

Table S6. Five-fold cross validation test results for the population consisting of G1 and G2.

Trait	Model	N	N		CV1	CV2	CV3	CV4	CV5	mean	SE
			G1	G2							
Tree height	BayesA	142	47	95	0.53	0.59	0.51	0.69	0.55	0.57	0.03
	BayesB	142	47	95	0.51	0.52	0.54	0.64	0.72	0.59	0.04
	BayesC	142	47	95	0.58	0.58	0.31	0.66	0.48	0.52	0.05
	BL	142	47	95	0.45	0.44	0.63	0.53	0.66	0.54	0.04
	BRR	142	47	95	0.54	0.69	0.63	0.74	0.42	0.60	0.05
Wood stiffness	BayesA	145	44	101	0.57	0.55	0.58	0.59	0.57	0.57	0.01
	BayesB	145	44	101	0.53	0.54	0.44	0.64	0.65	0.56	0.03
	BayesC	145	44	101	0.37	0.73	0.32	0.67	0.49	0.52	0.07
	BL	145	44	101	0.59	0.67	0.36	0.53	0.41	0.51	0.05
	BRR	145	44	101	0.61	0.35	0.40	0.52	0.61	0.50	0.05
Male flower quantity	BayesA	148	47	101	0.58	0.25	0.56	0.54	0.36	0.46	0.06
	BayesB	148	47	101	0.48	0.45	0.56	0.23	0.68	0.48	0.06
	BayesC	148	47	101	0.65	0.37	0.40	0.44	0.42	0.46	0.05
	BL	148	47	101	0.58	0.43	0.26	0.57	0.43	0.45	0.05
	BRR	148	47	101	0.41	0.27	0.43	0.48	0.65	0.45	0.05

Table S7. (a) Five-fold cross validation test results for the population consisting of G1_parent and G2, (b) Five-fold cross validation test results for the population consisting of G1_unrelated and G2.**(a)G1_parent +G2**

Trait	Model	N	N		CV1	CV2	CV3	CV4	CV5	mean	SE
			G1	G2							
Tree height	BRR	116	21	95	0.68	0.41	0.32	0.32	0.48	0.44	0.06
Wood stiffness	BayesA	119	18	101	0.56	0.58	0.49	0.63	0.40	0.53	0.03
Male flower quantity	BayesB	122	21	101	0.35	0.35	0.26	0.56	0.33	0.37	0.05

(b)G1_unrelated +G2

Trait	Model	N	N		CV1	CV2	CV3	CV4	CV5	mean	SE
			G1	G2							
Tree height	BRR	121	26	95	0.49	0.54	0.68	0.71	0.82	0.65	0.05
Wood stiffness	BayesA	127	26	101	0.39	0.47	0.35	0.53	0.67	0.48	0.05
Male flower quantity	BayesB	127	26	101	0.73	0.72	0.23	0.42	0.49	0.52	0.08

G1_parent: G1 clones with G2 offspring. G1_unrelated: G1 clones that left no offspring in G2.

For each trait, the model providing the highest accuracy over the full dataset was used (See Table 2).