**Table S5.** The accuracy of genomic prediction for days to 100 kg (AGE) with different p values of GWAS as prior information on GFBLUP.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| p-value | SNP number | ref | tar | cor | varA | varE | varR | $$h^{2}$$ |
| 10-1 | 1408517 | LM+ZX | LM | 0.635  | 0.000  | 90.776  | 40.971  | 0.689  |
| 10-2 | 632538 | LM+ZX | LM | 0.634  | 0.000  | 78.055  | 42.158  | 0.649  |
| 10-3 | 302932 | LM+ZX | LM | 0.633  | 0.000  | 73.053  | 43.607  | 0.626  |
| 10-4 | 148881 | LM+ZX | LM | 0.625  | 0.000  | 75.812  | 45.170  | 0.627  |
| 10-5 | 75354 | LM+ZX | LM | 0.624  | 3.414  | 80.803  | 46.315  | 0.645  |
| 10-6 | 39032 | LM+ZX | LM | 0.619  | 10.867  | 85.358  | 46.946  | 0.672  |
| 10-7 | 20529 | LM+ZX | LM | 0.609  | 17.455  | 96.997  | 47.786  | 0.705  |
| 10-8 | 10834 | LM+ZX | LM | 0.601  | 23.187  | 112.684  | 48.352  | 0.738  |
| 10-9 | 5864 | LM+ZX | LM | 0.593  | 27.407  | 156.559  | 48.909  | 0.790  |
| 10-1 | 917617 | ZX | LM | 0.124  | 0.000  | 36.495  | 15.701  | 0.699  |
| 10-2 | 262020 | ZX | LM | 0.059  | 0.000  | 36.190  | 15.654  | 0.698  |
| 10-3 | 80115 | ZX | LM | -0.014  | 0.000  | 44.784  | 16.549  | 0.730  |
| 10-4 | 27385 | ZX | LM | -0.060  | 2.942  | 58.713  | 17.233  | 0.782  |
| 10-5 | 10898 | ZX | LM | -0.079  | 6.074  | 78.964  | 18.863  | 0.818  |
| 10-6 | 4148 | ZX | LM | -0.052  | 10.052  | 120.528  | 21.670  | 0.858  |
| 10-7 | 1945 | ZX | LM | -0.046  | 8.544  | 291.761  | 23.857  | 0.926  |
| 10-8 | 808 | ZX | LM | -0.056  | 14.411  | 546.162  | 23.875  | 0.959  |
| 10-9 | 449 | ZX | LM | 0.020  | 24.354  | 548.090  | 25.216  | 0.958  |
| 10-1 | 1356489 | LM | LM | 0.640  | 0.000  | 103.575  | 42.724  | 0.708  |
| 10-2 | 593467 | LM | LM | 0.636  | 0.000  | 90.614  | 43.748  | 0.674  |
| 10-3 | 280508 | LM | LM | 0.631  | 0.000  | 86.396  | 45.363  | 0.656  |
| 10-4 | 137439 | LM | LM | 0.626  | 2.735  | 82.573  | 47.148  | 0.644  |
| 10-5 | 66663 | LM | LM | 0.621  | 12.041  | 78.885  | 47.153  | 0.659  |
| 10-6 | 32921 | LM | LM | 0.619  | 20.780  | 83.643  | 47.712  | 0.686  |
| 10-7 | 16514 | LM | LM | 0.608  | 29.777  | 86.696  | 49.091  | 0.703  |
| 10-8 | 8763 | LM | LM | 0.595  | 37.008  | 84.311  | 50.390  | 0.707  |
| 10-9 | 4287 | LM | LM | 0.581  | 48.223  | 89.379  | 50.008  | 0.733  |

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.