Analysis Summary: morphology, chin_dimple

Phenotype Description

morphology, question chin_dimple

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]
chin_dimple	case	58032	29963	28069	8104	18584	14864	16480
	control	13457	8816	4641	2235	4725	3432	3065

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

Phenotype	Group	Total	v1/v2	v3	v4
chin_dimple	case	58032	7160	48440	2432
	control	13457	1569	11313	575

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	0.00829	0.000617	13.4	4.6×10^{-41}	181.9	1.9×10^{-41}
sexF	0.56989	0.020023	28.5	3.4×10^{-178}	836.5	6.2×10^{-184}
pc.0	−0.05713	0.010215	−5.6	2.2×10^{-8}	32.4	1.2×10^{-8}
pc.1	0.00910	0.009626	0.9	0.34	0.9	0.34
pc.2	−0.03572	0.009653	−3.7	0.00022	13.6	0.00023
pc.3	−0.01069	0.009668	−1.1	0.27	1.2	0.27
pc.4	−0.00738	0.009634	−0.8	0.44	0.6	0.44

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	−16567	13762500
failed to converge	−224739	13537761

Genetic Association Tests

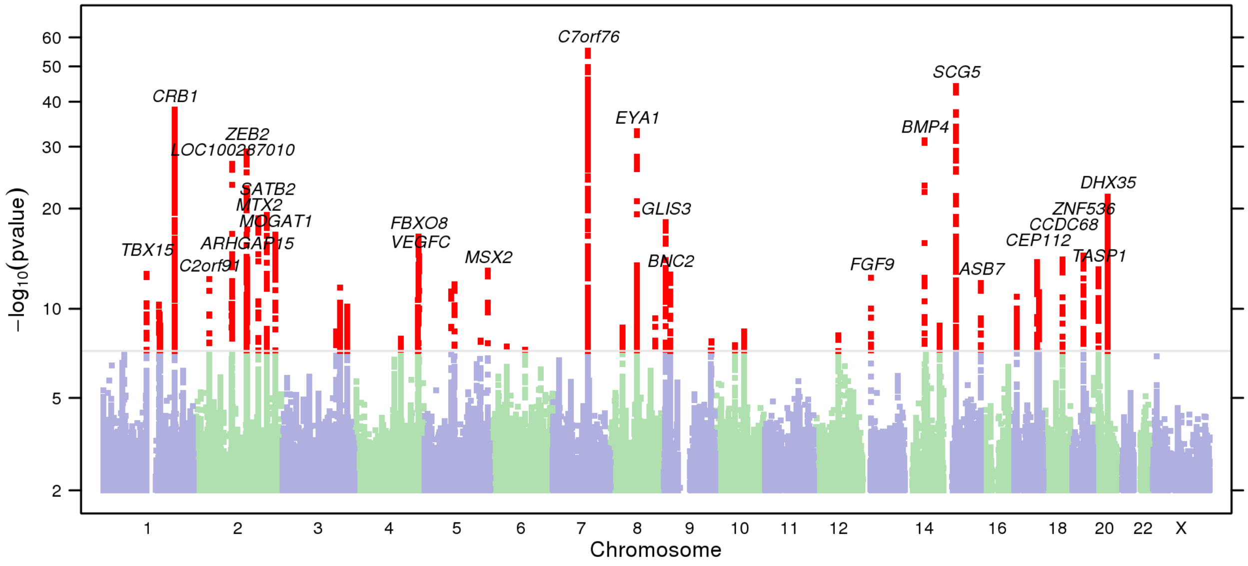
We performed logistic regression assuming an additive model for allelic effects, using the model:

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

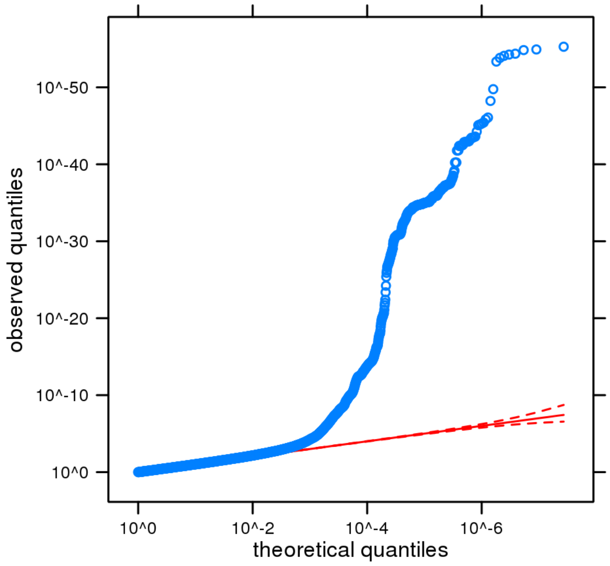
This genome-wide association analysis includes data from 58032 cases and 13457 controls of European ancestry, filtered to remove close relatives.

The results in this report have been adjusted for a genomic control inflation factor λ=1.071. The equivalent inflation factor for 1000 cases and 1000 controls λ_{1000}= 1.003 , and for 10000, λ_{10000}= 1.032 .

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
7q21.3	rs11768577	chr7	96143804	G/T	I	5.3×10^{-56}	1.352	[1.303,1.402]	C7orf76--[]---SHFM1

15q13.3	rs6494598	chr15	32995468	A/C	I	5.6×10^{-45}	1.222	[1.188,1.256]	SCG5-[]--GREM1
1q31.3	rs2476023	chr1	197351039	C/G	I	9.7×10^{-39}	0.793	[0.765,0.822]	[CRB1]
8q13.3	rs10504499	chr8	72036904	G/T	I	7.9×10^{-34}	1.292	[1.240,1.346]	XKR9---[]--EYA1
14q22.2	rs72678242	chr14	54255510	A/G	I	6.0×10^{-32}	0.785	[0.755,0.817]	DDHD1---[]---BMP4
2q22.3	rs17479393	chr2	145653287	A/T	I	8.1×10^{-30}	0.832	[0.806,0.858]	ZEB2---[]
2q12.1	rs10175706	chr2	104631814	C/T	I	1.3×10^{-27}	0.853	[0.829,0.878]	[]---LOC100287010
20q12	rs6028446	chr20	38101545	A/T	I	2.1×10^{-22}	0.871	[0.847,0.895]	DHX35---[]
2q33.1	rs13035389	chr2	199666111	C/T	I	6.8×10^{-20}	1.139	[1.107,1.171]	PLCL1---[]---SATB2
2q31.1	rs59156997	chr2	177371846	D/I	I	1.7×10^{-19}	0.834	[0.801,0.868]	MTX2---[]---HNRNPA3
9p24.2	rs4237150	chr9	4290085	C/G	I	5.6×10^{-19}	0.879	[0.855,0.905]	[GLIS3]
2q36.1	rs4674676	chr2	223529112	A/G	I	1.6×10^{-17}	0.841	[0.808,0.876]	FARSB-[]-MOGAT1
4q34.1	rs17275866	chr4	175071486	A/G	I	2.6×10^{-17}	0.875	[0.849,0.903]	HAND2---[]--FBXO8
19q12	rs55700449	chr19	30982165	A/G	I	2.8×10^{-15}	0.850	[0.817,0.886]	[ZNF536]
4q34.3	rs12509218	chr4	177587237	A/G	I	3.0×10^{-15}	0.838	[0.803,0.875]	SPCS3---[]--VEGFC
2q22.3	rs11688237	chr2	144560021	A/G	I	3.7×10^{-15}	0.894	[0.870,0.920]	ARHGAP15--[]---GTDC1
18q21.2	rs7243821	chr18	52655532	A/G	I	6.5×10^{-15}	1.130	[1.096,1.165]	CCDC68--[]---TCF4
17q24.1	rs11650175	chr17	63743650	C/T	I	1.1×10^{-14}	0.891	[0.865,0.918]	[CEP112]
20p12.1	rs2073323	chr20	13514434	C/G	I	6.1×10^{-14}	1.129	[1.094,1.165]	[TASP1]
5q35.2	rs4868444	chr5	174160113	C/T	I	7.4×10^{-14}	1.187	[1.134,1.242]	MSX2-[]---DRD1
1p12	rs1766786	chr1	119452500	G/T	I	1.6×10^{-13}	0.851	[0.816,0.888]	[TBX15]
9p22.2	rs10962767	chr9	16958463	A/C	I	1.8×10^{-13}	0.900	[0.875,0.925]	BNC2--[]---CNTLN
13q12.11	rs73168105	chr13	22713708	G/T	I	3.3×10^{-13}	1.149	[1.107,1.193]	FGF9---[]
2p21	rs6740960	chr2	42181679	A/T	I	4.3×10^{-13}	1.117	[1.084,1.151]	C2orf91[]--PKDCC
15q26.3	rs7167736	chr15	101206638	G/T	I	8.8×10^{-13}	0.880	[0.850,0.912]	ASB7--[]---ALDH1A3
5q14.2	rs10078545	chr5	82124190	A/T	I	1.2×10^{-12}	1.112	[1.080,1.145]	ATP6AP1L---[]---TMEM167A
3q25.32	rs11713363	chr3	157828322	C/T	I	2.3×10^{-12}	0.890	[0.861,0.920]	[RSRC1]
5q13.3	rs199880074	chr5	73483120	D/I	I	4.9×10^{-12}	0.893	[0.865,0.922]	ARHGEF28---[]---ENC1
17q24.3	rs56347314	chr17	69123106	C/T	I	5.4×10^{-12}	1.108	[1.076,1.140]	KCNJ2---[]---SOX9
17p13.1	rs80067372	chr17	7452752	A/G	I	1.2×10^{-11}	1.115	[1.080,1.150]	[TNFSF12-TNFSF13]
4q34.1	rs12505328	chr4	174378004	C/T	I	2.1×10^{-11}	1.106	[1.074,1.139]	SCRG1--[]--HAND2
1q22	rs11589479	chr1	155033308	A/G	I	4.7×10^{-11}	1.131	[1.090,1.173]	[ADAM15]
3q26.32	rs2133593	chr3	177301992	A/C	I	6.6×10^{-11}	0.904	[0.878,0.932]	TBL1XR1---[]---KCNMB2
8q24.13	rs12541121	chr8	123101743	A/G	I	4.7×10^{-10}	1.095	[1.064,1.127]	HAS2---[]---ZHX2
14q32.13	rs7161418	chr14	95479889	G/T	I	1.4×10^{-9}	1.106	[1.070,1.143]	GSC---[]--DICER1
1q23.1	rs1336149	chr1	156939175	C/T	I	1.5×10^{-9}	1.093	[1.062,1.125]	[ARHGEF11]
8p12	rs2347498	chr8	32353180	C/T	I	1.8×10^{-9}	0.915	[0.888,0.942]	[]--NRG1
10q22.3	rs11001765	chr10	78150285	A/C	I	3.5×10^{-9}	0.884	[0.848,0.921]	[C10orf11]
3q24	rs12495832	chr3	147829477	A/G	I	3.6×10^{-9}	0.870	[0.830,0.911]	ZIC1---[]---AGTR1
12q14.3	rs141753469	chr12	66397166	A/C	I	5.9×10^{-9}	1.111	[1.072,1.151]	HMGA2--[]---LLPH
4q28.1	rs145365164	chr4	126954652	C/T	I	9.6×10^{-9}	1.109	[1.070,1.148]	FAT4---[]
5q33.2	rs4958741	chr5	153868262	A/G	I	1.3×10^{-8}	1.108	[1.069,1.147]	HAND1--[]---LARP1
9q33.3	rs62578082	chr9	129277041	A/C	I	1.4×10^{-8}	1.140	[1.089,1.194]	MVB12B-[]--LMX1B
10q21.1	rs1194708	chr10	54199812	A/G	I	2.4×10^{-8}	0.910	[0.881,0.941]	DKK1---[]---MBL2
6p21.1	rs17336368	chr6	44751668	A/G	I	2.8×10^{-8}	0.915	[0.887,0.944]	CDC5L---[]--SUPT3H
6q16.1	rs112215522	chr6	94913574	C/T	I	4.2×10^{-8}	1.092	[1.058,1.127]	EPHA7---[]

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
rs11768577	FALSE	FALSE	FALSE					0.9852	0.9806	0.088	0.8466	v2v3v4
rs6494598	FALSE	FALSE	FALSE					0.9940	0.9852	0.56	0.5091	v2v3v4
rs2476023	FALSE	FALSE	FALSE					0.9758	0.9693	0.35	0.7839	v2v3v4
rs10504499	FALSE	FALSE	FALSE					0.9935	0.9874	0.73	0.8819	v2v3v4
rs72678242	FALSE	FALSE	FALSE					0.9733	0.9611	0.77	0.1288	v2v3v4
rs17479393	FALSE	FALSE	FALSE					0.9953	0.9937	0.90	0.2411	v2v3v4
rs10175706	FALSE	FALSE	FALSE					0.9950	0.9933	0.0033	0.5972	v2v3v4
rs6028446	FALSE	FALSE	FALSE					0.9963	0.9937	0.0040	0.4723	v2v3v4
rs13035389	TRUE	TRUE	TRUE	0.9996	0.13	0.24	0.5491	0.9969	0.9869	0.94	0.5497	v2v3v4
rs59156997	FALSE	FALSE	FALSE					0.9391	0.9242	0.017	0.8341	v2v3v4
rs4237150	FALSE	FALSE	FALSE					0.9941	0.9862	0.45	0.5795	v2v3v4
rs4674676	FALSE	FALSE	FALSE					0.9299	0.9246	0.062	0.8372	v2v3v4
rs17275866	FALSE	FALSE	FALSE					0.9909	0.9826	0.42	0.7043	v2v3v4
rs55700449	FALSE	FALSE	FALSE					0.9915	0.9881	0.28	0.8569	v2v3v4
rs12509218	FALSE	FALSE	FALSE					0.9948	0.9883	0.59	0.1055	v2v3v4
rs11688237	FALSE	FALSE	FALSE					0.9968	0.9951	0.89	0.5061	v2v3v4
rs7243821	FALSE	FALSE	FALSE					0.9899	0.9838	0.19	0.7239	v2v3v4
rs11650175	TRUE	TRUE	TRUE	0.9999	0.035	0.31	0.6516	0.9998	0.9993	0.17	0.6520	v2v3v4
rs2073323	FALSE	FALSE	FALSE					0.9987	0.9976	0.55	0.7521	v2v3v4
rs4868444	FALSE	FALSE	FALSE					0.9181	0.7897	6.3×10^{-5}	0.1216	v2v3v4
rs1766786	FALSE	FALSE	FALSE					0.9977	0.9899	0.065	0.1151	v2v3v4
rs10962767	FALSE	FALSE	FALSE					0.9780	0.9614	0.14	0.4331	v2v3v4
rs73168105	FALSE	FALSE	FALSE					0.9524	0.9249	0.0020	0.1817	v2v3v4
rs6740960	FALSE	FALSE	FALSE					0.8650	0.7734	3.3×10^{-11}	0.5062	v2v3v4
rs7167736	FALSE	FALSE	FALSE					0.9780	0.9547	0.24	0.7928	v2v3v4
rs10078545	FALSE	FALSE	FALSE					0.9809	0.9626	0.0081	0.6650	v2v3v4
rs11713363	TRUE	TRUE	TRUE	0.9997	0.024	0.22	0.7554	0.9914	0.9839	0.25	0.7571	v2v3v4
rs199880074	FALSE	FALSE	FALSE					0.9639	0.9506	0.39	0.7326	v2v3v4
rs56347314	FALSE	FALSE	FALSE					0.9138	0.8815	0.00037	0.4775	v2v3v4
rs80067372	FALSE	FALSE	FALSE					0.9622	0.9556	0.042	0.7290	v2v3v4
rs12505328	FALSE	FALSE	FALSE					0.9507	0.9307	0.068	0.6471	v2v3v4

rs11589479	FALSE	FALSE	FALSE					0.9600	0.8585	0.0070	0.8266	v2v3v4
rs2133593	FALSE	FALSE	FALSE					0.9090	0.8957	0.37	0.3556	v2v3v4
rs12541121	TRUE	TRUE	TRUE	0.9985	0.096	0.022	0.3874	0.9996	0.9985	0.0087	0.3858	v2v3v4
rs7161418	FALSE	FALSE	FALSE					0.9842	0.9468	0.047	0.2482	v2v3v4
rs1336149	TRUE	TRUE	FALSE	0.9895	5.4×10^{-105}	4.8×10^{-5}	0.4743	0.9301	0.9151	0.023	0.4847	v2v3v4
rs2347498	FALSE	FALSE	FALSE					0.9820	0.9794	0.043	0.6220	v2v3v4
rs11001765	FALSE	FALSE	FALSE					0.9925	0.9847	0.00019	0.8570	v2v3v4
rs12495832	FALSE	FALSE	FALSE					0.9254	0.8745	0.12	0.8871	v2v3v4
rs141753469	FALSE	FALSE	FALSE					0.9489	0.8948	0.35	0.2086	v2v3v4
rs145365164	FALSE	FALSE	FALSE					0.9733	0.9707	0.65	0.8073	v2v3v4
rs4958741	FALSE	FALSE	FALSE					0.9973	0.9965	0.51	0.8134	v2v3v4
rs62578082	FALSE	FALSE	FALSE					0.9582	0.9340	0.0042	0.1134	v2v3v4
rs1194708	FALSE	FALSE	FALSE					0.9878	0.9859	0.019	0.7586	v2v3v4
rs17336368	FALSE	FALSE	FALSE					0.9618	0.9547	0.44	0.7096	v2v3v4
rs112215522	FALSE	FALSE	FALSE					0.9605	0.9503	0.14	0.2849	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
rs11768577				13457	0.8166				58032	0.8560
rs6494598				13457	0.4676				58032	0.5169
rs2476023				13457	0.8114				58032	0.7749
rs10504499				13457	0.8597				58032	0.8872
rs72678242				13457	0.1528				58032	0.1249
rs17479393				13457	0.2687				58032	0.2355
rs10175706				13457	0.6327				58032	0.5951
rs6028446				13457	0.5048				58032	0.4691
rs13035389	3034	6777	3640	13457	0.5226	11476	28756	17782	58032	0.5544
rs59156997				13457	0.8531				58032	0.8305
rs4237150				13457	0.6059				58032	0.5752
rs4674676				13457	0.8538				58032	0.8330
rs17275866				13457	0.7251				58032	0.6984
rs55700449				13457	0.8681				58032	0.8495
rs12509218				13457	0.1193				58032	0.1016
rs11688237				13457	0.5253				58032	0.4994
rs7243821				13457	0.7060				58032	0.7295
rs11650175	1429	5901	6125	13457	0.6743	7147	26451	24428	58032	0.6489
rs2073323				13457	0.7339				58032	0.7571
rs4868444				13457	0.1087				58032	0.1247
rs1766786				13457	0.1259				58032	0.1099
rs10962767				13457	0.4558				58032	0.4303
rs73168105				13457	0.1667				58032	0.1868
rs6740960				13457	0.4927				58032	0.5150
rs7167736				13457	0.8082				58032	0.7881
rs10078545				13457	0.6457				58032	0.6691
rs11713363	714	4725	8015	13457	0.7725	3723	21530	32755	58032	0.7516
rs199880074				13457	0.7479				58032	0.7274
rs56347314				13457	0.4555				58032	0.4788
rs80067372				13457	0.7097				58032	0.7318
rs12505328				13457	0.6321				58032	0.6540
rs11589479				13457	0.8149				58032	0.8317
rs2133593				13457	0.3736				58032	0.3532
rs12541121	5339	6297	1816	13457	0.3690	21521	27769	8710	58032	0.3895
rs7161418				13457	0.2320				58032	0.2500
rs1336149	3829	6161	2744	13457	0.4663	15421	26443	13046	58032	0.4874
rs2347498				13457	0.6422				58032	0.6223
rs11001765				13457	0.8737				58032	0.8581
rs12495832				13457	0.8978				58032	0.8852
rs141753469				13457	0.1954				58032	0.2113
rs145365164				13457	0.7953				58032	0.8106
rs4958741				13457	0.8009				58032	0.8166
rs62578082				13457	0.1038				58032	0.1160
rs1194708				13457	0.7767				58032	0.7597
rs17336368				13457	0.7223				58032	0.7054
rs112215522				13457	0.2700				58032	0.2865

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
1q31.3	197351039	rs2476023	9.7×10^{-39}	−25131	0.841	rs2786098	2.0×10^{-13}	20032318	Asthma	DENND1B, CRB1
9p24.2	4290085	rs4237150	5.6×10^{-19}	−2619	0.671	rs7041847	2.0×10^{-14}	22158537	Type 2 diabetes	GLIS3
9p24.2	4290085	rs4237150	5.6×10^{-19}	−1035	0.708	rs7034200	7.0×10^{-7}	22581228	Fasting glucose-related traits (interaction with BMI)	GLIS3
9p24.2	4290085	rs4237150	5.6×10^{-19}	−1035	0.708	rs7034200	1.0×10^{-13}	20081858	Fasting glucose-related traits	GLIS3
9p24.2	4290085	rs4237150	5.6×10^{-19}	1662	0.677	rs7020673	5.0×10^{-12}	19430480	Type 1 diabetes	GLIS3
9p24.2	4290085	rs4237150	5.6×10^{-19}	1998	0.973	rs10758593	3.0×10^{-6}	18840781	Type 1 diabetes	GLIS3
9p24.2	4290085	rs4237150	5.6×10^{-19}	3065	0.681	rs10814916	6.0×10^{-12}	22961080	Type 2 diabetes	GLIS3
19q12	30982165	rs55700449	2.8×10^{-15}	8535	0.604	rs3786800	3.0×10^{-12}	23049088	Myopia (pathological)	ZNF536
17q24.3	69123106	rs56347314	5.4×10^{-12}	−14353	0.687	rs1859962	3.0×10^{-11}	21743057	Prostate cancer	Intergenic
17q24.3	69123106	rs56347314	5.4×10^{-12}	−14353	0.687	rs1859962	2.0×10^{-16}	19767753	Prostate cancer	
17q24.3	69123106	rs56347314	5.4×10^{-12}	−14353	0.687	rs1859962	1.0×10^{-6}	18264097	Prostate cancer	Intergenic
17q24.3	69123106	rs56347314	5.4×10^{-12}	−14353	0.687	rs1859962	3.0×10^{-10}	17603485	Prostate cancer	Intergenic

17p13.1	7452752	rs80067372	1.2×10^{-11}	38425	0.541	rs4227	4.0×10^{-10}	22197929	IgA nephropathy	MPDU1
17p13.1	7452752	rs80067372	1.2×10^{-11}	69163	0.656	rs12150660	6.0×10^{-30}	22829776	Sex hormone-binding globulin levels	SHBG
17p13.1	7452752	rs80067372	1.2×10^{-11}	69163	0.656	rs12150660	1.0×10^{-41}	21998597	Testosterone levels	SHBG
3q26.32	177301992	rs2133593	6.6×10^{-11}	2306	0.792	rs7620503	1.0×10^{-8}	23291589	Corneal structure	TBL1XR1, KCNMB2
6p21.1	44751668	rs17336368	2.8×10^{-8}	26023	0.743	rs10948172	6.0×10^{-7}	22763110	Osteoarthritis	SUPT3H, CDC5L

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
1q22	155033308	rs11589479	4.7×10^{-11}	−6366	0.589	rs6427128	ADAM15	K191T
1q23.1	156939175	rs1336149	1.5×10^{-9}	−32094	0.744	rs945508	ARHGEF11	H1467R
9q33.3	129277041	rs62578082	1.4×10^{-8}	−11135	0.503	rs3841410	MVB12B	?442?

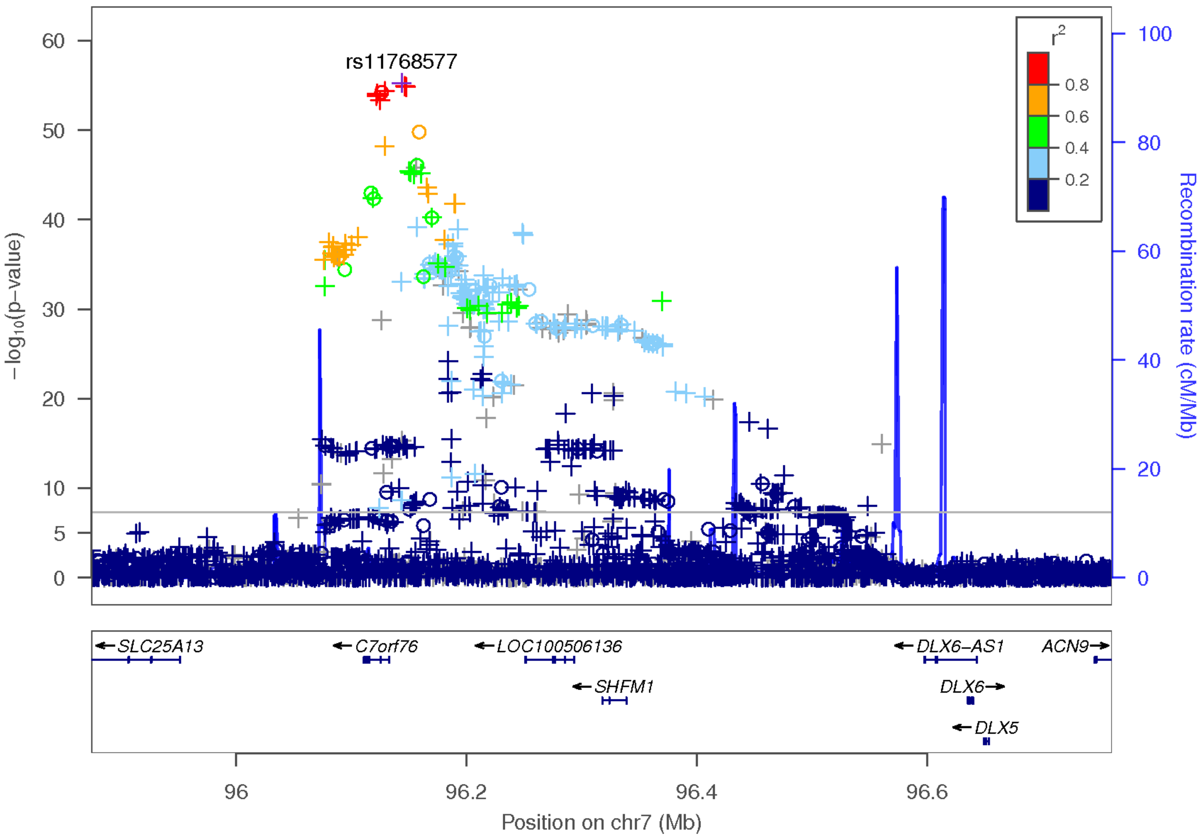
Nearby Expression QTLs

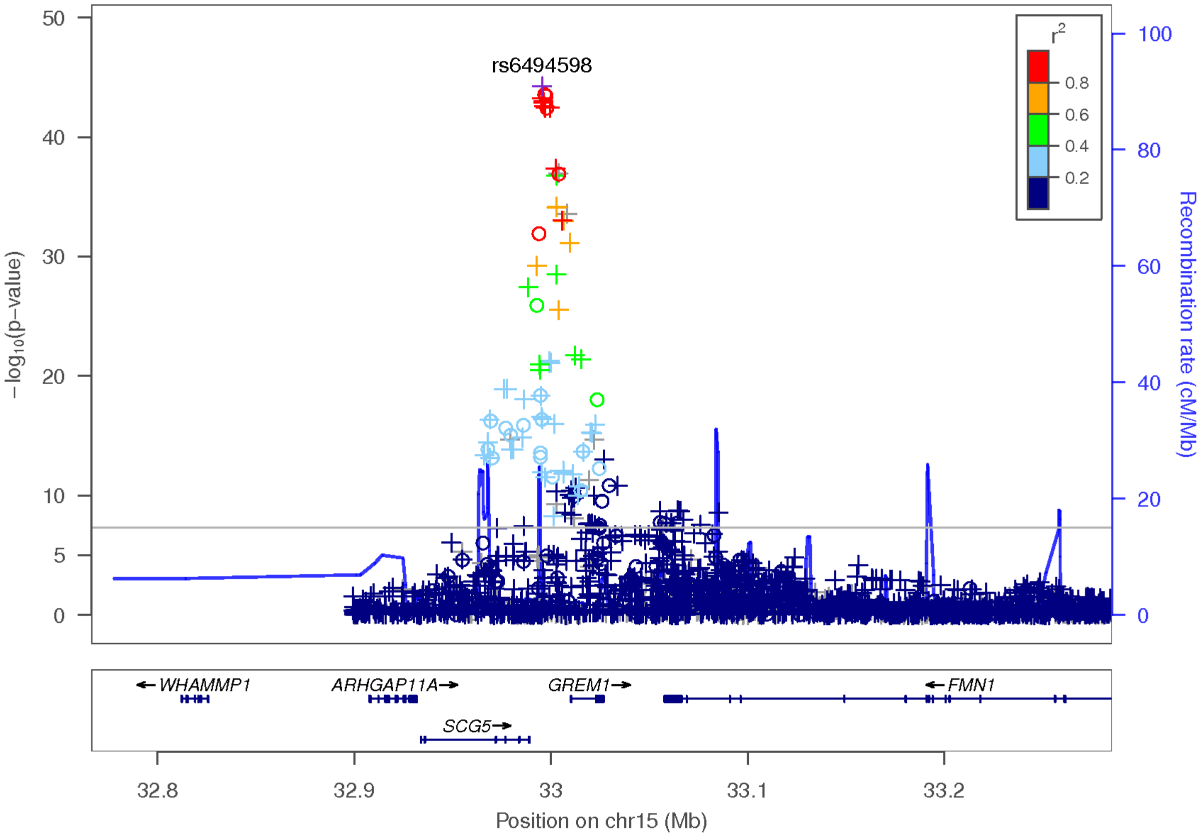
region	position	our.name	our.pval	dist	rsqr	assay.name	eqtl.dist	eqtl.gene	eqtl.pval	eqtl.rsqr	tissue	pubmed.id
3q25.32	157828322	rs11713363	2.3×10^{-12}	−160965	0.623	rs4362677	160504	RSRC1	3.5×10^{-10}	0.029	Monocyte	20502693
17p13.1	7452752	rs80067372	1.2×10^{-11}	−1642	0.911	rs34790908	9881	TNFSF12	0.00012	0.052	B-Cell	22446964
17p13.1	7452752	rs80067372	1.2×10^{-11}	−1642	0.911	rs34790908	9881	TNFSF12	1.8×10^{-27}	0.344	Monocyte	22446964
17p13.1	7452752	rs80067372	1.2×10^{-11}	2784	0.643	rs4511593	0	TNFSF12	1.5×10^{-73}	0.205	Monocyte	20502693
17p13.1	7452752	rs80067372	1.2×10^{-11}	2784	0.643	rs4511593	3161	TNFSF13	0.00026	0.168	Fibroblast	19644074
17p13.1	7452752	rs80067372	1.2×10^{-11}	15464	0.530	rs4968212	23404	SOX15	4.3×10^{-6}	0.073	Monocyte	22446964
17p13.1	7452752	rs80067372	1.2×10^{-11}	15464	0.530	rs4968212	297085	CYB5D1	0.00014	0.051	B-Cell	22446964
17p13.1	7452752	rs80067372	1.2×10^{-11}	24725	0.516	rs4968214	930844	MED31	9.3×10^{-5}	0.190	T-cell	19644074
17p13.1	7452752	rs80067372	1.2×10^{-11}	38425	0.541	rs4227	38609	SAT2	2.2×10^{-5}	0.062	Monocyte	22446964
5q33.2	153868262	rs4958741	1.3×10^{-8}	5298	0.504	rs283438	364546	CNOT8	0.00014	0.181	Lymphoblastoid	19644074
6p21.1	44751668	rs17336368	2.8×10^{-8}	26023	0.743	rs10948172	18995	SUPT3H	4.8×10^{-8}	0.101	B-Cell	22446964
6p21.1	44751668	rs17336368	2.8×10^{-8}	173625	0.608	rs12210292	−723741	SLC29A1	0.00016	0.050	Monocyte	22446964
6p21.1	44751668	rs17336368	2.8×10^{-8}	300292	0.720	rs17423748	−147514	SUPT3H	2.3×10^{-9}	0.224	Brain Frontal Cortex	20485568

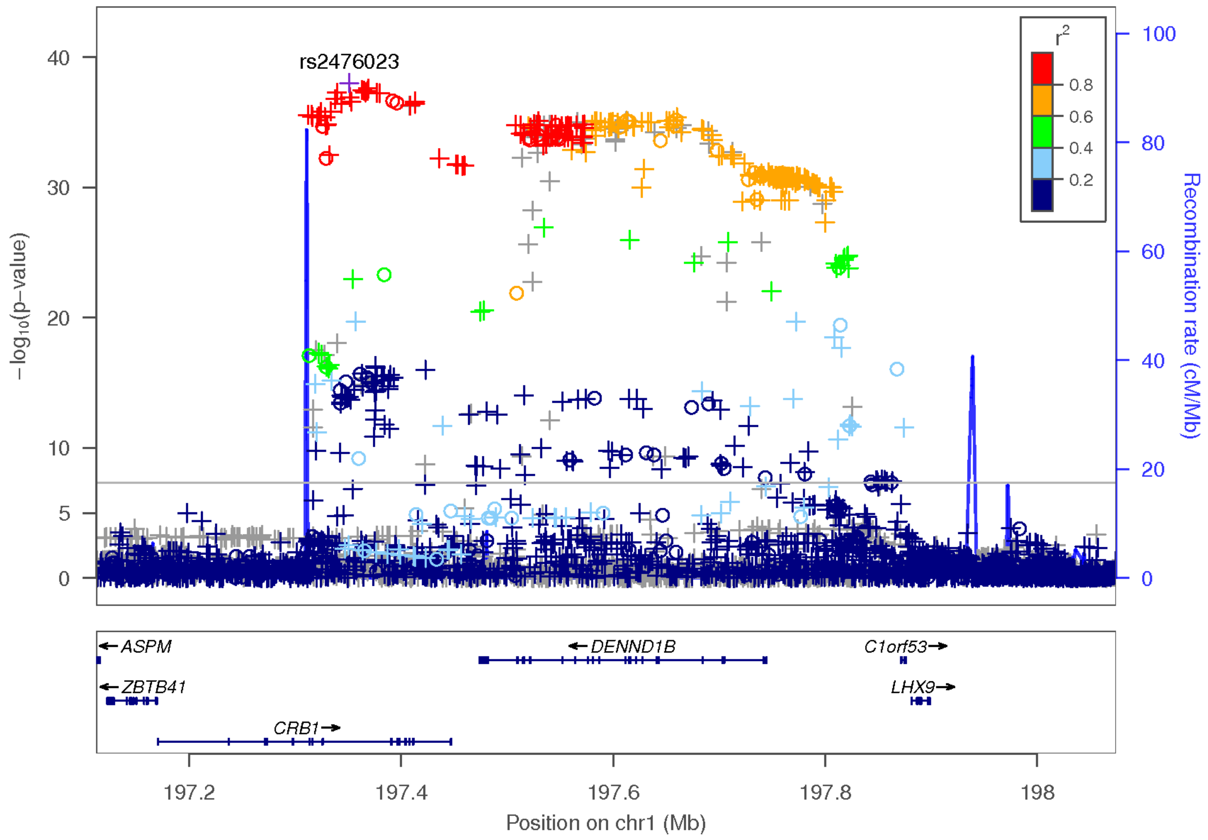
Nearby Clinical Variants

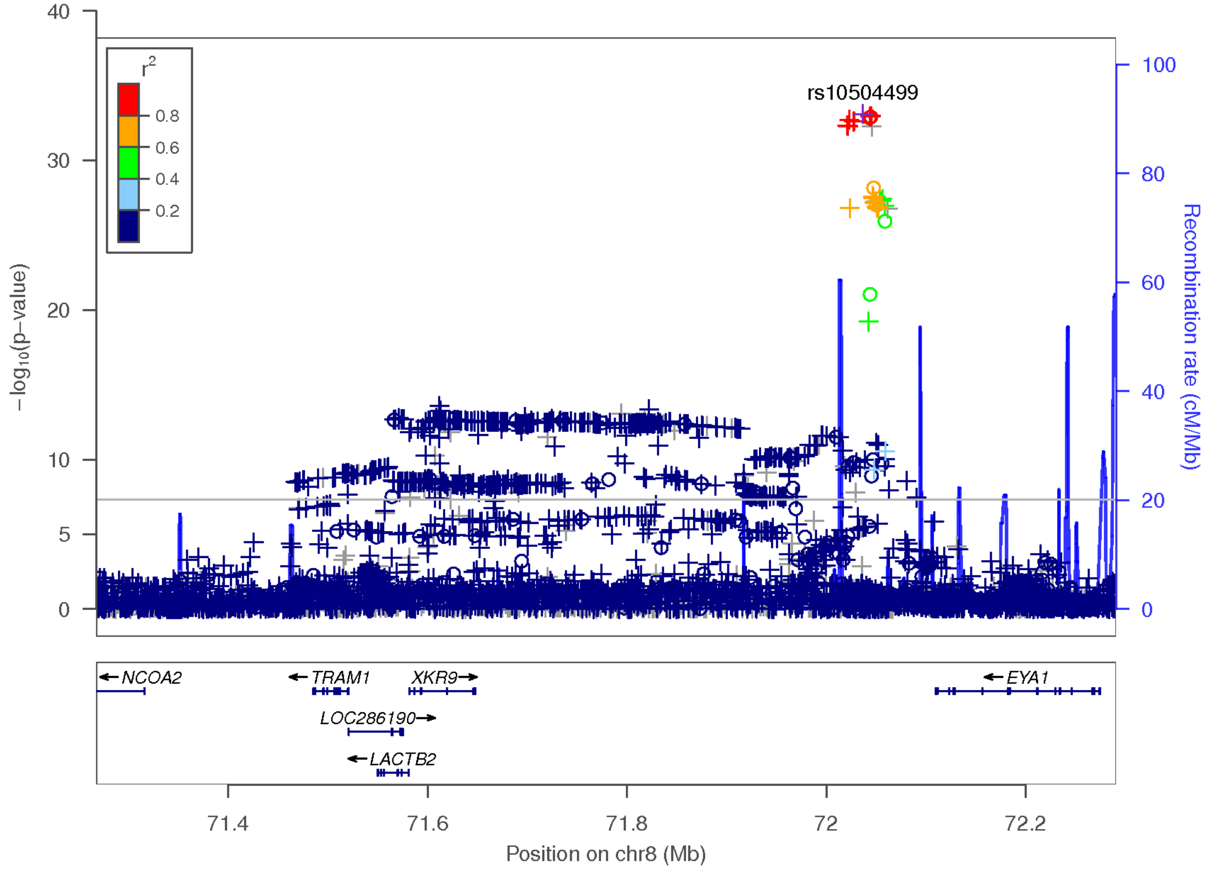
no hits were found for clinical variants

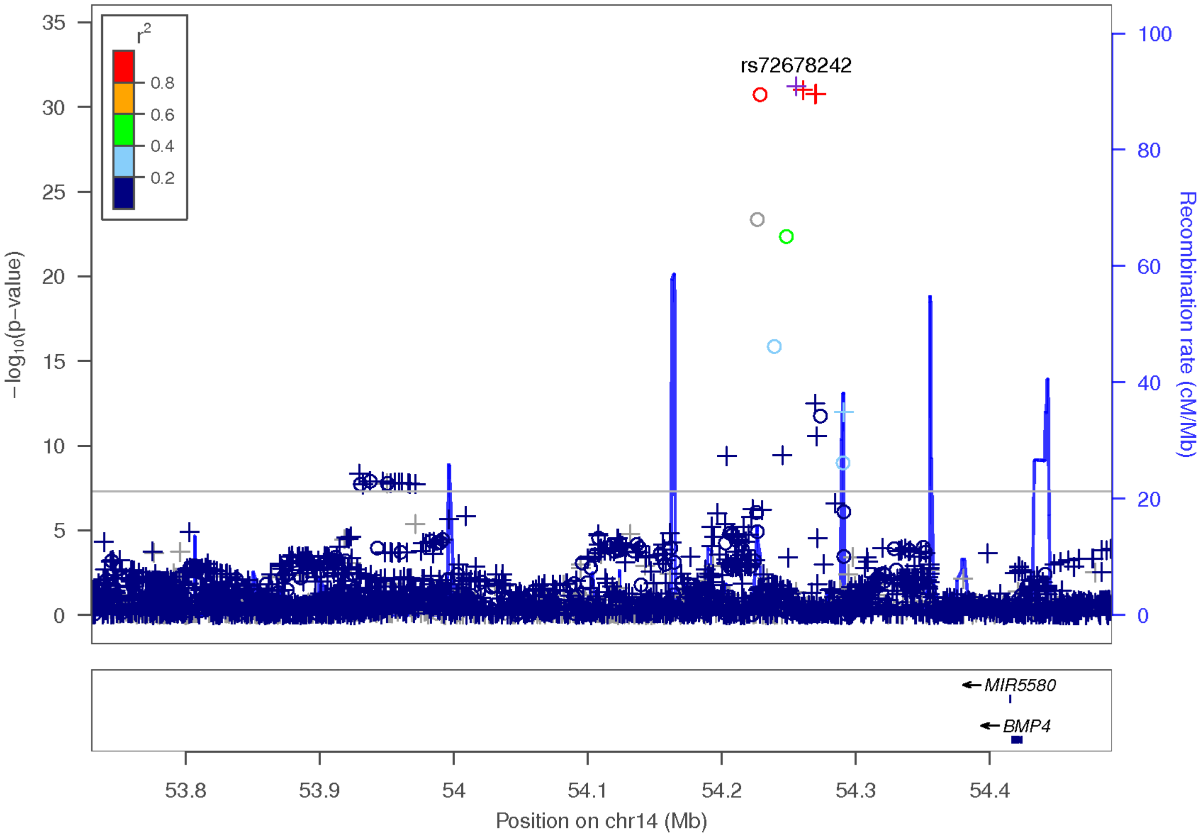
Regional Association Plots

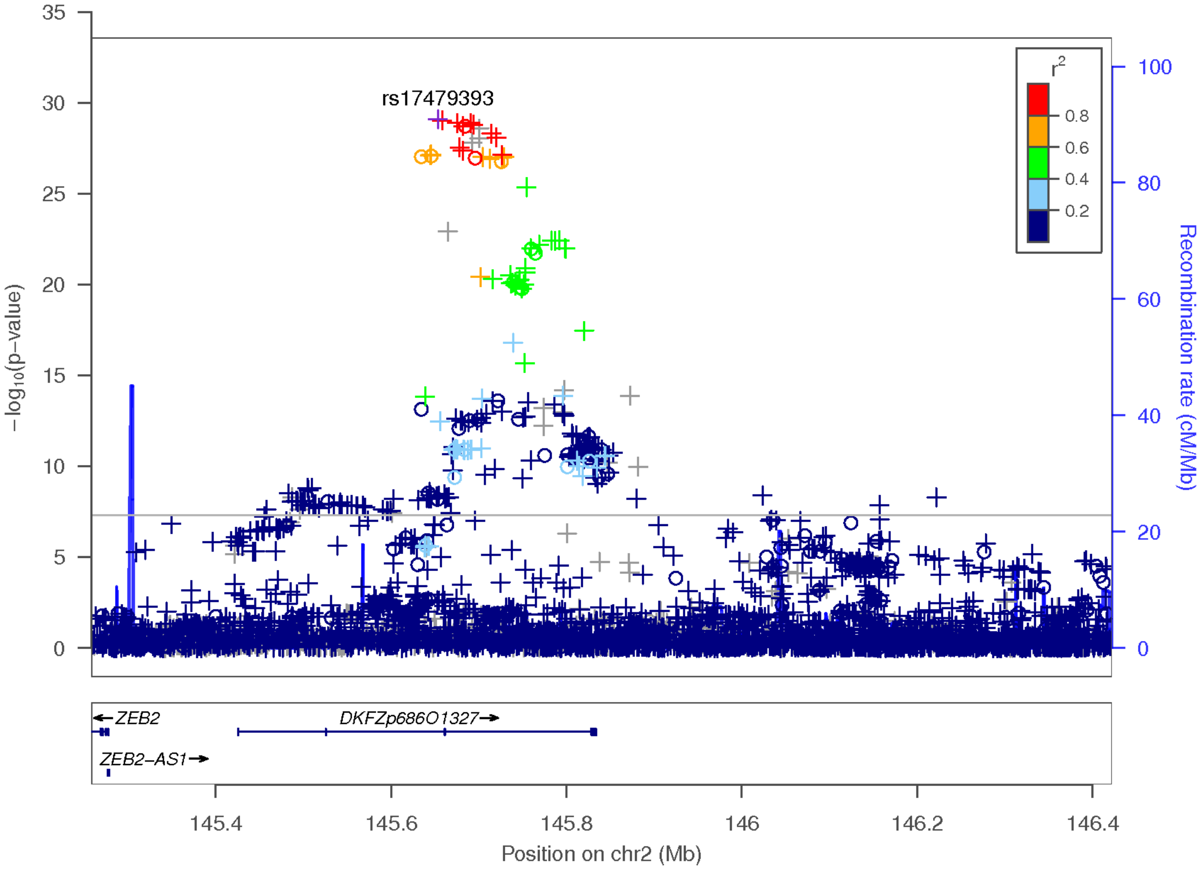

rs11768577
−log₁₀(p−value)
0
5
10
20
30
40
50
60
r²
0.8
0.6
0.4
0.2
Recombination rate (cM/Mb)
0
20
40
60
80
100
←SLC25A13
←C7orf76
←LOC100506136
←SHFM1
←DLX6−AS1
ACN9→
DLX6→
←DLX5
96
96.2
96.4
96.6
Position on chr7 (Mb)

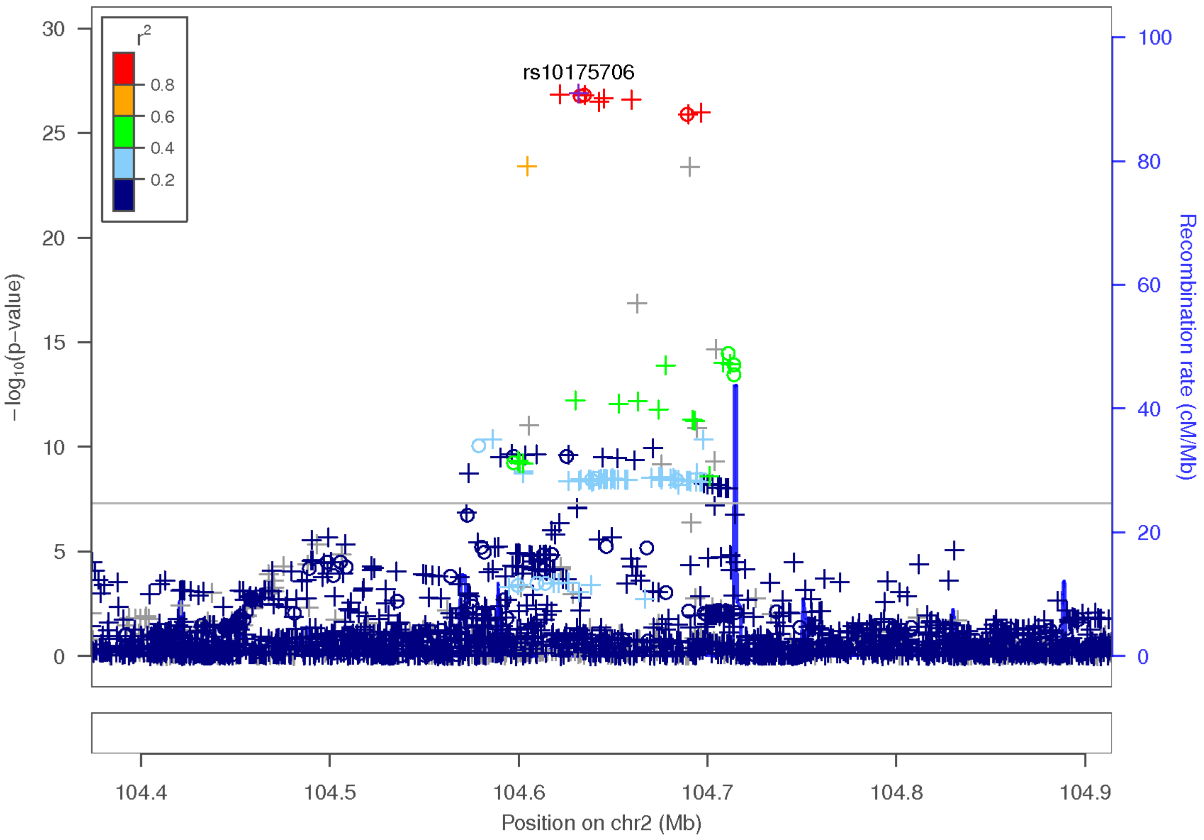

rs6494598
−log₁₀(p−value)
0
5
10
20
30
40
50
r²
0.8
0.6
0.4
0.2
Recombination rate (cM/Mb)
0
20
40
60
80
100
←WHAMMP1
ARHGAP11A→
GREM1→
←FMN1
SCG5→
32.8
32.9
33
33.1
33.2
Position on chr15 (Mb)

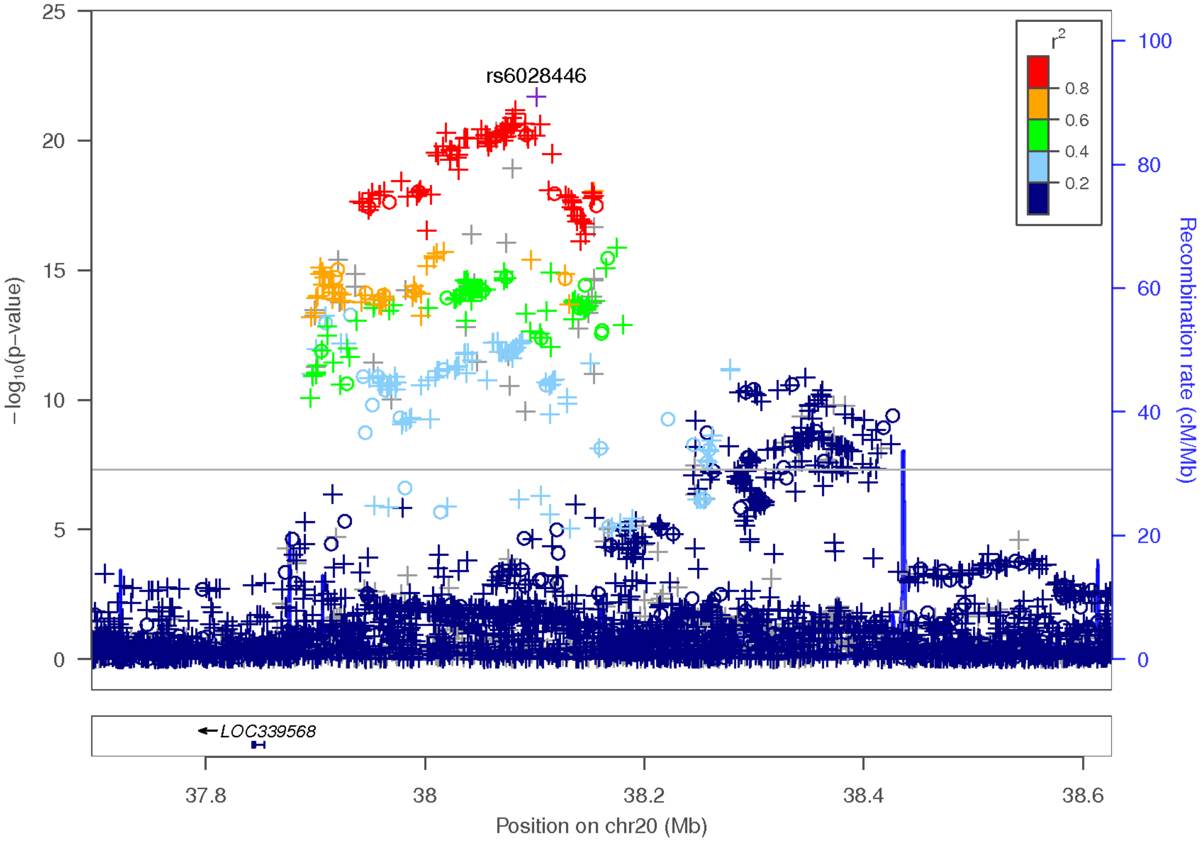

rs2476023
−log10(p−value)
40
30
20
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
ASPM
ZBTB41
CRB1
DENND1B
C1orf53
LHX9
197.2
197.4
197.6
197.8
198
Position on chr1 (Mb)

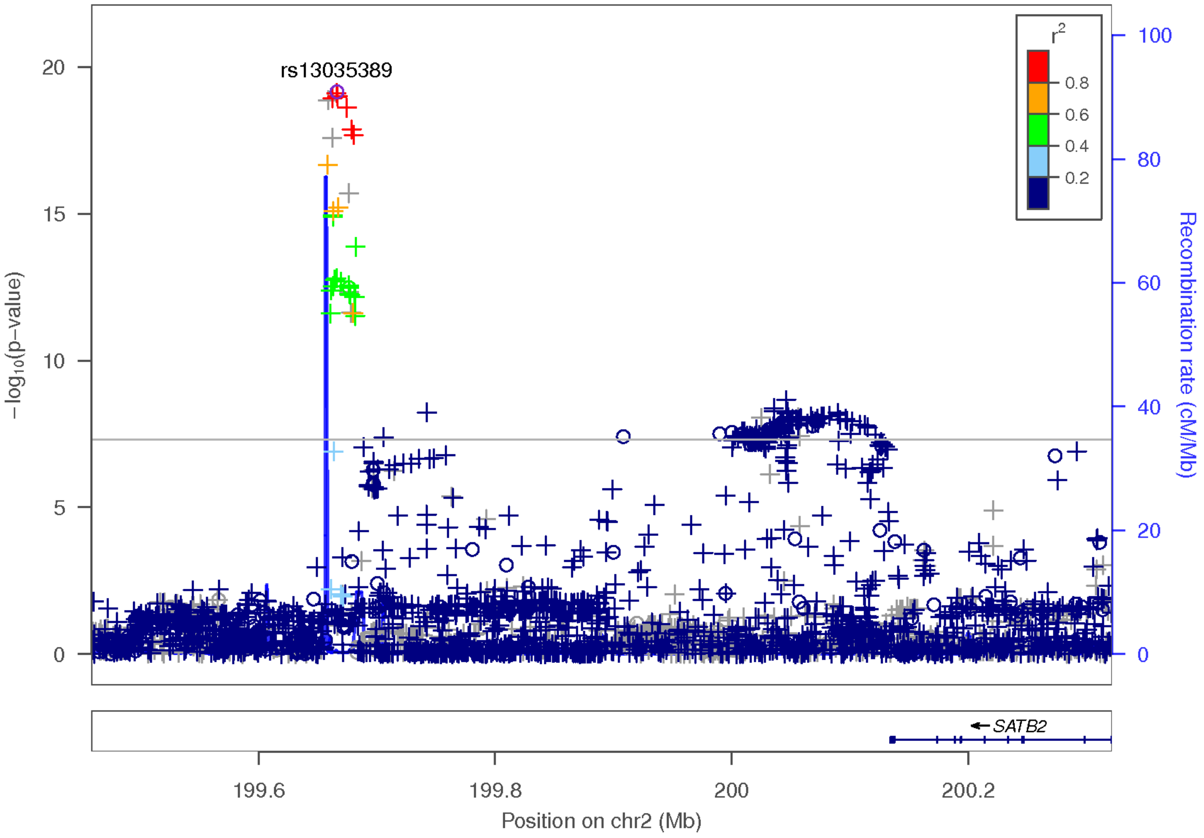

rs10504499
−log10(p−value)
40
30
20
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
r2
0.8
0.6
0.4
0.2
NCOA2
TRAM1
XKR9
LOC286190
LACTB2
EYA1
71.4
71.6
71.8
72
72.2
Position on chr8 (Mb)

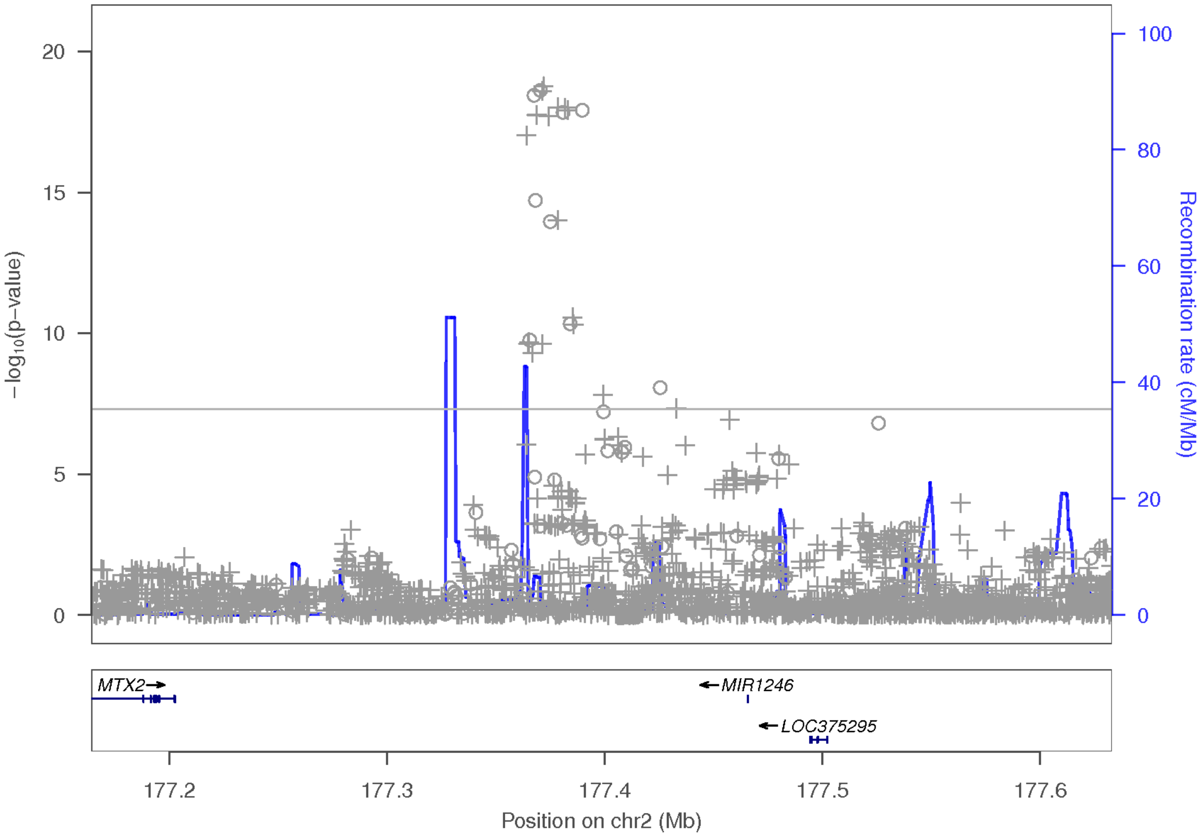

rs72678242
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
5
10
15
20
25
30
35
Recombination rate (cM/Mb)
0
20
40
60
80
100
MIR5580
BMP4
53.8
53.9
54
54.1
54.2
54.3
54.4
Position on chr14 (Mb)

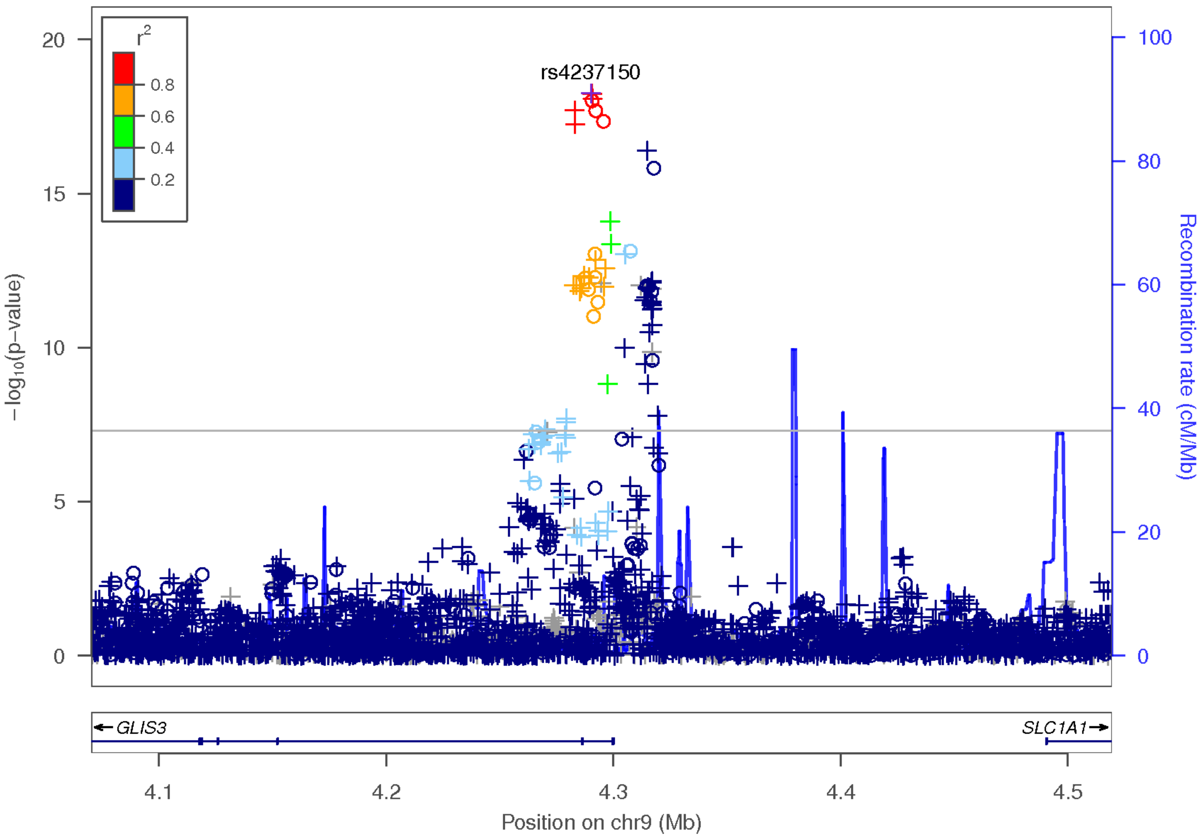

rs17479393
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
5
10
15
20
25
30
35
Recombination rate (cM/Mb)
0
20
40
60
80
100
ZEB2
DKFZp686O1327
ZEB2−AS1
145.4
145.6
145.8
146
146.2
146.4
Position on chr2 (Mb)

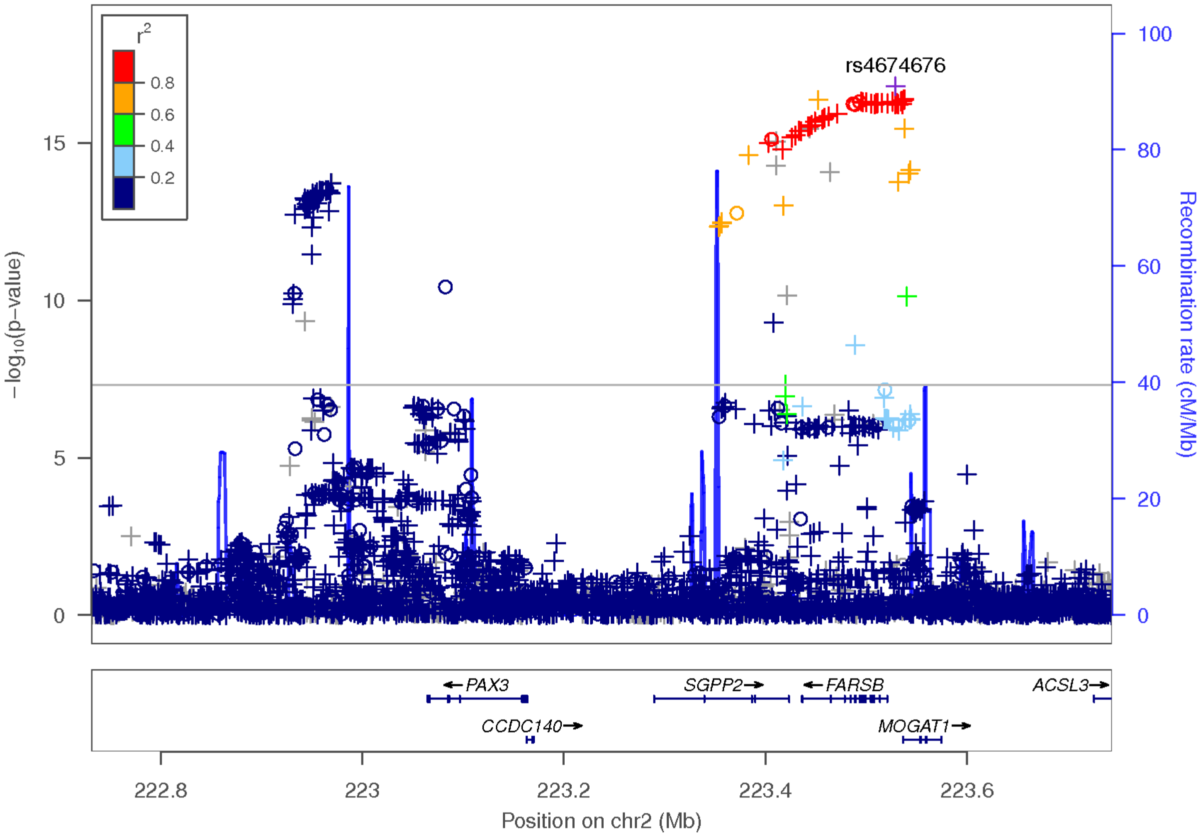

r2
0.8
0.6
0.4
0.2
rs10175706
−log10(p−value)
30
25
20
15
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
104.4
104.5
104.6
104.7
104.8
104.9
Position on chr2 (Mb)

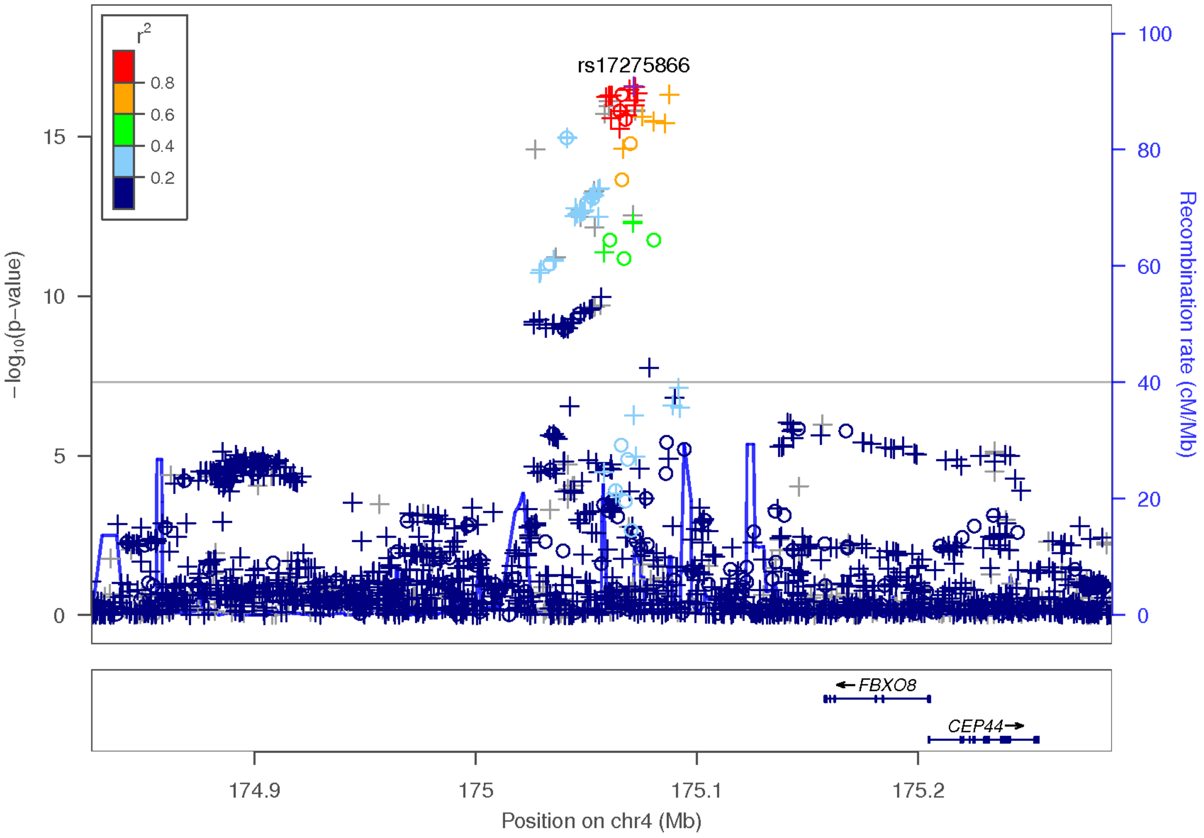

r2
0.8
0.6
0.4
0.2
rs6028446
−log10(p−value)
25
20
15
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
LOC339568
37.8
38
38.2
38.4
38.6
Position on chr20 (Mb)

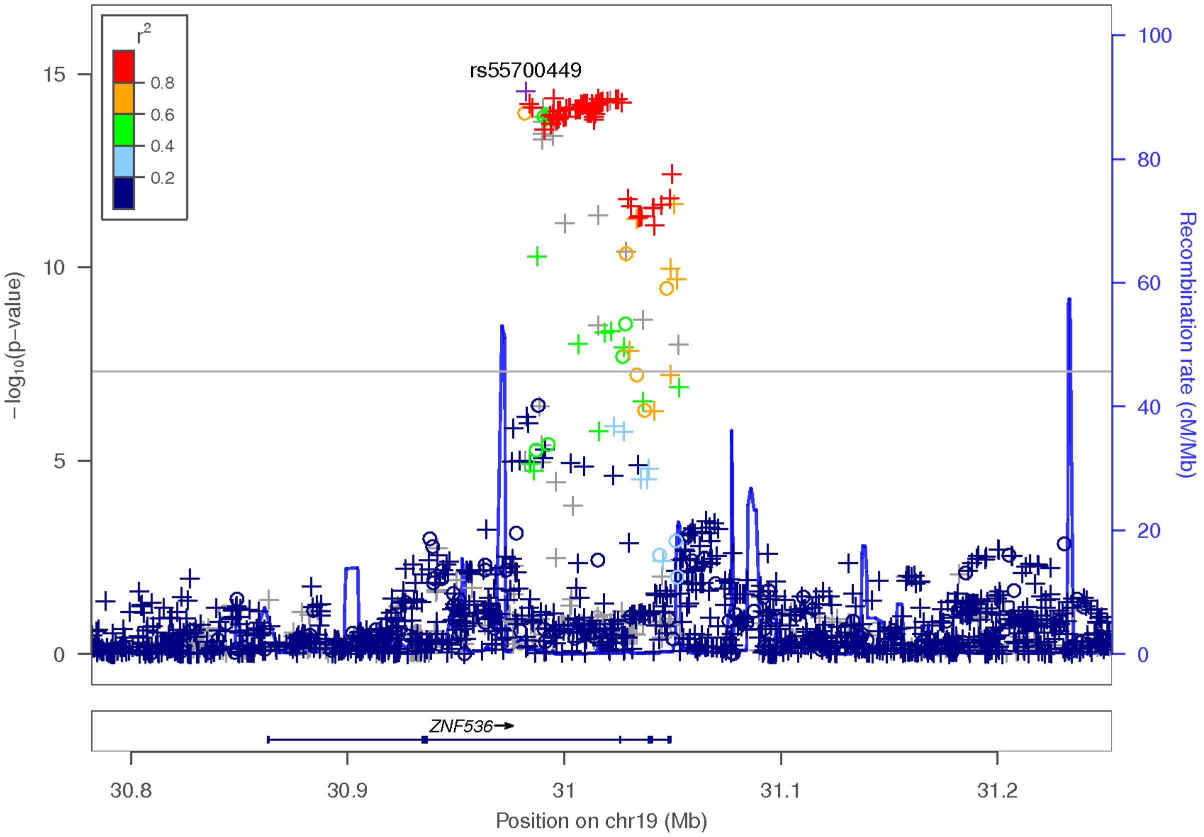

rs13035389
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
20
15
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
SATB2
199.6
199.8
200
200.2
Position on chr2 (Mb)

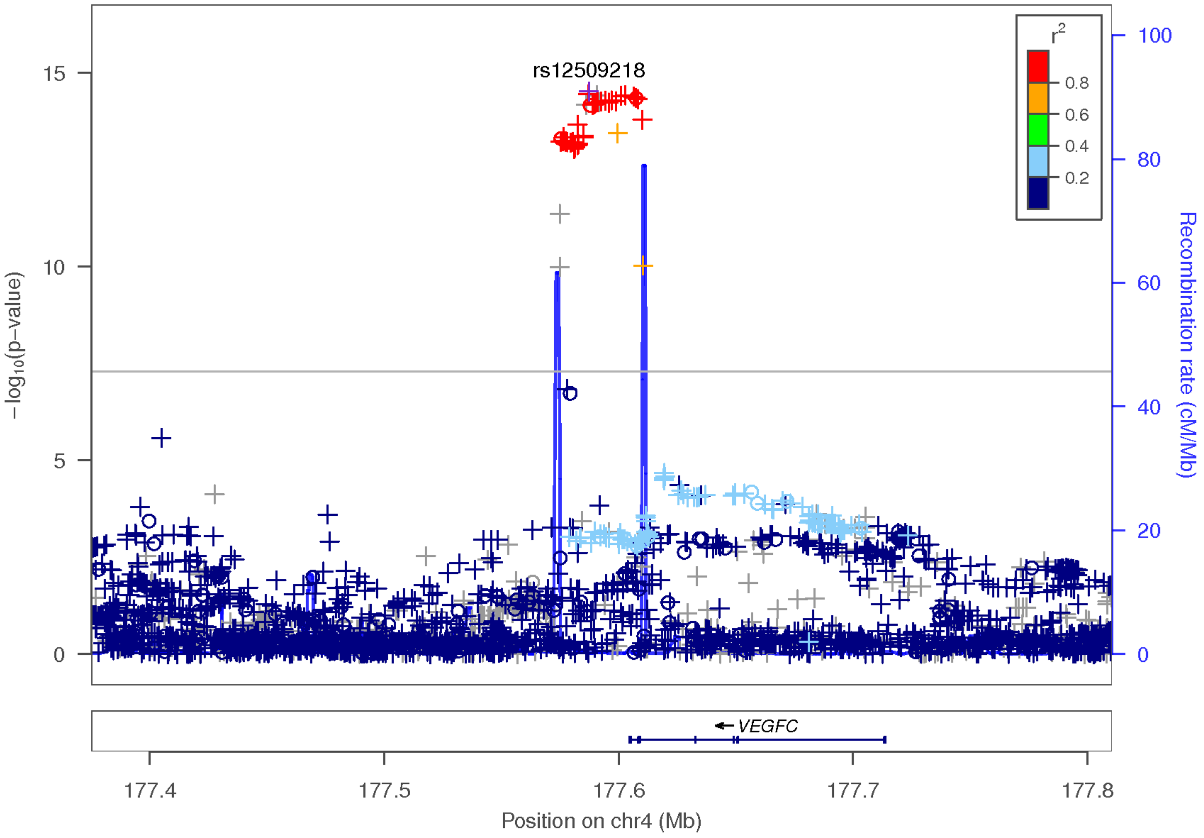

−log₁₀(p−value)
20
15
10
5
0
Recombination rate (cM/Mb)
100
80
60
40
20
0
MTX2
MIR1246
LOC375295
177.2
177.3
177.4
177.5
177.6
Position on chr2 (Mb)

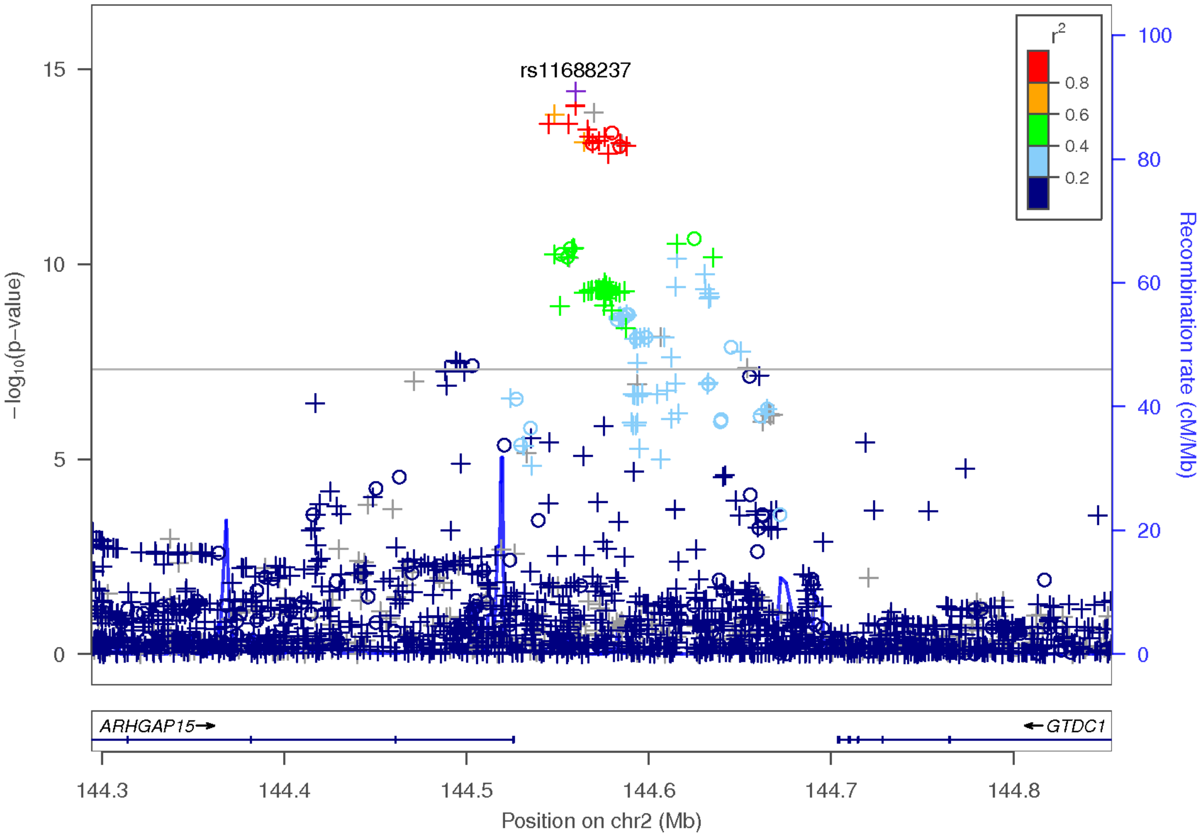

r2
0.8
0.6
0.4
0.2
rs4237150
−log10(p−value)
Recombination rate (cM/Mb)
0
5
10
15
20
0
20
40
60
80
100
GLIS3
SLC1A1
4.1
4.2
4.3
4.4
4.5
Position on chr9 (Mb)

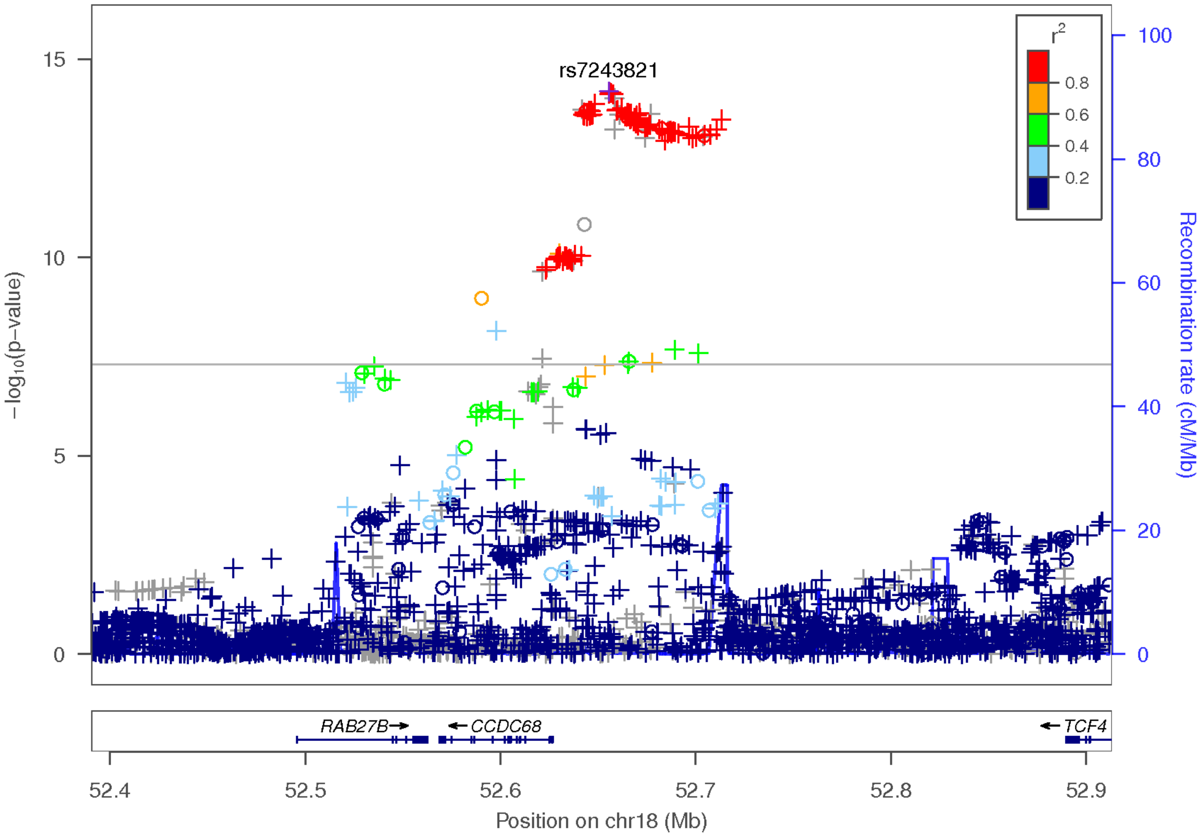

r2
0.8
0.6
0.4
0.2
rs4674676
−log10(p−value)
Recombination rate (cM/Mb)
0
5
10
15
0
20
40
60
80
100
PAX3
SGPP2
FARSB
ACSL3
CCDC140
MOGAT1
222.8
223
223.2
223.4
223.6
Position on chr2 (Mb)

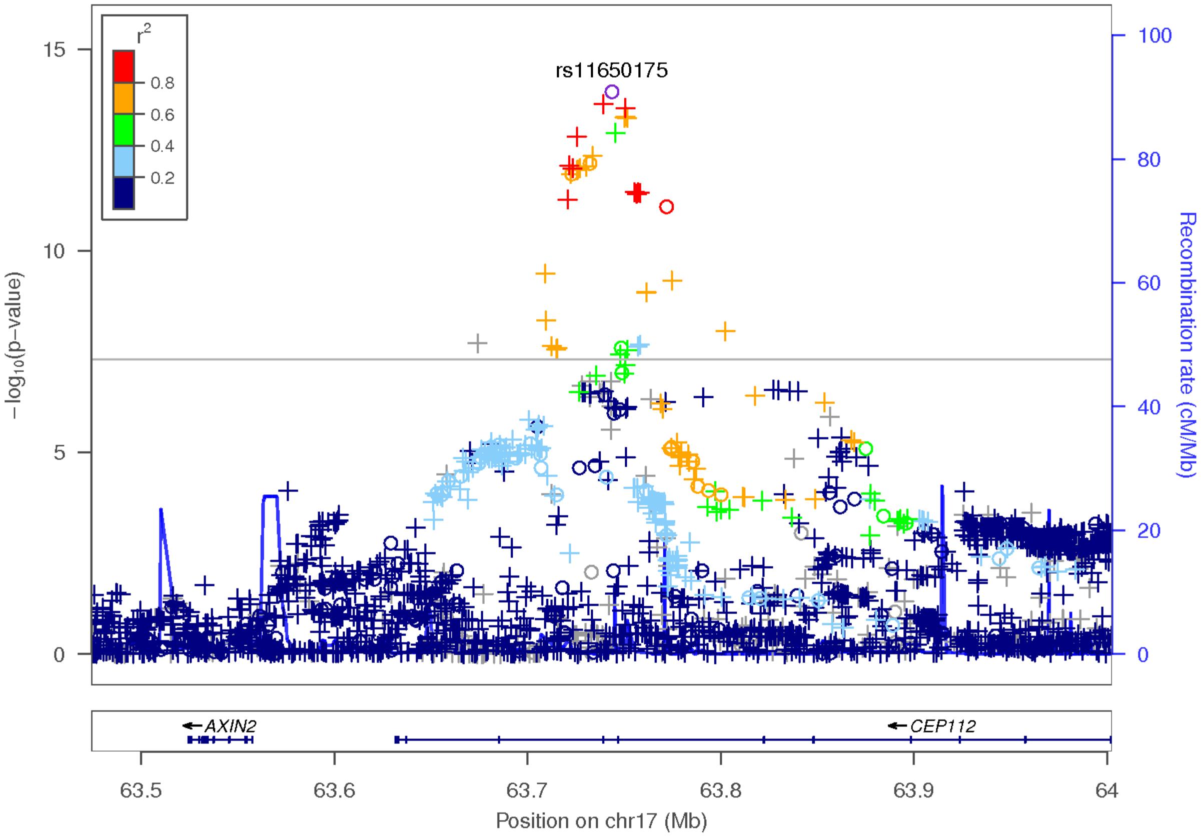

r2
0.8
0.6
0.4
0.2
rs17275866
−log10(p−value)
15
10
5
0
100
80
60
40
20
0
Recombination rate (cM/Mb)
FBXO8
CEP44
174.9
175
175.1
175.2
Position on chr4 (Mb)

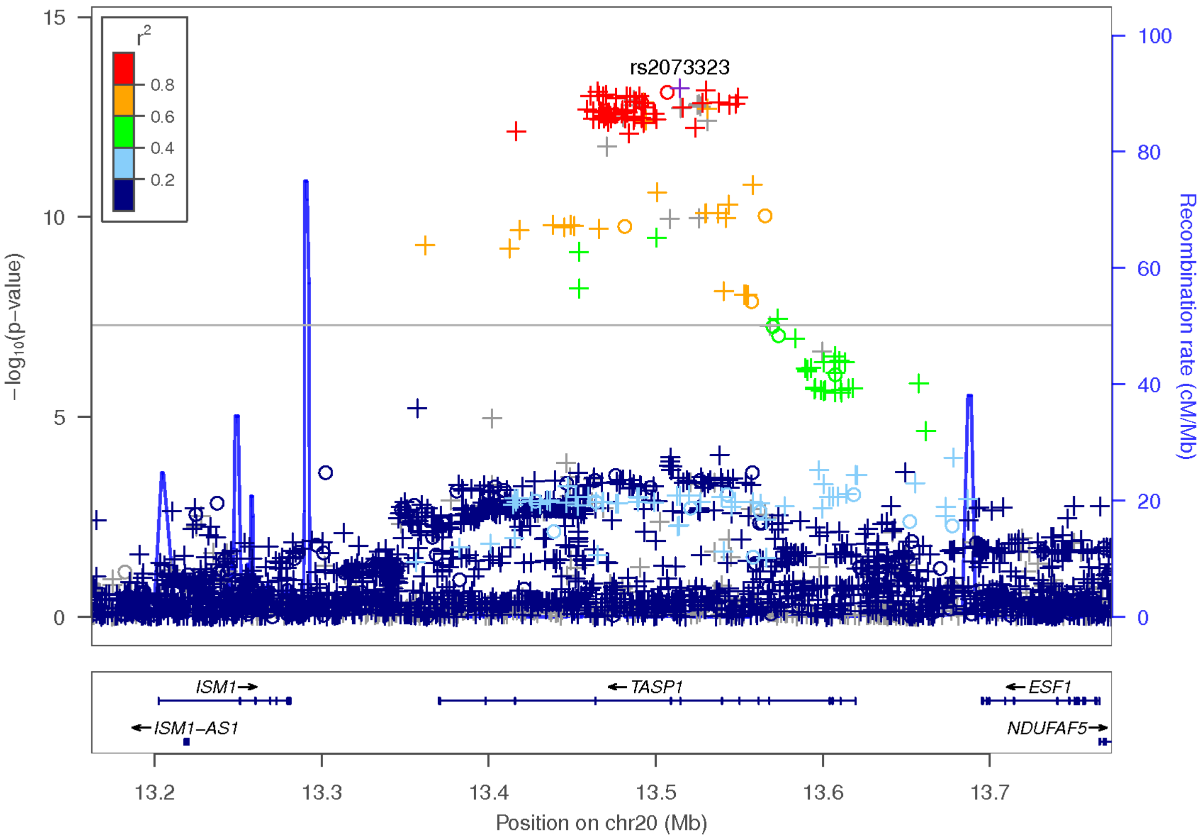

r2
0.8
0.6
0.4
0.2
rs55700449
−log10(p−value)
15
10
5
0
100
80
60
40
20
0
Recombination rate (cM/Mb)
ZNF536
30.8
30.9
31
31.1
31.2
Position on chr19 (Mb)


rs12509218
r²
0.8
0.6
0.4
0.2
15
10
5
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
VEGFC
177.4
177.5
177.6
177.7
177.8
Position on chr4 (Mb)

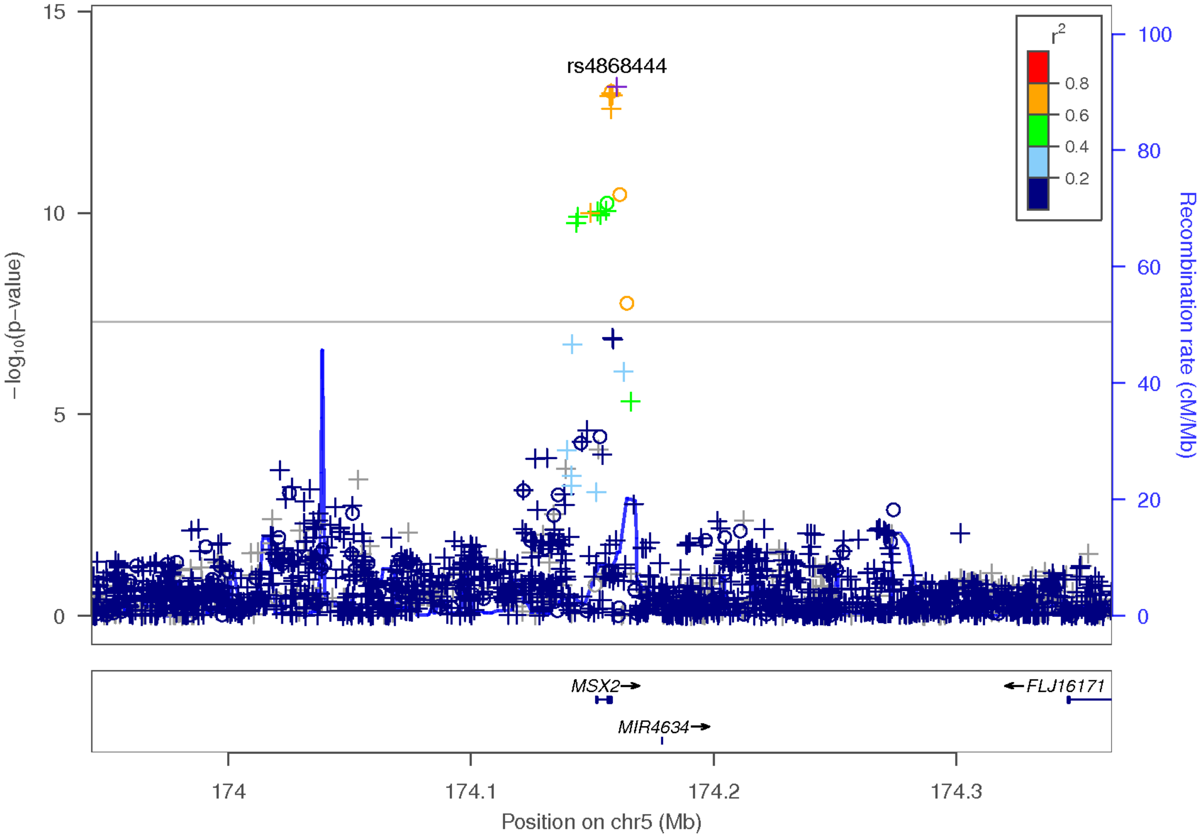

rs11688237
r²
0.8
0.6
0.4
0.2
15
10
5
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
ARHGAP15
GTDC1
144.3
144.4
144.5
144.6
144.7
144.8
Position on chr2 (Mb)


rs7243821
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
15
10
5
0
100
80
60
40
20
0
Recombination rate (cM/Mb)
RAB27B
CCDC68
TCF4
52.4
52.5
52.6
52.7
52.8
52.9
Position on chr18 (Mb)

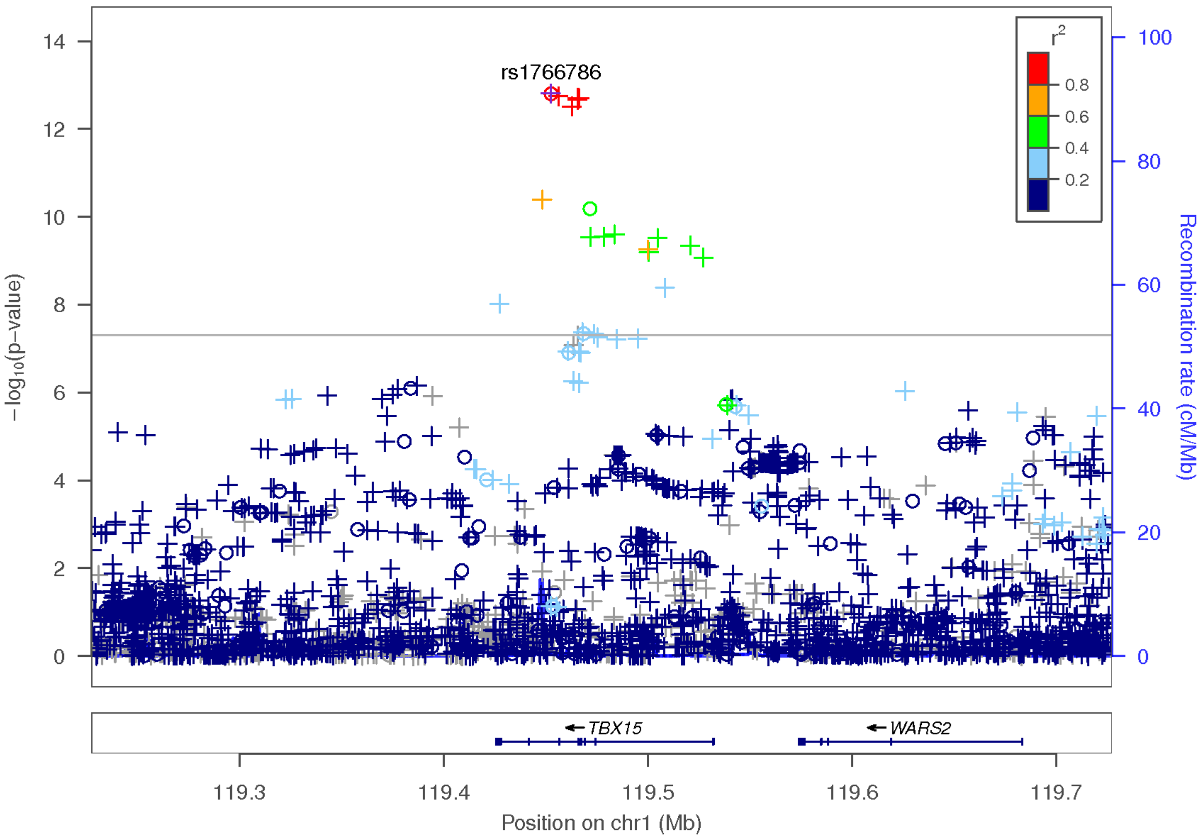

rs11650175
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
15
10
5
0
100
80
60
40
20
0
Recombination rate (cM/Mb)
AXIN2
CEP112
63.5
63.6
63.7
63.8
63.9
64
Position on chr17 (Mb)

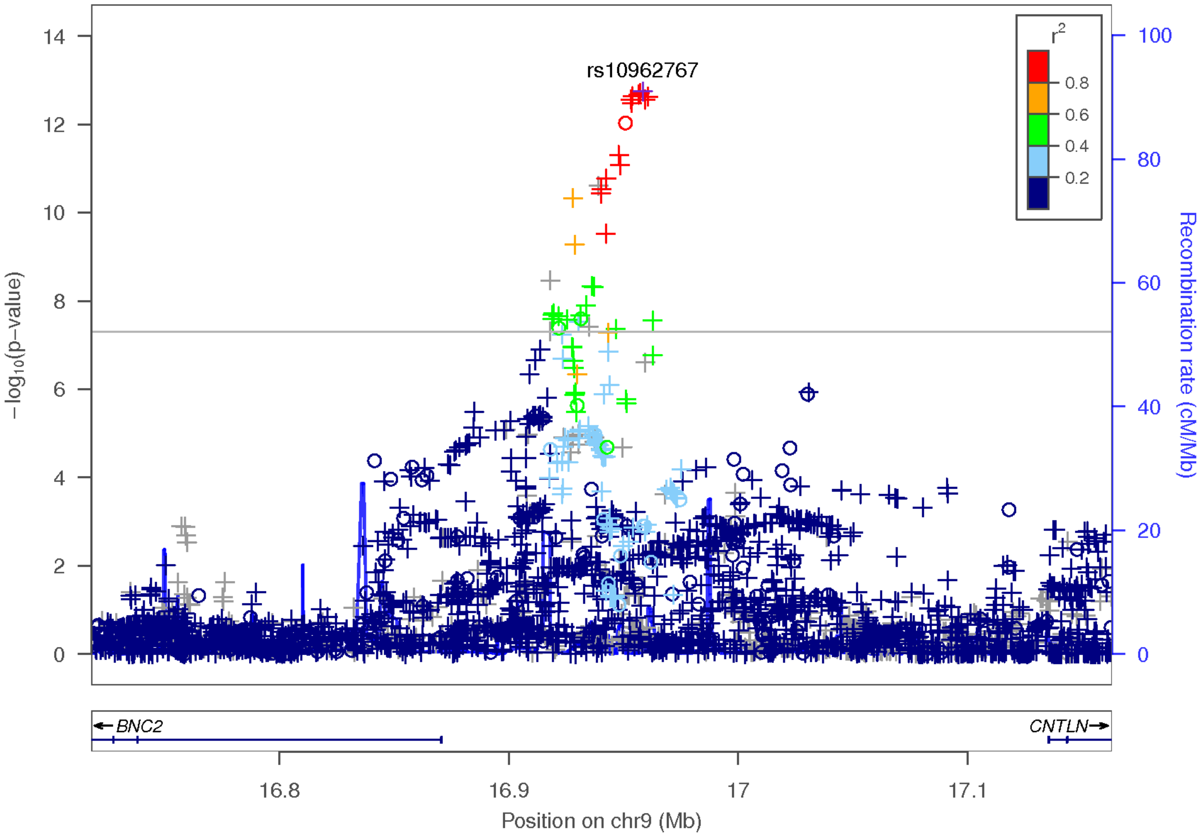


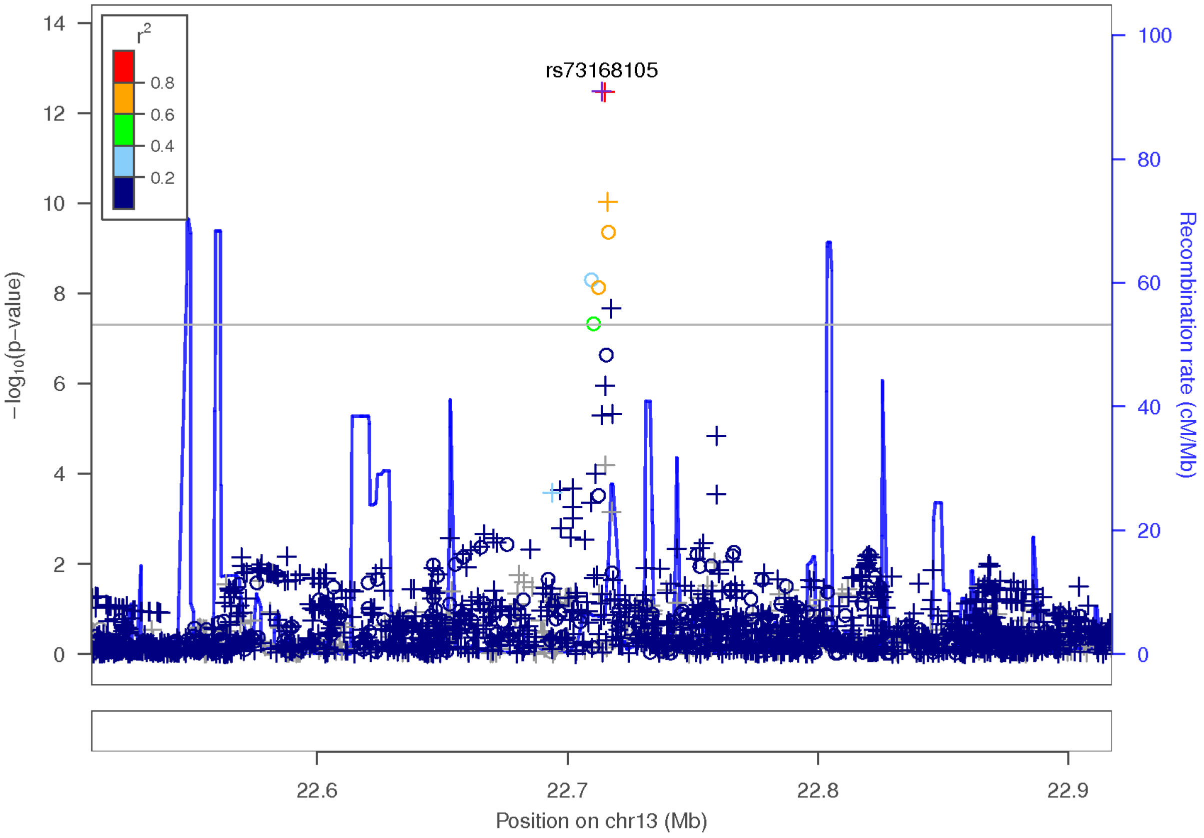
15
10
5
0
−log₁₀(p−value)
r^2
0.8
0.6
0.4
0.2
rs2073323
100
80
60
40
20
0
Recombination rate (cM/Mb)
ISM1→
←TASP1
←ESF1
←ISM1−AS1
NDUFAF5→
13.2
13.3
13.4
13.5
13.6
13.7
Position on chr20 (Mb)

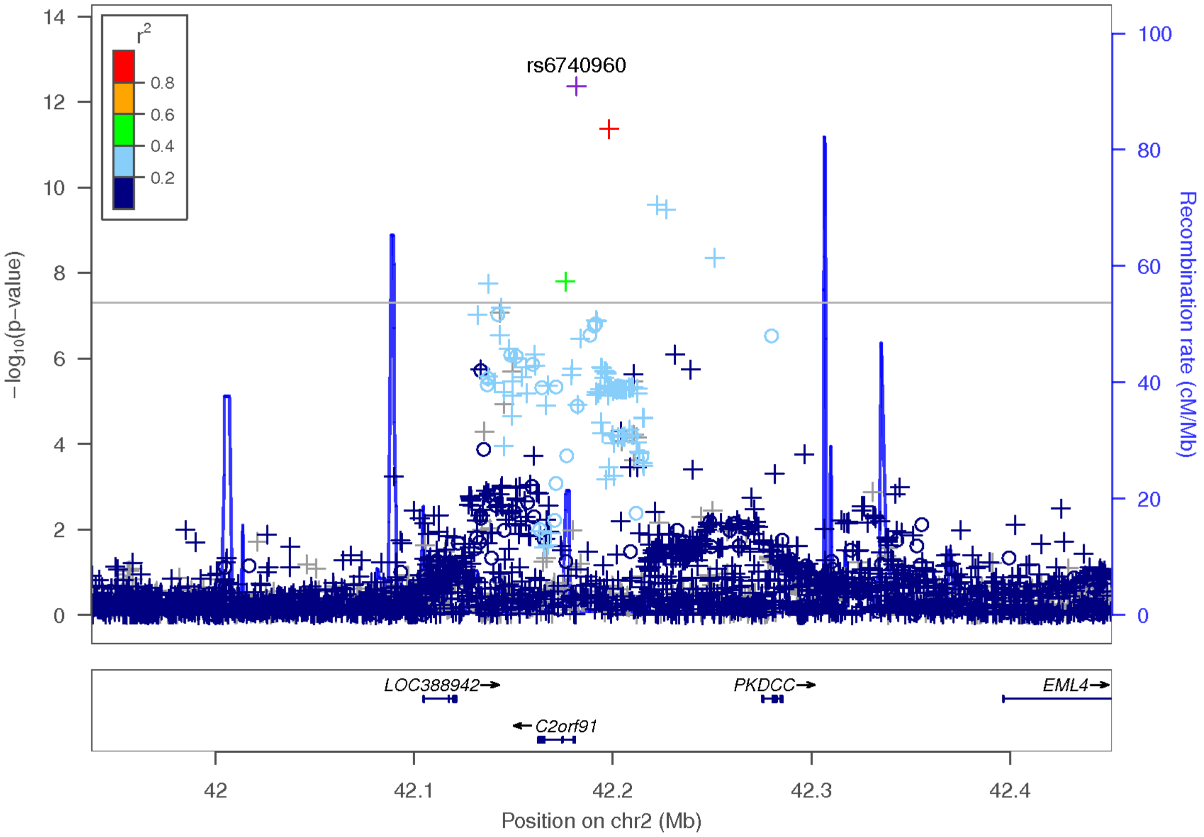


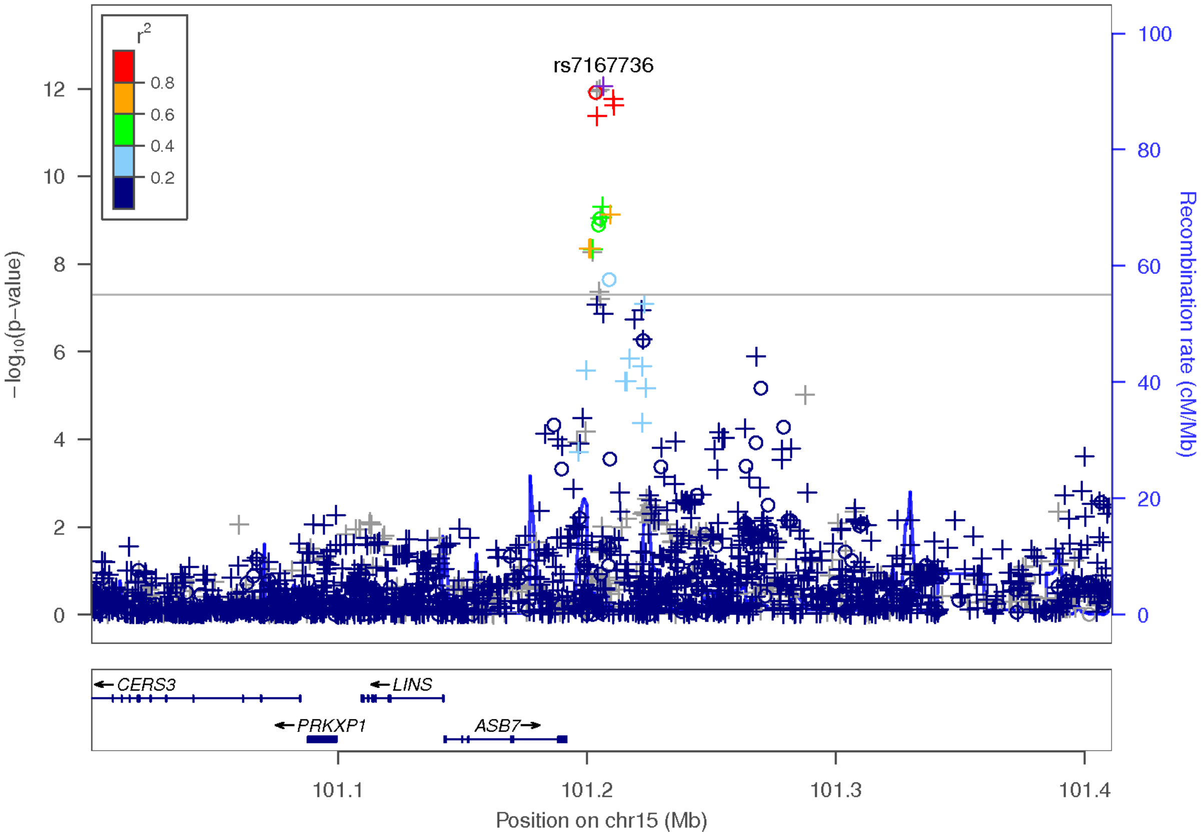
15
10
5
0
−log₁₀(p−value)
r^2
0.8
0.6
0.4
0.2
rs4868444
100
80
60
40
20
0
Recombination rate (cM/Mb)
MSX2→
←FLJ16171
MIR4634→
174
174.1
174.2
174.3
Position on chr5 (Mb)

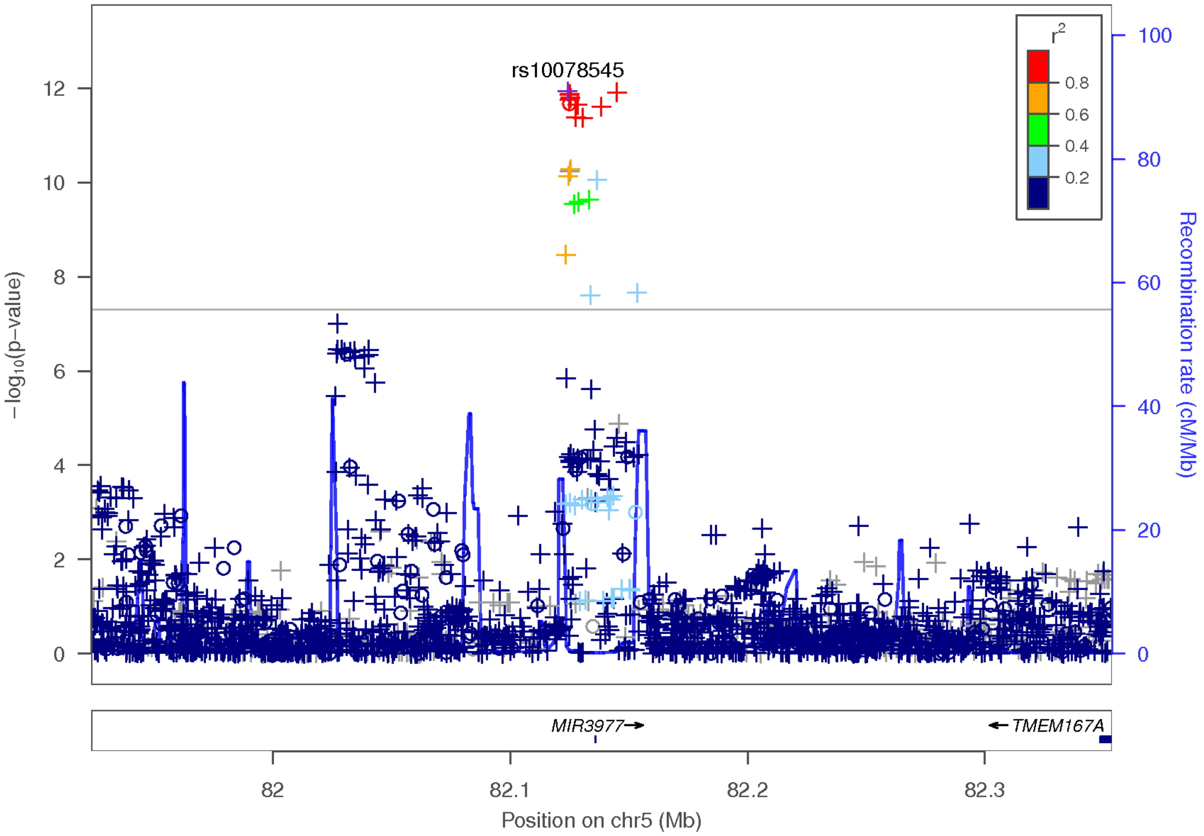

rs1766786
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
10
12
14
0
20
40
60
80
100
TBX15
WARS2
119.3
119.4
119.5
119.6
119.7
Position on chr1 (Mb)

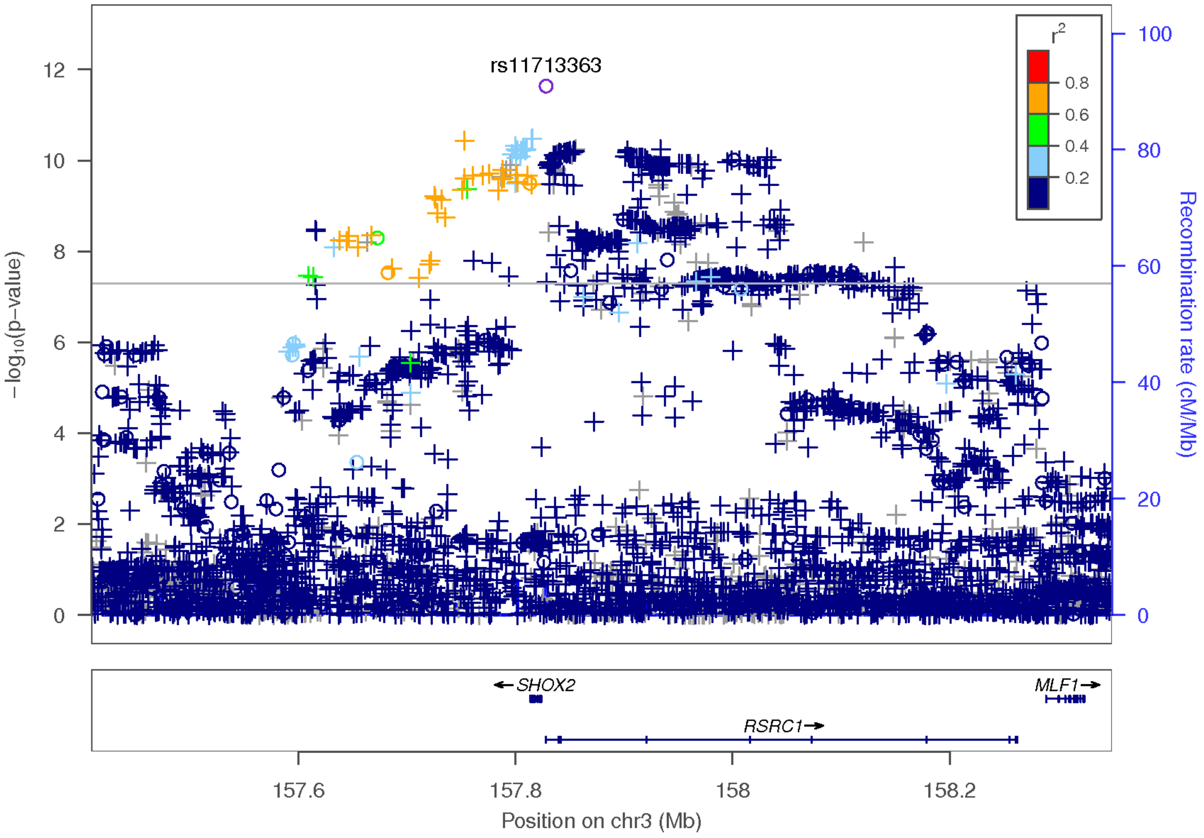

rs10962767
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
10
12
14
0
20
40
60
80
100
BNC2
CNTLN
16.8
16.9
17
17.1
Position on chr9 (Mb)

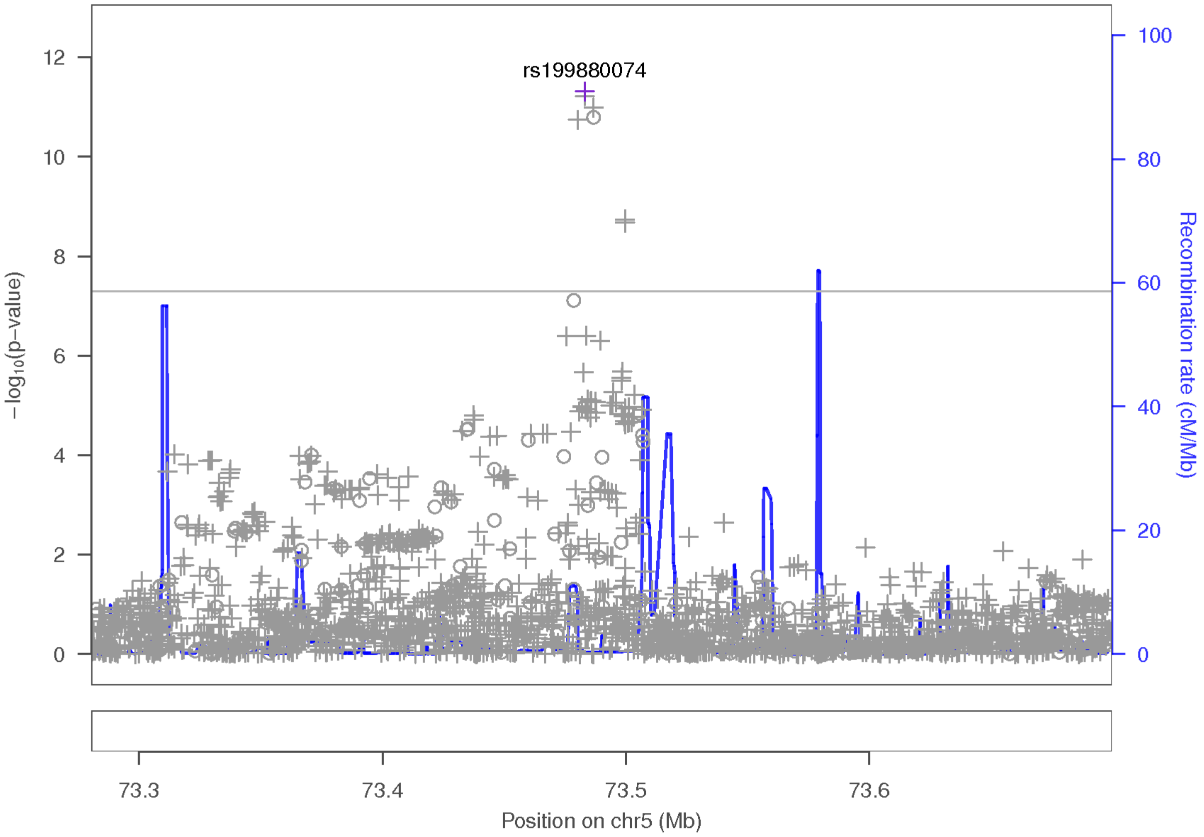

r²
0.8
0.6
0.4
0.2
rs73168105
14
12
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
22.6
22.7
22.8
22.9
Position on chr13 (Mb)

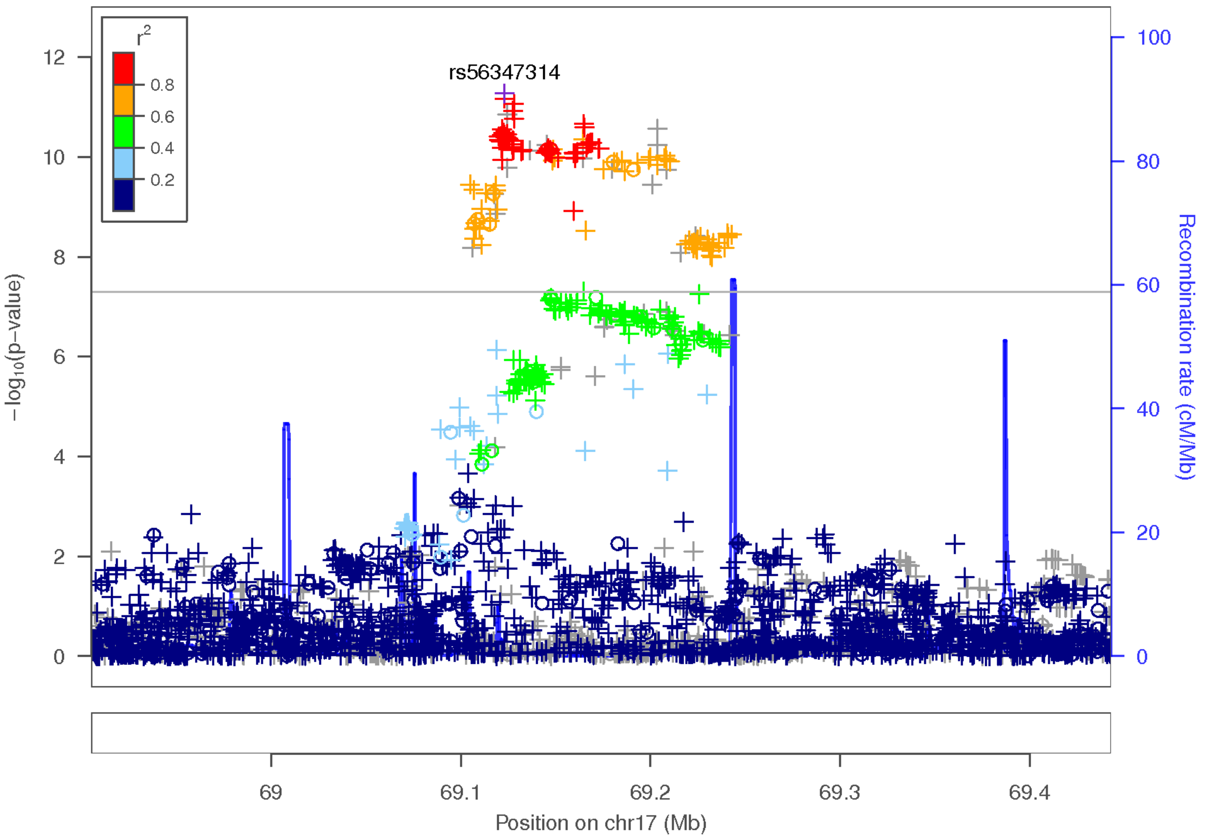

r²
0.8
0.6
0.4
0.2
rs6740960
14
12
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
LOC388942→
PKDCC→
EML4→
←C2orf91
42
42.1
42.2
42.3
42.4
Position on chr2 (Mb)

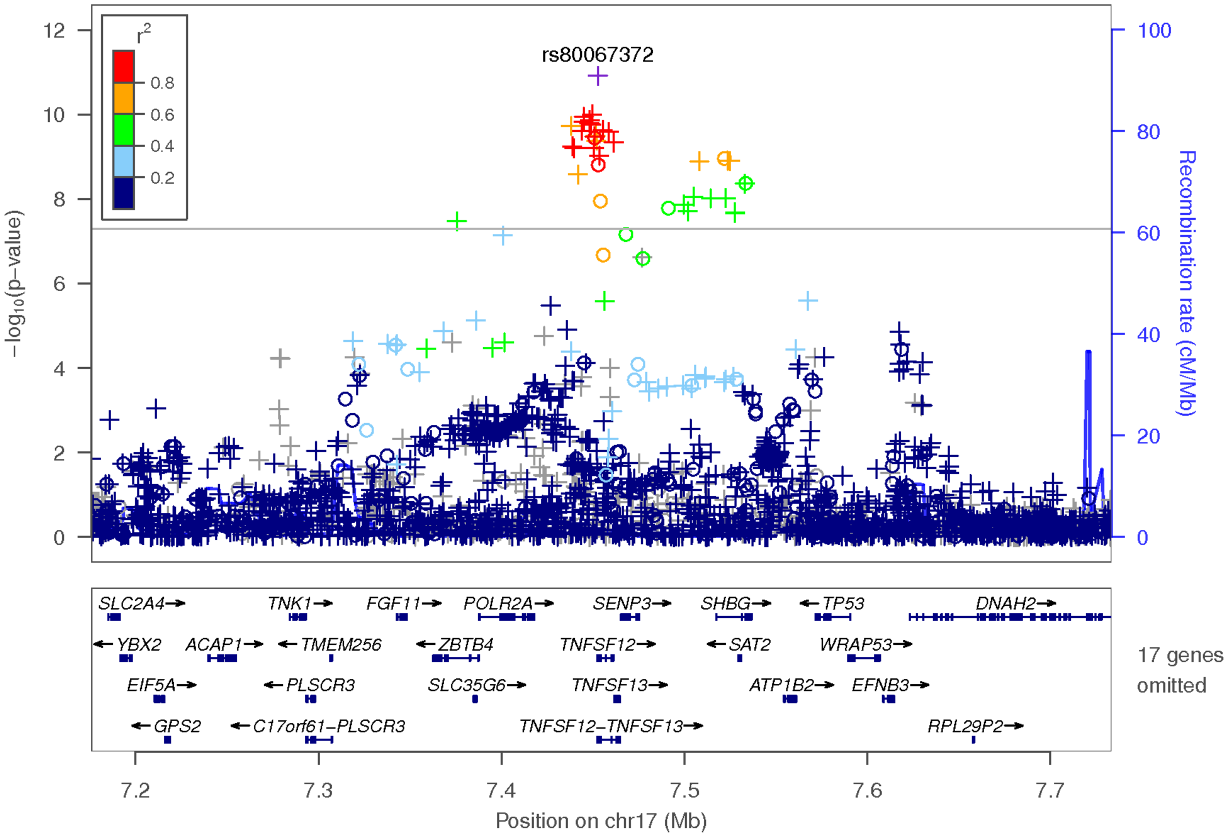

r2
0.8
0.6
0.4
0.2
rs7167736
−log10(p−value)
0
2
4
6
8
10
12
100
80
60
40
20
0
Recombination rate (cM/Mb)
CERS3
LINS
PRKXP1
ASB7
101.1
101.2
101.3
101.4
Position on chr15 (Mb)

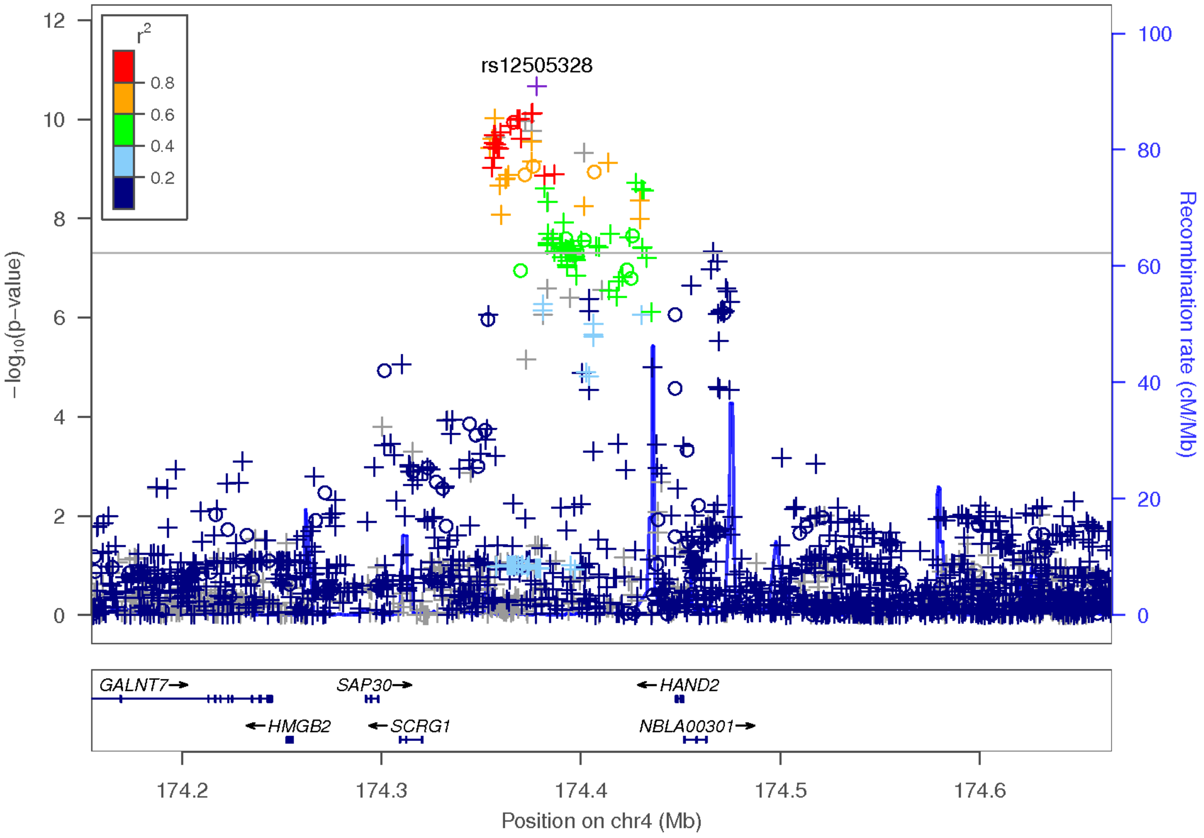

r2
0.8
0.6
0.4
0.2
rs10078545
−log10(p−value)
0
2
4
6
8
10
12
100
80
60
40
20
0
Recombination rate (cM/Mb)
MIR3977
TMEM167A
82
82.1
82.2
82.3
Position on chr5 (Mb)


rs11713363
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
10
12
0
20
40
60
80
100
SHOX2
MLF1
RSRC1
157.6
157.8
158
158.2
Position on chr3 (Mb)

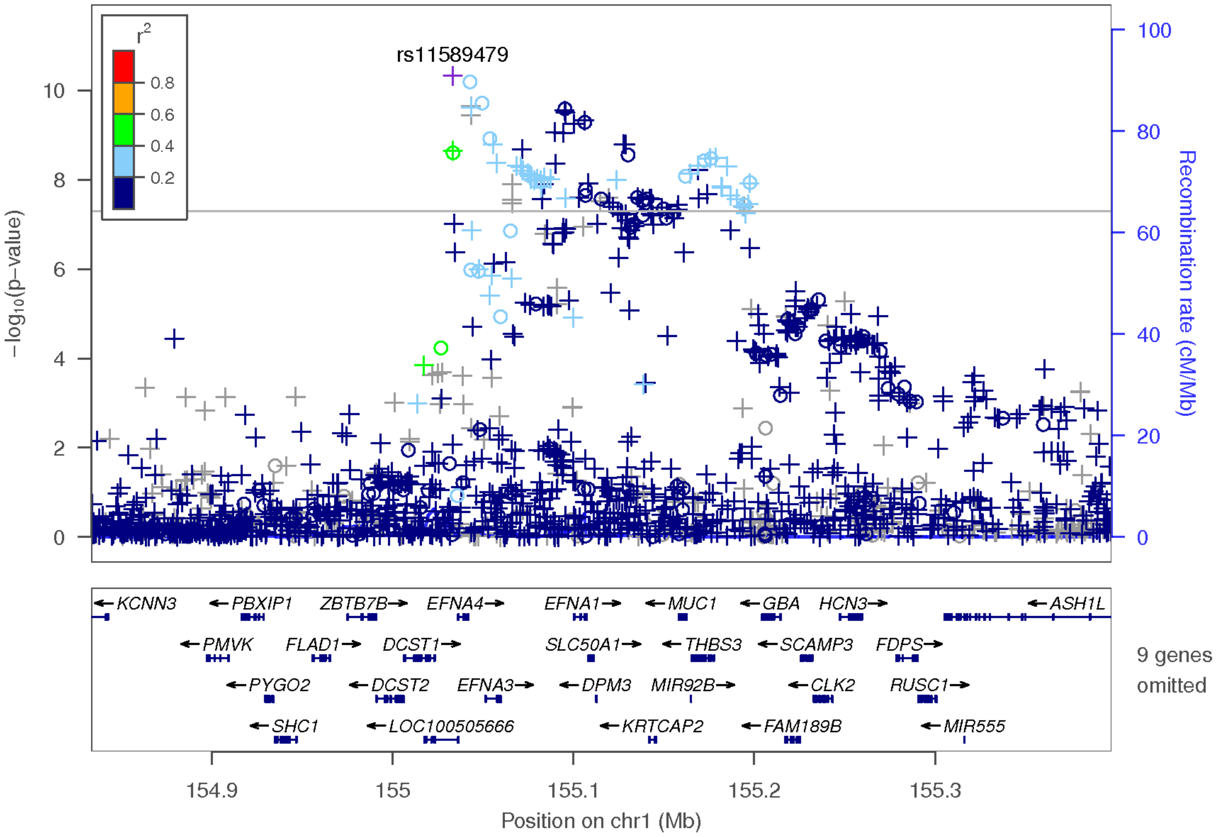

rs199880074
−log₁₀(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
10
12
0
20
40
60
80
100
73.3
73.4
73.5
73.6
Position on chr5 (Mb)


r²
0.8
0.6
0.4
0.2
rs56347314
−log₁₀(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
69
69.1
69.2
69.3
69.4
Position on chr17 (Mb)

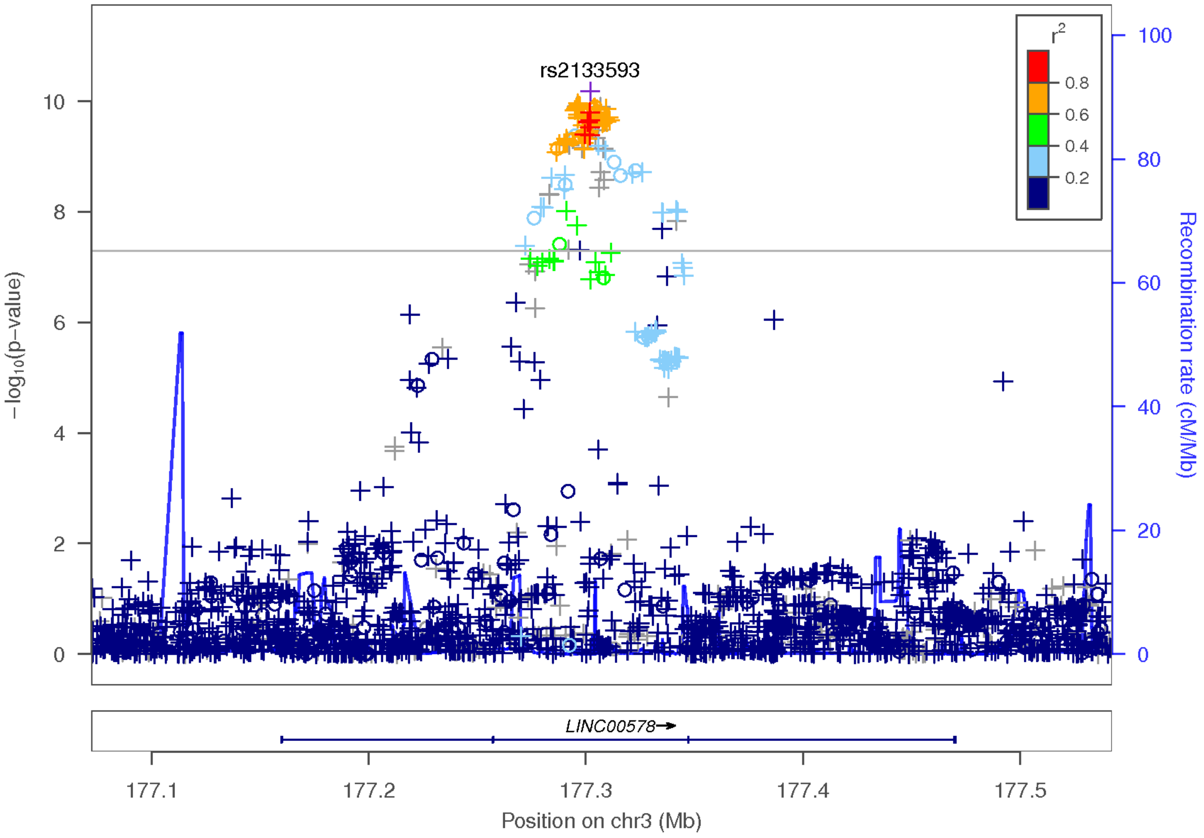

r²
0.8
0.6
0.4
0.2
rs80067372
−log₁₀(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
SLC2A4→
TNK1→
FGF11→
POLR2A→
SENP3→
SHBG→
←TP53
DNAH2→
←YBX2
ACAP1→
←TMEM256
←ZBTB4
TNFSF12→
←SAT2
WRAP53→
EIF5A→
←PLSCR3
SLC35G6→
TNFSF13→
ATP1B2→
EFNB3→
←GPS2
←C17orf61−PLSCR3
TNFSF12−TNFSF13→
RPL29P2→
17 genes omitted
7.2
7.3
7.4
7.5
7.6
7.7
Position on chr17 (Mb)

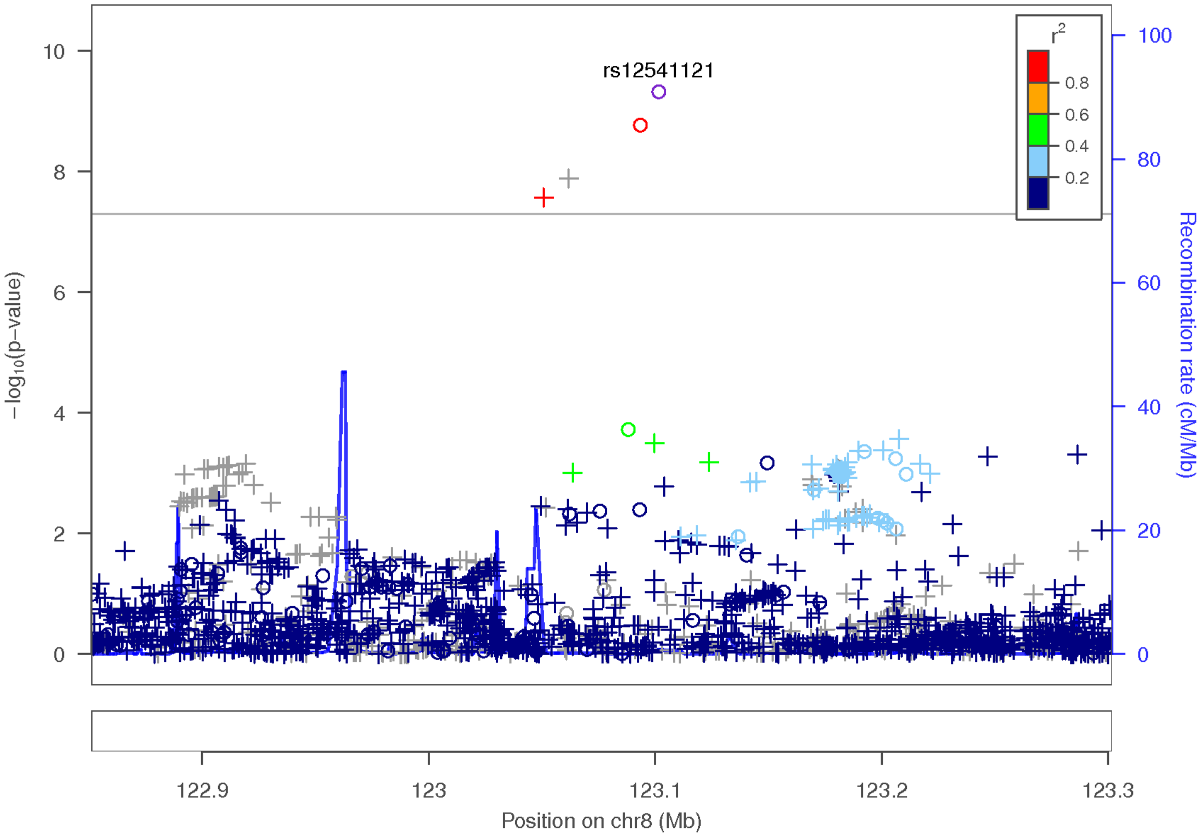


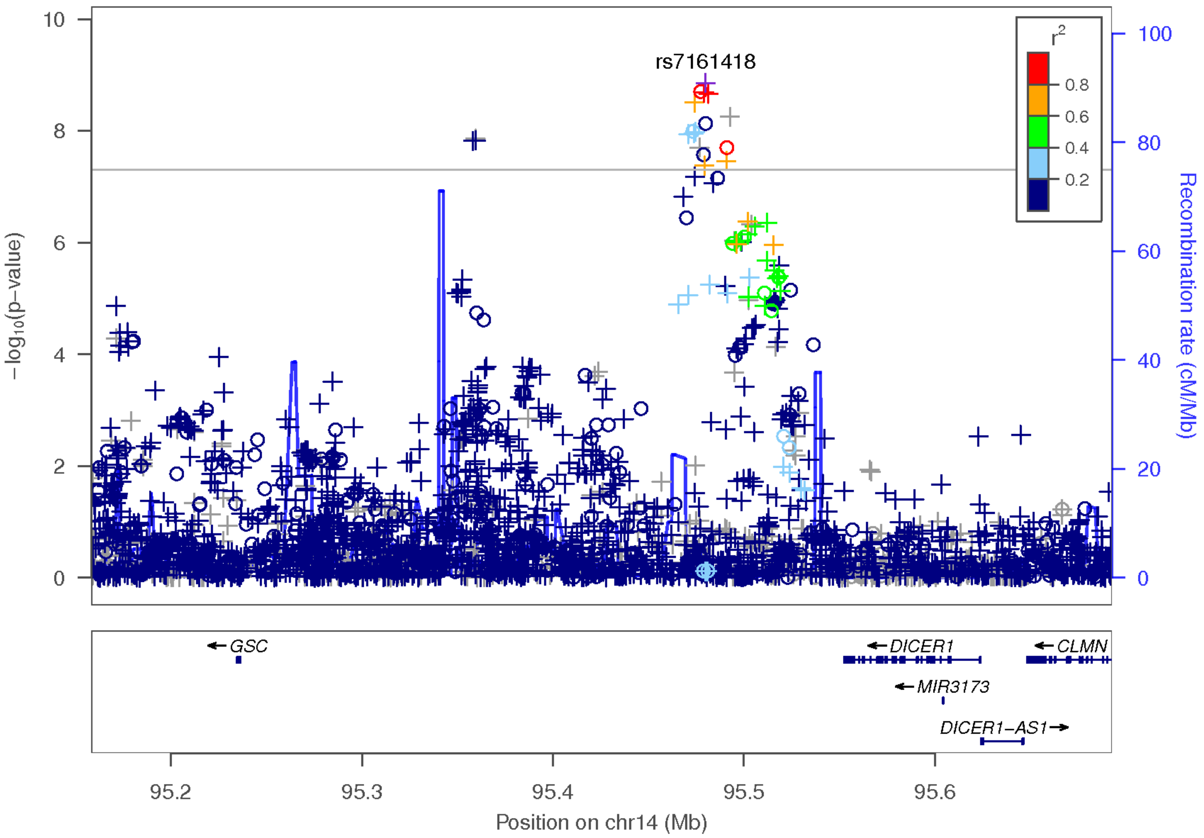
r²
0.8
0.6
0.4
0.2
rs12505328
−log₁₀(p−value)
0
2
4
6
8
10
12
Recombination rate (cM/Mb)
0
20
40
60
80
100
GALNT7
SAP30
HAND2
HMGB2
SCRG1
NBLA00301
174.2
174.3
174.4
174.5
174.6
Position on chr4 (Mb)



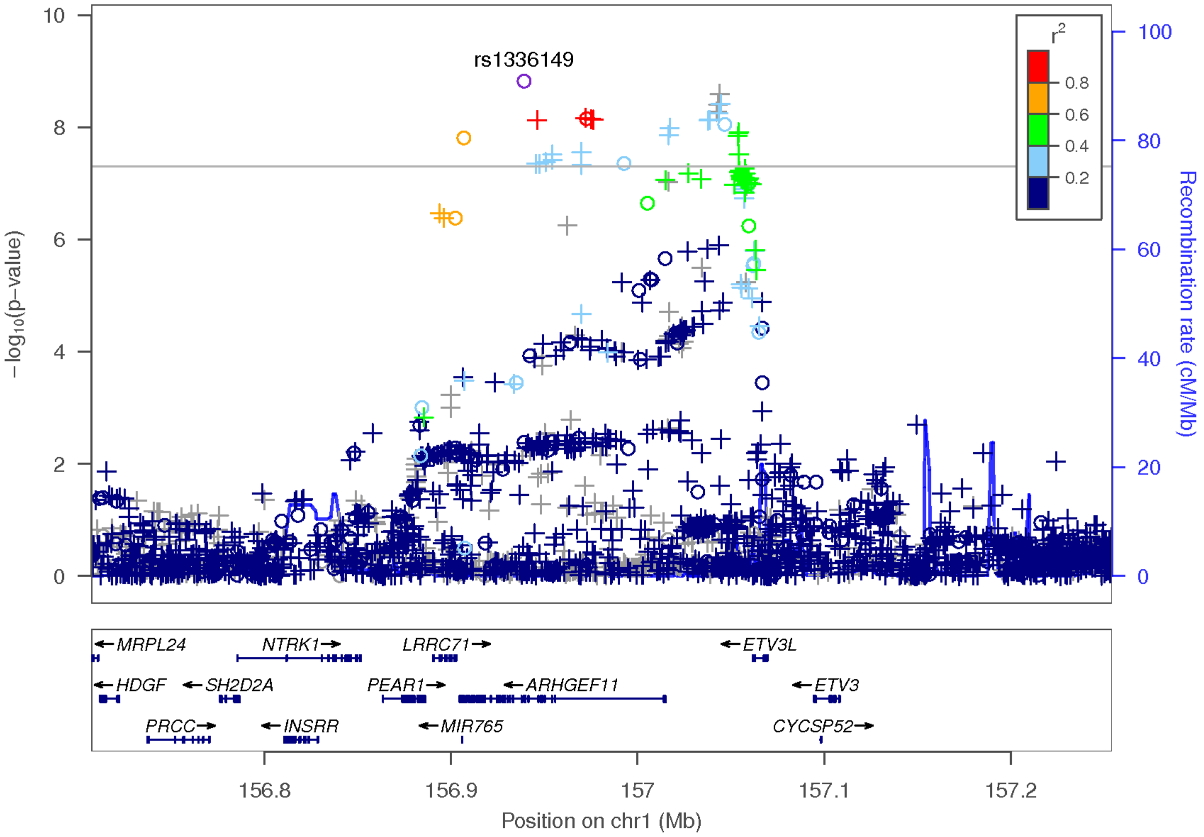
r²
0.8
0.6
0.4
0.2
rs11589479
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
KCNN3
PBXIP1
ZBTB7B
EFNA4
EFNA1
MUC1
GBA
HCN3
ASH1L
PMVK
FLAD1
DCST1
SLC50A1
THBS3
SCAMP3
FDPS
PYGO2
DCST2
EFNA3
DPM3
MIR92B
CLK2
RUSC1
SHC1
LOC100505666
KRTCAP2
FAM189B
MIR555
9 genes omitted
154.9
155
155.1
155.2
155.3
Position on chr1 (Mb)


rs2133593
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
LINC00578→
177.1
177.2
177.3
177.4
177.5
Position on chr3 (Mb)

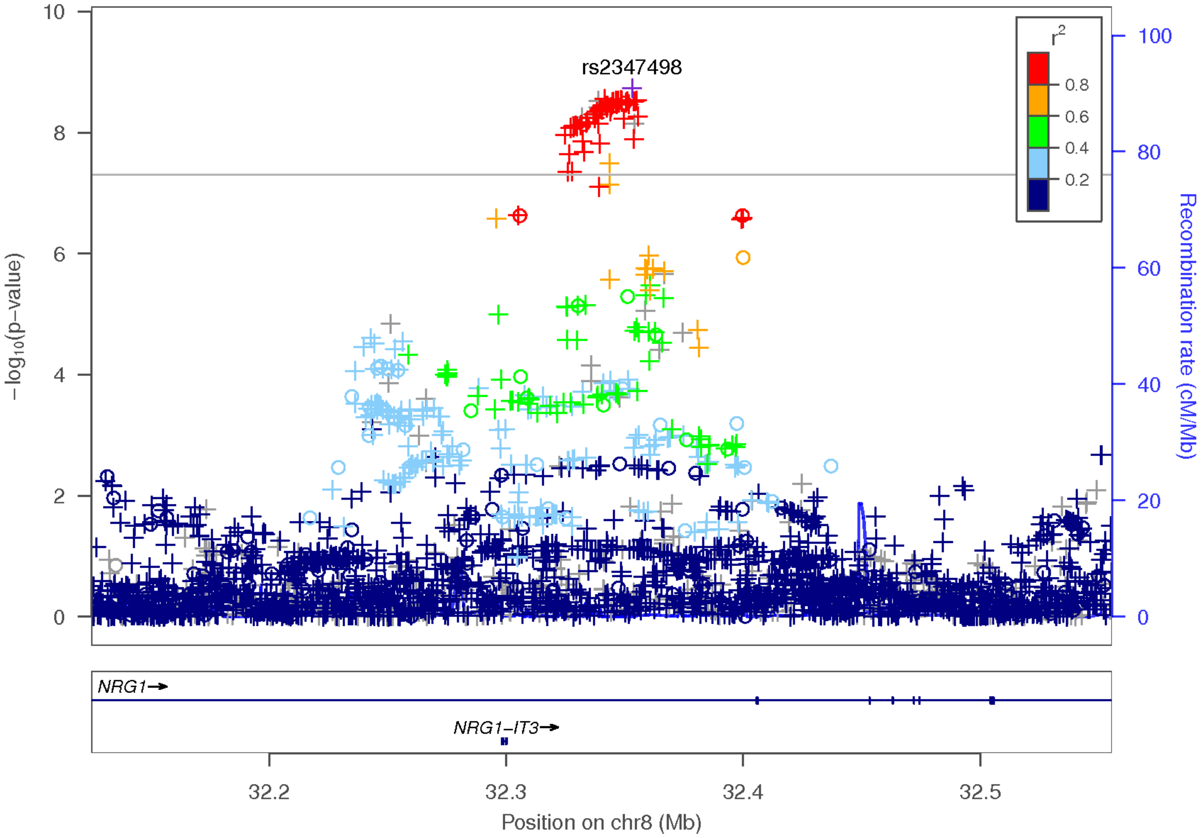

rs12541121
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
122.9
123
123.1
123.2
123.3
Position on chr8 (Mb)

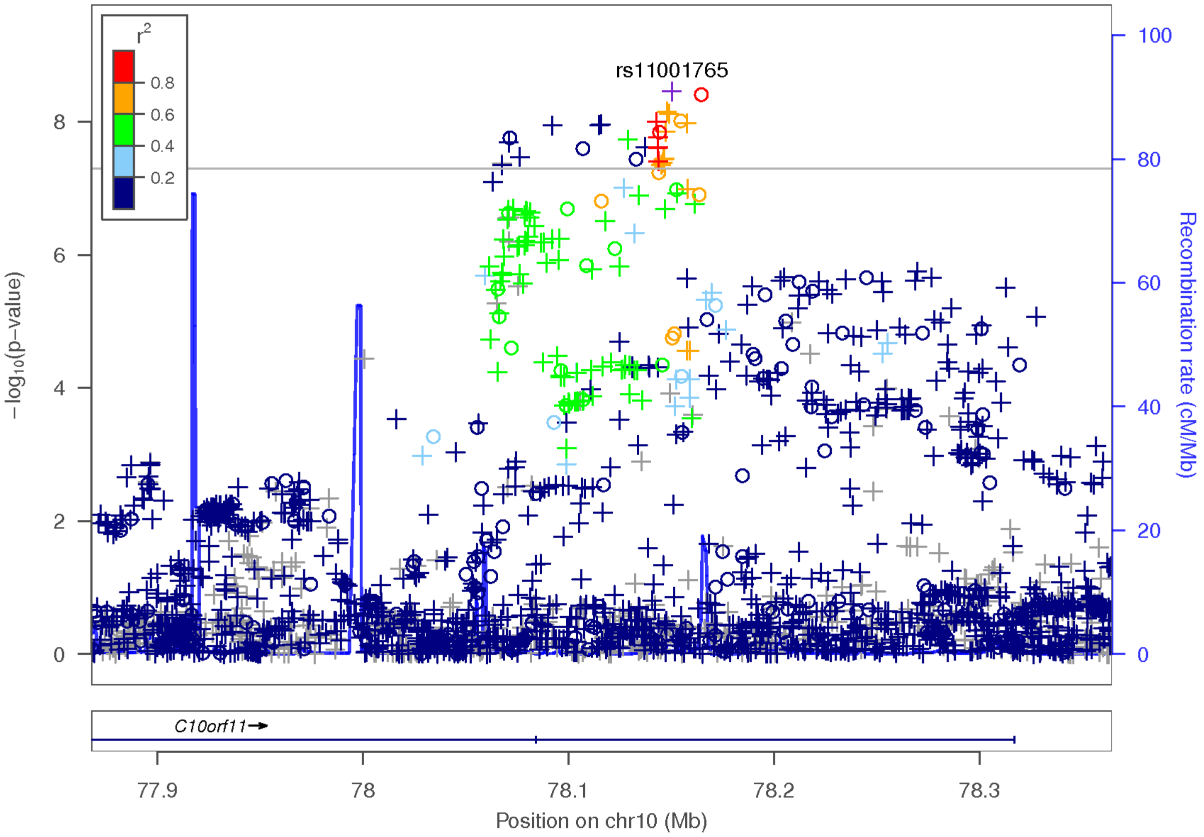


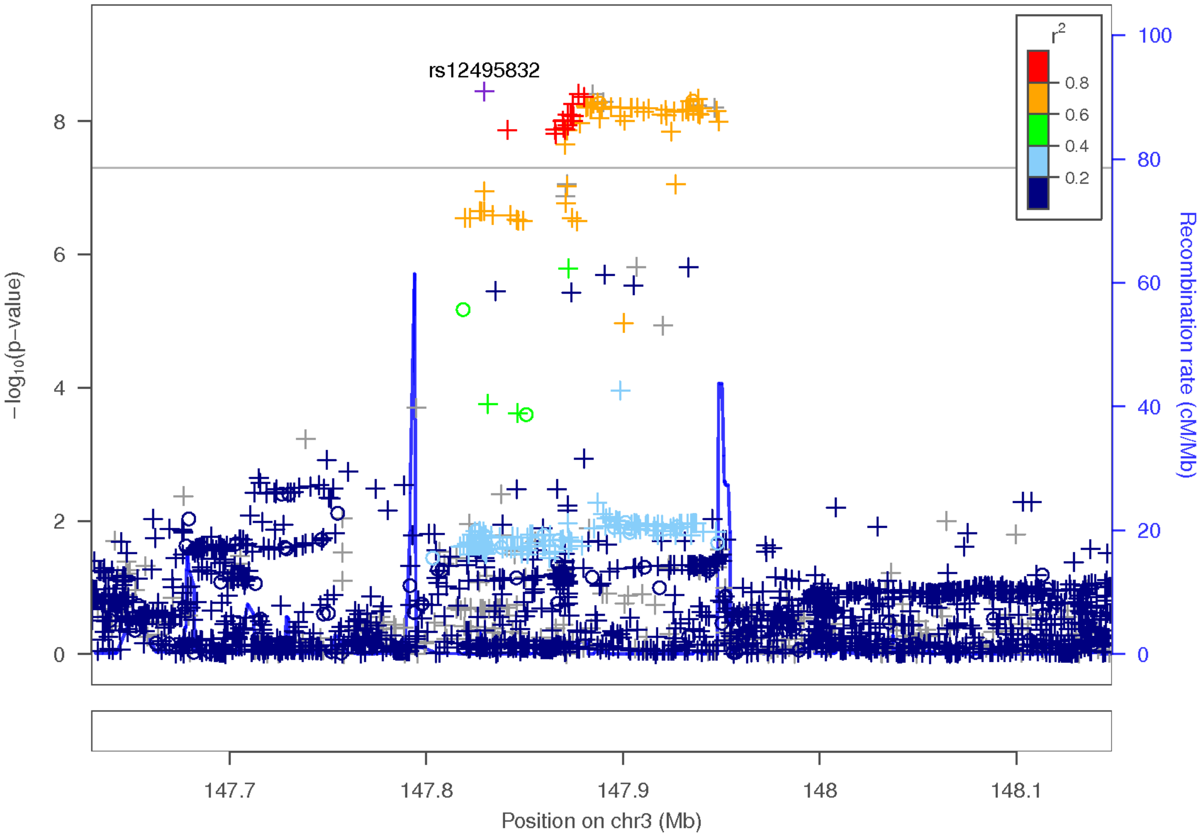
rs7161418
r2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
GSC
DICER1
CLMN
MIR3173
DICER1−AS1
95.2
95.3
95.4
95.5
95.6
Position on chr14 (Mb)

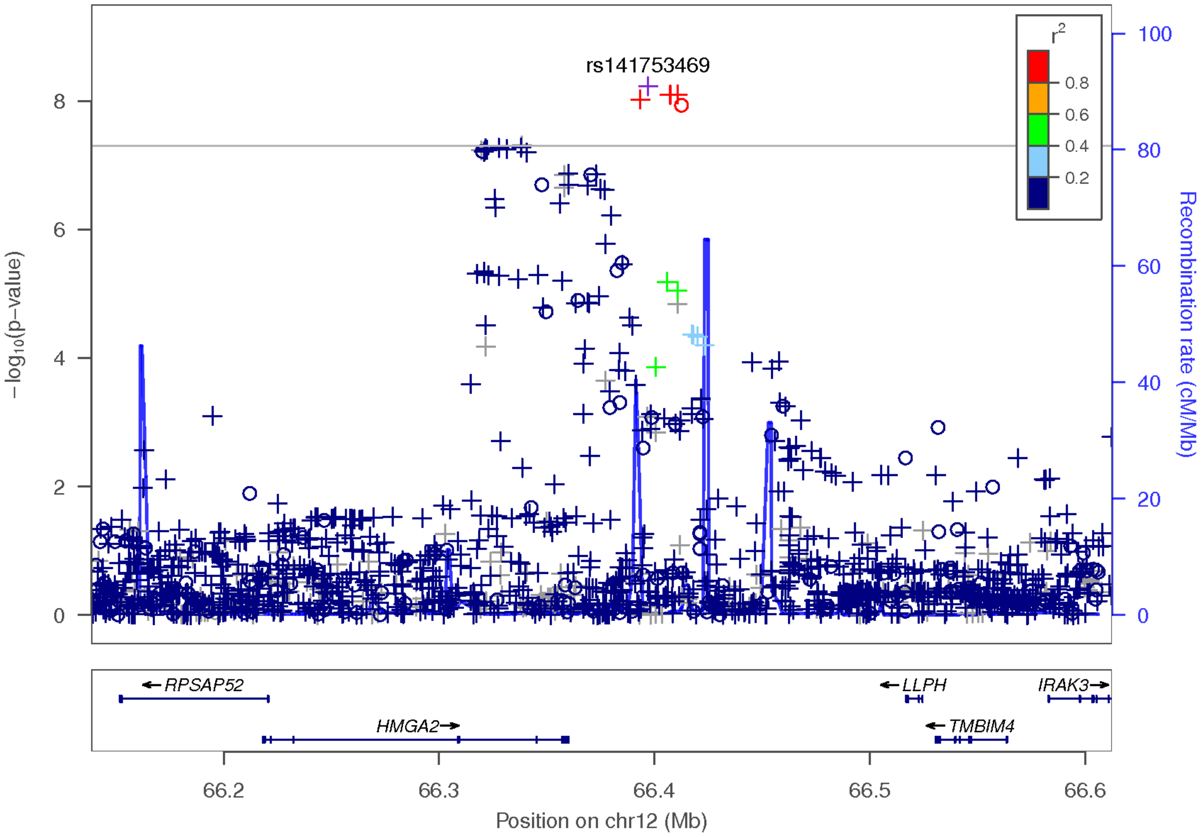


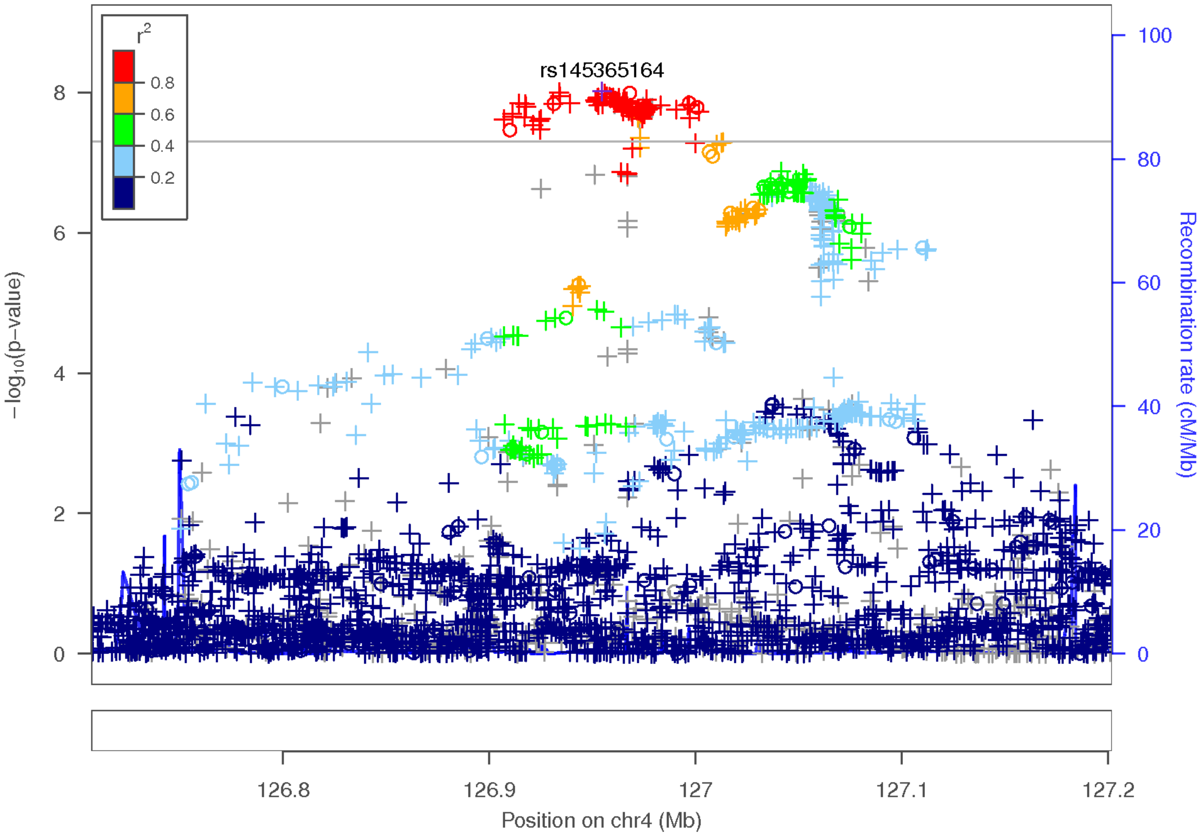
rs1336149
r2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
MRPL24
NTRK1
LRRC71
ETV3L
HDGF
SH2D2A
PEAR1
ARHGEF11
ETV3
PRCC
INSRR
MIR765
CYCSP52
156.8
156.9
157
157.1
157.2
Position on chr1 (Mb)


rs2347498
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
NRG1→
NRG1−IT3→
32.2
32.3
32.4
32.5
Position on chr8 (Mb)

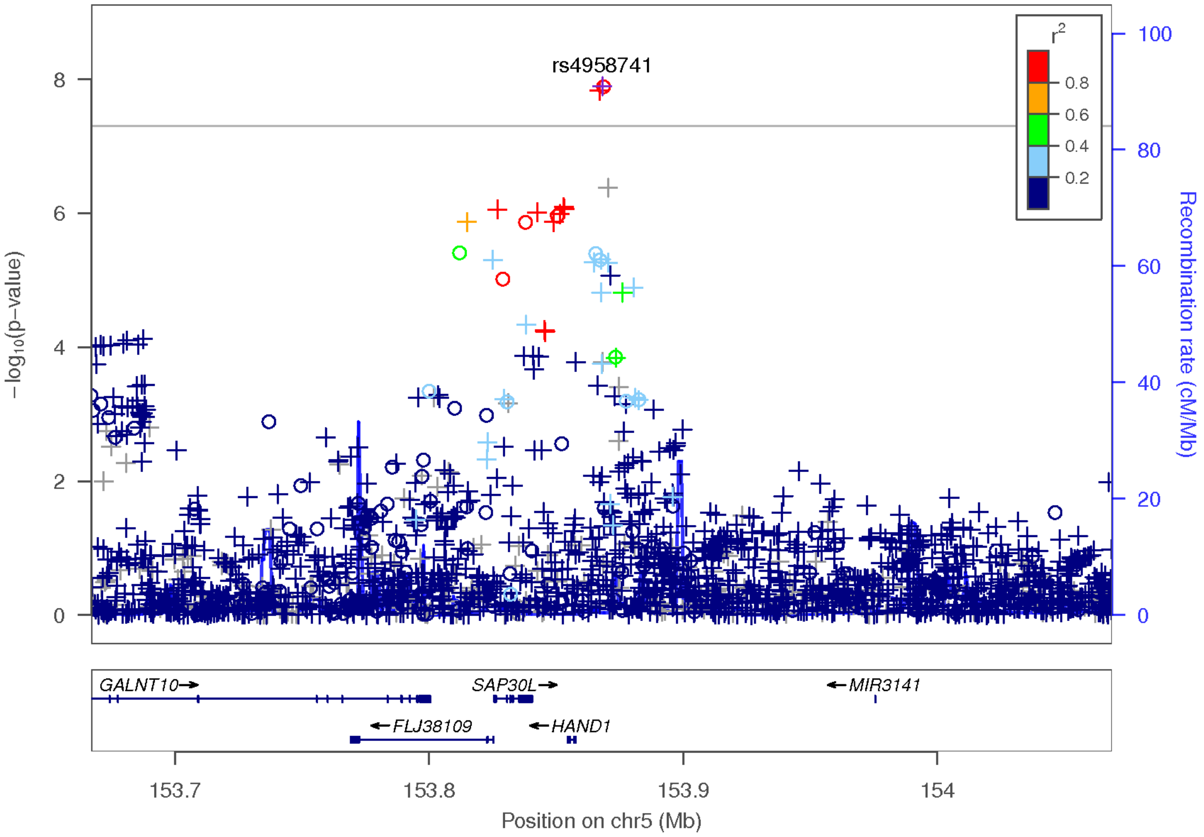

rs11001765
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
C10orf11→
77.9
78
78.1
78.2
78.3
Position on chr10 (Mb)


rs12495832
r^2
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
147.7
147.8
147.9
148
148.1
Position on chr3 (Mb)

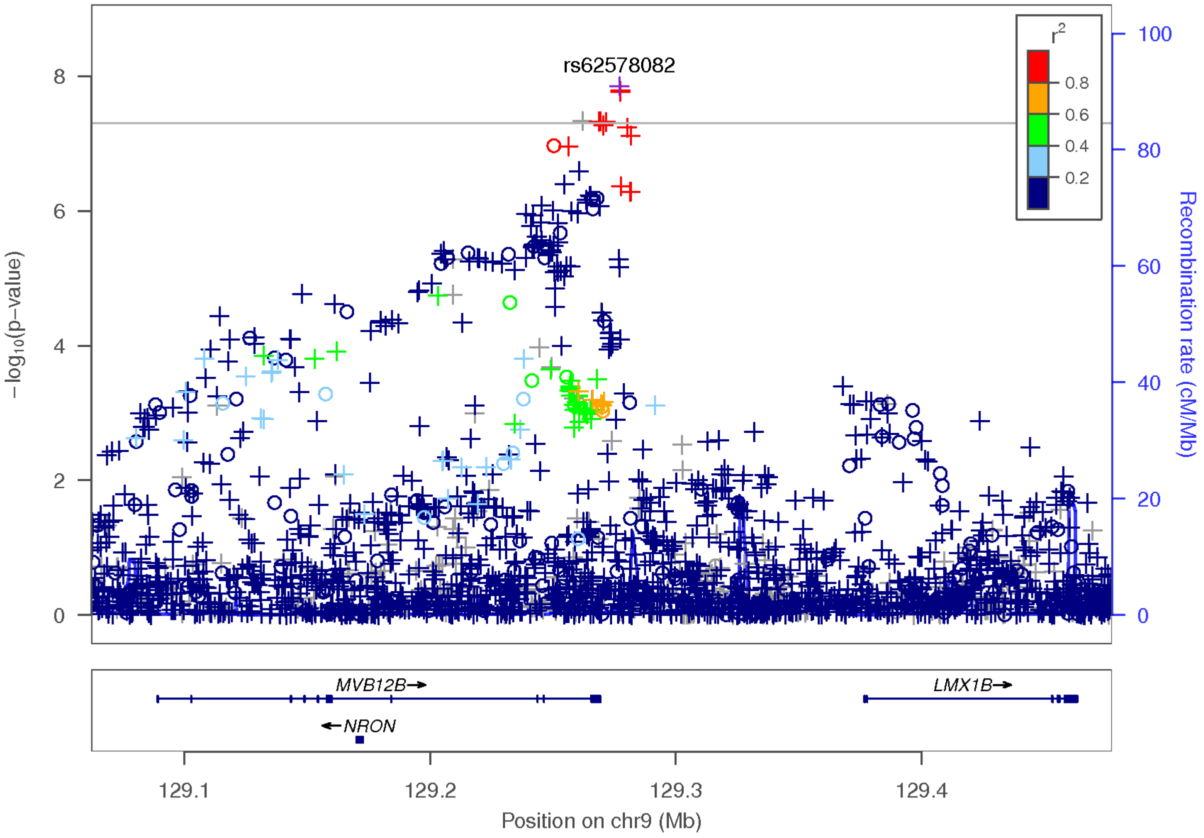

rs141753469
r^2
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
RPSAP52
HMGA2
LLPH
IRAK3
TMBIM4
66.2
66.3
66.4
66.5
66.6
Position on chr12 (Mb)

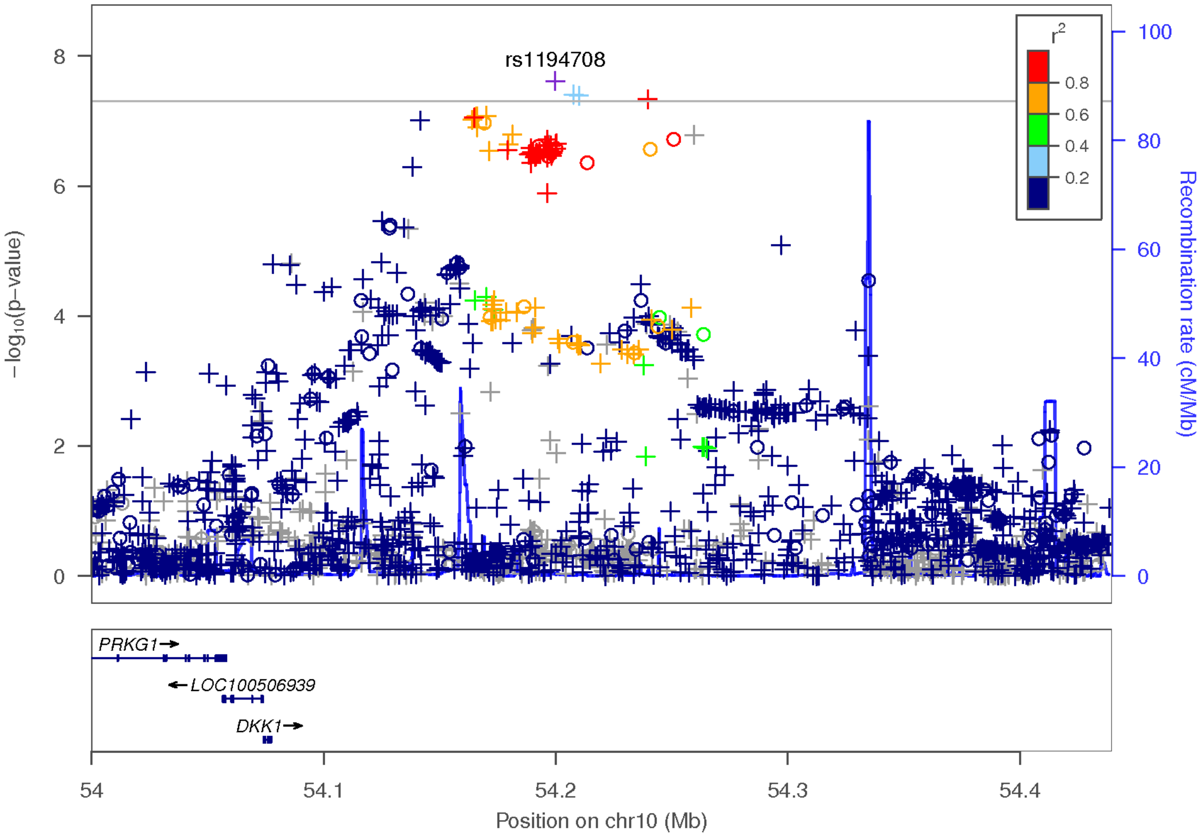


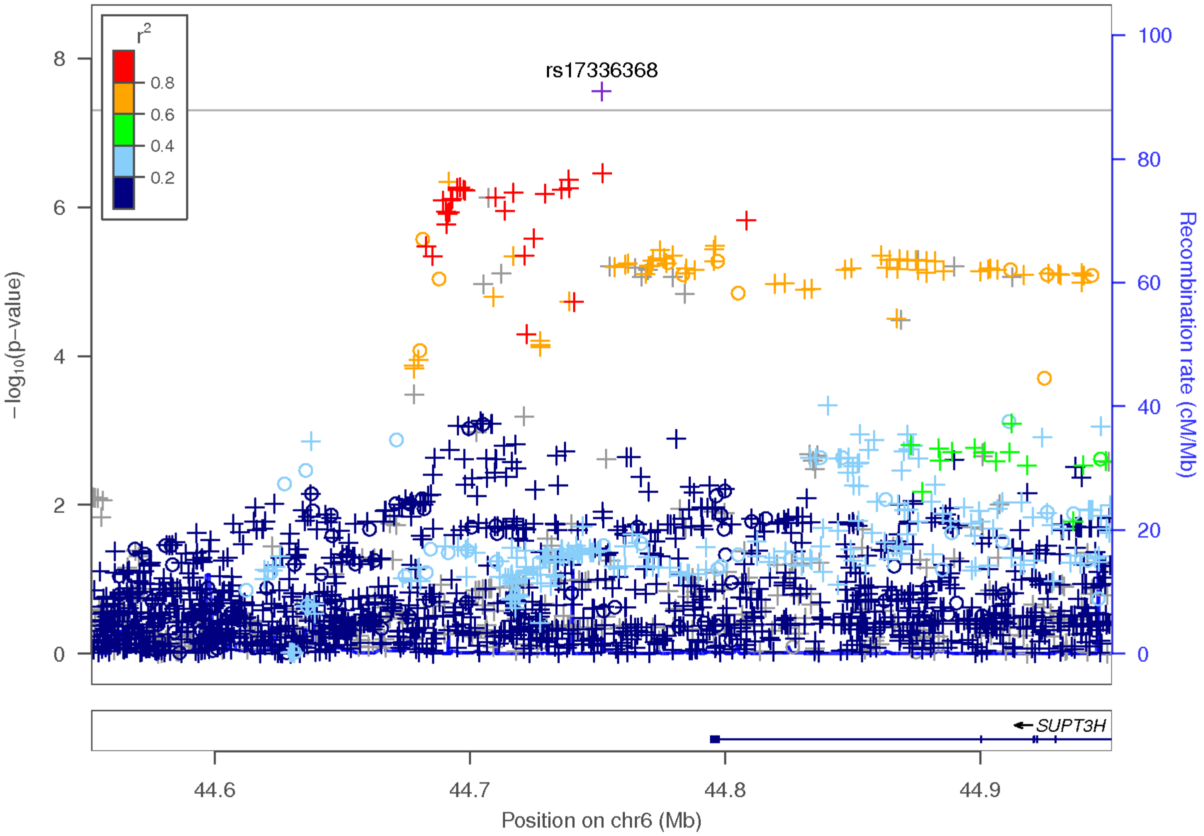
r²
0.8
0.6
0.4
0.2
rs145365164
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
126.8
126.9
127
127.1
127.2
Position on chr4 (Mb)

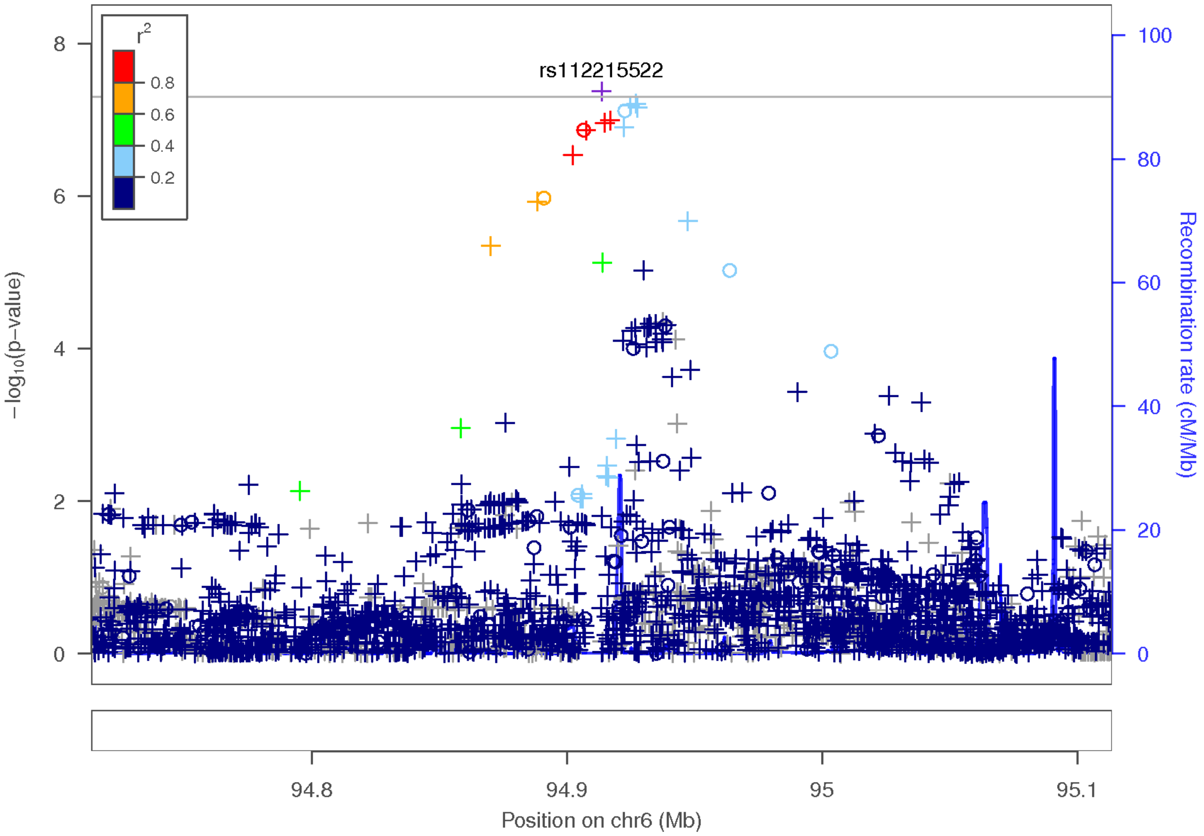


rs4958741
r²
0.8
0.6
0.4
0.2
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
GALNT10→
SAP30L→
←MIR3141
←FLJ38109
←HAND1
153.7
153.8
153.9
154
Position on chr5 (Mb)


rs62578082
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
MVB12B→
←NRON
LMX1B→
129.1
129.2
129.3
129.4
Position on chr9 (Mb)


rs1194708
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
PRKG1→
←LOC100506939
DKK1→
54
54.1
54.2
54.3
54.4
Position on chr10 (Mb)


r²
0.8
0.6
0.4
0.2
rs17336368
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
SUPT3H
44.6
44.7
44.8
44.9
Position on chr6 (Mb)


r²
0.8
0.6
0.4
0.2
rs112215522
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
94.8
94.9
95
95.1
Position on chr6 (Mb)