**Table S3.** The accuracy of genomic prediction for number of piglets born alive (NBA) with different QTL lengths as prior information on GFBLUP.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| QTL length(kb) | SNP number | ref | tar | cor | varA | varE | varR | $$h^{2}$$ |
| 100 | 1545 | LM+XD | LM | 0.478  | 1.198  | 0.039  | 0.457  | 0.730  |
| 500 | 15714 | LM+XD | LM | 0.472  | 1.233  | 0.000  | 0.455  | 0.730  |
| 1000 | 21017 | LM+XD | LM | 0.472  | 1.234  | 0.000  | 0.455  | 0.731  |
| 100 | 1545 | LM+XD | XD | 0.407  | 1.198  | 0.039  | 0.457  | 0.730  |
| 500 | 15714 | LM+XD | XD | 0.403  | 1.233  | 0.000  | 0.455  | 0.730  |
| 1000 | 21017 | LM+XD | XD | 0.403  | 1.234  | 0.000  | 0.455  | 0.731  |
| 100 | 1545 | XD | LM | -0.018  | 0.598  | 0.000  | 0.227  | 0.725  |
| 500 | 15714 | XD | LM | -0.022  | 0.584  | 0.017  | 0.227  | 0.726  |
| 1000 | 21017 | XD | LM | -0.017  | 0.598  | 0.000  | 0.227  | 0.725  |
| 100 | 1545 | XD | XD | 0.396  | 0.598  | 0.000  | 0.227  | 0.725  |
| 500 | 15714 | XD | XD | 0.398  | 0.584  | 0.017  | 0.227  | 0.726  |
| 1000 | 21017 | XD | XD | 0.395  | 0.598  | 0.000  | 0.227  | 0.725  |
| 100 | 1545 | LM | LM | 0.473  | 1.578  | 0.016  | 0.502  | 0.761  |
| 500 | 15714 | LM | LM | 0.470  | 1.598  | 0.000  | 0.500  | 0.762  |
| 1000 | 21017 | LM | LM | 0.470  | 1.600  | 0.000  | 0.500  | 0.762  |
| 100 | 1545 | LM | XD | 0.163  | 1.578  | 0.016  | 0.502  | 0.761  |
| 500 | 15714 | LM | XD | 0.160  | 1.598  | 0.000  | 0.500  | 0.762  |
| 1000 | 21017 | LM | XD | 0.160  | 1.600  | 0.000  | 0.500  | 0.762  |

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.