

An ensemble-based likelihood ratio approach for family-based genomic risk prediction

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Table S1 Significant interaction effects identified by logistic regression in the genome-wide prediction

	Estimate	S.E.	P value
<i>rs4546404:rs11647668</i>	2.4106	0.9370	0.0101
<i>rs4546404:rs2708919</i>	-2.7864	0.8619	0.0012
<i>rs4546404:rs870488</i>	2.2240	1.1028	0.0437
<i>rs4546404:rs755101</i>	4.4802	1.8256	0.0141
<i>rs184817:rs10492664</i>	-6.1239	3.0418	0.0441
<i>rs184817:rs12910488</i>	2.6292	1.1788	0.0257
<i>rs184817:rs1389660</i>	-3.6426	1.2971	0.0050
<i>rs184817:rs8002852</i>	9.4209	3.9425	0.0169
<i>rs184817:rs1317508</i>	-3.9708	1.4344	0.0056
<i>rs184817:rs2833834</i>	2.4553	1.2067	0.0419
<i>rs10492664:rs12910488</i>	-3.6646	1.8187	0.0439
<i>rs10492664:rs13058781</i>	-4.9072	2.2105	0.0264
<i>rs12910488:rs13058781</i>	-2.5370	0.8899	0.0044
<i>rs1389660:rs4078017</i>	5.8247	2.6567	0.0283
<i>rs13058781:rs755101</i>	5.1839	1.6973	0.0023
<i>rs8002852:rs755101</i>	19.8486	8.4126	0.0183
<i>rs1487044:rs4078017</i>	-20.7386	8.5690	0.0155
<i>rs1487044:rs2833834</i>	6.1731	3.0511	0.0431
<i>rs11647668:rs870488</i>	-2.8489	1.1567	0.0138
<i>rs11647668:rs17636733</i>	2.5013	0.8700	0.0040
<i>rs11647668:rs2833834</i>	2.4180	1.1431	0.0344

<i>rs2708919:rs2833834</i>	-1.7021	0.7760	0.0283
<i>rs870488:rs4078017</i>	-9.1475	3.0954	0.0031
<i>rs870488:rs2833834</i>	2.5804	1.1409	0.0237
<i>rs755101:rs4078017</i>	7.2114	2.9689	0.0151
<i>rs755101:rs17636733</i>	-3.9611	1.2933	0.0022
<i>rs755101:rs7595103</i>	8.0003	3.2795	0.0147
<i>rs1882668:rs1317508</i>	3.9526	1.4694	0.0071
<i>rs1317508:rs4078017</i>	-10.3021	3.8606	0.0076
<i>rs1317508:rs9396888</i>	2.1063	1.0018	0.0355
<i>rs4078017:rs17636733</i>	13.1547	3.6915	0.0004
