In the following tables, the second and third column contain the percentage of the 5000 traits for which the corresponding heritability estimates ($\hat{h}_r^2$ and $\hat{h}_m^2$) were contained in the intervals in the first column. The remaining columns show the correlation ($r$) between simulated and predicted genetic effects, averaged over these traits. 20 QTLs were simulated, which explained 50 percent of the genetic variance. Each trait was simulated for a randomly drawn training (200 accessions) and validation set (50 accessions). Genetic effects were predicted using G-BLUP, based on either a mixed model for the individual plants (replicates) or for the genotypic means.

Table S5(a) :  Prediction accuracy ($r$) of G-BLUP for 5000 simulated traits, for the structured regmap population, and a simulated heritability of 0.2.

<table>
<thead>
<tr>
<th>interval</th>
<th>$\hat{h}_r^2$</th>
<th>$\hat{h}_m^2$</th>
<th>$r$ (replicates) Training set</th>
<th>$r$ (means) Training set</th>
<th>$r$ (replicates) Validation set</th>
<th>$r$ (means) Validation set</th>
</tr>
</thead>
<tbody>
<tr>
<td>[0, 0.1)</td>
<td>3.08 %</td>
<td>9.88 %</td>
<td>0.637</td>
<td>0.654</td>
<td>0.216</td>
<td>0.218</td>
</tr>
<tr>
<td>[0.1, 0.3)</td>
<td>93.96 %</td>
<td>76.38 %</td>
<td>0.770</td>
<td>0.770</td>
<td>0.280</td>
<td>0.279</td>
</tr>
<tr>
<td>[0.3, 0.5)</td>
<td>2.96 %</td>
<td>13.52 %</td>
<td>0.816</td>
<td>0.803</td>
<td>0.325</td>
<td>0.313</td>
</tr>
<tr>
<td>[0.5, 0.7)</td>
<td>0 %</td>
<td>0.22 %</td>
<td>0.782</td>
<td>0.782</td>
<td>0.287</td>
<td>0.287</td>
</tr>
<tr>
<td>[0.7, 0.9]</td>
<td>0 %</td>
<td>0 %</td>
<td>0.767</td>
<td>0.763</td>
<td>0.279</td>
<td>0.278</td>
</tr>
<tr>
<td>[0, 1]</td>
<td>100 %</td>
<td>100 %</td>
<td>0.767</td>
<td>0.763</td>
<td>0.279</td>
<td>0.278</td>
</tr>
</tbody>
</table>

Table S5(b) :  Prediction accuracy ($r$) of G-BLUP for 5000 simulated traits, for the structured regmap population and a simulated heritability of 0.5.

<table>
<thead>
<tr>
<th>interval</th>
<th>$\hat{h}_r^2$</th>
<th>$\hat{h}_m^2$</th>
<th>$r$ (replicates) Training set</th>
<th>$r$ (means) Training set</th>
<th>$r$ (replicates) Validation set</th>
<th>$r$ (means) Validation set</th>
</tr>
</thead>
<tbody>
<tr>
<td>[0, 0.1)</td>
<td>0 %</td>
<td>0.04 %</td>
<td>0.709</td>
<td>0.709</td>
<td>0.328</td>
<td>0.328</td>
</tr>
<tr>
<td>[0.1, 0.3)</td>
<td>0 %</td>
<td>5.24 %</td>
<td>0.836</td>
<td>0.836</td>
<td>0.269</td>
<td>0.269</td>
</tr>
<tr>
<td>[0.3, 0.5)</td>
<td>51.42 %</td>
<td>46.54 %</td>
<td>0.886</td>
<td>0.887</td>
<td>0.302</td>
<td>0.302</td>
</tr>
<tr>
<td>[0.5, 0.7)</td>
<td>48.58 %</td>
<td>42.12 %</td>
<td>0.905</td>
<td>0.903</td>
<td>0.333</td>
<td>0.337</td>
</tr>
<tr>
<td>[0.7, 0.9)</td>
<td>0 %</td>
<td>5.84 %</td>
<td>0.905</td>
<td>0.905</td>
<td>0.343</td>
<td>0.343</td>
</tr>
<tr>
<td>[0.9, 1]</td>
<td>0 %</td>
<td>0.22 %</td>
<td>0.888</td>
<td>0.888</td>
<td>0.386</td>
<td>0.386</td>
</tr>
<tr>
<td>[0, 1]</td>
<td>100 %</td>
<td>100 %</td>
<td>0.895</td>
<td>0.892</td>
<td>0.317</td>
<td>0.317</td>
</tr>
</tbody>
</table>

Table S5(c) :  Prediction accuracy ($r$) of G-BLUP for 5000 simulated traits, for the structured regmap population and a simulated heritability of 0.8.

<table>
<thead>
<tr>
<th>interval</th>
<th>$\hat{h}_r^2$</th>
<th>$\hat{h}_m^2$</th>
<th>$r$ (replicates) Training set</th>
<th>$r$ (means) Training set</th>
<th>$r$ (replicates) Validation set</th>
<th>$r$ (means) Validation set</th>
</tr>
</thead>
<tbody>
<tr>
<td>[0, 0.1)</td>
<td>0 %</td>
<td>0 %</td>
<td>0.877</td>
<td>0.877</td>
<td>0.299</td>
<td>0.299</td>
</tr>
<tr>
<td>[0.1, 0.3)</td>
<td>0 %</td>
<td>0.02 %</td>
<td>0.930</td>
<td>0.930</td>
<td>0.283</td>
<td>0.283</td>
</tr>
<tr>
<td>[0.3, 0.5)</td>
<td>0 %</td>
<td>1.42 %</td>
<td>0.955</td>
<td>0.955</td>
<td>0.400</td>
<td>0.400</td>
</tr>
<tr>
<td>[0.5, 0.7)</td>
<td>0.04 %</td>
<td>19.26 %</td>
<td>0.964</td>
<td>0.964</td>
<td>0.343</td>
<td>0.344</td>
</tr>
<tr>
<td>[0.7, 0.9)</td>
<td>99.96 %</td>
<td>59.26 %</td>
<td>0.965</td>
<td>0.965</td>
<td>0.365</td>
<td>0.365</td>
</tr>
<tr>
<td>[0.9, 1]</td>
<td>0 %</td>
<td>20.04 %</td>
<td>0.962</td>
<td>0.962</td>
<td>0.343</td>
<td>0.343</td>
</tr>
<tr>
<td>[0, 1]</td>
<td>100 %</td>
<td>100 %</td>
<td>0.964</td>
<td>0.964</td>
<td>0.343</td>
<td>0.343</td>
</tr>
</tbody>
</table>
Table S5(d): Prediction accuracy \( (r) \) of G-BLUP for 5000 simulated traits, for the HapMap population and a simulated heritability of 0.2.

<table>
<thead>
<tr>
<th>interval</th>
<th>( h_r^2 )</th>
<th>( h_m^2 )</th>
<th>( r ) (replicates)</th>
<th>( r ) (means)</th>
</tr>
</thead>
<tbody>
<tr>
<td>([0, 0.1)]</td>
<td>(1.74%)</td>
<td>(28.64%)</td>
<td>0.616</td>
<td>0.632</td>
</tr>
<tr>
<td>([0.1, 0.3)]</td>
<td>(96.7%)</td>
<td>(40.7%)</td>
<td>0.673</td>
<td>0.674</td>
</tr>
<tr>
<td>([0.3, 0.5)]</td>
<td>(1.56%)</td>
<td>(17.8%)</td>
<td>0.711</td>
<td>0.684</td>
</tr>
<tr>
<td>([0.5, 0.7)]</td>
<td>(0%)</td>
<td>(5.8%)</td>
<td>0.681</td>
<td>0.364</td>
</tr>
<tr>
<td>([0.7, 0.9)]</td>
<td>(0%)</td>
<td>(2.84%)</td>
<td>0.675</td>
<td>0.362</td>
</tr>
<tr>
<td>([0.9, 1]]</td>
<td>(0%)</td>
<td>(4.22%)</td>
<td>0.669</td>
<td>0.357</td>
</tr>
<tr>
<td>([0, 1]]</td>
<td>(100%)</td>
<td>(100%)</td>
<td>0.672</td>
<td>0.664</td>
</tr>
</tbody>
</table>

Table S5(e): Prediction accuracy \( (r) \) of G-BLUP for 5000 simulated traits, for the HapMap population and a simulated heritability of 0.5.

<table>
<thead>
<tr>
<th>interval</th>
<th>( h_r^2 )</th>
<th>( h_m^2 )</th>
<th>( r ) (replicates)</th>
<th>( r ) (means)</th>
</tr>
</thead>
<tbody>
<tr>
<td>([0, 0.1)]</td>
<td>(0%)</td>
<td>(6%)</td>
<td>0.811</td>
<td>0.851</td>
</tr>
<tr>
<td>([0.1, 0.3)]</td>
<td>(0%)</td>
<td>(21.02%)</td>
<td>0.862</td>
<td>0.867</td>
</tr>
<tr>
<td>([0.3, 0.5)]</td>
<td>(51.78%)</td>
<td>(22.56%)</td>
<td>0.877</td>
<td>0.871</td>
</tr>
<tr>
<td>([0.5, 0.7)]</td>
<td>(48.22%)</td>
<td>(17.5%)</td>
<td>0.873</td>
<td>0.416</td>
</tr>
<tr>
<td>([0.7, 0.9)]</td>
<td>(0%)</td>
<td>(10.86%)</td>
<td>0.871</td>
<td>0.426</td>
</tr>
<tr>
<td>([0.9, 1]]</td>
<td>(0%)</td>
<td>(22.06%)</td>
<td>0.869</td>
<td>0.422</td>
</tr>
<tr>
<td>([0, 1]]</td>
<td>(100%)</td>
<td>(100%)</td>
<td>0.863</td>
<td>0.405</td>
</tr>
</tbody>
</table>

Table S5(f) (given as Table 6 in the main text): Prediction accuracy \( (r) \) of G-BLUP for 5000 simulated traits, for the HapMap population and a simulated heritability of 0.8.

<table>
<thead>
<tr>
<th>interval</th>
<th>( h_r^2 )</th>
<th>( h_m^2 )</th>
<th>( r ) (replicates)</th>
<th>( r ) (means)</th>
</tr>
</thead>
<tbody>
<tr>
<td>([0, 0.1)]</td>
<td>(0%)</td>
<td>(2.58%)</td>
<td>0.890</td>
<td>0.890</td>
</tr>
<tr>
<td>([0.1, 0.3)]</td>
<td>(0%)</td>
<td>(8.34%)</td>
<td>0.937</td>
<td>0.937</td>
</tr>
<tr>
<td>([0.3, 0.5)]</td>
<td>(0%)</td>
<td>(12.34%)</td>
<td>0.954</td>
<td>0.954</td>
</tr>
<tr>
<td>([0.5, 0.7)]</td>
<td>(0.04%)</td>
<td>(15.9%)</td>
<td>0.942</td>
<td>0.959</td>
</tr>
<tr>
<td>([0.7, 0.9)]</td>
<td>(99.96%)</td>
<td>(15.62%)</td>
<td>0.961</td>
<td>0.961</td>
</tr>
<tr>
<td>([0.9, 1]]</td>
<td>(0%)</td>
<td>(45.22%)</td>
<td>0.961</td>
<td>0.431</td>
</tr>
<tr>
<td>([0, 1]]</td>
<td>(100%)</td>
<td>(100%)</td>
<td>0.956</td>
<td>0.431</td>
</tr>
</tbody>
</table>