**Table S8.** The accuracy of genomic prediction for total number of piglets born (TNB) 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 | 1419825 | LM+XD | LM | 0.455  | 0.000  | 1.348  | 0.529  | 0.718  |
| 10-2 | 560256 | LM+XD | LM | 0.448  | 0.000  | 1.202  | 0.541  | 0.690  |
| 10-3 | 237134 | LM+XD | LM | 0.435  | 0.000  | 1.161  | 0.567  | 0.672  |
| 10-4 | 106843 | LM+XD | LM | 0.423  | 0.123  | 1.282  | 0.583  | 0.707  |
| 10-5 | 50828 | LM+XD | LM | 0.409  | 0.269  | 1.521  | 0.583  | 0.754  |
| 10-6 | 24754 | LM+XD | LM | 0.405  | 0.402  | 1.817  | 0.584  | 0.792  |
| 10-7 | 12341 | LM+XD | LM | 0.404  | 0.500  | 2.191  | 0.594  | 0.819  |
| 10-8 | 6299 | LM+XD | LM | 0.377  | 0.608  | 2.630  | 0.594  | 0.845  |
| 10-9 | 3025 | LM+XD | LM | 0.359  | 0.700  | 2.505  | 0.620  | 0.838  |
| 10-1 | 1419825 | LM+XD | XD | 0.485  | 0.000  | 1.348  | 0.529  | 0.718  |
| 10-2 | 560256 | LM+XD | XD | 0.494  | 0.000  | 1.202  | 0.541  | 0.690  |
| 10-3 | 237134 | LM+XD | XD | 0.481  | 0.000  | 1.161  | 0.567  | 0.672  |
| 10-4 | 106843 | LM+XD | XD | 0.466  | 0.123  | 1.282  | 0.583  | 0.707  |
| 10-5 | 50828 | LM+XD | XD | 0.469  | 0.269  | 1.521  | 0.583  | 0.754  |
| 10-6 | 24754 | LM+XD | XD | 0.454  | 0.402  | 1.817  | 0.584  | 0.792  |
| 10-7 | 12341 | LM+XD | XD | 0.417  | 0.500  | 2.191  | 0.594  | 0.819  |
| 10-8 | 6299 | LM+XD | XD | 0.409  | 0.608  | 2.630  | 0.594  | 0.845  |
| 10-9 | 3025 | LM+XD | XD | 0.431  | 0.700  | 2.505  | 0.620  | 0.838  |
| 10-1 | 1219182 | XD | LM | -0.064  | 0.000  | 0.639  | 0.179  | 0.781  |
| 10-2 | 402480 | XD | LM | -0.055  | 0.000  | 0.508  | 0.184  | 0.734  |
| 10-3 | 140643 | XD | LM | -0.098  | 0.000  | 0.448  | 0.202  | 0.689  |
| 10-4 | 48583 | XD | LM | -0.109  | 0.000  | 0.388  | 0.230  | 0.628  |
| 10-5 | 17265 | XD | LM | -0.050  | 0.000  | 0.413  | 0.242  | 0.630  |
| 10-6 | 5911 | XD | LM | -0.048  | 0.041  | 0.425  | 0.243  | 0.657  |
| 10-7 | 1904 | XD | LM | -0.049  | 0.080  | 0.355  | 0.253  | 0.632  |
| 10-8 | 649 | XD | LM | 0.009  | 0.066  | 0.384  | 0.288  | 0.609  |
| 10-9 | 221 | XD | LM | -0.123  | 0.076  | 0.543  | 0.321  | 0.659  |
| 10-1 | 1219182 | XD | XD | 0.422  | 0.000  | 0.639  | 0.179  | 0.781  |
| 10-2 | 402480 | XD | XD | 0.420  | 0.000  | 0.508  | 0.184  | 0.734  |
| 10-3 | 140643 | XD | XD | 0.414  | 0.000  | 0.448  | 0.202  | 0.689  |
| 10-4 | 48583 | XD | XD | 0.432  | 0.000  | 0.388  | 0.230  | 0.628  |
| 10-5 | 17265 | XD | XD | 0.425  | 0.000  | 0.413  | 0.242  | 0.630  |
| 10-6 | 5911 | XD | XD | 0.398  | 0.041  | 0.425  | 0.243  | 0.657  |
| 10-7 | 1904 | XD | XD | 0.404  | 0.080  | 0.355  | 0.253  | 0.632  |
| 10-8 | 649 | XD | XD | 0.389  | 0.066  | 0.384  | 0.288  | 0.609  |
| 10-9 | 221 | XD | XD | 0.369  | 0.076  | 0.543  | 0.321  | 0.659  |
| 10-1 | 1410194 | LM | LM | 0.458  | 0.000  | 1.789  | 0.598  | 0.750  |
| 10-2 | 544820 | LM | LM | 0.459  | 0.000  | 1.632  | 0.612  | 0.727  |
| 10-3 | 226150 | LM | LM | 0.439  | 0.038  | 1.603  | 0.649  | 0.717  |
| 10-4 | 99201 | LM | LM | 0.417  | 0.301  | 1.765  | 0.655  | 0.759  |
| 10-5 | 47437 | LM | LM | 0.401  | 0.437  | 2.260  | 0.654  | 0.805  |
| 10-6 | 22383 | LM | LM | 0.400  | 0.558  | 2.880  | 0.658  | 0.839  |
| 10-7 | 11496 | LM | LM | 0.403  | 0.689  | 3.608  | 0.664  | 0.866  |
| 10-8 | 4506 | LM | LM | 0.394  | 0.830  | 3.138  | 0.689  | 0.852  |
| 10-9 | 1864 | LM | LM | 0.405  | 0.878  | 2.876  | 0.711  | 0.841  |
| 10-1 | 1410194 | LM | XD | 0.267  | 0.000  | 1.789  | 0.598  | 0.750  |
| 10-2 | 544820 | LM | XD | 0.273  | 0.000  | 1.632  | 0.612  | 0.727  |
| 10-3 | 226150 | LM | XD | 0.282  | 0.038  | 1.603  | 0.649  | 0.717  |
| 10-4 | 99201 | LM | XD | 0.228  | 0.301  | 1.765  | 0.655  | 0.759  |
| 10-5 | 47437 | LM | XD | 0.199  | 0.437  | 2.260  | 0.654  | 0.805  |
| 10-6 | 22383 | LM | XD | 0.130  | 0.558  | 2.880  | 0.658  | 0.839  |
| 10-7 | 11496 | LM | XD | 0.048  | 0.689  | 3.608  | 0.664  | 0.866  |
| 10-8 | 4506 | LM | XD | 0.013  | 0.830  | 3.138  | 0.689  | 0.852  |
| 10-9 | 1864 | LM | XD | 0.028  | 0.878  | 2.876  | 0.711  | 0.841  |

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.