<table>
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<th>Tag length</th>
<th>Fragment size</th>
<th>Total tags sequenced*</th>
<th>Tags mapped allowing ≤500 matches (% of total tags sequenced)</th>
<th>Tags with unique match (% of total mapped tags)</th>
<th>Tags with 2-5 matches (% of total mapped tags)</th>
<th>Tags with 6-10 matches (% of total mapped tags)</th>
<th>Tags with 10-100 matches (% of total mapped tags)</th>
<th>Tags with 101-500 matches (% of total mapped tags)</th>
<th>Total repeated tags (% of total mapped tags)</th>
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<tbody>
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<td>36</td>
<td>62</td>
<td>35'821'593</td>
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<td>512'919 (9.67)</td>
<td>180'369 (3.40)</td>
<td>432'009 (8.14)</td>
<td>136'792 (2.58)</td>
<td>1'262'089 (23.79)</td>
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<td>147</td>
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<td>19'954'694 (95.76)</td>
<td>629'445 (3.02)</td>
<td>98'477 (0.47)</td>
<td>125'129 (0.60)</td>
<td>31'301 (0.15)</td>
<td>884'352 (4.24)</td>
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<td>BRF2</td>
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<td>141</td>
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<td>19'953'829 (55.53)</td>
<td>18'971'092 (95.07)</td>
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<td>32'528 (0.16)</td>
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<td>21'278'323 (95.46)</td>
<td>706'998 (3.17)</td>
<td>21'021 (0.54)</td>
<td>150'075 (0.67)</td>
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<td>10'652'047 (94.04)</td>
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<td>474'514 (3.23)</td>
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<td>2'735'214 (11.41)</td>
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<td>798'559 (3.06)</td>
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</tr>
</tbody>
</table>

Table S3. Number of tags with unique and repeated matches mapped onto the genome. * tags sequenced multiple times were counted only once.