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Genomic prediction in a backcross population using relationship matrices

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Supplementary Table S1. Mean performance of the models in various scenarios of heritabilities and marker densities in simulations of backcross populations

Simulated					Estimated parameters				
h^2	MD	σ_g^2	σ_e^2	Model	$\hat{\sigma}_a^2$ (rMSE)	$\sigma_{\hat{g}}^2$ (rMSE)	$\hat{\sigma}_e^2$ (rMSE)	Accuracy ($r_{\hat{g},g}$)	rMSE of GEBV
Independent simulation									
220	0.17	3.27	16	G-BLUP	3.19(0.89)	1.78(1.62)	16.09(1.12)	0.76	1.2
				CAG-BLUP	4.3(1.78)	1.7(1.69)	16.77(1.33)	0.74	1.23
				GASI-BLUP	3.04(1.01)	2.11(1.34)	16.14(1.12)	0.78	1.14
				GASC-BLUP	6.14(5.46)	2.01(1.43)	16.67(1.28)	0.77	1.18
	0.7	3.27	1.4	G-BLUP	2.79(0.56)	2.67(0.66)	1.53(0.18)	0.93	0.65
				CAG-BLUP	8.53(5.57)	2.59(0.74)	1.75(0.38)	0.92	0.72
				GASI-BLUP	2.66(0.68)	2.79(0.55)	1.54(0.19)	0.94	0.6
				GASC-BLUP	19.66(17.8)	2.75(0.59)	1.52(0.21)	0.94	0.63
440	0.17	3.27	16	G-BLUP	3.27(0.91)	1.81(1.59)	16.03(1.11)	0.77	1.18
				CAG-BLUP	4.33(1.84)	1.72(1.68)	16.78(1.33)	0.75	1.22
				GASI-BLUP	3.15(1.03)	2.13(1.33)	16.08(1.11)	0.79	1.13
				GASC-BLUP	6.38(5.69)	2.02(1.42)	16.67(1.28)	0.77	1.18
	0.7	3.27	1.4	G-BLUP	3.04(0.39)	2.72(0.61)	1.43(0.12)	0.94	0.62
				CAG-BLUP	9.31(6.36)	2.62(0.71)	1.73(0.35)	0.92	0.7
				GASI-BLUP	2.94(0.49)	2.85(0.5)	1.44(0.12)	0.95	0.57
				GASC-BLUP	24.18(23.05)	2.78(0.56)	1.45(0.2)	0.94	0.61
Dependent simulation									
220	0.17	6.54	31.93	G-BLUP	6.47(1.29)	4.2(2.57)	31.3(2.24)	0.81	1.51
				CAG-BLUP	8.97(3.05)	4.39(2.39)	32.31(2.13)	0.83	1.43
				GASI-BLUP	4.78(2.26)	5.66(1.49)	31.74(2.09)	0.92	1.04
				GASC-BLUP	12.51(14.72)	5.6(1.49)	32.17(2.09)	0.92	1.05
	0.7	6.54	2.8	G-BLUP	4.39(2.18)	5.73(0.91)	2.78(0.22)	0.95	0.79
				CAG-BLUP	9.26(3.1)	5.66(0.96)	3.16(0.43)	0.95	0.84
				GASI-BLUP	3.11(3.45)	6.14(0.6)	2.92(0.24)	0.97	0.6
				GASC-BLUP	28.55(23.75)	6.15(0.59)	2.72(0.25)	0.97	0.59
440	0.17	6.54	31.93	G-BLUP	6.57(1.33)	4.24(2.53)	31.21(2.25)	0.82	1.49
				CAG-BLUP	9(3.07)	4.41(2.38)	32.34(2.13)	0.84	1.42
				GASI-BLUP	4.99(2.18)	5.69(1.48)	31.63(2.1)	0.92	1.01
				GASC-BLUP	12.72(13.83)	5.61(1.49)	32.19(2.1)	0.92	1.03
	0.7	6.54	2.8	G-BLUP	4.61(1.97)	5.79(0.86)	2.66(0.25)	0.95	0.77
				CAG-BLUP	9.47(3.29)	5.69(0.94)	3.16(0.42)	0.95	0.82
				GASI-BLUP	3.26(3.32)	6.2(0.57)	2.81(0.2)	0.98	0.55
				GASC-BLUP	36.11(32.04)	6.19(0.57)	2.62(0.31)	0.98	0.57

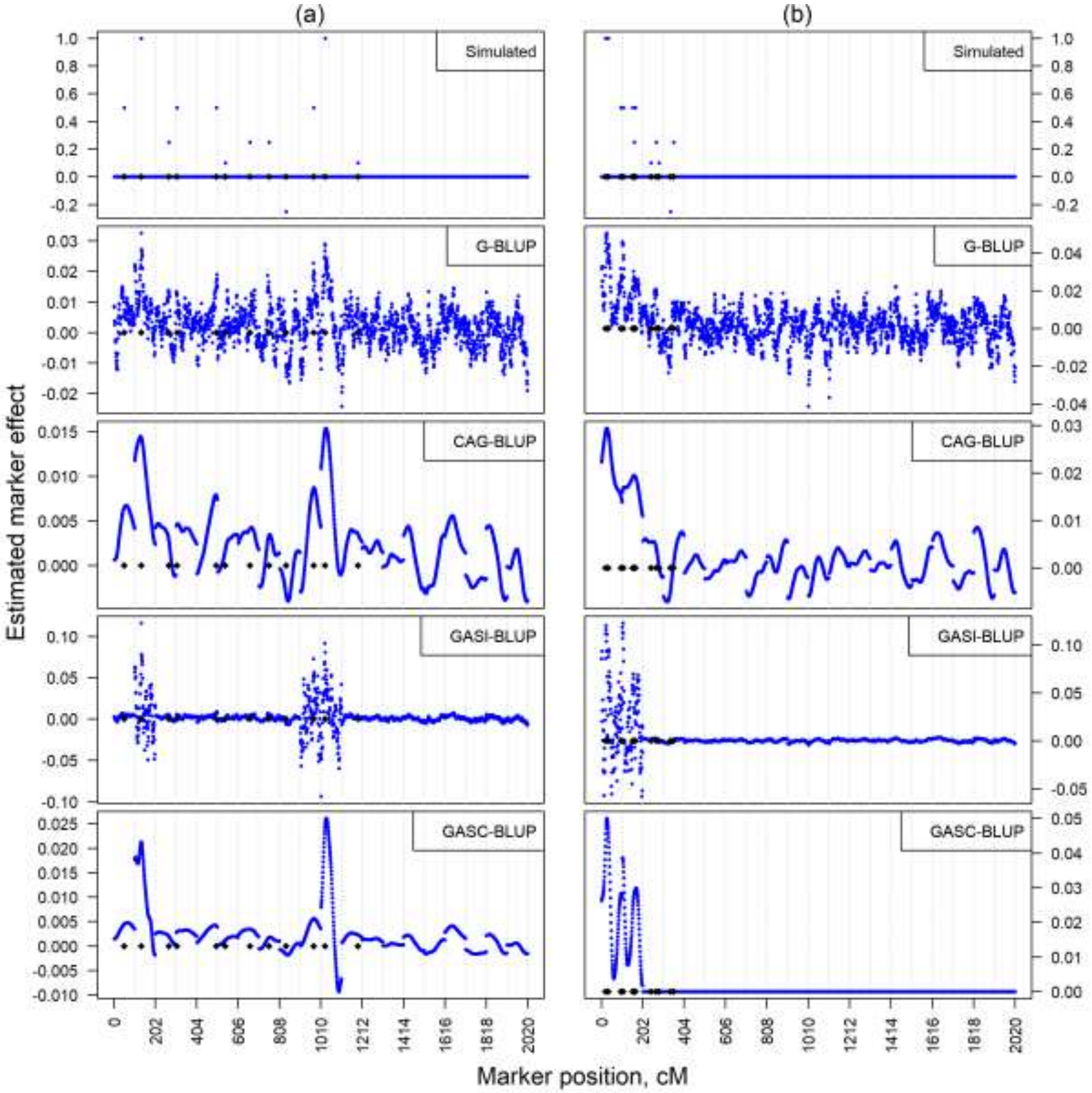
σ_g^2 : true genetic (Mendelian sampling) variance; σ_e^2 : true residual variance; $\hat{\sigma}_a^2$ and $\hat{\sigma}_e^2$: mean estimated additive and residual variance components, respectively; $\sigma_{\hat{g}}^2$: mean estimated genetic (Mendelian sampling) variance; rMSE: root mean squared error, indicating the deviation of estimated variances from true values; h^2 : heritability; MD: marker density; GEBV: genomic estimated breeding values; Accuracy ($r_{\hat{g},g}$): correlation between GEBV and true breeding values, indicating the precision of GEBV in predicting true breeding values.

Supplementary Table S2. Power (%) to detect a QTL-carrying chromosome in independent and dependent simulations of backcross populations

		h^2 = 0.17		h^2 = 0.29		h^2 = 0.70	
Chr	QE	G-BLUP	CAG-BLUP	G-BLUP	CAG-BLUP	G-BLUP	CAG-BLUP
Independent simulation							
1	0.5	5	5	29	27.5	89.5	89.5
2	1.0	88	86	99.5	99.5	100	100
3	0.25	0.5	1	2	2.5	7.5	7
4	0.50	5	4	19.5	15	86	79.5
5	0.50	8.5	6	22.5	20	83	78.5
6	0.1	-	-	-	-	-	-
7	0.25	1.5	1	1.5	1.5	11	12
8	0.25	1.5	1	1.5	1.5	7.5	8
9	-0.25	1.5	1	3	3	11.5	13.5
10	0.5	7.5	8	29.5	29.5	90.5	86.5
11	1.0	83.5	82	99	99	100	100
12	0.1	-	-	-	-	0.5	0.5
16	-	0	0.5	-	0.5	-	0.5
Dependent simulation							
1	1.0, 1.0, 0.5	100	100	100	100	100	100
2	0.5, 0.5, 0.25, 0.5	93	91.5	100	100	100	100
3	0.1, 0.25, 0.1	1	1	2	3	20	19.5
4	-0.25, 0.25	-	-	-	-	0.5	0.5
5	-	-	-	-	-	0.5	0.5
11	-	0	0.5	0	0.5	-	-
12	-	0.5	0.5	0.5	0.5	0.5	0.5
14	-	0.5	0	0.5	-	-	-
16	-	0	0.5	0.5	0.5	-	-
17	-	-	-	-	-	0.5	0.5
19	-	0.5	0.5	0.5	0.5	0.5	0.5

h^2 = heritability; QE = simulated QTL effect size; Chr = chromosome.

Results presented are for scenarios with a marker density of 2020 markers and chromosomes with entries.



Supplementary Figure S1. Simulated and estimated marker effects of a randomly selected replicate in independent (panel a) and dependent (panel b) simulations with a 1 cM marker distance and heritability of 0.29. The black diamonds are the quantitative trait loci positions.