Analysis Summary: nose size

Phenotype Description

The nose size phenotype comes from one question

- "Morphology" survey
  - "Looking at your nose in profile, which image best matches the shape, NOT the size, of your nose in profile? (You may need to take a picture or use two mirrors to get a better view of your nose from the side. If you have had surgery that may have altered the shape of your nose, please answer for how your nose looked prior to the surgery or surgeries." (16 pictures (a-p) plus "I'm not sure" and "None of the above" options)

The nose size phenotype is scored from 0—3, with 0 encompassing the six smallest pictures (a, b, c, d, e, f), 1 the next five largest (g, h, i, j, n), 2 the next three largest (o, k, l), and 3 the two biggest (m, p).

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]
nose_size	small	29205	11760	17445	4376	9224	7424	8181
	normal	26425	16028	10397	3635	8729	6826	7235
	large	10773	7459	3314	1454	3430	2906	2983
	huge	620	452	168	59	151	196	214

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

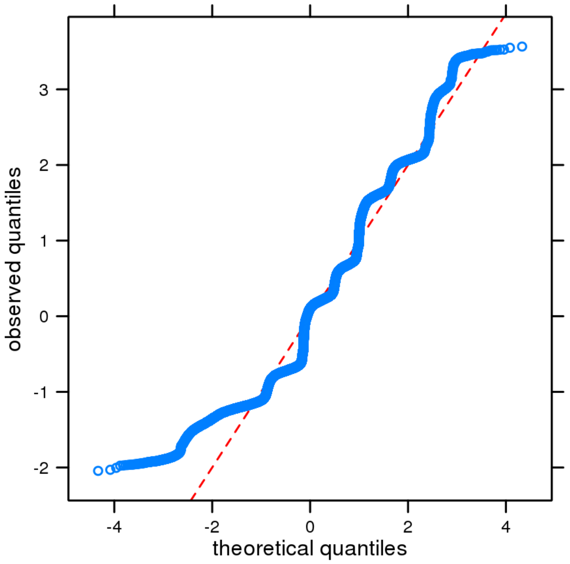
Phenotype	Group	Total	v1/v2	v3	v4
nose_size	small	29205	3422	24437	1346
	normal	26425	3198	22096	1131
	large	10773	1241	9125	407
	huge	620	101	491	28

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	t value	Pr(>|t|)
age	0.00147	0.000177	8.3	8.2×10^{-17}
sexF	−0.33297	0.005606	−59.4	0.0
pc.0	−0.12359	0.002799	−44.2	0.0
pc.1	0.01629	0.002812	5.8	7.0×10^{-9}
pc.2	0.01375	0.002810	4.9	1.0×10^{-6}
pc.3	0.00463	0.002802	1.7	0.099
pc.4	0.01133	0.002802	4.0	5.3×10^{-5}

Q-Q plot of scaled residuals



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	−16867	13762200
MAF < 0.1%	−1722709	12039491

Genetic Association Tests

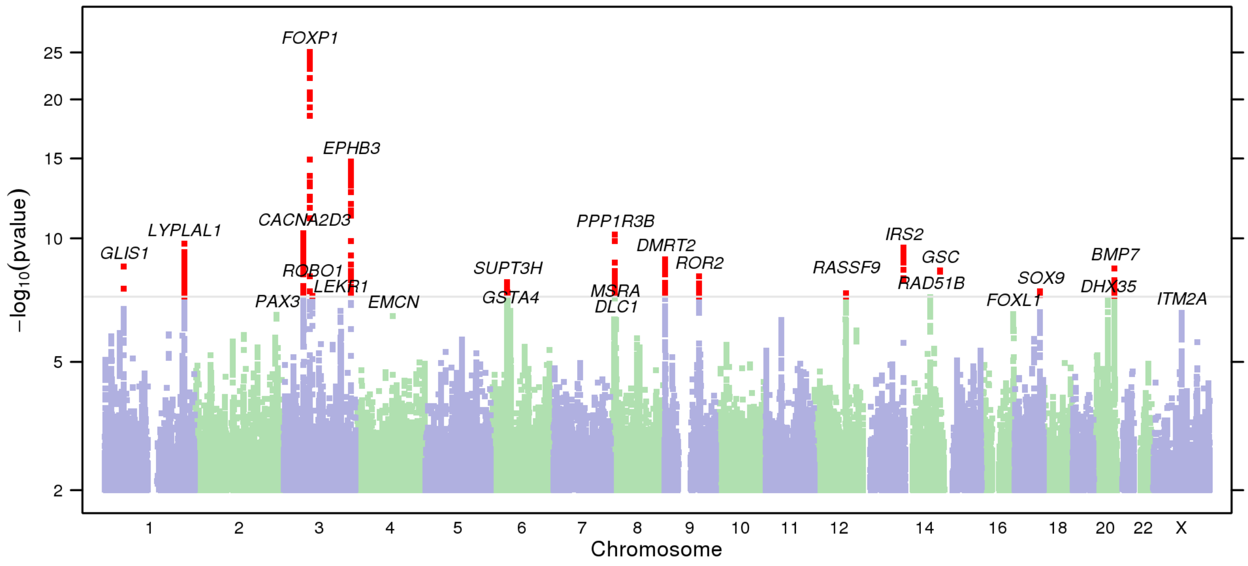
We performed linear regression assuming an additive model for allelic effects, using the model:

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

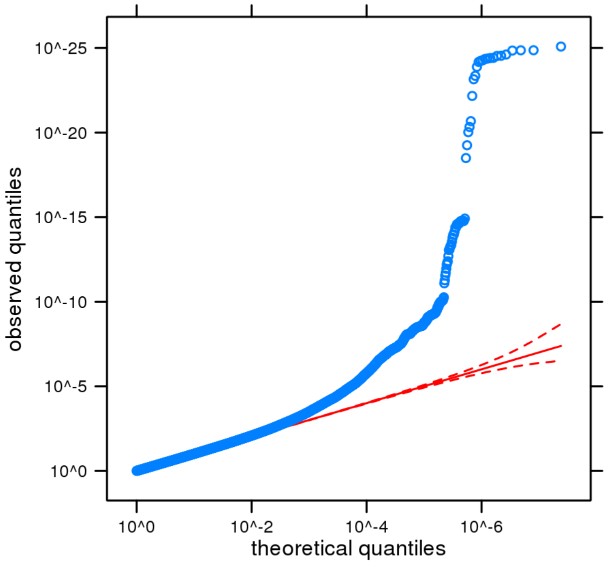
This genome-wide association analysis includes data from 67023 individuals of European ancestry, filtered to remove close relatives.

The results in this report have been adjusted for a genomic control inflation factor λ=1.088. The equivalent inflation factor rescaled for a sample size of 2000 would be λ_{2000}= 1.003 , and for 20000, λ_{20000}= 1.026 .

Manhattan Plot



Q-Q Plot of GWAS Results



Index SNPs for Strongest Associations

cytoband	assay.name	scaffold	position	alleles	src	pvalue	effect	95% CI	gene.context
3p13	3:71227306:T_TGA	chr3	71227306	D/I	I	8.2×10^{-26}	0.049	[0.040,0.059]	FOXP1--[]---EIF4E3
3q27.1	rs13097965	chr3	184339757	C/T	I	1.7×10^{-15}	−0.033	[-0.041,-0.025]	EPHB3--[]--MAGEF1
3p14.3	rs56063440	chr3	54731374	C/G	I	5.5×10^{-11}	0.030	[0.021,0.039]	[CACNA2D3]
8p23.1	rs2929451	chr8	9085295	A/T	I	6.4×10^{-11}	0.027	[0.019,0.035]	PPP1R3B--[]---TNKS
1q41	rs5781117	chr1	219642187	D/I	I	1.9×10^{-10}	0.028	[0.020,0.037]	LYPLAL1---[]---SLC30A10
13q34	rs146188897	chr13	110372691	D/I	I	3.0×10^{-10}	0.030	[0.021,0.039]	MYO16---[]--IRS2
9p24.3	rs10809266	chr9	1106093	A/G	I	1.1×10^{-9}	0.027	[0.018,0.036]	DMRT2--[]---SMARCA2
1p32.3	rs702489	chr1	54197688	A/G	I	2.5×10^{-9}	0.038	[0.025,0.050]	[GLIS1]
20q13.31	rs35130793	chr20	55792165	A/C	I	2.9×10^{-9}	0.025	[0.017,0.033]	[BMP7]
14q32.13	rs2224309	chr14	95333678	A/C	I	3.8×10^{-9}	−0.031	[-0.041,-0.021]	GSC--[]---DICER1
9q22.31	rs10761129	chr9	94486321	C/T	I	6.9×10^{-9}	−0.026	[-0.034,-0.017]	[ROR2]
6p21.1	6:44820741:AG_A	chr6	44820741	D/I	I	1.2×10^{-8}	−0.024	[-0.032,-0.016]	[SUPT3H]
17q24.3	rs34091987	chr17	70025587	C/T	I	3.1×10^{-8}	0.025	[0.016,0.034]	[]--SOX9
12q21.31	rs10779169	chr12	85967804	A/G	I	3.6×10^{-8}	−0.023	[-0.031,-0.015]	ALX1---[]---RASSF9
3p12.3	rs424737	chr3	78815906	A/G	I	4.6×10^{-8}	−0.025	[-0.033,-0.016]	[ROBO1]
14q24.1	rs34702092	chr14	68991747	D/I	I	5.1×10^{-8}	−0.026	[-0.035,-0.016]	[RAD51B]
20q12	rs6101567	chr20	38105055	A/G	I	6.7×10^{-8}	0.023	[0.014,0.031]	DHX35---[]

3q25.31	rs11717138	chr3	156534628	C/T	I	1.8×10^{-7}	−0.025	[-0.035,-0.016]	TIPARP---[]-LEKR1
6p12.2	rs142900698	chr6	52834739	C/G	I	1.8×10^{-7}	−0.267	[-0.367,-0.166]	GSTA3--[]-GSTA4
Xq21.1	rs5959351	chrX	78675583	C/T	I	2.1×10^{-7}	0.018	[0.011,0.025]	ITM2A--[]---TBX22
16q24.1	rs61646804	chr16	86608897	D/I	I	2.4×10^{-7}	0.029	[0.018,0.041]	FOXC2-[]-FOXL1
2q36.1	rs34460569	chr2	223026935	C/T	I	2.5×10^{-7}	−0.025	[-0.035,-0.016]	EPHA4---[]--PAX3
4q24	rs6851148	chr4	101218062	A/C	I	2.8×10^{-7}	−0.023	[-0.032,-0.014]	DDIT4L---[]--EMCN
8p23.1	rs11782517	chr8	10113507	C/T	I	3.8×10^{-7}	0.024	[0.015,0.034]	[MSRA]
8p22	rs767764	chr8	13199810	C/G	I	4.0×10^{-7}	0.025	[0.016,0.035]	[DLC1]

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
3:71227306:T_TGA	FALSE	FALSE	FALSE					0.8571	0.8514	0.00026	0.3393	v2v3v4
rs13097965	TRUE	TRUE	TRUE	0.9997	0.48	0.64	0.5292	0.9994	0.9968	0.62	0.5271	v2v3v4
rs56063440	FALSE	FALSE	FALSE					0.9829	0.9764	0.073	0.7192	v2v3v4
rs2929451	FALSE	FALSE	FALSE					0.9987	0.9980	0.21	0.5182	v2v3v4
rs5781117	FALSE	FALSE	FALSE					0.9682	0.9650	0.44	0.6763	v2v3v4
rs146188897	FALSE	FALSE	FALSE					0.9809	0.9783	0.79	0.2529	v2v3v4
rs10809266	FALSE	FALSE	FALSE					0.9506	0.9037	3.5×10^{-10}	0.3371	v2v3v4
rs702489	FALSE	TRUE	TRUE	0.9998	0.0055	0.56	0.8663	0.9542	0.7763	0.072	0.8669	v2v3v4
rs35130793	FALSE	FALSE	FALSE					0.9454	0.9304	0.0016	0.4843	v2v3v4
rs2224309	FALSE	FALSE	FALSE					0.9596	0.9337	0.74	0.7981	v2v3v4
rs10761129	FALSE	TRUE	FALSE	0.9993	0.045	0.74	0.6651	0.9906	0.9091	0.57	0.6653	v2v3v4
6:44820741:AG_A	FALSE	FALSE	FALSE					0.9880	0.9856	0.41	0.4788	v2v3v4
rs34091987	FALSE	FALSE	FALSE					0.9877	0.9839	0.48	0.3072	v2v3v4
rs10779169	FALSE	FALSE	FALSE					0.9961	0.9955	0.67	0.4156	v2v3v4
rs424737	FALSE	FALSE	FALSE					0.9901	0.9824	0.44	0.6996	v2v3v4
rs34702092	FALSE	FALSE	FALSE					0.9842	0.9748	0.093	0.2650	v2v3v4
rs6101567	FALSE	FALSE	FALSE					0.9850	0.9806	0.077	0.5081	v2v3v4
rs11717138	FALSE	FALSE	FALSE					0.9892	0.9787	0.69	0.2389	v2v3v4
rs142900698	FALSE	FALSE	FALSE					0.9821	0.9180	2.1×10^{-5}	0.9983	v2v3v4
rs5959351	FALSE	FALSE	FALSE					0.9895	0.9848	0.0030	0.6179	v2v3v4
rs61646804	FALSE	FALSE	FALSE					0.8464	0.7628	5.1×10^{-16}	0.8133	v2v3v4
rs34460569	FALSE	FALSE	FALSE					0.9863	0.9737	0.079	0.2299	v2v3v4
rs6851148	FALSE	FALSE	FALSE					0.9155	0.8283	3.1×10^{-10}	0.3718	v2v3v4
rs11782517	FALSE	FALSE	FALSE					0.9919	0.9762	0.40	0.7549	v2v3v4
rs767764	FALSE	FALSE	FALSE					0.9973	0.9914	0.72	0.2123	v2v3v4

SNP Statistics in the GWAS Sample

assay.name	AA.0	AB.0	BB.0	im.num.0	dose.b.0
3:71227306:T_TGA				67023	0.3338
rs13097965	14920	33304	18779	67023	0.5288
rs56063440				67023	0.7153
rs2929451				67023	0.5169
rs5781117				67023	0.6743
rs146188897				67023	0.2563
rs10809266				67023	0.3418
rs702489	1096	13372	44576	67023	0.8704
rs35130793				67023	0.4863
rs2224309				67023	0.7976
rs10761129	6233	25019	24849	67023	0.6671
6:44820741:AG_A				67023	0.4766
rs34091987				67023	0.3081
rs10779169				67023	0.4140
rs424737				67023	0.7006
rs34702092				67023	0.2683
rs6101567				67023	0.5034
rs11717138				67023	0.2385
rs142900698				67023	0.9983
rs5959351				67023	0.6164
rs61646804				67023	0.8122
rs34460569				67023	0.2309
rs6851148				67023	0.3661
rs11782517				67023	0.7554
rs767764				67023	0.2137

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
1q41	219642187	rs5781117	1.9×10^{-10}	2037	0.866	rs2605100	3.0×10^{-8}	19557161	Adiposity	LYPLAL1
1q41	219642187	rs5781117	1.9×10^{-10}	51033	0.527	rs2820464	7.0×10^{-9}	23563607	Waist-hip ratio	LYPLAL1
1q41	219642187	rs5781117	1.9×10^{-10}	58332	0.522	rs2785980	2.0×10^{-8}	22581228	Fasting insulin-related traits (interaction with BMI)	LYPLAL1
1q41	219642187	rs5781117	1.9×10^{-10}	85592	0.558	rs3001032	4.0×10^{-8}	22479202	Adiponectin levels	LYPLAL1

14q24.1	68991747	rs34702092	$5.1{\times}10^{-8}$	−5590	0.951	rs11624164	$5.0{\times}10^{-6}$	23251661	Obesity-related traits	RAD51L1
14q24.1	68991747	rs34702092	$5.1{\times}10^{-8}$	42935	0.787	rs999737	$3.0{\times}10^{-19}$	23535729	Breast cancer	RAD51L1
14q24.1	68991747	rs34702092	$5.1{\times}10^{-8}$	42935	0.787	rs999737	$2.0{\times}10^{-7}$	19330030	Breast cancer	RAD51L1
Xq21.1	78675583	rs5959351	$2.1{\times}10^{-7}$	−26390	0.749	rs1474563	$3.0{\times}10^{-6}$	18391951	Height	ITM2A

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
9q22.31	94486321	rs10761129	$6.9{\times}10^{-9}$	0	1.000	rs10761129	ROR2	V819I

Nearby Expression QTLs

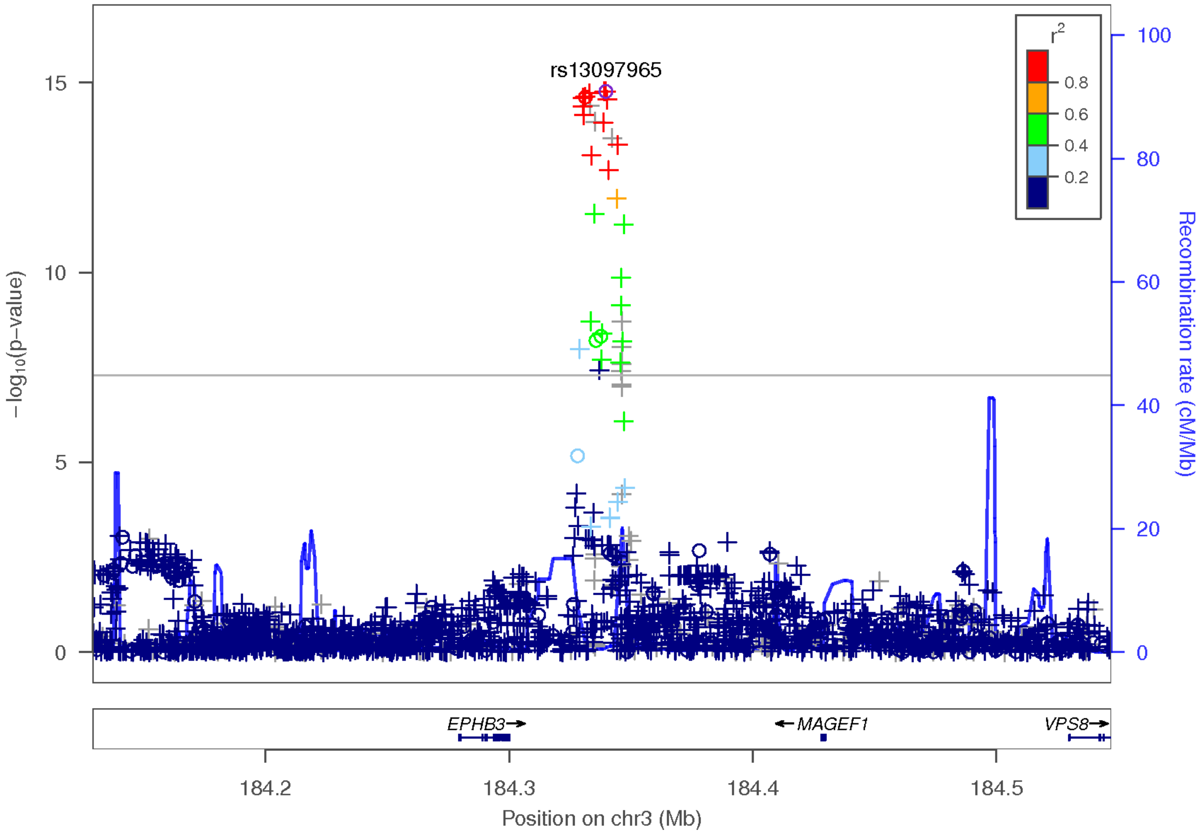
region	position	our.name	our.pval	dist	rsqr	assay.name	eqtl.dist	eqtl.gene	eqtl.pval	eqtl.rsqr	tissue	pubmed.id
3p14.3	54731374	rs56063440	$5.5{\times}10^{-11}$	50257	0.618	rs11914780	−2222994	NT5DC2	0.00071	0.040	B-Cell	22446964
8p23.1	9085295	rs2929451	$6.4{\times}10^{-11}$	−55882	0.650	rs435581	−2285766	DEFA4	0.00052	0.042	B-Cell	22446964
8p23.1	9085295	rs2929451	$6.4{\times}10^{-11}$	−55882	0.650	rs435581	−281782	MFHAS1	$4.6{\times}10^{-7}$	0.087	B-Cell	22446964
8p23.1	9085295	rs2929451	$6.4{\times}10^{-11}$	−78	0.924	rs2929305	−523730	CLDN23	$1.6{\times}10^{-5}$	0.065	Monocyte	22446964
8p23.1	9085295	rs2929451	$6.4{\times}10^{-11}$	0	1.000	rs2929451	334164	MFHAS1	$2.2{\times}10^{-10}$	0.029	Monocyte	20502693
20q13.31	55792165	rs35130793	$2.9{\times}10^{-9}$	14175	0.574	rs186659	−183952	HS.132453	0.00020	0.048	Monocyte	22446964
9q22.31	94486321	rs10761129	$6.9{\times}10^{-9}$	0	1.000	rs10761129	568474	SNORA84	0.00011	0.052	Monocyte	22446964

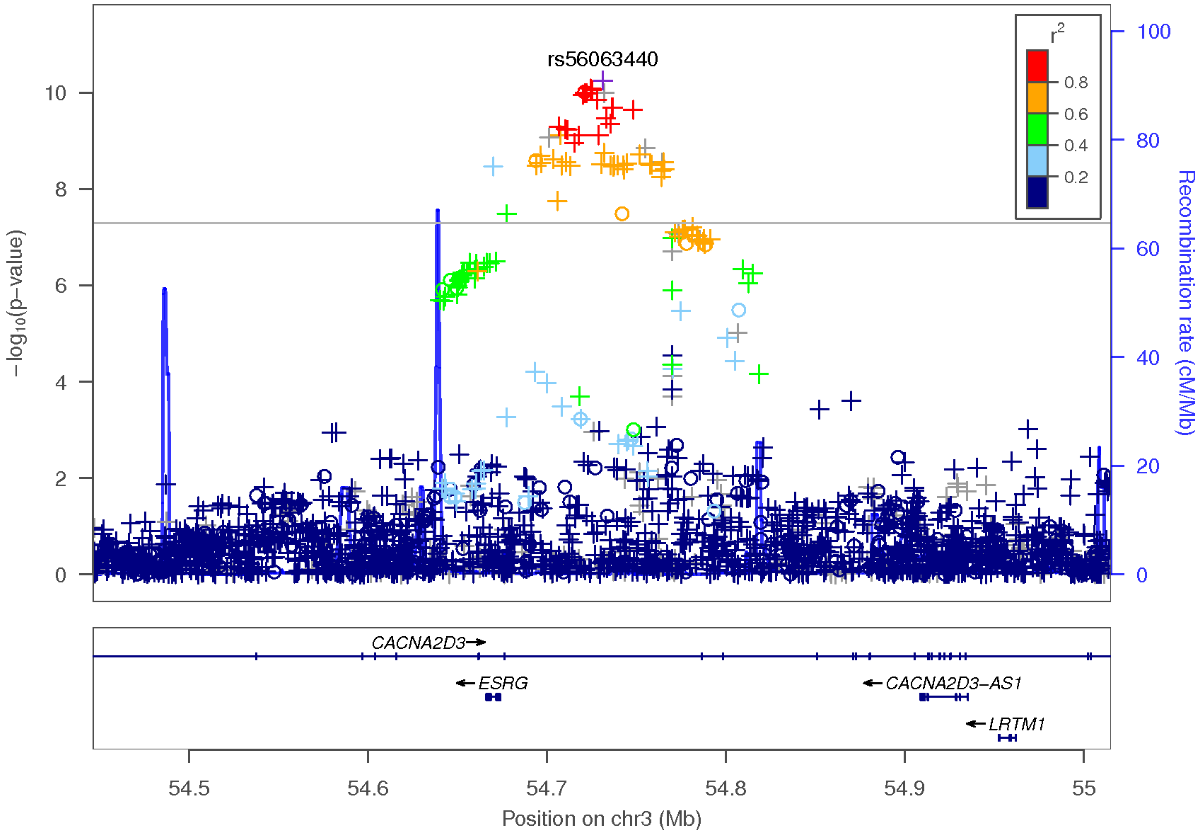
Nearby Clinical Variants

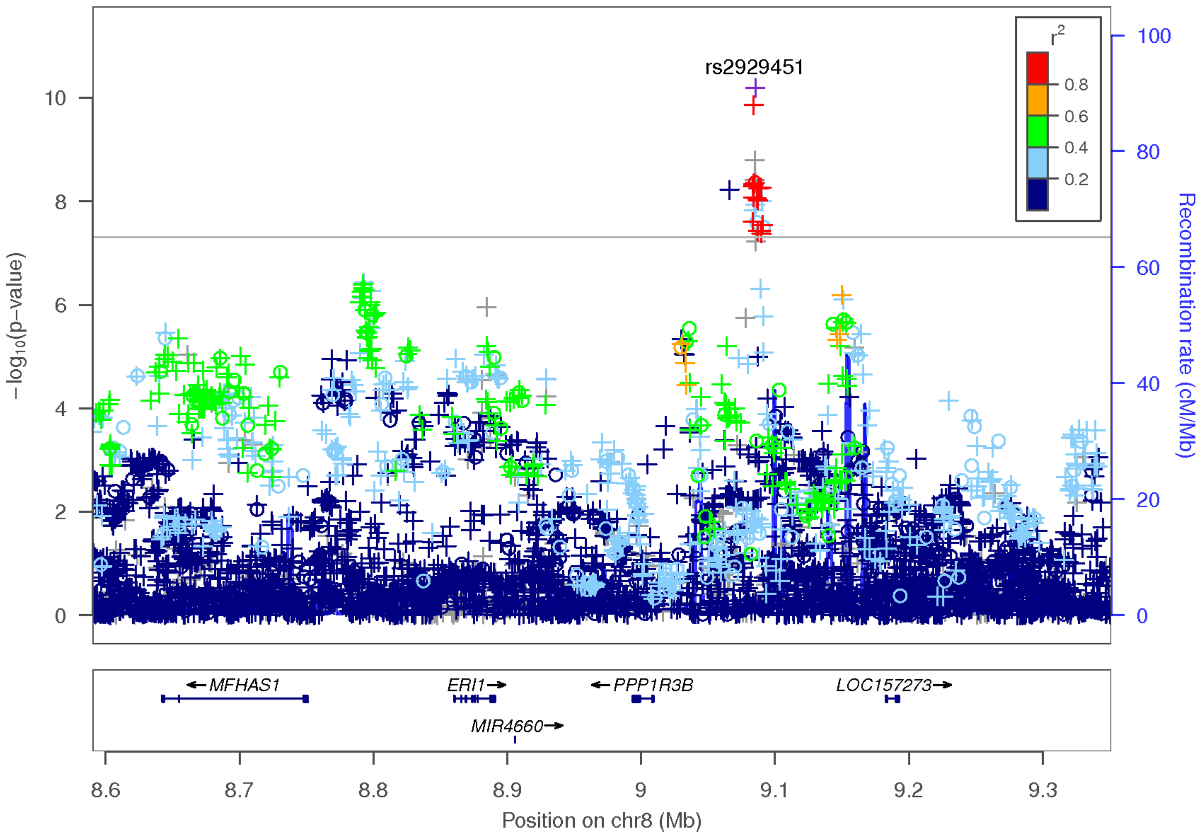
no hits were found for clinical variants

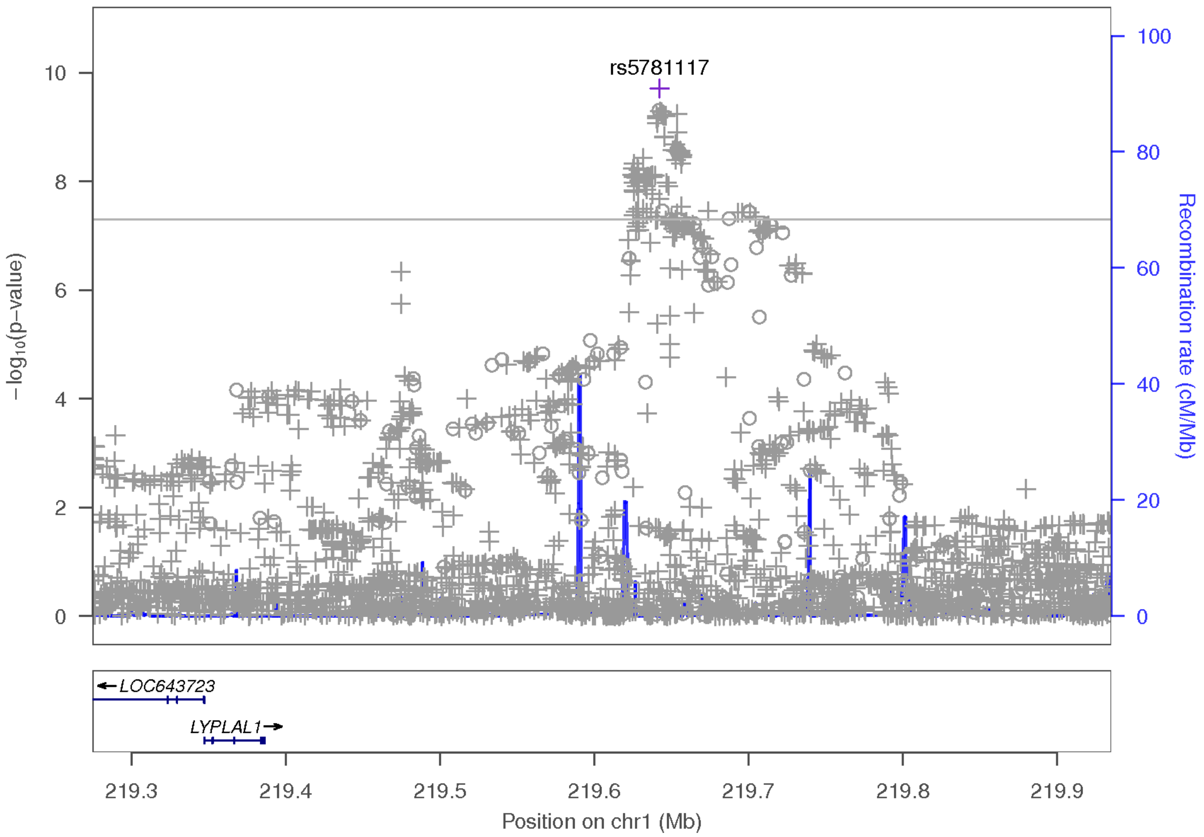
Regional Association Plots

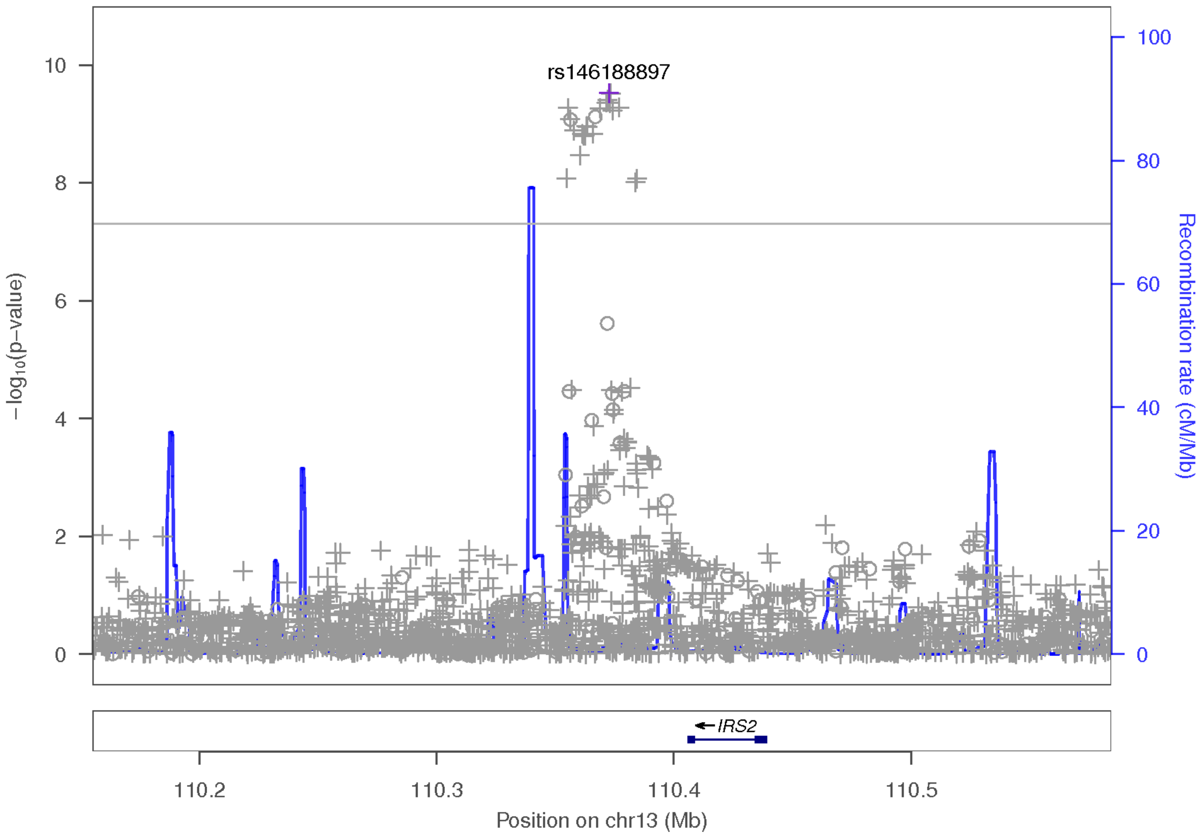
locuszoom plot for 3:71227306:T_TGA failed

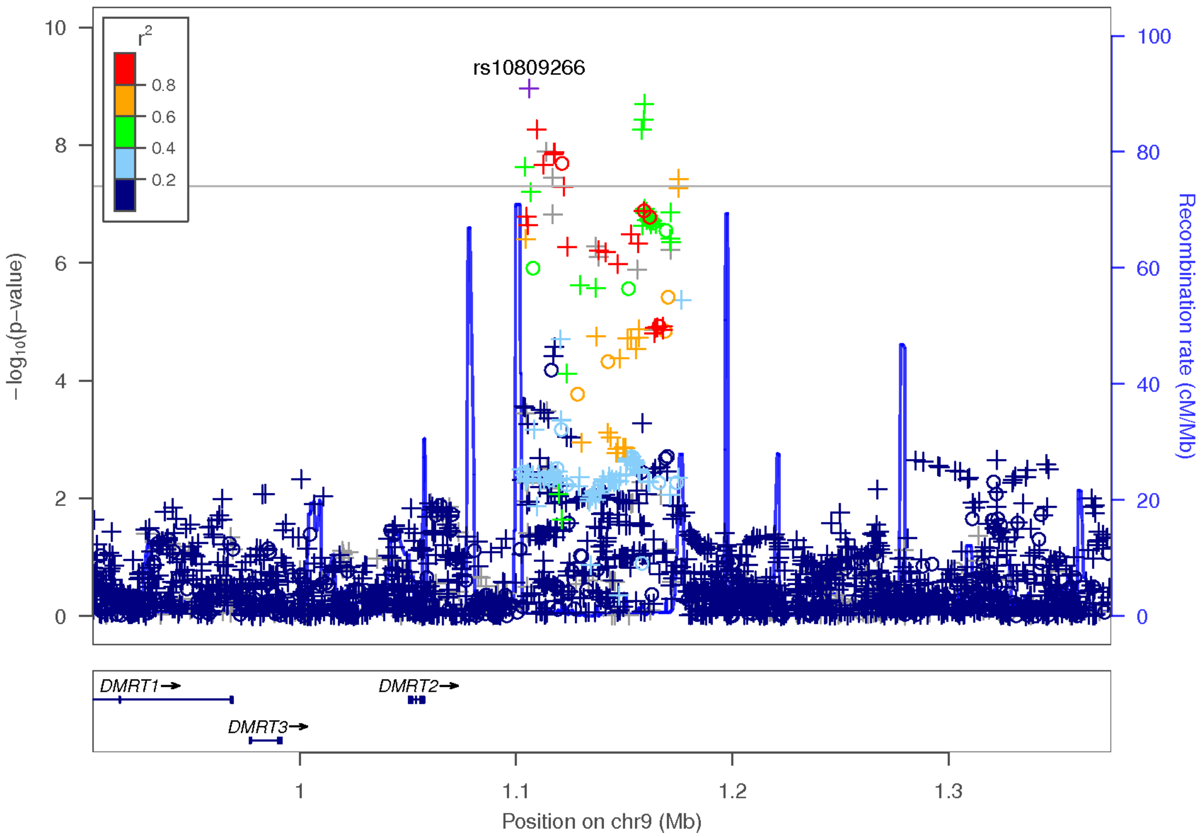

rs13097965
r2
0.8
0.6
0.4
0.2
15
10
5
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
EPHB3→
←MAGEF1
VPS8→
184.2
184.3
184.4
184.5
Position on chr3 (Mb)

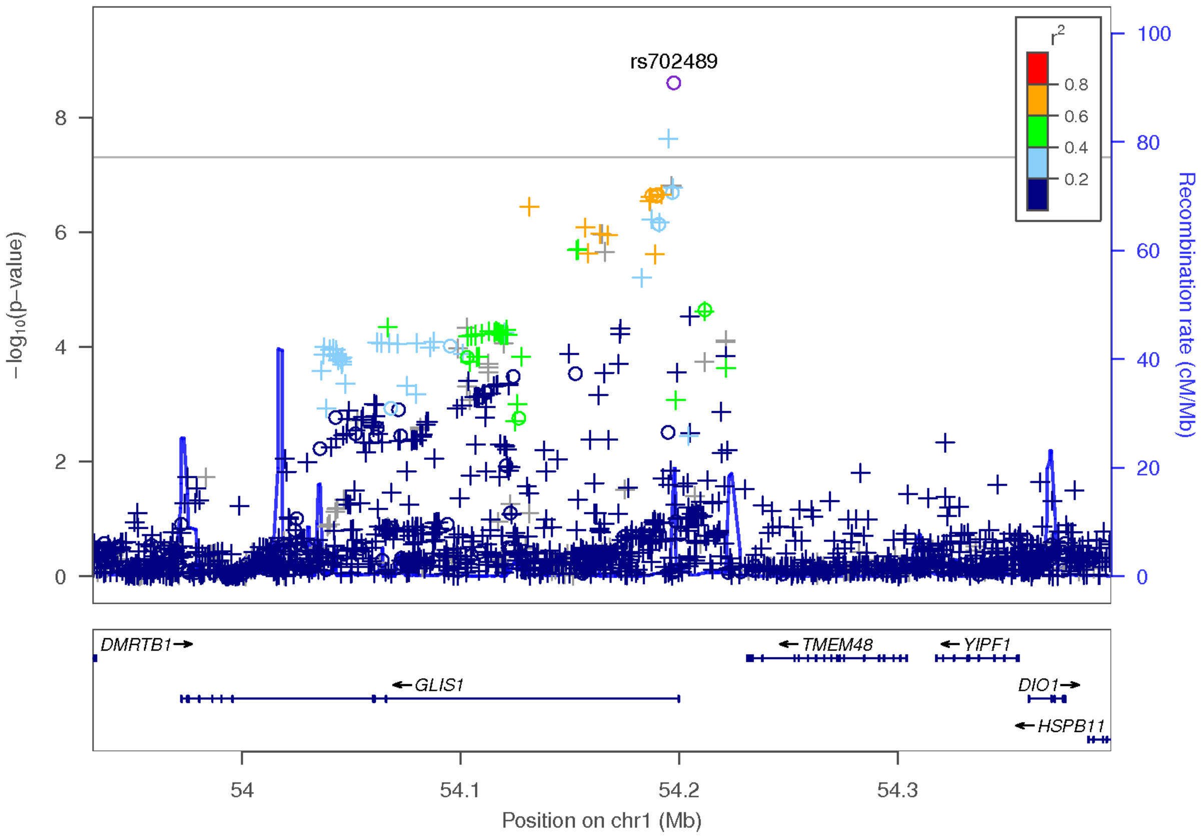

rs56063440
r2
0.8
0.6
0.4
0.2
10
8
6
4
2
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
CACNA2D3→
←ESRG
←CACNA2D3−AS1
←LRTM1
54.5
54.6
54.7
54.8
54.9
55
Position on chr3 (Mb)

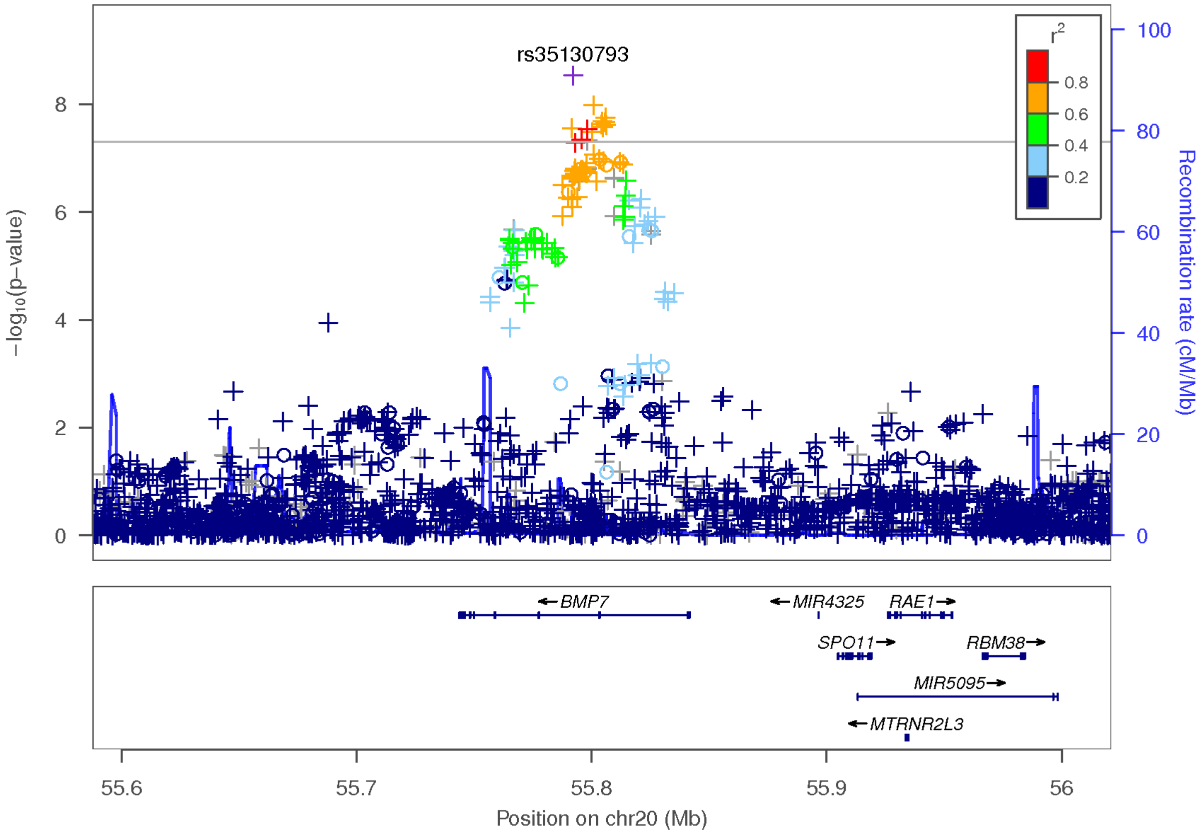

rs2929451
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
MFHAS1
ERI1
PPP1R3B
LOC157273
MIR4660
8.6
8.7
8.8
8.9
9
9.1
9.2
9.3
Position on chr8 (Mb)

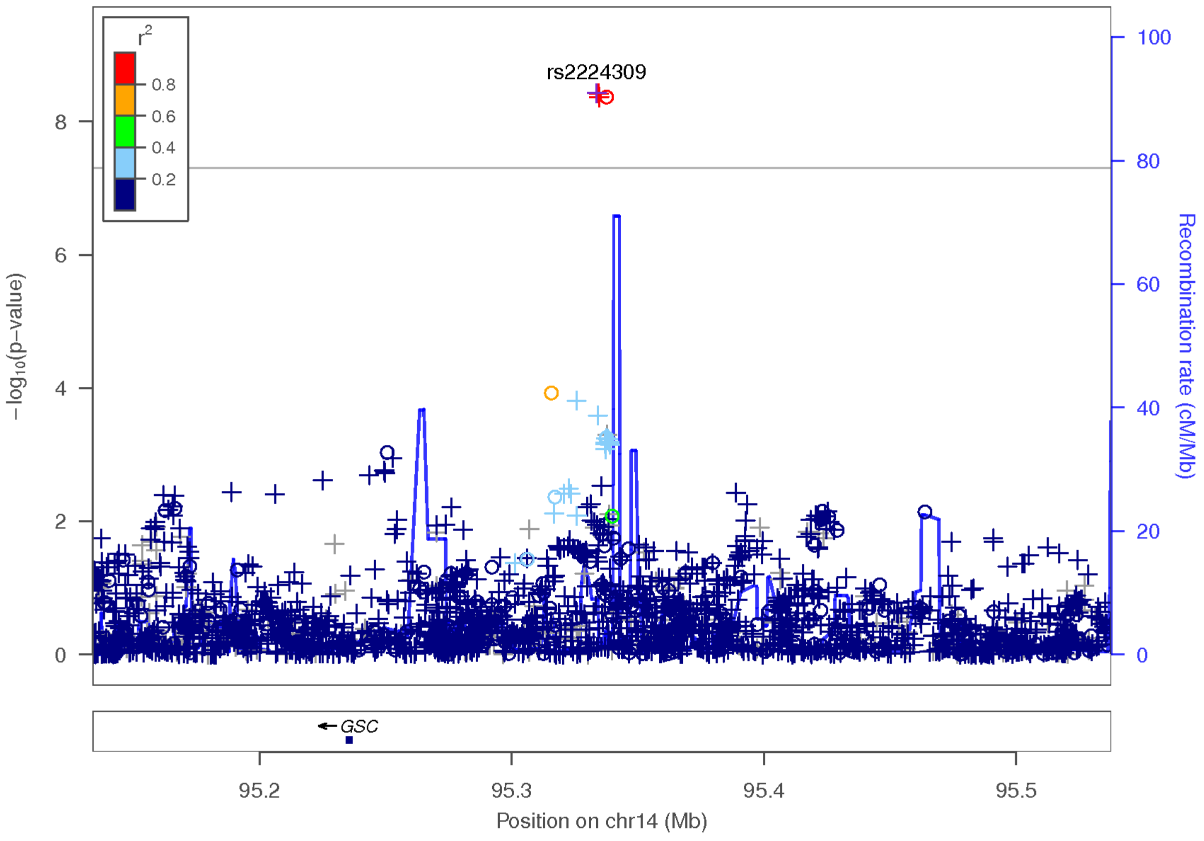

rs5781117
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
LOC643723
LYPLAL1
219.3
219.4
219.5
219.6
219.7
219.8
219.9
Position on chr1 (Mb)

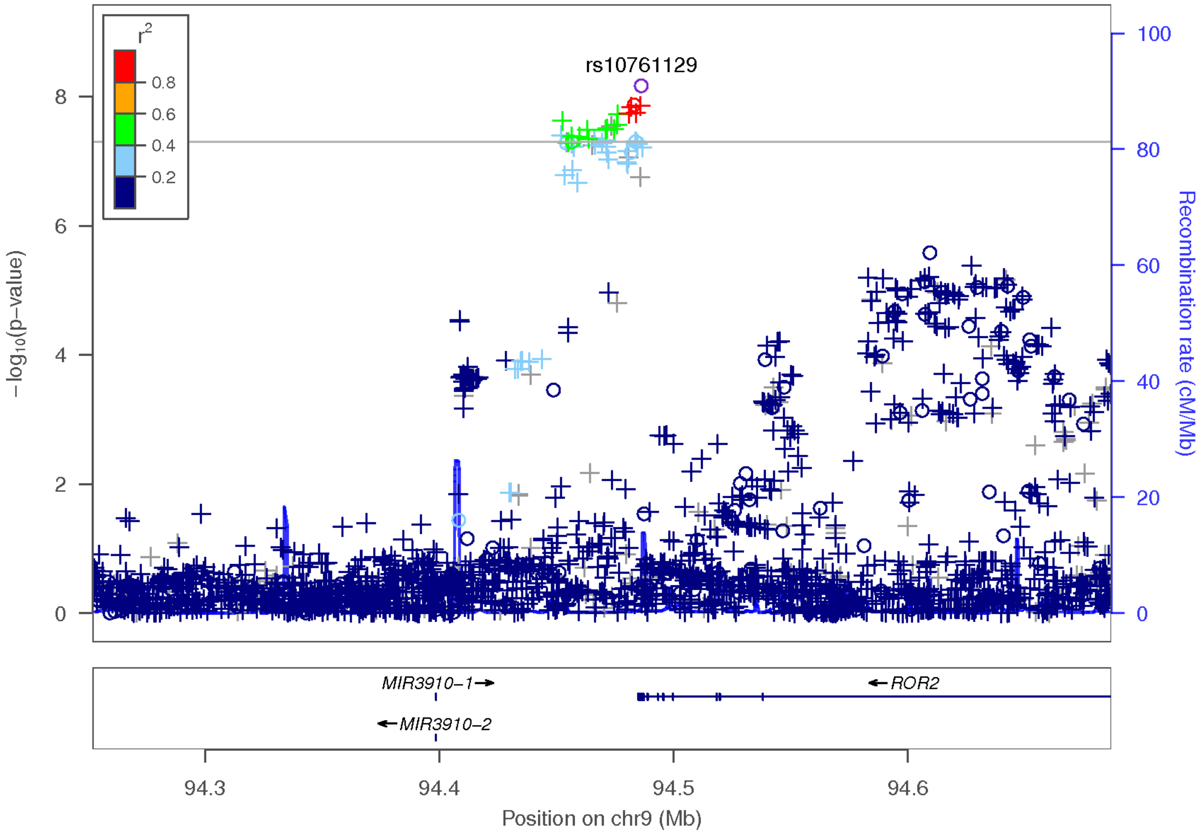

rs146188897
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
IRS2
110.2
110.3
110.4
110.5
Position on chr13 (Mb)


r²
0.8
0.6
0.4
0.2
rs10809266
−log₁₀(p−value)
0
2
4
6
8
10
Recombination rate (cM/Mb)
0
20
40
60
80
100
DMRT1
DMRT2
DMRT3
1
1.1
1.2
1.3
Position on chr9 (Mb)

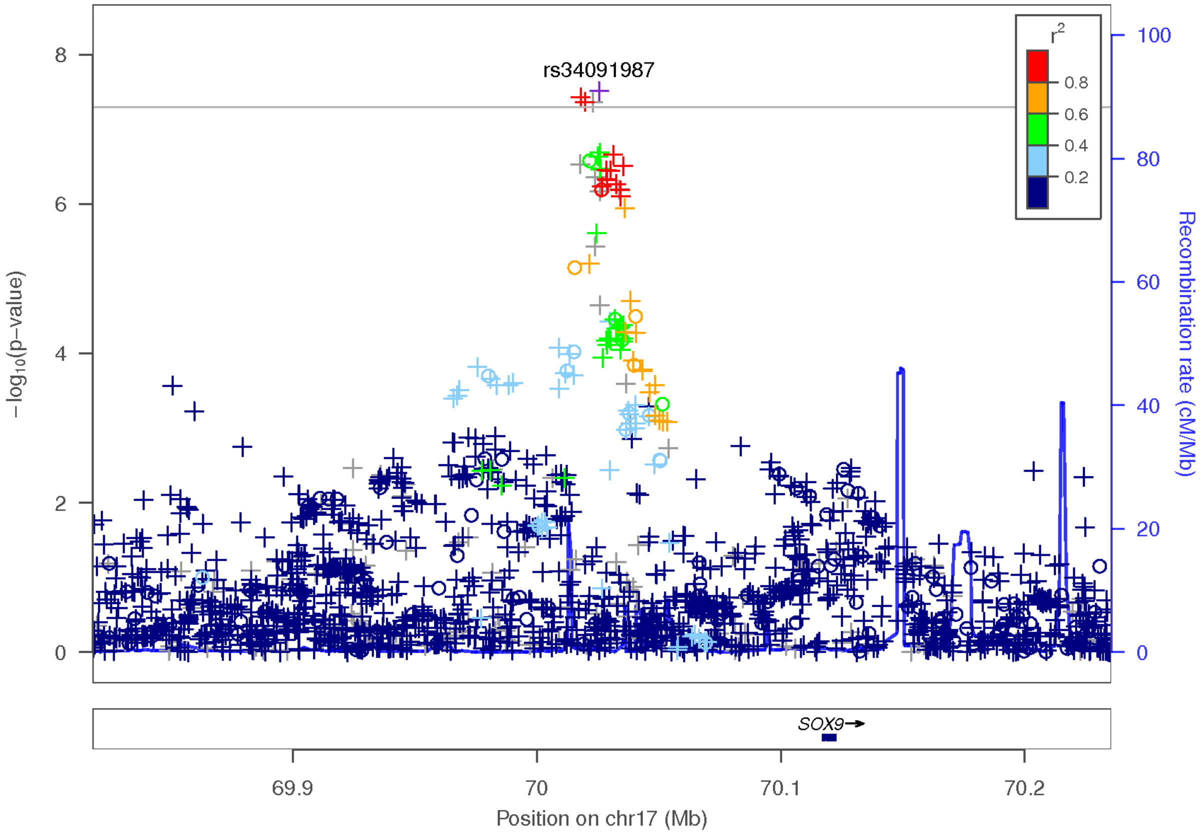

rs702489
r^2
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
DMRTB1→
←GLIS1
←TMEM48
←YIPF1
DIO1→
←HSPB11
54
54.1
54.2
54.3
Position on chr1 (Mb)

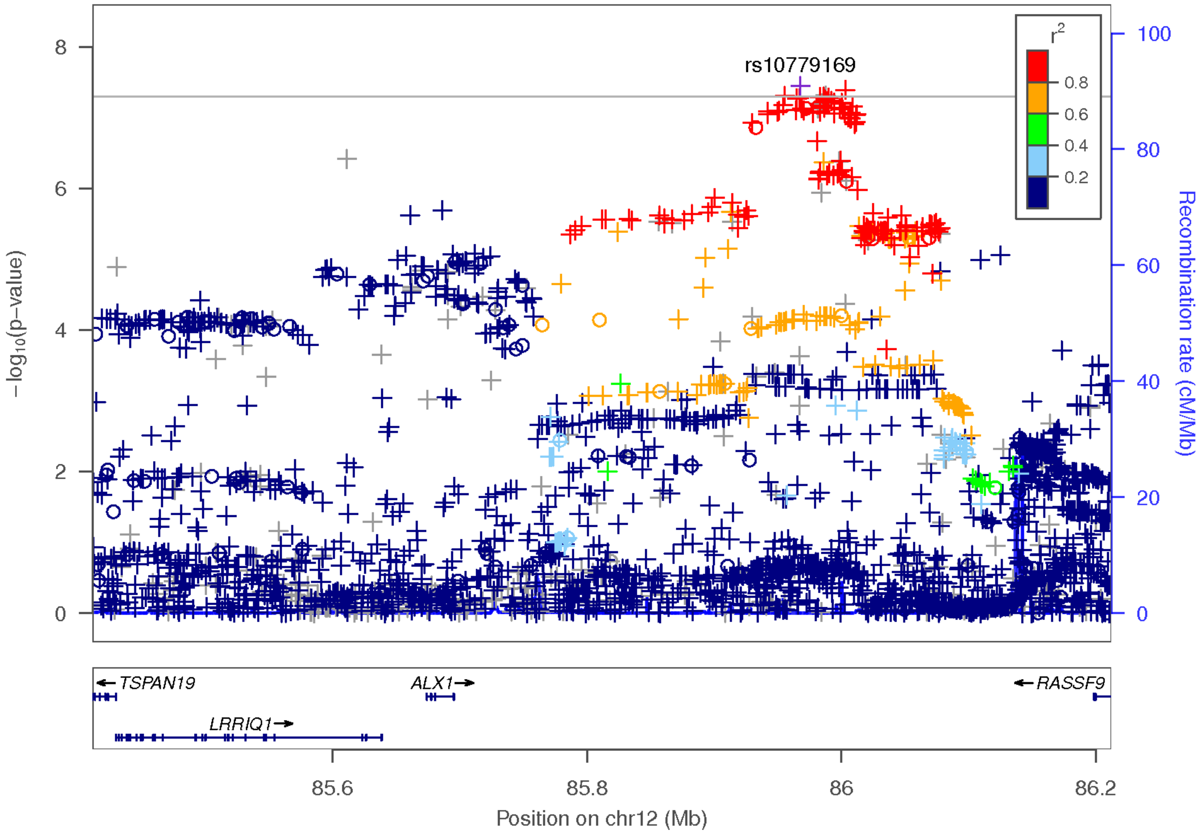

rs35130793
r^2
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
←BMP7
←MIR4325
RAE1→
SPO11→
RBM38→
MIR5095→
←MTRNR2L3
55.6
55.7
55.8
55.9
56
Position on chr20 (Mb)

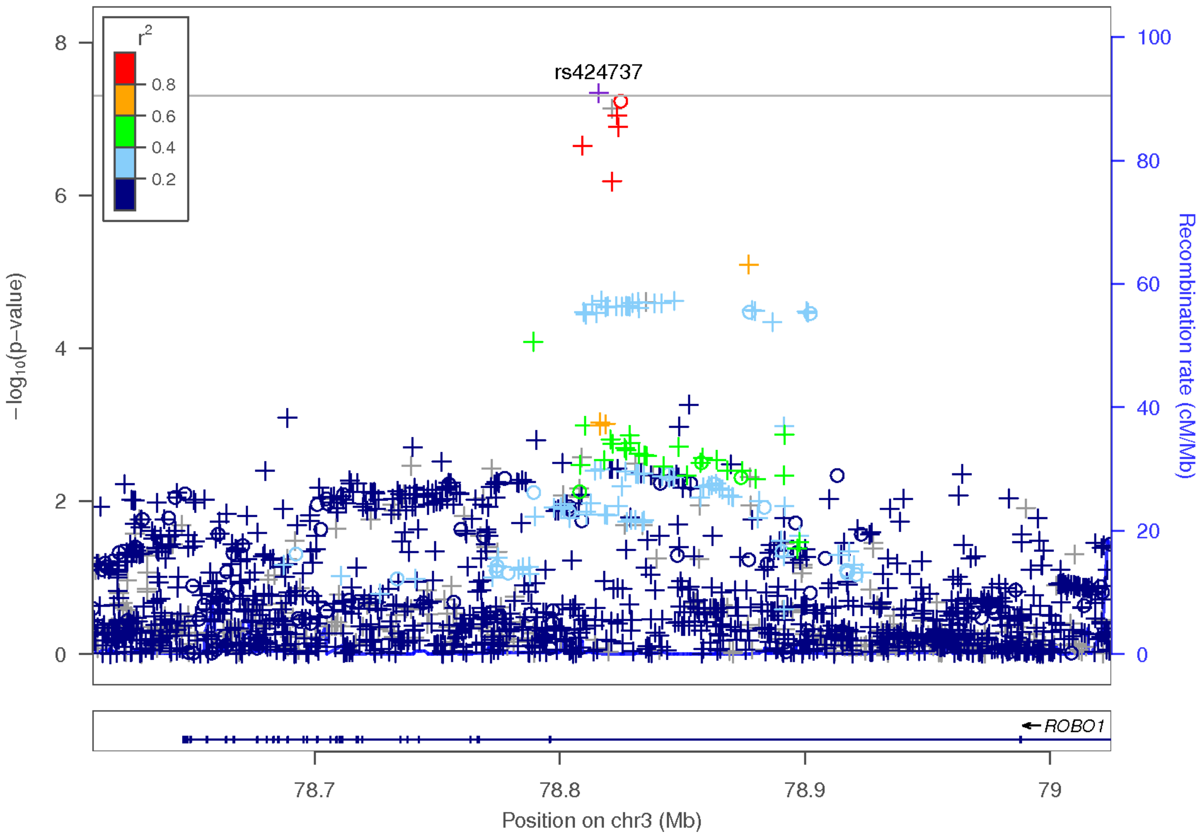


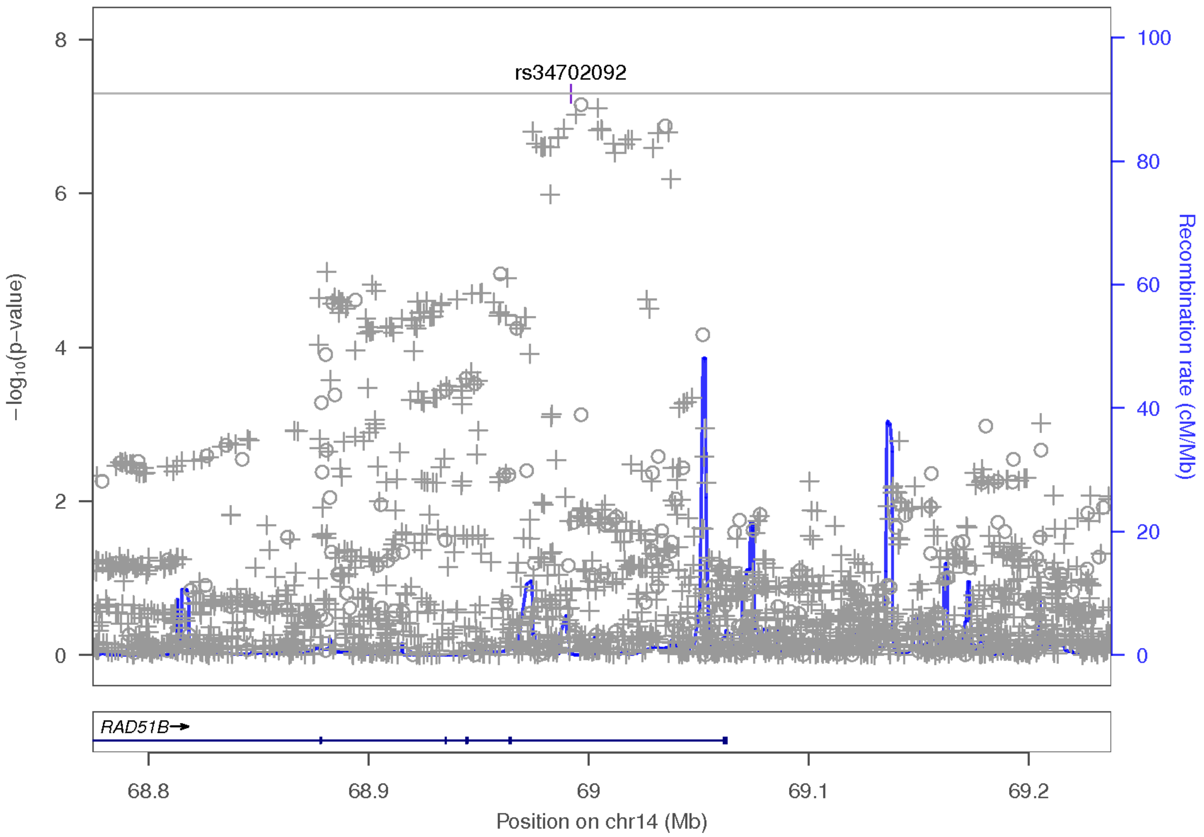


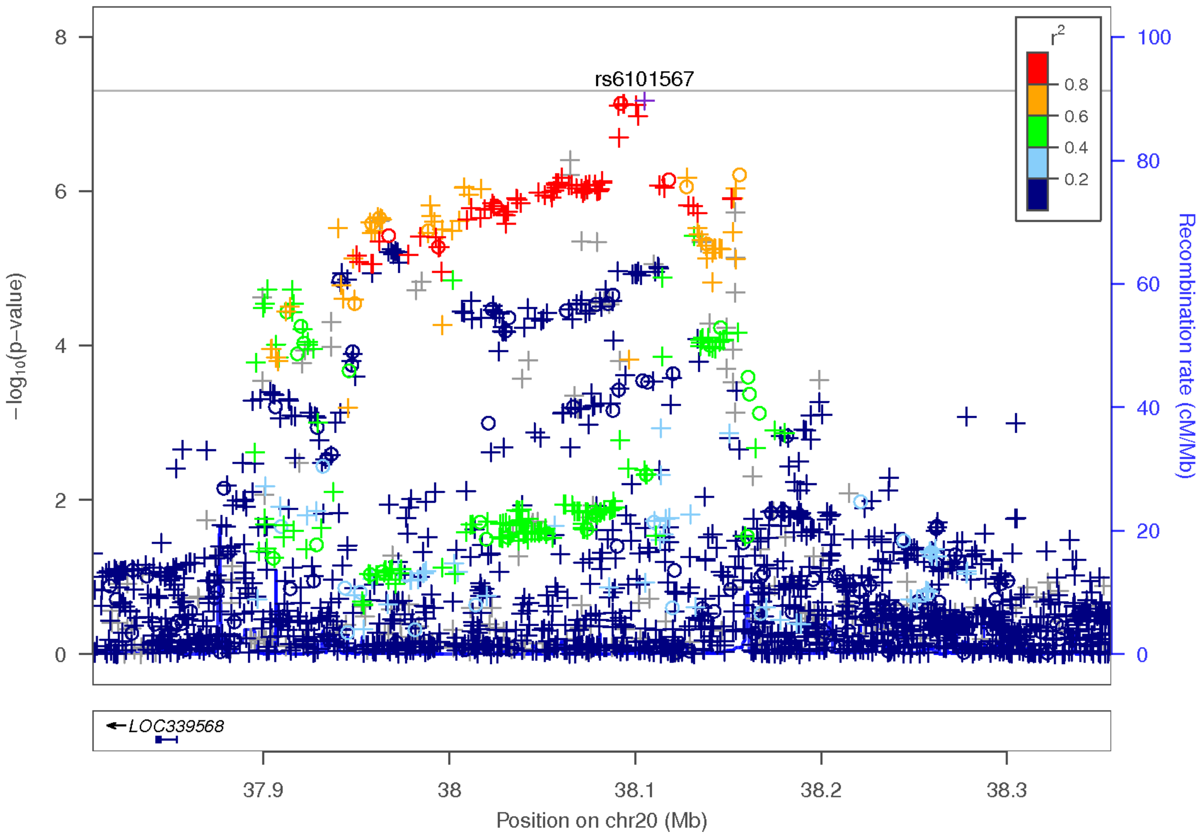
locuszoom plot for 6:44820741:AG_A failed

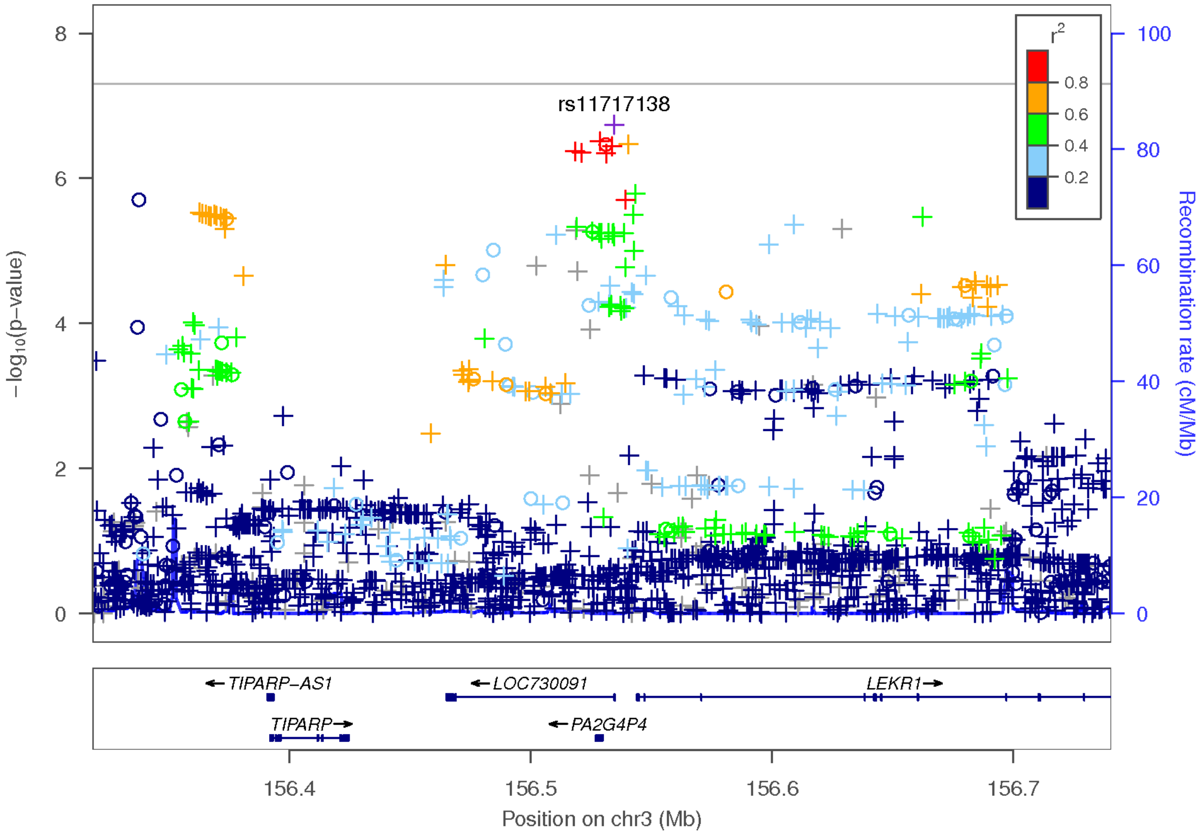

rs34091987
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
8
6
4
2
0
100
80
60
40
20
0
SOX9
69.9
70
70.1
70.2
Position on chr17 (Mb)

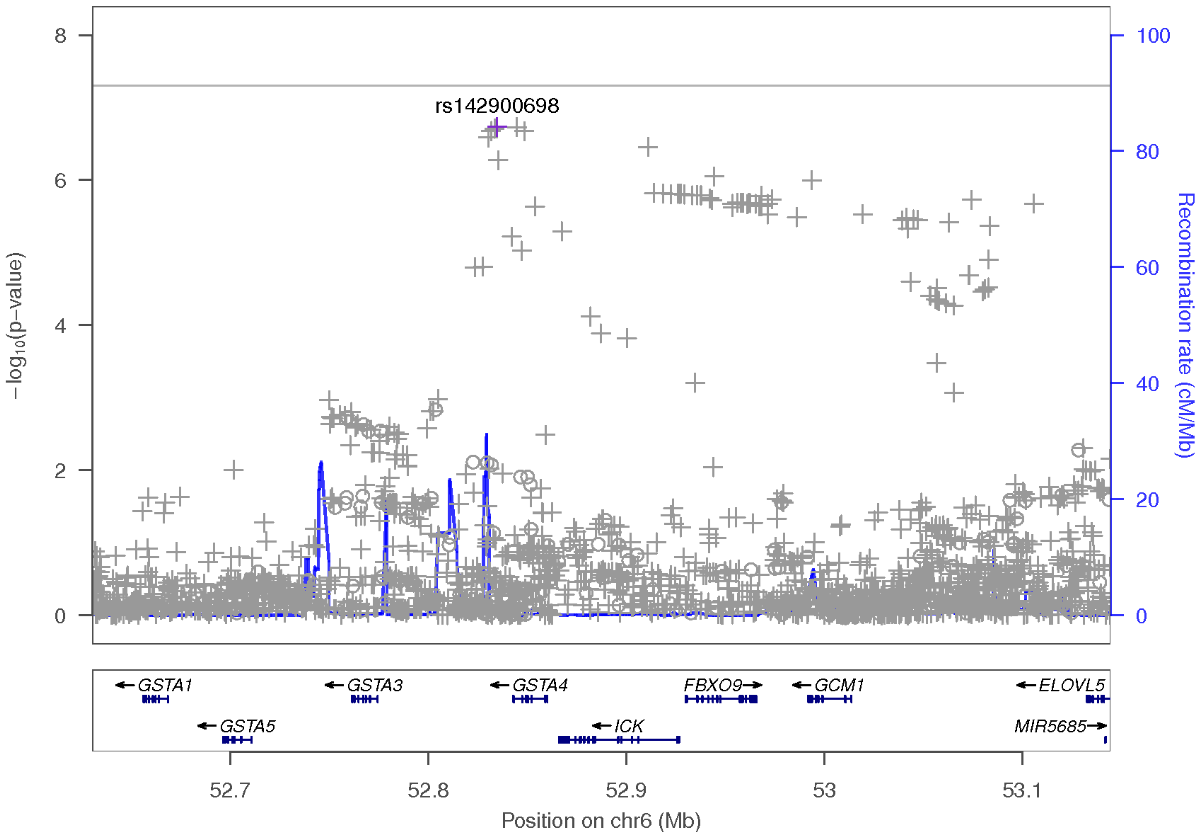

rs10779169
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
8
6
4
2
0
100
80
60
40
20
0
TSPAN19
ALX1
RASSF9
LRRIQ1
85.6
85.8
86
86.2
Position on chr12 (Mb)

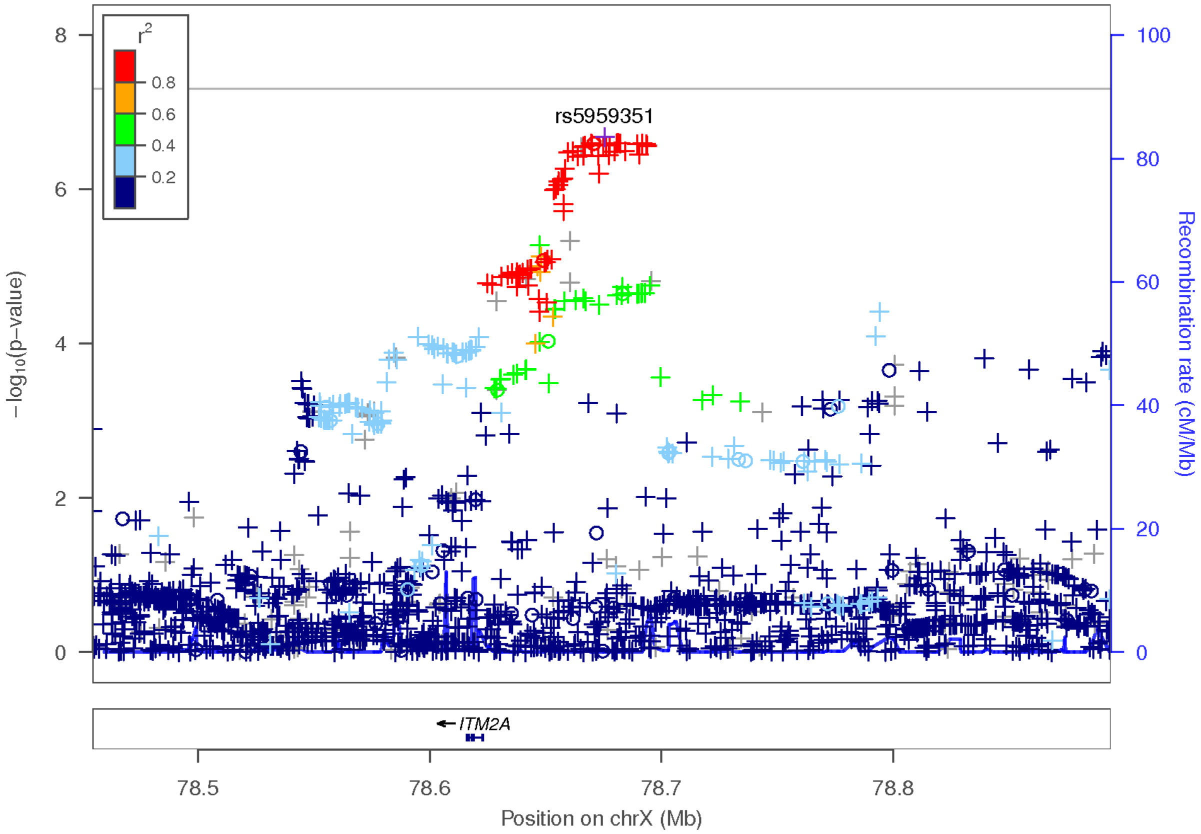

rs424737
r²
0.8
0.6
0.4
0.2
−log₁₀(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
ROBO1
78.7
78.8
78.9
79
Position on chr3 (Mb)

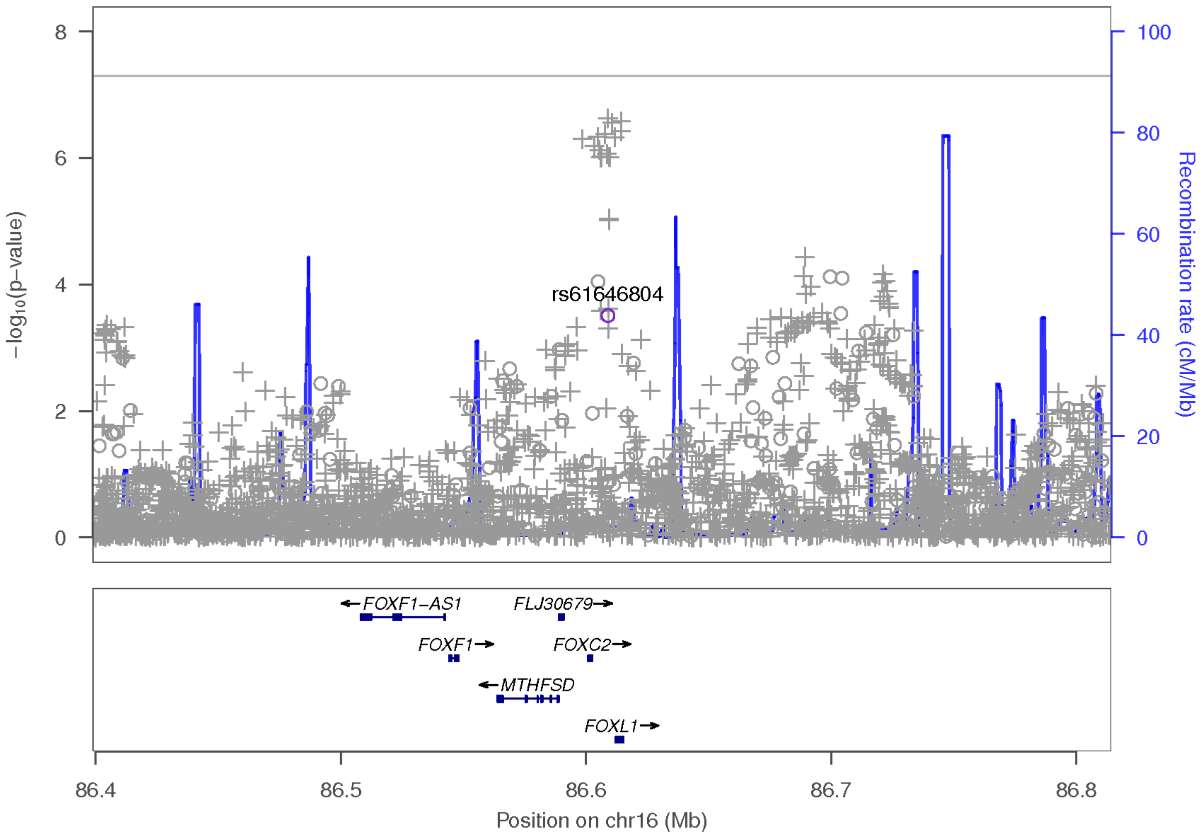

rs34702092
−log₁₀(p−value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
80
100
RAD51B
68.8
68.9
69
69.1
69.2
Position on chr14 (Mb)

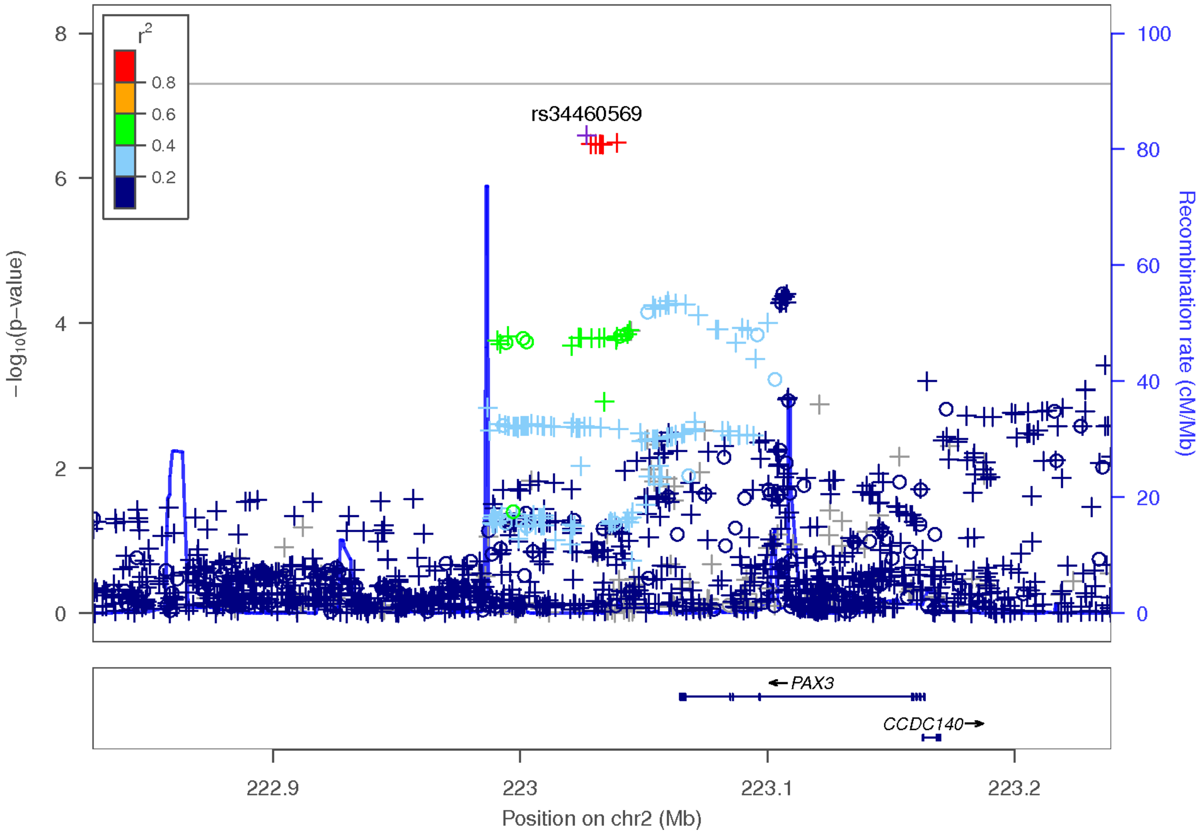

rs6101567
r^2
0.8
0.6
0.4
0.2
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
←LOC339568
37.9
38
38.1
38.2
38.3
Position on chr20 (Mb)

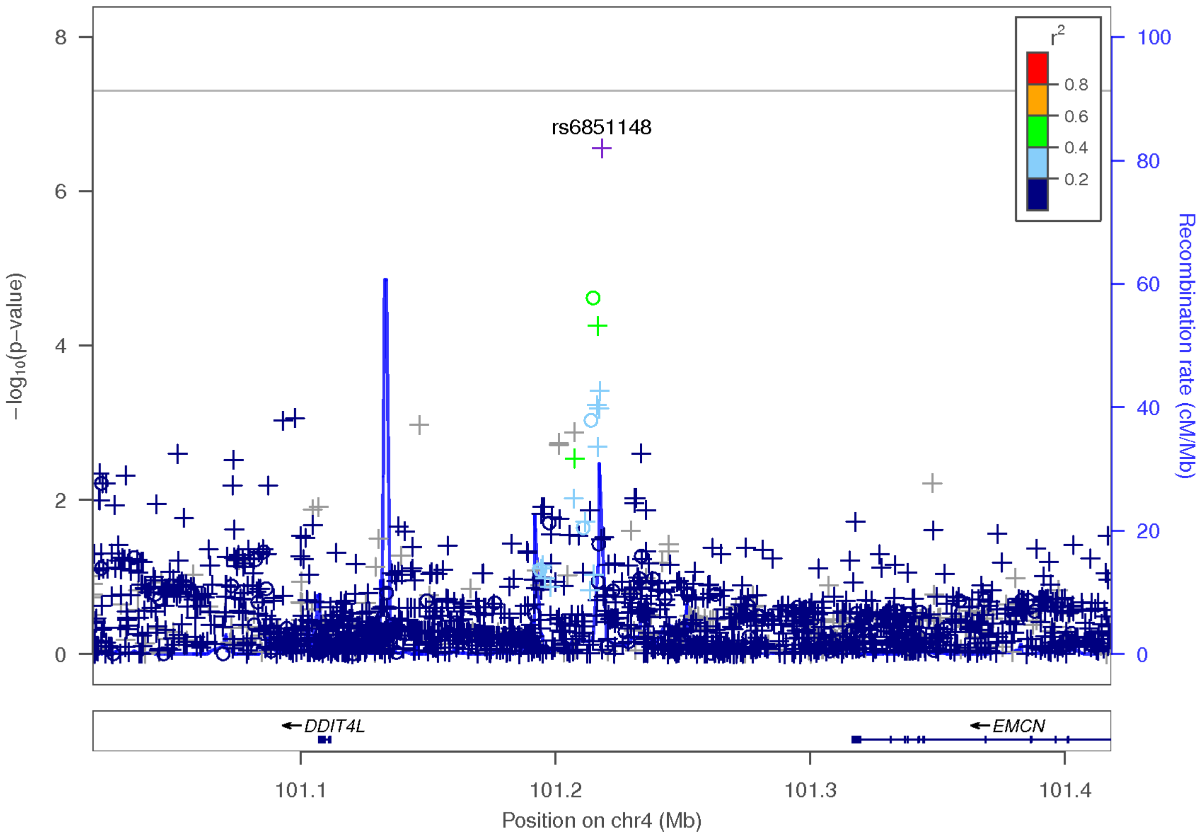

rs11717138
r^2
0.8
0.6
0.4
0.2
8
6
4
2
0
−log₁₀(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
←TIPARP−AS1
←LOC730091
LEKR1→
TIPARP→
←PA2G4P4
156.4
156.5
156.6
156.7
Position on chr3 (Mb)

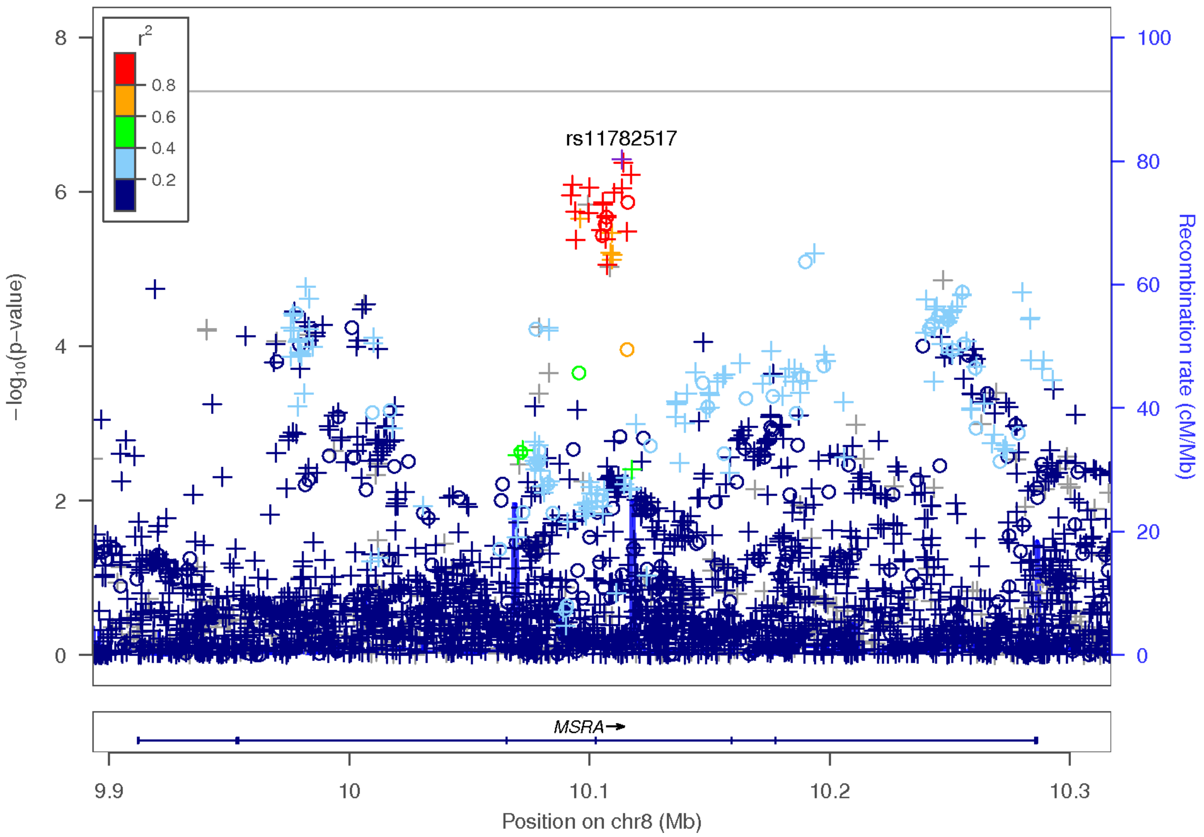

rs142900698
−log10(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
0
20
40
60
80
100
GSTA1
GSTA5
GSTA3
GSTA4
ICK
FBXO9
GCM1
ELOVL5
MIR5685
52.7
52.8
52.9
53
53.1
Position on chr6 (Mb)

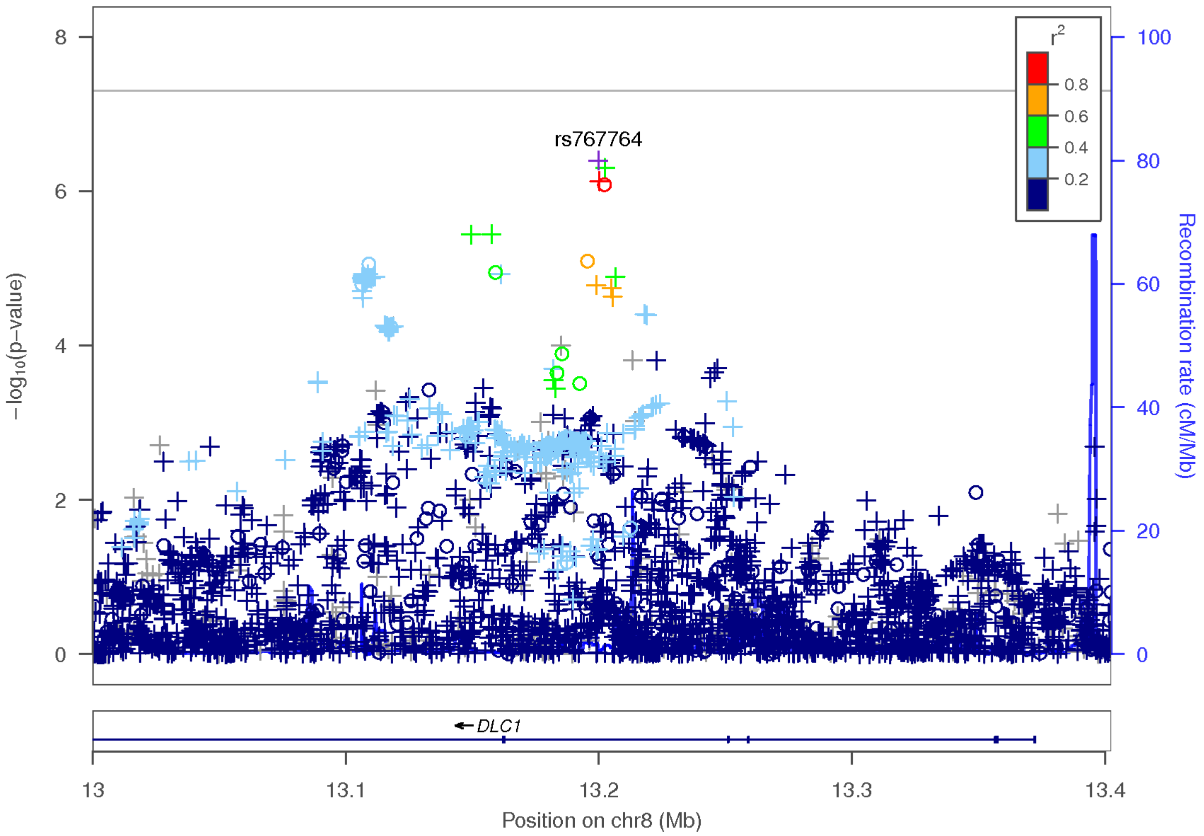

r2
0.8
0.6
0.4
0.2
rs5959351
−log10(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
0
20
40
60
80
100
ITM2A
78.5
78.6
78.7
78.8
Position on chrX (Mb)


rs61646804
−log₁₀(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
0
20
40
60
80
100
FOXF1−AS1
FLJ30679
FOXF1
FOXC2
MTHFSD
FOXL1
86.4
86.5
86.6
86.7
86.8
Position on chr16 (Mb)


r²
0.8
0.6
0.4
0.2
rs34460569
−log₁₀(p−value)
Recombination rate (cM/Mb)
0
2
4
6
8
0
20
40
60
80
100
PAX3
CCDC140
222.9
223
223.1
223.2
Position on chr2 (Mb)


rs6851148
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
DDIT4L
EMCN
101.1
101.2
101.3
101.4
Position on chr4 (Mb)


rs11782517
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
MSRA
9.9
10
10.1
10.2
10.3
Position on chr8 (Mb)


rs767764
r^2
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)
DLC1
13
13.1
13.2
13.3
13.4
Position on chr8 (Mb)