Supplementary Table S1. Summary of the linkage map for QTL analysis

<table>
<thead>
<tr>
<th>Chromosome</th>
<th>Used markers</th>
<th>Polymorphic markers</th>
<th>Polymorphism (%)</th>
<th>Anchored markers</th>
<th>Length (cM)</th>
<th>AMI (cM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>850</td>
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<td>13.33</td>
<td>46</td>
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<td>683</td>
<td>102</td>
<td>14.93</td>
<td>57</td>
<td>116.93</td>
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<tr>
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<td>51</td>
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<tr>
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<tr>
<td><strong>Total</strong></td>
<td><strong>7098</strong></td>
<td><strong>1024</strong></td>
<td><strong>14.42</strong></td>
<td><strong>498 (41.5)</strong></td>
<td><strong>1064.82</strong></td>
<td><strong>2.1</strong></td>
</tr>
</tbody>
</table>

\(^a\) Number of markers selected  
\(^b\) Length: chromosomal length  
\(^c\) Average marker interval