**Table S1.** The accuracy of genomic prediction for days to 100 kg (AGE) with different QTL lengths as prior information on GFBLUP.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL length(kb) | SNP number | ref | tar | cor | varA | varE | varR | $$h^{2}$$ |
| 100 | 4 | LM+ZX | LM | 0.633  | 119.780  | 3.408  | 42.857  | 0.742  |
| 500 | 1217 | LM+ZX | LM | 0.638  | 120.153  | 0.000  | 43.046  | 0.736  |
| 1000 | 1217 | LM+ZX | LM | 0.638  | 120.153  | 0.000  | 43.046  | 0.736  |
| 100 | 4 | ZX | LM | 0.164  | 44.916  | 0.000  | 19.678  | 0.695  |
| 500 | 1217 | ZX | LM | 0.155  | 43.111  | 2.603  | 20.102  | 0.695  |
| 1000 | 1217 | ZX | LM | 0.155  | 43.111  | 2.603  | 20.102  | 0.695  |
| 100 | 4 | LM | LM | 0.637  | 136.726  | 4.268  | 44.720  | 0.759  |
| 500 | 1217 | LM | LM | 0.642  | 137.728  | 0.000  | 44.817  | 0.754  |
| 1000 | 1217 | LM | LM | 0.642  | 137.728  | 0.000  | 44.817  | 0.754  |

ref: reference population; tar: validation population;

cor: accuracy of genomic prediction;

varA: variance components accounted for by the remaining genome;

varE: variance components accounted for by the variants in the genomic feature;

varR: residual variance component.