Additional File 1 - Read lengths and mapping results from the Illumina GAIIx reads of the reduced representation libraries of eight flax genotypes. Read mapping was performed against the new whole genome shotgun sequence assembly (LinUsi_v1.1) of CDC Bethune using Bowtie.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Read length (bp)</th>
<th>Mapped</th>
<th>Unmapped</th>
<th>Suppressed</th>
<th>Total</th>
<th>Length (Mbp)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Number of PET reads (percent)</td>
<td>Length (Mbp)</td>
<td>Number of PET reads (percent)</td>
<td>Length (Mbp)</td>
<td>Number of PET reads (percent)</td>
<td>Length (Mbp)</td>
</tr>
<tr>
<td>CDC Bethune</td>
<td>50</td>
<td>10,353,767 (60.4)</td>
<td>1,035</td>
<td>3,905,439 (22.8)</td>
<td>391</td>
<td>2,886,188 (16.8)</td>
</tr>
<tr>
<td>MacBeth</td>
<td>50</td>
<td>9,884,782 (60.2)</td>
<td>988</td>
<td>4,152,965 (25.3)</td>
<td>415</td>
<td>2,370,197 (14.4)</td>
</tr>
<tr>
<td>SP2047</td>
<td>50</td>
<td>9,535,745 (53.6)</td>
<td>954</td>
<td>5,091,315 (28.6)</td>
<td>509</td>
<td>3,158,246 (17.8)</td>
</tr>
<tr>
<td>UGG5-5</td>
<td>50</td>
<td>9,104,662 (56.8)</td>
<td>910</td>
<td>4,501,814 (28.1)</td>
<td>450</td>
<td>2,416,809 (15.1)</td>
</tr>
<tr>
<td>Double Low</td>
<td>75</td>
<td>14,214,503 (50.2)</td>
<td>2,132</td>
<td>11,444,119 (40.4)</td>
<td>1,717</td>
<td>2,676,274 (9.4)</td>
</tr>
<tr>
<td>Crepitam Tabor</td>
<td>75</td>
<td>14,615,616 (50.4)</td>
<td>2,192</td>
<td>11,957,292 (41.3)</td>
<td>1,794</td>
<td>2,414,164 (8.3)</td>
</tr>
<tr>
<td>G-1186/94</td>
<td>100</td>
<td>12,686,427 (43.8)</td>
<td>2,537</td>
<td>13,460,180 (46.5)</td>
<td>2,692</td>
<td>2,787,215 (9.6)</td>
</tr>
<tr>
<td>Atlas</td>
<td>100</td>
<td>12,405,940 (43.6)</td>
<td>2,481</td>
<td>13,987,831 (49.2)</td>
<td>2,798</td>
<td>2,056,559 (7.2)</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>92,801,442</td>
<td>13,229</td>
<td>68,500,955</td>
<td>10,766</td>
<td>20,765,652</td>
</tr>
</tbody>
</table>