SUPPLEMENTARY INFORMATION

Multiple common variants for celiac disease influencing immune gene expression

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Supplementary Note

Detailed description of case and control subjects:

GWAS: UK(1) celiac cases were previously described[1], with removal of additional individuals showing genetic relatedness to UK(2) individuals, and were matched to 1958 Birth Cohort population controls genotyped by the Type 1 Diabetes Genetics Consortium[2]. Details of Dutch and Italian cohorts were previously described[3,4]. UK(2) celiac cases were partly previously described[5], with additional individuals recruited through Celiac UK membership. UK(2) controls comprised 2434 population controls from the 1958 Birth Cohort and 2502 National Service population controls. Finnish affected individuals (sporadic cases, or unrelateds from affected families across Finland) were partly previously described[6]. Finnish population controls comprised 904 samples from Finrisk (Corogene, excluding coronary heart disease) and 925 samples from Health 2000 (excluding metabolic syndrome and positive celiac disease serology).

Follow-up: USA comprised 525 celiac cases and 340 controls from the Mayo Clinic (Minnesota), and 448 celiac cases and 215 controls from the University of California Irvine[7]. Polish celiac cases were diagnosed in hospital clinics, and controls from donors at the Children's Memorial Health Institute (Warsaw), excluding celiac serology positive samples. Italian samples comprised 377 celiac cases and 94 controls from Rome, and 637 celiac cases and 711 celiac serology negative controls from Naples[8]. Irish celiac cases and controls were as described, with additional samples[9]. 259 Finnish celiac cases were recruited similarly to GWAS samples, and controls were an additional 653 population controls from the Finrisk study. 965 Hungarian celiac cases were collected from Budapest and Debrecen children clinic, and 1067 controls representative of the Hungarian population were selected from an epidemiological study. Part of the Hungarian cohorts have been described earlier[6]. Spanish celiac cases were recruited in Madrid hospitals, controls were donors and hospital employees[10].

Detailed description of genotype calling:

To minimize calling biases arising from batch effects and the use of different genotyping platforms, we attempted to call cases and controls together from the same collections if possible, and maximized samples size to reduce problems when clustering rare variants. Genotypes were called separately in the following five pools from normalized R, theta data: pool A (n=2199: 778 UK1 cases together with 1421 1958 birth cohort controls genotyped on the Illumina Hap550v1-1 platform as described in our previous study[1]. Genotype data from the 1421 controls was then discarded and UK1 case data subsequently merged with UK1 controls for analysis. UK1 controls were called separately in pool B (2596 1958 birth cohort individuals genotyped for the Type 1 Diabetes Genetics Consortium on the Illumina Hap550-2v3 platform)[2]. Separate calling of UK1 case and UK1 control individuals was required due to differences in genotype cluster intensity characteristics observed for UK1 case data (Hap300v1-1) and controls (Hap550-2v3). Pool C comprised UK3 cases and controls (n=6963, 1894 cases on Human 670-QuadCustom_v1 and 5069 controls on 1.2M-DuoCustom_v1). Pool D comprised Dutch and Italian cases and controls (n=2917 on 670-QuadCustom_v1). Pool E comprised Health2000 and Finrisk cohorts and Finnish cases (n=6760, 674 cases on Human 670-QuadCustom_v1, 912 Finrisk

controls, 927 Health2000 controls, 4247 additional Finrisk and H2000 cases and internal controls- Human 610-Quad). The 4247 additional samples were then discarded.

Detailed description of expression probe re-mapping:

We used Ensembl52 to obtain, for each annotated gene, the transcript with the largest number of exons and included this main spliced transcript in our reference set. Second, we added one sequence per intron, extending intron boundaries 40 bp on each side to allow mapping of the 50 bp probe sequences, overlapping exon-intron junctions. Last, a version of the reference DNA genome with masked annotated transcripts was included. Probe sequences were mapped versus the composite reference using novoalign v2.05.12 (www.novocraft.com) permitting alignment against all possible sequences originating from the same transcript (parameters -t 150 -v 20 20 200 [>]([^_]*)_). For each probe we determined whether it mapped uniquely to one particular genomic locus, or, if multiple hits were present (e.g. across exons) that these resided < 250kb from the probe.

References for Supplementary Information

1. van Heel, D.A. et al. A genome-wide association study for celiac disease identifies risk variants in the region harboring IL2 and IL21. *Nat Genet* **39**, 827-9 (2007).
2. Barrett, J.C. et al. Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes. *Nat Genet* (2009).
3. Coenen, M.J. et al. Common and different genetic background for rheumatoid arthritis and coeliac disease. *Hum Mol Genet* (2009).
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5. Hunt, K.A. et al. Newly identified genetic risk variants for celiac disease related to the immune response. *Nat Genet* **40**, 395-402 (2008).
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7. Garner, C.P. et al. Replication of celiac disease UK genome-wide association study results in a US population. *Hum Mol Genet* **18**, 4219-25 (2009).
8. Megiorni, F. et al. HLA-DQ and susceptibility to celiac disease: evidence for gender differences and parent-of-origin effects. *Am J Gastroenterol* **103**, 997-1003 (2008).
9. Hunt, K.A. et al. Large scale replication of a genome-wide association study in celiac disease. *American Society of Human Genetics Meeting*, platform talk 26 (2007).
10. Dema, B. et al. Association of IL18RAP and CCR3 with coeliac disease in the Spanish population. *J Med Genet* **46**, 617-9 (2009).

Supplementary Table 1 Subjects used in eQTL mapping analysis.
Numbers are shown after quality control steps.

Case/Control	Population	Number of individuals	Genotype platform	Expression platform
Controls	Dutch	324	Hap370	HT-12
Amyotrophic Lateral Sclerosis	Dutch	414	Hap370	HT-12
Ulcerative Colitis	Dutch	49	610-Quad	HT-12
Chronic Obstructive Pulmonary Disease	Dutch	453	610-Quad	HT-12
Celiac disease	UK	111	Hap300	Ref-8 v2
Amyotrophic Lateral Sclerosis	Dutch	59	Hap300	Ref-8 v2
Controls	Dutch	59	Hap300	Ref-8 v2

Supplementary Table 2 Conditional logistic regression to test for multiple independent associations.

Locus	Chr	Position (bp, B36)	LD block (Mb)	SNP	Pairwise SNP[a] r^2	Pairwise SNP[a] D'	$P_{combined}$ (CMH analysis)	$P_{combined}$[b] (logistic regression)	$P_{combined}$ conditioned on alternate SNP[c] (logistic regression)
Residual evidence of multiple independent SNPs at a locus ($p<10^{-3}$, both before and after conditioning on alternate SNP)									
REL	2	60972975	60.78-61.74	rs842647	0.247	0.906	$2.88x10^{-8}$	$2.40x10^{-12}$	$6.82 x10^{-4}$
		61040333		rs13003464			$3.71x10^{-13}$	$1.03x10^{-16}$	$3.00x10^{-8}$
CCR1/CCR3	3	46210205	45.90-46.57	rs13098911	0.135	0.781	$3.26x10^{-17}$	$1.49x10^{-16}$	$7.77 x10^{-8}$
		46327388		rs6441961			$2.93x10^{-15}$	$3.87x10^{-18}$	$1.39x10^{-9}$
IL12A[d]	3	161147744	161.07-161.23	rs17810546	*0.160*	*0.957*	*$4.56x10^{-18}$*	*$2.34x10^{-15}$*	*$5.66 x10^{-9}$*
		161179692		rs9811792			*$1.03x10^{-11}$*	*$1.66x10^{-10}$*	*$2.83x10^{-4}$*
IRF4	6	328546	0.32-0.40	rs1033180	0.079	0.880	$5.58x10^{-08}$	$1.60x10^{-8}$	$1.02x10^{-4}$
		356064		rs872071			$8.22x10^{-07}$	$9.12x10^{-13}$	$4.26x10^{-9}$
THEMIS / PTPRK	6	128320491	127.99-128.32	rs802734	0.077	0.993	$2.62x10^{-14}$	$2.43x10^{-12}$	$9.00x10^{-8}$
		128337195		rs7738609			$2.88x10^{-10}$	$1.63x10^{-12}$	$4.07x10^{-8}$
ETS1	11	127886184	127.84-127.89	rs11221332	0.196	0.934	$5.28x10^{-16}$	$2.04x10^{-16}$	$4.98x10^{-9}$
		127926136		rs4245079			$5.34x10^{-10}$	$2.46x10^{-11}$	$6.83x10^{-4}$

[a]pairwise LD estimated for 6785 individuals from UK 2 GWAS
[b]logistic regression performed with sample collections as binary dummy covariates
[c]logistic regression perfomed as for b, conditioned on alternate SNP at locus
[d]no follow-up data for rs9811792, all SNP analyses confined to GWAS collections

Supplementary Table 3 Details of Illumina expression probes corresponding to Table 3 findings.

Unique Identifier	HGNC Name	Platform	ILMN Code	Array Address ID	Probe Sequence
650452	PLCH2	HumanHT12	ILMN_2061565	650452	CTTCGAGGCTGGCCCTGCCAGGCAGTTTTCCCGGCGTTTTAGGATCTGTA
6520725	TNFRSF14	HumanHT12	ILMN_1697409	6520725	AGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCAC
2070246	MMEL1	HumanHT12	ILMN_1718488	2070246	TTCTTCATCAACTATGCCCAGGTGTGGTGCGGGTCCTACCGGCCCGAGTT
Human_RefSeq-8_v2-6250338	C1orf93	Human_RefSeq-8_v2	ILMN_12752	6250338	GTGGGTGGGTGTGACAGCAGGAGCATTGCCATCTTGGACAAACATGGCCA
610193	PARK7	HumanHT12	ILMN_1744713	610193	AATTGTTGAAGCCCTGAATGGCAAGGAGGTGGCGGCTCAAGTGAAGGCTC
6290400	CD247	HumanHT12	ILMN_1676924	6290400	AAACCCGTCAATGTACTAGGATACTGCTGCGTCATTACAGGGCACAGGCC
3890689	CD247	HumanHT12	ILMN_2377669	3890689	ACTGCTGCGTCATTACAGGGCACAGGCCATGGATGGAAAACGCTCTCTGC
1300279	DDX59	HumanHT12	ILMN_1748077	1300279	CTGGGATATTGCAAAACGAGTAAAGCCCACAGGATCCATTCTTCCCCCTC
1170220	AHSA2	HumanHT12	ILMN_1798308	1170220	GGGAACTGGCCAGAAGAACACTATGCCATGGTTGCACTGAATTTTGTGCC
4810020	PLEK	HumanHT12	ILMN_1795762	4810020	GCCCTCCCTCAATTCCCCTGTAACATTCCTGAAGCTGTTCCCACTCCCAG
6520180	IL18RAP	HumanHT12	ILMN_1721762	6520180	GGGTACTTTCAGTACACAACACCCCTAAGATTTCCCAGTGGTCCGAGCAG
1780433	UBE2E3	HumanHT12	ILMN_1733142	1780433	GGGTGTCCTTGTCCTCTCCTAGTCACCACTTGTGCAAACAGCGAAAGTTT
6550333	CXCR6	HumanHT12	ILMN_1674640	6550333	TGCTGGCACCACCAGGCACCTCACAGAAATGAGATCAGGCTCTGCCTCAC
2190671	CCR3	HumanHT12	ILMN_1763322	2190671	GCCTTCCACACTCACCTCTAAAACAGTCCTTCAAACTTCCAGTGCAACAC
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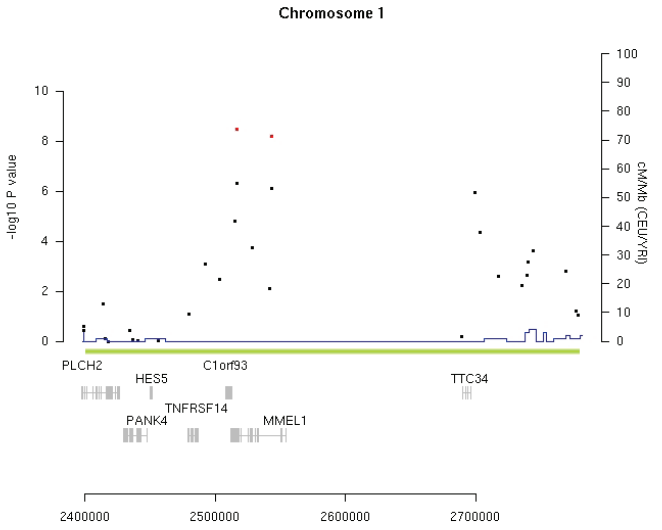
3850161	KTELC1	HumanHT12	ILMN_1774800	3850161	TGATGGCTTCATGATCCAGCACAGTGCCTCACACAAAGAACTATTGGGTG
6550288	KTELC1	HumanHT12	ILMN_1811104	6550288	GGATTTCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTC
3520349	BACH2	HumanHT12	ILMN_1777792	3520349	AGCTGTCTGCTTCAGAAAGTGAGGGCTCCAGGAATGAGGAGAATCTTCAA
4860242	TAGAP	HumanHT12	ILMN_1676408	4860242	ATAAGCTCCCCCGGCCCAACCTCCTGCTACTCAAGCACTTGGTCTATGTG
5890739	TAGAP	HumanHT12	ILMN_1739985	5890739	ATGAGAAATCCCCAACTTATGATCTCACCATCTGTTTGCCAAGTCCAGGC
5360364	TAGAP	HumanHT12	ILMN_2333774	5360364	TGGCCATCTGCATTGGACCCAACATGCTCACCCTGGAGAATGACCAGAGC
2750154	ELMO1	HumanHT12	ILMN_1784320	2750154	AGCGTTTGGTGTTACCTTCTCCTGGGAGGTCCTGCTGCAACTCAAGTTCC
2450131	ZMIZ1	HumanHT12	ILMN_1771627	2450131	CGTACACACATAAACACACCCACCAGTGCAGCCTGAAGTAACTCCCACAG
6560301	SH2B3///ATXN2	HumanHT12	ILMN_1752046	6560301	AAGGCCTTGGACTCTTCCCTGAGGGTTGCCTGAAATTCCTTCATGCTTTC
Human_RefSeq-8_v2-3190129	TMEM116	Human_RefSeq-8_v2	ILMN_23612	3190129	CCACCAACTAAAGCAGGAGGCTCGGCGTGATGCAGATACCCAGACACCAT
2070736	TMEM116	HumanHT12	ILMN_2052871	2070736	GCAGGGGCTTAAATTCACTGGAATCCACCCTGACTTTTCCTGCCAGTACT
840253	ALDH2	HumanHT12	ILMN_1793859	840253	GCAAGCTTCCTCCCTCAGCCATTGATGGAAAGTTCAGCAAGATCAGCAAC
4540072	AC009121.6	HumanHT12	ILMN_1790537	4540072	CGGCCCCTGAAAGACAACAGCTCCCTTTCTGCTTCGGACACCACTCAAAC

4070615	WNT3	HumanHT12	ILMN_1803593	4070615	ACGCGTGGTAAATGACCCAGACCCAACTCGCCTGTGGACGGGGAGGCTCT
3520672	ARL17///LRRC37A ///LRRC37A2	HumanHT12	ILMN_1783673	3520672	AACAGCCCCACACACAGCAGGGGCCTGAGAAGTTAGCGGGAAACGCCGTC
4880037	LOC388397	HumanHT12	ILMN_1678312	4880037	CCCCACCTCCCAAAAGGGCTGGGGACAGCAGGTGTATCCTTGTTAGTTCC
5260138	NSF	HumanHT12	ILMN_1680353	5260138	CCTGTGATTCCTGGTGGCCAGTATCCTGGATTCCTCTAAGATCTTGCCTC
1410484	NSF	HumanHT12	ILMN_1680687	1410484	TCAGCACCACCATCCACGTGCCCAACATTGCCACAGGAGAGCAGCTGTTG
Human_RefSeq-8_v2-7200373	RRP1///AP001053.1	Human_RefSeq-8_v2	ILMN_15485	7200373	GTGGCGGGGAGACAGAGGGGCGATGGCCCAGTTTCTTTTGGGCTGAAAAT
1230242	UBE2L3	HumanHT12	ILMN_1677877	1230242	TTCACACCCGCCTGGTTTCTTGAAGTGTGCTGGGTCCTTCCCTCTGCTCC
6480360	TLR8	HumanHT12	ILMN_1657892	6480360	CAGTTGGTCATCAACTATTTTCCCTTGACTGCTGTCCTGGGATGGCCTGC
3390612	TLR8	HumanHT12	ILMN_1705047	3390612	GCTCCATCCTCCAGTGGCCTGACAACCCGAAGGCAGAAGGCTTGTTTTGG

Supplementary Figure 1 LD structure, genes and association results for 39 non-HLA coeliac disease associated regions.
Chromosomal positions based on NCBI Build 36 co-ordinates. P_{GWAS} values (left Y axis and black points) are from 4,533 cases and 10,750 controls. $P_{combined}$ values (left Y axis and red points) are from 9,451 cases and 16,434 controls. Recombination rate (HapMap) shown in blue (right Y axis). The green bar indicates the narrow linkage disequilibrium block as reported in **Table 2**, the complete X axis shows an additional 0.05% of base positions for clarity. All genes with HUGO identifiers are displayed (as annotated in Ensembl v54), for multiple transcripts only the largest is shown.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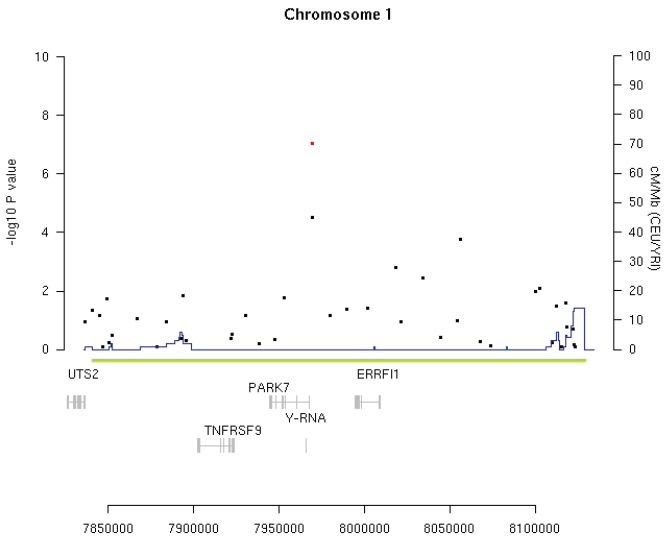
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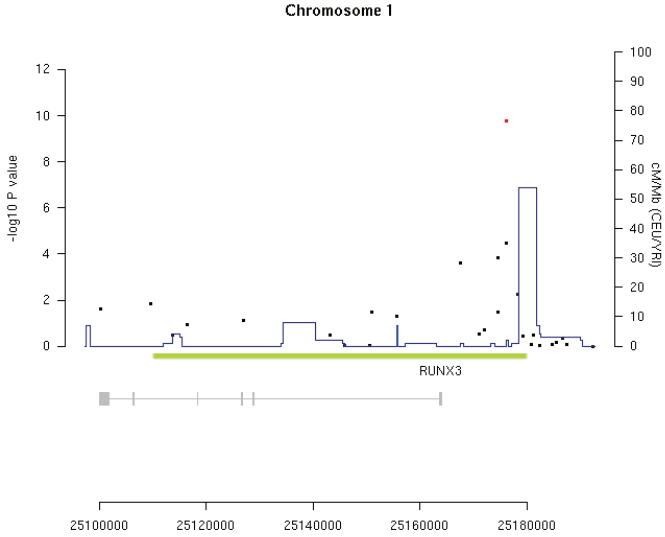
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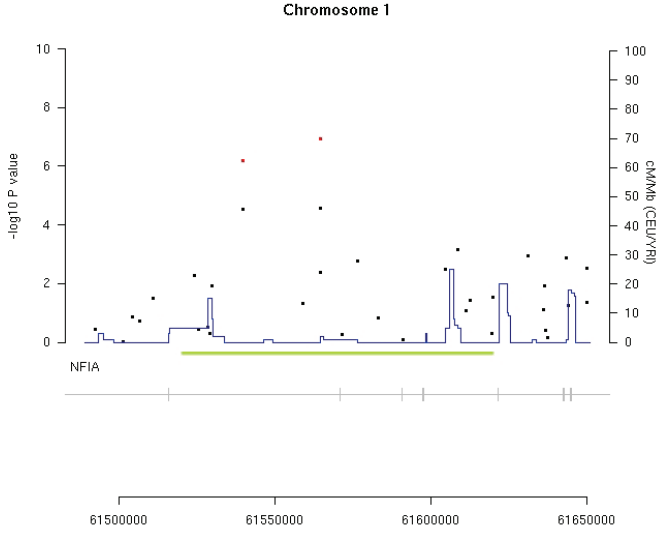
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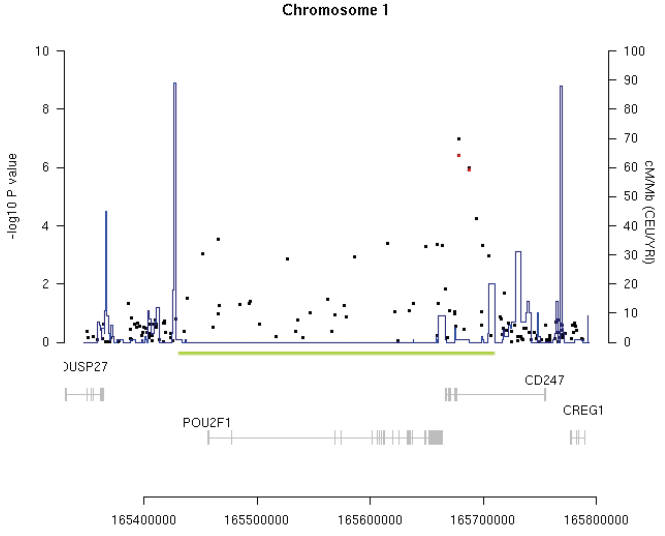
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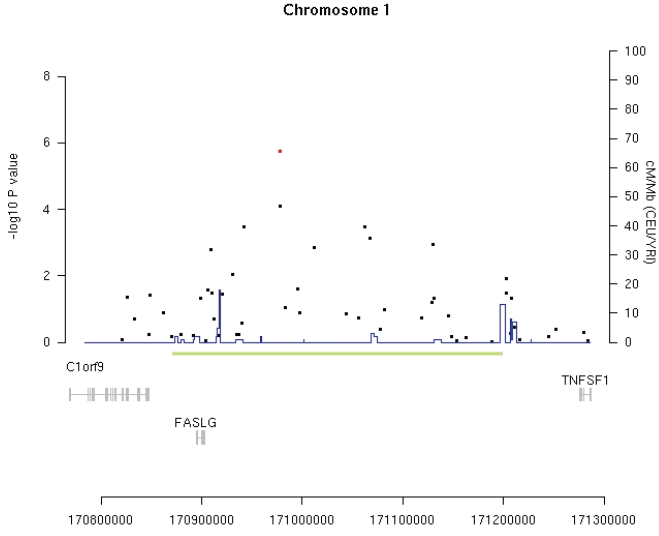
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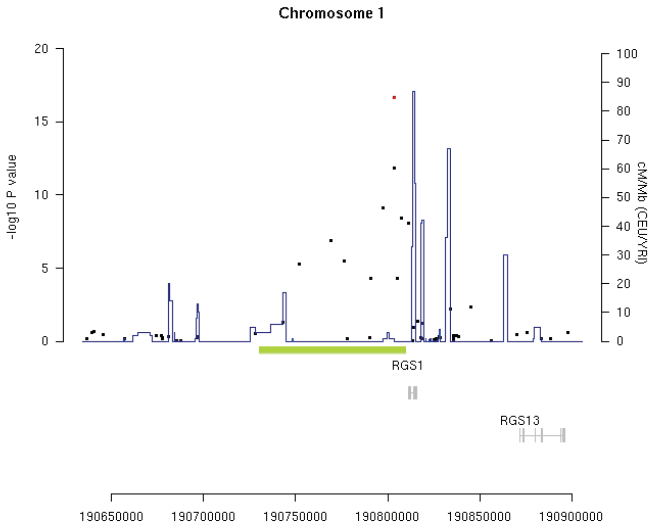
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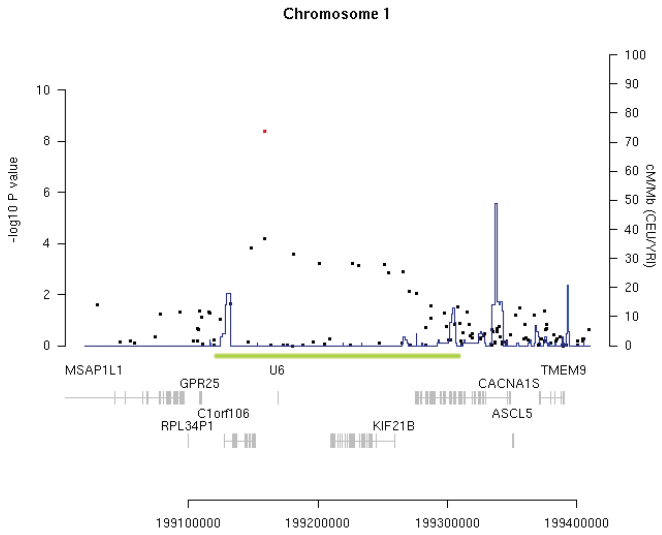
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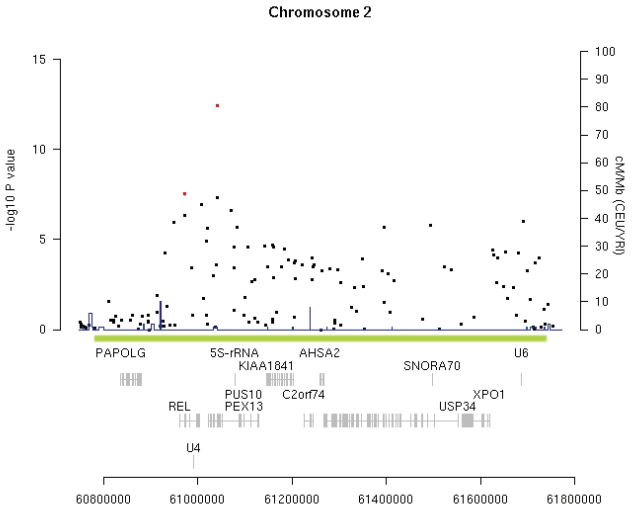
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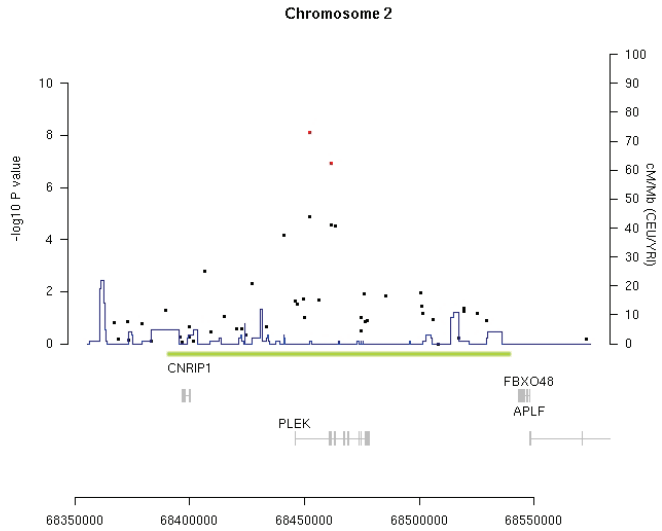
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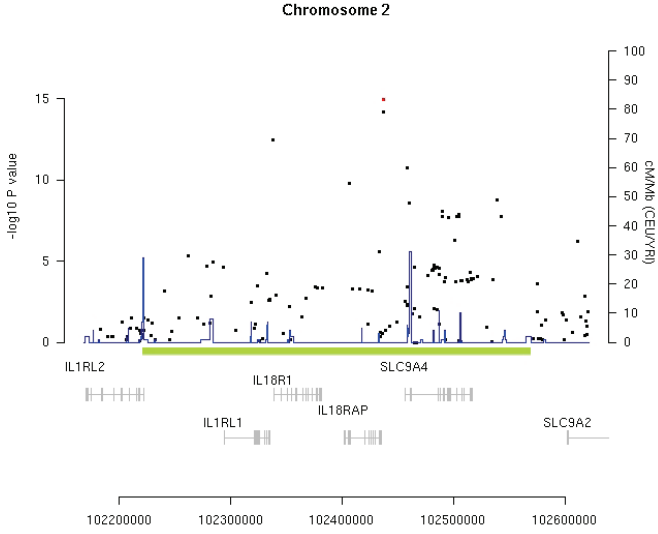
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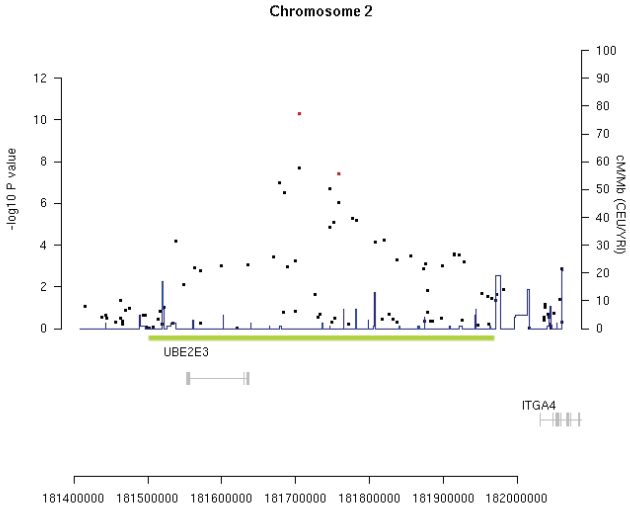
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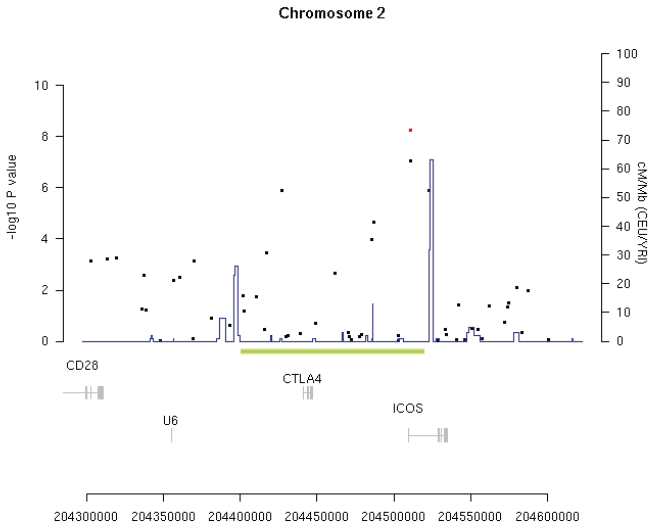
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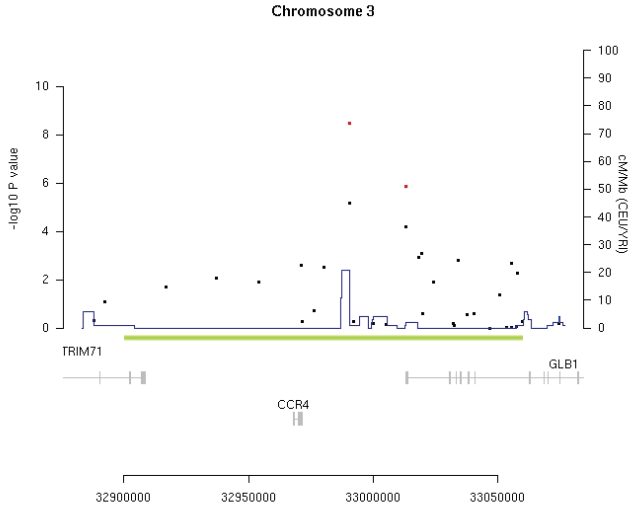
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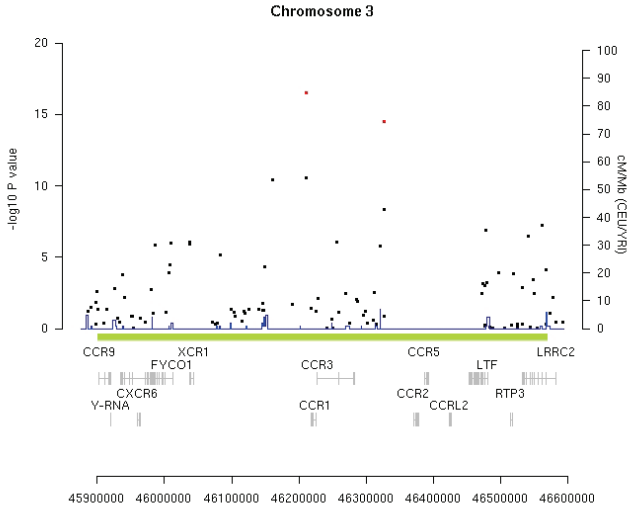
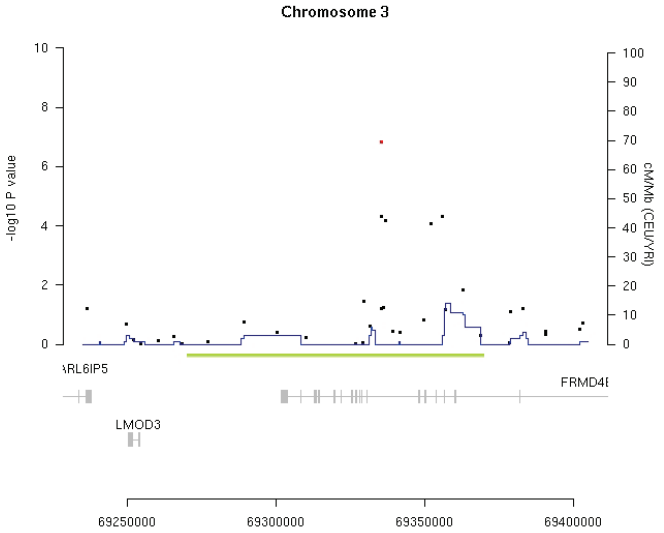
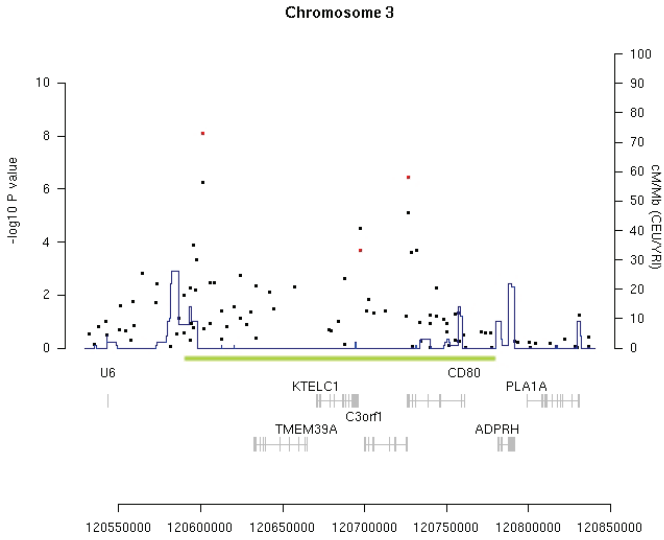
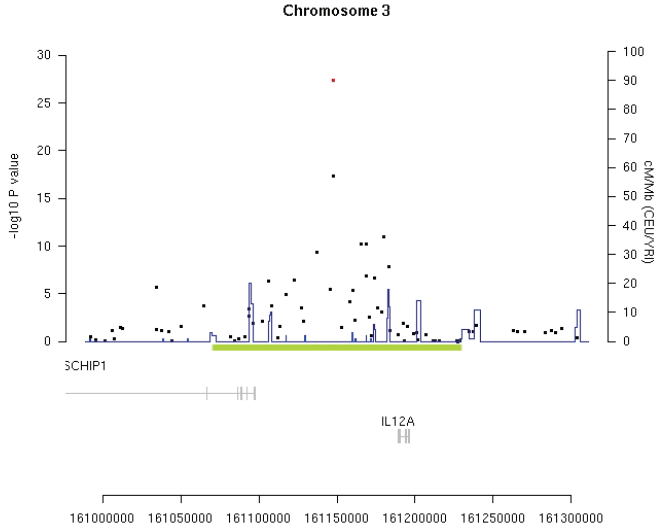
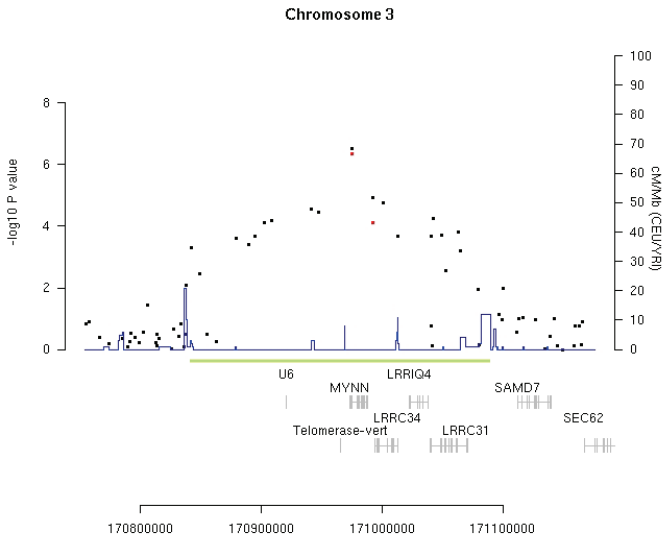
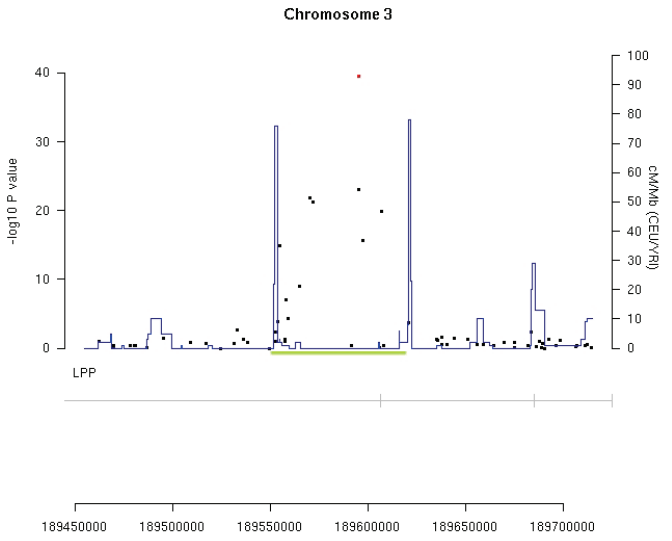

Chromosome 3
-log10 P value
cM/Mb (CEU/YRI)
CCR9
XCR1
FYCO1
CXCR6
Y-RNA
CCR3
CCR1
CCR5
CCR2
CCRL2
LTF
RTP3
LRRC2
45900000
46000000
46100000
46200000
46300000
46400000
46500000
46600000

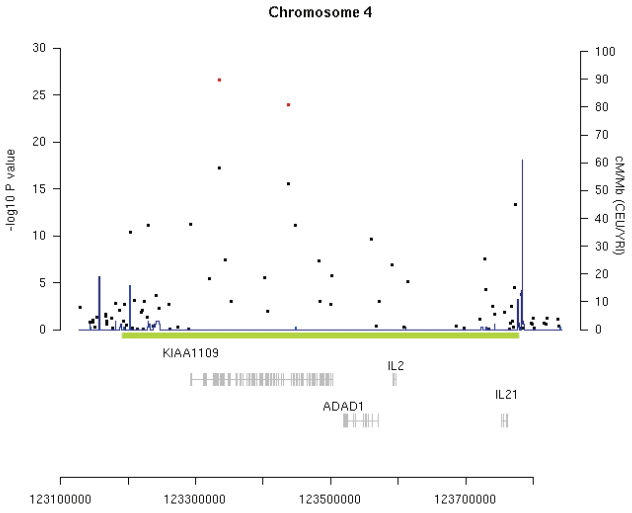

Chromosome 3
-log10 P value
cM/Mb (CEU/YRI)
LMOD3
69250000
69300000
69350000
69400000

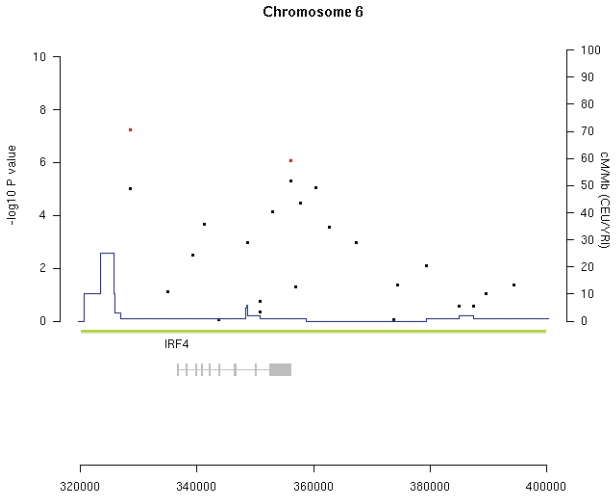

Chromosome 3
-log10 P value
cM/Mb (CEU/YRI)
U6
KTELC1
C3orf1
TMEM39A
CD80
PLA1A
ADPRH
120550000
120600000
120650000
120700000
120750000
120800000
120850000

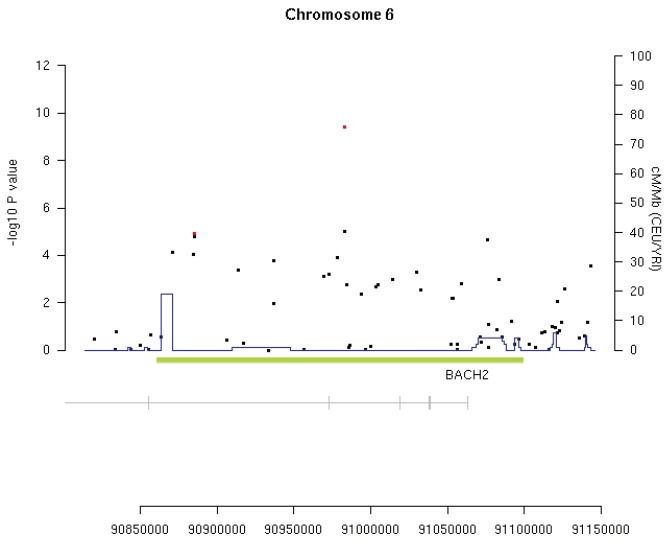

Chromosome 3
-log10 P value
cM/Mb (CEU/YRI)
IL12A
161000000
161050000
161100000
161150000
161200000
161250000
161300000

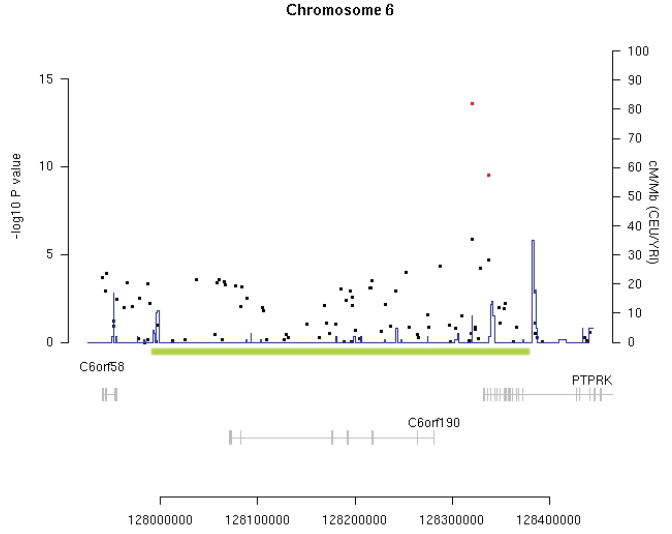

Chromosome 3
-log10 P value
cM/Mb (CEU/YRI)
U6
LRRIQ4
MYNN
SAMD7
LRRC34
SEC62
Telomerase-vert
LRRC31
170800000
170900000
171000000
171100000

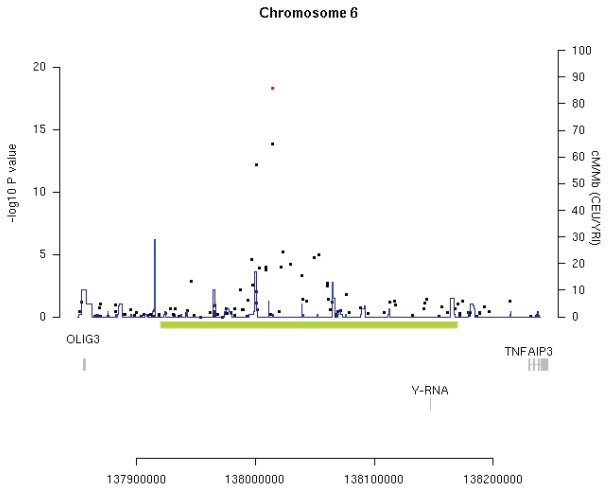

Chromosome 3
-log10 P value
cM/Mb (CEU/YRI)
LPP
189450000
189500000
189550000
189600000
189650000
189700000

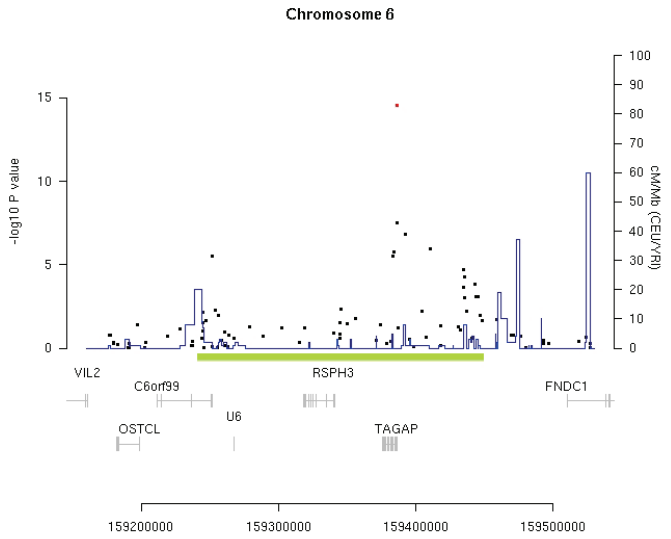

Chromosome 4
-log10 P value
cM/Mb (CEU/YRI)
KIAA1109
IL2
IL21
ADAD1
123100000
123300000
123500000
123700000

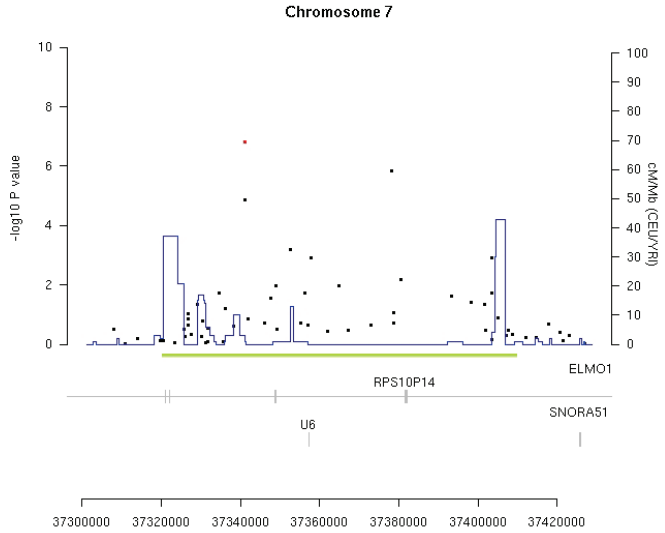

Chromosome 6
-log10 P value
cM/Mb (CEU/YRI)
IRF4
320000
340000
360000
380000
400000

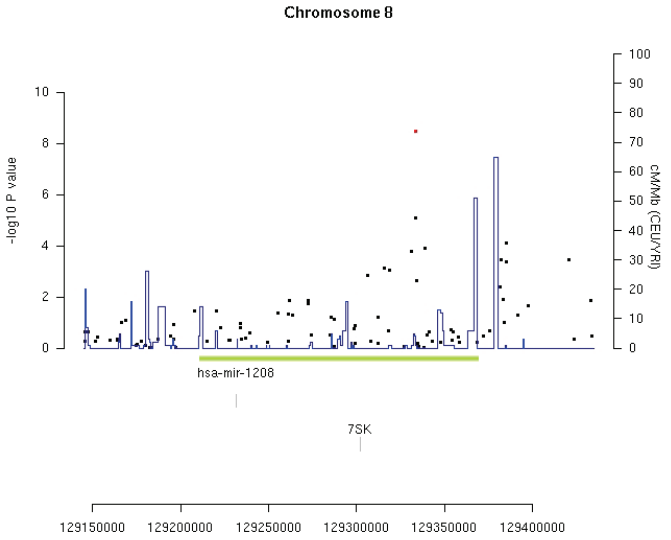

Chromosome 6
-log10 P value
cM/Mb (CEU/YRI)
BACH2
90850000
90900000
90950000
91000000
91050000
91100000
91150000

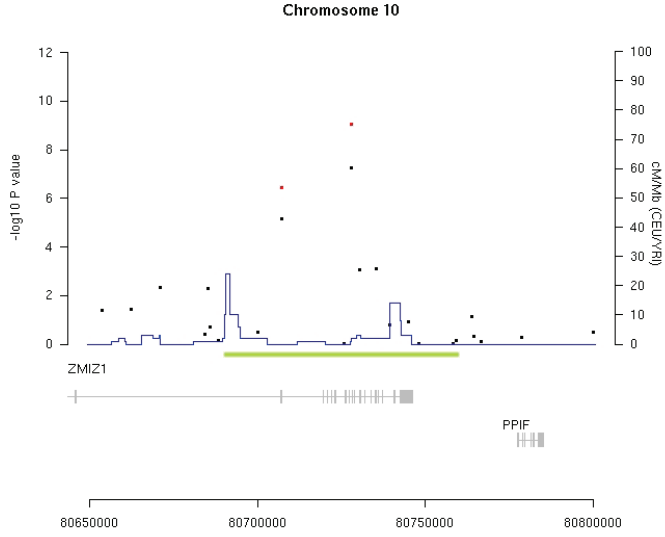

Chromosome 6
-log10 P value
cM/Mb (CEU/YRI)
C6orf58
PTPRK
C6orf190
128000000
128100000
128200000
128300000
128400000

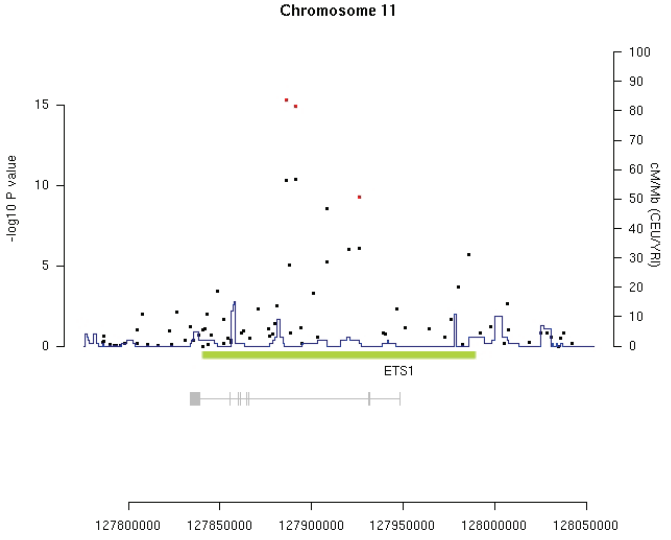

Chromosome 6
-log10 P value
cM/Mb (CEU/YRI)
OLIG3
TNFAIP3
Y-RNA
137900000
138000000
138100000
138200000

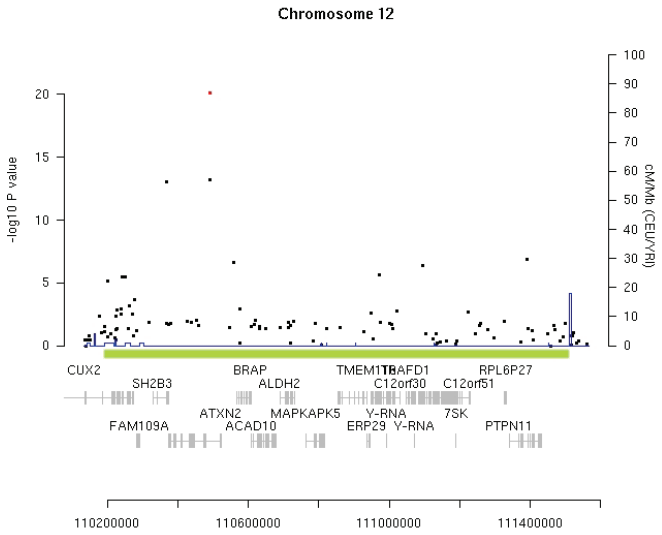

Chromosome 6
-log10 P value
cM/Mb (CEU/YRI)
VIL2
C6orf99
RSPH3
FNDC1
U6
OSTCL
TAGAP
159200000
159300000
159400000
159500000

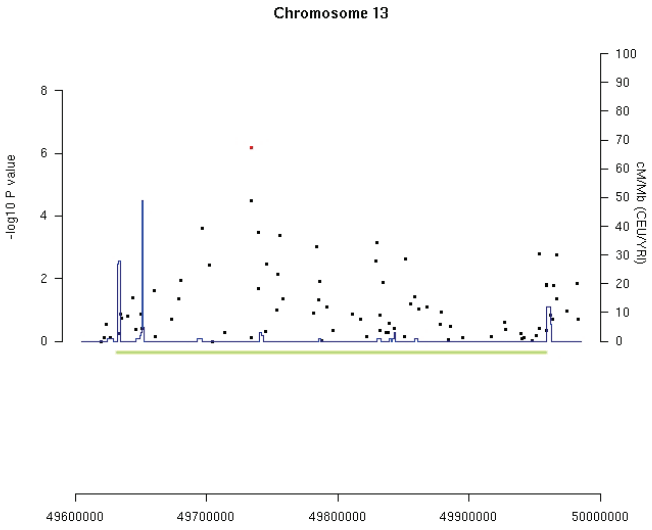

Chromosome 7
-log10 P value
cM/Mb (CEU/YRI)
ELMO1
RPS10P14
SNORA51
U6
37300000
37320000
37340000
37360000
37380000
37400000
37420000

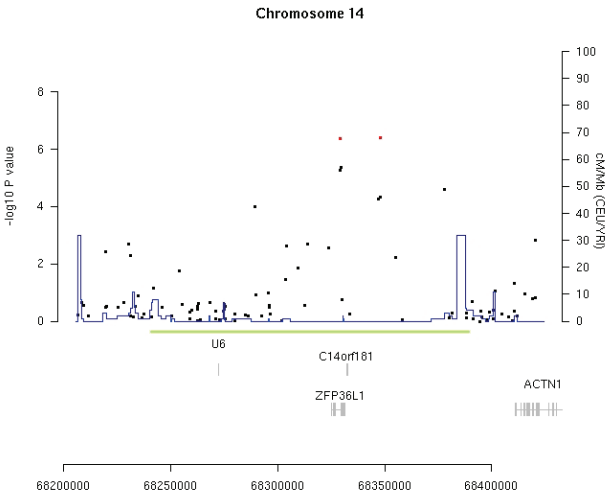

Chromosome 8
-log10 P value
cM/Mb (CEU/YRI)
hsa-mir-1208
7SK
129150000
129200000
129250000
129300000
129350000
129400000

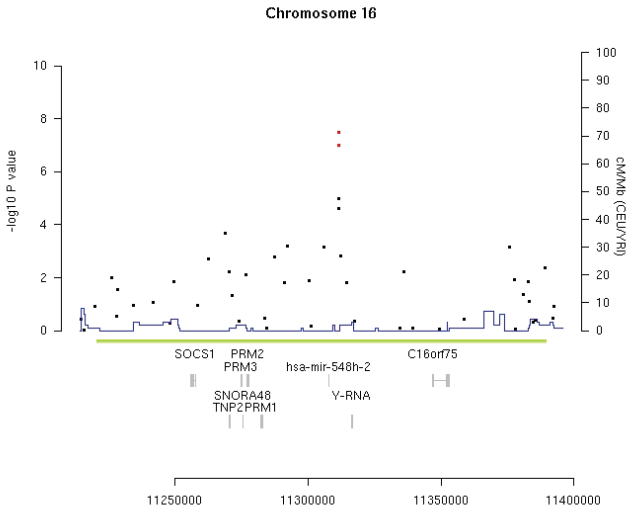

Chromosome 10
-log10 P value
cM/Mb (CEU/YRI)
ZMIZ1
PPIF
80650000
80700000
80750000
80800000

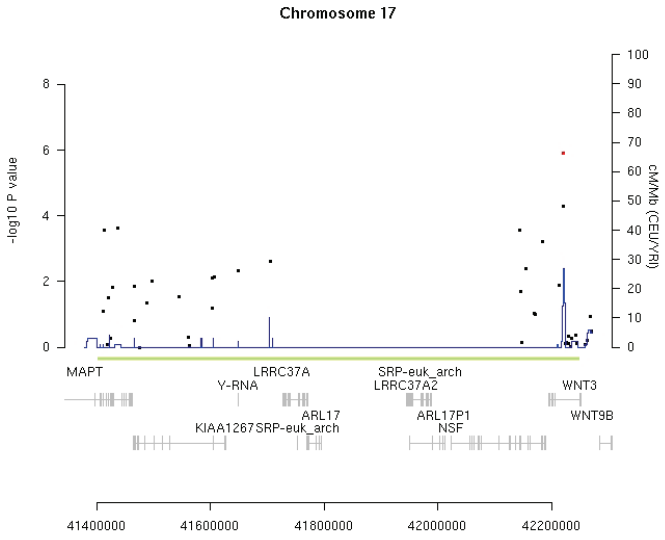

Chromosome 11
-log10 P value
cM/Mb (CEU/YRI)
ETS1
127800000
127850000
127900000
127950000
128000000
128050000

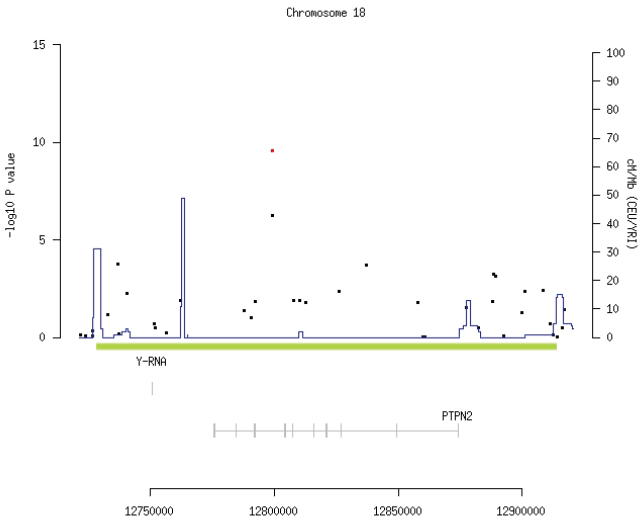

Chromosome 12
-log10 P value
cM/Mb (CEU/YRI)
CUX2
SH2B3
BRAP
ALDH2
TMEM116
AFD1
C12orf30
C12orf51
RPL6P27
ATXN2
MAPKAPK5
Y-RNA
7SK
FAM109A
ACAD10
ERP29
Y-RNA
PTPN11
110200000
110600000
111000000
111400000

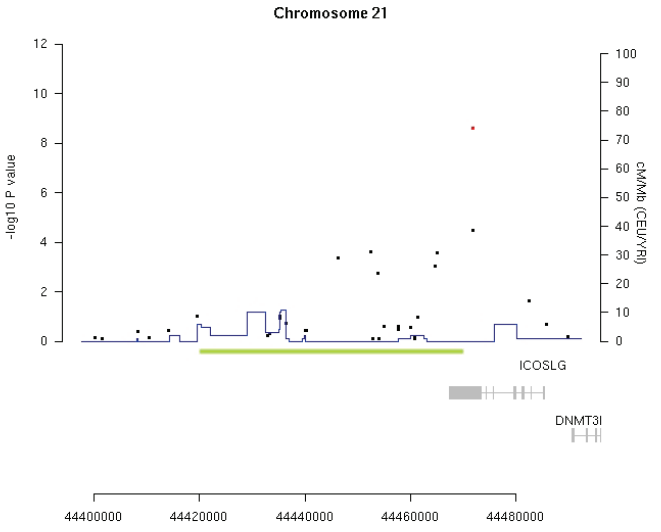

Chromosome 13
-log10 P value
cM/Mb (CEU/YRI)
49600000
49700000
49800000
49900000
50000000

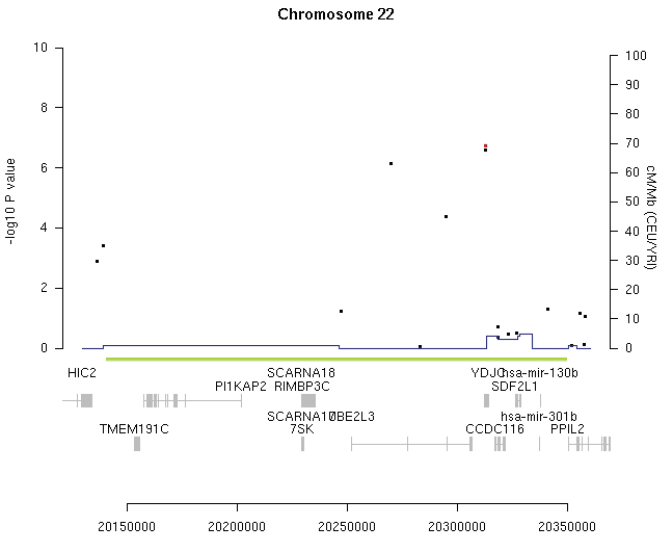

Chromosome 14
-log10 P value
cM/Mb (CEU/YRI)
U6
C14orf181
ZFP36L1
ACTN1
68200000
68250000
68300000
68350000
68400000

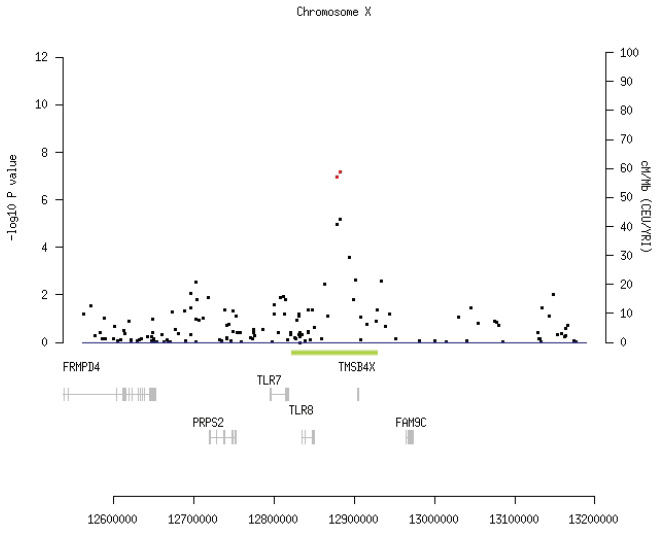

Chromosome 16
-log10 P value
cM/Mb (CEU/YRI)
SOCS1
PRM2
PRM3
hsa-mir-548h-2
C16orf75
SNORA48
TNP2
PRM1
Y-RNA
11250000
11300000
11350000
11400000


Chromosome 17
-log10 P value
cM/Mb (CEU/YRI)
MAPT
Y-RNA
LRRC37A
SRP-euk_arch
LRRC37A2
WNT3
ARL17
KIAA1267
SRP-euk_arch
ARL17P1
NSF
WNT9B
41400000
41600000
41800000
42000000
42200000


Chromosome 18
-log10 P value
cM/Mb (CEU/YRI)
Y-RNA
PTPN2
12750000
12800000
12850000
12900000


Chromosome 21
-log10 P value
cM/Mb (CEU/YRI)
ICOSLG
DNMT3L
44400000
44420000
44440000
44460000
44480000


Chromosome 22
-log10 P value
cM/Mb (CEU/YRI)
HIC2
SCARNA18
PI1KAP2
RIMBP3C
YDJC
hsa-mir-130b
SDF2L1
SCARNA10
BE2L3
hsa-mir-301b
TMEM191C
7SK
CCDC116
PPIL2
20150000
20200000
20250000
20300000
20350000

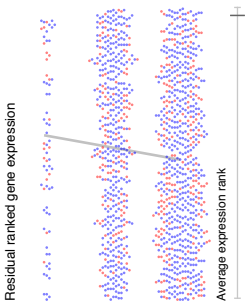

Chromosome X
-log10 P value
cM/Mb (CEU/YRI)
FRMPD4
TMSB4X
TLR7
TLR8
PRPS2
FAM9C
12600000
12700000
12800000
12900000
13000000
13100000
13200000

Supplementary Figure 2 Detailed eQTL genotype - expression correlation analyses. Individual level gene expression data (residual variance after Transcriptional Components removed) from 1469 PAXgene samples. Spearman Rank Correlation coefficients and *P* values shown for HT-12 and Ref8 data, and meta-analysis results. Right Y axis, average expression rank, is a measure of how strongly the tested probe is expressed amongst all probes in the dataset. eQTL plots are presented in descending *P* value order.

Females
Males

SNP rs2074404 (chr. 17, 42220599 bp)
Probe 4070615 (chr. 17, 42194044 - 42251980 bp), WNT3
P-Value 0.003

HT-12



CC (72) CA (473) AA (692)
Corr: -0.085 **R2:** 0.007
Z-Score: -2.984 **P-Value:** 0.003

Ref-8v2

eQTL not available

Probe not present.

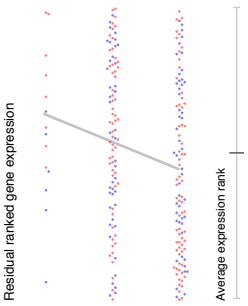
SNP rs4819388 (chr. 21, 44471849 bp)
Probe Human_RefSeq-8_v2-7200373 (chr. 21, 44044003 - 44055131 bp), RRP1///AP001053.1
P-Value 0.003

HT-12

eQTL not available

Probe not present.

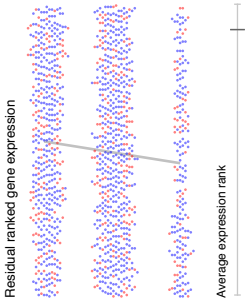
Ref-8v2



TT (14) TC (100) CC (115)
Corr: -0.199 **R2:** 0.039
Z-Score: -3.018 **P-Value:** 0.003

SNP rs1738074 (chr. 6, 159385965 bp)
Probe 4860242 (chr. 6, 159375017 - 159387172 bp), TAGAP
P-Value 0.002

HT-12



GG (455) GA (588) AA (196)
Corr: -0.087 **R2:** 0.008
Z-Score: -3.063 **P-Value:** 0.002

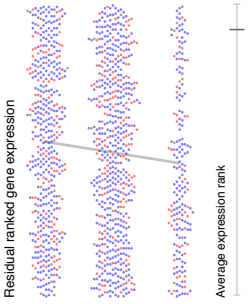
Ref-8v2

eQTL not available

Probe not present.

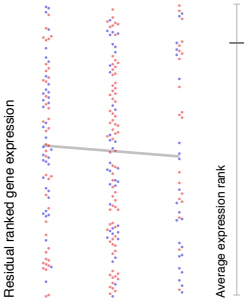
SNP rs1738074 (chr. 6, 159385965 bp)
Probe 5890739 (chr. 6, 159380068 - 159380068 bp), -
P-Value 0.0019881284915475735

HT-12



GG (455) GA (588) AA (196)
Corr: -0.088 **R2:** 0.008
Z-Score: -3.089 **P-Value:** 0.002

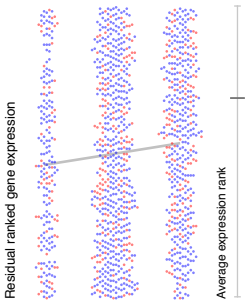
Ref-8v2



GG (78) GA (108) AA (43)
Corr: -0.041 **R2:** 0.002
Z-Score: -0.617 **P-Value:** 0.537

SNP rs10806425 (chr. 6, 90983333 bp)
Probe 3520349 (chr. 6, 90691969 - 91064182 bp), BACH2
P-Value 0.002

HT-12



AA (212) AC (584) CC (444)
Corr: 0.088 **R2:** 0.008
Z-Score: 3.118 **P-Value:** 0.002

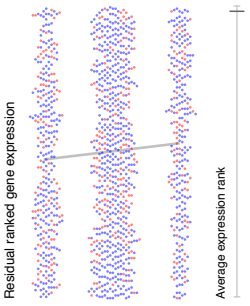
Ref-8v2

eQTL not available

Probe not present.

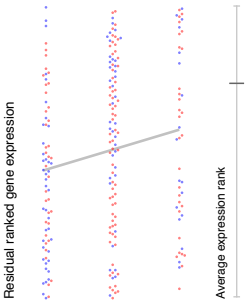
SNP rs1250552 (chr. 10, 80728033 bp)
Probe 2450131 (chr. 10, 80497798 - 80747282 bp), ZMIZ1
P-Value 0.002

HT-12



AA (322) AG (643) GG (275)
Corr: 0.065 **R2:** 0.004
Z-Score: 2.302 **P-Value:** 0.021

Ref-8v2



TT (75) TC (107) CC (47)
Corr: 0.169 **R2:** 0.029
Z-Score: 2.569 **P-Value:** 0.01

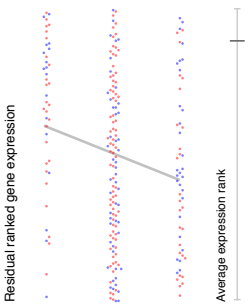
SNP rs653178 (chr. 12, 110492139 bp)
Probe Human_RefSeq-8_v2-3190129 (chr. 12, 110852486 - 110936326 bp), TMEM116
P-Value 0.002

HT-12

eQTL not available

Probe not present.

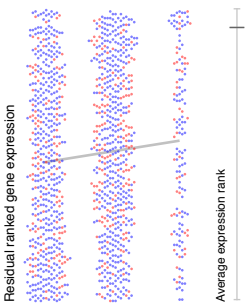
Ref-8v2



AA (43) AG (129) GG (56)
Corr: -0.208 **R2:** 0.043
Z-Score: -3.162 **P-Value:** 0.002

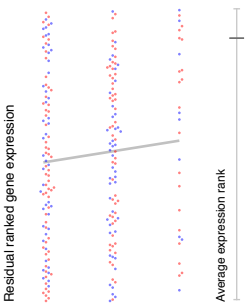
SNP rs3748816 (chr. 1, 2516606 bp)
Probe 6520725 (chr. 1, 2478153 - 2487757 bp), TNFRSF14
P-Value 0.001

HT-12



AA (522) AG (572) GG (145)
Corr: 0.083 **R2:** 0.007
Z-Score: 2.932 **P-Value:** 0.003

Ref-8v2



TT (104) TC (97) CC (28)
Corr: 0.089 **R2:** 0.008
Z-Score: 1.335 **P-Value:** 0.182

Females
Males

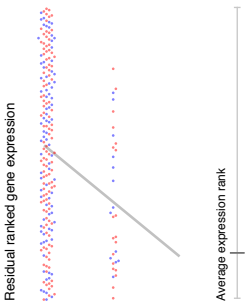
SNP rs13098911 (chr. 3, 46210205 bp)
Probe Human_RefSeq-8_v2-7570670 (chr. 3, 46226186 - 46284166 bp), CCR3
P-Value 5.69E-4

HT-12

eQTL not available

Probe not present.

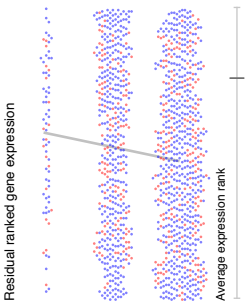
Ref-8v2



CC (197) CT (32) TT (0)
Corr: -0.226 **R2:** 0.051
Z-Score: -3.448 **P-Value:** 5.64E-4

SNP rs2074404 (chr. 17, 42220599 bp)
Probe 1410484 (chr. 17, 42022391 - 42191000 bp), NSF
P-Value 4.28E-4

HT-12



CC (72) CA (473) AA (692)
Corr: -0.099 **R2:** 0.01
Z-Score: -3.497 **P-Value:** 4.7E-4

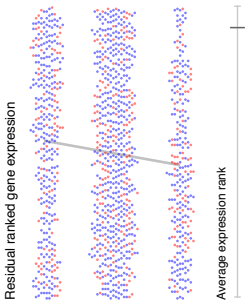
Ref-8v2

eQTL not available

Probe not present.

SNP rs653178 (chr. 12, 110492139 bp)
Probe 2070736 (chr. 12, 110852486 - 110936326 bp), TMEM116
P-Value 3.68E-4

HT-12



AA (351) AG (622) GG (267)
Corr: -0.1 **R2:** 0.01
Z-Score: -3.533 **P-Value:** 4.11E-4

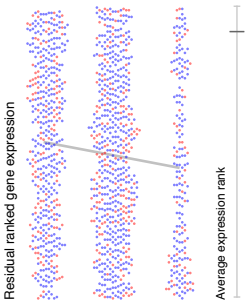
Ref-8v2

eQTL not available

Probe not present.

SNP rs1738074 (chr. 6, 159385965 bp)
Probe 5360364 (chr. 6, 159375017 - 159387172 bp), TAGAP
P-Value 3.23E-4

HT-12



GG (455) GA (588) AA (196)
Corr: -0.101 **R2:** 0.01
Z-Score: -3.573 **P-Value:** 3.53E-4

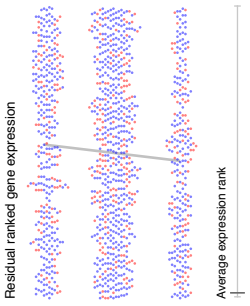
Ref-8v2

eQTL not available

Probe not present.

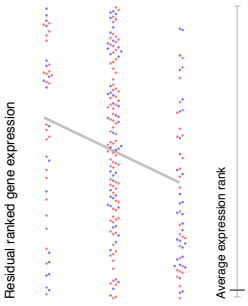
SNP rs653178 (chr. 12, 110492139 bp)
Probe 840253 (chr. 12, 110687729 - 110733165 bp), ALDH2
P-Value 1.44E-4

HT-12



AA (351) AG (622) GG (267)
Corr: -0.07 **R2:** 0.005
Z-Score: -2.477 **P-Value:** 0.013

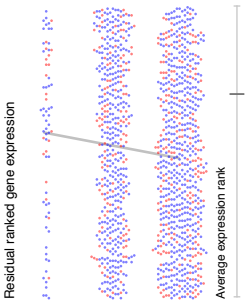
Ref-8v2



AA (43) AG (129) GG (56)
Corr: -0.25 **R2:** 0.062
Z-Score: -3.811 **P-Value:** 1.38E-4

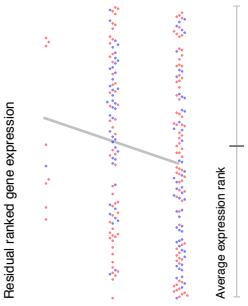
SNP rs2074404 (chr. 17, 42220599 bp)
Probe 3520672 (chr. 17, 41796319 - 41852371 bp), ARL17///LRRC37A///LRRC37A2
P-Value 1.17E-4

HT-12



CC (72) CA (473) AA (692)
Corr: -0.091 **R2:** 0.008
Z-Score: -3.194 **P-Value:** 0.001

Ref-8v2



GG (9) GT (94) TT (126)
Corr: -0.152 **R2:** 0.023
Z-Score: -2.3 **P-Value:** 0.021

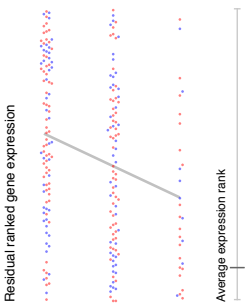
SNP rs3748816 (chr. 1, 2516606 bp)
Probe Human_RefSeq-8_v2-6250338 (chr. 1, 2507097 - 2513762 bp), C1orf93
P-Value 1.16E-4

HT-12

eQTL not available

Probe not present.

Ref-8v2



TT (104) TC (97) CC (28)
Corr: -0.253 **R2:** 0.064
Z-Score: -3.87 **P-Value:** 1.09E-4

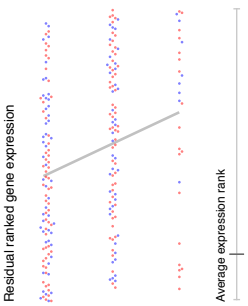
SNP rs6441961 (chr. 3, 46327388 bp)
Probe Human_RefSeq-8_v2-7570670 (chr. 3, 46226186 - 46284166 bp), CCR3
P-Value 1.02E-4

HT-12

eQTL not available

Probe not present.

Ref-8v2

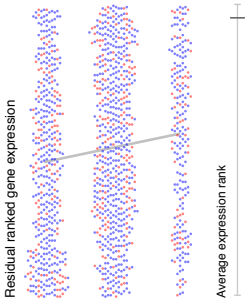


CC (105) CT (97) TT (27)
Corr: 0.254 **R2:** 0.064
Z-Score: 3.883 **P-Value:** 1.03E-4

Females
Males

SNP rs13010713 (chr. 2, 181704290 bp)
Probe 1780433 (chr. 2, 181557026 - 181630704 bp), UBE2E3
P-Value 4.93E-5

HT-12



AA (425) AG (597) GG (218)
Corr: 0.115 **R2:** 0.013
Z-Score: 4.075 **P-Value:** 4.61E-5

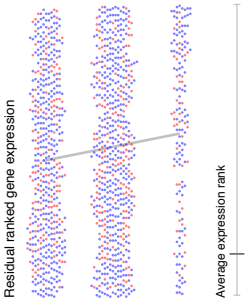
Ref-8v2

eQTL not available

Probe not present.

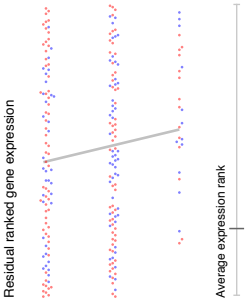
SNP rs296547 (chr. 1, 199158760 bp)
Probe 1300279 (chr. 1, 198880146 - 198880146 bp), -
P-Value 2.44519143035054E-5

HT-12



GG (489) GA (594) AA (157)
Corr: 0.107 **R2:** 0.011
Z-Score: 3.782 **P-Value:** 1.55E-4

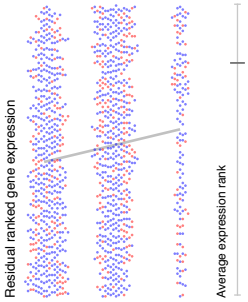
Ref-8v2



GG (96) GA (107) AA (26)
Corr: 0.127 **R2:** 0.016
Z-Score: 1.917 **P-Value:** 0.055

SNP rs3748816 (chr. 1, 2516606 bp)
Probe 650452 (chr. 1, 2396614 - 2427829 bp), PLCH2
P-Value 1.66E-5

HT-12



AA (522) AG (572) GG (145)
Corr: 0.122 **R2:** 0.015
Z-Score: 4.319 **P-Value:** 1.57E-5

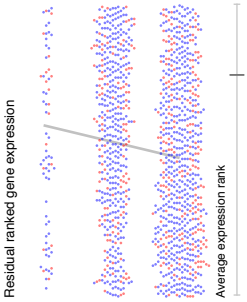
Ref-8v2

eQTL not available

Probe not present.

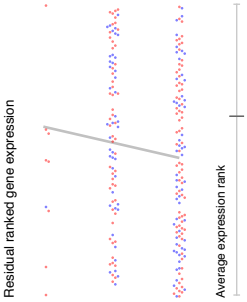
SNP rs2074404 (chr. 17, 42220599 bp)
Probe 5260138 (chr. 17, 42022391 - 42191000 bp), NSF
P-Value 1.2E-5

HT-12



CC (72) CA (473) AA (692)
Corr: -0.116 **R2:** 0.013
Z-Score: -4.073 **P-Value:** 4.65E-5

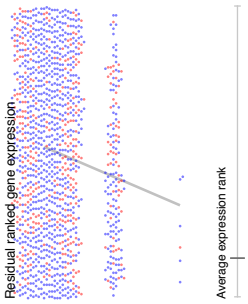
Ref-8v2



GG (9) GT (94) TT (126)
Corr: -0.104 **R2:** 0.011
Z-Score: -1.569 **P-Value:** 0.117

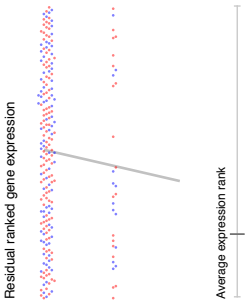
SNP rs13098911 (chr. 3, 46210205 bp)
Probe 6550333 (chr. 3, 45964449 - 45964449 bp), -
P-Value 9.662114013555729E-6

HT-12



GG (1062) GA (172) AA (6)
Corr: -0.124 **R2:** 0.015
Z-Score: -4.384 **P-Value:** 1.17E-5

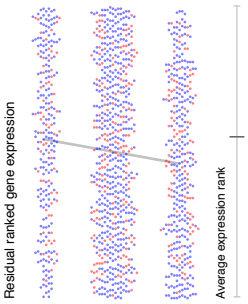
Ref-8v2



CC (197) CT (32) TT (0)
Corr: -0.062 **R2:** 0.004
Z-Score: -0.939 **P-Value:** 0.348

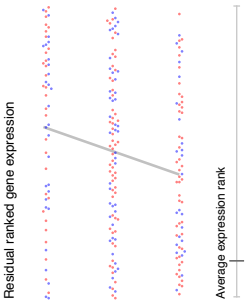
SNP rs11922594 (chr. 3, 120608512 bp)
Probe 3850161 (chr. 3, 120669489 - 120697240 bp), KTELC1
P-Value 7.34E-6

HT-12



AA (256) AG (620) GG (364)
Corr: -0.099 **R2:** 0.01
Z-Score: -3.499 **P-Value:** 4.68E-4

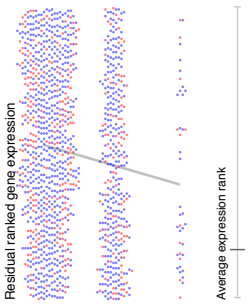
Ref-8v2



TT (58) TC (101) CC (70)
Corr: -0.207 **R2:** 0.043
Z-Score: -3.147 **P-Value:** 0.002

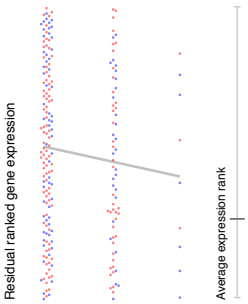
SNP rs6974491 (chr. 7, 37341035 bp)
Probe 2750154 (chr. 7, 36859486 - 37456036 bp), ELMO1
P-Value 5.4E-6

HT-12



GG (833) GA (365) AA (41)
Corr: -0.122 **R2:** 0.015
Z-Score: -4.322 **P-Value:** 1.54E-5

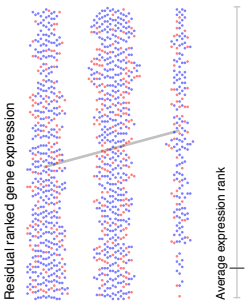
Ref-8v2



GG (151) GA (69) AA (9)
Corr: -0.095 **R2:** 0.009
Z-Score: -1.429 **P-Value:** 0.153

SNP rs864537 (chr. 1, 165678008 bp)
Probe 3890689 (chr. 1, 165665509 - 165755456 bp), CD247
P-Value 2.93E-7

HT-12



AA (481) AG (572) GG (187)
Corr: 0.145 **R2:** 0.021
Z-Score: 5.143 **P-Value:** 2.7E-7

Ref-8v2

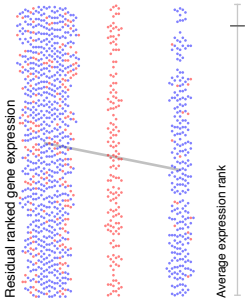
eQTL not available

Probe not present.

Females
Males

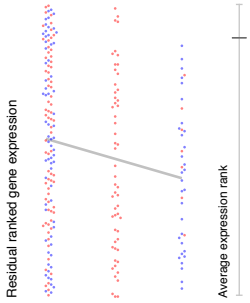
SNP rs5979785 (chr. 23, 12881445 bp)
Probe 3390612 (chr. 23, 12833679 - 12852209 bp), TLR8
P-Value 1.07E-7

HT-12



AA (826) AG (155) GG (259)
Corr: -0.132 **R2:** 0.017
Z-Score: -4.663 **P-Value:** 3.12E-6

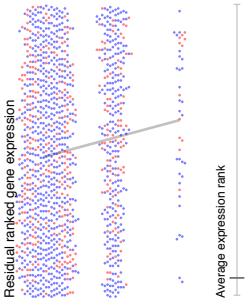
Ref-8v2



TT (136) TC (55) CC (38)
Corr: -0.173 **R2:** 0.03
Z-Score: -2.617 **P-Value:** 0.009

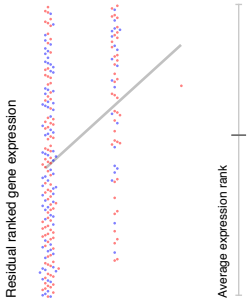
SNP rs12928822 (chr. 16, 11311394 bp)
Probe 4540072 (chr. 16, 11317137 - 11354118 bp), AC009121.6
P-Value 1.02E-8

HT-12



GG (865) GA (334) AA (41)
Corr: 0.115 **R2:** 0.013
Z-Score: 4.063 **P-Value:** 4.85E-5

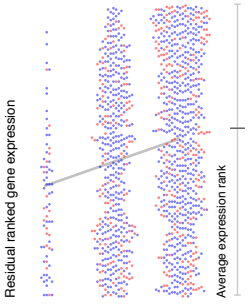
Ref-8v2



CC (167) CT (61) TT (1)
Corr: 0.327 **R2:** 0.107
Z-Score: 5.065 **P-Value:** 4.09E-7

SNP rs2074404 (chr. 17, 42220599 bp)
Probe 4880037 (chr. 17, 42485154 - 42485154 bp), -
P-Value 1.77898649876006 41E-9

HT-12



CC (72) CA (473) AA (692)
Corr: 0.17 **R2:** 0.029
Z-Score: 6.034 **P-Value:** 1.6E-9

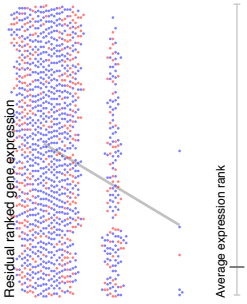
Ref-8v2

eQTL not available

Probe not present.

SNP rs13098911 (chr. 3, 46210205 bp)
Probe 2190671 (chr. 3, 46226186 - 46284166 bp), CCR3
P-Value 5.5E-10

HT-12



GG (1062) GA (172) AA (6)
Corr: -0.174 **R2:** 0.03
Z-Score: -6.18 **P-Value:** 6.4E-10

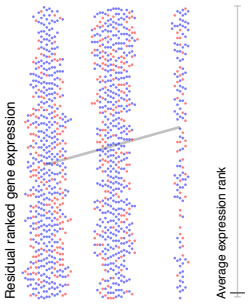
Ref-8v2

eQTL not available

Probe not present.

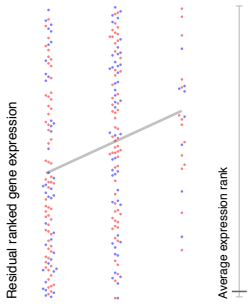
SNP rs842647 (chr. 2, 60972975 bp)
Probe 1170220 (chr. 2, 61257057 - 61270564 bp), AHSA2
P-Value 3.3E-10

HT-12



AA (542) AG (557) GG (140)
Corr: 0.151 **R2:** 0.023
Z-Score: 5.328 **P-Value:** 9.91E-8

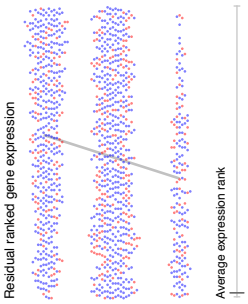
Ref-8v2



AA (101) AG (106) GG (22)
Corr: 0.235 **R2:** 0.055
Z-Score: 3.582 **P-Value:** 3.41E-4

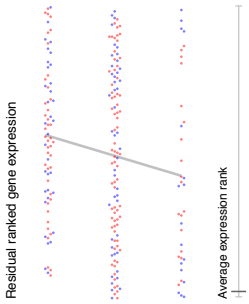
SNP rs13003464 (chr. 2, 61040333 bp)
Probe 1170220 (chr. 2, 61257057 - 61270564 bp), AHSA2
P-Value 6.39E-11

HT-12



AA (452) AG (611) GG (176)
Corr: -0.17 **R2:** 0.029
Z-Score: -6.026 **P-Value:** 1.68E-9

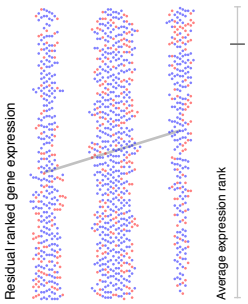
Ref-8v2



AA (75) AG (118) GG (36)
Corr: -0.162 **R2:** 0.026
Z-Score: -2.458 **P-Value:** 0.014

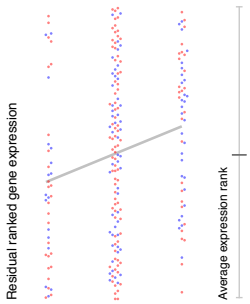
SNP rs653178 (chr. 12, 110492139 bp)
Probe 6560301 (chr. 12, 110350268 - 110448836 bp), SH2B3///ATXN2
P-Value 9.24E-12

HT-12



AA (351) AG (622) GG (267)
Corr: 0.171 **R2:** 0.029
Z-Score: 6.057 **P-Value:** 1.38E-9

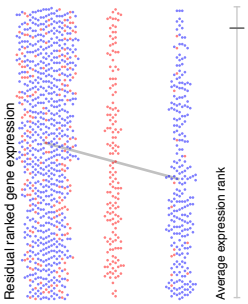
Ref-8v2



AA (43) AG (129) GG (56)
Corr: 0.215 **R2:** 0.046
Z-Score: 3.268 **P-Value:** 0.001

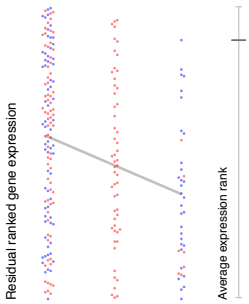
SNP rs5979785 (chr. 23, 12881445 bp)
Probe 6480360 (chr. 23, 12833679 - 12852209 bp), TLR8
P-Value 3.88E-13

HT-12



AA (826) AG (155) GG (259)
Corr: -0.174 **R2:** 0.03
Z-Score: -6.171 **P-Value:** 6.79E-10

Ref-8v2

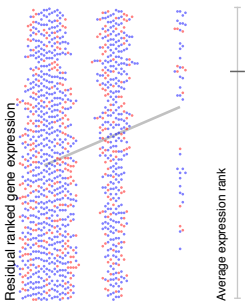


TT (136) TC (55) CC (38)
Corr: -0.259 **R2:** 0.067
Z-Score: -3.958 **P-Value:** 7.55E-5

Females
Males

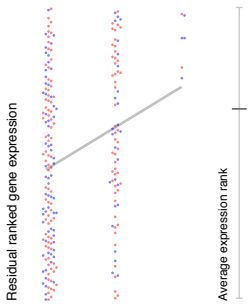
SNP rs12727642 (chr. 1, 7969259 bp)
Probe 610193 (chr. 1, 7943348 - 7968928 bp), PARK7
P-Value 9.76E-15

HT-12



CC (796) CA (399) AA (45)
Corr: 0.19 **R2:** 0.036
Z-Score: 6.739 **P-Value:** 1.6E-11

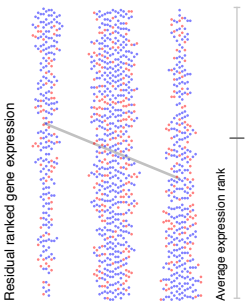
Ref-8v2



CC (147) CA (76) AA (6)
Corr: 0.26 **R2:** 0.068
Z-Score: 3.984 **P-Value:** 6.78E-5

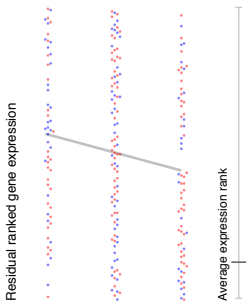
SNP rs11922594 (chr. 3, 120608512 bp)
Probe 6550288 (chr. 3, 120669489 - 120697240 bp), KTELC1
P-Value 5.09E-17

HT-12



AA (256) AG (620) GG (364)
Corr: -0.227 **R2:** 0.051
Z-Score: -8.075 **P-Value:** 6.76E-16

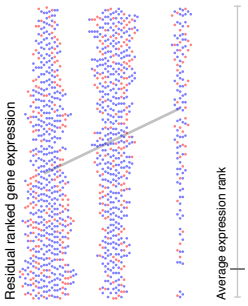
Ref-8v2



TT (58) TC (101) CC (70)
Corr: -0.158 **R2:** 0.025
Z-Score: -2.399 **P-Value:** 0.016

SNP rs6441961 (chr. 3, 46327388 bp)
Probe 2190671 (chr. 3, 46226186 - 46284166 bp), CCR3
P-Value 2.87E-19

HT-12



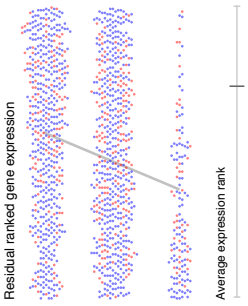
GG (584) GA (523) AA (133)
Corr: 0.251 **R2:** 0.063
Z-Score: 8.98 **P-Value:** 2.71E-19

Ref-8v2
eQTL not available

Probe not present.

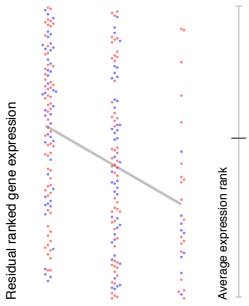
SNP rs3748816 (chr. 1, 2516606 bp)
Probe 2070246 (chr. 1, 2510941 - 2555289 bp), MMEL1
P-Value 1.03E-20

HT-12



AA (522) AG (572) GG (145)
Corr: -0.227 **R2:** 0.051
Z-Score: -8.072 **P-Value:** 6.91E-16

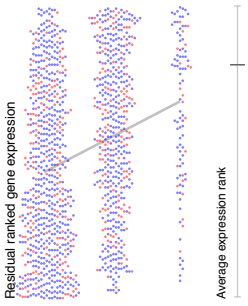
Ref-8v2



TT (104) TC (97) CC (28)
Corr: -0.312 **R2:** 0.098
Z-Score: -4.821 **P-Value:** 1.43E-6

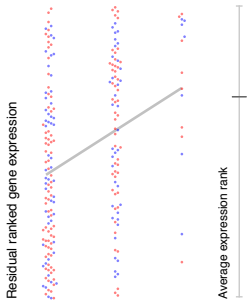
SNP rs3816281 (chr. 2, 68461451 bp)
Probe 4810020 (chr. 2, 68444826 - 68479088 bp), PLEK
P-Value 7.97E-26

HT-12



CC (667) CA (476) AA (97)
Corr: 0.263 **R2:** 0.069
Z-Score: 9.408 **P-Value:** 5.07E-21

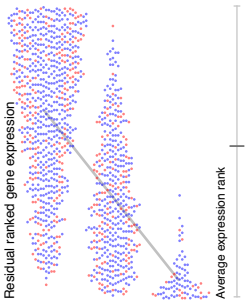
Ref-8v2



GG (127) GT (87) TT (15)
Corr: 0.31 **R2:** 0.096
Z-Score: 4.776 **P-Value:** 1.78E-6

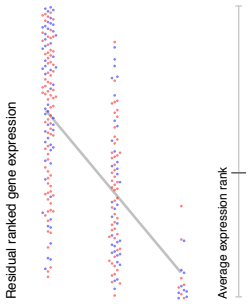
SNP rs917997 (chr. 2, 102437000 bp)
Probe 6520180 (chr. 2, 102400686 - 102436457 bp), IL18RAP
P-Value 7.35E-87

HT-12



GG (723) GA (435) AA (82)
Corr: -0.617 **R2:** 0.381
Z-Score: -17.244 **P-Value:** 5.5E-131

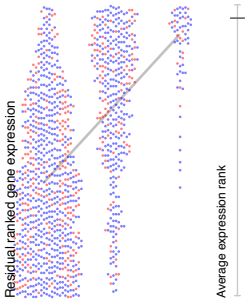
Ref-8v2



GG (128) GA (85) AA (16)
Corr: -0.593 **R2:** 0.351
Z-Score: -9.898 **P-Value:** 4.26E-23

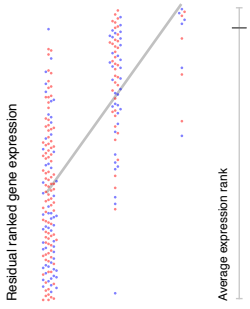
SNP rs2298428 (chr. 22, 20312892 bp)
Probe 1230242 (chr. 22, 20308188 - 20308188 bp), -
P-Value 1.955586158829425E-90

HT-12



GG (796) GA (380) AA (63)
Corr: 0.508 **R2:** 0.258
Z-Score: 17.244 **P-Value:** 2.93E-82

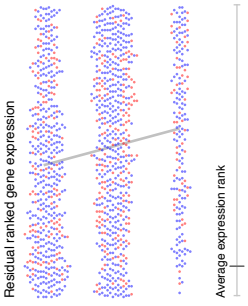
Ref-8v2



CC (148) CT (70) TT (11)
Corr: 0.642 **R2:** 0.412
Z-Score: 10.968 **P-Value:** 5.45E-28

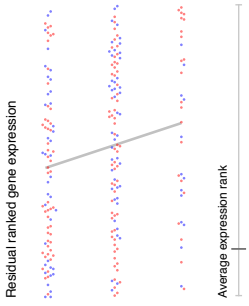
SNP rs864537 (chr. 1, 165678008 bp)
Probe 6290400 (chr. 1, 165665509 - 165755456 bp), CD247
P-Value 1.77E-9

HT-12



AA (481) AG (572) GG (187)
Corr: 0.151 **R2:** 0.023
Z-Score: 5.357 **P-Value:** 8.45E-8

Ref-8v2



TT (89) TC (105) CC (35)
Corr: 0.185 **R2:** 0.034
Z-Score: 2.807 **P-Value:** 0.005

Supplementary Figure 3 Co-localisation of case/control association and genotype-expression correlation (eQTL) signals.

Plots shown for regions described in Table 3. Chromosomal positions based on NCBI Build 36 co-ordinates. P_{GWAS} values (black points and black line) are from 4,533 cases and 10,750 controls. $P_{combined}$ values (red points) are from 9,451 cases and 16,434 controls. Genotype-expression correlation P values for SNP positions across the genome at each tested eQTL are shown in a different colour for each probe (annotated with Illumina ArrayAddressID and gene name).

Chromosome 1

rs3748816 - 2070246 - MMEL1

rs6667605 - 6520725 - TNFRSF14

rs2840528 - 650452 - PLCH2

rs3748816

rs3748816

rs6667605 - Human_RefSeq-8_v2-6250338 - C1orf93

-Log10(P-Value)

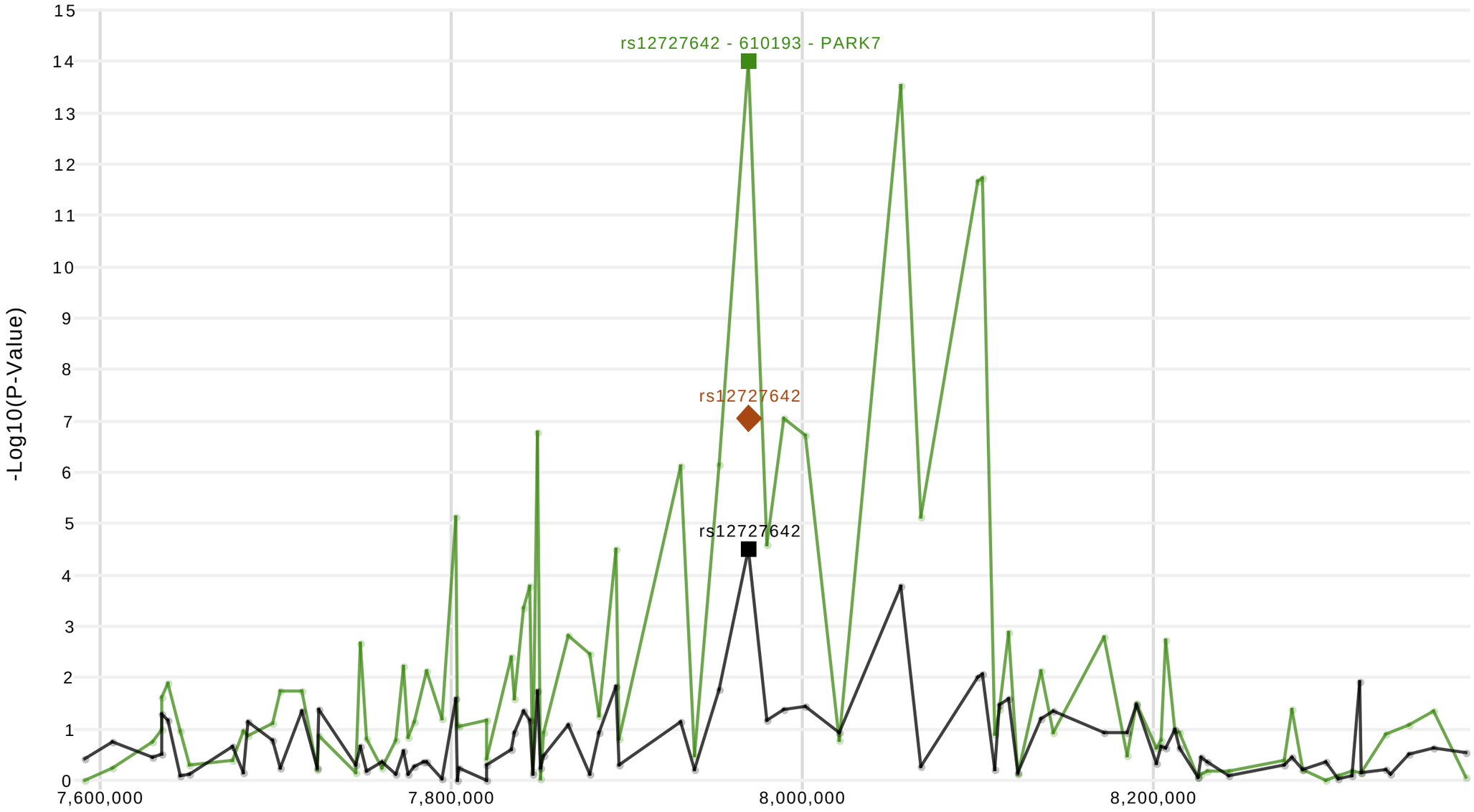
20
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
0

2,200,000
2,400,000
2,600,000
2,800,000
3,000,000

Genomic position (bp)

650452 - PLCH2
2070246 - MMEL1
Human_RefSeq-8_v2-6250338 - C1orf93
6520725 - TNFRSF14

Chromosome 1



Chromosome 1

-Log10(P-Value)

14
13
12
11
10
9
8
7
6
5
4
3
2
1
0

rs1554669 - 6290400 - CD247

rs1554669 - 3890689 - CD247

rs864537

rs864537

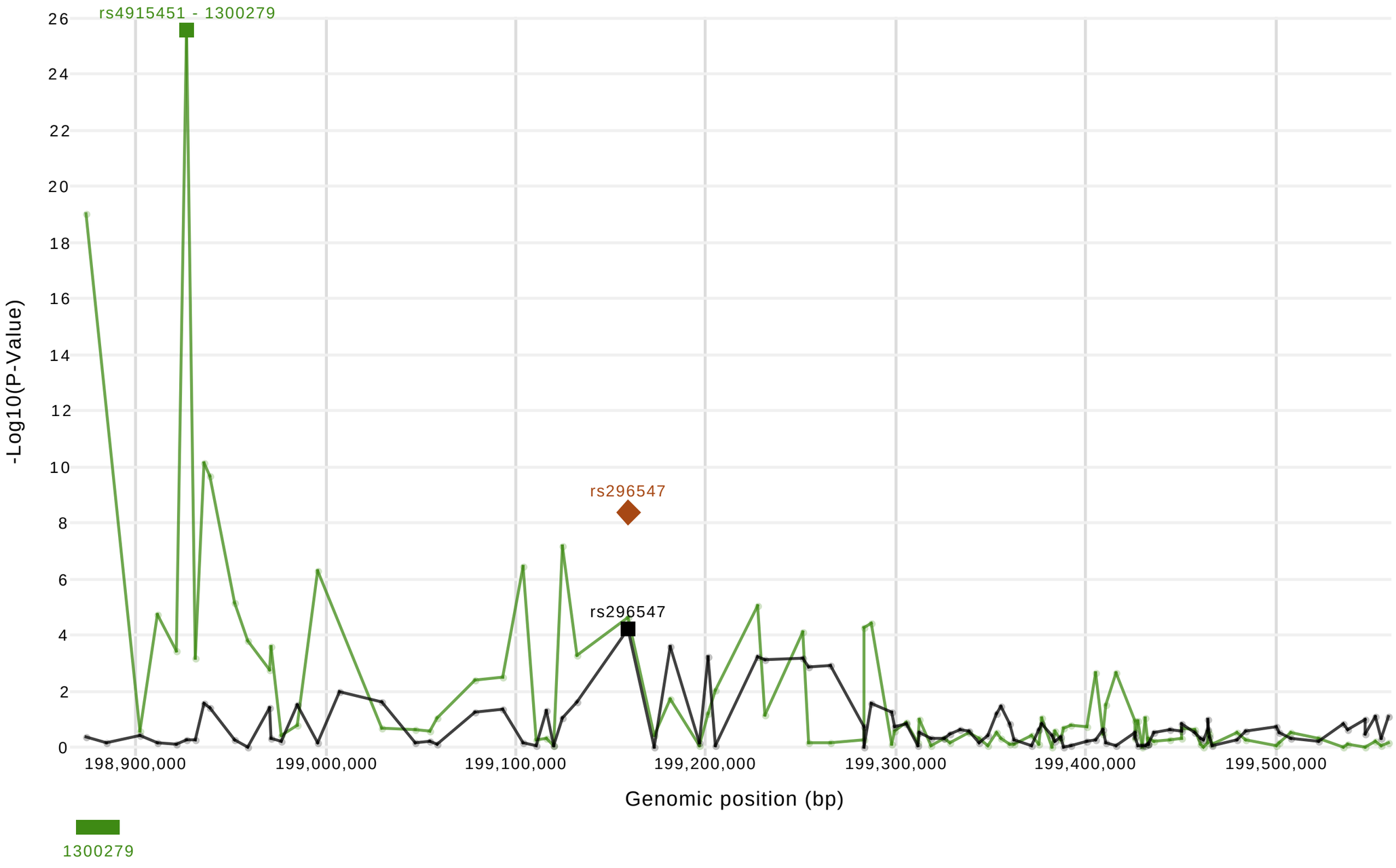
165,200,000
165,400,000
165,600,000
165,800,000

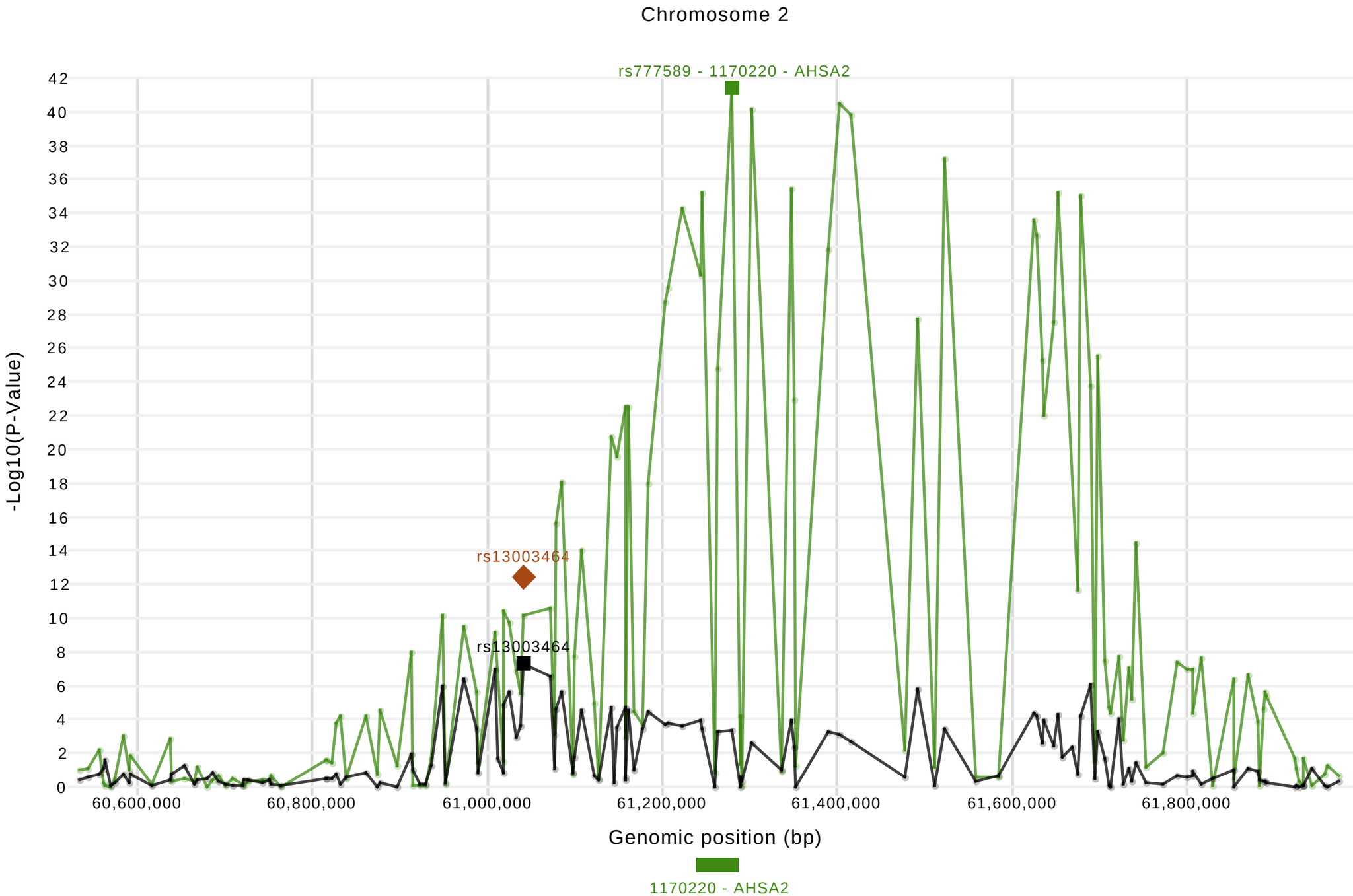
Genomic position (bp)

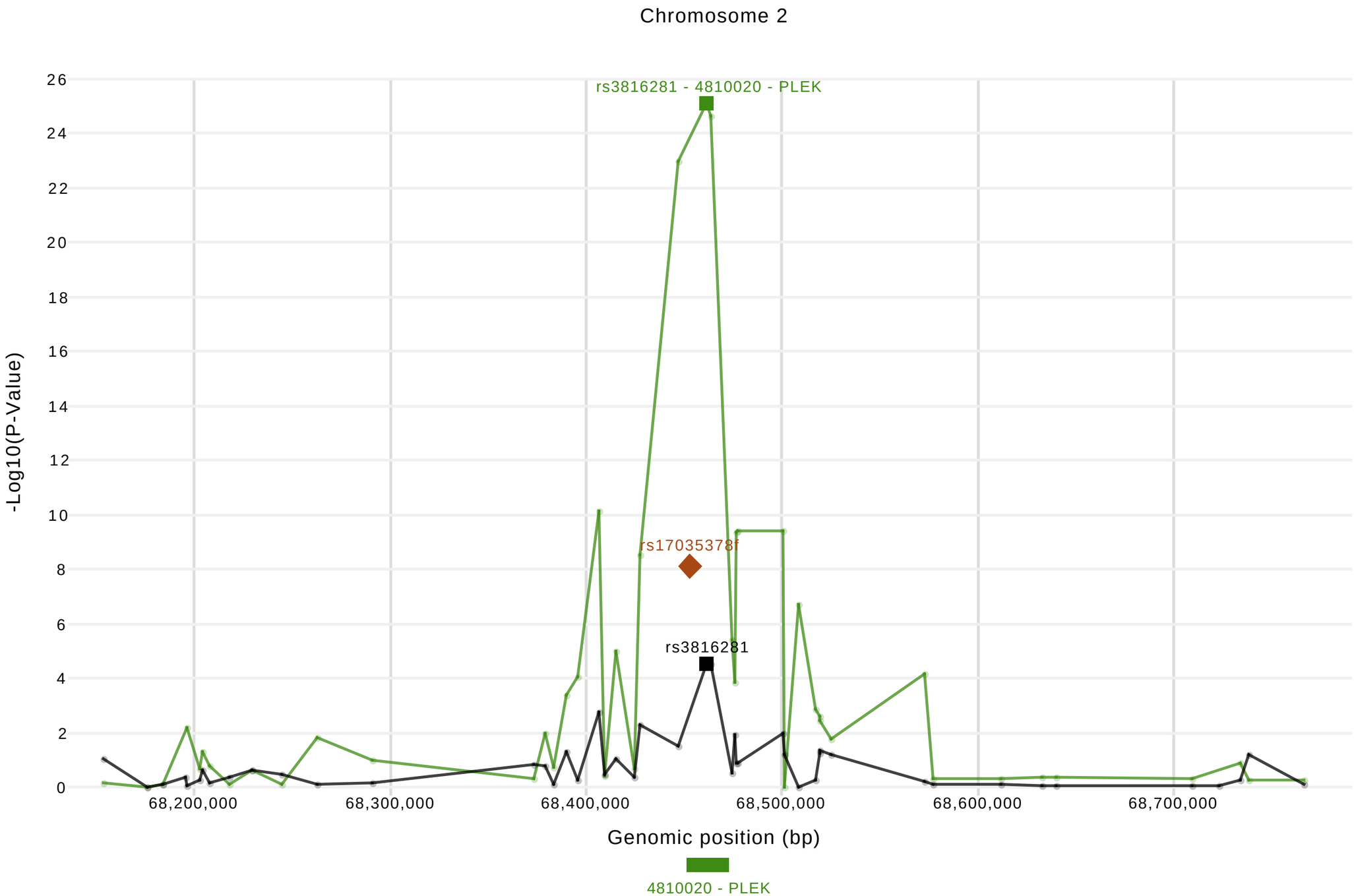
6290400 - CD247

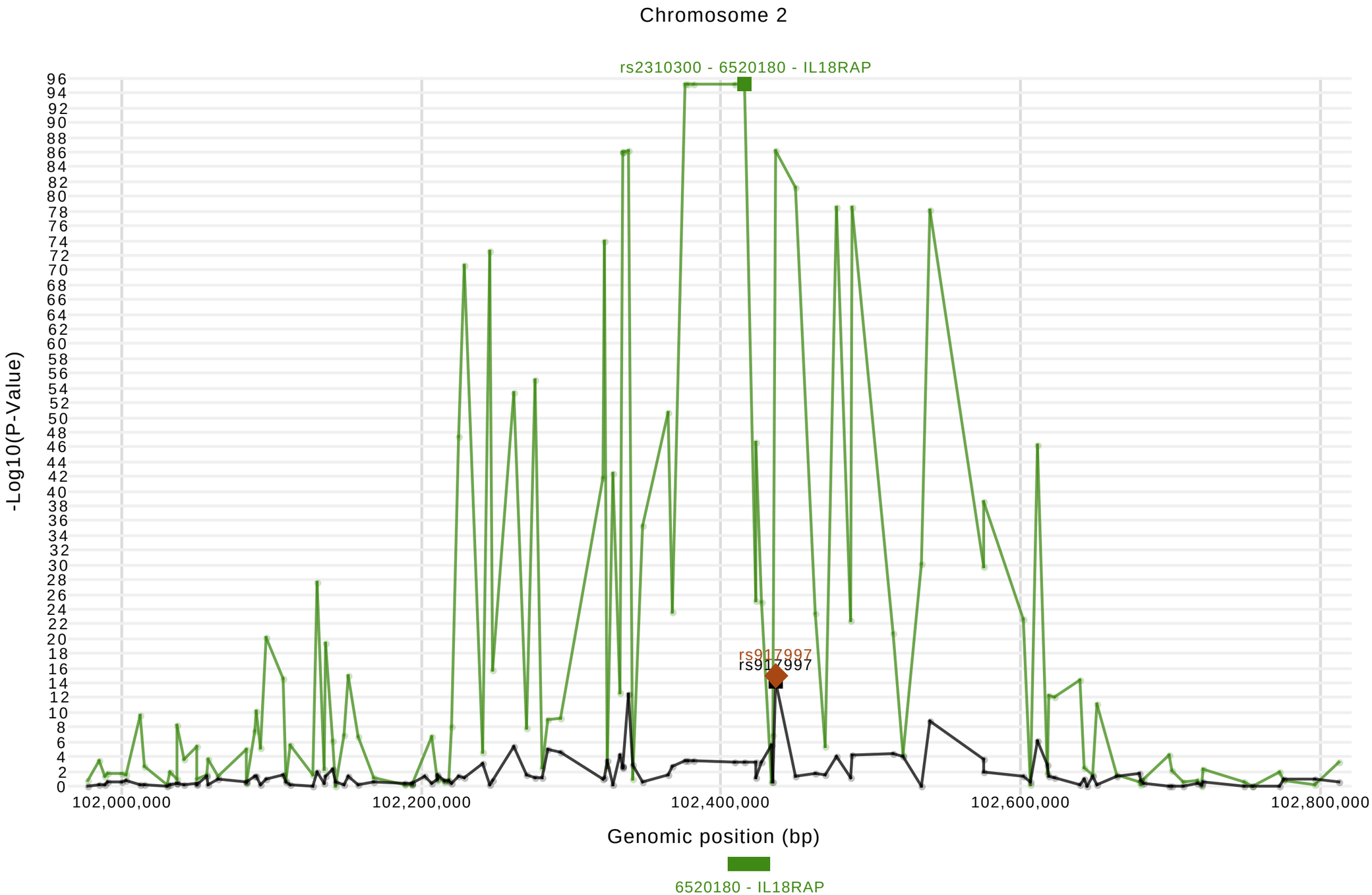
3890689 - CD247

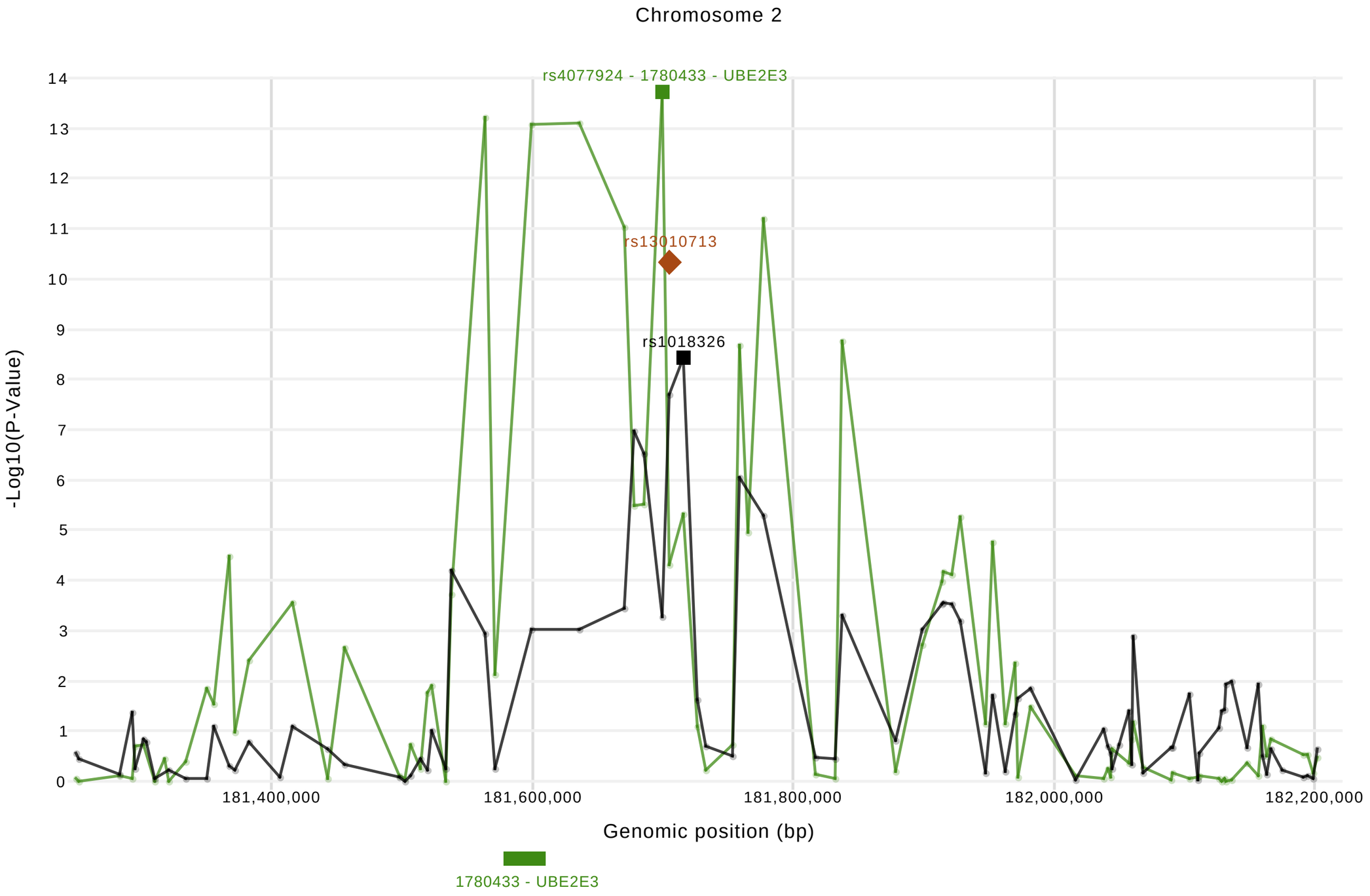
Chromosome 1

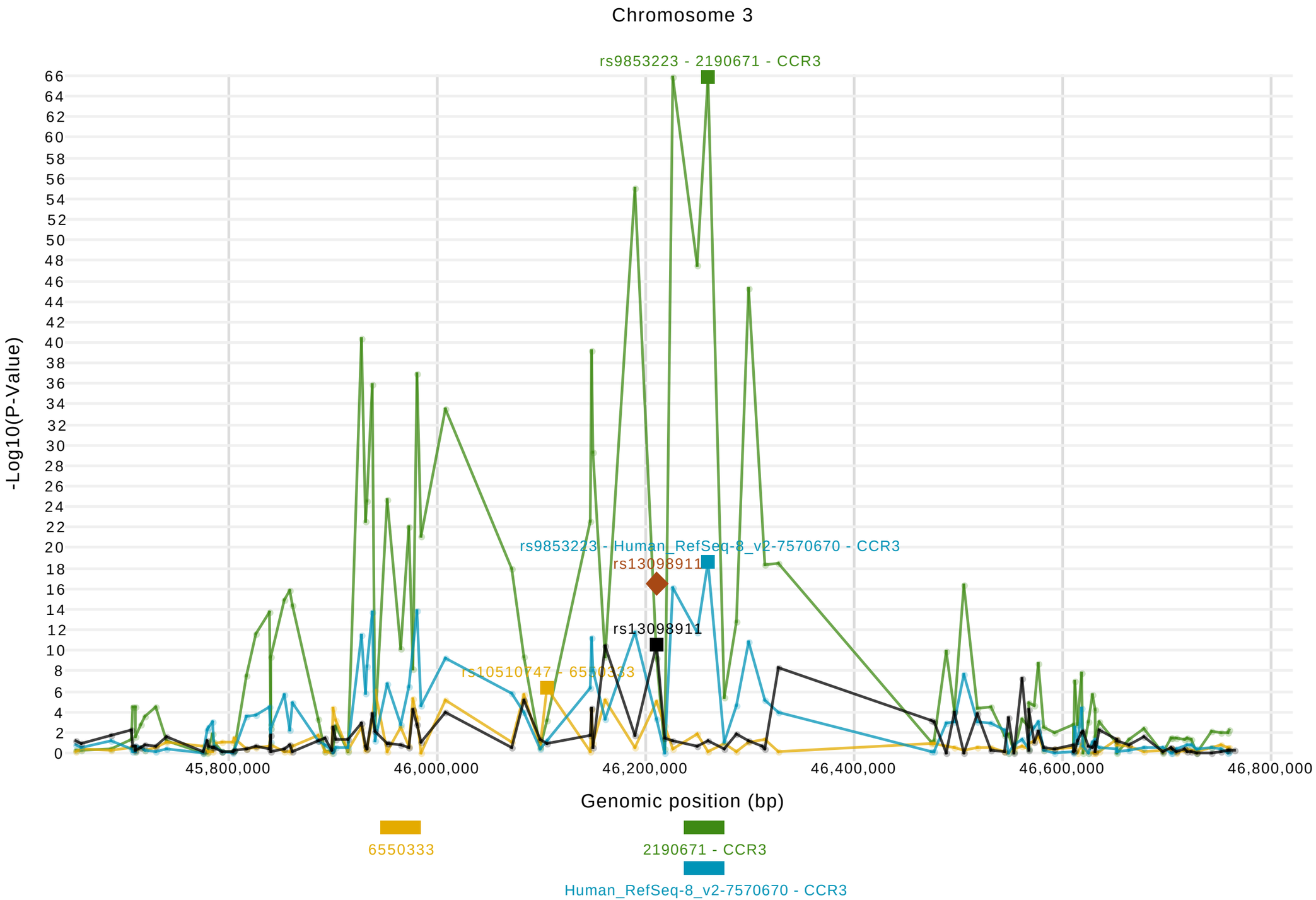


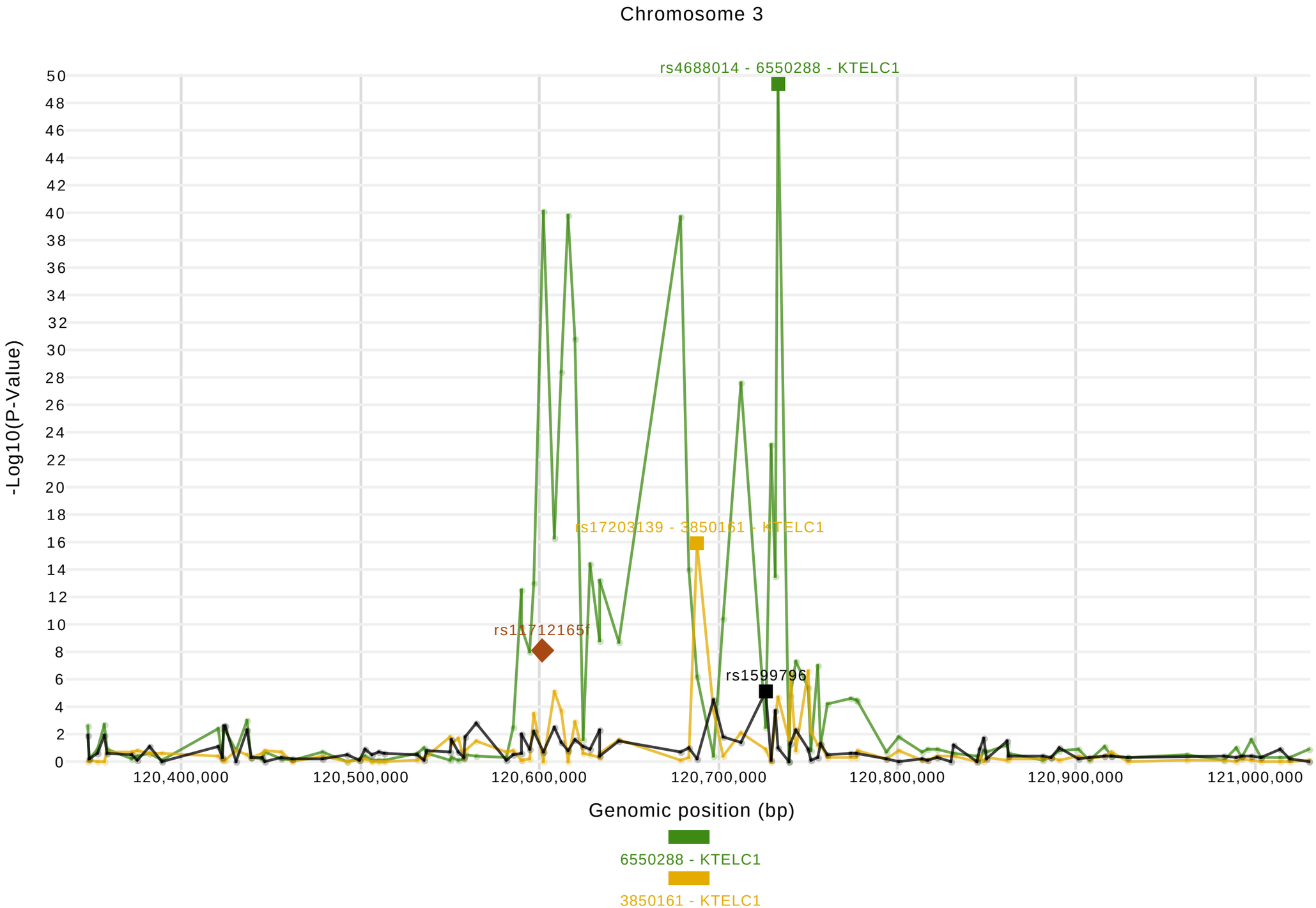

Chromosome 2
rs777589 - 1170220 - AHSA2
rs13003464
rs13003464
-Log10(P-Value)
42
40
38
36
34
32
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
60,600,000
60,800,000
61,000,000
61,200,000
61,400,000
61,600,000
61,800,000
Genomic position (bp)
1170220 - AHSA2

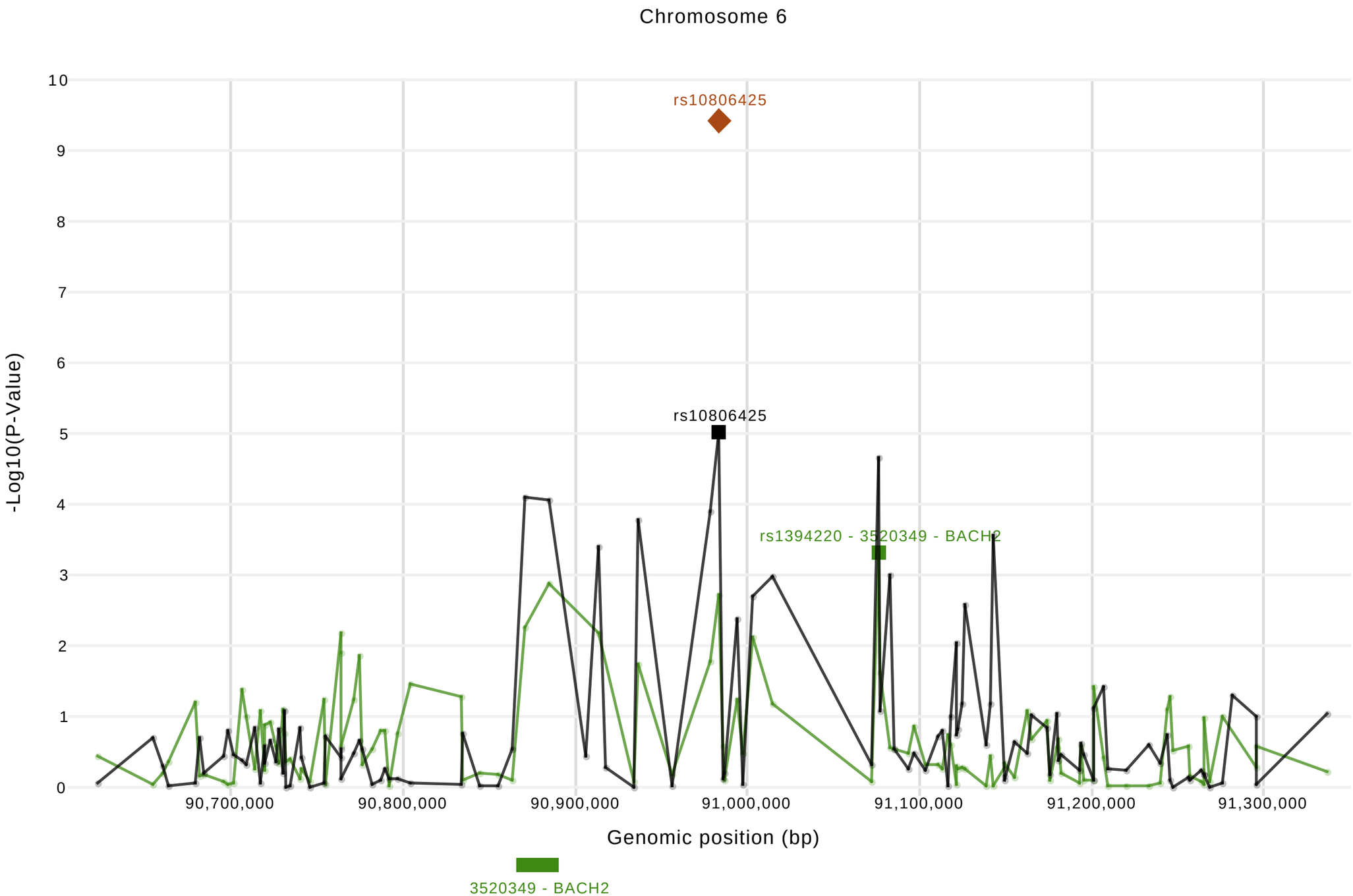

Chromosome 2
rs3816281 - 4810020 - PLEK
rs17035378f
rs3816281
-Log10(P-Value)
26
24
22
20
18
16
14
12
10
8
6
4
2
0
68,200,000
68,300,000
68,400,000
68,500,000
68,600,000
68,700,000
Genomic position (bp)
4810020 - PLEK


Chromosome 2
rs2310300 - 6520180 - IL18RAP
-Log10(P-Value)
96
94
92
90
88
86
84
82
80
78
76
74
72
70
68
66
64
62
60
58
56
54
52
50
48
46
44
42
40
38
36
34
32
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
rs917997
rs917997
102,000,000
102,200,000
102,400,000
102,600,000
102,800,000
Genomic position (bp)
6520180 - IL18RAP

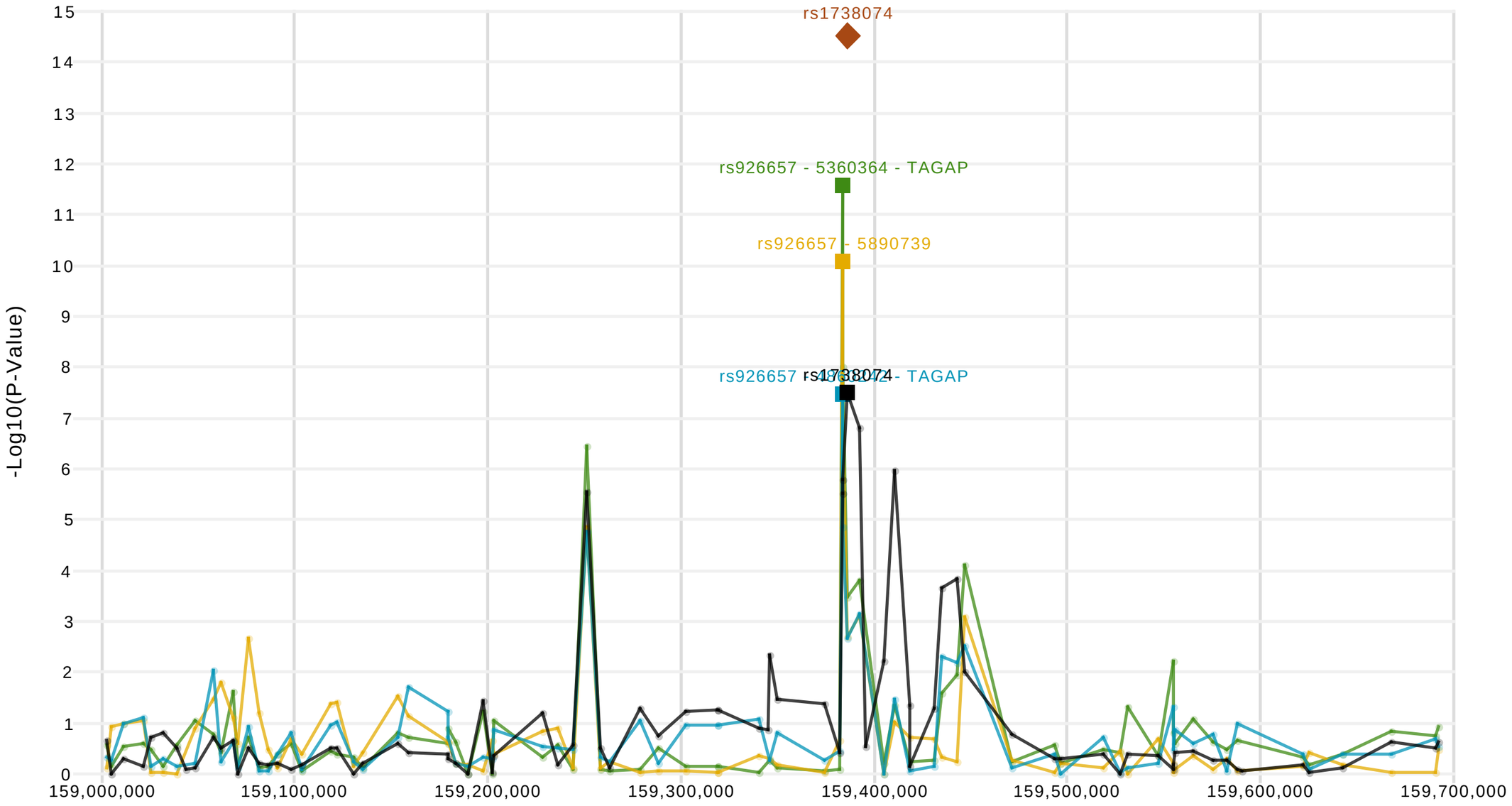

Chromosome 2
rs4077924 - 1780433 - UBE2E3
rs13010713
rs1018326
-Log10(P-Value)
14
13
12
11
10
9
8
7
6
5
4
3
2
1
0
181,400,000
181,600,000
181,800,000
182,000,000
182,200,000
Genomic position (bp)
1780433 - UBE2E3

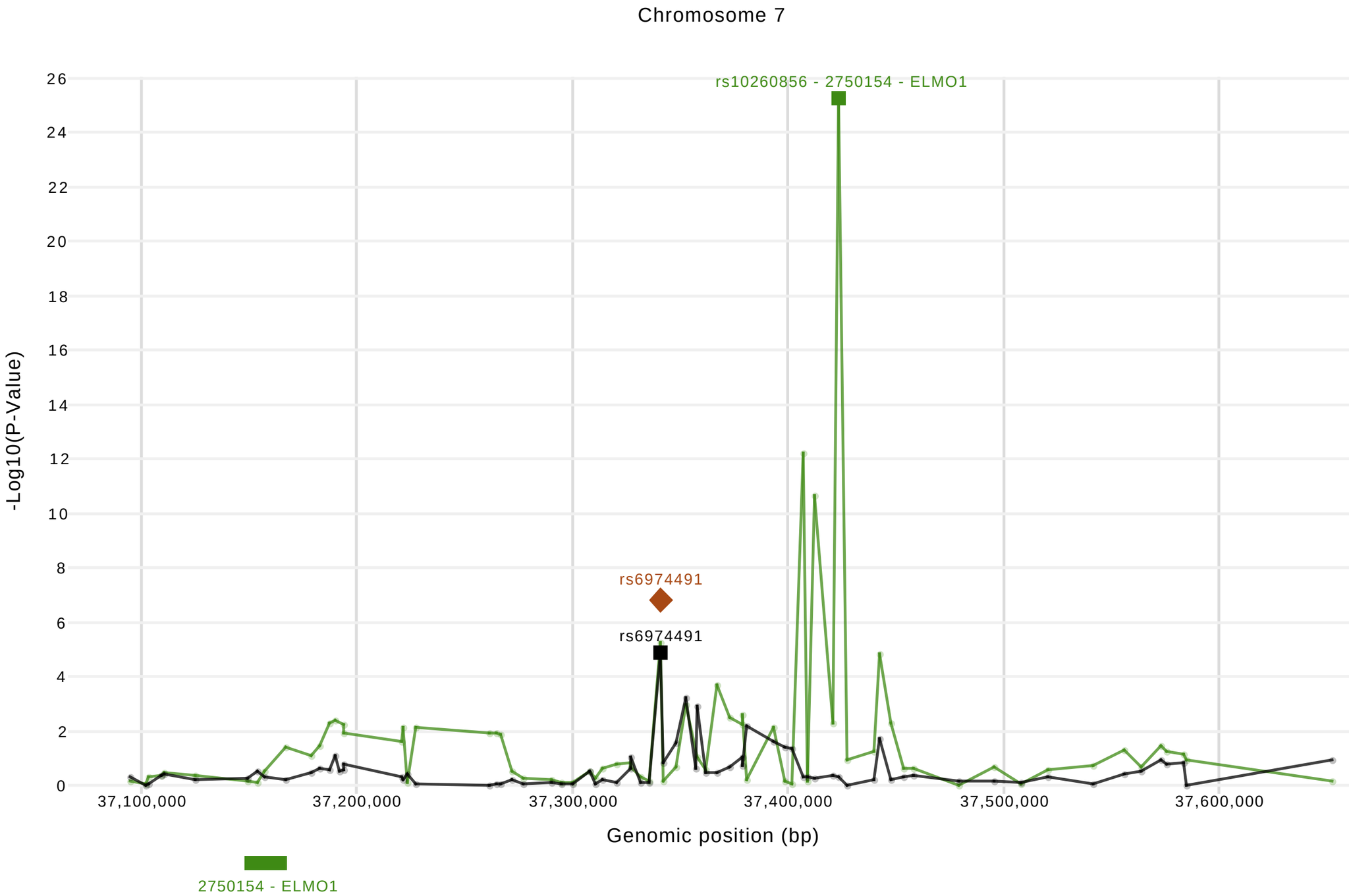

Chromosome 3
rs9853223 - 2190671 - CCR3
-Log10(P-Value)
66
64
62
60
58
56
54
52
50
48
46
44
42
40
38
36
34
32
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
rs9853223 - Human_RefSeq-8_v2-7570670 - CCR3
rs13098911
rs13098911
rs10510747 - 6550333
45,800,000
46,000,000
46,200,000
46,400,000
46,600,000
46,800,000
Genomic position (bp)
6550333
2190671 - CCR3
Human_RefSeq-8_v2-7570670 - CCR3


Chromosome 3
rs4688014 - 6550288 - KTELC1
rs17203139 - 3850161 - KTELC1
rs11712165f
rs1599796
-Log10(P-Value)
50
48
46
44
42
40
38
36
34
32
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
120,400,000
120,500,000
120,600,000
120,700,000
120,800,000
120,900,000
121,000,000
Genomic position (bp)
6550288 - KTELC1
3850161 - KTELC1

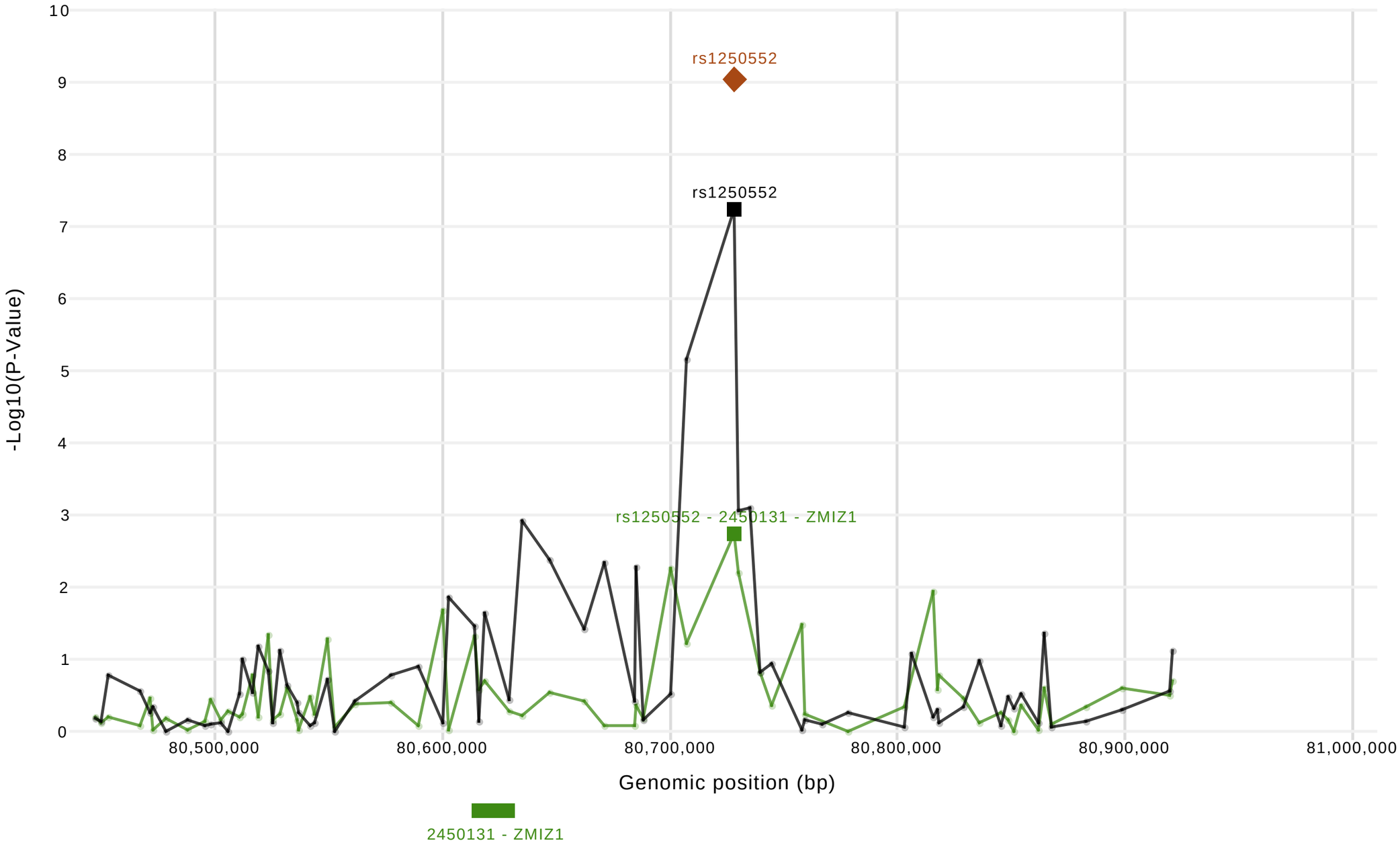

Chromosome 6
rs10806425
rs10806425
rs1394220 - 3520349 - BACH2
10
9
8
7
6
5
4
3
2
1
0
-Log10(P-Value)
90,700,000
90,800,000
90,900,000
91,000,000
91,100,000
91,200,000
91,300,000
Genomic position (bp)
3520349 - BACH2

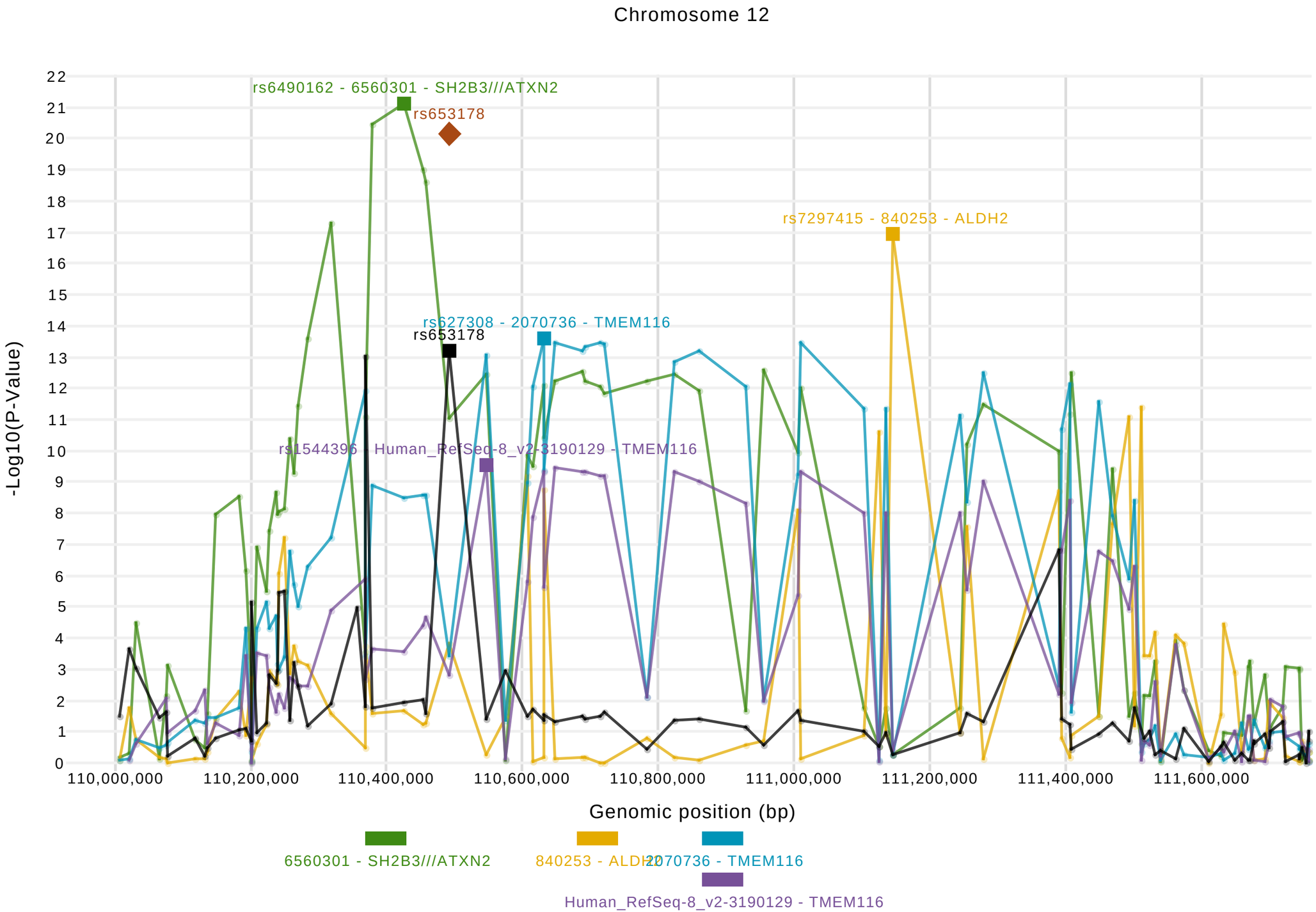
Chromosome 6



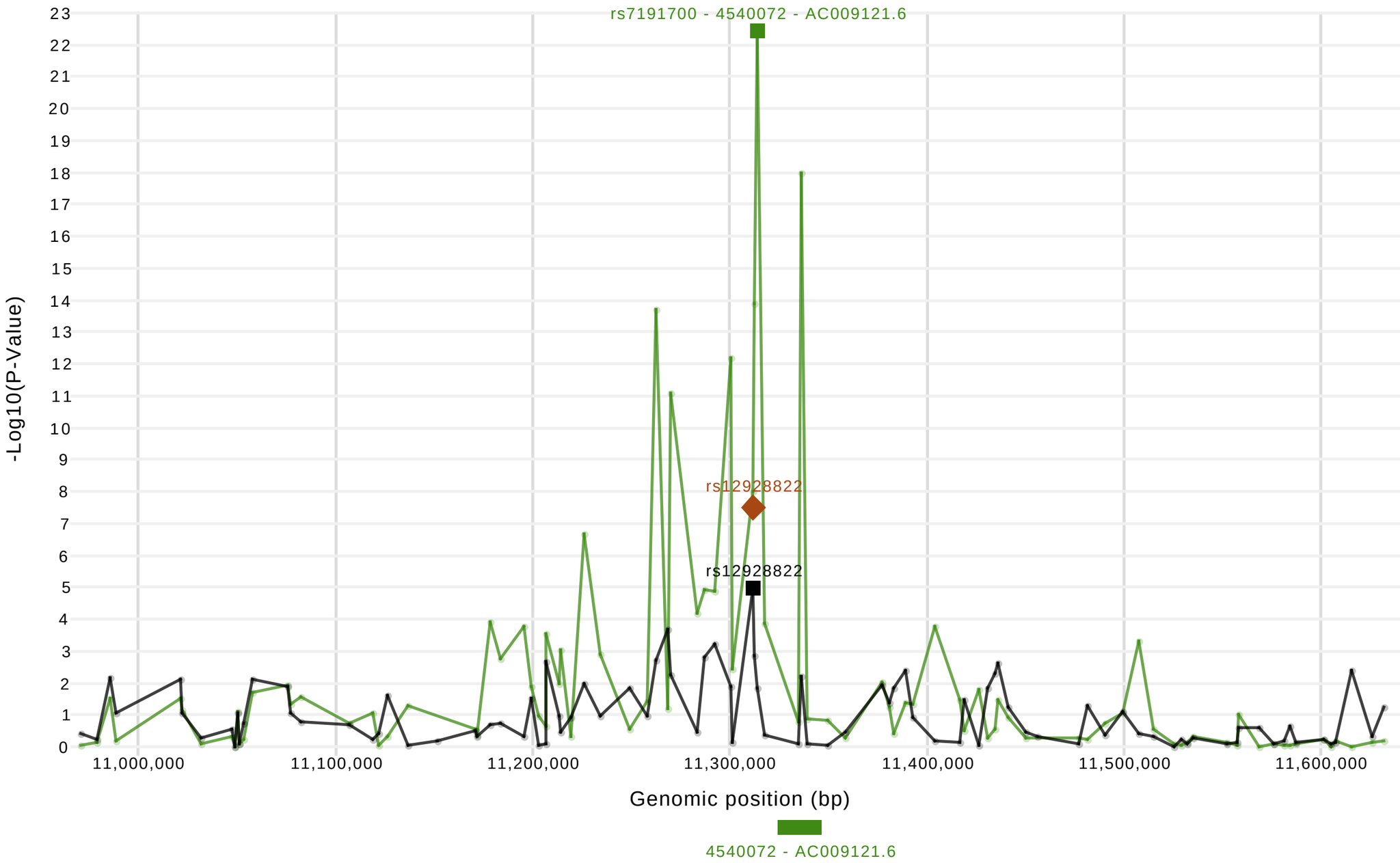

Chromosome 7
rs10260856 - 2750154 - ELMO1
rs6974491
rs6974491
-Log10(P-Value)
26
24
22
20
18
16
14
12
10
8
6
4
2
0
37,100,000
37,200,000
37,300,000
37,400,000
37,500,000
37,600,000
Genomic position (bp)
2750154 - ELMO1

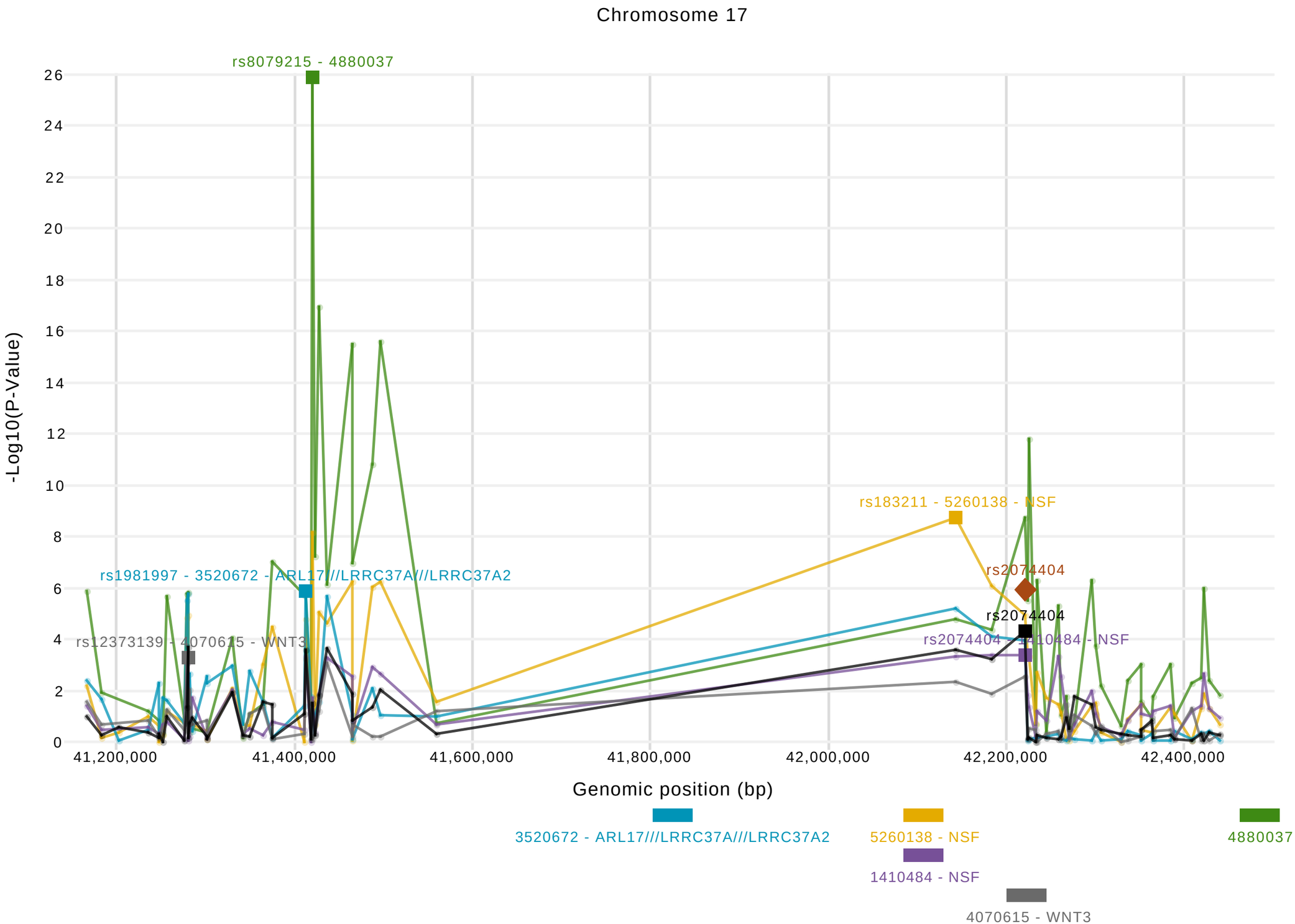
Chromosome 10

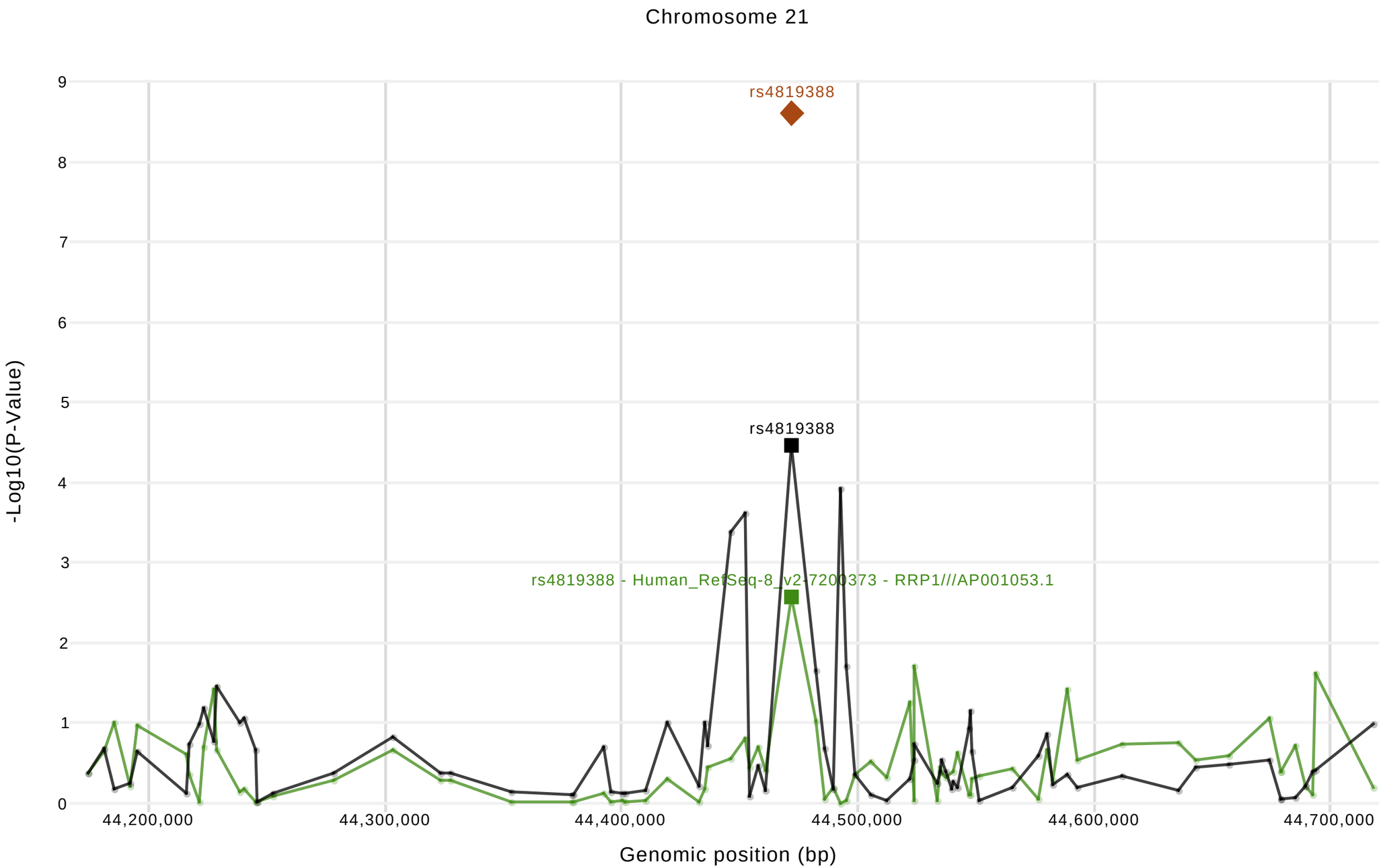



Chromosome 12
rs6490162 - 6560301 - SH2B3///ATXN2
rs653178
rs7297415 - 840253 - ALDH2
rs627308 - 2070736 - TMEM116
rs653178
rs11544396 - Human_RefSeq-8_v2-3190129 - TMEM116
-Log10(P-Value)
22
21
20
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
0
110,000,000
110,200,000
110,400,000
110,600,000
110,800,000
111,000,000
111,200,000
111,400,000
111,600,000
Genomic position (bp)
6560301 - SH2B3///ATXN2
840253 - ALDH2
2070736 - TMEM116
Human_RefSeq-8_v2-3190129 - TMEM116

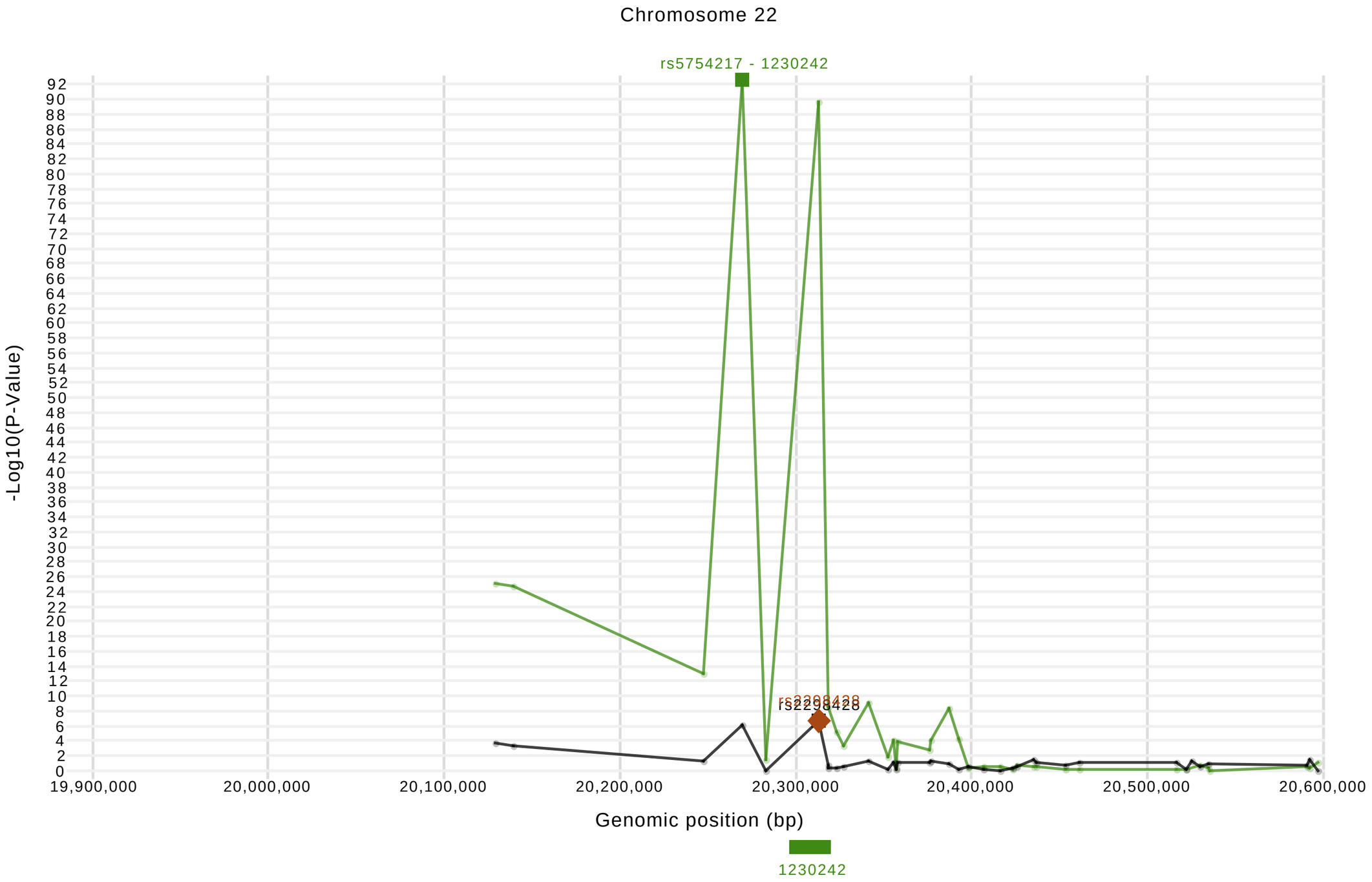
Chromosome 16

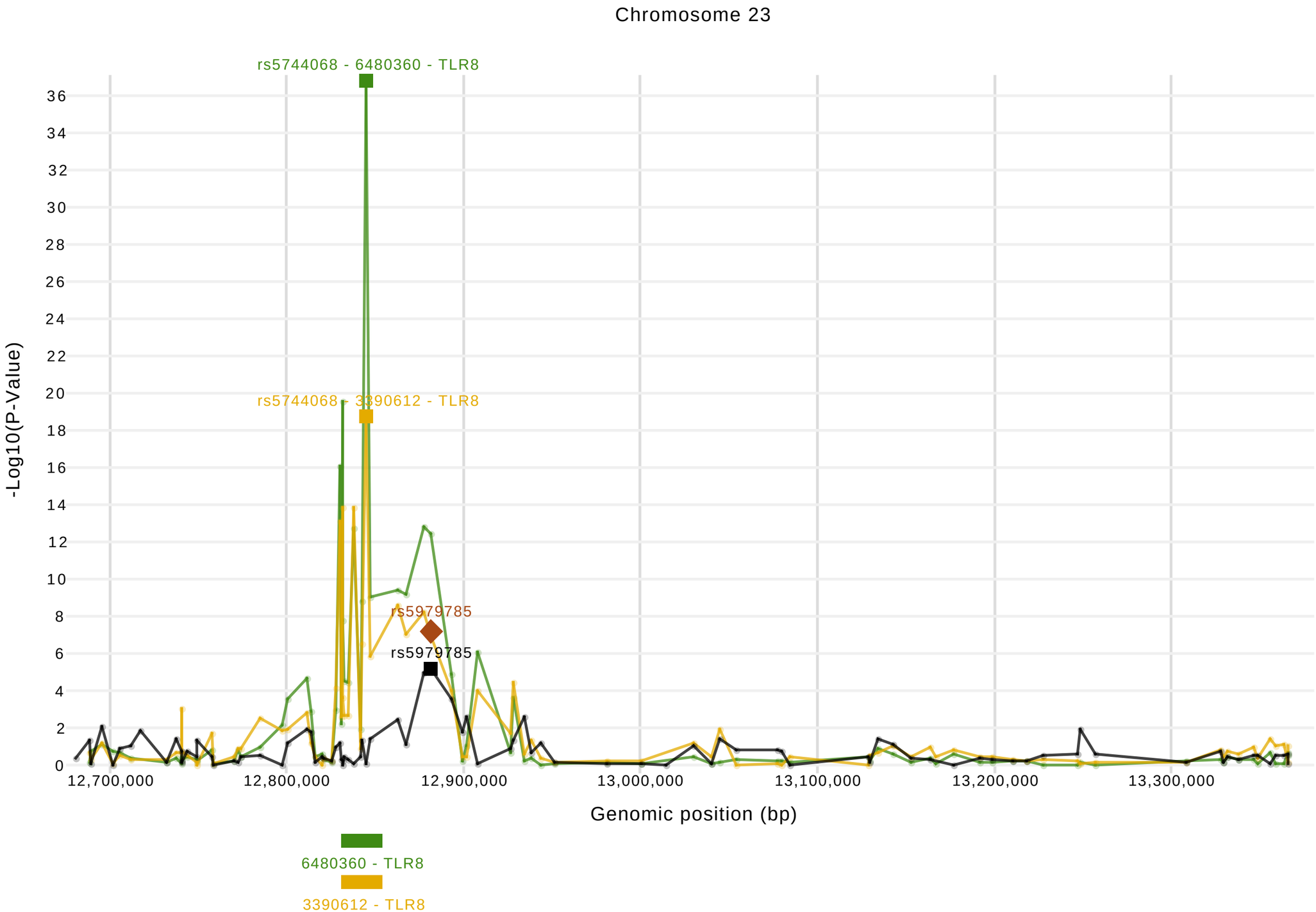



Chromosome 17
rs8079215 - 4880037
rs183211 - 5260138 - NSF
rs1981997 - 3520672 - ARL17///LRRC37A///LRRC37A2
rs2074404
rs2074404
rs12373139 - 4070615 - WNT3
rs2074404 - 1410484 - NSF
-Log10(P-Value)
26
24
22
20
18
16
14
12
10
8
6
4
2
0
41,200,000
41,400,000
41,600,000
41,800,000
42,000,000
42,200,000
42,400,000
Genomic position (bp)
3520672 - ARL17///LRRC37A///LRRC37A2
5260138 - NSF
4880037
1410484 - NSF
4070615 - WNT3



RP1///AP001053.1


Chromosome 22
rs5754217 - 1230242
-Log10(P-Value)
92
90
88
86
84
82
80
78
76
74
72
70
68
66
64
62
60
58
56
54
52
50
48
46
44
42
40
38
36
34
32
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
rs2298428
rs2298428
19,900,000
20,000,000
20,100,000
20,200,000
20,300,000
20,400,000
20,500,000
20,600,000
Genomic position (bp)
1230242


Chromosome 23
rs5744068 - 6480360 - TLR8
rs5744068 - 3390612 - TLR8
rs5979785
rs5979785
-Log10(P-Value)
36
34
32
30
28
26
24
22
20
18
16
14
12
10
8
6
4
2
0
12,700,000
12,800,000
12,900,000
13,000,000
13,100,000
13,200,000
13,300,000
Genomic position (bp)
6480360 - TLR8
3390612 - TLR8