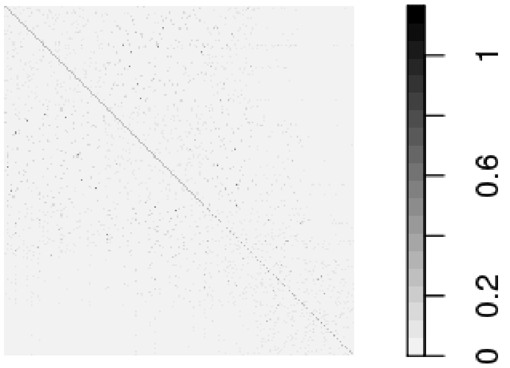

Figure S1 Pedigree relationship heat map of the 2000 reference (top left) and 1500 validation (bottom left) individuals in replicate 1 of the simulated dataset

Table S1 Accuracy of genomic prediction in simulated data estimated with different methods, where PLS is Partial Least Squares, BayesSSVS is Bayesian Stochastic Search Variable Selection, RR-BLUP is Ridge Regression, and BLUP (GBLUP) is (Genomic) Best Linear Unbiased Prediction.

Trait 1

	All Generations		Generation 6		Generation 8		Generation 10	
Method	cor	se	cor	se	cor	se	cor	se
Mean Genomic	0.449	0.002	0.551	0.003	0.418	0.003	0.360	0.002
PLS	0.431	0.011	0.530	0.011	0.398	0.016	0.348	0.015
BayesSSVS	0.449	0.013	0.550	0.014	0.419	0.019	0.361	0.016
BayesC	0.452	0.013	0.554	0.013	0.422	0.018	0.362	0.016
BayesB1	0.451	0.013	0.553	0.012	0.420	0.018	0.362	0.016
BayesA1	0.453	0.013	0.555	0.013	0.422	0.018	0.363	0.016
Lasso1	0.453	0.013	0.555	0.013	0.422	0.018	0.363	0.016
Lasso2	0.453	0.013	0.555	0.013	0.422	0.018	0.363	0.016
RR-BLUP	0.453	0.013	0.555	0.013	0.422	0.018	0.363	0.016
GBLUP	0.448	0.013	0.552	0.013	0.418	0.018	0.352	0.017
BLUP	0.290	0.014	0.440	0.020	0.212	0.025	0.110	0.023

Trait 2

	All Generations		Generation 6		Generation 8		Generation 10	
Method	cor	se	cor	se	cor	se	cor	se
Mean Genomic	0.483	0.017	0.580	0.012	0.447	0.019	0.401	0.022
PLS	0.424	0.011	0.527	0.014	0.387	0.021	0.331	0.016
BayesSSVS	0.517	0.027	0.603	0.020	0.489	0.040	0.448	0.029
BayesC	0.542	0.027	0.624	0.020	0.511	0.038	0.481	0.030
BayesB1	0.544	0.027	0.624	0.021	0.517	0.038	0.482	0.029
BayesA1	0.539	0.028	0.621	0.021	0.510	0.038	0.472	0.031
Lasso1	0.447	0.013	0.558	0.012	0.405	0.023	0.352	0.017
Lasso2	0.447	0.013	0.557	0.012	0.405	0.023	0.351	0.016
RR-BLUP	0.447	0.016	0.558	0.013	0.405	0.026	0.354	0.020
GBLUP	0.437	0.011	0.551	0.010	0.392	0.021	0.337	0.019
BLUP	0.297	0.016	0.463	0.011	0.206	0.030	0.099	0.019

Trait 3

	All Generations		Generation 6		Generation 8		Generation 10	
Method	cor	se	cor	se	cor	se	cor	se
Mean Genomic	0.386	0.003	0.484	0.005	0.339	0.002	0.306	0.003
PLS	0.366	0.009	0.447	0.016	0.325	0.018	0.304	0.018
BayesSSVS	0.378	0.010	0.480	0.015	0.333	0.021	0.290	0.016
BayesC	0.390	0.010	0.490	0.015	0.343	0.020	0.308	0.017
BayesB1	0.383	0.009	0.483	0.015	0.338	0.020	0.298	0.015
BayesA1	0.388	0.010	0.488	0.015	0.342	0.020	0.305	0.018
Lasso1	0.390	0.010	0.490	0.015	0.342	0.020	0.309	0.018
Lasso2	0.390	0.010	0.490	0.015	0.342	0.020	0.309	0.018
RR-BLUP	0.390	0.010	0.490	0.015	0.342	0.020	0.309	0.018
GBLUP	0.398	0.010	0.497	0.014	0.347	0.019	0.323	0.017
BLUP	0.257	0.010	0.406	0.015	0.160	0.025	0.094	0.028

Trait 4

	All Generations		Generation 6		Generation 8		Generation 10	
Method	cor	se	cor	se	cor	se	cor	se
Mean Genomic	0.448	0.016	0.559	0.013	0.409	0.016	0.339	0.021
PLS	0.391	0.017	0.507	0.018	0.350	0.028	0.273	0.012

BayesSSVS	0.480	0.014	0.586	0.012	0.442	0.027	0.381	0.018
BayesC	0.505	0.017	0.604	0.011	0.470	0.031	0.413	0.023
BayesB1	0.504	0.016	0.605	0.012	0.466	0.029	0.416	0.022
BayesA1	0.495	0.019	0.596	0.014	0.458	0.033	0.402	0.023
Lasso1	0.412	0.017	0.532	0.018	0.372	0.027	0.289	0.014
Lasso2	0.411	0.017	0.532	0.018	0.372	0.027	0.289	0.014
RR-BLUP	0.413	0.017	0.533	0.018	0.373	0.027	0.290	0.014
GBLUP	0.418	0.016	0.537	0.018	0.376	0.027	0.298	0.013
BLUP	0.287	0.017	0.449	0.019	0.204	0.027	0.043	0.029

Table S2 Slope of regression of true on predicted breeding values in simulated data estimated with different methods, where PLS is Partial Least Squares, BayesSSVS is Bayesian Stochastic Search Variable Selection, RR-BLUP is Ridge Regression, and BLUP (GBLUP) is Genomic Best Linear Unbiased Prediction.

Trait 1

	All Generations		Generation 6		Generation 8		Generation 10	
Method	slope	se	slope	se	slope	se	slope	se
Mean Genomic	1.028	0.065	1.023	0.065	1.057	0.067	1.008	0.063
PLS	0.519	0.014	0.513	0.015	0.534	0.019	0.519	0.023
BayesSSVS	1.202	0.068	1.186	0.058	1.243	0.078	1.192	0.089
BayesC	1.057	0.044	1.058	0.040	1.083	0.051	1.030	0.058
BayesB1	1.062	0.043	1.063	0.038	1.087	0.050	1.035	0.058
BayesA1	1.071	0.045	1.071	0.041	1.096	0.050	1.046	0.057
Lasso1	1.085	0.047	1.083	0.041	1.112	0.054	1.061	0.062
Lasso2	1.078	0.044	1.076	0.038	1.105	0.052	1.053	0.060
RR-BLUP	1.082	0.044	1.080	0.040	1.109	0.052	1.059	0.059
GBLUP	1.093	0.048	1.074	0.041	1.140	0.056	1.081	0.067
BLUP	1.018	0.057	1.002	0.044	1.036	0.133	1.059	0.212

Trait 2

	All Generations		Generation 6		Generation 8		Generation 10	
Method	slope	se	slope	se	slope	se	slope	se
Mean Genomic	0.961	0.059	0.953	0.059	0.958	0.058	0.966	0.061
PLS	0.503	0.013	0.493	0.015	0.511	0.032	0.504	0.026
BayesSSVS	1.006	0.095	0.981	0.077	1.012	0.110	1.038	0.124
BayesC	1.039	0.049	1.022	0.036	1.036	0.064	1.066	0.077
BayesB1	1.049	0.041	1.031	0.030	1.051	0.059	1.072	0.065
BayesA1	1.051	0.043	1.030	0.030	1.054	0.062	1.070	0.068
Lasso1	1.032	0.045	1.035	0.031	1.020	0.063	1.015	0.084
Lasso2	1.040	0.044	1.044	0.032	1.028	0.060	1.022	0.081
RR-BLUP	0.902	0.078	0.915	0.062	0.886	0.091	0.883	0.111
GBLUP	1.030	0.045	1.021	0.031	1.029	0.064	1.028	0.096
BLUP	1.041	0.051	1.059	0.048	0.960	0.114	0.880	0.149

Trait 3

	All Generations		Generation 6		Generation 8		Generation 10	
Method	slope	se	slope	se	slope	se	slope	se
Mean Genomic	0.887	0.058	0.912	0.061	0.854	0.056	0.871	0.055
PLS	0.429	0.013	0.429	0.019	0.413	0.024	0.449	0.031
BayesSSVS	0.988	0.062	1.030	0.049	0.963	0.107	0.932	0.077
BayesC	0.924	0.042	0.953	0.039	0.888	0.081	0.901	0.059
BayesB1	0.902	0.043	0.942	0.041	0.870	0.083	0.854	0.046
BayesA1	0.923	0.046	0.954	0.039	0.892	0.085	0.894	0.067
Lasso1	0.949	0.043	0.977	0.040	0.910	0.082	0.932	0.065
Lasso2	0.946	0.041	0.973	0.038	0.906	0.080	0.931	0.063
RR-BLUP	0.946	0.045	0.973	0.041	0.908	0.082	0.931	0.068
GBLUP	0.973	0.042	0.973	0.036	0.934	0.078	1.017	0.065
BLUP	0.896	0.053	0.925	0.036	0.764	0.132	0.951	0.289

Trait 4

	All Generations		Generation 6		Generation 8		Generation 10	
Method	slope	se	slope	se	slope	se	slope	se
Mean								
Genomic	0.929	0.061	0.985	0.064	0.893	0.058	0.855	0.059
PLS	0.454	0.026	0.481	0.022	0.440	0.044	0.410	0.027
BayesSSVS	1.091	0.056	1.142	0.067	1.055	0.072	1.033	0.055
BayesC	0.960	0.038	1.014	0.042	0.931	0.061	0.894	0.035
BayesB1	0.963	0.035	1.019	0.040	0.929	0.063	0.903	0.034
BayesA1	1.005	0.036	1.050	0.047	0.968	0.059	0.959	0.039
Lasso1	0.969	0.043	1.043	0.056	0.925	0.059	0.862	0.048
Lasso2	0.967	0.049	1.041	0.061	0.925	0.067	0.858	0.050
RR-BLUP	0.968	0.041	1.041	0.054	0.925	0.059	0.863	0.048
GBLUP	0.981	0.040	1.030	0.053	0.942	0.059	0.910	0.038
BLUP	0.966	0.053	1.020	0.053	0.895	0.119	0.287	0.259

Table S3 Length of chains, burn-in and hyper-parameters for Bayesian methods.

Method	Length of Chain	Burn-in	π	Effect dist. and parameters
BayesSSVS	100,000	10,000	0.999	Normal Var estimated
BayesC	160,000 5,200,000*	30,000 200,000*	Estimated	Normal Var estimated
BayesB1	160,000 5,200,000*	30,000 200,000*	Estimated	Scaled Student-t df= estimated Scale= estimated
BayesB2	5,200,000*	200,000*	estimated	Scaled Student-t df=4 Scale= estimated
BayesA1	160,000	30,000	-	Scaled Student-t df= estimated Scale= estimated
BayesA2	5,200,000*	200,000*	-	Scaled Student-t df= 4 Scale= estimated
Lasso1	160,000 5,200,000*	30,000 200,000*	-	Laplace rate=estimated
Lasso2	100,000	10,000	-	Laplace
RR-BLUP	100,000	10,000	0.0	Normal Var estimated

* chain used for analysis of pine and wheat dataset