Analysis Summary: Photic Sneeze

Phenotype Description

Photic sneeze cases were defined as saying "Yes" to at least one of the following questions:

- Ten Things About You ("Do you have a tendency to sneeze when exposed to bright sunlight?")
- Research Snippets ("Do you have a tendency to sneeze when exposed to bright sunlight?")

Controls were defined as saying "No" to either question above. Respondents who answered "Yes" to one question and "No" to the other were excluded.

Phenotype Statistics

The following table shows demographics of unrelated, European individuals included in the GWAS.

Phenotype	Group	Total	M	F	(0,30]	(30,45]	(45,60]	(60,Inf]
photic_sneeze	case	32446	16338	16108	4434	9839	9102	9071
	control	67249	33645	33604	7609	17784	18358	23498

The following table shows the phenotypic distribution across 23andMe genotyping platforms for individuals included in the GWAS.

Phenotype	Group	Total	v1/v2	v3	v4
photic_sneeze	case	32446	3696	24731	4019
	control	67249	7467	51201	8581

Null Model with Covariates

The following table shows results of fitting a model for the trait based on just the covariates. Principal coordinates have been standardized, so these effect sizes are in units of standard deviations.

	Estimate	Std. Error	z value	Pr(>|z|)	LRT	Pr(>Chi)
age	−0.01057	0.000431	−24.5	8.2×10^{-133}	606.0	8.4×10^{-134}
sexF	−0.00660	0.013611	−0.5	0.63	0.2	0.63
pc.0	0.08782	0.007203	12.2	3.4×10^{-34}	154.7	1.6×10^{-35}
pc.1	−0.06116	0.006979	−8.8	1.9×10^{-18}	78.3	8.8×10^{-19}
pc.2	−0.02523	0.007021	−3.6	0.00033	13.0	0.00032
pc.3	0.03191	0.006801	4.7	2.7×10^{-6}	22.0	2.7×10^{-6}
pc.4	0.00812	0.006777	1.2	0.23	1.4	0.23

SNP-level QC information

The following table shows results for QC filters on the genotyped data:

	failed	passed
no filters	0	1030430
not V1-only, chrM, chrY	4790	1025640
parent-offspring test	2129	1023511
MAF > 0%	3203	1020494
HWE > 1e-20	48225	972832
gt.rate > 90%	30775	952826
batch effects	28267	945446

The following table shows results for QC filters on the imputed dosage data:

	failed	passed
no filters	0	13733809
MAF > 0%	0	13733809

imputation quality	0	13733809
batch effects	2168	13731641

The following table shows results for QC filters on the merged association test results:

	passed	total
imputed only	12833621	12833621
both passed	898002	13731623
genotyped only	47444	13779067
no test result	−10843	13768224
failed to converge	−38367	13729857

Genetic Association Tests

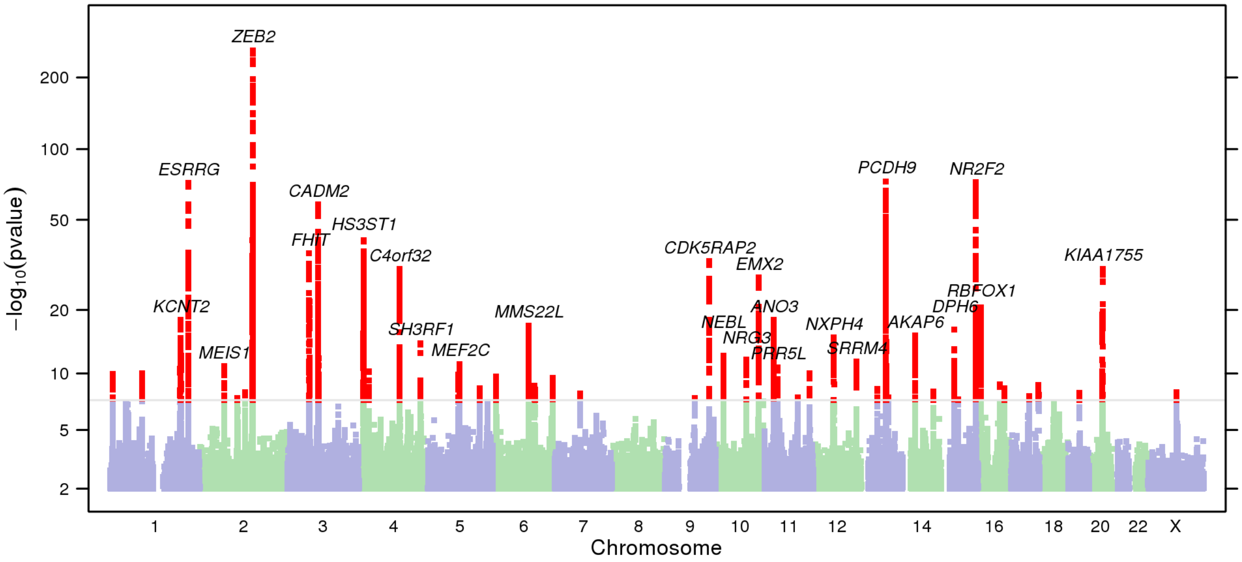
We performed logistic regression assuming an additive model for allelic effects, using the model:

photic_sneeze ~ age + sex + pc.0 + pc.1 + pc.2 + pc.3 + pc.4 + genotype

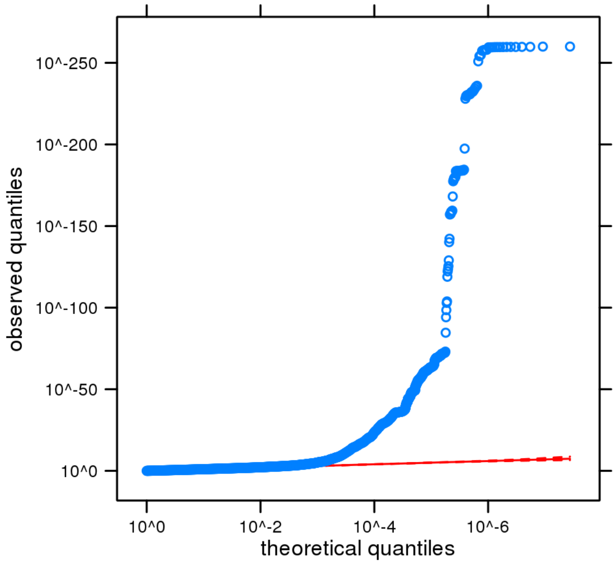
This genome-wide association analysis includes data from 32446 cases and 67249 controls of European ancestry, filtered to remove close relatives.

The results in this report have been adjusted for a genomic control inflation factor λ=1.118. The equivalent inflation factor for 1000 cases and 1000 controls λ_{1000}= 1.003 , and for 10000, λ_{10000}= 1.027 .

Manhattan Plot



Q-Q Plot of GWAS Results



Index SNPs for Strongest Associations

cytoband	assay.name	scaffold	position	alleles	src	pvalue	OR	95% CI	gene.context
2q22.3	rs1533426	chr2	146119018	A/G	I	1.0×10^{-260}	0.703	[0.689,0.717]	ZEB2---[]
13q21.32	rs9571757	chr13	67905237	A/C	I	8.6×10^{-74}	1.206	[1.182,1.231]	PCDH9---[]
15q26.2	rs1541995	chr15	96316457	A/C	I	3.5×10^{-73}	1.226	[1.199,1.253]	[]---NR2F2
1q41	rs12755398	chr1	217117146	A/G	I	1.0×10^{-72}	0.773	[0.751,0.795]	ESRRG---[]---GPATCH2
3p12.1	rs1146751	chr3	84889597	C/T	I	8.6×10^{-59}	1.179	[1.155,1.202]	[]---CADM2
4p15.33	rs9991510	chr4	12080930	C/T	I	1.9×10^{-41}	1.150	[1.127,1.174]	HS3ST1---[]
3p14.2	rs633798	chr3	59861871	C/T	I	2.0×10^{-36}	1.147	[1.123,1.172]	[FHIT]
9q33.2	rs887807	chr9	123050797	C/T	I	8.3×10^{-34}	1.326	[1.266,1.389]	DBC1---[]---CDK5RAP2
20q11.23	rs4811602	chr20	36849088	A/G	I	2.5×10^{-31}	0.886	[0.868,0.904]	[KIAA1755]
4q25	rs1376216	chr4	112659154	A/G	I	3.4×10^{-31}	1.130	[1.107,1.153]	[]---C4orf32
10q26.11	rs10886094	chr10	119283708	A/C	I	1.1×10^{-28}	1.134	[1.109,1.159]	PDZD8---[]--EMX2
16p13.3	rs368977885	chr16	7090929	D/I	I	2.6×10^{-21}	0.903	[0.885,0.923]	[]---RBFOX1
1q31.3	rs7534788	chr1	195835131	A/G	I	9.8×10^{-19}	1.097	[1.075,1.120]	[]---KCNT2
11p14.3	rs10642753	chr11	26062101	D/I	I	1.1×10^{-18}	1.141	[1.108,1.175]	LUZP2---[]---ANO3
6q16.1	rs1338552	chr6	98346633	C/T	I	1.0×10^{-17}	1.092	[1.070,1.115]	MMS22L---[]---POU3F2
15q14	rs144328717	chr15	36126406	D/I	I	6.3×10^{-17}	0.905	[0.884,0.926]	DPH6---[]---C15orf41
14q12	rs11850550	chr14	33137220	C/G	I	5.7×10^{-16}	0.919	[0.900,0.938]	[AKAP6]
12q13.3	rs55836402	chr12	57612766	D/I	I	1.2×10^{-15}	0.917	[0.898,0.937]	[NXPH4]
13q21.33	rs74677756	chr13	69606142	C/T	I	6.3×10^{-15}	1.089	[1.066,1.113]	[]---KLHL1
4q32.3	rs17626617	chr4	170013910	C/T	I	9.2×10^{-15}	1.112	[1.083,1.143]	CBR4--[]-SH3RF1
10p12.31	rs2148307	chr10	21052620	A/T	I	5.6×10^{-13}	0.929	[0.910,0.948]	PLXDC2---[]--NEBL
10q23.1	rs11814950	chr10	84722619	A/G	I	2.0×10^{-12}	0.860	[0.825,0.897]	[NRG3]
12q24.23	rs1568923	chr12	119419603	C/G	I	3.4×10^{-12}	0.926	[0.907,0.946]	[SRRM4]
5q14.3	rs10067451	chr5	87942506	A/G	I	7.3×10^{-12}	0.898	[0.871,0.926]	TMEM161B---[]--MEF2C
2p14	rs141078219	chr2	66857453	A/T	I	1.3×10^{-11}	1.080	[1.056,1.104]	MEIS1--[]---ETAA1
11p12	rs35407642	chr11	36473052	A/G	I	1.8×10^{-11}	0.932	[0.913,0.951]	[PRR5L]
1q31.3	rs61406265	chr1	193936939	C/T	I	2.8×10^{-11}	0.916	[0.893,0.940]	CDC73---[]
4p15.1	rs7697398	chr4	27813941	A/G	I	5.9×10^{-11}	1.091	[1.063,1.120]	STIM2---[]
1p22.3	rs12120466	chr1	88173984	G/T	I	9.7×10^{-11}	0.855	[0.816,0.896]	LMO4---[]---PKN2
11q24.2	rs7107770	chr11	125100438	C/G	I	1.0×10^{-10}	0.915	[0.890,0.940]	[PKNOX2]
1p36.23	rs10864302	chr1	7487277	C/T	I	1.1×10^{-10}	0.916	[0.892,0.941]	[CAMTA1]
5q14.3	rs67177172	chr5	84520674	A/C	I	1.4×10^{-10}	1.070	[1.048,1.092]	EDIL3---[]
6p24.3	rs1576263	chr6	8690217	G/T	I	2.0×10^{-10}	0.937	[0.919,0.956]	SLC35B3---[]
6q27	rs9347032	chr6	165157684	C/T	I	3.2×10^{-10}	1.069	[1.047,1.091]	[]---C6orf118
11p13	rs1174117	chr11	35686478	A/G	I	4.0×10^{-10}	0.934	[0.914,0.954]	[TRIM44]
16q21	rs3055140	chr16	60371500	D/I	I	1.5×10^{-9}	0.933	[0.912,0.954]	[]
17q25.3	rs35570576	chr17	77536946	C/G	I	1.7×10^{-9}	1.092	[1.061,1.124]	RBFOX3--[]---HP09025
6q22.1	rs4620151	chr6	115513803	A/C	I	2.2×10^{-9}	1.073	[1.049,1.099]	[]---FRK
5q31.3	rs4349753	chr5	144141555	A/T	I	4.0×10^{-9}	0.941	[0.923,0.960]	KCTD16---[]---PRELID2
16q22.3	rs7189864	chr16	73633936	C/G	I	4.1×10^{-9}	1.069	[1.046,1.094]	ZFHX3---[]---PSMD7
13q14.11	rs7319075	chr13	44166996	A/C	I	4.3×10^{-9}	1.085	[1.056,1.116]	[ENOX1]
14q31.2	rs11852029	chr14	83822726	A/G	I	7.8×10^{-9}	1.082	[1.053,1.111]	[]
2q14.3	rs13032103	chr2	125985244	G/T	I	8.6×10^{-9}	1.067	[1.044,1.091]	CNTNAP5---[]
Xq21.1	rs28417201	chrX	79956549	C/T	I	9.1×10^{-9}	1.057	[1.037,1.077]	[BRWD3]

19q12	rs36061463	chr19	31979737	D/I	I	1.1×10^{-8}	0.941	[0.921,0.961]	TSHZ3---[]---THEG5
7q11.22	rs10234796	chr7	70012519	A/G	I	1.2×10^{-8}	0.941	[0.921,0.961]	[AUTS2]
17q22	rs117147772	chr17	52061466	A/G	I	2.3×10^{-8}	1.137	[1.087,1.190]	KIF2B---[]---TOM1L1
13q22.1	rs9318213	chr13	74337218	C/T	I	2.6×10^{-8}	1.059	[1.038,1.081]	[KLF12]
11q14.3	11:92232901:G_GTA	chr11	92232901	D/I	I	2.8×10^{-8}	0.942	[0.923,0.962]	[FAT3]
2q12.1	rs266053	chr2	104090213	C/T	I	3.1×10^{-8}	1.060	[1.039,1.083]	TMEM182---[]---LOC100287010

Quality Statistics for Index SNPs

assay.name	is.v2	is.v3	is.v4	gt.rate	hw.p.value	p.date	freq.b	avg.rsqr	min.rsqr	p.batch	dose.b	qc.mask
rs1533426	FALSE	FALSE	FALSE					0.9981	0.9976	0.51	0.5450	v2v3v4
rs9571757	FALSE	TRUE	FALSE	0.9996	0.31	0.0079	0.5493	0.9824	0.9082	0.083	0.5497	v2v3v4
rs1541995	FALSE	FALSE	FALSE					0.9964	0.9947	0.058	0.7049	v2v3v4
rs12755398	FALSE	FALSE	FALSE					0.9826	0.9721	0.18	0.8558	v2v3v4
rs1146751	TRUE	TRUE	TRUE	0.9892	5.8×10^{-8}	0.0084	0.5112	1.0000	0.9998	0.46	0.5113	v2v3v4
rs9991510	FALSE	FALSE	FALSE					0.9625	0.9423	0.12	0.4739	v2v3v4
rs633798	FALSE	FALSE	FALSE					0.9457	0.9238	0.64	0.6364	v2v3v4
rs887807	TRUE	TRUE	TRUE	0.9999	0.010	0.24	0.9454	0.9993	0.9976	0.13	0.9447	v2v3v4
rs4811602	FALSE	FALSE	FALSE					0.9521	0.9276	0.081	0.5389	v2v3v4
rs1376216	FALSE	FALSE	FALSE					0.9871	0.9772	0.58	0.6051	v2v3v4
rs10886094	TRUE	TRUE	TRUE	0.9992	1.9×10^{-23}	0.0074	0.7151	0.9979	0.9965	0.20	0.7166	v2v3v4
rs368977885	FALSE	FALSE	FALSE					0.9447	0.9201	0.069	0.3945	v2v3v4
rs7534788	FALSE	FALSE	FALSE					0.9789	0.8948	0.0089	0.3795	v2v3v4
rs10642753	FALSE	FALSE	FALSE					0.9857	0.9810	0.44	0.8586	v2v3v4
rs1338552	FALSE	FALSE	FALSE					0.9673	0.9427	0.018	0.5159	v2v3v4
rs144328717	FALSE	FALSE	FALSE					0.9525	0.8615	0.23	0.7576	v2v3v4
rs11850550	FALSE	FALSE	FALSE					0.9418	0.9370	0.15	0.5113	v2v3v4
rs55836402	FALSE	FALSE	FALSE					0.9756	0.9680	0.77	0.3552	v2v3v4
rs74677756	FALSE	FALSE	FALSE					0.9821	0.9793	0.44	0.6614	v2v3v4
rs17626617	TRUE	TRUE	TRUE	0.9990	0.00051	0.11	0.8375	0.9998	0.9990	0.62	0.8389	v2v3v4
rs2148307	FALSE	FALSE	FALSE					0.9984	0.9924	0.31	0.4393	v2v3v4
rs11814950	FALSE	FALSE	FALSE					0.9941	0.9862	0.21	0.0614	v2v3v4
rs1568923	FALSE	FALSE	FALSE					0.8869	0.8486	0.31	0.6135	v2v3v4
rs10067451	FALSE	FALSE	FALSE					0.9596	0.9479	3.2×10^{-10}	0.8710	v2v3v4
rs141078219	FALSE	FALSE	FALSE					0.8764	0.8549	0.28	0.6383	v2v3v4
rs35407642	FALSE	FALSE	FALSE					0.9945	0.9914	0.58	0.3880	v2v3v4
rs61406265	FALSE	FALSE	FALSE					0.9568	0.9010	0.12	0.8100	v2v3v4
rs7697398	FALSE	FALSE	FALSE					0.9869	0.9719	0.24	0.1757	v2v3v4
rs12120466	FALSE	FALSE	FALSE					0.9975	0.9905	0.76	0.9555	v2v3v4
rs7107770	FALSE	FALSE	FALSE					0.9700	0.9523	0.38	0.8365	v2v3v4
rs10864302	FALSE	TRUE	FALSE	0.9997	2.6×10^{-8}	0.71	0.1720	0.9893	0.9530	0.00034	0.1733	v2v3v4
rs67177172	FALSE	FALSE	FALSE					0.9730	0.9688	0.088	0.3882	v2v3v4
rs1576263	FALSE	TRUE	FALSE	0.8209	0.0	0.0	0.4305	0.9935	0.9779	0.91	0.5192	v2v3v4
rs9347032	FALSE	FALSE	FALSE					0.9376	0.9266	0.65	0.4363	v2v3v4
rs1174117	FALSE	FALSE	FALSE					0.9445	0.8810	8.5×10^{-6}	0.3636	v2v3v4
rs3055140	FALSE	FALSE	FALSE					0.9814	0.9726	0.031	0.7291	v2v3v4
rs35570576	FALSE	FALSE	FALSE					0.8892	0.8233	1.0×10^{-21}	0.1868	v3v4
rs4620151	FALSE	FALSE	FALSE					0.7964	0.7407	0.00016	0.6451	v2v3v4
rs4349753	FALSE	FALSE	FALSE					0.9806	0.9757	0.16	0.5422	v2v3v4
rs7189864	FALSE	FALSE	FALSE					0.9454	0.9172	0.14	0.6929	v2v3v4
rs7319075	FALSE	FALSE	FALSE					0.9999	0.9994	0.0014	0.8341	v2v3v4
rs11852029	TRUE	TRUE	TRUE	0.9969	0.0020	0.67	0.1627	0.9999	0.9995	0.57	0.1622	v2v3v4
rs13032103	FALSE	FALSE	FALSE					0.9602	0.9420	0.17	0.6934	v2v3v4
rs28417201	FALSE	FALSE	FALSE					0.9882	0.9719	0.0091	0.2511	v2v3v4
rs36061463	FALSE	FALSE	FALSE					0.9656	0.8708	3.4×10^{-5}	0.3750	v2v3v4
rs10234796	FALSE	FALSE	FALSE					0.9875	0.9835	0.91	0.6481	v2v3v4
rs117147772	FALSE	FALSE	FALSE					0.9711	0.9621	0.21	0.9463	v2v3v4
rs9318213	FALSE	FALSE	FALSE					0.9881	0.9513	0.10	0.5749	v2v3v4
11:92232901:G_GTA	FALSE	FALSE	FALSE					0.9129	0.9002	0.068	0.4507	v2v3v4
rs266053	FALSE	FALSE	FALSE					0.9221	0.9118	0.33	0.5372	v2v3v4

SNP Statistics in the GWAS Sample

assay.name	AA.0	AB.0	BB.0	im.num.0	dose.b.0	AA.1	AB.1	BB.1	im.num.1	dose.b.1
rs1533426				67249	0.5683				32446	0.4795
rs9571757	11173	25391	14614	67249	0.5333	4371	11970	8378	32446	0.5785
rs1541995				67249	0.6890				32446	0.7296
rs12755398				67249	0.8663				32446	0.8343
rs1146751	16967	33074	16569	67249	0.4978	6901	15873	9338	32446	0.5383
rs9991510				67249	0.4618				32446	0.4942
rs633798				67249	0.6296				32446	0.6595
rs887807	241	7334	59667	67249	0.9419	63	2756	29620	32446	0.9556
rs4811602				67249	0.5474				32446	0.5179
rs1376216				67249	0.5977				32446	0.6257
rs10886094	6086	27309	33791	67249	0.7077	2418	12575	17417	32446	0.7326
rs368977885				67249	0.3998				32446	0.3754
rs7534788				67249	0.3719				32446	0.3928
rs10642753				67249	0.8543				32446	0.8697
rs1338552				67249	0.5089				32446	0.5298
rs144328717				67249	0.7628				32446	0.7444

rs11850550				67249	0.5195				32446	0.5007
rs55836402				67249	0.3605				32446	0.3418
rs74677756				67249	0.6579				32446	0.6782
rs17626617	1991	18758	46452	67249	0.8308	884	8351	23193	32446	0.8440
rs2148307				67249	0.4448				32446	0.4258
rs11814950				67249	0.0642				32446	0.0564
rs1568923				67249	0.6167				32446	0.6000
rs10067451				67249	0.8783				32446	0.8696
rs141078219				67249	0.6347				32446	0.6509
rs35407642				67249	0.3923				32446	0.3757
rs61406265				67249	0.8137				32446	0.8008
rs7697398				67249	0.1730				32446	0.1858
rs12120466				67249	0.9579				32446	0.9507
rs7107770				67249	0.8400				32446	0.8280
rs10864302	34871	14601	1721	67249	0.1772	17322	6712	688	32446	0.1654
rs67177172				67249	0.3817				32446	0.3968
rs1576263	10789	25688	5760	67249	0.5267	5534	12470	2706	32446	0.5115
rs9347032				67249	0.4312				32446	0.4455
rs1174117				67249	0.3656				32446	0.3497
rs3055140				67249	0.7320				32446	0.7182
rs35570576				59219	0.1814				28462	0.1916
rs4620151				67249	0.6397				32446	0.6521
rs4349753				67249	0.5423				32446	0.5255
rs7189864				67249	0.6893				32446	0.7023
rs7319075				67249	0.8349				32446	0.8478
rs11852029	47385	17964	1708	67249	0.1595	22284	9086	992	32446	0.1710
rs13032103				67249	0.6903				32446	0.7036
rs28417201				67249	0.2439				32446	0.2585
rs36061463				67249	0.3792				32446	0.3630
rs10234796				67249	0.6510				32446	0.6377
rs117147772				67249	0.9441				32446	0.9496
rs9318213				67249	0.5725				32446	0.5877
11:92232901:G_GTA				67249	0.4539				32446	0.4395
rs266053				67249	0.5358				32446	0.5505

Annotations from NHGRI GWAS Catalog

The following table shows, for each index SNP, all entries in the NHGRI GWAS Catalog that are within 500kb and in at least moderate linkage disequilibrium ($r^2 > 0.5$).

region	position	our.name	our.pval	dist	rsqr	assay.name	pvalue	pubmed.id	trait	genes
2q22.3	146119018	rs1533426	1.0×10^{-260}	6505	0.989	rs10427255	1.0×10^{-11}	20585627	Common traits (Other)	Intergenic
9q33.2	123050797	rs887807	8.3×10^{-34}	5840	0.975	rs4837752	6.0×10^{-6}	19875103	Response to antipsychotic therapy (extrapyramidal side effects)	Intergenic
20q11.23	36849088	rs4811602	2.5×10^{-31}	−5050	0.968	rs6127471	5.0×10^{-29}	23583979	Heart rate	KIAA1755
4q25	112659154	rs1376216	3.4×10^{-31}	−47404	0.685	rs10034228	8.0×10^{-13}	21505071	Myopia (pathological)	MYP11
6q16.1	98346633	rs1338552	1.0×10^{-17}	149319	0.732	rs2505059	5.0×10^{-6}	23648065	Adverse response to chemotherapy (neutropenia/leucopenia) (all anthracycline-based drugs)	MIR2113
7q11.22	70012519	rs10234796	1.2×10^{-8}	33422	0.525	rs10237317	5.0×10^{-6}	22925353	Bipolar disorder	AUTS2
2q12.1	104090213	rs266053	3.1×10^{-8}	208328	0.593	rs264943	7.0×10^{-6}	22174851	HIV-1 viral setpoint	Intergenic

Replication of GWAS Catalog Results

The following table shows, for each GWAS Catalog result for similar traits, our association test result for our best available proxy (distance < 100kb, $r^2 > 0.8$).

no relevant GWAS catalog terms were available

Nearby Nonsynonymous SNPs

region	position	our.name	our.pval	dist	rsqr	assay.name	gene	aa.chg
20q11.23	36849088	rs4811602	2.5×10^{-31}	−7174	0.916	rs3746471	KIAA1755	R1045W
20q11.23	36849088	rs4811602	2.5×10^{-31}	−3350	0.524	rs760998	KIAA1755	E940K
4q32.3	170013910	rs17626617	9.2×10^{-15}	23662	0.673	rs3811813	SH3RF1	P663S
10q23.1	84722619	rs11814950	2.0×10^{-12}	22307	1.000	rs17101193	NRG3	N552K
Xq21.1	79956549	rs28417201	9.1×10^{-9}	−257956	0.750	rs1113265	FAM46D	D185E

Nearby Expression QTLs

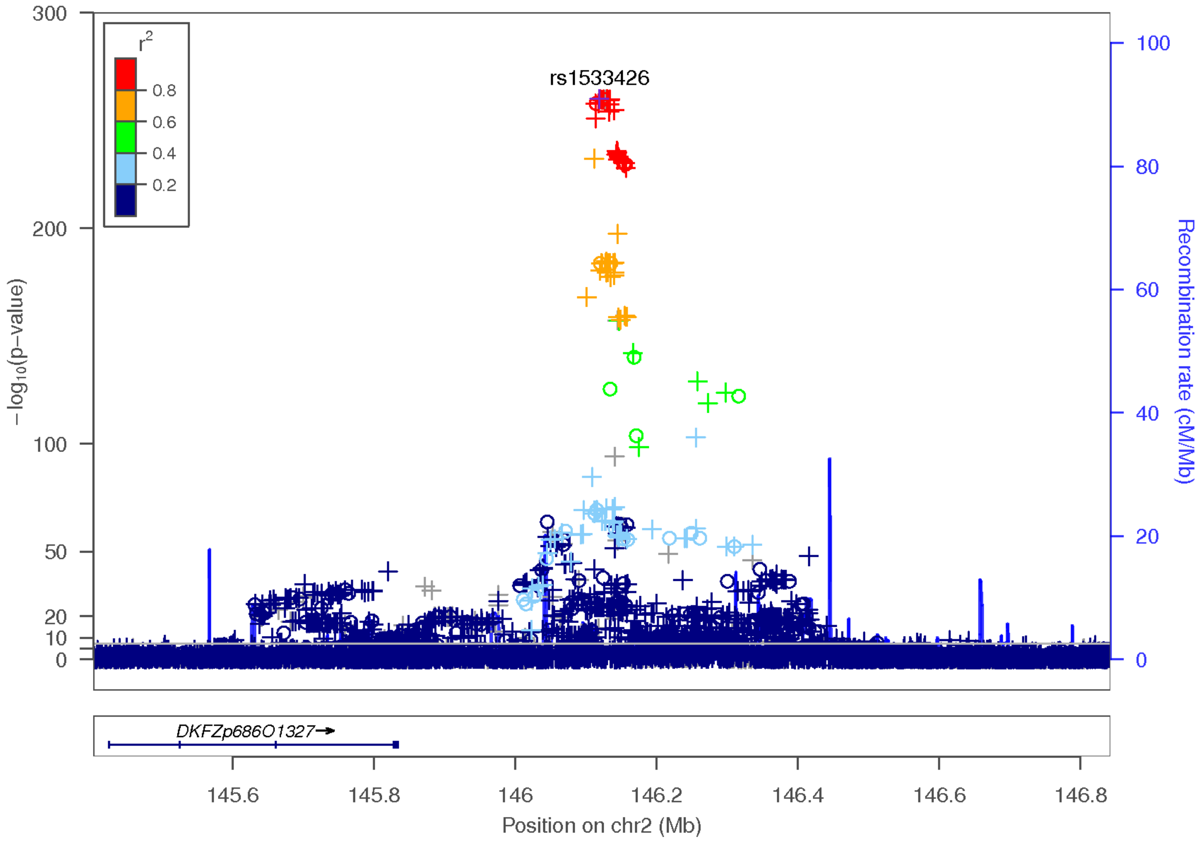
region	position	our.name	our.pval	dist	rsqr	assay.name	eqtl.dist	eqtl.gene	eqtl.pval	eqtl.rsqr	tissue	pubmed.id
4p15.33	12080930	rs9991510	1.9×10^{-41}	−62937	0.799	rs6448852	−1576156	ZNF518B	0.00026	0.047	B-Cell	22446964
6q16.1	98346633	rs1338552	1.0×10^{-17}	−17859	0.672	rs9401295	992929	FBXL4	0.00025	0.047	B-Cell	22446964

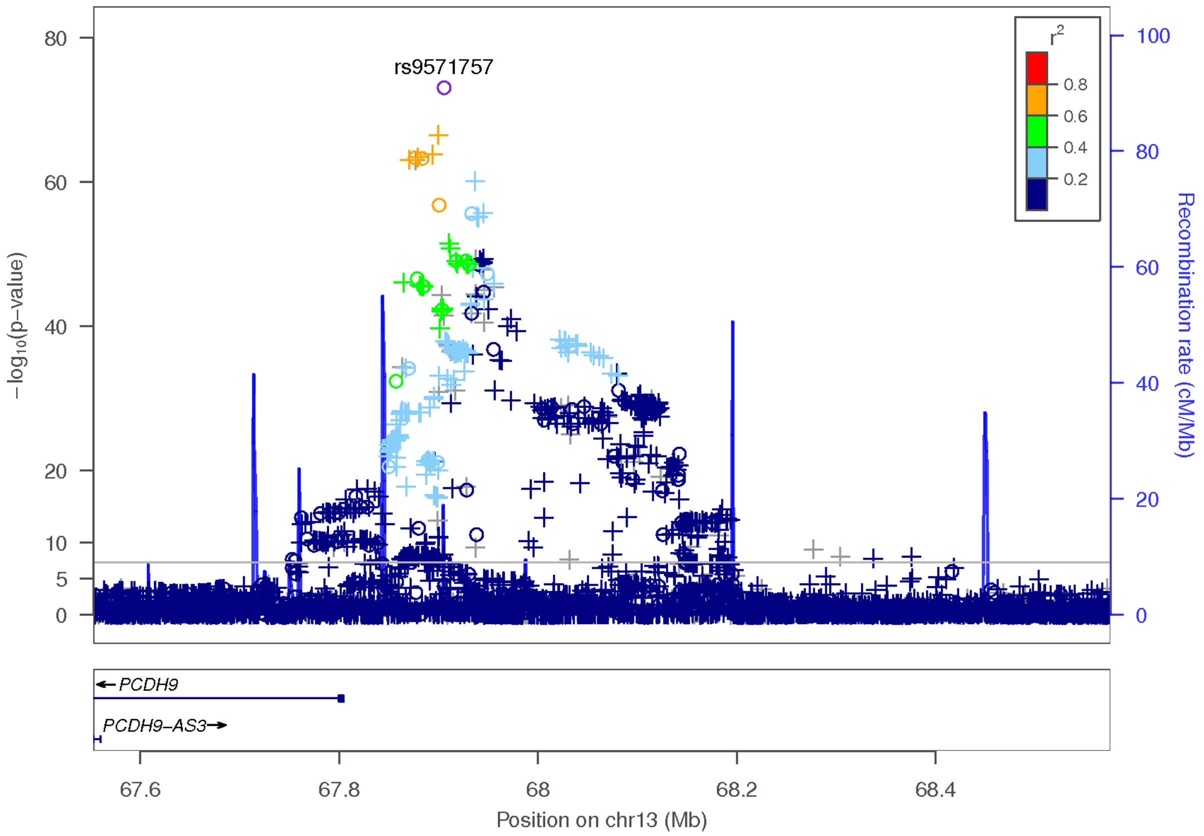
6p24.3	8690217	rs1576263	2.0×10^{-10}	2199	0.715	rs4960453	256791	SLC35B3	1.0×10^{-6}	0.018	Monocyte	20502693

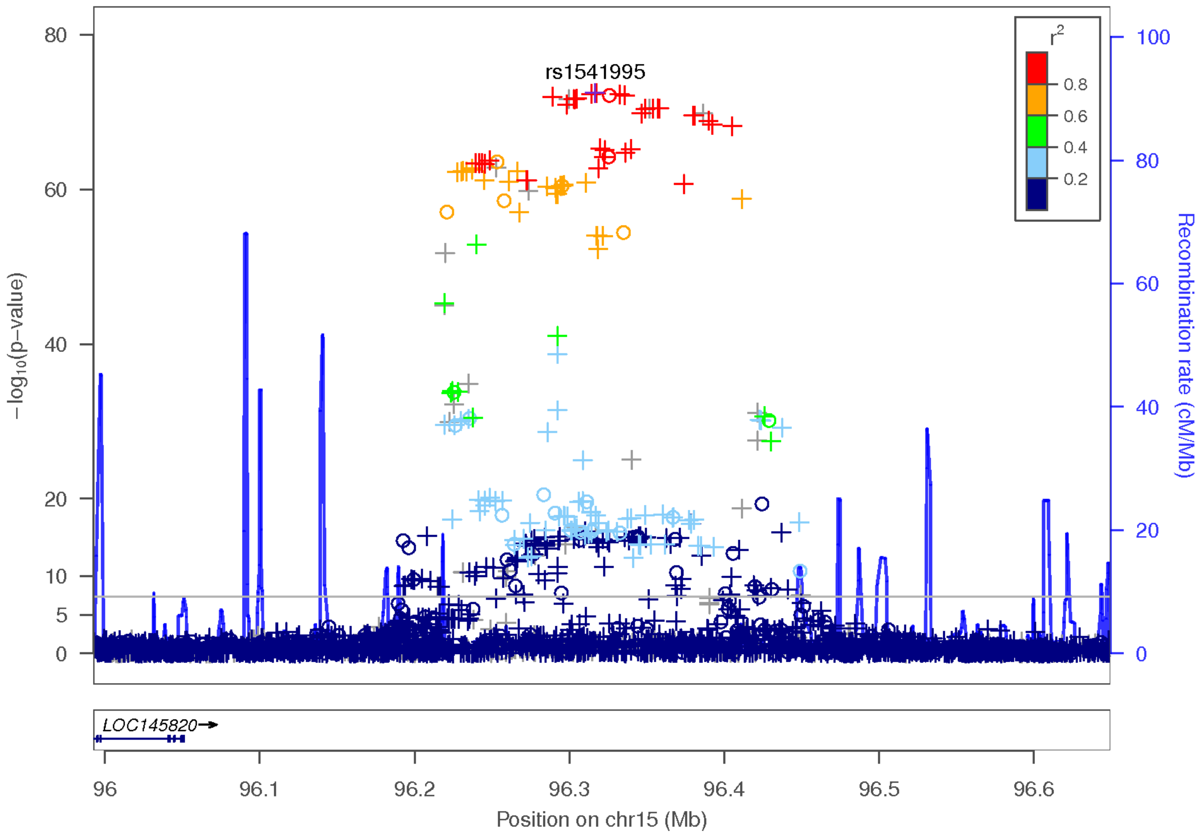
Nearby Clinical Variants

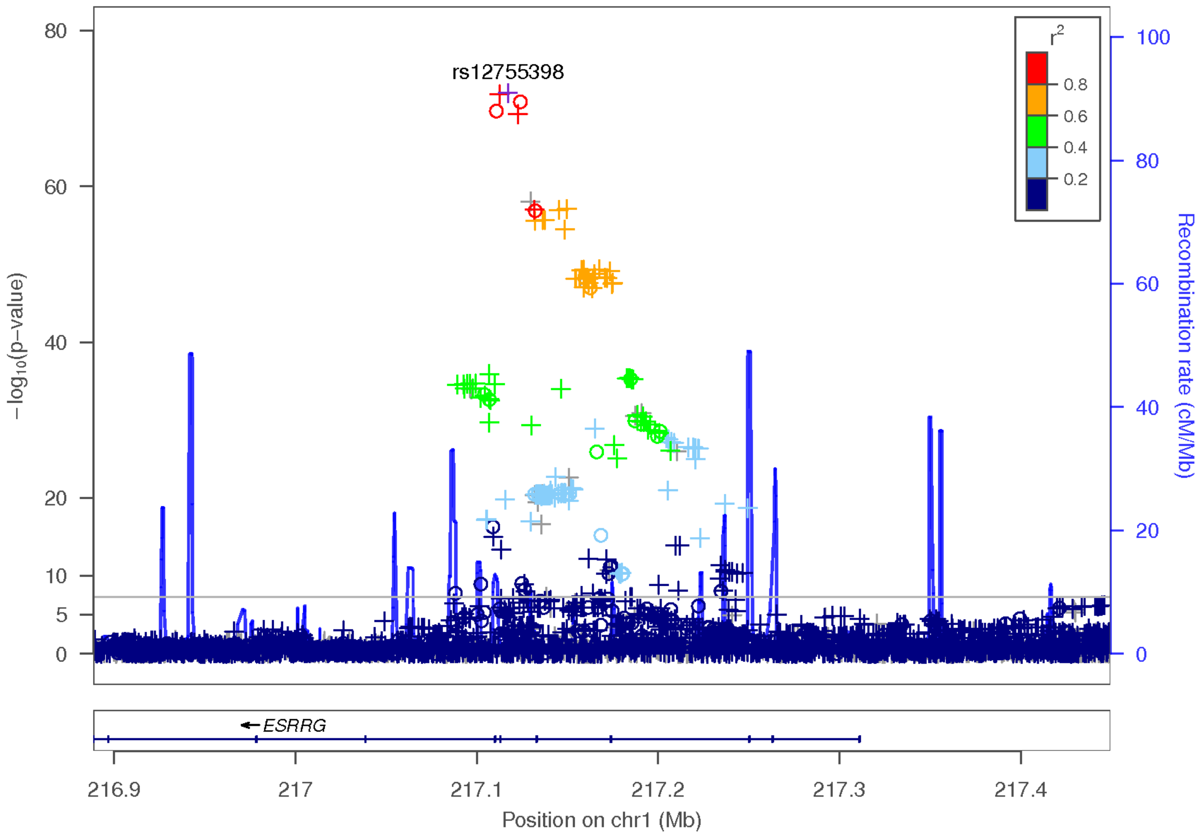
no hits were found for clinical variants

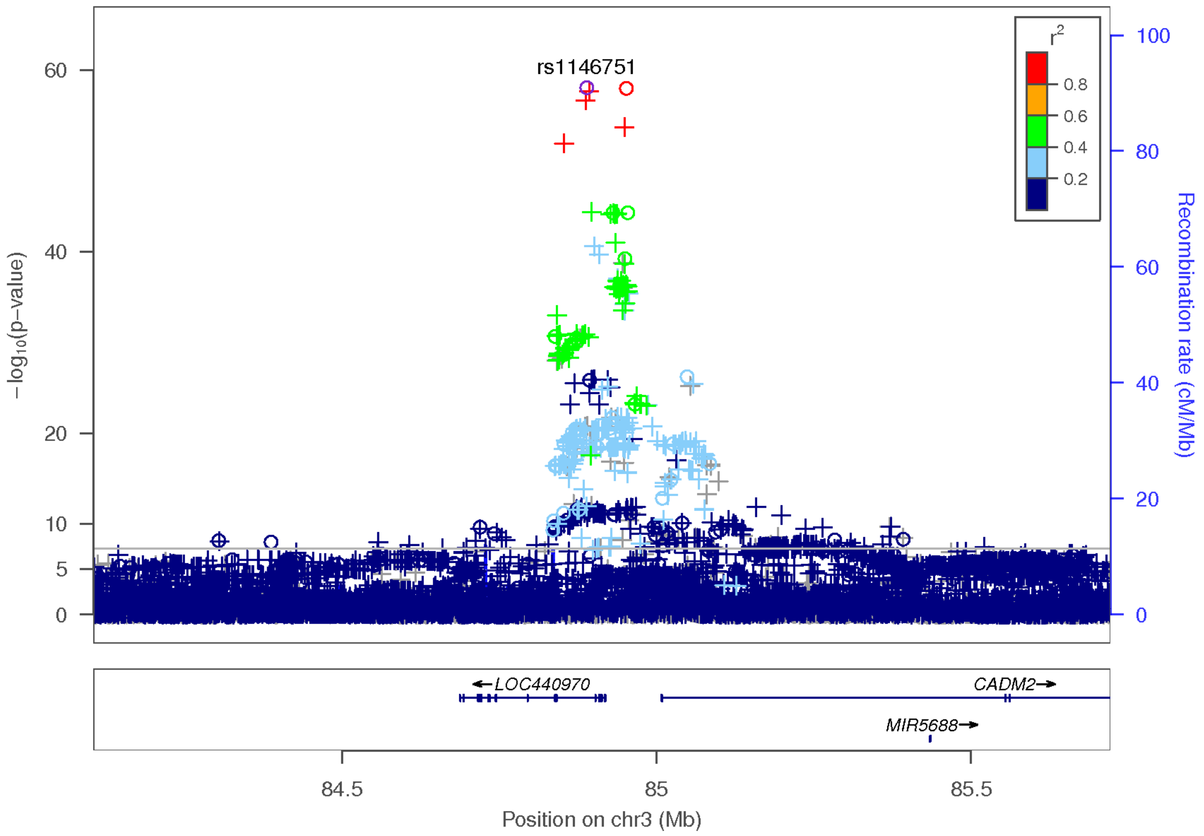
Regional Association Plots

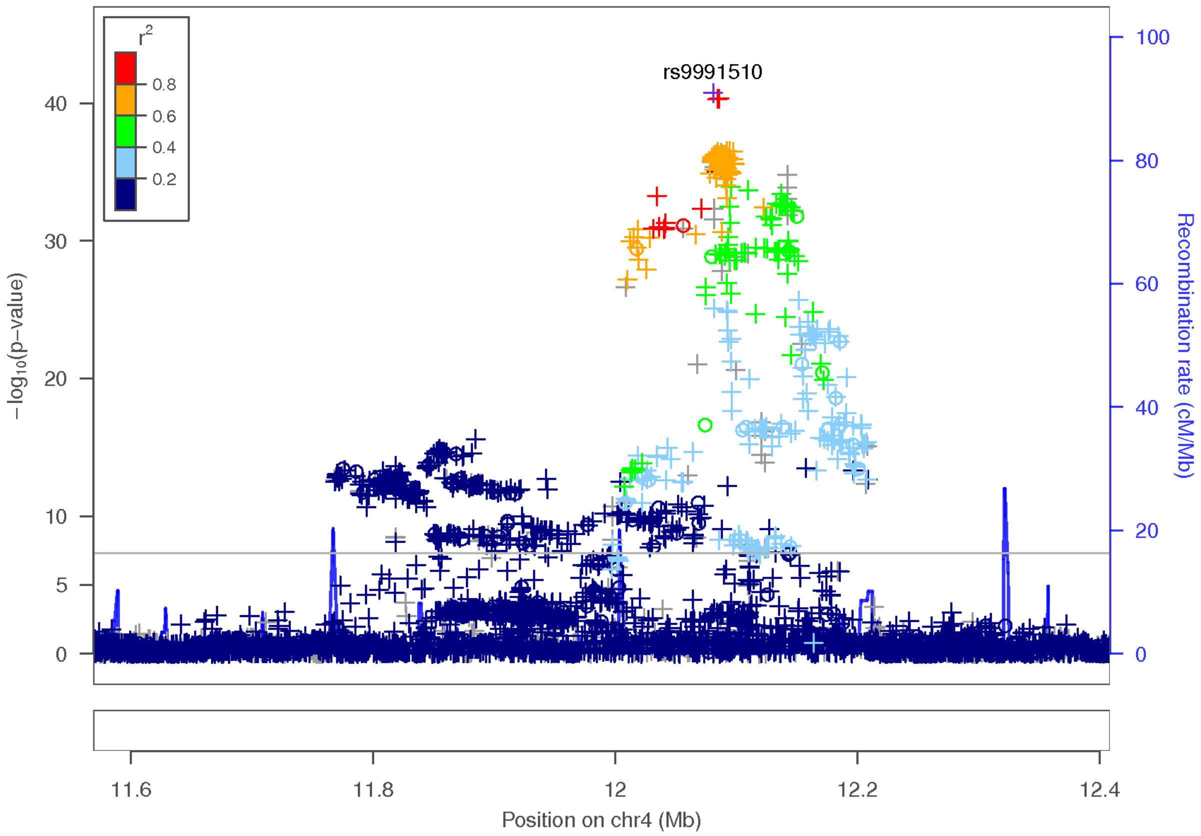


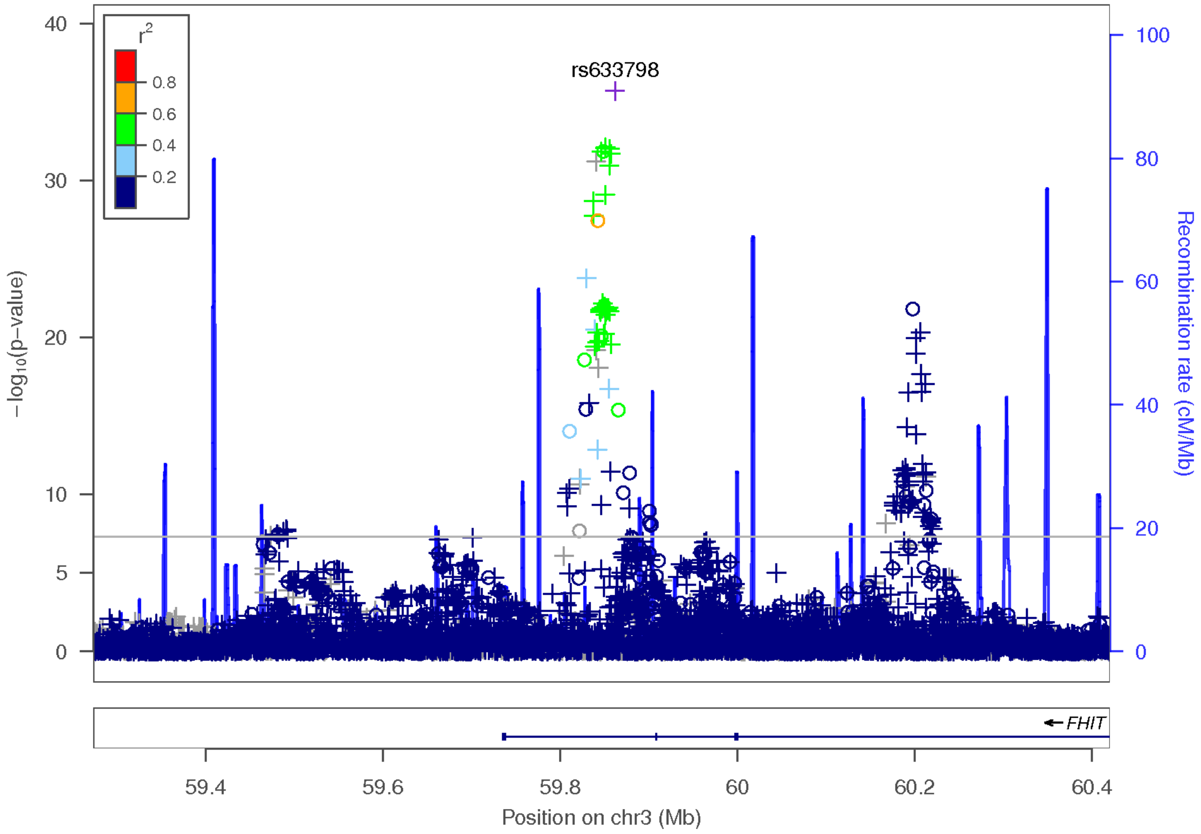

rs9571757
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
80
60
40
20
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
PCDH9
PCDH9−AS3
67.6
67.8
68
68.2
68.4
Position on chr13 (Mb)

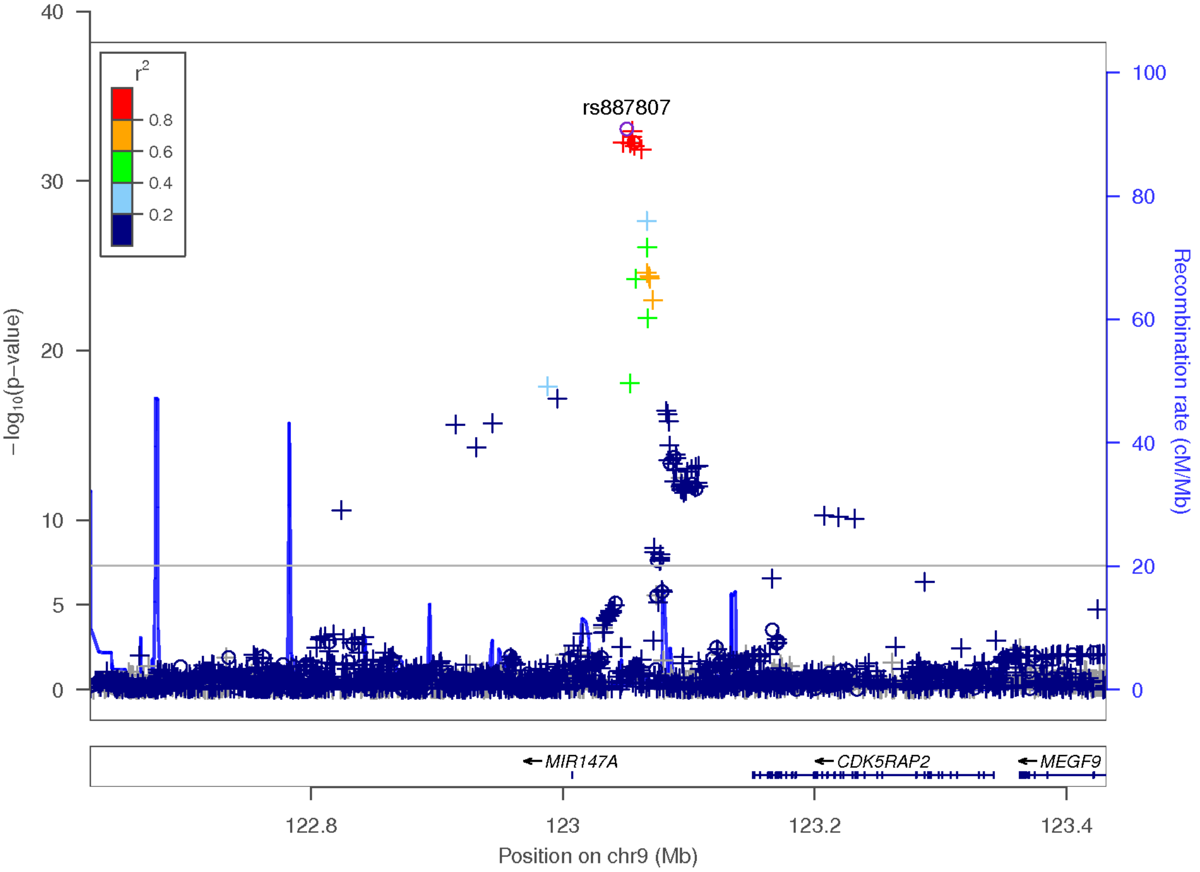

rs1541995
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
80
60
40
20
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
LOC145820
96
96.1
96.2
96.3
96.4
96.5
96.6
Position on chr15 (Mb)

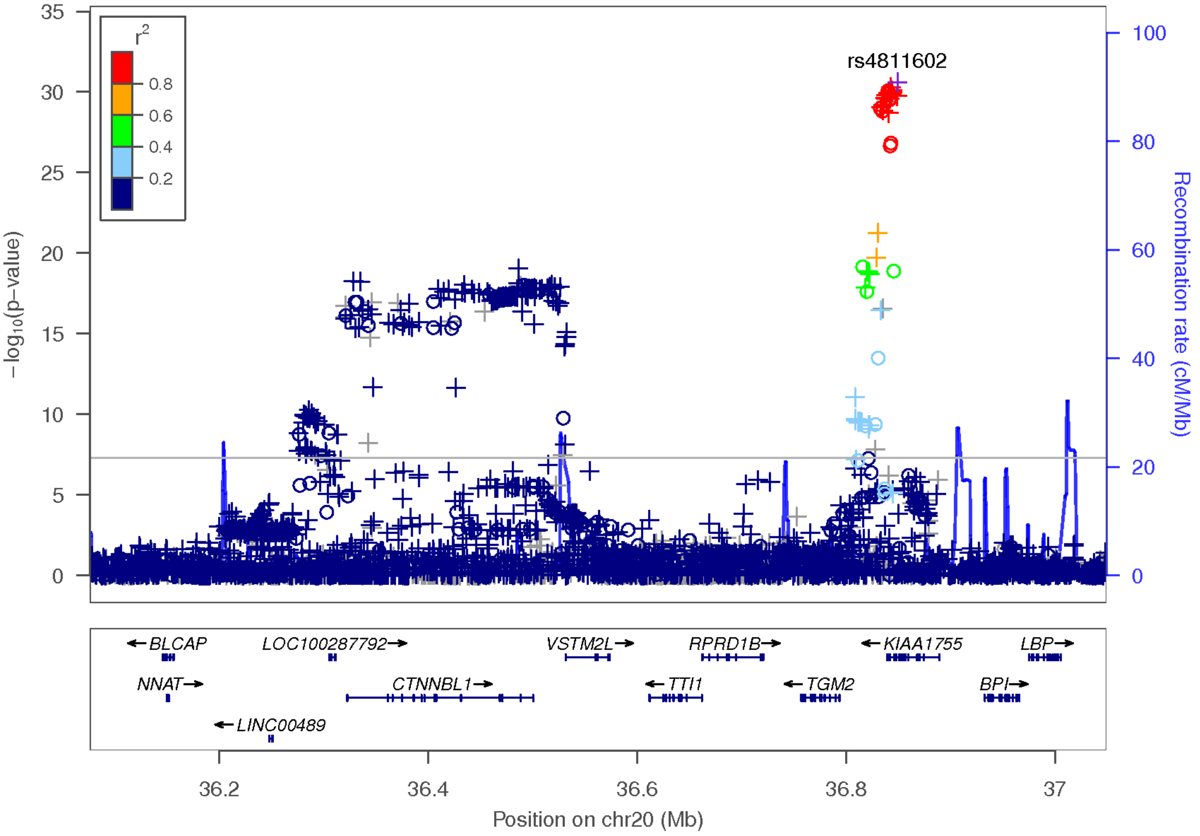

rs12755398
r2
0.8
0.6
0.4
0.2
80
60
40
20
10
5
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
ESRRG
216.9
217
217.1
217.2
217.3
217.4
Position on chr1 (Mb)

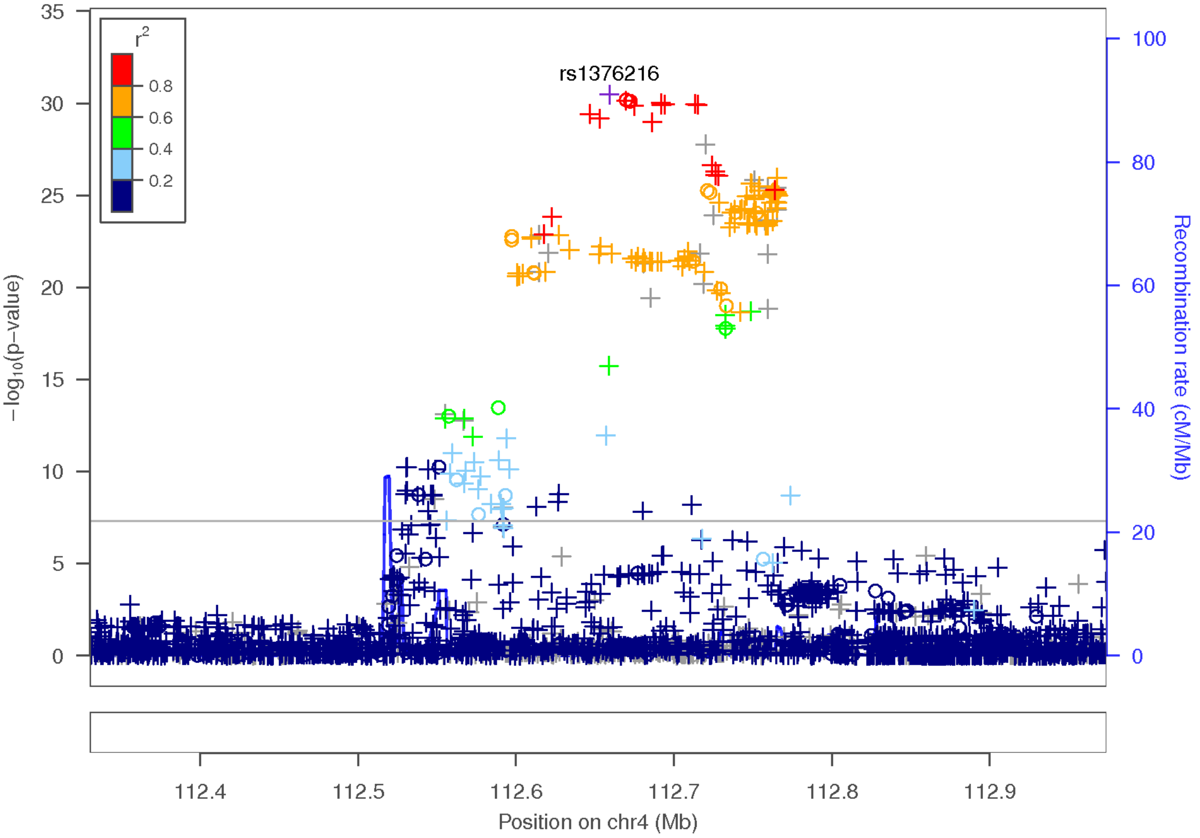

rs1146751
r2
0.8
0.6
0.4
0.2
60
40
20
10
5
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
LOC440970
CADM2
MIR5688
84.5
85
85.5
Position on chr3 (Mb)

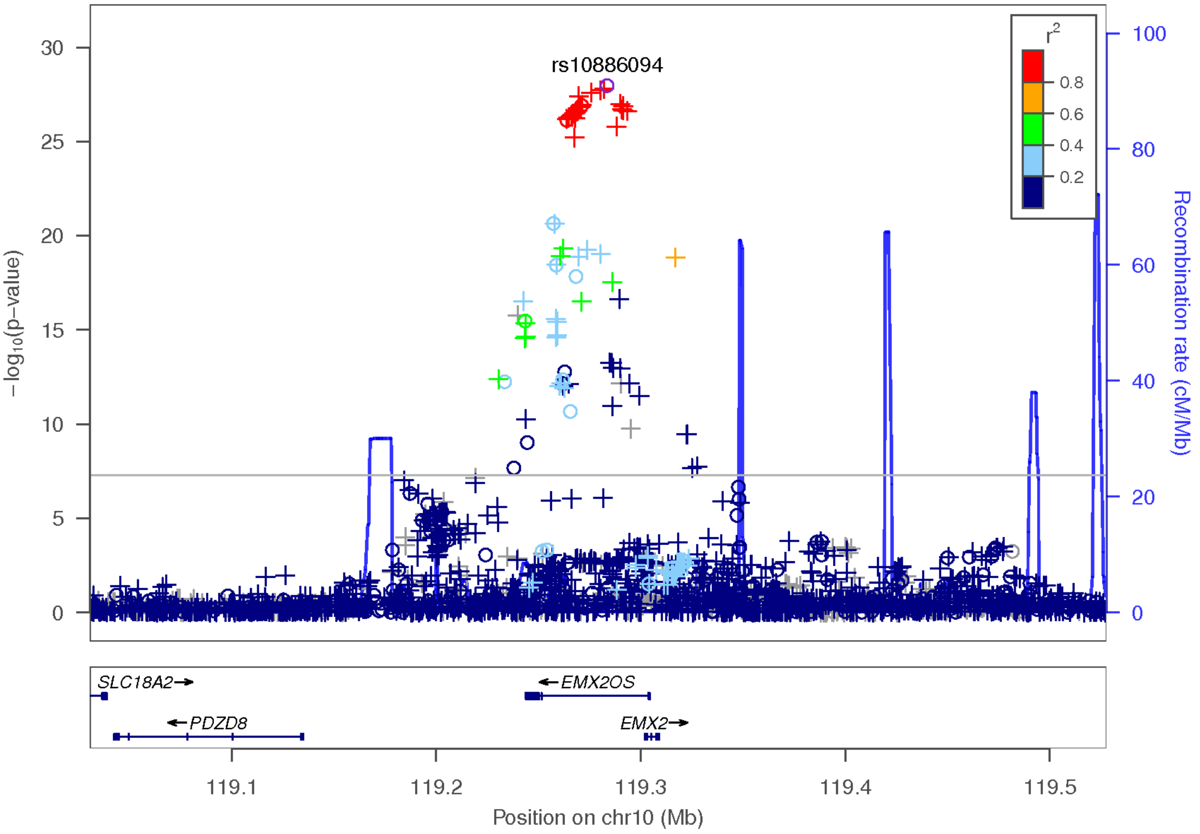

r2
0.8
0.6
0.4
0.2
rs9991510
− log10(p−value)
0
5
10
20
30
40
Recombination rate (cM/Mb)
0
20
40
60
80
100
11.6
11.8
12
12.2
12.4
Position on chr4 (Mb)


r2
0.8
0.6
0.4
0.2
rs633798
− log10(p−value)
0
5
10
20
30
40
Recombination rate (cM/Mb)
0
20
40
60
80
100
FHIT
59.4
59.6
59.8
60
60.2
60.4
Position on chr3 (Mb)

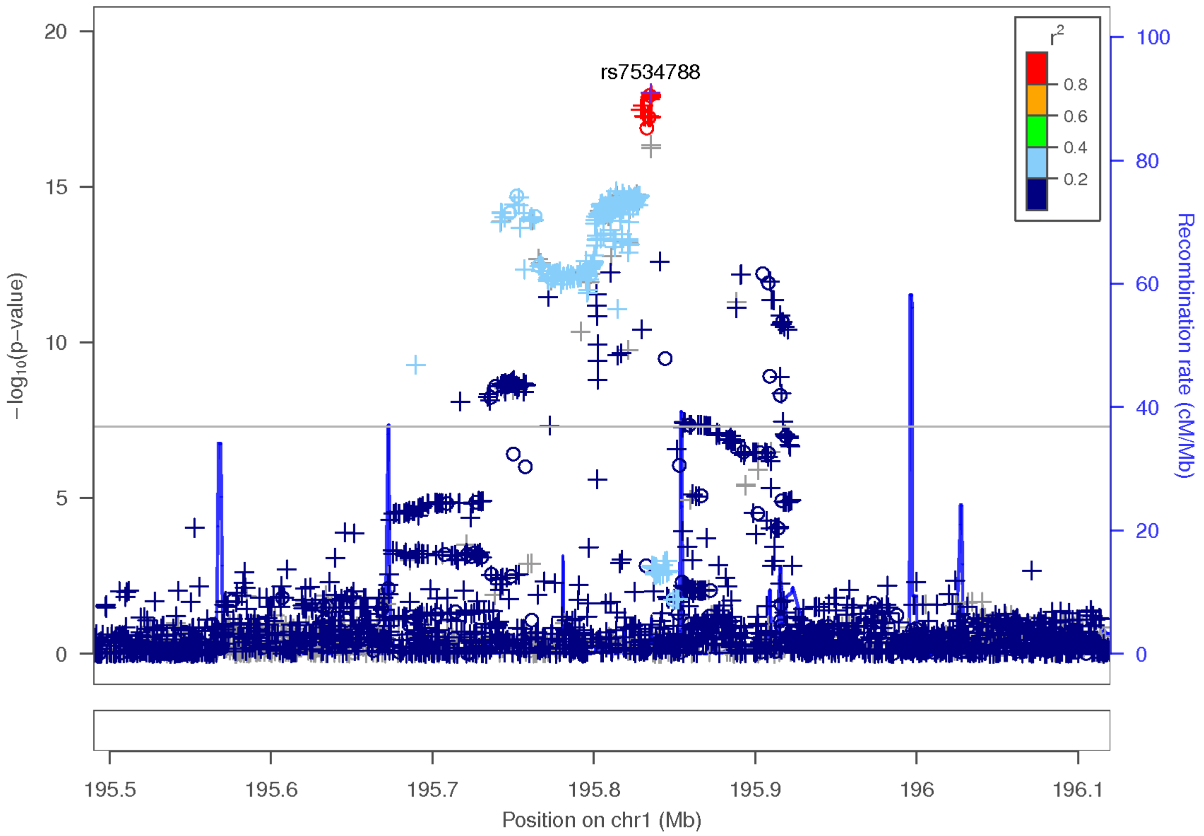

r^2
0.8
0.6
0.4
0.2
rs887807
−log$_{10}$(p−value)
0
5
10
20
30
40
Recombination rate (cM/Mb)
0
20
40
60
80
100
MIR147A
CDK5RAP2
MEGF9
122.8
123
123.2
123.4
Position on chr9 (Mb)

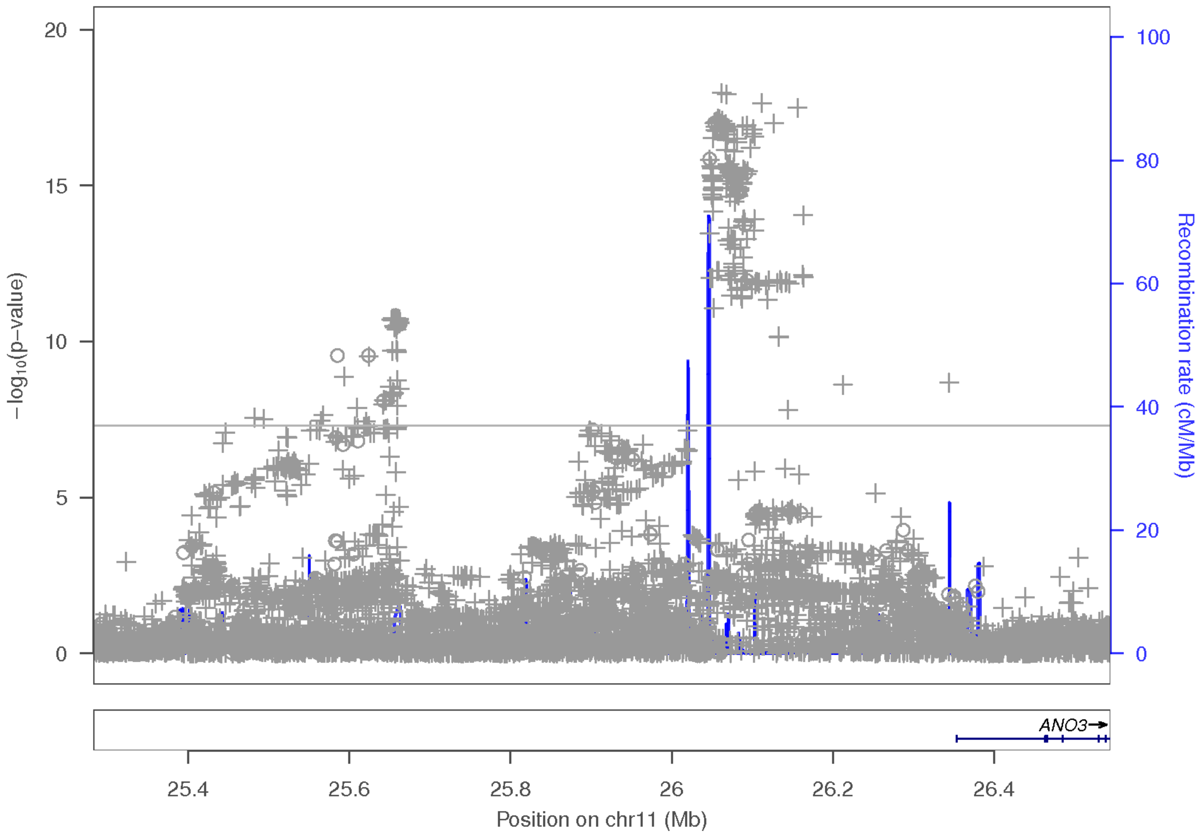

r^2
0.8
0.6
0.4
0.2
rs4811602
−log$_{10}$(p−value)
0
5
10
15
20
25
30
35
Recombination rate (cM/Mb)
0
20
40
60
80
100
BLCAP
LOC100287792
VSTM2L
RPRD1B
KIAA1755
LBP
NNAT
CTNNBL1
TTI1
TGM2
BPI
LINC00489
36.2
36.4
36.6
36.8
37
Position on chr20 (Mb)

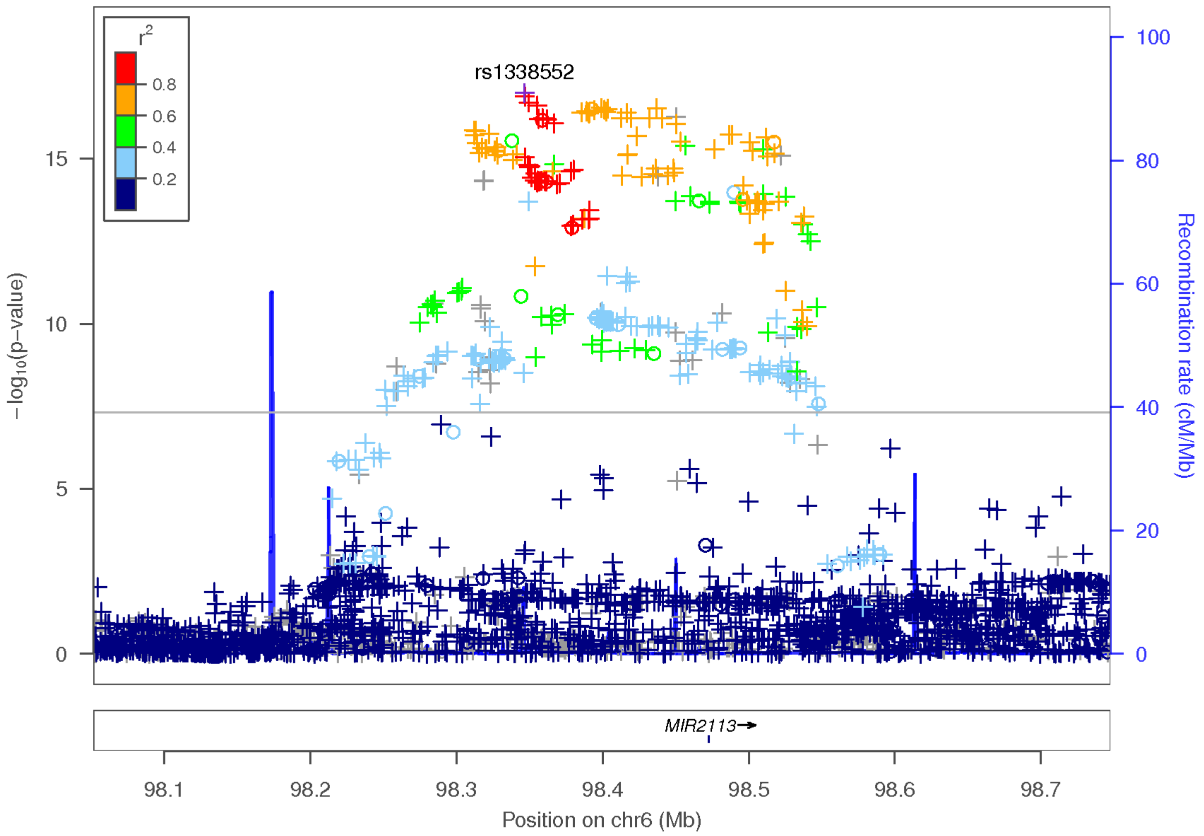


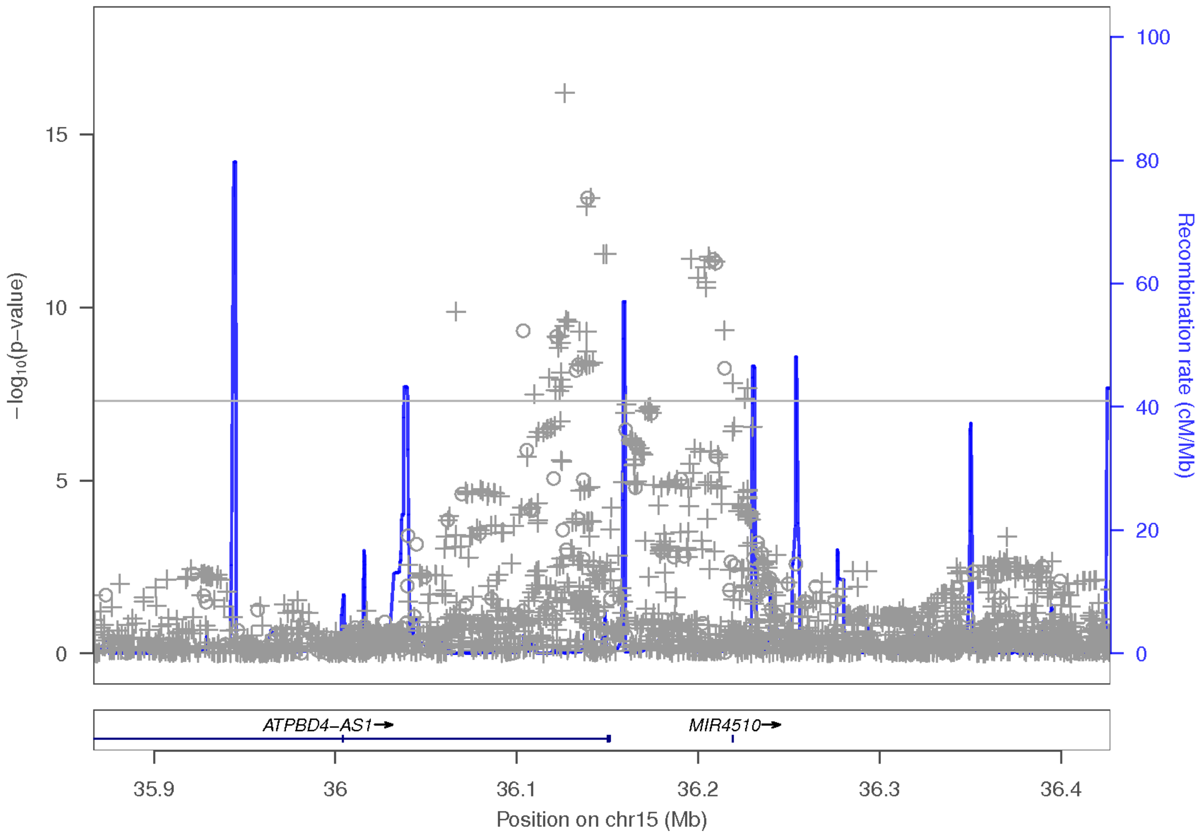


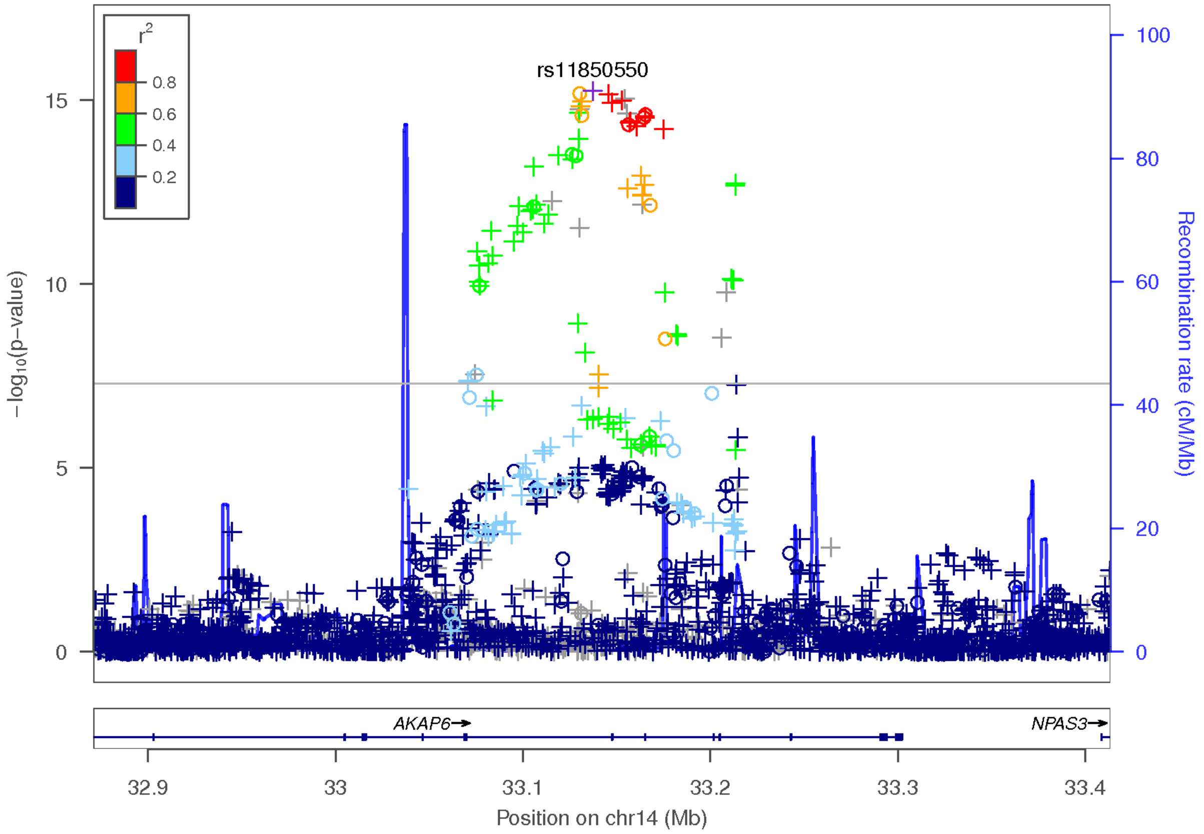
locuszoom plot for rs368977885 failed

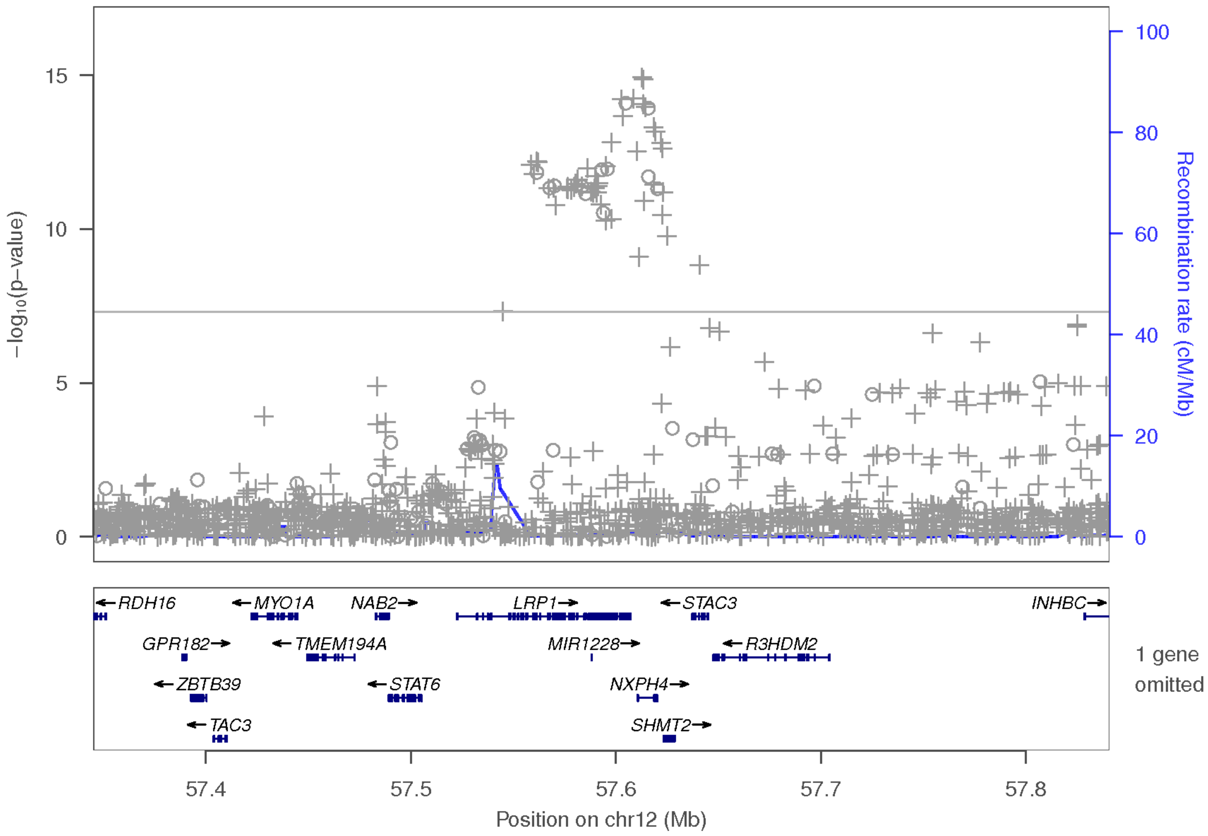

rs7534788
r2
0.8
0.6
0.4
0.2
20
15
10
5
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
195.5
195.6
195.7
195.8
195.9
196
196.1
Position on chr1 (Mb)

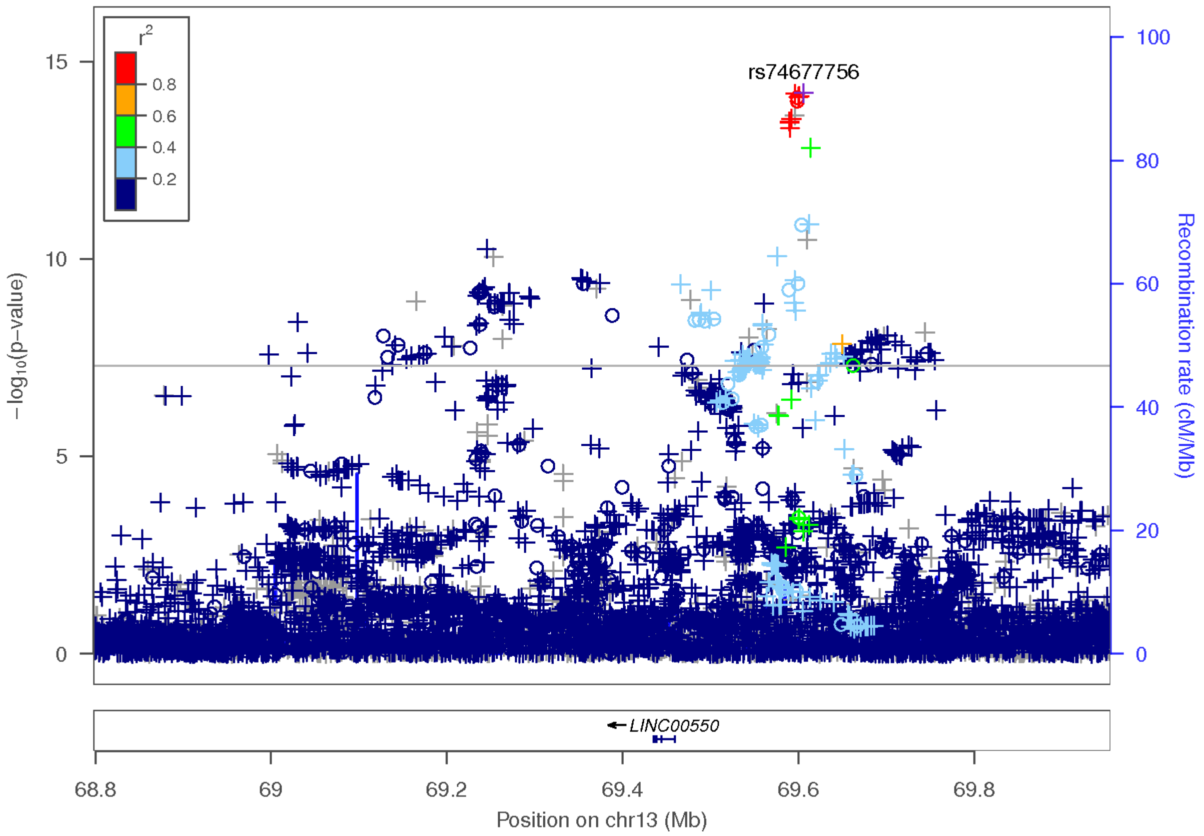

20
15
10
5
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
ANO3
25.4
25.6
25.8
26
26.2
26.4
Position on chr11 (Mb)

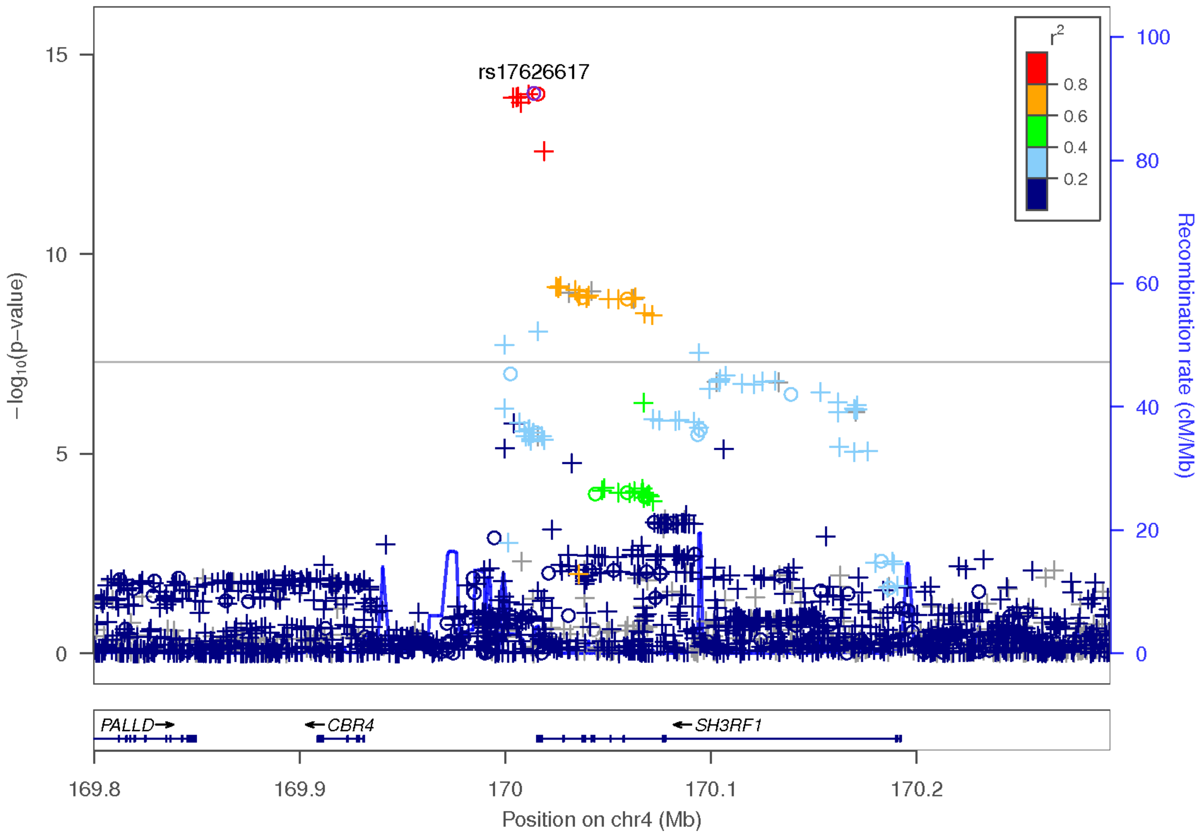

r²
0.8
0.6
0.4
0.2
rs1338552
−log₁₀(p−value)
0
5
10
15
Recombination rate (cM/Mb)
0
20
40
60
80
100
MIR2113
98.1
98.2
98.3
98.4
98.5
98.6
98.7
Position on chr6 (Mb)

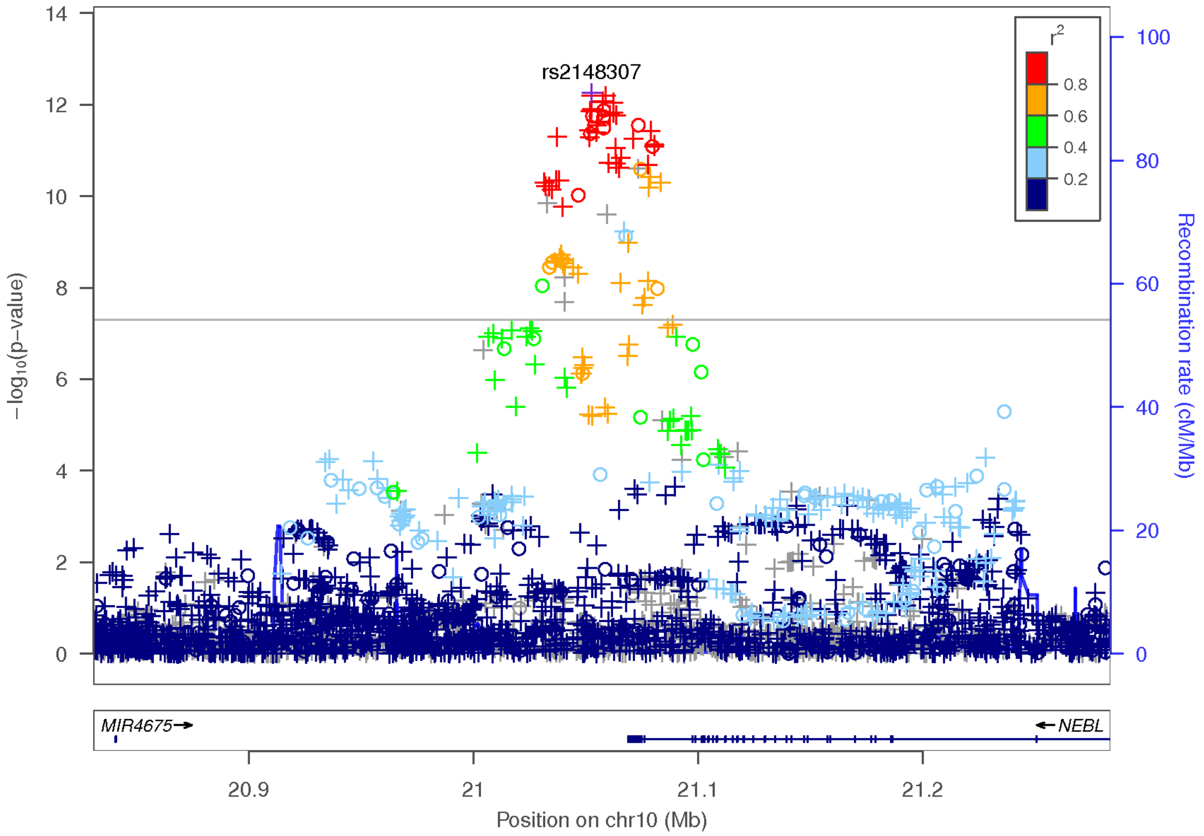

−log₁₀(p−value)
0
5
10
15
Recombination rate (cM/Mb)
0
20
40
60
80
100
ATPBD4−AS1
MIR4510
35.9
36
36.1
36.2
36.3
36.4
Position on chr15 (Mb)

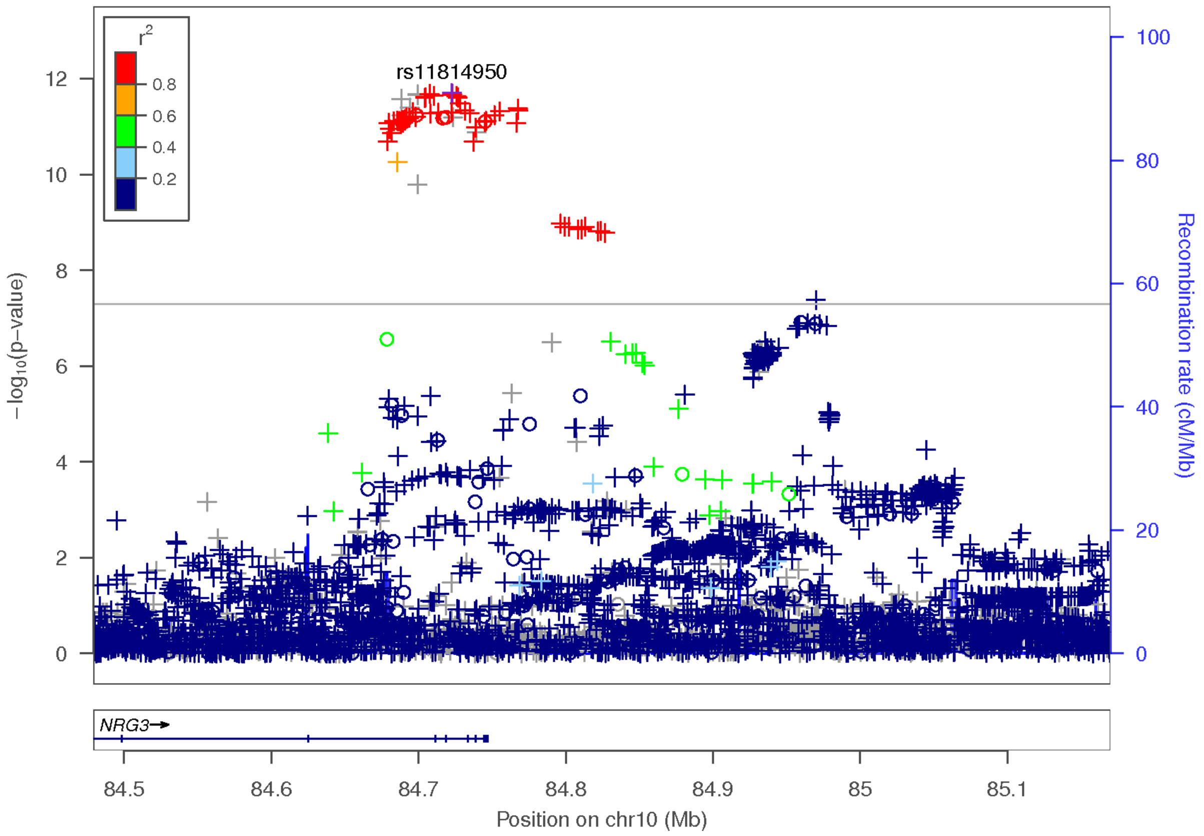

r²
0.8
0.6
0.4
0.2
rs11850550
−log₁₀(p−value)
0
5
10
15
Recombination rate (cM/Mb)
0
20
40
60
80
100
AKAP6→
NPAS3→
32.9
33
33.1
33.2
33.3
33.4
Position on chr14 (Mb)

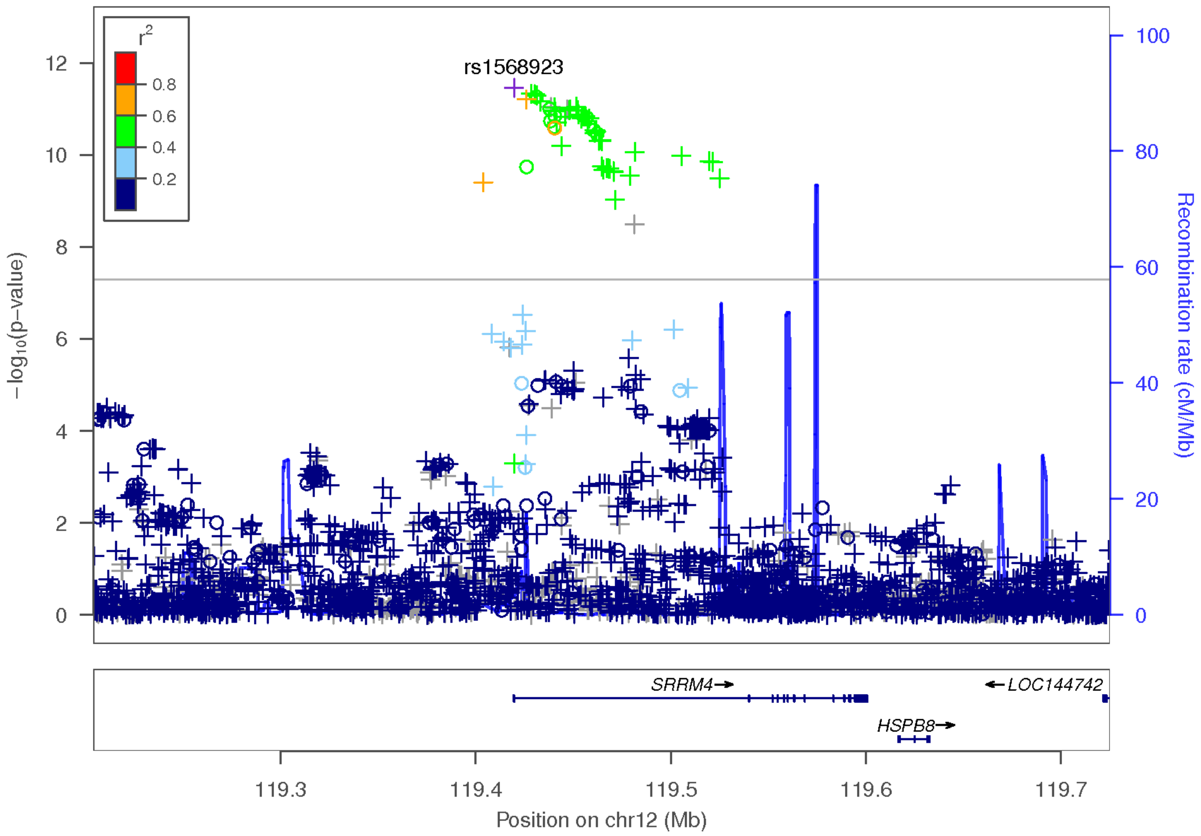

−log₁₀(p−value)
0
5
10
15
Recombination rate (cM/Mb)
0
20
40
60
80
100
←RDH16
←MYO1A
NAB2→
LRP1→
←STAC3
INHBC→
GPR182→
←TMEM194A
MIR1228→
←R3HDM2
←ZBTB39
←STAT6
NXPH4→
←TAC3
SHMT2→
1 gene omitted
57.4
57.5
57.6
57.7
57.8
Position on chr12 (Mb)

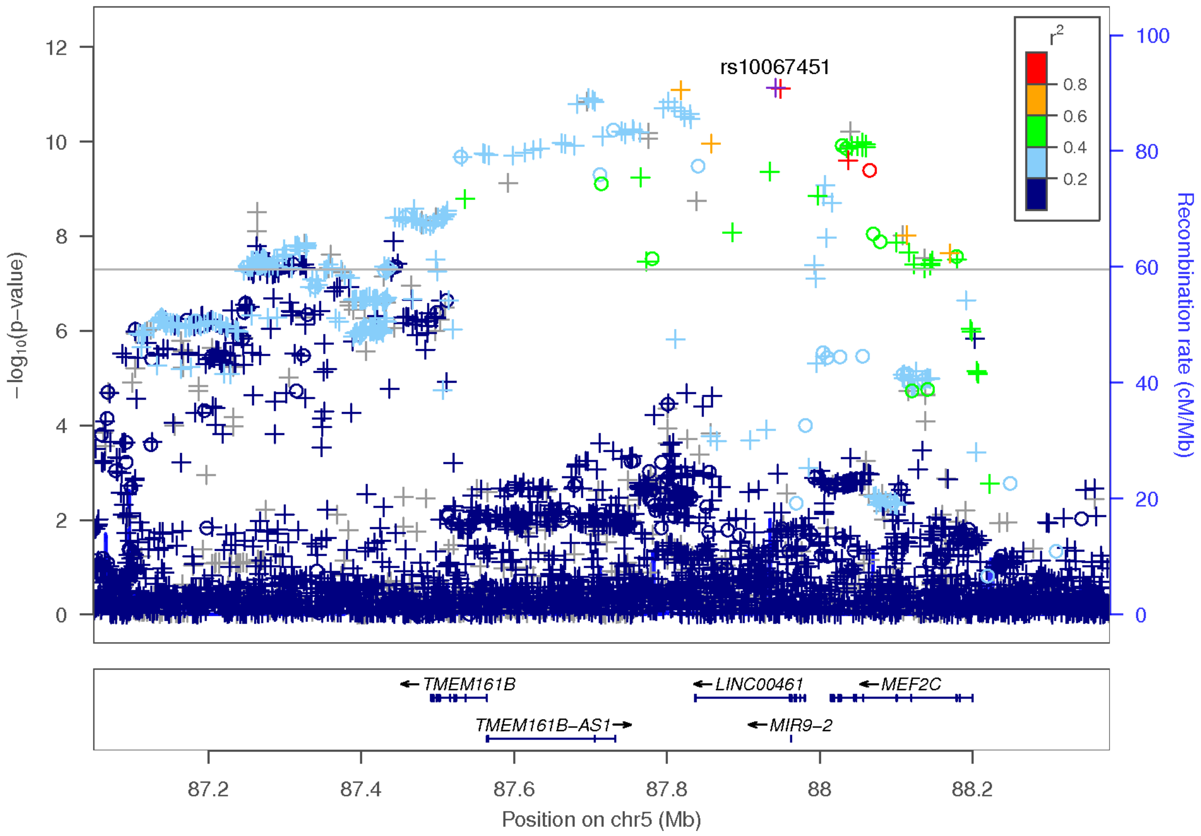

r2
0.8
0.6
0.4
0.2
rs74677756
15
10
5
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
LINC00550
68.8
69
69.2
69.4
69.6
69.8
Position on chr13 (Mb)

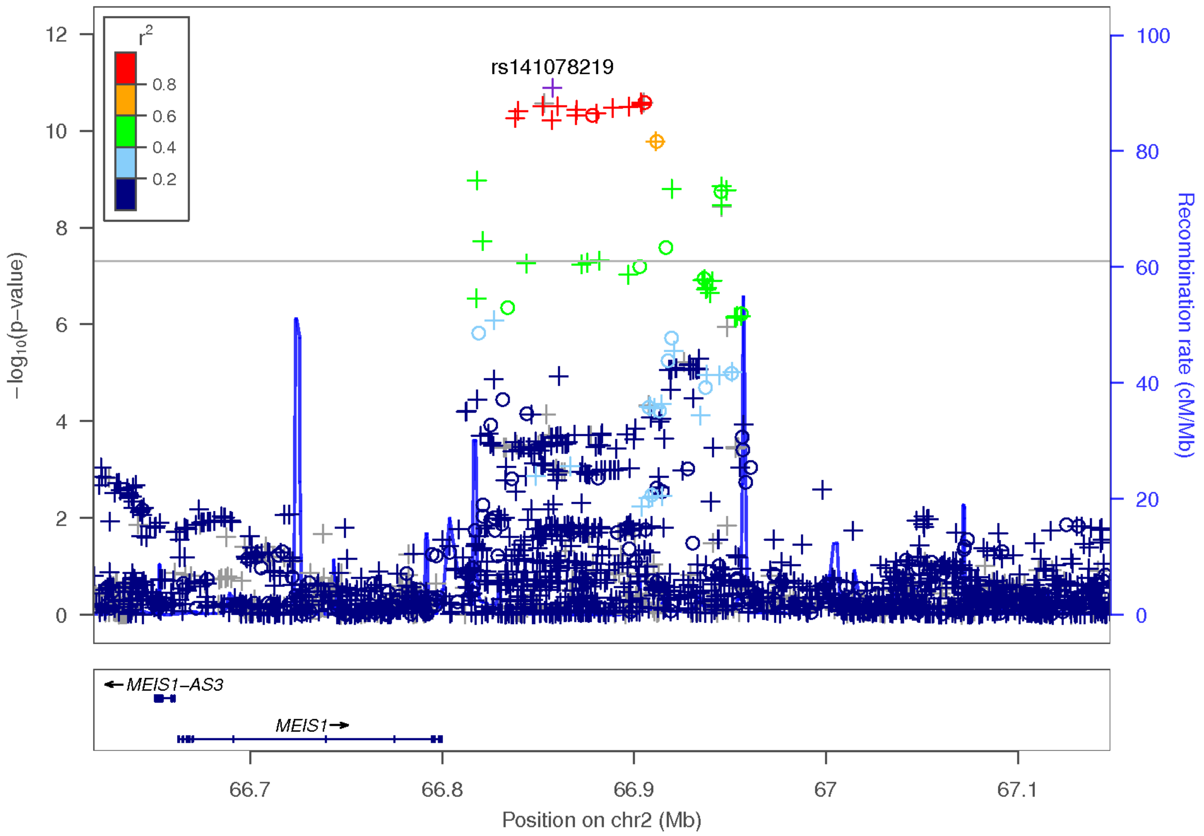

r2
0.8
0.6
0.4
0.2
rs17626617
15
10
5
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
PALLD
CBR4
SH3RF1
169.8
169.9
170
170.1
170.2
Position on chr4 (Mb)


rs2148307
r^2
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
12
14
Recombination rate (cM/Mb)
0
20
40
60
80
100
MIR4675→
←NEBL
20.9
21
21.1
21.2
Position on chr10 (Mb)

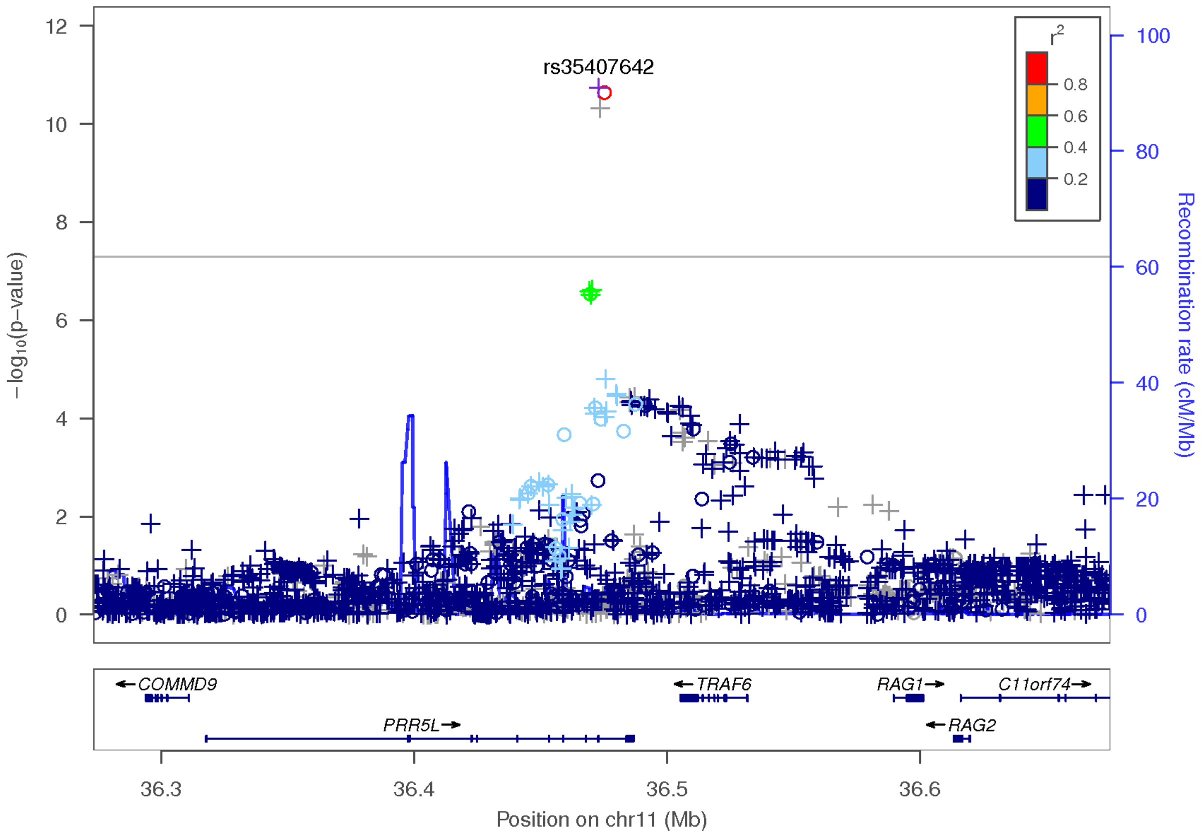

rs11814950
r^2
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
NRG3→
84.5
84.6
84.7
84.8
84.9
85
85.1
Position on chr10 (Mb)


rs1568923
r^2
0.8
0.6
0.4
0.2
12
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
SRRM4→
←LOC144742
HSPB8→
119.3
119.4
119.5
119.6
119.7
Position on chr12 (Mb)

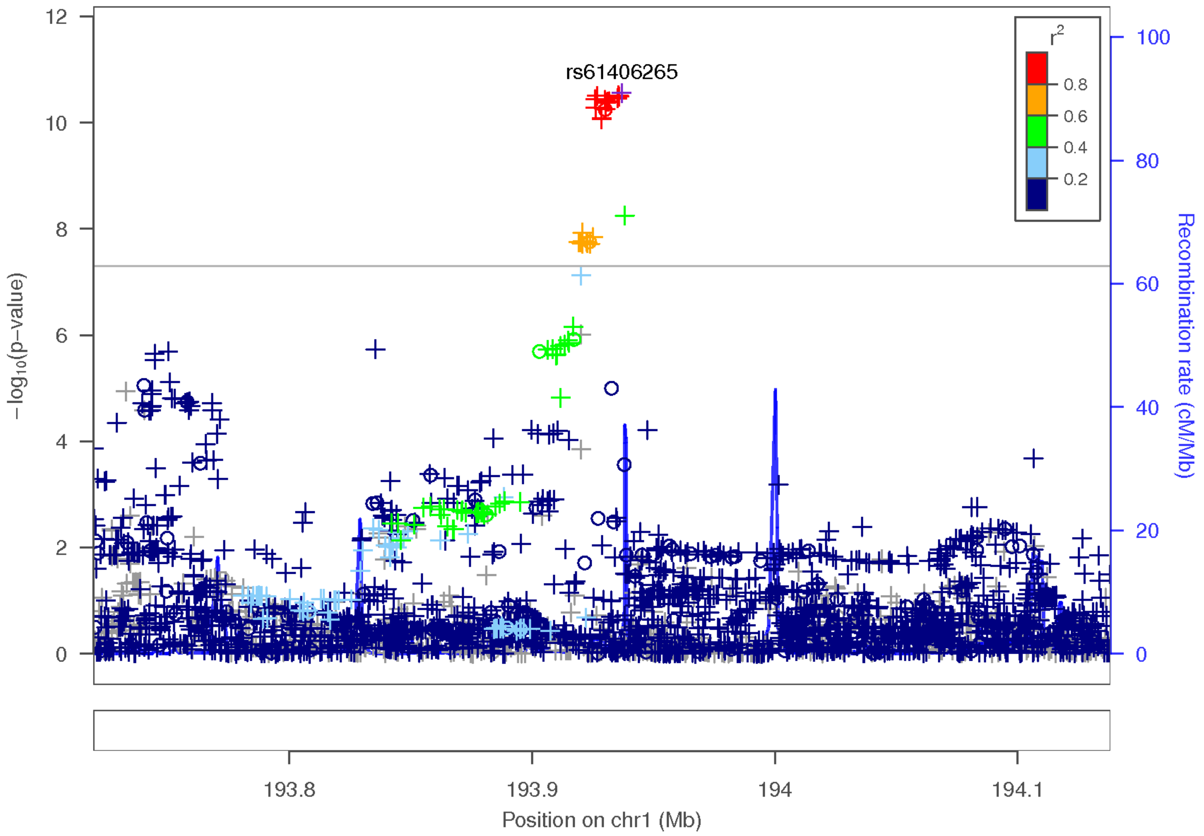

rs10067451
r^2
0.8
0.6
0.4
0.2
12
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
←TMEM161B
←LINC00461
←MEF2C
TMEM161B−AS1→
←MIR9−2
87.2
87.4
87.6
87.8
88
88.2
Position on chr5 (Mb)

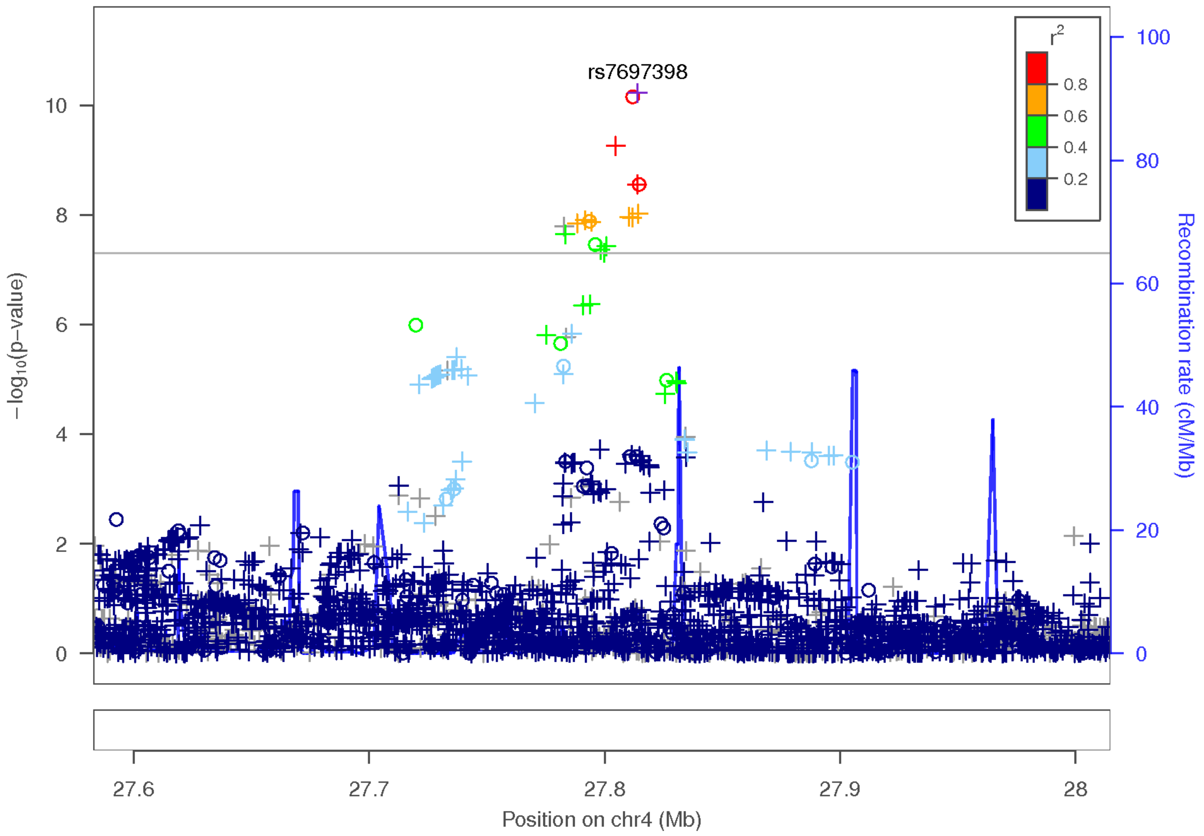


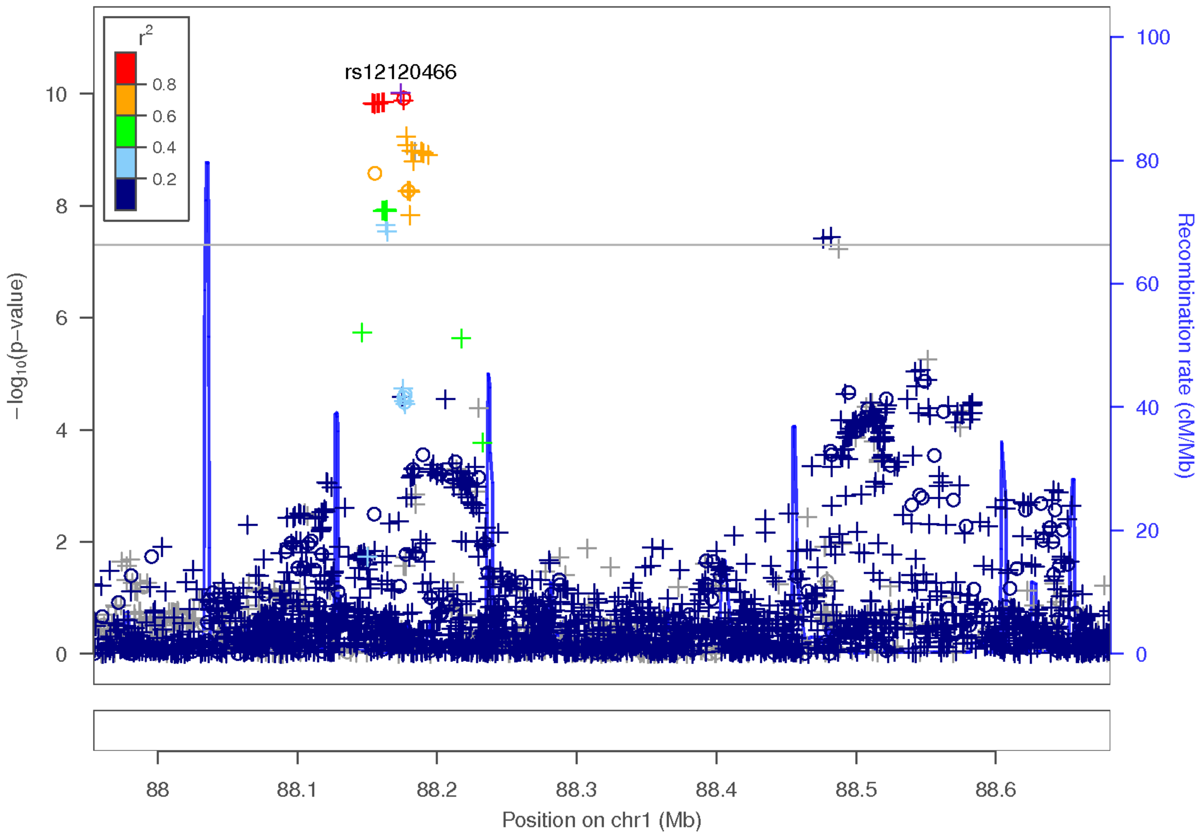
rs141078219
r^2
0.8
0.6
0.4
0.2
0
2
4
6
8
10
12
$-\log_{10}$(p-value)
0
20
40
60
80
100
Recombination rate (cM/Mb)
MEIS1-AS3
MEIS1
66.7
66.8
66.9
67
67.1
Position on chr2 (Mb)



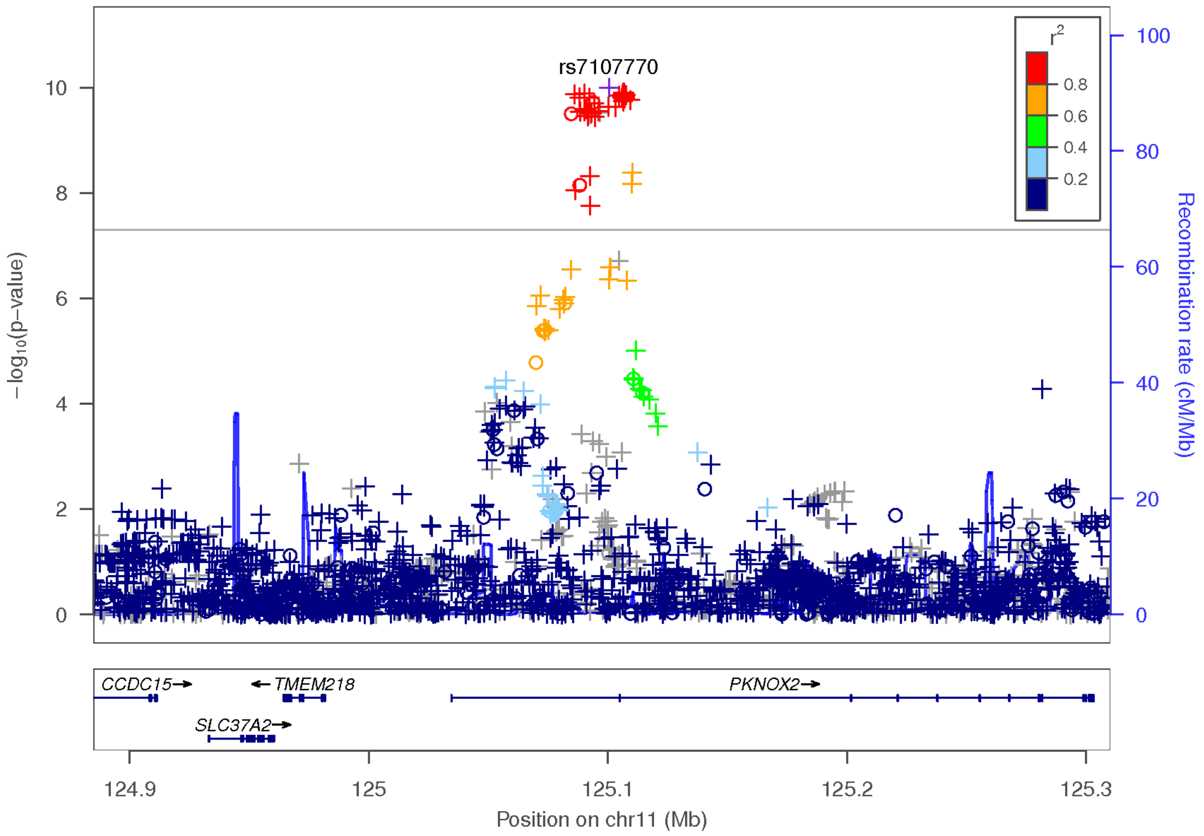
rs35407642
r^2
0.8
0.6
0.4
0.2
0
2
4
6
8
10
12
$-\log_{10}$(p-value)
0
20
40
60
80
100
Recombination rate (cM/Mb)
COMMD9
PRR5L
TRAF6
RAG1
RAG2
C11orf74
36.3
36.4
36.5
36.6
Position on chr11 (Mb)


rs61406265
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
193.8
193.9
194
194.1
Position on chr1 (Mb)

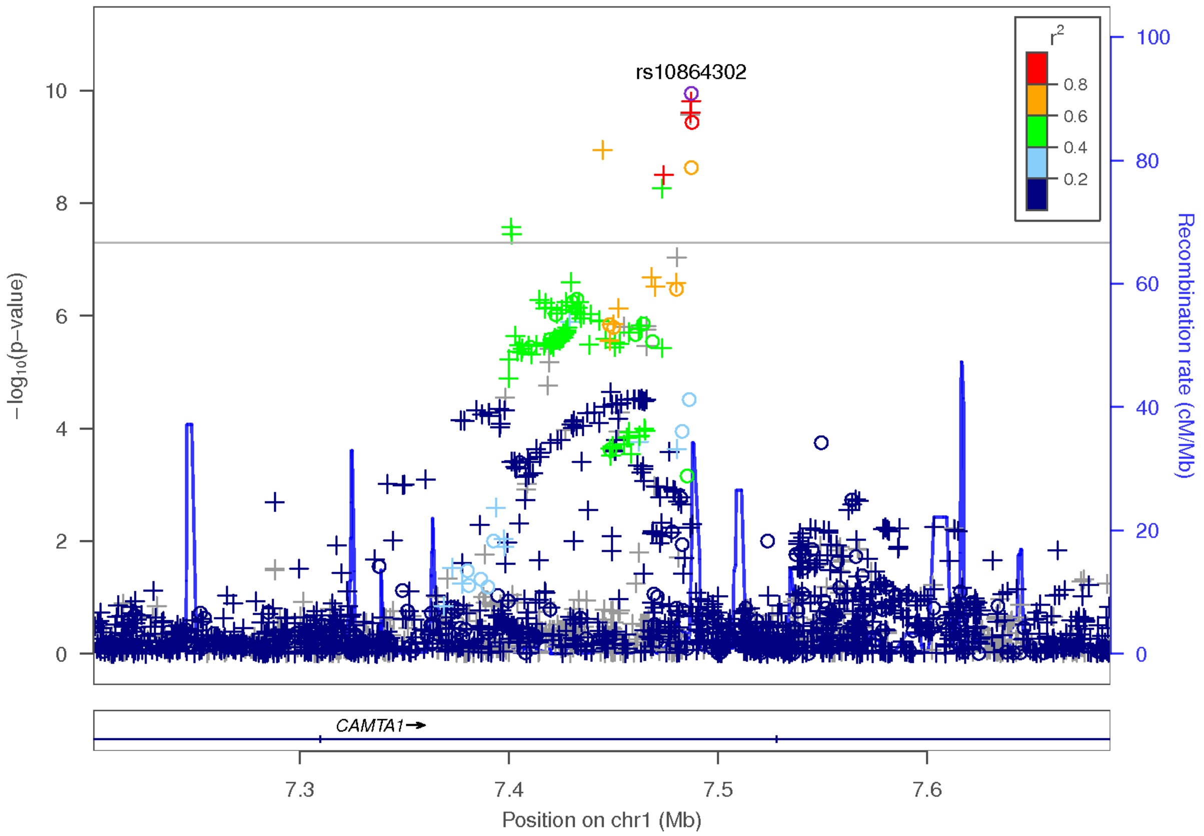

rs7697398
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
27.6
27.7
27.8
27.9
28
Position on chr4 (Mb)

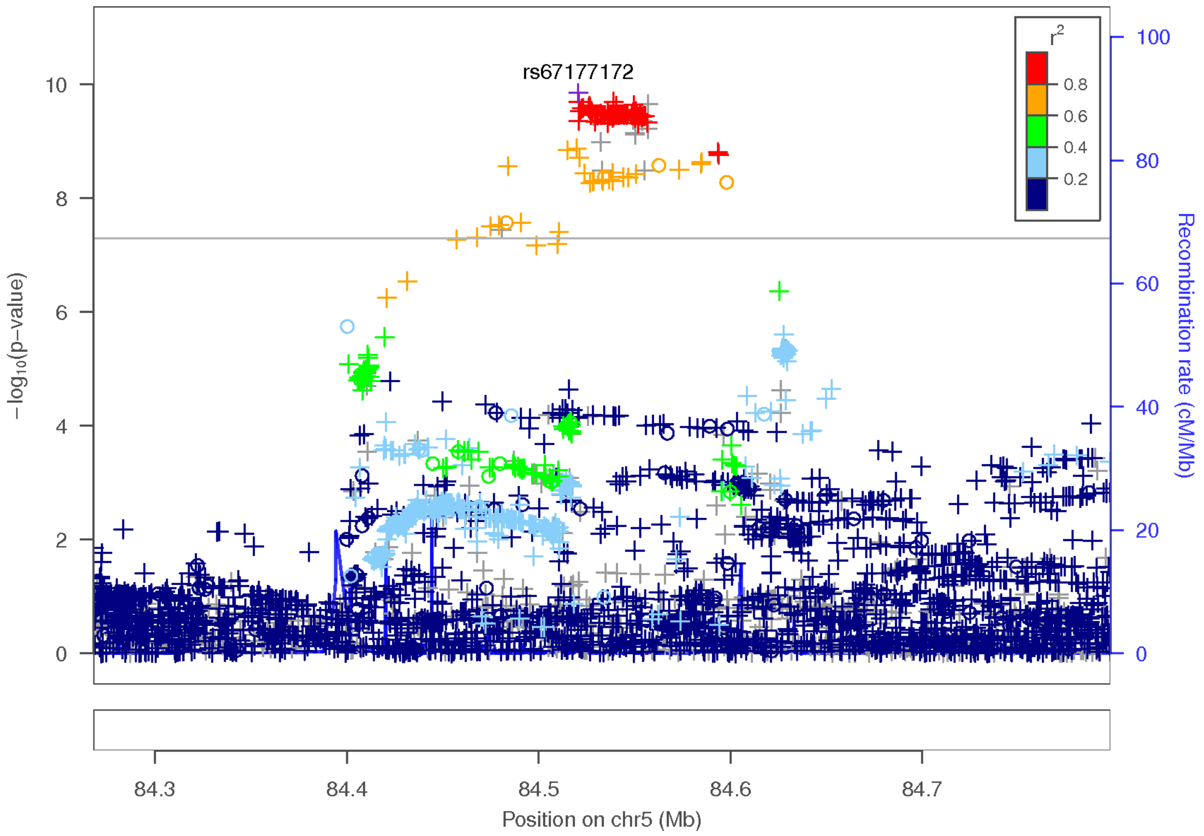


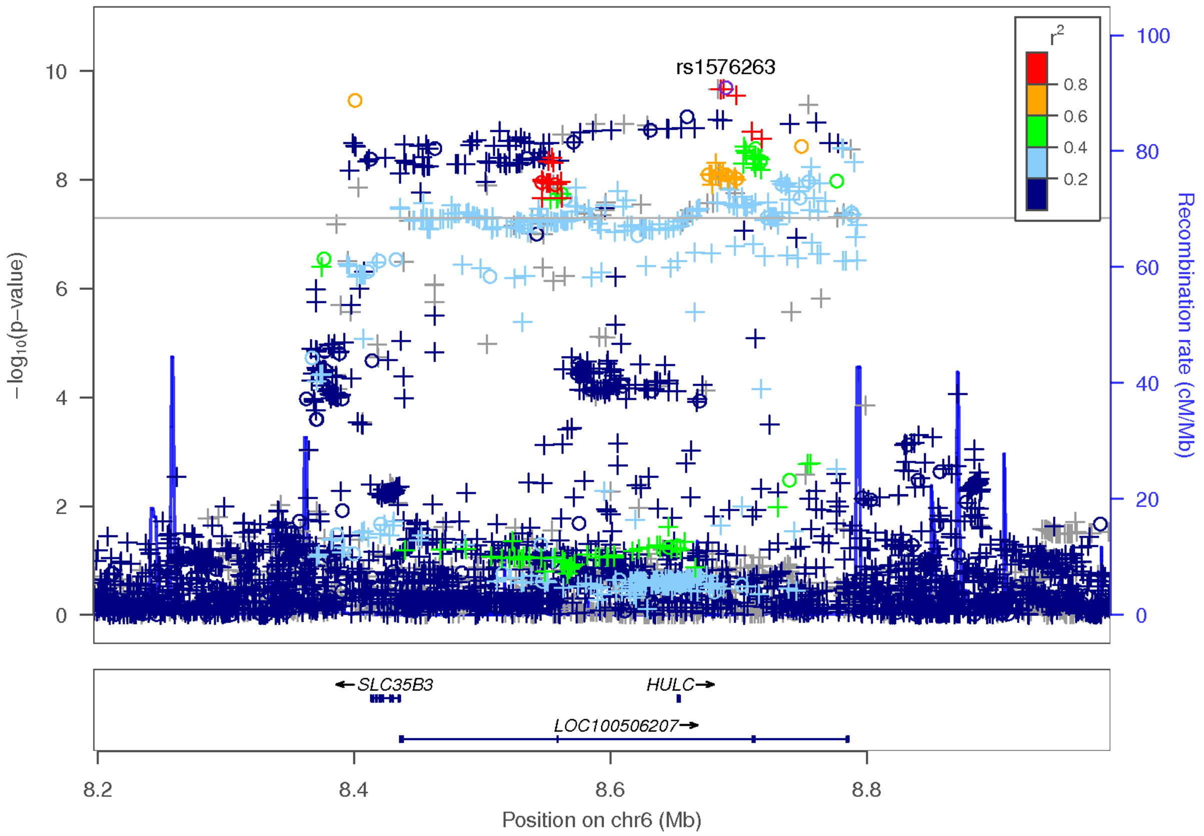
r²
0.8
0.6
0.4
0.2
rs12120466
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
88
88.1
88.2
88.3
88.4
88.5
88.6
Position on chr1 (Mb)

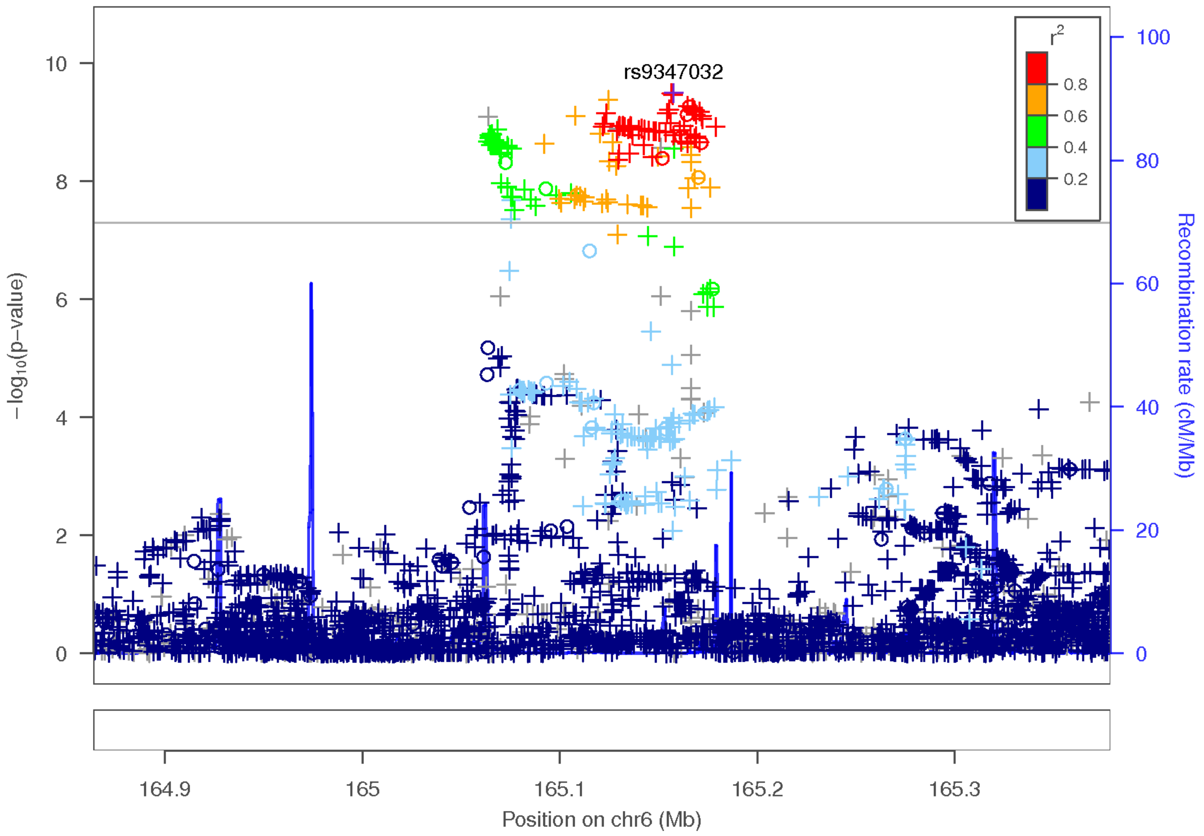


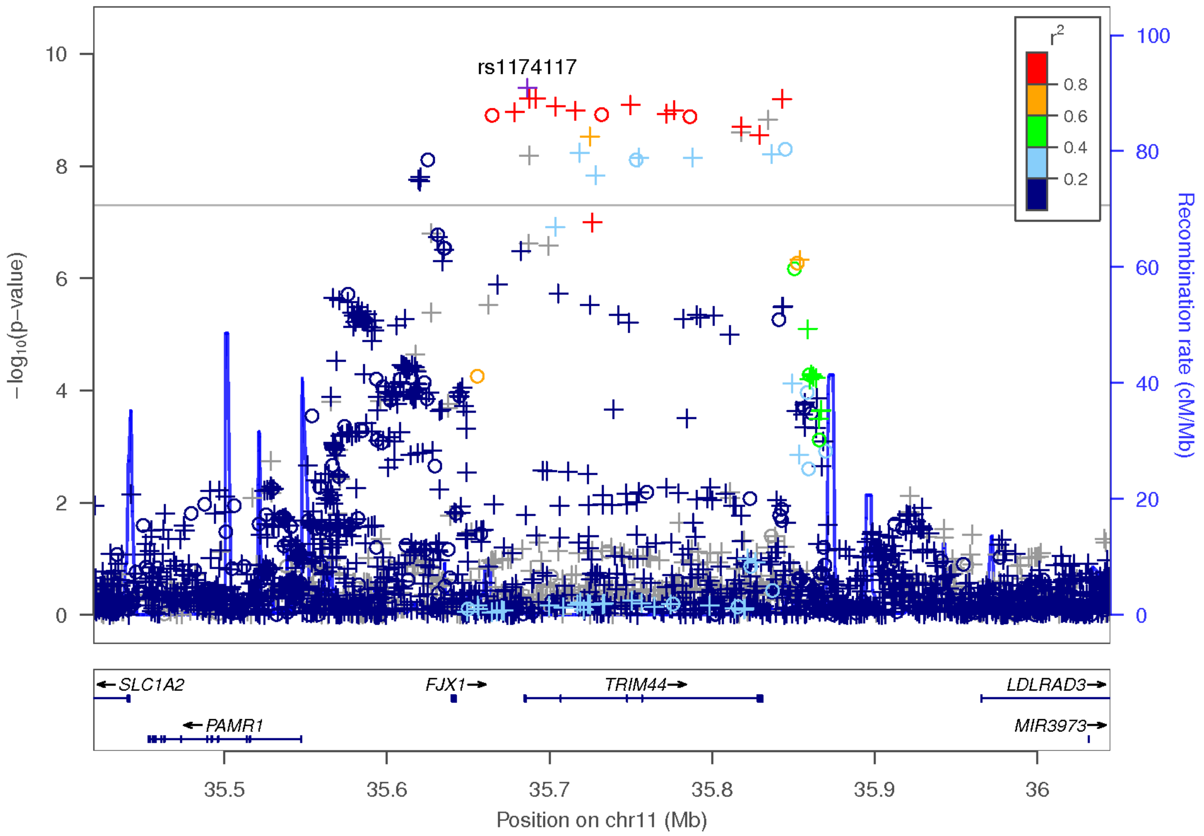
r²
0.8
0.6
0.4
0.2
rs7107770
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
CCDC15→
←TMEM218
PKNOX2→
SLC37A2→
124.9
125
125.1
125.2
125.3
Position on chr11 (Mb)

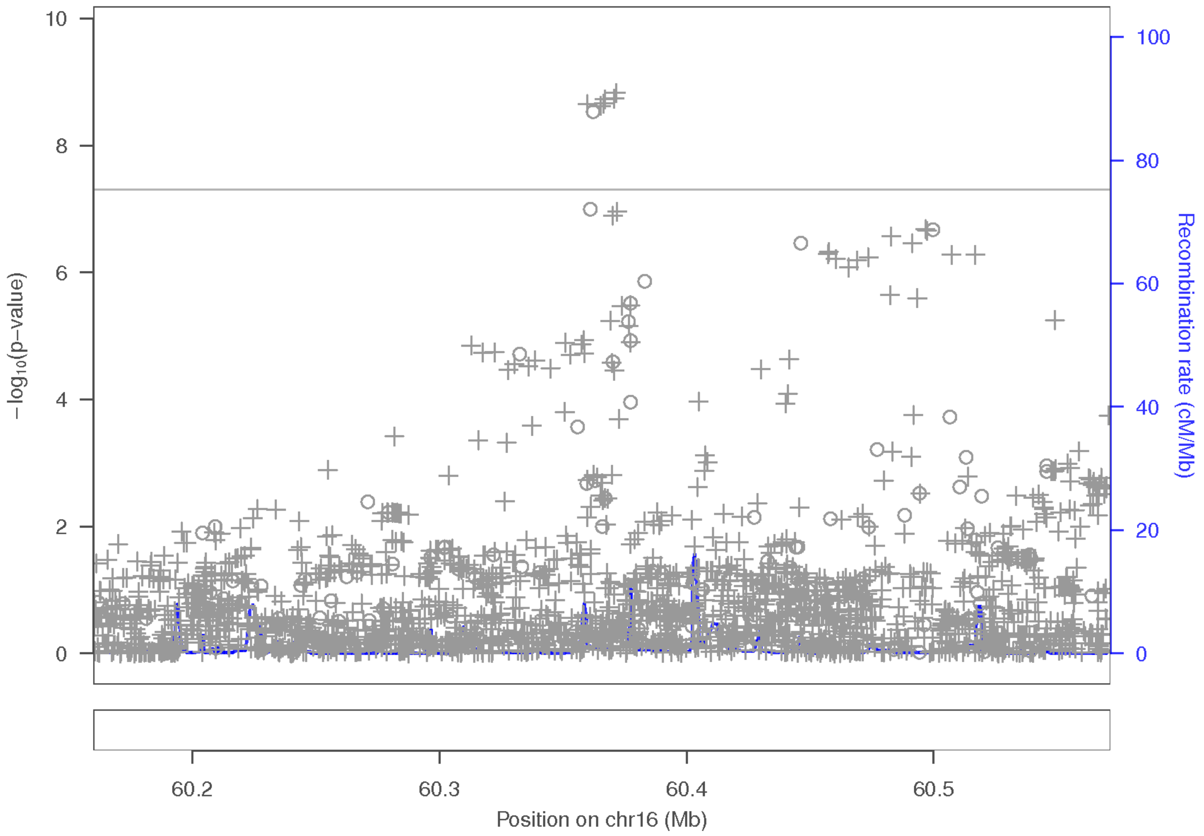

rs10864302
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
CAMTA1
7.3
7.4
7.5
7.6
Position on chr1 (Mb)

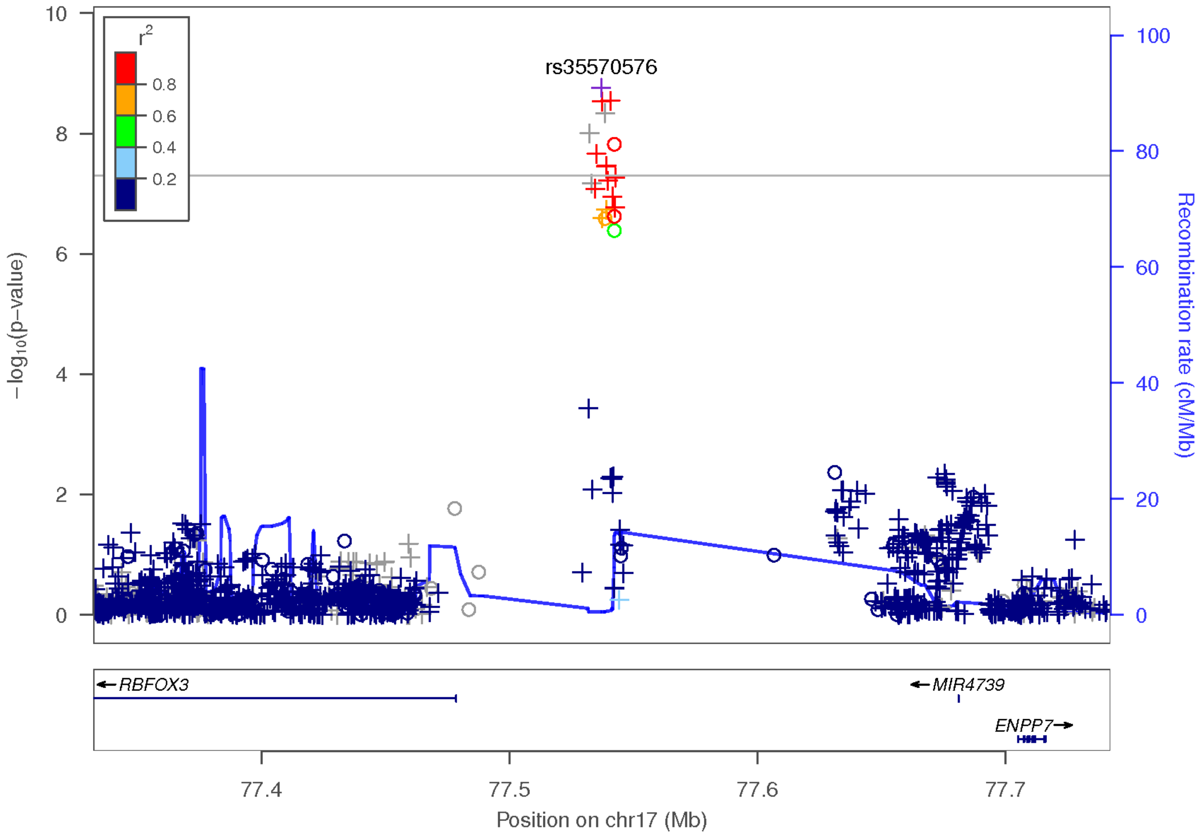

rs67177172
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
84.3
84.4
84.5
84.6
84.7
Position on chr5 (Mb)

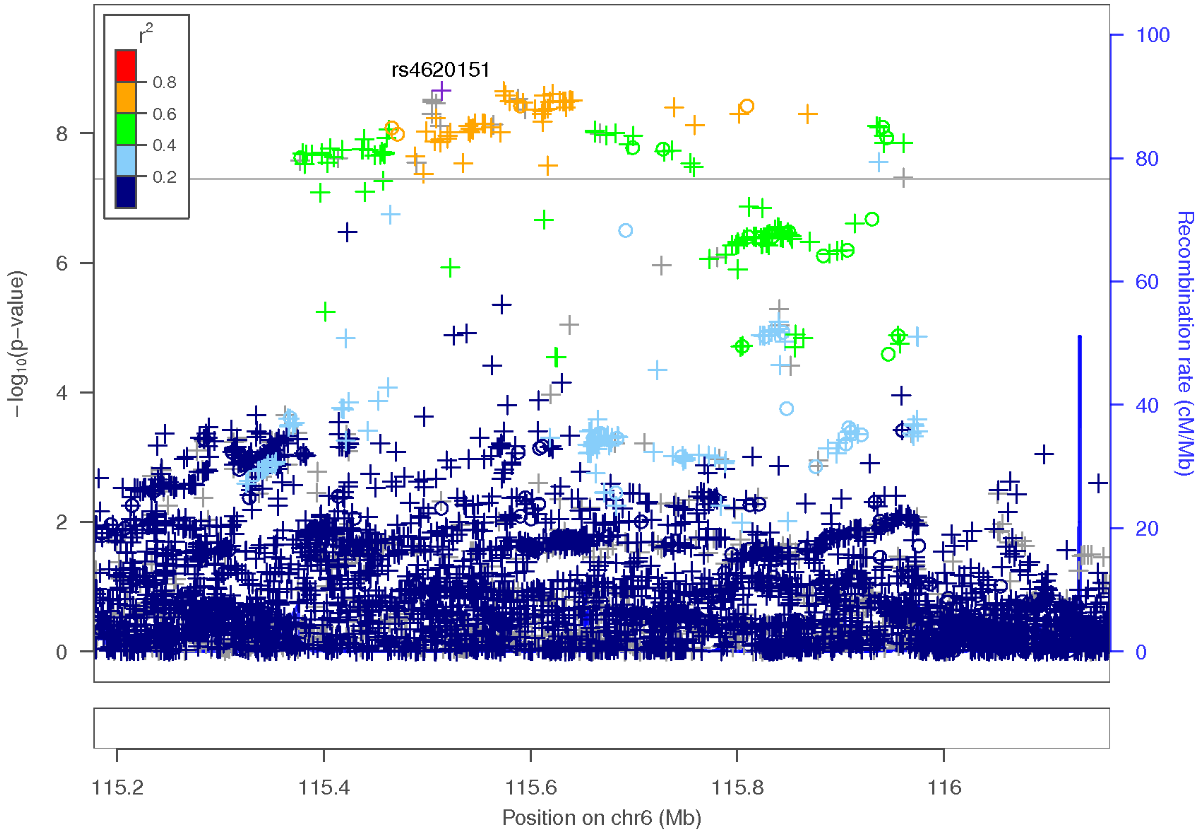

rs1576263
r^2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
10
0
20
40
60
80
100
SLC35B3
HULC
LOC100506207
8.2
8.4
8.6
8.8
Position on chr6 (Mb)

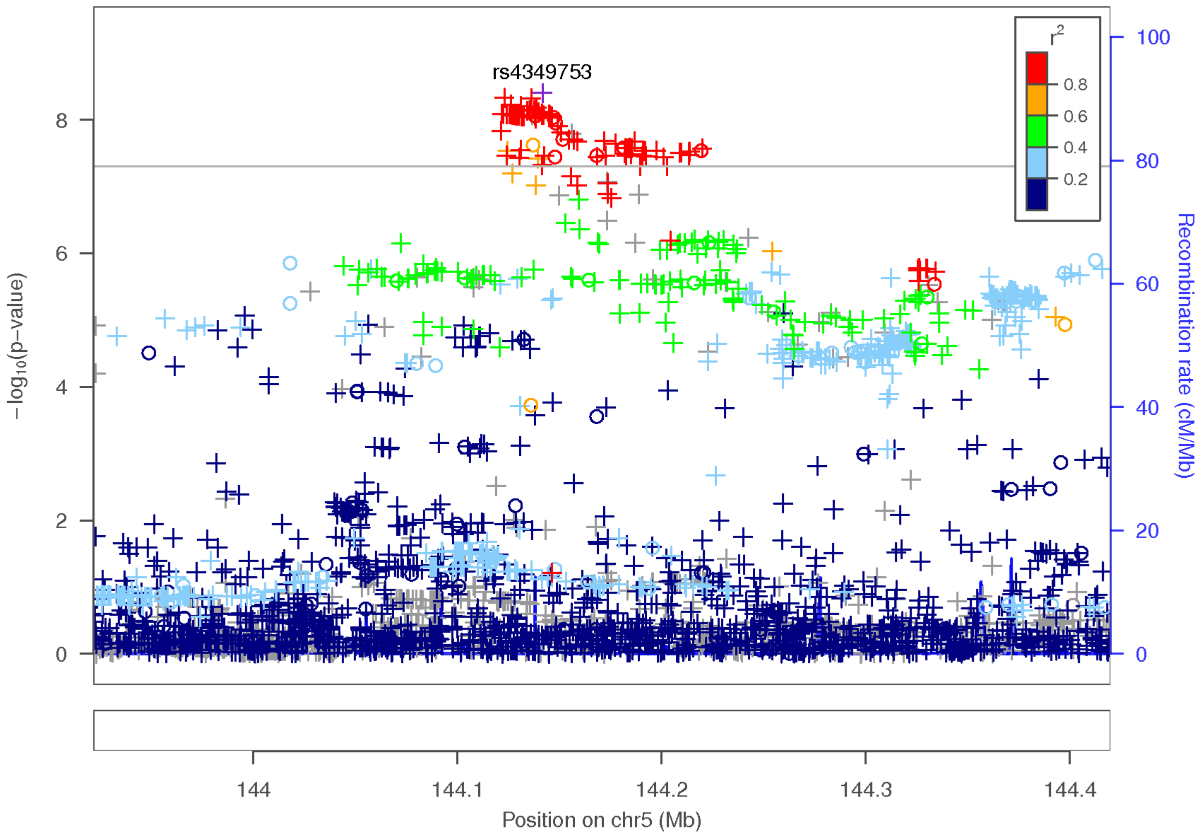

rs9347032
r^2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
10
0
20
40
60
80
100
164.9
165
165.1
165.2
165.3
Position on chr6 (Mb)

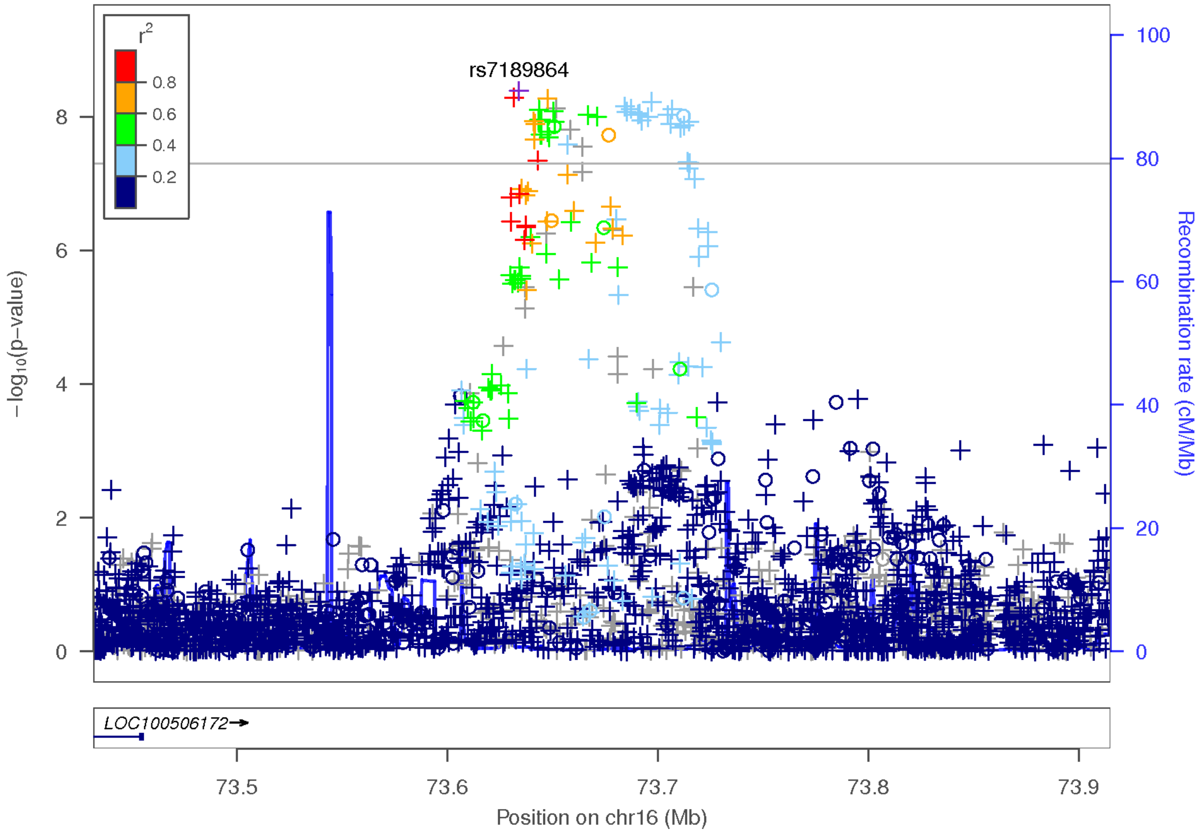

rs1174117
r2
0.8
0.6
0.4
0.2
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
SLC1A2
FJX1
TRIM44
LDLRAD3
PAMR1
MIR3973
35.5
35.6
35.7
35.8
35.9
36
Position on chr11 (Mb)

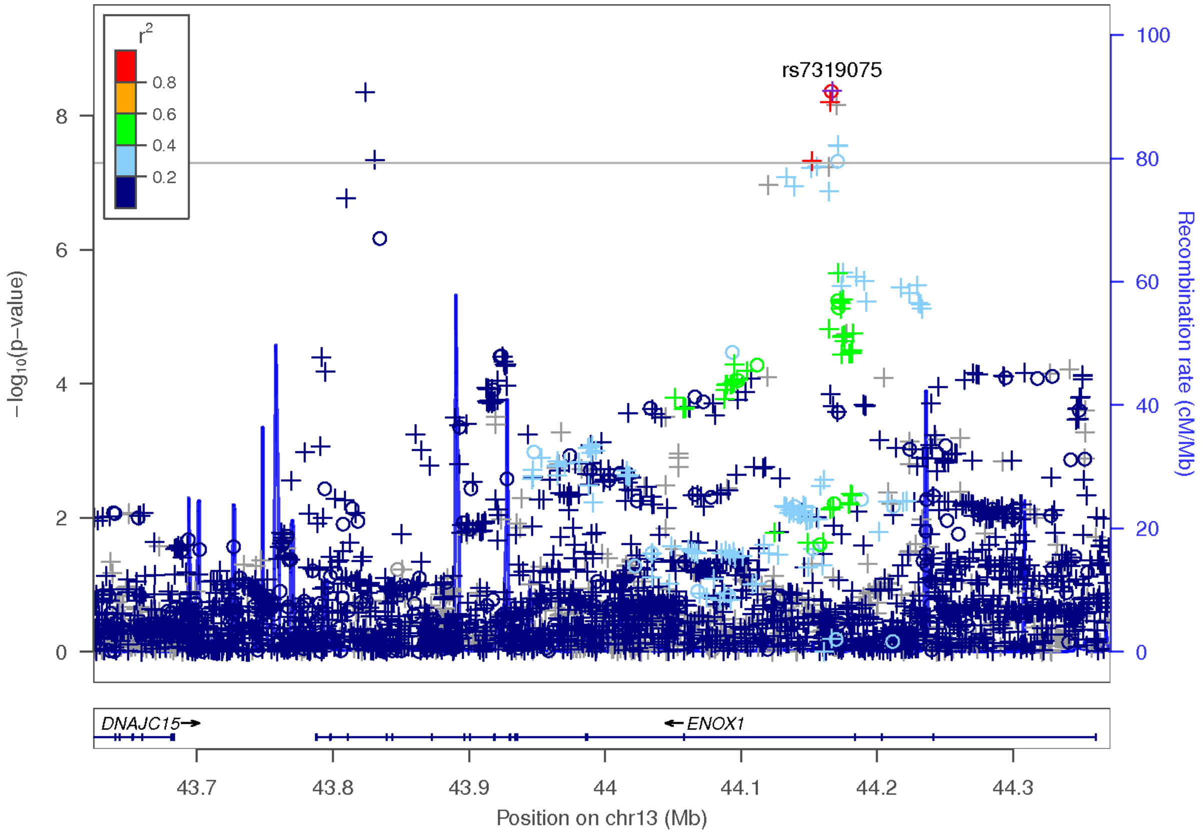

−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
60.2
60.3
60.4
60.5
Position on chr16 (Mb)

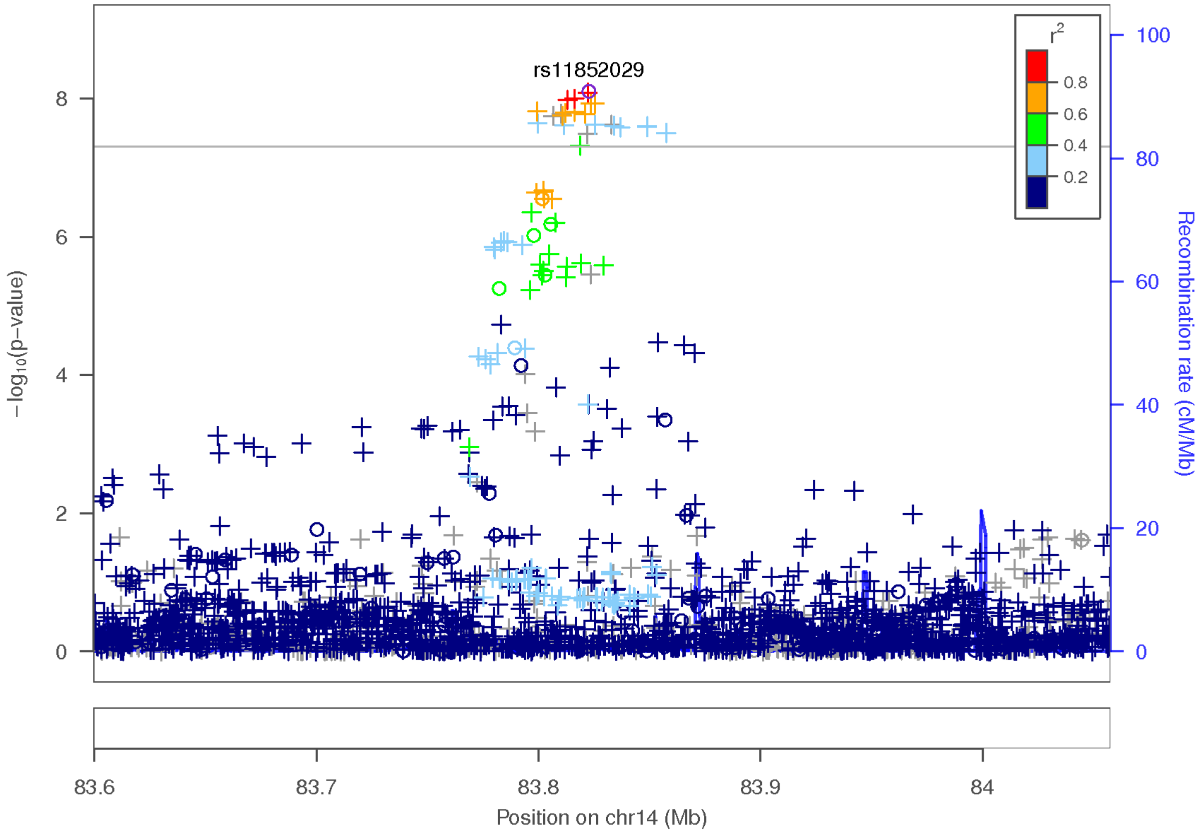

r2
0.8
0.6
0.4
0.2
rs35570576
−log10(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
RBFOX3
MIR4739
ENPP7
77.4
77.5
77.6
77.7
Position on chr17 (Mb)

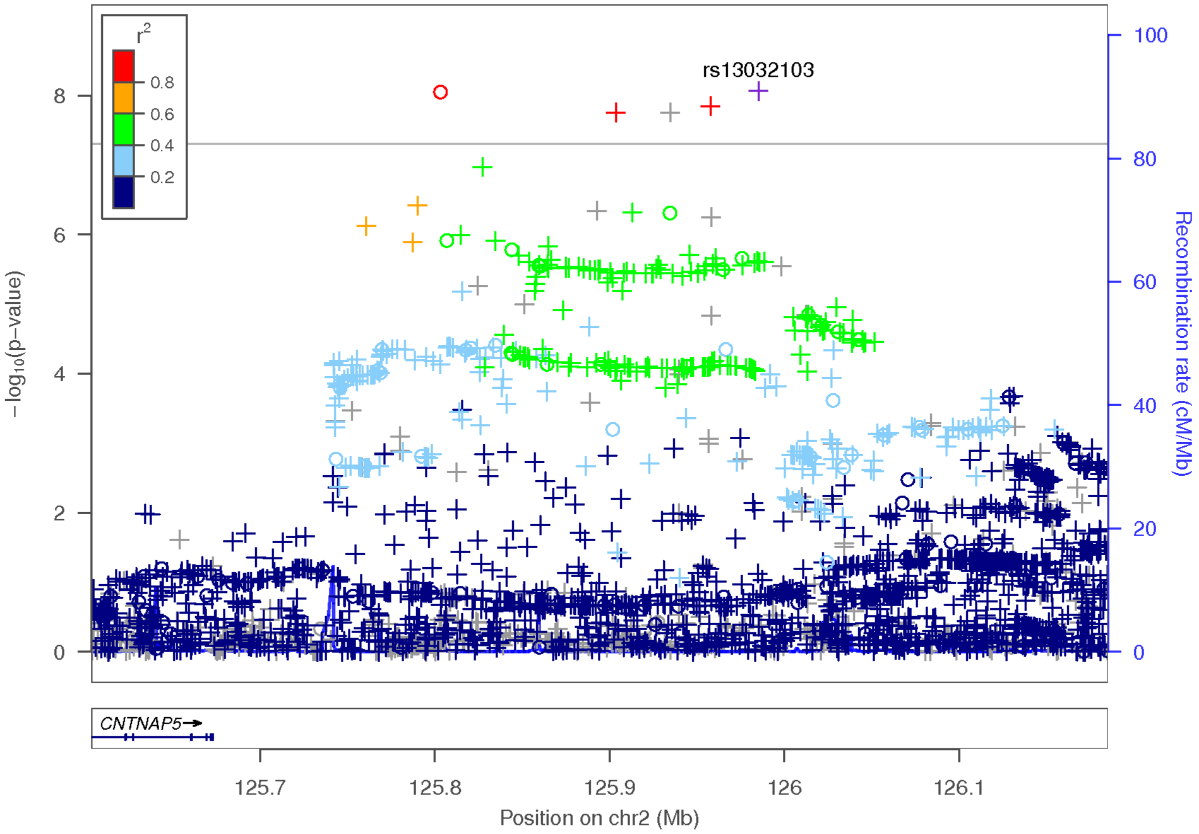

r2
0.8
0.6
0.4
0.2
rs4620151
−log10(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
115.2
115.4
115.6
115.8
116
Position on chr6 (Mb)


rs4349753
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
144
144.1
144.2
144.3
144.4
Position on chr5 (Mb)

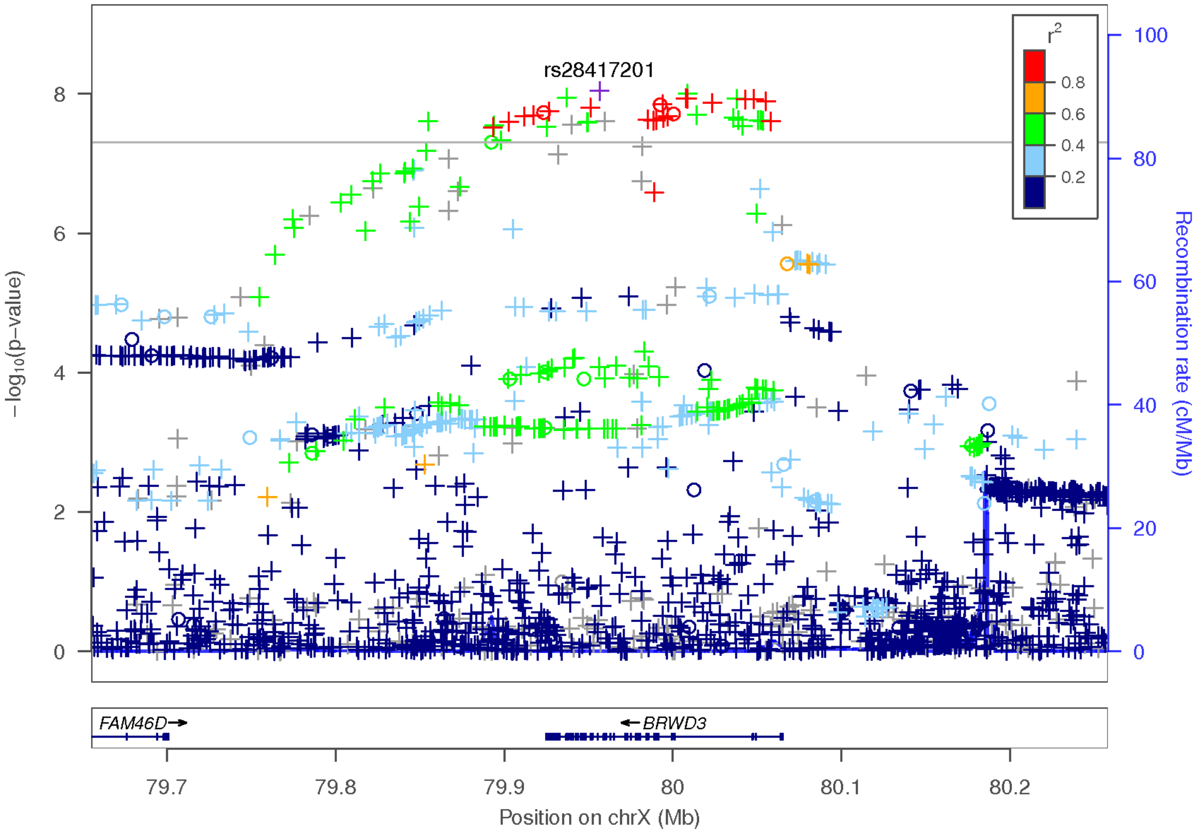

rs7189864
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
LOC100506172→
73.5
73.6
73.7
73.8
73.9
Position on chr16 (Mb)


r^2
0.8
0.6
0.4
0.2
rs7319075
−log₁₀(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
DNAJC15
ENOX1
43.7
43.8
43.9
44
44.1
44.2
44.3
Position on chr13 (Mb)

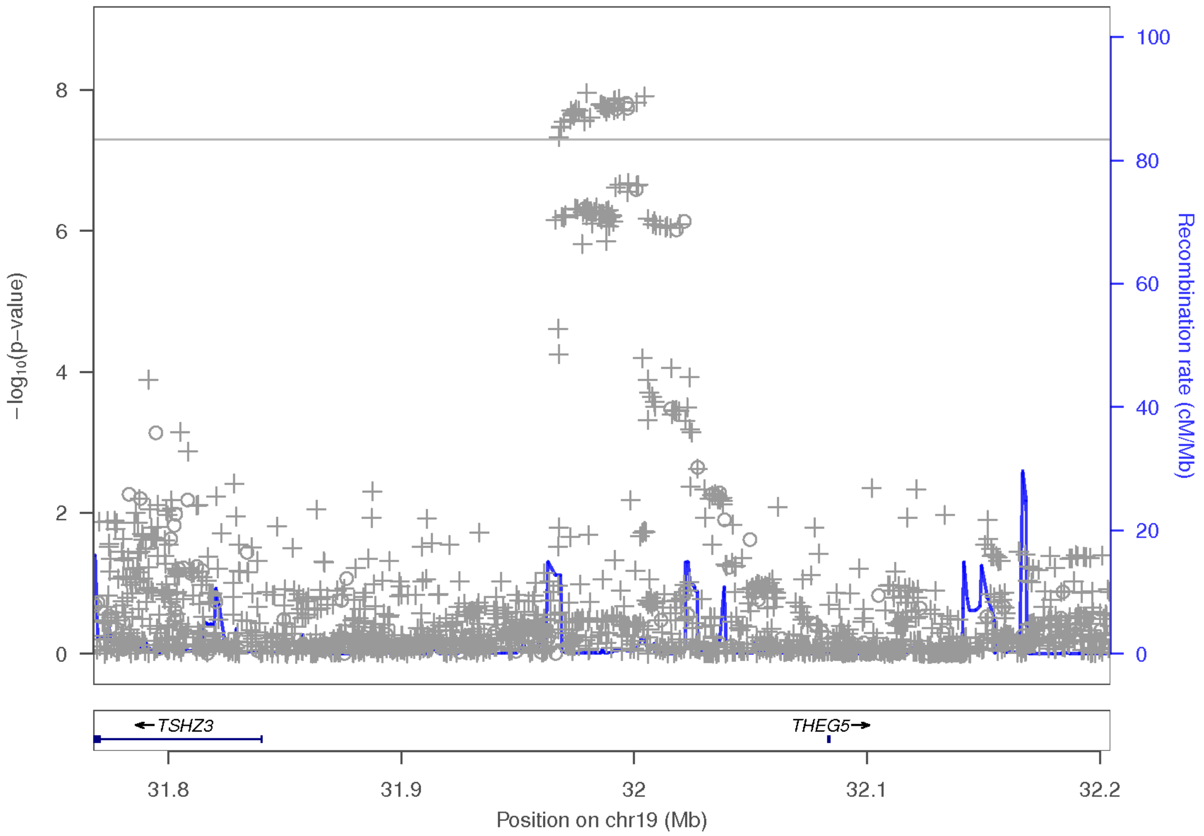

r^2
0.8
0.6
0.4
0.2
rs11852029
−log₁₀(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
83.6
83.7
83.8
83.9
84
Position on chr14 (Mb)

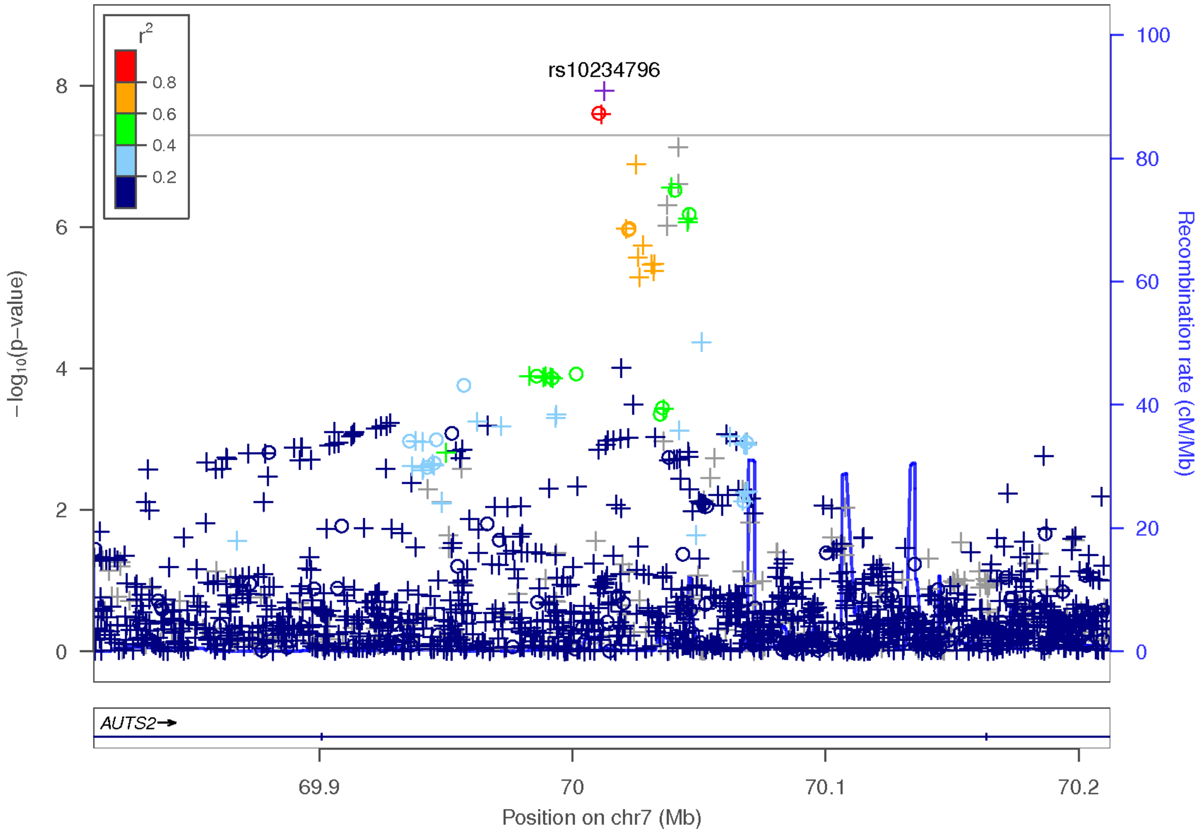


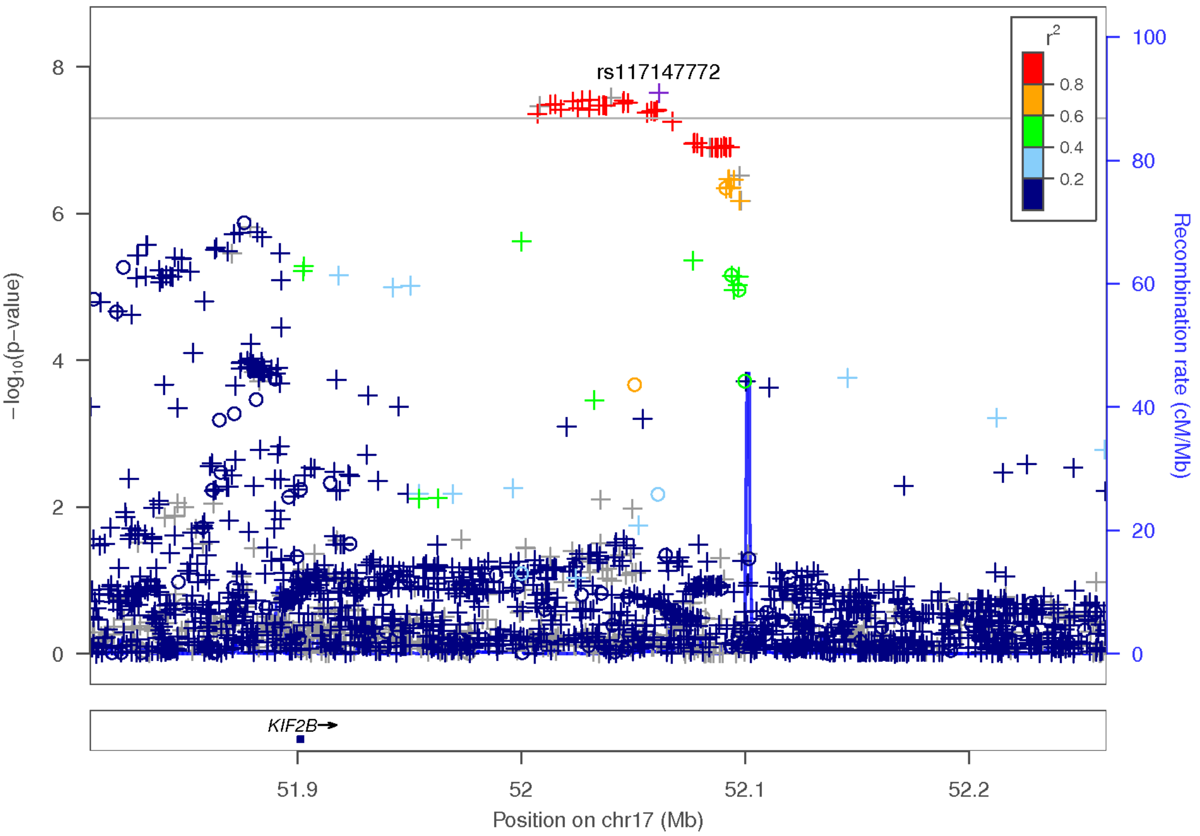
r2
0.8
0.6
0.4
0.2
rs13032103
−log10(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
CNTNAP5
125.7
125.8
125.9
126
126.1
Position on chr2 (Mb)

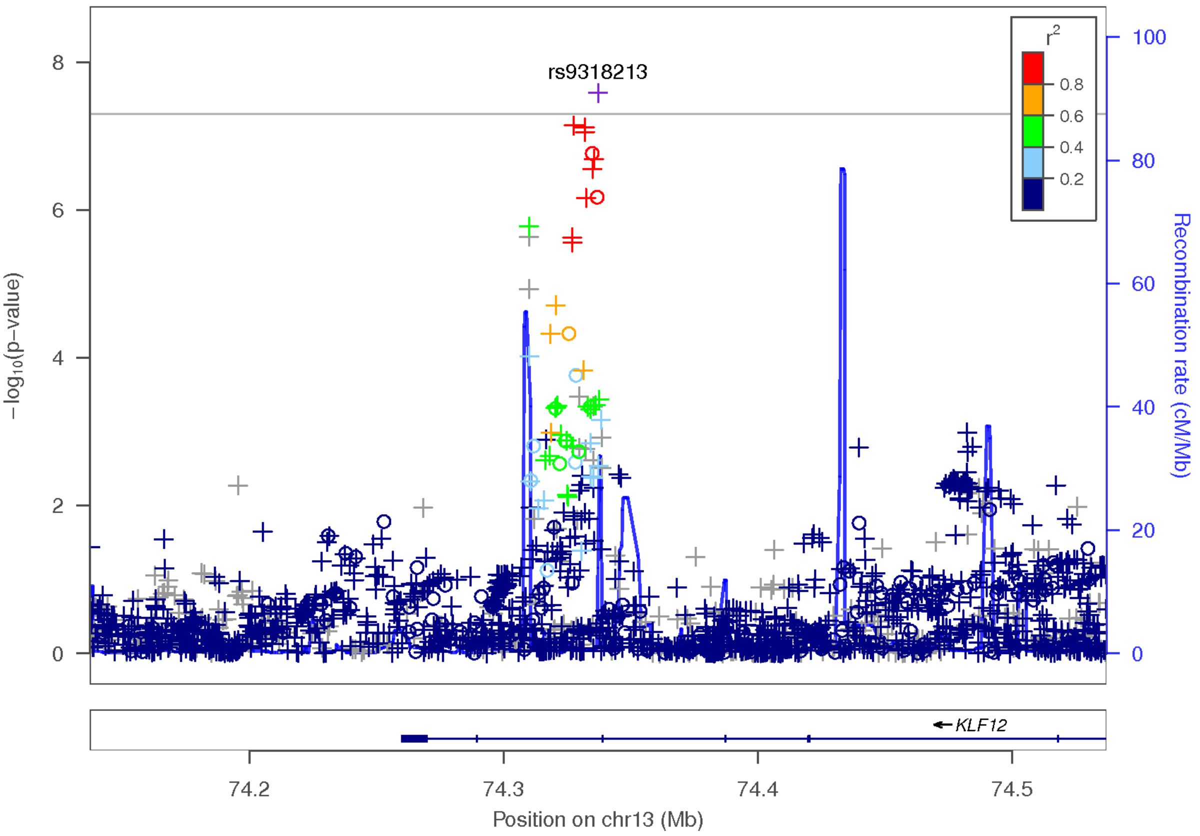


r2
0.8
0.6
0.4
0.2
rs28417201
−log10(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
FAM46D
BRWD3
79.7
79.8
79.9
80
80.1
80.2
Position on chrX (Mb)

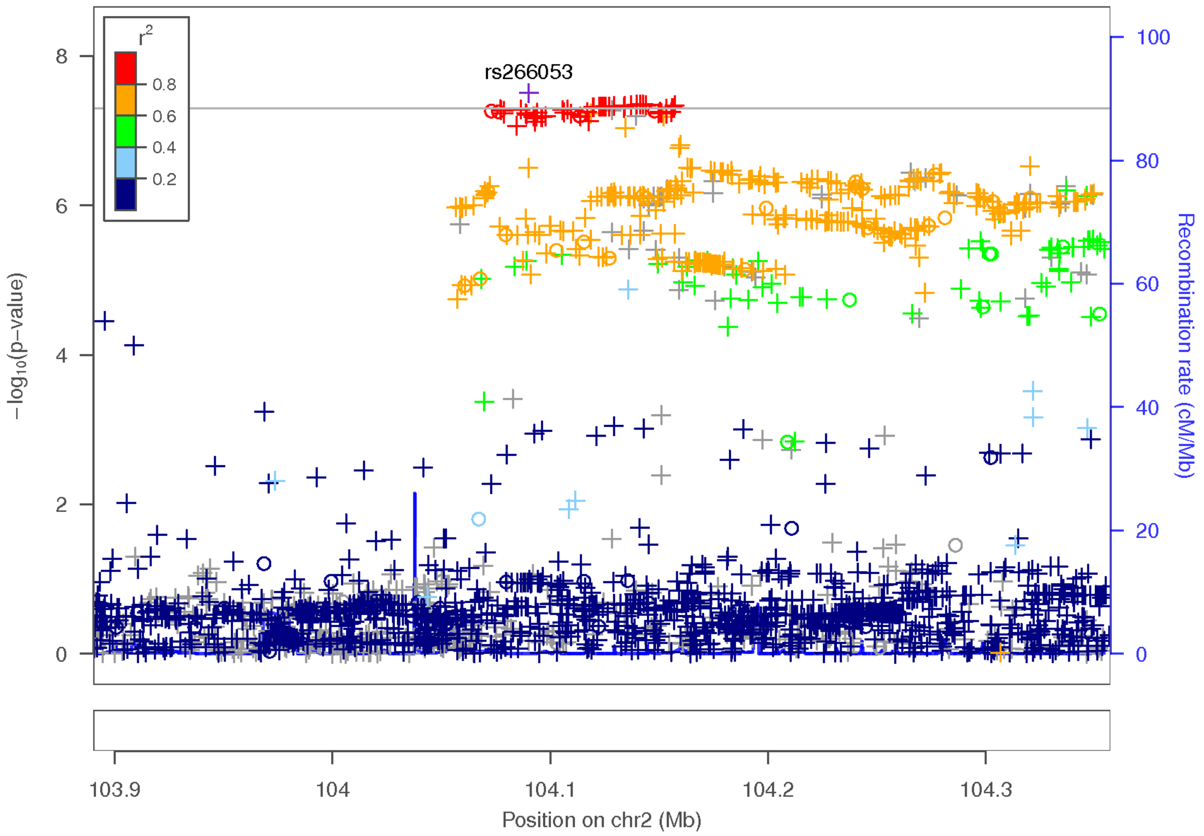

−log10(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
TSHZ3
THEG5
31.8
31.9
32
32.1
32.2
Position on chr19 (Mb)


r2
0.8
0.6
0.4
0.2
rs10234796
−log10(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
AUTS2
69.9
70
70.1
70.2
Position on chr7 (Mb)





locuszoom plot for 11:92232901:G_GTA failed


r2
0.8
0.6
0.4
0.2
rs266053
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
103.9
104
104.1
104.2
104.3
Position on chr2 (Mb)