

Supporting Files

Files S1-S6 are available for download at .

File S1 – Genotypic data.

File S2 – Pedigree data.

File S3 – Breeding values.

File S4 – Deregressed phenotypes.

File S5 – Random Regression Best Linear Unbiased Predictor (RR-BLUP) R script.

File S6 – Bayes A and Bayes C π R script.

Table S1 Predictive ability ($r_{\hat{y}y}$) and standard error (SE) of RR-BLUP model under two different cross validation schemes: 10-fold cross validation and leave one-out (L1-Out)

Trait Category	Trait	Methods			
		$r_{\hat{y}y}$ - 10-Fold	SE - 10-Fold	$r_{\hat{y}y}$ - L1-Out	SE - L1-Out
Growth	HT	0.39	0.029	0.38	0.029
	HTLC	0.45	0.027	0.46	0.027
	BHLC	0.49	0.026	0.49	0.026
	DBH	0.46	0.027	0.46	0.027
Development	CWAL	0.48	0.029	0.48	0.030
	CWAC	0.38	0.026	0.40	0.027
	BD	0.27	0.032	0.27	0.032
	BA	0.51	0.025	0.52	0.025
	Rootnum_bin	0.28	0.030	0.28	0.030
	Rootnum	0.24	0.031	0.24	0.031
Disease resistance	Rust_bin	0.29	0.032	0.29	0.033
	Rust_gall_vol	0.23	0.033	0.24	0.033
Wood	StiffnessTree	0.43	0.027	0.43	0.028
	Lignin	0.17	0.032	0.17	0.032
	Latewood%4	0.24	0.031	0.25	0.031
	Density	0.20	0.032	0.21	0.032
	C5C6	0.26	0.031	0.27	0.031

Table S2 Regression Beta and standard error (SE) of the RR-BLUP model under two different cross validation schemes: 10-fold cross validation and leave one-out (L1-Out)

Trait Category	Trait	Methods			
		Beta - 10-Fold	SE - 10-Fold	Beta - L1-Out	SE - L1-Out
Growth	HT	1.18	0.10	1.12	0.09
	HTLC	1.20	0.08	1.21	0.08
	BHLC	1.11	0.07	1.11	0.07
	DBH	1.19	0.08	1.17	0.08
Development	CWAL	1.04	0.06	1.03	0.06
	CWAC	1.10	0.09	1.13	0.09
	BD	1.23	0.15	1.19	0.15
	BA	1.13	0.07	1.13	0.06
	Rootnum_bin	1.36	0.15	1.31	0.15
	Rootnum	1.51	0.20	1.48	0.19
Disease resistance	Rust_bin	1.13	0.13	1.12	0.13
	Rust_gall_vol	1.29	0.19	1.23	0.18
Wood quality	StiffnessTree	1.12	0.08	1.10	0.08
	Lignin	1.00	0.19	0.96	0.19
	Latewood%4	1.01	0.14	1.03	0.13
	Density	1.26	0.20	1.27	0.20
	C5C6	1.22	0.15	1.23	0.15

Table S3 Standard error of the prediction models for the different methods tested.

Trait Category	Trait	Methods			
		RR-BLUP	BLASSO	Bayes A	Bayes Cπ
Growth	HT	0.029	0.029	0.029	0.029
	HTLC	0.027	0.027	0.028	0.028
	BHLC	0.026	0.026	0.026	0.026
	DBH	0.027	0.027	0.027	0.027
Development	CWAL	0.029	0.030	0.030	0.030
	CWAC	0.026	0.027	0.027	0.027
	BD	0.032	0.032	0.032	0.032
	BA	0.025	0.025	0.025	0.025
	Rootnum_bin	0.030	0.030	0.031	0.031
	Rootnum	0.031	0.031	0.031	0.031
Disease resistance	Rust_bin	0.032	0.033	0.031	0.031
	Rust_gall_vol	0.033	0.033	0.033	0.033
Wood	StiffnessTree	0.027	0.028	0.028	0.028
	Lignin	0.032	0.032	0.032	0.032
	Latewood%4	0.031	0.031	0.032	0.031
	Density	0.032	0.032	0.032	0.032
	C5C6	0.031	0.031	0.031	0.031

Table S4 Accuracies of Genome Wide Selection models in 17 different traits of Loblolly Pine. h^2_m represents the Mendelian segregation and was the correction factor used to convert predictive abilities into accuracies

Trait Category	Trait	h^2_m	Methods			
			RR-BLUP	BLASSO	Bayes A	Bayes Cπ
Growth	HT	0.66	0.48	0.47	0.47	0.47
	HTLC	0.53	0.62	0.60	0.60	0.60
	BHLC	0.52	0.68	0.68	0.68	0.68
	DBH	0.66	0.57	0.57	0.57	0.57
Development	CWAL	0.43	0.58	0.55	0.55	0.55
	CWAC	0.63	0.60	0.58	0.59	0.59
	BD	0.26	0.53	0.49	0.53	0.53
	BA	0.5	0.72	0.72	0.72	0.72
	Rootnum_bin	0.5	0.40	0.40	0.38	0.40
	Rootnum	0.43	0.37	0.40	0.38	0.37
Disease resistance	Rust_bin	0.21	0.63	0.61	0.74	0.74
	Rust_gall_vol	0.18	0.57	0.57	0.66	0.68
Wood	StiffnessTree	0.37	0.71	0.64	0.69	0.69
	Lignin	0.11	0.51	0.51	0.51	0.51
	Latewood%4	0.17	0.58	0.58	0.56	0.58
	Density	0.09	0.67	0.73	0.77	0.73
	C5C6	0.14	0.69	0.67	0.67	0.67

Table S5 Regression coefficients estimates of deregressed phenotypes regressed on Direct Genetic Values.

Estimates for the model RR-BLUP are presented in the Table S2.

Trait	BLASSO	SE (BLASSO)	Bayes A	SE (Bayes A)	BayesCπ	SE (Bayes Cπ)
HT	0.97	0.08	0.90	0.08	1.02	0.09
HTLC	0.98	0.07	0.93	0.06	1.00	0.07
BHLC	0.98	0.06	0.98	0.06	1.01	0.06
DBH	0.99	0.07	0.97	0.06	1.02	0.07
CWAL	0.90	0.08	0.87	0.08	0.95	0.08
CWAC	0.91	0.06	0.91	0.06	0.99	0.06
BD	0.97	0.13	0.97	0.12	1.08	0.13
BA	0.96	0.06	0.99	0.06	0.99	0.06
Rootnum_bin	1.01	0.11	0.85	0.10	1.04	0.12
Rootnum	1.01	0.13	1.04	0.14	1.05	0.14
Rust_bin	0.88	0.11	1.04	0.10	1.00	0.10
Rust_gall_vol	1.00	0.14	1.04	0.13	1.11	0.13
StiffnessTree	0.83	0.06	1.04	0.08	0.99	0.07
Lignin	1.01	0.20	0.87	0.17	1.11	0.21
Latewood%4	0.93	0.13	0.84	0.12	0.96	0.13
Density	0.95	0.14	0.99	0.14	1.04	0.15
C5C6	0.95	0.12	0.97	0.13	1.01	0.13

Table S6 Predictive abilities of RR-BLUP B when a reduced subset of markers was used compared to the predictive abilities of RR-BLUP

Trait	RR-BLUP	RR-BLUP B	Subset length
HT	0.38	0.38	4630
HTLC	0.45	0.45	3910
BHLC	0.49	0.50	1380
DBH	0.46	0.46	3800
CWAL	0.38	0.39	820
CWAC	0.48	0.47	590
BD	0.27	0.28	1110
BA	0.51	0.52	1040
Rootnum_bin	0.28	0.28	2550
Rootnum	0.23	0.24	3350
Rust_bin	0.29	0.33	310
Rust_gall_vol	0.23	0.37	100
StiffnessTree	0.43	0.44	1300
Lignin	0.17	0.17	4240
Latewood%4	0.24	0.24	3820
Density	0.20	0.24	240
C5C6	0.25	0.25	4790