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

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