Figure S5

A

	Genetic effect size					
	0.5	2	4	6	10	15
Lasso	2.87E-29	1.13E-21	1.30E-18	2.55E-11	2.22E-29	2.70E-30
Ridge	2.46E-30	2.13E-26	1.16E-26	1.26E-40	3.65E-33	2.41E-33
Random Forest	1.82E-23	5.45E-27	2.44E-17	1.56E-26	7.94E-29	8.92E-24
Elastic Net	8.28E-30	4.55E-24	7.09E-23	2.76E-19	8.34E-32	4.74E-31
mgRF	8.10E-07	1.50E-05	1.57E-05	1.37E-11	1.07E-**22**	4.70E-24

	Noise level					
	0.2	0.4	1	1.5	3	5
Lasso	1.33E-26	1.13E-21	7.75E-23	1.77E-19	2.65E-08	0.000243
Ridge	1.58E-29	2.13E-26	8.79E-27	4.93E-26	3.40E-30	1.35E-24
Random Forest	9.47E-30	5.45E-27	2.53E-27	7.77E-26	2.87E-30	1.75E-24
Elastic Net	2.33E-28	4.55E-24	5.34E-25	3.39E-23	7.30E-18	9.40E-11
mgRF	1.73E-06	1.50E-05	1.07E-08	2.87E-06	3.44E-07	4.17E-08

	Gene effect size					
	0.05	0.1	0.15	0.2	0.3	0.45
Lasso	8.68E-09	1.62E-26	1.68E-20	1.66E-28	1.29E-24	2.87E-29
Ridge	1.15E-23	6.38E-29	4.72E-26	8.79E-31	1.08E-25	2.46E-30
Random Forest	8.23E-16	1.40E-21	2.13E-19	1.52E-21	9.55E-18	1.82E-23
Elastic Net	5.50E-16	5.98E-31	1.73E-23	4.97E-30	4.48E-**25**	8.28E-30
mgRF	3.68E-07	8.27E-07	2.52E-06	8.72E-10	2.35E-07	8.10E-07

B

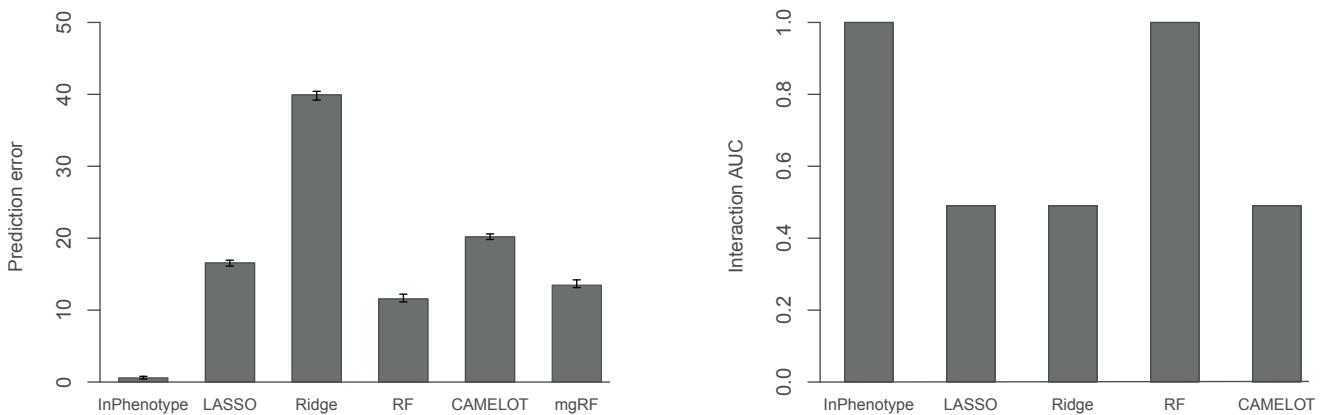**Figure S5**. **Performance comparisons.** (**A**) Shown are P-values of paired *t*-tests when comparing prediction errors of InPhenotype to prediction errors of other methods (rows) using one causal SNP. Each column refers to a different genetic effect size (**top left**), noise level (**top right**) and gene effect size (**bottom**). (**B**) prediction errors (**left**) and interaction AUCs (**right**) of various methods, for the simulation of joint gene-locus effect in the presence of epistasis.