

Past & Contemporary Patterns of Marine Biodiversity: Making Inferences from Anadromous Sea Lamprey Population Genomics & Publicly Archived Genetic Data

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Supplemental Information 3

SI.3.1. GO terms associated with pH and their biological functions as interpreted by ReviGo. The first detection method used enrichment analysis to detect statistically significant GO term/gene associations for variants associated with pH using LFMM2. The second detection method includes GO term/gene associations for variants found across LFMM2, pcadapt and F_{ST} outlier methods. No overlap was found between the two detection methods.

GO Term ID	Function Name	Detection Method
GO:0001501	skeletal system development	Subset 1
GO:0001505	regulation of neurotransmitter levels	Subset 1
GO:0001894	tissue homeostasis	Subset 1
GO:0060249	anatomical structure homeostasis	Subset 1
GO:0002009	morphogenesis of an epithelium	Subset 1
GO:0000902	cell morphogenesis	Subset 1
GO:0000904	cell morphogenesis involved in differentiation	Subset 1
GO:0007409	axonogenesis	Subset 1
GO:0007411	axon guidance	Subset 1
GO:0031175	neuron projection development	Subset 1

GO:0032989	cellular component morphogenesis	Subset 1
GO:0032990	cell part morphogenesis	Subset 1
GO:0048667	cell morphogenesis involved in neuron differentiation	Subset 1
GO:0048812	neuron projection morphogenesis	Subset 1
GO:0048858	cell projection morphogenesis	Subset 1
GO:0060026	convergent extension	Subset 1
GO:0061564	axon development	Subset 1
GO:0097485	neuron projection guidance	Subset 1
GO:0120039	plasma membrane bounded cell projection morphogenesis	Subset 1
GO:0005975	carbohydrate metabolic process	Subset 1
GO:0006468	protein phosphorylation	Subset 1
GO:0006816	calcium ion transport	Subset 1
GO:0006935	chemotaxis	Subset 1
GO:0042330	taxis	Subset 1
GO:0007155	cell adhesion	Subset 1
GO:0007167	enzyme-linked receptor protein signaling pathway	Subset 1
GO:0007215	glutamate receptor signaling pathway	Subset 1
GO:0007267	cell-cell signaling	Subset 1
GO:0007422	peripheral nervous system development	Subset 1

GO:0007610	behavior	Subset 1
GO:0007611	learning or memory	Subset 1
GO:0008037	cell recognition	Subset 1
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	Subset 1
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	Subset 1
GO:0016049	cell growth	Subset 1
GO:0048588	developmental cell growth	Subset 1
GO:0048589	developmental growth	Subset 1
GO:0048675	axon extension	Subset 1
GO:0048846	axon extension involved in axon guidance	Subset 1
GO:0060560	developmental growth involved in morphogenesis	Subset 1
GO:1902284	neuron projection extension involved in neuron projection guidance	Subset 1
GO:1990138	neuron projection extension	Subset 1
GO:0016052	carbohydrate catabolic process	Subset 1
GO:0016358	dendrite development	Subset 1
GO:0016477	cell migration	Subset 1
GO:0018108	peptidyl-tyrosine phosphorylation	Subset 1
GO:0018212	peptidyl-tyrosine modification	Subset 1
GO:0021675	nerve development	Subset 1

GO:0021954	central nervous system neuron development	Subset 1
GO:0007420	brain development	Subset 1
GO:0021537	telencephalon development	Subset 1
GO:0021761	limbic system development	Subset 1
GO:0021884	forebrain neuron development	Subset 1
GO:0030900	forebrain development	Subset 1
GO:0030198	extracellular matrix organization	Subset 1
GO:0030203	glycosaminoglycan metabolic process	Subset 1
GO:0030334	regulation of cell migration	Subset 1
GO:2000145	regulation of cell motility	Subset 1
GO:0030888	regulation of B cell proliferation	Subset 1
GO:0031290	retinal ganglion cell axon guidance	Subset 1
GO:0031344	regulation of cell projection organization	Subset 1
GO:0051129	negative regulation of cellular component organization	Subset 1
GO:0051130	positive regulation of cellular component organization	Subset 1
GO:0031345	negative regulation of cell projection organization	Subset 1
GO:0010975	regulation of neuron projection development	Subset 1
GO:0010976	positive regulation of neuron projection development	Subset 1
GO:0010977	negative regulation of neuron projection development	Subset 1

GO:0050770	regulation of axonogenesis	Subset 1
GO:0120035	regulation of plasma membrane bounded cell projection organization	Subset 1
GO:0031589	cell-substrate adhesion	Subset 1
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	Subset 1
GO:0098609	cell-cell adhesion	Subset 1
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	Subset 1
GO:0032880	regulation of protein localization	Subset 1
GO:0051050	positive regulation of transport	Subset 1
GO:0051222	positive regulation of protein transport	Subset 1
GO:0051223	regulation of protein transport	Subset 1
GO:0070201	regulation of establishment of protein localization	Subset 1
GO:1903829	positive regulation of protein localization	Subset 1
GO:1904951	positive regulation of establishment of protein localization	Subset 1
GO:1905475	regulation of protein localization to membrane	Subset 1
GO:0033674	positive regulation of kinase activity	Subset 1
GO:0034330	cell junction organization	Subset 1
GO:0034331	cell junction maintenance	Subset 1
GO:0007528	neuromuscular junction development	Subset 1
GO:0050808	synapse organization	Subset 1

GO:0038063	collagen-activated tyrosine kinase receptor signaling pathway	Subset 1
GO:0038065	collagen-activated signaling pathway	Subset 1
GO:0040007	growth	Subset 1
GO:0040012	regulation of locomotion	Subset 1
GO:0042391	regulation of membrane potential	Subset 1
GO:0043062	extracellular structure organization	Subset 1
GO:0043279	response to alkaloid	Subset 1
GO:0043534	blood vessel endothelial cell migration	Subset 1
GO:0043954	cellular component maintenance	Subset 1
GO:0045229	external encapsulating structure organization	Subset 1
GO:0048514	blood vessel morphogenesis	Subset 1
GO:0001568	blood vessel development	Subset 1
GO:0001944	vasculature development	Subset 1
GO:0007507	heart development	Subset 1
GO:0048638	regulation of developmental growth	Subset 1
GO:0048640	negative regulation of developmental growth	Subset 1
GO:0048841	regulation of axon extension involved in axon guidance	Subset 1
GO:0061387	regulation of extent of cell growth	Subset 1
GO:0048871	multicellular organismal-level homeostasis	Subset 1

GO:0050804	modulation of chemical synaptic transmission	Subset 1
GO:0048167	regulation of synaptic plasticity	Subset 1
GO:0050806	positive regulation of synaptic transmission	Subset 1
GO:0051966	regulation of synaptic transmission, glutamatergic	Subset 1
GO:0060291	long-term synaptic potentiation	Subset 1
GO:0050885	neuromuscular process controlling balance	Subset 1
GO:0051668	localization within membrane	Subset 1
GO:0051960	regulation of nervous system development	Subset 1
GO:0060021	roof of mouth development	Subset 1
GO:0060284	regulation of cell development	Subset 1
GO:0010720	positive regulation of cell development	Subset 1
GO:0010721	negative regulation of cell development	Subset 1
GO:0022603	regulation of anatomical structure morphogenesis	Subset 1
GO:0030517	negative regulation of axon extension	Subset 1
GO:0048843	negative regulation of axon extension involved in axon guidance	Subset 1
GO:0050767	regulation of neurogenesis	Subset 1
GO:0050768	negative regulation of neurogenesis	Subset 1
GO:0050769	positive regulation of neurogenesis	Subset 1
GO:0050771	negative regulation of axonogenesis	Subset 1

GO:0051094	positive regulation of developmental process	Subset 1
GO:0051961	negative regulation of nervous system development	Subset 1
GO:0051962	positive regulation of nervous system development	Subset 1
GO:0060322	head development	Subset 1
GO:0060348	bone development	Subset 1
GO:0048705	skeletal system morphogenesis	Subset 1
GO:0060349	bone morphogenesis	Subset 1
GO:0060350	endochondral bone morphogenesis	Subset 1
GO:0060351	cartilage development involved in endochondral bone morphogenesis	Subset 1
GO:0060384	innervation	Subset 1
GO:0021545	cranial nerve development	Subset 1
GO:0021602	cranial nerve morphogenesis	Subset 1
GO:0060385	axonogenesis involved in innervation	Subset 1
GO:0061061	muscle structure development	Subset 1
GO:0061351	neural precursor cell proliferation	Subset 1
GO:0070588	calcium ion transmembrane transport	Subset 1
GO:0072657	protein localization to membrane	Subset 1
GO:0043113	receptor clustering	Subset 1
GO:0090596	sensory organ morphogenesis	Subset 1

GO:0042471	ear morphogenesis	Subset 1
GO:0048562	embryonic organ morphogenesis	Subset 1
GO:0099177	regulation of trans-synaptic signaling	Subset 1
GO:0099536	synaptic signaling	Subset 1
GO:0007269	neurotransmitter secretion	Subset 1
GO:0016079	synaptic vesicle exocytosis	Subset 1
GO:0099643	signal release from synapse	Subset 1
GO:1902287	semaphorin-plexin signaling pathway involved in axon guidance	Subset 1
GO:1902285	semaphorin-plexin signaling pathway involved in neuron projection guidance	Subset 1
GO:2000243	positive regulation of reproductive process	Subset 1
GO:0000151	ubiquitin ligase complex	Subset 2
GO:0005576	extracellular region	Subset 2
GO:0005581	collagen trimer	Subset 2
GO:0005615	extracellular space	Subset 2
GO:0005622	intracellular anatomical structure	Subset 2
GO:0005634	nucleus	Subset 2
GO:0005667	transcription regulator complex	Subset 2
GO:0005737	cytoplasm	Subset 2

GO:0005764	lysosome	Subset 2
GO:0000323	lytic vacuole	Subset 2
GO:0005773	vacuole	Subset 2
GO:0005794	Golgi apparatus	Subset 2
GO:0005783	endoplasmic reticulum	Subset 2
GO:0005802	trans-Golgi network	Subset 2
GO:0005829	cytosol	Subset 2
GO:0005856	cytoskeleton	Subset 2
GO:0005886	plasma membrane	Subset 2
GO:0009986	cell surface	Subset 2
GO:0012505	endomembrane system	Subset 2
GO:0015630	microtubule cytoskeleton	Subset 2
GO:0005875	microtubule associated complex	Subset 2
GO:0030286	dynein complex	Subset 2
GO:0016020	membrane	Subset 2
GO:0019897	extrinsic component of plasma membrane	Subset 2
GO:0019898	extrinsic component of membrane	Subset 2
GO:0030054	cell junction	Subset 2
GO:0030117	membrane coat	Subset 2

GO:0030118	clathrin coat	Subset 2
GO:0030120	vesicle coat	Subset 2
GO:0030135	coated vesicle	Subset 2
GO:0005768	endosome	Subset 2
GO:0012506	vesicle membrane	Subset 2
GO:0030659	cytoplasmic vesicle membrane	Subset 2
GO:0031410	cytoplasmic vesicle	Subset 2
GO:0097708	intracellular vesicle	Subset 2
GO:0030136	clathrin-coated vesicle	Subset 2
GO:0030125	clathrin vesicle coat	Subset 2
GO:0030128	clathrin coat of endocytic vesicle	Subset 2
GO:0030662	coated vesicle membrane	Subset 2
GO:0030665	clathrin-coated vesicle membrane	Subset 2
GO:0030666	endocytic vesicle membrane	Subset 2
GO:0030669	clathrin-coated endocytic vesicle membrane	Subset 2
GO:0045334	clathrin-coated endocytic vesicle	Subset 2
GO:0030139	endocytic vesicle	Subset 2
GO:0030141	secretory granule	Subset 2
GO:0001669	acrosomal vesicle	Subset 2

GO:0070820	tertiary granule	Subset 2
GO:0030312	external encapsulating structure	Subset 2
GO:0031012	extracellular matrix	Subset 2
GO:0031090	organelle membrane	Subset 2
GO:0031461	cullin-RING ubiquitin ligase complex	Subset 2
GO:0019005	SCF ubiquitin ligase complex	Subset 2
GO:0031974	membrane-enclosed lumen	Subset 2
GO:0031981	nuclear lumen	Subset 2
GO:0005654	nucleoplasm	Subset 2
GO:0016604	nuclear body	Subset 2
GO:0043233	organelle lumen	Subset 2
GO:0070013	intracellular organelle lumen	Subset 2
GO:0031982	vesicle	Subset 2
GO:0031983	vesicle lumen	Subset 2
GO:0031984	organelle subcompartment	Subset 2
GO:0032045	guanyl-nucleotide exchange factor complex	Subset 2
GO:0032991	protein-containing complex	Subset 2
GO:0034708	methyltransferase complex	Subset 2
GO:0035097	histone methyltransferase complex	Subset 2

GO:0048188	Set1C/COMPASS complex	Subset 2
GO:0036126	sperm flagellum	Subset 2
GO:0097729	9+2 motile cilium	Subset 2
GO:0036477	somatodendritic compartment	Subset 2
GO:0042734	presynaptic membrane	Subset 2
GO:0042995	cell projection	Subset 2
GO:0043025	neuronal cell body	Subset 2
GO:0043226	organelle	Subset 2
GO:0043227	membrane-bounded organelle	Subset 2
GO:0043228	non-membrane-bounded organelle	Subset 2
GO:0043229	intracellular organelle	Subset 2
GO:0043231	intracellular membrane-bounded organelle	Subset 2
GO:0043232	intracellular non-membrane-bounded organelle	Subset 2
GO:0043235	receptor complex	Subset 2
GO:0044297	cell body	Subset 2
GO:0045111	intermediate filament cytoskeleton	Subset 2
GO:0045202	synapse	Subset 2
GO:0097060	synaptic membrane	Subset 2
GO:0098793	presynapse	Subset 2

GO:0048471	perinuclear region of cytoplasm	Subset 2
GO:0048475	coated membrane	Subset 2
GO:0060205	cytoplasmic vesicle lumen	Subset 2
GO:0034774	secretory granule lumen	Subset 2
GO:0062023	collagen-containing extracellular matrix	Subset 2
GO:0071944	cell periphery	Subset 2
GO:0090575	RNA polymerase II transcription regulator complex	Subset 2
GO:0098588	bounding membrane of organelle	Subset 2
GO:0098590	plasma membrane region	Subset 2
GO:0098791	Golgi apparatus subcompartment	Subset 2
GO:0098796	membrane protein complex	Subset 2
GO:0098797	plasma membrane protein complex	Subset 2
GO:0098802	plasma membrane signaling receptor complex	Subset 2
GO:0038037	G protein-coupled receptor dimeric complex	Subset 2
GO:0097648	G protein-coupled receptor complex	Subset 2
GO:1903143	adrenomedullin receptor complex	Subset 2
GO:1903439	calcitonin family receptor complex	Subset 2
GO:1990406	CGRP receptor complex	Subset 2
GO:0098833	presynaptic endocytic zone	Subset 2

GO:0098835	presynaptic endocytic zone membrane	Subset 2
GO:0098888	extrinsic component of presynaptic membrane	Subset 2
GO:0098894	extrinsic component of presynaptic endocytic zone membrane	Subset 2
GO:0098846	podocyte foot	Subset 2
GO:0099080	supramolecular complex	Subset 2
GO:0099243	extrinsic component of synaptic membrane	Subset 2
GO:0099503	secretory vesicle	Subset 2
GO:0099512	supramolecular fiber	Subset 2
GO:0005874	microtubule	Subset 2
GO:0005882	intermediate filament	Subset 2
GO:0045095	keratin filament	Subset 2
GO:0099081	supramolecular polymer	Subset 2
GO:0099513	polymeric cytoskeletal fiber	Subset 2
GO:0099568	cytoplasmic region	Subset 2
GO:0101002	ficolin-1-rich granule	Subset 2
GO:0110165	cellular anatomical entity	Subset 2
GO:0120025	plasma membrane bounded cell projection	Subset 2
GO:0005858	axonemal dynein complex	Subset 2
GO:0005929	cilium	Subset 2

GO:0005930	axoneme	Subset 2
GO:0030424	axon	Subset 2
GO:0031514	motile cilium	Subset 2
GO:0032838	plasma membrane bounded cell projection cytoplasm	Subset 2
GO:0036156	inner dynein arm	Subset 2
GO:0043005	neuron projection	Subset 2
GO:0097014	ciliary plasm	Subset 2
GO:0140513	nuclear protein-containing complex	Subset 2
GO:0140535	intracellular protein-containing complex	Subset 2
GO:1902494	catalytic complex	Subset 2
GO:1904724	tertiary granule lumen	Subset 2
GO:1904813	ficolin-1-rich granule lumen	Subset 2
GO:1990234	transferase complex	Subset 2

SI.3.2. GO terms associated with freshwater feeding behavior and their biological functions as interpreted by ReviGo. The first detection method used enrichment analysis to detect statistically significant GO term/gene associations for variants associated with freshwater feeding using LFMM2. The second detection method includes GO term/gene associations for variants found across LFMM2, pcadapt and F_{ST} outlier methods. An overlap of 5 GO terms (GO:0032940, GO:0034330, GO:0050808, GO:0099173, GO:0140352) was found between the two detection methods.

GO Term ID	Function Name	Detection Method
GO:0001655	urogenital system development	Subset 1
GO:0001775	cell activation	Subset 1
GO:0002009	morphogenesis of an epithelium	Subset 1
GO:0000902	cell morphogenesis	Subset 1
GO:0000904	cell morphogenesis involved in differentiation	Subset 1
GO:0007409	axonogenesis	Subset 1
GO:0007411	axon guidance	Subset 1
GO:0031175	neuron projection development	Subset 1
GO:0032989	cellular component morphogenesis	Subset 1
GO:0032990	cell part morphogenesis	Subset 1
GO:0048667	cell morphogenesis involved in neuron differentiation	Subset 1
GO:0048812	neuron projection morphogenesis	Subset 1
GO:0048858	cell projection morphogenesis	Subset 1
GO:0061564	axon development	Subset 1
GO:0097485	neuron projection guidance	Subset 1
GO:0120039	plasma membrane bounded cell projection morphogenesis	Subset 1
GO:0003013	circulatory system process	Subset 1
GO:0003018	vascular process in circulatory system	Subset 1

GO:0010232	vascular transport	Subset 1
GO:0043114	regulation of vascular permeability	Subset 1
GO:0043116	negative regulation of vascular permeability	Subset 1
GO:0150104	transport across blood-brain barrier	Subset 1
GO:0006836	neurotransmitter transport	Subset 1
GO:0006935	chemotaxis	Subset 1
GO:0042330	taxis	Subset 1
GO:0007155	cell adhesion	Subset 1
GO:0007272	ensheathment of neurons	Subset 1
GO:0007422	peripheral nervous system development	Subset 1
GO:0007612	learning	Subset 1
GO:0008037	cell recognition	Subset 1
GO:0008038	neuron recognition	Subset 1
GO:0014044	Schwann cell development	Subset 1
GO:0014037	Schwann cell differentiation	Subset 1
GO:0016477	cell migration	Subset 1
GO:0030001	metal ion transport	Subset 1
GO:0098655	monoatomic cation transmembrane transport	Subset 1
GO:0030010	establishment of cell polarity	Subset 1

GO:0090162	establishment of epithelial cell polarity	Subset 1
GO:0030029	actin filament-based process	Subset 1
GO:0030036	actin cytoskeleton organization	Subset 1
GO:0030155	regulation of cell adhesion	Subset 1
GO:0031344	regulation of cell projection organization	Subset 1
GO:0051129	negative regulation of cellular component organization	Subset 1
GO:0051130	positive regulation of cellular component organization	Subset 1
GO:0031345	negative regulation of cell projection organization	Subset 1
GO:0010975	regulation of neuron projection development	Subset 1
GO:0010977	negative regulation of neuron projection development	Subset 1
GO:0120035	regulation of plasma membrane bounded cell projection organization	Subset 1
GO:0007269	neurotransmitter secretion	Subset 1
GO:0023061	signal release	Subset 1
GO:0099643	signal release from synapse	Subset 1
GO:0035269	protein O-linked mannosylation	Subset 1
GO:0042391	regulation of membrane potential	Subset 1
GO:0042552	myelination	Subset 1
GO:0008366	axon ensheathment	Subset 1
GO:0043009	chordate embryonic development	Subset 1

GO:0009792	embryo development ending in birth or egg hatching	Subset 1
GO:0048701	embryonic cranial skeleton morphogenesis	Subset 1
GO:0048704	embryonic skeletal system morphogenesis	Subset 1
GO:0048706	embryonic skeletal system development	Subset 1
GO:0043087	regulation of GTPase activity	Subset 1
GO:0043547	positive regulation of GTPase activity	Subset 1
GO:0043588	skin development	Subset 1
GO:0050804	modulation of chemical synaptic transmission	Subset 1
GO:0050908	detection of light stimulus involved in visual perception	Subset 1
GO:0050962	detection of light stimulus involved in sensory perception	Subset 1
GO:0051056	regulation of small GTPase mediated signal transduction	Subset 1
GO:0051094	positive regulation of developmental process	Subset 1
GO:0051960	regulation of nervous system development	Subset 1
GO:0051962	positive regulation of nervous system development	Subset 1
GO:0051963	regulation of synapse assembly	Subset 1
GO:0051965	positive regulation of synapse assembly	Subset 1
GO:0060284	regulation of cell development	Subset 1
GO:0086001	cardiac muscle cell action potential	Subset 1
GO:0090596	sensory organ morphogenesis	Subset 1

GO:0007420	brain development	Subset 1
GO:0048562	embryonic organ morphogenesis	Subset 1
GO:0048592	eye morphogenesis	Subset 1
GO:0048705	skeletal system morphogenesis	Subset 1
GO:0098609	cell-cell adhesion	Subset 1
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	Subset 1
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	Subset 1
GO:0098660	inorganic ion transmembrane transport	Subset 1
GO:0098662	inorganic cation transmembrane transport	Subset 1
GO:0070588	calcium ion transmembrane transport	Subset 1
GO:0099003	vesicle-mediated transport in synapse	Subset 1
GO:0034329	cell junction assembly	Subset 1
GO:0099177	regulation of trans-synaptic signaling	Subset 1
GO:0099504	synaptic vesicle cycle	Subset 1
GO:0016079	synaptic vesicle exocytosis	Subset 1
GO:1901888	regulation of cell junction assembly	Subset 1
GO:1903305	regulation of regulated secretory pathway	Subset 1
GO:1903522	regulation of blood circulation	Subset 1
GO:0008016	regulation of heart contraction	Subset 1

GO:0061337	cardiac conduction	Subset 1
GO:0001501	skeletal system development	Subset 2
GO:0006139	nucleobase-containing compound metabolic process	Subset 2
GO:0006355	regulation of DNA-templated transcription	Subset 2
GO:0009889	regulation of biosynthetic process	Subset 2
GO:0010468	regulation of gene expression	Subset 2
GO:0010556	regulation of macromolecule biosynthetic process	Subset 2
GO:0019219	regulation of nucleobase-containing compound metabolic process	Subset 2
GO:0031323	regulation of cellular metabolic process	Subset 2
GO:0031326	regulation of cellular biosynthetic process	Subset 2
GO:0051171	regulation of nitrogen compound metabolic process	Subset 2
GO:0051252	regulation of RNA metabolic process	Subset 2
GO:0060255	regulation of macromolecule metabolic process	Subset 2
GO:0080090	regulation of primary metabolic process	Subset 2
GO:2001141	regulation of RNA biosynthetic process	Subset 2
GO:0006357	regulation of transcription by RNA polymerase II	Subset 2
GO:0006396	RNA processing	Subset 2
GO:0006397	mRNA processing	Subset 2
GO:0006399	tRNA metabolic process	Subset 2

GO:0008033	tRNA processing	Subset 2
GO:0034470	ncRNA processing	Subset 2
GO:0006508	proteolysis	Subset 2
GO:0006725	cellular aromatic compound metabolic process	Subset 2
GO:0006777	Mo-molybdopterin cofactor biosynthetic process	Subset 2
GO:0019720	Mo-molybdopterin cofactor metabolic process	Subset 2
GO:0032324	molybdopterin cofactor biosynthetic process	Subset 2
GO:0043545	molybdopterin cofactor metabolic process	Subset 2
GO:0006793	phosphorus metabolic process	Subset 2
GO:0006807	nitrogen compound metabolic process	Subset 2
GO:0006810	transport	Subset 2
GO:0051234	establishment of localization	Subset 2
GO:0055085	transmembrane transport	Subset 2
GO:0008152	metabolic process	Subset 2
GO:0008380	RNA splicing	Subset 2
GO:0008643	carbohydrate transport	Subset 2
GO:0009058	biosynthetic process	Subset 2
GO:0009451	RNA modification	Subset 2
GO:0009987	cellular process	Subset 2

GO:0010467	gene expression	Subset 2
GO:0016043	cellular component organization	Subset 2
GO:0016070	RNA metabolic process	Subset 2
GO:0016071	mRNA metabolic process	Subset 2
GO:0016073	snRNA metabolic process	Subset 2
GO:0016074	sno(s)RNA metabolic process	Subset 2
GO:0016192	vesicle-mediated transport	Subset 2
GO:0018130	heterocycle biosynthetic process	Subset 2
GO:0019222	regulation of metabolic process	Subset 2
GO:0019538	protein metabolic process	Subset 2
GO:0019637	organophosphate metabolic process	Subset 2
GO:0006796	phosphate-containing compound metabolic process	Subset 2
GO:0022406	membrane docking	Subset 2
GO:0023052	signaling	Subset 2
GO:0030198	extracellular matrix organization	Subset 2
GO:0031099	regeneration	Subset 2
GO:0031123	RNA 3'-end processing	Subset 2
GO:0032259	methylation	Subset 2
GO:0032501	multicellular organismal process	Subset 2

GO:0032502	developmental process	Subset 2
GO:0032879	regulation of localization	Subset 2
GO:0032880	regulation of protein localization	Subset 2
GO:0060341	regulation of cellular localization	Subset 2
GO:1900180	regulation of protein localization to nucleus	Subset 2
GO:1900182	positive regulation of protein localization to nucleus	Subset 2
GO:1903829	positive regulation of protein localization	Subset 2
GO:0032940	secretion by cell	Subset 1, Subset 2
GO:0006887	exocytosis	Subset 2
GO:0140029	exocytic process	Subset 2
GO:0033036	macromolecule localization	Subset 2
GO:0033967	box C/D RNA metabolic process	Subset 2
GO:0000494	box C/D RNA 3'-end processing	Subset 2
GO:0031126	sno(s)RNA 3'-end processing	Subset 2
GO:0034963	box C/D RNA processing	Subset 2
GO:0043144	sno(s)RNA processing	Subset 2
GO:0034330	cell junction organization	Subset 1, Subset 2
GO:0034641	cellular nitrogen compound metabolic process	Subset 2
GO:0034660	ncRNA metabolic process	Subset 2

GO:0040007	growth	Subset 2
GO:0040031	snRNA modification	Subset 2
GO:0043062	extracellular structure organization	Subset 2
GO:0043170	macromolecule metabolic process	Subset 2
GO:0043412	macromolecule modification	Subset 2
GO:0043414	macromolecule methylation	Subset 2
GO:0001510	RNA methylation	Subset 2
GO:0006400	tRNA modification	Subset 2
GO:0043484	regulation of RNA splicing	Subset 2
GO:0043628	regulatory ncRNA 3'-end processing	Subset 2
GO:0044237	cellular metabolic process	Subset 2
GO:0044238	primary metabolic process	Subset 2
GO:0044249	cellular biosynthetic process	Subset 2
GO:0045229	external encapsulating structure organization	Subset 2
GO:0046483	heterocycle metabolic process	Subset 2
GO:0046782	regulation of viral transcription	Subset 2
GO:0032897	negative regulation of viral transcription	Subset 2
GO:0048525	negative regulation of viral process	Subset 2
GO:0046903	secretion	Subset 2

GO:0046907	intracellular transport	Subset 2
GO:0006886	intracellular protein transport	Subset 2
GO:0008104	protein localization	Subset 2
GO:0015031	protein transport	Subset 2
GO:0045184	establishment of protein localization	Subset 2
GO:0051649	establishment of localization in cell	Subset 2
GO:0070727	cellular macromolecule localization	Subset 2
GO:0048518	positive regulation of biological process	Subset 2
GO:0048519	negative regulation of biological process	Subset 2
GO:0048522	positive regulation of cellular process	Subset 2
GO:0009891	positive regulation of biosynthetic process	Subset 2
GO:0009893	positive regulation of metabolic process	Subset 2
GO:0010557	positive regulation of macromolecule biosynthetic process	Subset 2
GO:0010604	positive regulation of macromolecule metabolic process	Subset 2
GO:0031325	positive regulation of cellular metabolic process	Subset 2
GO:0031328	positive regulation of cellular biosynthetic process	Subset 2
GO:0045893	positive regulation of DNA-templated transcription	Subset 2
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	Subset 2

GO:0045944	positive regulation of transcription by RNA polymerase II	Subset 2
GO:0051173	positive regulation of nitrogen compound metabolic process	Subset 2
GO:0051254	positive regulation of RNA metabolic process	Subset 2
GO:1902680	positive regulation of RNA biosynthetic process	Subset 2
GO:0048523	negative regulation of cellular process	Subset 2
GO:0000122	negative regulation of transcription by RNA polymerase II	Subset 2
GO:0009890	negative regulation of biosynthetic process	Subset 2
GO:0009892	negative regulation of metabolic process	Subset 2
GO:0010558	negative regulation of macromolecule biosynthetic process	Subset 2
GO:0010605	negative regulation of macromolecule metabolic process	Subset 2
GO:0031324	negative regulation of cellular metabolic process	Subset 2
GO:0031327	negative regulation of cellular biosynthetic process	Subset 2
GO:0045892	negative regulation of DNA-templated transcription	Subset 2
GO:0045934	negative regulation of nucleobase-containing compound metabolic process	Subset 2
GO:0051172	negative regulation of nitrogen compound metabolic process	Subset 2
GO:0051253	negative regulation of RNA metabolic process	Subset 2
GO:1902679	negative regulation of RNA biosynthetic process	Subset 2
GO:0048589	developmental growth	Subset 2

GO:0031101	fin regeneration	Subset 2
GO:0042246	tissue regeneration	Subset 2
GO:0048869	cellular developmental process	Subset 2
GO:0007275	multicellular organism development	Subset 2
GO:0048731	system development	Subset 2
GO:0048856	anatomical structure development	Subset 2
GO:0050684	regulation of mRNA processing	Subset 2
GO:0048024	regulation of mRNA splicing, via spliceosome	Subset 2
GO:0050792	regulation of viral process	Subset 2
GO:0050794	regulation of cellular process	Subset 2
GO:0050789	regulation of biological process	Subset 2
GO:0050808	synapse organization	Subset 1, Subset 2
GO:0001941	postsynaptic membrane organization	Subset 2
GO:0072578	neurotransmitter-gated ion channel clustering	Subset 2
GO:0072579	glycine receptor clustering	Subset 2
GO:0099173	postsynapse organization	Subset 1, Subset 2
GO:0051179	localization	Subset 2
GO:0051189	prosthetic group metabolic process	Subset 2
GO:0051640	organelle localization	Subset 2

GO:0051641	cellular localization	Subset 2
GO:0051668	localization within membrane	Subset 2
GO:0061024	membrane organization	Subset 2
GO:0065007	biological regulation	Subset 2
GO:0071702	organic substance transport	Subset 2
GO:0071704	organic substance metabolic process	Subset 2
GO:0071705	nitrogen compound transport	Subset 2
GO:0071840	cellular component organization or biogenesis	Subset 2
GO:0072657	protein localization to membrane	Subset 2
GO:0043113	receptor clustering	Subset 2
GO:0090304	nucleic acid metabolic process	Subset 2
GO:0090407	organophosphate biosynthetic process	Subset 2
GO:0140056	organelle localization by membrane tethering	Subset 2
GO:0006904	vesicle docking involved in exocytosis	Subset 2
GO:0048278	vesicle docking	Subset 2
GO:0140352	export from cell	Subset 1, Subset 2
GO:1901360	organic cyclic compound metabolic process	Subset 2
GO:1901362	organic cyclic compound biosynthetic process	Subset 2
GO:1901564	organonitrogen compound metabolic process	Subset 2

GO:1901566	organonitrogen compound biosynthetic process	Subset 2
GO:1901576	organic substance biosynthetic process	Subset 2
GO:1903311	regulation of mRNA metabolic process	Subset 2
GO:1904869	regulation of protein localization to Cajal body	Subset 2
GO:1904871	positive regulation of protein localization to Cajal body	Subset 2
GO:1905382	positive regulation of snRNA transcription by RNA polymerase II	Subset 2
GO:1905380	regulation of snRNA transcription by RNA polymerase II	Subset 2
GO:1990438	U6 2'-O-snRNA methylation	Subset 2
GO:0106349	snRNA methylation	Subset 2
GO:1990437	snRNA 2'-O-methylation	Subset 2