TABLE S5: Average within population prediction accuracies in interconnected biparental maize populations

<table>
<thead>
<tr>
<th>( N_p )</th>
<th>Trait</th>
<th>Pooling</th>
<th>( N_p )</th>
<th>Trait</th>
<th>Pooling</th>
<th>( N_p )</th>
<th>Trait</th>
<th>Pooling</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>no</td>
<td>partial</td>
<td>complete</td>
<td>no</td>
<td>partial</td>
<td>complete</td>
<td>no</td>
</tr>
<tr>
<td>31</td>
<td>EL</td>
<td>0.31(^a)</td>
<td>0.33(^b)</td>
<td>0.31(^a)</td>
<td>DON</td>
<td>0.38(^a)</td>
<td>0.44(^b)</td>
<td>0.46(^c)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>KR</td>
<td>0.46(^a)</td>
<td>0.50(^b)</td>
<td>0.52(^c)</td>
</tr>
<tr>
<td>62</td>
<td>EL</td>
<td>0.40(^a)</td>
<td>0.40(^b)</td>
<td>0.39(^a)</td>
<td>DON</td>
<td>0.47(^a)</td>
<td>0.51(^b)</td>
<td>0.51(^c)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>KR</td>
<td>0.53(^a)</td>
<td>0.56(^b)</td>
<td>0.58(^c)</td>
</tr>
<tr>
<td>95</td>
<td>EL</td>
<td>0.44(^a)</td>
<td>0.46(^b)</td>
<td>0.43(^a)</td>
<td>DON</td>
<td>0.51(^a)</td>
<td>0.53(^b)</td>
<td>0.53(^b)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>KR</td>
<td>0.56(^a)</td>
<td>0.58(^b)</td>
<td>0.59(^c)</td>
</tr>
</tbody>
</table>

Values shown are average within population prediction accuracies for test individuals, averaged over 100 random estimation-test data splits. Values within a row with common letters are not significantly different at an alpha level of 0.05 in a paired t-test. Standard errors of the averages were < 0.01. \( N_p \) denotes the average number of individuals per population in the training set. The traits were ear length (EL), deoxynivalenol content (DON), Giberella ear rot severity (GER) kernel rows (KR) and kernels per row (KpR)