## TABLE S1

Number of small RNA reads and tags in the various libraries: TTR16 – tetraploid parent (Genome BBAA), TQ113 – diploid parent (Genome DD), F1 – triploid hybrid (genome BAD), S1 – first generation of synthetic hexaploid (Genome BBAADD).

<table>
<thead>
<tr>
<th>Libraries:</th>
<th>TTR16</th>
<th>TQ113</th>
<th>Hybrid</th>
<th>Polyploid</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total reads</td>
<td>5,633,938</td>
<td>3,064,285</td>
<td>6,421,516</td>
<td>3,458,759</td>
<td>18,578,498</td>
</tr>
<tr>
<td>Total tags</td>
<td>3,726,879</td>
<td>1,879,921</td>
<td>3,068,481</td>
<td>1,092,783</td>
<td>-</td>
</tr>
<tr>
<td>Tags after QC&lt;sup&gt;a&lt;/sup&gt;</td>
<td>991,936</td>
<td>2,829,480</td>
<td>3,423,567</td>
<td>1,627,189</td>
<td>-</td>
</tr>
<tr>
<td>Tags with &gt;30 reads</td>
<td>7967</td>
<td>4292</td>
<td>6756</td>
<td>2772</td>
<td>-</td>
</tr>
<tr>
<td>Reads from tags with &gt;30 reads</td>
<td>1,576,108</td>
<td>1,202,651</td>
<td>1,689,159</td>
<td>1,561,663</td>
<td>6,029,581</td>
</tr>
</tbody>
</table>

<sup>a</sup>QC: Quality Control process including 1. Trimming of 3’ PCR primer; 2. Elimination of reads with >3Ns; 3. Assembly of reads with identical sequences into unique tags.