**Table S2.** The accuracy of genomic prediction for backfat thickness (BFT) with different QTL lengths as prior information on GFBLUP.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL length(kb) | SNP number | ref | tar | cor | varA | varE | varR | $$h^{2}$$ |
| 100 | 2738 | LM+ZX | LM | 0.443  | 3.592  | 0.083  | 1.690  | 0.685  |
| 500 | 26981 | LM+ZX | LM | 0.442  | 3.360  | 0.304  | 1.697  | 0.683  |
| 1000 | 81092 | LM+ZX | LM | 0.443  | 3.678  | 0.000  | 1.688  | 0.685  |
| 100 | 2738 | ZX | LM | 0.142  | 1.634  | 0.000  | 0.391  | 0.807  |
| 500 | 26981 | ZX | LM | 0.144  | 1.631  | 0.003  | 0.392  | 0.807  |
| 1000 | 81092 | ZX | LM | 0.137  | 1.637  | 0.000  | 0.391  | 0.807  |
| 100 | 2738 | LM | LM | 0.444  | 4.146  | 0.178  | 1.794  | 0.707  |
| 500 | 26981 | LM | LM | 0.444  | 4.087  | 0.199  | 1.801  | 0.704  |
| 1000 | 81092 | LM | LM | 0.443  | 4.322  | 0.000  | 1.790  | 0.707  |

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.