**Table S6.** The accuracy of genomic prediction for backfat thickness (BFT) 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 | 1212905 | LM+ZX | LM | 0.446  | 0.000  | 3.047  | 1.479  | 0.673  |
| 10-2 | 458875 | LM+ZX | LM | 0.437  | 0.000  | 2.723  | 1.495  | 0.646  |
| 10-3 | 186030 | LM+ZX | LM | 0.422  | 0.000  | 2.607  | 1.535  | 0.629  |
| 10-4 | 78470 | LM+ZX | LM | 0.405  | 0.034  | 2.593  | 1.571  | 0.626  |
| 10-5 | 32059 | LM+ZX | LM | 0.394  | 0.325  | 2.413  | 1.583  | 0.634  |
| 10-6 | 12642 | LM+ZX | LM | 0.395  | 0.428  | 2.606  | 1.613  | 0.653  |
| 10-7 | 4929 | LM+ZX | LM | 0.415  | 0.532  | 2.917  | 1.650  | 0.676  |
| 10-8 | 1820 | LM+ZX | LM | 0.452  | 0.663  | 3.691  | 1.696  | 0.720  |
| 10-9 | 618 | LM+ZX | LM | 0.433  | 1.134  | 2.945  | 1.735  | 0.702  |
| 10-1 | 1028035 | ZX | LM | 0.119  | 0.000  | 1.348  | 0.342  | 0.797  |
| 10-2 | 344848 | ZX | LM | 0.057  | 0.000  | 1.392  | 0.394  | 0.779  |
| 10-3 | 117607 | ZX | LM | 0.045  | 0.000  | 1.499  | 0.459  | 0.766  |
| 10-4 | 41558 | ZX | LM | 0.047  | 0.000  | 1.745  | 0.511  | 0.773  |
| 10-5 | 14980 | ZX | LM | 0.080  | 0.039  | 1.993  | 0.537  | 0.791  |
| 10-6 | 5162 | ZX | LM | 0.067  | 0.113  | 2.763  | 0.511  | 0.849  |
| 10-7 | 1965 | ZX | LM | 0.037  | 0.152  | 4.134  | 0.544  | 0.887  |
| 10-8 | 747 | ZX | LM | 0.055  | 0.343  | 4.381  | 0.575  | 0.891  |
| 10-9 | 98 | ZX | LM | -0.037  | 0.403  | 2.040  | 0.657  | 0.788  |
| 10-1 | 1239324 | LM | LM | 0.437  | 0.000  | 3.653  | 1.576  | 0.699  |
| 10-2 | 479616 | LM | LM | 0.433  | 0.000  | 3.318  | 1.592  | 0.676  |
| 10-3 | 197903 | LM | LM | 0.432  | 0.000  | 3.281  | 1.639  | 0.667  |
| 10-4 | 82603 | LM | LM | 0.416  | 0.140  | 3.129  | 1.683  | 0.660  |
| 10-5 | 33448 | LM | LM | 0.421  | 0.508  | 2.852  | 1.685  | 0.666  |
| 10-6 | 13835 | LM | LM | 0.432  | 0.593  | 3.356  | 1.698  | 0.699  |
| 10-7 | 5380 | LM | LM | 0.444  | 0.717  | 4.838  | 1.744  | 0.761  |
| 10-8 | 2403 | LM | LM | 0.439  | 0.737  | 8.745  | 1.815  | 0.839  |
| 10-9 | 1112 | LM | LM | 0.419  | 1.002  | 15.030  | 1.919  | 0.893  |

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.