

File S1

Additional description of populations and genomic patterns

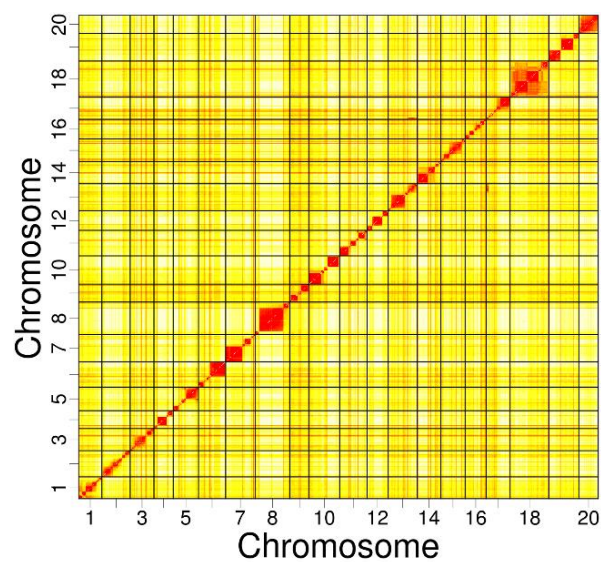


Fig. 1 SNP panel pairwise linkage disequilibrium among the 4077 markers in terms of r^2 in the SoyNAM population.

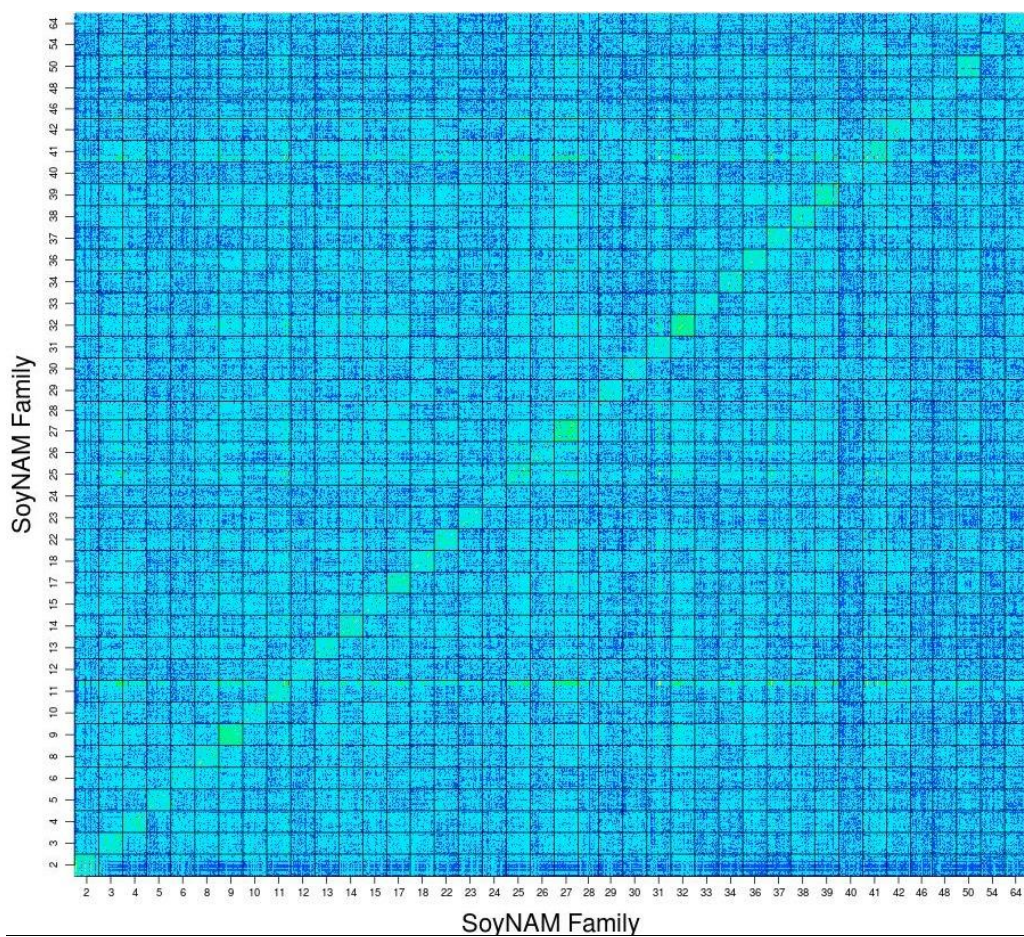


Fig. 2 Heatmap of the genomic relationship matrix of the SoyNAM population with delimitations indicating family.

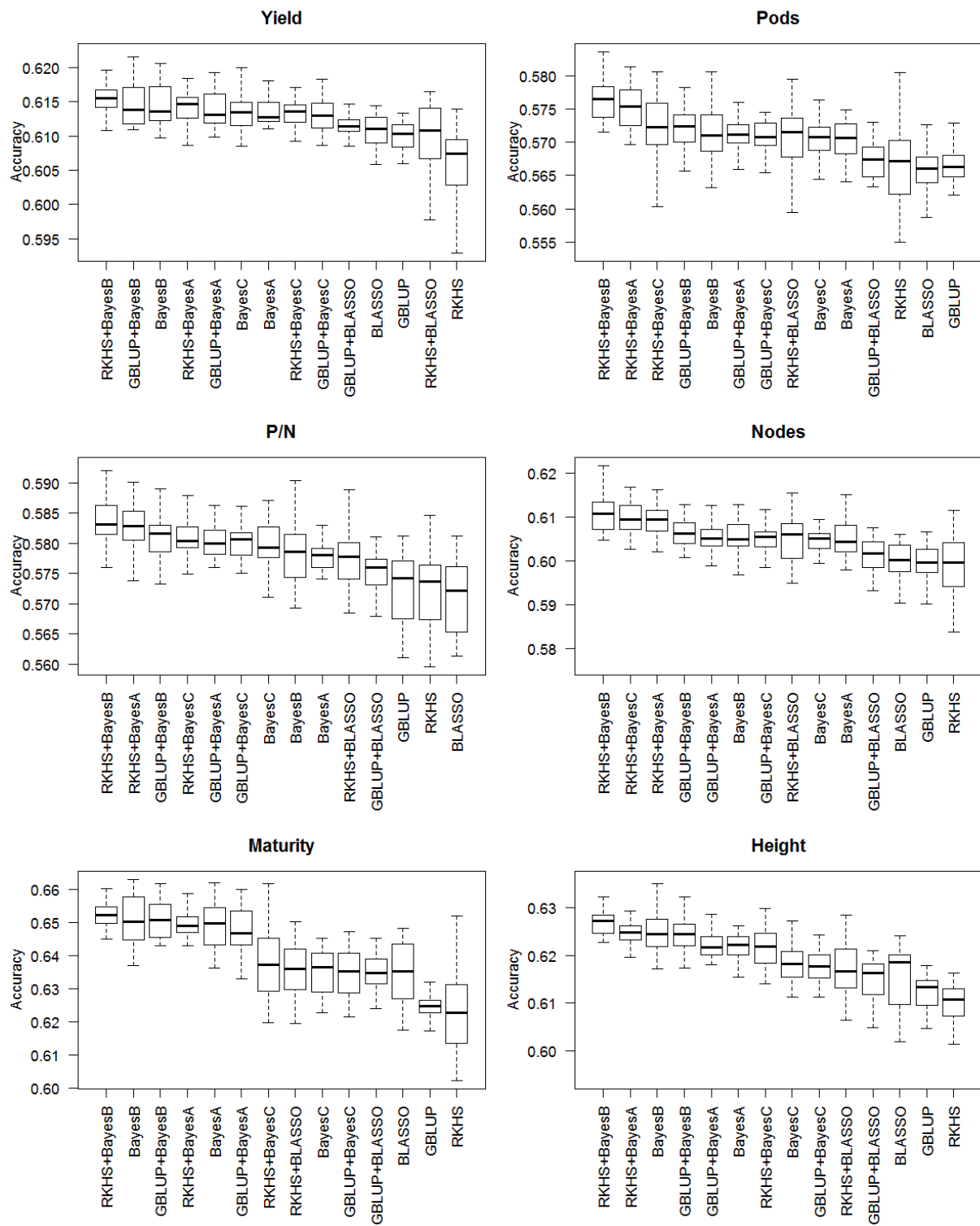


Fig. 3 The boxplot of accuracy of different genomic prediction models in soybeans across different scenarios (ie. combinations of trait, number of SNPs, environment and training population size). Whiskers represent the upper and lower limit, and the box represents the quartiles Q1 (25%), Q2 (median) and Q3 (75%). Models include additive methods (BayesA, BayesB, BayesC, BLASSO), kernel methods (GBLUP, RKHS) and each combination of both.

Table 1 Average accuracy of different prediction models for different soybean traits, comprising plant height (HT), days to maturity (R8), number of reproductive nodes (No), pods per node (PN), number of pods (Po), and grain yield (GY). Models include additive methods (BayesA, BayesB, BayesC, BLASSO), kernel methods (GBLUP, RKHS) and each combination of both.

	GY	Po	PN	No	R8	HT
BayesA	0.613	0.570	0.578	0.605	0.649	0.622
BayesB	0.614	0.572	0.579	0.606	0.651	0.625
BayesC	0.614	0.570	0.580	0.605	0.635	0.618
BLASSO	0.611	0.566	0.571	0.599	0.635	0.615
GBLUP	0.610	0.566	0.572	0.599	0.625	0.612
GBLUP+BayesA	0.614	0.571	0.580	0.606	0.648	0.622
GBLUP+BayesB	0.615	0.572	0.582	0.607	0.651	0.624
GBLUP+BayesC	0.613	0.571	0.580	0.605	0.635	0.618
GBLUP+BLASSO	0.612	0.567	0.575	0.601	0.635	0.615
RKHS	0.606	0.567	0.572	0.598	0.624	0.610
RKHS+BayesA	0.614	0.575	0.583	0.610	0.65	0.625
RKHS+BayesB	0.615	0.576	0.584	0.611	0.652	0.627
RKHS+BayesC	0.613	0.573	0.581	0.610	0.637	0.622
RKHS+BLASSO	0.610	0.571	0.577	0.605	0.636	0.617

Table 2 Average accuracy of different prediction models for different training population sizes in a soybean nested association mapping population. Models include additive methods (BayesA, BayesB, BayesC, BLASSO), kernel methods (GBLUP, RKHS) and each combination of both.

	250	500	1000	2000	3000	4000
BayesA	0.386	0.491	0.603	0.685	0.723	0.749
BayesB	0.389	0.496	0.604	0.685	0.724	0.748
BayesC	0.385	0.492	0.601	0.680	0.719	0.744
BLASSO	0.374	0.481	0.594	0.680	0.721	0.747
GBLUP	0.374	0.481	0.593	0.676	0.716	0.743
GBLUP+BayesA	0.387	0.494	0.603	0.685	0.723	0.749
GBLUP+BayesB	0.390	0.496	0.606	0.686	0.724	0.749
GBLUP+BayesC	0.386	0.492	0.600	0.680	0.719	0.745
GBLUP+BLASSO	0.379	0.486	0.595	0.679	0.720	0.747
RKHS	0.374	0.485	0.593	0.672	0.711	0.741
RKHS+BayesA	0.389	0.497	0.605	0.686	0.725	0.753
RKHS+BayesB	0.391	0.499	0.607	0.687	0.726	0.754
RKHS+BayesC	0.388	0.495	0.602	0.681	0.720	0.749
RKHS+BLASSO	0.380	0.490	0.597	0.678	0.720	0.751

Table 3 Average accuracy of different prediction models for 3 genotyping densities in a soybean nested association mapping population. Models include additive methods (BayesA, BayesB, BayesC, BLASSO), kernel methods (GBLUP, RKHS) and each combination of both.

	1020	2039	4077
BayesA	0.601	0.606	0.611
BayesB	0.602	0.608	0.613
BayesC	0.600	0.605	0.607
BLASSO	0.595	0.600	0.603
GBLUP	0.593	0.599	0.600
GBLUP+BayesA	0.602	0.608	0.611
GBLUP+BayesB	0.603	0.609	0.613
GBLUP+BayesC	0.600	0.605	0.607
GBLUP+BLASSO	0.597	0.602	0.604
RKHS	0.592	0.598	0.598
RKHS+BayesA	0.605	0.611	0.613
RKHS+BayesB	0.606	0.612	0.615
RKHS+BayesC	0.601	0.608	0.609
RKHS+BLASSO	0.599	0.604	0.605

Table 3 Average accuracy of 3 genotyping densities across population size in a soybean nested association mapping population.

	1020	2039	4077
250	0.388	0.388	0.375
500	0.496	0.497	0.480
1000	0.603	0.602	0.596
2000	0.682	0.680	0.683
3000	0.722	0.723	0.717
4000	0.739	0.757	0.747

Table 4 Average predictive ability (standard deviation) of 3 prediction models including BayesB (BB), GBLUP (G) and the combination of both, for grain yield in two years, in a 10-fold cross-validation scheme repeated 20 times, for each SoyNAM family.

Family	2013			2014		
	BB	G	BB+G	BB	G	BB+G
NAM2	0.318 (0.212)	0.337 (0.207)	0.322 (0.200)	0.545 (0.199)	0.549 (0.201)	0.542 (0.210)
NAM3	0.385 (0.209)	0.359 (0.218)	0.368 (0.215)	0.559 (0.178)	0.534 (0.190)	0.551 (0.177)
NAM4	0.246 (0.269)	0.245 (0.262)	0.259 (0.263)	0.134 (0.223)	0.135 (0.226)	0.141 (0.223)
NAM5	0.358 (0.186)	0.372 (0.202)	0.360 (0.191)	0.106 (0.369)	0.107 (0.363)	0.092 (0.374)
NAM6	0.103 (0.209)	0.135 (0.230)	0.110 (0.213)	0.359 (0.150)	0.380 (0.153)	0.359 (0.154)
NAM8	0.258 (0.246)	0.283 (0.234)	0.249 (0.247)	0.433 (0.225)	0.423 (0.222)	0.427 (0.221)
NAM9	0.152 (0.247)	0.154 (0.258)	0.157 (0.242)	0.456 (0.252)	0.473 (0.243)	0.459 (0.241)
NAM10	0.330 (0.181)	0.329 (0.155)	0.338 (0.160)	0.465 (0.182)	0.464 (0.181)	0.461 (0.189)
NAM11	0.506 (0.180)	0.520 (0.178)	0.503 (0.187)	0.336 (0.163)	0.345 (0.158)	0.337 (0.179)
NAM12	0.556 (0.160)	0.549 (0.158)	0.558 (0.163)	0.136 (0.251)	0.112 (0.253)	0.134 (0.242)
NAM13	0.315 (0.248)	0.309 (0.239)	0.317 (0.250)	0.451 (0.154)	0.432 (0.162)	0.443 (0.163)
NAM14	0.292 (0.218)	0.300 (0.207)	0.301 (0.212)	0.224 (0.197)	0.203 (0.207)	0.243 (0.206)
NAM15	0.246 (0.231)	0.257 (0.235)	0.238 (0.234)	0.280 (0.213)	0.268 (0.217)	0.263 (0.214)
NAM17	0.296 (0.288)	0.287 (0.287)	0.300 (0.290)	0.453 (0.157)	0.419 (0.153)	0.442 (0.150)
NAM18	0.199 (0.324)	0.211 (0.303)	0.195 (0.321)	0.075 (0.273)	0.089 (0.259)	0.071 (0.278)
NAM22	0.299 (0.228)	0.279 (0.209)	0.304 (0.221)	0.250 (0.271)	0.242 (0.290)	0.265 (0.274)
NAM23	0.350 (0.207)	0.319 (0.219)	0.333 (0.212)	0.374 (0.248)	0.370 (0.227)	0.369 (0.251)
NAM24	0.297 (0.225)	0.263 (0.217)	0.274 (0.222)	0.455 (0.141)	0.430 (0.155)	0.455 (0.142)
NAM25	0.619 (0.121)	0.615 (0.113)	0.620 (0.115)	0.001 (0.332)	0.029 (0.315)	0.001 (0.327)
NAM26	0.288 (0.178)	0.249 (0.189)	0.271 (0.179)	0.128 (0.291)	0.138 (0.270)	0.127 (0.301)
NAM27	0.372 (0.229)	0.372 (0.216)	0.382 (0.228)	0.195 (0.279)	0.194 (0.284)	0.199 (0.288)
NAM28	0.093 (0.317)	0.077 (0.297)	0.106 (0.320)	0.182 (0.333)	0.179 (0.311)	0.184 (0.329)
NAM29	0.204 (0.166)	0.240 (0.154)	0.224 (0.165)	-0.127 (0.251)	-0.148 (0.250)	-0.116 (0.289)
NAM30	0.106 (0.233)	0.084 (0.248)	0.106 (0.239)	0.356 (0.198)	0.344 (0.197)	0.367 (0.203)
NAM31	0.189 (0.335)	0.226 (0.334)	0.176 (0.316)	0.298 (0.233)	0.306 (0.234)	0.301 (0.241)
NAM32	0.018 (0.267)	0.032 (0.269)	0.026 (0.278)	-0.039 (0.284)	-0.042 (0.303)	-0.036 (0.285)
NAM33	0.183 (0.207)	0.182 (0.207)	0.176 (0.218)	-0.070 (0.246)	-0.066 (0.226)	-0.079 (0.238)
NAM34	0.264 (0.295)	0.268 (0.291)	0.260 (0.297)	0.383 (0.166)	0.361 (0.175)	0.385 (0.164)
NAM36	0.016 (0.274)	-0.014 (0.264)	0.016 (0.263)	-0.035 (0.374)	-0.022 (0.355)	-0.042 (0.356)
NAM37	0.177 (0.245)	0.199 (0.228)	0.184 (0.230)	0.155 (0.277)	0.161 (0.284)	0.168 (0.280)
NAM38	0.255 (0.305)	0.201 (0.321)	0.256 (0.318)	0.382 (0.229)	0.406 (0.212)	0.377 (0.240)
NAM39	0.163 (0.207)	0.113 (0.217)	0.177 (0.183)	0.213 (0.261)	0.248 (0.278)	0.240 (0.253)
NAM40	0.100 (0.295)	0.110 (0.288)	0.087 (0.275)	0.087 (0.282)	0.100 (0.276)	0.088 (0.274)
NAM41	0.352 (0.292)	0.350 (0.298)	0.360 (0.296)	0.314 (0.234)	0.315 (0.220)	0.319 (0.231)
NAM42	0.357 (0.283)	0.369 (0.268)	0.356 (0.272)	0.196 (0.315)	0.218 (0.291)	0.205 (0.313)
NAM46	-0.012 (0.244)	-0.002 (0.252)	-0.016 (0.254)	0.123 (0.225)	0.144 (0.221)	0.129 (0.233)
NAM48	0.157 (0.246)	0.190 (0.252)	0.152 (0.239)	0.237 (0.223)	0.196 (0.233)	0.192 (0.247)
NAM50	0.170 (0.296)	0.145 (0.321)	0.173 (0.311)	0.197 (0.246)	0.191 (0.266)	0.199 (0.262)
NAM54	0.124 (0.188)	0.130 (0.173)	0.129 (0.182)	0.152 (0.237)	0.171 (0.231)	0.148 (0.242)
NAM64	0.024 (0.138)	0.002 (0.146)	0.035 (0.143)	0.194 (0.268)	0.185 (0.278)	0.209 (0.259)