

Table S1. The mean accuracy and standard error of genomic prediction from a five-fold cross-validation using seven models

Model	BL	BH	CC	WC	AC	LMA	LMD	BF
GBLUP	0.499 (0.002)	0.474 (0.001)	0.494 (0.001)	0.497 (0.001)	0.491 (0.003)	0.421 (0.006)	0.432 (0.005)	0.369 (0.004)
ssGBLUP	0.502 (0.002)	0.477 (0.001)	0.497 (0.001)	0.499 (0.001)	0.494 (0.003)	0.422 (0.006)	0.434 (0.005)	0.371 (0.004)
BayesA	0.498 (0.002)	0.473 (0.001)	0.494 (0.001)	0.497 (0.001)	0.492 (0.003)	0.418 (0.006)	0.429 (0.005)	0.366 (0.003)
BayesB	0.499 (0.002)	0.474 (0.001)	0.495 (0.001)	0.497 (0.001)	0.492 (0.003)	0.419 (0.006)	0.430 (0.005)	0.368 (0.004)
BayesC	0.499 (0.002)	0.474 (0.001)	0.494 (0.001)	0.497 (0.001)	0.491 (0.003)	0.419 (0.006)	0.431 (0.005)	0.369 (0.004)
Bayesian LASSO	0.498 (0.002)	0.474 (0.001)	0.494 (0.001)	0.496 (0.001)	0.490 (0.003)	0.418 (0.006)	0.428 (0.004)	0.366 (0.004)
BayesR	0.499 (0.002)	0.475 (0.001)	0.495 (0.001)	0.497 (0.001)	0.491 (0.003)	0.419 (0.006)	0.431 (0.005)	0.368 (0.004)