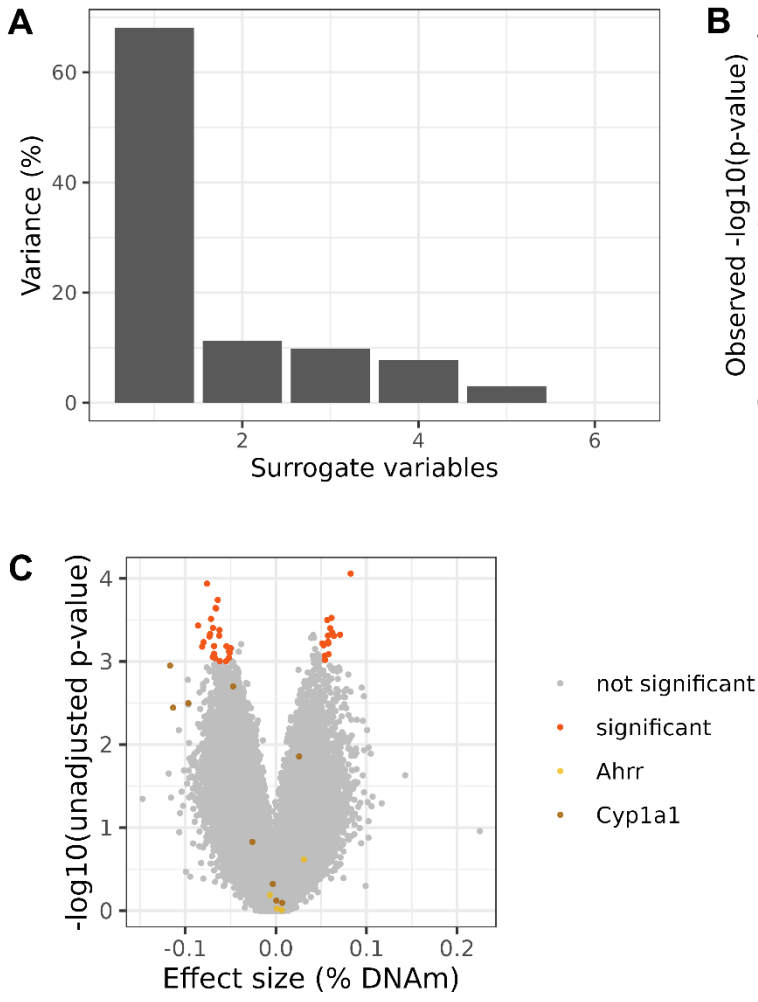
7: Appendices

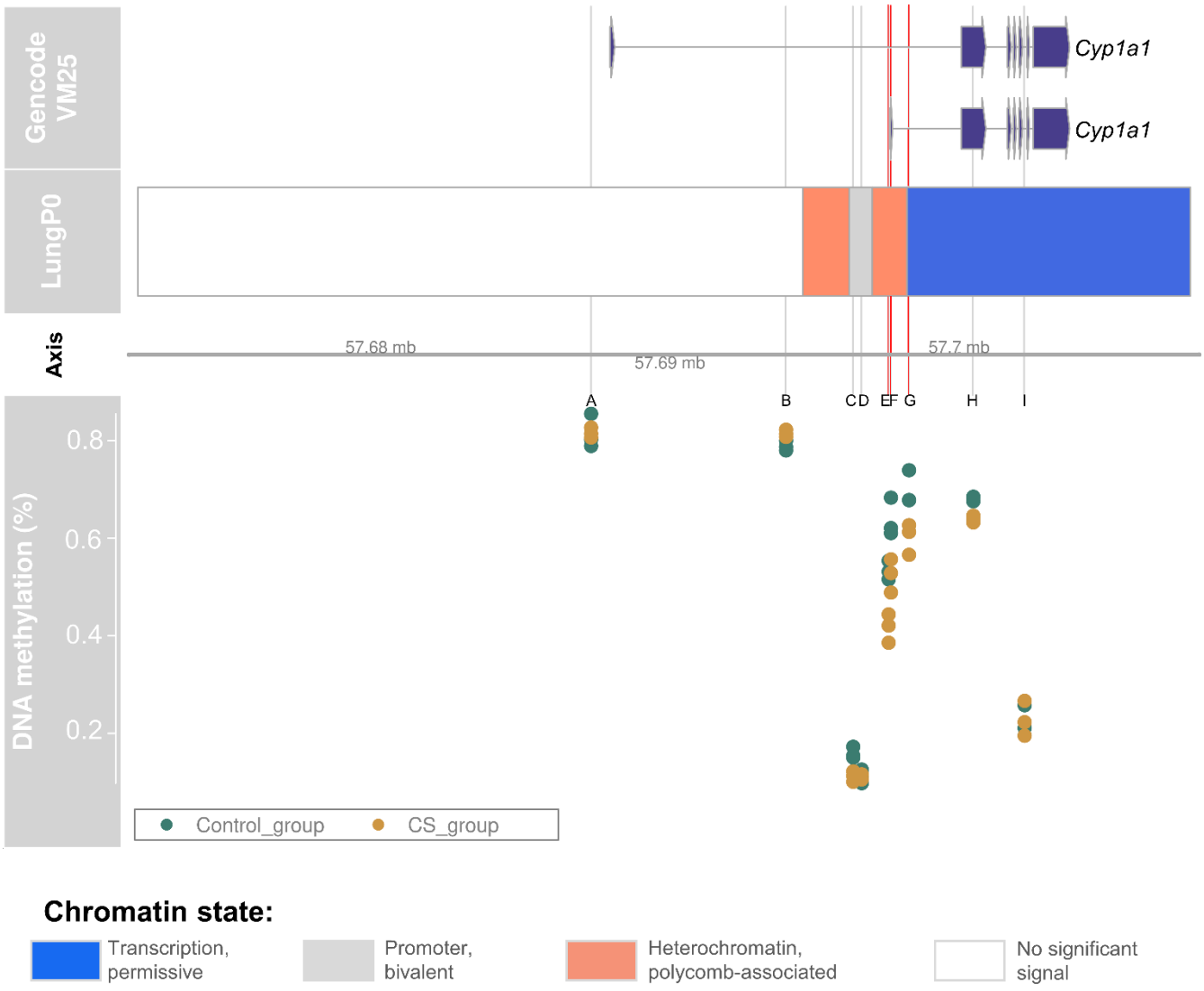
Appendix 2. 1: Sample information.

Number ID	Exposure group	Last day of cigarette smoke exposure	Mom endpoint
97205	Cigarette smoke	March 20, 2020	March 22, 2020
97203	Cigarette smoke	March 20, 2020	March 22, 2020
97192	Cigarette smoke	March 20, 2020	March 22, 2020
97183	Control	March 20, 2020	March 22, 2020
97185	Control	March 20, 2020	March 22, 2020
97181	Control	March 20, 2020	March 22, 2020
97198	Cigarette smoke	March 20, 2020	March 22, 2020
97190	Control	March 20, 2020	March 22, 2020
97187	Control	March 20, 2020	March 22, 2020
97202	Cigarette smoke	March 20, 2020	March 22, 2020
97180	Control	March 20, 2020	March 23, 2020
97182	Control	March 20, 2020	March 23, 2020
97206	Cigarette smoke	March 20, 2020	March 23, 2020
97199	Cigarette smoke	March 20, 2020	March 23, 2020
97200	Cigarette smoke	March 20, 2020	March 23, 2020
97194	Cigarette smoke	March 20, 2020	March 23, 2020
97179	Control	March 20, 2020	March 23, 2020
97189	Control	March 20, 2020	March 23, 2020
97193	Cigarette smoke	March 20, 2020	July 6, 2020
97184	Control	March 20, 2020	July 6, 2020
97201	Cigarette smoke	March 20, 2020	July 7, 2020
97186	Control	March 20, 2020	July 7, 2020
97191	Cigarette smoke	March 20, 2020	July 8, 2020
97178	Control	March 20, 2020	July 8, 2020
97175	Control	March 20, 2020	July 6, 2020
97176	Control	March 20, 2020	July 3, 2020
97177	Control	March 20, 2020	July 6, 2020
195	Cigarette smoke	March 20, 2020	July 3, 2020
97196	Cigarette smoke	March 20, 2020	July 7, 2020
97197	Cigarette smoke	March 20, 2020	July 7, 2020

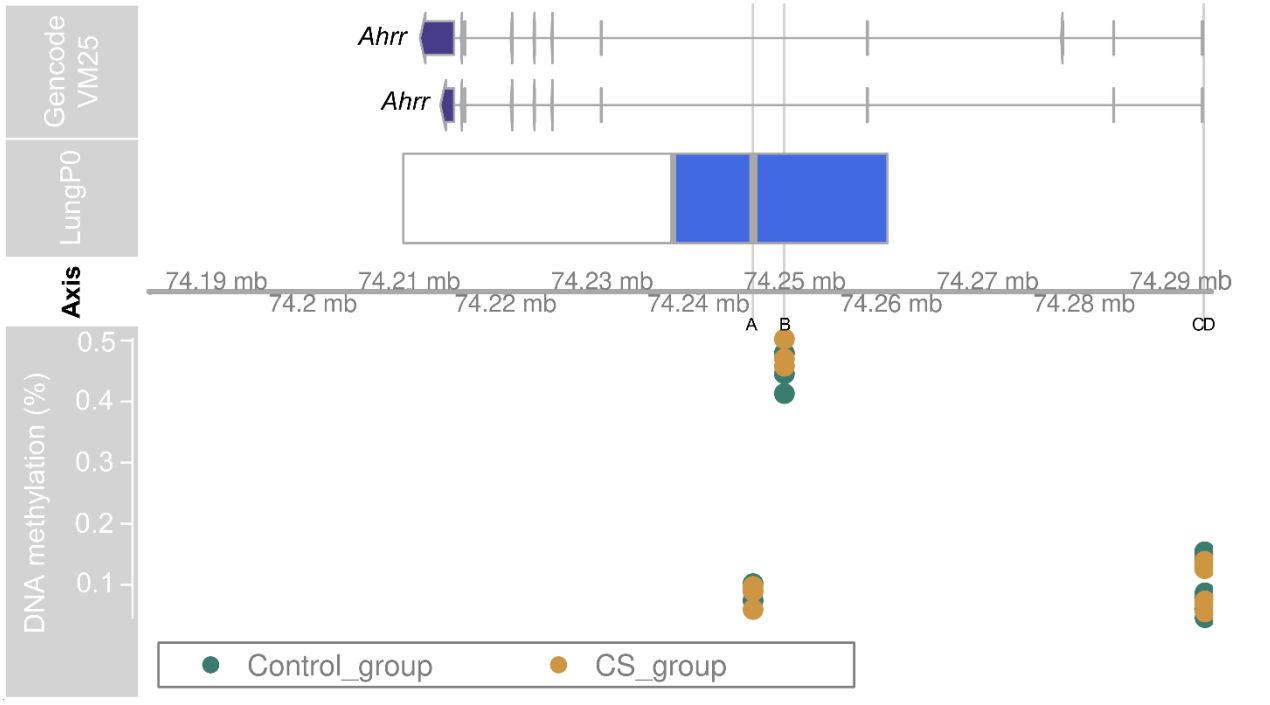
Information displayed is for the 30 dams used in this study as they had their litters within one week of each other (N = 15 Control and N = 15 CS-exposed dams). Dam endpoints were either immediately after 9 weeks of smoke exposure (March 2020) or 15 weeks after smoking cessation (July 2020).



Appendix 2. 2: Linear regression models were adequately fit to measure effects of heavy smoking on dam lung DNAm in autosomal probes.
N = 3 per group. (A) Surrogate Variable Analysis (SVA) identified 5 technical variables in dam lungs immediately after 9 weeks of heavy smoking. We included the first variable only to our regression model based on SVA recommendations. (B) QQ-plot showed a slightly deflated but adequate fit in our limma model, upon inclusion of the surrogate variable. (C) 40 differentially methylated CpGs (highlighted in orange), non-significant CpGs (grey), *Ahrr* CpGs (yellow) and *Cyp1a1* CpGs (brown). DNAm differences were measured using multivariable linear regression, from the limma package in R. Significance was determined using value cutoff of p < 1e-3 and effect size > 5%.

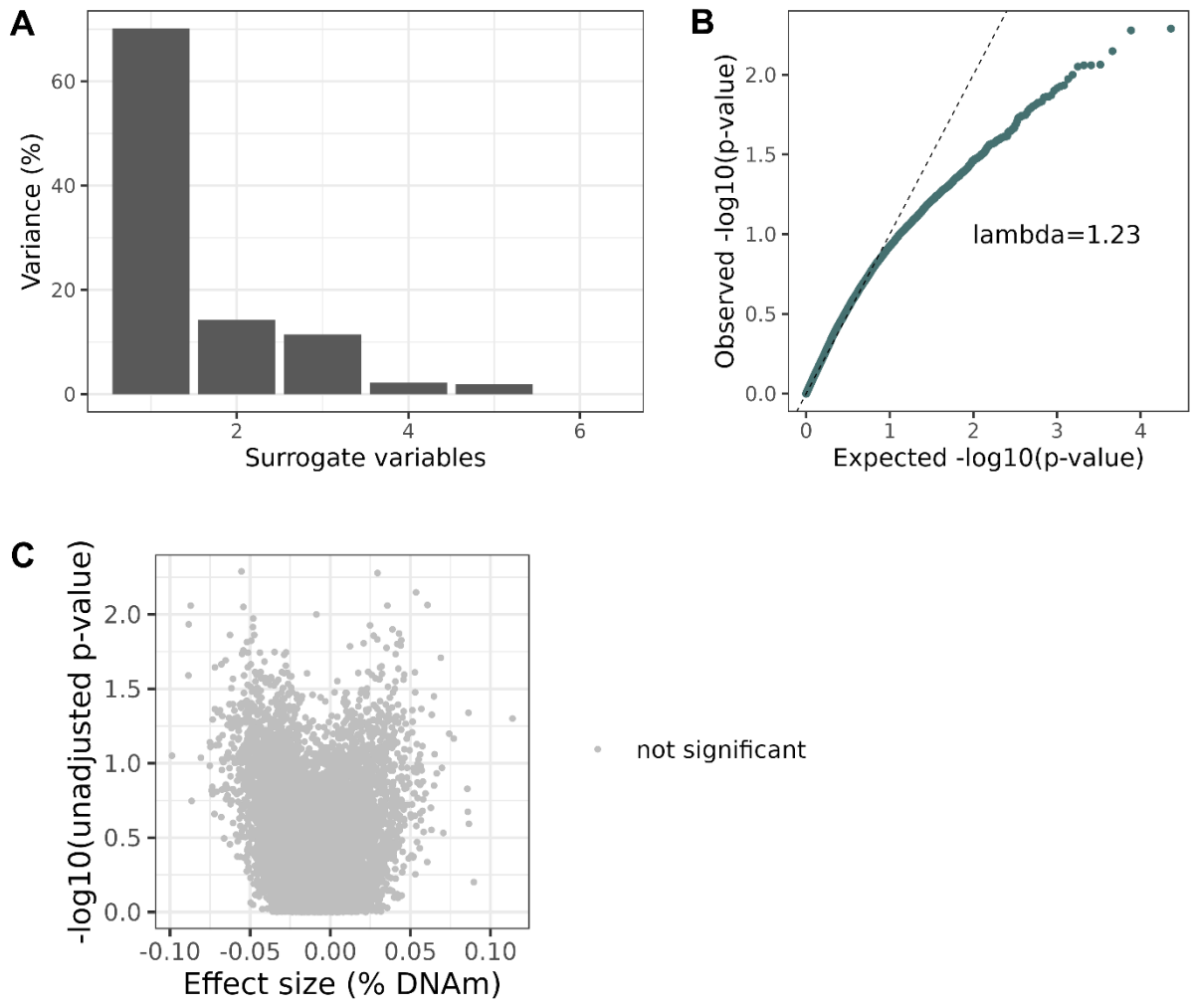


Appendix 2. 3: Chromatin state, genomic locations and DNAm levels at 9 *Cyp1a1* positions on the Illumina mouse methylation microarray.
Cyp1a1 sites from the Illumina mouse array are labelled A-I, the 3 sites with the greatest effect sizes are highlighted in red (sites E, F and G), while the other 6 are highlighted in grey. The genomic locations of the 9 *Cyp1a1* array sites are as follows: A: 57687270, B: 57694012, C: 57696335, D: 57696629, E: 57697560, F: 57697641, G: 57698266, H: 57700489 and I: 57702263. Our candidate CpG is at position 57696231. Information on chromatin state was obtained from UCSC genome browser using mouse genome build GRCm38/mm10. Chromatin state displayed here is from mouse lungs at postnatal day 0, as it is the latest timepoint currently available.



Chromatin state:

Appendix 2. 4: Chromatin state, genomic locations and DNAm levels at 4 *Ahrr* positions on the Illumina mouse methylation microarray.
Ahrr sites from the Illumina mouse array are labelled A-D and highlighted in grey. The genomic locations of the 4 *Ahrr* array sites are as follows: A: 74245665, B: 74248917, C: 74292502, D: 74292541. Our candidate CpG is at position 74260517. Information on chromatin state was obtained from UCSC genome browser using mouse genome build GRCm38/mm10. Chromatin state displayed here is from mouse lungs at postnatal day 0, as it is the latest timepoint currently available.



Appendix 2. 5: Linear regression models to measure effects of heavy smoking on dam lung DNAm in female X chromosome probes.

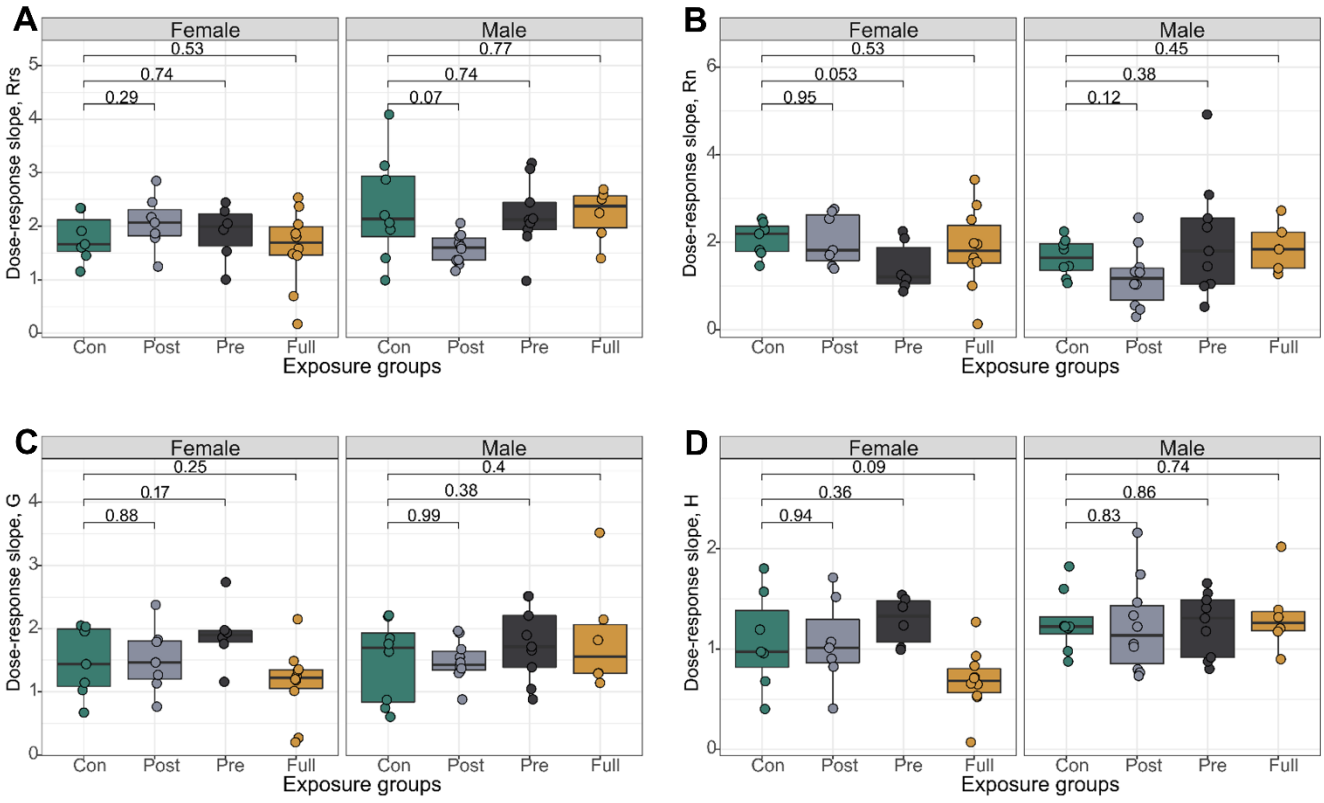
N = 3 per group. (A) Surrogate Variable Analysis (SVA) identified 5 technical variables in dam lungs immediately after 9 weeks of heavy smoking. We included the first variable only to our regression model based on SVA recommendations. (B) QQ-plot showed a slightly deflated fit in our limma model, upon inclusion of the surrogate variable. (C) Volcano plot showing no significantly differentially methylated CpGs. DNAm differences were measured using multivariable linear regression, from the limma package in R. Significance was determined using value cutoff of p < 1e-3 and effect size > 5%.

Appendix 3. 1: Mouse pyrosequencing primers

Gene	Primer sequence
Ahrr	Forward: AGTTGTTGTGGTTTTTGATAAAAAGAG
	Reverse: /5BiosG/AAACACAATATACAAAAATCCAACTCAT
	Sequencing: AGGGATTTATTGGGG
Cyp1a1	Forward: TTTTGTTTGAGAGTAAAGGTTTGAATAG
	Reverse: /5BiosG/ACACCTACAAAACAACCAACTAA
	Sequencing: GTTTATATTTTTAGTGGTAGGAT
Prkaa1	Forward: AGGAAGTTTGGAGTTGATAAGAA
	Reverse: /5BiosG/CTCCCCTAAAAATAACACAACAAC
	Sequencing: ATTATATAGTAAGTTAATTGAGTTT

Appendix 3. 2: Mouse qPCR primers

Gene	Primer sequence
Ahrr	Forward: GGACAAACAGATAGGAGCCACT
	Reverse: GCTGTTCTGTGCTCCAGTTCA
Cyp1a1	Forward: CAAGCGAAAGTGCATCGGAG
	Reverse: GAGGACCAGAAGACCGCATC
β -actin	Forward: AGAAGAGCTATGAGCTGCCTG
	Reverse: TAGAGGTCTTTACGGATGTCAACG
Eif2a	Forward: TCCCAAAAGCAGTTTGCCTTG
	Reverse: TTGTAGGTTAGGCGTCCCAG



Appendix 3. 3: Methacholine dose response slope analyses for lung function measurements in male and female offspring at 16 weeks.

A) Dose-response slope calculation for total lung resistance B) Dose-response slope for airway resistance C) Dose-response slope calculation for tissue resistance D) Dose-response slope calculation for alveolar elastance. N=6-10 per group. $p<0.05$ (t-test) was significant.

Appendix 3. 4: Male offspring echocardiography parameters

	Control	Prenatal Smoke	Postnatal Smoke	Prenatal and Postnatal Smoke	Prenatal Smoke	Postnatal Smoke	Interaction
Body Weight (g)	26.0 ± 0.13	25.9 ± 0.13	25.7 ± 0.06	25.7 ± 0.12	0.8872	0.4964	0.8655
LV mass (mg)	89.1 ± 0.9	89.2 ± 1.4	85.6 ± 0.8	82.6 ± 1.3	0.6957	0.1840	0.6716
LVPWd (mm)	0.75 ± 0.01	0.76 ± 0.01	0.73 ± 0.01	0.67 ± 0.01	0.4383	0.1099	0.3685
LVAWd (mm)	0.74 ± 0.01	0.75 ± 0.01	0.79 ± 0.01	0.73 ± 0.01	0.4717	0.5564	0.2913
IVSd (mm)	0.66 ± 0.01	0.69 ± 0.01	0.71 ± 0.01	0.68 ± 0.01	0.9911	0.5504	0.2704
LVIDd (mm)	4.10 ± 0.02	4.06 ± 0.02	4.02 ± 0.01	4.00 ± 0.01	0.5881	0.2374	0.9119
LV Vol (ul)	73.5 ± 0.5	69.8 ± 0.8	68.8 ± 0.6	66.6 ± 0.5	0.2022	0.0914	0.7522
EF (%)	51.8 ± 0.6	56.2 ± 0.7	53.5 ± 0.5	54.9 ± 0.4	0.0352	0.3285	0.8389
FS (%)	26.3 ± 0.4	29.2 ± 0.5	28.2 ± 0.3	29.2 ± 0.3	0.1095	0.4307	0.4225
CO (ml/min)	14.9 ± 0.3	17.0 ± 0.2	15.8 ± 0.1	16.3 ± 0.2	0.0347	0.8675	0.2108
SV (ul)	38.5 ± 0.6	40.5 ± 0.5	37.9 ± 0.4	39.5 ± 0.4	0.1241	0.6471	0.4787
IVCT (ms)	8.1 ± 0.3	9.9 ± 0.2	12.1 ± 0.3	11.3 ± 0.3	0.6817	0.0198	0.2509
IVRT (ms)	15.2 ± 0.3	13.7 ± 0.3	15.3 ± 0.2	14.2 ± 0.2	0.1118	0.7505	0.8026
E/A	2.47 ± 0.07	2.05 ± 0.05	1.88 ± 0.03	2.16 ± 0.05	0.6882	0.1546	0.0419
E'/A'	1.15 ± 0.03	1.12 ± 0.03	1.03 ± 0.02	1.00 ± 0.02	0.5589	0.1929	0.8663
E/E'	47.2 ± 0.6	42.8 ± 0.9	41.1 ± 0.5	40.3 ± 0.8	0.2331	0.0520	0.3970
MPI	0.44 ± 0.01	0.43 ± 0.01	0.51 ± 0.01	0.46 ± 0.01	0.3947	0.0944	0.4189
PAT (ms)	15.8 ± 0.2	15.7 ± 0.2	16.8 ± 0.2	15.7 ± 0.1	0.3675	0.4982	0.4769
PET (ms)	62.2 ± 0.5	60.3 ± 0.4	61.2 ± 0.3	59.6 ± 0.5	0.2517	0.5760	0.9120
PAT/PET	0.26 ± 0.01	0.26 ± 0.01	0.27 ± 0.01	0.26 ± 0.01	0.8646	0.2981	0.5046
PV Peak Velocity (mmHg)	608.0 ± 6.1	669.9 ± 7.7	637.3 ± 5.1	639.0 ± 3.0	0.1371	0.9716	0.1595
PV Peak Pressure (mmHg)	1.49 ± 0.03	1.70 ± 0.04	1.65 ± 0.03	1.64 ± 0.02	0.3104	0.6548	0.2682
RVWT (mm)	0.50 ± 0.01	0.52 ± 0.01	0.53 ± 0.00	0.57 ± 0.01	0.0005	< 0.0001	0.2881
RVOT (mm)	1.24 ± 0.01	1.19 ± 0.01	1.15 ± 0.01	1.20 ± 0.01	0.9959	0.2501	0.1421
MPAP (mmHg)	80.2 ± 0.13	80.3 ± 0.12	79.6 ± 0.11	80.3 ± 0.08	0.3678	0.4982	0.4769

HR (bpm)	390 ± 4.1	405 ± 3.8	413 ± 2.6	416 ± 3.6	0.7402	0.9087	0.2510

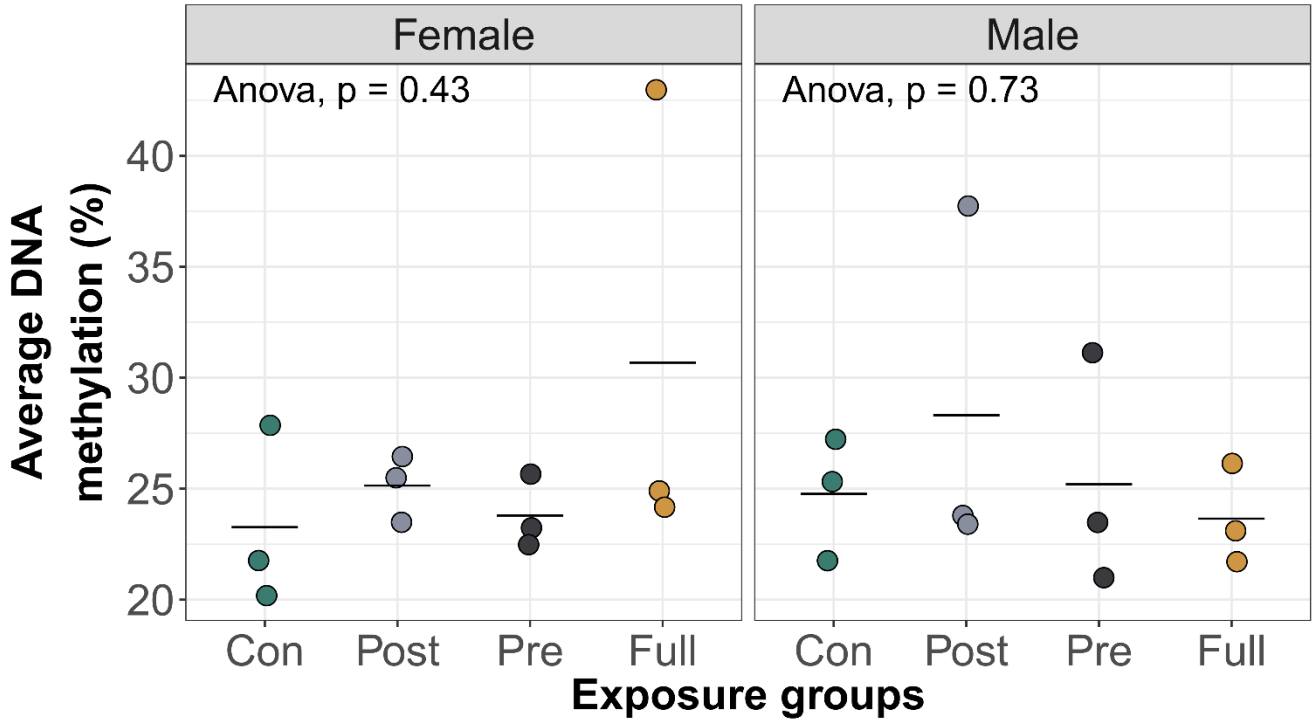
Abbreviations: HR-heart rate; LV- left ventricle; LVID- LV internal diameter; LVAW- LV anterior wall; LVPW- LV posterior wall; IVS- interventricular septum; EF- ejection fraction; FS- fractional shortening; CO- cardiac output; SV- stroke volume; IVRT- isovolumic relaxation time; E/A; ratio of mitral valve peak velocities measured by pulsed wave doppler during the early (E) and atrial (A) peaks; E'/A'- ratio of mitral valve peak velocities measured by tissue doppler during the early (E') and atrial (A') peaks; E/E'- ratio of early mitral inflow velocity (E) and mitral annular early diastolic velocity (E') measured by tissue doppler; MPI- myocardial performance index; LV Vol- end diastolic volume; bpm- beats per minute; PAT- pulmonary acceleration time; PET- pulmonary ejection time; RVWT- right ventricle wall thickness; RVOT- right ventricular outflow tract; MPAP- Mean pulmonary arterial pressure

Appendix 3. 5: Female offspring echocardiography parameters

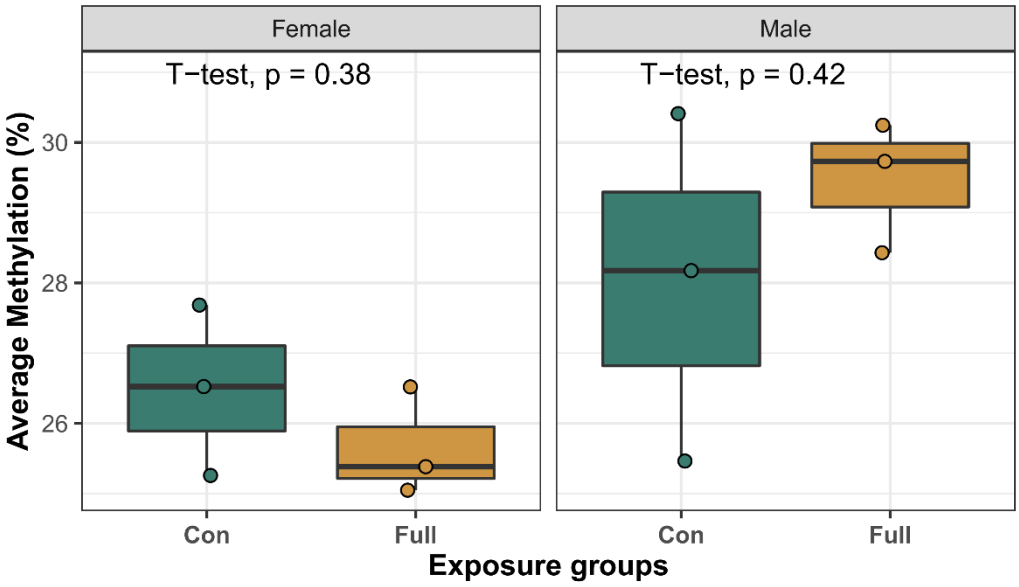
	Control	Prenatal Smoke	Postnatal Smoke	Prenatal and Postnatal Smoke	Prenatal Smoke	Postnatal Smoke	Interaction
Body Weight (g)	21.4 ± 0.04	21.3 ± 0.07	21.1 ± 0.06	20.5 ± 0.07	0.2274	0.0658	0.4613
LV mass (mg)	68.1 ± 0.3	67.5 ± 0.5	69.0 ± 0.5	68.0 ± 0.6	0.7459	0.6094	0.9065
LVPWd (mm)	0.61 ± 0.002	0.63 ± 0.003	0.66 ± 0.005	0.69 ± 0.005	0.1866	0.0010	0.9604
LVAWd (mm)	0.65 ± 0.003	0.61 ± 0.003	0.65 ± 0.003	0.67 ± 0.005	0.5532	0.0733	0.1731
IVSd (mm)	0.65 ± 0.003	0.62 ± 0.003	0.67 ± 0.003	0.65 ± 0.004	0.05	0.1592	0.6054
LVIDd (mm)	3.7 ± 0.01	3.6 ± 0.01	3.7 ± 0.01	3.6 ± 0.01	0.0072	0.5422	0.3386
LV Vol (ul)	57.8 ± 0.15	55.9 ± 0.28	58.9 ± 0.34	53.9 ± 0.38	0.0112	0.7292	0.2413
EF (%)	57.1 ± 0.2	57.0 ± 0.4	55.3 ± 0.3	59.2 ± 0.3	0.1831	0.8515	0.1593
FS (%)	29.0 ± 0.1	28.7 ± 0.2	28.4 ± 0.2	30.9 ± 0.2	0.2157	0.3742	0.1142
CO (ml/min)	13.4 ± 0.07	12.5 ± 0.09	13.2 ± 0.09	13.2 ± 0.11	0.3023	0.5938	0.2920
SV (ul)	34.1 ± 0.13	32.9 ± 0.25	33.3 ± 0.24	33.2 ± 0.24	0.5342	0.8299	0.6036
IVCT (ms)	10.6 ± 0.14	10.3 ± 0.16	11.4 ± 0.15	9.4 ± 0.18	0.1162	0.9182	0.2574
IVRT (ms)	13.9 ± 0.09	14.8 ± 0.14	13.4 ± 0.10	14.0 ± 0.12	0.1287	0.1935	0.7663
E/A	2.44 ± 0.02	2.37 ± 0.03	2.38 ± 0.03	2.07 ± 0.03	0.2039	0.2141	0.2858
E'/A'	1.04 ± 0.01	1.08 ± 0.01	1.05 ± 0.01	1.11 ± 0.01	0.3278	0.6450	0.8636
E/E'	41.0 ± 0.31	39.9 ± 0.40	41.2 ± 0.33	39.5 ± 0.40	0.4263	0.9619	0.8685
MPI	0.44 ± 0.003	0.44 ± 0.004	0.45 ± 0.004	0.44 ± 0.004	0.6185	0.9261	0.9677
PAT (ms)	16.9 ± 0.10	15.9 ± 0.08	15.5 ± 0.07	15.0 ± 0.08	0.0888	0.0105	0.4307
PET (ms)	63.0 ± 0.14	64.2 ± 0.17	62.1 ± 0.22	62.0 ± 0.17	0.5380	0.0826	0.4368
PAT/PET	0.27 ± 0.002	0.25 ± 0.001	0.25 ± 0.001	0.24 ± 0.001	0.0903	0.0894	0.3316
PV Peak Vel (mm/s)	580.0 ± 2.3	615.1 ± 3.9	605.6 ± 2.7	635.6 ± 3.4	0.0294	0.1213	0.8618
PV Peak Pressure (mmHg)	1.36 ± 0.01	1.58 ± 0.02	1.53 ± 0.01	1.69 ± 0.02	0.0080	0.0494	0.7303
RVWT (mm)	0.46 ± 0.000	0.49 ± 0.002	0.51 ± 0.003	0.54 ± 0.002	0.0004	< 0.0001	0.2874
RVOT (mm)	1.08 ± 0.004	1.13 ± 0.004	1.10 ± 0.004	1.14 ± 0.005	0.0609	0.4914	0.5624
MPAP (mmHg)	79.5 ± 0.06	79.7 ± 0.07	80.1 ± 0.05	80.5 ± 0.06	0.4103	0.0265	0.7468

HR (bpm)	393 ± 1.1	389 ± 1.5	398 ± 1.6	397 ± 1.3	0.7349	0.3194	0.8034

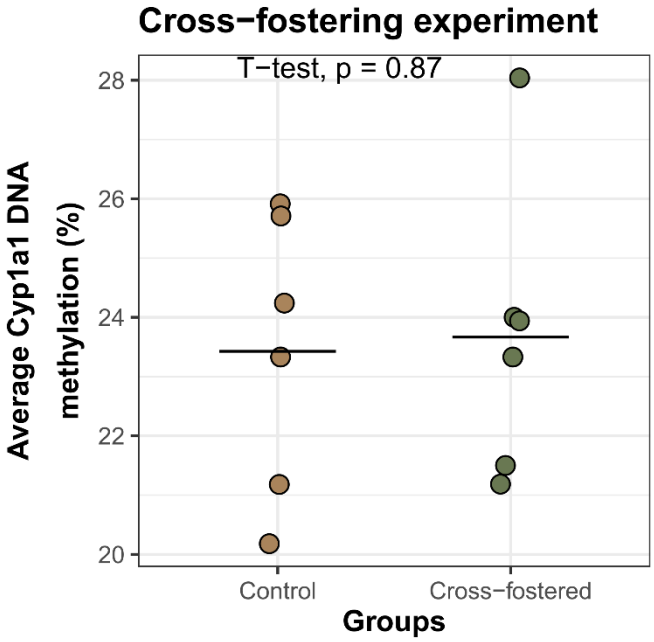
Abbreviations: HR-heart rate; LV- left ventricle; LVID- LV internal diameter; LVAW- LV anterior wall; LVPW- LV posterior wall; IVS- interventricular septum; EF- ejection fraction; FS- fractional shortening; CO- cardiac output; SV- stroke volume; IVRT- isovolumic relaxation time; E/A; ratio of mitral valve peak velocities measured by pulsed wave doppler during the early (E) and atrial (A) peaks; E'/A'- ratio of mitral valve peak velocities measured by tissue doppler during the early (E') and atrial (A') peaks; E/E'- ratio of early mitral inflow velocity (E) and mitral annular early diastolic velocity (E') measured by tissue doppler; MPI- myocardial performance index; LV Vol- end diastolic volume; bpm- beats per minute; PAT- pulmonary acceleration time; PET- pulmonary ejection time; RVWT- right ventricle wall thickness; RVOT- right ventricular outflow tract; MPAP- Mean pulmonary arterial pressure



Appendix 3. 6: Smoking did not alter *Ahrr* DNA methylation (DNAm) in offspring blood 13 weeks after smoke cessation.
N=3 per group. Differences in DNAm were measured using one-way ANOVA.

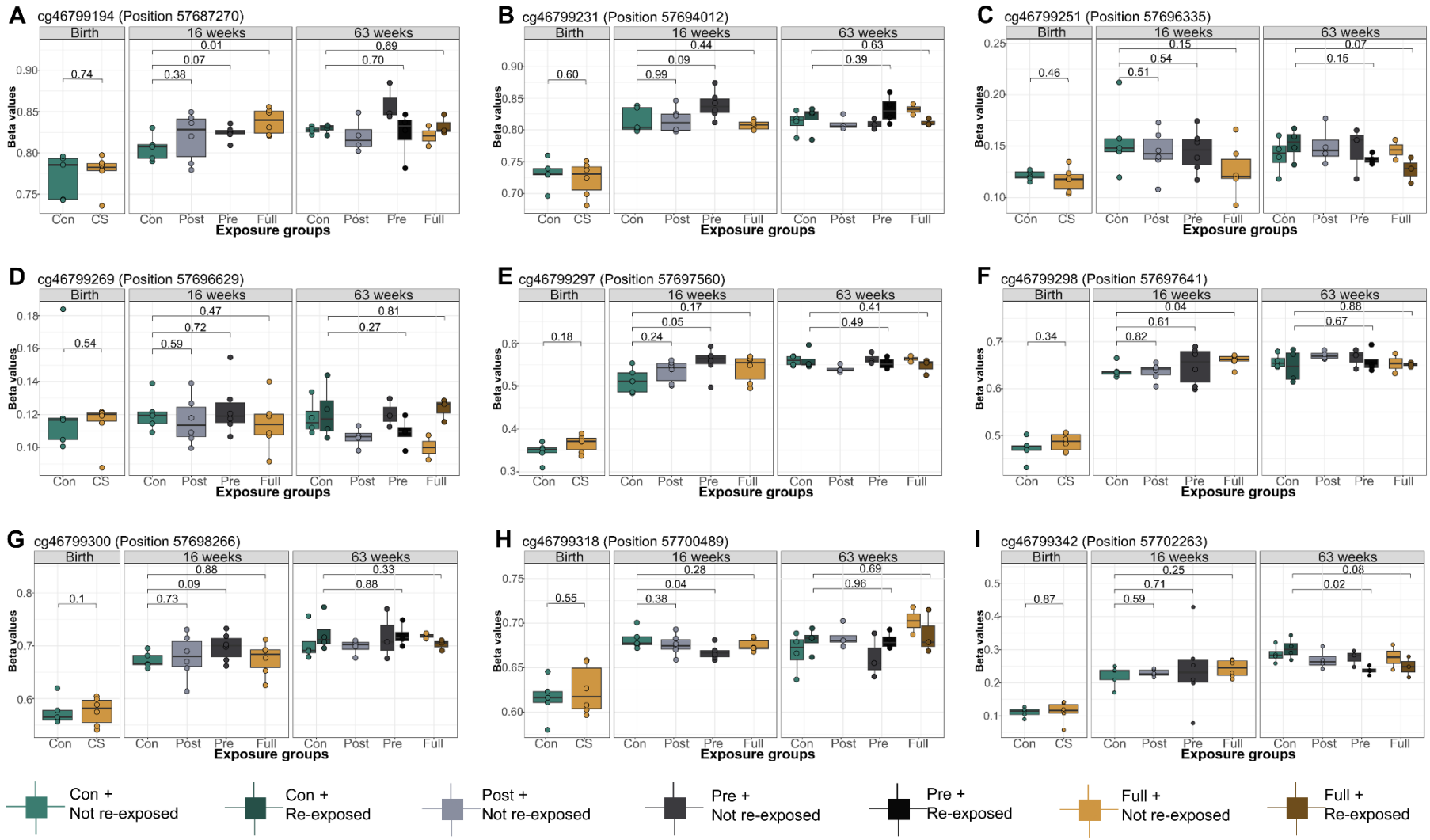


Appendix 3. 7: Early life exposure to CS did not significantly alter offspring lung DNAm at the control gene, *Prkaa1*.
N=3 per group. Differences in DNAm were measured using a student t-test. $p<0.05$ was considered significant.



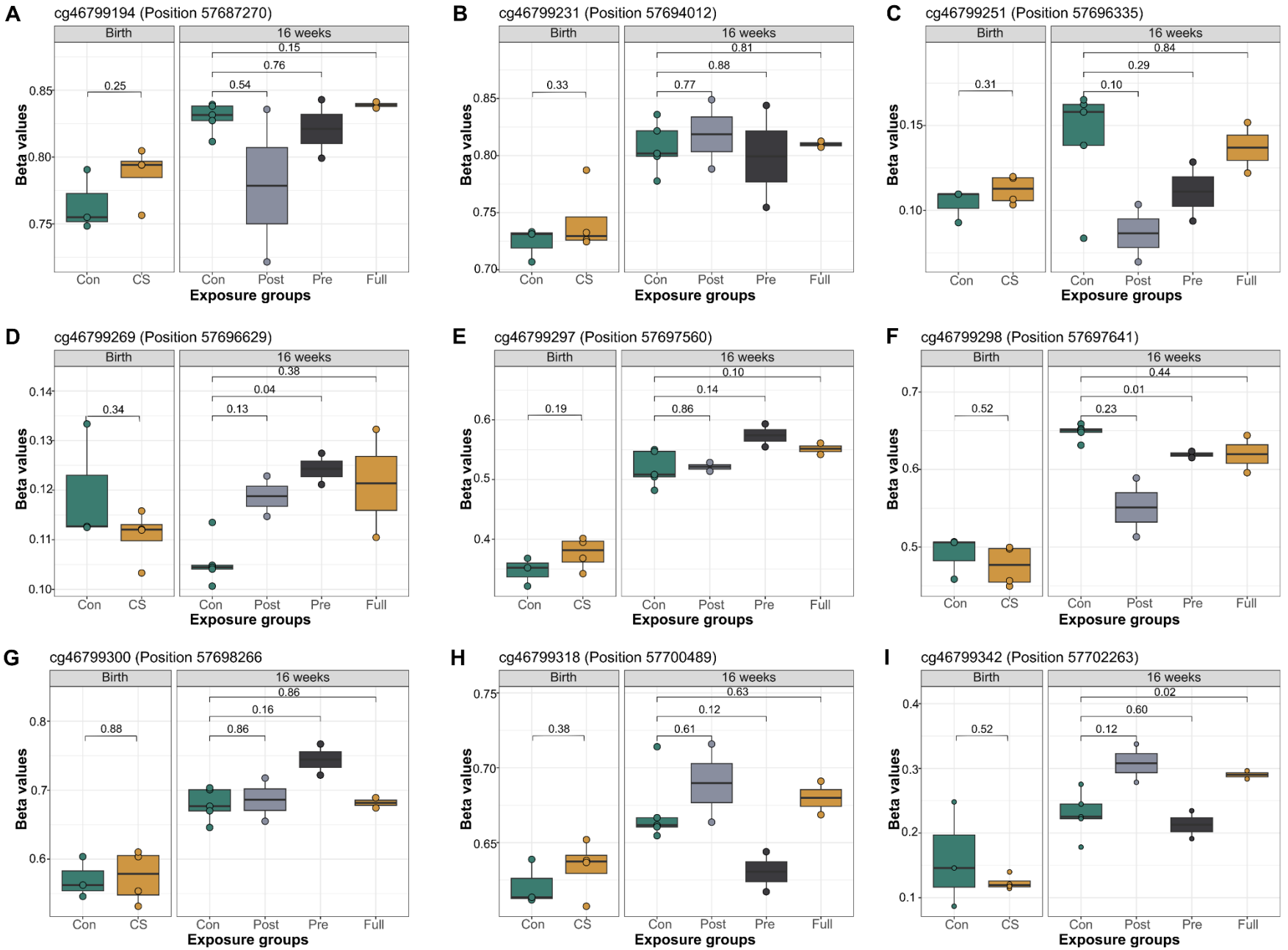
Appendix 3. 8: Cross-fostering did not significantly affect *Cyp1a1* DNAm in mouse lungs.

To rule out potential effects of cross-fostering on offspring DNAm, we measured *Cyp1a1* DNAm in lungs of cross-fostered (N=6) and non-cross fostered (N=6) control Balb/C mice at 8 weeks of age. Differences in DNAm were measured using a student t-test. $p<0.05$ was considered significant.



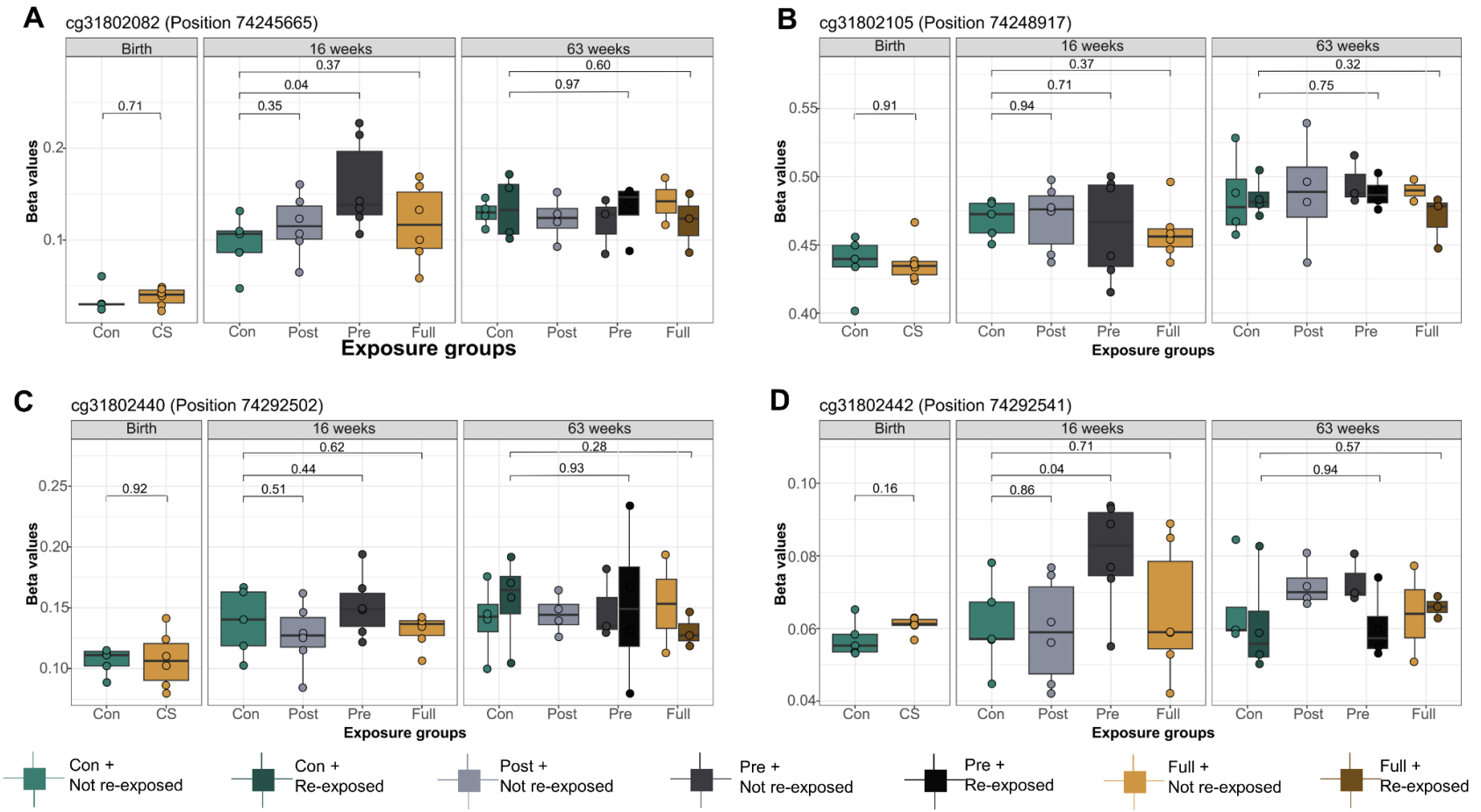
Appendix 3. 9: *Cyp1a1* DNAm in lungs of female offspring exposed to CS, at positions A to I on the Illumina mouse methylation array. N = 2-6 per group.

(A) DNAm measurements at position 57687270 (B) DNAm measurements at position 57694012 (C) DNAm measurements at position 57696335 (D) DNAm measurements at position 57696629 (E) DNAm measurements at position 57697560 (F) DNAm measurements at position 57697641 (G) DNAm measurements at position 57698266 (H) DNAm measurements at position 57700489 (I) DNAm measurements at position 57702263. Differences in DNAm were calculated using a one-way ANOVA, followed by two-group comparisons with t-tests. $p<0.05$ was considered significant.


A
cg46799194 (Position 57687270)
B
cg46799231 (Position 57694012)
C
cg46799251 (Position 57696335)
D
cg46799269 (Position 57696629)
E
cg46799297 (Position 57697560)
F
cg46799298 (Position 57697641)
G
cg46799300 (Position 57698266)
H
cg46799318 (Position 57700489)
I
cg46799342 (Position 57702263)
Birth
16 weeks
Beta values
Con
CS
Post
Pre
Full
Exposure groups

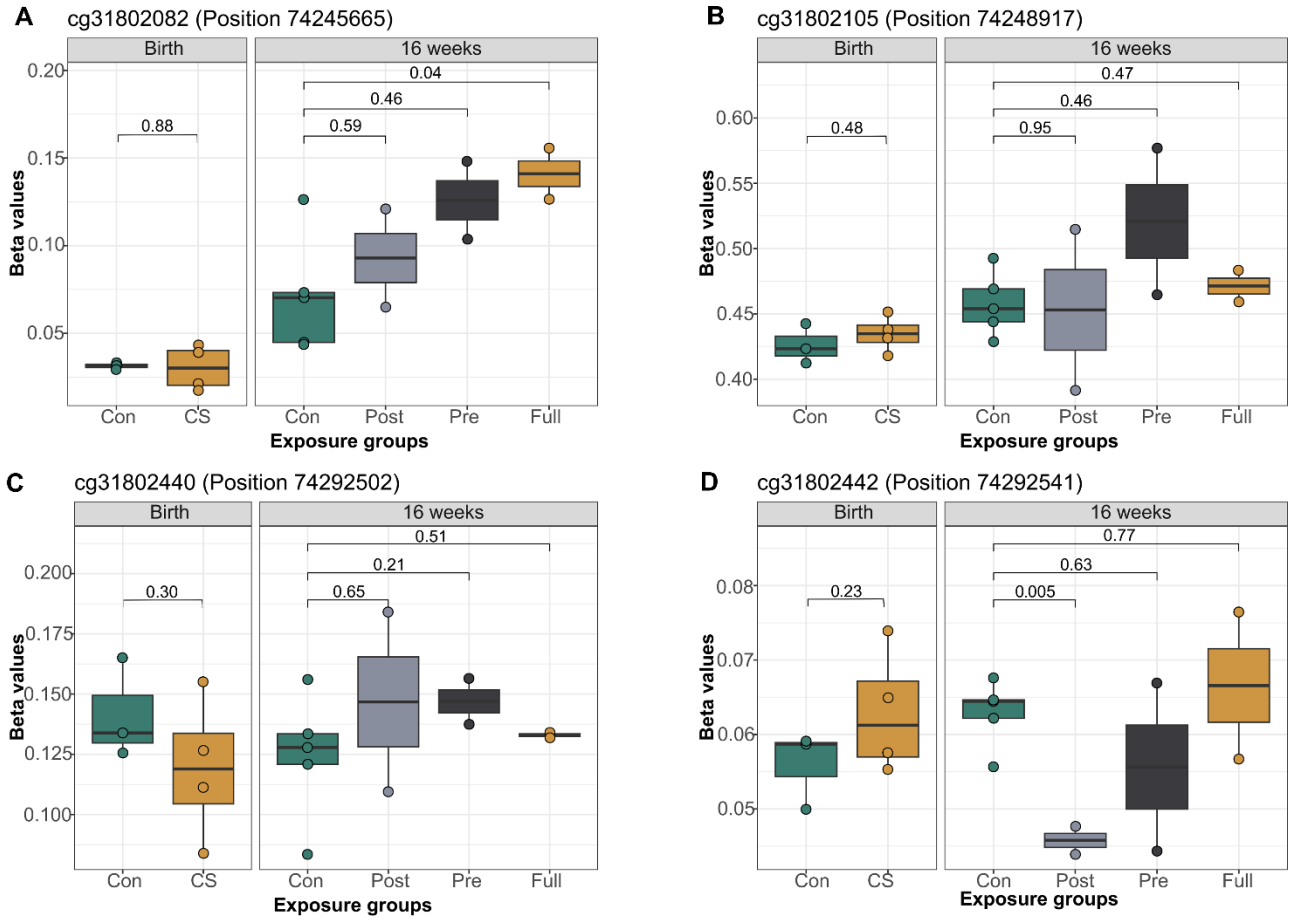
Appendix 3. 10: *Cyp1a1* DNAm in lungs of male offspring exposed to CS, at positions A to I on the Illumina mouse methylation array.

N = 2-6 per group. (A) DNAm measurements at position 57687270 (B) DNAm measurements at position 57694012 (C) DNAm measurements at position 57696335 (D) DNAm measurements at position 57696629 (E) DNAm measurements at position 57697560 (F) DNAm measurements at position 57697641 (G) DNAm measurements at position 57698266 (H) DNAm measurements at position 57700489 (I) DNAm measurements at position 57702263. Differences in DNAm were calculated using a one-way ANOVA, followed by two-group comparisons with t-tests. $p<0.05$ was considered significant.

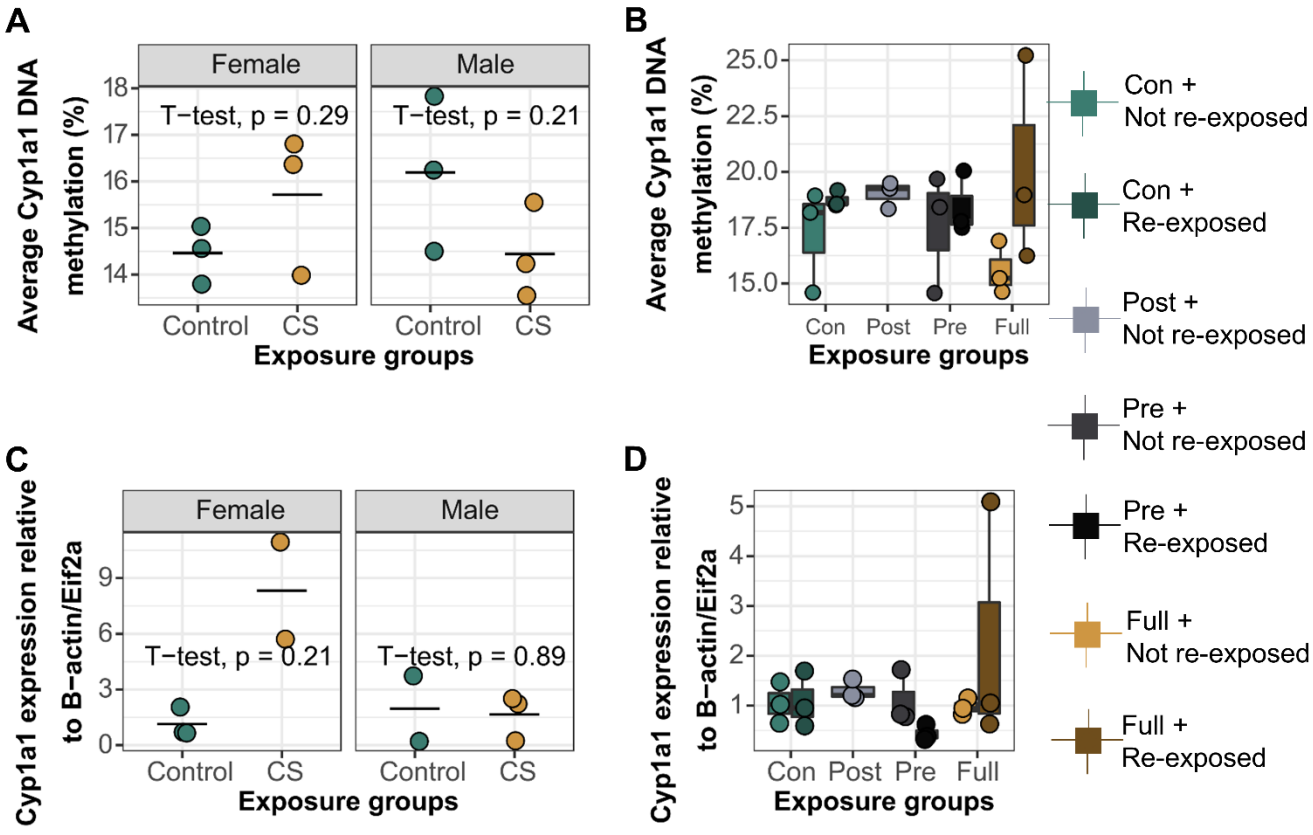


Appendix 3. 11: *Ahrr* DNAm in lungs of female offspring exposed to CS, at positions A to D on the Illumina mouse methylation array.

N = 2-6 per group. (A) DNAm measurements at position 74245665 (B) DNAm measurements at position 74248917 (C) DNAm measurements at position 74292502 (D) DNAm measurements at position 74292541. Differences in DNAm were calculated using a one-way ANOVA, followed by two-group comparisons with t-tests. $p<0.05$ was considered significant.



Appendix 3. 12: *Ahrr* DNAm in lungs of male offspring exposed to CS, at positions A to D on the Illumina mouse methylation array.
N = 2-6 per group. (A) DNAm measurements at position 74245665 (B) DNAm measurements at position 74248917 (C) DNAm measurements at position 74292502 (D) DNAm measurements at position 74292541. Differences in DNAm were calculated using a one-way ANOVA, followed by two-group comparisons with t-tests. $p<0.05$ was considered significant.



Appendix 3. 13: Smoke exposure did not significantly alter *Cyp1a1* (position 57696231) DNAm and expression in mouse livers at birth or 63 weeks of age.
(A) *Cyp1a1* DNAm in offspring livers at birth (N=12) was not significantly altered by prenatal CS exposure (B) Re-exposure to CS in adulthood did not significantly alter *Cyp1a1* DNAm in the livers of mouse offspring (N=21) (C) *Cyp1a1* expression in offspring livers at birth (N=10) was not significantly altered by prenatal CS exposure (D) Re-exposure to CS in adulthood did not significantly alter *Cyp1a1* expression in the livers of mouse offspring (N=21). Differences in DNAm and expression were calculated using a one-way ANOVA, followed by two-group comparisons. $p<0.05$ was considered significant.

Appendix 3. 14: Summary of results from offspring

		Birth		16 weeks						60 weeks	
		Male	Female	Male			Female			Female	
		CS	CS	Post	Pre	Full	Post	Pre	Full	Pre	Full
Lung function at baseline	Rrs										↑
	Rn						↑				
	G									↑	↑
	H			↑							
Lung function with methacholine	Rrs			↓		↑					
	Rn			↓				↓	↓		
	G										
	H			↓							
Lung immune cell infiltration	Macrophages										
	Eosinophils						↑				
	Lymphocytes					↑					
	Total cells										
Lung DNAm	*Cyp1a1* DNAm						↑*	↑	↓*		↓
Lung gene expression	*Cyp1a1* expression	↑	↑				↑	↑*			

At birth and 16 weeks, arrow directions are relative to control groups. At 60 weeks, arrows are relative to early-life control offspring exposed to CS in adulthood only.
* = borderline significance.

Appendix 4. 1: Significantly altered CpGs in female lungs at birth, due to prenatal CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg29603573_BC21	0.000498	-0.05203	Lower		chr11	-	tss_body	59475131
2	cg30015312_BC21	0.000481	-0.05117	Lower	Thra	chr11	+	tss_body	98750250
3	cg32604772_TC11	0.000549	-0.05622	Lower	Elp3	chr14	-	tss_body	65572375
4	cg34180489_BC21	0.000754	-0.05943	Lower	Drd3	chr16	+	tss_body	43762222
5	cg35854416_TC11	0.00095	-0.11565	Lower	Mc4r	chr18	-	tss_body	66859734
6	cg38266008_TC21	0.000486	0.061559	Higher	C230014O12Rik	chr2	-	tss_body	34098840
7	cg38605900_TC21	0.000739	0.067861	Higher	Pde1a	chr2	-	tss_body	79865161
8	cg40971505_BC21	0.000452	-0.05164	Lower	Kif12	chr4	-	tss_body	63171157
9	cg41115380_BC21	8.95E-06	0.059982	Higher	Ifna9	chr4	-	tss_200	88592545
10	cg41591846_TC11	0.000157	-0.05505	Lower	Nbl1	chr4	-	tss_body	1.39E+08
11	cg42012629_TC21	0.000885	-0.05098	Lower					33558421
12	cg43808744_BC21	0.000183	-0.06898	Lower	Cntn4	chr6	+	tss_body	1.06E+08
13	cg46209676_TC21	6.28E-05	0.0501	Higher	Wwox	chr8	+	tss_body	1.15E+08
14	cg46573144_TC11	0.000199	0.057868	Higher		chr9	-	tss_body	31997598
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47855939_BC21	0.000485	0.074497	Higher	Yipf6	chrX	+	tss_1500	98937325

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e-3$ and effect size > 0.05.

Appendix 4. 2: Significantly altered CpGs in male lungs at birth, due to prenatal CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28735362_TC21	9.31E-05	-0.06626	Lower	Dapk3	chr10	+	tss_body	81190411
2	cg28737921_BC11	0.000267	0.071053	Higher	Pip5k1c	chr10	+	tss_body	81310735
3	cg28747964_BC21	0.000727	-0.06942	Lower	Gm15608	chr10	+	tss_body	82199410
4	cg28764613_BC21	0.000199	-0.06427	Lower	1500009L16Rik	chr10	+	tss_body	83737933
5	cg28985440_BC21	0.000838	0.050464	Higher					1.11E+08
6	cg29369207_BC21	0.000246	-0.05833	Lower	Stc2	chr11	-	tss_1500	31370829
7	cg29375539_BC21	0.000108	0.064294	Higher					32121355
8	cg29701092_TC21	0.000432	-0.05119	Lower	Gucy2e	chr11	-	tss_body	69232780
9	cg29752132_TC21	0.000383	0.069092	Higher		chr11	+	tss_body	74104889
10	cg29895506_TC21	0.000433	-0.07491	Lower	Gm34064	chr11	-	tss_body	87795099
11	cg30001621_BC21	0.000909	-0.0512	Lower	Lasp1	chr11	+	tss_1500	97798170
12	cg30033118_TC21	0.000621	-0.08894	Lower	chr11-100319667-100320531	chr11	*	NShelf	1E+08
13	cg30871961_TC21	0.000963	-0.07646	Lower					82064124
14	cg30919992_BC21	0.000264	-0.11119	Lower		chr12	-	tss_body	86305964
15	cg31089679_BC21	0.0009	0.053448	Higher					1.07E+08
16	cg31223076_TC21	0.000232	0.056912	Higher	Akr1c12	chr13	-	tss_body	4272588
17	cg31330291_TC21	0.000832	-0.05324	Lower	Zscan12	chr13	+	tss_body	21363562
18	cg31473890_BC11	0.000223	0.051802	Higher					40387706
19	cg31687083_BC21	0.000142	0.09848	Higher	Agtpbp1	chr13	-	tss_body	59467990
20	cg31763090_BC11	0.000802	0.060779	Higher	H3BJF3	chr13	+	tss_body	69555439
21	cg32253169_TC21	0.000906	-0.05911	Lower	Dupd1	chr14	-	tss_body	21686649
22	cg32410489_TC11	0.000231	0.064931	Higher	LOC108168152	chr14	+	tss_body	43212944
23	cg32818432_BC21	0.000387	-0.06074	Lower					97293450
24	cg32981047_TC21	0.000624	-0.06633	Lower	Gm41253	chr14	-	tss_body	1.21E+08
25	cg33081643_TC21	0.000739	-0.05823	Lower	Gm34618	chr15	-	tss_200	11964244
26	cg34751213_TC21	0.000764	0.065106	Higher	Wdr24	chr17	+	tss_body	25824656

27	cg34775784_TC21	0.000365	0.050774	Higher	A0A338P783	chr17	-	tss_body	27521063
28	cg35300001_TC21	0.000514	0.067267	Higher	Slc3a1	chr17	+	tss_body	85059807
29	cg36844890_BC21	0.000619	-0.066	Lower	Gm3646	chr1	-	tss_1500	39806525
30	cg36977839_BC21	0.000486	-0.07463	Lower		chr1	-	tss_body	59492295
31	cg37649479_BC21	0.000885	-0.05142	Lower	Axdnd1	chr1	-	tss_1500	1.56E+08
32	cg38155722_BC21	0.000439	0.067583	Higher	Fut7	chr2	+	tss_body	25425633
33	cg38628392_TC21	0.000836	-0.06834	Lower	Itgav	chr2	+	tss_body	83801815
34	cg39051271_BC21	0.000544	0.057542	Higher	Bfsp1	chr2	-	tss_body	1.44E+08
35	cg39339180_BC21	0.000344	-0.0799	Lower	Dok5	chr2	+	tss_1500	1.71E+08
36	cg39441128_TC21	0.000399	0.054694	Higher					3139087
37	cg39532867_TC21	0.000211	-0.05373	Lower	Gm42189	chr3	+	tss_body	19695554
38	cg39679411_BC21	0.000709	-0.05074	Lower	1700017G19Rik	chr3	-	tss_200	40522952
39	cg39719440_BC11	0.000649	0.092015	Higher	1700018B24Rik	chr3	-	tss_body	48608982
40	cg41399455_BC11	0.000616	0.091994	Higher	Epha10	chr4	+	tss_body	1.25E+08
41	cg41683918_TC11	0.000927	-0.08172	Lower	Ptchd2	chr4	-	tss_body	1.48E+08
42	cg42590956_TC21	0.000246	-0.07777	Lower					1.12E+08
43	cg42647826_BC21	0.000708	-0.0989	Lower	Sirt4	chr5	-	tss_1500	1.15E+08
44	cg42918882_TC11	0.000117	-0.10283	Lower	Tfr2	chr5	+	tss_body	1.38E+08
45	cg44314619_BC21	0.000492	-0.09818	Lower	Zfp109	chr7	-	tss_body	24237076
46	cg44504323_TC21	0.000427	0.063148	Higher	Pold1	chr7	-	tss_body	44537879
47	cg44515468_BC11	0.000726	0.082848	Higher	Slc17a7	chr7	+	tss_body	45172102
48	cg44670207_TC21	0.000451	0.053276	Higher	Gm33926	chr7	-	tss_body	67435841
49	cg45000014_BC21	0.000211	-0.07857	Lower					1.12E+08
50	cg45313944_TC21	0.000957	0.091737	Higher	Zfp358	chr8	+	tss_body	3496386
51	cg45556641_BC21	0.000776	-0.05465	Lower	Gsr	chr8	+	tss_body	33655145
52	cg46104911_BC21	0.000462	0.0679	Higher	Lcat	chr8	-	tss_200	1.06E+08
53	cg46470757_BC11	0.000526	0.058079	Higher	Muc16	chr9	-	tss_body	18655053
54	cg46673402_TC21	0.000224	0.090505	Higher	Foxr1	chr9	-	tss_200	44441004
55	cg46884318_TC11	0.000959	-0.05881	Lower		chr9	+	tss_body	65671779
56	cg47212354_BC21	0.000934	-0.0672	Lower	D030055H07Rik	chr9	+	tss_body	1.06E+08
57	cg47217347_BC21	0.000705	-0.05442	Lower	Parp3	chr9	-	tss_body	1.06E+08

58	cg47219329_BC21	0.00083	0.069188	Higher	Grm2	chr9	-	tss_body	1.07E+08
59	cg47261365_TC21	0.000665	0.069555	Higher	Kif9	chr9	+	tss_body	1.1E+08
60	cg47366616_TC21	0.000714	0.069968	Higher					1.2E+08
61	cg47369200_TC11	0.000468	0.083069	Higher	Eif1b	chr9	+	tss_body	1.2E+08
62	cg47380557_BC21	0.000958	-0.06525	Lower	Trak1	chr9	+	tss_body	1.21E+08

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 3: Significantly altered CpGs in female lungs at 8 weeks due to prenatal CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28687516_TC21	0.000441	-0.05913	Lower	Tspear	chr10	+	tss_body	77795703
2	cg29846197_TC21	0.000515	0.076111	Higher	Unc45b	chr11	+	tss_1500	82910689
3	cg29853438_TC21	7.49E-06	0.07031	Higher		chr11	+	tss_body	83701416
4	cg29853507_TC21	0.000571	-0.05755	Lower					83715245
5	cg30859964_BC21	0.000779	-0.09312	Lower					80785145
6	cg31235933_BC21	0.000254	0.053057	Higher	Pitrm1	chr13	+	tss_body	6573181
7	cg32433123_BC21	0.000409	0.098736	Higher	D330046F09Rik	chr14	-	tss_body	46673507
8	cg33094946_BC11	0.000389	0.078906	Higher	Cdh6	chr15	-	tss_body	13064478
9	cg33841668_TC21	0.000456	0.062747	Higher	Smug1	chr15	-	tss_body	1.03E+08
10	cg35443599_TC21	0.000357	-0.05119	Lower	Gm36490	chr18	+	tss_body	12955858
11	cg35611449_BC21	0.000923	0.107082	Higher	Gm37013	chr18	+	tss_body	37308539
12	cg35652807_TC21	0.00045	-0.06578	Lower					42353322
13	cg37512030_TC21	0.000823	-0.05975	Lower	Ascl5	chr1	+	tss_200	1.36E+08
14	cg37656389_BC21	0.000267	0.064016	Higher		chr1	-	tss_body	1.57E+08
15	cg37997219_TC21	0.000781	0.101048	Higher					3277606
16	cg38499186_TC21	1.78E-06	0.312315	Higher	Cers6	chr2	+	tss_body	69018018
17	cg43086952_TC21	6.75E-05	0.139148	Higher	Hepacam2	chr6	-	tss_body	3470166
18	cg43349457_BC21	0.000137	0.084498	Higher	1700074P13Rik	chr6	-	tss_body	40940476
19	cg44181243_BC11	0.000308	-0.07195	Lower	Nlrp12	chr7	-	tss_body	3249609
20	cg44188200_BC21	0.000897	0.06202	Higher	Ttyh1	chr7	+	tss_body	4123892
21	cg44368673_TC21	0.00075	0.050377	Higher	Fbxo17	chr7	+	tss_body	28735628
22	cg45495459_TC21	0.000915	0.058303	Higher	Fgfr1	chr8	+	tss_body	25545458
23	cg46118131_BC21	9.47E-05	0.090476	Higher	Tmed6	chr8	-	tss_body	1.07E+08
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47453902_TC21	0.000334	0.050916	Higher	Gm14483	chrX	+	tss_1500	11298097
2	cg47568510_BC21	0.000418	0.132661	Higher		chrX	+	tss_body	38762876

3	cg48190254_TC21	7.57E-05	0.069179	Higher	Ofd1	chrX	-	tss_body	1.66E+08

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 4: Significantly altered CpGs in female lung autosomes at 8 weeks due to postnatal CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg29189744_TC21	0.00083249	0.06695279	Higher	Lif	chr11	+	tss_body	4269443
2	cg29570402_BC21	0.00097741	-0.10988202	Lower	LOC105244170	chr11	+	tss_body	56064766
3	cg29845151_BC21	0.00026349	-0.05726636	Lower	Rffl	chr11	-	tss_body	82845965
4	cg29853438_TC21	6.6585E-05	0.06214065	Higher		chr11	+	tss_body	83701416
5	cg30658512_BC21	0.00041835	0.06868851	Higher					54445103
6	cg31012555_BC21	0.00033743	0.07427018	Higher	Tdp1	chr12	+	tss_body	99916410
7	cg31165825_TC21	0.00083022	0.08715505	Higher	Pld4	chr12	+	tss_body	112760990
8	cg32012649_TC11	0.00097969	-0.05736583	Lower		chr13	-	tss_body	103970112
9	cg32038635_BC21	0.00025986	0.05049649	Higher	Gm32090	chr13	-	tss_body	107653755
10	cg32106796_BC21	0.00053049	0.05470398	Higher	4930467J12Rik	chr13	-	tss_body	114596794
11	cg32240244_BC21	0.00046471	-0.05589384	Lower	Fam149b	chr14	+	tss_body	20378515
12	cg32433123_BC21	4.4182E-05	0.12383551	Higher	D330046F09Rik	chr14	-	tss_body	46673507
13	cg33000153_BC21	0.00041906	0.08963466	Higher	Clybl	chr14	+	tss_body	122337205
14	cg33547630_TC11	0.00053984	-0.12866702	Lower	Gm10863	chr15	+	tss_body	79177055
15	cg33709089_BC21	0.00014399	0.06321721	Higher					93229536
16	cg33841668_TC21	0.0006865	0.06287868	Higher	Smug1	chr15	-	tss_body	103157899
17	cg34785431_TC21	0.00061564	0.08695661	Higher					28101765
18	cg34804233_TC21	0.00084397	0.06911472	Higher	Mtch1	chr17	-	tss_body	29336223
19	cg34837176_BC21	0.00047977	-0.05131207	Lower	Sik1	chr17	-	tss_body	31853865
20	cg35443597_BC11	0.00034619	-0.0696373	Lower	Gm36490	chr18	+	tss_body	12955791
21	cg35652807_TC21	0.00042553	-0.06126045	Lower					42353322
22	cg36944627_BC21	0.00043541	0.0532479	Higher	Boll	chr1	-	tss_body	55360644
23	cg37836173_TC21	0.00046285	-0.06039494	Lower	Smyd3	chr1	-	tss_body	179146855
24	cg37982175_TC21	0.00064483	0.06955985	Higher	Syt14	chr1	-	tss_body	193001698
25	cg38030658_BC21	0.00090206	-0.08071152	Lower	Celf2	chr2	-	tss_body	6722176
26	cg38499186_TC21	0.0003262	0.23610062	Higher	Cers6	chr2	+	tss_body	69018018

27	cg38531381_BC21	2.924E-05	0.105495	Higher	Rapgef4	chr2	+	tss_body	72092533
28	cg39409528_TC21	0.00057118	0.06729287	Higher	chr2-17929 3552-17929 3754	chr2	*	Island	179293753
29	cg40142097_BC21	0.00022078	0.08681099	Higher	St7l	chr3	+	tss_body	104887743
30	cg40705709_TC21	0.00062798	0.06569299	Higher		chr4	-	tss_body	28560567
31	cg42249886_TC21	0.00045276	0.08689939	Higher	Atp8a1	chr5	-	tss_body	67648053
32	cg42886265_TC21	0.00038927	0.08644803	Higher	Mlxipl	chr5	+	tss_body	135121823
33	cg43936939_BC21	0.0003253	-0.05753243	Lower	Slc6a13	chr6	+	tss_body	121336693
34	cg44047904_BC21	8.4175E-05	-0.06745312	Lower	Gm36533	chr6	-	tss_body	135197745
35	cg44235943_BC21	0.00049535	0.14503148	Higher		chr7	-	tss_body	12399731
36	cg44258846_BC11	0.00090582	-0.05533655	Lower	Slc8a2	chr7	+	tss_body	16158950
37	cg44674639_BC21	9.352E-05	-0.1165492	Lower	Gm34350	chr7	+	tss_body	67803850
38	cg44760524_BC21	7.6789E-05	0.0648363	Higher	Rlbp1	chr7	-	tss_body	79375625
39	cg45237140_BC21	0.00042924	-0.06801769	Lower					137715351
40	cg45409053_BC21	0.00071175	-0.06236622	Lower	Dlgap2	chr8	+	tss_body	14159472
41	cg45609243_TC21	0.00072317	0.10469374	Higher	Zdhhc2	chr8	+	tss_body	40427239
42	cg45830017_BC21	0.00092558	-0.08059123	Lower	B3gnt3	chr8	-	tss_body	71692928
43	cg45913609_TC21	0.00046473	-0.10492398	Lower	Pkn1	chr8	-	tss_body	83668855
44	cg46840460_BC21	0.0003826	0.07883557	Higher	Gm34828	chr9	-	tss_body	61756994
45	cg46993421_BC21	1.8233E-05	-0.05901869	Lower	Gsta4	chr9	+	tss_body	78195444
46	cg47120055_TC21	0.00096696	-0.06060512	Lower	Zbtb38	chr9	-	tss_body	96696787
47	cg47364371_BC21	0.00019756	0.05973007	Higher	Slc25a38	chr9	+	tss_body	120119598
48	cg47365584_BC21	0.00085916	-0.07352258	Lower		chr9	+	tss_body	120202385
49	cg47397977_TC21	0.00033478	0.06474842	Higher	Tmem42	chr9	+	tss_body	123023459
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47615728_BC11	0.00061817	0.08061342	Higher	Gm595	chrX	-	tss_body	48841550
2	cg47750718_TC21	0.00054137	-0.0538367	Lower					75643959
3	cg47911777_BC21	7.378E-05	-0.06082772	Lower	Lpar4	chrX	+	tss_body	106920742
4	cg48190254_TC21	0.00014401	0.06668919	Higher	Ofd1	chrX	-	tss_body	166393265

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e-3$ and effect size > 0.05.

Appendix 4. 5: Significantly altered CpGs in female lungs at 8 weeks due to full CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28176766_TC21	0.00068294	0.06391407	Higher		chr10	+	tss_200	11609242
2	cg28281162_TC21	4.7337E-05	0.09154205	Higher	Ctgf	chr10	+	tss_body	24597596
3	cg29249895_TC21	0.00043063	-0.0831749	Lower	Ikzf1	chr11	+	tss_body	11686928
4	cg29459890_BC21	0.00022657	0.06463331	Higher	Adra1b	chr11	-	tss_body	43817628
5	cg29752582_TC21	0.00055814	0.08238938	Higher	Olfr403	chr11	+	tss_body	74186491
6	cg29787895_TC21	0.00099247	0.06471176	Higher	Ssh2	chr11	+	tss_body	77423475
7	cg29853438_TC21	0.00010535	0.0675692	Higher		chr11	+	tss_body	83701416
8	cg32558733_TC11	0.0002406	-0.10054364	Lower	Mipepos	chr14	-	tss_body	60782270
9	cg32817566_TC21	0.00077826	0.07703791	Higher					97107630
10	cg35443597_BC11	0.00097118	-0.06295673	Lower	Gm36490	chr18	+	tss_body	12955791
11	cg35443599_TC21	0.00023288	-0.05395854	Lower	Gm36490	chr18	+	tss_body	12955858
12	cg35503773_TC11	0.00044865	-0.05278497	Lower	Nol4	chr18	-	tss_body	22850918
13	cg38499186_TC21	2.118E-05	0.31514294	Higher	Cers6	chr2	+	tss_body	69018018
14	cg39409528_TC21	0.00057599	0.06758401	Higher	chr2-179293552-179293754	chr2	*	Island	179293753
15	cg39903889_TC21	0.0007228	0.08024916	Higher	Fstl5	chr3	+	tss_body	76527825
16	cg40928338_TC21	0.00045098	0.05761982	Higher	Ptpn3	chr4	-	tss_body	57297324
17	cg42785718_BC11	8.9015E-05	0.05002954	Higher					125186463
18	cg44555480_BC21	0.00093369	-0.06156818	Lower	Nav2	chr7	+	tss_body	49088613
19	cg44674639_BC21	0.00037889	-0.09830811	Lower	Gm34350	chr7	+	tss_body	67803850
20	cg45064578_BC21	0.00017143	-0.06432671	Lower	Abca15	chr7	+	tss_1500	120327779
21	cg45226715_BC11	0.00097617	-0.05770094	Lower					136825860
22	cg45609243_TC21	0.00098102	0.09722627	Higher	Zdhhc2	chr8	+	tss_body	40427239
23	cg45913609_TC21	0.00073692	-0.10605951	Lower	Pkn1	chr8	-	tss_body	83668855
24	cg47216650_BC21	0.00055347	-0.07425332	Lower	Abhd14a	chr9	-	tss_body	106448227
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**

1	cg47568510_BC21	0.00025151	0.16249222	Higher		chrX	+	tss_body	38762876
2	cg47576216_BC21	0.00027971	0.08940008	Higher					40762749
3	cg48190254_TC21	0.0002279	0.05998324	Higher	Ofd1	chrX	-	tss_body	166393265

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 6: Significantly altered CpGs in male lungs at 8 weeks due to prenatal CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28641882_TC21	0.00069501	-0.05027121	Lower	Pcdh15	chr10	+	tss_body	73101882
2	cg28896224_BC21	0.00030321	-0.07788396	Lower					98214845
3	cg30959542_BC21	0.00029577	0.05540674	Higher	Ston2	chr12	-	tss_body	91684452
4	cg32012651_BC21	0.00024919	0.07066308	Higher		chr13	-	tss_1500	103970333
5	cg32693432_BC21	0.00067045	0.07700774	Higher					75870104
6	cg34072001_TC21	0.00025121	-0.05638638	Lower	Xxylt1	chr16	-	tss_body	31007707
7	cg34691197_TC11	0.00067356	0.05344082	Higher	Spaca6	chr17	+	tss_body	17829436
8	cg34927432_TC11	9.4306E-05	0.10317124	Higher	Tnfrsf21	chr17	+	tss_body	43077233
9	cg35962189_TC21	0.00042628	0.06333189	Higher	F830208F22Rik	chr18	-	tss_body	77796122
10	cg36391012_BC21	0.00022352	0.09812593	Higher	Blnk	chr19	-	tss_body	40964141
11	cg36471460_BC21	0.00029209	0.10095624	Higher	Neurl1a	chr19	+	tss_body	47222481
12	cg40502995_TC21	0.00052404	-0.050418	Lower	Gipc2	chr3	-	tss_body	152152020
13	cg40520484_TC11	0.00087539	-0.06318826	Lower	St6galnac3	chr3	-	tss_body	153675246
14	cg42941557_TC21	0.00060509	-0.09917986	Lower					139575524
15	cg44177869_TC11	0.00079427	0.05652447	Higher	2810474O19Rik	chr6	+	tss_body	149311190
16	cg44271640_BC21	0.00037419	-0.06771595	Lower	Psg16	chr7	+	tss_body	17093497
17	cg44276383_TC21	7.0598E-05	-0.06037411	Lower	Igfl3	chr7	+	tss_body	18179483
18	cg44939118_BC21	0.00065371	-0.07194298	Lower	Olfr586	chr7	-	tss_body	103122400
19	cg45830215_BC11	0.00064028	-0.12453166	Lower	B3gnt3	chr8	-	tss_body	71701592
20	cg47191038_TC21	0.00055391	-0.05125885	Lower	Gm29154	chr9	-	tss_body	103931970
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47462396_TC21	0.00032163	-0.06396873	Lower	Bcor	chrX	-	tss_body	12100269
2	cg47642465_BC21	0.00066993	0.05184226	Higher	Plac1	chrX	-	tss_body	53200321
3	cg47938392_TC21	0.00079923	0.10491814	Higher		chrX	-	tss_body	113225566
4	cg48055456_TC21	0.00016247	-0.0540094	Lower	Frmpd3	chrX	+	tss_body	140358009
5	cg48058292_TC21	0.00026338	-0.06456499	Lower	Mid2	chrX	+	tss_body	140677907

6	cg48192320_TC21	0.00090329	0.13206555	Higher					166652451
7	cg48200713_TC21	0.00094847	-0.06128818	Lower	Frmpd4	chrX	-	tss_body	168351991
Y chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48214002_TC21	0.00042266	0.06579284	Higher	Uty	chrY	-	tss_body	1110499
2	cg48214962_TC21	0.00051924	-0.05240843	Lower	Ddx3y	chrY	-	tss_1500	1286900
3	cg48215644_TC21	5.5102E-05	-0.15570673	Lower	Usp9y	chrY	-	tss_body	1459767
4	cg48223085_BC21	0.00098685	0.09368274	Higher					4020968
5	cg48231845_BC21	0.00023719	0.09479298	Higher					5690429

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 7: Significantly altered CpGs in male lungs at 8 weeks due to postnatal CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28290538_TC21	0.00059852	0.06145683	Higher	Epb41l2	chr10	+	tss_body	25499909
2	cg28374598_BC11	0.00083627	0.05421105	Higher	Slc16a10	chr10	-	tss_1500	40142526
3	cg28778632_TC11	0.00097563	-0.06931747	Lower	Mterf2	chr10	-	tss_1500	85128938
4	cg29548174_TC21	0.00074179	-0.06719636	Lower					53646485
5	cg30200131_TC21	0.00063695	-0.05841641	Lower					114628255
6	cg31054048_BC11	0.0004668	0.05586332	Higher	Serpina3j	chr12	+	tss_body	104320421
7	cg31773194_BC21	0.0003024	-0.06170286	Lower	Gm36474	chr13	+	tss_body	70676933
8	cg32648646_BC21	6.4716E-05	-0.06073668	Lower	Sorbs3	chr14	-	tss_body	70204183
9	cg32815358_TC21	4.466E-05	-0.06948995	Lower					96607458
10	cg34862808_BC11	0.00046985	-0.08494396	Lower	H2-Ob	chr17	+	tss_1500	34239788
11	cg35560821_TC21	0.00086036	0.05546333	Higher		chr18	-	tss_body	32112167
12	cg35612996_BC11	0.00093134	0.10351933	Higher	Gm37013	chr18	+	tss_body	37484067
13	cg36119206_TC21	0.00033594	0.0585174	Higher	Macrod1	chr19	+	tss_body	7183657
14	cg36318907_TC21	5.3873E-05	-0.07876174	Lower	Sgms1	chr19	-	tss_body	32180218
15	cg36595392_BC21	0.00068046	0.05546591	Higher	E330013P04Rik	chr19	+	tss_body	60144742
16	cg36790947_BC21	0.00039804	-0.05311308	Lower	LOC108167618	chr1	-	tss_1500	34757661
17	cg36825285_TC11	0.00013748	0.05977021	Higher	chr1-38129048-38130208	chr1	*	SShore	38132174
18	cg36832699_TC21	0.00093371	0.05113467	Higher					38764484
19	cg37084498_BC21	0.0001075	-0.06638188	Lower					74227624
20	cg37394627_TC21	0.00060444	0.06918159	Higher					121388658
21	cg37516628_TC21	0.00098794	-0.06732885	Lower	9230116N13Rik	chr1	-	tss_body	136414699
22	cg37840450_TC21	0.00032276	-0.08441539	Lower	Smyd3	chr1	-	tss_1500	179518262
23	cg39994399_TC21	0.00029134	0.06449593	Higher	Lmna	chr3	-	tss_body	88484722
24	cg40101030_TC11	4.347E-05	-0.06954759	Lower		chr3	+	tss_200	100692599
25	cg40101031_TC21	3.4639E-05	-0.07861758	Lower		chr3	+	tss_200	100692615

26	cg40157597_BC21	5.7694E-05	-0.07258299	Lower	Kcna2	chr3	+	tss_body	107103188
27	cg40372758_BC21	0.0005731 6	-0.05687206	Lower					135719292
28	cg41376863_BC21	0.0006439 3	-0.06436204	Lower					123003720
29	cg41661052_TC21	0.0001312 3	-0.08596246	Lower		chr4	+	tss_body	144587376
30	cg42565889_BC21	0.000989	-0.08444978	Lower	Gm8493	chr5	-	tss_body	109549934
31	cg42849366_BC21	0.0008157 2	-0.05283373	Lower	Gm29681	chr5	-	tss_1500	131415455
32	cg42919988_BC21	7.6164E-06	-0.06012823	Lower	Lrch4	chr5	+	tss_body	137639158
33	cg42994057_BC21	0.0003210 6	-0.06484231	Lower	Eif2ak1	chr5	+	tss_body	143894931
34	cg43507365_BC11	0.0006440 4	0.06044384	Higher	Grid2	chr6	+	tss_body	64663184
35	cg43698694_TC21	0.0003182 8	-0.06829486	Lower					91291570
36	cg44368244_TC21	0.0005291 1	0.11561721	Higher					28704630
37	cg44503171_TC21	0.0007266 6	-0.08817092	Lower	Lrrc4b	chr7	+	tss_body	44462799
38	cg45257357_BC21	0.0006172 1	-0.08510134	Lower	Adgra1	chr7	+	tss_body	139847538
39	cg45686701_TC21	0.0002533	-0.05269578	Lower					49035770
40	cg45879527_BC21	0.0003928 5	0.05246893	Higher	Zfp827	chr8	+	tss_body	79033766
41	cg46071266_BC21	8.1949E-05	-0.06790448	Lower					101949829
42	cg46301361_BC11	0.0007082 3	0.0678042	Higher	Gm22	chr8	+	tss_body	122091936
43	cg46312644_TC11	1.2569E-05	-0.08360459	Lower	C230057M02Rik	chr8	-	tss_body	122738123
44	cg46658697_BC21	0.0001737 2	-0.05628462	Lower	D630033O11Rik	chr9	+	tss_body	43270766
45	cg46788925_TC21	1.0599E-05	-0.06017746	Lower	Lingo1	chr9	-	tss_body	56795131
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47617508_BC21	0.0001231 4	0.0792107	Higher	Enox2	chrX	-	tss_body	49165381
2	cg47627442_TC21	0.0006968 3	-0.10469569	Lower					51046779
3	cg47963377_BC11	0.0005336 9	-0.07482833	Lower					119543348
4	cg48026181_TC21	0.0006384 7	-0.06473853	Lower					135278901
5	cg48031331_BC21	0.0006627	0.06241448	Higher	Bex1	chrX	-	tss_body	136214811
Y chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48214591_BC21	0.0009312 8	0.05735156	Higher	Uty	chrY	-	tss_body	1237802

2	cg48214610_BC11	0.00069927	-0.06661959	Lower	Uty	chrY	-	tss_body	1241858

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

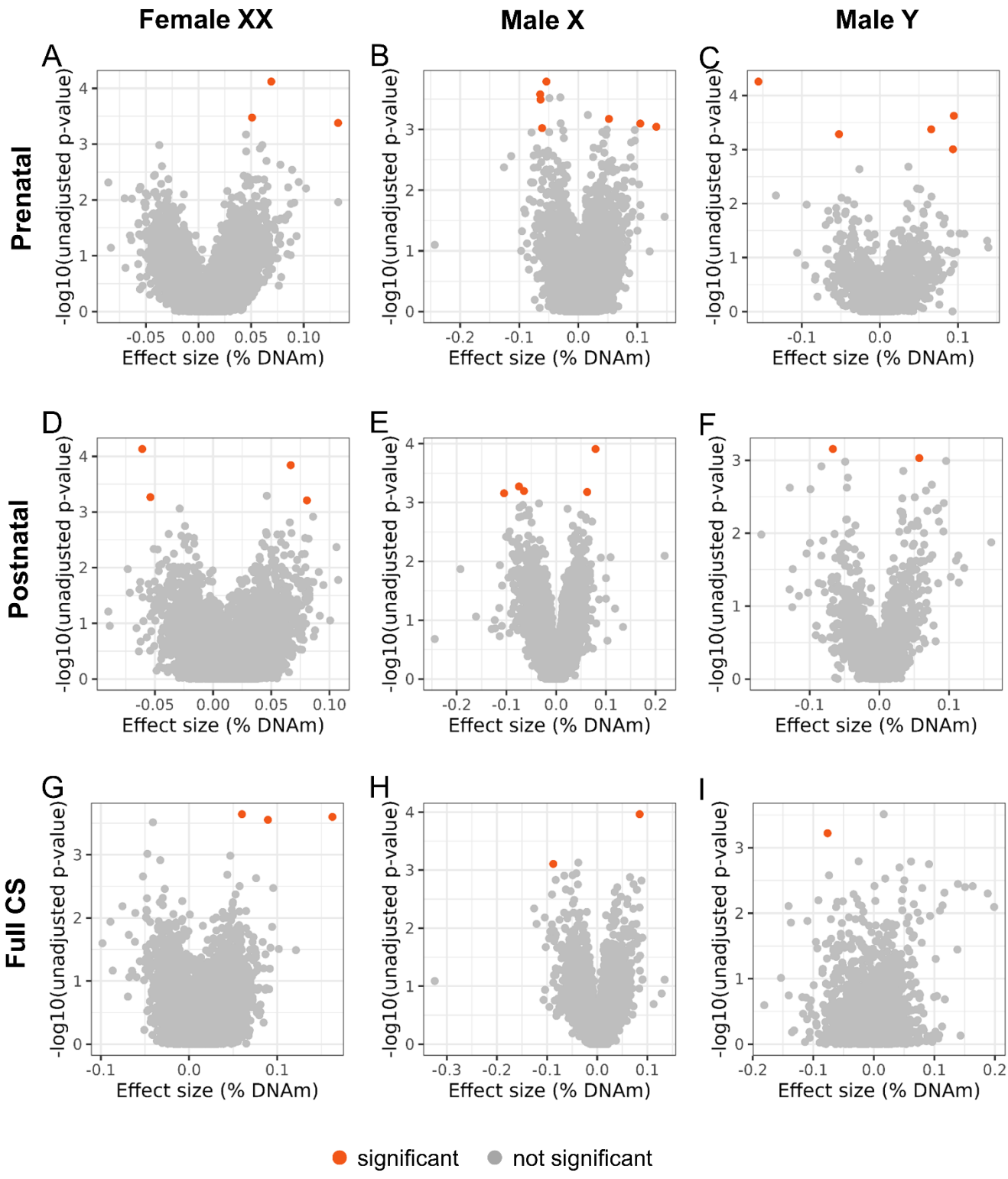
Appendix 4. 8: Significantly altered CpGs in male lungs at 8 weeks due to full CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28239862_BC11	0.000465	-0.05479	Lower	Map3k5	chr10	+	tss_body	20123471
2	cg28753128_BC11	0.000729	0.090758	Higher	Txnrd1	chr10	+	tss_body	82860348
3	cg28904813_TC21	0.000623	-0.07456	Lower	Gm34574	chr10	-	tss_body	99222830
4	cg29482745_BC11	0.000981	0.084554	Higher	Itk	chr11	-	tss_body	46355794
5	cg29525292_TC21	0.000628	0.12228	Higher	Nhp2	chr11	+	tss_body	51621624
6	cg29696405_BC21	0.00055	0.075022	Higher	Arhgef15	chr11	-	tss_body	68939271
7	cg30294115_TC21	0.000744	-0.11177	Lower	Mafg	chr11	-	tss_1500	1.21E+08
8	cg30922199_TC21	0.000271	-0.06516	Lower	Esrrb	chr12	+	tss_body	86470431
9	cg32460761_TC21	0.000883	-0.08161	Lower	1700011H14Rik	chr14	-	tss_body	49232185
10	cg32711834_BC21	0.000285	-0.05863	Lower	Enox1	chr14	+	tss_body	77580296
11	cg32852453_BC21	0.000583	0.050461	Higher	Lmo7	chr14	+	tss_body	1.02E+08
12	cg33416878_BC21	0.000216	0.057503	Higher					63768957
13	cg33469133_TC21	0.00056	-0.07883	Lower	Trappc9	chr15	-	tss_body	72809419
14	cg34190053_BC21	0.000186	0.067606	Higher					44689461
15	cg34589597_BC21	0.000903	-0.10364	Lower	Synj2	chr17	+	tss_body	6037775
16	cg34889769_BC21	8.33E-05	0.091264	Higher		chr17	-	tss_body	36138956
17	cg35048656_TC21	0.000294	-0.06534	Lower	Stap2	chr17	-	tss_body	56005465
18	cg36582690_TC21	0.00022	-0.08335	Lower	Pnliprp2	chr19	+	tss_body	58775192
19	cg39020411_BC21	0.000335	0.068887	Higher	LOC102636024	chr2	+	tss_body	1.38E+08
20	cg39383111_BC21	0.000147	-0.05884	Lower	Gnas	chr2	+	tss_body	1.74E+08
21	cg39598551_BC21	0.000655	-0.05468	Lower	Mecom	chr3	-	tss_body	30411157
22	cg39744011_BC21	9.1E-05	-0.08611	Lower	Maml3	chr3	-	tss_body	51839142
23	cg40329548_TC21	0.000537	-0.06379	Lower	Col25a1	chr3	+	tss_body	1.31E+08
24	cg40371678_TC11	0.000599	-0.07107	Lower	Nfkb1	chr3	-	tss_body	1.36E+08
25	cg40502995_TC21	0.000384	-0.06697	Lower	Gipc2	chr3	-	tss_body	1.52E+08
26	cg41661052_TC21	0.000306	-0.07555	Lower		chr4	+	tss_body	1.45E+08
27	cg42279805_BC21	0.000808	-0.0834	Lower	Tec	chr5	-	tss_body	72855648
28	cg42480003_BC21	0.000494	0.053986	Higher	Cops4	chr5	+	tss_body	1.01E+08

29	cg42705935_TC21	0.000137	-0.07207	Lower	Tbx3	chr5	+	tss_body	1.2E+08
30	cg43110740_TC21	0.000101	-0.05039	Lower	Gm20619	chr6	+	tss_body	6298810
31	cg43373704_TC21	0.00024	0.06407	Higher	Cntnap2	chr6	+	tss_body	46052081
32	cg43627880_BC21	0.000448	-0.09482	Lower	Ankrd53	chr6	+	tss_200	83762635
33	cg43688668_TC21	9.6E-05	-0.05259	Lower	Vmn1r51	chr6	+	tss_body	90128266
34	cg43954532_BC21	0.000452	-0.0538	Lower	Vmn2r24	chr6	+	tss_body	1.24E+08
35	cg44108787_BC21	0.000289	-0.08096	Lower	Slco1a6	chr6	-	tss_body	1.42E+08
36	cg44624465_BC21	9.69E-05	-0.08209	Lower	Gm9801	chr7	-	tss_body	62209517
37	cg44969216_BC21	0.000638	-0.05168	Lower	Olfr514	chr7	-	tss_body	1.09E+08
38	cg45125872_BC21	0.000399	-0.05835	Lower	Sez6l2	chr7	+	tss_body	1.27E+08
39	cg45320587_BC21	2.52E-05	-0.06892	Lower	Map2k7	chr8	+	tss_body	4240622
40	cg45462851_TC21	0.000337	-0.06748	Lower	Slc20a2	chr8	+	tss_body	22545171
41	cg45686701_TC21	0.00039	-0.0539	Lower					49035770
42	cg45830215_BC11	0.000322	-0.1753	Lower	B3gnt3	chr8	-	tss_body	71701592
43	cg45972490_BC21	8.39E-05	-0.05878	Lower	Sall1	chr8	-	tss_body	89032107
44	cg46150124_BC21	0.000395	0.058626	Higher	Atxn1l	chr8	-	tss_body	1.1E+08
45	cg46262980_TC21	0.001	-0.05113	Lower	Tldc1	chr8	-	tss_1500	1.2E+08
46	cg46498508_BC21	0.00072	-0.05578	Lower	Dock6	chr9	-	tss_body	21849614
47	cg46645436_TC21	0.000364	-0.06966	Lower	Sorl1	chr9	-	tss_body	42122944
48	cg47261389_BC21	0.000742	-0.05358	Lower	Kif9	chr9	+	tss_body	1.1E+08
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47817675_TC11	0.000783	-0.08766	Lower					91210536
2	cg47951321_BC21	0.000109	0.084593	Higher	Cpxcr1	chrX	+	tss_body	1.16E+08
Y chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48213788_TC21	0.0006	-0.07647	Lower		chrY	+	tss_1500	1048046

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within

the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e-3$ and effect size > 0.05.



Appendix 4. 9: Differentially methylated CpGs due to early life CS exposure in lung sex chromosomes at 8 weeks.

(A) 3 CpGs (3 higher, 0 lower) are differentially methylated due to prenatal CS exposure on the X chromosome of female offspring lungs at 8 weeks (B) 7 CpGs (3 higher, 4 lower) are differentially methylated due to prenatal CS exposure on the X chromosome of male offspring lungs at 8 weeks (C) 5 CpGs (3 higher, 2 lower) are differentially methylated due to prenatal

CS exposure on the Y chromosome of male offspring lungs at 8 weeks (D) 4 CpGs (2 higher, 2 lower) are differentially methylated due to postnatal CS exposure on the X chromosome of female offspring lungs at 8 weeks (E) 5 CpGs (2 higher, 3 lower) are differentially methylated due to postnatal CS exposure on the X chromosome of male offspring lungs at 8 weeks (F) 2 CpGs (1 higher, 1 lower) are differentially methylated due to postnatal CS exposure on the Y chromosome of male offspring lungs at 8 weeks (G) 3 CpGs (3 higher, 0 lower) are differentially methylated due to full CS exposure on the X chromosome of female offspring lungs at 8 weeks (H) 2 CpGs (1 higher, 1 lower) are differentially methylated due to full CS exposure on the Y chromosome of male offspring lungs at 8 weeks (I) 1 CpG (0 higher, 1 lower) is differentially methylated due to full CS exposure on the Y chromosome of male offspring lungs at 8 weeks . DNAm differences were analyzed using linear regression, and CpGs were considered differentially methylated at $p < 10e\text{-}3$ and effect size > 0.05. Delta beta (effect size) was calculated by subtracting beta values of exposed offspring from control mean betas. N = 3-4 per group. Significant CpGs are highlighted in orange, while non-significant ones are highlighted in grey.

Appendix 4. 10: Significantly altered CpGs in female lungs at 16 weeks due to prenatal CS exposure

Autosomes									
	CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	Feature	CpG position
1	cg28508810_BC21	0.000707	0.063409	Higher	Mcu	chr10	-	tss_body	59611630
2	cg29210334_BC21	0.000908	0.065257	Higher	Camk2b	chr11	-	tss_body	6029371
3	cg29321868_BC21	3.39E-05	0.051324	Higher	Cct4	chr11	+	tss_body	22992293
4	cg29919327_TC21	0.000548	0.052466	Higher	Ankfn1	chr11	-	tss_body	89720861
5	cg30218059_TC11	0.000845	0.050958	Higher	Llgl2	chr11	+	tss_body	1.16E+08
6	cg31182912_BC21	0.000338	-0.07933	Lower		chr12	+	tss_1500	1.15E+08
7	cg31342331_BC21	0.000279	-0.05727	Lower	Q8R271	chr13	+	tss_1500	23159166
8	cg31512395_TC21	0.000168	0.069342	Higher	Gm33489	chr13	-	tss_body	44018564
9	cg32638045_TC21	0.000993	-0.05427	Lower	1700092C10Rik	chr14	-	tss_body	69165894
10	cg32733173_TC21	3.39E-05	0.057265	Higher	Mir759	chr14	+	tss_1500	79737940
11	cg33816422_TC21	0.000919	-0.05697	Lower	Ankrd33	chr15	+	tss_body	1.01E+08
12	cg34150460_BC11	0.000974	0.061291	Higher	Arhgap31	chr16	-	tss_1500	38714322
13	cg34744733_BC11	0.000412	0.053187	Higher	Cacna1h	chr17	-	tss_body	25385729
14	cg35261601_TC21	0.000231	0.051064	Higher	Tmem178	chr17	+	tss_body	80969357
15	cg35311317_BC11	0.000344	0.086111	Higher					85932961
16	cg36461815_BC21	6.97E-05	0.084955	Higher	Arl3	chr19	-	tss_body	46534050
17	cg38576030_BC11	0.000281	0.050609	Higher	Pde11a	chr2	-	tss_body	76338665
18	cg39782533_BC21	4.54E-06	0.078227	Higher	Nbea	chr3	-	tss_body	55729905
19	cg41210063_TC11	0.000117	0.070832	Higher	Sgip1	chr4	+	tss_body	1.03E+08
20	cg43934380_BC21	0.000152	0.050068	Higher	Mical3	chr6	-	tss_body	1.21E+08
21	cg44187534_BC21	0.000593	-0.06052	Lower	Lair1	chr7	-	tss_body	4027045
22	cg44575042_BC21	0.000477	0.100507	Higher		chr7	+	tss_1500	51746362
23	cg44702083_BC21	0.000307	0.099439	Higher	Gm36011	chr7	-	tss_body	71116470
24	cg44903805_BC21	0.000413	0.05724	Higher					99366810
25	cg45641235_BC21	0.000142	-0.06419	Lower	Gm30504	chr8	+	tss_200	45110432
26	cg46500497_TC21	0.000467	0.071367	Higher	Rgl3	chr9	-	tss_body	21987681
27	cg47278650_BC21	6.09E-05	0.057877	Higher	Arpp21	chr9	-	tss_body	1.12E+08

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are

sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 11: Significantly altered CpGs in female lungs at 16 weeks due to postnatal CS exposure

Autosomes									
	CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	Feature	CpG position
1	cg28237096_TC21	0.000351	0.077398	Higher	Pex7	chr10	-	tss_body	19877966
2	cg28548905_BC21	0.000605	-0.06287	Lower	Stox1	chr10	-	tss_body	62665063
3	cg28752287_TC21	2.78E-05	0.072728	Higher					82805072
4	cg28873918_BC21	0.000415	0.054629	Higher	Cradd	chr10	-	tss_body	95314753
5	cg29954713_BC21	0.000978	0.068479	Higher	Acsf2	chr11	-	tss_body	94565366
6	cg30173248_BC21	0.000988	0.052101	Higher					1.13E+08
7	cg31071864_TC21	0.000607	-0.06029	Lower	Ak7	chr12	+	tss_body	1.06E+08
8	cg31182912_BC21	0.000828	-0.06035	Lower		chr12	+	tss_1500	1.15E+08
9	cg31502620_BC21	2.83E-05	0.058896	Higher	Gfod1	chr13	-	tss_body	43200483
10	cg33644329_BC21	0.000179	-0.0674	Lower					86673250
11	cg33907038_BC21	0.000876	0.05937	Higher	Clec16a	chr16	+	tss_body	10736529
12	cg33929849_TC21	0.000305	0.063611	Higher	Parn	chr16	-	tss_body	13610831
13	cg34070272_TC21	0.000819	0.051471	Higher		chr16	+	tss_body	30849838
14	cg34613661_TC21	0.000654	0.052065	Higher		chr17	+	tss_body	8368791
15	cg34876625_BC21	6.75E-05	0.070455	Higher	Aif1	chr17	-	tss_body	35175997
16	cg35287324_BC21	0.000756	0.059795	Higher	8430430B14Rik	chr17	+	tss_200	83998373
17	cg36063508_TC21	0.000572	-0.0582	Lower	1700030N03Rik	chr19	-	tss_body	3160247
18	cg36242770_BC21	0.000181	0.060082	Higher	Apba1	chr19	+	tss_body	23941496
19	cg36272404_TC21	0.000553	-0.07385	Lower	LOC108168409	chr19	+	tss_body	26844660
20	cg36461815_BC21	0.000303	0.064143	Higher	Arl3	chr19	-	tss_body	46534050
21	cg36801200_TC21	0.000266	0.062923	Higher	Gm39624	chr1	-	tss_body	36060919
22	cg37968196_TC21	0.000792	0.064596	Higher	Gm32200	chr1	-	tss_body	1.91E+08
23	cg38526180_BC21	0.00072	0.057595	Higher					71628921
24	cg38694036_TC21	0.000955	0.061217	Higher	Cd82	chr2	-	tss_body	93446751
25	cg38872198_BC21	0.000486	0.076005	Higher	Sptbn5	chr2	-	tss_body	1.2E+08
26	cg40795385_TC21	0.000977	0.071031	Higher	Arid3c	chr4	-	tss_body	41725512
27	cg41077948_TC21	0.000459	0.052233	Higher	Ccdc171	chr4	+	tss_body	83597634
28	cg41210063_TC11	7.53E-05	0.052036	Higher	Sgip1	chr4	+	tss_body	1.03E+08

29	cg41305287_BC21	0.000683	-0.06855	Lower	Cyp4x1	chr4	-	tss_body	1.15E+08
30	cg41478477_TC21	0.000917	0.064733	Higher					1.31E+08
31	cg41603283_BC11	3.78E-05	-0.06269	Lower	LOC108168982	chr4	+	tss_body	1.4E+08
32	cg42169678_TC21	0.000655	-0.05694	Lower		chr5	-	tss_body	55723355
33	cg42769149_TC21	7.64E-06	0.061127	Higher	Abcb9	chr5	-	tss_body	1.24E+08
34	cg43033349_TC21	0.00019	0.059627	Higher	Urad	chr5	-	tss_body	1.47E+08
35	cg43619818_TC21	0.000315	0.062962	Higher	Rtkn	chr6	+	tss_1500	83135332
36	cg44027956_TC21	0.000921	-0.0705	Lower	Tas2r121	chr6	-	tss_body	1.33E+08
37	cg44575042_BC21	0.000404	0.061903	Higher		chr7	+	tss_1500	51746362
38	cg44774180_BC21	0.000522	0.055846	Higher	Man2a2	chr7	-	tss_body	80361055
39	cg44903805_BC21	2.06E-05	0.051838	Higher					99366810
40	cg45107220_TC21	2.12E-05	0.058278	Higher					1.25E+08
41	cg45252956_BC21	0.000399	0.052699	Higher	Inpp5a	chr7	+	tss_body	1.39E+08
42	cg45284223_TC11	7.03E-05	0.075006	Higher	Tnnt3	chr7	+	tss_body	1.43E+08
43	cg45560129_TC21	0.00099	-0.07932	Lower	Rbpms	chr8	-	tss_body	33917999
44	cg45583330_TC21	0.000339	0.056509	Higher	D8Ertd82e	chr8	+	tss_body	36110117
45	cg45882119_TC21	0.000116	0.090278	Higher	1700011L22Rik	chr8	-	tss_body	79248503
46	cg46029882_BC21	9.51E-05	0.066136	Higher					94898990
47	cg46498077_BC21	5.99E-06	0.050907	Higher	Dock6	chr9	-	tss_body	21825491
48	cg46500497_TC21	0.00032	0.050841	Higher	Rgl3	chr9	-	tss_body	21987681
49	cg46674980_TC21	0.000729	0.061407	Higher	Q04683	chr9	-	tss_body	44545133
50	cg47362842_BC21	0.000806	0.063956	Higher	Gm33800	chr9	+	tss_body	1.2E+08
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47635490_TC21	7.09E-05	0.055619	Higher	Gpc3	chrX	-	tss_body	52275157
2	cg47668183_BC21	0.000989	0.060684	Higher	Gm36522	chrX	+	tss_body	58162882
3	cg47720696_BC21	0.000964	0.063927	Higher					70589322
4	cg47866866_TC21	0.000214	0.079443	Higher	Awat2	chrX	-	tss_body	1E+08
5	cg48051258_BC21	0.000337	0.062648	Higher	Cldn2	chrX	+	tss_body	1.4E+08
6	cg48111442_BC21	0.000957	0.057111	Higher	Huwe1	chrX	+	tss_body	1.52E+08
7	cg48131498_TC21	9.01E-05	-0.07049	Lower	Ptchd1	chrX	-	tss_body	1.56E+08

8	cg48154710_TC21	0.000584	-0.0607	Lower					1.6E+08

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 12: Significantly altered CpGs in female lungs at 16 weeks due to full CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28508810_BC21	0.00028683	0.05081725	Higher	Mcu	chr10	-	tss_body	59611630
2	cg28884038_TC21	0.00047268	0.0635387	Higher	Gm40748	chr10	-	tss_1500	96309183
3	cg29565119_TC21	2.8021E-05	0.07861456	Higher					55387028
4	cg29732911_BC21	0.00043237	-0.0532471	Lower	Wscd1	chr11	+	tss_body	71772266
5	cg29891469_TC21	0.00048222	0.05861006	Higher	Tex14	chr11	+	tss_body	87463479
6	cg30202933_TC21	0.00029277	-0.05672578	Lower	Btbd17	chr11	-	tss_body	114798315
7	cg30209565_TC21	0.0002947	-0.07853681	Lower	Otop2	chr11	+	tss_body	115318561
8	cg30256416_BC21	0.0005817	-0.06574186	Lower	Cyth1	chr11	-	tss_body	118221105
9	cg30489851_TC11	0.000638	-0.05387037	Lower					28402091
10	cg31792683_TC21	5.0169E-05	0.0624664	Higher					73242539
11	cg33544246_TC21	0.00014708	0.05056625	Higher	Triobp	chr15	+	tss_body	78987075
12	cg34414610_BC21	0.00042111	-0.05442642	Lower					82468801
13	cg35248308_BC21	0.00031019	0.06217056	Higher		chr17	+	tss_1500	79810438
14	cg35311317_BC11	0.0009797	0.05730439	Higher					85932961
15	cg35543036_TC21	0.00065009	-0.06262465	Lower					29307899
16	cg36563547_TC21	2.6324E-05	0.05333394	Higher	Ablim1	chr19	-	tss_body	57135017
17	cg38207175_TC21	0.00023142	0.06719404	Higher	Cercam	chr2	+	tss_body	29845737
18	cg38217444_BC21	0.00063659	0.0553829	Higher					30567724
19	cg39313925_BC21	0.00012893	0.05218821	Higher	Zfp64	chr2	-	tss_body	168935495
20	cg40602118_TC21	0.00060207	0.06435496	Higher	Gdf6	chr4	+	tss_body	9857335
21	cg41641009_BC21	0.00022325	0.0732739	Higher	Kazn	chr4	-	tss_body	142181093
22	cg41802396_BC21	0.00052227	0.05239708	Higher	Agrn	chr4	-	tss_body	156193936
23	cg42271121_TC21	0.00047686	-0.06027305	Lower	Gabrb1	chr5	+	tss_body	71881105
24	cg43654208_TC21	0.00099231	0.06802354	Higher	LOC108169150	chr6	+	tss_body	86624235
25	cg44297084_TC21	0.00022545	0.06078619	Higher	Bcl3	chr7	-	tss_body	19809724
26	cg44328980_BC11	0.00093904	-0.06366328	Lower	Pou2f2	chr7	-	tss_1500	25180348
27	cg45122215_TC21	0.00079832	-0.06501037	Lower	chr7-126704763-	chr7	*	SShelf	126708167

					126704981				
28	cg45284223_TC11	0.00010499	0.0657465	Higher	Tnnt3	chr7	+	tss_body	142509652
29	cg45483118_BC21	0.0006439	0.05113305	Higher	Gm30757	chr8	-	tss_body	24430348
30	cg45641235_BC21	1.5806E-05	-0.06897455	Lower	Gm30504	chr8	+	tss_200	45110432
31	cg45796965_BC11	0.00093076	-0.05456326	Lower	Slc18a1	chr8	-	tss_body	69088250
32	cg45829952_TC21	0.0008678	0.05871078	Higher	Jak3	chr8	+	tss_body	71690134
33	cg47246159_BC21	0.00031081	0.05469084	Higher					108820513
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47736120_TC21	0.00044267	0.05409179	Higher	Zfp92	chrX	+	tss_body	73421967
2	cg47906568_TC21	8.2943E-05	-0.05354549	Lower	Cox7b	chrX	+	tss_body	106015924

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e-3$ and effect size > 0.05.

Appendix 4. 13: Significantly altered CpGs in male lungs at 16 weeks due to prenatal CS exposure

Autosomes									
	CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	Feature	CpG position
1	cg09884843_TC21	0.00049744	0.10364629	Higher	Hat1	chr2	+	tss_body	71418967
2	cg16884658_BC21	2.2888E-06	-0.05682275	Lower	Bcl11a	chr11	+	tss_body	24164881
3	cg20138186_TC21	0.00039493	-0.22602563	Lower					44900527
4	cg28113901_TC21	0.00020436	0.09501009	Higher	Plekhg1	chr10	+	tss_body	3909234
5	cg28140621_BC21	0.00081326	-0.06536754	Lower	Cnksr3	chr10	-	tss_body	7183873
6	cg28156229_BC21	0.00057817	-0.10143435	Lower	Sash1	chr10	-	tss_body	8792597
7	cg28169677_BC21	6.2026E-05	-0.17897783	Lower	Rab32	chr10	-	tss_body	10546436
8	cg28187943_TC21	0.00082596	0.05275547	Higher	A0A0A6YWE3	chr10	+	tss_body	13087243
9	cg28190126_TC21	0.00032961	0.11039267	Higher	Phactr2	chr10	-	tss_body	13300971
10	cg28222382_TC21	0.00078416	0.05318761	Higher	Ccdc28a	chr10	-	tss_body	18219473
11	cg28225956_TC11	0.00013022	-0.07054065	Lower	Nhsl1	chr10	+	tss_body	18531495
12	cg28228446_TC21	0.0002492	0.06329462	Higher	Perp	chr10	+	tss_body	18846947
13	cg28230365_TC21	0.00063759	-0.0727166	Lower		chr10	-	tss_body	19094510
14	cg28246082_TC21	0.00080326	0.11502914	Higher	Pde7b	chr10	-	tss_body	20695799
15	cg28255176_TC21	0.00070884	-0.05456191	Lower	1700020N01Rik	chr10	+	tss_body	21605889
16	cg28301681_TC21	0.00077082	0.12687908	Higher	Lama2	chr10	-	tss_body	26984318
17	cg28309927_BC21	0.00070846	0.09848055	Higher	Ptprk	chr10	+	tss_body	28492951
18	cg28315202_TC21	0.0006598	-0.08679853	Lower					29402821
19	cg28334389_BC21	0.00010387	-0.11473881	Lower					33071553
20	cg28366498_TC21	0.00048544	-0.06617847	Lower		chr10	-	tss_200	39323447
21	cg28369763_BC21	0.00022573	0.05006535	Higher	Gm16365	chr10	-	tss_body	39612964
22	cg28372981_TC21	8.7195E-05	0.14639468	Higher	Mfsd4b5	chr10	-	tss_body	39975425
23	cg28395821_BC21	0.00037136	0.12223181	Higher					42143959
24	cg28402229_BC21	3.7331E-05	-0.1330802	Lower	D3Z790	chr10	+	tss_body	42628732
25	cg28464938_TC21	0.00051095	-0.06892209	Lower	Nus1	chr10	+	tss_body	52426707
26	cg28495298_BC21	0.00055769	0.08443179	Higher	Smpdl3a	chr10	+	tss_body	57795975
27	cg28506227_TC11	0.00064931	0.0979834	Higher	Pla2g12b	chr10	+	tss_body	59403763
28	cg28510935_TC21	0.00019999	-0.0535682	Lower	Micu1	chr10	+	tss_body	59798508

29	cg28518811_BC21	0.00096818	-0.13134475	Lower	Cdh23	chr10	-	tss_body	60371709
30	cg28524725_TC21	0.00050603	0.05024449	Higher	Unc5b	chr10	-	tss_body	60819809
31	cg28526016_BC21	0.00053099	-0.07205461	Lower					60913845
32	cg28532315_BC21	0.00013867	-0.050323	Lower	Nodal	chr10	+	tss_body	61421402
33	cg28537078_TC21	0.00017365	-0.12966556	Lower	H2afy2	chr10	-	tss_body	61767349
34	cg28551435_BC21	0.00096178	0.05232588	Higher	Tet1	chr10	-	tss_body	62887284
35	cg28563411_TC21	0.00039811	-0.05959092	Lower	Ctnna3	chr10	+	tss_body	64040338
36	cg28588785_TC21	0.00088993	-0.16622832	Lower	Gm32438	chr10	+	tss_body	67703301
37	cg28594748_BC21	0.00083036	-0.09379188	Lower	Arid5b	chr10	-	tss_body	68193096
38	cg28616058_BC21	5.3283E-05	-0.05940778	Lower	Ccdc6	chr10	+	tss_body	70128997
39	cg28623052_TC21	0.00014912	-0.07922141	Lower					70709444
40	cg28630561_BC11	0.0003549	-0.0639208	Lower	Ipmk	chr10	+	tss_body	71350814
41	cg28663378_BC21	0.00022165	-0.06199644	Lower					76801554
42	cg28676048_TC21	0.00053065	-0.06419718	Lower	Pcbp3	chr10	-	tss_body	76962050
43	cg28677530_TC21	3.1016E-05	0.06006132	Higher	Gm35664	chr10	+	tss_200	77012101
44	cg28678093_BC11	7.2203E-05	-0.06006958	Lower	Gm3137	chr10	-	tss_body	77243778
45	cg28680990_BC11	0.00023536	-0.06242033	Lower					77583879
46	cg28685272_TC21	0.00069739	-0.11021968	Lower	Pttg1ip	chr10	+	tss_body	77716347
47	cg28686991_TC21	5.0673E-05	0.07188692	Higher	Tspear	chr10	+	tss_body	77900227
48	cg28688608_BC21	0.00087543	0.09245833	Higher	Lrrc3	chr10	-	tss_body	78037829
49	cg28690521_TC21	5.9674E-05	-0.06340128	Lower	Aire	chr10	-	tss_body	78055314
50	cg28690779_TC21	0.00026665	-0.07895975	Lower	Dnmt3l	chr10	+	tss_body	78138155
51	cg28691674_TC21	0.0008496	-0.05263187	Lower		chr10	-	tss_200	79612378
52	cg28703612_TC21	0.00051474	0.06666161	Higher	C2cd4c	chr10	-	tss_body	79639929
53	cg28704178_TC21	0.00087018	-0.07381844	Lower	Odf3l2	chr10	-	tss_body	80020053
54	cg28712058_TC21	0.00049813	-0.09796213	Lower	Hmha1	chr10	+	tss_body	80188591
55	cg28715881_TC21	0.00056911	-0.12565113	Lower	Efna2	chr10	+	tss_body	80256642
56	cg28717035_BC21	0.00032354	-0.10542174	Lower	Ndufs7	chr10	+	tss_body	80301249
57	cg28717946_TC21	0.00035624	0.07188794	Higher	Apc2	chr10	+	tss_body	80301897
58	cg28717954_TC21	0.00079883	-0.11335916	Lower	Apc2	chr10	+	tss_body	80315075
59	cg28718344_TC21	0.00037822	-0.0607065	Lower	Apc2	chr10	+	tss_body	81022155

60	cg28731961_TC21	0.00023954	-0.06298901	Lower	Diras1	chr10	-	tss_body	81027642
61	cg28732083_TC21	0.00024287	0.07098982	Higher	chr10-81031112-81031665	chr10	*	NShelf	81325869
62	cg28738416_BC21	0.00021941	-0.08176556	Lower	Cactin	chr10	+	tss_body	81628515
63	cg28744456_TC21	8.555E-05	-0.05954577	Lower	Sirt6	chr10	-	tss_1500	83119019
64	cg28756860_BC21	0.00035829	-0.12429126	Lower	Chst11	chr10	+	tss_body	84391540
65	cg28770147_BC21	4.4302E-05	0.08610892	Higher	Nuak1	chr10	-	tss_body	84533157
66	cg28771954_TC11	0.00048518	0.06244672	Higher	Ckap4	chr10	-	tss_body	86335937
67	cg28790092_BC21	0.00062121	0.07095494	Higher	Syn3	chr10	-	tss_body	87128768
68	cg28797416_BC21	6.0188E-05	-0.06144422	Lower	1700113H08Rik	chr10	+	tss_body	87230543
69	cg28798228_BC21	6.2945E-05	-0.06770365	Lower	1700113H08Rik	chr10	+	tss_body	88350009
70	cg28806717_BC21	0.00010045	0.09710081	Higher	Dram1	chr10	-	tss_body	88446635
71	cg28808117_BC21	0.00033585	0.12355613	Higher	Gnptab	chr10	+	tss_body	88671450
72	cg28810335_TC21	0.00094391	-0.05654636	Lower		chr10	-	tss_200	89756598
73	cg28819830_BC21	0.00015932	-0.0564701	Lower	Uhrf1bp1l	chr10	+	tss_body	90575618
74	cg28825588_BC21	0.00022318	0.08216104	Higher	Anks1b	chr10	+	tss_body	92103909
75	cg28839136_TC21	0.00047794	-0.12874145	Lower	Rmst	chr10	-	tss_body	93035526
76	cg28846771_TC21	0.000788	0.0545561	Higher	Cfap54	chr10	-	tss_body	93084152
77	cg28847336_BC21	1.3796E-06	0.0864051	Higher	Cfap54	chr10	-	tss_1500	95112357
78	cg28871462_BC21	0.00041533	0.07621902	Higher					95460566
79	cg28875950_TC21	0.00057325	-0.0998759	Lower		chr10	-	tss_body	95561067
80	cg28877143_BC21	0.00024466	-0.06918082	Lower	Nudt4	chr10	-	tss_body	100576355
81	cg28915970_BC21	0.00061611	0.11268863	Higher	4930430F08Rik	chr10	-	tss_body	102365701
82	cg28924314_BC21	0.00035083	0.15571917	Higher	Mgat4c	chr10	+	tss_body	107860410
83	cg28955595_TC21	0.0006487	-0.06594465	Lower	Otogl	chr10	-	tss_body	108884466
84	cg28965273_BC21	0.00063499	-0.07074686	Lower	Syt1	chr10	-	tss_body	110733828
85	cg28977237_BC11	0.00027893	-0.11486656	Lower					110931115
86	cg28979681_BC11	0.00025379	0.08737603	Higher	Csrp2	chr10	+	tss_body	111654858
87	cg28988145_TC11	4.0347E-05	0.14483169	Higher					111800055
88	cg28989562_TC21	0.00058771	0.08239562	Higher		chr10	+	tss_body	116771886
89	cg29028280_BC11	1.0793E-05	-0.06231358	Lower					117642184

90	cg29039885_BC11	0.00022053	-0.06317444	Lower	Cpm	chr10	+	tss_body	118121573
91	cg29046663_TC21	0.00087089	-0.08071452	Lower		chr10	+	tss_body	118121754
92	cg29046671_BC21	0.00056031	-0.05412603	Lower		chr10	+	tss_body	118435357
93	cg29049696_TC21	0.00033034	0.0547175	Higher					119496198
94	cg29061901_BC21	0.00012746	-0.06141246	Lower	Grip1	chr10	+	tss_body	119806095
95	cg29065738_BC21	0.00024394	-0.10117696	Lower	Grip1	chr10	+	tss_body	120416662
96	cg29074081_TC21	0.00018999	0.09803363	Higher	Hmga2	chr10	-	tss_body	122679248
97	cg29102689_BC21	0.00024776	0.06349652	Higher	Ppm1h	chr10	+	tss_body	123883160
98	cg29114933_BC11	0.00021969	0.06286658	Higher					126709271
99	cg29136023_BC21	0.00010722	0.16397511	Higher					127060508
100	cg29141167_TC11	0.00074334	0.08419641	Higher	March9	chr10	-	tss_1500	127508662
101	cg29148419_BC11	0.0001487	0.10396404	Higher	Stac3	chr10	+	tss_body	127510118
102	cg29148470_TC11	7.4815E-05	-0.09219369	Lower	chr10-127512785-127513196	chr10	*	NShelf	127866468
103	cg29153934_TC21	0.00069393	-0.06923323	Lower	BC089597	chr10	+	tss_200	127970181
104	cg29154927_TC21	0.00035444	0.07931066	Higher	Gm40806	chr10	-	tss_body	3540889
105	cg29181100_BC21	0.00012544	-0.05796551	Lower	Gm33983	chr11	+	tss_body	4098346
106	cg29187387_BC21	0.0005164	-0.09024733	Lower	Sec14l2	chr11	-	tss_body	5106338
107	cg29199185_TC21	8.6897E-06	-0.07222491	Lower	Emid1	chr11	-	tss_body	5244301
108	cg29201125_TC21	0.00023513	0.16046856	Higher	Kremen1	chr11	-	tss_body	5803518
109	cg29207068_BC21	0.00068105	-0.0934749	Lower	Pgam2	chr11	-	tss_body	5874833
110	cg29208019_TC21	0.00080464	-0.06024146	Lower	Pold2	chr11	-	tss_body	11668640
111	cg29249597_TC21	0.00018996	0.05024456	Higher	Gm11999	chr11	-	tss_body	11822271
112	cg29251115_TC11	0.00074994	0.13250119	Higher	Ddc	chr11	-	tss_body	11884928
113	cg29251780_TC21	0.00039776	0.15059496	Higher	Ddc	chr11	-	tss_body	19008232
114	cg29289323_TC11	0.00035414	-0.14964416	Lower	Meis1	chr11	-	tss_body	19783764
115	cg29295759_BC21	0.00094735	-0.12225844	Lower		chr11	+	tss_body	20648016
116	cg29304932_BC21	0.0003863	-0.09351648	Lower	Sertad2	chr11	+	tss_body	22348015
117	cg29317119_BC21	0.00051893	-0.05966427	Lower					22860979
118	cg29320667_TC21	0.00089978	0.08952877	Higher	B3gnt2	chr11	-	tss_1500	22973866
119	cg29321596_TC11	0.00067597	0.07274812	Higher	Commd1	chr11	-	tss_body	22973947

120	cg29321599_TC21	0.00073835	0.05430656	Higher	Commd1	chr11	-	tss_body	23519922
121	cg29325936_BC21	4.8524E-05	-0.10715134	Lower	1700093K21Rik	chr11	-	tss_body	27229648
122	cg29347536_BC21	9.8176E-05	0.05008111	Higher					33122805
123	cg29386043_TC21	0.00038719	-0.05211031	Lower	Fgf18	chr11	-	tss_body	34170036
124	cg29396116_TC21	0.00011978	0.15314119	Higher					36214619
125	cg29415956_BC21	0.00027895	0.16260516	Higher	Tenm2	chr11	-	tss_body	45241680
126	cg29471896_BC21	4.1286E-05	0.06505418	Higher					46838255
127	cg29486285_BC21	0.00031598	0.07858865	Higher	Timd4	chr11	+	tss_body	47270019
128	cg29488552_BC21	0.00016467	0.09251841	Higher	Sgcd	chr11	-	tss_body	48290186
129	cg29493584_BC21	0.00080355	-0.05614257	Lower		chr11	-	tss_body	48595215
130	cg29495221_TC21	0.00015041	-0.07203199	Lower		chr11	+	tss_200	48805905
131	cg29496976_BC21	0.00050022	0.0791327	Higher	Rack1	chr11	+	tss_body	48997671
132	cg29498974_BC21	0.00027273	-0.0703626	Lower	Q8VGD6	chr11	+	tss_body	49070802
133	cg29499183_TC21	0.00093585	-0.05047735	Lower	Olfr56	chr11	+	tss_body	53478671
134	cg29545754_BC21	8.497E-05	0.06554906	Higher	Sowaha	chr11	-	tss_body	53478691
135	cg29545755_TC11	0.00012715	0.0713441	Higher	Sowaha	chr11	-	tss_body	53539376
136	cg29546696_TC21	0.00054381	-0.10159051	Lower	Sept8	chr11	+	tss_body	53759421
137	cg29549368_TC21	0.00041825	0.1491937	Higher					54744750
138	cg29558109_TC11	0.0006811	0.07146483	Higher	Cdc42se2	chr11	-	tss_body	55406045
139	cg29565309_TC21	0.00042851	-0.08398449	Lower	Sparc	chr11	-	tss_body	57573966
140	cg29580489_TC21	0.00053623	0.11445737	Higher		chr11	+	tss_body	57778058
141	cg29583297_TC21	5.0191E-05	-0.07578352	Lower	Galnt10	chr11	+	tss_body	57880833
142	cg29584972_TC21	0.00064893	-0.05078042	Lower		chr11	+	tss_200	58097862
143	cg29587422_BC21	0.00022937	0.10889903	Higher	Cnot8	chr11	+	tss_body	60872947
144	cg29619078_TC21	0.00046449	0.05701836	Higher	Tmem11	chr11	-	tss_body	61304266
145	cg29624278_TC21	0.00025592	-0.09499798	Lower	Slc47a2	chr11	-	tss_body	61362994
146	cg29625009_BC21	0.00048857	-0.06934746	Lower	Slc47a1	chr11	-	tss_body	61407981
147	cg29625608_BC21	0.00053611	0.05793126	Higher	chr11-61407999-61408727	chr11	*	NShore	62513118
148	cg29636353_BC21	0.00022354	-0.16779214	Lower	Pigl	chr11	+	tss_body	63953573
149	cg29650820_BC21	0.00077157	-0.05810214	Lower					65205208

150	cg29661768_TC21	0.00015586	-0.07857102	Lower	Myocd	chr11	-	tss_body	66956628
151	cg29674113_BC11	0.00016595	0.05233099	Higher	9130409J20Rik	chr11	+	tss_1500	67695539
152	cg29682169_BC21	0.00036236	-0.05133565	Lower	Glp2r	chr11	-	tss_body	68114300
153	cg29686439_TC11	0.00018798	0.08439455	Higher	Stx8	chr11	+	tss_body	69658966
154	cg29708399_TC21	4.127E-05	-0.07616379	Lower	Mpdu1	chr11	-	tss_body	70466078
155	cg29720959_BC21	0.00049285	0.09325491	Higher	Zmynd15	chr11	+	tss_body	70509866
156	cg29721404_TC21	7.1596E-05	0.05551662	Higher	Tm4sf5	chr11	+	tss_body	70552704
157	cg29722094_BC21	8.5001E-05	-0.0601182	Lower	Pld2	chr11	+	tss_body	71594606
158	cg29731427_BC21	0.00048016	-0.05683512	Lower					72031522
159	cg29735324_BC21	3.6756E-05	-0.10680486	Lower	Aipl1	chr11	-	tss_body	72438118
160	cg29739934_BC21	3.7717E-05	-0.10799958	Lower	Ggt6	chr11	+	tss_body	72497332
161	cg29740804_BC21	0.00035689	-0.07670582	Lower		chr11	-	tss_body	73989784
162	cg29751640_BC21	0.00050392	-0.05180842	Lower	Q8VFY0	chr11	-	tss_body	74659751
163	cg29756721_TC21	0.00065849	-0.05435267	Lower	Cluh	chr11	+	tss_body	75167309
164	cg29761693_BC21	0.00012657	-0.20822923	Lower	Hic1	chr11	-	tss_body	75868584
165	cg29771739_TC21	0.0004828	-0.06815593	Lower	Rph3al	chr11	-	tss_body	76748957
166	cg29782154_BC21	7.6154E-06	-0.06176423	Lower	Gosr1	chr11	-	tss_body	76896553
167	cg29783511_BC21	0.00034477	-0.06556801	Lower	Tmigd1	chr11	+	tss_body	77483677
168	cg29788695_BC21	0.00039905	-0.06891091	Lower	Ankrd13b	chr11	-	tss_body	77786761
169	cg29792091_BC11	3.6163E-05	0.07913774	Higher	Myo18a	chr11	+	tss_body	77941319
170	cg29794376_TC21	4.3561E-05	-0.05569678	Lower	Sez6	chr11	+	tss_body	78023094
171	cg29795514_BC21	1.4437E-05	-0.0550989	Lower	Phf12	chr11	+	tss_body	79016146
172	cg29807346_TC21	8.2366E-05	-0.05265212	Lower	Ksr1	chr11	-	tss_body	79225133
173	cg29810089_BC11	0.00086438	-0.05468375	Lower	Gm30470	chr11	+	tss_body	79273760
174	cg29810621_BC21	2.9366E-05	0.17134772	Higher		chr11	-	tss_body	81199304
175	cg29830927_BC21	0.00041005	-0.07530663	Lower	Asic2	chr11	-	tss_body	82251305
176	cg29839004_TC21	6.1677E-05	-0.05419635	Lower		chr11	-	tss_body	82840686
177	cg29845081_BC21	0.00014602	0.05976117	Higher	Rffl	chr11	-	tss_body	83644672
178	cg29853141_TC21	0.00034501	-0.05900778	Lower					84709278
179	cg29863890_BC21	0.00035948	-0.09561913	Lower					87463528
180	cg29891470_TC21	0.00072418	0.07669502	Higher	Tex14	chr11	+	tss_body	87567528

181	cg29892355_BC21	6.4468E-05	-0.05498335	Lower	Sept4	chr11	+	tss_body	87622925
182	cg29893289_BC21	0.00068227	0.09185824	Higher	Hsf5	chr11	+	tss_body	87697987
183	cg29894002_BC21	0.00031999	0.10870388	Higher	Rnf43	chr11	+	tss_body	87802570
184	cg29895631_BC21	0.00065872	-0.08843646	Lower	Mpo	chr11	+	tss_body	88799796
185	cg29908733_BC21	0.00041341	0.07052246	Higher					90109654
186	cg29922477_BC21	0.00072659	-0.06541058	Lower	Gm34726	chr11	-	tss_body	90392271
187	cg29925747_TC21	0.00030469	-0.07629348	Lower	Hlf	chr11	-	tss_1500	93763494
188	cg29945224_BC21	0.00064923	-0.05109932	Lower					94137423
189	cg29948556_BC11	5.5613E-06	0.1132219	Higher	B230206L02Rik	chr11	+	tss_body	94566455
190	cg29954737_TC21	0.00027627	-0.082674	Lower	Acsf2	chr11	-	tss_body	96006133
191	cg29973879_BC21	4.1477E-06	0.06665627	Higher	Igf2bp1	chr11	-	tss_200	96139553
192	cg29975605_TC21	0.00050297	-0.06419331	Lower	Ttll6	chr11	+	tss_body	96713418
193	cg29984286_BC21	0.00042594	0.06737381	Higher	Skap1	chr11	+	tss_body	96790571
194	cg29985460_TC21	0.00028721	-0.10507838	Lower	Cbx1	chr11	+	tss_body	97016695
195	cg29988815_TC21	0.00022498	0.07468502	Higher	Sp6	chr11	+	tss_body	97534548
196	cg29996728_TC11	0.00054383	-0.18555312	Lower	Srcin1	chr11	-	tss_body	97542503
197	cg29996950_BC21	8.5764E-05	-0.07872585	Lower	Srcin1	chr11	-	tss_body	98018455
198	cg30004657_BC21	4.4068E-05	-0.09973243	Lower	Cacnb1	chr11	-	tss_body	98028977
199	cg30004951_TC21	0.000159	-0.05917682	Lower	Rpl19	chr11	+	tss_body	98384228
200	cg30009848_BC21	0.00066763	-0.07617003	Lower	Tcap	chr11	+	tss_body	98414936
201	cg30010400_TC21	0.00017487	0.05480046	Higher	Erbb2	chr11	+	tss_body	99127996
202	cg30021477_TC11	0.00017596	-0.14605759	Lower					99666329
203	cg30027579_TC21	0.0004204	-0.08151805	Lower	Krtap4-6	chr11	-	tss_1500	100704586
204	cg30038841_TC21	0.00043287	-0.08137408	Lower	Dhx58	chr11	-	tss_1500	100705791
205	cg30038870_TC21	0.0006616	0.08161651	Higher	Kat2a	chr11	-	tss_body	100854315
206	cg30041231_BC21	1.3422E-05	0.08652161	Higher	Stat5b	chr11	-	tss_body	101030237
207	cg30043568_TC21	0.00044183	0.05298101	Higher	Atp6v0a1	chr11	+	tss_body	101068358
208	cg30044113_TC21	0.00054284	-0.13018901	Lower	chr11-101069883-101070493	chr11	*	NShore	101419378
209	cg30049469_BC21	0.00057271	0.07155763	Higher	Ptges3l	chr11	-	tss_body	101575178
210	cg30051522_BC21	0.00031661	-0.08907725	Lower	Nbr1	chr11	+	tss_body	101886654

211	cg30055652_BC21	0.00099801	-0.1007529	Lower	Meox1	chr11	-	tss_body	102196786
212	cg30060424_BC21	0.00038879	0.07209601	Higher	Hdac5	chr11	-	tss_body	102435855
213	cg30064650_TC21	5.0898E-05	-0.06570173	Lower	Grn	chr11	+	tss_body	102637415
214	cg30067470_TC21	0.0006658	-0.06268078	Lower					102639076
215	cg30067490_TC21	0.00075768	-0.06383902	Lower					102957080
216	cg30072057_BC21	0.00031696	-0.05934765	Lower					103325028
217	cg30077797_BC21	0.00010126	0.159634	Higher					105966370
218	cg30104680_TC21	0.00058683	-0.06604611	Lower	Gm11651	chr11	-	tss_body	106389507
219	cg30110228_TC21	0.00040711	-0.13139839	Lower	Icam2	chr11	-	tss_1500	106762803
220	cg30114751_TC21	7.3406E-05	-0.09461799	Lower	Milr1	chr11	+	tss_body	106763080
221	cg30114756_BC21	0.00077785	-0.10040495	Lower	Milr1	chr11	+	tss_body	106804818
222	cg30115426_BC21	0.00079161	-0.05263394	Lower	Cep95	chr11	+	tss_body	107014512
223	cg30117456_BC21	0.00024951	-0.05660013	Lower	chr11-107012600-107012831	chr11	*	SShore	107353322
224	cg30122074_TC21	0.00034923	-0.10514162	Lower	Pitpnc1	chr11	-	tss_body	107738323
225	cg30127215_BC21	0.00021703	-0.08347256	Lower	Cacng4	chr11	-	tss_body	109070013
226	cg30140894_TC21	0.00085005	0.09735601	Higher					109348407
227	cg30144209_BC21	0.00081337	-0.06330846	Lower	1700096J18Rik	chr11	+	tss_body	111658379
228	cg30165622_BC21	0.00066153	-0.06176358	Lower	Gm30219	chr11	-	tss_body	113166742
229	cg30179683_BC21	0.00061377	-0.10796404	Lower	2610035D17Rik	chr11	-	tss_body	113635025
230	cg30186853_TC21	0.00059394	-0.0500521	Lower	Slc39a11	chr11	-	tss_body	113709836
231	cg30188222_BC21	0.00092052	0.08514598	Higher	Cpsf4l	chr11	-	tss_body	113835573
232	cg30190188_BC21	0.00071061	0.10781639	Higher	Sdk2	chr11	-	tss_body	114043970
233	cg30192887_BC21	0.00025844	-0.06136481	Lower	Sdk2	chr11	-	tss_body	114135769
234	cg30194157_BC21	0.00083685	0.05141793	Higher					114361222
235	cg30196810_TC11	0.00026891	0.08154796	Higher					114728947
236	cg30201766_TC11	0.00025944	-0.11781829	Lower	Dnaic2	chr11	+	tss_body	114786358
237	cg30202620_TC11	0.00015078	0.06543473	Higher	Kif19a	chr11	+	tss_body	115282288
238	cg30209024_BC21	0.00034152	-0.06016498	Lower	Fads6	chr11	-	tss_body	115605242
239	cg30214308_BC11	0.0003886	0.06119633	Higher	Gga3	chr11	-	tss_1500	115622777
240	cg30214691_BC21	0.00033354	-0.10594062	Lower	Slc25a19	chr11	-	tss_body	115887565

241	cg30219103_BC21	1.6079E-05	-0.08507	Lower	Myo15b	chr11	+	tss_body	116006609
242	cg30220952_BC21	5.2561E-05	0.09895346	Higher	Itgb4	chr11	+	tss_body	116197233
243	cg30224382_BC21	0.00025275	-0.05680338	Lower	Acox1	chr11	-	tss_body	116222541
244	cg30224851_TC21	0.00073258	-0.09571849	Lower	Evpl	chr11	-	tss_body	116511598
245	cg30230014_BC21	0.00049062	-0.05703851	Lower					116985686
246	cg30237834_BC21	0.00050612	-0.05297436	Lower	Mgat5b	chr11	+	tss_body	116990300
247	cg30237908_TC11	0.00026093	-0.05013631	Lower					117694187
248	cg30248118_BC21	0.00074284	0.1433671	Higher	Tnrc6c	chr11	+	tss_body	117709414
249	cg30248242_BC21	0.00051809	-0.05823925	Lower	Tnrc6c	chr11	+	tss_body	117777279
250	cg30249131_BC21	6.2133E-05	-0.20487218	Lower	Tmc6	chr11	-	tss_body	117894929
251	cg30251175_BC11	5.4172E-05	-0.12328119	Lower	Gm11725	chr11	+	tss_body	118005516
252	cg30252966_BC21	0.00053078	-0.05798034	Lower	Pgs1	chr11	+	tss_body	118803201
253	cg30264787_BC21	0.00036789	0.14943736	Higher	Rbfox3	chr11	-	tss_body	119543123
254	cg30277184_BC21	0.00089545	-0.09769686	Lower	Nptx1	chr11	-	tss_body	120251566
255	cg30287396_TC21	0.00095691	-0.10113468	Lower	Bahcc1	chr11	+	tss_body	120749630
256	cg30296060_BC21	0.00038748	0.0546235	Higher					3171757
257	cg30310317_BC21	0.00037297	-0.0613716	Lower		chr12	+	tss_200	3899363
258	cg30317299_TC21	0.00025519	0.12796683	Higher	Dnmt3a	chr12	+	tss_body	4849052
259	cg30326689_TC21	0.00039304	-0.0903301	Lower	BC068281	chr12	+	tss_body	5247320
260	cg30330951_TC21	0.00088132	-0.05253319	Lower	Klhl29	chr12	-	tss_body	5304767
261	cg30331555_TC21	0.00089429	-0.07274989	Lower	Klhl29	chr12	-	tss_body	8268366
262	cg30347469_BC21	0.00031404	-0.08479912	Lower	Ldah	chr12	+	tss_body	8353447
263	cg30348835_BC21	2.825E-05	0.1099515	Higher					8445678
264	cg30349627_BC11	0.00016436	-0.11498277	Lower					12589160
265	cg30376961_TC21	0.00099014	-0.06844031	Lower					17034176
266	cg30406372_TC21	0.00064641	-0.07377997	Lower					17280371
267	cg30408802_TC21	0.00030952	-0.06792533	Lower	Pdia6	chr12	+	tss_body	17308596
268	cg30409084_TC21	6.3774E-05	0.06329942	Higher	Atp6v1c2	chr12	-	tss_body	17470142
269	cg30410661_TC21	0.00032699	-0.10035298	Lower					25240707
270	cg30469482_TC21	0.00046124	-0.05990531	Lower					26211605
271	cg30475854_TC21	0.00098298	0.10409157	Higher	Gm29687	chr12	-	tss_1500	27501321

272	cg30484969_TC21	0.00011341	0.09938875	Higher					28776043
273	cg30493652_TC21	0.00065624	-0.05387369	Lower	Tssc1	chr12	+	tss_body	29084208
274	cg30496381_TC21	0.00031844	-0.06368763	Lower	Gm31333	chr12	+	tss_body	29699389
275	cg30501011_TC21	0.00057859	0.1041672	Higher	Myt1l	chr12	+	tss_body	30348576
276	cg30506221_BC21	0.00038305	0.08018113	Higher	Sntg2	chr12	-	tss_body	31240882
277	cg30512774_TC21	0.00011912	-0.06382335	Lower	A0A1W2P738	chr12	+	tss_body	32105026
278	cg30520919_BC21	0.00042292	-0.10620889	Lower	5430401H09Rik	chr12	-	tss_body	32111514
279	cg30520964_TC21	0.00012299	-0.11656733	Lower	5430401H09Rik	chr12	-	tss_body	35925610
280	cg30548414_TC21	0.00049915	0.18123505	Higher	Agr3	chr12	+	tss_200	36214924
281	cg30551116_TC21	0.00072255	-0.08948254	Lower	Lrrc72	chr12	-	tss_body	39301459
282	cg30566758_BC21	0.0003417	-0.15855244	Lower					46817225
283	cg30607694_BC11	0.00036233	0.0782884	Higher	Nova1	chr12	-	tss_body	53501083
284	cg30649710_BC21	0.00011617	-0.06135598	Lower	Npas3	chr12	+	tss_body	54316469
285	cg30657324_BC11	0.00029997	0.09550718	Higher	chr12-54313169-54313370	chr12	*	SShelf	55640366
286	cg30670477_BC21	0.00046699	0.10298547	Higher	Ralgapa1	chr12	-	tss_body	56589628
287	cg30678041_TC21	0.0007638	-0.12827743	Lower	Gm26973	chr12	+	tss_body	57571522
288	cg30686574_BC21	0.00013956	-0.14292689	Lower	Ttc6	chr12	+	tss_body	69145487
289	cg30745744_TC21	0.00012737	0.16609981	Higher					69756688
290	cg30753175_BC21	1.2705E-05	0.1004623	Higher	Cdkl1	chr12	-	tss_body	71252834
291	cg30769850_TC21	0.00036596	-0.05100458	Lower	2700049A03Rik	chr12	+	tss_body	72238830
292	cg30780200_TC21	0.00021058	0.06997587	Higher	Rtn1	chr12	-	tss_body	72382289
293	cg30781740_BC11	0.00061648	0.06481055	Higher	Rtn1	chr12	-	tss_body	72409082
294	cg30782070_BC21	8.8156E-05	-0.06430211	Lower	Rtn1	chr12	-	tss_200	75203418
295	cg30807007_TC21	8.7409E-05	-0.06281993	Lower					76546989
296	cg30822155_TC21	0.00091674	0.15937058	Higher	Plekhg3	chr12	+	tss_body	76606393
297	cg30823045_BC11	5.643E-05	-0.13013293	Lower	Sptb	chr12	-	tss_body	79066633
298	cg30842349_BC21	9.055E-05	0.0703045	Higher	Plekhh1	chr12	+	tss_body	79536079
299	cg30846681_TC21	0.00047789	0.151519	Higher	Rad51b	chr12	+	tss_body	79974985
300	cg30850793_TC21	0.00064969	-0.06763265	Lower					80081524
301	cg30851811_TC21	0.00029296	0.09100861	Higher	Gm36660	chr12	-	tss_body	80220403

302	cg30853730_BC21	0.00045455	0.14132669	Higher	Actn1	chr12	-	tss_body	80406705
303	cg30855703_TC11	0.00095894	0.0866095	Higher	Dcaf5	chr12	-	tss_body	80653916
304	cg30858292_BC21	0.0005256	0.14042247	Higher	Slc39a9	chr12	+	tss_body	81205472
305	cg30863998_TC21	0.00040557	0.0963239	Higher	Slc8a3	chr12	-	tss_body	83504740
306	cg30886046_TC21	1.2201E-05	-0.05113951	Lower		chr12	+	tss_1500	84053055
307	cg30892325_BC21	0.00011588	0.10974613	Higher	Acot3	chr12	+	tss_body	84642493
308	cg30899823_BC21	0.00071987	-0.08662305	Lower	Vrtn	chr12	+	tss_body	85462250
309	cg30910036_TC21	0.0001058	-0.08154755	Lower					85523841
310	cg30910931_BC21	2.3558E-05	0.1638013	Higher					86074694
311	cg30917013_BC21	0.0002536	0.05311608	Higher	Tgfb3	chr12	-	tss_body	86244286
312	cg30919303_TC21	0.00042592	-0.07926773	Lower	Gpatch2l	chr12	+	tss_body	86806531
313	cg30925986_TC21	0.00066014	0.08358537	Higher					86988384
314	cg30928637_BC11	8.943E-05	-0.06652588	Lower	Zdhhc22	chr12	-	tss_body	87038526
315	cg30929300_BC21	0.00046257	-0.10625281	Lower	Tmem63c	chr12	+	tss_body	87862233
316	cg30935464_TC21	0.00011479	-0.05795798	Lower	Gm1995	chr12	+	tss_body	90408674
317	cg30949928_TC21	2.0238E-05	0.10678724	Higher	Gm40538	chr12	-	tss_body	91746006
318	cg30960256_BC21	0.0009913	-0.05027466	Lower	Ston2	chr12	-	tss_body	91923991
319	cg30962387_BC21	0.00015503	-0.09162367	Lower					98745291
320	cg30998932_TC21	0.00010315	0.08190669	Higher	chr12-98746804-98747423	chr12	*	NShore	98992964
321	cg31001095_BC21	0.00014509	-0.07593889	Lower		chr12	-	tss_body	99046694
322	cg31001573_BC21	0.00026804	0.08122778	Higher	Gm40554	chr12	+	tss_body	100179270
323	cg31015715_BC21	0.00037561	0.15412563	Higher	Gm36263	chr12	-	tss_body	100290381
324	cg31017196_TC21	0.00060548	0.08401902	Higher	Gm10432	chr12	+	tss_body	100403700
325	cg31018420_TC21	3.1417E-05	-0.07025758	Lower	Ttc7b	chr12	-	tss_body	100479643
326	cg31019114_BC21	0.00021296	0.08832587	Higher	Ttc7b	chr12	-	tss_body	100785954
327	cg31021807_BC21	0.00093469	-0.08713948	Lower	9030617O03Rik	chr12	+	tss_body	102290082
328	cg31034008_TC21	0.00095435	-0.07698411	Lower	Rin3	chr12	+	tss_body	102678813
329	cg31038717_TC21	2.2842E-05	-0.1101116	Lower	Itpk1	chr12	-	tss_body	103437263
330	cg31047476_TC21	0.00068243	0.12011569	Higher	Ifi27l2a	chr12	-	tss_body	103688837
331	cg31049410_TC21	0.00057299	-0.10512836	Lower	LOC108168025	chr12	+	tss_body	104780809

332	cg31059495_TC11	4.1015E-06	-0.09728755	Lower	Clmn	chr12	-	tss_body	104835699
333	cg31060274_BC21	0.00028348	0.0953717	Higher	Clmn	chr12	-	tss_body	105031070
334	cg31063046_BC21	0.00028265	-0.05470371	Lower	Snhg10	chr12	-	tss_body	105297905
335	cg31066070_TC21	0.0009544	0.13261351	Higher					105643860
336	cg31070811_TC21	0.00063052	0.05339263	Higher	Atg2b	chr12	-	tss_body	107372413
337	cg31092069_TC21	0.00061711	0.05687153	Higher					109526526
338	cg31119408_TC21	4.909E-05	0.10256379	Higher	Gm3408 1	chr12	-	tss_body	109533574
339	cg31119563_BC21	0.00065943	0.10517281	Higher	Gm3408 1	chr12	-	tss_body	109613283
340	cg31120745_TC21	0.00068855	-0.07914371	Lower	Rian	chr12	+	tss_body	109945774
341	cg31124147_BC21	0.00058541	-0.05979983	Lower	Gm3455 4	chr12	+	tss_body	110381484
342	cg31129634_BC11	1.4905E-05	-0.1747574	Lower					110674043
343	cg31134594_TC21	0.00042826	-0.10795481	Lower	1700001 K19Rik	chr12	-	tss_body	111299633
344	cg31143211_TC21	2.6982E-05	-0.05511995	Lower	Cdc42bp b	chr12	-	tss_body	111417743
345	cg31145412_TC21	0.00051804	0.06621024	Higher	Exoc3l4	chr12	+	tss_1500	111687194
346	cg31149197_BC21	0.00062756	0.06262047	Higher					111916863
347	cg31152738_TC21	0.00028314	-0.10167926	Lower					112175716
348	cg31156523_TC21	3.9195E-05	-0.0788137	Lower	Kif26a	chr12	+	tss_body	112541462
349	cg31161881_BC21	1.7841E-05	0.05734667	Higher					112654327
350	cg31163738_BC21	3.7202E-05	-0.07195016	Lower	Akt1	chr12	-	tss_body	112765009
351	cg31165859_TC21	0.00025825	-0.0501574	Lower	Pld4	chr12	+	tss_body	116367008
352	cg31189399_BC21	0.00067722	-0.07536571	Lower	Esyt2	chr12	+	tss_body	116927101
353	cg31193043_TC21	0.00090208	-0.11420465	Lower	Ptprn2	chr12	+	tss_body	117886810
354	cg31201098_TC21	0.00080554	-0.08294085	Lower	Dnah11	chr12	-	tss_body	6649665
355	cg31236807_BC21	0.00038109	-0.05672403	Lower	Pfkp	chr13	-	tss_1500	11653547
356	cg31266683_BC21	0.00068859	0.17822951	Higher	Ryr2	chr13	-	tss_body	13995230
357	cg31284760_BC21	4.4616E-05	0.07363511	Higher	B3galnt2	chr13	+	tss_body	15211789
358	cg31291174_BC11	0.00018892	0.11603032	Higher					19733001
359	cg31317963_BC21	0.00017272	-0.0667301	Lower	A530099 J19Rik	chr13	-	tss_200	28719111
360	cg31379956_TC21	0.00034387	0.17648464	Higher	2610307 P16Rik	chr13	-	tss_body	28836863
361	cg31381076_TC21	0.00049311	-0.08033381	Lower	2610307 P16Rik	chr13	-	tss_body	30211324
362	cg31393704_TC21	0.00036091	-0.08230122	Lower	Mboat1	chr13	+	tss_body	32615821

363	cg31412871_TC21	1.1268E-05	-0.15235233	Lower					32898192
364	cg31414835_BC11	9.4028E-05	0.10596914	Higher	Serpinb1c	chr13	-	tss_body	33086906
365	cg31415822_TC21	0.00034397	0.07641882	Higher	Serpinb1b	chr13	+	tss_body	33159792
366	cg31416142_TC21	0.00076095	0.09365143	Higher	Serpinb9c	chr13	-	tss_1500	34239292
367	cg31422434_BC21	0.00073639	0.18743681	Higher	Slc22a23	chr13	-	tss_body	35868443
368	cg31434819_BC21	0.00015374	-0.05679197	Lower	Cdyl	chr13	+	tss_body	38554368
369	cg31459367_BC21	0.00074636	0.14239959	Higher	Gm40922	chr13	+	tss_1500	38614535
370	cg31460055_BC21	0.00028305	-0.12827715	Lower	Bloc1s5	chr13	-	tss_body	41491845
371	cg31486148_TC21	0.00018131	0.08735438	Higher	Gm32401	chr13	+	tss_body	44321342
372	cg31515818_TC21	0.00012035	-0.05376441	Lower					44556509
373	cg31518528_TC21	0.00088638	-0.11795625	Lower	Gm34276	chr13	-	tss_body	44586558
374	cg31518870_BC21	0.00037846	-0.09972663	Lower	Gm40931	chr13	-	tss_body	44903192
375	cg31522038_TC11	0.00055969	-0.0861272	Lower	Jarid2	chr13	+	tss_body	46752546
376	cg31541651_BC21	0.00093612	-0.06438435	Lower	Kif13a	chr13	-	tss_body	47010523
377	cg31545251_TC21	0.00038265	-0.05618691	Lower		chr13	+	tss_body	48292148
378	cg31558485_BC21	0.00056563	-0.06639536	Lower					48508729
379	cg31560740_TC21	0.00013373	-0.1012322	Lower	Zfp169	chr13	-	tss_body	48626264
380	cg31562055_TC21	0.00095856	-0.06168052	Lower	Ptpdc1	chr13	-	tss_1500	49607814
381	cg31573102_TC21	0.00048896	0.1020419	Higher	Cenpp	chr13	-	tss_body	51704832
382	cg31590044_BC21	2.0304E-05	-0.06933443	Lower	Sema4d	chr13	-	tss_body	52080088
383	cg31594932_BC11	0.00050194	-0.05161678	Lower					52829344
384	cg31602828_BC21	0.00015733	0.05187169	Higher	Gm33315	chr13	+	tss_body	53016386
385	cg31605770_TC21	0.00061179	-0.10464257	Lower	Gm33424	chr13	+	tss_body	53969063
386	cg31617339_BC11	0.00056213	-0.06265051	Lower		chr13	+	tss_body	55247879
387	cg31633880_TC21	0.00088052	-0.08035691	Lower	Nsd1	chr13	+	tss_body	56329977
388	cg31649821_BC21	0.00035159	0.07975923	Higher					56888084
389	cg31656831_BC21	0.00082045	-0.06977548	Lower	Trpc7	chr13	-	tss_body	57580220
390	cg31663748_TC11	0.00025176	-0.05632035	Lower	Spock1	chr13	-	tss_body	58000145
391	cg31668749_BC11	0.00017961	0.0723111	Higher					58115012
392	cg31670513_BC21	0.00041166	-0.11938233	Lower	Klhl3	chr13	-	tss_body	58442758
393	cg31674961_TC11	3.8047E-05	-0.08942322	Lower		chr13	+	tss_1500	59738893

394	cg31690478_BC11	0.0006853	0.10109184	Higher		chr13	+	tss_body	60757027
395	cg31701790_BC21	0.00039369	0.12575133	Higher	Dapk1	chr13	+	tss_body	60936687
396	cg31702854_TC11	0.00012352	-0.14576264	Lower	Ctla2a	chr13	-	tss_200	63049104
397	cg31716011_TC21	0.0009033	0.10907777	Higher	2010111I01Rik	chr13	+	tss_body	73836778
398	cg31798672_BC21	6.8639E-05	0.09996698	Higher	Nkd2	chr13	-	tss_body	74049878
399	cg31800688_BC11	3.7449E-05	-0.05631711	Lower	Cep72	chr13	-	tss_body	75876971
400	cg31811294_TC21	0.00021747	-0.05241566	Lower	Rhobtb3	chr13	-	tss_body	81768766
401	cg31843445_BC21	0.00011394	-0.06597243	Lower					82068700
402	cg31845359_TC11	0.00058804	0.46407326	Higher					84690614
403	cg31859167_BC21	7.7007E-05	-0.14598978	Lower	Gm34196	chr13	-	tss_body	92305978
404	cg31898342_TC21	8.0599E-05	-0.06476382	Lower	Msh3	chr13	-	tss_body	93744295
405	cg31911445_TC21	0.00034151	0.0635539	Higher	Dmgdh	chr13	+	tss_body	95495226
406	cg31930639_TC11	0.00081551	0.06752597	Higher					95616388
407	cg31932089_BC21	0.00091062	-0.05009953	Lower	F2r	chr13	-	tss_body	98516670
408	cg31962489_TC21	0.00012867	-0.08374856	Lower					99505201
409	cg31973849_TC21	0.0008503	-0.06128302	Lower	Map1b	chr13	-	tss_body	99607573
410	cg31975019_TC21	0.00039693	-0.05762772	Lower					99880206
411	cg31977527_TC11	0.0006367	0.13306458	Higher					100153883
412	cg31980402_BC21	0.00034566	0.14654522	Higher	Naip2	chr13	-	tss_body	105271010
413	cg32023128_TC21	0.00071719	0.07306531	Higher	Rnf180	chr13	-	tss_body	107569133
414	cg32037759_TC21	0.00044483	-0.10890416	Lower	Gm31920	chr13	+	tss_body	111659656
415	cg32072899_BC21	0.00053893	0.05184638	Higher					112832078
416	cg32087099_TC21	0.00033193	0.16985938	Higher	Plpp1	chr13	+	tss_body	113209707
417	cg32091660_TC21	0.00030852	-0.11079986	Lower	Gm41069	chr13	-	tss_body	116441796
418	cg32119025_TC21	3.2245E-05	0.13391127	Higher					7822888
419	cg32160935_TC21	5.0084E-05	-0.0965751	Lower	Flnb	chr14	+	tss_body	8206768
420	cg32165266_BC21	0.00042696	-0.05591402	Lower					9597527
421	cg32173885_BC11	0.00014706	-0.08677963	Lower	Fhit	chr14	-	tss_body	11710982
422	cg32186140_TC21	0.00016191	-0.05501768	Lower	Ptprg	chr14	+	tss_body	11941660
423	cg32188201_BC21	0.00079393	0.13983278	Higher	Ptprg	chr14	+	tss_body	12111907
424	cg32189586_BC21	1.6247E-05	0.09814462	Higher	Ptprg	chr14	+	tss_body	12455602

425	cg32192702_TC21	0.00050295	0.11885382	Higher	Cadps	chr14	-	tss_body	14659082
426	cg32206002_BC21	7.9327E-05	-0.05166141	Lower		chr14	+	tss_200	18327378
427	cg32225794_TC11	0.000168	0.11345814	Higher	Ube2e1	chr14	-	tss_body	19920749
428	cg32235746_BC21	0.00016041	0.10824422	Higher	Gng2	chr14	-	tss_body	20838554
429	cg32245421_TC21	0.00024414	-0.10743287	Lower	Plau	chr14	+	tss_body	21714783
430	cg32253495_TC21	0.00013622	-0.17888469	Lower	Dupd1	chr14	-	tss_1500	22148051
431	cg32258206_TC11	0.00028533	-0.09806933	Lower	1700112E06Rik	chr14	+	tss_body	24014866
432	cg32270956_TC21	8.2738E-05	-0.09265192	Lower	LOC108168142	chr14	-	tss_body	24532598
433	cg32275671_BC21	3.1006E-05	-0.08185917	Lower					24833779
434	cg32277572_TC21	3.5721E-05	-0.09417389	Lower	Gm32008	chr14	+	tss_body	27151412
435	cg32298527_TC21	0.00036764	-0.10391275	Lower	Arhgef3	chr14	+	tss_body	28434763
436	cg32308694_BC21	0.00025677	-0.08172679	Lower	Erc2	chr14	+	tss_body	29788848
437	cg32318685_BC21	0.00065866	-0.08408074	Lower	Gm35281	chr14	-	tss_body	30609136
438	cg32327780_BC21	7.9325E-05	-0.06545879	Lower	Prkcd	chr14	-	tss_body	30889897
439	cg32330768_BC21	0.00041834	-0.07416311	Lower	Itih4	chr14	+	tss_body	31176435
440	cg32334028_BC21	0.00037373	-0.05558669	Lower	Nisch	chr14	-	tss_body	31414674
441	cg32337218_BC21	0.0005347	-0.10148228	Lower	Sh3bp5	chr14	-	tss_body	31414847
442	cg32337222_BC21	0.00060053	-0.12933228	Lower	Sh3bp5	chr14	-	tss_body	31415007
443	cg32337226_BC21	0.00016952	-0.15043864	Lower	Sh3bp5	chr14	-	tss_body	32016779
444	cg32343345_BC21	0.00014182	-0.06933353	Lower					32046354
445	cg32343678_TC21	1.4885E-05	-0.06908387	Lower	Galnt15	chr14	+	tss_body	33328516
446	cg32356927_BC21	0.00018477	-0.1269422	Lower	Arhgap22	chr14	+	tss_body	34599868
447	cg32369155_BC11	0.00097795	-0.08260021	Lower	Opn4	chr14	-	tss_body	45643777
448	cg32424382_TC21	0.00074226	0.05710562	Higher	Ddhd1	chr14	-	tss_body	46224505
449	cg32429088_BC21	0.00060863	0.06112949	Higher	Gm34499	chr14	+	tss_body	46623319
450	cg32432636_BC21	0.00027806	-0.09916639	Lower	4933425B07Rik	chr14	-	tss_body	47005184
451	cg32437202_TC21	0.0002152	-0.0895847	Lower	Samd4	chr14	+	tss_body	47379585
452	cg32441536_BC21	0.00033109	-0.0687264	Lower	Lgals3	chr14	+	tss_body	48344876
453	cg32451798_BC21	0.00078253	-0.0604304	Lower					48387876
454	cg32452247_TC21	0.00024814	0.12001112	Higher		chr14	-	tss_body	49116937
455	cg32459734_BC21	0.00017357	-0.05668605	Lower		chr14	-	tss_body	52017987

456	cg32479085_BC21	0.00040127	-0.06657721	Lower	Zfp219	chr14	-	tss_body	52066589
457	cg32479642_TC11	7.4479E-05	0.10362586	Higher					52265740
458	cg32481748_TC21	8.2654E-05	0.05104797	Higher	Rab2b	chr14	-	tss_body	54157234
459	cg32493000_BC21	0.00087613	0.05618057	Higher		chr14	+	tss_1500	55085418
460	cg32505831_TC21	6.9801E-05	0.07354666	Higher	Zfhx2	chr14	-	tss_body	57538428
461	cg32530526_TC21	0.00021345	-0.07301744	Lower	Il17d	chr14	+	tss_body	59094311
462	cg32543246_BC21	0.00052449	-0.09368722	Lower					62292431
463	cg32572578_TC21	0.00088453	0.22569184	Higher	Dleu7	chr14	-	tss_body	62944106
464	cg32578285_BC21	0.00033757	-0.06447143	Lower	Wdfy2	chr14	+	tss_body	67307219
465	cg32622448_BC21	0.00069838	-0.19621825	Lower	Ebf2	chr14	+	tss_body	67536698
466	cg32624901_BC21	0.00046735	-0.14897233	Lower					69697219
467	cg32641735_TC11	0.00013955	0.18388913	Higher					69767644
468	cg32642581_TC11	3.5096E-05	0.07413942	Higher	Tnfrsf10b	chr14	+	tss_body	70081171
469	cg32647039_BC21	0.00038135	0.05024564	Higher	Egr3	chr14	+	tss_body	70395468
470	cg32650531_TC21	7.2587E-05	-0.17048262	Lower	Piwil2	chr14	-	tss_body	70604587
471	cg32653557_TC21	0.00082011	-0.08367211	Lower	Dmtn	chr14	-	tss_body	72342007
472	cg32664780_BC21	0.00084227	0.06045	Higher					73049309
473	cg32669876_TC21	0.00070574	-0.18135152	Lower	Cysltr2	chr14	-	tss_200	73107799
474	cg32670323_BC11	0.00061536	0.08840857	Higher					73166410
475	cg32670974_TC21	0.00089921	-0.08128565	Lower	Rcbtb2	chr14	+	tss_body	73173952
476	cg32671065_BC21	0.00077106	-0.07958075	Lower	Rcbtb2	chr14	+	tss_body	73518096
477	cg32674366_TC21	0.00015904	0.06181845	Higher	Med4	chr14	+	tss_body	74451773
478	cg32679292_BC21	0.00055431	-0.09546737	Lower		chr14	-	tss_1500	74890577
479	cg32682961_BC21	0.00077202	-0.05479305	Lower	Lrch1	chr14	-	tss_body	75851156
480	cg32693248_TC21	0.00075166	-0.06894579	Lower					76526813
481	cg32701291_BC21	2.8117E-05	-0.097161	Lower		chr14	+	tss_body	77155822
482	cg32707289_BC21	0.00092748	0.12356757	Higher	Enox1	chr14	+	tss_body	77474433
483	cg32710680_TC21	0.00087211	0.05398698	Higher	Enox1	chr14	+	tss_body	82921281
484	cg32748938_TC21	1.4395E-05	-0.05895916	Lower					87613832
485	cg32774362_BC21	0.00047645	-0.08854724	Lower					97107630
486	cg32817566_TC21	0.00080045	0.10308447	Higher					99219845

487	cg32831221_TC21	0.00022576	0.13199843	Higher	Pibf1	chr14	+	tss_body	99578728
488	cg32835052_BC11	0.00054952	0.20408447	Higher	Gm33997	chr14	+	tss_body	102835328
489	cg32858627_TC21	0.0003048	0.08101563	Higher	Gm34589	chr14	-	tss_1500	113526921
490	cg32921584_TC21	0.00047505	0.12596618	Higher					115094267
491	cg32930571_BC21	0.00091552	0.12751421	Higher	Gpc5	chr14	+	tss_body	118474104
492	cg32956521_TC21	0.00045312	0.07469914	Higher	chr14-118473814-118474116	chr14	*	Island	119285987
493	cg32967164_BC21	0.00069979	-0.1073702	Lower	Hs6st3	chr14	+	tss_body	120855693
494	cg32982031_BC21	0.00061074	-0.07809832	Lower					121683466
495	cg32992689_TC11	0.00024683	-0.06758092	Lower	Dock9	chr14	-	tss_body	10952598
496	cg33073345_TC21	0.00026611	-0.10449518	Lower	Gm34315	chr15	-	tss_body	12196593
497	cg33084122_BC21	8.2612E-05	-0.0768715	Lower		chr15	-	tss_body	25026515
498	cg33152524_BC21	0.00026222	0.05849876	Higher	Gm2824	chr15	-	tss_body	25373026
499	cg33155380_BC21	0.00042938	-0.06516817	Lower	Basp1	chr15	-	tss_body	25411708
500	cg33155793_TC21	0.00072918	-0.05103443	Lower	Basp1	chr15	-	tss_body	25768584
501	cg33160278_BC21	0.00074609	-0.07390916	Lower	Myo10	chr15	+	tss_body	31577643
502	cg33206420_TC11	0.00056229	0.11251504	Higher	Cmbl	chr15	+	tss_body	36309082
503	cg33237608_TC21	0.00072932	0.06011775	Higher		chr15	-	tss_200	36497093
504	cg33239447_TC21	9.5277E-05	0.08129961	Higher	Ankrd46	chr15	-	tss_1500	36886022
505	cg33243737_BC21	0.00079308	0.0507414	Higher					37234868
506	cg33247817_BC21	0.0002111	0.05116022	Higher	Grhl2	chr15	+	tss_body	38472037
507	cg33259896_BC21	0.00093006	-0.12482721	Lower	Gm41308	chr15	+	tss_1500	38937844
508	cg33263063_BC21	0.00083477	0.09370745	Higher	Baalc	chr15	+	tss_body	39674884
509	cg33268660_BC21	0.00072461	-0.07141302	Lower	Rims2	chr15	+	tss_body	41722442
510	cg33282346_TC21	0.00040984	0.05054337	Higher	Oxr1	chr15	+	tss_body	52038484
511	cg33333102_TC11	0.00015092	0.06315246	Higher	chr15-52040030-52040580	chr15	*	NShore	54943746
512	cg33351652_TC21	2.5288E-05	-0.08541395	Lower	Enpp2	chr15	-	tss_body	55363302
513	cg33356136_BC21	0.00012005	0.16671213	Higher	Col14a1	chr15	+	tss_body	56004139
514	cg33360835_BC21	0.00061347	0.07689852	Higher		chr15	+	tss_body	58192316

515	cg33376330_BC11	0.00053942	-0.09400244	Lower	Fbxo32	chr15	-	tss_body	58271191
516	cg33377153_TC21	0.00040544	-0.1136098	Lower		chr15	+	tss_body	59040614
517	cg33385687_TC21	0.00011434	-0.08325263	Lower	Mtss1	chr15	-	tss_body	59994906
518	cg33395657_BC21	0.00083721	0.13128791	Higher		chr15	-	tss_200	60851189
519	cg33400265_TC21	0.0001178	-0.0569101	Lower		chr15	-	tss_body	64376958
520	cg33422756_TC21	0.0007748	-0.05943389	Lower	Asap1	chr15	-	tss_body	65200661
521	cg33427578_TC21	5.6645E-05	-0.10774071	Lower		chr15	-	tss_200	66729855
522	cg33435993_BC21	0.00010094	-0.08111637	Lower	Tg	chr15	+	tss_body	72809502
523	cg33469136_BC11	0.0003193	-0.07273411	Lower	Trappc9	chr15	-	tss_body	73628069
524	cg33478087_TC11	0.00089927	0.10212768	Higher	Slc45a4	chr15	-	tss_body	74956737
525	cg33492728_BC21	0.00025668	-0.12879222	Lower	Ly6e	chr15	+	tss_body	75239803
526	cg33494466_BC21	0.00046027	-0.09520433	Lower		chr15	-	tss_1500	75903455
527	cg33501085_TC21	0.00035143	-0.08272287	Lower	Eef1d	chr15	-	tss_body	75974843
528	cg33502294_BC21	5.4099E-05	-0.06808412	Lower	Zfp707	chr15	+	tss_body	76173788
529	cg33505910_TC21	0.00047178	-0.07007784	Lower	Plec	chr15	-	tss_body	76215515
530	cg33507122_BC21	0.0004246	0.11249102	Higher	Plec	chr15	-	tss_body	76433125
531	cg33510918_BC21	0.00058039	-0.12469468	Lower	Mroh1	chr15	+	tss_body	77339492
532	cg33523294_BC11	9.5247E-05	0.11367179	Higher					77405788
533	cg33524141_TC21	0.00034857	-0.10206277	Lower	Apol9a	chr15	-	tss_body	77781093
534	cg33526945_TC21	9.7164E-05	-0.08115105	Lower	Myh9	chr15	-	tss_body	78170064
535	cg33532451_BC21	0.00049923	-0.10079353	Lower	Ift27	chr15	-	tss_body	78257803
536	cg33533599_TC21	0.00016929	0.05997735	Higher	Ncf4	chr15	+	tss_body	78285212
537	cg33533855_TC21	0.00046857	-0.07824013	Lower	Csf2rb2	chr15	-	tss_body	78387336
538	cg33534732_BC21	0.00023224	-0.08371553	Lower	Tex33	chr15	-	tss_body	78430193
539	cg33535376_BC21	0.00075896	-0.10696868	Lower	Kctd17	chr15	+	tss_body	78619251
540	cg33537975_BC21	0.0005714	-0.05563691	Lower	Cyth4	chr15	+	tss_body	78687430
541	cg33539071_BC21	9.4942E-05	-0.18855441	Lower	Elfn2	chr15	-	tss_body	79305359
542	cg33549573_TC21	0.00022437	0.07235799	Higher	Pla2g6	chr15	-	tss_body	79694233
543	cg33555696_TC21	0.0009105	-0.11966785	Lower	Gtpbp1	chr15	+	tss_body	79900519
544	cg33558764_TC21	0.00039417	-0.05106802	Lower	Apobec3	chr15	+	tss_body	79929924
545	cg33559255_BC21	0.00044862	-0.08265254	Lower	Cbx7	chr15	-	tss_body	80414644

546	cg33566644_BC21	0.00046557	-0.07872046	Lower					81863659
547	cg33583122_TC21	0.00017806	-0.07336963	Lower	chr15-81859644-81859877	chr15	*	SShelf	81937821
548	cg33584041_TC21	0.00033361	-0.09456988	Lower	Csdc2	chr15	+	tss_body	81996027
549	cg33584852_TC21	0.00011956	-0.10382949	Lower	Xrcc6	chr15	+	tss_body	82742077
550	cg33593260_BC21	0.00041429	-0.07837966	Lower		chr15	-	tss_body	83429071
551	cg33601291_TC11	0.00027855	0.09470651	Higher	Pacsin2	chr15	-	tss_body	83602840
552	cg33603800_TC21	0.00082089	-0.10640079	Lower	Scube1	chr15	-	tss_body	84274978
553	cg33613246_BC11	0.00072474	-0.06231325	Lower	Parvb	chr15	+	tss_body	84755650
554	cg33619500_TC21	1.0987E-05	-0.06507665	Lower	Arhgap8	chr15	+	tss_body	84806023
555	cg33620210_BC21	2.4235E-05	-0.05433134	Lower	Phf21b	chr15	-	tss_body	85220232
556	cg33625221_TC21	0.00041723	-0.05287994	Lower	Fbln1	chr15	+	tss_body	85537681
557	cg33628904_BC21	3.5463E-05	-0.10425859	Lower	Wnt7b	chr15	-	tss_body	85600913
558	cg33630016_BC21	4.9909E-05	-0.14721459	Lower					88613054
559	cg33662534_BC21	0.000649	-0.05620153	Lower					88852253
560	cg33665697_BC21	0.0009122	0.05908091	Higher					88935509
561	cg33667039_BC21	0.00017976	-0.05822276	Lower	Ttll8	chr15	-	tss_body	89104098
562	cg33669442_TC21	0.00020678	-0.05288454	Lower	Tubgcp6	chr15	-	tss_body	89334480
563	cg33672951_TC21	0.00088627	0.06866367	Higher	Miox	chr15	+	tss_body	92679718
564	cg33703748_BC11	0.00059451	0.1214019	Higher	Pdzrn4	chr15	+	tss_body	92946243
565	cg33706099_TC11	0.0009935	0.05824365	Higher		chr15	+	tss_body	93105908
566	cg33707570_TC21	0.00067218	0.0584281	Higher					95843705
567	cg33738131_TC21	0.00017745	0.09770146	Higher	Ano6	chr15	+	tss_body	96643946
568	cg33748926_BC21	0.00020586	0.14611152	Higher	Slc38a1	chr15	-	tss_1500	96948800
569	cg33753160_TC11	0.00071079	0.10876291	Higher					97742264
570	cg33764499_BC21	1.8081E-05	-0.11316484	Lower	Gm33531	chr15	+	tss_body	97965366
571	cg33768218_BC11	0.00026205	0.07137234	Higher	Tmem106c	chr15	+	tss_body	98221587
572	cg33772044_TC21	0.0003439	-0.0776852	Lower	Olfr287	chr15	-	tss_1500	99124425
573	cg33786162_BC21	0.00018209	-0.10183153	Lower	Spats2	chr15	+	tss_1500	99568454
574	cg33793231_BC11	0.00014537	0.05744336	Higher					99814892
575	cg33797263_TC21	6.9659E-05	-0.08173104	Lower	Lima1	chr15	-	tss_body	99820064

576	cg33797344_TC21	0.00022896	-0.13762637	Lower	Lima1	chr15	-	tss_body	100528204
577	cg33806537_BC21	0.0003516	-0.13975253	Lower	Tfcp2	chr15	-	tss_body	100681175
578	cg33809015_BC21	1.8321E-05	0.07615381	Higher	Cela1	chr15	-	tss_body	101073898
579	cg33815700_BC21	0.00019118	0.15706696	Higher	Fignl2	chr15	-	tss_body	101364491
580	cg33820221_BC21	0.00038119	-0.12014595	Lower	Krt80	chr15	-	tss_body	101627838
581	cg33823141_BC21	0.00015664	-0.13177061	Lower	Gm5414	chr15	-	tss_body	102251346
582	cg33830745_BC21	0.00079013	0.08070686	Higher	Rarg	chr15	-	tss_body	102667852
583	cg33835294_BC21	0.00073612	0.11679198	Higher	Atp5g2	chr15	-	tss_body	103171915
584	cg33841914_BC21	0.00093179	-0.05101783	Lower	chr15-103170129-103170423	chr15	*	SShore	3976536
585	cg33853376_TC21	0.00076079	-0.0800946	Lower	Nlrc3	chr16	-	tss_body	4034186
586	cg33853976_TC21	0.00013486	-0.05367085	Lower		chr16	-	tss_body	4276441
587	cg33855988_TC21	0.00077621	-0.10033178	Lower	Gm36359	chr16	-	tss_body	4714638
588	cg33860750_TC21	0.0006027	-0.09513463	Lower	Nmral1	chr16	-	tss_body	4958037
589	cg33863384_BC21	0.00030233	-0.06965968	Lower	Anks3	chr16	-	tss_body	6532290
590	cg33875913_TC21	9.4278E-05	-0.06377104	Lower	Rbfox1	chr16	+	tss_body	8613458
591	cg33889498_TC21	0.00067187	0.05568894	Higher	Abat	chr16	+	tss_body	8625286
592	cg33889648_BC21	0.00016144	-0.18310487	Lower		chr16	-	tss_body	9274058
593	cg33895828_TC21	0.00010901	-0.06053324	Lower					10792159
594	cg33907757_BC21	0.00042504	-0.05882693	Lower	Prm3	chr16	-	tss_1500	11143662
595	cg33911457_BC21	1.9373E-05	-0.10227423	Lower	Zc3h7a	chr16	-	tss_body	11395238
596	cg33914002_TC21	0.00073946	0.08031417	Higher	Snx29	chr16	+	tss_body	14365699
597	cg33936433_BC21	0.0005827	-0.08171683	Lower	Abcc1	chr16	+	tss_body	15194640
598	cg33940518_BC21	0.00015353	-0.08440378	Lower					17144405
599	cg33953149_BC21	0.00070419	-0.06567898	Lower	Ccdc116	chr16	-	tss_body	18069585
600	cg33963529_BC21	0.00095559	-0.0642188	Lower	Dgcr6	chr16	+	tss_body	18079982
601	cg33963638_BC21	0.00027762	-0.07321434	Lower	Prodh	chr16	-	tss_body	18105925
602	cg33963925_BC21	0.00080218	-0.1018911	Lower					18416611
603	cg33967593_TC21	6.068E-05	-0.06243864	Lower	Comt	chr16	-	tss_body	19407540
604	cg33975725_BC21	0.00051792	0.10493938	Higher	Olfr165	chr16	-	tss_body	19956946
605	cg33978582_TC21	0.00020663	-0.08075887	Lower	Klhl6	chr16	-	tss_body	20679218

606	cg33985954_BC21	8.7642E-05	-0.07505231	Lower	Eif4g1	chr16	+	tss_body	22956054
607	cg34009583_BC21	0.00047982	-0.0726537	Lower	Hrg	chr16	+	tss_body	23302964
608	cg34012933_TC21	6.3856E-05	0.12481719	Higher	St6gal1	chr16	+	tss_body	23780198
609	cg34016591_BC21	0.00013475	-0.17648475	Lower		chr16	-	tss_200	28842931
610	cg34049088_BC21	9.1436E-05	-0.05684713	Lower	Mb21d2	chr16	-	tss_body	28880550
611	cg34049655_TC21	0.0007872	0.09061907	Higher	Mb21d2	chr16	-	tss_body	29834837
612	cg34058189_BC21	0.00097812	-0.05346994	Lower	Gm32679	chr16	-	tss_body	30736943
613	cg34069095_TC21	0.00043349	-0.09238255	Lower					31651359
614	cg34079554_BC11	0.00074169	0.05652376	Higher					32017613
615	cg34083229_BC21	0.00056228	0.06416244	Higher	Pak2	chr16	-	tss_body	32267487
616	cg34085922_BC21	0.00015999	-0.15961783	Lower	Mir1946a	chr16	-	tss_body	38057088
617	cg34142766_TC21	0.00085009	0.11223031	Higher	LOC108168284	chr16	-	tss_body	38342159
618	cg34145649_BC21	0.00077257	0.05326585	Higher	Maats1	chr16	-	tss_1500	38654890
619	cg34149695_TC21	0.00012734	0.16655829	Higher	Arhgap31	chr16	-	tss_body	38901490
620	cg34152326_BC21	7.6292E-05	0.07862164	Higher	Igsf11	chr16	+	tss_body	48993633
621	cg34215598_BC11	0.0002098	0.05738743	Higher	Dzip3	chr16	-	tss_body	56881869
622	cg34264096_TC21	0.00010812	0.05468234	Higher	Tmem45a	chr16	-	tss_body	63864115
623	cg34305611_BC21	0.00069865	0.05710286	Higher	Epha3	chr16	-	tss_body	70954206
624	cg34343455_BC21	0.00047025	-0.1057517	Lower	Gm29823	chr16	+	tss_1500	72088885
625	cg34348737_TC21	0.00095893	-0.08448418	Lower	Robo1	chr16	+	tss_body	74371814
626	cg34364564_BC21	0.00057865	0.08683882	Higher	Robo2	chr16	-	tss_body	76532240
627	cg34379299_TC21	0.00041513	-0.16276166	Lower					76547850
628	cg34379450_TC21	0.0005109	0.05531779	Higher	Gm30726	chr16	+	tss_1500	84972435
629	cg34428566_TC21	0.00028076	-0.10396559	Lower	App	chr16	-	tss_body	89046923
630	cg34458000_TC21	0.00049389	0.06950415	Higher					90524106
631	cg34474858_TC21	0.0001069	-0.06264326	Lower	chr16-90524263-90524485	chr16	*	NShore	91134843
632	cg34483156_TC21	0.00057572	-0.09910477	Lower	Gm41492	chr16	-	tss_body	91526932
633	cg34488695_BC21	0.00036304	-0.07150746	Lower					91616754
634	cg34490273_BC21	0.00027828	-0.10081936	Lower	Dnajc28	chr16	-	tss_body	92121108
635	cg34497589_TC21	0.00065363	-0.05977046	Lower	A0A338P7H3	chr16	+	tss_body	92126190

636	cg34497648_BC21	0.00049846	-0.0739476	Lower	Gm41496	chr16	+	tss_body	92352339
637	cg34500536_BC21	0.00028898	-0.07029396	Lower	Kcne1	chr16	-	tss_body	92359399
638	cg34500654_TC21	0.00036677	0.10424531	Higher	Kcne1	chr16	-	tss_body	92359499
639	cg34500656_TC21	0.00041272	0.15072921	Higher	Gm30163	chr16	+	tss_body	92604885
640	cg34504287_TC21	0.00019894	0.16377325	Higher	Runx1	chr16	-	tss_body	93788710
641	cg34518639_BC21	0.00062472	-0.0730586	Lower	Dopey2	chr16	+	tss_body	93929644
642	cg34520682_BC21	0.00013399	0.05876741	Higher	Cldn14	chr16	-	tss_body	95225857
643	cg34536605_TC21	0.00064933	0.07949458	Higher	Gm31641	chr16	-	tss_body	5175734
644	cg34578779_BC21	0.000394	-0.08196037	Lower	Arid1b	chr17	+	tss_body	5291008
645	cg34580324_TC21	0.00026469	-0.11794295	Lower	Arid1b	chr17	+	tss_body	5317974
646	cg34580638_TC21	0.00025017	0.08279875	Higher	Arid1b	chr17	+	tss_body	5829185
647	cg34586645_BC21	0.00075731	0.08213202	Higher					7144035
648	cg34601960_BC21	0.00061213	-0.0825203	Lower	Rps6ka2	chr17	+	tss_body	7162713
649	cg34602183_BC21	0.00055733	-0.09241783	Lower	Rps6ka2	chr17	+	tss_body	8924041
650	cg34619765_BC21	0.00072053	0.12543656	Higher	Pde10a	chr17	+	tss_body	9485544
651	cg34624390_TC21	0.00084383	-0.05310879	Lower					9759668
652	cg34626157_BC21	0.00015905	-0.05091608	Lower	4930452A19Rik	chr17	-	tss_body	10398595
653	cg34631823_BC21	0.00021704	0.11686141	Higher					12132908
654	cg34646066_TC21	0.00091765	-0.06357785	Lower	Agpat4	chr17	+	tss_body	12169348
655	cg34646492_BC21	0.00016638	-0.06687075	Lower	Agpat4	chr17	+	tss_body	14703698
656	cg34669634_BC21	0.00012953	-0.06359166	Lower					14875016
657	cg34670717_TC21	0.00049066	-0.10745151	Lower	Wdr27	chr17	-	tss_body	15598099
658	cg34677811_TC21	0.0005851	-0.07998258	Lower		chr17	+	tss_body	23835664
659	cg34724166_BC21	0.00074621	-0.11289975	Lower	Prss33	chr17	-	tss_body	25081423
660	cg34740477_TC21	0.00020397	-0.08314145	Lower	Ift140	chr17	+	tss_body	25803640
661	cg34750763_BC21	0.0001583	0.07990758	Higher	Gm41551	chr17	+	tss_body	25846770
662	cg34751816_BC21	0.00030118	-0.06546	Lower	Wdr90	chr17	-	tss_body	25847825
663	cg34751833_TC21	2.5211E-06	-0.0701058	Lower	Wdr90	chr17	-	tss_body	25928960
664	cg34753092_BC21	0.00089112	-0.07129226	Lower	Pigq	chr17	-	tss_body	26570860
665	cg34761327_TC21	0.0008246	-0.08738201	Lower	Ergic1	chr17	+	tss_body	26596365
666	cg34761689_BC21	0.00079449	-0.08624155	Lower	Ergic1	chr17	+	tss_body	26861466

667	cg34764896_BC11	0.00084529	-0.06666305	Lower	Gm17382	chr17	-	tss_body	27716707
668	cg34779468_TC21	0.00056324	0.05044923	Higher	Spdef	chr17	-	tss_body	28297137
669	cg34788935_TC21	0.00056771	-0.05618087	Lower	Ppard	chr17	+	tss_body	28300482
670	cg34789024_BC21	0.00013257	-0.06250951	Lower	Ppard	chr17	+	tss_body	28318036
671	cg34789335_BC21	0.00036485	-0.05193904	Lower	Fance	chr17	+	tss_body	28866902
672	cg34797278_TC21	0.0004265	0.06124875	Higher	Pnpla1	chr17	+	tss_body	28884263
673	cg34797551_BC11	0.00044723	-0.09491548	Lower	Pnpla1	chr17	+	tss_body	28935431
674	cg34798338_TC21	0.0009575	-0.06527002	Lower	Gm16191	chr17	+	tss_body	29147365
675	cg34801230_BC21	0.00085748	-0.08423363	Lower	Rab44	chr17	+	tss_body	29317195
676	cg34803900_BC21	0.00034222	-0.07345295	Lower	D3Z6T6	chr17	+	tss_1500	31198043
677	cg34828267_TC11	0.00017617	0.08969485	Higher	Tmprss3	chr17	-	tss_body	31477562
678	cg34831884_TC21	5.9706E-05	-0.08092132	Lower					31588473
679	cg34833587_TC11	0.00015721	-0.09327295	Lower	Pknox1	chr17	+	tss_body	31677806
680	cg34834986_TC21	8.4235E-05	-0.06494551	Lower	Cryaa	chr17	+	tss_200	32452845
681	cg34844395_BC21	0.00062019	0.05040525	Higher	Cyp4f39	chr17	+	tss_body	33749797
682	cg34854542_BC21	0.00026004	-0.08211186	Lower	Rab11b	chr17	-	tss_body	34147871
683	cg34861465_BC21	0.00087101	0.08569028	Higher	H2-DMb2	chr17	+	tss_body	34190652
684	cg34862013_TC21	1.9682E-05	-0.05940196	Lower	Tap1	chr17	+	tss_body	34193787
685	cg34862073_TC21	0.00053986	-0.08047077	Lower	Tap1	chr17	+	tss_body	34600574
686	cg34866258_BC21	0.00018603	0.08959691	Higher	Ager	chr17	+	tss_body	34607784
687	cg34866493_TC21	0.00055871	-0.06100041	Lower	Agpat1	chr17	+	tss_body	34610995
688	cg34866567_BC11	0.00038873	0.09232416	Higher	Agpat1	chr17	+	tss_body	34614897
689	cg34866641_BC21	0.00074107	-0.05876202	Lower	Egfl8	chr17	-	tss_body	34623260
690	cg34866765_BC21	0.00054323	-0.07835576	Lower	Ppt2	chr17	-	tss_body	34650737
691	cg34867397_TC21	0.00018617	-0.05497947	Lower	Atf6b	chr17	+	tss_body	34858487
692	cg34870654_BC21	0.00023265	-0.15965074	Lower	Cfb	chr17	-	tss_body	34905357
693	cg34871478_BC21	3.2962E-05	-0.0544469	Lower	Ehmt2	chr17	+	tss_body	34911625
694	cg34871652_BC21	5.3563E-05	-0.0963391	Lower	Ehmt2	chr17	+	tss_body	34931995
695	cg34871999_BC11	0.00074645	0.1110895	Higher	Neu1	chr17	+	tss_body	35015440
696	cg34873622_BC21	0.00024155	-0.05543641	Lower	Vars	chr17	+	tss_body	35061317
697	cg34874422_BC21	0.00013727	-0.0530285	Lower	Ddah2	chr17	+	tss_body	35065848

698	cg34874517_TC21	0.00054762	0.05010159	Higher	G6b	chr17	-	tss_body	35155058
699	cg34876157_TC21	0.00052394	-0.06578985	Lower	Prrc2a	chr17	-	tss_body	35159229
700	cg34876262_BC21	0.00063445	0.10308481	Higher	Prrc2a	chr17	-	tss_body	35779128
701	cg34884547_BC21	0.00090566	-0.066094	Lower	4833427F10Rik	chr17	+	tss_body	36839239
702	cg34894236_BC21	0.00030187	-0.07658082	Lower	Trim26	chr17	+	tss_body	43399152
703	cg34930382_BC21	0.00030586	-0.08198495	Lower	Adgrf5	chr17	+	tss_body	43577911
704	cg34932112_BC21	0.00011364	-0.05145681	Lower	Pla2g7	chr17	+	tss_body	44442007
705	cg34940218_TO21	0.00082047	0.12027393	Higher					44490241
706	cg34940666_TC21	0.00088897	0.08038192	Higher					46239016
707	cg34961753_TC21	1.4985E-05	-0.05261062	Lower	Xpo5	chr17	+	tss_body	47738551
708	cg34985739_TC21	0.00023291	0.05519606	Higher	Tfeb	chr17	+	tss_body	47979052
709	cg34989559_TC21	0.00028509	0.0634815	Higher	chr17-47975244-47975582	chr17	*	SShelf	48264543
710	cg34992454_TC21	3.6017E-05	-0.07349967	Lower	Treml4	chr17	+	tss_body	48359843
711	cg34993376_BC21	0.0001776	-0.07155015	Lower	Treml1	chr17	+	tss_200	48389640
712	cg34993621_BC21	0.00010975	-0.05229737	Lower	Nfya	chr17	-	tss_body	49206862
713	cg35002105_TC21	0.00091251	0.05888632	Higher					49809217
714	cg35007995_TC21	0.00059871	-0.0885713	Lower	Kif6	chr17	+	tss_body	49887306
715	cg35008865_TC21	0.00048831	-0.11540226	Lower	Kif6	chr17	+	tss_body	49975856
716	cg35009907_BC21	0.00035507	0.067317	Higher		chr17	+	tss_body	51986447
717	cg35026837_TC21	3.7216E-05	-0.05756832	Lower		chr17	+	tss_body	55445255
718	cg35044928_TC21	1.8638E-05	0.05032269	Higher	St6gal2	chr17	+	tss_1500	55768293
719	cg35046739_TC21	0.00086679	-0.07466866	Lower	Adgre4	chr17	+	tss_body	56000124
720	cg35048578_BC21	6.5227E-05	0.07127188	Higher	Stap2	chr17	-	tss_body	56000649
721	cg35048600_TC21	0.00042052	0.05333475	Higher	Stap2	chr17	-	tss_body	56116409
722	cg35050148_TC21	0.00055999	0.05217099	Higher	Plin5	chr17	-	tss_body	56124822
723	cg35050429_TC11	8.9426E-05	-0.23124369	Lower	Sema6b	chr17	-	tss_body	56124853
724	cg35050433_BC21	2.7476E-05	-0.17176854	Lower	Sema6b	chr17	-	tss_body	56459105
725	cg35055682_BC21	2.0224E-05	-0.10338942	Lower	Ptprs	chr17	-	tss_body	56547952
726	cg35057137_TC21	0.00014314	-0.06022379	Lower					57190503
727	cg35065839_BC21	0.00065869	-0.0583344	Lower	Tnfsf14	chr17	-	tss_body	62787197

728	cg35095172_BC21	0.00076345	-0.05068027	Lower	Efna5	chr17	-	tss_body	64467421
729	cg35110729_BC11	0.00036133	0.1178772	Higher					65683078
730	cg35121970_TC21	2.1093E-05	-0.06225298	Lower	Rab31	chr17	-	tss_body	66868500
731	cg35136695_BC21	0.00081131	-0.06159401	Lower	Ptprm	chr17	-	tss_body	67723968
732	cg35145377_TC21	0.00088918	0.10238094	Higher	Lama1	chr17	+	tss_body	67950828
733	cg35148365_TC21	2.566E-06	-0.07807405	Lower	Arhgap28	chr17	-	tss_body	70750371
734	cg35171769_TC21	0.00037566	0.08952658	Higher	Dlgap1	chr17	+	tss_body	70878194
735	cg35173658_BC21	0.00021079	-0.07119281	Lower	Gm26510	chr17	-	tss_body	71856291
736	cg35184960_BC21	0.00049862	-0.11995859	Lower	Clip4	chr17	+	tss_body	72917180
737	cg35194432_BC21	0.00046557	-0.05945551	Lower	Gm30375	chr17	-	tss_body	72933279
738	cg35194701_BC21	0.00053579	-0.07992979	Lower	Lbh	chr17	+	tss_body	72967616
739	cg35195063_BC21	0.0002685	-0.08272963	Lower					74629416
740	cg35209748_TC21	0.00088837	0.11086791	Higher	Birc6	chr17	+	tss_body	78107757
741	cg35230488_TC21	0.00063121	0.13488525	Higher		chr17	+	tss_1500	78268102
742	cg35232263_BC11	0.00055508	0.13319852	Higher	Crim1	chr17	+	tss_body	79509378
743	cg35245466_BC21	0.00037545	-0.10183509	Lower	Gm10494	chr17	-	tss_body	79580689
744	cg35246008_TC21	0.00098035	0.05440459	Higher	Gm41623	chr17	-	tss_body	79582200
745	cg35246032_TC21	0.00083236	-0.07469987	Lower	Gm41623	chr17	-	tss_body	80601618
746	cg35257567_TC21	0.00052262	0.05449093	Higher	Map4k3	chr17	-	tss_body	81001013
747	cg35261998_BC11	0.00096235	-0.06379009	Lower	Tmem178	chr17	+	tss_body	83166675
748	cg35276333_BC11	0.0006261	-0.05489702	Lower					83513321
749	cg35280486_BC21	0.0001763	-0.10158326	Lower	Cox7a2l	chr17	-	tss_body	83831707
750	cg35285007_BC21	0.00021177	-0.05770009	Lower	Haao	chr17	-	tss_body	83854652
751	cg35285354_BC21	0.0002681	-0.06136041	Lower	C430042M11Rik	chr17	-	tss_body	83952554
752	cg35286691_TC21	0.00035403	-0.08977184	Lower	Gm41639	chr17	-	tss_body	83961124
753	cg35286804_TC21	0.00059868	-0.15472232	Lower	Gm41638	chr17	-	tss_1500	85868804
754	cg35310593_TC21	0.0001419	-0.12401625	Lower	Gm30117	chr17	-	tss_body	85931303
755	cg35311276_BC11	0.00084037	-0.05837272	Lower					86298954
756	cg35315548_TC21	0.00033461	-0.05790454	Lower	Prkce	chr17	+	tss_body	86303302
757	cg35315625_BC21	0.0009608	-0.06249691	Lower	Prkce	chr17	+	tss_body	86404593
758	cg35316928_BC21	0.00016057	0.06203883	Higher	Prkce	chr17	+	tss_body	86966208

759	cg35324447_TC11	0.00066141	0.14515302	Higher	Rhoq	chr17	+	tss_body	87276230
760	cg35328490_BC11	5.415E-05	0.11571711	Higher	4833418N02Rik	chr17	-	tss_body	87296136
761	cg35328916_BC21	0.00054154	0.06098995	Higher	Ttc7	chr17	+	tss_body	87502731
762	cg35332123_TC21	0.00077622	-0.09403526	Lower					91088940
763	cg35359621_TC21	0.00067067	-0.08548013	Lower	Nrxn1	chr17	-	tss_body	3511602
764	cg35378861_TC21	0.00070623	-0.14771981	Lower	Bambi	chr18	+	tss_body	5079910
765	cg35388898_TC21	0.00093533	0.11003358	Higher	Svil	chr18	+	tss_body	10536645
766	cg35422887_BC21	0.00041391	-0.13712209	Lower	Greb1l	chr18	+	tss_body	10785573
767	cg35424859_BC21	0.00076776	0.08661304	Higher	Mib1	chr18	+	tss_body	11221927
768	cg35428161_TC21	0.00039156	-0.07488638	Lower					12927799
769	cg35443253_TC21	0.00014497	-0.08815851	Lower	Osbpl1a	chr18	-	tss_body	19079865
770	cg35481050_BC21	0.00043661	-0.06274782	Lower					21162872
771	cg35493654_BC21	0.00023962	-0.05172728	Lower	Garem	chr18	-	tss_body	23857085
772	cg35510375_BC11	0.00013386	0.07607646	Higher	Mapre2	chr18	+	tss_body	24081739
773	cg35512683_TC21	0.00034376	-0.09760264	Lower		chr18	-	tss_body	24246232
774	cg35514207_TC11	0.00097609	0.06341903	Higher	Galnt1	chr18	+	tss_body	24868204
775	cg35519994_TC21	0.00038697	-0.07141266	Lower	Fhod3	chr18	+	tss_body	32036693
776	cg35560232_BC11	0.00053282	0.07588219	Higher	Myo7b	chr18	-	tss_body	32701525
777	cg35565822_TC21	0.00044498	0.08540401	Higher	4930455D15Rik	chr18	-	tss_body	33297150
778	cg35569915_TC21	4.0796E-05	0.08010189	Higher	LOC108168400	chr18	+	tss_body	35757731
779	cg35594563_BC21	9.3089E-05	0.13485075	Higher					35862104
780	cg35595950_BC21	1.7153E-05	-0.11561358	Lower	chr18-35860500-35860796	chr18	*	SShore	35895154
781	cg35596537_TC21	6.6561E-05	-0.07607992	Lower					36533191
782	cg35603961_TC11	0.00049421	0.05270335	Higher	Slc4a9	chr18	+	tss_body	36664048
783	cg35604877_TC21	0.00020586	0.05513106	Higher	Eif4ebp3	chr18	+	tss_200	36676459
784	cg35605010_TC21	0.00087124	-0.06764685	Lower	Apbb3	chr18	-	tss_body	36973817
785	cg35608491_TC21	1.042E-05	-0.09270867	Lower	Pcdha1	chr18	+	tss_body	36975177
786	cg35608550_BC21	0.00013525	-0.07352181	Lower	Pcdha1	chr18	+	tss_body	37132456
787	cg35610001_TC21	0.00087732	0.12919025	Higher	Pcdha1	chr18	+	tss_body	37357495
788	cg35612025_BC21	0.00028347	-0.09324294	Lower	Gm37013	chr18	+	tss_body	37474502

789	cg35612855_BC21	1.8213E-05	0.08824451	Higher	Gm37013	chr18	+	tss_body	37714737
790	cg35615454_TC21	0.00042981	-0.05498169	Lower	Gm37013	chr18	+	tss_body	37765916
791	cg35616802_TC21	0.00038504	0.10483952	Higher	Gm37013	chr18	+	tss_body	37820416
792	cg35617601_TC21	3.7056E-05	0.09585705	Higher	Gm37013	chr18	+	tss_body	38338147
793	cg35624093_TC11	0.0006654	0.09831184	Higher	Gnpda1	chr18	-	tss_body	38795648
794	cg35629232_BC21	0.00095105	-0.07572341	Lower	Arhgap26	chr18	+	tss_body	39150110
795	cg35632890_BC21	0.00060274	-0.10507928	Lower	Arhgap26	chr18	+	tss_body	44812902
796	cg35671415_BC21	4.0608E-05	0.12979726	Higher	Mcc	chr18	-	tss_1500	46176107
797	cg35679310_BC21	0.00056411	-0.11207794	Lower	Trim36	chr18	-	tss_body	46335802
798	cg35681003_TC11	0.00078309	0.07961559	Higher					47334749
799	cg35690973_BC21	0.00077262	-0.05971452	Lower	Sema6a	chr18	-	tss_body	47733157
800	cg35694848_BC21	0.00054281	-0.05633902	Lower	Gm41720	chr18	+	tss_body	54576702
801	cg35740170_BC21	0.00068653	0.06040235	Higher					56696189
802	cg35757575_BC21	0.00043396	-0.15239527	Lower					58106417
803	cg35771538_TC21	1.6488E-05	-0.05830227	Lower	Fbn2	chr18	-	tss_body	60835143
804	cg35791427_BC21	3.4522E-05	-0.06739523	Lower	Tcof1	chr18	-	tss_body	60937668
805	cg35792848_BC21	0.00093699	0.06794327	Higher	Camk2a	chr18	+	tss_body	61037900
806	cg35794369_BC21	0.00019395	-0.06129014	Lower	chr18-61035675-61036479	chr18	*	SShore	61056874
807	cg35794668_BC21	0.00013044	-0.10229469	Lower	Pdgfrb	chr18	+	tss_body	61315523
808	cg35798040_TC21	0.00026971	-0.07839748	Lower	Ppargc1b	chr18	-	tss_body	64659449
809	cg35830834_TC21	4.848E-05	0.050441	Higher	Atp8b1	chr18	-	tss_body	64962598
810	cg35833893_TC21	1.3162E-05	-0.10314283	Lower	Nedd4l	chr18	+	tss_body	65378241
811	cg35838979_TC21	0.00081071	0.07286741	Higher	Alpk2	chr18	-	tss_body	65580066
812	cg35841110_TC21	0.00018639	0.12743196	Higher	Zfp532	chr18	+	tss_1500	66495269
813	cg35851428_BC11	0.00028292	-0.06381074	Lower					66509648
814	cg35851619_BC21	0.00020975	-0.06652638	Lower	Gm9926	chr18	+	tss_body	67311603
815	cg35859173_TC21	0.00025335	-0.1229393	Lower	Impa2	chr18	+	tss_body	68202227
816	cg35869399_BC21	9.2303E-06	-0.09635705	Lower	Ldlrad4	chr18	+	tss_body	69961906
817	cg35887175_BC21	0.00093546	-0.09672339	Lower	Ccdc68	chr18	+	tss_body	75187319
818	cg35930267_BC21	0.00046592	0.05516725	Higher	Dym	chr18	+	tss_body	76085722

819	cg35942199_BC21	0.00037224	-0.20959593	Lower	Zbtb7c	chr18	+	tss_body	76604325
820	cg35947754_BC11	0.00028032	0.06023164	Higher					76751173
821	cg35949463_TC21	0.00023306	0.05455254	Higher					77515937
822	cg35958495_TC21	0.00020919	-0.16459172	Lower	Rnf165	chr18	-	tss_body	80440873
823	cg35986763_BC21	0.00017903	-0.05917881	Lower	Ctdp1	chr18	-	tss_body	80565830
824	cg35988459_BC21	0.0005546	0.07999635	Higher					81849844
825	cg36003090_TC21	7.2215E-05	0.05897207	Higher	Gm30454	chr18	-	tss_body	82564692
826	cg36009903_BC21	5.7519E-05	0.09889287	Higher	Mbp	chr18	+	tss_body	83060440
827	cg36017423_TC21	0.00074687	0.05321236	Higher	LOC108168396	chr18	+	tss_body	83131685
828	cg36018297_BC21	0.00017565	-0.17547706	Lower					84409151
829	cg36032247_TC11	0.00075646	0.08831647	Higher	Zfp407	chr18	-	tss_body	3334390
830	cg36065096_TC21	4.1312E-05	-0.05427548	Lower	Cpt1a	chr19	+	tss_body	3767595
831	cg36069780_BC11	0.00010459	0.07664065	Higher	Suv420h1	chr19	+	tss_body	3992585
832	cg36072497_TC21	0.00020413	-0.19056182	Lower	Tbx10	chr19	+	tss_1500	4263193
833	cg36076583_TC21	0.00062423	0.06796685	Higher	Ssh3	chr19	-	tss_body	4263954
834	cg36076601_TC21	0.00078132	0.0538754	Higher	Ssh3	chr19	-	tss_body	4289606
835	cg36076989_BC21	0.00082372	-0.10291527	Lower	Adrbk1	chr19	-	tss_body	4601990
836	cg36080076_TC21	0.00089295	-0.09430263	Lower	Pcx	chr19	+	tss_body	4990562
837	cg36085621_BC21	7.9388E-07	-0.07505087	Lower	Npas4	chr19	-	tss_body	5070131
838	cg36086967_TC21	0.00039207	-0.05590919	Lower	Cd248	chr19	+	tss_body	5655721
839	cg36096057_BC21	0.00095315	0.11216066	Higher	Sipa1	chr19	-	tss_body	6284672
840	cg36106543_TC11	0.00044605	-0.10221491	Lower	Ehd1	chr19	+	tss_body	6386461
841	cg36108368_BC11	0.00035012	0.06547429	Higher	Pygm	chr19	+	tss_body	6449273
842	cg36109713_TC21	0.00039324	-0.08494585	Lower	Nrxn2	chr19	+	tss_body	6464593
843	cg36109935_BC21	0.00070973	-0.09563071	Lower	Nrxn2	chr19	+	tss_body	6491519
844	cg36110396_TC21	0.00047348	-0.05088666	Lower	Nrxn2	chr19	+	tss_body	6907964
845	cg36114290_BC21	0.00071146	0.17254893	Higher	Prdx5	chr19	-	tss_body	7167523
846	cg36119019_BC21	0.0003314	-0.05628187	Lower	Macrod1	chr19	+	tss_body	8839249
847	cg36132866_BC21	0.00027864	0.07817354	Higher	Bscl2	chr19	+	tss_body	9087892
848	cg36135914_TC21	0.00058944	0.19489493	Higher	Scgb1a1	chr19	-	tss_body	9100789
849	cg36136038_TC21	0.00026675	-0.0722081	Lower	Gm41805	chr19	+	tss_body	10042755

850	cg36142165_TC21	0.00064504	0.06121128	Higher	Fads3	chr19	+	tss_body	10240924
851	cg36144507_BC21	0.00016277	0.06200894	Higher	Myrf	chr19	-	tss_200	10535127
852	cg36148302_BC21	3.444E-05	0.12116876	Higher	Cpsf7	chr19	+	tss_body	10965865
853	cg36153370_TC21	9.3581E-05	-0.05478293	Lower	Ms4a10	chr19	-	tss_body	12671353
854	cg36164098_TC21	0.00087898	-0.05949033	Lower	Q0VEV7	chr19	+	tss_body	16491014
855	cg36188473_BC21	0.0004927	0.06530851	Higher	Gna14	chr19	+	tss_body	17645906
856	cg36198307_TC21	0.00027519	0.08265869	Higher	Pcsk5	chr19	-	tss_body	20824345
857	cg36216803_TC21	0.00012687	0.09363927	Higher	Tmc1	chr19	-	tss_body	21792942
858	cg36224649_TC21	9.4404E-05	-0.10231712	Lower	Tmem2	chr19	+	tss_body	25406739
859	cg36259386_BC21	0.00010771	0.06413379	Higher	Kank1	chr19	+	tss_body	27222127
860	cg36275319_BC21	0.00037086	-0.06593899	Lower	Gm35438	chr19	-	tss_body	30261113
861	cg36305204_BC21	0.00086968	-0.07868058	Lower					32648672
862	cg36323957_TC21	0.0004345	-0.06594995	Lower	Papss2	chr19	+	tss_body	34970187
863	cg36340328_BC21	0.00063281	0.05445312	Higher	Kif20b	chr19	+	tss_body	36368634
864	cg36348999_TC21	0.00052896	-0.05748901	Lower	Pcgf5	chr19	+	tss_body	37526705
865	cg36360685_BC11	0.00014097	0.08756697	Higher		chr19	+	tss_body	37918571
866	cg36365131_BC11	6.744E-05	-0.15675995	Lower	Myof	chr19	-	tss_body	38385428
867	cg36369984_TC21	0.00019992	-0.12584859	Lower		chr19	-	tss_body	38398899
868	cg36370179_TC21	0.0009466	-0.08047922	Lower	Slc35g1	chr19	+	tss_body	38583308
869	cg36372101_TC21	0.00052793	0.06552712	Higher	Plce1	chr19	+	tss_body	40382830
870	cg36384065_BC21	0.00093071	0.15926729	Higher	Sorbs1	chr19	-	tss_body	41063895
871	cg36392070_BC21	0.00050705	-0.05302764	Lower	Opalin	chr19	-	tss_body	41077307
872	cg36392250_TC21	0.00068281	-0.05827152	Lower	Opalin	chr19	-	tss_200	41800524
873	cg36400896_BC21	5.9983E-05	0.09707127	Higher	Arhgap19	chr19	-	tss_body	42526510
874	cg36411257_TC11	0.00015999	-0.11107874	Lower	R3hcc1l	chr19	+	tss_body	43573369
875	cg36420692_BC11	0.00053649	0.07104482	Higher		chr19	-	tss_200	43920544
876	cg36426137_BC21	8.6428E-05	-0.12318985	Lower	Dnmbp	chr19	-	tss_body	44453054
877	cg36432732_BC21	0.00055558	-0.05867521	Lower	Gm35406	chr19	+	tss_1500	45086656
878	cg36442350_BC21	7.7761E-05	-0.11561592	Lower		chr19	+	tss_body	46279225
879	cg36457636_BC21	0.00055987	-0.05589918	Lower	Gbf1	chr19	+	tss_body	47442218
880	cg36475046_BC21	1.3096E-06	-0.06955376	Lower	Sh3pxd2a	chr19	-	tss_body	47870228

881	cg36481047_TC21	0.00025399	0.12345085	Higher	Gsto2	chr19	+	tss_body	47896341
882	cg36481461_TC21	0.00023287	-0.10329281	Lower	Itprip	chr19	-	tss_body	53010554
883	cg36513925_BC21	0.00049391	-0.10018314	Lower	Xpnpep1	chr19	-	tss_body	53059384
884	cg36514792_BC21	0.00074271	-0.1391743	Lower	Gm30234	chr19	-	tss_body	57396380
885	cg36567175_TC21	0.00094316	0.0632662	Higher					58051122
886	cg36574956_BC21	3.9425E-05	-0.09046212	Lower	Atrnl1	chr19	+	tss_body	13290455
887	cg36661192_BC21	0.00053016	-0.12258921	Lower	Ncoa2	chr1	-	tss_body	13314187
888	cg36661453_BC21	2.4E-05	0.06084597	Higher	Ncoa2	chr1	-	tss_body	15312661
889	cg36674782_TC21	9.3316E-05	-0.08357328	Lower	Kcnb2	chr1	+	tss_body	35891865
890	cg36799616_TC11	0.00025872	-0.05514724	Lower					36321912
891	cg36804601_BC11	0.00010189	0.05709961	Higher	Arid5a	chr1	+	tss_body	36475201
892	cg36806517_BO21	0.00030121	0.11670915	Higher	Cnnm4	chr1	+	tss_body	36589699
893	cg36808547_TC21	0.00063331	-0.07862871	Lower	Fam178b	chr1	-	tss_body	37611605
894	cg36819927_TC21	0.00039068	-0.1080552	Lower					37697172
895	cg36821105_TC21	0.000968 1	0.14451683	Higher	2010300C02Rik	chr1	-	tss_body	38939248
896	cg36834574_BC21	0.00031798	0.10330623	Higher	Nms	chr1	+	tss_body	39845728
897	cg36845321_TC21	0.00019902	0.07204349	Higher	1700066B17Rik	chr1	-	tss_body	39972718
898	cg36847030_BC21	0.00080029	0.25373327	Higher	Map4k4	chr1	+	tss_body	40460754
899	cg36851717_TC21	0.000299 1	-0.08459799	Lower	Il1rl1	chr1	+	tss_body	42611056
900	cg36867485_TC21	8.1654E-05	0.10178892	Higher	Gm30248	chr1	-	tss_body	43146749
901	cg36873165_BC21	6.7861E-05	-0.05528977	Lower	Fhl2	chr1	-	tss_body	48527492
902	cg36901949_TC21	2.0325E-05	0.10497526	Higher		chr1	+	tss_200	52172379
903	cg36921867_BC21	0.00080526	-0.07173119	Lower	Gls	chr1	-	tss_body	55733765
904	cg36947404_BC21	0.00012311	-0.11852651	Lower	Plcl1	chr1	+	tss_body	59094835
905	cg36973555_TC21	0.000474 8	-0.07589505	Lower	Als2cr11	chr1	-	tss_body	59395120
906	cg36976568_BC21	0.00013343	0.08681954	Higher	Gm33724	chr1	-	tss_body	61203672
907	cg36991065_BC21	0.00070123	-0.12222989	Lower					61418116
908	cg36992572_TC11	0.00030877	0.06175847	Higher					62380376
909	cg36998056_BC21	3.8778E-05	-0.05378126	Lower	Pard3b	chr1	+	tss_body	63261254
910	cg37006138_BC11	0.00092527	0.10006717	Higher	Zdbf2	chr1	+	tss_body	63686584
911	cg37009795_TC21	0.00081844	0.07717588	Higher	Dytn	chr1	-	tss_body	64115938

912	cg37012905_BC21	0.00022558	-0.10749638	Lower	Klf7	chr1	-	tss_body	67585096
913	cg37036438_BC21	0.00028947	-0.07276549	Lower		chr1	+	tss_body	69548703
914	cg37046710_TC21	0.00023112	-0.09429289	Lower	Ikzf2	chr1	-	tss_body	72739469
915	cg37072123_BC21	0.00023888	0.06388975	Higher					72946816
916	cg37074359_BC21	0.0001298	0.16122667	Higher	Gm31047	chr1	+	tss_body	74194723
917	cg37084105_BC21	0.00089828	0.08446034	Higher	Cxcr1	chr1	-	tss_body	75253572
918	cg37096418_BC21	0.00024133	-0.08852165	Lower	Ptprn	chr1	-	tss_body	75685808
919	cg37103199_TC21	8.9516E-05	-0.08045661	Lower					80530253
920	cg37138909_BC21	0.00018224	0.20402039	Higher	Dock10	chr1	-	tss_body	81744563
921	cg37145201_BC21	0.00023712	0.16263528	Higher					83631648
922	cg37158372_TC21	0.00079468	-0.12601539	Lower					87183180
923	cg37185863_TC11	0.00077948	0.07165561	Higher	Prss56	chr1	+	tss_body	87205602
924	cg37186236_BC21	0.00015712	-0.05959446	Lower	Chrng	chr1	+	tss_1500	87620451
925	cg37190273_TC21	0.00089019	-0.06801675	Lower	Inpp5d	chr1	+	tss_body	88153211
926	cg37194339_BC21	0.00030637	0.0705512	Higher	Ugt1a10	chr1	+	tss_body	88269429
927	cg37195376_BC11	0.00097683	0.0728707	Higher	Hjurp	chr1	-	tss_body	88656396
928	cg37198993_BC21	0.00010615	0.05918297	Higher		chr1	+	tss_body	89930276
929	cg37213680_BC21	6.4515E-05	0.05115048	Higher	Gbx2	chr1	-	tss_body	89968920
930	cg37214580_BC21	0.00078346	-0.15039325	Lower	Asb18	chr1	-	tss_body	90810176
931	cg37223118_BC21	0.00045486	0.13628802	Higher	Col6a3	chr1	-	tss_body	91299618
932	cg37228315_BC21	0.00024792	-0.06839003	Lower	Scly	chr1	+	tss_body	91299674
933	cg37228316_BC21	0.00078707	-0.11742112	Lower	Scly	chr1	+	tss_body	93373683
934	cg37250693_TC21	0.00071507	0.05145086	Higher	Ano7	chr1	+	tss_1500	93826633
935	cg37255400_TC11	0.00010983	-0.11038207	Lower	D2hgdh	chr1	+	tss_body	118483940
936	cg37367507_TC21	0.00092324	0.15938522	Higher	Clasp1	chr1	+	tss_body	118916853
937	cg37371488_TC21	0.00081494	0.11273695	Higher	Gli2	chr1	-	tss_body	120504717
938	cg37387401_BC21	0.00069404	-0.14325063	Lower	Marco	chr1	-	tss_body	121335962
939	cg37394196_TC21	0.00037514	0.06721367	Higher					125489113
940	cg37414444_TC21	0.0001292	0.15364656	Higher					126822484
941	cg37424135_TC21	0.00042535	0.16675304	Higher	Nckap5	chr1	-	tss_body	130886890
942	cg37452766_TC21	6.4763E-05	0.12376012	Higher	Il24	chr1	-	tss_body	131217271

943	cg37456396_BC21	0.0003359	-0.07254553	Lower	Rassf5	chr1	-	tss_body	131503734
944	cg37458375_TC21	0.00075548	0.05816886	Higher	Srgap2	chr1	-	tss_body	133171475
945	cg37477654_BC21	0.00057299	-0.05745901	Lower	Plekha6	chr1	+	tss_body	133201310
946	cg37478056_BC21	0.00039864	-0.14567008	Lower	Plekha6	chr1	+	tss_body	133269655
947	cg37478868_TC21	0.0004722	-0.08516961	Lower	Plekha6	chr1	+	tss_body	133386271
948	cg37480537_BC21	0.00023723	-0.10863741	Lower	Sox13	chr1	-	tss_body	133882420
949	cg37486021_BC21	0.00067242	-0.13762893	Lower	Gm31515	chr1	+	tss_body	134107785
950	cg37488834_BC21	0.00079088	0.06148488	Higher					135096480
951	cg37499943_BC21	0.00037659	-0.24303802	Lower	Lgr6	chr1	-	tss_body	135162691
952	cg37500981_TC21	0.0007187	0.09986346	Higher	Gpr37l1	chr1	-	tss_body	135167700
953	cg37501022_TC21	0.00046308	-0.06338014	Lower	Gpr37l1	chr1	-	tss_200	135604636
954	cg37506537_TC21	0.00077784	-0.05593917	Lower	Nav1	chr1	-	tss_body	135858719
955	cg37509828_TC21	9.4114E-05	0.0662247	Higher					136073820
956	cg37512325_BC21	0.00013888	-0.21093627	Lower	Cacna1s	chr1	+	tss_body	136126433
957	cg37512978_TC21	0.00081402	-0.10036159	Lower		chr1	-	tss_body	138832415
958	cg37536817_BC21	0.0008099	-0.05870823	Lower	Lhx9	chr1	-	tss_body	151192953
959	cg37597641_BC21	0.00090444	-0.07038372	Lower	A0A286YD13	chr1	+	tss_body	151699606
960	cg37602733_BC21	0.00019269	-0.11348199	Lower	Fam129a	chr1	+	tss_body	152386849
961	cg37609890_TC21	0.00024238	0.05768913	Higher	Tsen15	chr1	-	tss_200	153155513
962	cg37618561_TC21	0.00011753	-0.12638193	Lower	Lamc2	chr1	-	tss_body	153258979
963	cg37619889_BC21	0.00021277	-0.0526021	Lower	Lamc1	chr1	-	tss_body	156222629
964	cg37647583_TC11	0.00070232	0.13651361	Higher	Gm30472	chr1	+	tss_body	156476783
965	cg37650124_BC21	0.00062102	-0.06725888	Lower	Gm39682	chr1	+	tss_body	156956751
966	cg37655487_BC21	0.00062471	0.11391131	Higher					159686770
967	cg37674216_TC21	0.0005024	-0.14416082	Lower	Tnr	chr1	+	tss_body	161181231
968	cg37684798_BC21	1.0804E-05	0.07199122	Higher		chr1	+	tss_body	165660645
969	cg37721852_BC21	0.00043556	0.12815938	Higher	Rcsd1	chr1	-	tss_body	165775661
970	cg37723305_TC21	0.00025292	0.07632951	Higher					166238685
971	cg37728003_TC11	0.00031434	-0.06829206	Lower	Mael	chr1	-	tss_body	167289427
972	cg37737981_TC11	0.00092925	0.06585558	Higher	Mir6347	chr1	+	tss_1500	167382277
973	cg37739279_TC21	0.00058551	0.07178086	Higher	Mgst3	chr1	-	tss_body	169462666

974	cg37756326_TC21	7.3623E-05	-0.11759768	Lower	Gm34535	chr1	+	tss_1500	170538906
975	cg37765824_TC21	0.00064105	-0.10806492	Lower	Nos1ap	chr1	-	tss_body	170912578
976	cg37769650_BC21	0.00023868	0.05356419	Higher	Fcrlb	chr1	-	tss_body	171282256
977	cg37774713_BC11	0.00091273	0.09858291	Higher	Ppox	chr1	-	tss_1500	171338361
978	cg37775454_BC21	0.0001447	-0.14196342	Lower	Dedd	chr1	+	tss_body	172406585
979	cg37787354_BC21	0.00011872	0.20810218	Higher					172556201
980	cg37789469_BC21	0.00074628	0.11212574	Higher	Vsig8	chr1	+	tss_1500	178358569
981	cg37828426_TC21	0.00023434	-0.05768107	Lower					180182726
982	cg37847180_BC21	0.00010711	-0.05550557	Lower	Adck3	chr1	-	tss_body	180763159
983	cg37854631_TC21	0.00090593	0.0593208	Higher	Gm38293	chr1	-	tss_body	181852965
984	cg37867216_TC11	0.00043347	0.08634604	Higher		chr1	-	tss_body	183656754
985	cg37887327_TC11	0.000129	0.12762212	Higher	Gm39724	chr1	+	tss_body	184037357
986	cg37890200_TC21	0.00044038	-0.09695837	Lower	Dusp10	chr1	+	tss_body	186435001
987	cg37913600_BC21	0.00072609	-0.08229072	Lower					190165667
988	cg37952230_BC21	0.00084008	-0.05675249	Lower	Prox1	chr1	-	tss_body	190180804
989	cg37952631_BC21	0.00014917	-0.08159684	Lower	LOC102632463	chr1	+	tss_body	190785269
990	cg37959334_BC21	6.2714E-05	-0.08777605	Lower	Rps6kc1	chr1	-	tss_body	191029652
991	cg37962583_TC21	0.00035289	0.14467894	Higher	A230020J21Rik	chr1	+	tss_body	191036507
992	cg37962641_BC21	0.00040696	-0.0511352	Lower	Spata45	chr1	+	tss_1500	191058898
993	cg37962851_TC21	0.00027782	-0.0548591	Lower	Tatdn3	chr1	-	tss_body	191896984
994	cg37972787_TC11	0.00048659	-0.0848813	Lower	1700034H15Rik	chr1	-	tss_body	191992773
995	cg37973969_BC21	0.00016411	-0.09971479	Lower		chr1	+	tss_200	192515714
996	cg37978038_TC11	0.00043217	0.08086565	Higher	Hhat	chr1	-	tss_body	192604596
997	cg37978647_BC21	0.00017436	-0.05038884	Lower	Hhat	chr1	-	tss_body	192612184
998	cg37978712_BC21	0.00032536	0.1613708	Higher	Hhat	chr1	-	tss_body	192800707
999	cg37980506_TC11	0.00048965	-0.06189685	Lower					4227740
1000	cg38005017_TC21	0.00050283	-0.08613321	Lower	Frmd4a	chr2	+	tss_body	4340562
1001	cg38006003_BC21	0.00022552	0.09113552	Higher	Frmd4a	chr2	+	tss_body	4547153
1002	cg38008146_BC21	0.0006439	0.08356894	Higher	Frmd4a	chr2	+	tss_body	4551288
1003	cg38008206_BC21	0.00020957	-0.09002749	Lower	Frmd4a	chr2	+	tss_body	4860047
1004	cg38011713_TC21	0.00077009	-0.053151	Lower					5327286

1005	cg38016643_TC21	0.00079105	0.16341012	Higher	Camk1d	chr2	-	tss_body	6133967
1006	cg38024746_BC21	4.0189E-05	-0.0668795	Lower	Gm10857	chr2	+	tss_body	7395757
1007	cg38035143_BC21	1.9904E-05	-0.16857141	Lower	Celf2	chr2	-	tss_body	9868855
1008	cg38048756_BC21	0.00029852	-0.06490662	Lower	Gata3	chr2	-	tss_body	10251066
1009	cg38053237_BC21	0.00056675	-0.06152568	Lower	Itih5	chr2	+	tss_body	13168932
1010	cg38075939_BC21	0.00063315	0.07219305	Higher	Rsu1	chr2	-	tss_body	17871658
1011	cg38101667_BC21	0.00013373	0.10993546	Higher					22976189
1012	cg38136889_BC21	0.000856 9	-0.08795255	Lower	Abi1	chr2	-	tss_body	25214284
1013	cg38152397_TC21	0.00055244	0.0513938	Higher	Stpg3	chr2	-	tss_body	26384877
1014	cg38167288_TC21	0.00045836	-0.06579847	Lower	Sdccag3	chr2	-	tss_body	26561094
1015	cg38169604_TC21	0.00066886	-0.06251047	Lower					26604937
1016	cg38170252_BC21	0.00046489	-0.09753147	Lower	Agpat2	chr2	-	tss_1500	26913621
1017	cg38172770_BC21	0.00058817	0.16169954	Higher	Surf1	chr2	-	tss_body	26927169
1018	cg38172956_TC21	0.00027906	-0.05776624	Lower	Surf4	chr2	-	tss_body	27165323
1019	cg38175603_TC21	0.00092541	-0.05619552	Lower	Dbh	chr2	+	tss_200	27248484
1020	cg38176529_BC21	1.1217E-05	-0.07714847	Lower	Sardh	chr2	-	tss_1500	27554523
1021	cg38180518_TC21	3.0795E-05	-0.15222172	Lower					28046604
1022	cg38185969_TC21	0.00076982	-0.08693154	Lower					28188600
1023	cg38187402_TC11	0.00038735	0.05456016	Higher					28497772
1024	cg38190925_BC21	0.00094246	-0.06683238	Lower	Gbgt1	chr2	+	tss_body	28597968
1025	cg38192391_TC21	0.00068876	-0.05973421	Lower					28616007
1026	cg38192623_TC21	0.0001178	0.0634453	Higher	Gfi1b	chr2	-	tss_body	28686969
1027	cg38193420_TC21	0.00053747	-0.05718775	Lower	Tsc1	chr2	+	tss_body	29186702
1028	cg38199600_TC21	0.00023871	-0.05828563	Lower					29564224
1029	cg38203854_BC21	0.00078146	0.06512799	Higher					29845633
1030	cg38207169_BC21	0.00023408	0.05914543	Higher	Cercam	chr2	+	tss_body	30677671
1031	cg38218876_TC21	0.00085 34	-0.08623079	Lower	Gm14486	chr2	-	tss_body	30924389
1032	cg38222546_BC21	0.00028792	-0.05795383	Lower	Gm39785	chr2	-	tss_body	31006427
1033	cg38223800_BC21	0.00063501	-0.07084219	Lower	Usp20	chr2	+	tss_body	31261026
1034	cg38227428_BC21	0.00016841	-0.08865208	Lower	Ncs1	chr2	+	tss_body	31660275
1035	cg38232990_BC21	0.00067163	-0.08748112	Lower		chr2	+	tss_200	31925175

1036	cg38236454_BC21	0.00029975	0.06449341	Higher	Lamc3	chr2	+	tss_body	32213893
1037	cg38240594_TC21	0.00013129	-0.07073847	Lower	Prrc2b	chr2	+	tss_body	32336337
1038	cg38242573_BC21	0.00026818	-0.09515709	Lower	Dnm1	chr2	-	tss_body	32336401
1039	cg38242574_BC21	0.00038434	0.09417266	Higher	Dnm1	chr2	-	tss_body	32687973
1040	cg38247933_BC21	9.597E-05	-0.13859029	Lower	Fpgs	chr2	-	tss_body	33605820
1041	cg38259616_TC21	0.00039668	-0.09202114	Lower	Lmx1b	chr2	-	tss_body	33887834
1042	cg38263807_TC21	0.00027946	0.1091636	Higher	Mvb12b	chr2	-	tss_body	35283168
1043	cg38277783_TC11	0.00063331	-0.07114969	Lower	Gsn	chr2	+	tss_body	35286773
1044	cg38277823_BC21	0.00022152	0.13204232	Higher	Gsn	chr2	+	tss_body	35483123
1045	cg38279895_TC11	8.2039E-05	-0.05041477	Lower					35581216
1046	cg38280979_TC21	0.00038651	0.12124152	Higher	Dab2ip	chr2	+	tss_body	35651553
1047	cg38282042_TC21	0.00029111	0.10644052	Higher	Dab2ip	chr2	+	tss_body	35863375
1048	cg38284656_TC21	0.00050868	0.09357247	Higher	Ttll11	chr2	-	tss_body	38701452
1049	cg38304296_TC21	0.00021991	-0.05693023	Lower	Nr5a1	chr2	-	tss_body	38714483
1050	cg38304659_BC21	3.4599E-05	-0.06114626	Lower	Nr5a1	chr2	-	tss_body	38784571
1051	cg38305133_BC21	0.00054678	0.12195607	Higher	Nr6a1	chr2	-	tss_body	49700518
1052	cg38362438_BC21	0.00073442	-0.08446238	Lower	Kif5c	chr2	+	tss_body	52991527
1053	cg38389649_TC21	0.00065562	-0.09966386	Lower	Fmnl2	chr2	+	tss_body	57997661
1054	cg38415978_BC21	3.2779E-05	0.11167	Higher	Gm33594	chr2	-	tss_body	58447034
1055	cg38419042_TC21	0.00013758	-0.06876527	Lower	Acvr1	chr2	-	tss_body	58487070
1056	cg38419525_TC21	1.3325E-05	0.12132149	Higher	Acvr1	chr2	-	tss_body	59647639
1057	cg38430685_BC21	0.00016036	-0.17788907	Lower	Tanc1	chr2	+	tss_body	59689021
1058	cg38431273_TC21	0.00086092	-0.07100154	Lower	Tanc1	chr2	+	tss_body	61059740
1059	cg38445975_TC11	0.00011181	0.07039113	Higher					69135856
1060	cg38500248_BC21	0.00024543	-0.10010632	Lower	Nostrin	chr2	+	tss_body	71875447
1061	cg38529075_BC21	0.00051222	-0.13022763	Lower	Pdk1	chr2	+	tss_body	72326306
1062	cg38534131_TC21	0.00011043	0.0742977	Higher	Zak	chr2	+	tss_body	73131737
1063	cg38542663_TC21	6.5034E-05	-0.07877622	Lower	Ola1	chr2	-	tss_body	74135851
1064	cg38552870_BC21	0.00067401	0.05177111	Higher		chr2	+	tss_body	75209199
1065	cg38564655_BC21	0.00062357	-0.08295508	Lower	LOC102635707	chr2	+	tss_body	77768841
1066	cg38591696_BC11	0.00035613	-0.05462952	Lower	Zfp385b	chr2	-	tss_body	84948811

1067	cg38637954_TC21	0.00085421	-0.0661008	Lower	Slc43a3	chr2	+	tss_body	85001633
1068	cg38638372_BC21	0.00062552	-0.13241385	Lower	P2rx3	chr2	-	tss_body	85196684
1069	cg38640263_TC11	8.8058E-05	-0.06534955	Lower	Lrrc55	chr2	-	tss_body	86923183
1070	cg38647492_BC11	0.00062526	-0.05595536	Lower	Olfr1098	chr2	-	tss_body	87372012
1071	cg38649316_TC21	0.00022963	-0.06292819	Lower	Olfr1121	chr2	+	tss_body	87753694
1072	cg38651123_TC21	0.00084976	0.10472428	Higher	Olfr1141	chr2	-	tss_body	90816363
1073	cg38665708_TC21	0.00023595	-0.05940634	Lower	Agbl2	chr2	+	tss_body	90905779
1074	cg38666767_TC11	5.0119E-05	0.08450963	Higher	Kbtbd4	chr2	+	tss_body	91328584
1075	cg38671584_BC21	0.00027235	-0.09541417	Lower	1110051M20Rik	chr2	-	tss_body	91452529
1076	cg38672479_BC21	0.00088296	0.0748176	Higher					91645808
1077	cg38674473_BC21	0.0001216	-0.14292163	Lower	Zfp408	chr2	-	tss_body	91945716
1078	cg38677275_BC21	0.00021251	-0.0823297	Lower	Dgkz	chr2	-	tss_body	92387272
1079	cg38682173_BC21	0.00013082	-0.08331925	Lower	Mapk8ip1	chr2	-	tss_body	92927406
1080	cg38687877_TC21	0.00031845	-0.05551258	Lower	Syt13	chr2	+	tss_body	93099288
1081	cg38690024_BC21	0.00062229	-0.12809565	Lower		chr2	-	tss_1500	93099578
1082	cg38690028_BC21	0.00091541	0.15398057	Higher		chr2	-	tss_1500	93304123
1083	cg38692422_TC21	0.00011604	-0.05006767	Lower	Tspan18	chr2	-	tss_body	103300362
1084	cg38749916_TC21	0.00088893	0.0674534	Higher	Ehf	chr2	-	tss_body	103896671
1085	cg38755625_TC21	0.00078274	0.12160097	Higher	Gm34948	chr2	-	tss_body	104220144
1086	cg38758959_TC21	0.00050756	-0.17147592	Lower	D430041D05Rik	chr2	-	tss_body	112501133
1087	cg38811026_TC21	0.00028264	-0.08454665	Lower	Chrm5	chr2	-	tss_body	115477508
1088	cg38830573_BC21	0.00036197	0.13294698	Higher					115724349
1089	cg38832483_TC11	1.973E-05	0.07388088	Higher	BC052040	chr2	+	tss_body	115963413
1090	cg38834717_TC21	0.0007006	-0.06669654	Lower	Meis2	chr2	-	tss_body	116852554
1091	cg38840726_BC21	0.00010283	-0.09589648	Lower	Gm13990	chr2	-	tss_body	118512716
1092	cg38854035_BC21	0.00069481	0.10681572	Higher					118996889
1093	cg38860446_BC21	9.6968E-05	-0.06149799	Lower	Gm14089	chr2	+	tss_200	119336633
1094	cg38864608_TC21	0.00018203	-0.06637847	Lower	chr2-119337792-119338215	chr2	*	NShore	127252362
1095	cg38930355_TC21	0.00081087	-0.06447334	Lower	Tmem127	chr2	+	tss_body	127524093
1096	cg38933298_BC21	0.00038709	-0.10559017	Lower	Gm35478	chr2	+	tss_body	128156849

1097	cg38939281_BC21	0.00072533	-0.08108831	Lower	Bcl2l11	chr2	+	tss_body	129038834
1098	cg38947766_BC21	0.00057698	0.05220247	Higher	Gm14025	chr2	-	tss_body	129204525
1099	cg38949945_TC21	0.00039925	-0.07309734	Lower	Slc20a1	chr2	+	tss_body	130003707
1100	cg38957131_TC21	2.7509E-05	0.06576181	Higher	Tgm3	chr2	+	tss_body	130309714
1101	cg38960010_TC21	0.00031721	-0.08476087	Lower	Ebf4	chr2	+	tss_body	131490894
1102	cg38972131_TC11	0.00027968	0.09667726	Higher	Gm30679	chr2	-	tss_body	138819516
1103	cg39022494_BC21	0.00017008	-0.06991024	Lower	Mir1952	chr2	+	tss_1500	144488066
1104	cg39058265_BC21	0.00021408	-0.06634347	Lower	Dzank1	chr2	-	tss_body	147382119
1105	cg39081967_BC21	0.00013514	0.11136421	Higher		chr2	+	tss_body	147928866
1106	cg39085287_BC21	0.00059231	0.07846359	Higher					151572483
1107	cg39107960_TC21	0.00095866	0.17977531	Higher	Sdcbp2	chr2	+	tss_1500	152686810
1108	cg39121127_BC21	1.8659E-05	-0.1015342	Lower	H13	chr2	+	tss_body	153561213
1109	cg39131647_TC11	0.00032681	0.06684091	Higher					153900328
1110	cg39135345_BC21	0.00041854	-0.08280461	Lower	Bpifb6	chr2	+	tss_200	154236764
1111	cg39137940_BC21	0.00011996	-0.07049254	Lower	Cdk5rap1	chr2	-	tss_body	155506487
1112	cg39150310_TC21	8.5729E-05	-0.10776988	Lower	Ggt7	chr2	-	tss_body	157020403
1113	cg39170339_BC21	2.6048E-05	-0.08542103	Lower	Soga1	chr2	-	tss_body	157074944
1114	cg39171214_TC21	0.00099181	-0.14406533	Lower	Soga1	chr2	-	tss_body	157243709
1115	cg39173351_TC21	0.0004945	-0.07317854	Lower	Mroh8	chr2	-	tss_body	157457068
1116	cg39176103_TC11	1.9375E-05	0.09981033	Higher	Src	chr2	+	tss_body	157569328
1117	cg39177712_TC21	0.00061213	-0.10447131	Lower	G3UWQ6	chr2	-	tss_body	157905545
1118	cg39181404_BC21	0.00056104	-0.05049337	Lower					158010766
1119	cg39182795_BC21	8.3564E-05	-0.06766497	Lower	Tti1	chr2	-	tss_body	158229634
1120	cg39185445_TC21	0.00093243	-0.0534059	Lower	D630003M21Rik	chr2	-	tss_1500	158824142
1121	cg39192817_BC21	0.00079355	0.10682291	Higher	Dhx35	chr2	+	tss_body	159004740
1122	cg39194703_TC21	0.00044215	-0.08894924	Lower					160880963
1123	cg39209456_BC11	0.00036466	-0.07851489	Lower	Lpin3	chr2	+	tss_body	162546202
1124	cg39221425_TC21	0.00029747	-0.06607661	Lower	Ptprt	chr2	-	tss_body	162912064
1125	cg39224961_TC21	0.00045775	-0.1114516	Lower	chr2-162908307-162908538	chr2	*	SShelf	163143645
1126	cg39228194_BC21	0.00092574	0.07612929	Higher	Gm11454	chr2	+	tss_body	164199868

1127	cg39242448_BC21	0.00025428	-0.08143628	Lower	Wfdc15a	chr2	-	tss_body	164400963
1128	cg39244509_BC21	0.00073277	-0.07954239	Lower	Matn4	chr2	-	tss_body	164846767
1129	cg39250966_TC21	0.0009181	0.07560155	Higher	Pltp	chr2	-	tss_body	164986404
1130	cg39253567_TC21	0.00041604	-0.06202349	Lower	Slc12a5	chr2	+	tss_body	165405476
1131	cg39260579_BC21	0.00083158	-0.14586185	Lower	Slc13a3	chr2	-	tss_body	166085042
1132	cg39270096_BC21	9.0192E-05	-0.0729987	Lower	Sulf2	chr2	-	tss_body	166322174
1133	cg39273710_TC21	0.00090393	0.05568441	Higher					167053227
1134	cg39284080_BC21	0.00061381	-0.07012962	Lower	Znfx1	chr2	-	tss_body	167351203
1135	cg39288714_TC11	0.00063311	0.10156216	Higher	chr2-167348898-167349851	chr2	*	SShore	167754120
1136	cg39294870_BC21	0.00073832	-0.07158506	Lower					167853439
1137	cg39296466_BC21	0.0005983	-0.05785791	Lower	Gm32845	chr2	+	tss_body	167987917
1138	cg39298513_TC21	0.00037957	0.07684104	Higher	Fam65c	chr2	-	tss_body	168226158
1139	cg39302157_TC21	0.00071505	0.05642439	Higher	Dpm1-adnp	chr2	-	tss_body	168474939
1140	cg39305879_BC21	0.00040718	-0.09578931	Lower					168546421
1141	cg39306989_BC21	1.3618E-05	-0.12043189	Lower	Nfatc2	chr2	-	tss_body	168563529
1142	cg39307302_TC21	0.00017345	-0.05042518	Lower	Nfatc2	chr2	-	tss_body	168618707
1143	cg39308309_BC21	0.00017869	-0.06346239	Lower	chr2-168619254-168619522	chr2	*	NShore	169357741
1144	cg39319702_BC21	0.00059111	0.06004625	Higher					170488200
1145	cg39335689_BC21	0.00028597	0.06014565	Higher	Cyp24a1	chr2	-	tss_body	172974879
1146	cg39365635_BC21	0.00041822	-0.08254463	Lower					173286146
1147	cg39370633_TC21	3.0784E-05	-0.07593726	Lower					174256197
1148	cg39381866_TC21	0.00070124	-0.14125321	Lower					174299168
1149	cg39382666_TC21	0.00019397	-0.13871747	Lower	Gnas	chr2	+	tss_body	174326886
1150	cg39383022_TC21	0.00065305	0.0589421	Higher	Gnas	chr2	+	tss_body	178193134
1151	cg39399139_BC21	0.00012113	-0.06130524	Lower	Phactr3	chr2	+	tss_body	179512699
1152	cg39411965_TC21	0.00097961	-0.11026026	Lower	Cdh4	chr2	+	tss_body	179569409
1153	cg39412654_TC21	0.0004632	-0.11822418	Lower	Cdh4	chr2	+	tss_body	179680145
1154	cg39414031_TC21	1.0631E-05	0.12412791	Higher	Cdh4	chr2	+	tss_body	179776150

1155	cg39415145_BC21	2.0888E-06	0.07311179	Higher	Cdh4	chr2	+	tss_body	180545413
1156	cg39425481_TC21	0.00031073	-0.0934674	Lower	Gm30144	chr2	-	tss_body	181483722
1157	cg39435780_BC11	0.00049253	-0.09704709	Lower	Zbtb46	chr2	-	tss_body	181579166
1158	cg39436663_BC11	0.00019507	0.07989443	Higher	Uckl1	chr2	-	tss_body	3919428
1159	cg39445087_BC21	0.00012147	-0.05111909	Lower					8628254
1160	cg39467931_BC11	0.00048585	0.09096246	Higher	Gm32496	chr3	+	tss_body	8990925
1161	cg39471833_BC21	0.00021265	-0.07218815	Lower	Tpd52	chr3	-	tss_body	9865829
1162	cg39481894_BC21	0.00049824	-0.05892831	Lower					10143692
1163	cg39484335_BC11	0.00012275	-0.13911465	Lower					10232243
1164	cg39485085_TC21	0.00063695	-0.05158945	Lower		chr3	+	tss_body	10242001
1165	cg39485199_TC21	0.00022861	0.05822826	Higher		chr3	+	tss_body	10344743
1166	cg39486314_BC21	0.00015606	-0.05199458	Lower	Zfand1	chr3	-	tss_body	19159709
1167	cg39528801_BC21	0.00043826	-0.05860432	Lower	Armc1	chr3	-	tss_body	21466525
1168	cg39542383_BC21	0.00012592	-0.11985012	Lower	Gm31610	chr3	-	tss_body	22024004
1169	cg39545659_BC21	0.00077997	-0.13448281	Lower					27665843
1170	cg39577996_BC21	3.4709E-05	-0.07652534	Lower	Fndc3b	chr3	-	tss_body	27783692
1171	cg39579466_BC21	7.1012E-05	0.0722901	Higher	Gm42194	chr3	+	tss_body	28124710
1172	cg39582364_TC21	0.00071153	-0.05062763	Lower	Pld1	chr3	+	tss_body	28430854
1173	cg39584916_BC11	0.00027185	0.11947598	Higher	Tnik	chr3	+	tss_body	30997798
1174	cg39604564_BC11	0.00099574	0.09843015	Higher	Prkci	chr3	+	tss_body	31054424
1175	cg39605185_BC21	0.00027691	0.08943896	Higher					33217717
1176	cg39623221_BC21	0.00097204	-0.0619741	Lower					35545846
1177	cg39642440_BC21	0.00017434	-0.15398184	Lower		chr3	+	tss_200	36395374
1178	cg39649063_TC21	0.00076791	0.05095322	Higher	Gm42209	chr3	-	tss_body	36835802
1179	cg39653310_TC21	0.00018811	-0.0638577	Lower					38888102
1180	cg39669659_TC21	0.00011132	0.0596223	Higher	Fat4	chr3	+	tss_body	41284930
1181	cg39685374_TC21	0.00086989	-0.15194588	Lower					52416650
1182	cg39751476_TC21	0.00038409	0.07891103	Higher					53625480
1183	cg39764036_TC21	0.00078613	-0.12416686	Lower	Frem2	chr3	-	tss_body	54633364
1184	cg39771756_TC21	0.00050745	-0.07772659	Lower		chr3	-	tss_body	55350031
1185	cg39779151_TC21	0.000520 6	-0.07566008	Lower	Dclk1	chr3	+	tss_body	56756117

1186	cg39788147_TC21	0.00034931	-0.14019342	Lower					60737434
1187	cg39813383_BC21	0.00093843	0.06425815	Higher					62395637
1188	cg39821578_TC21	2.3886E-05	0.08262578	Higher	Arhgef26	chr3	+	tss_body	63295512
1189	cg39826089_BC11	0.00071361	0.0813422	Higher	Mme	chr3	+	tss_1500	64142697
1190	cg39831280_BC21	0.00054576	0.07503629	Higher	Vmn2r1	chr3	+	tss_body	65201556
1191	cg39836069_TC21	0.00063259	0.09357899	Higher	Kcnab1	chr3	+	tss_body	65665763
1192	cg39839934_TC21	0.00074374	-0.06145913	Lower	Lekr1	chr3	+	tss_body	67103955
1193	cg39850518_TC21	0.00060196	-0.05072624	Lower	Rsrc1	chr3	+	tss_body	69543171
1194	cg39871135_BC21	0.00032882	-0.11506835	Lower	Ppm1l	chr3	+	tss_body	71620828
1195	cg39882273_TC21	0.00033914	-0.0578063	Lower					79582752
1196	cg39920638_BC21	0.00040154	-0.05485299	Lower		chr3	+	tss_body	82073409
1197	cg39934776_BC21	0.00032793	-0.06756964	Lower	Gucy1b3	chr3	-	tss_body	82540414
1198	cg39937697_TC21	0.00061485	0.13552036	Higher	Npy2r	chr3	-	tss_body	85172116
1199	cg39961902_TC21	2.0807E-05	0.15267124	Higher	E9QAY5	chr3	-	tss_body	85553352
1200	cg39965279_BC11	0.00063767	-0.13243122	Lower	Gm3740	chr3	-	tss_body	86002316
1201	cg39969136_TC21	8.9695E-05	-0.11127419	Lower	Sh3d19	chr3	+	tss_body	87357504
1202	cg39980551_TC21	2.3126E-05	-0.06260596	Lower	Gm31940	chr3	-	tss_body	87783842
1203	cg39984851_TC21	0.00029679	-0.09146514	Lower	Ntrk1	chr3	-	tss_body	88636624
1204	cg39996732_TC21	0.00011028	-0.06219219	Lower	Arhgef2	chr3	+	tss_body	89224117
1205	cg40003699_TC21	0.00088316	-0.06120848	Lower	Thbs3	chr3	+	tss_body	89409001
1206	cg40007195_TC11	0.00069775	-0.07939633	Lower	Flad1	chr3	-	tss_body	89648394
1207	cg40010374_TC21	0.00020427	-0.0757158	Lower	Kcnn3	chr3	+	tss_body	94377664
1208	cg40040294_TC21	4.6588E-05	-0.08454637	Lower	Rorc	chr3	+	tss_body	95734730
1209	cg40054855_BC21	0.00098376	-0.05751342	Lower	Ecm1	chr3	-	tss_body	95880745
1210	cg40056533_BC21	0.00040874	0.05390423	Higher	C920021L13Rik	chr3	+	tss_body	95944239
1211	cg40057587_TC21	0.00024108	-0.06575423	Lower	Anp32e	chr3	+	tss_body	97216609
1212	cg40073393_TC21	0.00040681	0.11113543	Higher	Bcl9	chr3	-	tss_body	97971918
1213	cg40081350_BC21	0.00020839	-0.1142041	Lower					98035209
1214	cg40082088_TC21	0.00057779	0.15762595	Higher	Notch2	chr3	+	tss_body	100704473
1215	cg40101144_BC21	0.00039898	0.05666538	Higher					101307197
1216	cg40107875_BC21	0.00049196	-0.0888225	Lower		chr3	-	tss_200	101404168

1217	cg40109059_TC21	0.000593	0.0574206	Higher	Igsf3	chr3	+	tss_body	102063034
1218	cg40116533_BC21	0.00043578	-0.11765039	Lower					102527004
1219	cg40121023_TC21	2.7196E-05	-0.13799136	Lower					103594508
1220	cg40130495_TC21	0.00030282	-0.07544351	Lower	Syt6	chr3	+	tss_body	103616443
1221	cg40130726_TC21	0.00070665	0.06014225	Higher	Syt6	chr3	+	tss_body	105459236
1222	cg40147111_TC21	3.7176E-05	-0.05152988	Lower	Kcnd3	chr3	+	tss_body	107756264
1223	cg40164062_BC21	0.00030911	-0.06610957	Lower	Gm40121	chr3	+	tss_body	108412816
1224	cg40172041_TC21	0.00073683	-0.05076733	Lower	Celsr2	chr3	-	tss_body	116726957
1225	cg40221218_TC21	0.00077169	-0.08089859	Lower					117361006
1226	cg40226446_TC21	0.00033586	0.10824185	Higher	Plppr4	chr3	-	tss_200	121295169
1227	cg40250690_BC21	0.00047745	-0.09601426	Lower	Alg14	chr3	+	tss_body	121438224
1228	cg40252511_BC21	0.00071693	-0.0768292	Lower	Cnn3	chr3	+	tss_body	121532299
1229	cg40253764_TC11	0.00094936	0.05965058	Higher	Slc44a3	chr3	-	tss_body	121715075
1230	cg40255735_TC11	0.00030098	0.15601955	Higher					121941142
1231	cg40258339_BC21	0.00048295	0.0890429	Higher					122207903
1232	cg40261334_BC21	5.3597E-05	-0.06880838	Lower	LOC108168894	chr3	-	tss_body	122334560
1233	cg40263035_BC11	0.00040357	-0.1314762	Lower		chr3	+	tss_body	123035054
1234	cg40270248_TC21	0.00057454	-0.07829917	Lower	Myoz2	chr3	-	tss_200	130962613
1235	cg40334106_TC21	0.00068308	0.09388899	Higher					133598849
1236	cg40358077_TC11	0.00086255	0.07539499	Higher					137622987
1237	cg40385381_TC21	0.00020444	0.10984225	Higher	Ddit4l	chr3	+	tss_1500	137921311
1238	cg40388314_BC21	0.00099451	-0.08462182	Lower	Lamtor3	chr3	+	tss_body	138833332
1239	cg40398943_BC11	0.00061103	0.08678576	Higher	Tspan5	chr3	+	tss_body	141837279
1240	cg40415783_TC21	4.8409E-05	-0.06517096	Lower	Bmpr1b	chr3	-	tss_body	146856364
1241	cg40464412_TC21	8.9195E-05	0.06194227	Higher	Ttll7	chr3	+	tss_body	148202374
1242	cg40474098_TC21	0.00074764	-0.09619519	Lower					148463002
1243	cg40475931_BC21	0.0003989	-0.0590099	Lower					152152020
1244	cg40502995_TC21	8.9472E-05	-0.10587757	Lower	Gipc2	chr3	-	tss_body	152516290
1245	cg40507508_TC21	0.00071381	0.12455439	Higher	Ak5	chr3	-	tss_body	154695608
1246	cg40531057_BC21	0.00020052	0.09280717	Higher	F6QRE9	chr3	+	tss_body	6901454
1247	cg40579861_TC21	2.2489E-05	-0.09590142	Lower	Tox	chr4	-	tss_body	9161386

1248	cg40596498_TC21	0.00097744	-0.07911975	Lower	Clvs1	chr4	+	tss_body	9617963
1249	cg40599952_TC21	0.00062281	0.06705349	Higher	Asph	chr4	-	tss_body	10960141
1250	cg40608610_TC21	0.00022193	0.07667685	Higher					13784398
1251	cg40629792_TC21	6.9419E-05	0.07727934	Higher	Runx1t1	chr4	+	tss_body	15608717
1252	cg40640579_BC21	5.8086E-06	-0.11573287	Lower					21931653
1253	cg40672554_TC21	0.00043025	0.09495186	Higher	Faxc	chr4	+	tss_body	33053972
1254	cg40735879_BC11	0.00035729	0.05859281	Higher		chr4	-	tss_body	41659925
1255	cg40793993_TC21	7.2725E-05	-0.17715373	Lower	Cntfr	chr4	-	tss_body	43447489
1256	cg40806991_TC21	0.00033618	0.0510612	Higher	Tesk1	chr4	+	tss_body	44123223
1257	cg40815814_TC21	0.00086498	-0.06646895	Lower	Gm12504	chr4	+	tss_body	44703414
1258	cg40822604_BC21	0.00092473	0.05502431	Higher	Pax5	chr4	-	tss_body	44905753
1259	cg40824162_TC21	0.00093718	-0.11188276	Lower	Zcchc7	chr4	+	tss_body	47881647
1260	cg40860603_TC21	0.00058204	0.08816225	Higher		chr4	-	tss_body	48663538
1261	cg40868000_TC21	0.00081472	0.12881671	Higher	Murc	chr4	+	tss_body	49282963
1262	cg40872352_TC21	0.00010458	0.06941901	Higher	Plppr1	chr4	+	tss_body	57221942
1263	cg40927222_BC11	0.00025022	0.1080605	Higher	Ptpn3	chr4	-	tss_body	57300610
1264	cg40928481_TC11	0.00044572	0.07290995	Higher	Ptpn3	chr4	-	tss_body	62274326
1265	cg40961891_BC21	0.00042337	-0.05878162	Lower	Q9D524	chr4	+	tss_body	62891298
1266	cg40968694_BC21	6.4804E-05	-0.05298244	Lower					63167510
1267	cg40971449_BC21	0.000440 9	-0.06215137	Lower	Kif12	chr4	-	tss_body	66171736
1268	cg40990121_BC21	0.00032491	-0.05176279	Lower	Astn2	chr4	-	tss_body	71072612
1269	cg41013201_BC21	0.00070478	-0.07167042	Lower		chr4	+	tss_200	84130014
1270	cg41082603_TC21	3.3118E-05	-0.05371169	Lower	Gm12414	chr4	-	tss_body	86774345
1271	cg41102154_BC21	0.00093553	0.15364601	Higher	Dennd4c	chr4	+	tss_body	88237169
1272	cg41113149_TC21	0.00010949	-0.05387315	Lower	Focad	chr4	+	tss_body	88640985
1273	cg41115586_BC21	0.00040532	0.05457954	Higher					89455265
1274	cg41122240_TC21	0.000429	-0.05580421	Lower	Gm12610	chr4	+	tss_body	94385754
1275	cg41145769_TC21	0.00022191	-0.12964864	Lower	LOC108168967	chr4	-	tss_body	95318619
1276	cg41152483_TC21	0.00084973	0.05873161	Higher					97786734
1277	cg41165883_BC21	4.5107E-05	0.07253784	Higher	Nfia	chr4	+	tss_body	98182333
1278	cg41169110_BC21	0.00028576	-0.05180624	Lower					100325583

1279	cg41189343_TC21	3.7806E-05	0.14248578	Higher	Ror1	chr4	+	tss_body	102856074
1280	cg41210063_TC11	0.0007693	0.11778307	Higher	Sgip1	chr4	+	tss_body	103026897
1281	cg41211624_BC11	0.00014978	0.06529398	Higher	Insl5	chr4	-	tss_200	105283279
1282	cg41230725_TC21	0.00026808	0.19654646	Higher					105313194
1283	cg41230938_BC21	0.00064276	-0.16154699	Lower	Gm40217	chr4	-	tss_body	105365342
1284	cg41231454_BC21	0.00010312	-0.05169252	Lower					105790649
1285	cg41234399_TC21	0.0003722	0.07386097	Higher	V9GX31	chr4	+	tss_body	106619324
1286	cg41242459_BC21	0.00057797	-0.10285153	Lower	chr4-106622395-106623099	chr4	*	NShelf	106938388
1287	cg41246675_BC21	0.00031014	-0.05706763	Lower	Ssbp3	chr4	+	tss_body	107001620
1288	cg41247356_TC21	0.00088066	0.05185422	Higher	Ssbp3	chr4	+	tss_body	107097761
1289	cg41248596_TC21	0.00088518	-0.09575592	Lower	Cdcp2	chr4	+	tss_body	107589214
1290	cg41255164_BC21	0.00018099	0.13648373	Higher	Glis1	chr4	+	tss_body	107668251
1291	cg41256081_BC21	0.00030648	-0.06319177	Lower					107757604
1292	cg41257295_BC21	0.00050337	-0.06895415	Lower		chr4	+	tss_body	108169544
1293	cg41262316_TC21	2.2793E-05	-0.05390731	Lower	Echdc2	chr4	+	tss_body	109860369
1294	cg41276247_TC21	0.00083197	0.06004174	Higher	Faf1	chr4	+	tss_body	114841638
1295	cg41302146_BC21	0.00041816	-0.06236637	Lower	Gm12830	chr4	+	tss_body	116004395
1296	cg41311773_BC21	0.00069572	0.07078226	Higher	Faah	chr4	-	tss_body	117004453
1297	cg41321117_BC21	2.0026E-05	-0.0907799	Lower	Hectd3	chr4	+	tss_body	117278896
1298	cg41324681_BC21	0.00049327	0.06926277	Higher	Rnf220	chr4	-	tss_body	117343407
1299	cg41325720_TC21	0.00086284	0.10301218	Higher	Rnf220	chr4	-	tss_body	117353270
1300	cg41325851_TC21	0.00022191	-0.05091245	Lower	Rnf220	chr4	-	tss_body	117374477
1301	cg41326142_TC21	0.0003564	-0.05739285	Lower	Rnf220	chr4	-	tss_body	117882146
1302	cg41331975_BC21	0.00038818	0.07549844	Higher	B4galt2	chr4	-	tss_body	118540384
1303	cg41342169_TC21	0.00089361	0.09884957	Higher	chr4-118541901-118542148	chr4	*	NShore	119009782
1304	cg41345983_BC21	0.00014371	0.09461842	Higher					119018797
1305	cg41346088_BC11	0.00072396	0.07451544	Higher					120614432
1306	cg41362756_BC21	0.00070011	-0.0831833	Lower		chr4	+	tss_1500	120877979

1307	cg41365735_TC21	0.00068369	-0.08031601	Lower	Rims3	chr4	+	tss_body	124481260
1308	cg41393350_BC11	0.00029431	-0.0522676	Lower	1700057H15Rik	chr4	-	tss_body	126105299
1309	cg41415644_BC21	0.0008251	0.11005621	Higher	Stk40	chr4	+	tss_body	126613853
1310	cg41422292_TC21	0.00098341	-0.0863632	Lower	5730409E04Rik	chr4	+	tss_body	126648493
1311	cg41422710_TC21	0.00067017	-0.08107352	Lower					126823660
1312	cg41424875_TC21	7.4218E-05	-0.05665731	Lower	AU040320	chr4	+	tss_body	127330882
1313	cg41430688_TC21	0.00087618	0.08857024	Higher	Gm40251	chr4	+	tss_body	128616341
1314	cg41445131_BC21	4.9051E-05	-0.0740018	Lower	Tlr12	chr4	-	tss_body	129557568
1315	cg41459254_BC11	0.00023998	0.13744032	Higher	Lck	chr4	-	tss_body	129626392
1316	cg41460302_TC21	6.3083E-06	-0.05014794	Lower	Txlna	chr4	-	tss_body	129933704
1317	cg41464252_BC21	0.00017892	-0.05274126	Lower	Spocd1	chr4	+	tss_body	130222476
1318	cg41468817_BC21	0.00058848	-0.0804748	Lower	Gm853	chr4	-	tss_200	131919644
1319	cg41487175_BC21	0.00071115	-0.05851067	Lower	Gm12992	chr4	-	tss_body	134402982
1320	cg41522263_TC21	3.8021E-05	-0.06213771	Lower	Pafah2	chr4	+	tss_body	134642220
1321	cg41526277_BC21	0.00067899	0.10447921	Higher	Man1c1	chr4	-	tss_body	135302559
1322	cg41536593_TC11	0.00044534	0.06148644	Higher					135491031
1323	cg41539436_TC21	5.9319E-05	-0.13941182	Lower	Nipal3	chr4	-	tss_body	135909817
1324	cg41545675_BC21	0.00038892	-0.05749046	Lower	Cnr2	chr4	+	tss_body	136090186
1325	cg41548411_TC21	0.00015982	0.08477576	Higher					137681158
1326	cg41571163_TC21	0.00039613	0.09276806	Higher	Rap1gap	chr4	+	tss_body	137717680
1327	cg41571802_BC21	0.00077111	-0.08252927	Lower	Rap1gap	chr4	+	tss_body	138167338
1328	cg41578381_BC21	0.00029067	0.08462422	Higher	Eif4g3	chr4	+	tss_body	138267733
1329	cg41579972_TC21	0.00067968	-0.11479922	Lower	Kif17	chr4	+	tss_body	138719613
1330	cg41586534_TC21	0.0008915	-0.08952203	Lower	Ubxn10	chr4	-	tss_body	138780358
1331	cg41587418_BC21	0.00016737	-0.1095143	Lower	Pla2g2d	chr4	+	tss_body	138819153
1332	cg41587909_TC21	0.00021103	0.08760963	Higher	Pla2g5	chr4	-	tss_body	139597225
1333	cg41599439_TC21	0.00030725	-0.09342396	Lower	Iffo2	chr4	+	tss_body	139923309
1334	cg41604320_TC21	0.00082497	-0.06717745	Lower	LOC102636380	chr4	+	tss_body	140462164
1335	cg41612054_TC21	0.00022641	-0.08204809	Lower					140742265
1336	cg41616785_TC21	0.00020626	-0.06717222	Lower	Padi6	chr4	-	tss_body	141088301
1337	cg41622780_TC11	0.00047186	-0.06233893	Lower	Spata21	chr4	+	tss_200	141202487

1338	cg41624484_TC21	0.00044788	0.10250254	Higher	Fbxo42	chr4	+	tss_body	141240734
1339	cg41625043_BC21	0.00051112	0.07558642	Higher	Arhgef19	chr4	+	tss_body	141361164
1340	cg41627284_BC11	0.00038422	-0.06897617	Lower					141365775
1341	cg41627366_TC21	0.00037311	-0.06788159	Lower	chr4-141368138-141368541	chr4	*	NShelf	141395468
1342	cg41627908_TC21	0.00047986	-0.08255292	Lower	Clcnka	chr4	-	tss_body	141398089
1343	cg41627951_TC21	0.00060622	-0.0768708	Lower	Clcnka	chr4	-	tss_body	141600131
1344	cg41631956_TC21	0.0007431	0.12737359	Higher	Fblim1	chr4	-	tss_body	141603284
1345	cg41632006_BC21	0.00087713	-0.10256404	Lower	Fblim1	chr4	-	tss_body	142143341
1346	cg41640424_TC21	0.00092679	-0.06794761	Lower	Kazn	chr4	-	tss_body	142159398
1347	cg41640679_TC21	0.0007994	0.09823272	Higher	Kazn	chr4	-	tss_body	142171932
1348	cg41640877_TC11	0.00078165	0.08482226	Higher	Kazn	chr4	-	tss_body	142303925
1349	cg41642671_BC21	0.00037542	-0.08267539	Lower					144213803
1350	cg41659101_TC21	0.00059062	-0.09820161	Lower	C87977	chr4	-	tss_1500	147920757
1351	cg41678439_BC21	9.5442E-05	-0.06864328	Lower	Plod1	chr4	-	tss_body	148125744
1352	cg41681455_BC21	0.00017383	-0.11815375	Lower	Draxin	chr4	-	tss_body	148306788
1353	cg41684456_BC21	0.00071263	-0.10610702	Lower		chr4	+	tss_200	148359740
1354	cg41685144_TC21	6.5342E-05	-0.05245368	Lower		chr4	-	tss_1500	151420594
1355	cg41731416_TC21	3.1297E-05	-0.17307947	Lower	Camta1	chr4	-	tss_body	151822077
1356	cg41736761_TC11	9.0896E-05	0.05396349	Higher	Camta1	chr4	-	tss_body	152062985
1357	cg41741297_TC21	0.00082966	0.17707026	Higher					152083879
1358	cg41741564_TC21	0.00064198	-0.0991662	Lower	Plekhg5	chr4	+	tss_body	152126745
1359	cg41742547_BC21	0.00011603	-0.06135484	Lower	Espn	chr4	-	tss_body	153712674
1360	cg41765654_BC11	0.00016238	0.11872438	Higher					154153914
1361	cg41772008_BC21	0.00021745	-0.05343806	Lower	Wrap73	chr4	+	tss_body	154231747
1362	cg41773254_BC21	7.5052E-05	0.05796872	Higher	Megf6	chr4	+	tss_body	154627091
1363	cg41779189_TC21	0.00013076	-0.10843302	Lower	Prdm16	chr4	-	tss_body	154731553
1364	cg41780739_TC21	5.999E-05	-0.07251107	Lower					154781340
1365	cg41781358_BC21	0.00027013	-0.09178395	Lower					155302036
1366	cg41789426_BC21	8.487E-05	0.07321165	Higher	Prkcz	chr4	-	tss_body	155992033
1367	cg41799406_BC11	7.4316E-05	-0.05422895	Lower	B3galt6	chr4	-	tss_body	156172576

1368	cg41802018_BC21	0.00056947	-0.09104227	Lower	Agrn	chr4	-	tss_body	156225332
1369	cg41803077_BC21	5.9992E-05	-0.05060629	Lower	Plekhn1	chr4	-	tss_body	156249019
1370	cg41803705_BC21	0.00063969	-0.10632441	Lower	Samd11	chr4	-	tss_body	3651107
1371	cg41810295_TC21	0.00018269	0.14589411	Higher	A0A0G2JDS4	chr5	-	tss_body	15933427
1372	cg41876357_TC21	0.00036366	0.14302109	Higher	Gm3510	chr5	-	tss_body	16149305
1373	cg41877801_BC21	0.00054297	0.10947312	Higher	Cacna2d1	chr5	+	tss_body	24482374
1374	cg41935762_BC11	0.00089716	-0.05207291	Lower	Agap3	chr5	+	tss_body	24591753
1375	cg41937553_BC21	0.00085029	-0.08513113	Lower	Chpf2	chr5	+	tss_body	30092901
1376	cg41976972_TC21	0.00019386	-0.10695357	Lower	Gm4961	chr5	+	tss_200	30798888
1377	cg41984989_BC21	0.00034368	-0.06226885	Lower	Dpysl5	chr5	+	tss_body	31200309
1378	cg41990676_TC21	6.1169E-05	-0.11876963	Lower	Zfp513	chr5	-	tss_body	32049480
1379	cg41998043_TC21	3.8939E-05	0.06558229	Higher	Bre	chr5	+	tss_body	33443652
1380	cg42011179_BC21	0.00025312	0.10537324	Higher	chr5-33442909-33443471	chr5	*	SShore	34635064
1381	cg42022941_TC21	0.00074584	-0.0838673	Lower	Mfsd10	chr5	-	tss_body	34635088
1382	cg42022942_TC21	0.00067984	-0.0913433	Lower	Mfsd10	chr5	-	tss_body	35472723
1383	cg42031352_BC21	0.00019578	0.07801153	Higher					35814526
1384	cg42035380_BC21	0.00037324	-0.08200655	Lower	Ablim2	chr5	+	tss_body	35840923
1385	cg42035687_BC21	0.00096545	-0.073224	Lower	Ablim2	chr5	+	tss_body	38550672
1386	cg42064655_BC21	0.00030056	0.11994092	Higher	Wdr1	chr5	-	tss_body	44286943
1387	cg42098141_BC21	0.00053409	0.15445098	Higher					45175811
1388	cg42103646_TC21	0.00079062	-0.06012613	Lower	D5Ertd615e	chr5	-	tss_body	51277730
1389	cg42135118_TC21	4.6954E-05	0.13259139	Higher					52992235
1390	cg42150753_BC21	0.00078245	0.05495753	Higher	5033403H07Rik	chr5	-	tss_body	53148080
1391	cg42152330_TC21	0.00085301	-0.07318768	Lower	Sel1l3	chr5	-	tss_body	53150518
1392	cg42152359_TC21	5.4515E-05	-0.08816631	Lower	Sel1l3	chr5	-	tss_body	53178877
1393	cg42152730_BC21	9.6015E-05	-0.08038905	Lower	Sel1l3	chr5	-	tss_body	53690569
1394	cg42158467_TC21	0.00090823	0.07749571	Higher					53726315
1395	cg42158860_TC21	0.0003554	0.09345239	Higher					53996271
1396	cg42160906_BC21	0.00028025	-0.09109703	Lower	Gm30601	chr5	+	tss_body	57760370
1397	cg42178583_BC21	0.00041243	-0.09804042	Lower	Pcdh7	chr5	+	tss_body	62108973

1398	cg42197205_TC21	0.00068266	0.14462956	Higher					64487948
1399	cg42213351_BC11	9.3999E-05	-0.08069922	Lower					64751900
1400	cg42215810_TC21	0.00079136	-0.11778295	Lower		chr5	-	tss_body	65782205
1401	cg42227404_BC21	0.00016276	0.0826756	Higher	N4bp2	chr5	+	tss_body	66800205
1402	cg42239748_BC11	0.00077147	0.13481863	Higher	Limch1	chr5	+	tss_body	68275185
1403	cg42254477_TC21	1.1536E-05	0.08556538	Higher					73211161
1404	cg42284666_TC21	0.00054778	0.06141583	Higher	Fryl	chr5	-	tss_body	73913497
1405	cg42292851_BC21	0.00026005	-0.06098676	Lower	1700019F05Rik	chr5	+	tss_body	74194933
1406	cg42296047_TC21	9.0845E-05	0.06625174	Higher	Rasl11b	chr5	+	tss_1500	75900734
1407	cg42314450_BC21	0.00038175	-0.06159985	Lower					76840423
1408	cg42324314_TC21	0.00024555	0.08888879	Higher	C530008M17Rik	chr5	+	tss_body	90794781
1409	cg42405091_TC21	5.8623E-06	0.14383017	Higher	Cxcl15	chr5	+	tss_body	92503640
1410	cg42420225_TC21	0.00024462	-0.1177438	Lower	Scarb2	chr5	-	tss_body	93296514
1411	cg42429394_BC21	0.00064572	0.11262856	Higher					97935269
1412	cg42453614_BC21	5.5772E-05	-0.0715883	Lower	Antxr2	chr5	-	tss_body	99403141
1413	cg42466823_TC21	0.00094087	-0.06214415	Lower	A930011G23Rik	chr5	-	tss_body	100751273
1414	cg42482799_TC21	0.00036047	0.12194595	Higher	Gm36619	chr5	+	tss_body	101817231
1415	cg42494475_TC11	0.00084247	-0.05171778	Lower	Cds1	chr5	+	tss_body	102514382
1416	cg42502168_TC21	0.00014008	0.05435027	Higher	Arhgap24	chr5	+	tss_body	103365993
1417	cg42509769_TC11	0.00067451	0.13653076	Higher					105777224
1418	cg42532958_TC11	0.00069095	0.11915668	Higher	Lrrc8d	chr5	+	tss_body	107251269
1419	cg42549054_TC21	0.00051766	0.07594971	Higher	Tgfbr3	chr5	-	tss_body	107726013
1420	cg42553530_BC11	0.00058272	0.05726687	Higher	Gfi1	chr5	-	tss_body	107844610
1421	cg42554398_BC21	0.00059441	0.11538975	Higher	Evi5	chr5	-	tss_body	108448807
1422	cg42559481_BC21	3.8019E-05	0.06919757	Higher	Mfsd7a	chr5	-	tss_body	108655544
1423	cg42561115_TC21	2.7462E-05	-0.14587116	Lower	Dgkq	chr5	-	tss_body	111578615
1424	cg42588019_TC11	0.00037115	-0.10610662	Lower					112167128
1425	cg42594562_BC21	0.00048506	-0.11321155	Lower					112174909
1426	cg42594652_BC21	6.6214E-05	-0.05215424	Lower					112228487
1427	cg42595299_BC11	0.00059202	0.05948802	Higher	Miat	chr5	-	tss_body	112861918
1428	cg42604041_TC21	0.00082272	-0.07438312	Lower	Myo18b	chr5	-	tss_body	112896351

1429	cg42604482_BC21	0.00026586	-0.053265	Lower	Myo18b	chr5	-	tss_body	113116465
1430	cg42607481_BC21	0.00052301	-0.05765932	Lower	2900026A02Rik	chr5	-	tss_body	113245081
1431	cg42609705_BC21	0.00074006	-0.0798471	Lower	Sgsm1	chr5	-	tss_body	113301830
1432	cg42610615_BC21	0.00022005	0.10938001	Higher	Sgsm1	chr5	-	tss_body	113643598
1433	cg42615396_BC21	0.00012538	-0.07597855	Lower	Cmklr1	chr5	-	tss_body	114165739
1434	cg42624225_TC21	0.00032626	-0.07252312	Lower	Acacb	chr5	+	tss_body	114422230
1435	cg42629046_BC21	0.00077097	0.09585622	Higher					114786057
1436	cg42635896_TC21	0.00033	-0.06213206	Lower	Ankrd13a	chr5	+	tss_body	115055409
1437	cg42640198_BC21	0.00030764	-0.06098798	Lower	Sppl3	chr5	+	tss_body	115523439
1438	cg42648433_BC21	0.00036604	-0.0887454	Lower	Pxn	chr5	+	tss_body	115581026
1439	cg42649747_TC21	0.00013511	0.05602012	Higher	Gcn1l1	chr5	+	tss_body	115643125
1440	cg42651118_TC21	0.00030258	-0.06415216	Lower	Rab35	chr5	+	tss_body	116271945
1441	cg42660819_BC21	0.00097762	-0.06282043	Lower	Ccdc60	chr5	-	tss_body	116968463
1442	cg42669008_BC21	7.7372E-05	-0.07279646	Lower					117509604
1443	cg42677339_TC21	0.00082206	-0.06815186	Lower	Ksr2	chr5	+	tss_body	117670542
1444	cg42679497_TC21	0.00065074	-0.05616816	Lower	Ksr2	chr5	+	tss_body	117896844
1445	cg42682422_TC21	0.00030692	-0.14368581	Lower	Nos1	chr5	+	tss_body	118463788
1446	cg42690896_BC21	0.00039407	-0.11901658	Lower					119179491
1447	cg42699950_BC21	0.00014866	-0.09354743	Lower					120698613
1448	cg42720921_TC21	0.00046938	-0.05273106	Lower	Dtx1	chr5	-	tss_body	121242715
1449	cg42727012_TC21	0.00071882	-0.10647605	Lower	Gm15800	chr5	+	tss_body	121604393
1450	cg42731910_BC11	0.00032324	0.05062576	Higher	Acad12	chr5	-	tss_body	122514766
1451	cg42746115_TC21	3.8291E-05	-0.06696219	Lower	LOC102635658	chr5	+	tss_body	122529925
1452	cg42746342_TC21	0.00057818	-0.07885644	Lower					123572715
1453	cg42761771_TC21	6.6919E-05	-0.06540754	Lower	Vps33a	chr5	-	tss_body	123865352
1454	cg42765840_TC21	0.00042059	0.07150864	Higher	Hcar2	chr5	-	tss_body	124072615
1455	cg42769072_TC21	0.00076019	0.10771244	Higher	Abcb9	chr5	-	tss_body	124224772
1456	cg42771642_TC21	0.00071404	-0.12886612	Lower	Pitpnm2	chr5	-	tss_body	124608374
1457	cg42777271_TC21	0.00045685	-0.07310947	Lower	Tctn2	chr5	+	tss_body	124883930
1458	cg42780682_TC21	0.00076998	-0.08136274	Lower	Zfp664	chr5	+	tss_body	125066318
1459	cg42783556_TC11	6.8645E-05	0.0503843	Higher	Ncor2	chr5	-	tss_body	125176934

1460	cg42785404_TC21	0.00047755	0.06726508	Higher	Ncor2	chr5	-	tss_body	125448222
1461	cg42789665_TC21	0.00045778	-0.05562146	Lower	Bri3bp	chr5	+	tss_body	127578346
1462	cg42808118_TC21	0.0002863	-0.10929478	Lower		chr5	+	tss_1500	128780764
1463	cg42820776_TC21	0.00075949	-0.08899101	Lower	Rimbp2	chr5	-	tss_body	130149406
1464	cg42837996_BC21	7.6599E-05	-0.06076137	Lower	Kctd7	chr5	+	tss_body	132098745
1465	cg42856685_BC21	0.00058291	-0.10801239	Lower	Auts2	chr5	-	tss_body	134227489
1466	cg42873300_BC21	0.00096665	-0.05382297	Lower	Ncf1	chr5	-	tss_body	134368401
1467	cg42875619_TC21	0.00026594	-0.10670126	Lower	Gtf2ird1	chr5	-	tss_body	134377262
1468	cg42875711_TC21	0.00083907	0.05233149	Higher	Gtf2ird1	chr5	-	tss_body	135350247
1469	cg42889160_TC21	2.5343E-05	-0.05320689	Lower	Fkbp6	chr5	-	tss_body	135525104
1470	cg42891759_BC11	7.9923E-05	-0.05472197	Lower	Hip1	chr5	-	tss_body	135945909
1471	cg42897482_BC21	0.00054706	-0.10935383	Lower					135995952
1472	cg42898250_BC21	0.00014879	-0.06360055	Lower	Dtx2	chr5	+	tss_body	136458221
1473	cg42904019_TC21	0.00023646	-0.09530944	Lower	Cux1	chr5	-	tss_body	136495205
1474	cg42904308_TC21	7.2915E-06	0.09211676	Higher	Cux1	chr5	-	tss_body	136503919
1475	cg42904380_TC21	0.00065635	-0.11794321	Lower	Cux1	chr5	-	tss_body	136539575
1476	cg42904651_TC21	0.00047829	0.09095644	Higher	Cux1	chr5	-	tss_body	136717732
1477	cg42906852_TC21	1.9667E-05	-0.05870551	Lower					136989653
1478	cg42910686_TC21	0.00011825	-0.08242261	Lower	Plod3	chr5	+	tss_body	137027041
1479	cg42911200_BC21	6.6206E-05	0.05087332	Higher	Vgf	chr5	+	tss_body	137297121
1480	cg42914557_TC21	0.00032075	-0.05507821	Lower	Srrt	chr5	-	tss_body	138258701
1481	cg42926466_BC21	0.00046992	-0.09435413	Lower	Lamtor4	chr5	+	tss_body	139081680
1482	cg42934186_BC21	0.00025899	-0.10666228	Lower	Prkar1b	chr5	-	tss_body	139112640
1483	cg42934499_TC21	0.00064333	-0.05719432	Lower	Prkar1b	chr5	-	tss_body	139204948
1484	cg42935847_BC21	0.00057585	0.16512539	Higher	Sun1	chr5	+	tss_body	139945546
1485	cg42946903_BC21	3.1299E-05	0.09894403	Higher	Elfn1	chr5	+	tss_body	140647086
1486	cg42955330_BC11	0.00068348	-0.08859755	Lower	Ttyh3	chr5	-	tss_body	140892968
1487	cg42958590_BC11	0.00030557	-0.05466446	Lower	Card11	chr5	-	tss_body	142782543
1488	cg42978586_TC21	0.00026649	0.14110007	Higher	Tnrc18	chr5	-	tss_body	143147458
1489	cg42983769_BC21	0.00043978	-0.08214334	Lower	A0A2I3BPT7	chr5	-	tss_body	143195102
1490	cg42984449_BC21	0.00013299	0.05889649	Higher	Spdye4b	chr5	+	tss_body	143288127

1491	cg42986132_BC11	0.00090529	0.06290039	Higher	Zfp853	chr5	-	tss_body	143518012
1492	cg42989734_TC21	0.00056855	-0.08678404	Lower	Rac1	chr5	-	tss_body	143633769
1493	cg42991332_BC21	0.000959 1	-0.10248013	Lower	Cyth3	chr5	+	tss_body	144203438
1494	cg42998061_TC11	0.00036362	-0.21469279	Lower	Tecpr1	chr5	-	tss_body	145344641
1495	cg43012843_TC21	0.00027979	-0.0544708	Lower	Cyp3a57	chr5	+	tss_1500	146860936
1496	cg43026030_TC21	0.00027035	0.08219681	Higher	Gm38748	chr5	+	tss_body	147539354
1497	cg43035946_TC21	0.00019994	-0.0956671	Lower	Pan3	chr5	+	tss_body	147634070
1498	cg43037284_BC21	0.00073265	0.06291582	Higher	Flt1	chr5	-	tss_body	148453808
1499	cg43048616_TC21	0.00082233	0.07538229	Higher					148674191
1500	cg43051310_BC21	0.000893 4	-0.08663533	Lower					149411822
1501	cg43061457_BC21	0.00053237	-0.05393292	Lower	Medag	chr5	+	tss_body	150152805
1502	cg43070616_TC21	0.00065124	-0.08868318	Lower	Fry	chr5	+	tss_body	150196641
1503	cg43071063_BC11	0.00034388	0.05391071	Higher	Fry	chr5	+	tss_body	150294387
1504	cg43072241_TC21	0.00022314	-0.0845259	Lower	Fry	chr5	+	tss_body	150620238
1505	cg43075977_TC11	0.00010653	0.05466834	Higher	N4bp2l2	chr5	-	tss_body	5167673
1506	cg43100289_BC21	0.00072794	-0.09766292	Lower					5491862
1507	cg43103321_TC21	0.000339 5	-0.06068327	Lower	Pdk4	chr6	-	tss_body	6691721
1508	cg43113632_TC21	0.00091757	0.10362886	Higher		chr6	-	tss_200	7831144
1509	cg43121539_TC21	8.8318E-06	0.17373281	Higher					14389904
1510	cg43157202_TC21	0.00030606	-0.05962801	Lower		chr6	-	tss_body	16733343
1511	cg43170105_BC11	0.00079975	0.05544724	Higher					17307396
1512	cg43174255_TC11	0.00069979	0.08726508	Higher	Cav1	chr6	+	tss_1500	28846194
1513	cg43243226_BC21	0.00041573	0.06031438	Higher	Snd1	chr6	+	tss_body	29274946
1514	cg43248395_BC21	0.00047993	-0.0813545	Lower	Hilpda	chr6	+	tss_body	29288169
1515	cg43248540_TC21	0.00048048	0.13477997	Higher	Fam71f2	chr6	+	tss_body	31605286
1516	cg43273247_TC21	0.00068272	-0.06899309	Lower	Gm31486	chr6	+	tss_body	31719464
1517	cg43274359_BC21	0.00067101	-0.08301794	Lower	Gm13846	chr6	+	tss_body	31786572
1518	cg43274777_TC21	0.00059293	-0.05391988	Lower		chr6	+	tss_body	33167238
1519	cg43285369_BC21	4.4648E-05	0.06002274	Higher					37096745
1520	cg43315556_BC21	2.5946E-05	0.10147363	Higher	Dgki	chr6	-	tss_body	39379529
1521	cg43337443_TC21	0.00012948	-0.14322479	Lower	chr6-39377419-	chr6	*	SShore	45758704

					39377777				
1522	cg43372653_BC21	0.00063249	0.1287733	Higher	Cntnap2	chr6	+	tss_body	45794225
1523	cg43372777_BC21	6.4551E-05	0.10587715	Higher	Cntnap2	chr6	+	tss_body	48508292
1524	cg43388720_BC21	0.00029184	-0.09181133	Lower	Zfp862-ps	chr6	+	tss_body	48932119
1525	cg43392950_TC21	0.00080151	-0.09074803	Lower	1600015I10Rik	chr6	+	tss_body	50585704
1526	cg43408085_TC21	0.00056185	0.07500001	Higher	5430402O13Rik	chr6	+	tss_body	50822000
1527	cg43410524_BC21	0.00020857	0.07873855	Higher	Gm31455	chr6	-	tss_body	52213321
1528	cg43426559_BC21	2.344E-05	0.09204678	Higher	Hoxaas3	chr6	+	tss_body	52213336
1529	cg43426560_TC11	1.4746E-05	0.0710719	Higher	Hoxaas3	chr6	+	tss_body	52213380
1530	cg43426562_TC21	7.1801E-05	0.05708842	Higher	Hoxaas3	chr6	+	tss_body	53200952
1531	cg43436966_TC21	0.00058208	-0.11043563	Lower					53449338
1532	cg43439304_TC21	0.00014743	-0.05665491	Lower	Creb5	chr6	+	tss_body	53761184
1533	cg43442245_BC21	0.00057683	-0.12561199	Lower					54408450
1534	cg43448958_BC21	0.00013952	-0.06820799	Lower	9130019P16Rik	chr6	-	tss_body	54509476
1535	cg43450212_TC21	0.00012421	-0.05889432	Lower	Scrn1	chr6	-	tss_body	54964530
1536	cg43454948_BC21	0.00056861	-0.05173186	Lower	Nod1	chr6	-	tss_body	55132948
1537	cg43457018_BC11	0.00087549	0.13304367	Higher	Crhr2	chr6	-	tss_body	55309186
1538	cg43458765_BC21	0.00032418	-0.05058151	Lower	Fam188b	chr6	+	tss_body	58907433
1539	cg43480561_BC11	0.00014271	-0.0712005	Lower	Herc3	chr6	+	tss_body	65133616
1540	cg43510819_TC21	0.00029176	-0.07356832	Lower	Hpgds	chr6	-	tss_body	65859138
1541	cg43515245_TC21	0.00031821	-0.05942619	Lower	Prdm5	chr6	+	tss_body	71216938
1542	cg43545496_TC21	0.00025339	-0.11545977	Lower	Smyd1	chr6	-	tss_body	71293646
1543	cg43546226_BC21	0.00091359	-0.1805548	Lower	Gm1070	chr6	+	tss_body	72348643
1544	cg43556891_BC21	0.00098571	-0.09635741	Lower	0610030E20Rik	chr6	+	tss_body	72520994
1545	cg43558968_BC21	0.00033949	-0.06529835	Lower	Sh2d6	chr6	-	tss_body	73279786
1546	cg43568013_BC21	0.00029367	-0.1365396	Lower					82947184
1547	cg43616917_BC11	0.00020296	-0.07008209	Lower	M1ap	chr6	+	tss_body	83086971
1548	cg43618920_TC11	0.00010471	0.08093775	Higher	Lbx2	chr6	+	tss_body	83121043
1549	cg43619572_BC21	0.00079404	0.08419439	Higher	Wbp1	chr6	-	tss_body	84226369
1550	cg43632253_TC21	0.00080601	-0.05666715	Lower		chr6	+	tss_body	88204646
1551	cg43672070_BC21	0.00066429	0.05262704	Higher	Gata2	chr6	+	tss_body	88242817

1552	cg43672560_BC11	0.00021982	0.12052702	Higher	A0A0N4SVT8	chr6	+	tss_body	88436393
1553	cg43673886_TC21	0.00046107	-0.11107761	Lower	Eefsec	chr6	-	tss_body	88760148
1554	cg43677275_TC21	0.00054079	-0.05311614	Lower	Mgll	chr6	+	tss_body	88811651
1555	cg43678047_TC21	0.00033618	-0.06467355	Lower	Mgll	chr6	+	tss_body	89661662
1556	cg43686173_BC11	0.00058615	0.12851607	Higher	Txnrd3	chr6	+	tss_body	90660894
1557	cg43693390_BC21	0.00070366	-0.11222205	Lower	Iqsec1	chr6	-	tss_body	91922845
1558	cg43705401_TC21	0.00048625	-0.06066523	Lower	4930590J08Rik	chr6	+	tss_body	93224533
1559	cg43716062_TC21	0.00085208	-0.0714692	Lower	Gm38863	chr6	+	tss_body	94204818
1560	cg43723940_TC21	0.00024044	0.08422948	Higher	Magi1	chr6	-	tss_body	94674025
1561	cg43728479_TC21	0.00061046	0.09218027	Higher	Lrig1	chr6	-	tss_body	97586418
1562	cg43750523_BC21	0.00074921	0.13602633	Higher	Frmd4b	chr6	-	tss_body	98667486
1563	cg43758842_TC21	0.00030117	0.07541142	Higher		chr6	-	tss_body	99950636
1564	cg43772881_BC21	0.00013576	-0.12924459	Lower		chr6	-	tss_body	100335722
1565	cg43776909_TC21	0.00074773	0.07822281	Higher					108445210
1566	cg43824342_TC21	0.00054461	-0.08579719	Lower	Itpr1	chr6	+	tss_body	112401923
1567	cg43845209_TC21	0.00010438	-0.05520995	Lower					113329324
1568	cg43854302_TC21	0.00016908	0.05924472	Higher	Ogg1	chr6	+	tss_body	113435909
1569	cg43855758_BC21	0.00034433	-0.10844707	Lower	Cidec	chr6	-	tss_1500	113563564
1570	cg43857529_BC21	8.44E-05	-0.07395274	Lower	Fancd2	chr6	+	tss_body	113719937
1571	cg43859585_BC21	0.00079267	0.05210701	Higher	Ghrl	chr6	-	tss_1500	113883323
1572	cg43861383_TC21	0.00099902	-0.06425398	Lower	Atp2b2	chr6	-	tss_body	115797728
1573	cg43880451_BC21	0.00051739	-0.05040712	Lower	Cand2	chr6	+	tss_body	115969408
1574	cg43882498_TC21	0.00063479	0.07825551	Higher	Plxnd1	chr6	-	tss_body	116821375
1575	cg43889527_BC21	0.00083601	-0.08504673	Lower	Gm36873	chr6	+	tss_body	117210855
1576	cg43892875_BC21	0.00077988	0.07398608	Higher					117277050
1577	cg43893455_TC21	0.00055014	-0.06111347	Lower					118205109
1578	cg43902530_BC21	0.00083299	-0.05598478	Lower					118609983
1579	cg43906723_BC21	0.00010268	0.07493373	Higher	Cacna1c	chr6	-	tss_body	120554793
1580	cg43927346_TC21	0.00085165	-0.06940026	Lower	1700072O05Rik	chr6	+	tss_200	120836093
1581	cg43929928_BC21	0.00022294	0.08771684	Higher	Gm38889	chr6	-	tss_body	121081747
1582	cg43933608_TC21	0.00039637	-0.0583742	Lower	Mical3	chr6	-	tss_body	122114058

1583	cg43942360_TC21	0.00073034	-0.08044902	Lower					122567486
1584	cg43946580_TC21	0.00017926	-0.06129873	Lower		chr6	-	tss_body	124812992
1585	cg43963158_TC21	0.00063742	0.11361605	Higher	Tpi1	chr6	-	tss_body	124912206
1586	cg43964824_TC21	0.00024345	-0.06129325	Lower	Lag3	chr6	-	tss_body	124961245
1587	cg43965660_TC21	0.00045982	-0.06817542	Lower	Cops7a	chr6	-	tss_body	125218706
1588	cg43969716_TC21	0.00070254	-0.05022502	Lower	Vamp1	chr6	+	tss_body	125483304
1589	cg43973410_BC21	0.00063777	0.05273971	Higher	Cd9	chr6	-	tss_body	126142530
1590	cg43979511_TC21	3.0494E-05	-0.10205601	Lower	Ntf3	chr6	-	tss_body	126534355
1591	cg43982345_BC21	0.00019348	-0.0591878	Lower	Kcna5	chr6	-	tss_body	126769495
1592	cg43985094_BC21	0.00014267	-0.11554162	Lower	LOC102636795	chr6	+	tss_body	127308049
1593	cg43991396_TC21	0.00051261	0.14844892	Higher	Gm38404	chr6	-	tss_200	127991975
1594	cg43999048_BC11	0.00032539	-0.05800137	Lower	Tspan9	chr6	-	tss_body	129451767
1595	cg44012477_BC21	0.0002026	-0.06265179	Lower	Clec1a	chr6	-	tss_body	131382855
1596	cg44021914_TC21	0.00088587	0.05016806	Higher	Ybx3	chr6	-	tss_body	134053938
1597	cg44034558_TC21	3.5853E-05	-0.06300488	Lower	Etv6	chr6	+	tss_body	134715811
1598	cg44042119_BC21	0.00080156	0.05634566	Higher	Dusp16	chr6	-	tss_body	134826982
1599	cg44043241_BC21	0.00012079	0.06361082	Higher	chr6-134829938-134830535	chr6	*	NShelf	135168119
1600	cg44047602_TC11	0.00046495	0.05550198	Higher	Hebp1	chr6	-	tss_body	136149269
1601	cg44056795_BC21	0.00048537	-0.12623242	Lower	Grin2b	chr6	-	tss_body	136560853
1602	cg44060953_BC21	5.9085E-05	-0.10260713	Lower	Atf7ip	chr6	+	tss_body	137581557
1603	cg44073210_BC11	0.0004224	0.10934148	Higher	Eps8	chr6	-	tss_body	139143506
1604	cg44085256_BC21	0.00090785	-0.10531544	Lower					141278773
1605	cg44104327_TC21	0.00044006	0.0707413	Higher	Pde3a	chr6	+	tss_body	142564152
1606	cg44112610_BC21	0.00058571	-0.06589648	Lower					142995176
1607	cg44117582_TC21	0.00038687	0.21244478	Higher					144107618
1608	cg44130052_BC21	2.1535E-06	-0.08201818	Lower	Sox5	chr6	-	tss_body	145359130
1609	cg44144440_TC21	0.00015706	-0.09821673	Lower					145381341
1610	cg44144765_TC21	6.6382E-05	-0.11801526	Lower	E9PY33	chr6	-	tss_body	146463319
1611	cg44156148_BC21	0.00022662	-0.17969735	Lower	Itpr2	chr6	-	tss_body	146976588
1612	cg44161172_BC21	0.00058107	0.08366507	Higher	Ppfibp1	chr6	+	tss_body	148943805

1613	cg44175243_TC21	0.00042179	0.06211713	Higher	Fam60a	chr6	-	tss_body	149215586
1614	cg44177292_TC21	0.00017932	-0.05501236	Lower		chr6	-	tss_1500	4132466
1615	cg44188312_BC21	0.00072822	-0.09598624	Lower	Ttyh1	chr7	+	tss_body	4504706
1616	cg44191542_TC11	0.00045885	-0.07343748	Lower	Tnnt1	chr7	-	tss_body	4523163
1617	cg44191883_BC21	6.7292E-05	0.12969413	Higher	Tnni3	chr7	-	tss_1500	4789269
1618	cg44195330_BC21	0.00055144	0.06737322	Higher	Tmem238	chr7	-	tss_body	5089961
1619	cg44200207_BO21	0.00013826	-0.05443241	Lower	Epn1	chr7	+	tss_body	6133003
1620	cg44205950_BC21	0.00012499	-0.08888697	Lower	Zfp787	chr7	-	tss_body	6229993
1621	cg44207179_BC21	0.00013493	-0.09198846	Lower	Zscan5b	chr7	+	tss_body	6729171
1622	cg44211871_TC21	0.00055865	-0.0936474	Lower	Peg3	chr7	-	tss_body	12305124
1623	cg44235492_BC21	5.5084E-05	0.05086906	Higher	Vmn1r82	chr7	+	tss_body	13299189
1624	cg44243207_TC11	0.00047238	-0.06624591	Lower	Lig1	chr7	+	tss_body	16158950
1625	cg44258846_BC11	0.00055594	0.0524135	Higher	Slc8a2	chr7	+	tss_body	16272711
1626	cg44260340_TC21	0.00070933	0.09190056	Higher	Inafm1	chr7	-	tss_body	16581764
1627	cg44264332_BC21	0.00096613	-0.06079135	Lower	Arhgap35	chr7	-	tss_body	18351161
1628	cg44277334_TC21	0.00021528	-0.05190359	Lower	Psg18	chr7	-	tss_body	18526762
1629	cg44278537_BC21	1.4337E-05	-0.05234872	Lower	Psg25	chr7	-	tss_body	18884854
1630	cg44280721_TC21	0.00030091	0.05750697	Higher	Pglyrp1	chr7	+	tss_body	18939024
1631	cg44281516_TC21	0.00063984	-0.13996133	Lower	Nova2	chr7	+	tss_body	19120577
1632	cg44284840_BC21	7.8992E-05	-0.0842285	Lower	Fbxo46	chr7	+	tss_body	19202026
1633	cg44286214_BC21	0.00024824	-0.06448985	Lower	Eml2	chr7	+	tss_body	19463059
1634	cg44291165_TC21	0.00024266	-0.06502626	Lower	Exoc3l2	chr7	+	tss_200	19517575
1635	cg44292240_BC21	0.00022078	0.05331342	Higher	Nkpd1	chr7	+	tss_body	19744693
1636	cg44295980_TC21	0.00038008	-0.14537677	Lower	Nectin2	chr7	-	tss_body	24082203
1637	cg44313157_BC11	0.00066737	0.08204343	Higher	Zfp180	chr7	+	tss_body	24617456
1638	cg44320707_BC21	0.00099518	-0.08371095	Lower	Phldb3	chr7	+	tss_body	25003410
1639	cg44325932_BC21	0.00089701	-0.05003791	Lower	Atp1a3	chr7	-	tss_body	25003655
1640	cg44325940_TC21	0.00044494	-0.07813736	Lower	Atp1a3	chr7	-	tss_body	25274789
1641	cg44330793_TC21	0.00023807	0.0799301	Higher	Cic	chr7	+	tss_body	25289529
1642	cg44331223_BC21	6.3432E-05	-0.10158487	Lower	Cic	chr7	+	tss_body	25787141
1643	cg44337697_TC21	0.000762	0.07092092	Higher	Axl	chr7	-	tss_body	25835571

1644	cg44338344_TC21	0.00056901	-0.16463996	Lower					26757087
1645	cg44343485_BC11	0.00066505	-0.15496684	Lower	Cyp2b19	chr7	+	tss_200	27198830
1646	cg44347209_BC21	8.4238E-05	0.09794045	Higher	BC024978	chr7	+	tss_body	27602324
1647	cg44353884_BC21	0.00080117	0.06410533	Higher	Akt2	chr7	+	tss_body	27604981
1648	cg44353910_TC21	0.00069699	-0.05757537	Lower	Akt2	chr7	+	tss_body	27703858
1649	cg44355409_TC21	0.00013581	-0.06204173	Lower	C030039L03Rik	chr7	+	tss_body	28496276
1650	cg44365426_TC21	0.00099163	-0.09320048	Lower	1700028B04Rik	chr7	+	tss_1500	28796683
1651	cg44369697_BC21	0.00039054	-0.09690775	Lower	Rinl	chr7	+	tss_body	28911496
1652	cg44371551_TC21	0.00084027	-0.12470438	Lower	Actn4	chr7	-	tss_body	29023987
1653	cg44373088_BC21	4.6966E-06	-0.07217684	Lower	Ryr1	chr7	-	tss_body	29024148
1654	cg44373098_BC21	0.00076984	-0.09389077	Lower	Ryr1	chr7	-	tss_body	29083330
1655	cg44374169_BC21	2.8532E-07	-0.16111836	Lower	Ryr1	chr7	-	tss_body	29150218
1656	cg44375209_TC21	0.00051573	-0.1088466	Lower	Rasgrp4	chr7	+	tss_body	29289566
1657	cg44377558_TC21	0.00079353	0.05207851	Higher	LOC108167414	chr7	-	tss_1500	29987731
1658	cg44386136_TC21	0.00067711	-0.07167064	Lower	Zfp568	chr7	+	tss_body	30313982
1659	cg44390842_TC11	7.3988E-05	-0.05072045	Lower	Alkbh6	chr7	+	tss_body	30440056
1660	cg44392668_TC21	0.00018821	-0.05603329	Lower	Aplp1	chr7	-	tss_body	30493785
1661	cg44393649_BC21	0.00062379	-0.05316608	Lower	Prodh2	chr7	+	tss_body	30543694
1662	cg44394508_BC21	0.00024359	-0.09194566	Lower	Proser3	chr7	-	tss_body	30556598
1663	cg44394730_BC21	0.00020266	-0.06854643	Lower	Lin37	chr7	-	tss_body	30811861
1664	cg44398219_TC21	0.0007881	-0.08300312	Lower					30861388
1665	cg44398848_TC21	0.00028448	-0.09578154	Lower	Ffar1	chr7	-	tss_body	30989307
1666	cg44400576_TC21	0.00023078	-0.07002329	Lower	Fam187b	chr7	+	tss_body	31040220
1667	cg44401030_TC21	0.00057495	-0.06083584	Lower	Fxyd5	chr7	-	tss_body	35141417
1668	cg44429159_BC21	0.00012376	-0.05024682	Lower	Gm35724	chr7	+	tss_body	42951936
1669	cg44489159_TC21	0.00083956	-0.05381768	Lower		chr7	+	tss_body	43504218
1670	cg44493427_BC11	0.00026705	0.07687792	Higher	4931406B18Rik	chr7	-	tss_body	43998943
1671	cg44498066_BC21	0.00027383	-0.06814821	Lower	Klk1b11	chr7	+	tss_body	44248268
1672	cg44499826_TC11	0.00026194	0.07168138	Higher	2410002F23Rik	chr7	+	tss_body	44551330
1673	cg44504682_BC21	0.00069426	-0.07243533	Lower	Nr1h2	chr7	-	tss_body	45021397
1674	cg44512648_TC21	0.00026152	-0.1125125	Lower	Rras	chr7	+	tss_body	45061829

1675	cg44513484_TC11	0.00058622	0.12108003	Higher	Prrg2	chr7	-	tss_body	45176961
1676	cg44515620_TC21	0.0002086	0.05251652	Higher	Pth2	chr7	+	tss_1500	45231274
1677	cg44516532_BC21	0.00042637	-0.05398384	Lower	Tead2	chr7	+	tss_body	45422802
1678	cg44519967_BC21	0.00033359	-0.07483195	Lower	Ruvbl2	chr7	-	tss_body	45448447
1679	cg44520471_BC21	0.00031939	-0.06934005	Lower	Gys1	chr7	+	tss_body	45788204
1680	cg44526223_BC21	0.00015936	-0.09608329	Lower	Lmtk3	chr7	+	tss_body	45792324
1681	cg44526277_BC21	0.00096443	-0.10565186	Lower	Lmtk3	chr7	+	tss_body	46031732
1682	cg44530161_BC21	0.00038843	-0.0551527	Lower	Abcc6	chr7	-	tss_1500	46743985
1683	cg44540045_BC21	0.00042265	0.07728072	Higher	Saa1	chr7	-	tss_1500	52161838
1684	cg44577554_BC21	0.00045019	0.08963536	Higher					62392427
1685	cg44625518_TC21	0.00029123	-0.08425923	Lower	Gm32061	chr7	-	tss_body	63668102
1686	cg44632793_BC21	0.00025178	-0.05117158	Lower	Otud7a	chr7	+	tss_body	65893813
1687	cg44654683_TC21	8.8102E-05	-0.10814649	Lower	Pcsk6	chr7	+	tss_body	66247530
1688	cg44658754_TC21	3.1431E-05	-0.08208199	Lower		chr7	-	tss_body	67443736
1689	cg44670307_BC21	0.00051187	-0.07274023	Lower		chr7	-	tss_body	67755452
1690	cg44673934_BC11	0.00019516	0.10569536	Higher	Synm	chr7	-	tss_body	68771580
1691	cg44685745_TC21	7.8247E-05	0.07768053	Higher					70357874
1692	cg44695968_TC21	0.00065908	-0.12715673	Lower	Nr2f2	chr7	-	tss_body	73630680
1693	cg44721117_TC21	0.00018221	0.17198784	Higher		chr7	+	tss_body	75365343
1694	cg44733684_TC21	0.00047021	-0.0729075	Lower		chr7	+	tss_1500	75612181
1695	cg44735557_TC21	0.00097725	-0.08564812	Lower	Akap13	chr7	+	tss_body	79386559
1696	cg44760653_TC21	2.9789E-05	-0.16959903	Lower	Rlbp1	chr7	-	tss_body	79698666
1697	cg44765146_TC21	0.00059665	-0.07485895	Lower	Kif7	chr7	-	tss_body	79826262
1698	cg44767058_TC21	0.00049286	-0.1101688	Lower	Anpep	chr7	-	tss_body	80629408
1699	cg44777786_BC21	0.00097182	-0.12460122	Lower	Crtc3	chr7	-	tss_body	80859193
1700	cg44780608_TC21	0.00040782	-0.08623639	Lower	chr7-80861061-80861321	chr7	*	NShore	80889254
1701	cg44781046_TC21	0.00037875	-0.0758683	Lower					80907627
1702	cg44781378_BC21	0.00031485	-0.10597849	Lower	Nmb	chr7	-	tss_body	81057462
1703	cg44782802_BC11	0.00095829	0.1502387	Higher	Alpk3	chr7	+	tss_200	81161721
1704	cg44784129_BC21	0.00032948	-0.09229267	Lower	Slc28a1	chr7	+	tss_body	81585408

1705	cg44788538_TC21	0.00077372	-0.05183978	Lower	Whamm	chr7	+	tss_body	82870439
1706	cg44801595_TC21	3.1936E-05	-0.18830626	Lower	Mex3b	chr7	+	tss_body	84410392
1707	cg44813013_BC21	0.00036235	0.09190738	Higher	Arnt2	chr7	-	tss_1500	89747994
1708	cg44838257_BC21	0.0007921	-0.11426867	Lower	Me3	chr7	+	tss_body	90026946
1709	cg44840648_TC21	8.6924E-05	0.07054772	Higher		chr7	+	tss_body	92688288
1710	cg44855896_TC21	0.00079093	0.2005948	Higher					96816620
1711	cg44878662_BC21	2.0197E-05	0.08787638	Higher	Tenm4	chr7	+	tss_body	97407154
1712	cg44883262_TC11	0.00019626	0.12941819	Higher	Ndufc2	chr7	+	tss_body	98199429
1713	cg44890811_BC21	0.00027601	-0.10389871	Lower	B3gnt6	chr7	-	tss_body	98437771
1714	cg44892729_BC11	6.6892E-05	-0.16005996	Lower	Gm39053	chr7	+	tss_body	99326381
1715	cg44903254_BC21	0.00051305	0.06028169	Higher	Map6	chr7	+	tss_body	99349344
1716	cg44903555_TC21	2.5162E-05	-0.05775081	Lower	Serpinh1	chr7	-	tss_body	99863313
1717	cg44909573_TC21	0.00075806	-0.08911445	Lower	Spcs2	chr7	-	tss_body	100964450
1718	cg44920874_TC21	0.00045048	-0.05754714	Lower	P2ry6	chr7	-	tss_body	103937438
1719	cg44942875_TC21	7.338E-05	-0.05788398	Lower	Olfr632	chr7	+	tss_body	107930677
1720	cg44965333_BC21	0.00093926	-0.0711519	Lower	Q8VG44	chr7	+	tss_body	108626777
1721	cg44968410_TC21	0.00043108	-0.08362249	Lower					109017680
1722	cg44970664_BC21	0.00020073	-0.12342871	Lower	Tub	chr7	+	tss_body	110659058
1723	cg44985231_BC21	0.00024794	0.1707145	Higher					111779505
1724	cg44994486_BC21	0.00034911	0.07258554	Higher	Galnt18	chr7	-	tss_body	112713806
1725	cg45003094_TC21	0.00015103	0.12599991	Higher	Tead1	chr7	+	tss_body	113270744
1726	cg45008819_TC21	0.00065514	0.05208212	Higher	Arntl	chr7	+	tss_body	118584404
1727	cg45050246_TC21	0.0001605	0.05492153	Higher	Tmc7	chr7	-	tss_body	120931280
1728	cg45069791_BC21	0.00049724	-0.06589343	Lower	Polr3e	chr7	+	tss_body	122527743
1729	cg45085853_BC21	0.0003489	-0.06862186	Lower	Prkcb	chr7	+	tss_body	122847240
1730	cg45088673_BC21	0.00094853	0.08479606	Higher					125445646
1731	cg45107889_BC21	4.5655E-05	-0.06551874	Lower	Kdm8	chr7	+	tss_body	126777843
1732	cg45123149_BC21	0.00052462	-0.17761956	Lower	Ypel3	chr7	+	tss_body	126816253
1733	cg45123852_TC21	8.8319E-05	-0.053955	Lower	Fam57b	chr7	+	tss_body	127214778
1734	cg45129675_BC21	0.00034522	-0.08577346	Lower	Sept1	chr7	-	tss_body	128129341
1735	cg45142204_TC21	0.00022333	-0.07717096	Lower	Itgax	chr7	+	tss_1500	128268987

1736	cg45143940_TC21	0.00019183	-0.06462286	Lower	Slc5a2	chr7	+	tss_body	128688556
1737	cg45148558_BC11	0.00081726	-0.0940772	Lower	Inpp5f	chr7	+	tss_body	130058723
1738	cg45159798_TC11	9.9132E-05	0.12881124	Higher					130326322
1739	cg45162936_TC21	0.00030776	0.07549888	Higher	Gm33661	chr7	-	tss_body	130449008
1740	cg45163928_TC21	0.00081189	-0.05486477	Lower	Ate1	chr7	-	tss_body	130772187
1741	cg45167707_BC21	6.0849E-06	-0.05975674	Lower	F2Z480	chr7	-	tss_body	133038289
1742	cg45190708_TC21	0.00027859	0.10354433	Higher	Ctbp2	chr7	-	tss_body	133062370
1743	cg45191001_BC21	0.00039278	-0.05985206	Lower	Ctbp2	chr7	-	tss_body	134499006
1744	cg45204565_BC21	0.00094225	0.20975926	Higher	D7Ertd443e	chr7	-	tss_body	136455362
1745	cg45223097_TC21	0.000846	-0.11539236	Lower					136946074
1746	cg45227954_BC21	0.00058959	0.07081776	Higher	Mgmt	chr7	+	tss_body	137129717
1747	cg45230068_TC21	3.8013E-05	-0.07196115	Lower	P26187	chr7	+	tss_body	138856670
1748	cg45246440_TC21	0.00079576	-0.1947088	Lower	Ppp2r2d	chr7	+	tss_body	138924835
1749	cg45247139_BC21	0.00062553	-0.05565325	Lower					139252672
1750	cg45250697_TC11	0.00084883	0.05961775	Higher	Pwwp2b	chr7	+	tss_body	139910754
1751	cg45258031_TC21	0.00064532	-0.13571395	Lower	Kndc1	chr7	+	tss_body	139957767
1752	cg45258821_BC21	7.6711E-05	-0.2088628	Lower	LOC102635948	chr7	+	tss_body	140813172
1753	cg45265419_TC21	0.00015135	-0.10119904	Lower	Zfp941	chr7	-	tss_body	140844648
1754	cg45265733_BC21	0.00057946	-0.12236486	Lower	C330022C24Rik	chr7	-	tss_body	140947090
1755	cg45267367_BC21	0.00084054	-0.05140051	Lower	Athl1	chr7	+	tss_body	141152663
1756	cg45270215_TC21	4.6661E-05	-0.05384762	Lower	Ptdss2	chr7	+	tss_body	141464878
1757	cg45274806_BC11	0.00052735	0.06304399	Higher	Cracr2b	chr7	+	tss_body	141701349
1758	cg45277610_BC21	0.00065044	0.05905881	Higher	Muc2	chr7	+	tss_body	141839194
1759	cg45278478_TC21	0.00040126	-0.09641637	Lower	Muc5b	chr7	+	tss_body	142582086
1760	cg45285159_TC21	3.121E-05	-0.11895417	Lower					142675023
1761	cg45286251_BC21	0.00049269	-0.06588477	Lower					143285692
1762	cg45290514_BC21	0.00095269	-0.08156141	Lower	Kcnq1	chr7	+	tss_body	144284377
1763	cg45299986_TC21	0.000565	-0.08268097	Lower	Shank2	chr7	+	tss_body	144765055
1764	cg45304406_TC21	0.00019139	0.05070008	Higher	D930030F02Rik	chr7	+	tss_body	144838116
1765	cg45305125_BC21	0.00033856	0.06162216	Higher	Fgf3	chr7	+	tss_1500	145136068
1766	cg45308246_BC21	0.00041585	-0.0514572	Lower					145159463

1767	cg45308409_BC11	0.00039867	0.07712763	Higher					3459303
1768	cg45313456_TC21	0.00029067	-0.07566563	Lower	Pex11g	chr8	-	tss_body	8231654
1769	cg45340760_BC21	0.00048883	-0.07006244	Lower		chr8	-	tss_body	8488453
1770	cg45342956_BC21	9.7889E-05	0.22843989	Higher		chr8	+	tss_body	8598047
1771	cg45344157_BC21	3.9534E-05	-0.24979254	Lower					10006874
1772	cg45357659_TC21	0.00019065	-0.05960492	Lower	Tnfsf13b	chr8	+	tss_body	10434266
1773	cg45361250_TC21	0.00055253	-0.14725476	Lower	Myo16	chr8	+	tss_body	11149250
1774	cg45368957_TC21	0.00043584	0.05811824	Higher		chr8	-	tss_200	11406045
1775	cg45372435_TC21	0.00010711	-0.12868482	Lower	Col4a2	chr8	+	tss_body	11701352
1776	cg45376827_TC21	0.00068781	-0.12414388	Lower	A0A087WQK3	chr8	-	tss_1500	12002973
1777	cg45380489_BC21	0.00028086	0.08741295	Higher					12429401
1778	cg45385998_TC21	0.000975	0.05060348	Higher	Gm5607	chr8	+	tss_body	12607432
1779	cg45388134_BC11	0.00042832	0.05315778	Higher					12720592
1780	cg45389607_TC21	0.00050702	0.07516902	Higher	Gm15348	chr8	-	tss_1500	13598236
1781	cg45401758_BC11	0.00062336	-0.05791963	Lower	Rasa3	chr8	-	tss_body	13899553
1782	cg45405574_BC11	9.5446E-06	-0.07614421	Lower					14894827
1783	cg45416390_BC21	0.00061362	-0.07640595	Lower	Cln8	chr8	+	tss_body	15042772
1784	cg45419253_BC21	0.00048808	0.08131974	Higher	BB014433	chr8	-	tss_body	18907370
1785	cg45443760_TC21	4.4912E-05	-0.07677802	Lower		chr8	-	tss_1500	25019560
1786	cg45488756_TC21	0.00025904	0.05726556	Higher	Tm2d2	chr8	+	tss_body	25091160
1787	cg45489634_TC21	7.2056E-05	-0.11833417	Lower	Plekha2	chr8	-	tss_body	27008499
1788	cg45512119_BC21	0.0006438	0.07206566	Higher	Gm32389	chr8	+	tss_body	31991001
1789	cg45544868_TC21	0.00096172	0.05184547	Higher	Nrg1	chr8	-	tss_body	32381474
1790	cg45547572_TC21	0.00035607	-0.08724906	Lower	Nrg1	chr8	-	tss_body	33598117
1791	cg45555665_TC21	0.00063401	-0.06299979	Lower	chr8-33599493-33600228	chr8	*	NShore	35411045
1792	cg45576078_TC21	0.00063139	-0.10883127	Lower	Gm34911	chr8	-	tss_body	41827491
1793	cg45620738_BC21	0.00059588	0.06245433	Higher	2810404M03Rik	chr8	+	tss_body	44757428
1794	cg45636636_TC21	0.00027927	-0.06067922	Lower	Gm30397	chr8	-	tss_body	45037221
1795	cg45640214_TC21	0.00018324	-0.06175993	Lower	Fat1	chr8	+	tss_body	45037290
1796	cg45640219_BC21	7.3768E-05	0.06287204	Higher	Fat1	chr8	+	tss_body	47218103

1797	cg45662637_BC21	8.3779E-05	-0.09378288	Lower	Stox2	chr8	-	tss_body	48563853
1798	cg45681590_BC21	0.00030658	-0.06318618	Lower	Tenm3	chr8	-	tss_body	49465599
1799	cg45689574_TC21	0.00081242	0.07046221	Higher	4930555F03Rik	chr8	+	tss_body	57636826
1800	cg45730760_BC21	0.00010931	-0.0550593	Lower	Galnt7	chr8	-	tss_body	66511848
1801	cg45780933_BC11	0.00035166	-0.05506157	Lower	Tktl2	chr8	+	tss_body	69240155
1802	cg45798326_BC11	0.00042674	-0.12214221	Lower		chr8	-	tss_200	70285151
1803	cg45808706_TC21	0.00079235	-0.06882086	Lower	Homer3	chr8	+	tss_body	70501363
1804	cg45812324_BC21	0.00010358	-0.07270597	Lower	Crlf1	chr8	+	tss_body	70756017
1805	cg45816832_BC21	0.00026257	-0.10110537	Lower	Rab3a	chr8	+	tss_body	70758303
1806	cg45816879_BC21	0.00055529	-0.10738919	Lower	Rab3a	chr8	+	tss_body	70768890
1807	cg45817176_BC21	0.00011126	0.05204441	Higher	Pik3r2	chr8	-	tss_body	70783322
1808	cg45817628_TC21	0.00016853	-0.14221976	Lower	Mast3	chr8	-	tss_body	71558476
1809	cg45827179_TC21	0.00029985	0.05482059	Higher	Tmem221	chr8	-	tss_body	71925660
1810	cg45831947_TC21	0.00022069	0.13409818	Higher	Zfp617	chr8	+	tss_body	72268516
1811	cg45834482_TC21	0.00088101	-0.11634315	Lower					74269802
1812	cg45845848_TC21	0.00072253	-0.05683247	Lower		chr8	+	tss_1500	75057268
1813	cg45849944_TC21	0.00040201	-0.17922601	Lower	Tom1	chr8	+	tss_body	78001765
1814	cg45869230_BC21	0.0007171	-0.05270433	Lower					83291514
1815	cg45909708_TC21	0.00014764	-0.06214635	Lower	Ucp1	chr8	+	tss_body	83902729
1816	cg45916815_BC21	0.00030577	-0.07225218	Lower	Adgrl1	chr8	+	tss_body	83929919
1817	cg45917216_BC21	0.00013327	-0.09033473	Lower	Adgrl1	chr8	+	tss_body	83990653
1818	cg45918031_BO21	0.00035746	-0.08239209	Lower	Prkaca	chr8	+	tss_body	84012012
1819	cg45918775_BC11	5.8373E-05	0.06252026	Higher	Mir1199	chr8	-	tss_1500	85152198
1820	cg45935936_TC21	0.00042977	-0.05485022	Lower	Cks1brt	chr8	+	tss_body	86902427
1821	cg45949211_BC21	1.3989E-05	-0.14349886	Lower		chr8	+	tss_200	87588956
1822	cg45955306_BC11	0.00027384	0.08442171	Higher	4933402J07Rik	chr8	+	tss_body	87926403
1823	cg45959625_BC21	6.795E-05	-0.10387319	Lower	Zfp423	chr8	-	tss_body	91149013
1824	cg45991098_TC21	0.00011307	-0.14528177	Lower		chr8	-	tss_body	91689473
1825	cg45997577_BC21	0.00019972	-0.05558864	Lower		chr8	+	tss_1500	91799474
1826	cg45998910_BC21	0.00013406	-0.11822328	Lower	Irx3	chr8	-	tss_body	91865064
1827	cg45999945_TC21	8.7386E-05	-0.08869443	Lower	LOC108167544	chr8	+	tss_body	91997086

1828	cg46001334_BC11	0.00086026	0.14403617	Higher	Gm36843	chr8	+	tss_1500	94191398
1829	cg46022002_TC11	0.00036642	-0.13231863	Lower					94691825
1830	cg46027375_TC21	0.0008028	-0.0567652	Lower	Pllp	chr8	-	tss_body	94692217
1831	cg46027381_BC21	0.00029358	-0.06202491	Lower	Pllp	chr8	-	tss_body	94904105
1832	cg46029969_TC21	2.09E-06	-0.09671632	Lower	Ccdc102a	chr8	-	tss_body	97693839
1833	cg46052640_BC21	0.00047796	0.08729175	Higher					102781146
1834	cg46075158_TC21	0.00049521	0.06842066	Higher	Cdh11	chr8	-	tss_body	105484192
1835	cg46098900_TC21	0.00062573	0.13271731	Higher	Zdhhc1	chr8	-	tss_body	106264820
1836	cg46108872_TC21	0.00074473	-0.0522234	Lower	Smpd3	chr8	-	tss_body	106572034
1837	cg46112241_BC21	0.00022208	0.06336812	Higher					106878133
1838	cg46115737_BC21	8.0442E-05	-0.05366918	Lower	Has3	chr8	+	tss_body	107164382
1839	cg46119394_TC21	0.00084401	0.10696245	Higher	Cyb5b	chr8	+	tss_body	108068346
1840	cg46129162_TC21	9.7983E-05	-0.06773336	Lower	E9QMD3	chr8	+	tss_body	108766374
1841	cg46137019_BC21	0.00012261	0.05498007	Higher	Zfhx3	chr8	+	tss_body	108794950
1842	cg46137584_TC21	0.00075539	-0.05125936	Lower	Zfhx3	chr8	+	tss_body	109986608
1843	cg46152696_TC21	0.00051312	0.06000057	Higher					110756637
1844	cg46162046_TC11	0.00050255	0.11354184	Higher	Il34	chr8	-	tss_body	110863799
1845	cg46163356_BC21	0.00075602	-0.0838198	Lower	Cog4	chr8	+	tss_body	110941389
1846	cg46164435_TC21	0.00051576	-0.07840487	Lower	St3gal2	chr8	+	tss_body	110957886
1847	cg46164695_BC21	0.0001176	-0.11196519	Lower	St3gal2	chr8	+	tss_body	114682027
1848	cg46201867_BC21	2.7179E-06	-0.05815288	Lower	Wwox	chr8	+	tss_body	117016774
1849	cg46227344_BC21	0.00056966	-0.13252136	Lower	Pkd1l2	chr8	-	tss_body	117198761
1850	cg46229885_BC21	0.00026824	-0.08623439	Lower	Gan	chr8	+	tss_body	117436860
1851	cg46233814_BC11	0.00022666	-0.14153214	Lower	Cmip	chr8	+	tss_body	117538545
1852	cg46235285_BC11	0.00021727	0.0799612	Higher	Plcg2	chr8	+	tss_body	117590150
1853	cg46235986_TC21	0.00019015	-0.05930178	Lower	Plcg2	chr8	+	tss_body	117646752
1854	cg46236842_BC21	0.00062368	0.11781432	Higher					118701436
1855	cg46248744_BC11	0.00088288	-0.11942298	Lower	Cdh13	chr8	+	tss_body	119028646
1856	cg46252386_BC21	0.00032363	-0.05643507	Lower	Cdh13	chr8	+	tss_body	119626354
1857	cg46260680_BC21	0.0002826	-0.05013718	Lower	Kcng4	chr8	-	tss_body	119992534
1858	cg46266235_BC11	0.00097737	0.14156066	Higher	Crispld2	chr8	+	tss_body	120018610

1859	cg46266644_BC21	0.00068666	0.06711914	Higher	Crispld2	chr8	+	tss_body	120144985
1860	cg46268558_BC21	0.00013994	-0.05059372	Lower	6430548M08Rik	chr8	+	tss_body	120255982
1861	cg46270332_TC21	0.00040645	0.09357433	Higher	Gse1	chr8	+	tss_body	120439513
1862	cg46273291_BC21	0.00022671	0.08941672	Higher	Gse1	chr8	+	tss_body	120991111
1863	cg46282669_BC21	0.00025372	-0.05561464	Lower	Q6PB93	chr8	+	tss_body	121128143
1864	cg46285667_BC21	2.1491E-05	0.16286326	Higher	Foxl1	chr8	+	tss_body	121128159
1865	cg46285668_BC21	0.00070463	0.17478138	Higher	Foxl1	chr8	+	tss_body	121252722
1866	cg46287573_TC21	0.00012491	-0.0702254	Lower	Q6PB93	chr8	+	tss_body	121530995
1867	cg46291865_TC21	0.00011853	-0.06886446	Lower	1700018B08Rik	chr8	-	tss_body	122339437
1868	cg46305614_TC21	0.000176 8	-0.08158767	Lower	Q6PB93	chr8	+	tss_body	122471842
1869	cg46307846_BC21	0.00069441	0.05908777	Higher	Rnf166	chr8	-	tss_body	122575606
1870	cg46309876_BC21	0.00092563	-0.05838874	Lower	Aprt	chr8	-	tss_body	122752234
1871	cg46312865_BC21	0.00062388	0.06546931	Higher	C230057M02Rik	chr8	-	tss_body	123256564
1872	cg46320249_BC21	0.00041914	-0.06582899	Lower	Zfp276	chr8	+	tss_body	123454315
1873	cg46323765_BC21	9.577E-05	-0.05352357	Lower	Def8	chr8	+	tss_body	124023960
1874	cg46331918_TC21	2.394E-05	-0.06747035	Lower	Urb2	chr8	+	tss_body	125730345
1875	cg46355064_TC21	0.00019545	0.11304109	Higher	Ntpcr	chr8	+	tss_body	126340058
1876	cg46362144_TC21	0.00097516	-0.06419848	Lower	Slc35f3	chr8	+	tss_body	126914350
1877	cg46368672_BC21	0.00018105	-0.14036719	Lower					128799017
1878	cg46381818_TC21	0.00027685	0.09200702	Higher	LOC105242417	chr8	-	tss_body	7830030
1879	cg46409224_BC21	0.00059266	-0.06820257	Lower	Birc2	chr9	-	tss_body	15036959
1880	cg46450195_BC21	0.00075625	-0.15294407	Lower	Panx1	chr9	-	tss_body	20672272
1881	cg46481461_BC11	0.00025317	-0.10013345	Lower	Olfm2	chr9	-	tss_body	20976457
1882	cg46485737_BC21	0.00074315	0.05014794	Higher	S1pr2	chr9	-	tss_body	21934165
1883	cg46499564_TC21	1.6961E-05	-0.0692697	Lower	Ccdc159	chr9	+	tss_body	21990217
1884	cg46500617_BC11	0.00029218	-0.10693935	Lower	Rgl3	chr9	-	tss_1500	22026371
1885	cg46501165_TC21	0.00075906	-0.06822465	Lower	Elavl3	chr9	-	tss_body	22204448
1886	cg46503825_TC21	0.00092268	-0.05290824	Lower		chr9	-	tss_body	27005726
1887	cg46534799_TC21	0.00038167	0.08855217	Higher	Thyn1	chr9	+	tss_body	27308764
1888	cg46537790_TC21	0.00065007	-0.16226046	Lower	Igsf9b	chr9	+	tss_body	27783900
1889	cg46541065_BC11	9.2871E-05	-0.12919963	Lower					31030269

1890	cg46563438_TC21	0.00091015	0.05609182	Higher	Gm29724	chr9	-	tss_body	32372579
1891	cg46576498_TC11	0.00016932	0.08392295	Higher	Gm31755	chr9	-	tss_body	33297033
1892	cg46584028_BC21	0.00091595	0.07844503	Higher		chr9	+	tss_body	35016651
1893	cg46594520_TC21	0.00020104	-0.06219362	Lower	Kirrel3	chr9	+	tss_body	35516880
1894	cg46599387_TC21	0.00014325	0.15173346	Higher	A0A140LHF2	chr9	-	tss_body	37018245
1895	cg46607941_TC21	0.00017958	-0.05262185	Lower	Pknox2	chr9	-	tss_body	40324034
1896	cg46626335_BC21	0.00057137	-0.05304445	Lower	Gramd1b	chr9	-	tss_body	40374679
1897	cg46626965_BC21	0.00079606	0.1267342	Higher	Gramd1b	chr9	-	tss_body	41079529
1898	cg46635136_BC21	0.0001428	-0.11154064	Lower	Ubash3b	chr9	-	tss_body	42808739
1899	cg46653156_BC21	0.00095032	-0.10805535	Lower	Grik4	chr9	-	tss_body	42886435
1900	cg46654012_TC21	0.00068322	-0.07010541	Lower	Grik4	chr9	-	tss_body	43115931
1901	cg46656746_TC21	0.00037929	-0.07161804	Lower	Tmem136	chr9	-	tss_body	43741095
1902	cg46663845_BC21	0.00097946	-0.05938438	Lower	LOC102631930	chr9	-	tss_body	43921535
1903	cg46666357_TC21	0.00098173	-0.14507616	Lower					43993628
1904	cg46667165_TC21	9.4756E-05	-0.05456636	Lower		chr9	+	tss_1500	44384736
1905	cg46672600_TC11	0.00033721	0.10210682	Higher	Hyou1	chr9	+	tss_body	44878869
1906	cg46679529_BC21	0.00078998	-0.14005046	Lower	Kmt2a	chr9	-	tss_body	45266730
1907	cg46684036_BC21	3.529E-05	-0.06888307	Lower	Il10ra	chr9	-	tss_body	45380473
1908	cg46685310_TC21	0.00021479	-0.06663601	Lower	Fxyd6	chr9	+	tss_body	45679936
1909	cg46688835_BC21	0.00049073	0.11182081	Higher	Dscaml1	chr9	+	tss_body	45943008
1910	cg46692045_TC11	8.0163E-05	-0.08091517	Lower	Sidt2	chr9	-	tss_body	46046853
1911	cg46693459_TC21	0.00095477	0.05892878	Higher	Sik3	chr9	+	tss_body	46243100
1912	cg46695585_BC21	3.0295E-05	-0.05490827	Lower	Apoa4	chr9	+	tss_body	46504709
1913	cg46698585_BC11	0.0004275	-0.05292363	Lower	Gm31432	chr9	+	tss_body	48675691
1914	cg46719627_BC21	0.00011283	-0.05143023	Lower	Zbtb16	chr9	-	tss_body	49032570
1915	cg46724079_BC21	0.00099941	-0.06647106	Lower	Usp28	chr9	+	tss_body	49777537
1916	cg46730689_TC11	8.8044E-05	-0.07167782	Lower	Ncam1	chr9	-	tss_body	50597129
1917	cg46737315_TC21	0.00011189	0.10175734	Higher	Sdhd	chr9	-	tss_body	50808776
1918	cg46740229_TC21	0.00043891	-0.05839032	Lower	Alg9	chr9	+	tss_body	56423292
1919	cg46784966_TC21	0.00032128	0.07421702	Higher	Hmg20a	chr9	+	tss_body	56710612
1920	cg46788036_TC21	0.00090642	0.05499205	Higher	Lingo1	chr9	-	tss_body	56795131

1921	cg46788925_TC21	1.7066E-05	-0.06658749	Lower	Lingo1	chr9	-	tss_body	57107423
1922	cg46792569_TC21	0.00069117	-0.07758715	Lower	Sin3a	chr9	+	tss_body	57139251
1923	cg46792912_BC21	0.0001982	-0.12924218	Lower	Man2c1	chr9	+	tss_body	57140524
1924	cg46792928_TC21	0.00072653	-0.07132323	Lower	Man2c1	chr9	+	tss_body	57143576
1925	cg46792976_TC21	0.00010026	-0.05105021	Lower	Neil1	chr9	-	tss_body	57334082
1926	cg46794930_BC21	2.662E-05	-0.07301441	Lower		chr9	+	tss_200	57683452
1927	cg46799154_TC21	0.00086947	0.16026778	Higher	Cyp1a2	chr9	-	tss_body	58134826
1928	cg46804073_BC21	0.00030164	-0.08923142	Lower	Stra6	chr9	+	tss_body	58422812
1929	cg46807412_TC21	0.0006377	-0.06918715	Lower					61164451
1930	cg46833753_BC21	2.1254E-05	-0.1245576	Lower					62282039
1931	cg46845855_BC21	0.00058399	-0.06730571	Lower	Spesp1	chr9	-	tss_body	62416647
1932	cg46847690_BC21	0.000168	-0.10233497	Lower	Gm40523	chr9	-	tss_1500	63074538
1933	cg46854560_BC11	0.00074772	-0.08652687	Lower					63399460
1934	cg46858735_TC11	0.00095326	0.07095922	Higher	Gm16759	chr9	+	tss_body	63849692
1935	cg46863524_TC21	0.00074581	-0.05740319	Lower					63927749
1936	cg46864468_TC21	0.00036855	0.05247824	Higher		chr9	-	tss_body	63936959
1937	cg46864555_TC11	0.00062297	-0.07626761	Lower	Gm36033	chr9	-	tss_body	63936959
1938	cg46864555_TO21	4.7384E-05	-0.06842518	Lower	Gm36033	chr9	-	tss_body	64078919
1939	cg46866711_TC21	8.8667E-05	-0.10357165	Lower					64454084
1940	cg46870805_BC11	0.00071622	0.13242383	Higher	Megf11	chr9	+	tss_body	64512302
1941	cg46871447_BC21	0.0002294	-0.09257094	Lower	Megf11	chr9	+	tss_body	64666570
1942	cg46872939_BC21	5.7468E-05	-0.19451088	Lower	Megf11	chr9	+	tss_body	64951664
1943	cg46875523_BC21	0.00028634	-0.0929747	Lower	Slc24a1	chr9	-	tss_200	65094776
1944	cg46877033_BC21	6.023E-05	-0.08447123	Lower		chr9	-	tss_1500	65515184
1945	cg46882383_TC21	0.00028346	-0.07597441	Lower	Ankdd1a	chr9	-	tss_body	66985293
1946	cg46895376_TC21	0.00059999	-0.12049859	Lower					67330739
1947	cg46899035_BC21	2.1758E-05	-0.06702657	Lower	Tln2	chr9	-	tss_body	69303208
1948	cg46916919_BC21	0.00053393	0.06200381	Higher	Rora	chr9	+	tss_body	70405717
1949	cg46928764_TC21	0.0005878	-0.087106	Lower	Mir5626	chr9	-	tss_body	72615274
1950	cg46947570_TC21	0.00095322	-0.07185533	Lower	Rfx7	chr9	+	tss_body	74976226
1951	cg46966793_BC11	0.00011302	0.05041957	Higher	Fam214a	chr9	+	tss_body	76013962

1952	cg46976224_BC21	6.8924E-05	0.08569584	Higher	Hmgcll1	chr9	+	tss_1500	77553898
1953	cg46986145_BC21	0.00043176	0.06398778	Higher		chr9	-	tss_200	81438400
1954	cg47015608_BC21	0.00076121	-0.08926913	Lower					85782706
1955	cg47043249_TC21	0.00045174	-0.06024919	Lower		chr9	-	tss_200	86619321
1956	cg47049844_TC21	0.00093542	-0.06857015	Lower	Me1	chr9	-	tss_body	86626707
1957	cg47049923_TC21	0.00084081	0.07403314	Higher	Me1	chr9	-	tss_body	86756384
1958	cg47051131_TC11	0.00024117	-0.06623927	Lower	Prss35	chr9	+	tss_body	89729484
1959	cg47071544_TC21	0.00043491	0.05106567	Higher	Ankrd34c	chr9	-	tss_body	90170139
1960	cg47075869_TC21	0.00049562	-0.08729436	Lower	Adamts7	chr9	+	tss_body	96445633
1961	cg47117143_BC21	0.00020398	0.07537843	Higher		chr9	-	tss_body	96527270
1962	cg47118214_TC21	0.0007911	0.16266033	Higher	LOC108167675	chr9	+	tss_body	96995832
1963	cg47124146_BC21	3.1859E-06	-0.0841628	Lower	Spsb4	chr9	-	tss_body	98388332
1964	cg47135628_TC21	0.00012747	-0.18947907	Lower	Nmnat3	chr9	+	tss_body	99682384
1965	cg47149849_BC11	0.00070791	0.11289554	Higher					99710102
1966	cg47150161_BC21	5.5773E-05	0.11234471	Higher	Cldn18	chr9	-	tss_body	99710182
1967	cg47150162_TC11	0.0009418	0.05855907	Higher	Cldn18	chr9	-	tss_body	99717317
1968	cg47150247_TC21	0.00017662	-0.06820534	Lower	Cldn18	chr9	-	tss_200	99947384
1969	cg47152599_TC11	0.0008087	-0.08424156	Lower		chr9	-	tss_body	102262721
1970	cg47171647_BC21	2.9709E-05	0.09439739	Higher	Ephb1	chr9	-	tss_body	103305592
1971	cg47184390_TC21	0.0002403	0.05065995	Higher	Topbp1	chr9	+	tss_body	104035814
1972	cg47192201_BC21	6.3937E-05	-0.12256941	Lower	Nphp3	chr9	+	tss_body	104035976
1973	cg47192207_BC21	0.00099421	-0.1112451	Lower	Nphp3	chr9	+	tss_body	105650880
1974	cg47206579_TC21	7.2167E-05	0.08321778	Higher	Pik3r4	chr9	+	tss_body	106157532
1975	cg47212360_TC11	0.00099683	-0.11740898	Lower	D030055H07Rik	chr9	+	tss_body	106243484
1976	cg47213665_BC21	0.00065275	-0.14434281	Lower	Alas1	chr9	-	tss_body	107309384
1977	cg47224959_TC21	0.00089347	-0.08472067	Lower					107444250
1978	cg47226756_TC21	5.1803E-05	-0.13792654	Lower	Cacna2d2	chr9	+	tss_body	107484672
1979	cg47227331_BC21	0.00096201	-0.10246137	Lower	Cacna2d2	chr9	+	tss_body	107544189
1980	cg47228397_TC21	4.3434E-06	-0.13109808	Lower	Nprl2	chr9	+	tss_body	107544891
1981	cg47228418_TC11	0.00015112	-0.11874128	Lower	Nprl2	chr9	+	tss_body	107659793
1982	cg47230731_TC21	0.00070571	-0.0698409	Lower	Slc38a3	chr9	-	tss_body	107665363

1983	cg47230802_BC21	0.00013268	-0.14355514	Lower	Slc38a3	chr9	-	tss_body	107941250
1984	cg47234073_BC21	0.00050188	0.09615483	Higher	Camkv	chr9	+	tss_body	108083352
1985	cg47236151_TC21	0.00051333	-0.09418723	Lower	Mst1	chr9	+	tss_body	108393015
1986	cg47240375_BC21	0.00010033	-0.063536	Lower	1700102P08Rik	chr9	+	tss_body	108857014
1987	cg47247039_TC21	0.00041229	-0.06637564	Lower	Slc26a6	chr9	+	tss_body	110740684
1988	cg47264576_BC21	0.00085659	-0.06346414	Lower	Pth1r	chr9	-	tss_body	111182247
1989	cg47270249_BC21	0.00019056	0.08258156	Higher	Lrrfip2	chr9	+	tss_body	112187653
1990	cg47278954_TC21	0.00081084	0.09353082	Higher	Arpp21	chr9	-	tss_body	113981422
1991	cg47292197_BC11	0.00028157	0.09643173	Higher	Fbxl2	chr9	-	tss_body	115054016
1992	cg47305560_BC21	0.00028557	-0.06394836	Lower	Osbpl10	chr9	+	tss_body	118633353
1993	cg47342737_BC21	3.888E-05	-0.08528928	Lower	Itga9	chr9	+	tss_body	118807246
1994	cg47344801_BC21	0.00025215	-0.0569923	Lower	Itga9	chr9	+	tss_body	119145701
1995	cg47350341_TC21	0.00059246	0.12695068	Higher	Dlec1	chr9	+	tss_body	119157033
1996	cg47350596_BC21	0.00021823	0.1180051	Higher	Acaa1b	chr9	-	tss_body	120372545
1997	cg47367593_TC11	0.00020232	0.10054049	Higher	Myrip	chr9	+	tss_body	121706388
1998	cg47384463_TC11	3.2921E-05	0.0817699	Higher	Sec22c	chr9	-	tss_1500	121792364
1999	cg47385900_TC11	0.00033922	-0.06579866	Lower	Hhatl	chr9	-	tss_body	122315874
2000	cg47391509_BC21	6.8019E-05	-0.08225329	Lower	Gm35289	chr9	+	tss_1500	75822390
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47433385_BC21	0.00073922	-0.20465667	Lower	Wdr13	chrX	-	tss_body	8131601
2	cg47453080_BC21	0.00080668	-0.10635038	Lower					11187909
3	cg47454751_TC21	0.00030505	-0.13987231	Lower					11432865
4	cg47455400_TC21	0.00070398	-0.10522341	Lower	Gm39496	chrX	-	tss_body	11507006
5	cg47457632_BC21	0.00066623	-0.17694706	Lower					11739297
6	cg47459954_TC21	0.00020953	-0.13848699	Lower					11981391
7	cg47472698_BC21	8.6464E-05	-0.08379044	Lower	2010308F09Rik	chrX	-	tss_body	13235129
8	cg47497821_TC21	0.00088443	-0.0920067	Lower					18640970
9	cg47498643_TC21	4.4402E-05	-0.09421149	Lower					18847437
10	cg47498648_TC21	0.00040057	-0.21012242	Lower					18847763
11	cg47508392_TC21	1.4437E-05	-0.05380317	Lower					20789890

12	cg47513951_TC21	0.00042416	-0.05380388	Lower					21859468
13	cg47556869_BC21	0.00078865	-0.05211416	Lower	Sept6	chrX	-	tss_body	36983423
14	cg47561766_TC21	0.00030539	0.07187193	Higher	Rhox6	chrX	+	tss_body	37827666
15	cg47569060_TC21	0.00021159	-0.1222413	Lower	6030498E09Rik	chrX	+	tss_body	38867297
16	cg47620538_BC21	0.00012467	-0.14030677	Lower	Igsf1	chrX	-	tss_body	49794629
17	cg47641246_TC21	0.00086406	-0.10944063	Lower		chrX	-	tss_body	53052350
18	cg47652508_BC21	0.00064736	-0.05456217	Lower	3830403N18Rik	chrX	+	tss_1500	55838445
19	cg47656898_BC11	0.00087597	0.09590178	Higher	Gm648	chrX	-	tss_body	56560870
20	cg47659485_TC11	6.5132E-05	0.11691802	Higher	B7ZCC9	chrX	+	tss_200	56870139
21	cg47671780_TC21	0.00098799	-0.10556637	Lower					58900663
22	cg47680297_TC21	2.3085E-05	0.09721002	Higher		chrX	+	tss_body	60701865
23	cg47685506_TC21	0.00027662	-0.20461595	Lower					61712365
24	cg47712606_TC21	0.00062655	0.13517327	Higher					68730324
25	cg47740643_BC21	0.0006523	-0.08182105	Lower	Hcfc1	chrX	-	tss_body	73951453
26	cg47759500_TC21	0.00015402	0.14709389	Higher					77412735
27	cg47821652_TC21	0.00053646	-0.0546534	Lower	Mageb18	chrX	-	tss_body	92196212
28	cg47824263_TC11	0.00029287	-0.10652241	Lower					92863987
29	cg47828487_BC21	0.00074125	-0.11113911	Lower	Pcyt1b	chrX	+	tss_body	93655211
30	cg47844846_TC21	0.00036913	-0.178393	Lower	F630028O10Rik	chrX	+	tss_body	96242638
31	cg47852098_TC21	0.00094627	-0.07161328	Lower					98096189
32	cg47859934_TC21	0.00010688	-0.06209481	Lower					99350681
33	cg47862607_TC21	0.00086233	0.13688095	Higher					99604531
34	cg47871172_TC11	0.00024995	0.10432854	Higher	Tex11	chrX	-	tss_body	101006028
35	cg47873016_BC21	0.00010054	-0.12610413	Lower	Foxo4	chrX	+	tss_body	101259169
36	cg47873099_BC21	0.00095093	-0.12456434	Lower	Il2rg	chrX	-	tss_body	101268074
37	cg47876443_BC21	0.00054017	-0.12863907	Lower					101620594
38	cg47876735_TC21	0.00012687	0.0501311	Higher	Ogt	chrX	+	tss_body	101647084
39	cg47880212_TC21	0.00035004	-0.1052012	Lower	Nhsl2	chrX	+	tss_body	102029947
40	cg47880238_TC11	0.00026973	0.08300661	Higher	Nhsl2	chrX	+	tss_body	102032773
41	cg47882199_BC21	0.00060608	-0.0714542	Lower	Cited1	chrX	-	tss_body	102247953
42	cg47886653_TC21	0.00029973	0.17282345	Higher	Dmrtc1a	chrX	-	tss_body	102905537

43	cg47891153_BC11	7.2417E-05	0.05121191	Higher	Jpx	chrX	+	tss_body	103500303
44	cg47891591_TC11	0.00039152	0.07275961	Higher	Gm9159	chrX	+	tss_body	103546801
45	cg47900704_TC21	0.00012751	-0.10264108	Lower	5530601H04Rik	chrX	-	tss_body	105059627
46	cg47913064_TC21	0.00086327	-0.06253972	Lower		chrX	+	tss_body	107233661
47	cg47934556_BC21	0.00031415	-0.09208367	Lower	Satl1	chrX	-	tss_body	112405817
48	cg47986459_TC21	0.00090683	-0.05858016	Lower	4932411N23Rik	chrX	-	tss_body	126814462
49	cg47992187_TC21	8.4122E-05	-0.07332207	Lower		chrX	+	tss_200	128261371
50	cg48017590_TC21	6.9521E-05	0.17679887	Higher	A0A0R4J1X7	chrX	-	tss_body	134146638
51	cg48021187_BC21	0.00053025	-0.09407564	Lower	Btk	chrX	-	tss_body	134552086
52	cg48035493_BC21	0.00021791	0.12548511	Higher					136841620
53	cg48040375_BC21	0.00034851	-0.08847695	Lower	Il1rapl2	chrX	+	tss_body	137620551
54	cg48046212_BC21	0.00034127	-0.05214651	Lower	Nrk	chrX	+	tss_body	138999855
55	cg48104040_BC21	0.00022558	-0.10444628	Lower	Pfkfb1	chrX	+	tss_body	150588856
56	cg48151464_BC21	0.0008516	-0.15457143	Lower	Sh3kbp1	chrX	+	tss_body	159697213
57	cg48170592_TC21	2.0102E-05	0.11031058	Higher	Ctps2	chrX	+	tss_1500	162900616
58	cg48177924_TC21	0.00060851	-0.08316035	Lower	Tmem27	chrX	+	tss_body	164091873
59	cg48181118_TC21	0.00029574	0.18985154	Higher					164560080
60	cg48182479_TC21	0.00050345	-0.05424968	Lower		chrX	+	tss_body	164863743
61	cg48183114_TC21	0.0009963	-0.08995046	Lower	Mospd2	chrX	-	tss_body	164963177
62	cg48184225_BC21	0.00046817	0.06608592	Higher	Glra2	chrX	-	tss_body	165183592
63	cg48196835_BC21	0.00055475	-0.06371255	Lower					167434268
64	cg48197038_TC21	0.00051858	0.07275658	Higher	Frmpd4	chrX	-	tss_body	167478030
65	cg48203988_BC21	8.7119E-05	0.07676415	Higher	Arhgap6	chrX	+	tss_body	168990687
66	cg48204492_TC21	0.0006983	-0.06023783	Lower	Arhgap6	chrX	+	tss_body	169098808
Y chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48212271_TC11	0.00083907	0.06249264	Higher					809720
2	cg48214012_BC21	7.3189E-05	0.07380451	Higher	Uty	chrY	-	tss_body	1111263
3	cg48217471_BC21	0.00035651	0.08476459	Higher		chrY	+	tss_body	1960679
4	cg48219462_TC21	0.00016984	-0.12253094	Lower					2390460
5	cg48222264_TC21	5.0981E-05	0.06297294	Higher					3887159

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 14: Significantly altered CpGs in male lungs at 16 weeks due to postnatal CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28109245_TC21	0.00032508	0.0932258 3	Higher	Gm29826	chr10	+	tss_body	3291621
2	cg28114907_TC21	0.00064733	0.0544394 6	Higher	Mthfd1l	chr10	+	tss_body	3997138
3	cg28122137_TC21	0.00029213	0.0506016 7	Higher	Esr1	chr10	+	tss_body	4620915
4	cg28139359_TC21	0.00068631	0.0978374 4	Higher					7068806
5	cg28155671_BC21	0.00021672	-0.063108	Lower	Sash1	chr10	-	tss_body	8756685
6	cg28169677_BC21	0.00019948	-0.0859378 9	Lower	Rab32	chr10	-	tss_body	10546436
7	cg28179259_BC21	0.00036299	-0.0657157 7	Lower		chr10	-	tss_body	12009363
8	cg28188014_BC21	0.00057332	-0.0836748 3	Lower	Plagl1	chr10	+	tss_200	13090764
9	cg28192106_BC21	0.00087277	0.0567283	Higher	Fuca2	chr10	+	tss_body	13507325
10	cg28193183_BC21	0.00024184	0.0898239 1	Higher					13616207
11	cg28222382_TC21	0.00015786	0.0682343 1	Higher	Ccdc28a	chr10	-	tss_body	18219473
12	cg28237096_TC21	0.00025031	0.1466346 3	Higher	Pex7	chr10	-	tss_body	19877966
13	cg28238171_TC21	0.00063077	0.0894549 6	Higher	Map3k5	chr10	+	tss_body	19970188
14	cg28255176_TC21	0.00072112	-0.0972706 7	Lower	1700020N01Rik	chr10	+	tss_body	21605889
15	cg28271368_BC21	0.00016777	0.0614639 7	Higher					23403832
16	cg28309925_TC21	0.00037822	0.0987534 3	Higher	Ptprk	chr10	+	tss_body	28492769
17	cg28337586_TC11	0.00084105	-0.0686094 4	Lower	Sult3a2	chr10	-	tss_body	33783689
18	cg28360904_BC21	0.00096243	-0.0580210 4	Lower		chr10	-	tss_1500	38434402
19	cg28376180_TC21	0.00049047	-0.0640491 4	Lower	Amd1	chr10	-	tss_body	40297526
20	cg28415771_TC21	0.00025849	0.0532400 1	Higher		chr10	+	tss_1500	43820741
21	cg28424112_TC21	0.00075806	0.0548869 1	Higher		chr10	+	tss_body	44698658
22	cg28464938_TC21	0.00057886	-0.0637424 7	Lower	Nus1	chr10	+	tss_body	52426707
23	cg28464939_TC21	0.00023672	0.1195809 2	Higher	Nus1	chr10	+	tss_body	52426813

24	cg28469145_BC21	0.00043747	-0.1056925	Lower	Gm4064 9	chr10	+	tss_body	53181246
25	cg28494049_TC21	0.00019164	-0.0607786 9	Lower					57569420
26	cg28504881_BC21	0.00092546	-0.0794964 7	Lower					59279882
27	cg28509023_TC21	0.00038651	0.0581633 5	Higher					59622729
28	cg28512110_BC11	0.00036913	-0.0668043 7	Lower	Dnajb12	chr10	+	tss_body	59882071
29	cg28526564_BC21	4.4858E-05	-0.0836928 9	Lower					60958149
30	cg28533317_BC21	0.00043021	-0.0645041 6	Lower	Lrrc20	chr10	+	tss_body	61494744
31	cg28538739_TC21	0.00099358	0.0810583 7	Higher	Col13a1	chr10	-	tss_body	61881472
32	cg28560812_BC21	0.0005124	-0.0620409 2	Lower	Ctnna3	chr10	+	tss_body	63694404
33	cg28648790_TC21	0.00010126	-0.0714578 9	Lower	Pcdh15	chr10	+	tss_body	74416228
34	cg28659985_BC21	0.00081629	-0.0637871 2	Lower	Lrrc75b	chr10	-	tss_body	75553963
35	cg28664911_TC21	0.00029321	-0.0877570 8	Lower	Mmp11	chr10	-	tss_body	75925827
36	cg28665445_BC21	6.1538E-05	-0.0623702 1	Lower	Gm5134	chr10	+	tss_body	75954598
37	cg28665629_TC21	0.00080085	-0.0567877 5	Lower	Gm5134	chr10	+	tss_body	75969721
38	cg28678331_BC21	0.00032975	0.0501848 1	Higher	Slc19a1	chr10	+	tss_1500	77032712
39	cg28680752_TC21	0.00060867	-0.0859040 6	Lower	Gm3583 7	chr10	+	tss_body	77225904
40	cg28683213_TC21	0.0005175	0.0699037 4	Higher	Gm1776 9	chr10	+	tss_body	77418670
41	cg28684754_BC21	0.00058216	0.0979036 2	Higher	Itgb2	chr10	+	tss_body	77543328
42	cg28721028_BC21	0.0003886	-0.0547260 9	Lower	Tcf3	chr10	-	tss_body	80426757
43	cg28722897_TC11	0.00090693	0.0917134 2	Higher	Atp8b3	chr10	-	tss_body	80528543
44	cg28724591_TC11	0.00022293	-0.0829742 6	Lower	Adat3	chr10	+	tss_body	80607606
45	cg28736734_TC21	0.0002562	0.0714435 5	Higher	Matk	chr10	+	tss_body	81262845
46	cg28742201_TC11	0.0005732	-0.0718792 7	Lower	S1pr4	chr10	-	tss_body	81499416
47	cg28751541_TC21	0.00046861	-0.0574428	Lower	Hcfc2	chr10	+	tss_body	82747228

48	cg28762750_BC11	0.00021286	-0.10576063	Lower	A230046K03Rik	chr10	+	tss_body	83590940
49	cg28763683_TC21	0.00012156	0.1308124	Higher		chr10	+	tss_body	83659451
50	cg28772168_TC21	0.00022154	-0.0590178	Lower					84542941
51	cg28775532_TC21	0.00033712	0.14305237	Higher	Rfx4	chr10	+	tss_body	84822511
52	cg28805568_TC21	0.00043532	0.08723119	Higher	Ccdc53	chr10	+	tss_body	88241535
53	cg28810447_BC21	0.00035577	0.06712143	Higher	D3YYM5	chr10	-	tss_200	88685079
54	cg28826404_TC21	0.00077525	0.08871764	Higher	Anks1b	chr10	+	tss_body	90680327
55	cg28838015_BC21	0.00025195	0.09208749	Higher	Gm31592	chr10	+	tss_body	91923614
56	cg28849670_BC21	9.0358E-05	-0.13828941	Lower	Elk3	chr10	-	tss_body	93284892
57	cg28851119_BC11	0.00038821	0.05448726	Higher					93418312
58	cg28853431_TC21	0.00060365	-0.1234937	Lower	Ccdc38	chr10	+	tss_body	93581259
59	cg28949914_TC21	0.00025272	0.09102053	Higher	Acss3	chr10	-	tss_body	106989431
60	cg28954004_BC11	0.00025739	-0.05053808	Lower	Gm36177	chr10	+	tss_body	107610545
61	cg28956114_BC21	0.00036911	0.10739226	Higher	Otogl	chr10	-	tss_body	107912079
62	cg28960719_TC21	4.1E-05	0.11056309	Higher	Pawr	chr10	+	tss_body	108388362
63	cg28963884_TC21	0.00072033	0.06433764	Higher	Syt1	chr10	-	tss_body	108680039
64	cg29031068_BC21	0.00062046	-0.0559114	Lower	D630029K05Rik	chr10	+	tss_body	116966253
65	cg29032480_BC21	0.00085289	0.10675921	Higher	Cct2	chr10	-	tss_body	117054898
66	cg29034383_BC21	0.00062991	-0.05887077	Lower					117199616
67	cg29074286_TC11	0.00022826	-0.15046094	Lower	Hmga2	chr10	-	tss_body	120428784
68	cg29136833_TC21	0.00026991	-0.05498643	Lower	4930484H19Rik	chr10	-	tss_body	126793663
69	cg29136834_TC21	0.00025703	-0.05219515	Lower	4930484H19Rik	chr10	-	tss_body	126793674
70	cg29139017_TC21	0.00035527	0.0850219	Higher					126953179
71	cg29143466_TC21	0.00029469	0.07493207	Higher	Slc26a10	chr10	-	tss_body	127180535
72	cg29154282_TC21	0.00072741	-0.08456948	Lower	Sdr9c7	chr10	+	tss_body	127904632
73	cg29154927_TC21	0.00098056	0.06980587	Higher	Gm40806	chr10	-	tss_body	127970181
74	cg29159360_TC11	0.00022018	-0.05960418	Lower	Il23a	chr10	-	tss_200	128298146

75	cg29177304_BC21	0.00063754	0.08107752	Higher	Eif4enif1	chr11	+	tss_body	3243894
76	cg29197588_BC21	0.00050443	0.08833236	Higher	Ap1b1	chr11	+	tss_body	4996907
77	cg29199652_BC21	9.1066E-05	-0.06557809	Lower	Emid1	chr11	-	tss_body	5144382
78	cg29229005_TO21	0.00056967	-0.11333213	Lower					8209282
79	cg29249728_BC21	0.00077881	-0.06207811	Lower	Gm11999	chr11	-	tss_body	11685359
80	cg29252485_BC11	0.00095775	-0.08291572	Lower	Grb10	chr11	-	tss_body	11962076
81	cg29268796_TC21	0.00063188	0.06736024	Higher					15416819
82	cg29289323_TC11	0.00016939	-0.08245742	Lower	Meis1	chr11	-	tss_body	19008232
83	cg29304663_BC21	0.00070255	0.0790007	Higher	Sertad2	chr11	+	tss_body	20628248
84	cg29322137_TC21	0.00091738	0.08204053	Higher	Fam161a	chr11	+	tss_body	23020132
85	cg29323090_BC21	3.4873E-05	0.0769491	Higher					23147334
86	cg29345200_TC11	0.00091955	-0.09251182	Lower					26746331
87	cg29374132_TC21	0.00056355	-0.08975986	Lower	4930524B15Rik	chr11	+	tss_body	31965849
88	cg29380998_TC21	0.00074081	-0.08066307	Lower	Stk10	chr11	+	tss_body	32603742
89	cg29403022_TC11	0.00042622	-0.13619582	Lower	Slit3	chr11	+	tss_body	35124602
90	cg29466662_BC11	0.00033599	-0.14877975	Lower	Ebf1	chr11	+	tss_body	44620409
91	cg29479060_BC11	0.00056564	-0.053864	Lower	Adam19	chr11	+	tss_body	46061304
92	cg29495221_TC21	3.1143E-05	-0.07892048	Lower		chr11	+	tss_200	48595215
93	cg29496825_BC21	0.00066949	0.09375529	Higher	Gm36109	chr11	-	tss_body	48797669
94	cg29517447_TC21	0.00076515	0.06464028	Higher	Grm6	chr11	+	tss_body	50857201
95	cg29518969_TC21	0.00026963	-0.0546825	Lower	Olfr51	chr11	+	tss_body	51007795
96	cg29528648_TC21	0.00077162	-0.08363884	Lower					51875664
97	cg29545754_BC21	0.00057157	0.13966819	Higher	Sowaha	chr11	-	tss_body	53478671
98	cg29545755_TC11	4.093E-05	0.09763675	Higher	Sowaha	chr11	-	tss_body	53478691
99	cg29549368_TC21	0.0006931	0.07686893	Higher					53759421
100	cg29557921_BC21	0.00093694	0.05258642	Higher	Cdc42se2	chr11	-	tss_body	54722138

101	cg29560096_BC21	0.0005547	-0.0547535	Lower	Tnip1	chr11	-	tss_body	54928891
102	cg29605416_BC11	0.0007172	-0.0993932	Lower					59632140
103	cg29608273_BC21	0.0001854 1	-0.1217550 2	Lower		chr11	+	tss_200	59898257
104	cg29621032_BC21	0.0004044 9	-0.1356704	Lower	Kcnj12	chr11	+	tss_body	61025732
105	cg29626480_BC11	0.0005655 4	0.1008967 8	Higher	Mfap4	chr11	+	tss_200	61485333
106	cg29631787_TC21	5.1927E-05	0.0691325 8	Higher	Specc1	chr11	+	tss_body	62015178
107	cg29644077_BC11	0.0009556 3	0.0865878 5	Higher					63217255
108	cg29660249_BC21	0.0009942 6	-0.0549709 6	Lower	Arhgap44	chr11	-	tss_body	65059734
109	cg29677987_TC21	0.0004470 5	0.0651706 8	Higher	Myh8	chr11	+	tss_body	67277395
110	cg29681673_TC21	0.0005670 4	-0.0784752 6	Lower	Gas7	chr11	+	tss_body	67651808
111	cg29685533_TC21	0.0002814 6	0.1064641 3	Higher	Stx8	chr11	+	tss_body	68023718
112	cg29717860_TC21	0.0005739 9	0.0633649	Higher	Mir497b	chr11	-	tss_1500	70235768
113	cg29718897_BC21	0.0007831	-0.0689313 8	Lower	Alox12e	chr11	-	tss_body	70316183
114	cg29740241_BC21	0.0007956 7	0.1256742 3	Higher	Spns2	chr11	-	tss_body	72456838
115	cg29767888_TC21	0.0003169 9	0.1111452 2	Higher	Slc43a2	chr11	+	tss_body	75564079
116	cg29780141_BC21	0.0006902 7	-0.0536279 7	Lower		chr11	-	tss_body	76587768
117	cg29821336_TC21	0.0008605 5	0.1163774 5	Higher					80283925
118	cg29839004_TC21	0.0006299 8	0.0747029 2	Higher		chr11	-	tss_body	82251305
119	cg29852214_BC21	0.0005698 1	-0.0544379 6	Lower	Gm32650	chr11	+	tss_body	83530257
120	cg29895270_BC21	0.0002193 4	-0.0595377 9	Lower	Bzrap1	chr11	+	tss_body	87776063
121	cg29895352_BC21	0.000929	-0.0698258	Lower	Bzrap1	chr11	+	tss_body	87779902
122	cg29952294_TC21	0.0006615 9	-0.0961382 9	Lower	Cacna1g	chr11	-	tss_body	94417524
123	cg29962916_TC11	0.0001266 6	0.0749072 3	Higher	LOC102640586	chr11	-	tss_body	95198207
124	cg29994868_BC21	0.0007967 4	-0.0769363 3	Lower	Arhgap23	chr11	+	tss_body	97424441
125	cg30004657_BC21	7.8423E-05	-0.0883244 4	Lower	Cacnb1	chr11	-	tss_body	98018455

126	cg30004950_TC21	0.0005878 4	-0.0629854 4	Lower	Rpl19	chr11	+	tss_body	98028930
127	cg30013063_TC21	0.0008454 7	0.1178613 9	Higher	chr11-9858703 2-9858743 4	chr11	*	SShelf	98589449
128	cg30020457_TC21	0.0006365 3	0.0636211 7	Higher	Igfbp4	chr11	+	tss_body	99045862
129	cg30028634_TC21	0.0003265 6	0.0605261 3	Higher	Gm1156 7	chr11	+	tss_body	99879925
130	cg30036331_TC21	8.6473E-05	0.1335031	Higher	Acly	chr11	-	tss_body	10052587 7
131	cg30040460_BC21	0.0008036 2	-0.0723852 8	Lower	Stat5b	chr11	-	tss_body	10080705 6
132	cg30042877_TC21	0.0009918 2	0.0850245 6	Higher	Ptrf	chr11	-	tss_1500	10097131 2
133	cg30046798_TC21	0.0006368 9	0.0800148 5	Higher	Ezh1	chr11	-	tss_body	10121969 4
134	cg30059257_BC21	0.0006483 5	-0.0772065 1	Lower					10211691 0
135	cg30070175_BC21	0.0007930 7	0.0805228 6	Higher	Higd1b	chr11	+	tss_1500	10283595 3
136	cg30070284_BC21	0.0002440 3	-0.0836459 4	Lower	Eftud2	chr11	-	tss_body	10284417 5
137	cg30085808_BC21	0.0005937	-0.0995042 9	Lower					10396210 9
138	cg30086376_BC21	0.0009784 7	0.1093310 3	Higher					10400683 8
139	cg30093306_TC21	0.0007906 5	0.0597691 3	Higher	Itgb3	chr11	+	tss_body	10462518 2
140	cg30109094_TC11	0.0003748 4	-0.0579760 5	Lower	Gh	chr11	-	tss_body	10630200 6
141	cg30109656_TC21	0.0006802 2	0.1045101 7	Higher	Scn4a	chr11	-	tss_body	10634525 5
142	cg30110108_TC21	0.00094	-0.0566037 9	Lower	Icam2	chr11	-	tss_body	10638045 2
143	cg30110228_TC21	0.0006263 3	-0.0555435 2	Lower	Icam2	chr11	-	tss_1500	10638950 7
144	cg30114756_BC21	0.0005419 9	-0.0524640 2	Lower	Milr1	chr11	+	tss_body	10676308 0
145	cg30122074_TC21	4.1109E-05	-0.0895485 2	Lower	Pitpnc1	chr11	-	tss_body	10735332 2
146	cg30141706_TC21	4.4527E-06	-0.1314430 7	Lower	E030025 P04Rik	chr11	-	tss_200	10914444 3
147	cg30188222_BC21	0.0002979 9	0.0764485 2	Higher	Cpsf4l	chr11	-	tss_body	11370983 6
148	cg30204912_BC21	0.0006383 4	-0.0982390 5	Lower	Cd300ld	chr11	-	tss_body	11498986 6
149	cg30205297_TC21	0.0006660 6	0.1655879 8	Higher	Cd300e	chr11	-	tss_body	11505934 5

150	cg30206116_BC21	0.00011012	-0.0866249	Lower	Rab37	chr11	+	tss_body	115118462
151	cg30209679_TC11	0.00048968	0.06043618	Higher	Otop2	chr11	+	tss_body	115322196
152	cg30224851_TC21	0.00017833	-0.0791672 5	Lower	Evpl	chr11	-	tss_body	116222541
153	cg30227853_BC21	0.0007791	0.07780599	Higher	Rnf157	chr11	-	tss_body	116387139
154	cg30233070_TC21	0.00055644	0.09169872	Higher	P70277	chr11	-	tss_body	116676273
155	cg30249131_BC21	0.00053191	0.07579575	Higher	Tmc6	chr11	-	tss_body	117777279
156	cg30249825_TC21	0.00072207	-0.057273	Lower	Syngr2	chr11	+	tss_body	117812564
157	cg30251762_BC21	0.00082721	-0.1034978	Lower					117935652
158	cg30258344_BC21	0.00058987	0.05223957	Higher	Timp2	chr11	-	tss_body	118349825
159	cg30261861_TC21	0.0004228	-0.0780124 6	Lower	Rbfox3	chr11	-	tss_body	118576704
160	cg30283910_TC21	0.00078646	0.06590558	Higher	Cep131	chr11	-	tss_body	120068231
161	cg30290648_BC21	0.00018847	-0.0698296 2	Lower	Pde6g	chr11	-	tss_1500	120453763
162	cg30294216_TC21	0.00037075	-0.0695708 9	Lower	Pycr1	chr11	-	tss_body	120641724
163	cg30303127_BC21	0.00067289	-0.0540757	Lower	Foxk2	chr11	+	tss_body	121307661
164	cg30304067_BC21	0.00052189	0.07655041	Higher	Rab40b	chr11	-	tss_body	121387389
165	cg30304163_TC21	0.0003293	-0.0762534 4	Lower					121392546
166	cg30329142_BC21	0.00019582	-0.0775559 2	Lower	Klhl29	chr12	-	tss_body	5088130
167	cg30353898_BC21	0.00023324	-0.1013830 9	Lower					8859251
168	cg30358550_TC21	0.00048686	0.11359796	Higher	Gm7099	chr12	+	tss_body	9429876
169	cg30403771_TC21	0.00044105	0.07564172	Higher	Greb1	chr12	-	tss_body	16760447
170	cg30468895_TC21	0.00066194	0.09829417	Higher	Gm36287	chr12	+	tss_body	25181896
171	cg30478716_BC21	0.00087017	-0.1080682 1	Lower					26551668
172	cg30484020_BC21	0.00099958	0.05022142	Higher	Gm30855	chr12	+	tss_body	27351547
173	cg30484294_TC21	0.00071897	0.10684658	Higher					27392059
174	cg30491594_TC21	0.00049588	-0.0683522 9	Lower	Colec11	chr12	-	tss_body	28607857
175	cg30529604_TC21	0.00050271	0.08724723	Higher	Atxn7l1	chr12	+	tss_body	33213827
176	cg30629834_TC21	0.00070265	-0.1123589 7	Lower					51276717

177	cg30633954_BC21	0.00084547	-0.05540045	Lower	Ap4s1	chr12	+	tss_body	51717094
178	cg30655960_TC21	0.00097863	-0.10520102	Lower	Egln3	chr12	-	tss_body	54188187
179	cg30669032_BC21	0.00069612	-0.0520545	Lower					55513685
180	cg30757781_BC11	0.00028199	-0.1105351	Lower					70136695
181	cg30789374_BC21	1.132E-05	0.12374423	Higher	Six4	chr12	-	tss_body	73103861
182	cg30815869_TC21	0.00066356	0.09918043	Higher	Syne2	chr12	+	tss_body	76072113
183	cg30825588_BC21	0.00058261	0.06966299	Higher	Gpx2	chr12	-	tss_1500	76795917
184	cg30843162_BC21	0.00020734	0.07229849	Higher	Arg2	chr12	+	tss_body	79150327
185	cg30847641_TC21	0.00078343	0.0777862	Higher	Rad51b	chr12	+	tss_body	79663431
186	cg30859895_TC11	0.00012015	-0.08917536	Lower					80778324
187	cg30861333_BC21	0.00057561	0.08924437	Higher	Srsf5	chr12	+	tss_body	80948419
188	cg30873876_TC21	0.00087697	0.08112125	Higher	Sipa1l1	chr12	+	tss_body	82232098
189	cg30876440_TC21	0.00061816	0.05801307	Higher		chr12	-	tss_body	82496461
190	cg30896827_BC21	0.00047693	-0.05059509	Lower	Entpd5	chr12	-	tss_body	84379267
191	cg30897119_TC21	0.00061408	0.11128105	Higher	Entpd5	chr12	-	tss_body	84401127
192	cg30907193_TC21	0.00059911	-0.08141552	Lower	Eif2b2	chr12	+	tss_body	85223728
193	cg30911977_TC11	0.00075496	-0.1052468	Lower	Jdp2	chr12	+	tss_body	85602494
194	cg30919303_TC21	0.00030786	-0.05261683	Lower	Gpatch2l	chr12	+	tss_body	86244286
195	cg30920803_BC21	0.00043025	0.05668405	Higher	Esrrb	chr12	+	tss_body	86366028
196	cg30924543_BC21	0.00092386	-0.0672236	Lower	Vash1	chr12	+	tss_body	86682085
197	cg30927524_TC21	0.00098499	0.08554898	Higher					86906817
198	cg30968496_TC21	0.00045358	0.0593489	Higher					93116921
199	cg31014319_BC21	0.00054479	-0.0836983	Lower		chr12	-	tss_body	100084485
200	cg31017989_TC21	0.00080625	-0.05924368	Lower	Ttc7b	chr12	-	tss_body	100360990
201	cg31019114_BC21	5.6664E-05	0.11621964	Higher	Ttc7b	chr12	-	tss_body	100479643
202	cg31038717_TC21	3.9046E-05	-0.06184337	Lower	Itpk1	chr12	-	tss_body	102678813
203	cg31049145_BC21	0.00049992	0.07562993	Higher	Serpina6	chr12	-	tss_body	103656546

204	cg31068874_TC21	0.00015762	-0.07211299	Lower					105511715
205	cg31073673_TC11	0.00049272	-0.06630352	Lower	chr12-105862675-105862932	chr12	*	Island	105862820
206	cg31116673_TC21	0.00083362	0.09660666	Higher					109254652
207	cg31119721_TC21	0.00044804	-0.05994584	Lower	Meg3	chr12	+	tss_body	109542279
208	cg31120321_BC21	0.00078295	-0.0731242	Lower	Mir3070b	chr12	+	tss_1500	109588311
209	cg31142603_TC21	0.00056956	0.09035271	Higher	Amn	chr12	+	tss_body	111273584
210	cg31161753_TC21	0.00023864	-0.06755619	Lower					112533676
211	cg31193043_TC21	0.00012798	-0.08193668	Lower	Ptprn2	chr12	+	tss_body	116927101
212	cg31200415_TC11	0.00013292	-0.07243887	Lower		chr12	+	tss_body	117821829
213	cg31205997_TC21	0.00043865	-0.05882551	Lower		chr12	+	tss_200	118602670
214	cg31266683_BC21	0.00010106	0.11827833	Higher	Ryr2	chr13	-	tss_body	11653547
215	cg31272859_BC21	0.0009351	-0.06401624	Lower					12369350
216	cg31293557_BC21	9.7283E-05	0.09395457	Higher	Gli3	chr13	+	tss_body	15576909
217	cg31351423_BC21	0.00076719	-0.08390017	Lower	Lrrc16a	chr13	-	tss_body	24082154
218	cg31370524_BC21	0.0009493	-0.06159568	Lower	Hdgfl1	chr13	-	tss_body	26770104
219	cg31420981_BC21	0.00082888	-0.10193624	Lower	chr13-34077688-34078152	chr13	*	SShore	34080023
220	cg31428338_BC21	0.00020435	0.0518582	Higher	Eci3	chr13	-	tss_body	34963622
221	cg31446936_TC21	0.00048204	-0.05411828	Lower	Gm30863	chr13	-	tss_body	37509790
222	cg31447398_TC21	0.00039582	-0.07346922	Lower	Gm30918	chr13	+	tss_body	37547804
223	cg31448806_TC21	0.00045403	0.11398958	Higher					37680523
224	cg31557543_TC21	0.00092529	0.05240763	Higher	A330033J07Rik	chr13	-	tss_body	48227166
225	cg31559681_BC21	0.00039872	-0.06287692	Lower		chr13	-	tss_body	48408359

226	cg31571402_BC21	0.0005682	-0.0699366	Lower	Bicd2	chr13	+	tss_body	49383080
227	cg31585454_BC21	0.0009989	0.0769331	Higher	LOC108168083	chr13	+	tss_body	51312129
228	cg31590044_BC21	0.0001671	-0.0500935	Lower	Sema4d	chr13	-	tss_body	51704832
229	cg31604387_BC21	0.0003442	-0.0590155	Lower	Auh	chr13	-	tss_body	52922135
230	cg31610799_BC21	0.0004361	0.0968025	Higher	Gm2762	chr13	+	tss_body	53395275
231	cg31613698_BC21	0.0009905	-0.1173092	Lower					53634695
232	cg31621276_TC21	0.0004378	-0.0509356	Lower	Cplx2	chr13	+	tss_body	54323182
233	cg31625162_TC21	0.0009758	0.0694586	Higher	Faf2	chr13	+	tss_body	54633216
234	cg31625630_TC21	0.0004443	0.0527045	Higher					54676995
235	cg31632671_TC11	0.0006557	-0.0549123	Lower	Fgfr4	chr13	+	tss_body	55161671
236	cg31633170_BC21	0.0009682	-0.0637447	Lower					55194731
237	cg31635651_TC21	0.0009771	0.0739716	Higher	Slc34a1	chr13	+	tss_body	55400472
238	cg31638882_BC11	0.0007907	0.0591695	Higher	Tmed9	chr13	+	tss_1500	55592576
239	cg31671871_BC21	0.0002016	0.0520899	Higher	Ubqln1	chr13	-	tss_body	58198104
240	cg31674961_TC11	9.7668E-05	-0.0623020	Lower		chr13	+	tss_1500	58442758
241	cg31698718_TC21	0.0003467	0.0988999	Higher	A530001N23Rik	chr13	-	tss_body	60493884
242	cg31743344_TC21	0.0002145	0.0593684	Higher	Zfp759	chr13	+	tss_body	67128985
243	cg31773032_TC21	0.0009854	0.1141190	Higher	Gm36377	chr13	-	tss_body	70655841
244	cg31793183_BC11	0.0001373	0.0986932	Higher	Irx4	chr13	+	tss_body	73268568
245	cg31797804_TC21	9.3427E-05	0.0770753	Higher	Slc12a7	chr13	+	tss_body	73763206
246	cg31804647_TC21	0.0001065	-0.0878163	Lower	LOC108168101	chr13	-	tss_body	74617462
247	cg31804965_TC21	0.0002586	0.0553012	Higher	Erap1	chr13	+	tss_body	74666548
248	cg31816168_TC21	0.0001275	0.1128143	Higher	Mctp1	chr13	+	tss_body	76724015
249	cg31824994_BC21	0.0005069	-0.0587759	Lower		chr13	+	tss_body	78273677
250	cg31845359_TC11	3.4995E-05	0.7106019	Higher					82068700
251	cg31905671_BC21	0.0003043	-0.0934488	Lower	Cmya5	chr13	-	tss_body	93095063
252	cg31925292_TC21	0.0008924	0.1118377	Higher	Wdr41	chr13	+	tss_body	94990622

253	cg31937551_TC21	0.00082312	0.06335101	Higher	Sv2c	chr13	-	tss_body	96126855
254	cg31944712_TC21	0.00086096	-0.07310636	Lower					96989641
255	cg31955291_TC21	0.00062738	0.05383474	Higher	Arhgef28	chr13	-	tss_body	97938741
256	cg31959335_TC21	0.00078466	0.08251709	Higher	LOC102637808	chr13	+	tss_body	98279927
257	cg32013108_BC21	0.00037798	0.07984427	Higher					104018586
258	cg32019149_TC21	0.00034847	0.0788899	Higher	Cwc27	chr13	-	tss_body	104799335
259	cg32030354_BC21	0.0001293	-0.10239086	Lower	Gm30411	chr13	-	tss_body	106760159
260	cg32043024_TC21	0.00049555	0.05107527	Higher		chr13	+	tss_200	107996188
261	cg32050473_BC21	0.00057484	-0.09777935	Lower	Pde4d	chr13	+	tss_body	108860110
262	cg32074298_BC21	0.00076762	-0.06001044	Lower	Map3k1	chr13	-	tss_body	111755488
263	cg32076131_TC21	0.00068585	0.08843813	Higher		chr13	+	tss_1500	111856494
264	cg32135131_TC21	0.00056458	0.06183109	Higher					118894297
265	cg32140101_TC21	3.5211E-05	0.11447588	Higher	Ccl28	chr13	+	tss_body	119639169
266	cg32141464_BC21	4.5925E-05	-0.06431942	Lower	Gm41077	chr13	+	tss_body	119767472
267	cg32190471_TC21	0.00057411	-0.05694442	Lower	Ptprg	chr14	+	tss_body	12202431
268	cg32203671_BC11	0.00042454	-0.07009238	Lower		chr14	-	tss_body	14294593
269	cg32261871_TC11	0.00050975	0.14362765	Higher	1700112E06Rik	chr14	+	tss_body	22633995
270	cg32288475_TC21	0.00011212	0.0864033	Higher					25825317
271	cg32348660_TC21	0.00040436	-0.0728671	Lower	Ercc6	chr14	+	tss_body	32531783
272	cg32365275_TC21	0.0008567	-0.0593465	Lower	Syt15	chr14	+	tss_body	34226070
273	cg32370792_BC21	0.00013005	-0.14523657	Lower		chr14	+	tss_body	34770075
274	cg32395736_TC21	5.8637E-05	-0.09330294	Lower	1700109I08Rik	chr14	+	tss_body	39655796
275	cg32439094_BC21	0.00078939	0.05472579	Higher	Gch1	chr14	-	tss_body	47175092
276	cg32474575_BC21	0.00022192	-0.0728096	Lower	Gm7247	chr14	+	tss_body	51435242
277	cg32478884_BC21	0.00057974	0.10329115	Higher	Zfp219	chr14	-	tss_body	52010978
278	cg32480858_TC21	0.00021105	0.06897244	Higher	Supt16	chr14	-	tss_body	52190289
279	cg32499351_TC21	0.00039484	-0.09855193	Lower	Psmb11	chr14	+	tss_body	54628337

280	cg32503857_BC21	3.6628E-05	-0.09408484	Lower	Myh6	chr14	-	tss_body	54949115
281	cg32505387_TC21	0.00025679	-0.06887909	Lower	Gm20687	chr14	+	tss_body	55062990
282	cg32564080_TC11	0.00039809	-0.20132357	Lower	Arl11	chr14	+	tss_body	61309901
283	cg32584731_TC21	0.00026069	0.11458076	Higher	Tdh	chr14	-	tss_body	63509062
284	cg32589378_TC21	0.00065967	0.11931097	Higher	4930578I06Rik	chr14	-	tss_200	63987889
285	cg32591154_BC21	0.00092397	-0.07410816	Lower	Msra	chr14	-	tss_body	64173402
286	cg32594765_BC21	0.00034677	-0.06397704	Lower	Mir124a-1hg	chr14	+	tss_body	64591183
287	cg32610027_TC21	0.00053114	0.0732336	Higher	Ephx2	chr14	-	tss_body	66089177
288	cg32623271_TC11	0.00067499	-0.14318895	Lower	Ebf2	chr14	+	tss_body	67371412
289	cg32624901_BC21	0.00046274	-0.09679358	Lower					67536698
290	cg32638295_TC21	0.00065785	0.10557665	Higher					69181656
291	cg32676348_TC21	0.00089436	-0.09741631	Lower		chr14	+	tss_body	73812760
292	cg32686832_TC21	0.00038874	-0.06825944	Lower	Cpb2	chr14	+	tss_body	75257659
293	cg32697902_BC21	0.0004665	-0.09048336	Lower					76279313
294	cg32717598_BC21	0.00027891	-0.09472528	Lower					78216256
295	cg32733070_BC21	0.000269	-0.1112459	Lower					79725752
296	cg32734850_BC21	0.00013307	0.08779514	Higher	LOC328448	chr14	+	tss_1500	79890487
297	cg32771742_BC21	0.00030221	-0.09406476	Lower					87292136
298	cg32778236_TC21	0.00093825	0.11553292	Higher	Pcdh20	chr14	-	tss_body	88467312
299	cg32820991_BC21	0.00044239	0.08607426	Higher	Dach1	chr14	-	tss_body	97795533
300	cg32858594_BC21	0.00051693	-0.08055585	Lower	Gm34589	chr14	-	tss_body	102832552
301	cg32875027_BC21	8.6826E-05	-0.06413417	Lower	D130009I18Rik	chr14	+	tss_body	104715775
302	cg32890153_BC21	0.00045194	-0.05950003	Lower		chr14	-	tss_body	106555939
303	cg32975903_TC11	0.00024492	-0.07756772	Lower	Mbnl2	chr14	+	tss_body	120286492

304	cg33099783_TC21	0.00071645	0.0519672	Higher		chr15	-	tss_body	13758785
305	cg33102115_BC21	0.00083892	0.1024860 4	Higher					14311940
306	cg33147938_TC21	0.00080007	-0.0589308 3	Lower					24119960
307	cg33150002_BC21	0.00056708	0.0941718 3	Higher					24547369
308	cg33158723_TC21	0.00025079	-0.0735943 7	Lower	Myo10	chr15	+	tss_body	25657810
309	cg33181253_BC21	0.00065804	0.0885568 7	Higher	Trio	chr15	-	tss_body	27995732
310	cg33272921_BC21	0.00046716	-0.0712123	Lower	Gm33301	chr15	+	tss_body	40167607
311	cg33349060_BC11	0.00030689	0.0613901 8	Higher	Mal2	chr15	+	tss_body	54571592
312	cg33409552_BC21	0.00058717	-0.0595517	Lower		chr15	+	tss_body	62332349
313	cg33469198_BC21	0.00080826	-0.0535058 3	Lower	Trappc9	chr15	-	tss_body	72810540
314	cg33477309_BC21	0.00099496	-0.0648414 2	Lower	Dennd3	chr15	+	tss_body	73564937
315	cg33497182_BC11	0.00051622	-0.0950802 7	Lower	Gm38506	chr15	+	tss_body	75643440
316	cg33500639_BC21	0.00053786	-0.0579918 3	Lower	Mroh6	chr15	-	tss_body	75884009
317	cg33501025_BC21	0.00010123	0.075269	Higher	Eef1d	chr15	-	tss_body	75900404
318	cg33501060_BC21	7.2497E-05	-0.0852359	Lower	Eef1d	chr15	-	tss_body	75902763
319	cg33505306_TC11	0.00068094	0.0621598 9	Higher	BC024139	chr15	-	tss_body	76125284
320	cg33506085_TC21	1.2179E-05	-0.0730654 7	Lower	Plec	chr15	-	tss_body	76177122
321	cg33506459_BC21	0.00080689	-0.0504455 5	Lower	Plec	chr15	-	tss_body	76183686
322	cg33509542_TC21	0.00080827	-0.0513592 8	Lower	Maf1	chr15	+	tss_body	76352606
323	cg33526200_BC11	1.8699E-05	-0.0986584 5	Lower	Apol9b	chr15	+	tss_body	77732971
324	cg33534152_TC21	0.0008157	-0.0764577 8	Lower	Csf2rb	chr15	+	tss_200	78325909
325	cg33544878_BC21	0.00078297	-0.0535675	Lower	Gm17753	chr15	-	tss_body	79025791
326	cg33565841_BC21	0.00026963	-0.0710664 8	Lower	Cacna1i	chr15	+	tss_body	80359027
327	cg33569890_BC21	0.00060939	0.0655733 5	Higher	Fam83f	chr15	+	tss_body	80679382
328	cg33603153_BC21	0.00029472	0.0669598 9	Higher	Tspo	chr15	+	tss_1500	83562482
329	cg33613629_TC21	0.00037659	0.1021741 9	Higher	Parvb	chr15	+	tss_body	84298074

330	cg33615355_BC21	0.00063588	0.10003023	Higher	1810041L15Rik	chr15	-	tss_body	84430135
331	cg33622247_BC21	6.0491E-05	0.07196252	Higher	5031439G07Rik	chr15	-	tss_body	84947878
332	cg33624578_BC11	1.7517E-05	-0.05883723	Lower					85166555
333	cg33699257_BC21	0.00057817	-0.10101325	Lower	Cntn1	chr15	+	tss_body	92161317
334	cg33771431_TC21	0.00066637	0.05555922	Higher	Ccdc184	chr15	+	tss_body	98168486
335	cg33773280_TC21	0.0008519	-0.07298814	Lower	Olfr284	chr15	-	tss_1500	98341152
336	cg33788236_TC21	0.00076922	0.06187725	Higher	Mcrs1	chr15	-	tss_body	99244661
337	cg33792312_BC21	0.00033264	0.0606957	Higher	Faim2	chr15	-	tss_body	99502212
338	cg33792692_BC21	0.00037864	-0.05345383	Lower	Faim2	chr15	-	tss_body	99526304
339	cg33793380_BC21	0.00055246	-0.06322241	Lower	Gm34765	chr15	-	tss_body	99579000
340	cg33813510_BC21	0.00084271	-0.06577077	Lower	Scn8a	chr15	+	tss_body	100957004
341	cg33825595_BC21	0.00022427	-0.0518986	Lower	Krt76	chr15	-	tss_200	101892923
342	cg33827401_TC21	0.00068841	0.0511396	Higher					102034495
343	cg33839082_TC21	5.751E-05	0.07796254	Higher	Hoxc10	chr15	+	tss_body	102967557
344	cg33839964_TC21	0.00086795	-0.09488362	Lower	Hoxc6	chr15	+	tss_body	103010855
345	cg33841914_BC21	0.00087007	-0.05370348	Lower	chr15-103170129-103170423	chr15	*	SShore	103171915
346	cg33843815_BC21	0.00014811	0.07833252	Higher	Zfp385a	chr15	-	tss_body	103339787
347	cg33863432_TC21	0.00095761	0.08637084	Higher	Anks3	chr16	-	tss_body	4962961
348	cg33889648_BC21	0.00081403	-0.08325091	Lower		chr16	-	tss_body	8625286
349	cg33911457_BC21	1.1064E-05	-0.08228846	Lower	Zc3h7a	chr16	-	tss_body	11143662
350	cg33914002_TC21	0.00083495	0.06366747	Higher	Snx29	chr16	+	tss_body	11395238
351	cg33915221_TC21	0.00085331	0.07630678	Higher	Snx29	chr16	+	tss_body	11530518
352	cg33933288_TC21	0.00057325	-0.06769946	Lower	Ifitm7	chr16	-	tss_body	13985198
353	cg33934959_TC21	0.00039432	0.07681136	Higher	Myh11	chr16	-	tss_body	14195597
354	cg33954720_TC21	0.00014792	0.05397637	Higher	Tmem191c	chr16	+	tss_body	17276555

355	cg33961451_TC21	0.0009592	-0.05119609	Lower	Dgcr14	chr16	-	tss_body	17904985
356	cg33984681_BC21	0.0002542 8	-0.0674688	Lower	Vwa5b2	chr16	+	tss_body	20602091
357	cg33987033_BC11	0.0007172 5	0.0825915 3	Higher	Chrd	chr16	+	tss_body	20737406
358	cg34012933_TC21	0.0007006	0.0511078	Higher	St6gal1	chr16	+	tss_body	23302964
359	cg34014734_TC21	0.0002707 7	-0.0740263 6	Lower	Masp1	chr16	-	tss_body	23506831
360	cg34016591_BC21	0.0009592 3	-0.0649134 8	Lower		chr16	-	tss_200	23780198
361	cg34020807_BC21	0.0003485 5	0.0538497 8	Higher	Gm3181 4	chr16	-	tss_body	24232319
362	cg34022583_TC11	0.0002354 5	-0.0644363 9	Lower	Lpp	chr16	+	tss_body	24439298
363	cg34023222_TC21	0.0007389	-0.0508472 7	Lower	Lpp	chr16	+	tss_body	24506884
364	cg34079224_BC21	0.0003696 1	-0.0861167 4	Lower	Gm536	chr16	+	tss_1500	31617547
365	cg34085770_TC11	0.0007824 9	-0.0787843	Lower	Wdr53	chr16	+	tss_body	32250926
366	cg34111615_TC11	0.0008282 7	-0.0550067 7	Lower	Ropn1	chr16	+	tss_body	34669375
367	cg34117739_BC21	0.0009012 5	-0.0688105 2	Lower	Adcy5	chr16	+	tss_body	35229747
368	cg34121898_BC11	0.0006345 4	-0.1184068 6	Lower	Sema5b	chr16	+	tss_body	35584256
369	cg34127650_BC21	0.0007101 1	-0.0634417 7	Lower	Ccdc58	chr16	+	tss_body	36081441
370	cg34348737_TC21	0.0009533 5	-0.0561963 5	Lower	Robo1	chr16	+	tss_body	72088885
371	cg34366780_TC21	0.0004319	0.0687204 7	Higher	Robo2	chr16	-	tss_body	74739781
372	cg34376991_TC11	0.0007617 4	-0.0856371	Lower	Nrip1	chr16	-	tss_body	76323625
373	cg34395052_BC21	0.0007373 8	-0.0739363 5	Lower	D16Ertd472e	chr16	-	tss_body	78564204
374	cg34423201_BC21	0.0004000 4	-0.0595798 7	Lower	4930553E22Rik	chr16	+	tss_body	84371289
375	cg34426971_BC21	0.0007823 5	0.0548746 5	Higher	Jam2	chr16	+	tss_body	84824695
376	cg34449033_BC21	0.0005535 4	0.0760531 4	Higher	Gm3292 5	chr16	+	tss_body	87741583
377	cg34466747_TC21	0.0003282 7	-0.0714003	Lower	Tiam1	chr16	-	tss_body	89988843
378	cg34488706_BC21	0.0002280 8	-0.0844269 7	Lower	Mir6367	chr16	-	tss_body	91527458

379	cg34489109_BC21	0.00015986	-0.07177378	Lower	Ifngr2	chr16	+	tss_body	91549991
380	cg34491684_BC21	0.00096669	0.05242341	Higher	Gm10785	chr16	+	tss_body	91708744
381	cg34497648_BC21	0.00027064	-0.05661899	Lower	Gm41496	chr16	+	tss_body	92126190
382	cg34504287_TC21	3.186E-05	0.1143909	Higher	Runx1	chr16	-	tss_body	92604885
383	cg34515988_TC21	0.00086062	-0.05395712	Lower					93581408
384	cg34538045_TC11	0.00066577	-0.05994804	Lower	Erg	chr16	-	tss_body	95364849
385	cg34547676_BC21	0.00049164	0.06258299	Higher	Sh3bgr	chr16	+	tss_body	96206452
386	cg34568992_TC21	0.00070395	0.05977356	Higher					4008467
387	cg34574294_BC21	0.00061934	0.12107276	Higher		chr17	-	tss_body	4792692
388	cg34615997_BC21	0.00032089	0.05277276	Higher	Pde10a	chr17	+	tss_body	8558038
389	cg34619454_TC21	0.00017154	0.05949596	Higher	Pde10a	chr17	+	tss_body	8893511
390	cg34652578_BC21	0.00096054	-0.06322983	Lower	Igf2r	chr17	-	tss_body	12693157
391	cg34653101_BC21	0.00071518	-0.08885569	Lower	Igf2r	chr17	-	tss_body	12741390
392	cg34676680_TC21	0.000469	0.08339901	Higher	Psmb1	chr17	-	tss_body	15496420
393	cg34680398_BC21	0.00054767	0.05525736	Higher	Rgmb	chr17	-	tss_body	15831302
394	cg34721284_TC21	0.00078637	0.07700334	Higher	Ccdc64b	chr17	+	tss_body	23661245
395	cg34725718_TC21	0.00084866	0.05462961	Higher	Prss22	chr17	-	tss_body	23998490
396	cg34727537_BC21	0.0002588	-0.08923791	Lower	chr17-24169074-24169782	chr17	*	SShelf	24172515
397	cg34731205_BC21	0.00022788	-0.06722607	Lower	Dnase1l2	chr17	-	tss_1500	24444268
398	cg34735929_TC21	0.00019027	-0.08968561	Lower	Rpl3l	chr17	+	tss_body	24728413
399	cg34741624_BC21	0.00015237	-0.05988596	Lower	Ccdc154	chr17	+	tss_body	25171526
400	cg34756603_BC21	0.00094178	-0.05330471	Lower	Pdia2	chr17	-	tss_body	26197001
401	cg34764894_TC21	0.00072637	-0.09992996	Lower	Gm17382	chr17	-	tss_body	26861185
402	cg34764896_BC11	0.00076834	-0.05296731	Lower	Gm17382	chr17	-	tss_body	26861466

403	cg34769799_TC21	0.00042492	-0.11902681	Lower		chr17	+	tss_body	27139630
404	cg34778830_BC21	0.00084168	0.0777593	Higher	Pacsin1	chr17	+	tss_body	27679990
405	cg34788792_TC21	0.00022292	-0.09080314	Lower	Ppard	chr17	+	tss_body	28288004
406	cg34794653_BC21	0.00098526	0.0643436	Higher	Mapk14	chr17	+	tss_1500	28690896
407	cg34806032_BC21	9.565E-05	-0.11398236	Lower	Gm36199	chr17	+	tss_body	29457859
408	cg34815879_TC21	0.00088742	0.05022942	Higher	Zfand3	chr17	+	tss_body	30188234
409	cg34832519_TC21	0.00039726	0.07659121	Higher	Ndufv3	chr17	+	tss_body	31521773
410	cg34836850_BC21	0.0004817	0.0775509	Higher	Gm41564	chr17	+	tss_body	31837344
411	cg34852811_BC11	0.00038935	-0.11472151	Lower	Myo1f	chr17	+	tss_200	33555668
412	cg34853533_BC11	0.00029745	-0.1002297	Lower	Pram1	chr17	+	tss_body	33640268
413	cg34853641_TC21	0.000592	-0.05033375	Lower	Hnrnpm	chr17	-	tss_body	33650125
414	cg34866141_TC21	5.2475E-05	0.12266654	Higher	Pbx2	chr17	+	tss_body	34594354
415	cg34866493_TC21	0.00069913	0.14857583	Higher	Agpat1	chr17	+	tss_body	34607784
416	cg34871619_TC21	0.00042338	0.07978757	Higher	Ehmt2	chr17	+	tss_body	34910558
417	cg34875973_BC21	0.00074879	-0.05841338	Lower	Bag6	chr17	+	tss_body	35142028
418	cg34883732_TC21	0.00073475	-0.12971848	Lower	Ddr1	chr17	-	tss_body	35703721
419	cg34885962_BC21	0.00041901	-0.09157557	Lower	Ppp1r18	chr17	+	tss_body	35868741
420	cg34895085_TC21	0.00077279	-0.05544726	Lower	1700031A10Rik	chr17	+	tss_body	36927852
421	cg34912755_TC21	0.0002039	0.09389406	Higher		chr17	+	tss_1500	40447966
422	cg34916589_TC11	0.00050625	0.09311318	Higher					41161504
423	cg34952529_TC21	0.00060552	-0.06024463	Lower	Slc29a1	chr17	-	tss_body	45587296
424	cg34957049_TC11	0.0003434	-0.10311798	Lower	Gm41584	chr17	+	tss_body	45886386
425	cg34977949_BC21	0.00046719	-0.09126211	Lower	Trerf1	chr17	+	tss_body	47226473
426	cg34980876_BC11	0.00083492	-0.07642892	Lower	1700001C19Rik	chr17	-	tss_body	47421756
427	cg34993704_BC21	0.00079202	-0.05751648	Lower	Nfya	chr17	-	tss_body	48399014

428	cg35047742_BC21	4.8597E-05	0.06936839	Higher	Zfp119b	chr17	-	tss_body	55945869
429	cg35050226_BC21	5.0276E-05	-0.05852152	Lower	Lrg1	chr17	-	tss_body	56119833
430	cg35053509_TC21	0.00089685	-0.09743294	Lower	Uhrf1	chr17	+	tss_body	56315417
431	cg35071963_TC21	0.00050349	0.09517283	Higher	Cntnap5c	chr17	+	tss_body	58334790
432	cg35159535_TC21	0.00021004	0.11954705	Higher	Epb41l3	chr17	+	tss_body	69255801
433	cg35195063_BC21	0.00075445	-0.05668453	Lower					72967616
434	cg35204299_TC21	8.1579E-06	0.0777527	Higher	Srd5a2	chr17	-	tss_body	74028592
435	cg35209748_TC21	0.00039982	0.05838292	Higher	Birc6	chr17	+	tss_body	74629416
436	cg35275405_TC21	0.00070165	0.08308994	Higher					83085323
437	cg35293565_BC11	0.00033716	-0.0706416	Lower	Plekhh2	chr17	+	tss_body	84552572
438	cg35294702_BC21	0.00010472	0.08726225	Higher	Dync2li1	chr17	+	tss_body	84636645
439	cg35300000_TC21	2.9333E-05	0.0525368	Higher	Slc3a1	chr17	+	tss_body	85059801
440	cg35300001_TC21	0.00033714	0.06493313	Higher	Slc3a1	chr17	+	tss_body	85059807
441	cg35313785_BC21	0.00065321	-0.1148862	Lower	Prkce	chr17	+	tss_body	86170179
442	cg35321960_BC21	0.00087693	-0.06948522	Lower	Epas1	chr17	+	tss_body	86785742
443	cg35322027_BC21	0.00049851	-0.05671344	Lower	Epas1	chr17	+	tss_body	86789812
444	cg35473653_BC21	0.00091757	0.08542606	Higher					17390775
445	cg35492750_TC21	0.00021015	0.05405406	Higher	Mep1b	chr18	+	tss_body	21072383
446	cg35518777_BC21	0.00074185	0.05720717	Higher	Fhod3	chr18	+	tss_body	24713799
447	cg35537377_TC21	0.00056512	-0.06629233	Lower					27987620
448	cg35557169_BC11	0.00097503	0.07161969	Higher	Ammecr1l	chr18	+	tss_body	31761125
449	cg35560821_TC21	0.00059133	0.05513132	Higher		chr18	-	tss_body	32112167
450	cg35585600_BC21	0.00029157	0.06166536	Higher	Reep2	chr18	+	tss_200	34840403
451	cg35588334_BC21	0.00011331	0.07094882	Higher	Gm3587	chr18	-	tss_body	35087085
452	cg35596666_BC21	0.00063108	-0.05042929	Lower		chr18	+	tss_body	35913173
453	cg35603898_BC21	0.00080309	0.05130858	Higher	Slc4a9	chr18	+	tss_body	36529202
454	cg35619348_BC21	0.00092075	-0.08570494	Lower	Arap3	chr18	-	tss_body	37974447
455	cg35642335_TC21	6.7708E-05	0.08591374	Higher		chr18	+	tss_body	40540706

456	cg35671415_BC21	0.00049861	0.06467988	Higher	Mcc	chr18	-	tss_1500	44812902
457	cg35688618_BC21	8.2623E-06	0.08454938	Higher	Q3UTM6	chr18	+	tss_body	47098379
458	cg35761886_BC21	0.00096029	0.05966352	Higher	Megf10	chr18	+	tss_1500	57132673
459	cg35794292_TC21	0.00021125	0.0584872	Higher	Cdx1	chr18	-	tss_body	61036114
460	cg35797139_BC11	0.00077252	-0.09197552	Lower	Pde6a	chr18	+	tss_body	61245579
461	cg35803669_TC11	6.3531E-05	-0.07193002	Lower	Afap1l1	chr18	-	tss_body	61759272
462	cg35812257_BC21	0.00022896	-0.05308176	Lower	Spink13	chr18	-	tss_body	62719905
463	cg35819557_TC21	0.00089342	0.06554845	Higher					63493343
464	cg35825367_TC21	0.00057473	0.10347298	Higher	St8sia3os	chr18	-	tss_body	64171569
465	cg35843824_TC21	0.00014573	-0.07468806	Lower					65783388
466	cg35851619_BC21	0.00056938	-0.06103775	Lower	Gm9926	chr18	+	tss_body	66509648
467	cg35898565_TC21	0.00023047	0.09033806	Higher	Dcc	chr18	-	tss_body	71663371
468	cg35911900_TC21	0.00056119	-0.07084611	Lower	Gm32548	chr18	+	tss_1500	73711026
469	cg35930267_BC21	0.00055672	0.06203174	Higher	Dym	chr18	+	tss_body	75187319
470	cg35939934_TC21	0.00043619	0.05749148	Higher	Zbtb7c	chr18	+	tss_body	75898338
471	cg35956477_BC21	0.00047036	0.06517078	Higher	Loxhd1	chr18	+	tss_body	77359091
472	cg35958039_TC21	0.00074964	-0.05073385	Lower	Rnf165	chr18	-	tss_body	77484295
473	cg35981508_TC21	0.00034469	0.09083988	Higher	Pard6g	chr18	+	tss_body	80098762
474	cg35982740_TC21	1.2888E-05	0.08274328	Higher	LOC105246506	chr18	+	tss_body	80187211
475	cg36001667_TC21	0.00017581	0.05868948	Higher		chr18	+	tss_body	81708561
476	cg36009618_TC21	0.00073849	0.05414356	Higher	Mbp	chr18	+	tss_body	82549792
477	cg36070590_BC21	0.00067	-0.10220893	Lower		chr19	-	tss_body	3837711
478	cg36075296_TC21	0.00083279	-0.06324908	Lower	Carns1	chr19	-	tss_body	4170093
479	cg36089794_TC21	0.00028644	0.11368871	Higher	Gal3st3	chr19	+	tss_body	5298345
480	cg36111411_BC21	0.00087359	0.06147729	Higher	Slc22a12	chr19	-	tss_200	6543239
481	cg36114862_TC21	4.6693E-05	-0.07830859	Lower	Kcnk4	chr19	-	tss_body	6932999

482	cg36143712_BC21	0.00084372	-0.08774616	Lower	Fads1	chr19	+	tss_body	10188282
483	cg36150060_BC21	0.00091846	-0.073962	Lower	Vps37c	chr19	+	tss_body	10692557
484	cg36166963_TC21	0.00013808	0.09127543	Higher	Olfr1462	chr19	+	tss_body	13190679
485	cg36173320_TC21	0.0008865	-0.05715045	Lower	Tle4	chr19	-	tss_body	14481224
486	cg36285470_TC21	0.00059494	0.08706999	Higher	Glis3	chr19	-	tss_body	28436698
487	cg36290643_BC21	0.00098304	0.05448292	Higher	Slc1a1	chr19	+	tss_body	28902356
488	cg36293390_BC21	0.00063269	-0.07673336	Lower	Rcl1	chr19	+	tss_body	29125245
489	cg36295952_TC21	0.00019659	0.08053073	Higher	Plgrkt	chr19	-	tss_body	29361275
490	cg36305203_BC21	0.00091379	-0.06043678	Lower					30261064
491	cg36392250_TC21	0.00087579	-0.0609051	Lower	Opalin	chr19	-	tss_200	41077307
492	cg36401440_BC21	5.8732E-05	-0.08034536	Lower	chr19-41829931-41830950	chr19	*	SShelf	41833238
493	cg36408699_BC21	0.00079679	0.05773041	Higher	Crtac1	chr19	-	tss_body	42345298
494	cg36409100_TC21	0.00094659	0.05726912	Higher	Crtac1	chr19	-	tss_body	42379142
495	cg36426137_BC21	7.8844E-05	-0.09686933	Lower	Dnmbp	chr19	-	tss_body	43920544
496	cg36440270_BC21	0.00083355	0.0656714	Higher	Sema4g	chr19	+	tss_body	44989661
497	cg36447448_TC21	0.00072212	-0.08111642	Lower	Btrc	chr19	+	tss_body	45476420
498	cg36469344_BC21	0.00096982	-0.05912826	Lower	Taf5	chr19	+	tss_body	47075032
499	cg36484480_TC21	0.00062583	-0.08783267	Lower		chr19	+	tss_200	48117337
500	cg36489045_BC21	0.00066965	-0.08717453	Lower	Sorcs3	chr19	+	tss_body	48650066
501	cg36520101_BC21	0.00055494	0.09825968	Higher					53413730
502	cg36521113_BC21	0.00069298	0.08545531	Higher		chr19	+	tss_1500	53482041
503	cg36557907_TC21	0.00022528	0.05516091	Higher					56733993
504	cg36564282_BC21	0.00039083	0.05480626	Higher	Ablim1	chr19	-	tss_body	57195758
505	cg36579282_BC21	0.00078571	-0.08001439	Lower	Gfra1	chr19	-	tss_body	58420135
506	cg36581263_TC11	0.000725	-0.07833743	Lower	1810007D17Rik	chr19	+	tss_1500	58606060

507	cg36670076_BC21	0.00072387	-0.06063878	Lower					14486037
508	cg36811274_TC11	0.00077464	-0.11660241	Lower	Tmem131	chr1	-	tss_body	36814626
509	cg36811324_TC11	0.00020633	-0.06095419	Lower	Tmem131	chr1	-	tss_body	36818668
510	cg36814224_BC21	0.00082488	-0.06344513	Lower	Vwa3b	chr1	+	tss_body	37106627
511	cg36816058_BC21	0.00048589	-0.11569475	Lower					37272294
512	cg36822807_TC21	0.00058691	0.07654714	Higher	Mitd1	chr1	-	tss_body	37881900
513	cg36845321_TC21	2.2305E-05	0.07737608	Higher	1700066B17Rik	chr1	-	tss_body	39845728
514	cg36873682_TC11	0.00042251	0.05494351	Higher	Fhl2	chr1	-	tss_body	43197209
515	cg36915655_BC11	9.1035E-05	0.05225822	Higher					51499071
516	cg36925712_TC21	0.00013605	0.0925439	Higher	Mfsd6	chr1	-	tss_body	52709019
517	cg36954336_TC21	0.00020661	0.06017949	Higher	Satb2	chr1	-	tss_body	56910070
518	cg36954727_BC21	0.00047025	-0.11941135	Lower	Satb2	chr1	-	tss_body	56956032
519	cg36990489_BC11	0.00054795	-0.05748027	Lower					61140122
520	cg37005079_TC21	0.00080719	-0.09861591	Lower	Ndufs1	chr1	-	tss_body	63162288
521	cg37005639_BC21	0.0009628	0.08730562	Higher	Gpr1	chr1	-	tss_body	63214527
522	cg37006150_BC21	0.00047435	-0.0738299	Lower	Zdbf2	chr1	+	tss_body	63261553
523	cg37007700_BC21	0.00079952	-0.07816051	Lower					63441406
524	cg37022794_TC21	0.00057497	0.0601045	Higher	Pth2r	chr1	+	tss_body	65282017
525	cg37039563_BC21	0.00060529	-0.08173779	Lower	Erbb4	chr1	-	tss_body	68245222
526	cg37085060_BC21	0.00057093	-0.06208253	Lower	Gpbar1	chr1	+	tss_body	74278680
527	cg37095455_TC21	0.00034614	-0.0620567	Lower	Ankzf1	chr1	+	tss_body	75196172
528	cg37095964_BC21	0.00093484	0.08165199	Higher	A630095N17Rik	chr1	-	tss_body	75227469
529	cg37096614_BC21	0.00089937	-0.10605764	Lower	Ptprn	chr1	-	tss_1500	75264768
530	cg37099089_TC21	0.00012484	0.06627519	Higher	Speg	chr1	+	tss_body	75423439
531	cg37120814_TC21	0.00030344	0.05100167	Higher	Pax3	chr1	-	tss_body	78189752
532	cg37127203_TC21	0.00045906	0.05929663	Higher	Gm29536	chr1	-	tss_body	78821242

533	cg37133267_BC11	0.00014879	-0.10291448	Lower	Mrpl44	chr1	+	tss_body	79778107
534	cg37147442_BC21	8.2563E-05	0.06244883	Higher					82182797
535	cg37169010_TC21	0.00098257	-0.06073057	Lower	A530040E14Rik	chr1	+	tss_body	85270111
536	cg37178314_BC21	0.00033487	0.06358399	Higher					86377025
537	cg37194729_BC21	0.00018387	-0.09948427	Lower	Ugt1a10	chr1	+	tss_body	88205798
538	cg37195790_TC11	0.00015836	0.06585775	Higher		chr1	+	tss_body	88302820
539	cg37205411_BC21	0.0001744	-0.05138695	Lower					89281765
540	cg37206315_BC21	0.00051663	-0.07451286	Lower	C030007H22Rik	chr1	-	tss_body	89394668
541	cg37210497_TC21	0.00083786	-0.05527644	Lower	Agap1	chr1	+	tss_body	89702725
542	cg37229439_TC21	0.00018492	-0.05222015	Lower	Fam132b	chr1	+	tss_body	91370913
543	cg37241600_BC21	0.00063874	-0.0545822	Lower	Q8VET3	chr1	+	tss_body	92590931
544	cg37247727_TC11	0.00010856	-0.08080778	Lower	Gm36472	chr1	+	tss_body	93115714
545	cg37250572_BC21	0.00062482	0.07063559	Higher	Ppp1r7	chr1	+	tss_body	93362008
546	cg37252925_BC21	0.00062028	0.06238655	Higher	Farp2	chr1	+	tss_body	93620534
547	cg37390534_TC21	0.00060056	0.07035956	Higher	Gm29345	chr1	+	tss_body	120842465
548	cg37397597_BC21	0.00024288	-0.0678498	Lower					121709430
549	cg37414444_TC21	0.0009586	0.05891193	Higher					125489113
550	cg37424015_TC21	0.00052318	0.08614841	Higher	Nckap5	chr1	-	tss_body	126806237
551	cg37429968_TC11	0.0006046	-0.087927	Lower	Tmem163	chr1	-	tss_body	127508568
552	cg37456185_BC11	0.00079454	-0.08606767	Lower	Rassf5	chr1	-	tss_body	131200084
553	cg37485318_BC21	0.00028815	0.1173079	Higher					133817690
554	cg37485452_TC21	0.00080818	0.09148486	Higher					133832041
555	cg37489661_TC21	0.00056878	-0.05229835	Lower	Chil1	chr1	+	tss_body	134182892
556	cg37490856_BC21	0.00061421	0.11971644	Higher	Gm32221	chr1	-	tss_1500	134277268
557	cg37504834_TC21	0.00062116	-0.05846821	Lower	Nav1	chr1	-	tss_body	135477797
558	cg37505008_BC21	0.00039751	0.07981576	Higher	Nav1	chr1	-	tss_body	135491006

559	cg37507896_TC21	0.00088155	-0.06020899	Lower	Q4FJX4	chr1	+	tss_200	135719882
560	cg37509828_TC21	0.00015651	0.05591905	Higher					135858719
561	cg37512239_TC21	0.00099926	0.0557565	Higher	Cacna1s	chr1	+	tss_body	136065309
562	cg37514747_TC21	0.00012405	-0.07392547	Lower		chr1	+	tss_body	136247708
563	cg37544155_BC21	0.00092718	-0.08307135	Lower	Cfhr2	chr1	-	tss_body	139839713
564	cg37584869_TC21	9.8983E-06	-0.06022963	Lower		chr1	+	tss_body	149173078
565	cg37618222_TC21	0.00083439	0.07233676	Higher	Lamc2	chr1	-	tss_body	153130608
566	cg37640795_TC21	0.00091559	0.07022359	Higher	Gm5532	chr1	-	tss_200	155527130
567	cg37648598_TC11	0.00018529	-0.06717484	Lower	Nphs2	chr1	+	tss_200	156310521
568	cg37660309_BC21	0.00072649	0.07211289	Higher	Sec16b	chr1	+	tss_body	157533071
569	cg37660582_TC21	0.00040327	0.06966356	Higher	Sec16b	chr1	+	tss_body	157556566
570	cg37674812_BC21	0.00087991	-0.06448496	Lower	Tnr	chr1	+	tss_body	159773731
571	cg37684798_BC21	1.0983E-05	0.06135845	Higher		chr1	+	tss_body	161181231
572	cg37713951_BC11	0.00033055	0.08090364	Higher	Gm32652	chr1	-	tss_body	164863120
573	cg37739279_TC21	0.00045427	0.05146744	Higher	Mgst3	chr1	-	tss_body	167382277
574	cg37758475_BC21	0.00065554	0.09303206	Higher	Rgs4	chr1	-	tss_body	169742053
575	cg37773918_TC21	0.0007397	-0.06595321	Lower	Ndufs2	chr1	-	tss_body	171238023
576	cg37779523_BC21	0.00069739	-0.11844369	Lower	Cd48	chr1	+	tss_body	171699221
577	cg37827223_BC21	0.00016433	-0.07113793	Lower	Q9D291	chr1	+	tss_body	178256376
578	cg37847991_BC21	0.00029681	-0.08200526	Lower	Psen2	chr1	-	tss_body	180245701
579	cg37856509_BC21	0.00012455	0.08686586	Higher	Lefty2	chr1	+	tss_body	180898098
580	cg37858774_TC21	0.00088349	0.08716981	Higher	Nvl	chr1	-	tss_body	181091168
581	cg37897883_BC21	0.00029866	0.09000945	Higher	Marc2	chr1	-	tss_body	184822520
582	cg37914253_TC11	0.00035783	-0.08792533	Lower					186508472
583	cg37938874_TC21	0.00059072	0.06875048	Higher	Kctd3	chr1	-	tss_1500	189008101
584	cg37947415_TC21	0.00029211	0.05739166	Higher	Ptpn14	chr1	+	tss_body	189812963

585	cg37959127_TC21	0.00091492	0.05159411	Higher	Gm3973 8	chr1	+	tss_body	190765537
586	cg37964419_BC21	0.00023773	-0.07854199	Lower	Fam71a	chr1	-	tss_body	191164735
587	cg37996562_BC21	0.00084517	-0.05404821	Lower	Fam171a 1	chr2	+	tss_body	3196628
588	cg38000334_BC21	0.00066265	0.06730421	Higher	LOC1081 68726	chr2	+	tss_body	3613723
589	cg38005998_TC21	0.00091095	0.07763873	Higher	Frmd4a	chr2	+	tss_body	4340008
590	cg38011861_BC21	0.00015409	0.11433649	Higher					4872488
591	cg38055908_TC21	4.544E-05	0.07236118	Higher	Sfmbt2	chr2	+	tss_body	10465976
592	cg38103602_TC21	9.8411E-05	0.07631472	Higher	Mllt10	chr2	+	tss_body	18055240
593	cg38110621_BC21	0.00073691	-0.08767154	Lower	Pip4k2a	chr2	-	tss_body	18856637
594	cg38123863_TC11	0.00080579	-0.07528022	Lower	Etl4	chr2	+	tss_body	20722454
595	cg38158621_BC21	0.00047957	0.05121108	Higher	Ccdc183	chr2	-	tss_body	25611385
596	cg38164086_BC21	0.00035751	-0.06503112	Lower	C330006 A16Rik	chr2	-	tss_body	26138639
597	cg38166398_TC21	0.00091488	0.09055215	Higher	Gpsm1	chr2	+	tss_body	26319830
598	cg38168562_TC21	0.00036797	0.10778782	Higher	Notch1	chr2	-	tss_body	26475012
599	cg38170111_BC21	0.00075481	-0.08865522	Lower	Agpat2	chr2	-	tss_body	26600184
600	cg38170642_TC21	0.00019121	0.06870954	Higher	Fam69b	chr2	+	tss_body	26635662
601	cg38173254_BC21	0.00097059	0.07889833	Higher	Stkld1	chr2	+	tss_body	26951737
602	cg38187613_BC21	0.00061333	0.10018129	Higher	Olfm1	chr2	+	tss_body	28203190
603	cg38192391_TC21	0.00032249	-0.05722018	Lower					28597968
604	cg38208394_BC21	0.0006852	-0.12880704	Lower	Gle1	chr2	+	tss_1500	29935012
605	cg38221399_BC11	8.3389E-05	-0.13405503	Lower	Prrx2	chr2	+	tss_1500	30844821
606	cg38221877_TC11	0.00013381	-0.18503497	Lower	Prrx2	chr2	+	tss_body	30874173
607	cg38240599_BC21	8.6456E-05	-0.0755544	Lower	Prrc2b	chr2	+	tss_body	32213998
608	cg38241212_BC21	0.00021026	-0.05532513	Lower	Pomt1	chr2	+	tss_body	32248378
609	cg38242573_BC21	0.00046617	-0.06197845	Lower	Dnm1	chr2	-	tss_body	32336337
610	cg38254762_TC21	0.00020838	0.08741503	Higher	Ralgps1	chr2	-	tss_body	33180611

611	cg38259616_TC21	0.00034394	-0.05900087	Lower	Lmx1b	chr2	-	tss_body	33605820
612	cg38262675_TC21	0.0004318	-0.07735177	Lower	Mvb12b	chr2	-	tss_body	33801524
613	cg38303946_TC21	0.0008291	-0.11509302	Lower	Adgrd2-ps	chr2	+	tss_body	38672230
614	cg38320638_TC21	0.00016472	-0.08942174	Lower	Lrp1b	chr2	-	tss_body	42125007
615	cg38337138_TC21	0.0006699	-0.05468341	Lower	Zeb2	chr2	-	tss_body	45055268
616	cg38358436_BC21	0.00082093	-0.05459839	Lower	Mbd5	chr2	+	tss_body	49246192
617	cg38415978_BC21	0.00034691	0.05170776	Higher	Gm33594	chr2	-	tss_body	57997661
618	cg38425630_BC21	0.00033256	-0.15456997	Lower	Pkp4	chr2	+	tss_body	59187103
619	cg38426698_BC11	0.00098441	-0.05008875	Lower	Pkp4	chr2	+	tss_body	59293750
620	cg38446179_TC21	0.00048338	-0.07674871	Lower					61100951
621	cg38466161_TC21	0.00074516	0.07556145	Higher	Gm13575	chr2	-	tss_body	64390045
622	cg38469235_BC21	0.00069588	-0.0852489	Lower	Grb14	chr2	-	tss_body	64917309
623	cg38480751_BC21	0.00043676	-0.07344862	Lower	Scn1a	chr2	-	tss_body	66272966
624	cg38513673_BC21	0.00035861	0.13859141	Higher	Gad1os	chr2	-	tss_body	70499204
625	cg38527248_TC21	0.0009474	-0.05376583	Lower	Gm17250	chr2	-	tss_body	71735134
626	cg38528255_TC21	0.00085118	-0.05441799	Lower	Itga6	chr2	+	tss_body	71811867
627	cg38536531_TC21	0.00021257	-0.12077513	Lower					72530141
628	cg38542663_TC21	3.745E-05	-0.0812871	Lower	Ola1	chr2	-	tss_body	73131737
629	cg38565563_BC21	0.00046325	-0.08704728	Lower	LOC102635707	chr2	+	tss_body	75315660
630	cg38570217_TC21	0.00064193	0.07443008	Higher					75758465
631	cg38588097_BC11	0.00020592	-0.05636656	Lower					77401611
632	cg38623081_TC11	0.00022999	-0.08230307	Lower	Fsip2	chr2	+	tss_body	82943746
633	cg38634932_BC21	0.00035525	-0.08007884	Lower	Clp1	chr2	-	tss_body	84724042

634	cg38636040_TC21	0.00026556	0.0876525 3	Higher	Smtnl1	chr2	-	tss_body	84816849
635	cg38653068_TC21	0.0009998 1	-0.0679671 8	Lower	Olfr1170	chr2	-	tss_1500	88225919
636	cg38659815_BC21	0.0005158 5	0.0739764 4	Higher	Olfr1258	chr2	+	tss_body	89926861
637	cg38660271_BC21	0.0002391 3	-0.0518372 2	Lower	Olfr140	chr2	-	tss_body	90052082
638	cg38662908_TC21	0.0008380 4	0.0533858 4	Higher	Ptprj	chr2	-	tss_body	90538645
639	cg38669508_TC21	0.0006431 3	-0.0545743 4	Lower	Madd	chr2	-	tss_body	91154508
640	cg38690031_BC21	0.0005120 3	0.0613907 6	Higher		chr2	-	tss_1500	93099711
641	cg38692895_BC21	0.0008327 9	0.0703462 5	Higher	Tspan18	chr2	-	tss_1500	93334819
642	cg38742838_TC11	0.0002062 6	0.0557369 7	Higher	Trim44	chr2	-	tss_body	102400539
643	cg38769262_TC21	0.0007077 9	0.0622006 1	Higher	Them7	chr2	+	tss_body	105311607
644	cg38857624_BC21	0.0004505 4	-0.0598457 4	Lower	Disp2	chr2	+	tss_body	118780212
645	cg38884011_BC21	0.0007911 2	0.0510404 1	Higher	Strc	chr2	-	tss_body	121365822
646	cg38893058_TC21	0.0001741 1	-0.0844357 3	Lower	Duox2	chr2	-	tss_body	122298207
647	cg38916373_TC21	0.0002830 5	0.0613168 1	Higher	Shc4	chr2	-	tss_body	125666275
648	cg38931537_TC21	0.0007863 5	0.0531853 8	Higher	Adra2b	chr2	+	tss_body	127364666
649	cg38946578_TC21	0.0008437 6	0.0590496 7	Higher	Fbln7	chr2	+	tss_body	128892934
650	cg38955662_BC21	0.0005262	0.0980518 4	Higher					129833194
651	cg38967357_TC21	0.0004922	0.0695414 3	Higher	Gfra4	chr2	-	tss_body	131040479
652	cg38970814_TC11	0.0001732 4	0.0832283 8	Higher	Rnf24	chr2	-	tss_body	131322772
653	cg38975305_TC21	0.0009820 6	-0.0528386 1	Lower	5330413P13Rik	chr2	-	tss_200	131847772
654	cg38975426_TC21	5.843E-05	-0.0531225 9	Lower	Erv3	chr2	-	tss_body	131859824
655	cg38980504_TC11	0.0004742 8	0.0863845	Higher	A2AMQ7	chr2	-	tss_body	132340629
656	cg38982260_BC21	0.0007306 1	0.0537036	Higher	Gpcpd1	chr2	-	tss_body	132533767
657	cg39000113_BC11	0.0003823 5	-0.0635251 2	Lower	Plcb1	chr2	+	tss_body	135297869
658	cg39013926_BC21	0.0003163 4	-0.0960017 8	Lower					137244025
659	cg39014403_TC11	0.0001677 5	-0.0982674 4	Lower					137331851
660	cg39085018_TC21	0.0003501 4	0.1067949 3	Higher	Gm3552 8	chr2	+	tss_body	147878561

661	cg39107739_TC11	6.4265E-05	-0.1324882	Lower	Fkbp1a	chr2	+	tss_body	151544018
662	cg39109767_BC21	7.1936E-05	-0.0710972 5	Lower	Psmf1	chr2	-	tss_1500	151744642
663	cg39118685_BC11	0.0007874 7	-0.0919148 4	Lower	Defb22	chr2	-	tss_body	152485930
664	cg39120434_BC21	0.0009674 8	0.0587700 2	Higher	chr2-152634450-152634683	chr2	*	SShore	152636183
665	cg39121127_BC21	0.0003174	-0.0534844 3	Lower	H13	chr2	+	tss_body	152686810
666	cg39121262_TC21	1.9628E-06	0.1204826 6	Higher	H13	chr2	+	tss_body	152693734
667	cg39131823_TC21	0.0008659 1	0.0675375 4	Higher					153575964
668	cg39156884_TC21	0.0008045 5	0.0603674 8	Higher	6430550D23Rik	chr2	-	tss_body	156003790
669	cg39177345_TC21	0.0007706 4	0.083211	Higher					157553081
670	cg39185599_TC21	0.0009000 1	-0.1145935 8	Lower					158243284
671	cg39189725_BC11	0.0009761	0.0538903 6	Higher	Slc32a1	chr2	+	tss_body	158614212
672	cg39190160_BC21	0.0003501 7	-0.0844460 7	Lower	Actr5	chr2	+	tss_body	158633624
673	cg39221425_TC21	0.0006568 5	-0.0531048 9	Lower	Ptprt	chr2	-	tss_body	162546202
674	cg39222744_BC21	0.0009896 3	-0.0549993 2	Lower	9430021M05Rik	chr2	+	tss_body	162672450
675	cg39226025_BC21	0.0009954 2	-0.0554017 4	Lower					162977966
676	cg39243174_BC21	0.0002931 7	-0.0727394 4	Lower					164281966
677	cg39247696_BC21	0.0005966 8	-0.0510024 8	Lower	Wfdc8	chr2	-	tss_body	164612562
678	cg39255560_BC21	0.0002826 3	-0.1019415 6	Lower	Cdh22	chr2	-	tss_body	165114822
679	cg39260508_BC21	0.0006418 1	-0.0558521 6	Lower	Ocstamp	chr2	-	tss_200	165400551
680	cg39266625_TC21	0.0003208 7	0.0880990 9	Higher	Zmynd8	chr2	-	tss_body	165831987
681	cg39287380_TC21	0.0001727 6	0.0711219 3	Higher					167262377
682	cg39291794_TC21	0.0003868 7	-0.1324744 6	Lower	Gm11476	chr2	+	tss_body	167570593
683	cg39295260_BC21	0.0001626	-0.0769923 4	Lower	Gm32287	chr2	-	tss_body	167775388

684	cg39302921_TC21	9.4537E-05	-0.0888846	Lower	Kcng1	chr2	-	tss_body	168268528
685	cg39307302_TC21	0.0007509	-0.0548076	Lower	Nfatc2	chr2	-	tss_body	168563529
686	cg39368014_BC21	2.6571E-05	-0.0924137	Lower	Gm40011	chr2	+	tss_body	173119139
687	cg39371924_BC21	0.0006748	-0.0750700	Lower					173382400
688	cg39374354_BC21	0.0009230	0.0669833	Higher	Ankrd60	chr2	-	tss_body	173572626
689	cg39382183_TC11	0.0001145	-0.1209238	Lower	Nespas	chr2	-	tss_body	174283967
690	cg39382200_BC21	0.0008074	-0.0882205	Lower	Nespas	chr2	-	tss_body	174284343
691	cg39382521_BC21	0.0005502	-0.0875831	Lower	Gnas	chr2	+	tss_body	174296217
692	cg39382642_TC21	1.3704E-06	-0.1263014	Lower	Gnas	chr2	+	tss_body	174298821
693	cg39382778_TC21	0.0002589	-0.0742849	Lower	Gnas	chr2	+	tss_body	174300643
694	cg39401893_BC21	0.0001575	-0.0840621	Lower					178506328
695	cg39415145_BC21	1.7746E-05	0.0526298	Higher	Cdh4	chr2	+	tss_body	179776150
696	cg39433417_BC21	0.0003934	-0.0693983	Lower	Helz2	chr2	-	tss_body	181237930
697	cg39435858_BC21	0.0006908	-0.0643901	Lower	Zbtb46	chr2	-	tss_1500	181493733
698	cg39437664_BC21	0.0002589	-0.0557052	Lower	Sox18	chr2	-	tss_body	181670397
699	cg39446934_BC21	0.0002813	0.1083407	Higher		chr3	+	tss_1500	4337955
700	cg39468674_TC21	0.0003659	0.1053723	Higher	Gm32561	chr3	-	tss_body	8685858
701	cg39485085_TC21	0.0002098	-0.0601545	Lower		chr3	+	tss_body	10232243
702	cg39535450_BC21	0.0003067	-0.0636243	Lower	Hltf	chr3	+	tss_body	20081467
703	cg39583516_BC11	0.0001217	0.0541779	Higher	Tnik	chr3	+	tss_1500	28262562
704	cg39643095_TC21	0.0009850	-0.0702286	Lower	Gm6639	chr3	-	tss_body	35636668
705	cg39651828_TC21	0.0005239	-0.0605927	Lower	Trpc3	chr3	-	tss_body	36671154
706	cg39812677_TC21	0.0003358	-0.0543539	Lower	Mbnl1	chr3	+	tss_body	60602957

707	cg39861363_BC21	0.00088648	-0.07886495	Lower	Gm21949	chr3	+	tss_body	68584356
708	cg39896744_BC21	0.00096036	-0.05946727	Lower	Zbbx	chr3	-	tss_body	75053247
709	cg39907390_TC21	0.00058856	-0.07182825	Lower					77378595
710	cg39938800_BC21	0.0001596	-0.09887568	Lower					82723756
711	cg39952464_TC21	0.00025844	0.05647916	Higher	Trim2	chr3	-	tss_body	84235575
712	cg39952466_TC21	0.00099448	0.0629961	Higher	Trim2	chr3	-	tss_body	84235646
713	cg39953456_TC21	0.00051703	0.08975172	Higher					84315718
714	cg39977731_TC21	0.00042508	0.0995577	Higher		chr3	+	tss_body	87054517
715	cg39988400_BC21	0.00024875	-0.09370205	Lower	Hapln2	chr3	-	tss_body	88025170
716	cg39992198_TC21	0.00036926	0.08696863	Higher	Cct3	chr3	+	tss_body	88320891
717	cg40001626_TC21	0.00012293	-0.05238619	Lower	Fdps	chr3	-	tss_body	89096102
718	cg40064103_BC21	0.00097716	-0.058371	Lower	BC107364	chr3	-	tss_body	96436664
719	cg40085027_TC21	0.0001121	-0.06182315	Lower	Hmgcs2	chr3	+	tss_body	98297074
720	cg40107875_BC21	0.00092738	-0.0714219	Lower		chr3	-	tss_200	101307197
721	cg40112836_TC21	0.00029688	-0.05154333	Lower					101713031
722	cg40120933_TC21	0.00049825	-0.05128321	Lower	Ngf	chr3	+	tss_body	102520119
723	cg40125839_BC21	0.00035993	-0.05559989	Lower	Dennd2c	chr3	+	tss_body	103124092
724	cg40149099_TC21	0.00028186	-0.05074228	Lower	Ddx20	chr3	-	tss_body	105681042
725	cg40164595_TC21	0.00059154	-0.06114354	Lower	Gm40121	chr3	+	tss_body	107812198
726	cg40166989_TC21	1.857E-05	0.06113185	Higher	Gstm4	chr3	-	tss_200	108045140
727	cg40171150_TC21	0.00017124	0.08403524	Higher	Mybphl	chr3	+	tss_1500	108364632
728	cg40177964_BC21	0.00078707	-0.09922911	Lower	Henmt1	chr3	+	tss_body	108939925
729	cg40252961_BC21	0.00091896	-0.17974637	Lower	Slc44a3	chr3	-	tss_body	121467305
730	cg40271026_TC21	4.3258E-06	0.11312033	Higher	Synpo2	chr3	-	tss_body	123112858

731	cg40309213_TC21	0.00050805	-0.09461915	Lower					12852065 8
732	cg40343145_BC21	0.0008513	0.08598596	Higher					131719460
733	cg40365042_TC21	0.0004958 3	-0.07045943	Lower	Tacr3	chr3	+	tss_body	134906911
734	cg40398211_BC21	0.0003526 4	0.11203851	Higher	Tspan5	chr3	+	tss_body	138782819
735	cg40398212_TC21	0.0006714 2	0.09582531	Higher	Tspan5	chr3	+	tss_body	138782875
736	cg40566210_TC21	0.0005753 7	0.11347148	Higher	Gm33057	chr4	+	tss_body	4538769
737	cg40577706_BC21	0.0007096 2	-0.09139298	Lower		chr4	+	tss_body	6539698
738	cg40640579_BC21	3.5636E-05	-0.06049413	Lower					15608717
739	cg40683750_TC21	0.0008869 4	-0.10378493	Lower					23895552
740	cg40731064_BC21	0.0005079 7	-0.08208967	Lower	Casp8ap2	chr4	+	tss_body	32639614
741	cg40748707_TC21	0.0005895	0.08165076	Higher	Rars2	chr4	+	tss_body	34629859
742	cg40751477_TC21	0.0005008 8	0.07588053	Higher	Cga	chr4	+	tss_body	34897210
743	cg40754068_TC21	0.0005247 9	0.05117316	Higher	Mob3b	chr4	-	tss_body	35136369
744	cg40792760_BC21	0.0005530 4	-0.06251203	Lower	Fam219a	chr4	-	tss_body	41568133
745	cg40807614_BC21	0.0003216 5	0.1163291	Higher	Arhgef39	chr4	-	tss_body	43496549
746	cg40820765_BC21	0.0002086 6	-0.13467509	Lower	Pax5	chr4	-	tss_body	44561342
747	cg40821241_BC21	0.0002916 5	0.09412418	Higher	Pax5	chr4	-	tss_body	44594828
748	cg40837588_BC21	0.0002534 3	-0.06608196	Lower	Tdrd7	chr4	+	tss_body	45968050
749	cg40842015_TC21	0.0009330 6	-0.06961709	Lower	Gm42280	chr4	+	tss_1500	46327265
750	cg40852382_TC21	7.7607E-05	-0.08807158	Lower	Anks6	chr4	-	tss_body	47041961
751	cg40856814_TC21	0.0005956 9	0.09804236	Higher					47450336
752	cg40864885_TC21	0.0001226 5	-0.06929824	Lower	Invs	chr4	+	tss_body	48392143
753	cg40974216_BC21	0.0004631 3	-0.0578245	Lower	Akna	chr4	-	tss_body	63402698
754	cg41036063_TC21	0.0002174 8	0.06599415	Higher	Ptprd	chr4	-	tss_body	76179846
755	cg41164166_BC21	0.0002192 1	-0.08783078	Lower	Nfia	chr4	+	tss_body	97618759

756	cg41245381_BC21	0.00025976	-0.08996914	Lower		chr4	-	tss_body	106843073
757	cg41256314_TC21	0.00057392	-0.06152973	Lower	Dmrtb1	chr4	-	tss_body	107683545
758	cg41276247_TC21	0.00076322	0.06242043	Higher	Faf1	chr4	+	tss_body	109860369
759	cg41279297_TC11	0.00095832	-0.05660441	Lower	Elavl4	chr4	-	tss_body	110225549
760	cg41311773_BC21	0.00039903	0.09511031	Higher	Faah	chr4	-	tss_body	116004395
761	cg41312122_TC21	0.00051152	0.08679313	Higher					116030517
762	cg41349205_BC11	0.00099835	-0.11387379	Lower	Cldn19	chr4	+	tss_body	119261976
763	cg41365509_TC21	0.00097937	-0.09994053	Lower	Rims3	chr4	+	tss_body	120856769
764	cg41415072_BC11	0.00070557	-0.08352002	Lower	Oscp1	chr4	+	tss_body	126072125
765	cg41418672_TC11	0.00017414	-0.07448352	Lower	Col8a2	chr4	+	tss_body	126300488
766	cg41427377_TC11	0.00076462	0.09851827	Higher	Zmym6	chr4	+	tss_body	127077631
767	cg41435847_TC21	0.00065208	-0.09798668	Lower					127806695
768	cg41445398_TC11	0.00046332	-0.12765875	Lower	Gm12958	chr4	+	tss_body	128637327
769	cg41460060_TC21	0.00067805	-0.07805768	Lower	Dcdc2b	chr4	-	tss_body	129610627
770	cg41465805_TC21	0.00015722	-0.06434034	Lower	Adgrb2	chr4	+	tss_body	130015724
771	cg41468005_TC11	0.00081414	-0.08519845	Lower	Tinagl1	chr4	-	tss_body	130166048
772	cg41474232_BC21	0.00060771	-0.06559149	Lower					130837636
773	cg41502089_TC21	0.00061656	-0.05330357	Lower	Ahdc1	chr4	+	tss_body	133061869
774	cg41502888_TC21	0.00025911	0.11464219	Higher					133103305
775	cg41505389_TC21	0.00019092	0.09761341	Higher	Tmem222	chr4	-	tss_body	133271227
776	cg41528068_TC21	0.0003084	-0.07328608	Lower	Ldlrap1	chr4	-	tss_body	134749985
777	cg41532355_TC21	0.00058826	-0.05047373	Lower					135032223
778	cg41536952_BC21	0.00056395	0.07977946	Higher	Srrm1	chr4	-	tss_body	135327095
779	cg41537864_BC21	0.00036317	0.08557794	Higher	Ncmap	chr4	-	tss_body	135385615

780	cg41539785_BC21	0.0001138	0.07994166	Higher	Stpg1	chr4	+	tss_body	135508183
781	cg41542652_BC21	0.0006738 1	-0.0738213 9	Lower	Ifnlr1	chr4	+	tss_body	135698916
782	cg41545493_BC21	0.0005877 8	-0.1462072 3	Lower	Cnr2	chr4	+	tss_body	135895659
783	cg41545539_TC21	0.0007247	-0.0851726 9	Lower	Cnr2	chr4	+	tss_body	135898682
784	cg41547321_BC21	0.0006256 2	-0.0687868 2	Lower	Tceb3	chr4	-	tss_body	136006337
785	cg41567577_TC21	0.0006868 6	0.06674533	Higher	Gm13010	chr4	-	tss_body	137461931
786	cg41574165_BC21	0.0006354 9	-0.0751513 5	Lower	Ece1	chr4	+	tss_body	137875629
787	cg41587128_BC21	0.0004767 1	-0.0680292 1	Lower	Pla2g2f	chr4	-	tss_body	138757496
788	cg41592239_TC21	0.0001519 5	0.07047713	Higher	Minos1	chr4	-	tss_body	139112663
789	cg41597619_TC11	0.0005429 5	0.0629955	Higher	Ubr4	chr4	+	tss_body	139480836
790	cg41611251_TC11	0.0003835 3	-0.1247649 1	Lower					140403180
791	cg41618168_TC21	0.0008017 6	-0.0972517 2	Lower	Padi1	chr4	-	tss_body	140823701
792	cg41619671_BC21	4.3056E-05	0.05142447	Higher	Padi2	chr4	+	tss_body	140925391
793	cg41623331_BC21	0.0001926	0.06893216	Higher	Szrd1	chr4	-	tss_body	141125176
794	cg41625104_BC21	0.0009973 7	-0.0693065 5	Lower	Arhgef19	chr4	+	tss_body	141244000
795	cg41632228_BC21	0.0001201 2	0.05304111	Higher	Tmem82	chr4	-	tss_body	141617653
796	cg41651225_BC21	0.0003733 7	0.06314179	Higher	Prdm2	chr4	-	tss_body	143135187
797	cg41665823_TC21	0.0001162 2	0.09091495	Higher	Gm36233	chr4	-	tss_body	145258525
798	cg41681455_BC21	0.0006402 2	-0.0546029 7	Lower	Draxin	chr4	-	tss_body	148125744
799	cg41689588_TC21	0.0007714 8	-0.1020378 2	Lower	Gm572	chr4	+	tss_body	148667080
800	cg41707301_TC21	0.0006581 7	0.05781414	Higher	Slc25a33	chr4	-	tss_body	149773017
801	cg41710945_BC21	0.0006619 1	-0.0515419 3	Lower	H6pd	chr4	-	tss_body	150001341
802	cg41713986_TC21	0.0007646 9	0.09066206	Higher					150174177
803	cg41768247_BC21	0.0005182 9	-0.1328032	Lower		chr4	+	tss_body	153907698
804	cg41770724_TC21	0.0006240 9	0.13712829	Higher	Trp73	chr4	-	tss_body	154071366

805	cg41777844_BC21	0.00019	-0.08636826	Lower	Prdm16	chr4	-	tss_body	154541734
806	cg41840863_BC21	0.00010895	0.05701159	Higher	Dbf4	chr5	-	tss_body	8420009
807	cg41876514_BC21	0.0006778	0.06428157	Higher	Gm3510	chr5	-	tss_1500	15935436
808	cg41894681_BC11	0.00086255	-0.06112288	Lower	Magi2	chr5	+	tss_body	19504896
809	cg41904537_BC21	0.00042325	-0.10788648	Lower	A0A0G2JEI9	chr5	-	tss_200	20956468
810	cg41918556_TC21	0.00046424	0.05020771	Higher	Orc5	chr5	-	tss_body	22550304
811	cg41957339_BC21	0.00042846	0.05123831	Higher	Dpp6	chr5	+	tss_body	27160734
812	cg41974823_TC21	0.00089223	0.07599991	Higher	Dnajb6	chr5	+	tss_body	29758251
813	cg41976243_BC21	7.1464E-05	-0.12594323	Lower		chr5	-	tss_body	30001405
814	cg41977980_BC21	0.00058475	0.06294978	Higher	Hadhb	chr5	+	tss_body	30165429
815	cg41981583_BC11	0.00030837	0.11063821	Higher	Cib4	chr5	-	tss_body	30521413
816	cg41983663_BC21	0.00083021	0.07513428	Higher					30698490
817	cg41984989_BC21	9.0931E-05	0.074143	Higher	Dpysl5	chr5	+	tss_body	30798888
818	cg41990705_BC21	0.00065467	0.0916699	Higher	Zfp513	chr5	-	tss_body	31200775
819	cg42031971_BC21	0.0003964	-0.06764509	Lower	Cpz	chr5	-	tss_1500	35526009
820	cg42039947_BC11	0.00020692	-0.05593827	Lower	Sorcs2	chr5	-	tss_body	36228687
821	cg42061741_BC21	0.00069198	-0.07147701	Lower	Tmem128	chr5	+	tss_body	38268372
822	cg42103646_TC21	0.00073189	0.0698213	Higher	D5Ertd615e	chr5	-	tss_body	45175811
823	cg42116437_BC21	6.396E-05	-0.07730222	Lower		chr5	+	tss_body	47634785
824	cg42228653_BC21	0.00017171	-0.07732024	Lower					65900219
825	cg42269819_BC21	0.00089405	0.08251813	Higher	Gabra4	chr5	-	tss_body	71628370
826	cg42277403_TC21	0.00023294	-0.06232051	Lower	Cnga1	chr5	-	tss_body	72631408
827	cg42353923_TC21	5.4987E-05	0.09063186	Higher	Adgrl3	chr5	+	tss_body	81736263
828	cg42381920_TC11	0.00056736	-0.0534931	Lower	Sult1d1	chr5	-	tss_body	87560392
829	cg42402199_BC21	0.00034211	0.06961767	Higher	Afp	chr5	+	tss_body	90497278
830	cg42405091_TC21	1.0104E-05	0.10106765	Higher	Cxcl15	chr5	+	tss_body	90794781
831	cg42448025_BC21	0.00047187	0.07071465	Higher	Paqr3	chr5	-	tss_body	97109429

832	cg42465151_BC21	0.0001839	-0.0922542	Lower	Rasgef1b	chr5	-	tss_body	99247439
833	cg42493915_TC21	0.0001348	0.1354259	Higher	Cds1	chr5	+	tss_body	101778451
834	cg42510370_BC21	0.0009051	0.0937837	Higher					103418758
835	cg42530910_TC21	0.0006528	0.0998647	Higher					105632358
836	cg42546431_BC21	0.0009435	-0.0724752	Lower					107017720
837	cg42547902_TC21	0.0007265	-0.0920535	Lower	Tgfbr3	chr5	-	tss_body	107146326
838	cg42581456_BC21	0.0002504	0.0850833	Higher	Ttc28	chr5	+	tss_body	111123684
839	cg42634867_BC21	0.0007040	0.0959973	Higher	Git2	chr5	-	tss_body	114738575
840	cg42637190_BC21	0.0004099	0.051751	Higher	4930519G04Rik	chr5	+	tss_body	114853864
841	cg42682422_TC21	0.0001406	-0.0888467	Lower	Nos1	chr5	+	tss_body	117896844
842	cg42705966_BC11	0.0006495	-0.1283710	Lower	Tbx3	chr5	+	tss_body	119675677
843	cg42707692_BC11	0.0002662	-0.1385937	Lower	Tbx5	chr5	+	tss_body	119800659
844	cg42725128_BC21	0.0002982	-0.0712273	Lower					121092743
845	cg42727858_TC11	0.0008810	0.0570806	Higher	Gm15800	chr5	+	tss_body	121322133
846	cg42729711_BC21	0.0007496	-0.1035385	Lower	Erp29	chr5	-	tss_body	121450066
847	cg42741527_TC21	2.6609E-05	-0.1306113	Lower	Hvcn1	chr5	+	tss_body	122210205
848	cg42747700_BC11	0.0004472	-0.1076875	Lower	P2rx7	chr5	+	tss_body	122643917
849	cg42771715_TC21	0.0001379	0.0943627	Higher	Pitpnm2	chr5	-	tss_body	124231230
850	cg42781360_BC11	0.0002189	-0.0727286	Lower					124931340
851	cg42784906_TC21	0.0003783	0.1841268	Higher	Ncor2	chr5	-	tss_body	125149241
852	cg42829573_BC11	0.0007921	-0.0515153	Lower					129470307
853	cg42834408_TC21	0.0009397	-0.0767801	Lower	Chchd2	chr5	-	tss_body	129886206
854	cg42859650_TC21	0.0004328	-0.0571852	Lower	Auts2	chr5	-	tss_body	132467204
855	cg42873366_BC21	0.0009957	-0.1086491	Lower					134233181

856	cg42880083_BC21	0.00041602	-0.07441131	Lower	Limk1	chr5	-	tss_body	134675729
857	cg42892263_TC21	0.00036992	-0.07000111	Lower	Ccl26	chr5	-	tss_body	135563325
858	cg42898250_BC21	0.00037903	0.10091612	Higher	Dtx2	chr5	+	tss_body	135995952
859	cg42917124_TC21	0.00022282	0.06131845	Higher	Gm38725	chr5	+	tss_1500	137477066
860	cg42925266_BC21	0.00023954	0.0563163	Higher	Mcm7	chr5	-	tss_body	138165536
861	cg42931922_TC21	0.00026486	-0.07061401	Lower					138912218
862	cg42947969_TC21	0.00010857	0.0810021	Higher	Mad1l1	chr5	-	tss_body	140023891
863	cg42952925_BC21	0.00039981	-0.07665899	Lower	LOC101055939	chr5	+	tss_body	140488879
864	cg42954001_TC21	0.00012622	0.08019457	Higher	Gm32158	chr5	+	tss_body	140565428
865	cg42959404_BC21	0.00089304	0.10911899	Higher	Card11	chr5	-	tss_body	140966474
866	cg42959765_TC21	0.00039178	0.08814099	Higher	Gm38729	chr5	-	tss_body	141006967
867	cg42981933_TC21	0.00053053	-0.05315267	Lower	Fscn1	chr5	+	tss_body	142968280
868	cg43006793_BC21	0.00099107	0.05465972	Higher	Trrap	chr5	+	tss_body	144851130
869	cg43006872_TC21	7.1139E-05	0.10855022	Higher	Trrap	chr5	+	tss_body	144856456
870	cg43029926_BC21	0.00027049	-0.10410651	Lower	Polr1d	chr5	+	tss_body	147100793
871	cg43036275_BC21	9.18E-05	0.08027665	Higher	Flt1	chr5	-	tss_body	147563645
872	cg43040335_TC21	0.00025035	-0.07762565	Lower					147839882
873	cg43046282_BC21	0.000339	-0.15716523	Lower	Mtus2	chr5	+	tss_body	148303284
874	cg43051310_BC21	0.00056394	-0.07900315	Lower					148674191
875	cg43059010_BC21	7.7941E-05	-0.08226803	Lower	Uspl1	chr5	+	tss_body	149215265
876	cg43059645_TC21	0.00060897	-0.08189077	Lower					149259116
877	cg43060518_TC21	0.00079507	0.07185974	Higher					149338820
878	cg43060835_TC21	0.00074539	-0.05843106	Lower	Gm38753	chr5	-	tss_body	149364360
879	cg43068872_BC21	0.00051137	-0.06087752	Lower	Rxfp2	chr5	+	tss_1500	150017853
880	cg43075674_TC21	0.00066869	0.12027023	Higher	chr5-150593653-	chr5	*	SShelf	150597220

					150594699				
881	cg43078651_TC21	0.00086574	0.09430577	Higher					150948481
882	cg43094419_TC21	0.00092586	0.05589033	Higher	Casd1	chr6	+	tss_1500	4600535
883	cg43100314_BC21	0.00014833	0.07334114	Higher	Pon1	chr6	-	tss_body	5169886
884	cg43102835_TC21	0.00083655	-0.08203208	Lower					5437945
885	cg43105038_BC21	0.00091661	-0.06860868	Lower	Dync1i1	chr6	+	tss_body	5730366
886	cg43109782_BC21	9.0707E-05	0.13739137	Higher	Slc25a13	chr6	-	tss_body	6194922
887	cg43121539_TC21	0.00026192	0.0657672	Higher					7831144
888	cg43219358_TC21	0.00012094	0.06874014	Higher	Asb15	chr6	+	tss_body	24562712
889	cg43245162_BC21	0.00029969	0.09632212	Higher		chr6	+	tss_body	29002437
890	cg43258809_BC11	4.8802E-05	0.0896552	Higher	Ube2h	chr6	-	tss_body	30212719
891	cg43295086_BC21	0.00012317	-0.07005481	Lower					34343741
892	cg43320355_BC21	0.00040356	0.06635808	Higher					37603309
893	cg43322730_BC21	0.00021803	0.06318166	Higher	Trim24	chr6	+	tss_body	37944828
894	cg43345280_TC21	0.00039711	0.06893575	Higher	Tmem178b	chr6	+	tss_body	40230256
895	cg43350031_TC21	0.00063878	0.09375246	Higher		chr6	+	tss_body	41087489
896	cg43357184_TC21	0.00020193	-0.1139131	Lower	Zyx	chr6	+	tss_body	42356194
897	cg43372653_BC21	0.00042841	0.07437767	Higher	Cntnap2	chr6	+	tss_body	45758704
898	cg43372777_BC21	1.6273E-05	0.09811304	Higher	Cntnap2	chr6	+	tss_body	45794225
899	cg43383366_TC21	0.00087341	0.06297602	Higher	Zfp282	chr6	+	tss_body	47905082
900	cg43392379_TC21	0.00052683	-0.09623251	Lower	Gm7932	chr6	+	tss_body	48863208
901	cg43429492_BC21	0.00061325	-0.07645391	Lower		chr6	-	tss_body	52357716
902	cg43431754_BC21	0.00057382	-0.06403159	Lower	Hibadh	chr6	-	tss_body	52593808
903	cg43434440_TC21	0.0003017	-0.07835123	Lower	Jazf1	chr6	-	tss_body	52900838
904	cg43480497_TC21	0.00041066	0.07768486	Higher	Herc3	chr6	+	tss_body	58906085
905	cg43480516_TC21	8.626E-05	-0.09011369	Lower	Herc3	chr6	+	tss_body	58906758
906	cg43480544_BC21	0.00062054	-0.08911836	Lower	Herc3	chr6	+	tss_body	58907095

907	cg43545665_TC21	0.00054518	-0.06312716	Lower	Smyd1	chr6	-	tss_body	71235318
908	cg43555163_TC21	0.0004885	0.05967022	Higher	Atoh8	chr6	-	tss_body	72218501
909	cg43556891_BC21	0.00013264	-0.07454965	Lower	0610030E20Rik	chr6	+	tss_body	72348643
910	cg43560604_TC21	0.0006983	-0.11300329	Lower	Tcf7l1	chr6	-	tss_body	72647059
911	cg43591135_TC21	0.00016558	0.07527505	Higher	Reg3d	chr6	-	tss_200	78378874
912	cg43598859_TC11	0.00051532	-0.07223345	Lower	Lrrtm4	chr6	+	tss_body	80166626
913	cg43622881_BC11	0.00030735	-0.07728466	Lower	Bola3	chr6	+	tss_body	83351678
914	cg43628008_BC21	0.00023322	-0.06243718	Lower	Tex261	chr6	-	tss_body	83770784
915	cg43633704_TC21	0.00045848	0.09422647	Higher					84394043
916	cg43639818_BC21	0.00035031	-0.10566822	Lower	Emx1	chr6	+	tss_body	85192375
917	cg43656066_TC21	0.0003614	0.08900317	Higher	Anxa4	chr6	-	tss_body	86776630
918	cg43664122_TC21	0.00037244	0.07167622	Higher					87544798
919	cg43667430_TC21	0.00025108	0.05410841	Higher	Cnbp	chr6	-	tss_body	87847479
920	cg43670664_BC21	0.00068647	-0.0571013	Lower					88117141
921	cg43691205_BC21	0.00043161	-0.06884672	Lower	Klf15	chr6	+	tss_1500	90461609
922	cg43691468_TC21	0.0005119	-0.06076651	Lower	Klf15	chr6	+	tss_body	90470075
923	cg43698154_BC21	0.00014087	0.08740632	Higher	Fbln2	chr6	+	tss_body	91246811
924	cg43730535_TC21	0.00056128	0.05352213	Higher					94877845
925	cg43745312_BC21	0.00050497	-0.09138099	Lower					97101664
926	cg43768749_BC21	0.00032255	0.06135107	Higher	H3BJN7	chr6	-	tss_body	99600426
927	cg43823045_BC21	0.00054294	0.06593225	Higher	Itpr1	chr6	+	tss_body	108330683
928	cg43830395_TC21	4.0494E-05	-0.10481158	Lower		chr6	+	tss_body	109125766
929	cg43855220_TC21	0.00094953	-0.06140766	Lower	Ttll3	chr6	+	tss_body	113398035
930	cg43865326_BC11	0.00052583	-0.06890513	Lower	LOC108169162	chr6	+	tss_body	114274488
931	cg43871151_BC21	0.00052414	-0.05488373	Lower	Atg7	chr6	+	tss_body	114846506

932	cg43880352_BC11	0.00092524	-0.0980961	Lower	Cand2	chr6	+	tss_body	115792085
933	cg43881651_TC21	0.0002092	0.09093087	Higher	Ift122	chr6	+	tss_body	115914801
934	cg43908250_BC21	0.00019238	0.07658597	Higher	Cacna1c	chr6	-	tss_body	118757904
935	cg43909839_TC11	0.00063378	-0.10280749	Lower	Cacna1c	chr6	-	tss_body	118899776
936	cg43923792_TC21	0.00065416	0.05166697	Higher	B4galnt3	chr6	-	tss_body	120250970
937	cg43942360_TC21	1.5669E-05	-0.0895308	Lower					122114058
938	cg43949634_BC11	0.00091213	0.16069792	Higher	Foxj2	chr6	+	tss_body	122822553
939	cg43971212_TC21	0.00014859	0.05846138	Higher	Scnn1a	chr6	+	tss_body	125321688
940	cg43982499_BC21	0.00056343	0.09475423	Higher					126544844
941	cg43999825_TC21	0.00057595	-0.06736554	Lower	Tspan9	chr6	-	tss_body	128045163
942	cg44012477_BC21	0.00035469	-0.06208648	Lower	Clec1a	chr6	-	tss_body	129451767
943	cg44045809_BC21	2.6858E-05	-0.0762793	Lower	Ddx47	chr6	+	tss_body	135019014
944	cg44105408_BC21	0.0006406	-0.05915581	Lower	Pde3a	chr6	+	tss_body	141434508
945	cg44115889_BC21	0.00024322	0.10246822	Higher	St8sia1	chr6	-	tss_body	142835400
946	cg44145090_BC21	0.00061699	-0.05709345	Lower	Lmntd1	chr6	-	tss_body	145414414
947	cg44150808_TC21	0.00035852	0.08960954	Higher					145889566
948	cg44160134_TC11	5.6371E-05	-0.0511736	Lower	Smco2	chr6	+	tss_body	146862980
949	cg44161593_BC21	0.00024658	0.06132111	Higher	Ppfibp1	chr6	+	tss_body	147016603
950	cg44180988_BC21	0.00044028	0.13357083	Higher	D7Ertd143e	chr7	+	tss_body	3219602
951	cg44180995_BC21	0.00026003	-0.07715661	Lower	D7Ertd143e	chr7	+	tss_body	3220415
952	cg44181342_BC21	0.00041779	-0.11526196	Lower		chr7	-	tss_body	3265180
953	cg44183217_BC21	0.0001072	-0.0785147	Lower	Cacng8	chr7	+	tss_body	3408969
954	cg44191089_TC21	0.00087086	-0.06309899	Lower	Eps8l1	chr7	+	tss_body	4479068
955	cg44209239_BC11	0.00056645	-0.0930227	Lower	Smim17	chr7	+	tss_body	6417976
956	cg44211952_TC11	4.705E-05	0.15426532	Higher	Usp29	chr7	+	tss_body	6730824
957	cg44260186_BC11	0.00029588	-0.09782325	Lower	C5ar1	chr7	-	tss_body	16259022

958	cg44264332_BC21	0.00040983	-0.0593082	Lower	Arhgap35	chr7	-	tss_body	16581764
959	cg44268440_TC21	0.00089579	-0.0680175	Lower	Dact3	chr7	+	tss_body	16884915
960	cg44269178_TC21	3.7201E-05	0.0963727	Higher	Calm3	chr7	-	tss_body	16917003
961	cg44295273_BC21	0.00026765	0.0696885	Higher	Apoe	chr7	-	tss_1500	19700497
962	cg44313073_BC21	0.00051944	-0.0911513	Lower	Gm36694	chr7	-	tss_body	24073353
963	cg44317526_BC11	7.714E-05	-0.0916947	Lower	Irgc1	chr7	-	tss_body	24433147
964	cg44328526_BC21	0.00078571	-0.0856774	Lower	Pou2f2	chr7	-	tss_body	25154756
965	cg44329497_BC21	0.00043016	-0.0694447	Lower	Dedd2	chr7	-	tss_body	25217585
966	cg44333350_BC21	2.4079E-05	-0.0635234	Lower	4732471J01Rik	chr7	+	tss_body	25422818
967	cg44346390_TC21	0.00021798	0.0513538	Higher	Cyp2t4	chr7	+	tss_body	27155137
968	cg44353884_BC21	0.00020642	0.0627554	Higher	Akt2	chr7	+	tss_body	27602324
969	cg44369686_TC21	0.0008344	-0.0686142	Lower	Rinl	chr7	+	tss_body	28796218
970	cg44374169_BC21	0.00036929	0.0677930	Higher	Ryr1	chr7	-	tss_body	29083330
971	cg44377566_TC21	0.00059946	0.0673309	Higher	LOC108167414	chr7	-	tss_1500	29289676
972	cg44390869_BC21	0.00043305	0.0526005	Higher	Syne4	chr7	+	tss_body	30314939
973	cg44393649_BC21	6.6404E-05	-0.0678901	Lower	Prodh2	chr7	+	tss_body	30493785
974	cg44398219_TC21	5.8114E-05	-0.0883864	Lower					30811861
975	cg44401264_BC21	0.00059296	-0.0543510	Lower	Gm38984	chr7	+	tss_body	31052998
976	cg44401533_TC21	0.00086645	-0.1004889	Lower	Lgi4	chr7	+	tss_body	31069842
977	cg44422560_BC21	8.3569E-05	0.0716177	Higher					34633771
978	cg44471231_BC21	0.00082482	-0.0565509	Lower		chr7	-	tss_body	39740463
979	cg44508863_TC21	0.00031362	-0.0996009	Lower	Gm21948	chr7	+	tss_body	44839573
980	cg44508904_TC11	0.00030355	-0.1606492	Lower	Gm21948	chr7	+	tss_body	44840009
981	cg44514893_BC21	0.00094916	-0.0674902	Lower	Aldh16a1	chr7	-	tss_body	45144649

982	cg44523447_BC11	0.0005962	-0.0698650 4	Lower	Rasip1	chr7	+	tss_body	45635902
983	cg44528046_BC11	0.0009879 2	0.1445010 7	Higher	Grin2d	chr7	-	tss_body	45870058
984	cg44529525_TC21	0.0004052 4	-0.0836504 6	Lower	Abcc6	chr7	-	tss_body	45980007
985	cg44535845_TC21	0.0004341 6	0.0634182 8	Higher	Kcnc1	chr7	+	tss_body	46422353
986	cg44536277_BC21	0.0003011 5	-0.0882984 8	Lower	Sergef	chr7	-	tss_body	46449419
987	cg44561763_TC21	1.2709E-05	-0.0521607 4	Lower	Nav2	chr7	+	tss_body	49609455
988	cg44594170_TC21	7.4923E-05	0.0776223	Higher	Cyfip1	chr7	+	tss_body	55907324
989	cg44626049_BC21	0.0007675 2	-0.0962386 4	Lower	Peg12	chr7	-	tss_body	62463716
990	cg44638699_TC21	0.0008527	-0.1486960 2	Lower	Trpm1	chr7	+	tss_body	64268532
991	cg44682046_TC21	0.0004418 4	0.0629502	Higher	Fam169b	chr7	+	tss_body	68355574
992	cg44739010_BC21	0.0008305 9	0.1156481 2	Higher					75984165
993	cg44765474_TC11	0.0002152	-0.1071223 4	Lower	Kif7	chr7	-	tss_body	79714091
994	cg44767537_TC21	0.0004756 7	0.0663123 1	Higher					79863147
995	cg44770141_TC21	4.9289E-05	-0.0752956 3	Lower	Zfp710	chr7	+	tss_body	80081962
996	cg44771607_BC21	0.0003880 9	0.0628168 3	Higher	Sema4b	chr7	+	tss_body	80196461
997	cg44801595_TC21	0.0004595 3	-0.0768334 2	Lower	Mex3b	chr7	+	tss_body	82870439
998	cg44843448_BC21	0.0003139 8	0.0789663 4	Higher	Sytl2	chr7	+	tss_body	90348611
999	cg44857249_BC21	4.4647E-05	0.0581758 1	Higher	Ddias	chr7	-	tss_body	92857722
1000	cg44890326_TC21	0.0005871 5	-0.1056475 7	Lower	Capn5	chr7	-	tss_body	98165567
1001	cg44904106_TC21	0.0007050 7	0.0694585	Higher	Gdpd5	chr7	+	tss_body	99385721
1002	cg44936269_BC21	1.4918E-05	-0.0817444 2	Lower	Olfr550	chr7	+	tss_body	102578863
1003	cg44948995_BC21	0.0007099 6	0.0666065 5	Higher	A0A2I3BS13	chr7	-	tss_body	105092169
1004	cg44953031_BC21	0.0001446 5	-0.0690994 2	Lower	Timm10b	chr7	+	tss_body	105651665
1005	cg44969054_BC11	0.0008342 6	-0.0898044 3	Lower					108793277
1006	cg44972600_BC21	0.0005191 1	-0.0667056 6	Lower					109230888

1007	cg45003429_TC21	0.00075139	-0.0535683	Lower	Tead1	chr7	+	tss_body	112743273
1008	cg45015246_TC21	0.00019411	-0.0575093	Lower	Rras2	chr7	-	tss_body	114096049
1009	cg45039592_BC21	0.00035193	-0.0775713	Lower	Xylt1	chr7	+	tss_body	117393522
1010	cg45040295_TC21	9.2118E-05	0.0779756	Higher	Xylt1	chr7	+	tss_body	117465090
1011	cg45051691_BC21	0.00031412	0.1473724	Higher	Ccp110	chr7	+	tss_body	118715364
1012	cg45055031_BC11	0.00055714	-0.0688253	Lower	Gprc5b	chr7	-	tss_body	118984290
1013	cg45091814_BC21	0.00094814	-0.0507984	Lower	Tnrc6a	chr7	+	tss_body	123162846
1014	cg45103891_TC21	0.00071154	-0.0811683	Lower					124914888
1015	cg45121762_TC21	0.00092123	0.1046119	Higher	Sult1a1	chr7	-	tss_body	126685227
1016	cg45124807_TC21	0.00037001	-0.0647391	Lower	Taok2	chr7	-	tss_body	126871535
1017	cg45125113_TC21	0.00062263	-0.0728514	Lower	Tmem219	chr7	-	tss_body	126896867
1018	cg45131984_TC21	0.00014321	0.0925522 3	Higher	chr7-127363670-127363908	chr7	*	Island	127363793
1019	cg45131991_BC21	3.4642E-05	0.1436253 4	Higher	chr7-127363670-127363908	chr7	*	Island	127363894
1020	cg45134307_BC21	0.00011673	0.0863236 4	Higher	Srcap	chr7	+	tss_body	127552875
1021	cg45143872_TC21	0.00086121	-0.0736147 6	Lower	Slc5a2	chr7	+	tss_1500	128265374
1022	cg45148558_BC11	0.00090968	-0.0621989 9	Lower	Inpp5f	chr7	+	tss_body	128688556
1023	cg45159798_TC11	8.7887E-05	0.0795350 3	Higher					130058723
1024	cg45182395_TC21	0.00062438	-0.0861641 7	Lower	Chst15	chr7	-	tss_body	132262981
1025	cg45187959_TC21	0.00017246	-0.0804071 8	Lower	Fam53b	chr7	-	tss_body	132776309
1026	cg45195025_BC21	0.00055758	0.0761258 1	Higher					133444508
1027	cg45200989_TC21	2.4071E-05	0.0836049 9	Higher	Adam12	chr7	-	tss_body	134023462
1028	cg45207164_TC11	0.00087324	-0.0512901 6	Lower	Dock1	chr7	+	tss_body	134777613

1029	cg45211795_BC21	0.00089425	-0.05438771	Lower	A0A1B0GRF8	chr7	+	tss_1500	135258470
1030	cg45217751_TC21	0.00071359	0.06027858	Higher	6330420H09Rik	chr7	+	tss_1500	135852827
1031	cg45219258_TC21	9.1312E-05	0.09534076	Higher					136024176
1032	cg45258031_TC21	0.00043745	-0.0736684	Lower	Kndc1	chr7	+	tss_body	139910754
1033	cg45258966_TC21	0.00099366	0.07232394	Higher	LOC102635948	chr7	+	tss_body	139968997
1034	cg45260522_BC21	0.00070111	-0.09367681	Lower	Caly	chr7	-	tss_body	140081962
1035	cg45263646_TC21	0.00089213	0.05500382	Higher	Olfr536	chr7	-	tss_body	140506804
1036	cg45266180_BC21	0.00057178	-0.09777056	Lower	Sirt3	chr7	-	tss_body	140866455
1037	cg45270367_TC21	7.0953E-05	-0.10330939	Lower	Rnh1	chr7	-	tss_body	141164645
1038	cg45272009_TC11	0.00044568	-0.06613829	Lower	Cdhr5	chr7	-	tss_body	141273712
1039	cg45277610_BC21	0.00024708	0.05024938	Higher	Muc2	chr7	+	tss_body	141701349
1040	cg45277616_BC21	0.0001153	0.08121552	Higher	Muc2	chr7	+	tss_body	141702112
1041	cg45285595_TC21	0.0006183	-0.08767835	Lower					142634066
1042	cg45285789_BC11	0.0002895	0.11976226	Higher	Igf2	chr7	-	tss_body	142656114
1043	cg45289160_TC21	0.00073638	0.08017835	Higher	Trpm5	chr7	-	tss_body	143094633
1044	cg45289163_BC21	0.00048987	-0.10065502	Lower	Trpm5	chr7	-	tss_1500	143094725
1045	cg45318645_TC21	0.00095218	0.06191375	Higher		chr8	+	tss_200	4018865
1046	cg45320442_BC21	0.00035253	-0.0729412	Lower	Lrrc8e	chr8	+	tss_body	4235400
1047	cg45348730_TC21	0.00096379	-0.06315606	Lower					8985611
1048	cg45365159_BC21	0.00029499	0.10741797	Higher					10837863
1049	cg45373915_BC21	0.00057523	0.06752389	Higher	Carkd	chr8	+	tss_body	11506564
1050	cg45375048_TC21	0.00053103	-0.13642358	Lower	Ing1	chr8	+	tss_body	11561846
1051	cg45376378_BC11	0.00061959	-0.06362964	Lower	1700016D06Rik	chr8	-	tss_body	11660537
1052	cg45386253_BC21	0.00078552	-0.07108732	Lower					12445153
1053	cg45413377_BC21	0.00087042	0.0847109	Higher	Dlgap2	chr8	+	tss_body	14610641
1054	cg45420713_BC11	0.00034281	-0.08858024	Lower		chr8	+	tss_body	15189494

1055	cg45441950_TC21	0.00014685	-0.07280729	Lower	Mcph1	chr8	+	tss_body	18741399
1056	cg45444907_TC21	8.9343E-05	0.08021065	Higher	Defb39	chr8	-	tss_200	19064933
1057	cg45461259_TC21	0.00045809	0.06372178	Higher	Mrps31	chr8	+	tss_body	22423915
1058	cg45465757_TC21	0.00051962	-0.11655842	Lower	Plat	chr8	+	tss_body	22771715
1059	cg45494205_BC21	0.00058173	-0.07576258	Lower	Gm30978	chr8	-	tss_body	25454053
1060	cg45515489_TC21	0.00034936	-0.08391032	Lower	Adrb3	chr8	-	tss_body	27229164
1061	cg45577937_BC21	0.00067097	0.06478905	Higher	Mfhas1	chr8	+	tss_body	35589860
1062	cg45579826_TC21	0.00022087	-0.0703407	Lower	Gm19410	chr8	+	tss_body	35773666
1063	cg45584415_BC21	0.00021361	0.10075005	Higher	Gm35520	chr8	+	tss_body	36196444
1064	cg45646655_TC11	0.00017891	0.05770056	Higher	Sorbs2	chr8	+	tss_body	45752298
1065	cg45646851_BC21	0.00031104	0.05982124	Higher	Sorbs2	chr8	+	tss_body	45769795
1066	cg45670382_BC21	0.00037402	-0.0529575	Lower					47784694
1067	cg45676693_TC21	0.00076265	0.10956043	Higher	Tenm3	chr8	-	tss_body	48228524
1068	cg45810928_TC21	8.0902E-05	-0.1073453	Lower	Crtc1	chr8	-	tss_body	70419116
1069	cg45811388_BC21	0.00093601	0.07944352	Higher	Klhl26	chr8	-	tss_body	70452880
1070	cg45814840_TC21	8.749E-05	-0.09103689	Lower					70645774
1071	cg45819506_TC21	0.00069887	-0.05496276	Lower	Ccdc124	chr8	-	tss_body	70868450
1072	cg45823593_BC11	0.00060687	-0.08312749	Lower	Use1	chr8	+	tss_body	71369186
1073	cg45826455_TC21	0.00057531	-0.08891314	Lower	Plvap	chr8	-	tss_200	71511936
1074	cg45829533_TC21	0.00049621	0.0579661	Higher	Jak3	chr8	+	tss_body	71678377
1075	cg45841904_BC11	0.00056876	-0.08120682	Lower	Large	chr8	-	tss_body	73303134
1076	cg45851084_BC21	0.00023449	-0.09265593	Lower		chr8	+	tss_body	75201597
1077	cg45861330_BC21	0.0004579	-0.06249096	Lower	Nr3c2	chr8	+	tss_body	77186140
1078	cg45929043_BC21	0.00083407	0.07360418	Higher	Nfix	chr8	-	tss_body	84752467
1079	cg45929578_BC21	0.00065277	-0.11463002	Lower	Nfix	chr8	-	tss_body	84784685
1080	cg45948343_TC21	4.6299E-05	0.0757816	Higher	Gm39215	chr8	-	tss_body	86826085

1081	cg45955306_BC11	0.00010857	0.0673575 1	Higher	4933402J07Rik	chr8	+	tss_body	87588956
1082	cg45967621_TC21	0.00041876	-0.0744345 8	Lower	Nkd1	chr8	+	tss_body	88592492
1083	cg45991252_TC21	9.4251E-05	0.1131926 9	Higher		chr8	-	tss_body	91160107
1084	cg45993864_BC21	0.00041722	0.1102553 3	Higher	Fto	chr8	+	tss_body	91406857
1085	cg45996991_TC21	0.00039344	0.0925855 1	Higher	Fto	chr8	+	tss_body	91649371
1086	cg46012112_BC11	0.00057926	-0.0973603 4	Lower	Ces1a	chr8	-	tss_body	93031949
1087	cg46014905_TC21	0.00039366	-0.0689583 8	Lower	Ces5a	chr8	-	tss_body	93523648
1088	cg46021554_TC21	0.00017386	-0.1404139 6	Lower	Gm39227	chr8	-	tss_body	94171438
1089	cg46022002_TC11	0.00013106	-0.1004308 8	Lower					94191398
1090	cg46032758_BC21	8.5599E-05	0.0617194 2	Higher	Kifc3	chr8	-	tss_body	95110557
1091	cg46037373_BC21	3.0079E-05	0.1291603	Higher	Csnk2a2	chr8	-	tss_body	95487650
1092	cg46042379_TC21	0.00014938	-0.0923423 1	Lower	Got2	chr8	-	tss_body	95875402
1093	cg46087073_TC21	0.00071163	0.0876792 4	Higher	Cmtm3	chr8	+	tss_body	104347272
1094	cg46091843_TC21	0.00030666	0.0818421	Higher	Ces2c	chr8	+	tss_1500	104846154
1095	cg46097137_TC21	0.00077231	-0.0904554 6	Lower	Slc9a5	chr8	+	tss_body	105355545
1096	cg46097544_TC21	0.00079434	0.0734229 3	Higher	Plekhg4	chr8	+	tss_body	105377569
1097	cg46100553_TC11	5.168E-05	-0.0603307 5	Lower	Fam65a	chr8	+	tss_body	105618838
1098	cg46104713_TC11	0.0007252	-0.0610680 3	Lower	Ctrl	chr8	-	tss_body	105933629
1099	cg46104867_BC21	4.9086E-05	0.0706220 5	Higher	Lcat	chr8	-	tss_body	105941687
1100	cg46104907_BC21	1.3099E-05	-0.0907510 6	Lower	Lcat	chr8	-	tss_200	105943434
1101	cg46115840_BC21	0.00044773	-0.0573797 6	Lower	Chtf8	chr8	-	tss_body	106886342
1102	cg46115867_BC21	0.00067221	-0.0970927 3	Lower	Chtf8	chr8	-	tss_body	106889030
1103	cg46128783_BC21	0.00049367	-0.0905898 9	Lower	E9QMD3	chr8	+	tss_body	108027916
1104	cg46173287_BC11	1.5509E-05	-0.1302129	Lower	Ctrb1	chr8	-	tss_body	111689875
1105	cg46215955_BC21	0.00024167	-0.0714564 5	Lower					115899802

1106	cg46227344_BC21	0.00079465	-0.0777756	Lower	Pkd1l2	chr8	-	tss_body	117016774
1107	cg46229885_BC21	0.00020273	-0.0637480 2	Lower	Gan	chr8	+	tss_body	117198761
1108	cg46231955_BC21	0.00081393	-0.0593578 6	Lower	Cmip	chr8	+	tss_body	117322659
1109	cg46242250_TC21	0.00021294	0.0545955 4	Higher					118091134
1110	cg46252798_BC21	0.00081112	-0.0757531 4	Lower	Cdh13	chr8	+	tss_body	119064855
1111	cg46254458_BC21	0.0002434	-0.1019293 5	Lower	Cdh13	chr8	+	tss_body	119221476
1112	cg46259372_TC21	0.00050134	-0.0502044 9	Lower	Mbtps1	chr8	-	tss_1500	119560238
1113	cg46261674_TC21	0.00055717	0.0874145 3	Higher	Atp2c2	chr8	+	tss_1500	119699513
1114	cg46269940_BC11	0.00026176	-0.1186062 1	Lower	Gse1	chr8	+	tss_body	120230064
1115	cg46273292_BC21	0.00086591	0.1257439 5	Higher	Gse1	chr8	+	tss_body	120439534
1116	cg46273461_BC21	0.00026052	-0.0762274 1	Lower	Gse1	chr8	+	tss_body	120450065
1117	cg46286320_BC21	0.00021167	-0.0594527 2	Lower	Q6PB93	chr8	+	tss_body	121170412
1118	cg46306843_TC21	0.00059089	0.0655192 2	Higher	Il17c	chr8	+	tss_body	122422288
1119	cg46314535_TC21	0.00017111	0.0821080 7	Higher	Cdh15	chr8	+	tss_body	122864944
1120	cg46332764_BC21	0.00042925	0.1276602 8	Higher	Q6PB93	chr8	+	tss_body	124099361
1121	cg46351905_TC21	0.00079013	-0.0856813 4	Lower	Sipa1l2	chr8	-	tss_body	125485259
1122	cg46368240_TC21	0.00099489	-0.1054762 9	Lower	Gm31718	chr8	-	tss_body	126867906
1123	cg46381818_TC21	0.0004137	0.0552968	Higher	LOC105242417	chr8	-	tss_body	128799017
1124	cg46454209_BC11	0.00026004	-0.0905112 2	Lower	Smco4	chr9	+	tss_body	15506967
1125	cg46474610_TC21	0.00045842	0.1079176 4	Higher	Q8VGG6	chr9	-	tss_200	19541187
1126	cg46475333_TC21	0.00017262	-0.1039161 5	Lower		chr9	+	tss_200	19690464
1127	cg46484247_TC21	0.00095412	-0.0805377 4	Lower	Ppan	chr9	+	tss_body	20892119
1128	cg46509936_TC11	0.00050837	0.0960082 3	Higher	Bbs9	chr9	+	tss_body	22830844
1129	cg46607941_TC21	0.00052603	-0.0545932 6	Lower	Pknox2	chr9	-	tss_body	37018245
1130	cg46610030_BC21	0.00017072	0.0572865 2	Higher	Slc37a2	chr9	-	tss_body	37245097

1131	cg46626965_BC21	0.00019457	0.10802497	Higher	Gramd1b	chr9	-	tss_body	40374679
1132	cg46630384_BC21	0.00054122	0.09484959	Higher	Clmp	chr9	+	tss_1500	40685237
1133	cg46635746_BC21	0.00035516	0.07297014	Higher	Ubash3b	chr9	-	tss_body	41130271
1134	cg46658035_BC21	0.00093173	-0.05166536	Lower	Oaf	chr9	-	tss_body	43223963
1135	cg46670601_BC21	0.00030666	-0.07578395	Lower	Nlrx1	chr9	-	tss_body	44266694
1136	cg46677265_BC21	0.00056524	0.07597233	Higher	Phldb1	chr9	-	tss_body	44721258
1137	cg46678302_TC21	0.0002903	-0.06382972	Lower	Tmem25	chr9	-	tss_body	44796530
1138	cg46685273_TC21	0.00019321	0.0913391	Higher	Fxyd6	chr9	+	tss_body	45376658
1139	cg46685414_TC21	0.00048878	-0.08351316	Lower	Fxyd6	chr9	+	tss_body	45387876
1140	cg46685603_BC21	0.00036517	-0.1041632	Lower	Fxyd2	chr9	+	tss_body	45402830
1141	cg46688835_BC21	0.00027324	0.06418418	Higher	Dscaml1	chr9	+	tss_body	45679936
1142	cg46695462_BC21	0.00079066	0.05220886	Higher	Apoc3	chr9	-	tss_body	46233226
1143	cg46708966_BC21	0.00021138	0.06163352	Higher	Cadm1	chr9	+	tss_body	47618557
1144	cg46721187_BC21	0.00048844	-0.08489586	Lower	Zbtb16	chr9	-	tss_body	48793070
1145	cg46771718_BC11	0.00058835	-0.10511886	Lower					54782754
1146	cg46794116_TC21	0.00083798	-0.06801866	Lower	1700017B05Rik	chr9	-	tss_body	57256607
1147	cg46794388_TC21	0.00059871	-0.06566467	Lower					57268283
1148	cg46795715_TC21	0.000903	-0.0668423	Lower	Ppcdc	chr9	-	tss_body	57428487
1149	cg46807741_TC21	0.00045224	-0.07357148	Lower	4930461G14Rik	chr9	+	tss_200	58455010
1150	cg46817409_BC21	0.00063114	0.06268091	Higher	Gm33180	chr9	-	tss_1500	59513558
1151	cg46817515_TC21	0.00039189	0.06469748	Higher	Tmem202	chr9	-	tss_body	59525752
1152	cg46858734_BC11	0.00094915	0.06563485	Higher	2300009A05Rik	chr9	-	tss_200	63399419
1153	cg46863524_TC21	0.00066924	-0.06134642	Lower					63849692
1154	cg46864756_BC21	2.6206E-05	-0.11486127	Lower	Smad6	chr9	-	tss_body	63953681
1155	cg46889174_TC21	0.00035573	0.14157482	Higher	Dapk2	chr9	+	tss_body	66242650
1156	cg46950374_TC11	0.00083107	-0.05433291	Lower	Prtg	chr9	+	tss_body	72856914

1157	cg46976224_BC21	0.00019809	0.07444348	Higher	Hmgcll1	chr9	+	tss_1500	76013962
1158	cg46977999_TC21	0.00040482	0.05235619	Higher	Hcrtr2	chr9	-	tss_body	76323507
1159	cg47000344_BC21	0.00033248	-0.08219913	Lower		chr9	-	tss_body	78936744
1160	cg47027320_TC21	0.00019308	0.06642839	Higher	Gm2087	chr9	+	tss_body	83447796
1161	cg47072735_BC21	0.00084722	0.07444224	Higher					89875621
1162	cg47091723_BC21	0.00060193	0.10021122	Higher	4933400C23Rik	chr9	+	tss_body	92718884
1163	cg47124137_TC21	0.00015483	-0.07525583	Lower	Spsb4	chr9	-	tss_body	96995674
1164	cg47124146_BC21	6.1171E-06	-0.07062831	Lower	Spsb4	chr9	-	tss_body	96995832
1165	cg47125036_BC21	0.00039057	0.09974	Higher		chr9	-	tss_body	97059192
1166	cg47175897_TC21	0.00040228	0.11611325	Higher	Anapc13	chr9	+	tss_body	102634161
1167	cg47177325_BC21	0.00060914	-0.05103286	Lower	Gm5627	chr9	+	tss_body	102739805
1168	cg47185465_BC21	0.00081485	0.0535924	Higher					103398867
1169	cg47200539_TC21	0.00061433	-0.07552087	Lower	Cpne4	chr9	+	tss_body	104995051
1170	cg47217155_TC21	0.00030888	-0.06500653	Lower	Gpr62	chr9	-	tss_body	106466117
1171	cg47227192_TC21	6.7987E-05	0.07400564	Higher	Cacna2d2	chr9	+	tss_body	107476551
1172	cg47227878_BC21	0.00058767	-0.10809597	Lower	Cacna2d2	chr9	+	tss_body	107521693
1173	cg47231156_TC21	0.0006251	-0.06328293	Lower	Sema3f	chr9	-	tss_body	107682948
1174	cg47232144_TC21	0.00040419	-0.05659956	Lower	Rbm5	chr9	-	tss_body	107744087
1175	cg47234031_BC21	0.0009401	-0.08202713	Lower	Camkv	chr9	+	tss_body	107937254
1176	cg47234613_TC21	0.00080647	0.06668851	Higher	Uba7	chr9	+	tss_body	107978474
1177	cg47236366_TC21	0.00087548	0.06471296	Higher	LOC108167685	chr9	+	tss_1500	108094644
1178	cg47242366_BC11	0.00023107	0.06955587	Higher	Qrich1	chr9	+	tss_body	108518162
1179	cg47244189_TC21	0.00026056	0.06424975	Higher		chr9	-	tss_1500	108654680
1180	cg47265090_BC21	0.00087256	0.12738256	Higher	Myl3	chr9	+	tss_body	110768824
1181	cg47278088_BC21	0.00022676	0.07843267	Higher	Arpp21	chr9	-	tss_body	112095105
1182	cg47342737_BC21	6.2925E-05	-0.05353553	Lower	Itga9	chr9	+	tss_body	118633353

1183	cg47395211_TC21	0.0008534	0.0762954	Higher	Gm35501	chr9	+	tss_body	122686808
1184	cg47406903_TC21	0.0004574	-0.0618397	Lower	LOC108167320	chr9	-	tss_body	124442192
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47520568_TC21	0.0002558	0.0554866	Higher					23404896
2	cg47578637_TC21	0.0008951	-0.0562605	Lower	Gria3	chrX	+	tss_body	41402822
3	cg47620358_BC21	0.0008553	-0.0536001	Lower					49768766
4	cg47633832_TC21	0.0007086	-0.1013973	Lower	Gpc4	chrX	-	tss_body	52053879
5	cg47634370_BC21	0.0009399	0.0517104	Higher	Gpc4	chrX	-	tss_body	52128685
6	cg47634421_TC21	0.0001952	0.0761416	Higher	Gpc4	chrX	-	tss_body	52136704
7	cg47645856_TC11	0.0009023	-0.0830175	Lower	Xlr	chrX	-	tss_200	53797727
8	cg47719174_BC21	0.0001958	0.1146922	Higher					70327574
9	cg47860946_TC11	0.0006593	0.0703845	Higher	Gm30798	chrX	+	tss_body	99456505
10	cg47901320_TC21	0.0006475	-0.0546036	Lower	Magee1	chrX	+	tss_body	105123155
11	cg47943853_BC21	0.0004217	-0.0668575	Lower	Klhl4	chrX	+	tss_body	114551512
12	cg48017410_BC21	0.0009787	-0.0559147	Lower	Nox1	chrX	-	tss_body	134119638
13	cg48018391_TC21	0.0005044	-0.0630482	Lower	Trmt2b	chrX	-	tss_body	134244977
14	cg48030336_TC21	0.0009301	-0.1054732	Lower	Nxf3	chrX	-	tss_body	136085193
15	cg48044319_TC21	0.0007523	0.0804220	Higher	Il1rapl2	chrX	+	tss_body	138651585
16	cg48046212_BC21	0.0001368	-0.0573317	Lower	Nrk	chrX	+	tss_body	138999855
17	cg48067677_BC21	0.0001681	0.1022329	Higher					142476564
18	cg48070676_BC21	0.0007797	0.0597000	Higher	Tmem164	chrX	+	tss_body	142839791
19	cg48116023_BC21	0.0008462	-0.0622539	Lower	Shroom2	chrX	-	tss_body	152623078
20	cg48175474_BC21	0.0006776	-0.0796296	Lower		chrX	-	tss_body	163778404
21	cg48205167_TC21	0.0009481	-0.0701093	Lower	Arhgap6	chrX	+	tss_body	169255513

Y chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48217471_BC21	8.1979E-06	0.11820814	Higher		chrY	+	tss_body	1960679

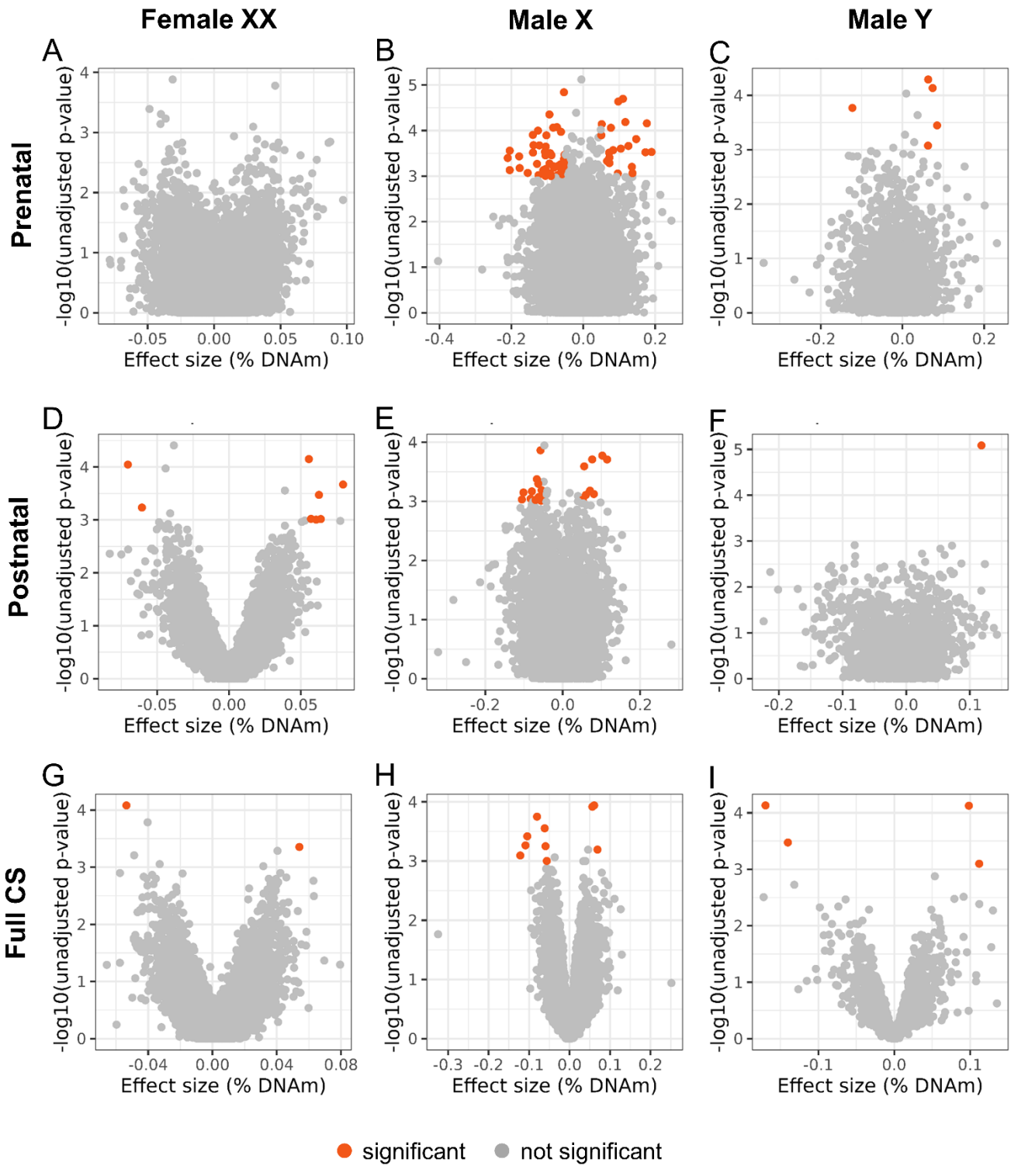
Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 15: Significantly altered CpGs in male lungs at 16 weeks due to full CS exposure

Autosomes									
	CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	Feature	CpG position
1	cg28696378_TC21	0.000994	0.07904	Higher	Olfr1358	chr10	+	tss_body	78520134
2	cg29268796_TC21	0.000511	0.052206	Higher					15416819
3	cg29289063_TC21	0.000368	0.052414	Higher	Meis1	chr11	-	tss_body	18973968
4	cg30130752_TC21	0.000416	0.052589	Higher	Prkca	chr11	-	tss_body	1.08E+08
5	cg30760310_TC11	0.000454	0.061388	Higher	Gm32151	chr12	+	tss_body	70347981
6	cg31061762_TC21	0.000384	0.056538	Higher	Syne3	chr12	-	tss_body	1.05E+08
7	cg32471934_TC21	0.000626	-0.05335	Lower	E9Q0Z1	chr14	-	tss_body	51074379
8	cg34113166_TC11	0.000821	0.053709	Higher	Mylk	chr16	+	tss_body	34824879
9	cg34844222_BC11	0.000339	0.068871	Higher					32434525
10	cg35248308_BC21	0.00043	0.081736	Higher		chr17	+	tss_1500	79810438
11	cg35595055_BC21	0.000853	0.074279	Higher		chr18	+	tss_body	35814934
12	cg36075302_BC21	0.000971	-0.0774	Lower	Carns1	chr19	-	tss_body	4170366
13	cg36520101_BC21	0.000746	0.085591	Higher					53413730
14	cg36796439_BC21	0.00032	0.062526	Higher					35472963
15	cg37624108_BC11	0.000711	0.084958	Higher	Rgs8	chr1	+	tss_200	1.54E+08
16	cg37684366_BC11	0.000688	0.070481	Higher	Ankrd45	chr1	+	tss_body	1.61E+08
17	cg39234132_BC21	0.000489	0.055694	Higher	Hnf4a	chr2	+	tss_body	1.64E+08
18	cg40924194_BC11	0.00092	0.054795	Higher	Frrs1l	chr4	-	tss_1500	56990608
19	cg41495568_TC21	0.000386	-0.05418	Lower	Ptafr	chr4	+	tss_1500	1.33E+08
20	cg41503067_BC21	0.00077	0.05972	Higher					1.33E+08
21	cg42091454_BC21	0.000421	0.074251	Higher	C1qtnf7	chr5	+	tss_200	43515539
22	cg42722996_TC21	0.000215	0.056327	Higher	Oas1g	chr5	-	tss_200	1.21E+08
23	cg42945152_TC21	6.48E-05	0.063742	Higher	LOC108169079	chr5	+	tss_1500	1.4E+08
24	cg43315556_BC21	0.000211	0.072224	Higher	Dgki	chr6	-	tss_body	37096745
25	cg43372777_BC21	0.000217	0.052585	Higher	Cntnap2	chr6	+	tss_body	45794225
26	cg43473236_TC21	1.44E-05	0.100384	Higher	Herc6	chr6	+	tss_body	57581096
27	cg44197369_TC11	0.00049	0.064299	Higher	Nat14	chr7	+	tss_body	4924346
28	cg44390869_BC21	0.000187	0.065889	Higher	Syne4	chr7	+	tss_body	30314939

29	cg44954718_BC21	3.21E-05	0.071637	Higher	Mrpl17	chr7	-	tss_body	1.06E+08
30	cg46347459_BC11	0.000451	0.070611	Higher	Disc1	chr8	+	tss_body	1.25E+08
31	cg46730689_TC11	0.000617	0.055122	Higher	Ncam1	chr9	-	tss_body	49777537
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47498648_TC21	0.000178	-0.08035	Lower					18847763
2	cg47508392_TC21	0.00028	-0.06146	Lower					20789890
3	cg47675154_TC21	0.000561	-0.05936	Lower		chrX	-	tss_200	59693556
4	cg47726582_TC21	0.000382	-0.10448	Lower					71624551
5	cg47874257_BC21	0.000641	0.068977	Higher					1.01E+08
6	cg48052239_TC21	0.000115	0.060758	Higher	Rbm41	chrX	-	tss_body	1.4E+08
7	cg48082394_TC21	0.000121	0.056273	Higher	Zcchc16	chrX	+	tss_body	1.45E+08
8	cg48101692_BC21	0.000805	-0.12169	Lower					1.5E+08
9	cg48122829_BC21	0.000544	-0.10886	Lower					1.54E+08
10	cg48129303_TC21	0.000995	-0.05621	Lower					1.55E+08
Y chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48214003_BC11	0.000797	0.111967	Higher	Uty	chrY	-	tss_body	1110542
2	cg48216952_TC21	7.39E-05	-0.1697	Lower					1879627
3	cg48219835_TC21	7.48E-05	0.098359	Higher					2458037
4	cg48235951_BC21	0.000335	-0.1402	Lower					6541886

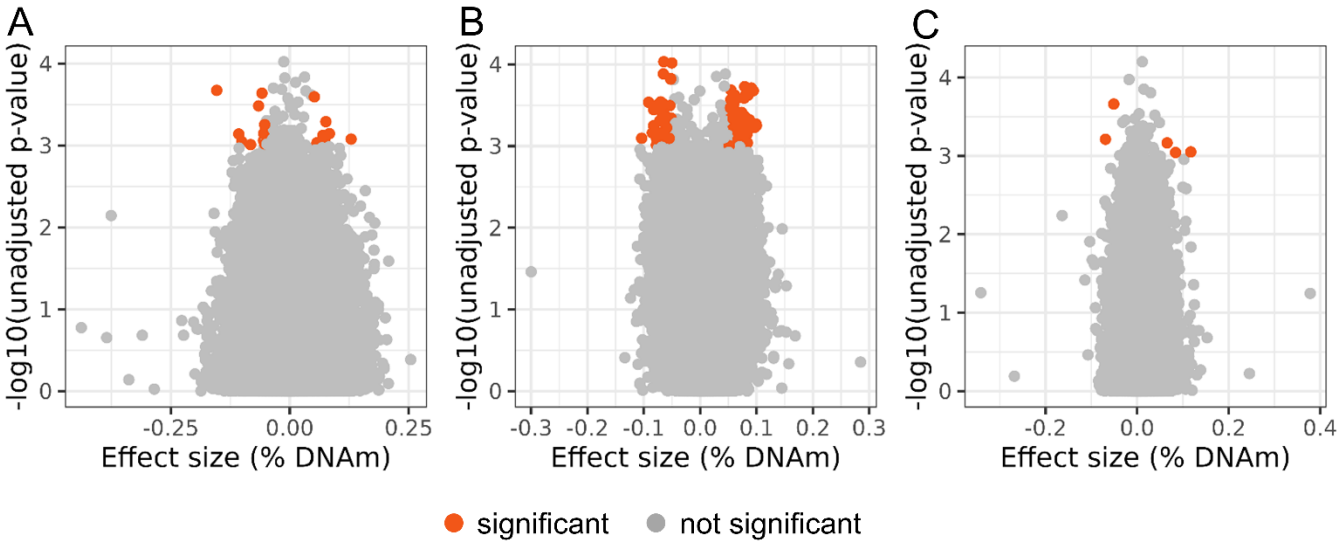
Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.



Appendix 4. 16: Differentially methylated CpGs due to early life CS exposure in lung sex chromosomes at 16 weeks.

(A) There were no differentially methylated CpGs due to prenatal CS exposure on the X chromosome of female offspring lung at 16 weeks (B) 66 CpGs (20 higher, 46 lower) are differentially methylated due to prenatal CS exposure on the X chromosome of male offspring lung at 16 weeks (C) 5 CpGs (4 higher, 1 lower) are differentially methylated due to prenatal

CS exposure on the Y chromosome of male offspring lung at 16 weeks (D) 8 CpGs (6 higher, 2 lower) are differentially methylated due to postnatal CS exposure on the X chromosome of female offspring lung at 16 weeks (E) 21 CpGs (8 higher, 13 lower) are differentially methylated due to postnatal CS exposure on the X chromosome of male offspring lung at 16 weeks (F) 1 CpG (1 higher, 0 lower) is differentially methylated due to postnatal CS exposure on the Y chromosome of male offspring lung at 16 weeks (G) 2 CpGs (1 higher, 1 lower) are differentially methylated due to full CS exposure on the X chromosome of female offspring lung at 16 weeks (H) 10 CpGs (3 higher, 7 lower) are differentially methylated due to full CS exposure on the Y chromosome of male offspring lung at 16 weeks (I) 4 CpGs (2 higher, 2 lower) are differentially methylated due to full CS exposure on the Y chromosome of male offspring lung at 16 weeks. DNAm differences were analyzed using linear regression, and CpGs were considered differentially methylated at $p < 10e\text{-}3$ and effect size > 0.05. Delta beta (effect size) was calculated by subtracting beta values of exposed offspring from control mean betas. N = 2-6 per group. Significant CpGs are highlighted in orange, while non-significant ones are highlighted in grey.



Appendix 4. 17: Differentially methylated CpGs due to early life CS exposure in lung autosomes of a reduced number of female offspring at 16 weeks (sensitivity analysis).

(A) 20 CpGs (9 higher, 11 lower) are differentially methylated due to prenatal CS exposure on the autosomes of female offspring lung at 16 weeks (B) 89 CpGs (53 higher, 36 lower) are differentially methylated due to postnatal CS exposure on the autosomes of female offspring lung at 16 weeks (C) 5 CpGs (3 higher, 2 lower) are differentially methylated due to full CS exposure on the autosomes of female offspring lung at 16 weeks DNAm differences were analyzed using linear regression, and CpGs were considered differentially methylated at $p <$ 10e-3 and effect size > 0.05. Delta beta (effect size) was calculated by subtracting beta values of exposed offspring from control mean betas. N = 5 control, 2 prenatal, 2 postnatal, 2 full CS. Significant CpGs are highlighted in orange, while non-significant ones are highlighted in grey.

Appendix 4. 18: Significantly altered CpGs in female lungs at 63 weeks due to prenatal CS exposure

Autosomes									
	CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	Feature	CpG position
1	cg04056615_TC21	0.000798	-0.05061	Lower	Celf3	chr3	+	tss_body	94484297
2	cg28690445_TC21	1.52E-05	0.092968	Higher	Aire	chr10	-	tss_body	78031949
3	cg28711694_BC21	0.000331	0.058914	Higher	Abca7	chr10	+	tss_body	80002702
4	cg28725096_TC21	0.000725	-0.0531	Lower	Csnk1g2	chr10	+	tss_body	80638507
5	cg28795853_TC21	9.19E-05	0.056949	Higher	Stab2	chr10	-	tss_body	86974363
6	cg29034922_TC21	0.000303	-0.05891	Lower	Gm31963	chr10	+	tss_body	1.17E+08
7	cg29840782_TC21	9.27E-05	0.051027	Higher	Tmem132e	chr11	+	tss_body	82423770
8	cg30251175_BC11	0.000708	-0.05682	Lower	Gm11725	chr11	+	tss_body	1.18E+08
9	cg30359570_TC11	0.00044	-0.06992	Lower	Osr1	chr12	+	tss_body	9580130
10	cg30841665_TC11	0.000598	0.067541	Higher	Tmem229b	chr12	-	tss_1500	79008009
11	cg31089458_TC21	0.000239	0.050096	Higher					1.07E+08
12	cg31118594_TC11	0.000563	0.072624	Higher	Dlk1	chr12	+	tss_body	1.09E+08
13	cg31162145_TC21	0.000964	-0.05262	Lower					1.13E+08
14	cg31401165_BC21	0.000762	-0.11966	Lower	Gm35302	chr13	+	tss_body	31082105
15	cg31403382_BC21	5.04E-06	-0.09009	Lower	G630018N14Rik	chr13	-	tss_body	31408925
16	cg31426156_BC21	0.000625	0.068361	Higher					34705652
17	cg31616668_BC21	7.55E-05	0.057692	Higher					53898758
18	cg31680002_BC21	0.000869	0.083979	Higher	Ntrk2	chr13	+	tss_body	58844222
19	cg31702693_TC21	0.000159	0.055919	Higher	Tpbpb	chr13	-	tss_body	60902188
20	cg31960217_BC11	0.000801	0.053024	Higher	Foxd1	chr13	+	tss_1500	98353799
21	cg32005605_BC21	0.000157	-0.07049	Lower	Mast4	chr13	-	tss_body	1.03E+08
22	cg32518464_TC21	0.00046	-0.05673	Lower	Gzmg	chr14	-	tss_body	56157252
23	cg32980380_TC21	0.000102	0.070213	Higher					1.21E+08
24	cg33395766_BC21	0.000293	-0.05112	Lower	4933412E24Rik	chr15	-	tss_200	60016630
25	cg33655237_BC21	0.000362	0.059609	Higher	Gm35599	chr15	+	tss_body	87831652
26	cg34084439_TC11	0.00032	-0.08264	Lower					32129848
27	cg34101092_TC11	0.000124	-0.1047	Lower	Heg1	chr16	+	tss_body	33691724
28	cg34228024_BC21	0.000127	-0.05953	Lower	4930542D17Rik	chr16	+	tss_body	50645430

29	cg34731705_TC21	0.000405	-0.08411	Lower	Mlst8	chr17	-	tss_body	24474098
30	cg34860661_TC21	0.000633	0.050145	Higher	Brd2	chr17	-	tss_body	34116908
31	cg34895367_BC11	1.41E-05	0.065757	Higher	Rnf39	chr17	+	tss_body	36947513
32	cg35053184_BC21	0.000629	0.051472	Higher	Arrdc5	chr17	-	tss_body	56297805
33	cg35242342_BC21	0.000321	-0.0549	Lower					79136053
34	cg35446079_TC21	0.000252	-0.05458	Lower		chr18	-	tss_200	13306418
35	cg35592236_TC21	0.000842	0.054491	Higher	Snhg4	chr18	+	tss_body	35554655
36	cg35593178_BC21	0.000259	0.114755	Higher	Prob1	chr18	-	tss_body	35651613
37	cg35792874_BC21	0.000284	0.055737	Higher	Camk2a	chr18	+	tss_body	60941684
38	cg35843124_BC21	0.000246	0.051718	Higher	Oacyl	chr18	+	tss_body	65715890
39	cg35845375_TC21	0.000393	0.131442	Higher					65906218
40	cg36799857_TC11	0.000227	0.053054	Higher					35918269
41	cg36803879_TC11	0.000527	0.092031	Higher	Neurl3	chr1	-	tss_body	36269715
42	cg36849232_TC21	0.000413	0.071564	Higher					40179230
43	cg37006138_BC11	0.000198	-0.05604	Lower	Zdbf2	chr1	+	tss_body	63261254
44	cg37191000_TC21	0.000131	0.063657	Higher	Inpp5d	chr1	+	tss_body	87695382
45	cg37214886_TC11	0.000131	-0.06473	Lower	Asb18	chr1	-	tss_body	89993031
46	cg37253717_TC21	7.82E-05	0.054459	Higher	Bok	chr1	+	tss_body	93689452
47	cg37785443_TC21	0.000961	-0.06501	Lower	Atp1a2	chr1	-	tss_body	1.72E+08
48	cg37799500_BC21	0.00075	0.063678	Higher	Olfr417	chr1	+	tss_1500	1.74E+08
49	cg37839755_BC21	0.000491	0.09504	Higher	Smyd3	chr1	-	tss_body	1.79E+08
50	cg37880407_BC21	0.000143	0.052925	Higher	Tlr5	chr1	+	tss_body	1.83E+08
51	cg37907117_TC21	0.000935	-0.07978	Lower					1.86E+08
52	cg38196075_BC11	0.00072	0.055168	Higher	chr2-28909689-28910009	chr2	*	NShelf	28906783
53	cg38527101_TC21	3.36E-05	-0.06946	Lower	Platr26	chr2	+	tss_body	71719666
54	cg38569434_TC21	0.000527	-0.05379	Lower	Nfe2l2	chr2	-	tss_body	75687528
55	cg38834870_TC21	0.000455	-0.05697	Lower	Meis2	chr2	-	tss_body	1.16E+08
56	cg39010442_BC21	0.000768	-0.11492	Lower	Snap25	chr2	+	tss_body	1.37E+08
57	cg39177451_TC21	0.00023	0.076965	Higher	Blcap	chr2	-	tss_body	1.58E+08
58	cg39234132_BC21	0.000348	-0.05194	Lower	Hnf4a	chr2	+	tss_body	1.64E+08
59	cg39351755_TC21	0.000428	-0.06261	Lower		chr2	-	tss_body	1.72E+08

60	cg39750545_TC21	0.000985	-0.05655	Lower	Foxo1	chr3	+	tss_body	52340473
61	cg40117414_TC21	5.66E-05	0.08167	Higher					1.02E+08
62	cg40149438_TC21	8.07E-06	0.05724	Higher	Fam212b	chr3	+	tss_1500	1.06E+08
63	cg40292382_BC21	0.000304	-0.06025	Lower	Camk2d	chr3	+	tss_body	1.27E+08
64	cg41054616_TC21	0.000214	-0.05322	Lower					80446820
65	cg41337956_BC11	0.000849	-0.05117	Lower	Ptprf	chr4	-	tss_body	1.18E+08
66	cg41343796_BC11	7.65E-05	0.059262	Higher	L7MU75	chr4	+	tss_1500	1.19E+08
67	cg41359583_BC21	0.000224	0.052192	Higher	Foxo6	chr4	-	tss_body	1.2E+08
68	cg41705774_BC21	0.000277	0.100369	Higher	Pik3cd	chr4	-	tss_body	1.5E+08
69	cg41918952_BC21	0.000961	0.050261	Higher		chr5	+	tss_body	22611973
70	cg42658214_BC21	0.000948	-0.0525	Lower	Tmem233	chr5	-	tss_body	1.16E+08
71	cg42731685_TC21	5.12E-05	-0.06776	Lower	Aldh2	chr5	-	tss_body	1.22E+08
72	cg42830830_BC21	0.000185	0.055796	Higher	Sfswap	chr5	+	tss_body	1.3E+08
73	cg42858079_TC21	0.000193	0.063952	Higher	Auts2	chr5	-	tss_body	1.32E+08
74	cg43394833_TC21	0.000302	0.06496	Higher	Malsu1	chr6	+	tss_body	49131976
75	cg43420321_TC21	0.00059	0.068783	Higher					51680733
76	cg43480504_BC21	5.41E-05	0.052282	Higher	Herc3	chr6	+	tss_body	58906529
77	cg43728479_TC21	0.000874	-0.05516	Lower	Lrig1	chr6	-	tss_body	94674025
78	cg43904183_TC21	0.00032	-0.06289	Lower					1.18E+08
79	cg43945543_BC21	0.000305	-0.06479	Lower	Rimklb	chr6	-	tss_1500	1.22E+08
80	cg44356429_TC21	0.000584	0.057768	Higher	Zfp626	chr7	+	tss_body	27808062
81	cg44455662_BC21	0.000128	-0.05621	Lower	Zfp536	chr7	-	tss_body	37466702
82	cg44458934_TC21	6.24E-05	-0.06478	Lower	Zfp536	chr7	-	tss_body	37743481
83	cg44495119_BC21	0.000952	-0.06288	Lower	Ctu1	chr7	+	tss_body	43675345
84	cg44516596_BC11	0.000782	0.070804	Higher	Cd37	chr7	-	tss_body	45234353
85	cg44779726_TC21	0.000223	0.068296	Higher	Iqgap1	chr7	-	tss_body	80777408
86	cg44958331_TC21	0.000684	0.052979	Higher	Q7TRN3	chr7	-	tss_body	1.07E+08
87	cg45007652_TC21	0.00019	0.054578	Higher					1.13E+08
88	cg45316032_TC21	4.09E-05	-0.07123	Lower	Retn	chr8	+	tss_body	3657840
89	cg45808368_BC21	0.000892	-0.06208	Lower	Sugp2	chr8	+	tss_body	70257675
90	cg45839022_TC21	4.71E-05	0.06174	Higher	Sin3b	chr8	+	tss_body	72753908

91	cg45996620_BC21	6.06E-05	-0.06369	Lower	Fto	chr8	+	tss_body	91626067
92	cg46018659_TC21	0.000755	-0.0794	Lower	Gnao1	chr8	+	tss_body	93918034
93	cg46095071_TC11	0.000881	0.059873	Higher	Tradd	chr8	-	tss_body	1.05E+08
94	cg46368710_TC11	0.000566	0.076663	Higher					1.27E+08
95	cg46463090_BC21	0.000107	-0.05236	Lower					16888213
96	cg47120580_TC21	0.000709	-0.06166	Lower	Zbtb38	chr9	-	tss_body	96726613
97	cg47166957_TC21	0.000915	-0.05154	Lower					1.02E+08
98	cg47234055_TC21	7.71E-05	-0.05519	Lower	Camkv	chr9	+	tss_body	1.08E+08
99	cg47294788_BC21	0.000207	-0.05048	Lower					1.14E+08
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47427942_TC21	0.000338	-0.06796	Lower	Wdr45	chrX	+	tss_1500	7721990
2	cg47489270_BC21	0.000756	0.061359	Higher	Maob	chrX	-	tss_200	16817510
3	cg47511567_BC21	0.000446	-0.07564	Lower	Gm6938	chrX	-	tss_200	21334742
4	cg47562473_TC21	4.94E-05	-0.13328	Lower					37908803
5	cg47575004_TC21	0.000598	-0.08162	Lower		chrX	+	tss_body	40407821
6	cg47626157_TC21	0.000614	-0.05688	Lower	Stk26	chrX	+	tss_body	50884199
7	cg47632691_TC21	0.000178	-0.05777	Lower					51895795
8	cg47657337_BC21	0.00036	-0.10129	Lower	Slc9a6	chrX	+	tss_body	56609994
9	cg47667002_BC21	0.000322	-0.05132	Lower	Zic3	chrX	+	tss_body	58029063
10	cg47677954_BC21	0.000842	-0.07397	Lower	Atp11c	chrX	-	tss_body	60266392
11	cg47741246_TC21	0.000549	-0.05395	Lower	Irak1	chrX	-	tss_body	74021027
12	cg47743038_BC21	0.000434	-0.11594	Lower	Dnase1l1	chrX	-	tss_body	74273985
13	cg47749679_BC21	0.000426	0.084461	Higher	Brcc3	chrX	+	tss_body	75416898
14	cg47794447_BC21	0.000205	0.070173	Higher	Tab3	chrX	+	tss_body	85574516
15	cg48018338_BC21	7.05E-05	-0.08031	Lower	Trmt2b	chrX	-	tss_body	1.34E+08
16	cg48034707_BC21	0.000587	-0.07702	Lower	Morf4l2	chrX	-	tss_body	1.37E+08
17	cg48037561_BC21	0.000807	-0.05877	Lower		chrX	-	tss_body	1.37E+08
18	cg48037906_BC21	0.000765	-0.06312	Lower	Esx1	chrX	-	tss_body	1.37E+08
19	cg48204404_BC21	0.000136	-0.07	Lower	Arhgap6	chrX	+	tss_body	1.69E+08

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are

sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 19: Significantly altered CpGs in female lungs at 63 weeks due to postnatal CS exposure

Autosomes									
	CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	Feature	CpG position
1	cg28587407_BC21	0.000593	0.064611	Higher	LOC105245193	chr10	-	tss_body	67570584
2	cg29166603_TC21	7.87E-05	-0.05256	Lower	Dnajc14	chr10	+	tss_body	1.29E+08
3	cg29290990_TC21	6.9E-05	-0.06246	Lower					19178969
4	cg30779576_TC21	0.000956	-0.05478	Lower	Ccdc175	chr12	-	tss_body	72185012
5	cg32468817_TC21	1.64E-05	-0.05316	Lower	Ttc5	chr14	-	tss_body	50776182
6	cg32473369_BC21	0.000985	-0.05358	Lower	Rnase2a	chr14	-	tss_body	51255677
7	cg33178210_TC21	0.000507	-0.05744	Lower	Trio	chr15	-	tss_body	27796254
8	cg34102287_BC11	0.000452	0.050508	Higher		chr16	-	tss_body	33785503
9	cg34398520_TC21	0.000112	-0.05597	Lower	Tmprss15	chr16	-	tss_body	79091035
10	cg34909837_BC11	7.25E-05	0.05735	Higher		chr17	+	tss_body	39844389
11	cg36834032_BC21	0.000663	-0.05032	Lower	Chst10	chr1	-	tss_body	38885445
12	cg37186079_TC21	0.000101	-0.05042	Lower	Chrnd	chr1	+	tss_body	87191549
13	cg37920875_TC11	0.000559	0.068084	Higher	Spata17	chr1	-	tss_body	1.87E+08
14	cg38383428_BC21	0.000863	0.071601	Higher	LOC108168754	chr2	+	tss_1500	52378296
15	cg38437107_BC21	0.000737	-0.06741	Lower	Baz2b	chr2	-	tss_body	60173366
16	cg38552868_BC21	0.000688	-0.07379	Lower		chr2	+	tss_body	74135810
17	cg38975136_BC21	0.000206	-0.05064	Lower	5330413P13Rik	chr2	-	tss_body	1.32E+08
18	cg39429188_TC21	0.000805	-0.05276	Lower	Gm14342	chr2	-	tss_body	1.81E+08
19	cg41355441_BC21	7.71E-05	-0.05903	Lower	Hivep3	chr4	+	tss_body	1.2E+08
20	cg42164070_BC21	0.000172	-0.06568	Lower					54411463
21	cg43380935_BC21	0.000538	0.078826	Higher					47606056
22	cg44144665_BC11	0.000489	0.058216	Higher	LOC105247329	chr6	-	tss_body	1.45E+08
23	cg44320080_BC21	0.000887	-0.07527	Lower	Zfp575	chr7	-	tss_body	24585592
24	cg44416130_BC11	0.000284	0.055854	Higher	Scgb2b27	chr7	-	tss_body	34013353
25	cg44797941_TC21	8.46E-05	0.070582	Higher	Adamtsl3	chr7	+	tss_body	82465632
26	cg44998063_BC21	0.00068	-0.06665	Lower	Mical2	chr7	+	tss_1500	1.12E+08
27	cg45653386_TC21	0.000948	-0.06088	Lower	Gm30931	chr8	+	tss_1500	46363042
28	cg46018659_TC21	0.000137	-0.07758	Lower	Gnao1	chr8	+	tss_body	93918034

29	cg47390980_TC11	0.00023	-0.06212	Lower	Ano10	chr9	-	tss_body	1.22E+08
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47472437_TC21	0.000191	-0.11529	Lower					13207360
2	cg47628518_BC21	0.000483	-0.05583	Lower	Mbnl3	chrX	-	tss_body	51189840
3	cg47638657_TC21	0.000413	0.057826	Higher	Mir363	chrX	-	tss_1500	52742477
4	cg47720211_BC11	0.000108	0.056743	Higher	BC023829	chrX	-	tss_body	70476909
5	cg47745239_BC21	0.000696	0.057423	Higher		chrX	+	tss_body	74567289
6	cg47882406_BC11	0.000719	0.068731	Higher	Cited1	chrX	-	tss_body	1.02E+08
7	cg48074189_BC21	0.000539	0.058644	Higher	Chrdl1	chrX	-	tss_body	1.43E+08

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 20: Significantly altered CpGs in female lungs at 63 weeks due to full CS exposure

Autosomes									
	CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	Feature	CpG position
1	cg12044283_TC21	0.00012	-0.06685	Lower	Gm28578	chr19	-	tss_body	45330028
2	cg20138186_TC21	0.000278	0.070724	Higher					44900527
3	cg28300281_TC21	0.000381	-0.0617	Lower	Arhgap18	chr10	+	tss_body	26785669
4	cg28355659_TC21	1.87E-05	0.052167	Higher					37251190
5	cg28471146_TC21	0.000479	0.051063	Higher	Gm36280	chr10	+	tss_200	53488123
6	cg28558004_TC11	0.00021	-0.06805	Lower	Q9R022	chr10	+	tss_body	63410442
7	cg28612785_TC21	0.000223	-0.06207	Lower	Ank3	chr10	+	tss_body	69901457
8	cg28690445_TC21	0.000172	0.073335	Higher	Aire	chr10	-	tss_body	78031949
9	cg28880711_BC21	0.00014	-0.07675	Lower	Gm33377	chr10	+	tss_body	95893328
10	cg28959315_TC21	0.000724	-0.08308	Lower					1.08E+08
11	cg29022528_TC21	5.49E-05	-0.05891	Lower	Ptprb	chr10	+	tss_body	1.16E+08
12	cg29100534_TC11	0.000191	0.261588	Higher	Avpr1a	chr10	+	tss_1500	1.22E+08
13	cg29164617_TC21	0.000278	0.058178	Higher	Ikzf4	chr10	-	tss_body	1.29E+08
14	cg29178996_BC21	0.000181	-0.06567	Lower	Limk2	chr11	-	tss_body	3368756
15	cg29197045_TC21	0.000662	0.064048	Higher	Ap1b1	chr11	+	tss_body	4949549
16	cg29252451_BC21	0.000139	0.074761	Higher	Grb10	chr11	-	tss_body	11957070
17	cg29297828_TC21	6.1E-05	-0.05821	Lower	Spred2	chr11	+	tss_body	19955747
18	cg29314303_BC11	7.31E-05	-0.05048	Lower	Otx1	chr11	-	tss_body	21996261
19	cg29376878_TC11	0.000457	0.09117	Higher	Rhbdf1	chr11	-	tss_body	32219006
20	cg29428350_BC11	0.000115	0.137128	Higher					38120928
21	cg29582848_TC21	5.62E-05	0.056667	Higher	Galnt10	chr11	+	tss_body	57751164
22	cg29681068_BC11	0.00065	0.081118	Higher	Gas7	chr11	+	tss_body	67589948
23	cg29706202_BC21	8.29E-05	0.09704	Higher	Dnah2	chr11	-	tss_body	69527097
24	cg29708327_BC11	0.000864	0.087717	Higher	Sox15	chr11	+	tss_body	69655569
25	cg29745520_TC21	0.000349	0.051736	Higher	Camkk1	chr11	+	tss_body	73037251
26	cg29747941_TC21	0.000298	-0.05167	Lower	Trpv1	chr11	+	tss_body	73238284
27	cg29760826_TC21	0.000424	-0.06325	Lower	Smg6	chr11	+	tss_body	75071418
28	cg29763258_BC11	0.000844	0.055379	Higher	Rtn4rl1	chr11	+	tss_body	75245587

29	cg29861614_BC21	0.000164	-0.06162	Lower	Lhx1	chr11	-	tss_body	84522122
30	cg29978669_BC21	0.000973	0.088326	Higher	Hoxb5os	chr11	-	tss_body	96305223
31	cg30069111_BC21	0.000599	-0.05124	Lower	Adam11	chr11	+	tss_body	1.03E+08
32	cg30078889_BC21	0.000189	0.053314	Higher	Plekhm1	chr11	-	tss_body	1.03E+08
33	cg30111960_BC21	0.000248	-0.05426	Lower	Tex2	chr11	-	tss_body	1.07E+08
34	cg30112251_TC21	9.24E-05	0.054484	Higher	Tex2	chr11	-	tss_body	1.07E+08
35	cg30112662_TC21	0.000491	0.058291	Higher	Tex2	chr11	-	tss_body	1.07E+08
36	cg30136214_TC11	6.13E-05	-0.05889	Lower	Cep112	chr11	+	tss_body	1.09E+08
37	cg30138431_BC21	0.000322	0.061581	Higher	LOC108167934	chr11	-	tss_body	1.09E+08
38	cg30175990_BC21	0.000225	0.101424	Higher	LOC108167938	chr11	+	tss_body	1.13E+08
39	cg30219161_TC21	0.000419	0.081245	Higher	Myo15b	chr11	+	tss_body	1.16E+08
40	cg30239448_TC21	0.000874	-0.06358	Lower					1.17E+08
41	cg30243594_TC21	4.59E-05	-0.0694	Lower	Sept9	chr11	+	tss_body	1.17E+08
42	cg30259126_BC11	0.000713	0.065869	Higher	Cant1	chr11	-	tss_body	1.18E+08
43	cg30260678_TC21	0.000234	0.054055	Higher	Rbfox3	chr11	-	tss_body	1.19E+08
44	cg30278583_TC11	6.6E-05	0.067261	Higher	Rptor	chr11	+	tss_body	1.2E+08
45	cg30287912_BC21	0.000293	-0.05262	Lower	Bahcc1	chr11	+	tss_body	1.2E+08
46	cg30482431_BC21	0.000271	0.05528	Higher	Gm9866	chr12	-	tss_body	27160471
47	cg30751288_TC11	0.000534	0.061295	Higher	Vcpkmt	chr12	-	tss_1500	69583638
48	cg30923252_BC21	7.56E-05	-0.12744	Lower					86559089
49	cg31002138_TC21	0.000867	-0.05899	Lower					99097404
50	cg31077270_BC21	0.000185	0.059553	Higher					1.06E+08
51	cg31103515_TC21	9.81E-05	0.074536	Higher	Ccdc85c	chr12	-	tss_body	1.08E+08
52	cg31257492_BC21	0.000256	-0.05138	Lower	Chrm3	chr13	-	tss_body	9878969
53	cg31405776_BC11	8.73E-05	0.07251	Higher	Foxf2	chr13	+	tss_body	31629426
54	cg31486768_TC21	0.000985	-0.06537	Lower	Gm32184	chr13	-	tss_body	41560032
55	cg31605050_BC21	0.000995	-0.0602	Lower	Nfil3	chr13	-	tss_body	52976415
56	cg31645345_TC21	0.000496	-0.05028	Lower		chr13	+	tss_body	56024904
57	cg31686159_TC21	0.000577	-0.05462	Lower					59388087
58	cg31702693_TC21	9.05E-05	0.06987	Higher	Tpbpb	chr13	-	tss_body	60902188
59	cg31723131_BC21	0.000592	-0.07503	Lower	LOC108168093	chr13	-	tss_body	63901772

60	cg31837287_BC21	0.000858	0.059419	Higher	9330111N05Rik	chr13	+	tss_1500	80963764
61	cg31879636_BC21	0.00072	0.086425	Higher					89427902
62	cg31972732_BC11	0.000284	0.06588	Higher	Map1b	chr13	-	tss_body	99421817
63	cg32245475_TC21	0.000185	-0.05654	Lower	Plau	chr14	+	tss_body	20842909
64	cg32253169_TC21	0.000486	-0.07684	Lower	Dupd1	chr14	-	tss_body	21686649
65	cg32284667_TC21	0.000313	0.073636	Higher	Zmiz1	chr14	+	tss_body	25524818
66	cg32462514_BC21	0.000114	0.089939	Higher	Slc35f4	chr14	-	tss_body	49525558
67	cg32654102_TC11	0.000213	0.130736	Higher	Gm38605	chr14	+	tss_body	70636816
68	cg32673886_TC21	7.94E-05	-0.06342	Lower	Gm35450	chr14	+	tss_body	73475684
69	cg32732802_BC21	0.000786	0.074335	Higher	4930452G13Rik	chr14	+	tss_body	79703756
70	cg32936562_TC21	0.000437	0.064836	Higher	Gpc5	chr14	+	tss_body	1.16E+08
71	cg33069242_BC21	0.000537	-0.07611	Lower	Ttc23l	chr15	-	tss_body	10533718
72	cg33072421_TC11	0.000397	0.099051	Higher		chr15	+	tss_body	10823650
73	cg33182008_TC21	0.000519	-0.06182	Lower		chr15	+	tss_body	28041030
74	cg33183782_BC21	0.000761	0.071352	Higher	Dnah5	chr15	+	tss_body	28229640
75	cg33203070_BC21	0.000216	-0.05182	Lower					31286881
76	cg33353666_BC21	0.000368	-0.07701	Lower	Deptor	chr15	+	tss_body	55121109
77	cg33503308_TC21	0.00021	-0.05604	Lower	Fam83h	chr15	-	tss_body	76014234
78	cg33527557_BC21	0.000557	-0.06367	Lower	Myh9	chr15	-	tss_body	77819933
79	cg33538704_TC21	0.000879	-0.10219	Lower	Elfn2	chr15	-	tss_body	78672051
80	cg33554308_BC11	0.000241	0.093238	Higher	Fam227a	chr15	-	tss_body	79617414
81	cg33561950_TC21	0.000243	0.063783	Higher	Gm31134	chr15	-	tss_body	80091856
82	cg33595928_TC21	0.000117	0.072783	Higher	Nfam1	chr15	-	tss_body	83003121
83	cg33622646_BC21	0.000437	-0.05353	Lower	5031439G07Rik	chr15	-	tss_body	84973649
84	cg33765833_BC11	0.00039	-0.09631	Lower	Hdac7	chr15	-	tss_body	97813059
85	cg33765834_BC21	0.000476	-0.07531	Lower	Hdac7	chr15	-	tss_body	97813097
86	cg33952840_TC11	1.11E-05	0.081986	Higher	2610318N02Rik	chr16	-	tss_body	17124481
87	cg33982213_BC21	2.32E-06	-0.05323	Lower	Abcc5	chr16	-	tss_body	20392886
88	cg33992356_TC21	1.8E-05	0.067874	Higher					21362811
89	cg34020561_TC21	0.000626	0.053511	Higher	Gm31814	chr16	-	tss_body	24205460
90	cg34284589_TC21	0.000605	-0.06028	Lower	Epha6	chr16	-	tss_body	59688596

91	cg34493984_BC21	0.000882	0.063388	Higher	Itsn1	chr16	+	tss_body	91868775
92	cg34538475_BC21	0.000737	-0.05802	Lower	Erg	chr16	-	tss_body	95403602
93	cg34538528_TC21	0.000218	-0.06085	Lower	Erg	chr16	-	tss_body	95408405
94	cg34576750_BC21	0.000501	0.052473	Higher	Arid1b	chr17	+	tss_body	5004419
95	cg34589015_BC21	0.000637	0.06457	Higher	Synj2	chr17	+	tss_body	5996879
96	cg34624722_BC21	1.63E-05	-0.07906	Lower					9539077
97	cg34660538_BC21	7.47E-05	-0.06723	Lower		chr17	-	tss_body	13683791
98	cg34733471_TC21	0.00068	-0.06511	Lower	Pkd1	chr17	+	tss_body	24591145
99	cg34736633_BC21	9.24E-05	-0.08602	Lower		chr17	+	tss_body	24779751
100	cg34761893_BC21	0.000848	-0.07937	Lower	Ergic1	chr17	+	tss_body	26611502
101	cg34864454_BC21	0.000132	0.057379	Higher	BC051142	chr17	+	tss_body	34417490
102	cg34870820_BC21	0.000265	0.107284	Higher	C2	chr17	-	tss_body	34873636
103	cg34883379_TC21	0.000342	0.054125	Higher	Ddr1	chr17	-	tss_body	35686453
104	cg35061388_TC21	0.000723	-0.05964	Lower	Rfx2	chr17	-	tss_body	56829988
105	cg35176658_BC21	0.000394	-0.06201	Lower	Myom1	chr17	+	tss_body	71103089
106	cg35287173_TC11	0.000404	0.097903	Higher					83986353
107	cg35289736_BC21	0.000784	0.095731	Higher	Gm41640	chr17	-	tss_body	84180315
108	cg35306893_BC21	0.000157	-0.0586	Lower	Six3os1	chr17	-	tss_body	85612591
109	cg35414684_TC11	6.83E-05	0.065412	Higher	Fzd8	chr18	+	tss_body	9215132
110	cg35436706_TC21	0.000456	-0.06638	Lower	Npc1	chr18	-	tss_body	12233207
111	cg35512803_TC21	0.000896	-0.06269	Lower					24095213
112	cg35529587_TC21	0.000135	-0.05271	Lower	Gm33228	chr18	+	tss_body	26178704
113	cg35744979_BC21	0.000366	-0.06404	Lower	Gm4221	chr18	+	tss_body	55096324
114	cg35789303_BC21	1.39E-07	-0.06029	Lower	Ndst1	chr18	-	tss_body	60695237
115	cg35840234_TC21	0.000183	-0.05539	Lower	Gm41758	chr18	+	tss_body	65505355
116	cg35993364_BC11	0.000834	0.06973	Higher	Sall3	chr18	-	tss_body	80972081
117	cg36030890_BC21	7.05E-05	0.053911	Higher	Zfp407	chr18	-	tss_body	84264730
118	cg36079252_TC21	7.42E-05	-0.05003	Lower					4492936
119	cg36094169_BC21	4.08E-06	0.069297	Higher	Ovol1	chr19	-	tss_body	5553567
120	cg36104860_TC21	0.000418	-0.05688	Lower	Batf2	chr19	+	tss_200	6164317
121	cg36146503_BC21	1.16E-05	0.071133	Higher	Syt7	chr19	+	tss_body	10395481

122	cg36160877_BC21	0.000616	-0.05504	Lower	Olfr1428	chr19	-	tss_body	12109508
123	cg36186367_TC21	0.000182	-0.06255	Lower	Gnaq	chr19	+	tss_body	16255369
124	cg36408505_BC21	0.000857	-0.0602	Lower	Crtac1	chr19	-	tss_body	42332602
125	cg36463708_BC11	0.000524	-0.0572	Lower	Wbp1l	chr19	+	tss_body	46654649
126	cg36475596_TC21	0.000465	0.073211	Higher					47473355
127	cg36554052_TC21	0.000616	-0.07082	Lower	Plekhs1	chr19	+	tss_body	56461198
128	cg36664824_TC11	0.000336	0.056691	Higher	Lactb2	chr1	-	tss_body	13646304
129	cg36666447_TC11	0.00034	0.086334	Higher	Gm31195	chr1	+	tss_body	13859960
130	cg36680457_TC21	0.000465	-0.05489	Lower					16202657
131	cg36715762_BC21	0.000234	0.054619	Higher	Rims1	chr1	-	tss_body	22306457
132	cg36785974_TC21	0.000386	0.077844	Higher	Dst	chr1	+	tss_body	34290372
133	cg36785975_TC11	0.000262	0.117337	Higher	Dst	chr1	+	tss_body	34290402
134	cg36791371_BC21	0.000845	-0.07627	Lower	Arhgef4	chr1	+	tss_1500	34801247
135	cg36792115_TC21	0.00052	0.079882	Higher	Plekhb2	chr1	+	tss_body	34853144
136	cg36840463_BC21	0.000278	-0.08108	Lower	Tbc1d8	chr1	-	tss_body	39450178
137	cg36927885_TC21	5.7E-05	-0.05536	Lower					53037692
138	cg36959034_BC21	0.000896	-0.05243	Lower					57449198
139	cg37021053_TC21	0.000117	-0.06913	Lower	Crygd	chr1	-	tss_body	65062866
140	cg37084105_BC21	0.000237	-0.05881	Lower	Cxcr1	chr1	-	tss_body	74194723
141	cg37194731_BC21	0.00097	0.062338	Higher	Ugt1a10	chr1	+	tss_body	88205863
142	cg37317587_BC21	8.6E-05	0.053468	Higher	Bcl2	chr1	-	tss_body	1.07E+08
143	cg37408205_TC21	0.000195	-0.07135	Lower	Dpp10	chr1	-	tss_body	1.24E+08
144	cg37451389_BC21	0.000714	0.056612	Higher	Pfkfb2	chr1	-	tss_body	1.31E+08
145	cg37482045_BC21	0.000643	-0.05096	Lower					1.34E+08
146	cg37490547_TC11	0.000469	0.07325	Higher					1.34E+08
147	cg37496044_TC21	0.00012	0.126887	Higher	Syt2	chr1	+	tss_body	1.35E+08
148	cg37514395_TC11	0.000444	-0.05347	Lower	5730559C18Rik	chr1	-	tss_body	1.36E+08
149	cg37648598_TC11	0.000659	0.06948	Higher	Nphs2	chr1	+	tss_200	1.56E+08
150	cg37714201_BC21	0.000274	0.053614	Higher	Gm32652	chr1	-	tss_body	1.65E+08
151	cg38018781_BC21	0.00026	-0.05038	Lower	Camk1d	chr2	-	tss_body	5579737
152	cg38060428_BC21	0.000282	0.05099	Higher		chr2	+	tss_200	11090805

153	cg38123240_TC21	0.000659	-0.05863	Lower	Etl4	chr2	+	tss_body	20649722
154	cg38169749_TC11	0.000345	0.06497	Higher					26575127
155	cg38173187_BC21	0.000309	-0.06901	Lower	Stkld1	chr2	+	tss_body	26943898
156	cg38239673_BC21	0.000925	0.053159	Higher	Prrc2b	chr2	+	tss_body	32157282
157	cg38255705_BC21	0.000609	0.069791	Higher	Ralgps1	chr2	-	tss_body	33265937
158	cg38263560_TC21	0.00033	-0.06827	Lower	Mvb12b	chr2	-	tss_body	33876558
159	cg38277823_BC21	5.19E-05	-0.0671	Lower	Gsn	chr2	+	tss_body	35286773
160	cg38320046_BC21	0.000568	-0.06132	Lower	Lrp1b	chr2	-	tss_body	41988730
161	cg38557782_BC21	0.000169	-0.06	Lower	Hoxd12	chr2	+	tss_body	74675515
162	cg38633051_BC21	0.00094	0.08752	Higher		chr2	-	tss_body	84530316
163	cg38663671_TC21	0.000185	-0.05021	Lower					90612297
164	cg38664172_BC21	0.000205	-0.05899	Lower	Gm39871	chr2	-	tss_1500	90670534
165	cg38687137_TC11	0.000454	0.061844	Higher	Gm13791	chr2	-	tss_body	92849121
166	cg38688527_TC21	0.000244	-0.07524	Lower	Prdm11	chr2	-	tss_body	92983536
167	cg38843590_BC21	0.000424	-0.06537	Lower					1.17E+08
168	cg38933413_BC21	0.000141	-0.06436	Lower	Prom2	chr2	-	tss_body	1.28E+08
169	cg39257930_TC21	9.17E-05	-0.07375	Lower					1.65E+08
170	cg39261217_BC21	9.09E-05	0.058425	Higher	Slc13a3	chr2	-	tss_body	1.65E+08
171	cg39289015_BC11	0.000519	0.052344	Higher					1.67E+08
172	cg39363766_BC21	4.6E-05	-0.06245	Lower	Gm36254	chr2	-	tss_body	1.73E+08
173	cg39370558_BC21	0.000722	0.05188	Higher					1.73E+08
174	cg39780022_TC21	0.000307	0.060782	Higher	Dclk1	chr3	+	tss_body	55442701
175	cg39994401_BC11	0.000121	0.062255	Higher	Lmna	chr3	-	tss_body	88484752
176	cg40001299_BC21	0.000172	0.055651	Higher	Rusc1	chr3	-	tss_body	89084543
177	cg40015413_BC21	0.000311	-0.05768	Lower	4933434E20Rik	chr3	+	tss_body	90062748
178	cg40022036_TC21	0.00045	-0.05031	Lower	Pglyrp4	chr3	+	tss_1500	90726704
179	cg40056553_BC21	0.000871	0.078339	Higher	C920021L13Rik	chr3	+	tss_body	95881923
180	cg40143403_TC21	6.4E-05	-0.09276	Lower	Cttnbp2nl	chr3	-	tss_body	1.05E+08
181	cg40293531_TC21	0.00018	0.065101	Higher	Camk2d	chr3	+	tss_body	1.27E+08
182	cg40391942_BC21	0.000956	-0.05553	Lower	Adh7	chr3	+	tss_body	1.38E+08
183	cg40611586_TC21	5.5E-05	-0.05263	Lower	Ints8	chr4	-	tss_body	11225628

184	cg40974101_TC21	6.36E-05	0.118908	Higher	Akna	chr4	-	tss_body	63395090
185	cg41192859_TC21	0.000518	0.084	Higher	Cachd1	chr4	+	tss_body	1.01E+08
186	cg41337956_BC11	0.000192	-0.12107	Lower	Ptprf	chr4	-	tss_body	1.18E+08
187	cg41343796_BC11	0.000592	0.070071	Higher	L7MU75	chr4	+	tss_1500	1.19E+08
188	cg41464445_TC21	1.99E-05	-0.07931	Lower	Spocd1	chr4	+	tss_body	1.3E+08
189	cg41485520_TC21	0.000301	0.094758	Higher	Ptpru	chr4	-	tss_body	1.32E+08
190	cg41533007_BC11	0.000331	0.100739	Higher					1.35E+08
191	cg41543871_TC21	1.63E-05	0.089764	Higher	Myom3	chr4	+	tss_body	1.36E+08
192	cg41578956_TC21	0.000151	-0.08043	Lower	chr4-138216399-138217685	chr4	*	NShelf	1.38E+08
193	cg41614986_BC11	5.98E-06	0.133194	Higher	Arhgef10l	chr4	-	tss_body	1.41E+08
194	cg41616312_TC21	0.000649	-0.05127	Lower	Rcc2	chr4	+	tss_body	1.41E+08
195	cg41777305_BC21	0.000426	-0.06648	Lower	Prdm16	chr4	-	tss_body	1.55E+08
196	cg41964123_TC21	0.000146	-0.06878	Lower	En2	chr5	+	tss_body	28170175
197	cg41975691_TC11	0.000138	-0.05655	Lower		chr5	-	tss_body	29891928
198	cg41977120_TC21	0.00016	0.053131	Higher	3110082J24Rik	chr5	-	tss_body	30105458
199	cg42051725_BC21	7.77E-05	0.096184	Higher	Crmp1	chr5	+	tss_body	37242963
200	cg42065447_BC21	8.89E-05	0.050675	Higher					38634558
201	cg42289906_BC21	0.000267	0.050707	Higher	Lrrc66	chr5	-	tss_1500	73633304
202	cg42404810_TC11	0.000426	0.063993	Higher	Ppbp	chr5	+	tss_200	90768482
203	cg42420225_TC21	0.000497	-0.06905	Lower	Scarb2	chr5	-	tss_body	92503640
204	cg42446074_TC21	0.000543	0.069292	Higher					96948868
205	cg42531954_TC21	0.000964	-0.06455	Lower	Lrrc8d	chr5	+	tss_body	1.06E+08
206	cg42550579_BC21	0.000295	-0.05837	Lower	Gm17202	chr5	-	tss_body	1.07E+08
207	cg42590608_TC11	4.1E-05	-0.05866	Lower	Gm36535	chr5	+	tss_body	1.12E+08
208	cg42609231_BC21	0.000331	-0.11414	Lower	2900026A02Rik	chr5	-	tss_body	1.13E+08
209	cg42731685_TC21	0.000218	-0.06482	Lower	Aldh2	chr5	-	tss_body	1.22E+08
210	cg42736554_BC21	0.000262	-0.05786	Lower	Cux2	chr5	-	tss_body	1.22E+08
211	cg42744114_TC21	0.000101	0.054352	Higher	Gpn3	chr5	+	tss_body	1.22E+08
212	cg42747912_TC21	0.000318	-0.06154	Lower	P2rx7	chr5	+	tss_body	1.23E+08
213	cg42763078_TC21	0.000775	-0.05568	Lower	Clip1	chr5	-	tss_body	1.24E+08
214	cg42940734_BC21	0.000277	0.053072	Higher	Uncx	chr5	+	tss_1500	1.4E+08

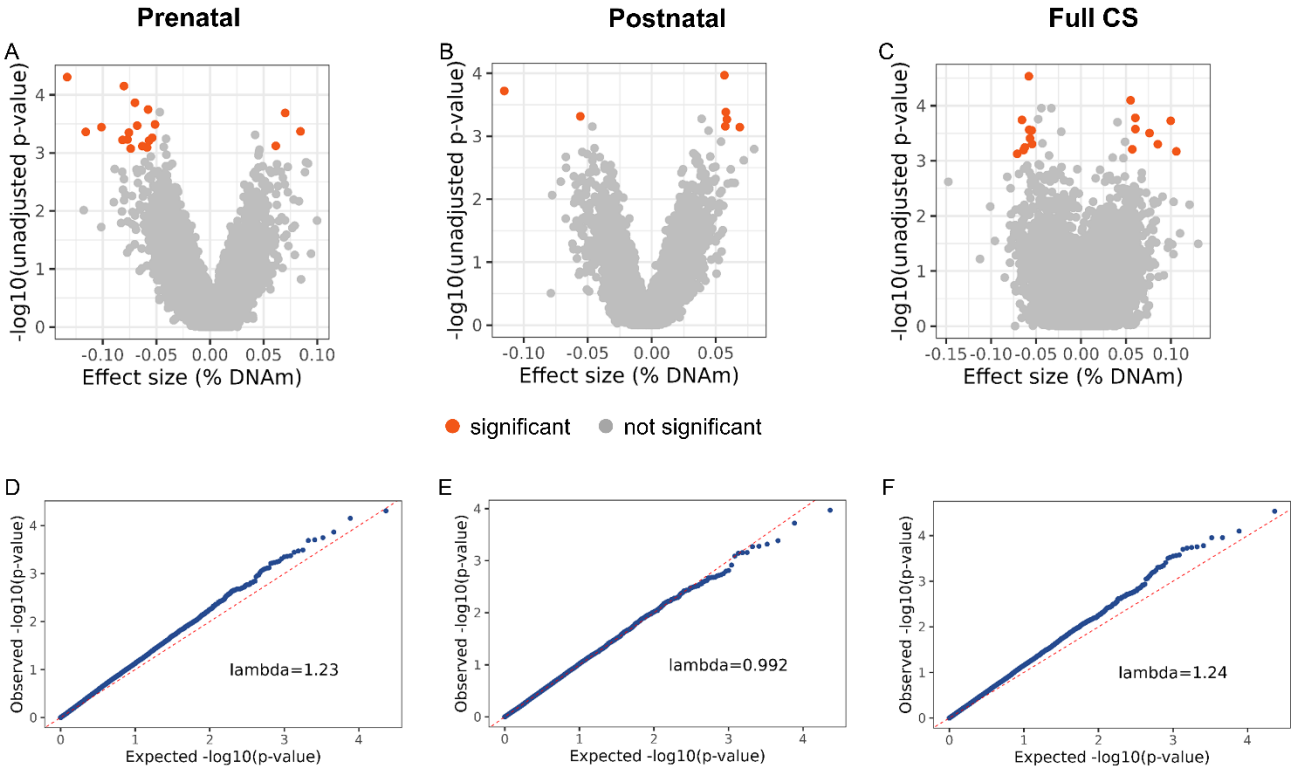
215	cg42952201_TC21	0.000574	-0.05343	Lower	Eif3b	chr5	+	tss_body	1.4E+08
216	cg42956861_TC21	0.000342	0.074489	Higher	Amz1	chr5	+	tss_body	1.41E+08
217	cg42984318_TC21	0.000458	0.091032	Higher	Spdye4b	chr5	+	tss_1500	1.43E+08
218	cg42992970_TC21	0.000125	0.114136	Higher	Usp42	chr5	-	tss_body	1.44E+08
219	cg42992971_TC21	0.000345	0.10482	Higher	Usp42	chr5	-	tss_body	1.44E+08
220	cg42997884_TC21	1.41E-05	-0.06125	Lower	Bhlha15	chr5	+	tss_body	1.44E+08
221	cg43006793_BC21	1.46E-05	0.083015	Higher	Trrap	chr5	+	tss_body	1.45E+08
222	cg43030693_TC21	0.000844	-0.05248	Lower	Gm34994	chr5	+	tss_body	1.47E+08
223	cg43121539_TC21	0.000963	-0.05568	Lower					7831144
224	cg43381095_TC21	0.000843	-0.05243	Lower		chr6	+	tss_200	47637017
225	cg43391351_TC21	7.78E-05	0.063729	Higher	Gimap5	chr6	+	tss_body	48746220
226	cg43405996_TC21	9.33E-05	-0.0586	Lower	Osbpl3	chr6	-	tss_body	50382876
227	cg43615508_BC21	1.8E-05	-0.08126	Lower	Gm38843	chr6	-	tss_1500	82806250
228	cg43640515_TC21	0.000699	-0.06286	Lower	Sfxn5	chr6	-	tss_body	85254144
229	cg43643466_TC21	0.000673	0.068843	Higher	Fbxo41	chr6	-	tss_body	85498537
230	cg43677384_BC21	8.35E-06	-0.09962	Lower	Mgll	chr6	+	tss_body	88766809
231	cg43683455_TC21	0.000832	-0.05181	Lower		chr6	+	tss_body	89309063
232	cg43856375_BC21	0.000143	-0.09261	Lower	Il17rc	chr6	+	tss_body	1.13E+08
233	cg43867668_BC21	9.42E-05	0.057434	Higher	Hrh1	chr6	+	tss_body	1.14E+08
234	cg43870711_TC21	0.000407	0.077761	Higher	Atg7	chr6	+	tss_body	1.15E+08
235	cg43916343_TC11	0.000636	0.079104	Higher	Wnt5b	chr6	-	tss_body	1.19E+08
236	cg43991146_TC21	0.000502	-0.08067	Lower					1.27E+08
237	cg44198236_TC21	0.000664	0.066053	Higher	Zfp579	chr7	-	tss_body	4994585
238	cg44199524_TC21	0.000548	-0.07217	Lower	Ccdc106	chr7	+	tss_body	5054343
239	cg44270164_TC21	5.24E-05	-0.06984	Lower					16974237
240	cg44281613_TC11	0.000239	0.090752	Higher	Nova2	chr7	+	tss_body	18948429
241	cg44281806_BC21	0.000122	0.094226	Higher	Nova2	chr7	+	tss_body	18957993
242	cg44289908_TC21	0.000193	0.055495	Higher	Klc3	chr7	-	tss_body	19396551
243	cg44321467_TC11	0.000461	0.067687	Higher		chr7	+	tss_1500	24665392
244	cg44360395_TC21	7.84E-06	-0.09868	Lower	Dyrk1b	chr7	+	tss_body	28184960
245	cg44370775_TC21	8.06E-05	-0.06308	Lower	Lgals7	chr7	+	tss_1500	28863803

246	cg44378620_TC11	0.000476	0.078529	Higher	Sipa1l3	chr7	-	tss_body	29345971
247	cg44402178_BC21	0.00012	0.079691	Higher	Scn1b	chr7	-	tss_body	31117436
248	cg44417071_TC21	0.000658	0.059694	Higher	Wtip	chr7	-	tss_body	34130278
249	cg44508914_TC21	0.000167	0.088297	Higher	Gm21948	chr7	+	tss_body	44840146
250	cg44516596_BC11	0.000678	0.076105	Higher	Cd37	chr7	-	tss_body	45234353
251	cg44558893_TC21	0.000501	-0.05219	Lower	Nav2	chr7	+	tss_body	49397787
252	cg44883413_TC21	0.000224	-0.06819	Lower	Thrsp	chr7	-	tss_1500	97418745
253	cg44890325_TC21	0.000172	0.075223	Higher	Capn5	chr7	-	tss_body	98165537
254	cg44922022_BC21	0.000229	0.052982	Higher					1.01E+08
255	cg44971210_BC21	0.000135	0.08396	Higher	Ric3	chr7	-	tss_200	1.09E+08
256	cg45017341_TC21	0.000174	0.068044	Higher	4933406I18Rik	chr7	-	tss_body	1.14E+08
257	cg45085353_TC21	0.000357	-0.05954	Lower	Prkcb	chr7	+	tss_body	1.22E+08
258	cg45092084_BC21	9.82E-05	-0.06016	Lower	Tnrc6a	chr7	+	tss_body	1.23E+08
259	cg45121762_TC21	0.00059	0.058998	Higher	Sult1a1	chr7	-	tss_body	1.27E+08
260	cg45190391_TC21	1.95E-05	0.074108	Higher	Ctbp2	chr7	-	tss_body	1.33E+08
261	cg45471099_BC21	0.000271	0.052552	Higher	Nkx6-3	chr8	+	tss_body	23156759
262	cg45513759_BC21	0.000637	-0.06668	Lower	Adgra2	chr8	+	tss_body	27121089
263	cg45644441_BC11	0.000802	0.056138	Higher					45477677
264	cg45809434_BC11	0.000164	0.061334	Higher	Cers1	chr8	+	tss_body	70330794
265	cg45825657_BC21	0.000408	-0.06843	Lower	Ano8	chr8	-	tss_body	71477517
266	cg45833964_TC21	0.000816	-0.0558	Lower	Cib3	chr8	-	tss_body	72210633
267	cg45947680_TC21	4.39E-05	-0.06981	Lower					86757552
268	cg46018659_TC21	7.62E-05	-0.08579	Lower	Gnao1	chr8	+	tss_body	93918034
269	cg46098315_TC21	0.000946	0.07886	Higher	Lrrc36	chr8	+	tss_body	1.05E+08
270	cg46166242_BC21	0.00011	-0.0808	Lower	Gm38523	chr8	-	tss_1500	1.11E+08
271	cg46205434_TC11	0.000142	0.058789	Higher	Wwox	chr8	+	tss_body	1.15E+08
272	cg46259982_TC11	0.000586	0.110703	Higher	Dnaaf1	chr8	+	tss_body	1.2E+08
273	cg46274825_TC21	7.83E-05	0.058319	Higher	Gse1	chr8	+	tss_body	1.21E+08
274	cg46279954_BC11	0.000637	0.063434	Higher	Q6PB93	chr8	+	tss_body	1.21E+08
275	cg46290197_TC21	6.9E-05	0.076641	Higher	Gm26747	chr8	+	tss_200	1.21E+08
276	cg46290706_TC21	0.00039	-0.05886	Lower	Q6PB93	chr8	+	tss_body	1.21E+08

277	cg46321823_BC21	0.000314	0.058677	Higher	Spire2	chr8	+	tss_body	1.23E+08
278	cg46337270_TC21	0.000468	0.068239	Higher	Pgbd5	chr8	-	tss_body	1.24E+08
279	cg46580278_TC21	0.000111	-0.05095	Lower	Ets1	chr9	+	tss_body	32715975
280	cg46664079_BC11	0.000295	0.054678	Higher	LOC102631930	chr9	-	tss_body	43746400
281	cg46681936_BC21	0.000237	-0.06158	Lower	Amica1	chr9	+	tss_body	45081234
282	cg46705827_TC11	0.000353	0.072797	Higher	Gm31816	chr9	-	tss_body	47348771
283	cg46801220_BC11	0.000426	0.070225	Higher					57876930
284	cg46836382_TC11	0.000983	0.05786	Higher	Tle3	chr9	+	tss_body	61384935
285	cg47041430_TC11	0.000747	-0.05893	Lower		chr9	-	tss_body	85552043
286	cg47141551_TC21	0.000432	-0.07659	Lower	chr9-98954990-98957445	chr9	*	SShelf	98960297
287	cg47157009_TC21	0.000583	-0.06757	Lower	Il20rb	chr9	-	tss_body	1E+08
288	cg47267273_BC21	0.000886	-0.05536	Lower					1.11E+08
289	cg47303884_TC21	0.000669	-0.05701	Lower	Gpd1l	chr9	-	tss_body	1.15E+08
290	cg47334265_BC21	9.08E-05	0.062663	Higher	Rbms3	chr9	-	tss_body	1.18E+08
291	cg47384292_BC11	0.000391	0.083142	Higher	Sec22c	chr9	-	tss_body	1.22E+08
292	cg47397977_TC21	5.6E-05	-0.05033	Lower	Tmem42	chr9	+	tss_body	1.23E+08
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47427389_BC11	0.000266	0.060364	Higher	Magix	chrX	-	tss_body	7674839
2	cg47428422_TC11	0.000676	0.105936	Higher		chrX	-	tss_body	7750535
3	cg47445069_BC21	2.92E-05	-0.05814	Lower	Sytl5	chrX	+	tss_body	9846108
4	cg47540313_TC21	0.000274	-0.05775	Lower					31764898
5	cg47566244_BC21	0.000638	-0.06392	Lower	Lamp2	chrX	-	tss_body	38456215
6	cg47620959_TC21	0.000281	-0.0549	Lower					49896206
7	cg47873549_BC21	0.000499	0.085341	Higher	Nlgn3	chrX	+	tss_body	1.01E+08
8	cg47894568_TC21	0.000181	-0.06572	Lower					1.04E+08
9	cg47941763_TC21	0.000314	0.076112	Higher		chrX	-	tss_body	1.14E+08
10	cg48005767_BC11	0.000166	0.060316	Higher					1.32E+08
11	cg48030590_BC21	0.000748	-0.07106	Lower					1.36E+08
12	cg48037071_BC11	0.000496	-0.05448	Lower	Fam199x	chrX	+	tss_body	1.37E+08

13	cg48050340_TC21	0.000188	0.099683	Higher	Tbc1d8b	chrX	+	tss_body	1.4E+08
14	cg48137755_BC21	0.000619	0.056982	Higher	Phex	chrX	-	tss_body	1.57E+08
15	cg48140840_TC21	0.000391	-0.0568	Lower	Smpx	chrX	+	tss_body	1.58E+08
16	cg48172527_BC11	0.000571	-0.06257	Lower					1.63E+08
17	cg48175315_BC21	7.98E-05	0.0551	Higher	Rnf138rt1	chrX	-	tss_body	1.64E+08

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.



Appendix 4. 21: Effects of early life CS exposure on DNAm in female lung X chromosomes at 63 weeks.

(A) 19 CpGs (3 higher, 16 lower) are differentially methylated due to prenatal CS exposure in female offspring lung X chromosome probes at 63 weeks (B) 7 CpGs (5 higher, 2 lower) are differentially methylated due to postnatal CS exposure in female offspring lung X chromosome probes at 63 weeks (C) 17 CpGs (8 higher, 9 lower) are differentially methylated due to full CS exposure in female offspring lung X chromosome probes at 63 weeks (D) QQ-plot showed an inflated fit in our limma model used to identify effects of prenatal CS on DNAm in female lung autosomes (E) QQ-plot showed an adequate fit in our limma model used to identify effects of postnatal CS on DNAm in female lung autosomes (F) QQ-plot showed an inflated fit in our limma model used to identify effects of full CS on DNAm in female lung autosomes. DNAm differences were analyzed using linear regression, and CpGs were considered differentially methylated at $p < 10e\text{-}3$ and effect size > 0.05. Delta beta (effect size) was calculated by subtracting beta values of exposed offspring from control mean betas. N = 3-4 per group. Significant CpGs are highlighted in orange, while non-significant ones are highlighted in grey.

Appendix 4. 22: Significantly altered CpGs in male blood at 8 weeks due to prenatal CS exposure

Autosomes									
	CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	Feature	CpG position
1	cg28434480_BC21	2.79E-05	-0.06368	Lower					46071394
2	cg28570884_BC11	0.000679	-0.05899	Lower					65537154
3	cg28632159_BC21	0.0004	0.060422	Higher		chr10	-	tss_body	71477517
4	cg28666646_TC21	0.000311	0.071014	Higher					76047416
5	cg28687711_BC11	0.000224	-0.06548	Lower	Tspear	chr10	+	tss_body	77815698
6	cg28780003_TC21	0.000153	-0.05635	Lower		chr10	-	tss_body	85266223
7	cg28783377_TC21	0.000594	0.051604	Higher	Btbd11	chr10	+	tss_body	85598682
8	cg28916444_TC11	0.000176	-0.09577	Lower					1.01E+08
9	cg28926982_TC21	0.00054	0.072803	Higher					1.03E+08
10	cg29065926_BC11	0.000422	-0.06938	Lower	Grip1	chr10	+	tss_body	1.2E+08
11	cg29168513_BC21	2.07E-05	-0.06635	Lower					1.29E+08
12	cg29171407_BC21	0.000707	-0.05778	Lower	Q8VGJ1	chr10	-	tss_body	1.3E+08
13	cg29565489_TC21	0.00088	-0.05317	Lower	Sparc	chr11	-	tss_1500	55421325
14	cg29594824_BC21	0.000374	0.066498	Higher	2810021J22Rik	chr11	+	tss_body	58867318
15	cg29604948_BC11	0.000182	-0.10314	Lower	Q7TS30	chr11	-	tss_body	59576036
16	cg29618485_BC21	0.000436	-0.05233	Lower	Gm12618	chr11	-	tss_1500	60819892
17	cg29735452_BC11	0.000717	-0.05834	Lower	Fam64a	chr11	+	tss_1500	72042131
18	cg29735467_BC21	0.000942	-0.09583	Lower	Fam64a	chr11	+	tss_200	72042334
19	cg29958546_TC21	0.000262	-0.05574	Lower	Col1a1	chr11	+	tss_200	94936164
20	cg29998199_BC11	0.00086	-0.08704	Lower	2410003L11Rik	chr11	+	tss_body	97619568
21	cg30045797_TC11	0.000614	-0.11985	Lower	Plekhh3	chr11	-	tss_body	1.01E+08
22	cg30097654_BC11	0.000876	-0.06092	Lower					1.05E+08
23	cg30209567_TC21	9.99E-05	-0.08756	Lower	Otop2	chr11	+	tss_body	1.15E+08
24	cg30330577_BC11	0.000368	-0.05291	Lower	Klhl29	chr12	-	tss_body	5216641
25	cg30482158_TC21	0.000149	-0.05677	Lower	Gm30401	chr12	+	tss_body	27127505
26	cg30513195_TC21	9.53E-05	-0.05169	Lower	Lamb1	chr12	+	tss_body	31271406
27	cg30589924_TC11	7.26E-05	-0.05421	Lower					43472405
28	cg30786568_BC21	4.59E-05	0.06739	Higher					72853799

29	cg30878064_TC11	0.000881	-0.0518	Lower	Rgs6	chr12	+	tss_body	82674816
30	cg30941165_BC11	0.000346	-0.05873	Lower	Nrxn3	chr12	+	tss_body	88731762
31	cg31051789_TC21	0.000131	0.060986	Higher	Serpina11	chr12	-	tss_body	1.04E+08
32	cg31089008_TC21	0.000301	0.08107	Higher	Gm16086	chr12	-	tss_body	1.07E+08
33	cg31344028_BC21	0.000379	0.084827	Higher					23388819
34	cg31451165_BC21	0.000438	0.059424	Higher	Rreb1	chr13	+	tss_body	37880874
35	cg31562962_TC21	1.71E-05	-0.05229	Lower					48686850
36	cg31622713_TC21	0.000206	0.05339	Higher					54439471
37	cg31682876_TC21	0.000127	-0.06974	Lower	Ntrk2	chr13	+	tss_body	59090575
38	cg31697929_BC21	0.000871	-0.06698	Lower	Gm35333	chr13	-	tss_body	60427761
39	cg31819938_BC21	0.000326	-0.0695	Lower	2210408I21Rik	chr13	+	tss_body	77439372
40	cg31859487_TC21	0.000774	-0.05035	Lower	Gm34196	chr13	-	tss_body	84758986
41	cg32133160_TC11	0.000926	0.057808	Higher	1700003P14Rik	chr13	+	tss_1500	1.19E+08
42	cg32279121_BC21	0.000996	0.05425	Higher					24999746
43	cg32304793_TC21	0.000888	0.073908	Higher	Erc2	chr14	+	tss_body	27844742
44	cg32312489_TC21	2.49E-05	-0.0511	Lower	Cacna2d3	chr14	-	tss_body	28953749
45	cg32322269_BC21	3.65E-05	-0.05501	Lower	Cacna1d	chr14	-	tss_body	30109282
46	cg32465551_BC21	0.000744	-0.05918	Lower	A2RTN7	chr14	+	tss_body	50123339
47	cg32554194_TC21	0.000255	-0.0542	Lower	Amer2	chr14	+	tss_body	60383974
48	cg32835566_TC21	7.05E-05	-0.10639	Lower		chr14	-	tss_1500	99631363
49	cg33177908_BC21	0.000309	-0.07276	Lower	Trio	chr15	-	tss_body	27777427
50	cg33235739_TC11	0.00042	0.059971	Higher	Rgs22	chr15	-	tss_body	36140211
51	cg33438066_BC21	0.000135	-0.07189	Lower					67018543
52	cg33603283_BC11	0.000338	0.051625	Higher	Tspo	chr15	+	tss_body	83570488
53	cg33612987_BC21	0.000702	0.072008	Higher	Parvb	chr15	+	tss_body	84256757
54	cg33798751_BC21	6.51E-05	0.061449	Higher	1700030F18Rik	chr15	-	tss_body	99927735
55	cg33814851_TC21	1.42E-05	-0.08237	Lower	Scn8a	chr15	+	tss_body	1.01E+08
56	cg33991183_TC11	0.000957	-0.05169	Lower	Gm16863	chr16	-	tss_body	21255944
57	cg34103557_BC21	0.000368	0.058655	Higher	Itgb5	chr16	+	tss_body	33886997
58	cg34279974_TC21	0.000936	-0.05142	Lower		chr16	-	tss_200	59102044
59	cg34664715_BC21	0.00012	-0.09612	Lower	Dact2	chr17	-	tss_body	14204129

60	cg34703150_BC11	0.000197	-0.11106	Lower	E9PZJ7	chr17	+	tss_body	20378930
61	cg34741669_TC11	0.000491	-0.08324	Lower	Gm38655	chr17	-	tss_body	25175584
62	cg34761349_BC21	0.0001	0.051188	Higher	Ergic1	chr17	+	tss_body	26572416
63	cg34791132_BC11	5.91E-05	0.055263	Higher	Fkbp5	chr17	-	tss_body	28420600
64	cg34873389_BC21	0.00051	0.052833	Higher	Vars	chr17	+	tss_body	35003771
65	cg34894232_TC21	0.000228	0.071205	Higher	Trim26	chr17	+	tss_body	36838948
66	cg35131761_BC21	0.000749	0.058793	Higher	Mtcl1	chr17	-	tss_body	66447385
67	cg35142670_BC21	0.000198	-0.06348	Lower					67473339
68	cg35149967_TC21	0.000835	0.054415	Higher		chr17	-	tss_body	68114337
69	cg35473653_BC21	0.000119	-0.05471	Lower					17390775
70	cg35597105_TC21	0.000155	-0.0551	Lower	chr18-35939614-35939888	chr18	*	NShelf	35936583
71	cg35608462_BC11	0.000627	-0.14189	Lower	Pcdha1	chr18	+	tss_body	36969909
72	cg35624093_TC11	0.000705	0.050739	Higher	Gnpda1	chr18	-	tss_body	38338147
73	cg35650056_BC21	0.000786	-0.05239	Lower	Sh3rf2	chr18	+	tss_body	42053606
74	cg35747308_TC21	0.000846	0.056997	Higher	Gm34233	chr18	+	tss_body	55422598
75	cg35805977_TC11	0.000446	-0.057	Lower	Sh3tc2	chr18	+	tss_body	61953649
76	cg35807882_TC21	1.67E-05	-0.07313	Lower					62149780
77	cg35814910_BC21	0.000743	-0.10763	Lower	Napg	chr18	+	tss_1500	62977502
78	cg36080472_BC21	1.94E-06	-0.05852	Lower	Pcx	chr19	+	tss_body	4618310
79	cg36080483_BC21	0.000231	-0.06761	Lower	Pcx	chr19	+	tss_body	4618451
80	cg36135058_TC21	0.000399	0.077735	Higher	Ahnak	chr19	+	tss_1500	8988990
81	cg36291483_BC21	0.000462	-0.05611	Lower	chr19-28975069-28975404	chr19	*	Island	28975073
82	cg36799480_TC21	0.000908	-0.05303	Lower	1110002O04Rik	chr1	+	tss_body	35879908
83	cg36800730_TC21	3.67E-05	-0.09236	Lower	Gm33222	chr1	-	tss_body	36009301
84	cg36873625_BC11	0.000397	-0.10314	Lower	Fhl2	chr1	-	tss_body	43191241
85	cg36975130_TC11	6.95E-05	-0.08338	Lower					59247328
86	cg37269951_TC11	0.000702	-0.06855	Lower	Slco4c1	chr1	-	tss_body	96846179
87	cg37520498_BC21	6.13E-05	0.055955	Higher	Platr22	chr1	+	tss_1500	1.37E+08
88	cg37747508_TC21	1.22E-05	-0.08751	Lower	Pbx1	chr1	-	tss_body	1.68E+08
89	cg38022736_BC21	0.000497	0.055307	Higher	Dhtkd1	chr2	-	tss_body	5942773

90	cg38022738_TC21	8.42E-05	0.05987	Higher	Dhtkd1	chr2	-	tss_body	5942802
91	cg38078957_BC21	0.000205	0.060843	Higher	LOC105244085	chr2	+	tss_body	13559130
92	cg38164903_BC11	3.7E-05	-0.07043	Lower	Lhx3	chr2	-	tss_body	26200256
93	cg38165067_TC11	0.000313	-0.11728	Lower	Lhx3	chr2	-	tss_body	26204558
94	cg38230283_BC11	0.000381	0.065607	Higher	Ass1	chr2	+	tss_body	31472812
95	cg38538744_BC21	1.95E-05	-0.05103	Lower	6430710C18Rik	chr2	-	tss_body	72752217
96	cg38540036_BC21	2.08E-05	0.072843	Higher					72886478
97	cg38549853_TC21	0.000193	0.054799	Higher					73792420
98	cg38587235_TC21	0.000116	0.054379	Higher					77313156
99	cg38807756_BC21	0.000197	-0.07748	Lower	Olfr1314	chr2	-	tss_body	1.12E+08
100	cg38809150_TC11	0.000364	-0.07589	Lower	Slc12a6	chr2	+	tss_body	1.12E+08
101	cg38868496_TC11	0.000285	0.085052	Higher	Itpka	chr2	+	tss_body	1.2E+08
102	cg38877587_TC21	0.000717	-0.05063	Lower	Stard9	chr2	+	tss_body	1.21E+08
103	cg38903505_BC21	5.2E-05	-0.10644	Lower	Sema6d	chr2	+	tss_body	1.24E+08
104	cg38931202_BC21	5.13E-05	-0.05097	Lower	Astl	chr2	+	tss_body	1.27E+08
105	cg38944536_TC11	0.000816	-0.06528	Lower	Gm39931	chr2	-	tss_body	1.29E+08
106	cg38955541_TC21	1.88E-06	0.302885	Higher	Stk35	chr2	+	tss_body	1.3E+08
107	cg38956028_BC11	0.000641	-0.06591	Lower					1.3E+08
108	cg38974309_TC11	0.000774	-0.07129	Lower	Gm30986	chr2	+	tss_1500	1.32E+08
109	cg38975125_BC21	0.000247	0.053238	Higher	5330413P13Rik	chr2	-	tss_body	1.32E+08
110	cg39007822_TC21	0.000512	-0.06708	Lower	Pak7	chr2	-	tss_body	1.36E+08
111	cg39022858_BC11	0.000619	0.074783	Higher					1.39E+08
112	cg39107600_TC21	0.000247	-0.05815	Lower	chr2-151542372-151543206	chr2	*	NShelf	1.52E+08
113	cg39208433_BC21	7.89E-05	0.109054	Higher	Plcg1	chr2	+	tss_body	1.61E+08
114	cg39438728_TC21	0.000461	-0.0576	Lower	Myt1	chr2	+	tss_body	1.82E+08
115	cg39442495_TC21	5.63E-05	-0.08804	Lower					3349532
116	cg39500993_TC21	0.000497	-0.06903	Lower	Ralyl	chr3	+	tss_1500	13472133
117	cg39620920_TC21	0.000221	-0.05823	Lower	Usp13	chr3	+	tss_body	32915297
118	cg39754979_BC21	0.000203	-0.05989	Lower	Gm2447	chr3	+	tss_body	52767000
119	cg39800116_TC21	0.000863	0.064485	Higher	Selt	chr3	+	tss_body	58583212

120	cg39902527_TC21	0.00097	0.066503	Higher	Fstl5	chr3	+	tss_body	76174001
121	cg39905391_BC21	4.59E-05	-0.07511	Lower		chr3	+	tss_body	76885122
122	cg39973321_BC11	0.00089	0.082573	Higher	Lrba	chr3	+	tss_body	86547210
123	cg39976668_BC11	0.00025	-0.06207	Lower	Dclk2	chr3	-	tss_1500	86921581
124	cg40048245_BC21	0.000404	0.050216	Higher	Mir8099-1	chr3	-	tss_1500	95140190
125	cg40091280_TC21	0.000612	0.057514	Higher	Tbx15	chr3	+	tss_body	99263521
126	cg40159422_TC21	0.000173	0.071125	Higher	Rbm15	chr3	-	tss_body	1.07E+08
127	cg40369886_BC21	0.000361	0.050767	Higher	Manba	chr3	+	tss_body	1.35E+08
128	cg41167411_BC21	8.06E-05	-0.06741	Lower	Nfia	chr4	+	tss_body	97974349
129	cg41366896_TC21	0.000633	0.061316	Higher	Smap2	chr4	-	tss_body	1.21E+08
130	cg41542081_TC11	0.000296	-0.05552	Lower					1.36E+08
131	cg41690476_BC21	0.000318	0.056428	Higher	chr4-148724379-148724585	chr4	*	Island	1.49E+08
132	cg41917625_TC21	0.000281	-0.05232	Lower		chr5	-	tss_body	22403371
133	cg41983569_BC21	0.000786	0.092696	Higher					30686832
134	cg42039836_BC21	0.000107	0.053638	Higher	Sorcs2	chr5	-	tss_body	36221347
135	cg42043721_BC11	0.000211	0.064802	Higher	Tbc1d14	chr5	-	tss_body	36574239
136	cg42143828_TC11	0.000877	0.096857	Higher	Sod3	chr5	+	tss_body	52368751
137	cg42445830_TC21	0.00014	0.057081	Higher	Gm33370	chr5	-	tss_body	96922356
138	cg42718662_TC21	0.000376	0.07346	Higher	Tpcn1	chr5	-	tss_body	1.21E+08
139	cg42724182_BC21	0.000222	-0.0762	Lower	Rph3a	chr5	-	tss_body	1.21E+08
140	cg42780929_TC21	0.000846	-0.07459	Lower	Gm40320	chr5	+	tss_body	1.25E+08
141	cg42938053_TC21	0.000256	0.053642	Higher	3110082I17Rik	chr5	-	tss_body	1.39E+08
142	cg42958524_BC21	0.000181	0.067598	Higher	Card11	chr5	-	tss_body	1.41E+08
143	cg43119450_BC11	0.000951	-0.10269	Lower	Tac1	chr6	+	tss_body	7555136
144	cg43131025_BC21	5.17E-06	-0.05172	Lower	Nxph1	chr6	+	tss_body	9070471
145	cg43147431_BC21	0.000685	0.053368	Higher	Thsd7a	chr6	-	tss_body	12565450
146	cg43171581_BC11	0.000877	-0.07672	Lower					16979023
147	cg43668590_TC21	0.000579	-0.0521	Lower					87948115
148	cg43739358_TC21	5.15E-05	-0.05303	Lower	2900060L22Rik	chr6	-	tss_body	96115502
149	cg43973536_BC11	0.00052	-0.05595	Lower	Cd9	chr6	-	tss_body	1.25E+08

150	cg44038750_TC11	0.000202	-0.06899	Lower	Bcl2l14	chr6	+	tss_body	1.34E+08
151	cg44193003_BC21	0.000136	0.117413	Higher					4624684
152	cg44211968_TC11	0.000947	-0.06611	Lower	Usp29	chr7	+	tss_body	6731248
153	cg44393279_TC11	0.000524	-0.06805	Lower	Nphs1	chr7	+	tss_body	30467976
154	cg44393643_TC11	0.000162	-0.07702	Lower	Prodh2	chr7	+	tss_1500	30493447
155	cg44412858_TC21	0.000391	0.065858	Higher		chr7	+	tss_1500	33422910
156	cg44519801_TC11	0.000214	0.117189	Higher	Ntf5	chr7	+	tss_body	45415757
157	cg44579867_TC11	0.00043	0.087447	Higher					52713964
158	cg44635133_TC11	0.000918	0.137718	Higher	Klf13	chr7	-	tss_body	63905762
159	cg44787589_TC11	7.23E-05	-0.06112	Lower	BC048679	chr7	-	tss_body	81498191
160	cg44980108_BC21	0.000801	-0.05589	Lower	Zfp143	chr7	+	tss_body	1.1E+08
161	cg45010453_BC21	0.000904	-0.05218	Lower					1.14E+08
162	cg45140060_BC11	3.86E-05	-0.23533	Lower	Kat8	chr7	+	tss_body	1.28E+08
163	cg45375946_TC21	7.5E-05	0.070808	Higher	Ankrd10	chr8	-	tss_body	11633847
164	cg45659384_BC21	0.000811	0.063242	Higher					46893664
165	cg45821428_TC21	0.000342	0.073998	Higher	Gm17576	chr8	-	tss_body	71044081
166	cg45874948_TC21	0.000997	-0.05515	Lower	Slc10a7	chr8	+	tss_body	78585137
167	cg45920458_BC11	0.00037	-0.06094	Lower	Podnl1	chr8	+	tss_200	84125792
168	cg45953801_TC21	0.000996	-0.0742	Lower	Gm19872	chr8	+	tss_200	87460373
169	cg45996571_TC11	0.000243	-0.05845	Lower	Fto	chr8	+	tss_body	91623959
170	cg46021554_TC21	7.85E-05	0.086553	Higher	Gm39227	chr8	-	tss_body	94171438
171	cg46022002_TC11	2.87E-05	0.079453	Higher					94191398
172	cg46036778_TC11	0.000929	0.055453	Higher	Cfap20	chr8	-	tss_body	95427760
173	cg46339766_BC11	0.000812	0.050228	Higher	Capn9	chr8	+	tss_body	1.25E+08
174	cg46419050_BC21	0.000531	0.076423	Higher		chr9	-	tss_body	9495405
175	cg46473950_BC21	0.000901	-0.06813	Lower	Olfr847	chr9	-	tss_body	19378053
176	cg46527351_TC21	0.000465	-0.08351	Lower	Eepd1	chr9	+	tss_body	25516605
177	cg46577765_BC21	8E-05	0.078596	Higher	Fli1	chr9	-	tss_body	32496246
178	cg46782830_BC11	0.000252	-0.05701	Lower	Tspan3	chr9	-	tss_1500	56161326
179	cg46818416_BC21	0.00036	0.072949	Higher	Celf6	chr9	+	tss_body	59603161
180	cg46835876_TC21	0.000557	0.061613	Higher	chr9-61370646-61371649	chr9	*	NShelf	61368190

181	cg46845557_TC11	0.000258	0.056567	Higher					62253965
182	cg46887798_TC21	0.000723	-0.05003	Lower	Snx1	chr9	-	tss_body	66110165
183	cg47072754_TC21	0.000227	0.136971	Higher					89877107
184	cg47072866_BC21	0.000894	0.115142	Higher					89882170
185	cg47134365_TC21	0.000451	0.051121	Higher					98276420
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47426861_BC21	5.85E-06	-0.06811	Lower	Syp	chrX	+	tss_body	7641201
2	cg47469903_BC21	0.000389	-0.09583	Lower					12873363
3	cg47472705_BC11	0.000474	0.058017	Higher	2010308F09Rik	chrX	-	tss_body	13236090
4	cg47480933_TC21	0.000736	-0.06696	Lower		chrX	+	tss_body	14796809
5	cg47515337_TC11	0.000869	0.051367	Higher					22172339
6	cg47619718_TC11	0.000187	-0.10802	Lower					49619685
7	cg47628382_BC11	0.000477	-0.0689	Lower	Mbnl3	chrX	-	tss_body	51169985
8	cg47642162_BC21	0.000248	-0.10667	Lower	Gm35988	chrX	+	tss_body	53159137
9	cg47663864_TC21	0.000636	0.197835	Higher					57522194
10	cg47671374_TC21	0.000182	-0.06339	Lower					58795082
11	cg47683122_BC11	2.12E-06	0.074773	Higher	C230004F18Rik	chrX	+	tss_200	61116350
12	cg47736119_BC21	0.000353	-0.08096	Lower	Zfp92	chrX	+	tss_body	73421950
13	cg47736262_BC21	0.00011	-0.06101	Lower	Trex2	chrX	-	tss_body	73435303
14	cg47742031_TC21	3.14E-05	0.056328	Higher	Tex28	chrX	-	tss_body	74153053
15	cg47778672_BC11	0.000573	-0.07381	Lower					81621061
16	cg47828485_BC21	0.000812	-0.07298	Lower	Pcyt1b	chrX	+	tss_body	93655144
17	cg47863622_BC21	5.5E-05	-0.09524	Lower					99763116
18	cg47909147_TC21	0.000231	-0.07888	Lower		chrX	-	tss_body	1.06E+08
19	cg47920991_TC21	0.000442	-0.05888	Lower	5730416F02Rik	chrX	+	tss_200	1.09E+08
20	cg47949472_BC11	1.7E-05	-0.07878	Lower					1.16E+08
21	cg47957345_BC21	0.000435	-0.05102	Lower					1.18E+08
22	cg47965560_BC21	0.000304	-0.06226	Lower					1.2E+08
23	cg47993424_TC11	0.000874	0.057943	Higher					1.29E+08
24	cg48046195_TC21	0.000281	0.076047	Higher	Nrk	chrX	+	tss_body	1.39E+08

25	cg48060010_TC21	5.49E-05	0.052577	Higher	Vsig1	chrX	+	tss_body	1.41E+08
26	cg48066232_BC21	0.00012	0.089388	Higher					1.42E+08
27	cg48076850_BC21	0.00035	-0.06728	Lower	Dcx	chrX	-	tss_body	1.44E+08
28	cg48114992_BC21	0.000825	-0.05729	Lower	3010001F23Rik	chrX	+	tss_body	1.52E+08
29	cg48140840_TC21	0.000958	0.057633	Higher	Smpx	chrX	+	tss_body	1.58E+08
30	cg48157134_TC11	0.000394	-0.08348	Lower					1.61E+08
31	cg48208694_TC11	0.000665	-0.12794	Lower	Mid1	chrX	+	tss_body	1.7E+08
Y chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48236752_TC21	0.00095	-0.21192	Lower		chrY	-	tss_body	6724899

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e-3$ and effect size > 0.05.

Appendix 4. 23: Significantly altered CpGs in male blood at 8 weeks due to postnatal CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28698102_TC21	0.00086981	-0.08629253	Lower	Ccdc105	chr10	-	tss_body	78748289
2	cg29168513_BC21	0.00085884	-0.0545449	Lower					129002283
3	cg29172527_BC21	0.00092845	0.06165668	Higher	Olfr816	chr10	-	tss_body	129911692
4	cg29459319_TC11	0.00073341	0.0758964	Higher					43761951
5	cg29586682_TC21	0.00016317	-0.0630246	Lower	Larp1	chr11	+	tss_body	58022259
6	cg29624784_TC21	0.00012878	-0.05380005	Lower	Slc47a2	chr11	-	tss_1500	61342940
7	cg29722460_TC21	0.00040686	0.07726787	Higher	Mink1	chr11	+	tss_body	70578833
8	cg29748693_TC21	0.00068156	-0.07526436	Lower	Aspa	chr11	-	tss_body	73326765
9	cg29892590_BC11	0.00093137	0.0615336	Higher	Sept4	chr11	+	tss_body	87583368
10	cg29952742_TC21	0.00031845	0.08129594	Higher	Cacna1g	chr11	-	tss_body	94447126
11	cg30142815_TC21	0.00077853	0.0674928	Higher	Rgs9	chr11	-	tss_body	109239089
12	cg30222406_BC21	0.00083968	-0.05254854	Lower	Wbp2	chr11	-	tss_1500	116088300
13	cg30386980_TC21	0.00051414	-0.05545711	Lower		chr12	-	tss_1500	13792516
14	cg30490922_BC21	0.00043431	0.07001	Higher	Dcdc2c	chr12	-	tss_body	28547477
15	cg30762903_BC21	0.00058874	-0.05009279	Lower					70633200
16	cg31074017_BC21	0.00035107	-0.05428396	Lower					105884904
17	cg31199342_BC11	0.00013405	-0.08223681	Lower	Rapgef5	chr12	+	tss_body	117688829
18	cg31367030_BC21	0.00096232	0.05218415	Higher		chr13	-	tss_body	25968630
19	cg31824037_TC21	0.00074362	-0.06922575	Lower	Nr2f1	chr13	-	tss_body	78194030
20	cg32235005_BC21	0.0002147	-0.0576655	Lower	chr14-19823347-19823956	chr14	*	SShelf	19827390
21	cg32416771_BC11	0.00074739	0.05714634	Higher	E9Q207	chr14	-	tss_body	44743573

22	cg32474105_TC21	0.00099165	0.05922655	Higher	Gm7247	chr14	+	tss_body	51361734
23	cg32588793_BC21	0.00047515	-0.07394164	Lower	chr14-63943359-63944306	chr14	*	NShore	63941605
24	cg32603120_BC21	0.00011651	0.05977205	Higher	Pnoc	chr14	-	tss_body	65405184
25	cg32715023_TC11	0.00028792	-0.05777757	Lower	Epsti1	chr14	+	tss_body	77904344
26	cg32817044_TC21	0.00017094	0.05097969	Higher		chr14	-	tss_200	96992302
27	cg33238224_BC21	0.00090053	0.07500592	Higher		chr15	-	tss_body	36390153
28	cg33324762_BC21	0.00056887	-0.05699436	Lower	Trps1	chr15	-	tss_body	50889657
29	cg33346487_TC21	0.00083842	0.06356143	Higher					54069848
30	cg33838986_BC11	0.00024358	-0.0627456	Lower	chr15-102967304-102967662	chr15	*	NShelf	102965061
31	cg34118239_TC21	0.00036061	0.06078177	Higher	Adcy5	chr16	+	tss_body	35273065
32	cg34153965_BC21	2.968E-06	-0.06882308	Lower					39062480
33	cg34683510_BC21	0.00044203	-0.06519782	Lower	Gm41534	chr17	+	tss_body	16452796
34	cg34931562_TC21	0.00078279	-0.07461454	Lower					43519120
35	cg35508529_TC21	0.00034197	0.08477041	Higher	Dtna	chr18	+	tss_body	23647301
36	cg36722004_BC21	7.3117E-05	-0.0646021	Lower					23321518
37	cg37520498_BC21	8.5995E-05	0.05350328	Higher	Platr22	chr1	+	tss_1500	136694865
38	cg37691184_TC21	0.00057253	-0.05246831	Lower	Dnm3	chr1	-	tss_body	162005359
39	cg37702330_TC21	0.00089538	0.07719392	Higher					163449200
40	cg37707905_TC11	0.00014623	0.06551566	Higher	F5	chr1	+	tss_body	164192289
41	cg38071562_BC21	0.00089422	0.05495957	Higher	Fam188a	chr2	-	tss_1500	12420003
42	cg38291158_TC21	0.00058909	0.05823443	Higher					36696850
43	cg38711917_BC21	0.00076896	0.06911009	Higher					95937540
44	cg38794157_TC21	0.00017122	0.08221077	Higher					109458036
45	cg38795330_TC21	0.00022087	-0.0591973	Lower	Bdnf	chr2	+	tss_1500	109675039
46	cg38836332_BC21	0.00070266	0.09259338	Higher					116107856

47	cg38892385_BC21	0.00021554	-0.06176231	Lower	Sord	chr2	+	tss_body	122242193
48	cg38955541_TC21	9.179E-06	0.34172356	Higher	Stk35	chr2	+	tss_body	129819498
49	cg39213616_TC11	0.00083488	0.06419056	Higher		chr2	+	tss_body	161331338
50	cg39382585_BC21	0.00049076	0.06913154	Higher	Gnas	chr2	+	tss_body	174297850
51	cg39411013_TC21	0.00026549	-0.05098367	Lower	Cdh4	chr2	+	tss_1500	179442123
52	cg39519451_TC21	0.00057991	-0.0673731	Lower	Gm30340	chr3	-	tss_body	17325007
53	cg40159837_TC21	0.00098778	0.07361973	Higher					107356629
54	cg40333950_TC11	0.0005581	0.08645481	Higher					130947198
55	cg40556508_TC21	1.6888E-05	-0.05421482	Lower					3051396
56	cg40683387_TC21	0.00056269	0.08059623	Higher	Gm31145	chr4	-	tss_body	23816649
57	cg41828870_TC21	0.0002259	0.08466542	Higher					6169203
58	cg42028848_BC21	5.4761E-05	-0.06059437	Lower	Adra2c	chr5	+	tss_body	35280242
59	cg42112813_TC21	0.00098249	0.06007632	Higher					46774546
60	cg42757212_BC21	0.00096661	-0.05212587	Lower	Gm42025	chr5	+	tss_body	123252023
61	cg43393332_TC21	0.00089968	-0.07383726	Lower	4930563H07Rik	chr6	-	tss_body	48986849
62	cg43972064_BC11	0.0008608	0.09085207	Higher	Plekhg6	chr6	-	tss_body	125372943
63	cg44054755_BC21	0.00018347	0.06276328	Higher	Grin2b	chr6	-	tss_body	135926461
64	cg44261588_BC21	0.00024302	0.05812257	Higher	Sae1	chr7	-	tss_body	16332170
65	cg44453541_BC11	0.00055963	0.05570772	Higher	Gm38439	chr7	+	tss_body	37299196
66	cg44709988_BC21	0.00042903	-0.06749393	Lower	Mctp2	chr7	-	tss_body	72305829
67	cg44750917_TC21	0.00067648	-0.07612541	Lower	Ntrk3	chr7	-	tss_body	78498120
68	cg44771814_BC11	0.0001571	0.07243144	Higher	Sema4b	chr7	+	tss_body	80206363
69	cg45334737_TC11	0.00020952	0.09811988	Higher					6952760
70	cg45972279_TC21	0.00067729	-0.07172191	Lower	Mir8110	chr8	+	tss_body	89024764
71	cg46287781_BC21	0.00061539	-0.05898386	Lower	Gm33823	chr8	-	tss_body	121263580
72	cg46354720_TC21	0.0006594	0.05483793	Higher					125702648

73	cg46418960_BC11	0.00099008	0.09754613	Higher		chr9	-	tss_body	9475517
74	cg46577765_BC21	0.0003693	0.05555398	Higher	Fli1	chr9	-	tss_body	32496246
75	cg46617762_TC21	5.0815E-05	-0.10510187	Lower	Olfr914	chr9	+	tss_1500	38604705
76	cg46668144_TC21	0.00073457	0.05088907	Higher	Gm39325	chr9	-	tss_body	44081858
77	cg47127756_TC21	0.00015165	0.05065404	Higher	Trim42	chr9	-	tss_200	97370026
78	cg47391226_TC21	0.00090265	0.05027569	Higher	Ano10	chr9	-	tss_body	122287940
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47441404_TC21	0.0003815	-0.08342353	Lower	Gm33602	chrX	-	tss_body	9253963
2	cg47461826_BC11	0.00068203	-0.10667197	Lower	Bcor	chrX	-	tss_body	12083119
3	cg47498019_BC21	0.00096393	-0.0534532	Lower					18691107
4	cg47511325_BC21	0.00024315	-0.06375814	Lower					21288746
5	cg47586487_BC11	0.00061491	0.05756667	Higher	Tenm1	chrX	-	tss_body	42666296
6	cg47618293_TC21	0.00048894	-0.05627861	Lower	Gm14696	chrX	-	tss_body	49330317
7	cg47654906_TC21	0.00066274	0.05244649	Higher	16000 25M17 Rik	chrX	+	tss_body	56317699
8	cg47677245_TC11	0.00086617	0.05781502	Higher	Mcf2	chrX	-	tss_body	60142393
9	cg47728724_BC11	0.00040326	0.05696853	Higher	Prrg3	chrX	+	tss_body	71972268
10	cg47799420_TC21	0.00041035	0.06372423	Higher					86500892
11	cg47819497_BC11	0.00095921	0.05517713	Higher	Gm14781	chrX	+	tss_body	91627200
12	cg47844283_BC21	0.00092199	-0.06378543	Lower	Msn	chrX	+	tss_body	96128881
13	cg47860387_BC21	3.6522E-05	-0.07145162	Lower					99403073
14	cg47880212_TC21	0.00068685	0.05875531	Higher	Nhsl2	chrX	+	tss_body	102029947
15	cg47957345_BC21	0.00017612	-0.05722944	Lower					117981905
16	cg48046195_TC21	0.00021103	0.13735452	Higher	Nrk	chrX	+	tss_body	138997832
17	cg48052312_TC21	6.9494E-05	-0.06447062	Lower	Rbm41	chrX	-	tss_body	139935560

Y chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48222360_TC21	0.0007397	0.05392302	Higher					3902410
2	cg48343126_BC21	0.00023135	-0.06209386	Lower					90719266

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 24: Significantly altered CpGs in male blood at 8 weeks due to full CS exposure

Autosomes									
	CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	Feature	CpG position
1	cg28165706_TC21	0.00091238	-0.0686107	Lower	Stxbp5	chr10	-	tss_body	9899823
2	cg28295897_TC11	0.0006591	0.0885732	Higher	Samd3	chr10	+	tss_body	26242735
3	cg28372975_BC21	0.00014655	-0.0678815	Lower	Mfsd4b5	chr10	-	tss_body	39975179
4	cg28414294_TC21	0.00011774	-0.0812148	Lower		chr10	+	tss_body	43667281
5	cg28434480_BC21	2.0963E-05	-0.0643245	Lower					46071394
6	cg28686957_BC21	0.00099971	0.0718091	Higher	Tspear	chr10	+	tss_body	77710609
7	cg28916444_TC11	0.00023266	-0.0953651	Lower					100629962
8	cg28926982_TC21	0.00099123	0.0667310	Higher					102878934
9	cg28969648_TC21	0.00072763	-0.0593286	Lower	Gm4075 7	chr10	+	tss_body	109641444
10	cg29222742_BC21	0.0006705	-0.0774660	Lower	Adcy1	chr11	+	tss_body	7161931
11	cg29624784_TC21	0.00013928	-0.0502781	Lower	Slc47a2	chr11	-	tss_1500	61342940
12	cg29648001_TC21	0.00029664	0.0555765	Higher					63691254
13	cg29735452_BC11	0.00070384	-0.0575991	Lower	Fam64a	chr11	+	tss_1500	72042131
14	cg29735467_BC21	0.00094808	-0.0955348	Lower	Fam64a	chr11	+	tss_200	72042334
15	cg29902070_BC21	0.00070161	-0.0598500	Lower	Ccdc18 2	chr11	+	tss_200	88293993
16	cg30209567_TC21	0.00064559	-0.0658374	Lower	Otop2	chr11	+	tss_body	115318597
17	cg30363806_BC21	0.00047497	-0.0629591	Lower					10438654
18	cg30894677_BC21	0.00011914	-0.0657572	Lower	Elmsan1	chr12	-	tss_body	84207421
19	cg31145489_BC21	0.00037374	-0.0740547	Lower	Exoc3l4	chr12	+	tss_body	111423455
20	cg31199342_BC11	0.00043289	-0.0654559	Lower	Rapgef5	chr12	+	tss_body	117688829

21	cg31512652_BC21	0.00017806	-0.0582035	Lower	Gm3348	chr13	-	tss_body	44040858
22	cg31611668_BC11	0.00078655	-0.0610391	Lower	Gm3376	chr13	+	tss_body	53468819
23	cg31759324_BC21	0.00033907	-0.0534176	Lower	Gm2684	chr13	+	tss_body	69141297
24	cg31837079_BC11	0.00075262	-0.0560733	Lower	5430425K12Rik	chr13	+	tss_body	80940885
25	cg31964794_TC21	0.00088477	-0.0763848	Lower	Tmem171	chr13	-	tss_body	98695080
26	cg32279121_BC21	0.00086033	0.0593909	Higher					24999746
27	cg32330668_TC21	7.2625E-05	-0.0744574	Lower	Mustn1	chr14	+	tss_body	30881534
28	cg32728657_TC11	0.00075086	0.0529549	Higher					79314332
29	cg33346487_TC21	0.00029519	0.0618094	Higher					54069848
30	cg33511505_TC21	0.00087777	-0.0613167	Lower	Bop1	chr15	-	tss_body	76462525
31	cg33519600_BC21	4.299E-05	-0.0919489	Lower					76956346
32	cg33751900_TC11	0.00066732	0.0562146	Higher	Gm3267	chr15	+	tss_body	96842088
33	cg33814851_TC21	1.6218E-05	-0.0852846	Lower	Scn8a	chr15	+	tss_body	101039850
34	cg33814852_BC21	0.00094443	-0.0543099	Lower	Scn8a	chr15	+	tss_body	101039894
35	cg34343048_TC21	0.00027787	-0.0686173	Lower					70881084
36	cg34831362_TC21	0.00093514	-0.0553512	Lower	Pde9a	chr17	+	tss_body	31434408
37	cg34988380_TC11	1.3729E-05	-0.0648112	Lower	Foxp4	chr17	-	tss_body	47909811
38	cg35305453_TC21	0.00026271	-0.0724601	Lower	chr17-85486587-85486944	chr17	*	NShore	85486407
39	cg35597105_TC21	0.00023945	-0.0500572	Lower	chr18-35939614-35939888	chr18	*	NShelf	35936583
40	cg35614635_TC21	0.00034411	-0.0732943	Lower	Gm3701	chr18	+	tss_body	37668849
41	cg35666692_BC11	0.00044126	0.0749540	Higher	Gm4171	chr18	-	tss_body	44269959
42	cg35742526_TC11	0.0003217	-0.0972486	Lower					54847578

43	cg35776494_TC11	0.00022749	-0.07008053	Lower					58697180
44	cg35861116_BC21	0.00068469	-0.06646562	Lower	Afg3l2	chr18	-	tss_1500	67450017
45	cg36161905_TC21	0.00069884	-0.08867168	Lower	A0A140LHS9	chr19	-	tss_body	12335613
46	cg36384309_BC21	0.00089467	-0.05012069	Lower	Sorbs1	chr19	-	tss_body	40402280
47	cg36402381_TC21	0.00031475	0.0673932	Higher	Rrp12	chr19	-	tss_body	41895182
48	cg36688740_BC21	0.00063755	0.05096835	Higher	Pi15	chr1	+	tss_body	17602000
49	cg36709453_TC11	0.00083737	-0.05589806	Lower	Gm28836	chr1	-	tss_body	21240568
50	cg37100346_BC11	6.7336E-05	-0.05267984	Lower	Obsl1	chr1	-	tss_body	75486773
51	cg37613237_BC21	5.1303E-05	-0.06189118	Lower	Rgl1	chr1	-	tss_body	152682852
52	cg37666716_TC21	0.00035392	-0.05927959	Lower	Astn1	chr1	+	tss_body	158489503
53	cg37747508_TC21	0.00041447	-0.05399796	Lower	Pbx1	chr1	-	tss_body	168221396
54	cg37769525_TC11	0.00092491	-0.09141626	Lower	Fcrlb	chr1	-	tss_body	170907684
55	cg37816090_TC11	0.00011696	0.1057292	Higher	Sdccag8	chr1	+	tss_body	176835683
56	cg38115856_TC21	0.00060953	-0.05060929	Lower					19456978
57	cg38123859_BC21	0.00063692	-0.07647009	Lower	Etl4	chr2	+	tss_body	20722358
58	cg38427913_BC21	6.0812E-05	0.05070147	Higher		chr2	+	tss_body	59396912
59	cg38648897_BC21	0.00093182	-0.06281797	Lower	A0A1L1SRZ5	chr2	+	tss_body	87272993
60	cg38955541_TC21	1.5647E-06	0.30861735	Higher	Stk35	chr2	+	tss_body	129819498
61	cg39022858_BC11	0.00016673	0.09135339	Higher					138903039
62	cg39068351_BC21	0.00035574	-0.06102326	Lower	Rin2	chr2	+	tss_body	145860618
63	cg39084985_BC21	0.00061517	-0.06543275	Lower	Gm35528	chr2	+	tss_body	147877080
64	cg39357674_BC21	0.00031085	-0.08486503	Lower	Rtfdc1	chr2	+	tss_body	172441492
65	cg39382584_TC21	0.00075836	0.05641789	Higher	Gnas	chr2	+	tss_body	174297823

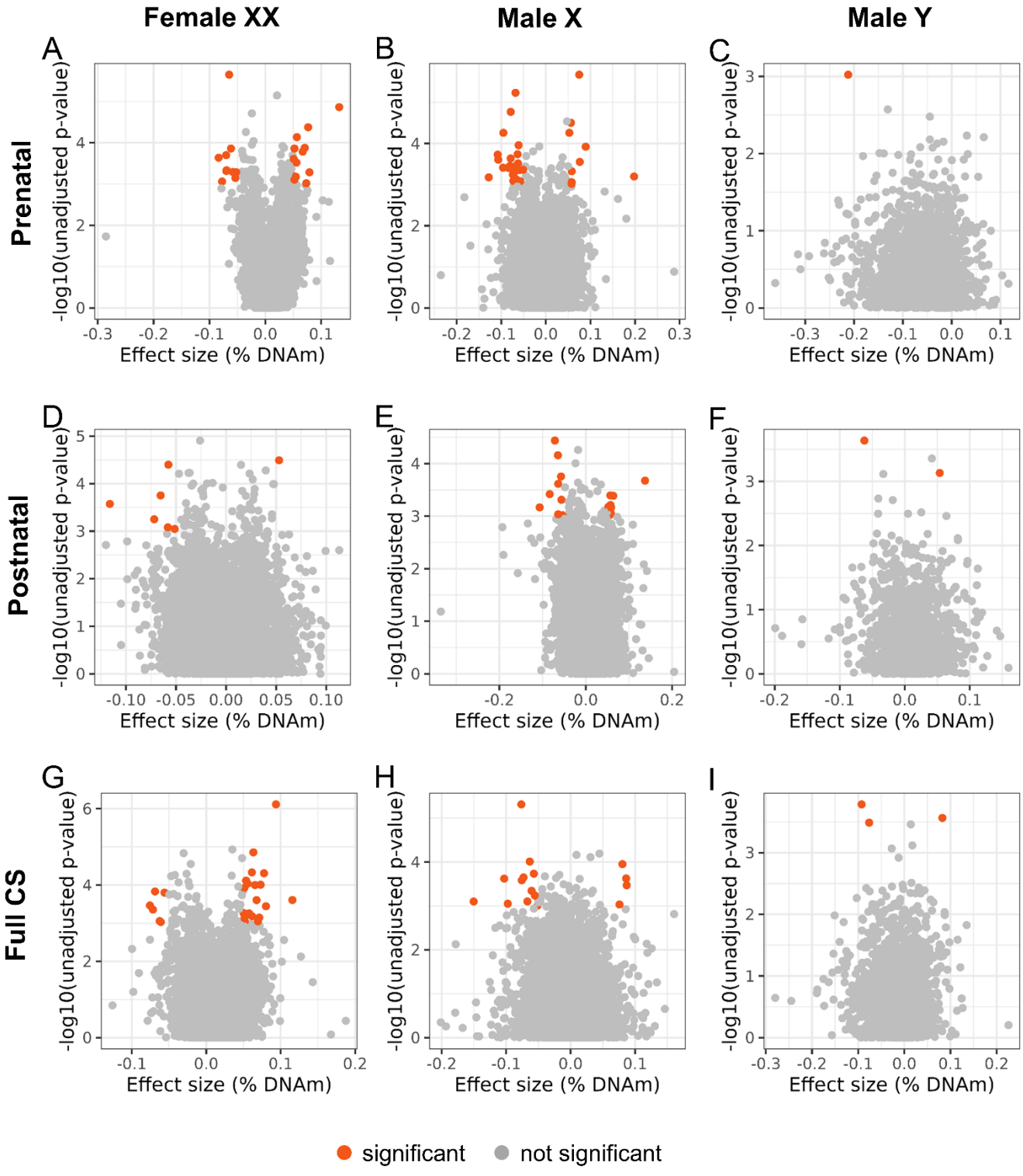
66	cg39438728_TC21	0.00077403	-0.0521452	Lower	Myt1	chr2	+	tss_body	181797663
67	cg39442495_TC21	0.00032718	-0.0686919	Lower					3349532
68	cg39621333_TC21	0.00092051	-0.1070704	Lower	Pex5l	chr3	-	tss_body	32966076
69	cg39641434_BC21	0.00059586	-0.0580985	Lower	Gm3851	chr3	-	tss_body	35405766
70	cg39754979_BC21	0.00025252	-0.0587785	Lower	Gm2447	chr3	+	tss_body	52767000
71	cg39799962_TC21	0.00010683	0.0753829	Higher	Selt	chr3	+	tss_1500	58576128
72	cg39902527_TC21	0.00055517	0.0790383	Higher	Fstl5	chr3	+	tss_body	76174001
73	cg40383437_TC21	0.00063206	-0.0504745	Lower					137322676
74	cg40683387_TC21	0.00020875	0.0600748	Higher	Gm3114	chr4	-	tss_body	23816649
75	cg40875723_BC21	0.00039295	-0.0518680	Lower	Grin3a	chr4	-	tss_body	49717853
76	cg41359048_TC21	0.00088769	-0.0517357	Lower	Gm3613	chr4	-	tss_body	120225821
77	cg41370858_TC21	0.00092767	-0.0697676	Lower	Gm1288	chr4	-	tss_body	121618300
78	cg41384056_TC11	0.00042326	0.0580160	Higher	Macf1	chr4	-	tss_body	123677231
79	cg41648098_TC21	0.00061379	-0.0712535	Lower		chr4	-	tss_body	142829673
80	cg41717622_TC21	0.00065888	-0.0583279	Lower	Rere	chr4	+	tss_body	150488581
81	cg42027863_BC21	0.00095679	-0.0551331	Lower					35189362
82	cg42039836_BC21	4.5262E-05	0.0604962	Higher	Sorcs2	chr5	-	tss_body	36221347
83	cg42220057_TC21	0.00085212	-0.0549199	Lower	Klhl5	chr5	+	tss_body	65130922
84	cg42252138_BC21	0.00082502	-0.0511865	Lower	Atp8a1	chr5	-	tss_1500	67848004
85	cg42300038_TC21	0.00028132	-0.0597404	Lower	Lnx1	chr5	-	tss_body	74623468
86	cg42423927_TC21	0.00081572	-0.0512561	Lower	Shroom3	chr5	+	tss_body	92856694
87	cg42548725_BC21	0.00069427	-0.0540486	Lower	Tgfbr3	chr5	-	tss_body	107222131
88	cg42724182_BC21	0.00021768	-0.0789998	Lower	Rph3a	chr5	-	tss_body	121008514

89	cg43410312_BC21	0.00085967	-0.0521802	Lower	C530044C16Rik	chr6	+	tss_body	50807797
90	cg43571174_TC21	0.0004502	-0.0848137	Lower					73803785
91	cg43713942_TC11	0.00083531	-0.0978317	Lower	Adamts9	chr6	-	tss_body	92940259
92	cg43923057_BC21	0.00081325	0.0554309	Higher	Ninj2	chr6	+	tss_body	120189531
93	cg44191732_TC21	0.00036935	-0.0519393	Lower	Tnnt1	chr7	-	tss_body	4513512
94	cg44314622_BC21	1.1696E-05	-0.0878202	Lower	Zfp109	chr7	-	tss_body	24237179
95	cg44393279_TC11	0.00087111	-0.0670838	Lower	Nphs1	chr7	+	tss_body	30467976
96	cg44523447_BC11	0.00079634	-0.0531595	Lower	Rasip1	chr7	+	tss_body	45635902
97	cg44978110_BC21	0.00045711	-0.0691153	Lower	Scube2	chr7	-	tss_body	109865101
98	cg45140060_BC11	4.1656E-05	-0.2382745	Lower	Kat8	chr7	+	tss_body	127922816
99	cg45375946_TC21	0.00096499	0.0500287	Higher	Ankrd10	chr8	-	tss_body	11633847
100	cg45623829_BC21	0.0007467	-0.0834798	Lower					42567388
101	cg45810285_TC11	0.00060543	-0.0530120	Lower	Comp	chr8	+	tss_body	70376086
102	cg45829155_TC21	0.00012904	-0.0588761	Lower	Unc13a	chr8	-	tss_body	71660519
103	cg46287781_BC21	0.00033993	-0.0670501	Lower	Gm33823	chr8	-	tss_body	121263580
104	cg46339766_BC11	0.0003897	0.0669424	Higher	Capn9	chr8	+	tss_body	124618061
105	cg46461724_TC21	0.00021276	-0.0656093	Lower					16599530
106	cg46577765_BC21	0.00010148	0.071479	Higher	Fli1	chr9	-	tss_body	32496246
107	cg46793218_BC21	0.00048187	0.0617158	Higher	Commd4	chr9	-	tss_body	57158233
108	cg46798108_BC11	0.00017195	0.0644284	Higher	Gm32392	chr9	+	tss_body	57607934
109	cg47134365_TC21	0.00013469	0.0608792	Higher					98276420
110	cg47200491_TC21	9.5877E-05	-0.0672245	Lower	Cpne4	chr9	+	tss_body	104986678
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**

1	cg47426861_BC21	4.8893E-06	-0.0764538 7	Lower	Syp	chrX	+	tss_body	7641201
2	cg47441291_BC21	0.00098995	-0.0512847 6	Lower	Gm3360 2	chrX	-	tss_body	9243382
3	cg47461826_BC11	0.00024005	-0.1029614 8	Lower	Bcor	chrX	-	tss_body	12083119
4	cg47490290_TC21	0.00023822	0.0861501 4	Higher					17065982
5	cg47604072_TC21	0.00089487	-0.0973848 8	Lower					47253163
6	cg47618293_TC21	0.00079211	-0.0670166 8	Lower	Gm1469 6	chrX	-	tss_body	49330317
7	cg47628382_BC11	0.00063747	-0.0517462 3	Lower	Mbnl3	chrX	-	tss_body	51169985
8	cg47736696_BC11	0.00018518	-0.057029	Lower	Atp2b3	chrX	+	tss_1500	73502795
9	cg47757743_BC21	0.00093087	0.0757650 5	Higher					77009801
10	cg47778672_BC11	0.0002615	-0.0757570 2	Lower					81621061
11	cg47856401_BC21	9.8093E-05	-0.0633474 3	Lower					98989413
12	cg48046195_TC21	0.00033969	0.0870020 3	Higher	Nrk	chrX	+	tss_body	138997832
13	cg48066232_BC21	0.00011229	0.0803680 6	Higher					142290410
14	cg48076850_BC21	0.00045333	-0.0605518 5	Lower	Dcx	chrX	-	tss_body	143882189
15	cg48157134_TC11	0.00057902	-0.0555103 4	Lower					160601339
16	cg48198816_TC21	0.00022525	-0.0730448 7	Lower	Frmpd4	chrX	-	tss_body	167899087
17	cg48208694_TC11	0.00079629	-0.1503100 2	Lower	Mid1	chrX	+	tss_body	169978880
Y chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48211792_BC21	0.00027315	0.0824864	Higher					711293
2	cg48229855_TC21	0.00032591	-0.0761515 1	Lower					5330826
3	cg48343126_BC21	0.00016453	-0.0924761 9	Lower					90719266

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome

browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.



Appendix 4. 25: Differentially methylated CpGs due to early life CS exposure in blood sex chromosomes at 8 weeks.

(A) 23 CpGs (13 higher, 10 lower) are differentially methylated due to prenatal CS exposure on the X chromosome of female offspring blood at 8 weeks (B) 31 CpGs (10 higher, 21 lower) are differentially methylated due to prenatal CS exposure on the X chromosome of male offspring blood at 8 weeks (C) 1 CpGs (0 higher, 1 lower) are differentially methylated due to

prenatal CS exposure on the Y chromosome of male offspring blood at 8 weeks (D) 7 CpGs (1 higher, 6 lower) are differentially methylated due to postnatal CS exposure on the X chromosome of female offspring blood at 8 weeks (E) 17 CpGs (8 higher, 9 lower) are differentially methylated due to postnatal CS exposure on the X chromosome of male offspring blood at 8 weeks (F) 2 CpGs (1 higher, 1 lower) are differentially methylated due to postnatal CS exposure on the Y chromosome of male offspring blood at 8 weeks (G) 25 CpGs (19 higher, 6 lower) are differentially methylated due to full CS exposure on the X chromosome of female offspring blood at 8 weeks (H) 13 CpGs (6 higher, 7 lower) are differentially methylated due to full CS exposure on the Y chromosome of male offspring blood at 8 weeks (I) 3 CpGs (1 higher, 2 lower) are differentially methylated due to full CS exposure on the Y chromosome of male offspring blood at 8 weeks. DNAm differences were analyzed using linear regression, and CpGs were considered differentially methylated at $p < 10e\text{-}3$ and effect size > 0.05. Delta beta (effect size) was calculated by subtracting beta values of exposed offspring from control mean betas. N = 3-4 per group. Significant CpGs are highlighted in orange, while non-significant ones are highlighted in grey.

Appendix 4. 26: Significantly altered CpGs in female blood at 8 weeks due to prenatal CS exposure

Autosomes									
	CpG name	P value	Effect size	Direction	Gene	Chromosome	Strand	Feature	CpG position
1	cg28120976_TC21	0.00063657	-0.05922686	Lower	Ccdc170	chr10	+	tss_body	4490307
2	cg28402135_BC11	0.00029368	-0.05062964	Lower	D3Z790	chr10	+	tss_body	42618018
3	cg28665445_BC21	0.00030117	0.08360601	Higher	Gm5134	chr10	+	tss_body	75954598
4	cg28665446_TC21	0.00046539	0.05668825	Higher	Gm5134	chr10	+	tss_body	75954663
5	cg29051138_TC21	0.00043088	0.0683473	Higher					118596032
6	cg29220931_TC21	0.00064504	0.06251148	Higher					6990682
7	cg29385607_BC21	0.00015839	-0.0516947	Lower		chr11	+	tss_body	33079507
8	cg30080889_BC21	0.00020879	0.0718224	Higher	Gm884	chr11	-	tss_body	103627781
9	cg31596091_BC21	0.00032084	-0.0509857	Lower					52191325
10	cg31743284_TC21	0.00053056	-0.08324599	Lower	A0A286YDZ7	chr13	+	tss_body	67122601
11	cg31789574_TC21	0.00090743	-0.09053791	Lower	D730050B12Rik	chr13	-	tss_200	72816771
12	cg31974447_TC21	0.00024361	0.05981473	Higher					99546792
13	cg31988148_TC21	0.00049334	-0.05879968	Lower	Gm41042	chr13	+	tss_body	101019456
14	cg32237864_BC21	0.00061443	-0.05713873	Lower	Kcnk5	chr14	-	tss_body	20153030
15	cg32427342_TC21	2.7987E-05	-0.05113746	Lower		chr14	+	tss_body	45989291
16	cg33699256_TC11	0.00014416	-0.07063054	Lower	Cntn1	chr15	+	tss_body	92161291
17	cg33699258_BC21	0.0009532	-0.07398933	Lower	Cntn1	chr15	+	tss_body	92161382
18	cg33824013_TC11	0.00014721	0.05351027	Higher	Krt71	chr15	-	tss_body	101742986
19	cg34190381_BC21	0.0006123	-0.06223915	Lower	Nepro	chr16	+	tss_body	44725479
20	cg34207876_BC11	1.058E-05	-0.06695791	Lower					47765981
21	cg34427814_BC21	0.00056723	-0.06845257	Lower					84890334
22	cg34536916_BC21	0.00081607	-0.05581688	Lower	Gm31641	chr16	-	tss_body	95259679
23	cg35051314_TC21	0.00048731	-0.0525482	Lower	Tnfaip8l1	chr17	+	tss_body	56171976
24	cg35653163_TC21	0.00054781	0.0716148	Higher					42382577
25	cg37452536_BC21	0.00083795	-0.05481383	Lower	Fcmr	chr1	+	tss_200	130865651
26	cg38387387_BC21	0.00097279	0.06075583	Higher					52757231
27	cg38499186_TC21	1.6198E-06	0.25289436	Higher	Cers6	chr2	+	tss_body	69018018
28	cg39899427_TC21	0.00045574	-0.05056619	Lower	Serpini1	chr3	+	tss_body	75628187

29	cg40008005_BC21	0.00035655	0.07653576	Higher	Pmvk	chr3	+	tss_body	89458613
30	cg41807246_BC11	0.00022671	-0.07374751	Lower	Cdk6	chr5	+	tss_body	3386405
31	cg42042825_TC21	0.00070725	-0.05675335	Lower	Tada2b	chr5	-	tss_1500	36485774
32	cg42230996_TC11	0.00055165	-0.0586595	Lower	Rbm47	chr5	-	tss_body	66084919
33	cg42923809_BC21	0.0009772	-0.06086709	Lower	Azgp1	chr5	+	tss_body	137981692
34	cg43086952_TC21	0.00055781	0.07072743	Higher	Hepacam2	chr6	-	tss_body	3470166
35	cg43878315_BC21	0.00085266	0.06384397	Higher	Mkrn2	chr6	+	tss_1500	115601661
36	cg43983500_BC21	1.4545E-05	-0.08311417	Lower	Kcna1	chr6	-	tss_body	126642028
37	cg43983512_BC21	9.1805E-05	-0.0634297	Lower	Kcna1	chr6	-	tss_body	126642436
38	cg44200993_TC11	0.00095978	-0.06548912	Lower	Vmn1r56	chr7	-	tss_body	5195844
39	cg45162018_BC21	0.0007017	-0.05211905	Lower	Fgfr2	chr7	-	tss_body	130262166
40	cg45382861_BC21	0.00069628	-0.06212297	Lower					12209624
41	cg46127313_TC21	0.00053163	0.05523616	Higher					107904666
42	cg46618993_BC21	0.00071378	-0.06699133	Lower					38896083
43	cg46793322_BC11	0.00091584	-0.0519611	Lower					57172578
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47462473_TC21	0.00086907	-0.07737506	Lower	Bcor	chrX	-	tss_body	12108095
2	cg47475803_BC11	0.00065528	0.05206694	Higher	Cask	chrX	-	tss_body	13676954
3	cg47505933_TC21	0.00013839	-0.06143642	Lower	Jade3	chrX	+	tss_body	20470178
4	cg47591964_BC21	0.00020037	-0.07003326	Lower					44020950
5	cg47606588_BC21	0.00046425	-0.0693859	Lower	Smarca1	chrX	-	tss_body	47851733
6	cg47634087_TC21	4.2287E-05	0.0767461	Higher	Gpc4	chrX	-	tss_body	52089275
7	cg47640095_BC21	0.0003039	0.05581889	Higher	Phf6	chrX	+	tss_body	52912584
8	cg47651137_TC11	0.0007124	-0.05351484	Lower					55523175
9	cg47756657_TC11	0.00023129	-0.08350775	Lower					76746484
10	cg47862063_BC21	0.00095959	0.07340445	Higher	Gm31155	chrX	+	tss_body	99557370
11	cg47879608_BC21	0.0006685	0.05466826	Higher	Nhsl2	chrX	+	tss_body	101956232
12	cg47888890_TC21	7.3386E-05	0.05655556	Higher	4930519F16Rik	chrX	-	tss_body	103227883
13	cg47889189_BC21	0.00052084	0.07905036	Higher		chrX	-	tss_body	103280560
14	cg48103246_BC21	0.00013307	0.07065442	Higher	Tmem29	chrX	-	tss_body	150463988

15	cg48119210_TC21	0.00078504	0.05221118	Higher	Rragb	chrX	+	tss_body	153172939
16	cg48120711_BC21	0.0005111	-0.05809819	Lower	Klf8	chrX	+	tss_body	153394815
17	cg48137504_TC11	0.00016539	0.06695969	Higher	Phex	chrX	-	tss_body	157222287
18	cg48142205_BC21	0.00024742	0.050848	Higher	Cnksr2	chrX	-	tss_body	157958654
19	cg48160830_BC21	0.00048417	-0.06978681	Lower	LOC108168453	chrX	+	tss_body	161297969
20	cg48181891_BC21	2.2589E-06	-0.06473922	Lower					164733752
21	cg48188882_TC21	0.00013827	0.05214344	Higher	Gemin8	chrX	+	tss_body	166189246
22	cg48189968_BC11	0.00051806	-0.05223406	Lower	Gpm6b	chrX	+	tss_body	166352089
23	cg48208953_TC21	1.3779E-05	0.13238468	Higher	Mid1	chrX	+	tss_body	169987518

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 27: Significantly altered CpGs in female blood at 8 weeks due to postnatal CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg30401631_BC21	0.00046459	0.12153195	Higher	Lpin1	chr12	-	tss_body	16569561
2	cg31787244_TC21	0.00097061	-0.11158424	Lower	Gm38580	chr13	-	tss_body	72558339
3	cg33088697_TC21	0.00072996	-0.05993079	Lower	Pdzd2	chr15	-	tss_body	12552085
4	cg34742631_BC21	0.00017821	-0.06759528	Lower	Gnptg	chr17	-	tss_body	25235757
5	cg34989687_BC21	0.00037324	-0.08106147	Lower	Gm41591	chr17	-	tss_body	47988698
6	cg35937058_TC21	0.00058822	-0.06734277	Lower	Ctif	chr18	-	tss_body	75661774
7	cg37288050_TC21	0.00063985	0.05618178	Higher					100690990
8	cg38499186_TC21	9.7782E-06	0.10771313	Higher	Cers6	chr2	+	tss_body	69018018
9	cg39959999_BC21	0.00017975	-0.08955004	Lower	Fbxw7	chr3	+	tss_body	84952336
10	cg44966968_BC11	0.00058702	-0.06085906	Lower	Olfr491	chr7	+	tss_1500	108316552
11	cg46342358_BC21	0.00054263	-0.09109388	Lower					124776287
12	cg46835257_TC21	0.0006933	-0.05265477	Lower	Gm34264	chr9	-	tss_body	61312773
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47550863_BC21	3.9933E-05	-0.05764102	Lower		chrX	-	tss_1500	36214053
2	cg47576002_BC21	0.00089596	-0.05137024	Lower					40697523
3	cg47825742_BC21	0.00082999	-0.05819516	Lower					93212665
4	cg47843281_TC21	0.00017678	-0.0653837	Lower	Las1l	chrX	-	tss_body	95955728
5	cg47921738_BC21	0.0002672	-0.11618513	Lower	Sh3bgrl	chrX	+	tss_body	109136935
6	cg48103769_TC21	0.00056135	-0.07179586	Lower	Apex2	chrX	-	tss_body	150552404
7	cg48173324_BC21	3.2271E-05	0.05296454	Higher		chrX	-	tss_1500	163389265

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 28: Significantly altered CpGs in female blood at 8 weeks due to full CS exposure

Autosomes									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28379604_BC21	0.00075301	0.05028352	Higher	Ddo	chr10	+	tss_body	40630305
2	cg28677455_BC11	0.00081962	-0.05567638	Lower	Pcbp3	chr10	-	tss_body	76960760
3	cg29290711_TC11	0.00038473	-0.06374746	Lower					19140939
4	cg29536516_TO21	0.00056542	0.05420428	Higher	Gm30366	chr11	+	tss_body	52579503
5	cg30080889_BC21	0.00076507	0.06007095	Higher	Gm884	chr11	-	tss_body	103627781
6	cg30249564_TC21	0.00042514	-0.05331729	Lower	6030468B19Rik	chr11	+	tss_1500	117797070
7	cg30822240_TC21	0.00063979	-0.06046535	Lower	Plekhg3	chr12	+	tss_body	76552709
8	cg31069367_BC21	0.00028579	-0.05887655	Lower					105546691
9	cg31077188_BC21	0.0005758	0.05804106	Higher	Gm32635	chr12	-	tss_body	106098876
10	cg31335229_TC21	0.00015781	0.05375731	Higher					21924892
11	cg31629534_BC21	0.00072661	0.05938286	Higher		chr13	-	tss_body	54926865
12	cg31747830_TC21	0.00016431	-0.06653915	Lower		chr13	-	tss_body	67766831
13	cg32347720_TC11	4.383E-06	-0.07343094	Lower	Chat	chr14	-	tss_body	32461956
14	cg34288092_BC21	0.00097896	-0.06057533	Lower	Epha6	chr16	-	tss_body	60368669
15	cg34348193_TC11	0.00047551	-0.06988565	Lower					71986131
16	cg35181928_TC21	0.00091526	-0.05387984	Lower	Gm30091	chr17	-	tss_body	71611752
17	cg35236167_TC11	0.00087511	-0.09126581	Lower	Vit	chr17	+	tss_body	78585288
18	cg35608354_TC21	0.00079282	0.0719504	Higher	Pcdha1	chr18	+	tss_body	36967565
19	cg35608785_BC21	0.00050387	-0.06530781	Lower	Pcdha1	chr18	+	tss_body	36992333
20	cg35615599_TC21	0.00010347	-0.05038431	Lower	Gm37013	chr18	+	tss_body	37721661
21	cg35653163_TC21	0.00067237	0.06736272	Higher					42382577

22	cg36165707_BC11	0.00044627	-0.05627758	Lower	Q8VF19	chr19	+	tss_1500	12949625
23	cg36584620_TC21	0.00012018	-0.09784168	Lower	Hspa12a	chr19	-	tss_body	58933683
24	cg36790907_BC21	0.00052377	-0.07104669	Lower	LOC108167618	chr1	-	tss_body	34752731
25	cg37119969_TC21	0.00047378	-0.05559741	Lower	Pax3	chr1	-	tss_body	78110744
26	cg37836060_BC21	0.00031679	0.07204552	Higher	Smyd3	chr1	-	tss_body	179136978
27	cg37905983_BC21	0.00065539	0.05703199	Higher					185469664
28	cg38499186_TC21	1.4747E-06	0.30073905	Higher	Cers6	chr2	+	tss_body	69018018
29	cg39356818_TC11	0.00095904	-0.08303159	Lower	Cstf1	chr2	+	tss_body	172381916
30	cg39389852_BC21	0.00070757	0.05343117	Higher					174897807
31	cg40065495_BC21	0.0008227	-0.07238883	Lower	Hfe2	chr3	+	tss_body	96528225
32	cg41345924_BC21	0.00013934	-0.05992102	Lower					119005526
33	cg41517165_TC21	0.00014194	0.05266586	Higher	Aim1l	chr4	+	tss_1500	134060325
34	cg41930887_BC11	0.00013669	0.13765676	Higher	Klhl7	chr5	+	tss_body	24101048
35	cg41930896_BC21	0.00072948	0.12120364	Higher	Klhl7	chr5	+	tss_body	24101169
36	cg41988946_TC21	0.00035597	0.05259178	Higher	Slc30a3	chr5	-	tss_body	31088290
37	cg42317251_BC21	0.00042178	-0.07599931	Lower					76177943
38	cg42318458_BC21	0.00013507	0.05319518	Higher	Clock	chr5	-	tss_1500	76305992
39	cg43104173_BC21	0.00026026	-0.0524425	Lower					5599276
40	cg43271503_TC11	0.00076757	-0.05357862	Lower	Mkln1	chr6	+	tss_body	31415590
41	cg43594187_BC21	0.00046178	0.05789056	Higher					79101885
42	cg44185525_TC11	0.00014093	-0.05981321	Lower	Tmc4	chr7	-	tss_body	3666947
43	cg44340894_BC11	0.00067239	-0.05153731	Lower	Vmn1r184	chr7	+	tss_200	26266797
44	cg44403820_BC21	0.00041884	-0.05447609	Lower	Scgb2b1	chr7	+	tss_1500	31263529
45	cg44916175_BC21	0.00089093	0.05144572	Higher	Dnajb13	chr7	-	tss_body	100511650
46	cg44982532_TC21	0.00026856	0.05222376	Higher		chr7	+	tss_200	110301935

47	cg45162018_BC21	6.4249E-05	-0.07834879	Lower	Fgfr2	chr7	-	tss_body	130262166
48	cg45737034_TC11	0.00051078	-0.05585607	Lower	Galntl6	chr8	-	tss_body	58734560
49	cg45798326_BC11	0.00046396	-0.05015782	Lower		chr8	-	tss_200	69240155
50	cg46432937_TC21	0.00043598	-0.05339134	Lower					12529748
51	cg46479432_TC21	0.00069362	-0.08578061	Lower	Zfp26	chr9	-	tss_1500	20461613
52	cg46973169_TC11	2.7081E-05	-0.06301591	Lower	Tmod2	chr9	-	tss_body	75593687
53	cg47165358_TC21	0.00086849	0.05138564	Higher					101518164
X chromosome									
	CpG name	**P value**	**Effect size**	**Direction**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47415226_BC21	0.00036056	0.0802124	Higher		chrX	+	tss_body	5665665
2	cg47488822_TC11	0.00054061	0.05004776	Higher					16706135
3	cg47503747_BC21	0.00015853	-0.05602593	Lower	Chst7	chrX	+	tss_body	20088844
4	cg47505933_TC21	0.00014808	-0.06874589	Lower	Jade3	chrX	+	tss_body	20470178
5	cg47509707_BC21	4.9253E-05	0.07764544	Higher	Elk1	chrX	-	tss_200	20950790
6	cg47626858_BC21	0.00034387	-0.07561128	Lower					50979284
7	cg47661083_TC21	9.1767E-05	0.0556883	Higher	Vgll1	chrX	+	tss_body	57104009
8	cg47749596_TC21	0.00044109	-0.0715391	Lower	Cmc4	chrX	-	tss_body	75409447
9	cg47804630_TC21	0.00088124	-0.06253943	Lower	Il1rapl1	chrX	-	tss_body	88021914
10	cg47839695_BC21	0.00089965	0.05192978	Higher	Arhgef9	chrX	-	tss_body	95196763
11	cg47843323_TC21	0.00011918	0.05128977	Higher	Las1l	chrX	-	tss_body	95956940
12	cg47855844_BC21	0.00024888	0.06759527	Higher					98927818
13	cg47888890_TC21	7.722E-07	0.09370465	Higher	4930519F16Rik	chrX	-	tss_body	103227883
14	cg47906744_BC21	0.000716	0.07132358	Higher	Atp7a	chrX	+	tss_body	106036502
15	cg47918910_BC21	0.00093373	-0.06100166	Lower		chrX	-	tss_body	108548937
16	cg48014720_BC21	0.00055377	0.05761525	Higher					133711132
17	cg48037925_TC21	1.3949E-05	0.06336057	Higher	Esx1	chrX	-	tss_body	137121029

18	cg48068292_TC21	0.0001004	0.06554258	Higher					142561808
19	cg48103246_BC21	0.00089392	0.06947434	Higher	Tmem29	chrX	-	tss_body	150463988
20	cg48121355_TC21	7.6854E-05	0.05349248	Higher	Ubqln2	chrX	+	tss_body	153500322
21	cg48122403_TC21	4.6745E-05	0.06132483	Higher					153706494
22	cg48137504_TC11	9.8183E-05	0.0730517	Higher	Phex	chrX	-	tss_body	157222287
23	cg48156926_TC21	0.0007328	0.05133694	Higher	Phka2	chrX	+	tss_body	160575812
24	cg48189175_BC11	0.00065941	0.06159605	Higher	Gpm6b	chrX	+	tss_1500	166238718
25	cg48208953_TC21	0.0002477	0.11570671	Higher	Mid1	chrX	+	tss_body	169987518

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Direction: direction of DNAm change in CS exposure group compared to controls. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.05.

Appendix 4. 29: Persistently altered CpGs in female lungs, identified by student t-tests

T-test longitudinal analysis: CpGs identified as significently altered by prenatal CS in female autosomes at birth, and persistently altered till 63 weeks					
	CpG	Birth	8 weeks	16 weeks	63 weeks
1	cg29603573_BC21	Negative	NotSus	NotSus	NotSus
2	cg30015312_BC21	Negative	NotSus	NotSus	NotSus
3	cg32604772_TC11	Negative	Sus_Pos	NotSus	NotSus
4	cg34180489_BC21	Negative	NotSus	NotSus	NotSus
5	cg35854416_TC11	Negative	NotSus	NotSus	NotSus
6	cg38266008_TC21	Positive	NotSus	Sus_Pos	NotSus
7	cg38605900_TC21	Positive	NotSus	NotSus	NotSus
8	cg40971505_BC21	Negative	NotSus	NotSus	NotSus
9	cg41115380_BC21	Positive	NotSus	NotSus	NotSus
10	cg41591846_TC11	Negative	NotSus	NotSus	NotSus
11	cg42012629_TC21	Negative	NotSus	NotSus	NotSus
12	cg43808744_BC21	Negative	Sus_Neg	NotSus	NotSus
13	cg46209676_TC21	Positive	NotSus	NotSus	NotSus
14	cg46573144_TC11	Positive	NotSus	NotSus	Sus_Neg
T-test longitudinal analysis: CpGs identified as significently altered by prenatal CS in female autosomes at 63 weeks, and persistently altered at birth					
	CpG	Birth	8 weeks	16 weeks	63 weeks
1	cg04056615_TC21	NotSus	NotSus	Sus_Neg	Negative
2	cg28690445_TC21	NotSus	NotSus	NotSus	Positive
3	cg28711694_BC21	NotSus	NotSus	NotSus	Positive
4	cg28725096_TC21	NotSus	NotSus	NotSus	Negative
5	cg28795853_TC21	NotSus	NotSus	NotSus	Positive
6	cg29034922_TC21	NotSus	Sus_Pos	NotSus	Negative
7	cg29840782_TC21	NotSus	NotSus	NotSus	Positive
8	cg30251175_BC11	NotSus	Sus_Pos	NotSus	Negative
9	cg30359570_TC11	NotSus	NotSus	NotSus	Negative
10	cg30841665_TC11	NotSus	NotSus	NotSus	Positive
11	cg31089458_TC21	NotSus	NotSus	NotSus	Positive
12	cg31118594_TC11	NotSus	NotSus	NotSus	Positive
13	cg31162145_TC21	NotSus	NotSus	NotSus	Negative
14	cg31401165_BC21	NotSus	NotSus	NotSus	Negative
15	cg31403382_BC21	NotSus	NotSus	NotSus	Negative
16	cg31426156_BC21	NotSus	Sus_Pos	NotSus	Positive
17	cg31616668_BC21	NotSus	NotSus	NotSus	Positive
18	cg31680002_BC21	NotSus	NotSus	NotSus	Positive
19	cg31702693_TC21	NotSus	NotSus	NotSus	Positive
20	cg31960217_BC11	NotSus	NotSus	NotSus	Positive
21	cg32005605_BC21	NotSus	NotSus	NotSus	Negative
22	cg32518464_TC21	NotSus	NotSus	NotSus	Negative

23	cg32980380_TC21	NotSus	NotSus	Sus_Pos	Positive
24	cg33395766_BC21	NotSus	NotSus	NotSus	Negative
25	cg33655237_BC21	NotSus	NotSus	NotSus	Positive
26	cg34084439_TC11	NotSus	NotSus	NotSus	Negative
27	cg34101092_TC11	NotSus	NotSus	NotSus	Negative
28	cg34228024_BC21	NotSus	NotSus	NotSus	Negative
29	cg34731705_TC21	NotSus	NotSus	NotSus	Negative
30	cg34860661_TC21	NotSus	NotSus	NotSus	Positive
31	cg34895367_BC11	NotSus	NotSus	NotSus	Positive
32	cg35053184_BC21	NotSus	NotSus	NotSus	Positive
33	cg35242342_BC21	NotSus	NotSus	NotSus	Negative
34	cg35446079_TC21	NotSus	NotSus	NotSus	Negative
35	cg35592236_TC21	NotSus	NotSus	NotSus	Positive
36	cg35593178_BC21	NotSus	NotSus	NotSus	Positive
37	cg35792874_BC21	NotSus	NotSus	NotSus	Positive
38	cg35843124_BC21	NotSus	NotSus	NotSus	Positive
39	cg35845375_TC21	NotSus	NotSus	NotSus	Positive
40	cg36799857_TC11	NotSus	NotSus	NotSus	Positive
41	cg36803879_TC11	NotSus	NotSus	NotSus	Positive
42	cg36849232_TC21	NotSus	NotSus	Sus_Pos	Positive
43	cg37006138_BC11	NotSus	NotSus	NotSus	Negative
44	cg37191000_TC21	NotSus	NotSus	NotSus	Positive
45	cg37214886_TC11	NotSus	NotSus	NotSus	Negative
46	cg37253717_TC21	NotSus	NotSus	NotSus	Positive
47	cg37785443_TC21	NotSus	NotSus	NotSus	Negative
48	cg37799500_BC21	NotSus	NotSus	NotSus	Positive
49	cg37839755_BC21	NotSus	NotSus	NotSus	Positive
50	cg37880407_BC21	NotSus	NotSus	NotSus	Positive
51	cg37907117_TC21	NotSus	NotSus	NotSus	Negative
52	cg38196075_BC11	NotSus	NotSus	NotSus	Positive
53	cg38527101_TC21	NotSus	NotSus	NotSus	Negative
54	cg38569434_TC21	NotSus	NotSus	NotSus	Negative
55	cg38834870_TC21	NotSus	NotSus	NotSus	Negative
56	cg39010442_BC21	NotSus	NotSus	NotSus	Negative
57	cg39177451_TC21	NotSus	Sus_Pos	NotSus	Positive
58	cg39234132_BC21	NotSus	NotSus	NotSus	Negative
59	cg39351755_TC21	NotSus	NotSus	NotSus	Negative
60	cg39750545_TC21	NotSus	NotSus	NotSus	Negative
61	cg40117414_TC21	NotSus	NotSus	Sus_Pos	Positive
62	cg40149438_TC21	NotSus	NotSus	NotSus	Positive
63	cg40292382_BC21	NotSus	NotSus	NotSus	Negative
64	cg41054616_TC21	NotSus	NotSus	NotSus	Negative
65	cg41337956_BC11	Sus_Neg	NotSus	NotSus	Negative

66	cg41343796_BC11	NotSus	NotSus	NotSus	Positive
67	cg41359583_BC21	NotSus	Sus_Neg	NotSus	Positive
68	cg41705774_BC21	NotSus	NotSus	NotSus	Positive
69	cg41918952_BC21	NotSus	NotSus	NotSus	Positive
70	cg42658214_BC21	NotSus	NotSus	Sus_Neg	Negative
71	cg42731685_TC21	NotSus	NotSus	NotSus	Negative
72	cg42830830_BC21	NotSus	NotSus	NotSus	Positive
73	cg42858079_TC21	NotSus	NotSus	NotSus	Positive
74	cg43394833_TC21	NotSus	NotSus	NotSus	Positive
75	cg43420321_TC21	NotSus	NotSus	NotSus	Positive
76	cg43480504_BC21	NotSus	NotSus	NotSus	Positive
77	cg43728479_TC21	NotSus	NotSus	NotSus	Negative
78	cg43904183_TC21	NotSus	NotSus	NotSus	Negative
79	cg43945543_BC21	NotSus	NotSus	NotSus	Negative
80	cg44356429_TC21	NotSus	NotSus	NotSus	Positive
81	cg44455662_BC21	NotSus	NotSus	NotSus	Negative
82	cg44458934_TC21	NotSus	NotSus	NotSus	Negative
83	cg44495119_BC21	NotSus	NotSus	NotSus	Negative
84	cg44516596_BC11	NotSus	NotSus	Sus_Pos	Positive
85	cg44779726_TC21	NotSus	NotSus	NotSus	Positive
86	cg44958331_TC21	NotSus	NotSus	NotSus	Positive
87	cg45007652_TC21	NotSus	NotSus	NotSus	Positive
88	cg45316032_TC21	NotSus	NotSus	NotSus	Negative
89	cg45808368_BC21	NotSus	NotSus	Sus_Neg	Negative
90	cg45839022_TC21	NotSus	NotSus	NotSus	Positive
91	cg45996620_BC21	NotSus	NotSus	NotSus	Negative
92	cg46018659_TC21	NotSus	NotSus	NotSus	Negative
93	cg46095071_TC11	NotSus	NotSus	NotSus	Positive
94	cg46368710_TC11	NotSus	NotSus	NotSus	Positive
95	cg46463090_BC21	NotSus	NotSus	NotSus	Negative
96	cg47120580_TC21	NotSus	NotSus	NotSus	Negative
97	cg47166957_TC21	NotSus	NotSus	NotSus	Negative
98	cg47234055_TC21	NotSus	NotSus	NotSus	Negative
99	cg47294788_BC21	NotSus	Sus_Pos	NotSus	Negative
T-test longitudinal analysis: CpGs identified as significently altered by prenatal CS in female X chromosome probes at birth, and persistently altered till 63 weeks					
	CpG	Birth	8 weeks	16 weeks	63 weeks
1	cg47855939_BC21	Positive	NotSus	NotSus	NotSus
T-test longitudinal analysis: CpGs identified as significently altered by prenatal CS in female X chromosome probes at 63 weeks, and persistently altered at birth					
	CpG	Birth	8 weeks	16 weeks	63 weeks
1	cg47427942_TC21	NotSus	NotSus	NotSus	Negative

2	cg47489270_BC21	NotSus	NotSus	NotSus	Positive
3	cg47511567_BC21	NotSus	NotSus	NotSus	Negative
4	cg47562473_TC21	NotSus	NotSus	NotSus	Negative
5	cg47575004_TC21	NotSus	NotSus	NotSus	Negative
6	cg47626157_TC21	NotSus	NotSus	NotSus	Negative
7	cg47632691_TC21	NotSus	NotSus	NotSus	Negative
8	cg47657337_BC21	NotSus	NotSus	NotSus	Negative
9	cg47667002_BC21	NotSus	NotSus	NotSus	Negative
10	cg47677954_BC21	NotSus	NotSus	NotSus	Negative
11	cg47741246_TC21	NotSus	Sus_Pos	NotSus	Negative
12	cg47743038_BC21	NotSus	NotSus	Sus_Pos	Negative
13	cg47749679_BC21	NotSus	NotSus	NotSus	Positive
14	cg47794447_BC21	NotSus	NotSus	NotSus	Positive
15	cg48018338_BC21	NotSus	NotSus	NotSus	Negative
16	cg48034707_BC21	NotSus	NotSus	NotSus	Negative
17	cg48037561_BC21	NotSus	NotSus	NotSus	Negative
18	cg48037906_BC21	NotSus	NotSus	NotSus	Negative
19	cg48204404_BC21	NotSus	NotSus	Sus_Pos	Negative

DNAm differences were initially calculated by limma at each end timepoint (birth and 63 weeks in females and birth and 16 weeks in males), and significant CpGs were identified a $p < 1e\text{-}3$ and effect size > 0.05. Student t-test was used to determine whether CpGs which were significantly altered at birth or at the end timepoint (63 weeks for females and 16 weeks for males) were persistently altered within the other individual timepoints. Sus_Pos = Sustained/persistent with positive effect size compared to controls, Sus_Neg = Sustained/persistent with negative effect size compared to controls, NotSus = Not sustained/persistent. ‘Positive’ and ‘Negative’ denote the direction of DNAm change compared to controls at each timepoint. Persistently altered CpGs were identified at a cutoff of $p < 0.05$.

Appendix 4. 30: Persistently altered CpGs in male lungs, identified by student t-tests

T-test longitudinal analysis: CpGs identified as significently altered by prenatal CS in male autosomes at birth, and persistently altered till 16 weeks				
	CpG	Birth	8 weeks	16 weeks
1	cg28735362_TC21	Negative	NotSus	NotSus
2	cg28737921_BC11	Positive	NotSus	NotSus
3	cg28747964_BC21	Negative	NotSus	NotSus
4	cg28764613_BC21	Negative	NotSus	NotSus
5	cg28985440_BC21	Positive	NotSus	Sus_Pos
6	cg29369207_BC21	Negative	NotSus	NotSus
7	cg29375539_BC21	Positive	NotSus	NotSus
8	cg29701092_TC21	Negative	Sus_Pos	NotSus
9	cg29752132_TC21	Positive	NotSus	NotSus
10	cg29895506_TC21	Negative	NotSus	NotSus
11	cg30001621_BC21	Negative	NotSus	NotSus
12	cg30033118_TC21	Negative	NotSus	NotSus
13	cg30871961_TC21	Negative	Sus_Pos	NotSus
14	cg30919992_BC21	Negative	NotSus	Sus_Neg
15	cg31089679_BC21	Positive	NotSus	NotSus
16	cg31223076_TC21	Positive	NotSus	NotSus
17	cg31330291_TC21	Negative	NotSus	NotSus
18	cg31473890_BC11	Positive	NotSus	NotSus
19	cg31687083_BC21	Positive	NotSus	NotSus
20	cg31763090_BC11	Positive	NotSus	Sus_Neg
21	cg32253169_TC21	Negative	NotSus	NotSus
22	cg32410489_TC11	Positive	NotSus	NotSus
23	cg32818432_BC21	Negative	NotSus	Sus_Pos
24	cg32981047_TC21	Negative	NotSus	NotSus
25	cg33081643_TC21	Negative	Sus_Neg	NotSus
26	cg34751213_TC21	Positive	NotSus	NotSus
27	cg34775784_TC21	Positive	NotSus	NotSus
28	cg35300001_TC21	Positive	NotSus	NotSus
29	cg36844890_BC21	Negative	NotSus	NotSus
30	cg36977839_BC21	Negative	NotSus	NotSus
31	cg37649479_BC21	Negative	NotSus	NotSus
32	cg38155722_BC21	Positive	NotSus	NotSus
33	cg38628392_TC21	Negative	NotSus	Sus_Pos
34	cg39051271_BC21	Positive	Sus_Pos	NotSus
35	cg39339180_BC21	Negative	NotSus	NotSus
36	cg39441128_TC21	Positive	NotSus	NotSus
37	cg39532867_TC21	Negative	NotSus	NotSus
38	cg39679411_BC21	Negative	NotSus	NotSus
39	cg39719440_BC11	Positive	NotSus	NotSus

40	cg41399455_BC11	Positive	NotSus	NotSus
41	cg41683918_TC11	Negative	NotSus	NotSus
42	cg42590956_TC21	Negative	NotSus	NotSus
43	cg42647826_BC21	Negative	NotSus	NotSus
44	cg42918882_TC11	Negative	Sus_Pos	NotSus
45	cg44314619_BC21	Negative	NotSus	NotSus
46	cg44504323_TC21	Positive	NotSus	NotSus
47	cg44515468_BC11	Positive	NotSus	NotSus
48	cg44670207_TC21	Positive	NotSus	NotSus
49	cg45000014_BC21	Negative	NotSus	NotSus
50	cg45313944_TC21	Positive	NotSus	NotSus
51	cg45556641_BC21	Negative	NotSus	NotSus
52	cg46104911_BC21	Positive	Sus_Neg	Sus_Pos
53	cg46470757_BC11	Positive	NotSus	Sus_Neg
54	cg46673402_TC21	Positive	NotSus	NotSus
55	cg46884318_TC11	Negative	NotSus	NotSus
56	cg47212354_BC21	Negative	NotSus	NotSus
57	cg47217347_BC21	Negative	NotSus	NotSus
58	cg47219329_BC21	Positive	NotSus	NotSus
59	cg47261365_TC21	Positive	NotSus	NotSus
60	cg47366616_TC21	Positive	NotSus	NotSus
61	cg47369200_TC11	Positive	NotSus	NotSus
62	cg47380557_BC21	Negative	NotSus	NotSus
T-test longitudinal analysis: CpGs identified as significently altered by prenatal CS in male autosomes at 16 weeks, and persistently altered at birth				
	CpG	Birth	8 weeks	16 weeks
1	cg09884843_TC21	NotSus	NotSus	Positive
2	cg16884658_BC21	NotSus	NotSus	Negative
3	cg20138186_TC21	NotSus	NotSus	Negative
4	cg28113901_TC21	NotSus	NotSus	Positive
5	cg28140621_BC21	NotSus	NotSus	Negative
6	cg28156229_BC21	NotSus	NotSus	Negative
7	cg28169677_BC21	NotSus	NotSus	Negative
8	cg28187943_TC21	NotSus	NotSus	Positive
9	cg28190126_TC21	NotSus	NotSus	Positive
10	cg28222382_TC21	NotSus	NotSus	Positive
11	cg28225956_TC11	NotSus	NotSus	Negative
12	cg28228446_TC21	NotSus	NotSus	Positive
13	cg28230365_TC21	NotSus	NotSus	Negative
14	cg28246082_TC21	NotSus	NotSus	Positive
15	cg28255176_TC21	NotSus	NotSus	Negative
16	cg28301681_TC21	NotSus	NotSus	Positive
17	cg28309927_BC21	NotSus	NotSus	Positive

18	cg28315202_TC21	NotSus	NotSus	Negative
19	cg28334389_BC21	NotSus	NotSus	Negative
20	cg28366498_TC21	Sus_Pos	NotSus	Negative
21	cg28369763_BC21	NotSus	NotSus	Positive
22	cg28372981_TC21	NotSus	NotSus	Positive
23	cg28395821_BC21	NotSus	NotSus	Positive
24	cg28402229_BC21	NotSus	NotSus	Negative
25	cg28464938_TC21	NotSus	NotSus	Negative
26	cg28495298_BC21	NotSus	NotSus	Positive
27	cg28506227_TC11	NotSus	NotSus	Positive
28	cg28510935_TC21	NotSus	NotSus	Negative
29	cg28518811_BC21	NotSus	Sus_Neg	Negative
30	cg28524725_TC21	NotSus	NotSus	Positive
31	cg28526016_BC21	NotSus	NotSus	Negative
32	cg28532315_BC21	NotSus	NotSus	Negative
33	cg28537078_TC21	NotSus	NotSus	Negative
34	cg28551435_BC21	NotSus	NotSus	Positive
35	cg28563411_TC21	NotSus	NotSus	Negative
36	cg28588785_TC21	NotSus	NotSus	Negative
37	cg28594748_BC21	NotSus	NotSus	Negative
38	cg28616058_BC21	NotSus	NotSus	Negative
39	cg28623052_TC21	NotSus	NotSus	Negative
40	cg28630561_BC11	NotSus	NotSus	Negative
41	cg28663378_BC21	NotSus	NotSus	Negative
42	cg28676048_TC21	NotSus	NotSus	Negative
43	cg28677530_TC21	NotSus	NotSus	Positive
44	cg28678093_BC11	NotSus	NotSus	Negative
45	cg28680990_BC11	NotSus	Sus_Pos	Negative
46	cg28685272_TC21	NotSus	NotSus	Negative
47	cg28686991_TC21	NotSus	NotSus	Positive
48	cg28688608_BC21	NotSus	NotSus	Positive
49	cg28690521_TC21	NotSus	NotSus	Negative
50	cg28690779_TC21	NotSus	NotSus	Negative
51	cg28691674_TC21	NotSus	NotSus	Negative
52	cg28703612_TC21	NotSus	NotSus	Positive
53	cg28704178_TC21	NotSus	NotSus	Negative
54	cg28712058_TC21	NotSus	NotSus	Negative
55	cg28715881_TC21	NotSus	NotSus	Negative
56	cg28717035_BC21	NotSus	NotSus	Negative
57	cg28717946_TC21	NotSus	Sus_Neg	Positive
58	cg28717954_TC21	NotSus	NotSus	Negative
59	cg28718344_TC21	NotSus	NotSus	Negative
60	cg28731961_TC21	NotSus	NotSus	Negative

61	cg28732083_TC21	NotSus	NotSus	Positive
62	cg28738416_BC21	NotSus	NotSus	Negative
63	cg28744456_TC21	NotSus	NotSus	Negative
64	cg28756860_BC21	NotSus	NotSus	Negative
65	cg28770147_BC21	NotSus	NotSus	Positive
66	cg28771954_TC11	NotSus	NotSus	Positive
67	cg28790092_BC21	NotSus	NotSus	Positive
68	cg28797416_BC21	NotSus	NotSus	Negative
69	cg28798228_BC21	NotSus	NotSus	Negative
70	cg28806717_BC21	NotSus	NotSus	Positive
71	cg28808117_BC21	NotSus	NotSus	Positive
72	cg28810335_TC21	NotSus	NotSus	Negative
73	cg28819830_BC21	NotSus	NotSus	Negative
74	cg28825588_BC21	NotSus	NotSus	Positive
75	cg28839136_TC21	NotSus	NotSus	Negative
76	cg28846771_TC21	NotSus	NotSus	Positive
77	cg28847336_BC21	NotSus	NotSus	Positive
78	cg28871462_BC21	NotSus	NotSus	Positive
79	cg28875950_TC21	NotSus	NotSus	Negative
80	cg28877143_BC21	NotSus	NotSus	Negative
81	cg28915970_BC21	NotSus	NotSus	Positive
82	cg28924314_BC21	NotSus	NotSus	Positive
83	cg28955595_TC21	NotSus	NotSus	Negative
84	cg28965273_BC21	NotSus	NotSus	Negative
85	cg28977237_BC11	NotSus	NotSus	Negative
86	cg28979681_BC11	NotSus	NotSus	Positive
87	cg28988145_TC11	NotSus	Sus_Pos	Positive
88	cg28989562_TC21	NotSus	NotSus	Positive
89	cg29028280_BC11	NotSus	NotSus	Negative
90	cg29039885_BC11	NotSus	NotSus	Negative
91	cg29046663_TC21	NotSus	NotSus	Negative
92	cg29046671_BC21	NotSus	NotSus	Negative
93	cg29049696_TC21	NotSus	NotSus	Positive
94	cg29061901_BC21	NotSus	Sus_Pos	Negative
95	cg29065738_BC21	NotSus	NotSus	Negative
96	cg29074081_TC21	NotSus	NotSus	Positive
97	cg29102689_BC21	NotSus	NotSus	Positive
98	cg29114933_BC11	NotSus	NotSus	Positive
99	cg29136023_BC21	NotSus	NotSus	Positive
100	cg29141167_TC11	NotSus	NotSus	Positive
101	cg29148419_BC11	NotSus	NotSus	Positive
102	cg29148470_TC11	NotSus	Sus_Pos	Negative
103	cg29153934_TC21	Sus_Pos	NotSus	Negative

104	cg29154927_TC21	NotSus	NotSus	Positive
105	cg29181100_BC21	NotSus	NotSus	Negative
106	cg29187387_BC21	NotSus	NotSus	Negative
107	cg29199185_TC21	NotSus	NotSus	Negative
108	cg29201125_TC21	NotSus	Sus_Pos	Positive
109	cg29207068_BC21	NotSus	NotSus	Negative
110	cg29208019_TC21	NotSus	NotSus	Negative
111	cg29249597_TC21	NotSus	NotSus	Positive
112	cg29251115_TC11	NotSus	NotSus	Positive
113	cg29251780_TC21	NotSus	NotSus	Positive
114	cg29289323_TC11	NotSus	NotSus	Negative
115	cg29295759_BC21	NotSus	NotSus	Negative
116	cg29304932_BC21	NotSus	NotSus	Negative
117	cg29317119_BC21	NotSus	NotSus	Negative
118	cg29320667_TC21	NotSus	NotSus	Positive
119	cg29321596_TC11	NotSus	NotSus	Positive
120	cg29321599_TC21	NotSus	NotSus	Positive
121	cg29325936_BC21	NotSus	Sus_Pos	Negative
122	cg29347536_BC21	NotSus	NotSus	Positive
123	cg29386043_TC21	NotSus	NotSus	Negative
124	cg29396116_TC21	NotSus	NotSus	Positive
125	cg29415956_BC21	NotSus	NotSus	Positive
126	cg29471896_BC21	NotSus	NotSus	Positive
127	cg29486285_BC21	NotSus	NotSus	Positive
128	cg29488552_BC21	NotSus	NotSus	Positive
129	cg29493584_BC21	NotSus	NotSus	Negative
130	cg29495221_TC21	NotSus	NotSus	Negative
131	cg29496976_BC21	NotSus	NotSus	Positive
132	cg29498974_BC21	NotSus	NotSus	Negative
133	cg29499183_TC21	NotSus	Sus_Pos	Negative
134	cg29545754_BC21	NotSus	NotSus	Positive
135	cg29545755_TC11	NotSus	NotSus	Positive
136	cg29546696_TC21	NotSus	NotSus	Negative
137	cg29549368_TC21	NotSus	NotSus	Positive
138	cg29558109_TC11	NotSus	Sus_Pos	Positive
139	cg29565309_TC21	NotSus	NotSus	Negative
140	cg29580489_TC21	NotSus	NotSus	Positive
141	cg29583297_TC21	NotSus	Sus_Pos	Negative
142	cg29584972_TC21	NotSus	NotSus	Negative
143	cg29587422_BC21	NotSus	NotSus	Positive
144	cg29619078_TC21	NotSus	NotSus	Positive
145	cg29624278_TC21	NotSus	NotSus	Negative
146	cg29625009_BC21	NotSus	Sus_Neg	Negative

147	cg29625608_BC21	NotSus	NotSus	Positive
148	cg29636353_BC21	NotSus	NotSus	Negative
149	cg29650820_BC21	NotSus	NotSus	Negative
150	cg29661768_TC21	NotSus	NotSus	Negative
151	cg29674113_BC11	NotSus	NotSus	Positive
152	cg29682169_BC21	NotSus	NotSus	Negative
153	cg29686439_TC11	NotSus	NotSus	Positive
154	cg29708399_TC21	NotSus	NotSus	Negative
155	cg29720959_BC21	NotSus	Sus_Pos	Positive
156	cg29721404_TC21	NotSus	NotSus	Positive
157	cg29722094_BC21	NotSus	NotSus	Negative
158	cg29731427_BC21	NotSus	NotSus	Negative
159	cg29735324_BC21	NotSus	NotSus	Negative
160	cg29739934_BC21	Sus_Pos	NotSus	Negative
161	cg29740804_BC21	NotSus	NotSus	Negative
162	cg29751640_BC21	NotSus	NotSus	Negative
163	cg29756721_TC21	NotSus	NotSus	Negative
164	cg29761693_BC21	NotSus	NotSus	Negative
165	cg29771739_TC21	NotSus	Sus_Pos	Negative
166	cg29782154_BC21	NotSus	NotSus	Negative
167	cg29783511_BC21	NotSus	NotSus	Negative
168	cg29788695_BC21	NotSus	NotSus	Negative
169	cg29792091_BC11	NotSus	NotSus	Positive
170	cg29794376_TC21	NotSus	NotSus	Negative
171	cg29795514_BC21	NotSus	NotSus	Negative
172	cg29807346_TC21	NotSus	NotSus	Negative
173	cg29810089_BC11	NotSus	NotSus	Negative
174	cg29810621_BC21	NotSus	NotSus	Positive
175	cg29830927_BC21	NotSus	NotSus	Negative
176	cg29839004_TC21	Sus_Neg	NotSus	Negative
177	cg29845081_BC21	NotSus	NotSus	Positive
178	cg29853141_TC21	NotSus	NotSus	Negative
179	cg29863890_BC21	NotSus	NotSus	Negative
180	cg29891470_TC21	NotSus	NotSus	Positive
181	cg29892355_BC21	NotSus	NotSus	Negative
182	cg29893289_BC21	NotSus	NotSus	Positive
183	cg29894002_BC21	NotSus	NotSus	Positive
184	cg29895631_BC21	NotSus	Sus_Neg	Negative
185	cg29908733_BC21	NotSus	NotSus	Positive
186	cg29922477_BC21	NotSus	NotSus	Negative
187	cg29925747_TC21	NotSus	NotSus	Negative
188	cg29945224_BC21	Sus_Neg	NotSus	Negative
189	cg29948556_BC11	NotSus	NotSus	Positive

190	cg29954737_TC21	NotSus	NotSus	Negative
191	cg29973879_BC21	NotSus	NotSus	Positive
192	cg29975605_TC21	NotSus	NotSus	Negative
193	cg29984286_BC21	NotSus	Sus_Pos	Positive
194	cg29985460_TC21	Sus_Pos	NotSus	Negative
195	cg29988815_TC21	NotSus	NotSus	Positive
196	cg29996728_TC11	NotSus	NotSus	Negative
197	cg29996950_BC21	NotSus	NotSus	Negative
198	cg30004657_BC21	NotSus	NotSus	Negative
199	cg30004951_TC21	NotSus	NotSus	Negative
200	cg30009848_BC21	NotSus	NotSus	Negative
201	cg30010400_TC21	NotSus	NotSus	Positive
202	cg30021477_TC11	NotSus	NotSus	Negative
203	cg30027579_TC21	NotSus	NotSus	Negative
204	cg30038841_TC21	NotSus	NotSus	Negative
205	cg30038870_TC21	NotSus	NotSus	Positive
206	cg30041231_BC21	NotSus	NotSus	Positive
207	cg30043568_TC21	NotSus	NotSus	Positive
208	cg30044113_TC21	NotSus	NotSus	Negative
209	cg30049469_BC21	NotSus	NotSus	Positive
210	cg30051522_BC21	NotSus	NotSus	Negative
211	cg30055652_BC21	NotSus	NotSus	Negative
212	cg30060424_BC21	NotSus	NotSus	Positive
213	cg30064650_TC21	NotSus	NotSus	Negative
214	cg30067470_TC21	NotSus	NotSus	Negative
215	cg30067490_TC21	NotSus	NotSus	Negative
216	cg30072057_BC21	NotSus	NotSus	Negative
217	cg30077797_BC21	NotSus	NotSus	Positive
218	cg30104680_TC21	NotSus	NotSus	Negative
219	cg30110228_TC21	NotSus	Sus_Pos	Negative
220	cg30114751_TC21	NotSus	NotSus	Negative
221	cg30114756_BC21	NotSus	NotSus	Negative
222	cg30115426_BC21	NotSus	NotSus	Negative
223	cg30117456_BC21	NotSus	NotSus	Negative
224	cg30122074_TC21	NotSus	NotSus	Negative
225	cg30127215_BC21	NotSus	NotSus	Negative
226	cg30140894_TC21	NotSus	NotSus	Positive
227	cg30144209_BC21	NotSus	NotSus	Negative
228	cg30165622_BC21	NotSus	NotSus	Negative
229	cg30179683_BC21	NotSus	NotSus	Negative
230	cg30186853_TC21	NotSus	NotSus	Negative
231	cg30188222_BC21	NotSus	NotSus	Positive
232	cg30190188_BC21	NotSus	NotSus	Positive

233	cg30192887_BC21	NotSus	NotSus	Negative
234	cg30194157_BC21	NotSus	NotSus	Positive
235	cg30196810_TC11	NotSus	NotSus	Positive
236	cg30201766_TC11	NotSus	NotSus	Negative
237	cg30202620_TC11	NotSus	NotSus	Positive
238	cg30209024_BC21	NotSus	NotSus	Negative
239	cg30214308_BC11	Sus_Pos	NotSus	Positive
240	cg30214691_BC21	NotSus	NotSus	Negative
241	cg30219103_BC21	NotSus	NotSus	Negative
242	cg30220952_BC21	NotSus	NotSus	Positive
243	cg30224382_BC21	NotSus	NotSus	Negative
244	cg30224851_TC21	NotSus	NotSus	Negative
245	cg30230014_BC21	NotSus	NotSus	Negative
246	cg30237834_BC21	NotSus	NotSus	Negative
247	cg30237908_TC11	NotSus	NotSus	Negative
248	cg30248118_BC21	NotSus	NotSus	Positive
249	cg30248242_BC21	NotSus	NotSus	Negative
250	cg30249131_BC21	NotSus	NotSus	Negative
251	cg30251175_BC11	NotSus	Sus_Pos	Negative
252	cg30252966_BC21	NotSus	NotSus	Negative
253	cg30264787_BC21	NotSus	NotSus	Positive
254	cg30277184_BC21	NotSus	NotSus	Negative
255	cg30287396_TC21	NotSus	NotSus	Negative
256	cg30296060_BC21	NotSus	NotSus	Positive
257	cg30310317_BC21	NotSus	NotSus	Negative
258	cg30317299_TC21	NotSus	NotSus	Positive
259	cg30326689_TC21	NotSus	NotSus	Negative
260	cg30330951_TC21	NotSus	Sus_Pos	Negative
261	cg30331555_TC21	NotSus	NotSus	Negative
262	cg30347469_BC21	NotSus	NotSus	Negative
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265	cg30376961_TC21	NotSus	NotSus	Negative
266	cg30406372_TC21	Sus_Pos	NotSus	Negative
267	cg30408802_TC21	NotSus	NotSus	Negative
268	cg30409084_TC21	NotSus	NotSus	Positive
269	cg30410661_TC21	NotSus	NotSus	Negative
270	cg30469482_TC21	NotSus	NotSus	Negative
271	cg30475854_TC21	Sus_Neg	NotSus	Positive
272	cg30484969_TC21	NotSus	NotSus	Positive
273	cg30493652_TC21	NotSus	NotSus	Negative
274	cg30496381_TC21	NotSus	NotSus	Negative
275	cg30501011_TC21	NotSus	NotSus	Positive

276	cg30506221_BC21	NotSus	NotSus	Positive
277	cg30512774_TC21	NotSus	NotSus	Negative
278	cg30520919_BC21	NotSus	NotSus	Negative
279	cg30520964_TC21	NotSus	NotSus	Negative
280	cg30548414_TC21	NotSus	NotSus	Positive
281	cg30551116_TC21	NotSus	NotSus	Negative
282	cg30566758_BC21	NotSus	NotSus	Negative
283	cg30607694_BC11	NotSus	NotSus	Positive
284	cg30649710_BC21	NotSus	NotSus	Negative
285	cg30657324_BC11	NotSus	NotSus	Positive
286	cg30670477_BC21	NotSus	NotSus	Positive
287	cg30678041_TC21	NotSus	NotSus	Negative
288	cg30686574_BC21	NotSus	NotSus	Negative
289	cg30745744_TC21	Sus_Pos	NotSus	Positive
290	cg30753175_BC21	NotSus	NotSus	Positive
291	cg30769850_TC21	NotSus	NotSus	Negative
292	cg30780200_TC21	NotSus	NotSus	Positive
293	cg30781740_BC11	NotSus	NotSus	Positive
294	cg30782070_BC21	NotSus	NotSus	Negative
295	cg30807007_TC21	NotSus	NotSus	Negative
296	cg30822155_TC21	NotSus	Sus_Pos	Positive
297	cg30823045_BC11	NotSus	NotSus	Negative
298	cg30842349_BC21	NotSus	NotSus	Positive
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300	cg30850793_TC21	NotSus	NotSus	Negative
301	cg30851811_TC21	NotSus	NotSus	Positive
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303	cg30855703_TC11	NotSus	NotSus	Positive
304	cg30858292_BC21	NotSus	NotSus	Positive
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306	cg30886046_TC21	NotSus	NotSus	Negative
307	cg30892325_BC21	NotSus	NotSus	Positive
308	cg30899823_BC21	NotSus	NotSus	Negative
309	cg30910036_TC21	NotSus	Sus_Pos	Negative
310	cg30910931_BC21	NotSus	NotSus	Positive
311	cg30917013_BC21	NotSus	NotSus	Positive
312	cg30919303_TC21	NotSus	NotSus	Negative
313	cg30925986_TC21	NotSus	NotSus	Positive
314	cg30928637_BC11	NotSus	NotSus	Negative
315	cg30929300_BC21	NotSus	NotSus	Negative
316	cg30935464_TC21	NotSus	NotSus	Negative
317	cg30949928_TC21	NotSus	NotSus	Positive
318	cg30960256_BC21	NotSus	NotSus	Negative

319	cg30962387_BC21	NotSus	NotSus	Negative
320	cg30998932_TC21	NotSus	NotSus	Positive
321	cg31001095_BC21	NotSus	NotSus	Negative
322	cg31001573_BC21	NotSus	NotSus	Positive
323	cg31015715_BC21	NotSus	NotSus	Positive
324	cg31017196_TC21	NotSus	NotSus	Positive
325	cg31018420_TC21	NotSus	NotSus	Negative
326	cg31019114_BC21	NotSus	NotSus	Positive
327	cg31021807_BC21	NotSus	NotSus	Negative
328	cg31034008_TC21	NotSus	NotSus	Negative
329	cg31038717_TC21	NotSus	NotSus	Negative
330	cg31047476_TC21	NotSus	NotSus	Positive
331	cg31049410_TC21	NotSus	NotSus	Negative
332	cg31059495_TC11	NotSus	NotSus	Negative
333	cg31060274_BC21	NotSus	NotSus	Positive
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336	cg31070811_TC21	NotSus	NotSus	Positive
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345	cg31145412_TC21	NotSus	NotSus	Positive
346	cg31149197_BC21	NotSus	NotSus	Positive
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348	cg31156523_TC21	NotSus	NotSus	Negative
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351	cg31165859_TC21	NotSus	NotSus	Negative
352	cg31189399_BC21	NotSus	NotSus	Negative
353	cg31193043_TC21	NotSus	NotSus	Negative
354	cg31201098_TC21	NotSus	NotSus	Negative
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356	cg31266683_BC21	NotSus	NotSus	Positive
357	cg31284760_BC21	NotSus	NotSus	Positive
358	cg31291174_BC11	NotSus	NotSus	Positive
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360	cg31379956_TC21	NotSus	NotSus	Positive
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362	cg31393704_TC21	NotSus	NotSus	Negative
363	cg31412871_TC21	NotSus	NotSus	Negative
364	cg31414835_BC11	NotSus	NotSus	Positive
365	cg31415822_TC21	NotSus	NotSus	Positive
366	cg31416142_TC21	NotSus	NotSus	Positive
367	cg31422434_BC21	NotSus	NotSus	Positive
368	cg31434819_BC21	NotSus	NotSus	Negative
369	cg31459367_BC21	NotSus	Sus_Pos	Positive
370	cg31460055_BC21	NotSus	NotSus	Negative
371	cg31486148_TC21	NotSus	NotSus	Positive
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373	cg31518528_TC21	NotSus	NotSus	Negative
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375	cg31522038_TC11	NotSus	NotSus	Negative
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383	cg31594932_BC11	NotSus	NotSus	Negative
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386	cg31617339_BC11	NotSus	NotSus	Negative
387	cg31633880_TC21	NotSus	NotSus	Negative
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391	cg31668749_BC11	NotSus	NotSus	Positive
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393	cg31674961_TC11	NotSus	NotSus	Negative
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395	cg31701790_BC21	NotSus	NotSus	Positive
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399	cg31800688_BC11	NotSus	NotSus	Negative
400	cg31811294_TC21	NotSus	NotSus	Negative
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403	cg31859167_BC21	NotSus	NotSus	Negative
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405	cg31911445_TC21	NotSus	NotSus	Positive
406	cg31930639_TC11	NotSus	NotSus	Positive
407	cg31932089_BC21	NotSus	NotSus	Negative
408	cg31962489_TC21	NotSus	NotSus	Negative
409	cg31973849_TC21	NotSus	Sus_Pos	Negative
410	cg31975019_TC21	NotSus	NotSus	Negative
411	cg31977527_TC11	NotSus	NotSus	Positive
412	cg31980402_BC21	NotSus	NotSus	Positive
413	cg32023128_TC21	NotSus	NotSus	Positive
414	cg32037759_TC21	NotSus	NotSus	Negative
415	cg32072899_BC21	NotSus	NotSus	Positive
416	cg32087099_TC21	NotSus	NotSus	Positive
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418	cg32119025_TC21	NotSus	NotSus	Positive
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420	cg32165266_BC21	NotSus	NotSus	Negative
421	cg32173885_BC11	NotSus	NotSus	Negative
422	cg32186140_TC21	NotSus	NotSus	Negative
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426	cg32206002_BC21	NotSus	NotSus	Negative
427	cg32225794_TC11	NotSus	NotSus	Positive
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431	cg32258206_TC11	NotSus	NotSus	Negative
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433	cg32275671_BC21	NotSus	NotSus	Negative
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435	cg32298527_TC21	NotSus	NotSus	Negative
436	cg32308694_BC21	NotSus	NotSus	Negative
437	cg32318685_BC21	NotSus	NotSus	Negative
438	cg32327780_BC21	NotSus	NotSus	Negative
439	cg32330768_BC21	Sus_Pos	NotSus	Negative
440	cg32334028_BC21	NotSus	NotSus	Negative
441	cg32337218_BC21	NotSus	NotSus	Negative
442	cg32337222_BC21	Sus_Neg	NotSus	Negative
443	cg32337226_BC21	NotSus	NotSus	Negative
444	cg32343345_BC21	NotSus	NotSus	Negative
445	cg32343678_TC21	NotSus	NotSus	Negative
446	cg32356927_BC21	NotSus	NotSus	Negative
447	cg32369155_BC11	NotSus	NotSus	Negative

448	cg32424382_TC21	NotSus	NotSus	Positive
449	cg32429088_BC21	NotSus	NotSus	Positive
450	cg32432636_BC21	NotSus	NotSus	Negative
451	cg32437202_TC21	NotSus	NotSus	Negative
452	cg32441536_BC21	NotSus	NotSus	Negative
453	cg32451798_BC21	NotSus	NotSus	Negative
454	cg32452247_TC21	NotSus	NotSus	Positive
455	cg32459734_BC21	NotSus	NotSus	Negative
456	cg32479085_BC21	NotSus	NotSus	Negative
457	cg32479642_TC11	NotSus	NotSus	Positive
458	cg32481748_TC21	Sus_Pos	NotSus	Positive
459	cg32493000_BC21	NotSus	Sus_Neg	Positive
460	cg32505831_TC21	NotSus	NotSus	Positive
461	cg32530526_TC21	NotSus	NotSus	Negative
462	cg32543246_BC21	NotSus	NotSus	Negative
463	cg32572578_TC21	NotSus	NotSus	Positive
464	cg32578285_BC21	NotSus	NotSus	Negative
465	cg32622448_BC21	NotSus	NotSus	Negative
466	cg32624901_BC21	NotSus	NotSus	Negative
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468	cg32642581_TC11	NotSus	NotSus	Positive
469	cg32647039_BC21	NotSus	NotSus	Positive
470	cg32650531_TC21	NotSus	NotSus	Negative
471	cg32653557_TC21	NotSus	NotSus	Negative
472	cg32664780_BC21	NotSus	NotSus	Positive
473	cg32669876_TC21	NotSus	NotSus	Negative
474	cg32670323_BC11	NotSus	NotSus	Positive
475	cg32670974_TC21	NotSus	NotSus	Negative
476	cg32671065_BC21	NotSus	NotSus	Negative
477	cg32674366_TC21	NotSus	NotSus	Positive
478	cg32679292_BC21	NotSus	NotSus	Negative
479	cg32682961_BC21	NotSus	NotSus	Negative
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482	cg32707289_BC21	NotSus	NotSus	Positive
483	cg32710680_TC21	NotSus	NotSus	Positive
484	cg32748938_TC21	NotSus	NotSus	Negative
485	cg32774362_BC21	NotSus	NotSus	Negative
486	cg32817566_TC21	NotSus	NotSus	Positive
487	cg32831221_TC21	NotSus	Sus_Pos	Positive
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489	cg32858627_TC21	Sus_Neg	NotSus	Positive
490	cg32921584_TC21	NotSus	NotSus	Positive

491	cg32930571_BC21	NotSus	NotSus	Positive
492	cg32956521_TC21	NotSus	Sus_Pos	Positive
493	cg32967164_BC21	NotSus	NotSus	Negative
494	cg32982031_BC21	NotSus	NotSus	Negative
495	cg32992689_TC11	NotSus	NotSus	Negative
496	cg33073345_TC21	NotSus	NotSus	Negative
497	cg33084122_BC21	NotSus	NotSus	Negative
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499	cg33155380_BC21	NotSus	NotSus	Negative
500	cg33155793_TC21	NotSus	NotSus	Negative
501	cg33160278_BC21	NotSus	NotSus	Negative
502	cg33206420_TC11	NotSus	NotSus	Positive
503	cg33237608_TC21	NotSus	NotSus	Positive
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506	cg33247817_BC21	NotSus	NotSus	Positive
507	cg33259896_BC21	NotSus	NotSus	Negative
508	cg33263063_BC21	NotSus	NotSus	Positive
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511	cg33333102_TC11	NotSus	NotSus	Positive
512	cg33351652_TC21	NotSus	NotSus	Negative
513	cg33356136_BC21	NotSus	NotSus	Positive
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515	cg33376330_BC11	NotSus	NotSus	Negative
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519	cg33400265_TC21	NotSus	NotSus	Negative
520	cg33422756_TC21	NotSus	Sus_Neg	Negative
521	cg33427578_TC21	NotSus	NotSus	Negative
522	cg33435993_BC21	NotSus	NotSus	Negative
523	cg33469136_BC11	NotSus	NotSus	Negative
524	cg33478087_TC11	NotSus	NotSus	Positive
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526	cg33494466_BC21	Sus_Pos	NotSus	Negative
527	cg33501085_TC21	NotSus	NotSus	Negative
528	cg33502294_BC21	NotSus	NotSus	Negative
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530	cg33507122_BC21	NotSus	NotSus	Positive
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532	cg33523294_BC11	NotSus	NotSus	Positive
533	cg33524141_TC21	NotSus	NotSus	Negative

534	cg33526945_TC21	NotSus	NotSus	Negative
535	cg33532451_BC21	NotSus	NotSus	Negative
536	cg33533599_TC21	NotSus	NotSus	Positive
537	cg33533855_TC21	NotSus	NotSus	Negative
538	cg33534732_BC21	NotSus	NotSus	Negative
539	cg33535376_BC21	NotSus	NotSus	Negative
540	cg33537975_BC21	NotSus	NotSus	Negative
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542	cg33549573_TC21	NotSus	NotSus	Positive
543	cg33555696_TC21	NotSus	NotSus	Negative
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545	cg33559255_BC21	NotSus	NotSus	Negative
546	cg33566644_BC21	NotSus	NotSus	Negative
547	cg33583122_TC21	NotSus	NotSus	Negative
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549	cg33584852_TC21	NotSus	NotSus	Negative
550	cg33593260_BC21	NotSus	NotSus	Negative
551	cg33601291_TC11	NotSus	NotSus	Positive
552	cg33603800_TC21	NotSus	NotSus	Negative
553	cg33613246_BC11	NotSus	NotSus	Negative
554	cg33619500_TC21	NotSus	NotSus	Negative
555	cg33620210_BC21	NotSus	NotSus	Negative
556	cg33625221_TC21	NotSus	NotSus	Negative
557	cg33628904_BC21	NotSus	NotSus	Negative
558	cg33630016_BC21	NotSus	NotSus	Negative
559	cg33662534_BC21	NotSus	Sus_Pos	Negative
560	cg33665697_BC21	NotSus	NotSus	Positive
561	cg33667039_BC21	NotSus	NotSus	Negative
562	cg33669442_TC21	NotSus	NotSus	Negative
563	cg33672951_TC21	NotSus	NotSus	Positive
564	cg33703748_BC11	NotSus	NotSus	Positive
565	cg33706099_TC11	NotSus	NotSus	Positive
566	cg33707570_TC21	Sus_Neg	NotSus	Positive
567	cg33738131_TC21	NotSus	NotSus	Positive
568	cg33748926_BC21	NotSus	NotSus	Positive
569	cg33753160_TC11	NotSus	NotSus	Positive
570	cg33764499_BC21	NotSus	NotSus	Negative
571	cg33768218_BC11	NotSus	NotSus	Positive
572	cg33772044_TC21	NotSus	NotSus	Negative
573	cg33786162_BC21	NotSus	Sus_Pos	Negative
574	cg33793231_BC11	NotSus	NotSus	Positive
575	cg33797263_TC21	NotSus	NotSus	Negative
576	cg33797344_TC21	NotSus	NotSus	Negative

577	cg33806537_BC21	NotSus	NotSus	Negative
578	cg33809015_BC21	NotSus	NotSus	Positive
579	cg33815700_BC21	NotSus	NotSus	Positive
580	cg33820221_BC21	NotSus	NotSus	Negative
581	cg33823141_BC21	NotSus	NotSus	Negative
582	cg33830745_BC21	NotSus	NotSus	Positive
583	cg33835294_BC21	NotSus	NotSus	Positive
584	cg33841914_BC21	NotSus	NotSus	Negative
585	cg33853376_TC21	NotSus	NotSus	Negative
586	cg33853976_TC21	NotSus	NotSus	Negative
587	cg33855988_TC21	NotSus	NotSus	Negative
588	cg33860750_TC21	NotSus	NotSus	Negative
589	cg33863384_BC21	NotSus	NotSus	Negative
590	cg33875913_TC21	NotSus	NotSus	Negative
591	cg33889498_TC21	NotSus	NotSus	Positive
592	cg33889648_BC21	NotSus	NotSus	Negative
593	cg33895828_TC21	NotSus	NotSus	Negative
594	cg33907757_BC21	Sus_Pos	NotSus	Negative
595	cg33911457_BC21	NotSus	NotSus	Negative
596	cg33914002_TC21	NotSus	NotSus	Positive
597	cg33936433_BC21	NotSus	NotSus	Negative
598	cg33940518_BC21	NotSus	NotSus	Negative
599	cg33953149_BC21	NotSus	NotSus	Negative
600	cg33963529_BC21	NotSus	NotSus	Negative
601	cg33963638_BC21	NotSus	NotSus	Negative
602	cg33963925_BC21	NotSus	NotSus	Negative
603	cg33967593_TC21	NotSus	NotSus	Negative
604	cg33975725_BC21	NotSus	NotSus	Positive
605	cg33978582_TC21	NotSus	NotSus	Negative
606	cg33985954_BC21	NotSus	NotSus	Negative
607	cg34009583_BC21	NotSus	NotSus	Negative
608	cg34012933_TC21	NotSus	NotSus	Positive
609	cg34016591_BC21	NotSus	NotSus	Negative
610	cg34049088_BC21	NotSus	Sus_Pos	Negative
611	cg34049655_TC21	NotSus	NotSus	Positive
612	cg34058189_BC21	NotSus	NotSus	Negative
613	cg34069095_TC21	NotSus	NotSus	Negative
614	cg34079554_BC11	NotSus	NotSus	Positive
615	cg34083229_BC21	NotSus	NotSus	Positive
616	cg34085922_BC21	NotSus	NotSus	Negative
617	cg34142766_TC21	NotSus	NotSus	Positive
618	cg34145649_BC21	NotSus	NotSus	Positive
619	cg34149695_TC21	NotSus	NotSus	Positive

620	cg34152326_BC21	NotSus	NotSus	Positive
621	cg34215598_BC11	NotSus	NotSus	Positive
622	cg34264096_TC21	NotSus	NotSus	Positive
623	cg34305611_BC21	NotSus	NotSus	Positive
624	cg34343455_BC21	NotSus	NotSus	Negative
625	cg34348737_TC21	NotSus	Sus_Pos	Negative
626	cg34364564_BC21	NotSus	NotSus	Positive
627	cg34379299_TC21	NotSus	NotSus	Negative
628	cg34379450_TC21	NotSus	NotSus	Positive
629	cg34428566_TC21	Sus_Neg	NotSus	Negative
630	cg34458000_TC21	NotSus	NotSus	Positive
631	cg34474858_TC21	NotSus	NotSus	Negative
632	cg34483156_TC21	NotSus	NotSus	Negative
633	cg34488695_BC21	NotSus	NotSus	Negative
634	cg34490273_BC21	Sus_Pos	NotSus	Negative
635	cg34497589_TC21	NotSus	NotSus	Negative
636	cg34497648_BC21	NotSus	NotSus	Negative
637	cg34500536_BC21	NotSus	NotSus	Negative
638	cg34500654_TC21	NotSus	NotSus	Positive
639	cg34500656_TC21	NotSus	NotSus	Positive
640	cg34504287_TC21	Sus_Neg	NotSus	Positive
641	cg34518639_BC21	Sus_Pos	NotSus	Negative
642	cg34520682_BC21	NotSus	NotSus	Positive
643	cg34536605_TC21	NotSus	NotSus	Positive
644	cg34578779_BC21	NotSus	NotSus	Negative
645	cg34580324_TC21	NotSus	NotSus	Negative
646	cg34580638_TC21	NotSus	NotSus	Positive
647	cg34586645_BC21	NotSus	NotSus	Positive
648	cg34601960_BC21	NotSus	NotSus	Negative
649	cg34602183_BC21	NotSus	NotSus	Negative
650	cg34619765_BC21	NotSus	NotSus	Positive
651	cg34624390_TC21	NotSus	NotSus	Negative
652	cg34626157_BC21	NotSus	NotSus	Negative
653	cg34631823_BC21	NotSus	Sus_Neg	Positive
654	cg34646066_TC21	NotSus	NotSus	Negative
655	cg34646492_BC21	NotSus	NotSus	Negative
656	cg34669634_BC21	NotSus	NotSus	Negative
657	cg34670717_TC21	NotSus	NotSus	Negative
658	cg34677811_TC21	NotSus	NotSus	Negative
659	cg34724166_BC21	Sus_Pos	NotSus	Negative
660	cg34740477_TC21	NotSus	NotSus	Negative
661	cg34750763_BC21	NotSus	NotSus	Positive
662	cg34751816_BC21	NotSus	NotSus	Negative

663	cg34751833_TC21	NotSus	NotSus	Negative
664	cg34753092_BC21	NotSus	NotSus	Negative
665	cg34761327_TC21	NotSus	NotSus	Negative
666	cg34761689_BC21	NotSus	NotSus	Negative
667	cg34764896_BC11	NotSus	NotSus	Negative
668	cg34779468_TC21	NotSus	NotSus	Positive
669	cg34788935_TC21	NotSus	NotSus	Negative
670	cg34789024_BC21	NotSus	Sus_Pos	Negative
671	cg34789335_BC21	NotSus	NotSus	Negative
672	cg34797278_TC21	NotSus	NotSus	Positive
673	cg34797551_BC11	NotSus	NotSus	Negative
674	cg34798338_TC21	NotSus	NotSus	Negative
675	cg34801230_BC21	NotSus	NotSus	Negative
676	cg34803900_BC21	NotSus	NotSus	Negative
677	cg34828267_TC11	NotSus	NotSus	Positive
678	cg34831884_TC21	NotSus	NotSus	Negative
679	cg34833587_TC11	NotSus	NotSus	Negative
680	cg34834986_TC21	NotSus	NotSus	Negative
681	cg34844395_BC21	NotSus	NotSus	Positive
682	cg34854542_BC21	NotSus	NotSus	Negative
683	cg34861465_BC21	NotSus	NotSus	Positive
684	cg34862013_TC21	NotSus	NotSus	Negative
685	cg34862073_TC21	NotSus	Sus_Pos	Negative
686	cg34866258_BC21	NotSus	NotSus	Positive
687	cg34866493_TC21	NotSus	NotSus	Negative
688	cg34866567_BC11	NotSus	NotSus	Positive
689	cg34866641_BC21	NotSus	NotSus	Negative
690	cg34866765_BC21	NotSus	NotSus	Negative
691	cg34867397_TC21	NotSus	NotSus	Negative
692	cg34870654_BC21	NotSus	NotSus	Negative
693	cg34871478_BC21	NotSus	NotSus	Negative
694	cg34871652_BC21	NotSus	Sus_Pos	Negative
695	cg34871999_BC11	NotSus	NotSus	Positive
696	cg34873622_BC21	NotSus	NotSus	Negative
697	cg34874422_BC21	NotSus	NotSus	Negative
698	cg34874517_TC21	NotSus	NotSus	Positive
699	cg34876157_TC21	NotSus	NotSus	Negative
700	cg34876262_BC21	NotSus	NotSus	Positive
701	cg34884547_BC21	NotSus	NotSus	Negative
702	cg34894236_BC21	NotSus	NotSus	Negative
703	cg34930382_BC21	NotSus	NotSus	Negative
704	cg34932112_BC21	NotSus	NotSus	Negative
705	cg34940218_TO21	NotSus	NotSus	Positive

706	cg34940666_TC21	NotSus	NotSus	Positive
707	cg34961753_TC21	NotSus	NotSus	Negative
708	cg34985739_TC21	NotSus	NotSus	Positive
709	cg34989559_TC21	NotSus	NotSus	Positive
710	cg34992454_TC21	NotSus	NotSus	Negative
711	cg34993376_BC21	NotSus	NotSus	Negative
712	cg34993621_BC21	NotSus	NotSus	Negative
713	cg35002105_TC21	NotSus	NotSus	Positive
714	cg35007995_TC21	NotSus	NotSus	Negative
715	cg35008865_TC21	NotSus	NotSus	Negative
716	cg35009907_BC21	NotSus	NotSus	Positive
717	cg35026837_TC21	Sus_Neg	NotSus	Negative
718	cg35044928_TC21	NotSus	NotSus	Positive
719	cg35046739_TC21	NotSus	NotSus	Negative
720	cg35048578_BC21	NotSus	NotSus	Positive
721	cg35048600_TC21	NotSus	Sus_Pos	Positive
722	cg35050148_TC21	NotSus	NotSus	Positive
723	cg35050429_TC11	NotSus	NotSus	Negative
724	cg35050433_BC21	NotSus	NotSus	Negative
725	cg35055682_BC21	NotSus	NotSus	Negative
726	cg35057137_TC21	NotSus	NotSus	Negative
727	cg35065839_BC21	NotSus	Sus_Neg	Negative
728	cg35095172_BC21	NotSus	NotSus	Negative
729	cg35110729_BC11	NotSus	NotSus	Positive
730	cg35121970_TC21	NotSus	NotSus	Negative
731	cg35136695_BC21	NotSus	NotSus	Negative
732	cg35145377_TC21	NotSus	NotSus	Positive
733	cg35148365_TC21	NotSus	NotSus	Negative
734	cg35171769_TC21	NotSus	NotSus	Positive
735	cg35173658_BC21	NotSus	NotSus	Negative
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737	cg35194432_BC21	NotSus	NotSus	Negative
738	cg35194701_BC21	NotSus	NotSus	Negative
739	cg35195063_BC21	NotSus	NotSus	Negative
740	cg35209748_TC21	NotSus	NotSus	Positive
741	cg35230488_TC21	NotSus	NotSus	Positive
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744	cg35246008_TC21	NotSus	NotSus	Positive
745	cg35246032_TC21	NotSus	NotSus	Negative
746	cg35257567_TC21	NotSus	NotSus	Positive
747	cg35261998_BC11	NotSus	NotSus	Negative
748	cg35276333_BC11	NotSus	NotSus	Negative

749	cg35280486_BC21	NotSus	NotSus	Negative
750	cg35285007_BC21	NotSus	NotSus	Negative
751	cg35285354_BC21	NotSus	NotSus	Negative
752	cg35286691_TC21	NotSus	NotSus	Negative
753	cg35286804_TC21	NotSus	NotSus	Negative
754	cg35310593_TC21	NotSus	NotSus	Negative
755	cg35311276_BC11	NotSus	NotSus	Negative
756	cg35315548_TC21	NotSus	NotSus	Negative
757	cg35315625_BC21	NotSus	Sus_Pos	Negative
758	cg35316928_BC21	NotSus	NotSus	Positive
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760	cg35328490_BC11	NotSus	NotSus	Positive
761	cg35328916_BC21	NotSus	NotSus	Positive
762	cg35332123_TC21	NotSus	NotSus	Negative
763	cg35359621_TC21	NotSus	NotSus	Negative
764	cg35378861_TC21	NotSus	NotSus	Negative
765	cg35388898_TC21	NotSus	NotSus	Positive
766	cg35422887_BC21	NotSus	NotSus	Negative
767	cg35424859_BC21	NotSus	NotSus	Positive
768	cg35428161_TC21	NotSus	NotSus	Negative
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770	cg35481050_BC21	NotSus	NotSus	Negative
771	cg35493654_BC21	NotSus	NotSus	Negative
772	cg35510375_BC11	NotSus	NotSus	Positive
773	cg35512683_TC21	NotSus	NotSus	Negative
774	cg35514207_TC11	NotSus	NotSus	Positive
775	cg35519994_TC21	NotSus	NotSus	Negative
776	cg35560232_BC11	NotSus	Sus_Pos	Positive
777	cg35565822_TC21	NotSus	NotSus	Positive
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779	cg35594563_BC21	NotSus	NotSus	Positive
780	cg35595950_BC21	NotSus	NotSus	Negative
781	cg35596537_TC21	NotSus	NotSus	Negative
782	cg35603961_TC11	NotSus	NotSus	Positive
783	cg35604877_TC21	NotSus	NotSus	Positive
784	cg35605010_TC21	NotSus	NotSus	Negative
785	cg35608491_TC21	NotSus	NotSus	Negative
786	cg35608550_BC21	NotSus	NotSus	Negative
787	cg35610001_TC21	NotSus	NotSus	Positive
788	cg35612025_BC21	NotSus	NotSus	Negative
789	cg35612855_BC21	NotSus	NotSus	Positive
790	cg35615454_TC21	NotSus	NotSus	Negative
791	cg35616802_TC21	NotSus	NotSus	Positive

792	cg35617601_TC21	NotSus	NotSus	Positive
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794	cg35629232_BC21	NotSus	NotSus	Negative
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796	cg35671415_BC21	NotSus	NotSus	Positive
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798	cg35681003_TC11	NotSus	NotSus	Positive
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800	cg35694848_BC21	NotSus	NotSus	Negative
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808	cg35798040_TC21	NotSus	NotSus	Negative
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812	cg35841110_TC21	NotSus	NotSus	Positive
813	cg35851428_BC11	NotSus	NotSus	Negative
814	cg35851619_BC21	NotSus	NotSus	Negative
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816	cg35869399_BC21	NotSus	NotSus	Negative
817	cg35887175_BC21	NotSus	NotSus	Negative
818	cg35930267_BC21	NotSus	NotSus	Positive
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823	cg35986763_BC21	NotSus	NotSus	Negative
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825	cg36003090_TC21	NotSus	NotSus	Positive
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827	cg36017423_TC21	NotSus	NotSus	Positive
828	cg36018297_BC21	NotSus	NotSus	Negative
829	cg36032247_TC11	NotSus	NotSus	Positive
830	cg36065096_TC21	NotSus	NotSus	Negative
831	cg36069780_BC11	NotSus	NotSus	Positive
832	cg36072497_TC21	NotSus	NotSus	Negative
833	cg36076583_TC21	NotSus	NotSus	Positive
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835	cg36076989_BC21	NotSus	NotSus	Negative
836	cg36080076_TC21	NotSus	NotSus	Negative
837	cg36085621_BC21	NotSus	NotSus	Negative
838	cg36086967_TC21	NotSus	NotSus	Negative
839	cg36096057_BC21	NotSus	NotSus	Positive
840	cg36106543_TC11	NotSus	Sus_Pos	Negative
841	cg36108368_BC11	NotSus	NotSus	Positive
842	cg36109713_TC21	NotSus	NotSus	Negative
843	cg36109935_BC21	NotSus	NotSus	Negative
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846	cg36119019_BC21	Sus_Neg	NotSus	Negative
847	cg36132866_BC21	NotSus	NotSus	Positive
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850	cg36142165_TC21	NotSus	NotSus	Positive
851	cg36144507_BC21	NotSus	NotSus	Positive
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855	cg36188473_BC21	NotSus	NotSus	Positive
856	cg36198307_TC21	NotSus	NotSus	Positive
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858	cg36224649_TC21	Sus_Pos	NotSus	Negative
859	cg36259386_BC21	NotSus	NotSus	Positive
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861	cg36305204_BC21	NotSus	NotSus	Negative
862	cg36323957_TC21	NotSus	NotSus	Negative
863	cg36340328_BC21	NotSus	NotSus	Positive
864	cg36348999_TC21	Sus_Neg	NotSus	Negative
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866	cg36365131_BC11	NotSus	NotSus	Negative
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868	cg36370179_TC21	NotSus	NotSus	Negative
869	cg36372101_TC21	NotSus	NotSus	Positive
870	cg36384065_BC21	NotSus	NotSus	Positive
871	cg36392070_BC21	Sus_Pos	NotSus	Negative
872	cg36392250_TC21	NotSus	NotSus	Negative
873	cg36400896_BC21	NotSus	NotSus	Positive
874	cg36411257_TC11	NotSus	NotSus	Negative
875	cg36420692_BC11	NotSus	NotSus	Positive
876	cg36426137_BC21	NotSus	NotSus	Negative
877	cg36432732_BC21	NotSus	NotSus	Negative

878	cg36442350_BC21	NotSus	NotSus	Negative
879	cg36457636_BC21	NotSus	NotSus	Negative
880	cg36475046_BC21	NotSus	NotSus	Negative
881	cg36481047_TC21	NotSus	NotSus	Positive
882	cg36481461_TC21	NotSus	NotSus	Negative
883	cg36513925_BC21	NotSus	NotSus	Negative
884	cg36514792_BC21	NotSus	NotSus	Negative
885	cg36567175_TC21	NotSus	NotSus	Positive
886	cg36574956_BC21	NotSus	NotSus	Negative
887	cg36661192_BC21	NotSus	NotSus	Negative
888	cg36661453_BC21	NotSus	NotSus	Positive
889	cg36674782_TC21	NotSus	NotSus	Negative
890	cg36799616_TC11	NotSus	NotSus	Negative
891	cg36804601_BC11	NotSus	NotSus	Positive
892	cg36806517_BO21	NotSus	NotSus	Positive
893	cg36808547_TC21	NotSus	Sus_Pos	Negative
894	cg36819927_TC21	Sus_Pos	NotSus	Negative
895	cg36821105_TC21	NotSus	NotSus	Positive
896	cg36834574_BC21	NotSus	NotSus	Positive
897	cg36845321_TC21	NotSus	NotSus	Positive
898	cg36847030_BC21	NotSus	NotSus	Positive
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900	cg36867485_TC21	NotSus	NotSus	Positive
901	cg36873165_BC21	NotSus	NotSus	Negative
902	cg36901949_TC21	NotSus	NotSus	Positive
903	cg36921867_BC21	NotSus	Sus_Pos	Negative
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920	cg37138909_BC21	NotSus	NotSus	Positive

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923	cg37185863_TC11	NotSus	NotSus	Positive
924	cg37186236_BC21	NotSus	NotSus	Negative
925	cg37190273_TC21	NotSus	NotSus	Negative
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936	cg37367507_TC21	NotSus	NotSus	Positive
937	cg37371488_TC21	NotSus	NotSus	Positive
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939	cg37394196_TC21	NotSus	NotSus	Positive
940	cg37414444_TC21	NotSus	NotSus	Positive
941	cg37424135_TC21	NotSus	NotSus	Positive
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943	cg37456396_BC21	NotSus	NotSus	Negative
944	cg37458375_TC21	NotSus	NotSus	Positive
945	cg37477654_BC21	NotSus	NotSus	Negative
946	cg37478056_BC21	NotSus	NotSus	Negative
947	cg37478868_TC21	NotSus	NotSus	Negative
948	cg37480537_BC21	NotSus	NotSus	Negative
949	cg37486021_BC21	NotSus	NotSus	Negative
950	cg37488834_BC21	NotSus	NotSus	Positive
951	cg37499943_BC21	NotSus	NotSus	Negative
952	cg37500981_TC21	NotSus	NotSus	Positive
953	cg37501022_TC21	NotSus	NotSus	Negative
954	cg37506537_TC21	NotSus	NotSus	Negative
955	cg37509828_TC21	NotSus	NotSus	Positive
956	cg37512325_BC21	NotSus	NotSus	Negative
957	cg37512978_TC21	NotSus	NotSus	Negative
958	cg37536817_BC21	NotSus	NotSus	Negative
959	cg37597641_BC21	NotSus	NotSus	Negative
960	cg37602733_BC21	NotSus	NotSus	Negative
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962	cg37618561_TC21	NotSus	NotSus	Negative
963	cg37619889_BC21	NotSus	NotSus	Negative

964	cg37647583_TC11	NotSus	NotSus	Positive
965	cg37650124_BC21	NotSus	NotSus	Negative
966	cg37655487_BC21	NotSus	NotSus	Positive
967	cg37674216_TC21	NotSus	NotSus	Negative
968	cg37684798_BC21	NotSus	NotSus	Positive
969	cg37721852_BC21	NotSus	NotSus	Positive
970	cg37723305_TC21	NotSus	NotSus	Positive
971	cg37728003_TC11	NotSus	NotSus	Negative
972	cg37737981_TC11	NotSus	NotSus	Positive
973	cg37739279_TC21	NotSus	NotSus	Positive
974	cg37756326_TC21	NotSus	NotSus	Negative
975	cg37765824_TC21	NotSus	NotSus	Negative
976	cg37769650_BC21	NotSus	NotSus	Positive
977	cg37774713_BC11	NotSus	NotSus	Positive
978	cg37775454_BC21	NotSus	NotSus	Negative
979	cg37787354_BC21	NotSus	NotSus	Positive
980	cg37789469_BC21	NotSus	NotSus	Positive
981	cg37828426_TC21	NotSus	NotSus	Negative
982	cg37847180_BC21	NotSus	NotSus	Negative
983	cg37854631_TC21	NotSus	Sus_Neg	Positive
984	cg37867216_TC11	NotSus	Sus_Neg	Positive
985	cg37887327_TC11	Sus_Pos	NotSus	Positive
986	cg37890200_TC21	NotSus	NotSus	Negative
987	cg37913600_BC21	NotSus	NotSus	Negative
988	cg37952230_BC21	NotSus	NotSus	Negative
989	cg37952631_BC21	Sus_Pos	NotSus	Negative
990	cg37959334_BC21	NotSus	NotSus	Negative
991	cg37962583_TC21	NotSus	NotSus	Positive
992	cg37962641_BC21	NotSus	NotSus	Negative
993	cg37962851_TC21	NotSus	NotSus	Negative
994	cg37972787_TC11	NotSus	NotSus	Negative
995	cg37973969_BC21	NotSus	NotSus	Negative
996	cg37978038_TC11	NotSus	NotSus	Positive
997	cg37978647_BC21	NotSus	NotSus	Negative
998	cg37978712_BC21	NotSus	NotSus	Positive
999	cg37980506_TC11	NotSus	NotSus	Negative
1000	cg38005017_TC21	NotSus	NotSus	Negative
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1002	cg38008146_BC21	NotSus	NotSus	Positive
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1006	cg38024746_BC21	NotSus	NotSus	Negative

1007	cg38035143_BC21	NotSus	NotSus	Negative
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1009	cg38053237_BC21	NotSus	NotSus	Negative
1010	cg38075939_BC21	NotSus	NotSus	Positive
1011	cg38101667_BC21	NotSus	NotSus	Positive
1012	cg38136889_BC21	NotSus	NotSus	Negative
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1015	cg38169604_TC21	NotSus	NotSus	Negative
1016	cg38170252_BC21	NotSus	NotSus	Negative
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1021	cg38180518_TC21	NotSus	NotSus	Negative
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1028	cg38199600_TC21	NotSus	NotSus	Negative
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1095	cg38930355_TC21	NotSus	NotSus	Negative
1096	cg38933298_BC21	NotSus	NotSus	Negative
1097	cg38939281_BC21	NotSus	NotSus	Negative
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1168	cg39542383_BC21	NotSus	Sus_Pos	Negative
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1181	cg39685374_TC21	NotSus	NotSus	Negative
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1222	cg40147111_TC21	NotSus	NotSus	Negative
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1267	cg40971449_BC21	NotSus	NotSus	Negative
1268	cg40990121_BC21	NotSus	NotSus	Negative
1269	cg41013201_BC21	NotSus	NotSus	Negative
1270	cg41082603_TC21	NotSus	NotSus	Negative
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1353	cg41684456_BC21	NotSus	NotSus	Negative
1354	cg41685144_TC21	NotSus	NotSus	Negative
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1373	cg41877801_BC21	NotSus	NotSus	Positive
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1375	cg41937553_BC21	NotSus	NotSus	Negative
1376	cg41976972_TC21	NotSus	NotSus	Negative
1377	cg41984989_BC21	NotSus	NotSus	Negative
1378	cg41990676_TC21	NotSus	NotSus	Negative
1379	cg41998043_TC21	NotSus	NotSus	Positive
1380	cg42011179_BC21	NotSus	NotSus	Positive
1381	cg42022941_TC21	NotSus	NotSus	Negative
1382	cg42022942_TC21	NotSus	NotSus	Negative
1383	cg42031352_BC21	NotSus	NotSus	Positive
1384	cg42035380_BC21	NotSus	NotSus	Negative
1385	cg42035687_BC21	NotSus	NotSus	Negative
1386	cg42064655_BC21	NotSus	NotSus	Positive
1387	cg42098141_BC21	NotSus	NotSus	Positive
1388	cg42103646_TC21	NotSus	NotSus	Negative
1389	cg42135118_TC21	Sus_Pos	NotSus	Positive
1390	cg42150753_BC21	NotSus	NotSus	Positive
1391	cg42152330_TC21	NotSus	NotSus	Negative
1392	cg42152359_TC21	NotSus	NotSus	Negative
1393	cg42152730_BC21	NotSus	NotSus	Negative

1394	cg42158467_TC21	NotSus	NotSus	Positive
1395	cg42158860_TC21	NotSus	NotSus	Positive
1396	cg42160906_BC21	NotSus	NotSus	Negative
1397	cg42178583_BC21	NotSus	NotSus	Negative
1398	cg42197205_TC21	NotSus	NotSus	Positive
1399	cg42213351_BC11	NotSus	NotSus	Negative
1400	cg42215810_TC21	NotSus	NotSus	Negative
1401	cg42227404_BC21	NotSus	NotSus	Positive
1402	cg42239748_BC11	NotSus	NotSus	Positive
1403	cg42254477_TC21	Sus_Pos	NotSus	Positive
1404	cg42284666_TC21	NotSus	Sus_Pos	Positive
1405	cg42292851_BC21	NotSus	NotSus	Negative
1406	cg42296047_TC21	NotSus	NotSus	Positive
1407	cg42314450_BC21	NotSus	NotSus	Negative
1408	cg42324314_TC21	NotSus	NotSus	Positive
1409	cg42405091_TC21	NotSus	NotSus	Positive
1410	cg42420225_TC21	NotSus	NotSus	Negative
1411	cg42429394_BC21	NotSus	NotSus	Positive
1412	cg42453614_BC21	NotSus	NotSus	Negative
1413	cg42466823_TC21	NotSus	NotSus	Negative
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1416	cg42502168_TC21	NotSus	NotSus	Positive
1417	cg42509769_TC11	NotSus	NotSus	Positive
1418	cg42532958_TC11	NotSus	NotSus	Positive
1419	cg42549054_TC21	NotSus	NotSus	Positive
1420	cg42553530_BC11	NotSus	NotSus	Positive
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1422	cg42559481_BC21	NotSus	NotSus	Positive
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1424	cg42588019_TC11	NotSus	Sus_Pos	Negative
1425	cg42594562_BC21	NotSus	NotSus	Negative
1426	cg42594652_BC21	NotSus	NotSus	Negative
1427	cg42595299_BC11	NotSus	Sus_Pos	Positive
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1441	cg42660819_BC21	NotSus	NotSus	Negative
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1443	cg42677339_TC21	NotSus	NotSus	Negative
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1445	cg42682422_TC21	NotSus	NotSus	Negative
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1447	cg42699950_BC21	NotSus	NotSus	Negative
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1453	cg42761771_TC21	NotSus	NotSus	Negative
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1464	cg42837996_BC21	NotSus	NotSus	Negative
1465	cg42856685_BC21	NotSus	NotSus	Negative
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1476	cg42904651_TC21	NotSus	NotSus	Positive
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1480	cg42914557_TC21	NotSus	NotSus	Negative
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1488	cg42978586_TC21	NotSus	NotSus	Positive
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1490	cg42984449_BC21	NotSus	NotSus	Positive
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1494	cg42998061_TC11	NotSus	NotSus	Negative
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1497	cg43035946_TC21	NotSus	NotSus	Negative
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1507	cg43103321_TC21	NotSus	NotSus	Negative
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1523	cg43372777_BC21	NotSus	NotSus	Positive
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1525	cg43392950_TC21	NotSus	NotSus	Negative
1526	cg43408085_TC21	Sus_Neg	NotSus	Positive
1527	cg43410524_BC21	NotSus	NotSus	Positive
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1530	cg43426562_TC21	NotSus	NotSus	Positive
1531	cg43436966_TC21	NotSus	NotSus	Negative
1532	cg43439304_TC21	NotSus	Sus_Pos	Negative
1533	cg43442245_BC21	NotSus	NotSus	Negative
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1539	cg43480561_BC11	NotSus	NotSus	Negative
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1562	cg43750523_BC21	NotSus	NotSus	Positive
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1611	cg44156148_BC21	NotSus	NotSus	Negative
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1613	cg44175243_TC21	NotSus	NotSus	Positive
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1619	cg44200207_BO21	NotSus	NotSus	Negative
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1654	cg44373098_BC21	Sus_Pos	NotSus	Negative
1655	cg44374169_BC21	NotSus	NotSus	Negative
1656	cg44375209_TC21	NotSus	NotSus	Negative
1657	cg44377558_TC21	NotSus	Sus_Pos	Positive
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1666	cg44400576_TC21	NotSus	NotSus	Negative
1667	cg44401030_TC21	NotSus	NotSus	Negative
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1671	cg44498066_BC21	Sus_Pos	NotSus	Negative
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1676	cg44515620_TC21	NotSus	NotSus	Positive
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1730	cg45088673_BC21	NotSus	NotSus	Positive
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1736	cg45143940_TC21	Sus_Pos	Sus_Neg	Negative
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1741	cg45167707_BC21	NotSus	NotSus	Negative
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1746	cg45227954_BC21	NotSus	NotSus	Positive
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1766	cg45308246_BC21	NotSus	NotSus	Negative
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1775	cg45372435_TC21	NotSus	NotSus	Negative
1776	cg45376827_TC21	NotSus	NotSus	Negative
1777	cg45380489_BC21	NotSus	NotSus	Positive
1778	cg45385998_TC21	NotSus	NotSus	Positive
1779	cg45388134_BC11	NotSus	NotSus	Positive
1780	cg45389607_TC21	NotSus	NotSus	Positive

1781	cg45401758_BC11	NotSus	NotSus	Negative
1782	cg45405574_BC11	NotSus	NotSus	Negative
1783	cg45416390_BC21	NotSus	Sus_Neg	Negative
1784	cg45419253_BC21	NotSus	NotSus	Positive
1785	cg45443760_TC21	NotSus	NotSus	Negative
1786	cg45488756_TC21	NotSus	NotSus	Positive
1787	cg45489634_TC21	NotSus	NotSus	Negative
1788	cg45512119_BC21	NotSus	NotSus	Positive
1789	cg45544868_TC21	NotSus	NotSus	Positive
1790	cg45547572_TC21	NotSus	NotSus	Negative
1791	cg45555665_TC21	NotSus	NotSus	Negative
1792	cg45576078_TC21	NotSus	NotSus	Negative
1793	cg45620738_BC21	NotSus	NotSus	Positive
1794	cg45636636_TC21	NotSus	NotSus	Negative
1795	cg45640214_TC21	NotSus	NotSus	Negative
1796	cg45640219_BC21	NotSus	NotSus	Positive
1797	cg45662637_BC21	NotSus	NotSus	Negative
1798	cg45681590_BC21	NotSus	NotSus	Negative
1799	cg45689574_TC21	NotSus	NotSus	Positive
1800	cg45730760_BC21	NotSus	NotSus	Negative
1801	cg45780933_BC11	Sus_Pos	NotSus	Negative
1802	cg45798326_BC11	NotSus	NotSus	Negative
1803	cg45808706_TC21	NotSus	NotSus	Negative
1804	cg45812324_BC21	NotSus	NotSus	Negative
1805	cg45816832_BC21	NotSus	NotSus	Negative
1806	cg45816879_BC21	NotSus	Sus_Pos	Negative
1807	cg45817176_BC21	NotSus	NotSus	Positive
1808	cg45817628_TC21	NotSus	NotSus	Negative
1809	cg45827179_TC21	NotSus	Sus_Pos	Positive
1810	cg45831947_TC21	NotSus	NotSus	Positive
1811	cg45834482_TC21	NotSus	NotSus	Negative
1812	cg45845848_TC21	NotSus	NotSus	Negative
1813	cg45849944_TC21	NotSus	NotSus	Negative
1814	cg45869230_BC21	NotSus	NotSus	Negative
1815	cg45909708_TC21	NotSus	NotSus	Negative
1816	cg45916815_BC21	NotSus	NotSus	Negative
1817	cg45917216_BC21	NotSus	NotSus	Negative
1818	cg45918031_BO21	NotSus	NotSus	Negative
1819	cg45918775_BC11	NotSus	NotSus	Positive
1820	cg45935936_TC21	NotSus	NotSus	Negative
1821	cg45949211_BC21	NotSus	NotSus	Negative
1822	cg45955306_BC11	NotSus	NotSus	Positive
1823	cg45959625_BC21	NotSus	NotSus	Negative

1824	cg45991098_TC21	Sus_Neg	NotSus	Negative
1825	cg45997577_BC21	NotSus	NotSus	Negative
1826	cg45998910_BC21	NotSus	NotSus	Negative
1827	cg45999945_TC21	NotSus	NotSus	Negative
1828	cg46001334_BC11	NotSus	Sus_Pos	Positive
1829	cg46022002_TC11	NotSus	NotSus	Negative
1830	cg46027375_TC21	NotSus	NotSus	Negative
1831	cg46027381_BC21	NotSus	NotSus	Negative
1832	cg46029969_TC21	NotSus	NotSus	Negative
1833	cg46052640_BC21	NotSus	NotSus	Positive
1834	cg46075158_TC21	NotSus	NotSus	Positive
1835	cg46098900_TC21	NotSus	NotSus	Positive
1836	cg46108872_TC21	NotSus	NotSus	Negative
1837	cg46112241_BC21	NotSus	NotSus	Positive
1838	cg46115737_BC21	NotSus	NotSus	Negative
1839	cg46119394_TC21	NotSus	NotSus	Positive
1840	cg46129162_TC21	NotSus	NotSus	Negative
1841	cg46137019_BC21	NotSus	NotSus	Positive
1842	cg46137584_TC21	NotSus	NotSus	Negative
1843	cg46152696_TC21	NotSus	NotSus	Positive
1844	cg46162046_TC11	NotSus	NotSus	Positive
1845	cg46163356_BC21	NotSus	NotSus	Negative
1846	cg46164435_TC21	NotSus	NotSus	Negative
1847	cg46164695_BC21	NotSus	NotSus	Negative
1848	cg46201867_BC21	NotSus	NotSus	Negative
1849	cg46227344_BC21	NotSus	NotSus	Negative
1850	cg46229885_BC21	NotSus	NotSus	Negative
1851	cg46233814_BC11	NotSus	Sus_Neg	Negative
1852	cg46235285_BC11	NotSus	NotSus	Positive
1853	cg46235986_TC21	NotSus	NotSus	Negative
1854	cg46236842_BC21	NotSus	NotSus	Positive
1855	cg46248744_BC11	NotSus	NotSus	Negative
1856	cg46252386_BC21	NotSus	NotSus	Negative
1857	cg46260680_BC21	NotSus	NotSus	Negative
1858	cg46266235_BC11	NotSus	NotSus	Positive
1859	cg46266644_BC21	NotSus	NotSus	Positive
1860	cg46268558_BC21	NotSus	NotSus	Negative
1861	cg46270332_TC21	NotSus	NotSus	Positive
1862	cg46273291_BC21	NotSus	NotSus	Positive
1863	cg46282669_BC21	NotSus	NotSus	Negative
1864	cg46285667_BC21	NotSus	NotSus	Positive
1865	cg46285668_BC21	NotSus	NotSus	Positive
1866	cg46287573_TC21	NotSus	NotSus	Negative

1867	cg46291865_TC21	NotSus	NotSus	Negative
1868	cg46305614_TC21	NotSus	NotSus	Negative
1869	cg46307846_BC21	NotSus	NotSus	Positive
1870	cg46309876_BC21	NotSus	NotSus	Negative
1871	cg46312865_BC21	NotSus	NotSus	Positive
1872	cg46320249_BC21	NotSus	NotSus	Negative
1873	cg46323765_BC21	NotSus	NotSus	Negative
1874	cg46331918_TC21	NotSus	NotSus	Negative
1875	cg46355064_TC21	NotSus	NotSus	Positive
1876	cg46362144_TC21	NotSus	NotSus	Negative
1877	cg46368672_BC21	NotSus	NotSus	Negative
1878	cg46381818_TC21	NotSus	NotSus	Positive
1879	cg46409224_BC21	NotSus	NotSus	Negative
1880	cg46450195_BC21	NotSus	NotSus	Negative
1881	cg46481461_BC11	NotSus	NotSus	Negative
1882	cg46485737_BC21	NotSus	NotSus	Positive
1883	cg46499564_TC21	NotSus	NotSus	Negative
1884	cg46500617_BC11	NotSus	NotSus	Negative
1885	cg46501165_TC21	NotSus	NotSus	Negative
1886	cg46503825_TC21	NotSus	NotSus	Negative
1887	cg46534799_TC21	NotSus	NotSus	Positive
1888	cg46537790_TC21	NotSus	NotSus	Negative
1889	cg46541065_BC11	Sus_Neg	NotSus	Negative
1890	cg46563438_TC21	NotSus	NotSus	Positive
1891	cg46576498_TC11	NotSus	NotSus	Positive
1892	cg46584028_BC21	NotSus	NotSus	Positive
1893	cg46594520_TC21	NotSus	NotSus	Negative
1894	cg46599387_TC21	NotSus	NotSus	Positive
1895	cg46607941_TC21	NotSus	NotSus	Negative
1896	cg46626335_BC21	NotSus	NotSus	Negative
1897	cg46626965_BC21	NotSus	NotSus	Positive
1898	cg46635136_BC21	NotSus	NotSus	Negative
1899	cg46653156_BC21	NotSus	NotSus	Negative
1900	cg46654012_TC21	NotSus	NotSus	Negative
1901	cg46656746_TC21	NotSus	NotSus	Negative
1902	cg46663845_BC21	NotSus	NotSus	Negative
1903	cg46666357_TC21	NotSus	NotSus	Negative
1904	cg46667165_TC21	NotSus	Sus_Pos	Negative
1905	cg46672600_TC11	NotSus	NotSus	Positive
1906	cg46679529_BC21	NotSus	NotSus	Negative
1907	cg46684036_BC21	NotSus	NotSus	Negative
1908	cg46685310_TC21	NotSus	NotSus	Negative
1909	cg46688835_BC21	NotSus	Sus_Neg	Positive

1910	cg46692045_TC11	NotSus	NotSus	Negative
1911	cg46693459_TC21	NotSus	NotSus	Positive
1912	cg46695585_BC21	NotSus	NotSus	Negative
1913	cg46698585_BC11	NotSus	NotSus	Negative
1914	cg46719627_BC21	NotSus	NotSus	Negative
1915	cg46724079_BC21	NotSus	NotSus	Negative
1916	cg46730689_TC11	NotSus	NotSus	Negative
1917	cg46737315_TC21	NotSus	NotSus	Positive
1918	cg46740229_TC21	NotSus	NotSus	Negative
1919	cg46784966_TC21	NotSus	NotSus	Positive
1920	cg46788036_TC21	NotSus	NotSus	Positive
1921	cg46788925_TC21	NotSus	NotSus	Negative
1922	cg46792569_TC21	NotSus	NotSus	Negative
1923	cg46792912_BC21	NotSus	NotSus	Negative
1924	cg46792928_TC21	NotSus	NotSus	Negative
1925	cg46792976_TC21	NotSus	NotSus	Negative
1926	cg46794930_BC21	NotSus	NotSus	Negative
1927	cg46799154_TC21	NotSus	NotSus	Positive
1928	cg46804073_BC21	NotSus	NotSus	Negative
1929	cg46807412_TC21	NotSus	NotSus	Negative
1930	cg46833753_BC21	NotSus	NotSus	Negative
1931	cg46845855_BC21	NotSus	NotSus	Negative
1932	cg46847690_BC21	NotSus	NotSus	Negative
1933	cg46854560_BC11	NotSus	NotSus	Negative
1934	cg46858735_TC11	NotSus	NotSus	Positive
1935	cg46863524_TC21	NotSus	NotSus	Negative
1936	cg46864468_TC21	NotSus	Sus_Pos	Positive
1937	cg46864555_TC11	Sus_Pos	NotSus	Negative
1938	cg46864555_TO21	NotSus	NotSus	Negative
1939	cg46866711_TC21	NotSus	NotSus	Negative
1940	cg46870805_BC11	NotSus	NotSus	Positive
1941	cg46871447_BC21	NotSus	NotSus	Negative
1942	cg46872939_BC21	NotSus	Sus_Neg	Negative
1943	cg46875523_BC21	NotSus	NotSus	Negative
1944	cg46877033_BC21	NotSus	NotSus	Negative
1945	cg46882383_TC21	NotSus	NotSus	Negative
1946	cg46895376_TC21	NotSus	NotSus	Negative
1947	cg46899035_BC21	NotSus	NotSus	Negative
1948	cg46916919_BC21	NotSus	NotSus	Positive
1949	cg46928764_TC21	NotSus	NotSus	Negative
1950	cg46947570_TC21	NotSus	NotSus	Negative
1951	cg46966793_BC11	NotSus	NotSus	Positive
1952	cg46976224_BC21	NotSus	NotSus	Positive

1953	cg46986145_BC21	NotSus	NotSus	Positive
1954	cg47015608_BC21	NotSus	NotSus	Negative
1955	cg47043249_TC21	NotSus	NotSus	Negative
1956	cg47049844_TC21	NotSus	Sus_Pos	Negative
1957	cg47049923_TC21	NotSus	NotSus	Positive
1958	cg47051131_TC11	NotSus	NotSus	Negative
1959	cg47071544_TC21	NotSus	NotSus	Positive
1960	cg47075869_TC21	NotSus	NotSus	Negative
1961	cg47117143_BC21	NotSus	NotSus	Positive
1962	cg47118214_TC21	NotSus	NotSus	Positive
1963	cg47124146_BC21	NotSus	NotSus	Negative
1964	cg47135628_TC21	NotSus	NotSus	Negative
1965	cg47149849_BC11	NotSus	NotSus	Positive
1966	cg47150161_BC21	NotSus	NotSus	Positive
1967	cg47150162_TC11	NotSus	NotSus	Positive
1968	cg47150247_TC21	NotSus	NotSus	Negative
1969	cg47152599_TC11	NotSus	NotSus	Negative
1970	cg47171647_BC21	NotSus	NotSus	Positive
1971	cg47184390_TC21	NotSus	NotSus	Positive
1972	cg47192201_BC21	NotSus	NotSus	Negative
1973	cg47192207_BC21	NotSus	NotSus	Negative
1974	cg47206579_TC21	NotSus	NotSus	Positive
1975	cg47212360_TC11	NotSus	NotSus	Negative
1976	cg47213665_BC21	NotSus	NotSus	Negative
1977	cg47224959_TC21	NotSus	NotSus	Negative
1978	cg47226756_TC21	NotSus	NotSus	Negative
1979	cg47227331_BC21	NotSus	NotSus	Negative
1980	cg47228397_TC21	NotSus	NotSus	Negative
1981	cg47228418_TC11	NotSus	NotSus	Negative
1982	cg47230731_TC21	NotSus	NotSus	Negative
1983	cg47230802_BC21	NotSus	NotSus	Negative
1984	cg47234073_BC21	NotSus	NotSus	Positive
1985	cg47236151_TC21	NotSus	NotSus	Negative
1986	cg47240375_BC21	NotSus	NotSus	Negative
1987	cg47247039_TC21	NotSus	NotSus	Negative
1988	cg47264576_BC21	NotSus	NotSus	Negative
1989	cg47270249_BC21	NotSus	NotSus	Positive
1990	cg47278954_TC21	NotSus	NotSus	Positive
1991	cg47292197_BC11	NotSus	Sus_Pos	Positive
1992	cg47305560_BC21	NotSus	NotSus	Negative
1993	cg47342737_BC21	NotSus	NotSus	Negative
1994	cg47344801_BC21	NotSus	NotSus	Negative
1995	cg47350341_TC21	NotSus	NotSus	Positive

1996	cg47350596_BC21	Sus_Neg	NotSus	Positive
1997	cg47367593_TC11	NotSus	NotSus	Positive
1998	cg47384463_TC11	NotSus	Sus_Neg	Positive
1999	cg47385900_TC11	NotSus	NotSus	Negative
2000	cg47391509_BC21	NotSus	NotSus	Negative
T-test longitudinal analysis: CpGs identified as significently altered by prenatal CS in male X chromosome probes at 16 weeks, and persistently altered at birth				
	CpG	Birth	8 weeks	16 weeks
1	cg47433385_BC21	Sus_Pos	NotSus	Negative
2	cg47453080_BC21	NotSus	NotSus	Negative
3	cg47454751_TC21	NotSus	NotSus	Negative
4	cg47455400_TC21	NotSus	NotSus	Negative
5	cg47457632_BC21	NotSus	NotSus	Negative
6	cg47459954_TC21	NotSus	NotSus	Negative
7	cg47472698_BC21	NotSus	NotSus	Negative
8	cg47497821_TC21	NotSus	NotSus	Negative
9	cg47498643_TC21	NotSus	NotSus	Negative
10	cg47498648_TC21	NotSus	NotSus	Negative
11	cg47508392_TC21	NotSus	NotSus	Negative
12	cg47513951_TC21	NotSus	NotSus	Negative
13	cg47556869_BC21	NotSus	NotSus	Negative
14	cg47561766_TC21	NotSus	NotSus	Positive
15	cg47569060_TC21	NotSus	NotSus	Negative
16	cg47620538_BC21	Sus_Neg	NotSus	Negative
17	cg47641246_TC21	NotSus	NotSus	Negative
18	cg47652508_BC21	NotSus	NotSus	Negative
19	cg47656898_BC11	NotSus	NotSus	Positive
20	cg47659485_TC11	NotSus	NotSus	Positive
21	cg47671780_TC21	NotSus	NotSus	Negative
22	cg47680297_TC21	NotSus	NotSus	Positive
23	cg47685506_TC21	Sus_Pos	NotSus	Negative
24	cg47712606_TC21	NotSus	NotSus	Positive
25	cg47740643_BC21	NotSus	NotSus	Negative
26	cg47759500_TC21	NotSus	NotSus	Positive
27	cg47821652_TC21	NotSus	NotSus	Negative
28	cg47824263_TC11	NotSus	NotSus	Negative
29	cg47828487_BC21	NotSus	NotSus	Negative
30	cg47844846_TC21	NotSus	Sus_Neg	Negative
31	cg47852098_TC21	NotSus	NotSus	Negative
32	cg47859934_TC21	Sus_Pos	NotSus	Negative
33	cg47862607_TC21	NotSus	NotSus	Positive
34	cg47871172_TC11	NotSus	NotSus	Positive
35	cg47873016_BC21	NotSus	Sus_Pos	Negative

36	cg47873099_BC21	NotSus	NotSus	Negative
37	cg47876443_BC21	NotSus	NotSus	Negative
38	cg47876735_TC21	NotSus	NotSus	Positive
39	cg47880212_TC21	NotSus	NotSus	Negative
40	cg47880238_TC11	Sus_Pos	NotSus	Positive
41	cg47882199_BC21	NotSus	NotSus	Negative
42	cg47886653_TC21	NotSus	NotSus	Positive
43	cg47891153_BC11	NotSus	NotSus	Positive
44	cg47891591_TC11	NotSus	NotSus	Positive
45	cg47900704_TC21	NotSus	NotSus	Negative
46	cg47913064_TC21	NotSus	Sus_Neg	Negative
47	cg47934556_BC21	NotSus	NotSus	Negative
48	cg47986459_TC21	NotSus	NotSus	Negative
49	cg47992187_TC21	NotSus	NotSus	Negative
50	cg48017590_TC21	NotSus	NotSus	Positive
51	cg48021187_BC21	NotSus	NotSus	Negative
52	cg48035493_BC21	NotSus	NotSus	Positive
53	cg48040375_BC21	NotSus	NotSus	Negative
54	cg48046212_BC21	NotSus	NotSus	Negative
55	cg48104040_BC21	NotSus	NotSus	Negative
56	cg48151464_BC21	NotSus	NotSus	Negative
57	cg48170592_TC21	NotSus	NotSus	Positive
58	cg48177924_TC21	NotSus	NotSus	Negative
59	cg48181118_TC21	NotSus	NotSus	Positive
60	cg48182479_TC21	NotSus	NotSus	Negative
61	cg48183114_TC21	NotSus	NotSus	Negative
62	cg48184225_BC21	NotSus	NotSus	Positive
63	cg48196835_BC21	NotSus	NotSus	Negative
64	cg48197038_TC21	NotSus	NotSus	Positive
65	cg48203988_BC21	NotSus	NotSus	Positive
66	cg48204492_TC21	NotSus	NotSus	Negative
T-test longitudinal analysis: CpGs identified as significently altered by prenatal CS in male Y chromosome probes at 16 weeks, and persistently altered at birth				
	CpG	Birth	8 weeks	16 weeks
1	cg48212271_TC11	NotSus	NotSus	Positive
2	cg48214012_BC21	NotSus	NotSus	Positive
3	cg48217471_BC21	NotSus	NotSus	Positive
4	cg48219462_TC21	NotSus	NotSus	Negative
5	cg48222264_TC21	NotSus	NotSus	Positive

DNAm differences were initially calculated by limma at each end timepoint (birth and 63 weeks in females and birth and 16 weeks in males), and significant CpGs were identified a $p < 1e\text{-}3$ and effect size > 0.05. Student t-test was used to determine whether CpGs which were significantly altered at birth or at the end timepoint (63 weeks for females and 16 weeks for

males) were persistently altered within the other individual timepoints. Sus_Pos = Sustained/persistent with positive effect size compared to controls, Sus_Neg = Sustained/persistent with negative effect size compared to controls, NotSus = Not sustained/persistent. ‘Positive’ and ‘Negative’ denote the direction of DNAm change compared to controls at each timepoint. Persistently altered CpGs were identified at a cutoff of $p < 0.05$.

Appendix 4. 31: CpGs which are persistently differentially methylated across the lifespan by prenatal CS exposure in female lungs, identified by limma

Autosomes								
	CpG name	P value	Effect size	Gene	Chromosome	Strand	Feature	CpG position
1	cg29007456_TC21	0.000662	-0.02547	Trhde	chr10	-	tss_body	1.15E+08
2	cg29067981_TC21	0.000281	0.036136	Grip1	chr10	+	tss_body	1.2E+08
3	cg29207068_BC21	0.000327	-0.02754	Pgam2	chr11	-	tss_body	5803518
4	cg29592104_TC21	0.000571	0.032548	M9MMK5	chr11	-	tss_body	58545377
5	cg29730013_TC21	0.00047	-0.03005	Gm33249	chr11	+	tss_body	71390401
6	cg29800793_BC21	0.000375	0.035396	Slc13a2os	chr11	+	tss_body	78404744
7	cg29804762_BC21	0.000118	0.026747					78789243
8	cg30060917_TC11	0.000133	0.051439	Hdac5	chr11	-	tss_body	1.02E+08
9	cg30218076_TC21	0.000199	0.030891	Llgl2	chr11	+	tss_body	1.16E+08
10	cg30317968_TC21	6.52E-05	-0.03251	Pomc	chr12	+	tss_200	3954889
11	cg30358000_TC21	9.06E-07	-0.02714					9338997
12	cg30849798_BC21	0.000688	0.0357	LOC108168012	chr12	+	tss_body	79881369
13	cg31176160_TC21	0.000936	0.030342	A0A075B5Q1	chr12	-	tss_1500	1.14E+08
14	cg31222385_TC11	0.000721	0.033536	Akr1c18	chr13	-	tss_body	4132805
15	cg31447323_BC21	0.000147	0.032687	Gm30918	chr13	+	tss_body	37541378
16	cg31503029_BC21	0.000443	0.027067	Gfod1	chr13	-	tss_body	43230435
17	cg31557541_BC21	2.88E-05	-0.03406	A330033J07Rik	chr13	-	tss_body	48227119
18	cg31679582_BC21	0.000352	-0.02612	Ntrk2	chr13	+	tss_body	58810141
19	cg32197807_BC21	0.000189	-0.02677	Synpr	chr14	+	tss_body	13358311
20	cg32344040_BC21	0.000177	0.034621	Dph3	chr14	-	tss_body	32081074
21	cg32418104_TC21	0.000761	0.041991	Ptger2	chr14	+	tss_200	44987984
22	cg32480517_BC21	0.000329	-0.03166	Rpgrip1	chr14	+	tss_body	52149786
23	cg32825210_BC21	0.000462	0.033266					98533755
24	cg32985255_BC21	0.000146	0.037144	Farp1	chr14	+	tss_body	1.21E+08
25	cg33072421_TC11	0.000248	0.04183		chr15	+	tss_body	10823650
26	cg33634839_BC21	0.000884	-0.02543	Celsr1	chr15	-	tss_body	85903905
27	cg33738827_TC21	4.49E-05	0.044493	Ano6	chr15	+	tss_body	95904361
28	cg33776661_TC21	0.000994	0.036632	Adcy6	chr15	-	tss_body	98606817

29	cg33835209_TC21	0.000782	0.037854	Gm4544	chr15	+	tss_body	1.03E+08
30	cg33854820_BC21	0.000343	0.025648	Crebbp	chr16	-	tss_body	4128321
31	cg34514212_BC21	7.61E-05	0.036796	1700029J03Rik	chr16	-	tss_body	93426155
32	cg34517576_BC21	5.5E-05	0.053921	Dopey2	chr16	+	tss_body	93716080
33	cg34804233_TC21	0.000338	0.032196	Mtch1	chr17	-	tss_body	29336223
34	cg34806353_BC21	0.000207	0.027278		chr17	-	tss_body	29476797
35	cg34886473_BC21	0.000722	0.048106	2310061I04Rik	chr17	-	tss_body	35896407
36	cg34890974_BC21	0.000254	-0.02979	chr17-36248872-36249182	chr17	*	NShore	36248596
37	cg35449240_TC21	4.09E-05	0.055581	Zfp521	chr18	-	tss_body	13740489
38	cg35582720_BC21	3.81E-05	0.040387	4933408B17Rik	chr18	-	tss_body	34597521
39	cg36378509_TC21	0.000244	0.028441	Cyp2c39	chr19	+	tss_200	39510787
40	cg36429123_BC21	5.87E-05	-0.03565	Bloc1s2	chr19	-	tss_200	44146594
41	cg36461815_BC21	0.000116	0.034934	Arl3	chr19	-	tss_body	46534050
42	cg36849232_TC21	0.000553	0.044424					40179230
43	cg37084256_BC21	0.000869	-0.02841	Mir1928	chr1	-	tss_200	74206796
44	cg37907117_TC21	0.00078	-0.0262					1.86E+08
45	cg37973883_BC21	0.000841	-0.02594	Rd3	chr1	+	tss_body	1.92E+08
46	cg38176514_TC11	2.98E-05	0.044843	Sardh	chr2	-	tss_body	27246738
47	cg38207174_TC11	0.000907	0.030616	Cercam	chr2	+	tss_body	29845714
48	cg38245840_TC11	0.000649	0.025505	Fam102a	chr2	+	tss_body	32559543
49	cg38274618_TC21	5.55E-05	0.043878					34982923
50	cg38487693_TC21	0.00099	-0.02554					67544796
51	cg38499186_TC21	0.000149	0.048637	Cers6	chr2	+	tss_body	69018018
52	cg38527566_BC21	0.000969	0.037657		chr2	+	tss_body	71762469
53	cg38688527_TC21	0.000767	-0.0376	Prdm11	chr2	-	tss_body	92983536
54	cg38781372_TC21	0.000396	0.028739	Mpped2	chr2	+	tss_body	1.07E+08
55	cg38871223_TC21	0.000104	0.026132	Mapkbp1	chr2	+	tss_body	1.2E+08
56	cg38939271_TC21	0.000303	0.043438	Bcl2l11	chr2	+	tss_body	1.28E+08
57	cg39332892_TC21	0.000245	0.028596					1.7E+08
58	cg39438802_BC21	0.000301	0.037776	Myt1	chr2	+	tss_body	1.82E+08
59	cg39469907_BC21	0.000465	0.04225	Mrps28	chr3	-	tss_body	8805768

60	cg39469910_BC21	3.85E-05	0.047673	Mrps28	chr3	-	tss_body	8805813
61	cg39956963_BC21	0.000843	0.040093	E9QAY5	chr3	-	tss_body	84629191
62	cg40002023_TC21	0.000131	-0.03193	chr3-89132363-89132635	chr3	*	Island	89132464
63	cg40009811_BC21	0.000823	-0.02741	Kcnn3	chr3	+	tss_body	89601047
64	cg40117414_TC21	0.00032	0.02953					1.02E+08
65	cg40139051_TC11	0.000734	0.048133					1.05E+08
66	cg41283005_TC21	0.000957	0.033692	Agbl4	chr4	+	tss_body	1.11E+08
67	cg41508250_TC21	0.000232	-0.02625	Fam46b	chr4	+	tss_1500	1.33E+08
68	cg41690314_TC21	8.27E-05	-0.04032		chr4	+	tss_body	1.49E+08
69	cg41737767_TC21	0.000615	-0.02585					1.52E+08
70	cg41774137_TC21	7.82E-06	0.03279	Arhgef16	chr4	-	tss_body	1.54E+08
71	cg41789054_BC21	0.000279	0.029651	Prkcz	chr4	-	tss_body	1.55E+08
72	cg41819996_BC21	0.00017	0.02864	Cdk14	chr5	-	tss_body	4934487
73	cg41837008_BC21	0.000666	-0.02595		chr5	-	tss_body	7923821
74	cg42320870_BC21	0.000722	0.031333	Exoc1	chr5	+	tss_body	76561481
75	cg42331716_BC21	0.000306	0.045514	Igfbp7	chr5	-	tss_body	77401074
76	cg43264257_TC21	1.42E-05	0.036298	Cep41	chr6	-	tss_1500	30711643
77	cg43754611_BC21	0.000171	-0.0373					98089493
78	cg43861383_TC21	0.000131	-0.02687	Atp2b2	chr6	-	tss_body	1.14E+08
79	cg44091397_TC21	0.000854	0.028102	Plcz1	chr6	-	tss_body	1.4E+08
80	cg44199548_TC21	0.000269	0.036697	Ccdc106	chr7	+	tss_body	5056064
81	cg44497828_TC21	6.06E-05	-0.03488	Klk1b8	chr7	+	tss_body	43953087
82	cg44516596_BC11	0.000736	0.047272	Cd37	chr7	-	tss_body	45234353
83	cg44543899_BC21	8.87E-05	0.055939	LOC102637012	chr7	-	tss_body	47074307
84	cg44760194_BC21	0.000648	0.027792	Abhd2	chr7	+	tss_body	79350344
85	cg44808188_BC21	0.000563	0.02905	Gm39043	chr7	+	tss_body	83835012
86	cg44932296_TC21	0.000449	0.033749	Art1	chr7	+	tss_body	1.02E+08
87	cg45516763_TC21	0.000245	-0.02948					27362049
88	cg45562131_BC21	0.000336	0.037	Mboat4	chr8	+	tss_body	34115161
89	cg45641235_BC21	9.92E-06	-0.03395	Gm30504	chr8	+	tss_200	45110432
90	cg45808368_BC21	0.000242	-0.03001	Sugp2	chr8	+	tss_body	70257675

91	cg45910272_BC21	0.000221	-0.03011	Mgat4d	chr8	+	tss_200	83348514
92	cg46118131_BC21	0.000595	0.031602	Tmed6	chr8	-	tss_body	1.07E+08
93	cg46272194_TC21	0.000681	0.027959	Gse1	chr8	+	tss_body	1.2E+08
94	cg46358182_TC21	0.000217	-0.02869					1.26E+08
95	cg46492375_TC21	8.97E-05	0.025712	Ilf3	chr9	+	tss_body	21399185
96	cg46914735_BC21	5.82E-06	-0.02915	Rora	chr9	+	tss_body	69110656
97	cg46942155_TC21	0.000629	0.02587	Tcf12	chr9	-	tss_body	71922839
98	cg47133779_TC21	0.000359	-0.03311		chr9	-	tss_body	98186914
X chromosome								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47418818_TC21	0.00098	-0.0256	Shroom4	chrX	+	tss_1500	6399818
2	cg47575004_TC21	0.000414	-0.0295		chrX	+	tss_body	40407821
3	cg47583043_BC21	0.000905	-0.02922		chrX	-	tss_200	42130770
4	cg47623302_TC21	0.000261	-0.02696	Olfr1324	chrX	-	tss_body	50426076
5	cg47626298_BC21	0.000233	-0.02552	Frmd7	chrX	-	tss_body	50901510
6	cg47628556_TC11	1.81E-05	0.034382	Mbnl3	chrX	-	tss_body	51195010
7	cg47694853_TC21	0.000713	-0.03234					64165579
8	cg47757743_BC21	0.000556	-0.02768					77009801
9	cg47771676_BC21	0.000485	-0.02703		chrX	-	tss_body	79903547
10	cg47833621_BC11	0.000927	0.03226	Klhl15	chrX	+	tss_1500	94235009
11	cg47836657_BC21	0.000211	0.034703	Q8BQF5	chrX	+	tss_body	94639434
12	cg47930268_BC21	0.000669	0.035199	Rps6ka6	chrX	-	tss_body	1.11E+08
13	cg47932053_TC21	0.00027	-0.02647					1.12E+08
14	cg47992884_TC11	3.71E-05	-0.03671					1.28E+08
15	cg48057161_TC21	0.00098	-0.02806	Tsc22d3	chrX	-	tss_body	1.41E+08
16	cg48063988_TC21	0.000603	0.03008		chrX	-	tss_body	1.42E+08
17	cg48128983_BC21	0.000957	0.045775					1.55E+08

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500

= 200-1500 bases upstream of transcriptional start site). Significance was determined at p < 1e-3 and effect size > 0.025.

Appendix 4. 32: CpGs which are persistently differentially methylated across the lifespan by postnatal CS exposure in female lungs, identified by limma

Autosomes								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28394563_TC21	0.00084543	0.02984688					42041540
2	cg29792281_TC21	0.00087688	-0.02542317	Myo18a	chr11	+	tss_body	77801585
3	cg29912664_BC21	0.00015179	-0.02819048	Gm525	chr11	+	tss_body	89074998
4	cg30931990_TC21	0.00093022	0.03310354	Ism2	chr12	-	tss_body	87286915
5	cg31619267_BC21	0.00094849	0.03738208					54154322
6	cg31792683_TC21	0.00011786	0.03574975					73242539
7	cg31917269_TC21	0.0005748	-0.03066704	Gm32089	chr13	-	tss_body	94294097
8	cg32282923_BC21	0.00051862	0.03835161	Zmiz1os1	chr14	-	tss_body	25379637
9	cg32493539_BC21	0.00030912	-0.04848251	A0A0G2JER2	chr14	+	tss_1500	54205109
10	cg32495844_TC21	0.00017908	0.0302586	Slc7a7	chr14	-	tss_body	54401393
11	cg32811809_BC21	0.00057643	-0.02730387					95791448
12	cg33066930_TC21	0.00092001	-0.02957584	Prlr	chr15	+	tss_body	10249460
13	cg33487989_BC21	0.00092739	0.02737188	Adgrb1	chr15	+	tss_body	74527787
14	cg33816819_BC21	0.00074511	0.02900336	Acvrl1	chr15	+	tss_body	101142649
15	cg34574775_TC21	4.0833E-06	-0.02709686		chr17	-	tss_body	4854520
16	cg34802999_TC21	0.00045493	0.02814615	Ppil1	chr17	-	tss_body	29257982
17	cg35246430_TC21	0.00096153	-0.02708637	Rmdn2	chr17	+	tss_body	79621560
18	cg35616485_BC21	0.00031736	-0.02603525	Gm37013	chr18	+	tss_body	37753887
19	cg35995116_BC11	0.0004543	0.0388207		chr18	+	tss_body	81083362
20	cg36242770_BC21	9.4641E-05	0.03679688	Apba1	chr19	+	tss_body	23941496
21	cg36560791_TC21	0.00055407	0.02847008	Afap1l2	chr19	-	tss_body	56923966
22	cg36560807_TC21	0.00062925	0.03563828	Afap1l2	chr19	-	tss_body	56925637
23	cg36588129_BC21	0.00063899	0.03109757					59238153
24	cg37487780_TC21	0.00051199	0.05256249	Fmod	chr1	+	tss_200	134037453
25	cg37679569_BC21	0.00059203	-0.02651615	Rabgap1l	chr1	-	tss_body	160441997
26	cg37808506_BC21	0.00055459	-0.03708496	Wdr64	chr1	+	tss_body	175726968
27	cg38167997_BC21	0.00056504	0.02718137	Sec16a	chr2	-	tss_body	26439834
28	cg38176514_TC11	0.00015625	0.03593735	Sardh	chr2	-	tss_body	27246738

29	cg38288212_TC21	3.2806E-05	0.0469018	Mrrf	chr2	+	tss_body	36172235
30	cg38499186_TC21	0.00033033	0.05584133	Cers6	chr2	+	tss_body	69018018
31	cg38735151_BC21	0.00055764	0.04507441	Rag2	chr2	+	tss_body	101629775
32	cg38871223_TC21	0.00016407	0.02800853	Mapkbp1	chr2	+	tss_body	120012939
33	cg39297744_TC21	0.00085684	-0.03184247	Ptpn1	chr2	+	tss_body	167933677
34	cg39841168_BC21	0.00086583	0.03654278		chr3	-	tss_body	65832716
35	cg39867398_BC11	0.00053966	-0.03705511					69205932
36	cg40140795_TC21	0.00086682	0.05457027	Fam19a3	chr3	-	tss_body	104776860
37	cg40383232_TC21	4.7255E-07	-0.0351488	Gm567	chr3	+	tss_body	137290025
38	cg41263545_BC21	0.00034373	0.03116752	Zyg11b	chr4	-	tss_body	108299389
39	cg41329326_TC21	0.00044616	0.02547606	Eri3	chr4	+	tss_body	117659472
40	cg42595671_BC21	0.00061719	0.04612558	Cryba4	chr5	-	tss_body	112252460
41	cg43221346_TC21	0.00074918	-0.02538668		chr6	+	tss_body	24837727
42	cg43380935_BC21	0.00063873	0.04585975					47606056
43	cg43426292_BC21	0.00090149	0.05091156	Hoxa3	chr6	-	tss_body	52205107
44	cg44760194_BC21	0.00063526	0.03399736	Abhd2	chr7	+	tss_body	79350344
45	cg45124360_TC21	0.00076361	-0.03101921	Doc2a	chr7	+	tss_body	126848607
46	cg45226715_BC11	0.00013971	-0.03681452					136825860
47	cg45237140_BC21	0.00086143	-0.03364596					137715351
48	cg45365894_TC21	0.00099422	0.02934747	Gm2814	chr8	-	tss_body	10900476
49	cg46045669_BC21	0.00062674	0.04474559					96296129
50	cg46283862_TC11	0.00031876	0.03532908	Fendrr	chr8	-	tss_body	121066066
51	cg46698593_BC21	0.00066538	0.0265842	Gm31432	chr9	+	tss_body	46505098
52	cg46705818_TC21	0.0009684	0.03372346	Gm31816	chr9	-	tss_body	47348280
53	cg46798477_BC21	0.00063912	0.03473588	Csk	chr9	-	tss_body	57631551
X chromosome								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47618336_TC21	4.7331E-05	-0.0407155	Gm14696	chrX	-	tss_body	49340559
2	cg47858202_TC21	3.0263E-05	0.03469745					99163667
3	cg47913837_TC21	0.00062313	-0.02621546		chrX	-	tss_body	107406123
4	cg48127908_BC21	0.00012274	0.03697675	Cldn34b1	chrX	-	tss_body	154891430

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.025.

Appendix 4. 33: CpGs which are persistently differentially methylated across the lifespan by full CS exposure in female lungs, identified by limma

Autosomes								
	CpG name	P value	Effect size	Gene	Chromosome	Strand	Feature	CpG position
1	cg28394563_TC21	0.00015275	0.03370196					42041540
2	cg28783379_BC21	0.00097108	-0.02865425	Btbd11	chr10	+	tss_body	85598704
3	cg28959315_TC21	0.00010837	-0.03324716					108294688
4	cg29100534_TC11	0.00095893	0.05302696	Avpr1a	chr10	+	tss_1500	122448285
5	cg29376878_TC11	0.00062718	0.04101473	Rhbdf1	chr11	-	tss_body	32219006
6	cg29845151_BC21	0.00069152	-0.02673785	Rffl	chr11	-	tss_body	82845965
7	cg30060917_TC11	0.00096326	0.0564002	Hdac5	chr11	-	tss_body	102224783
8	cg30214719_TC21	0.00065878	0.0267679	Slc25a19	chr11	-	tss_body	115624014
9	cg31477928_BC21	0.00076927	-0.03478879		chr13	-	tss_body	40754964
10	cg31488211_BC21	0.00010519	0.02975792					41707746
11	cg31792683_TC21	0.00026527	0.04473659					73242539
12	cg32077401_TC21	0.00096721	0.0302475	chr13-111977845-111978120	chr13	*	Island	111977846
13	cg32165757_TC21	4.781E-06	0.045	Acox2	chr14	-	tss_body	8243767
14	cg32430329_BC11	0.00040267	-0.03995573	Bmp4	chr14	-	tss_body	46385875
15	cg32555880_BC11	0.00078265	0.03025468	Spata13	chr14	+	tss_body	60554069
16	cg33437524_BC11	6.5199E-05	0.03570117	Ndrg1	chr15	-	tss_body	66961862
17	cg33507292_TC11	0.00065948	0.04974154	Plec	chr15	-	tss_body	76229448
18	cg33787835_TC21	0.00036088	-0.02621478	LOC108168265	chr15	-	tss_body	99225080
19	cg33809129_BC21	0.00022469	0.03826386	Cela1	chr15	-	tss_body	100687886
20	cg34488934_TC11	0.00041587	0.02628499		chr16	-	tss_1500	91541434
21	cg34546895_BC21	0.00052329	-0.02596161	Wrb	chr16	+	tss_body	96148269
22	cg34619823_TC21	0.00053943	0.03288652	Pde10a	chr17	+	tss_body	8927803
23	cg34643699_BC21	0.00055536	-0.0274764	Park2	chr17	+	tss_body	11918628
24	cg34736633_BC21	0.00086882	-0.02680467		chr17	+	tss_body	24779751
25	cg34971865_BC21	0.00046028	0.02708763	Gltscr1l	chr17	-	tss_body	46815263
26	cg35289193_BC21	0.0006734	0.03183925	Gm19696	chr17	-	tss_body	84137904
27	cg35543036_TC21	0.00014843	-0.04138244					29307899

28	cg35635132_BC21	0.00077965	0.04129914					39394819
29	cg36080493_BC21	0.00013948	0.03601278	Pcx	chr19	+	tss_body	4619169
30	cg36279367_TC21	0.00025039	-0.02726365					27693907
31	cg36400195_TC21	0.00083877	-0.02611419	Slit1	chr19	-	tss_body	41743277
32	cg36419071_TC21	0.00016717	0.02575863	Cnnm1	chr19	+	tss_body	43463720
33	cg37679569_BC21	0.00012056	-0.02730086	Rabgap1l	chr1	-	tss_body	160441997
34	cg37964579_BC21	0.00017486	0.03923584	Atf3	chr1	-	tss_body	191179984
35	cg38302477_BC21	0.00048996	0.03081425	Nek6	chr2	+	tss_body	38529516
36	cg38499186_TC21	0.00021927	0.07728807	Cers6	chr2	+	tss_body	69018018
37	cg38518301_BC21	5.7618E-06	0.03250641					70940926
38	cg39069569_BC21	0.00038795	-0.02788929	B7ZCD7	chr2	+	tss_body	145971725
39	cg39298807_BC11	0.00016858	0.03631039	Fam65c	chr2	-	tss_body	168006201
40	cg39303706_BC11	0.0004457	-0.03047281					168315189
41	cg40036047_TC21	0.00014582	0.03145371	Gm40093	chr3	-	tss_1500	93598042
42	cg41246378_TC21	0.00024474	0.04204709	Ssbp3	chr4	+	tss_body	106913661
43	cg42549054_TC21	0.00025488	0.04690892	Tgfbr3	chr5	-	tss_body	107251269
44	cg42597888_TC11	0.00059119	0.05109122	Asphd2	chr5	-	tss_body	112385514
45	cg42954218_BC21	0.00035126	0.02570781	Gm32158	chr5	+	tss_body	140583734
46	cg44091397_TC21	0.00012559	0.04250821	Plcz1	chr6	-	tss_body	140016210
47	cg44494846_BC21	0.00029513	0.03832521	Siglece	chr7	-	tss_body	43652927
48	cg45052418_TC21	6.2452E-05	0.02824233	9030624J02Rik	chr7	+	tss_body	118763870
49	cg45272968_TC11	0.00032401	0.05141928	Eps8l2	chr7	+	tss_body	141339154
50	cg45641235_BC21	0.00051488	-0.04006054	Gm30504	chr8	+	tss_200	45110432
51	cg45848223_BC21	0.00035636	0.02933783		chr8	-	tss_200	74833977
52	cg45874031_TC21	0.00038546	-0.0349562	Rbmxl1	chr8	-	tss_body	78506857
53	cg46259982_TC11	0.00077809	0.06039307	Dnaaf1	chr8	+	tss_body	119588955
54	cg46274825_TC21	0.00025005	0.04527127	Gse1	chr8	+	tss_body	120521394
55	cg46511764_BC21	0.00086586	-0.03141686	Gm36743	chr9	+	tss_body	23068091
56	cg46804919_BC21	0.00062622	-0.02734961	Islr2	chr9	-	tss_body	58202939
57	cg46848754_BC21	0.00042952	0.02820081	Coro2b	chr9	-	tss_body	62510573
58	cg47199766_BC21	0.00030379	0.0289013	Cpne4	chr9	+	tss_body	104872772

X chromosome								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47417399_TC21	0.00064765	-0.03658377	Gm26618	chrX	-	tss_200	6092249
2	cg47519914_BC21	0.00089566	-0.02862888	Klhl13	chrX	-	tss_body	23266578
3	cg47562411_BC21	0.00018679	0.03057385	Rhox9	chrX	-	tss_1500	37902042
4	cg47576398_TC21	0.00016773	-0.03958889					40811430
5	cg47685458_TC21	0.00061538	0.03305197	Ldoc1	chrX	+	tss_200	61709600
6	cg47712350_TC21	0.00088009	-0.02951927	Fmr1	chrX	+	tss_body	68679733
7	cg47913837_TC21	0.00040942	-0.02596989		chrX	-	tss_body	107406123
8	cg48153063_TC21	0.00047174	-0.03697195	Sh3kbp1	chrX	+	tss_body	159951962

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.025.

Appendix 4. 34: CpGs which are persistently differentially methylated across the lifespan by prenatal CS exposure in male lungs, identified by limma

Autosomes								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg28113478_TC21	2.6729E-05	-0.0379362	Plekhg1	chr10	+	tss_body	3859037
2	cg28140488_BC21	0.00024735	-0.03957812	Cnksr3	chr10	-	tss_body	7172710
3	cg28196547_TC21	0.00036469	-0.05655475	Hivep2	chr10	+	tss_body	13971643
4	cg28229706_TC21	0.00057512	0.04721716	Tnfaip3	chr10	-	tss_body	19012102
5	cg28239647_BC21	6.5241E-06	-0.04148668	Map3k5	chr10	+	tss_body	20109060
6	cg28239931_BC11	0.00035181	-0.04496862	Map3k5	chr10	+	tss_body	20127421
7	cg28290026_BC21	8.58E-05	0.02962752	Epb41l2	chr10	+	tss_body	25448770
8	cg28309927_BC21	0.00016588	0.04291968	Ptprk	chr10	+	tss_body	28492951
9	cg28356118_BC21	0.00010016	-0.02917383	Gm26535	chr10	+	tss_body	37337826
10	cg28363459_TC11	0.00030871	-0.04676815	Lama4	chr10	+	tss_1500	38964929
11	cg28367756_TC21	0.0002478	-0.02861585	Fyn	chr10	+	tss_body	39445940
12	cg28373074_TC21	0.00012112	-0.04594821	Mfsd4b5	chr10	-	tss_200	39986654
13	cg28377598_TC21	0.00090607	-0.03406665	Cdk19	chr10	+	tss_body	40422934
14	cg28382463_BC21	0.0002441	-0.03268003	Wasf1	chr10	+	tss_body	40909350
15	cg28416310_BC21	0.00020015	-0.03931091	Qrsl1	chr10	-	tss_body	43874634
16	cg28422076_BC21	0.00072092	-0.03398618	Prdm1	chr10	-	tss_body	44459898
17	cg28432956_BC21	0.00012357	0.02875618	D030045P18Rik	chr10	+	tss_200	45807695
18	cg28490569_TC21	2.0251E-05	-0.06597618					56921021
19	cg28506227_TC11	0.00011345	0.03004042	Pla2g12b	chr10	+	tss_body	59403763
20	cg28563411_TC21	0.00039404	-0.04570716	Ctnna3	chr10	+	tss_body	64040338
21	cg28581132_TC21	2.1929E-05	0.05608337	Reep3	chr10	-	tss_body	67056603
22	cg28657373_TC21	0.00035364	-0.05777945	Adora2a	chr10	+	tss_body	75324244
23	cg28659937_BC21	6.4179E-05	-0.07245506	Lrrc75b	chr10	-	tss_body	75551196
24	cg28660293_BC21	0.00080132	-0.02930488	Ggt1	chr10	+	tss_body	75571480
25	cg28661750_BC21	0.00015698	-0.02964065	Cabin1	chr10	-	tss_body	75684265
26	cg28665635_BC21	0.00027271	-0.03011818	Gm5134	chr10	+	tss_body	75969907
27	cg28679596_TC21	0.00049338	0.03184025	Col18a1	chr10	-	tss_body	77131036
28	cg28695739_TC11	0.00071799	-0.03584615	Pdxk	chr10	-	tss_body	78457179

29	cg28707103_BC21	0.0001097	-0.04201057	Prss57	chr10	-	tss_body	79791091
30	cg28707784_TC21	0.00031672	-0.02721931	Misp	chr10	+	tss_body	79826608
31	cg28708915_BC21	0.00061332	-0.03207117	Elane	chr10	+	tss_body	79886746
32	cg28714076_TC21	0.0008353	0.04548171	Cbarp	chr10	-	tss_body	80131071
33	cg28725764_TC21	2.8836E-05	0.03831848	Mknk2	chr10	-	tss_body	80672156
34	cg28732083_TC21	0.00038815	0.02685573	chr10-81031112-81031665	chr10	*	NShelf	81027642
35	cg28738501_BC11	0.00019249	0.05032442	Tbxa2r	chr10	+	tss_body	81332258
36	cg28741349_BC21	0.00021103	-0.02752206	Celf5	chr10	-	tss_body	81461222
37	cg28790122_TC21	0.00018151	0.04883733	Syn3	chr10	-	tss_body	86339395
38	cg28797416_BC21	0.00027017	-0.029422	1700113H08Rik	chr10	+	tss_body	87128768
39	cg28812015_TC21	0.00037704	-0.0276085	Utp20	chr10	-	tss_body	88817198
40	cg28817556_BC21	0.00054121	-0.05019684	Nr1h4	chr10	-	tss_body	89533503
41	cg28848693_BC21	0.00067487	0.03310269	Cdk17	chr10	+	tss_body	93213541
42	cg28859528_TC21	0.00030519	0.05238943	Fgd6	chr10	+	tss_body	94072431
43	cg28873260_BC21	0.00064226	-0.03827854	Cradd	chr10	-	tss_body	95266445
44	cg28877132_TC21	5.6299E-05	0.03871686	Nudt4	chr10	-	tss_body	95560303
45	cg28877143_BC21	2.2272E-06	-0.03814751	Nudt4	chr10	-	tss_body	95561067
46	cg28906590_BC21	0.00051166	0.02839565		chr10	+	tss_body	99354148
47	cg28924314_BC21	0.00019932	0.03303434	Mgat4c	chr10	+	tss_body	102365701
48	cg28955595_TC21	0.0001179	-0.03227374	Otogl	chr10	-	tss_body	107860410
49	cg28958838_TC21	0.00020634	0.03543479	Ppp1r12a	chr10	+	tss_body	108253491
50	cg28969998_TC21	0.00072361	-0.06877022	Nav3	chr10	-	tss_body	109684209
51	cg28977237_BC11	0.00019264	-0.03133775					110733828
52	cg29018084_TC21	0.00091194	0.02767434	Tspan8	chr10	+	tss_1500	115816604
53	cg29055107_TC21	0.00087013	0.02893044					118933595
54	cg29057175_TC21	0.00034545	-0.03002264					119108142
55	cg29061901_BC21	0.00083116	-0.04203869	Grip1	chr10	+	tss_body	119496198
56	cg29083981_BC21	0.00055325	0.0482877	LOC102642038	chr10	-	tss_body	121161114
57	cg29141167_TC11	4.6645E-05	0.02563643	March9	chr10	-	tss_1500	127060508
58	cg29146439_TC21	2.15E-07	-0.04924214	Gli1	chr10	-	tss_body	127336411
59	cg29150818_BC21	0.00047115	-0.03156375	Lrp1	chr10	-	tss_body	127614140

60	cg29157526_TC21	7.2093E-06	0.03198674	Rbms2	chr10	-	tss_body	128180222
61	cg29165407_BC21	0.00099056	-0.05374938	Cdk2	chr10	-	tss_1500	128706107
62	cg29166678_TC21	0.00031293	-0.03060827	Dnajc14	chr10	+	tss_body	128816728
63	cg29173424_TC21	0.0003675	0.026097		chr10	+	tss_body	130120456
64	cg29177459_TC21	0.0002685	0.02797441	Drg1	chr11	-	tss_body	3264883
65	cg29194212_BC21	0.00047192	-0.05966745	Zmat5	chr11	+	tss_body	4735571
66	cg29194678_TC21	8.6377E-05	-0.03083939					4755138
67	cg29199185_TC21	0.00034408	-0.03029041	Emid1	chr11	-	tss_body	5106338
68	cg29232312_BC11	0.0007723	0.07177838	Tns3	chr11	-	tss_body	8591581
69	cg29251209_BC21	3.8734E-05	0.04619514	Ddc	chr11	-	tss_body	11831220
70	cg29275415_TC21	0.00048445	-0.0372072	Egfr	chr11	+	tss_body	16794880
71	cg29296311_TC21	0.00039278	0.0347703					19829124
72	cg29299699_BC21	0.00027988	-0.04039344					20117493
73	cg29304932_BC21	0.00032825	-0.03164677	Sertad2	chr11	+	tss_body	20648016
74	cg29309214_BC21	0.00092336	-0.04602616					21175323
75	cg29331965_TC21	0.00079557	-0.04553958	Gm33440	chr11	+	tss_body	24243230
76	cg29377574_TC21	0.00073627	0.07134768					32272504
77	cg29393903_BC11	8.3493E-05	0.03531883	Kcnip1	chr11	-	tss_body	33928830
78	cg29393963_TC21	0.00036781	-0.05336384	Kcnip1	chr11	-	tss_body	33932502
79	cg29394877_TC21	0.00069658	-0.04104219		chr11	-	tss_body	34031440
80	cg29396343_TC21	4.2646E-05	-0.04326182	Foxi1	chr11	-	tss_body	34206019
81	cg29398420_BC21	0.00042721	0.03142218	Dock2	chr11	-	tss_body	34420995
82	cg29416811_BC21	0.00021571	-0.04175568	Tenm2	chr11	-	tss_body	36293153
83	cg29482745_BC11	5.0098E-05	0.04469423	Itk	chr11	-	tss_body	46355794
84	cg29511540_TC11	0.00091395	-0.05684332	chr11-50359091-50359865	chr11	*	SShelf	50362205
85	cg29513285_TC21	4.9742E-05	-0.03362902					50495942
86	cg29527953_BC11	0.00062468	-0.03985317	Jade2	chr11	-	tss_body	51833731
87	cg29527955_BC11	0.00033666	-0.03489837	Jade2	chr11	-	tss_body	51833880
88	cg29538480_TC21	0.00037229	0.02544859	Fstl4	chr11	+	tss_body	52765404
89	cg29558186_TC21	0.00088017	0.05104188	Cdc42se2	chr11	-	tss_body	54756532
90	cg29569784_TC21	3.9906E-05	-0.02543731	LOC105244170	chr11	+	tss_body	55974024

91	cg29580474_BC11	0.00095477	0.02680987		chr11	+	tss_body	57572570
92	cg29599294_TC21	0.00039474	-0.04918493	Iba57	chr11	-	tss_body	59155598
93	cg29602381_TC21	0.00017369	-0.0300182					59366847
94	cg29608276_TC21	0.00051559	-0.0409315		chr11	+	tss_body	59898521
95	cg29609864_BC21	0.00070307	-0.03487203	Pemt	chr11	-	tss_body	60033924
96	cg29610437_TC21	6.5439E-05	-0.04486492					60089142
97	cg29625009_BC21	0.00017212	-0.0338546	Slc47a1	chr11	-	tss_body	61362994
98	cg29626475_TC21	0.00013363	-0.05882207	Mfap4	chr11	+	tss_1500	61484917
99	cg29626534_BC21	0.0004532	-0.03210205	Mfap4	chr11	+	tss_body	61487990
100	cg29650820_BC21	9.3282E-06	-0.04232737					63953573
101	cg29678542_TC21	9.1416E-06	0.03822783	Myh13	chr11	+	tss_body	67327114
102	cg29683298_BC21	0.00097721	-0.02792937	Gm40032	chr11	-	tss_body	67820899
103	cg29689461_TC21	0.00017923	-0.02818507	Ntn1	chr11	-	tss_body	68372545
104	cg29694969_BC21	0.00041027	-0.03615166	Myh10	chr11	+	tss_body	68814469
105	cg29705231_BC21	0.00094173	-0.02946609	Dnah2	chr11	-	tss_body	69464788
106	cg29710908_TC21	0.00024064	0.04990167	Gm39566	chr11	-	tss_1500	69816783
107	cg29715151_BC21	4.2475E-06	-0.03606395	Dlg4	chr11	+	tss_body	70028378
108	cg29735324_BC21	5.1883E-05	-0.02780125	Aipl1	chr11	-	tss_body	72031522
109	cg29739934_BC21	0.00038861	-0.02701719	Ggt6	chr11	+	tss_body	72438118
110	cg29740804_BC21	0.00079085	-0.03570406		chr11	-	tss_body	72497332
111	cg29748250_TC21	0.0001546	0.04171253	Trpv3	chr11	+	tss_200	73267485
112	cg29770261_TC21	0.00075726	0.04412602	Ywhae	chr11	+	tss_body	75746349
113	cg29772508_BC21	0.00027213	-0.02892915	Rph3al	chr11	-	tss_body	75936144
114	cg29777239_TC21	5.6981E-05	-0.03469991	Nxn	chr11	-	tss_body	76352672
115	cg29784321_TC21	0.00062646	0.02795705	Blmh	chr11	+	tss_body	76983613
116	cg29788695_BC21	2.5683E-06	-0.04320932	Ankrd13b	chr11	-	tss_body	77483677
117	cg29789708_TC21	0.00063115	-0.03663489	Abhd15	chr11	+	tss_body	77519251
118	cg29798048_TC21	0.00015738	-0.03291346	Proca1	chr11	+	tss_1500	78194205
119	cg29813946_TC21	0.00089635	-0.02760658	Rab11fip4	chr11	+	tss_body	79645194
120	cg29815728_BC21	0.00022509	-0.07050917	LOC105242790	chr11	-	tss_body	79753310
121	cg29827123_TC21	0.00080711	-0.0283986					80832664

122	cg29837622_BC21	0.00036296	-0.04136763	Ccl11	chr11	+	tss_200	82057711
123	cg29845081_BC21	0.00016301	0.02810045	Rffl	chr11	-	tss_body	82840686
124	cg29857162_TC21	6.2006E-06	-0.05824094	Synrg	chr11	+	tss_body	84040853
125	cg29877803_TC21	0.00087432	-0.02709425	Gm20759	chr11	-	tss_1500	86025610
126	cg29887186_TC21	0.00056035	-0.04397265	Gdpd1	chr11	-	tss_body	87045791
127	cg29892455_BC21	4.8725E-05	-0.03303693	Sept4	chr11	+	tss_body	87574799
128	cg29901999_BC21	0.00024443	-0.02870856					88288935
129	cg29906111_TC21	0.00060718	-0.04073292	Msi2	chr11	-	tss_body	88608023
130	cg29921379_BC21	0.00095296	0.04418461	Pctp	chr11	-	tss_body	89996961
131	cg29925747_TC21	2.3369E-06	-0.03564498	Hlf	chr11	-	tss_1500	90392271
132	cg29945224_BC21	0.00028166	-0.04069983					93763494
133	cg29948556_BC11	0.00014888	0.05311308	B230206L02Rik	chr11	+	tss_body	94137423
134	cg29952742_TC21	6.0082E-05	-0.04683086	Cacna1g	chr11	-	tss_body	94447126
135	cg29960091_TC21	0.00046161	0.03905965	Samd14	chr11	+	tss_body	95024411
136	cg29979500_TC21	2.9825E-05	0.03050887	Hoxb3	chr11	+	tss_body	96344775
137	cg29982178_TC11	0.00093295	0.02628542	Skap1	chr11	+	tss_body	96554045
138	cg29996728_TC11	0.00039988	-0.07960724	Srcin1	chr11	-	tss_body	97534548
139	cg29996950_BC21	2.6502E-06	-0.0407461	Srcin1	chr11	-	tss_body	97542503
140	cg30003989_TC21	0.00011783	-0.030619	Plxdc1	chr11	-	tss_body	97983434
141	cg30010131_TC21	0.0005598	-0.02725019	Pgap3	chr11	-	tss_body	98399717
142	cg30024086_BC21	0.00072754	-0.06493809	Krt26	chr11	-	tss_body	99337667
143	cg30026686_TC21	1.7517E-06	0.06550585	A2A592	chr11	-	tss_200	99559641
144	cg30058099_BC21	0.00049062	0.03585432	Cd300lg	chr11	+	tss_body	102044724
145	cg30072057_BC21	0.00070293	-0.03444437					102957080
146	cg30102621_TC21	0.000389	-0.03074389	Tanc2	chr11	+	tss_body	105637003
147	cg30108487_BC21	0.0003005	-0.04213976	Smarcd2	chr11	-	tss_body	106265754
148	cg30140033_BC21	0.000405	0.03248103	Gm36876	chr11	+	tss_body	108984948
149	cg30165622_BC21	2.0102E-05	-0.05817601	Gm30219	chr11	-	tss_body	111658379
150	cg30175387_BC21	0.00080218	-0.03829423	Gm30562	chr11	-	tss_body	112806780
151	cg30194091_BC11	3.8498E-05	-0.02664383					114129709
152	cg30198655_TC21	0.00065697	-0.05144119					114512826

153	cg30199182_BC21	0.00010756	-0.06231023	Gm31724	chr11	-	tss_body	114554074
154	cg30200562_BC21	3.4653E-05	-0.0805968					114657444
155	cg30214308_BC11	0.00028234	0.03636891	Gga3	chr11	-	tss_1500	115605242
156	cg30230014_BC21	2.5523E-05	-0.03355323					116511598
157	cg30230524_BC21	1.5082E-05	0.02707315	Sphk1	chr11	+	tss_body	116535765
158	cg30232898_TC21	0.00092267	-0.0288302					116668645
159	cg30237558_BC21	2.4113E-05	-0.04091153	Mgat5b	chr11	+	tss_body	116968800
160	cg30245320_TC21	2.8053E-05	-0.05654475	LOC108167873	chr11	-	tss_body	117462392
161	cg30246313_TC21	1.7426E-05	-0.05575649					117543584
162	cg30247299_BC21	0.00020363	-0.03030241	Gm35170	chr11	-	tss_body	117627208
163	cg30249131_BC21	0.00079319	-0.05490188	Tmc6	chr11	-	tss_body	117777279
164	cg30250781_TC21	0.00072641	-0.03639324	Tha1	chr11	-	tss_body	117872393
165	cg30251175_BC11	6.0532E-05	-0.03794312	Gm11725	chr11	+	tss_body	117894929
166	cg30271978_TC21	0.00043606	0.02618495	Tbc1d16	chr11	-	tss_body	119210869
167	cg30287227_BC21	9.2577E-05	-0.07924405	Bahcc1	chr11	+	tss_body	120241257
168	cg30302004_BC21	3.233E-05	-0.03352183	Hexdc	chr11	+	tss_body	121219779
169	cg30315376_TC21	7.7194E-05	-0.03216476	Dtnb	chr12	+	tss_body	3749283
170	cg30348835_BC21	0.00028468	0.02782856					8353447
171	cg30367955_TC21	3.9318E-05	-0.05856686	Kcns3	chr12	-	tss_body	11151301
172	cg30374523_BC11	7.1412E-06	-0.06055058	Fam49a	chr12	+	tss_body	12287896
173	cg30379133_TC21	0.00070821	-0.04794857	Gm35155	chr12	+	tss_body	12813194
174	cg30400252_BC21	0.00028505	-0.05804169					16387216
175	cg30402095_TC21	0.00042677	-0.04949025	Lpin1	chr12	-	tss_body	16604043
176	cg30402912_TC21	5.1663E-05	-0.02994236	Greb1	chr12	-	tss_body	16680403
177	cg30463060_BC21	0.00021046	-0.05170179	Cys1	chr12	-	tss_body	24680231
178	cg30469482_TC21	0.00038145	-0.04338761					25240707
179	cg30470027_TC21	0.00027211	0.02993308	LOC108167993	chr12	+	tss_body	25304569
180	cg30490740_TC21	5.5764E-05	0.04388453	Dcdc2c	chr12	-	tss_body	28520211
181	cg30492383_TC21	0.00043322	-0.03448837	chr12-28675146-28675589	chr12	*	NShelf	28671767
182	cg30493802_TC21	1.4947E-05	0.07348276	Tssc1	chr12	+	tss_body	28790528
183	cg30501011_TC21	7.5744E-05	0.03612516	Myt1l	chr12	+	tss_body	29699389

184	cg30512694_TC21	9.2161E-05	-0.02677147		chr12	+	tss_200	31234472
185	cg30520919_BC21	0.00019329	-0.04541007	5430401H09Rik	chr12	-	tss_body	32105026
186	cg30552430_BC21	0.00090854	0.02663948	Ispd	chr12	+	tss_body	36381991
187	cg30581573_TC21	4.1275E-05	0.02875708	Immp2l	chr12	+	tss_body	41486792
188	cg30653787_BC21	0.00022957	-0.03144789	Npas3	chr12	+	tss_body	53982352
189	cg30671587_TC21	0.00098931	-0.04258153	Ralgapa1	chr12	-	tss_body	55821515
190	cg30745744_TC21	1.912E-05	0.06451025					69145487
191	cg30769850_TC21	0.00010478	-0.03007946	2700049A03Rik	chr12	+	tss_body	71252834
192	cg30770919_TC21	7.5946E-06	-0.03283885	Gm33016	chr12	+	tss_body	71337610
193	cg30771509_BC21	0.00029365	-0.03561556		chr12	+	tss_body	71399905
194	cg30781545_TC11	0.00012024	0.03145736	Rtn1	chr12	-	tss_body	72363581
195	cg30782070_BC21	4.8939E-06	-0.04525073	Rtn1	chr12	-	tss_200	72409082
196	cg30795870_BC21	0.00093231	0.04558615	Prkch	chr12	+	tss_body	73699405
197	cg30822155_TC21	5.1915E-07	0.0260049	Plekhg3	chr12	+	tss_body	76546989
198	cg30840381_BC21	0.00028064	-0.05287661	Plek2	chr12	-	tss_body	78891359
199	cg30849646_BC21	0.00091687	-0.03247044	Gm36132	chr12	-	tss_body	79864513
200	cg30850230_TC21	0.00057325	-0.05494552	9430078K24Rik	chr12	-	tss_body	79924794
201	cg30850231_TC21	0.00015763	-0.05061488	9430078K24Rik	chr12	-	tss_body	79924888
202	cg30853730_BC21	0.00033482	0.06071165	Actn1	chr12	-	tss_body	80220403
203	cg30877250_TC11	0.00095682	-0.0618327	A0A0J9YU74	chr12	+	tss_body	82589076
204	cg30903103_BC21	0.0002771	0.03664876		chr12	+	tss_body	84881889
205	cg30906410_BC11	0.00073208	-0.05539541	Pgf	chr12	-	tss_body	85173073
206	cg30909522_TC21	2.8504E-05	-0.03486489	LOC105242442	chr12	+	tss_body	85426381
207	cg30910036_TC21	4.5316E-05	-0.03946965					85462250
208	cg30941866_TC21	0.00068505	-0.04907008	Nrxn3	chr12	+	tss_body	88860919
209	cg30948433_TC11	0.00052136	-0.04234806	Nrxn3	chr12	+	tss_body	90129174
210	cg30949928_TC21	0.00038668	0.03937804	Gm40538	chr12	-	tss_body	90408674
211	cg31001079_TC21	0.00055426	0.04297052		chr12	-	tss_body	98991967
212	cg31001373_BC11	0.00050433	0.0268071	Gm40554	chr12	+	tss_body	99024532
213	cg31015715_BC21	0.00015601	0.04250105	Gm36263	chr12	-	tss_body	100179270
214	cg31026270_TC21	0.0003601	-0.04781535		chr12	+	tss_body	101221990

215	cg31039252_TC21	0.00074315	-0.03617331		chr12	-	tss_body	102707318
216	cg31047476_TC21	0.00034433	0.0333947	Ifi27l2a	chr12	-	tss_body	103437263
217	cg31049177_TC21	0.00035617	0.03984185					103660195
218	cg31049410_TC21	5.8568E-05	-0.04009619	LOC108168025	chr12	+	tss_body	103688837
219	cg31070223_TC21	0.00097412	-0.09053885	Bdkrb1	chr12	+	tss_200	105604054
220	cg31093182_BC11	0.00089165	-0.04889645		chr12	-	tss_body	107484192
221	cg31107082_TC21	5.2269E-05	-0.04924325	Eml1	chr12	+	tss_body	108450187
222	cg31119531_BC21	0.00051352	-0.03588864	Gm34081	chr12	-	tss_body	109530849
223	cg31121849_BC21	0.00076078	-0.02779682	Mir544	chr12	+	tss_1500	109728600
224	cg31134594_TC21	0.0001322	-0.04309123	1700001K19Rik	chr12	-	tss_body	110674043
225	cg31151868_TC21	0.00082292	-0.02559449	Ppp1r13b	chr12	-	tss_body	111840979
226	cg31153933_BC21	1.5496E-05	-0.02537853	Tdrd9	chr12	+	tss_body	112007665
227	cg31155305_BC21	0.00011391	-0.02801154	Aspg	chr12	+	tss_body	112120037
228	cg31157781_TC21	6.7848E-05	-0.03006998	Gm36894	chr12	+	tss_body	112260405
229	cg31165859_TC21	8.6041E-05	-0.02608249	Pld4	chr12	+	tss_body	112765009
230	cg31172451_BC11	0.00015456	0.07304053	Crip1	chr12	+	tss_1500	113150918
231	cg31220758_TC21	0.00017128	0.02689225	Net1	chr13	-	tss_body	3887366
232	cg31242956_BC21	0.00036456	0.03444921					7820038
233	cg31285395_BC11	0.0001928	0.03541109	Ggps1	chr13	-	tss_1500	14063987
234	cg31356801_BC11	0.00080824	-0.02657279	Fam65b	chr13	+	tss_body	24662067
235	cg31379956_TC21	5.9766E-05	0.03783503	2610307P16Rik	chr13	-	tss_body	28719111
236	cg31398820_BC21	0.00059015	0.04038963	Exoc2	chr13	-	tss_body	30793679
237	cg31405749_BC21	0.00014511	-0.0549063	Foxf2	chr13	+	tss_body	31629060
238	cg31412871_TC21	7.2358E-08	-0.06844541					32615821
239	cg31416142_TC21	0.00051745	0.04922825	Serpinb9c	chr13	-	tss_1500	33159792
240	cg31428338_BC21	0.00093043	-0.03084262	Eci3	chr13	-	tss_body	34963622
241	cg31432333_TC21	0.00018525	-0.02522188		chr13	-	tss_body	35614957
242	cg31446936_TC21	0.00091056	-0.04166924	Gm30863	chr13	-	tss_body	37509790
243	cg31448657_BC21	0.0009391	-0.027528	AI463229	chr13	-	tss_body	37667641
244	cg31453160_TC21	0.00033446	0.02823294	Cage1	chr13	-	tss_body	38033447
245	cg31459367_BC21	6.8919E-05	0.03841858	Gm40922	chr13	+	tss_1500	38554368

246	cg31460055_BC21	3.8948E-05	-0.04221198	Bloc1s5	chr13	-	tss_body	38614535
247	cg31476588_TC21	0.0002493	0.04005576					40698180
248	cg31478680_BC21	0.00030713	-0.03187642	Gm35160	chr13	+	tss_body	40850772
249	cg31481726_BC21	0.00092487	-0.02771741		chr13	+	tss_200	41091366
250	cg31487648_TC21	0.00073289	0.05441387	Gm5082	chr13	+	tss_body	41655635
251	cg31489106_TC21	0.00040655	-0.04020932	Adtrp	chr13	-	tss_body	41796194
252	cg31502575_BC21	0.00016463	-0.06003677	Gfod1	chr13	-	tss_body	43197408
253	cg31508555_TC21	0.00023189	-0.0622557		chr13	+	tss_body	43684919
254	cg31513546_TC21	0.00031758	-0.03314627	Gm5083	chr13	+	tss_body	44121192
255	cg31518528_TC21	0.00031943	-0.05523473	Gm34276	chr13	-	tss_body	44556509
256	cg31518870_BC21	0.00022562	-0.03120139	Gm40931	chr13	-	tss_body	44586558
257	cg31522428_BC21	0.00070909	0.02515404	Dtnbp1	chr13	-	tss_body	44939860
258	cg31534603_BC21	0.00053196	-0.04696291					46043290
259	cg31539383_BC11	0.00060963	0.05697511	Cap2	chr13	+	tss_body	46548264
260	cg31545311_TC21	0.00021413	-0.03712342	Nhlrc1	chr13	-	tss_body	47013774
261	cg31554833_TC21	0.00057179	0.03147143	Gm40938	chr13	-	tss_body	47943889
262	cg31558485_BC21	0.0009168	-0.04745439					48292148
263	cg31560740_TC21	1.0524E-05	-0.06457739	Zfp169	chr13	-	tss_body	48508729
264	cg31565012_TC21	0.00014236	-0.03515633	Phf2	chr13	-	tss_body	48842201
265	cg31567678_BC21	4.0628E-05	-0.04401508	Wnk2	chr13	-	tss_body	49079367
266	cg31569360_BC21	0.00089952	-0.03451252					49200716
267	cg31581924_TC21	0.00071844	-0.02899145					51016633
268	cg31588347_BC21	0.00010221	-0.03501415					51574202
269	cg31602828_BC21	1.1172E-05	0.03178016	Gm33315	chr13	+	tss_body	52829344
270	cg31605770_TC21	0.00015756	-0.04684488	Gm33424	chr13	+	tss_body	53016386
271	cg31663748_TC11	0.00064404	-0.03818595	Spock1	chr13	-	tss_body	57580220
272	cg31670513_BC21	0.00082269	-0.06399099	Klhl3	chr13	-	tss_body	58115012
273	cg31676276_TC21	2.8309E-05	-0.03960629					58542554
274	cg31690136_TC21	4.8863E-05	-0.03257797	Spata31d1b	chr13	+	tss_1500	59712045
275	cg31692375_BC21	0.00070356	-0.04508199	Gm19866	chr13	-	tss_body	59892458
276	cg31700172_BC11	0.00018068	0.0279582	Dapk1	chr13	+	tss_body	60628684

277	cg31718089_TC21	4.0201E-05	0.03759946	2010111I01Rik	chr13	+	tss_body	63301171
278	cg31754959_BC21	0.00035712	-0.04767628	Mtrr	chr13	-	tss_body	68572928
279	cg31798434_TC21	6.7343E-05	-0.0277612	Slc12a7	chr13	+	tss_body	73816185
280	cg31808317_TC21	0.00077942	-0.06263267					75368457
281	cg31810414_TC21	0.00092253	-0.02743492	Ell2	chr13	+	tss_body	75756370
282	cg31859167_BC21	2.0204E-05	-0.03858243	Gm34196	chr13	-	tss_body	84690614
283	cg31870910_BC21	0.0005986	0.02812523		chr13	+	tss_body	87307764
284	cg31942092_TC21	0.00066461	-0.04029462	Hmgcr	chr13	-	tss_body	96669590
285	cg31957151_BC11	0.00094933	0.03106167	Arhgef28	chr13	-	tss_body	98096418
286	cg31975045_TC21	2.1866E-06	-0.06478157					99609633
287	cg31977527_TC11	0.0007831	0.0261074					99880206
288	cg31980402_BC21	8.2141E-06	0.03748887	Naip2	chr13	-	tss_body	100153883
289	cg31980408_BC21	0.00096717	0.02683014	Naip2	chr13	-	tss_body	100154469
290	cg31994224_TC21	2.4034E-05	-0.03635567					101813691
291	cg32037759_TC21	0.00024284	-0.04395742	Gm31920	chr13	+	tss_body	107569133
292	cg32039168_BC21	0.00017979	-0.02539516					107700236
293	cg32045590_TC21	0.00096876	0.03833975	Elovl7	chr13	+	tss_body	108218216
294	cg32066976_TC21	0.00028477	-0.03731089	Gm38397	chr13	+	tss_body	110903887
295	cg32077188_TC21	0.00027677	-0.04142082					111954321
296	cg32083172_TC21	0.00027854	0.0619831	Il6st	chr13	+	tss_body	112473362
297	cg32091660_TC21	0.0009658	-0.03218682	Gm41069	chr13	-	tss_body	113209707
298	cg32160935_TC21	1.7794E-05	-0.02514033	Flnb	chr14	+	tss_body	7822888
299	cg32165900_TC21	2.383E-05	-0.04073631	Acox2	chr14	-	tss_body	8258169
300	cg32190471_TC21	0.00081355	-0.0299979	Ptprg	chr14	+	tss_body	12202431
301	cg32203680_BC21	0.00040777	-0.02938265		chr14	-	tss_1500	14295081
302	cg32225794_TC11	0.00021544	0.02965765	Ube2e1	chr14	-	tss_body	18327378
303	cg32238562_TC21	0.00088603	-0.0343981		chr14	+	tss_200	20215415
304	cg32241407_BC21	0.00068731	0.02588168	Anxa7	chr14	-	tss_body	20476057
305	cg32245421_TC21	0.0001349	-0.06434416	Plau	chr14	+	tss_body	20838554
306	cg32252882_BC21	0.00041177	0.02831925	Kat6b	chr14	+	tss_body	21664539
307	cg32258206_TC11	0.00022581	-0.0553835	1700112E06Rik	chr14	+	tss_body	22148051

308	cg32267012_TC21	0.0004183	-0.04964723	Kcnma1	chr14	-	tss_body	23493982
309	cg32277572_TC21	0.0005366	-0.03112984	Gm32008	chr14	+	tss_body	24833779
310	cg32278232_TC21	0.00035697	-0.03609522					24907733
311	cg32334527_BC21	0.00066018	0.03520228	Tnnc1	chr14	+	tss_body	31208348
312	cg32337222_BC21	4.9165E-06	-0.04150052	Sh3bp5	chr14	-	tss_body	31414847
313	cg32344854_BC21	1.3843E-05	-0.02898001	Msmb	chr14	+	tss_body	32154893
314	cg32369155_BC11	0.00016837	-0.03333955	Opn4	chr14	-	tss_body	34599868
315	cg32403845_BC21	0.0007726	-0.04108442		chr14	+	tss_body	41148939
316	cg32426672_BC21	0.00098798	-0.05039434		chr14	+	tss_body	45903150
317	cg32432636_BC21	0.00023839	-0.04977073	4933425B07Rik	chr14	-	tss_body	46623319
318	cg32437202_TC21	0.00054638	-0.03518088	Samd4	chr14	+	tss_body	47005184
319	cg32460786_TC21	0.00044204	-0.02772734	1700011H14Rik	chr14	-	tss_body	49235307
320	cg32471891_TC21	0.00077328	0.03885196	Olfr750	chr14	-	tss_200	51071476
321	cg32472044_BC21	0.00018169	-0.04792037					51084384
322	cg32479642_TC11	0.00011269	0.03126624					52066589
323	cg32483720_BC11	0.00097173	0.02690385	Olfr1507	chr14	-	tss_body	52495469
324	cg32506343_BC21	0.00025641	-0.03744645	Jph4	chr14	-	tss_body	55110185
325	cg32506376_TC21	0.00089635	-0.05073288	Jph4	chr14	-	tss_body	55113428
326	cg32506567_TC11	0.00085848	-0.03612056	Jph4	chr14	-	tss_1500	55117139
327	cg32522486_TC11	0.00027165	0.02896171	Mphosph8	chr14	+	tss_body	56690849
328	cg32530526_TC21	0.00026426	-0.05491591	Il17d	chr14	+	tss_body	57538428
329	cg32545044_BC21	4.904E-05	-0.0559321	Phf11c	chr14	-	tss_body	59388870
330	cg32564074_TC21	0.00076602	-0.05155649	Arl11	chr14	+	tss_body	61309588
331	cg32570577_TC11	0.00039538	-0.02745206	Gm35307	chr14	+	tss_body	62037065
332	cg32572969_BC21	0.00010393	-0.02917842	Rnaseh2b	chr14	+	tss_body	62334962
333	cg32591413_TC21	3.2905E-05	-0.03738049	Msra	chr14	-	tss_body	64201299
334	cg32591956_BC21	2.9374E-05	-0.02595609	Msra	chr14	-	tss_body	64268440
335	cg32621834_TC21	6.6166E-05	-0.02752345	Ebf2	chr14	+	tss_body	67255699
336	cg32622448_BC21	0.00023284	-0.06802595	Ebf2	chr14	+	tss_body	67307219
337	cg32624901_BC21	0.00018788	-0.07288265					67536698
338	cg32641735_TC11	0.00088436	0.07725604					69697219

339	cg32683942_TC21	0.00015441	-0.04455903	Gm4278	chr14	+	tss_body	74976550
340	cg32694328_BC21	0.00038976	0.04009405	Gtf2f2	chr14	-	tss_body	75955000
341	cg32708758_BC21	0.00093337	-0.08997786	Enox1	chr14	+	tss_body	77273984
342	cg32734857_TC21	0.00048191	0.03551208	LOC328448	chr14	+	tss_body	79891104
343	cg32735403_BC11	0.00026059	0.03047984	LOC328448	chr14	+	tss_body	79972788
344	cg32737817_TC21	0.00031916	-0.02642624	LOC108168183	chr14	+	tss_body	80342712
345	cg32805816_TC21	0.00034193	0.03058467					94466431
346	cg32867803_TC21	0.00048318	-0.03364992	Gm35197	chr14	+	tss_body	103816997
347	cg32921584_TC21	1.3003E-05	0.05120897					113526921
348	cg32937043_TC21	0.00065417	0.0498483	Gpc5	chr14	+	tss_body	116295842
349	cg32953324_TC21	0.00096677	-0.03349981	Sox21	chr14	-	tss_body	118234232
350	cg32956521_TC21	2.0294E-07	0.02514508	chr14-118473814-118474116	chr14	*	Island	118474104
351	cg32973230_TC21	0.00020493	-0.03906212	Oxgr1	chr14	-	tss_body	120023319
352	cg32976047_BC21	0.00025877	0.06595142	Mbnl2	chr14	+	tss_body	120296752
353	cg32985580_BC21	0.00066301	0.02507253	Farp1	chr14	+	tss_body	121129139
354	cg32986013_BC21	4.2204E-06	-0.04141049	Farp1	chr14	+	tss_body	121164825
355	cg32991112_TC21	0.00041098	-0.03917156	Dock9	chr14	-	tss_body	121567052
356	cg33068238_TC21	0.00072817	0.03626488	Dnajc21	chr15	-	tss_body	10452351
357	cg33068329_TC11	0.00016916	-0.0298875	Dnajc21	chr15	-	tss_body	10461252
358	cg33084122_BC21	1.6954E-06	-0.03353883		chr15	-	tss_body	12196593
359	cg33084416_TC21	0.00057958	0.03035187	Mtmr12	chr15	+	tss_body	12210234
360	cg33154362_BC21	0.00096989	-0.06205812	4930445E18Rik	chr15	-	tss_body	25282473
361	cg33155793_TC21	0.0008077	-0.03640626	Basp1	chr15	-	tss_body	25411708
362	cg33160080_TC21	8.1152E-05	-0.03305632	Myo10	chr15	+	tss_body	25756671
363	cg33160278_BC21	0.0003659	-0.03238833	Myo10	chr15	+	tss_body	25768584
364	cg33175199_BC21	0.00082518	-0.04097504	Ank	chr15	+	tss_body	27581958
365	cg33230186_TC21	0.00030598	-0.03391296	Osr2	chr15	+	tss_body	35300433
366	cg33239447_TC21	5.2257E-05	0.04115416	Ankrd46	chr15	-	tss_1500	36497093
367	cg33246989_BC11	0.00037976	-0.04728042	chr15-37175906-37176318	chr15	*	NShore	37175216
368	cg33259896_BC21	0.00026257	-0.04770731	Gm41308	chr15	+	tss_1500	38472037

369	cg33263063_BC21	0.00074893	0.03937463	Baalc	chr15	+	tss_body	38937844
370	cg33280605_BC21	0.000497	0.02699926	Oxr1	chr15	+	tss_body	41451851
371	cg33334123_BC21	0.00073572	0.05185955					52156926
372	cg33356136_BC21	0.00046775	0.05461228	Col14a1	chr15	+	tss_body	55363302
373	cg33360835_BC21	0.0002494	0.03438692		chr15	+	tss_body	56004139
374	cg33370306_BC21	0.00068841	0.04186509	Zhx2	chr15	+	tss_body	57697732
375	cg33385687_TC21	0.00078452	-0.03674396	Mtss1	chr15	-	tss_body	59040614
376	cg33395657_BC21	0.00010904	0.02707252		chr15	-	tss_200	59994906
377	cg33400265_TC21	0.00025779	-0.06357505		chr15	-	tss_body	60851189
378	cg33409118_BC11	8.051E-05	0.06279062	Pvt1	chr15	+	tss_body	62258701
379	cg33412840_TC21	0.00069158	0.04062937					63007125
380	cg33427578_TC21	0.00022139	-0.02928873		chr15	-	tss_200	65200661
381	cg33437740_BC11	0.00050293	-0.03995205	LOC105245970	chr15	+	tss_body	66972254
382	cg33491236_TC11	0.00014455	0.03166658	Ly6k	chr15	-	tss_body	74797259
383	cg33504602_TC21	0.00028271	-0.05593417	Nrbp2	chr15	-	tss_body	76087831
384	cg33504649_TC11	0.00067568	-0.09380746	Nrbp2	chr15	-	tss_body	76089969
385	cg33505436_BC21	0.00024351	-0.04222747					76136466
386	cg33510046_TC21	1.0852E-05	-0.02523627	chr15-76380219-76380523	chr15	*	NShelf	76377542
387	cg33515176_BC21	0.00024212	-0.03450418	Kifc2	chr15	+	tss_body	76667172
388	cg33532451_BC21	8.4103E-05	-0.03105309	Ift27	chr15	-	tss_body	78170064
389	cg33534732_BC21	1.0554E-05	-0.04499943	Tex33	chr15	-	tss_body	78387336
390	cg33534877_BC21	0.00047876	0.03745356	Tst	chr15	-	tss_body	78402438
391	cg33535601_TC11	0.00070225	-0.03241871	Tmprss6	chr15	-	tss_body	78442290
392	cg33542455_BC21	0.00067528	0.03036534	Gga1	chr15	+	tss_body	78892018
393	cg33556556_BC21	0.00084473	-0.05683404	Gm16576	chr15	+	tss_body	79751964
394	cg33561950_TC21	0.00023452	-0.0532431	Gm31134	chr15	-	tss_body	80091856
395	cg33562072_TC21	5.1363E-06	-0.04462381	Syngr1	chr15	+	tss_body	80098987
396	cg33562073_TC21	5.7799E-06	-0.05389779	Syngr1	chr15	+	tss_body	80099010
397	cg33563703_BC21	0.0005104	-0.02960855	Mgat3	chr15	+	tss_body	80212309
398	cg33567983_BC11	0.0004305	-0.05730753	Enthd1	chr15	-	tss_body	80531146
399	cg33572188_TC21	0.00056722	0.05546436	Tnrc6b	chr15	+	tss_body	80939890

400	cg33574135_TC21	8.5236E-06	-0.04915554	Mkl1	chr15	-	tss_body	81106165
401	cg33588591_TC21	0.00010295	-0.03389075	Tnfrsf13c	chr15	-	tss_body	82221918
402	cg33594178_TC21	0.00047512	-0.03280299	Tcf20	chr15	-	tss_body	82897981
403	cg33597103_TC21	3.6933E-05	-0.03741613		chr15	+	tss_200	83089358
404	cg33599129_BC21	6.0085E-05	0.03667047	A4galt	chr15	-	tss_body	83242680
405	cg33619500_TC21	8.8748E-07	-0.02749529	Arhgap8	chr15	+	tss_body	84755650
406	cg33629010_BC21	0.00016252	-0.03517502	Wnt7b	chr15	-	tss_body	85543891
407	cg33630016_BC21	3.6521E-05	-0.04210999					85600913
408	cg33636248_TC21	8.3915E-05	-0.0418075	Celsr1	chr15	-	tss_body	85997242
409	cg33637216_BC21	5.0646E-05	-0.04995416	Gm41375	chr15	-	tss_body	86056552
410	cg33639772_BC11	4.7045E-05	-0.05248021					86204660
411	cg33673739_TC21	0.00048794	0.03256007	Tymp	chr15	-	tss_200	89377056
412	cg33692983_TC21	0.00068775	0.02767874	Slc2a13	chr15	-	tss_body	91443537
413	cg33703748_BC11	0.00080397	0.03364989	Pdzrn4	chr15	+	tss_body	92679718
414	cg33706099_TC11	0.00031122	0.02785757		chr15	+	tss_body	92946243
415	cg33714777_TC21	0.00020012	-0.05116261					93632587
416	cg33748728_TC11	0.00035842	-0.04476723	Slc38a1	chr15	-	tss_body	96640509
417	cg33750728_TC21	0.00095528	0.03577114					96749037
418	cg33758471_BC21	0.00060089	0.04458852	Pced1b	chr15	+	tss_body	97315292
419	cg33759214_BC21	5.7159E-05	-0.0304654	Pced1b	chr15	+	tss_body	97361077
420	cg33762078_BC21	3.7076E-05	-0.04431469					97583222
421	cg33764186_TC21	3.7748E-05	-0.05203164	Endou	chr15	-	tss_body	97721349
422	cg33764499_BC21	1.8266E-05	-0.03955268	Gm33531	chr15	+	tss_body	97742264
423	cg33772044_TC21	0.00042982	-0.0292059	Olfr287	chr15	-	tss_1500	98221587
424	cg33793231_BC11	0.00039078	0.02884924					99568454
425	cg33797048_BC21	0.0001913	0.03015049	Lima1	chr15	-	tss_body	99800763
426	cg33819764_TC21	0.00014224	-0.04029397		chr15	+	tss_body	101317554
427	cg33819771_TC21	5.4629E-05	-0.04261032		chr15	+	tss_body	101317704
428	cg33821041_TC21	0.00075152	-0.02751124	Q6IMF0	chr15	-	tss_body	101431052
429	cg33833833_TC11	0.00029916	0.0839705	Pcbp2	chr15	+	tss_body	102473443
430	cg33835199_TC21	0.00099445	0.02702802	Gm4544	chr15	+	tss_1500	102656511

431	cg33839638_BC21	0.00026583	-0.03231579	Hoxc8	chr15	+	tss_body	102992583
432	cg33840844_BC21	0.00035725	-0.03102583	chr15-103085923-103086798	chr15	*	NShelf	103082598
433	cg33841859_BC21	0.00024299	-0.03468906	Smug1	chr15	-	tss_1500	103170140
434	cg33852581_BC21	0.00048984	-0.03979082	Naa60	chr16	+	tss_body	3894398
435	cg33853376_TC21	0.00029535	-0.04616788	Nlrc3	chr16	-	tss_body	3976536
436	cg33863384_BC21	5.7995E-06	-0.02535981	Anks3	chr16	-	tss_body	4958037
437	cg33874617_BC11	0.00016071	-0.02694823	Rbfox1	chr16	+	tss_body	6348172
438	cg33879056_TC21	0.00058914	0.07148023	Rbfox1	chr16	+	tss_body	7052257
439	cg33909236_BC21	9.5636E-06	-0.05464252		chr16	-	tss_body	10938344
440	cg33911457_BC21	9.5391E-05	-0.04899743	Zc3h7a	chr16	-	tss_body	11143662
441	cg33928476_BC21	4.7764E-06	-0.0822404	Gm32817	chr16	+	tss_body	13449547
442	cg33936433_BC21	0.00069722	-0.02741072	Abcc1	chr16	+	tss_body	14365699
443	cg33946889_BC21	0.0003383	-0.0491453	Pkp2	chr16	+	tss_body	16223841
444	cg33948880_TC21	1.6784E-05	-0.03151037	Fgd4	chr16	-	tss_body	16560153
445	cg33953149_BC21	0.00024705	-0.02976668	Ccdc116	chr16	-	tss_body	17144405
446	cg33968335_BC21	0.00083789	-0.03763811		chr16	+	tss_body	18484570
447	cg33976135_BC11	0.00084159	0.02934864		chr16	-	tss_body	19521198
448	cg33978582_TC21	0.00026361	-0.02739297	Klhl6	chr16	-	tss_body	19956946
449	cg34011276_TC21	0.00024182	-0.03140101	Adipoq	chr16	+	tss_body	23146630
450	cg34016591_BC21	4.1644E-06	-0.05003047		chr16	-	tss_200	23780198
451	cg34052833_TC21	0.00025529	0.03314894	Hrasls	chr16	+	tss_body	29226230
452	cg34061439_BC21	0.00055628	-0.0417467					30081806
453	cg34063214_TC21	0.00026991	-0.04033985					30233282
454	cg34063228_BC21	4.2251E-05	-0.03469441					30234328
455	cg34076900_TC21	0.00069027	-0.03536262	Bdh1	chr16	+	tss_body	31427923
456	cg34085922_BC21	2.4483E-05	-0.04580816	Mir1946a	chr16	-	tss_body	32267487
457	cg34099800_BC21	0.00059085	-0.04648421	Slc12a8	chr16	+	tss_body	33563444
458	cg34102392_BC21	8.4141E-05	-0.03345729	Muc13	chr16	+	tss_body	33794382
459	cg34122618_BC11	0.00034362	-0.06325783	Sema5b	chr16	+	tss_body	35645351
460	cg34127650_BC21	0.00059455	-0.04533982	Ccdc58	chr16	+	tss_body	36081441
461	cg34149695_TC21	0.00097826	0.03333535	Arhgap31	chr16	-	tss_body	38654890

462	cg34150196_BC21	0.00064632	0.06675456	Arhgap31	chr16	-	tss_body	38700425
463	cg34151458_TC21	0.00031976	0.02740871	Upk1b	chr16	-	tss_1500	38800535
464	cg34152326_BC21	0.00054077	0.0382773	Igsf11	chr16	+	tss_body	38901490
465	cg34190066_BC21	0.00034393	-0.04858894					44691646
466	cg34191706_BC21	3.717E-05	0.02718406	Cd200r3	chr16	+	tss_body	44958380
467	cg34201600_TC21	0.00075915	-0.05623363	Nectin3	chr16	-	tss_body	46438061
468	cg34209957_BC21	0.00045822	-0.03306336	6430553K19Rik	chr16	-	tss_body	48158431
469	cg34220686_BC21	0.00021325	-0.05893955	Gm16619	chr16	+	tss_body	49818823
470	cg34236142_BC21	6.3466E-05	0.09281549	Cblb	chr16	+	tss_body	52078904
471	cg34265359_TC21	0.00091876	0.02549486					57106442
472	cg34327298_TC21	1.1755E-05	0.05333706		chr16	-	tss_body	67736776
473	cg34348737_TC21	0.00051068	-0.04819633	Robo1	chr16	+	tss_body	72088885
474	cg34428566_TC21	3.7618E-05	-0.04245393	App	chr16	-	tss_body	84972435
475	cg34435463_BC11	0.00032968	-0.0298597					85807669
476	cg34449158_BC21	0.00075575	-0.02611754	Gm32925	chr16	+	tss_body	87751377
477	cg34477599_BC21	0.00091775	-0.0421281	Mrap	chr16	+	tss_body	90743192
478	cg34488921_BC21	0.00042732	-0.06348016		chr16	-	tss_200	91540240
479	cg34500654_TC21	1.7303E-06	0.03339739	Kcne1	chr16	-	tss_body	92359399
480	cg34500656_TC21	0.00088728	0.04255983	Gm30163	chr16	+	tss_body	92359499
481	cg34518503_TC21	7.606E-05	-0.04207327	Dopey2	chr16	+	tss_body	93777644
482	cg34528577_BC21	0.0005061	-0.03570696	Gm31323	chr16	+	tss_body	94485276
483	cg34537372_TC21	1.4051E-05	-0.03922785		chr16	-	tss_body	95303676
484	cg34556225_TC21	0.00087896	0.03308575	Bace2	chr16	+	tss_body	97415071
485	cg34556468_TC21	3.6843E-05	-0.060259	Mx1	chr16	-	tss_body	97455493
486	cg34588745_TC21	5.6045E-05	-0.03569108	Synj2	chr17	+	tss_body	5975466
487	cg34588748_BC21	0.00018509	-0.04465027	Synj2	chr17	+	tss_body	5975559
488	cg34590380_BC21	0.00057081	-0.02665505					6098032
489	cg34596803_BC21	0.00077122	-0.02819982	Sytl3	chr17	+	tss_body	6731142
490	cg34598657_TC11	4.5482E-05	-0.06520292					6864834
491	cg34605822_TC21	0.00098418	-0.04082895					7521414
492	cg34646492_BC21	0.00080575	-0.03455699	Agpat4	chr17	+	tss_body	12169348

493	cg34653260_TC21	0.0007472	0.0518658	Igf2r	chr17	-	tss_body	12750659
494	cg34669634_BC21	0.00039768	-0.02908575					14703698
495	cg34680630_BC21	0.00070094	0.03068415					15864413
496	cg34721681_BC21	0.00015236	-0.03108013	Cldn6	chr17	+	tss_200	23679226
497	cg34751833_TC21	1.9996E-05	-0.03452073	Wdr90	chr17	-	tss_body	25847825
498	cg34764260_BC21	0.00037123	-0.02875441					26828288
499	cg34766893_BC21	0.00070653	-0.03929208	Zbtb9	chr17	+	tss_body	26974130
500	cg34773358_BC21	9.7929E-07	-0.03249841					27380184
501	cg34783977_BC21	0.00077643	0.05176265	Anks1	chr17	+	tss_body	28020242
502	cg34789177_TC21	0.00058237	-0.03391338	Fance	chr17	+	tss_1500	28312966
503	cg34797551_BC11	9.2142E-05	-0.03292532	Pnpla1	chr17	+	tss_body	28884263
504	cg34800288_TC21	3.3948E-07	0.03218073	Trp53cor1	chr17	-	tss_body	29079103
505	cg34827585_TC21	0.00051701	-0.03890792	Tff2	chr17	-	tss_body	31141194
506	cg34831665_BC21	0.00011386	-0.05526924	Pde9a	chr17	+	tss_body	31457374
507	cg34833587_TC11	1.4892E-05	-0.03858661	Pknox1	chr17	+	tss_body	31588473
508	cg34838418_BC21	0.00013633	0.03198467					31939450
509	cg34839398_BC21	0.00022725	-0.02535234	Rrp1b	chr17	+	tss_body	32040644
510	cg34859931_TC21	0.00046635	-0.03347176	Col11a2	chr17	+	tss_body	34065702
511	cg34862013_TC21	5.5941E-06	-0.03397298	Tap1	chr17	+	tss_body	34190652
512	cg34862808_BC11	4.8605E-05	-0.0594538	H2-Ob	chr17	+	tss_1500	34239788
513	cg34863671_BC21	0.00063943	-0.03348738	H2-Eb2	chr17	+	tss_body	34325765
514	cg34866135_TC21	0.00023124	-0.03363998	Pbx2	chr17	+	tss_body	34594289
515	cg34866258_BC21	0.00044133	0.03596749	Ager	chr17	+	tss_body	34600574
516	cg34866668_BC21	8.7101E-05	-0.03704057	Egfl8	chr17	-	tss_body	34616500
517	cg34867539_BC21	0.00096754	-0.06850573					34657685
518	cg34870654_BC21	0.00026291	-0.03366618	Cfb	chr17	-	tss_body	34858487
519	cg34872807_BC21	0.00016882	-0.0273312	Hspa1a	chr17	-	tss_1500	34972922
520	cg34873590_BC21	0.00029121	0.0336709	Vars	chr17	+	tss_body	35014052
521	cg34879966_BC21	1.0388E-05	-0.04908599	H2-Q6	chr17	+	tss_body	35425706
522	cg34890974_BC21	0.00094844	0.03665477	chr17-36248872-36249182	chr17	*	NShore	36248596
523	cg34891237_BC21	0.00061473	0.03942726	Trim39	chr17	-	tss_body	36263868

524	cg34895085_TC21	0.00022974	-0.02970807	1700031A10Rik	chr17	+	tss_body	36927852
525	cg34896527_TC21	0.00083906	-0.04651677	Gabbr1	chr17	+	tss_body	37047498
526	cg34911101_TC21	0.00071296	-0.04614881					40052152
527	cg34932670_TC21	0.00013315	-0.03495336	Tdrd6	chr17	-	tss_body	43624617
528	cg34942201_BC21	2.7486E-05	-0.04906777	Runx2	chr17	-	tss_body	44631428
529	cg34951932_TC21	0.00051779	-0.0479255	Nfkbie	chr17	+	tss_body	45558288
530	cg34954619_BC21	0.00068478	-0.03804002	Gm35456	chr17	-	tss_body	45719751
531	cg34960002_TC11	0.00086778	-0.06006093					46104723
532	cg34976713_TC21	0.00090074	-0.03344081	Trerf1	chr17	+	tss_body	47148705
533	cg34982290_TC21	0.00019641	0.03317714	Ccnd3	chr17	+	tss_body	47512775
534	cg34993376_BC21	0.00030346	-0.02778227	Treml1	chr17	+	tss_200	48359843
535	cg35000236_BC21	0.00081399	-0.02552448	Lrfn2	chr17	+	tss_body	48994803
536	cg35006756_TC21	0.00024806	0.0801685	Kif6	chr17	+	tss_body	49691465
537	cg35006762_TC11	6.8191E-05	0.08434292	Kif6	chr17	+	tss_body	49691652
538	cg35013138_TC21	0.00032822	-0.04609045	AY702103	chr17	+	tss_body	50244771
539	cg35026125_TC21	0.0004724	-0.02544938	Gm20098	chr17	+	tss_body	51906958
540	cg35026837_TC21	4.7614E-06	-0.035185		chr17	+	tss_body	51986447
541	cg35026838_TC21	0.00077346	-0.03723178		chr17	+	tss_body	51986459
542	cg35046739_TC21	0.00098505	-0.02784388	Adgre4	chr17	+	tss_body	55768293
543	cg35050429_TC11	0.00098726	-0.07755961	Sema6b	chr17	-	tss_body	56124822
544	cg35050433_BC21	0.00086144	-0.04380658	Sema6b	chr17	-	tss_body	56124853
545	cg35057137_TC21	0.0004932	-0.03174255					56547952
546	cg35065815_BC21	4.3317E-05	-0.04257759					57189044
547	cg35099859_TC21	0.00099046	-0.03812029	Fbxl17	chr17	-	tss_body	63220867
548	cg35115166_BC21	0.0005725	-0.07192844					64915999
549	cg35120856_TC21	0.0005484	0.05418031	Vapa	chr17	-	tss_body	65601105
550	cg35148365_TC21	0.00034921	-0.04113292	Arhgap28	chr17	-	tss_body	67950828
551	cg35245466_BC21	0.00012195	-0.05712941	Gm10494	chr17	-	tss_body	79509378
552	cg35261998_BC11	5.2383E-05	-0.05889174	Tmem178	chr17	+	tss_body	81001013
553	cg35276308_BC21	9.9135E-05	-0.05170001					83164577
554	cg35278811_BC21	0.0003117	0.02589251					83343329

555	cg35286804_TC21	4.7594E-06	-0.07394988	Gm41638	chr17	-	tss_1500	83961124
556	cg35313122_TC21	0.00011996	0.06955913	Srbd1	chr17	-	tss_body	86136116
557	cg35314960_TC21	0.00056982	-0.04094589	Prkce	chr17	+	tss_body	86256877
558	cg35315638_TC21	0.00097105	-0.03972424	Prkce	chr17	+	tss_body	86303896
559	cg35324447_TC11	7.7858E-05	0.04124426	Rhoq	chr17	+	tss_body	86966208
560	cg35336686_TC11	0.00050508	0.04016026		chr17	+	tss_body	87826231
561	cg35336692_BC11	0.00027085	0.05941055		chr17	+	tss_body	87826364
562	cg35348746_BC21	0.00019961	0.03122601					88966231
563	cg35359621_TC21	2.3923E-05	-0.03815149	Nrxn1	chr17	-	tss_body	91088940
564	cg35404105_TC21	0.00081204	-0.04018638	Armc4	chr18	-	tss_body	7297421
565	cg35406328_TC21	0.00092121	-0.03023941					7636795
566	cg35443749_BC11	0.0002011	-0.02557236	Impact	chr18	+	tss_body	12973000
567	cg35453586_TC21	0.00062395	-0.02533466	8430422H06Rik	chr18	+	tss_200	14232195
568	cg35459599_BC21	0.00053594	-0.03127926	Kctd1	chr18	-	tss_body	15001889
569	cg35463205_BC11	0.00099208	0.04112527	Aqp4	chr18	-	tss_body	15401142
570	cg35486110_BC21	3.5517E-05	-0.05424121					20214163
571	cg35510375_BC11	6.8722E-06	0.05844557	Mapre2	chr18	+	tss_body	23857085
572	cg35512683_TC21	0.00086279	-0.03731442		chr18	-	tss_body	24081739
573	cg35525053_BC11	0.00028537	-0.0254851	Celf4	chr18	-	tss_body	25554628
574	cg35525707_BC11	5.096E-06	0.0623778	Celf4	chr18	-	tss_body	25607686
575	cg35557789_TC21	0.00092827	0.05431007	Wdr33	chr18	+	tss_body	31825349
576	cg35564237_TC21	1.9982E-05	0.03216006	Gm35060	chr18	-	tss_body	32462509
577	cg35564878_TC21	3.7235E-05	0.03964333	Gypc	chr18	-	tss_body	32547790
578	cg35588001_BC11	0.00018473	0.03690275	Gm36037	chr18	+	tss_body	35046877
579	cg35588396_BC21	0.00041937	-0.04665115		chr18	+	tss_body	35092998
580	cg35595950_BC21	0.00046658	-0.03439268	chr18-35860500-35860796	chr18	*	SShore	35862104
581	cg35596537_TC21	1.0016E-06	-0.07498542					35895154
582	cg35601962_BC21	0.00073019	-0.03380617	Cystm1	chr18	+	tss_1500	36348381
583	cg35605279_TC21	0.00086043	0.0252711	E230025N22Rik	chr18	-	tss_body	36692213
584	cg35612025_BC21	0.00013913	-0.02930341	Gm37013	chr18	+	tss_body	37357495
585	cg35616800_BC21	0.00018914	0.04738638	Gm37013	chr18	+	tss_body	37765901

586	cg35617601_TC21	0.00017161	0.03961354	Gm37013	chr18	+	tss_body	37820416
587	cg35623059_TC21	0.00044719	0.05211958	0610009O20Rik	chr18	+	tss_body	38250977
588	cg35623099_BC21	2.7808E-06	-0.03158094	0610009O20Rik	chr18	+	tss_body	38253716
589	cg35629231_BC21	0.00023704	-0.05014067	Arhgap26	chr18	+	tss_body	38795621
590	cg35629232_BC21	0.00015949	-0.03576585	Arhgap26	chr18	+	tss_body	38795648
591	cg35632890_BC21	3.6826E-05	-0.03091759	Arhgap26	chr18	+	tss_body	39150110
592	cg35633788_BC21	3.0654E-07	-0.03958393	Arhgap26	chr18	+	tss_body	39251042
593	cg35686882_TC21	2.9314E-05	-0.04734907					46915040
594	cg35694158_TC21	0.00042137	-0.04928002	Gm5095	chr18	+	tss_body	47646616
595	cg35721855_TC21	0.0008197	0.02996103	Zfp474	chr18	+	tss_body	52616043
596	cg35757575_BC21	0.00080554	-0.07005684					56696189
597	cg35790052_BC11	4.2181E-05	0.02567983	Ndst1	chr18	-	tss_body	60746512
598	cg35793138_BC21	0.00047698	-0.05563693	Camk2a	chr18	+	tss_body	60963439
599	cg35794369_BC21	2.7752E-05	-0.03196164	chr18-61035675-61036479	chr18	*	SShore	61037900
600	cg35794668_BC21	3.3184E-05	-0.04286588	Pdgfrb	chr18	+	tss_body	61056874
601	cg35798040_TC21	1.1367E-05	-0.03355492	Ppargc1b	chr18	-	tss_body	61315523
602	cg35803854_BC11	0.00025331	0.04771633	Afap1l1	chr18	-	tss_body	61776706
603	cg35826377_BC21	0.00068536	0.03063667		chr18	-	tss_body	64288409
604	cg35831324_TC21	0.00059397	0.05121368		chr18	-	tss_body	64700014
605	cg35832502_TC21	0.00025363	-0.05824738	LOC108168399	chr18	+	tss_body	64858551
606	cg35838956_TC21	1.2473E-05	-0.04236171	Alpk2	chr18	-	tss_body	65376227
607	cg35848420_BC21	0.00055896	-0.04527504	Ccbe1	chr18	-	tss_body	66190916
608	cg35851619_BC21	0.00091727	-0.0384326	Gm9926	chr18	+	tss_body	66509648
609	cg35868888_BC21	6.0239E-05	-0.04934098	Ldlrad4	chr18	+	tss_body	68160132
610	cg35871912_BC21	0.00028054	-0.03408568	Gm29677	chr18	+	tss_body	68472082
611	cg35882359_TC21	0.00052739	-0.0526721	Tcf4	chr18	+	tss_body	69519350
612	cg35897621_TC11	0.00038594	0.03864027	Dcc	chr18	-	tss_body	71491035
613	cg35911618_TC21	0.00092731	0.07997547	Smad4	chr18	-	tss_body	73700485
614	cg35912902_BC21	0.00058135	0.04576428	Me2	chr18	-	tss_body	73781626
615	cg35937184_TC21	0.00091312	-0.0430955	Ctif	chr18	-	tss_body	75669714
616	cg35942199_BC21	9.6591E-05	-0.10475281	Zbtb7c	chr18	+	tss_body	76085722

617	cg35947367_BC21	4.83E-06	0.03711609					76560096
618	cg35988459_BC21	6.3506E-06	0.02991196					80565830
619	cg35996383_BC21	0.0002393	0.03171401					81192734
620	cg36009903_BC21	0.00010082	0.03999217	Mbp	chr18	+	tss_body	82564692
621	cg36017677_BC21	0.00096429	-0.03536901	LOC108168396	chr18	+	tss_body	83076530
622	cg36045367_BC21	0.00012143	-0.03116503	Neto1	chr18	+	tss_body	86499020
623	cg36064484_TC11	0.00055222	0.04412076	Mrpl21	chr19	+	tss_body	3289132
624	cg36072497_TC21	1.8124E-05	-0.07786652	Tbx10	chr19	+	tss_1500	3992585
625	cg36073679_BC11	0.00058119	-0.03232413	Cabp2	chr19	+	tss_body	4083594
626	cg36094509_TC21	0.00095252	0.04762551	Ap5b1	chr19	+	tss_body	5567205
627	cg36096153_TC11	0.00067416	-0.05035684	Sipa1	chr19	-	tss_body	5660949
628	cg36109935_BC21	0.00077261	-0.03391713	Nrxn2	chr19	+	tss_body	6464593
629	cg36117439_TC21	0.00032416	-0.02567159	Macrod1	chr19	+	tss_body	7069577
630	cg36119316_TC21	0.00017691	-0.03416525	Macrod1	chr19	+	tss_body	7189804
631	cg36135914_TC21	0.00064284	0.08432318	Scgb1a1	chr19	-	tss_body	9087892
632	cg36147289_BC21	0.00013409	-0.06073851	Syt7	chr19	+	tss_body	10451108
633	cg36149480_BC21	0.00024244	0.03547364	Vwce	chr19	+	tss_body	10642565
634	cg36152756_BC21	0.00085067	-0.03134967	Zp1	chr19	-	tss_body	10916834
635	cg36165183_TC21	0.00072297	0.03753957	A0A494BA26	chr19	+	tss_body	12846828
636	cg36174321_BC21	0.0001661	-0.04766183	Tle4	chr19	-	tss_1500	14599414
637	cg36187925_BC21	0.00061886	-0.03540928	Gna14	chr19	+	tss_body	16436859
638	cg36194026_BC21	0.00061691	-0.06992354	Prune2	chr19	+	tss_body	17137447
639	cg36239860_BC21	0.00032681	-0.02942585	Ptar1	chr19	+	tss_body	23700043
640	cg36243664_BC21	0.00090077	0.06153052	Fam189a2	chr19	-	tss_body	24024798
641	cg36247698_TC21	0.00055732	-0.04122326	Pip5k1b	chr19	-	tss_body	24339644
642	cg36285037_BC21	0.00023744	-0.0421085	Glis3	chr19	-	tss_body	28383080
643	cg36318896_BC21	0.00026009	0.0603983	Sgms1	chr19	-	tss_body	32179184
644	cg36348999_TC21	3.0279E-05	-0.03715133	Pcgf5	chr19	+	tss_body	36368634
645	cg36355756_TC21	3.8994E-05	-0.06010268	Cpeb3	chr19	-	tss_body	37073670
646	cg36362488_BC21	0.00080486	-0.04007279	Gm32342	chr19	-	tss_body	37686656
647	cg36365185_TC21	0.00050963	-0.03111318	Myof	chr19	-	tss_body	37923639

648	cg36384358_BC11	0.0003056	-0.04957218	Sorbs1	chr19	-	tss_body	40406035
649	cg36420590_BC21	0.00061751	0.04249955	Gm34636	chr19	-	tss_body	43567436
650	cg36426137_BC21	3.0516E-05	-0.06373714	Dnmbp	chr19	-	tss_body	43920544
651	cg36429899_TC11	0.00099339	-0.03017243	Pkd2l1	chr19	-	tss_body	44238287
652	cg36434530_BC21	0.00082699	-0.02776					44583746
653	cg36440188_TC21	0.0007669	-0.05614909	Sema4g	chr19	+	tss_1500	44988185
654	cg36442350_BC21	1.4632E-08	-0.0326068		chr19	+	tss_body	45086656
655	cg36451687_TC21	1.6793E-06	0.03604844	Mgea5	chr19	-	tss_body	45765605
656	cg36481047_TC21	0.00012041	0.04640692	Gsto2	chr19	+	tss_body	47870228
657	cg36487086_TC21	0.00069493	0.03119754	Sorcs3	chr19	+	tss_body	48378299
658	cg36491152_BC21	0.00060394	0.03947896		chr19	+	tss_200	48992018
659	cg36514792_BC21	0.00096937	-0.03821047	Gm30234	chr19	-	tss_body	53059384
660	cg36520722_TC21	0.00023028	-0.03754351	Mirt1	chr19	-	tss_body	53451334
661	cg36522208_TC21	0.00026627	-0.03968851					53552619
662	cg36525247_BC11	8.718E-05	0.04298618	Rbm20	chr19	+	tss_body	53793316
663	cg36526548_BC21	0.00092676	0.02673629	Gm30990	chr19	-	tss_body	53894644
664	cg36541907_BC21	0.00027687	-0.0642803	Vti1a	chr19	+	tss_body	55552996
665	cg36564121_TC21	0.00078206	0.08336544	Ablim1	chr19	-	tss_body	57182287
666	cg36574956_BC21	0.00022195	-0.05414018	Atrnl1	chr19	+	tss_body	58051122
667	cg36578422_TC21	0.00069521	-0.04291947	Gfra1	chr19	-	tss_body	58345221
668	cg36579235_BC21	0.00022305	0.0401529	Gfra1	chr19	-	tss_body	58415330
669	cg36587375_BC21	0.00025102	-0.03753373	4930442E04Rik	chr19	+	tss_1500	59171294
670	cg36634086_BC21	7.7029E-05	-0.02541803	Sntg1	chr1	-	tss_body	8963611
671	cg36689411_TC21	5.2643E-06	0.02638518	Crispld1	chr1	+	tss_body	17758611
672	cg36788409_BC21	0.00030867	-0.04286631	Prss39	chr1	+	tss_body	34502826
673	cg36804601_BC11	3.5836E-05	0.0258615	Arid5a	chr1	+	tss_body	36321912
674	cg36843166_TC21	0.00068027	-0.03278453					39663837
675	cg36847030_BC21	0.00042247	0.09152663	Map4k4	chr1	+	tss_body	39972718
676	cg36901949_TC21	0.00088737	0.04640327		chr1	+	tss_200	48527492
677	cg36939728_TC21	0.00053689	-0.0609458	Ankrd44	chr1	-	tss_body	54802904
678	cg36947404_BC21	0.00077239	-0.04843888	Plcl1	chr1	+	tss_body	55733765

679	cg36959034_BC21	0.00056718	-0.04107507					57449198
680	cg36964169_BC21	0.00021332	-0.04086253	Aox1	chr1	+	tss_body	58054967
681	cg36991065_BC21	0.00073165	-0.04499326					61203672
682	cg36995391_BC21	2.9953E-05	-0.03806209	Pard3b	chr1	+	tss_body	61912274
683	cg37083501_TC21	0.00054449	-0.02597437	Rufy4	chr1	+	tss_body	74133602
684	cg37086724_BC21	0.00024669	0.04283165	Ctdsp1	chr1	+	tss_body	74394145
685	cg37095620_TC21	0.00012412	-0.05214057	Glb1l	chr1	-	tss_body	75209635
686	cg37096615_BC21	0.00017533	-0.05171723	Ptprn	chr1	-	tss_1500	75264782
687	cg37103199_TC21	0.00014542	-0.03382286					75685808
688	cg37111352_TC21	0.00030811	-0.05994271		chr1	-	tss_body	76975910
689	cg37115115_TC21	0.00067016	-0.04150624	Epha4	chr1	-	tss_body	77446714
690	cg37115703_BC21	0.00067504	-0.02751665	Epha4	chr1	-	tss_body	77512993
691	cg37136517_BC21	0.00069577	-0.02982193		chr1	+	tss_body	80186898
692	cg37164442_BC21	0.00019895	0.03200919	Dner	chr1	-	tss_body	84690529
693	cg37185858_BC21	2.3818E-05	-0.05268001	Prss56	chr1	+	tss_1500	87182835
694	cg37186236_BC21	0.00012277	-0.03474887	Chrng	chr1	+	tss_1500	87205602
695	cg37190273_TC21	0.00056833	-0.03722646	Inpp5d	chr1	+	tss_body	87620451
696	cg37198993_BC21	4.6704E-05	0.03215733		chr1	+	tss_body	88656396
697	cg37200103_TC21	0.00016829	-0.0636623					88757232
698	cg37206315_BC21	0.00014284	-0.03447482	C030007H22Rik	chr1	-	tss_body	89394668
699	cg37208566_TC21	9.2734E-05	-0.06691261	Agap1	chr1	+	tss_body	89579759
700	cg37214580_BC21	0.00030748	-0.0365781	Asb18	chr1	-	tss_body	89968920
701	cg37224789_TC21	0.000835	-0.05278663		chr1	-	tss_body	90975094
702	cg37247587_TC21	0.00042497	-0.07475785	Kif1a	chr1	-	tss_1500	93102783
703	cg37251863_TC21	0.00056992	0.05039006	Sept2	chr1	+	tss_body	93487772
704	cg37275268_TC21	0.00022384	0.03144692	F6TGI4	chr1	-	tss_body	97802687
705	cg37316964_BC21	1.2302E-05	0.0265826	Bcl2	chr1	-	tss_body	106630458
706	cg37367507_TC21	0.00028756	0.06685002	Clasp1	chr1	+	tss_body	118483940
707	cg37369081_TC21	8.0849E-05	0.03132535	Tfcp2l1	chr1	+	tss_body	118669070
708	cg37388624_BC11	3.0006E-05	-0.04645543	En1	chr1	+	tss_body	120607917
709	cg37421770_BC21	7.9033E-05	-0.03747851	Nckap5	chr1	-	tss_body	126493072

710	cg37438699_TC21	0.00035739	-0.04252077					128567818
711	cg37456347_TC21	3.8436E-05	-0.02762952	Rassf5	chr1	-	tss_body	131212575
712	cg37457282_TC21	0.00097368	-0.04519749	Ikbke	chr1	-	tss_body	131279249
713	cg37465773_TC21	0.00082263	-0.07587509	Gm29695	chr1	+	tss_body	132198320
714	cg37478056_BC21	6.4175E-06	-0.05143463	Plekha6	chr1	+	tss_body	133201310
715	cg37479942_TC21	0.00073819	-0.02677458	Ren1	chr1	+	tss_body	133350850
716	cg37506027_TC21	0.00035299	0.03237478	Nav1	chr1	-	tss_body	135568407
717	cg37506267_BC21	0.00067921	-0.03534969	Nav1	chr1	-	tss_body	135585104
718	cg37511525_TC21	0.00026835	-0.0327645	Igfn1	chr1	-	tss_body	136008254
719	cg37512450_TC21	0.00017911	0.04518246	Cacna1s	chr1	+	tss_body	136086016
720	cg37512978_TC21	0.00048267	-0.0406279		chr1	-	tss_body	136126433
721	cg37521323_BC21	0.00017577	-0.03773723		chr1	-	tss_1500	136758946
722	cg37526138_BC21	0.00034911	-0.03962833					137221216
723	cg37536817_BC21	0.00039527	-0.03084128	Lhx9	chr1	-	tss_body	138832415
724	cg37562440_TC21	0.00034527	-0.05856751					143916643
725	cg37597641_BC21	2.4977E-05	-0.02811704	A0A286YD13	chr1	+	tss_body	151192953
726	cg37624755_TC21	0.00064262	-0.03597771					153705182
727	cg37625988_TC21	0.00085447	0.03432947	Rgsl1	chr1	-	tss_body	153822676
728	cg37633518_BC21	0.00061083	-0.03894497	Cacna1e	chr1	-	tss_body	154791463
729	cg37647583_TC11	0.00053463	0.04707131	Gm30472	chr1	+	tss_body	156222629
730	cg37650124_BC21	0.00074809	-0.0338397	Gm39682	chr1	+	tss_body	156476783
731	cg37714560_TC21	0.00069946	-0.04124634	Xcl1	chr1	-	tss_1500	164935833
732	cg37721136_TC21	0.00018019	-0.06360458	Mpzl1	chr1	-	tss_body	165618779
733	cg37723305_TC21	1.0294E-05	0.02606435					165775661
734	cg37736982_TC21	0.00079293	0.04374886	Uck2	chr1	-	tss_body	167235754
735	cg37739279_TC21	0.00019513	0.03524625	Mgst3	chr1	-	tss_body	167382277
736	cg37744696_TC11	0.00034891	0.03419901					167893572
737	cg37756326_TC21	2.0846E-05	-0.03955639	Gm34535	chr1	+	tss_1500	169462666
738	cg37763557_BC21	9.5139E-05	-0.02695558					170294944
739	cg37769602_TC21	0.00012049	-0.03252019	Fcrlb	chr1	-	tss_body	170908785
740	cg37773796_BC21	0.00075567	0.04614383	Fcer1g	chr1	-	tss_body	171230693

741	cg37774713_BC11	0.00018888	0.02887306	Ppox	chr1	-	tss_1500	171282256
742	cg37781657_TC11	6.2742E-05	0.03887573					171983268
743	cg37787354_BC21	5.3763E-06	0.04713626					172406585
744	cg37794765_BC21	0.00027975	-0.03802797	Aim2	chr1	+	tss_body	173420439
745	cg37815435_TC21	0.00086837	0.04915835	Cep170	chr1	-	tss_body	176754590
746	cg37816935_BC11	3.0189E-05	-0.04903249	Sdccag8	chr1	+	tss_body	176934652
747	cg37850400_BC21	0.00028139	-0.03975398	Itpkb	chr1	+	tss_body	180421277
748	cg37856881_TC21	0.00015749	0.04605123					180919895
749	cg37857447_BC21	3.1705E-05	0.04878513	Tmem63a	chr1	+	tss_body	180958169
750	cg37887327_TC11	9.8362E-05	0.04855686	Gm39724	chr1	+	tss_body	183656754
751	cg37892937_BC21	0.00043234	-0.05184702		chr1	+	tss_200	184358310
752	cg37922386_BC21	0.0003143	-0.04770261	Gpatch2	chr1	+	tss_body	187303021
753	cg37943995_BC21	0.00076319	-0.06919687					189550272
754	cg37984274_TC21	0.0005313	-0.02762874	Hsd11b1	chr1	-	tss_body	193241630
755	cg37985099_BC21	0.00075846	-0.05760995	Lamb3	chr1	+	tss_body	193338385
756	cg37991541_BC21	0.00094366	-0.03203058	Plxna2	chr1	+	tss_body	194635626
757	cg38005998_TC21	0.00065447	-0.03716521	Frmd4a	chr2	+	tss_body	4340008
758	cg38007126_TC21	0.00024579	-0.04959351	Frmd4a	chr2	+	tss_body	4454616
759	cg38008146_BC21	8.0666E-06	0.04765667	Frmd4a	chr2	+	tss_body	4547153
760	cg38016643_TC21	0.00063029	0.04462951	Camk1d	chr2	-	tss_body	5327286
761	cg38035143_BC21	0.00016671	-0.06196174	Celf2	chr2	-	tss_body	7395757
762	cg38037454_TC21	7.7217E-07	0.02598969					7866375
763	cg38066534_TC21	0.0005676	-0.05842228	Il15ra	chr2	+	tss_body	11712721
764	cg38076415_BC21	0.00017594	0.02517837	Rsu1	chr2	-	tss_body	13222218
765	cg38107896_BC21	7.2082E-05	0.03582976					18635009
766	cg38145010_TC21	0.00052738	-0.03828049	Pax8	chr2	-	tss_body	24475144
767	cg38165312_BC21	6.7236E-05	0.0393728	Qsox2	chr2	-	tss_body	26222483
768	cg38167502_BC21	0.0008237	0.02528316	Pmpca	chr2	+	tss_body	26393521
769	cg38169960_TC21	0.00029935	-0.02700614	Egfl7	chr2	+	tss_body	26587698
770	cg38172770_BC21	0.00083502	0.0255396	Surf1	chr2	-	tss_body	26913621
771	cg38180518_TC21	0.0002789	-0.05019928					27554523

772	cg38186721_TC11	0.000558	0.05841208	F730016J06Rik	chr2	+	tss_body	28119414
773	cg38209960_TC21	0.00022082	-0.02597168	Set	chr2	+	tss_1500	30061534
774	cg38218479_TC11	0.00049226	0.03264179	Gm32316	chr2	-	tss_body	30655054
775	cg38218876_TC21	0.00069508	-0.03977158	Gm14486	chr2	-	tss_body	30677671
776	cg38224879_TC21	7.4922E-05	0.03530275	Fnbp1	chr2	-	tss_body	31080839
777	cg38225725_BC21	0.00045849	-0.03550959	Fnbp1	chr2	-	tss_body	31140326
778	cg38236454_BC21	0.00015973	0.0539393	Lamc3	chr2	+	tss_body	31925175
779	cg38243308_TC21	0.00014049	0.0551077	Ciz1	chr2	+	tss_body	32374073
780	cg38247235_BC21	7.7721E-05	-0.03229594					32640725
781	cg38247933_BC21	0.00076352	-0.03914382	Fpgs	chr2	-	tss_body	32687973
782	cg38249143_TC11	0.00085565	0.09389603	Sh2d3c	chr2	+	tss_body	32751988
783	cg38252430_TC21	0.00029075	-0.08561818	Rpl12	chr2	+	tss_body	32962930
784	cg38263561_TC21	0.00085877	-0.04126399	Mvb12b	chr2	-	tss_body	33876578
785	cg38272105_TC21	0.00019164	0.02621913	Hspa5	chr2	+	tss_body	34774392
786	cg38277518_TC21	4.606E-05	-0.03281541	Gsn	chr2	+	tss_body	35260076
787	cg38277621_BC21	0.00014429	0.02814392	Gsn	chr2	+	tss_body	35269104
788	cg38282042_TC21	0.00030724	0.0695217	Dab2ip	chr2	+	tss_body	35651553
789	cg38300911_BC21	0.00068489	0.02554306	Lhx2	chr2	+	tss_body	38366724
790	cg38302562_BC21	0.00069495	-0.03788267	Nek6	chr2	+	tss_body	38536169
791	cg38359367_BC21	0.00023403	0.02863986					49368265
792	cg38363741_TC21	0.00010829	-0.03509786	Lypd6b	chr2	+	tss_body	49803633
793	cg38367026_BC21	0.00022556	-0.05220507	Lypd6	chr2	+	tss_body	50184664
794	cg38379485_TC21	3.9306E-05	-0.03787448	chr2-51934710-51935070	chr2	*	SShelf	51938635
795	cg38409942_TC21	2.9416E-06	-0.03063403	Nr4a2	chr2	-	tss_1500	57124759
796	cg38419554_BC21	0.00071376	0.06267722	Acvr1	chr2	-	tss_body	58489285
797	cg38430685_BC21	8.9343E-07	-0.07192383	Tanc1	chr2	+	tss_body	59647639
798	cg38431273_TC21	5.1047E-05	-0.06045751	Tanc1	chr2	+	tss_body	59689021
799	cg38438559_BC21	0.00091155	0.03991666	Ly75	chr2	-	tss_body	60317329
800	cg38442804_TC21	0.00021563	0.03281026					60747512
801	cg38443740_TC11	0.00039609	0.04408482	Rbms1	chr2	-	tss_body	60827410
802	cg38527406_BC11	0.00059852	-0.02582567	Gm17250	chr2	-	tss_body	71748574

803	cg38529075_BC21	3.2895E-05	-0.05825355	Pdk1	chr2	+	tss_body	71875447
804	cg38544388_TC21	0.00067261	-0.0709123		chr2	+	tss_body	73281420
805	cg38563323_BC21	0.00067603	-0.04658645					75090377
806	cg38564655_BC21	0.00048547	-0.02667834	LOC102635707	chr2	+	tss_body	75209199
807	cg38572185_TC21	4.0003E-05	-0.05988843					75960708
808	cg38582239_TC21	0.00029773	-0.03474367	Ttn	chr2	-	tss_body	76814404
809	cg38583623_TC21	0.00068944	0.06225032	Ttn	chr2	-	tss_body	76932238
810	cg38586728_BC21	0.00013052	-0.03345193	Sestd1	chr2	-	tss_body	77265931
811	cg38590300_TC11	0.00034616	-0.02911499	Zfp385b	chr2	-	tss_body	77618299
812	cg38603474_TC11	0.00074536	0.03173565					79528519
813	cg38632610_TC21	0.0007775	0.03918563	Tfpi	chr2	-	tss_body	84474080
814	cg38633051_BC21	0.00025566	-0.03193329		chr2	-	tss_body	84530316
815	cg38644477_BC21	0.0003597	-0.02577627	Olfr1040	chr2	-	tss_1500	86148133
816	cg38651123_TC21	6.0275E-05	0.025796	Olfr1141	chr2	-	tss_body	87753694
817	cg38652099_TC11	0.00065547	0.04008441	Olfr74	chr2	-	tss_body	87974564
818	cg38656603_BC11	0.00076954	-0.02560737	Olfr1222	chr2	-	tss_body	89125300
819	cg38668514_TC21	0.00051483	-0.0552951					91079333
820	cg38668546_BC21	0.00047837	-0.05469632	Spi1	chr2	+	tss_1500	91082022
821	cg38690706_TC21	0.00019106	0.04211282					93170289
822	cg38712640_BC21	0.00045766	0.03547437					96105272
823	cg38749916_TC21	2.7322E-05	0.03149655	Ehf	chr2	-	tss_body	103300362
824	cg38752712_BC11	0.00024908	-0.04531353	Abtb2	chr2	+	tss_body	103595249
825	cg38758959_TC21	1.078E-06	-0.07863689	D430041D05Rik	chr2	-	tss_body	104220144
826	cg38762439_BC21	3.3083E-05	-0.03634597		chr2	-	tss_body	104583642
827	cg38794243_TC21	0.00018386	0.03699318		chr2	+	tss_body	109477097
828	cg38850116_TC21	0.00094128	-0.04248185	Thbs1	chr2	+	tss_body	118125548
829	cg38874336_BC21	0.00051872	-0.06373755	Pla2g4f	chr2	-	tss_body	120302804
830	cg38910905_BC21	0.00091181	0.03274491	Slc12a1	chr2	+	tss_body	125153974
831	cg38939508_BC21	0.00013405	0.03153026	Gm14009	chr2	+	tss_body	128172504
832	cg38953481_TC21	8.3528E-05	-0.05190489	Sirpa	chr2	+	tss_body	129602054
833	cg38954191_TC21	4.7642E-05	0.03341985					129677650

834	cg38957472_BC21	0.00072222	-0.02822363	Tgm3	chr2	+	tss_body	130040435
835	cg38959845_BC21	0.00060793	-0.02646993	Ebf4	chr2	+	tss_body	130297070
836	cg38960010_TC21	6.7497E-05	-0.03587723	Ebf4	chr2	+	tss_body	130309714
837	cg38961058_TC21	0.0001232	-0.03010313	Tmem239	chr2	+	tss_1500	130405755
838	cg38963002_TC21	0.00057479	-0.0557707	chr2-130580656-130581246	chr2	*	NShore	130579468
839	cg38967491_BC21	0.0001193	-0.02638674	Gfra4	chr2	-	tss_body	131042895
840	cg38969541_BC11	0.00012034	-0.02908057	Cdc25b	chr2	+	tss_body	131191173
841	cg38976264_TC21	0.00039757	-0.02500423	Prn	chr2	+	tss_body	131955531
842	cg38989543_TC21	0.00063543	-0.03012095					133473094
843	cg39038948_TC21	0.00042314	0.02725289	Macrod2	chr2	+	tss_body	141837500
844	cg39057554_BC21	0.0003162	0.0353636	LOC108168801	chr2	-	tss_1500	144422280
845	cg39073814_TC21	0.00075864	-0.06156046	Ralgapa2	chr2	-	tss_body	146415539
846	cg39085287_BC21	1.0542E-06	0.04817513					147928866
847	cg39088453_BC21	1.8449E-05	-0.03925223	Sstr4	chr2	+	tss_200	148395194
848	cg39111055_TC11	0.00047284	0.03121479	Rspo4	chr2	+	tss_body	151871948
849	cg39126495_TC21	0.00020618	-0.02878233	Hck	chr2	+	tss_body	153108860
850	cg39128618_BC11	0.00020984	0.03421818	Kif3b	chr2	+	tss_body	153308688
851	cg39133277_BC11	0.00032905	-0.07271388					153694693
852	cg39133278_BC21	0.00066478	-0.04085125					153694712
853	cg39150310_TC21	0.00082993	-0.03945287	Ggt7	chr2	-	tss_body	155506487
854	cg39153185_TC21	9.6731E-07	0.02662312					155735409
855	cg39162328_TC21	0.00014106	0.03739987	Epb41l1	chr2	+	tss_body	156446191
856	cg39171082_TC21	0.00062675	-0.0391012	Soga1	chr2	-	tss_body	157064150
857	cg39171481_BC21	0.00015494	-0.0525413	Tldc2	chr2	+	tss_body	157079840
858	cg39206433_TC21	4.8107E-05	-0.02883369					160537608
859	cg39208516_TC21	0.00052979	-0.03513249	Plcg1	chr2	+	tss_body	160744743
860	cg39213697_BC21	0.00010724	-0.025715					161340396
861	cg39222009_BC21	0.00099442	0.04498284	Ptprt	chr2	-	tss_body	162610823
862	cg39224961_TC21	0.00068541	-0.03118243	chr2-162908307-162908538	chr2	*	SShelf	162912064
863	cg39240796_BC21	0.0001602	0.03811793	Stk4	chr2	+	tss_body	164082495

864	cg39244860_TC21	0.00091017	-0.02782156					164419179
865	cg39253567_TC21	0.00042034	-0.02618053	Slc12a5	chr2	+	tss_body	164986404
866	cg39272146_BC11	0.00054853	-0.05459394		chr2	-	tss_1500	166209426
867	cg39274210_TC11	0.00056141	-0.05256127	Gm14268	chr2	-	tss_body	166354135
868	cg39282276_BC11	0.00038532	0.05259249	Gm31204	chr2	-	tss_body	166905707
869	cg39284881_BC11	0.00076415	0.03191699	Kcnb1	chr2	-	tss_body	167105024
870	cg39286124_BC21	0.00074649	-0.03976466	Kcnb1	chr2	-	tss_body	167186911
871	cg39288502_BC21	0.00094892	-0.02999995	B4galt5	chr2	-	tss_body	167345329
872	cg39305879_BC21	0.00015813	-0.04076702					168474939
873	cg39308309_BC21	0.00023259	-0.03009544	chr2-168619254-168619522	chr2	*	NShore	168618707
874	cg39321350_BC21	0.00027811	-0.03388027	Gm34112	chr2	-	tss_body	169494177
875	cg39338287_TC21	0.00068252	-0.03039728		chr2	-	tss_1500	170662789
876	cg39341702_TC21	0.00022699	-0.03386612					170923691
877	cg39362172_TC21	0.00036823	-0.04636628					172758029
878	cg39365635_BC21	3.1978E-05	-0.03544903					172974879
879	cg39374577_BC21	0.00025918	-0.05747589	Ppp4r1l-ps	chr2	-	tss_body	173585640
880	cg39381866_TC21	0.0008184	-0.04537638					174256197
881	cg39382297_BC21	0.00037077	-0.03824916	Nespas	chr2	-	tss_body	174285861
882	cg39389142_TC21	0.00044114	-0.03791377		chr2	-	tss_body	174841091
883	cg39399139_BC21	0.0002465	-0.04033168	Phactr3	chr2	+	tss_body	178193134
884	cg39411965_TC21	7.1199E-06	-0.04530653	Cdh4	chr2	+	tss_body	179512699
885	cg39412654_TC21	0.00024951	-0.06317024	Cdh4	chr2	+	tss_body	179569409
886	cg39414031_TC21	0.00034658	0.02957016	Cdh4	chr2	+	tss_body	179680145
887	cg39418296_TC21	0.00024807	-0.05296485	Lsm14b	chr2	+	tss_body	180026447
888	cg39424466_BC21	0.00086779	0.04491119	Slco4a1	chr2	+	tss_body	180460828
889	cg39425481_TC21	5.4189E-05	-0.03603158	Gm30144	chr2	-	tss_body	180545413
890	cg39431210_TC21	7.9516E-06	-0.0531506	Chrna4	chr2	-	tss_body	181043268
891	cg39434089_TC21	0.00023851	-0.05183652	Stmn3	chr2	-	tss_body	181307823
892	cg39435883_BC21	0.00064529	-0.05082685	Zbtb46	chr2	-	tss_1500	181494419
893	cg39450966_TC21	0.00089373	-0.0356144	Zfhx4	chr3	+	tss_body	5221482
894	cg39468295_BC21	4.4812E-05	-0.0949824	Hey1	chr3	-	tss_body	8664413

895	cg39471833_BC21	0.00096892	-0.03864076	Tpd52	chr3	-	tss_body	8990925
896	cg39477911_BC21	0.00016143	-0.0550603	Zfp704	chr3	-	tss_body	9522941
897	cg39484335_BC11	0.00072093	-0.02990307					10143692
898	cg39503887_BC21	0.00084122	-0.03356128	Ralyl	chr3	+	tss_body	14098668
899	cg39514975_TC21	0.00053268	-0.03325188					16334267
900	cg39577996_BC21	3.9058E-05	-0.02845701	Fndc3b	chr3	-	tss_body	27665843
901	cg39584916_BC11	0.00055856	0.03767589	Tnik	chr3	+	tss_body	28430854
902	cg39596406_BC21	0.0002626	0.03373734	Mecom	chr3	-	tss_body	30173905
903	cg39605185_BC21	0.00072083	0.06273447					31054424
904	cg39611665_TC21	0.00078463	-0.0302735	Kcnmb2	chr3	+	tss_body	31902641
905	cg39618381_TC21	0.00055699	0.02954513					32668738
906	cg39642440_BC21	3.1338E-08	-0.05446295		chr3	+	tss_200	35545846
907	cg39651273_BC21	0.00027305	0.06747836	Bbs7	chr3	-	tss_1500	36613882
908	cg39669975_BC21	4.6644E-05	0.03232451	Fat4	chr3	+	tss_body	38916378
909	cg39688555_TC11	0.00020521	-0.05679865	Jade1	chr3	+	tss_body	41567694
910	cg39735508_BC21	0.00075901	0.02973399	Gm40044	chr3	-	tss_1500	51221578
911	cg39748837_TC21	0.00083119	-0.07522991		chr3	-	tss_body	52198277
912	cg39761100_TC21	0.00043656	-0.05269172					53382125
913	cg39779056_BC21	0.00077845	-0.03083705	Dclk1	chr3	+	tss_body	55343247
914	cg39783013_BC21	0.00036369	-0.09086965	Nbea	chr3	-	tss_body	55782388
915	cg39805756_TC21	0.00041924	-0.04756537	Med12l	chr3	+	tss_body	59208546
916	cg39812067_BC21	1.5125E-05	0.04055589	Mbnl1	chr3	+	tss_body	60513588
917	cg39861232_BC11	0.00078715	0.03502842	Gm21949	chr3	+	tss_body	68574923
918	cg39871135_BC21	0.00064244	-0.03574529	Ppm1l	chr3	+	tss_body	69543171
919	cg39874243_TC21	0.00048691	-0.03285333					69895653
920	cg39919526_BC11	0.00015276	0.05981472	Fnip2	chr3	-	tss_body	79489104
921	cg39934776_BC21	0.00034472	-0.05111991	Gucy1b3	chr3	-	tss_body	82073409
922	cg39950519_BC21	0.00080479	0.03463267	Gm30352	chr3	+	tss_body	84048661
923	cg39955611_BC21	0.00038757	0.0266776	Fhdc1	chr3	-	tss_1500	84481407
924	cg39967156_TC11	0.00048704	0.08842963	Fam160a1	chr3	-	tss_1500	85786770
925	cg39975634_TC21	0.00060741	-0.04313126	Dclk2	chr3	-	tss_body	86832372

926	cg39976670_BC21	6.705E-05	-0.05997714	Dclk2	chr3	-	tss_1500	86921637
927	cg39978122_BC21	0.0003653	-0.02698983	Kirrel	chr3	-	tss_body	87088293
928	cg39986700_BC21	0.00098009	0.05046671	Rrnad1	chr3	-	tss_body	87928037
929	cg39990054_BC21	0.00031235	0.03912057	Mef2d	chr3	+	tss_body	88146296
930	cg40001523_TC21	0.00038307	-0.06376611	Rusc1	chr3	-	tss_body	89091819
931	cg40036627_TC21	0.00034967	0.03637381					93708702
932	cg40054870_TC21	0.00074944	-0.02908756	Ecm1	chr3	-	tss_body	95735392
933	cg40057587_TC21	0.00066844	-0.03136229	Anp32e	chr3	+	tss_body	95944239
934	cg40061343_BC21	0.00010767	-0.07843262		chr3	+	tss_body	96247465
935	cg40081350_BC21	2.3155E-06	-0.05674276					97971918
936	cg40084270_BC21	0.00059561	-0.04368655	Reg4	chr3	+	tss_body	98223998
937	cg40109156_TC21	9.5333E-05	-0.02694474	Igsf3	chr3	+	tss_body	101410040
938	cg40118001_TC11	0.00050897	-0.06141279	Vangl1	chr3	-	tss_body	102193496
939	cg40119719_TC21	0.00083222	0.03435232		chr3	+	tss_body	102369147
940	cg40121023_TC21	7.1279E-06	-0.03961151					102527004
941	cg40150047_TC21	0.00068634	-0.02770412	Rap1a	chr3	-	tss_body	105798911
942	cg40158603_TC21	0.0002133	0.0339785	Prok1	chr3	-	tss_body	107234578
943	cg40166635_BC21	5.9443E-05	0.0622497	Gstm1	chr3	-	tss_body	108014594
944	cg40179939_BC21	0.00036235	-0.04791196	Slc25a24	chr3	+	tss_body	109126184
945	cg40215691_TC21	0.00044637	-0.05043327	Gpr88	chr3	-	tss_body	116253462
946	cg40226445_TC21	0.00041766	-0.02843865	Plppr4	chr3	-	tss_200	117360943
947	cg40252511_BC21	0.00026843	-0.03741032	Cnn3	chr3	+	tss_body	121438224
948	cg40263035_BC11	0.00017667	-0.05416755		chr3	+	tss_body	122334560
949	cg40318493_TC21	0.00070526	-0.02539227	Elovl6	chr3	+	tss_body	129582789
950	cg40323823_TC21	0.00073208	0.05074706	Sec24b	chr3	-	tss_body	129998129
951	cg40358507_BC21	9.5513E-06	-0.03831141	Gm40153	chr3	-	tss_body	133663765
952	cg40361894_TC21	4.7374E-05	-0.0346434					134272005
953	cg40370084_BC21	6.8726E-05	-0.04219534	Manba	chr3	+	tss_body	135514269
954	cg40388314_BC21	0.00062616	-0.0282325	Lamtor3	chr3	+	tss_body	137921311
955	cg40397738_BC21	0.00077948	0.05362643	Tspan5	chr3	+	tss_body	138745672
956	cg40398744_TC21	0.00073434	-0.04117021	Tspan5	chr3	+	tss_body	138818812

957	cg40398943_BC11	0.00039082	0.03065923	Tspan5	chr3	+	tss_body	138833332
958	cg40439433_TC21	0.00021535	-0.03767992	Sep15	chr3	+	tss_body	144594625
959	cg40454033_BC21	9.2117E-06	0.04061176	Gm40166	chr3	-	tss_body	146027512
960	cg40475931_BC21	0.00011517	-0.05168545					148463002
961	cg40502995_TC21	0.00018585	-0.05237357	Gipc2	chr3	-	tss_body	152152020
962	cg40579861_TC21	0.00097769	-0.04553047	Tox	chr4	-	tss_body	6901454
963	cg40593839_TC21	1.7247E-05	-0.07098666	chr4-8911252-8911702	chr4	*	SShore	8912472
964	cg40643255_BC21	0.00083309	0.03661409	Osgin2	chr4	-	tss_body	16010431
965	cg40679356_BC21	0.00033557	0.02840968	Gm30886	chr4	+	tss_1500	22938197
966	cg40734220_TC21	0.00015608	-0.04397683	Ankrd6	chr4	-	tss_body	32926067
967	cg40785497_BC21	0.0007551	-0.03255637	Spink4	chr4	+	tss_200	40920055
968	cg40791708_TC21	9.3056E-05	-0.04042974	AI464131	chr4	-	tss_body	41497575
969	cg40792230_TC21	0.0007466	0.04281414	Fam219a	chr4	-	tss_body	41520352
970	cg40805571_TC21	7.919E-05	-0.04892921	LOC108168937	chr4	-	tss_body	43374891
971	cg40806991_TC21	8.5161E-05	0.04181107	Tesk1	chr4	+	tss_body	43447489
972	cg40815814_TC21	7.7276E-05	-0.02792743	Gm12504	chr4	+	tss_body	44123223
973	cg40837767_BC21	0.00031424	-0.02927335	Tdrd7	chr4	+	tss_body	45976806
974	cg40851902_TC21	0.00087389	-0.03749625		chr4	-	tss_200	47010825
975	cg40868000_TC21	7.5284E-05	0.0466705	Murc	chr4	+	tss_body	48663538
976	cg40904421_TC21	0.00075153	-0.02930942		chr4	-	tss_1500	54646544
977	cg40911685_TC21	0.00022676	0.04350201		chr4	-	tss_1500	55466016
978	cg40928598_TC21	0.00064022	-0.06985227	Ptpn3	chr4	-	tss_body	57305683
979	cg40933064_TC11	0.0008176	0.02723035	Pakap	chr4	+	tss_body	57739343
980	cg40946999_BC21	0.00061345	-0.05317529	Gm35578	chr4	-	tss_body	59281017
981	cg40968694_BC21	0.00053719	-0.05233169					62891298
982	cg40973626_TC11	0.00021523	0.02690063	Orm3	chr4	+	tss_body	63358911
983	cg41014046_BC21	0.00057552	-0.03064869					71291593
984	cg41080268_TC21	0.00048736	-0.02643815	Gm11415	chr4	-	tss_body	83888697
985	cg41080563_BC21	0.00091929	0.0448063					83925930
986	cg41082603_TC21	4.9783E-05	-0.02933429	Gm12414	chr4	-	tss_body	84130014
987	cg41091388_TC21	7.6948E-05	0.02646715	Sh3gl2	chr4	+	tss_body	85226783

988	cg41117776_BC21	0.00039884	0.02579553	LOC106557447	chr4	-	tss_body	88918436
989	cg41166891_TC21	0.00028892	0.06622824	Nfia	chr4	+	tss_body	97910768
990	cg41186906_TC21	0.00078049	-0.05966724					100036111
991	cg41207246_BC21	0.00079603	0.05684072	Pde4b	chr4	+	tss_body	102496393
992	cg41225008_TC21	0.00079664	-0.05109112	Dab1	chr4	+	tss_body	104702987
993	cg41236186_BC21	5.3678E-05	-0.07437984					106019852
994	cg41242459_BC21	0.00022676	-0.05984029	chr4-106622395-106623099	chr4	*	NShelf	106619324
995	cg41243291_BC21	0.00015514	-0.04828665	Ttc4	chr4	-	tss_body	106678248
996	cg41243621_TC21	0.00073852	-0.02891565	Mroh7	chr4	-	tss_body	106704158
997	cg41245607_BC21	0.00057789	-0.04047514					106862054
998	cg41248574_BC21	0.00085483	-0.0342772	Cdcp2	chr4	+	tss_1500	107096323
999	cg41256445_TC21	0.00026954	-0.03273925	LOC102633724	chr4	+	tss_1500	107688182
1000	cg41260151_BC21	0.00021997	-0.04295615	Slc1a7	chr4	+	tss_200	107968222
1001	cg41278537_BC11	0.00017886	-0.04771871					110120902
1002	cg41299110_BC21	2.1393E-06	-0.03071895	Trabd2b	chr4	+	tss_body	114457340
1003	cg41303141_BC21	0.00091863	-0.0474273	Foxd2os	chr4	+	tss_body	114913001
1004	cg41305088_BC21	0.00083121	-0.03281725	Pdzk1ip1	chr4	+	tss_body	115089620
1005	cg41329468_TC21	0.00036637	-0.02561184	Eri3	chr4	+	tss_body	117673564
1006	cg41330345_TC21	0.00056565	0.06178553	Klf17	chr4	-	tss_body	117765627
1007	cg41332930_TC21	0.00045554	-0.03509757	Artn	chr4	-	tss_body	117927254
1008	cg41335649_BC21	0.00010507	0.02690625	St3gal3	chr4	-	tss_body	118122325
1009	cg41343454_BC21	0.00020784	-0.02970639	Ebna1bp2	chr4	+	tss_body	118624299
1010	cg41356206_BC21	0.00096909	-0.05624384	Hivep3	chr4	+	tss_body	119970418
1011	cg41358069_TC21	0.00038734	0.04941788	Hivep3	chr4	+	tss_body	120132016
1012	cg41359347_BC21	0.00029856	-0.03614851	Gm36134	chr4	-	tss_body	120254543
1013	cg41366059_BC21	0.00010293	-0.02564508					120910387
1014	cg41368943_TC21	0.00082613	0.03843086		chr4	-	tss_200	121227477
1015	cg41394627_BC21	8.7771E-05	-0.05002161	Gm2164	chr4	-	tss_body	124586874
1016	cg41422292_TC21	0.0007765	-0.03802098	5730409E04Rik	chr4	+	tss_body	126613853
1017	cg41449449_BC21	0.00020119	-0.03469919	Trim62	chr4	+	tss_body	128899547

1018	cg41450862_BC21	0.00064056	-0.0600569	chr4-128993046-128993583	chr4	*	NShelf	128989366
1019	cg41464749_TC21	0.00048121	-0.05023425					129967245
1020	cg41508873_BC21	0.00013835	0.04034012					133509279
1021	cg41519981_BC21	0.00038143	-0.02838655	Grrp1	chr4	-	tss_body	134253985
1022	cg41523942_BC21	0.00024012	-0.04114701	Paqr7	chr4	+	tss_body	134502027
1023	cg41529044_BC21	2.8927E-05	0.02786855	Tmem57	chr4	-	tss_body	134813672
1024	cg41539436_TC21	0.00024504	-0.05894637	Nipal3	chr4	-	tss_body	135491031
1025	cg41545695_BC21	0.00087568	-0.0540696	Cnr2	chr4	+	tss_body	135911735
1026	cg41551354_BC21	0.0002158	-0.05574405	Tcea3	chr4	+	tss_body	136262118
1027	cg41571802_BC21	0.00086076	-0.05072857	Rap1gap	chr4	+	tss_body	137717680
1028	cg41587909_TC21	4.8971E-05	0.03916053	Pla2g5	chr4	-	tss_body	138819153
1029	cg41588619_BC21	0.0001192	0.03626336	Gm13030	chr4	-	tss_body	138873735
1030	cg41593392_BC11	0.00010227	0.06748377	Capzb	chr4	+	tss_body	139198259
1031	cg41622780_TC11	0.00023302	-0.02909209	Spata21	chr4	+	tss_200	141088301
1032	cg41627316_BC21	0.00028696	-0.05081711					141362809
1033	cg41627366_TC21	7.8637E-07	-0.05697806	chr4-141368138-141368541	chr4	*	NShelf	141365775
1034	cg41627908_TC21	0.00023633	-0.0471077	Clcnka	chr4	-	tss_body	141395468
1035	cg41641009_BC21	0.00097381	-0.09032137	Kazn	chr4	-	tss_body	142181093
1036	cg41642671_BC21	0.00036346	-0.03528144					142303925
1037	cg41650006_TC21	3.2136E-06	-0.02956273		chr4	-	tss_body	143030008
1038	cg41681455_BC21	0.00084999	-0.03988915	Draxin	chr4	-	tss_body	148125744
1039	cg41681872_TC21	3.7175E-05	-0.05366862	Fbxo6	chr4	-	tss_body	148147363
1040	cg41682076_TC21	3.3182E-05	-0.03367523	Fbxo44	chr4	-	tss_body	148157076
1041	cg41684455_BC21	0.00069307	-0.05402867		chr4	+	tss_200	148306776
1042	cg41684456_BC21	0.00040584	-0.04173742		chr4	+	tss_200	148306788
1043	cg41692578_BC21	0.0009406	-0.03302345	Casz1	chr4	+	tss_body	148842375
1044	cg41693365_BC21	0.00012132	-0.0829905	Casz1	chr4	+	tss_body	148891127
1045	cg41710768_BC11	0.00090696	0.04971269	H6pd	chr4	-	tss_body	149991428
1046	cg41721339_BC21	0.0001347	-0.06102967	Gm36806	chr4	-	tss_body	150779577
1047	cg41731416_TC21	1.7343E-06	-0.0429829	Camta1	chr4	-	tss_body	151420594

1048	cg41741297_TC21	4.3944E-05	0.06332812					152062985
1049	cg41742551_TC21	0.00013752	-0.07297154	Espn	chr4	-	tss_body	152126853
1050	cg41754316_TC11	0.00010646	-0.05513836					152823997
1051	cg41785772_TC21	0.00079261	0.0412382	Rer1	chr4	-	tss_body	155080014
1052	cg41789426_BC21	5.1164E-05	0.02522263	Prkcz	chr4	-	tss_body	155302036
1053	cg41803077_BC21	0.00028655	-0.03991269	Plekhn1	chr4	-	tss_body	156225332
1054	cg41822321_BC21	9.7082E-05	-0.04516285	Cdk14	chr5	-	tss_body	5266285
1055	cg41847769_TC21	0.00088657	-0.03476405	9330182L06Rik	chr5	+	tss_body	9346739
1056	cg41886786_TC21	0.00086044	-0.02564018	Gnat3	chr5	+	tss_body	17990749
1057	cg41906473_TC21	0.00084367	-0.02745322	Gsap	chr5	+	tss_1500	21175526
1058	cg41943473_BC21	0.00068318	-0.0708397	Prkag2	chr5	-	tss_body	25059336
1059	cg41989440_BC11	0.00060068	0.03639779	Trim54	chr5	+	tss_body	31116935
1060	cg41998043_TC21	3.8648E-06	0.02628452	Bre	chr5	+	tss_body	32049480
1061	cg42021268_TC21	0.00016216	-0.03186038	Fam193a	chr5	+	tss_body	34465873
1062	cg42022225_TC21	0.0001616	0.02860813	chr5-34573412-34574182	chr5	*	NShelf	34570973
1063	cg42022942_TC21	0.00014449	-0.03263793	Mfsd10	chr5	-	tss_body	34635088
1064	cg42041361_BC21	0.00022935	-0.08029171	Sorcs2	chr5	-	tss_body	36373572
1065	cg42042482_BC21	0.000441	0.05275986	Grpel1	chr5	+	tss_body	36470408
1066	cg42046106_BC21	8.4E-05	-0.03505505	Man2b2	chr5	-	tss_body	36817685
1067	cg42058627_BC21	3.7189E-05	-0.02585516					37964308
1068	cg42067388_BC21	2.455E-05	-0.03933776	Clnk	chr5	-	tss_body	38840955
1069	cg42135118_TC21	8.1207E-05	0.03912254					51277730
1070	cg42144977_BC21	7.8917E-05	-0.03771812	Ccdc149	chr5	-	tss_1500	52471921
1071	cg42150753_BC21	1.8612E-05	0.03185177	5033403H07Rik	chr5	-	tss_body	52992235
1072	cg42152359_TC21	0.00075033	-0.02516337	Sel1l3	chr5	-	tss_body	53150518
1073	cg42172158_TC21	2.1812E-06	-0.02588942					56284446
1074	cg42213351_BC11	0.00019314	-0.04649062					64487948
1075	cg42227404_BC21	0.00021044	0.03339228	N4bp2	chr5	+	tss_body	65782205
1076	cg42275853_TC21	0.00036282	-0.03203512	Corin	chr5	-	tss_body	72497076
1077	cg42277515_TC11	0.00017452	0.03101219	Cnga1	chr5	-	tss_1500	72643752
1078	cg42279384_BC21	0.00083624	-0.03399523	Tec	chr5	-	tss_body	72808910

1079	cg42304970_TC21	0.00042405	-0.05143665	Gsx2	chr5	+	tss_1500	75075304
1080	cg42421390_TC21	0.00099091	-0.02527569	Stbd1	chr5	+	tss_body	92605731
1081	cg42429394_BC21	0.00060589	0.02981547					93296514
1082	cg42450370_TC21	0.00026715	-0.03397239	4930467D21Rik	chr5	+	tss_body	97410444
1083	cg42453614_BC21	0.00012545	-0.04831268	Antxr2	chr5	-	tss_body	97935269
1084	cg42466823_TC21	0.0001209	-0.05009698	A930011G23Rik	chr5	-	tss_body	99403141
1085	cg42494200_TC21	0.00044278	-0.0352033	Cds1	chr5	+	tss_body	101798331
1086	cg42498024_BC21	0.00095474	0.0401479	Wdfy3	chr5	-	tss_body	102054757
1087	cg42530870_TC21	0.00018003	-0.03840994					105627326
1088	cg42546779_BC21	4.2189E-05	-0.04017223	Gm33371	chr5	-	tss_1500	107047018
1089	cg42561115_TC21	0.00038452	-0.03340954	Dgkq	chr5	-	tss_body	108655544
1090	cg42573234_TC21	0.00077476	-0.04161439	Fbrsl1	chr5	-	tss_body	110386227
1091	cg42589127_TC21	6.7286E-05	0.03767589					111675942
1092	cg42594295_BC21	0.00071548	-0.03777274					112144897
1093	cg42619181_BC21	0.00034613	0.03313165	Coro1c	chr5	-	tss_body	113865070
1094	cg42621499_BC21	0.0002421	-0.04031834	Dao	chr5	+	tss_body	114003919
1095	cg42635896_TC21	1.9054E-07	-0.03362302	Ankrd13a	chr5	+	tss_body	114786057
1096	cg42639863_BC21	2.9751E-05	0.04472779	Sppl3	chr5	+	tss_body	115015321
1097	cg42648554_BC21	0.00015498	-0.05684728	Pxn	chr5	+	tss_body	115529141
1098	cg42663307_BC21	0.0001821	-0.03125451	Srrm4os	chr5	+	tss_body	116461185
1099	cg42672405_TC21	1.5641E-05	-0.04825321	Taok3	chr5	+	tss_body	117203337
1100	cg42690704_TC21	0.00015608	-0.03361967					118446672
1101	cg42690896_BC21	0.00061345	-0.03825704					118463788
1102	cg42699950_BC21	0.00037719	-0.03650584					119179491
1103	cg42717593_TC21	0.00036619	0.04284737	Slc8b1	chr5	+	tss_body	120517754
1104	cg42748405_TC21	0.00064407	0.048521	P2rx7	chr5	+	tss_body	122690805
1105	cg42766316_TC21	0.00012371	0.03391628					123896746
1106	cg42768165_BC11	0.00087049	0.02510845	Vps37b	chr5	-	tss_body	124014002
1107	cg42803420_TC11	0.00070486	0.0405573	Gm33491	chr5	-	tss_1500	127107807
1108	cg42820776_TC21	0.00034173	-0.02553513	Rimbp2	chr5	-	tss_body	128780764
1109	cg42910686_TC21	0.00010823	-0.0284012	Plod3	chr5	+	tss_body	136989653

1110	cg42921401_TC11	0.0001498	-0.03619641	Nyap1	chr5	-	tss_body	137736026
1111	cg42926799_BC21	0.00017279	0.03375755	Stag3	chr5	+	tss_body	138275852
1112	cg42934186_BC21	5.9826E-05	-0.03340647	Prkar1b	chr5	-	tss_body	139081680
1113	cg42938147_TC21	0.00022478	0.03150427	3110082I17Rik	chr5	-	tss_body	139374715
1114	cg42956446_TC21	3.9133E-05	0.03397011	Brat1	chr5	+	tss_body	140710311
1115	cg42958262_TC21	0.00085081	-0.06458801	Gm30804	chr5	+	tss_body	140872058
1116	cg42958590_BC11	0.00015364	-0.02549862	Card11	chr5	-	tss_body	140892968
1117	cg42970181_TC21	0.00051151	-0.02846814	Sdk1	chr5	+	tss_body	142169746
1118	cg42976694_TC21	0.00073224	-0.02706542	Wipi2	chr5	+	tss_body	142666961
1119	cg42995878_TC21	0.00038204	0.05278261	Ocm	chr5	-	tss_body	144026649
1120	cg42998061_TC11	0.00048208	-0.04129264	Tecpr1	chr5	-	tss_body	144203438
1121	cg43002739_BC21	0.00020556	-0.02836334	Nptx2	chr5	+	tss_body	144551655
1122	cg43017772_TC21	0.00027961	-0.0407722		chr5	-	tss_body	146191038
1123	cg43048181_BC21	0.00019024	-0.03632307					148419123
1124	cg43051310_BC21	0.00014294	-0.04615154					148674191
1125	cg43059711_BC21	0.0004112	-0.0372549	Alox5ap	chr5	+	tss_1500	149264508
1126	cg43100289_BC21	0.00039341	-0.03646684					5167673
1127	cg43121539_TC21	5.6268E-05	0.0490011					7831144
1128	cg43127173_BC11	0.00059723	0.05878475	Glcci1	chr6	+	tss_body	8573212
1129	cg43174255_TC11	6.0401E-05	0.03064751	Cav1	chr6	+	tss_1500	17307396
1130	cg43182253_TC21	6.6139E-05	0.02707833	Cttnbp2	chr6	-	tss_body	18372914
1131	cg43210814_BC21	1.2048E-05	-0.05587126	Cadps2	chr6	-	tss_body	23273280
1132	cg43240011_TC21	0.00031622	0.02995813		chr6	-	tss_1500	28468321
1133	cg43242948_BC21	9.5068E-06	-0.06245065	Snd1	chr6	+	tss_body	28831641
1134	cg43261338_BC21	1.6447E-05	-0.08240577	1700012C14Rik	chr6	+	tss_body	30461009
1135	cg43274777_TC21	0.00014275	-0.02649054		chr6	+	tss_body	31786572
1136	cg43298556_BC21	0.0006883	-0.0374733	Cald1	chr6	+	tss_body	34709563
1137	cg43361320_BC21	3.2615E-05	-0.05324478		chr6	+	tss_body	43094922
1138	cg43383857_TC21	0.00071647	-0.02500798	Zfp783	chr6	+	tss_body	47943782
1139	cg43388720_BC21	6.8278E-05	-0.04142662	Zfp862-ps	chr6	+	tss_body	48508292
1140	cg43388997_BC11	2.7997E-05	-0.0426229	Zfp862-ps	chr6	+	tss_body	48530227

1141	cg43390290_BC21	0.00060764	-0.03327771	AI854703	chr6	+	tss_200	48628110
1142	cg43412057_BC21	2.0703E-05	-0.02847791	Gm38809	chr6	-	tss_body	50981942
1143	cg43435859_TC21	0.00015531	-0.03185625	Jazf1	chr6	-	tss_body	53067581
1144	cg43436966_TC21	0.00019985	-0.04192739					53200952
1145	cg43442245_BC21	7.9882E-06	-0.05339367					53761184
1146	cg43443797_TC21	0.00076094	-0.08310372	Cpvl	chr6	-	tss_body	53907145
1147	cg43447044_TC21	0.00081498	0.03675723	Chn2	chr6	+	tss_body	54224475
1148	cg43448958_BC21	0.00038608	-0.04266146	9130019P16Rik	chr6	-	tss_body	54408450
1149	cg43455295_BC21	0.00038722	-0.02652014	Ggct	chr6	-	tss_body	54991300
1150	cg43459688_BC21	0.00068583	0.06864397	6430584L05Rik	chr6	+	tss_body	55400141
1151	cg43480561_BC11	4.0265E-06	-0.04593718	Herc3	chr6	+	tss_body	58907433
1152	cg43543845_BC11	0.00013108	-0.02806675					71026191
1153	cg43544553_BC21	0.00099698	-0.05561819	Gm38826	chr6	-	tss_200	71106674
1154	cg43545496_TC21	0.00015251	-0.04369987	Smyd1	chr6	-	tss_body	71216938
1155	cg43546226_BC21	1.4242E-05	-0.0444763	Gm1070	chr6	+	tss_body	71293646
1156	cg43548561_TC21	0.0009422	0.02600136					71530671
1157	cg43558968_BC21	0.00028481	-0.02839053	Sh2d6	chr6	-	tss_body	72520994
1158	cg43613724_TC21	0.0009012	-0.02557687	Pole4	chr6	-	tss_body	82649306
1159	cg43616917_BC11	0.00039978	-0.02935617	M1ap	chr6	+	tss_body	82947184
1160	cg43617672_BC21	0.00088665	-0.04262933	Dok1	chr6	-	tss_body	83032431
1161	cg43620171_TC21	0.00014704	-0.02682448	Wdr54	chr6	-	tss_body	83154479
1162	cg43620308_TC11	0.00058294	-0.02857307	1700003E16Rik	chr6	+	tss_body	83161273
1163	cg43628782_TC21	3.1042E-05	-0.0362036		chr6	-	tss_body	83845066
1164	cg43632253_TC21	0.00018713	-0.04924786		chr6	+	tss_body	84226369
1165	cg43663987_BC21	0.00091104	-0.07297792	Arhgap25	chr6	-	tss_body	87533154
1166	cg43670664_BC21	0.000446	-0.04912331					88117141
1167	cg43672560_BC11	0.0001041	0.03419808	A0A0N4SVT8	chr6	+	tss_body	88242817
1168	cg43693390_BC21	0.00048753	-0.05706291	Iqsec1	chr6	-	tss_body	90660894
1169	cg43699398_BC21	0.00010045	-0.0300649	Wnt7a	chr6	-	tss_body	91365885
1170	cg43719591_BC21	1.1255E-05	-0.05833415	Magi1	chr6	-	tss_body	93717434
1171	cg43741590_BC21	0.00091747	-0.03292449	Fam19a1	chr6	+	tss_body	96485165

1172	cg43750523_BC21	0.00039861	0.03376811	Frmd4b	chr6	-	tss_body	97586418
1173	cg43758530_BC21	8.3879E-05	-0.05617395		chr6	-	tss_body	98632263
1174	cg43763212_TC21	0.00029993	-0.02623101	Foxp1	chr6	-	tss_body	99097160
1175	cg43765454_TC11	0.00031596	-0.02701084	Foxp1	chr6	-	tss_body	99310690
1176	cg43766438_BC11	0.00049269	0.02719448	Foxp1	chr6	-	tss_body	99403259
1177	cg43767456_BC21	0.00096183	-0.06331622	Foxp1	chr6	-	tss_body	99490463
1178	cg43772881_BC21	1.4467E-05	-0.06209288		chr6	-	tss_body	99950636
1179	cg43814105_TC11	0.00088141	-0.04601376	Crbn	chr6	-	tss_body	106794171
1180	cg43824342_TC21	0.00067289	-0.05224402	Itpr1	chr6	+	tss_body	108445210
1181	cg43855161_BC21	0.0001643	-0.04023057	Ttll3	chr6	+	tss_body	113393120
1182	cg43855758_BC21	0.00014318	-0.04459372	Cidec	chr6	-	tss_1500	113435909
1183	cg43863135_BC21	0.00041097	-0.02692263	Gm15083	chr6	+	tss_body	114050050
1184	cg43870625_BC21	0.00080918	-0.05506785	Atg7	chr6	+	tss_body	114791074
1185	cg43903647_TC21	0.00078003	-0.03521024					118324469
1186	cg43926578_BC21	0.00055365	-0.02548126	Cecr6	chr6	-	tss_1500	120494184
1187	cg43929523_BC21	0.00066804	-0.03123288	Atp6v1e1	chr6	-	tss_body	120797427
1188	cg43929928_BC21	2.6353E-06	0.02540419	Gm38889	chr6	-	tss_body	120836093
1189	cg43933608_TC21	0.00029838	-0.0356668	Mical3	chr6	-	tss_body	121081747
1190	cg43936200_BC21	0.00087898	-0.03604135		chr6	-	tss_200	121272736
1191	cg43937141_TC11	0.00011295	0.03344637	Slc6a12	chr6	+	tss_body	121352922
1192	cg43939740_BC21	0.00061399	0.04098943	A2m	chr6	+	tss_1500	121635851
1193	cg43966164_BC21	0.00012519	-0.03645048	Pianp	chr6	+	tss_body	124998412
1194	cg43982345_BC21	0.00089119	-0.03124487	Kcna5	chr6	-	tss_body	126534355
1195	cg43984702_BC11	0.00089336	-0.03588706	Kcna6	chr6	-	tss_body	126738659
1196	cg43985094_BC21	0.00045891	-0.04738701	LOC102636795	chr6	+	tss_body	126769495
1197	cg44048945_BC21	0.00071386	-0.03466157					135271181
1198	cg44130052_BC21	0.0001339	-0.03418478	Sox5	chr6	-	tss_body	144107618
1199	cg44131173_TC21	0.0002976	-0.03376112	Sox5	chr6	-	tss_body	144204235
1200	cg44131277_BC11	0.00010637	0.04502298	Sox5	chr6	-	tss_body	144210933
1201	cg44144765_TC21	0.0003748	-0.07520969	E9PY33	chr6	-	tss_body	145381341
1202	cg44161888_BC21	0.00037545	0.0398086	Mrps35	chr6	+	tss_body	147043357

1203	cg44177292_TC21	0.00015526	-0.02527964		chr6	-	tss_1500	149215586
1204	cg44183052_BC21	0.00065174	-0.02579164	Cacng8	chr7	+	tss_body	3394734
1205	cg44183584_BC21	2.8628E-05	0.02976933	Cacng6	chr7	+	tss_1500	3424062
1206	cg44185638_TC21	0.00015889	0.02855135	Tmc4	chr7	-	tss_body	3675040
1207	cg44192278_TC11	0.00094758	-0.04223922	Syt5	chr7	-	tss_body	4546474
1208	cg44205950_BC21	3.6813E-05	-0.03243274	Zfp787	chr7	-	tss_body	6133003
1209	cg44211880_BC21	0.00025129	-0.03125244	Peg3	chr7	-	tss_body	6729451
1210	cg44256119_TC21	6.8176E-05	0.02549945	Ehd2	chr7	-	tss_body	15951183
1211	cg44267234_TC21	4.4193E-05	-0.04068394	Fkrp	chr7	-	tss_body	16811701
1212	cg44277334_TC21	0.00011066	-0.0265956	Psg18	chr7	-	tss_body	18351161
1213	cg44281516_TC21	0.00070302	-0.04147066	Nova2	chr7	+	tss_body	18939024
1214	cg44290234_TC21	0.00080381	0.02713056	Ckm	chr7	+	tss_body	19413712
1215	cg44291165_TC21	0.00052575	-0.02978814	Exoc3l2	chr7	+	tss_200	19463059
1216	cg44292240_BC21	0.00032087	0.03529513	Nkpd1	chr7	+	tss_body	19517575
1217	cg44298827_BC21	0.00020424	-0.03251384					19934577
1218	cg44316161_BC21	0.00044094	-0.04072897	Lypd5	chr7	+	tss_body	24352475
1219	cg44320336_TC21	9.6075E-05	-0.04391413	Ethe1	chr7	+	tss_body	24595143
1220	cg44323110_TC21	3.6104E-05	-0.02616026	Gm5893	chr7	+	tss_200	24818627
1221	cg44330793_TC21	2.3871E-05	0.04683153	Cic	chr7	+	tss_body	25274789
1222	cg44338344_TC21	0.00018245	-0.06968771					25835571
1223	cg44347415_TC21	0.00081928	-0.03834312	Itpkc	chr7	-	tss_body	27219942
1224	cg44353417_BC21	0.00024985	-0.03620553	2310022A10Rik	chr7	+	tss_body	27565718
1225	cg44371916_TC21	0.00093263	0.03634376	Actn4	chr7	-	tss_body	28949254
1226	cg44377566_TC21	0.00097427	-0.03680269	LOC108167414	chr7	-	tss_1500	29289676
1227	cg44390436_TC21	0.00051894	0.02787729	Clip3	chr7	+	tss_1500	30291448
1228	cg44392418_BC11	0.00012103	-0.03575238	Nfkbid	chr7	+	tss_body	30423305
1229	cg44398848_TC21	9.3889E-05	-0.02974482	Ffar1	chr7	-	tss_body	30861388
1230	cg44418731_TC21	0.00015862	-0.03072991	4931406P16Rik	chr7	-	tss_body	34245360
1231	cg44427374_BC21	0.00062999	-0.05015311	Pepd	chr7	+	tss_body	35005246
1232	cg44492501_TC21	0.00066772	-0.02734631	Nkg7	chr7	+	tss_1500	43436594
1233	cg44499977_TC21	0.00087909	-0.0304527	Acpt	chr7	-	tss_body	44261140

1234	cg44503353_TC11	0.0003721	0.02504183		chr7	+	tss_1500	44472331
1235	cg44512648_TC21	0.00017956	-0.03985917	Rras	chr7	+	tss_body	45021397
1236	cg44513484_TC11	1.3559E-05	0.0314984	Prrg2	chr7	-	tss_body	45061829
1237	cg44516321_BC21	3.9789E-05	-0.03160505	Tead2	chr7	+	tss_body	45216754
1238	cg44519189_BC21	0.00030202	-0.02801281	Snrnp70	chr7	-	tss_body	45383232
1239	cg44527703_BC21	1.0191E-05	-0.05349605	Grin2d	chr7	-	tss_body	45856775
1240	cg44530161_BC21	0.00052039	-0.04399604	Abcc6	chr7	-	tss_1500	46031732
1241	cg44558735_TC21	0.00029639	-0.03717631	Nav2	chr7	+	tss_body	49382816
1242	cg44594554_TC11	2.0443E-05	0.03816863	Nipa2	chr7	-	tss_body	55954031
1243	cg44644827_TC21	0.00024406	-0.03882715	Fam189a1	chr7	-	tss_body	64925675
1244	cg44645078_TC21	0.0002562	-0.03707721	Fam189a1	chr7	-	tss_body	64956986
1245	cg44675226_TC21	6.138E-05	-0.03813985	Gm39027	chr7	-	tss_200	67850025
1246	cg44685745_TC21	0.00060677	0.02534297					68771580
1247	cg44689659_TC21	4.8362E-05	-0.04892415	Gm38584	chr7	-	tss_body	69488950
1248	cg44727031_TC21	5.4243E-05	-0.06056955	Slco3a1	chr7	-	tss_body	74325374
1249	cg44736679_TC21	0.0006295	-0.06425396	Akap13	chr7	+	tss_body	75752676
1250	cg44758208_BC21	0.00050396	-0.07848379					79191044
1251	cg44760653_TC21	8.9167E-05	-0.04161969	Rlbp1	chr7	-	tss_body	79386559
1252	cg44767058_TC21	2.5449E-06	-0.04735826	Anpep	chr7	-	tss_body	79826262
1253	cg44771166_TC21	0.0003078	0.03534607					80160115
1254	cg44771167_TC21	0.00013391	0.03816009					80160223
1255	cg44777786_BC21	6.4296E-05	-0.06688259	Crtc3	chr7	-	tss_body	80629408
1256	cg44782517_BC21	0.00038501	-0.02521591	Zfp592	chr7	+	tss_body	81025198
1257	cg44801052_TC21	0.00083779	-0.03690219	Gm36584	chr7	-	tss_body	82842827
1258	cg44801567_TC21	0.00050226	-0.0753614	Mex3b	chr7	+	tss_body	82869912
1259	cg44801595_TC21	3.1819E-05	-0.09147742	Mex3b	chr7	+	tss_body	82870439
1260	cg44805939_TC21	0.00077802	0.02651913	Gm10610	chr7	-	tss_body	83550138
1261	cg44806815_TC21	0.0008877	-0.04724499	Il16	chr7	-	tss_body	83655459
1262	cg44835045_BC21	0.00040574	0.02719136	Tmem135	chr7	-	tss_body	89323382
1263	cg44862885_BC21	0.00042124	-0.04269829	Gm32647	chr7	+	tss_body	94042708
1264	cg44889532_BC11	0.00070835	-0.03730786	Myo7a	chr7	-	tss_body	98111350

1265	cg44892515_TC21	0.00034043	-0.06521749	LOC108167447	chr7	-	tss_body	98415826
1266	cg44892729_BC11	0.00099621	-0.05175781	Gm39053	chr7	+	tss_body	98437771
1267	cg44893281_BC21	0.0001047	-0.06950709	Lrrc32	chr7	+	tss_1500	98489244
1268	cg44895680_TC21	0.00022058	-0.04788474	LOC105243004	chr7	-	tss_1500	98728489
1269	cg44904536_TC21	0.00054377	-0.03246638	Gdpd5	chr7	+	tss_body	99423924
1270	cg44909573_TC21	0.00062058	-0.03163092	Spcs2	chr7	-	tss_body	99863313
1271	cg44911398_BC11	0.00039811	-0.04074233	Chrdl2	chr7	+	tss_body	100033864
1272	cg44921128_BC21	0.0007836	-0.03327767					100987717
1273	cg44925102_TC21	0.00026878	-0.03531409	F7D3W5	chr7	+	tss_body	101414103
1274	cg44926646_TC21	0.00091594	-0.05079484	Gm35363	chr7	-	tss_body	101538345
1275	cg44932431_TC21	0.00010644	0.03574586	Chrna10	chr7	-	tss_body	102116728
1276	cg44942328_BC21	0.00021748	0.04012856	Hbb-bt	chr7	-	tss_body	103813919
1277	cg44970664_BC21	1.2496E-05	-0.03834124	Tub	chr7	+	tss_body	109017680
1278	cg44984896_TC21	1.064E-05	-0.03213111	Adm	chr7	+	tss_body	110629456
1279	cg45000102_BC21	0.00021953	0.0516975	Parva	chr7	+	tss_1500	112427223
1280	cg45003094_TC21	2.2276E-07	0.0603082	Tead1	chr7	+	tss_body	112713806
1281	cg45017091_TC21	0.0005224	0.03525241					114290755
1282	cg45025226_BC21	2.1303E-05	-0.05326128	Sox6	chr7	-	tss_body	115539340
1283	cg45029252_TC21	2.9325E-05	-0.04785355	Plekha7	chr7	-	tss_body	116131583
1284	cg45048502_TC21	0.00044882	0.02625674	Syt17	chr7	-	tss_body	118442157
1285	cg45059060_TC21	2.1019E-05	-0.0290548	Acsm2	chr7	+	tss_body	119561750
1286	cg45065811_TC21	0.00037778	-0.03893095		chr7	+	tss_200	120553115
1287	cg45085853_BC21	2.2999E-06	-0.06309734	Prkcb	chr7	+	tss_body	122527743
1288	cg45090471_BC21	0.00014618	-0.06004392	Tnrc6a	chr7	+	tss_body	123032091
1289	cg45113861_BC21	0.00071229	-0.06049433	Gsg1l	chr7	-	tss_body	126038723
1290	cg45120773_BC21	1.5156E-05	-0.03556678	Cln3	chr7	-	tss_body	126585024
1291	cg45120780_TC21	7.662E-05	-0.03924286	Cln3	chr7	-	tss_body	126585405
1292	cg45121672_TC21	0.00027053	0.04586494	Sult1a1	chr7	-	tss_body	126676730
1293	cg45123210_TC21	0.00058436	-0.02572694	Tbx6	chr7	+	tss_200	126781478
1294	cg45123701_TC21	9.1639E-05	0.04980214	Aldoa	chr7	-	tss_body	126807457
1295	cg45125400_TC11	0.00040063	0.03315026	Tmem219	chr7	-	tss_body	126923132

1296	cg45128597_BC21	0.00058107	-0.05893177	Spn	chr7	-	tss_body	127136519
1297	cg45130867_TC21	0.00035498	-0.03852928					127278746
1298	cg45144523_BC21	0.00066811	-0.02843513					128313207
1299	cg45183883_BC21	0.00043155	-0.03260154	Gm39101	chr7	+	tss_1500	132404663
1300	cg45203448_BC21	5.4269E-05	0.04225492	D7Ertd443e	chr7	-	tss_body	134349512
1301	cg45204565_BC21	2.7764E-06	0.07172378	D7Ertd443e	chr7	-	tss_body	134499006
1302	cg45208747_TC11	6.2755E-05	-0.04798319	Dock1	chr7	+	tss_body	134932904
1303	cg45220870_TC21	0.00073764	-0.04137363					136209622
1304	cg45223097_TC21	0.00020127	-0.03366998					136455362
1305	cg45258821_BC21	5.3991E-06	-0.06513583	LOC102635948	chr7	+	tss_body	139957767
1306	cg45266580_TC11	0.000529	0.02622191	Psmd13	chr7	+	tss_body	140894413
1307	cg45267480_BC21	1.3365E-05	0.03080475	A0A1B0GT68	chr7	-	tss_body	140953598
1308	cg45269161_TC21	0.00076341	0.03907221	Pkp3	chr7	+	tss_body	141078264
1309	cg45270246_BC21	0.00016006	-0.03324603	Ptdss2	chr7	+	tss_body	141154649
1310	cg45282614_BC21	0.00013394	-0.04328142	Ifitm10	chr7	-	tss_body	142342390
1311	cg45285404_BC21	0.00018905	-0.06274091	Gm33148	chr7	+	tss_body	142612076
1312	cg45285804_BC21	0.00096955	-0.04003897	Igf2	chr7	-	tss_body	142657283
1313	cg45287869_TC21	0.00061949	-0.04158255	Ascl2	chr7	-	tss_body	142966898
1314	cg45289142_TC11	0.00029187	-0.05397423	Trpm5	chr7	-	tss_body	143091810
1315	cg45289905_BC21	0.0001421	-0.04885582	Kcnq1	chr7	+	tss_body	143179676
1316	cg45290904_BC21	0.000589	-0.0576744	Kcnq1	chr7	+	tss_body	143325199
1317	cg45292214_BC21	0.00021998	-0.02926595	Cdkn1c	chr7	-	tss_body	143458618
1318	cg45292897_BC21	0.00064487	-0.05542481	Slc22a18	chr7	+	tss_body	143490780
1319	cg45308290_BC21	0.00070609	0.03903862					145141545
1320	cg45342952_BC11	0.00024014	0.05643083		chr8	+	tss_body	8488327
1321	cg45342956_BC21	0.00021553	0.05880082		chr8	+	tss_body	8488453
1322	cg45344157_BC21	9.4346E-05	-0.07840109					8598047
1323	cg45346063_BC21	0.00067388	-0.05341958	Gm39127	chr8	+	tss_body	8745744
1324	cg45357659_TC21	0.00021723	-0.04431129	Tnfsf13b	chr8	+	tss_body	10006874
1325	cg45367036_TC21	0.00090286	0.03843412	Irs2	chr8	-	tss_body	10996108
1326	cg45369206_TC21	0.00055505	-0.06039523					11172847

1327	cg45380489_BC21	7.9967E-05	0.02757973					12002973
1328	cg45405574_BC11	0.00095764	-0.05346951					13899553
1329	cg45418192_TC21	0.00050091	0.0450248	Arhgef10	chr8	+	tss_body	14992857
1330	cg45446096_BC21	0.00014391	0.03817583	Defb3	chr8	+	tss_1500	19292315
1331	cg45455522_BC21	0.00065636	-0.02628588	Defb2	chr8	+	tss_body	21842887
1332	cg45456468_BC11	0.00048741	0.03359103					21992477
1333	cg45465974_BC21	0.00078389	-0.03344213	Ap3m2	chr8	-	tss_body	22789132
1334	cg45467127_BC21	0.00048411	0.04728597	Kat6a	chr8	+	tss_body	22862568
1335	cg45481218_BC21	0.00088392	-0.04612334		chr8	+	tss_body	24220543
1336	cg45482165_BC21	1.7324E-05	0.04058459					24335490
1337	cg45488756_TC21	1.8061E-05	0.04042267	Tm2d2	chr8	+	tss_body	25019560
1338	cg45499346_TC21	0.000146	-0.05853252	Ash2l	chr8	-	tss_1500	25848553
1339	cg45515327_TC21	0.00064534	-0.06375081	Got1l1	chr8	-	tss_200	27224011
1340	cg45517493_TC21	0.00084207	-0.03133729	Poteg	chr8	+	tss_body	27447746
1341	cg45582244_TC21	2.698E-05	-0.05037202					36019235
1342	cg45591880_TC21	0.00016962	-0.04428358	Dlc1	chr8	-	tss_body	36953080
1343	cg45639245_BC21	8.8094E-05	0.03856524	Fat1	chr8	+	tss_body	44985447
1344	cg45640214_TC21	0.00056666	-0.03049951	Fat1	chr8	+	tss_body	45037221
1345	cg45652599_BC11	0.00055238	0.04547407		chr8	+	tss_200	46299081
1346	cg45662637_BC21	0.00027811	-0.04390881	Stox2	chr8	-	tss_body	47218103
1347	cg45682912_BC21	0.00059111	-0.02515546	Tenm3	chr8	-	tss_body	48674425
1348	cg45779814_BC21	0.00063251	-0.04319263	March1	chr8	+	tss_body	66334555
1349	cg45792546_TC21	0.00034219	-0.03682029	Csgalnact1	chr8	-	tss_body	68421059
1350	cg45807709_TC21	0.00045039	-0.03641837	Slc25a42	chr8	-	tss_body	70198309
1351	cg45817169_TC21	0.0002283	-0.05136854	Pik3r2	chr8	-	tss_body	70768818
1352	cg45817628_TC21	0.0004926	-0.0328527	Mast3	chr8	-	tss_body	70783322
1353	cg45824130_TC11	0.0005043	0.03703527	Nr2f6	chr8	-	tss_1500	71382766
1354	cg45840443_BC21	0.00085745	-0.02866042	Large	chr8	-	tss_body	73016551
1355	cg45849944_TC21	0.00061419	-0.05967014	Tom1	chr8	+	tss_body	75057268
1356	cg45869230_BC21	0.00073448	-0.02805862					78001765
1357	cg45870569_BC21	4.5718E-05	-0.05728431					78149087

1358	cg45885196_BC11	0.0004581	-0.03253258		chr8	-	tss_1500	79551377
1359	cg45928102_TC11	0.00060357	-0.07143638	Lyl1	chr8	+	tss_body	84701612
1360	cg45929549_BC11	2.8332E-05	-0.09476496	Nfix	chr8	-	tss_body	84784358
1361	cg45958149_BC21	0.00050653	0.0306935	Zfp423	chr8	-	tss_body	87803832
1362	cg45959625_BC21	0.0004515	-0.03934383	Zfp423	chr8	-	tss_body	87926403
1363	cg45959793_TC21	0.0008551	0.03137773	Zfp423	chr8	-	tss_body	87940187
1364	cg45991098_TC21	2.3043E-06	-0.06570987		chr8	-	tss_body	91149013
1365	cg45997577_BC21	0.0002232	-0.02614603		chr8	+	tss_1500	91689473
1366	cg45999945_TC21	0.00022781	-0.03984875	LOC108167544	chr8	+	tss_body	91865064
1367	cg46023267_BC21	0.00049347	-0.04497483	Slc12a3	chr8	+	tss_body	94329289
1368	cg46028917_TC21	0.00028552	0.03370276	Ciapin1	chr8	-	tss_body	94832829
1369	cg46029969_TC21	6.201E-07	-0.02899543	Ccdc102a	chr8	-	tss_body	94904105
1370	cg46031209_TC21	0.00092998	-0.04442252	Adgrg1	chr8	+	tss_body	94995870
1371	cg46031499_BC21	0.00035082	-0.03452816	Adgrg3	chr8	+	tss_body	95017757
1372	cg46037373_BC21	0.0005738	0.05728164	Csnk2a2	chr8	-	tss_body	95487650
1373	cg46052640_BC21	0.00012916	0.03233164					97693839
1374	cg46087535_BC21	0.00018122	-0.03386121	Cmtm4	chr8	-	tss_body	104381428
1375	cg46093455_BC21	0.00014652	0.03443758	Ces4a	chr8	+	tss_200	105131613
1376	cg46095485_BC11	7.0284E-05	-0.05788675	Hsf4	chr8	+	tss_body	105272476
1377	cg46095580_TC11	0.00094265	-0.03713001	Nol3	chr8	+	tss_body	105277586
1378	cg46095974_BC21	0.00042646	-0.03872286	Exoc3l	chr8	-	tss_body	105293342
1379	cg46104912_BC21	0.0007195	0.03629992	Lcat	chr8	-	tss_200	105943577
1380	cg46108872_TC21	0.00032031	-0.04107095	Smpd3	chr8	-	tss_body	106264820
1381	cg46136291_BC21	0.00052337	0.04968246	Zfhx3	chr8	+	tss_body	108718467
1382	cg46140142_TC21	0.00030678	-0.03043622	Zfhx3	chr8	+	tss_body	108936885
1383	cg46151036_TC21	0.0002724	0.03108134	Ap1g1	chr8	+	tss_body	109843354
1384	cg46163356_BC21	7.0221E-05	-0.0326815	Cog4	chr8	+	tss_body	110863799
1385	cg46169099_BC21	2.2541E-05	-0.04266574	Mlkl	chr8	-	tss_1500	111338583
1386	cg46201867_BC21	0.00089178	-0.06156246	Wwox	chr8	+	tss_body	114682027
1387	cg46227344_BC21	6.2645E-05	-0.04236431	Pkd1l2	chr8	-	tss_body	117016774
1388	cg46233814_BC11	0.00069178	-0.04737526	Cmip	chr8	+	tss_body	117436860

1389	cg46236842_BC21	0.00056843	0.02538269					117646752
1390	cg46263698_TC21	0.00063694	-0.02518455	Cotl1	chr8	-	tss_body	119826443
1391	cg46264177_TC21	7.8173E-05	-0.05072243					119858059
1392	cg46266235_BC11	0.00017106	0.03526103	Crispld2	chr8	+	tss_body	119992534
1393	cg46268105_TC21	3.7277E-05	-0.02626814	6430548M08Rik	chr8	+	tss_1500	120112668
1394	cg46270739_BC21	0.00098495	-0.06414694	Gse1	chr8	+	tss_body	120277355
1395	cg46271678_BC21	0.00067555	-0.04335263	Gse1	chr8	+	tss_body	120337841
1396	cg46285667_BC21	2.042E-06	0.03341219	Foxl1	chr8	+	tss_body	121128143
1397	cg46291865_TC21	0.0006483	-0.04280521	1700018B08Rik	chr8	-	tss_body	121530995
1398	cg46302868_BC21	0.00017388	-0.03359028	Gm22	chr8	+	tss_body	122194674
1399	cg46311454_BC21	9.0257E-05	-0.06552932	Cbfa2t3	chr8	-	tss_body	122665096
1400	cg46311676_TC21	0.00011676	0.06035743	Cbfa2t3	chr8	-	tss_body	122677882
1401	cg46312076_BC21	0.00012846	-0.06576119	Cbfa2t3	chr8	-	tss_body	122699230
1402	cg46322714_TC21	0.00067992	-0.03255386	Tcf25	chr8	+	tss_body	123398052
1403	cg46327131_BC21	0.00053913	-0.04216343	Q6PB93	chr8	+	tss_body	123702100
1404	cg46352326_TC21	2.8135E-05	-0.02846077	Sipa1l2	chr8	-	tss_body	125518654
1405	cg46352908_TC21	0.00027874	0.04119741	Sipa1l2	chr8	-	tss_body	125563109
1406	cg46353178_TC21	6.6233E-06	-0.03873284	Sipa1l2	chr8	-	tss_1500	125571141
1407	cg46366420_TC21	0.00060838	0.04963939					126685461
1408	cg46368678_TC21	0.000304	-0.06136508					126914859
1409	cg46390852_BC11	0.00032567	-0.05568221					4209772
1410	cg46410628_TC21	0.00092929	0.03573782	Yap1	chr9	-	tss_body	7976520
1411	cg46440003_TC11	0.00036155	0.05361109	Fam76b	chr9	+	tss_body	13839337
1412	cg46447810_TC11	0.00013991	0.03661556	1700012B09Rik	chr9	-	tss_body	14770951
1413	cg46450195_BC21	0.00086421	-0.05427272	Panx1	chr9	-	tss_body	15036959
1414	cg46452677_BC21	0.00056109	0.05447813	Cep295	chr9	-	tss_body	15330309
1415	cg46457772_BC21	0.00018637	-0.04849747	Fat3	chr9	-	tss_body	15938343
1416	cg46469675_BC21	0.00099592	0.02521468	Ubtfl1	chr9	+	tss_body	18408372
1417	cg46492635_TC21	0.00064391	0.04574074	Qtrt1	chr9	+	tss_body	21415332
1418	cg46492684_BC21	0.00042415	-0.02630371	Qtrt1	chr9	+	tss_body	21419439
1419	cg46497453_BC11	0.00083561	-0.02782074	Kank2	chr9	-	tss_body	21792905

1420	cg46500617_BC11	5.8991E-05	-0.05274904	Rgl3	chr9	-	tss_1500	21990217
1421	cg46536497_BC11	0.00013004	0.02558811	Jam3	chr9	-	tss_200	27155492
1422	cg46537790_TC21	0.0003319	-0.05854004	Igsf9b	chr9	+	tss_body	27308764
1423	cg46541065_BC11	5.3115E-05	-0.05460085					27783900
1424	cg46599387_TC21	9.7354E-05	0.04879173	A0A140LHF2	chr9	-	tss_body	35516880
1425	cg46606668_TC21	0.00063582	0.05060734	Fez1	chr9	+	tss_body	36870255
1426	cg46626335_BC21	0.00093949	-0.04523965	Gramd1b	chr9	-	tss_body	40324034
1427	cg46635136_BC21	0.00018013	-0.05824351	Ubash3b	chr9	-	tss_body	41079529
1428	cg46656805_TC21	0.00043898	-0.0376965	Tmem136	chr9	-	tss_1500	43116916
1429	cg46666357_TC21	0.00043797	-0.04150791					43921535
1430	cg46670897_TC11	0.0003321	-0.03310544	Abcg4	chr9	-	tss_body	44287349
1431	cg46685414_TC21	0.00032457	-0.05794086	Fxyd6	chr9	+	tss_body	45387876
1432	cg46695585_BC21	0.00051262	-0.0299319	Apoa4	chr9	+	tss_body	46243100
1433	cg46719627_BC21	7.6035E-06	-0.02700415	Zbtb16	chr9	-	tss_body	48675691
1434	cg46734920_BC21	0.00040436	0.03553339					50376184
1435	cg46740229_TC21	0.00040078	-0.04660315	Alg9	chr9	+	tss_body	50808776
1436	cg46742414_TC21	0.00058775	-0.03145488	Gm32681	chr9	+	tss_body	51052254
1437	cg46768314_TO21	0.00054917	-0.02628131	Dmxl2	chr9	-	tss_body	54474249
1438	cg46778881_TC21	0.00014092	-0.03314899	Isl2	chr9	+	tss_body	55542762
1439	cg46807412_TC21	2.6321E-05	-0.04855416					58422812
1440	cg46822910_BC21	6.3782E-05	-0.0404167	Thsd4	chr9	-	tss_body	60139656
1441	cg46833753_BC21	7.1952E-06	-0.0629474					61164451
1442	cg46836250_TC21	0.00072692	-0.03844754	Tle3	chr9	+	tss_body	61375221
1443	cg46838813_BC21	0.00042745	-0.03451711					61602902
1444	cg46839536_BC21	0.00043025	-0.04203983	Gm34770	chr9	-	tss_1500	61662668
1445	cg46845855_BC21	0.00087069	-0.02542779	Spesp1	chr9	-	tss_body	62282039
1446	cg46848752_TC21	0.00095665	-0.03574577	Coro2b	chr9	-	tss_body	62510475
1447	cg46848908_BC21	0.00099752	-0.03389391	Coro2b	chr9	-	tss_body	62522307
1448	cg46871447_BC21	0.00024213	-0.02886416	Megf11	chr9	+	tss_body	64512302
1449	cg46872939_BC21	4.8726E-07	-0.10562291	Megf11	chr9	+	tss_body	64666570
1450	cg46877033_BC21	1.4579E-05	-0.05973537		chr9	-	tss_1500	65094776

1451	cg46877455_BC21	0.00096724	-0.03925311	Igdcc4	chr9	+	tss_body	65122679
1452	cg46879476_BC21	0.00033495	-0.02881145	Gm36538	chr9	-	tss_body	65265562
1453	cg46882383_TC21	0.00014555	-0.04365359	Ankdd1a	chr9	-	tss_body	65515184
1454	cg46895376_TC21	0.00082729	-0.03063409					66985293
1455	cg46899035_BC21	0.00012787	-0.03360831	Tln2	chr9	-	tss_body	67330739
1456	cg46925706_TC21	0.0004062	-0.05058238	Fam81a	chr9	-	tss_1500	70142693
1457	cg46947915_BC21	0.0005454	0.0315111					72653113
1458	cg47075869_TC21	1.2889E-05	-0.03953206	Adamts7	chr9	+	tss_body	90170139
1459	cg47092634_TC21	0.00047537	0.02753752		chr9	+	tss_body	92895890
1460	cg47118214_TC21	0.00031604	0.03598688	LOC108167675	chr9	+	tss_body	96527270
1461	cg47119459_TC21	0.00069926	0.04020499					96649719
1462	cg47124146_BC21	0.00022571	-0.03147999	Spsb4	chr9	-	tss_body	96995832
1463	cg47135628_TC21	0.00067808	-0.06366681	Nmnat3	chr9	+	tss_body	98388332
1464	cg47136010_TC21	0.00056285	0.04261745	Rbp1	chr9	+	tss_200	98422853
1465	cg47141519_TC21	0.00058499	-0.02978031	Q2TVT7	chr9	+	tss_body	98958330
1466	cg47149849_BC11	0.00049638	0.02802958					99682384
1467	cg47150161_BC21	0.00011056	0.02524664	Cldn18	chr9	-	tss_body	99710102
1468	cg47150247_TC21	0.00088856	-0.03068482	Cldn18	chr9	-	tss_200	99717317
1469	cg47157957_TC21	0.00011739	0.03374324	Slc35g2	chr9	-	tss_body	100569836
1470	cg47192201_BC21	0.00027899	-0.03193142	Nphp3	chr9	+	tss_body	104035814
1471	cg47214924_TC21	8.434E-05	0.02534644	Poc1a	chr9	+	tss_body	106338278
1472	cg47227331_BC21	0.00012439	-0.03374469	Cacna2d2	chr9	+	tss_body	107484672
1473	cg47228397_TC21	9.703E-06	-0.03364049	Nprl2	chr9	+	tss_body	107544189
1474	cg47240375_BC21	0.00042915	-0.03259271	1700102P08Rik	chr9	+	tss_body	108393015
1475	cg47241556_BC21	0.00035063	-0.02889489	Lamb2	chr9	+	tss_body	108486804
1476	cg47244578_TC21	0.00039344	0.03096984	A0A0A6YWE5	chr9	+	tss_1500	108688614
1477	cg47264827_BC21	0.00021422	-0.05988326	Pth1r	chr9	-	tss_body	110746955
1478	cg47266285_TC21	3.3043E-05	-0.05786027	Prss50	chr9	+	tss_body	110858425
1479	cg47266964_TC11	0.00048478	-0.05242938	Als2cl	chr9	+	tss_body	110897760
1480	cg47270249_BC21	0.00072996	0.03006618	Lrrfip2	chr9	+	tss_body	111182247
1481	cg47274295_BC21	0.00062231	-0.02558251	Stac	chr9	-	tss_body	111575045

1482	cg47301499_TC21	5.1082E-05	0.0329212	Cmtm7	chr9	-	tss_body	114761963
1483	cg47317911_TC21	1.0353E-05	0.05346704	Tgfbr2	chr9	-	tss_body	116150893
1484	cg47344801_BC21	0.0008311	-0.0262231	Itga9	chr9	+	tss_body	118807246
1485	cg47350341_TC21	1.1119E-05	0.03828066	Dlec1	chr9	+	tss_body	119145701
1486	cg47350526_BC21	8.7926E-05	0.04166935	Acaa1b	chr9	-	tss_body	119155763
1487	cg47369455_BC11	7.999E-05	-0.0610926					120516908
1488	cg47380470_BC11	0.00010782	0.0552318	Trak1	chr9	+	tss_body	121398493
1489	cg47384463_TC11	2.1963E-06	0.03158481	Sec22c	chr9	-	tss_1500	121706388
1490	cg47391509_BC21	0.00011175	-0.0636192	Gm35289	chr9	+	tss_1500	122315874
1491	cg47395208_BC21	0.0005212	-0.03483813	Gm35501	chr9	+	tss_body	122686532
1492	cg47400998_BC21	0.00063465	0.02612465	Lars2	chr9	+	tss_body	123377790
X chromosome								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47426861_BC21	8.222E-06	-0.02891676	Syp	chrX	+	tss_body	7641201
2	cg47453080_BC21	0.00095065	-0.0275628					11187909
3	cg47454751_TC21	0.0004533	-0.05582261					11432865
4	cg47458439_TC21	0.00021837	-0.05355901					11818597
5	cg47459954_TC21	3.2451E-05	-0.03631598					11981391
6	cg47470742_BC21	0.00062923	0.06844096					12964423
7	cg47495399_BC21	0.0007321	0.03740234	Gm41891	chrX	-	tss_body	18146200
8	cg47557325_TC21	3.1221E-05	0.02539686		chrX	-	tss_200	37037365
9	cg47558215_TC21	0.00021508	0.02729383					37114643
10	cg47621549_BC11	0.0009125	0.03055915					50037851
11	cg47626514_TC21	0.00010298	-0.047832	Frmd7	chrX	-	tss_body	50927790
12	cg47641246_TC21	0.00070442	-0.03157726		chrX	-	tss_body	53052350
13	cg47655468_TC21	2.9838E-06	-0.02524233					56385873
14	cg47663859_TC21	0.00049841	0.06348852					57522065
15	cg47685477_BC21	0.00066493	-0.04219884	Ldoc1	chrX	+	tss_body	61709886
16	cg47708532_BC11	0.00070059	-0.03758793	Gm1140	chrX	-	tss_1500	67694488
17	cg47736044_TC21	1.1345E-05	0.07043004	Zfp92	chrX	+	tss_body	73411587
18	cg47822885_BC21	0.00094772	-0.04857743	Mageb18	chrX	-	tss_body	92509550

19	cg47838575_TC11	0.0008563	0.04684217	chrX-94990585-94990809	chrX	*	SShore	94991466
20	cg47851630_TC21	0.00013833	-0.04140865					97949085
21	cg47868168_BC21	2.4573E-05	0.02623389	Awat1	chrX	+	tss_body	100574961
22	cg47875250_TC21	0.00039124	0.03455865					101468301
23	cg48021187_BC21	0.0001477	-0.04435903	Btk	chrX	-	tss_body	134552086
24	cg48025963_TC11	0.0002995	0.02908613					135227395
25	cg48036611_BC21	0.00055757	0.02977297	Slc25a53	chrX	-	tss_body	136998071
26	cg48072374_BC21	0.00082577	-0.03180186	Rgag1	chrX	+	tss_body	143066246
27	cg48078643_TC21	0.00075936	-0.04041622		chrX	-	tss_200	144233584
28	cg48087405_BC21	0.00021372	-0.04655305		chrX	+	tss_body	145994874
29	cg48114075_BC21	0.00082144	-0.02734465	Kdm5c	chrX	+	tss_body	152267124
30	cg48151464_BC21	0.00036582	-0.06068796	Sh3kbp1	chrX	+	tss_body	159697213
31	cg48152293_BC21	9.6345E-05	-0.03261418	Sh3kbp1	chrX	+	tss_body	159829248
32	cg48194673_BC21	0.00018436	-0.0307952					167103898
Y chromosome								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48212684_TC21	0.00042527	-0.02799399					880537
2	cg48214234_TC11	0.00025806	-0.03053818	Uty	chrY	-	tss_body	1166836
3	cg48216350_BC11	0.00092108	-0.02832163					1766886
4	cg48216476_TC21	0.00075308	-0.03618824		chrY	+	tss_body	1788804
5	cg48216944_BC21	0.00097982	-0.09106302					1876723
6	cg48217446_BC21	0.00049409	-0.03668305		chrY	+	tss_body	1954502
7	cg48219462_TC21	8.9001E-05	-0.02767257					2390460
8	cg48219983_BC21	0.00078438	-0.03395765					2490628
9	cg48223313_TC21	0.00019152	0.0480721					4055925
10	cg48226982_BC21	0.00041159	-0.06420794					4796506
11	cg48230288_TC21	0.00015318	-0.0314154					5434281
12	cg48231845_BC21	0.00029018	0.03584674					5690429
13	cg48242543_BC21	3.8679E-05	0.07166283					8496332
14	cg48333104_BC21	9.2319E-05	-0.03411529	LOC105247287	chrY	+	tss_body	83536486

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.025.

Appendix 4. 35: CpGs which are persistently differentially methylated across the lifespan by postnatal CS exposure in male lungs, identified by limma

Autosomes								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg03755602_TC21	0.00012674	0.05650196	Foxp2	chr6	+	tss_body	15193448
2	cg22758731_BC11	0.00073626	-0.03624298	Adk	chr14	+	tss_body	21369281
3	cg28118640_TC21	0.00021886	0.09063164	Akap12	chr10	+	tss_body	4321548
4	cg28119071_BC21	0.00012354	-0.03439434	Akap12	chr10	+	tss_body	4353759
5	cg28121151_BC21	3.0598E-05	-0.03486396	Ccdc170	chr10	+	tss_body	4511643
6	cg28135224_BC21	0.00015526	0.04257613	Gm3213	chr10	+	tss_body	6367674
7	cg28138683_TC11	0.00098805	0.0431532	Oprm1	chr10	+	tss_body	6976588
8	cg28179259_BC21	5.0081E-05	-0.04253964		chr10	-	tss_body	12009363
9	cg28237096_TC21	0.00042318	0.08164112	Pex7	chr10	-	tss_body	19877966
10	cg28238120_TC21	0.00091479	0.04909821	Map3k5	chr10	+	tss_body	19965840
11	cg28253279_BC21	0.00034062	0.0305729		chr10	-	tss_1500	21411012
12	cg28253365_TC21	0.00028127	-0.05067731		chr10	+	tss_body	21419539
13	cg28284149_BC11	0.00017415	-0.0335166	Med23	chr10	+	tss_body	24873820
14	cg28284790_BC21	0.00028881	-0.06519937	Arg1	chr10	-	tss_body	24923054
15	cg28313788_BC21	0.00053876	-0.05900317	Soga3	chr10	+	tss_body	29197162
16	cg28314972_TC21	0.0002991	0.02599433	Rnf146	chr10	-	tss_body	29362386
17	cg28315004_BC21	0.00061485	0.04051676	Gm4062 1	chr10	+	tss_1500	29367174
18	cg28337586_TC11	0.00031295	-0.0378295	Sult3a2	chr10	-	tss_body	33783689
19	cg28397670_BC21	0.00031528	-0.05982948	Foxo3	chr10	-	tss_body	42274771
20	cg28417237_BC21	9.0949E-05	0.04378996	Aim1	chr10	-	tss_body	43953771
21	cg28422076_BC21	0.00091317	-0.0381115	Prdm1	chr10	-	tss_body	44459898
22	cg28458543_BC21	0.00084033	-0.06071422		chr10	+	tss_body	51456047
23	cg28470035_TC21	0.00081827	-0.07395427	Cep85l	chr10	-	tss_body	53344031
24	cg28492253_BC21	2.1093E-06	-0.04633067		chr10	-	tss_body	57266721
25	cg28497221_TC11	0.00080146	-0.06609854	Lims1	chr10	+	tss_body	58394545
26	cg28498851_TC11	0.00076421	0.04439407	Edar	chr10	-	tss_body	58610295
27	cg28501612_TC21	0.00077907	0.03002127	Sh3rf3	chr10	+	tss_body	58896278
28	cg28504881_BC21	1.3129E-05	-0.05360831					59279882
29	cg28506791_TC21	0.00018504	-0.02772984	Mcu	chr10	-	tss_body	59447568
30	cg28526564_BC21	0.00069099	-0.04160569					60958149
31	cg28529848_BC21	0.00048731	0.04230135	Adamts1 4	chr10	-	tss_body	61247451
32	cg28541010_BC21	0.00015525	0.03013965	Gm5424	chr10	+	tss_body	62071039
33	cg28541880_TC11	0.0005021	0.05006456	Neurog3	chr10	+	tss_body	62133843
34	cg28541943_BC21	0.0005296	-0.0458763	F8WHN9	chr10	-	tss_body	62139392
35	cg28547368_BC11	0.00015006	-0.08958674	H3BIY2	chr10	-	tss_body	62543463
36	cg28608820_TC21	0.00029474	0.02744572	Ank3	chr10	+	tss_body	69541002
37	cg28612947_BC11	0.00018373	0.07932663	Ank3	chr10	+	tss_body	69916688

38	cg28632594_TC11	0.00033318	0.04001955					71523869
39	cg28665277_TC21	0.00026233	0.04843964	D3Z6J4	chr10	+	tss_body	75945690
40	cg28683213_TC21	0.00014487	0.03243895	Gm17769	chr10	+	tss_body	77418670
41	cg28684935_BC21	0.0002176	-0.03380713	Itgb2	chr10	+	tss_body	77557512
42	cg28705011_BC21	0.00013084	0.02638553	Gzmm	chr10	+	tss_200	79689014
43	cg28707784_TC21	0.00080706	-0.03428115	Misp	chr10	+	tss_body	79826608
44	cg28709269_BC21	0.00056644	0.039608	Med16	chr10	-	tss_body	79903287
45	cg28719052_BC21	0.00098651	-0.04204519	Adamtsl5	chr10	-	tss_body	80341835
46	cg28720702_TC21	0.00049937	-0.05453583	Uqcr11	chr10	-	tss_1500	80407956
47	cg28726203_TC21	0.00075895	-0.04280793	Mob3a	chr10	-	tss_body	80696926
48	cg28737724_BC21	0.00038306	-0.03154983	Pip5k1c	chr10	+	tss_body	81301369
49	cg28740307_TC11	0.00048763	-0.05376406	Nfic	chr10	-	tss_body	81407607
50	cg28743524_BC11	0.00085081	-0.029145	Tle2	chr10	+	tss_1500	81574678
51	cg28747223_TC21	0.00092618	-0.04539015	BC024063	chr10	+	tss_200	82083177
52	cg28751541_TC21	9.9495E-06	-0.02995048	Hcfc2	chr10	+	tss_body	82747228
53	cg28756650_TC21	0.00046846	0.05974215	Chst11	chr10	+	tss_body	83102970
54	cg28778632_TC11	8.0569E-05	-0.07453348	Mterf2	chr10	-	tss_1500	85128938
55	cg28810447_BC21	2.4555E-05	0.03590526	D3YYM5	chr10	-	tss_200	88685079
56	cg28824323_TC21	0.00060539	0.05997025	Anks1b	chr10	+	tss_body	90380764
57	cg28826404_TC21	0.00092707	0.04504326	Anks1b	chr10	+	tss_body	90680327
58	cg28842295_BC21	0.00045595	0.04430632					92516667
59	cg28849670_BC21	1.912E-05	-0.07447619	Elk3	chr10	-	tss_body	93284892
60	cg28849847_BC21	0.00082367	-0.04576471	Elk3	chr10	-	tss_body	93298030
61	cg28853431_TC21	7.0164E-05	-0.06459497	Ccdc38	chr10	+	tss_body	93581259
62	cg28865074_BC21	0.00031944	-0.04277088	Tmcc3	chr10	+	tss_body	94523361
63	cg28865198_BC11	0.00015564	0.05141666	Tmcc3	chr10	+	tss_body	94533508
64	cg28879804_TC21	0.00058474	-0.02716606	4732465J04Rik	chr10	+	tss_body	95785147
65	cg28884225_BC21	0.00038341	0.04894483	Gm33782	chr10	+	tss_body	96334300
66	cg28894355_TC21	0.00048811	-0.03929854	Gm10754	chr10	-	tss_body	97797624
67	cg28924314_BC21	0.00011745	0.07091064	Mgat4c	chr10	+	tss_body	102365701
68	cg28967830_TC21	0.0006649	-0.05039816		chr10	-	tss_200	109326901
69	cg29032480_BC21	0.00036514	0.05191026	Cct2	chr10	-	tss_body	117054898
70	cg29040331_TC21	0.00029343	0.06294696	Cpm	chr10	+	tss_body	117671729
71	cg29074286_TC11	3.6469E-05	-0.07660183	Hmga2	chr10	-	tss_body	120428784
72	cg29104472_TC21	0.00016853	-0.07148979	Ppm1h	chr10	+	tss_body	122815483
73	cg29127041_TC21	0.00096171	0.06792241					125782883
74	cg29141351_TC21	0.00061362	-0.0297071	Tspan31	chr10	-	tss_body	127068159
75	cg29144705_BC11	0.00065667	-0.0365174	Kif5a	chr10	-	tss_body	127243674

76	cg29148275_BC21	0.00080395	-0.04161304	Stac3	chr10	+	tss_1500	127501407
77	cg29148902_BC11	0.00029944	-0.02654331	chr10-127526221-127526946	chr10	*	NShore	127525378
78	cg29150675_TC21	0.00044065	-0.05898939	Lrp1	chr10	-	tss_body	127605193
79	cg29150818_BC21	0.00057728	-0.03147942	Lrp1	chr10	-	tss_body	127614140
80	cg29152040_BC21	0.00048516	0.0759874	Tmem194	chr10	+	tss_body	127695475
81	cg29162649_TC21	0.00071001	-0.05690065	Esyt1	chr10	-	tss_body	128515932
82	cg29167425_TC21	0.00021727	-0.04994693	Q549D0	chr10	+	tss_body	128904325
83	cg29189745_TC21	0.00059458	-0.03548657	Lif	chr11	+	tss_body	4270022
84	cg29191915_BC21	0.00083571	0.02819062	Mtmr3	chr11	-	tss_body	4497960
85	cg29197588_BC21	0.00079687	0.07373799	Ap1b1	chr11	+	tss_body	4996907
86	cg29222600_TC21	0.00020263	0.04299918	Adcy1	chr11	+	tss_body	7150124
87	cg29278272_TC21	0.00025074	0.0359849	Ppp3r1	chr11	+	tss_body	17187526
88	cg29323090_BC21	0.00078928	0.0603942					23147334
89	cg29394728_BC21	0.00090139	-0.04180921		chr11	-	tss_body	34009696
90	cg29395000_BC21	0.00010718	-0.07119781	Lcp2	chr11	+	tss_body	34047313
91	cg29466662_BC11	0.00015568	-0.0716056	Ebf1	chr11	+	tss_body	44620409
92	cg29481477_BC21	0.00042014	-0.03964071	Cyfip2	chr11	-	tss_body	46254591
93	cg29497789_TC21	0.00036065	-0.04026582	Trim7	chr11	+	tss_body	48849546
94	cg29518969_TC21	0.00015931	-0.0366658	Olfr51	chr11	+	tss_body	51007795
95	cg29599764_BC21	0.0004309	-0.02950008	Gjc2	chr11	-	tss_body	59182847
96	cg29608273_BC21	0.00043512	-0.0342178		chr11	+	tss_200	59898257
97	cg29615608_BC21	0.00074069	-0.03264964	Myo15	chr11	+	tss_body	60509899
98	cg29616284_BC21	0.00054963	-0.02921921	chr11-60575380-60575667	chr11	*	NShelf	60572780
99	cg29621032_BC21	0.00035058	-0.05835232	Kcnj12	chr11	+	tss_body	61025732
100	cg29623288_TC21	0.00019366	0.03864099	Aldh3a1	chr11	+	tss_body	61214856
101	cg29669621_BC21	0.00037773	0.03475415	LOC102633054	chr11	+	tss_body	66278659
102	cg29675419_BC21	0.00029618	-0.03300495					67075209
103	cg29691631_BC21	0.00069016	0.03658241	Pik3r6	chr11	+	tss_body	68531629
104	cg29697668_BC21	0.00026157	0.03607715	Ctc1	chr11	+	tss_body	69031425
105	cg29711008_BC21	0.00032591	-0.04007927	Spem1	chr11	-	tss_200	69822198
106	cg29713449_TC21	0.00063247	-0.02866689	Slc2a4	chr11	-	tss_body	69944258
107	cg29723465_BC21	0.0007908	-0.04606545	Rnf167	chr11	+	tss_body	70650777
108	cg29725816_TC21	0.00058042	-0.03374156	Scimp	chr11	-	tss_body	70805001

109	cg29726855_TC21	0.00033195	-0.02742116	Rabep1	chr11	+	tss_body	70934453
110	cg29740241_BC21	0.00016196	0.06136173	Spns2	chr11	-	tss_body	72456838
111	cg29747901_BC21	0.00012203	-0.05506858	Trpv1	chr11	+	tss_body	73234255
112	cg29767968_BC21	0.00089674	0.05145225	Slc43a2	chr11	+	tss_body	75569336
113	cg29772434_TC21	0.00029979	0.08218828	Rph3al	chr11	-	tss_body	75929807
114	cg29783167_TC21	0.00018652	0.07440231					76854674
115	cg29788695_BC21	1.8828E-05	-0.0356687	Ankrd13b	chr11	-	tss_body	77483677
116	cg29799693_TC21	7.8668E-05	0.05252366	Aldoc	chr11	+	tss_body	78325520
117	cg29801705_BC21	0.00092021	-0.02784453	Sarm1	chr11	-	tss_body	78482135
118	cg29802520_BC21	0.00029993	-0.06956679	Tnfaip1	chr11	-	tss_body	78530720
119	cg29804653_BC21	0.00014123	0.05995956					78778314
120	cg29812786_BC21	5.047E-05	-0.02719726	Nf1	chr11	+	tss_body	79546770
121	cg29813739_TC21	0.00021579	-0.06332184	Rab11fip4	chr11	+	tss_body	79625246
122	cg29817164_BC21	0.00036823	0.04607884					79885924
123	cg29838322_BC21	0.00094073	-0.0360813	Ccl1	chr11	-	tss_1500	82180037
124	cg29844621_TC21	0.00055761	0.03890922	Lig3	chr11	+	tss_body	82802018
125	cg29889349_BC21	0.00023297	-0.052428	Ppm1e	chr11	-	tss_body	87260089
126	cg29894989_BC21	0.00063861	-0.04771375	Bzrap1	chr11	+	tss_body	87760855
127	cg29969161_TC21	0.00053631	-0.03730576	Phb	chr11	+	tss_body	95670579
128	cg29978381_TC21	0.00016844	0.03503249	Hoxb5os	chr11	-	tss_body	96298799
129	cg29985059_BC11	0.00076978	0.05055379	Snx11	chr11	-	tss_body	96769412
130	cg29986328_TC21	0.00041143	0.04755097	Copz2	chr11	+	tss_body	96857811
131	cg29991518_TC21	0.00083619	0.03343141	Kpnb1	chr11	-	tss_body	97165841
132	cg30000480_TC21	0.00064925	-0.0378554	Pip4k2b	chr11	-	tss_body	97726586
133	cg30004657_BC21	0.0007645	-0.03616124	Cacnb1	chr11	-	tss_body	98018455
134	cg30013063_TC21	0.00062625	0.05497972	chr11-98587032-98587434	chr11	*	SShelf	98589449
135	cg30016053_BC11	0.00038531	0.04387654	chr11-98794754-98796475	chr11	*	NShore	98793025
136	cg30021854_TC11	0.00024796	-0.06259203	Ccr7	chr11	-	tss_body	99150621

137	cg30027059_TC21	0.00054096	0.0405589	LOC105246886	chr11	+	tss_body	99603746
138	cg30030765_TC21	0.00031067	0.06790846					100114720
139	cg30031809_BC21	0.00033437	0.0384711	Krt14	chr11	-	tss_body	100204250
140	cg30038229_TC21	9.1698E-05	-0.05184421	Zfp385c	chr11	-	tss_body	100653917
141	cg30041051_BC21	0.00074204	-0.0315247	Stat5b	chr11	-	tss_body	100849090
142	cg30057036_BC21	0.00073193	-0.04627358	Dusp3	chr11	-	tss_body	101981690
143	cg30059257_BC21	0.00045003	-0.03620715					102116910
144	cg30070284_BC21	0.00031931	-0.03719726	Eftud2	chr11	-	tss_body	102844175
145	cg30072908_TC21	0.0007294	-0.03658118	Dcakd	chr11	-	tss_body	103015982
146	cg30074487_TC21	4.8042E-05	0.070041	chr11-103116397-103116657	chr11	*	NShelf	103114068
147	cg30078271_TC21	0.00062336	0.07605476	Arhgap27	chr11	-	tss_body	103355421
148	cg30085808_BC21	0.00038706	-0.05778623					103962109
149	cg30089248_BC21	0.00090587	-0.02644559	Mapt	chr11	+	tss_body	104233920
150	cg30109316_TC21	0.00016634	0.03549254	Scn4a	chr11	-	tss_body	106320590
151	cg30109656_TC21	0.00014388	0.0728601	Scn4a	chr11	-	tss_body	106345255
152	cg30110108_TC21	0.00075393	-0.03802766	Icam2	chr11	-	tss_body	106380452
153	cg30123452_TC11	0.0007557	0.0329789	Pitpnc1	chr11	-	tss_body	107453929
154	cg30140334_BC21	0.00054695	-0.03227281	Gm36876	chr11	+	tss_body	109012124
155	cg30164752_TC21	2.8517E-05	0.03568843					111539796
156	cg30187390_BC21	0.00054254	0.03363389	Cog1	chr11	+	tss_body	113661200
157	cg30200131_TC21	0.00057052	-0.0545217					114628255
158	cg30204912_BC21	0.00013524	-0.06461161	Cd300ld	chr11	-	tss_body	114989866
159	cg30205297_TC21	8.6019E-06	0.09451529	Cd300e	chr11	-	tss_body	115059345
160	cg30206116_BC21	5.1918E-06	-0.04660439	Rab37	chr11	+	tss_body	115118462
161	cg30209679_TC11	6.3702E-05	0.03891696	Otop2	chr11	+	tss_body	115322196
162	cg30223028_TC21	0.00059661	-0.03696901		chr11	-	tss_body	116120527
163	cg30233070_TC21	5.9262E-05	0.04005115	P70277	chr11	-	tss_body	116676273
164	cg30241340_TC11	0.00032762	0.04823437	Sept9	chr11	+	tss_body	117204969
165	cg30251106_BC21	0.00018547	-0.02771996	Gm11725	chr11	+	tss_body	117891078
166	cg30261861_TC21	0.00034081	-0.06714071	Rbfox3	chr11	-	tss_body	118576704

167	cg30280519_TC21	6.0085E-05	-0.0394736	Rptor	chr11	+	tss_body	119833978
168	cg30289802_BC21	7.3868E-05	-0.02874197	Faap100	chr11	-	tss_body	120377712
169	cg30298895_BC11	0.00025057	-0.03707333	Slc16a3	chr11	+	tss_1500	120948732
170	cg30304067_BC21	0.0005779	0.05270815	Rab40b	chr11	-	tss_body	121387389
171	cg30328929_TC21	0.00010771	0.02632708		chr12	-	tss_200	5067488
172	cg30353898_BC21	5.1136E-05	-0.06384231					8859251
173	cg30358550_TC21	0.00016167	0.06478746	Gm7099	chr12	+	tss_body	9429876
174	cg30378297_TO21	0.00065203	-0.06025772	Gm40270	chr12	-	tss_body	12725223
175	cg30399104_BC21	0.00087028	-0.02562434		chr12	+	tss_body	16186860
176	cg30411035_TC21	0.00086478	0.0335471					17510415
177	cg30440139_BC21	0.00098612	-0.07507275	Asap2	chr12	+	tss_body	21141830
178	cg30484020_BC21	0.00015382	0.03382242	Gm30855	chr12	+	tss_body	27351547
179	cg30484294_TC21	0.00066328	0.05179043					27392059
180	cg30496730_TC21	0.00079534	-0.0335907	Gm31333	chr12	+	tss_body	29129445
181	cg30507191_BC21	9.1509E-05	0.03094927		chr12	-	tss_body	30486794
182	cg30520682_BC21	7.9138E-05	-0.0348029	Gm33111	chr12	-	tss_body	32080999
183	cg30538375_TC21	0.00060953	0.04100118	Hdac9	chr12	-	tss_body	34373091
184	cg30547016_BC11	0.00016415	-0.03424276	9130015A21Rik	chr12	-	tss_body	35674705
185	cg30627789_BC21	0.00089486	-0.029392		chr12	-	tss_body	50999900
186	cg30629834_TC21	0.00010174	-0.07440281					51276717
187	cg30633261_TC11	7.3987E-05	0.0306254	Strn3	chr12	-	tss_body	51627825
188	cg30675847_TC21	0.00071587	-0.06264818					56373131
189	cg30682982_TC21	0.00074813	0.04100567	Slc25a21	chr12	-	tss_body	57160803
190	cg30785434_BC21	0.00011582	-0.03359529	A0A1Y7VL98	chr12	+	tss_body	72758558
191	cg30792700_BC21	0.00052572	0.02662979	Gm34080	chr12	+	tss_body	73456954
192	cg30793699_BC21	0.00013516	0.02574483					73536582
193	cg30820629_BC21	0.00021882	-0.04848302	Ppp1r36	chr12	+	tss_body	76431119
194	cg30840026_BC21	0.00078233	0.06821622	Atp6v1d	chr12	-	tss_body	78848913
195	cg30851834_BC21	1.009E-05	-0.04787145	Gm36660	chr12	-	tss_body	80084452
196	cg30856916_TC21	0.00066663	-0.04231624	Galnt16	chr12	+	tss_body	80523786
197	cg30868350_TC21	0.0004609	0.02637648	Map3k9	chr12	-	tss_body	81732127

198	cg30872348_BC21	0.0001422	-0.04575821	Gm30799	chr12	+	tss_body	82097723
199	cg30877495_TC11	0.00013928	0.02899233	Rgs6	chr12	+	tss_1500	82616748
200	cg30903103_BC21	0.00080454	0.04694065		chr12	+	tss_body	84881889
201	cg31014319_BC21	0.00087867	-0.05057651		chr12	-	tss_body	100084485
202	cg31014320_BC21	0.00092475	-0.06145302		chr12	-	tss_body	100084497
203	cg31047841_BC21	0.00090993	-0.03815477					103494636
204	cg31049410_TC21	0.00075933	-0.03819298	LOC108168025	chr12	+	tss_body	103688837
205	cg31053032_BC11	0.0006312	0.03970712	Serpina3b	chr12	+	tss_body	104127908
206	cg31057227_TC21	0.00084661	-0.04038022					104615609
207	cg31083852_BC21	9.3685E-05	-0.02559346					106597972
208	cg31103026_TC21	0.00032304	-0.04481576	Ccdc85c	chr12	-	tss_body	108221063
209	cg31119721_TC21	0.00062909	-0.03308334	Meg3	chr12	+	tss_body	109542279
210	cg31119827_BC21	0.00057876	-0.06040051	Meg3	chr12	+	tss_body	109549080
211	cg31129899_TC11	0.0007375	-0.05837428					110398502
212	cg31134262_BC21	0.00041614	0.04361022	Dync1h1	chr12	+	tss_body	110658104
213	cg31145412_TC21	4.3532E-05	0.05615128	Exoc3l4	chr12	+	tss_1500	111417743
214	cg31145648_BC11	0.00021847	-0.03211908	Exoc3l4	chr12	+	tss_body	111428946
215	cg31153112_BC21	0.00011662	-0.04382226	Gm36757	chr12	+	tss_1500	111944794
216	cg31159868_BC21	0.00029917	0.04212576	E330035G20Rik	chr12	-	tss_body	112404174
217	cg31161279_BC21	0.00027146	-0.02695764	Tmem179	chr12	-	tss_body	112502494
218	cg31166425_BC21	0.00092948	0.05686054	Ahnak2	chr12	-	tss_body	112797469
219	cg31203203_TC11	0.00069621	-0.02875269	Dnah11	chr12	-	tss_body	118198332
220	cg31231255_BC21	0.00023346	-0.02541049	1700016G22Rik	chr13	-	tss_body	5857980
221	cg31239250_BC21	0.0007756	-0.0299173					7093299
222	cg31319821_BC21	0.0002371	-0.05043658					20049880
223	cg31327884_TC11	0.00094752	0.04972552					21162788
224	cg31328099_BC21	0.00045295	-0.06692676					21174162
225	cg31332244_BC11	0.00096365	0.04813306	Olfr1362	chr13	-	tss_1500	21612316
226	cg31344450_TC21	0.00028034	-0.0306534	Abt1	chr13	-	tss_body	23422133
227	cg31380800_TC21	3.5016E-07	-0.02980247	2610307P16Rik	chr13	-	tss_body	28806399
228	cg31446936_TC21	0.00031782	-0.04933782	Gm30863	chr13	-	tss_body	37509790

229	cg31448806_TC21	1.0682E-05	0.04846945					37680523
230	cg31452933_BC21	0.00019578	0.06363232	Cage1	chr13	-	tss_body	38012859
231	cg31477198_TC21	4.314E-05	-0.02672898	Tfap2a	chr13	-	tss_body	40729433
232	cg31544037_TC21	0.00018019	-0.04383953	Kif13a	chr13	-	tss_body	46925712
233	cg31550001_BC21	9.3696E-05	0.03799184		chr13	+	tss_1500	47360819
234	cg31553244_TC21	0.00070642	0.03062834					47747534
235	cg31566269_BC21	0.0009679	0.04125557	Fam120a	chr13	-	tss_body	48958416
236	cg31567248_BC21	0.00023752	-0.03667682	Wnk2	chr13	-	tss_body	49042691
237	cg31567678_BC21	0.00022925	-0.0530553	Wnk2	chr13	-	tss_body	49079367
238	cg31568259_BC21	0.00045997	-0.04568943	Wnk2	chr13	-	tss_body	49132708
239	cg31571376_BC21	0.00054203	-0.06229896	Bicd2	chr13	+	tss_body	49380080
240	cg31575830_TC21	0.00066189	-0.05203758		chr13	-	tss_body	49945303
241	cg31581924_TC21	0.00022943	-0.0611398					51016633
242	cg31610799_BC21	4.5672E-05	0.04823052	Gm2762	chr13	+	tss_body	53395275
243	cg31617339_BC11	0.00038754	-0.03544391		chr13	+	tss_body	53969063
244	cg31621276_TC21	0.00064793	-0.02732723	Cplx2	chr13	+	tss_body	54323182
245	cg31635651_TC21	0.00071278	0.03225716	Slc34a1	chr13	+	tss_body	55400472
246	cg31637068_BC21	0.00021104	-0.03514587	Prr7	chr13	+	tss_body	55473021
247	cg31674988_BC21	8.1005E-05	-0.06134953	Gm33875	chr13	-	tss_body	58444436
248	cg31686564_BC21	0.00071143	-0.03644721					59423654
249	cg31692375_BC21	0.00032206	-0.04869053	Gm19866	chr13	-	tss_body	59892458
250	cg31718129_TC21	0.00076054	0.03883364	2010111I01Rik	chr13	+	tss_body	63305342
251	cg31723131_BC21	0.00093142	-0.02862194	LOC108168093	chr13	-	tss_body	63901772
252	cg31727315_BC21	0.00033798	-0.0470997	Aaed1	chr13	-	tss_body	64310117
253	cg31741866_TC21	9.7634E-05	0.03649911	Mterf3	chr13	-	tss_body	66927507
254	cg31767961_TC21	0.00075976	0.0280619	1700084F23Rik	chr13	-	tss_body	70026448
255	cg31771672_BC11	0.00074572	-0.0551621					70510373
256	cg31797804_TC21	0.00022105	0.04321394	Slc12a7	chr13	+	tss_body	73763206
257	cg31804647_TC21	2.1146E-05	-0.04706962	LOC108168101	chr13	-	tss_body	74617462
258	cg31808317_TC21	0.00032364	-0.07521564					75368457
259	cg31824994_BC21	0.00032008	-0.03573128		chr13	+	tss_body	78273677

260	cg31925292_TC21	0.00070034	0.07793086	Wdr41	chr13	+	tss_body	94990622
261	cg31928643_BC21	0.0008594	0.05159984	Zbed3	chr13	+	tss_body	95328635
262	cg31943493_BC21	0.00074488	-0.03492013	Ankrd31	chr13	+	tss_body	96870640
263	cg31944614_BC11	0.00071739	-0.06800664	Gm4102 7	chr13	-	tss_body	96984008
264	cg31944712_TC21	0.00053453	-0.03245121					96989641
265	cg31945312_BC21	0.00042682	-0.04104908	Gm4102 8	chr13	+	tss_body	97054036
266	cg31953839_BC21	0.00011841	0.03899976		chr13	-	tss_body	97806028
267	cg31968996_BC21	0.00040048	-0.04230176	Gm807	chr13	+	tss_body	99102269
268	cg31999714_BC21	0.00017643	-0.06659128					10265615 2
269	cg32013108_BC21	0.00044298	0.0388544					10401858 6
270	cg32016573_TC21	0.00014754	-0.06229576	Adamts6	chr13	+	tss_body	10449365 7
271	cg32019149_TC21	0.00027067	0.04323382	Cwc27	chr13	-	tss_body	10479933 5
272	cg32042087_TC21	0.0004232	0.06585718	Gm4105 3	chr13	+	tss_1500	10792290 7
273	cg32044666_BC21	0.00045998	0.02666199	Ndufaf2	chr13	-	tss_body	10814586 0
274	cg32053924_TC21	0.00023057	-0.04431762	Pde4d	chr13	+	tss_body	10934208 8
275	cg32076313_BC21	0.00056289	-0.03053061	Gm1532 6	chr13	+	tss_body	11187118 8
276	cg32076988_BC11	0.0001899	-0.03408696					11193610 6
277	cg32081346_BC21	0.00084702	0.08117021	Ankrd55	chr13	+	tss_body	11231701 1
278	cg32086034_TC21	0.0006065	0.03138952					11274786 5
279	cg32141464_BC21	3.4625E-05	-0.03311018	Gm4107 7	chr13	+	tss_body	11976747 2
280	cg32250904_BC21	0.00051935	-0.03443326	S4R2Q8	chr14	+	tss_body	21491182
281	cg32257308_BC21	0.00079211	-0.03804583	1700112 E06Rik	chr14	+	tss_body	22048900
282	cg32261871_TC11	0.000453	0.07677158	1700112 E06Rik	chr14	+	tss_body	22633995
283	cg32272878_TC21	0.00036446	-0.03100003	Dlg5	chr14	-	tss_body	24214512
284	cg32276489_BC21	8.7096E-05	0.03361104		chr14	+	tss_body	24645373
285	cg32280460_BC21	0.00056209	-0.03933534	Gm3222 4	chr14	+	tss_1500	25127640
286	cg32298927_BC21	0.00015776	0.04807117	Arhgef3	chr14	+	tss_body	27184567
287	cg32299494_TC21	0.00016114	-0.05093869	Arhgef3	chr14	+	tss_body	27238007
288	cg32337222_BC21	2.9946E-05	-0.06548737	Sh3bp5	chr14	-	tss_body	31414847
289	cg32338966_TC21	0.00042691	-0.04131103	Colq	chr14	-	tss_body	31564911
290	cg32340118_TC21	0.0007767	-0.06318845	Btd	chr14	+	tss_body	31661958

291	cg32344040_BC21	0.00066923	0.0296816	Dph3	chr14	-	tss_body	32081074
292	cg32348660_TC21	0.00032852	-0.04644662	Ercc6	chr14	+	tss_body	32531783
293	cg32365180_BC21	0.00096531	-0.05072605	Syt15	chr14	+	tss_1500	34219710
294	cg32373940_BC21	0.00016769	-0.06344378	Grid1	chr14	+	tss_body	35093863
295	cg32385542_BC21	0.0002279	0.06468664					37295725
296	cg32395736_TC21	2.3413E-07	-0.05569175	1700109I08Rik	chr14	+	tss_body	39655796
297	cg32447024_BC21	0.00024944	0.04804281	4930447J18Rik	chr14	+	tss_body	47911377
298	cg32470109_TC21	8.412E-05	0.0583986	Klhl33	chr14	-	tss_body	50896780
299	cg32490491_BC21	0.00034756	-0.06187143					53805047
300	cg32503247_TC11	0.00036794	0.02600259	Slc22a17	chr14	-	tss_body	54913571
301	cg32506418_TC11	0.00041497	0.07077794	Jph4	chr14	-	tss_body	55113926
302	cg32516034_BC21	8.6083E-06	0.04791756	Nynrin	chr14	+	tss_body	55866547
303	cg32526170_BC21	1.8695E-05	0.02675746	Gjb2	chr14	-	tss_body	57104696
304	cg32546818_TC21	0.00049816	0.03389812	Shisa2	chr14	+	tss_200	59625114
305	cg32548093_TC21	0.00082233	-0.03233058	Atp8a2	chr14	-	tss_body	59736010
306	cg32553099_TC21	0.0002906	0.05733264	Gm38641	chr14	+	tss_body	60262013
307	cg32557741_BC21	0.00067835	-0.06035423	Spata13	chr14	+	tss_body	60709370
308	cg32564080_TC11	1.9243E-06	-0.10535129	Arl11	chr14	+	tss_body	61309901
309	cg32566768_BC21	0.00064745	0.03626901	Trim13	chr14	+	tss_body	61602011
310	cg32567836_TC21	9.5572E-05	-0.04319297	Gm35196	chr14	-	tss_body	61689620
311	cg32578622_BC21	0.00077281	-0.03449187		chr14	+	tss_body	62973866
312	cg32583869_BC11	7.3103E-05	-0.06897934					63427904
313	cg32584731_TC21	0.00066734	0.03524682	Tdh	chr14	-	tss_body	63509062
314	cg32590249_BC21	0.00072342	-0.04193978					64070622
315	cg32607175_TC21	0.00041888	-0.02682377	Pbk	chr14	+	tss_body	65812345
316	cg32609377_BC11	0.00051031	-0.05722078					66023651
317	cg32653053_TC21	0.00053288	0.02887055	chr14-70577466-70578210	chr14	*	NShore	70576017
318	cg32653900_TC21	0.00019886	0.05665258	Dmtn	chr14	-	tss_body	70626171
319	cg32683942_TC21	0.00079961	-0.0434587	Gm4278	chr14	+	tss_body	74976550
320	cg32731024_BC21	0.0005099	0.04058329	Elf1	chr14	+	tss_body	79527404

321	cg32733070_BC21	0.00084075	-0.06054129					79725752
322	cg32805816_TC21	0.00095876	0.03640441					94466431
323	cg32858594_BC21	0.00047292	-0.04091313	Gm3458 9	chr14	-	tss_body	10283255 2
324	cg32961499_BC21	0.00036517	-0.0593849	Cldn10	chr14	+	tss_body	11879736 4
325	cg32976071_TC21	0.00057956	0.0585871	Mbnl2	chr14	+	tss_body	12029773 8
326	cg32986123_BC11	0.00079419	0.06745946	Farp1	chr14	+	tss_body	12117273 2
327	cg32988705_BC21	0.00011881	-0.03711365	Stk24	chr14	-	tss_body	12135866 2
328	cg33059141_BC21	0.00065131	-0.05683425	Ranbp3l	chr15	+	tss_body	8994810
329	cg33059744_TC21	0.0005468	-0.03844293	Nadk2	chr15	+	tss_body	9088039
330	cg33181147_TC11	0.00033234	0.03951107	Trio	chr15	-	tss_body	27989044
331	cg33195283_BC21	0.00074158	-0.05090248	Ctnnd2	chr15	+	tss_body	30387571
332	cg33204808_BC21	0.00020488	-0.08004252					31418260
333	cg33230186_TC21	0.00014157	-0.04900849	Osr2	chr15	+	tss_body	35300433
334	cg33245717_BC21	0.00068107	-0.02759754					37053394
335	cg33251424_BC11	0.00030275	0.04145403	Ncald	chr15	-	tss_body	37604133
336	cg33253194_TC21	0.000934	-0.04489493	Ncald	chr15	-	tss_body	37792540
337	cg33269150_TC11	0.00070973	0.03866164	Dcstamp	chr15	+	tss_body	39746204
338	cg33298170_BC21	0.00071511	-0.03012885	Sybu	chr15	-	tss_body	44752247
339	cg33356786_TC21	6.6472E-05	0.04446976	Col14a1	chr15	+	tss_body	55442476
340	cg33370853_BC21	0.00090612	0.02707863	Zhx2	chr15	+	tss_body	57744956
341	cg33407492_TC21	0.00086813	0.04700379	Pvt1	chr15	+	tss_body	62092637
342	cg33495810_BC21	0.00041596	-0.02755978	Gm3459 3	chr15	+	tss_body	75498845
343	cg33506085_TC21	0.00099001	-0.03257182	Plec	chr15	-	tss_body	76177122
344	cg33506459_BC21	0.0001695	-0.03238266	Plec	chr15	-	tss_body	76183686
345	cg33511842_TC11	0.00079716	-0.04380496	Hsf1	chr15	+	tss_body	76478631
346	cg33524179_TC21	0.00023929	0.03559853	Apol9a	chr15	-	tss_body	77408833
347	cg33526200_BC11	0.00083902	-0.04859089	Apol9b	chr15	+	tss_body	77732971
348	cg33532518_TC21	8.6887E-05	-0.05887769	Ift27	chr15	-	tss_body	78173465
349	cg33533855_TC21	0.00023188	-0.02632049	Csf2rb2	chr15	-	tss_body	78285212
350	cg33547472_TC21	5.1849E-05	-0.03268569	Gm1086 3	chr15	+	tss_1500	79165457
351	cg33560469_BC21	0.00037715	-0.07682212	Pdgfb	chr15	-	tss_body	80000451

352	cg33562072_TC21	0.00038009	-0.03557638	Syngr1	chr15	+	tss_body	80098987
353	cg33575248_BC21	0.00013818	0.04093606	Gm31608	chr15	+	tss_200	81217119
354	cg33580565_BC21	0.00057583	-0.05303584	Chadl	chr15	-	tss_body	81697239
355	cg33596037_TC21	9.4186E-05	-0.02570033	Nfam1	chr15	-	tss_body	83011202
356	cg33597416_BC21	4.9841E-05	-0.02676512	Serhl	chr15	+	tss_body	83112898
357	cg33615355_BC21	0.00051085	0.05823326	1810041L15Rik	chr15	-	tss_body	84430135
358	cg33641823_TC21	0.0001273	-0.04781735	Tbc1d22a	chr15	+	tss_body	86396921
359	cg33671081_TC11	0.00097505	-0.02791392	Plxnb2	chr15	-	tss_1500	89182408
360	cg33694784_TC11	0.00037597	0.0396036					91614558
361	cg33722351_TC21	0.00097889	0.03732727	Adamts20	chr15	-	tss_body	94356697
362	cg33771431_TC21	0.00018873	0.0325603	Ccdc184	chr15	+	tss_body	98168486
363	cg33794246_BC21	0.0007122	0.03224219	Racgap1	chr15	-	tss_body	99626482
364	cg33798177_BC21	0.00012968	0.05125088		chr15	+	tss_200	99880068
365	cg33800417_BC21	0.00016938	0.08840844	Dip2b	chr15	+	tss_body	100081901
366	cg33808540_BC21	0.00019203	-0.04201508	Bin2	chr15	-	tss_body	100649061
367	cg33821671_TC11	0.00048194	-0.04139662	Krt86	chr15	+	tss_body	101479791
368	cg33825901_BC11	0.0005811	0.05915249	Krt4	chr15	-	tss_200	101924767
369	cg33838197_TC21	0.00037446	-0.05846274	chr15-102927187-102927519	chr15	*	SShelf	102931359
370	cg33838986_BC11	0.00032245	-0.03108859	chr15-102967304-102967662	chr15	*	NShelf	102965061
371	cg33839082_TC21	0.00039088	0.03515738	Hoxc10	chr15	+	tss_body	102967557
372	cg33841859_BC21	0.00026862	-0.02521088	Smug1	chr15	-	tss_1500	103170140
373	cg33843815_BC21	1.5975E-05	0.03976193	Zfp385a	chr15	-	tss_body	103339787
374	cg33854628_BC21	7.0556E-05	0.0416873	Crebbp	chr16	-	tss_body	4096582
375	cg33863379_BC21	0.00012946	0.04097401	Anks3	chr16	-	tss_body	4957645
376	cg33886974_TC21	0.00033725	0.03727946					8380046
377	cg33888187_TC11	0.00074149	0.03381307					8492512
378	cg33911457_BC21	6.0335E-05	-0.05175219	Zc3h7a	chr16	-	tss_body	11143662
379	cg33915220_TC21	0.00069593	0.02775891	Snx29	chr16	+	tss_body	11530328

380	cg33934498_TC21	9.5969E-05	-0.05694508	Marf1	chr16	-	tss_body	14157843
381	cg33952927_TC21	0.00080947	-0.04319705	Sdf2l1	chr16	-	tss_body	17130855
382	cg33954720_TC21	5.9997E-06	0.02745756	Tmem191c	chr16	+	tss_body	17276555
383	cg33964251_TC11	0.0002052	0.0747637	Rtn4r	chr16	+	tss_body	18128518
384	cg33970361_BC21	0.00091641	-0.05215978	Gp1bb	chr16	-	tss_body	18622327
385	cg33991015_BC11	0.00076313	-0.03920498		chr16	+	tss_body	21247019
386	cg33992856_BC21	0.00012267	0.04266363					21405314
387	cg33998985_BC11	0.00073458	-0.03665633	Liph	chr16	-	tss_body	21976186
388	cg34000406_BC21	0.00078006	-0.03443271	Igf2bp2	chr16	-	tss_body	22097531
389	cg34014734_TC21	1.2973E-05	-0.03813441	Masp1	chr16	-	tss_body	23506831
390	cg34049523_TC21	0.00071248	0.0276282	Mb21d2	chr16	-	tss_body	28871229
391	cg34065183_BC11	0.00091926	0.04194788	A0A2R8VJX0	chr16	-	tss_1500	30406233
392	cg34101625_BC21	0.00020127	0.06729226	Heg1	chr16	+	tss_body	33728655
393	cg34108738_TC21	0.00046061	-0.04887519	Kalrn	chr16	-	tss_body	34361002
394	cg34127650_BC21	0.00017267	-0.04843372	Ccdc58	chr16	+	tss_body	36081441
395	cg34130280_TC11	0.0007888	-0.05794458	Casr	chr16	-	tss_body	36531817
396	cg34131822_BC21	0.00039684	-0.04698032	Ildr1	chr16	+	tss_body	36709405
397	cg34140472_TC21	0.00074825	-0.04002009	Gm41452	chr16	-	tss_body	37845342
398	cg34149678_BC21	0.00086623	-0.04982492	Arhgap31	chr16	-	tss_body	38653780
399	cg34163587_BC21	0.00094245	-0.03198421		chr16	+	tss_body	40968434
400	cg34170614_BC21	0.00039874	0.04079952					48797461
401	cg34214647_TC21	0.00062045	0.04735579	Trat1	chr16	-	tss_body	54002829
402	cg34245948_BC21	0.00038728	0.04870439					55888192
403	cg34256279_TC11	0.00089826	-0.03574946	Nxpe3	chr16	-	tss_body	70862794
404	cg34342950_TC21	0.00012578	0.05215577					72694833
405	cg34352749_BC21	0.0008891	-0.03874044	Robo1	chr16	+	tss_body	79091035
406	cg34398520_TC21	0.00087694	0.04596053	Tmprss15	chr16	-	tss_body	85899376
407	cg34436113_BC21	0.00033649	-0.0330808	Adamts5	chr16	-	tss_body	87763124
408	cg34449343_TC21	0.00035098	0.05910104	Gm32925	chr16	+	tss_body	89988843
409	cg34466747_TC21	1.438E-05	-0.05036352	Tiam1	chr16	-	tss_body	90085835
410	cg34468318_TC21	0.00073233	0.05173272	Tiam1	chr16	-	tss_body	91160849

411	cg34483440_BC21	0.00051285	-0.03476493	Gm41492	chr16	-	tss_body	91268870
412	cg34485066_BC21	0.00047861	-0.03557256	Olig1	chr16	+	tss_1500	91453534
413	cg34487667_BC21	0.00074303	0.03868229		chr16	-	tss_body	91527458
414	cg34488706_BC21	0.00029368	-0.06344959	Mir6367	chr16	-	tss_body	92604885
415	cg34504287_TC21	0.00038168	0.08783206	Runx1	chr16	-	tss_body	92694618
416	cg34505700_BC21	0.00072768	0.05211063	Runx1	chr16	-	tss_body	93089780
417	cg34510361_TC21	0.00064488	-0.02941358					93777644
418	cg34518503_TC21	0.00041242	-0.0372117	Dopey2	chr16	+	tss_body	95101143
419	cg34535393_BC21	0.00065034	-0.0601636		chr16	+	tss_1500	96206452
420	cg34547676_BC21	0.00094971	0.05721038	Sh3bgr	chr16	+	tss_body	3101677
421	cg34561694_TC21	0.00084752	-0.03688904		chr17	-	tss_body	4854437
422	cg34574773_BC21	0.00016749	0.04262088		chr17	-	tss_body	5975757
423	cg34588755_BC21	0.00080629	-0.06023248	Synj2	chr17	+	tss_body	6731142
424	cg34596803_BC21	0.00035736	-0.03285773	Sytl3	chr17	+	tss_body	6808495
425	cg34598087_BC21	0.00058192	0.08222107	LOC102640250	chr17	-	tss_1500	7353111
426	cg34604687_TC21	0.00022892	0.0289552	Ttll2	chr17	-	tss_body	7645397
427	cg34606894_BC21	0.0009946	0.05811662		chr17	+	tss_body	8337858
428	cg34613170_BC21	0.00062237	0.0250679		chr17	+	tss_body	9669332
429	cg34625455_BC11	0.00016745	-0.03461154	Pabpc6	chr17	-	tss_body	10450035
430	cg34632402_BC21	0.0008837	0.05139639	Pacrg	chr17	-	tss_body	11613800
431	cg34640852_TC21	0.00096133	-0.05850524	Park2	chr17	+	tss_body	12044737
432	cg34645025_BC21	0.00054607	-0.02689556	Park2	chr17	+	tss_body	12669923
433	cg34652290_TC21	0.00029841	-0.02677424	Slc22a1	chr17	-	tss_body	14279338
434	cg34665537_BC21	0.00069602	0.03439061	Smoc2	chr17	+	tss_200	15194192
435	cg34673519_BC21	0.00092577	0.07580775	Gm35502	chr17	+	tss_1500	23642216
436	cg34720990_TC11	0.00032677	-0.02613196	Mmp25	chr17	-	tss_body	24156797
437	cg34727211_BC21	0.0008554	-0.04449416	Pdpk1	chr17	-	tss_1500	24179895
438	cg34727602_BC21	0.00038699	-0.04748746	Tbc1d24	chr17	-	tss_body	25171526
439	cg34741624_BC21	2.2934E-06	-0.0444995	Ccdc154	chr17	+	tss_body	26828288
440	cg34764260_BC21	0.00062519	-0.03396465					26935257
441	cg34765989_BC21	3.6464E-05	-0.02821985	Phf1	chr17	+	tss_body	26994662

442	cg34767122_BC21	0.00094938	-0.02938342	Q8CDC7	chr17	+	tss_body	28077040
443	cg34784958_BC21	8.7073E-05	-0.03613919	Tcp11	chr17	-	tss_body	28245020
444	cg34788080_BC21	0.00082853	-0.03288255	Ppard	chr17	+	tss_body	28522253
445	cg34792384_TC21	0.00036949	0.04660539	LOC102639076	chr17	+	tss_body	28690896
446	cg34794653_BC21	0.00044493	0.02883934	Mapk14	chr17	+	tss_1500	29280915
447	cg34803419_TC11	0.00053534	-0.05450215	BC004004	chr17	+	tss_body	29500661
448	cg34806844_BC21	0.00019696	-0.04611314					30465648
449	cg34819031_BC11	0.00055929	-0.0504146	Btbd9	chr17	-	tss_body	31319178
450	cg34829872_BC21	0.00086147	0.069633	Slc37a1	chr17	+	tss_body	31521773
451	cg34832519_TC21	0.00080884	0.04540549	Ndufv3	chr17	+	tss_body	31642953
452	cg34834454_BC11	0.00011008	-0.05297633					32363091
453	cg34843293_BC21	0.00034617	0.03621404	Wiz	chr17	-	tss_body	33468619
454	cg34852022_BC21	0.00056934	-0.04580119		chr17	-	tss_body	33555668
455	cg34852811_BC11	3.9942E-05	-0.07515732	Myo1f	chr17	+	tss_200	33640268
456	cg34853533_BC11	0.00021544	-0.04382779	Pram1	chr17	+	tss_body	33650125
457	cg34853641_TC21	0.00054707	-0.03053711	Hnrnpm	chr17	-	tss_body	35204704
458	cg34877083_TC21	0.00086743	-0.05720857	Lta	chr17	-	tss_body	35425706
459	cg34879966_BC21	0.00080454	-0.03338643	H2-Q6	chr17	+	tss_body	38134440
460	cg34901870_BC21	1.3225E-06	-0.02991297	Q7TRI8	chr17	-	tss_body	39627016
461	cg34908719_TC11	0.00032621	0.04740226					40598705
462	cg34913423_TC21	0.00033293	0.04497867	Esp4	chr17	+	tss_body	45209734
463	cg34947218_TC21	0.000731	-0.02610516		chr17	+	tss_1500	45667804
464	cg34953741_TC21	0.00066662	0.03348467	Tmem63b	chr17	-	tss_body	47267097
465	cg34978593_TC21	0.00090679	0.02816198	Trerf1	chr17	+	tss_body	47480521
466	cg34981740_TC21	0.00027158	-0.03167766					47592774
467	cg34983294_BC21	0.00097113	0.04633458	Ccnd3	chr17	+	tss_body	56315072
468	cg35053503_BC21	0.00064007	0.03183975	Uhrf1	chr17	+	tss_body	56315417
469	cg35053509_TC21	0.00041945	-0.04510192	Uhrf1	chr17	+	tss_body	56509812
470	cg35056641_TC21	1.8538E-05	-0.05229038	chr17-56511298-56512467	chr17	*	NShore	58855549
471	cg35074227_TC11	5.7328E-05	0.0370032					64622353

472	cg35112463_BC11	0.00056106	-0.05078781	Man2a1	chr17	+	tss_body	73012696
473	cg35195518_BC21	0.00071434	-0.04493221					74028592
474	cg35204299_TC21	1.7809E-05	0.03458058	Srd5a2	chr17	-	tss_body	79580689
475	cg35246008_TC21	0.00054276	0.03440032	Gm4162 3	chr17	-	tss_body	79918446
476	cg35249475_BC21	0.00037711	0.04489294	Gm4162 5	chr17	-	tss_body	83741172
477	cg35283700_TC21	0.00043064	0.03516256	Mta3	chr17	+	tss_body	85059807
478	cg35300001_TC21	0.00015756	0.040757	Slc3a1	chr17	+	tss_body	88664558
479	cg35346251_TC11	0.00073542	-0.05529377	Gtf2a1l	chr17	+	tss_1500	90088143
480	cg35354182_TC21	0.00033257	-0.08753041	Nrxn1	chr17	-	tss_body	12287088
481	cg35437234_BC11	0.00030346	0.05956806	Ankrd29	chr18	-	tss_body	12643242
482	cg35440351_TC21	0.0006575	0.03464595	Ttc39c	chr18	+	tss_1500	17028695
483	cg35472033_BC11	0.00046023	0.04603995		chr18	+	tss_body	20375835
484	cg35486871_TC21	0.00030494	-0.04507926	Dsg1b	chr18	+	tss_1500	20956669
485	cg35491721_BC21	0.00033643	-0.05294006	Rnf125	chr18	+	tss_body	25554628
486	cg35525053_BC11	0.00010901	-0.03043445	Celf4	chr18	-	tss_body	27987620
487	cg35537377_TC21	0.00074752	-0.04004492					32112167
488	cg35560821_TC21	0.00048517	0.05057547		chr18	-	tss_body	33297150
489	cg35569915_TC21	0.00056836	0.03399263	LOC1081 68400	chr18	+	tss_body	33988476
490	cg35576078_TC21	8.9415E-05	0.05634109	Epb41l4a	chr18	-	tss_body	35933577
491	cg35597061_BC21	0.00027318	-0.03859067	chr18-3593038 0-3593085 3	chr18	*	SShelf	36664048
492	cg35604877_TC21	0.00018299	0.03531128	Eif4ebp3	chr18	+	tss_200	36696057
493	cg35605321_BC21	0.00036026	-0.04641478	E230025 N22Rik	chr18	-	tss_body	37434375
494	cg35612458_TC21	0.0009132	0.06044102	Gm3701 3	chr18	+	tss_body	37473534
495	cg35612835_BC21	0.00012491	-0.05162536	Gm3701 3	chr18	+	tss_body	37484067
496	cg35612996_BC11	2.0952E-05	0.09376869	Gm3701 3	chr18	+	tss_body	38184208
497	cg35621845_TC21	0.00025273	-0.06054634	chr18-3818598 8-3818627 9	chr18	*	NShore	38203224
498	cg35622263_BC21	0.00022098	-0.03732486	Pcdh1	chr18	-	tss_body	38213469
499	cg35622573_TC21	6.6894E-05	0.05136606	2010320 O07Rik	chr18	+	tss_body	38284467

500	cg35623507_BC21	0.00029516	-0.03798241	Rnf14	chr18	+	tss_body	38795648
501	cg35629232_BC21	0.0001731	-0.07282771	Arhgap26	chr18	+	tss_body	42105651
502	cg35650517_BC21	2.8349E-05	0.04392814	Sh3rf2	chr18	+	tss_body	47019856
503	cg35687980_BC21	0.00047023	-0.02879779	Commd10	chr18	+	tss_body	47349148
504	cg35691157_TC21	9.536E-05	-0.04483604	Sema6a	chr18	-	tss_body	52750887
505	cg35722888_TC21	0.00073384	-0.03772452					54952466
506	cg35743595_TC11	0.00027175	0.07232933	Zfp608	chr18	-	tss_body	56600901
507	cg35756537_TC21	0.00012963	-0.04482662		chr18	-	tss_body	60300347
508	cg35785364_BC21	0.00053423	-0.05427385	F830016B08Rik	chr18	+	tss_body	61220437
509	cg35796892_BC21	8.2991E-05	-0.04787363	Pde6a	chr18	+	tss_200	61402055
510	cg35799179_BC21	0.00056864	0.06015474	Ppargc1b	chr18	-	tss_1500	61759272
511	cg35803669_TC11	0.00037403	-0.04547332	Afap1l1	chr18	-	tss_body	62172787
512	cg35808081_BC21	0.00068766	-0.03607004					64489766
513	cg35828957_TC21	0.00042125	0.04716423	Fech	chr18	-	tss_1500	65783388
514	cg35843824_TC21	0.00041142	-0.03061284					67007581
515	cg35855528_TC21	0.00029711	0.0547158					68304689
516	cg35870584_TC21	0.0003492	0.04403476	Rnmt	chr18	+	tss_body	70707817
517	cg35893379_BC21	0.00085479	-0.03608061		chr18	-	tss_1500	74823340
518	cg35925532_BC21	0.00093011	-0.05279596					75187319
519	cg35930267_BC21	0.00013575	0.05274607	Dym	chr18	+	tss_body	75502906
520	cg35935053_BC21	0.00091234	-0.04519611	Ctif	chr18	-	tss_body	75554640
521	cg35935744_TC21	2.9279E-05	0.02580974	Ctif	chr18	-	tss_body	77281919
522	cg35955631_TC11	0.00075837	-0.03771592	Loxhd1	chr18	+	tss_200	77359091
523	cg35956477_BC21	0.00046073	0.03730171	Loxhd1	chr18	+	tss_body	84944411
524	cg36037379_TC21	0.0003981	-0.0346748	Fbxo15	chr18	+	tss_body	89257236
525	cg36057015_BC21	0.00086993	-0.03554849	Cd226	chr18	+	tss_body	3283025
526	cg36064396_BC21	0.00017922	0.02549204	Mrpl21	chr19	+	tss_200	3413505
527	cg36065940_TC21	2.2504E-05	-0.03741615	Gal	chr19	-	tss_body	4170093
528	cg36075296_TC21	0.00024091	-0.03186555	Carns1	chr19	-	tss_body	5051366
529	cg36086650_BC21	0.00045256	-0.02507487	Rin1	chr19	+	tss_body	5298345
530	cg36089794_TC21	1.0012E-05	0.0574978	Gal3st3	chr19	+	tss_body	5554002

531	cg36094181_BC11	0.00095252	0.02616541	Ovol1	chr19	-	tss_body	5745681
532	cg36097929_BC21	0.00065294	-0.02845532	Ltbp3	chr19	+	tss_body	5877948
533	cg36100119_BC21	0.00022603	-0.05744548	Slc25a45	chr19	+	tss_1500	7095147
534	cg36117818_BC21	0.00051258	-0.03668748	Macrod1	chr19	+	tss_body	8540770
535	cg36129491_TC21	0.00046315	-0.03929803		chr19	-	tss_body	8875199
536	cg36133327_BC21	0.00032759	0.02661422	Ubxn1	chr19	+	tss_body	9559137
537	cg36138816_BC21	0.00059159	-0.03002536	Stxbp3-ps	chr19	-	tss_body	9938946
538	cg36141002_TC11	0.00076655	-0.09232578	Gm36913	chr19	-	tss_body	10188282
539	cg36143712_BC21	0.00037478	-0.05632153	Fads1	chr19	+	tss_body	11874669
540	cg36158794_TC21	2.1333E-05	0.04967015	Q7TQS2	chr19	-	tss_body	14481224
541	cg36173320_TC21	0.00090344	-0.02522176	Tle4	chr19	-	tss_body	14665687
542	cg36174845_BC21	0.00031363	0.04024608					15954717
543	cg36183424_BC11	0.00099827	0.03072266					16174172
544	cg36185731_BC21	0.00069003	-0.02539975	Gnaq	chr19	+	tss_body	16436859
545	cg36187925_BC21	0.00019441	-0.04398121	Gna14	chr19	+	tss_body	16449429
546	cg36188063_BC21	0.00016844	-0.06521194	Gna14	chr19	+	tss_body	22106198
547	cg36227082_BC21	3.4611E-05	0.10209085					23282145
548	cg36236458_BC21	0.00030853	-0.03269741		chr19	+	tss_body	25300048
549	cg36257875_BC21	0.00070428	0.03763023	Kank1	chr19	+	tss_body	28262571
550	cg36283821_TC21	0.00013213	0.04028394	Glis3	chr19	-	tss_body	30420051
551	cg36306444_BC21	0.00093891	0.04097875					38246410
552	cg36368659_BC21	0.0004071	0.0311596					40873134
553	cg36390105_BC21	0.00059752	-0.04468099	LOC108168428	chr19	+	tss_body	41014053
554	cg36391538_TO11	0.00045173	0.03718319	LOC100861913	chr19	-	tss_body	42158073
555	cg36406048_BC21	0.00067989	-0.06848418					42211985
556	cg36406852_TC21	0.00081653	-0.0455301					42379142
557	cg36409100_TC21	0.0005547	0.03282624	Crtac1	chr19	-	tss_body	42752604
558	cg36413792_BC11	0.00059594	0.05397188	Pyroxd2	chr19	-	tss_body	43889186
559	cg36425647_BC21	0.00026474	0.08844636	Dnmbp	chr19	-	tss_body	43893142
560	cg36425720_TC21	0.00061904	0.03659979	Dnmbp	chr19	-	tss_body	43920544
561	cg36426137_BC21	9.2906E-06	-0.0645706	Dnmbp	chr19	-	tss_body	44694939

562	cg36436192_BC21	0.00027827	-0.0352922	Gm26644	chr19	-	tss_body	45323157
563	cg36445977_TC21	0.00021205	-0.03925261		chr19	-	tss_body	45765605
564	cg36451687_TC21	3.2758E-05	0.02645896	Mgea5	chr19	-	tss_body	47510995
565	cg36476184_BC21	0.00042934	-0.07078045	Obfc1	chr19	-	tss_body	47661311
566	cg36478113_BC21	0.00028223	0.02576037	Col17a1	chr19	-	tss_body	49090704
567	cg36491706_TC21	0.00028749	-0.04719791		chr19	+	tss_body	56724389
568	cg36557776_BC21	0.00017181	-0.04600837	Adrb1	chr19	+	tss_body	57875040
569	cg36573110_BC21	0.00049256	0.06817229	Atrnl1	chr19	+	tss_body	58830434
570	cg36583398_TC21	0.00040726	0.05422637	Hspa12a	chr19	-	tss_body	59366059
571	cg36589413_BC21	0.00092963	-0.03711879					10056660
572	cg36641404_BC21	0.00024301	-0.04700474	Cspp1	chr1	+	tss_body	13052377
573	cg36658500_BC21	0.0003587	-0.06307949					35806866
574	cg36798717_BC21	0.00037475	0.04938963		chr1	+	tss_200	36103996
575	cg36801889_TC21	0.00086683	0.03743153	Hs6st1	chr1	+	tss_body	36663962
576	cg36809178_BC21	0.00056108	0.03748896	Fam178b	chr1	-	tss_body	36814626
577	cg36811274_TC11	0.00021076	-0.06821706	Tmem131	chr1	-	tss_body	55132593
578	cg36942887_BC21	0.00085341	0.03653647	Mob4	chr1	+	tss_body	57899722
579	cg36962780_TC21	0.0001296	0.04990121	Spats2l	chr1	+	tss_body	58734805
580	cg36970575_BC21	0.00030345	0.04101474	Cflar	chr1	+	tss_body	61374497
581	cg36992191_TC21	0.00050111	-0.05112938					62706101
582	cg37000623_BC21	0.00039012	-0.03432701	Nrp2	chr1	+	tss_body	63267965
583	cg37006273_BC21	0.0004977	-0.03838112	Zdbf2	chr1	+	tss_body	72814408
584	cg37072853_BC21	2.082E-05	-0.02944604	Gm30847	chr1	+	tss_body	75196172
585	cg37095455_TC21	1.6656E-05	-0.03411277	Ankzf1	chr1	+	tss_body	75375040
586	cg37098066_TC21	0.00068088	-0.08882333	Speg	chr1	+	tss_1500	76069846
587	cg37106153_BC21	0.00078882	-0.04874536	Gm32622	chr1	+	tss_body	88205798
588	cg37194729_BC21	0.00027282	-0.05756414	Ugt1a10	chr1	+	tss_body	88277027
589	cg37195492_TC21	0.00034493	-0.04821907	Hjurp	chr1	-	tss_body	89394668
590	cg37206315_BC21	2.0082E-05	-0.03501321	C030007H22Rik	chr1	-	tss_body	89538687
591	cg37208068_BC21	0.00080993	-0.02658635	Agap1	chr1	+	tss_body	90204513
592	cg37217179_TC21	7.4339E-05	0.03376412	Ackr3	chr1	+	tss_body	90260020

593	cg37217796_BC21	0.00029714	-0.03298603	Gm34930	chr1	+	tss_body	92663248
594	cg37242324_BC21	0.00068291	-0.04535152					93168598
595	cg37248309_TC21	7.7775E-05	-0.05337651	Crocc2	chr1	+	tss_body	119995370
596	cg37381932_TC21	0.00063548	-0.06069796	Cfap221	chr1	-	tss_body	121388658
597	cg37394627_TC21	5.9387E-06	0.05056797					126806237
598	cg37424015_TC21	0.00031256	0.06191281	Nckap5	chr1	-	tss_body	132261258
599	cg37466541_BC21	0.00060884	-0.04452366					134277268
600	cg37490856_BC21	0.00041618	0.06824894	Gm32221	chr1	-	tss_1500	134299258
601	cg37491160_TC21	0.00072787	-0.11012582	Ppfia4	chr1	-	tss_body	134987595
602	cg37498773_BC21	0.00047688	-0.05308975	Lgr6	chr1	-	tss_body	135477797
603	cg37504834_TC21	0.00052629	-0.02689844	Nav1	chr1	-	tss_body	135660312
604	cg37507081_BC21	0.00080504	-0.05439872	Nav1	chr1	-	tss_body	135740837
605	cg37508167_BC11	0.00053315	-0.02757345	Csrp1	chr1	+	tss_body	136130899
606	cg37513025_TC21	0.00011702	-0.04713981	Gm15850	chr1	-	tss_body	151287621
607	cg37598502_TC21	0.00034242	-0.08175681					155529656
608	cg37640832_BC21	0.00072952	-0.03283714					156310521
609	cg37648598_TC11	0.00011543	-0.04493827	Nphs2	chr1	+	tss_200	157533071
610	cg37660309_BC21	0.00064752	0.03938292	Sec16b	chr1	+	tss_body	163725261
611	cg37704038_TC21	2.3962E-06	-0.05770847	Mettl11b	chr1	-	tss_200	164863120
612	cg37713951_BC11	0.00029647	0.03663952	Gm32652	chr1	-	tss_body	167893572
613	cg37744696_TC11	0.00027349	0.050424					170510741
614	cg37765524_BC21	0.00010444	-0.05875636	Nos1ap	chr1	-	tss_body	171979190
615	cg37781612_BC21	0.00058751	0.04136128					172307395
616	cg37785730_TC11	3.1483E-05	-0.03422188	G3UYZ1	chr1	+	tss_body	172526427
617	cg37788969_TC21	0.00059441	-0.05374307	Cfap45	chr1	+	tss_body	173983476
618	cg37797508_BC21	0.00014576	0.02911147	Ifi202b	chr1	-	tss_1500	180884005
619	cg37856284_TC21	0.00073525	-0.05017625	Gm39714	chr1	-	tss_body	182866498
620	cg37879225_BC21	0.00095291	0.04306189	Susd4	chr1	+	tss_body	185797738
621	cg37908858_BC21	0.00024752	0.05388003					189008101
622	cg37938874_TC21	4.0129E-05	0.04912161	Kctd3	chr1	-	tss_1500	191164735
623	cg37964419_BC21	0.00010413	-0.04182129	Fam71a	chr1	-	tss_body	193194045

624	cg37983914_TC21	0.00064366	0.02562199	Traf3ip3	chr1	-	tss_body	6046901
625	cg38023620_BC21	0.00011285	0.02724683	Upf2	chr2	+	tss_body	9828224
626	cg38048325_BC21	0.00067663	0.04784242					11193455
627	cg38061378_BC21	0.00059104	-0.06038647	Prkcq	chr2	+	tss_body	16738418
628	cg38095239_BC21	0.00084309	-0.0557091	Plxdc2	chr2	+	tss_body	18055240
629	cg38103602_TC21	6.9487E-05	0.0451364	Mllt10	chr2	+	tss_body	20510376
630	cg38122130_BC21	0.00013675	-0.02664865	Etl4	chr2	+	tss_body	20807026
631	cg38124506_BC11	0.00010319	0.0297434	Etl4	chr2	+	tss_body	23207277
632	cg38138576_BC21	0.00066254	-0.03480965	4931423 N10Rik	chr2	+	tss_body	25362064
633	cg38154771_BC21	0.00038334	-0.03900682	Uap1l1	chr2	-	tss_body	26397912
634	cg38167541_BC21	9.7957E-05	-0.03829542	Inpp5e	chr2	-	tss_body	26470080
635	cg38168484_TC11	9.2117E-05	-0.04942921	Notch1	chr2	-	tss_body	26475012
636	cg38168562_TC21	0.00048011	0.0447015	Notch1	chr2	-	tss_body	26584154
637	cg38169850_BC11	6.1766E-05	-0.07137325	Egfl7	chr2	+	tss_body	26600184
638	cg38170111_BC21	0.00026835	-0.05142761	Agpat2	chr2	-	tss_body	28203190
639	cg38187613_BC21	0.00064135	0.04454465	Olfm1	chr2	+	tss_body	28530639
640	cg38191409_TC21	0.00031731	0.07087551	Ralgds	chr2	+	tss_body	29378695
641	cg38201815_BC21	7.3984E-05	0.03449854	Med27	chr2	+	tss_body	29716025
642	cg38205466_BC11	0.00015353	0.05845587	Rapgef1	chr2	+	tss_body	30844821
643	cg38221399_BC11	0.00080557	-0.07486463	Prrx2	chr2	+	tss_1500	32192400
644	cg38240201_TC21	0.00087991	0.04325936	Prrc2b	chr2	+	tss_body	32282436
645	cg38241668_TC11	8.5769E-05	-0.06290169	Swi5	chr2	-	tss_body	32452498
646	cg38244505_TC21	0.00064063	-0.04128331	Naif1	chr2	+	tss_body	32653987
647	cg38247424_TC11	0.00016787	-0.02988656	Eng	chr2	+	tss_body	33868150
648	cg38263445_BC21	0.00080868	0.03302078	Mvb12b	chr2	-	tss_body	33978241
649	cg38264792_BC21	0.00068579	-0.02923653	LOC105244124	chr2	+	tss_body	34871680
650	cg38273274_BC11	0.00028558	-0.05956856	Psmd5	chr2	-	tss_1500	35269104
651	cg38277621_BC21	0.00079858	0.03658742	Gsn	chr2	+	tss_body	36176256
652	cg38288254_TC21	0.00019888	0.03562745	Mrrf	chr2	+	tss_body	36217737
653	cg38288729_TC21	0.00044745	-0.02938111	Ptgs1	chr2	+	tss_body	37776766
654	cg38296809_BC21	2.8635E-05	-0.02664582	Crb2	chr2	+	tss_body	38514674

655	cg38302305_BC11	0.0006544	-0.04076348	Nek6	chr2	+	tss_body	38536169
656	cg38302562_BC21	0.00075069	-0.0560033	Nek6	chr2	+	tss_body	44860745
657	cg38335612_TC21	0.00087295	0.02781333	Gtdc1	chr2	-	tss_body	62412513
658	cg38454957_TC21	0.00084193	-0.05530331	Dpp4	chr2	-	tss_200	62507652
659	cg38455744_BC21	0.00099066	0.04589852	Fap	chr2	-	tss_body	65113733
660	cg38470695_BC21	0.00074165	-0.03029912	Cobll1	chr2	-	tss_body	72305834
661	cg38533867_TC21	0.00027181	0.03564116	Zak	chr2	+	tss_body	74669637
662	cg38557630_TC21	0.00074493	-0.03080402	Hoxd13	chr2	+	tss_body	74697416
663	cg38558473_BC11	0.00026383	-0.07404221	Hoxd9	chr2	+	tss_1500	75060737
664	cg38563007_TC21	0.00040851	0.05122792	LOC108168769	chr2	+	tss_1500	75269679
665	cg38565188_TC21	0.00091001	-0.02739327	LOC102635707	chr2	+	tss_body	75960708
666	cg38572185_TC21	5.1993E-05	-0.06650398					76254970
667	cg38575248_BC21	0.0005071	-0.04073694	Pde11a	chr2	-	tss_body	76814565
668	cg38582242_BC21	0.00088739	-0.05138644	Ttn	chr2	-	tss_body	87388106
669	cg38649392_TC21	0.00025314	0.02853789	Olfr1122	chr2	+	tss_body	89125300
670	cg38656603_BC11	0.00056192	-0.03012377	Olfr1222	chr2	-	tss_body	90751108
671	cg38665016_BC21	0.00054886	0.02886098	Fnbp4	chr2	+	tss_body	91096897
672	cg38668736_TC21	0.00066628	-0.05005181	Spi1	chr2	+	tss_body	93304123
673	cg38692422_TC21	0.00055315	-0.0320945	Tspan18	chr2	-	tss_body	93334819
674	cg38692895_BC21	0.00017612	0.04615446	Tspan18	chr2	-	tss_1500	93635065
675	cg38696228_BC21	0.00017402	0.03421648					98329624
676	cg38721928_BC21	0.00021647	-0.03486729					116950473
677	cg38841538_BC21	4.5767E-07	-0.03549136					118775193
678	cg38857556_BC21	0.00025184	-0.0301617	Phgr1	chr2	+	tss_body	122298207
679	cg38893058_TC21	0.00070473	-0.04160544	Duox2	chr2	-	tss_body	125645040
680	cg38916106_TC21	0.00016033	-0.04397153	Shc4	chr2	-	tss_body	125666275
681	cg38916373_TC21	0.00043734	0.04100735	Shc4	chr2	-	tss_body	128185759
682	cg38939656_BC11	0.00050524	-0.07024954	Gm14009	chr2	+	tss_body	128588210
683	cg38943670_BC21	0.00081042	-0.02722744	Gm36203	chr2	-	tss_body	129833194
684	cg38955662_BC21	0.00026507	0.07602333					140783185
685	cg39033839_BC21	0.00095504	-0.03965219	Macrod2	chr2	+	tss_body	142956355

686	cg39045310_TC21	0.00060082	0.06828744					145398041
687	cg39064552_BC21	0.00052186	-0.03375435	Slc24a3	chr2	+	tss_body	145613157
688	cg39065993_TC21	0.00038816	-0.04339864	Slc24a3	chr2	+	tss_body	147928866
689	cg39085287_BC21	0.00026371	0.03806063					151544018
690	cg39107739_TC11	0.00012362	-0.06644148	Fkbp1a	chr2	+	tss_body	151704239
691	cg39109350_BC21	0.00027878	-0.03173167	Tmem74b	chr2	+	tss_body	151744617
692	cg39109766_BC21	0.00043007	-0.06470461	Psmf1	chr2	-	tss_1500	151744642
693	cg39109767_BC21	0.0001023	-0.05159249	Psmf1	chr2	-	tss_1500	152324370
694	cg39116290_BC21	0.0001475	-0.02788357	Rbck1	chr2	-	tss_body	152485930
695	cg39118685_BC11	0.00046352	-0.04459694	Defb22	chr2	-	tss_body	152636183
696	cg39120434_BC21	0.00038818	0.03482251	chr2-152634450-152634683	chr2	*	SShore	156809555
697	cg39167590_BC21	0.00030721	-0.05716199					157021238
698	cg39170382_BC21	0.00035394	-0.04131559	Soga1	chr2	-	tss_body	157058414
699	cg39170996_BC21	0.00012876	0.05024491	Soga1	chr2	-	tss_body	157088587
700	cg39171579_TC11	0.00052244	0.04921786	Tldc2	chr2	+	tss_body	158168762
701	cg39184618_TC21	0.00016816	-0.03513241					158633624
702	cg39190160_BC21	0.00070439	-0.03641974	Actr5	chr2	+	tss_body	158696099
703	cg39191047_BC21	0.00096	-0.04256706	Ppp1r16b	chr2	+	tss_body	161607436
704	cg39215553_TC21	0.00052797	0.02934595	Ptprt	chr2	-	tss_body	162546202
705	cg39221425_TC21	0.00081689	-0.02934656	Ptprt	chr2	-	tss_body	163703207
706	cg39235932_TC21	6.3137E-06	0.03143881	Pkig	chr2	+	tss_body	164612562
707	cg39247696_BC21	0.00033156	-0.03566392	Wfdc8	chr2	-	tss_body	164643348
708	cg39247992_TC21	3.2213E-05	0.0364138		chr2	-	tss_200	164656092
709	cg39248176_BC21	0.00090484	-0.04317415	Wfdc9	chr2	-	tss_body	164828630
710	cg39250574_BC21	0.00097793	-0.04453911	Spata25	chr2	-	tss_200	164854394
711	cg39251067_BC21	1.6703E-05	0.02787829	Pltp	chr2	-	tss_body	166820963
712	cg39281163_TC21	0.00015529	-0.05942995	Arfgef2	chr2	+	tss_body	166974854
713	cg39283023_TC21	0.00051431	0.03132574	Stau1	chr2	-	tss_body	167559765
714	cg39291619_BC21	5.9655E-06	0.05506592	Gm11476	chr2	+	tss_body	167727317
715	cg39294534_BC11	0.00079283	-0.05028881	Gm38464	chr2	+	tss_body	168879785

716	cg39312885_BC21	0.00086835	-0.03240305					168894302
717	cg39313085_TC11	0.00078943	-0.04544179	Gm38422	chr2	-	tss_body	172030698
718	cg39352177_BC21	0.00019594	-0.03905605					172350888
719	cg39356237_BC21	0.00033971	-0.03442905	Fam210b	chr2	+	tss_body	173119139
720	cg39368014_BC21	1.861E-05	-0.04008932	Gm40011	chr2	+	tss_body	173248889
721	cg39369835_BC21	0.00086097	-0.04377449	Pmepa1	chr2	-	tss_body	173562019
722	cg39374167_TC21	0.0006469	-0.03413279					174283902
723	cg39382179_BC21	0.00050758	-0.03747014	Nespas	chr2	-	tss_body	174298821
724	cg39382642_TC21	0.00056963	-0.05703705	Gnas	chr2	+	tss_body	174300643
725	cg39382778_TC21	9.6721E-05	-0.03475131	Gnas	chr2	+	tss_body	177081692
726	cg39394642_TC21	0.00067084	0.04587114	Gm14403	chr2	+	tss_body	179817123
727	cg39415570_TC21	0.00030955	0.04390722	Cdh4	chr2	+	tss_body	180824636
728	cg39428665_BC21	0.00069744	-0.03317911		chr2	-	tss_200	181237930
729	cg39433417_BC21	8.796E-06	-0.04892902	Helz2	chr2	-	tss_body	181493733
730	cg39435858_BC21	0.00056309	-0.03659437	Zbtb46	chr2	-	tss_1500	181670397
731	cg39437664_BC21	0.00044229	-0.05135003	Sox18	chr2	-	tss_body	8685858
732	cg39468674_TC21	0.00012357	0.06919063	Gm32561	chr3	-	tss_body	9343744
733	cg39475923_BC21	0.00071921	-0.02712618	Gm41997	chr3	-	tss_body	10205970
734	cg39484839_BC21	0.00085885	-0.0455834	Fabp4	chr3	-	tss_body	11362344
735	cg39491820_BC21	4.2394E-05	-0.02961503					23183609
736	cg39552126_TC21	0.0006153	-0.04610173					26920510
737	cg39570196_TC21	9.7865E-05	0.03729413	Spata16	chr3	+	tss_body	28781075
738	cg39587820_BC21	0.00031743	-0.0296044	Eif5a2	chr3	+	tss_1500	30867084
739	cg39603224_TC21	0.00049458	0.03235973	Gpr160	chr3	+	tss_body	34323615
740	cg39630697_BC21	0.00014468	-0.03125909	Gm38505	chr3	-	tss_body	38820573
741	cg39668919_BC11	0.00026174	0.03692419					51400930
742	cg39738279_TC21	0.00067775	-0.04602651					51401085
743	cg39738281_TC21	1.0457E-07	-0.04206546					51403193
744	cg39738317_TC21	0.00094265	-0.04008193		chr3	-	tss_200	57294864
745	cg39790639_BC21	2.7838E-06	-0.09196979	Tm4sf1	chr3	-	tss_body	60529163
746	cg39812176_TC11	0.00080366	0.10265615	Mbnl1	chr3	+	tss_body	65564090

747	cg39838866_TC11	0.0002803	-0.02699147					69543171
748	cg39871135_BC21	0.00018885	-0.06007327	Ppm1l	chr3	+	tss_body	77378595
749	cg39907390_TC21	0.0004649	-0.04041486					83014195
750	cg39941034_BC21	0.00032627	-0.04605084	Fgg	chr3	+	tss_body	85186668
751	cg39962080_TC21	0.00076647	-0.04760251	E9QAY5	chr3	-	tss_body	87927017
752	cg39986689_BC11	0.00089358	0.02505934	Rrnad1	chr3	-	tss_body	88048311
753	cg39988633_TC21	0.00089488	0.05116069	Gpatch4	chr3	+	tss_body	88238868
754	cg39991229_BC21	0.00066586	0.03752022	chr3-88240996-88241413	chr3	*	NShelf	88320891
755	cg39992198_TC21	0.0002839	0.06529412	Cct3	chr3	+	tss_body	89095123
756	cg40001612_TC21	0.00034598	-0.03201583	Fdps	chr3	-	tss_body	89422286
757	cg40007459_TC21	0.00042558	0.04297668	Shc1	chr3	+	tss_body	92572575
758	cg40030194_TC11	0.00084735	-0.0444241	Ivl	chr3	-	tss_body	99352567
759	cg40091869_BC21	7.3366E-05	-0.02730482	Tbx15	chr3	+	tss_body	101089053
760	cg40105365_BC21	3.0113E-05	0.03662424	Ptgfrn	chr3	-	tss_body	104366592
761	cg40137072_TC21	0.00013405	0.05874041		chr3	-	tss_body	104432089
762	cg40137714_BC21	0.00054737	-0.03733867	A0A0G2JG33	chr3	-	tss_body	105681042
763	cg40149099_TC21	1.8978E-05	-0.0278109	Ddx20	chr3	-	tss_body	105709507
764	cg40149536_TC21	0.00090714	0.02772138	Fam212b	chr3	+	tss_body	107103188
765	cg40157597_BC21	1.438E-05	-0.06217881	Kcna2	chr3	+	tss_body	107324809
766	cg40159378_BC21	0.00080195	0.03266908	Rbm15	chr3	-	tss_body	108045140
767	cg40166989_TC21	0.00011583	0.02619117	Gstm4	chr3	-	tss_200	108475640
768	cg40173067_BC21	0.00017173	0.03652837	5330417C22Rik	chr3	-	tss_body	108722778
769	cg40175821_TC21	0.00057434	0.04939906	Gpsm2	chr3	-	tss_1500	108939925
770	cg40177964_BC21	0.00063762	-0.05369192	Henmt1	chr3	+	tss_body	112846933
771	cg40197931_BC21	0.00092891	0.03181792					121467305
772	cg40252961_BC21	0.00035793	-0.11518536	Slc44a3	chr3	-	tss_body	121483933
773	cg40253186_BC21	0.00029267	-0.0579002	Slc44a3	chr3	-	tss_body	121532299
774	cg40253764_TC11	0.00012358	0.03139799	Slc44a3	chr3	-	tss_body	122895332
775	cg40268942_TC21	0.0008032	0.05432574	4933405D12Rik	chr3	-	tss_body	126367473
776	cg40290210_BC21	0.00014065	0.06370333	Arsj	chr3	+	tss_body	127545133

777	cg40300299_BC21	0.00038217	-0.03027956	Larp7	chr3	-	tss_body	135514269
778	cg40370084_BC21	0.00014377	-0.04586131	Manba	chr3	+	tss_body	138610579
779	cg40396206_TC21	0.00021875	-0.05826071					138690073
780	cg40397030_TC21	0.00098497	0.04050936					143576839
781	cg40429161_TC21	0.00060089	0.05451965	Gm33651	chr3	+	tss_body	144697409
782	cg40440565_BC21	0.00018273	-0.04918344	Sh3glb1	chr3	-	tss_body	152113847
783	cg40502584_BC21	0.00034193	-0.02935105	Gipc2	chr3	-	tss_body	4538769
784	cg40566210_TC21	3.4242E-05	0.05971811	Gm33057	chr4	+	tss_body	9419227
785	cg40598361_TC21	0.00031489	0.03361999	Clvs1	chr4	+	tss_body	12009094
786	cg40618742_BC21	0.00094728	-0.04125561	LOC105247602	chr4	-	tss_body	20779240
787	cg40665417_BC11	0.0004302	-0.04535987	Nkain3	chr4	-	tss_body	23261040
788	cg40680773_BC21	0.00054863	-0.0369144	Gm38450	chr4	+	tss_body	32832293
789	cg40733113_TC21	3.3449E-05	0.04043762	Ankrd6	chr4	-	tss_body	41568133
790	cg40792760_BC21	2.6678E-05	-0.03852236	Fam219a	chr4	-	tss_body	43447489
791	cg40806991_TC21	0.00036724	0.04114062	Tesk1	chr4	+	tss_body	43568112
792	cg40808911_BC21	8.1107E-05	0.03118533	Gba2	chr4	-	tss_body	44561342
793	cg40820765_BC21	0.00023004	-0.06814632	Pax5	chr4	-	tss_body	44645956
794	cg40821838_BC21	0.00030163	0.04530011	Pax5	chr4	-	tss_body	46008403
795	cg40838009_BC21	0.00072821	-0.05183214	Tdrd7	chr4	+	tss_body	47041961
796	cg40852382_TC21	2.3555E-06	-0.04681479	Anks6	chr4	-	tss_body	47311041
797	cg40855532_TC11	0.00052422	-0.03524065	Col15a1	chr4	+	tss_body	47450336
798	cg40856814_TC21	0.00029141	0.05364816					48392143
799	cg40864885_TC21	0.00045266	-0.03232923	Invs	chr4	+	tss_body	58943470
800	cg40943603_BC21	0.00039072	0.03039524	Zkscan16	chr4	+	tss_200	62535642
801	cg40964714_TC21	0.00090358	-0.02678907	4933430I17Rik	chr4	+	tss_body	62705684
802	cg40966813_TC21	0.00072475	0.03564078		chr4	+	tss_1500	63420342
803	cg40974535_BC21	0.00029825	0.04362171	Whrn	chr4	-	tss_body	82537778
804	cg41067970_BC21	0.00023889	-0.0365477	A2ADI3	chr4	-	tss_body	84104623
805	cg41082355_BC21	0.00087768	0.03318146		chr4	+	tss_1500	89470182
806	cg41122347_BC21	0.00097837	0.03442048	Gm12610	chr4	+	tss_body	99062412
807	cg41177406_TC21	0.000612	0.05141076	Dock7	chr4	-	tss_body	99653778

808	cg41183661_BC21	8.2393E-05	0.04025217	chr4-99655945-99658098	chr4	*	NShelf	102870649
809	cg41210231_BC21	0.0008744	0.05353332	Sgip1	chr4	+	tss_body	104702987
810	cg41225008_TC21	0.00028221	-0.06591918	Dab1	chr4	+	tss_body	104715316
811	cg41225142_TC21	0.00059382	0.03320641	Dab1	chr4	+	tss_body	106619324
812	cg41242459_BC21	0.00019674	-0.07049692	chr4-106622395-106623099	chr4	*	NShelf	108164983
813	cg41262216_BC21	0.00033204	-0.04872151	Echdc2	chr4	+	tss_1500	110125701
814	cg41278586_TC21	0.00086478	-0.04321397					111691257
815	cg41286390_BC21	0.00091606	0.04481983					117927254
816	cg41332930_TC21	0.00048686	-0.02857965	Artn	chr4	-	tss_body	120856769
817	cg41365509_TC21	0.00028524	-0.05073406	Rims3	chr4	+	tss_body	126106941
818	cg41415667_BC21	0.00080066	0.07174308	Stk40	chr4	+	tss_body	127077631
819	cg41427377_TC11	0.00075891	0.04408965	Zmym6	chr4	+	tss_body	127258455
820	cg41429671_BC21	6.1525E-06	-0.0410377	Gm33269	chr4	+	tss_body	127487184
821	cg41432536_TC21	0.00022102	0.04360673	1700080G11Rik	chr4	+	tss_body	127806695
822	cg41435847_TC21	0.00075887	-0.06954863					128788300
823	cg41447690_BC21	0.00025835	-0.07339541	Zfp362	chr4	-	tss_body	131010725
824	cg41476534_TC11	0.00020879	0.03400722	A930031H19Rik	chr4	-	tss_1500	132140844
825	cg41489938_TC11	0.00025384	0.06321062	Oprd1	chr4	-	tss_body	133103889
826	cg41502901_TC11	0.00012345	0.04478114					134354280
827	cg41521494_BC21	0.00077984	-0.03758728	Slc30a2	chr4	+	tss_body	134813672
828	cg41529044_BC21	9.918E-06	0.05799328	Tmem57	chr4	-	tss_body	135327095
829	cg41536952_BC21	0.00019948	0.03385344	Srrm1	chr4	-	tss_body	135761725
830	cg41543564_BC21	0.00014223	0.04033266	Myom3	chr4	+	tss_body	136330736
831	cg41552364_TC21	0.00044875	0.029285	Hnrnpr	chr4	+	tss_body	136773004
832	cg41557784_TC21	0.00049488	-0.03764262	Ephb2	chr4	-	tss_body	137581905
833	cg41569806_BC21	0.00054878	-0.03553604	Ldlrad2	chr4	-	tss_body	138066586
834	cg41576997_BC21	0.00093754	-0.0526917	Eif4g3	chr4	+	tss_body	138290722
835	cg41580326_BC21	7.7267E-05	-0.02563125	Kif17	chr4	+	tss_body	138832185

836	cg41588095_BC21	0.00042071	-0.04182089	Pla2g5	chr4	-	tss_body	139086073
837	cg41591796_BC21	0.000313	-0.05230471	Nbl1	chr4	-	tss_body	139112663
838	cg41592239_TC21	6.7679E-05	0.05095876	Minos1	chr4	-	tss_body	140182808
839	cg41608061_TC21	0.00070796	0.04535117	Igsf21	chr4	-	tss_body	140356613
840	cg41610515_TC21	0.0006898	-0.06247543	Gm34074	chr4	+	tss_body	140403271
841	cg41611256_BC21	0.00071194	-0.03429162					141413492
842	cg41628214_TC21	0.00063071	0.02900454	Clcnkb	chr4	-	tss_body	142068001
843	cg41639339_BC21	0.00037924	0.03167008	Tmem51	chr4	-	tss_body	142210392
844	cg41641376_BC21	0.0002659	-0.0500907	Kazn	chr4	-	tss_body	143030008
845	cg41650006_TC21	3.2677E-05	-0.03102539		chr4	-	tss_body	143135187
846	cg41651225_BC21	0.00027351	0.04402511	Prdm2	chr4	-	tss_body	148077089
847	cg41680734_BC21	0.00083993	0.02799562	Gm13201	chr4	-	tss_1500	148306776
848	cg41684455_BC21	0.00014316	-0.09408		chr4	+	tss_200	148306788
849	cg41684456_BC21	0.00037136	-0.06605131		chr4	+	tss_200	149477403
850	cg41702472_TC21	0.00053532	-0.02873279	Nmnat1	chr4	-	tss_body	149758499
851	cg41707142_BC21	0.00040722	0.04510297	Slc25a33	chr4	-	tss_body	152062985
852	cg41741297_TC21	0.00052742	0.06643399					152126853
853	cg41742551_TC21	0.00035007	-0.04801558	Espn	chr4	-	tss_body	152131940
854	cg41742746_TC21	3.4667E-05	-0.03157658	Espn	chr4	-	tss_body	152405104
855	cg41748019_TC21	0.0005065	0.04118881	Kcnab2	chr4	-	tss_body	154409491
856	cg41775900_BC21	0.00065497	0.07462017	Prdm16	chr4	-	tss_body	154541734
857	cg41777844_BC21	0.00016938	-0.04764009	Prdm16	chr4	-	tss_body	154898694
858	cg41782901_TC21	4.4807E-05	-0.04082167	Fam213b	chr4	-	tss_body	155043488
859	cg41785243_TC11	0.00047979	-0.06626816	Plch2	chr4	-	tss_body	155739927
860	cg41795494_TC21	0.00098046	0.0278938	Tmem240	chr4	+	tss_body	155863400
861	cg41797546_BC11	0.0007223	0.03409901	Tas1r3	chr4	-	tss_200	156036249
862	cg41800139_TC21	0.00036498	-0.05691708	Ttll10	chr4	-	tss_body	156254680
863	cg41803818_TC21	0.00089209	-0.05446085	Samd11	chr4	-	tss_body	3844946
864	cg41811731_TC21	0.00087938	0.03036063	Lrrd1	chr5	+	tss_1500	23659184
865	cg41926160_TC21	0.00069467	0.02833426	Srpk2	chr5	-	tss_body	24337628
866	cg41933072_TC21	0.00060709	-0.0551926	Kcnh2	chr5	-	tss_body	25302506

867	cg41945805_BC21	0.00028441	0.05375559	Kmt2c	chr5	-	tss_body	26933000
868	cg41955971_TC21	4.0957E-05	-0.05589028	Dpp6	chr5	+	tss_body	31785019
869	cg41996263_BC21	0.00045861	0.07670658	Bre	chr5	+	tss_body	34666722
870	cg42023423_BC21	0.00087353	0.03316622	Grk4	chr5	+	tss_body	35526009
871	cg42031971_BC21	2.1784E-05	-0.0321686	Cpz	chr5	-	tss_1500	37894334
872	cg42058008_BC21	0.00087682	-0.02770828	Gm3405 5	chr5	+	tss_body	40367414
873	cg42074935_TC21	0.00092561	0.04809135					44428467
874	cg42099026_TC21	0.00064004	0.04811169	Gm3601 7	chr5	-	tss_1500	47634785
875	cg42116437_BC21	2.119E-05	-0.03689869		chr5	+	tss_body	52342325
876	cg42143472_TC21	0.00084048	-0.0509442		chr5	-	tss_body	56414155
877	cg42172630_BC21	0.00046434	-0.02500812		chr5	+	tss_200	63847327
878	cg42206247_TC21	0.00029627	0.03722825	0610040 J01Rik	chr5	+	tss_body	64822031
879	cg42216726_TC21	0.0009408	-0.03447008	Klf3	chr5	+	tss_body	67139264
880	cg42243647_TC21	0.00087518	-0.03682009					72989991
881	cg42281343_TC21	0.00089076	0.02770965					73007949
882	cg42281565_BC21	0.00055907	0.03481422	Slc10a4	chr5	+	tss_body	74305062
883	cg42297308_TC21	0.00023299	0.03472479	Scfd2	chr5	-	tss_body	76484183
884	cg42320066_BC11	0.0008751	-0.03063285	Gm7271	chr5	+	tss_body	86180480
885	cg42374487_BC11	0.00039151	0.03747757					88934691
886	cg42390727_BC21	0.00032681	-0.05742274	Slc4a4	chr5	+	tss_body	99203134
887	cg42464602_TC21	0.00012858	-0.03916928					10071060 0
888	cg42482277_TC21	0.00076722	0.0490866	Hpse	chr5	-	tss_body	10318588 1
889	cg42508114_BC21	0.00037896	0.04888026	Mapk10	chr5	-	tss_body	10337776 6
890	cg42509921_TC21	0.00054169	-0.06539757					10341875 8
891	cg42510370_BC21	9.2327E-05	0.05722592					10585794 5
892	cg42534074_TC21	7.4974E-05	0.04895607					10854225 0
893	cg42560171_TC21	0.00022872	-0.0439741	Cplx1	chr5	-	tss_body	10869214 4
894	cg42561566_TC21	6.2882E-05	-0.05569801	Gm4215 1	chr5	-	tss_body	11048102 7
895	cg42574420_BC21	0.00081552	-0.05877436	chr5-1104806 56-1104811 79	chr5	*	Island	11150323 6
896	cg42587195_BO21	0.00063661	0.04149105					11194028 8

897	cg42591982_TC11	0.0004776	0.03388603	Gm36794	chr5	-	tss_body	112219240
898	cg42595160_BC21	0.00018302	-0.02937373	Miat	chr5	-	tss_body	112649604
899	cg42601599_BC21	0.00031286	0.04433455	Gm30529	chr5	+	tss_body	112928557
900	cg42604884_BC21	0.00039012	-0.05285843	Adrbk2	chr5	-	tss_body	113152475
901	cg42608098_BC21	0.00024126	0.0386411	2900026A02Rik	chr5	-	tss_body	113175568
902	cg42608479_BC21	0.0008097	-0.03969432	2900026A02Rik	chr5	-	tss_body	113324491
903	cg42611058_TC21	0.00095428	0.03313117	Mir7229	chr5	-	tss_body	114996775
904	cg42639407_TC21	0.00012734	-0.06738412	Hnf1aos1	chr5	+	tss_body	115635418
905	cg42650990_TC21	0.00026966	-0.03672909	Rab35	chr5	+	tss_body	115645710
906	cg42651167_TC21	0.00091785	0.05143351	Rab35	chr5	+	tss_body	115685274
907	cg42651743_TC21	0.00046657	0.03300828	Ccdc64	chr5	-	tss_body	116829213
908	cg42667529_TC21	0.00028498	-0.0517206		chr5	-	tss_body	118190560
909	cg42687092_TC21	0.00088397	-0.04166358					120513244
910	cg42717518_BC21	0.00098936	-0.04673117	Slc8b1	chr5	+	tss_body	120749800
911	cg42721681_BC21	0.00036127	0.02969251	Oas2	chr5	-	tss_body	121450066
912	cg42729711_BC21	0.00041547	-0.05944275	Erp29	chr5	-	tss_body	121743033
913	cg42733706_BC21	0.00084997	0.03611141	Atxn2	chr5	+	tss_body	122210205
914	cg42741527_TC21	0.00023516	-0.07418217	Hvcn1	chr5	+	tss_body	122602513
915	cg42747096_BC21	0.00025585	-0.02696038	Ift81	chr5	-	tss_body	123863894
916	cg42765795_BC21	0.00046529	0.04539132	Hcar2	chr5	-	tss_body	124014002
917	cg42768165_BC11	0.00034387	0.03667701	Vps37b	chr5	-	tss_body	124931340
918	cg42781360_BC11	0.00073449	-0.03423295					125003277
919	cg42782283_BC21	3.3942E-05	-0.03196806	Fam101a	chr5	+	tss_200	125066318
920	cg42783556_TC11	0.00083257	0.029014	Ncor2	chr5	-	tss_body	125106200
921	cg42784228_BC21	0.00041357	-0.05372428	Ncor2	chr5	-	tss_body	125149241
922	cg42784906_TC21	3.2479E-05	0.08716622	Ncor2	chr5	-	tss_body	129272311
923	cg42827279_BC21	0.00023355	-0.02819281					134360519
924	cg42875509_TC21	0.00078817	-0.06237342	Gtf2ird1	chr5	-	tss_body	136862873
925	cg42908643_TC21	0.00068687	-0.05360267	Col26a1	chr5	-	tss_body	139912980
926	cg42946471_TC21	6.0201E-05	0.02953805	Elfn1	chr5	+	tss_body	140524192
927	cg42953495_BC21	6.4991E-05	-0.03275213	Chst12	chr5	+	tss_body	140763706

928	cg42957253_BC21	0.00011127	-0.05180841	Gna12	chr5	-	tss_body	143245063
929	cg42985138_TC21	0.00087842	-0.05293992	Zfp12	chr5	+	tss_body	143367746
930	cg42987518_TC21	4.214E-05	0.06103228	Grid2ip	chr5	+	tss_body	145203402
931	cg43011455_TC11	0.00072409	0.03216747	Zkscan14	chr5	-	tss_body	146781939
932	cg43024738_BC21	0.00026074	-0.04419931	Usp12	chr5	-	tss_body	147563645
933	cg43036275_BC21	2.3963E-05	0.05131264	Flt1	chr5	-	tss_body	147839882
934	cg43040335_TC21	0.00031237	-0.03896233					148419123
935	cg43048181_BC21	0.00027899	-0.04991827					149215265
936	cg43059010_BC21	0.00089422	-0.03677684	Uspl1	chr5	+	tss_body	149259116
937	cg43059645_TC21	0.00034086	-0.04027761					149320284
938	cg43060248_TC21	0.00022754	-0.0314329	Gm35620	chr5	-	tss_body	149338820
939	cg43060518_TC21	0.00047788	0.04746343					149364360
940	cg43060835_TC21	0.00077374	-0.03253555	Gm38753	chr5	-	tss_body	150948481
941	cg43078651_TC21	0.00054987	0.04245279					151247424
942	cg43081670_BC21	0.00083478	-0.04895516	Stard13	chr5	-	tss_body	4600535
943	cg43094419_TC21	0.00048266	0.04028415	Casd1	chr6	+	tss_1500	6623552
944	cg43113143_BC11	0.00025621	-0.04105144		chr6	-	tss_body	28758408
945	cg43242315_BC21	0.00058798	0.07735903	Snd1	chr6	+	tss_body	28768226
946	cg43242370_BC21	7.7992E-05	0.03194142	Snd1	chr6	+	tss_body	28846194
947	cg43243226_BC21	7.6864E-05	0.04773765	Snd1	chr6	+	tss_body	29042355
948	cg43245648_BC11	0.00017893	-0.08904198					30212719
949	cg43258809_BC11	0.00094651	0.04868545	Ube2h	chr6	-	tss_body	31103089
950	cg43267778_TC21	0.00066217	0.04931813	Lncpint	chr6	-	tss_body	31719464
951	cg43274359_BC21	8.2433E-05	-0.03661121	Gm13846	chr6	+	tss_body	34869748
952	cg43300026_TC21	0.0008388	-0.03168487	Tmem140	chr6	+	tss_body	35476543
953	cg43306068_TC11	0.00097151	-0.03518646					40230256
954	cg43345280_TC21	0.00090415	0.03156111	Tmem178b	chr6	+	tss_body	42356194
955	cg43357184_TC21	3.4765E-05	-0.05519006	Zyx	chr6	+	tss_body	42357319
956	cg43357201_BC21	0.00042787	0.05735642	Zyx	chr6	+	tss_body	45794225
957	cg43372777_BC21	0.0003066	0.06496647	Cntnap2	chr6	+	tss_body	47799251
958	cg43382198_TC21	0.00096232	-0.05109548	Pdia4	chr6	-	tss_body	48743078

959	cg43391311_TC21	3.4048E-06	-0.05326874	Gimap1	chr6	+	tss_body	49366481
960	cg43397395_BC11	0.00026475	-0.0554163	Fam221a	chr6	+	tss_1500	50822529
961	cg43410533_TC21	0.00026495	-0.04845749	Gm31455	chr6	-	tss_1500	52208576
962	cg43426400_BC21	0.000261	-0.03039994	Hoxa3	chr6	-	tss_body	52593808
963	cg43431754_BC21	0.00011929	-0.0448382	Hibadh	chr6	-	tss_body	53643754
964	cg43441107_TC21	3.2877E-05	0.06163728	Creb5	chr6	+	tss_body	54944334
965	cg43454734_BC21	0.00073443	-0.0390179	Nod1	chr6	-	tss_body	60772251
966	cg43489457_TC21	0.00064248	0.04582997	Snca	chr6	-	tss_body	67126716
967	cg43522696_TC21	0.00018937	0.06799144		chr6	+	tss_body	71352873
968	cg43546853_BC21	0.0006131	0.03461507		chr6	+	tss_200	71799524
969	cg43550948_BC21	0.00091329	0.03546049	Reep1	chr6	+	tss_body	71922594
970	cg43552106_TC21	0.00070032	0.06037093	Polr1a	chr6	+	tss_body	72103178
971	cg43553834_TC21	0.00099834	0.05064858	St3gal5	chr6	+	tss_body	84476504
972	cg43634394_TC21	0.00013003	0.0485946					88548629
973	cg43675248_BC21	0.00063635	-0.02712646	Kbtbd12	chr6	-	tss_body	89420576
974	cg43684660_TC21	0.00028988	0.04582269	Chchd6	chr6	-	tss_body	90541798
975	cg43692133_BC21	0.00045895	0.02589771		chr6	+	tss_body	93717434
976	cg43719591_BC21	0.00084345	-0.0350486	Magi1	chr6	-	tss_body	100247436
977	cg43775913_BC21	0.0004102	0.05874268	Rybp	chr6	-	tss_body	109125766
978	cg43830395_TC21	1.4629E-06	-0.04707653		chr6	+	tss_body	112900607
979	cg43849830_BC21	0.00047349	0.03762043	Srgap3	chr6	-	tss_body	113393120
980	cg43855161_BC21	2.0832E-05	0.06315812	Ttll3	chr6	+	tss_body	113495269
981	cg43856751_BC21	0.00020518	-0.0531589	Prrt3	chr6	-	tss_body	113857106
982	cg43861065_TC21	0.00079014	0.06013514	Atp2b2	chr6	-	tss_body	115908552
983	cg43881569_TC21	0.00067884	-0.02995619	Ift122	chr6	+	tss_body	118085252
984	cg43901061_BC21	0.00018034	-0.05927221	Rasgef1a	chr6	+	tss_body	118462199
985	cg43905069_TC21	0.00094332	0.04457643	Zfp9	chr6	-	tss_body	119962797
986	cg43921123_TC21	0.00014214	0.05353652	Wnk1	chr6	-	tss_body	120250970
987	cg43923792_TC21	0.00062652	0.05612189	B4galnt3	chr6	-	tss_body	122662017
988	cg43947553_BC21	0.00051827	-0.05330128					125069060
989	cg43967180_TC21	0.00087138	-0.04787519	Lpar5	chr6	+	tss_body	125232767

990	cg43969896_TC21	0.00027793	-0.06489712	E130112N10Rik	chr6	+	tss_body	125353689
991	cg43971696_BC21	0.00022874	-0.09192839	Tnfrsf1a	chr6	+	tss_body	125357798
992	cg43971768_TC21	0.00096637	0.03631674	Tnfrsf1a	chr6	+	tss_body	125661735
993	cg43975712_TC21	9.4278E-05	-0.0554947	Vwf	chr6	+	tss_body	127446894
994	cg43992877_BC21	0.0009787	-0.08370605	Parp11	chr6	+	tss_body	128004903
995	cg43999199_BC21	0.00084569	-0.08017632	Tspan9	chr6	-	tss_body	128137234
996	cg44001084_BC21	0.00014274	-0.06626838	Tspan9	chr6	-	tss_body	128339399
997	cg44003392_TC21	5.2945E-05	0.04496059	Tulp3	chr6	-	tss_body	129275319
998	cg44011521_BC21	0.00031659	-0.06075008	Cd69	chr6	-	tss_body	129397415
999	cg44012184_BC21	0.00062122	-0.0663538	Clec12b	chr6	-	tss_body	135048914
1000	cg44046167_TC21	0.00031858	-0.03962577					135352670
1001	cg44049776_TC21	0.00019818	-0.05339109					142806344
1002	cg44115492_TC21	0.00095958	-0.03922699					144210846
1003	cg44131275_BC11	0.00074437	-0.0500964	Sox5	chr6	-	tss_body	145750833
1004	cg44149078_TC21	1.8601E-05	0.02540832	Rassf8	chr6	+	tss_body	145916468
1005	cg44151020_BC21	0.00075785	0.04915156	Gm32675	chr6	+	tss_body	146397030
1006	cg44155426_TC21	0.00096458	0.02663116	Itpr2	chr6	-	tss_body	3219602
1007	cg44180988_BC21	0.00072846	0.09028287	D7Ertd143e	chr7	+	tss_body	4479068
1008	cg44191089_TC21	0.00010298	-0.04061485	Eps8l1	chr7	+	tss_body	4524317
1009	cg44191921_TC21	0.00041443	-0.04519707	Dnaaf3	chr7	-	tss_body	4530830
1010	cg44192047_BC21	0.0004828	-0.04413737	Dnaaf3	chr7	-	tss_body	4602881
1011	cg44192810_TC11	0.00068867	0.04779072	Ptprh	chr7	-	tss_body	5100065
1012	cg44200373_BC11	0.00084929	0.03371569					6228615
1013	cg44207153_BC21	0.00052229	-0.05057843	Zscan5b	chr7	+	tss_body	6343718
1014	cg44208345_BC21	5.0525E-05	0.03106473	Gm38944	chr7	-	tss_body	6417976
1015	cg44209239_BC11	0.00053694	-0.04368483	Smim17	chr7	+	tss_body	6730687
1016	cg44211948_TC21	0.00011902	0.07007167	Usp29	chr7	+	tss_body	6730824
1017	cg44211952_TC11	6.5265E-05	0.07719699	Usp29	chr7	+	tss_body	6731275
1018	cg44211969_TC21	0.0008759	0.02711648	Usp29	chr7	+	tss_body	12775375
1019	cg44237935_BC21	0.00045035	0.0313747	Zscan18	chr7	-	tss_body	13029407
1020	cg44240950_TC21	1.6202E-05	0.04101888	Trim28	chr7	+	tss_body	13324811

1021	cg44243360_TC21	0.00072546	0.02750517	Pla2g4c	chr7	+	tss_body	14187223
1022	cg44247321_BC21	0.00065831	-0.04245649		chr7	-	tss_body	16308769
1023	cg44261060_BC21	0.00078249	0.02706826	Bbc3	chr7	+	tss_1500	18526762
1024	cg44278537_BC21	0.00091461	-0.03503057	Psg25	chr7	-	tss_body	19264819
1025	cg44287061_TC11	2.3293E-05	0.02716678	Vasp	chr7	-	tss_body	19400150
1026	cg44289987_BC21	0.00014475	0.03457225	Klc3	chr7	-	tss_body	19463059
1027	cg44291165_TC21	0.00082976	-0.03707324	Exoc3l2	chr7	+	tss_200	19700497
1028	cg44295273_BC21	0.00031146	0.0363907	Apoe	chr7	-	tss_1500	19861270
1029	cg44297927_BC21	0.00029925	0.04150257	Ceacam16	chr7	-	tss_body	24073353
1030	cg44313073_BC21	3.7009E-05	-0.07115704	Gm36694	chr7	-	tss_body	24435427
1031	cg44317563_TC11	0.0001482	-0.04323715	Irgc1	chr7	-	tss_body	24448691
1032	cg44317737_TC21	0.00073819	0.05950403	Gm36159	chr7	+	tss_body	24601326
1033	cg44320415_BC21	0.00015048	-0.0298986	Ethe1	chr7	+	tss_body	25154756
1034	cg44328526_BC21	0.00049679	-0.04962158	Pou2f2	chr7	-	tss_body	25700947
1035	cg44336492_BC21	0.0007616	-0.05508958	Tgfb1	chr7	+	tss_body	25773892
1036	cg44337532_BC21	0.00032675	-0.02957223	Axl	chr7	-	tss_body	27385637
1037	cg44350387_BC21	0.00067045	-0.07279738	Sptbn4	chr7	-	tss_body	28464215
1038	cg44364963_TC21	0.00056042	0.03157284	Lrfn1	chr7	+	tss_body	28796218
1039	cg44369686_TC21	0.00010813	-0.06162558	Rinl	chr7	+	tss_body	29829806
1040	cg44384202_BC21	0.00087403	0.03060981	Zfp790	chr7	+	tss_body	30360569
1041	cg44391626_BC11	1.5812E-05	-0.0593784	Lrfn3	chr7	-	tss_body	30944488
1042	cg44399767_TC21	0.00043902	-0.05291331	Hamp	chr7	-	tss_1500	31052924
1043	cg44401260_BC21	0.00024126	-0.03365574	Gm38984	chr7	+	tss_body	31052998
1044	cg44401264_BC21	0.00025806	-0.03152186	Gm38984	chr7	+	tss_body	34353499
1045	cg44419617_BC21	0.00043461	0.04334319	Lsm14a	chr7	-	tss_body	34722083
1046	cg44423970_BC21	0.00028697	-0.0473388	Chst8	chr7	-	tss_body	37346249
1047	cg44454229_TC11	0.00067108	-0.03409701	Zfp536	chr7	-	tss_body	44306972
1048	cg44500523_BC21	0.00039976	-0.0423031	Shank1	chr7	+	tss_1500	44858567
1049	cg44509438_BC21	0.00068344	-0.03024487	Pnkp	chr7	+	tss_body	44984092
1050	cg44511729_TC21	0.00065909	-0.02550091	Prmt1	chr7	-	tss_body	45008156
1051	cg44512325_TC11	0.00030399	-0.04383369	Scaf1	chr7	-	tss_body	45021397

1052	cg44512648_TC21	0.00028221	-0.05039716	Rras	chr7	+	tss_body	45144649
1053	cg44514893_BC21	0.00065095	-0.04977736	Aldh16a1	chr7	-	tss_body	45172102
1054	cg44515468_BC11	0.00057566	-0.06421505	Slc17a7	chr7	+	tss_body	45233920
1055	cg44516579_BC21	0.00054888	-0.04205618	Cd37	chr7	-	tss_body	45920840
1056	cg44528740_BC21	0.00031694	0.02528883	Emp3	chr7	-	tss_body	45980007
1057	cg44529525_TC21	0.0004681	-0.04660862	Abcc6	chr7	-	tss_body	46449419
1058	cg44536277_BC21	0.00024425	-0.04303349	Sergef	chr7	-	tss_body	46751482
1059	cg44540134_TC21	0.00060917	0.03421896	Saa2	chr7	+	tss_1500	49654701
1060	cg44562421_TC21	0.00041223	-0.03000965					52001301
1061	cg44576777_BC21	8.1568E-05	0.07060682	Svip	chr7	-	tss_body	52238878
1062	cg44577891_TC21	0.00065723	-0.03674303					55903477
1063	cg44594132_TC21	0.00081675	0.02780508	Cyfip1	chr7	+	tss_body	55954031
1064	cg44594554_TC11	0.00032829	0.0338459	Nipa2	chr7	-	tss_body	58740312
1065	cg44609343_TC21	6.1458E-05	-0.02590108	Atp10a	chr7	+	tss_body	68469176
1066	cg44683197_TC21	0.00041332	-0.02808163		chr7	+	tss_body	68471261
1067	cg44683226_TC21	0.00088646	-0.03136621		chr7	+	tss_body	74388020
1068	cg44727627_BC21	0.00080293	-0.03610446	Slco3a1	chr7	-	tss_body	75827915
1069	cg44737488_BC21	0.00024041	-0.04527233					79714091
1070	cg44765474_TC11	0.00040478	-0.05285543	Kif7	chr7	-	tss_body	80373824
1071	cg44774512_TC21	7.0003E-05	-0.06818842	chr7-80370616-80371559	chr7	*	SShelf	82842827
1072	cg44801052_TC21	0.00061068	-0.05244337	Gm36584	chr7	-	tss_body	84925033
1073	cg44815859_TC21	0.0007995	-0.03555229					92777719
1074	cg44856639_TC21	7.6729E-06	-0.06238415	Rab30	chr7	+	tss_body	99625558
1075	cg44907111_BC21	0.00013066	-0.05644537	Tpbgl	chr7	-	tss_body	99944688
1076	cg44910370_BC21	0.00040087	-0.03615368	Rnf169	chr7	-	tss_body	102578863
1077	cg44936269_BC21	6.0891E-05	-0.05007462	Olfr550	chr7	+	tss_body	103893231
1078	cg44942690_TC21	5.4521E-05	0.02731336	Olfr64	chr7	-	tss_body	104141254
1079	cg44943969_TC21	0.00056474	-0.05056785	Ubqln3	chr7	-	tss_body	105334659
1080	cg44949994_TC21	0.00037377	0.04009516	Q8VH18	chr7	-	tss_1500	105617834
1081	cg44952569_BC21	0.00061607	-0.03161981	Trim3	chr7	-	tss_body	109230888

1082	cg44972600_BC21	0.00013244	-0.0409441					110301935
1083	cg44982532_TC21	1.0132E-05	0.03726593		chr7	+	tss_200	114712900
1084	cg45019550_BC21	0.0006403	-0.04081685					117465090
1085	cg45040295_TC21	2.6554E-05	0.04224097	Xylt1	chr7	+	tss_body	118141944
1086	cg45045941_TC21	0.00013153	0.04812838	Smg1	chr7	-	tss_body	118295005
1087	cg45047055_TC11	2.5767E-05	-0.0548817					119689961
1088	cg45059873_TC21	0.00043034	0.03795353	Acsm4	chr7	+	tss_200	122344838
1089	cg45083846_BC21	0.00052249	0.05291199	Prkcb	chr7	+	tss_body	122478922
1090	cg45085279_BC21	0.00088823	0.05678726	Prkcb	chr7	+	tss_body	123338523
1091	cg45093621_BC21	0.00047221	-0.04927538	Arhgap17	chr7	-	tss_body	126511337
1092	cg45119928_BC21	0.00035661	-0.05044377	LOC105243053	chr7	+	tss_body	126585024
1093	cg45120773_BC21	0.00050934	-0.03804101	Cln3	chr7	-	tss_body	126685227
1094	cg45121762_TC21	0.00017167	0.07232994	Sult1a1	chr7	-	tss_body	127042765
1095	cg45127463_TC21	0.00021997	-0.06116197	Kif22	chr7	-	tss_1500	127363894
1096	cg45131991_BC21	0.0003457	0.05891492	chr7-127363670-127363908	chr7	*	Island	127810984
1097	cg45138202_TC21	0.00089399	-0.0354535	Stx1b	chr7	-	tss_body	129439086
1098	cg45154471_BC21	0.00076366	-0.03336189					132262981
1099	cg45182395_TC21	0.00072174	-0.05462663	Chst15	chr7	-	tss_body	132304147
1100	cg45182805_TC21	0.00046035	-0.06963681	Chst15	chr7	-	tss_body	133399920
1101	cg45200259_BC21	0.00058621	0.03216267	Adam12	chr7	-	tss_body	134023462
1102	cg45200989_TC21	1.2419E-06	0.08052405	Adam12	chr7	-	tss_body	135601659
1103	cg45215005_TC21	0.00012576	0.07123636	Ptpre	chr7	+	tss_body	135762273
1104	cg45216796_BC21	0.00043079	-0.02839462		chr7	+	tss_body	136928972
1105	cg45227760_TC21	0.00011322	-0.03997084	Mgmt	chr7	+	tss_body	138413826
1106	cg45242682_TC21	0.00014615	0.02772337		chr7	+	tss_body	140081962
1107	cg45260522_BC21	0.00018443	-0.05449561	Caly	chr7	-	tss_body	140335201
1108	cg45262796_BC11	0.00024017	0.03675667	Olfr527	chr7	+	tss_1500	140894413
1109	cg45266580_TC11	0.00031153	0.03199253	Psmd13	chr7	+	tss_body	141016784
1110	cg45268260_TC21	0.00029366	0.04749264	Ifitm6	chr7	-	tss_body	141163232
1111	cg45270343_BC21	0.00027135	-0.04157512	Rnh1	chr7	-	tss_body	141343213

1112	cg45273029_BC21	0.00045575	-0.0579258	Eps8l2	chr7	+	tss_body	142656114
1113	cg45285789_BC11	0.0002736	0.06466616	Igf2	chr7	-	tss_body	142670137
1114	cg45286226_BC21	0.00077378	-0.03804971	Igf2os	chr7	+	tss_body	143340839
1115	cg45291058_TC21	0.00099737	-0.05257123	Kcnq1	chr7	+	tss_body	143340877
1116	cg45291059_BC21	0.00071275	-0.04013089	Kcnq1	chr7	+	tss_body	144628070
1117	cg45303254_TC21	0.00073159	-0.04506078	Ano1	chr7	-	tss_body	4205526
1118	cg45319945_BC21	0.00067974	-0.04835722	Evi5l	chr8	+	tss_body	4591954
1119	cg45323526_TC21	0.00082304	0.05165055					8985611
1120	cg45348730_TC21	7.4916E-05	-0.05441059					9098731
1121	cg45349811_TC21	0.00085555	0.0572542					10857455
1122	cg45365373_BC21	5.7595E-05	-0.02692106	Gm32540	chr8	-	tss_body	11395162
1123	cg45372271_BC11	0.00092536	-0.08321433	Col4a2	chr8	+	tss_body	11506564
1124	cg45373915_BC21	0.00019264	0.03407482	Carkd	chr8	+	tss_body	11559062
1125	cg45374995_TC21	2.4671E-05	-0.05919273	Ing1	chr8	+	tss_body	11629160
1126	cg45375899_TC21	0.00071196	0.06926919	Ankrd10	chr8	-	tss_body	12293677
1127	cg45383833_TC21	0.0008547	0.03674932					12445153
1128	cg45386253_BC21	0.00077397	-0.05123421					12537389
1129	cg45387360_TC21	0.00060458	0.03164126					12718769
1130	cg45389587_TC21	0.00066748	0.02621733	Gm15348	chr8	-	tss_body	19064933
1131	cg45444907_TC21	0.00032946	0.04799433	Defb39	chr8	-	tss_200	22217129
1132	cg45459166_TC21	0.0005037	-0.05569228	Vps36	chr8	+	tss_body	22423915
1133	cg45461259_TC21	2.7371E-05	0.04099373	Mrps31	chr8	+	tss_body	24816756
1134	cg45486880_BC21	0.00025331	-0.03946952	Adam5	chr8	-	tss_body	27229164
1135	cg45515489_TC21	0.00081353	-0.03828852	Adrb3	chr8	-	tss_body	31039256
1136	cg45537489_TC21	0.00061962	0.02969042					36187568
1137	cg45584316_BC21	0.00029423	0.08827043	Gm35520	chr8	+	tss_1500	36196444
1138	cg45584415_BC21	0.00028982	0.06344421	Gm35520	chr8	+	tss_body	36549239
1139	cg45588159_TC21	0.00022955	0.05275552	chr8-36549162-36549390	chr8	*	Island	45752298
1140	cg45646655_TC11	1.0831E-05	0.04127793	Sorbs2	chr8	+	tss_body	45769795
1141	cg45646851_BC21	4.8502E-06	0.02916576	Sorbs2	chr8	+	tss_body	46398097

1142	cg45653674_TC21	0.00045702	0.09427867					46448926
1143	cg45654126_TC21	0.00018642	0.05469478					47284076
1144	cg45663485_TC21	0.00095877	0.03337811	Stox2	chr8	-	tss_body	55659636
1145	cg45717904_TC21	4.9724E-05	0.04507201		chr8	+	tss_body	66494327
1146	cg45780791_BC21	0.0006364	0.05222227		chr8	+	tss_1500	68196094
1147	cg45791069_BC21	0.00083303	0.03899125	Psd3	chr8	-	tss_body	68634067
1148	cg45793774_TC21	3.1201E-05	0.04235321	Csgalnact1	chr8	-	tss_body	69894273
1149	cg45803994_TC21	0.00062025	-0.03415738	Ndufa13	chr8	-	tss_body	70198309
1150	cg45807709_TC21	5.4061E-05	-0.02683436	Slc25a42	chr8	-	tss_body	70297202
1151	cg45808889_TC11	0.0009785	-0.04132863	Ddx49	chr8	-	tss_body	70419116
1152	cg45810928_TC21	0.00057632	-0.04601567	Crtc1	chr8	-	tss_body	70454433
1153	cg45811409_TC21	0.00056462	0.03837675	Klhl26	chr8	-	tss_body	70475856
1154	cg45811644_TC21	0.00098514	0.04731041	Klhl26	chr8	-	tss_body	70645774
1155	cg45814840_TC21	0.00086392	-0.04896713					70808496
1156	cg45818270_BC21	0.00020881	-0.06918708	Il12rb1	chr8	+	tss_body	71348656
1157	cg45823309_TC21	0.00053004	0.05001014	Myo9b	chr8	+	tss_body	71378707
1158	cg45823847_TC21	0.00018025	-0.10693699	Nr2f6	chr8	-	tss_body	71505448
1159	cg45826292_BC21	0.0003446	-0.03981302	Plvap	chr8	-	tss_body	71511936
1160	cg45826455_TC21	0.00082507	-0.06921843	Plvap	chr8	-	tss_200	71566620
1161	cg45827397_BC21	0.00090299	0.04965941	Nxnl1	chr8	-	tss_body	71685814
1162	cg45829792_BC21	0.00023674	-0.02595961	Jak3	chr8	+	tss_body	72253283
1163	cg45834351_BC21	0.00028726	0.04658091	Ap1m1	chr8	+	tss_body	72429993
1164	cg45836118_TC21	0.00047384	0.04238268	LOC108167537	chr8	+	tss_body	79230725
1165	cg45881988_BC21	0.00037066	0.0374232	1700011L22Rik	chr8	-	tss_body	80086697
1166	cg45889206_BC21	0.000215	0.02693249		chr8	-	tss_body	83725951
1167	cg45914544_TC21	5.4504E-05	-0.04491608	Adgre5	chr8	-	tss_body	84094864
1168	cg45920043_BC21	0.00017053	-0.04947957	Rfx1	chr8	+	tss_body	84752467
1169	cg45929043_BC21	0.00031609	0.0679186	Nfix	chr8	-	tss_body	86353957
1170	cg45944193_TC21	0.00052813	0.0432251					86921138
1171	cg45949432_TC11	0.00081733	-0.04895441	Gm33391	chr8	+	tss_1500	88570863
1172	cg45967318_TC21	0.00076379	-0.04547163	Nkd1	chr8	+	tss_body	89386713

1173	cg45976293_BC21	0.0007274	-0.041801					90741763
1174	cg45986887_TC21	0.0001534	0.07060052	Gm35850	chr8	-	tss_1500	90855081
1175	cg45988000_TC21	0.00097912	-0.05291044	Chd9	chr8	+	tss_body	91406857
1176	cg45993864_BC21	0.00047437	0.06382451	Fto	chr8	+	tss_body	93930021
1177	cg46018798_BC21	0.0009989	-0.04879256	Gnao1	chr8	+	tss_body	94171438
1178	cg46021554_TC21	0.00022144	-0.07131195	Gm39227	chr8	-	tss_body	94377813
1179	cg46023851_BC21	0.00042669	-0.03713031		chr8	+	tss_200	95137395
1180	cg46033052_BC21	0.0008629	0.05393269	Kifc3	chr8	-	tss_body	95487650
1181	cg46037373_BC21	1.2537E-05	0.07666848	Csnk2a2	chr8	-	tss_body	97693839
1182	cg46052640_BC21	0.00083449	0.03830143					104704910
1183	cg46090997_BC21	0.00062422	-0.06233733		chr8	-	tss_body	105355545
1184	cg46097137_TC21	0.00062964	-0.05861347	Slc9a5	chr8	+	tss_body	105615749
1185	cg46100482_BC21	0.00054627	-0.04561547	Fam65a	chr8	+	tss_body	106054521
1186	cg46106441_TC21	0.00019941	-0.09545182					106574276
1187	cg46112276_TC21	8.1414E-06	0.02811829		chr8	-	tss_1500	106704964
1188	cg46113840_BC21	0.00068254	-0.03471685	Tango6	chr8	+	tss_body	107397932
1189	cg46121492_TC21	0.00054657	0.04299641	Nqo1	chr8	-	tss_body	109839378
1190	cg46151009_TC21	0.00068265	0.0699905	Ap1g1	chr8	+	tss_body	111338583
1191	cg46169099_BC21	0.00016961	-0.04367282	Mlkl	chr8	-	tss_1500	114522069
1192	cg46199550_TC21	0.00097064	0.03832473	Wwox	chr8	+	tss_body	116867014
1193	cg46225110_BC21	0.00021336	-0.0428029	chr8-116863490-116863709	chr8	*	SShelf	117016774
1194	cg46227344_BC21	2.2504E-05	-0.059101	Pkd1l2	chr8	-	tss_body	117126437
1195	cg46228825_TC21	0.00095318	0.03570486	Bco1	chr8	+	tss_body	117198761
1196	cg46229885_BC21	0.00037275	-0.04569703	Gan	chr8	+	tss_body	119064855
1197	cg46252798_BC21	0.00051081	-0.04284923	Cdh13	chr8	+	tss_body	120145014
1198	cg46268559_TC21	5.4193E-05	-0.07262673	6430548M08Rik	chr8	+	tss_body	120307363
1199	cg46271214_BC21	0.00098935	-0.04175672	Gse1	chr8	+	tss_body	121544169
1200	cg46292062_TC11	0.00036909	0.03169743	1700018B08Rik	chr8	-	tss_body	121584286
1201	cg46292943_BC21	0.00068513	0.07359733	Q6PB93	chr8	+	tss_body	121772486
1202	cg46296328_BC21	0.00015122	-0.03015143	Jph3	chr8	+	tss_body	122422288

1203	cg46306843_TC21	0.00056321	0.03975772	Il17c	chr8	+	tss_body	123522992
1204	cg46324937_BC21	0.00057876	-0.02968964	Gas8	chr8	+	tss_body	124265265
1205	cg46334927_TC11	0.00067535	-0.05483709	Galnt2	chr8	+	tss_body	125518654
1206	cg46352326_TC21	0.00014477	-0.03306186	Sipa1l2	chr8	-	tss_body	126673194
1207	cg46366305_TC21	0.00058775	-0.05164808					4663270
1208	cg46393261_TC21	4.7466E-05	0.04309563	Gria4	chr9	-	tss_body	6192455
1209	cg46400255_BC11	0.00092365	0.02818531	Pdgfd	chr9	+	tss_body	12059439
1210	cg46430530_TC21	0.00073001	-0.02948743					14694153
1211	cg46446843_BC21	0.00066304	0.02855944		chr9	+	tss_body	19541187
1212	cg46474610_TC21	2.7728E-05	0.05656781	Q8VGG6	chr9	-	tss_200	20892119
1213	cg46484247_TC21	0.00039784	-0.04175237	Ppan	chr9	+	tss_body	21792905
1214	cg46497453_BC11	8.737E-05	-0.04051425	Kank2	chr9	-	tss_body	22131781
1215	cg46502838_TC21	6.416E-05	0.03247281	Acp5	chr9	-	tss_body	22188054
1216	cg46503664_TC21	0.00045395	-0.05855343	Zfp872	chr9	+	tss_200	29014085
1217	cg46547992_BC21	0.00028374	-0.03211757	Ntm	chr9	-	tss_body	41091349
1218	cg46635278_BC21	0.00032909	-0.03980394	Ubash3b	chr9	-	tss_body	43270766
1219	cg46658697_BC21	0.00047773	-0.05132396	D630033O11Rik	chr9	+	tss_body	44072246
1220	cg46667989_BC21	0.00022462	-0.03145007	Gm39325	chr9	-	tss_body	44266694
1221	cg46670601_BC21	5.8565E-05	-0.04070394	Nlrx1	chr9	-	tss_body	45135264
1222	cg46682566_BC21	0.00020991	-0.02686415	Gm10684	chr9	-	tss_body	45368596
1223	cg46685153_BC21	0.0003683	-0.03269232	chr9-45370199-45370483	chr9	*	NShore	45370034
1224	cg46685161_BC21	0.00076192	-0.03171606	Fxyd6	chr9	+	tss_200	45387876
1225	cg46685414_TC21	8.0885E-05	-0.06277447	Fxyd6	chr9	+	tss_body	45402830
1226	cg46685603_BC21	7.5198E-05	-0.04478194	Fxyd2	chr9	+	tss_body	50755856
1227	cg46739474_BC21	0.00043733	0.03518263	Cryab	chr9	+	tss_body	53629707
1228	cg46761428_TC21	3.8723E-05	0.03712032	Cul5	chr9	-	tss_body	54735008
1229	cg46771131_TC21	0.00011693	-0.04440659	Wdr61	chr9	-	tss_1500	55542762
1230	cg46778881_TC21	0.00012947	-0.03673052	Isl2	chr9	+	tss_body	56192037
1231	cg46783086_TC21	0.00071071	-0.04255961					56828246
1232	cg46789417_BC21	0.00084229	-0.05666605					59513558

1233	cg46817409_BC21	0.00022439	0.03931713	Gm33180	chr9	-	tss_1500	60864380
1234	cg46830295_BC21	0.00053591	0.03393826	Uaca	chr9	+	tss_body	60936926
1235	cg46831129_TC11	8.2995E-05	-0.047719		chr9	+	tss_body	63399419
1236	cg46858734_BC11	4.5849E-05	0.02629344	2300009A05Rik	chr9	-	tss_200	63730779
1237	cg46861989_TC21	0.00071857	0.04783492	Smad3	chr9	-	tss_body	63803499
1238	cg46863002_TC21	0.00023243	0.04335289					63953681
1239	cg46864756_BC21	8.2091E-05	-0.05026844	Smad6	chr9	-	tss_body	64084823
1240	cg46866770_BC11	2.4665E-05	0.06012369	Scarletltr	chr9	+	tss_body	64638140
1241	cg46872662_TC21	0.00040031	-0.05373802	Megf11	chr9	+	tss_body	65128380
1242	cg46877598_BC21	0.00052077	-0.03001902	Igdcc4	chr9	+	tss_body	66131604
1243	cg46888058_TC21	0.0005666	0.04066868	Fam96a	chr9	+	tss_body	66272081
1244	cg46889424_TC21	0.0001135	0.04932342	Dapk2	chr9	+	tss_body	69366403
1245	cg46917658_TC21	0.00099136	0.03834113	Rora	chr9	+	tss_body	69453662
1246	cg46918463_BC21	0.00037938	0.04425035	Anxa2	chr9	+	tss_200	74868726
1247	cg46965600_BC21	0.00035104	-0.08155384	Onecut1	chr9	+	tss_body	86696158
1248	cg47050591_TC21	0.00042396	0.05450304	A330041J22Rik	chr9	+	tss_body	89826985
1249	cg47072327_TC21	0.00011088	0.03736785	4930524O08Rik	chr9	+	tss_body	92718884
1250	cg47091723_BC21	9.2958E-05	0.06444447	4933400C23Rik	chr9	+	tss_body	95705448
1251	cg47110302_BC11	0.00035373	-0.03328451	Trpc1	chr9	-	tss_body	96837786
1252	cg47121987_BC11	0.00038533	-0.04091095	Pxylp1	chr9	-	tss_body	96995832
1253	cg47124146_BC21	9.0676E-05	-0.04756124	Spsb4	chr9	-	tss_body	102307754
1254	cg47172065_BC21	0.0007185	-0.0470615	Ephb1	chr9	-	tss_body	105311871
1255	cg47203257_TC21	0.00055558	0.06304884	Nek11	chr9	-	tss_body	106338278
1256	cg47214924_TC21	0.00056417	0.0417334	Poc1a	chr9	+	tss_body	107521693
1257	cg47227878_BC21	0.0007055	-0.04967965	Cacna2d2	chr9	+	tss_body	107976399
1258	cg47234584_BC21	0.00027133	-0.03826612	Uba7	chr9	+	tss_body	107978474
1259	cg47234613_TC21	0.00026822	0.04142158	Uba7	chr9	+	tss_body	108094644
1260	cg47236366_TC21	0.00023905	0.02839915	LOC108167685	chr9	+	tss_1500	108486804
1261	cg47241556_BC21	0.00084025	-0.03426229	Lamb2	chr9	+	tss_body	108518162
1262	cg47242366_BC11	1.2091E-07	0.02777865	Qrich1	chr9	+	tss_body	109969197
1263	cg47255572_TC21	0.00010182	0.02600114	Map4	chr9	+	tss_body	113352135

1264	cg47286145_BC21	0.00014687	0.03569805	Gm36436	chr9	-	tss_body	115229829
1265	cg47307945_TC11	0.00027192	0.03088901	Osbpl10	chr9	+	tss_body	115229829
1266	cg47307945_TO11	0.00014734	0.02667955	Osbpl10	chr9	+	tss_body	116150893
1267	cg47317911_TC21	0.00063261	0.05701049	Tgfbr2	chr9	-	tss_body	116423985
1268	cg47320697_BC21	0.00063764	0.05001303					118731040
1269	cg47343952_TC21	0.00034458	-0.04674493	Itga9	chr9	+	tss_body	118908089
1270	cg47346095_BC21	0.00026315	-0.02782579		chr9	-	tss_body	118939631
1271	cg47346773_BC11	0.00034561	-0.0347928	Ctdspl	chr9	+	tss_body	119079979
1272	cg47349103_TC21	0.00069215	0.0796894	Plcd1	chr9	-	tss_body	119157033
1273	cg47350596_BC21	0.00015388	0.03113654	Acaa1b	chr9	-	tss_body	120867023
1274	cg47373682_BC21	0.00059135	-0.03428992	LOC105243573	chr9	-	tss_1500	121704566
1275	cg47384384_TC21	0.00027117	-0.03078657	Sec22c	chr9	-	tss_body	121790967
1276	cg47385868_BC21	0.00032256	-0.031728	Klhl40	chr9	+	tss_body	124442192
1277	cg47406903_TC21	0.00051654	-0.03568513	LOC108167320	chr9	-	tss_body	42262979
X chromosome								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47427989_TC11	5.362E-05	-0.04127371	Wdr45	chrX	+	tss_body	7724231
2	cg47429113_TC21	0.00039823	-0.06013277	Gripap1	chrX	+	tss_body	7801478
3	cg47430033_TC21	0.0004871	-0.10341424	Otud5	chrX	+	tss_body	7874269
4	cg47446368_BC21	0.00014534	0.04587566	Srpx	chrX	-	tss_body	10113229
5	cg47453519_TC11	9.925E-05	-0.05288344					11254296
6	cg47454817_TC21	7.3693E-05	-0.07593854	Gm34138	chrX	-	tss_1500	11437414
7	cg47464520_TC21	0.00046993	-0.03088164	chrX-12252439-12252771	chrX	*	NShelf	12249272
8	cg47466142_BC21	0.00060557	-0.03142123					12426560
9	cg47470796_BC21	0.00027683	-0.03755986	Gm41890	chrX	-	tss_body	12971839
10	cg47472849_TC21	1.9856E-05	-0.03806437	2010308F09Rik	chrX	-	tss_200	13247770
11	cg47511325_BC21	0.00045022	-0.08628569					21288746
12	cg47523223_TC21	0.00073551	0.02586163					24026166
13	cg47548942_BC21	0.00068021	-0.08948987	Dock11	chrX	+	tss_body	35904460
14	cg47552668_BC21	2.2407E-05	0.03691929	Gm14569	chrX	-	tss_body	36492103
15	cg47558215_TC21	5.5652E-05	0.03851824					37114643
16	cg47559793_TC21	0.00014633	-0.03719117	Rhox2b	chrX	+	tss_body	37413432
17	cg47578637_TC21	0.00046478	-0.04005633	Gria3	chrX	+	tss_body	41402822

18	cg47607613_TC21	0.00051038	-0.09903531					47980364
19	cg47608331_BC21	0.00066465	-0.07192652					48042714
20	cg47608976_BC21	0.00097168	0.02837761	Xpnpep2	chrX	+	tss_body	48123847
21	cg47611588_TC21	0.00057404	-0.05557059	Bcorl1	chrX	+	tss_body	48352225
22	cg47612670_BC21	0.00053758	-0.0300558	Elf4	chrX	-	tss_body	48449565
23	cg47632382_BC21	0.00065781	-0.0557013	Gm3572 7	chrX	+	tss_body	51846045
24	cg47634421_TC21	9.3369E-05	0.06469229	Gpc4	chrX	-	tss_body	52136704
25	cg47636113_BC21	0.00047122	0.07646973	Gpc3	chrX	-	tss_body	52377448
26	cg47656785_TC21	0.00042783	-0.09314239	Gm648	chrX	-	tss_body	56549543
27	cg47675407_TC21	0.00017196	0.0302405					59763400
28	cg47680088_TC21	0.00042734	-0.0569938		chrX	+	tss_body	60657808
29	cg47680398_BC21	0.00057941	-0.07621642		chrX	+	tss_body	60719947
30	cg47684742_BC21	0.00015837	0.05793826					61521591
31	cg47694801_BC21	0.00018757	-0.06179462	Gm6760	chrX	-	tss_200	64152256
32	cg47726582_TC21	0.00055996	-0.06972072					71624551
33	cg47737554_BC21	0.00033171	-0.05946704	LOC1081 68457	chrX	-	tss_1500	73636859
34	cg47743931_BC21	9.7385E-05	-0.04770937					74359295
35	cg47761340_BC21	0.0009583	0.03445602		chrX	+	tss_body	77733805
36	cg47770038_TC11	0.00028712	-0.05594088	Gm7173	chrX	-	tss_body	79517272
37	cg47775313_BC11	0.0009376	0.02744682					80790997
38	cg47778054_TC11	0.000331	0.05752269					81468672
39	cg47778764_BC21	0.00020762	-0.08102473					81644930
40	cg47794715_TC21	0.00040084	-0.02539041	Tab3	chrX	+	tss_body	85622090
41	cg47810471_TC21	5.5201E-05	0.04063899	Pet2	chrX	-	tss_200	89409737
42	cg47813938_TC21	0.00019909	-0.03658073					90257716
43	cg47823998_BC21	0.00018418	0.05777993					92810866
44	cg47839670_TC21	0.000779	0.07138962	Arhgef9	chrX	-	tss_body	95195470
45	cg47843712_BC21	6.0507E-05	0.06511559					96006611
46	cg47844530_TC21	0.0002102	-0.05671111	Msn	chrX	+	tss_body	96166213
47	cg47860816_BC21	0.00090847	-0.05542413	Gm1481 2	chrX	-	tss_body	99443783
48	cg47861500_BC21	0.00024346	-0.06070924					99498687
49	cg47862196_BC11	0.00023429	-0.04289332					99568002
50	cg47874273_TC21	0.00042039	-0.04322971	Gjb1	chrX	+	tss_1500	10137609 1
51	cg47881998_BC21	4.4647E-05	-0.06331211					10221613 7
52	cg47893435_BC11	0.0008623	0.03746041	Slc16a2	chrX	-	tss_body	10375150 5
53	cg47903160_BC21	0.00051006	0.04579026					10554168 5
54	cg47933199_TC21	0.00026348	-0.07375921	Tex16	chrX	+	tss_body	11211176 8
55	cg47937651_BC21	0.00052657	-0.0310555	Chm	chrX	-	tss_body	11308132 4
56	cg47953675_BC21	0.00059652	-0.04571523					11703297 1

57	cg47963377_BC11	0.00073361	-0.05853366					119543348
58	cg47963681_TC21	0.00069479	-0.0572809					119600832
59	cg48016351_TC21	0.00068708	-0.06953291	Sytl4	chrX	-	tss_body	133971382
60	cg48019623_BC21	0.00034345	0.0524712					134389022
61	cg48020508_TC21	2.1938E-05	-0.13519156	Taf7l	chrX	-	tss_1500	134476536
62	cg48030336_TC21	3.5975E-05	-0.05354661	Nxf3	chrX	-	tss_body	136085193
63	cg48031331_BC21	0.00038492	0.0638242	Bex1	chrX	-	tss_body	136214811
64	cg48040476_BC21	0.0004893	0.03270756	Il1rapl2	chrX	+	tss_body	137650103
65	cg48047122_BC21	0.00094033	0.03336875		chrX	-	tss_200	139202195
66	cg48051020_BC21	0.0009591	-0.05551665	Ripply1	chrX	-	tss_body	139782097
67	cg48066316_TC21	0.00031515	-0.02579056	Kcne1l	chrX	-	tss_body	142305241
68	cg48070023_BC21	0.00089928	-0.05003618	Tmem164	chrX	+	tss_body	142771028
69	cg48072591_TC21	0.00092119	0.09696963	Rgag1	chrX	+	tss_body	143088986
70	cg48103747_TC21	0.00030858	-0.07664677	Apex2	chrX	-	tss_body	150547235
71	cg48104323_BC21	0.00040038	-0.03793116	Tro	chrX	-	tss_body	150645495
72	cg48157223_BC21	0.00045194	-0.04352192					160617467
73	cg48166099_BC21	0.0008924	0.03656887					162240223
74	cg48177454_TC21	0.00027118	0.02869925					164044043
75	cg48203470_BC21	0.00013747	-0.04144176	Arhgap6	chrX	+	tss_body	168868776
Y chromosome								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48211859_BC21	0.0008034	0.0540572					721654
2	cg48212808_TC11	0.00072548	0.05102257	Kdm5d	chrY	+	tss_1500	897525
3	cg48215622_TC21	0.00055012	0.06542798	Usp9y	chrY	-	tss_body	1457367
4	cg48217641_BC11	0.00025212	0.07829942		chrY	+	tss_1500	2002803
5	cg48218986_BC21	0.00042558	0.03192273					2293551
6	cg48219683_BC21	3.4433E-05	0.05060307					2428341
7	cg48219761_TC21	0.00063286	0.03492703					2440750
8	cg48220131_TC21	0.00073649	0.05588987					2519789
9	cg48221173_BC11	0.00069889	-0.04688619					2743792
10	cg48222874_TC21	0.00019412	0.03393575					3997945
11	cg48222895_BC21	0.00025107	0.04595961					3999324
12	cg48224327_BC11	0.00052851	0.04771336					4283153
13	cg48226984_BC21	0.00072974	-0.05937521					4796577
14	cg48306067_TC11	0.00084606	-0.06750443					42376573

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e\text{-}3$ and effect size > 0.025.

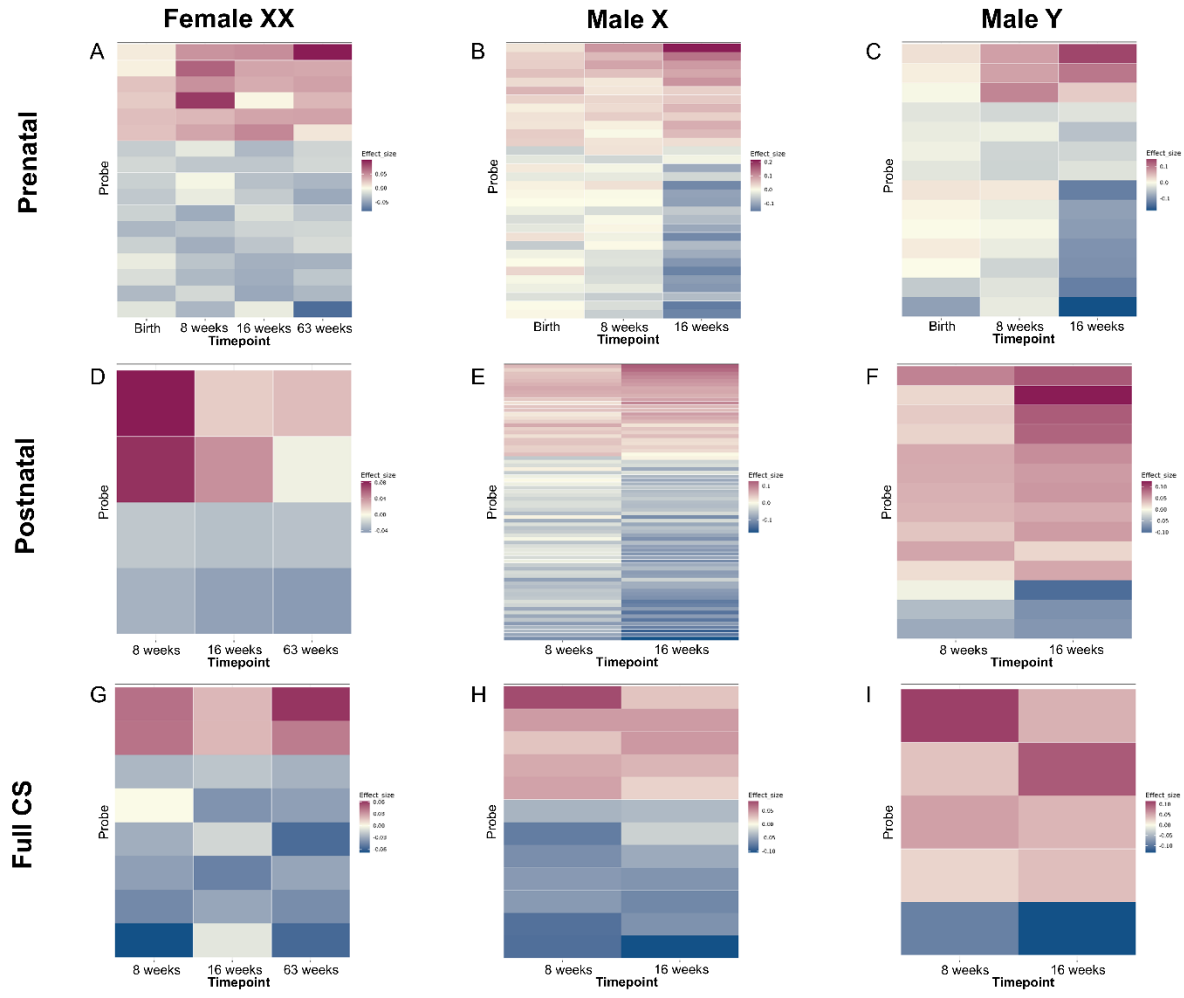
Appendix 4. 36: CpGs which are persistently differentially methylated across the lifespan by full CS exposure in male lungs, identified by limma

Autosomes								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg25794145_BC21	0.000465	0.032838	Setd5	chr6	+	tss_body	1.13E+08
2	cg28384042_BC11	0.000503	0.027451	Gpr6	chr10	-	tss_body	41071323
3	cg29482745_BC11	0.000623	0.050652	Itk	chr11	-	tss_body	46355794
4	cg29525292_TC21	0.000262	0.06819	Nhp2	chr11	+	tss_body	51621624
5	cg30027059_TC21	0.000722	0.04087	LOC105246886	chr11	+	tss_body	99603746
6	cg30664503_BC11	0.000197	0.031866	Baz1a	chr12	-	tss_body	55013976
7	cg30760310_TC11	0.000898	0.025335	Gm32151	chr12	+	tss_body	70347981
8	cg31870910_BC21	0.000279	0.033032		chr13	+	tss_body	87307764
9	cg31911919_BC21	0.000595	0.053188	Arsb	chr13	+	tss_body	93790461
10	cg33493582_TC11	0.000799	0.031343		chr15	+	tss_body	75071426
11	cg33886974_TC21	0.000945	0.045071					8380046
12	cg33963938_BC21	0.00084	-0.03688					18107810
13	cg33983733_TC21	0.000449	-0.034	Dvl3	chr16	+	tss_body	20531114
14	cg34047560_TC21	0.000595	0.035981	Fgf12	chr16	-	tss_body	28661801
15	cg34108738_TC21	0.000638	-0.03966	Kalrn	chr16	-	tss_body	34361002
16	cg34153902_TC21	2.08E-05	0.035529					39057142
17	cg34173105_TC21	0.000143	0.031602					42668444
18	cg34211078_TC21	0.000522	0.032077	Q9CWH0	chr16	+	tss_200	48303896
19	cg34496231_BC21	0.000219	-0.03802					92020129
20	cg34702083_BC21	0.000296	-0.05094		chr17	+	tss_1500	20078476
21	cg34787813_TC21	0.00069	-0.02521	chr17-28232542-28233035	chr17	*	NShore	28231135
22	cg34844222_BC11	0.000854	0.028183					32434525
23	cg35202884_BC21	0.000167	-0.0606		chr17	-	tss_body	73871062
24	cg35239997_BC11	0.000805	0.044479					78911845
25	cg35336699_TC11	0.000587	0.068515		chr17	+	tss_body	87826510
26	cg35594239_BC21	6.67E-05	0.056727	1700066B19Rik	chr18	+	tss_body	35728977
27	cg35734994_BC21	0.000577	0.036396	Csnk1g3	chr18	+	tss_body	53931780
28	cg35997481_TC11	0.000494	0.043978	Gm30192	chr18	+	tss_body	81321977
29	cg36061362_BC21	0.000548	0.029087		chr18	-	tss_body	90311691
30	cg37195492_TC21	0.00064	-0.03789	Hjurp	chr1	-	tss_body	88277027
31	cg38063996_TC21	0.000141	0.028151	Pfkfb3	chr2	-	tss_body	11480213
32	cg38425630_BC21	0.000536	-0.07698	Pkp4	chr2	+	tss_body	59187103
33	cg38977808_TC21	0.000807	-0.02595	Slc23a2	chr2	-	tss_body	1.32E+08
34	cg39428665_BC21	0.000628	-0.0378		chr2	-	tss_200	1.81E+08
35	cg40360951_TC11	0.000686	0.042535	Gm26691	chr3	-	tss_body	1.34E+08
36	cg40502995_TC21	7.56E-05	-0.05852	Gipc2	chr3	-	tss_body	1.52E+08
37	cg41116054_TC11	0.000482	0.061259	Klhl9	chr4	-	tss_body	88722428

38	cg41210695_TC21	0.000435	0.030792	Sgip1	chr4	+	tss_body	1.03E+08
39	cg41466892_BC21	0.000999	-0.05123	Col16a1	chr4	+	tss_body	1.3E+08
40	cg41495568_TC21	0.000904	-0.02779	Ptafr	chr4	+	tss_1500	1.33E+08
41	cg41542044_BC21	0.000405	0.032919					1.36E+08
42	cg41754316_TC11	0.000167	-0.04178					1.53E+08
43	cg41797010_TC11	0.000613	0.050813	Mxra8	chr4	+	tss_1500	1.56E+08
44	cg41803820_BC11	0.000831	-0.05136	Samd11	chr4	-	tss_body	1.56E+08
45	cg43237638_TC21	0.000639	-0.02714	Zfp800	chr6	-	tss_body	28244132
46	cg43410533_TC21	0.000185	-0.03369	Gm31455	chr6	-	tss_1500	50822529
47	cg44204392_TC11	0.000674	0.039056	Vmn1r64	chr7	-	tss_body	5883612
48	cg44286229_BC21	1.55E-05	-0.0327	Eml2	chr7	+	tss_body	19202635
49	cg44317567_TC21	0.000373	-0.04062	Irgc1	chr7	-	tss_body	24435831
50	cg44625694_TC21	0.000765	0.03481	Gm32061	chr7	-	tss_body	62418525
51	cg44954718_BC21	0.000172	0.044033	Mrpl17	chr7	-	tss_body	1.06E+08
52	cg45531463_TC21	0.000842	0.037734					29980130
53	cg45920878_BC21	0.000161	-0.04586	4930432K21Rik	chr8	+	tss_1500	84148270
54	cg45972026_BC21	0.000409	-0.05208	chr8-89006472-89006769	chr8	*	NShore	89005930
55	cg46330061_BC21	0.000924	-0.03587	Acta1	chr8	-	tss_body	1.24E+08
56	cg46474610_TC21	0.000787	0.03534	Q8VGG6	chr9	-	tss_200	19541187
57	cg46606668_TC21	0.000951	0.060707	Fez1	chr9	+	tss_body	36870255
58	cg47175897_TC21	0.000824	0.062054	Anapc13	chr9	+	tss_body	1.03E+08
59	cg47265666_BC21	0.000341	0.04364	Prss44	chr9	+	tss_body	1.11E+08
X chromosome								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg47478291_BC21	0.0003	-0.0463					14207132
2	cg47562723_BC21	6.67E-05	0.036137					37954565
3	cg47611588_TC21	0.000249	-0.05936	Bcorl1	chrX	+	tss_body	48352225
4	cg47632359_TC21	0.000701	-0.07368	Gm35727	chrX	+	tss_body	51842734
5	cg47726582_TC21	0.000116	-0.10006					71624551
6	cg47761340_BC21	0.000539	0.035972		chrX	+	tss_body	77733805
7	cg47832653_BC21	0.000305	0.035564	Zfx	chrX	-	tss_body	94134712
8	cg47904743_BC21	0.00064	-0.06691					1.06E+08
9	cg47951321_BC21	0.000574	0.06241	Cpxcr1	chrX	+	tss_body	1.16E+08
10	cg48045465_TC21	0.00035	-0.05981					1.39E+08
11	cg48076118_TC21	0.000128	0.028752	Pak3	chrX	+	tss_body	1.44E+08
12	cg48196835_BC21	0.000579	-0.04699					1.67E+08
Y chromosome								
	CpG name	**P value**	**Effect size**	**Gene**	**Chromosome**	**Strand**	**Feature**	**CpG position**
1	cg48212670_BC21	0.000306	0.04967					879036
2	cg48219472_BC21	5.74E-05	-0.10804					2392656

3	cg48219761_TC21	1.05E-05	0.08096					2440750
4	cg48219835_TC21	0.00076	0.067316					2458037
5	cg48222874_TC21	0.000884	0.025069					3997945

Differential DNAm was measured using LIMMA, after adjusting for the respective surrogate variables recommended by SVA and controlling for the timepoint variable. DNAm results are sorted by CpG name in ascending order. Gene: gene symbols as annotated by the UCSC Genome browser. Strand = direction of gene on the chromosome (+ = forward, - = reverse). Feature = gene region feature/location as annotated by the UCSC Genome browser (tss_body = within the gene body, tss_200 = 0-200 bases upstream of transcriptional start site, tss_1500 = 200-1500 bases upstream of transcriptional start site). Significance was determined at $p < 1e-3$ and effect size > 0.025.



Appendix 4. 37: Longitudinal DNAm changes over time in males and females amongst sex chromosome CpGs, identified by limma.

(A) 17 CpGs are persistently altered on the X chromosome in the lungs of female offspring exposed to prenatal CS (B) 32 CpGs are persistently altered on the X chromosome in the lungs of male offspring exposed to prenatal CS (C) 14 CpGs are persistently altered on the Y chromosome in the lungs of male offspring exposed to prenatal CS (D) 4 CpGs are persistently altered on the X chromosome in the lungs of female offspring exposed to postnatal CS (E) 75 CpGs are persistently altered on the X chromosome in the lungs of male offspring exposed to postnatal CS (F) 14 CpGs are persistently altered on the Y chromosome in the lungs of male offspring exposed to postnatal CS (G) 8 CpGs are persistently altered on the X chromosome in the lungs of female offspring exposed to full CS (H) 12 CpGs are persistently altered on the X chromosome in the lungs of male offspring exposed to full CS (I) 5 CpG are persistently altered on the Y chromosome in the lungs of male offspring exposed to full CS. Longitudinal DNAm changes were analyzed using Limma, and controlling for the timepoint variable. CpGs were significantly altered across time at $p < 1e\text{-}3$ and effect size > 0.025.

Appendix 4. 38: CpGs which are differentially methylated in lungs of offspring exposed to combined prenatal and adulthood CS

Autosomes									
	CpG	***p* value**	**Effect size**	**Direction of change**	**Gene name**	**Chromosome number**	**Chromosome strand**	**Feature**	**CpG position**
1	cg28123000_TC21	0.000625	-0.07077	Lower	Esr1	10	+	tss_body	4712512
2	cg28182580_TC21	0.000311	-0.05423	Lower	Utrn	10	-	tss_body	12550369
3	cg28220503_TC11	8.03E-05	-0.09056	Lower					18048092
4	cg28257261_BC21	0.000404	-0.07854	Lower					21810292
5	cg28396151_BC21	2.85E-05	0.065228	Higher					42177973
6	cg28690445_TC21	7.31E-05	-0.08986	Lower	Aire	10	-	tss_body	78031949
7	cg28693263_BC21	0.000392	-0.05886	Lower	Gm30122	10	-	tss_body	78256282
8	cg28706900_BC21	0.000523	-0.07111	Lower	Fstl3	10	+	tss_body	79779937
9	cg28711723_TC21	0.00099	-0.09797	Lower	Abca7	10	+	tss_body	80003287
10	cg28728010_BC21	0.000593	-0.05345	Lower	Jsrp1	10	-	tss_body	80810216
11	cg28795853_TC21	0.0005	-0.06331	Lower	Stab2	10	-	tss_body	86974363
12	cg28881488_BC21	9.75E-05	0.050141	Higher	Eea1	10	+	tss_body	95996658
13	cg29127636_TC21	0.000647	-0.10537	Lower					1.26E+08
14	cg29166214_BC21	0.000392	-0.06303	Lower					1.29E+08
15	cg29203995_BC11	0.000636	-0.08307	Lower	Ccdc117	11	-	tss_body	5540637
16	cg29290353_BC21	0.000699	-0.05693	Lower					19093185
17	cg29428369_TC21	0.000473	-0.05063	Lower					38123675
18	cg29560351_TC21	0.00094	-0.05141	Lower	Tnip1	11	-	tss_body	54947800
19	cg29578053_BC21	0.00024	0.127682	Higher	Gria1	11	+	tss_body	57309098
20	cg29631866_TC21	0.000824	-0.07207	Lower	Specc1	11	+	tss_body	62024338

21	cg29730013_TC21	0.000603	0.061843	Higher	Gm33249	11	+	tss_body	71390401
22	cg29744583_TC21	6.88E-05	-0.0837	Lower	Atp2a3	11	+	tss_body	72963193
23	cg29778162_TC11	0.000504	0.08287	Higher	Timm22	11	+	tss_body	76411220
24	cg29778665_BC21	0.000754	-0.07609	Lower	Abr	11	-	tss_body	76454667
25	cg29808508_TC21	2.63E-05	-0.07764	Lower	Ksr1	11	-	tss_body	79096222
26	cg29837798_BC11	0.000558	-0.06518	Lower					82086834
27	cg29850884_BC21	0.00031	0.074034	Higher	Rasl10b	11	+	tss_body	83419088
28	cg30116904_BC21	0.000251	-0.107	Lower		11	-	tss_body	1.07E+08
29	cg30181440_BC21	0.000675	0.051247	Higher	Slc39a11	11	-	tss_body	1.13E+08
30	cg30189719_BC21	0.000669	0.070831	Higher	Sdk2	11	-	tss_body	1.14E+08
31	cg30198816_BC21	0.000499	-0.06578	Lower	Gm31724	11	-	tss_body	1.15E+08
32	cg30203816_TC11	0.000606	0.0646	Higher	Gprc5c	11	+	tss_body	1.15E+08
33	cg30214863_TC21	1.46E-05	0.12708	Higher	chr11-115627761-115628034	11	*	SShelf	1.16E+08
34	cg30235053_BC21	0.000744	-0.11051	Lower	Mxra7	11	-	tss_body	1.17E+08
35	cg30243594_TC21	0.00057	0.05274	Higher	Sept9	11	+	tss_body	1.17E+08
36	cg30258304_BC21	0.000105	0.055695	Higher	Timp2	11	-	tss_body	1.18E+08
37	cg30721506_BC21	0.0005	-0.06025	Lower					64656493
38	cg30851676_BC21	0.000897	0.071581	Higher	Gm36660	12	-	tss_body	80064638
39	cg31064529_BC21	0.000112	0.054345	Higher	Tcl1b2	12	+	tss_1500	1.05E+08
40	cg31156701_BC11	2.25E-06	-0.09535	Lower	Kif26a	12	+	tss_body	1.12E+08
41	cg31159906_TC21	0.000677	-0.10753	Lower	E330035G20Rik	12	-	tss_body	1.12E+08
42	cg31352479_BC21	0.000607	-0.07504	Lower	Lrrc16a	13	-	tss_body	24199625
43	cg31408833_TC21	0.000425	-0.06725	Lower	Gmds	13	-	tss_body	31963888
44	cg31446351_BC21	0.000747	-0.05644	Lower					37457343

45	cg31562402_BC11	0.000906	-0.06645	Lower	Gm36606	13	-	tss_body	48659966
46	cg31569885_TC21	0.000492	0.067035	Higher	Susd3	13	-	tss_body	49241717
47	cg31650206_BC21	0.000669	-0.05096	Lower	Gm40960	13	-	tss_body	56356757
48	cg31686928_TC11	0.000838	0.067343	Higher	Agtpbp1	13	-	tss_body	59454229
49	cg31702693_TC21	0.00017	-0.0803	Lower	Tpbpb	13	-	tss_body	60902188
50	cg31716830_TC21	0.000258	-0.06149	Lower	2010111I01Rik	13	+	tss_body	63171464
51	cg31720345_TC21	0.000583	-0.06598	Lower	Ptch1	13	-	tss_body	63558744
52	cg32119025_TC21	6.92E-05	0.071105	Higher					1.16E+08
53	cg32129755_TC21	0.000731	-0.08749	Lower	Hcn1	13	+	tss_body	1.18E+08
54	cg32355969_BC11	0.00071	-0.06385	Lower	Arhgap22	14	+	tss_body	33247812
55	cg32401261_BC21	0.000704	-0.08111	Lower	Sh2d4b	14	-	tss_body	40853252
56	cg32505750_BC21	0.000928	-0.08079	Lower	Zfhx2	14	-	tss_body	55078680
57	cg32716442_BC21	0.000643	0.068688	Higher					78063181
58	cg32840508_BC21	0.000329	-0.08262	Lower	Klf12	14	-	tss_body	1E+08
59	cg32957734_TC11	0.000293	-0.06058	Lower	Abcc4	14	-	tss_body	1.19E+08
60	cg33065017_TC21	0.000292	-0.09922	Lower					9908433
61	cg33070309_TC21	0.00086	-0.07218	Lower	Rai14	15	-	tss_body	10623961
62	cg33201379_BC21	0.000162	-0.10198	Lower					31150856
63	cg33425502_BC21	0.000191	-0.06784	Lower	Adcy8	15	-	tss_body	64801276
64	cg33471264_BC21	0.000865	-0.09289	Lower	Trappc9	15	-	tss_body	73005208
65	cg33504303_TC21	0.00043	0.066453	Higher	Scrib	15	-	tss_1500	76070471
66	cg33506477_TC21	0.000437	0.055003	Higher	Plec	15	-	tss_body	76184258
67	cg33569106_TC21	0.000491	0.070447	Higher	Grap2	15	+	tss_body	80620452
68	cg33609733_BC21	0.000209	-0.06358	Lower	Efcab6	15	-	tss_body	84030215

69	cg33655237_BC21	0.000458	-0.06726	Lower	Gm35599	15	+	tss_body	87831652
70	cg33688006_BC21	0.000684	0.052588	Higher	Kif21a	15	-	tss_body	90956505
71	cg33737143_BC21	0.000982	-0.05209	Lower		15	+	tss_200	95775738
72	cg33768655_BC21	0.000477	-0.08906	Lower	Col2a1	15	-	tss_body	97990232
73	cg33779789_BC11	1.35E-06	-0.0585	Lower	Wnt10b	15	-	tss_1500	98778536
74	cg33786547_BC21	0.000291	-0.09129	Lower	Spats2	15	+	tss_body	99139311
75	cg33828490_TC21	9.4E-05	-0.06375	Lower	Tns2	15	+	tss_body	1.02E+08
76	cg33842441_BC21	0.00058	-0.08383	Lower	Cbx5	15	-	tss_body	1.03E+08
77	cg33842810_TC21	0.000422	0.061161	Higher	Nfe2	15	-	tss_body	1.03E+08
78	cg33863432_TC21	0.000824	0.051871	Higher	Anks3	16	-	tss_body	4962961
79	cg33900652_BC21	0.00028	-0.1252	Lower	Grin2a	16	-	tss_body	9992495
80	cg33908673_TC11	0.00067	0.05596	Higher	Q3UPE3	16	+	tss_body	10875719
81	cg33927554_TC21	4.86E-05	-0.06921	Lower	Mkl2	16	+	tss_body	13365062
82	cg34228024_BC21	6.64E-05	0.070652	Higher	4930542D17Rik	16	+	tss_body	50645430
83	cg34354004_TC21	0.00073	-0.07644	Lower	Robo1	16	+	tss_body	72828612
84	cg34427814_BC21	0.000403	-0.12757	Lower					84890334
85	cg34471888_TC11	2.24E-05	-0.09386	Lower		16	+	tss_body	90329317
86	cg34474866_BC21	0.000367	-0.05234	Lower	chr16-90524263-90524485	16	*	Island	90524276
87	cg34492210_BC21	0.000926	0.053643	Higher	Itsn1	16	+	tss_body	91735054
88	cg34525668_BC21	0.000737	0.052322	Higher	Hlcs	16	-	tss_body	94245965
89	cg34550275_TC21	0.000194	-0.08244	Lower	Pcp4	16	+	tss_body	96499084
90	cg34731705_TC21	0.000289	0.088584	Higher	Mlst8	17	-	tss_body	24474098
91	cg34807008_TC21	0.000131	-0.0759	Lower					29513136

92	cg34837114_BC21	0.000638	-0.09085	Lower	Sik1	17	-	tss_body	31851019
93	cg34860661_TC21	0.000119	-0.07855	Lower	Brd2	17	-	tss_body	34116908
94	cg34952888_TC21	0.000681	-0.07881	Lower					45607784
95	cg35022819_TC21	8.33E-05	-0.05356	Lower					51536472
96	cg35027436_TC21	0.000823	0.051212	Higher		17	+	tss_body	52078706
97	cg35100315_BC21	1.24E-05	-0.06703	Lower	Fbxl17	17	-	tss_body	63271194
98	cg35159636_BC11	0.000584	-0.06612	Lower	Epb41l3	17	+	tss_body	69262126
99	cg35159829_BC21	0.000491	0.069441	Higher	Epb41l3	17	+	tss_body	69274805
100	cg35311644_BC21	0.000434	-0.07707	Lower					85956527
101	cg35442630_TC21	0.000652	-0.10869	Lower	Osbpl1a	18	-	tss_body	12863190
102	cg35504634_TC21	0.000103	-0.0688	Lower	Nol4	18	-	tss_body	23022935
103	cg35743611_TC21	0.000375	-0.0894	Lower	Zfp608	18	-	tss_body	54953098
104	cg35845375_TC21	0.000521	-0.15826	Lower					65906218
105	cg35870620_BC21	0.000874	-0.0542	Lower	Rnmt	18	+	tss_body	68307490
106	cg35945579_TC21	0.000521	0.057777	Higher					76374581
107	cg35950679_BC21	0.000664	-0.07162	Lower	Skor2	18	+	tss_body	76857545
108	cg35995116_BC11	0.00019	-0.09882	Lower		18	+	tss_body	81083362
109	cg36080508_TC21	0.000204	0.061132	Higher	Pcx	19	+	tss_body	4619858
110	cg36095203_TC11	0.000706	-0.06878	Lower	Kat5	19	-	tss_body	5607924
111	cg36104861_BC21	0.000113	-0.06871	Lower	Batf2	19	+	tss_200	6164323
112	cg36113287_BC21	0.000489	-0.08456	Lower	Rps6ka4	19	-	tss_body	6830305
113	cg36162016_TC21	0.000355	-0.07721	Lower					12360358
114	cg36322862_TC21	0.00078	0.075362	Higher	Gm36419	19	+	tss_body	32548455
115	cg36412014_BC11	0.000444	-0.07519	Lower	Loxl4	19	-	tss_body	42608053

116	cg36452470_BC11	9.62E-05	-0.06393	Lower	Kcnip2	19	-	tss_body	45815787
117	cg36460610_TC21	7.4E-05	-0.09219	Lower	Sufu	19	+	tss_body	46459396
118	cg36487291_BC21	7.95E-05	-0.05379	Lower	Sorcs3	19	+	tss_body	48405034
119	cg36528343_TC21	0.000181	-0.06273	Lower	chr19-54045055-54047684	19	*	SShelf	54049925
120	cg36713841_BC21	0.00039	-0.05215	Lower	Kcnq5	1	-	tss_body	21962053
121	cg36720185_TC21	0.000384	-0.0891	Lower					23028099
122	cg36789132_BC21	0.000504	-0.07072	Lower	Amer3	1	+	tss_body	34580784
123	cg36832176_BC21	0.000642	-0.06317	Lower					38720476
124	cg36919032_BC11	0.000505	0.070926	Higher	Myo1b	1	-	tss_body	51896373
125	cg36922700_TC21	0.000239	0.084145	Higher		1	-	tss_body	52288735
126	cg37039563_BC21	0.00041	-0.08759	Lower	Erbb4	1	-	tss_body	68245222
127	cg37155593_TC21	0.000303	-0.05886	Lower	Ccl20	1	+	tss_body	83116773
128	cg37171714_BC11	5.09E-05	-0.11516	Lower	9930111H07Rik	1	+	tss_1500	85775063
129	cg37206740_TC21	0.000603	0.075835	Higher					89443534
130	cg37207691_TC21	0.000198	-0.06064	Lower	Agap1	1	+	tss_body	89510237
131	cg37214886_TC11	0.000745	0.068878	Higher	Asb18	1	-	tss_body	89993031
132	cg37222426_BC21	0.000794	-0.05904	Lower					90740732
133	cg37232412_BC21	0.000333	0.050999	Higher	Gm28380	1	+	tss_body	91611405
134	cg37375545_TC21	4.89E-05	0.06429	Higher					1.19E+08
135	cg37511293_TC21	0.000838	-0.09033	Lower	Igfn1	1	-	tss_body	1.36E+08
136	cg37516464_BC21	0.00068	-0.0879	Lower					1.36E+08
137	cg37541159_TC21	0.000876	0.061849	Higher	Crb1	1	-	tss_body	1.39E+08
138	cg37620132_TC21	0.000209	-0.06929	Lower	Lamc1	1	-	tss_body	1.53E+08

139	cg37697713_BC21	0.000769	0.060809	Higher					1.63E+08
140	cg37763318_TC11	0.000332	-0.15298	Lower	Gm6345	1	-	tss_200	1.7E+08
141	cg37772972_TC21	0.000879	-0.0609	Lower	Mpz	1	+	tss_body	1.71E+08
142	cg37839755_BC21	0.000126	-0.13707	Lower	Smyd3	1	-	tss_body	1.79E+08
143	cg37856881_TC21	0.000682	-0.11483	Lower					1.81E+08
144	cg37876033_TC21	0.00088	-0.05881	Lower	Capn8	1	+	tss_body	1.83E+08
145	cg38010642_BC21	0.000886	0.052224	Higher	Bend7	2	+	tss_body	4764233
146	cg38110621_BC21	0.000111	-0.08236	Lower	Pip4k2a	2	-	tss_body	18856637
147	cg38135667_TC11	0.000296	-0.08229	Lower	Apbb1ip	2	+	tss_body	22773935
148	cg38163122_BC11	0.000278	0.051362	Higher	Nacc2	2	-	tss_body	26060285
149	cg38175585_BC21	0.000604	-0.0766	Lower	Dbhos	2	-	tss_1500	27164020
150	cg38196075_BC11	0.000167	-0.07672	Lower	chr2-28909689-28910009	2	*	NShelf	28906783
151	cg38204592_BC21	0.000165	0.071926	Higher	Rapgef1	2	+	tss_body	29623110
152	cg38207953_TC21	0.000101	0.063621	Higher	Odf2	2	+	tss_body	29894755
153	cg38231073_BC11	0.000636	-0.12203	Lower					31526041
154	cg38255705_BC21	0.000304	-0.09042	Lower	Ralgps1	2	-	tss_body	33265937
155	cg38261132_BC21	0.000523	-0.05629	Lower					33690224
156	cg38285307_BC21	0.000758	-0.0517	Lower	Ttll11	2	-	tss_body	35928306
157	cg38334364_BC21	0.000106	-0.09084	Lower	Gtdc1	2	-	tss_body	44631304
158	cg38372894_BC21	0.00055	-0.08423	Lower					51049145
159	cg38482949_BC21	0.000364	0.05554	Higher	Scn9a	2	-	tss_body	66617184
160	cg38527101_TC21	0.000529	0.055395	Higher	Platr26	2	+	tss_body	71719666
161	cg38557976_TC11	0.000614	-0.06185	Lower	Hoxd11	2	+	tss_body	74682224
162	cg38572191_TC21	0.000569	-0.07824	Lower					75961099

163	cg38583622_BC21	0.000855	-0.09288	Lower	Ttn	2	-	tss_body	76932214
164	cg38652007_TC21	0.000931	-0.05772	Lower	A2AVC3	2	-	tss_body	87952550
165	cg38691284_BC11	0.000161	0.07403	Higher	Trp53i11	2	+	tss_body	93201280
166	cg38995024_TC11	0.000449	-0.09845	Lower					1.34E+08
167	cg39056514_TC21	0.000184	-0.07659	Lower	Ovol2	2	-	tss_1500	1.44E+08
168	cg39079932_BC21	0.000672	-0.05108	Lower	Nkx2-2	2	-	tss_body	1.47E+08
169	cg39120755_TC21	4.93E-05	-0.08152	Lower					1.53E+08
170	cg39121117_TC21	0.000666	0.094618	Higher	H13	2	+	tss_body	1.53E+08
171	cg39230316_TC21	0.000859	0.051619	Higher	Tox2	2	+	tss_body	1.63E+08
172	cg39327437_BC21	0.000613	-0.08472	Lower	Tshz2	2	+	tss_body	1.7E+08
173	cg39414631_BC21	0.000589	-0.1285	Lower	Cdh4	2	+	tss_body	1.8E+08
174	cg39471337_TC21	0.000586	0.059166	Higher	Tpd52	3	-	tss_body	8954471
175	cg39471985_TC21	0.000326	0.055833	Higher	Tpd52	3	-	tss_body	9001943
176	cg39534548_TC21	0.000444	-0.0518	Lower	Cp	3	+	tss_body	19982083
177	cg39920720_TC21	0.00098	-0.07607	Lower	Ppid	3	+	tss_1500	79590910
178	cg39950093_BC21	0.000511	0.074122	Higher	D930015E06Rik	3	-	tss_body	84022891
179	cg39958359_BC11	0.000416	-0.07491	Lower	Gm40079	3	+	tss_1500	84744718
180	cg39990755_TC11	0.000241	-0.08657	Lower		3	-	tss_body	88204142
181	cg39990771_TC21	0.000229	-0.05459	Lower	Gm3764	3	+	tss_1500	88206045
182	cg40022036_TC21	0.000767	0.05629	Higher	Pglyrp4	3	+	tss_1500	90726704
183	cg40030852_BC11	0.000494	-0.05422	Lower	A0A0A6YX29	3	-	tss_body	92738961
184	cg40067296_TC21	0.000643	0.06148	Higher	Itga10	3	+	tss_body	96652524
185	cg40072299_TC21	7.39E-05	-0.06238	Lower		3	-	tss_200	97126258
186	cg40104234_TC21	0.000623	-0.05742	Lower	Cd101	3	-	tss_body	1.01E+08

187	cg40117414_TC21	0.000677	-0.07913	Lower					1.02E+08
188	cg40149438_TC21	0.000229	-0.05435	Lower	Fam212b	3	+	tss_1500	1.06E+08
189	cg40429302_BC21	0.00085	-0.07902	Lower					1.44E+08
190	cg40512099_BC21	0.000371	-0.06885	Lower	St6galnac5	3	-	tss_body	1.53E+08
191	cg40535716_TC21	9.74E-05	-0.07766	Lower					1.55E+08
192	cg40561157_BC21	0.00093	-0.07297	Lower	Lyn	4	+	tss_body	3722235
193	cg40909842_TC21	0.000963	-0.07523	Lower		4	-	tss_body	55277076
194	cg40984181_TC21	0.000928	-0.07351	Lower					65069869
195	cg41167675_BC21	0.000346	-0.08599	Lower	Nfia	4	+	tss_body	98004013
196	cg41260290_BC21	0.000245	-0.0875	Lower	Slc1a7	4	+	tss_body	1.08E+08
197	cg41359583_BC21	0.000139	-0.10606	Lower	Foxo6	4	-	tss_body	1.2E+08
198	cg41385572_BC21	0.000971	0.082377	Higher	Rhbdl2	4	+	tss_body	1.24E+08
199	cg41406843_TC21	0.000123	-0.06144	Lower					1.25E+08
200	cg41495507_BC11	0.000268	0.079892	Higher					1.33E+08
201	cg41509200_BC21	0.000707	0.073598	Higher	Kdf1	4	+	tss_body	1.34E+08
202	cg41583659_BC21	0.000627	0.061024	Higher					1.38E+08
203	cg41593509_BC21	0.00092	0.068619	Higher	Capzb	4	+	tss_body	1.39E+08
204	cg41593803_TC21	0.000738	-0.05198	Lower	Capzb	4	+	tss_body	1.39E+08
205	cg41593905_TC21	0.000656	0.060326	Higher	Capzb	4	+	tss_body	1.39E+08
206	cg41628246_BC21	0.000738	-0.05385	Lower	Clcnkb	4	-	tss_body	1.41E+08
207	cg41640020_BC21	5.65E-05	0.065159	Higher	Kazn	4	-	tss_body	1.42E+08
208	cg41703909_TC21	0.000352	-0.09664	Lower		4	-	tss_1500	1.5E+08
209	cg41705774_BC21	0.000346	-0.16766	Lower	Pik3cd	4	-	tss_body	1.5E+08
210	cg41712689_BC21	0.000306	0.096396	Higher	Gpr157	4	+	tss_body	1.5E+08

211	cg41736279_TC21	0.000439	-0.07616	Lower	Camta1	4	-	tss_body	1.52E+08
212	cg41808575_BC21	0.000674	-0.06542	Lower	Cdk6	5	+	tss_body	3503400
213	cg41853550_BC21	0.000653	-0.08082	Lower		5	+	tss_200	10558345
214	cg41959829_BC21	0.000814	0.070214	Higher	Dpp6	5	+	tss_body	27652222
215	cg41982447_BC21	1.97E-06	-0.07589	Lower	Kcnk3	5	+	tss_body	30595135
216	cg41985865_TC21	0.00076	0.051634	Higher	Tmem214	5	+	tss_body	30873181
217	cg42001431_BC21	0.000423	-0.06797	Lower		5	-	tss_1500	32398114
218	cg42236130_BC21	0.000257	-0.07477	Lower	Apbb2	5	-	tss_body	66504619
219	cg42588741_BC21	0.000153	-0.07881	Lower					1.12E+08
220	cg42655874_TC21	0.000851	0.052217	Higher	Cit	5	+	tss_body	1.16E+08
221	cg42675448_BC21	0.000697	-0.06713	Lower	Rfc5	5	-	tss_body	1.17E+08
222	cg42684748_BC21	0.000961	-0.14986	Lower	Tesc	5	+	tss_body	1.18E+08
223	cg42697462_TC11	0.000502	-0.09907	Lower					1.19E+08
224	cg42697527_TC21	0.000814	-0.06074	Lower					1.19E+08
225	cg42709083_BC21	0.000872	-0.15509	Lower					1.2E+08
226	cg42750471_TC21	0.000601	-0.06211	Lower	Anapc5	5	-	tss_body	1.23E+08
227	cg42830830_BC21	0.000783	-0.06383	Lower	Sfswap	5	+	tss_body	1.3E+08
228	cg42858079_TC21	0.000516	-0.06546	Lower	Auts2	5	-	tss_body	1.32E+08
229	cg42873367_BC11	0.000324	-0.10637	Lower					1.34E+08
230	cg42914918_BC11	0.000244	-0.12267	Lower	Trip6	5	-	tss_body	1.37E+08
231	cg43033247_TC11	0.000408	-0.08681	Lower	Urad	5	-	tss_body	1.47E+08
232	cg43054403_BC11	0.000184	0.089674	Higher	Katnal1	5	-	tss_body	1.49E+08
233	cg43358315_TC21	0.000588	0.073323	Higher					42523598

234	cg43394833_TC21	0.000124	-0.10078	Lower	Malsu1	6	+	tss_body	49131976
235	cg43436804_BC21	0.000601	-0.05626	Lower		6	-	tss_1500	53172080
236	cg43480504_BC21	1.47E-05	-0.08273	Lower	Herc3	6	+	tss_body	58906529
237	cg43683112_TC21	0.000479	-0.06693	Lower	4930512J16Rik	6	-	tss_body	89272837
238	cg43689964_BC11	0.000601	0.060395	Higher	Uroc1	6	+	tss_body	90333358
239	cg43728479_TC21	0.000645	0.075501	Higher	Lrig1	6	-	tss_body	94674025
240	cg43863564_BC21	0.000371	0.084309	Higher	Gm36023	6	+	tss_1500	1.14E+08
241	cg43904183_TC21	0.000295	0.076142	Higher					1.18E+08
242	cg43944577_TC21	7.67E-07	0.061417	Higher		6	-	tss_body	1.22E+08
243	cg43945543_BC21	0.000495	0.065656	Higher	Rimklb	6	-	tss_1500	1.22E+08
244	cg43952169_BC21	0.000646	-0.07762	Lower	Clec4b2	6	+	tss_200	1.23E+08
245	cg44047003_BC21	2.65E-05	0.054324	Higher	Gprc5d	6	-	tss_200	1.35E+08
246	cg44232627_TC21	0.000536	-0.07722	Lower					11663857
247	cg44256119_TC21	0.000446	0.052798	Higher	Ehd2	7	-	tss_body	15951183
248	cg44279323_TC11	0.000619	-0.05477	Lower	Psg20	7	-	tss_1500	18686316
249	cg44336907_TC21	0.000159	0.05821	Higher	Hnrnpul1	7	-	tss_body	25727955
250	cg44504050_BC21	0.00052	-0.12292	Lower	Mybpc2	7	-	tss_1500	44525175
251	cg44507835_TC11	0.000215	-0.11768	Lower	Zfp473	7	-	tss_body	44747791
252	cg44527192_BC21	0.000922	-0.06197	Lower	Grin2d	7	-	tss_body	45832500
253	cg44645508_BC21	9.63E-05	-0.05097	Lower	Fam189a1	7	-	tss_body	65011339
254	cg44650849_BC21	0.000859	-0.08499	Lower					65532880
255	cg44764363_BC11	0.000575	-0.1574	Lower	Rhcg	7	-	tss_body	79617390
256	cg44779726_TC21	0.000144	-0.09617	Lower	Iqgap1	7	-	tss_body	80777408
257	cg44808497_TC21	0.00075	-0.09839	Lower		7	+	tss_body	83876525
258	cg44917224_TC21	0.000793	0.053266	Higher	Rab6a	7	+	tss_body	1.01E+08

259	cg44958088_BC21	0.000184	-0.08018	Lower		7	-	tss_body	1.07E+08
260	cg44972558_TC11	0.00042	0.095503	Higher		7	-	tss_body	1.09E+08
261	cg45007652_TC21	0.000792	-0.06314	Lower					1.13E+08
262	cg45057598_BC21	0.000557	-0.09219	Lower					1.19E+08
263	cg45070401_TC11	1.93E-05	-0.07453	Lower	493342 7G17Rik	7	+	tss_body	1.21E+08
264	cg45082538_TC21	0.000607	-0.06657	Lower	Chp2	7	+	tss_body	1.22E+08
265	cg45139335_TC21	0.000637	0.060624	Higher	Zfp646	7	+	tss_body	1.28E+08
266	cg45141470_TC11	0.000147	-0.05801	Lower		7	-	tss_1500	1.28E+08
267	cg45229089_BC21	0.000269	-0.05698	Lower	Mgmt	7	+	tss_body	1.37E+08
268	cg45250826_BC21	0.00056	0.058798	Higher	Pwwp2b	7	+	tss_body	1.39E+08
269	cg45270140_TC21	0.00085	0.089152	Higher	Ptdss2	7	+	tss_body	1.41E+08
270	cg45305645_TC21	0.000422	0.055864	Higher	Fgf4	7	+	tss_body	1.45E+08
271	cg45365670_TC21	0.000343	-0.05393	Lower	B930025P03Rik	8	-	tss_body	10881922
272	cg45384281_BC21	0.000722	-0.09497	Lower					12328620
273	cg45662723_TC21	0.000255	-0.06418	Lower	Stox2	8	-	tss_body	47225478
274	cg45804125_BC21	0.000643	-0.0809	Lower	Ndufa13	8	-	tss_body	69902357
275	cg45806010_TC21	0.000205	-0.05777	Lower	Hapln4	8	+	tss_body	70085023
276	cg45808368_BC21	0.000279	0.057256	Higher	Sugp2	8	+	tss_body	70257675
277	cg45817350_BC21	0.000183	0.054003	Higher	Pik3r2	8	-	tss_body	70774931
278	cg45823847_TC21	0.00042	-0.12364	Lower	Nr2f6	8	-	tss_body	71378707
279	cg45839022_TC21	3.17E-05	-0.0772	Lower	Sin3b	8	+	tss_body	72753908
280	cg45996620_BC21	0.000109	0.074326	Higher	Fto	8	+	tss_body	91626067
281	cg46037529_TC11	0.000375	-0.1057	Lower	Csnk2a2	8	-	tss_1500	95490173
282	cg46095071_TC11	0.000914	-0.0909	Lower	Tradd	8	-	tss_body	1.05E+08
283	cg46095485_BC11	0.00017	-0.06037	Lower	Hsf4	8	+	tss_body	1.05E+08

284	cg46209045_TC21	0.000678	0.05495	Higher	Wwox	8	+	tss_body	1.15E+08
285	cg46297853_BC21	0.00068	-0.07309	Lower	Gm34168	8	+	tss_body	1.22E+08
286	cg46316364_BC21	0.000365	0.064076	Higher	Ankrd11	8	-	tss_body	1.23E+08
287	cg46487545_BC21	0.000693	-0.0676	Lower		9	+	tss_body	21098202
288	cg46502924_BC21	9.28E-05	0.062522	Higher	Acp5	9	-	tss_body	22135236
289	cg46609822_TC21	0.00079	-0.0533	Lower	Tmem218	9	+	tss_body	37222434
290	cg46611487_TC11	0.000713	-0.13037	Lower	Robo3	9	-	tss_body	37429765
291	cg46710445_TC21	0.000589	0.083484	Higher	Cadm1	9	+	tss_body	47755308
292	cg46825251_TC21	0.000985	-0.08719	Lower	Thsd4	9	-	tss_body	60385002
293	cg46831043_BC11	0.000568	0.055784	Higher		9	+	tss_body	60926426
294	cg46838398_TC21	0.000856	0.058041	Higher					61561973
295	cg46881202_BC11	0.000869	-0.06722	Lower	Rasl12	9	+	tss_body	65409476
296	cg46914735_BC21	0.000195	0.082504	Higher	Rora	9	+	tss_body	69110656
297	cg47120580_TC21	0.00012	0.073316	Higher	Zbtb38	9	-	tss_body	96726613
298	cg47121158_TC21	0.000696	-0.07025	Lower	C430002N11Rik	9	+	tss_body	96769894
299	cg47207099_BC21	0.00013	0.052277	Higher	Pik3r4	9	+	tss_body	1.06E+08
300	cg47234055_TC21	0.000435	0.05226	Higher	Camkv	9	+	tss_body	1.08E+08
301	cg47236163_BC21	0.000258	0.07167	Higher	Mst1	9	+	tss_body	1.08E+08
302	cg47269462_BC11	0.000612	0.078085	Higher					1.11E+08
303	cg47363177_TC21	0.000226	0.061028	Higher	Q9Z0D9	9	-	tss_body	1.2E+08
304	cg47374018_BC21	0.000921	-0.07682	Lower					1.21E+08
X chromosome									
	CpG	***p* value**	**Effect size**	**Direction of change**	**Gene name**	**Chromosome number**	**Chromosome strand**	**Feature**	**CpG position**
1	cg47562473_TC21	0.00034	0.105476	Higher		X			37908803
2	cg47850059_TC21	0.000253	-0.06737	Lower		X			97528277
3	cg47889454_BC21	0.000568	0.068648	Higher	Cdx4	X	+	tss_body	1.03E+08
4	cg48034707_BC21	0.000473	0.080533	Higher	Morf4l2	X	-	tss_body	1.37E+08
5	cg48192413_BC21	9.47E-05	0.066153	Higher	Gm1720	X	+	tss_body	1.67E+08

Differences in DNA methylation were measured using linear regression contained within the LIMMA package in R. Differentially methylated sites were identified at p < 1e-3 and an effect size > 0.05. CpG = CpG ID on the Illumina mouse methylation microarray. *p* value = *p* value calculated following differential methylation analysis using LIMMA. Effect size = Difference in DNAm between groups. Direction of change - Direction of change in DNAm of CS groups relative to controls. Gene name = Gene name obtained from UCSC Genome Browser. Chromosome number = Chromosome containing the CpG as annotated by UCSC Genome Browser. Chromosome strand = Chromosomal strand on which CpG is located ('+' is the positive strand, '-' is the negative strand). Feature = Location of gene as annotated by the UCSC Genome Browser (tss_body = within gene body, tss_200 = 0-200 bases upstream of the transcription start site, tss_1500 = 200-1500 bases upstream of the transcription start site), Sshelf = 2-4kb downstream (3') of the stop site of a CpG island. CpG position = Genomic location of CpG.

Appendix 4. 39: Enriched biological processes in lungs of offspring exposed to combined prenatal and adulthood CS

ID	Description	P value	FDR	Gene ID	Gene count
GO:0007275	multicellular organism development	6.66E-13	2.33E-09	Esr1/Aire/Fstl3/Gria1/Specc1/Abr/Sdk2/Timp2/Kif26a/Agtpbp1/Ptch1/Hcn1/Arhgap22/Zfhx2/Trappc9/Scrib/Plec/Col2a1/Wnt10b/Tns2/Nfe2/Grin2a/Robo1/Itsn1/Pcp4/Sik1/Brd2/Epb41l3/Zfp608/Skor2/Kat5/Kcnip2/Sufu/Erbb4/Crb1/Lamc1/Mpz/Pip4k2a/Rapgef1/Odf2/Scn9a/Hoxd11/Ttn/Ovol2/Nkx2-2/Nkx2-2os/H13/Tshz2/Cdh4/Pglyrp4/Cd101/Lyn/Nfia/Foxo6/Kdf1/Pik3cd/Gpr157/Cdk6/Apbb2/Cit/Tesc/Auts2/Trip6/Igf2bp3/Lrig1/Iqgap1/Fgf4/Tssk6/Hapln4/Pik3r2/Nr2f6/Sin3b/Tradd/Wwox/Ankrd11/Acp5/Robo3/Cadm1/Rora/Mst1	80
GO:0048856	anatomical structure development	1.67E-12	2.92E-09	Esr1/Utrn/Aire/Fstl3/Gria1/Specc1/Abr/Sdk2/Timp2/Kif26a/Agtpbp1/Ptch1/Hcn1/Arhgap22/Zfhx2/Trappc9/Scrib/Plec/Col2a1/Wnt10b/Tns2/Nfe2/Grin2a/Robo1/Itsn1/Pcp4/Sik1/Brd2/Epb41l3/Zfp608/Skor2/Kat5/Batf2/Kcnip2/Sufu/Erbb4/Crb1/Lamc1/Mpz/Smyd3/Pip4k2a/Rapgef1/Odf2/Scn9a/Hoxd11/Ttn/Ovol2/Nkx2-2/Nkx2-2os/H13/Tshz2/Cdh4/Tpd52/Pglyrp4/Cd101/Lyn/Nfia/Foxo6/Kdf1/Capzb/Kazn/Pik3cd/Gpr157/Cdk6/Apbb2/Cit/Tesc/Auts2/Trip6/Igf2bp3/Lrig1/Gprc5d/Ehd2/Vrk3/Iqgap1/Fgf4/Tssk6/Hapln4/Pik3r2/Nr2f6/Sin3b/Fto/Tradd/Wwox/Ankrd11/Acp5/Robo3/Cadm1/Rora/Mst1	90
GO:0031323	regulation of cellular metabolic process	3.68E-12	4.29E-09	Esr1/Aire/Fstl3/Abca7/Ccdc117/Tnip1/Gria1/Ksr1/Timp2/Tcl1b2/Agtpbp1/Ptch1/Zfhx2/Klf12/Adcy8/Trappc9/Scrib/Puf60/Plec/Wnt10b/Cbx5/Nfe2/Robo1/Pcp4/Mlst8/Sik1/Brd2/Zfp608/Skor2/Pcx/Kat5/Batf2/Rps6ka4/Sufu/Erbb4/Smyd3/Pip4k2a/Nacc2/Hoxd11/Ttn/Ovol2/Nkx2-2/Tox2/Tshz2/Ppid/Lyn/Nfia/Foxo6/Camta1/Cdk6/Apbb2/Rfc5/Tesc/Sfswap/Auts2/Malsu1/Igf2bp3/Zfp473/Vrk3/Iqgap1/Chp2/Zfp668/Mgmt/Pwwp2b/Fgf4/Stox2/Ndufa13/Pik3r2/Nr2f6/Sin3b/Fto/Csnk2a2/Tradd/Hsf4/Wwox/Acp5/Cadm1/Rora/Zbtb38/Pik3r4	80
GO:0060255	regulation of macromolecule metabolic process	6.6E-12	5.78E-09	Esr1/Aire/Fstl3/Abca7/Ccdc117/Tnip1/Gria1/Atp2a3/Ksr1/Timp2/Tcl1b2/Agtpbp1/Ptch1/Zfhx2/Klf12/Adcy8/Trappc9/Scrib/Puf60/Plec/Col2a1/Wnt10b/Cbx5/Nfe2/Grin2a/Robo1/Pcp4/Mlst8/Sik1/Brd2/Zfp608/Skor2/Pcx/Kat5/Batf2/Rps6ka4/Sufu/Erbb4/Ccl20/Smyd3/Nacc2/Hoxd11/Ttn/Ovol2/Nkx2-2/Nkx2-2os/Tox2/Tshz2/Ppid/Pglyrp4/Lyn/Nfia/Foxo6/Pik3cd/Camta1/Cdk6/Apbb2/Rfc5/Tesc/Sfswap/Auts2/Malsu1/Igf2bp3/Zfp473/Vrk3/Iqgap1/Chp2/Zfp646/Zfp668/Mgmt/Pwwp2b/Fgf4/Stox2/Ndufa13/Pik3r2/Nr2f6/Sin3b/Fto/Csnk2a2/Tradd/Hsf4/Wwox/Acp5/Cadm1/Rora/Zbtb38/Mst1	87
GO:0032502	developmental process	1.16E-11	8.13E-09	Esr1/Utrn/Aire/Fstl3/Gria1/Specc1/Abr/Sdk2/Timp2/Kif26a/Agtpbp1/Ptch1/Hcn1/Arhgap22/Zfhx2/Rai14/Trappc9/Scrib/Plec/Col2a1/Wnt10b/Tns2/Nfe2/Grin2a/Robo1/Itsn1/Pcp4/Sik1/Brd2/Epb41l3/Zfp608/Skor2/Kat5/Batf2/Kcnip2/Sufu/Erbb4/Crb1/Lamc1/Mpz/Smyd3/Pip4k2a/Rapgef1/Odf2/Scn9a/Hoxd11/Ttn/Ovol2/Nkx2-2/Nkx2-2os/H13/Tshz2/Cdh4/Tpd52/Pglyrp4/Cd101/Lyn/Nfia/Foxo6/Kdf1/Capzb/Kazn/Pik3cd/Gpr157/Cdk6/Apbb2/Cit/Tesc/Auts2/Trip6/Katnal1/Igf2bp3/Lrig1/Gprc5d/Ehd2/Vrk3/Iqgap1/Fgf4/Tssk6/Hapln4/Pik3r2/Nr2f6/Sin3b/Fto/Tradd/Wwox/Ankrd11/Acp5/Robo3/Cadm1/Rora/Mst1	92
GO:0007399	nervous system development	1.91E-11	1.07E-08	Gria1/Abr/Sdk2/Timp2/Kif26a/Agtpbp1/Ptch1/Hcn1/Zfhx2/Trappc9/Scrib/Plec/Col2a1/Wnt10b/Grin2a/Robo1/Itsn1/Pcp4/Brd2/Epb41l3/Skor2/Kat5/Kcnip2/Sufu/Erbb4/Crb1/Lamc1/Mpz/Rapgef1/Ttn/Ovol2/Nkx2-2/Nkx2-2os/Cdh4/Lyn/Nfia/Foxo6/Gpr157/Cdk6/Apbb2/Cit/Auts2/Igf2bp3/Lrig1/Iqgap1/Hapln4/Nr2f6/Robo3/Cadm1/Rora	50
GO:0048518	positive regulation of	2.13E-11	1.07E-08	Esr1/Utrn/Aire/Fstl3/Abca7/Ccdc117/Tnip1/Gria1/Atp2a3/Abr/Ksr1/Rasl10b/Timp2/Tcl1b2/Agtpbp1/Ptch1/Hcn1/Klf12/Abcc4/A	90

	biological process			dcy8/Scrib/Wnt10b/Nfe2/Grin2a/Robo1/Itsn1/Pcp4/Mlst8/Sik1/Skor2/Pcx/Kat5/Rps6ka4/Kcnip2/Erbb4/Ccl20/Lamc1/Smyd3/Pip4k2a/Apbb1ip/Nacc2/Dbh/Rapgef1/Hoxd11/Ttn/Ovol2/Nkx2-2/Nkx2-2os/Tox2/Cdh4/Tpd52/Ppid/Cd101/Lyn/Nfia/Foxo6/Kdf1/Pik3cd/Camta1/Cdk6/Dpp6/Kcnk3/Apbb2/Cit/Rfc5/Tesc/Anapc5/Auts2/Trip6/Igf2bp3/Clec4b2/Ehd2/Vrk3/Grin2d/Iqgap1/Chp2/Mgmt/Pwwp2b/Fgf4/Ndufa13/Pik3r2/Fto/Tradd/Wwox/Acp5/Cadm1/Rora/Zbtb38/Pik3r4/Mst1	
GO:0019222	regulation of metabolic process	2.86E-11	1.25E-08	Esr1/Aire/Fstl3/Abca7/Ccdc117/Tnip1/Gria1/Atp2a3/Ksr1/Timp2/Tcl1b2/Agtpbp1/Ptch1/Zfhx2/Klf12/Adcy8/Trappc9/Scrib/Puf60/Plec/Col2a1/Wnt10b/Cbx5/Nfe2/Grin2a/Robo1/Pcp4/Mlst8/Sik1/Brd2/Zfp608/Skor2/Pcx/Kat5/Batf2/Rps6ka4/Sufu/Erbb4/Ccl20/Smyd3/Pip4k2a/Nacc2/Dbh/Hoxd11/Ttn/Ovol2/Nkx2-2/Nkx2-2os/Tox2/Tshz2/Ppid/Pglyrp4/Lyn/Nfia/Foxo6/Pik3cd/Camta1/Cdk6/Apbb2/Rfc5/Tesc/Sfswap/Auts2/Malsu1/Igf2bp3/Zfp473/Vrk3/Iqgap1/Chp2/Zfp646/Zfp668/Mgmt/Pwwp2b/Fgf4/Stox2/Ndufa13/Pik3r2/Nr2f6/Sin3b/Fto/Csnk2a2/Tradd/Hsf4/Wwox/Acp5/Cadm1/Rora/Zbtb38/Pik3r4/Mst1	90
GO:0048731	system development	3.77E-11	1.47E-08	Esr1/Aire/Gria1/Abr/Sdk2/Timp2/Kif26a/Agtpbp1/Ptch1/Hcn1/Arhgap22/Zfhx2/Trappc9/Scrib/Plec/Col2a1/Wnt10b/Tns2/Nfe2/Grin2a/Robo1/Itsn1/Pcp4/Sik1/Brd2/Epb41l3/Skor2/Kat5/Kcnip2/Sufu/Erbb4/Crb1/Lamc1/Mpz/Pip4k2a/Rapgef1/Hoxd11/Ttn/Ovol2/Nkx2-2/Nkx2-2os/Cdh4/Lyn/Nfia/Foxo6/Pik3cd/Gpr157/Cdk6/Apbb2/Cit/Tesc/Auts2/Igf2bp3/Lrig1/Iqgap1/Fgf4/Hapln4/Pik3r2/Nr2f6/Sin3b/Wwox/Ankrd11/Acp5/Robo3/Cadm1/Rora	66
GO:0010468	regulation of gene expression	6.65E-11	2.21E-08	Esr1/Aire/Fstl3/Tnip1/Gria1/Ptch1/Zfhx2/Klf12/Adcy8/Trappc9/Scrib/Puf60/Col2a1/Wnt10b/Cbx5/Nfe2/Robo1/Sik1/Brd2/Zfp608/Skor2/Pcx/Kat5/Batf2/Rps6ka4/Sufu/Erbb4/Ccl20/Smyd3/Nacc2/Hoxd11/Ttn/Ovol2/Nkx2-2/Nkx2-2os/Tox2/Tshz2/Ppid/Pglyrp4/Lyn/Nfia/Foxo6/Pik3cd/Camta1/Cdk6/Apbb2/Tesc/Sfswap/Auts2/Malsu1/Igf2bp3/Zfp473/Iqgap1/Chp2/Zfp646/Zfp668/Pwwp2b/Fgf4/Stox2/Ndufa13/Pik3r2/Nr2f6/Sin3b/Fto/Tradd/Hsf4/Wwox/Acp5/Cadm1/Rora/Zbtb38/Mst1	72
GO:0080090	regulation of primary metabolic process	6.93E-11	2.21E-08	Esr1/Aire/Fstl3/Abca7/Ccdc117/Tnip1/Atp2a3/Ksr1/Timp2/Tcl1b2/Agtpbp1/Ptch1/Zfhx2/Klf12/Adcy8/Trappc9/Scrib/Puf60/Plec/Wnt10b/Cbx5/Nfe2/Grin2a/Robo1/Pcp4/Mlst8/Sik1/Brd2/Zfp608/Skor2/Pcx/Kat5/Batf2/Rps6ka4/Sufu/Erbb4/Smyd3/Pip4k2a/Nacc2/Hoxd11/Ttn/Ovol2/Nkx2-2/Tox2/Tshz2/Ppid/Lyn/Nfia/Foxo6/Camta1/Cdk6/Apbb2/Rfc5/Tesc/Sfswap/Auts2/Malsu1/Igf2bp3/Zfp473/Vrk3/Iqgap1/Chp2/Zfp668/Mgmt/Pwwp2b/Fgf4/Stox2/Ndufa13/Pik3r2/Nr2f6/Sin3b/Fto/Csnk2a2/Tradd/Hsf4/Wwox/Cadm1/Rora/Zbtb38/Pik3r4	80
GO:0051171	regulation of nitrogen compound metabolic process	8.8E-11	2.57E-08	Esr1/Aire/Fstl3/Abca7/Ccdc117/Tnip1/Atp2a3/Ksr1/Timp2/Tcl1b2/Agtpbp1/Ptch1/Zfhx2/Klf12/Adcy8/Trappc9/Scrib/Puf60/Plec/Wnt10b/Cbx5/Nfe2/Grin2a/Robo1/Pcp4/Mlst8/Sik1/Brd2/Zfp608/Skor2/Kat5/Batf2/Rps6ka4/Sufu/Erbb4/Smyd3/Nacc2/Hoxd11/Ttn/Ovol2/Nkx2-2/Tox2/Tshz2/Ppid/Lyn/Nfia/Foxo6/Camta1/Cdk6/Apbb2/Rfc5/Tesc/Sfswap/Auts2/Malsu1/Igf2bp3/Zfp473/Vrk3/Iqgap1/Chp2/Zfp668/Mgmt/Pwwp2b/Fgf4/Stox2/Ndufa13/Pik3r2/Nr2f6/Sin3b/Fto/Csnk2a2/Tradd/Hsf4/Wwox/Acp5/Cadm1/Rora/Zbtb38	78
GO:0048522	positive regulation of cellular process	1.36E-10	3.67E-08	Esr1/Utrn/Aire/Fstl3/Abca7/Ccdc117/Tnip1/Gria1/Ksr1/Rasl10b/Timp2/Tcl1b2/Agtpbp1/Ptch1/Hcn1/Klf12/Abcc4/Adcy8/Scrib/Wnt10b/Grin2a/Robo1/Itsn1/Pcp4/Mlst8/Sik1/Skor2/Pcx/Kat5/Rps6ka4/Kcnip2/Erbb4/Ccl20/Lamc1/Smyd3/Pip4k2a/Apbb1ip/Nacc2/Rapgef1/Hoxd11/Ttn/Ovol2/Nkx2-2/Nkx2-2os/Tox2/Cdh4/Tpd52/Ppid/Cd101/Lyn/Nfia/Kdf1/Pik3cd/Camta1/Cdk6/Dpp6/Kcnk3/Apbb2/Cit/Rfc5/Tesc/Anapc5/Auts2/Trip6/Ehd2/Vrk3/Grin2d/Iqgap1/Chp2/Mgmt/Pwwp2b/Fgf4/Pik3r2/Fto/Tradd/Wwox/Acp5/Cadm1/Rora/Zbtb38/Pik3r4/Mst1	82

GO:0006357	regulation of transcription by RNA polymerase II	3.07E-10	7.69E-08	Esr1/Aire/Fstl3/Tnip1/Ptch1/Zfhx2/Klf12/Wnt10b/Cbx5/Nfe2/Sik1/Brd2/Zfp608/Skor2/Kat5/Batf2/Rps6ka4/Sufu/Smyd3/Nacc2/Hoxd11/Ovol2/Nkx2-2/Tox2/Tshz2/Ppid/Nfia/Foxo6/Camta1/Cdk6/Apbb2/Auts2/Zfp473/Chp2/Zfp668/Pwwp2b/Fgf4/Stox2/Pik3r2/Nr2f6/Sin3b/Hsf4/Wwox/Rora/Zbtb38	45
GO:0006366	transcription by RNA polymerase II	7.1E-10	1.56E-07	Esr1/Aire/Fstl3/Tnip1/Ptch1/Zfhx2/Klf12/Wnt10b/Cbx5/Nfe2/Sik1/Brd2/Zfp608/Skor2/Kat5/Batf2/Rps6ka4/Sufu/Smyd3/Nacc2/Hoxd11/Ovol2/Nkx2-2/Tox2/Tshz2/Ppid/Nfia/Foxo6/Camta1/Cdk6/Apbb2/Auts2/Zfp473/Chp2/Zfp668/Pwwp2b/Fgf4/Stox2/Pik3r2/Nr2f6/Sin3b/Hsf4/Wwox/Rora/Zbtb38	45
GO:0009889	regulation of biosynthetic process	7.12E-10	1.56E-07	Esr1/Aire/Fstl3/Abca7/Tnip1/Ptch1/Zfhx2/Klf12/Adcy8/Trappc9/Scrib/Wnt10b/Cbx5/Nfe2/Mlst8/Sik1/Brd2/Zfp608/Skor2/Pcx/Kat5/Batf2/Rps6ka4/Sufu/Erbb4/Ccl20/Smyd3/Nacc2/Hoxd11/Ovol2/Nkx2-2/Tox2/Tshz2/Ppid/Nfia/Foxo6/Camta1/Cdk6/Apbb2/Rfc5/Tesc/Auts2/Malsu1/Igf2bp3/Zfp473/Chp2/Zfp668/Pwwp2b/Fgf4/Stox2/Ndufa13/Pik3r2/Nr2f6/Sin3b/Fto/Tradd/Hsf4/Wwox/Acp5/Rora/Zbtb38	61
GO:0010556	regulation of macromolecule biosynthetic process	9.19E-10	1.89E-07	Esr1/Aire/Fstl3/Abca7/Tnip1/Ptch1/Zfhx2/Klf12/Adcy8/Trappc9/Scrib/Wnt10b/Cbx5/Nfe2/Sik1/Brd2/Zfp608/Skor2/Kat5/Batf2/Rps6ka4/Sufu/Erbb4/Ccl20/Smyd3/Nacc2/Hoxd11/Ovol2/Nkx2-2/Tox2/Tshz2/Ppid/Nfia/Foxo6/Camta1/Cdk6/Apbb2/Rfc5/Tesc/Auts2/Malsu1/Igf2bp3/Zfp473/Chp2/Zfp668/Pwwp2b/Fgf4/Stox2/Ndufa13/Pik3r2/Nr2f6/Sin3b/Fto/Tradd/Hsf4/Wwox/Rora/Zbtb38	58
GO:0019219	regulation of nucleobase-containing compound metabolic process	1.36E-09	2.64E-07	Esr1/Aire/Fstl3/Ccdc117/Tnip1/Ptch1/Zfhx2/Klf12/Adcy8/Trappc9/Puf60/Wnt10b/Cbx5/Nfe2/Mlst8/Sik1/Brd2/Zfp608/Skor2/Kat5/Batf2/Rps6ka4/Sufu/Erbb4/Smyd3/Nacc2/Hoxd11/Ovol2/Nkx2-2/Tox2/Tshz2/Ppid/Nfia/Foxo6/Camta1/Cdk6/Apbb2/Rfc5/Tesc/Sfswap/Auts2/Igf2bp3/Zfp473/Chp2/Zfp668/Mgmt/Pwwp2b/Fgf4/Stox2/Ndufa13/Pik3r2/Nr2f6/Sin3b/Fto/Tradd/Hsf4/Wwox/Rora/Zbtb38	59
GO:0010467	gene expression	1.54E-09	2.84E-07	Esr1/Aire/Fstl3/Tnip1/Gria1/Ptch1/Zfhx2/Klf12/Adcy8/Trappc9/Scrib/Puf60/Plec/Col2a1/Wnt10b/Cbx5/Nfe2/Robo1/Sik1/Brd2/Zfp608/Rnmt/Skor2/Pcx/Kat5/Batf2/Rps6ka4/Sufu/Erbb4/Ccl20/Crb1/Lamc1/Smyd3/Nacc2/Dbh/Hoxd11/Ttn/Ovol2/Nkx2-2/Nkx2-2os/H13/Mcts2/Tox2/Tshz2/Ppid/Pglyrp4/Lyn/Nfia/Foxo6/Pik3cd/Camta1/Cdk6/Apbb2/Tesc/Sfswap/Auts2/Malsu1/Igf2bp3/Hnrnpul1/Zfp473/Iqgap1/Chp2/Zfp646/Zfp668/Pwwp2b/Fgf4/Stox2/Ndufa13/Sugp2/Pik3r2/Nr2f6/Sin3b/Fto/Tradd/Hsf4/Wwox/Acp5/Cadm1/Rora/Zbtb38/Mst1	81
GO:0048523	negative regulation of cellular process	2.14E-09	3.74E-07	Esr1/Fstl3/Abca7/Jsrp1/Tnip1/Gria1/Abr/Timp2/Kif26a/Agtpbp1/Ptch1/Hcn1/Klf12/Adcy8/Scrib/Plec/Col2a1/Wnt10b/Tns2/Cbx5/Nfe2/Robo1/Itsn1/Pcp4/Mlst8/Sik1/Zfp608/Skor2/Kat5/Sufu/Sorcs3/Erbb4/Mpz/Smyd3/Pip4k2a/Nacc2/Rapgef1/Ovol2/Nkx2-2/Ppid/Pglyrp4/Lyn/Kdf1/Capzb/Cdk6/Apbb2/Cit/Tesc/Sfswap/Malsu1/Igf2bp3/Zfp473/Vrk3/Iqgap1/Zfp668/Mgmt/Fgf4/Ndufa13/Tssk6/Pik3r2/Nr2f6/Sin3b/Fto/Csnk2a2/Hsf4/Wwox/Acp5/Cadm1/Rora/Zbtb38/Mst1	71

Gene ontology was performed using the ClusterProfiler package in R. Altered biological processes/pathways were identified at FDR < 0.05. ID = Gene Ontology identification. Description = affected biological process/pathway. Gene ID = Genes involved in the altered biological process. Gene count = number of genes involved in the biological process

Appendix 4. 40: CpGs which are differentially methylated in lungs of offspring exposed to combined full and adulthood CS

Autosomes									
	CpG	***p* value**	**Effect size**	**Direction of change**	**Gene name**	**Chromosome number**	**Chromosome strand**	**Feature**	**CpG position**
1	cg28188072_BC21	8.43E-05	0.100858	Higher	Plagl1	10	+	tss_body	13091499
2	cg28375833_BC21	0.000979	0.056807	Higher	chr10-40257439-40257793	10	*	SShelf	40260762
3	cg28471146_TC21	0.000121	-0.06506	Lower	Gm36280	10	+	tss_200	53488123
4	cg28506344_TC21	0.00044	0.134814	Higher	Pla2g12b	10	+	tss_body	59413925
5	cg28605854_TC21	0.000196	0.051051	Higher					69306317
6	cg28686926_TC21	0.000996	-0.06084	Lower	Tspear	10	+	tss_body	77706056
7	cg28690445_TC21	0.000582	-0.078	Lower	Aire	10	-	tss_body	78031949
8	cg28725096_TC21	0.000726	-0.08149	Lower	Csnk1g2	10	+	tss_body	80638507
9	cg28880711_BC21	0.000976	0.062537	Higher	Gm33377	10	+	tss_body	95893328
10	cg28953917_BC21	0.000687	-0.0752	Lower	Gm36177	10	+	tss_body	1.08E+08
11	cg29177189_BC21	0.000945	0.064616	Higher	Eif4enif1	11	+	tss_body	3227467
12	cg29216175_BC21	0.000455	0.054768	Higher	Myo1g	11	-	tss_body	6519449
13	cg29428350_BC11	0.000189	-0.15589	Lower					38120928
14	cg29467473_BC21	0.000236	-0.0776	Lower	Ebf1	11	+	tss_body	44697470
15	cg29511409_BC21	0.000626	-0.0882	Lower	Q9CVN6	11	+	tss_1500	50354112
16	cg29582848_TC21	0.000502	-0.06391	Lower	Galnt10	11	+	tss_body	57751164
17	cg29634617_BC21	0.000515	0.056029	Higher	Ttc19	11	+	tss_body	62309323
18	cg29730351_TC21	8.6E-05	-0.0634	Lower	Gm16013	11	-	tss_body	71435977
19	cg29783556_BC21	0.000372	-0.0764	Lower	Tmigd1	11	+	tss_body	76901969
20	cg29989382_TC21	3.1E-05	0.056582	Higher	Lrrc46	11	-	tss_body	97040909
21	cg30039250_TC21	0.000371	0.054131	Higher	Rab5c	11	-	tss_body	1.01E+08
22	cg30039252_BC21	0.000816	0.067258	Higher	Rab5c	11	-	tss_body	1.01E+08
23	cg30069111_BC21	0.000115	0.054929	Higher	Adam11	11	+	tss_body	1.03E+08
24	cg30138431_BC21	0.0008	-0.05227	Lower	LOC108167934	11	-	tss_body	1.09E+08
25	cg30175990_BC21	7.1E-05	-0.11961	Lower	LOC108167938	11	+	tss_body	1.13E+08

26	cg30243594_TC21	2.61E-05	0.078163	Higher	Sept9	11	+	tss_body	1.17E+08
27	cg30278583_TC11	0.000399	-0.07455	Lower	Rptor	11	+	tss_body	1.2E+08
28	cg30284429_TC21	0.000803	-0.06416	Lower	Enthd2	11	-	tss_body	1.2E+08
29	cg30287588_TC21	0.000753	-0.055	Lower	Bahcc1	11	+	tss_body	1.2E+08
30	cg30330450_TC11	0.000255	-0.06205	Lower	Klhl29	12	-	tss_body	5210013
31	cg30374005_TC21	0.000345	-0.09102	Lower					12222990
32	cg30480322_TC21	0.000575	-0.15302	Lower	493340 9F18Rik	12	-	tss_body	26834126
33	cg30482657_BC21	0.000547	0.052652	Higher	Gm40872	12	-	tss_body	27191705
34	cg30530786_BC21	0.000826	-0.07393	Lower	Atxn7l1	12	+	tss_body	33315077
35	cg31013061_TC21	0.00018	0.062098	Higher					99956655
36	cg31064631_TC21	0.000225	-0.11037	Lower	Tcl1b1	12	+	tss_body	1.05E+08
37	cg31352479_BC21	0.000558	-0.08745	Lower	Lrrc16a	13	-	tss_body	24199625
38	cg31358928_BC21	0.000418	-0.0608	Lower	Tdp2	13	+	tss_body	24833249
39	cg31419613_BC21	0.000411	0.051176	Higher					33908594
40	cg31592452_BC21	0.000272	0.104086	Higher					51866628
41	cg31679540_TC21	0.000996	-0.06765	Lower	Ntrk2	13	+	tss_body	58808553
42	cg31702693_TC21	1.38E-05	-0.11497	Lower	Tpbpb	13	-	tss_body	60902188
43	cg31879636_BC21	0.000414	-0.10761	Lower					89427902
44	cg31948263_TC21	4.76E-05	0.099084	Higher					97275560
45	cg31967369_BC21	0.000515	0.073001	Higher	Gm35215	13	-	tss_200	98945990
46	cg32281862_TC21	0.000688	0.091356	Higher	Zmiz1os1	14	-	tss_body	25273047
47	cg32363423_TC21	0.000157	-0.0685	Lower	A630023A22Rik	14	-	tss_body	34052702
48	cg32414600_TC21	0.00086	0.05261	Higher	Gm32857	14	-	tss_body	44249284
49	cg32462514_BC21	0.000113	-0.1023	Lower	Slc35f4	14	-	tss_body	49525558
50	cg32513538_BC21	0.000509	-0.05323	Lower	Tgm1	14	-	tss_body	55707642
51	cg32584189_TC21	2.16E-05	-0.07892	Lower	Fam167a	14	+	tss_body	63456217
52	cg32654102_TC11	0.000707	-0.13621	Lower	Gm38605	14	+	tss_body	70636816
53	cg32757583_TC21	0.000845	0.058811	Higher					84886510
54	cg33001205_BC21	0.000917	-0.07378	Lower	Gm5089	14	-	tss_body	1.22E+08
55	cg33008861_BC21	0.000478	-0.08953	Lower	Itgbl1	14	+	tss_body	1.24E+08

56	cg33101971_BC21	0.000175	-0.07939	Lower					14274977
57	cg33183782_BC21	0.000618	-0.10517	Lower	Dnah5	15	+	tss_body	28229640
58	cg33394238_TC21	0.000844	-0.05997	Lower					59815262
59	cg33472488_BC21	0.000649	-0.07198	Lower	Chrac1	15	+	tss_body	73093615
60	cg33503308_TC21	0.00033	0.059924	Higher	Fam83h	15	-	tss_body	76014234
61	cg33547465_BC21	0.000706	-0.07329	Lower	Gm10863	15	+	tss_1500	79164921
62	cg33554308_BC11	0.000967	-0.09771	Lower	Fam227a	15	-	tss_body	79617414
63	cg33556729_BC11	0.000909	0.057281	Higher	Dnal4	15	-	tss_body	79765123
64	cg33566048_BC21	0.000223	-0.08861	Lower	Cacna1i	15	+	tss_body	80372556
65	cg33572379_TC21	4.08E-05	-0.08638	Lower	Adsl	15	+	tss_body	80952399
66	cg33612698_TC21	0.000175	0.075614	Higher	Parvb	15	+	tss_body	84237318
67	cg33615024_TC21	0.000414	-0.07541	Lower	1810041L15Rik	15	-	tss_body	84406681
68	cg33655237_BC21	8.3E-05	-0.08044	Lower	Gm35599	15	+	tss_body	87831652
69	cg33736569_BC21	0.000746	0.051187	Higher					95725931
70	cg33783789_BC21	0.000474	-0.09437	Lower	4930578M01Rik	15	+	tss_body	98987218
71	cg33793380_BC21	0.000291	0.078061	Higher	Gm34765	15	-	tss_body	99579000
72	cg33819331_BC21	0.000165	0.057208	Higher	Atg101	15	+	tss_body	1.01E+08
73	cg33820260_BC21	0.000627	0.089323	Higher	Krt80	15	-	tss_body	1.01E+08
74	cg33842441_BC21	0.000109	-0.10181	Lower	Cbx5	15	-	tss_body	1.03E+08
75	cg33859152_TC21	0.000742	-0.06304	Lower	LOC105246062	16	-	tss_body	4593545
76	cg33982213_BC21	7.37E-05	0.063392	Higher	Abcc5	16	-	tss_body	20392886
77	cg34091286_BC21	0.000949	-0.08446	Lower	Muc4	16	+	tss_body	32778966
78	cg34125074_BC21	0.000476	-0.08233	Lower					35829882
79	cg34131872_TC21	0.000359	0.064094	Higher	Ildr1	16	+	tss_body	36712055
80	cg34284589_TC21	0.000672	0.078218	Higher	Epha6	16	-	tss_body	59688596
81	cg34301664_BC21	0.000576	0.054858	Higher		16	+	tss_200	63111675
82	cg34449158_BC21	0.000219	0.052188	Higher	Gm32925	16	+	tss_body	87751377
83	cg34545384_BC21	1.33E-05	-0.05495	Lower	Brwd1	16	-	tss_body	96040754
84	cg34548485_BC21	0.000894	-0.07736	Lower	B3galt5	16	+	tss_body	96299435
85	cg34589015_BC21	0.000856	-0.10033	Lower	Synj2	17	+	tss_body	5996879

86	cg34624722_BC21	0.000253	0.071341	Higher					9539077
87	cg34738210_BC21	0.000245	0.052592	Higher	Mapk8ip3	17	-	tss_body	24899028
88	cg34757113_TC21	0.000905	0.070946	Higher	Fam234a	17	-	tss_body	26225387
89	cg34787061_BC21	0.000159	0.057089	Higher	Zfp523	17	+	tss_body	28185904
90	cg34798259_BC11	0.000906	0.068044	Higher	Gm16191	17	+	tss_body	28930696
91	cg34860306_BC21	0.000949	-0.05024	Lower	BC051537	17	-	tss_body	34091379
92	cg34864454_BC21	0.000732	-0.06387	Lower	BC051142	17	+	tss_body	34417490
93	cg34867975_BC21	0.000856	-0.0529	Lower	Tnxb	17	+	tss_body	34678674
94	cg34870820_BC21	7.63E-06	-0.18785	Lower	C2	17	-	tss_body	34873636
95	cg35064640_TC21	0.000976	-0.05887	Lower	Crb3	17	+	tss_body	57065285
96	cg35095691_TC21	9.58E-05	0.051657	Higher	Efna5	17	-	tss_body	62829144
97	cg35100315_BC21	4.54E-05	-0.06303	Lower	Fbxl17	17	-	tss_body	63271194
98	cg35424955_BC21	0.000197	-0.0856	Lower	Mib1	18	+	tss_body	10799847
99	cg35591722_BC21	0.000909	0.055376	Higher	Gm41691	18	-	tss_body	35504966
100	cg35629786_TC21	0.000426	-0.08622	Lower	Arhgap26	18	+	tss_body	38846959
101	cg35744979_BC21	0.000888	0.070842	Higher	Gm4221	18	+	tss_body	55096324
102	cg35789303_BC21	8.04E-06	0.065658	Higher	Ndst1	18	-	tss_body	60695237
103	cg35949472_TC21	0.00061	0.05407	Higher					76751643
104	cg36066719_TC11	0.000299	-0.06008	Lower	Ppp6r3	19	-	tss_body	3484840
105	cg36094169_BC21	1.97E-05	-0.08411	Lower	Ovol1	19	-	tss_body	5553567
106	cg36101011_BC21	0.000732	-0.08875	Lower					5937740
107	cg36104434_TC21	0.000216	0.057317	Higher	Arl2	19	-	tss_body	6137295
108	cg36115409_TC21	0.000637	-0.06121	Lower	Plcb3	19	-	tss_body	6956481
109	cg36146503_BC21	1.85E-06	-0.1081	Lower	Syt7	19	+	tss_body	10395481
110	cg36424786_TC21	0.000764	-0.06635	Lower	Abcc2	19	+	tss_body	43834972
111	cg36439044_TC21	0.000357	-0.1208	Lower					44881498
112	cg36492755_TC21	0.000474	-0.05019	Lower					49302184
113	cg36523451_TC21	0.000575	-0.06157	Lower	Rbm20	19	+	tss_body	53662492
114	cg36789132_BC21	0.000173	-0.08135	Lower	Amer3	1	+	tss_body	34580784
115	cg36800056_BC21	0.000154	-0.10297	Lower	Gm33176	1	+	tss_1500	35941711
116	cg36839456_TC21	0.000128	0.057348	Higher	Rpl31	1	+	tss_body	39371044

117	cg36840463_BC21	0.000368	0.092271	Higher	Tbc1d8	1	-	tss_body	39450178
118	cg36865872_TC21	0.000159	-0.08192	Lower	Gm36678	1	-	tss_body	42418641
119	cg36929811_TC21	0.000375	0.052154	Higher	Q8BFS9	1	-	tss_body	53342134
120	cg37203575_TC21	2.7E-05	0.084991	Higher	Sh3bp4	1	+	tss_body	89105134
121	cg37214137_TC21	0.000269	0.054015	Higher	chr1-89941589-89942209	1	*	SShore	89942649
122	cg37217388_BC21	0.000334	-0.0514	Lower					90222845
123	cg37235414_BC11	0.000415	0.057653	Higher					91872566
124	cg37317587_BC21	0.000248	-0.06382	Lower	Bcl2	1	-	tss_body	1.07E+08
125	cg37435528_BC21	0.000439	0.06078	Higher	R3hdm1	1	+	tss_body	1.28E+08
126	cg37453889_BC11	0.000322	0.065902	Higher	Il10	1	+	tss_1500	1.31E+08
127	cg37496044_TC21	0.000601	-0.14415	Lower	Syt2	1	+	tss_body	1.35E+08
128	cg37499637_BC21	0.000453	-0.0957	Lower	Lgr6	1	-	tss_body	1.35E+08
129	cg37659571_BC21	0.000879	-0.06517	Lower	BC026585	1	+	tss_body	1.57E+08
130	cg37794339_TC21	1.77E-05	-0.0656	Lower	Aim2	1	+	tss_body	1.73E+08
131	cg37798284_TC21	0.000744	-0.06027	Lower	E9Q4G0	1	+	tss_body	1.74E+08
132	cg38061470_TC21	0.000273	0.068757	Higher	Prkcq	2	+	tss_body	11203355
133	cg38150914_TC21	1.08E-05	-0.13072	Lower	Noxa1	2	-	tss_body	25094949
134	cg38227428_BC21	0.000381	0.055698	Higher	Ncs1	2	+	tss_body	31261026
135	cg38255705_BC21	0.000103	-0.11527	Lower	Ralgps1	2	-	tss_body	33265937
136	cg38406333_BC21	0.000154	-0.07972	Lower					56539962
137	cg38459620_BC21	0.000686	-0.0644	Lower	Gm34110	2	+	tss_body	63184515
138	cg38914483_BC21	0.000204	-0.0703	Lower	Fbn1	2	-	tss_body	1.26E+08
139	cg38950347_TC21	0.000486	-0.13012	Lower					1.29E+08
140	cg39070845_TC21	0.000156	-0.10086	Lower	A8Y5L4	2	+	tss_body	1.46E+08
141	cg39076276_BC21	0.000804	-0.06723	Lower					1.47E+08
142	cg39271092_TC11	0.000811	0.058482	Higher	Sulf2	2	-	tss_body	1.66E+08
143	cg39382173_TC21	0.000227	0.086383	Higher	Nespas	2	-	tss_body	1.74E+08
144	cg39383432_BC21	0.000888	0.051446	Higher	Gnas	2	+	tss_body	1.74E+08
145	cg39425367_BC21	0.000553	-0.09739	Lower	Ntsr1	2	+	tss_body	1.81E+08
146	cg39534548_TC21	0.00069	-0.05351	Lower	Cp	3	+	tss_body	19982083

147	cg39628672_BC11	0.000288	-0.08456	Lower	Dnajc19	3	-	tss_body	34079114
148	cg39651828_TC21	0.000572	0.077756	Higher	Trpc3	3	-	tss_body	36671154
149	cg39653965_BC11	0.00092	-0.16443	Lower	4932438A13Rik	3	+	tss_body	36936992
150	cg39668285_BC21	0.000407	0.052122	Higher					38733495
151	cg39733979_TC21	0.000261	-0.11191	Lower					51096116
152	cg39758130_BC21	0.000415	-0.05012	Lower	Lhfp	3	+	tss_body	53060359
153	cg40019657_BC11	0.000702	-0.06494	Lower	Npr1	3	-	tss_body	90455888
154	cg40022036_TC21	0.000134	0.074675	Higher	Pglyrp4	3	+	tss_1500	90726704
155	cg40049844_BC21	0.000255	0.075548	Higher	Bnipl	3	-	tss_body	95250855
156	cg40054101_BC21	5.74E-05	0.067288	Higher					95671462
157	cg40056553_BC21	0.000441	-0.07734	Lower	C920021L13Rik	3	+	tss_body	95881923
158	cg40143403_TC21	0.00026	0.100283	Higher	Cttnbp2nl	3	-	tss_body	1.05E+08
159	cg40203941_BC21	0.000515	-0.05674	Lower					1.14E+08
160	cg40293241_TC21	0.000736	-0.05397	Lower	Camk2d	3	+	tss_body	1.27E+08
161	cg40932533_TC21	0.000471	-0.07427	Lower	Palm2	4	+	tss_body	57688464
162	cg40973659_TC21	0.000192	0.061547	Higher	Orm2	4	+	tss_body	63362884
163	cg40984181_TC21	0.000778	-0.07764	Lower					65069869
164	cg41103180_TC21	0.000802	-0.07524	Lower	Acer2	4	+	tss_body	86887667
165	cg41210657_BC11	0.000887	0.058847	Higher	Sgip1	4	+	tss_body	1.03E+08
166	cg41461686_BC21	0.000815	-0.05637	Lower	Khdrbs1	4	-	tss_body	1.3E+08
167	cg41516235_BC21	0.00046	-0.05123	Lower	Dhdds	4	-	tss_body	1.34E+08
168	cg41526874_BC21	0.000315	-0.11818	Lower	Man1c1	4	-	tss_body	1.35E+08
169	cg41527953_BC21	0.000537	0.059523	Higher	Ldlrap1	4	-	tss_body	1.35E+08
170	cg41614986_BC11	4.51E-05	-0.19062	Lower	Arhgef10l	4	-	tss_body	1.41E+08
171	cg41616312_TC21	0.000211	0.068777	Higher	Rcc2	4	+	tss_body	1.41E+08
172	cg41640020_BC21	1.98E-05	0.080417	Higher	Kazn	4	-	tss_body	1.42E+08
173	cg41702081_BC21	0.000222	-0.05995	Lower	Rbp7	4	-	tss_body	1.49E+08
174	cg41799737_BC21	6.72E-05	0.058794	Higher	Sdf4	4	+	tss_body	1.56E+08
175	cg41826838_TC21	0.000474	-0.0541	Lower					5780511
176	cg41888536_BC21	0.000934	0.069031	Higher	Gnai1	5	-	tss_body	18314471
177	cg41975691_TC11	2.23E-05	0.08648	Higher		5	-	tss_body	29891928

178	cg41989895_BC21	0.000353	0.072194	Higher	Mpv17	5	-	tss_body	31146573
179	cg42022941_TC21	0.000731	0.061181	Higher	Mfsd10	5	-	tss_body	34635064
180	cg42034934_TC21	2.89E-05	0.067787	Higher	Ablim2	5	+	tss_body	35773318
181	cg42239730_TC21	0.000746	-0.07811	Lower	Limch1	5	+	tss_body	66797858
182	cg42289906_BC21	0.000945	-0.07943	Lower	Lrrc66	5	-	tss_1500	73633304
183	cg42442517_BC21	0.000238	-0.09113	Lower	Fras1	5	+	tss_body	96558379
184	cg42446074_TC21	0.000264	-0.08283	Lower					96948868
185	cg42493331_TC21	0.000872	-0.06931	Lower	9430085M18Rik	5	+	tss_body	1.02E+08
186	cg42572866_BC21	0.000233	0.068664	Higher	Fbrsl1	5	-	tss_body	1.1E+08
187	cg42590608_TC11	1.52E-05	0.076323	Higher	Gm36535	5	+	tss_body	1.12E+08
188	cg42630966_BC21	0.000583	0.117132	Higher					1.15E+08
189	cg42653827_TC11	0.000997	-0.06074	Lower	Cit	5	+	tss_body	1.16E+08
190	cg42675448_BC21	0.00025	-0.07902	Lower	Rfc5	5	-	tss_body	1.17E+08
191	cg42688679_BC21	0.00085	-0.05996	Lower					1.18E+08
192	cg42800602_BC21	0.000106	-0.07868	Lower	1700081B01Rik	5	+	tss_body	1.27E+08
193	cg42858079_TC21	0.000713	-0.06469	Lower	Auts2	5	-	tss_body	1.32E+08
194	cg42866081_TC21	0.000165	-0.11061	Lower					1.33E+08
195	cg42878416_BC21	0.000449	-0.06815	Lower	Syna	5	-	tss_body	1.35E+08
196	cg42879072_BC21	1.71E-05	-0.08015	Lower	Lat2	5	-	tss_body	1.35E+08
197	cg42924521_BC21	1.93E-05	0.054971	Higher	Zkscan1	5	+	tss_body	1.38E+08
198	cg43080579_BC21	0.000383	-0.08926	Lower	Stard13	5	-	tss_body	1.51E+08
199	cg43238366_TC21	0.000933	0.066945	Higher	Zfp800	6	-	tss_body	28319862
200	cg43264611_TC21	0.000883	0.077684	Higher	Mest	6	+	tss_body	30737200
201	cg43264624_BC11	0.000697	0.074261	Higher	Mest	6	+	tss_body	30737492
202	cg43391351_TC21	6.81E-05	-0.08926	Lower	Gimap5	6	+	tss_body	48746220
203	cg43412027_BC21	0.00047	-0.08365	Lower	Gm38809	6	-	tss_body	50977746
204	cg43615508_BC21	0.000276	0.080189	Higher	Gm38843	6	-	tss_1500	82806250
205	cg43652874_TC21	5.12E-05	-0.07021	Lower		6	+	tss_1500	86498241
206	cg43677384_BC21	2.1E-05	0.097488	Higher	Mgll	6	+	tss_body	88766809
207	cg43720095_TC21	0.000534	0.06458	Higher	Magi1	6	-	tss_body	93770968

208	cg43777906_TC21	0.000953	-0.06433	Lower					1E+08
209	cg43787998_BC21	0.000482	-0.06131	Lower	Pdzrn3	6	-	tss_body	1.01E+08
210	cg43856375_BC21	9.87E-05	0.094039	Higher	Il17rc	6	+	tss_body	1.13E+08
211	cg43859584_BC21	0.000742	0.082538	Higher	Ghrl	6	-	tss_body	1.14E+08
212	cg43970229_TC21	0.000228	-0.06837	Lower	Gm24175	6	-	tss_body	1.25E+08
213	cg43993782_TC21	0.00094	0.076616	Higher					1.28E+08
214	cg44198236_TC21	0.00022	-0.10288	Lower	Zfp579	7	-	tss_body	4994585
215	cg44241737_TC21	0.000819	-0.09375	Lower	Vmn1r85	7	-	tss_body	13085179
216	cg44360395_TC21	3.76E-05	0.124867	Higher	Dyrk1b	7	+	tss_body	28184960
217	cg44518605_TC21	0.000889	-0.09781	Lower	Ppfia3	7	-	tss_body	45356674
218	cg44520293_BC21	3.47E-05	0.053519	Higher	Gys1	7	+	tss_body	45439373
219	cg44537418_TC11	0.000255	-0.05539	Lower	Sergef	7	-	tss_body	46535579
220	cg44773937_TC21	5.46E-05	0.052974	Higher	Hddc3	7	+	tss_body	80345558
221	cg44890325_TC21	9.1E-05	-0.0959	Lower	Capn5	7	-	tss_body	98165537
222	cg44922022_BC21	7.32E-06	-0.0937	Lower					1.01E+08
223	cg45027956_TC21	0.000609	-0.05896	Lower	Sox6	7	-	tss_body	1.16E+08
224	cg45092084_BC21	0.000256	0.07567	Higher	Tnrc6a	7	+	tss_body	1.23E+08
225	cg45309778_BC21	0.000283	-0.08025	Lower	Mrgprf	7	+	tss_body	1.45E+08
226	cg45365670_TC21	5.48E-05	-0.07758	Lower	B930025P03Rik	8	-	tss_body	10881922
227	cg45483137_BC11	0.000683	-0.08893	Lower	Gm30757	8	-	tss_1500	24431933
228	cg45495107_BC21	8.45E-05	0.070329	Higher	Fgfr1	8	+	tss_body	25521901
229	cg45802604_BC21	0.000342	-0.08012	Lower	Gmip	8	+	tss_body	69821547
230	cg45816073_TC21	0.000408	0.089213	Higher	Gm16486	8	+	tss_body	70716663
231	cg45832715_TC21	0.000891	-0.06479	Lower		8	+	tss_1500	72036818
232	cg45866450_TC21	0.000814	0.051239	Higher	1700092C02Rik	8	+	tss_1500	77623962
233	cg45920043_BC21	0.000907	0.050103	Higher	Rfx1	8	+	tss_body	84094864
234	cg45947680_TC21	6.85E-05	0.079935	Higher					86757552
235	cg46018659_TC21	0.000191	0.075727	Higher	Gnao1	8	+	tss_body	93918034
236	cg46263698_TC21	7.66E-05	0.096962	Higher	Cotl1	8	-	tss_body	1.2E+08
237	cg46290197_TC21	1.17E-05	-0.12571	Lower	Gm26747	8	+	tss_200	1.21E+08

238	cg46321823_BC21	0.00015	-0.08214	Lower	Spire2	8	+	tss_body	1.23E+08
239	cg46344516_TC21	0.000854	0.061288	Higher	Egln1	8	-	tss_body	1.25E+08
240	cg46485446_BC21	2.71E-05	0.073875	Higher	Dnmt1	9	-	tss_body	20959347
241	cg46595673_BC21	0.000855	0.052802	Higher	Dcps	9	-	tss_body	35138305
242	cg46609822_TC21	0.000937	-0.06121	Lower	Tmem218	9	+	tss_body	37222434
243	cg47141551_TC21	0.000492	0.105221	Higher	chr9-98954990-98957445	9	*	SShelf	98960297
244	cg47142264_BC11	0.000791	0.05225	Higher	Gm1123	9	-	tss_body	99010600
245	cg47234603_BC21	0.000468	0.065872	Higher	Uba7	9	+	tss_body	1.08E+08
246	cg47317446_TC21	0.000255	0.095283	Higher	Tgfbr2	9	-	tss_body	1.16E+08
247	cg47391049_TC21	0.000547	0.056145	Higher	Ano10	9	-	tss_body	1.22E+08
X chromosome									
	CpG	***p* value**	**Effect size**	**Direction of change**	**Gene name**	**Chromosome number**	**Chromosome strand**	**Feature**	**CpG position**
1	cg47561448_BC21	0.000471	0.083607	Higher		X			37700518
2	cg47583639_BC21	0.000809	-0.09508	Lower	Stag2	X	+	tss_body	42183958
3	cg47588478_BC21	0.000442	-0.08778	Lower	Tenm1	X	-	tss_body	43167237
4	cg47604423_BC21	0.000293	-0.09246	Lower		X			47342322
5	cg47930516_BC21	0.000706	0.118774	Higher	Rps6ka6	X	-	tss_body	1.12E+08
6	cg48034703_TC21	0.000178	0.093435	Higher	Morf4l2	X	-	tss_body	1.37E+08
7	cg48037071_BC11	5.46E-05	0.100479	Higher	Fam199x	X	+	tss_body	1.37E+08
8	cg48106450_BC21	0.00038	0.084371	Higher	Gnl3l	X	-	tss_body	1.51E+08
9	cg48175315_BC21	0.000187	-0.06377	Lower	Rnf138rt1	X	-	tss_body	1.64E+08
10	cg48183380_TC21	0.000271	-0.08112	Lower	Fancb	X	+	tss_body	1.65E+08

Differences in DNA methylation were measured using linear regression contained within the LIMMA package in R. Differentially methylated sites were identified at p < 1e-3 and an effect size > 0.05. CpG = CpG ID on the Illumina mouse methylation microarray. *p* value = *p* value calculated following differential methylation analysis using LIMMA. Effect size = Difference in DNAm between groups. Direction of change - Direction of change in DNAm of CS groups relative to controls. Gene name = Gene name obtained from UCSC Genome Browser. Chromosome number = Chromosome containing the CpG as annotated by UCSC Genome Browser. Chromosome strand = Chromosomal strand on which CpG is located ('+' is the positive strand, '-' is the negative strand). Feature = Location of gene as annotated by the UCSC Genome Browser (tss_body = within gene body, tss_200 = 0-200 bases upstream of the transcription start site, tss_1500 = 200-1500 bases upstream of the transcription start site),

Sshelf = 2-4kb downstream (3') of the stop site of a CpG island. CpG position = Genomic location of CpG.

Appendix 4. 41: Enriched biological processes in lungs of offspring exposed to combined full and adulthood CS

ID	Description	P value	FDR	Gene ID	Gene count
GO:0048518	positive regulation of biological process	1.2E-09	4.28E-06	Plagl1/Aire/Csnk1g2/Eif4enif1/Myo1g/Ebf1/Rptor/Tcl1b1/Ntrk2/Tgm1/Fgf17/Dmtn/Fam83h/Sox10/Cacna1i/Aqp2/Atg101/Glis2/Muc20/Ildr1/Mapk8ip3/Zfp523/H2-Oa/Tnxb/C2/Crb3/Efna5/Mib1/Fgf1/Ndst1/Ovol1/Arl2/Syt7/Rbm20/Sh3bp4/Bcl2/Mir128-1/Il10/Syt2/Lgr6/Aim2/Prkcq/Ncs1/Fbn1/Sulf2/Gnas/Ntsr1/Trpc3/Npr1/Camk2d/Acer2/Sgip1/Khdrbs1/Ldlrap1/Arhgef10l/Rcc2/Gnai1/Ablim2/Limch1/Cit/Rfc5/Auts2/Lat2/Gimap5/Mgll/Magi1/Il17rc/Ghrl/Dyrk1b/Sox6/Tnrc6a/Fgfr1/Lpar2/Spire2/Egln1/Dnmt1/Dcps/Tgfbr2	78
GO:0048522	positive regulation of cellular process	5.7E-09	7.32E-06	Plagl1/Aire/Csnk1g2/Eif4enif1/Ebf1/Rptor/Tcl1b1/Ntrk2/Tgm1/Fgf17/Dmtn/Fam83h/Sox10/Cacna1i/Atg101/Glis2/Muc20/Ildr1/Mapk8ip3/Zfp523/H2-Oa/Tnxb/C2/Crb3/Efna5/Mib1/Fgf1/Ndst1/Ovol1/Arl2/Syt7/Rbm20/Sh3bp4/Bcl2/Mir128-1/Il10/Syt2/Lgr6/Prkcq/Ncs1/Fbn1/Sulf2/Gnas/Ntsr1/Trpc3/Npr1/Camk2d/Acer2/Khdrbs1/Ldlrap1/Arhgef10l/Rcc2/Gnai1/Ablim2/Limch1/Cit/Rfc5/Auts2/Gimap5/Magi1/Ghrl/Dyrk1b/Sox6/Tnrc6a/Fgfr1/Lpar2/Spire2/Egln1/Dnmt1/Dcps/Tgfbr2	71
GO:0051179	localization	6.15E-09	7.32E-06	Pla2g12b/Csnk1g2/Eif4enif1/Myo1g/Tmigd1/Rab5c/Adam11/Rptor/Ntrk2/Antxrl/Slc35f4/Dmtn/Dnah5/Fam83h/Cacna1i/Aqp2/Glis2/Abcc5/Ildr1/Synj2/Mapk8ip3/C2/Crb3/Efna5/Mib1/Arl2/Plcb3/Syt7/Abcc2/Sh3bp4/Bcl2/Syt2/Cadm3/Prkcq/Ncs1/Kcnh7/Fbn1/Gnas/Ntsr1/Cp/Dnajc19/Trpc3/Cttnbp2nl/Camk2d/Pakap/Sgip1/Khdrbs1/Ldlrap1/Rcc2/Rbp7/Sdf4/Gnai1/Mfsd10/Fras1/Lat2/Mest/Gimap5/Ghrl/Ppfia3/Sergef/Tnrc6a/Fgfr1/Gnao1/Spire2/Tgfbr2/Ano10	66
GO:0140352	export from cell	1.16E-07	0.000103	Myo1g/Rptor/Ntrk2/Dmtn/Cacna1i/Abcc5/Ildr1/Efna5/Syt7/Abcc2/Syt2/Prkcq/Ncs1/Fbn1/Gnas/Ntsr1/Sdf4/Lat2/Ghrl/Ppfia3/Sergef/Fgfr1/Gnao1	23
GO:0051234	establishment of localization	2.04E-07	0.000146	Pla2g12b/Csnk1g2/Eif4enif1/Myo1g/Rab5c/Adam11/Rptor/Ntrk2/Antxrl/Slc35f4/Dmtn/Dnah5/Cacna1i/Aqp2/Abcc5/Ildr1/Synj2/Mapk8ip3/C2/Efna5/Mib1/Arl2/Plcb3/Syt7/Abcc2/Sh3bp4/Bcl2/Syt2/Prkcq/Ncs1/Kcnh7/Fbn1/Gnas/Ntsr1/Cp/Dnajc19/Trpc3/Cttnbp2nl/Camk2d/Sgip1/Khdrbs1/Ldlrap1/Rcc2/Rbp7/Sdf4/Mfsd10/Fras1/Lat2/Gimap5/Ghrl/Ppfia3/Sergef/Fgfr1/Gnao1/Spire2/Tgfbr2/Ano10	57
GO:0006810	transport	3.64E-07	0.000216	Pla2g12b/Csnk1g2/Eif4enif1/Myo1g/Rab5c/Rptor/Ntrk2/Antxrl/Slc35f4/Dmtn/Dnah5/Cacna1i/Aqp2/Abcc5/Ildr1/Synj2/Mapk8ip3/C2/Efna5/Mib1/Arl2/Plcb3/Syt7/Abcc2/Sh3bp4/Bcl2/Syt2/Prkcq/Ncs1/Kcnh7/Fbn1/Gnas/Ntsr1/Cp/Dnajc19/Trpc3/Cttnbp2nl/Camk2d/Sgip1/Khdrbs1/Ldlrap1/Rbp7/Sdf4/Mfsd10/Fras1/Lat2/Gimap5/Ghrl/Ppfia3/Sergef/Fgfr1/Gnao1/Spire2/Tgfbr2/Ano10	55
GO:0046903	secretion	6.43E-07	0.000292	Pla2g12b/Myo1g/Rptor/Ntrk2/Dmtn/Cacna1i/Ildr1/Efna5/Syt7/Abcc2/Syt2/Prkcq/Ncs1/Fbn1/Gnas/Ntsr1/Sdf4/Lat2/Ghrl/Ppfia3/Sergef/Fgfr1/Gnao1	23
GO:0032940	secretion by cell	6.55E-07	0.000292	Myo1g/Rptor/Ntrk2/Dmtn/Cacna1i/Ildr1/Efna5/Syt7/Syt2/Prkcq/Ncs1/Fbn1/Gnas/Ntsr1/Sdf4/Lat2/Ghrl/Ppfia3/Sergef/Fgfr1/Gnao1	21
GO:0030036	actin cytoskeleton organization	8.89E-07	0.000353	Myo1g/Dmtn/Parvb/Aqp2/Efna5/Arhgap26/Bcl2/Prkcq/Pakap/Arhgef10l/Ablim2/Limch1/Cit/Auts2/Stard13/Ghrl/Cotl1/Spire2	18
GO:0030029	actin filament-based process	1E-06	0.000357	Myo1g/Dmtn/Parvb/Aqp2/Efna5/Arhgap26/Bcl2/Prkcq/Camk2d/Pakap/Arhgef10l/Ablim2/Limch1/Cit/Auts2/Stard13/Ghrl/Cotl1/Spire2	19
GO:0051641	cellular localization	1.57E-06	0.000508	Eif4enif1/Myo1g/Tmigd1/Rab5c/Adam11/Rptor/Ntrk2/Dmtn/Dnah5/Fam83h/Glis2/Ildr1/Synj2/Mapk8ip3/Crb3/Efna5/Arl2/Plcb3/Syt7/Sh3bp4/Bcl2/Syt2/Cadm3/Prkcq/Ncs1/Fbn1/Gnas/N	45

				tsr1/Dnajc19/Trpc3/Camk2d/Pakap/Khdrbs1/Ldlrap1/Rcc2/Gnai1/Fras1/Lat2/Gimap5/Ghrl/Ppfia3/Sergef/Tnrc6a/Gnao1/Spire2	
GO:0048856	anatomical structure development	2.56E-06	0.000762	Plagl1/Tspear/Aire/Ptprq/Eif4enif1/Ebf1/Tmigd1/Tdp2/Ntrk2/Tgm1/Fgf17/Dmtn/Dnah5/Fam83h/Sox10/Parvb/Aqp2/Krt80/Glis2/Muc4/Epha6/Brwd1/Synj2/Mapk8ip3/Zfp523/H2-Oa/Tnxb/Crb3/Efna5/Mib1/Fgf1/Ndst1/Ovol1/Rbm20/Bcl2/Il10/Syt2/Lgr6/Ncs1/Fbn1/Sulf2/Gnas/Dnajc19/Pglyrp4/Camk2d/Pakap/Kazn/Sdf4/Mpv17/Sgcb/Fras1/Cit/Auts2/Syna/Stard13/Zfp800/Gimap5/Mgll/Ghrl/Dyrk1b/Gys1/Sox6/Tnrc6a/Fgfr1/Egln1/Dnmt1/Tgfbr2	67
GO:0048513	animal organ development	2.91E-06	0.000798	Plagl1/Tspear/Aire/Ptprq/Ntrk2/Tgm1/Fgf17/Dnah5/Fam83h/Sox10/Aqp2/Krt80/Glis2/Synj2/Mapk8ip3/Efna5/Mib1/Fgf1/Ndst1/Ovol1/Rbm20/Bcl2/Il10/Fbn1/Sulf2/Gnas/Dnajc19/Camk2d/Kazn/Sdf4/Mpv17/Sgcb/Fras1/Syna/Zfp800/Ghrl/Dyrk1b/Gys1/Sox6/Fgfr1/Egln1/Tgfbr2	42
GO:0031323	regulation of cellular metabolic process	3.17E-06	0.000807	Plagl1/Aire/Ptprq/Eif4enif1/Ebf1/Tmigd1/Rptor/Tcl1b1/Ntrk2/Fgf17/Dmtn/Chrac1/Sox10/Atg101/Cbx5/Glis2/Ildr1/Brwd1/Mapk8ip3/Zfp523/Tnxb/Efna5/Fgf1/Ppp6r3/Ovol1/Arl2/Rbm20/Sh3bp4/Bcl2/Il10/Aim2/Prkcq/Noxa1/Fbn1/Gnas/Ntsr1/Dnajc19/Ciart/Camk2d/Acer2/Khdrbs1/Mpv17/Ablim2/Limch1/Rfc5/Auts2/Zkscan1/Gimap5/Zfp579/Dyrk1b/Sox6/Tnrc6a/Fgfr1/Rfx1/Spire2/Egln1/Dnmt1/Dcps/Tgfbr2	59
GO:0032502	developmental process	6.69E-06	0.001592	Plagl1/Tspear/Aire/Ptprq/Eif4enif1/Ebf1/Tmigd1/Tdp2/Ntrk2/Tgm1/Fgf17/Dmtn/Dnah5/Fam83h/Sox10/Parvb/Aqp2/Krt80/Glis2/Muc4/Epha6/Brwd1/Synj2/Mapk8ip3/Zfp523/H2-Oa/Tnxb/Crb3/Efna5/Mib1/Fgf1/Ndst1/Ovol1/Rbm20/Bcl2/Il10/Syt2/Lgr6/Ncs1/Fbn1/Sulf2/Gnas/Dnajc19/Pglyrp4/Camk2d/Pakap/Sgip1/Kazn/Sdf4/Mpv17/Sgcb/Fras1/Cit/Auts2/Syna/Stard13/Zfp800/Gimap5/Mgll/Ghrl/Dyrk1b/Gys1/Sox6/Tnrc6a/Fgfr1/Gnao1/Egln1/Dnmt1/Tgfbr2	69
GO:0032879	regulation of localization	9.03E-06	0.002011	Rab5c/Rptor/Ntrk2/Dmtn/Cacna1i/Aqp2/Glis2/Ildr1/C2/Efna5/Mib1/Plcb3/Syt7/Bcl2/Syt2/Prkcq/Ncs1/Kcnh7/Fbn1/Gnas/Ntsr1/Trpc3/Cttnbp2nl/Camk2d/Khdrbs1/Ldlrap1/Gnai1/Mest/Gimap5/Ghrl/Sergef/Fgfr1/Gnao1	33
GO:1903530	regulation of secretion by cell	9.58E-06	0.002011	Rptor/Ntrk2/Cacna1i/Ildr1/Efna5/Syt7/Syt2/Prkcq/Ncs1/Fbn1/Gnas/Ntsr1/Ghrl/Sergef/Fgfr1/Gnao1	16
GO:0033036	macromolecule localization	1.07E-05	0.002118	Pla2g12b/Eif4enif1/Tmigd1/Rab5c/Adam11/Rptor/Dmtn/Fam83h/Glis2/Ildr1/Mapk8ip3/Crb3/Efna5/Arl2/Syt7/Abcc2/Sh3bp4/Bcl2/Cadm3/Prkcq/Fbn1/Gnas/Ntsr1/Dnajc19/Camk2d/Pakap/Khdrbs1/Ldlrap1/Rcc2/Rbp7/Gnai1/Fras1/Mest/Ghrl/Sergef/Tnrc6a/Gnao1/Spire2/Tgfbr2	39
GO:0023051	regulation of signaling	1.22E-05	0.00225	Tspear/Csnk1g2/Rptor/Ntrk2/Dmtn/Sox10/Glis2/Muc4/Muc20/Ildr1/Mapk8ip3/Efna5/Fbxl17/Arhgap26/Fgf1/Ndst1/Syt7/Amer3/Sh3bp4/Bcl2/Mir128-1/Il10/Lgr6/Prkcq/Ncs1/Ralgps1/Fbn1/Sulf2/Gnas/Ntsr1/Npr1/Camk2d/Gnai1/Cit/Auts2/Stard13/Mgll/Ghrl/Ppfia3/Fgfr1/Lpar2/Gnao1/Egln1/Tgfbr2	44
GO:0010646	regulation of cell communication	1.26E-05	0.00225	Tspear/Csnk1g2/Rptor/Ntrk2/Dmtn/Sox10/Glis2/Muc4/Muc20/Ildr1/Mapk8ip3/Efna5/Fbxl17/Arhgap26/Fgf1/Ndst1/Syt7/Amer3/Sh3bp4/Bcl2/Mir128-1/Il10/Lgr6/Prkcq/Ncs1/Ralgps1/Fbn1/Sulf2/Gnas/Ntsr1/Npr1/Camk2d/Gnai1/Cit/Auts2/Stard13/Mgll/Ghrl/Ppfia3/Fgfr1/Lpar2/Gnao1/Egln1/Tgfbr2	44

Gene ontology was performed using the ClusterProfiler package in R. Altered biological processes/pathways were identified at FDR < 0.05. ID = Gene Ontology identification. Description = affected biological process/pathway. Gene ID = Genes involved in the altered biological process. Gene count = number of genes involved in the biological process

Appendix 4. 42: CpGs which asre differentially methylated by singular CS exposure in adulthood

Autosomes									
	CpG	*p* value	Effect size	Direction of change	Gene name	Chromosome number	Chromosome strand	Feature	CpG position
1	cg05728921_TC21	0.000457	-0.05704	Lower	Zfp407	18	-	tss_body	84547811
2	cg29058556_TC21	0.000596	-0.05068	Lower	Cand1	10	-	tss_body	1.19E+08
3	cg29578053_BC21	0.000479	-0.07131	Lower	Gria1	11	+	tss_body	57309098
4	cg30187073_TC21	0.000138	-0.05094	Lower	Slc39a11	11	-	tss_body	1.14E+08
5	cg30203816_TC11	0.000465	-0.05024	Lower	Gprc5c	11	+	tss_body	1.15E+08
6	cg30261794_BC21	0.000258	-0.06558	Lower	Rbfox3	11	-	tss_body	1.19E+08
7	cg30909951_TC21	0.000413	0.067973	Higher	Gm38543	12	+	tss_body	85456406
8	cg31516736_TC21	0.000449	-0.05491	Lower	Gm33958	13	-	tss_body	44399969
9	cg31702693_TC21	0.000687	0.054059	Higher	Tpbpb	13	-	tss_body	60902188
10	cg32119025_TC21	0.00073	-0.05585	Lower					1.16E+08
11	cg32204502_BC21	0.000163	-0.0524	Lower	A0A0U1RQ01	14	+	tss_body	14401392
12	cg33607144_BC21	0.000232	0.094048	Higher	Mpped1	15	+	tss_body	83837934
13	cg33655237_BC21	3.97E-05	0.054077	Higher	Gm35599	15	+	tss_body	87831652
14	cg33839465_TC21	0.000583	0.05742	Higher	Hoxc9	15	+	tss_body	1.03E+08
15	cg34630874_BC21	9.55E-05	-0.06204	Lower	1700110C19Rik	17	+	tss_200	10324583
16	cg34770321_TC21	0.000779	0.06363	Higher					27176650
17	cg34909837_BC11	0.000294	0.061712	Higher		17	+	tss_body	39844389
18	cg35726494_BC11	0.000644	0.055557	Higher					53161116
19	cg35995116_BC11	0.000181	0.067929	Higher		18	+	tss_body	81083362
20	cg37174803_BC21	0.000545	-0.06333	Lower					86059011
21	cg37471841_TC21	0.000798	0.05553	Higher	Nfasc	1	-	tss_body	1.33E+08
22	cg38255705_BC21	0.000297	0.059975	Higher	Ralgps1	2	-	tss_body	33265937

23	cg38840026_TC21	0.00062	-0.05923	Lower					1.17E+08
24	cg39425367_BC21	0.000404	0.053765	Higher	Ntsr1	2	+	tss_body	1.81E+08
25	cg40198583_TC21	0.000381	0.05489	Higher		3	+	tss_200	1.13E+08
26	cg40525493_BC21	0.000665	-0.05237	Lower	Slc44a5	3	+	tss_body	1.54E+08
27	cg41621454_TC21	0.000922	0.056635	Higher	Crocc	4	-	tss_body	1.41E+08
28	cg41705774_BC21	0.0006	0.098751	Higher	Pik3cd	4	-	tss_body	1.5E+08
29	cg41957876_TC21	0.000432	0.050341	Higher	Dpp6	5	+	tss_body	27261856
30	cg43708741_BC11	0.000436	-0.06089	Lower	Gm30688	6	+	tss_body	92269558
31	cg44998063_BC21	9.31E-05	-0.0783	Lower	Mical2	7	+	tss_1500	1.12E+08
32	cg45106295_BC21	0.000888	-0.05351	Lower					1.25E+08
33	cg45679400_TC21	0.000876	-0.0574	Lower	Tenm3	8	-	tss_body	48413553
34	cg45804125_BC21	0.000212	0.058935	Higher	Ndufa13	8	-	tss_body	69902357
35	cg45933778_BC21	0.000189	0.076232	Higher	Best2	8	-	tss_body	85011262
36	cg46018659_TC21	6.36E-05	-0.06324	Lower	Gnao1	8	+	tss_body	93918034
37	cg46148493_BC21	0.000406	0.058916	Higher	Pkd1l3	8	+	tss_body	1.1E+08
38	cg46510712_BC21	7.58E-05	-0.05628	Lower					22954760
39	cg46521764_BC21	0.000887	-0.0718	Lower	Tbx20	9	-	tss_body	24769664
40	cg47374018_BC21	0.00065	0.059192	Higher					1.21E+08
X chromosome									
	CpG	***p* value**	**Effect size**	**Direction of change**	**Gene name**	**Chromosome number**	**Chromosome strand**	**Feature**	**CpG position**
1	cg47447070_BC11	5.81E-05	0.079772	Higher	Rpgr	X	-	tss_1500	10216908
2	cg47452975_TC21	0.000226	-0.05702	Lower		X			11172046
3	cg47562473_TC21	0.000451	-0.08029	Lower		X			37908803
4	cg47622160_TC21	0.000835	-0.07706	Lower		X			50196036
5	cg47856464_TC21	0.000849	0.058847	Higher		X			98999308

6	cg47874392_BC11	0.000624	0.058408	Higher	Gjb1	X	+	tss_body	1.01E+08
7	cg47913719_BC21	0.000889	-0.05027	Lower		X			1.07E+08
8	cg47913830_TC21	0.000861	0.06396	Higher	Itm2a	X	-	tss_1500	1.07E+08
9	cg48050898_BC21	0.000345	-0.0669	Lower		X			1.4E+08
10	cg48072262_BC21	0.000699	0.07584	Higher	Rgag1	X	+	tss_body	1.43E+08
11	cg48091033_TC21	0.000685	0.0542	Higher	Htr2c	X	+	tss_body	1.47E+08

Differences in DNA methylation were measured using linear regression contained within the LIMMA package in R. Differentially methylated sites were identified at p < 1e-3 and an effect size > 0.05. CpG = CpG ID on the Illumina mouse methylation microarray. *p* value = *p* value calculated following differential methylation analysis using LIMMA. Effect size = Difference in DNAm between groups. Direction of change - Direction of change in DNAm of CS groups relative to controls. Gene name = Gene name obtained from UCSC Genome Browser. Chromosome number = Chromosome containing the CpG as annotated by UCSC Genome Browser. Chromosome strand = Chromosomal strand on which CpG is located ('+' is the positive strand, '-' is the negative strand). Feature = Location of gene as annotated by the UCSC Genome Browser (tss_body = within gene body, tss_200 = 0-200 bases upstream of the transcription start site, tss_1500 = 200-1500 bases upstream of the transcription start site), Sshelf = 2-4kb downstream (3') of the stop site of a CpG island. CpG position = Genomic location of CpG.

Appendix 4. 43: Enriched biological processes in lungs of offspring with singular CS exposure in adulthood

ID	Description	P value	FDR	Gene ID	Gene count
GO:1902495	transmembrane transporter complex	2.45E-05	0.002834	Gria1/Dpp6/Ndufa13/Best2/Pkd1l3	5
GO:1990351	transporter complex	3.22E-05	0.002834	Gria1/Dpp6/Ndufa13/Best2/Pkd1l3	5
GO:0098796	membrane protein complex	8.73E-05	0.00512	Gria1/Pik3cd/Dpp6/Ndufa13/Best2/Gnao1/Pkd1l3	7
GO:0034702	ion channel complex	0.00015	0.006603	Gria1/Dpp6/Best2/Pkd1l3	4
GO:0036477	somatodendritic compartment	0.000369	0.013003	Gria1/Rbfox3/Nfasc/Ntsr1/Dpp6/Gnao1	6
GO:0005886	plasma membrane	0.000515	0.01511	Gria1/Slc39a11/Gprc5c/Nfasc/Ralgps1/Ntsr1/Crocc/Pik3cd/Dpp6/Tenm3/Best2/Gnao1/Pkd1l3	13
GO:0044297	cell body	0.000928	0.023322	Gria1/Rbfox3/Ntsr1/Dpp6/Gnao1	5
GO:0071944	cell periphery	0.001195	0.02629	Gria1/Slc39a11/Gprc5c/Nfasc/Ralgps1/Ntsr1/Crocc/Pik3cd/Dpp6/Tenm3/Best2/Gnao1/Pkd1l3	13
GO:0043198	dendritic shaft	0.001902	0.037196	Gria1/Ntsr1	2
GO:0032991	protein-containing complex	0.002675	0.039986	Cand1/Gria1/Cog1/Gprc5c/Hoxc9/Pik3cd/Dpp6/Ndufa13/Tssk6/Best2/Gnao1/Pkd1l3	12
GO:0097454	Schwann cell microvillus	0.002726	0.039986	Nfasc	1
GO:0120219	subapical part of cell	0.002726	0.039986	Crocc	1
GO:0044308	axonal spine	0.003634	0.045678	Gria1	1
GO:0099544	perisynaptic space	0.003634	0.045678	Gria1	1
GO:0030425	dendrite	0.004502	0.048427	Gria1/Nfasc/Ntsr1/Gnao1	4
GO:0097447	dendritic tree	0.004565	0.048427	Gria1/Nfasc/Ntsr1/Gnao1	4
GO:0043025	neuronal cell body	0.004717	0.048427	Gria1/Rbfox3/Ntsr1/Dpp6	4
GO:0120025	plasma membrane bounded cell projection	0.004953	0.048427	Gria1/Nfasc/Ntsr1/Crocc/Tenm3/Best2/Gnao1	7

Gene ontology was performed using the ClusterProfiler package in R. Altered biological processes/pathways were identified at FDR < 0.05. ID = Gene Ontology identification. Description = affected biological process/pathway. Gene ID = Genes involved in the altered biological process. Gene count = number of genes involved in the biological process

Appendix 4. 44: CpGs which are differentially methylated in CS-reexposed versus non reexposed offspring exposed to early life full CS

Autosomes									
	CpG	***p* value**	**Effect size**	**Direction of change**	**Gene name**	**Chromosome number**	**Chromosome strand**	**Feature**	**CpG position**
1	cg12044283_TC21	0.00074	0.053217	Higher	Gm28578	19	-	tss_body	45330028
2	cg28225609_BC11	0.00047	-0.12237	Lower	Nhsl1	10	+	tss_body	18505692
3	cg28375833_BC21	0.00052	0.054179	Higher	chr10-40257439-40257793	10	*	SShelf	40260762
4	cg28558004_TC11	5.28E-05	0.058905	Higher	Q9R022	10	+	tss_body	63410442
5	cg28580996_BC21	9.28E-05	-0.07966	Lower	Reep3	10	-	tss_body	67046323
6	cg28725096_TC21	0.00043	-0.07574	Lower	Csnk1g2	10	+	tss_body	80638507
7	cg28734564_TC21	0.00068	0.066076	Higher	Pias4	10	-	tss_body	81154361
8	cg28769563_TC21	6.62E-05	0.065379	Higher					84339534
9	cg28772191_TC21	0.00059	-0.09073	Lower					84545100
10	cg28851119_BC11	0.00095	-0.0631	Lower					93418312
11	cg28880711_BC21	3.65E-05	0.058745	Higher	Gm33377	10	+	tss_body	95893328
12	cg28953917_BC21	0.00089	-0.06215	Lower	Gm36177	10	+	tss_body	1.08E+08
13	cg29138616_BC21	7.85E-05	-0.08823	Lower	chr10-126928336-126928636	10	*	NShelf	1.27E+08
14	cg29141909_TC11	9.35E-05	0.06156	Higher	Agap2	10	+	tss_body	1.27E+08
15	cg29147983_BC11	0.00029	0.0662	Higher	R3hdm2	10	+	tss_body	1.27E+08
16	cg29162681_BC21	0.00078	-0.07103	Lower	Esyt1	10	-	tss_body	1.29E+08
17	cg29216175_BC21	7.17E-05	0.054509	Higher	Myo1g	11	-	tss_body	6519449
18	cg29330004_TC21	0.00014 7	0.052466	Higher	Gm33232	11	-	tss_body	24075516
19	cg29365155_TC21	0.00043 5	-0.06176	Lower	Acyp2	11	-	tss_body	30649224
20	cg29391470_BC11	0.00051 5	-0.09171	Lower	Kcnip1	11	-	tss_body	33680456

21	cg29428350_BC11	0.000608	-0.12299	Lower					38120928
22	cg29455032_TC21	0.000129	0.061671	Higher					43388351
23	cg29465728_TC21	0.00086	-0.06803	Lower	Rnf145	11	+	tss_body	44551146
24	cg29530514_TC21	0.00048	-0.06667	Lower	Cdkl3	11	+	tss_body	52037298
25	cg29533556_TC21	0.000171	0.056175	Higher	Gm30217	11	+	tss_body	52318578
26	cg29560554_BC21	2.38E-06	0.052298	Higher	Tnip1	11	-	tss_1500	54963338
27	cg29567845_BC21	0.000623	-0.05319	Lower					55638539
28	cg29582848_TC21	8.65E-05	-0.07631	Lower	Galnt10	11	+	tss_body	57751164
29	cg29715182_BC21	5.77E-05	0.052554	Higher	Dlg4	11	+	tss_body	70029670
30	cg29744357_BC21	0.000608	-0.071	Lower	Gm34793	11	+	tss_body	72948049
31	cg29745520_TC21	8.77E-05	-0.07995	Lower	Camkk1	11	+	tss_body	73037251
32	cg29754373_TC21	0.00083	0.088094	Higher	Rap1gap2	11	-	tss_body	74465852
33	cg29819925_TC21	0.000321	0.056275	Higher					80146260
34	cg29861614_BC21	0.000382	0.05506	Higher	Lhx1	11	-	tss_body	84522122
35	cg29885592_BC21	0.000711	-0.05032	Lower					86899323
36	cg29885767_BC21	0.000943	-0.08701	Lower					86916550
37	cg29902227_TC21	0.000273	-0.09782	Lower					88304294
38	cg29995278_BC21	0.000339	-0.0938	Lower	Arhgap23	11	+	tss_body	97450313
39	cg30025969_BC21	0.000209	-0.0536	Lower	Krt23	11	-	tss_body	99481015
40	cg30039252_BC21	0.000409	0.050238	Higher	Rab5c	11	-	tss_body	1.01E+08
41	cg30069156_BC21	0.000294	0.076959	Higher	Adam11	11	+	tss_body	1.03E+08
42	cg30092657_TC21	0.000367	-0.09791	Lower	Myl4	11	+	tss_body	1.05E+08
43	cg30116743_TC11	0.000789	-0.08873	Lower					1.07E+08
44	cg30175990_BC21	9.74E-05	-0.10055	Lower	LOC108167938	11	+	tss_body	1.13E+08
45	cg30237306_BC21	0.000859	0.059629	Higher	Mgat5b	11	+	tss_body	1.17E+08

46	cg30243594_TC21	0.000121	0.053517	Higher	Sept9	11	+	tss_body	1.17E+08
47	cg30252131_BC21	0.000156	0.056362	Higher	chr11-117963365-117963770	11	*	NShore	1.18E+08
48	cg30284429_TC21	0.000845	-0.05312	Lower	Enthd2	11	-	tss_body	1.2E+08
49	cg30353768_BC21	0.000719	0.061311	Higher					8847099
50	cg30374005_TC21	8.8E-05	-0.07118	Lower					12222990
51	cg31013061_TC21	4.58E-05	0.064298	Higher					99956655
52	cg31064631_TC21	0.00012	-0.09584	Lower	Tcl1b1	12	+	tss_body	1.05E+08
53	cg31073704_TC21	0.000129	-0.06034	Lower	chr12-105862675-105862932	12	*	SShore	1.06E+08
54	cg31145492_TC21	0.000722	0.059021	Higher	Exoc3l4	12	+	tss_body	1.11E+08
55	cg31330291_TC21	0.000435	-0.13822	Lower	Zscan12	13	+	tss_body	21363562
56	cg31330891_BC21	0.000755	-0.05734	Lower	Pgbd1	13	-	tss_body	21439968
57	cg31405776_BC11	0.000421	-0.06133	Lower	Foxf2	13	+	tss_body	31629426
58	cg31468771_BC21	6.92E-05	-0.06213	Lower		13	+	tss_body	39650886
59	cg31493586_TC21	0.00086	0.065565	Higher					42258934
60	cg31569360_BC21	0.000557	0.080983	Higher					49200716
61	cg31592452_BC21	0.000107	0.10043	Higher					51866628
62	cg31679540_TC21	0.000402	-0.06184	Lower	Ntrk2	13	+	tss_body	58808553
63	cg31702693_TC21	0.000545	-0.06091	Lower	Tpbpb	13	-	tss_body	60902188
64	cg31705777_BC21	0.000249	-0.1066	Lower	Cts3	13	-	tss_body	61565301
65	cg31796133_BC21	0.000514	-0.0717	Lower	Slc6a3	13	+	tss_body	73577078
66	cg31842090_BC21	0.000284	-0.06062	Lower	Adgrv1	13	-	tss_body	81633285
67	cg31879636_BC21	7.51E-06	-0.14025	Lower					89427902

68	cg31948263_TC21	2.56E-06	0.095406	Higher					97275560
69	cg31963009_BC21	9.67E-05	0.058081	Higher	Gm41033	13	-	tss_body	98560070
70	cg31970024_BC21	0.00068	0.078853	Higher	Zfp366	13	+	tss_body	99196416
71	cg32013379_TC11	9.44E-05	0.062553	Higher	Nln	13	-	tss_body	1.04E+08
72	cg32079551_BC21	0.000659	0.0534	Higher					1.12E+08
73	cg32281862_TC21	5.33E-05	0.092589	Higher	Zmiz1os1	14	-	tss_body	25273047
74	cg32282839_TC21	0.000411	-0.08015	Lower	Zmiz1os1	14	-	tss_body	25377298
75	cg32363423_TC21	0.000178	-0.05111	Lower	A630023A22Rik	14	-	tss_body	34052702
76	cg32382747_BC21	0.000851	-0.06009	Lower	Ccser2	14	-	tss_body	36917221
77	cg32401710_TC21	9.19E-05	-0.13095	Lower	Tspan14	14	-	tss_body	40906740
78	cg32462514_BC21	2.75E-05	-0.09821	Lower	Slc35f4	14	-	tss_body	49525558
79	cg32561669_BC21	0.000912	-0.09509	Lower	Gm41168	14	+	tss_body	61068956
80	cg32580235_TC21	0.000252	0.062406	Higher	Ctsb	14	+	tss_body	63131363
81	cg32584189_TC21	7.43E-05	-0.05179	Lower	Fam167a	14	+	tss_body	63456217
82	cg32612591_BC21	0.000367	-0.0862	Lower	Gm41183	14	-	tss_body	66341095
83	cg32617501_BC21	0.000676	-0.06018	Lower	Dpysl2	14	-	tss_body	66870881
84	cg33101971_BC21	0.000213	-0.06606	Lower					14274977
85	cg33224786_BC21	0.000541	-0.08165	Lower	Pop1	15	+	tss_body	34496869
86	cg33244981_BC21	0.000565	-0.07382	Lower					36991473
87	cg33353666_BC21	0.000142	0.065457	Higher	Deptor	15	+	tss_body	55121109
88	cg33491564_TC21	0.000661	-0.05943	Lower	Gml2	15	+	tss_body	74841637
89	cg33501423_TC21	0.000434	-0.05335	Lower	Pycrl	15	-	tss_body	75916745
90	cg33549590_TC21	0.000674	0.060078	Higher	Pla2g6	15	-	tss_body	79305978
91	cg33566048_BC21	0.00038	-0.06339	Lower	Cacna1i	15	+	tss_body	80372556

92	cg33569910_TC21	0.000408	0.058946	Higher	Fam83f	15	+	tss_body	80681078
93	cg33572379_TC21	4.32E-05	-0.07323	Lower	Adsl	15	+	tss_body	80952399
94	cg33612698_TC21	2.87E-05	0.062409	Higher	Parvb	15	+	tss_body	84237318
95	cg33623252_BC21	0.000347	-0.07527	Lower	Upk3a	15	+	tss_1500	85016868
96	cg33641493_TC21	0.00039	0.05937	Higher	Tbc1d22a	15	+	tss_body	86363746
97	cg33747779_BC11	0.00088	-0.07193	Lower	Slc38a1	15	-	tss_body	96583922
98	cg33783789_BC21	0.000343	-0.07929	Lower	4930578M01Rik	15	+	tss_body	98987218
99	cg33793380_BC21	0.00074	0.056457	Higher	Gm34765	15	-	tss_body	99579000
100	cg33872882_BC21	0.000442	-0.0562	Lower	Rbfox1	16	+	tss_body	6084064
101	cg33912019_TC21	0.000811	-0.07071	Lower		16	+	tss_body	11186057
102	cg33992356_TC21	0.000651	-0.06277	Lower					21362811
103	cg34091286_BC21	0.000508	-0.0806	Lower	Muc4	16	+	tss_body	32778966
104	cg34284589_TC21	0.000659	0.055649	Higher	Epha6	16	-	tss_body	59688596
105	cg34285702_TC21	0.000431	0.068438	Higher	Epha6	16	-	tss_body	59872493
106	cg34480775_TC21	0.000568	-0.08955	Lower	Synj1	16	-	tss_body	90955569
107	cg34588755_BC21	0.000529	0.088787	Higher	Synj2	17	+	tss_body	5975757
108	cg34589015_BC21	0.000401	-0.07796	Lower	Synj2	17	+	tss_body	5996879
109	cg34691367_BC11	0.000998	-0.07265	Lower	Has1	17	-	tss_body	17844249
110	cg34720628_TC21	0.000873	0.051954	Higher	Zscan10	17	+	tss_body	23610613
111	cg34864454_BC21	5.04E-05	-0.06817	Lower	BC051142	17	+	tss_body	34417490
112	cg34870820_BC21	1.86E-05	-0.14999	Lower	C2	17	-	tss_body	34873636
113	cg34883379_TC21	0.00023	-0.06639	Lower	Ddr1	17	-	tss_body	35686453
114	cg34972159_BC21	0.000612	0.059191	Higher	Gltscr1l	17	-	tss_body	46832307
115	cg34988365_TC21	0.000722	0.0684	Higher	Foxp4	17	-	tss_body	47909606

116	cg35064640_TC21	0.000155	-0.05988	Lower	Crb3	17	+	tss_body	57065285
117	cg35257568_BC21	0.000521	-0.05915	Lower	Map4k3	17	-	tss_body	80601635
118	cg35322276_TC21	0.000671	-0.06775	Lower	Epas1	17	+	tss_body	86805290
119	cg35424955_BC21	8.66E-05	-0.0625	Lower	Mib1	18	+	tss_body	10799847
120	cg35523982_BC21	0.000239	-0.05615	Lower	Celf4	18	-	tss_body	25477667
121	cg35615203_BC11	0.000331	0.058668	Higher	Gm37013	18	+	tss_body	37694353
122	cg35680259_TC21	9.47E-05	-0.05942	Lower	Pggt1b	18	-	tss_body	46264293
123	cg35744979_BC21	0.0008	0.061962	Higher	Gm4221	18	+	tss_body	55096324
124	cg35793003_BC21	0.00032	0.073617	Higher	Camk2a	18	+	tss_body	60951583
125	cg35900296_TC21	0.000316	0.062965	Higher	Dcc	18	-	tss_body	71987206
126	cg35993364_BC11	0.000883	-0.08075	Lower	Sall3	18	-	tss_body	80972081
127	cg36030890_BC21	0.000511	-0.06769	Lower	Zfp407	18	-	tss_body	84264730
128	cg36094169_BC21	6.45E-06	-0.06497	Lower	Ovol1	19	-	tss_body	5553567
129	cg36104434_TC21	0.000146	0.052433	Higher	Arl2	19	-	tss_body	6137295
130	cg36146503_BC21	1.06E-05	-0.0773	Lower	Syt7	19	+	tss_body	10395481
131	cg36169598_BC21	0.000261	-0.07575	Lower	Olfr1497	19	-	tss_body	13795323
132	cg36177247_BC21	0.000387	-0.09991	Lower					15034518
133	cg36207359_BC21	0.000593	-0.07771	Lower	Rorb	19	-	tss_body	18969670
134	cg36307476_BC21	0.000352	-0.13791	Lower	Ppp1r2-ps3	19	-	tss_1500	30539926
135	cg36315616_TC21	0.000577	-0.07457	Lower	Prkg1	19	-	tss_body	31751469
136	cg36425561_BC21	0.000427	-0.11528	Lower	Dnmbp	19	-	tss_body	43883432
137	cg36788230_TC21	0.000513	0.050128	Higher	Gm32566	1	+	tss_body	34485953
138	cg36800056_BC21	0.000567	-0.07779	Lower	Gm33176	1	+	tss_1500	35941711

139	cg36855466_BC21	9.79E-05	-0.06314	Lower					40887876
140	cg36916593_TC21	0.000284	-0.09643	Lower	Gm31636	1	+	tss_body	51624301
141	cg37021053_TC21	0.000136	0.06935	Higher	Crygd	1	-	tss_body	65062866
142	cg37156032_BC21	0.000679	0.055781	Higher	Daw1	1	+	tss_body	83178087
143	cg37203575_TC21	1.31E-05	0.050655	Higher	Sh3bp4	1	+	tss_body	89105134
144	cg37214137_TC21	7.41E-06	0.061753	Higher	chr1-89941589-89942209	1	*	SShore	89942649
145	cg37235414_BC11	2.26E-05	0.060193	Higher					91872566
146	cg37247426_TC21	0.000163	-0.06064	Lower	Kif1a	1	-	tss_body	93096684
147	cg37372197_BC21	0.000836	0.053231	Higher	Gli2	1	-	tss_body	1.19E+08
148	cg37429392_BC21	0.000277	-0.08837	Lower	Mgat5	1	+	tss_body	1.27E+08
149	cg37434191_BC21	0.000361	-0.07301	Lower	Zranb3	1	-	tss_body	1.28E+08
150	cg37453889_BC11	6.88E-05	0.070785	Higher	Il10	1	+	tss_1500	1.31E+08
151	cg37496044_TC21	0.000281	-0.1285	Lower	Syt2	1	+	tss_body	1.35E+08
152	cg37746552_BC21	8.01E-05	-0.05393	Lower	Pbx1	1	-	tss_body	1.68E+08
153	cg37776649_TC21	0.000902	-0.05494	Lower	Usf1	1	+	tss_body	1.71E+08
154	cg37794339_TC21	7.61E-07	-0.06712	Lower	Aim2	1	+	tss_body	1.73E+08
155	cg37798284_TC21	0.000451	-0.06047	Lower	E9Q4G0	1	+	tss_body	1.74E+08
156	cg38015282_TC21	0.000338	-0.111	Lower	Ccdc3	2	+	tss_body	5161335
157	cg38018781_BC21	0.000116	0.064672	Higher	Camk1d	2	-	tss_body	5579737
158	cg38109999_TC21	0.000488	-0.08244	Lower	Carlr	2	-	tss_body	18801775
159	cg38150914_TC21	0.000658	-0.08344	Lower	Noxa1	2	-	tss_body	25094949
160	cg38235497_TC21	0.000332	-0.07087	Lower					31857332
161	cg38247031_BC11	0.000423	0.060935	Higher	Ak1	2	+	tss_body	32625480

162	cg38337226_BC11	0.000991	-0.07413	Lower	Zeb2	2	-	tss_body	45061857
163	cg38342166_BC21	0.000231	-0.08307	Lower					45776949
164	cg38703337_TC11	0.000491	-0.0625	Lower					94289854
165	cg39076276_BC21	0.000388	-0.05993	Lower					1.47E+08
166	cg39206102_BC21	0.000532	-0.06064	Lower					1.61E+08
167	cg39229622_TC21	0.000503	0.05494	Higher	Tox2	2	+	tss_body	1.63E+08
168	cg39252633_TC21	0.000745	0.063388	Higher	Mmp9	2	+	tss_body	1.65E+08
169	cg39265697_TC11	0.000354	0.114654	Higher					1.66E+08
170	cg39271092_TC11	0.000124	0.061912	Higher	Sulf2	2	-	tss_body	1.66E+08
171	cg39370558_BC21	0.00041	-0.07462	Lower					1.73E+08
172	cg39382173_TC21	8.18E-06	0.087552	Higher	Nespas	2	-	tss_body	1.74E+08
173	cg39383113_TC21	0.000978	0.070355	Higher	Gnas	2	+	tss_body	1.74E+08
174	cg39400795_BC21	0.000155	-0.08497	Lower	Ppp1r3d	2	-	tss_body	1.78E+08
175	cg39563667_TC21	1.77E-05	-0.0739	Lower	Nlgn1	3	-	tss_body	25730895
176	cg39597063_TC11	0.000686	0.056167	Higher	Mecom	3	-	tss_body	30246250
177	cg39628672_BC11	7.32E-06	-0.11147	Lower	Dnajc19	3	-	tss_body	34079114
178	cg39628672_BO21	0.000678	-0.0978	Lower	Dnajc19	3	-	tss_body	34079114
179	cg39644709_TC21	0.000326	-0.06581	Lower					35885787
180	cg39973310_BC21	0.000105	0.053726	Higher	Lrba	3	+	tss_body	86547076
181	cg39983155_TC21	0.000505	-0.07526	Lower	Arhgef11	3	+	tss_body	87618751
182	cg40017193_TC21	0.000678	-0.05368	Lower	Jtb	3	+	tss_body	90235387
183	cg40019657_BC11	0.000292	-0.0625	Lower	Npr1	3	-	tss_body	90455888
184	cg40022036_TC21	7.15E-05	0.057244	Higher	Pglyrp4	3	+	tss_1500	90726704
185	cg40049844_BC21	0.000345	0.060901	Higher	Bnipl	3	-	tss_body	95250855
186	cg40143403_TC21	0.000174	0.065968	Higher	Cttnbp2nl	3	-	tss_body	1.05E+08

187	cg40189694_TC21	0.00042	-0.07986	Lower					1.11E+08
188	cg40211529_BC11	0.000271	0.075684	Higher					1.16E+08
189	cg40734187_BC21	0.000199	-0.13001	Lower	Ankrd6	4	-	tss_body	32923483
190	cg40932533_TC21	0.00026	-0.07848	Lower	Palm2	4	+	tss_body	57688464
191	cg41492003_BC11	0.000189	-0.08686	Lower	Rab42	4	-	tss_body	1.32E+08
192	cg41526874_BC21	9.74E-05	-0.11916	Lower	Man1c1	4	-	tss_body	1.35E+08
193	cg41603187_BC11	0.000181	0.065421	Higher	LOC108168982	4	+	tss_body	1.4E+08
194	cg41611078_TC21	0.000222	-0.06589	Lower	LOC102637278	4	+	tss_body	1.4E+08
195	cg41614986_BC11	8.28E-05	-0.12997	Lower	Arhgef10l	4	-	tss_body	1.41E+08
196	cg41616312_TC21	0.000148	0.050359	Higher	Rcc2	4	+	tss_body	1.41E+08
197	cg41702601_TC21	6.45E-05	-0.05811	Lower	Nmnat1	4	-	tss_body	1.49E+08
198	cg41719744_BC21	0.000298	-0.08126	Lower					1.51E+08
199	cg41742574_TC11	0.000872	-0.06726	Lower	Espn	4	-	tss_body	1.52E+08
200	cg41753377_TC21	0.000307	-0.0668	Lower					1.53E+08
201	cg41888536_BC21	0.000691	0.05161	Higher	Gnai1	5	-	tss_body	18314471
202	cg41964123_TC21	0.000399	0.050462	Higher	En2	5	+	tss_body	28170175
203	cg41977120_TC21	0.000313	-0.05919	Lower	3110082J24Rik	5	-	tss_body	30105458
204	cg42100922_TC21	0.000411	-0.05314	Lower	Ldb2	5	-	tss_body	44696239
205	cg42169592_BC21	0.00087	-0.06548	Lower					55701103
206	cg42289235_BC21	0.000176	0.053326	Higher					73567184
207	cg42318588_BC21	0.000501	-0.08711	Lower	Pdcl2	5	-	tss_body	76324151
208	cg42328536_TC21	0.000835	-0.0697	Lower	Gm34598	5	-	tss_body	77158782
209	cg42481401_TC21	0.000777	-0.09602	Lower					1.01E+08

210	cg42572866_BC21	0.000105	0.050544	Higher	Fbrsl1	5	-	tss_body	1.1E+08
211	cg42614585_BC21	0.000263	-0.08949	Lower	Wscd2	5	+	tss_body	1.14E+08
212	cg42632275_TC21	0.00062	0.050307	Higher	Fam222a	5	+	tss_body	1.15E+08
213	cg42684300_TC21	0.000456	-0.06419	Lower					1.18E+08
214	cg42697766_BC11	0.00012	0.06334	Higher	chr5-119006032-119006424	5	*	Island	1.19E+08
215	cg42800602_BC21	0.000167	-0.0607	Lower	1700081B01Rik	5	+	tss_body	1.27E+08
216	cg42866081_TC21	0.000262	-0.07945	Lower					1.33E+08
217	cg42878416_BC21	0.000127	-0.06532	Lower	Syna	5	-	tss_body	1.35E+08
218	cg42879072_BC21	0.000124	-0.06348	Lower	Lat2	5	-	tss_body	1.35E+08
219	cg42933939_BC21	0.000439	0.059074	Higher	Prkar1b	5	-	tss_body	1.39E+08
220	cg42984318_TC21	0.000273	-0.10671	Lower	Spdye4b	5	+	tss_1500	1.43E+08
221	cg43006793_BC21	0.000152	-0.08119	Lower	Trrap	5	+	tss_body	1.45E+08
222	cg43056667_BC21	2.36E-05	-0.08367	Lower	Hmgb1	5	-	tss_body	1.49E+08
223	cg43057305_TC21	0.000196	0.063534	Higher	A0A0J9YUZ4	5	-	tss_body	1.49E+08
224	cg43067566_BC21	0.000829	-0.06962	Lower					1.5E+08
225	cg43080579_BC21	0.000688	-0.09384	Lower	Stard13	5	-	tss_body	1.51E+08
226	cg43175728_TC11	0.000264	-0.09537	Lower	Met	6	+	tss_body	17491191
227	cg43204880_TC21	0.000444	-0.07359	Lower					22443967
228	cg43240519_BC21	0.000829	-0.05419	Lower	Snd1	6	+	tss_body	28522132
229	cg43264561_BC21	0.0002	0.075943	Higher	Mest	6	+	tss_body	30735608
230	cg43264624_BC11	4.93E-05	0.068251	Higher	Mest	6	+	tss_body	30737492
231	cg43525571_TC21	0.000634	0.072574	Higher	chr6-675348633-67535660	6	*	NShelf	67532412

232	cg43635451_TC21	0.000436	0.07155	Higher	Cyp26b1	6	-	tss_body	84583804
233	cg43661954_TC21	0.00052	-0.08553	Lower	Gkn1	6	-	tss_body	87346626
234	cg43677384_BC21	6.07E-06	0.082437	Higher	Mgll	6	+	tss_body	88766809
235	cg43764831_BC21	0.00097	-0.05581	Lower	Foxp1	6	-	tss_body	99257208
236	cg43777906_TC21	0.000218	-0.05244	Lower					1E+08
237	cg43787998_BC21	4.25E-05	-0.06064	Lower	Pdzrn3	6	-	tss_body	1.01E+08
238	cg43813750_TC21	0.000964	0.073626	Higher	Il5ra	6	-	tss_1500	1.07E+08
239	cg43826367_TC21	0.000871	0.05505	Higher	0610040F04Rik	6	-	tss_body	1.09E+08
240	cg43856375_BC21	3.71E-05	0.069299	Higher	Il17rc	6	+	tss_body	1.13E+08
241	cg43934380_BC21	6.55E-05	0.074483	Higher	Mical3	6	-	tss_body	1.21E+08
242	cg43968839_TC11	0.000941	-0.08787	Lower	Iffo1	6	+	tss_body	1.25E+08
243	cg43983500_BC21	0.000507	-0.08181	Lower	Kcna1	6	-	tss_body	1.27E+08
244	cg44023521_BC11	0.000201	-0.08152	Lower	Tas2r104	6	-	tss_1500	1.32E+08
245	cg44099432_BC11	0.000754	-0.0919	Lower	Gm30215	6	+	tss_body	1.41E+08
246	cg44160952_BC21	0.000483	-0.07279	Lower	Ppfibp1	6	+	tss_body	1.47E+08
247	cg44198236_TC21	5.51E-05	-0.09423	Lower	Zfp579	7	-	tss_body	4994585
248	cg44281806_BC21	0.000177	-0.0908	Lower	Nova2	7	+	tss_body	18957993
249	cg44360395_TC21	6.03E-06	0.096473	Higher	Dyrk1b	7	+	tss_body	28184960
250	cg44398343_BC21	0.00069	0.078929	Higher	Ffar2	7	-	tss_body	30820320
251	cg44503171_TC21	0.000944	0.070613	Higher	Lrrc4b	7	+	tss_body	44462799
252	cg44540015_BC11	0.000403	0.059177	Higher					46740067
253	cg44635198_TC21	0.000358	0.070961	Higher	Klf13	7	-	tss_body	63911389
254	cg44654683_TC21	0.000527	0.057796	Higher	Pcsk6	7	+	tss_body	65893813
255	cg44772996_TC21	0.000997	0.080465	Higher	Vps33b	7	+	tss_body	80289988
256	cg44874396_TC21	0.000681	-0.05586	Lower	Tenm4	7	+	tss_body	96357913

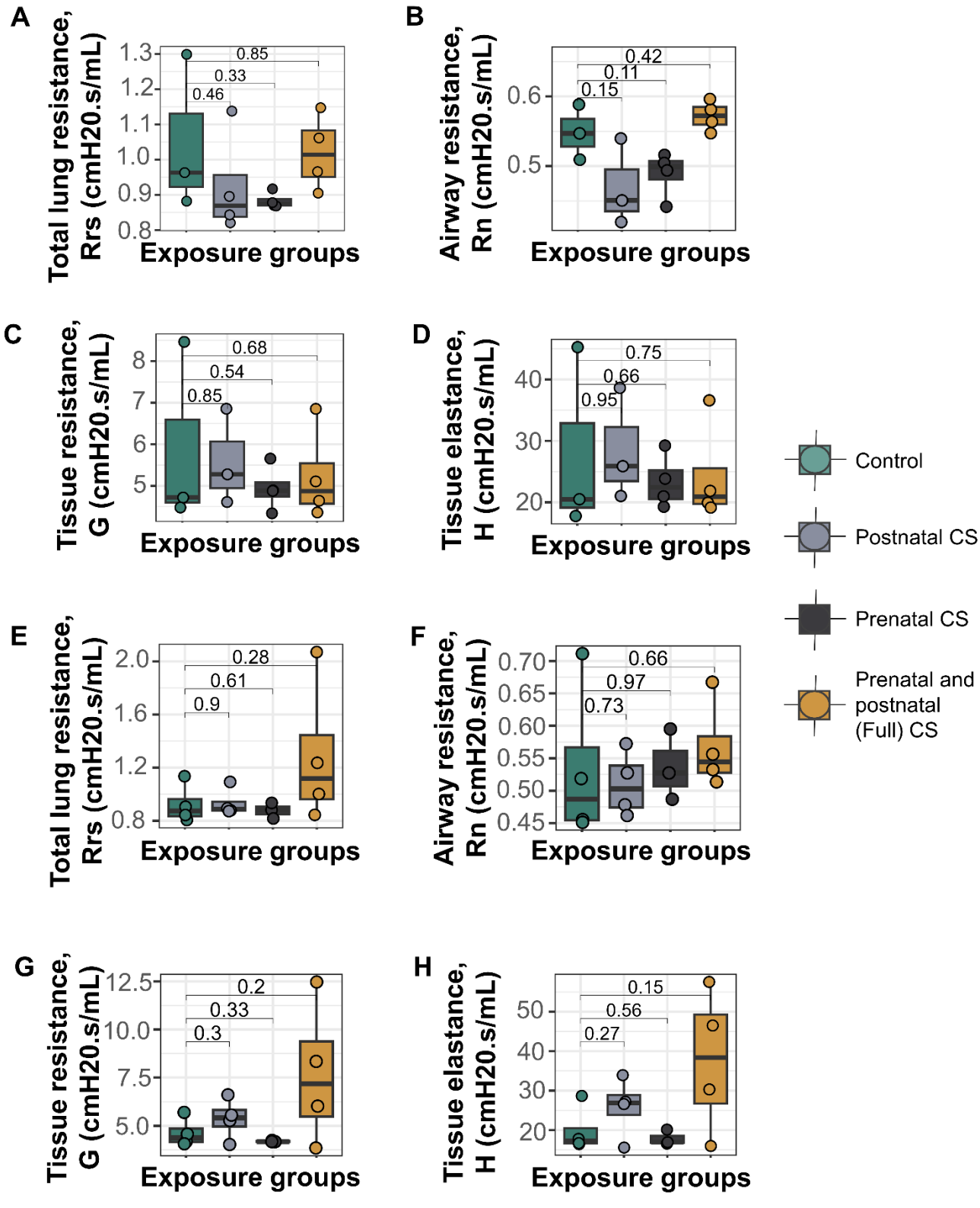
257	cg44890325_TC21	4.12E-05	-0.08715	Lower	Capn5	7	-	tss_body	98165537
258	cg44922022_BC21	1.05E-05	-0.07758	Lower					1.01E+08
259	cg44927008_TC21	0.000458	-0.06605	Lower	Art2b	7	-	tss_body	1.02E+08
260	cg44971210_BC21	0.000847	-0.0699	Lower	Ric3	7	-	tss_200	1.09E+08
261	cg44989325_TC11	0.000677	-0.08187	Lower	Eif4g2	7	-	tss_body	1.11E+08
262	cg45150073_TC21	7.76E-05	-0.09008	Lower		7	+	tss_body	1.29E+08
263	cg45219258_TC21	0.000692	0.05184	Higher					1.36E+08
264	cg45274235_BC21	5.74E-05	-0.06785	Lower	Slc25a22	7	-	tss_1500	1.41E+08
265	cg45283792_BC21	0.000892	0.060068	Higher	Lsp1	7	+	tss_body	1.42E+08
266	cg45309778_BC21	0.000308	-0.08109	Lower	Mrgprf	7	+	tss_body	1.45E+08
267	cg45387766_BC21	0.0002	-0.07341	Lower	Spaca7	8	+	tss_body	12573182
268	cg45471099_BC21	0.000621	-0.07013	Lower	Nkx6-3	8	+	tss_body	23156759
269	cg45495107_BC21	3.12E-05	0.056717	Higher	Fgfr1	8	+	tss_body	25521901
270	cg45651770_TC21	0.000966	-0.08414	Lower					46237844
271	cg45816073_TC21	0.000471	0.074479	Higher	Gm16486	8	+	tss_body	70716663
272	cg45816426_BC21	0.000117	-0.06325	Lower	Pde4c	8	+	tss_body	70742653
273	cg45823203_BC11	0.000642	-0.14227	Lower	Myo9b	8	+	tss_body	71338907
274	cg45832421_TC11	0.000664	-0.11076	Lower	Cyp4f18	8	-	tss_body	71993090
275	cg45947680_TC21	2.4E-06	0.081955	Higher					86757552
276	cg46098315_TC21	0.00011	-0.11136	Lower	Lrrc36	8	+	tss_body	1.05E+08
277	cg46148493_BC21	0.00024	0.089208	Higher	Pkd1l3	8	+	tss_body	1.1E+08
278	cg46263698_TC21	0.000959	0.061983	Higher	Cotl1	8	-	tss_body	1.2E+08
279	cg46290197_TC21	0.000282	-0.07482	Lower	Gm26747	8	+	tss_200	1.21E+08

280	cg46321823_BC21	0.000668	-0.06916	Lower	Spire2	8	+	tss_body	1.23E+08
281	cg46580278_TC21	9.52E-05	0.053784	Higher	Ets1	9	+	tss_body	32715975
282	cg46730767_TC21	0.00081	-0.08315	Lower	Ncam1	9	-	tss_body	49790798
283	cg46768314_TC11	0.000993	0.052984	Higher	Dmxl2	9	-	tss_body	54474249
284	cg46801097_BC21	0.000377	0.055149	Higher					57862120
285	cg46981687_BC21	0.001	-0.06573	Lower	Tinag	9	-	tss_1500	77046506
286	cg47007050_BC11	0.000812	-0.10238	Lower	Filip1	9	-	tss_body	79961607
287	cg47234603_BC21	0.000684	0.051522	Higher	Uba7	9	+	tss_body	1.08E+08
288	cg47235997_BC11	0.000171	-0.06413	Lower	Rnf123	9	-	tss_body	1.08E+08
289	cg47317446_TC21	0.000597	0.075874	Higher	Tgfbr2	9	-	tss_body	1.16E+08
290	cg47334265_BC21	0.000649	-0.05852	Lower	Rbms3	9	-	tss_body	1.18E+08
291	cg47367593_TC11	3.14E-05	-0.0777	Lower	Myrip	9	+	tss_body	1.2E+08
X chromosome									
	CpG	***p* value**	**Effect size**	**Direction of change**	**Gene name**	**Chromosome number**	**Chromosome strand**	**Feature**	**CpG position**
1	cg47428422_TC11	0.000331	-0.11276	Lower		X	-	tss_body	7750535
2	cg47430186_BC21	0.000817	0.056074	Higher	Pim2	X	+	tss_body	7881143
3	cg47430502_TC11	8.6E-05	0.088644	Higher	Timm17b	X	+	tss_1500	7899369
4	cg47551736_BC21	0.000845	-0.09299	Lower	Lonrf3	X	+	tss_body	36344697
5	cg47645560_BC11	0.000432	-0.05287	Lower	1700013H16Rik	X	-	tss_body	53757863
6	cg47663054_BC11	0.000714	0.065403	Higher	Rbmx	X	-	tss_body	57392915
7	cg47742973_TC21	0.000969	0.054526	Higher	Rpl10	X	+	tss_200	74270769
8	cg47902628_BC21	0.000929	-0.06354	Lower		X			1.05E+08
9	cg48034703_TC21	0.000209	0.056067	Higher	Morf4l2	X	-	tss_body	1.37E+08
10	cg48037071_BC11	5.67E-06	0.084149	Higher	Fam199x	X	+	tss_body	1.37E+08
11	cg48118438_TC21	0.000416	0.050342	Higher	9530051G07Rik	X	+	tss_200	1.53E+08
12	cg48165651_TC21	0.000401	0.067804	Higher	Nhs	X	-	tss_1500	1.62E+08

13	cg48169904_BC21	0.000167	0.070597	Higher	Txlng	X	-	tss_body	1.63E+08

Differences in DNA methylation were measured using linear regression contained within the LIMMA package in R. Differentially methylated sites were identified at p < 1e-3 and an effect size > 0.05. CpG = CpG ID on the Illumina mouse methylation microarray. *p* value = *p* value calculated following differential methylation analysis using LIMMA. Effect size = Difference in DNAm between groups. Direction of change - Direction of change in DNAm of CS groups relative to controls. Gene name = Gene name obtained from UCSC Genome Browser. Chromosome number = Chromosome containing the CpG as annotated by UCSC Genome Browser. Chromosome strand = Chromosomal strand on which CpG is located ('+' is the positive strand, '-' is the negative strand). Feature = Location of gene as annotated by the UCSC Genome Browser (tss_body = within gene body, tss_200 = 0-200 bases upstream of the transcription start site, tss_1500 = 200-1500 bases upstream of the transcription start site), Sshelf = 2-4kb downstream (3') of the stop site of a CpG island. CpG position = Genomic location of CpG.

Baseline lung function in offspring at 8 weeks of age (5 weeks after cessation of early life smoke exposure)



Appendix 4. 45: Effects of early life exposure to CS on offspring baseline lung function at 8 weeks of age.

Lung function parameters (A) Total lung resistance was not significantly altered by early life CS in females at baseline. (B) Airway resistance was not significantly altered by early life CS in females at baseline. (C) Tissue resistance was not significantly altered by early life CS in females at baseline. (D) Alveolar elastance was not significantly altered by early life CS in females at baseline. (E) Total lung resistance was not significantly altered by early life CS in males at baseline. (F) Airway resistance was not significantly altered by early life CS in males at baseline. (G) Tissue resistance was not significantly altered by early life CS in males at baseline. (H) Alveolar elastance was not significantly altered by early life CS in males at baseline. N = 3-4 per group. Lung function was assessed by taking 90^{th} percentile values in response to injection of saline into the lungs (baseline). Lung function data was analyzed in a sex-disaggregated manner using a two-way ANOVA, followed by multiple comparisons between groups at each methacholine dose where significant.