

Supplementary materials for:

Origin Specific Genomic Selection: a simple process to optimize the favorable contribution of parents to progeny.

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Table S1. Prediction summary across traits and methods. For each NAM family and trait, we predicted the marker effects for all (A), primary (P) and secondary (S) favorable alleles using rrBLUP, LASSO and BayesC π , and we evaluated the prediction accuracy via correlations between observed and predicted breeding values.

Fam.	Fam. Size	Prop. of favorable allele									Correlation (Obs. vs Pred.)									Trait
		rrBLUP			LASSO			BayesCπ			rrBLUP			LASSO			BayesCπ			
		A	P	S	A	P	S	A	P	S	A	P	S	A	P	S	A	P	S	
1	58	1.00	0.54	0.46	0.007	0.004	0.002	1.00	0.58	0.42	1.00	0.76	0.42	0.95	0.91	0.56	0.97	0.84	0.59	DTH
2	48	1.00	0.52	0.48	0.015	0.011	0.004	1.00	0.53	0.47	0.98	0.90	0.65	0.98	0.95	0.61	0.95	0.89	0.65	DTH
3	73	1.00	0.53	0.47	0.018	0.011	0.006	1.00	0.54	0.46	0.98	0.77	0.34	0.98	0.86	0.50	0.94	0.78	0.47	DTH
4	43	1.00	0.55	0.45	0.021	0.013	0.008	1.00	0.49	0.51	1.00	0.80	0.76	1.00	0.89	0.82	0.98	0.85	0.85	DTH
5	58	1.00	0.56	0.44	0.013	0.008	0.005	1.00	0.53	0.47	0.96	0.75	0.54	0.97	0.85	0.59	0.93	0.76	0.58	DTH
6	54	1.00	0.56	0.44	0.006	0.005	0.001	1.00	0.57	0.43	0.97	0.82	0.35	0.88	0.87	0.43	0.95	0.84	0.43	DTH
7	58	1.00	0.47	0.53	0.009	0.006	0.002	1.00	0.46	0.54	0.94	0.79	0.58	0.94	0.87	0.59	0.94	0.79	0.58	DTH
8	58	1.00	0.50	0.50	0.009	0.005	0.003	1.00	0.52	0.48	1.00	0.83	0.32	0.96	0.94	0.20	0.97	0.87	0.50	DTH
9	50	1.00	0.49	0.51	0.006	0.004	0.002	1.00	0.49	0.51	0.96	0.79	0.65	0.90	0.84	0.53	0.94	0.79	0.65	DTH
10	59	1.00	0.52	0.48	0.004	0.002	0.002	1.00	0.52	0.48	0.87	0.68	0.58	0.88	0.68	0.56	0.89	0.68	0.56	DTH
11	57	1.00	0.53	0.47	0.019	0.013	0.006	1.00	0.50	0.50	1.00	0.70	0.39	0.97	0.90	0.62	0.95	0.77	0.56	DTH
12	67	1.00	0.51	0.49	0.019	0.011	0.008	1.00	0.49	0.51	0.96	0.69	0.70	0.97	0.79	0.69	0.94	0.69	0.72	DTH
13	55	1.00	0.51	0.49	0.019	0.010	0.009	1.00	0.52	0.48	0.96	0.79	0.50	0.96	0.90	0.47	0.94	0.81	0.55	DTH
14	61	1.00	0.57	0.43	0.022	0.016	0.006	1.00	0.56	0.44	1.00	0.89	0.32	0.99	0.96	0.58	0.99	0.93	0.49	DTH
15	57	1.00	0.56	0.44	0.025	0.020	0.005	1.00	0.59	0.41	0.93	0.80	0.30	0.97	0.92	0.33	0.91	0.78	0.32	DTH
16	60	1.00	0.55	0.45	0.005	0.004	0.001	1.00	0.56	0.44	0.99	0.92	0.38	0.95	0.94	0.26	0.97	0.92	0.52	DTH
17	49	1.00	0.49	0.51	0.023	0.014	0.009	1.00	0.51	0.49	1.00	0.76	0.60	0.99	0.87	0.59	0.97	0.82	0.65	DTH
18	22	1.00	0.52	0.48	0.010	0.006	0.005	1.00	0.53	0.47	1.00	0.85	0.42	0.98	0.91	0.63	0.96	0.81	0.56	DTH
19	59	1.00	0.62	0.38	0.006	0.005	0.000	1.00	0.61	0.39	0.92	0.84	0.38	0.84	0.84	0.36	0.92	0.83	0.40	DTH
20	55	1.00	0.52	0.48	0.006	0.003	0.003	1.00	0.52	0.48	0.97	0.78	0.42	0.89	0.84	0.36	0.95	0.79	0.44	DTH
21	48	1.00	0.43	0.57	0.017	0.008	0.009	1.00	0.45	0.55	0.99	0.76	0.68	0.98	0.86	0.64	0.97	0.76	0.71	DTH
22	42	1.00	0.51	0.49	0.026	0.014	0.012	1.00	0.50	0.50	0.98	0.81	0.67	1.00	0.85	0.36	0.95	0.81	0.68	DTH
23	62	1.00	0.46	0.54	0.024	0.012	0.012	1.00	0.45	0.55	0.98	0.64	0.67	0.99	0.72	0.72	0.96	0.65	0.69	DTH
24	58	1.00	0.46	0.54	0.027	0.017	0.010	1.00	0.47	0.53	0.96	0.72	0.45	0.98	0.76	0.51	0.94	0.74	0.47	DTH
25	60	1.00	0.51	0.49	0.013	0.005	0.008	1.00	0.50	0.50	0.99	0.77	0.52	0.96	0.85	0.64	0.97	0.79	0.61	DTH
1	58	1.00	0.57	0.43	0.012	0.009	0.003	1.00	0.57	0.43	0.85	0.78	0.53	0.90	0.83	0.49	0.86	0.78	0.50	YLD
2	48	1.00	0.67	0.33	0.015	0.012	0.003	1.00	0.63	0.37	0.98	0.90	0.35	0.96	0.95	0.51	0.95	0.89	0.42	YLD
3	73	1.00	0.78	0.22	0.011	0.011	0.000	1.00	0.74	0.26	0.93	0.89	0.02	0.90	0.90	NA	0.92	0.88	0.05	YLD
4	43	1.00	0.56	0.44	0.007	0.005	0.002	1.00	0.59	0.41	0.82	0.78	0.43	0.89	0.87	0.19	0.89	0.81	0.41	YLD
5	58	1.00	0.55	0.45	0.013	0.012	0.001	1.00	0.60	0.40	0.99	0.90	0.32	0.96	0.95	0.44	0.96	0.90	0.47	YLD
6	54	1.00	0.72	0.28	0.009	0.006	0.003	1.00	0.64	0.36	0.87	0.78	0.37	0.90	0.85	0.43	0.88	0.78	0.33	YLD
7	58	1.00	0.66	0.34	0.008	0.008	0.000	1.00	0.63	0.37	0.88	0.79	0.17	0.87	0.87	0.13	0.89	0.79	0.16	YLD
8	58	1.00	0.61	0.39	0.004	0.003	0.001	1.00	0.60	0.40	0.97	0.86	0.29	0.84	0.83	0.11	0.94	0.86	0.33	YLD
9	50	1.00	0.63	0.38	0.004	0.003	0.001	1.00	0.63	0.37	0.77	0.76	0.51	0.77	0.69	0.28	0.87	0.82	0.51	YLD
10	59	1.00	0.59	0.41	0.029	0.023	0.006	1.00	0.61	0.39	0.95	0.89	0.49	0.98	0.93	0.51	0.94	0.88	0.52	YLD
11	57	1.00	0.65	0.35	0.007	0.006	0.001	1.00	0.63	0.37	0.96	0.88	0.25	0.85	0.84	0.29	0.94	0.87	0.32	YLD
12	67	1.00	0.54	0.46	0.023	0.016	0.007	1.00	0.54	0.46	0.93	0.76	0.52	0.96	0.86	0.55	0.92	0.76	0.53	YLD
13	55	1.00	0.70	0.30	0.027	0.021	0.006	1.00	0.68	0.32	0.95	0.89	0.09	0.99	0.94	0.16	0.93	0.88	0.20	YLD
14	61	1.00	0.61	0.39	0.004	0.003	0.001	1.00	0.61	0.39	0.90	0.83	0.44	0.84	0.81	0.40	0.90	0.83	0.45	YLD
15	57	1.00	0.68	0.32	0.018	0.017	0.002	1.00	0.66	0.34	0.96	0.89	0.02	0.98	0.95	0.29	0.94	0.88	0.08	YLD
16	60	1.00	0.67	0.33	0.024	0.022	0.002	1.00	0.68	0.32	0.99	0.90	0.18	0.99	0.97	0.35	0.95	0.89	0.36	YLD
17	49	1.00	0.58	0.42	0.007	0.005	0.001	1.00	0.58	0.42	0.94	0.87	0.54	0.90	0.86	0.53	0.94	0.86	0.58	YLD
18	22	1.00	0.58	0.42	0.017	0.010	0.007	1.00	0.60	0.40	1.00	0.96	0.59	1.00	0.95	0.72	0.96	0.93	0.73	YLD
19	59	1.00	0.48	0.52	0.024	0.013	0.012	1.00	0.53	0.47	0.95	0.80	0.52	0.97	0.88	0.43	0.94	0.79	0.54	YLD
20	55	1.00	0.65	0.35	0.012	0.011	0.002	1.00	0.68	0.32	0.99	0.92	0.11	0.98	0.97	0.39	0.97	0.91	0.28	YLD
21	48	1.00	0.70	0.30	0.021	0.020	0.001	1.00	0.69	0.31	0.99	0.95	0.22	1.00	0.99	0.27	0.96	0.94	0.35	YLD
22	42	1.00	0.63	0.37	0.034	0.026	0.008	1.00	0.61	0.39	0.95	0.88	0.54	1.00	0.88	0.46	0.94	0.86	0.54	YLD
23	62	1.00	0.61	0.39	0.016	0.014	0.002	1.00	0.61	0.39	0.93	0.86	0.39	0.96	0.90	0.43	0.92	0.85	0.41	YLD
24	58	1.00	0.66	0.34	0.019	0.017	0.002	1.00	0.63	0.37	0.98	0.79	0.36	0.98	0.88	0.43	0.96	0.81	0.41	YLD
25	60	1.00	0.66	0.34	0.017	0.015	0.001	1.00	0.66	0.34	0.97	0.92	0.13	0.97	0.96	0.28	0.94	0.91	0.18	YLD

1	194	1.00	0.49	0.51	0.099	0.050	0.050	1.00	0.49	0.51	0.88	0.41	0.50	0.92	0.49	0.57	0.88	0.42	0.51	DTS
2	196	1.00	0.51	0.49	0.055	0.028	0.027	1.00	0.51	0.49	0.76	0.50	0.35	0.76	0.60	0.41	0.77	0.50	0.34	DTS
3	191	1.00	0.60	0.40	0.066	0.046	0.020	1.00	0.59	0.41	0.89	0.74	0.16	0.86	0.79	0.33	0.88	0.75	0.17	DTS
4	196	1.00	0.61	0.39	0.096	0.073	0.023	1.00	0.62	0.38	0.92	0.78	0.12	0.93	0.83	0.34	0.92	0.79	0.15	DTS
5	187	1.00	0.60	0.40	0.046	0.033	0.013	1.00	0.59	0.41	0.90	0.78	0.23	0.85	0.82	0.21	0.90	0.79	0.24	DTS
6	185	1.00	0.56	0.44	0.108	0.075	0.033	1.00	0.56	0.44	0.93	0.64	0.22	0.94	0.71	0.34	0.92	0.65	0.23	DTS
7	193	1.00	0.60	0.40	0.071	0.052	0.020	1.00	0.60	0.40	0.83	0.66	0.30	0.82	0.70	0.39	0.84	0.66	0.31	DTS
8	196	1.00	0.65	0.35	0.072	0.047	0.025	1.00	0.64	0.36	0.87	0.76	0.11	0.92	0.81	0.19	0.87	0.77	0.12	DTS
9	189	1.00	0.63	0.37	0.053	0.039	0.014	1.00	0.63	0.37	0.84	0.68	0.25	0.80	0.73	0.30	0.84	0.69	0.26	DTS
10	192	1.00	0.48	0.52	0.076	0.029	0.047	1.00	0.48	0.52	0.91	0.56	0.53	0.90	0.63	0.62	0.91	0.57	0.54	DTS
11	194	1.00	0.45	0.55	0.075	0.036	0.039	1.00	0.45	0.55	0.90	0.44	0.62	0.91	0.54	0.66	0.90	0.45	0.62	DTS
12	193	1.00	0.55	0.45	0.041	0.027	0.014	1.00	0.56	0.44	0.90	0.80	0.20	0.85	0.82	0.18	0.90	0.80	0.20	DTS
13	126	1.00	0.58	0.42	0.043	0.032	0.012	1.00	0.58	0.42	0.90	0.70	0.41	0.87	0.78	0.50	0.90	0.71	0.42	DTS
14	196	1.00	0.58	0.42	0.115	0.065	0.050	1.00	0.59	0.41	0.90	0.64	0.39	0.95	0.67	0.45	0.90	0.64	0.42	DTS
15	185	1.00	0.58	0.42	0.042	0.031	0.011	1.00	0.58	0.42	0.87	0.71	0.16	0.83	0.77	0.30	0.87	0.72	0.17	DTS
16	194	1.00	0.58	0.42	0.089	0.058	0.031	1.00	0.57	0.43	0.86	0.69	0.15	0.89	0.77	0.26	0.86	0.70	0.16	DTS
17	192	1.00	0.63	0.37	0.080	0.062	0.017	1.00	0.63	0.37	0.93	0.80	-0.01	0.92	0.86	0.22	0.92	0.81	0.01	DTS
18	196	1.00	0.51	0.49	0.040	0.021	0.019	1.00	0.51	0.49	0.79	0.53	0.46	0.77	0.58	0.51	0.80	0.53	0.46	DTS
19	187	1.00	0.58	0.42	0.071	0.048	0.024	1.00	0.59	0.41	0.87	0.60	0.36	0.88	0.65	0.45	0.87	0.61	0.37	DTS
20	183	1.00	0.47	0.53	0.102	0.057	0.045	1.00	0.48	0.52	0.94	0.50	0.47	0.96	0.59	0.58	0.93	0.52	0.49	DTS
21	193	1.00	0.49	0.51	0.051	0.015	0.035	1.00	0.49	0.51	0.85	0.34	0.54	0.81	0.37	0.62	0.85	0.34	0.56	DTS
22	181	1.00	0.55	0.45	0.049	0.032	0.017	1.00	0.57	0.43	0.75	0.61	0.29	0.80	0.67	0.38	0.76	0.61	0.29	DTS
23	183	1.00	0.43	0.57	0.094	0.030	0.064	1.00	0.43	0.57	0.90	0.21	0.64	0.93	0.34	0.70	0.89	0.24	0.64	DTS
24	188	1.00	0.57	0.43	0.036	0.028	0.008	1.00	0.57	0.43	0.76	0.57	0.24	0.70	0.65	0.28	0.78	0.57	0.23	DTS
25	187	1.00	0.63	0.37	0.057	0.042	0.014	1.00	0.63	0.37	0.84	0.69	0.32	0.84	0.74	0.40	0.84	0.69	0.32	DTS
1	194	1.00	0.48	0.52	0.034	0.017	0.017	1.00	0.49	0.51	0.80	0.47	0.42	0.72	0.55	0.47	0.81	0.48	0.42	CL
2	196	1.00	0.48	0.52	0.026	0.009	0.017	1.00	0.47	0.53	0.81	0.39	0.59	0.71	0.47	0.61	0.81	0.39	0.59	CL
3	191	1.00	0.47	0.53	0.083	0.039	0.044	1.00	0.47	0.53	0.90	0.45	0.52	0.92	0.57	0.62	0.91	0.46	0.53	CL
4	196	1.00	0.54	0.46	0.056	0.036	0.020	1.00	0.54	0.46	0.84	0.49	0.52	0.82	0.56	0.61	0.84	0.49	0.53	CL
5	187	1.00	0.55	0.45	0.103	0.061	0.042	1.00	0.55	0.45	0.87	0.59	0.37	0.93	0.65	0.45	0.87	0.59	0.38	CL
6	185	1.00	0.50	0.50	0.045	0.022	0.024	1.00	0.50	0.50	0.81	0.54	0.42	0.81	0.63	0.51	0.81	0.54	0.42	CL
7	193	1.00	0.59	0.41	0.046	0.030	0.016	1.00	0.59	0.41	0.81	0.59	0.45	0.80	0.64	0.51	0.81	0.60	0.45	CL
8	196	1.00	0.57	0.43	0.057	0.033	0.024	1.00	0.57	0.43	0.78	0.55	0.40	0.84	0.58	0.48	0.79	0.55	0.40	CL
9	189	1.00	0.50	0.50	0.039	0.026	0.013	1.00	0.51	0.49	0.84	0.57	0.43	0.80	0.63	0.54	0.84	0.57	0.43	CL
10	192	1.00	0.55	0.45	0.107	0.058	0.049	1.00	0.55	0.45	0.88	0.43	0.55	0.94	0.47	0.55	0.88	0.43	0.56	CL
11	194	1.00	0.56	0.44	0.038	0.032	0.006	1.00	0.56	0.44	0.82	0.66	0.20	0.77	0.73	0.25	0.83	0.67	0.19	CL
12	193	1.00	0.50	0.50	0.048	0.024	0.024	1.00	0.50	0.50	0.80	0.57	0.46	0.80	0.61	0.52	0.80	0.57	0.46	CL
13	126	1.00	0.51	0.49	0.044	0.022	0.023	1.00	0.51	0.49	0.89	0.68	0.40	0.90	0.76	0.39	0.89	0.69	0.40	CL
14	196	1.00	0.46	0.54	0.059	0.023	0.036	1.00	0.45	0.55	0.86	0.45	0.61	0.85	0.50	0.67	0.86	0.45	0.61	CL
15	185	1.00	0.56	0.44	0.073	0.045	0.028	1.00	0.55	0.45	0.83	0.60	0.34	0.88	0.69	0.43	0.83	0.61	0.35	CL
16	194	1.00	0.43	0.57	0.066	0.032	0.034	1.00	0.44	0.56	0.81	0.42	0.54	0.82	0.53	0.60	0.81	0.42	0.54	CL
17	192	1.00	0.47	0.53	0.007	0.005	0.003	1.00	0.47	0.53	0.68	0.43	0.45	0.42	0.29	0.30	0.70	0.43	0.45	CL
18	196	1.00	0.51	0.49	0.052	0.022	0.030	1.00	0.49	0.51	0.77	0.45	0.48	0.80	0.54	0.53	0.78	0.46	0.48	CL
19	187	1.00	0.50	0.50	0.040	0.027	0.013	1.00	0.49	0.51	0.84	0.62	0.47	0.77	0.66	0.51	0.84	0.62	0.47	CL
20	183	1.00	0.57	0.43	0.058	0.038	0.020	1.00	0.57	0.43	0.89	0.58	0.45	0.84	0.65	0.54	0.89	0.59	0.46	CL
21	193	1.00	0.48	0.52	0.032	0.013	0.019	1.00	0.47	0.53	0.76	0.38	0.55	0.73	0.42	0.60	0.77	0.38	0.56	CL
22	181	1.00	0.48	0.52	0.073	0.037	0.036	1.00	0.47	0.53	0.85	0.36	0.55	0.85	0.52	0.60	0.84	0.37	0.56	CL
23	183	1.00	0.52	0.48	0.020	0.012	0.008	1.00	0.53	0.47	0.75	0.52	0.42	0.61	0.48	0.41	0.76	0.52	0.42	CL
24	188	1.00	0.50	0.50	0.068	0.042	0.025	1.00	0.50	0.50	0.86	0.50	0.48	0.87	0.58	0.59	0.86	0.51	0.49	CL
25	187	1.00	0.51	0.49	0.079	0.040	0.039	1.00	0.52	0.48	0.87	0.57	0.48	0.91	0.68	0.51	0.87	0.58	0.48	CL

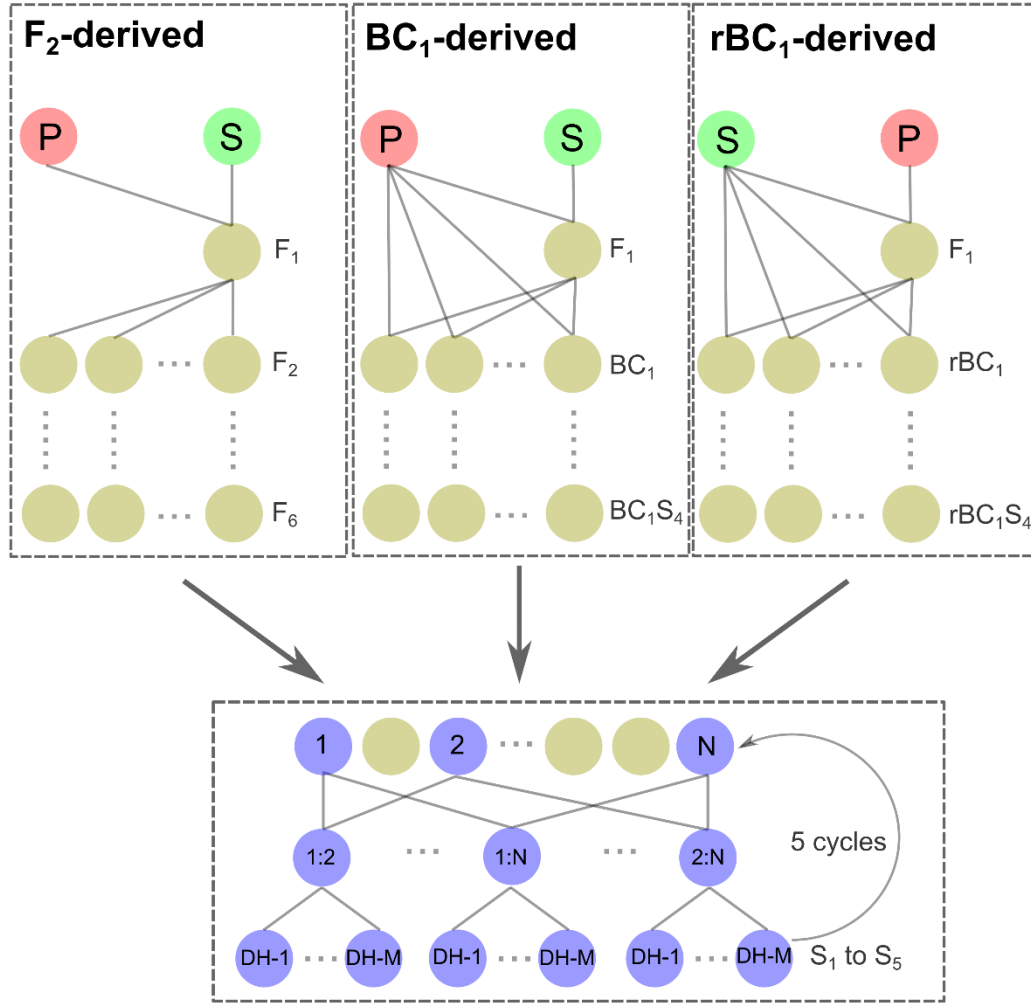


Figure S1: Selection process used in the simulation study. For each of the NAM family, F_2 -, BC_1 - and rBC_1 -derived populations, we selected N lines based on their breeding values determined from either genomic selection (GS) or origin specific genomic selection (OSGS). All possible half-diallel crosses were made among the N selected lines, and M double-haploids (DHs) were made from each cross. These DHs make up the population referred to as S_1 , which has $M \sum_{i=1}^{N-1} i$ lines. For any simulation involving recurrent selection, we took S_1 into next selection cycles. We evaluated the percentage of favourable primary and secondary QTL alleles and the true/estimated breeding values for each line at each generation. We set $N=5$ and $M=20$ for the NAM families and $N=10$ and $M=10$ for the simulated populations.

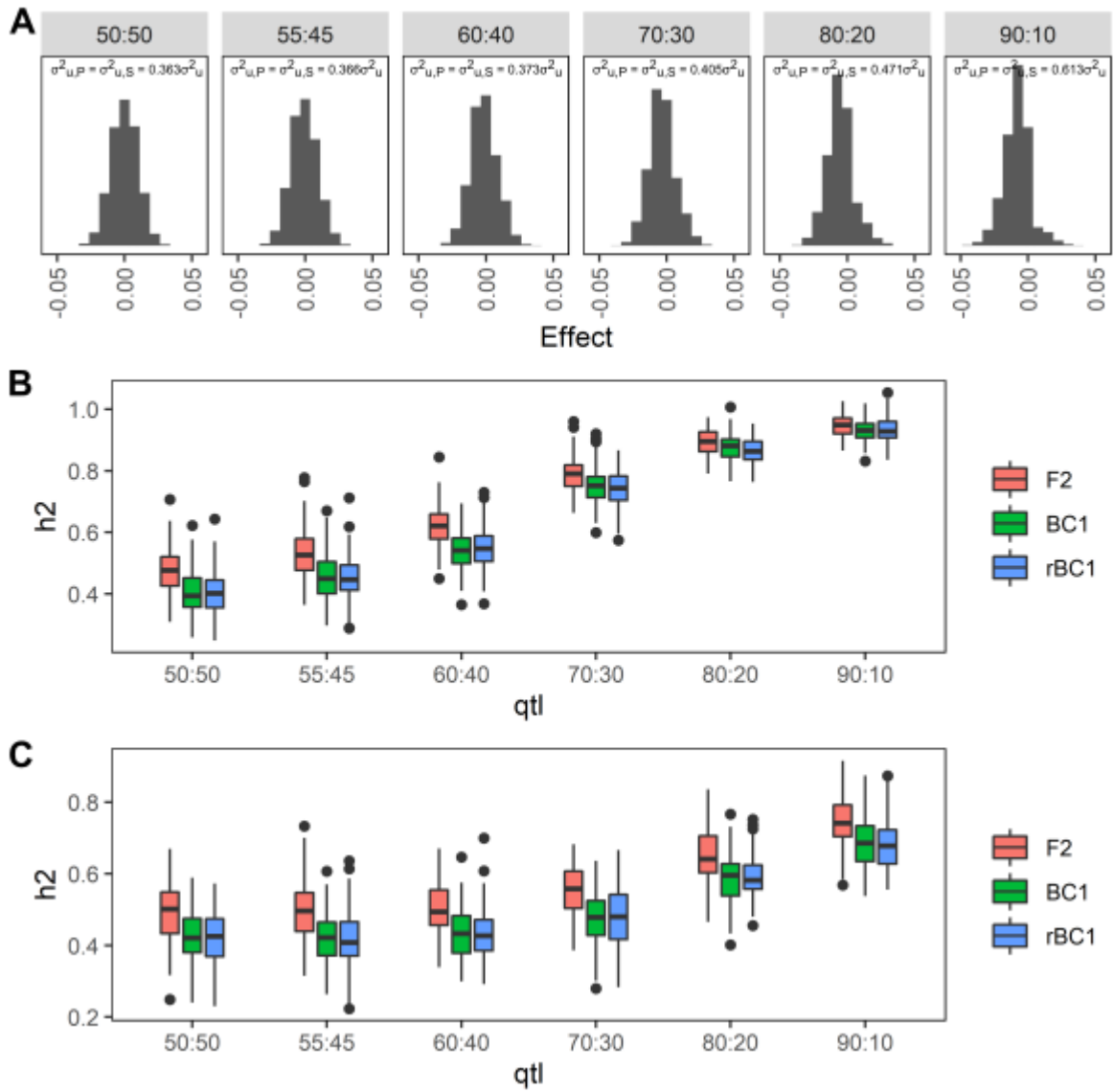


Figure S2. Simulated QTL effects and heritabilities for all P:S. [A] For each P:S, we simulated the QTL marker effects using a half-normal distribution with the same variance ($\sigma^2_{u,P} = \sigma^2_{u,S}$). In addition, we also restricted the simulated effects such that the aggregated distribution of P and S gives $\sigma^2_u = p^{-1}$, where p is the number of QTLs. This ensures that the genetic variance $\sigma^2_g = 1$ when P and S segregate equally. [B] Actual heritabilities of the simulated phenotypic trait under 2cM/QTL across all tested P:S proportions. [C] Actual heritabilities of the simulated phenotypic trait under 20cM/QTL across all tested P:S proportions.

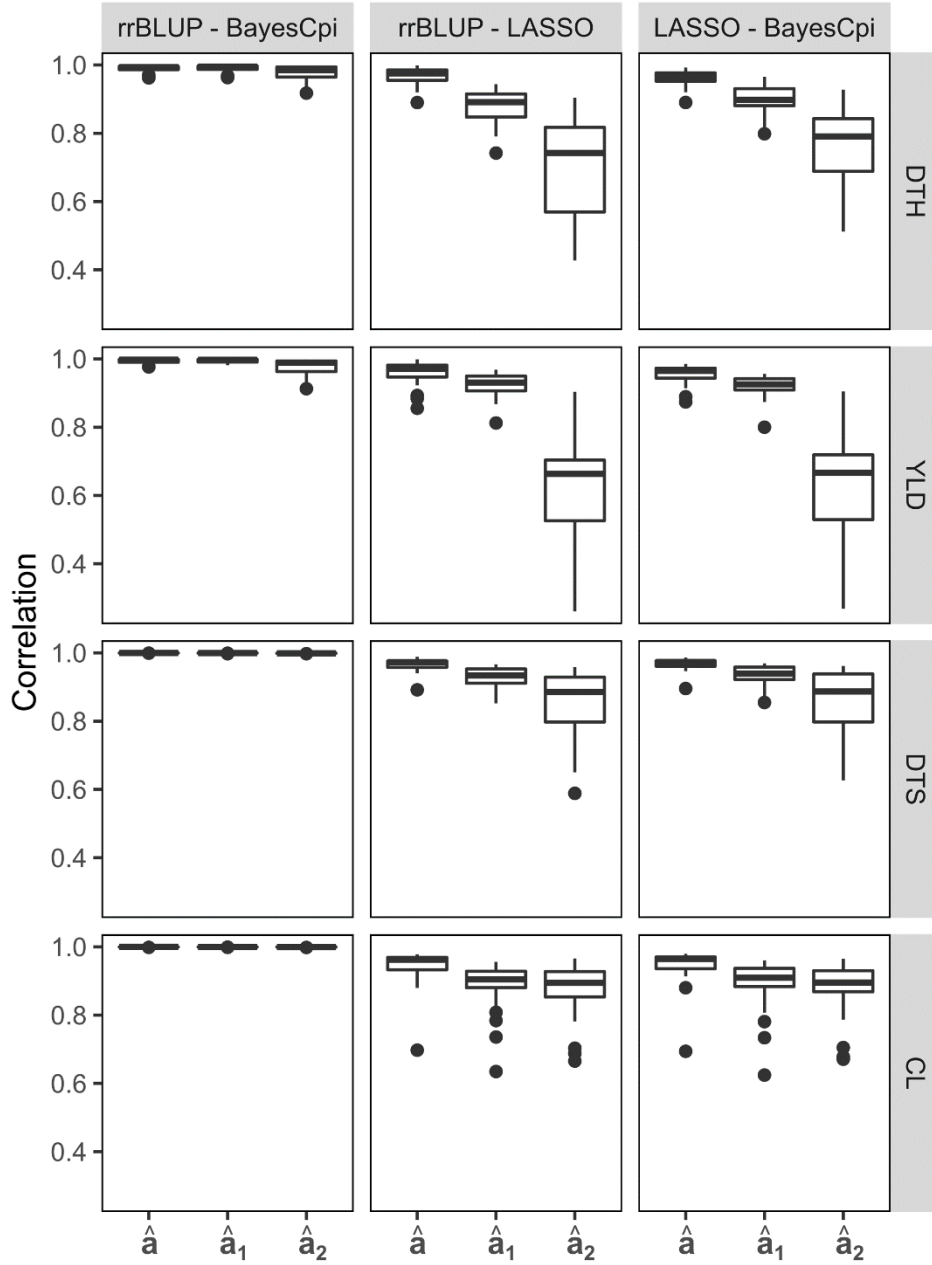


Figure S3. Correlations across three common GS methods. For each trait, we calculated the correlations of the predicted $\hat{a}$, $\hat{a}_1$ and $\hat{a}_2$ between any two methods. Predictions for $\hat{a}$, and $\hat{a}_1$ are highly similar across all three GS methods, but predictions for $\hat{a}_2$ are more similar between rrBLUP and BayesCpi than LASSO.

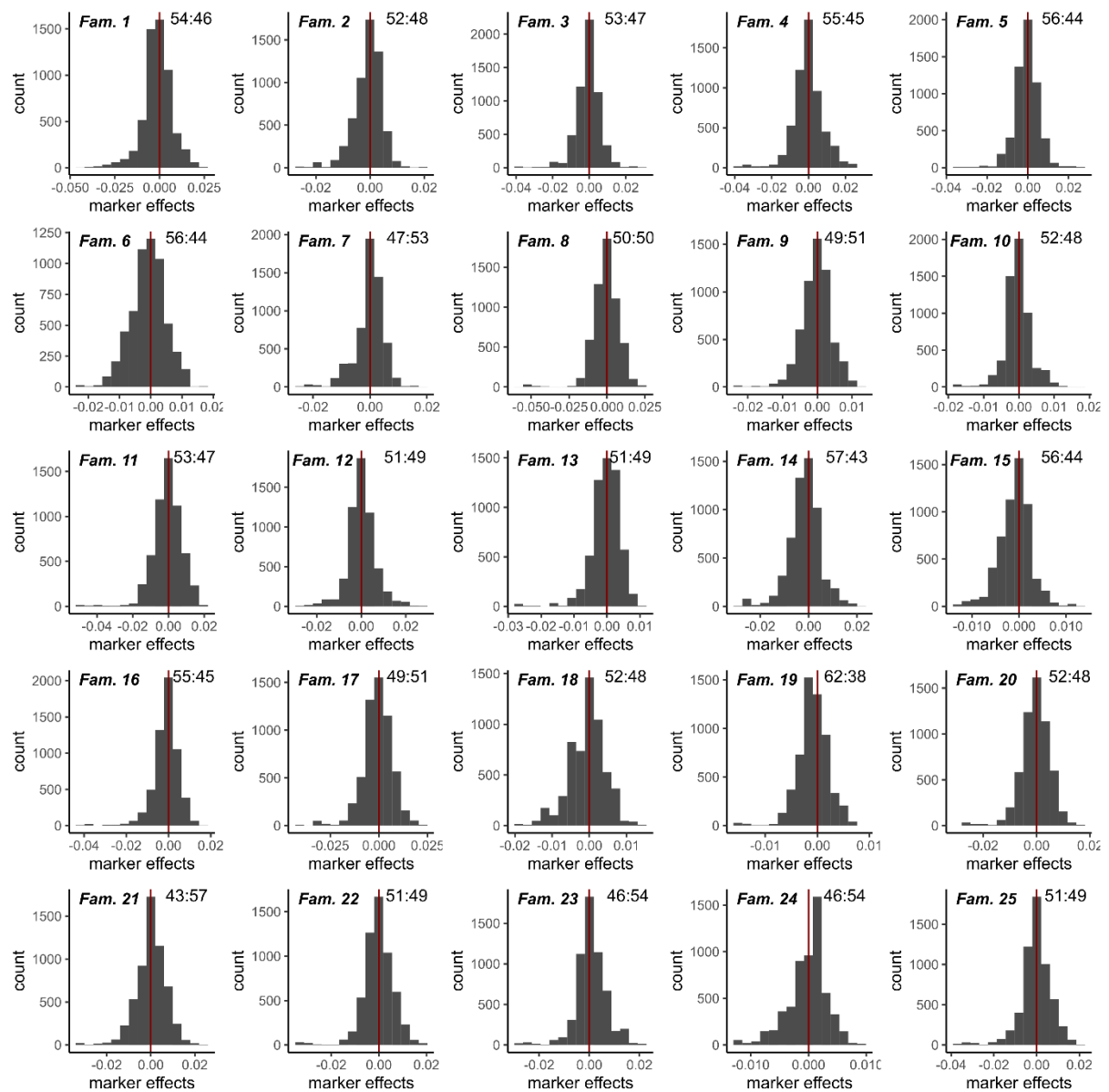


Figure S4. Distributions of marker effects for DTH. For DTH, negative marker effects represent favorable primary alleles and positive marker effects represent favourable secondary alleles.

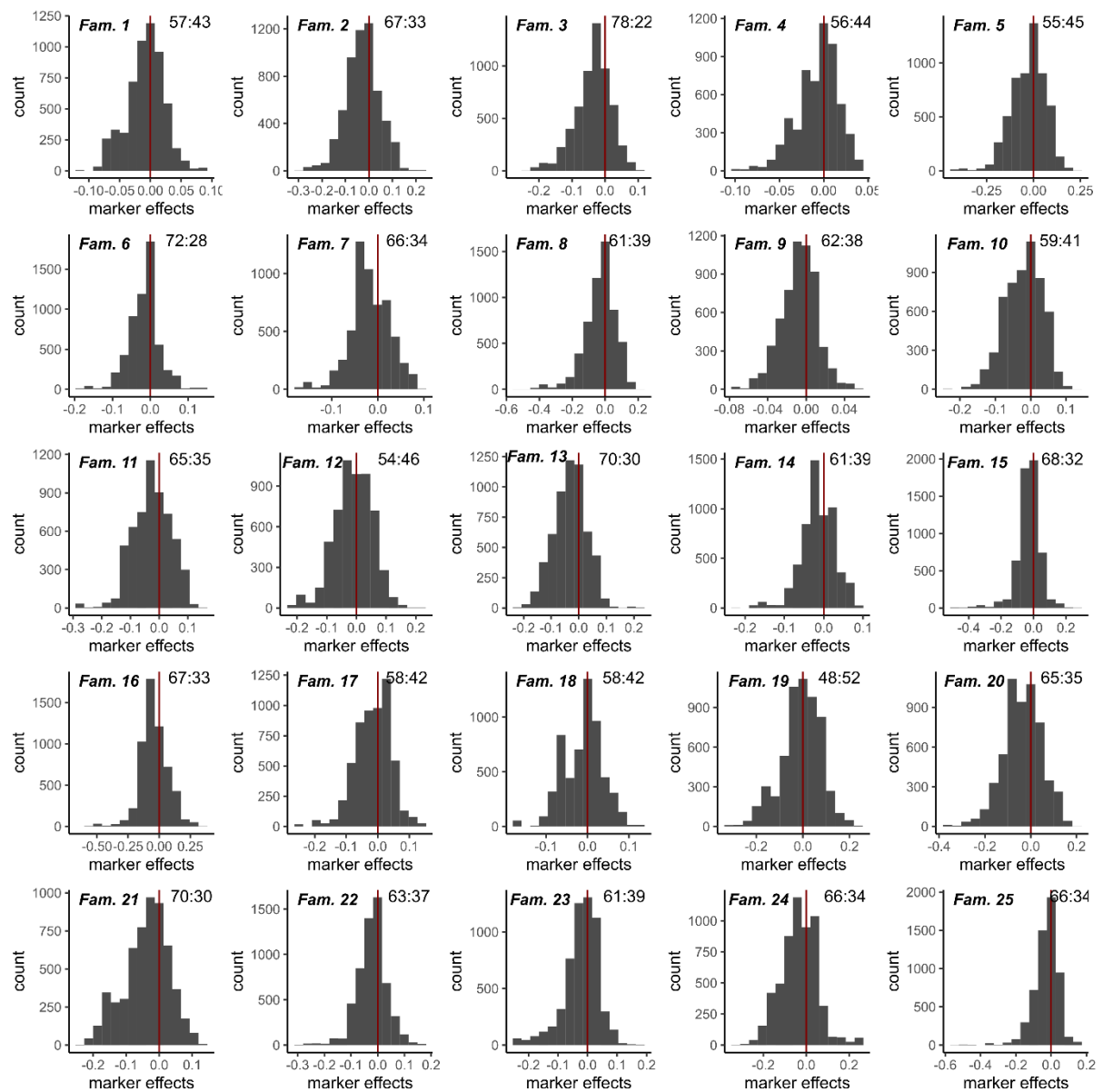


Figure S5. Distributions of marker effects for YLD. For YLD, negative marker effects represent favorable primary alleles and positive marker effects represent favourable secondary alleles.

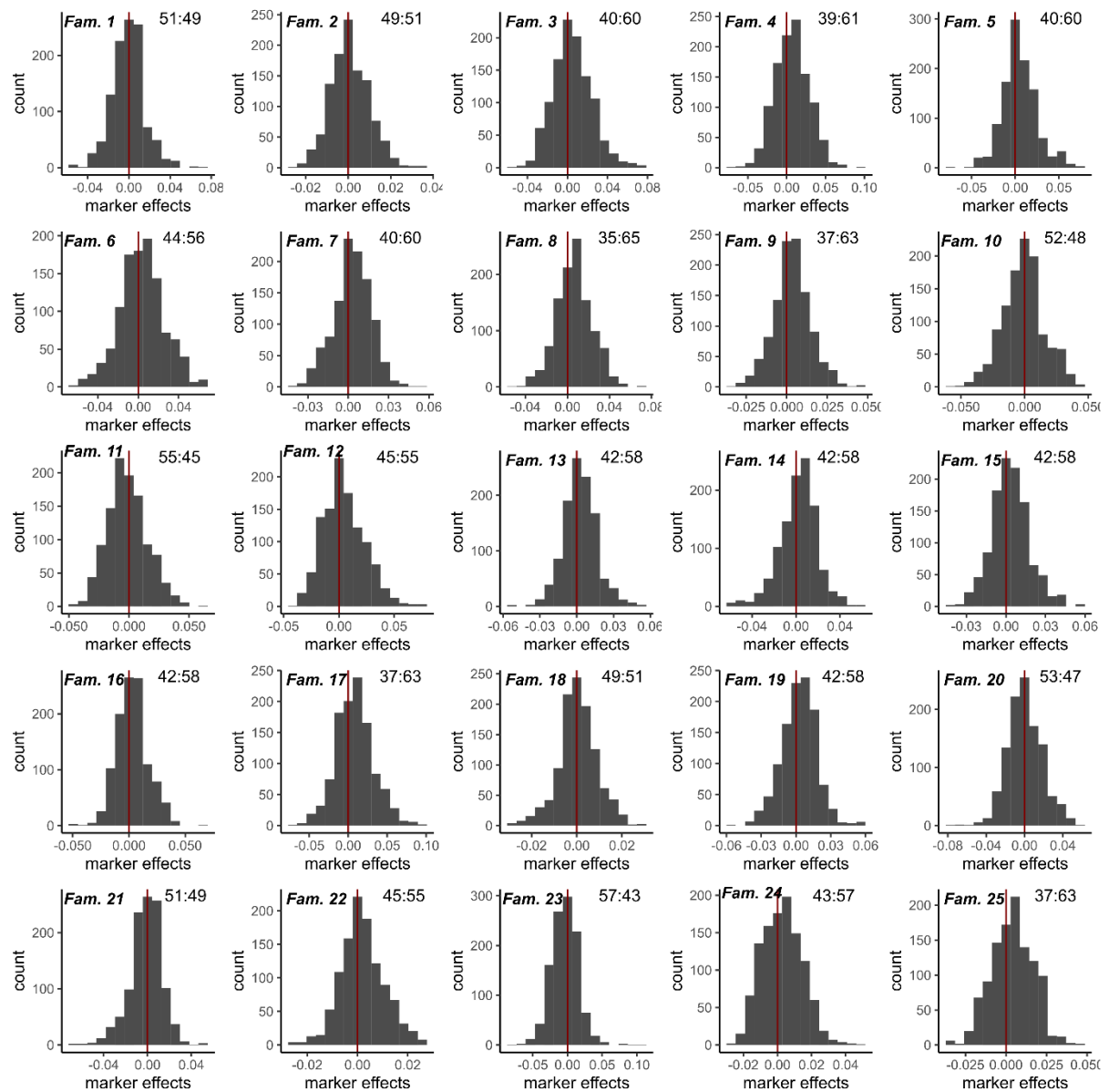


Figure S6. Distributions of marker effects for DTS. For DTS, positive marker effects represent favorable primary alleles and negative marker effects represent favourable secondary alleles.

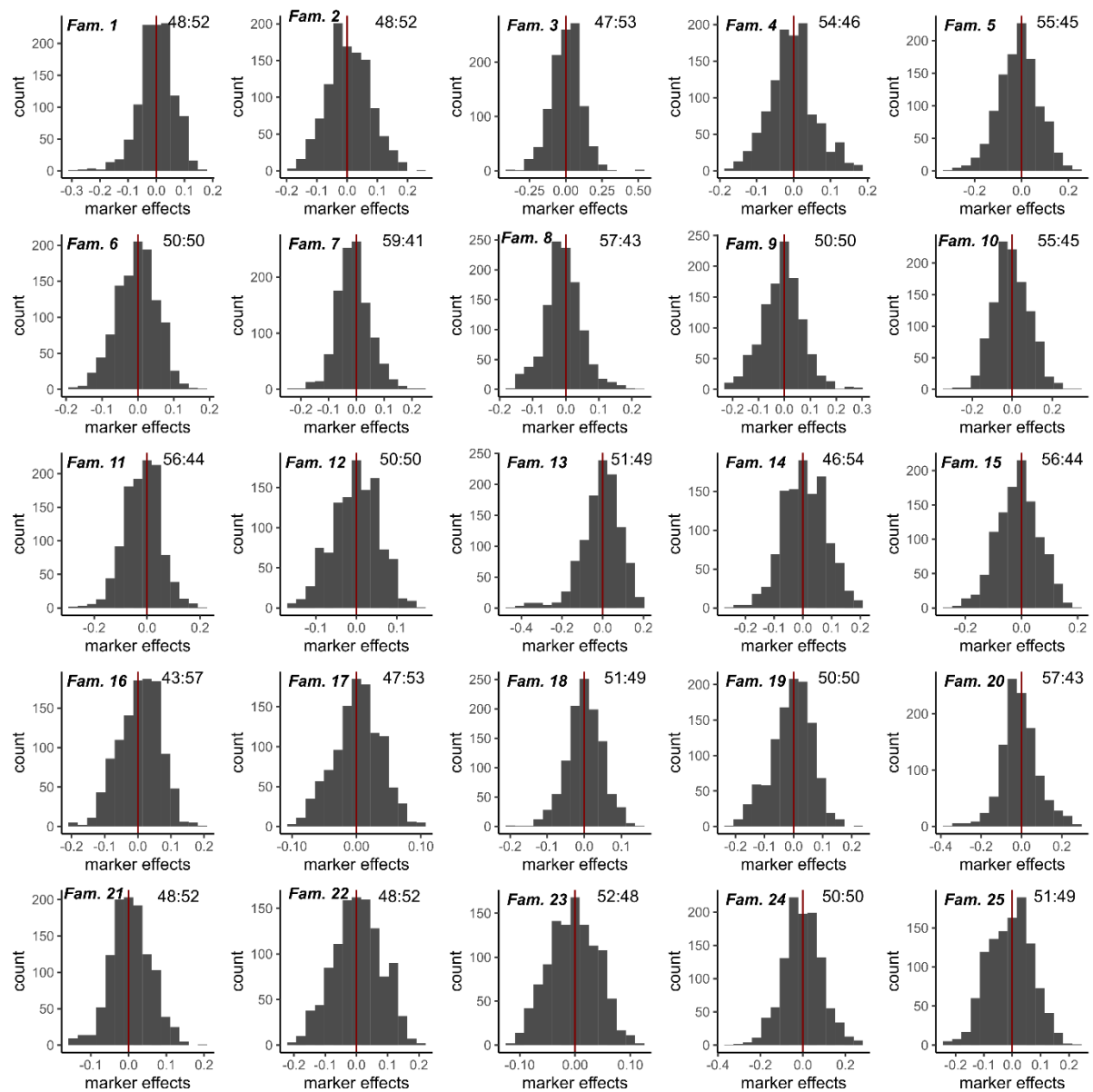


Figure S7. Distributions of marker effects for CL. For CL, negative marker effects represent favorable primary allele and positive marker effect represent favourable secondary allele.

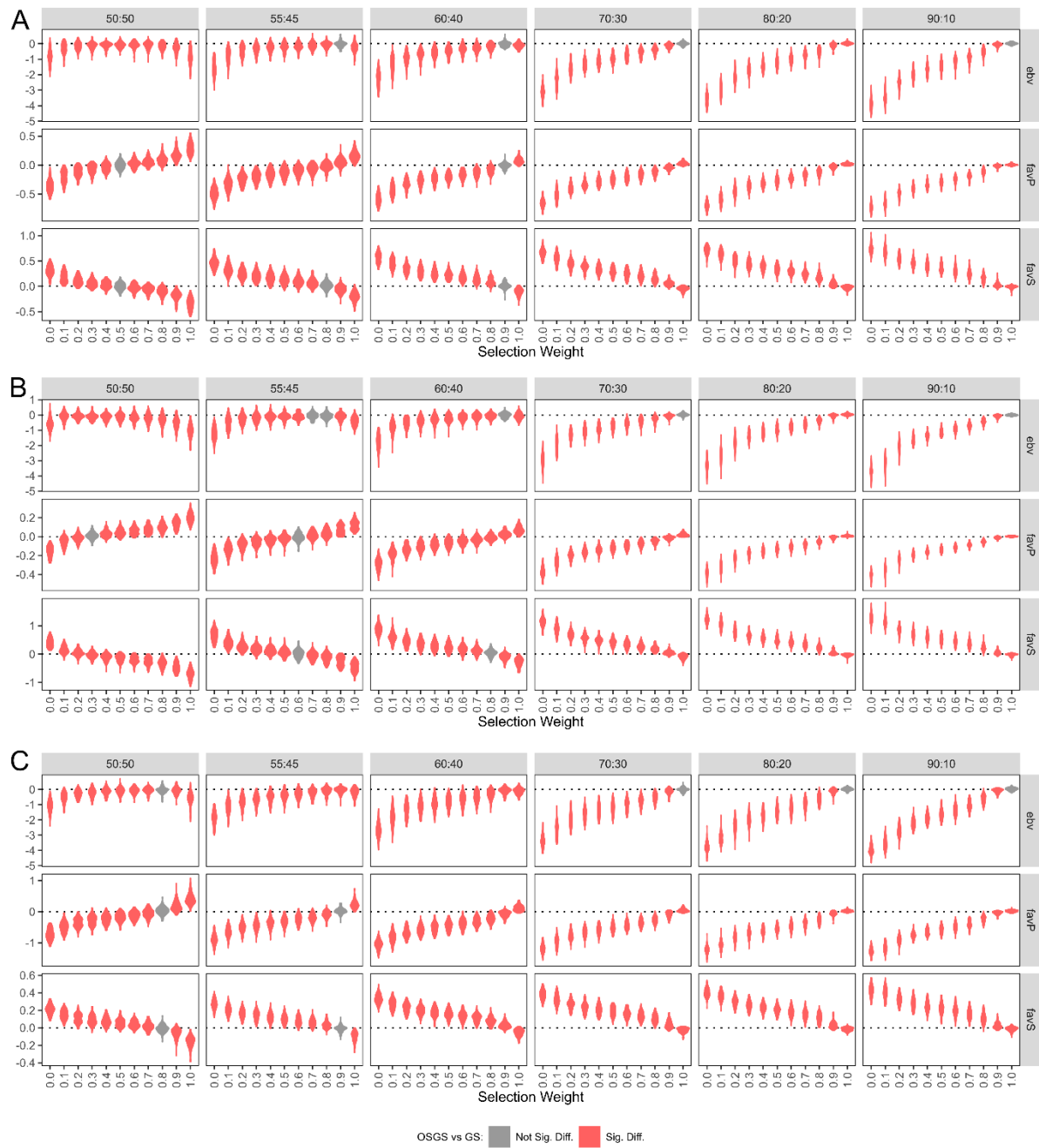


Figure S8. Performance comparison of OSGS under different ω against GS in simulated populations with 2cM/QTL. We applied a single generation of selection under OSGS/GS on 100 simulated [A] F₂, [B] BC₁ and [C] rBC₁ populations (2cM/QTL) and evaluated the change in true breeding value (ΔBV), P proportion (ΔP) and S proportion (ΔS). Significance is determined by t-test with Bonferroni correction ($p=0.05/25$).

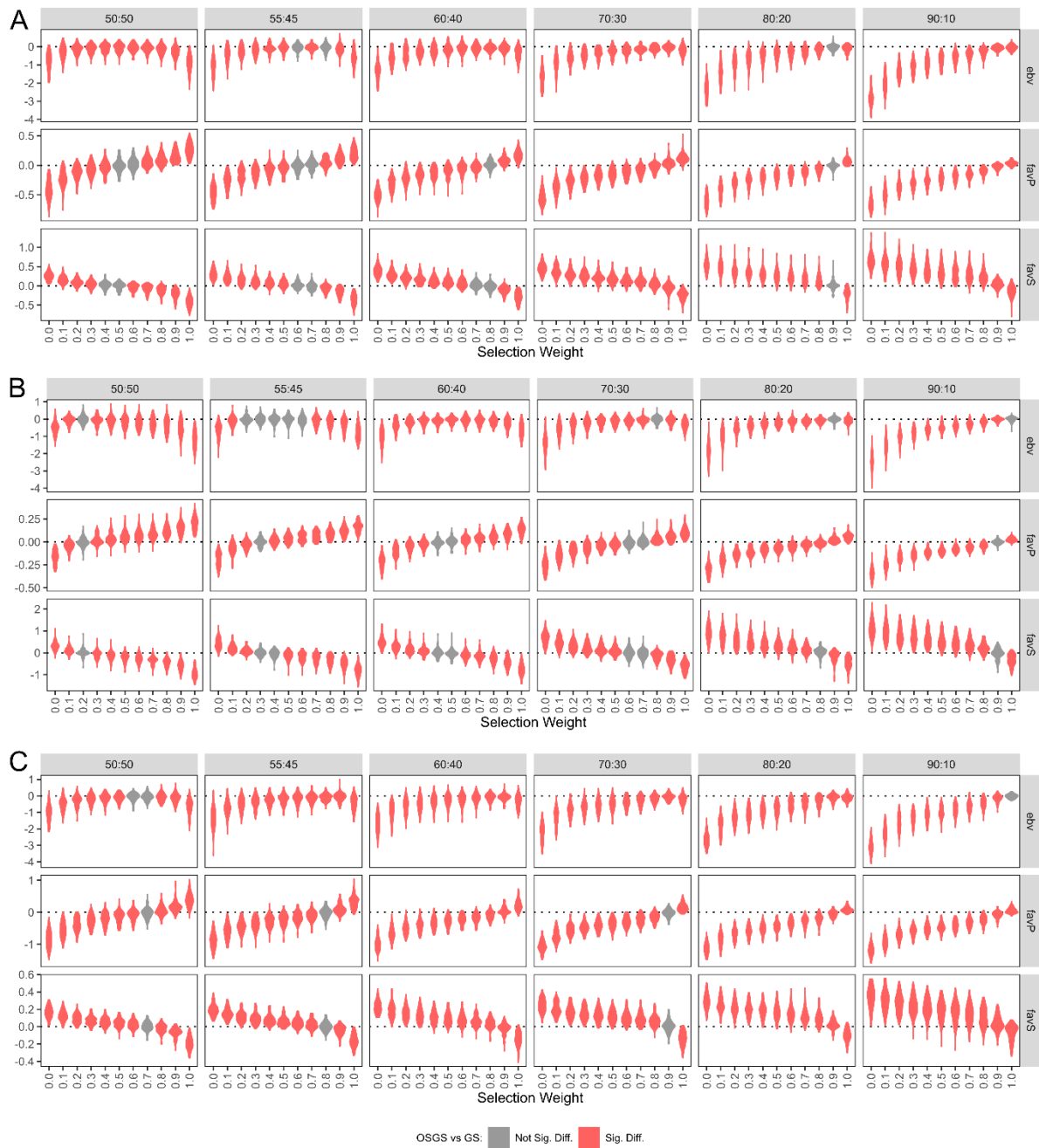


Figure S9. Performance comparison of OSGS under different ω against GS in simulated populations with 20cM/QTL. We applied a single generation of selection under OSGS/GS on 100 simulated **[A] F_2** , **[B] BC_1** and **[C] rBC_1** populations (20cM/QTL) and evaluated the change in true breeding value (ΔBV), P proportion (ΔP) and S proportion (ΔS). Significance is determined by t-test with Bonferroni correction ($p=0.05/25$).

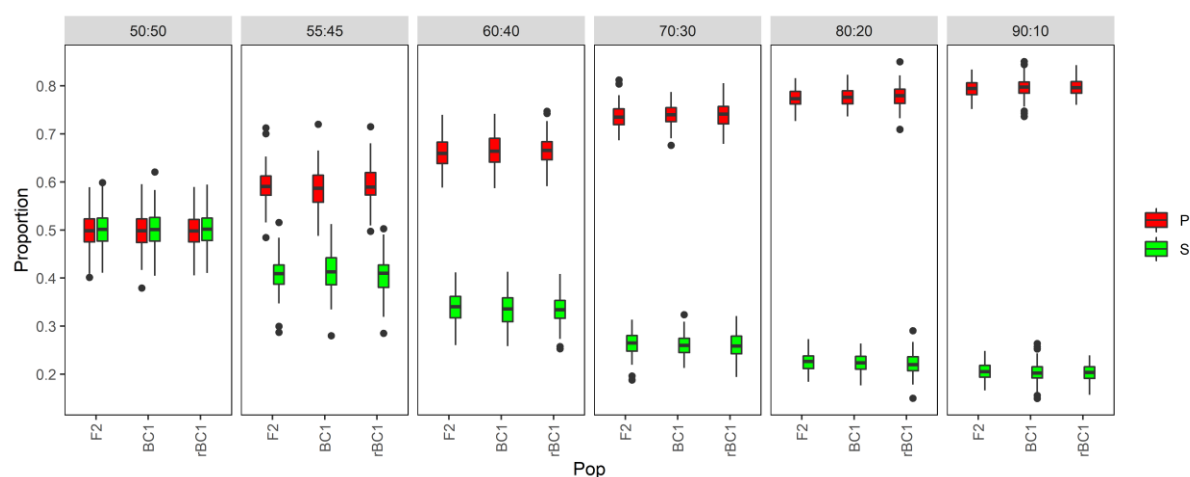


Figure S10. Comparison of true and estimated P:S proportions. Each boxplot represents the estimated P or S proportions from 100 simulations. The proportions estimated from rrBLUP match with the true proportions reasonably well. P is overestimated when the true P:S are 55:45 or 60:40, while P is underestimated when the true P:S are 80:20 or 90:10. There is little to no difference in the proportions estimated from F₂, BC₁ or rBC₁ populations.

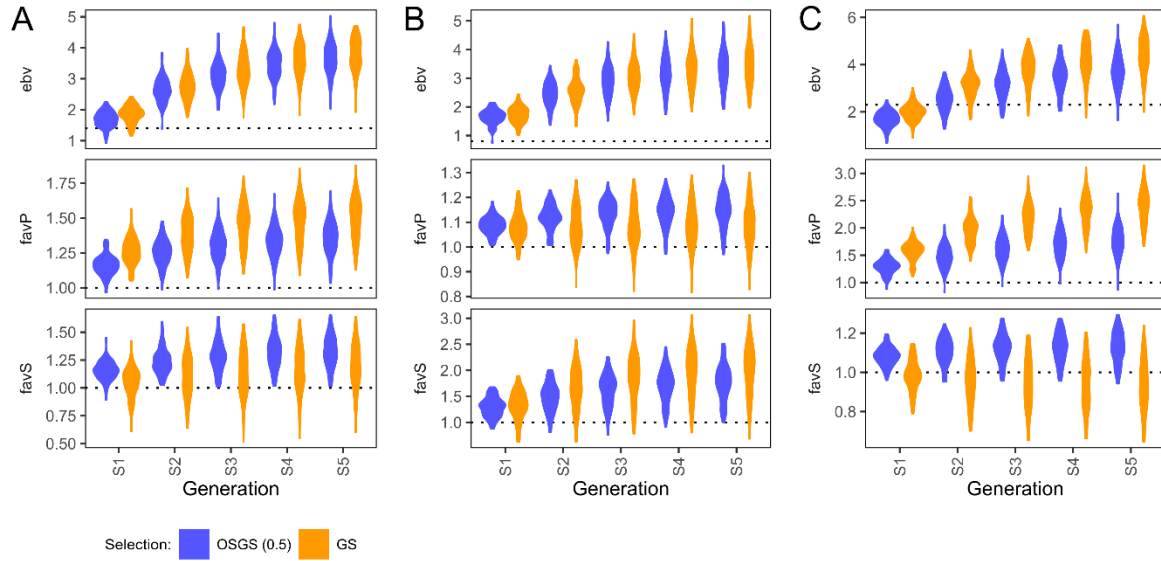


Figure S11. Performance comparison of OSGS against GS under recurrent selection. We applied five generations of recurrent selection under OSGS/GS on 100 simulated [A] F₂, [B] BC₁ and [C] rBC₁-derived populations (20cM/QTL) with P:S of 60:40. We showed the change in true breeding value (ΔBV_i), P proportion (ΔP_i) and S proportion (ΔS_i), where i is either OSGS with $\omega = 0.5$ or GS. ΔBV_i is calculated as $(\mu_{BV,i} - \sigma_{BV,0})/\mu_{BV,0}$, ΔP_i as $\mu_{P,i}/\mu_{P,0}$ and ΔS_i as $\mu_{S,i}/\mu_{S,0}$.