Analysis Summary: Nearsightedness

Phenotype Description

Nearsightedness cases are defined as having said "Yes" or checking nearsightedness to one of the following questions.

- Your Medical History ("Have you ever been diagnosed by a doctor with nearsightedness (near objects are clear, far objects are blurry)?" Yes)
- Research Snippets ("Are you nearsighted (near objects are clear, far objects are blurry)?" Yes)
- Refractive Error ("What vision problems do you have? Please check all that apply." Nearsightedness (near objects are clear, far objects are blurry)
- Refractive Error ("Prior to your LASIK eye surgery, what vision problems did you have? Please check all that apply." Nearsightedness (near objects are clear, far objects are blurry)

Controls are defined as having said "No" or not checking nearsightedness to at least one of the questions above. Discordant answers are removed.

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]
nearsightedness	case	106086	53935	52151	15103	33066	29503	28414
	control	85757	47488	38269	12935	24222	21975	26625

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

Phenotype	Group	Total	v1/v2	v3	v4
nearsightedness	case	106086	8140	82499	15447
	control	85757	6072	66218	13467

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	−0.00489	0.000287	−17.1	3.1×10^{-65}	291.4	2.5×10^{-65}
sexF	0.19536	0.009255	21.1	6.5×10^{-99}	446.4	4.3×10^{-99}
pc.0	−0.03665	0.004638	−7.9	2.7×10^{-15}	62.8	2.3×10^{-15}
pc.1	0.03886	0.004648	8.4	6.2×10^{-17}	70.2	5.3×10^{-17}
pc.2	−0.01167	0.004623	−2.5	0.012	6.4	0.012
pc.3	0.02378	0.004604	5.2	2.4×10^{-7}	26.7	2.4×10^{-7}
pc.4	0.03085	0.004601	6.7	2.0×10^{-11}	44.7	2.2×10^{-11}

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	−5807	13773260
failed to converge	−10335	13762925

Genetic Association Tests

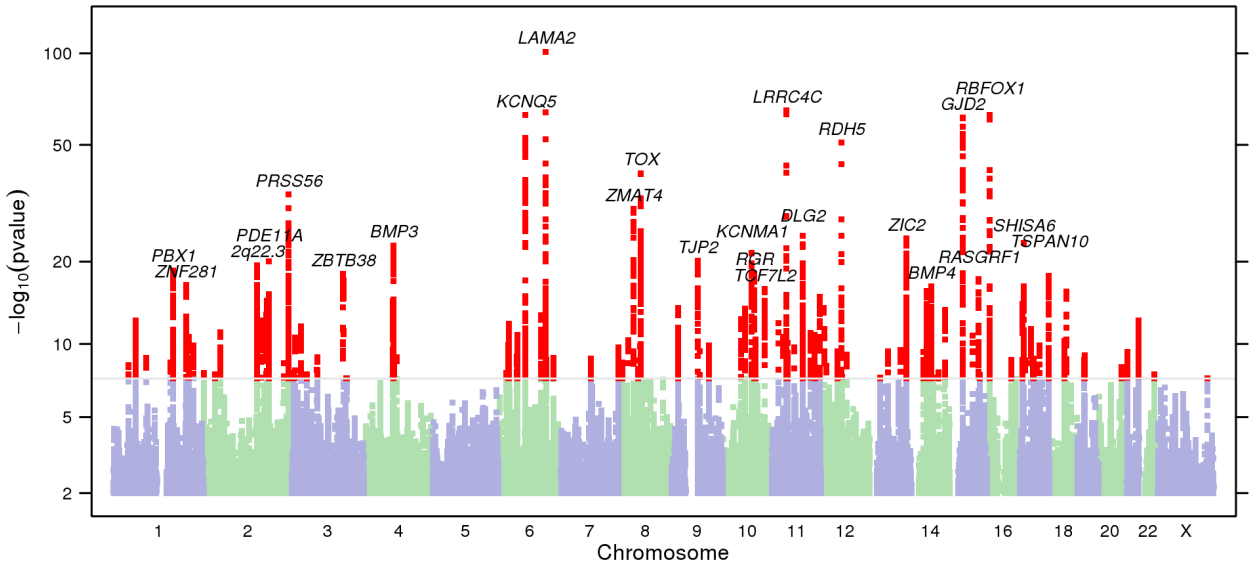
We performed logistic regression assuming an additive model for allelic effects, using the model:

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

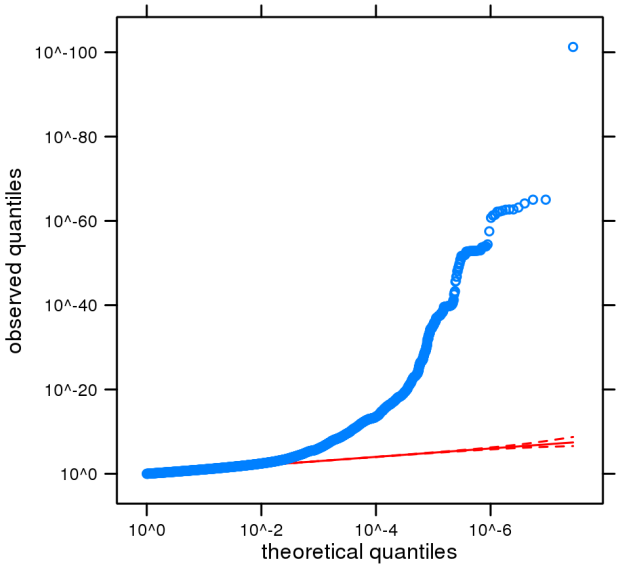
This genome-wide association analysis includes data from 106086 cases and 85757 controls of European ancestry, filtered to remove close relatives.

The results in this report have been adjusted for a genomic control inflation factor λ=1.230. The equivalent inflation factor for 1000 cases and 1000 controls λ_{1000}= 1.002 , and for 10000, λ_{10000}= 1.024 .

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
6q22.33	rs12193446	chr6	129820038	A/G	I	5.4×10^{-102}	0.769	[0.751,0.788]	[LAMA2]
11p12	rs11606250	chr11	40149300	A/G	I	9.2×10^{-66}	0.845	[0.829,0.862]	[LRRC4C]
6q13	rs7744813	chr6	73643289	A/C	I	1.9×10^{-63}	0.883	[0.871,0.896]	[KCNQ5]
16p13.3	rs10500355	chr16	7459347	A/T	I	2.0×10^{-63}	0.881	[0.868,0.894]	[RBFOX1]
15q14	rs524952	chr15	35005886	A/T	I	3.5×10^{-62}	0.886	[0.874,0.899]	GOLGA8B---[]--GJD2
12q13.2	rs3138141	chr12	56115778	A/C	I	1.5×10^{-51}	1.146	[1.126,1.167]	[RDH5]
8q12.1	rs10089517	chr8	60178721	A/C	I	6.0×10^{-41}	1.107	[1.091,1.124]	TOX---[]---CA8
2q37.1	rs1550094	chr2	233385396	A/G	I	9.2×10^{-35}	1.102	[1.085,1.119]	[PRSS56]
8p11.21	rs869422	chr8	40723970	A/G	I	4.0×10^{-31}	0.903	[0.887,0.918]	[ZMAT4]
11q14.1	rs2155413	chr11	84634790	A/C	I	2.3×10^{-25}	0.927	[0.914,0.941]	[DLG2]
13q32.3	rs9585327	chr13	100689354	A/G	I	8.9×10^{-25}	0.928	[0.915,0.941]	ZIC2--[]--PCCA
17p12	rs2908972	chr17	11407259	A/T	I	5.3×10^{-24}	0.927	[0.914,0.941]	[SHISA6]
4q21.21	rs5022942	chr4	81959966	A/G	I	1.6×10^{-23}	0.917	[0.901,0.932]	[BMP3]
10q22.3	rs10824518	chr10	79063542	A/T	I	3.3×10^{-22}	0.929	[0.916,0.943]	[KCNMA1]
9q21.11	rs11145488	chr9	71770939	A/G	I	6.7×10^{-21}	0.920	[0.904,0.936]	FXN--[]--TJP2
2q31.2	rs17400325	chr2	178565913	C/T	I	9.6×10^{-21}	0.844	[0.814,0.875]	[PDE11A]
2q22.3	rs61049169	chr2	146888708	A/G	I	3.4×10^{-20}	1.070	[1.054,1.085]	[]
1q23.3	rs1556867	chr1	164213686	C/T	I	2.7×10^{-19}	1.080	[1.062,1.098]	NUF2---[]---PBX1
10q23.1	rs10887265	chr10	86015573	C/G	I	5.6×10^{-19}	0.931	[0.917,0.946]	[RGR]
3q23	rs9866391	chr3	141076084	C/T	I	7.7×10^{-19}	1.069	[1.053,1.084]	[ZBTB38]
17q25.3	rs9747347	chr17	79606820	C/T	I	1.6×10^{-18}	1.074	[1.057,1.092]	NPLOC4-[]-TSPAN10
15q25.1	rs13380104	chr15	79378821	C/T	I	4.3×10^{-18}	1.066	[1.051,1.082]	[RASGRF1]
1q32.1	rs2808510	chr1	200336075	C/T	I	3.1×10^{-17}	1.065	[1.049,1.081]	NR5A2---[]--ZNF281
14q22.2	rs2181346	chr14	54552428	A/T	I	4.7×10^{-17}	1.079	[1.060,1.098]	BMP4---[]---CDKN3
10q25.2	rs56299331	chr10	114788436	C/T	I	1.1×10^{-16}	1.078	[1.059,1.098]	[TCF7L2]
14q21.1	rs34217772	chr14	42273570	C/G	I	2.0×10^{-16}	1.081	[1.061,1.102]	[LRFN5]
18q21.1	rs12965607	chr18	47391025	G/T	I	2.4×10^{-16}	0.918	[0.899,0.937]	[MYO5B]
11q25	rs1793639	chr11	131931531	A/G	I	9.7×10^{-16}	1.061	[1.046,1.076]	[NTM]
4q21.21	rs13129838	chr4	80508788	C/T	I	2.6×10^{-15}	1.068	[1.051,1.086]	GK2---[]---ANTXR2
2q31.1	rs17428076	chr2	172851936	C/G	I	3.2×10^{-15}	0.935	[0.919,0.951]	HAT1-[]--METAP1D
17p13.1	rs11658305	chr17	7429321	A/C	I	7.9×10^{-15}	1.062	[1.046,1.078]	POLR2A--[]--TNFSF12-TNFSF13
9p22.2	rs10511652	chr9	18362865	A/G	I	2.3×10^{-14}	1.058	[1.043,1.073]	SH3GL2---[]---ADAMTSL1
12p13.31	rs5442	chr12	6954864	A/G	I	2.3×10^{-14}	0.895	[0.870,0.921]	[GNB3]
10q21.1	rs4948523	chr10	60339098	A/C	I	2.8×10^{-14}	0.946	[0.933,0.960]	[BICC1]
14q32.12	rs34016308	chr14	92615741	D/I	I	4.1×10^{-14}	0.929	[0.911,0.947]	[CPSF2]
6q22.1	rs1064583	chr6	116446576	A/G	I	1.6×10^{-13}	1.056	[1.041,1.072]	[NT5DC1,COL10A1]
10q11.22	rs201140091	chr10	49408240	D/I	I	3.7×10^{-13}	1.068	[1.049,1.087]	[FRMPD2]
21q22.3	rs73157695	chr21	47371947	A/G	I	5.1×10^{-13}	0.944	[0.929,0.959]	PCBP3-[]--COL6A1
1p31.3	rs479445	chr1	61341632	A/T	I	5.7×10^{-13}	0.946	[0.932,0.960]	C1orf87---[]---NFIA
2q24.1	rs297589	chr2	157358750	A/T	I	5.8×10^{-13}	1.061	[1.044,1.078]	[GPD2]
11p15.1	rs1550870	chr11	18751041	C/T	I	9.9×10^{-13}	0.950	[0.936,0.963]	[PTPN5]
6p22.1	rs2799081	chr6	28270584	C/T	I	1.2×10^{-12}	0.943	[0.928,0.959]	PGBD1[]--ZSCAN31
3p24.2	rs826220	chr3	24268677	C/T	I	2.3×10^{-12}	0.949	[0.936,0.963]	[THRB]
17q11.2	rs10512441	chr17	31239645	C/T	I	3.8×10^{-12}	1.065	[1.046,1.084]	MYO1D--[]--TMEM98
12p13.31	rs7968679	chr12	9313304	A/G	I	3.8×10^{-12}	1.057	[1.040,1.073]	[PZP]
2p21	rs2342406	chr2	45152748	C/T	I	7.8×10^{-12}	1.065	[1.046,1.085]	CAMKMT---[]--SIX3
11q22.3	rs71041628	chr11	105665158	D/I	I	9.7×10^{-12}	1.055	[1.039,1.072]	[GRIA4]
11q23.3	rs10892173	chr11	117672561	C/T	I	1.4×10^{-11}	1.051	[1.036,1.066]	DSCAML1-[]--FXYD6-FXYD2
6p12.3	rs2207136	chr6	50809720	C/T	I	1.5×10^{-11}	1.051	[1.036,1.066]	[TFAP2B]

15q22.2	rs7162310	chr15	63571234	C/T	I	1.7×10^{-11}	0.943	[0.927,0.959]	[APH1B]

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
rs12193446	TRUE	TRUE	TRUE	1.0000	0.026	0.64	0.0954	0.9946	0.9882	0.76	0.0947	v2v3v4
rs11606250	FALSE	FALSE	FALSE					0.9716	0.9313	0.088	0.8297	v2v3v4
rs7744813	FALSE	TRUE	TRUE	0.9991	0.89	0.40	0.4079	0.9913	0.9309	0.27	0.4071	v2v3v4
rs10500355	FALSE	FALSE	FALSE					0.9860	0.9681	0.095	0.6333	v2v3v4
rs524952	FALSE	FALSE	TRUE	1.0000	0.013	0.25	0.5239	0.9958	0.9643	0.060	0.5262	v2v3v4
rs3138141	FALSE	FALSE	FALSE					0.9861	0.9721	7.8×10^{-5}	0.7712	v3v4
rs10089517	FALSE	FALSE	TRUE	0.9936	0.059	0.063	0.6494	0.9874	0.9728	0.025	0.6452	v2v3v4
rs1550094	FALSE	TRUE	TRUE	0.9652	6.8×10^{-10}	1.9×10^{-5}	0.3067	0.9926	0.9326	0.22	0.3052	v2v3v4
rs869422	TRUE	TRUE	FALSE	0.9999	0.41	0.74	0.2157	0.9961	0.9777	0.85	0.2153	v2v3v4
rs2155413	TRUE	TRUE	TRUE	0.9998	0.34	0.064	0.5361	0.9960	0.9939	0.30	0.5319	v2v3v4
rs9585327	FALSE	FALSE	FALSE					0.9929	0.9864	0.22	0.5556	v2v3v4
rs2908972	FALSE	FALSE	TRUE	1.0000	0.26	0.59	0.6010	0.9815	0.9718	0.28	0.5981	v2v3v4
rs5022942	FALSE	FALSE	TRUE	1.0000	2.3×10^{-5}	0.41	0.7771	0.9983	0.9930	1.2×10^{-5}	0.7721	v2v3v4
rs10824518	FALSE	FALSE	FALSE					0.9916	0.9903	0.59	0.6461	v2v3v4
rs11145488	FALSE	FALSE	FALSE					0.9966	0.9930	0.24	0.7902	v2v3v4
rs17400325	FALSE	TRUE	TRUE	0.9998	0.24	0.067	0.9583	0.9834	0.9249	1.7×10^{-10}	0.9565	v2v3v4
rs61049169	FALSE	FALSE	FALSE					0.9902	0.9787	0.63	0.5593	v2v3v4
rs1556867	TRUE	TRUE	TRUE	0.9997	0.58	0.48	0.2330	0.9996	0.9989	0.43	0.2328	v2v3v4
rs10887265	FALSE	FALSE	FALSE					0.9277	0.9238	0.78	0.6763	v2v3v4
rs9866391	FALSE	FALSE	FALSE					0.9811	0.9383	0.020	0.6175	v2v3v4
rs9747347	FALSE	FALSE	FALSE					0.8344	0.7649	0.070	0.3738	v2v3v4
rs13380104	FALSE	FALSE	FALSE					0.9953	0.9835	0.063	0.4036	v2v3v4
rs2808510	FALSE	FALSE	FALSE					0.9926	0.9871	0.73	0.3822	v2v3v4
rs2181346	FALSE	FALSE	FALSE					0.7408	0.6697	0.39	0.3119	v2v3v4
rs56299331	FALSE	FALSE	FALSE					0.9875	0.9785	0.27	0.2025	v2v3v4
rs34217772	FALSE	FALSE	FALSE					0.9984	0.9953	0.014	0.1745	v2v3v4
rs12965607	FALSE	FALSE	FALSE					0.9496	0.9022	0.19	0.8539	v2v3v4
rs1793639	FALSE	FALSE	FALSE					0.9830	0.9621	0.27	0.5773	v2v3v4
rs13129838	FALSE	FALSE	FALSE					0.9229	0.9074	0.088	0.2826	v2v3v4
rs17428076	FALSE	FALSE	TRUE	1.0000	0.84	0.16	0.2363	0.9942	0.9910	0.48	0.2348	v2v3v4
rs11658305	FALSE	FALSE	FALSE					0.9165	0.8846	0.025	0.6085	v2v3v4
rs10511652	TRUE	TRUE	FALSE	0.9713	5.8×10^{-13}	9.8×10^{-50}	0.5994	0.9971	0.9825	0.17	0.5880	v2v3v4
rs5442	TRUE	TRUE	TRUE	0.9991	0.56	0.59	0.9336	0.9952	0.9929	0.51	0.9335	v2v3v4
rs4948523	FALSE	FALSE	FALSE					0.9943	0.9930	0.0071	0.5275	v2v3v4
rs34016308	FALSE	FALSE	FALSE					0.9841	0.9783	0.40	0.1659	v2v3v4
rs1064583	TRUE	TRUE	TRUE	0.9987	0.94	0.76	0.3889	1.0000	0.9998	0.95	0.3882	v2v3v4
rs201140091	FALSE	FALSE	FALSE					0.8150	0.8005	0.033	0.2682	v2v3v4
rs73157695	FALSE	FALSE	FALSE					0.9809	0.9711	0.23	0.7020	v2v3v4
rs479445	FALSE	FALSE	FALSE					0.9975	0.9875	0.056	0.6745	v2v3v4
rs297589	FALSE	FALSE	FALSE					0.8998	0.8746	0.15	0.3093	v2v3v4
rs1550870	TRUE	TRUE	TRUE	0.9983	0.022	0.87	0.4609	0.9989	0.9951	0.35	0.4587	v2v3v4
rs2799081	FALSE	FALSE	FALSE					0.9982	0.9974	0.031	0.7354	v2v3v4
rs826220	FALSE	FALSE	FALSE					0.9975	0.9950	0.17	0.5968	v2v3v4
rs10512441	FALSE	TRUE	TRUE	0.9999	0.017	0.46	0.2012	0.9855	0.8263	0.075	0.2023	v2v3v4
rs7968679	FALSE	FALSE	FALSE					0.9814	0.9709	0.0021	0.3038	v2v3v4
rs2342406	FALSE	TRUE	FALSE	0.9995	0.91	0.27	0.8083	0.9851	0.9171	0.63	0.8091	v2v3v4
rs71041628	FALSE	FALSE	FALSE					0.8855	0.8746	0.0013	0.3810	v2v3v4
rs10892173	FALSE	FALSE	FALSE					0.9946	0.9857	0.32	0.4030	v2v3v4
rs2207136	FALSE	FALSE	FALSE					0.9824	0.9767	0.0054	0.5511	v2v3v4
rs7162310	FALSE	FALSE	FALSE					0.9990	0.9953	0.19	0.2212	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
rs12193446	68256	16488	1009	85757	0.1076	88839	16416	829	106086	0.0850
rs11606250				85757	0.8425				106086	0.8201
rs7744813	26276	39453	14100	85757	0.4231	36189	46636	15314	106086	0.3936
rs10500355				85757	0.6508				106086	0.6217
rs524952	2824	6710	3933	85757	0.5427	3760	7651	4036	106086	0.5136
rs3138141				79302	0.7588				97352	0.7825
rs10089517	1755	6231	5397	85757	0.6330	1757	6913	6679	106086	0.6555
rs1550094	37631	32437	6499	85757	0.2939	43744	41278	9228	106086	0.3140
rs869422	43456	25388	3444	85757	0.2226	57188	29475	3971	106086	0.2060
rs2155413	17704	42366	25665	85757	0.5430	23526	52969	29567	106086	0.5251
rs9585327				85757	0.5657				106086	0.5477
rs2908972	2029	6355	5083	85757	0.6097	2608	7428	5411	106086	0.5920
rs5022942	652	4533	8282	85757	0.7848	828	5347	9272	106086	0.7690
rs10824518				85757	0.6519				106086	0.6356
rs11145488				85757	0.7963				106086	0.7831
rs17400325	118	5802	73751	85757	0.9613	204	8276	89450	106086	0.9545
rs61049169				85757	0.5470				106086	0.5643
rs1556867	51303	30044	4390	85757	0.2263	61329	38716	6011	106086	0.2391
rs10887265				85757	0.6849				106086	0.6703
rs9866391				85757	0.6065				106086	0.6220
rs9747347				85757	0.3684				106086	0.3820
rs13380104				85757	0.3983				106086	0.4130
rs2808510				85757	0.3770				106086	0.3912
rs2181346				85757	0.3044				106086	0.3171
rs56299331				85757	0.1946				106086	0.2061
rs34217772				85757	0.1718				106086	0.1825
rs12965607				85757	0.8591				106086	0.8491
rs1793639				85757	0.5703				106086	0.5849
rs13129838				85757	0.2758				106086	0.2878
rs17428076	7809	4888	770	85757	0.2409	9148	5504	795	106086	0.2289
rs11658305				85757	0.6020				106086	0.6151

rs10511652	11281	34437	24438	85757	0.5820	13365	42754	32020	106086	0.5951
rs5442	365	10123	75187	85757	0.9363	502	13843	91640	106086	0.9295
rs4948523				85757	0.5364				106086	0.5221
rs34016308				85757	0.1702				106086	0.1607
rs1064583	32689	40395	12565	85757	0.3827	38774	50622	16569	106086	0.3953
rs201140091				85757	0.2638				106086	0.2738
rs73157695				85757	0.7082				106086	0.6970
rs479445				85757	0.6833				106086	0.6709
rs297589				85757	0.3034				106086	0.3145
rs1550870	24181	42482	18935	85757	0.4694	31415	52323	22166	106086	0.4563
rs2799081				85757	0.7429				106086	0.7316
rs826220				85757	0.6051				106086	0.5920
rs10512441	51846	24707	3124	85757	0.1945	61877	31944	4108	106086	0.2051
rs7968679				85757	0.2995				106086	0.3102
rs2342406	2633	20862	42691	85757	0.8037	2869	25185	54405	106086	0.8135
rs71041628				85757	0.3757				106086	0.3867
rs10892173				85757	0.3990				106086	0.4103
rs2207136				85757	0.5407				106086	0.5534
rs7162310				85757	0.2240				106086	0.2143

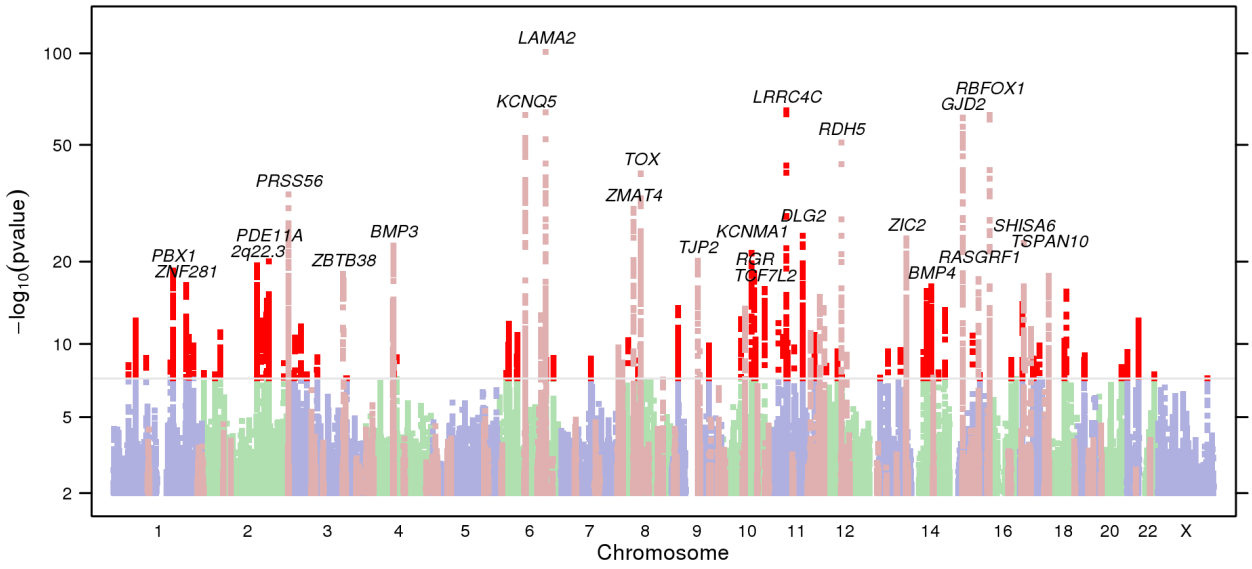
Annotations from NHGRI GWAS Catalog

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
6q22.33	129820038	rs12193446	5.4×10^{-102}	0	1.000	rs12193446	1.0×10^{-8}	24144296	Axial length	LAMA2, ARHGAP18
6q22.33	129820038	rs12193446	5.4×10^{-102}	14591	0.551	rs12205363	2.0×10^{-12}	23396134	Refractive error	LAMA2
6q13	73643289	rs7744813	1.9×10^{-63}	0	1.000	rs7744813	4.0×10^{-9}	23396134	Refractive error	KCNQ5
16p13.3	7459347	rs10500355	2.0×10^{-63}	0	1.000	rs10500355	4.0×10^{-9}	23474815	Refractive error	RBFOX1
16p13.3	7459347	rs10500355	2.0×10^{-63}	336	1.000	rs17648524	6.0×10^{-10}	23396134	Refractive error	RBFOX1
15q14	35005886	rs524952	3.5×10^{-62}	−16260	0.591	rs11073058	4.0×10^{-11}	24144296	Axial length	GJD2, ACTC1
15q14	35005886	rs524952	3.5×10^{-62}	0	1.000	rs524952	1.0×10^{-15}	23396134	Refractive error	GJD2
15q14	35005886	rs524952	3.5×10^{-62}	187	1.000	rs634990	2.0×10^{-14}	20835239	Refractive error	GJD2,ACTC1,GOLGA8B
8q12.1	60178721	rs10089517	6.0×10^{-41}	0	1.000	rs10089517	2.0×10^{-6}	22589738	Visceral adipose tissue/subcutaneous adipose tissue ratio	TOX
8q12.1	60178721	rs10089517	6.0×10^{-41}	365	0.576	rs7837791	4.0×10^{-12}	23396134	Refractive error	CHD7, TOX
8p11.21	40723970	rs869422	4.0×10^{-31}	2424	1.000	rs7829127	4.0×10^{-10}	23396134	Refractive error	ZMAT4
17p12	11407259	rs2908972	5.3×10^{-24}	642	0.621	rs2969180	7.0×10^{-11}	23396134	Refractive error	SHISA6
9q21.11	71770939	rs11145488	6.7×10^{-21}	−4346	1.000	rs11145465	7.0×10^{-9}	23396134	Refractive error	TJP2
3q23	141076084	rs9866391	7.7×10^{-19}	2104	0.685	rs9857275	2.0×10^{-6}	22210626	Prion diseases	ZBTB38, RASA2
3q23	141076084	rs9866391	7.7×10^{-19}	18125	0.547	rs6440003	2.0×10^{-10}	21998595	Height	ZBTB38
3q23	141076084	rs9866391	7.7×10^{-19}	18125	0.547	rs6440003	2.0×10^{-24}	18391952	Height	ZBTB38
3q23	141076084	rs9866391	7.7×10^{-19}	26749	0.542	rs6763931	2.0×10^{-8}	21743467	Prostate cancer	ZBTB38
3q23	141076084	rs9866391	7.7×10^{-19}	26749	0.542	rs6763931	3.0×10^{-12}	19343178	Height	ZBTB38
3q23	141076084	rs9866391	7.7×10^{-19}	26749	0.542	rs6763931	1.0×10^{-27}	18391951	Height	ZBTB38
3q23	141076084	rs9866391	7.7×10^{-19}	29486	0.542	rs724016	3.0×10^{-86}	20881960	Height	ZBTB38
3q23	141076084	rs9866391	7.7×10^{-19}	29486	0.542	rs724016	8.0×10^{-22}	18391950	Height	ZBTB38
3q23	141076084	rs9866391	7.7×10^{-19}	29486	0.542	rs724016	1.0×10^{-6}	18193045	Height	ZBTB38
3q23	141076084	rs9866391	7.7×10^{-19}	57366	0.509	rs1991431	4.0×10^{-47}	23563607	Height	ZBTB38
15q25.1	79378821	rs13380104	4.3×10^{-18}	−5946	0.899	rs4778879	4.0×10^{-11}	23396134	Refractive error	RASGRF1
15q25.1	79378821	rs13380104	4.3×10^{-18}	85026	0.660	rs1474256	6.0×10^{-6}	23897914	Bronchopulmonary dysplasia	RASGRF1, LOC729911
10q25.2	114788436	rs56299331	1.1×10^{-16}	−34348	0.543	rs7901695	1.0×10^{-6}	21347282	Coronary heart disease	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−34348	0.543	rs7901695	1.0×10^{-48}	17463249	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−32395	0.545	rs4506565	1.0×10^{-8}	20081858	Fasting glucose-related traits	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−32395	0.545	rs4506565	5.0×10^{-12}	17554300	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	2.0×10^{-15}	23945395	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	9.0×10^{-75}	23300278	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	1.0×10^{-35}	23209189	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	4.0×10^{-21}	22693455	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	3.0×10^{-6}	22581228	Fasting insulin-related traits (interaction with BMI)	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	2.0×10^{-14}	22581228	Fasting glucose-related traits (interaction with BMI)	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	2.0×10^{-15}	22101970	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	2.0×10^{-20}	21873549	Proinsulin levels	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	1.0×10^{-7}	20849430	Glycated hemoglobin levels	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	7.0×10^{-7}	20694148	Metabolic syndrome	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	2.0×10^{-51}	20581827	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	1.0×10^{-30}	19734900	Type 2 diabetes and other traits	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	8.0×10^{-12}	19401414	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	9.0×10^{-30}	19056611	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	3.0×10^{-23}	18372903	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	5.0×10^{-8}	17668382	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	1.0×10^{-8}	17463248	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	2.0×10^{-31}	17463246	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	2.0×10^{-10}	17460697	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	2.0×10^{-34}	17293876	Type 2 diabetes	TCF7L2
10q25.2	114788436	rs56299331	1.1×10^{-16}	379	0.687	rs12243326	1.0×10^{-7}	20081857	Two-hour glucose challenge	TCF7L2
4q21.21	80508788	rs13129838	2.6×10^{-15}	21883	0.618	rs9307551	1.0×10^{-8}	23396134	Refractive error	LOC100506035
17p13.1	7429321	rs11658305	7.9×10^{-15}	−11658	0.860	rs6761	3.0×10^{-7}	18464913	Protein quantitative trait loci	SHBG

10q21.1	60339098	rs4948523	2.8×10^{-14}	−73694	0.927	rs7084402	2.0×10^{-13}	23396134	Refractive error	BICC1
10q21.1	60339098	rs4948523	2.8×10^{-14}	−20201	0.948	rs1658442	3.0×10^{-6}	23322567	Corneal astigmatism	
6q22.1	116446576	rs1064583	1.6×10^{-13}	−2841	0.989	rs3812111	2.0×10^{-8}	23455636	Age-related macular degeneration	COL10A1
6p22.1	28270584	rs2799081	1.2×10^{-12}	51712	0.791	rs6903823	2.0×10^{-10}	21946350	Pulmonary function	ZKSCAN3, ZNF323
17q11.2	31239645	rs10512441	3.8×10^{-12}	−161373	0.924	rs17183295	1.0×10^{-10}	23396134	Refractive error	MYO1D

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, $r^2 > 0.8$).

region	position	our.name	our.pval	dist	rsqr	assay.name	pvalue	pubmed.id	trait	genes
1p21.3	99524047	rs10747502	0.37	0	1.000	rs10747502	1.0×10^{-9}	23049088	Myopia (pathological)	LOC100129620
1q42.2	230922951	rs12038826	0.75	0	1.000	rs12038826	7.0×10^{-6}	23049088	Myopia (pathological)	CAPN9
1q44	249168436	rs12032643	0.35	0	1.000	rs12032643	1.0×10^{-9}	23049088	Myopia (pathological)	Intergenic
2p16.2	54718181	rs4557020	0.070	0	1.000	rs4557020	3.0×10^{-7}	22685421	Myopia (pathological)	SPTBN1
2p13.1	74939176	rs1137	0.029	0	1.000	rs1137	4.0×10^{-6}	22685421	Myopia (pathological)	SEMA4F
3p14.2	59928851	rs931317	0.96	0	1.000	rs931317	3.0×10^{-6}	23049088	Myopia (pathological)	FHIT
3p12.1	86255672	rs7428796	0.018	0	1.000	rs7428796	2.0×10^{-18}	23049088	Myopia (pathological)	Intergenic
3q23	140247177	rs4683505	0.60	0	1.000	rs4683505	4.0×10^{-7}	23049088	Myopia (pathological)	CLSTN2
3q24	143902027	rs4839680	0.68	0	1.000	rs4839680	1.0×10^{-15}	23049088	Myopia (pathological)	Intergenic
3q26.32	177766464	rs7634528	0.65	0	1.000	rs7634528	1.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
3q27.3	186466252	rs1656966	0.99	0	1.000	rs1656966	4.0×10^{-21}	23049088	Myopia (pathological)	Intergenic
3q27.3	187687890	rs16862782	0.64	0	1.000	rs16862782	5.0×10^{-7}	23049088	Myopia (pathological)	Intergenic
4p16.1	10726853	rs16872571	0.92	0	1.000	rs16872571	2.0×10^{-10}	23049088	Myopia (pathological)	Intergenic
4p15.2	24578097	rs6841898	0.19	0	1.000	rs6841898	3.0×10^{-26}	23049088	Myopia (pathological)	DHX15
4q25	112611750	rs10034228	0.24	0	1.000	rs10034228	8.0×10^{-13}	21505071	Myopia (pathological)	MYP11
4q25	112702635	rs1585471	0.22	0	1.000	rs1585471	2.0×10^{-6}	21505071	Myopia (pathological)	MYP11
4q33	170880883	rs11723530	0.40	0	1.000	rs11723530	4.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
4q35.2	189120911	rs6857559	0.48	0	1.000	rs6857559	3.0×10^{-21}	23049088	Myopia (pathological)	Intergenic
5p15.31	7368845	rs13172324	0.87	0	1.000	rs13172324	3.0×10^{-10}	23049088	Myopia (pathological)	Intergenic
5p15.2	11169945	rs6885224	0.41	0	1.000	rs6885224	8.0×10^{-6}	21095009	Myopia (pathological)	CTNND2
5p13.1	39979172	rs10053502	0.096	0	1.000	rs10053502	1.0×10^{-16}	23049088	Myopia (pathological)	Intergenic
5q11.1	50026465	rs282544	0.0083	0	1.000	rs282544	4.0×10^{-6}	22685421	Myopia (pathological)	PARP8
5q31.3	141189168	rs248471	0.62	0	1.000	rs248471	2.0×10^{-6}	23406873	Myopia (pathological)	PCDH1
5q33.1	150473674	rs999556	0.32	0	1.000	rs999556	1.0×10^{-15}	23049088	Myopia (pathological)	Intergenic
6p24.3	7743663	rs9505270	0.69	0	1.000	rs9505270	4.0×10^{-7}	23049088	Myopia (pathological)	BMP6
6q21	108017671	rs12525668	0.52	0	1.000	rs12525668	8.0×10^{-11}	23049088	Myopia (pathological)	Intergenic
6q22.1	117605991	rs13201929	0.23	0	1.000	rs13201929	3.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
6q24.3	147971574	rs1302019	0.78	0	1.000	rs1302019	2.0×10^{-23}	23049088	Myopia (pathological)	Intergenic
7p14.1	38004406	rs1668357	0.46	0	1.000	rs1668357	4.0×10^{-8}	23049088	Myopia (pathological)	Intergenic
7q21.3	97422926	rs1229542	0.39	0	1.000	rs1229542	2.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
7q22.3	104758250	rs6968355	0.047	0	1.000	rs6968355	2.0×10^{-7}	23049088	Myopia (pathological)	SRPK2
7q36.3	157387441	rs10274279	0.53	0	1.000	rs10274279	4.0×10^{-11}	23049088	Myopia (pathological)	PTPRN2
7q36.3	158846929	rs2730260	0.0030	0	1.000	rs2730260	9.0×10^{-14}	23406873	Myopia (pathological)	VIPR2
8p23.1	8890098	rs1045529	6.8×10^{-6}	0	1.000	rs1045529	3.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
8p23.1	8990577	rs189798	0.089	0	1.000	rs189798	6.0×10^{-7}	23049088	Myopia (pathological)	PPP1R3B, MYP10, MIR4660, MIR124-1, MSRA
8p23.1	9814411	rs656319	0.0043	0	1.000	rs656319	3.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
8p23.1	11612698	rs804280	0.045	0	1.000	rs804280	4.0×10^{-6}	23049088	Myopia (pathological)	GATA4
8q12.1	56599548	rs4737395	0.80	0	1.000	rs4737395	5.0×10^{-9}	23049088	Myopia (pathological)	Intergenic
8q12.1	60961821	rs569688	0.083	0	1.000	rs569688	4.0×10^{-7}	23049088	Myopia (pathological)	Intergenic
8q13.1	66822030	rs6472235	0.017	0	1.000	rs6472235	1.0×10^{-7}	23049088	Myopia (pathological)	Intergenic
8q21.13	82151747	rs12216812	0.76	0	1.000	rs12216812	3.0×10^{-9}	23049088	Myopia (pathological)	Intergenic

8q23.1	110217266	rs7823896	0.57	0	1.000	rs7823896	3.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
8q24.12	121562418	rs7839488	0.00026	0	1.000	rs7839488	8.0×10^{-12}	23406873	Myopia (pathological)	SNTB1
8q24.12	121568921	rs4395927	0.00019	0	1.000	rs4395927	8.0×10^{-12}	23406873	Myopia (pathological)	SNTB1
8q24.12	121583283	rs4455882	7.9×10^{-5}	0	1.000	rs4455882	8.0×10^{-12}	23406873	Myopia (pathological)	SNTB1
9p24.1	7734250	rs10758892	0.66	0	1.000	rs10758892	9.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
9p23	9924724	rs7849581	0.79	0	1.000	rs7849581	9.0×10^{-7}	23049088	Myopia (pathological)	PTPRD
9q31.1	107588777	rs4149311	0.69	0	1.000	rs4149311	9.0×10^{-6}	23049088	Myopia (pathological)	ABCA1
9q33.3	126154354	rs872863	0.88	0	1.000	rs872863	2.0×10^{-11}	23049088	Myopia (pathological)	DENND1A
10p15.1	6315794	rs7077335	0.93	0	1.000	rs7077335	2.0×10^{-12}	23049088	Myopia (pathological)	Intergenic
10q25.3	115235114	rs1472750	0.31	0	1.000	rs1472750	5.0×10^{-9}	23049088	Myopia (pathological)	Intergenic
10q26.13	123913330	rs17103138	0.74	0	1.000	rs17103138	2.0×10^{-7}	23049088	Myopia (pathological)	TACC2
11q12.1	56242261	rs7939886	0.0057	0	1.000	rs7939886	2.0×10^{-7}	23049088	Myopia (pathological)	Intergenic
11q22.1	100043420	rs12803066	0.21	0	1.000	rs12803066	4.0×10^{-6}	23049088	Myopia (pathological)	CNTN5
11q24.1	122030190	rs577948	0.14	0	1.000	rs577948	2.0×10^{-7}	19779542	Myopia (pathological)	BLID, LOC399959
11q24.3	128582557	rs665440	0.66	0	1.000	rs665440	2.0×10^{-8}	23049088	Myopia (pathological)	FLI1
11q25	134482466	rs1944866	0.68	0	1.000	rs1944866	2.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
11q25	134626887	rs11223996	0.36	0	1.000	rs11223996	7.0×10^{-7}	23049088	Myopia (pathological)	Intergenic
12p13.31	6683287	rs1057510	0.16	0	1.000	rs1057510	6.0×10^{-6}	23049088	Myopia (pathological)	CHD4
12q21.2	77899510	rs17788937	0.52	0	1.000	rs17788937	4.0×10^{-15}	23049088	Myopia (pathological)	Intergenic
13q12.11	23294033	rs373767	0.29	0	1.000	rs373767	3.0×10^{-10}	22685421	Myopia (pathological)	ZC3H11B
13q12.12	24432467	rs9318086	0.41	0	1.000	rs9318086	2.0×10^{-16}	21640322	Myopia (pathological)	MIPEP, C1QTNF9B-AS1, C1QTNF9B
13q14.13	45900267	rs7323755	0.42	0	1.000	rs7323755	2.0×10^{-13}	23049088	Myopia (pathological)	Intergenic
13q22.1	73741149	rs11838472	0.50	0	1.000	rs11838472	3.0×10^{-17}	23049088	Myopia (pathological)	Intergenic
13q33.2	106096812	rs11618212	0.63	0	1.000	rs11618212	5.0×10^{-12}	23049088	Myopia (pathological)	Intergenic
15q21.3	58080617	rs1559777	0.39	0	1.000	rs1559777	1.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
15q24.1	74305966	rs8039584	0.12	0	1.000	rs8039584	5.0×10^{-8}	23049088	Myopia (pathological)	PML
16q21	60733603	rs17822114	0.36	0	1.000	rs17822114	3.0×10^{-18}	23049088	Myopia (pathological)	Intergenic
16q21	62100211	rs8050940	0.12	0	1.000	rs8050940	1.0×10^{-26}	23049088	Myopia (pathological)	Intergenic
17p13.2	3393068	rs923375	0.52	0	1.000	rs923375	4.0×10^{-16}	23049088	Myopia (pathological)	ASPA
17p12	11803461	rs4792192	0.77	0	1.000	rs4792192	3.0×10^{-6}	23049088	Myopia (pathological)	DNAH9
17q11.2	29333516	rs17826255	0.0093	0	1.000	rs17826255	8.0×10^{-9}	23049088	Myopia (pathological)	LOC646021
17q25.3	78737287	rs7215564	0.77	0	1.000	rs7215564	2.0×10^{-6}	23049088	Myopia (pathological)	KIAA1303
19q12	30990700	rs3786800	0.099	0	1.000	rs3786800	3.0×10^{-12}	23049088	Myopia (pathological)	ZNF536
19q13.31	44888276	rs4142248		0	1.000	rs4142248	3.0×10^{-15}	23049088	Myopia (pathological)	ZNF285A
21q22.13	37809377	rs9984974	0.32	0	1.000	rs9984974	2.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
22q12.2	29793641	rs2267138	0.87	0	1.000	rs2267138	3.0×10^{-6}	23049088	Myopia (pathological)	Intergenic
2q37.1	233379941	rs1656404	1.2×10^{-20}	0	1.000	rs1656404	8.0×10^{-11}	23396134	Refractive error	PRSS56
2q37.1	233406998	rs1881492	1.1×10^{-15}	0	1.000	rs1881492	5.0×10^{-11}	23396134	Refractive error	CHRNG, PRSS56
3p21.1	53847408	rs14165	1.9×10^{-5}	0	1.000	rs14165	2.0×10^{-8}	23396134	Refractive error	CACNA1D
4q21.21	80530671	rs9307551	3.7×10^{-14}	0	1.000	rs9307551	1.0×10^{-8}	23396134	Refractive error	LOC100506035
4q21.21	81930814	rs1960445	5.2×10^{-13}	0	1.000	rs1960445	1.0×10^{-6}	23396134	Refractive error	BMP3
6q13	73643289	rs7744813	1.9×10^{-63}	0	1.000	rs7744813	4.0×10^{-9}	23396134	Refractive error	KCNQ5
6q22.33	129834629	rs12205363	7.3×10^{-65}	0	1.000	rs12205363	2.0×10^{-12}	23396134	Refractive error	LAMA2
8p11.21	40726394	rs7829127	4.2×10^{-31}	0	1.000	rs7829127	4.0×10^{-10}	23396134	Refractive error	ZMAT4
8q12.1	60179086	rs7837791	1.4×10^{-23}	0	1.000	rs7837791	4.0×10^{-12}	23396134	Refractive error	CHD7, TOX
9q21.11	71766593	rs11145465	6.8×10^{-21}	0	1.000	rs11145465	7.0×10^{-9}	23396134	Refractive error	TJP2
9q21.13	77149837	rs7042950	4.3×10^{-10}	0	1.000	rs7042950	4.0×10^{-8}	23396134	Refractive error	RORB
10q21.1	60265404	rs7084402	1.6×10^{-13}	0	1.000	rs7084402	2.0×10^{-13}	23396134	Refractive error	BICC1
10q23.33	94924324	rs10882165	0.00081	0	1.000	rs10882165	1.0×10^{-11}	23396134	Refractive error	CYP26A1
11q22.3	105556598	rs11601239	1.1×10^{-8}	0	1.000	rs11601239	6.0×10^{-9}	23396134	Refractive error	GRIA4
12q13.2	56114769	rs3138144	2.4×10^{-25}	0	1.000	rs3138144	4.0×10^{-12}	23396134	Refractive error	RDH5
12q15	71249996	rs12229663	2.4×10^{-9}	0	1.000	rs12229663	5.0×10^{-9}	23396134	Refractive error	PTPRR
13q32.3	100818092	rs2184971	1.4×10^{-7}	0	1.000	rs2184971	2.0×10^{-8}	23396134	Refractive error	PCCA, ZIC2
14q23.1	60903757	rs1254319	1.7×10^{-6}	0	1.000	rs1254319	1.0×10^{-8}	23396134	Refractive error	SIX6
15q14	35005886	rs524952	3.5×10^{-62}	0	1.000	rs524952	1.0×10^{-15}	23396134	Refractive error	GJD2
15q14	35006073	rs634990	5.0×10^{-62}	0	1.000	rs634990	2.0×10^{-14}	20835239	Refractive error	GJD2,ACTC1,GOLGA8B
15q25.1	79372875	rs4778879	6.2×10^{-18}	0	1.000	rs4778879	4.0×10^{-11}	23396134	Refractive error	RASGRF1
15q25.1	79451869	rs939658	5.9×10^{-7}	0	1.000	rs939658	2.0×10^{-9}	20835236	Refractive error	RASGRF1
16p13.3	7459347	rs10500355	2.0×10^{-63}	0	1.000	rs10500355	4.0×10^{-9}	23474815	Refractive error	RBFOX1
16p13.3	7459683	rs17648524	2.2×10^{-63}	0	1.000	rs17648524	6.0×10^{-10}	23396134	Refractive error	RBFOX1
17p12	11407901	rs2969180	2.4×10^{-15}	0	1.000	rs2969180	7.0×10^{-11}	23396134	Refractive error	SHISA6
17q11.2	31078272	rs17183295	7.8×10^{-11}	0	1.000	rs17183295	1.0×10^{-10}	23396134	Refractive error	MYO1D
17q24.3	68718734	rs4793501	3.8×10^{-7}	0	1.000	rs4793501	3.0×10^{-8}	23396134	Refractive error	KCNJ2
18q22.3	72174023	rs12971120	0.034	0	1.000	rs12971120	2.0×10^{-7}	23396134	Refractive error	CNDP2
20p12.3	6761765	rs235770	3.0×10^{-5}	0	1.000	rs235770	2.0×10^{-8}	23396134	Refractive error	BMP2

Nearby Nonsynonymous SNPs

region	position	our.name	our.pval	dist	rsqr	assay.name	gene	aa.chg
2q37.1	233385396	rs1550094	9.2×10^{-35}	0	1.000	rs1550094	PRSS56	A30T
2q31.2	178565913	rs17400325	9.6×10^{-21}	0	1.000	rs17400325	PDE11A	Y727C
17q25.3	79606820	rs9747347	1.6×10^{-18}	5577	0.919	rs6420484	TSPAN10	Y139C
12p13.31	6954864	rs5442	2.3×10^{-14}	0	1.000	rs5442	GNB3	G272S
6q22.1	116446576	rs1064583	1.6×10^{-13}	0	1.000	rs1064583	COL10A1	M27T
2q24.1	157358750	rs297589	5.8×10^{-13}	47499	0.819	rs2116665	GPD2	R264H
6p22.1	28270584	rs2799081	1.2×10^{-12}	−921	0.720	rs1997660	PGBD1	I678V

6p22.1	28270584	rs2799081	1.2×10^{-12}	23966	0.521	rs853684	ZSCAN31	K205R
6p22.1	28270584	rs2799081	1.2×10^{-12}	87736	0.604	rs1361385	ZSCAN12	C583R
6p22.1	28270584	rs2799081	1.2×10^{-12}	87751	0.604	rs1416918	ZSCAN12	R578G
12p13.31	9313304	rs7968679	3.8×10^{-12}	−81036	0.692	rs669	A2M	I1000V
12p13.31	9313304	rs7968679	3.8×10^{-12}	−10008	0.981	rs10842971	PZP	I1443N

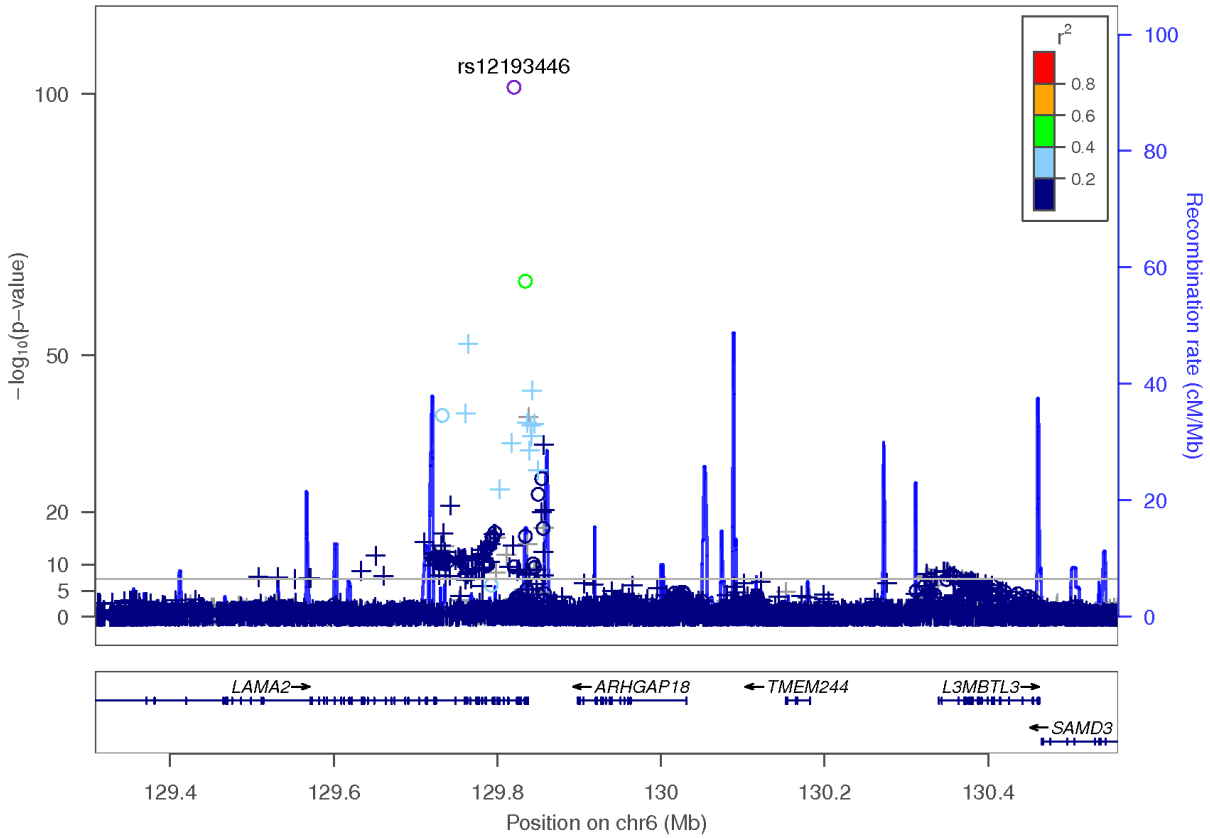
Nearby Expression QTLs

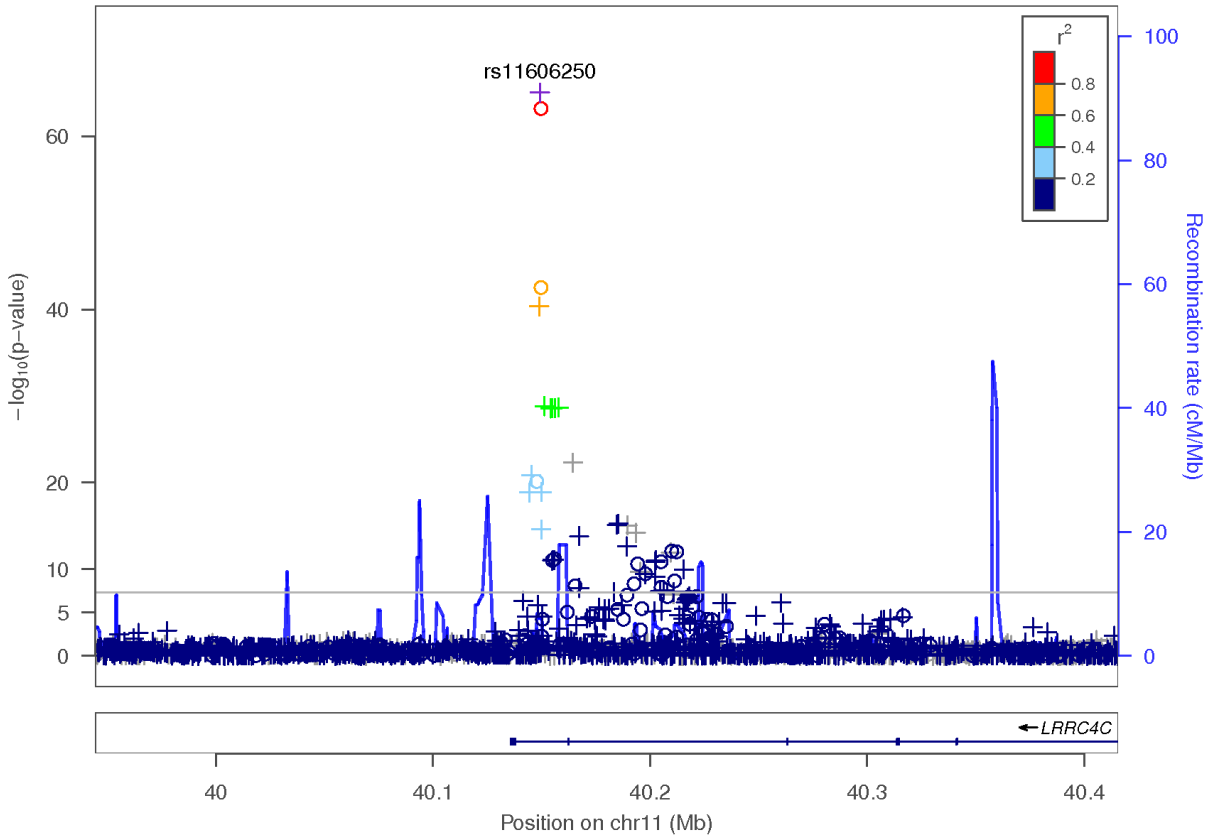
region	position	our.name	our.pval	dist	rsqr	assay.name	eqtl.dist	eqtl.gene	eqtl.pval	eqtl.rsqr	tissue	pubmed.id
12q13.2	56115778	rs3138141	1.5×10^{-51}	−193	0.975	rs3138142	728519	MIP	7.2×10^{-5}	0.055	B-Cell	22446964
12q13.2	56115778	rs3138141	1.5×10^{-51}	−193	0.975	rs3138142	2823	RDH5	2.7×10^{-42}	0.485	Monocyte	22446964
12q13.2	56115778	rs3138141	1.5×10^{-51}	−193	0.975	rs3138142	2823	RDH5	5.2×10^{-26}	0.329	B-Cell	22446964
2q37.1	233385396	rs1550094	9.2×10^{-35}	−9612	0.705	rs2117770	359210	ILMN_18124	0.00034	0.162	Lymphoblastoid	19644074
13q32.3	100689354	rs9585327	8.9×10^{-25}	2013	0.652	rs8000973	49970	PCCA	2.0×10^{-8}	0.024	Monocyte	20502693
3q23	141076084	rs9866391	7.7×10^{-19}	17201	0.612	rs7624084	368312	RNF7	0.0011	0.038	B-Cell	22446964
17p13.1	7429321	rs11658305	7.9×10^{-15}	−66233	0.624	rs9217	−2403	CHRNB1	2.4×10^{-22}	0.287	Monocyte	22446964
17p13.1	7429321	rs11658305	7.9×10^{-15}	−23187	0.662	rs11658168	45202	CHRNB1	3.1×10^{-66}	0.184	Monocyte	20502693
10q21.1	60339098	rs4948523	2.8×10^{-14}	−67274	0.588	rs7069916	318910	HS.100261	4.4×10^{-5}	0.058	Monocyte	22446964
6q22.1	116446576	rs1064583	1.6×10^{-13}	−23277	0.611	rs509002	143014	NT5DC1	0.0011	0.037	Monocyte	22446964
6q22.1	116446576	rs1064583	1.6×10^{-13}	−7356	0.577	rs515745	17221	NT5DC1	7.4×10^{-15}	0.151	Lymphoblastoid	24037378
6q22.1	116446576	rs1064583	1.6×10^{-13}	100348	0.540	rs1204804	235609	FAM26F	1.3×10^{-7}	0.021	Monocyte	20502693
6p22.1	28270584	rs2799081	1.2×10^{-12}	−83483	0.510	rs1736891	213941	ZSCAN23	0.00085	0.039	B-Cell	22446964
6p22.1	28270584	rs2799081	1.2×10^{-12}	29752	0.623	rs17312661	−460639	HIST1H3I	0.00018	0.049	B-Cell	22446964
6p22.1	28270584	rs2799081	1.2×10^{-12}	54724	0.723	rs6922111	0	ZKSCAN3	2.1×10^{-8}	0.024	Monocyte	20502693
6p22.1	28270584	rs2799081	1.2×10^{-12}	119646	0.590	rs16894095	590925	HIST1H4K	5.8×10^{-6}	0.016	Monocyte	20502693
6p22.1	28270584	rs2799081	1.2×10^{-12}	256071	0.558	rs414745	−429050	ZSCAN16	0.00030	0.046	Monocyte	22446964
6p22.1	28270584	rs2799081	1.2×10^{-12}	263362	0.558	rs418092	−728240	HIST1H2AK	0.00090	0.039	B-Cell	22446964
6p22.1	28270584	rs2799081	1.2×10^{-12}	272680	0.643	rs17336532	−273277	PGBD1	4.4×10^{-5}	0.058	B-Cell	22446964
6p22.1	28270584	rs2799081	1.2×10^{-12}	276368	0.722	rs16901848	−2261548	HIST1H4H	0.00031	0.045	Monocyte	22446964
17q11.2	31239645	rs10512441	3.8×10^{-12}	−203152	0.915	rs9912761	216865	MYO1D	1.5×10^{-6}	0.274	T-cell	19644074
17q11.2	31239645	rs10512441	3.8×10^{-12}	−52429	0.932	rs17781142	0	MYO1D	4.2×10^{-74}	0.204	Monocyte	20502693
12p13.31	9313304	rs7968679	3.8×10^{-12}	−199751	0.685	rs1805664	−14101	C12orf33	3.4×10^{-5}		Liver	18462017
12p13.31	9313304	rs7968679	3.8×10^{-12}	−94698	0.686	rs10771309	124548	PHC1	4.9×10^{-11}	0.031	Monocyte	20502693

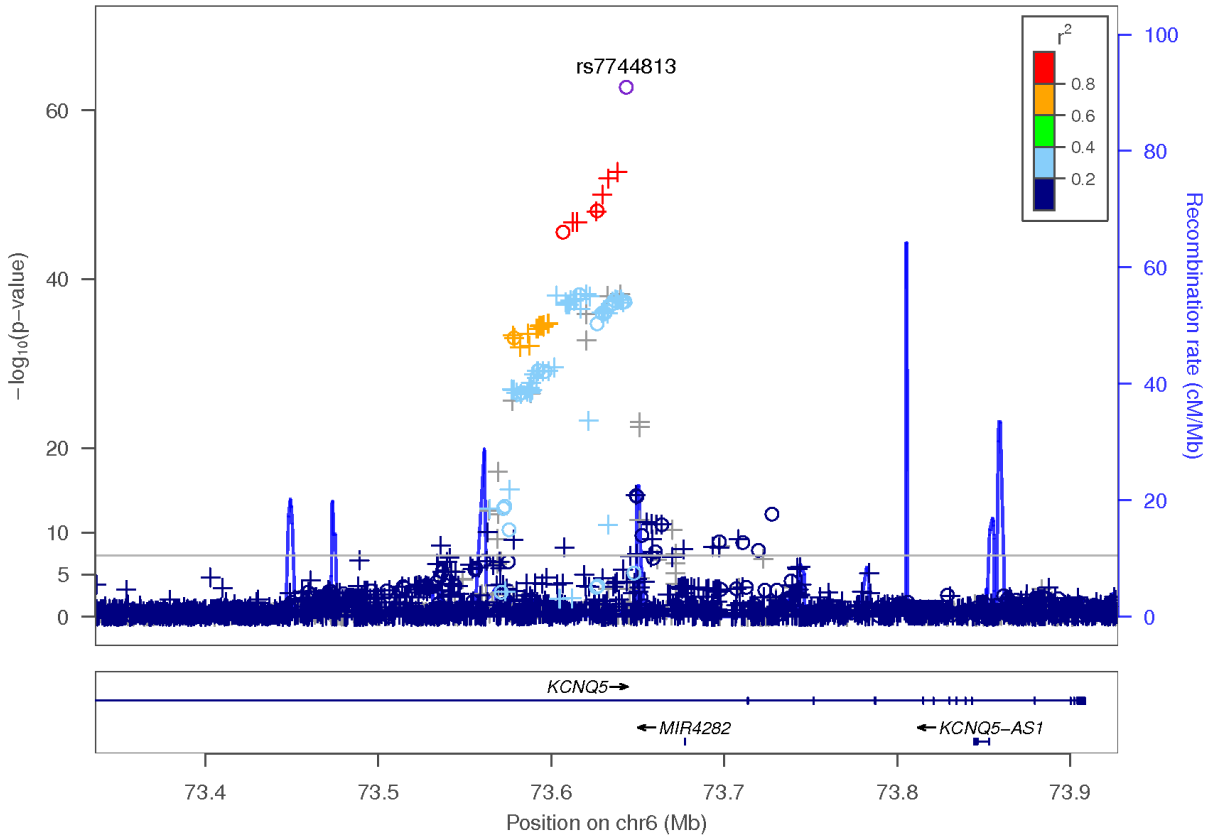
Nearby Clinical Variants

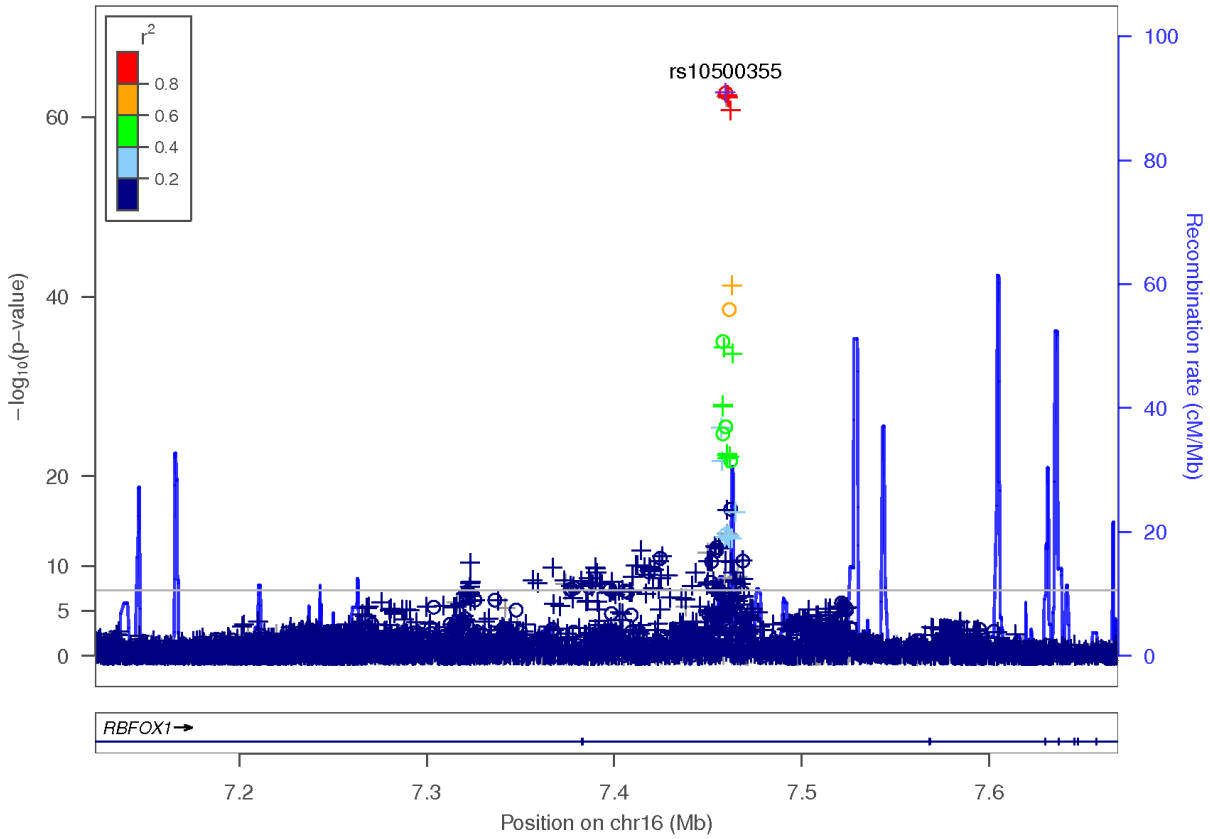
source	region	our.name	our.pval	dist	rsqr	assay.name	gene	phenotype	accession
clinvar	10q25.2	rs56299331	1.1×10^{-16}	−30087	0.593	rs7903146	TCF7L2	Diabetes mellitus type 2	SNOMED CT44054006
clinvar	10q25.2	rs56299331	1.1×10^{-16}	20466	0.665	rs12255372	TCF7L2	Diabetes mellitus type 2	SNOMED CT44054006
clinvar	12p13.31	rs7968679	3.8×10^{-12}	−81036	0.692	rs669	A2M	Alzheimer’s disease	SNOMED CT26929004
clinvar	12p13.31	rs7968679	3.8×10^{-12}	−81036	0.692	rs669	A2M	Alpha-2-macroglobulin deficiency	NCBI curation

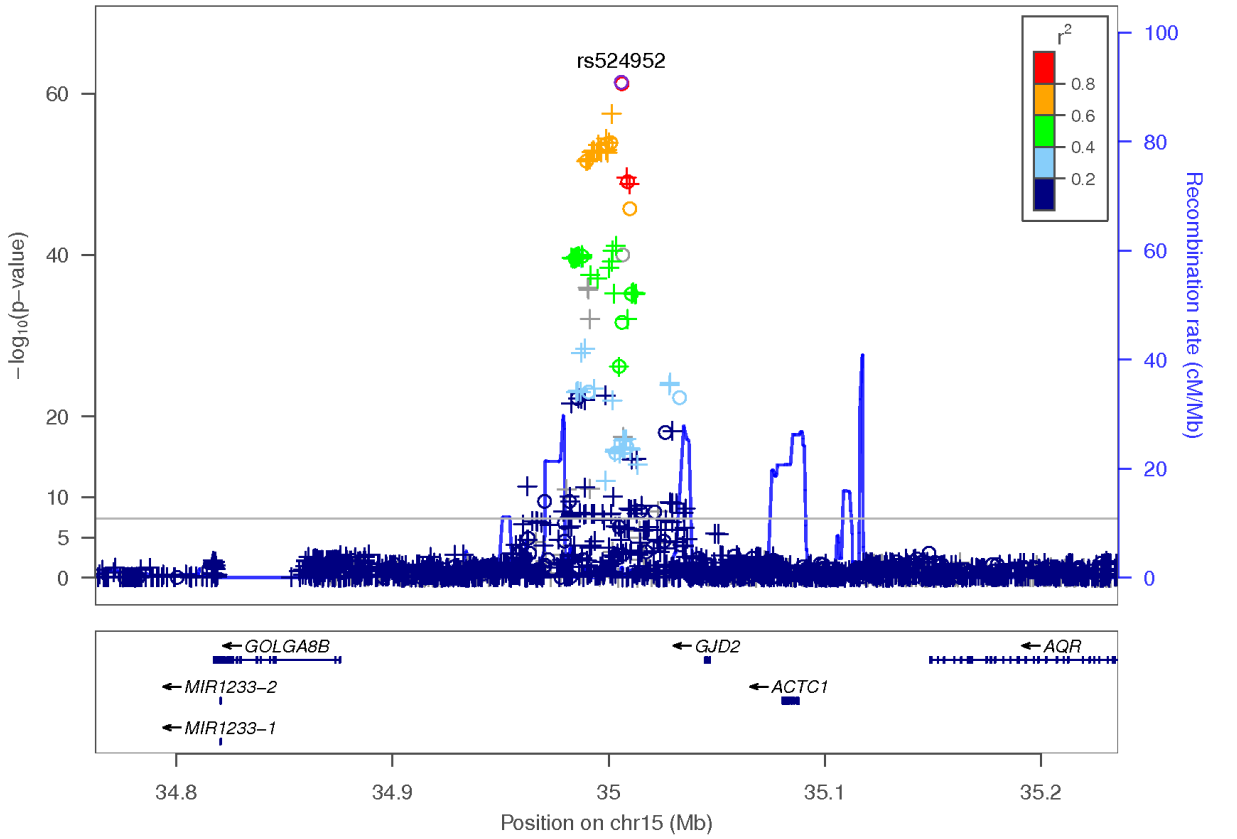
Regional Association Plots

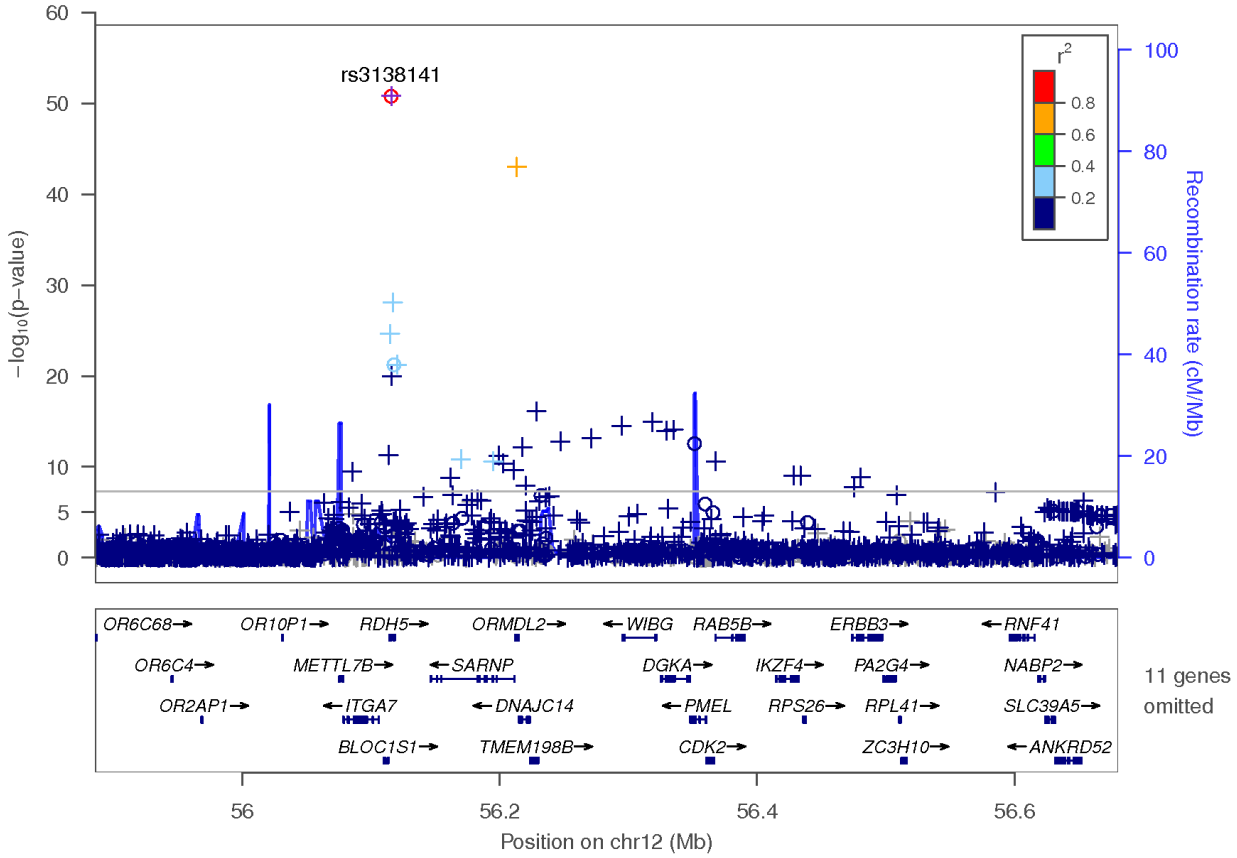

rs12193446
r²
0.8
0.6
0.4
0.2
100
50
20
10
5
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
LAMA2
ARHGAP18
TMEM244
L3MBTL3
SAMD3
129.4
129.6
129.8
130
130.2
130.4
Position on chr6 (Mb)

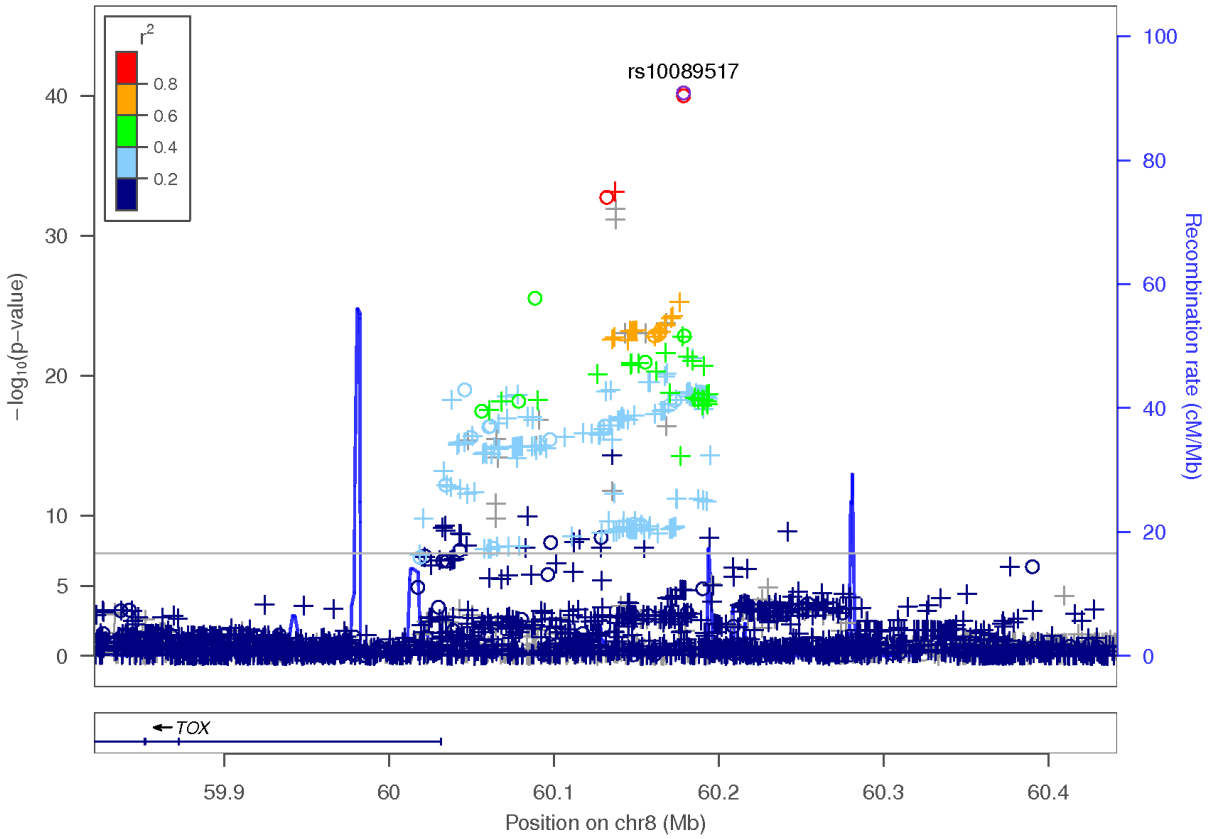

rs11606250
r²
0.8
0.6
0.4
0.2
60
40
20
10
5
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
LRRC4C
40
40.1
40.2
40.3
40.4
Position on chr11 (Mb)

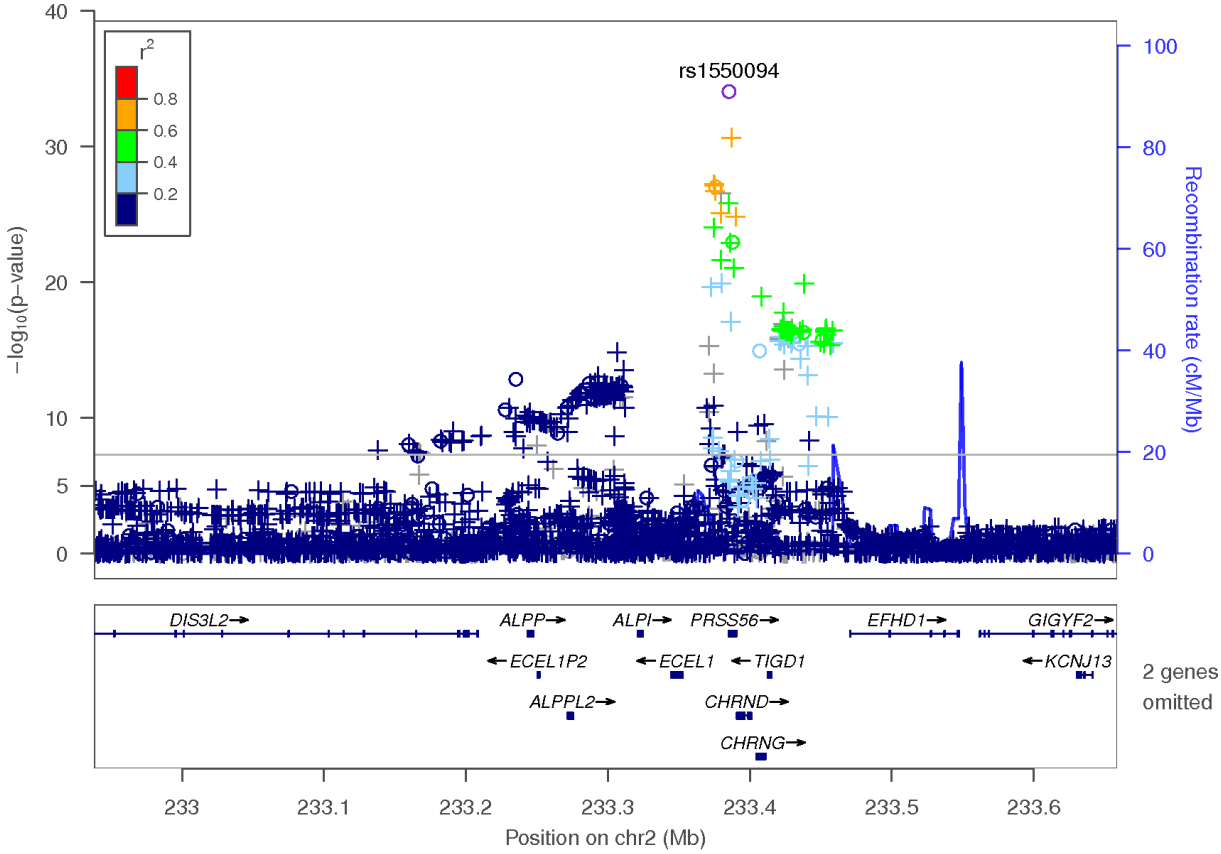

rs7744813
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
KCNQ5
MIR4282
KCNQ5−AS1
Position on chr6 (Mb)

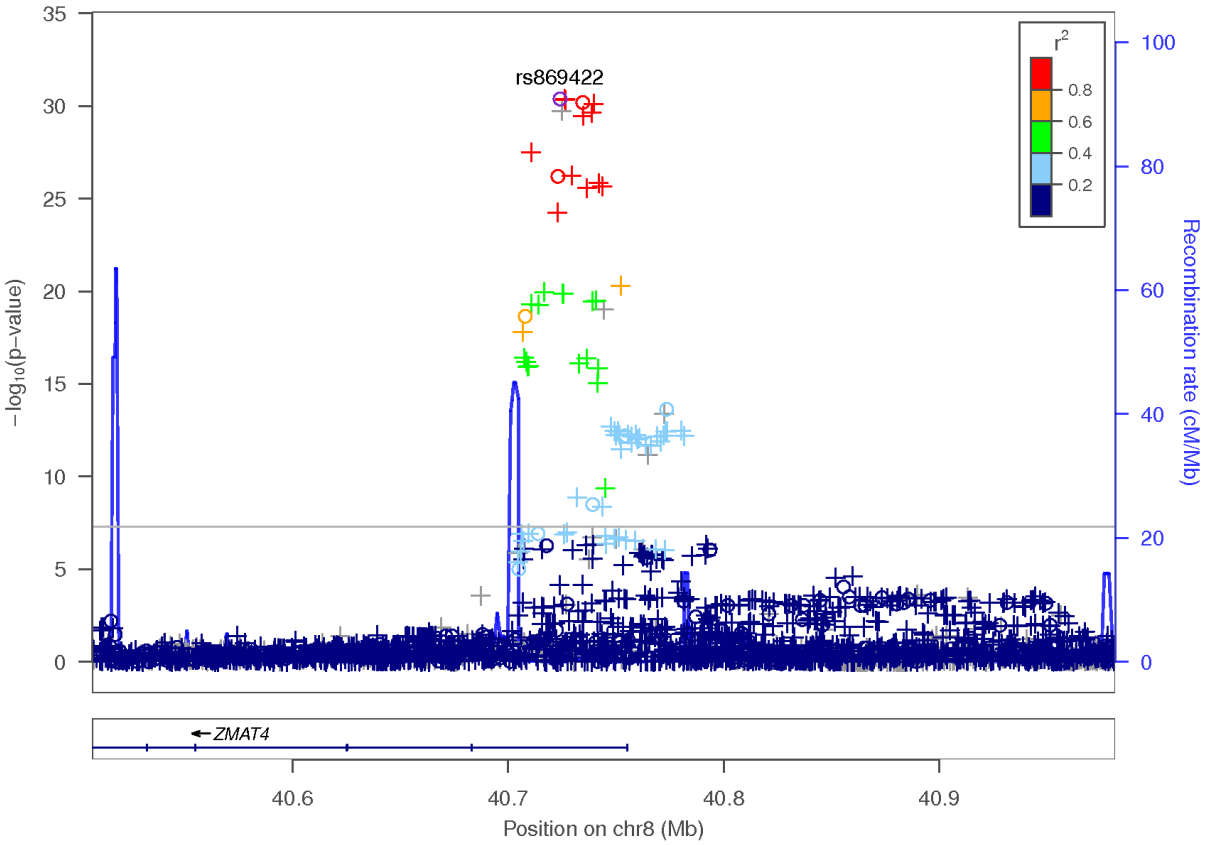

rs10500355
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
RBFOX1
Position on chr16 (Mb)

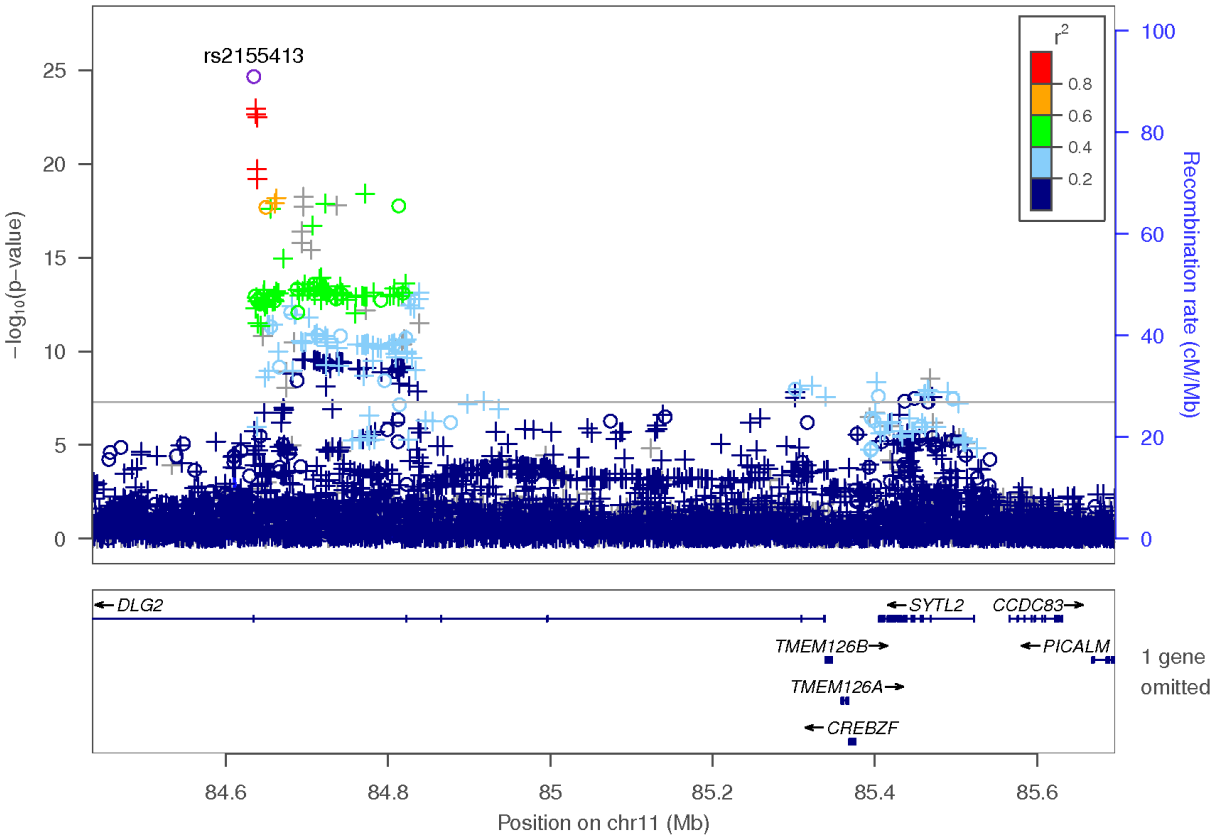

rs524952
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
GOLGA8B
GJD2
AQR
MIR1233−2
ACTC1
MIR1233−1
34.8
34.9
35
35.1
35.2
Position on chr15 (Mb)

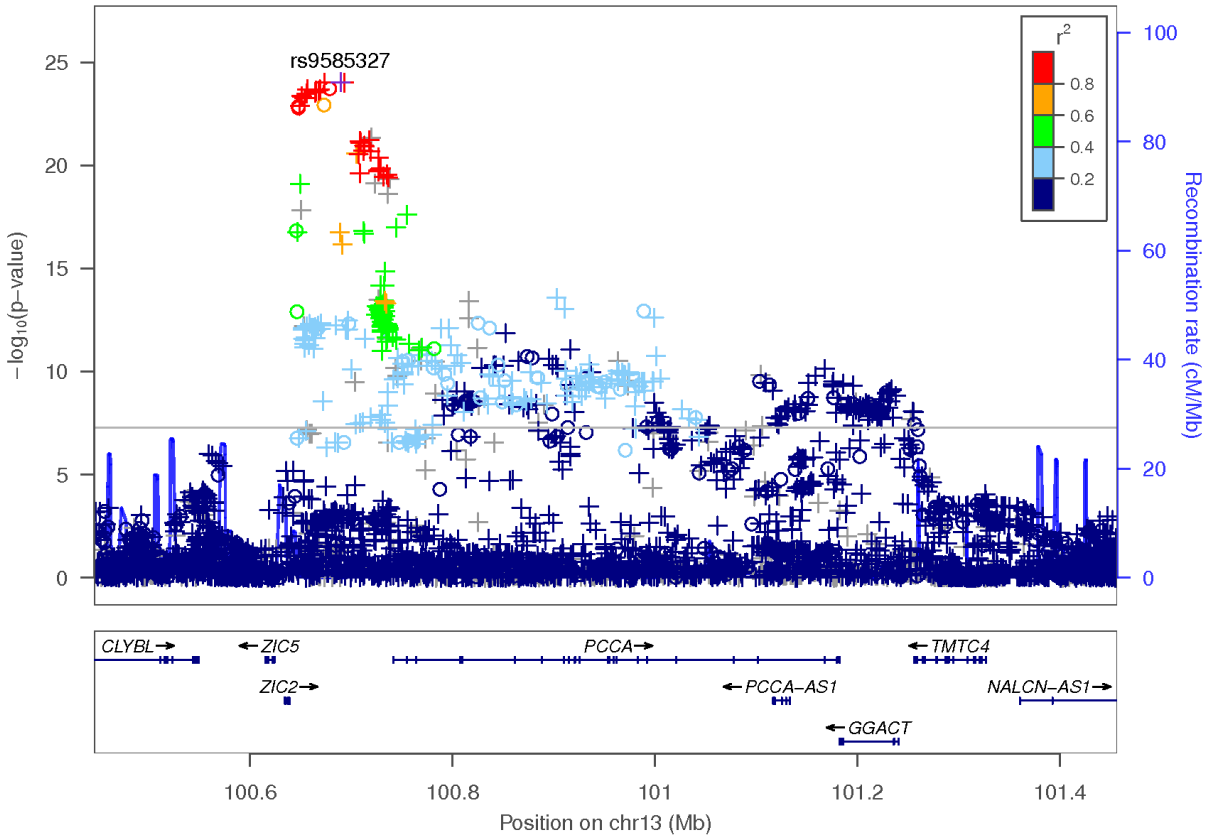

rs3138141
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
OR6C68
OR10P1
RDH5
ORMDL2
WIBG
RAB5B
ERBB3
RNF41
OR6C4
METTL7B
SARNP
DGKA
IKZF4
PA2G4
NABP2
OR2AP1
ITGA7
DNAJC14
PMEL
RPS26
RPL41
SLC39A5
BLOC1S1
TMEM198B
CDK2
ZC3H10
ANKRD52
11 genes
omitted
56
56.2
56.4
56.6
Position on chr12 (Mb)

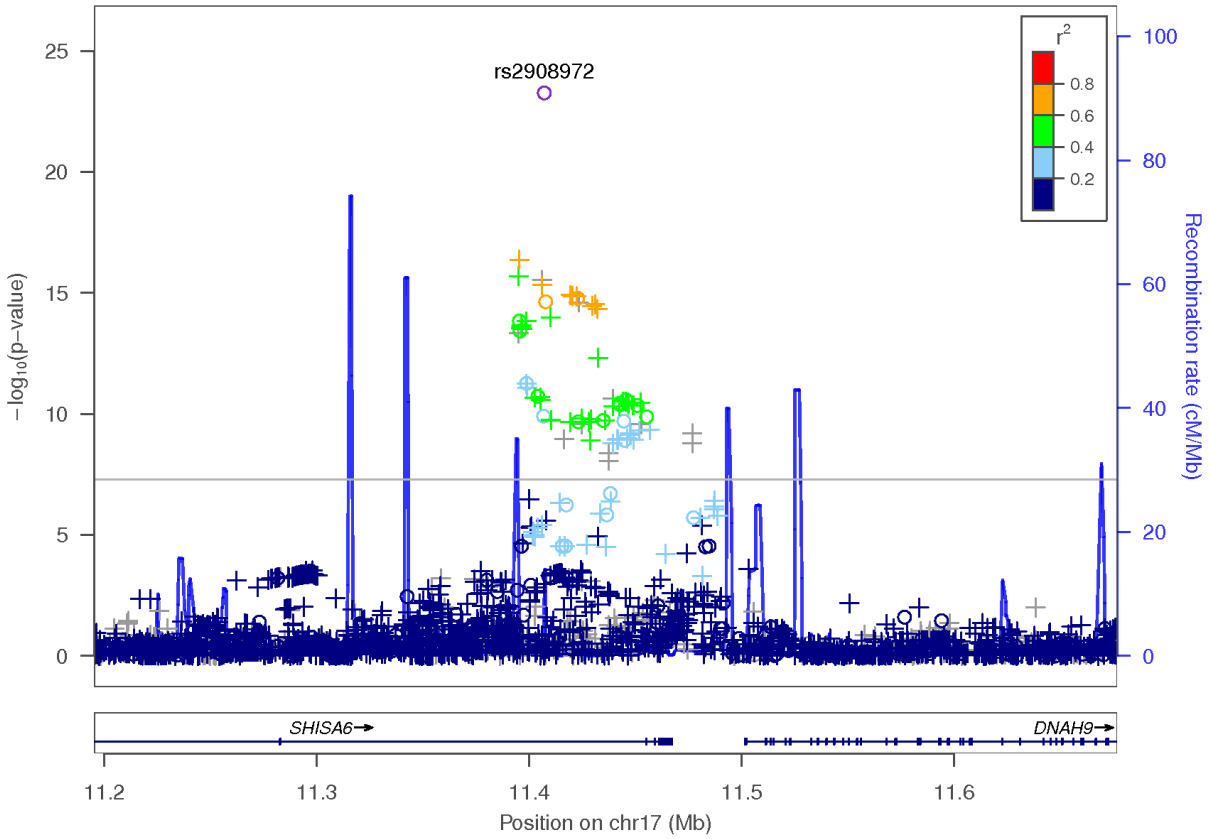

rs10089517
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
TOX
59.9
60
60.1
60.2
60.3
60.4
Position on chr8 (Mb)

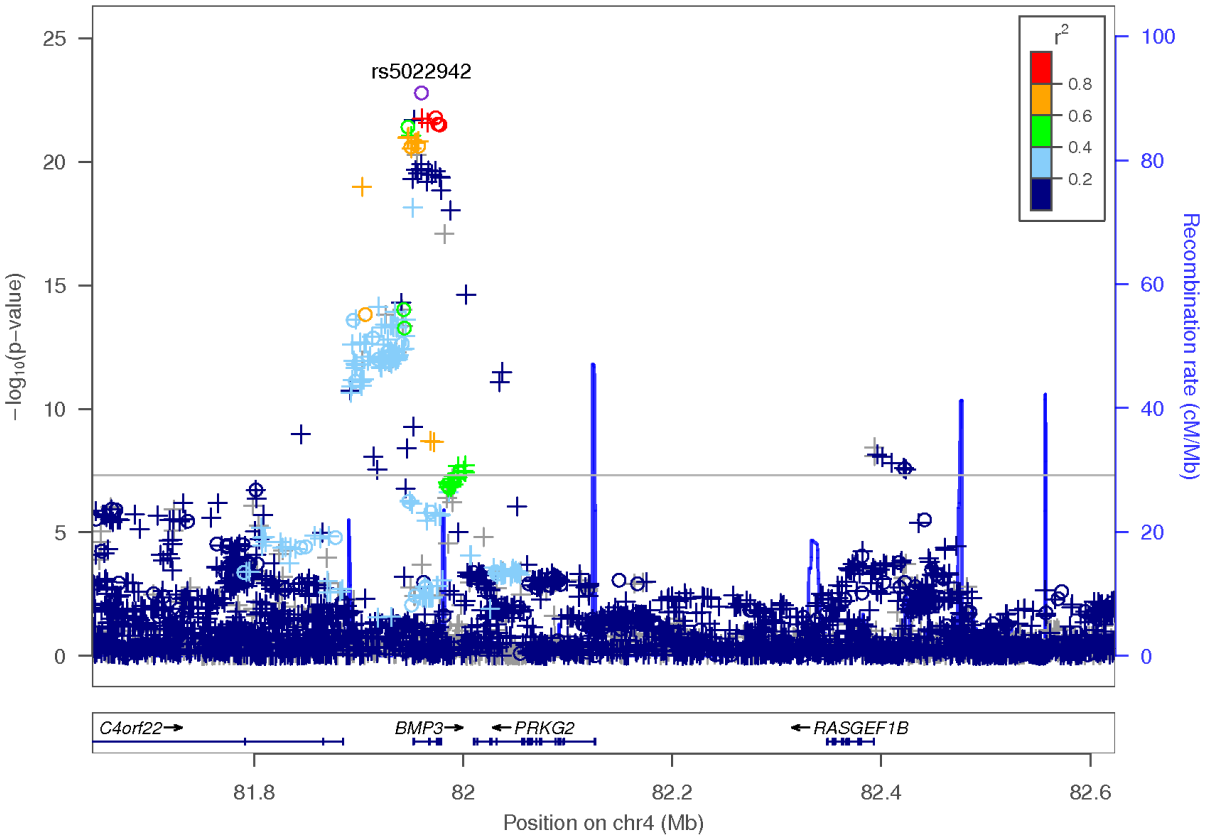

rs1550094
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
DIS3L2
ALPP
ALPI
PRSS56
EFHD1
GIGYF2
ECEL1P2
ECEL1
TIGD1
KCNJ13
ALPPL2
CHRND
CHRNG
2 genes omitted
233
233.1
233.2
233.3
233.4
233.5
233.6
Position on chr2 (Mb)

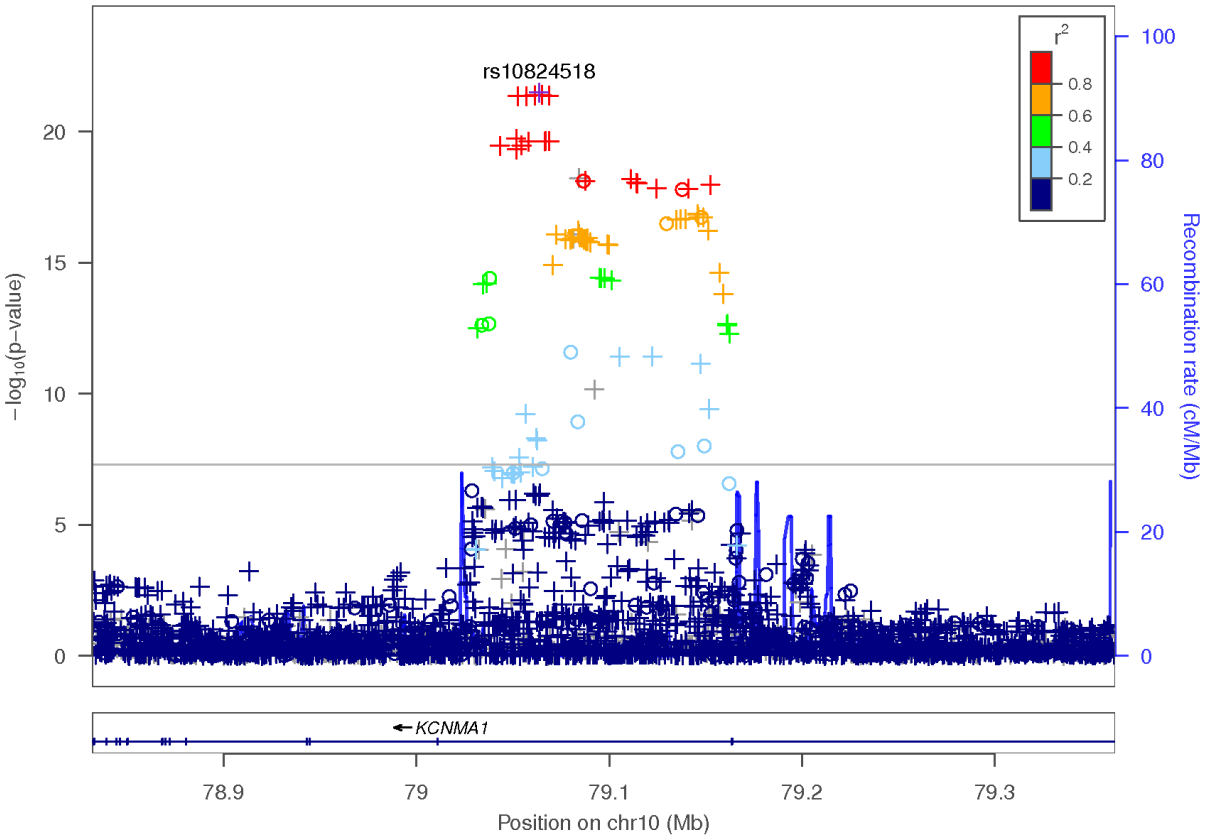

rs869422
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
ZMAT4
40.6
40.7
40.8
40.9
Position on chr8 (Mb)

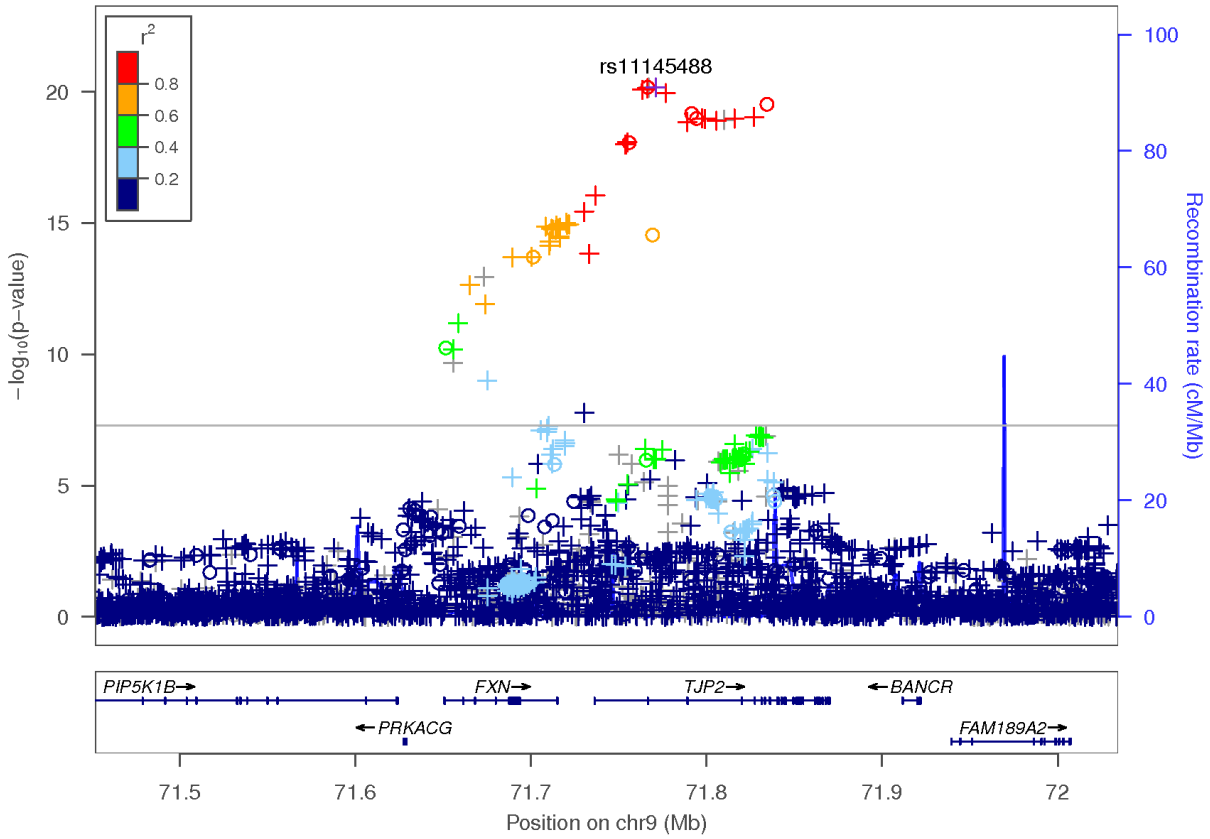

rs2155413
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
DLG2
SYTL2
CCDC83
TMEM126B
PICALM
TMEM126A
CREBZF
1 gene
omitted
84.6
84.8
85
85.2
85.4
85.6
Position on chr11 (Mb)

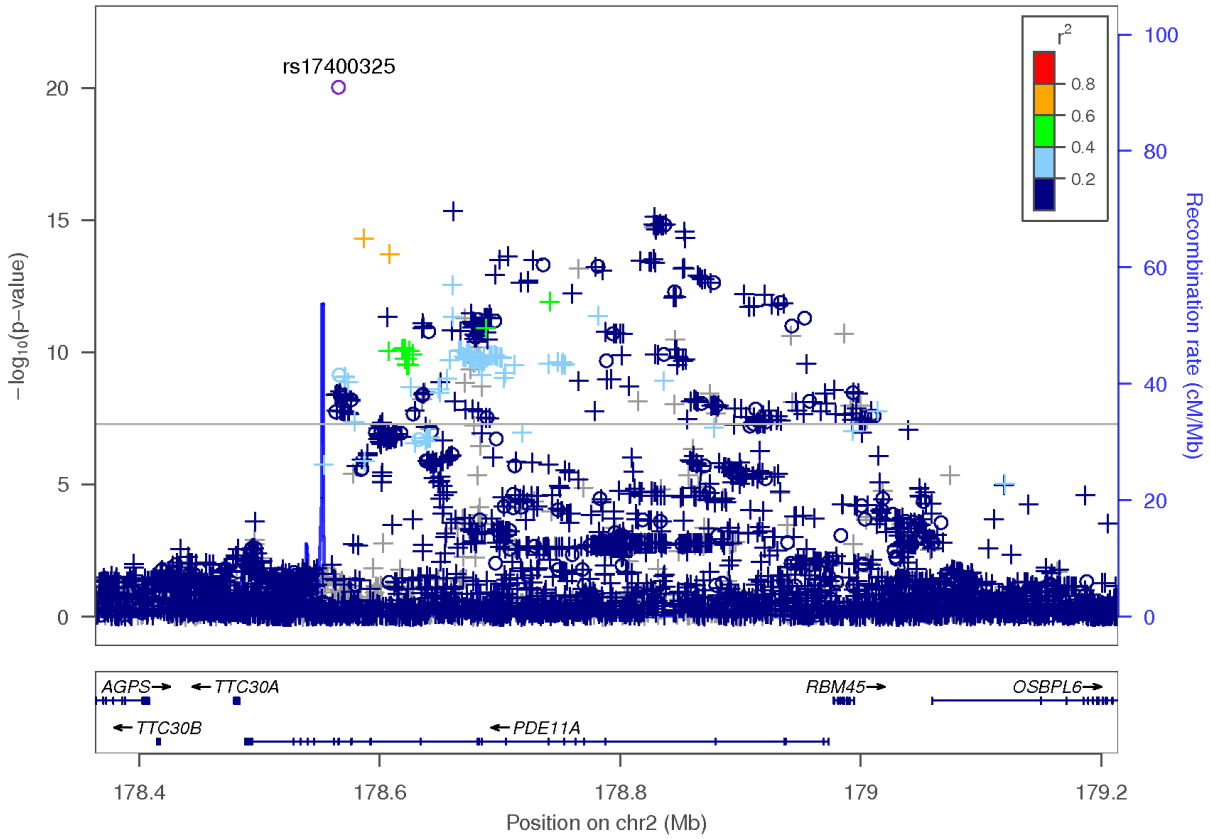

rs9585327
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
CLYBL
ZIC5
PCCA
TMTC4
ZIC2
PCCA−AS1
NALCN−AS1
GGACT
100.6
100.8
101
101.2
101.4
Position on chr13 (Mb)

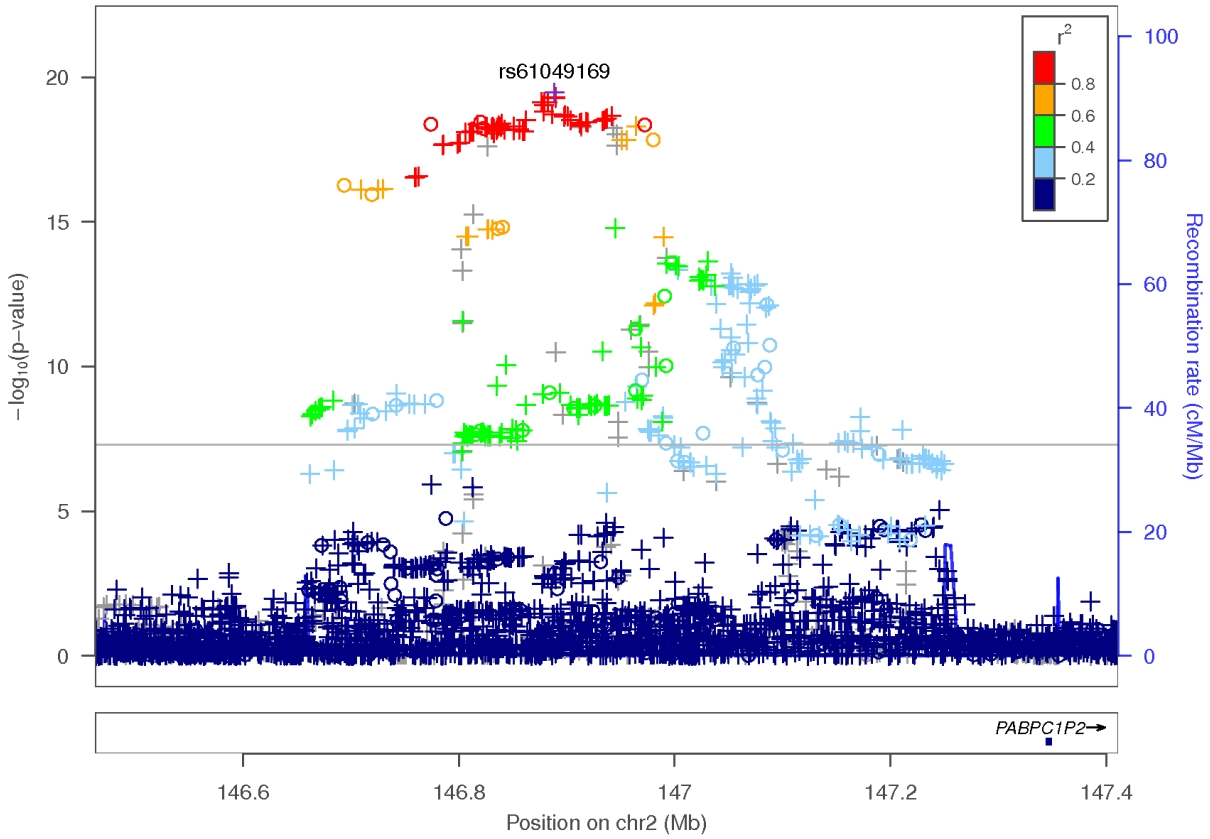

rs2908972
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
SHISA6
DNAH9
11.2
11.3
11.4
11.5
11.6
Position on chr17 (Mb)

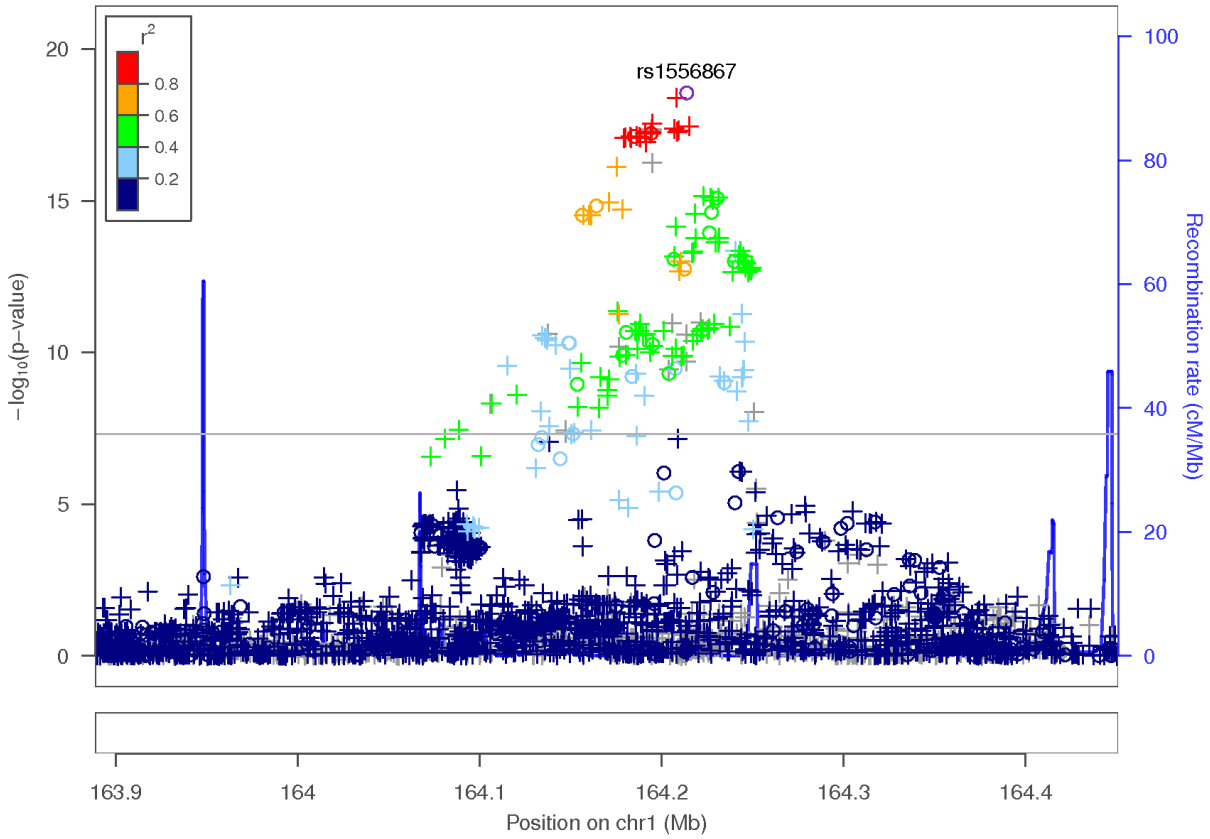

rs5022942
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
C4orf22
BMP3
PRKG2
RASGEF1B
81.8
82
82.2
82.4
82.6
Position on chr4 (Mb)

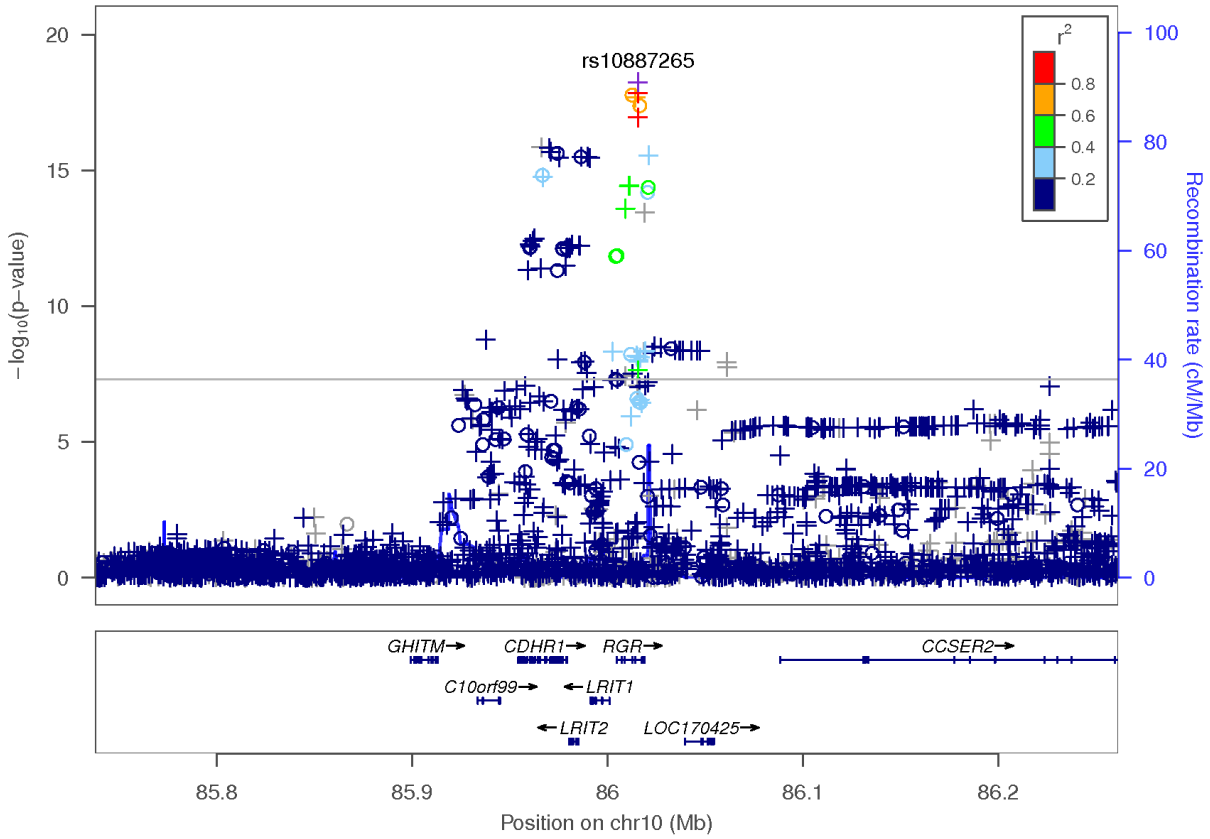

rs10824518
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
KCNMA1
78.9
79
79.1
79.2
79.3
Position on chr10 (Mb)

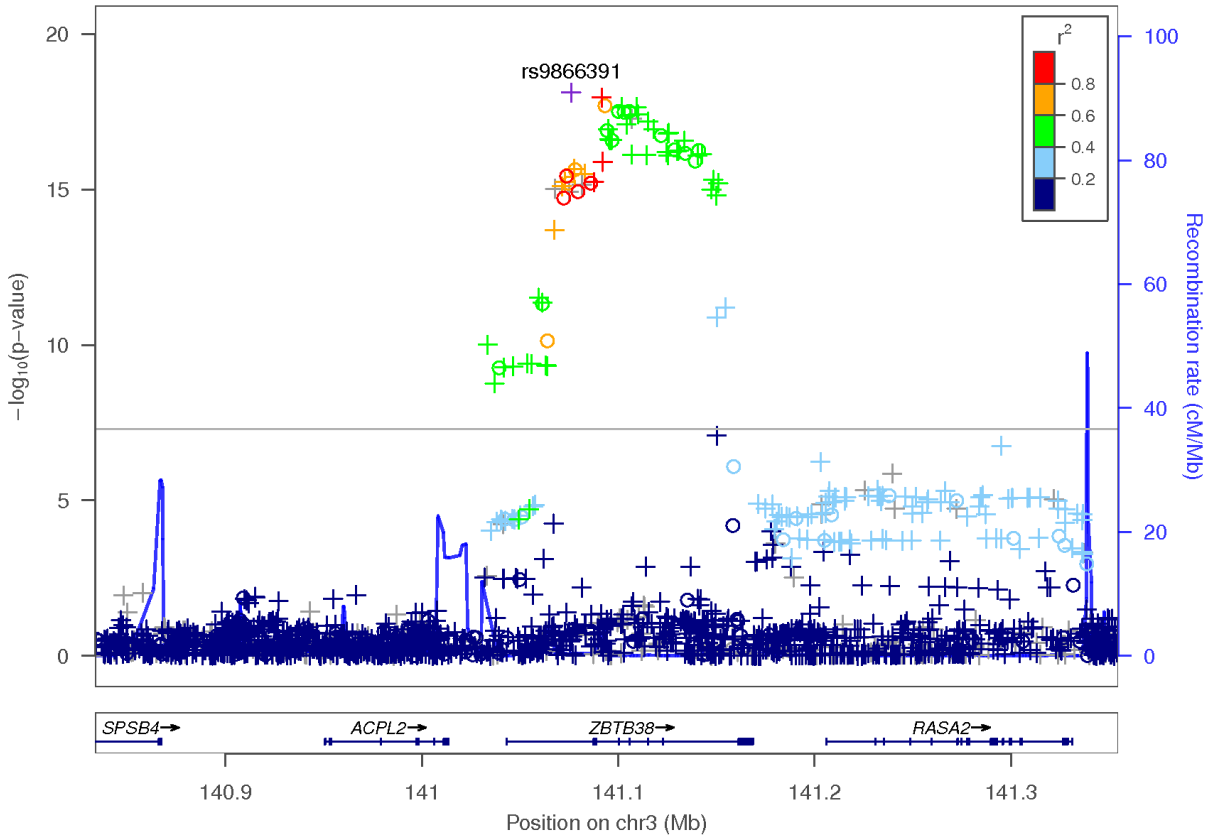

rs11145488
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
PIP5K1B
FXN
TJP2
BANCR
PRKACG
FAM189A2
71.5
71.6
71.7
71.8
71.9
72
Position on chr9 (Mb)

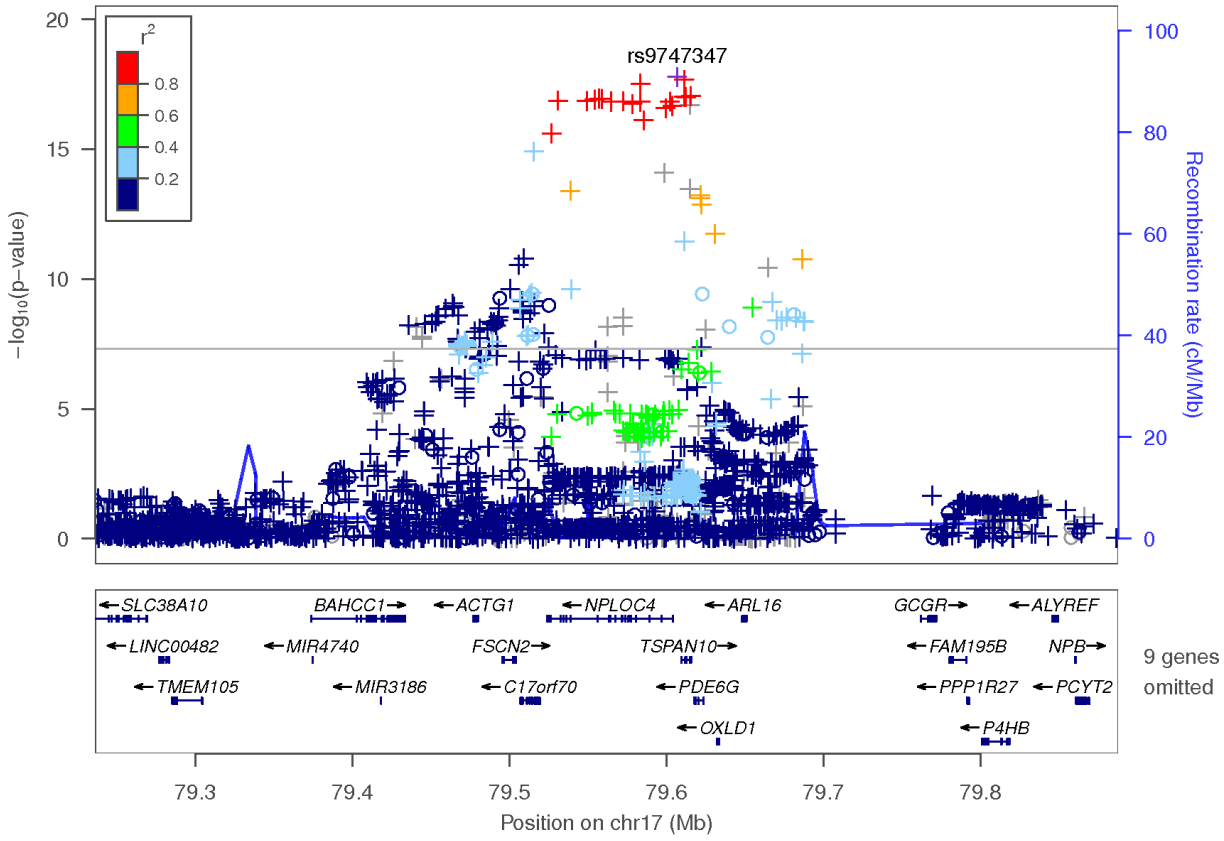

rs17400325
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
AGPS
TTC30A
RBM45
OSBPL6
TTC30B
PDE11A
178.4
178.6
178.8
179
179.2
Position on chr2 (Mb)

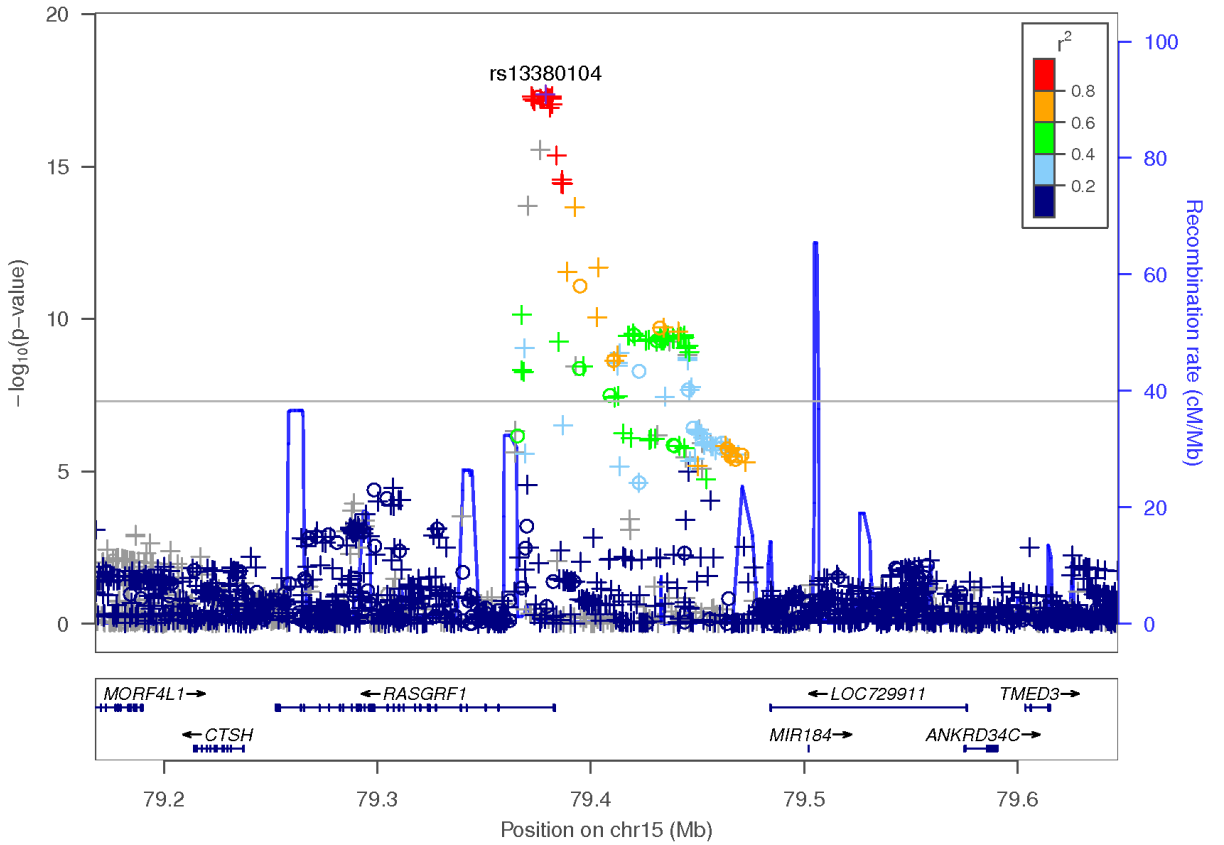

rs61049169
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
PABPC1P2
146.6
146.8
147
147.2
147.4
Position on chr2 (Mb)

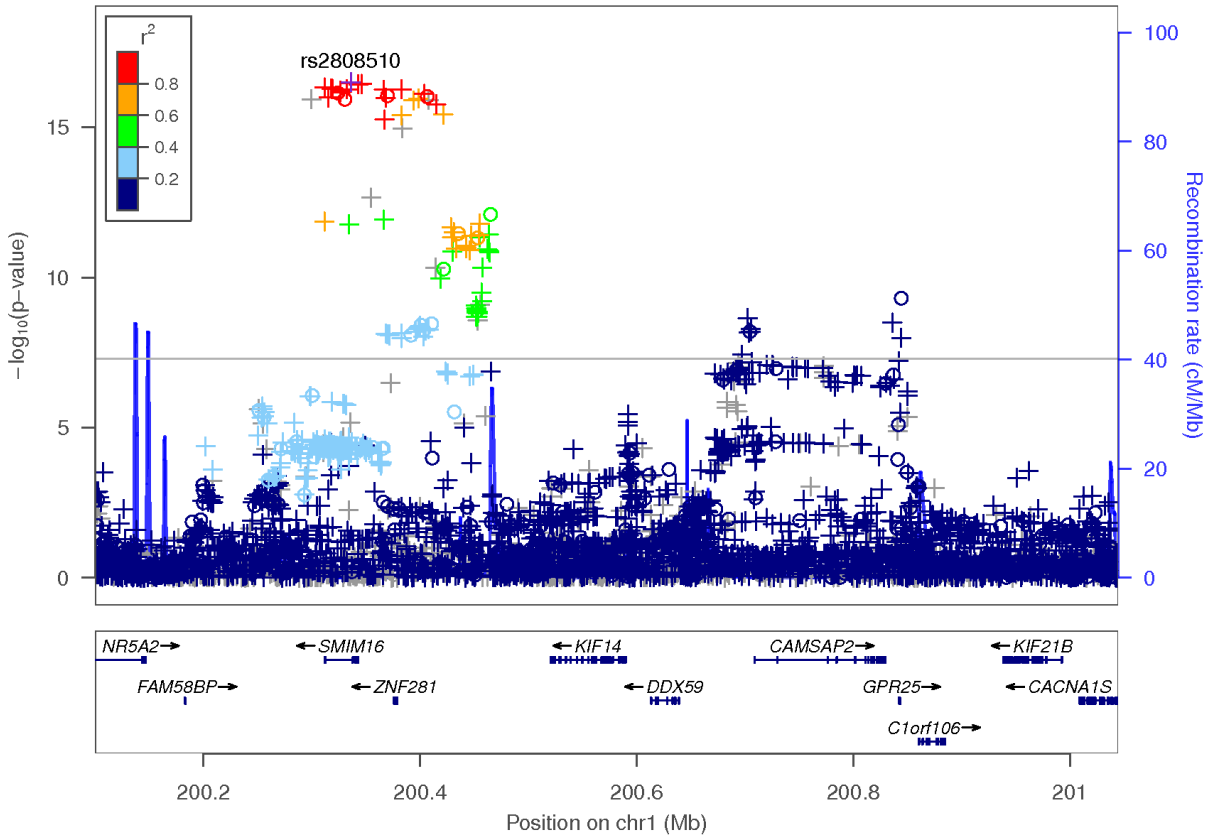

rs1556867
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
163.9
164
164.1
164.2
164.3
164.4
Position on chr1 (Mb)

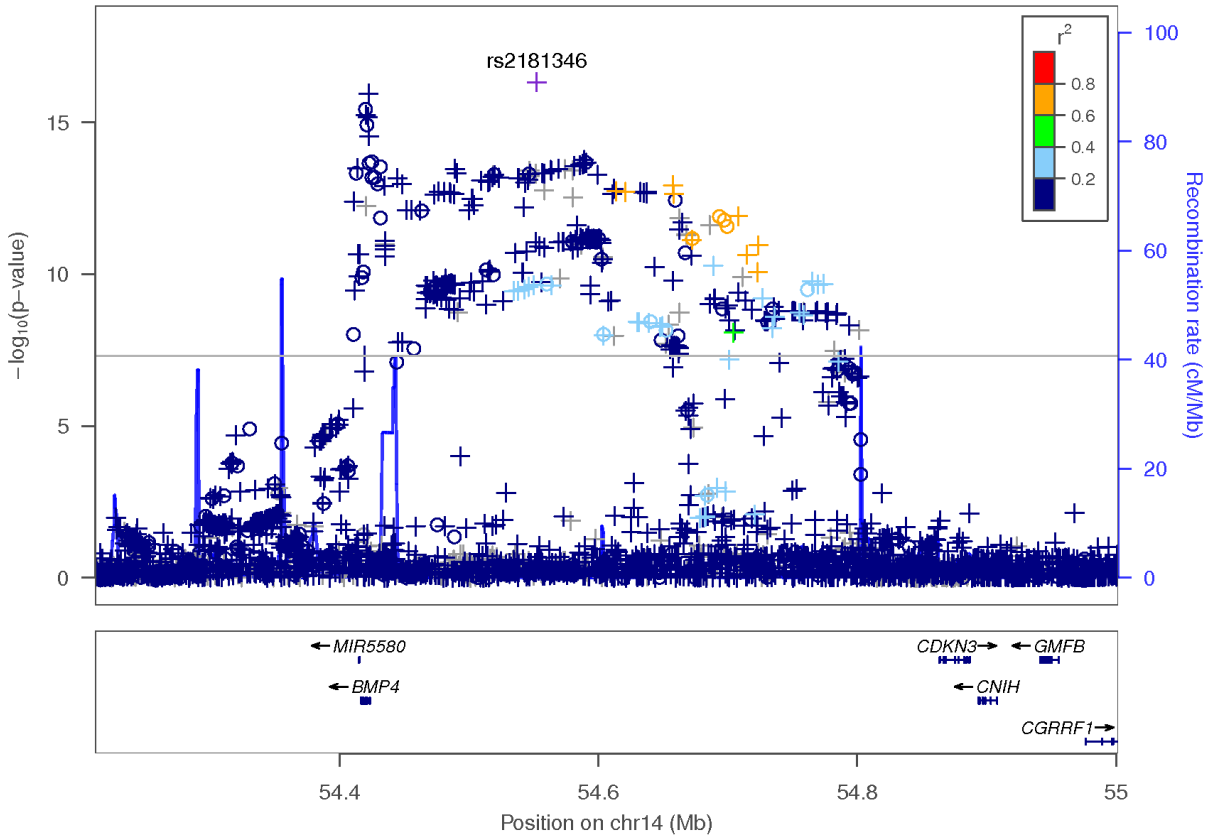

rs10887265
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
GHITM
CDHR1
RGR
CCSER2
C10orf99
LRIT1
LRIT2
LOC170425
Position on chr10 (Mb)

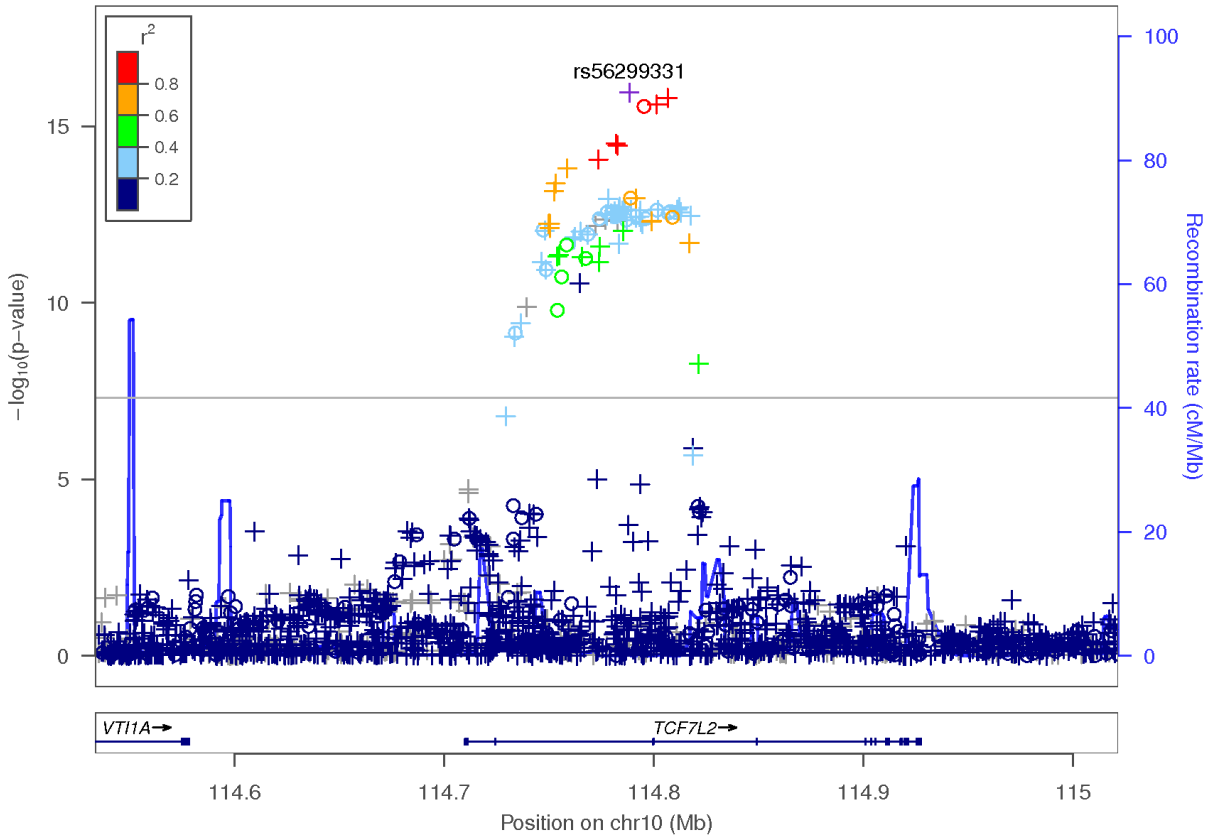

rs9866391
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
SPSB4
ACPL2
ZBTB38
RASA2
Position on chr3 (Mb)

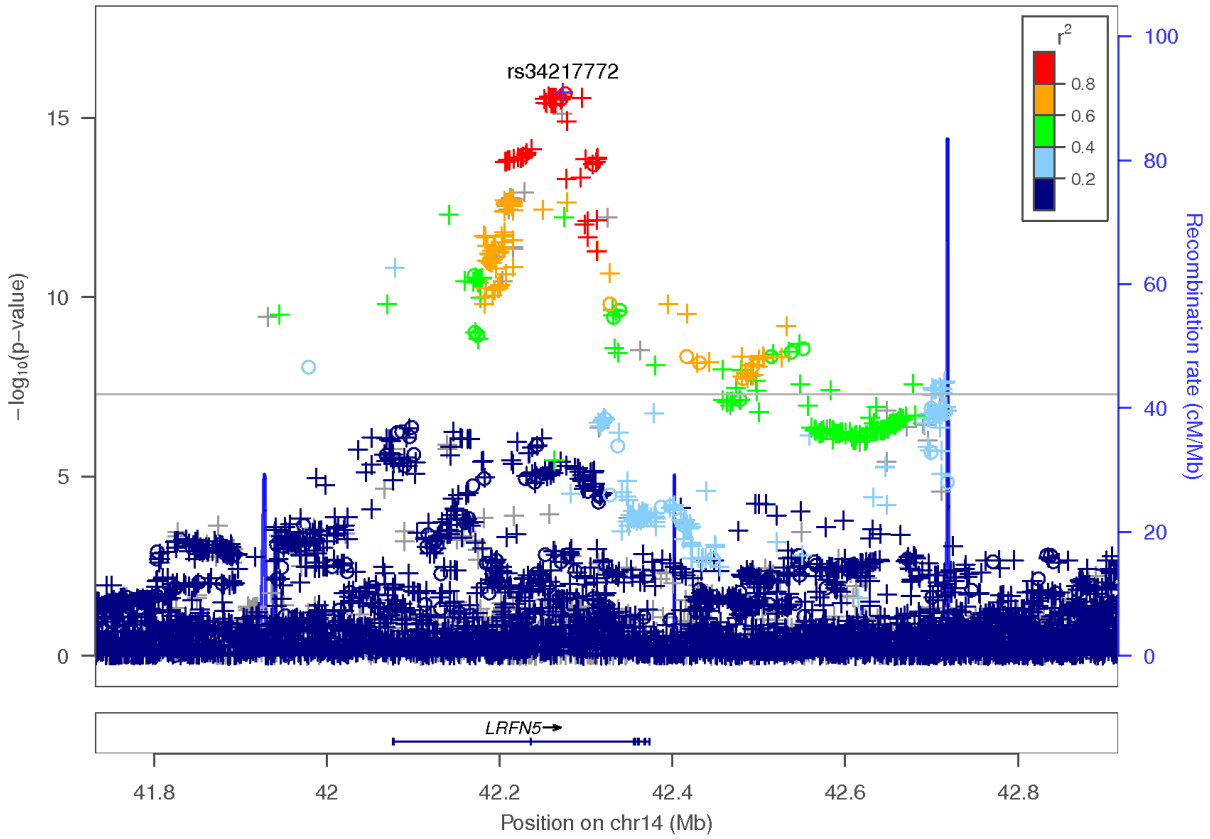

rs9747347
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
SLC38A10
BAHCC1
ACTG1
NPLOC4
ARL16
GCGR
ALYREF
LINC00482
MIR4740
FSCN2
TSPAN10
FAM195B
NPB
TMEM105
MIR3186
C17orf70
PDE6G
PPP1R27
PCYT2
OXLD1
P4HB
9 genes omitted
Position on chr17 (Mb)

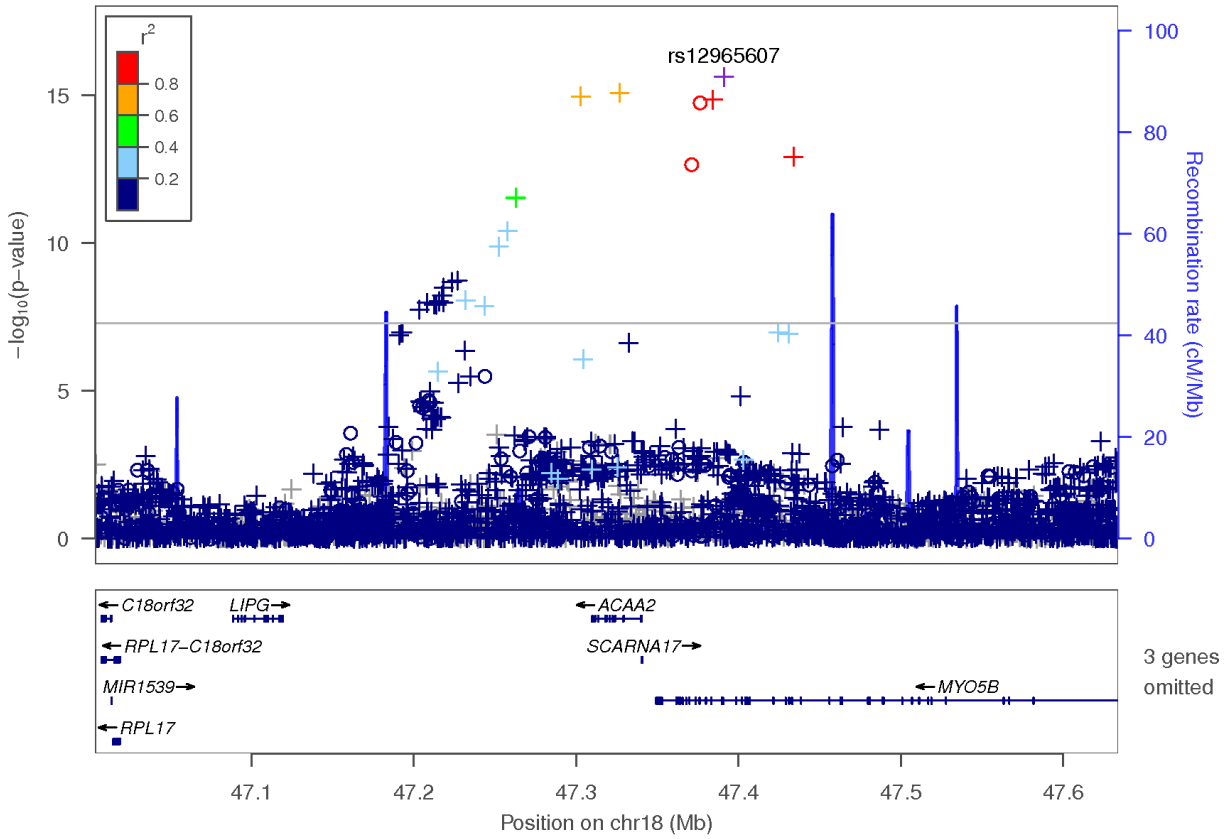

rs13380104
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
MORF4L1
RASGRF1
LOC729911
TMED3
CTSH
MIR184
ANKRD34C
Position on chr15 (Mb)

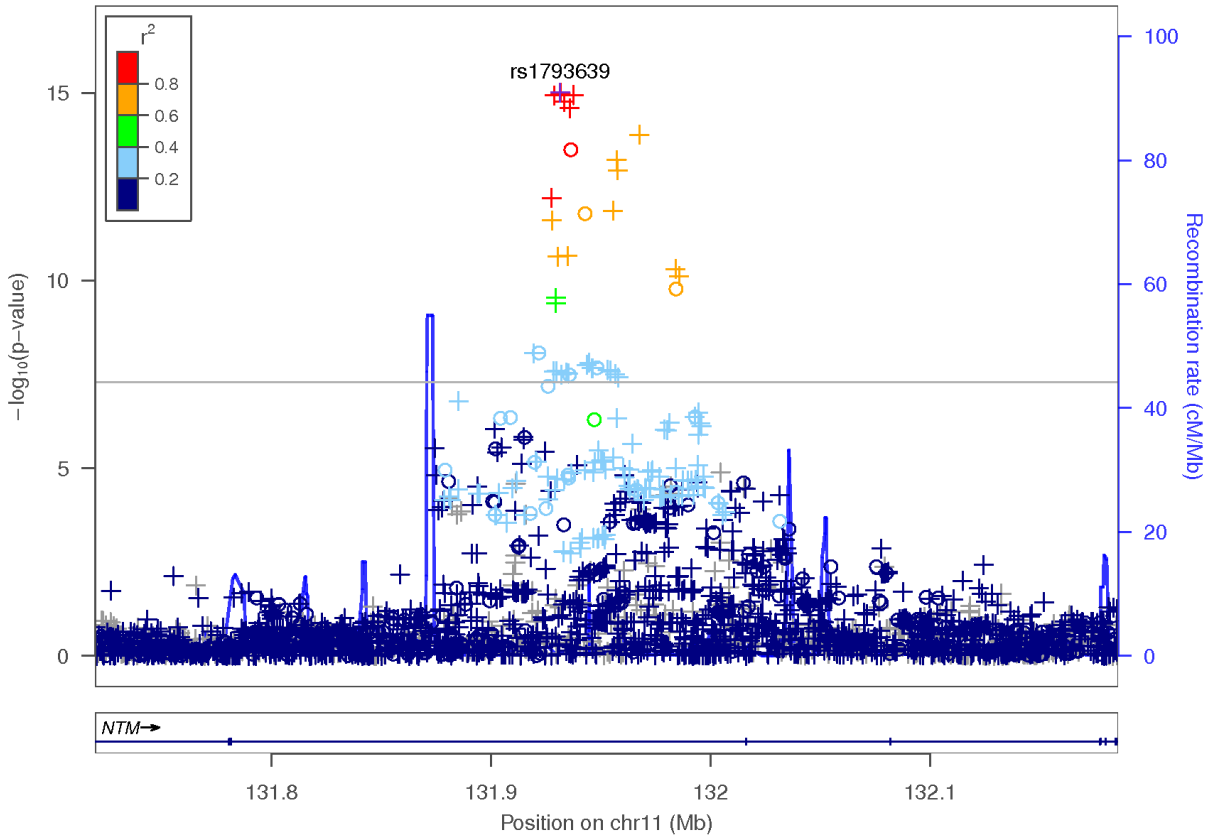

rs2808510
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
NR5A2
SMIM16
KIF14
CAMSAP2
KIF21B
FAM58BP
ZNF281
DDX59
GPR25
CACNA1S
C1orf106
200.2
200.4
200.6
200.8
201
Position on chr1 (Mb)

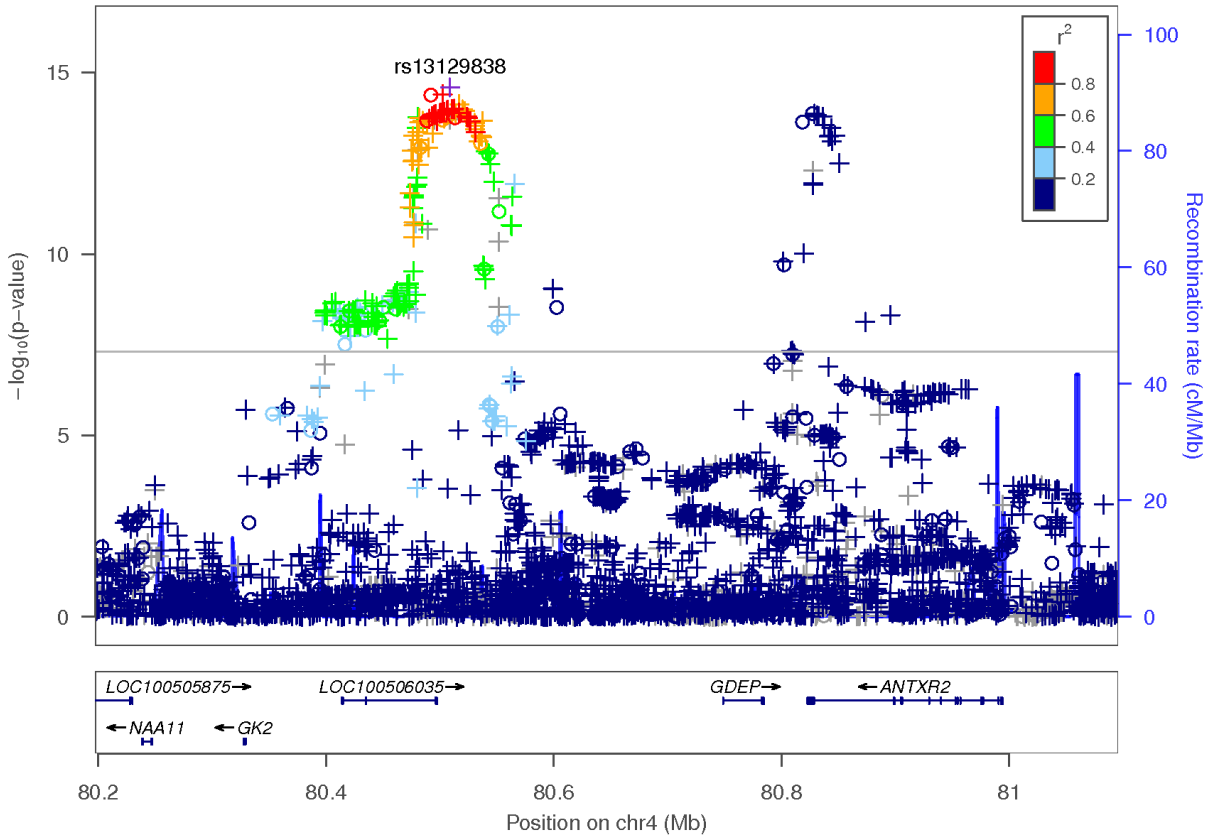

rs2181346
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
MIR5580
BMP4
CDKN3
GMFB
CNIH
CGRRF1
54.4
54.6
54.8
55
Position on chr14 (Mb)

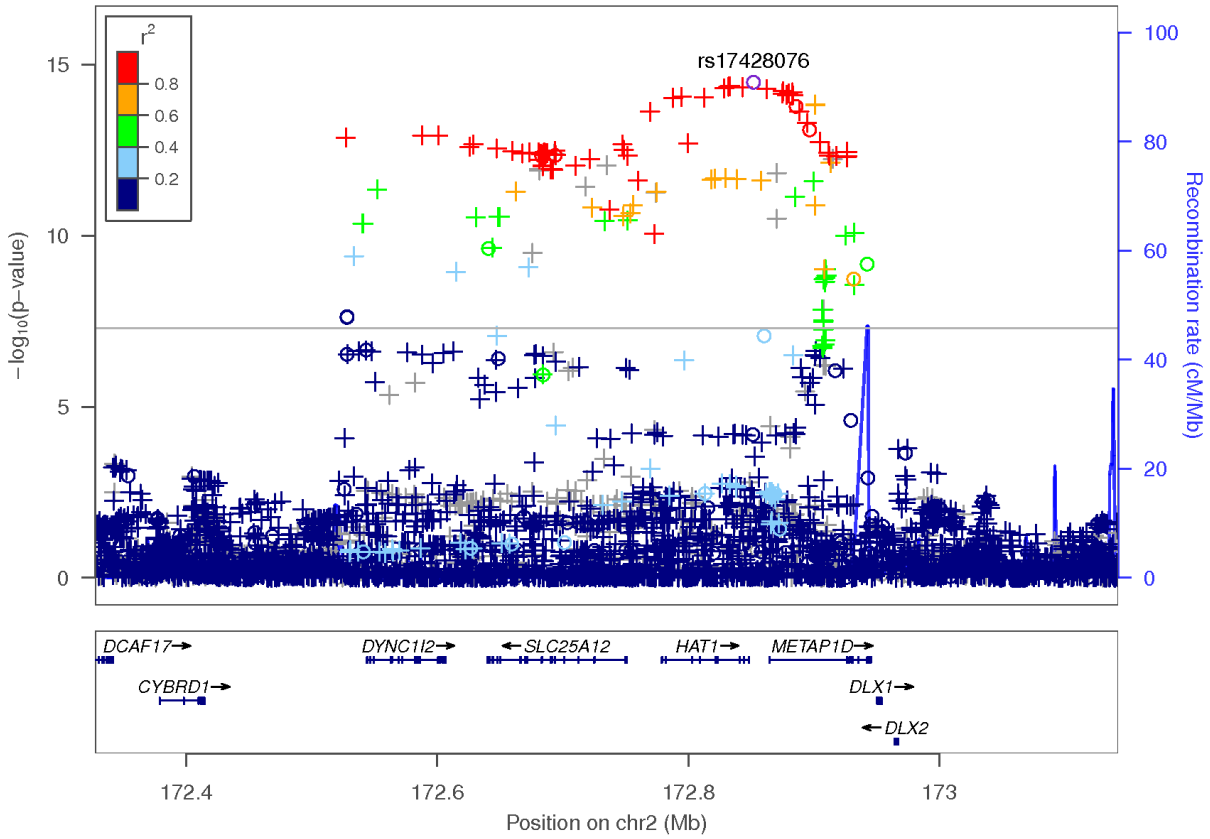

r²
0.8
0.6
0.4
0.2
rs56299331
15
10
5
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
VTI1A
TCF7L2
114.6
114.7
114.8
114.9
115
Position on chr10 (Mb)

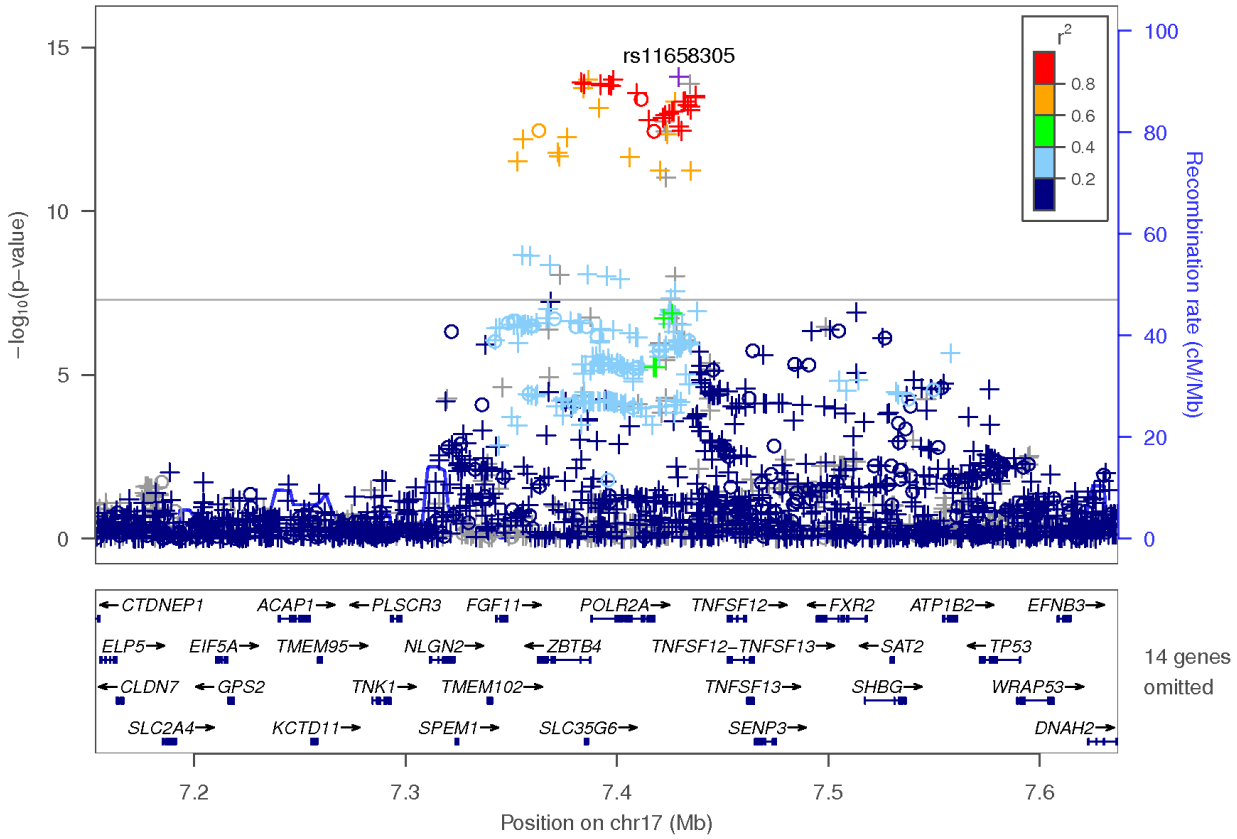

r²
0.8
0.6
0.4
0.2
rs34217772
15
10
5
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
LRFN5
41.8
42
42.2
42.4
42.6
42.8
Position on chr14 (Mb)

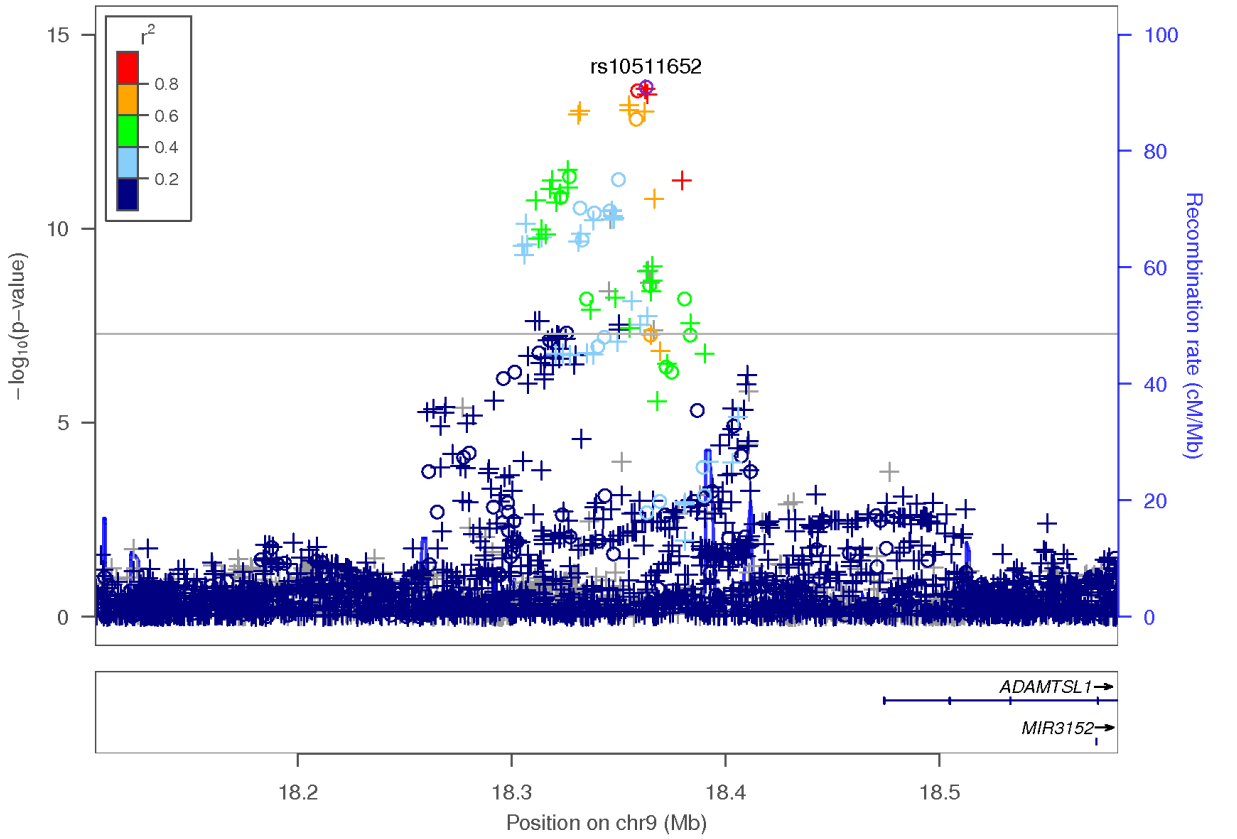

rs12965607
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
C18orf32
LIPG
ACAA2
RPL17−C18orf32
SCARNA17
MIR1539
MYO5B
RPL17
3 genes omitted
47.1
47.2
47.3
47.4
47.5
47.6
Position on chr18 (Mb)

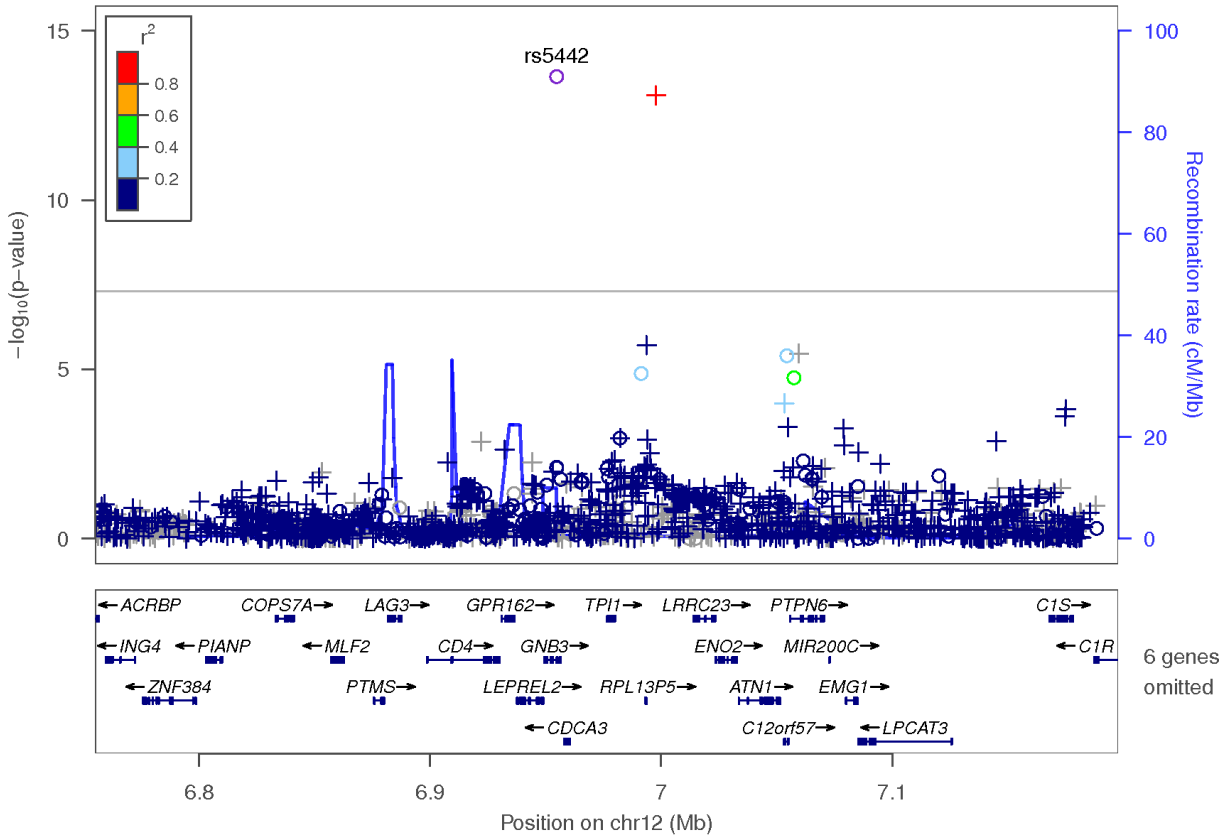

rs1793639
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
NTM
131.8
131.9
132
132.1
Position on chr11 (Mb)

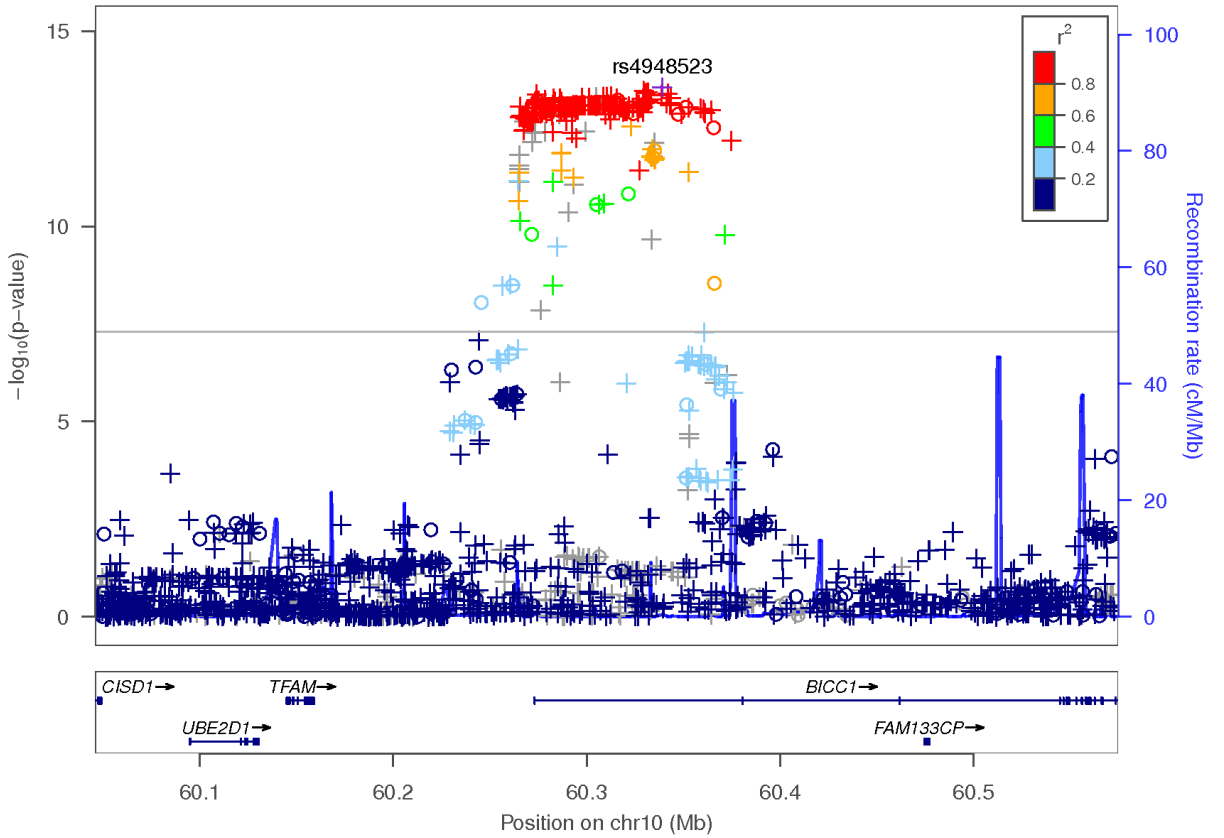

rs13129838
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
LOC100505875
LOC100506035
GDEP
ANTXR2
NAA11
GK2
Position on chr4 (Mb)

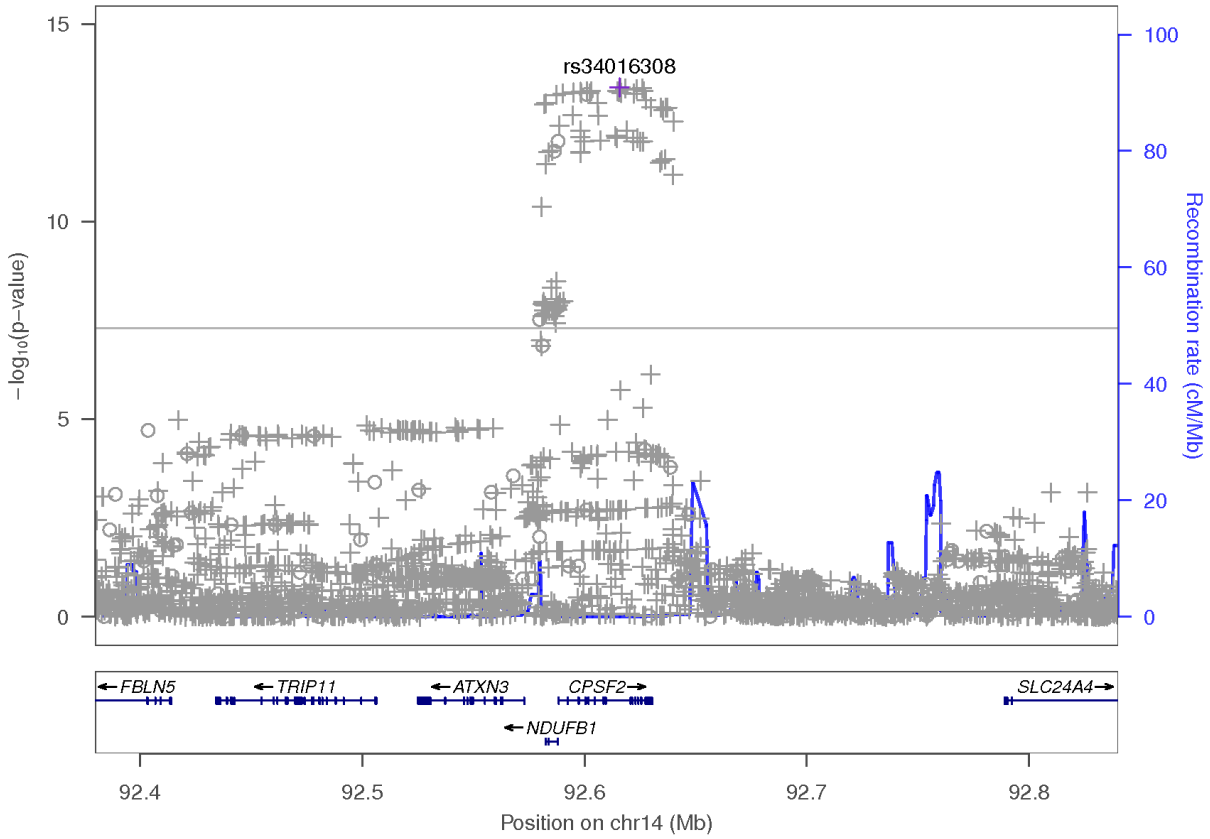

rs17428076
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
DCAF17
DYNC1I2
SLC25A12
HAT1
METAP1D
CYBRD1
DLX1
DLX2
Position on chr2 (Mb)

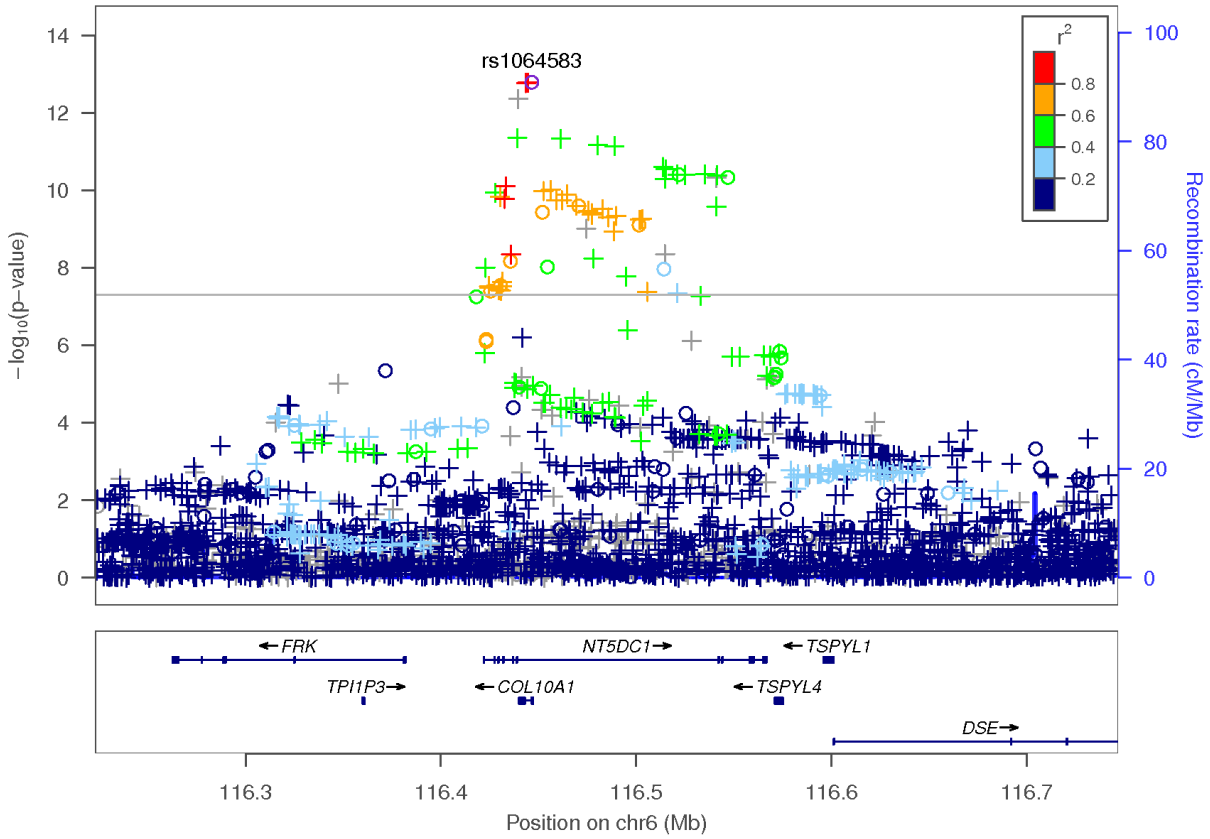

rs11658305
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
CTDNEP1
ACAP1
PLSCR3
FGF11
POLR2A
TNFSF12
FXR2
ATP1B2
EFNB3
ELP5
EIF5A
TMEM95
NLGN2
ZBTB4
TNFSF12−TNFSF13
SAT2
TP53
CLDN7
GPS2
TNK1
TMEM102
TNFSF13
SHBG
WRAP53
SLC2A4
KCTD11
SPEM1
SLC35G6
SENP3
DNAH2
14 genes
omitted
Position on chr17 (Mb)

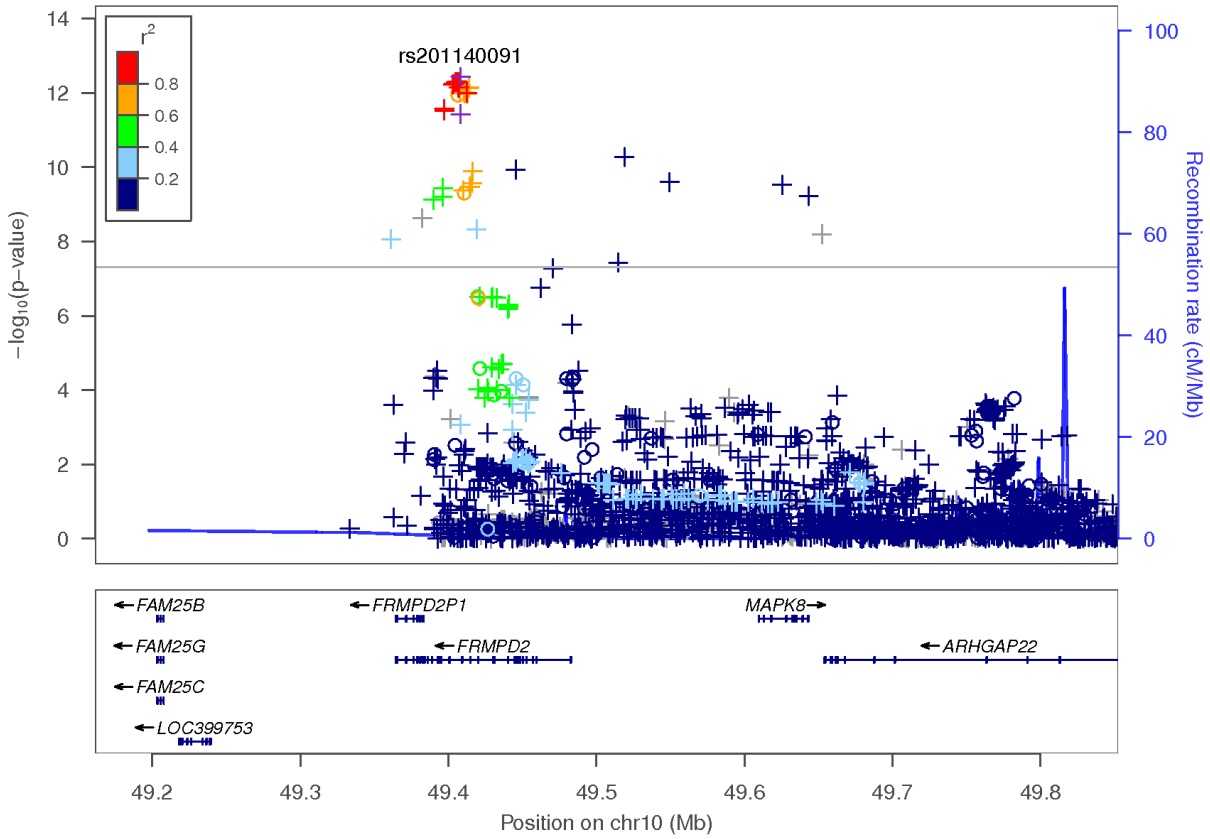

rs10511652
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ADAMTSL1
MIR3152
Position on chr9 (Mb)

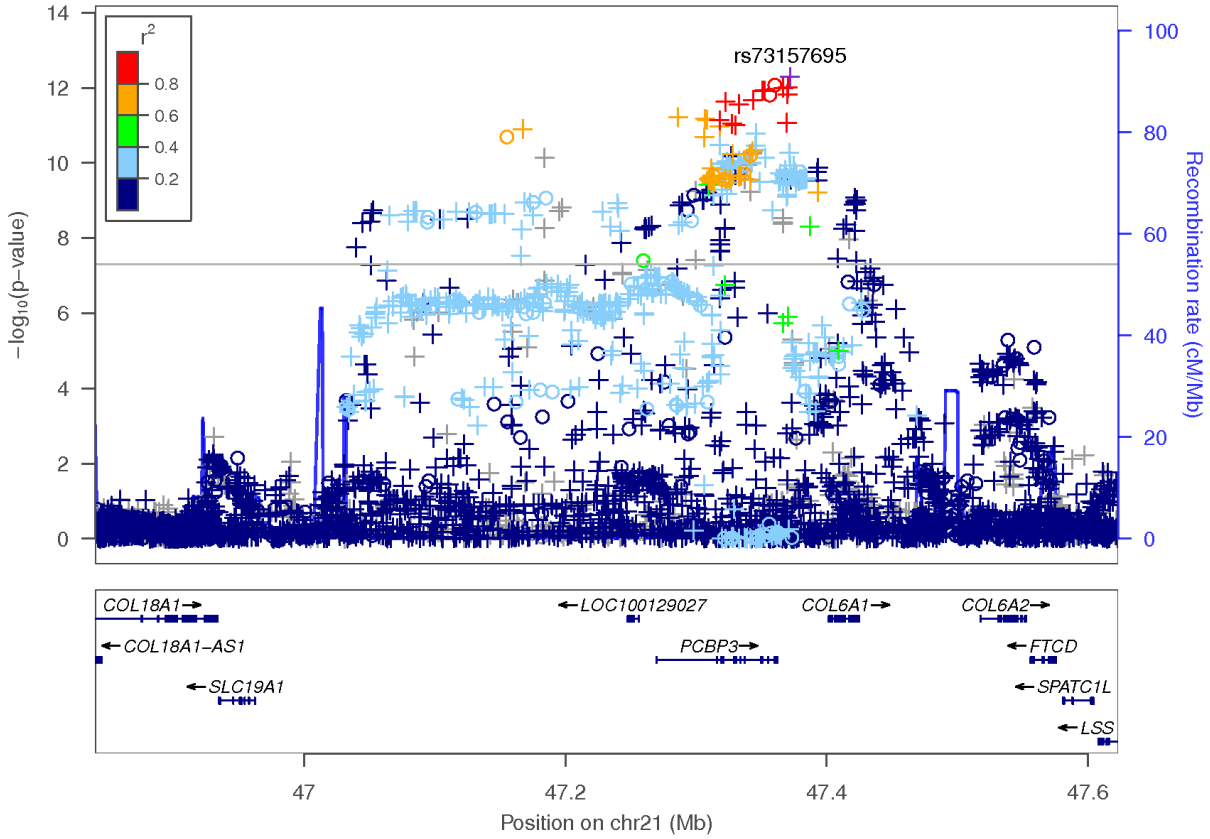

rs5442
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ACRBP
COPS7A
LAG3
GPR162
TPI1
LRRC23
PTPN6
C1S
ING4
PIANP
MLF2
CD4
GNB3
ENO2
MIR200C
C1R
ZNF384
PTMS
LEPREL2
RPL13P5
ATN1
EMG1
CDCA3
C12orf57
LPCAT3
6 genes omitted
Position on chr12 (Mb)

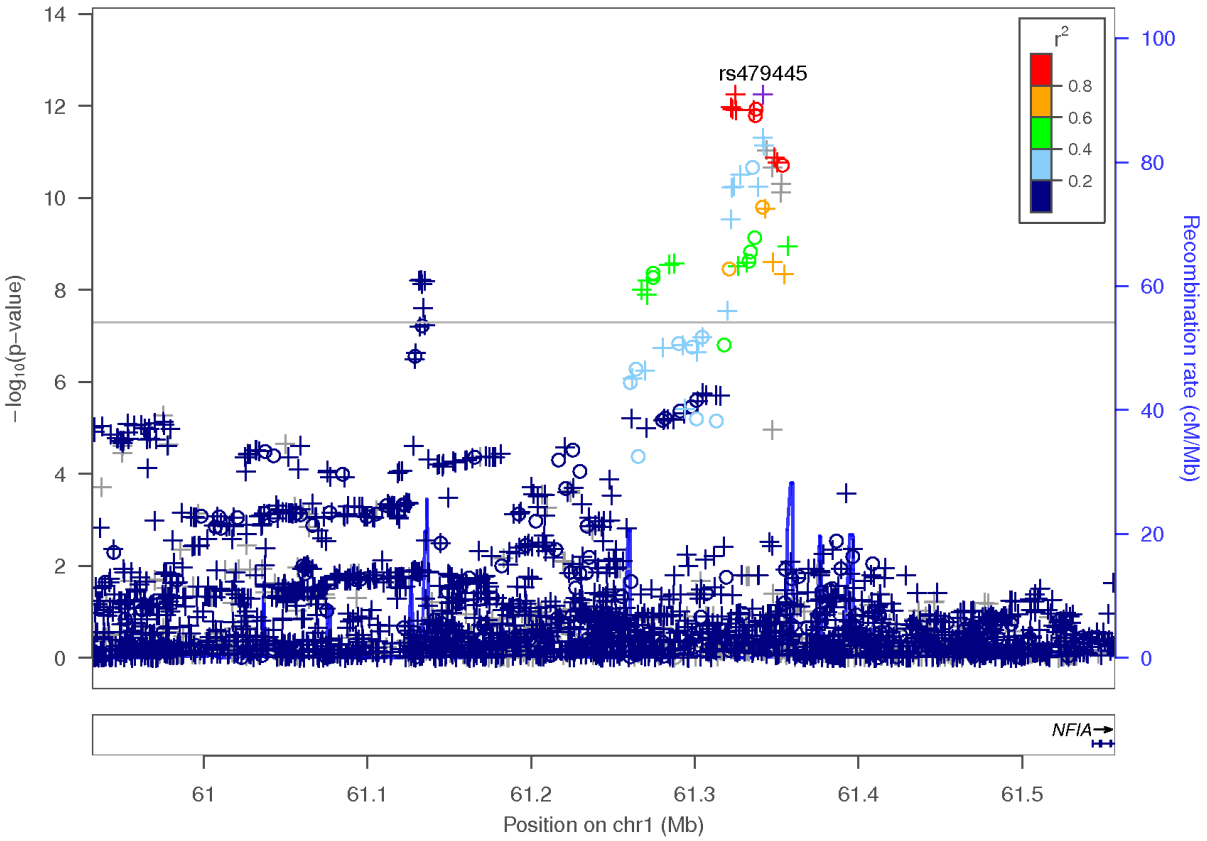

rs4948523
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
CISD1
TFAM
BICC1
UBE2D1
FAM133CP
Position on chr10 (Mb)

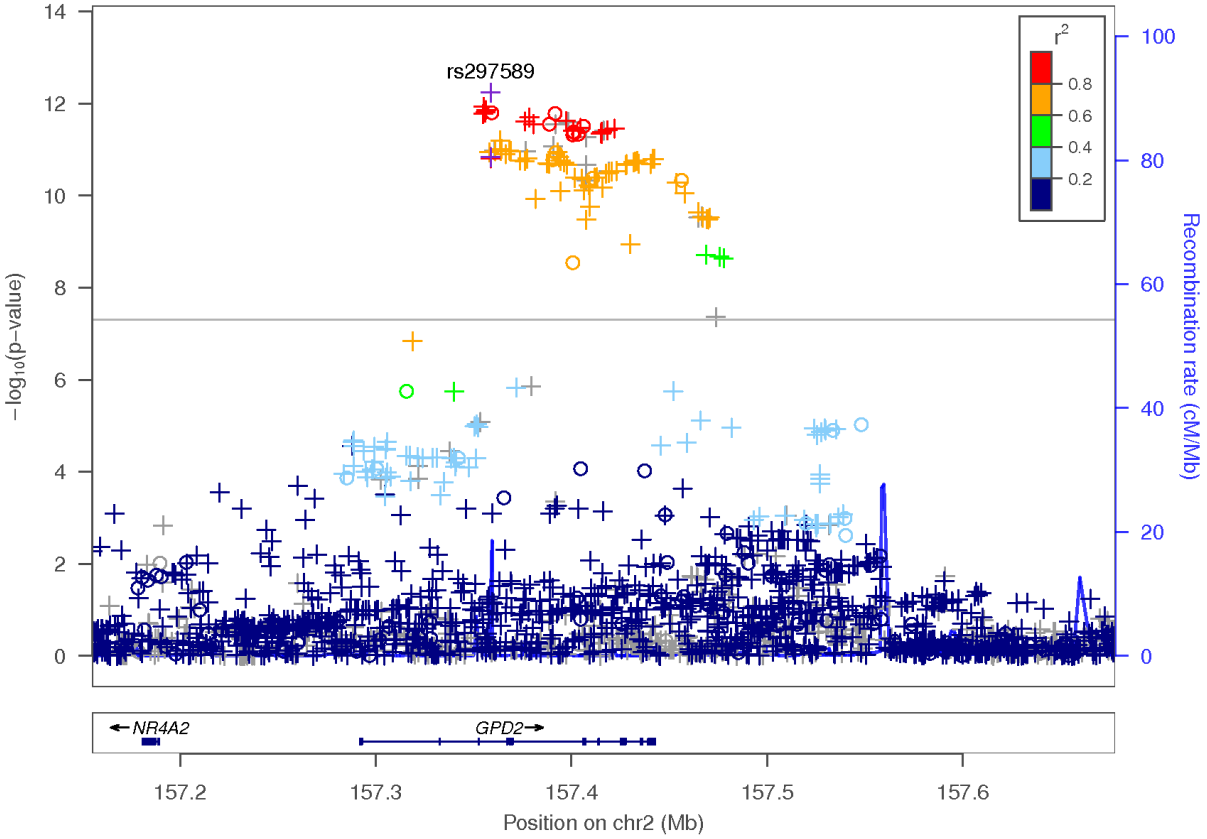

rs34016308
−log10(p−value)
Recombination rate (cM/Mb)
FBLN5
TRIP11
ATXN3
CPSF2
SLC24A4
NDUFB1
Position on chr14 (Mb)

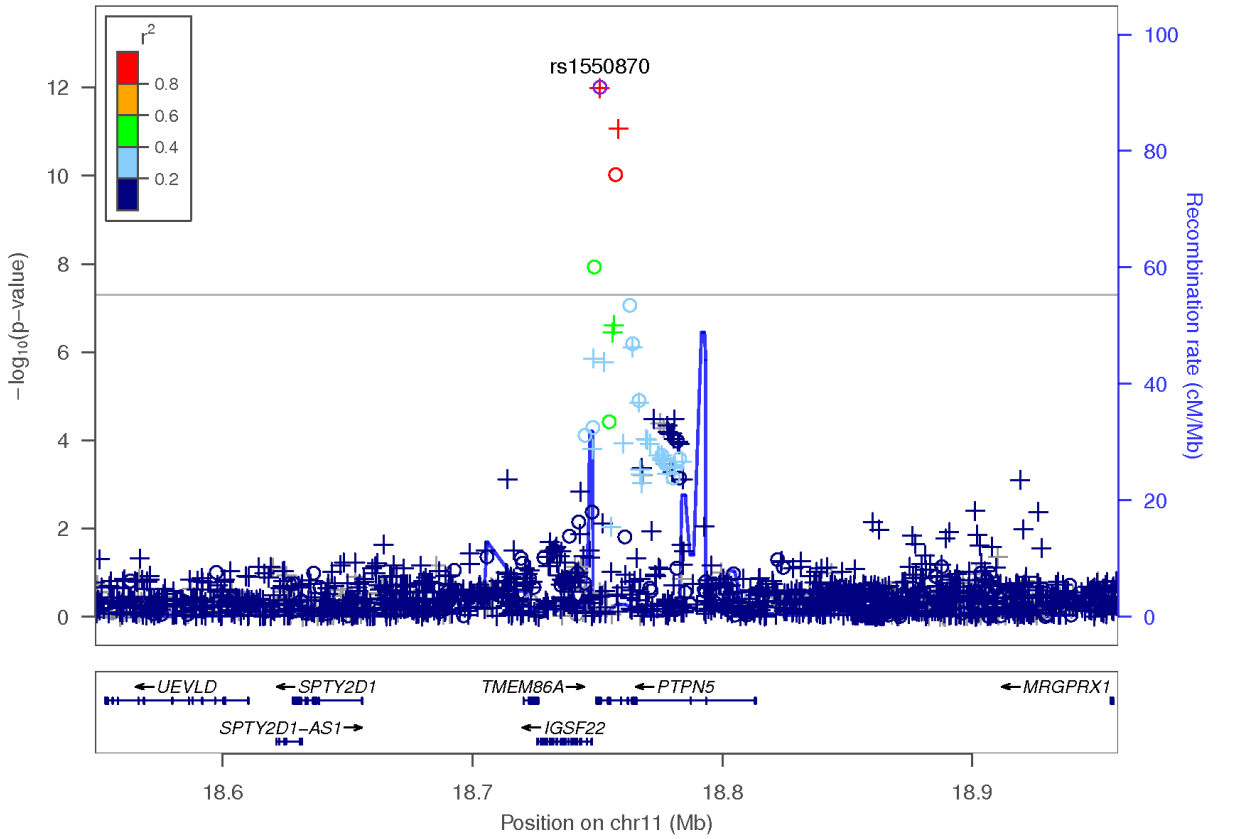

rs1064583
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
FRK
TPI1P3
NT5DC1
COL10A1
TSPYL1
TSPYL4
DSE
Position on chr6 (Mb)

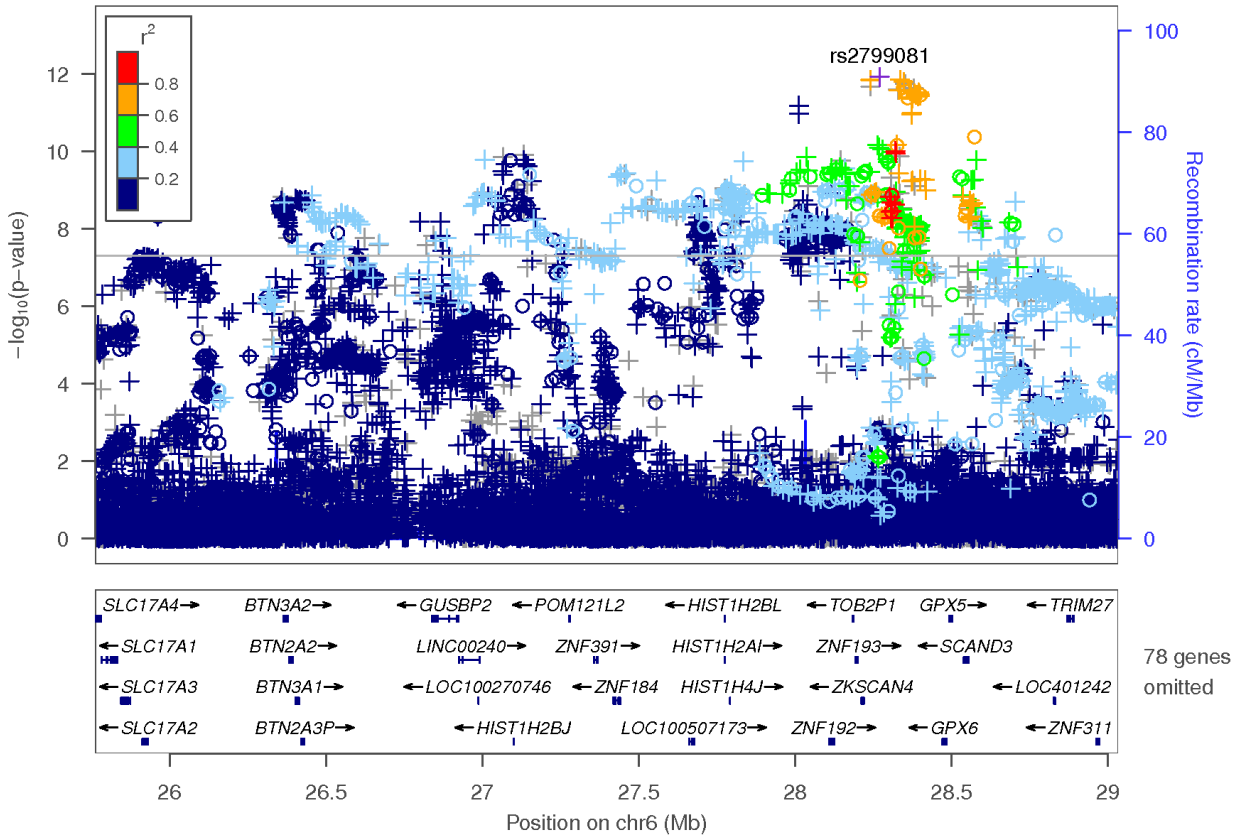

rs201140091
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
FAM25B
FAM25G
FAM25C
LOC399753
FRMPD2P1
FRMPD2
MAPK8
ARHGAP22
Position on chr10 (Mb)

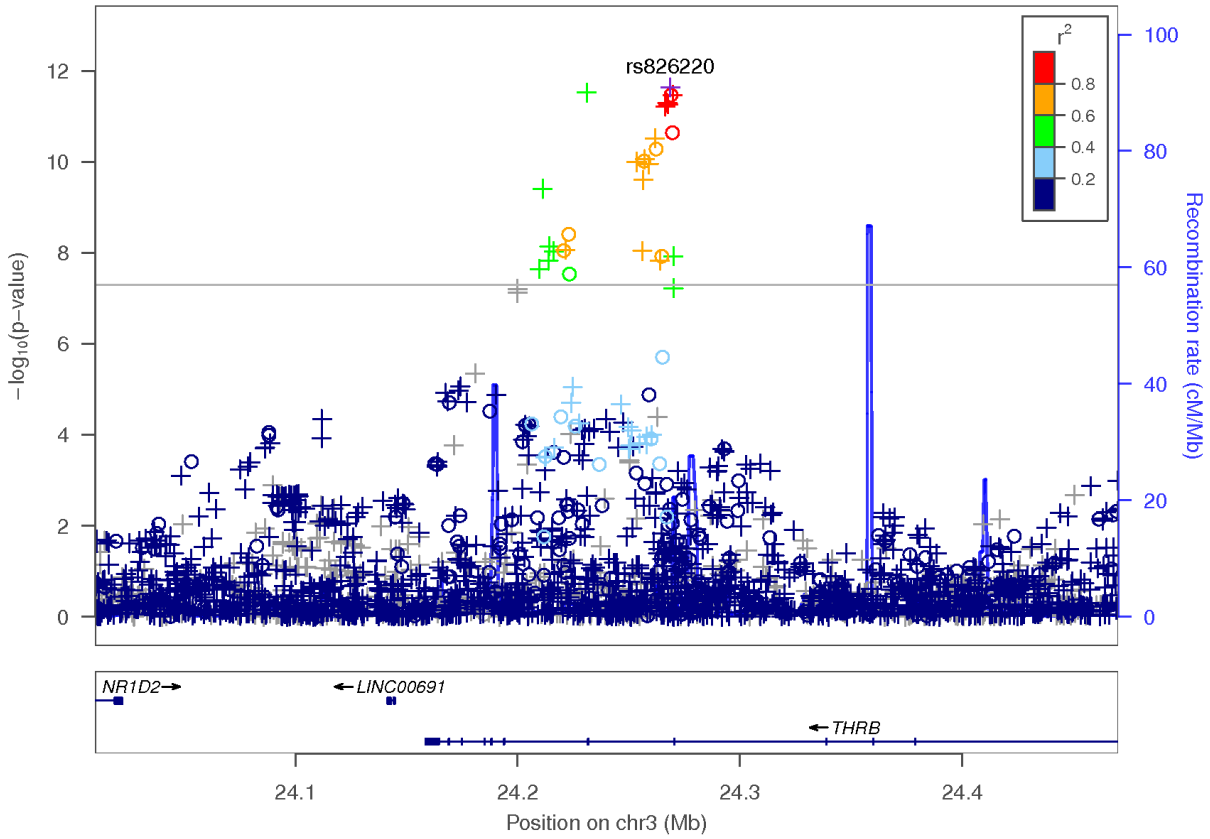

rs73157695
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
COL18A1
COL18A1−AS1
SLC19A1
LOC100129027
PCBP3
COL6A1
COL6A2
FTCD
SPATC1L
LSS
Position on chr21 (Mb)

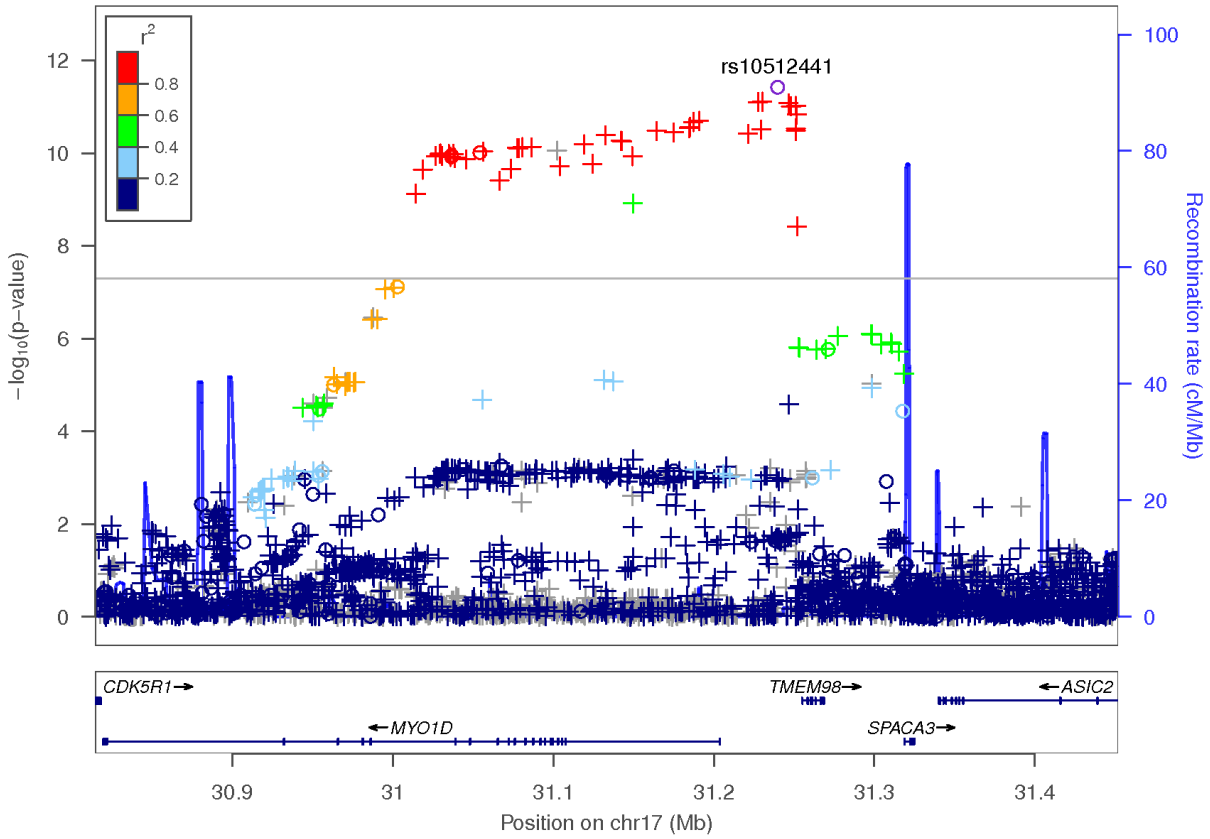

rs479445
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
NFIA
Position on chr1 (Mb)

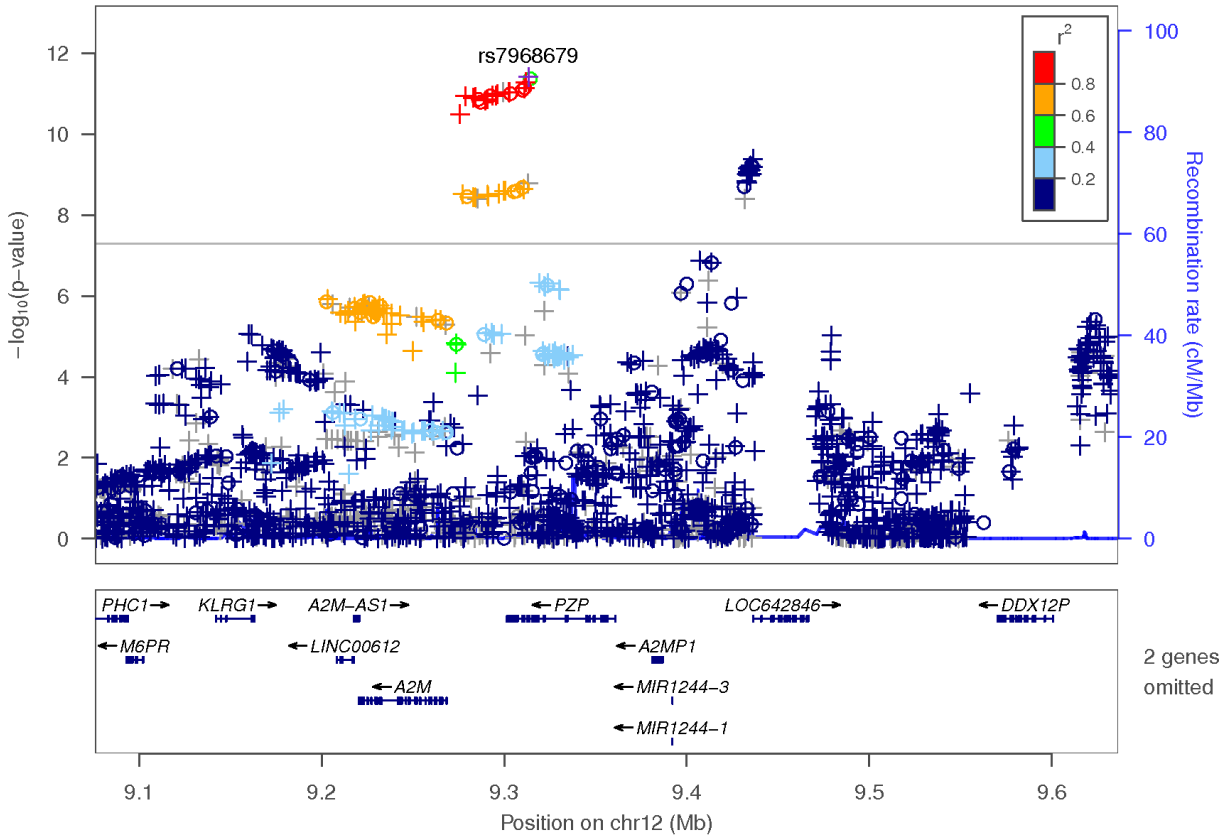

rs297589
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
NR4A2
GPD2
Position on chr2 (Mb)

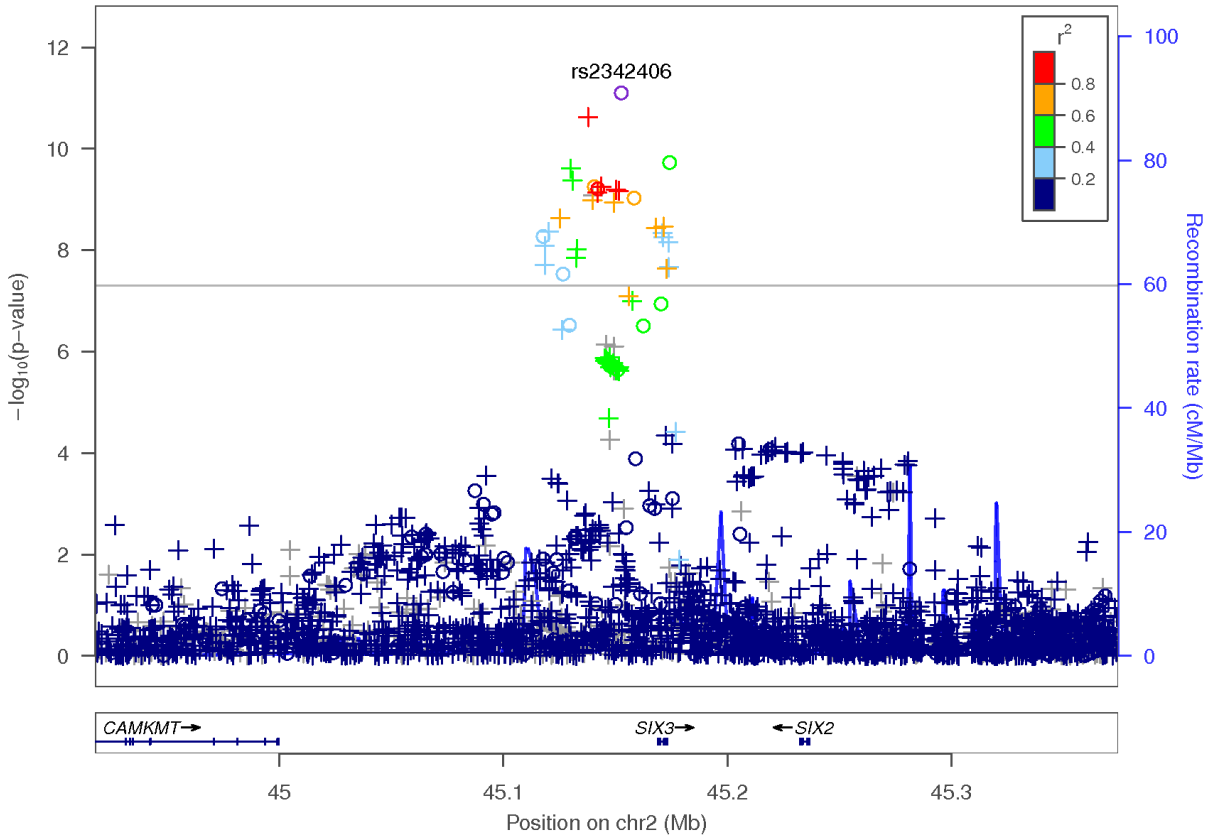

rs1550870
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
UEVLD
SPTY2D1
TMEM86A
PTPN5
MRGPRX1
SPTY2D1−AS1
IGSF22
18.6
18.7
18.8
18.9
Position on chr11 (Mb)

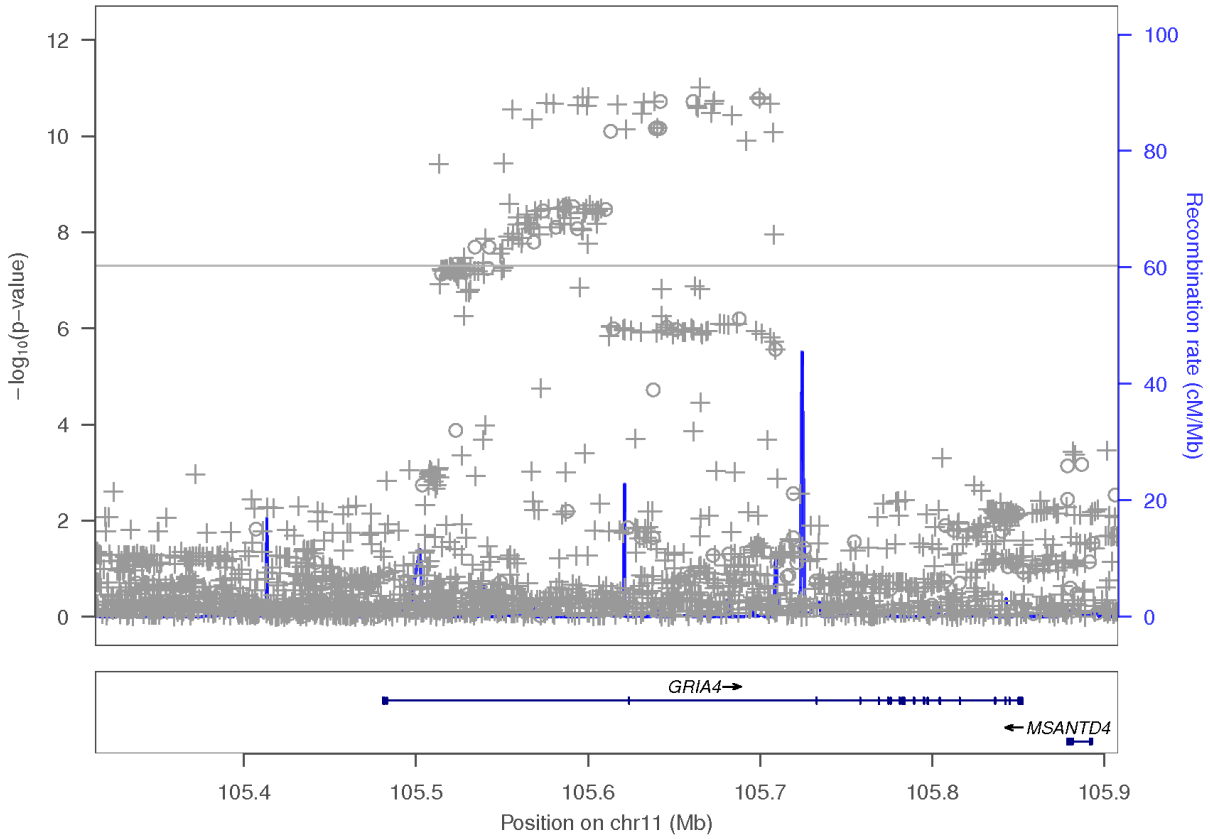

rs2799081
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
SLC17A4
BTN3A2
GUSBP2
POM121L2
HIST1H2BL
TOB2P1
GPX5
TRIM27
SLC17A1
BTN2A2
LINC00240
ZNF391
HIST1H2AI
ZNF193
SCAND3
SLC17A3
BTN3A1
LOC100270746
ZNF184
HIST1H4J
ZKSCAN4
LOC401242
SLC17A2
BTN2A3P
HIST1H2BJ
LOC100507173
ZNF192
GPX6
ZNF311
78 genes omitted
26
26.5
27
27.5
28
28.5
29
Position on chr6 (Mb)

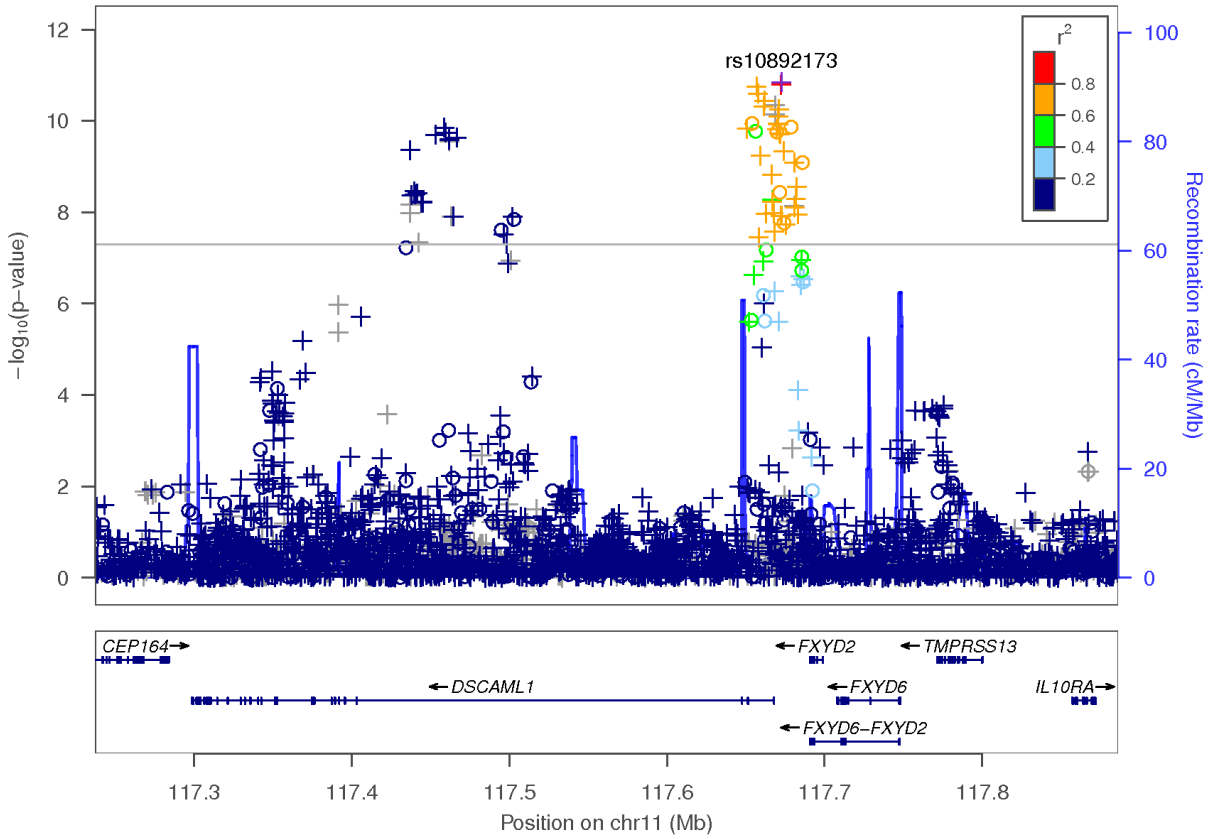

rs826220
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
NR1D2
LINC00691
THRB
24.1
24.2
24.3
24.4
Position on chr3 (Mb)

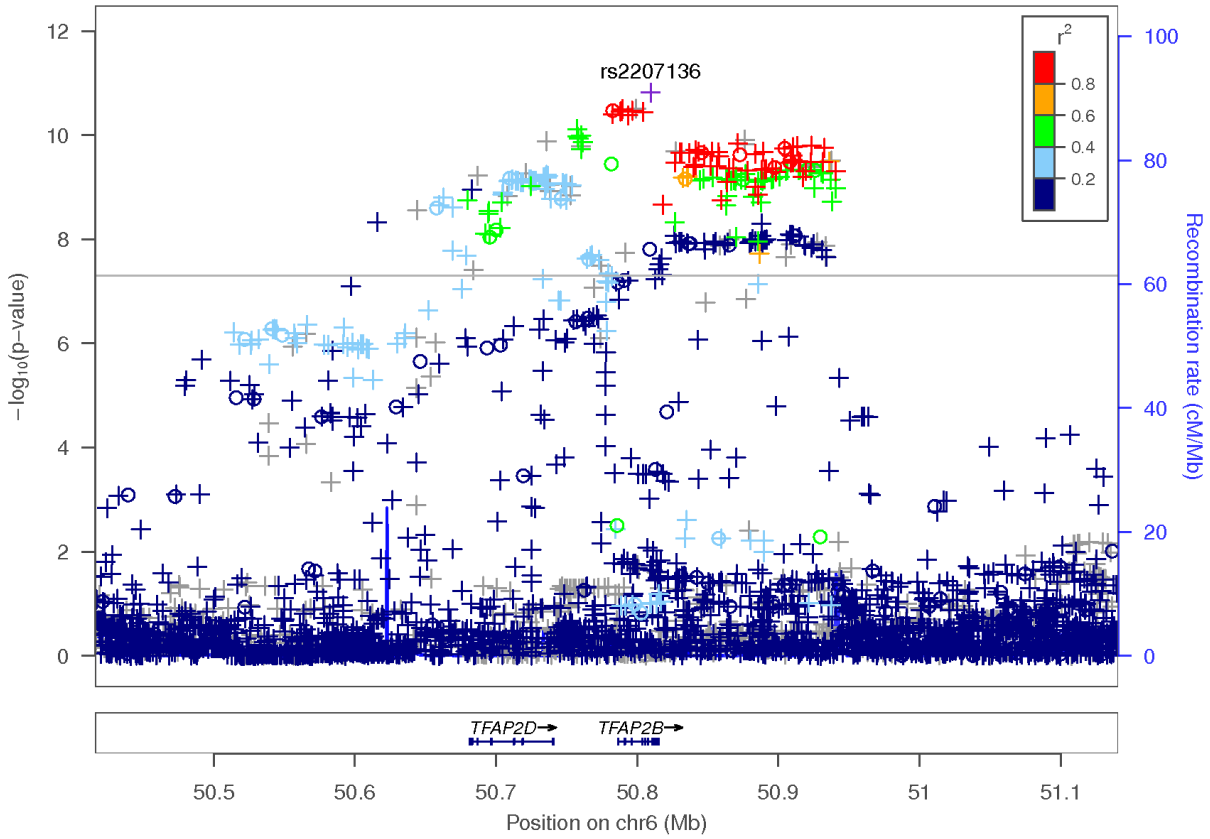

rs10512441
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
CDK5R1
MYO1D
TMEM98
SPACA3
ASIC2
30.9
31
31.1
31.2
31.3
31.4
Position on chr17 (Mb)

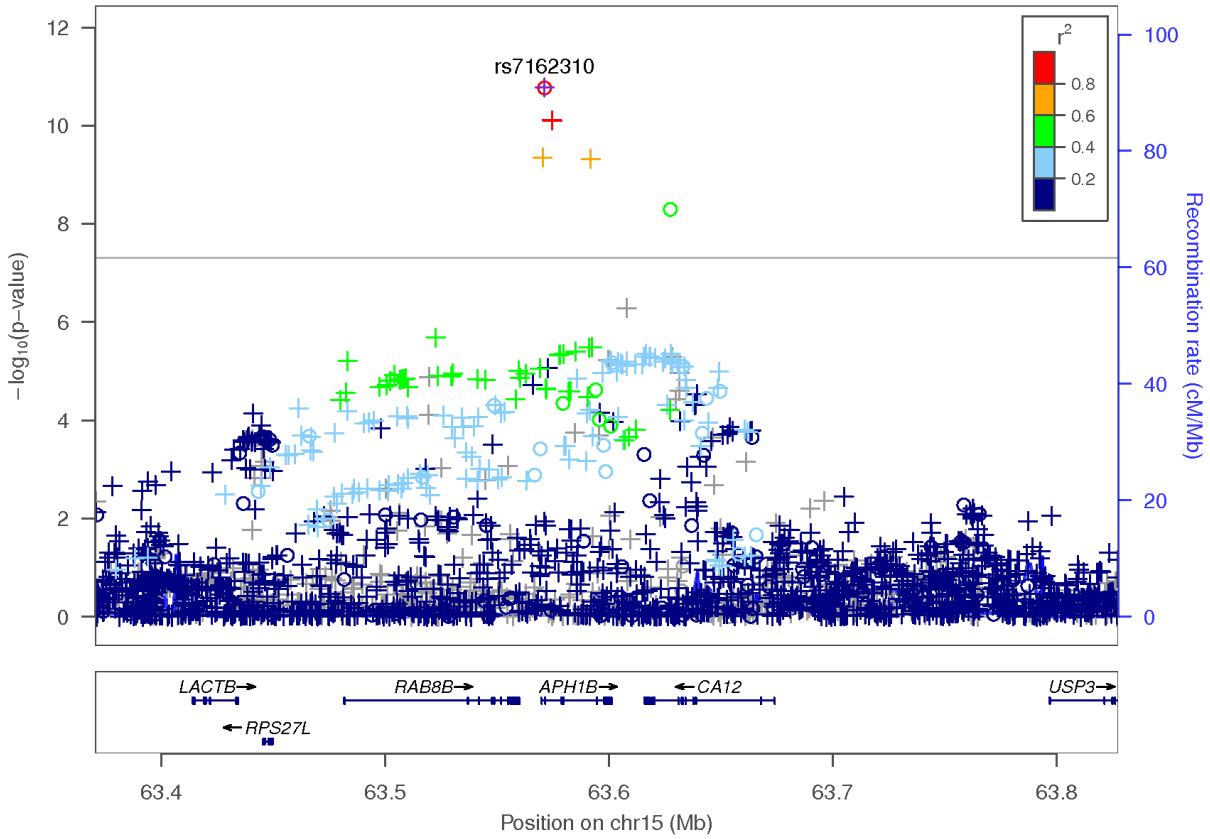

rs7968679
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
PHC1
KLRG1
A2M−AS1
PZP
LOC642846
DDX12P
M6PR
LINC00612
A2MP1
A2M
MIR1244−3
MIR1244−1
2 genes omitted
Position on chr12 (Mb)


rs2342406
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
CAMKMT
SIX3
SIX2
Position on chr2 (Mb)


12
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
GRIA4
MSANTD4
105.4
105.5
105.6
105.7
105.8
105.9
Position on chr11 (Mb)


rs10892173
r2
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)
CEP164
FXYD2
TMPRSS13
DSCAML1
FXYD6
IL10RA
FXYD6–FXYD2
117.3
117.4
117.5
117.6
117.7
117.8
Position on chr11 (Mb)


rs2207136
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
TFAP2D
TFAP2B
50.5
50.6
50.7
50.8
50.9
51
51.1
Position on chr6 (Mb)


rs7162310
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
Recombination rate (cM/Mb)
LACTB
RAB8B
APH1B
CA12
USP3
RPS27L
63.4
63.5
63.6
63.7
63.8
Position on chr15 (Mb)