### Table S6:
Potential sampling depth after filtering of residually heterozygous regions and those involved in obvious identity by descent.

<table>
<thead>
<tr>
<th></th>
<th>RAL</th>
<th>MW</th>
<th>SI</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>mean</td>
<td>max</td>
<td>M</td>
</tr>
<tr>
<td>X</td>
<td>34.92</td>
<td>35</td>
<td>7</td>
</tr>
<tr>
<td>2L</td>
<td>33.90</td>
<td>35</td>
<td>6</td>
</tr>
<tr>
<td>2R</td>
<td>34.97</td>
<td>36</td>
<td>6</td>
</tr>
<tr>
<td>3L</td>
<td>33.29</td>
<td>35</td>
<td>5</td>
</tr>
<tr>
<td>3R</td>
<td>32.95</td>
<td>34</td>
<td>5</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>33.95</td>
<td>35</td>
<td>5.76</td>
</tr>
</tbody>
</table>

### Table S7:
RAL allelic depth at Q40 plus the total numbers of assembled bp.

<table>
<thead>
<tr>
<th></th>
<th>X</th>
<th>2L</th>
<th>2R</th>
<th>3L</th>
<th>3R</th>
<th><strong>total</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>mean</strong></td>
<td>27.73</td>
<td>29.38</td>
<td>30.21</td>
<td>31.69</td>
<td>28.86</td>
<td>29.02</td>
</tr>
<tr>
<td><strong>median</strong></td>
<td>30</td>
<td>31</td>
<td>32</td>
<td>33</td>
<td>30</td>
<td>31</td>
</tr>
<tr>
<td><strong>bp</strong></td>
<td>285,009,253</td>
<td>437,320,403</td>
<td>330,471,088</td>
<td>401,221,253</td>
<td>440,908,643</td>
<td>1,894,930,640</td>
</tr>
</tbody>
</table>

### Table S8:
MW sampling depth at Q40 plus the total numbers of assembled bp.

<table>
<thead>
<tr>
<th></th>
<th>X</th>
<th>2L</th>
<th>2R</th>
<th>3L</th>
<th>3R</th>
<th><strong>total</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>mean</strong></td>
<td>5.84</td>
<td>5.22</td>
<td>5.21</td>
<td>4.14</td>
<td>4.20</td>
<td>4.84</td>
</tr>
<tr>
<td><strong>median</strong></td>
<td>6</td>
<td>6</td>
<td>6</td>
<td>5</td>
<td>5</td>
<td>5</td>
</tr>
<tr>
<td><strong>bp</strong></td>
<td>54,819,051</td>
<td>77,720,775</td>
<td>55,441,956</td>
<td>57,121,007</td>
<td>62,369,042</td>
<td>307,471,831</td>
</tr>
</tbody>
</table>