

Genetics of circulating inflammatory proteins identifies drivers of immune-mediated disease risk and therapeutic targets

In the format provided by the
authors and unedited

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Supplementary Note 1: Cohort details

INTERVAL. The INTERVAL study¹ is a prospective cohort study of blood donors. Volunteers were recruited and consented between 2012 and 2014 from 25 NHSBT (National Health Service Blood and Transplant) static donor centres across England. The INTERVAL study was approved by the Cambridge (East) Research Ethics Committee. A subset of 4,896 participants from INTERVAL with Olink inflammation panel data contributed to the present study. 2,907 were male and 1,989 female. These participants had an age range between 49 and 78 years (median 61, IQR=55-66). A complete list of the investigators and contributors to the INTERVAL trial is provided in reference².

Stabilization of Atherosclerotic Plaque by Initiation of Darapladib Therapy Trial (STABILITY). STABILITY is a randomized, controlled trial conducted in 15,828 patients with chronic coronary heart disease (CHD) comparing darapladib or placebo, in addition to standard of care (<https://clinicaltrials.gov/ct2/show/NCT00799903>)³. Data from 2,951 individuals with Olink inflammation panel and genotyping data contributed to this pQTL study. All participants gave written informed consent to the biomarker and genetic sub-studies and the study was approved by the National Ethics Committees in the participating countries.

Biomarkers For Identifying Neurodegenerative Disorders Early and Reliably (BioFINDER). The BioFINDER study⁴ is run by the Clinical Memory Research Unit and The Biomedical center, at Lund University, Sweden. Participants were recruited from the Memory and Neurology clinics at Skåne University Hospital and the Memory Clinic at Ängelholm's Hospital. Study participants comprised 1,496 individuals with mild cognitive symptoms, dementia or parkinsonian symptoms, and cognitively healthy elderly. The Ethics Committee of Lund University approved this study. All study participants gave written consent for participation in the study, which was performed in accordance with the Helsinki Declaration.

Cooperative Health Research in the Region of Augsburg (KORA). KORA is a series of independent population-based studies from the general population living in the region of Augsburg, Southern Germany. The KORA F4 study was conducted from 2006-2008 as a follow-up study to KORA S4 (1999-2001)⁵. 1,064 participants from KORA F4 contributed data to this study.

Orkney Complex Disease Study (ORCADES). The ORCADES is a family-based study in the isolated Scottish archipelago of Orkney, part of the Viking Genes studies (ed.ac.uk/viking). A total of 981 individuals with Olink inflammation panel data contributed to this pQTL study. All participants gave written informed consent and the study was approved by Research Ethics Committees in Orkney, Aberdeen (North of Scotland REC), and South East Scotland REC, NHS Lothian (reference: 12/SS/0151).

Northern Sweden Population Health Study (NSPHS). NSPHS is a cross-sectional study conducted in the communities of Karesuando (samples gathered in 2006) and Soppero (2009) in the subarctic region of the County of Norrbotten, Sweden⁶. Ethical approval was given by the local ethics committee at the University of Uppsala (Regionala Etikprövningsnämnden, Uppsala, Dnr 2005:325) in compliance with the Declaration of Helsinki. All participants gave

their written informed consent to the study. A total of 866 individuals with Olink inflammation panel data contributed to the present study.

VIS. CROATIA-Vis is a family-based, cross-sectional study in the island of Vis, Croatia. 899 participants with Olink Inflammation panel and genotyping data contributed to this pQTL study. All participants gave written informed consent and the study was approved by Research Ethics Committees in Croatia (Institutional Ethics Committee of the University of Split School of Medicine [protocol code 2181-198-03-04/10-11-0008] and Scotland).

STANLEY (SWEBIC). The SWEBIC cohort comprises participants meeting the diagnostic criteria for Bipolar disorder as per the DSM-IV recruited at Swedish sites in affiliation with the Stanley Medical Research Institute. In total, SWEBIC contributed 644 samples (cohort A [swe6]: 300, cohort B [lahl]: 344) with Olink inflammation panel data to this pQTL study. Ethical approval for SWEBIC was granted by the Regional Ethical Review Board in Stockholm, Sweden (2008/2009-31/2).

Estonian Biobank (EstBB). The EstBB cohort is a volunteer-based sample of the Estonian resident adult population (aged ≥ 18 years)⁷. A total of 487 participants contributed to this study. Ethical approval was given by the Estonian Committee on Bioethics and Human Research (1.1-12/624) and by the Research Ethics Committee of the University of Tartu (application number 262/T-3, October 2016), data extraction nr K29.

RECOMBINE/EIRA. The RECOMBINE/EIRA biobank was generated from participants with active rheumatoid arthritis recruited between February 2011 and May 2013 at the Karolinska University Hospital, Stockholm, Sweden as part of the Epidemiologic Investigation of Rheumatoid Arthritis (EIRA) study⁸. The study was approved by the Ethical Review Board at Karolinska Institutet, Stockholm, Sweden (reference numbers 2007-0889-31, 2007-1443-32 and 2015/1844-31/2). All participants gave written informed consent. At the time of recruitment, all participants were undergoing treatment initiation or escalation. 540 patients with Olink inflammation panel data contributed to this pQTL study.

ARISTOTLE. The Apixaban for reduction in stroke and other Thromboembolic events in atrial fibrillation (ARISTOTLE) trial was designed to investigate the safety and efficacy of the Factor Xa (FXa) inhibitor apixaban for secondary prevention of stroke in atrial fibrillation patients. Full details of the ARISTOTLE cohort are available at^{9,10}. In total, ARISTOTLE contributed 1,585 samples with Olink inflammation panel data for comparison with the pQTL discovery meta-analysis findings. All participants gave written informed consent to the biomarker and genetic sub-studies and the study was approved by the National Ethics Committees in the participating countries.

Supplementary Note 2: Comparison with pQTL study of Ferkingstad *et al.*

In addition to testing the pQTLs from our discovery meta-analysis for replication in the ARISTOTLE study, we also compared our results to those from the study by Ferkingstad *et al.*¹¹ from the deCODE group, hereafter referred to as the “deCODE study”. The deCODE study performed pQTL mapping in approximately 35,000 individuals from Iceland, with 4,907 proteins measured using the aptamer-based SomaScan V4 platform (whereas we used the

Olink Inflammation platform in our study).

72 of the 91 proteins in our study were measured in the deCODE study. Of the 180 significant locus-protein associations from our study, 158 were testable for replication in the deCODE summary statistics. Of these 158 variants, 75 were significant at $P < 5 \times 10^{-10}$, 78 at $P < 5 \times 10^{-8}$, and 96 at a more liberal P -value threshold of 2.8×10^{-4} (a Bonferroni-correction for the 180 pQTLs eligible for replication testing; P -values from linear regression). The numbers of pQTLs replicating in ARISTOTLE and in deCODE at varying P -value thresholds are shown in **Supplementary Note Table 1**. Overall, we replicated 126 (71%) of the 178 testable pQTLs in either ARISTOTLE or deCODE at $P < 2.8 \times 10^{-4}$.

Supplementary Note Table 1. The numbers of pQTLs replicating in ARISTOTLE and in deCODE at varying P -value thresholds (P -values from linear regression).

P-value threshold	No. pQTLs replicated in ARISTOTLE	No. pQTLs replicated in deCODE	No. pQTLs replicated in either ARISTOTLE or deCODE
5.0×10^{-10}	32	75	87
5.0×10^{-8}	39	78	92
2.78×10^{-4}	72	96	126
Number of testable pQTLs	174	158	178

Of note, 7 pQTLs replicated in ARISTOTLE with $P < 5 \times 10^{-8}$ and yet did not replicate in the deCODE study despite the larger sample size of the latter (**Supplementary Note Table 2**). 4 of these 7 were *cis*-pQTLs. Of the three *trans*-pQTLs, two have been reported in previous studies that use single protein ELISAs; i) the association of rs385076 with IL-18 levels was reported by Johansson *et al*¹², and ii) rs2228145, a variant in *IL6R* (the gene encoding the interleukin-6 receptor), is well known to affect soluble IL6 levels^{13,14}.

The lack of signal in the deCODE data (generated using the Somascan platform), despite convincing evidence of a pQTL in these instances (in both Olink and ELISA-based studies), may reflect platform effects. Consistent with this, rs2228145 was not significantly associated with plasma IL6 levels in the study of Sun *et al*¹⁵, which used an earlier version of the SomaScan platform. There are a number of possible explanations for the absence of detecting a pQTL using the SomaScan: i) the specific aptamer may lack sensitivity; ii) aptamers do not always measure their canonical target protein, and instead may target a cleavage product or the protein bound in complex to another protein; iii) aptamers are more vulnerable to off-target binding than the Olink platform used in our study. This is because the Olink platform uses a pair of antibodies, each with a complementary oligonucleotide tag, for each protein target. If,

and only if, both antibodies bind then the oligonucleotides hybridise and a qPCR read-out is generated.

Supplementary Note Table 2. Details of pQTLs which replicated at $P < 5 \times 10^{-8}$ in ARISTOTLE (n=1,585, Olink proteomics) but not in deCODE (n=35,556, SomaScan proteomics). *P*-values from linear regression.

Protein	rsID	P-value in ARISTOTLE	P-value in deCODE	<i>Cis</i> or <i>trans</i>
LTA	rs2229092	5.8×10^{-81}	0.56	<i>cis</i>
CCL3	rs8951	2.4×10^{-25}	0.0087	<i>cis</i>
GDNF	rs62360376	1.6×10^{-13}	0.48	<i>cis</i>
CCL13	rs3136676	3.1×10^{-10}	0.15	<i>cis</i>
IL18	rs385076	5.1×10^{-17}	0.42	<i>trans</i>
TNFSF10	rs28929474	1.6×10^{-9}	0.78	<i>trans</i>
IL6	rs2228145	3.0×10^{-8}	0.0022	<i>trans</i>

Supplementary Note 3: Additional information on potential mechanisms underpinning *cis*-pQTLs

Supplementary Note Table 3 provides information on whether the sentinel *cis*-pQTL variant was a protein-altering variant (PAV), or whether it was in high LD ($r^2 \geq 0.8$) with a PAV, and whether there was a colocalising eQTL in at least one tissue or cell type.

Of the 11 *cis*-pQTLs with sentinel variants that are PAVs, only 2 had a corresponding colocalising (PP H4 > 0.8) *cis*-eQTL. These were pQTLs for IL15RA and PLAUI. The remaining 9 did not (*cis*-pQTLs for ADA, CCL8, CCL25, CXCL10, HGF, LTA, MMP10, SIRT2, TGFB1).

For a further 10 *cis*-pQTLs, the sentinel variants were not themselves PAVs but were in high LD ($r^2 \geq 0.8$) with a PAV. However, 3 of these PAVs were not in the gene encoding the target protein but were instead in another nearby gene, and thus protein-altering effects could not account for the pQTL. Of the remaining 7 *cis*-pQTLs, 4 have a colocalising corresponding *cis*-eQTL (CD6, CCL11, CST5, CXCL5), whereas 3 do not (TNFSF14, CCL4, CASP8).

There were 27 *cis*-pQTLs without a corresponding colocalising *cis*-eQTL. 12 of the 27 *cis*-pQTLs without a colocalising eQTL are potentially explaining by PAVs, leaving 15 unexplained

by current available eQTL data.

Supplementary Note Table 3. Annotation of *cis*-pQTLs. The target protein is denoted by the non-italicised gene symbol of the encoding gene. PAV = protein-altering variant. LD = linkage disequilibrium. PP H4 = posterior probability of hypothesis 4 from coloc.

Sentinel pQTL variant	Target protein	Sentinel pQTL is a PAV	Sentinel pQTL is in high LD ($r^2 \geq 0.8$) with a PAV	Colocalising eQTL in at least 1 tissue (PP H4 ≥ 0.8)
rs11555566	ADA	Yes	N/A	No
rs6328	NGF	No	No	Yes
rs56328050	CASP8	No	Yes	No
rs79722574	CCL11	No	Yes	Yes
rs11574915	CCL19	No	Yes but in a different gene to that encoding target protein (<i>FAM205A</i>)	No
rs10207134	CCL20	No	No	Yes
rs712048	CCL23	No	No	No
rs2032887	CCL25	Yes	N/A	No
rs8064426	CCL4	No	Yes	No
rs11265493	CD244	No	No	Yes
rs1883832	CD40	No	No	Yes
rs674379	CD5	No	No	Yes
rs2074227	CD6	No	Yes	Yes
rs2276862	CDCP1	No	No	Yes
rs17610659	CSF1	No	No	Yes
rs4815244	CST5	No	Yes	Yes
rs671623	CX3CL1	No	No	Yes
rs1366949	CXCL1	No	No	Yes
rs11548618	CXCL10	Yes	N/A	No
rs6827617	CXCL11	No	Yes but in a different gene to that encoding target protein	No

			(SDAD1)	
rs450373	CXCL5	No	Yes	Yes
rs16850073	CXCL6	No	No	Yes
rs4241577	CXCL9	No	Yes but in a different gene to that encoding target protein (NAA)	Yes
rs62193248	DNER	No	No	Yes
rs3014874	S100A12	No	No	Yes
rs838131	FGF21	No	No	No
rs12509595	FGF5	No	No	Yes
rs62360376	GDNF	No	No	No
rs5745687	HGF	Yes	N/A	No
rs12123181	IL10	No	No	No
rs2266590	IL10RB	No	No	Yes
rs10076557	IL12B	No	No	No
rs2228059	IL15RA	Yes	No	Yes
rs17700884	IL17C	No	No	No
rs5744249	IL18	No	No	Yes
rs2270297	IL18R1	No	No	Yes
rs112359206	IL7	No	No	Yes
rs6446951	IL8	No	No	No
rs1800472	TGFB1	Yes	N/A	No
rs1133763	CCL8	Yes	N/A	No
rs7213460	CCL7	No	No	No
rs3136676	CCL13	No	No	No
rs8951	CCL3	No	No	Yes
rs471994	MMP1	No	No	Yes
rs17860955	MMP10	Yes	N/A	No
rs2247769	TNFRSF11B	No	No	No
rs822335	CD274	No	No	Yes

rs144373891	SIRT2	Yes	N/A	No
rs60094514	SLAMF1	No	No	No
rs149278	SULT1A1	No	No	Yes
rs72912115	TGFA	No	No	Yes
rs2229092	LTA	Yes	N/A	No
rs1776354	TNFRSF9	No	No	Yes
rs344562	TNFSF14	No	Yes	No
rs574044675	TNFSF10	No	No	No
rs4512994	TNFSF11	No	No	Yes
rs34790908	TNFSF12	No	No	Yes
rs55744193	PLAU	Yes	No	Yes
rs6921438	VEGFA	No	No	No

Supplementary Note 4: Protein-protein network analysis for TNFSF10

Plasma levels of TNFSF10 were associated with 7 genetic loci. To help identify the mediating genes at each of these loci, we constructed a protein-protein interaction network based on the candidate mediating genes at each loci and TNFSF10 itself using STRINGdb. We observed a cluster of eight interacting proteins (**Extended Data Figure 7a**), representing proteins encoded by 5 of the 7 loci with pQTLs for TNFSF10. The genes encoding these proteins highlight the plasminogen-activating system as a common feature. The relation of the trans-pQTLs for TNFSF10 and these are as follows: (i) rs4760 is a missense variant in *PLAUR*, which encodes the plasminogen-activator urokinase receptor; (ii) rs5030044 is intronic in *KNG1*, encoding kininogen 1 which is involved in bradykinin formation, which is regulated by plasmin; (iii) rs28929474 is a missense variant in *SERPINA1*, which encodes alpha1-antitrypsin, an anti-protease which can bind plasmin; (iv) rs8178824 is intronic to *APOH*, which encodes a cofactor for plasminogen activation^{16,17}; and (v) rs654488 is upstream of *MEP1B*, encoding meprin A, which is activated by the plasmin¹⁸. Together, these findings highlight the most likely mediating genes at 5 of the 7 regulatory loci and links TNFSF10 to the plasminogen-activating system.

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Supplementary Figure Titles

Supplementary Figure 1. Manhattan plots for the 91 proteins.

Supplementary Figure 2. Forest plots and regional association plots for the 180 pQTLs.

Supplementary Figure 3. Regional association plots comparing plasma *cis*-pQTLs and blood *cis*-eQTLs for the gene encoding the corresponding protein.

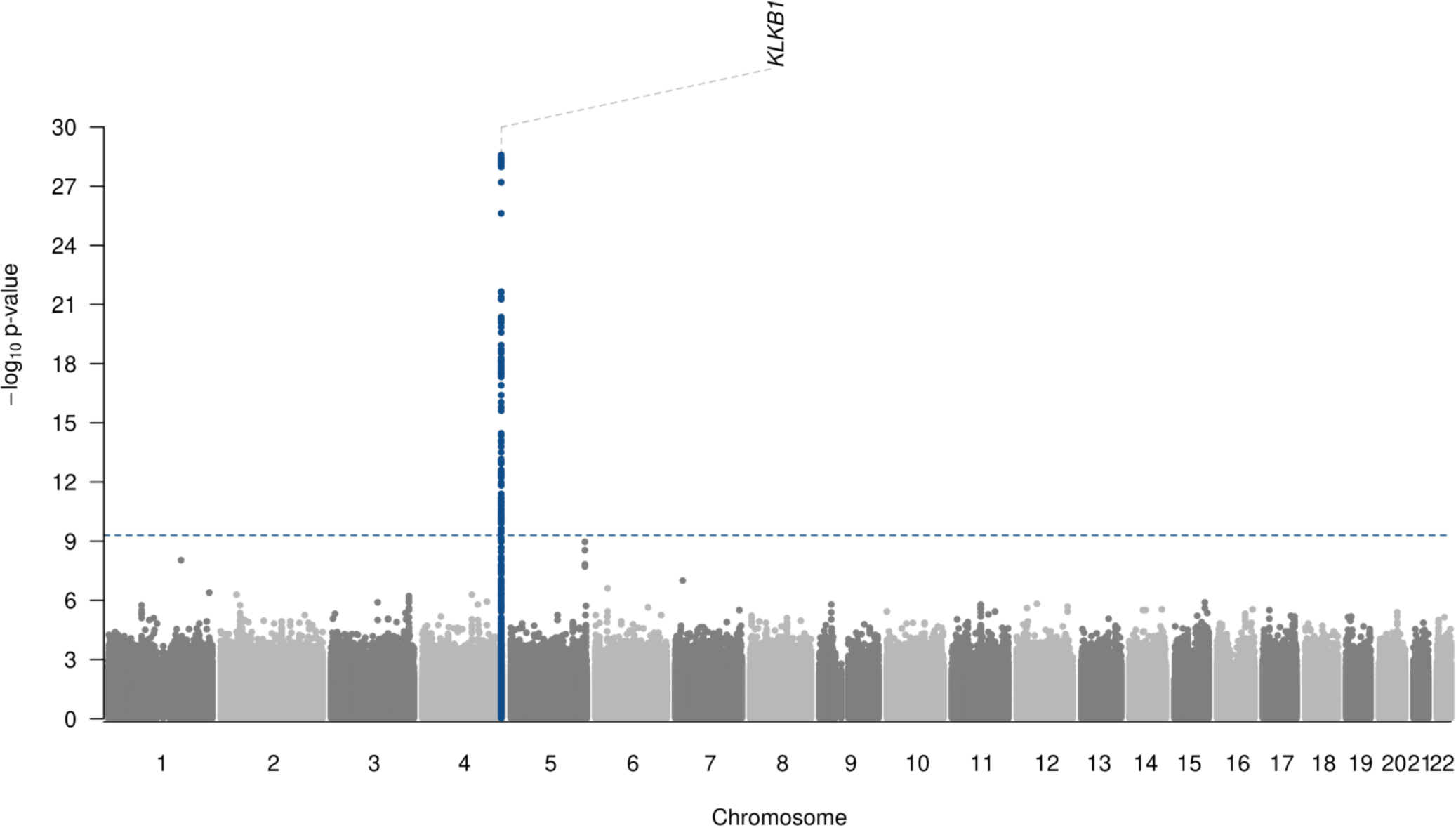
Supplementary Figure 4. Regional association plots comparing plasma *cis*-pQTLs and disease associations.

Supplementary Item. 3-dimensional interactive genomic map of pQTLs.

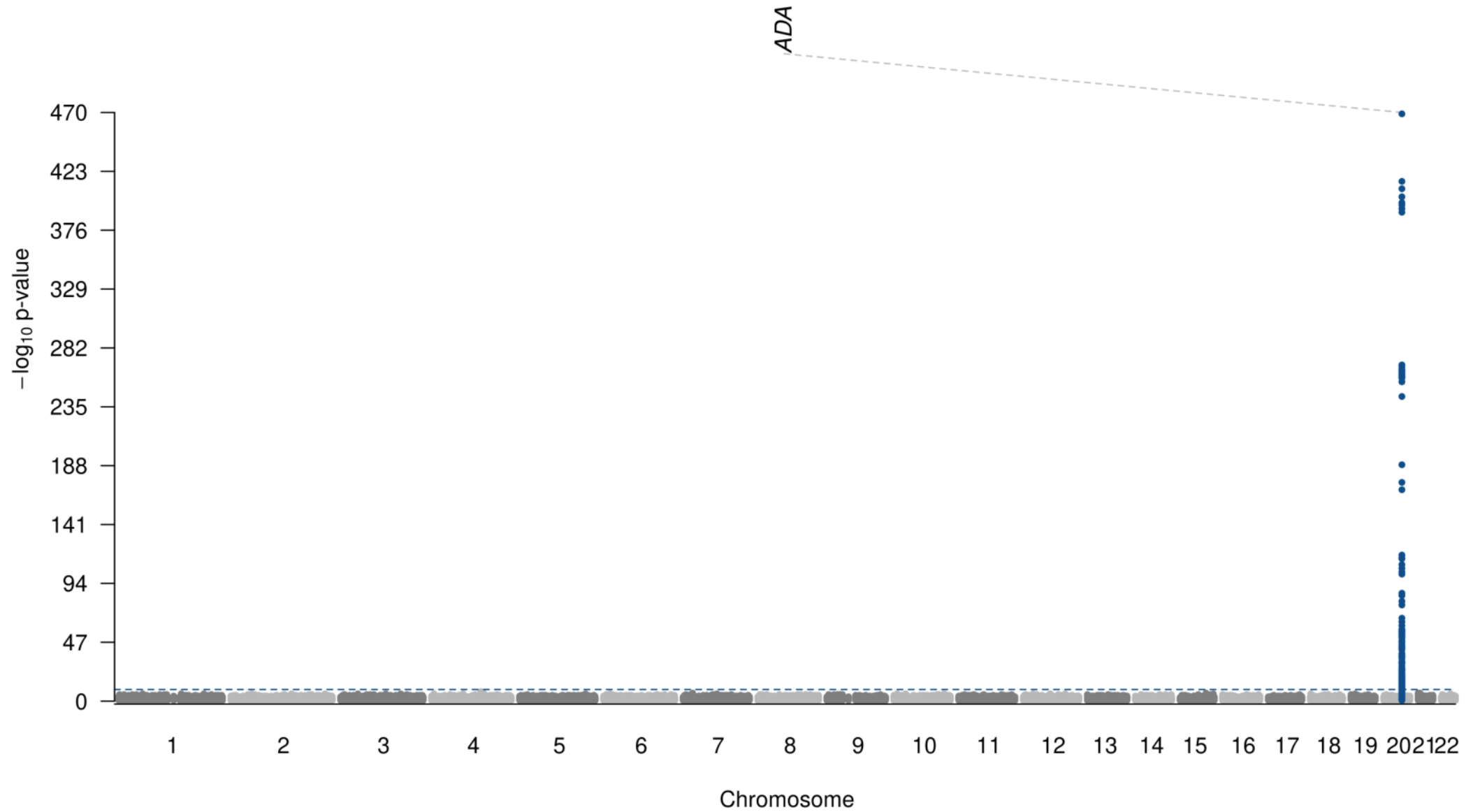
The html file (supplied separately) shows pQTL sentinel variant position in relation to the gene encoding the target protein and the strength of the statistical association (two-sided *P*-values are from meta-analysis of linear regression estimates). Hover over a point to see detailed information. The image can be rotated by holding at left clicking the mouse.

Supplementary Figure 1. Manhattan plots for the 91 proteins. Proteins are labelled with both the label provided by Olink, and with the encoding gene symbol in parentheses. Two-sided P -values are from meta-analysis of linear regression estimates. Horizontal dash blue line = $P=5 \times 10^{-10}$ (genome-wide significance after Bonferroni-correction for testing multiple proteins).

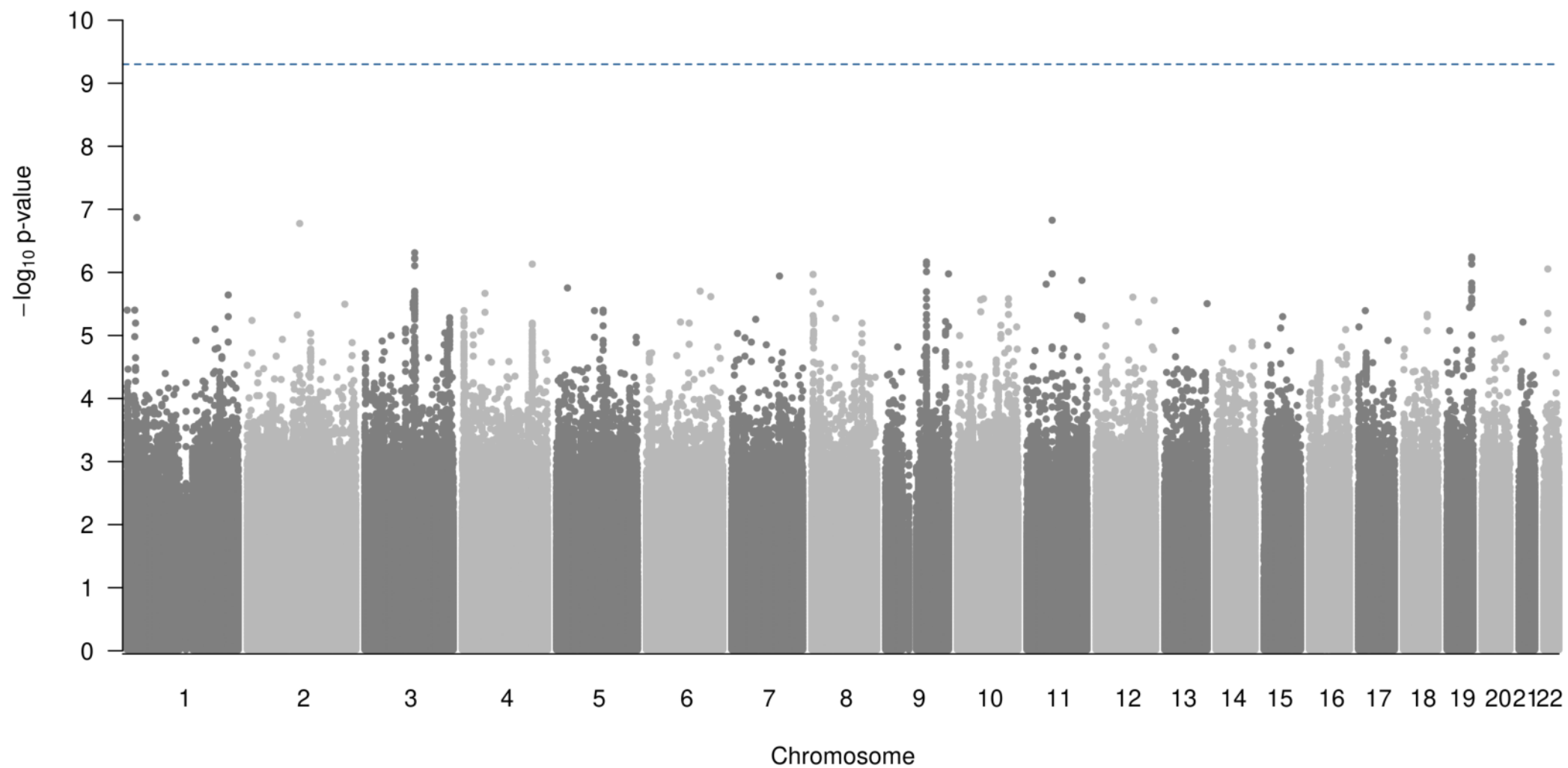
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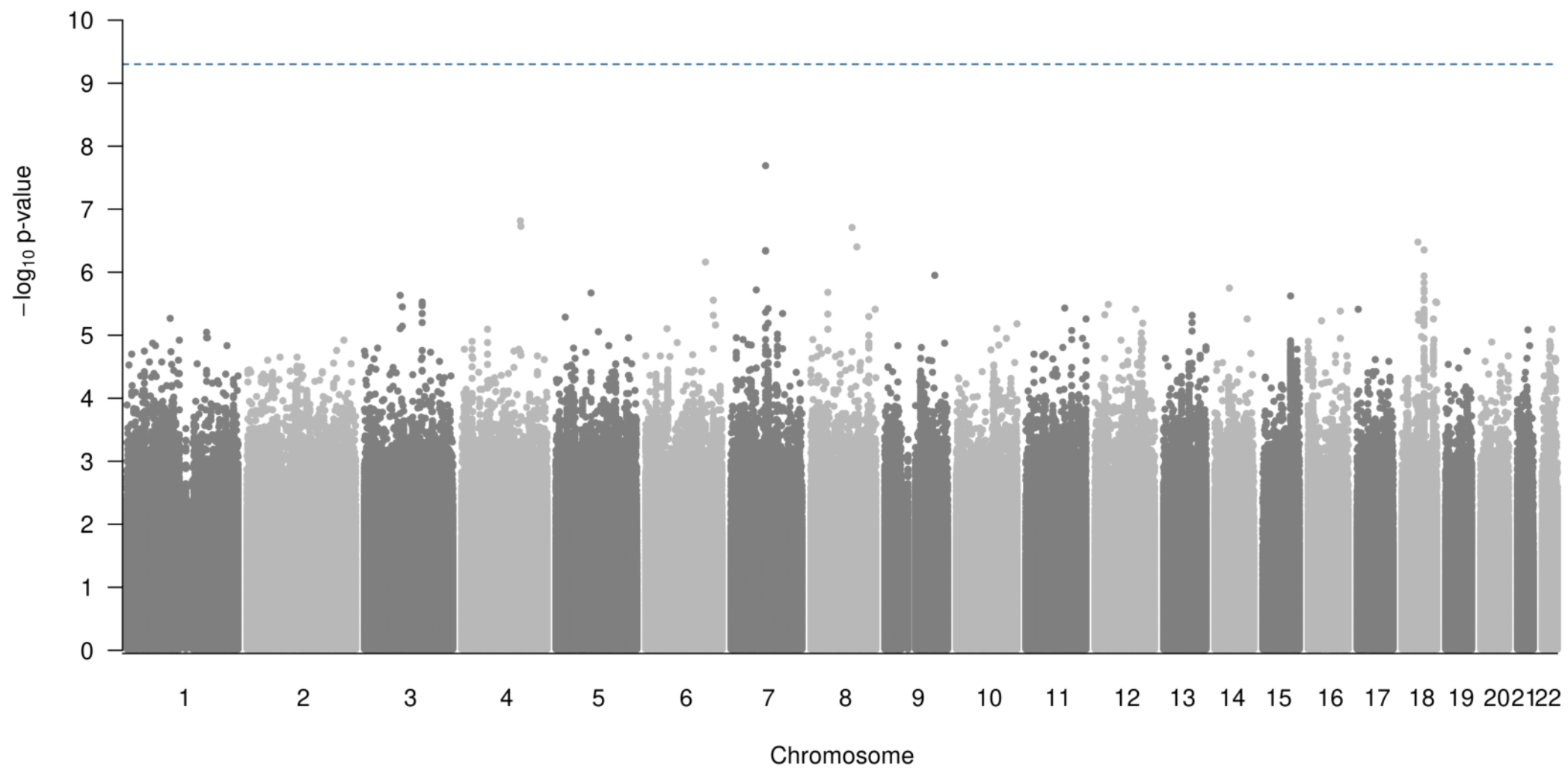
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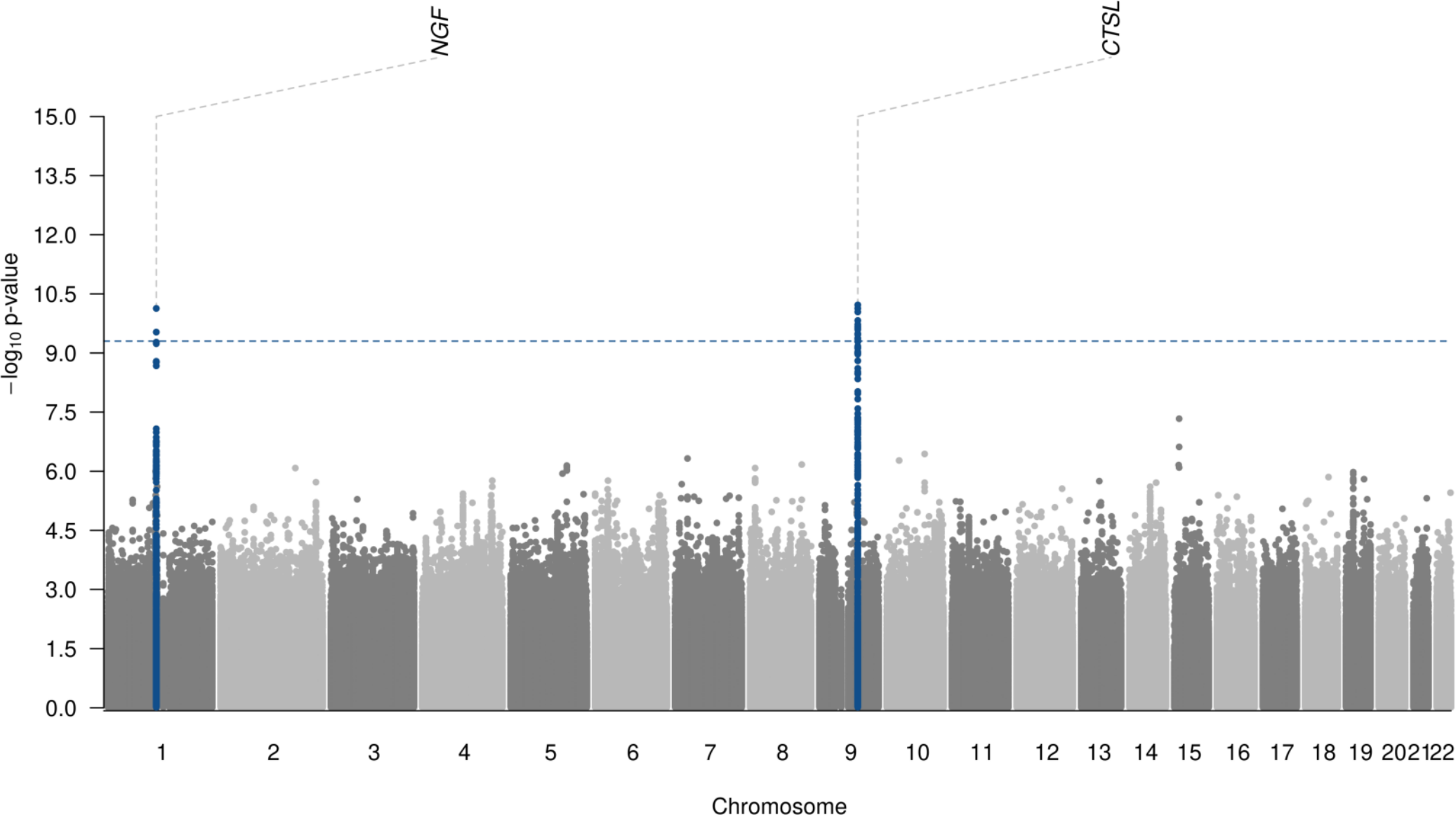
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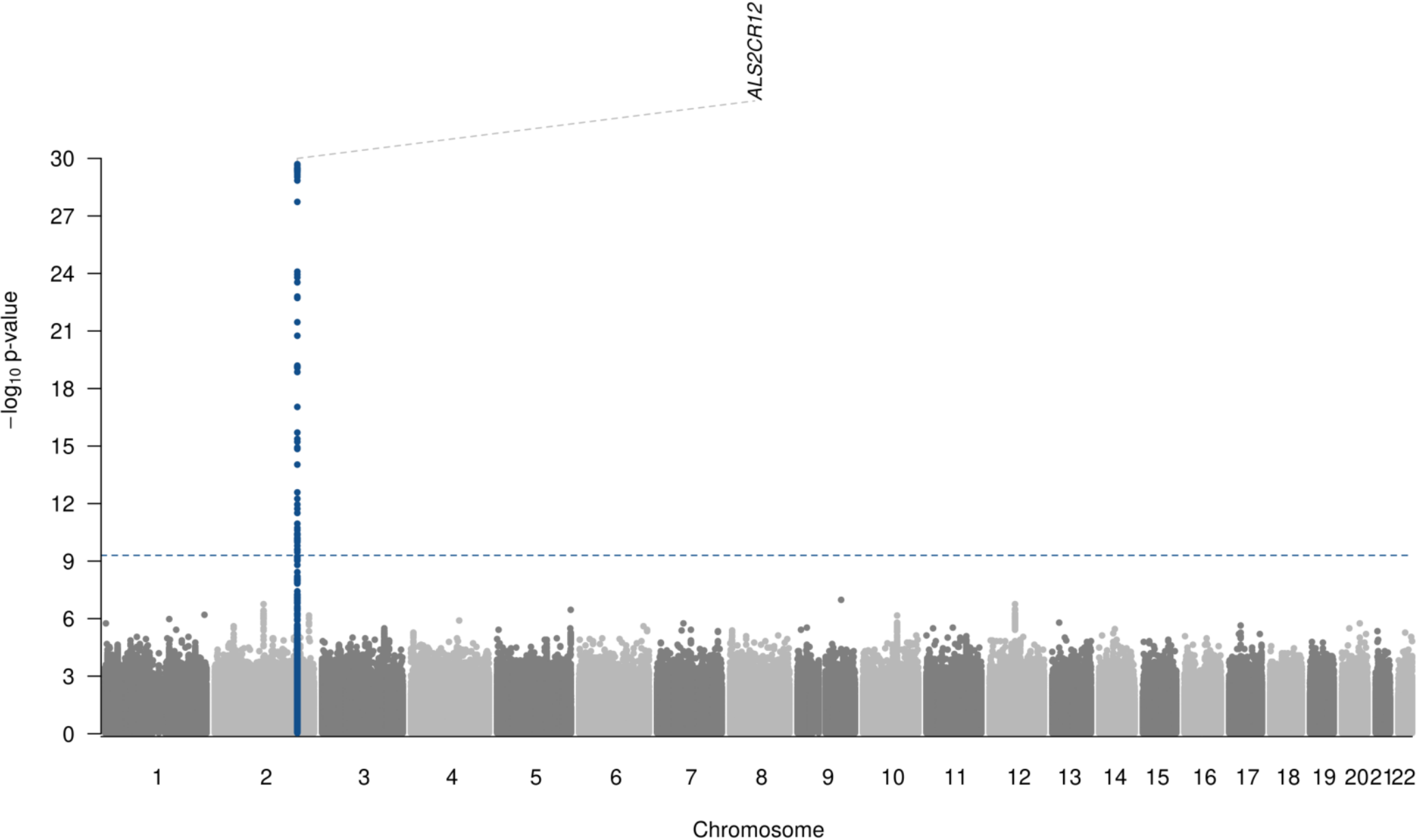
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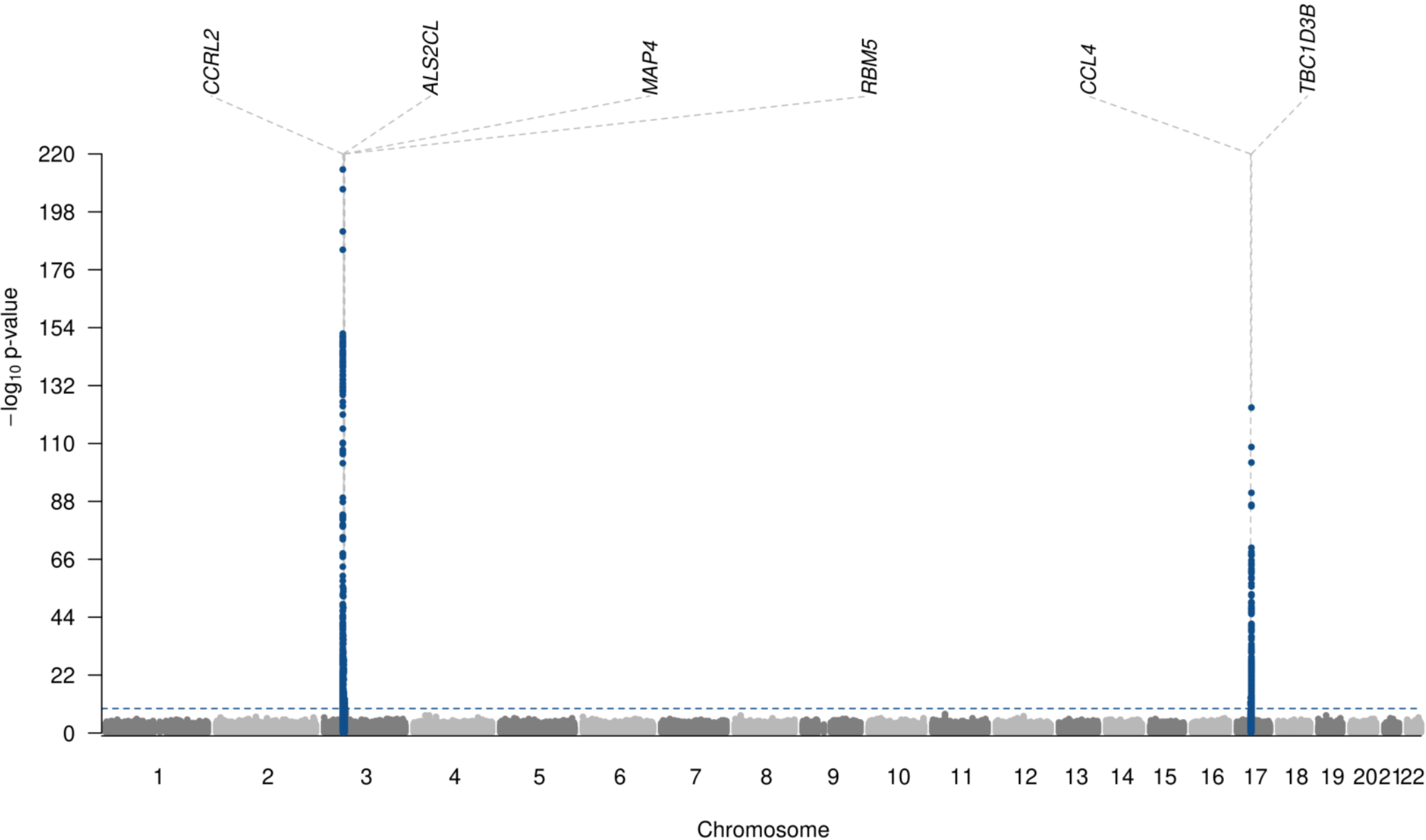
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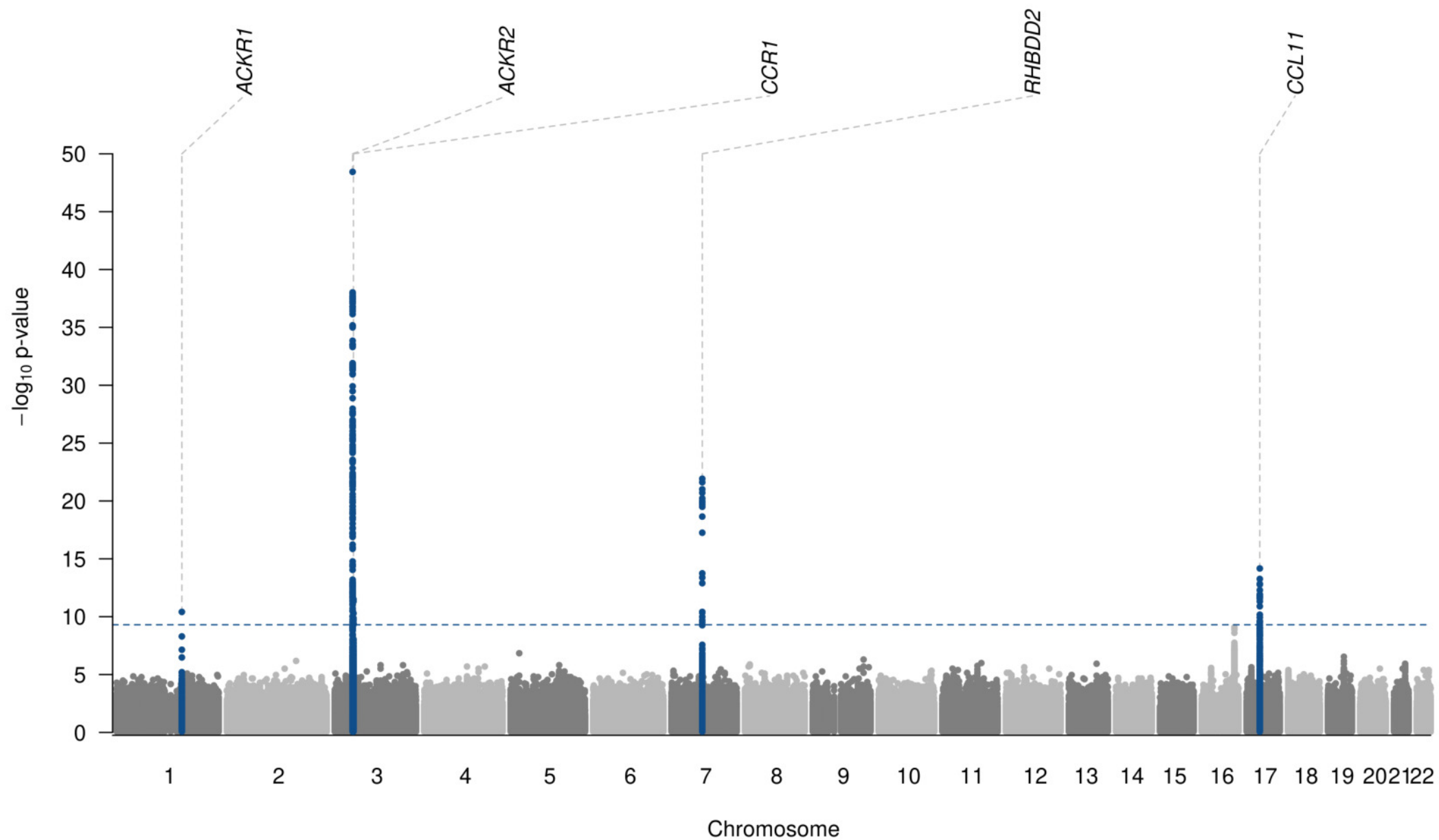
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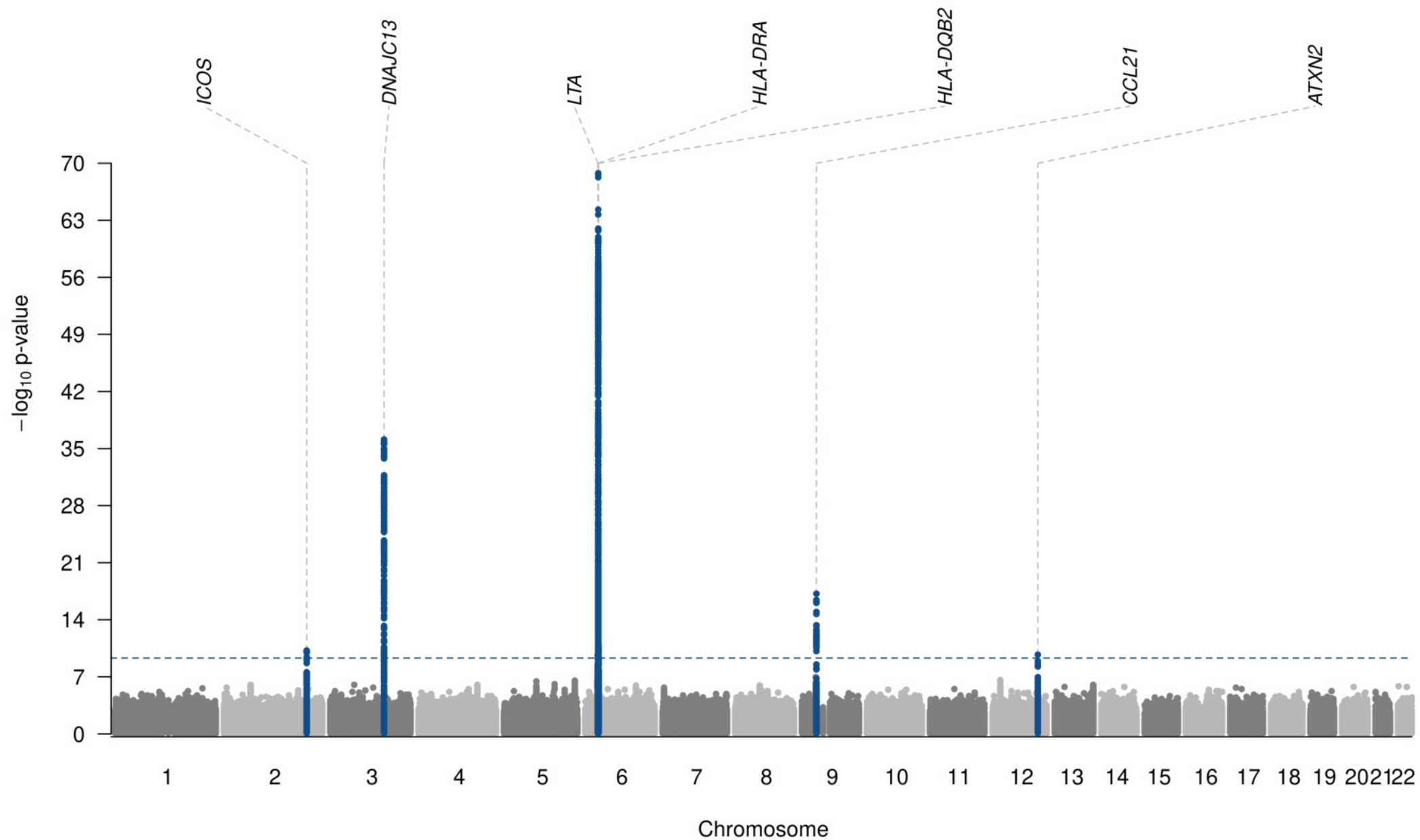
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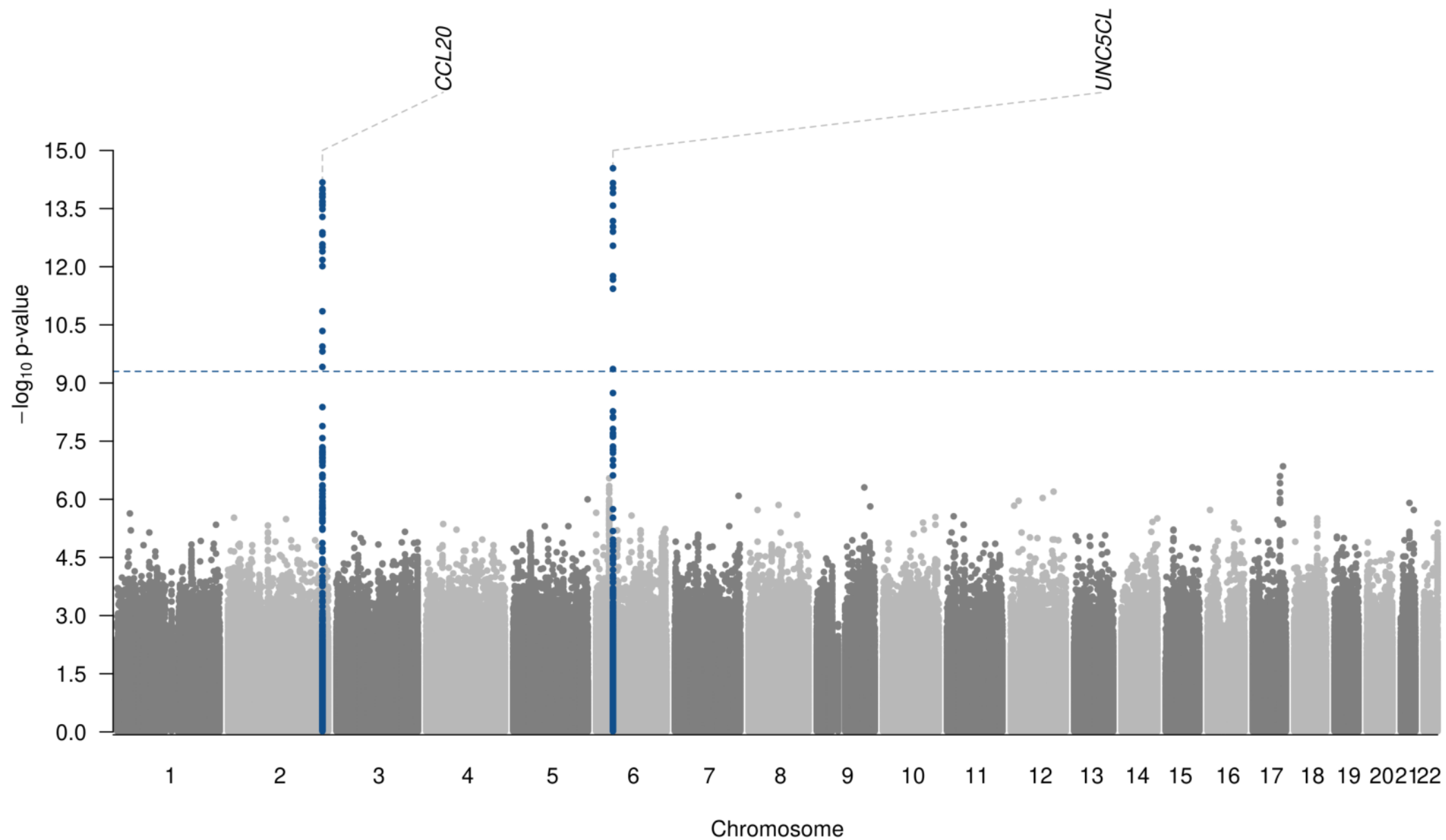
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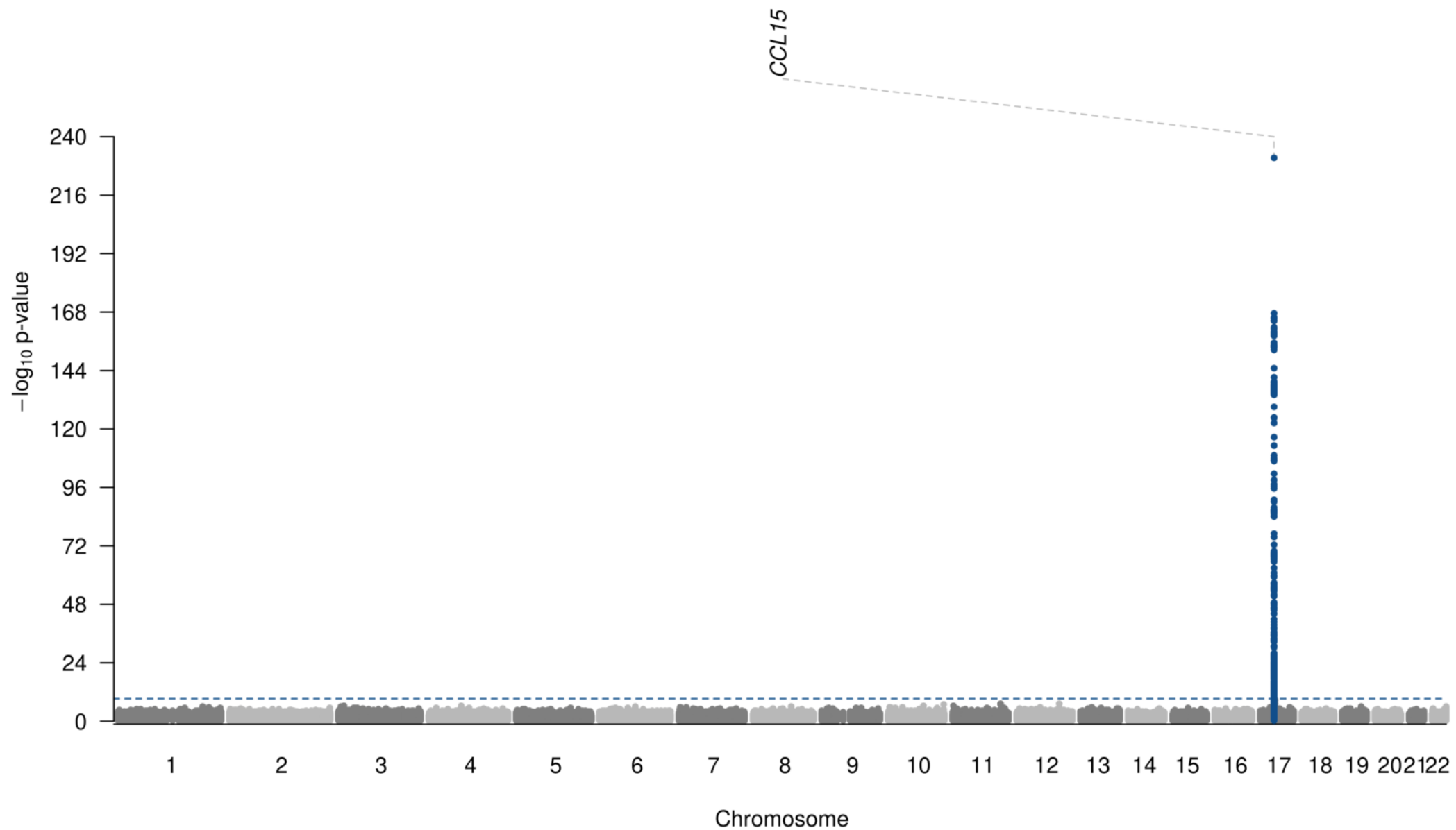
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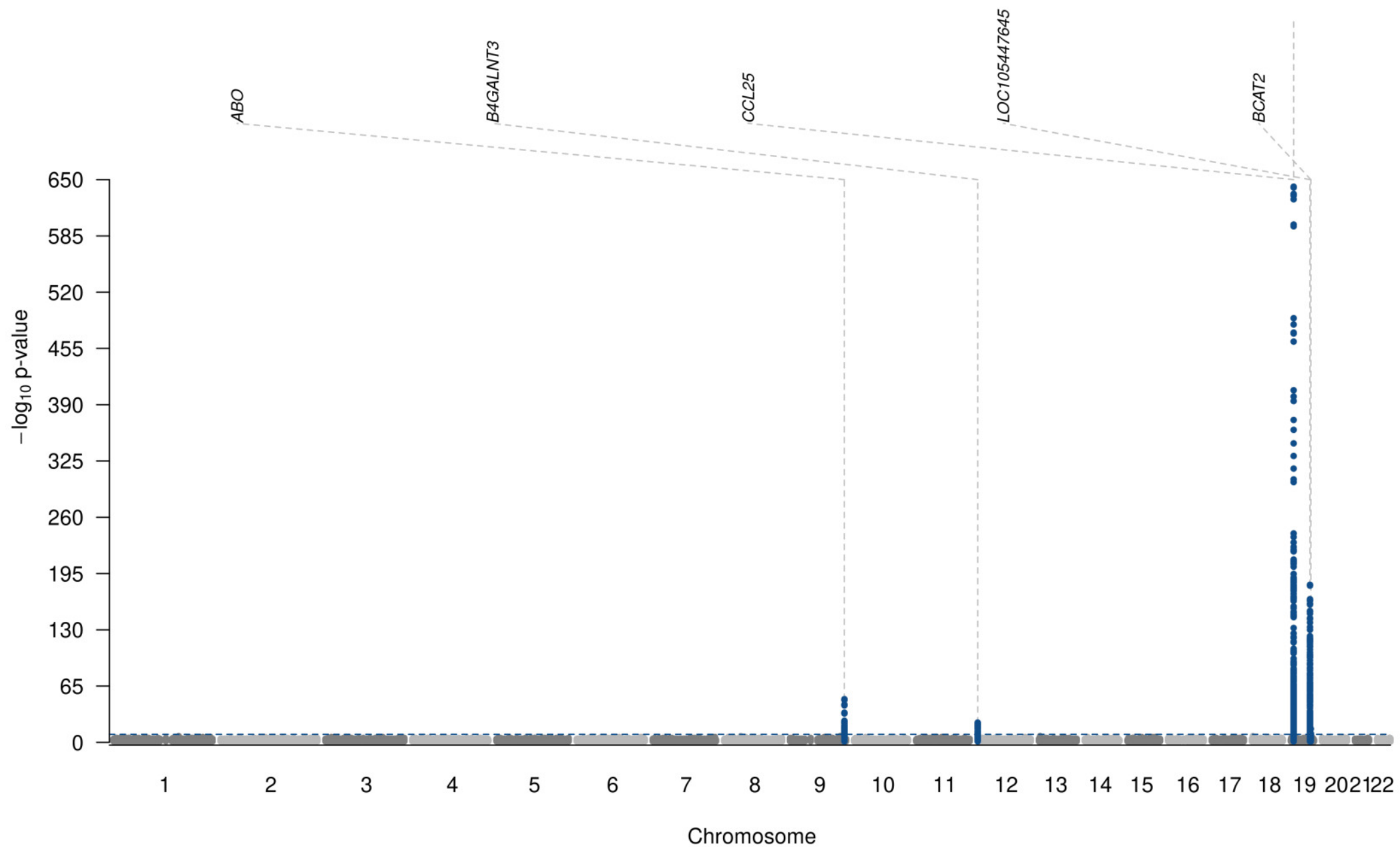
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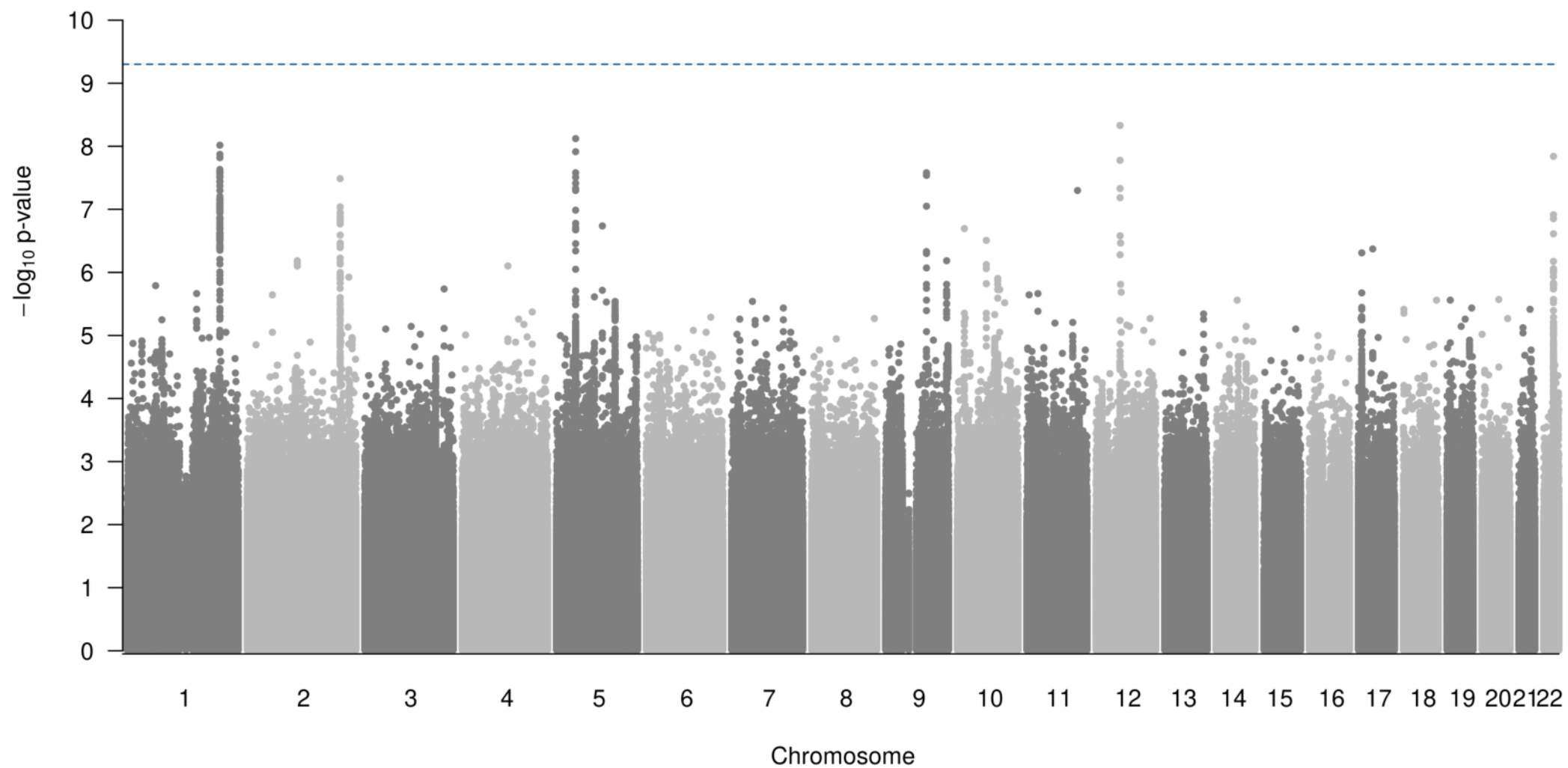
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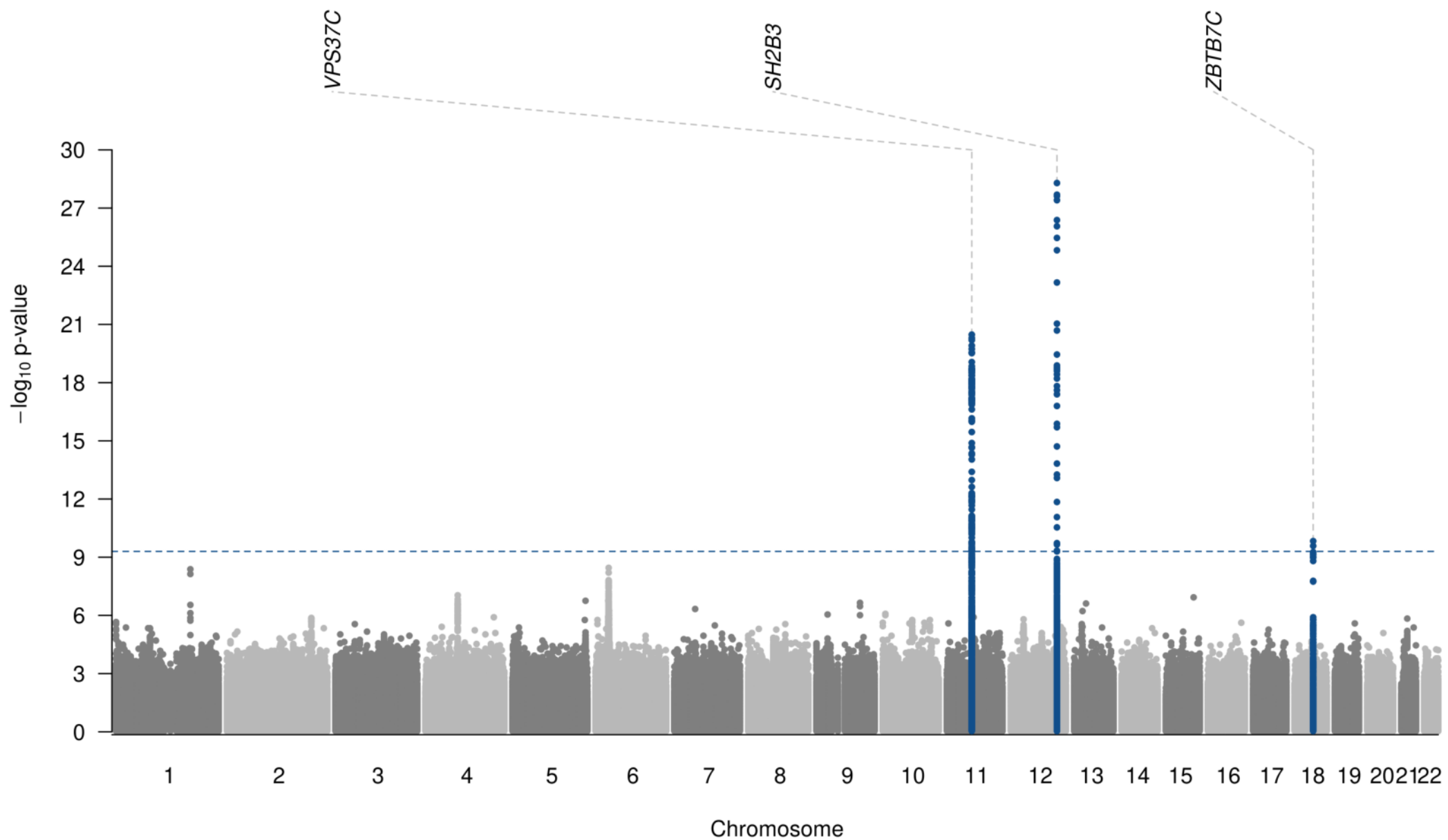
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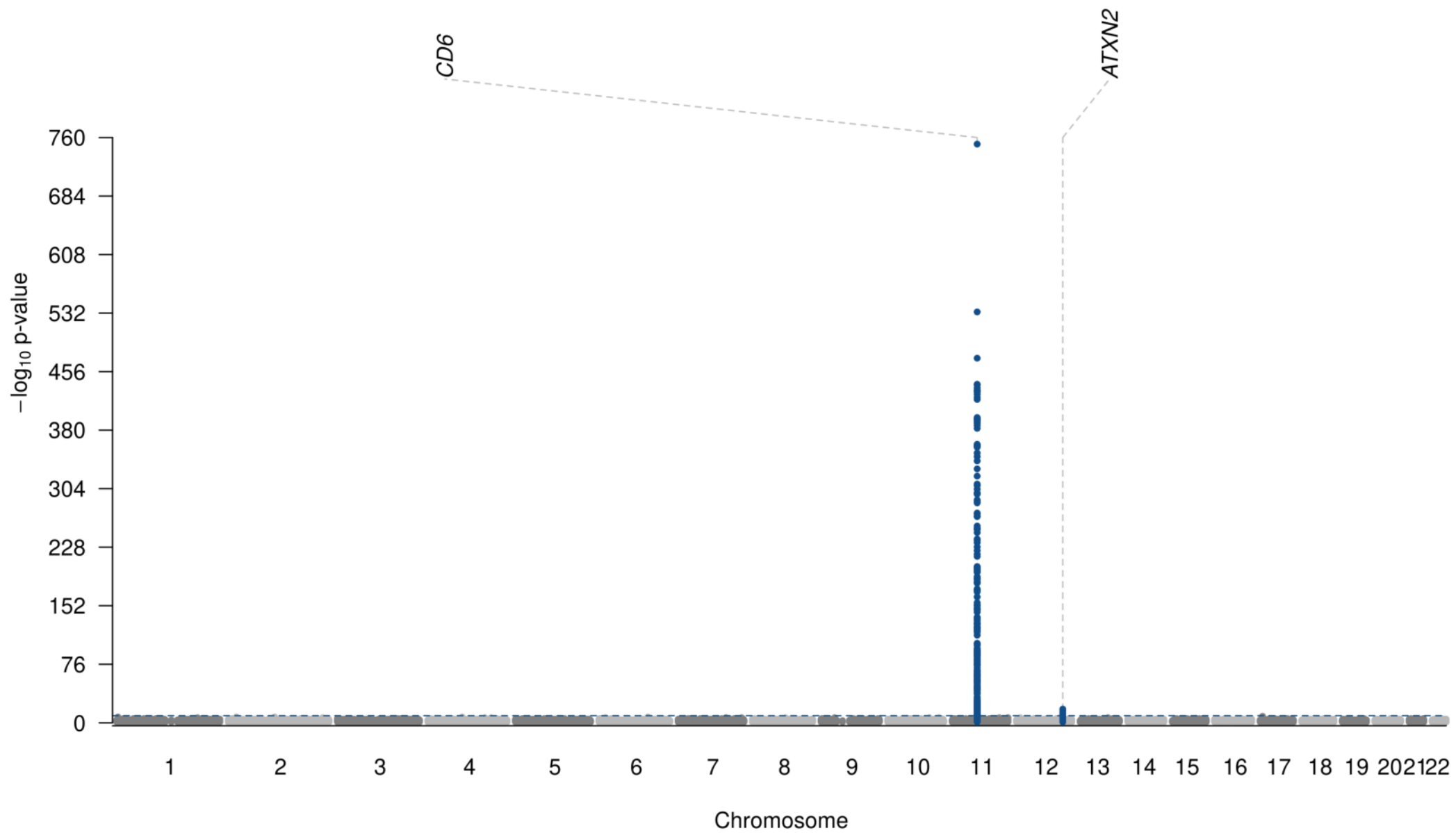
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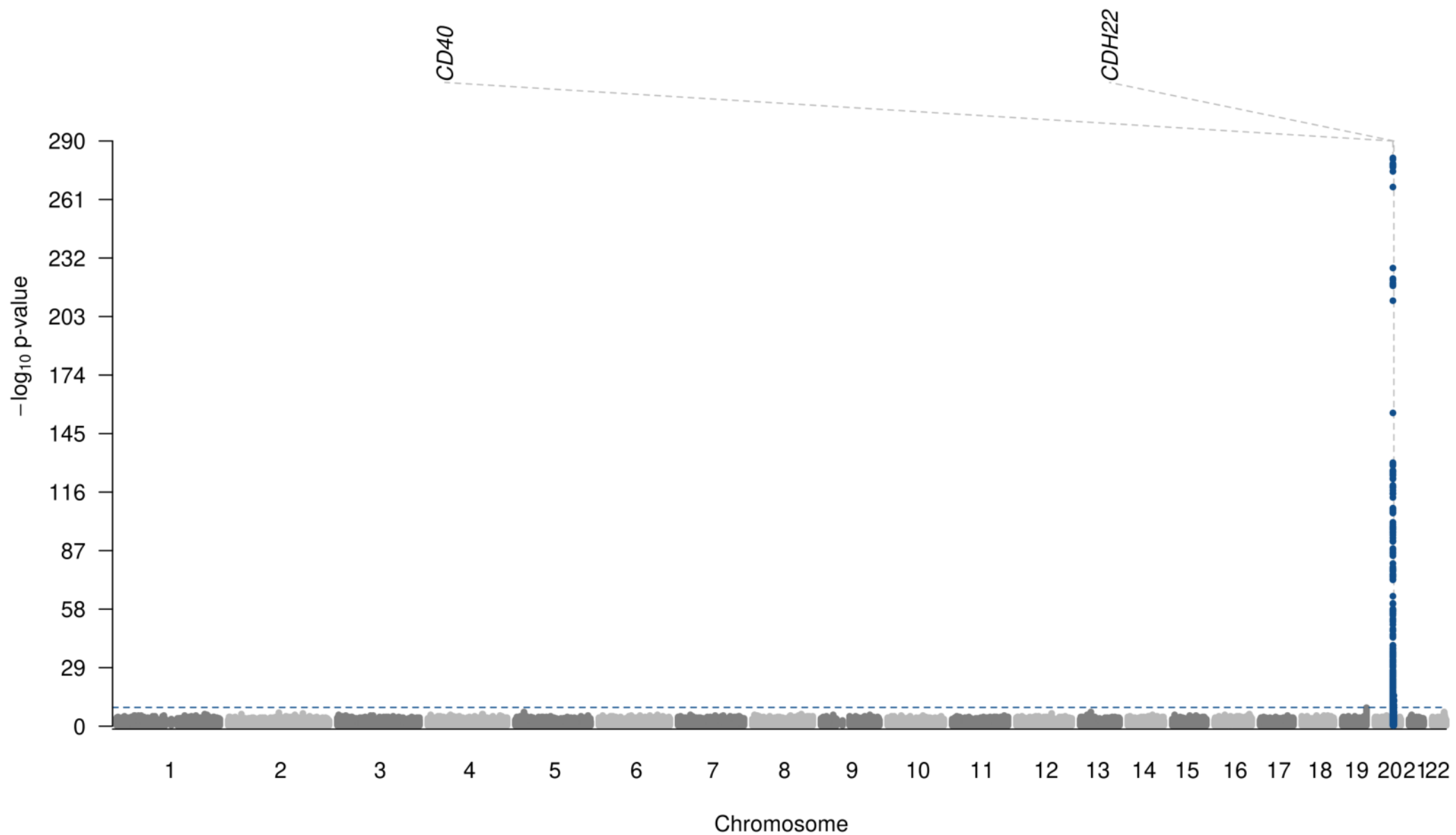
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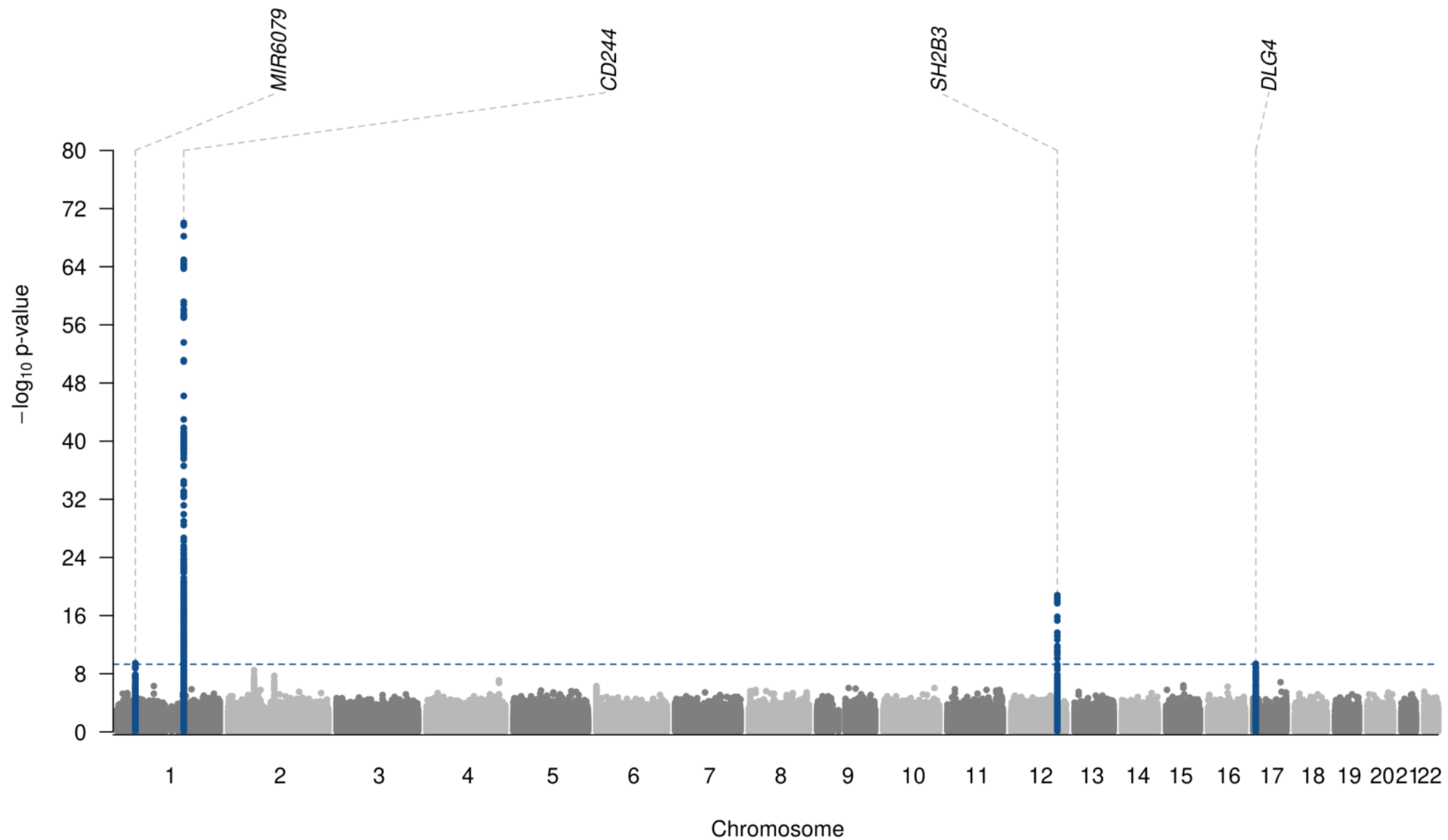
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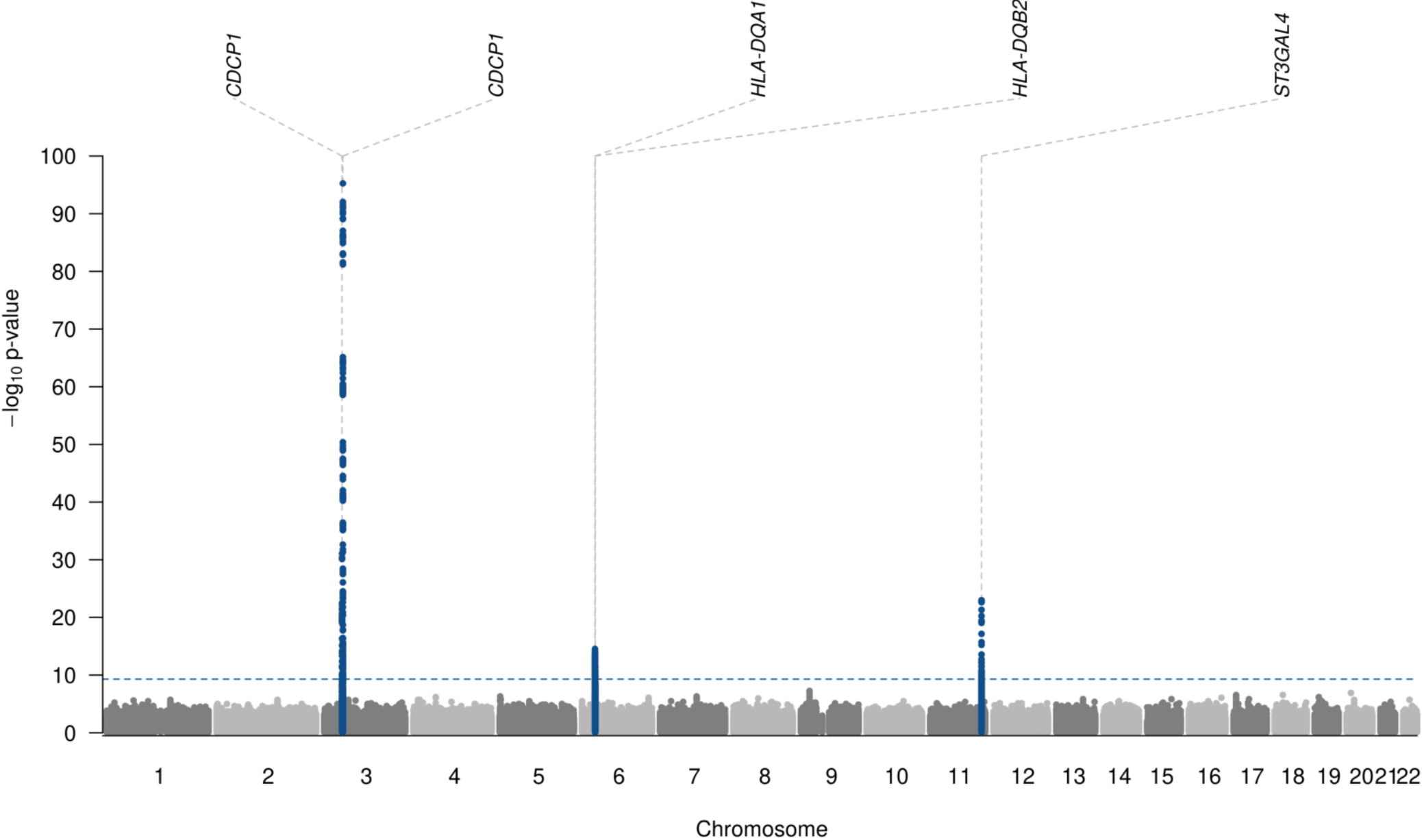
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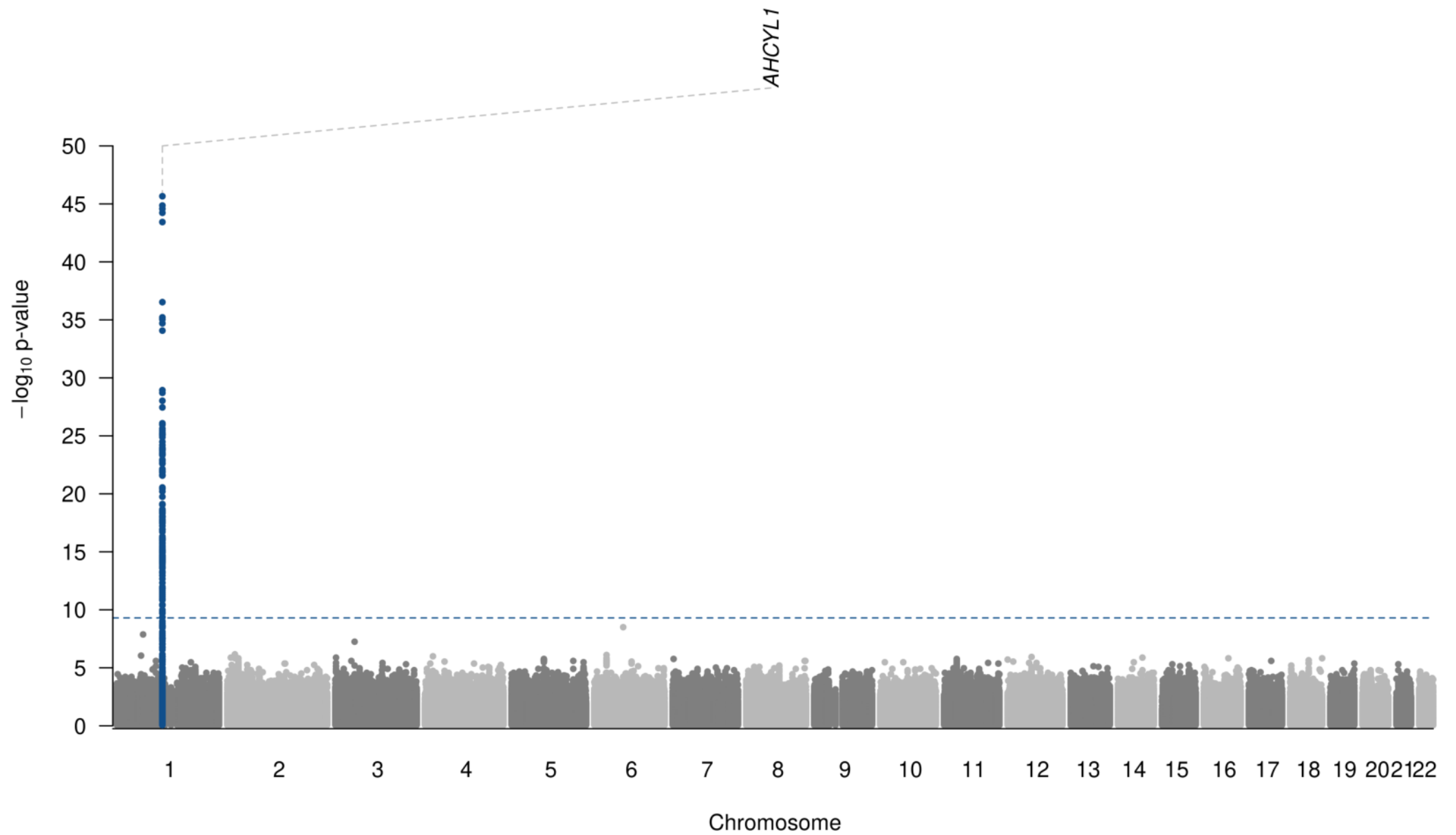
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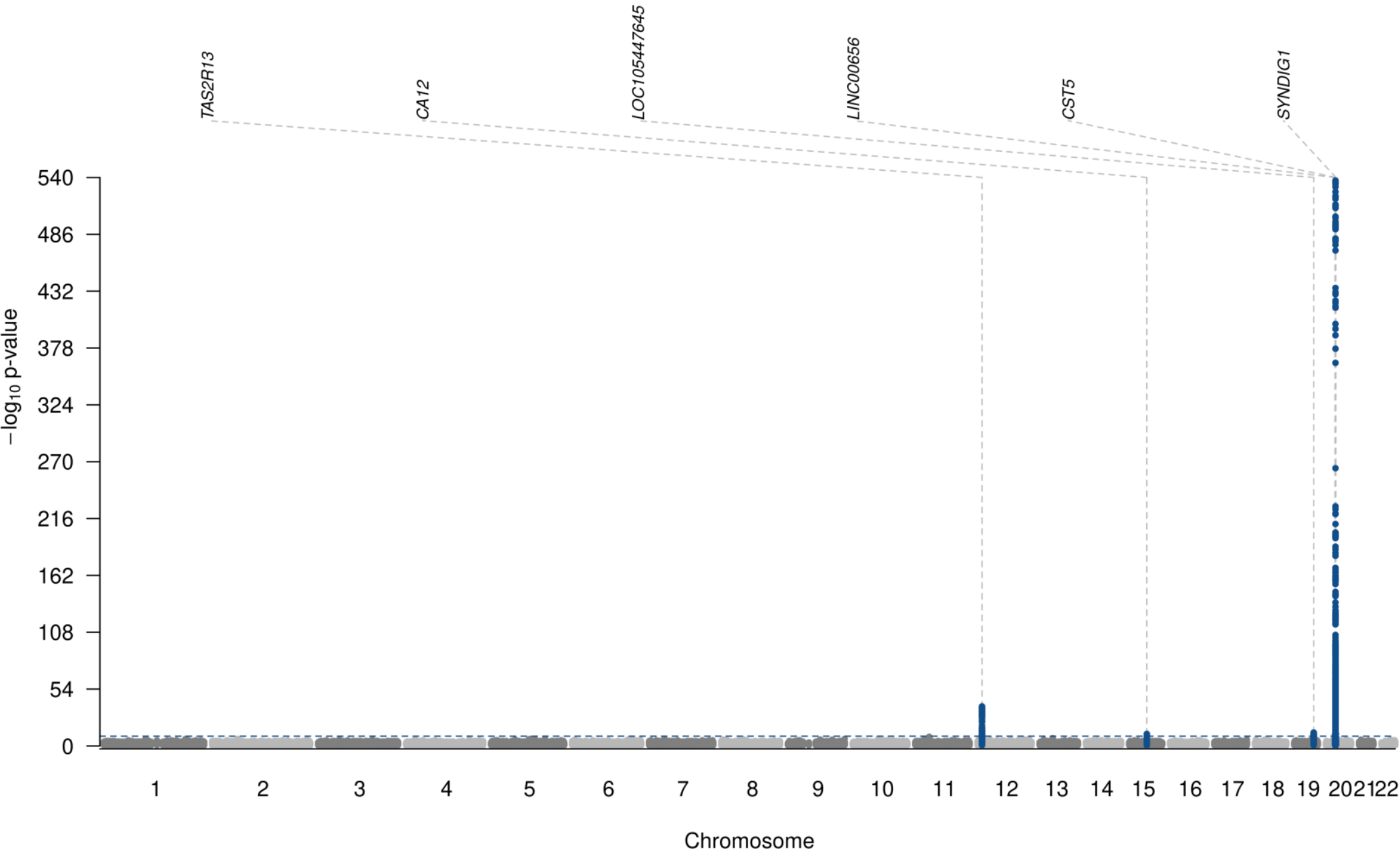
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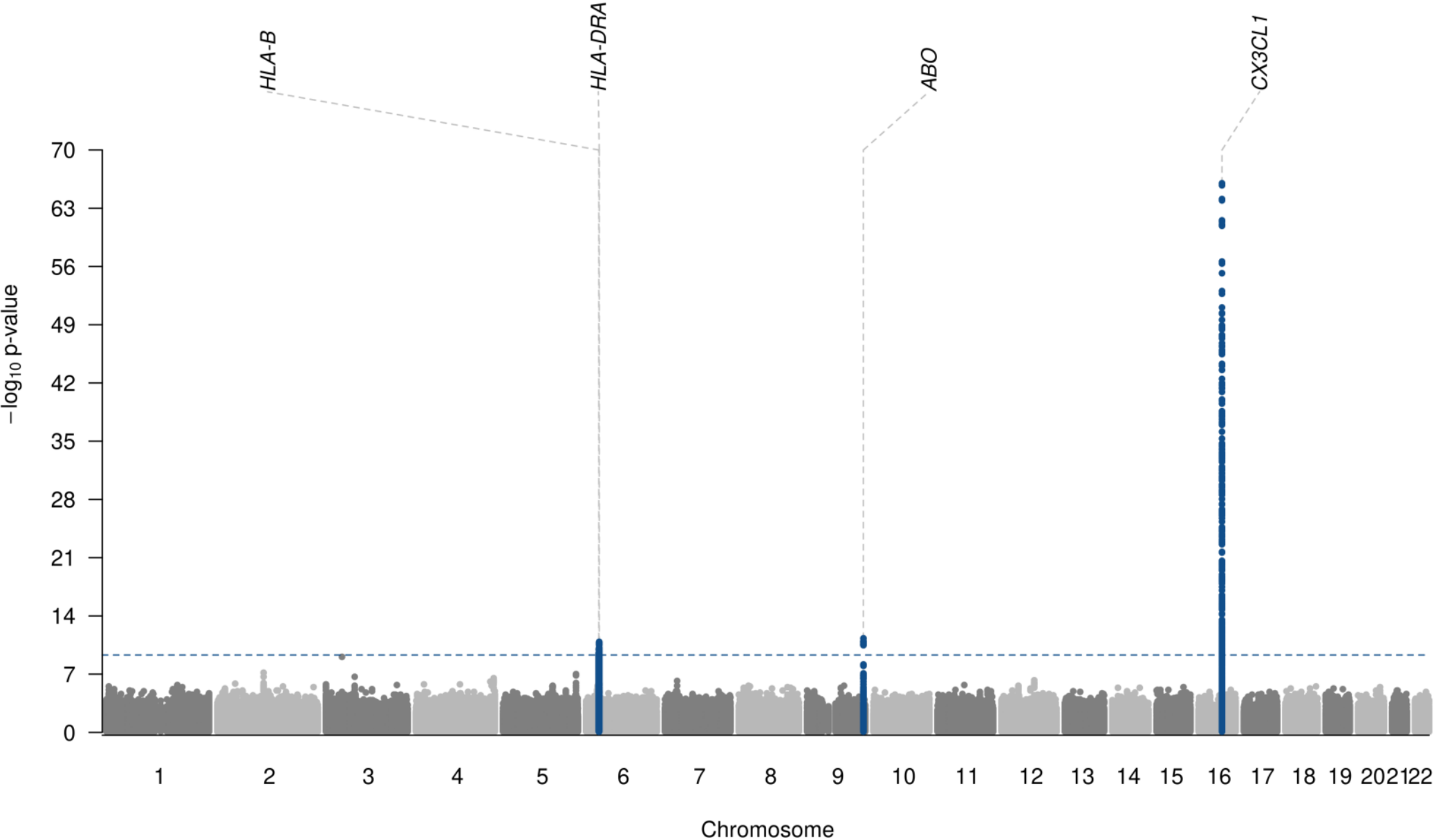
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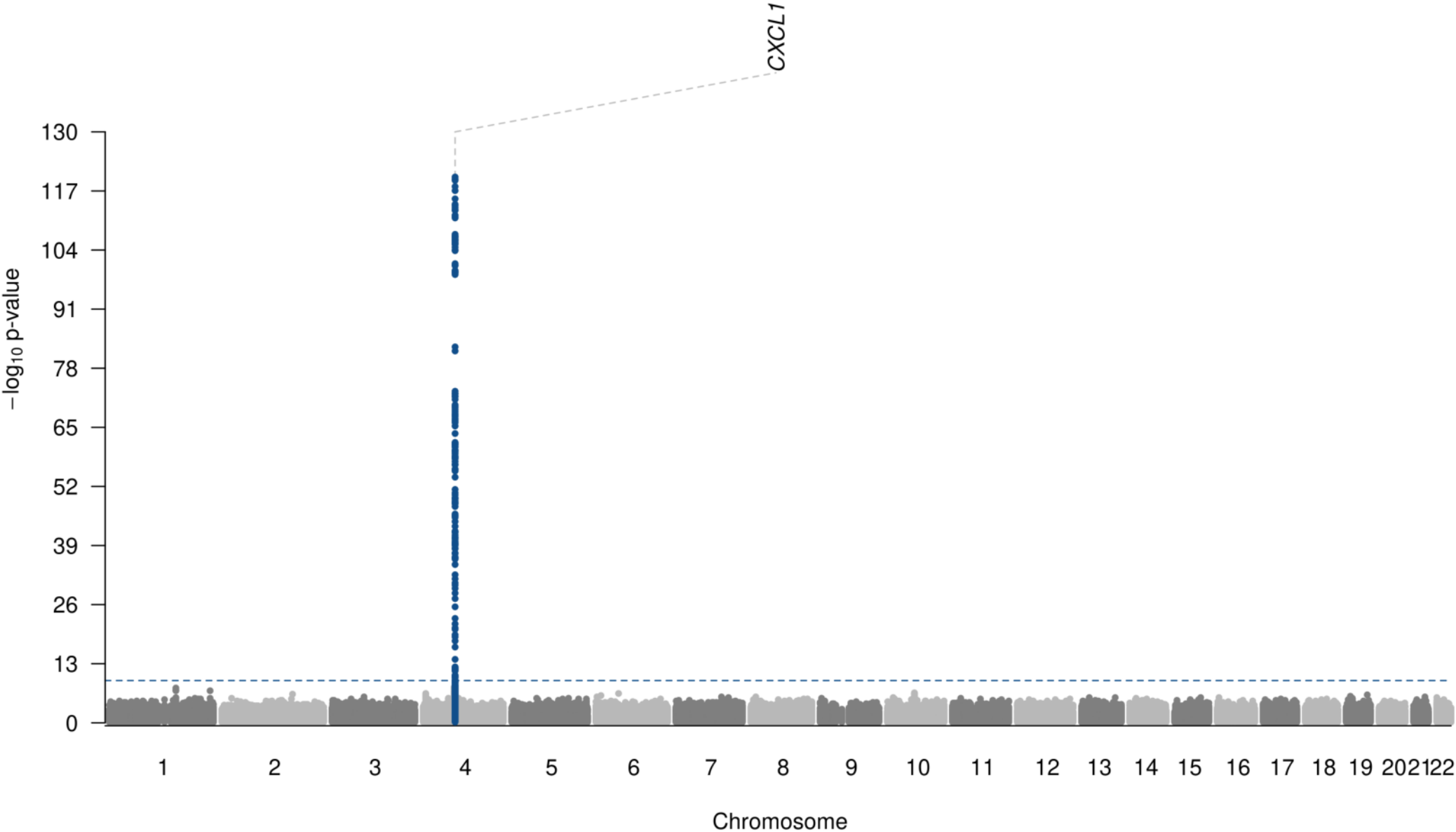
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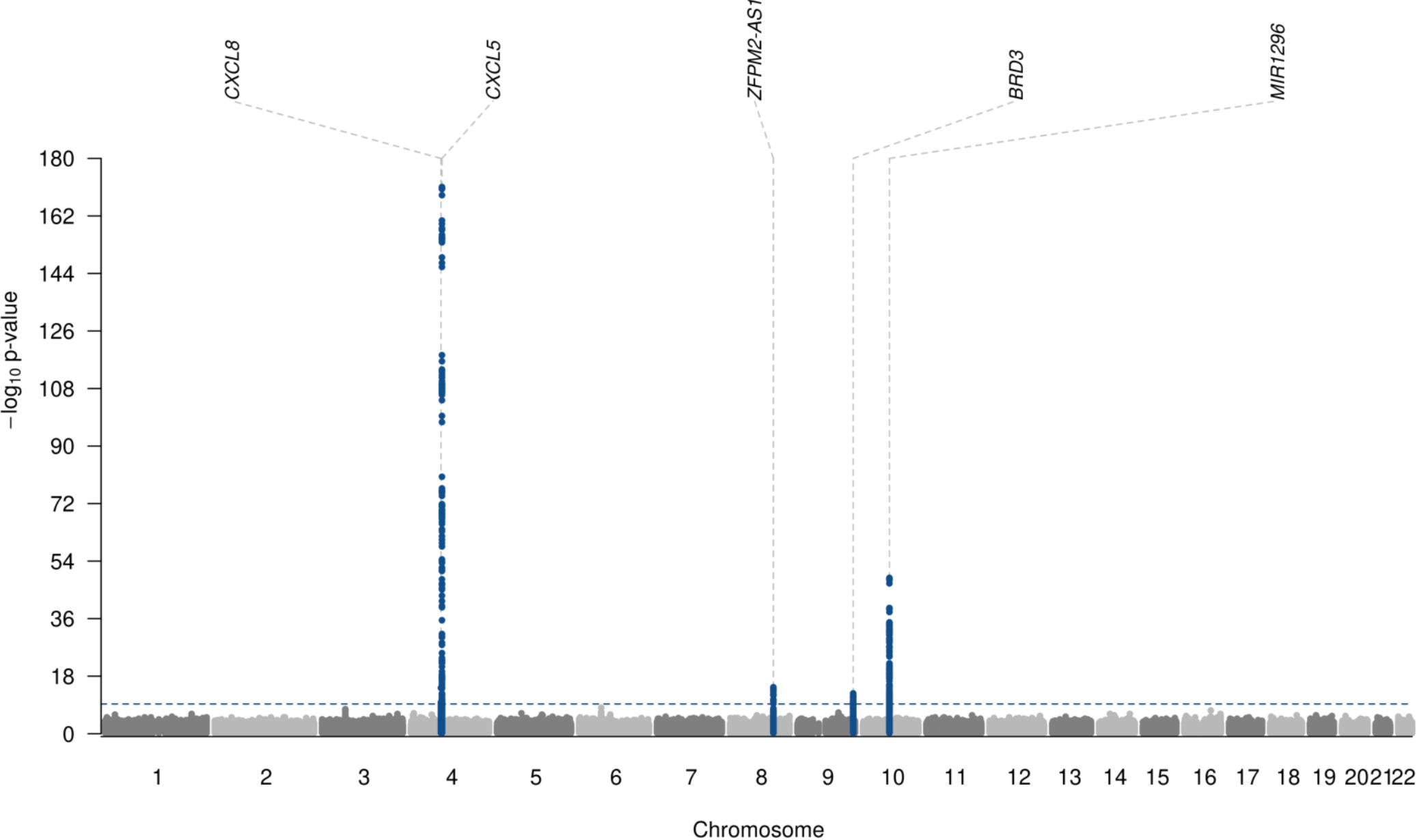
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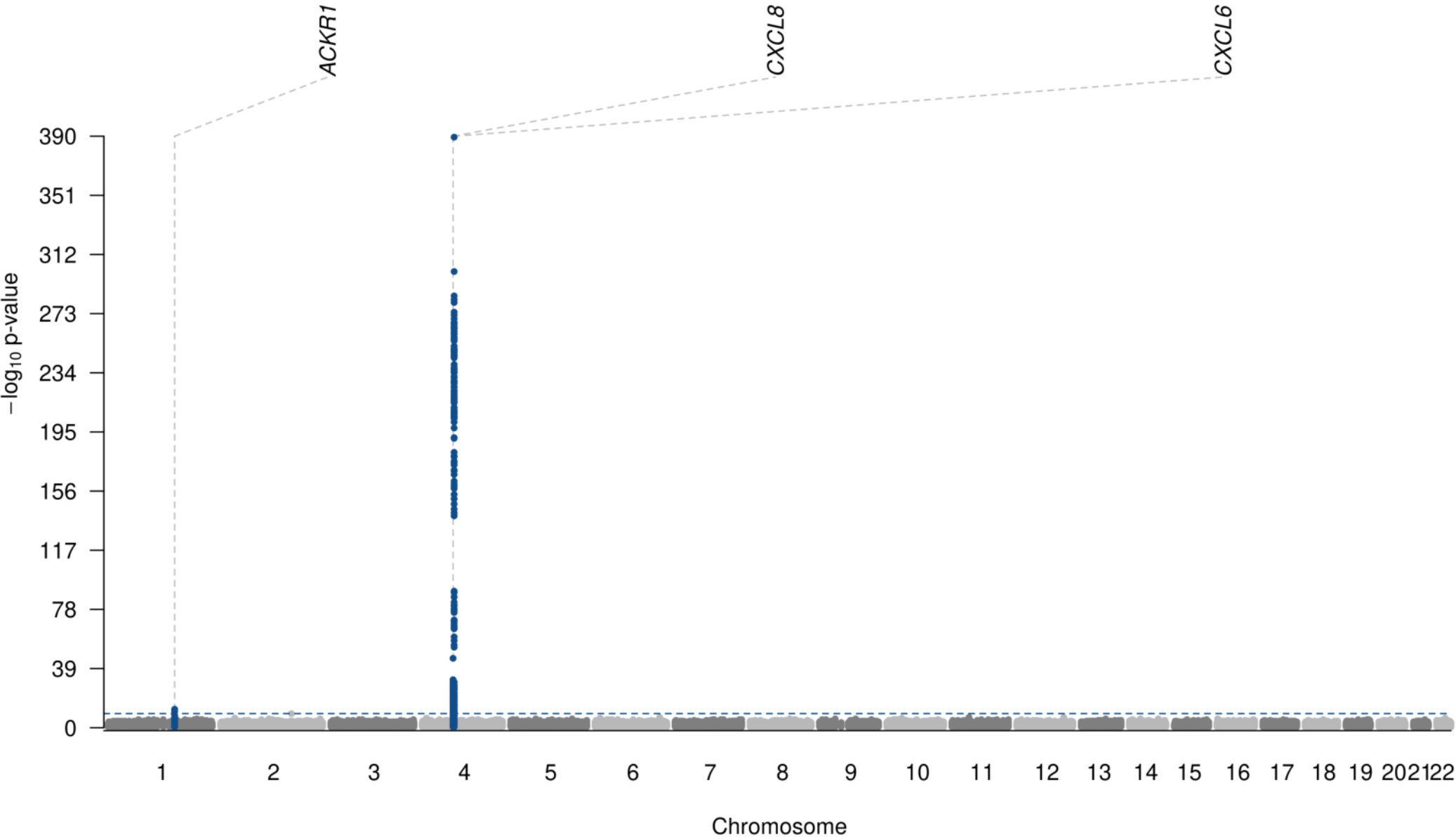
CXCL1 (CXCL1)



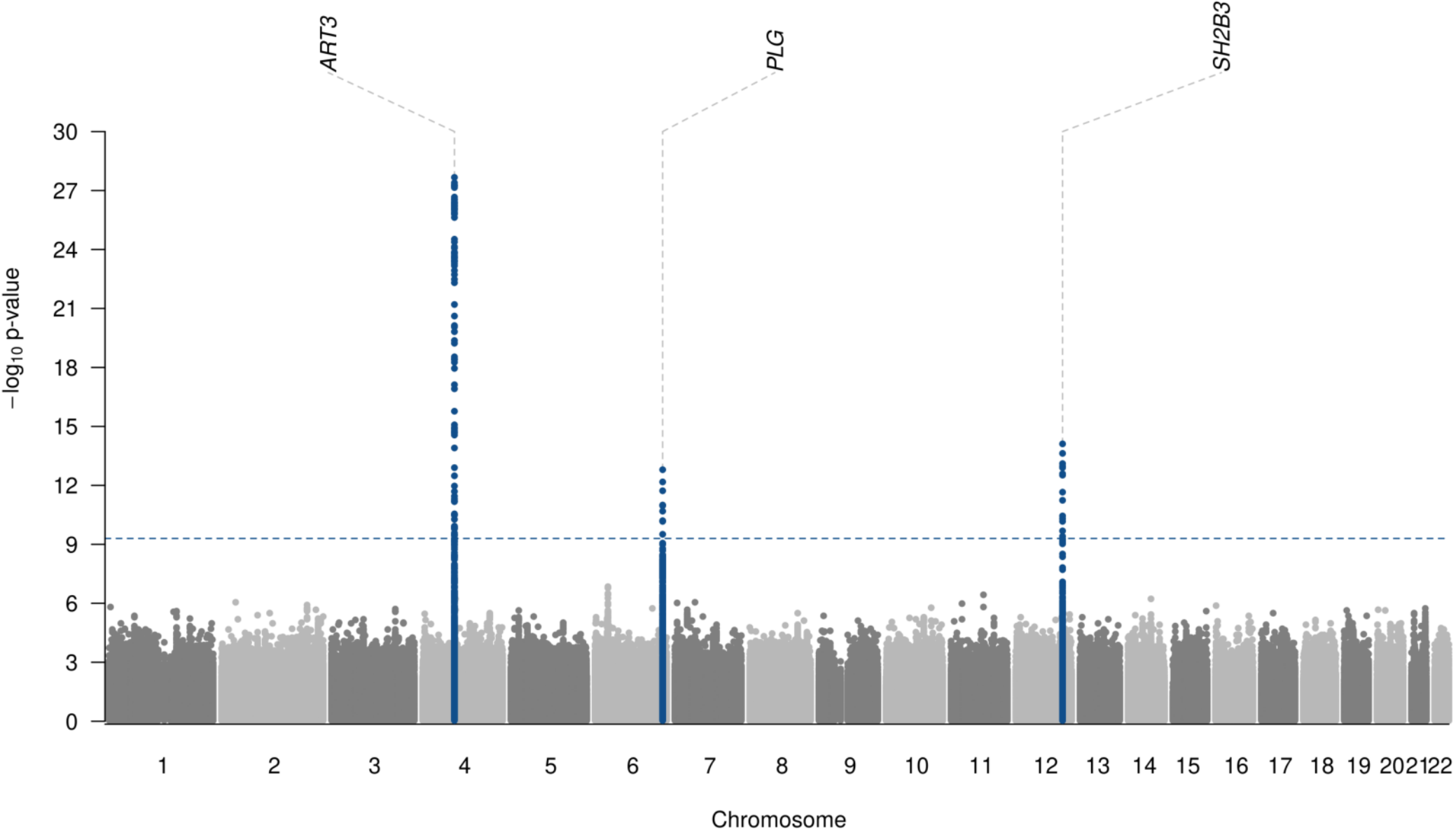
CXCL5 (CXCL5)



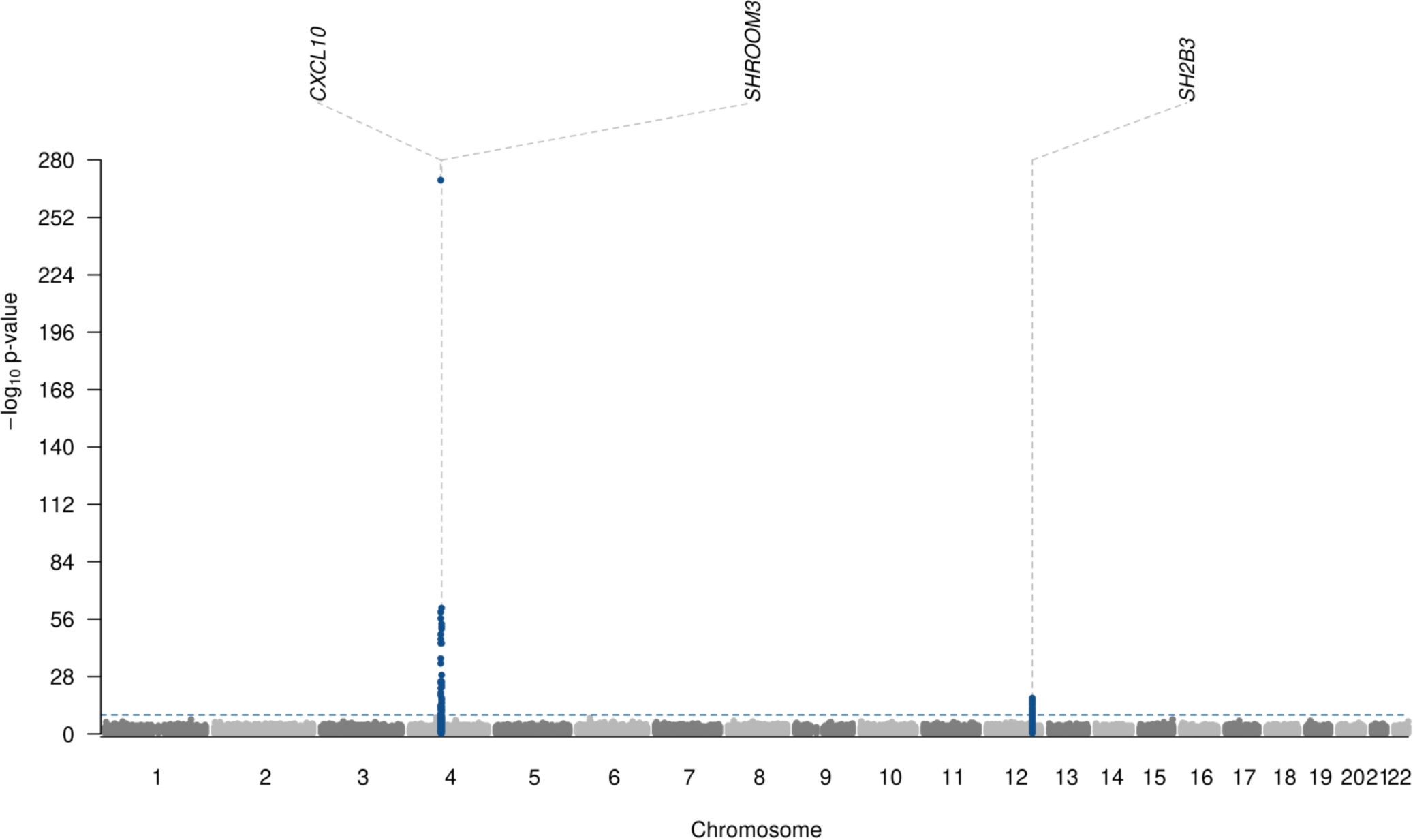
CXCL6 (CXCL6)



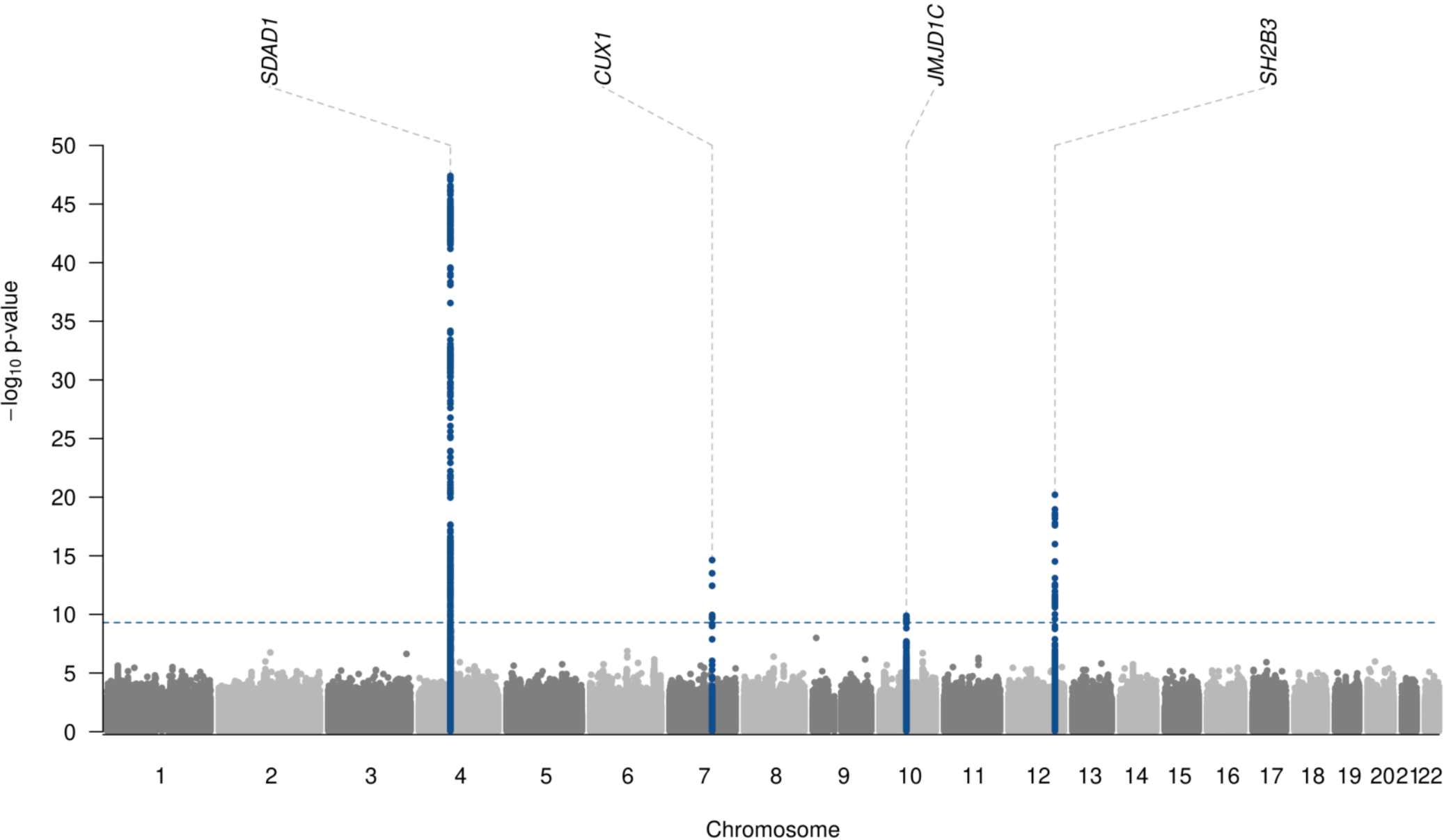
CXCL9 (CXCL9)



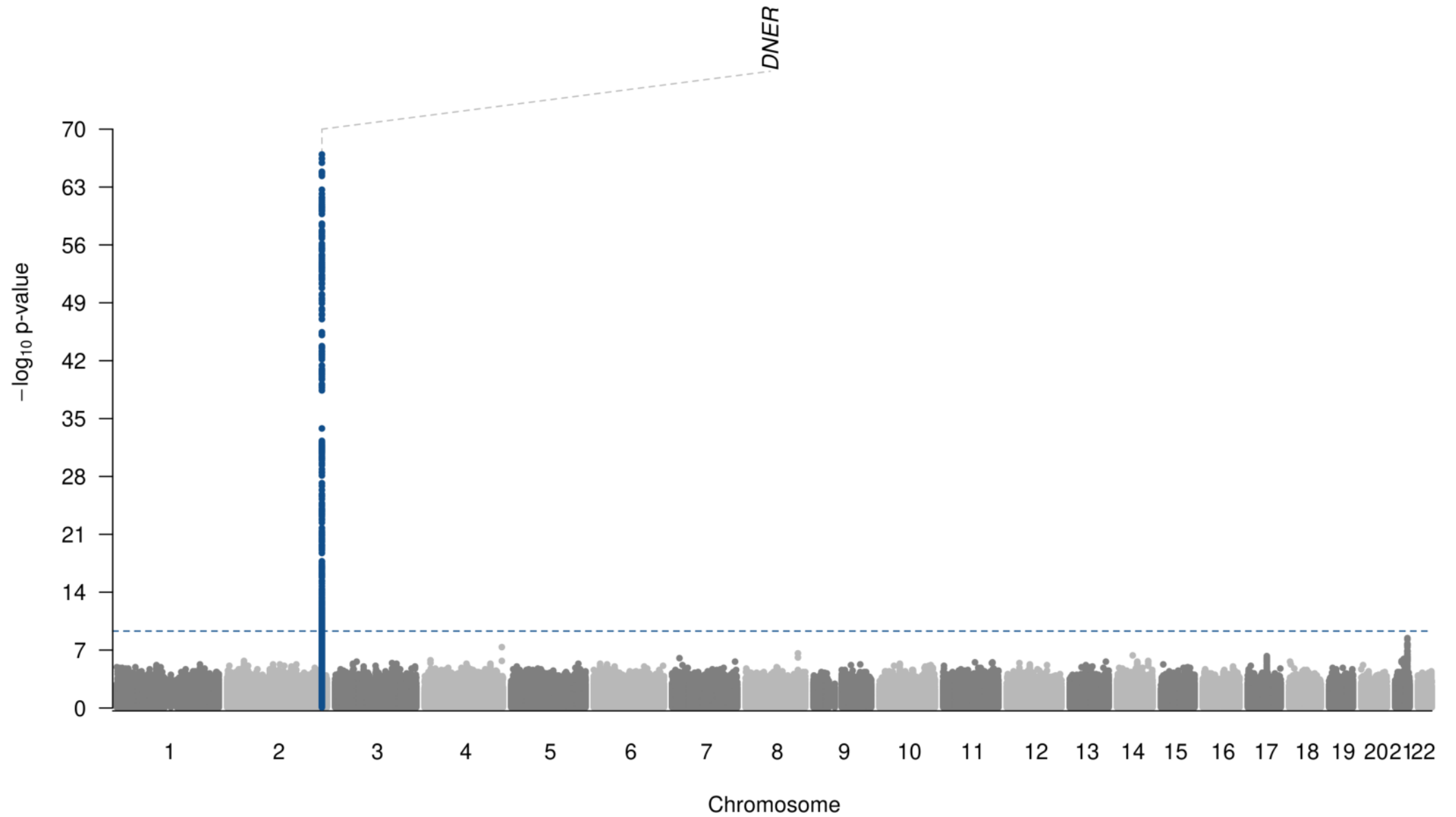
CXCL10 (CXCL10)



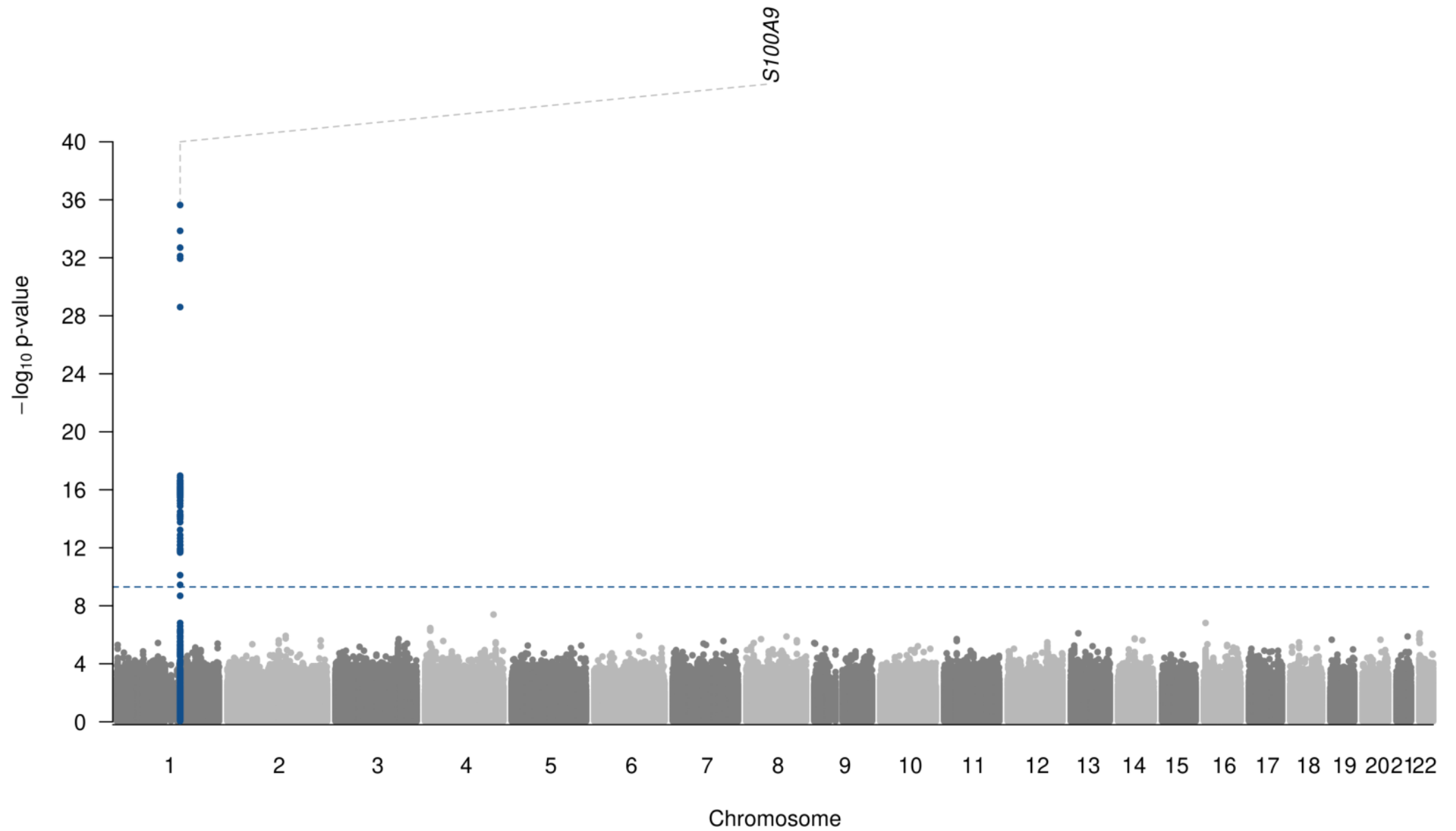
CXCL11 (CXCL11)



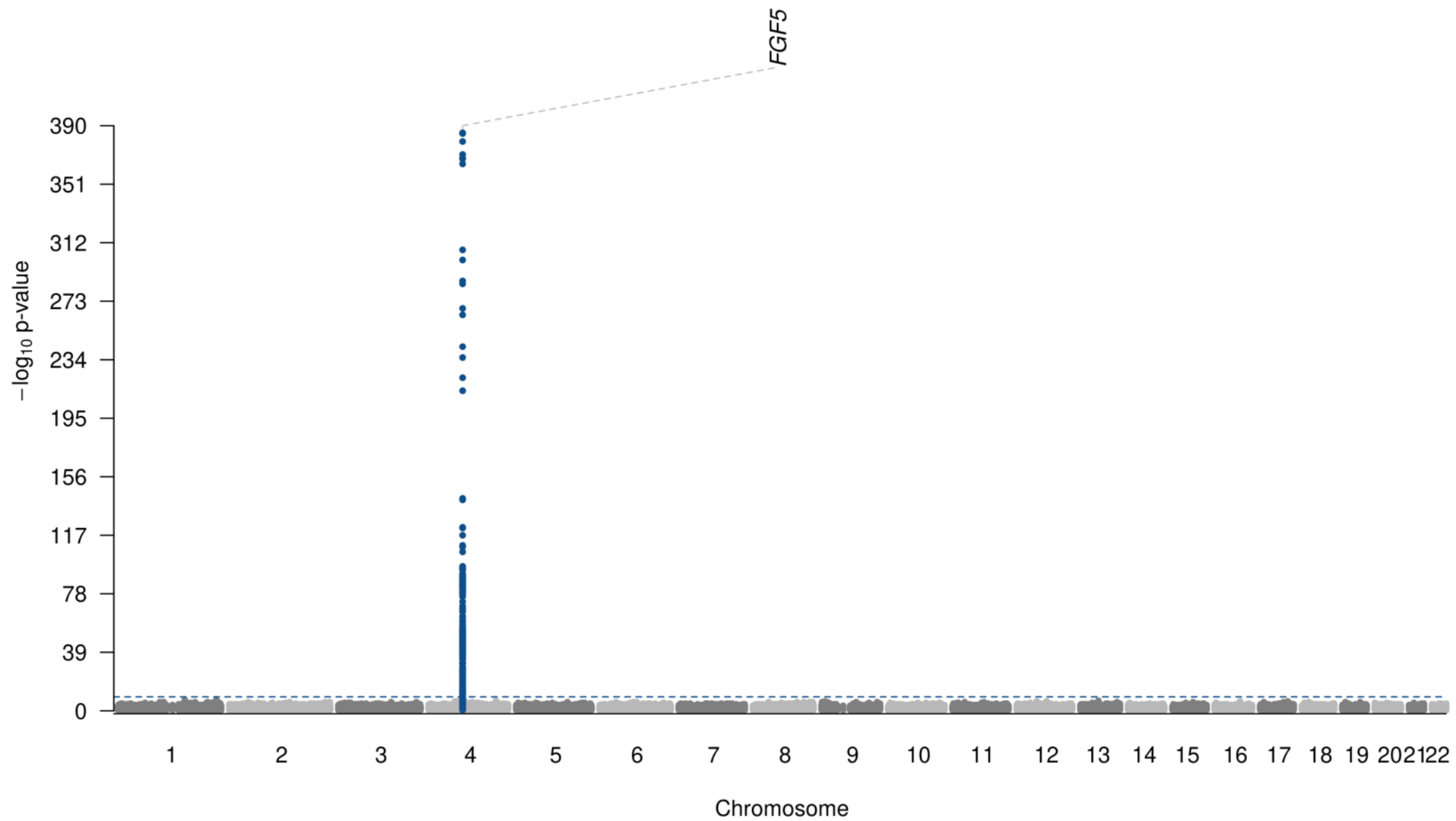
DNER (DNER)



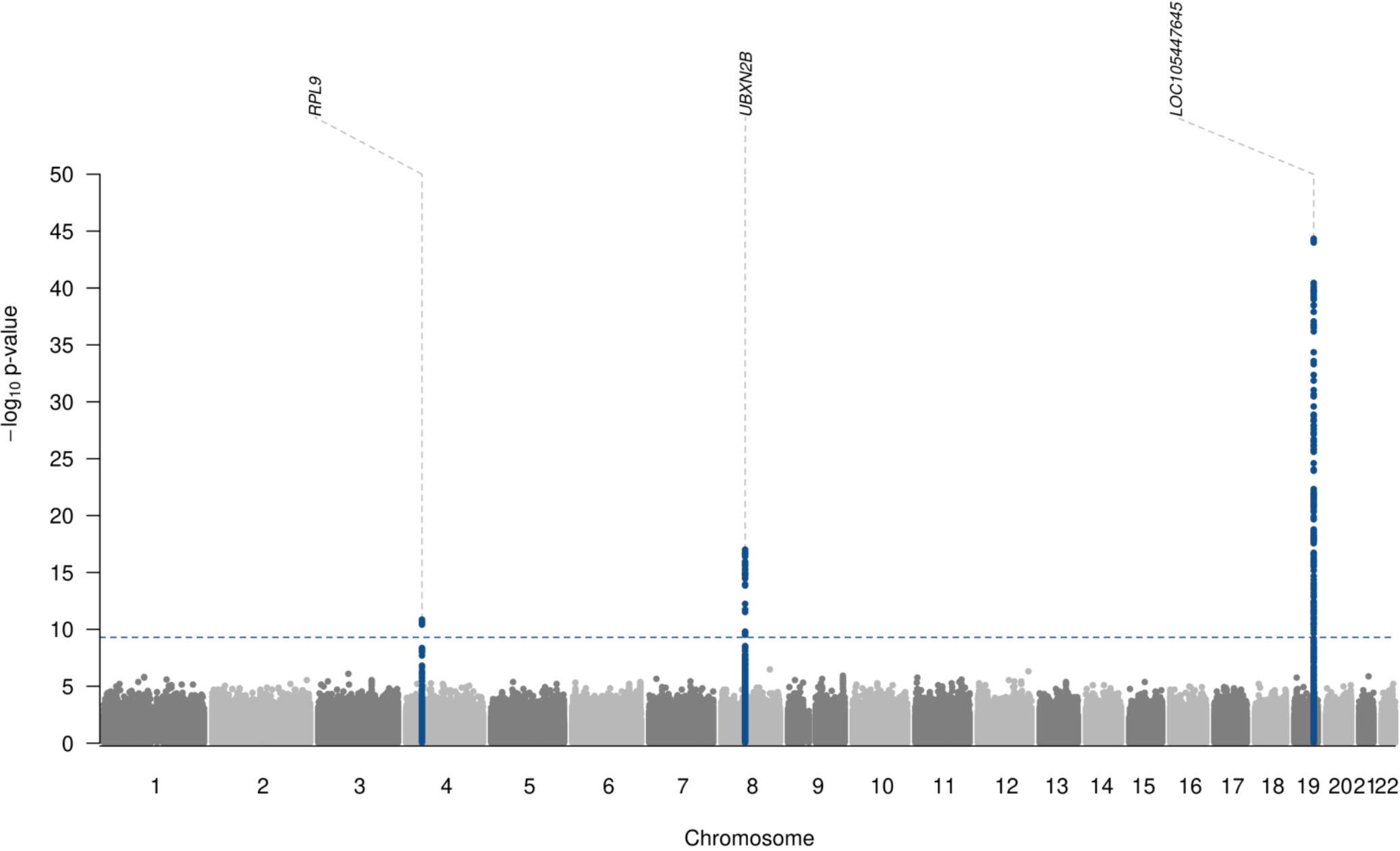
EN-RAGE (S100A12)



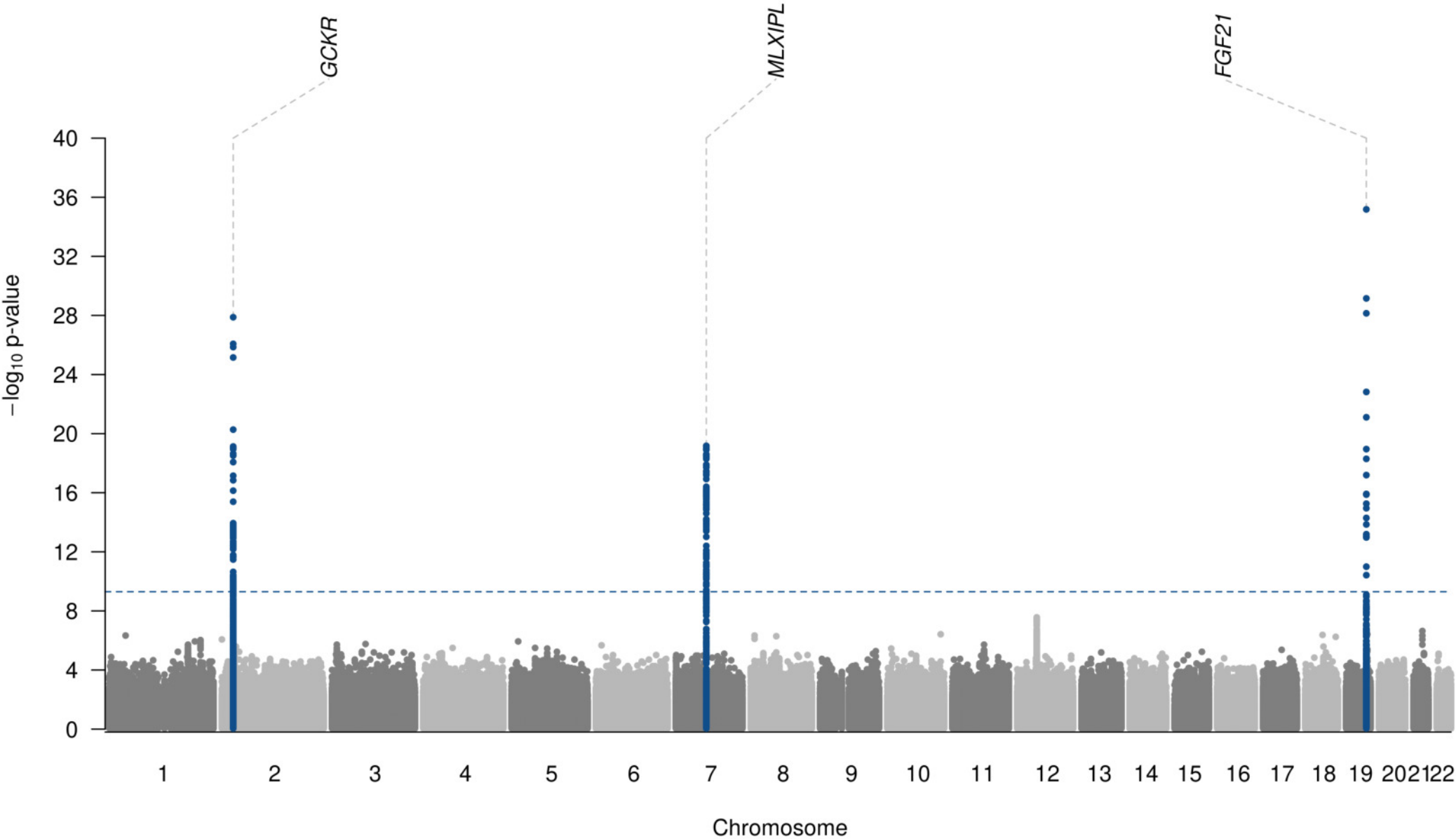
FGF-5 (FGF5)



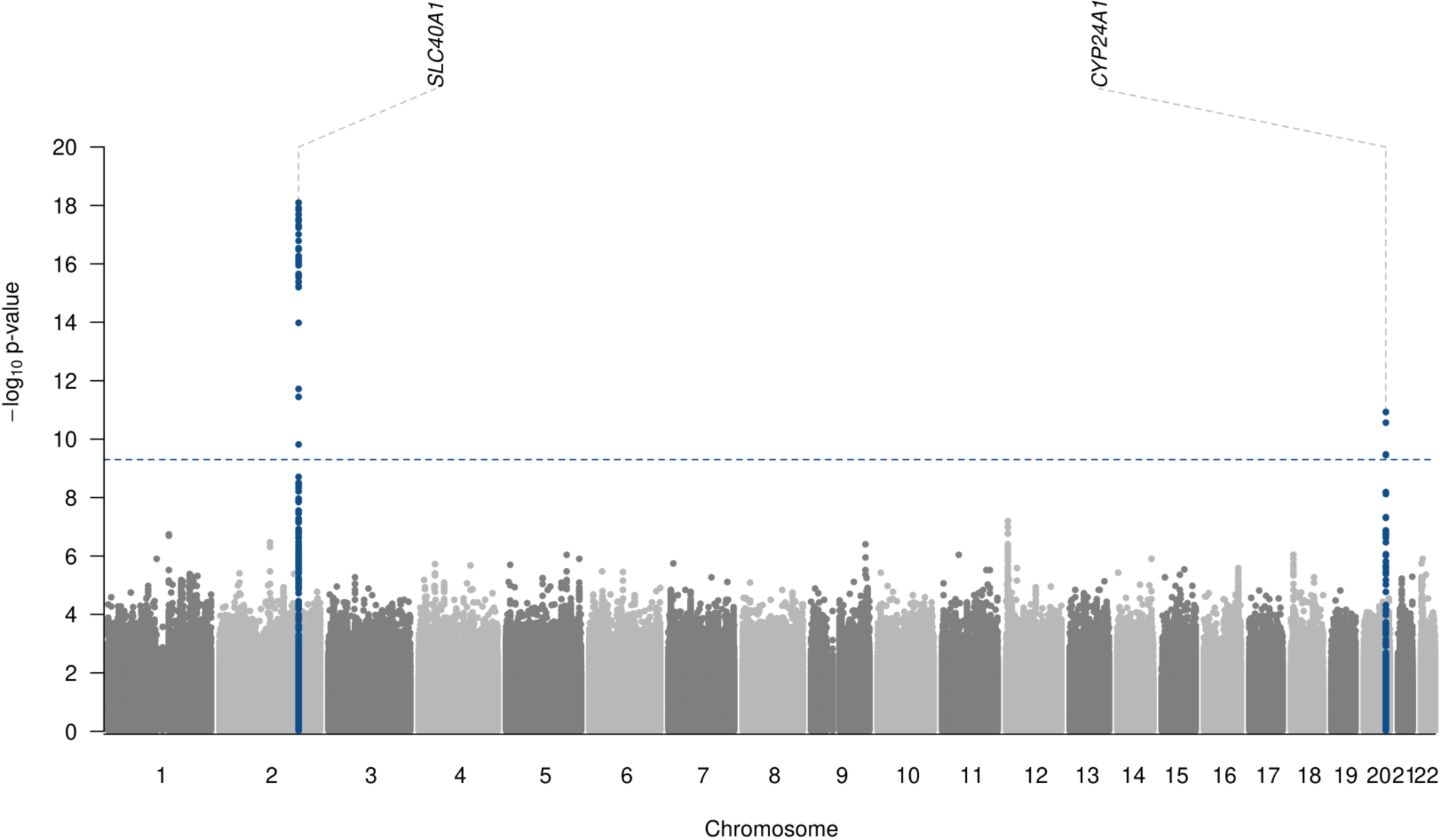
FGF-19 (FGF19)



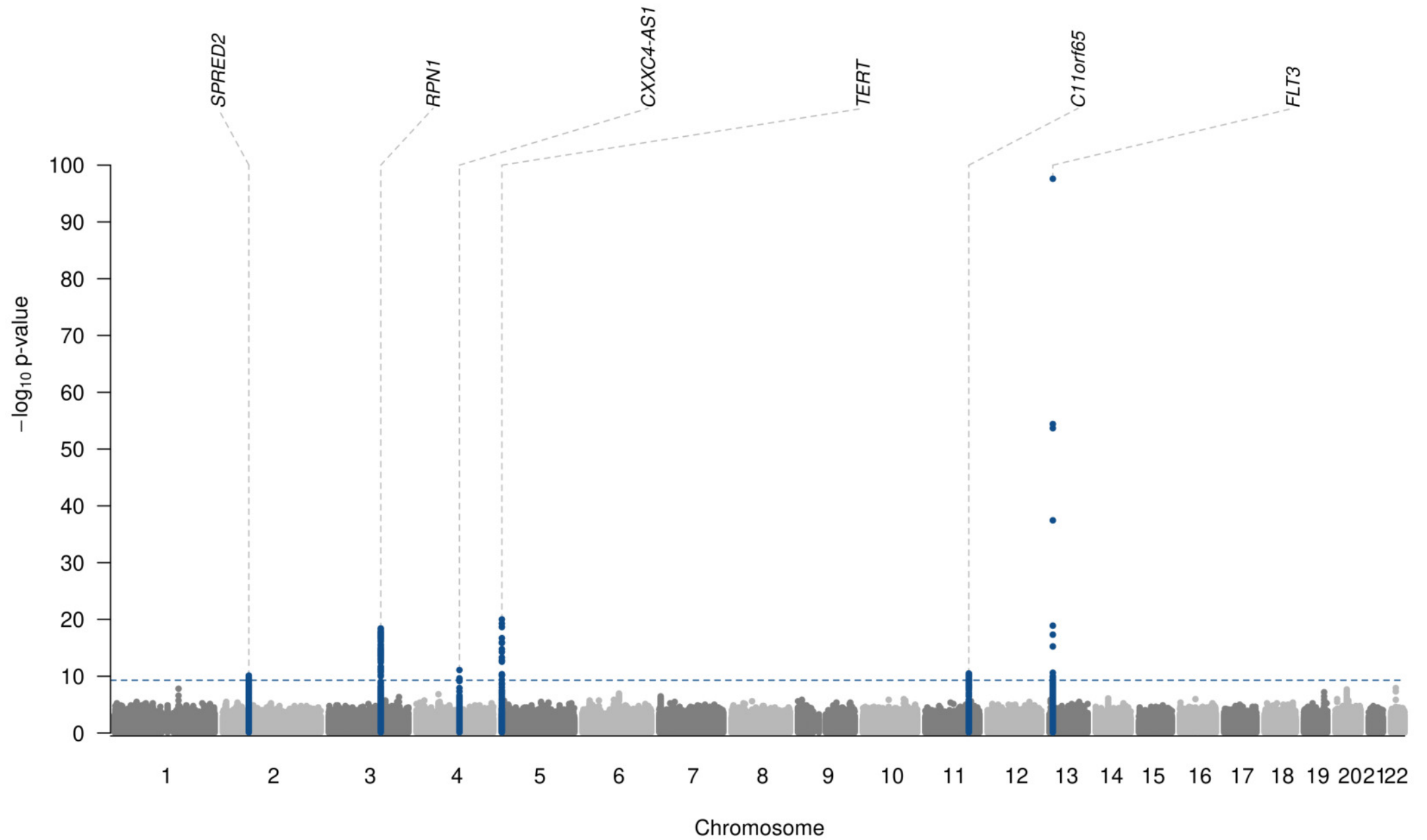
FGF-21 (FGF21)



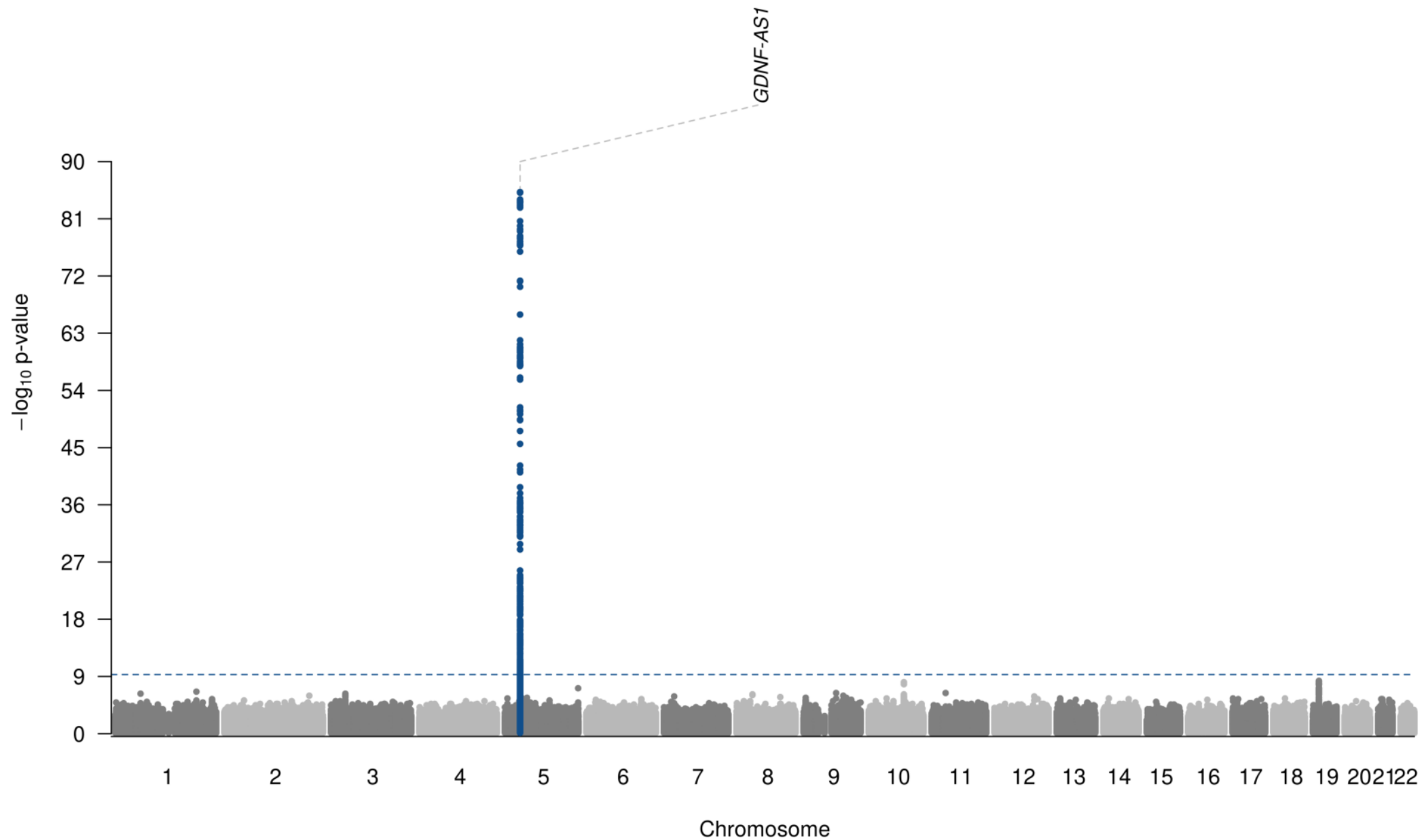
FGF-23 (FGF23)



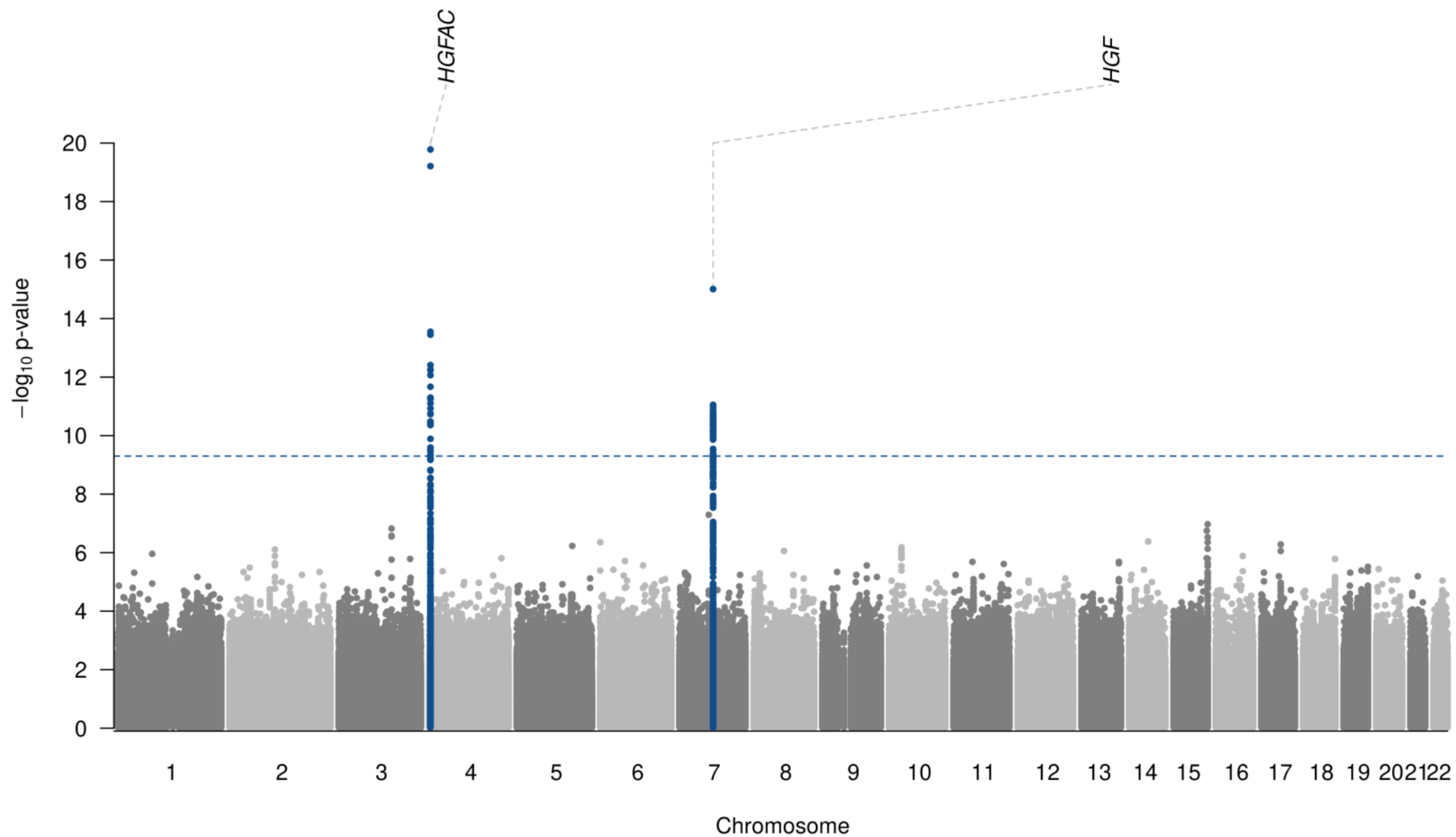
Flt3L (FLT3LG)



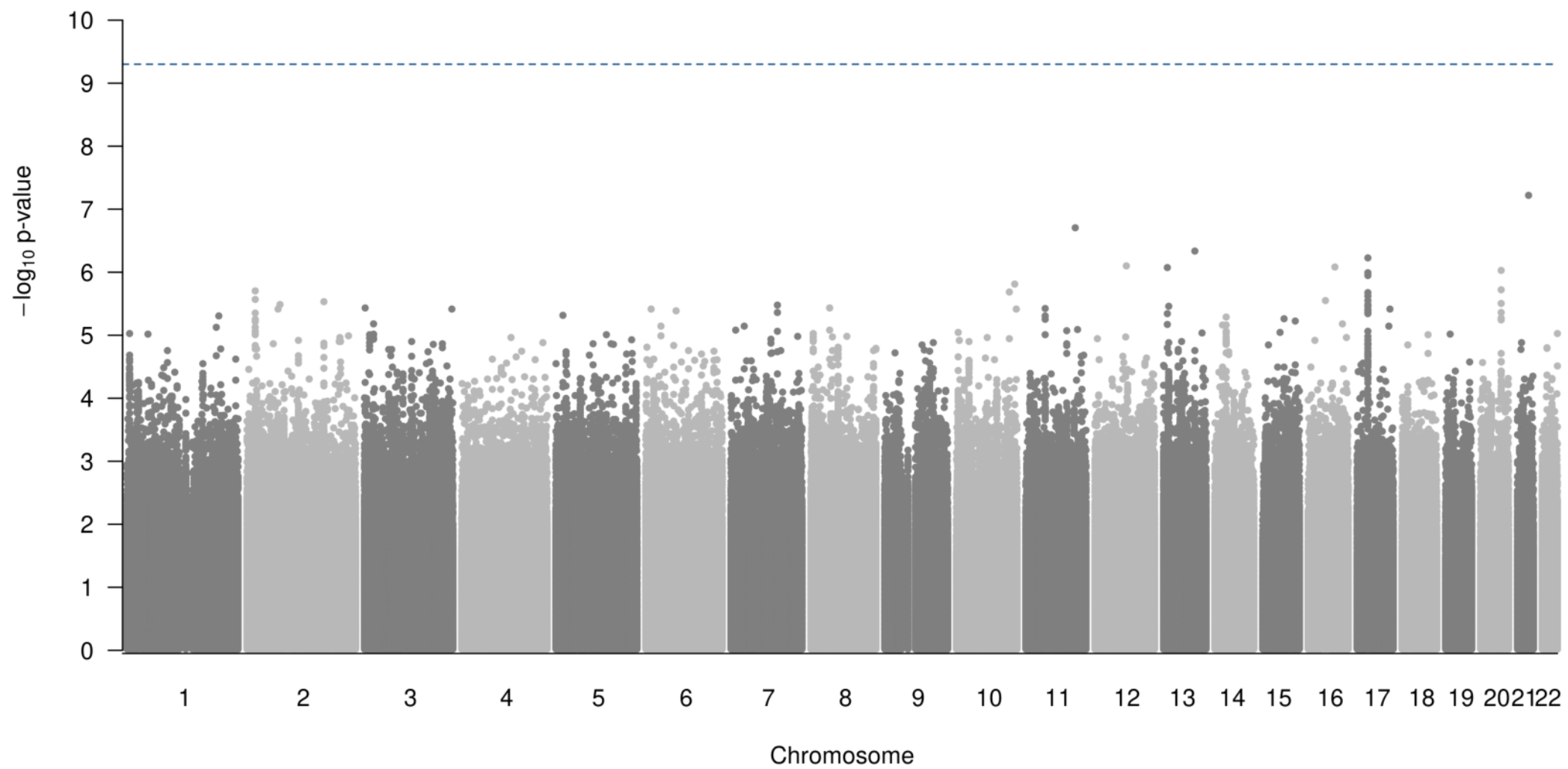
hGDNF (GDNF)



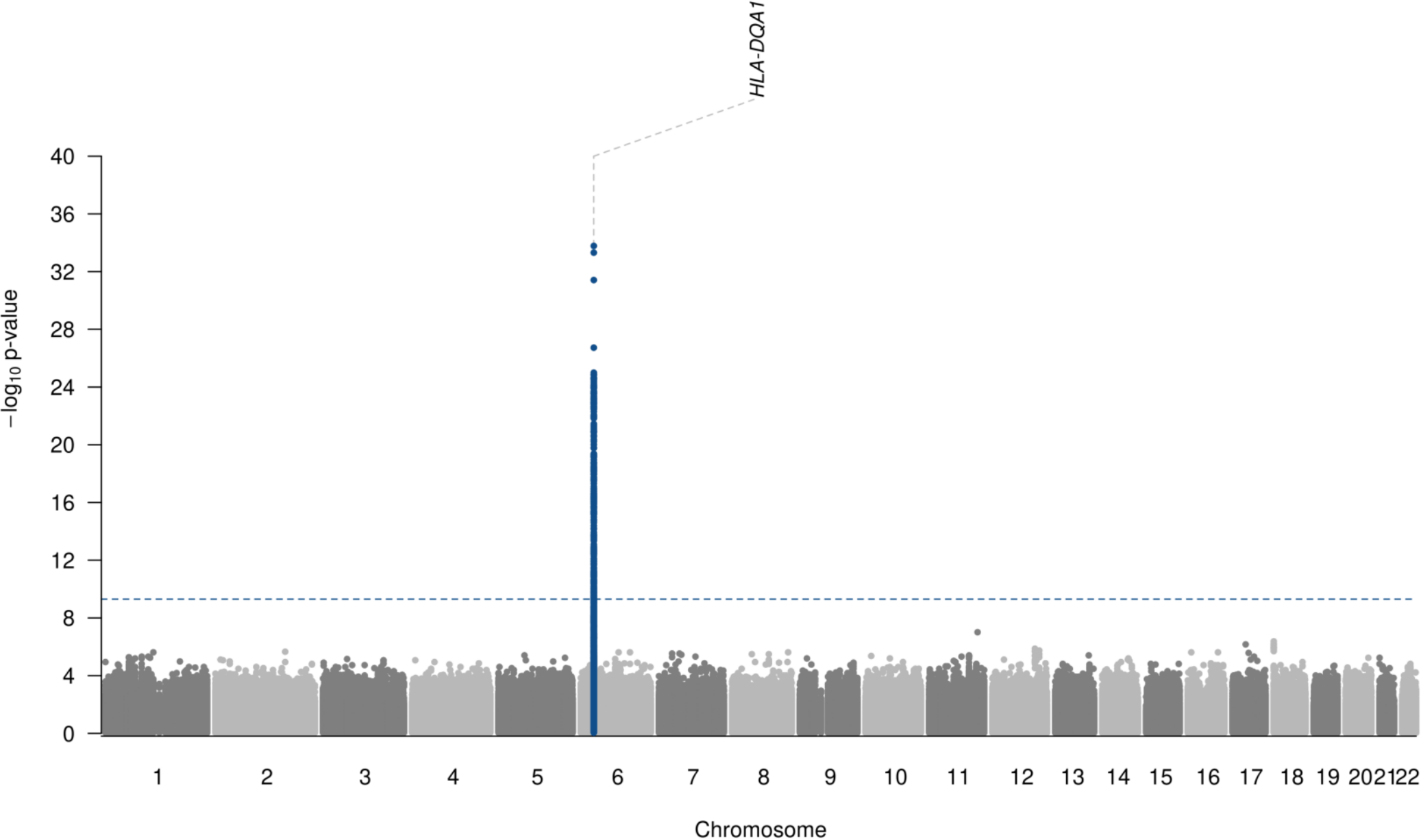
HGF (HGF)



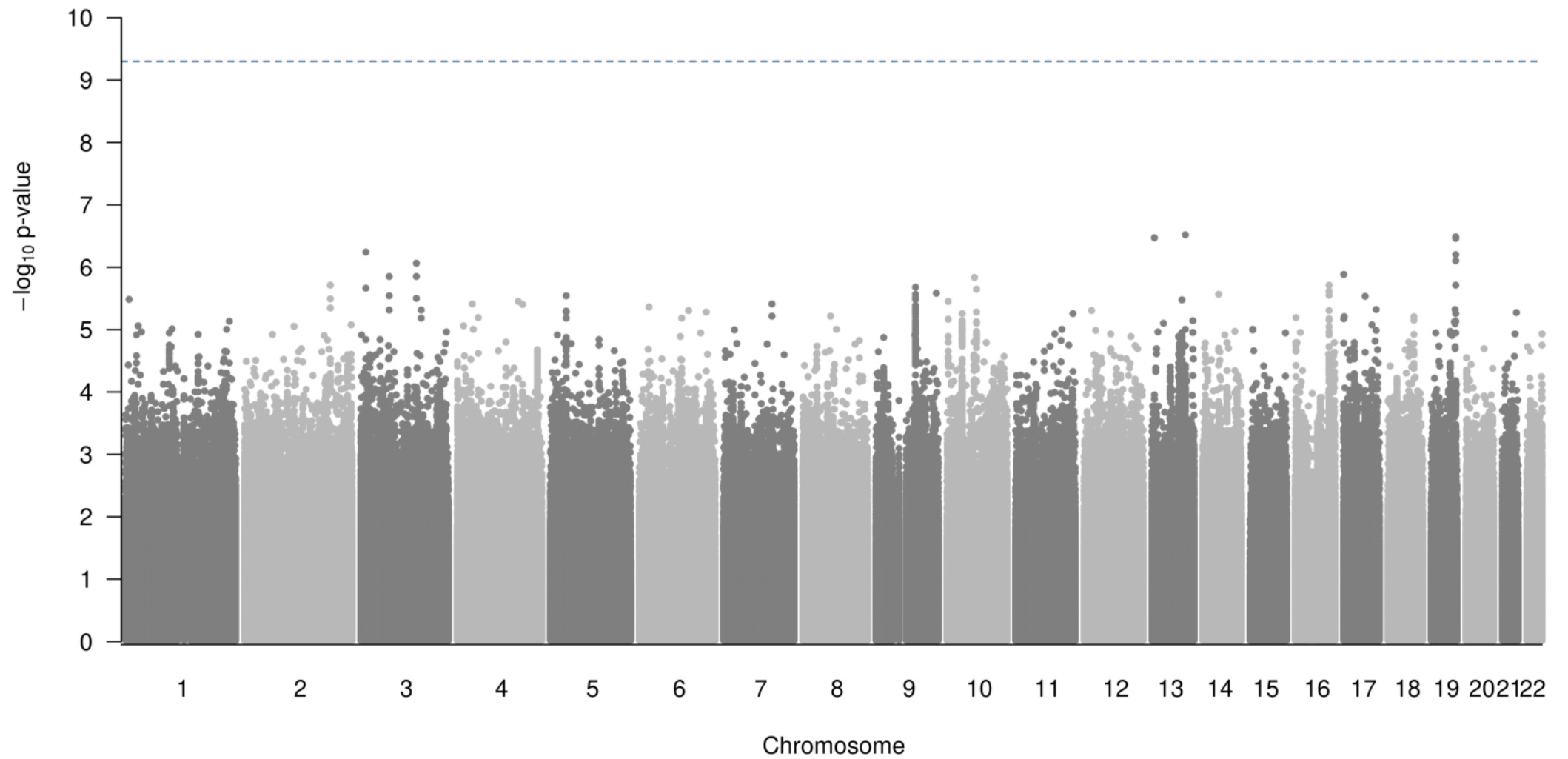
IFN-gamma (IFNG)



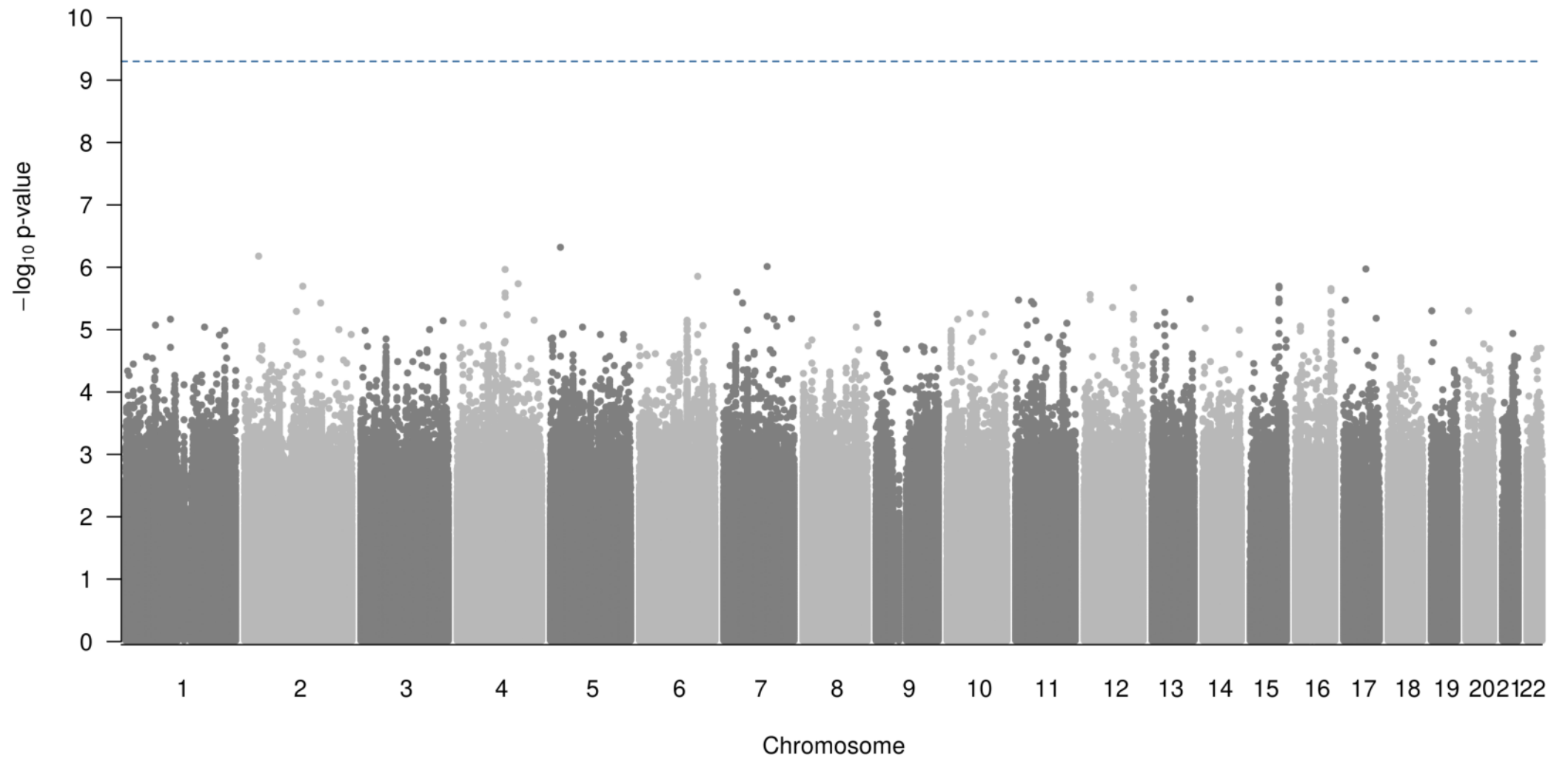
IL-1 (IL1A)



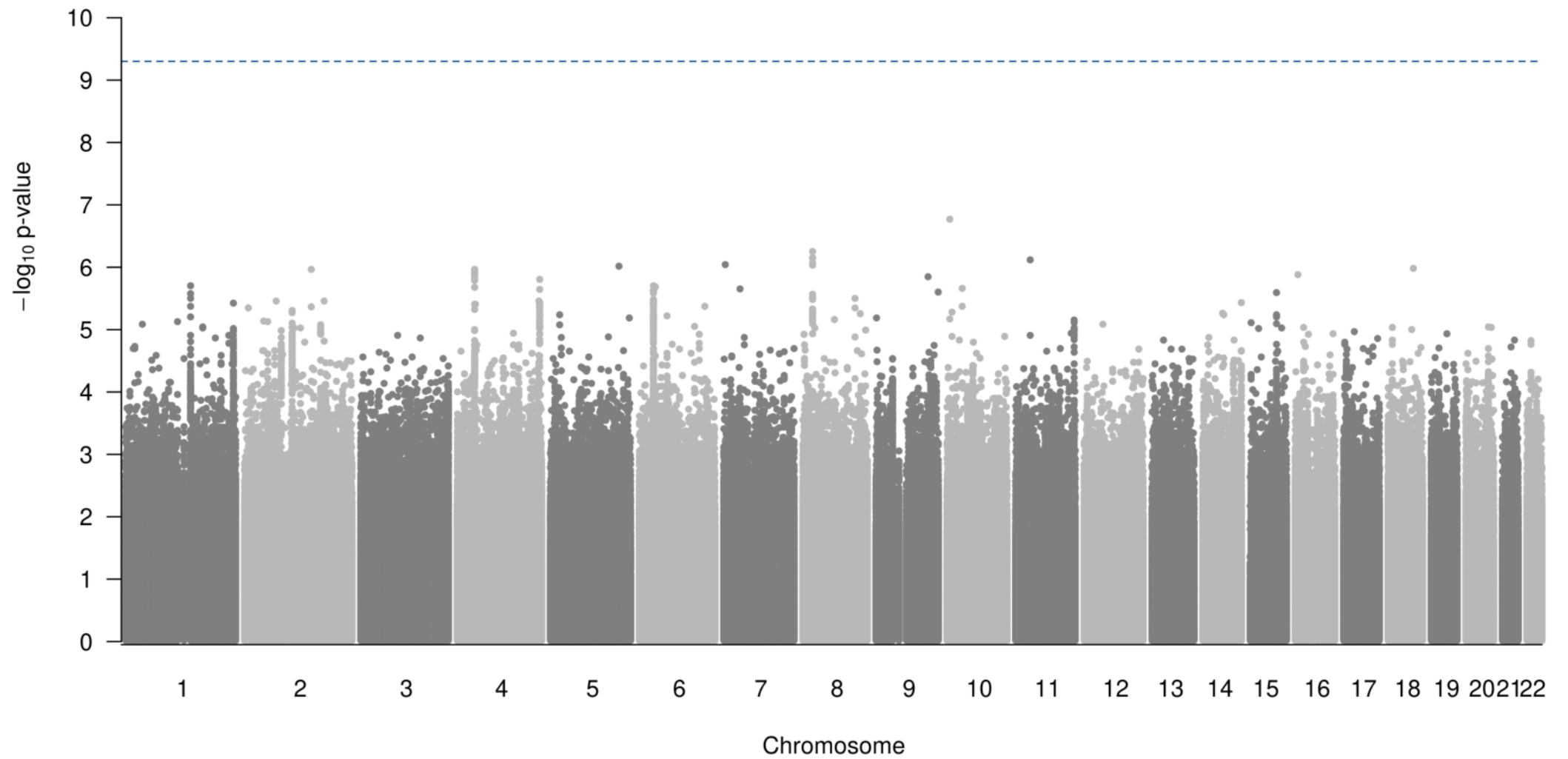
IL-2 (IL2)



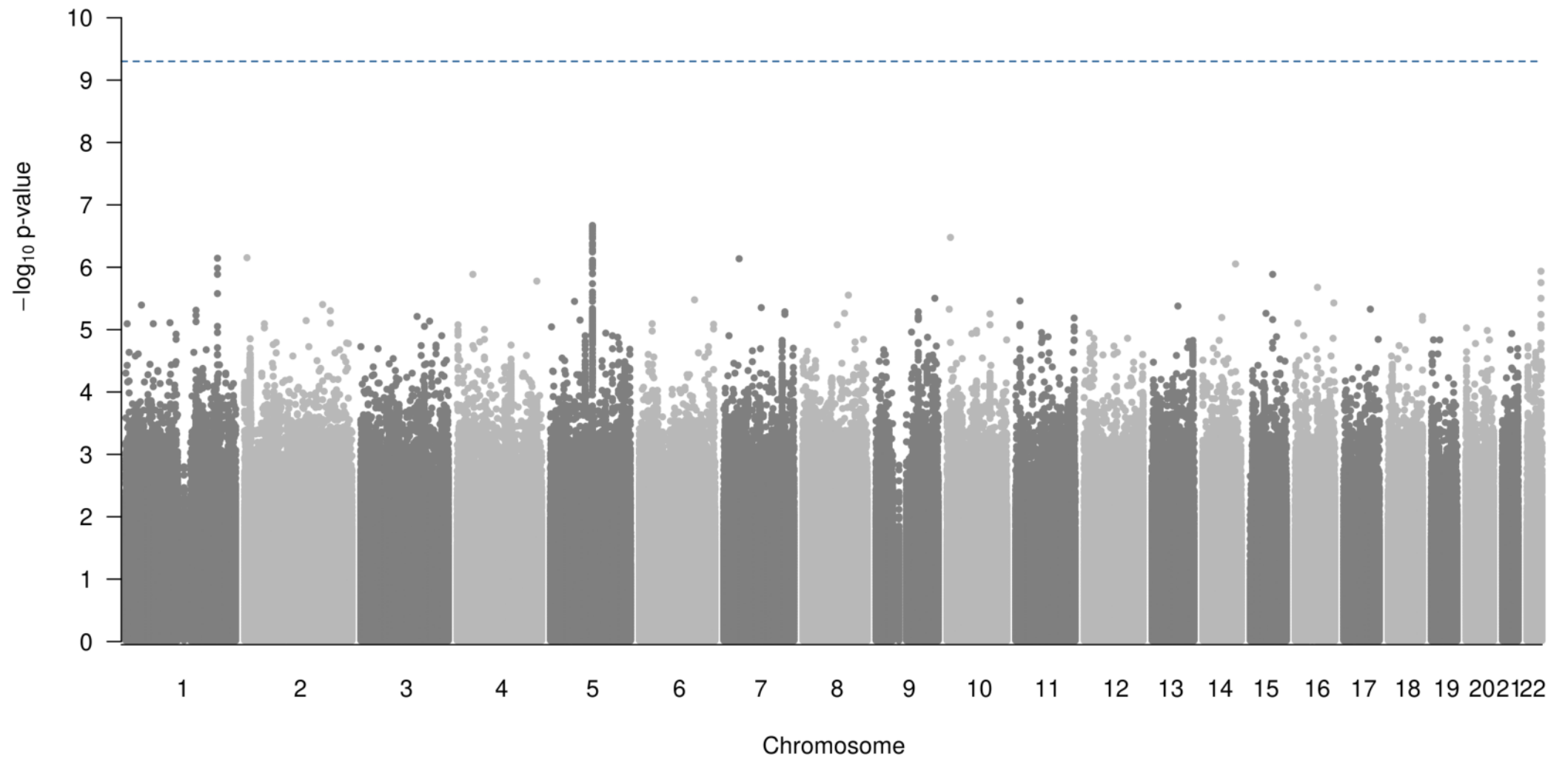
IL-2RB (IL2RB)



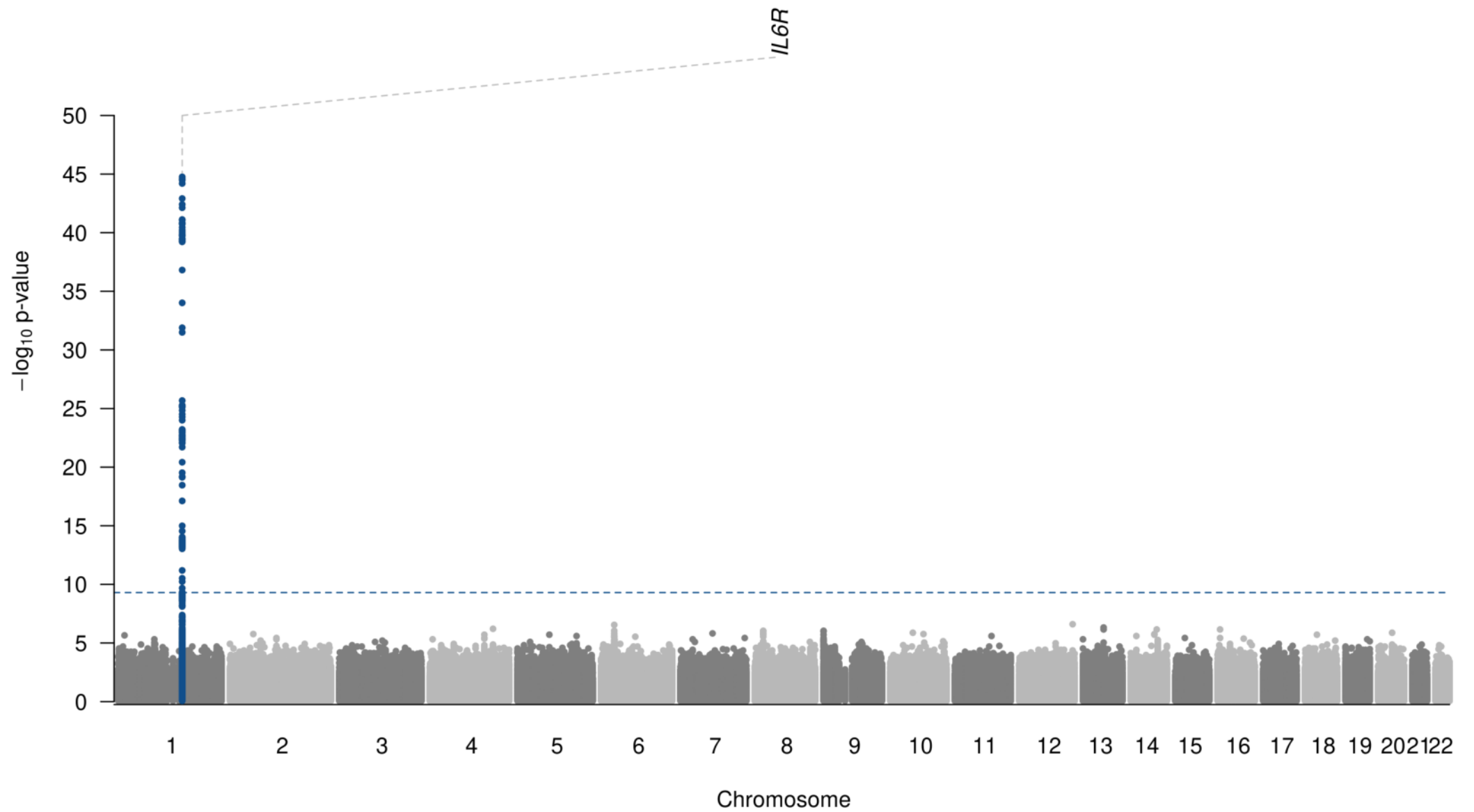
IL-4 (IL4)



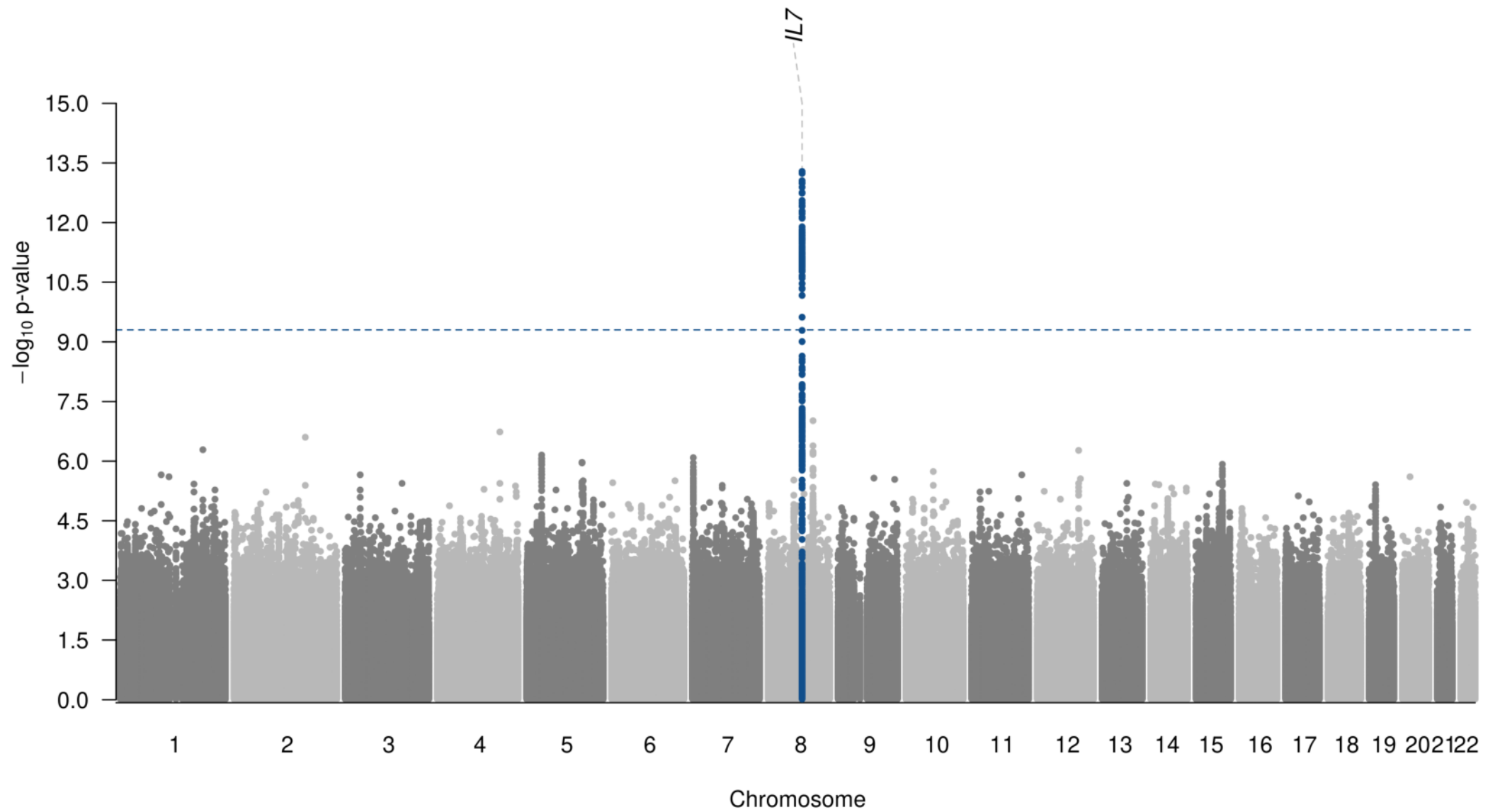
IL-5 (IL5)



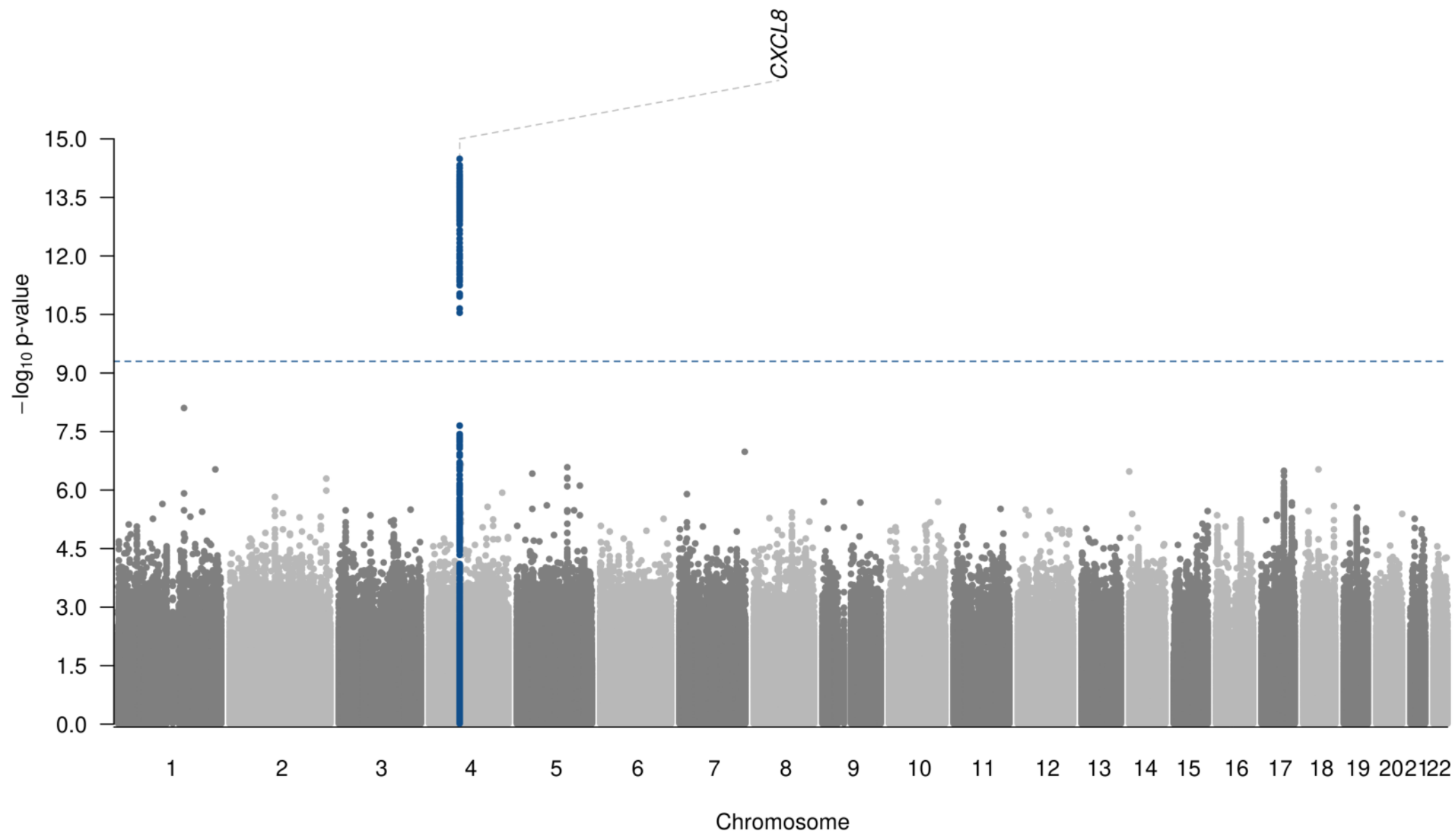
IL-6 (IL6)



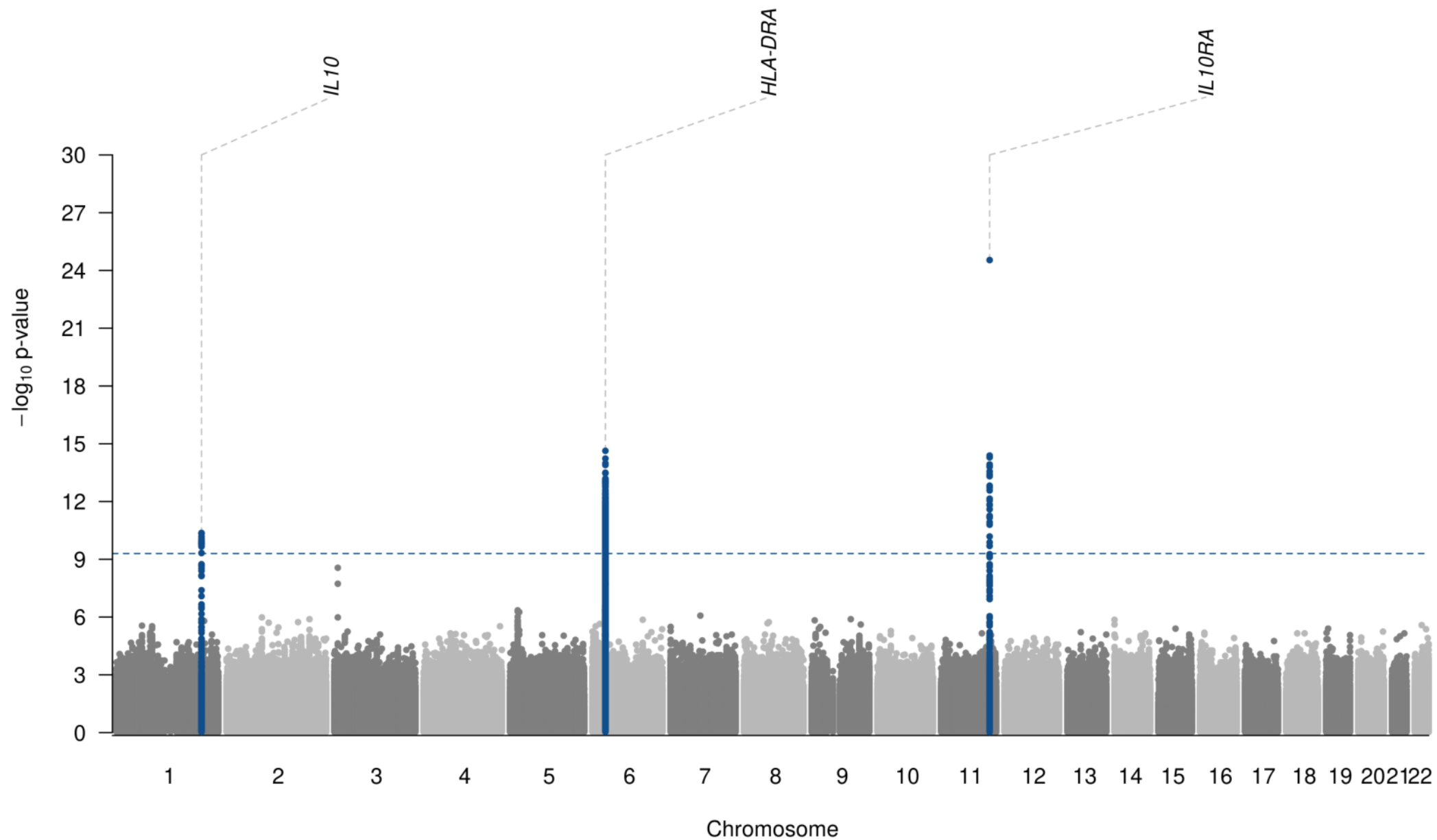
IL-7 (IL7)



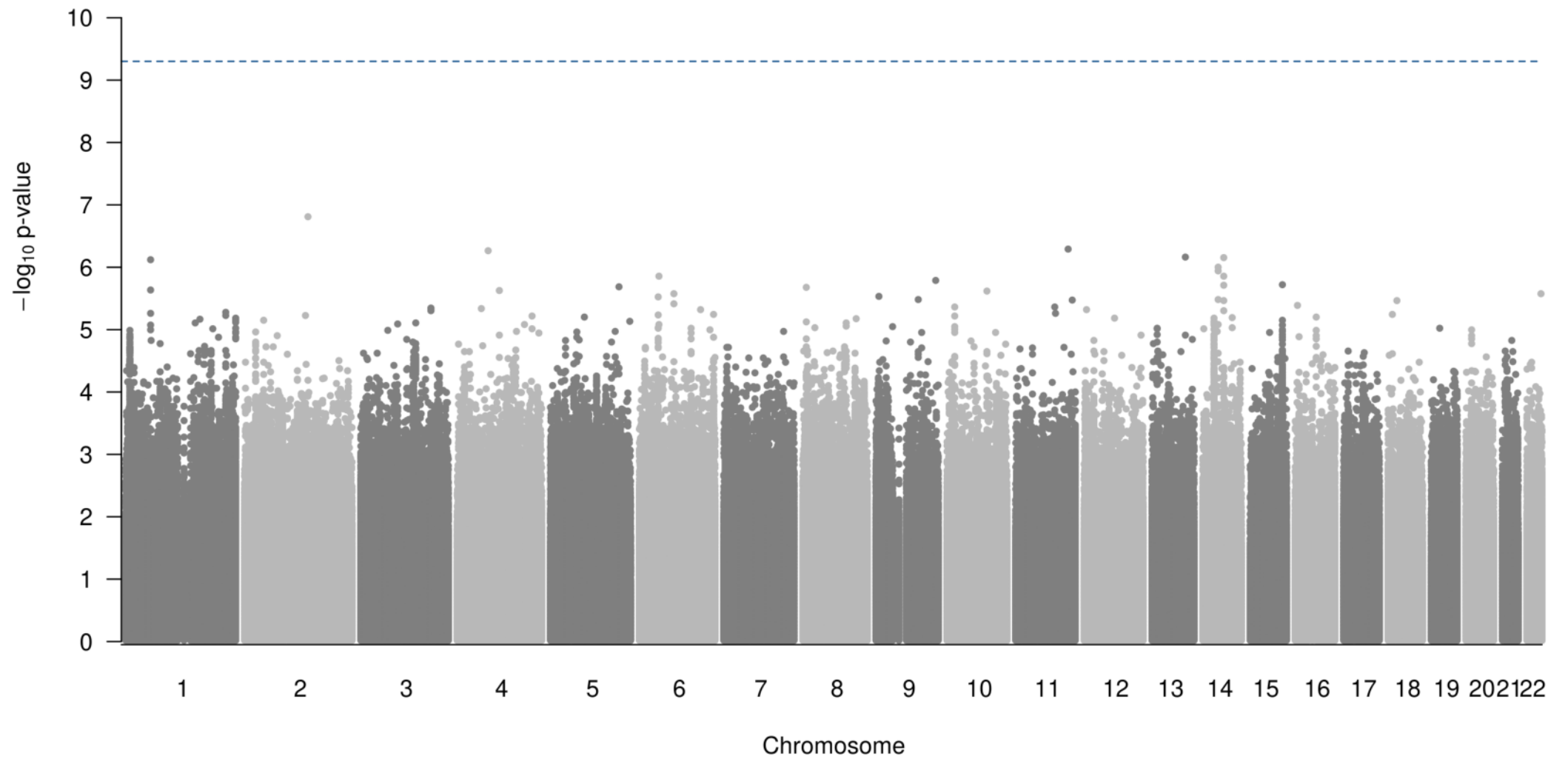
IL-8 (IL8)



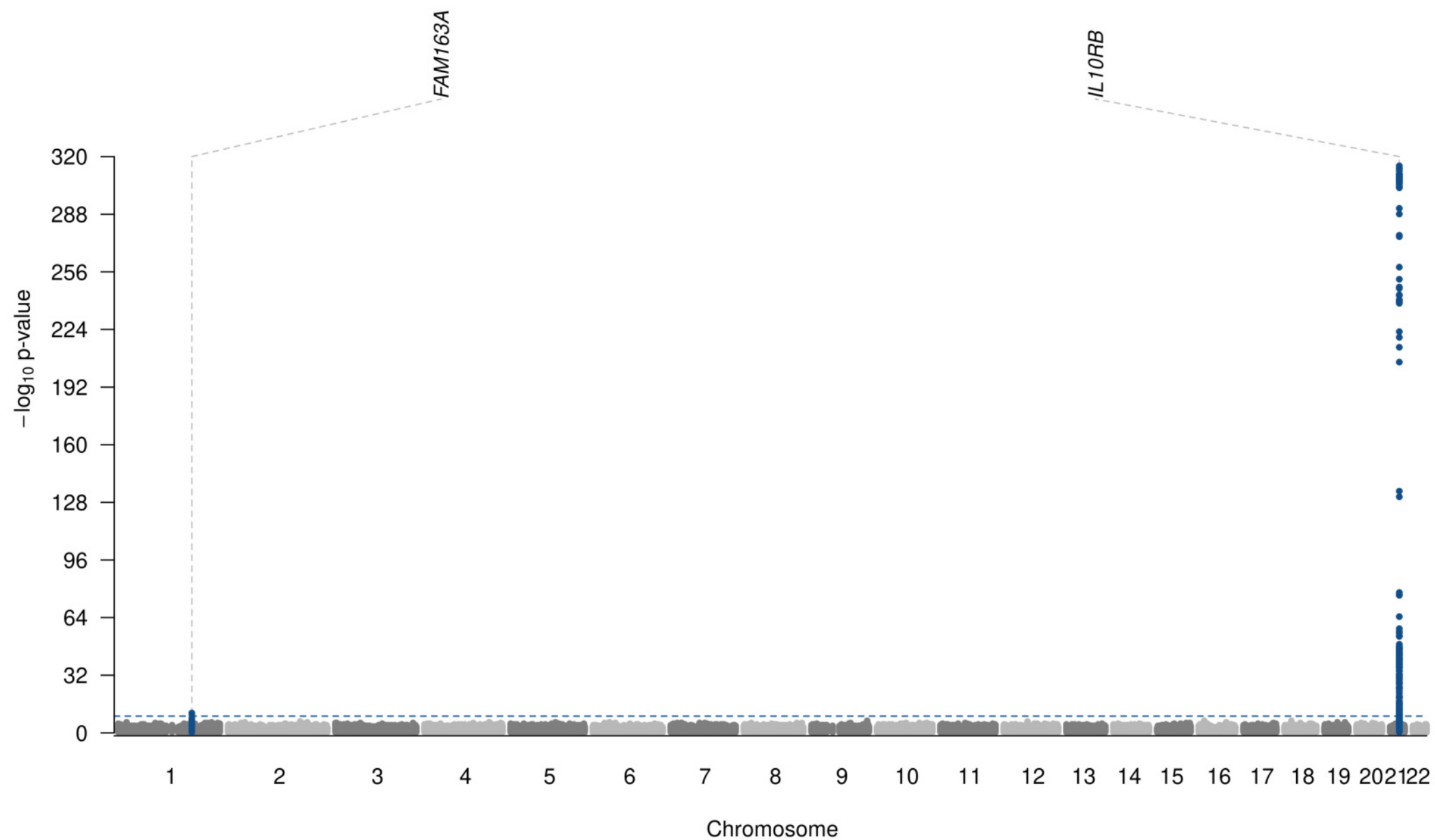
IL-10 (IL10)



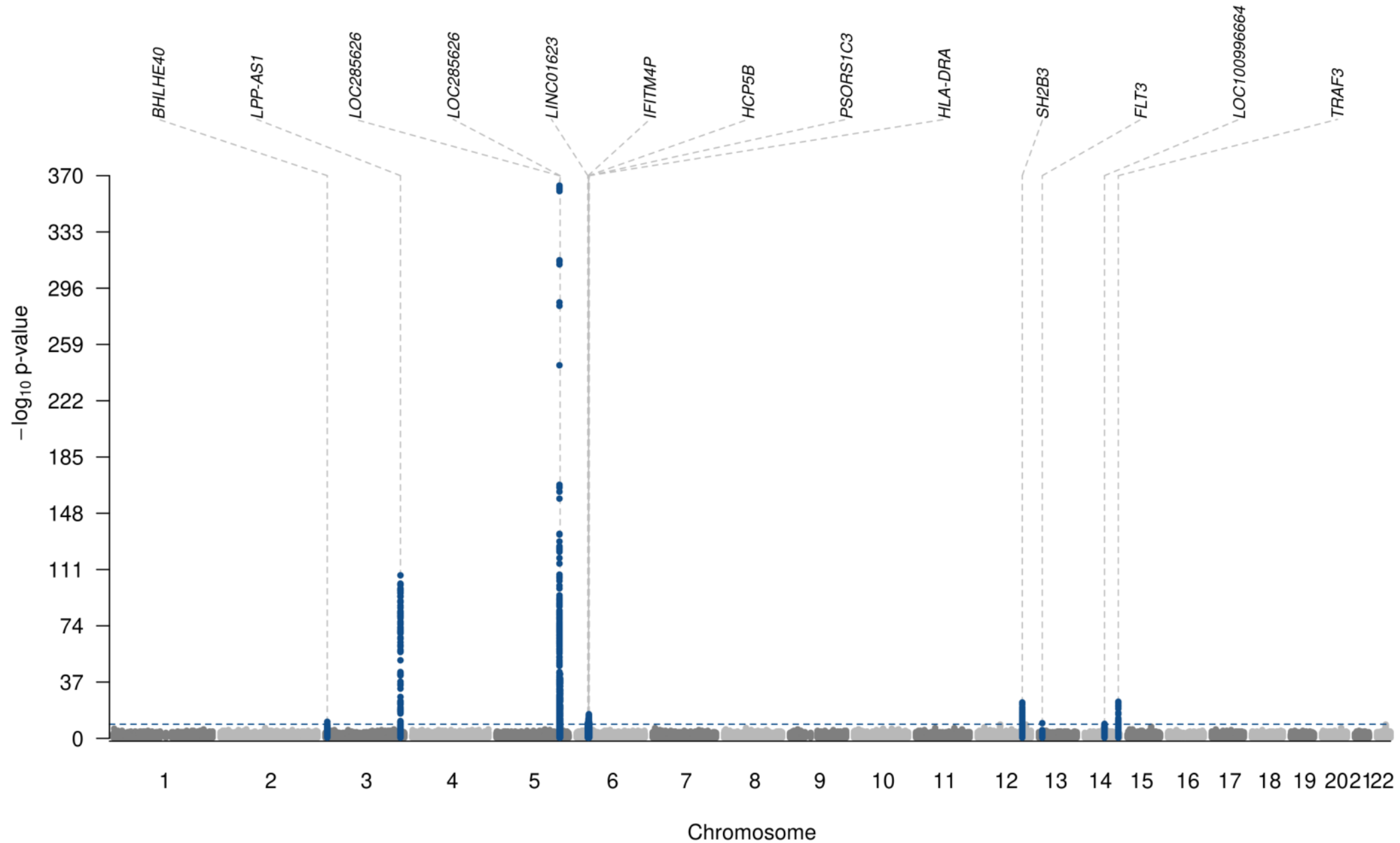
IL-10RA (IL10RA)



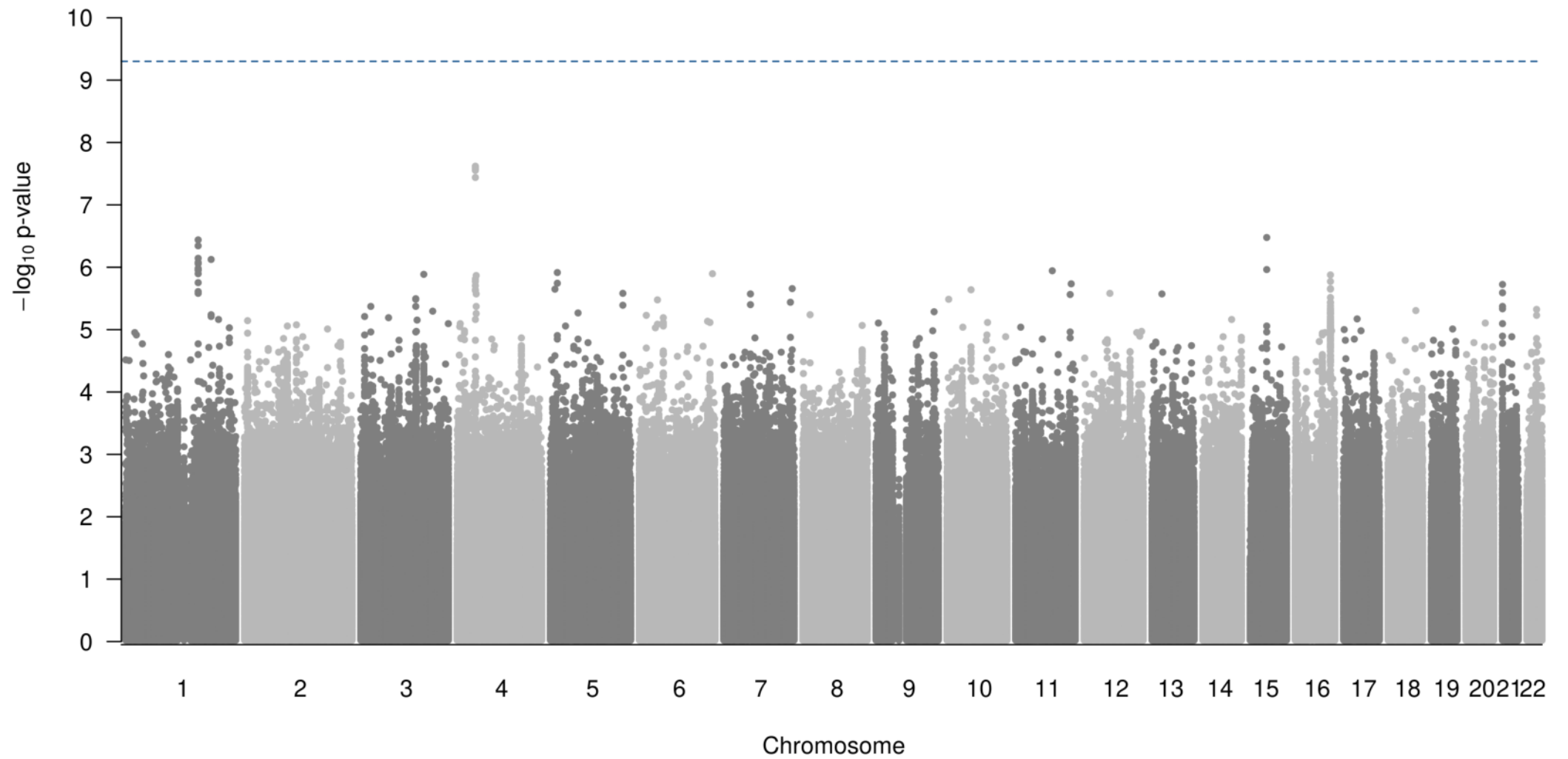
IL10RB (IL10RB)



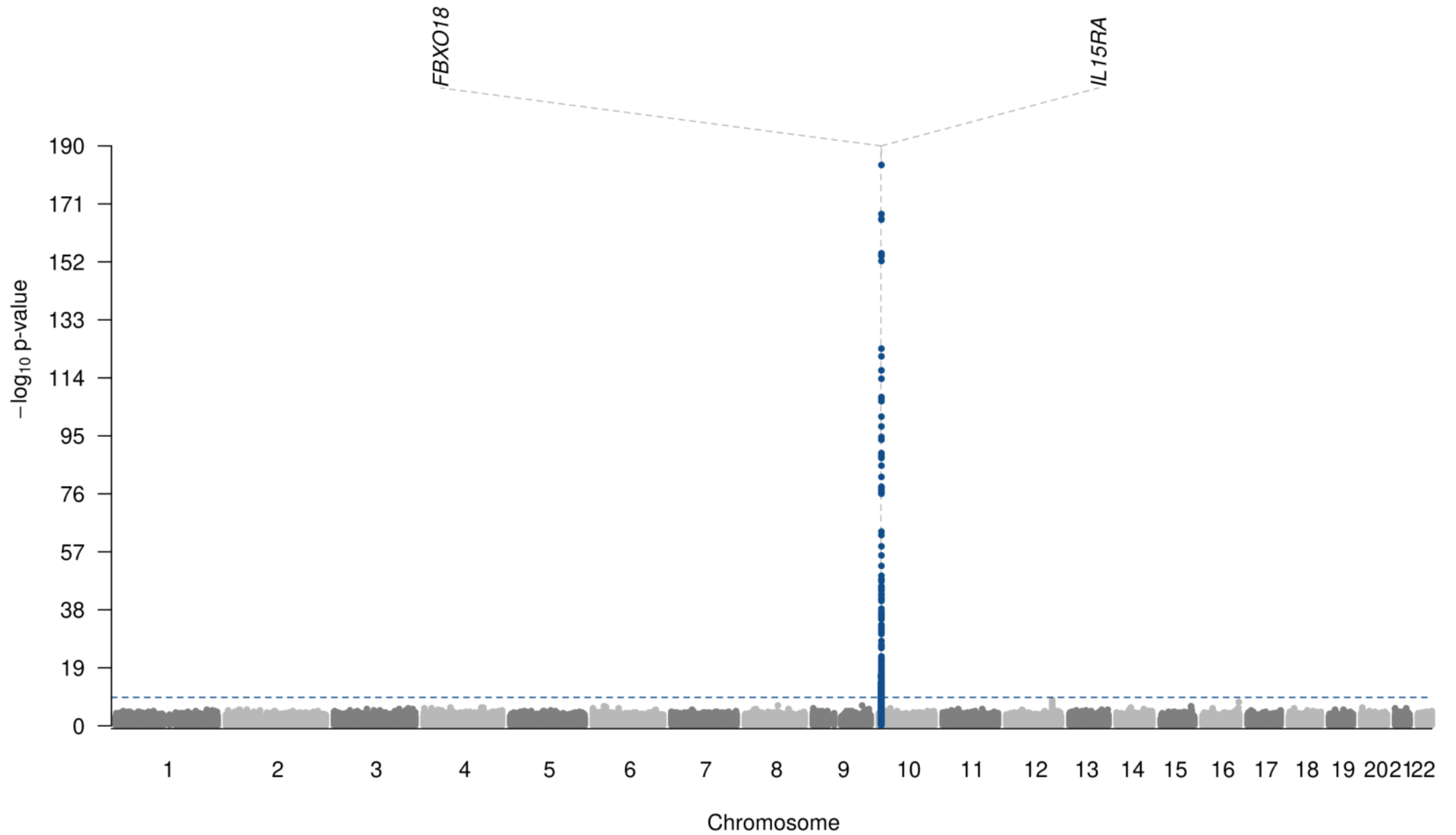
IL-12B (IL12B)



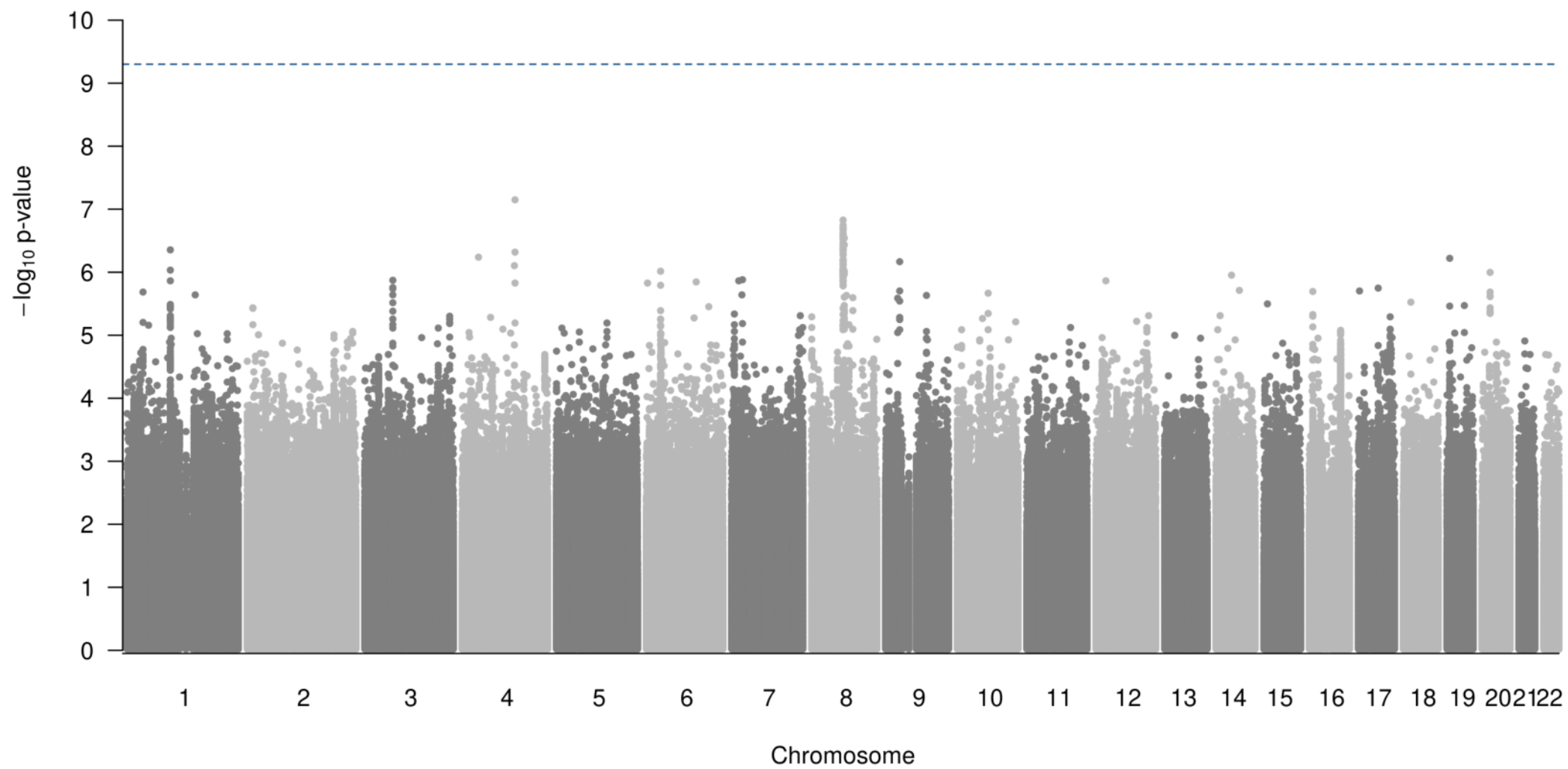
IL-13 (IL13)



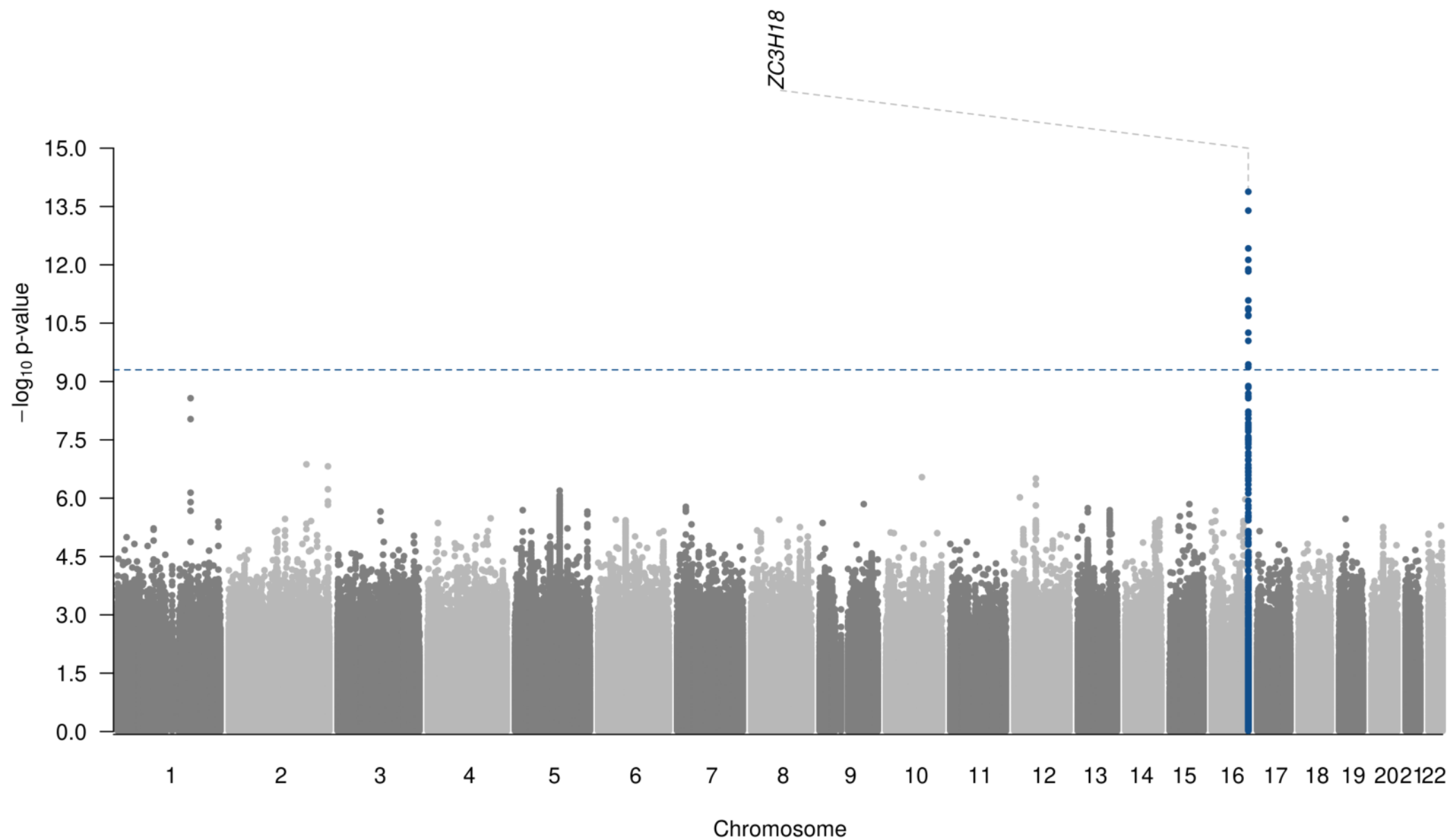
IL-15RA (IL15RA)



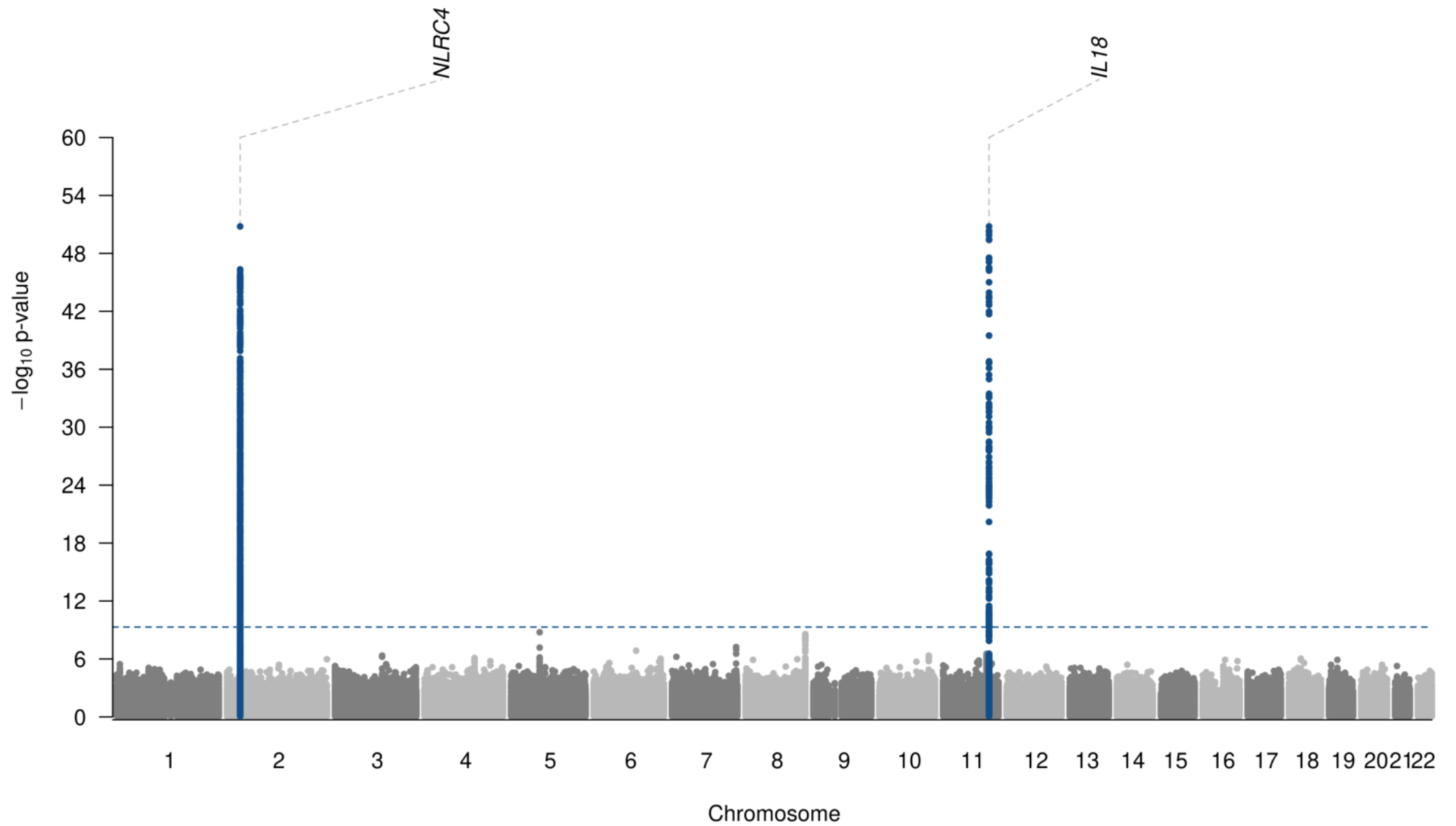
IL-17A (IL17A)



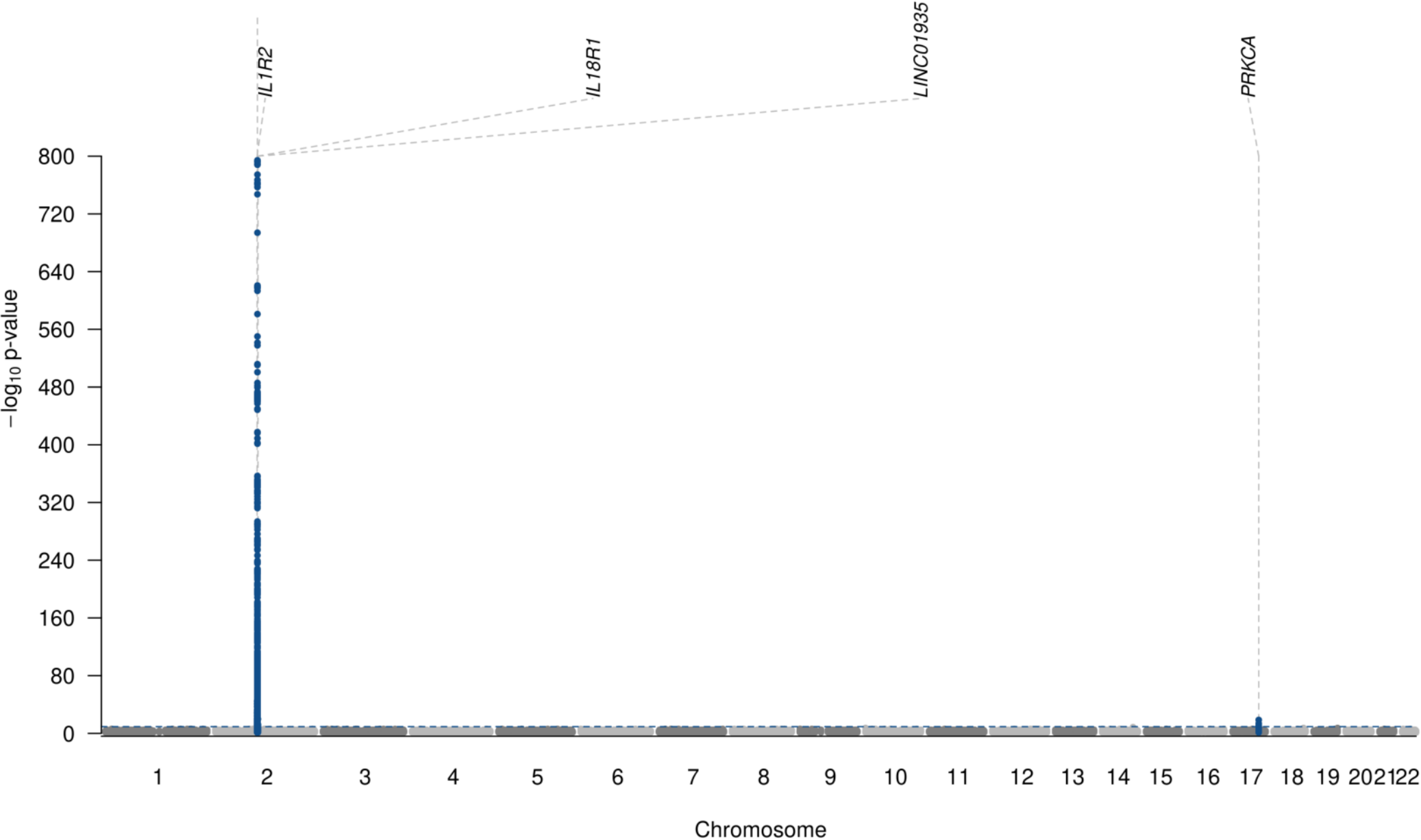
IL-17C (IL17C)



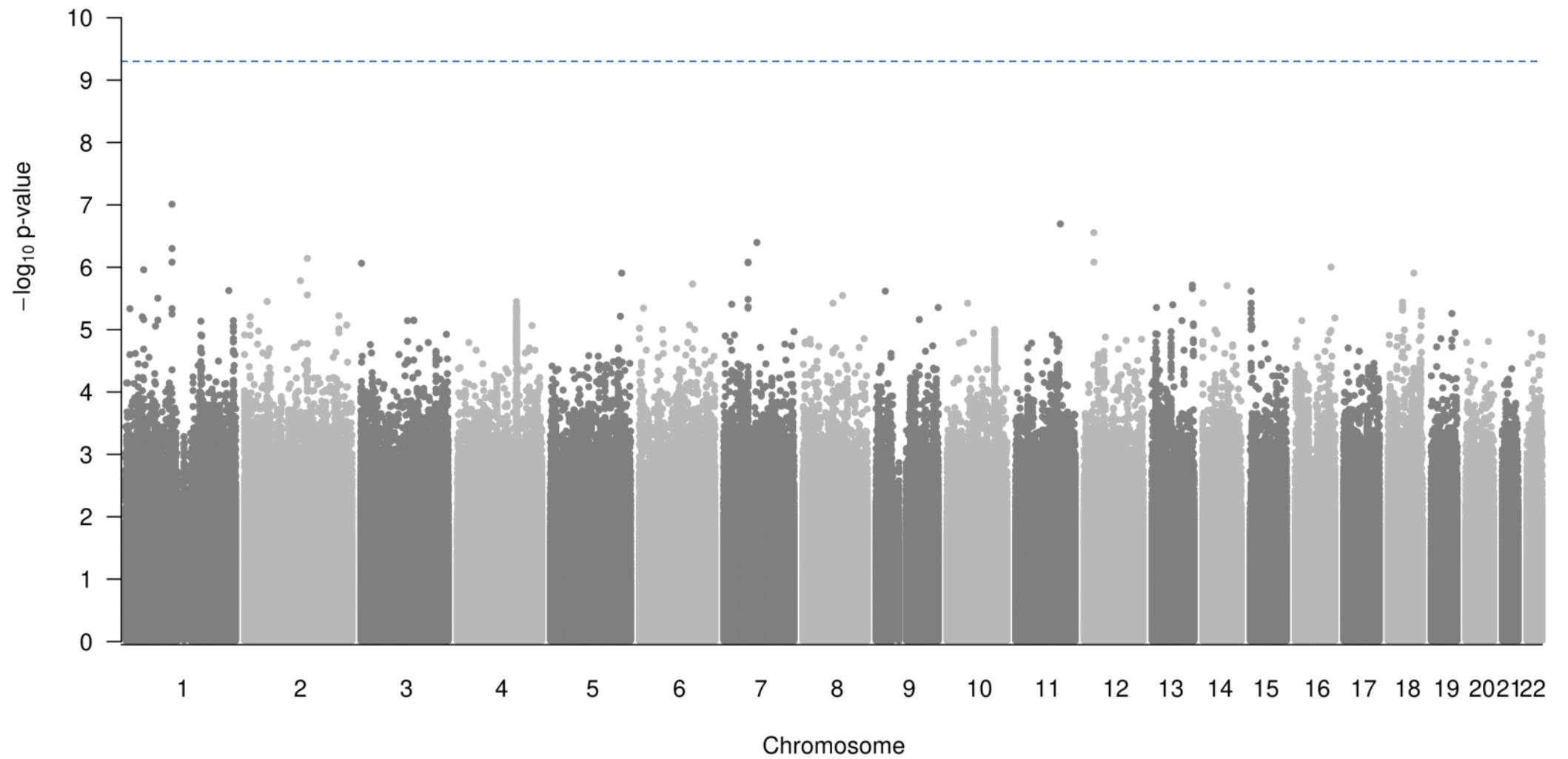
IL-18 (IL18)



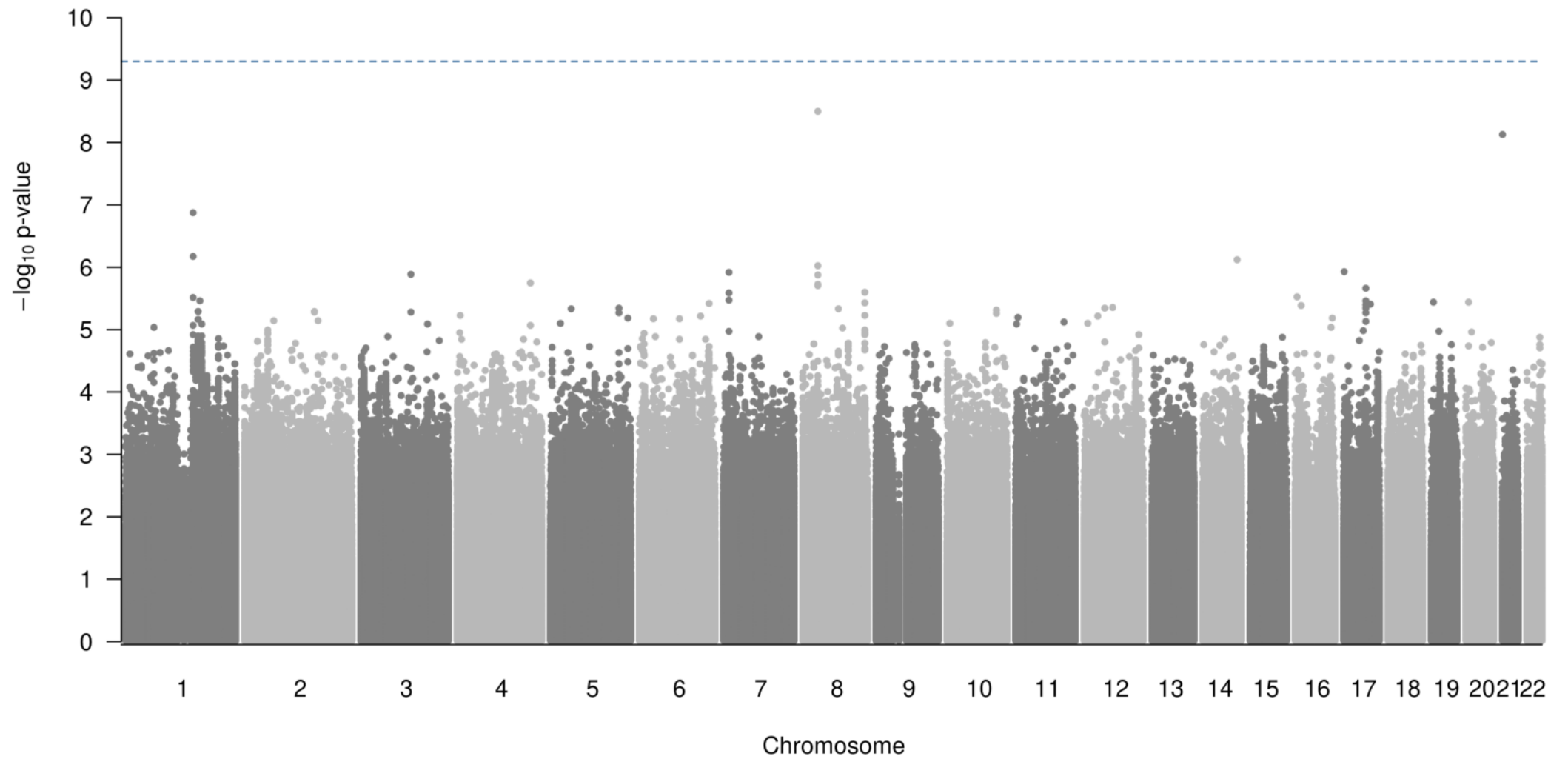
IL-18R1 (IL18R1)



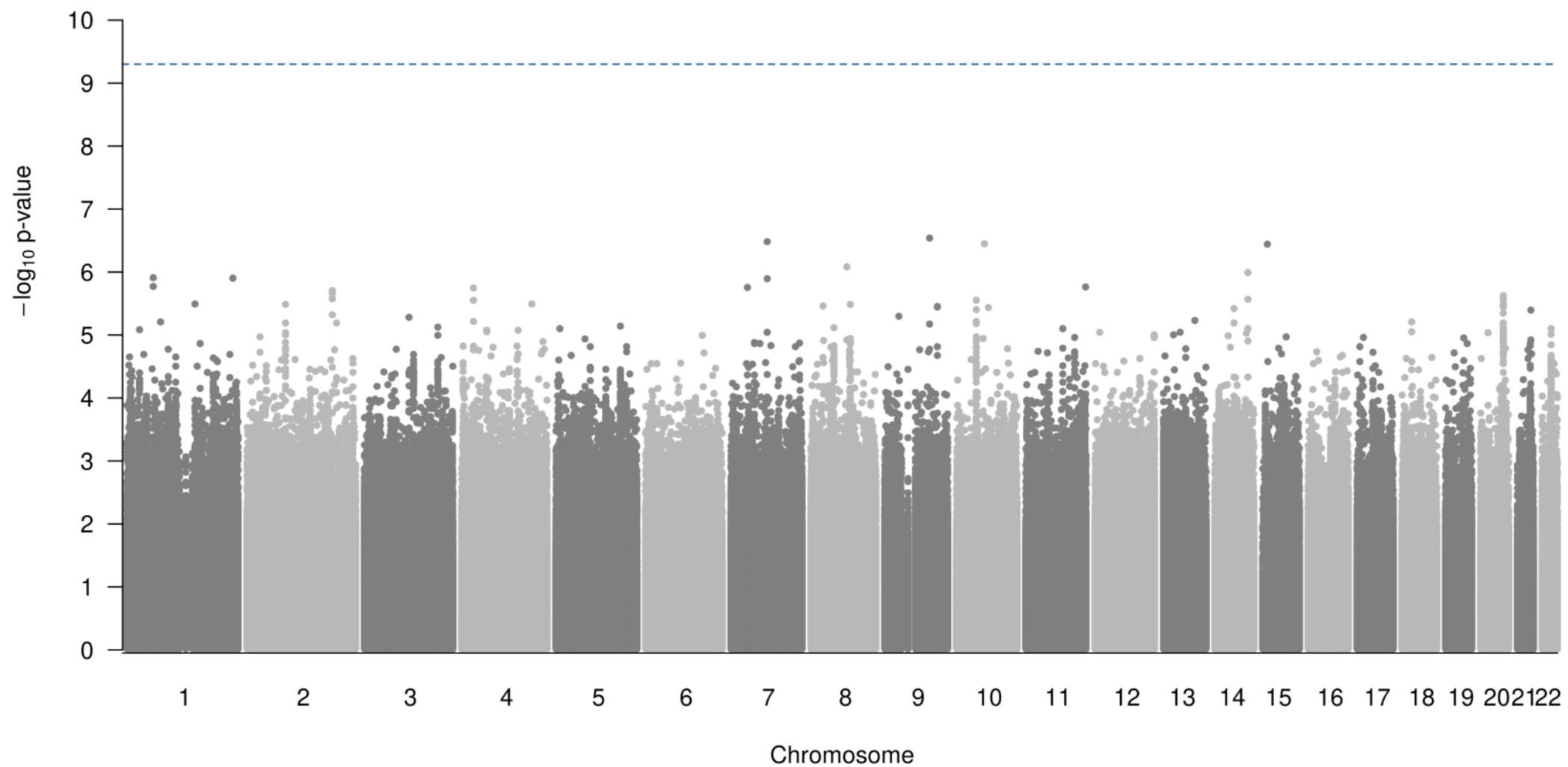
IL-20 (IL20)



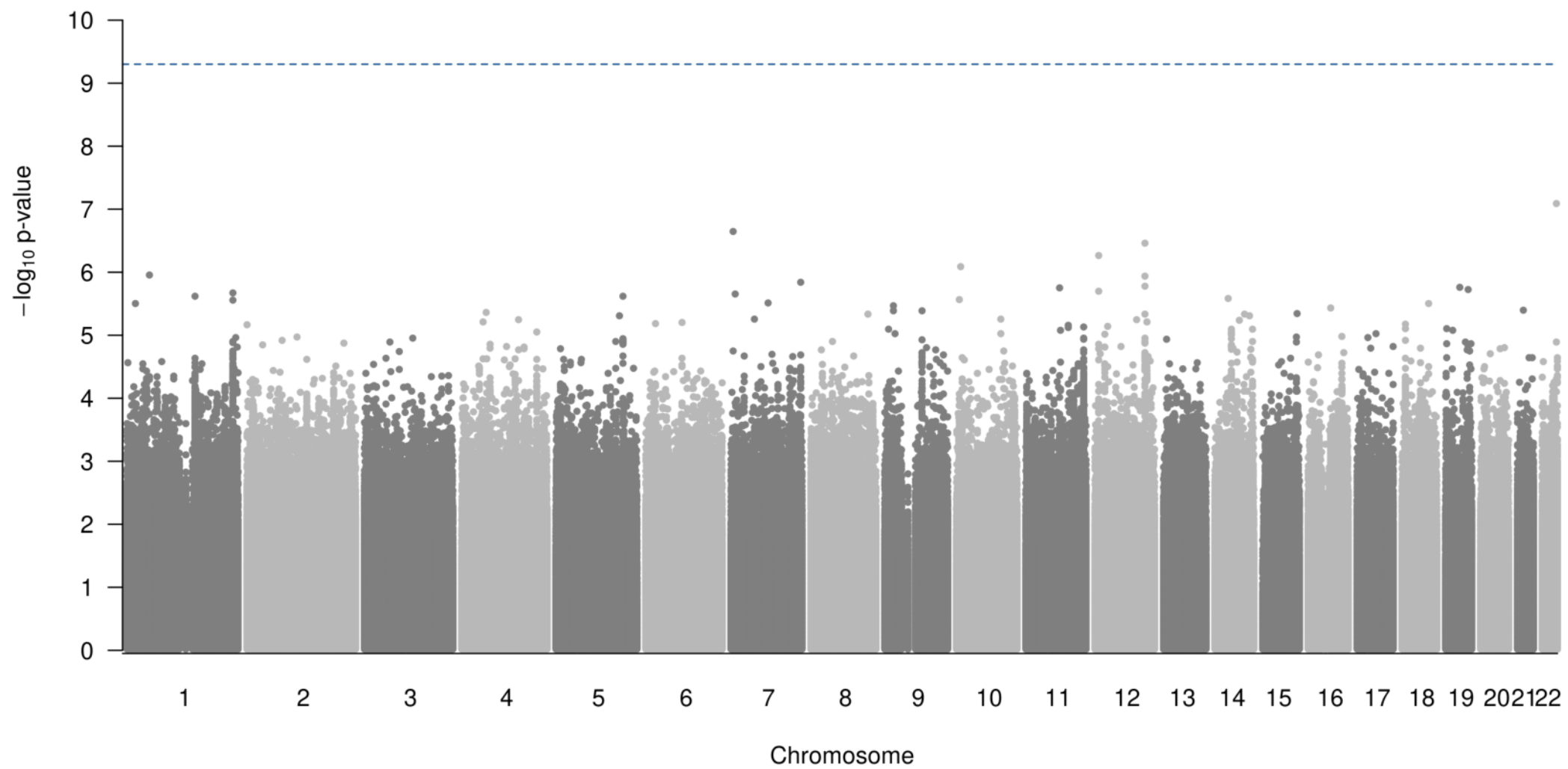
IL-20RA (IL20RA)



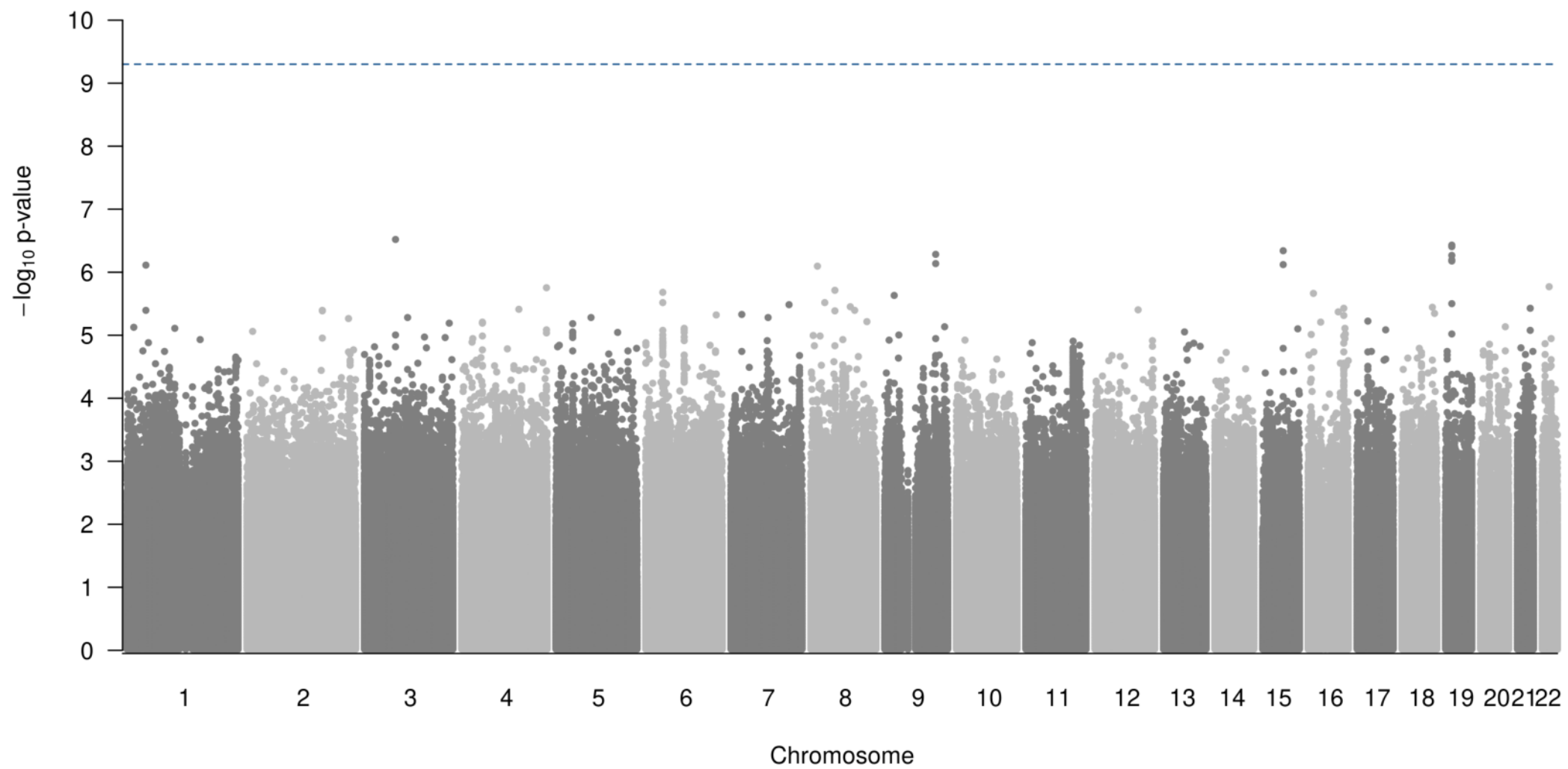
IL-22RA1 (IL22RA1)



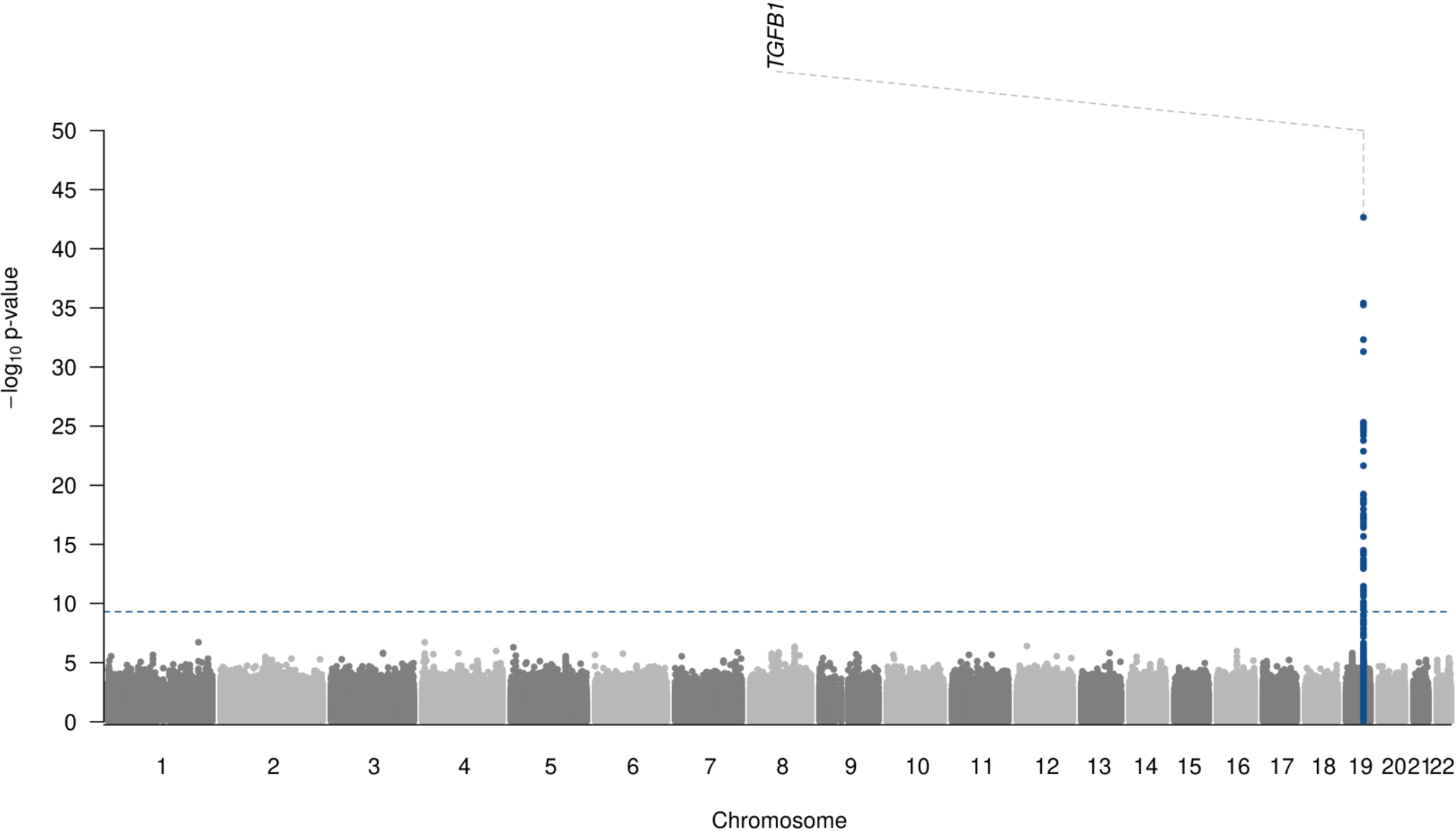
IL-24 (IL24)



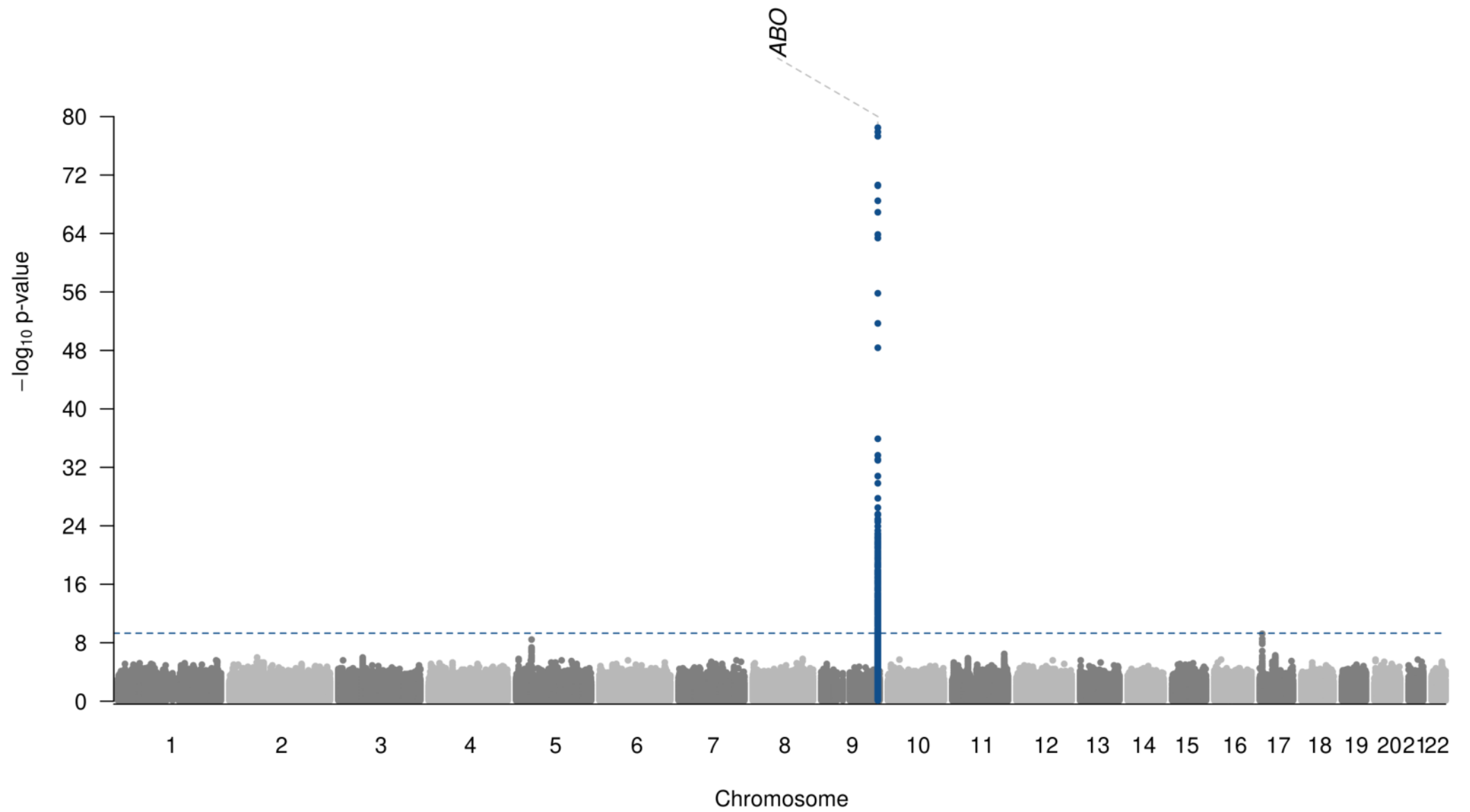
IL-33 (IL33)



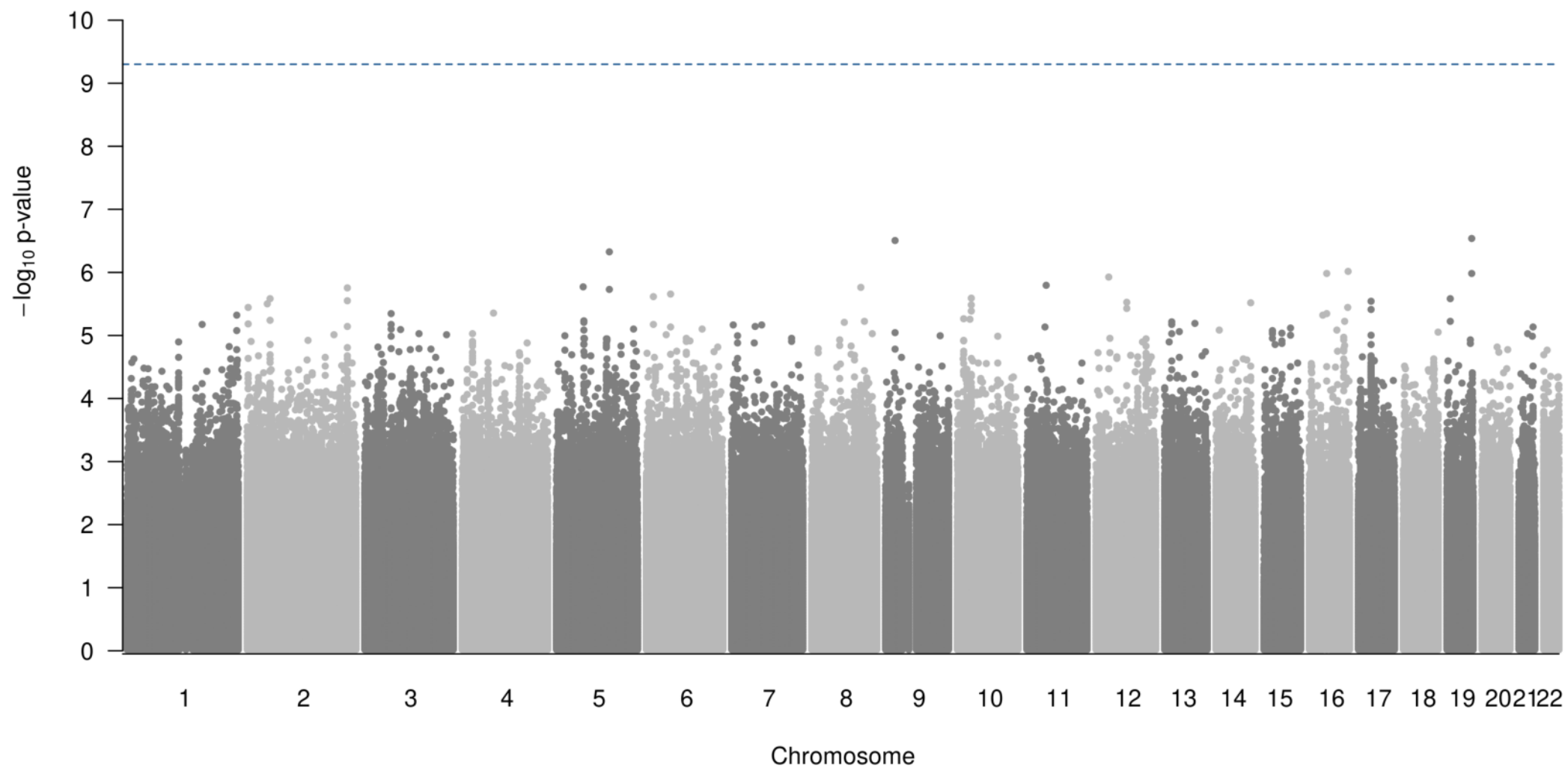
LAP (TGFB1)



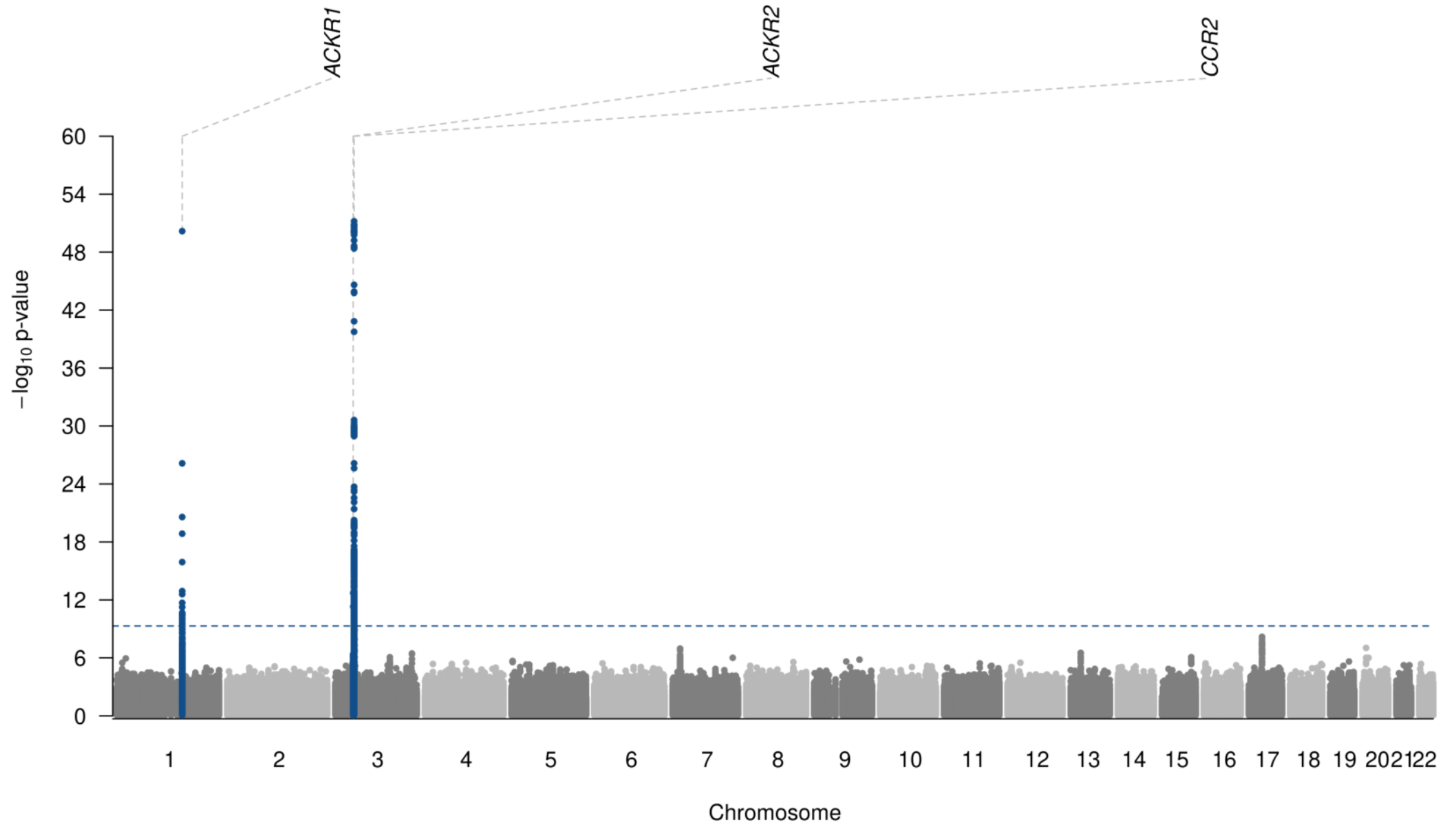
LIF-R (LIFR)



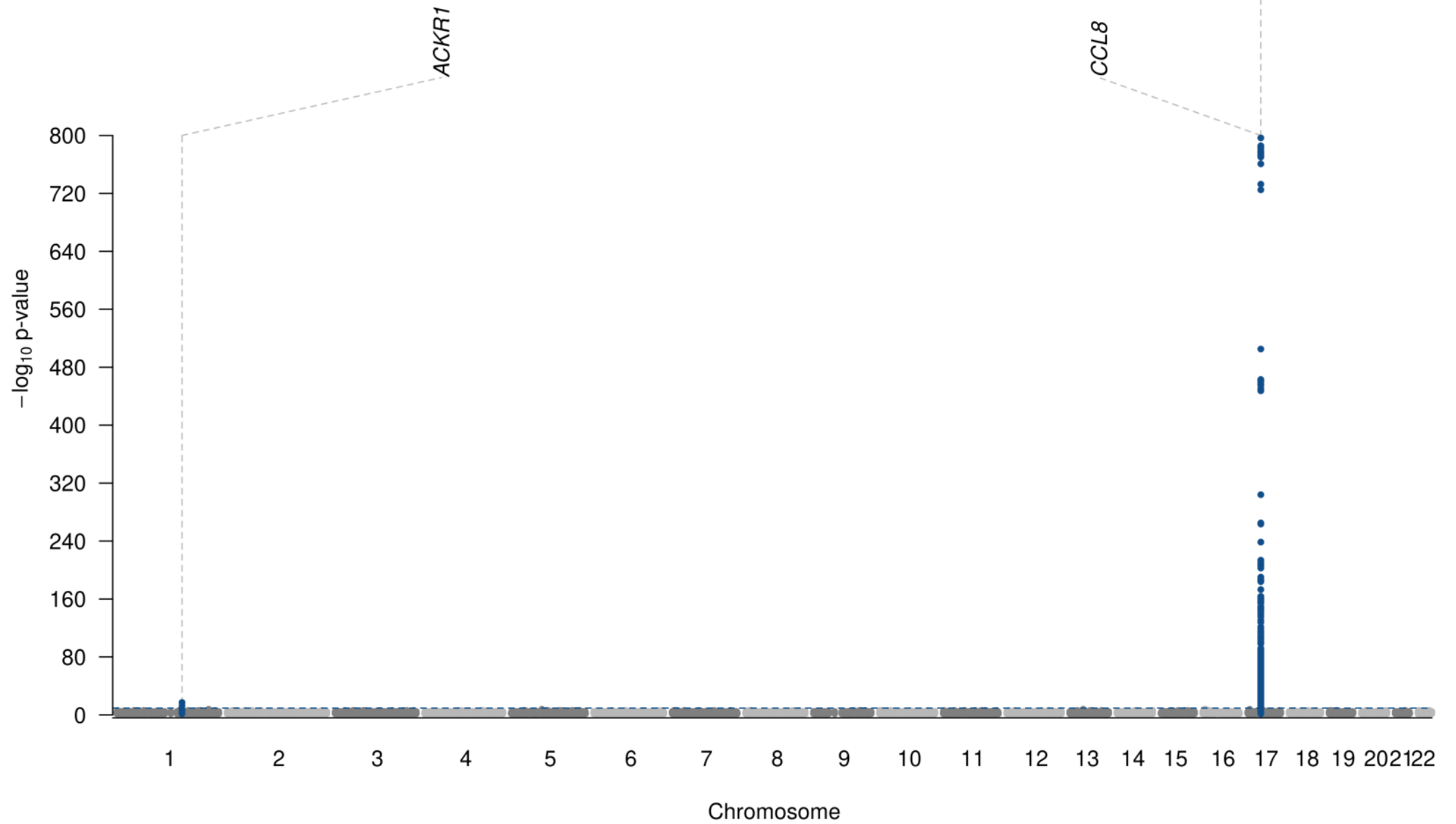
LIF (LIF)



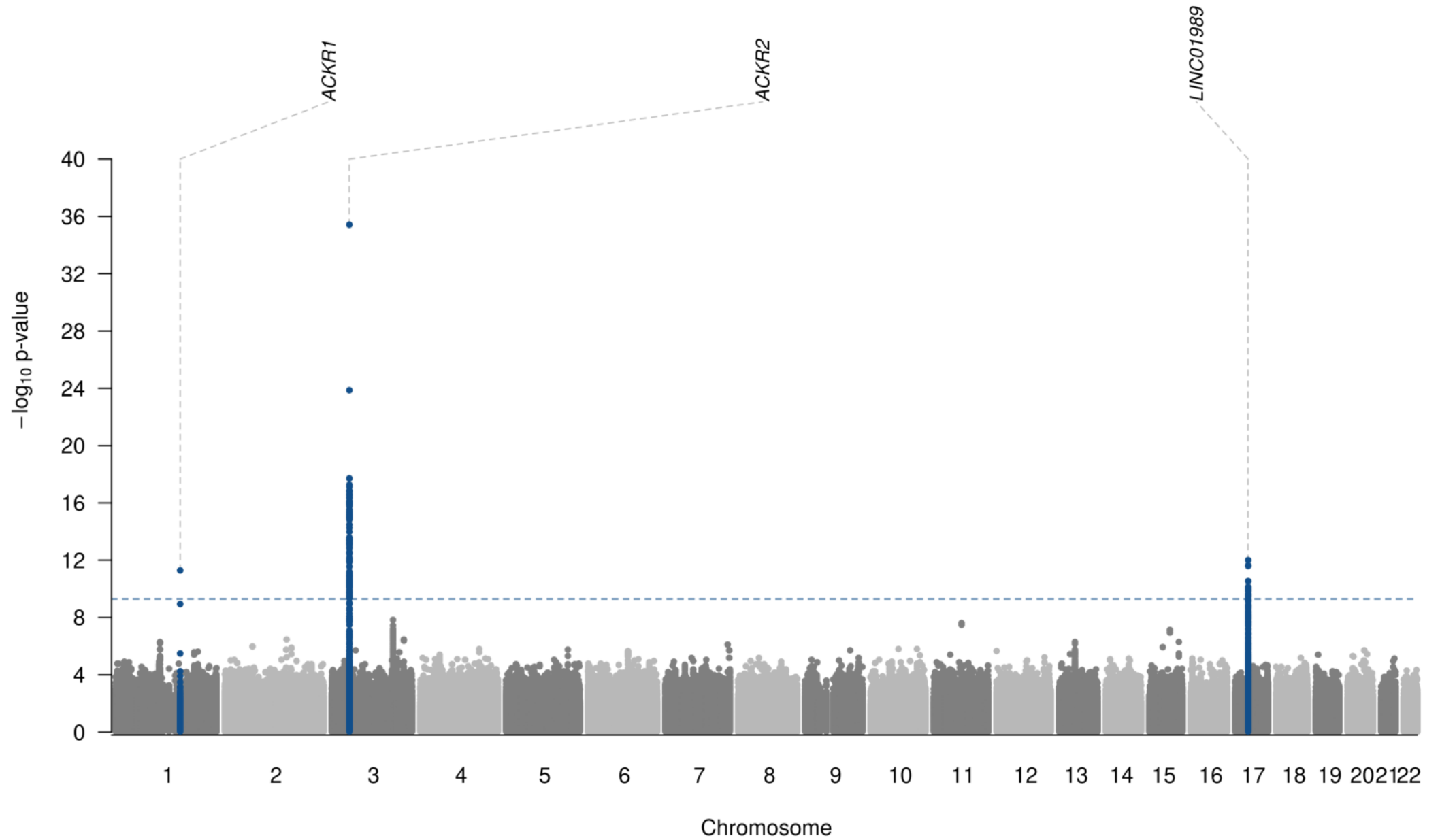
MCP-1 (CCL2)



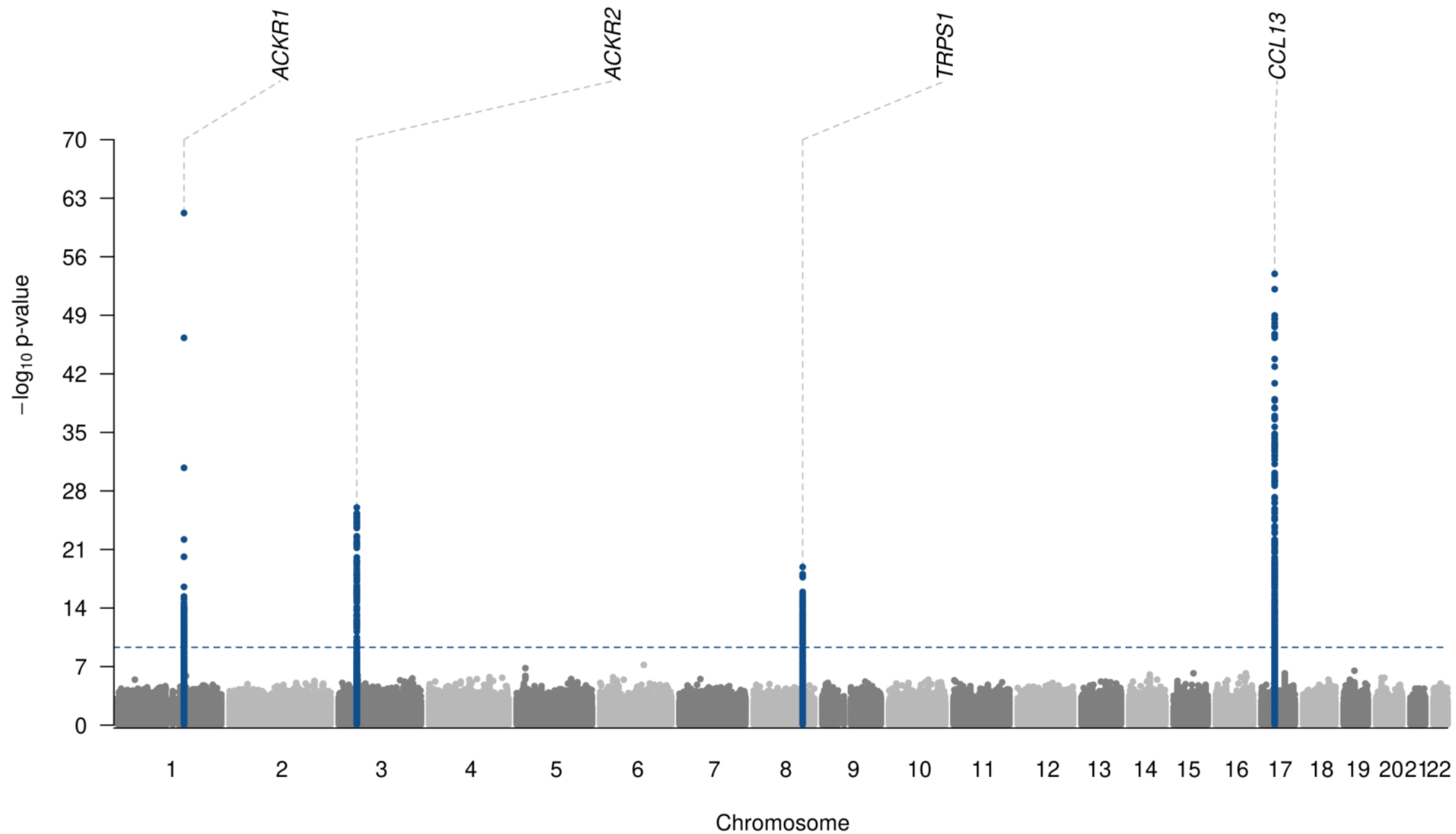
MCP-2 (CCL8)



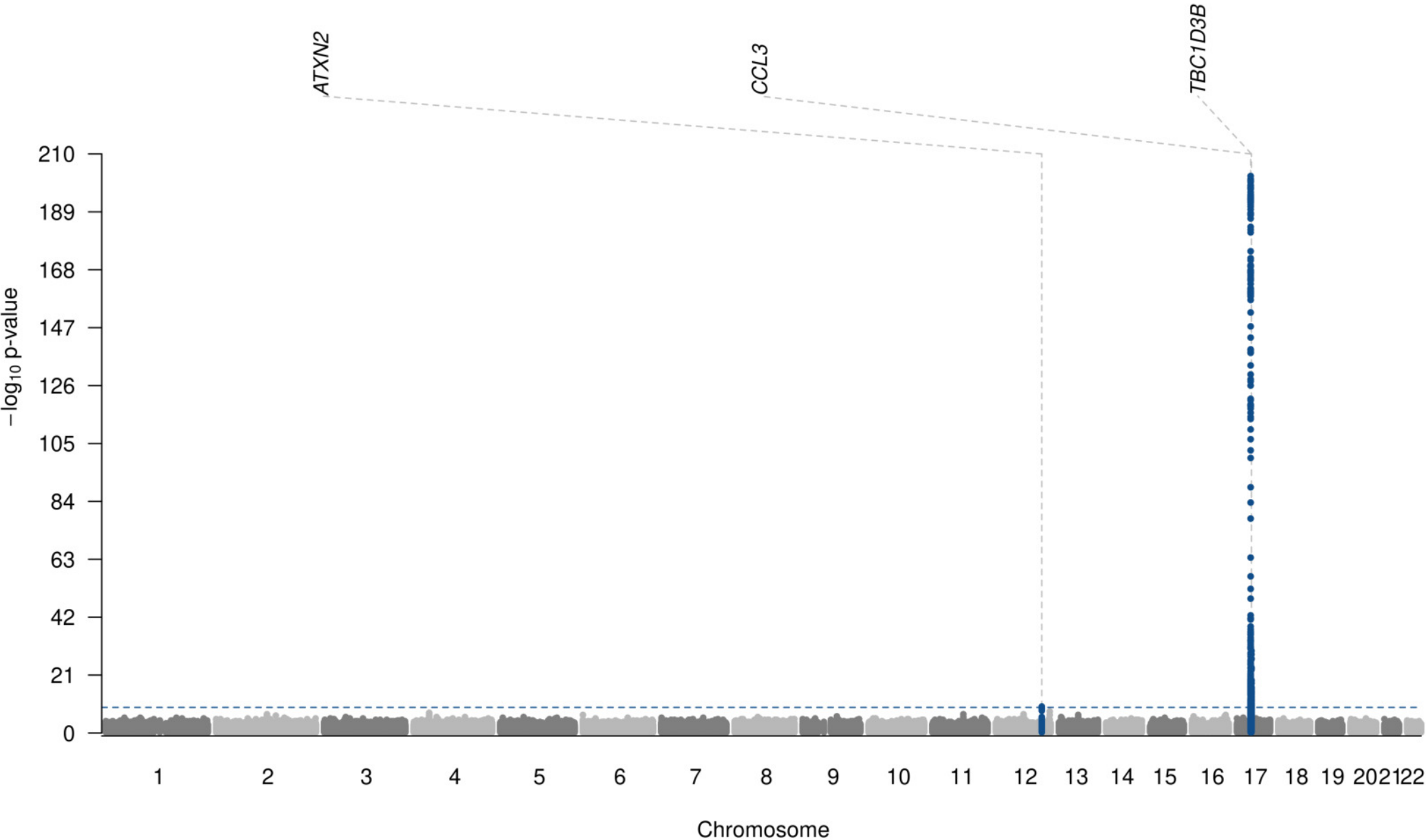
MCP-3 (CCL7)



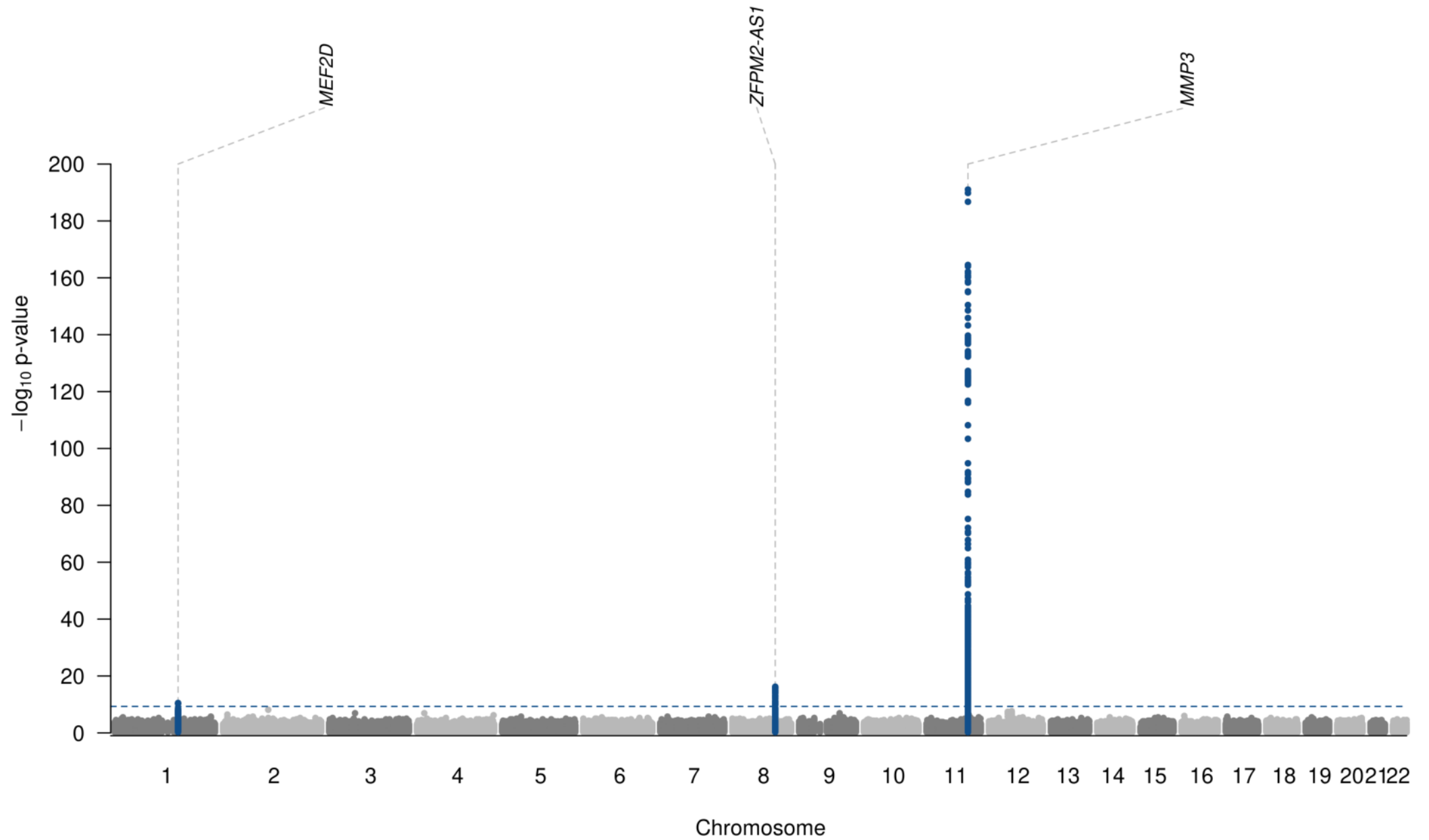
MCP-4 (CCL13)



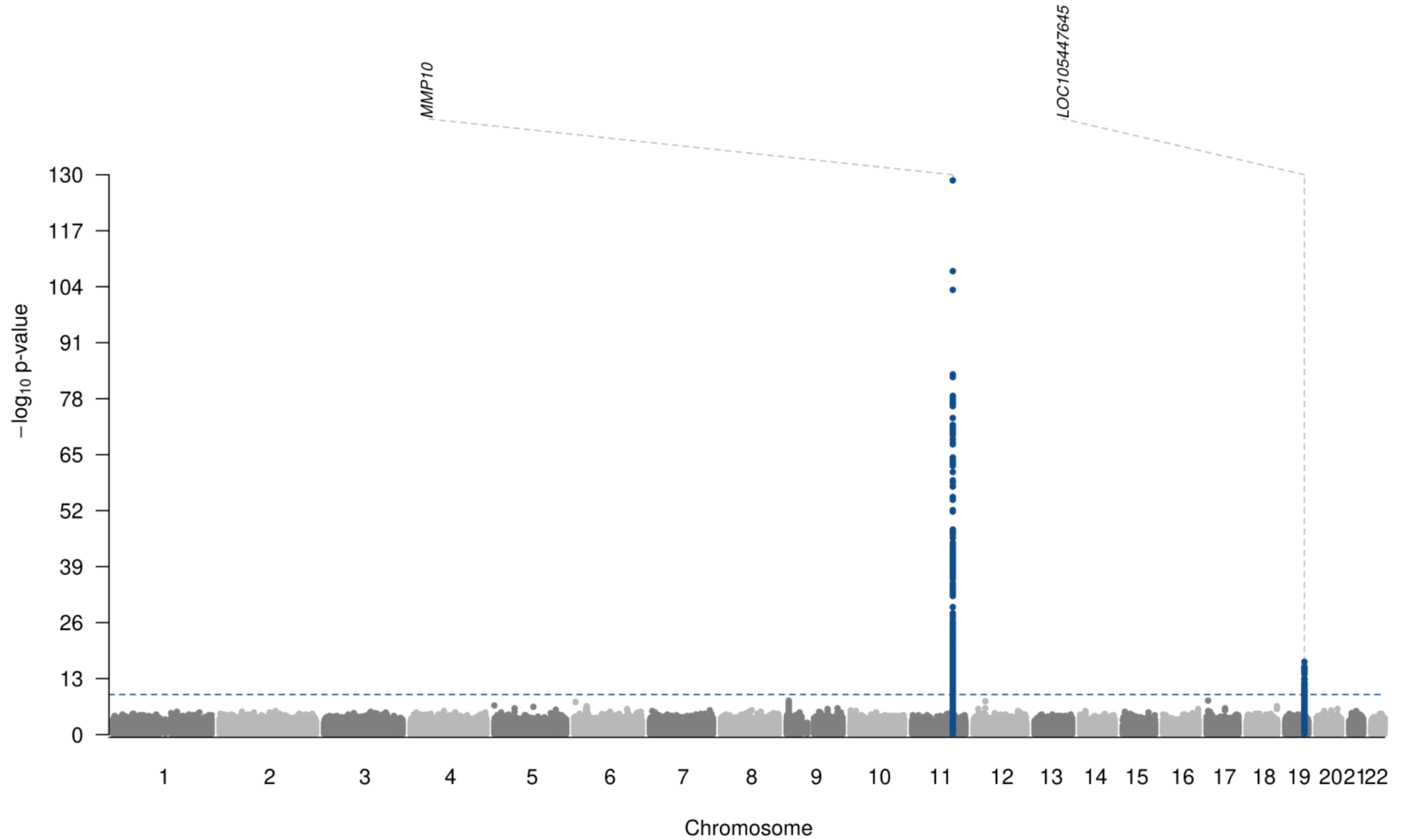
MIP-1 (CCL3)



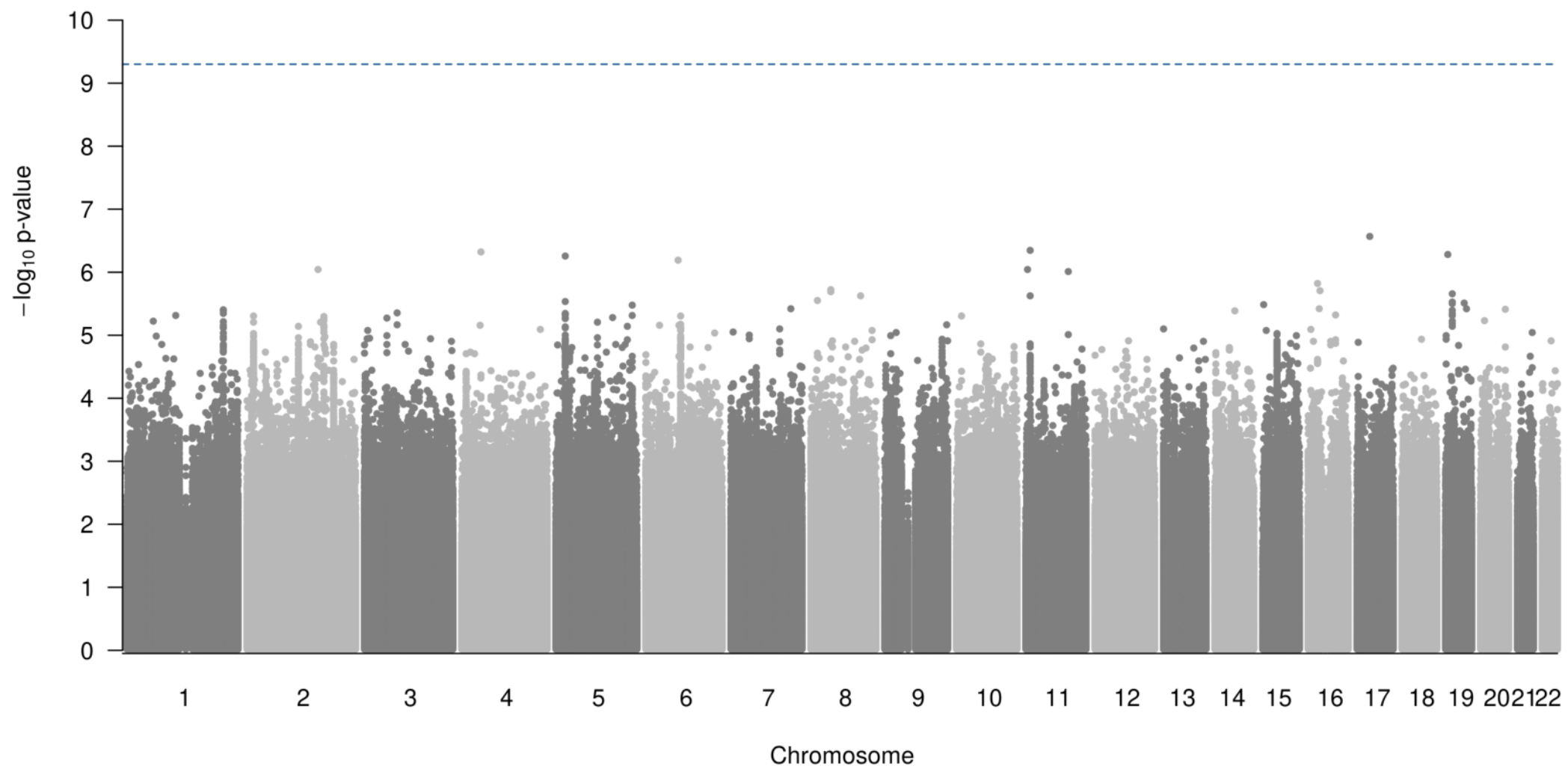
MMP-1 (MMP1)



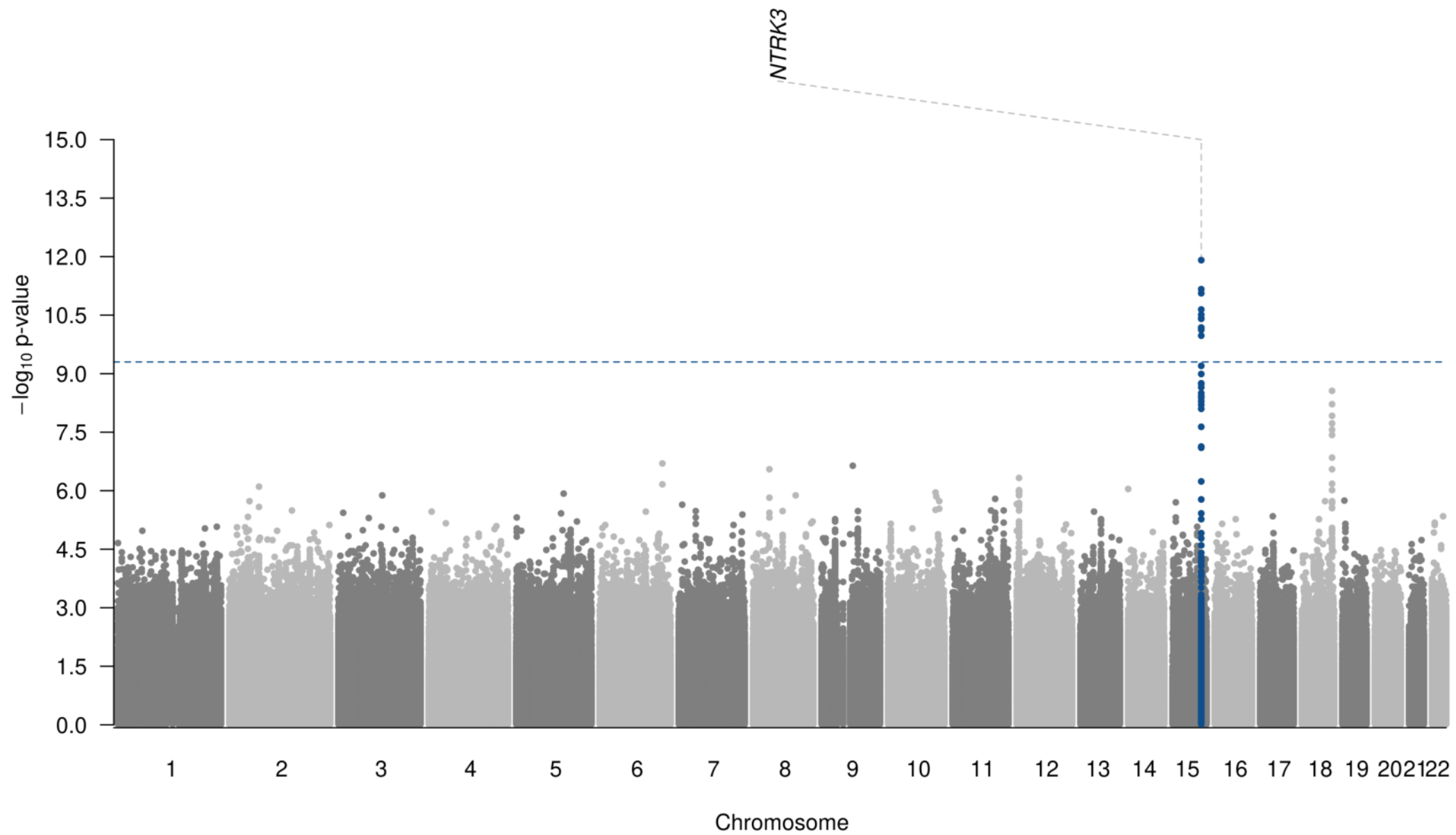
MMP-10 (MMP10)



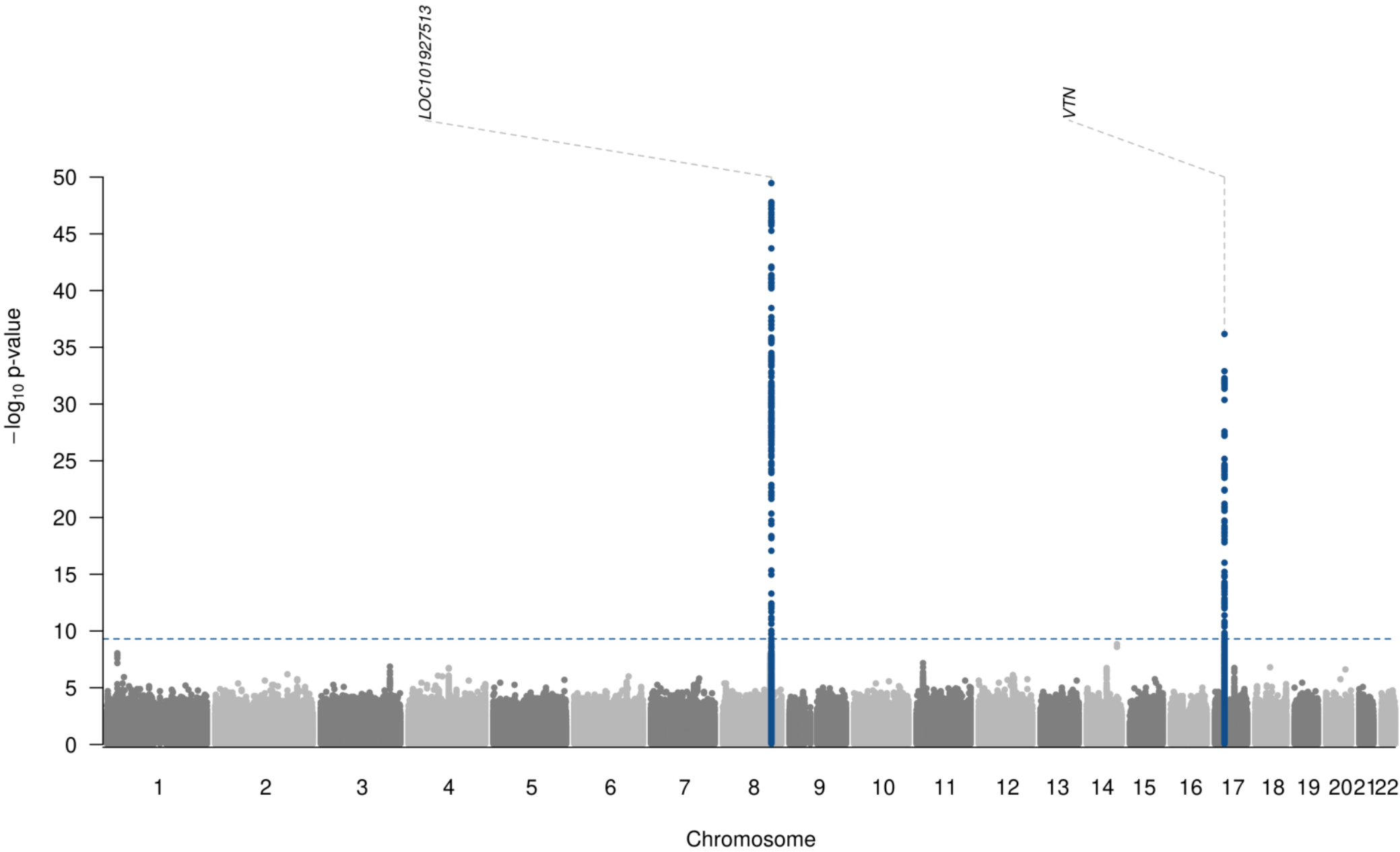
NRTN (NRTN)



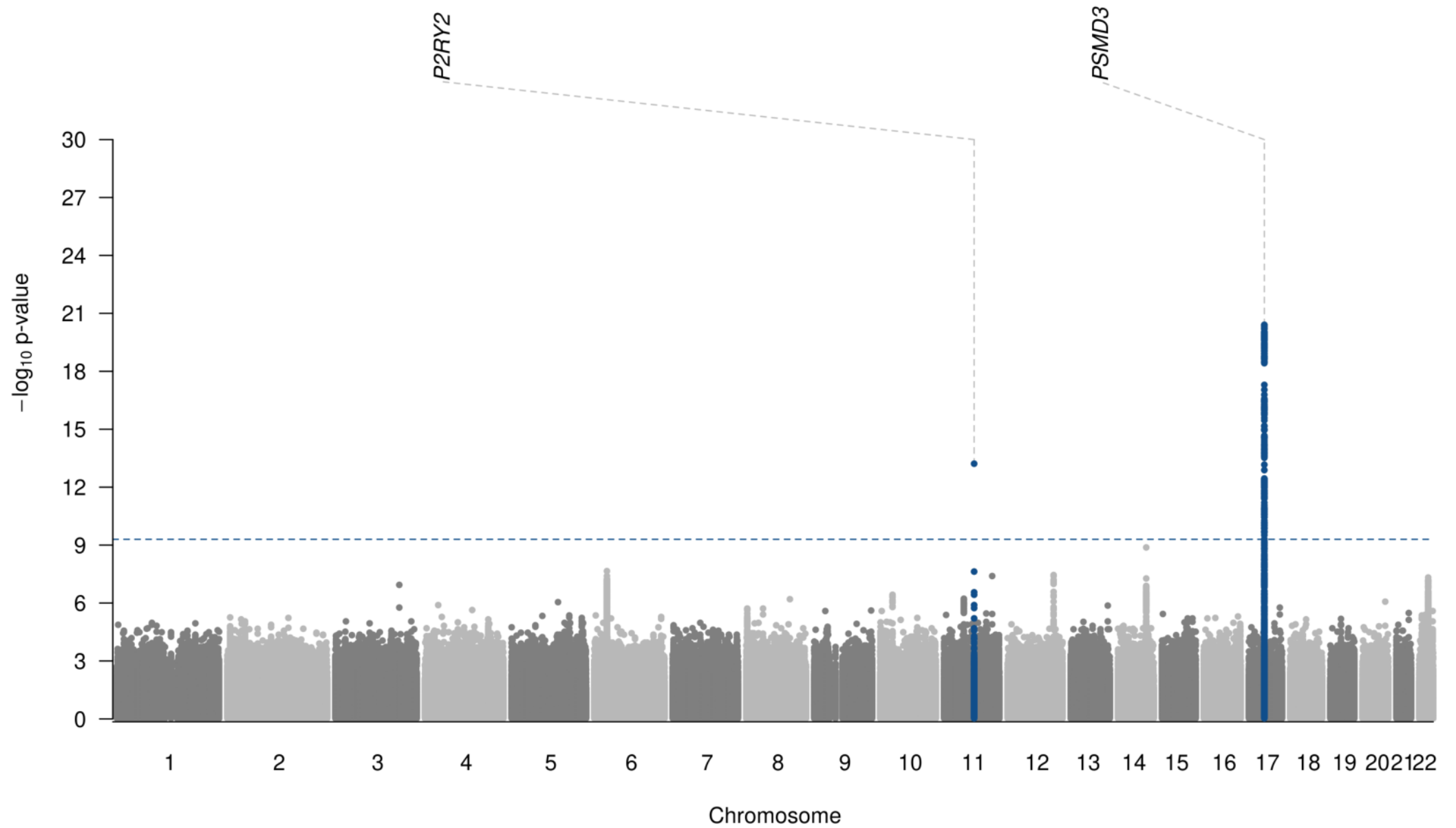
NT-3 (NTF3)



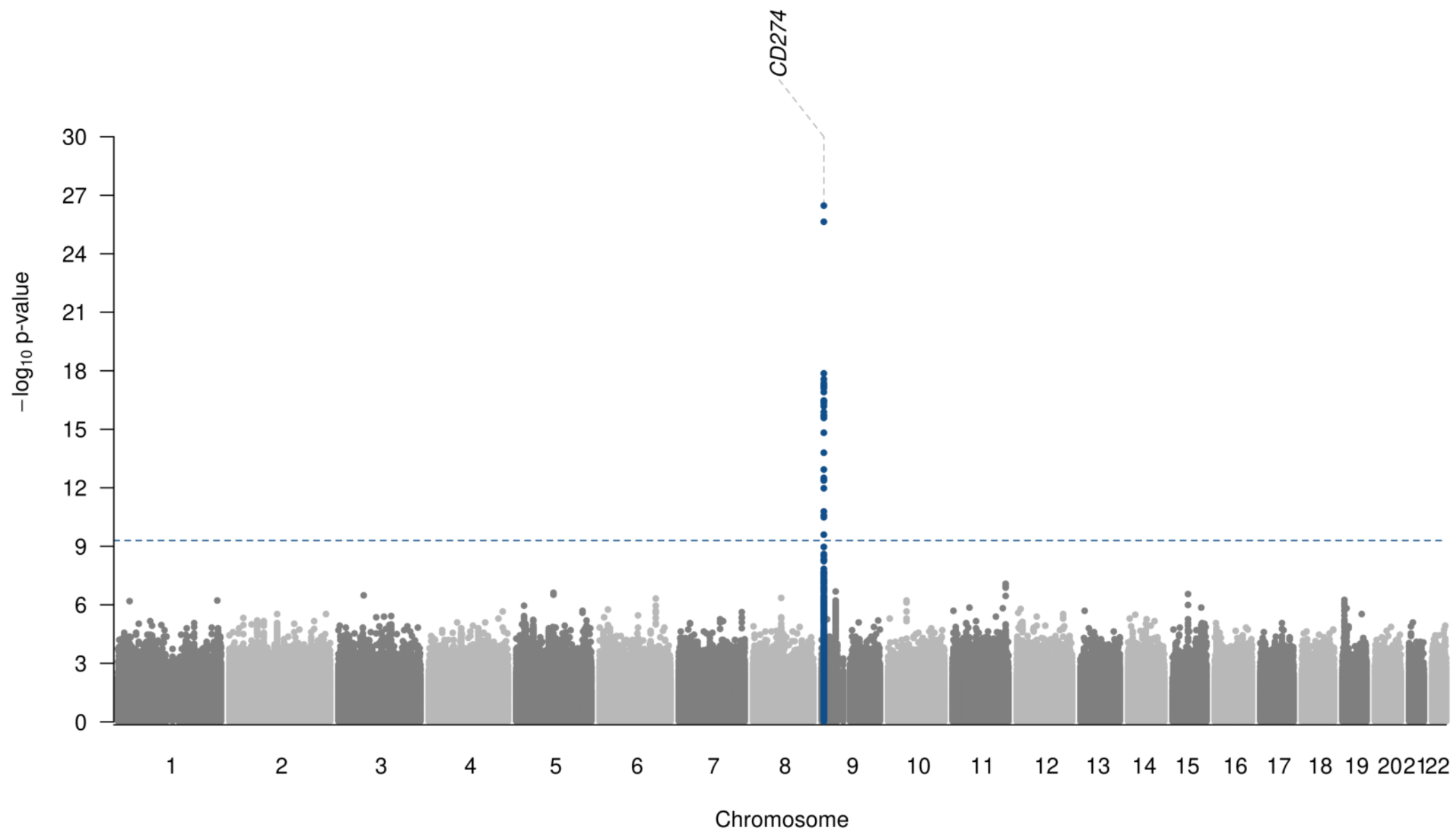
OPG (TNFRSF11B)



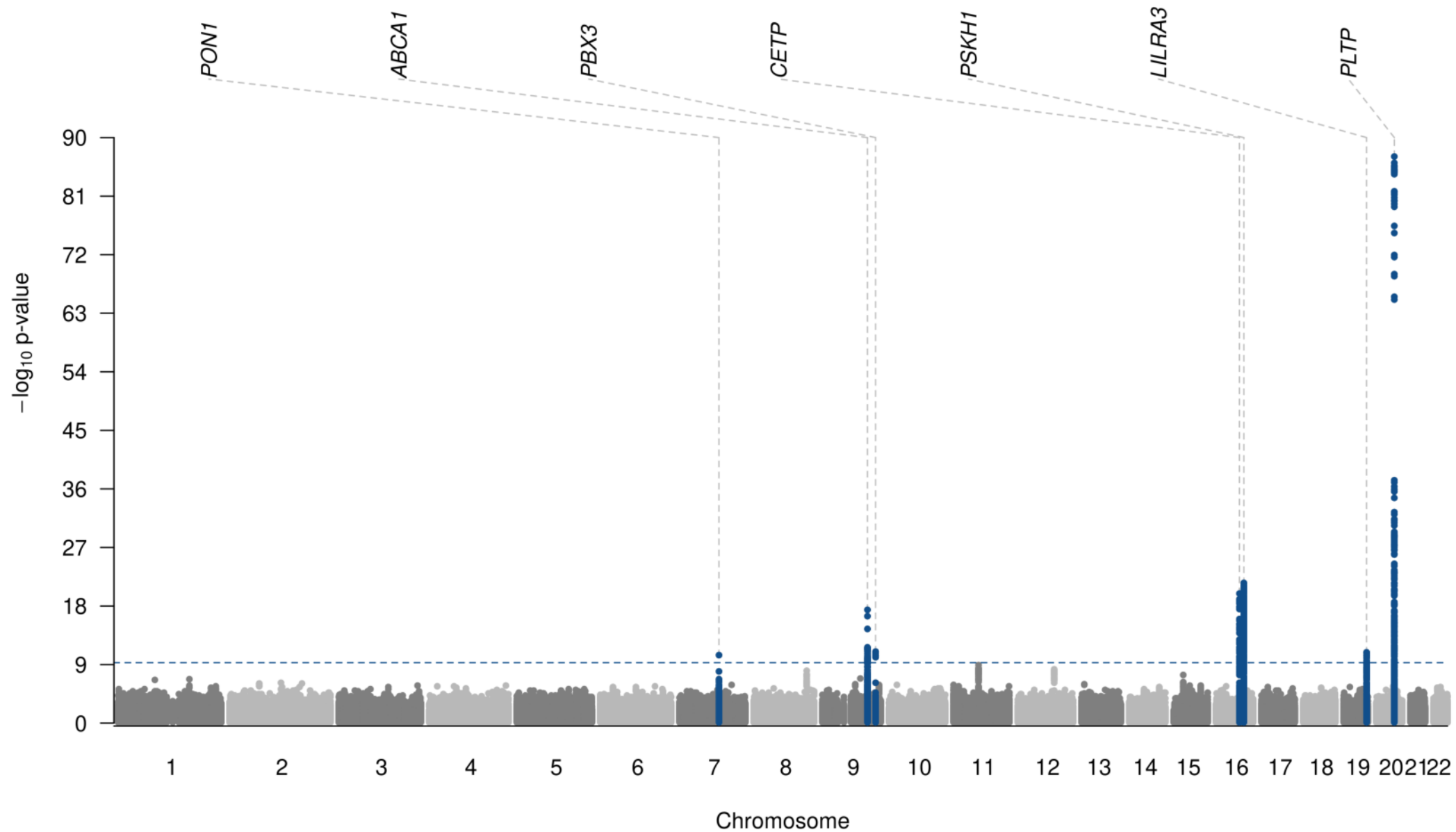
OSM (OSM)



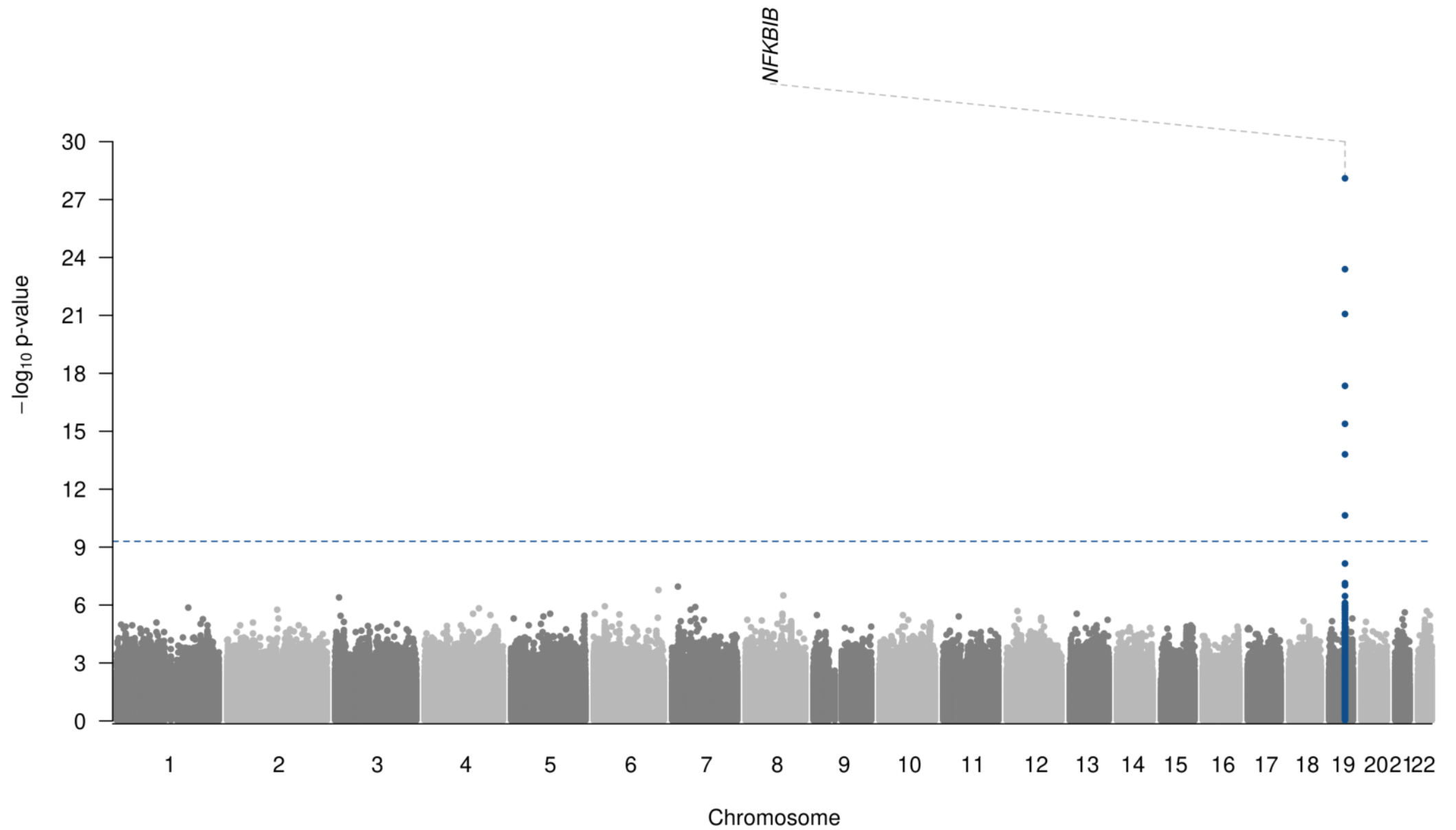
PD-L1 (CD274)



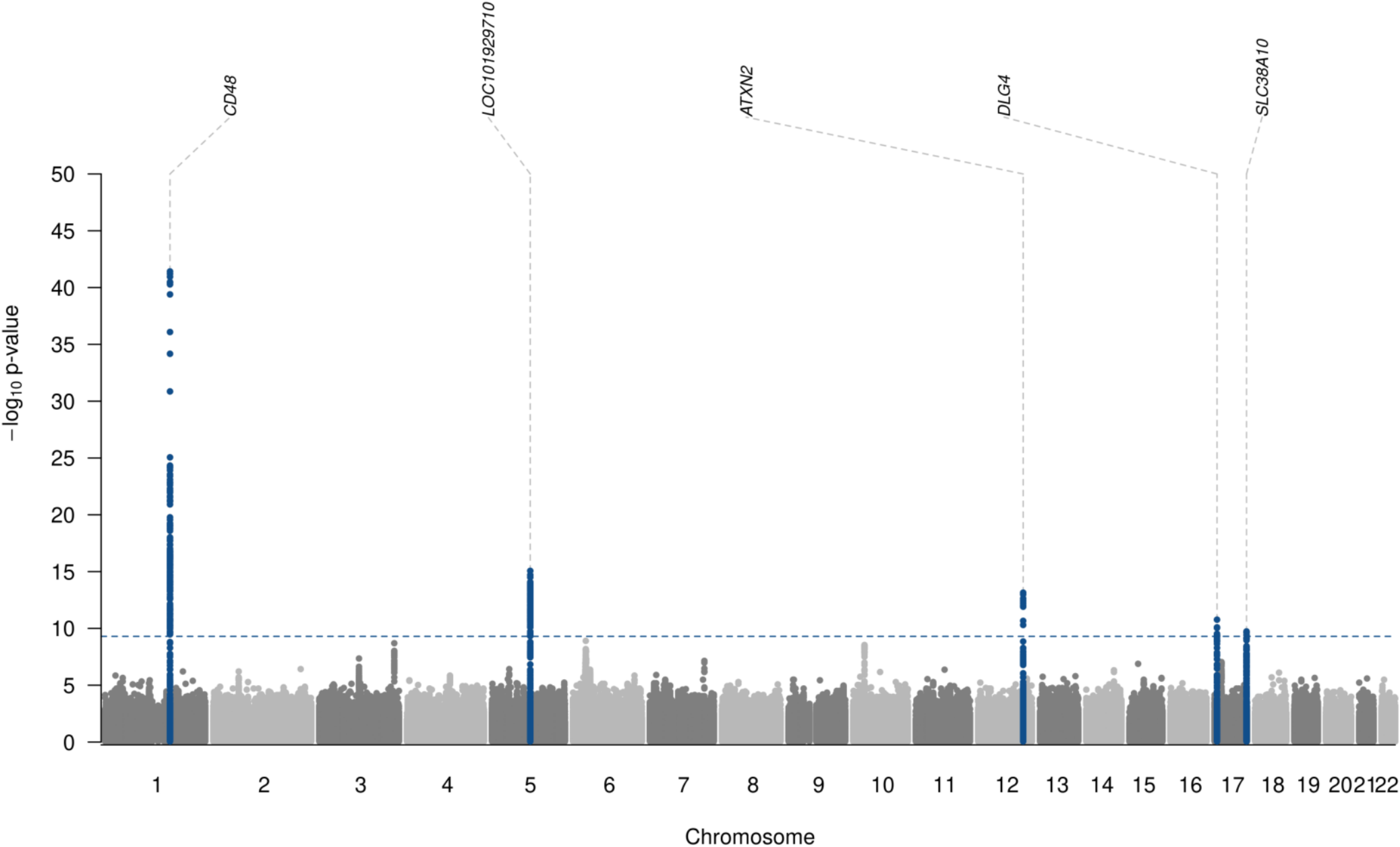
SCF (KITLG)



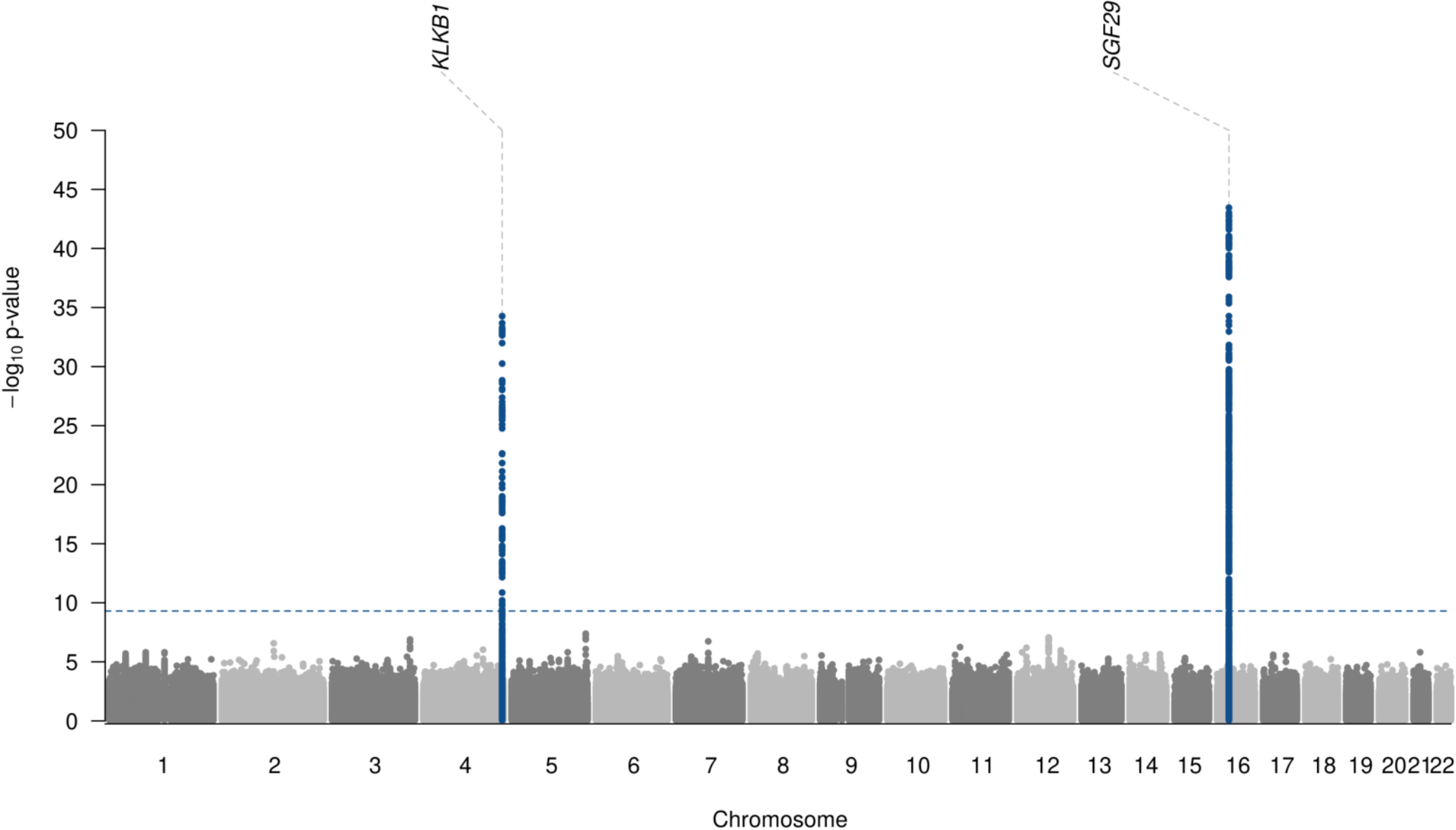
SIRT2 (SIRT2)



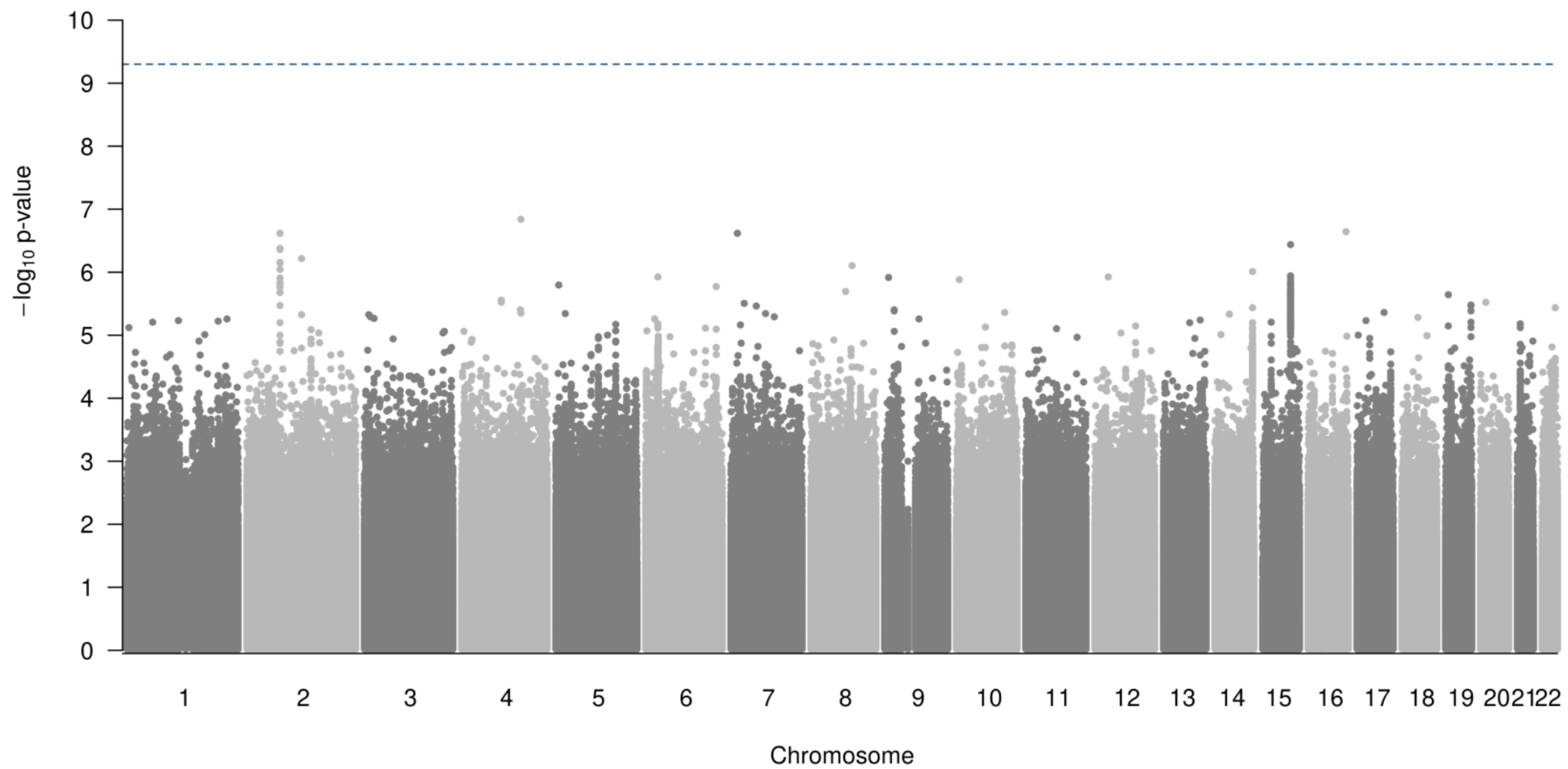
SLAMF1 (SLAMF1)



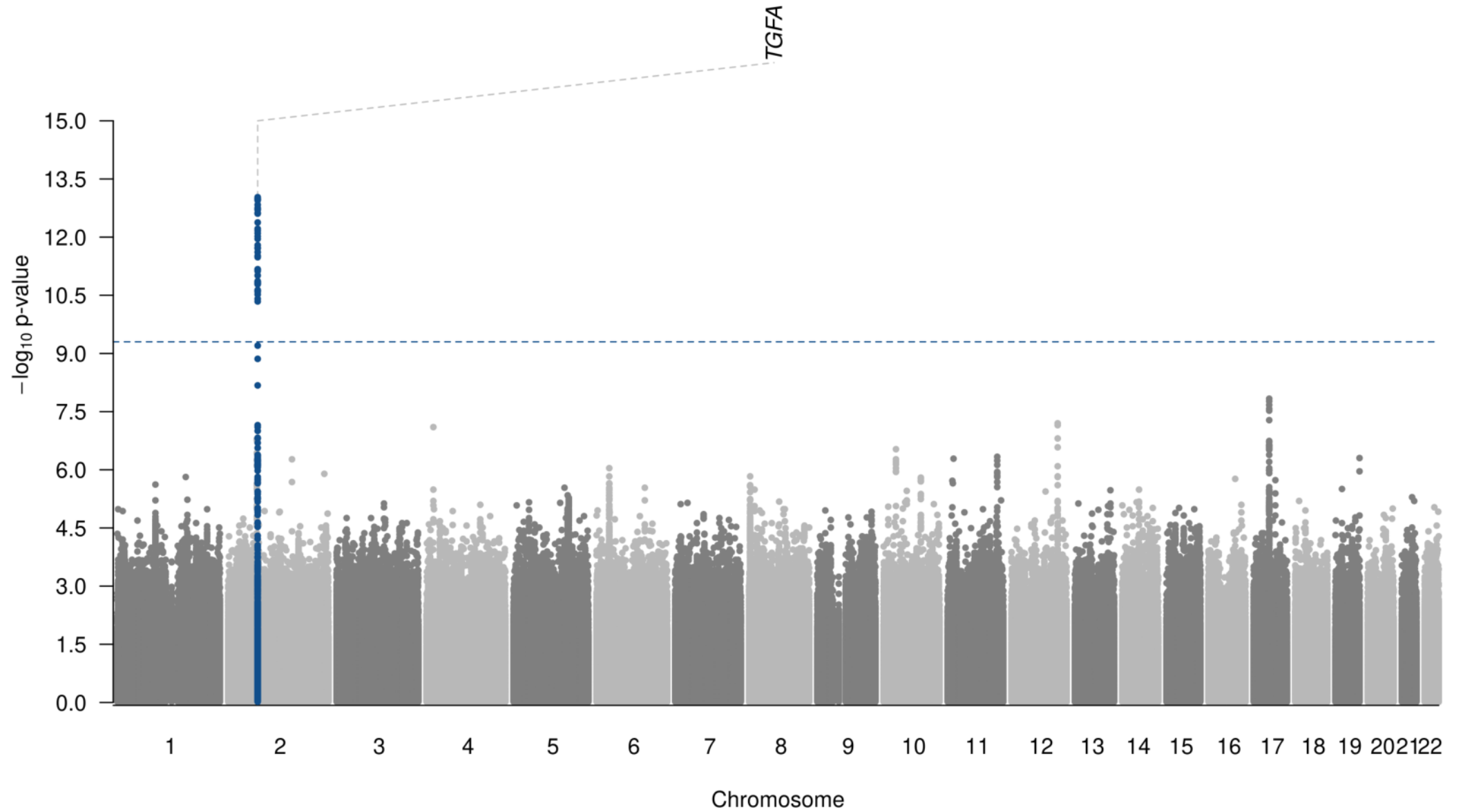
ST1A1 (SULT1A1)



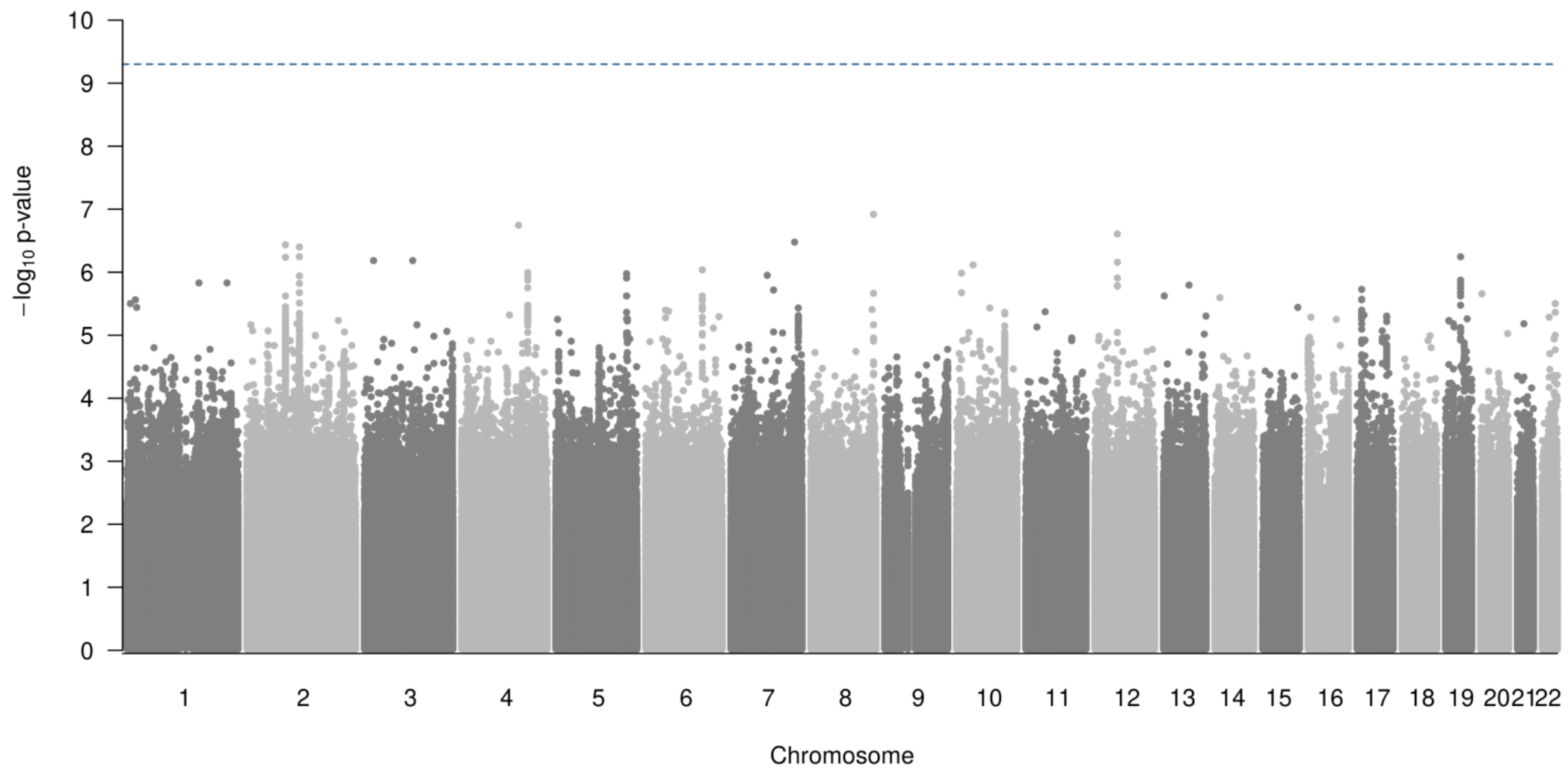
STAMPB (STAMPB)



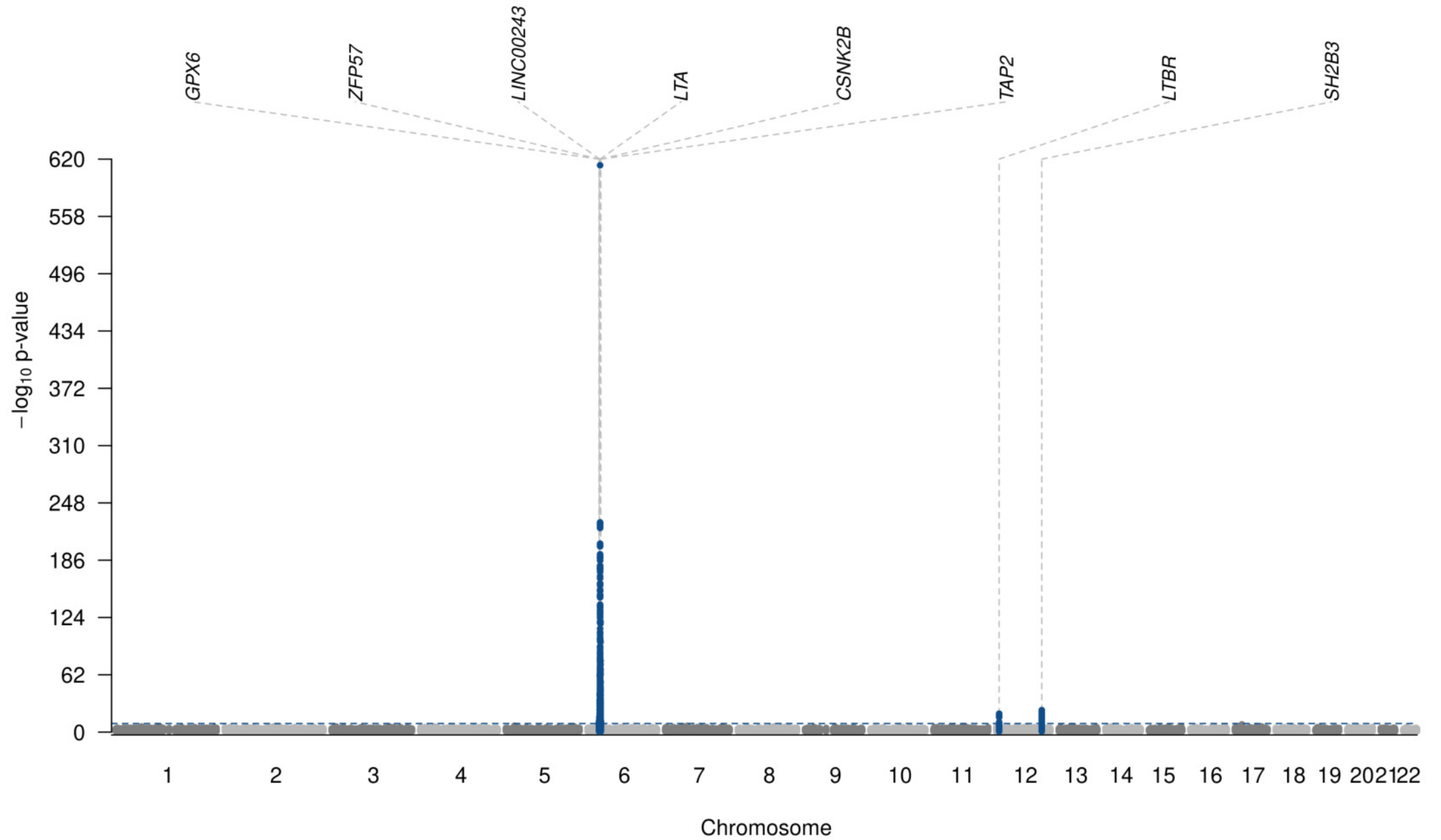
TGF-alpha (TGFA)



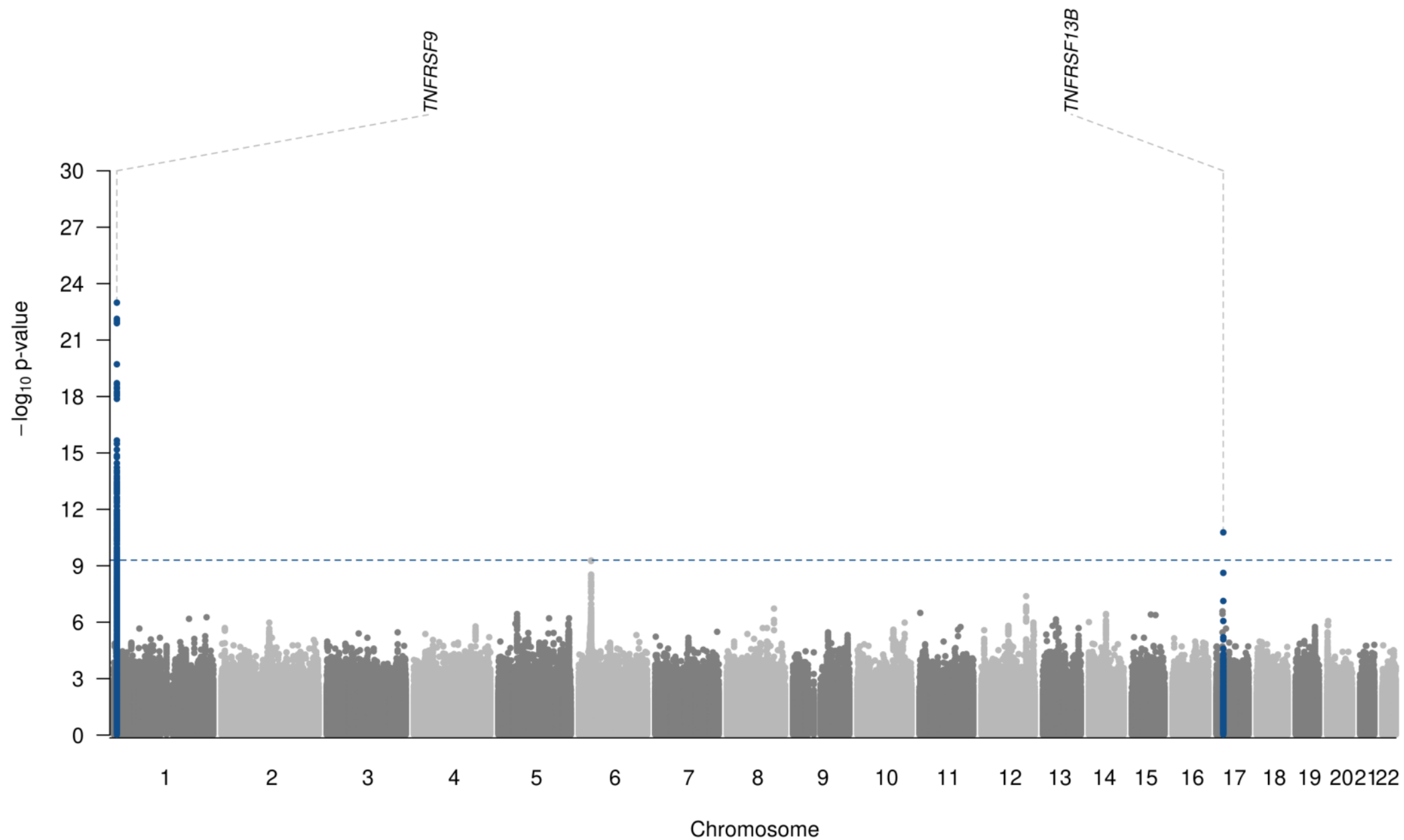
TNF (TNF)



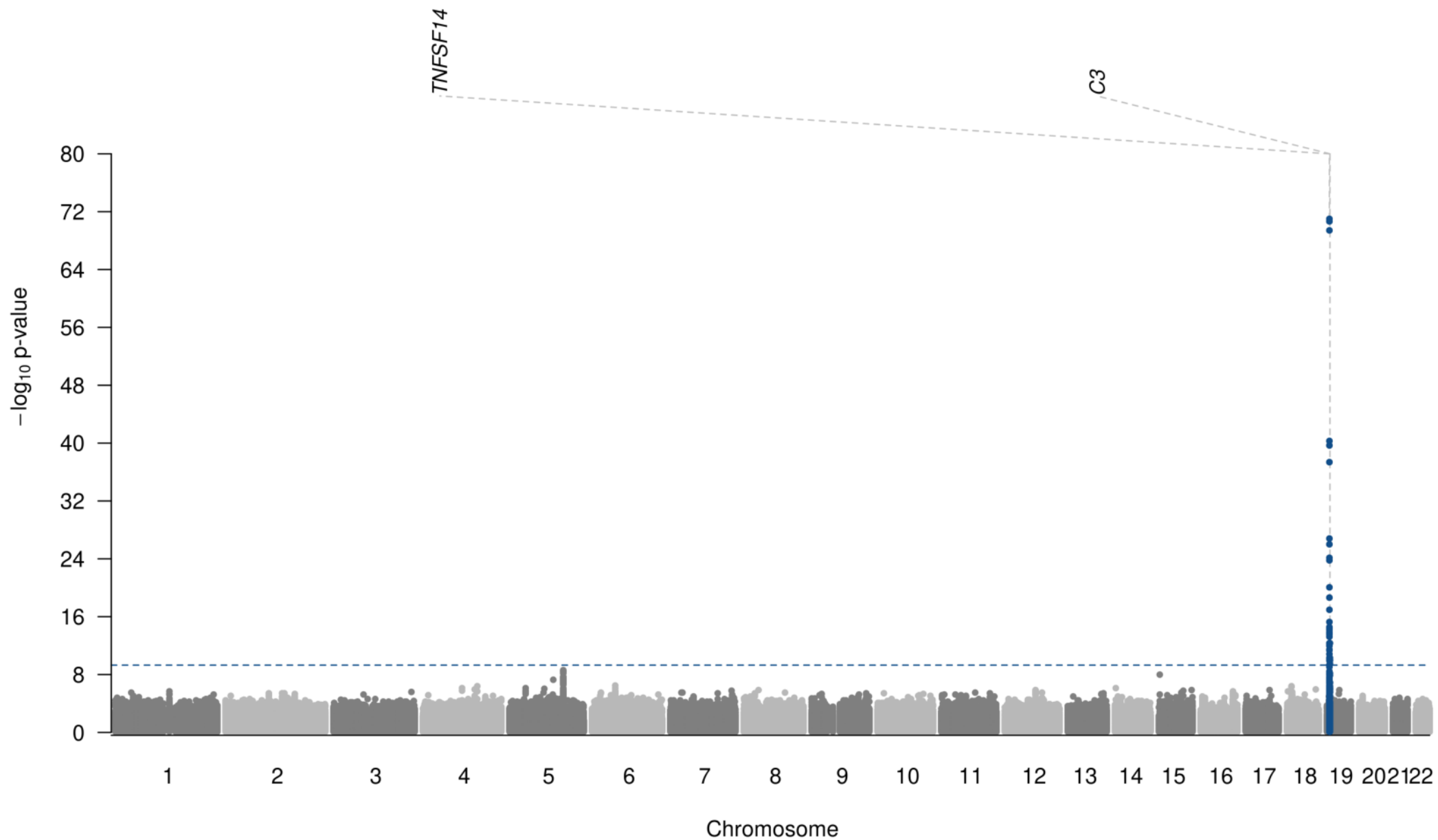
TNFB (LTA)



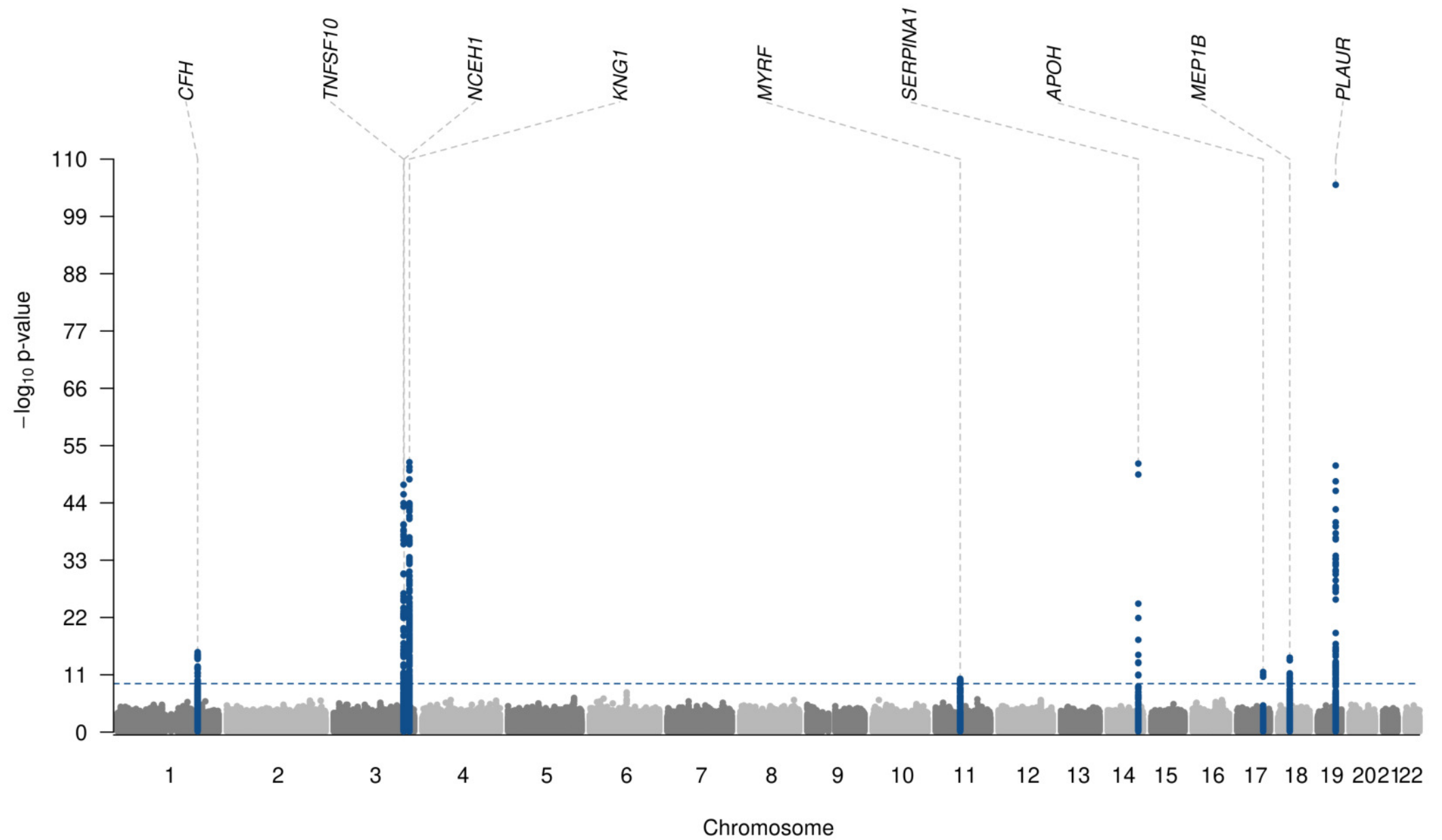
TNFRSF9 (TNFRSF9)



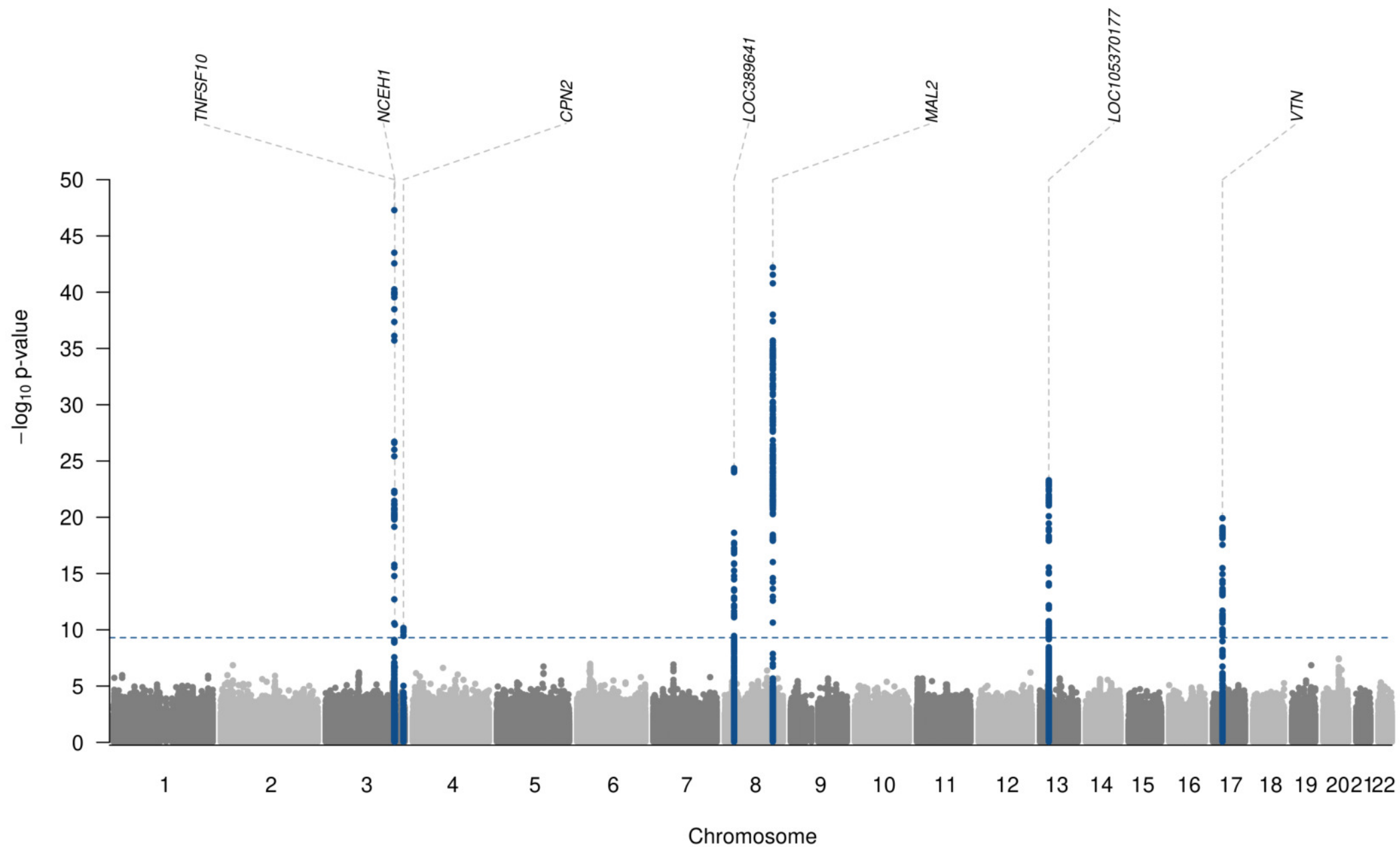
TNFSF14 (TNFSF14)



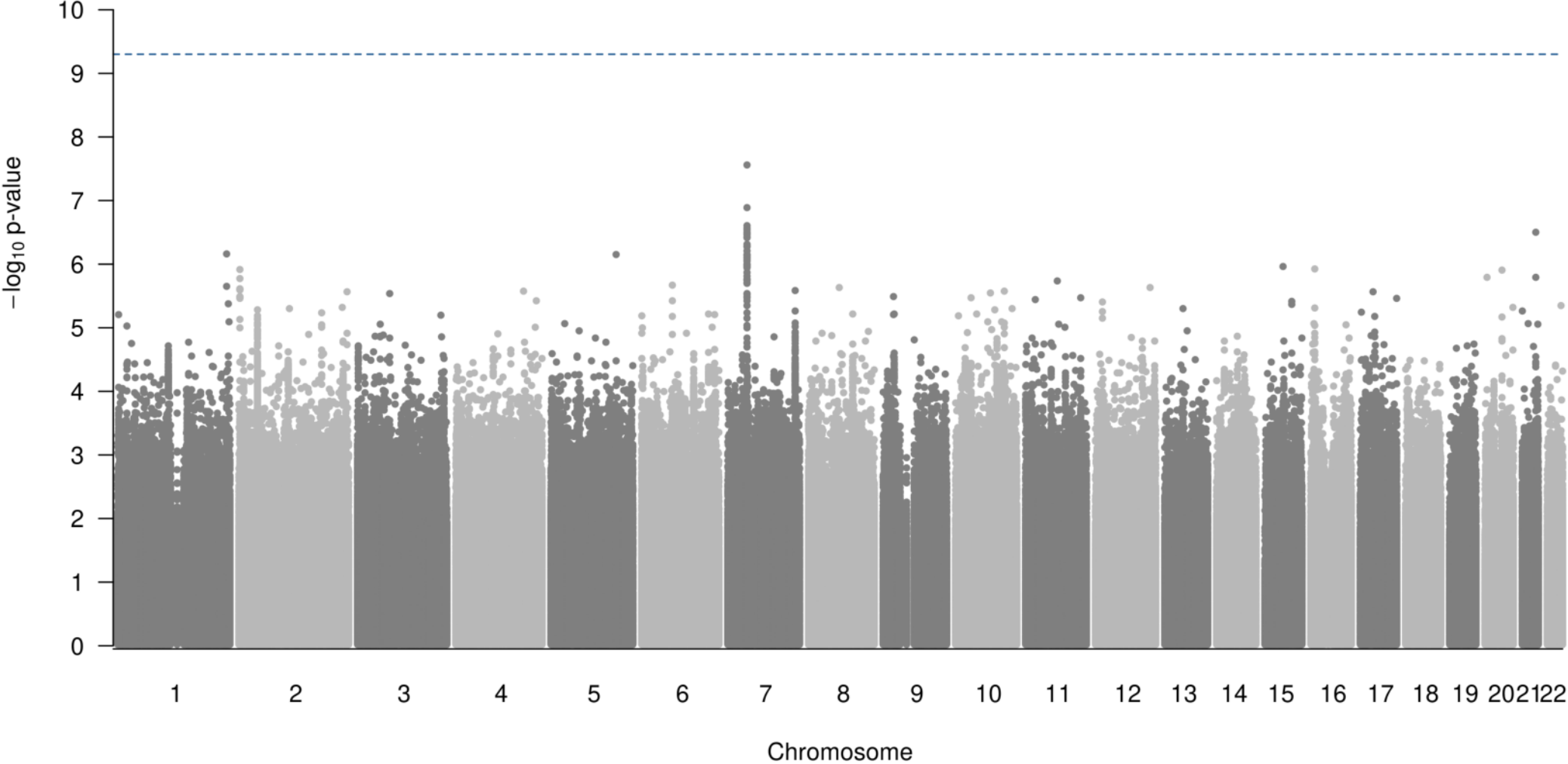
TRAIL (TNFSF10)



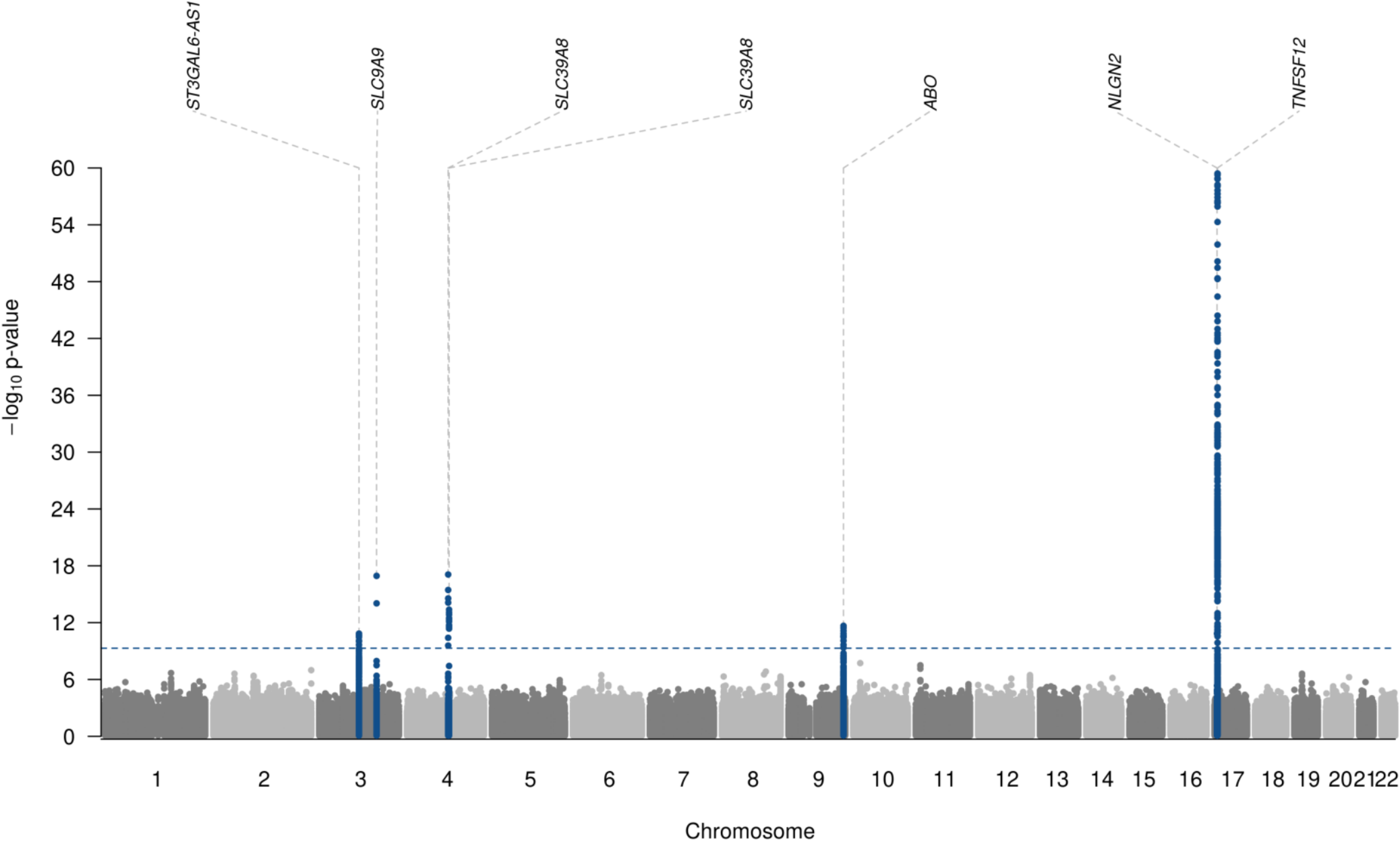
TRANSE (TNFSF11)



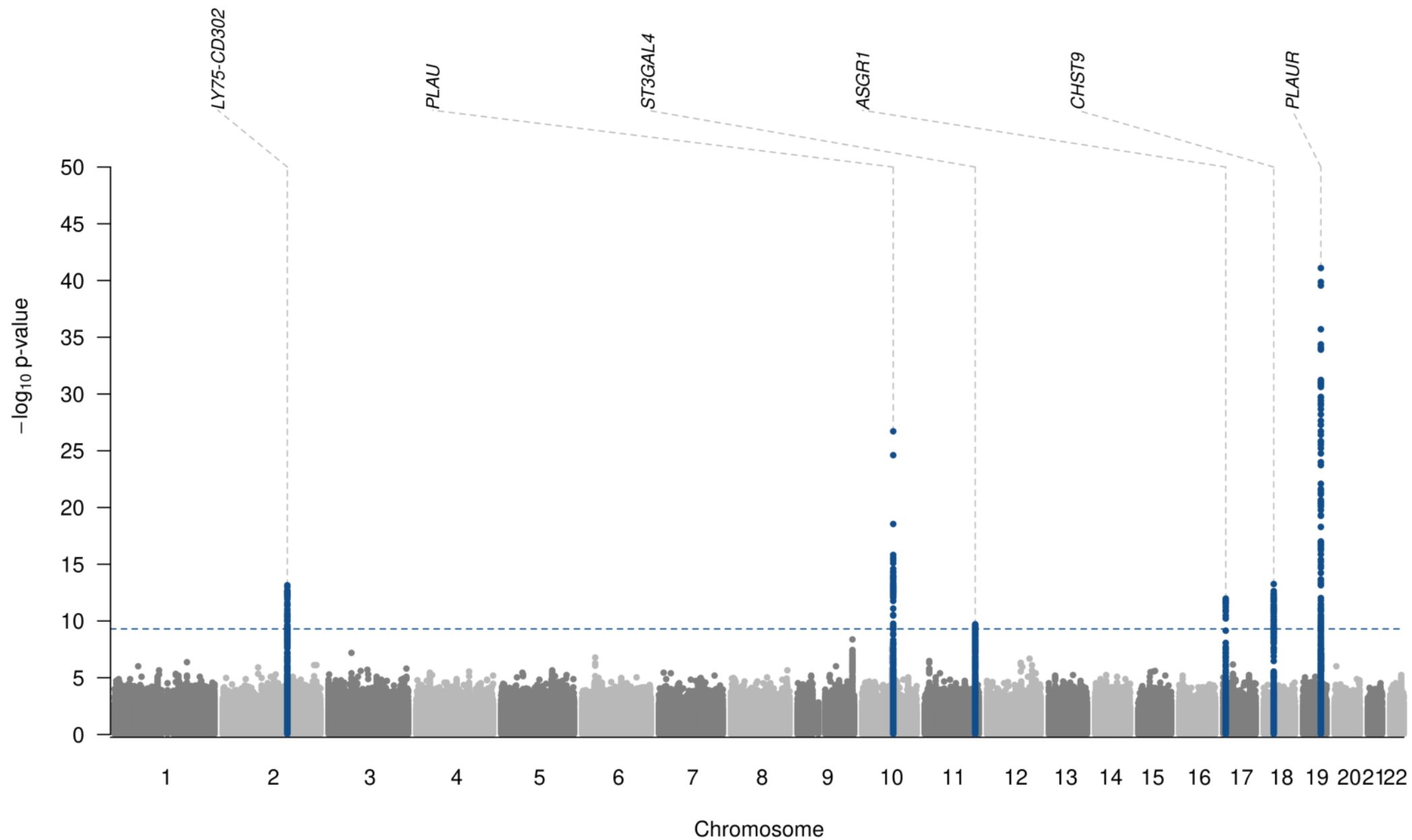
TSLP (TSLP)



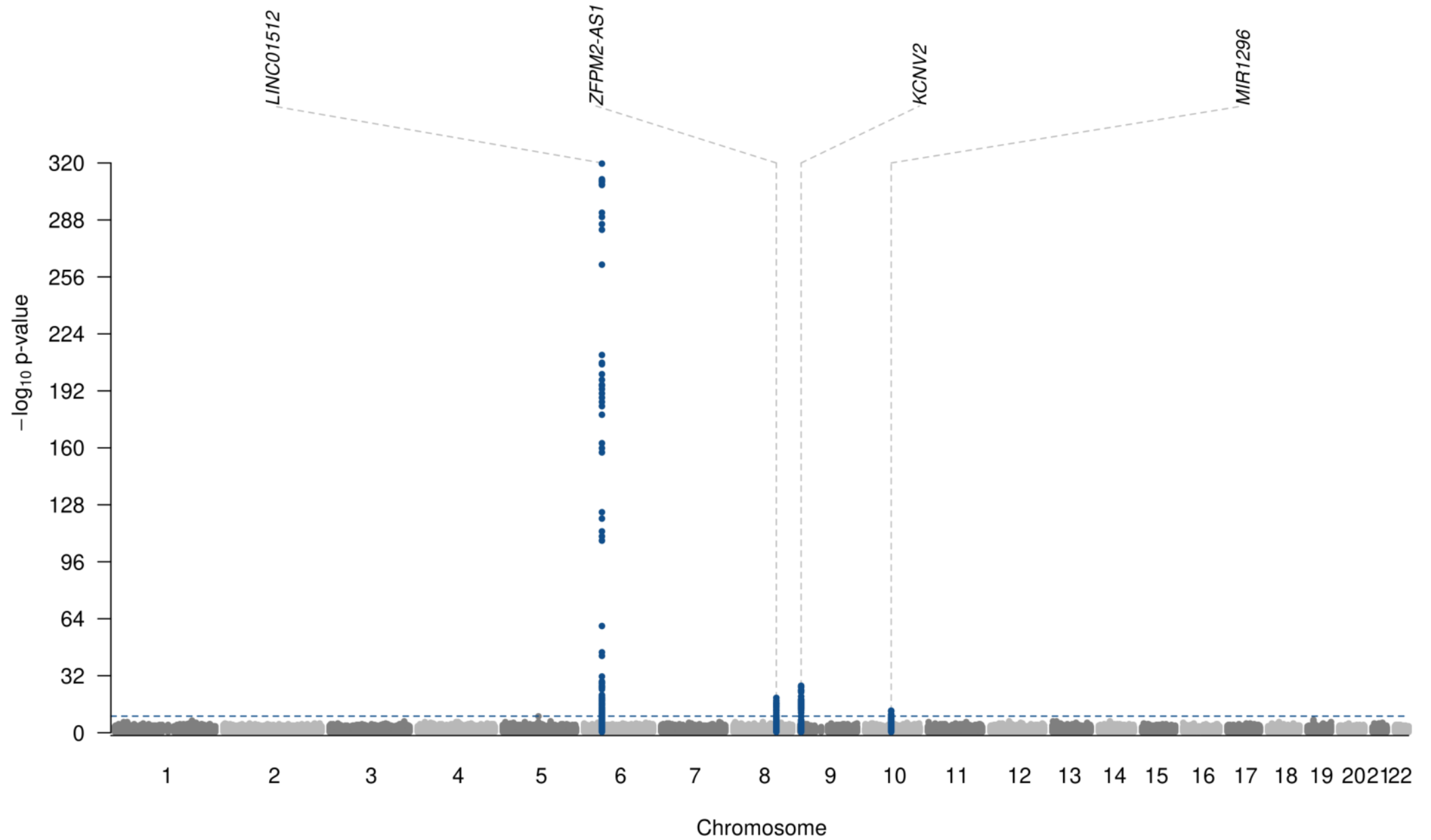
TWEAK (TNFSF12)



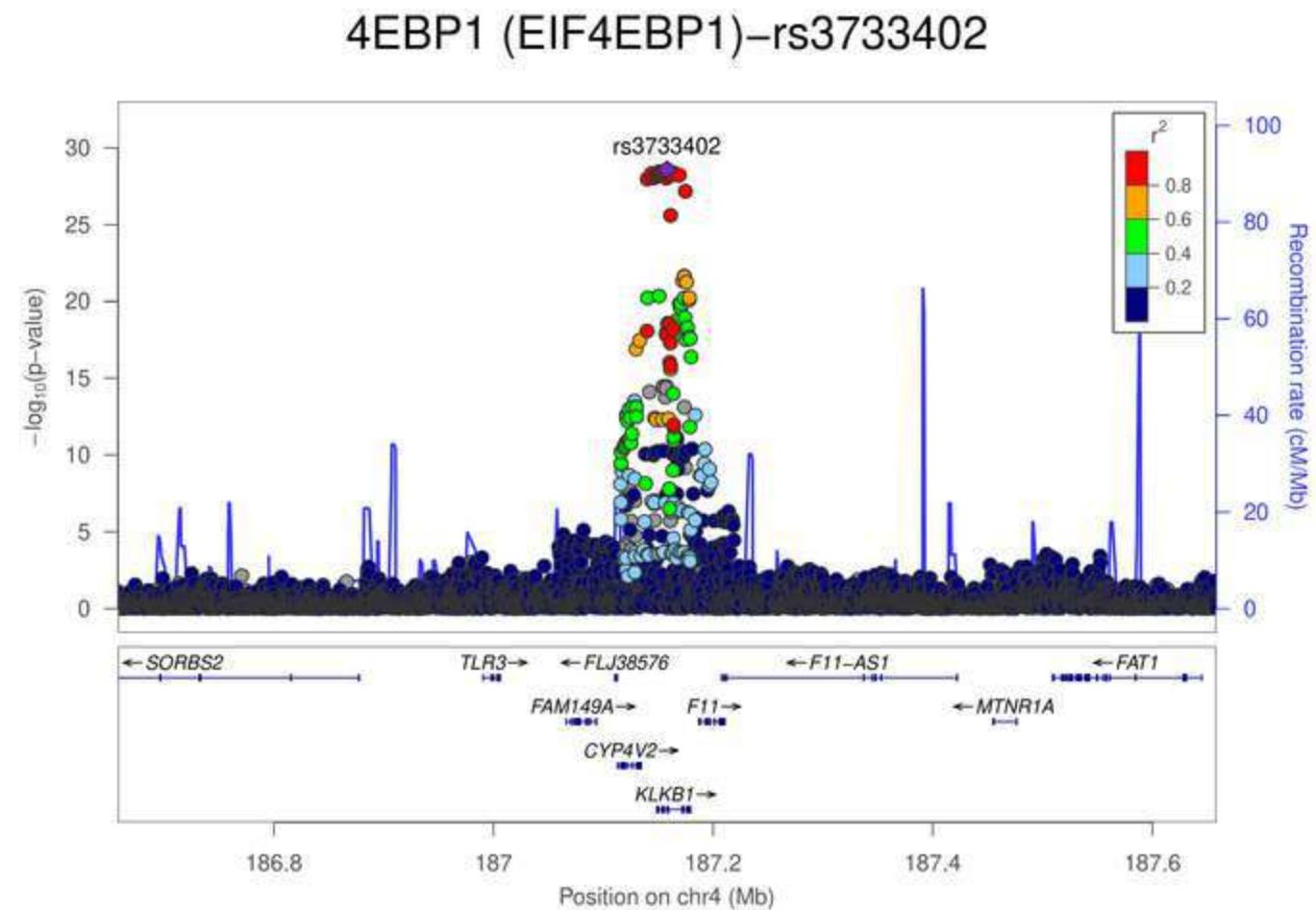
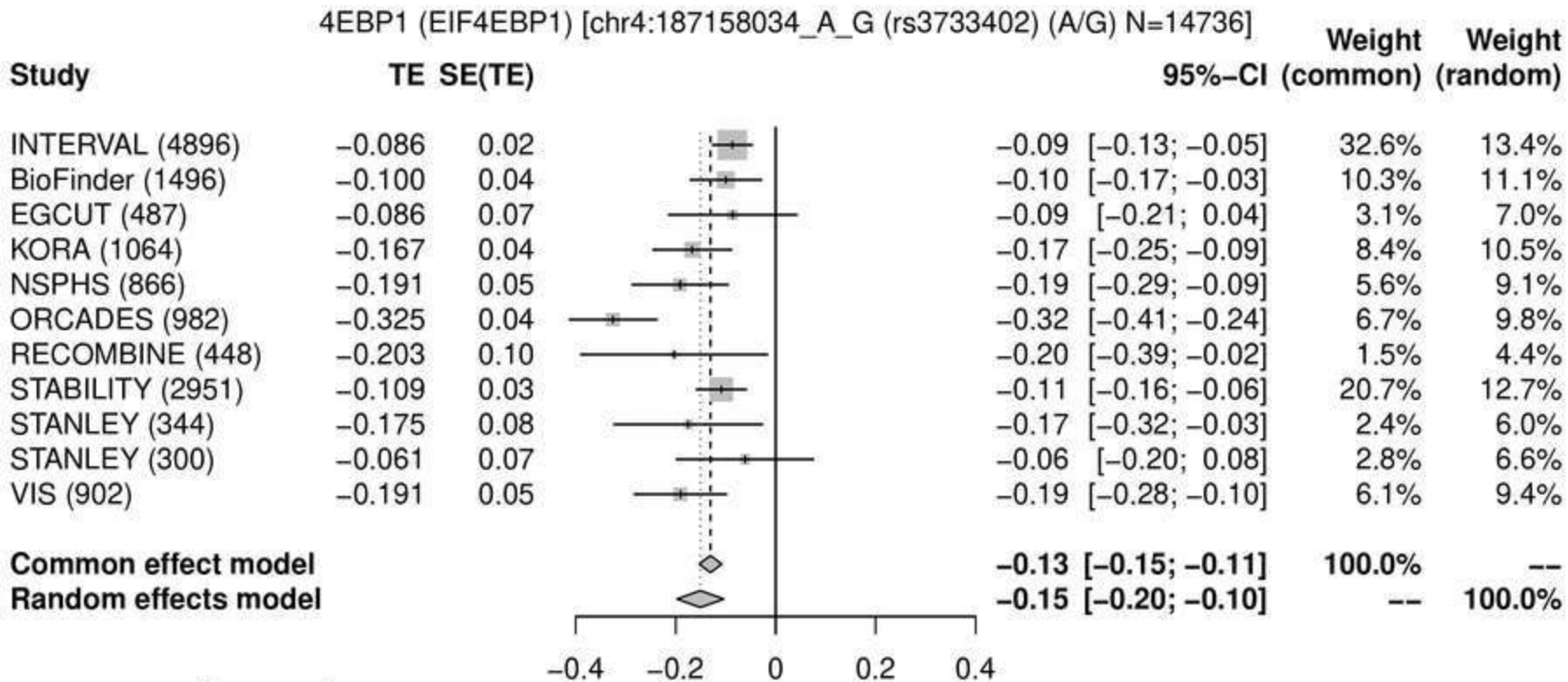
uPA (PLAU)

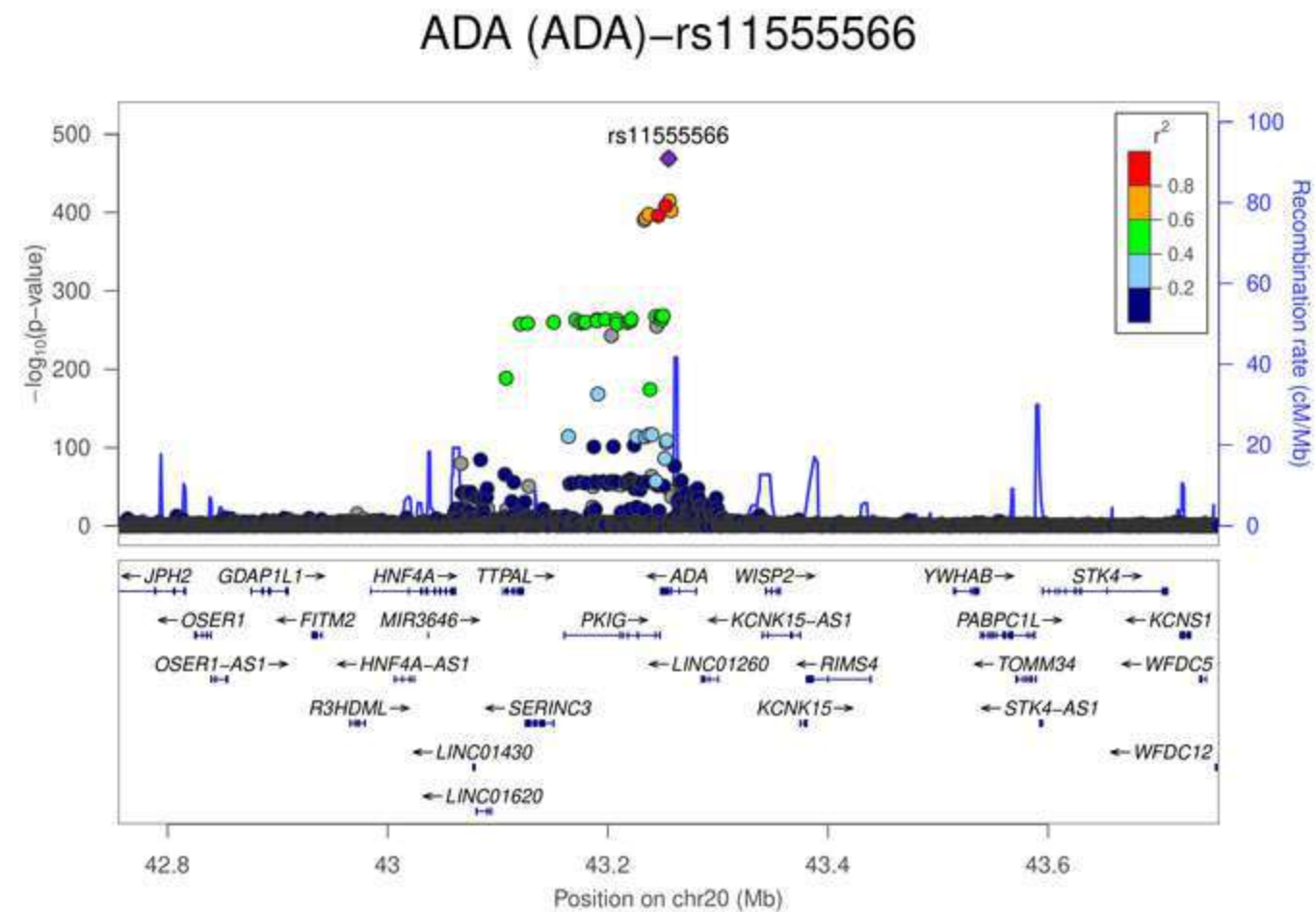
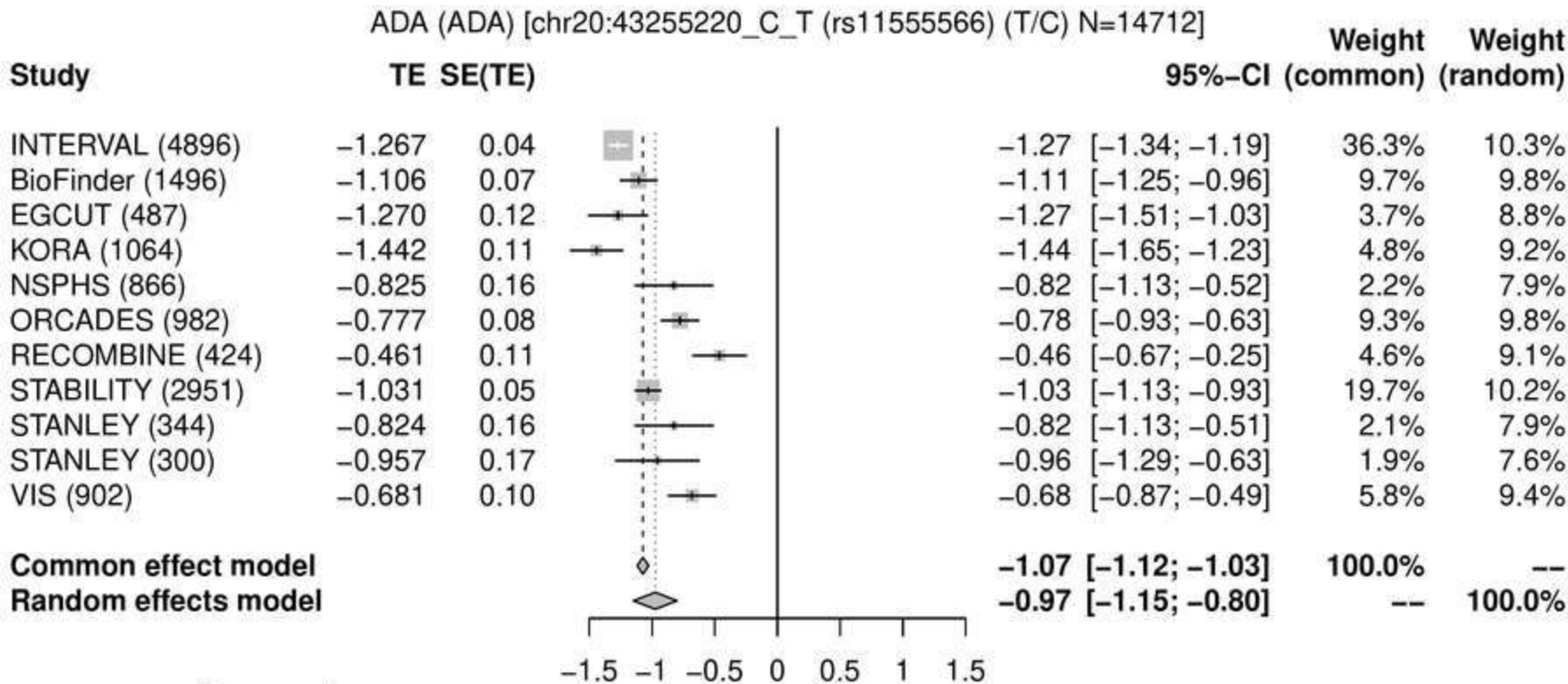


VEGF_A (VEGFA)

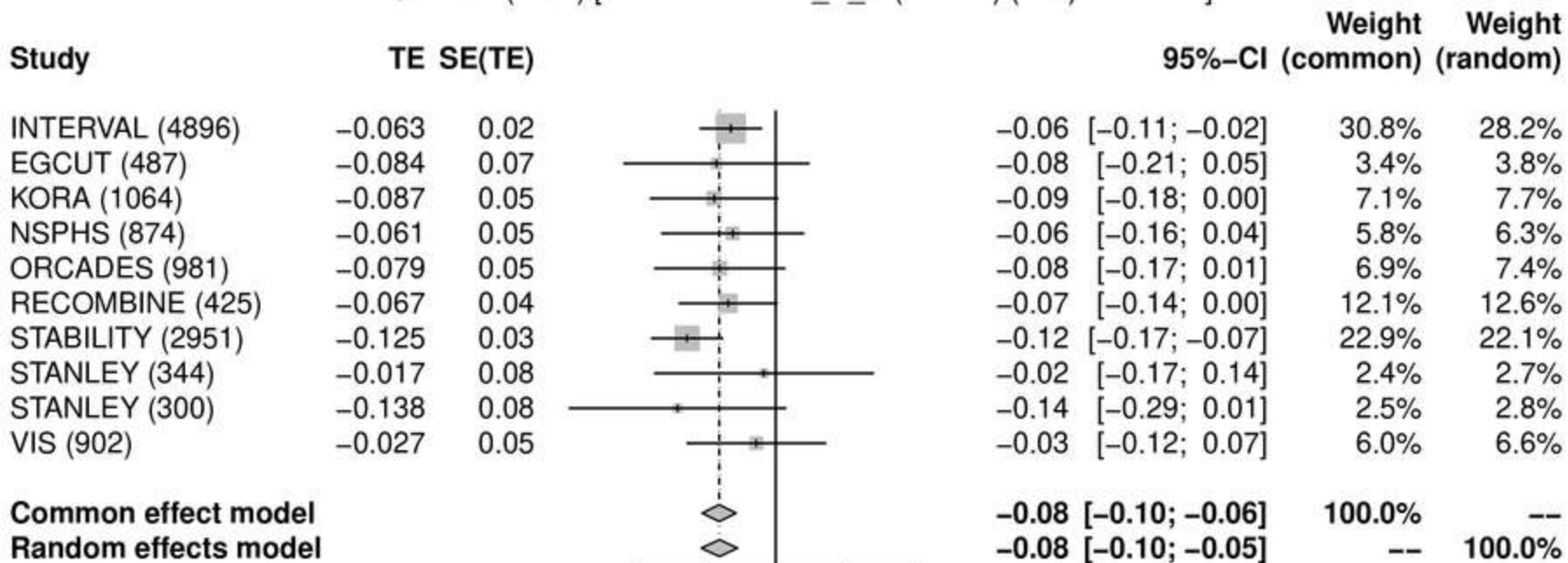


Supplementary Figure 2. Forest plots and regional association plots for the 180 pQTLs. Left panels: forest plots show the effect estimate and 95% confidence intervals in each cohort. Metrics of heterogeneity are provided. N= number of individuals. Right panels: locuszoom plots of the regional associations. Proteins are labelled with both the label provided by Olink, and with the encoding gene symbol in parentheses. Two-sided *P*-values are from meta-analysis of linear regression estimates.



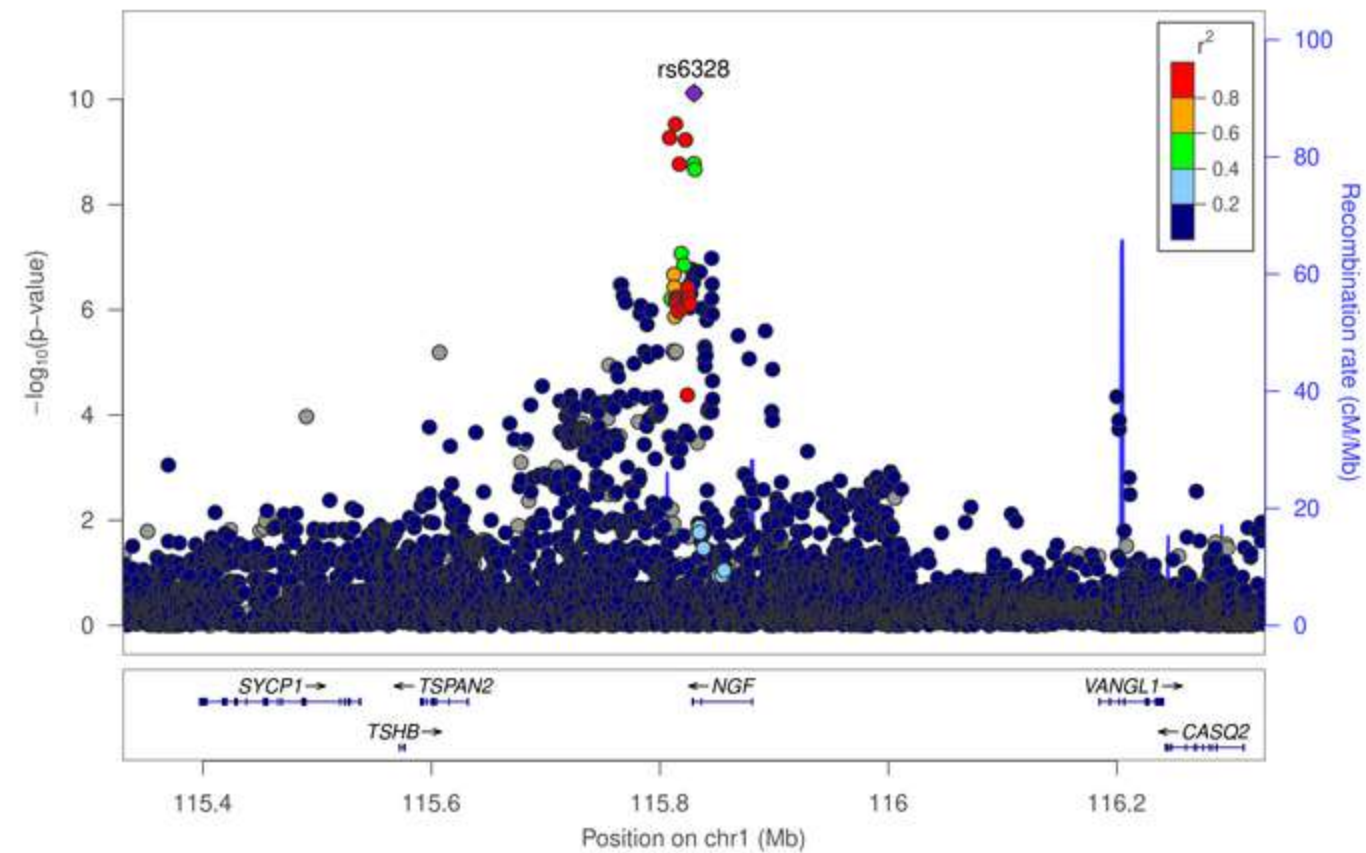


Beta-NGF (NGF) [chr1:115829943_A_C (rs6328) (A/C) N=13224]

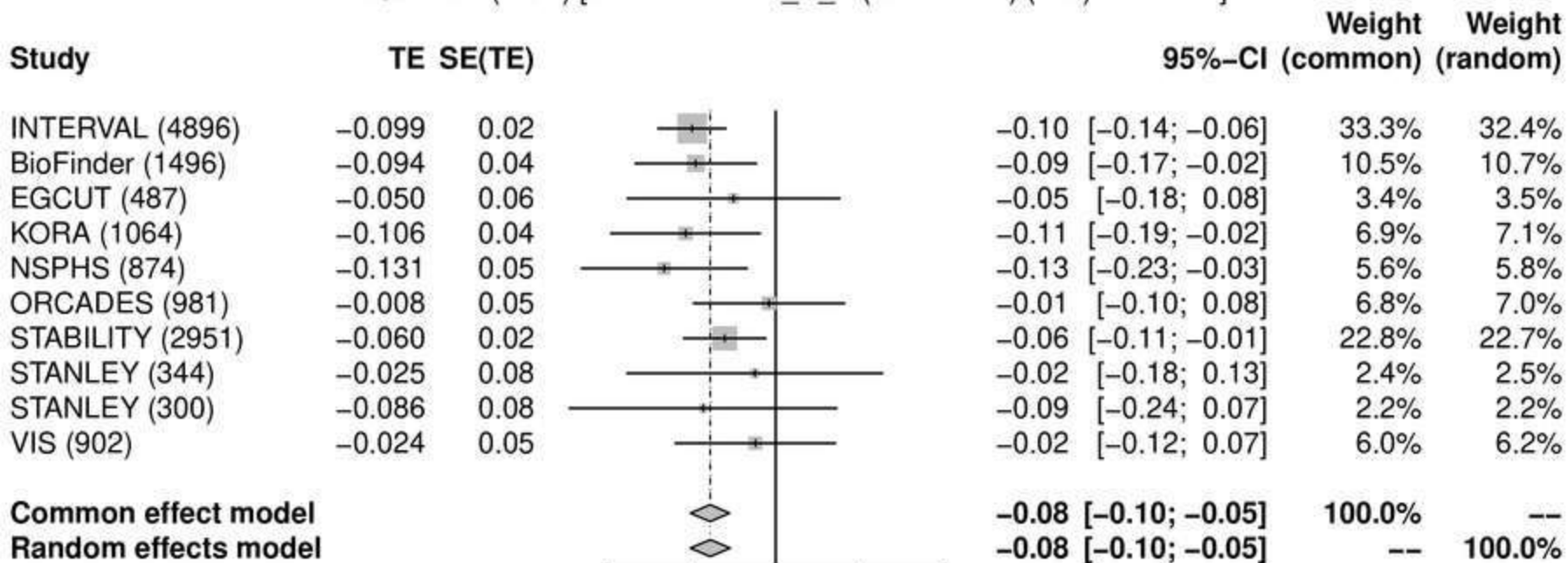


Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0.0001$, $p = 0.71$

Beta-NGF (NGF)-rs6328

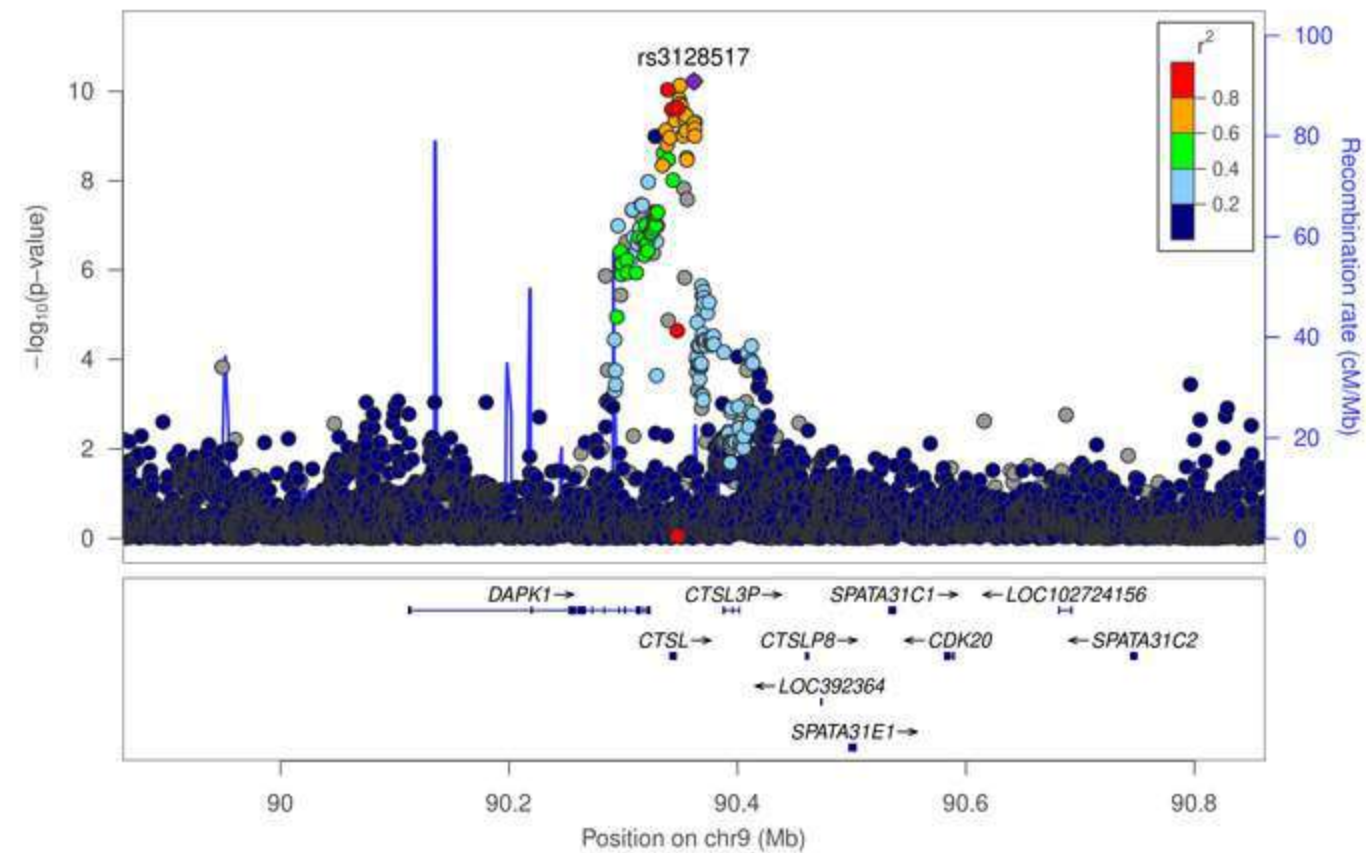


Beta-NGF (NGF) [chr9:90362040_C_T (rs3128517) (T/C) N=14295]



Heterogeneity: $I^2 = 0\%$, $\tau^2 < 0.0001$, $p = 0.57$

Beta-NGF (NGF)-rs3128517



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (874)

ORCADES (982)

RECOMBINE (447)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 35\%$, $\tau^2 = 0.0017$, $p = 0.12$

CASP-8 (CASP8) [chr2:202164805_C_G (rs56328050) (C/G) N=14743]

TE SE(TE)

-0.198 0.03

-0.218 0.05

-0.098 0.10

-0.368 0.06

-0.119 0.06

-0.248 0.07

-0.073 0.14

-0.180 0.04

-0.016 0.12

-0.108 0.10

-0.233 0.07

Weight
95%-CI (common) (random)

-0.20 [-0.26; -0.14] 33.1% 20.7%

-0.22 [-0.32; -0.11] 10.8% 11.9%

-0.10 [-0.29; 0.10] 3.0% 4.5%

-0.37 [-0.49; -0.25] 8.0% 9.8%

-0.12 [-0.24; 0.00] 7.8% 9.6%

-0.25 [-0.38; -0.12] 7.0% 8.9%

-0.07 [-0.36; 0.21] 1.5% 2.4%

-0.18 [-0.26; -0.10] 17.2% 15.6%

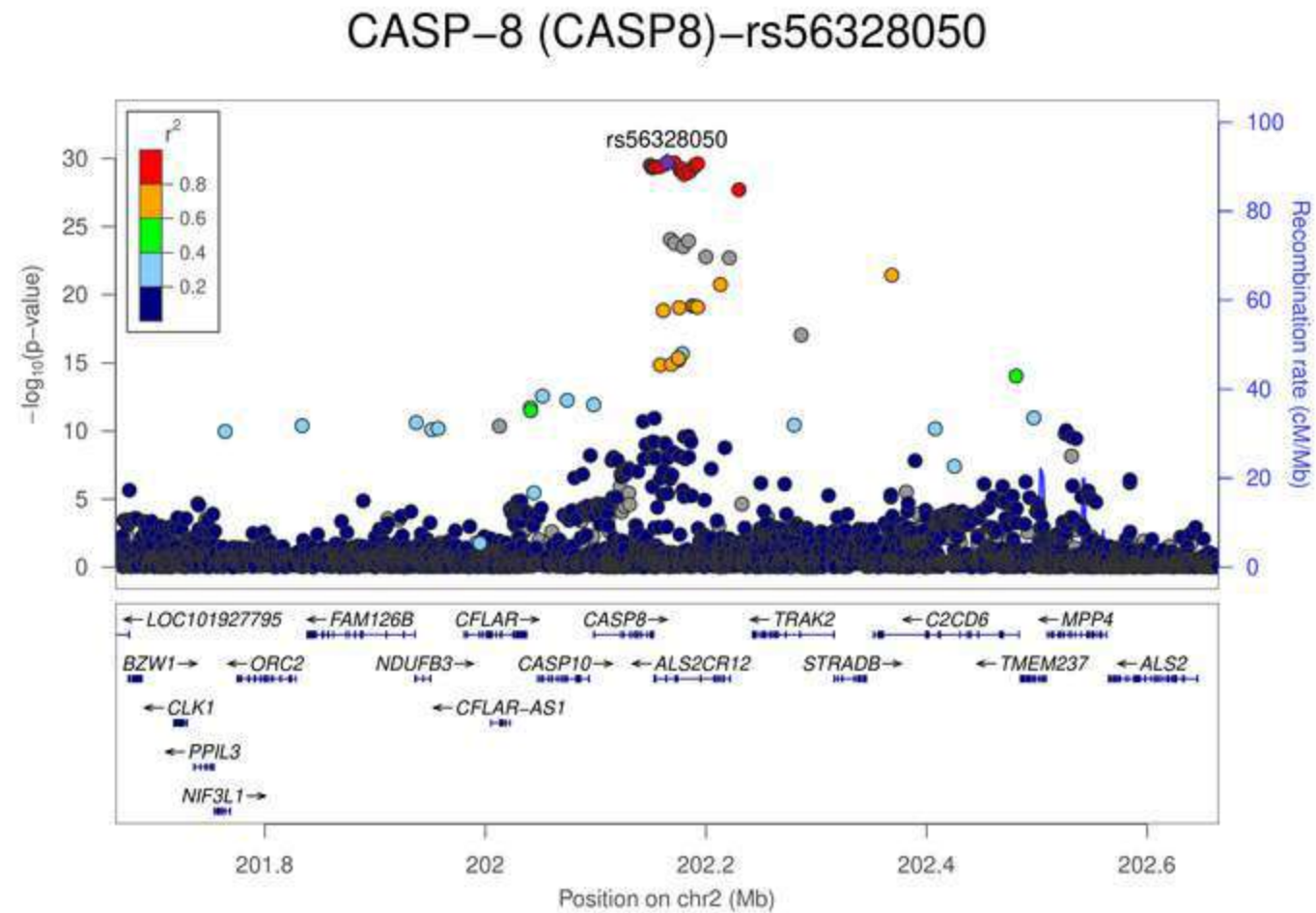
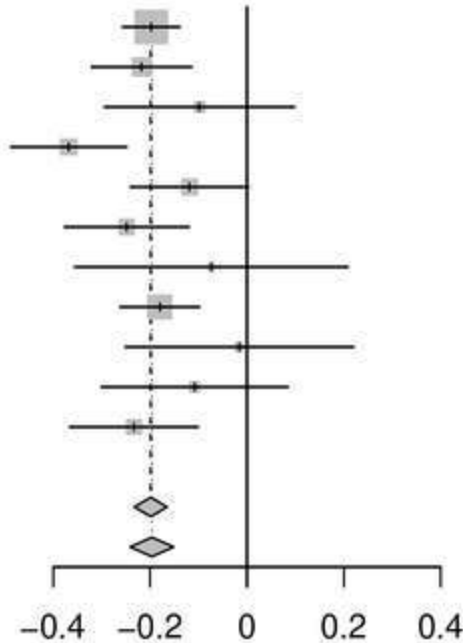
-0.02 [-0.25; 0.22] 2.1% 3.3%

-0.11 [-0.30; 0.08] 3.1% 4.7%

-0.23 [-0.37; -0.10] 6.6% 8.5%

-0.20 [-0.23; -0.16] 100.0% --

-0.20 [-0.24; -0.15] -- 100.0%



Study

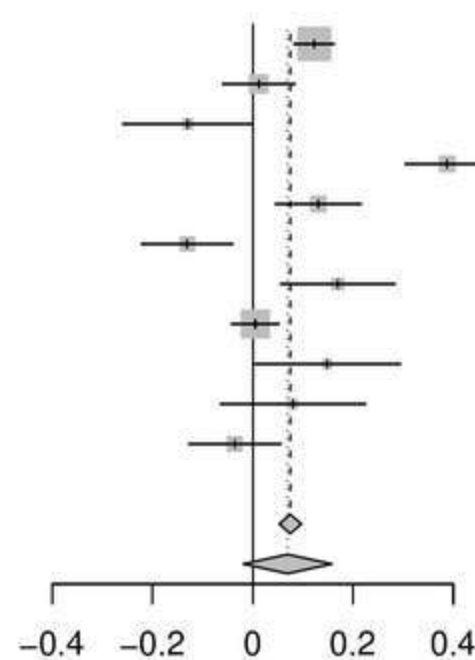
CCL11 (CCL11) [chr1:159175354_A_G (rs12075) (A/G) N=14731]

TE SE(TE)

INTERVAL (4896)	0.122	0.02
BioFinder (1496)	0.012	0.04
EGCUT (487)	-0.130	0.07
KORA (1064)	0.388	0.04
NSPHS (866)	0.131	0.04
ORCADES (981)	-0.131	0.05
RECOMBINE (445)	0.170	0.06
STABILITY (2951)	0.005	0.02
STANLEY (344)	0.148	0.07
STANLEY (300)	0.080	0.07
VIS (901)	-0.036	0.05

Common effect model

Random effects model

Heterogeneity: $I^2 = 91\%$, $\tau^2 = 0.0200$, $p < 0.01$ 

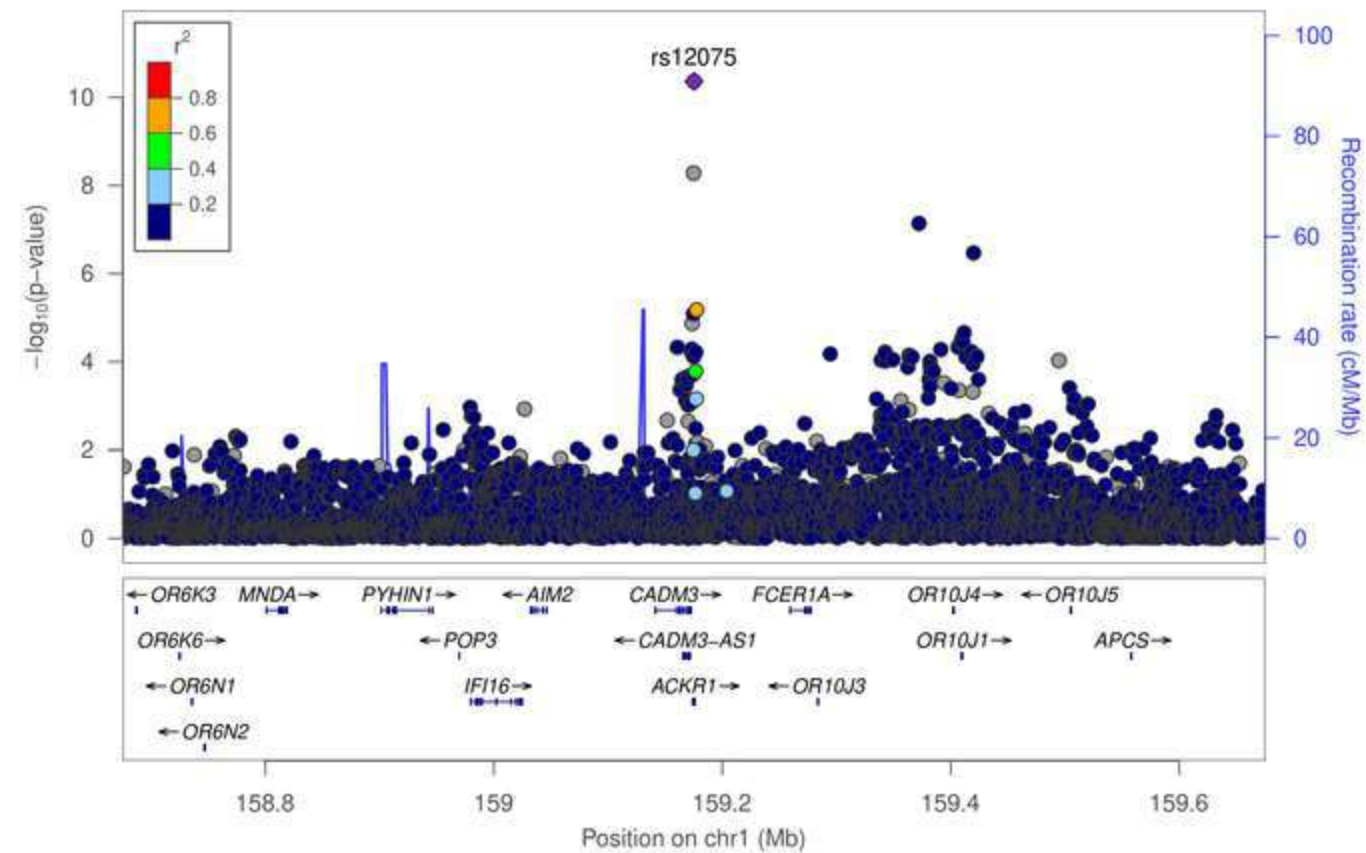
Weight 95%-CI (common) (random)

0.12	[0.08; 0.16]	31.2%	10.0%
0.01	[-0.06; 0.08]	9.5%	9.6%
-0.13	[-0.26; 0.00]	3.0%	8.4%
0.39	[0.30; 0.47]	7.1%	9.4%
0.13	[0.05; 0.22]	6.8%	9.3%
-0.13	[-0.22; -0.04]	6.0%	9.2%
0.17	[0.06; 0.28]	3.8%	8.8%
0.01	[-0.04; 0.05]	22.0%	9.9%
0.15	[0.00; 0.29]	2.3%	8.0%
0.08	[-0.06; 0.22]	2.4%	8.0%
-0.04	[-0.13; 0.06]	5.9%	9.2%

0.07 [0.05; 0.10] 100.0% --

0.07 [-0.02; 0.16] -- 100.0%

CCL11 (CCL11)-rs12075



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (981)

RECOMBINE (434)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 38\%$, $\tau^2 = 0.0014$, $p = 0.09$

CCL11 (CCL11) [chr17:32619052_C_T (rs79722574) (T/C) N=14720]

TE SE(TE)

-0.093 0.03

-0.170 0.05

0.008 0.09

-0.029 0.06

-0.165 0.06

-0.237 0.06

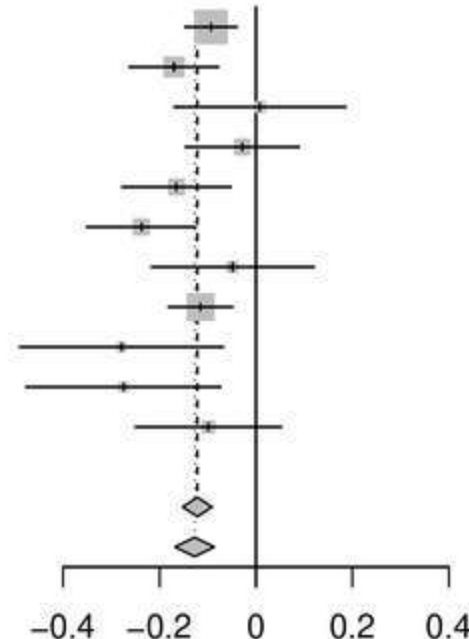
-0.048 0.09

-0.115 0.03

-0.278 0.11

-0.275 0.10

-0.099 0.08



95%-CI (common) (random)

-0.09 [-0.15; -0.04]

-0.17 [-0.26; -0.08]

0.01 [-0.17; 0.19]

-0.03 [-0.15; 0.09]

-0.16 [-0.28; -0.05]

-0.24 [-0.35; -0.12]

-0.05 [-0.22; 0.12]

-0.11 [-0.18; -0.05]

-0.28 [-0.49; -0.07]

-0.27 [-0.48; -0.07]

-0.10 [-0.25; 0.05]

-0.12 [-0.15; -0.09]

-0.13 [-0.17; -0.09]

Weight

Weight

31.9%

10.9%

3.0%

6.7%

7.3%

7.3%

3.3%

21.1%

2.1%

2.3%

4.1%

100.0%

--

Weight

Weight

20.6%

12.2%

4.5%

8.8%

9.3%

9.3%

5.0%

17.4%

3.4%

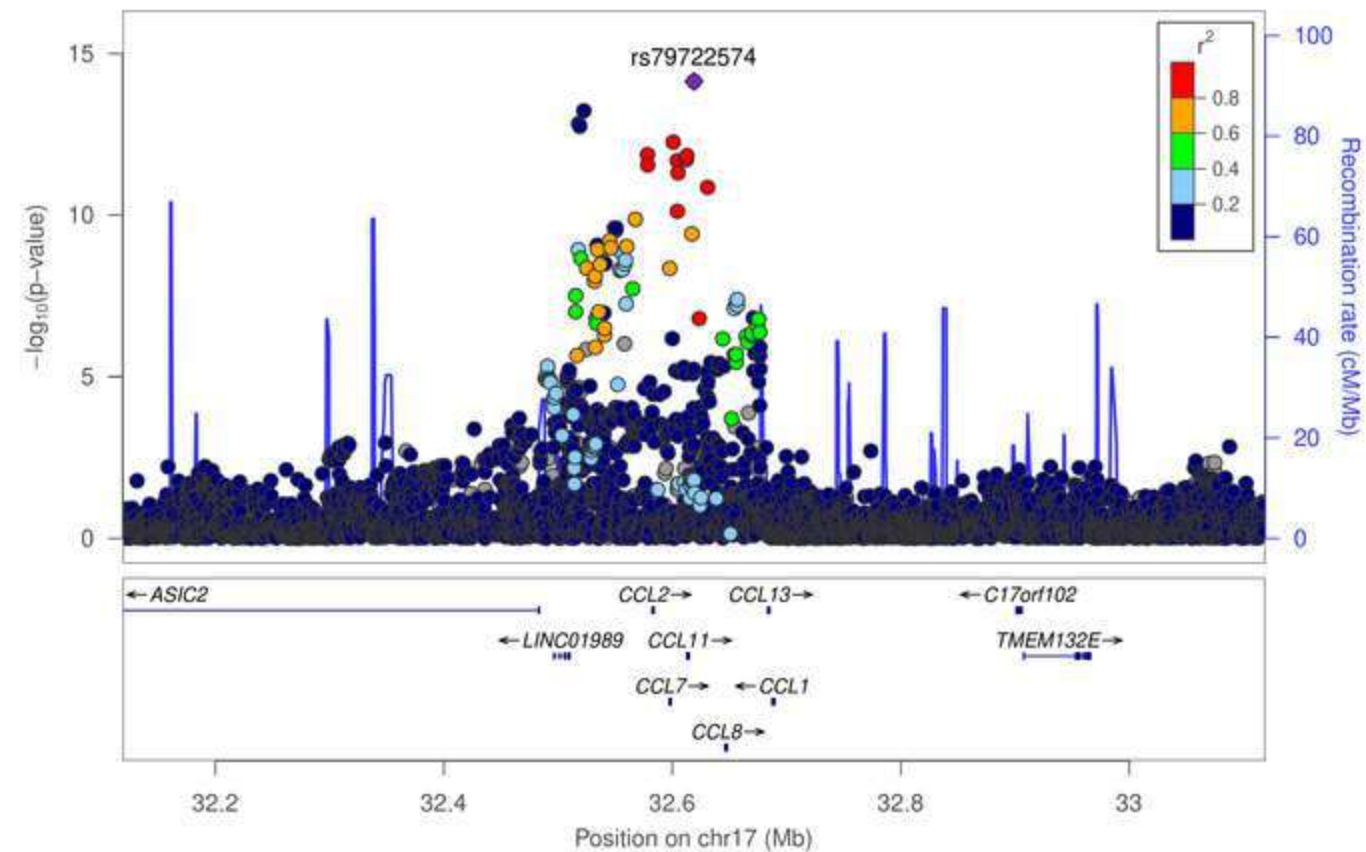
3.6%

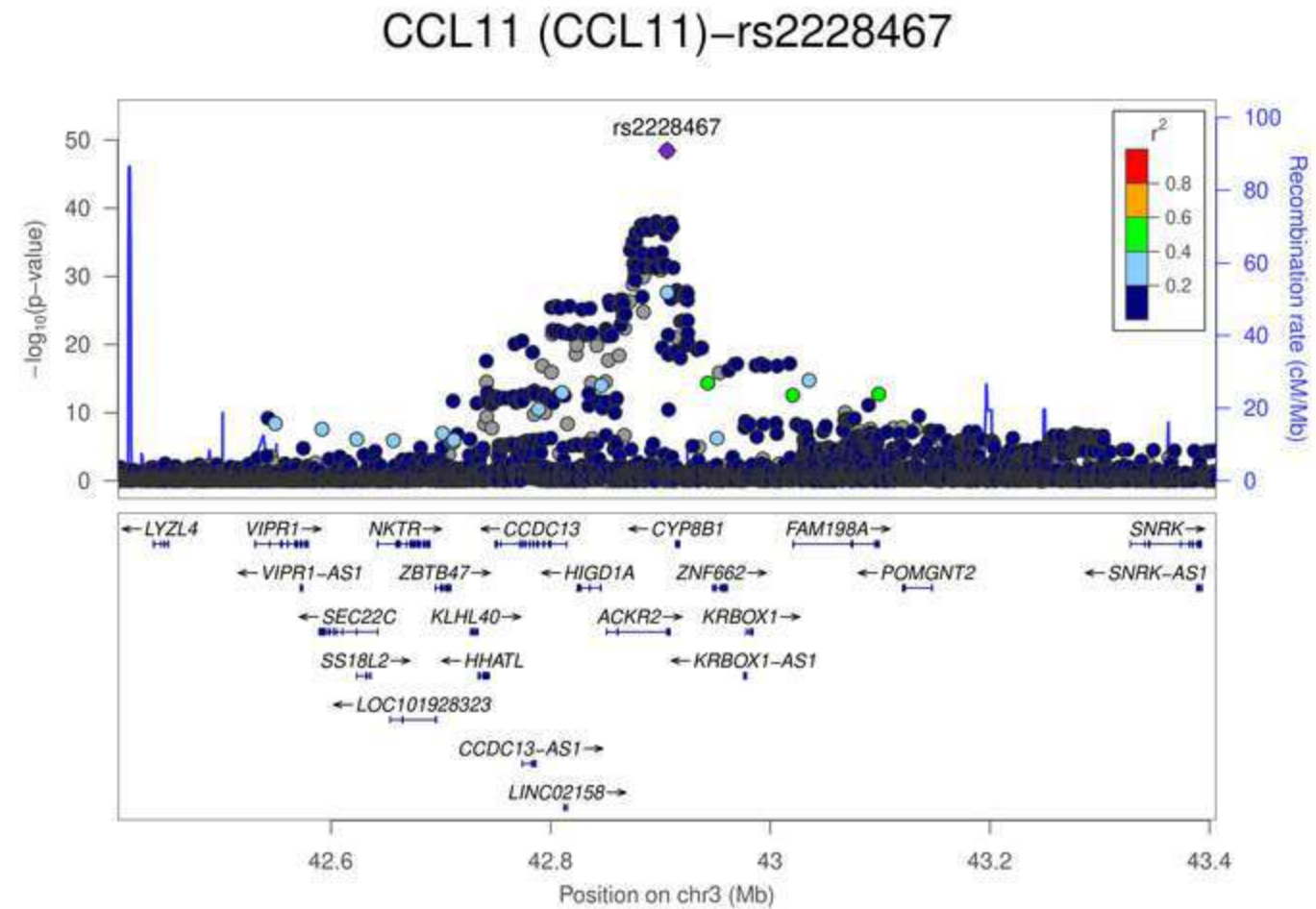
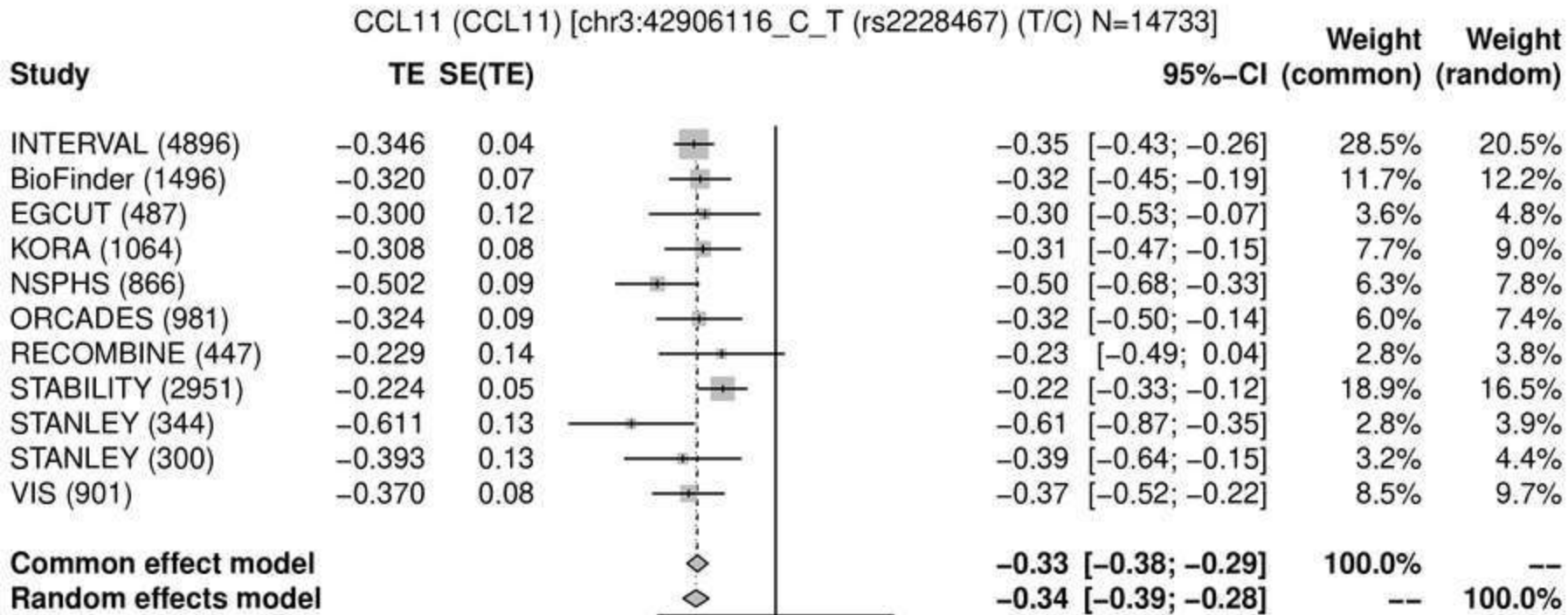
6.0%

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100.0%

CCL11 (CCL11)-rs79722574





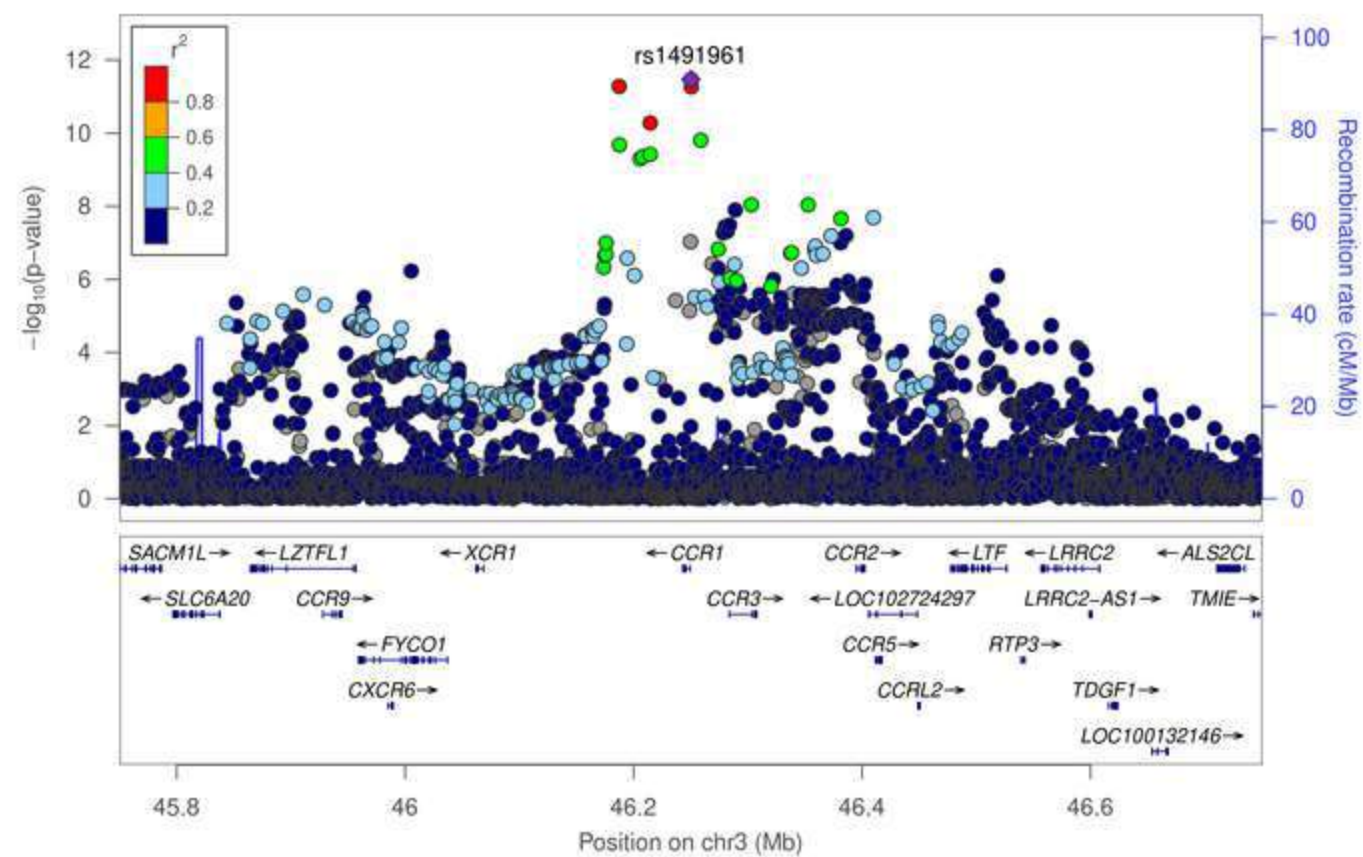
CCL11 (CCL11) [chr3:46250348_C_T (rs1491961) (T/C) N=14286]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.040	0.02	0.04 [-0.00; 0.08]	35.0%	19.1%
BioFinder (1496)	0.104	0.04	0.10 [0.02; 0.19]	10.1%	12.1%
EGCUT (487)	0.249	0.07	0.25 [0.11; 0.39]	3.6%	6.3%
KORA (1064)	0.118	0.05	0.12 [0.03; 0.21]	8.0%	10.7%
NSPHS (866)	0.164	0.05	0.16 [0.06; 0.27]	6.5%	9.5%
ORCADES (981)	0.079	0.06	0.08 [-0.03; 0.19]	5.7%	8.7%
STABILITY (2951)	0.085	0.03	0.09 [0.03; 0.14]	21.0%	16.6%
STANLEY (344)	0.185	0.10	0.18 [-0.02; 0.39]	1.7%	3.4%
STANLEY (300)	0.229	0.09	0.23 [0.05; 0.40]	2.2%	4.3%
VIS (901)	0.142	0.05	0.14 [0.04; 0.25]	6.2%	9.2%
Common effect model			0.09 [0.07; 0.12]	100.0%	--
Random effects model			0.11 [0.07; 0.15]	--	100.0%

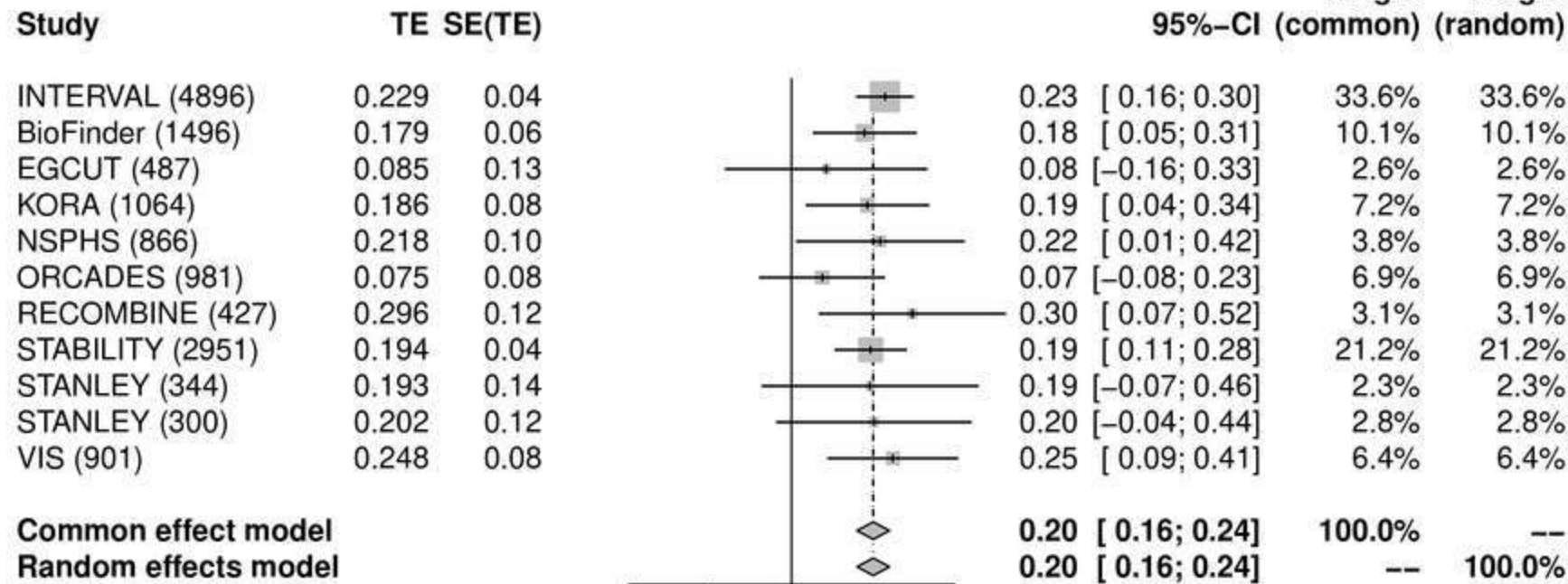
-0.4 -0.2 0 0.2 0.4

Heterogeneity: $I^2 = 46\%$, $\tau^2 = 0.0017$, $p = 0.05$

CCL11 (CCL11)-rs1491961

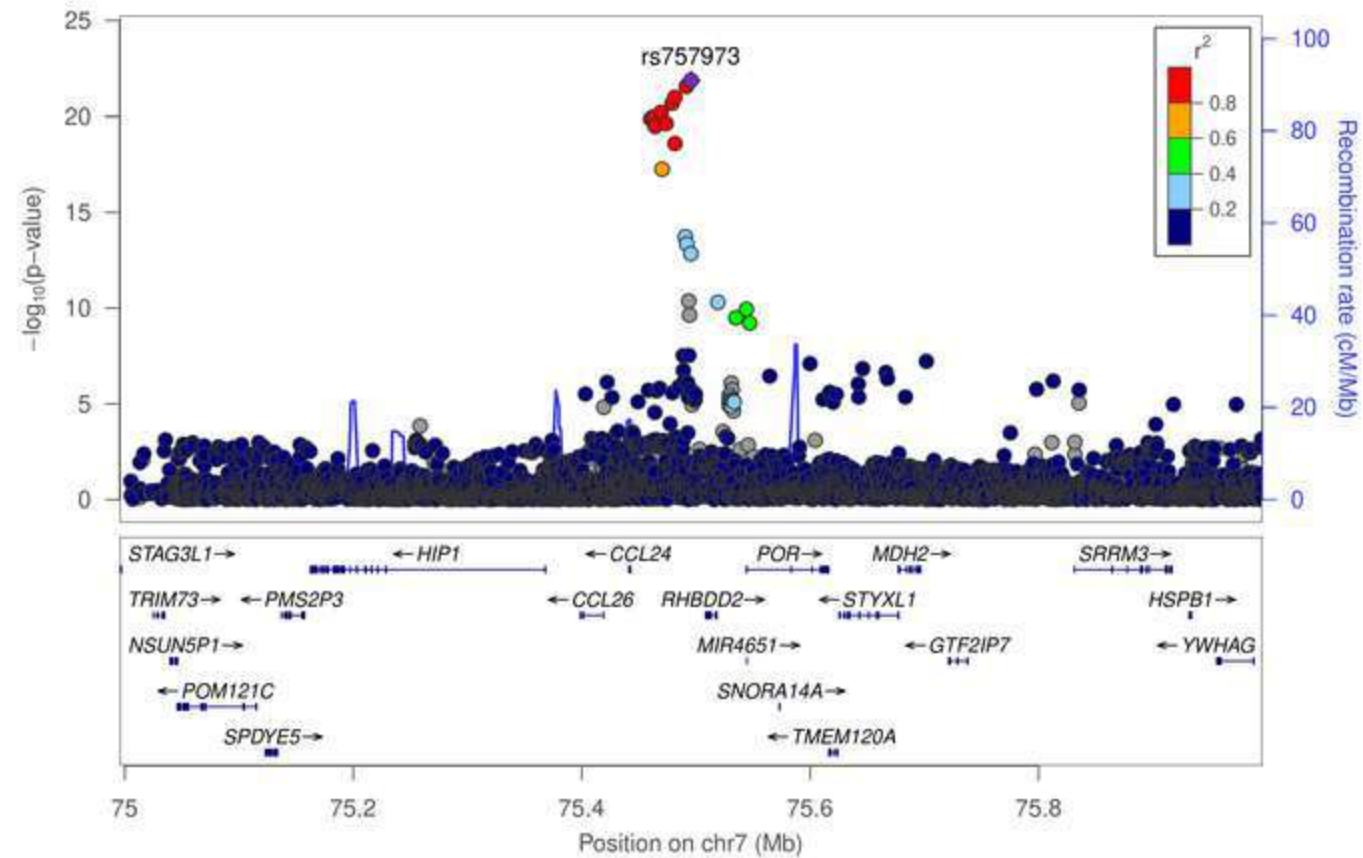


CCL11 (CCL11) [chr7:75495667_A_G (rs757973) (A/G) N=14713]

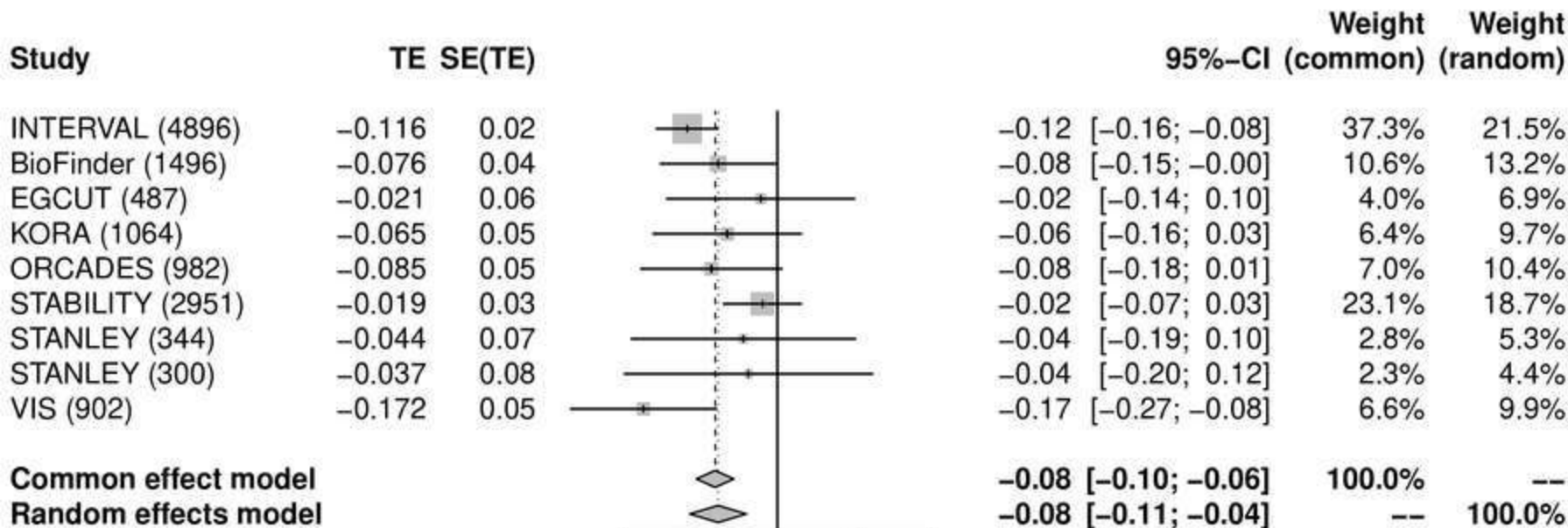


Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.87$

CCL11 (CCL11)-rs757973

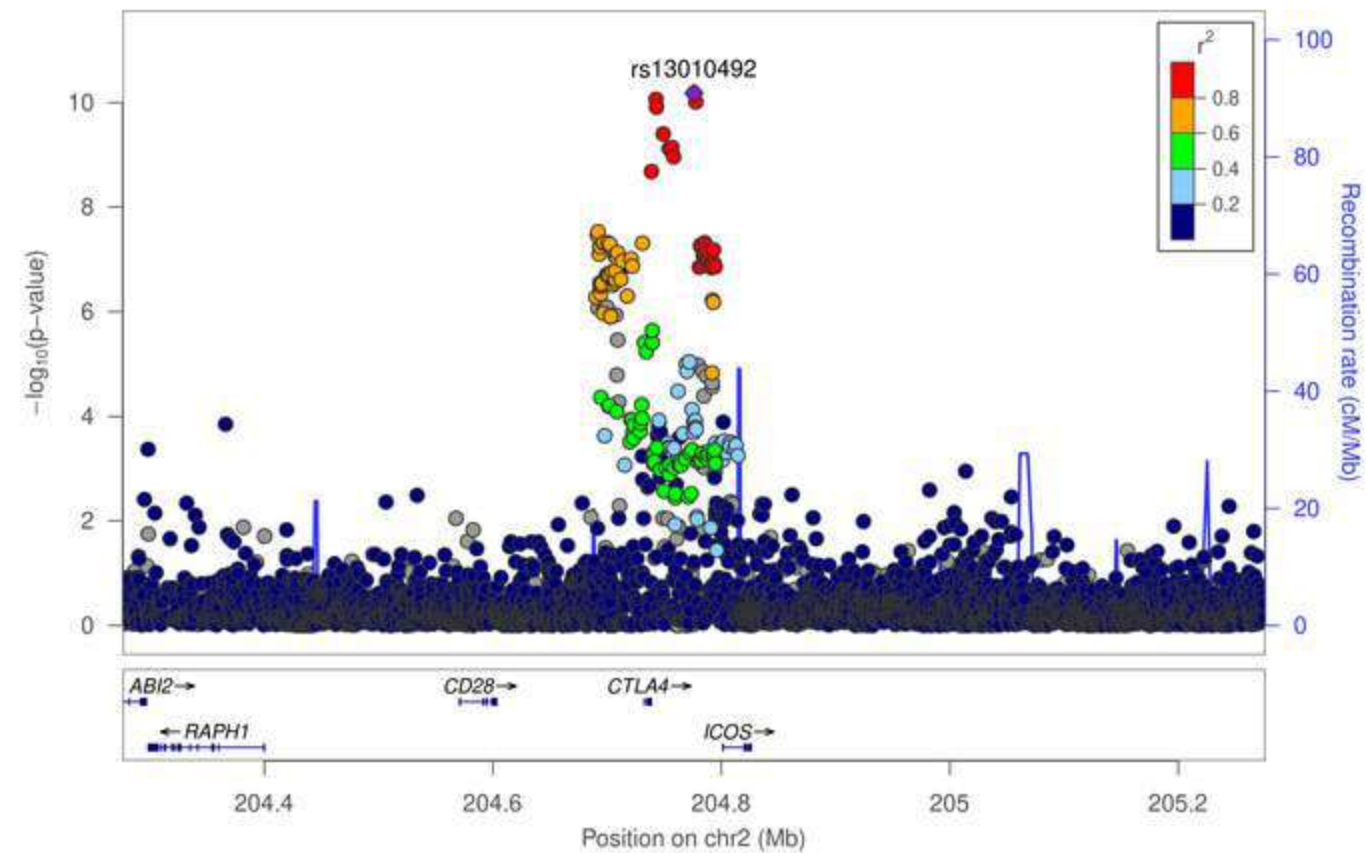


CCL19 (CCL19) [chr2:204776176_C_G (rs13010492) (C/G) N=13422]



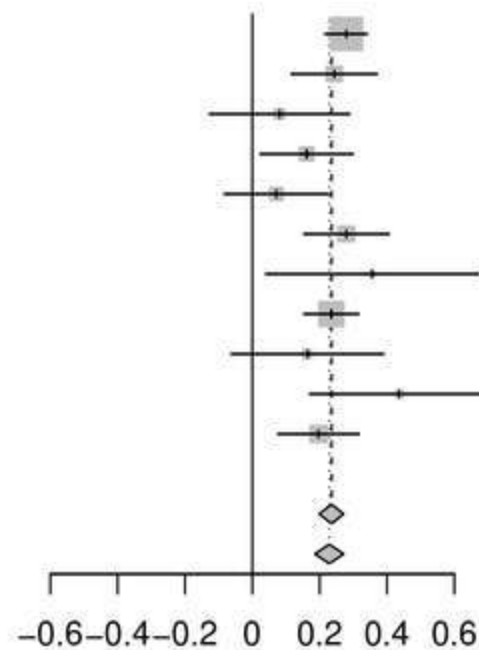
Heterogeneity: $I^2 = 43\%$, $\tau^2 = 0.0012$, $p = 0.08$

CCL19 (CCL19)-rs13010492

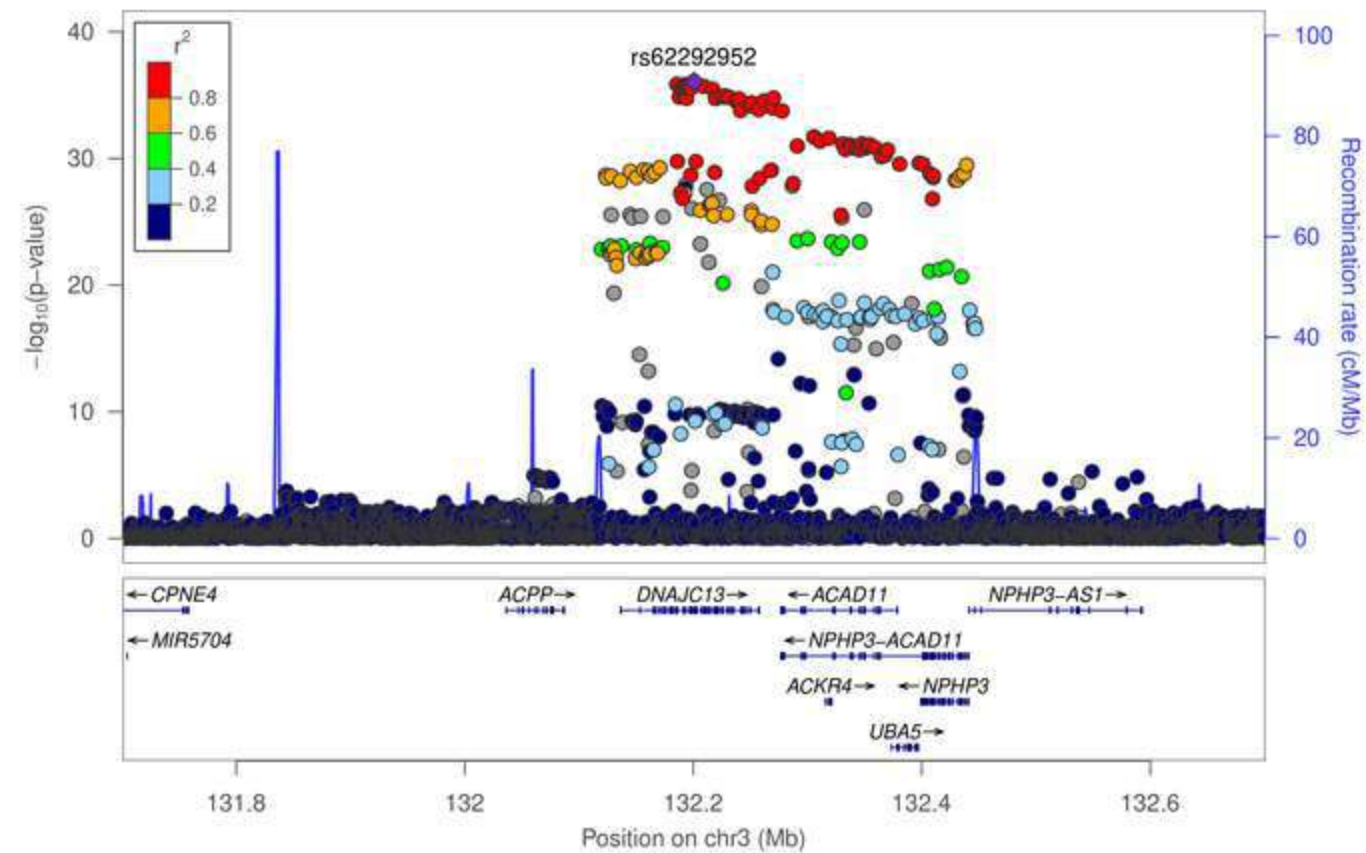


CCL19 (CCL19) [chr3:132200719_G_T (rs62292952) (T/G) N=14728]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.278	0.03	0.28 [0.22; 0.34]	33.6%
BioFinder (1496)	0.243	0.07	0.24 [0.12; 0.37]	8.1%
EGCUT (487)	0.081	0.11	0.08 [-0.13; 0.29]	3.0%
KORA (1064)	0.161	0.07	0.16 [0.02; 0.30]	6.9%
NSPHS (866)	0.071	0.08	0.07 [-0.08; 0.23]	5.5%
ORCADES (982)	0.279	0.06	0.28 [0.15; 0.41]	8.2%
RECOMBINE (440)	0.356	0.16	0.36 [0.04; 0.67]	1.3%
STABILITY (2951)	0.234	0.04	0.23 [0.15; 0.32]	19.8%
STANLEY (344)	0.163	0.12	0.16 [-0.06; 0.39]	2.6%
STANLEY (300)	0.436	0.14	0.44 [0.17; 0.70]	1.9%
VIS (902)	0.196	0.06	0.20 [0.08; 0.32]	9.1%
Common effect model			0.23 [0.20; 0.27]	100.0%
Random effects model			0.23 [0.19; 0.27]	-- 100.0%



CCL19 (CCL19)-rs62292952



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (447)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 19\%$, $\tau^2 < 0.0001$, $p = 0.26$

CCL19 (CCL19) [chr6:32444093_C_G (rs9469127) (C/G) N=14735]

TE SE(TE)

-0.525 0.06

-0.444 0.09

-0.542 0.12

-0.456 0.10

-0.502 0.07

-0.521 0.13

-0.737 0.22

-0.416 0.06

-0.620 0.16

-1.036 0.21

-0.392 0.11

SE(TE)

0.06

0.09

0.12

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0.07

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0.22

0.06

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SE(TE)

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Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (445)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 0\%$, $\tau^2 < 0.0001$, $p = 0.83$

CCL19 (CCL19) [chr9:34710084_A_C (rs11574915) (A/C) N=14733]

TE SE(TE)

-0.187

0.03

-0.092

0.06

-0.069

0.08

-0.143

0.06

-0.079

0.08

-0.093

0.06

-0.105

0.13

-0.170

0.04

-0.140

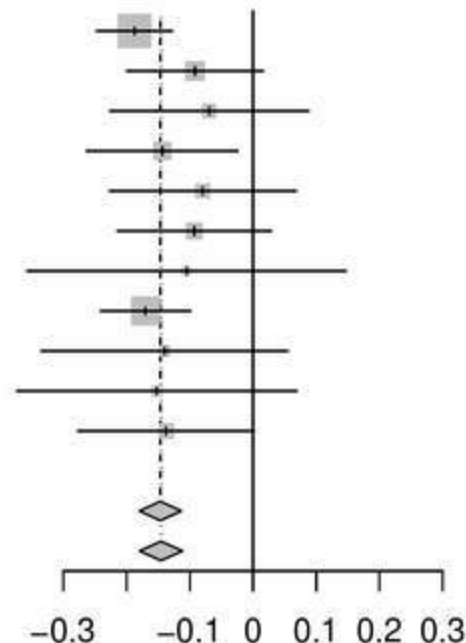
0.10

-0.152

0.11

-0.137

0.07

Weight
95%-CI (common) (random)

-0.19 [-0.25; -0.13]

30.9%

29.7%

-0.09 [-0.20; 0.02]

9.6%

9.8%

-0.07 [-0.23; 0.09]

4.5%

4.7%

-0.14 [-0.26; -0.02]

7.8%

8.0%

-0.08 [-0.23; 0.07]

5.1%

5.3%

-0.09 [-0.21; 0.03]

7.5%

7.7%

-0.11 [-0.36; 0.15]

1.7%

1.8%

-0.17 [-0.24; -0.10]

21.9%

21.6%

-0.14 [-0.33; 0.06]

2.9%

3.1%

-0.15 [-0.37; 0.07]

2.3%

2.4%

-0.14 [-0.28; 0.00]

5.7%

5.9%

-0.15 [-0.18; -0.11]

100.0%

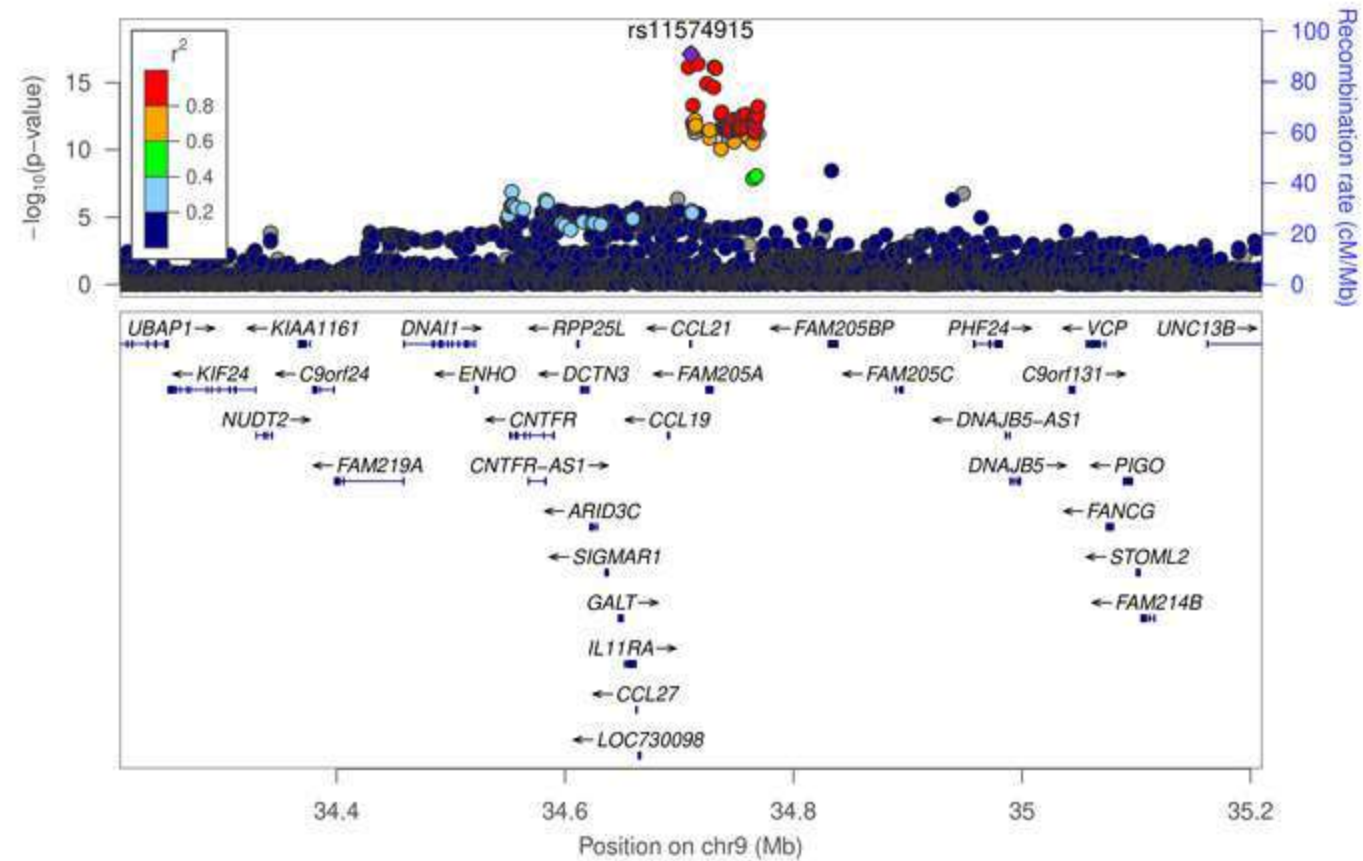
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-0.15 [-0.18; -0.11]

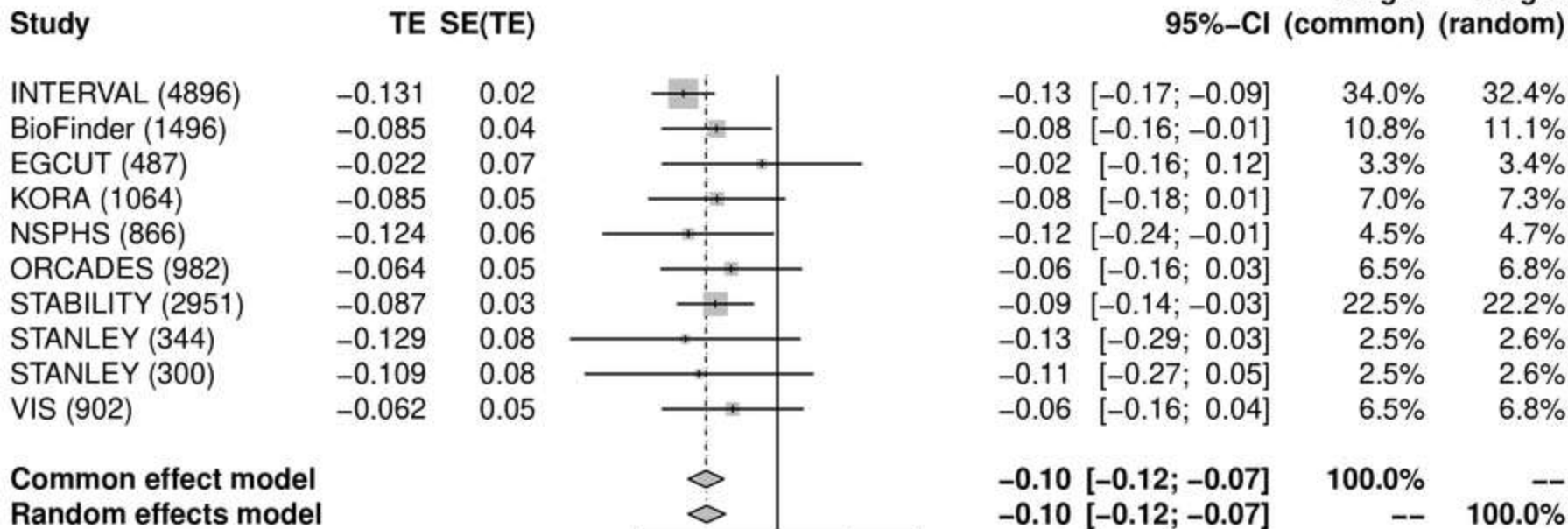
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100.0%

CCL19 (CCL19)-rs11574915

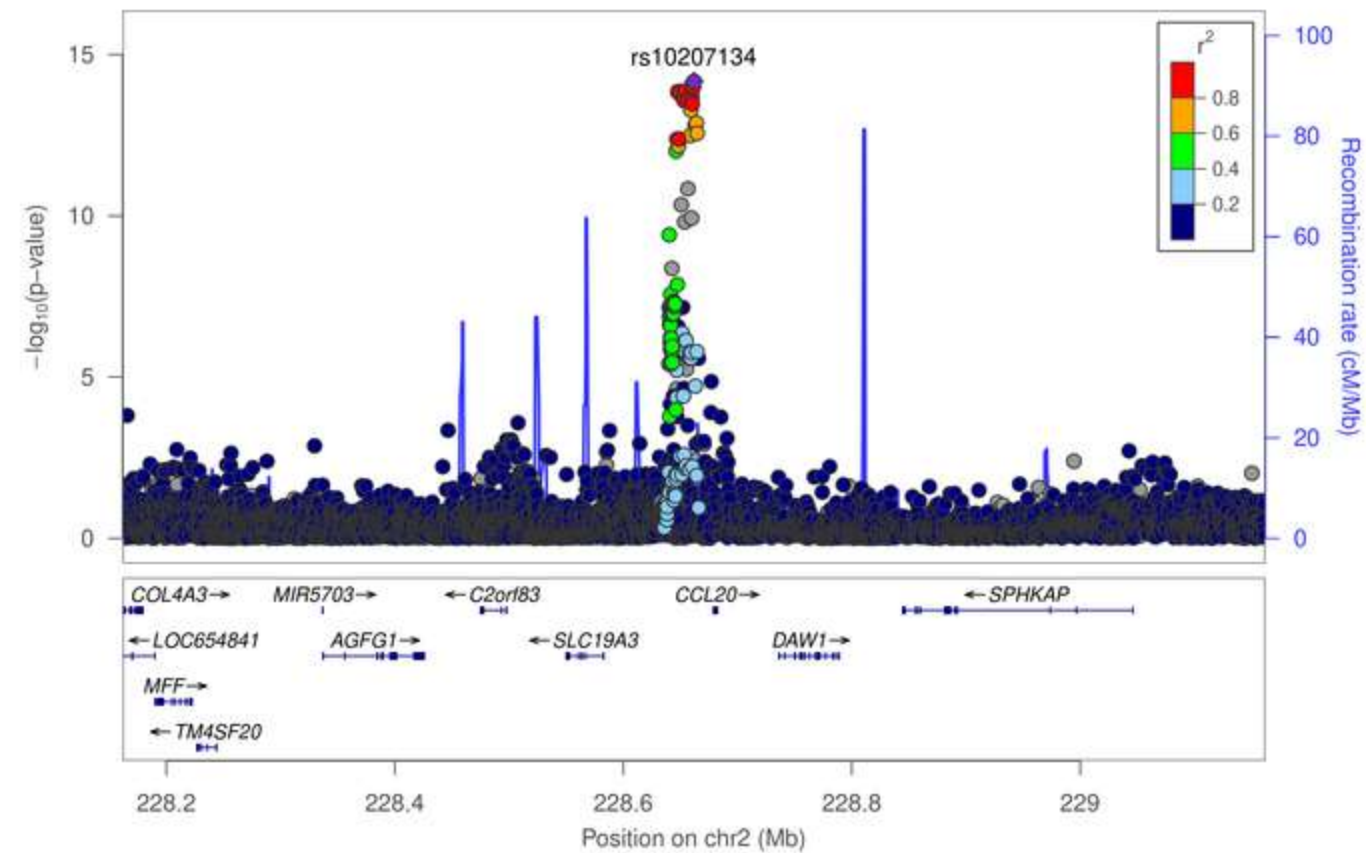


CCL20 (CCL20) [chr2:228661828_C_T (rs10207134) (T/C) N=14288]

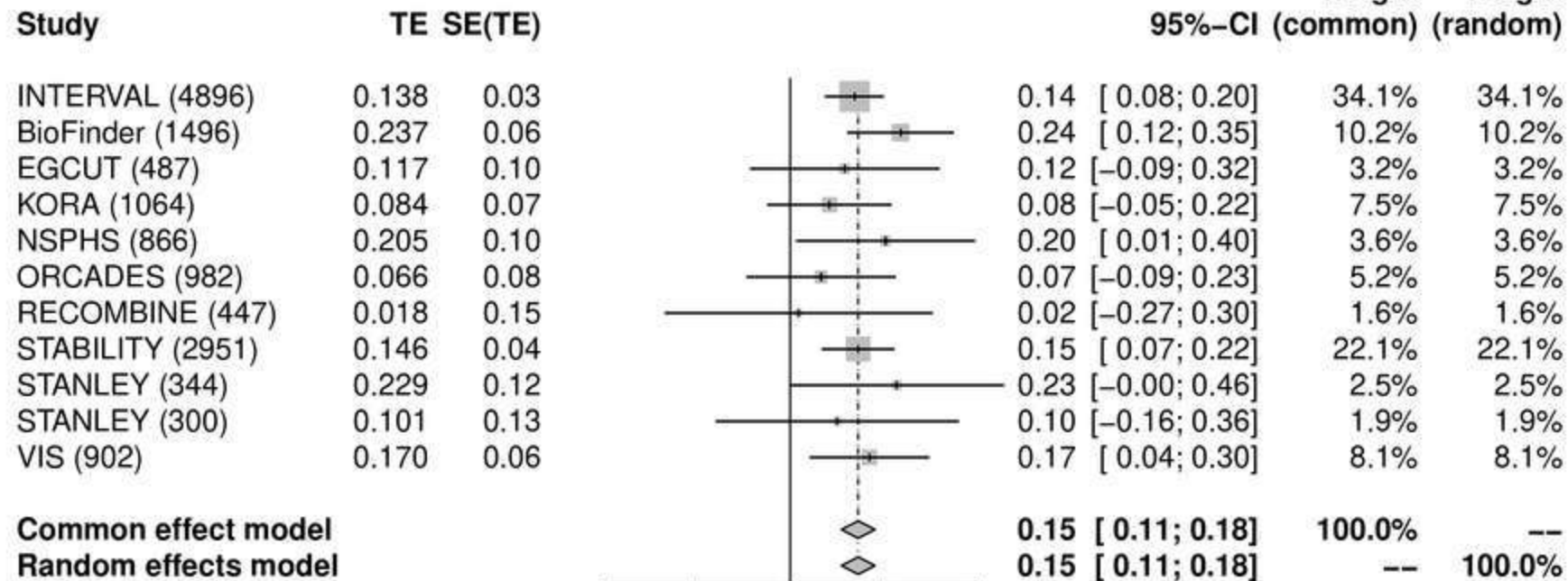


Heterogeneity: $I^2 = 0\%$, $\tau^2 < 0.0001$, $p = 0.82$

CCL20 (CCL20)-rs10207134

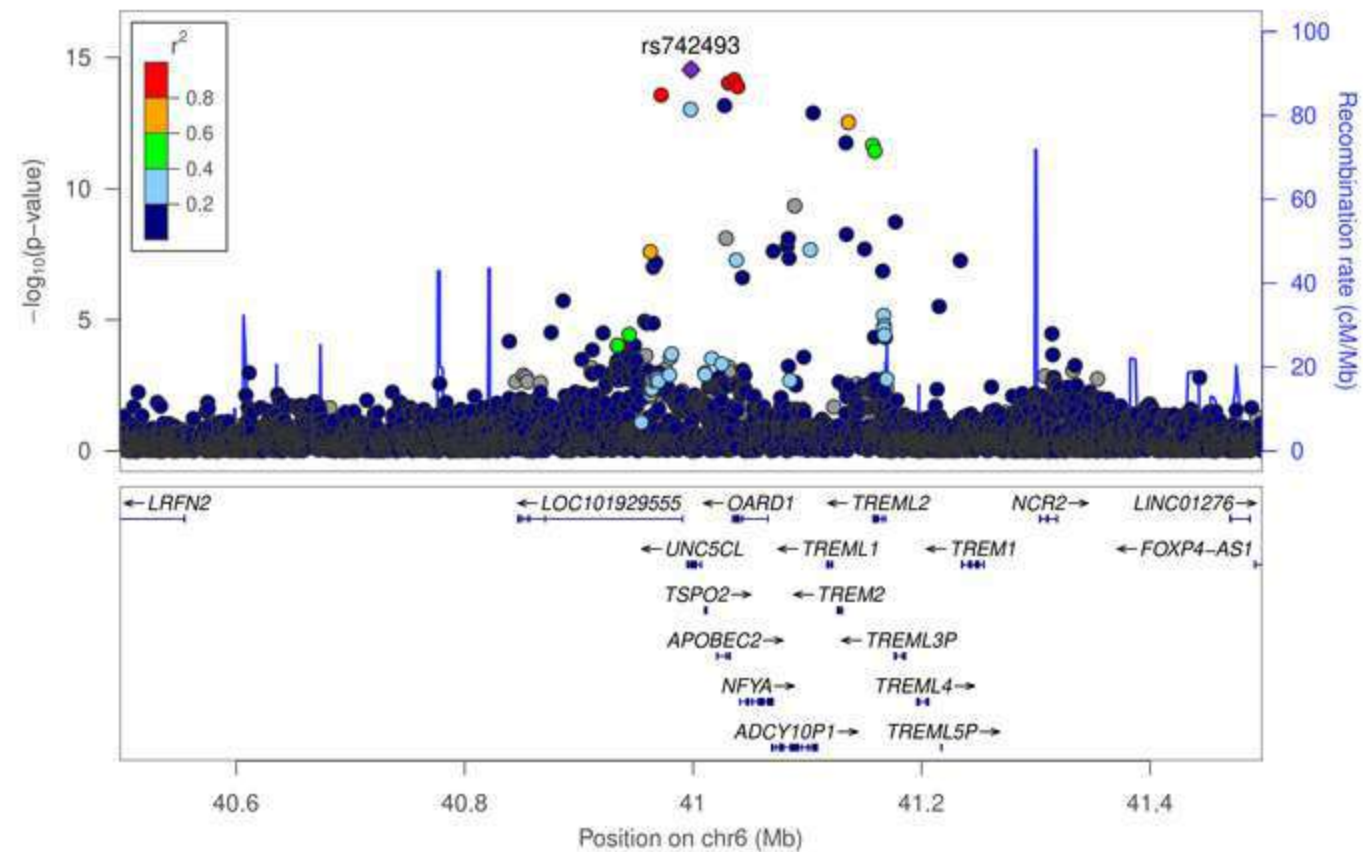


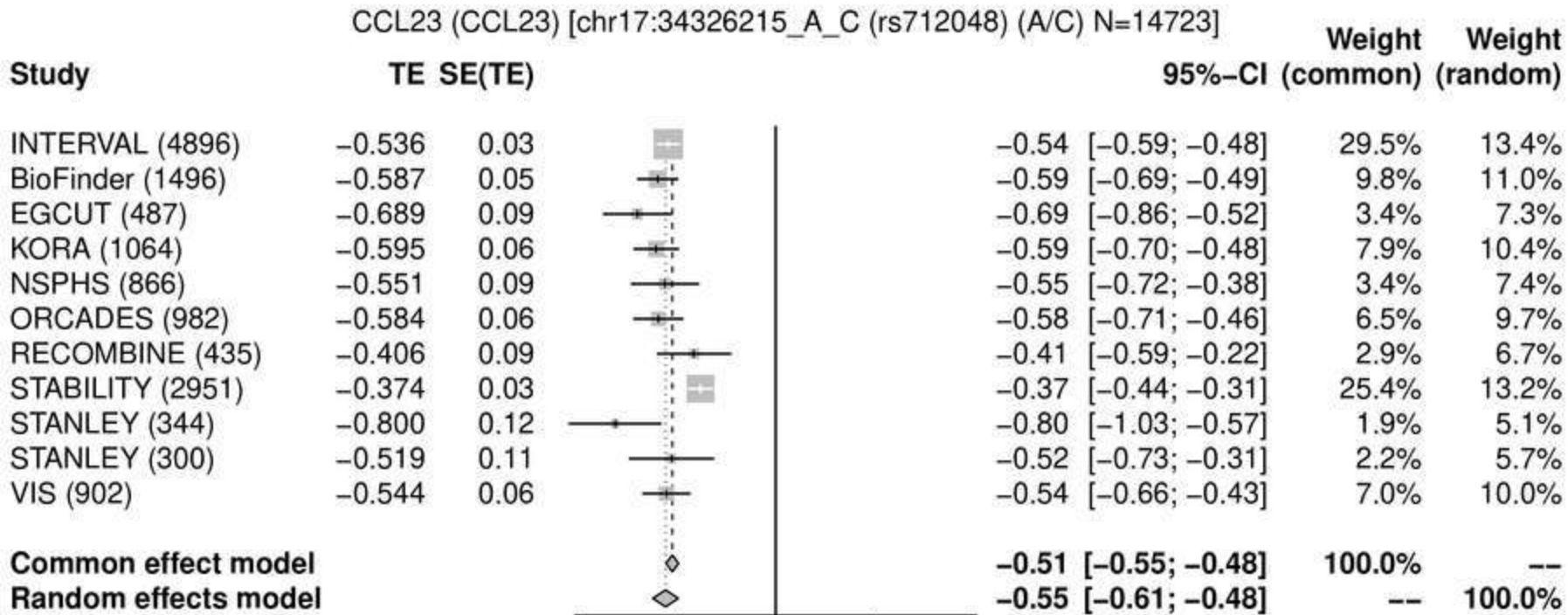
CCL20 (CCL20) [chr6:40998167_C_T (rs742493) (T/C) N=14735]



Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.79$

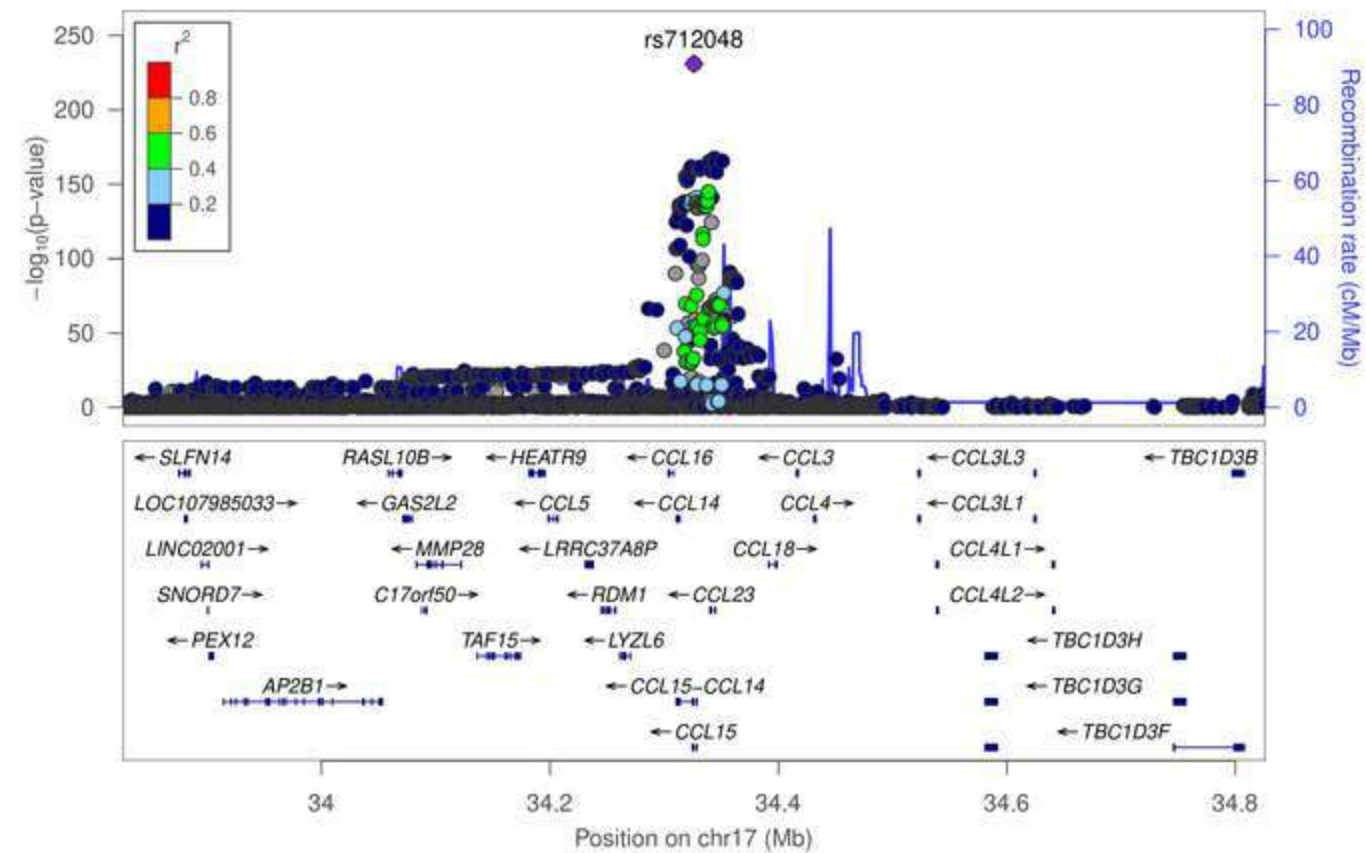
CCL20 (CCL20)-rs742493





Heterogeneity: $I^2 = 74\%$, $\tau^2 = 0.0070$, $p < 0.01$

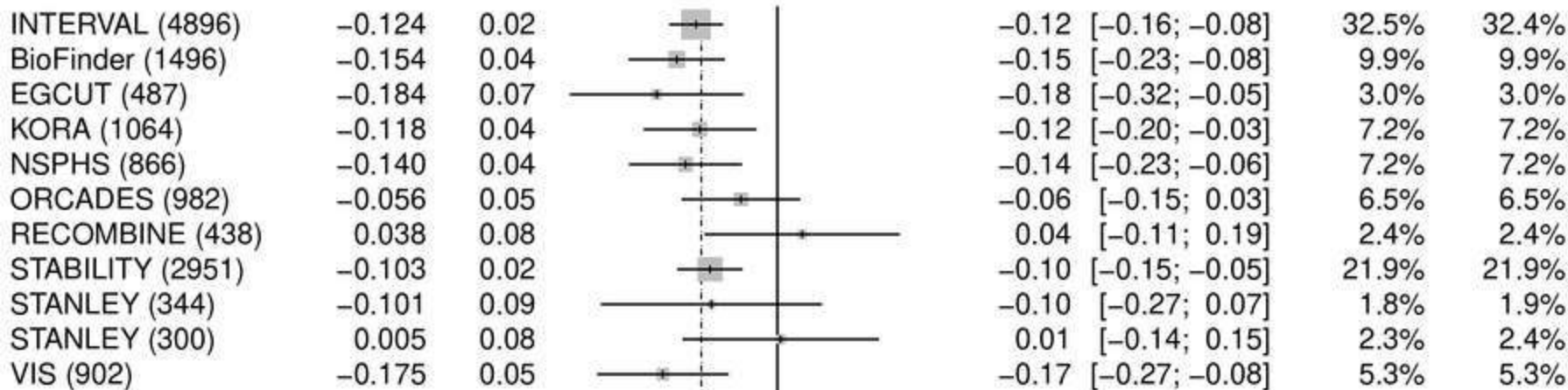
CCL23 (CCL23)-rs712048



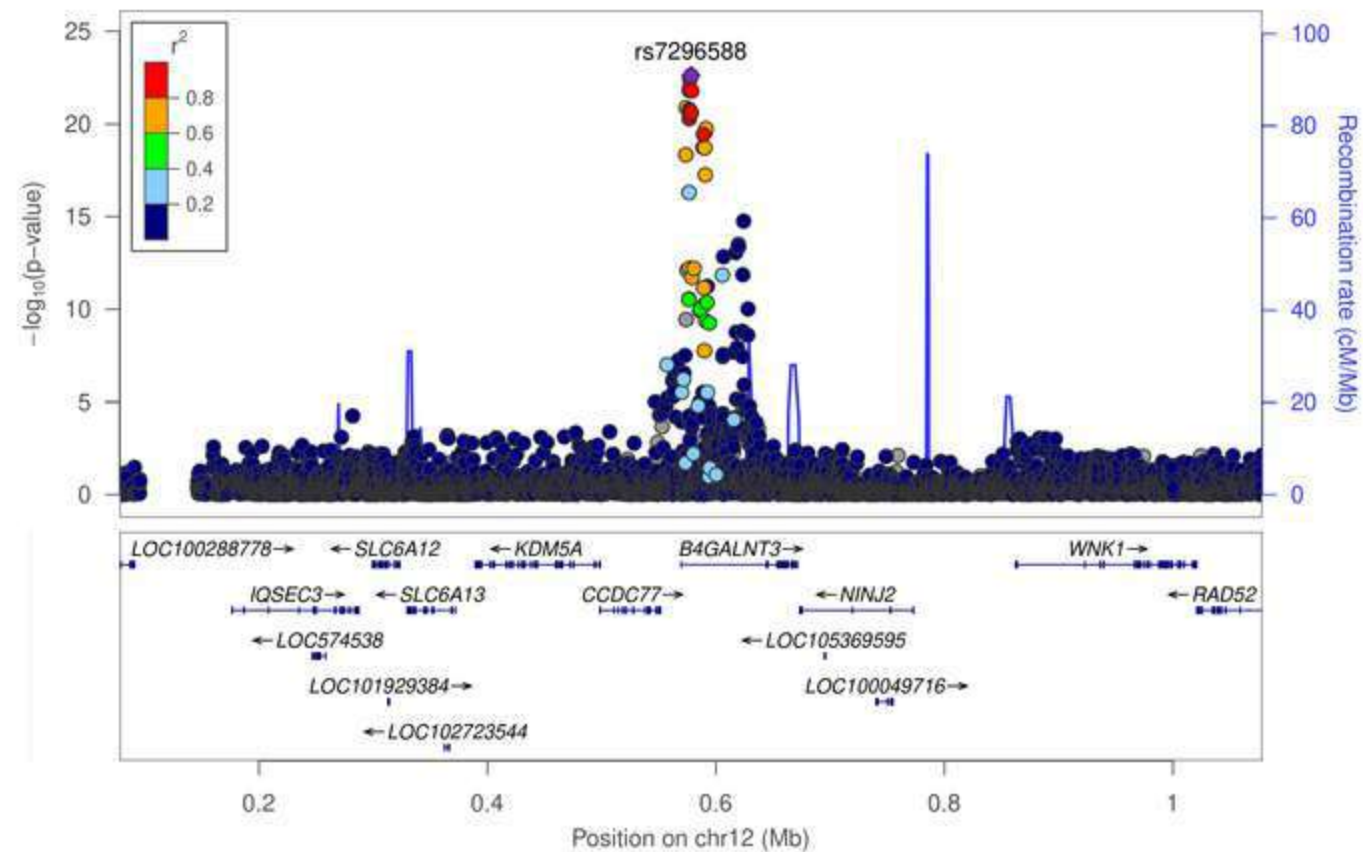
Study

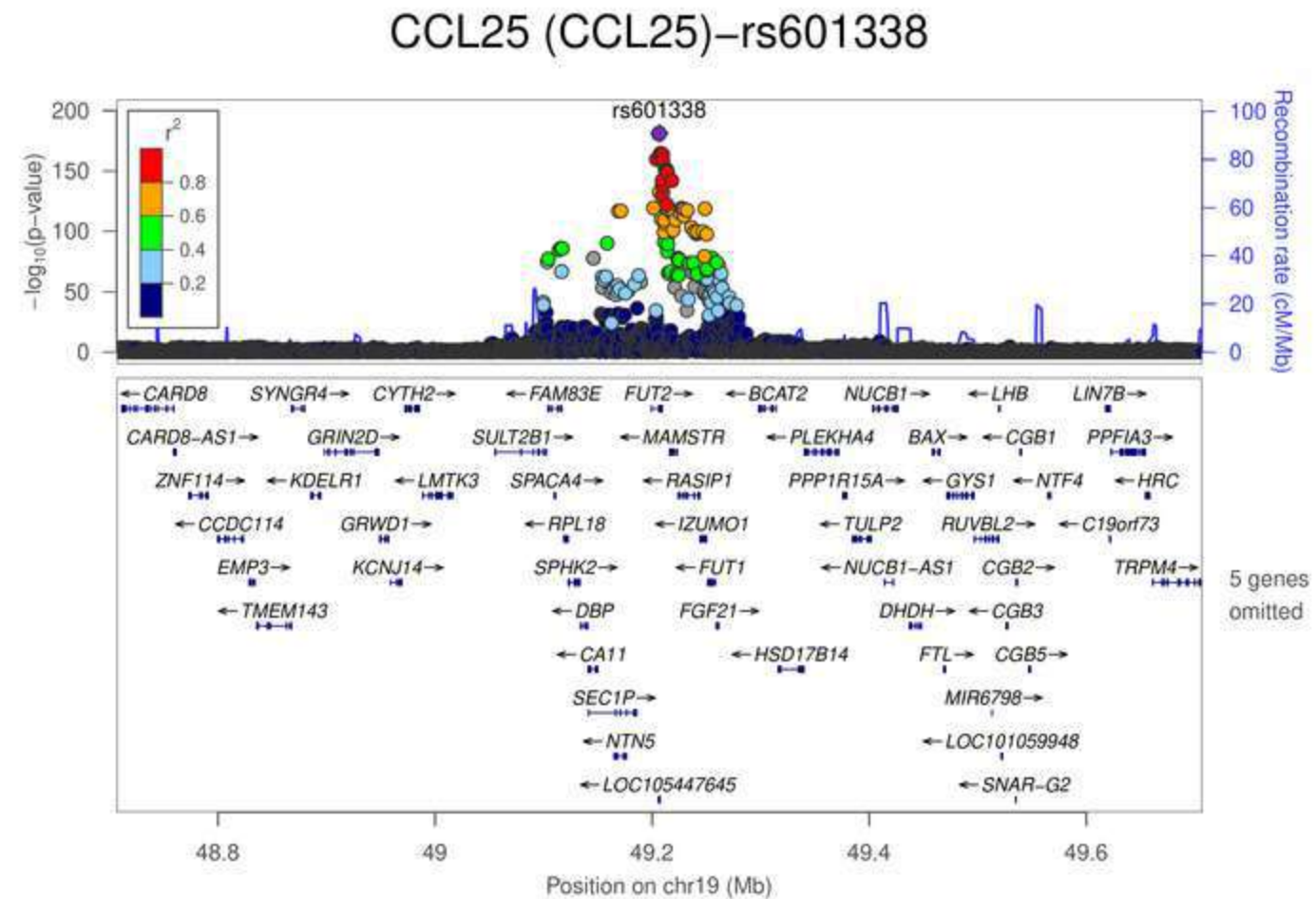
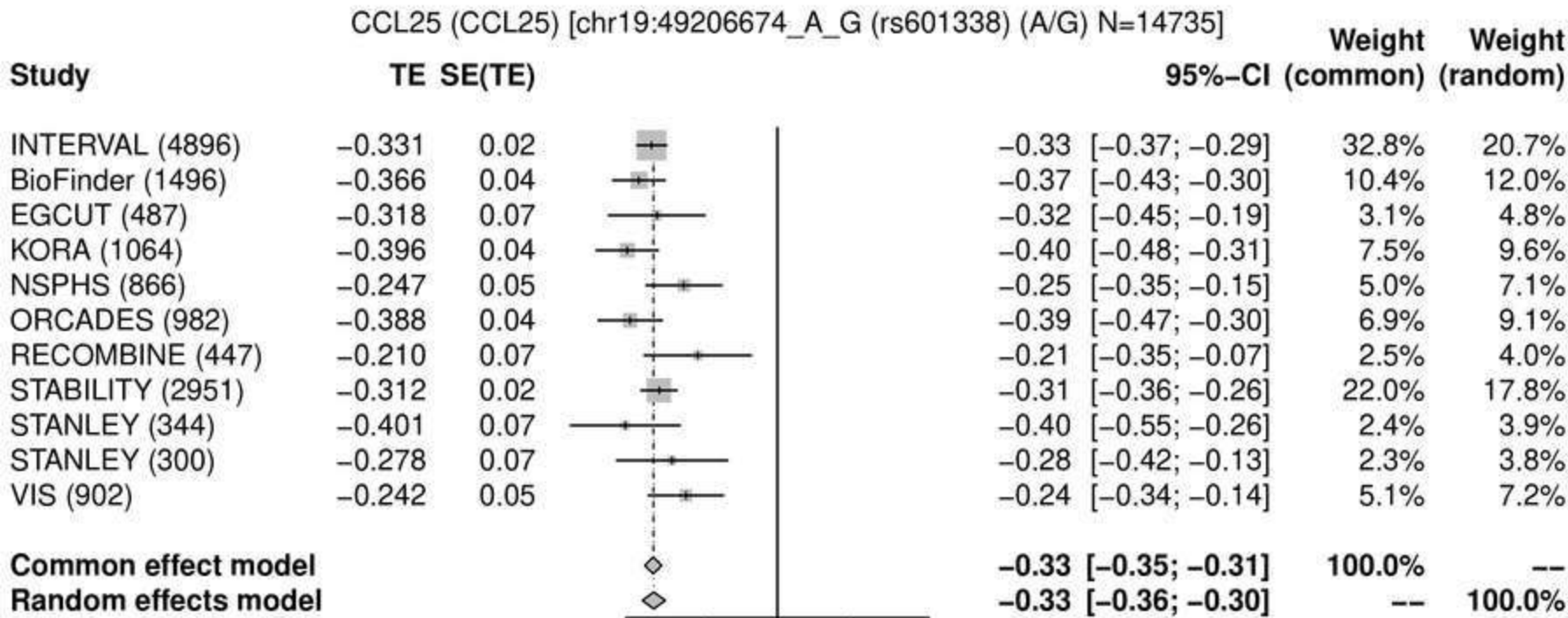
CCL25 (CCL25) [chr12:578100_A_G (rs7296588) (A/G) N=14726]

TE SE(TE)

Weight
95%-CI (common) Weight
(random)Common effect model
Random effects modelHeterogeneity: $I^2 = 21\%$, $\tau^2 < 0.0001$, $p = 0.25$

CCL25 (CCL25)-rs7296588





Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (446)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 87\%$, $\tau^2 = 0.0176$, $p < 0.01$

CCL25 (CCL25) [chr19:8121360_A_G (rs2032887) (A/G) N=14734]

TE SE(TE)

-0.853

0.02

-0.736

0.04

-0.650

0.07

-0.921

0.07

-0.582

0.05

-0.794

0.05

-0.368

0.09

-0.664

0.03

-0.861

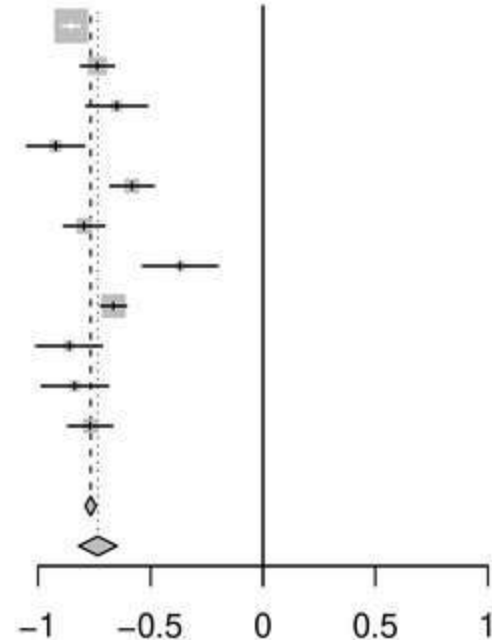
0.07

-0.836

0.08

-0.767

0.05

Weight
95%-CI (common) (random)

-0.85

[-0.89; -0.81]

37.8%

10.5%

-0.74

[-0.81; -0.66]

10.5%

9.9%

-0.65

[-0.79; -0.51]

3.2%

8.4%

-0.92

[-1.05; -0.79]

3.6%

8.6%

-0.58

[-0.68; -0.48]

6.2%

9.4%

-0.79

[-0.89; -0.70]

7.1%

9.6%

-0.37

[-0.54; -0.20]

2.1%

7.6%

-0.66

[-0.72; -0.61]

18.3%

10.3%

-0.86

[-1.01; -0.71]

2.7%

8.2%

-0.84

[-0.98; -0.69]

2.7%

8.1%

-0.77

[-0.87; -0.67]

6.0%

9.4%

-0.77 [-0.79; -0.74]

100.0%

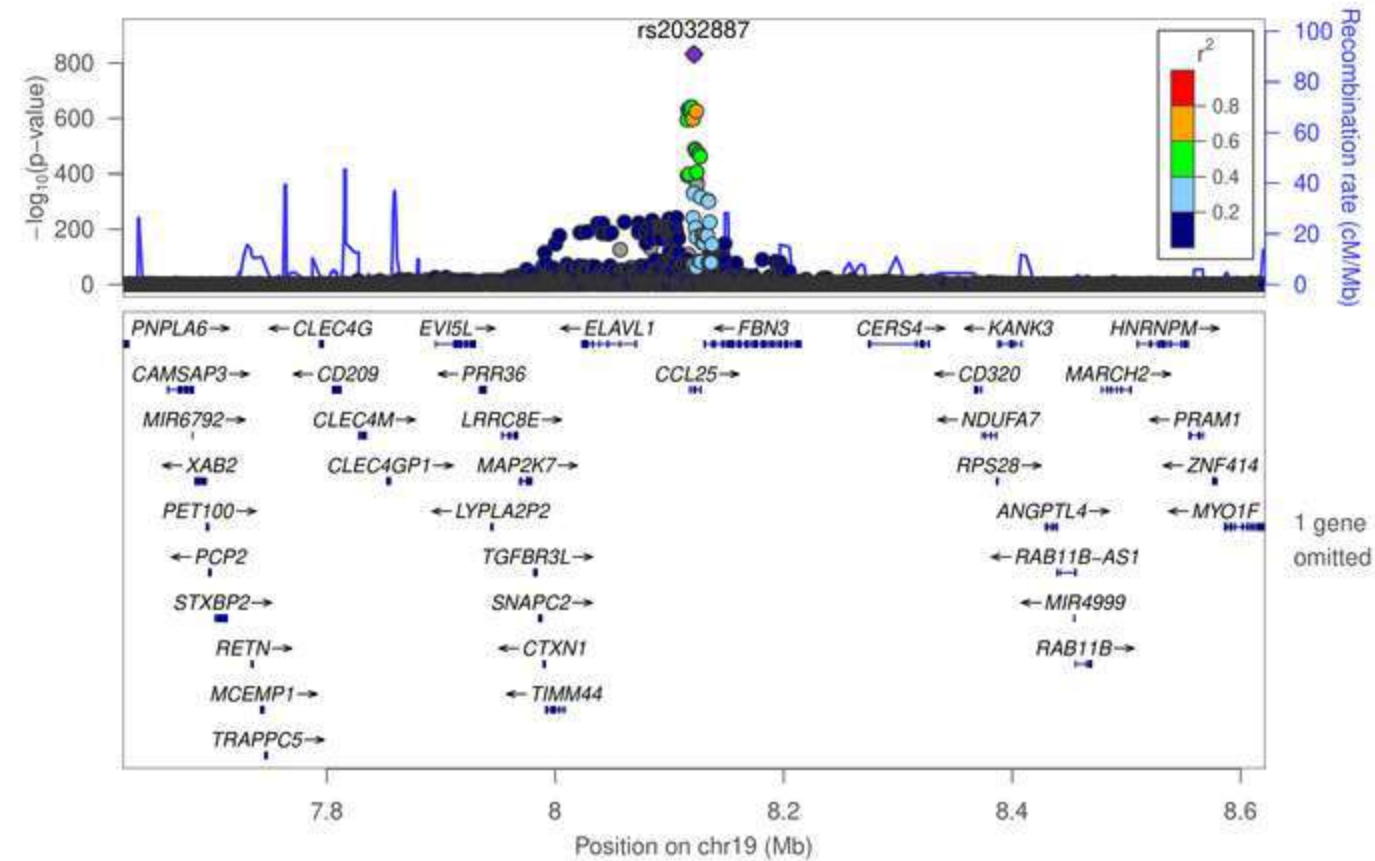
--

-0.73 [-0.82; -0.65]

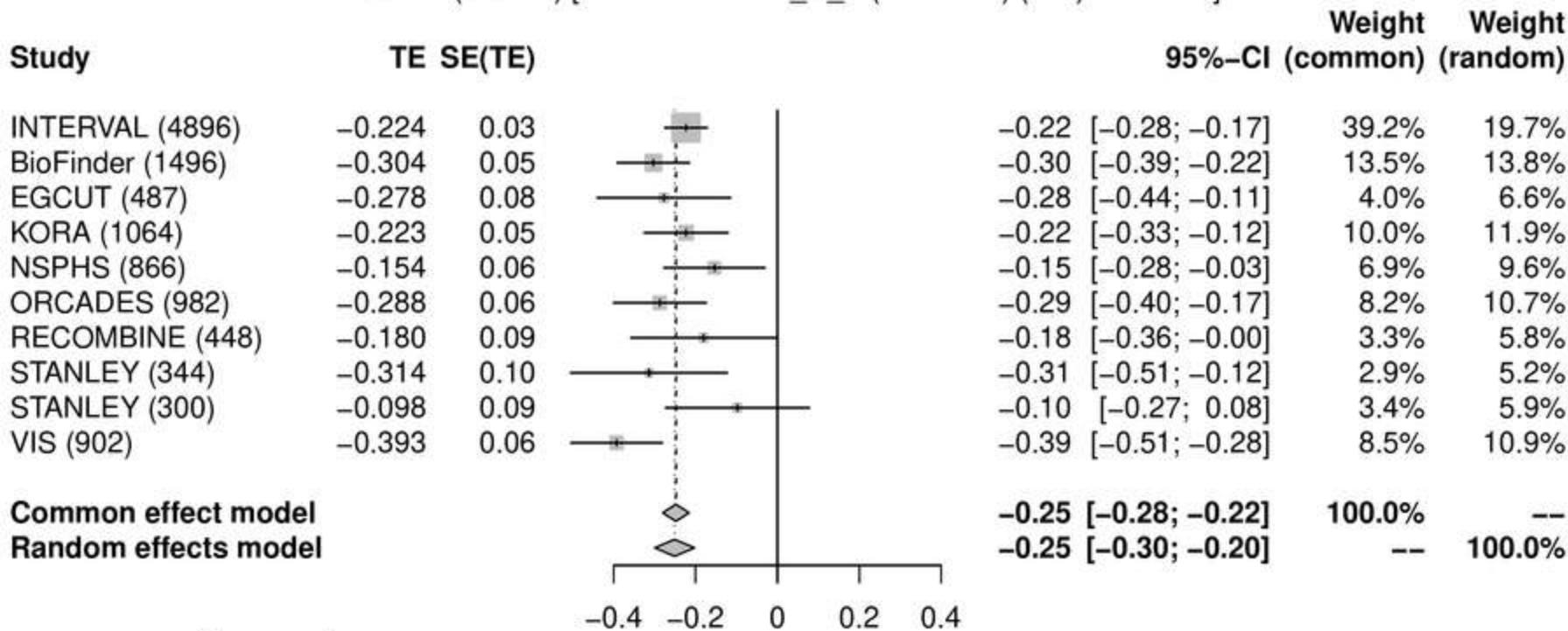
--

100.0%

CCL25 (CCL25)-rs2032887

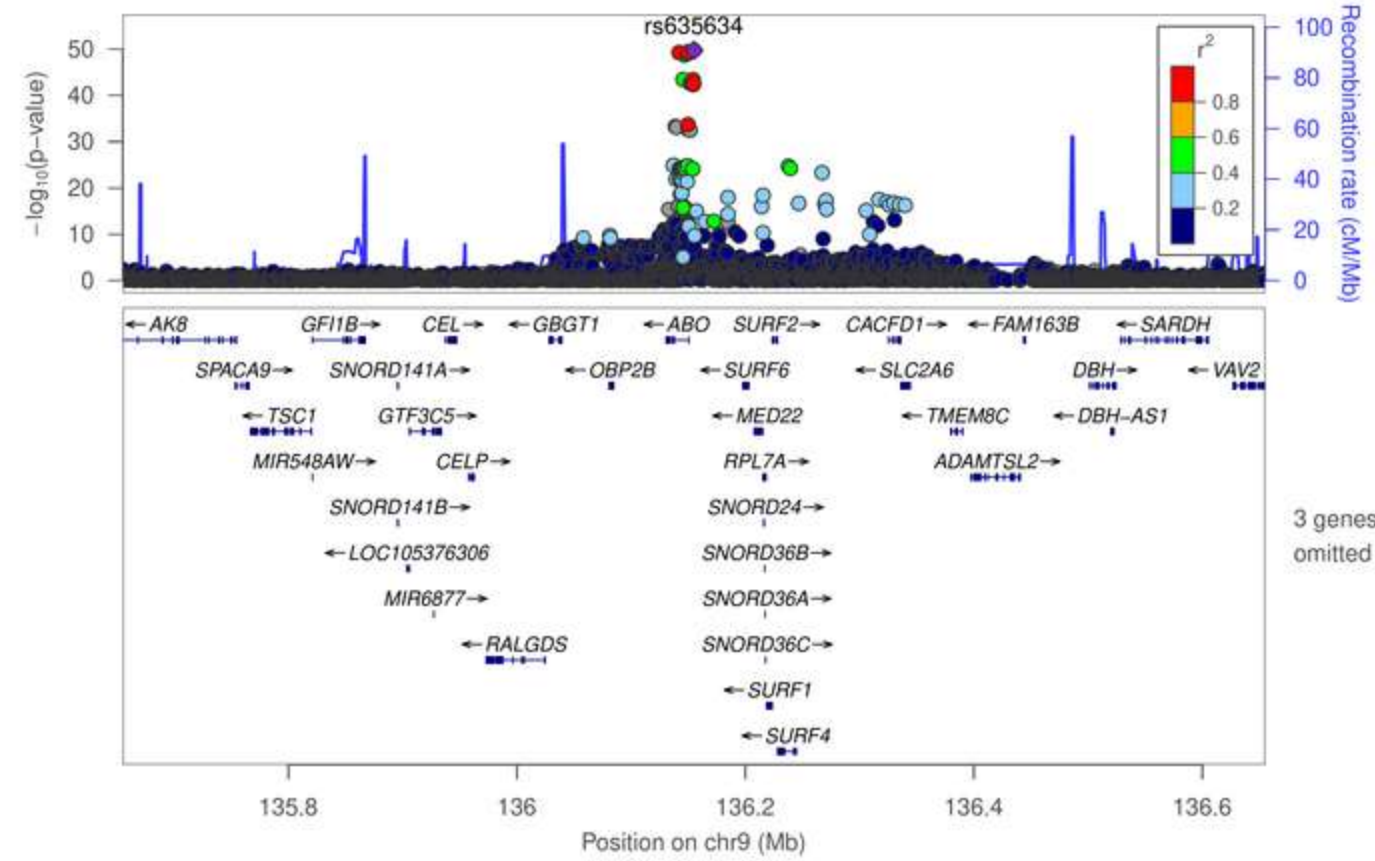


CCL25 (CCL25) [chr9:136155000_C_T (rs635634) (T/C) N=11785]

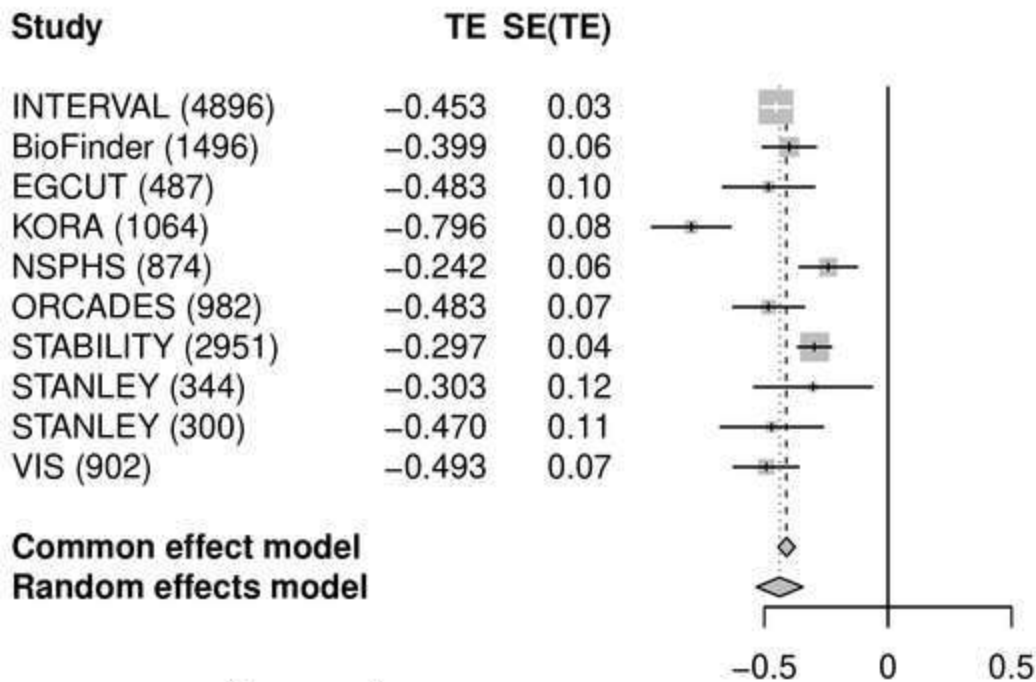


Heterogeneity: $I^2 = 43\%$, $\tau^2 = 0.0024$, $p = 0.07$

CCL25 (CCL25)-rs635634



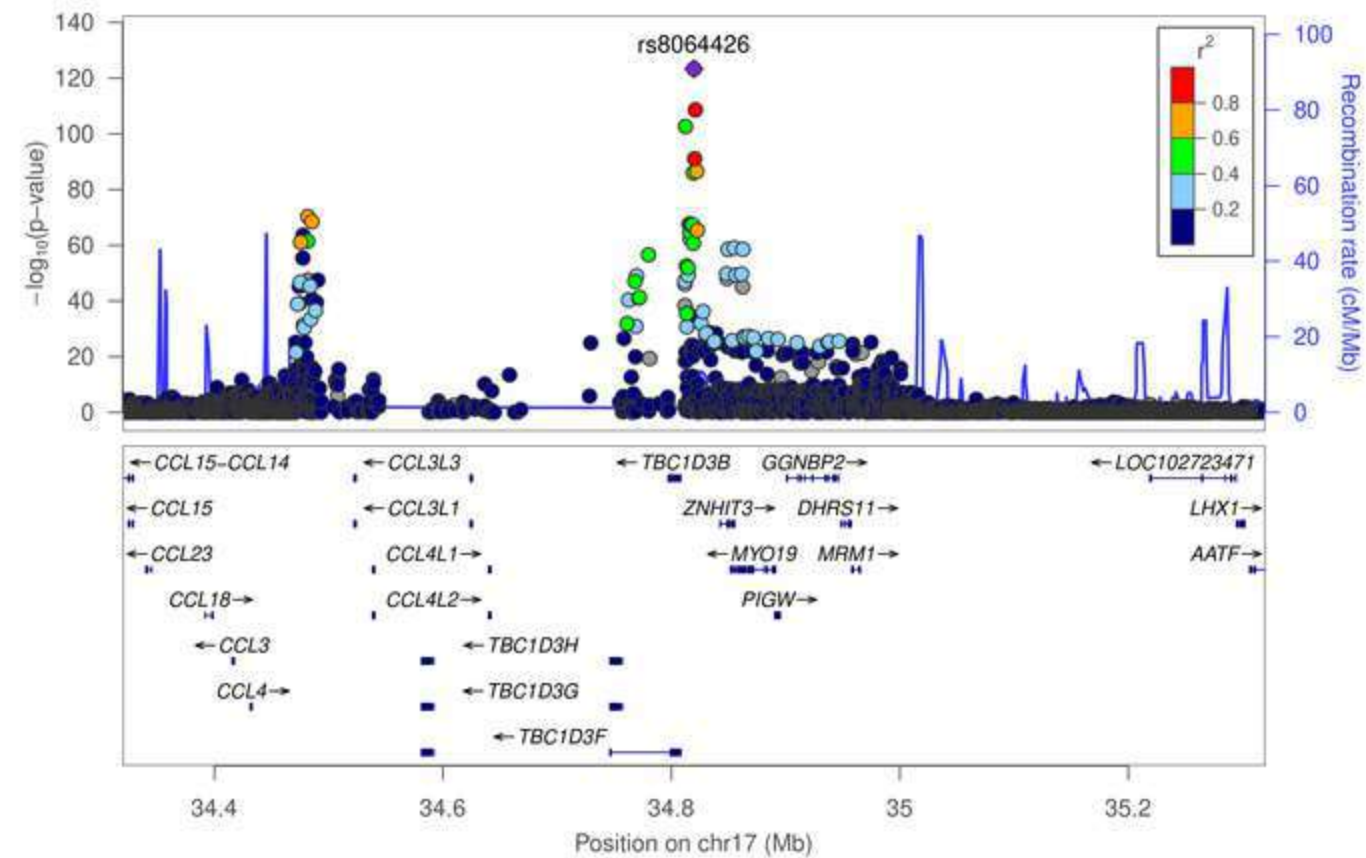
CCL4 (CCL4) [chr17:34819750_A_G (rs8064426) (A/G) N=14296]



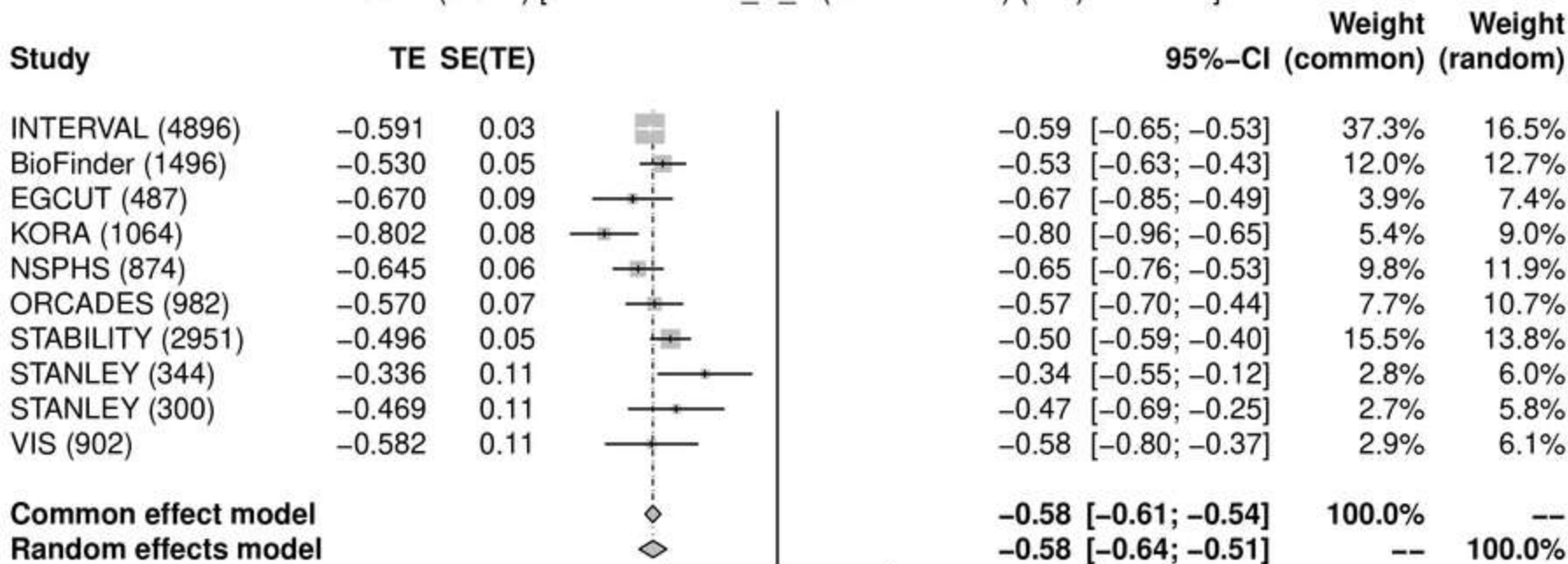
Heterogeneity: $I^2 = 81\%$, $\tau^2 = 0.0178$, $p < 0.01$

	Weight	Weight
95%-CI (common)	(common)	(random)
-0.45 [-0.51; -0.39]	32.9%	12.4%
-0.40 [-0.51; -0.29]	9.7%	11.1%
-0.48 [-0.67; -0.30]	3.3%	8.6%
-0.80 [-0.96; -0.64]	4.5%	9.5%
-0.24 [-0.36; -0.12]	8.4%	10.8%
-0.48 [-0.63; -0.34]	5.5%	10.0%
-0.30 [-0.37; -0.23]	24.4%	12.2%
-0.30 [-0.54; -0.06]	2.0%	7.1%
-0.47 [-0.68; -0.26]	2.6%	8.0%
-0.49 [-0.63; -0.36]	6.6%	10.4%
-0.41 [-0.44; -0.38]	100.0%	--
-0.44 [-0.53; -0.34]	--	100.0%

CCL4 (CCL4)-rs8064426

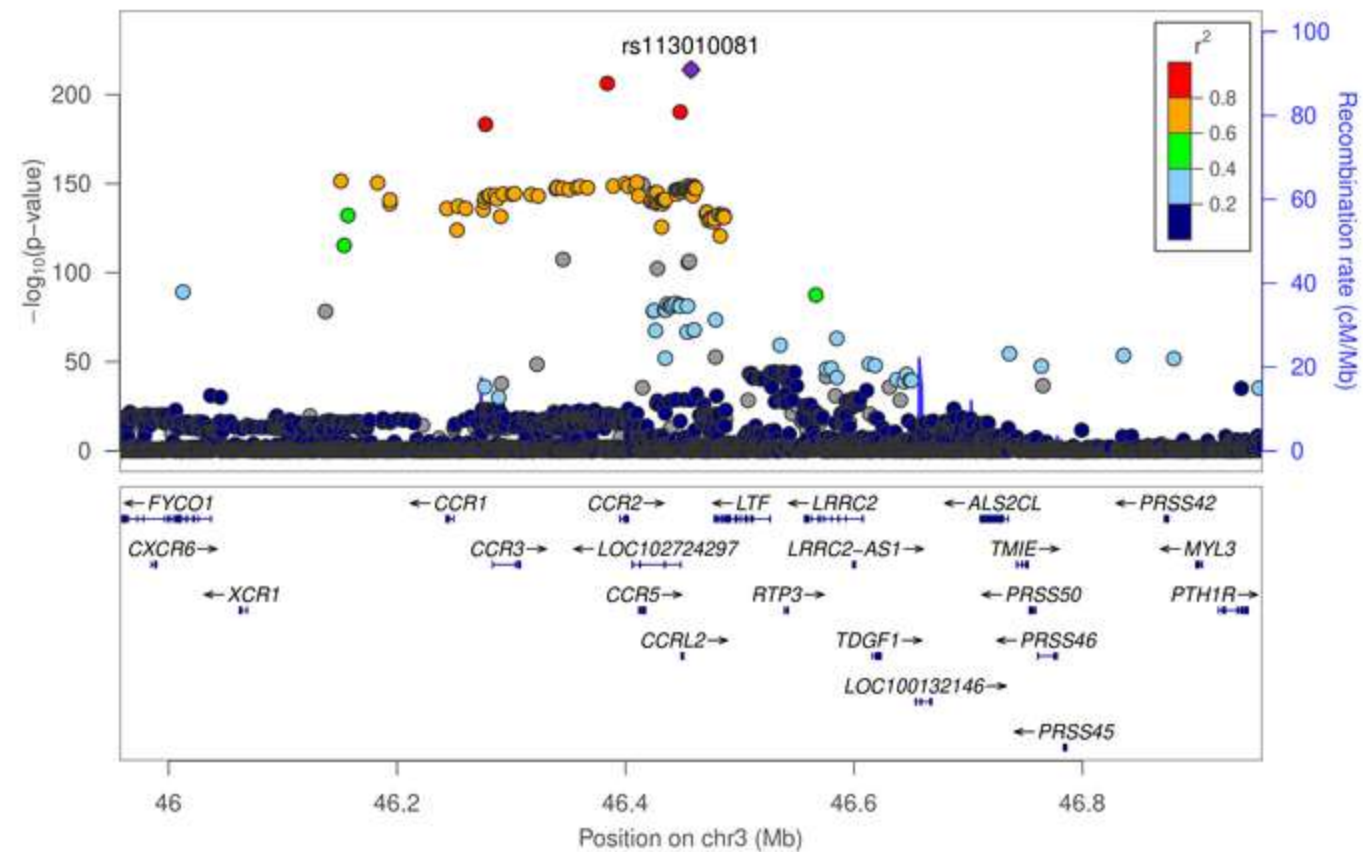


CCL4 (CCL4) [chr3:46457412_C_T (rs113010081) (T/C) N=14296]

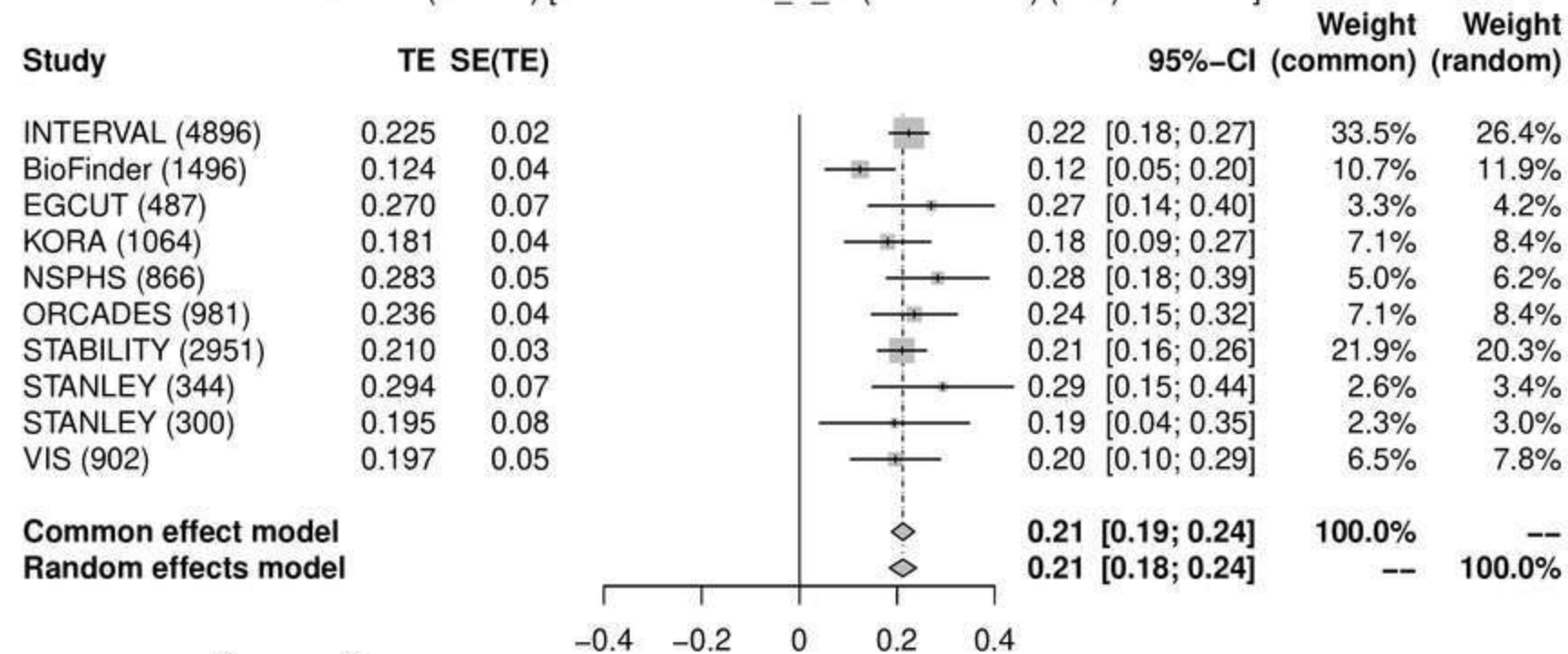


Heterogeneity: $I^2 = 55\%$, $\tau^2 = 0.0055$, $p = 0.02$

CCL4 (CCL4)-rs113010081

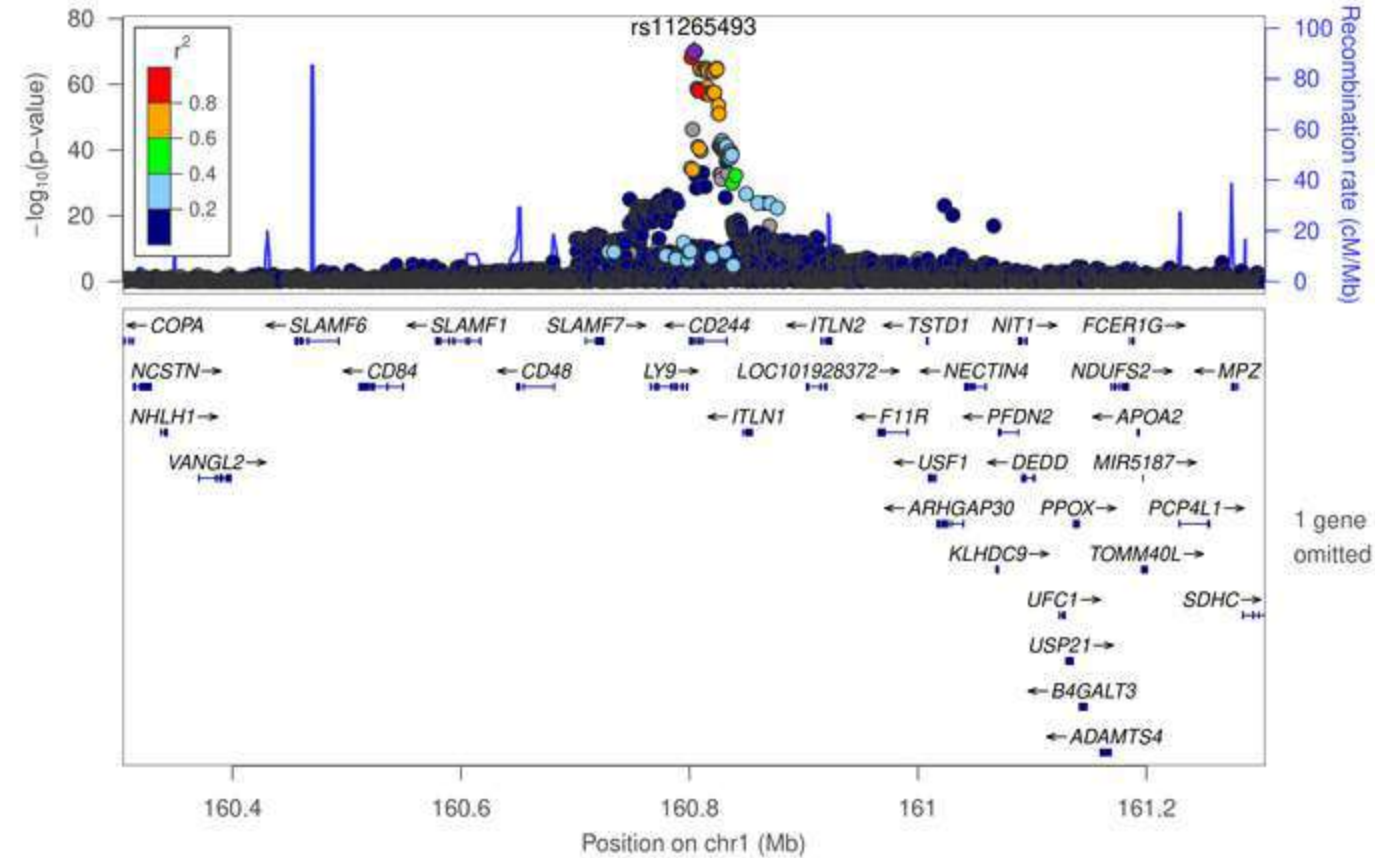


CD244 (CD244) [chr1:160803802_A_G (rs11265493) (A/G) N=14287]



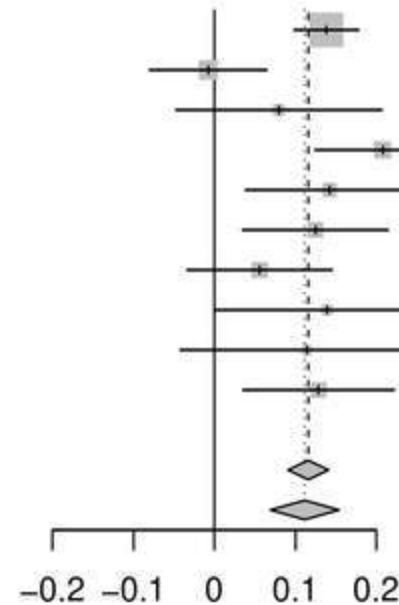
Heterogeneity: $I^2 = 17\%$, $\tau^2 = 0.0003$, $p = 0.28$

CD244 (CD244)-rs11265493



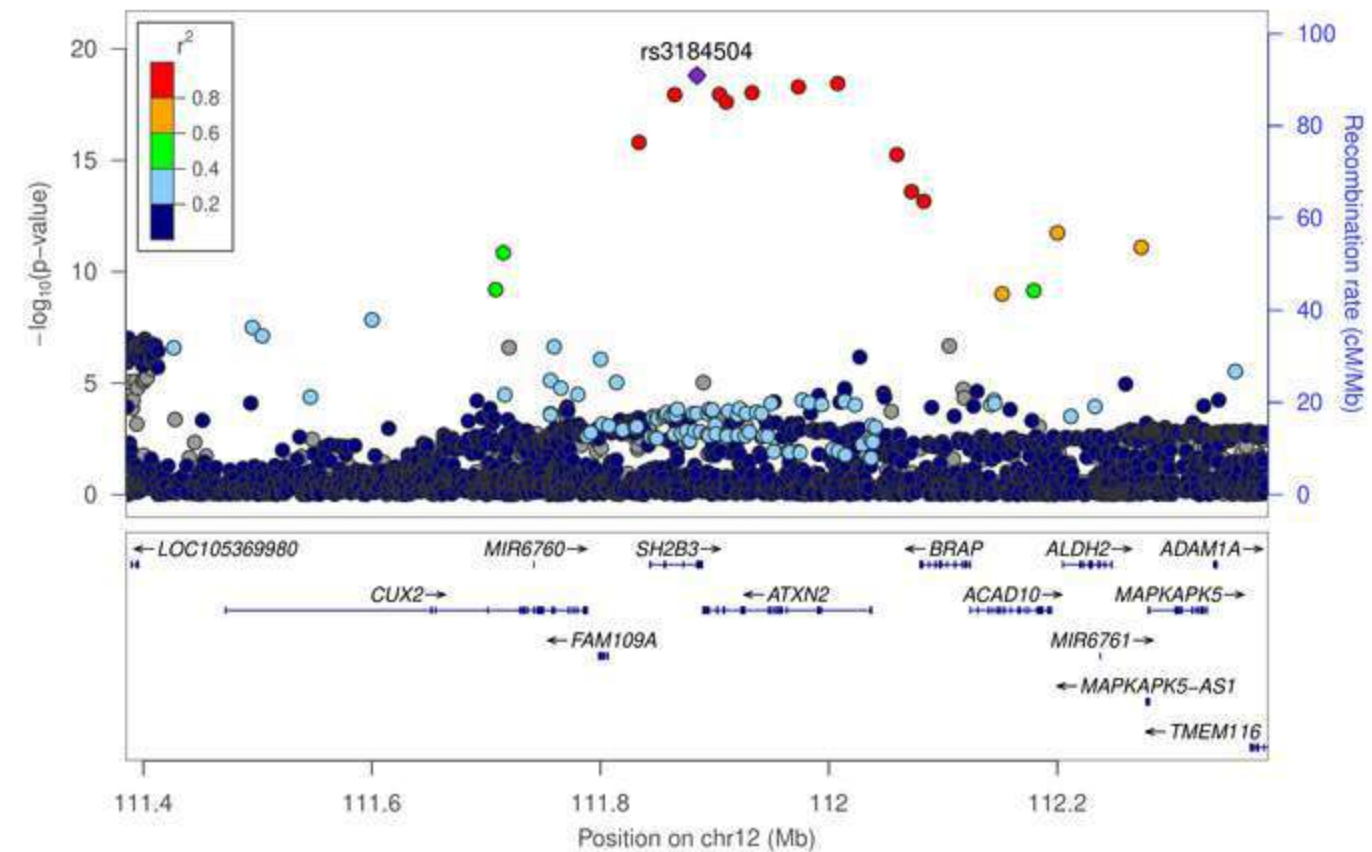
CD244 (CD244) [chr12:111884608_C_T (rs3184504) (T/C) N=11784]

Study	TE	SE(TE)		Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.138	0.02		0.14 [0.10; 0.18]	40.2% 16.9%
BioFinder (1496)	-0.008	0.04		-0.01 [-0.08; 0.06]	12.1% 12.6%
EGCUT (487)	0.080	0.06		0.08 [-0.05; 0.21]	3.9% 7.2%
KORA (1064)	0.208	0.04		0.21 [0.12; 0.29]	9.0% 11.2%
NSPHS (866)	0.142	0.05		0.14 [0.04; 0.25]	5.9% 9.1%
ORCADES (981)	0.125	0.05		0.12 [0.03; 0.21]	7.8% 10.5%
RECOMBINE (448)	0.056	0.05		0.06 [-0.03; 0.15]	7.9% 10.6%
STANLEY (344)	0.139	0.07		0.14 [0.00; 0.28]	3.3% 6.4%
STANLEY (300)	0.114	0.08		0.11 [-0.04; 0.27]	2.6% 5.4%
VIS (902)	0.129	0.05		0.13 [0.04; 0.22]	7.3% 10.1%
Common effect model				0.12 [0.09; 0.14]	100.0% --
Random effects model				0.11 [0.07; 0.15]	-- 100.0%

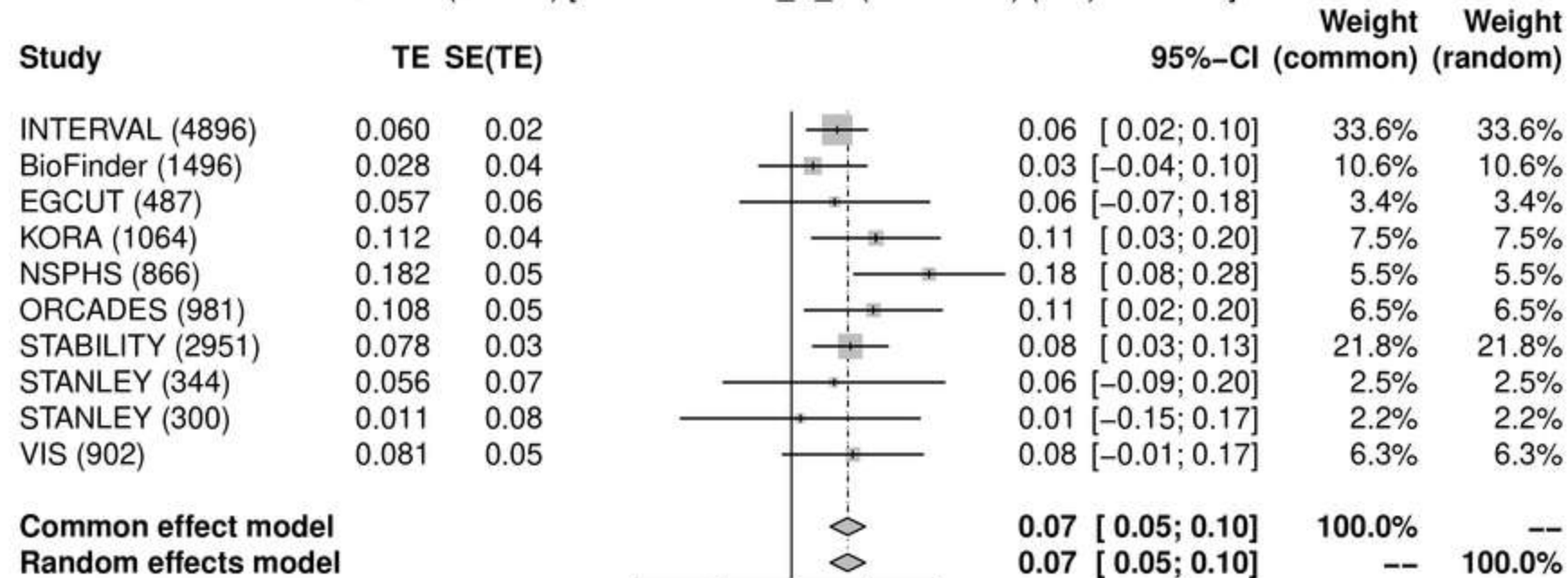


Heterogeneity: $I^2 = 54\%$, $\tau^2 = 0.0024$, $p = 0.02$

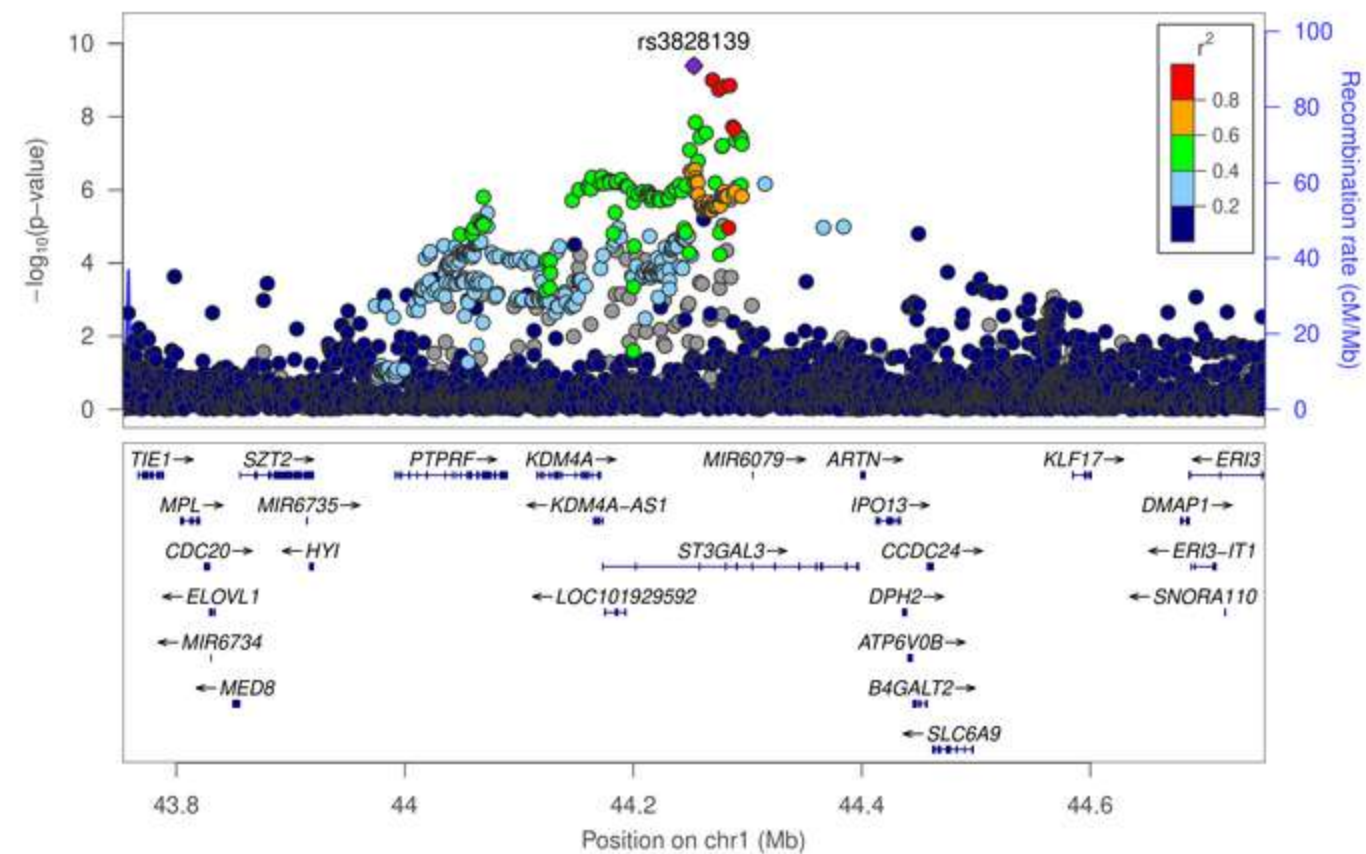
CD244 (CD244)-rs3184504



CD244 (CD244) [chr1:44253015_C_T (rs3828139) (T/C) N=14287]



CD244 (CD244)-rs3828139



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (448)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 87\%$, $\tau^2 = 0.0167$, $p < 0.01$

CD40 (CD40) [chr20:44746982_C_T (rs1883832) (T/C) N=14736]

TE SE(TE)

-0.453

0.02

-0.311

0.04

-0.590

0.07

-0.639

0.05

-0.557

0.06

-0.584

0.05

-0.234

0.05

-0.486

0.03

-0.299

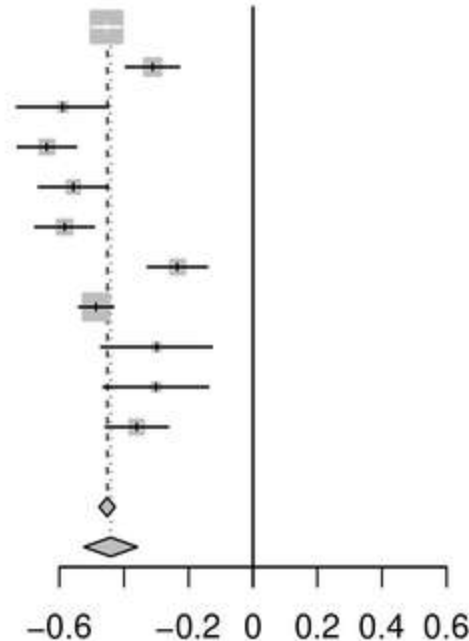
0.09

-0.301

0.08

-0.360

0.05



95%-CI (common)

Weight

Weight

-0.45 [-0.50; -0.41]

29.9%

10.4%

-0.31 [-0.39; -0.23]

8.8%

9.7%

-0.59 [-0.73; -0.45]

3.0%

8.1%

-0.64 [-0.73; -0.55]

7.3%

9.5%

-0.56 [-0.66; -0.45]

5.2%

9.1%

-0.58 [-0.68; -0.49]

7.2%

9.5%

-0.23 [-0.33; -0.14]

7.1%

9.4%

-0.49 [-0.54; -0.43]

20.9%

10.2%

-0.30 [-0.47; -0.13]

2.0%

7.3%

-0.30 [-0.46; -0.14]

2.3%

7.6%

-0.36 [-0.46; -0.26]

6.3%

9.3%

-0.45 [-0.48; -0.43]

100.0%

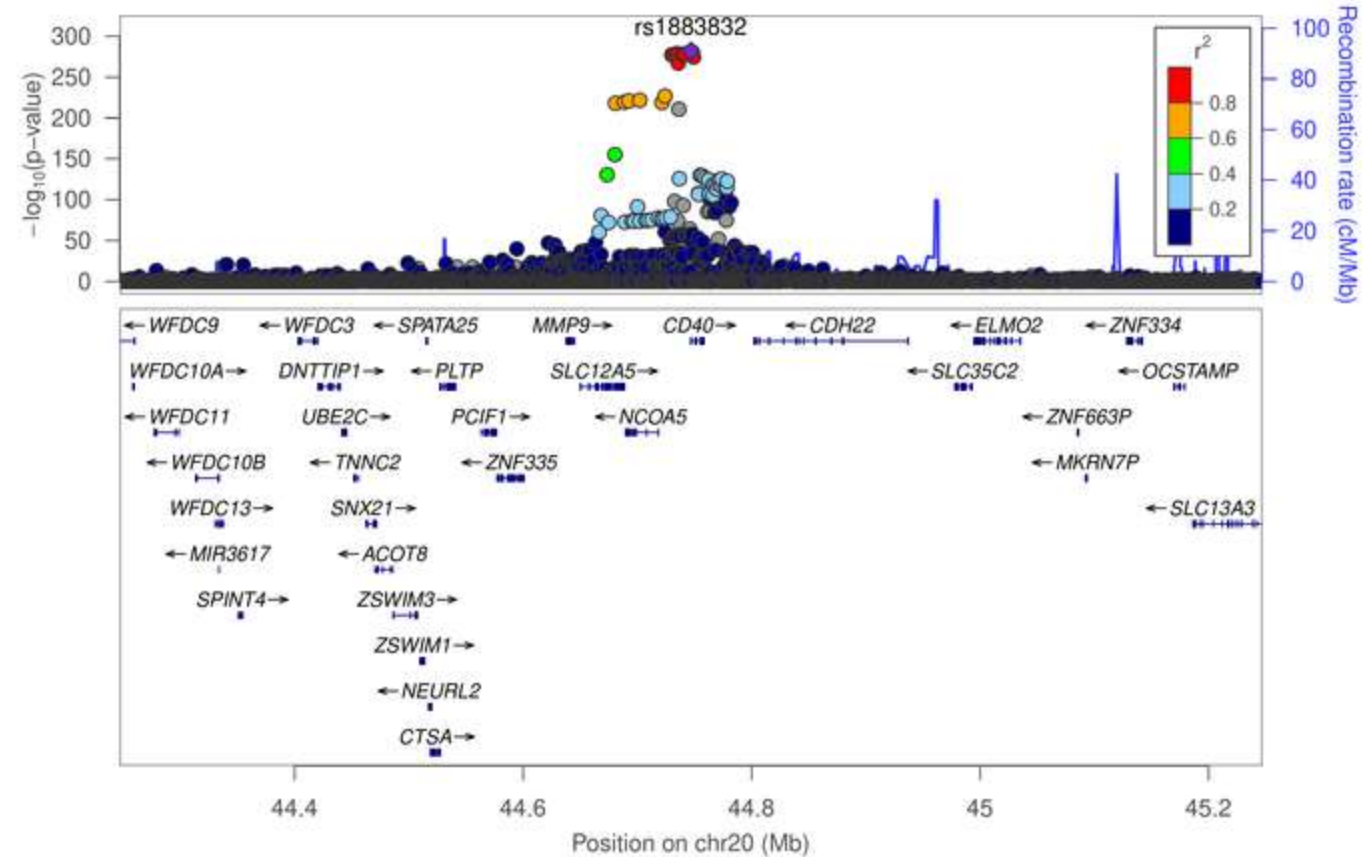
--

-0.44 [-0.52; -0.36]

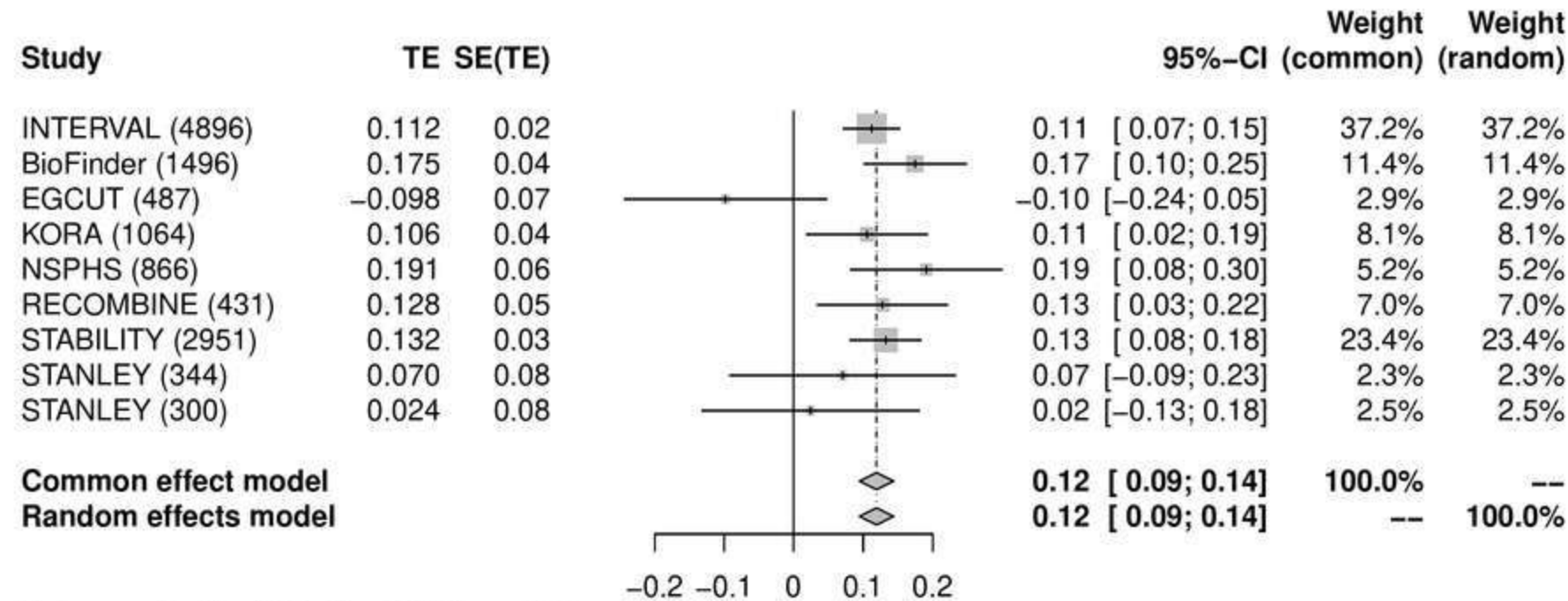
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100.0%

CD40 (CD40)-rs1883832

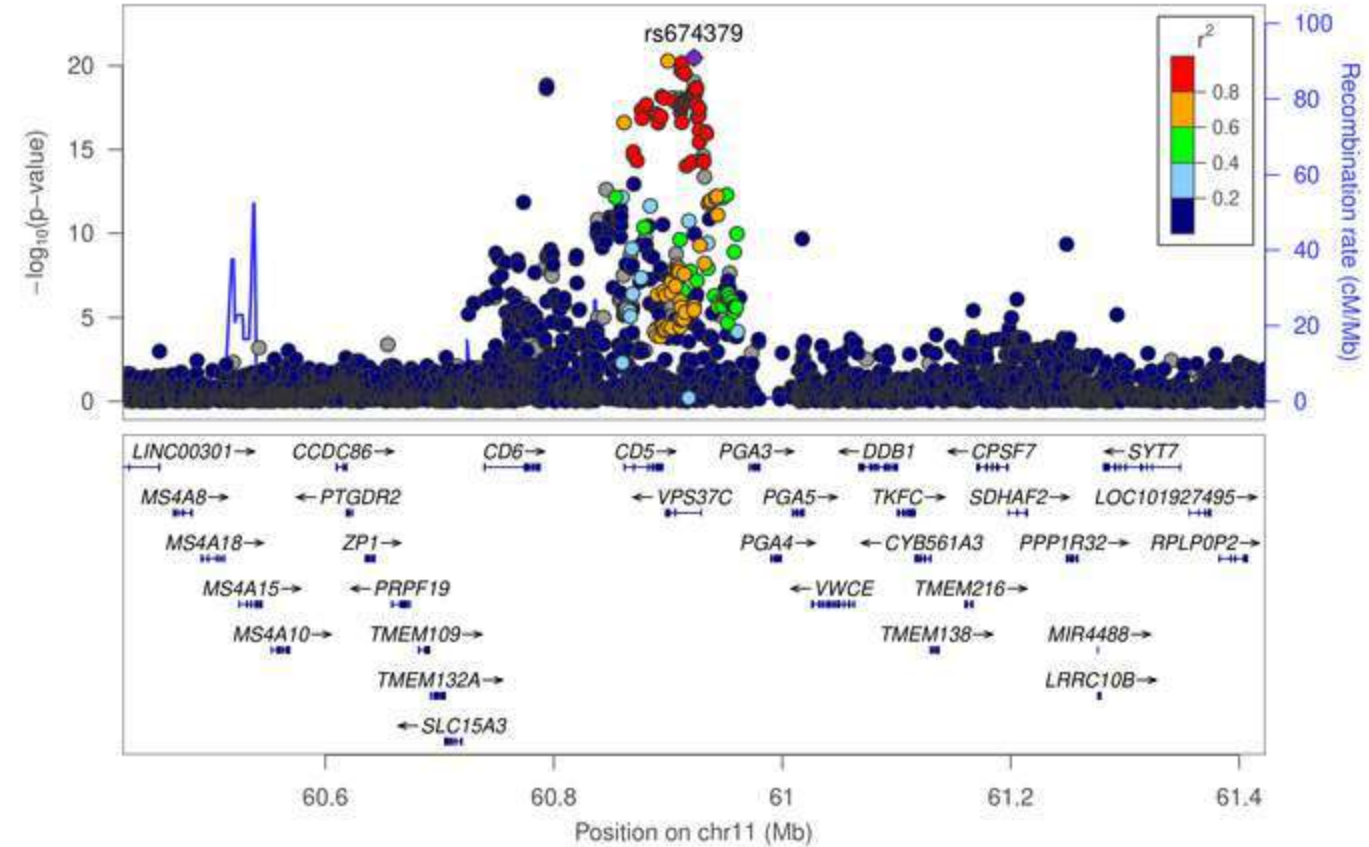


CD5 (CD5) [chr11:60922561_C_G (rs674379) (C/G) N=12835]

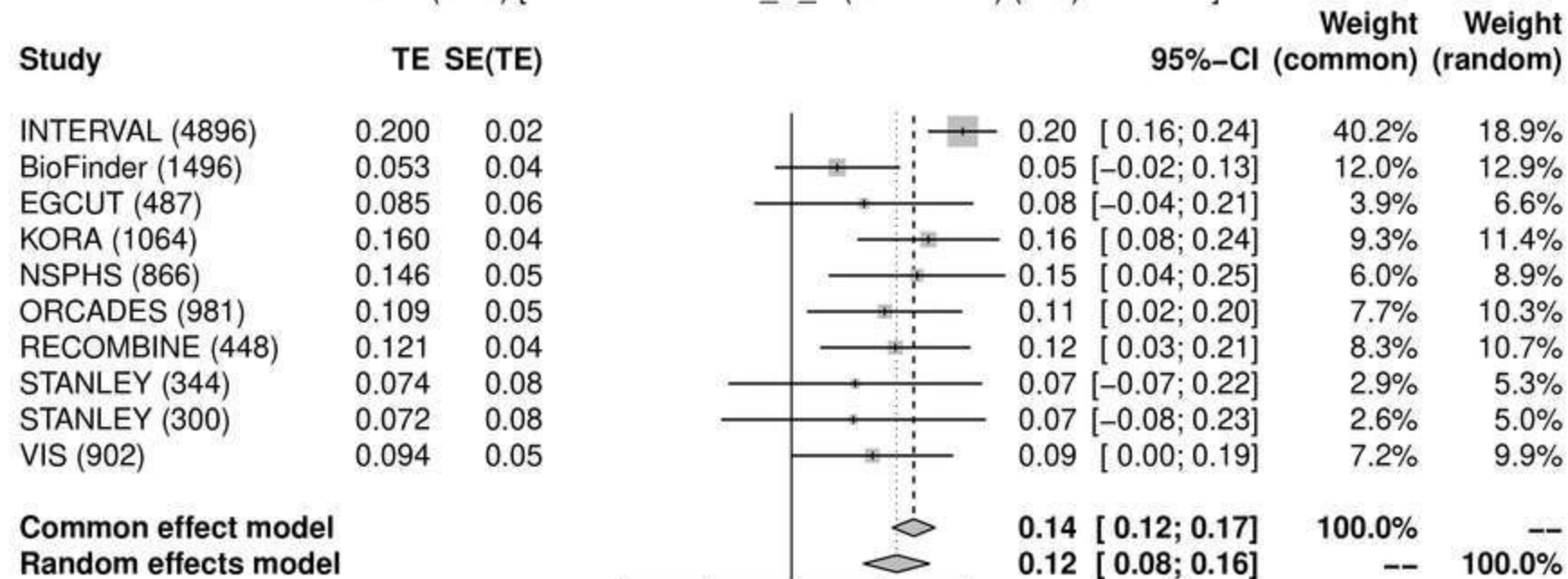


Heterogeneity: $I^2 = 45\%$, $\tau^2 < 0.0001$, $p = 0.07$

CD5 (CD5)-rs674379

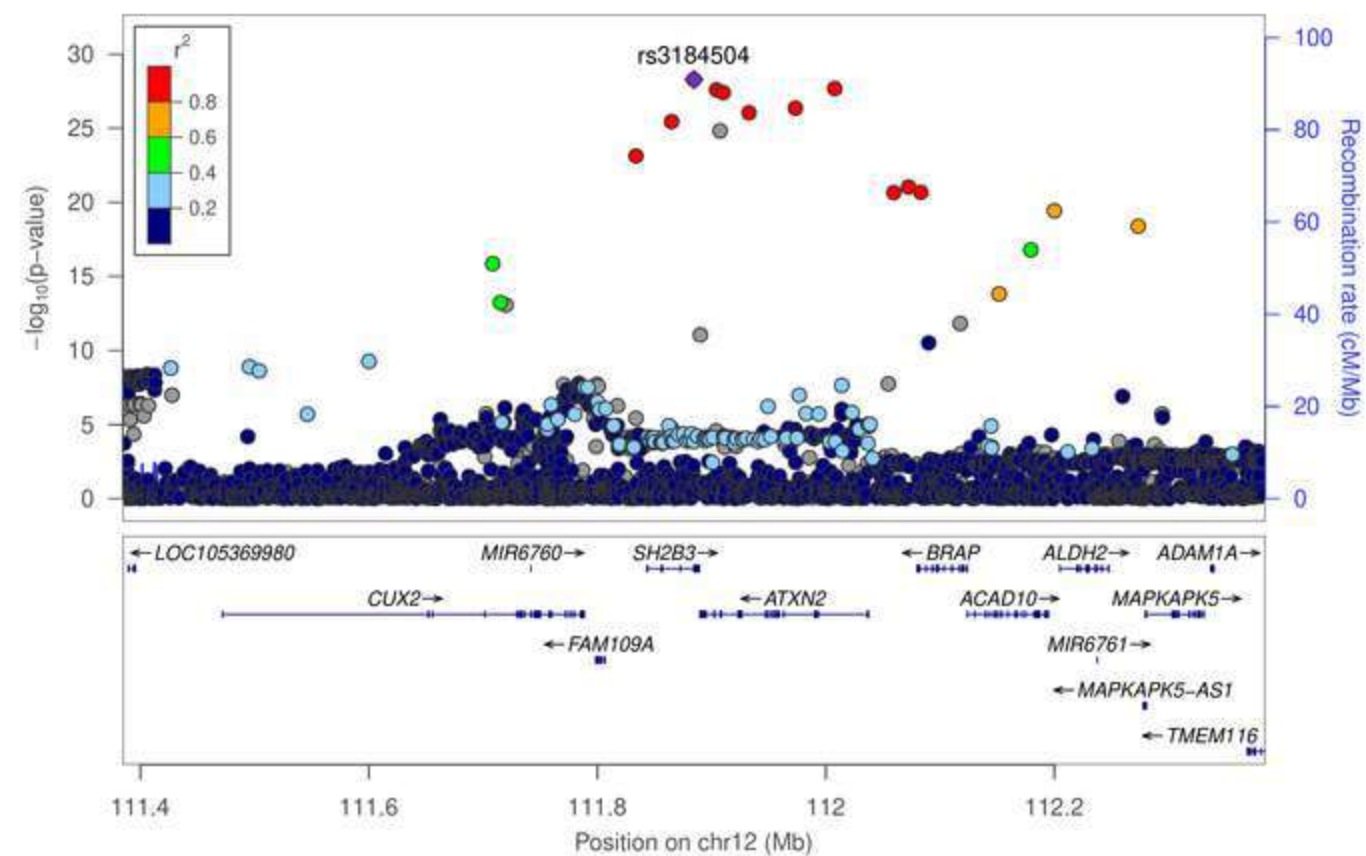


CD5 (CD5) [chr12:111884608_C_T (rs3184504) (T/C) N=11784]

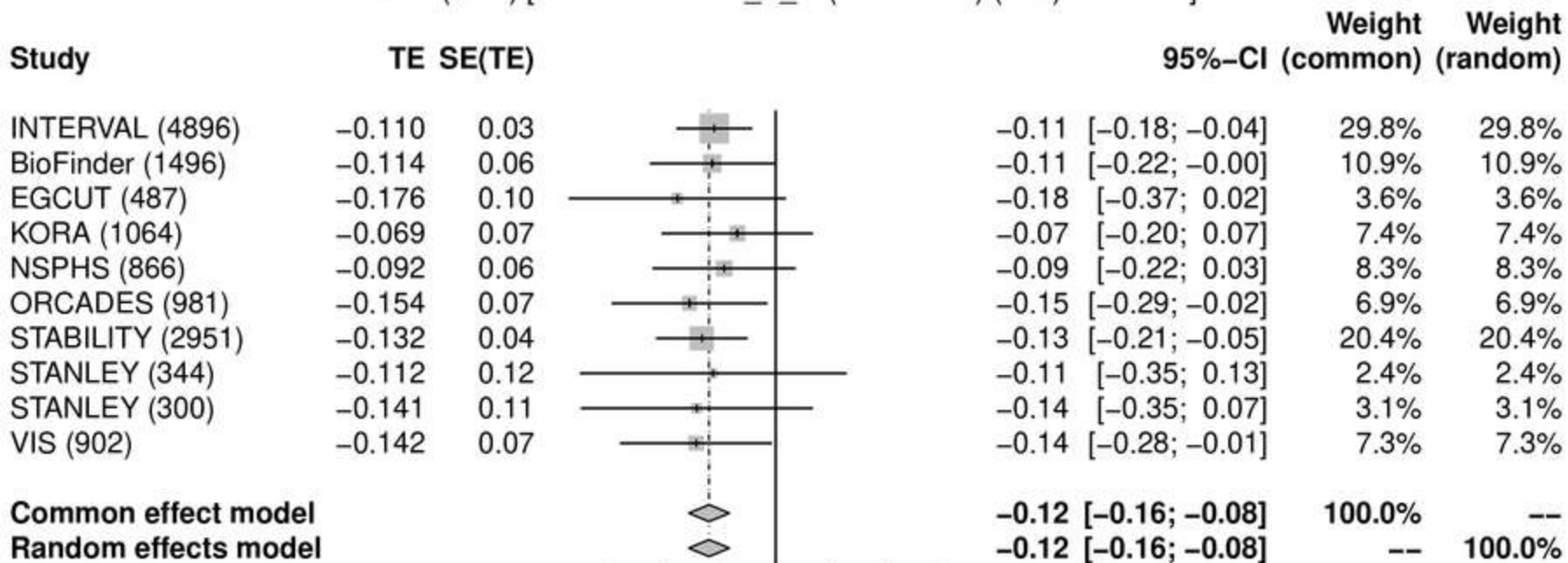


Heterogeneity: $I^2 = 51\%$, $\tau^2 = 0.0016$, $p = 0.03$

CD5 (CD5)-rs3184504

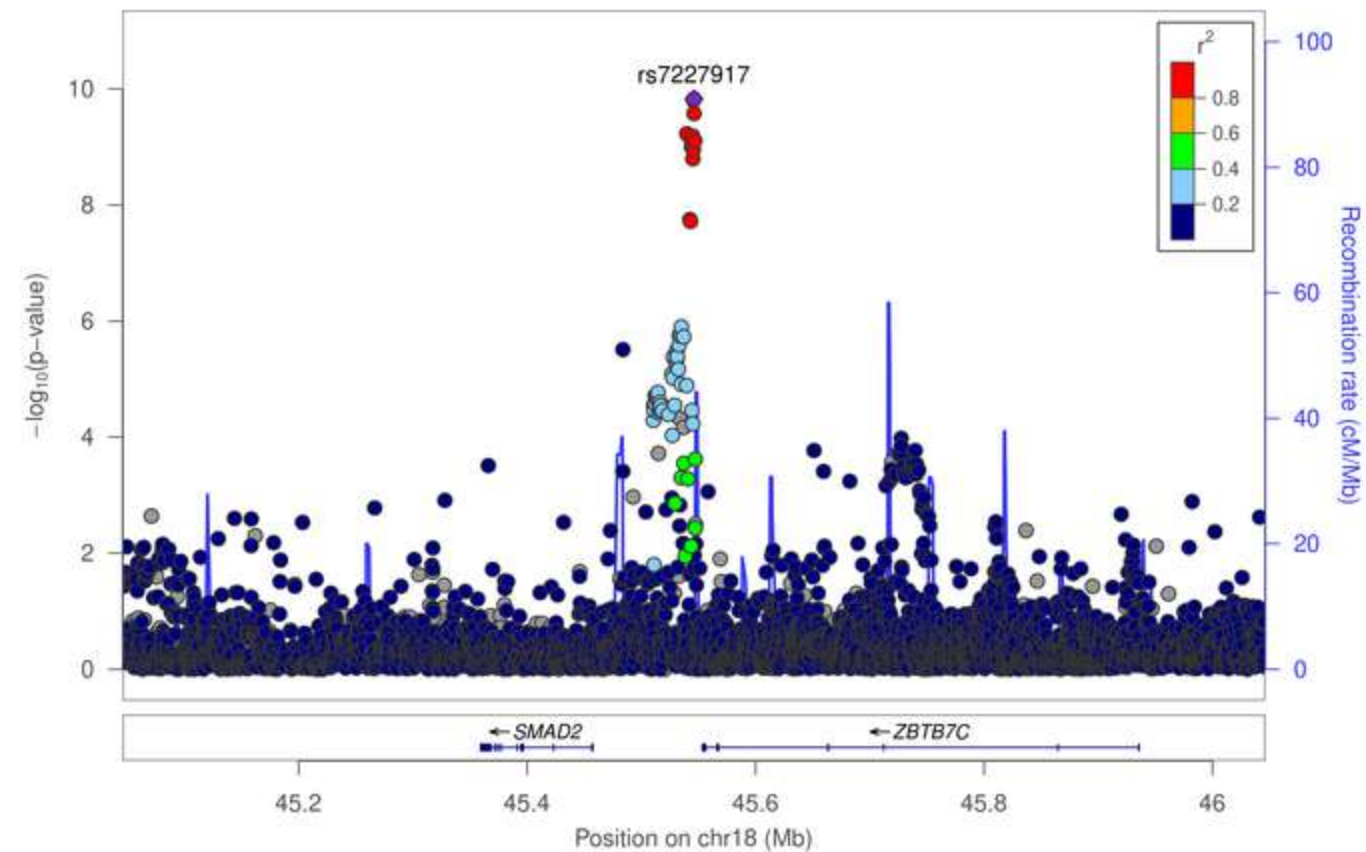


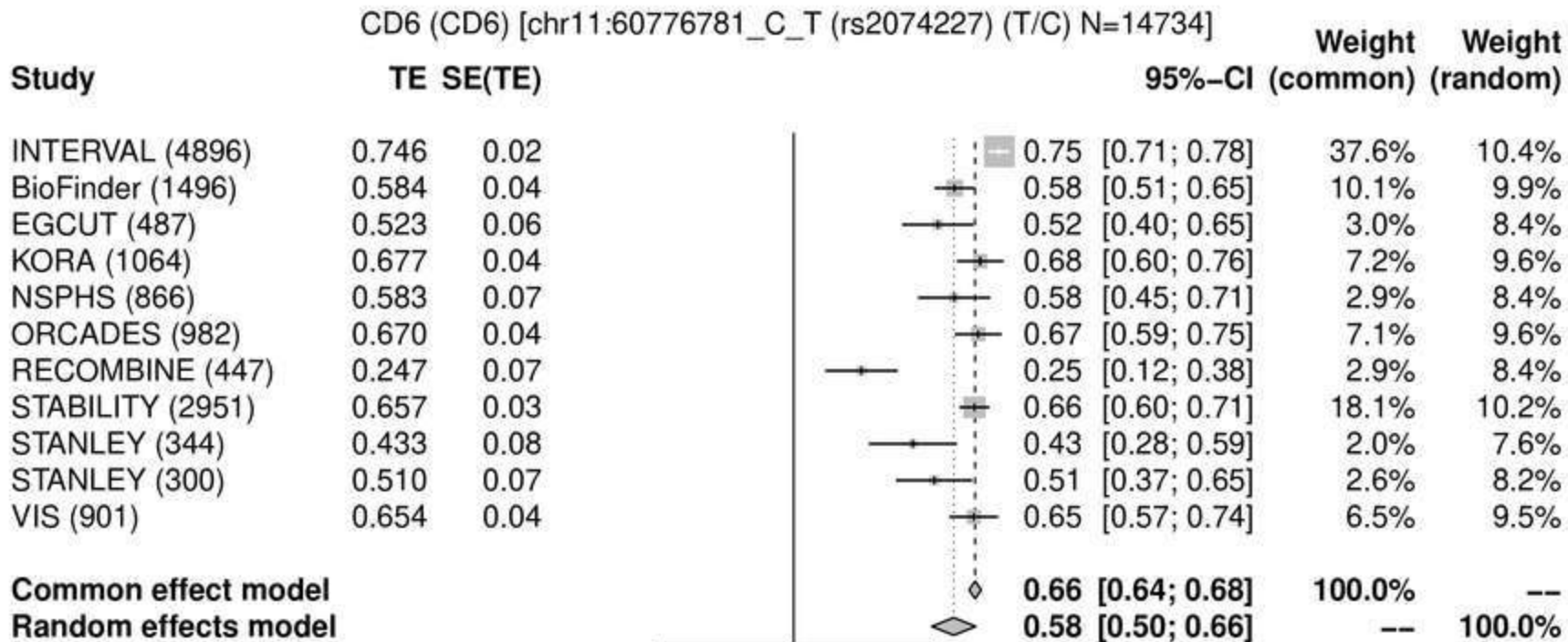
CD5 (CD5) [chr18:45546185_A_G (rs7227917) (A/G) N=14287]



Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 1.00$

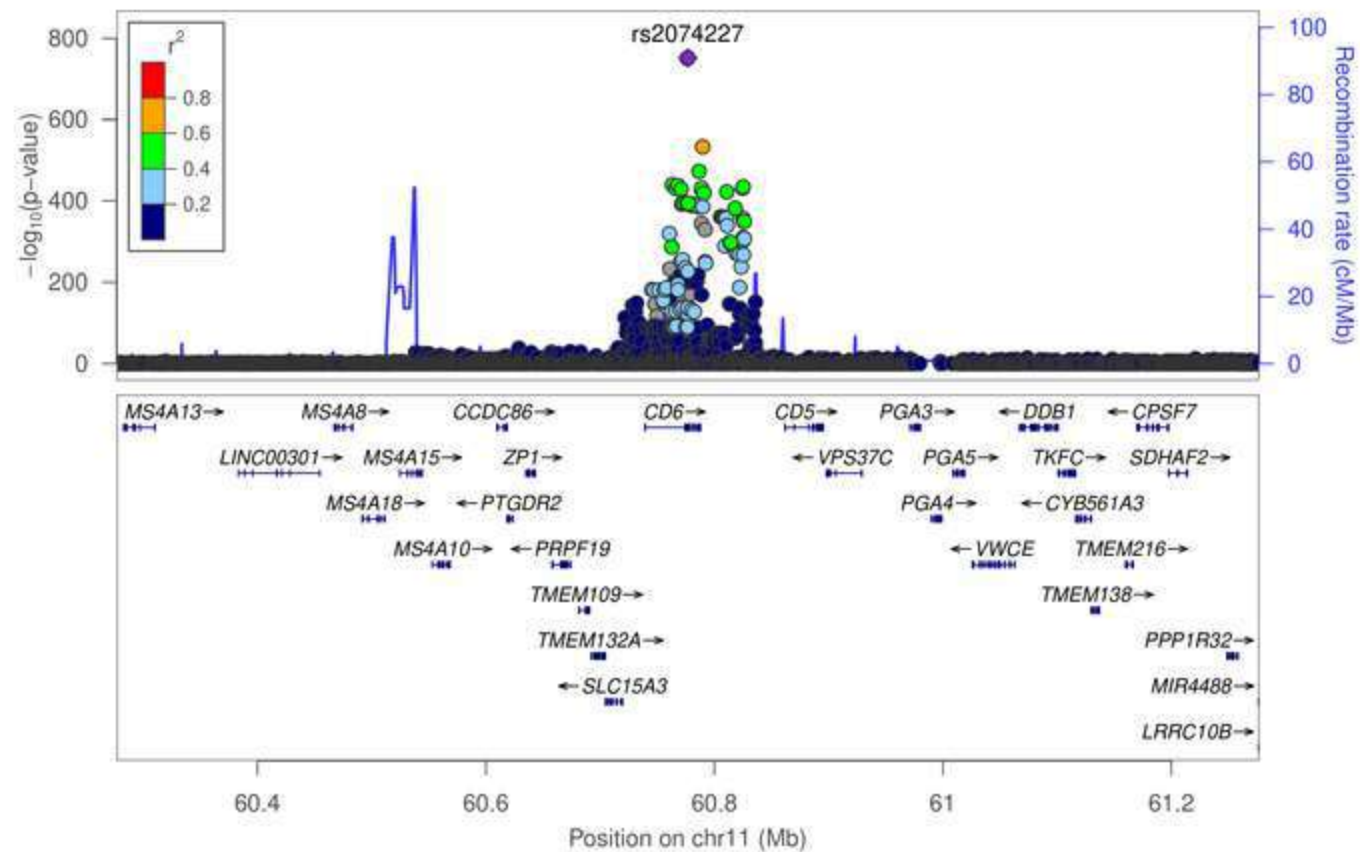
CD5 (CD5)-rs7227917



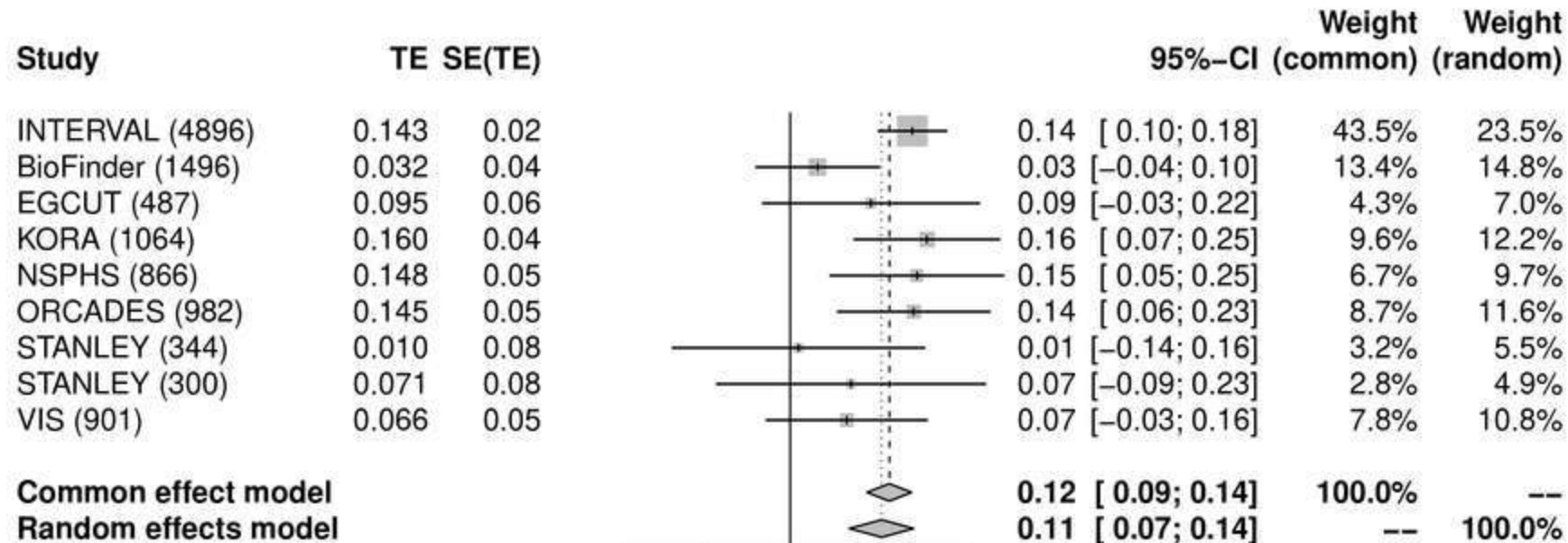


Heterogeneity: $I^2 = 88\%$, $\tau^2 = 0.0158$, $p < 0.01$

CD6 (CD6)-rs2074227

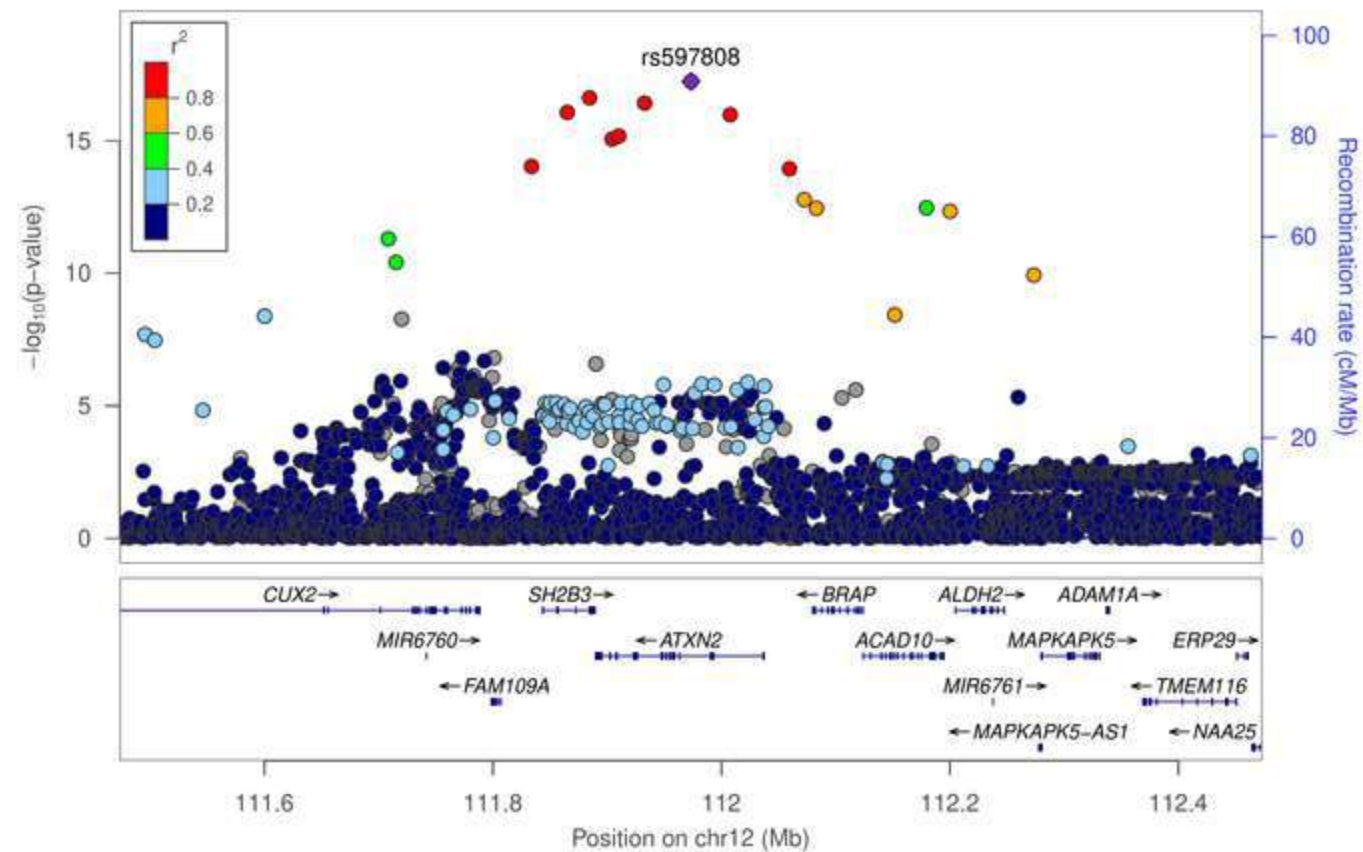


CD6 (CD6) [chr12:111973358_A_G (rs597808) (A/G) N=11336]

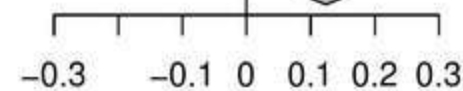
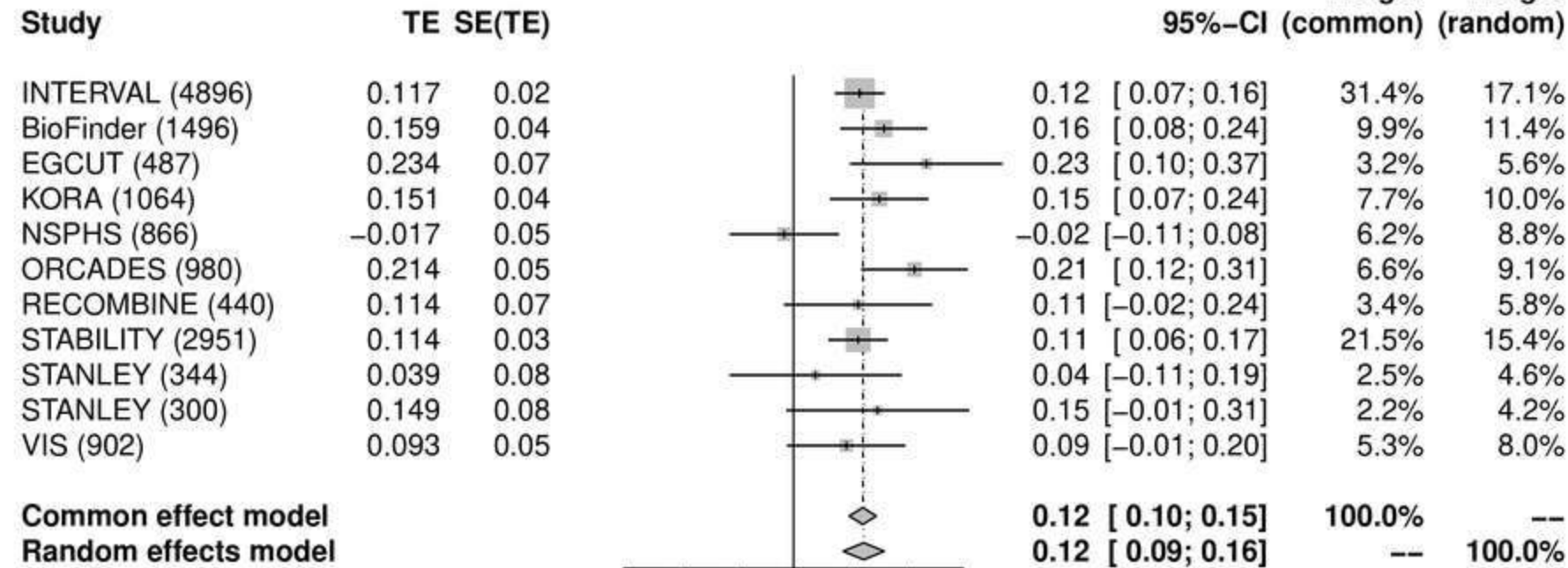


Heterogeneity: $I^2 = 35\%$, $\tau^2 = 0.0012$, $p = 0.14$

CD6 (CD6)-rs597808

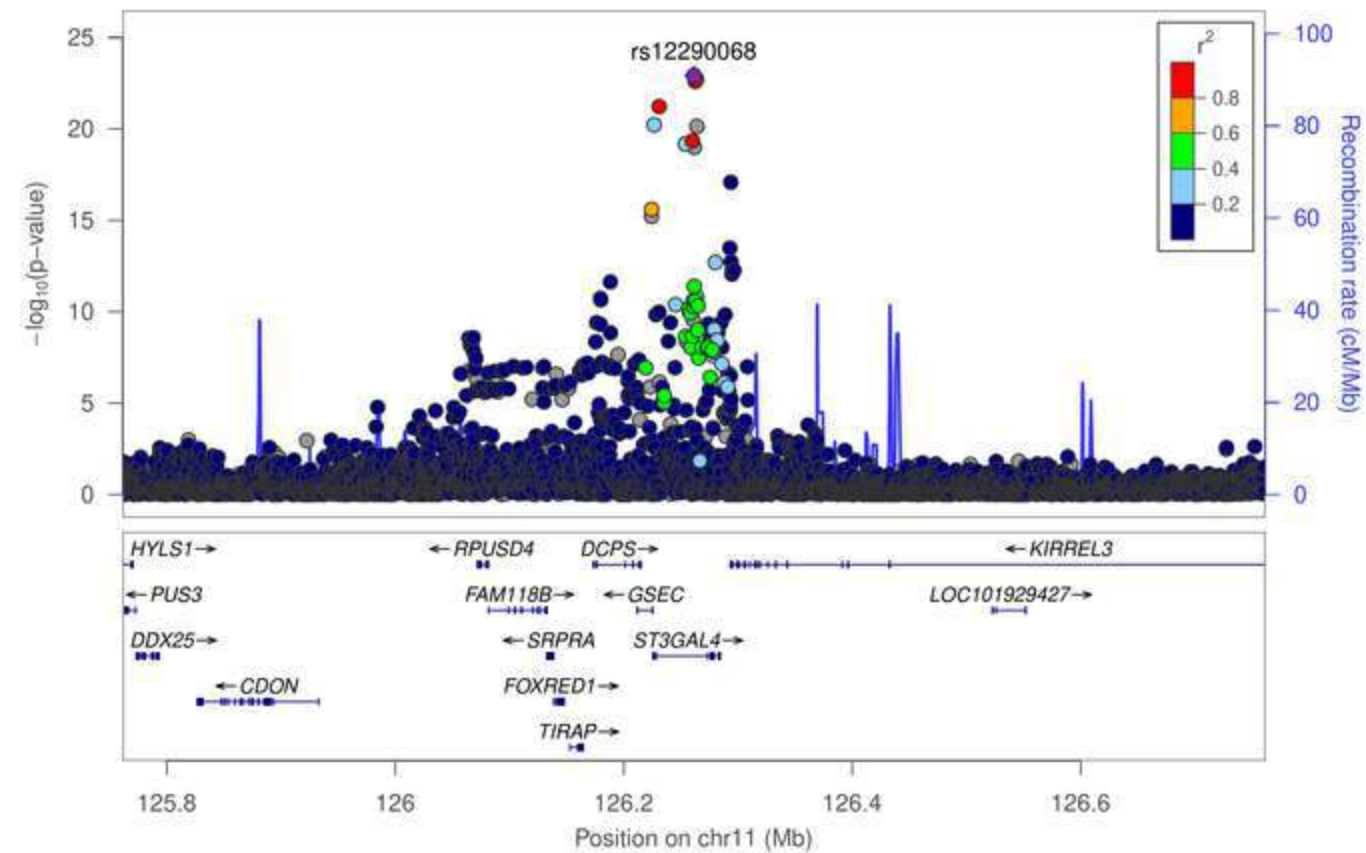


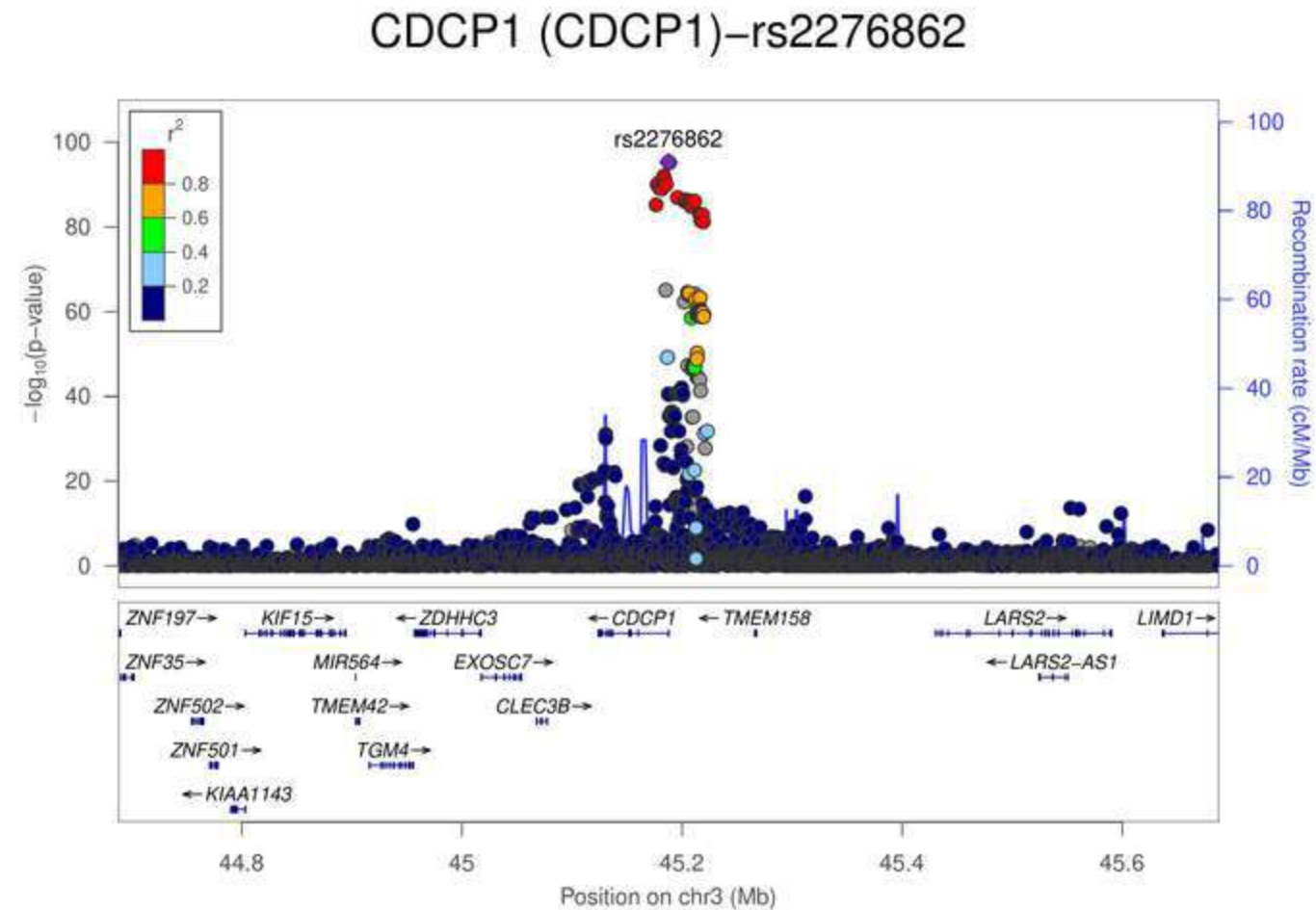
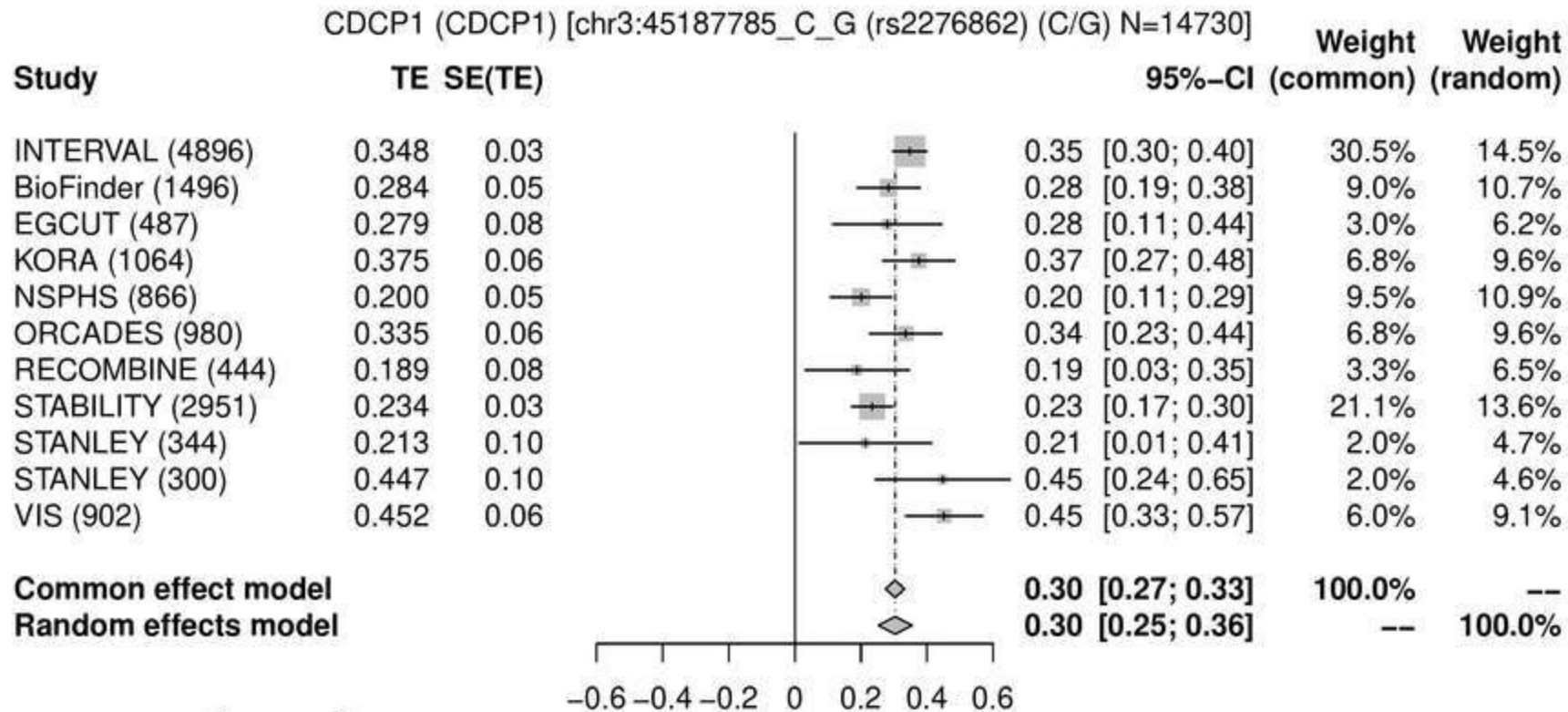
CDCP1 (CDCP1) [chr11:126261564_A_G (rs12290068) (A/G) N=14726]



Heterogeneity: $I^2 = 43\%$, $\tau^2 = 0.0016$, $p = 0.06$

CDCP1 (CDCP1)-rs12290068





Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (980)

RECOMBINE (447)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

CDCP1 (CDCP1) [chr6:32602396_C_T (rs9272226) (T/C) N=14733]

TE SE(TE)

-0.096 0.02

-0.100 0.04

-0.128 0.07

-0.125 0.04

-0.119 0.04

-0.126 0.05

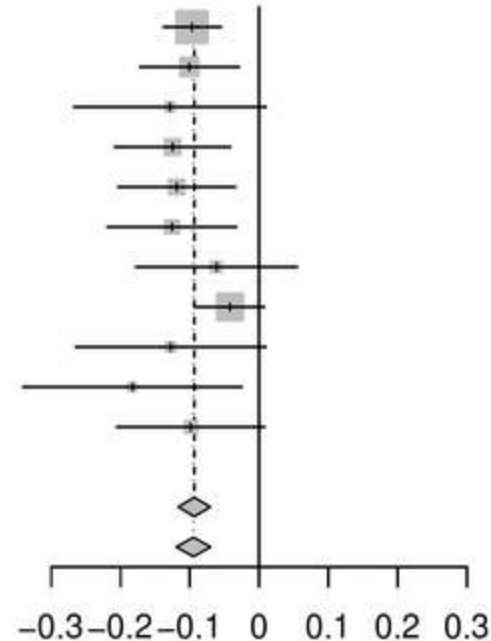
-0.061 0.06

-0.042 0.03

-0.127 0.07

-0.183 0.08

-0.098 0.05

Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0.0001$, $p = 0.69$ Weight
95%-CI (common) (random)

-0.10 [-0.14; -0.05] 30.6% 27.2%

-0.10 [-0.17; -0.03] 10.4% 11.0%

-0.13 [-0.27; 0.01] 2.8% 3.1%

-0.12 [-0.21; -0.04] 7.7% 8.2%

-0.12 [-0.20; -0.03] 7.5% 8.1%

-0.13 [-0.22; -0.03] 6.2% 6.7%

-0.06 [-0.18; 0.06] 3.9% 4.4%

-0.04 [-0.09; 0.01] 21.2% 20.3%

-0.13 [-0.26; 0.01] 2.8% 3.2%

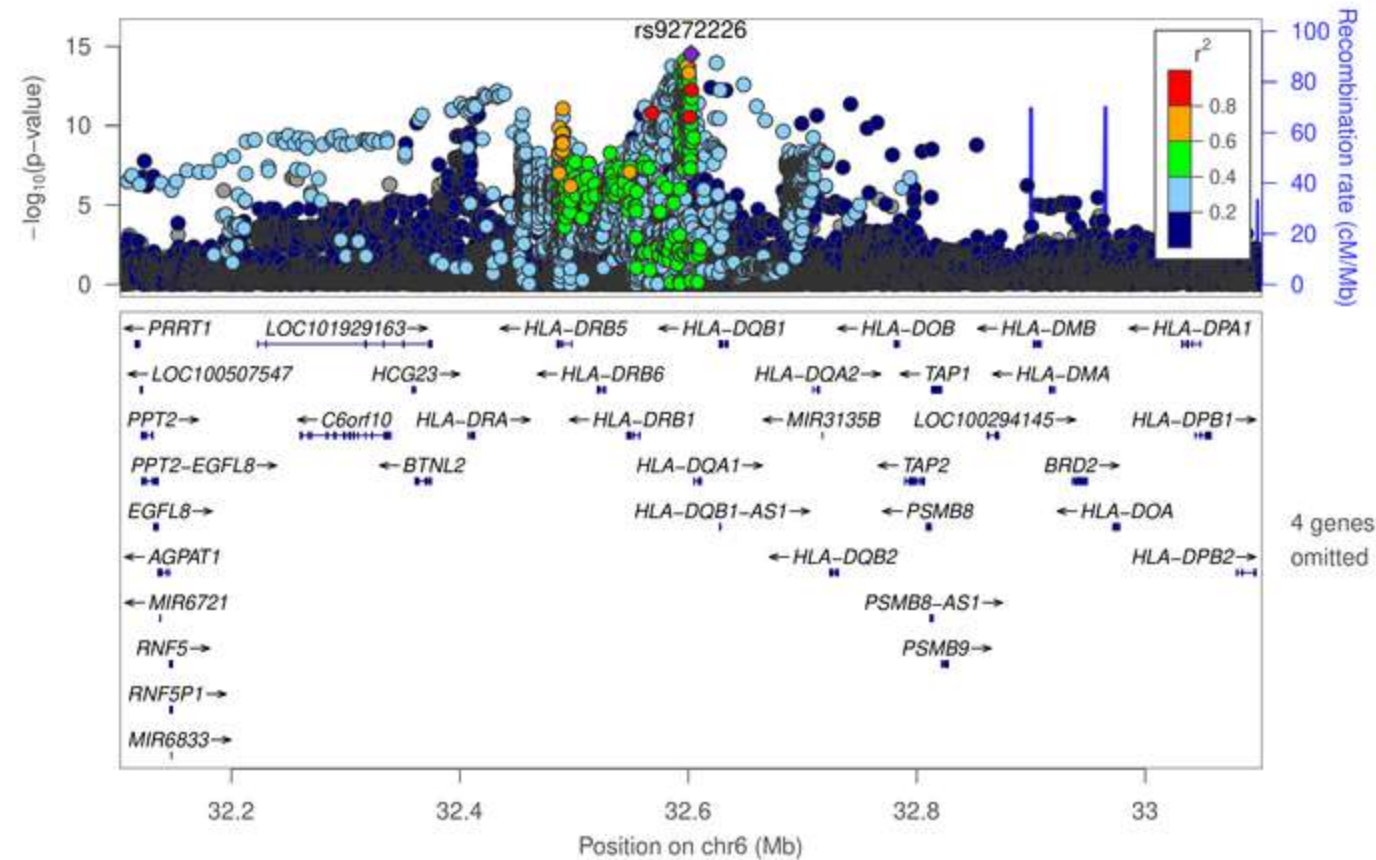
-0.18 [-0.34; -0.02] 2.1% 2.4%

-0.10 [-0.21; 0.01] 4.7% 5.2%

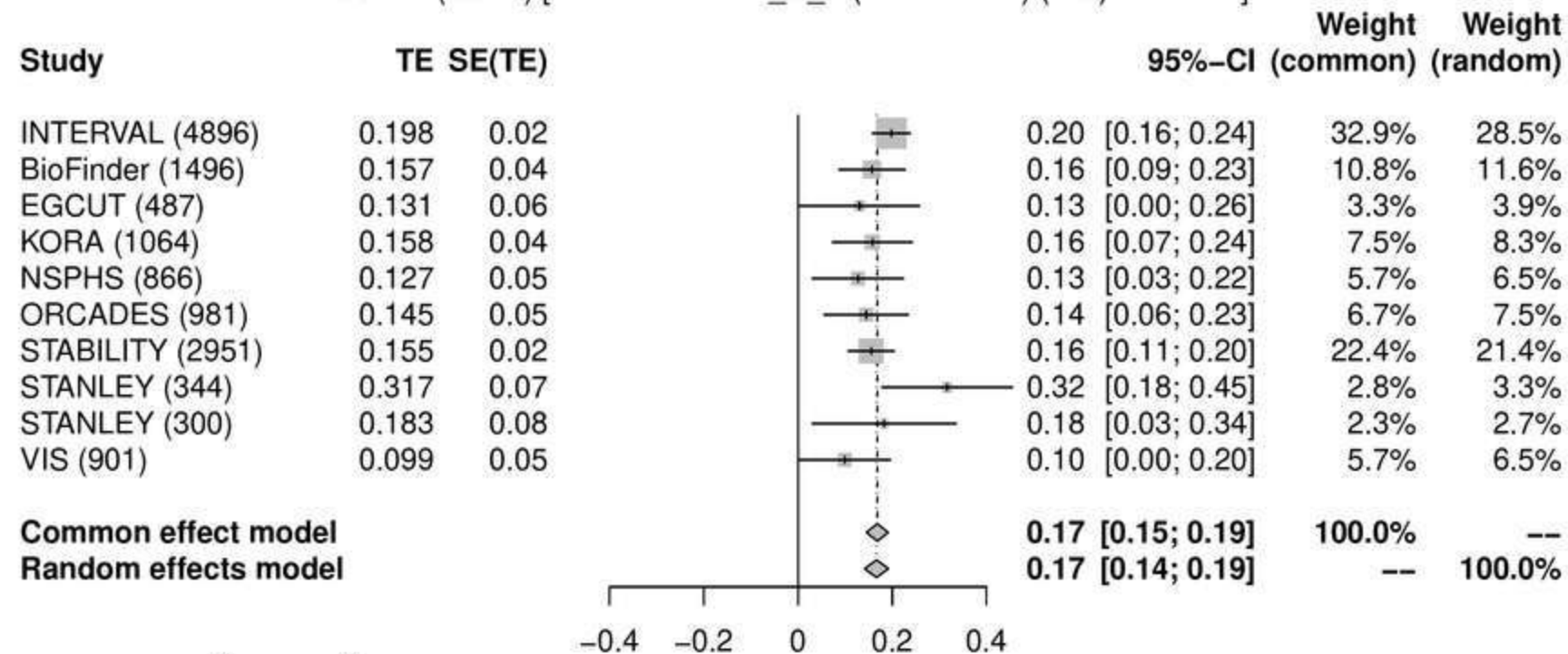
-0.09 [-0.12; -0.07] 100.0% --

-0.09 [-0.12; -0.07] -- 100.0%

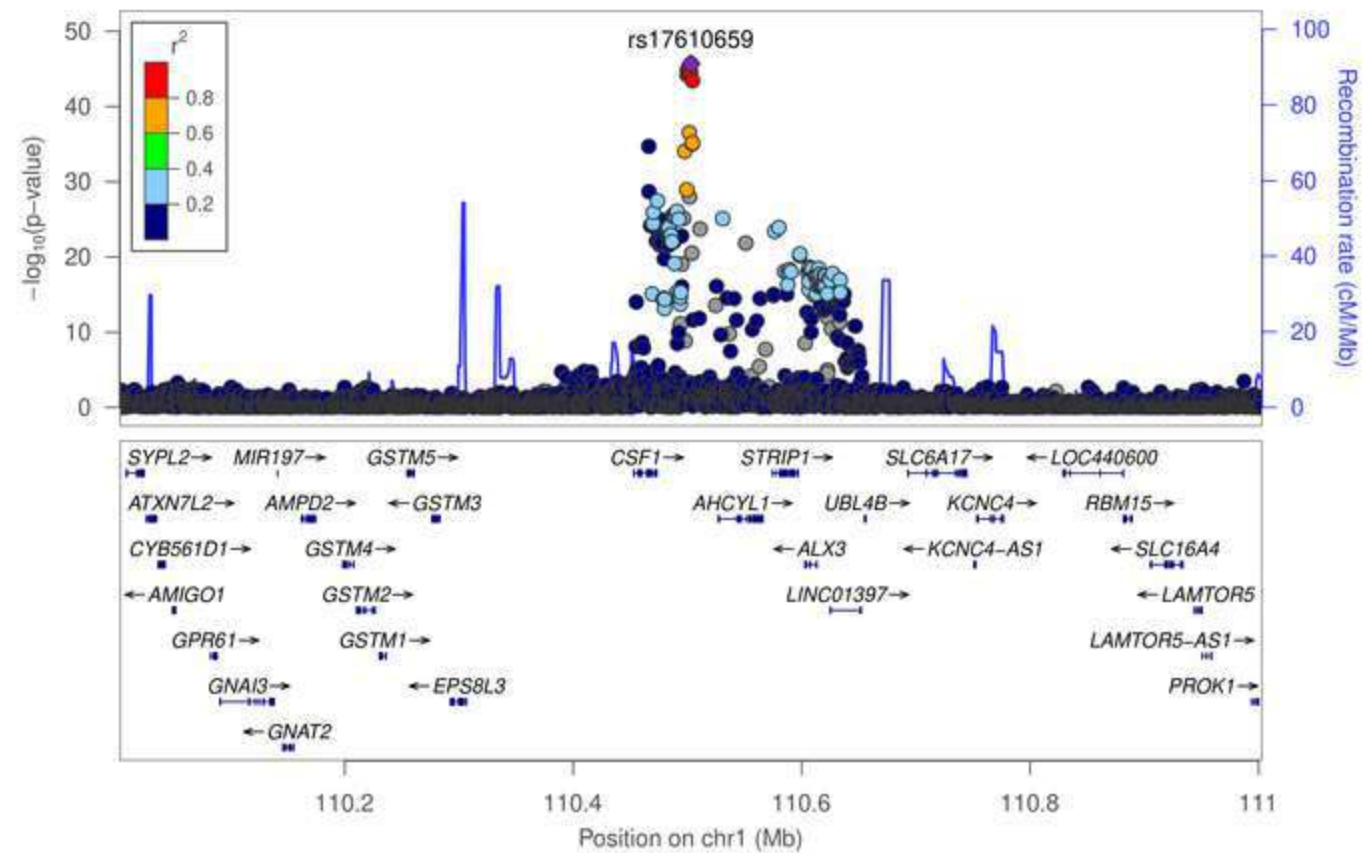
CDCP1 (CDCP1)-rs9272226



CSF-1 (CSF1) [chr1:110503296_C_T (rs17610659) (T/C) N=14286]

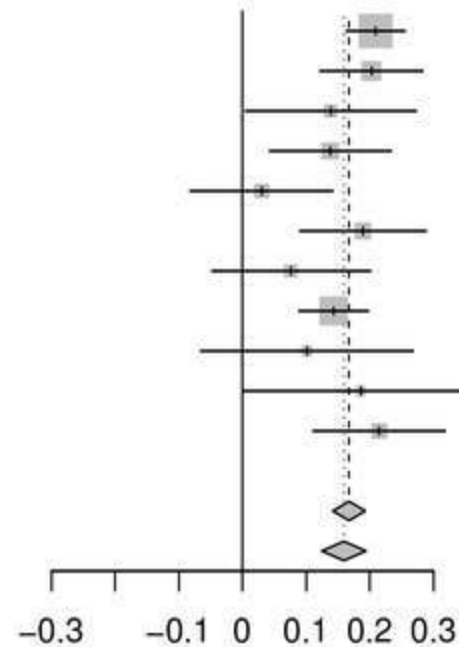


CSF-1 (CSF1)-rs17610659



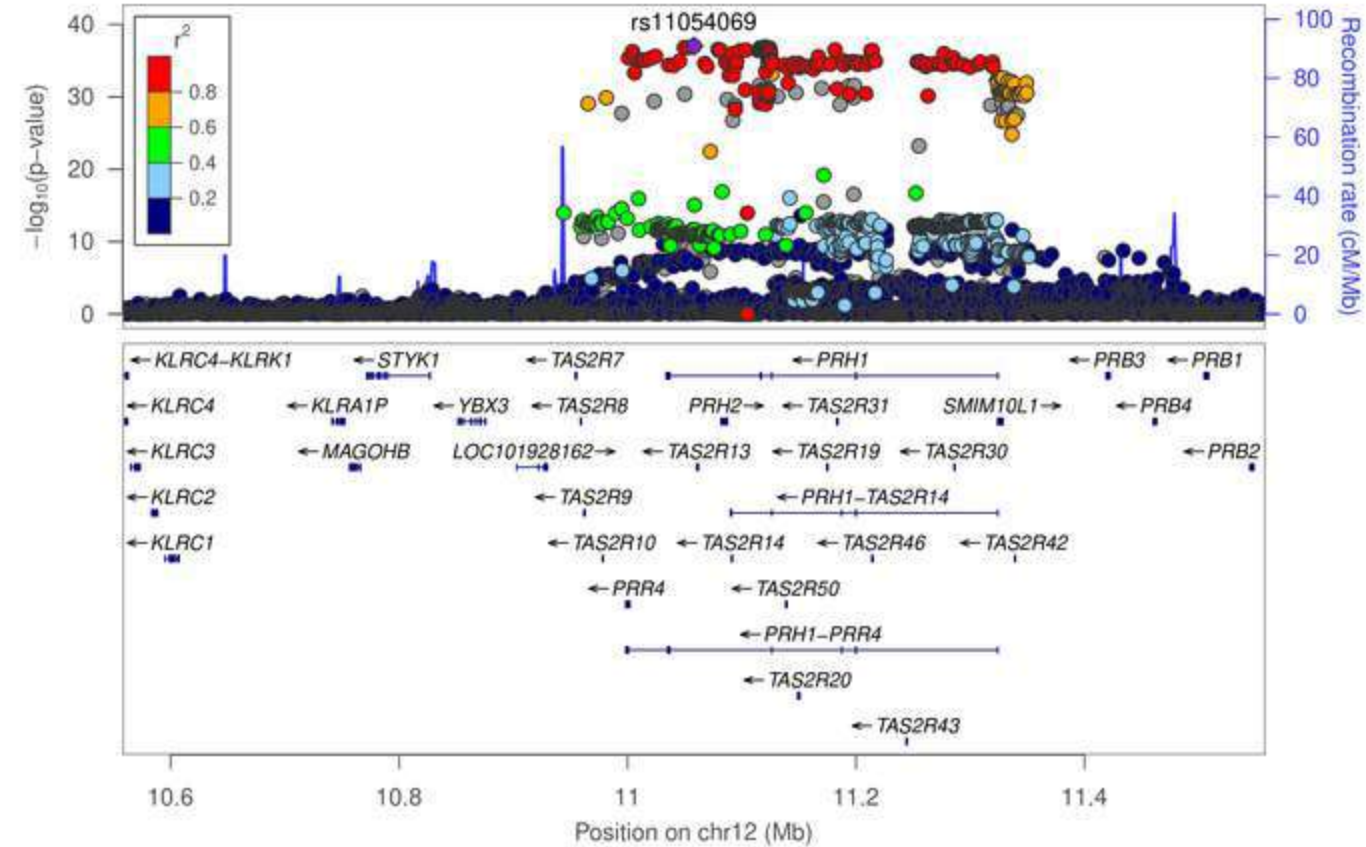
CST5 (CST5) [chr12:11058117_C_T (rs11054069) (T/C) N=14724]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.209	0.02	0.21 [0.16; 0.26]	30.8%	19.5%
BioFinder (1496)	0.202	0.04	0.20 [0.12; 0.28]	10.0%	11.4%
EGCUT (487)	0.139	0.07	0.14 [0.00; 0.27]	3.6%	5.5%
KORA (1064)	0.138	0.05	0.14 [0.04; 0.23]	7.2%	9.2%
NSPHS (866)	0.030	0.06	0.03 [-0.08; 0.14]	5.2%	7.3%
ORCADES (982)	0.189	0.05	0.19 [0.09; 0.29]	6.7%	8.7%
RECOMBINE (436)	0.076	0.06	0.08 [-0.05; 0.20]	4.2%	6.2%
STABILITY (2951)	0.143	0.03	0.14 [0.09; 0.20]	22.0%	17.1%
STANLEY (344)	0.101	0.09	0.10 [-0.07; 0.27]	2.3%	3.8%
STANLEY (300)	0.186	0.09	0.19 [0.00; 0.37]	1.9%	3.2%
VIS (902)	0.215	0.05	0.21 [0.11; 0.32]	6.1%	8.2%
Common effect model			0.17 [0.14; 0.19]	100.0%	--
Random effects model			0.16 [0.12; 0.19]	--	100.0%



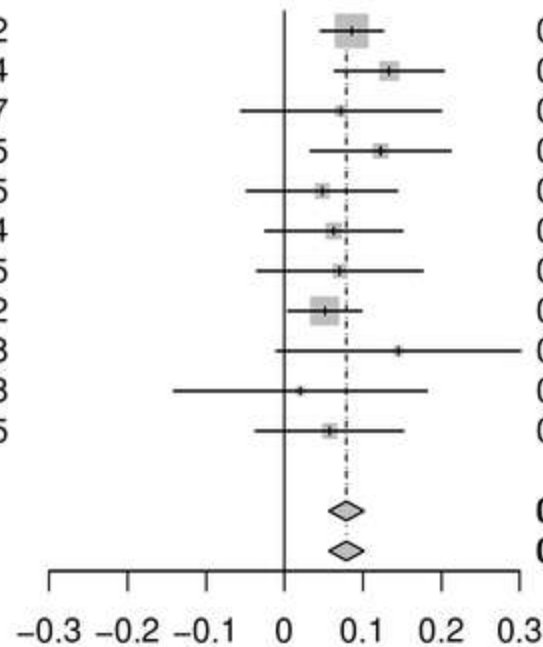
Heterogeneity: $I^2 = 32\%$, $\tau^2 = 0.0011$, $p = 0.15$

CST5 (CST5)-rs11054069



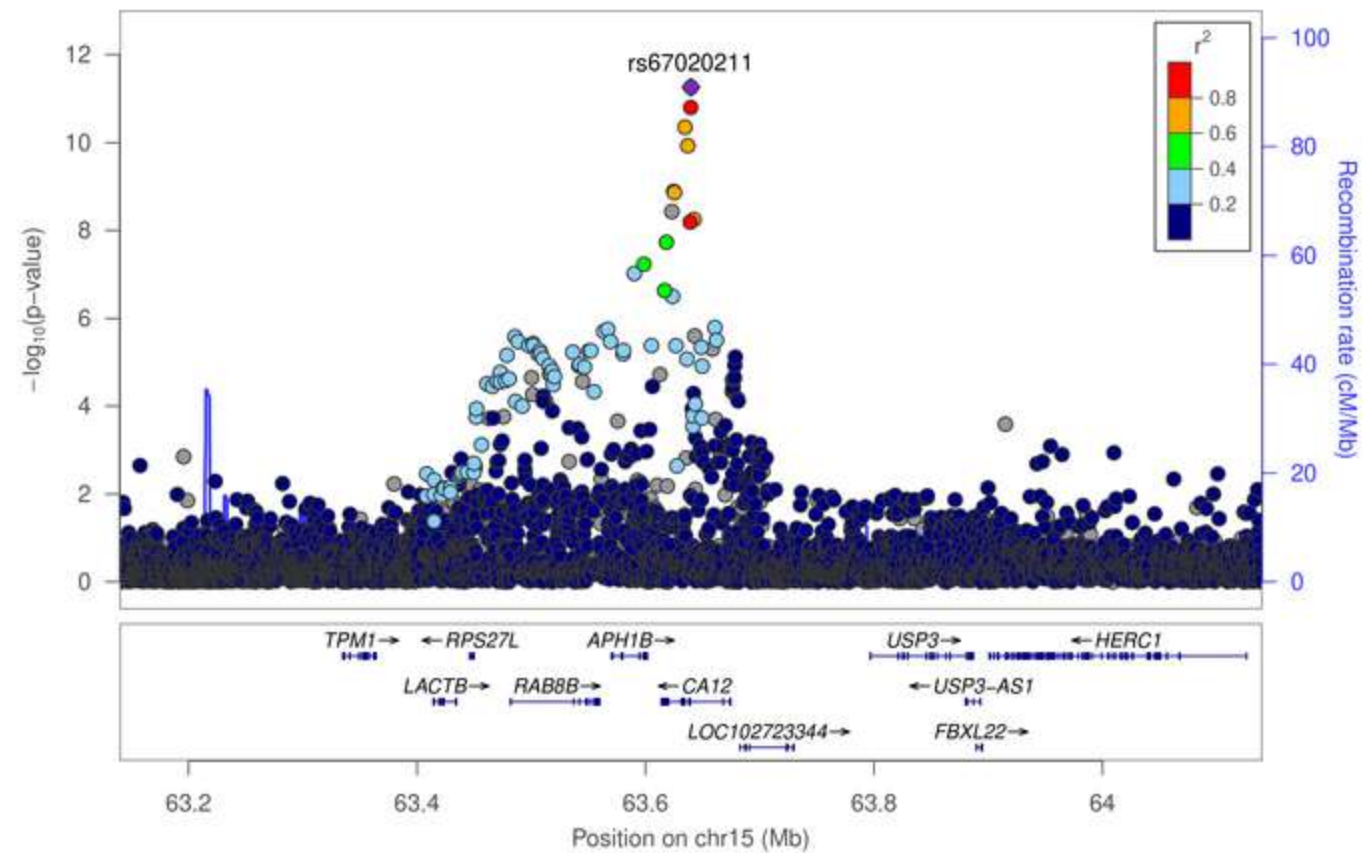
CST5 (CST5) [chr15:63639644_G_T (rs67020211) (T/G) N=14734]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.086	0.02	0.09 [0.05; 0.13]	31.3%
BioFinder (1496)	0.134	0.04	0.13 [0.06; 0.20]	10.4%
EGCUT (487)	0.072	0.07	0.07 [-0.06; 0.20]	3.1%
KORA (1064)	0.123	0.05	0.12 [0.03; 0.21]	6.3%
NSPHS (866)	0.048	0.05	0.05 [-0.05; 0.14]	5.5%
ORCADES (982)	0.063	0.04	0.06 [-0.02; 0.15]	6.6%
RECOMBINE (446)	0.071	0.05	0.07 [-0.04; 0.18]	4.5%
STABILITY (2951)	0.051	0.02	0.05 [0.00; 0.10]	22.7%
STANLEY (344)	0.145	0.08	0.15 [-0.01; 0.30]	2.1%
STANLEY (300)	0.020	0.08	0.02 [-0.14; 0.18]	1.9%
VIS (902)	0.057	0.05	0.06 [-0.04; 0.15]	5.7%
Common effect model			0.08 [0.06; 0.10]	100.0%
Random effects model			0.08 [0.06; 0.10]	-- 100.0%



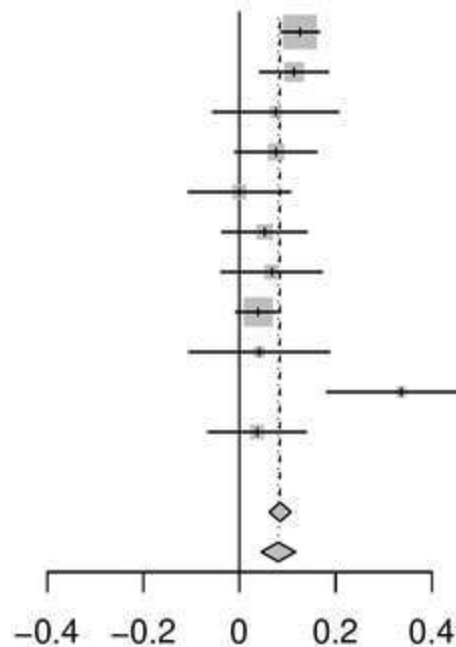
Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.76$

CST5 (CST5)-rs67020211



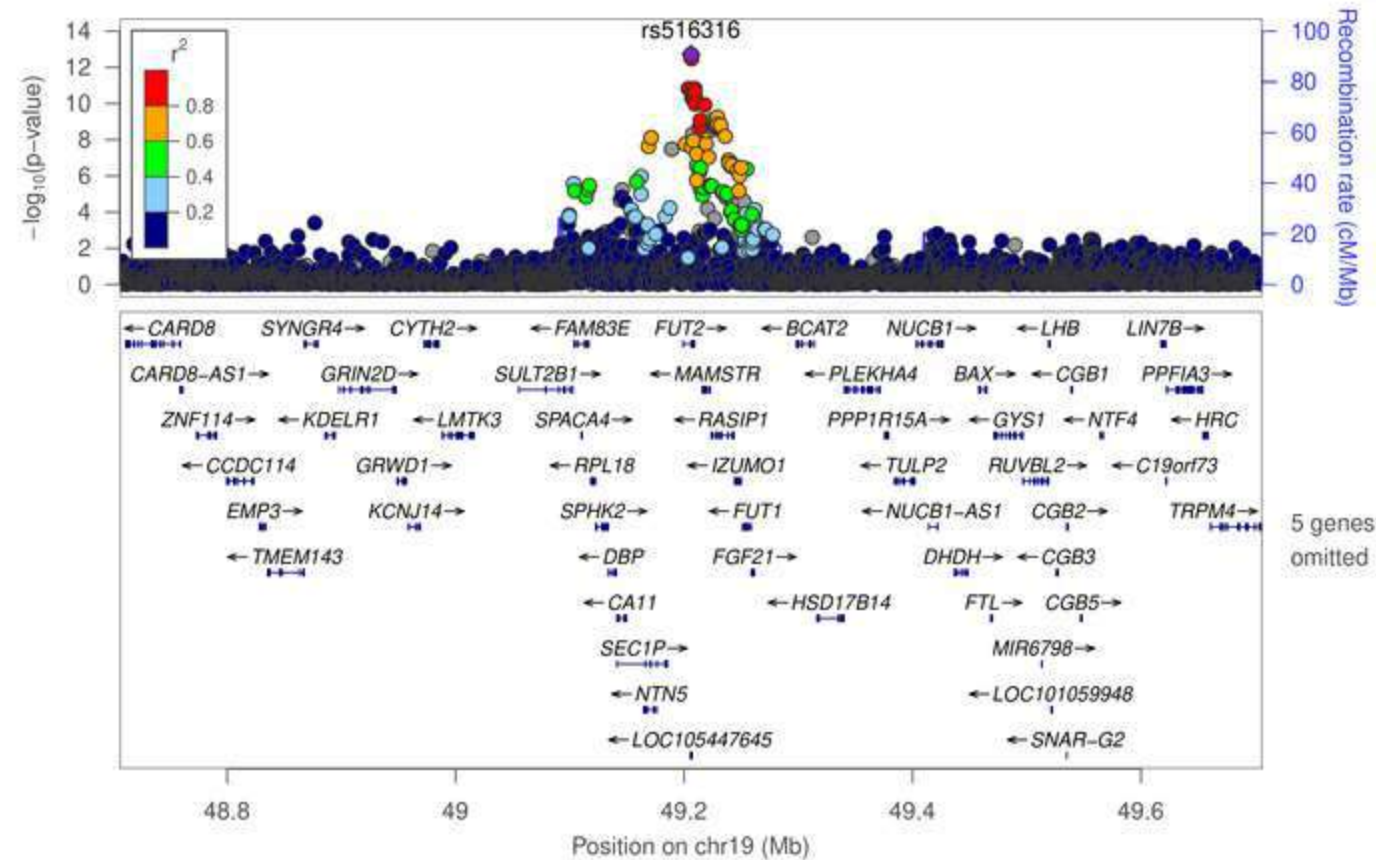
CST5 (CST5) [chr19:49206145_C_G (rs516316) (C/G) N=14734]

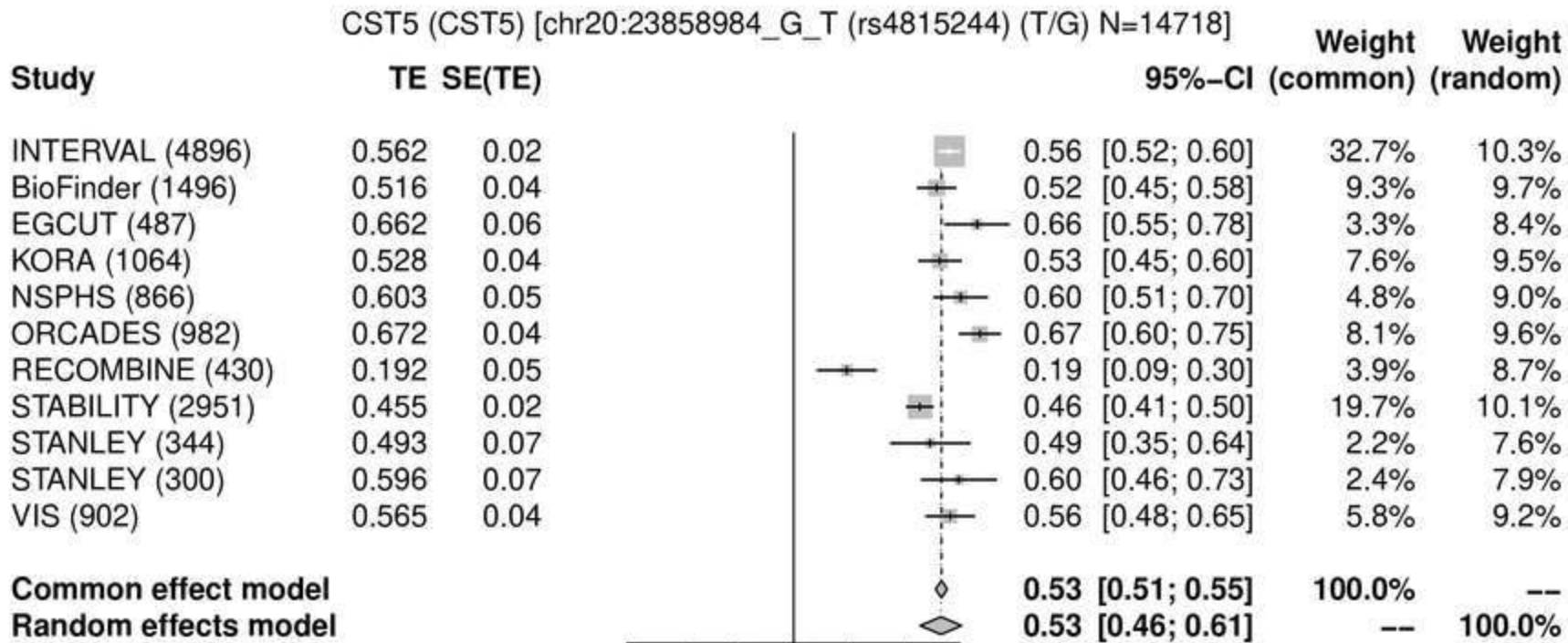
Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.126	0.02	0.13 [0.09; 0.17]	31.9%
BioFinder (1496)	0.114	0.04	0.11 [0.04; 0.18]	9.9%
EGCUT (487)	0.076	0.07	0.08 [-0.06; 0.21]	3.0%
KORA (1064)	0.076	0.04	0.08 [-0.01; 0.16]	6.9%
NSPHS (866)	0.000	0.05	0.00 [-0.11; 0.11]	4.5%
ORCADES (982)	0.052	0.05	0.05 [-0.04; 0.14]	6.5%
RECOMBINE (446)	0.067	0.05	0.07 [-0.04; 0.17]	4.6%
STABILITY (2951)	0.039	0.02	0.04 [-0.01; 0.09]	23.3%
STANLEY (344)	0.041	0.07	0.04 [-0.10; 0.19]	2.4%
STANLEY (300)	0.336	0.08	0.34 [0.18; 0.49]	2.1%
VIS (902)	0.037	0.05	0.04 [-0.07; 0.14]	4.9%
Common effect model			0.08 [0.06; 0.11]	100.0%
Random effects model			0.08 [0.05; 0.12]	-- 100.0%



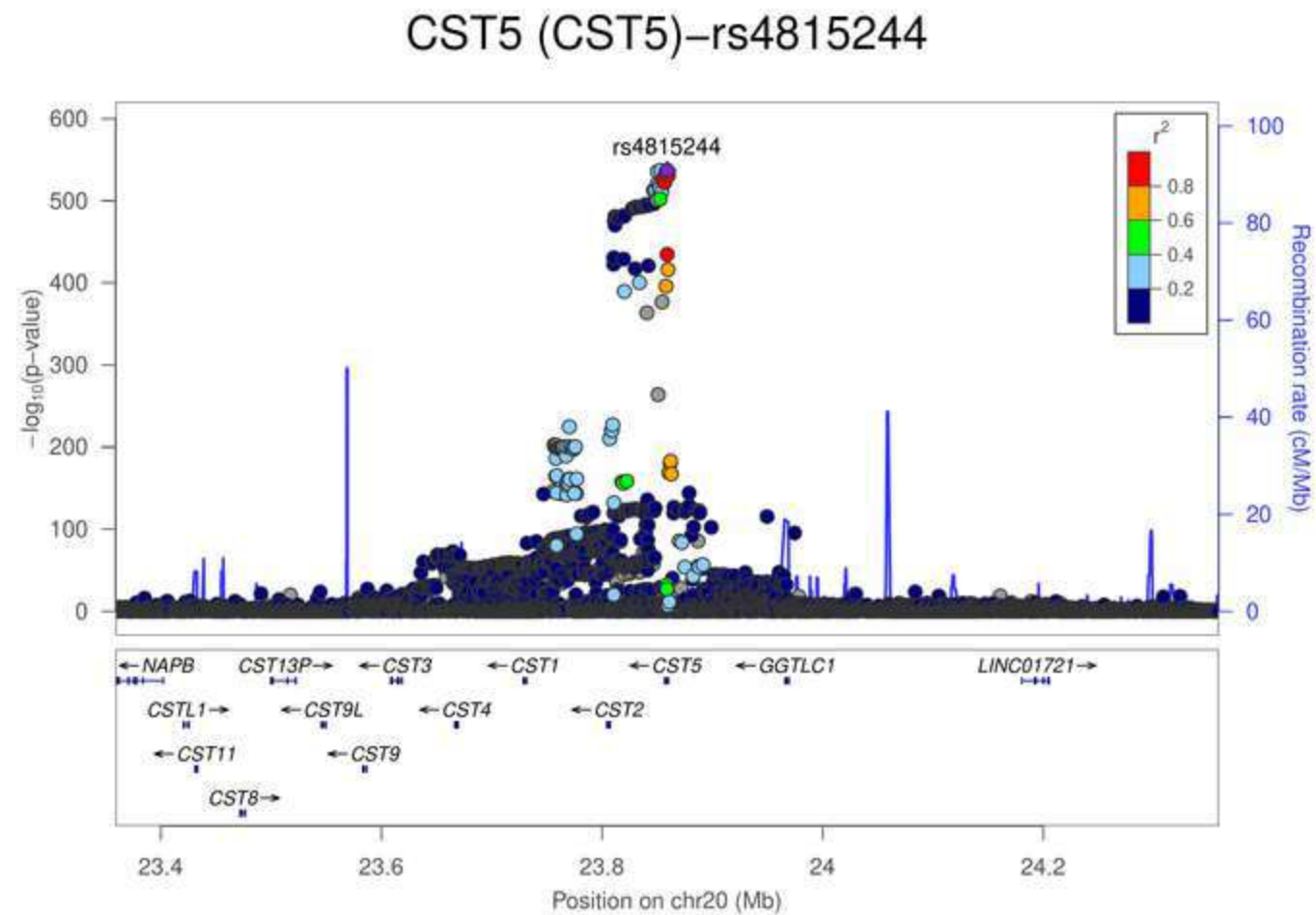
Heterogeneity: $I^2 = 57\%$, $\tau^2 = 0.0015$, $p = 0.01$

CST5 (CST5)-rs516316

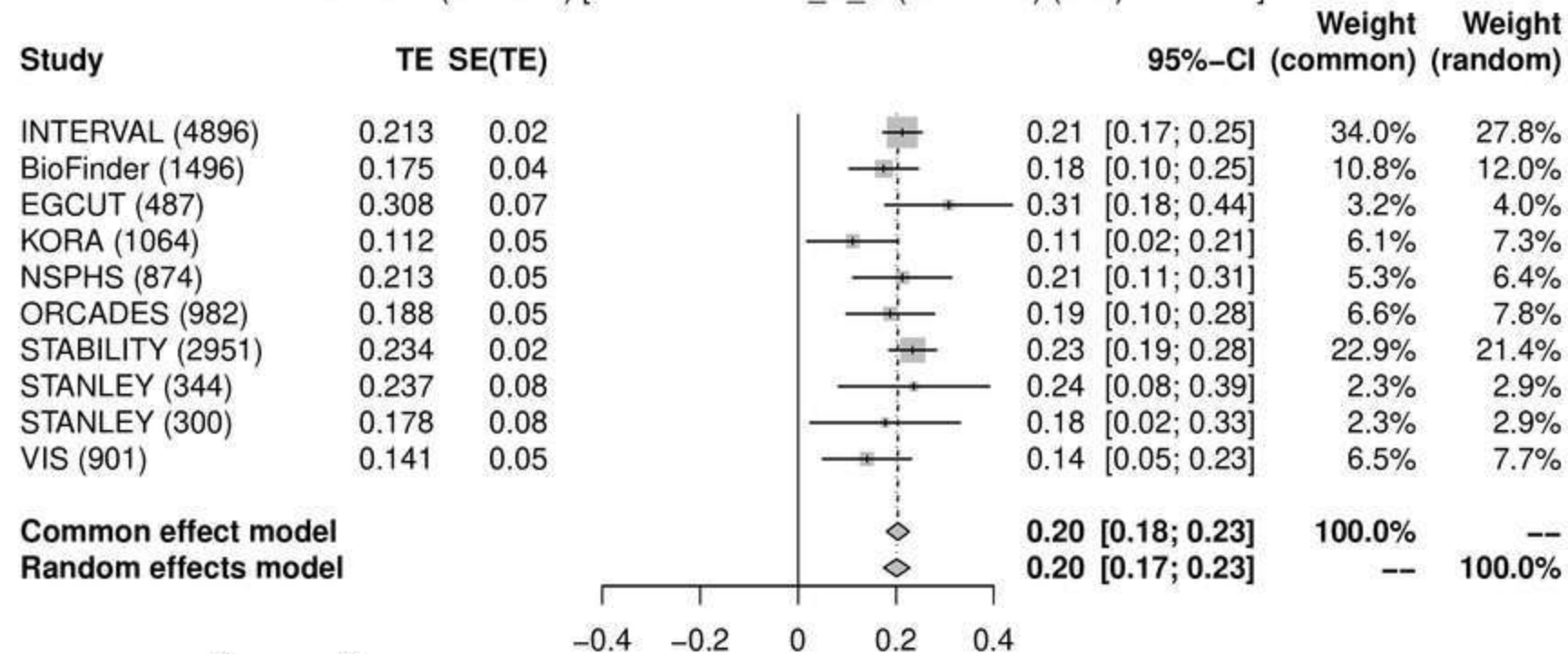




Heterogeneity: $I^2 = 87\%$, $\tau^2 = 0.0139$, $p < 0.01$

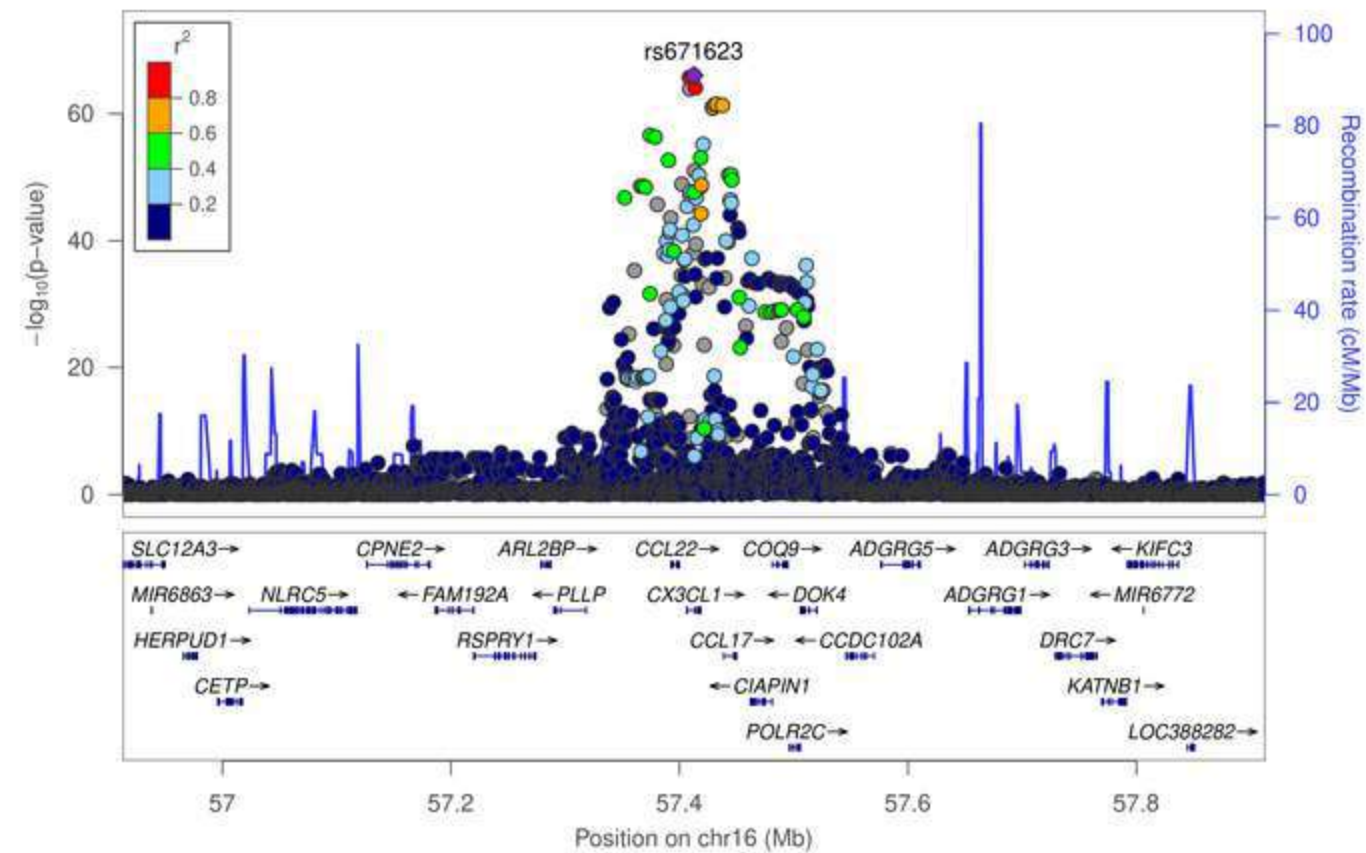


CX3CL1 (CX3CL1) [chr16:57412802_C_G (rs671623) (C/G) N=14295]

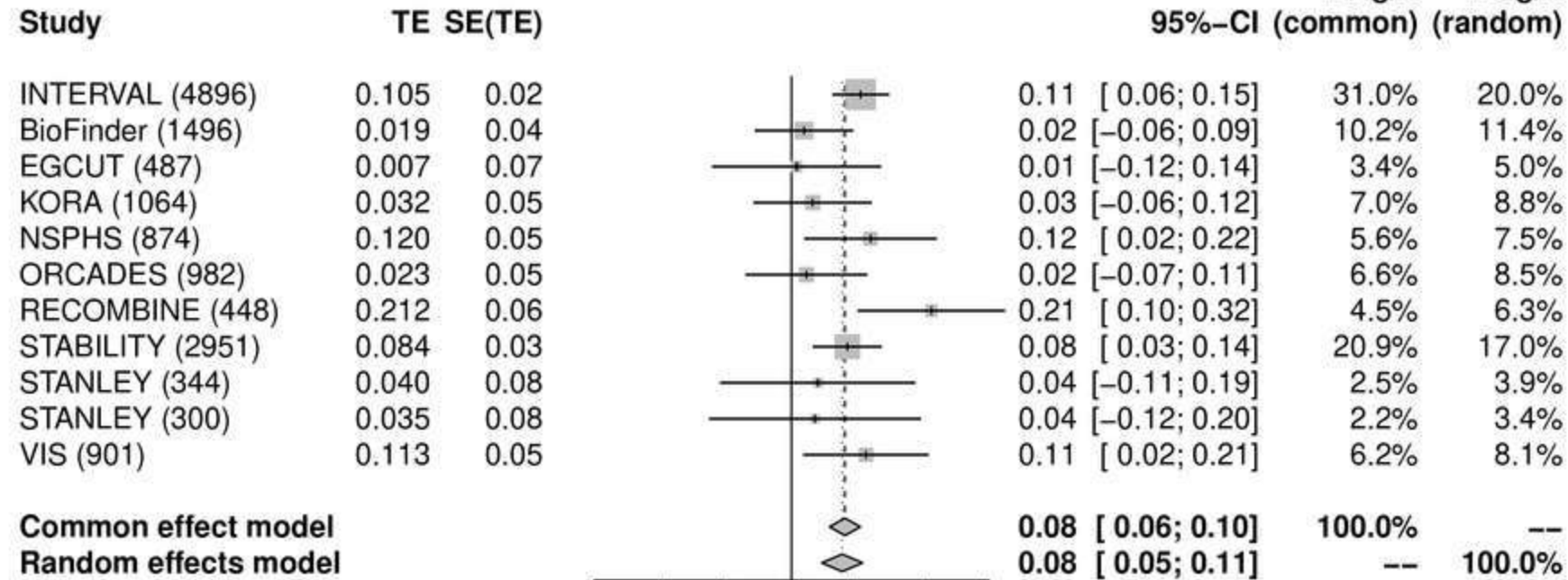


Heterogeneity: $I^2 = 17\%$, $\tau^2 = 0.0003$, $p = 0.29$

CX3CL1 (CX3CL1)-rs671623

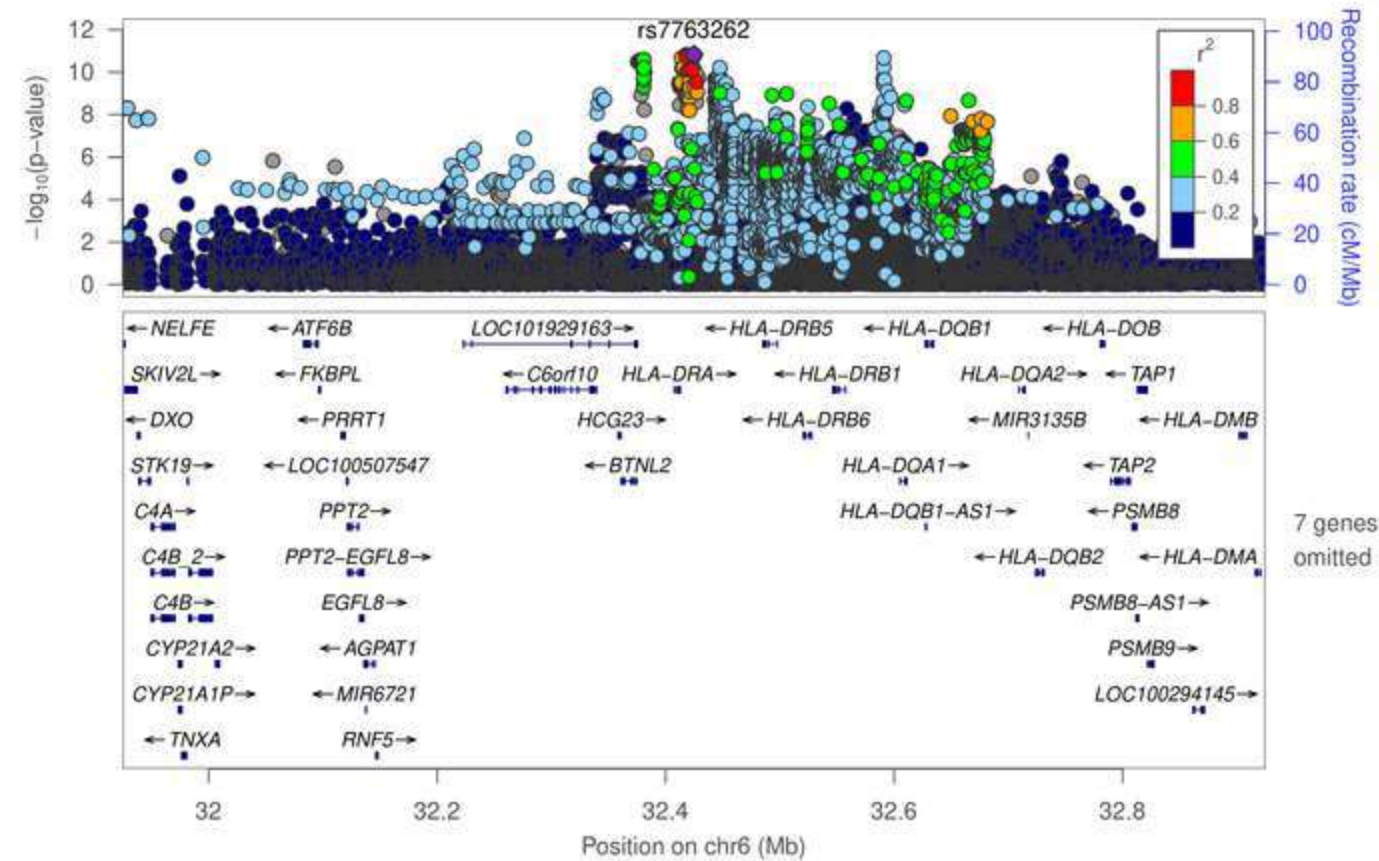


CX3CL1 (CX3CL1) [chr6:32424882_C_T (rs7763262) (T/C) N=14743]

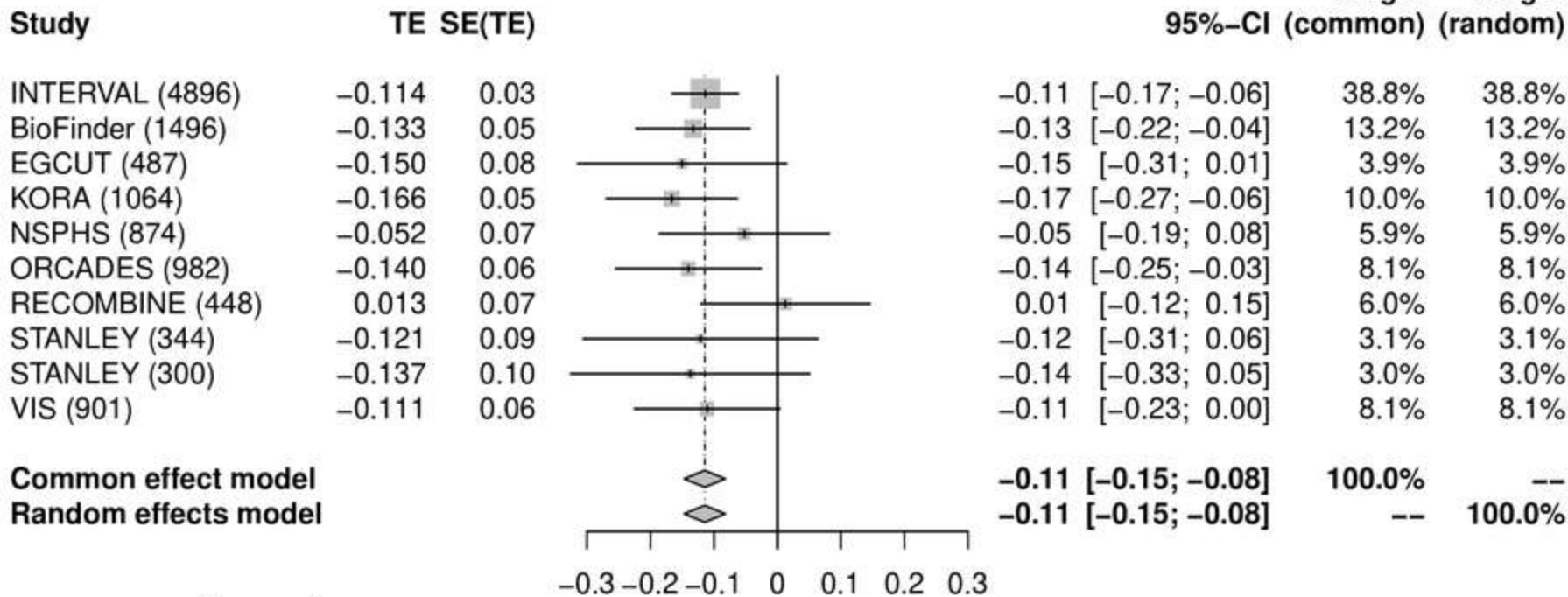


Heterogeneity: $I^2 = 33\%$, $\tau^2 = 0.0008$, $p = 0.13$

CX3CL1 (CX3CL1)-rs7763262

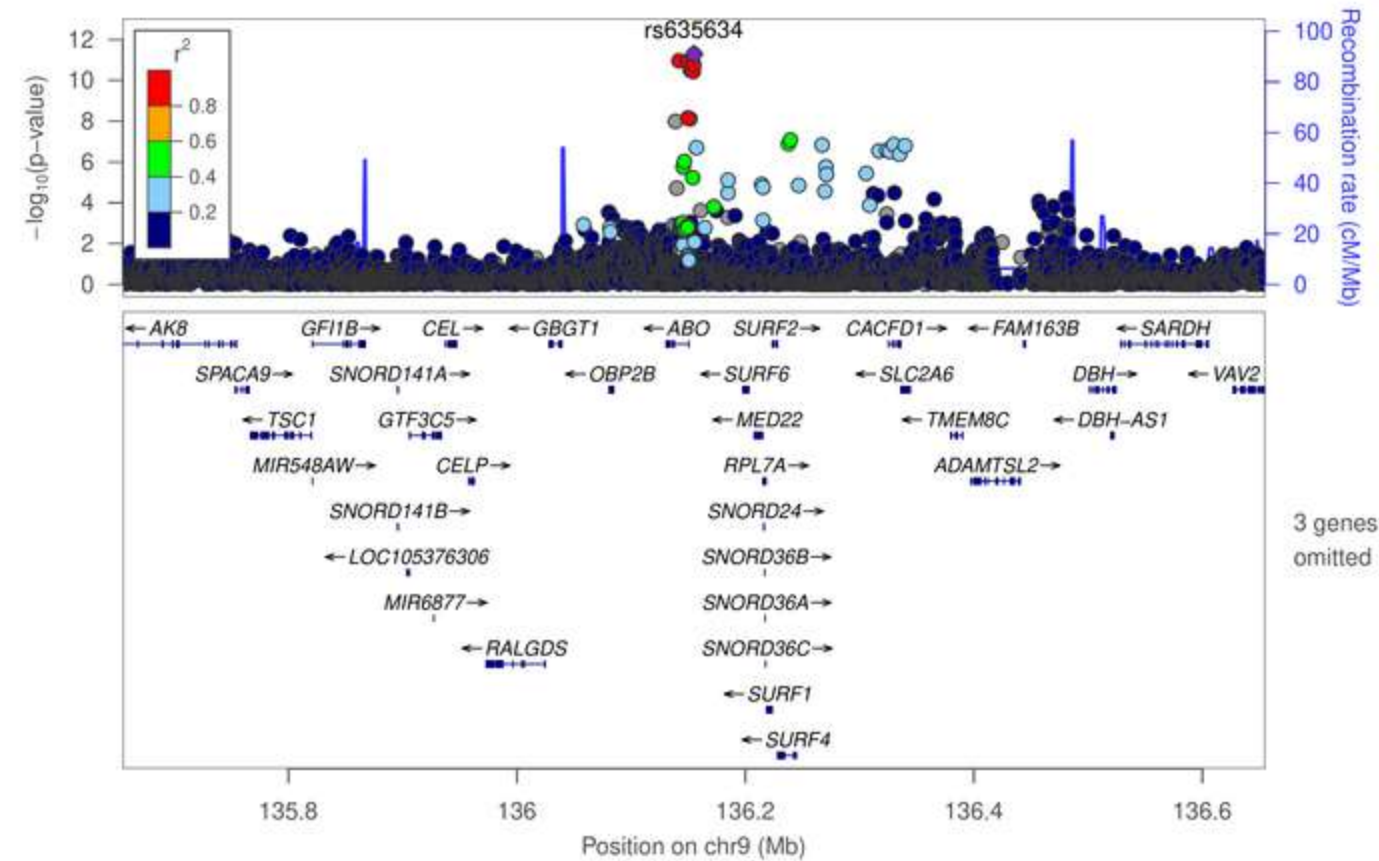


CX3CL1 (CX3CL1) [chr9:136155000_C_T (rs635634) (T/C) N=11792]

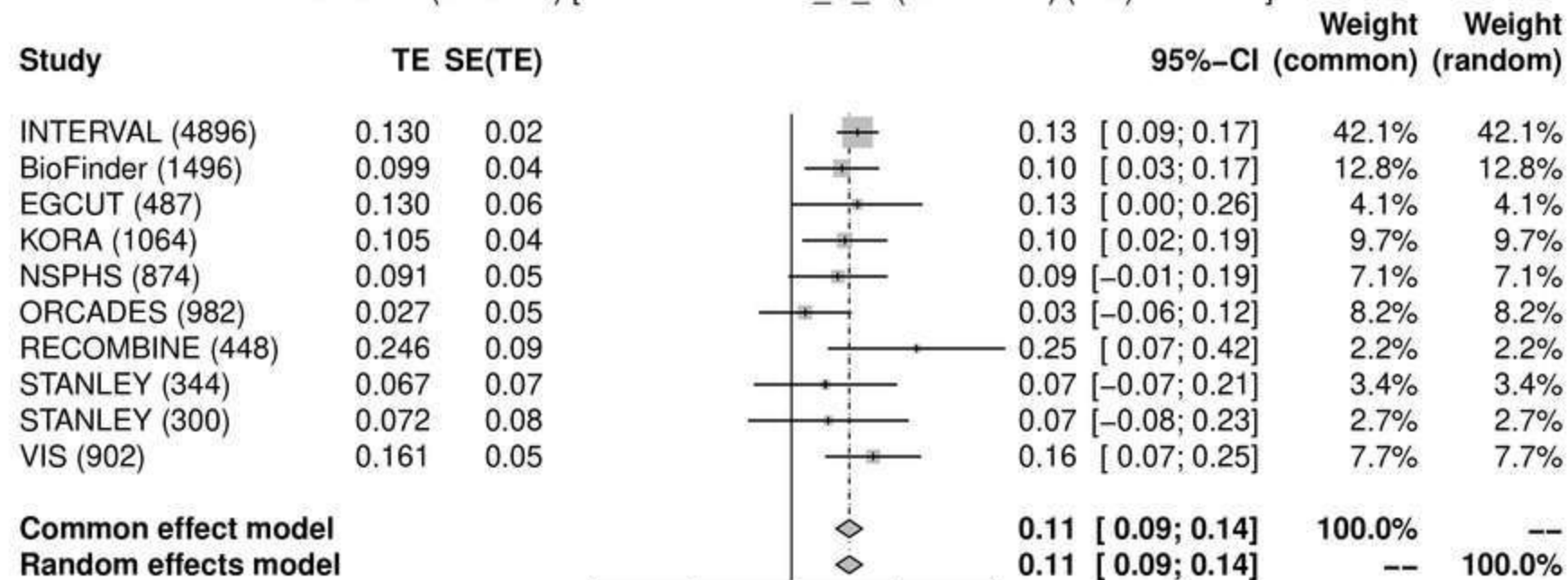


Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.75$

CX3CL1 (CX3CL1)-rs635634

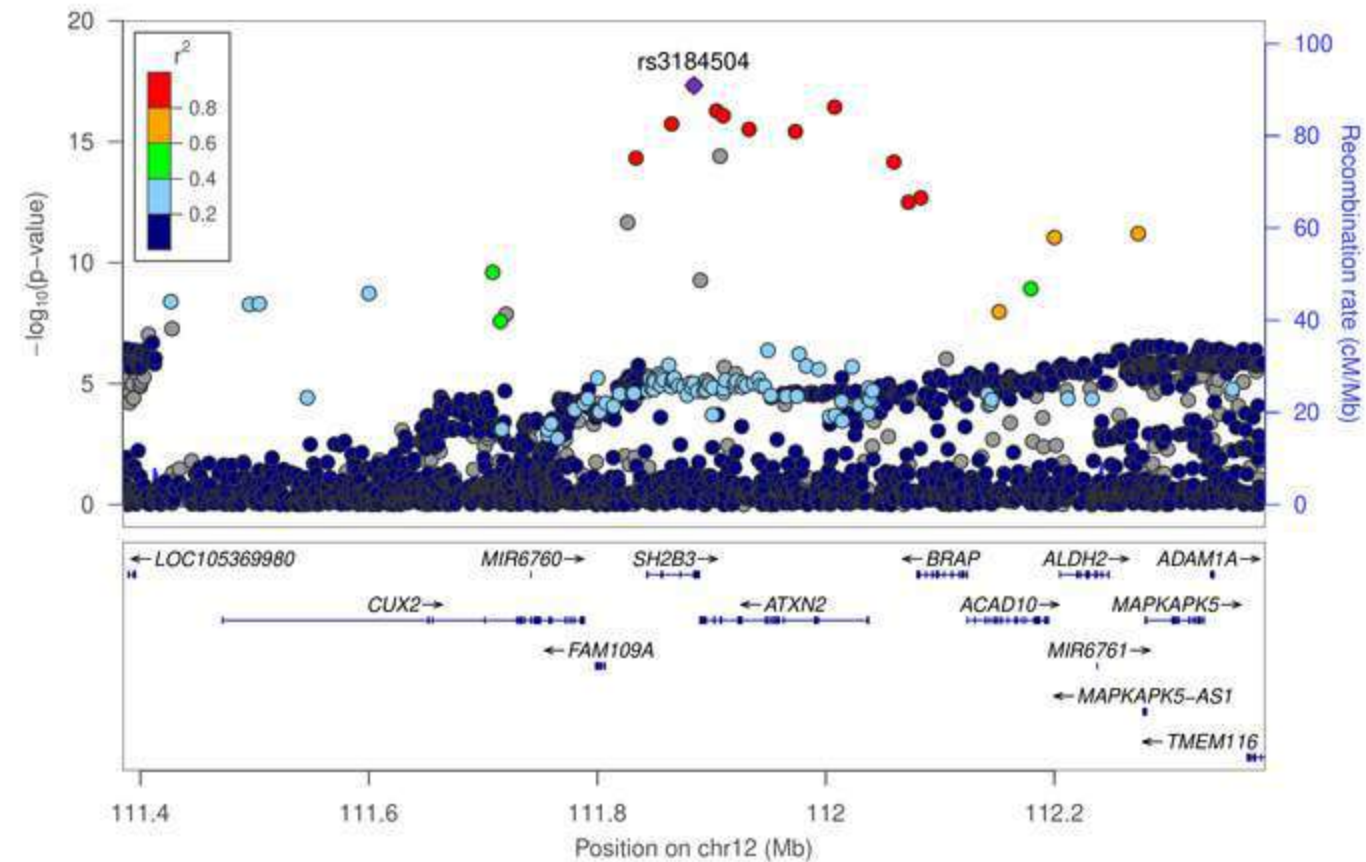


CXCL10 (CXCL10) [chr12:111884608_C_T (rs3184504) (T/C) N=11793]



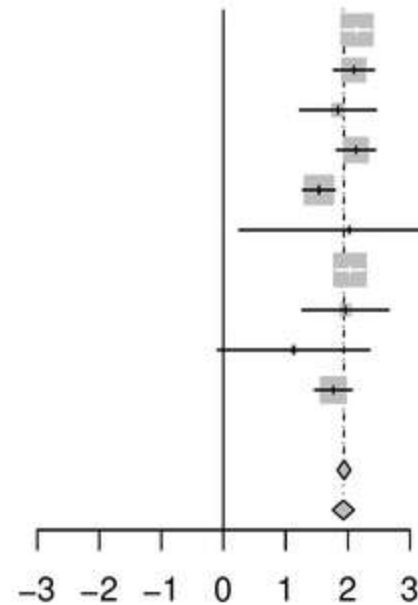
Heterogeneity: $I^2 = 0\%$, $\tau^2 < 0.0001$, $p = 0.47$

CXCL10 (CXCL10)-rs3184504



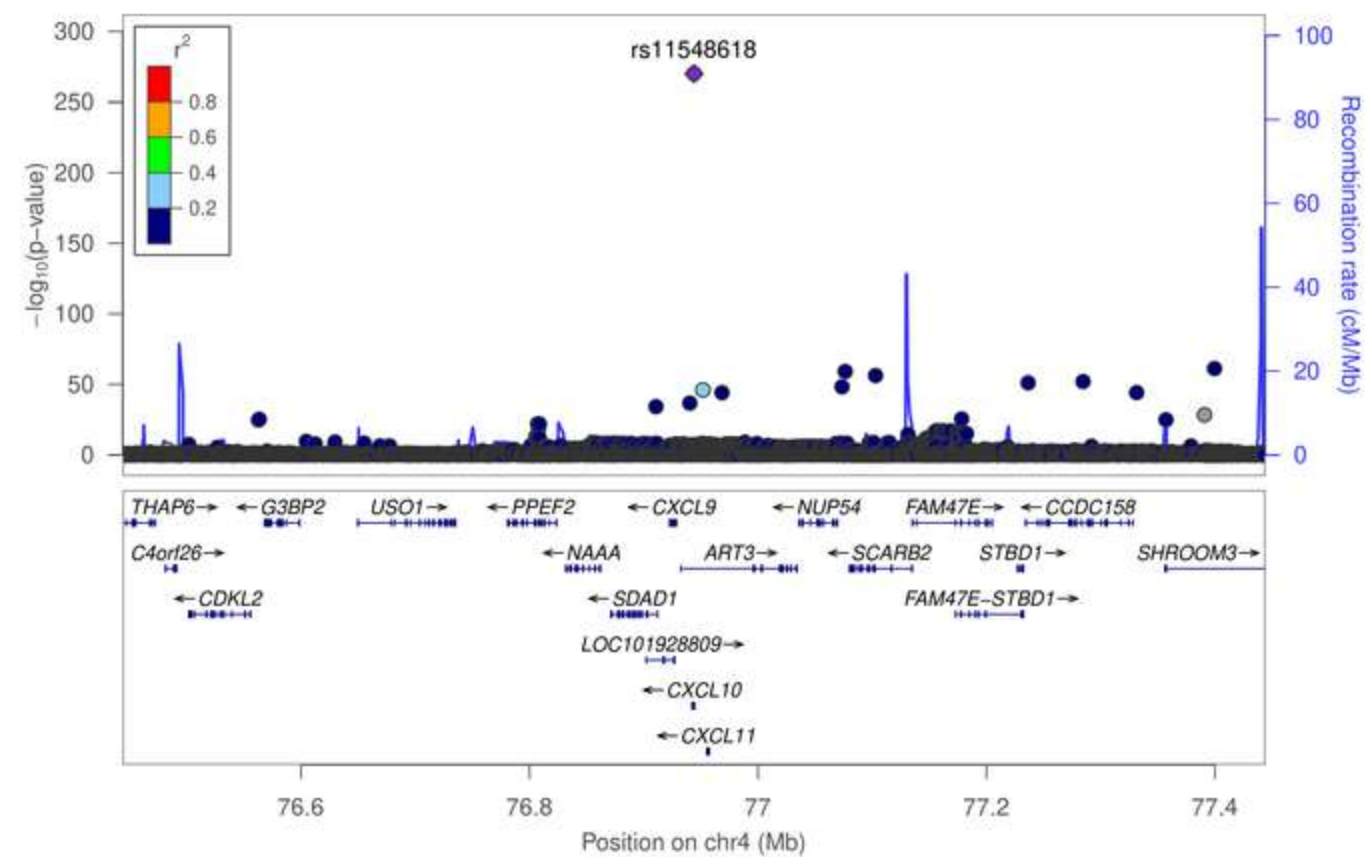
CXCL10 (CXCL10) [chr4:76943947_A_G (rs11548618) (A/G) N=14296]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	2.144	0.12	2.14 [1.90; 2.39]	19.8%
BioFinder (1496)	2.100	0.17	2.10 [1.77; 2.43]	10.9%
EGCUT (487)	1.843	0.31	1.84 [1.23; 2.46]	3.1%
KORA (1064)	2.133	0.16	2.13 [1.82; 2.45]	11.8%
NSPHS (874)	1.537	0.13	1.54 [1.28; 1.80]	17.2%
ORCADES (982)	2.027	0.91	2.03 [0.25; 3.80]	0.4%
STABILITY (2951)	2.036	0.12	2.04 [1.80; 2.27]	20.7%
STANLEY (344)	1.963	0.36	1.96 [1.26; 2.66]	2.4%
STANLEY (300)	1.129	0.62	1.13 [-0.10; 2.35]	0.8%
VIS (902)	1.769	0.15	1.77 [1.47; 2.07]	13.0%
Common effect model			1.94 [1.83; 2.05]	100.0%
Random effects model			1.93 [1.76; 2.10]	100.0%



Heterogeneity: $I^2 = 50\%$, $\tau^2 = 0.0346$, $p = 0.04$

CXCL10 (CXCL10)-rs11548618



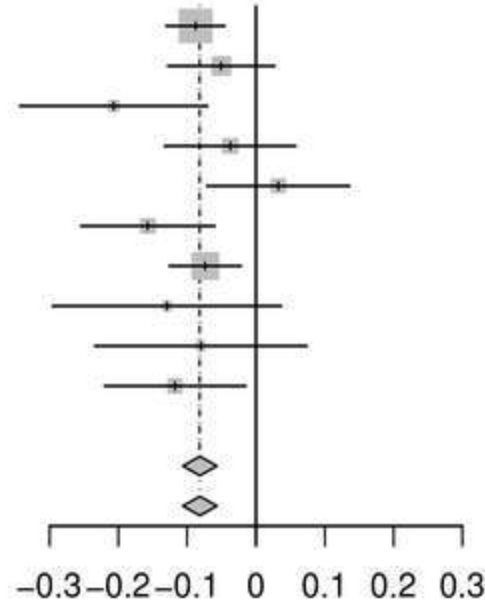
CXCL11 (CXCL11) [chr10:64948684_C_T (rs10733789) (T/C) N=14288]

Study

TE SE(TE)

INTERVAL (4896)
BioFinder (1496)
EGCUT (487)
KORA (1064)
NSPHS (866)
ORCADES (982)
STABILITY (2951)
STANLEY (344)
STANLEY (300)
VIS (902)

-0.088 0.02
-0.051 0.04
-0.207 0.07
-0.038 0.05
0.032 0.05
-0.157 0.05
-0.074 0.03
-0.130 0.08
-0.080 0.08
-0.117 0.05

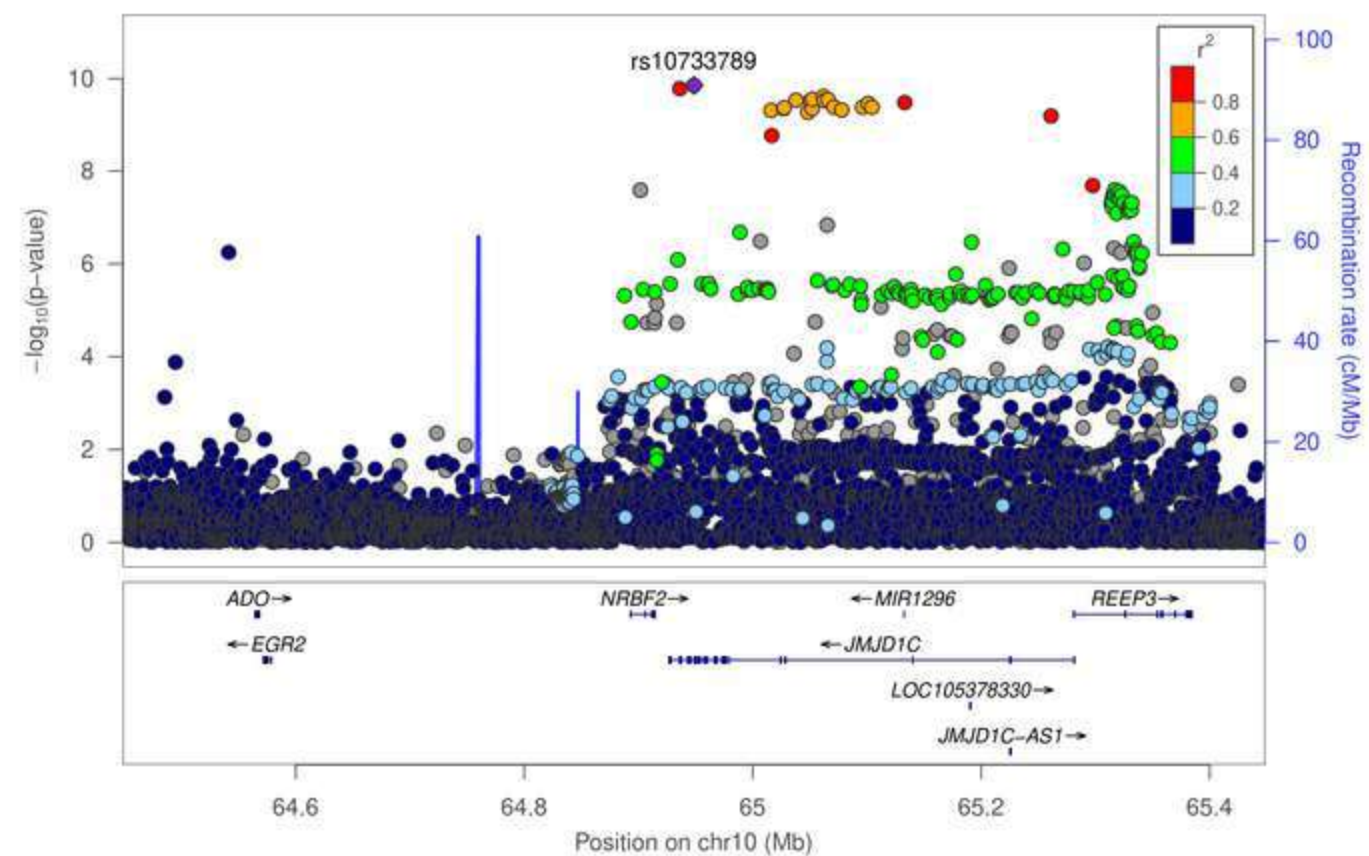


Common effect model
Random effects model

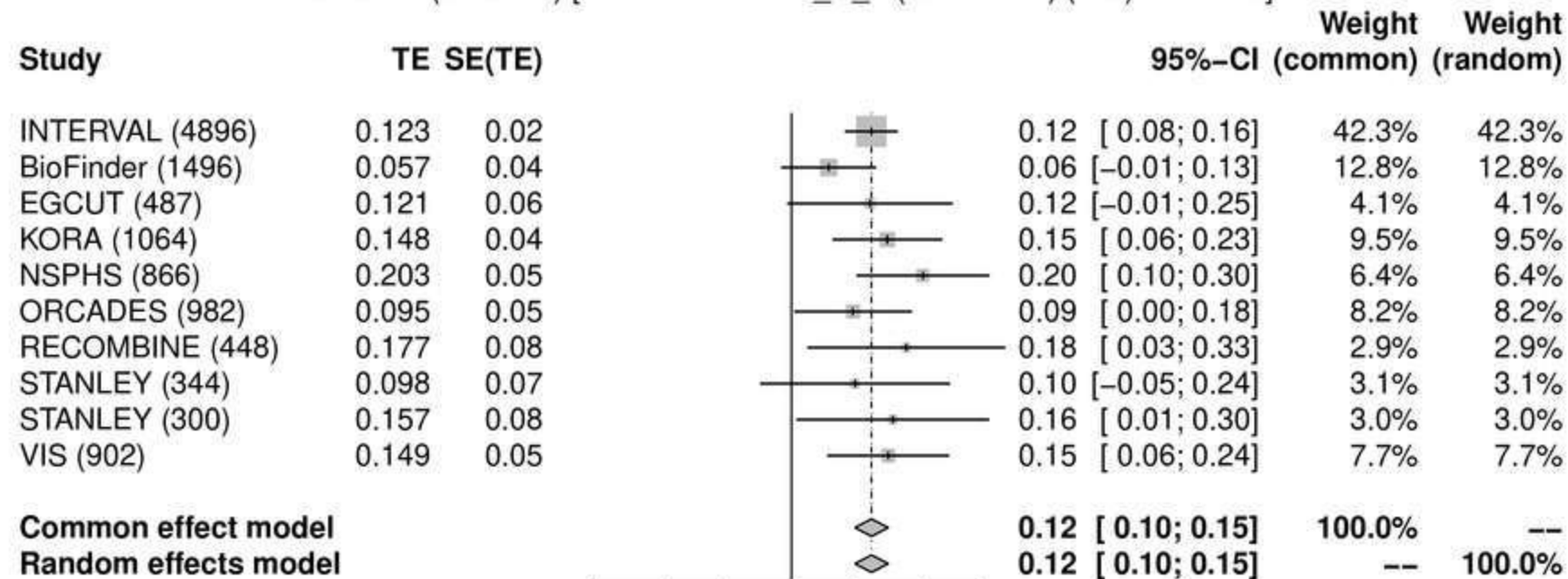
Weight	Weight
95%-CI (common)	(random)
-0.09 [-0.13; -0.05]	33.9%
-0.05 [-0.13; 0.03]	10.2%
-0.21 [-0.34; -0.07]	3.3%
-0.04 [-0.13; 0.06]	6.8%
0.03 [-0.07; 0.14]	5.8%
-0.16 [-0.25; -0.06]	6.5%
-0.07 [-0.13; -0.02]	22.7%
-0.13 [-0.30; 0.04]	2.2%
-0.08 [-0.23; 0.07]	2.6%
-0.12 [-0.22; -0.01]	5.9%
-0.08 [-0.11; -0.06]	100.0%
-0.08 [-0.11; -0.06]	-- 100.0%

Heterogeneity: $I^2 = 28\%$, $\tau^2 < 0.0001$, $p = 0.18$

CXCL11 (CXCL11)-rs10733789

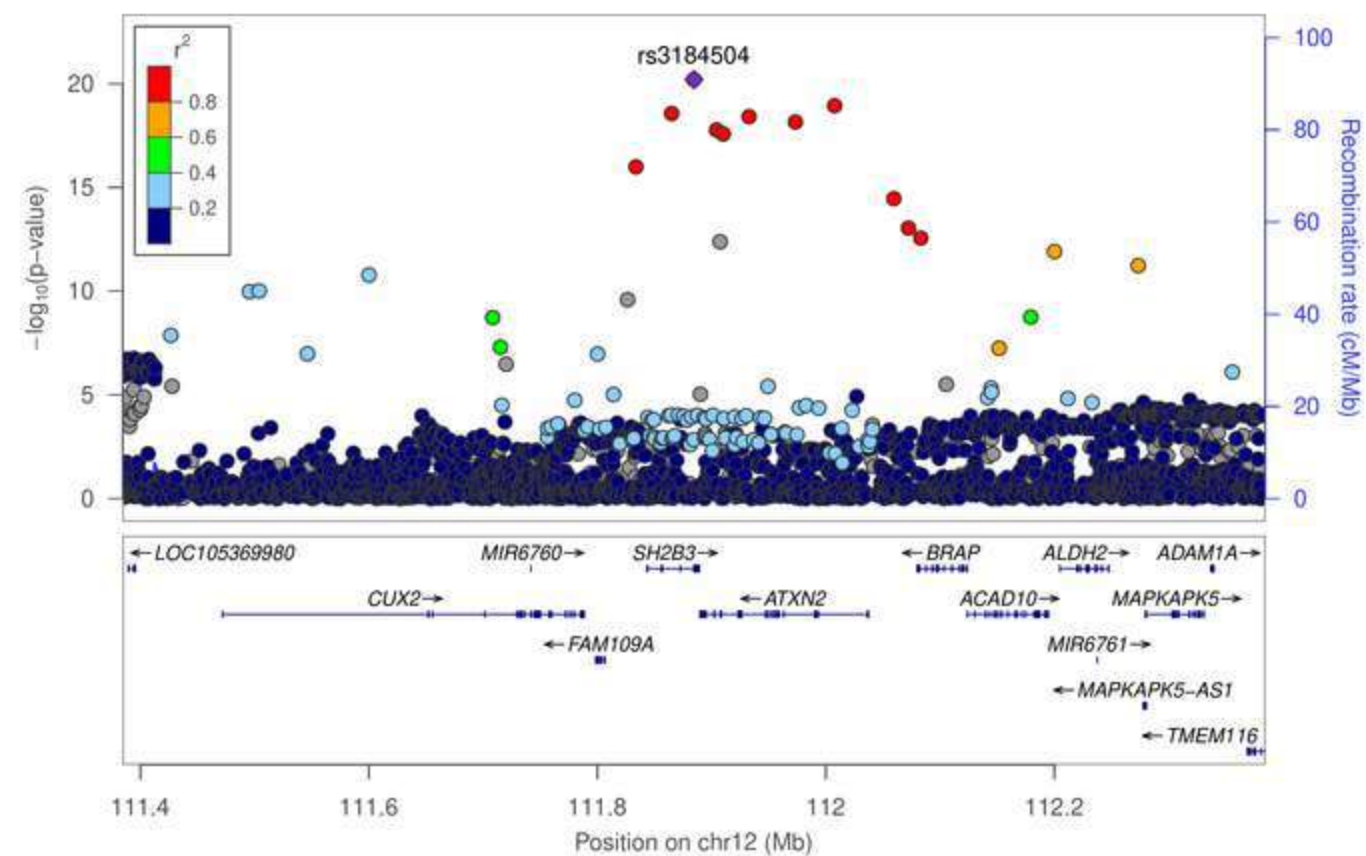


CXCL11 (CXCL11) [chr12:111884608_C_T (rs3184504) (T/C) N=11785]



Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.60$

CXCL11 (CXCL11)-rs3184504



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (430)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 79\%$, $\tau^2 = 0.0096$, $p < 0.01$

CXCL11 (CXCL11) [chr4:76916146_A_G (rs6827617) (A/G) N=14718]

TE SE(TE)

-0.157

0.02

-0.292

0.04

-0.339

0.06

-0.076

0.04

-0.036

0.05

-0.233

0.04

0.048

0.09

-0.136

0.03

-0.267

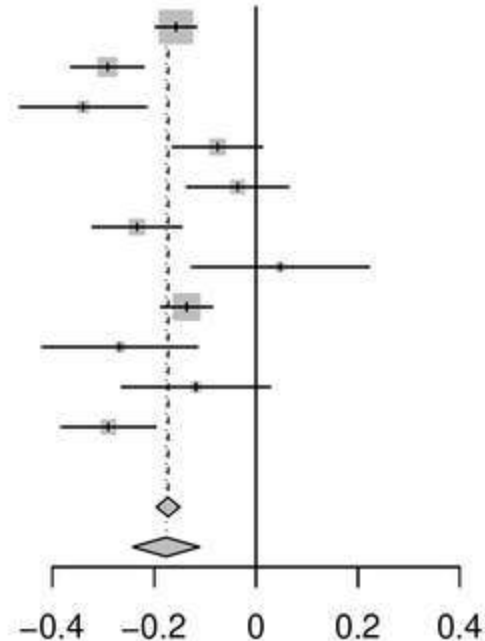
0.08

-0.118

0.07

-0.289

0.05

Weight
95%-CI (common) (random)

-0.16 [-0.20; -0.12]

33.1%

11.2%

-0.29 [-0.36; -0.22]

10.5%

10.3%

-0.34 [-0.46; -0.21]

3.5%

8.3%

-0.08 [-0.16; 0.01]

6.9%

9.7%

-0.04 [-0.14; 0.06]

5.4%

9.2%

-0.23 [-0.32; -0.15]

7.0%

9.7%

0.05 [-0.13; 0.22]

1.8%

6.4%

-0.14 [-0.19; -0.09]

20.8%

11.0%

-0.27 [-0.42; -0.11]

2.3%

7.2%

-0.12 [-0.26; 0.03]

2.5%

7.4%

-0.29 [-0.38; -0.20]

6.2%

9.5%

-0.17 [-0.20; -0.15]

100.0%

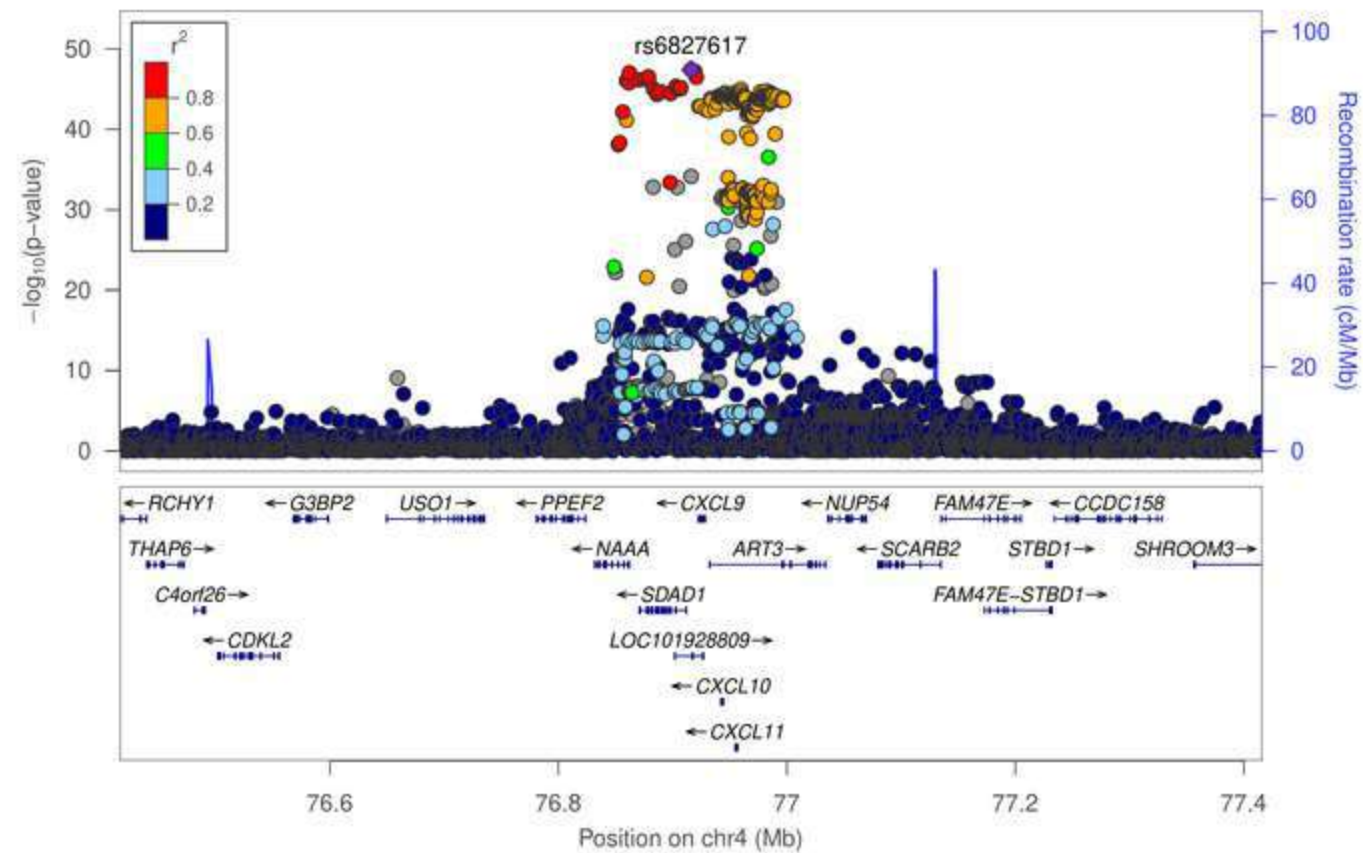
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-0.18 [-0.24; -0.11]

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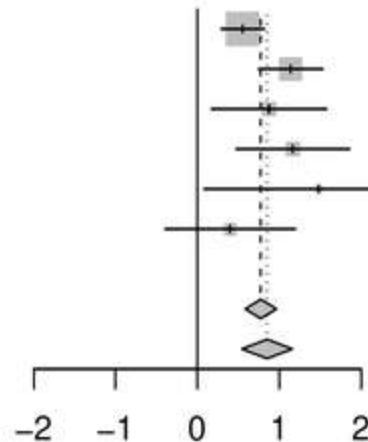
100.0%

CXCL11 (CXCL11)-rs6827617



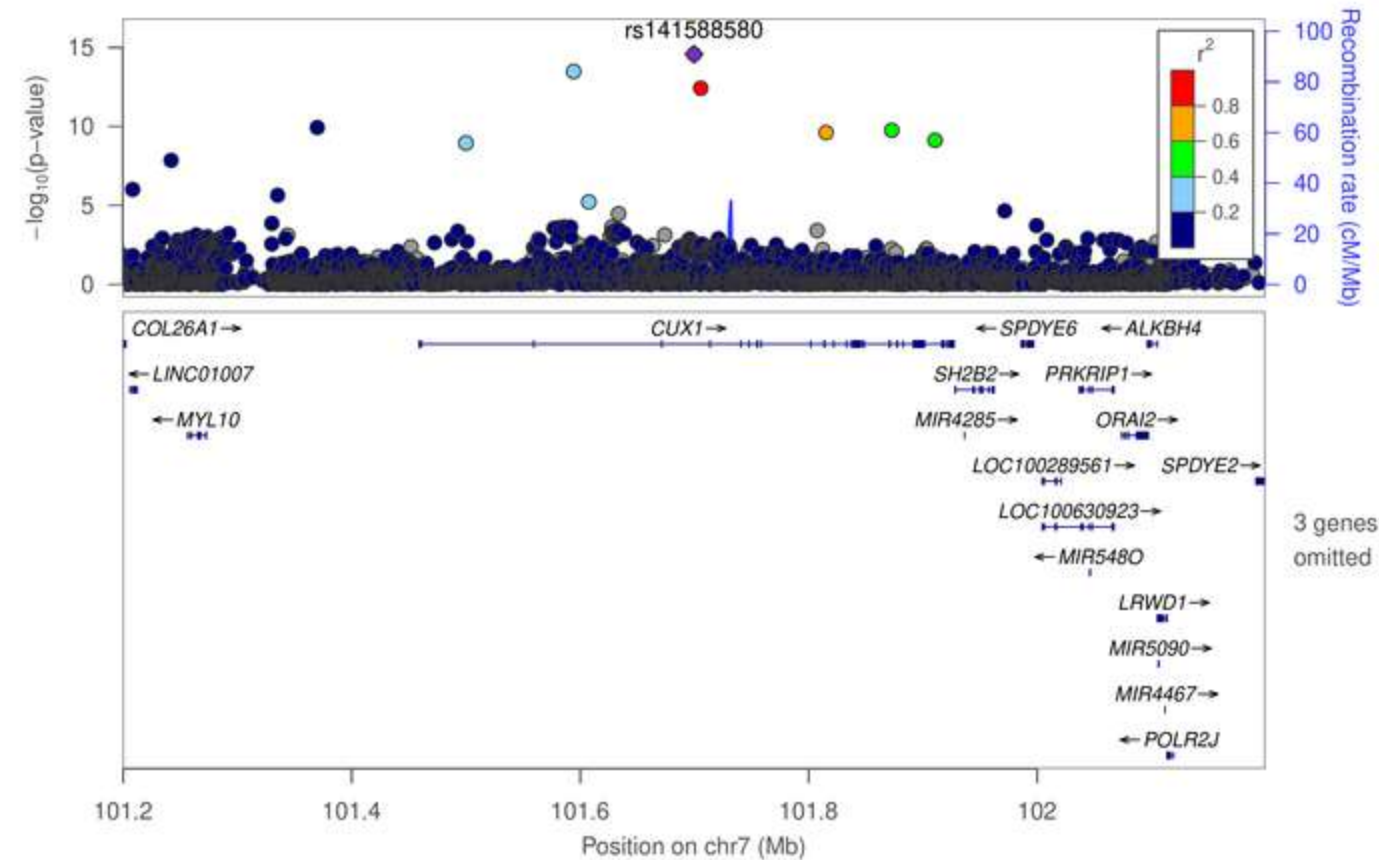
CXCL11 (CXCL11) [chr7:101699589_G_T (rs141588580) (T/G) N=9082]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.553	0.13	0.55 [0.29; 0.82]	53.0%	32.2%
BioFinder (1496)	1.139	0.20	1.14 [0.75; 1.53]	24.1%	25.2%
KORA (1064)	0.873	0.36	0.87 [0.17; 1.58]	7.4%	13.3%
ORCADES (982)	1.164	0.35	1.16 [0.47; 1.86]	7.7%	13.6%
STANLEY (344)	1.482	0.72	1.48 [0.08; 2.88]	1.9%	4.4%
STANLEY (300)	0.400	0.40	0.40 [-0.39; 1.19]	5.8%	11.2%
Common effect model			0.77 [0.58; 0.97]	100.0%	--
Random effects model			0.85 [0.54; 1.16]	--	100.0%



Heterogeneity: $I^2 = 46\%$, $\tau^2 = 0.0598$, $p = 0.10$

CXCL11 (CXCL11)-rs141588580



Study

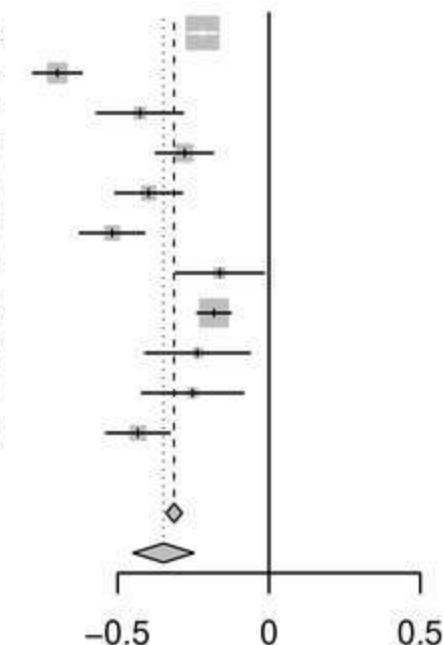
Study	TE	SE(TE)
INTERVAL (4896)	-0.220	0.02
BioFinder (1496)	-0.699	0.04
EGCUT (487)	-0.426	0.07
KORA (1064)	-0.279	0.05
NSPHS (866)	-0.398	0.06
ORCADES (982)	-0.518	0.05
RECOMBINE (443)	-0.163	0.07
STABILITY (2951)	-0.182	0.03
STANLEY (344)	-0.236	0.09
STANLEY (300)	-0.252	0.09
VIS (902)	-0.433	0.05

Common effect model
Random effects model

Heterogeneity: $I^2 = 93\%$, $\tau^2 = 0.0256$, $p < 0.01$

CXCL1 (CXCL1) [chr4:74739076_G_T (rs1366949) (T/G) N=14731]

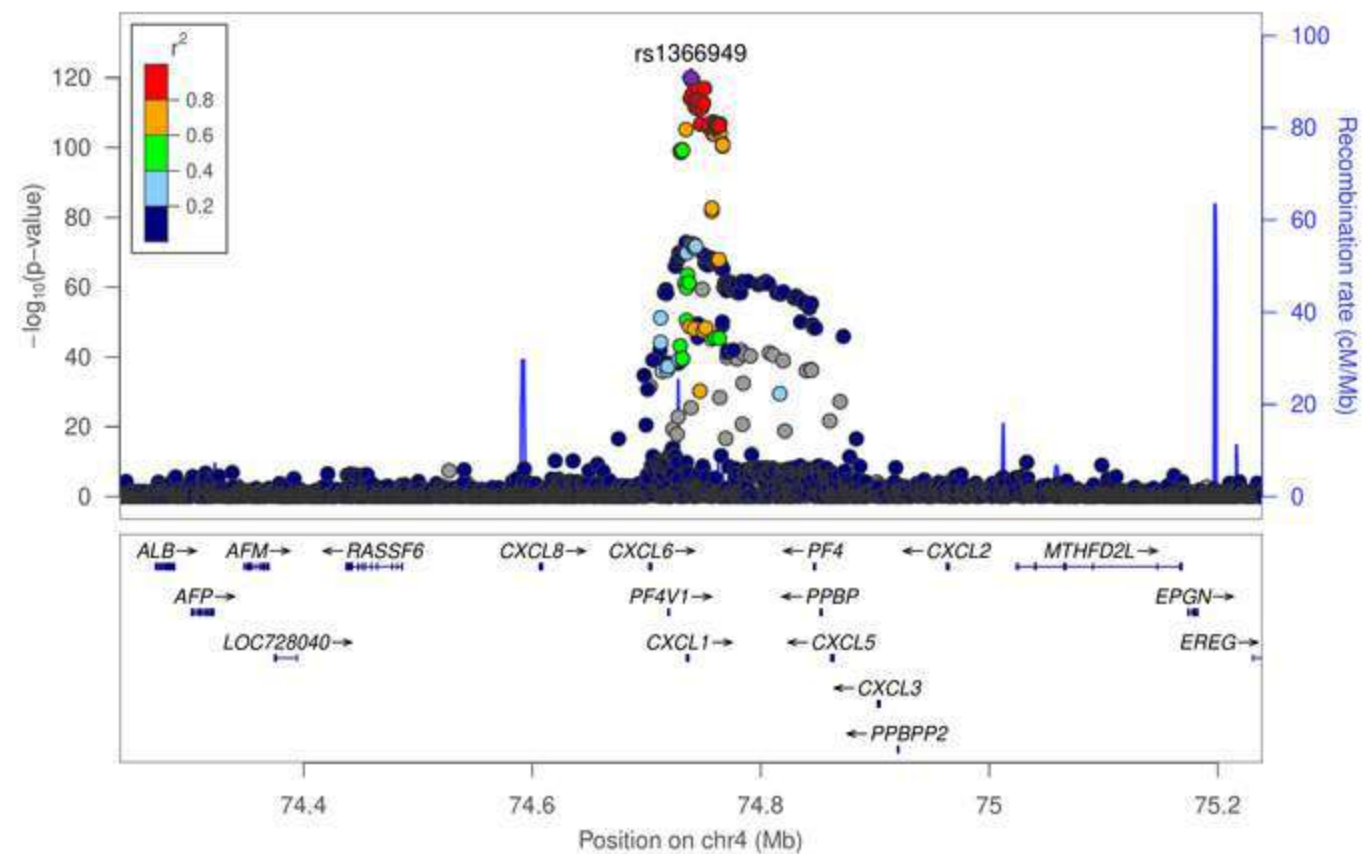
TE SE(TE)



Weight 95%-CI (common) Weight 95%-CI (random)

-0.22	[-0.27; -0.17]	30.5%	10.1%
-0.70	[-0.78; -0.62]	10.4%	9.7%
-0.43	[-0.57; -0.28]	3.4%	8.6%
-0.28	[-0.37; -0.18]	7.6%	9.5%
-0.40	[-0.51; -0.29]	5.6%	9.2%
-0.52	[-0.63; -0.41]	6.0%	9.3%
-0.16	[-0.31; -0.02]	3.2%	8.5%
-0.18	[-0.24; -0.13]	22.3%	10.0%
-0.24	[-0.41; -0.06]	2.3%	7.9%
-0.25	[-0.42; -0.08]	2.4%	8.0%
-0.43	[-0.54; -0.33]	6.2%	9.3%
-0.31	[-0.34; -0.29]	100.0%	--
-0.35	[-0.45; -0.25]	--	100.0%

CXCL1 (CXCL1)-rs1366949



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (448)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 53\%$, $\tau^2 = 0.0022$, $p = 0.02$

CXCL5 (CXCL5) [chr10:65077994_C_G (rs7090111) (C/G) N=14736]

TE SE(TE)

-0.137

0.02

-0.127

0.04

-0.236

0.07

-0.227

0.04

-0.318

0.05

-0.195

0.05

-0.124

0.09

-0.151

0.03

-0.162

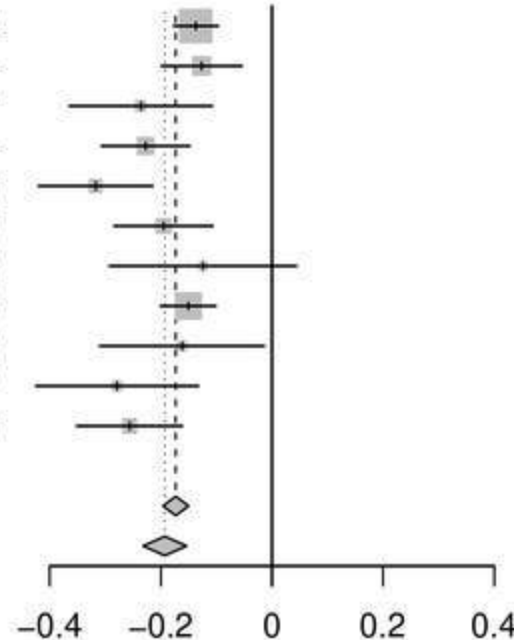
0.08

-0.279

0.07

-0.257

0.05

Weight
95%-CI (common) (random)

-0.14 [-0.18; -0.10]

33.0%

15.7%

-0.13 [-0.20; -0.05]

10.0%

11.5%

-0.24 [-0.37; -0.11]

3.2%

6.3%

-0.23 [-0.31; -0.15]

8.3%

10.6%

-0.32 [-0.42; -0.21]

5.0%

8.2%

-0.20 [-0.28; -0.11]

6.7%

9.6%

-0.12 [-0.29; 0.04]

1.9%

4.2%

-0.15 [-0.20; -0.10]

21.2%

14.4%

-0.16 [-0.31; -0.01]

2.4%

5.2%

-0.28 [-0.43; -0.13]

2.5%

5.2%

-0.26 [-0.35; -0.16]

5.8%

9.0%

-0.17 [-0.20; -0.15]

100.0%

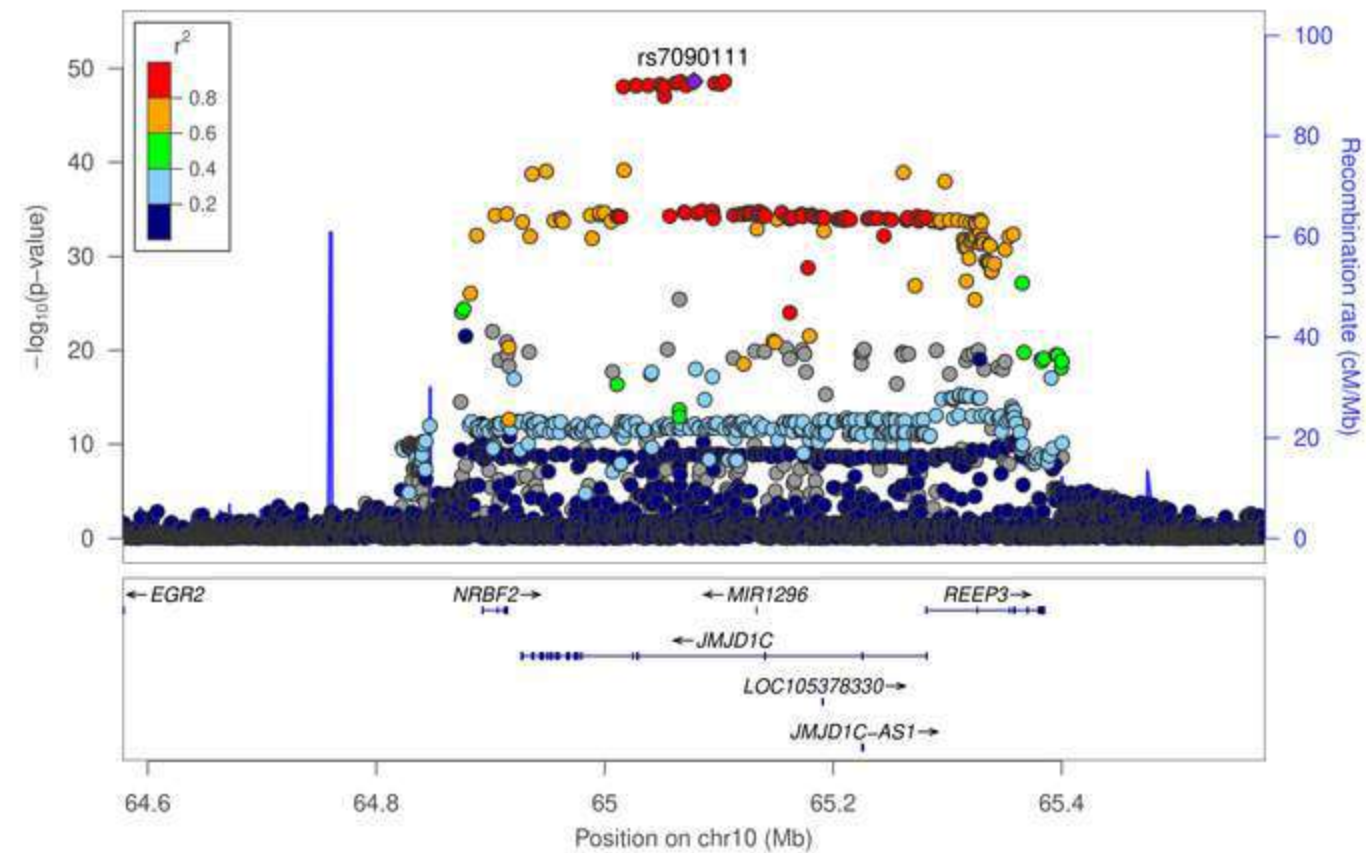
--

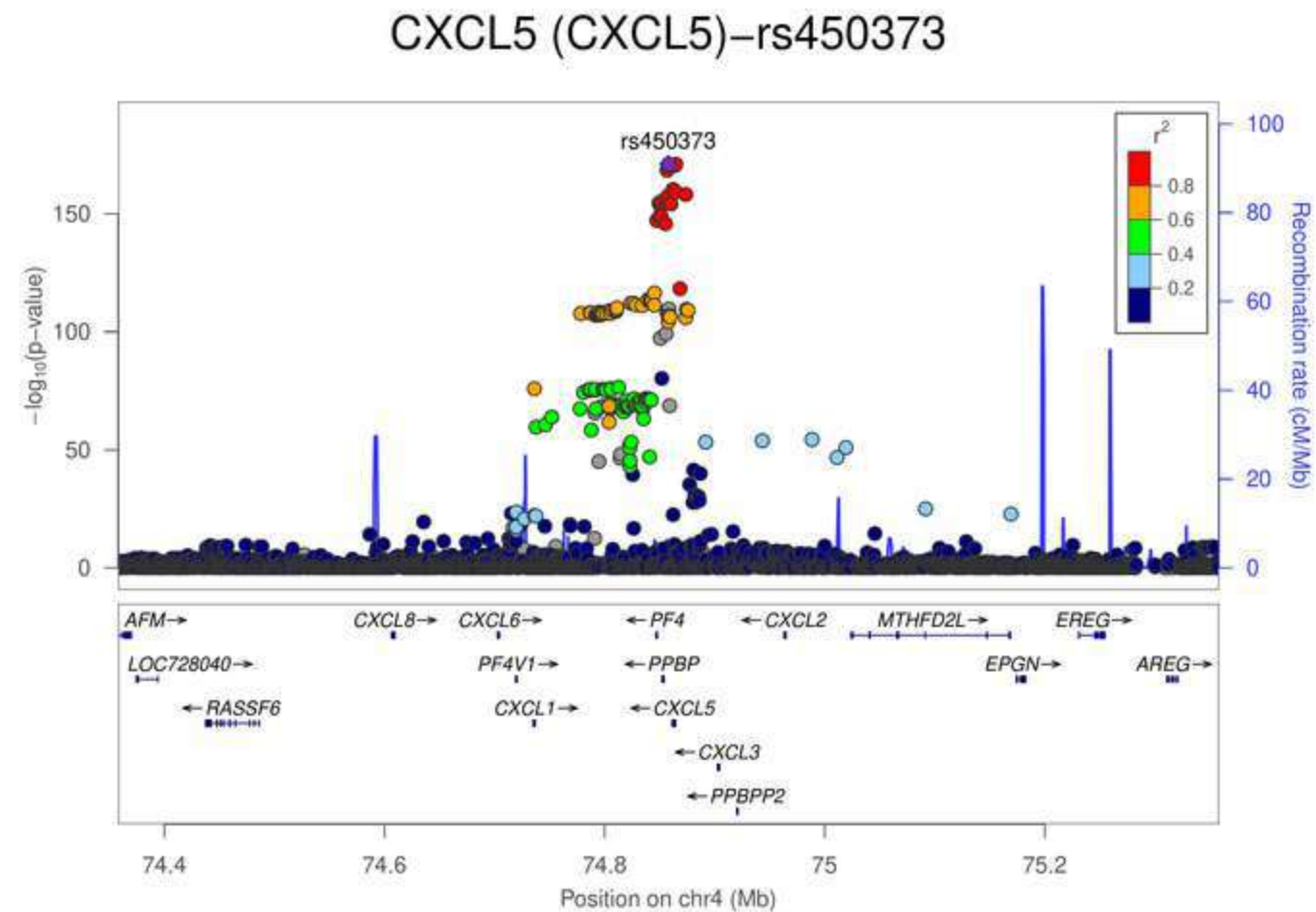
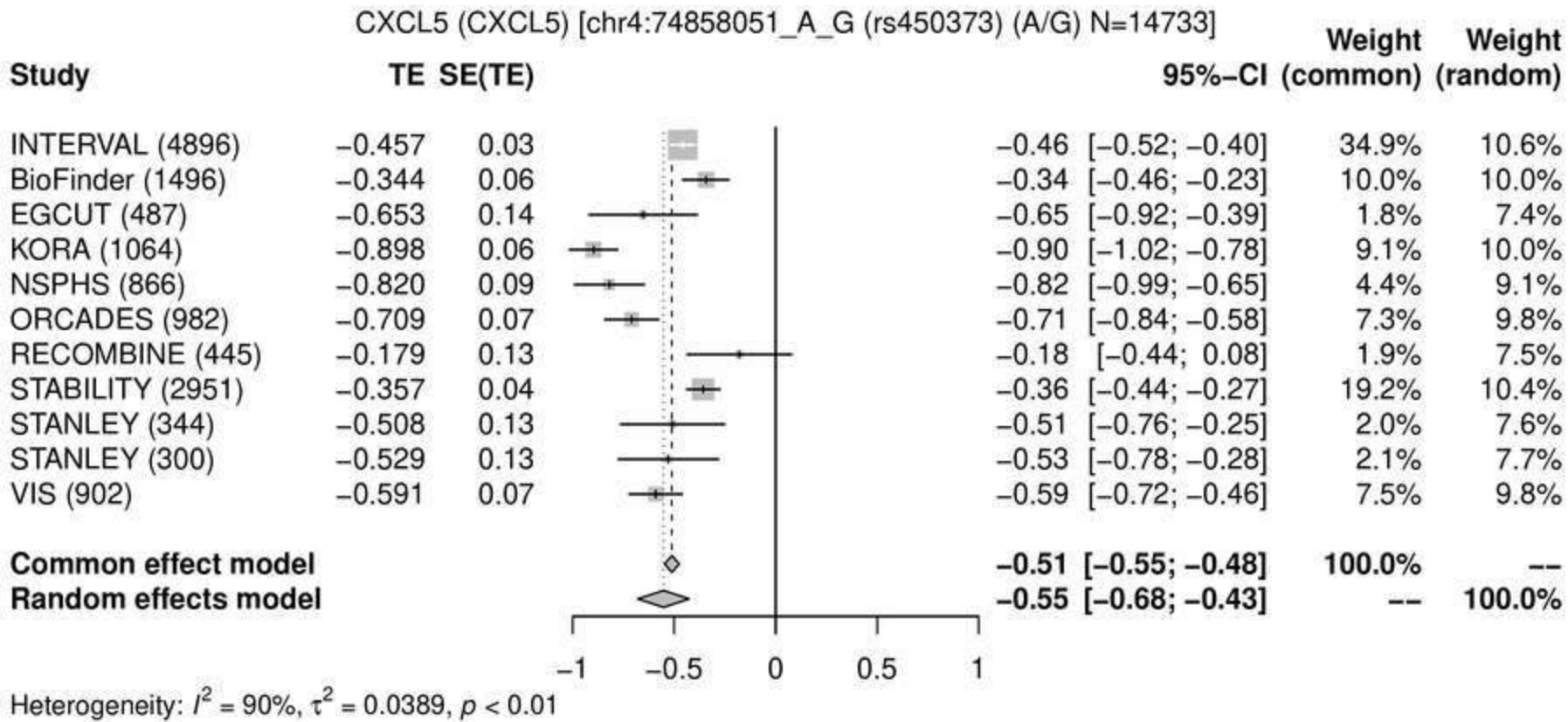
-0.19 [-0.23; -0.15]

--

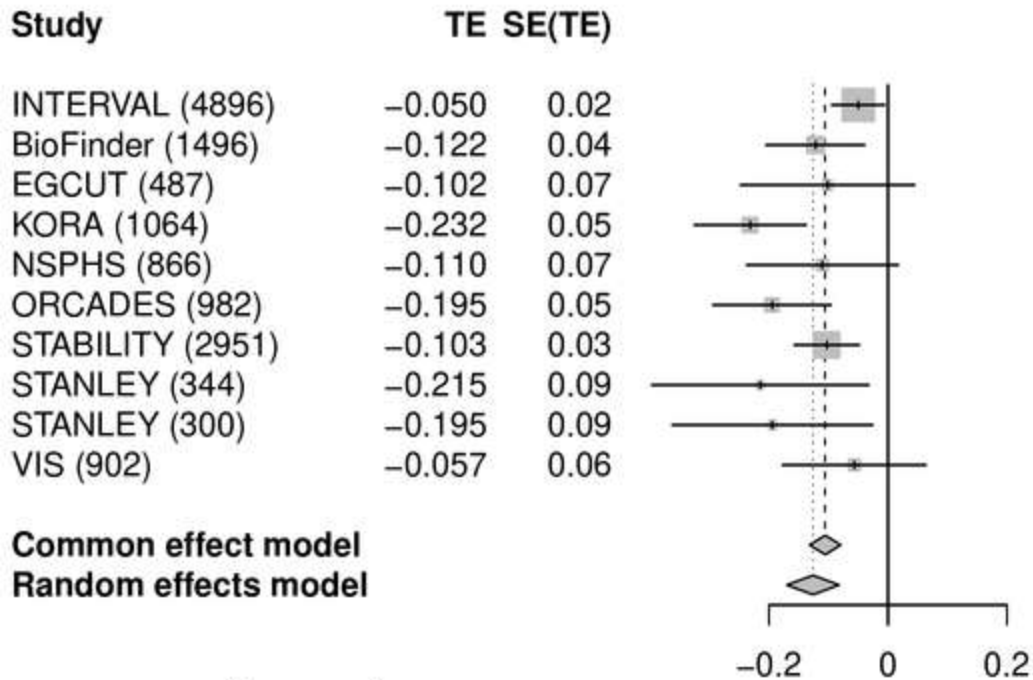
100.0%

CXCL5 (CXCL5)-rs7090111





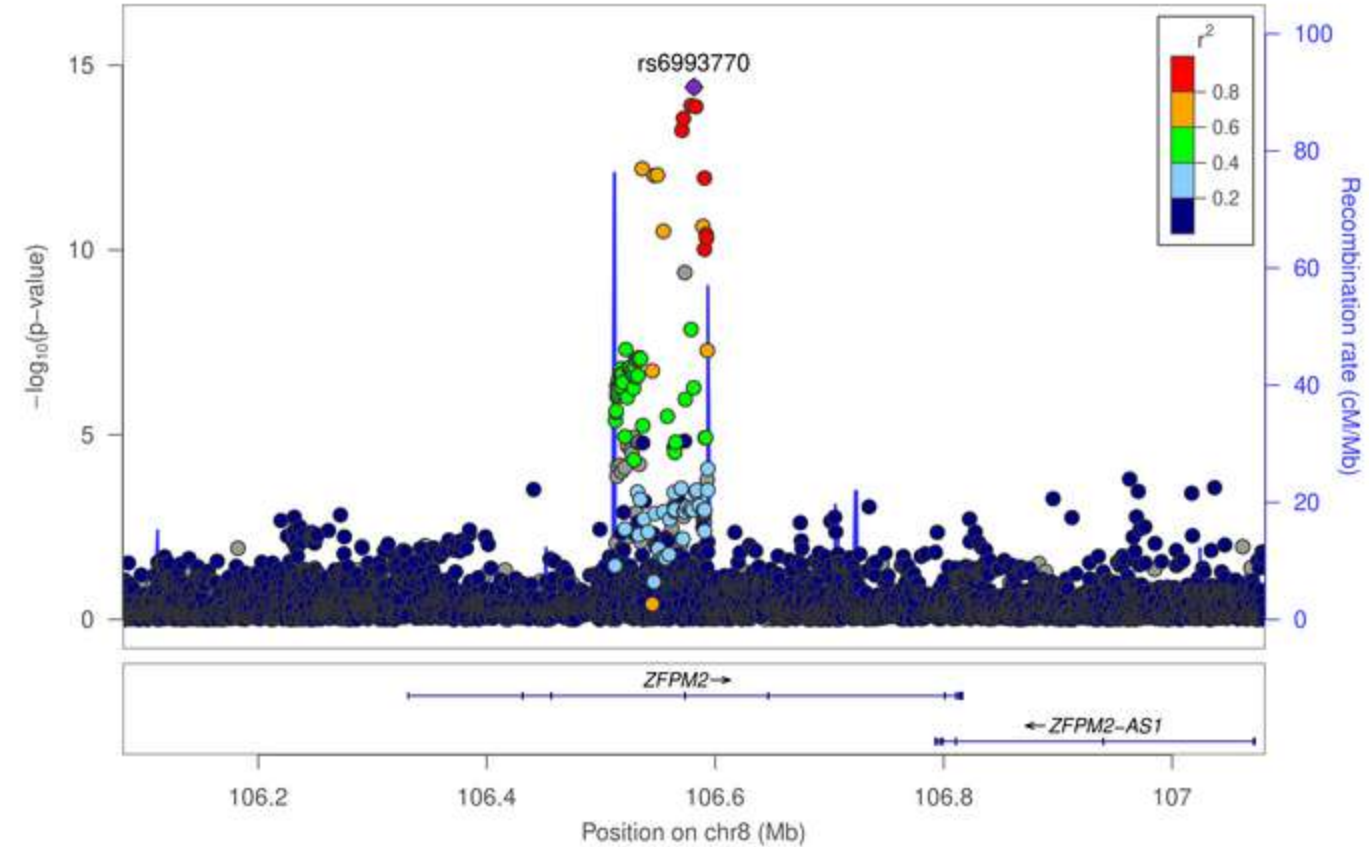
CXCL5 (CXCL5) [chr8:106581528_A_T (rs6993770) (A/T) N=14288]



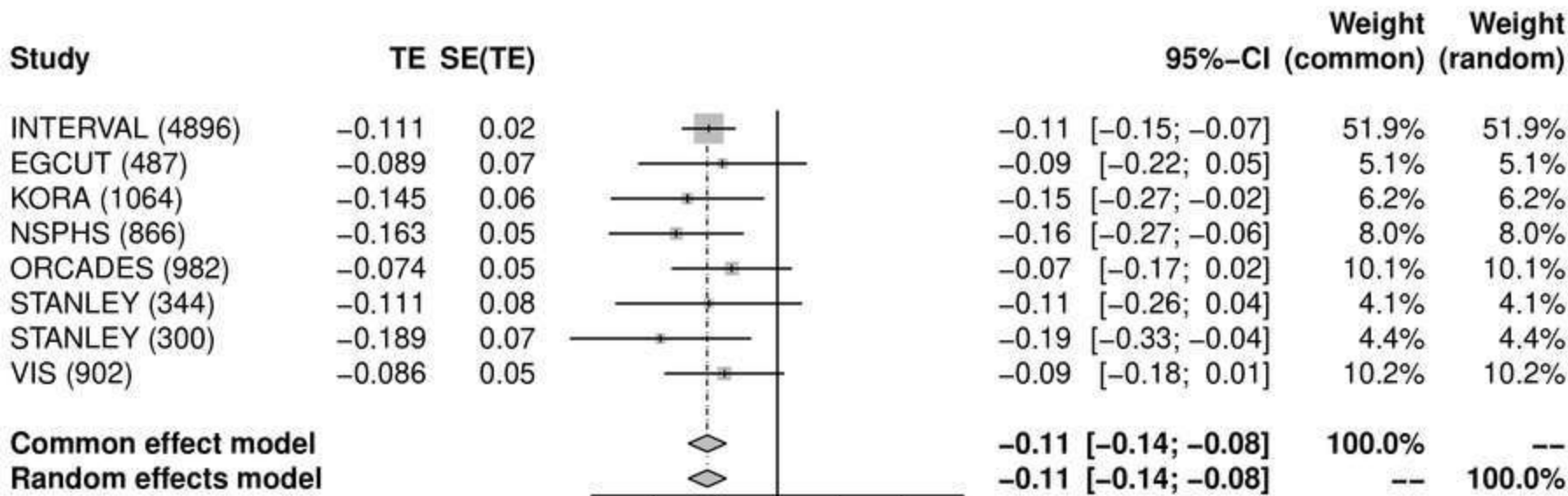
Heterogeneity: $I^2 = 53\%$, $\tau^2 = 0.0023$, $p = 0.02$

		Weight	Weight
	95%-CI	(common)	(random)
-0.05	[-0.09; -0.01]	35.0%	17.8%
-0.12	[-0.21; -0.04]	10.1%	12.3%
-0.10	[-0.25; 0.05]	3.2%	6.4%
-0.23	[-0.33; -0.14]	7.9%	11.0%
-0.11	[-0.24; 0.02]	4.3%	7.7%
-0.20	[-0.29; -0.10]	7.0%	10.4%
-0.10	[-0.16; -0.05]	23.2%	16.3%
-0.21	[-0.40; -0.03]	2.1%	4.6%
-0.19	[-0.36; -0.03]	2.4%	5.2%
-0.06	[-0.18; 0.06]	4.8%	8.3%
-0.11	[-0.13; -0.08]	100.0%	--
-0.13	[-0.17; -0.08]	--	100.0%

CXCL5 (CXCL5)-rs6993770

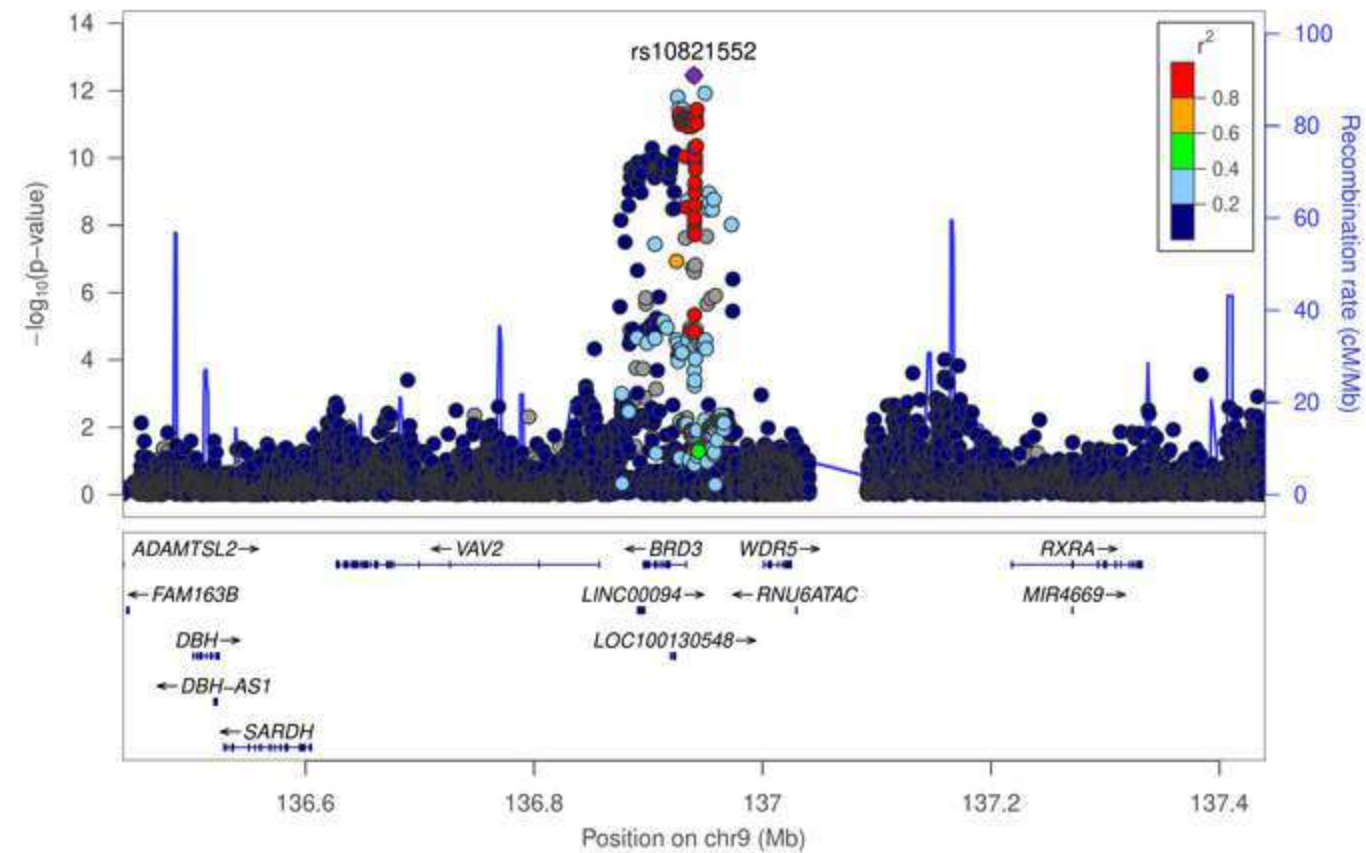


CXCL5 (CXCL5) [chr9:136939992_A_C (rs10821552) (A/C) N=9841]



Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.86$

CXCL5 (CXCL5)-rs10821552



Study

CXCL6 (CXCL6) [chr1:159175354_A_G (rs12075) (A/G) N=14741]

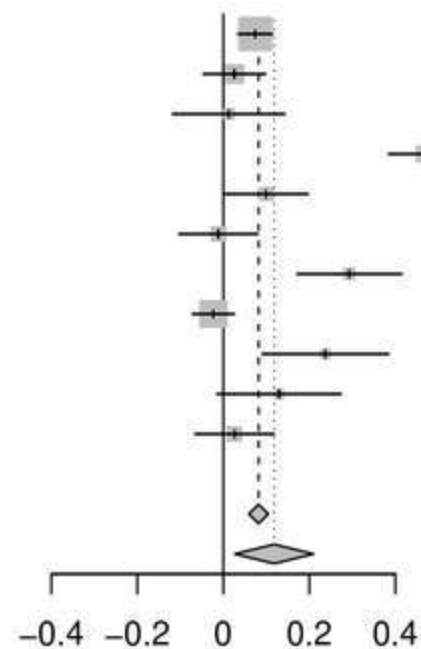
TE SE(TE)

Weight
95%-CI (common) Weight
(random)

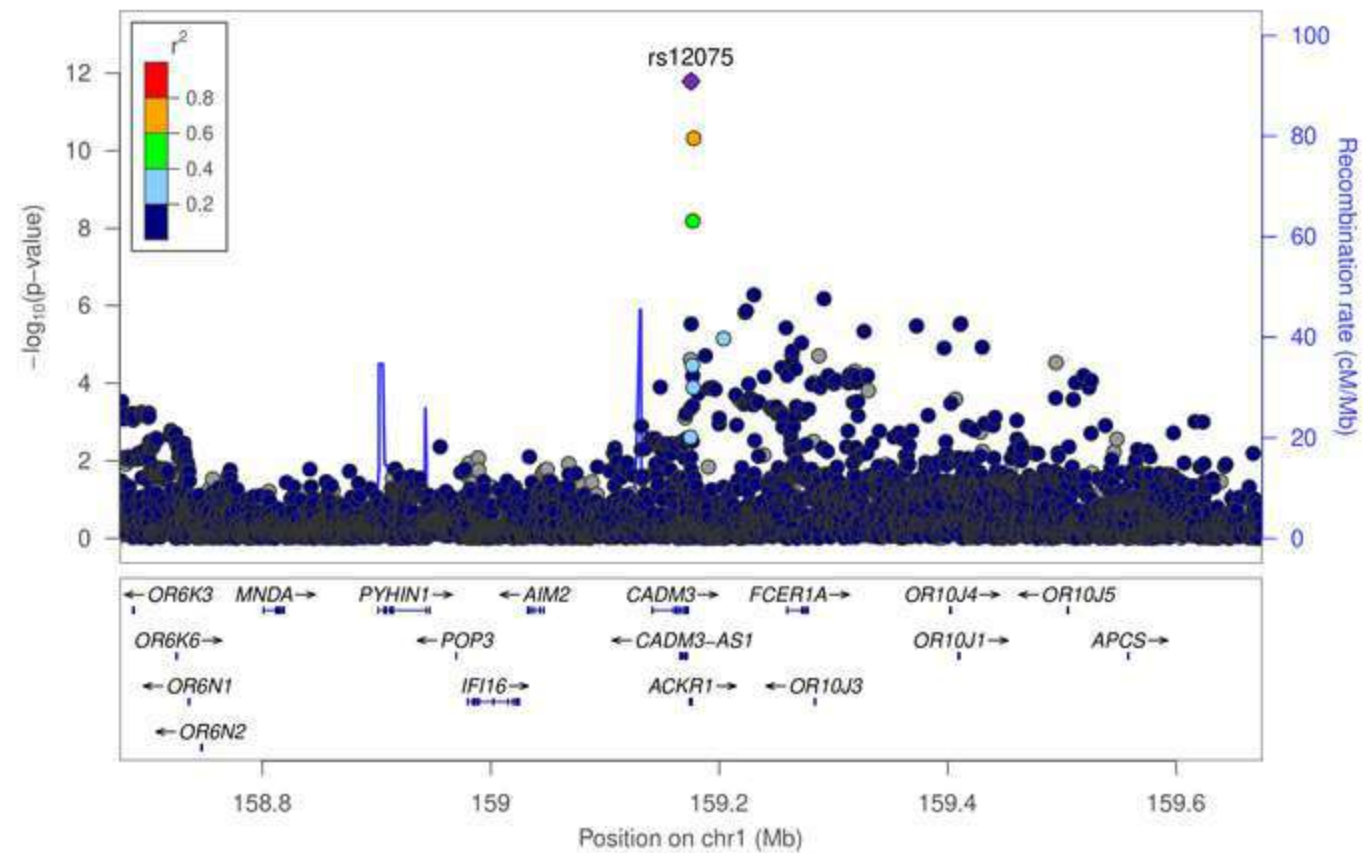
INTERVAL (4896)	0.074	0.02		0.07	[0.03; 0.11]	32.0%	10.0%
BioFinder (1496)	0.025	0.04		0.03	[-0.05; 0.10]	9.8%	9.6%
EGCUT (487)	0.012	0.07		0.01	[-0.12; 0.14]	3.0%	8.5%
KORA (1064)	0.467	0.04		0.47	[0.38; 0.55]	7.5%	9.4%
NSPHS (874)	0.099	0.05		0.10	[0.00; 0.20]	5.4%	9.1%
ORCADES (982)	-0.012	0.05		-0.01	[-0.10; 0.08]	6.1%	9.3%
RECOMBINE (445)	0.293	0.06		0.29	[0.17; 0.41]	3.5%	8.7%
STABILITY (2951)	-0.023	0.02		-0.02	[-0.07; 0.03]	21.7%	9.9%
STANLEY (344)	0.237	0.07		0.24	[0.09; 0.38]	2.4%	8.1%
STANLEY (300)	0.129	0.07		0.13	[-0.02; 0.27]	2.5%	8.2%
VIS (902)	0.026	0.05		0.03	[-0.07; 0.12]	6.1%	9.3%

Common effect model

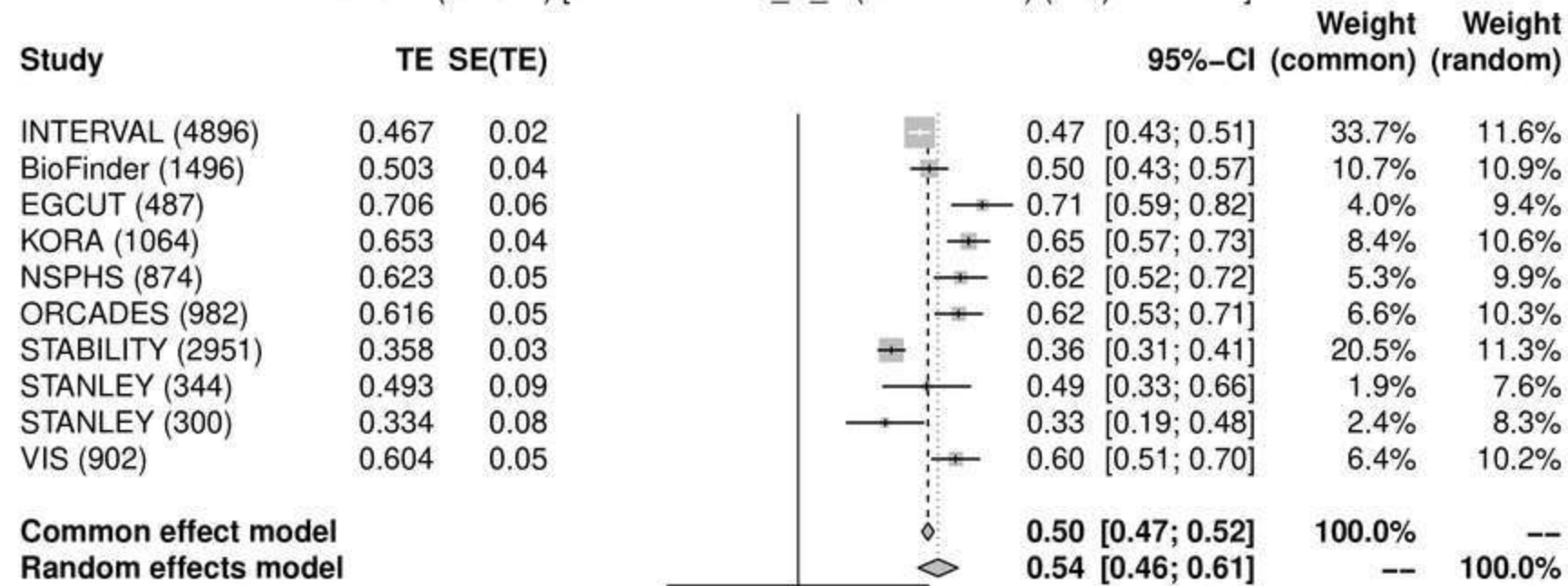
Random effects model

Heterogeneity: $I^2 = 92\%$, $\tau^2 = 0.0216$, $p < 0.01$ 

CXCL6 (CXCL6)-rs12075

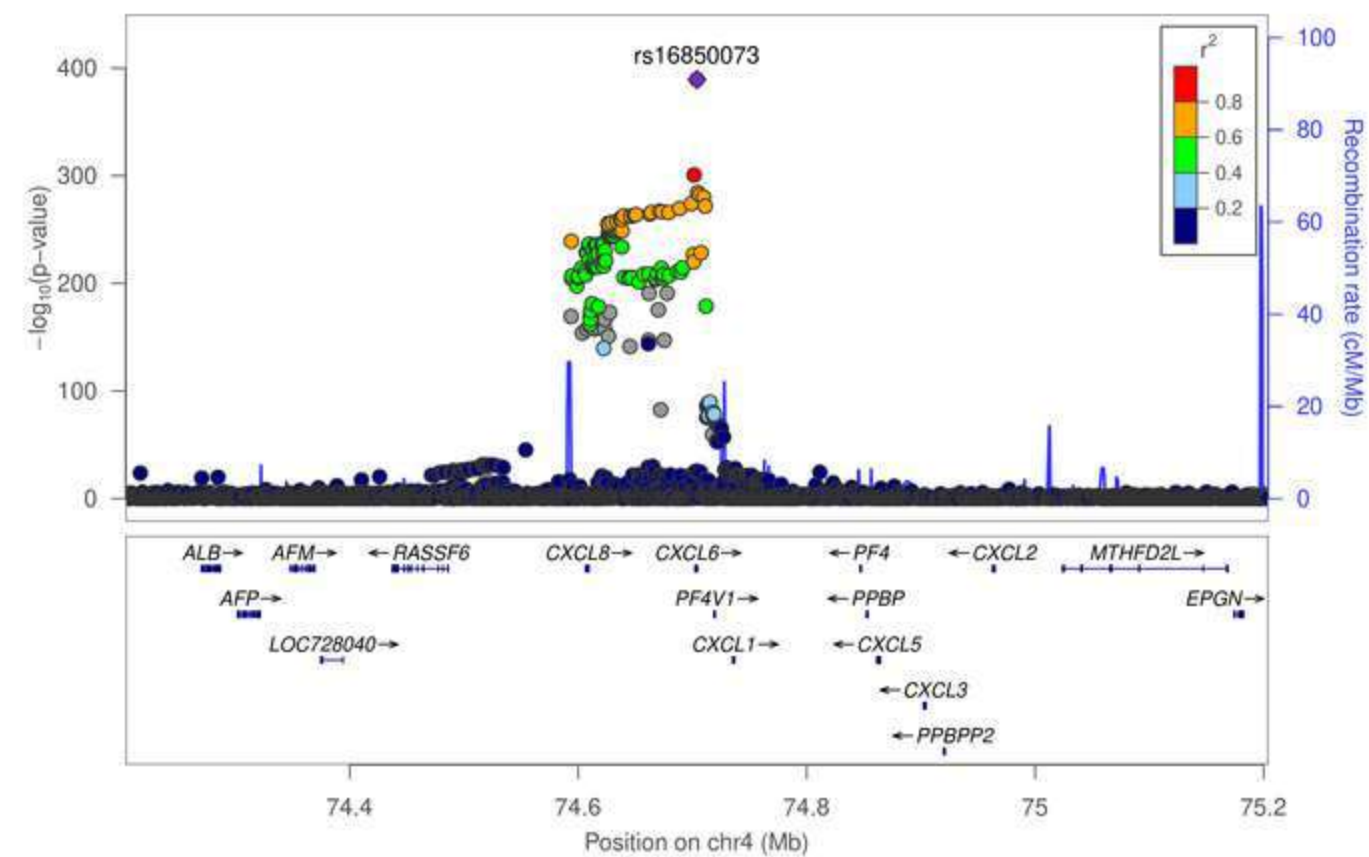


CXCL6 (CXCL6) [chr4:74703999_C_T (rs16850073) (T/C) N=14296]



Heterogeneity: $I^2 = 89\%$, $\tau^2 = 0.0128$, $p < 0.01$

CXCL6 (CXCL6)-rs16850073



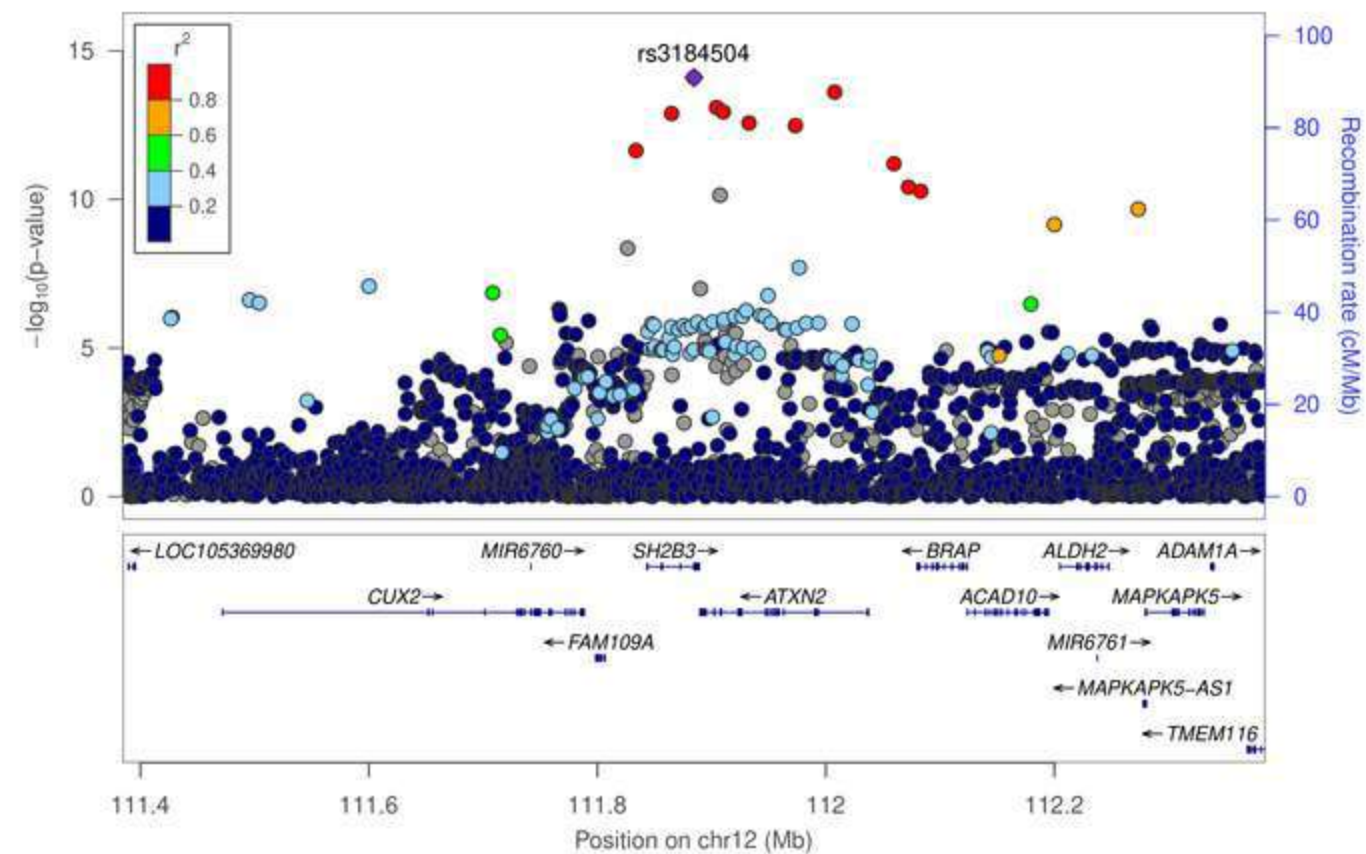
CXCL9 (CXCL9) [chr12:111884608_C_T (rs3184504) (T/C) N=11784]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.098	0.02	0.10 [0.06; 0.14]	40.9%
BioFinder (1496)	0.100	0.04	0.10 [0.03; 0.17]	12.4%
EGCUT (487)	0.134	0.06	0.13 [0.01; 0.26]	4.0%
KORA (1064)	0.073	0.04	0.07 [-0.01; 0.15]	10.5%
NSPHS (866)	0.090	0.05	0.09 [0.00; 0.18]	8.2%
ORCADES (982)	0.041	0.05	0.04 [-0.05; 0.13]	8.0%
RECOMBINE (448)	0.236	0.08	0.24 [0.08; 0.40]	2.5%
STANLEY (344)	0.036	0.07	0.04 [-0.10; 0.17]	3.5%
STANLEY (300)	0.040	0.08	0.04 [-0.12; 0.20]	2.4%
VIS (901)	0.217	0.05	0.22 [0.12; 0.31]	7.5%
Common effect model			0.10 [0.08; 0.13]	100.0%
Random effects model			0.10 [0.08; 0.13]	-- 100.0%



Heterogeneity: $I^2 = 29\%$, $\tau^2 < 0.0001$, $p = 0.18$

CXCL9 (CXCL9)-rs3184504



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (437)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0.0002$, $p = 0.44$

CXCL9 (CXCL9) [chr4:76930776_A_C (rs4241577) (A/C) N=14724]

TE SE(TE)

-0.169 0.02

-0.123 0.04

-0.197 0.07

-0.140 0.05

-0.121 0.05

-0.158 0.06

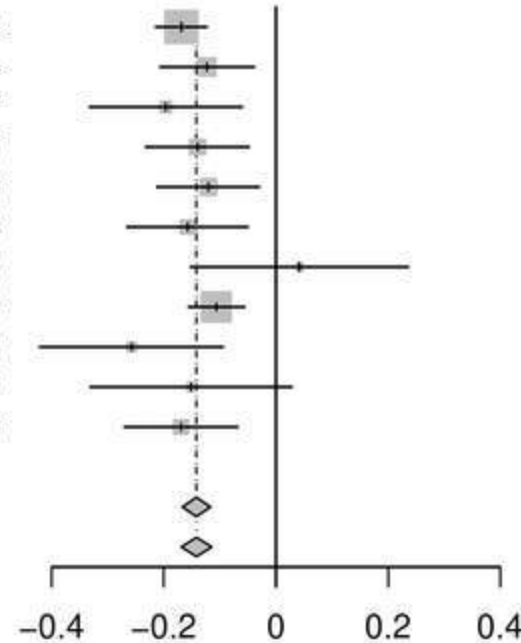
0.042 0.10

-0.106 0.03

-0.258 0.08

-0.151 0.09

-0.169 0.05



95%-CI (common) (random)

-0.17 [-0.21; -0.12]

-0.12 [-0.21; -0.04]

-0.20 [-0.33; -0.06]

-0.14 [-0.23; -0.05]

-0.12 [-0.21; -0.03]

-0.16 [-0.27; -0.05]

0.04 [-0.15; 0.24]

-0.11 [-0.16; -0.06]

-0.26 [-0.42; -0.09]

-0.15 [-0.33; 0.03]

-0.17 [-0.27; -0.07]

-0.14 [-0.17; -0.12]

-0.14 [-0.17; -0.11]

Weight

30.0%

8.9%

3.4%

7.4%

7.5%

5.4%

1.7%

25.1%

2.4%

2.0%

6.2%

100.0%

--

Weight

27.0%

9.6%

3.9%

8.1%

8.2%

6.0%

1.9%

23.4%

2.7%

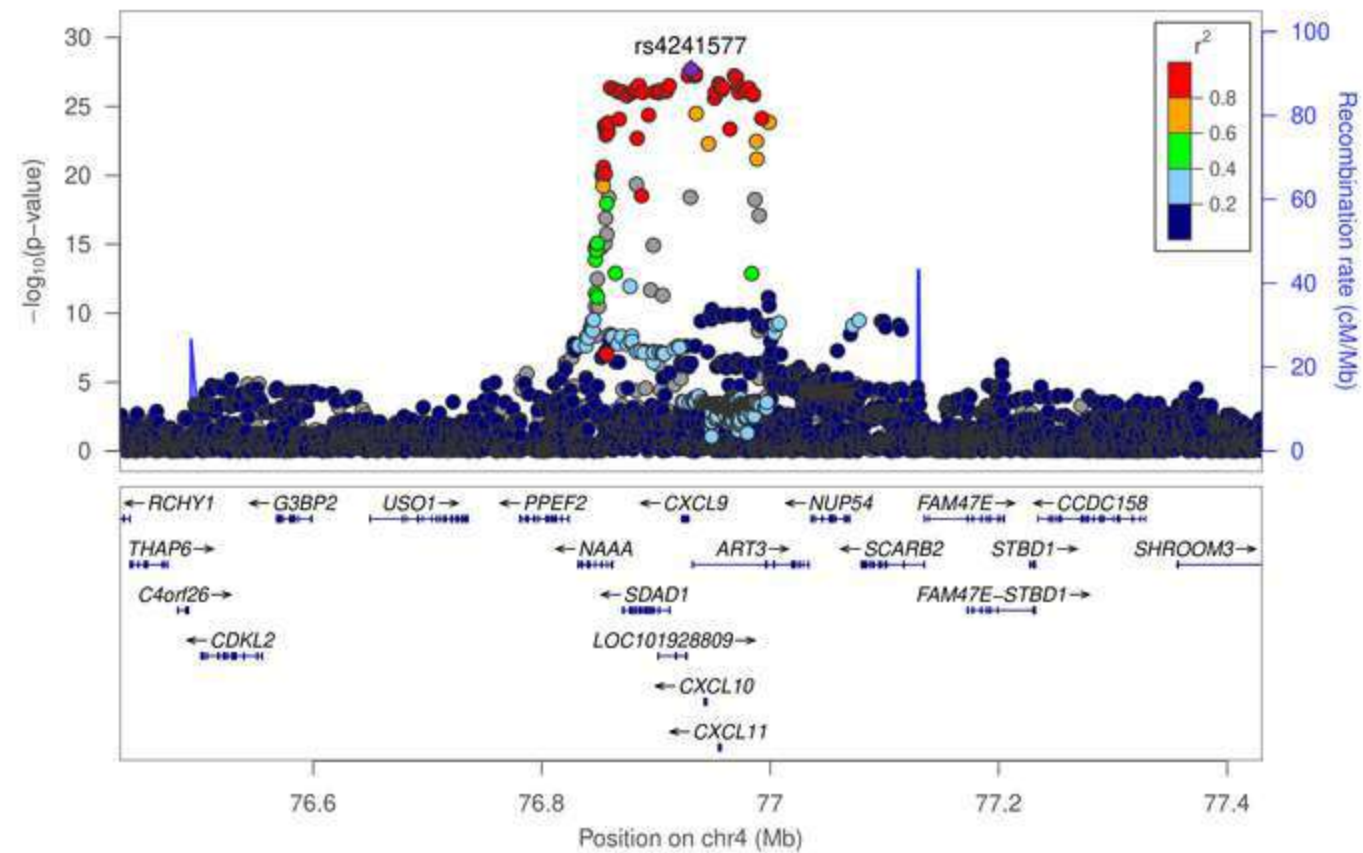
2.3%

6.8%

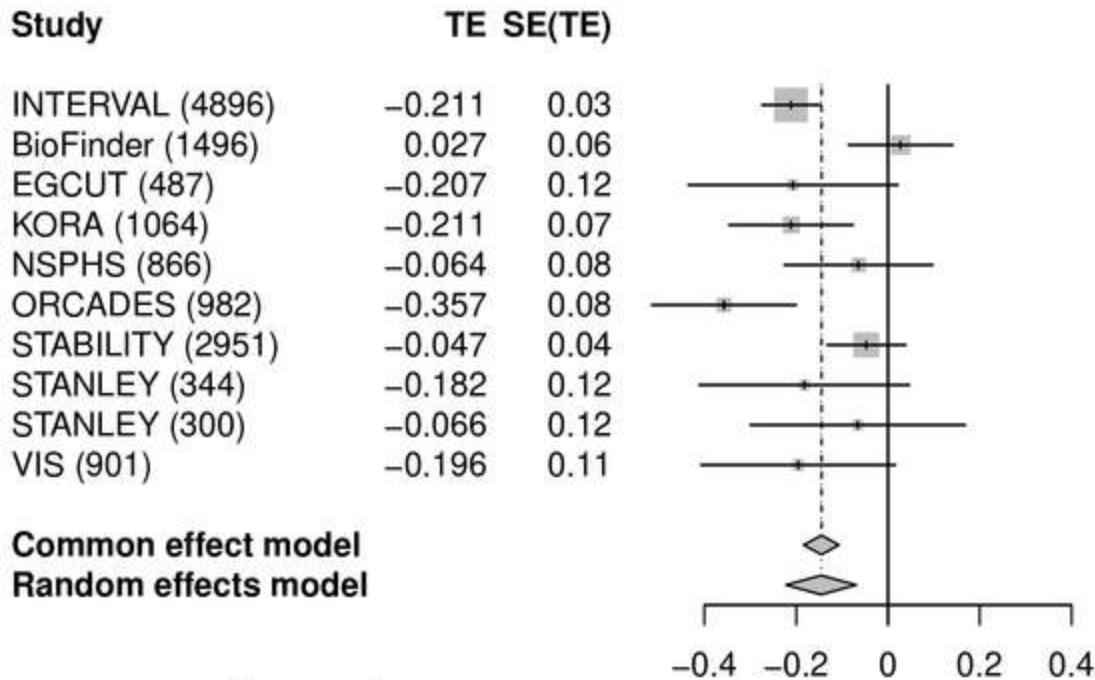
--

100.0%

CXCL9 (CXCL9)-rs4241577



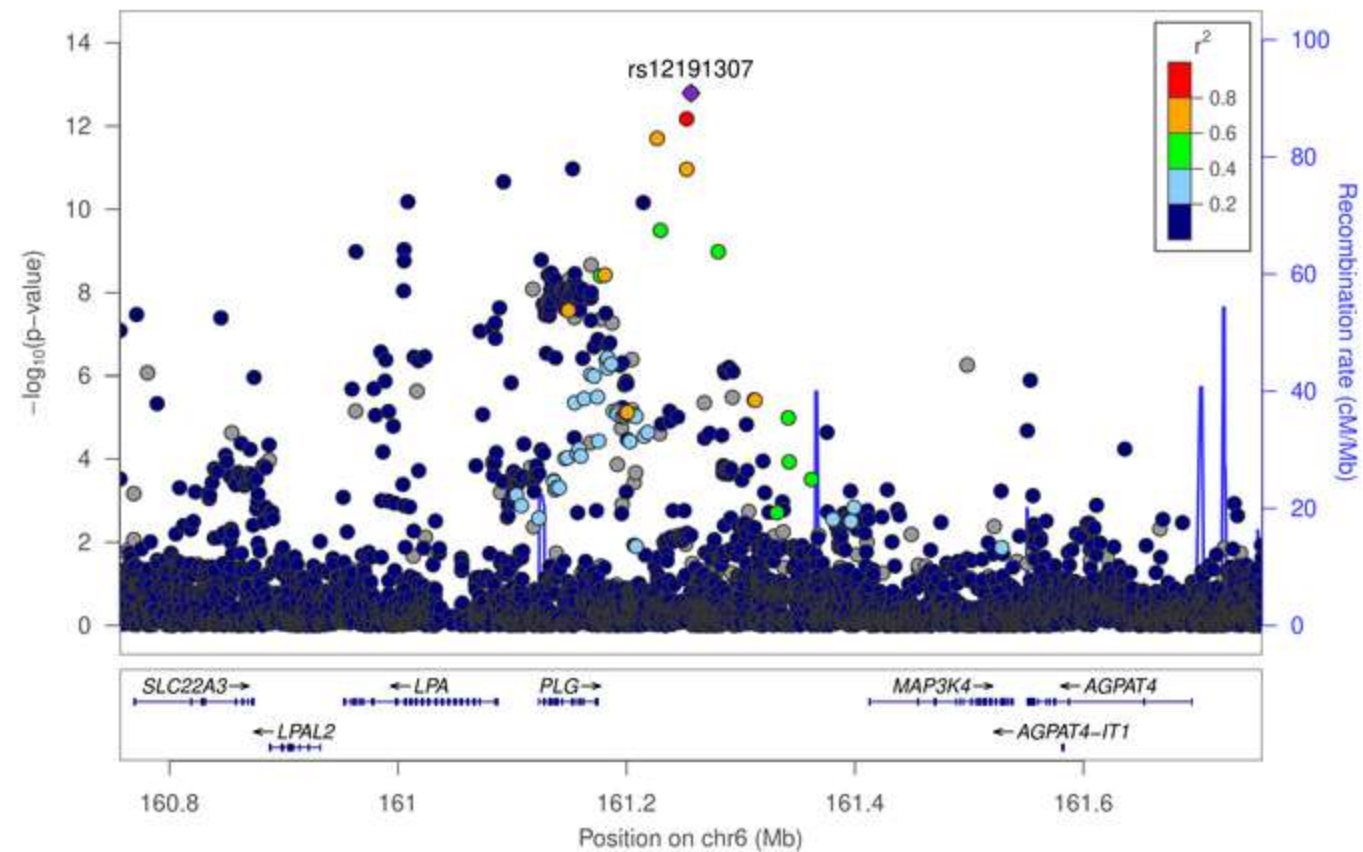
CXCL9 (CXCL9) [chr6:161256529_A_G (rs12191307) (A/G) N=14287]



Heterogeneity: $I^2 = 68\%$, $\tau^2 = 0.0091$, $p < 0.01$

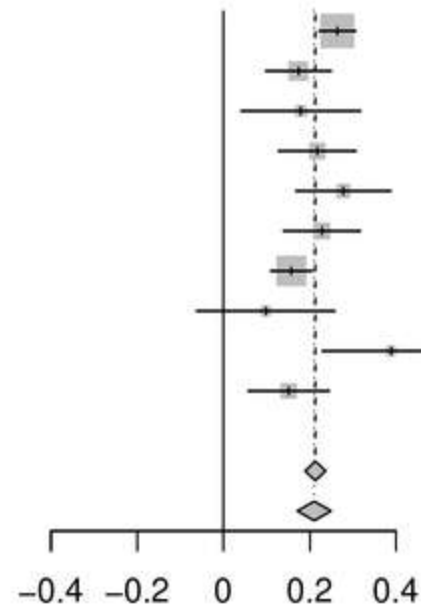
		Weight	Weight
	95%-CI	(common)	(random)
-0.21	[-0.27; -0.15]	36.6%	15.2%
0.03	[-0.09; 0.14]	11.6%	12.4%
-0.21	[-0.44; 0.02]	2.8%	6.8%
-0.21	[-0.35; -0.08]	8.1%	11.1%
-0.06	[-0.23; 0.10]	5.7%	9.7%
-0.36	[-0.51; -0.20]	6.0%	9.9%
-0.05	[-0.13; 0.04]	20.3%	14.0%
-0.18	[-0.41; 0.05]	2.8%	6.8%
-0.07	[-0.30; 0.17]	2.7%	6.6%
-0.20	[-0.41; 0.02]	3.3%	7.4%
-0.15	[-0.18; -0.11]	100.0%	--
-0.15	[-0.22; -0.07]	--	100.0%

CXCL9 (CXCL9)-rs12191307



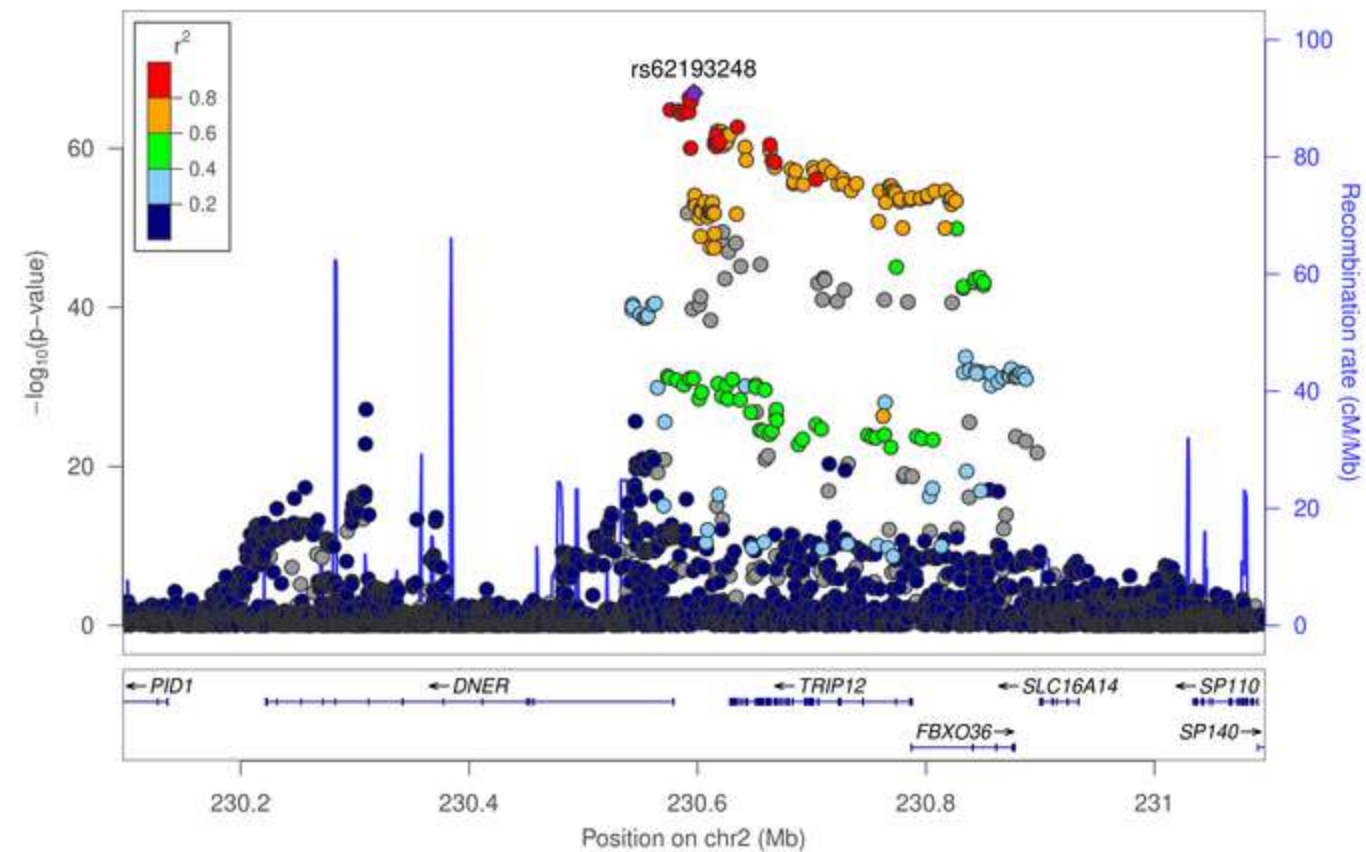
DNER (DNER) [chr2:230596917_A_T (rs62193248) (A/T) N=14287]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.264	0.02	0.26 [0.22; 0.31]	32.2%	17.5%
BioFinder (1496)	0.174	0.04	0.17 [0.10; 0.25]	10.0%	12.1%
EGCUT (487)	0.179	0.07	0.18 [0.04; 0.32]	3.0%	5.9%
KORA (1064)	0.217	0.05	0.22 [0.13; 0.31]	7.1%	10.2%
NSPHS (866)	0.278	0.06	0.28 [0.17; 0.39]	4.8%	8.1%
ORCADES (982)	0.228	0.05	0.23 [0.14; 0.32]	7.3%	10.3%
STABILITY (2951)	0.158	0.02	0.16 [0.11; 0.21]	24.6%	16.5%
STANLEY (344)	0.098	0.08	0.10 [-0.06; 0.26]	2.3%	4.7%
STANLEY (300)	0.389	0.08	0.39 [0.23; 0.55]	2.3%	4.8%
VIS (901)	0.151	0.05	0.15 [0.06; 0.25]	6.5%	9.7%
Common effect model			0.21 [0.19; 0.24]	100.0%	--
Random effects model			0.21 [0.17; 0.25]	--	100.0%

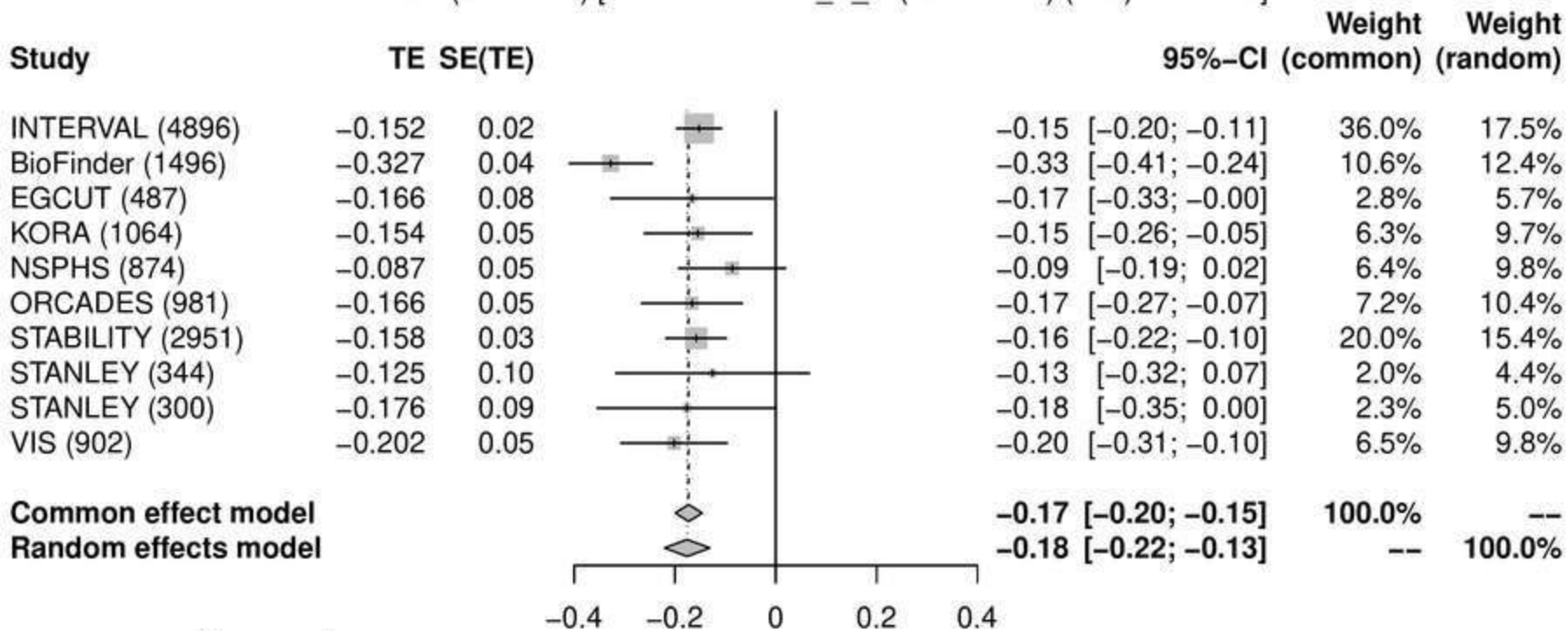


Heterogeneity: $I^2 = 58\%$, $\tau^2 = 0.0018$, $p = 0.01$

DNER (DNER)-rs62193248

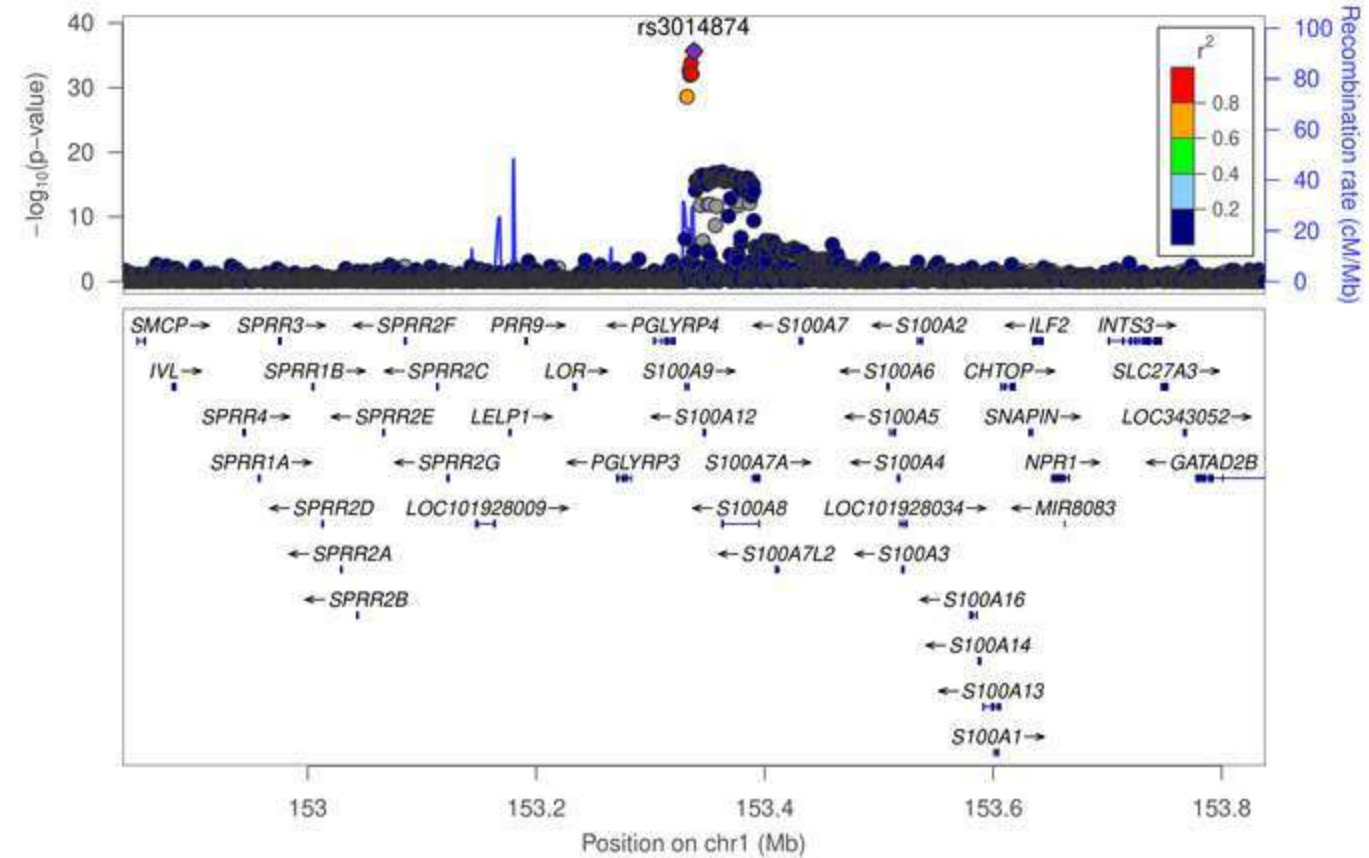


EN-RAGE (S100A12) [chr1:153337943_A_G (rs3014874) (A/G) N=14295]



Heterogeneity: $I^2 = 49\%$, $\tau^2 = 0.0025$, $p = 0.04$

EN-RAGE (S100A12)-rs3014874



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (874)

ORCADES (982)

RECOMBINE (448)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.83$

FGF-19 (FGF19) [chr19:49206172_C_T (rs516246) (T/C) N=14744]

TE SE(TE)

-0.173 0.02

-0.161 0.04

-0.142 0.07

-0.176 0.04

-0.104 0.05

-0.202 0.04

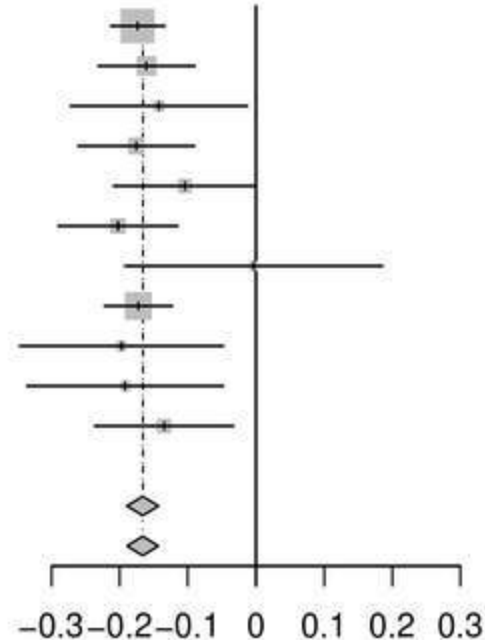
-0.003 0.10

-0.173 0.03

-0.197 0.08

-0.192 0.07

-0.135 0.05

Weight
95%-CI (common) (random)

-0.17 [-0.21; -0.13] 33.9% 33.9%

-0.16 [-0.23; -0.09] 10.6% 10.6%

-0.14 [-0.27; -0.01] 3.2% 3.2%

-0.18 [-0.26; -0.09] 7.3% 7.3%

-0.10 [-0.21; 0.00] 4.9% 4.9%

-0.20 [-0.29; -0.11] 7.0% 7.0%

-0.00 [-0.19; 0.19] 1.5% 1.5%

-0.17 [-0.22; -0.12] 21.5% 21.5%

-0.20 [-0.35; -0.05] 2.4% 2.4%

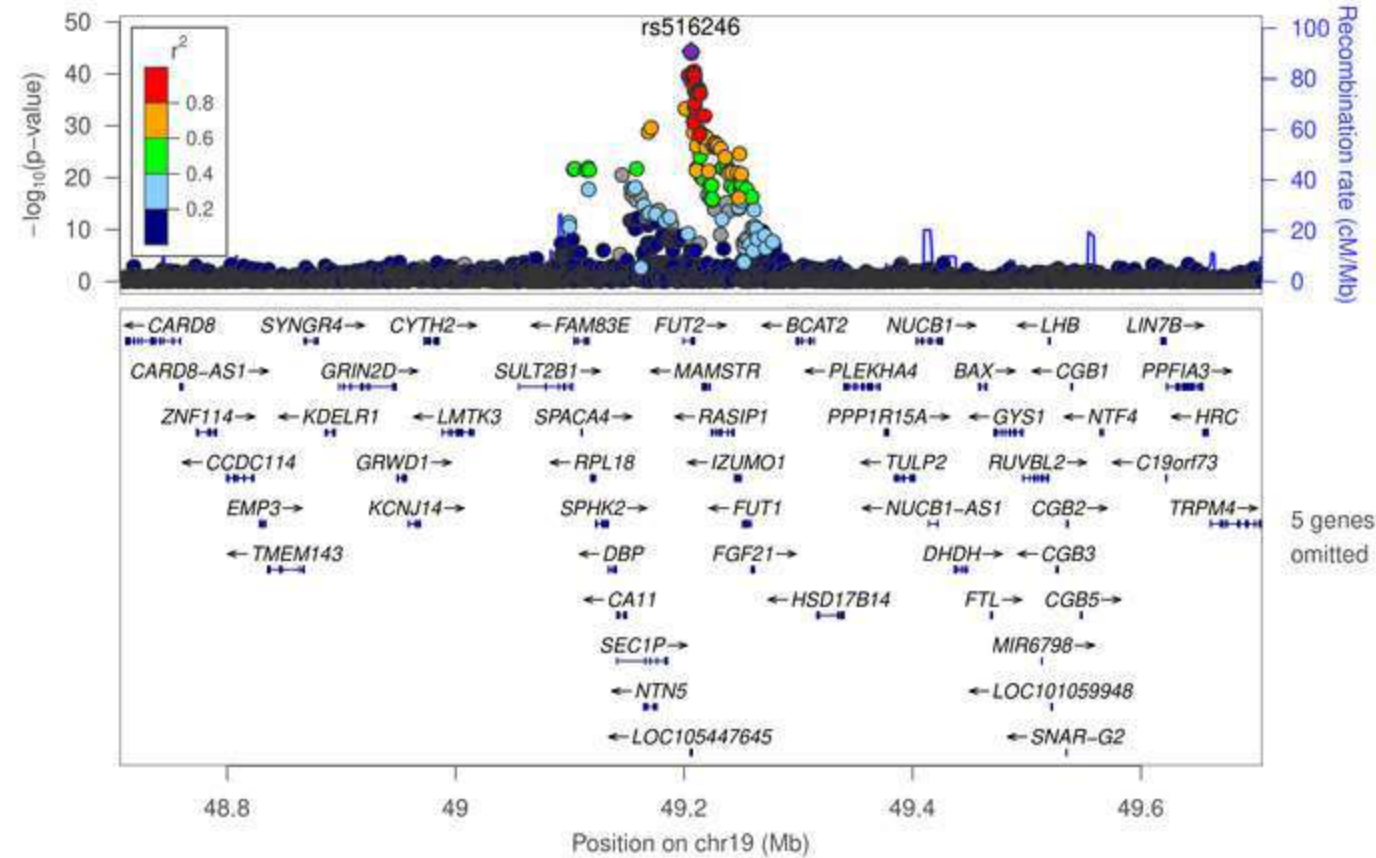
-0.19 [-0.34; -0.05] 2.6% 2.6%

-0.13 [-0.24; -0.03] 5.2% 5.2%

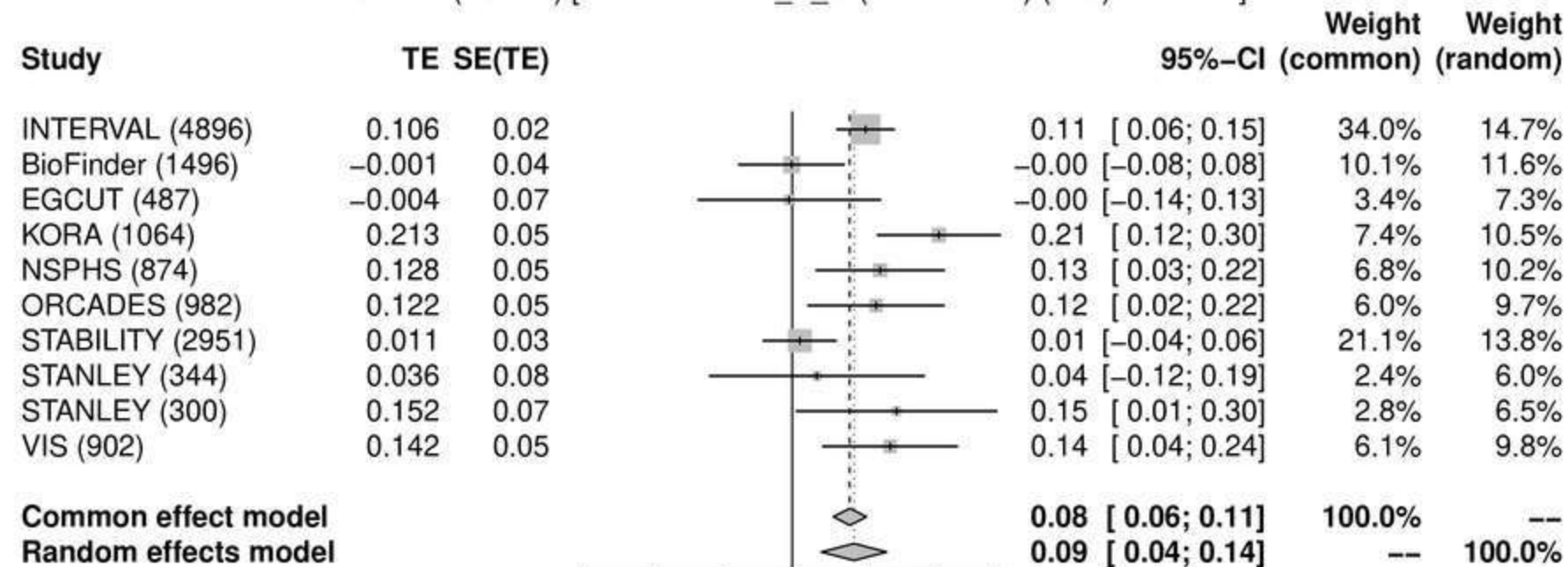
-0.17 [-0.19; -0.14] 100.0% --

-0.17 [-0.19; -0.14] -- 100.0%

FGF-19 (FGF19)-rs516246

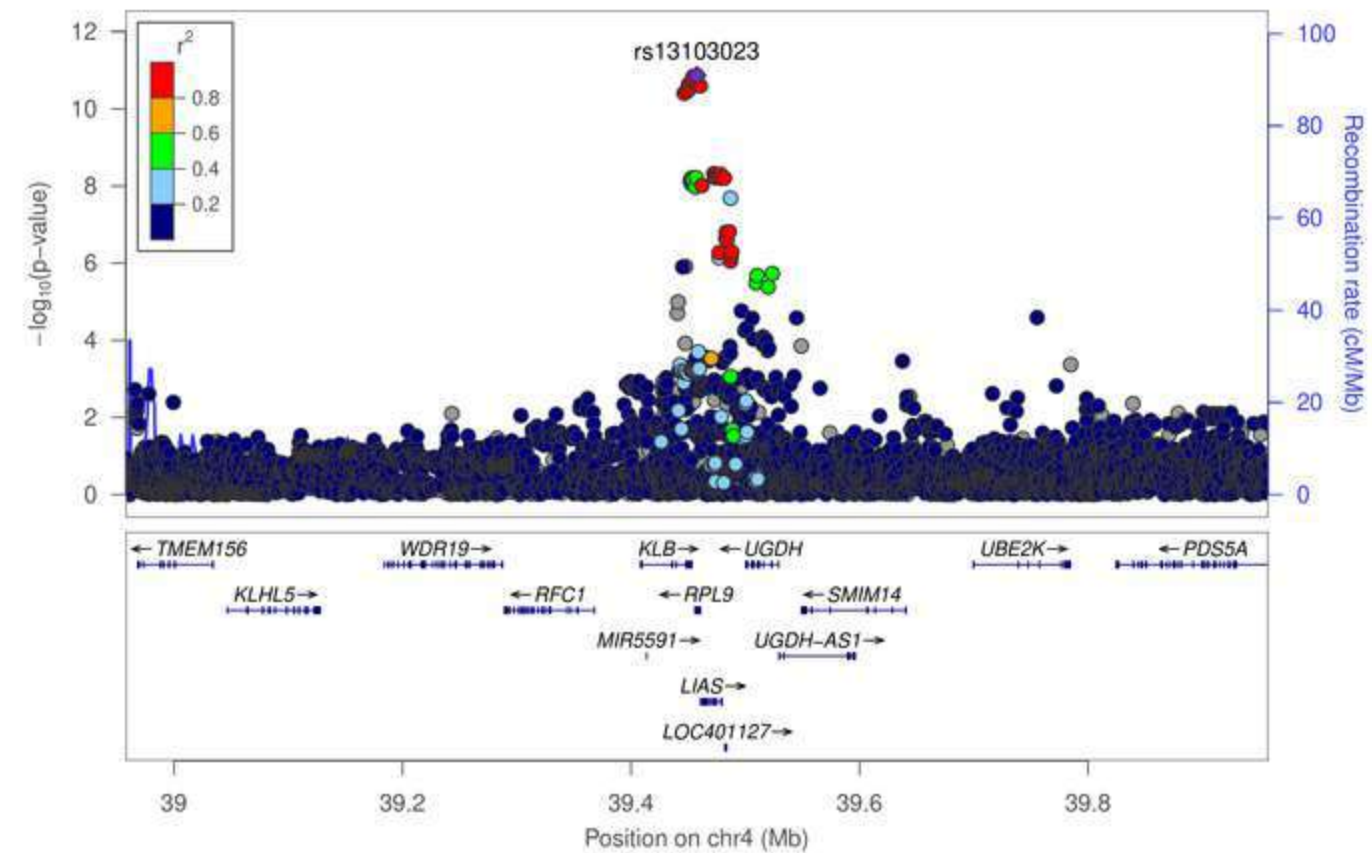


FGF-19 (FGF19) [chr4:39457617_A_G (rs13103023) (A/G) N=14296]



Heterogeneity: $I^2 = 67\%$, $\tau^2 = 0.0036$, $p < 0.01$

FGF-19 (FGF19)-rs13103023



Study

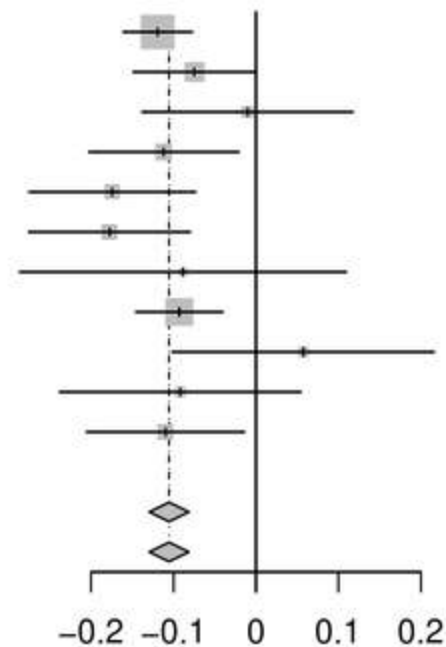
Study	TE	SE(TE)
INTERVAL (4896)	-0.119	0.02
BioFinder (1496)	-0.075	0.04
EGCUT (487)	-0.010	0.07
KORA (1064)	-0.112	0.05
NSPHS (874)	-0.174	0.05
ORCADES (982)	-0.178	0.05
RECOMBINE (448)	-0.089	0.10
STABILITY (2951)	-0.093	0.03
STANLEY (344)	0.057	0.08
STANLEY (300)	-0.092	0.07
VIS (902)	-0.110	0.05

Common effect model
Random effects model

Heterogeneity: $I^2 = 12\%$, $\tau^2 < 0.0001$, $p = 0.33$

FGF-19 (FGF19) [chr8:59382715_A_G (rs7005978) (A/G) N=14744]

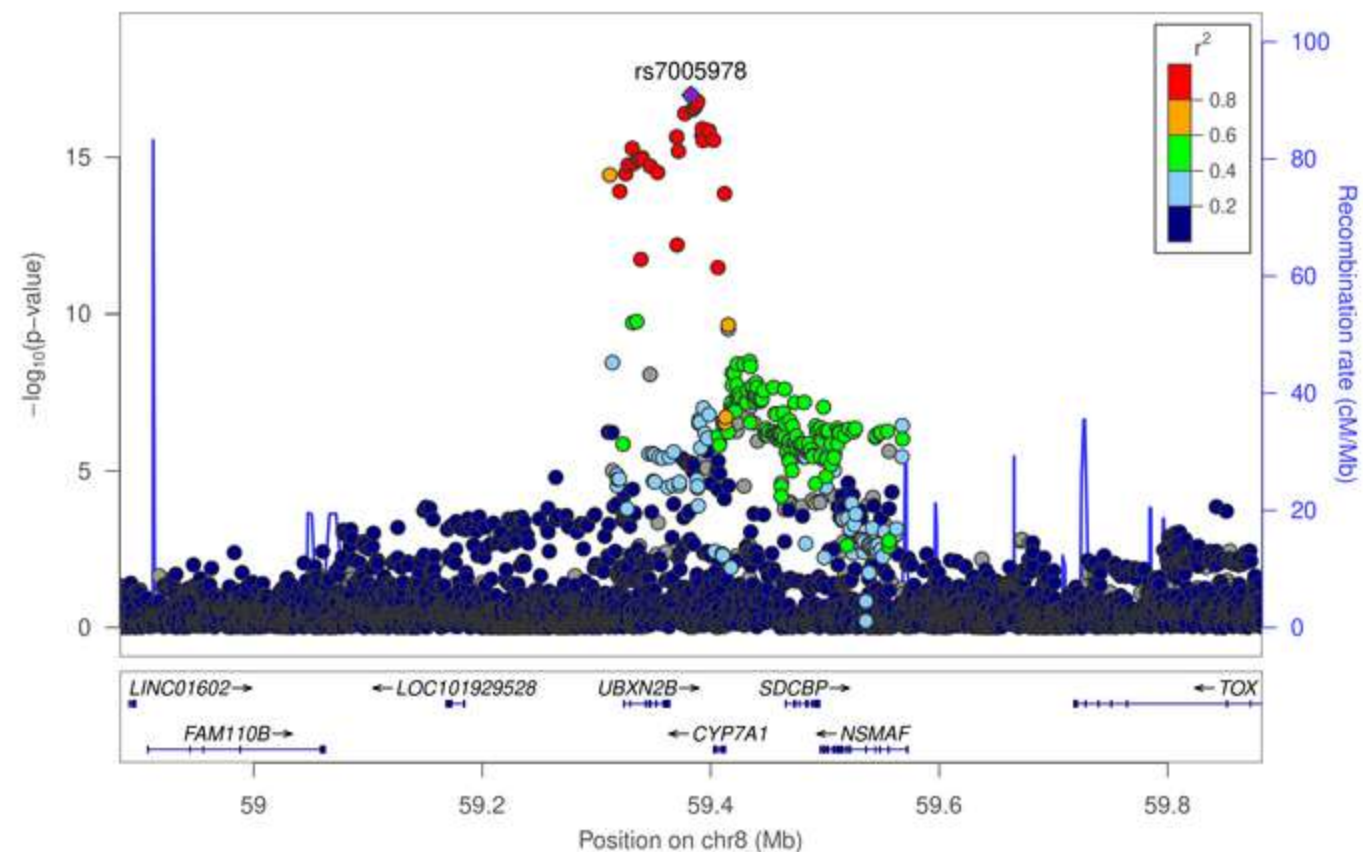
TE SE(TE)



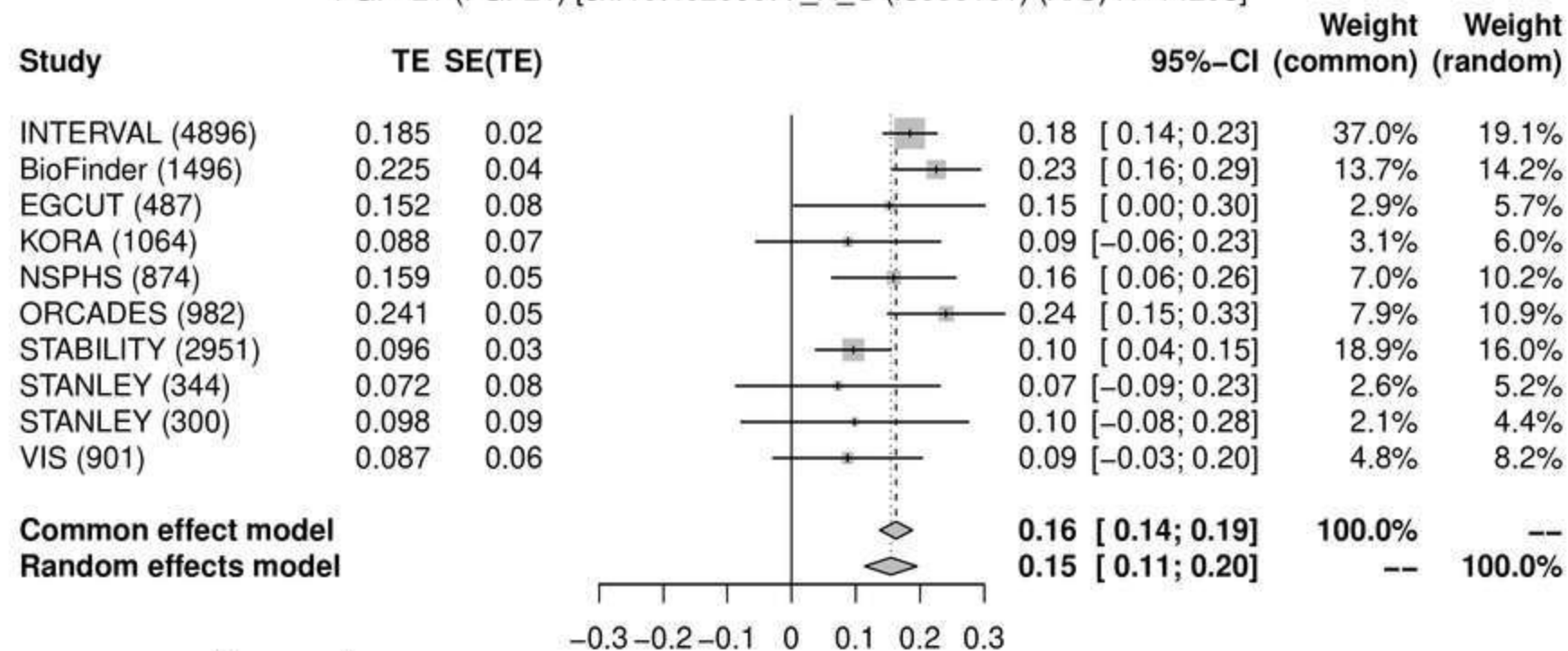
Weight 95%-CI (common) Weight 95%-CI (random)

-0.12	[-0.16; -0.08]	33.3%	33.2%
-0.07	[-0.15; -0.00]	10.5%	10.5%
-0.01	[-0.14; 0.12]	3.6%	3.6%
-0.11	[-0.20; -0.02]	7.0%	7.0%
-0.17	[-0.28; -0.07]	5.7%	5.7%
-0.18	[-0.28; -0.08]	6.1%	6.1%
-0.09	[-0.29; 0.11]	1.5%	1.5%
-0.09	[-0.15; -0.04]	21.0%	20.9%
0.06	[-0.10; 0.22]	2.3%	2.3%
-0.09	[-0.24; 0.05]	2.7%	2.7%
-0.11	[-0.21; -0.01]	6.4%	6.4%
-0.11	[-0.13; -0.08]	100.0%	--
-0.11	[-0.13; -0.08]	--	100.0%

FGF-19 (FGF19)-rs7005978

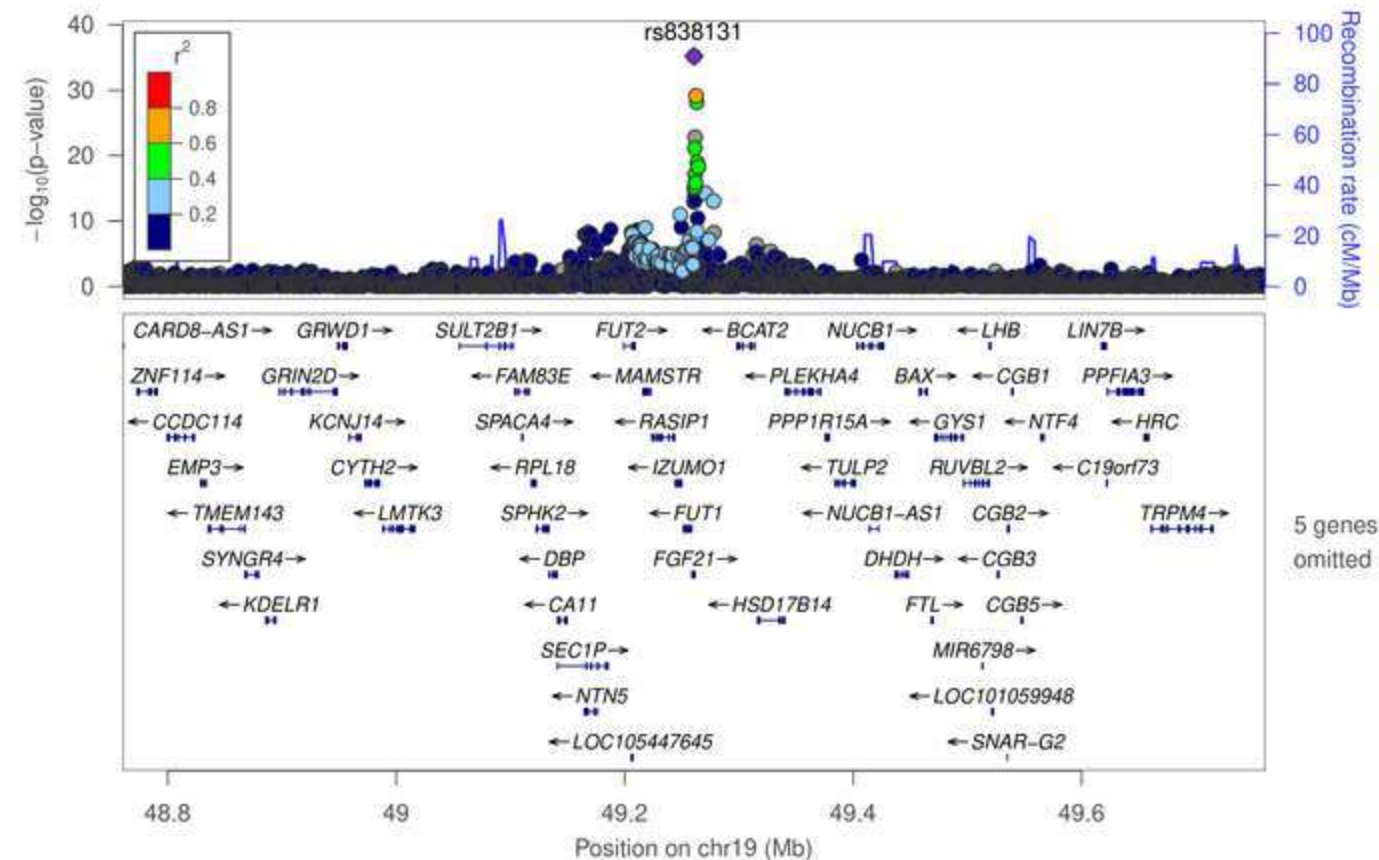


FGF-21 (FGF21) [chr19:49260677_A_C (rs838131) (A/C) N=14295]

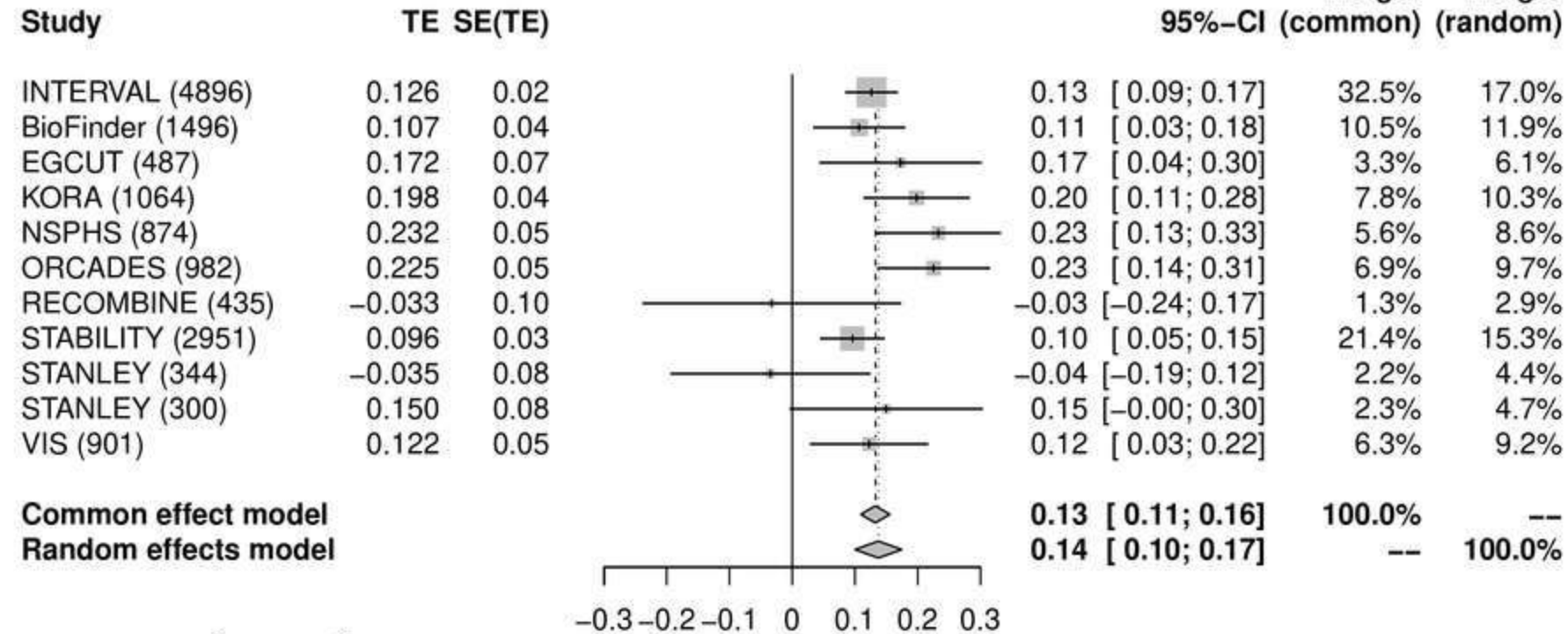


Heterogeneity: $I^2 = 45\%$, $\tau^2 = 0.0018$, $p = 0.06$

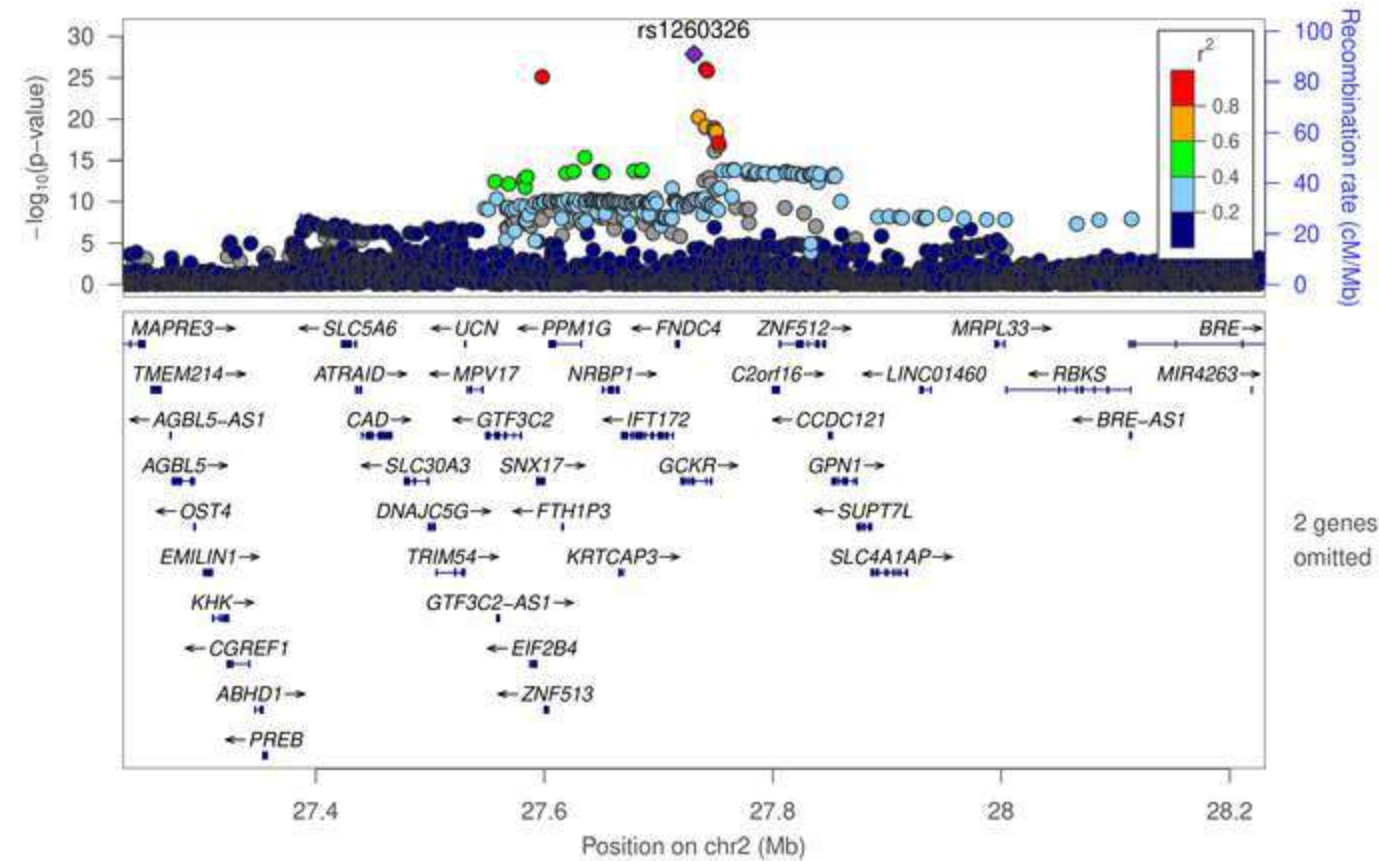
FGF-21 (FGF21)-rs838131



FGF-21 (FGF21) [chr2:27730940_C_T (rs1260326) (T/C) N=14730]



FGF-21 (FGF21)-rs1260326



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (874)

ORCADES (982)

RECOMBINE (448)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 0\%$, $\tau^2 < 0.0001$, $p = 0.65$

FGF-21 (FGF21) [chr7:73030175_A_G (rs13229619) (A/G) N=14743]

TE SE(TE)

-0.152 0.03

-0.192 0.05

-0.111 0.09

-0.181 0.07

-0.204 0.07

-0.192 0.06

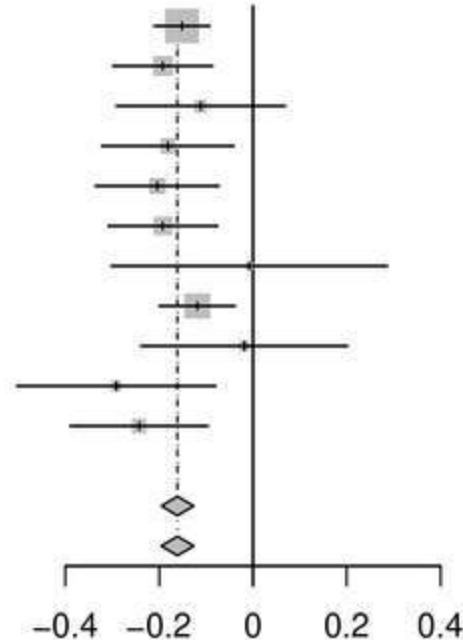
-0.008 0.15

-0.119 0.04

-0.019 0.11

-0.291 0.11

-0.243 0.08



95%-CI (common)

-0.15 [-0.21; -0.09]

-0.19 [-0.30; -0.09]

-0.11 [-0.29; 0.07]

-0.18 [-0.32; -0.04]

-0.20 [-0.34; -0.07]

-0.19 [-0.31; -0.08]

-0.01 [-0.30; 0.29]

-0.12 [-0.20; -0.04]

-0.02 [-0.24; 0.20]

-0.29 [-0.50; -0.08]

-0.24 [-0.39; -0.10]

-0.16 [-0.20; -0.13]

-0.16 [-0.20; -0.13]

Weight

33.8%

10.6%

3.7%

6.0%

6.9%

8.7%

1.4%

18.3%

2.5%

2.7%

5.5%

100.0%

--

Weight

33.8%

10.6%

3.7%

6.0%

6.9%

8.7%

1.4%

18.3%

2.5%

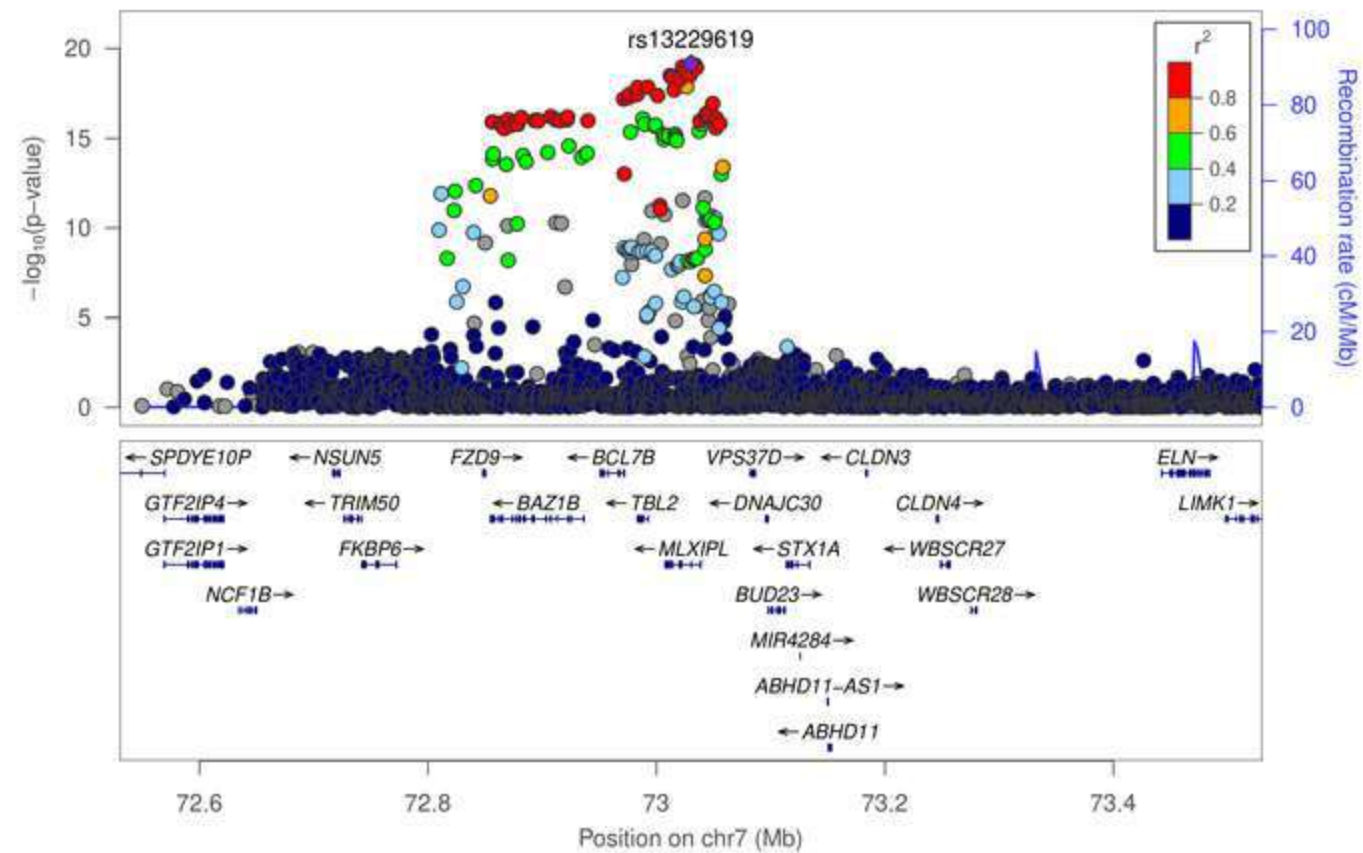
2.7%

5.5%

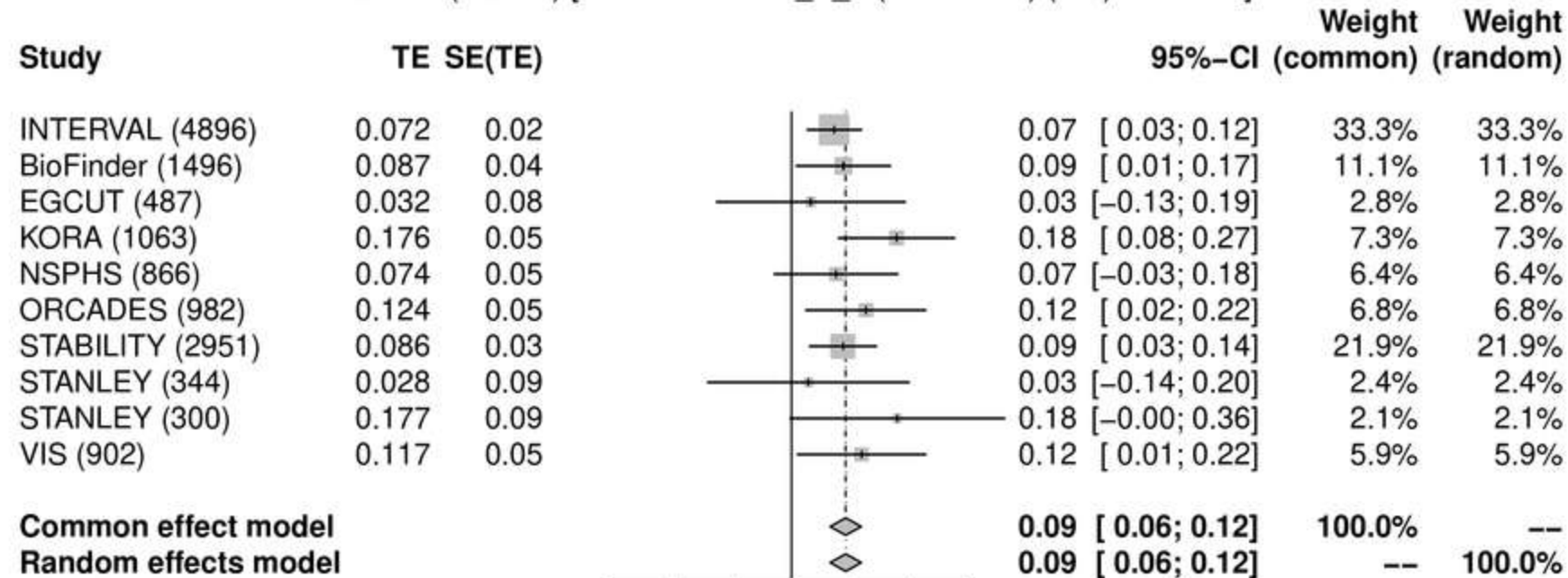
--

100.0%

FGF-21 (FGF21)-rs13229619

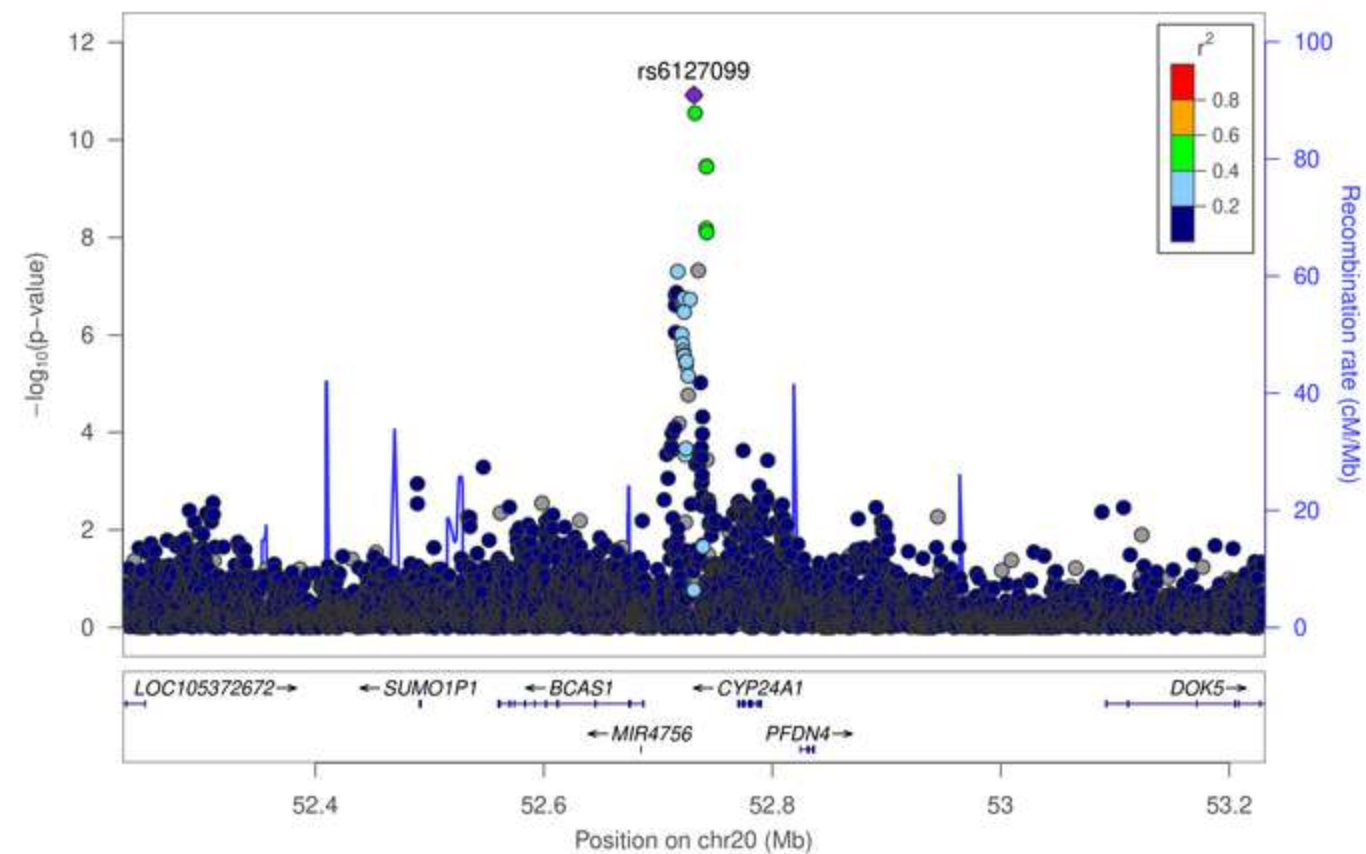


FGF-23 (FGF23) [chr20:52731402_A_T (rs6127099) (A/T) N=14287]

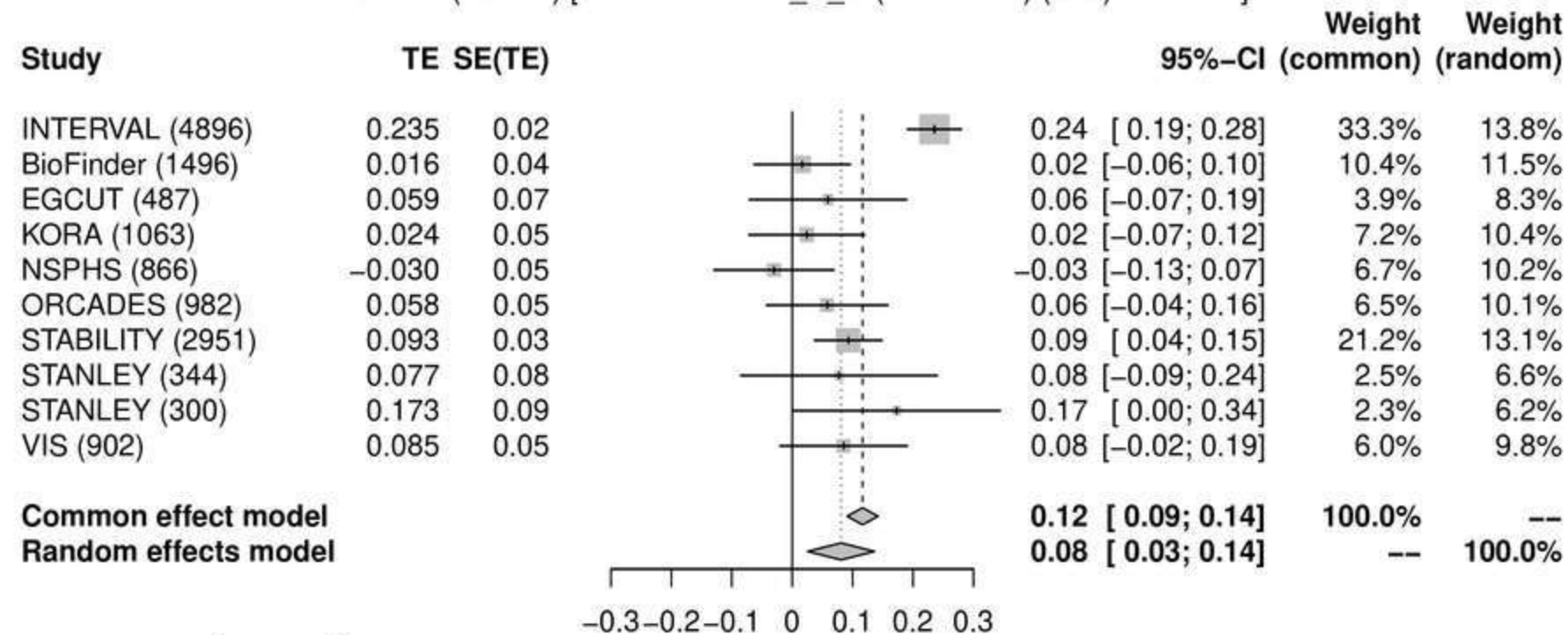


Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.70$

FGF-23 (FGF23)-rs6127099

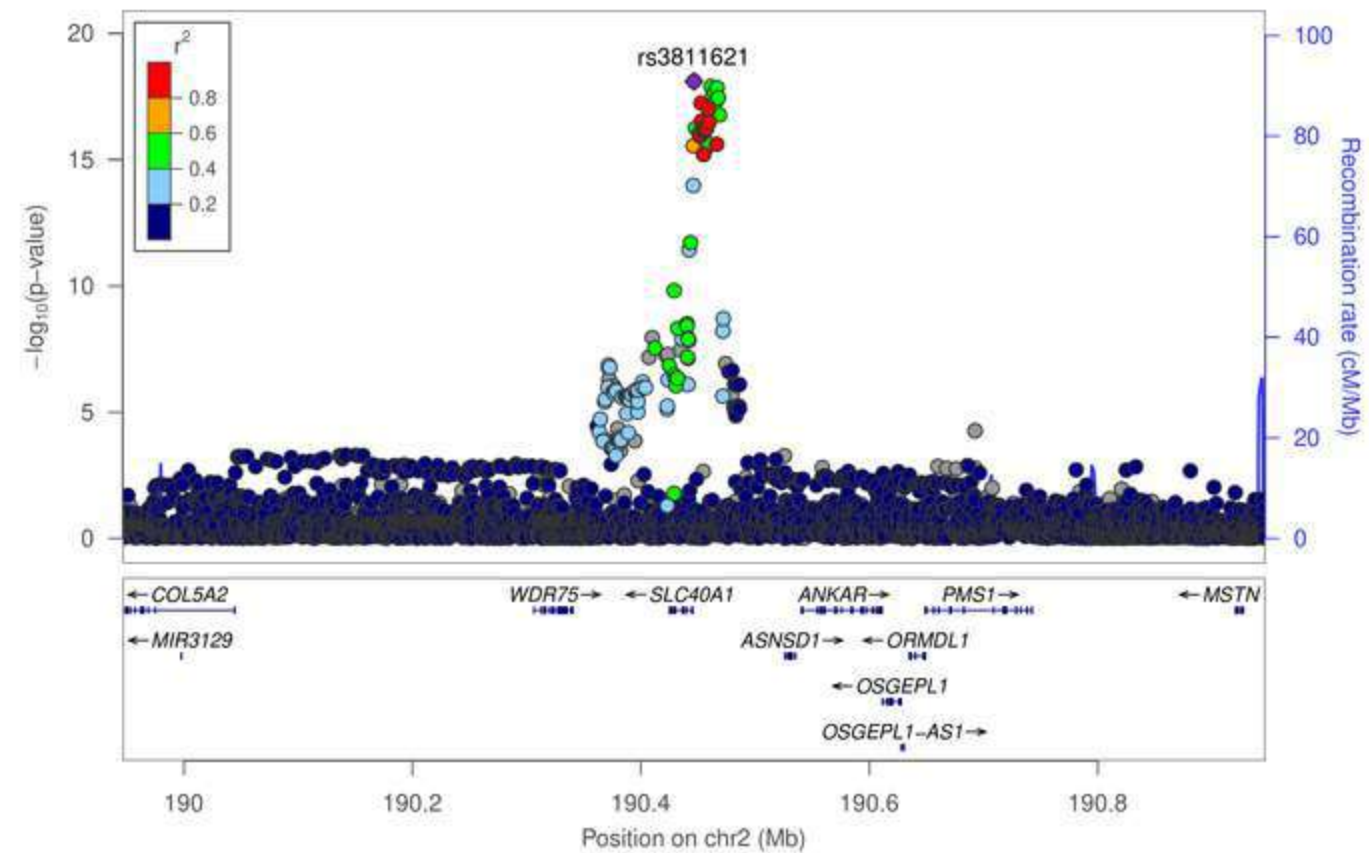


FGF-23 (FGF23) [chr2:190446541_C_G (rs3811621) (C/G) N=14287]

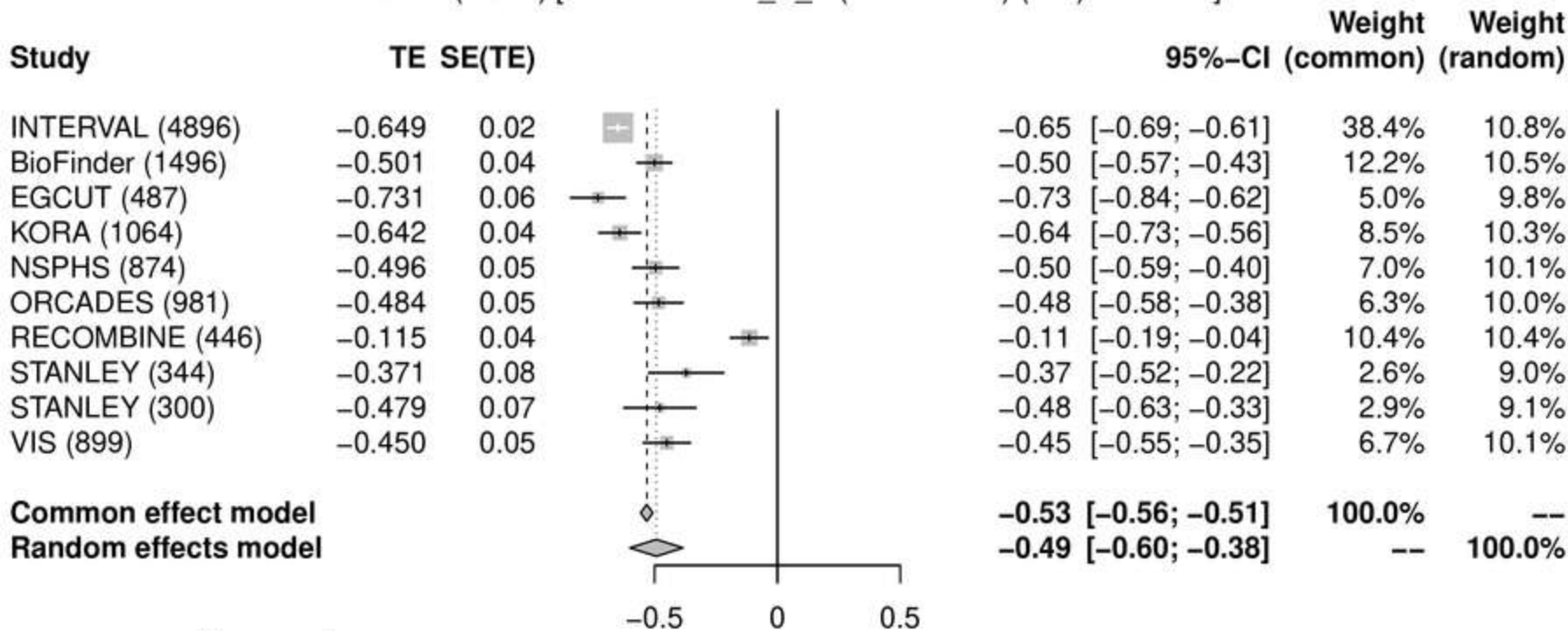


Heterogeneity: $I^2 = 82\%$, $\tau^2 = 0.0053$, $p < 0.01$

FGF-23 (FGF23)-rs3811621

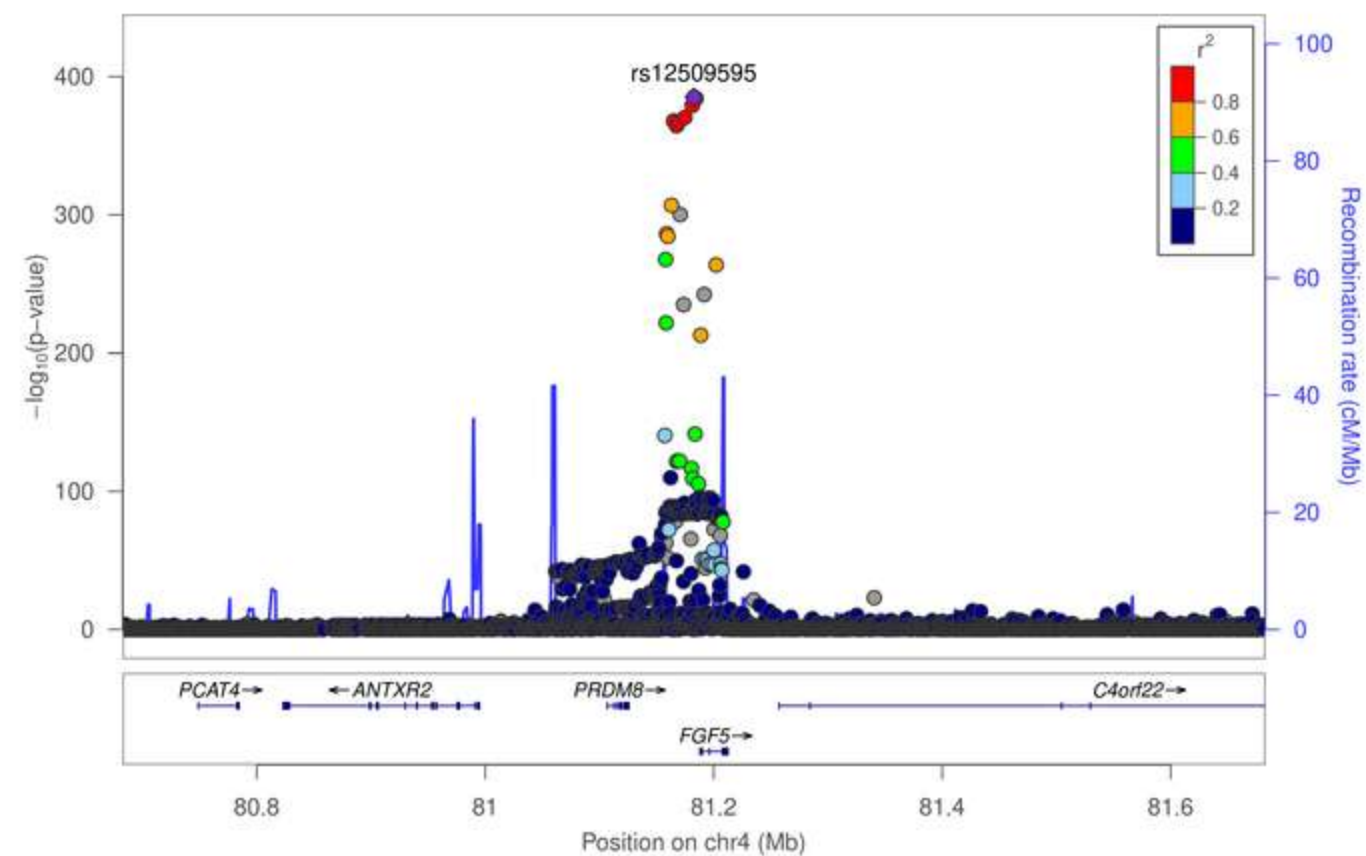


FGF-5 (FGF5) [chr4:81182554_C_T (rs12509595) (T/C) N=11787]



Heterogeneity: $I^2 = 95\%$, $\tau^2 = 0.0279$, $p < 0.01$

FGF-5 (FGF5)-rs12509595



Study

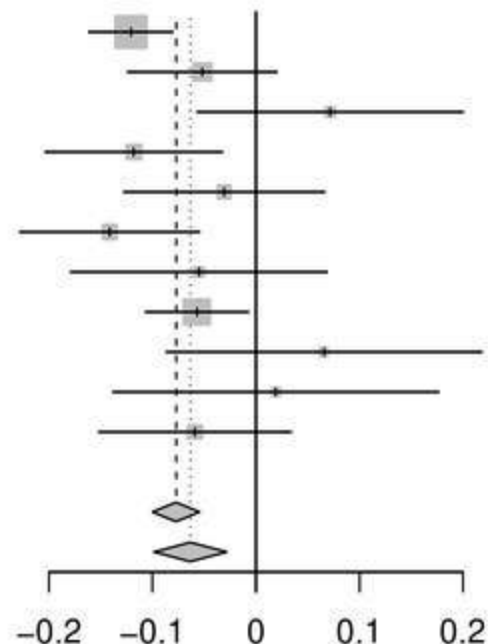
Study	TE	SE(TE)
INTERVAL (4896)	-0.121	0.02
BioFinder (1496)	-0.052	0.04
EGCUT (487)	0.072	0.07
KORA (1064)	-0.118	0.04
NSPHS (866)	-0.031	0.05
ORCADES (981)	-0.141	0.04
RECOMBINE (438)	-0.055	0.06
STABILITY (2951)	-0.057	0.03
STANLEY (344)	0.066	0.08
STANLEY (300)	0.019	0.08
VIS (901)	-0.059	0.05

Common effect model
Random effects model

Heterogeneity: $I^2 = 49\%$, $\tau^2 = 0.0015$, $p = 0.03$

Flt3L (FLT3LG) [chr11:108311965_A_G (rs11212636) (A/G) N=14724]

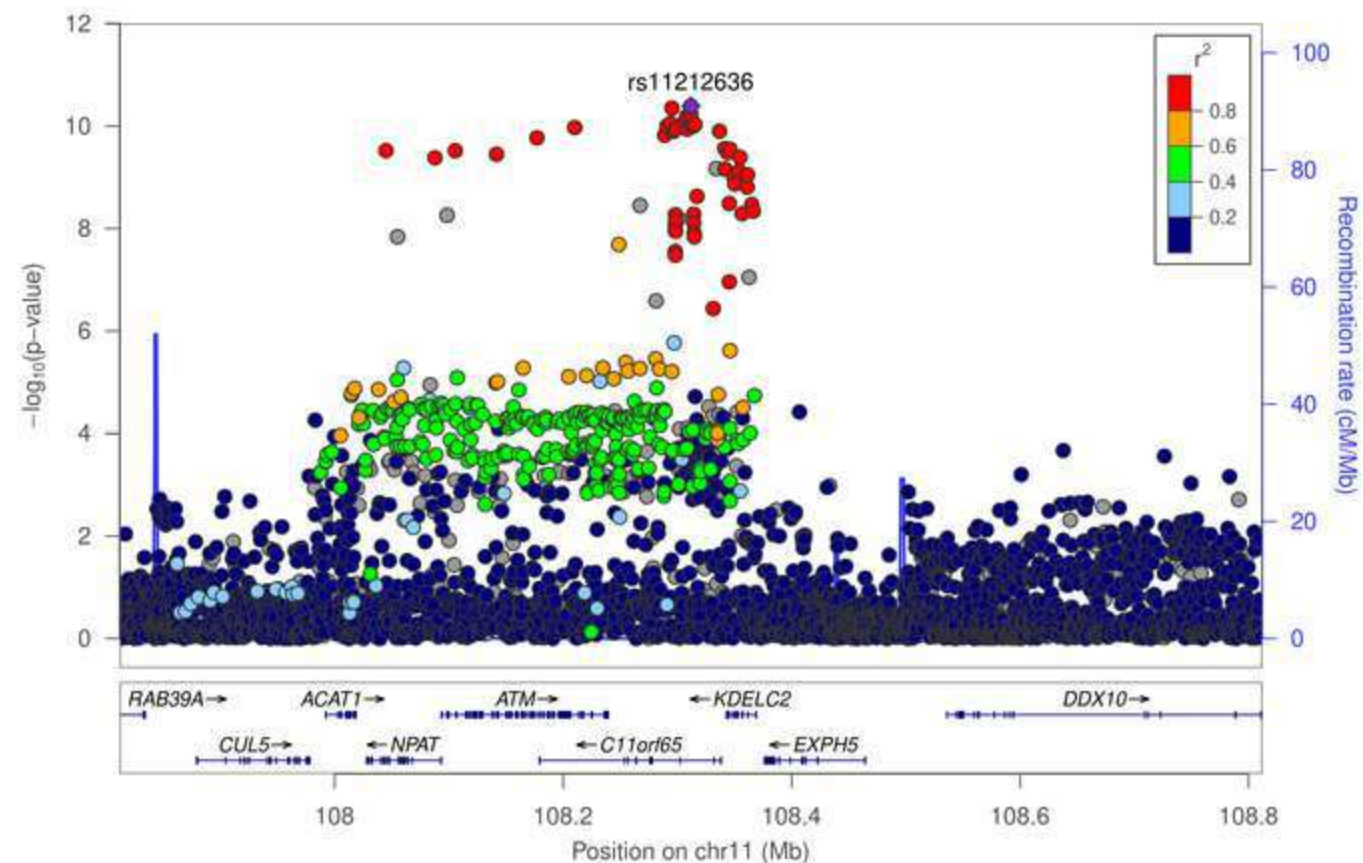
TE SE(TE)



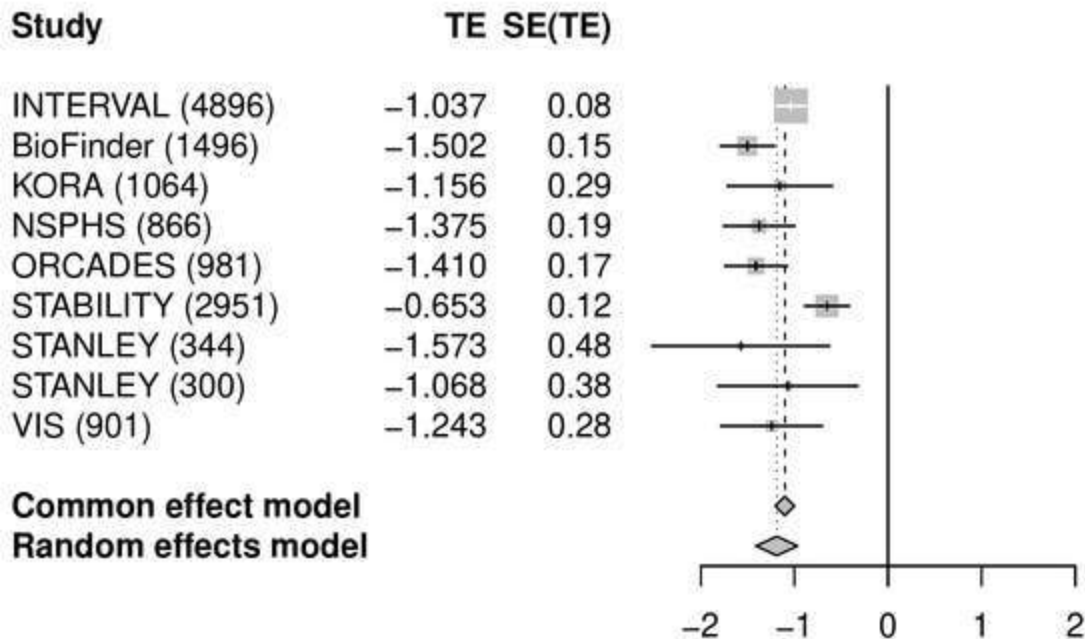
Weight Weight
95%-CI (common) (random)

-0.12	[-0.16; -0.08]	31.9%	17.1%
-0.05	[-0.12; 0.02]	10.1%	11.5%
0.07	[-0.06; 0.20]	3.2%	5.6%
-0.12	[-0.20; -0.03]	7.2%	9.6%
-0.03	[-0.13; 0.07]	5.6%	8.3%
-0.14	[-0.23; -0.05]	7.0%	9.5%
-0.06	[-0.18; 0.07]	3.4%	6.0%
-0.06	[-0.11; -0.01]	21.2%	15.3%
0.07	[-0.09; 0.22]	2.3%	4.3%
0.02	[-0.14; 0.18]	2.1%	4.1%
-0.06	[-0.15; 0.03]	6.1%	8.7%
-0.08	[-0.10; -0.05]	100.0%	--
-0.06	[-0.10; -0.03]	--	100.0%

Flt3L (FLT3LG)-rs11212636



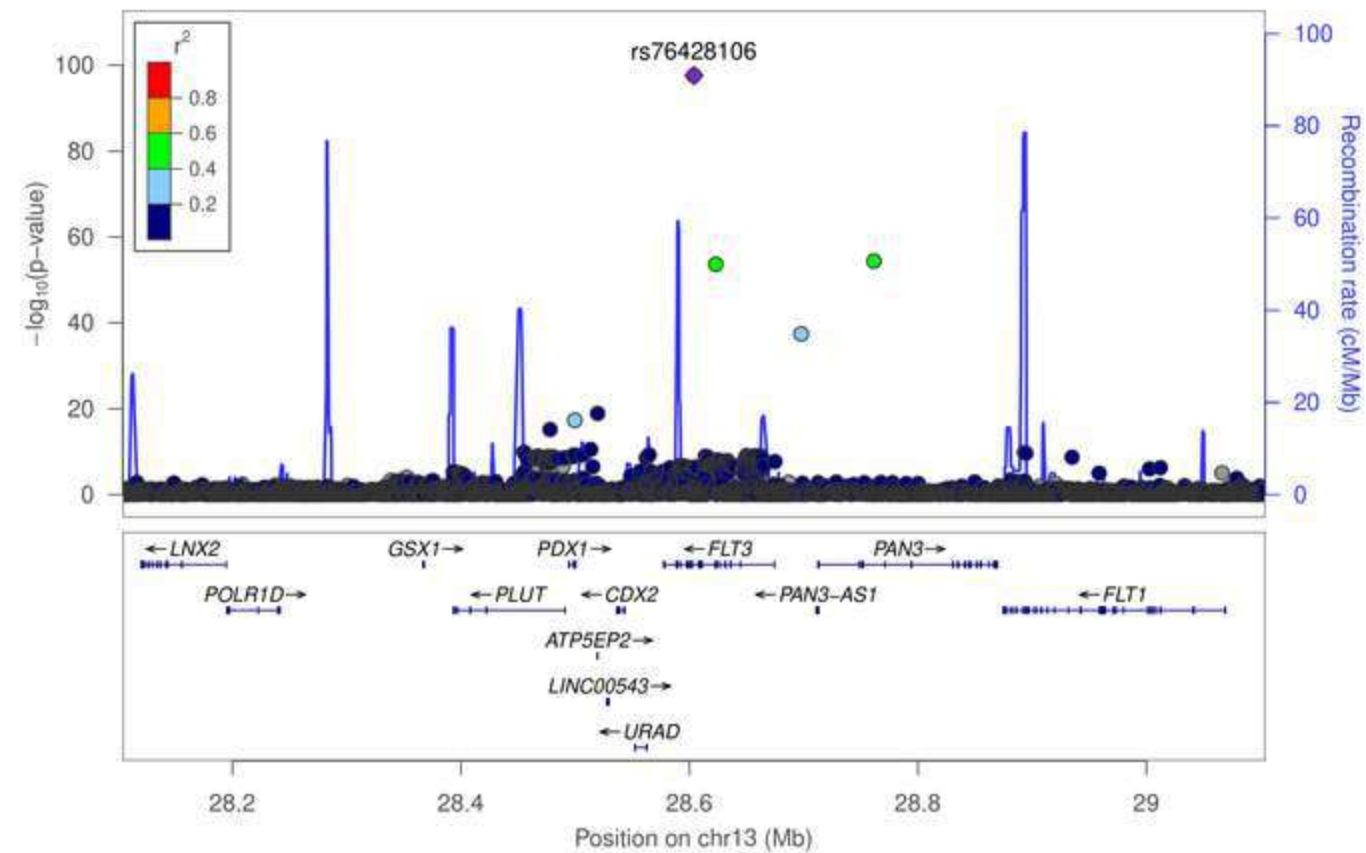
Flt3L (FLT3LG) [chr13:28604007_C_T (rs76428106) (T/C) N=13799]



Heterogeneity: $I^2 = 71\%$, $\tau^2 = 0.0685$, $p < 0.01$

	Weight 95%-CI	Weight (common)	Weight (random)
-1.04 [-1.19; -0.88]	42.4%	17.2%	
-1.50 [-1.79; -1.21]	12.6%	14.3%	
-1.16 [-1.72; -0.59]	3.3%	8.5%	
-1.37 [-1.76; -0.99]	7.2%	12.1%	
-1.41 [-1.74; -1.08]	9.4%	13.2%	
-0.65 [-0.89; -0.41]	18.5%	15.5%	
-1.57 [-2.52; -0.62]	1.2%	4.3%	
-1.07 [-1.82; -0.32]	1.9%	6.0%	
-1.24 [-1.79; -0.70]	3.6%	8.9%	
-1.10 [-1.20; -1.00]	100.0%	--	
-1.19 [-1.41; -0.96]	--	100.0%	

Flt3L (FLT3LG)-rs76428106



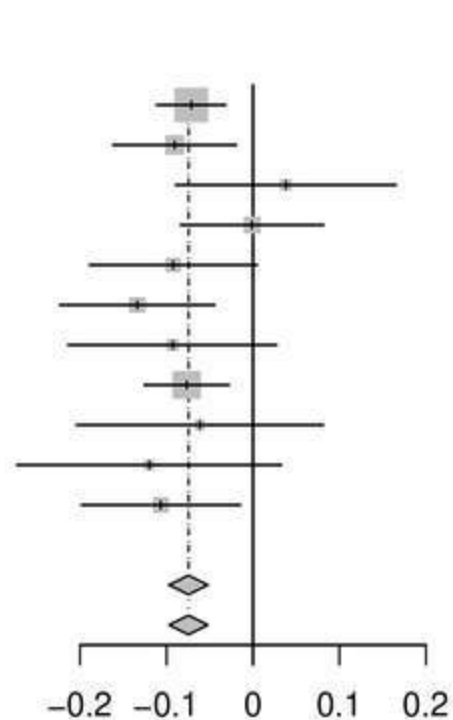
Study

Study	TE	SE(TE)
INTERVAL (4896)	-0.072	0.02
BioFinder (1496)	-0.090	0.04
EGCUT (487)	0.038	0.07
KORA (1064)	-0.001	0.04
NSPHS (866)	-0.092	0.05
ORCADES (981)	-0.134	0.05
RECOMBINE (446)	-0.093	0.06
STABILITY (2951)	-0.077	0.03
STANLEY (344)	-0.061	0.07
STANLEY (300)	-0.120	0.08
VIS (901)	-0.106	0.05

Common effect model
Random effects model

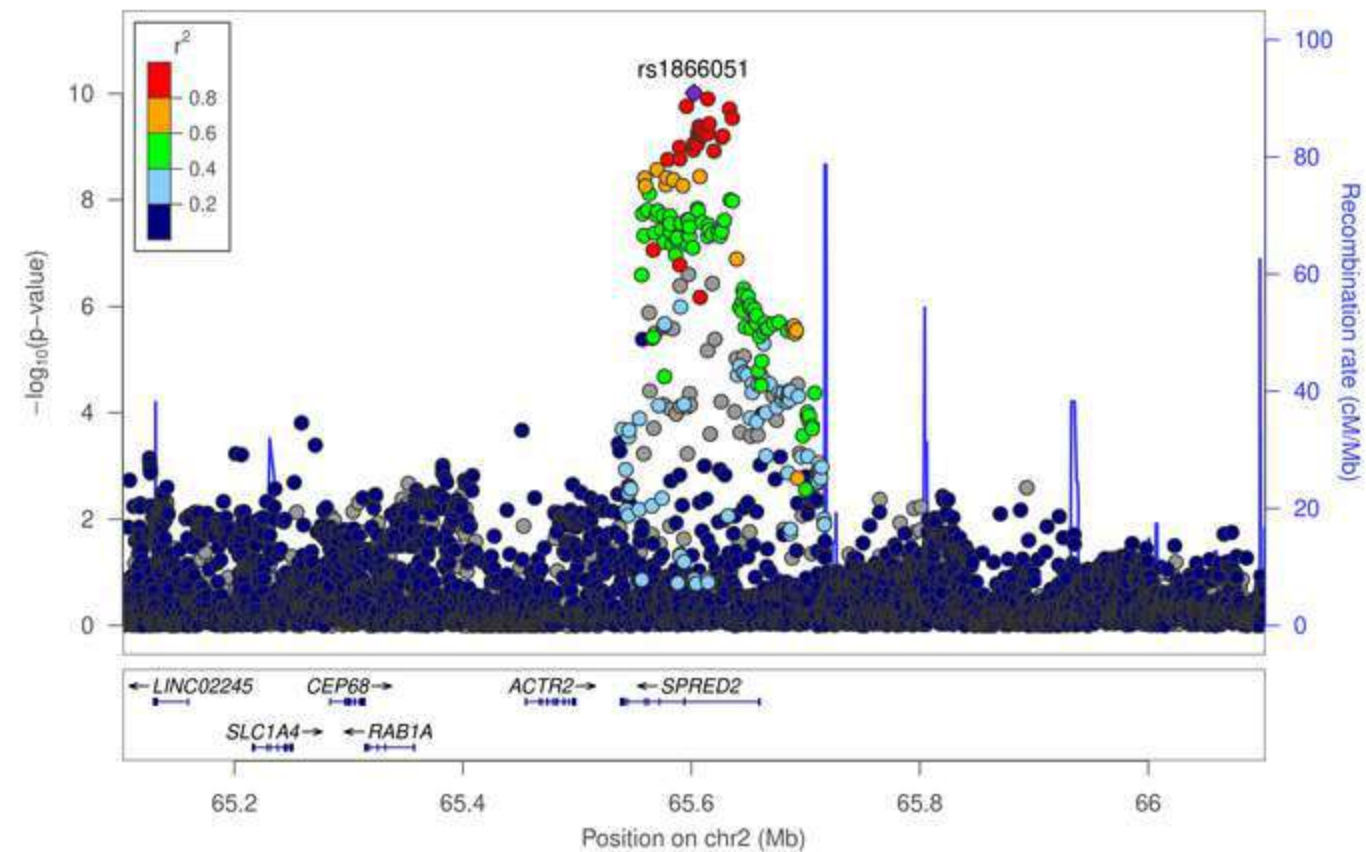
Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.54$

Flt3L (FLT3LG) [chr2:65602149_C_T (rs1866051) (T/C) N=14732]



	Weight	Weight
95%-CI (common)	(random)	
-0.07 [-0.11; -0.03]	32.2%	32.2%
-0.09 [-0.16; -0.02]	10.0%	10.0%
0.04 [-0.09; 0.17]	3.1%	3.1%
-0.00 [-0.08; 0.08]	7.5%	7.5%
-0.09 [-0.19; 0.00]	5.4%	5.4%
-0.13 [-0.22; -0.04]	6.4%	6.4%
-0.09 [-0.21; 0.03]	3.5%	3.5%
-0.08 [-0.13; -0.03]	21.2%	21.2%
-0.06 [-0.20; 0.08]	2.5%	2.5%
-0.12 [-0.27; 0.03]	2.2%	2.2%
-0.11 [-0.20; -0.01]	6.0%	6.0%
-0.07 [-0.10; -0.05]	100.0%	--
-0.07 [-0.10; -0.05]	--	100.0%

Flt3L (FLT3LG)-rs1866051



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (981)

RECOMBINE (433)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0.0002$, $p = 0.44$

Flt3L (FLT3LG) [chr3:128381886_G_T (rs7624160) (T/G) N=14719]

TE SE(TE)

-0.121 0.02

-0.180 0.04

-0.125 0.06

-0.083 0.05

-0.109 0.05

-0.088 0.05

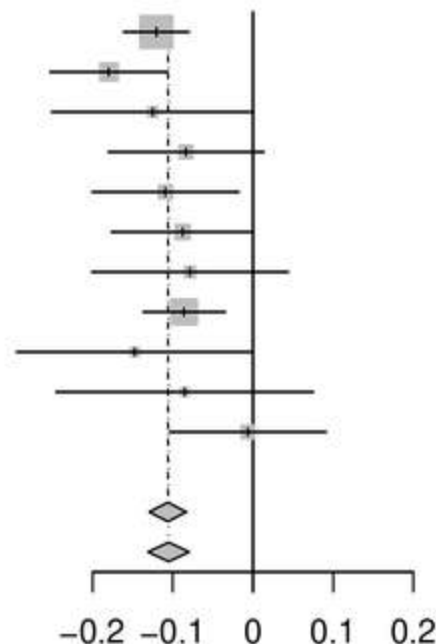
-0.078 0.06

-0.086 0.03

-0.147 0.07

-0.085 0.08

-0.006 0.05

Weight
95%-CI (common) (random)

-0.12 [-0.16; -0.08] 32.6% 27.5%

-0.18 [-0.25; -0.11] 10.1% 10.9%

-0.12 [-0.25; 0.00] 3.4% 4.0%

-0.08 [-0.18; 0.01] 5.8% 6.6%

-0.11 [-0.20; -0.02] 6.5% 7.3%

-0.09 [-0.18; 0.00] 6.9% 7.7%

-0.08 [-0.20; 0.04] 3.6% 4.2%

-0.09 [-0.14; -0.03] 20.8% 19.8%

-0.15 [-0.29; -0.00] 2.5% 3.0%

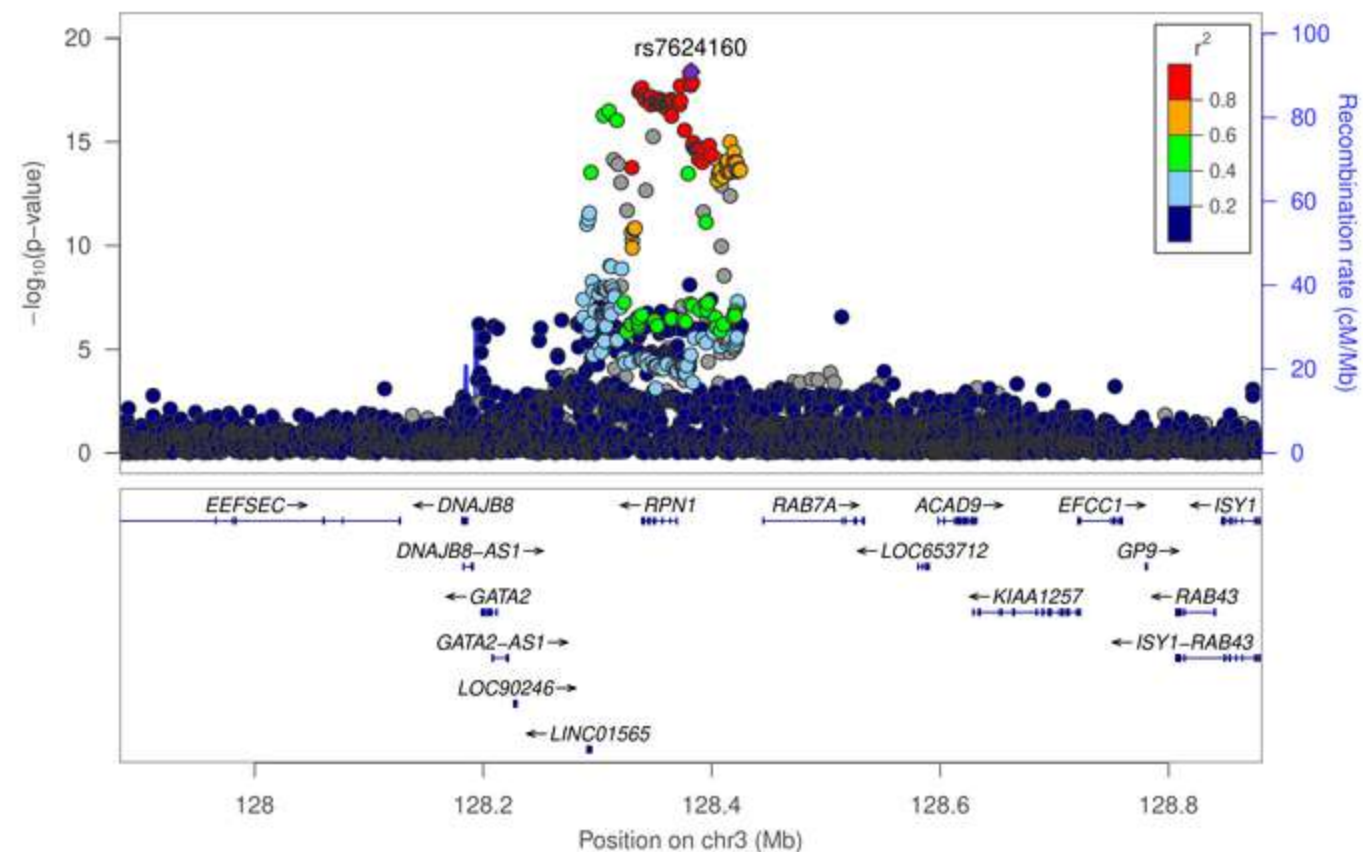
-0.09 [-0.25; 0.08] 2.1% 2.5%

-0.01 [-0.10; 0.09] 5.7% 6.5%

-0.11 [-0.13; -0.08] 100.0% --

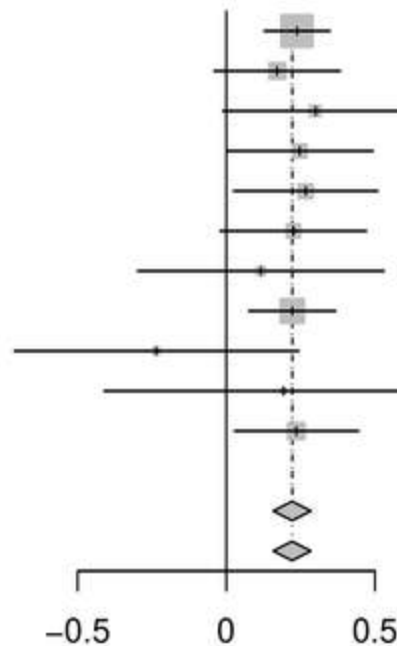
-0.11 [-0.13; -0.08] -- 100.0%

Flt3L (FLT3LG)-rs7624160



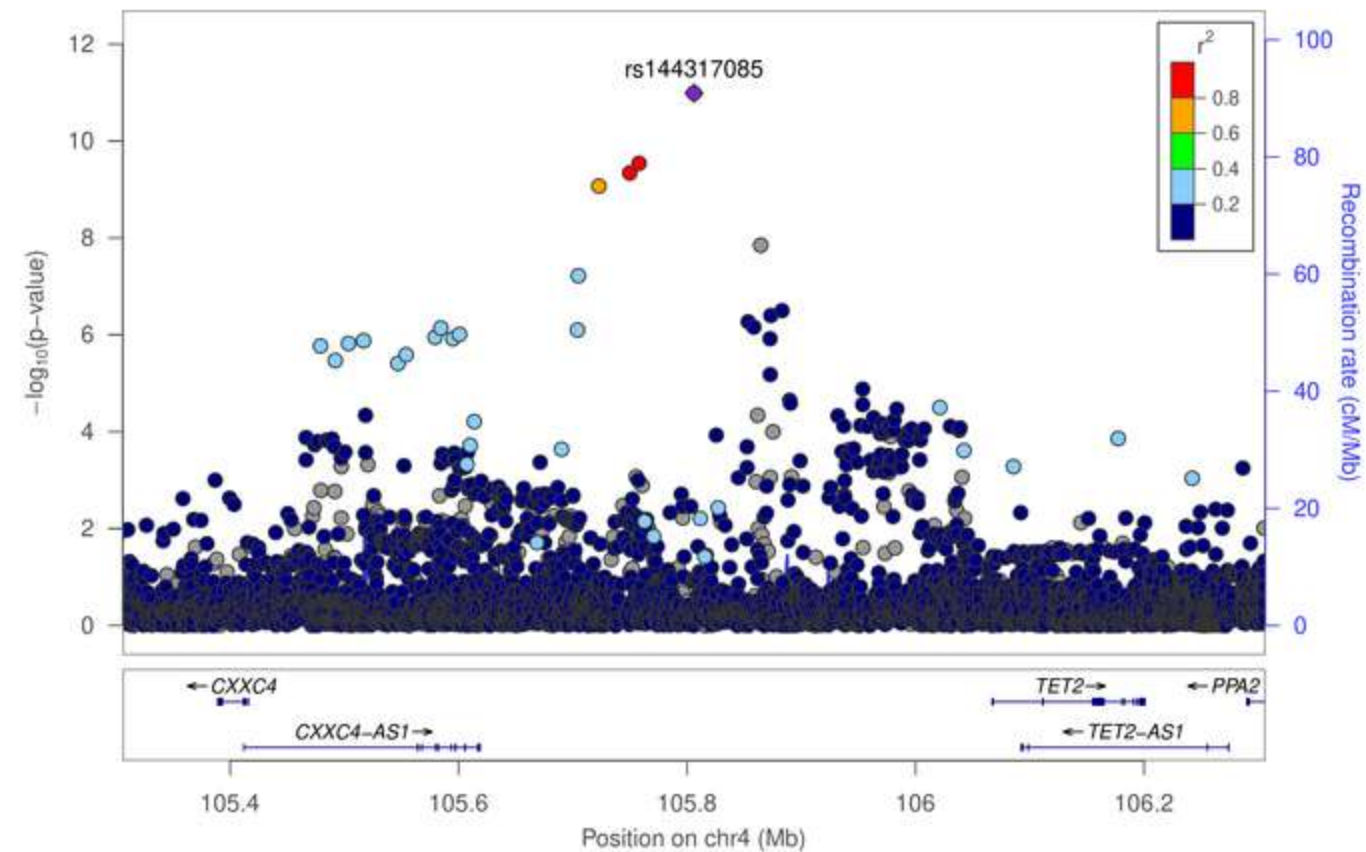
Flt3L (FLT3LG) [chr4:105806108_A_T (rs144317085) (A/T) N=14722]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight Weight (random)
INTERVAL (4896)	0.237	0.06	0.24 [0.13; 0.35]	33.2%
BioFinder (1496)	0.171	0.11	0.17 [-0.04; 0.38]	9.0%
EGCUT (487)	0.300	0.16	0.30 [-0.01; 0.61]	4.1%
KORA (1064)	0.246	0.13	0.25 [-0.00; 0.49]	6.6%
NSPHS (866)	0.266	0.12	0.27 [0.02; 0.51]	6.9%
ORCADES (981)	0.225	0.13	0.22 [-0.02; 0.47]	6.7%
RECOMBINE (436)	0.116	0.21	0.12 [-0.30; 0.53]	2.4%
STABILITY (2951)	0.221	0.07	0.22 [0.07; 0.37]	19.0%
STANLEY (344)	-0.235	0.24	-0.24 [-0.71; 0.24]	1.8%
STANLEY (300)	0.192	0.31	0.19 [-0.41; 0.79]	1.1%
VIS (901)	0.235	0.11	0.24 [0.03; 0.44]	9.3%
Common effect model			0.22 [0.16; 0.28]	100.0%
Random effects model			0.22 [0.16; 0.28]	-- 100.0%



Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.92$

Flt3L (FLT3LG)-rs144317085



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (981)

RECOMBINE (447)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 9\%$, $\tau^2 < 0.0001$, $p = 0.36$

Flt3L (FLT3LG) [chr5:1282319_A_C (rs7726159) (A/C) N=14733]

TE SE(TE)

-0.115 0.02

-0.160 0.04

-0.104 0.08

-0.231 0.06

-0.091 0.05

-0.129 0.05

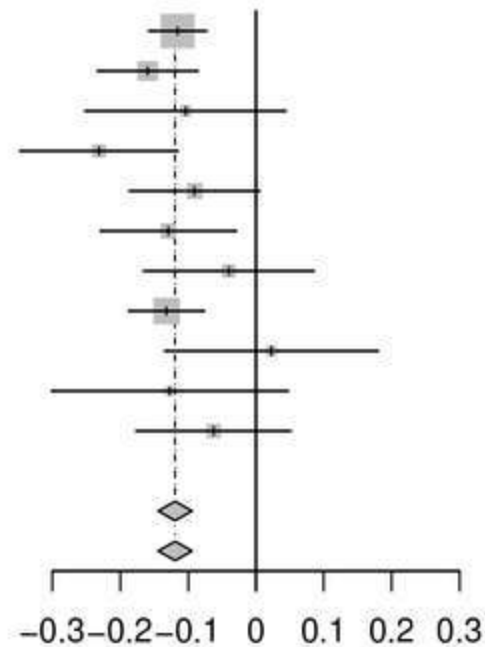
-0.040 0.06

-0.132 0.03

0.023 0.08

-0.127 0.09

-0.063 0.06

Weight
95%-CI (common) (random)

-0.12 [-0.16; -0.07] 34.5% 34.4%

-0.16 [-0.23; -0.09] 11.4% 11.4%

-0.10 [-0.25; 0.04] 2.9% 2.9%

-0.23 [-0.35; -0.12] 4.6% 4.6%

-0.09 [-0.19; 0.01] 6.8% 6.8%

-0.13 [-0.23; -0.03] 6.2% 6.3%

-0.04 [-0.17; 0.09] 4.0% 4.0%

-0.13 [-0.19; -0.08] 20.1% 20.1%

0.02 [-0.13; 0.18] 2.5% 2.5%

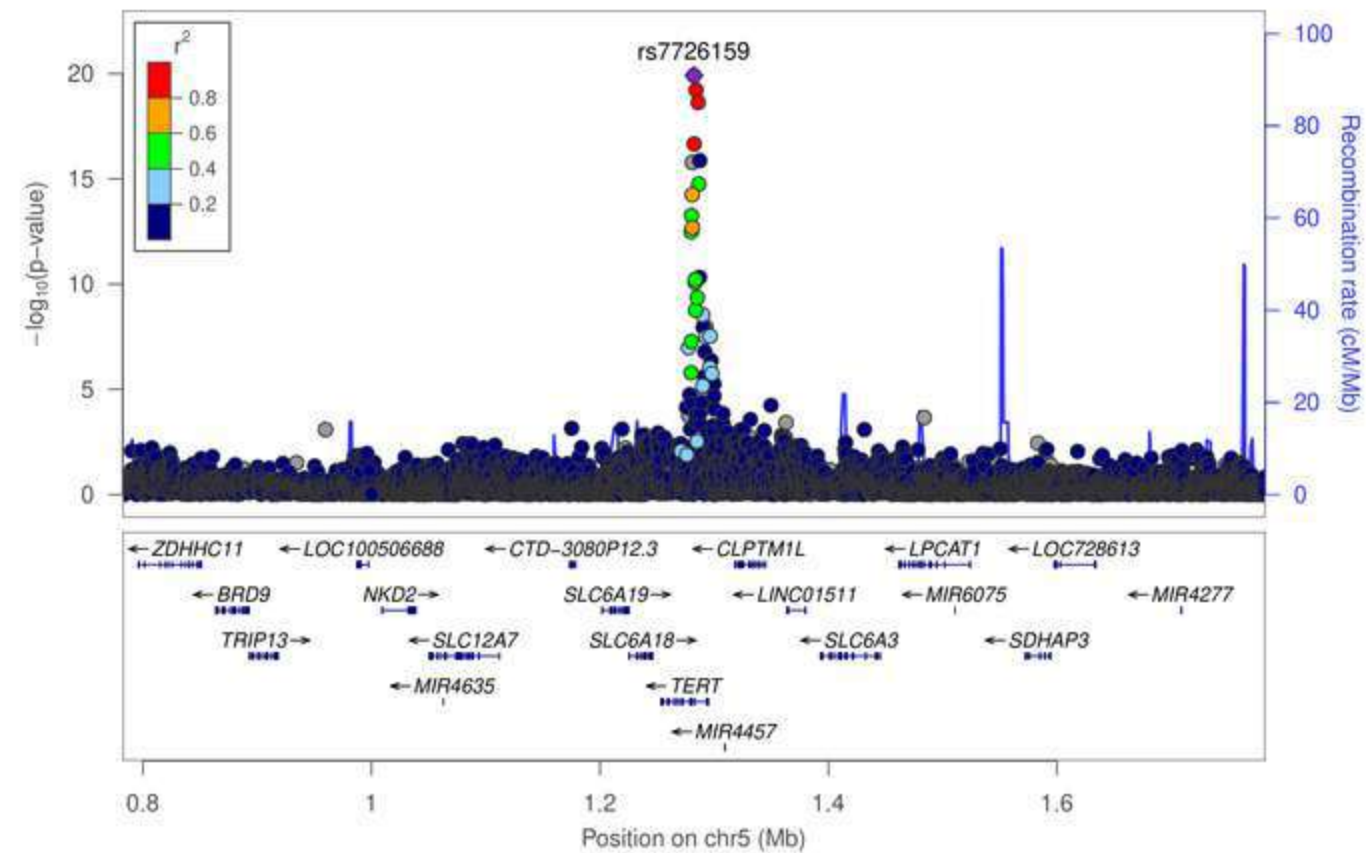
-0.13 [-0.30; 0.05] 2.1% 2.1%

-0.06 [-0.18; 0.05] 4.8% 4.8%

-0.12 [-0.14; -0.09] 100.0% --

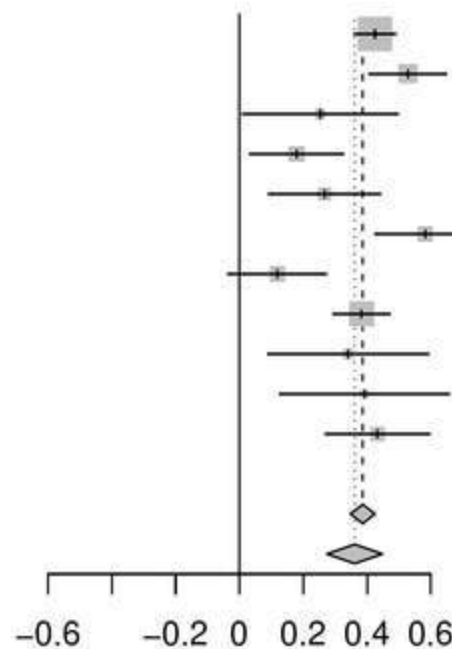
-0.12 [-0.14; -0.09] -- 100.0%

Flt3L (FLT3LG)-rs7726159



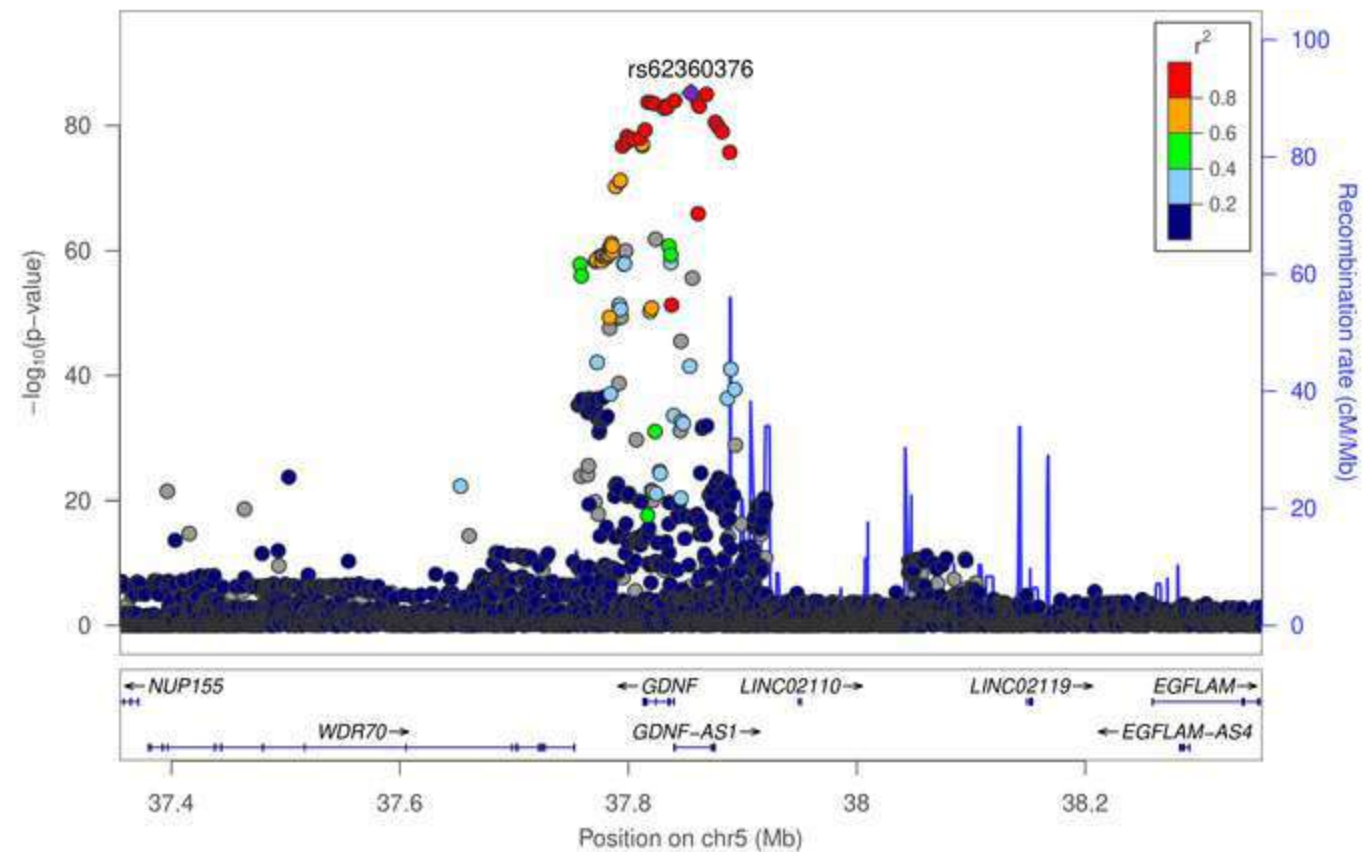
hGDNF (GDNF) [chr5:37854688_A_T (rs62360376) (A/T) N=14722]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.425	0.03	0.42 [0.36; 0.49]	34.8%
BioFinder (1496)	0.528	0.06	0.53 [0.41; 0.65]	10.1%
EGCUT (487)	0.253	0.12	0.25 [0.01; 0.50]	2.5%
KORA (1064)	0.179	0.08	0.18 [0.03; 0.33]	6.9%
NSPHS (866)	0.266	0.09	0.27 [0.09; 0.44]	4.8%
ORCADES (982)	0.583	0.08	0.58 [0.42; 0.74]	6.0%
RECOMBINE (434)	0.118	0.08	0.12 [-0.04; 0.27]	6.2%
STABILITY (2951)	0.383	0.05	0.38 [0.29; 0.47]	18.7%
STANLEY (344)	0.341	0.13	0.34 [0.09; 0.59]	2.3%
STANLEY (300)	0.392	0.14	0.39 [0.13; 0.66]	2.1%
VIS (902)	0.433	0.08	0.43 [0.27; 0.60]	5.5%
Common effect model			0.39 [0.35; 0.43]	100.0%
Random effects model			0.36 [0.27; 0.45]	-- 100.0%

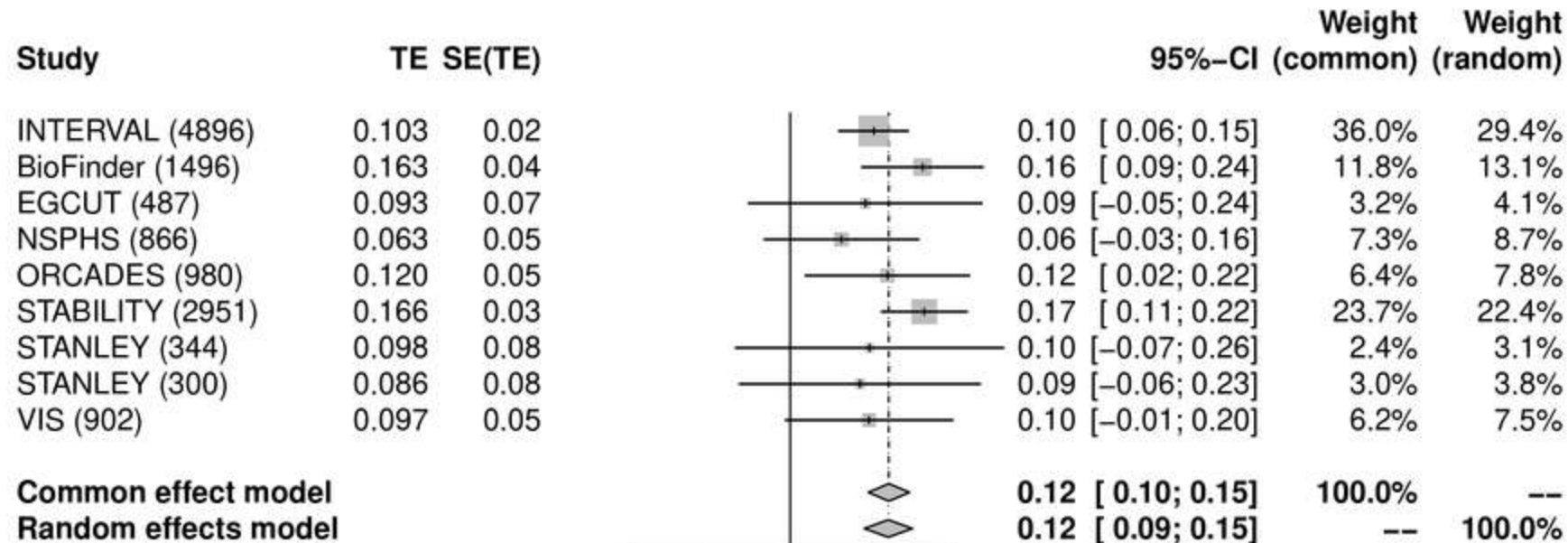


Heterogeneity: $I^2 = 71\%$, $\tau^2 = 0.0150$, $p < 0.01$

hGDNF (GDNF)-rs62360376

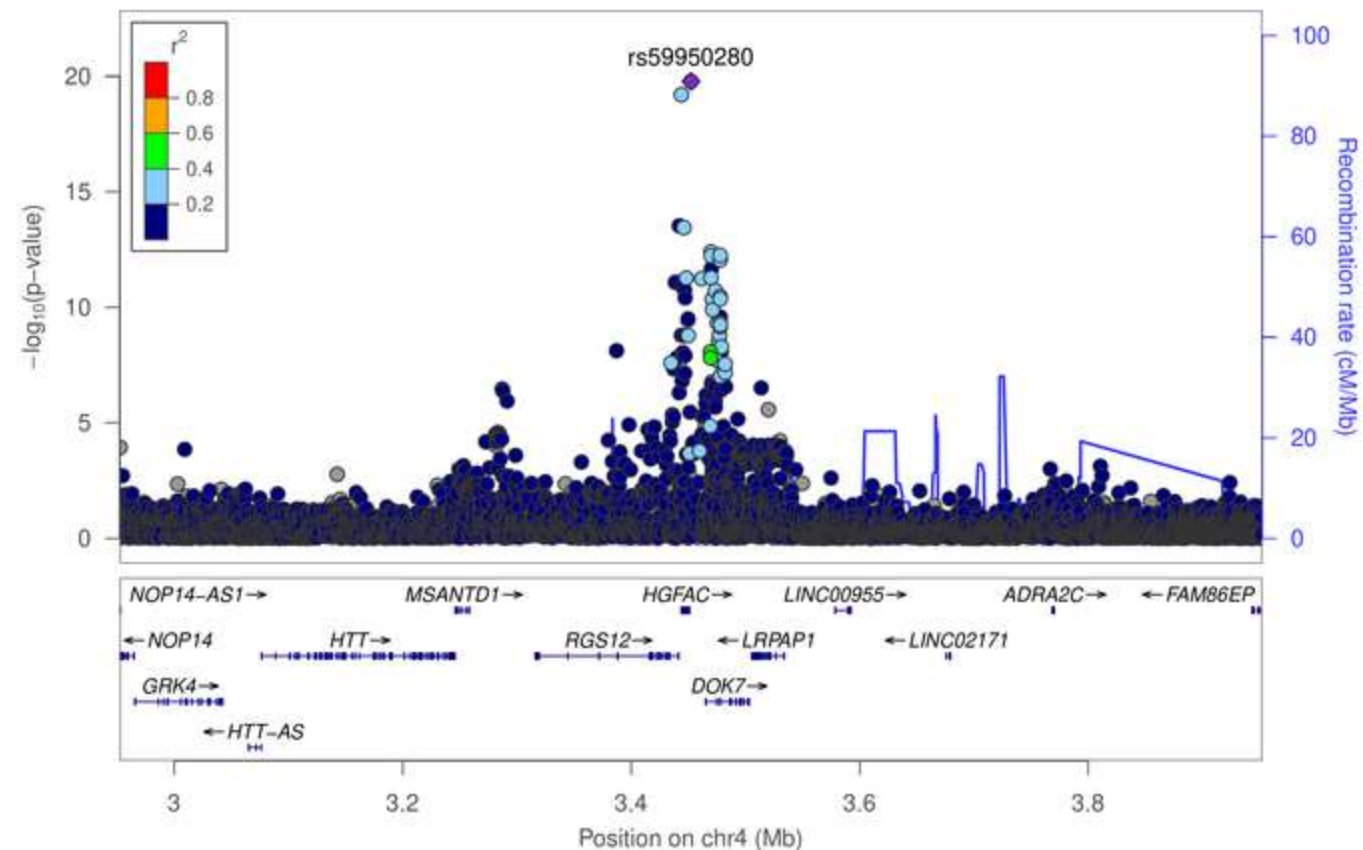


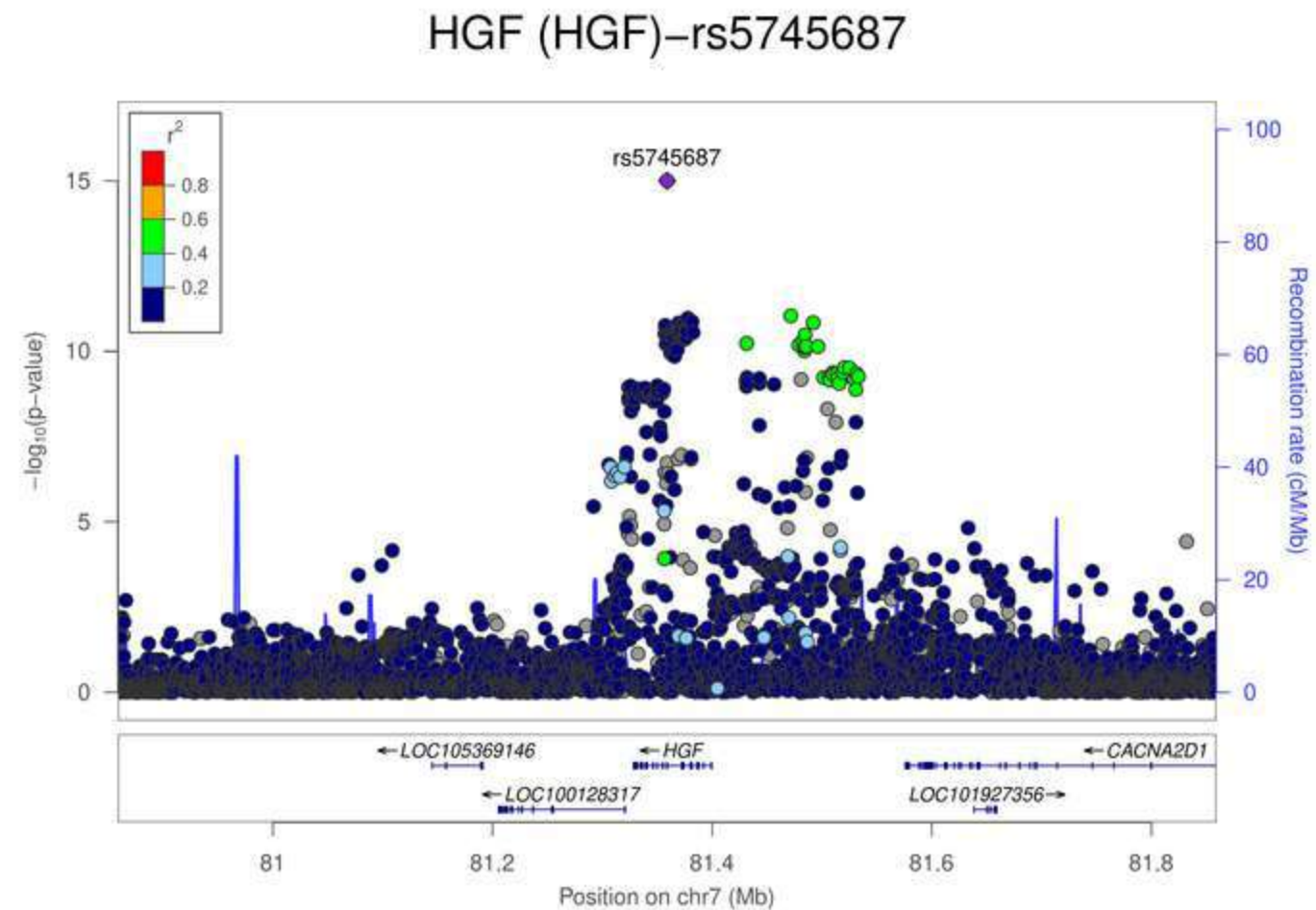
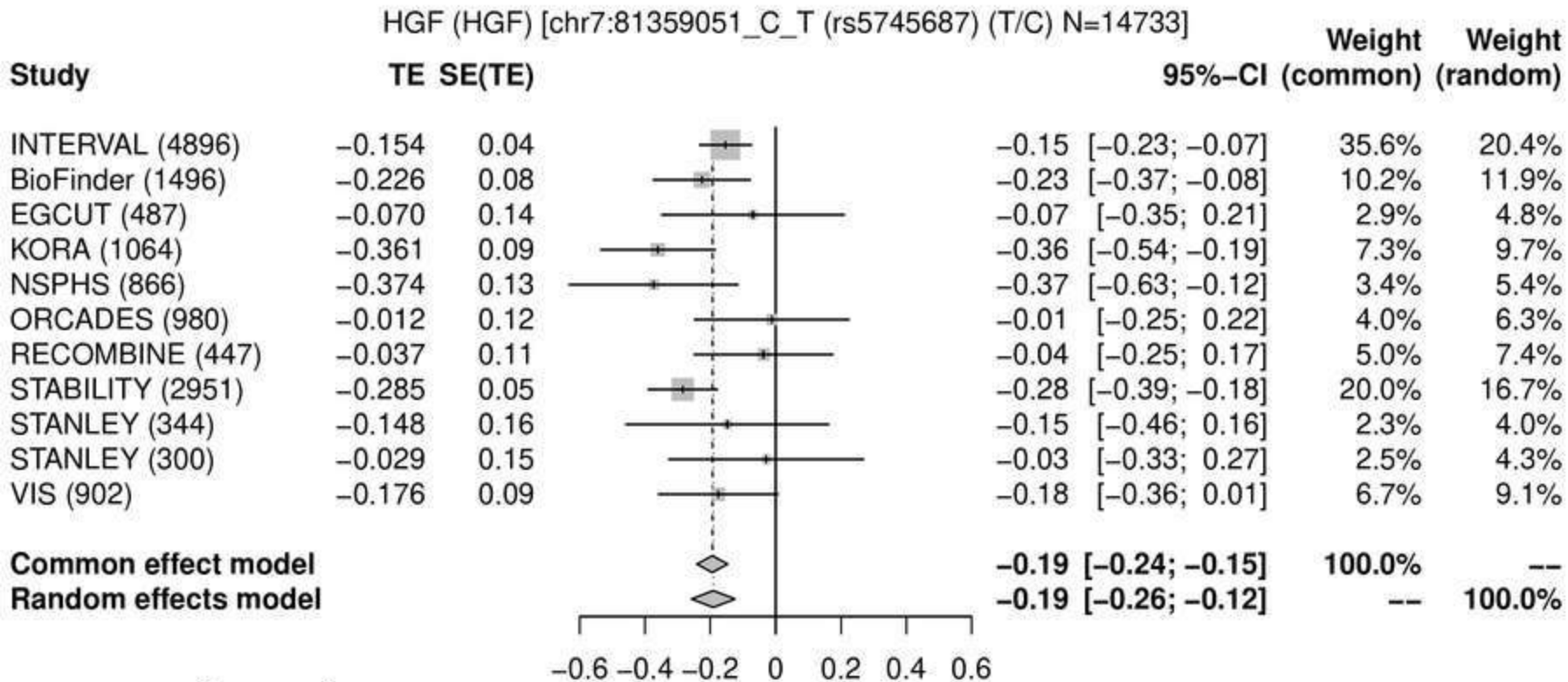
HGF (HGF) [chr4:3452345_A_G (rs59950280) (A/G) N=13222]

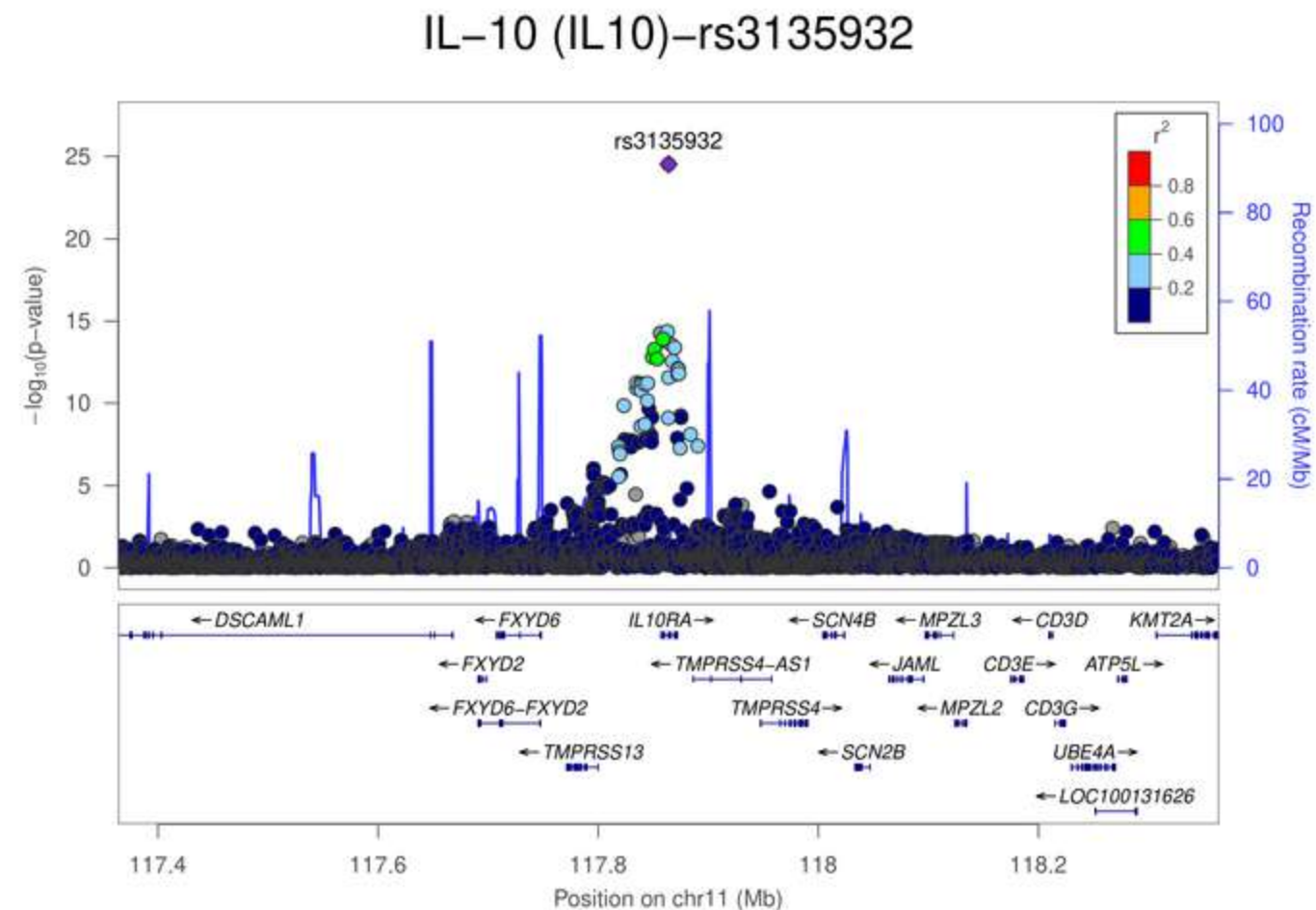
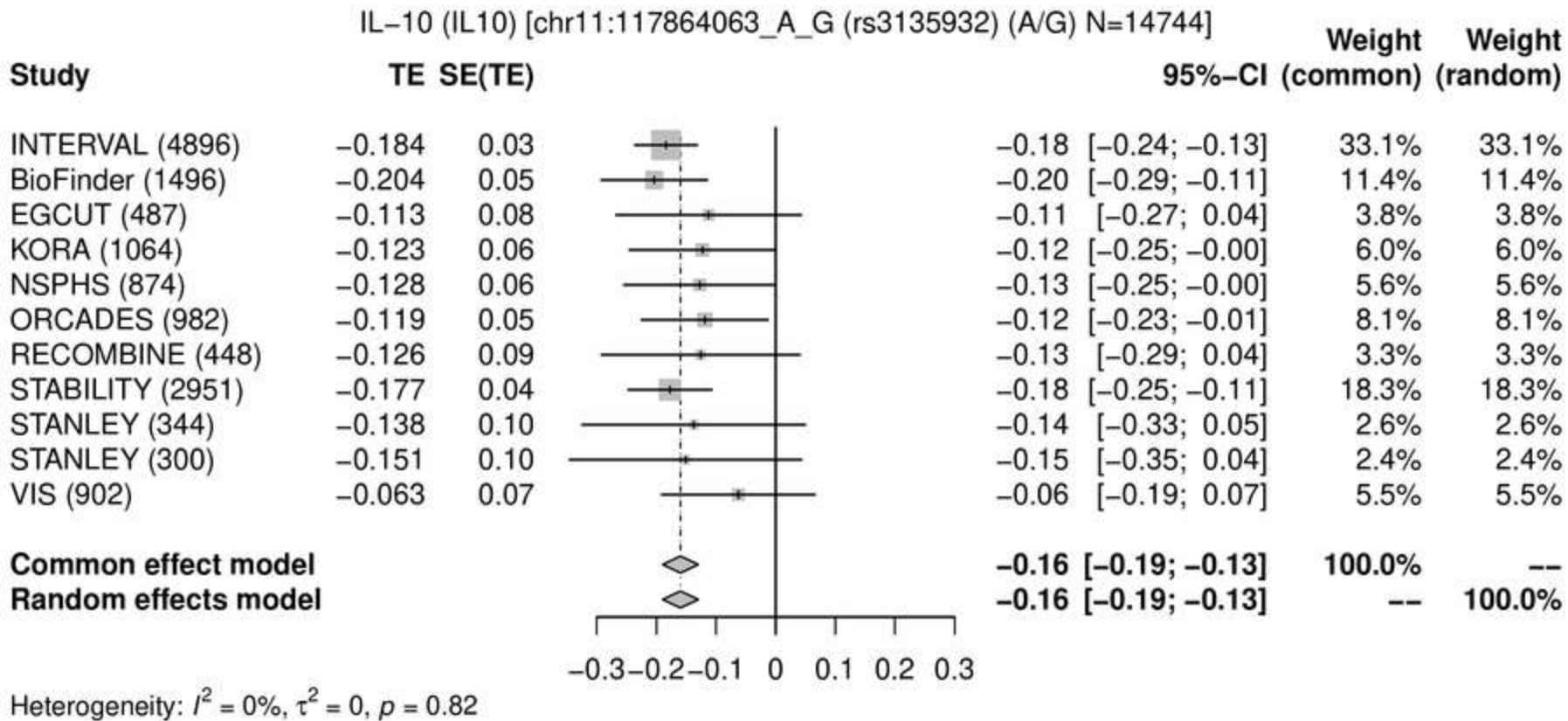


Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0.0003$, $p = 0.57$

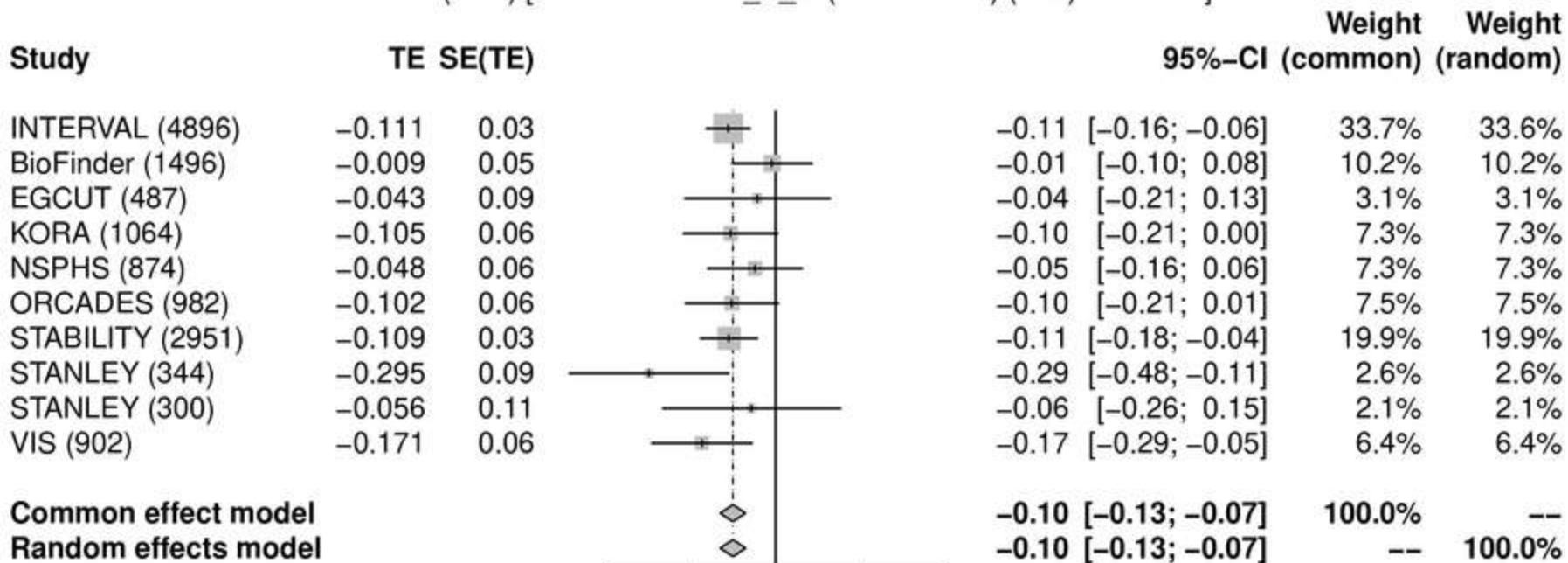
HGF (HGF)-rs59950280





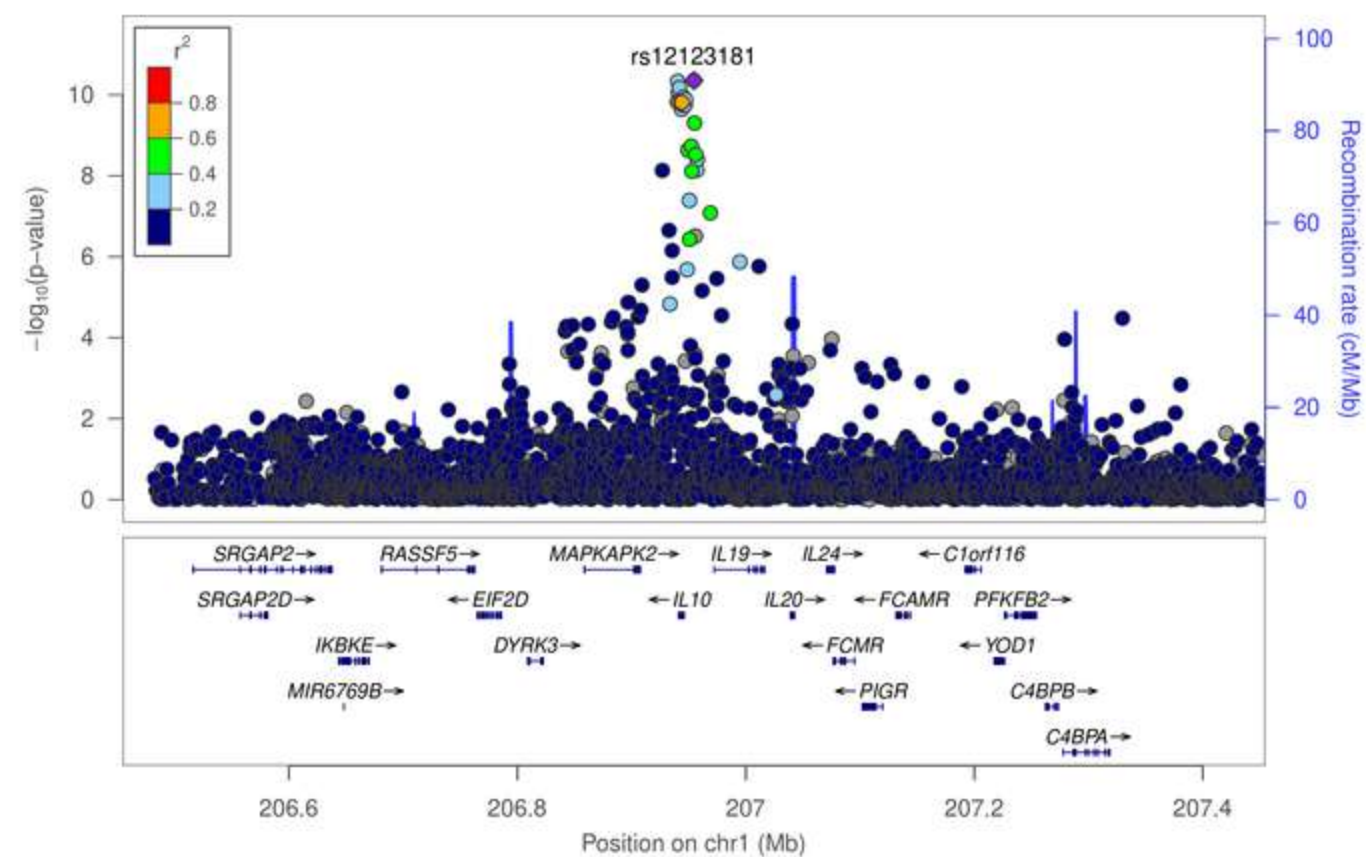


IL-10 (IL10) [chr1:206954566_A_G (rs12123181) (A/G) N=14296]

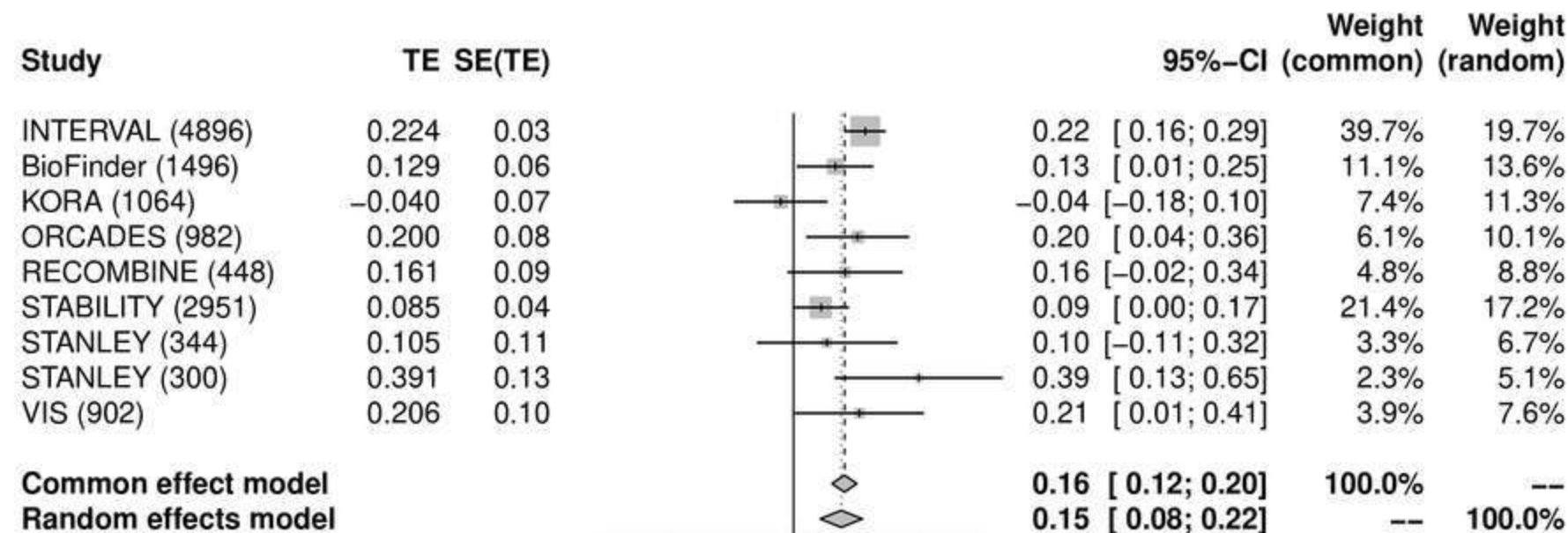


Heterogeneity: $I^2 = 19\%$, $\tau^2 < 0.0001$, $p = 0.27$

IL-10 (IL10)-rs12123181

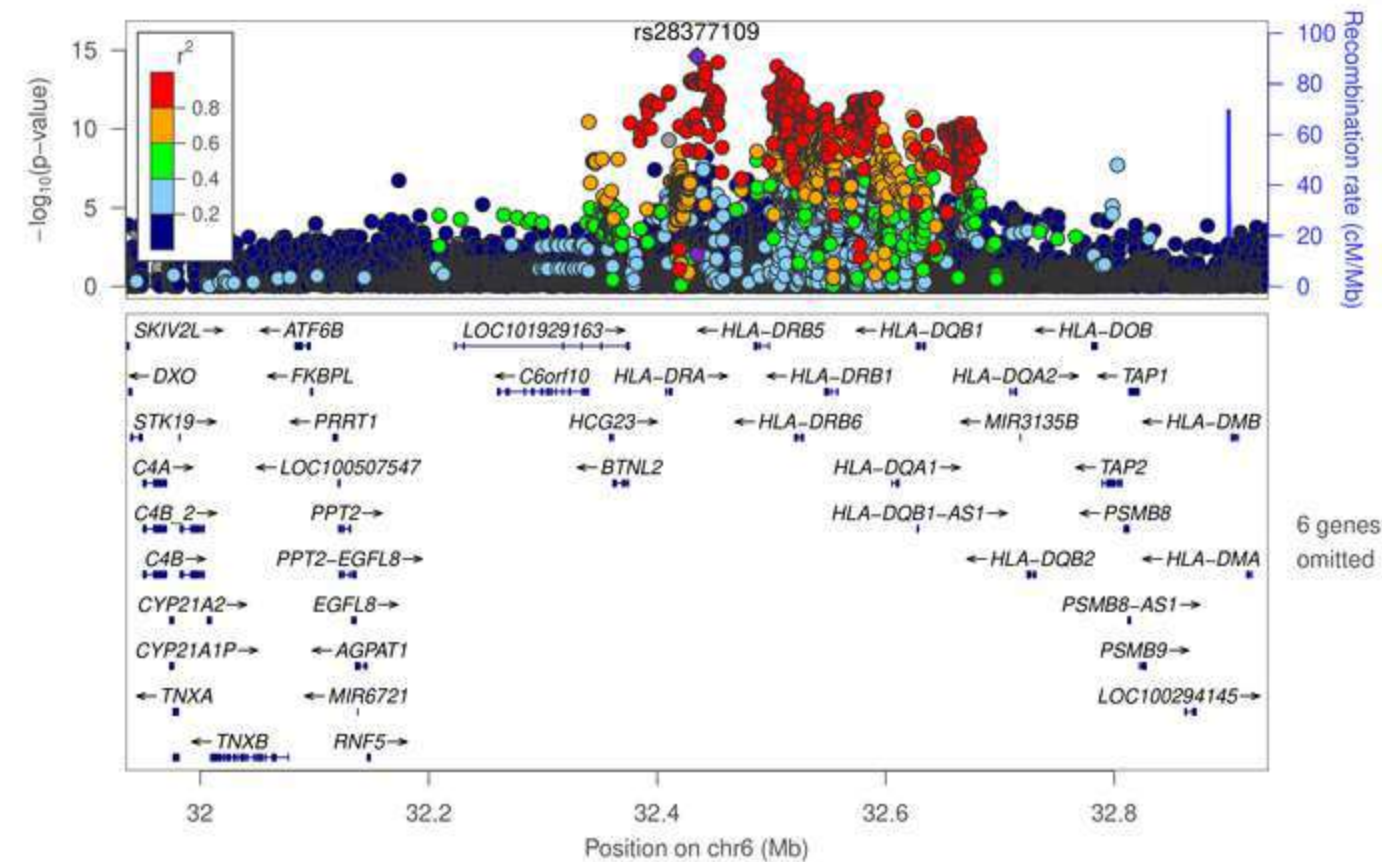


IL-10 (IL10) [chr6:32434716_A_C (rs28377109) (A/C) N=13383]

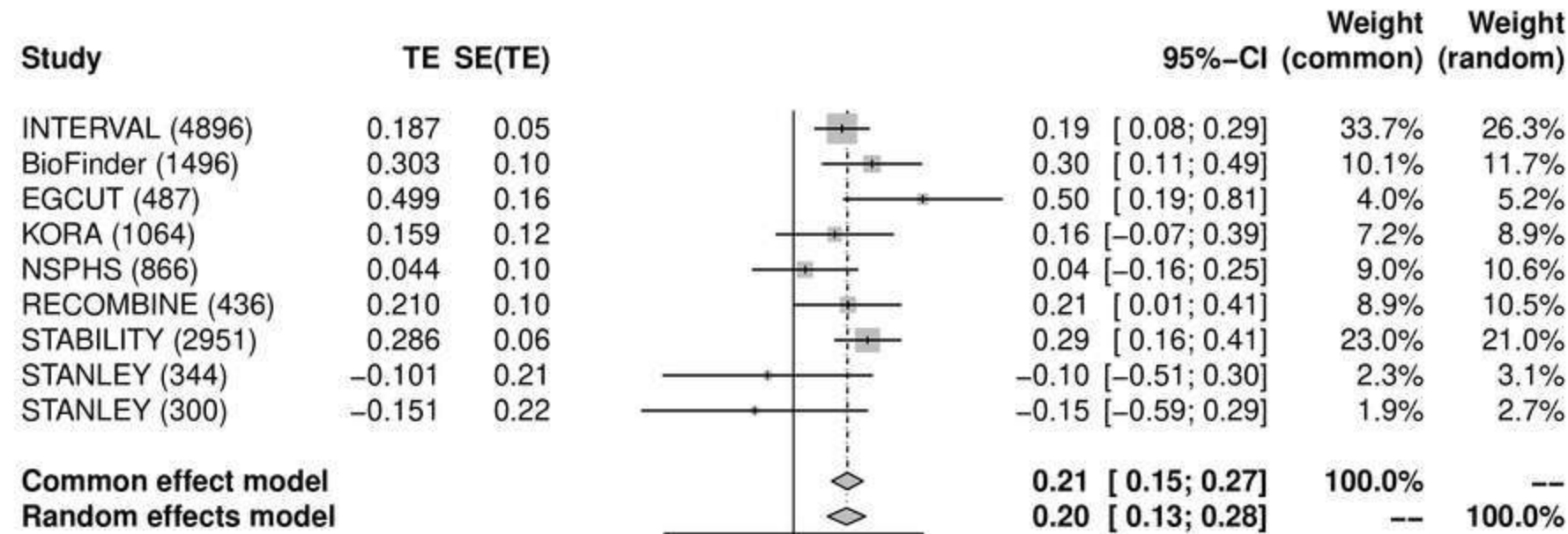


Heterogeneity: $I^2 = 56\%$, $\tau^2 = 0.0048$, $p = 0.02$

IL-10 (IL10)-rs28377109

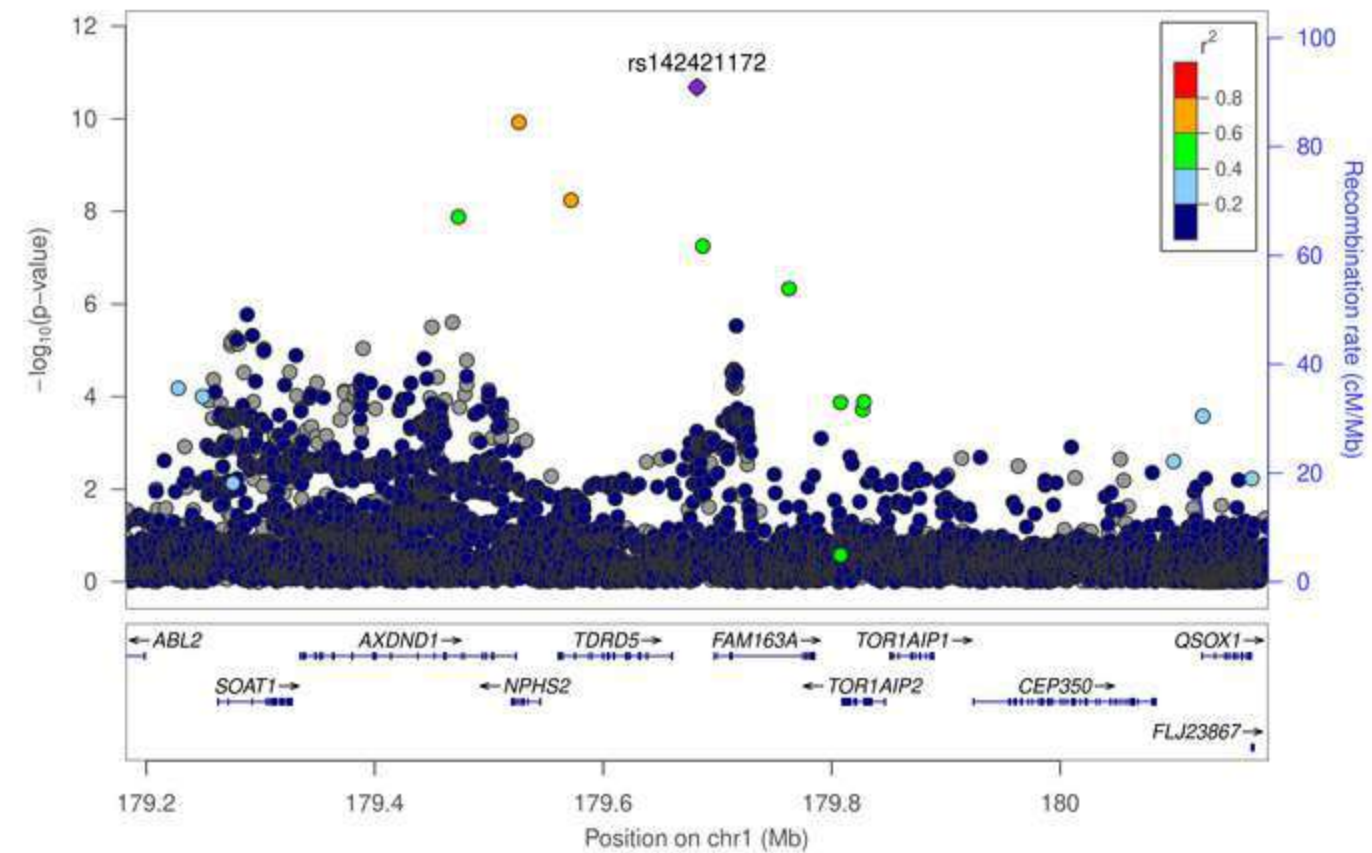


IL10RB (IL10RB) [chr1:179682087_A_G (rs142421172) (A/G) N=12840]



Heterogeneity: $I^2 = 41\%$, $\tau^2 = 0.0025$, $p = 0.09$

IL10RB (IL10RB)-rs142421172



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (981)

RECOMBINE (428)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 87\%$, $\tau^2 = 0.0086$, $p < 0.01$

IL10RB (IL10RB) [chr21:34659396_A_G (rs2266590) (A/G) N=14714]

TE SE(TE)

-0.493 0.02

-0.390 0.03

-0.533 0.06

-0.374 0.04

-0.423 0.05

-0.451 0.04

-0.143 0.04

-0.375 0.03

-0.377 0.06

-0.373 0.08

-0.405 0.05

SE(TE)

0.02

0.03

0.06

0.04

0.05

0.04

0.04

0.03

0.06

0.08

0.05

0.02

0.03

-0.6 -0.4 -0.2 0 0.2 0.4 0.6

95%-CI (common) (random)

-0.49 [-0.53; -0.46]

-0.39 [-0.46; -0.32]

-0.53 [-0.64; -0.42]

-0.37 [-0.46; -0.29]

-0.42 [-0.52; -0.33]

-0.45 [-0.53; -0.37]

-0.14 [-0.22; -0.07]

-0.38 [-0.42; -0.33]

-0.38 [-0.50; -0.25]

-0.37 [-0.53; -0.22]

-0.41 [-0.50; -0.32]

-0.41 [-0.43; -0.39]

-0.39 [-0.45; -0.33]

Weight

Weight

31.7%

9.7%

3.6%

6.7%

4.7%

6.7%

7.8%

18.6%

3.0%

1.9%

5.5%

100.0%

--

Weight

Weight

10.8%

9.9%

8.2%

9.4%

8.8%

9.4%

9.6%

10.5%

7.8%

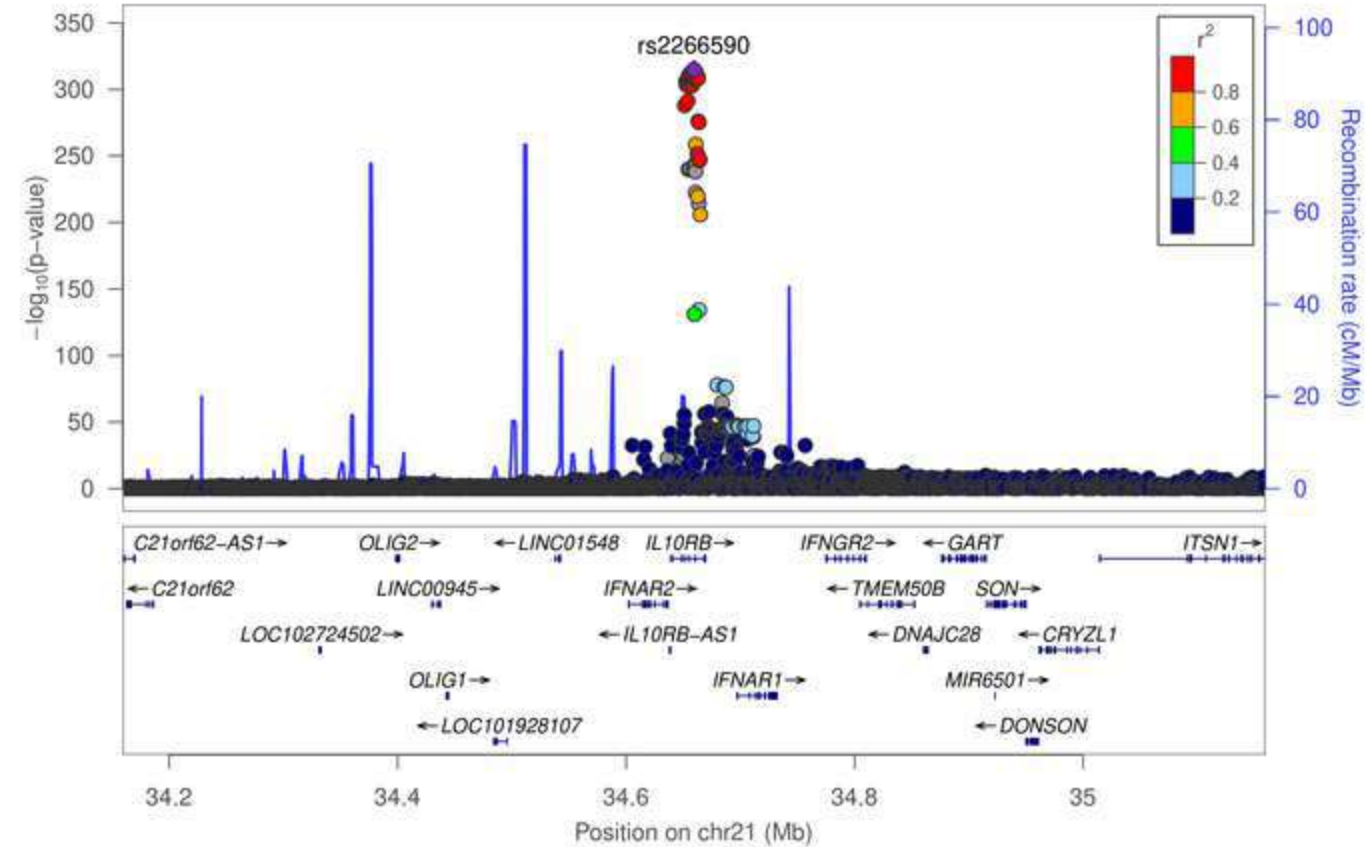
6.5%

9.1%

--

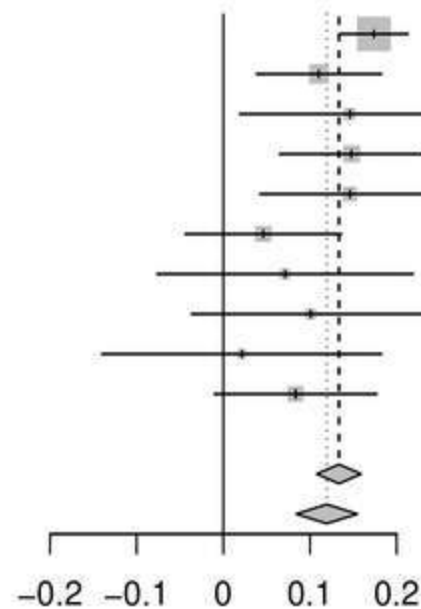
100.0%

IL10RB (IL10RB)-rs2266590



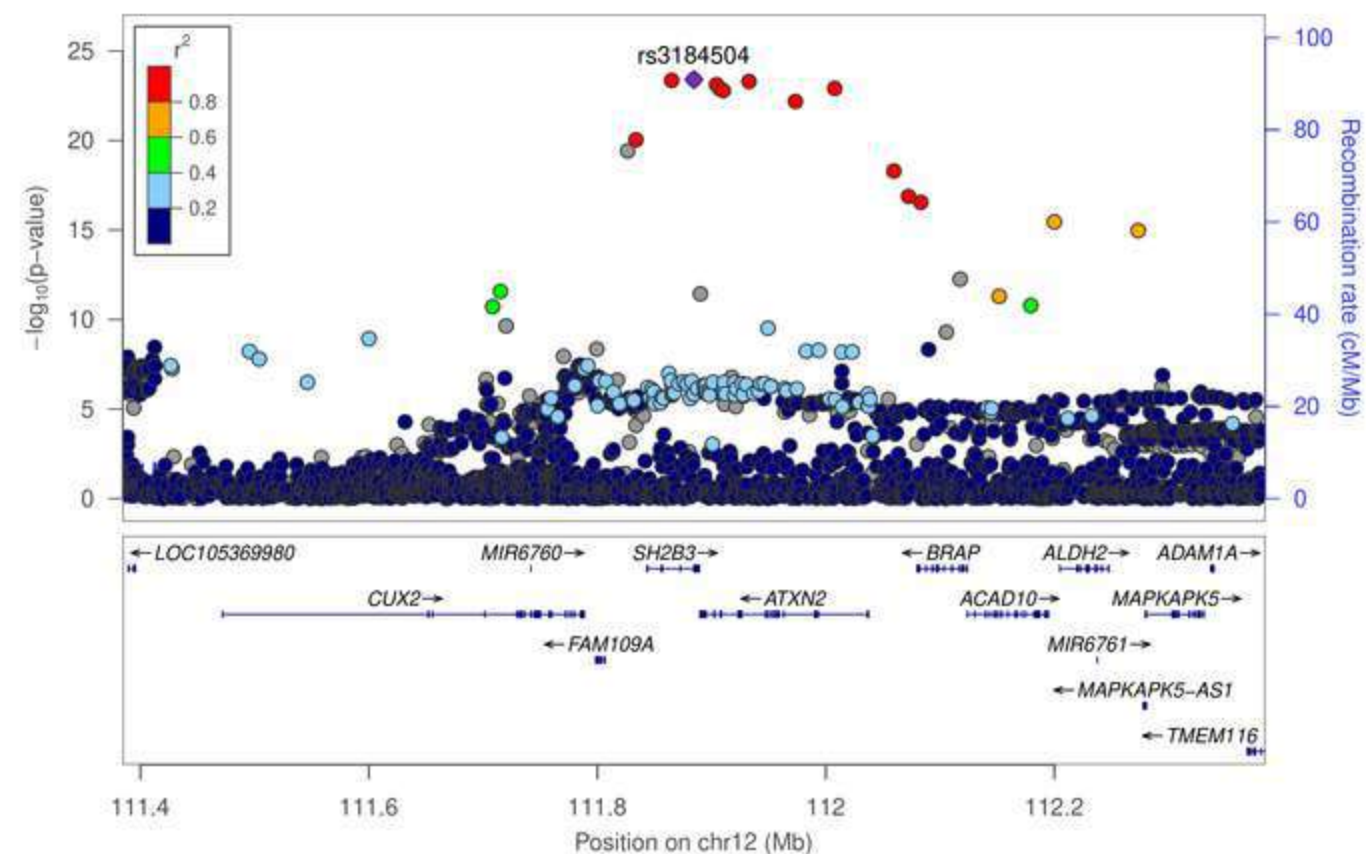
IL-12B (IL12B) [chr12:111884608_C_T (rs3184504) (T/C) N=11785]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.173	0.02	0.17 [0.13; 0.21]	42.4%
BioFinder (1496)	0.110	0.04	0.11 [0.04; 0.18]	12.8%
EGCUT (487)	0.146	0.06	0.15 [0.02; 0.27]	4.1%
KORA (1064)	0.148	0.04	0.15 [0.06; 0.23]	9.6%
NSPHS (866)	0.146	0.05	0.15 [0.04; 0.25]	6.2%
ORCADES (982)	0.046	0.05	0.05 [-0.04; 0.14]	8.2%
RECOMBINE (448)	0.071	0.08	0.07 [-0.08; 0.22]	3.0%
STANLEY (344)	0.101	0.07	0.10 [-0.04; 0.24]	3.5%
STANLEY (300)	0.021	0.08	0.02 [-0.14; 0.18]	2.5%
VIS (902)	0.083	0.05	0.08 [-0.01; 0.18]	7.6%
Common effect model			0.13 [0.11; 0.16]	100.0%
Random effects model			0.12 [0.08; 0.15]	-- 100.0%

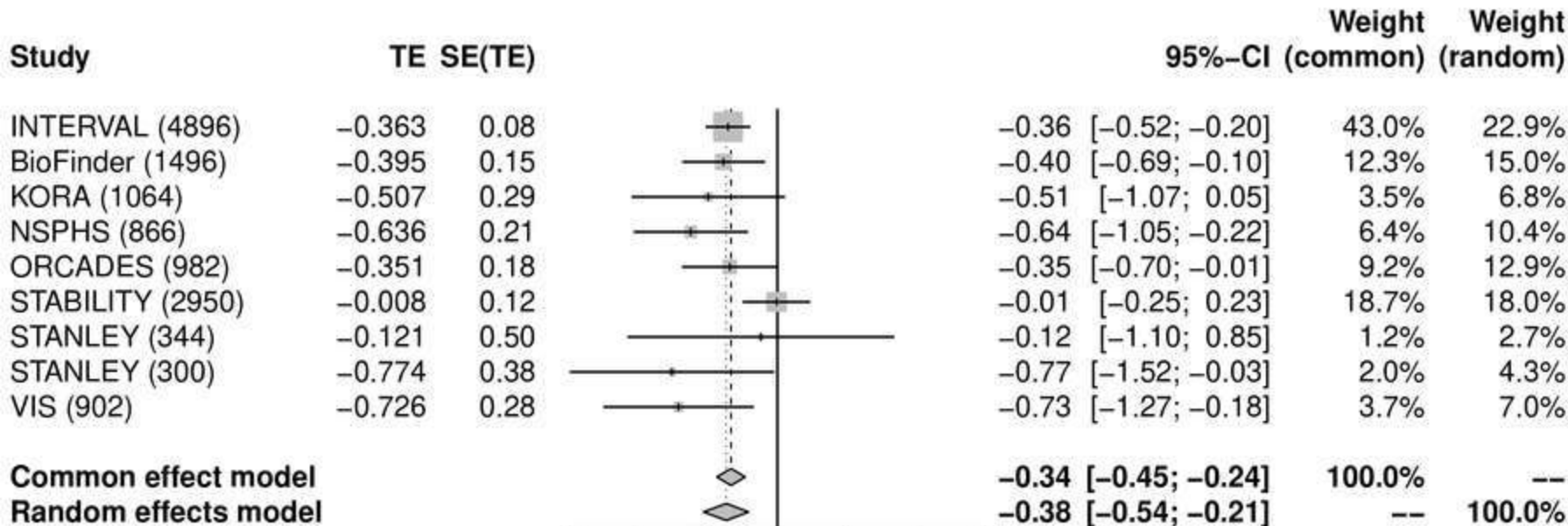


Heterogeneity: $I^2 = 25\%$, $\tau^2 = 0.0010$, $p = 0.21$

IL-12B (IL12B)-rs3184504

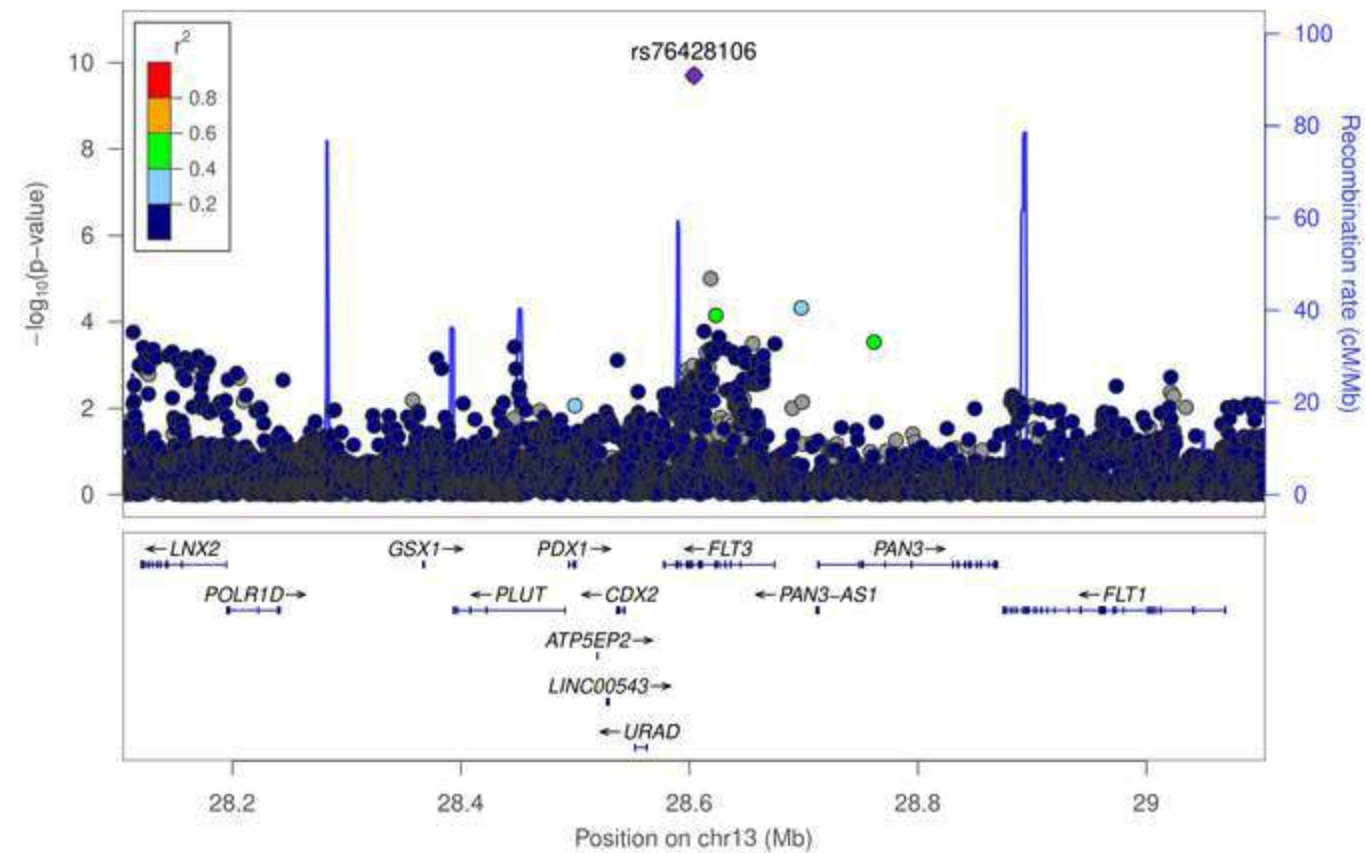


IL-12B (IL12B) [chr13:28604007_C_T (rs76428106) (T/C) N=13800]

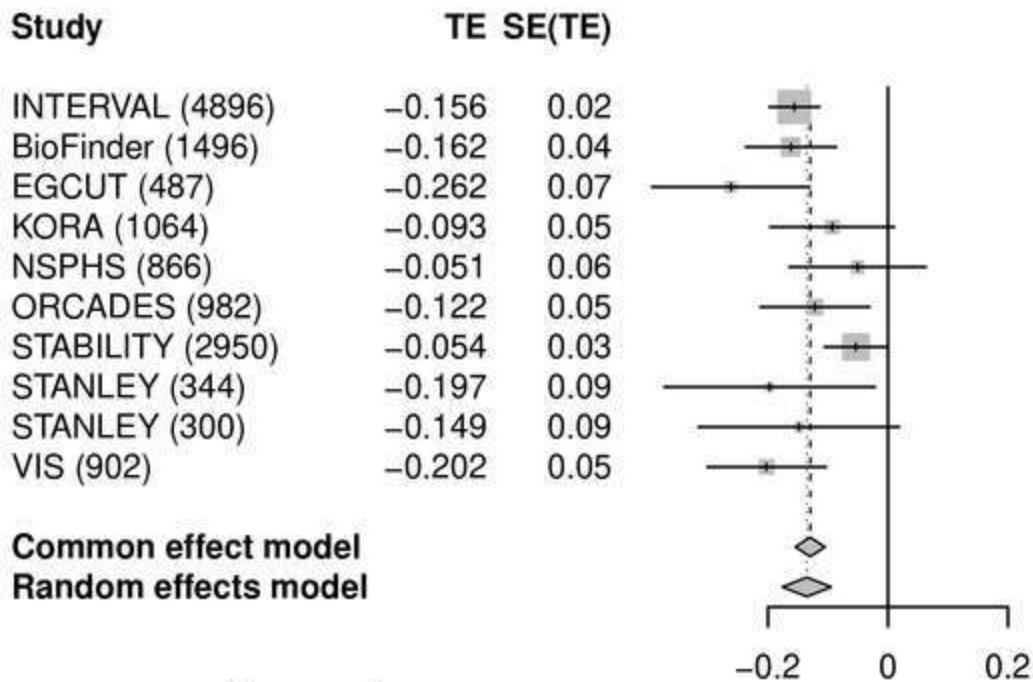


Heterogeneity: $I^2 = 39\%$, $\tau^2 = 0.0249$, $p = 0.11$

IL-12B (IL12B)-rs76428106



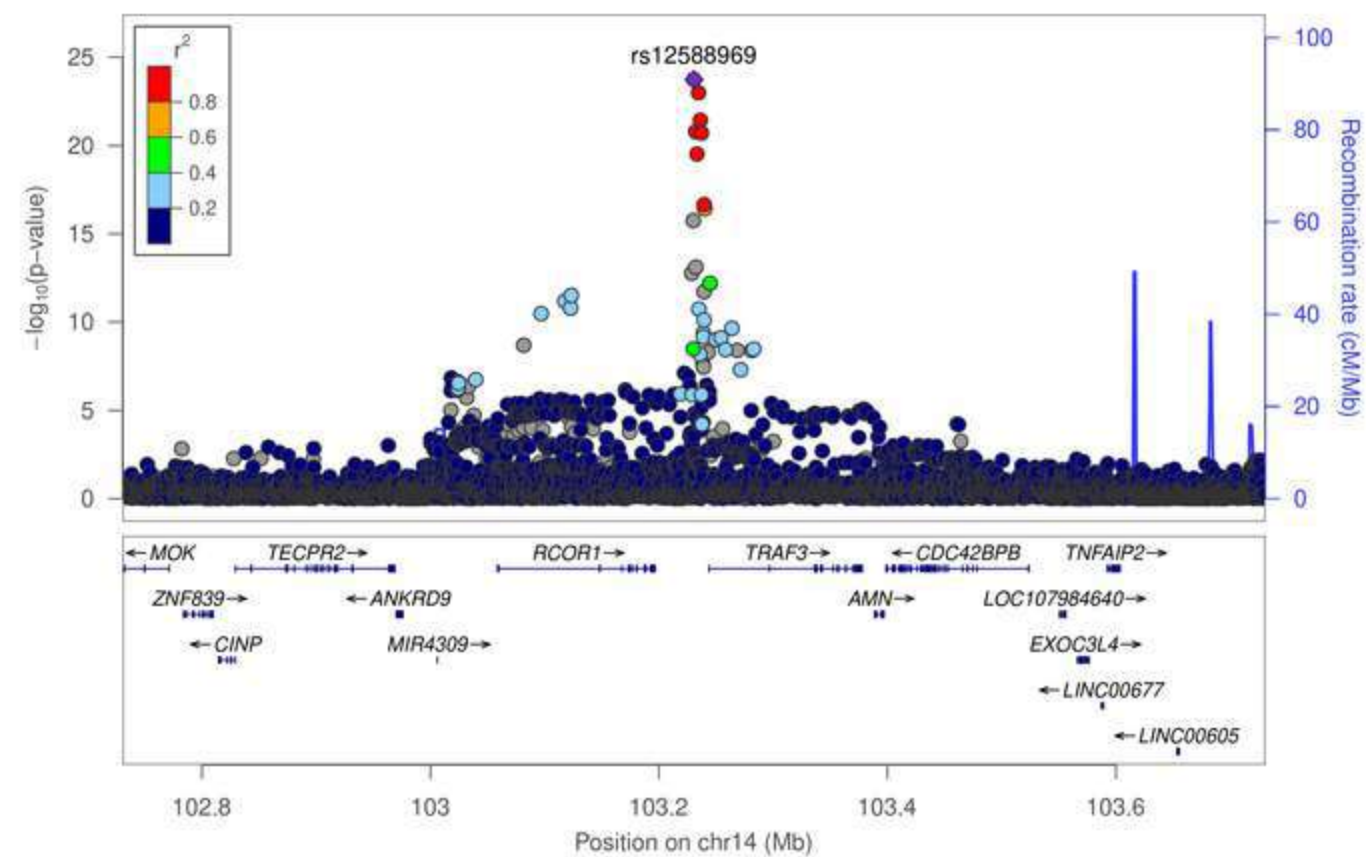
IL-12B (IL12B) [chr14:103230758_C_G (rs12588969) (C/G) N=14287]



Heterogeneity: $I^2 = 53\%$, $\tau^2 = 0.0020$, $p = 0.02$

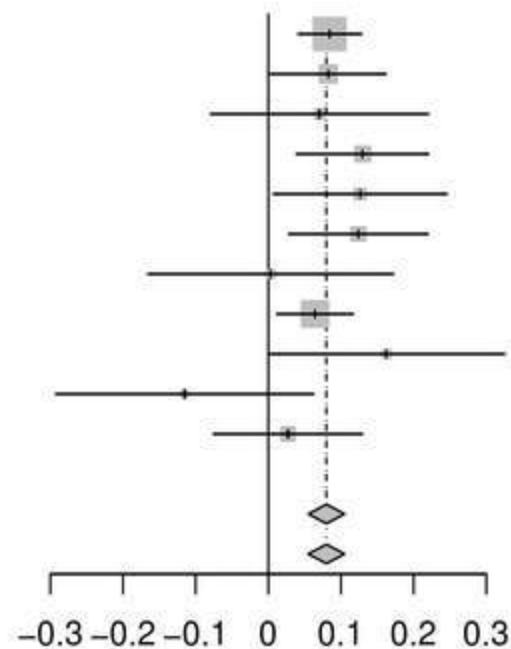
		Weight	Weight
	95%-CI	(common)	(random)
-0.16	[-0.20; -0.11]	34.6%	17.9%
-0.16	[-0.24; -0.09]	10.8%	12.6%
-0.26	[-0.39; -0.13]	3.6%	6.7%
-0.09	[-0.20; 0.01]	5.8%	9.1%
-0.05	[-0.16; 0.06]	4.8%	8.1%
-0.12	[-0.21; -0.03]	7.4%	10.5%
-0.05	[-0.11; -0.00]	22.6%	16.2%
-0.20	[-0.37; -0.02]	2.0%	4.4%
-0.15	[-0.32; 0.02]	2.2%	4.7%
-0.20	[-0.30; -0.10]	6.3%	9.6%
-0.13	[-0.15; -0.10]	100.0%	--
-0.14	[-0.18; -0.09]	--	100.0%

IL-12B (IL12B)-rs12588969



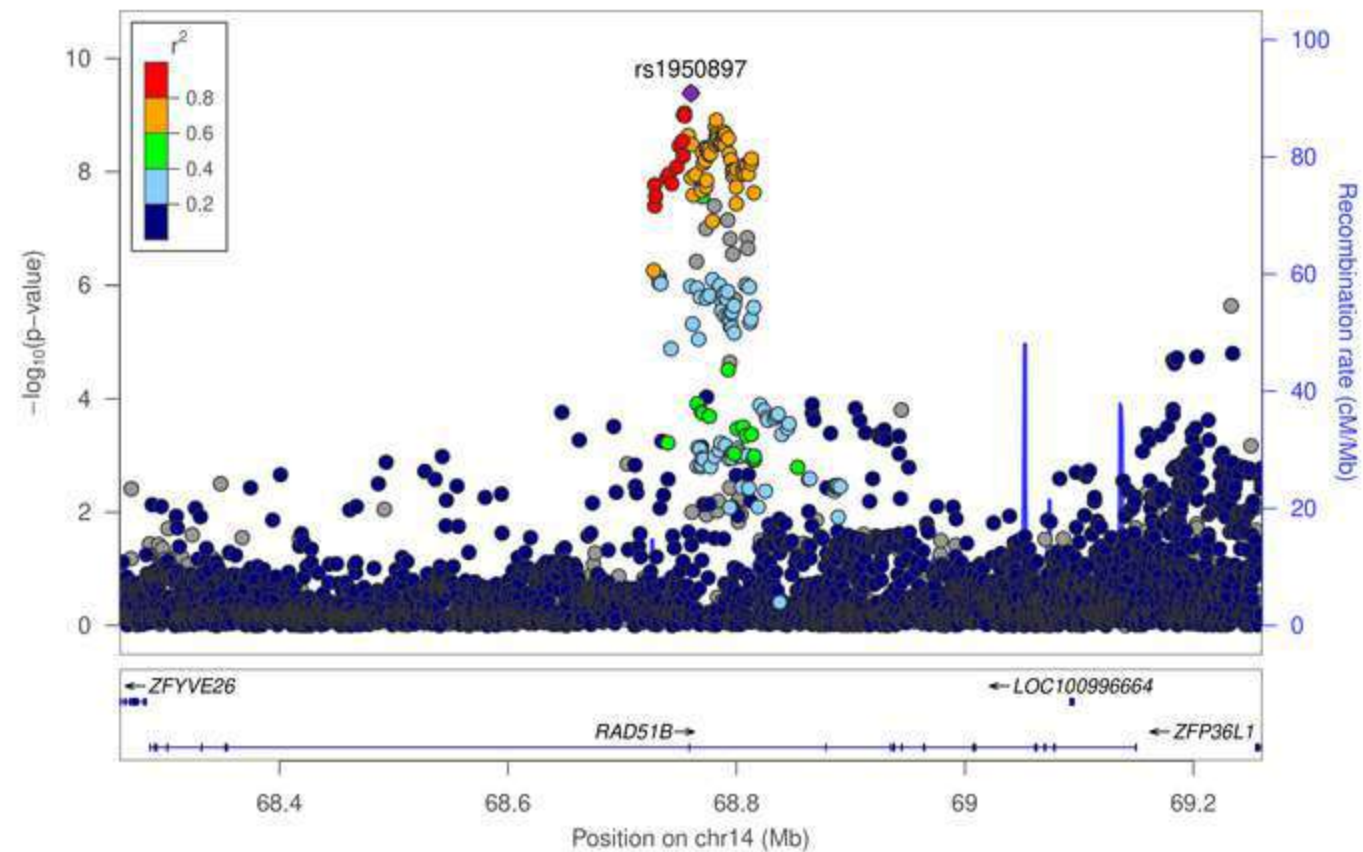
IL-12B (IL12B) [chr14:68760141_C_T (rs1950897) (T/C) N=14735]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight Weight (random)
INTERVAL (4896)	0.085	0.02	0.08 [0.04; 0.13]	33.4%
BioFinder (1496)	0.082	0.04	0.08 [0.00; 0.16]	9.9%
EGCUT (487)	0.070	0.08	0.07 [-0.08; 0.22]	2.8%
KORA (1064)	0.129	0.05	0.13 [0.04; 0.22]	7.6%
NSPHS (866)	0.126	0.06	0.13 [0.01; 0.25]	4.4%
ORCADES (982)	0.124	0.05	0.12 [0.03; 0.22]	6.8%
RECOMBINE (448)	0.003	0.09	0.00 [-0.17; 0.17]	2.2%
STABILITY (2950)	0.064	0.03	0.06 [0.01; 0.12]	22.7%
STANLEY (344)	0.162	0.08	0.16 [-0.00; 0.33]	2.4%
STANLEY (300)	-0.115	0.09	-0.12 [-0.29; 0.06]	2.0%
VIS (902)	0.027	0.05	0.03 [-0.08; 0.13]	6.0%
Common effect model			0.08 [0.05; 0.10]	100.0%
Random effects model			0.08 [0.05; 0.10]	100.0%



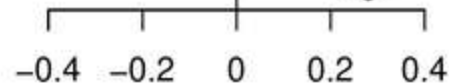
Heterogeneity: $I^2 = 4\%$, $\tau^2 < 0.0001$, $p = 0.41$

IL-12B (IL12B)-rs1950897



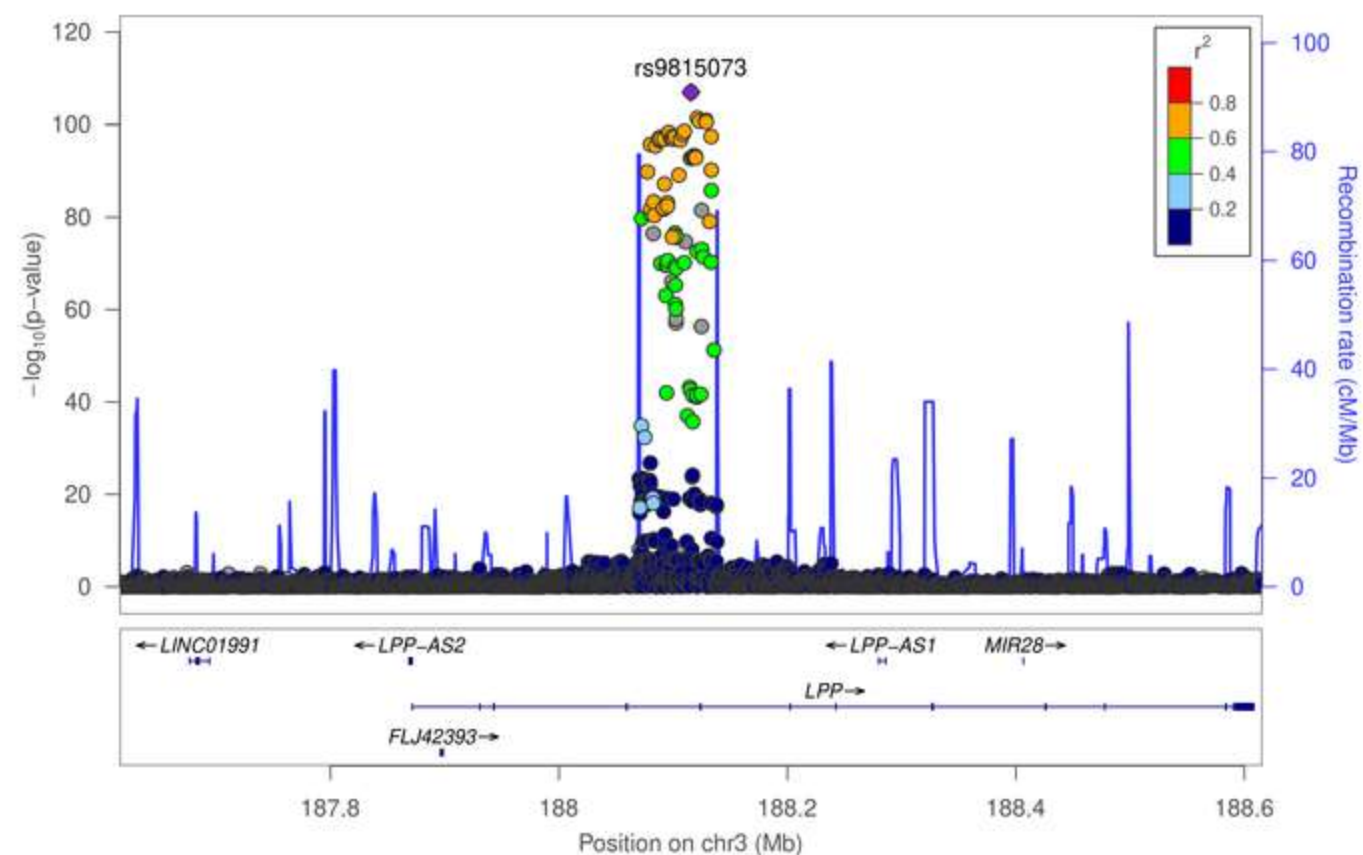
IL-12B (IL12B) [chr3:188115682_A_C (rs9815073) (A/C) N=14287]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.347	0.02	0.35 [0.30; 0.39]	33.9%	17.7%
BioFinder (1496)	0.240	0.04	0.24 [0.17; 0.31]	12.0%	13.0%
EGCUT (487)	0.364	0.07	0.36 [0.23; 0.50]	3.4%	6.4%
KORA (1064)	0.311	0.05	0.31 [0.22; 0.40]	7.3%	10.3%
NSPHS (866)	0.360	0.06	0.36 [0.24; 0.48]	4.8%	8.1%
ORCADES (982)	0.257	0.05	0.26 [0.16; 0.35]	7.2%	10.3%
STABILITY (2950)	0.210	0.03	0.21 [0.15; 0.27]	21.0%	15.8%
STANLEY (344)	0.249	0.09	0.25 [0.07; 0.43]	2.1%	4.4%
STANLEY (300)	0.210	0.09	0.21 [0.04; 0.38]	2.1%	4.5%
VIS (902)	0.247	0.05	0.25 [0.15; 0.35]	6.3%	9.5%
Common effect model			0.29 [0.26; 0.31]	100.0%	--
Random effects model			0.28 [0.24; 0.32]	--	100.0%



Heterogeneity: $I^2 = 57\%$, $\tau^2 = 0.0021$, $p = 0.01$

IL-12B (IL12B)-rs9815073



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (446)

STABILITY (2950)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

IL-12B (IL12B) [chr3:5026008_A_G (rs11130215) (A/G) N=14733]

TE SE(TE)

-0.141 0.03

-0.008 0.05

-0.008 0.08

-0.215 0.07

-0.087 0.06

-0.030 0.06

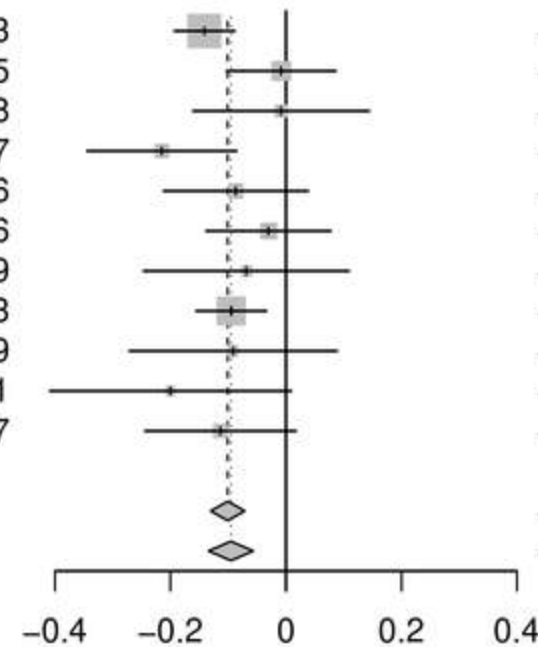
-0.069 0.09

-0.095 0.03

-0.091 0.09

-0.200 0.11

-0.114 0.07

Weight
95%-CI (common) (random)

-0.14 [-0.19; -0.09] 31.8% 21.5%

-0.01 [-0.10; 0.09] 9.8% 11.4%

-0.01 [-0.16; 0.14] 3.8% 5.5%

-0.21 [-0.34; -0.09] 5.2% 7.1%

-0.09 [-0.21; 0.04] 5.6% 7.6%

-0.03 [-0.14; 0.08] 7.5% 9.4%

-0.07 [-0.25; 0.11] 2.8% 4.2%

-0.09 [-0.16; -0.03] 23.7% 18.9%

-0.09 [-0.27; 0.09] 2.7% 4.1%

-0.20 [-0.41; 0.01] 2.0% 3.1%

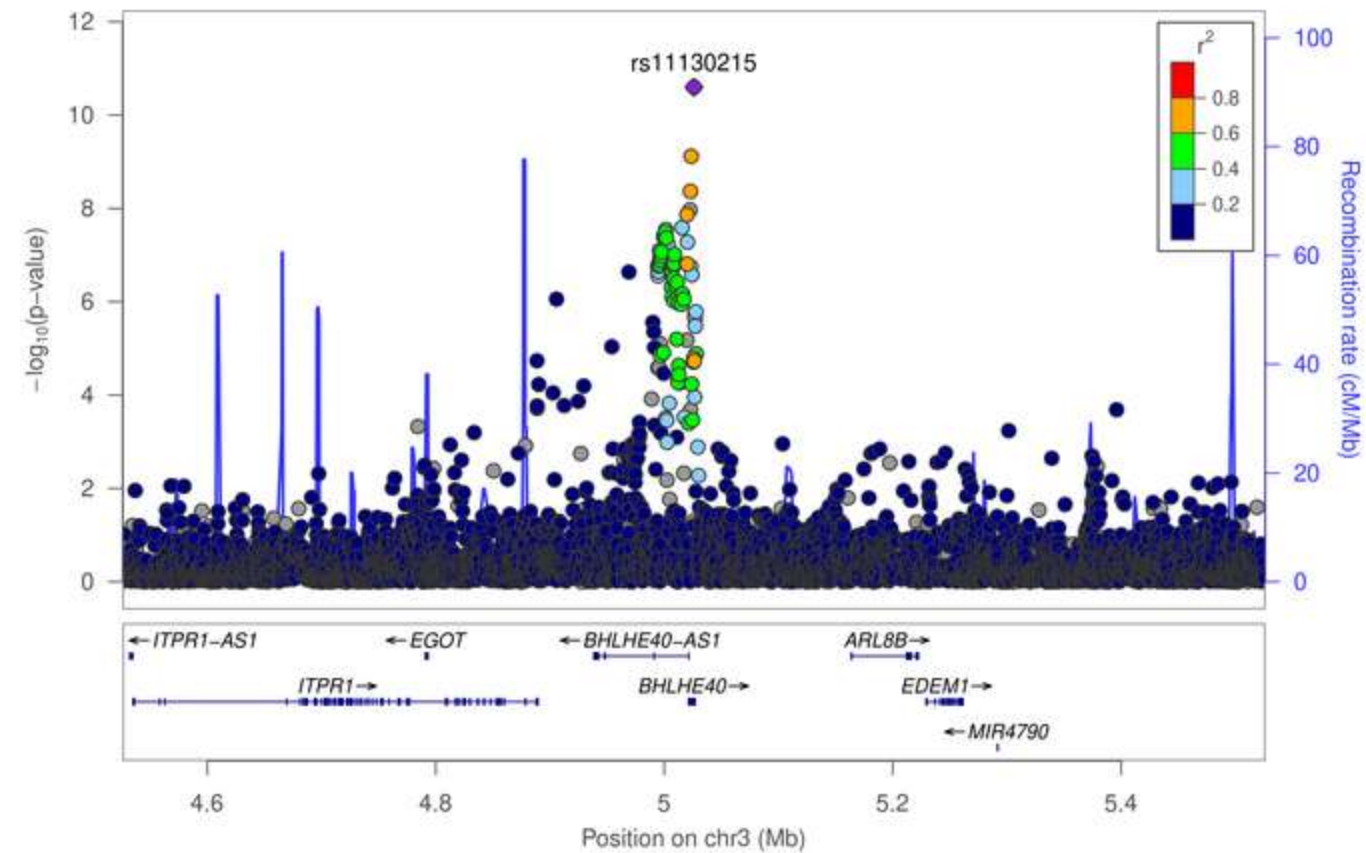
-0.11 [-0.24; 0.02] 5.1% 7.1%

-0.10 [-0.13; -0.07] 100.0% --

-0.10 [-0.13; -0.06] -- 100.0%

Heterogeneity: $I^2 = 23\%$, $\tau^2 = 0.0011$, $p = 0.22$

IL-12B (IL12B)-rs11130215



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (433)

STABILITY (2950)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 78\%$, $\tau^2 = 0.0038$, $p < 0.01$

IL-12B (IL12B) [chr5:158792819_C_G (rs10076557) (C/G) N=14720]

TE SE(TE)

-0.582 0.02

-0.447 0.04

-0.451 0.07

-0.508 0.04

-0.524 0.06

-0.470 0.05

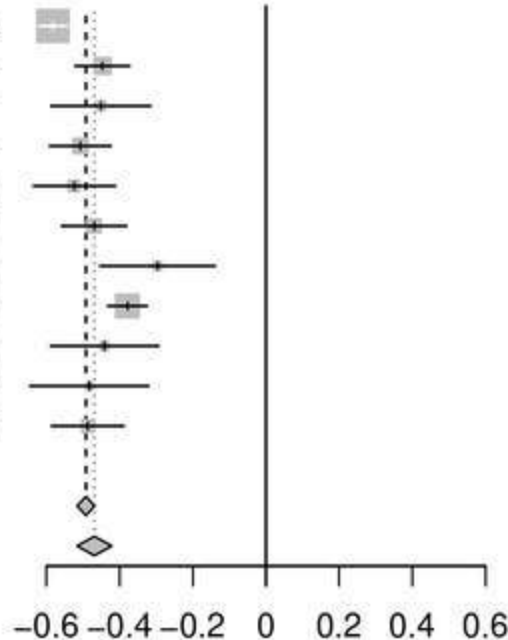
-0.296 0.08

-0.379 0.03

-0.441 0.08

-0.483 0.08

-0.487 0.05

Weight
95%-CI (common) (random)

-0.58 [-0.62; -0.54] 36.0% 13.9%

-0.45 [-0.52; -0.37] 10.0% 11.2%

-0.45 [-0.59; -0.31] 3.0% 6.8%

-0.51 [-0.59; -0.42] 7.8% 10.4%

-0.52 [-0.64; -0.41] 4.5% 8.3%

-0.47 [-0.56; -0.38] 7.0% 10.0%

-0.30 [-0.45; -0.14] 2.3% 5.7%

-0.38 [-0.43; -0.32] 19.1% 12.8%

-0.44 [-0.59; -0.29] 2.6% 6.2%

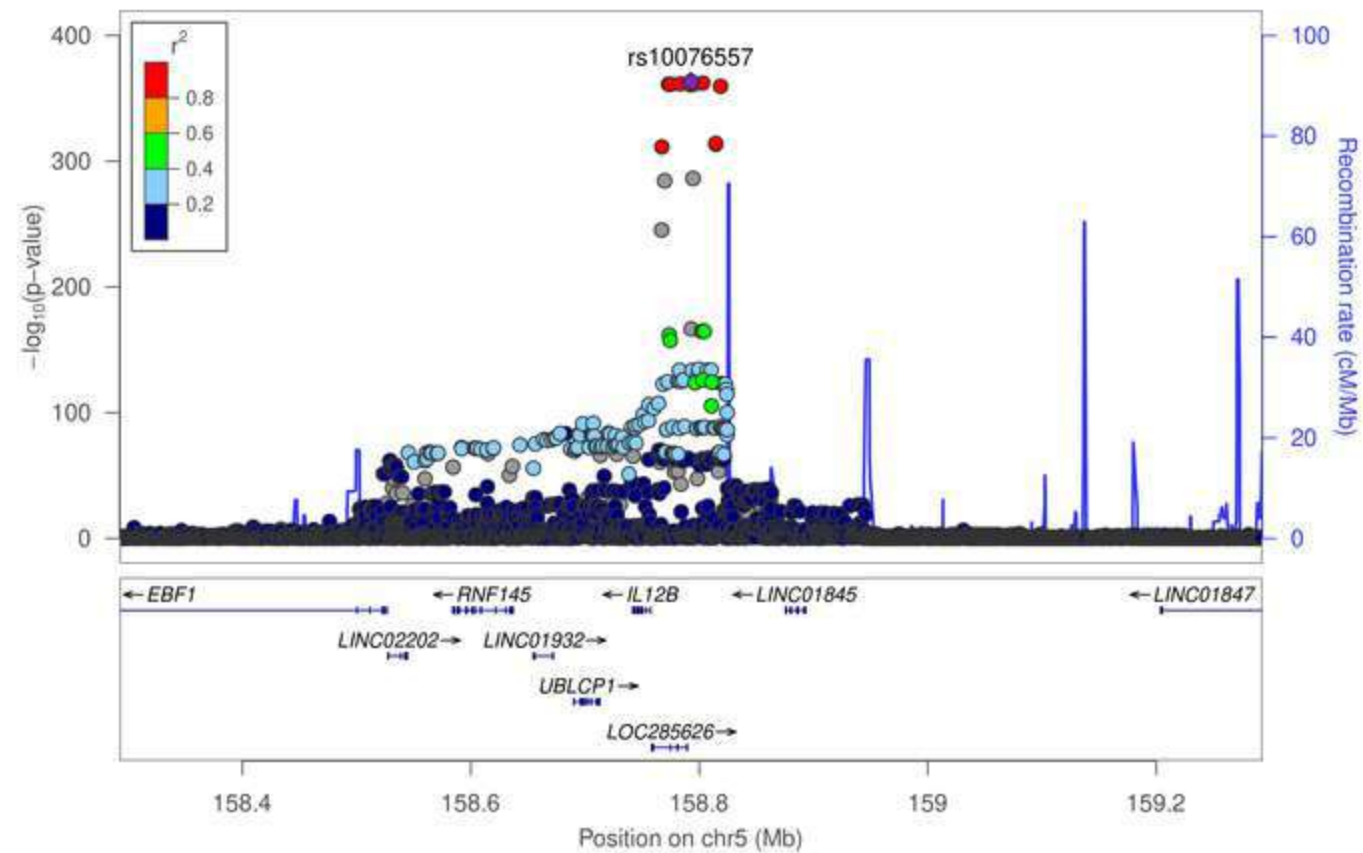
-0.48 [-0.65; -0.32] 2.1% 5.5%

-0.49 [-0.59; -0.39] 5.7% 9.2%

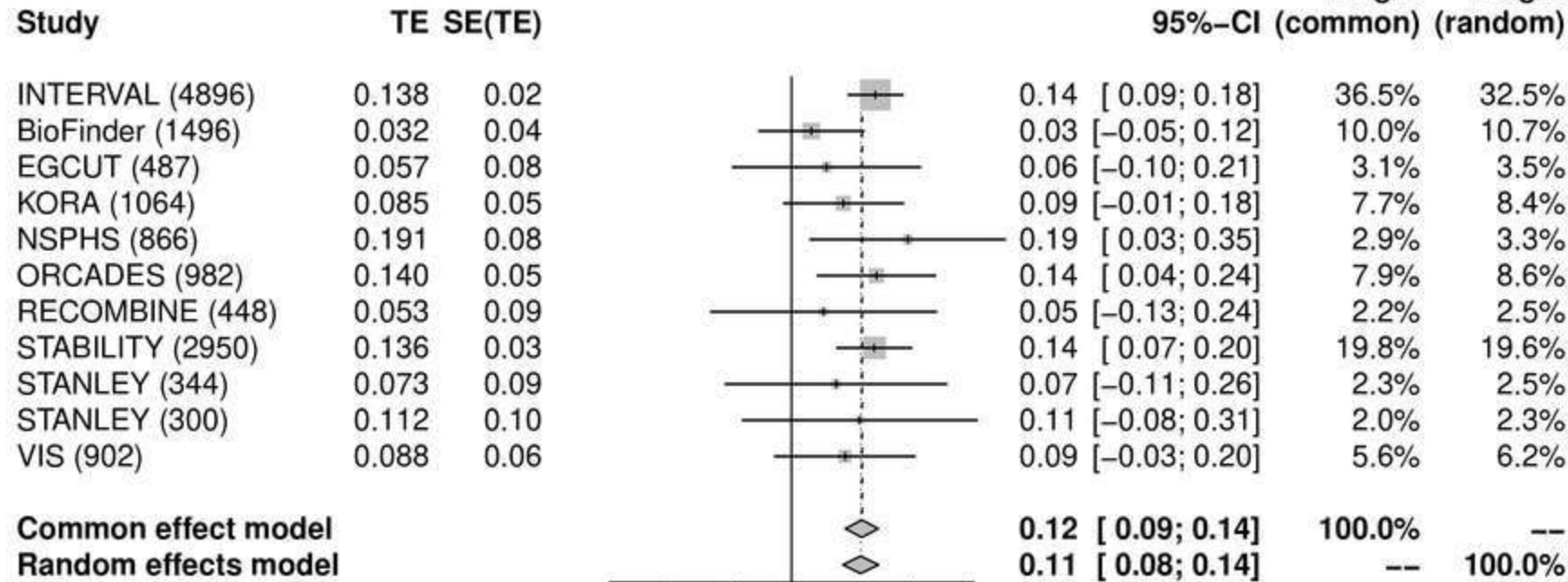
-0.49 [-0.52; -0.47] 100.0% --

-0.47 [-0.52; -0.42] -- 100.0%

IL-12B (IL12B)-rs10076557

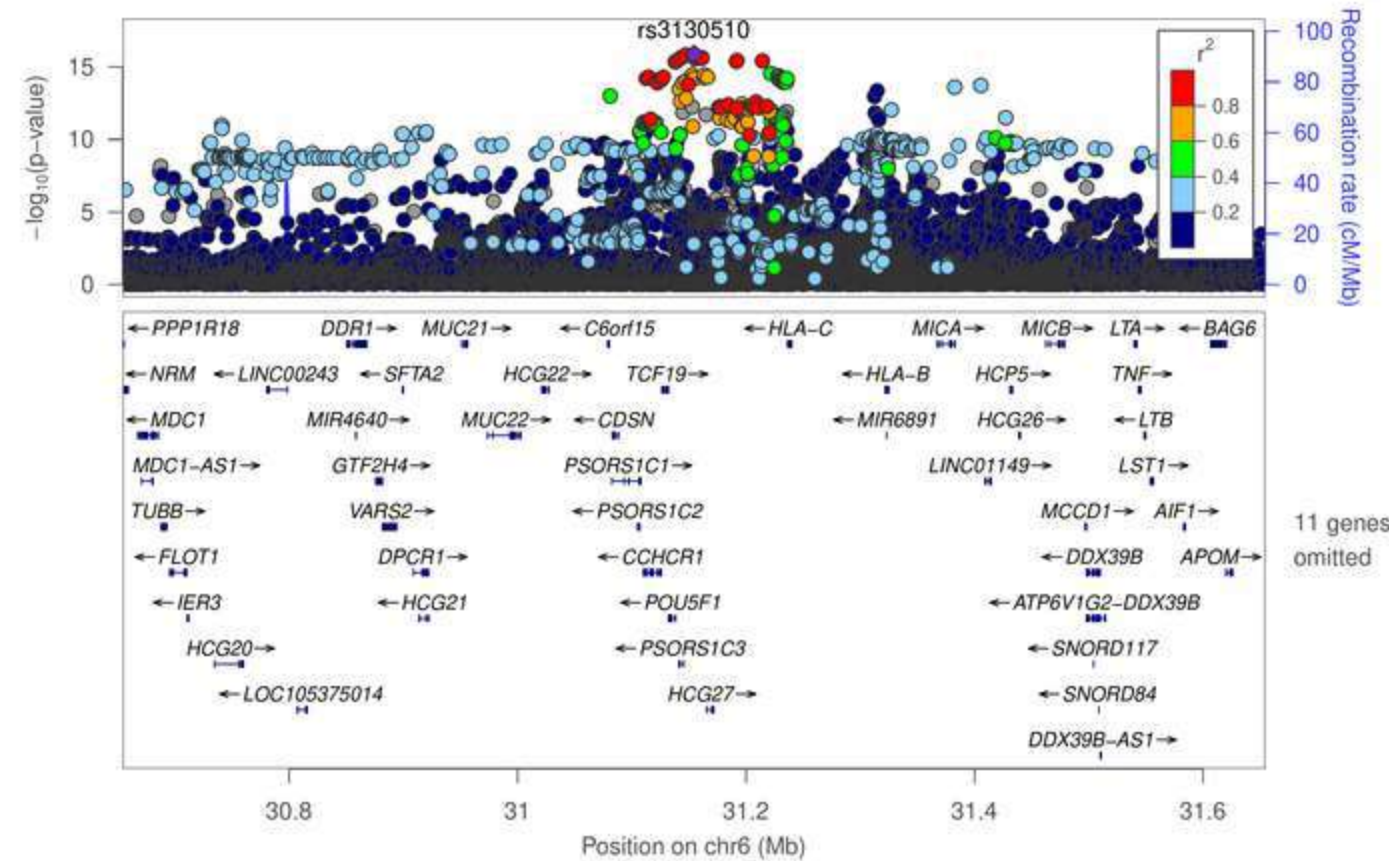


IL-12B (IL12B) [chr6:31154493_A_G (rs3130510) (A/G) N=14735]

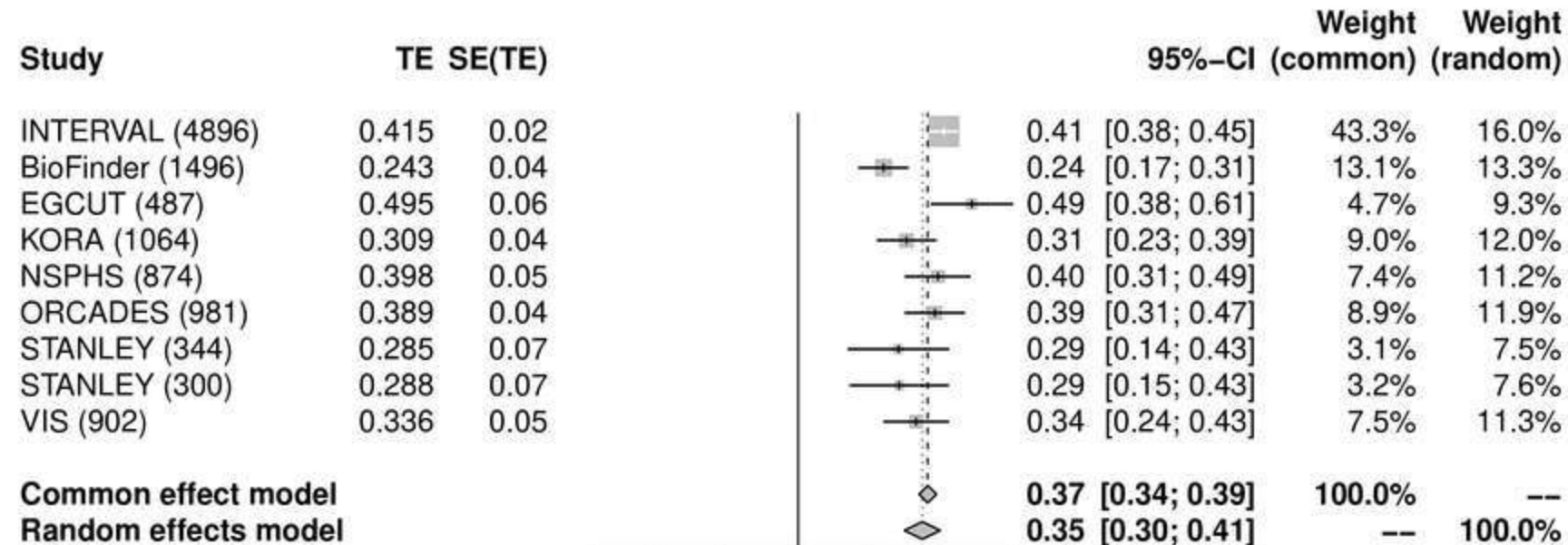


Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0.0002$, $p = 0.65$

IL-12B (IL12B)-rs3130510

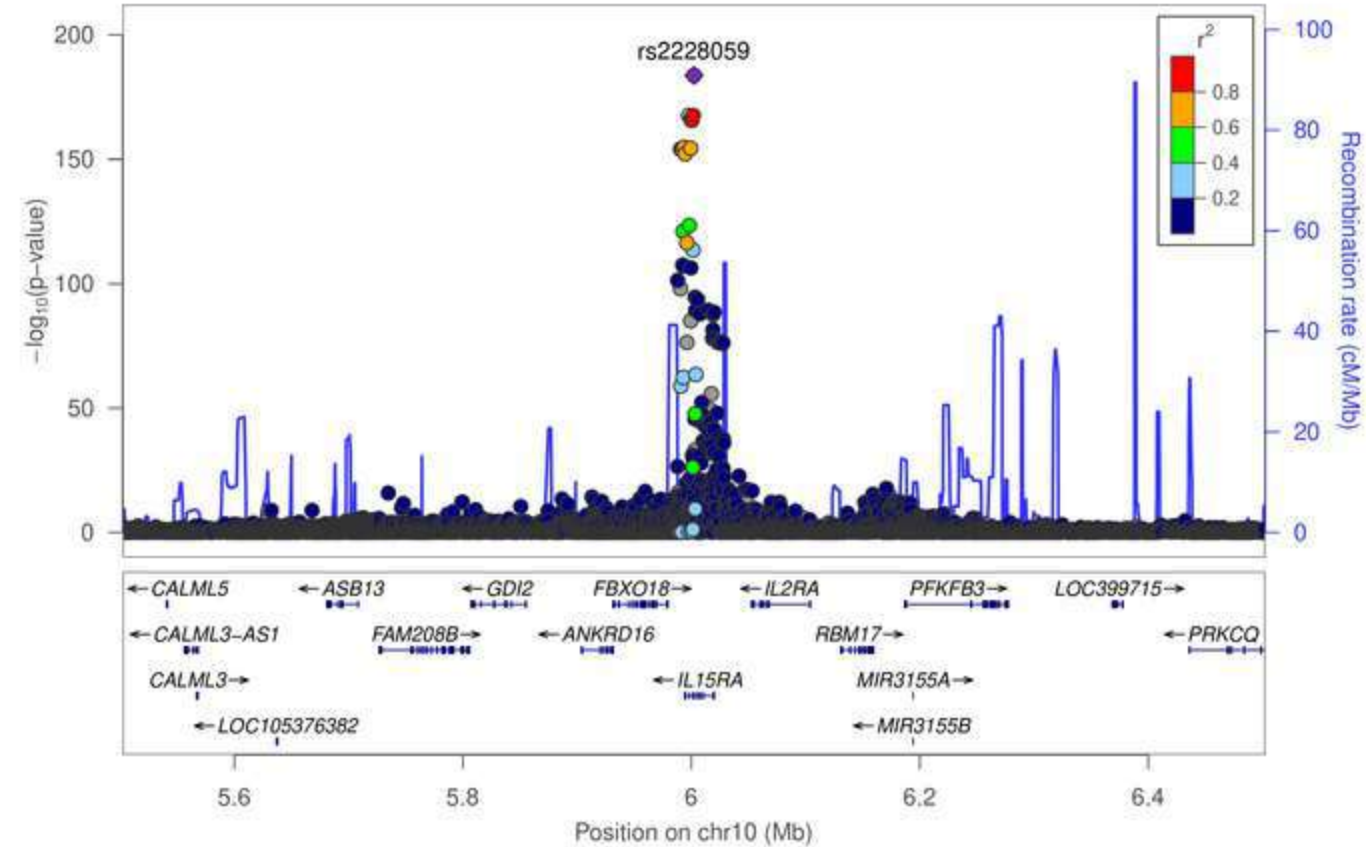


IL-15RA (IL15RA) [chr10:6002368_G_T (rs2228059) (T/G) N=11344]

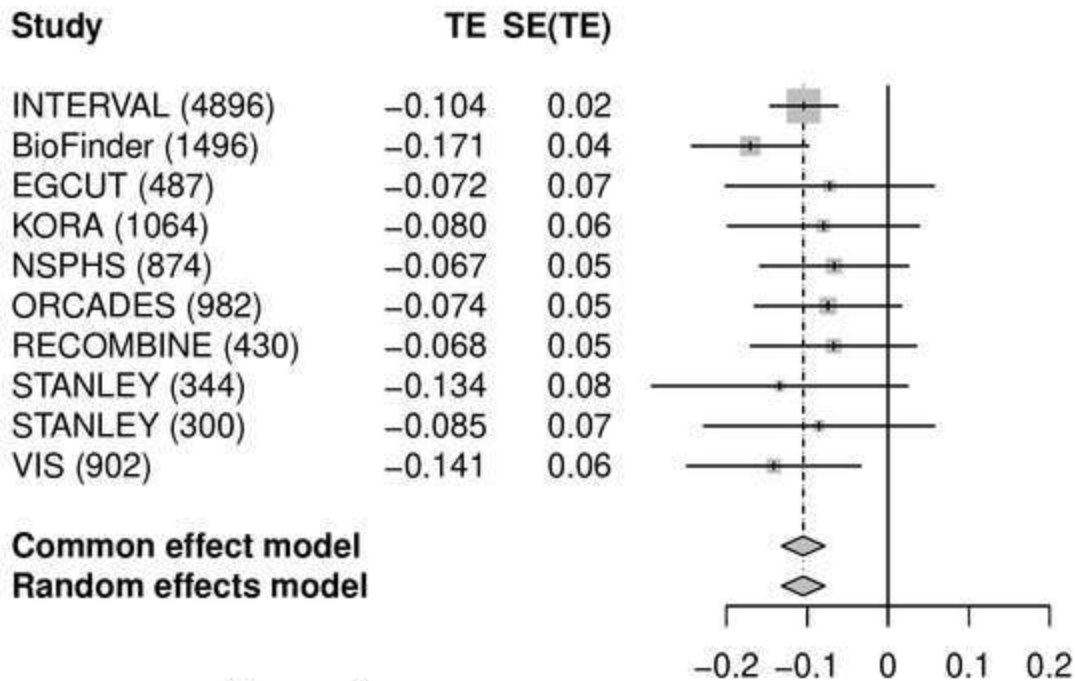


Heterogeneity: $I^2 = 72\%$, $\tau^2 = 0.0039$, $p < 0.01$

IL-15RA (IL15RA)-rs2228059



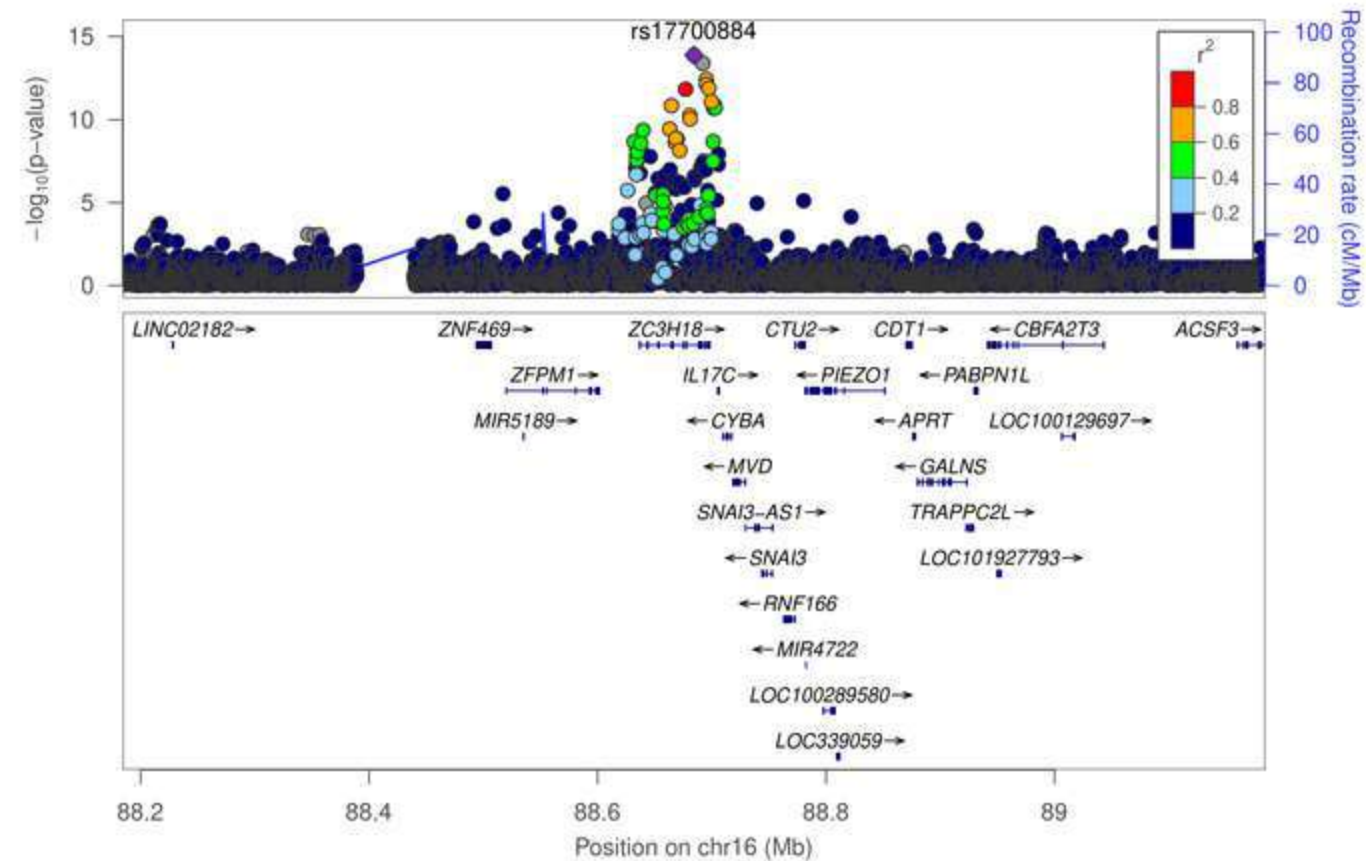
IL-17C (IL17C) [chr16:88684495_G_T (rs17700884) (T/G) N=11775]



Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.75$

		Weight	Weight
	95%-CI	(common)	(random)
-0.10	[-0.15; -0.06]	40.8%	40.8%
-0.17	[-0.24; -0.10]	13.7%	13.7%
-0.07	[-0.20; 0.06]	4.3%	4.3%
-0.08	[-0.20; 0.04]	5.1%	5.1%
-0.07	[-0.16; 0.03]	8.4%	8.4%
-0.07	[-0.17; 0.02]	8.6%	8.6%
-0.07	[-0.17; 0.04]	6.8%	6.8%
-0.13	[-0.29; 0.02]	2.8%	2.8%
-0.09	[-0.23; 0.06]	3.5%	3.5%
-0.14	[-0.25; -0.03]	6.1%	6.1%
-0.10	[-0.13; -0.08]	100.0%	--
-0.10	[-0.13; -0.08]	--	100.0%

IL-17C (IL17C)-rs17700884



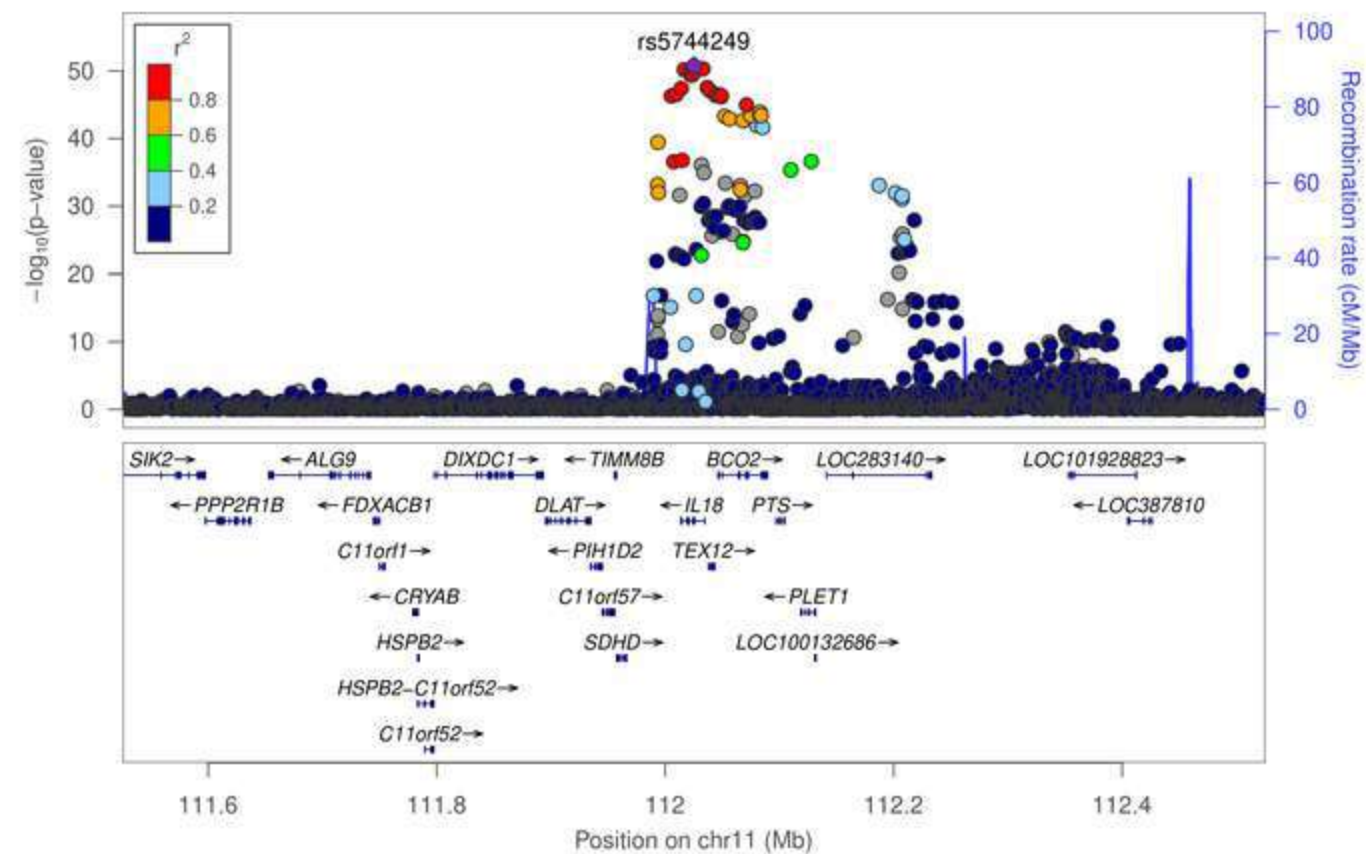
IL-18 (IL18) [chr11:112025306_A_C (rs5744249) (A/C) N=14742]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.104	0.02	0.10 [0.06; 0.15]	33.1%
BioFinder (1496)	0.334	0.04	0.33 [0.25; 0.42]	10.5%
EGCUT (487)	0.264	0.07	0.26 [0.12; 0.40]	3.5%
KORA (1064)	0.247	0.05	0.25 [0.15; 0.34]	7.6%
NSPHS (874)	0.283	0.06	0.28 [0.17; 0.40]	5.3%
ORCADES (982)	0.296	0.05	0.30 [0.20; 0.40]	7.0%
RECOMBINE (446)	0.156	0.07	0.16 [0.02; 0.29]	4.0%
STABILITY (2951)	0.242	0.03	0.24 [0.18; 0.30]	19.3%
STANLEY (344)	0.178	0.09	0.18 [-0.01; 0.36]	2.0%
STANLEY (300)	0.052	0.09	0.05 [-0.12; 0.22]	2.5%
VIS (902)	0.243	0.06	0.24 [0.13; 0.36]	5.1%
Common effect model			0.20 [0.18; 0.23]	100.0%
Random effects model			0.22 [0.17; 0.28]	-- 100.0%

-0.4 -0.2 0 0.2 0.4

Heterogeneity: $I^2 = 75\%$, $\tau^2 = 0.0047$, $p < 0.01$

IL-18 (IL18)-rs5744249



IL-18 (IL18) [chr2:32489851_C_T (rs385076) (T/C) N=14296]

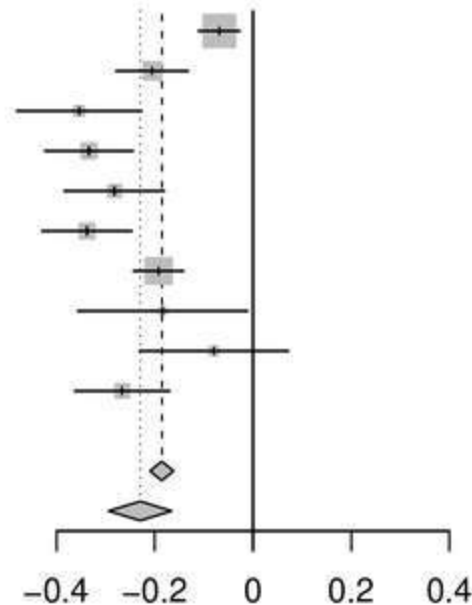
Study

TE SE(TE)

INTERVAL (4896)	-0.069	0.02
BioFinder (1496)	-0.205	0.04
EGCUT (487)	-0.353	0.06
KORA (1064)	-0.334	0.05
NSPHS (874)	-0.282	0.05
ORCADES (982)	-0.338	0.05
STABILITY (2951)	-0.192	0.03
STANLEY (344)	-0.184	0.09
STANLEY (300)	-0.079	0.08
VIS (902)	-0.266	0.05

Common effect model
Random effects model

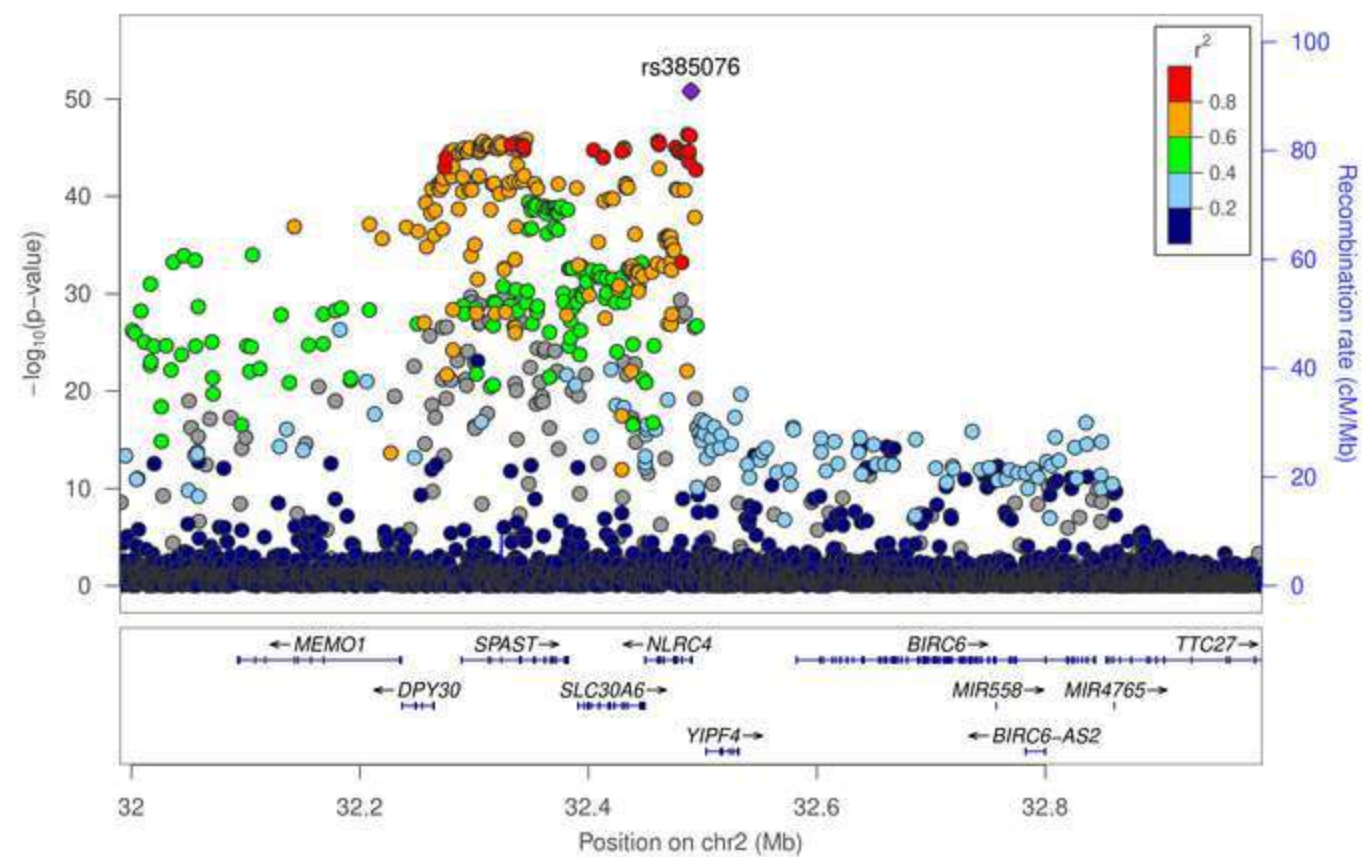
Heterogeneity: $I^2 = 86\%$, $\tau^2 = 0.0083$, $p < 0.01$



Weight Weight
95%-CI (common) (random)

-0.07	[-0.11; -0.03]	33.0%	12.5%
-0.21	[-0.28; -0.13]	10.7%	11.2%
-0.35	[-0.48; -0.23]	3.6%	8.7%
-0.33	[-0.42; -0.24]	7.2%	10.5%
-0.28	[-0.38; -0.18]	5.6%	9.9%
-0.34	[-0.43; -0.25]	6.9%	10.4%
-0.19	[-0.24; -0.14]	22.3%	12.2%
-0.18	[-0.36; -0.01]	1.9%	6.8%
-0.08	[-0.23; 0.07]	2.5%	7.6%
-0.27	[-0.36; -0.17]	6.2%	10.2%
-0.19	[-0.21; -0.16]	100.0%	--
-0.23	[-0.29; -0.17]	--	100.0%

IL-18 (IL18)-rs385076



Study

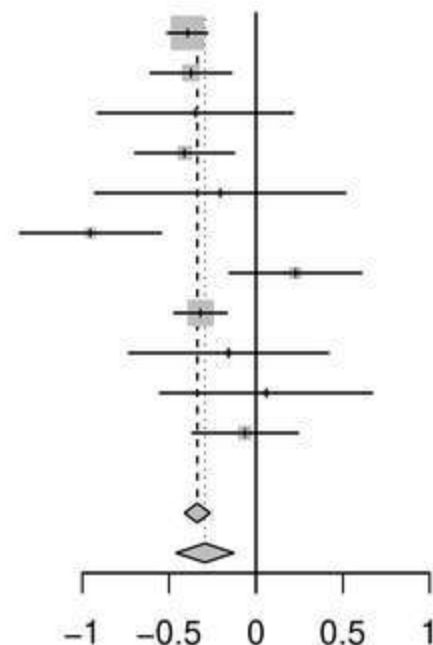
Study	TE	SE(TE)
INTERVAL (4896)	-0.395	0.06
BioFinder (1496)	-0.374	0.12
EGCUT (487)	-0.349	0.29
KORA (1064)	-0.412	0.15
NSPHS (874)	-0.206	0.37
ORCADES (982)	-0.953	0.21
RECOMBINE (448)	0.228	0.19
STABILITY (2950)	-0.320	0.08
STANLEY (344)	-0.158	0.29
STANLEY (300)	0.058	0.31
VIS (902)	-0.063	0.16

Common effect model
Random effects model

Heterogeneity: $I^2 = 58\%$, $\tau^2 = 0.0452$, $p < 0.01$

IL-18R1 (IL18R1) [chr17:64305051_A_G (rs78357146) (A/G) N=14743]

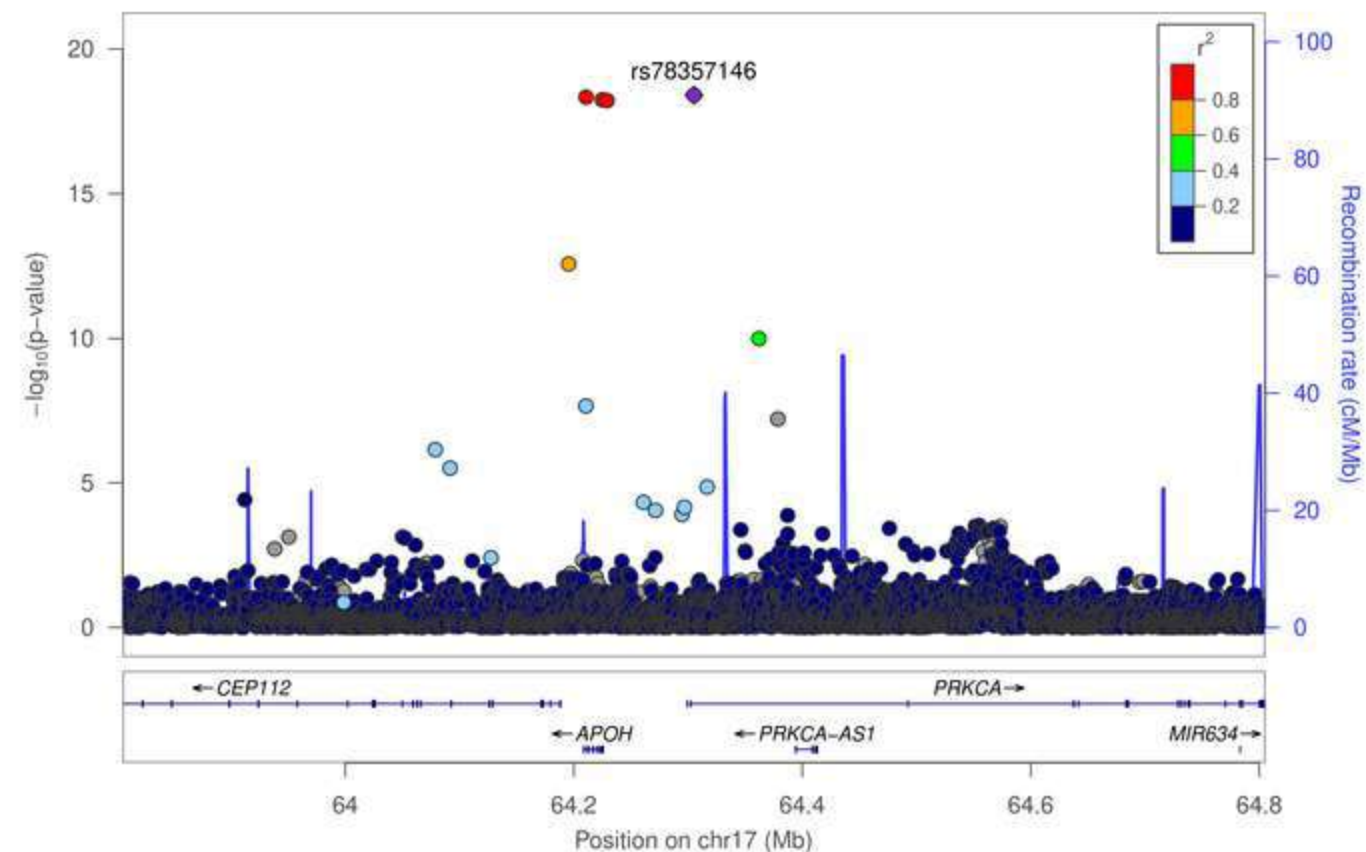
TE SE(TE)

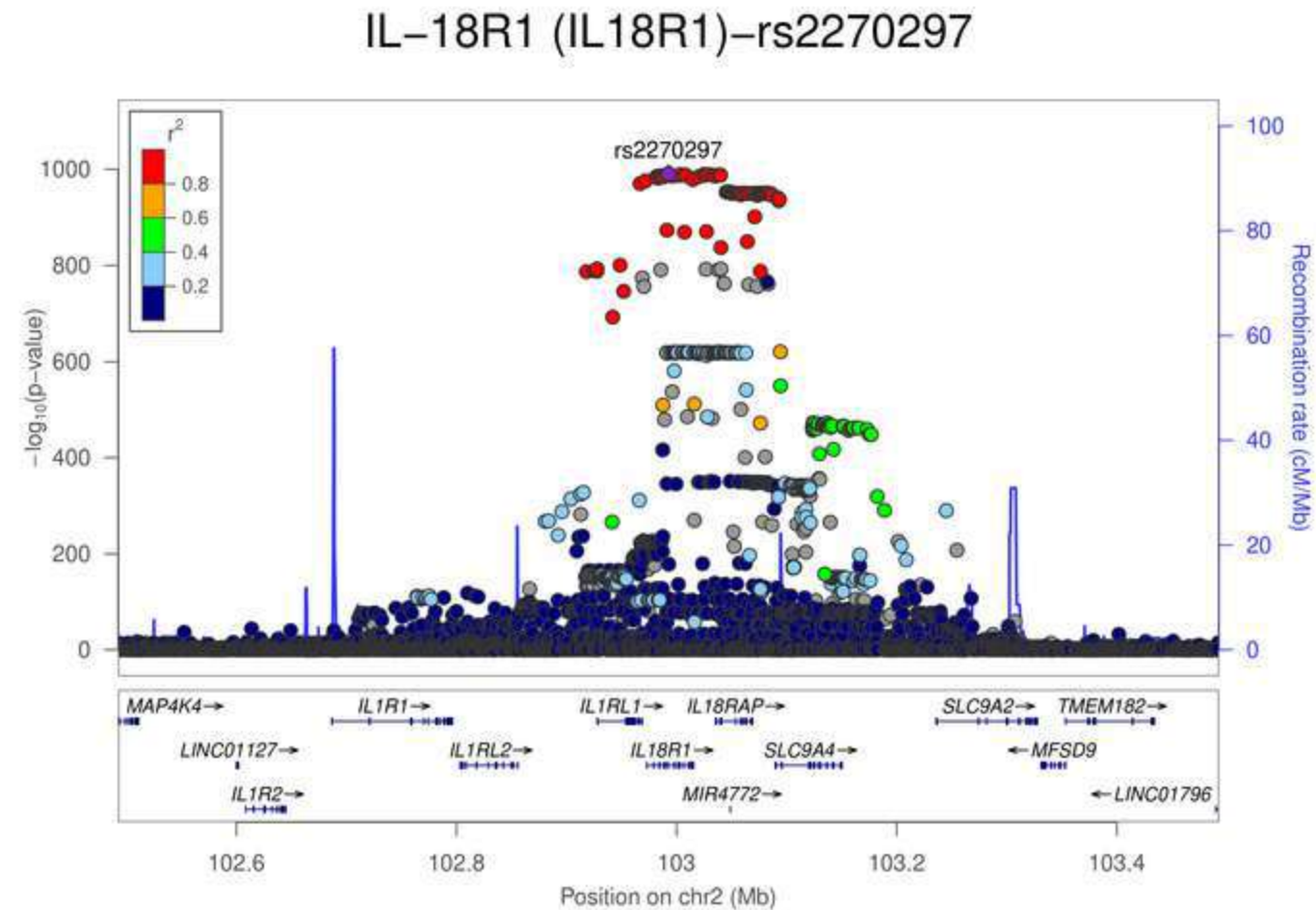
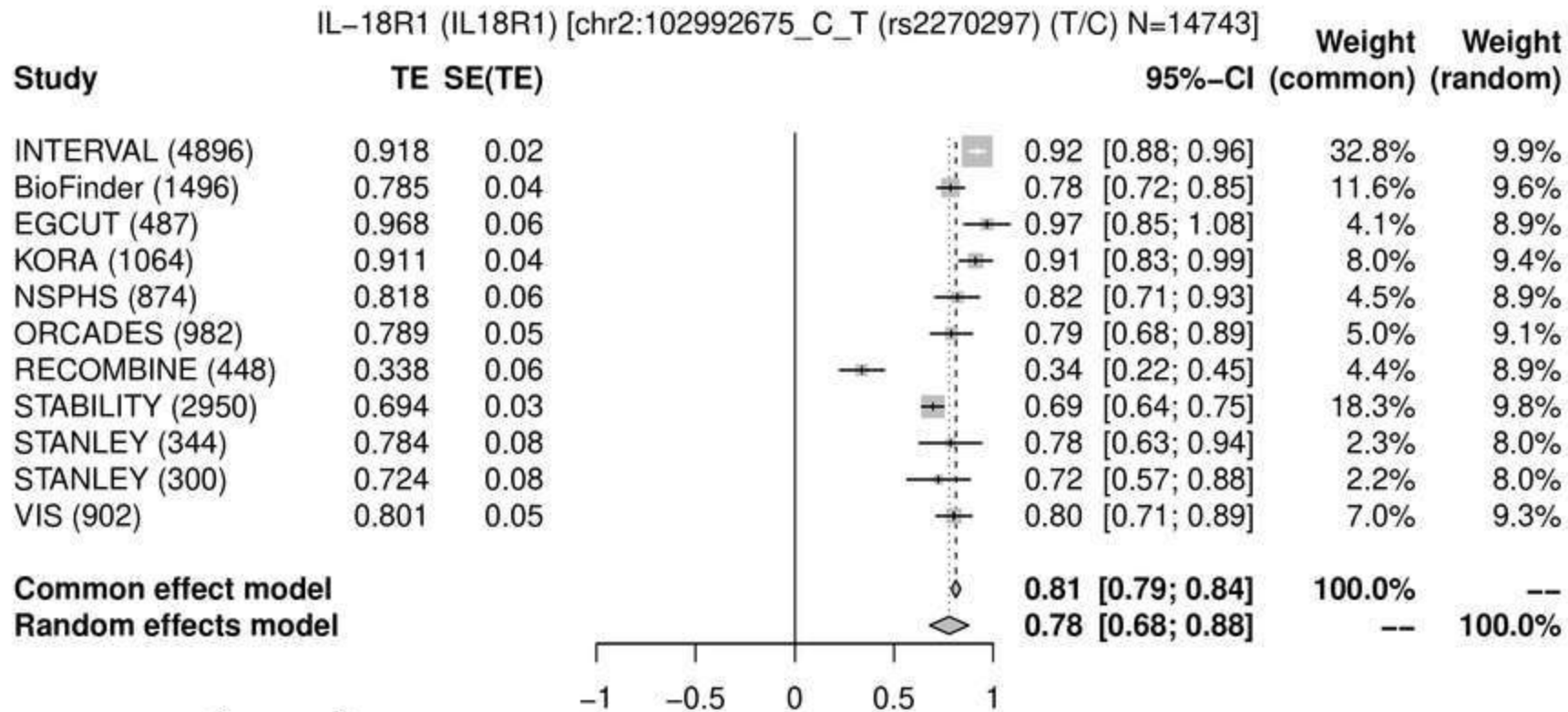


Weight
95%-CI (common) (random)

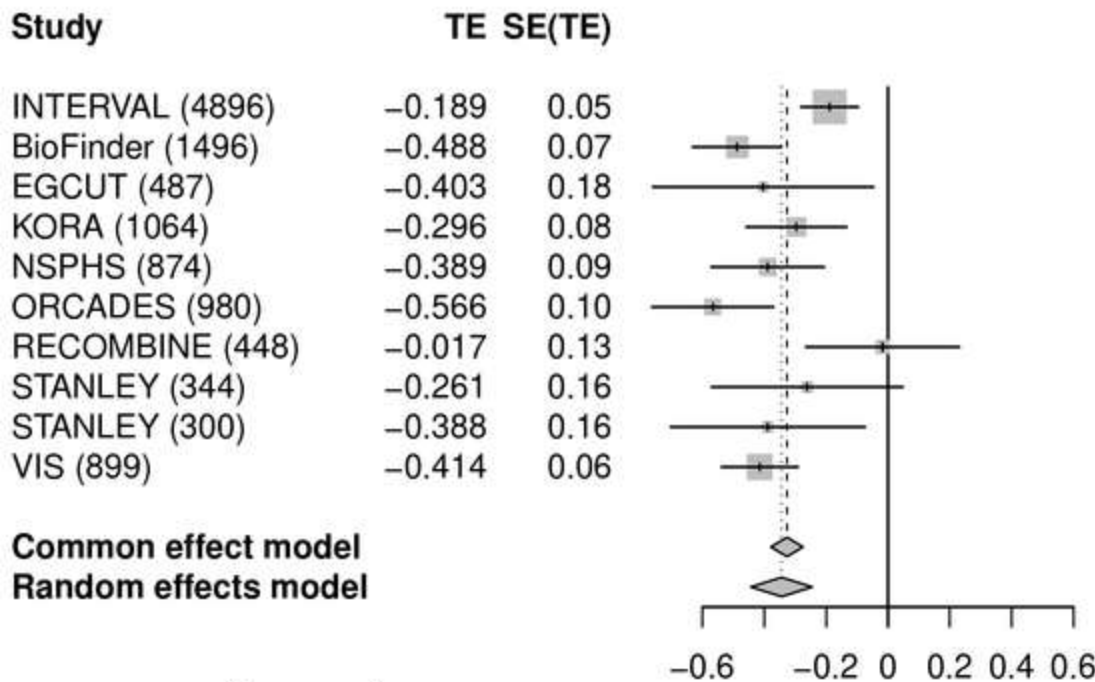
Weight	Weight
95%-CI (common)	(random)
-0.40 [-0.51; -0.28]	40.8%
-0.37 [-0.61; -0.14]	10.0%
-0.35 [-0.91; 0.22]	1.7%
-0.41 [-0.70; -0.13]	6.7%
-0.21 [-0.93; 0.52]	1.1%
-0.95 [-1.36; -0.55]	3.3%
0.23 [-0.15; 0.61]	3.8%
-0.32 [-0.47; -0.17]	23.6%
-0.16 [-0.73; 0.42]	1.7%
0.06 [-0.55; 0.67]	1.5%
-0.06 [-0.37; 0.24]	5.9%
-0.34 [-0.41; -0.26]	100.0%
-0.29 [-0.46; -0.13]	-- 100.0%

IL-18R1 (IL18R1)-rs78357146





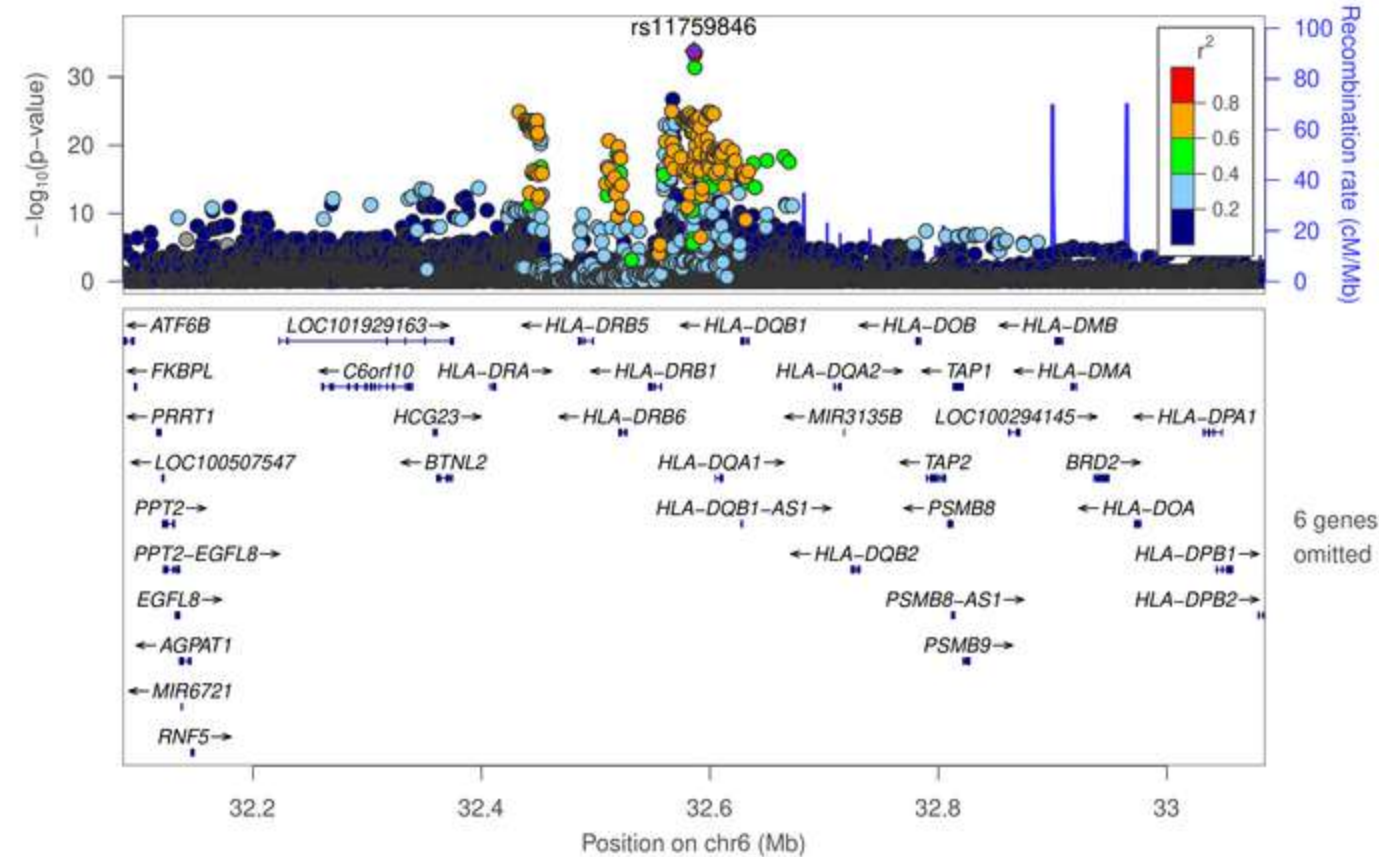
IL-1 alpha (IL1A) [chr6:32586222_A_G (rs11759846) (A/G) N=11788]

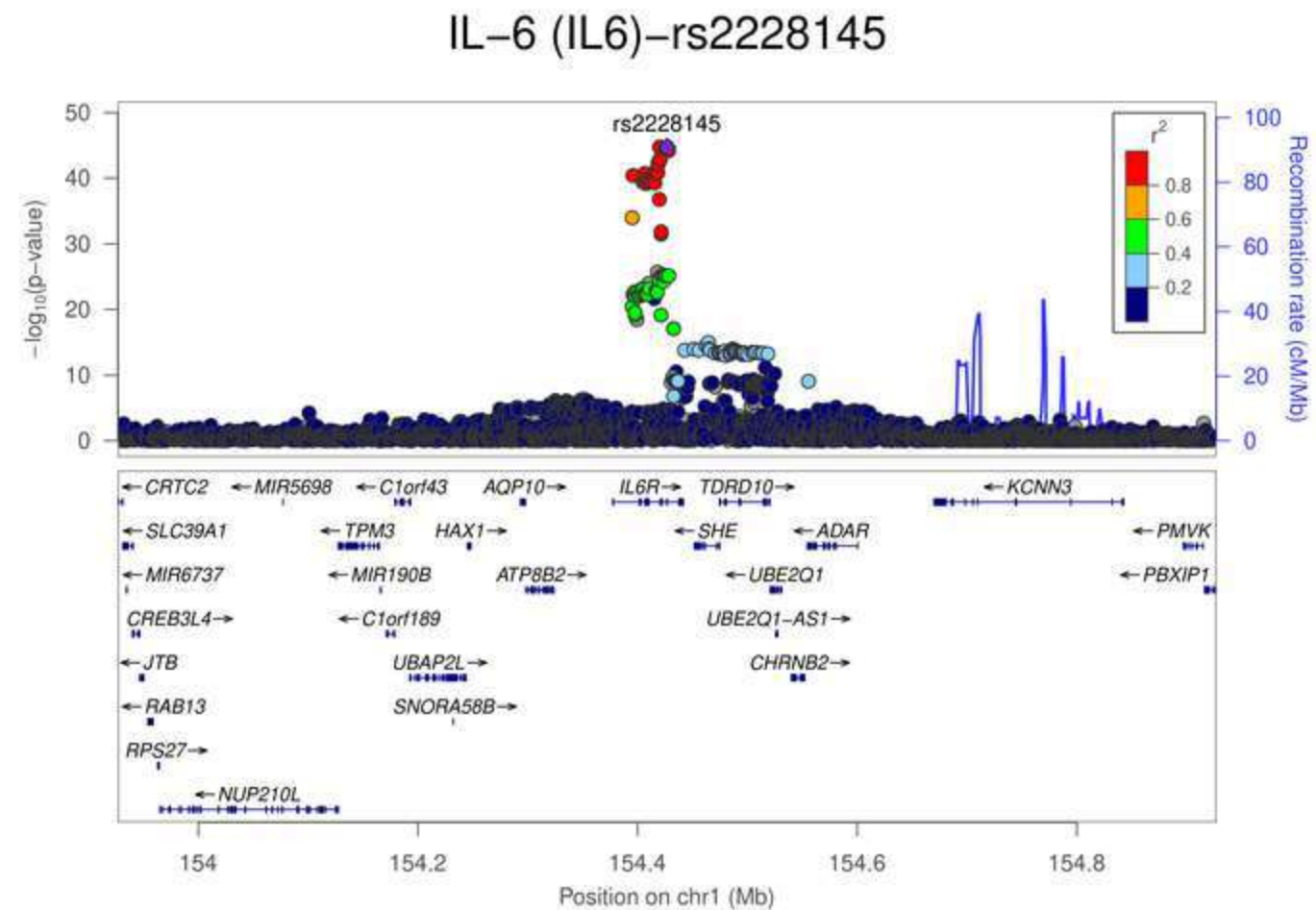
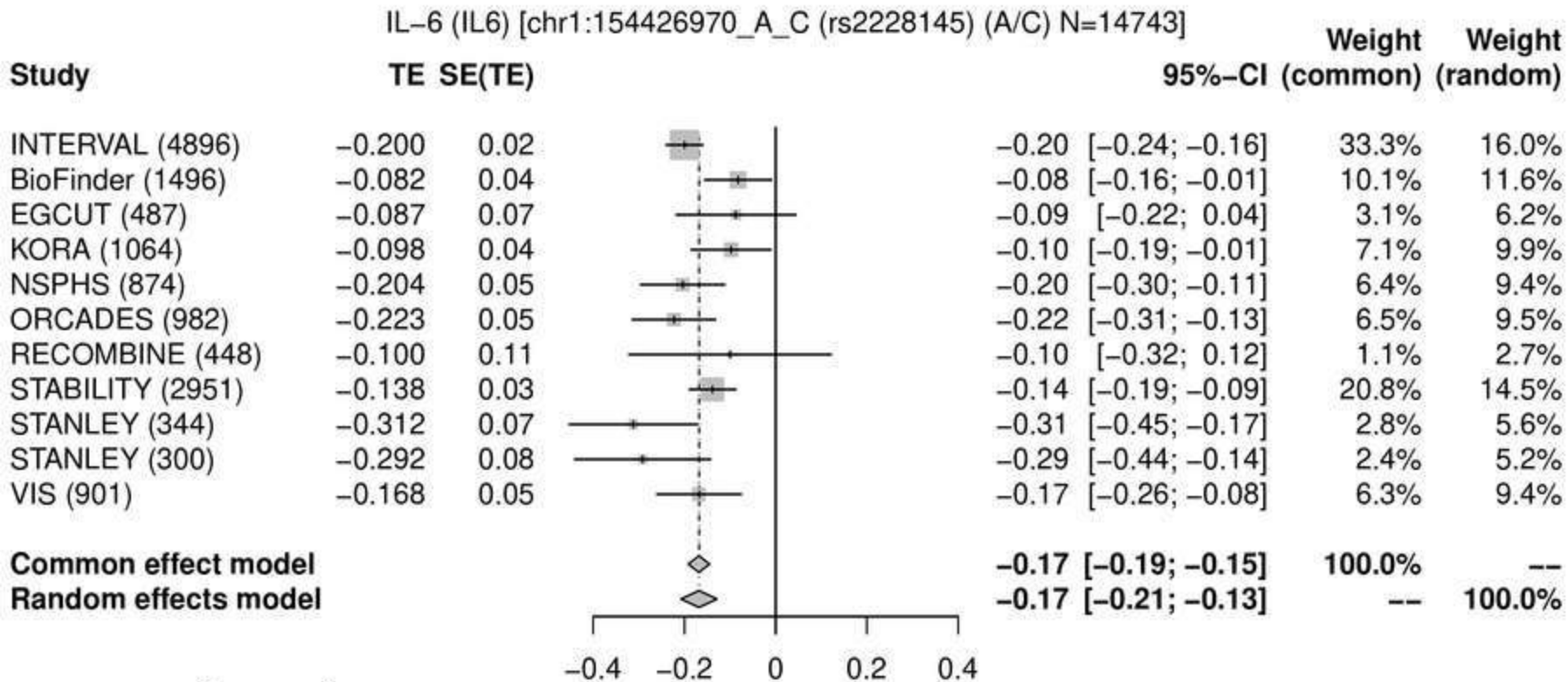


Heterogeneity: $I^2 = 68\%$, $\tau^2 = 0.0151$, $p < 0.01$

	Weight	Weight
95%-CI (common)	(common)	(random)
-0.19 [-0.28; -0.10]	31.5%	14.8%
-0.49 [-0.63; -0.34]	13.1%	12.6%
-0.40 [-0.76; -0.05]	2.1%	5.3%
-0.30 [-0.46; -0.13]	10.3%	11.7%
-0.39 [-0.57; -0.21]	8.1%	10.8%
-0.57 [-0.76; -0.37]	7.0%	10.2%
-0.02 [-0.27; 0.23]	4.4%	8.3%
-0.26 [-0.57; 0.05]	2.9%	6.4%
-0.39 [-0.70; -0.07]	2.8%	6.3%
-0.41 [-0.54; -0.29]	17.7%	13.5%
-0.33 [-0.38; -0.27]	100.0%	--
-0.34 [-0.44; -0.24]	--	100.0%

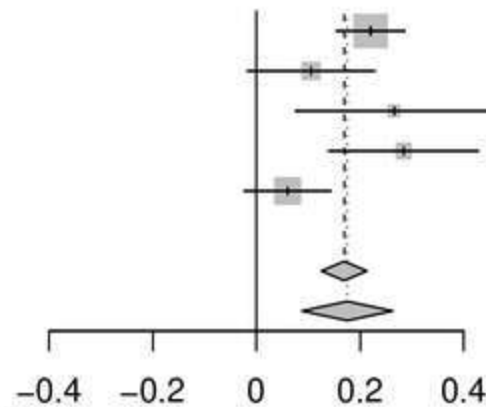
IL-1 (alpha)-rs11759846





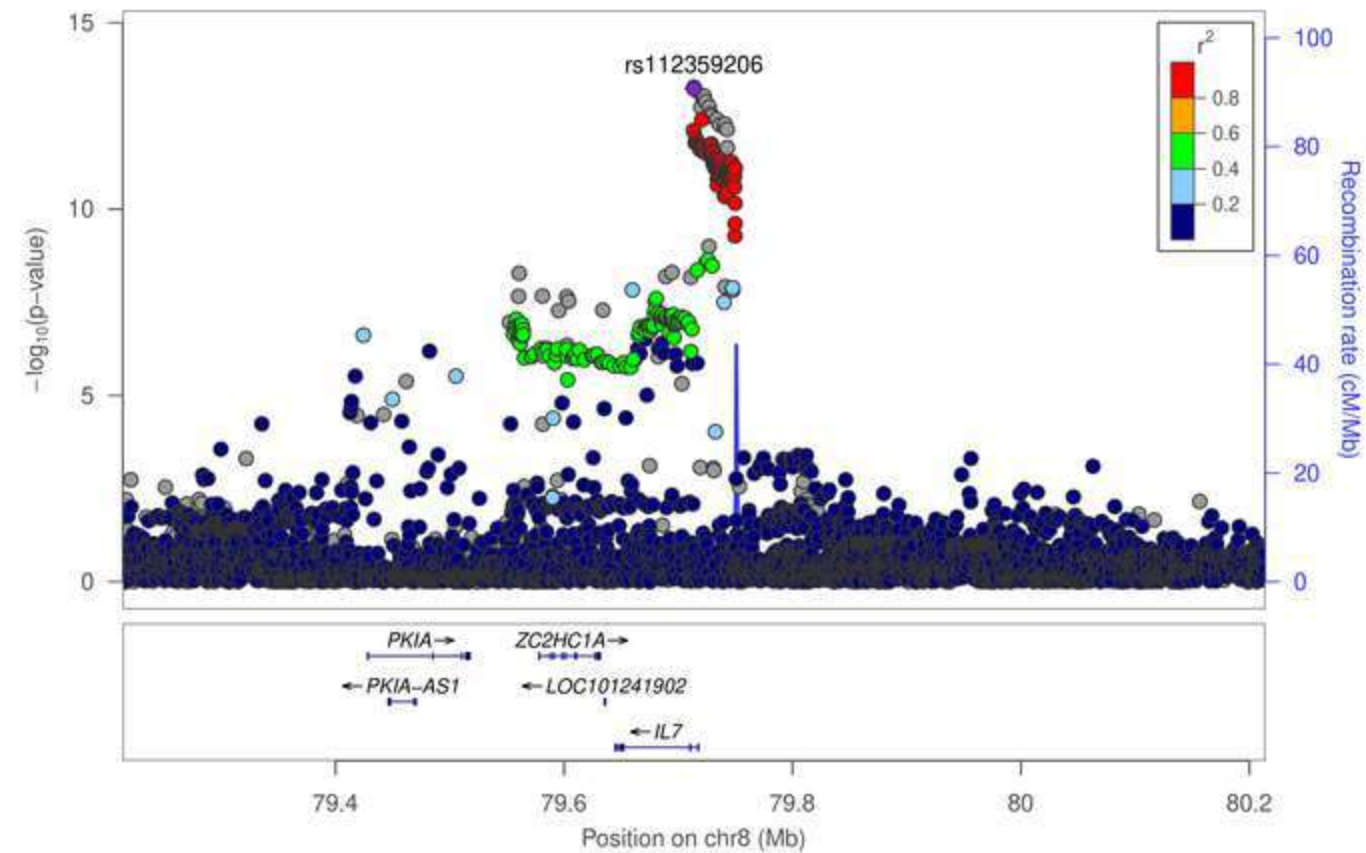
IL-7 (IL7) [chr8:79713766_A_G (rs112359206) (A/G) N=10894]

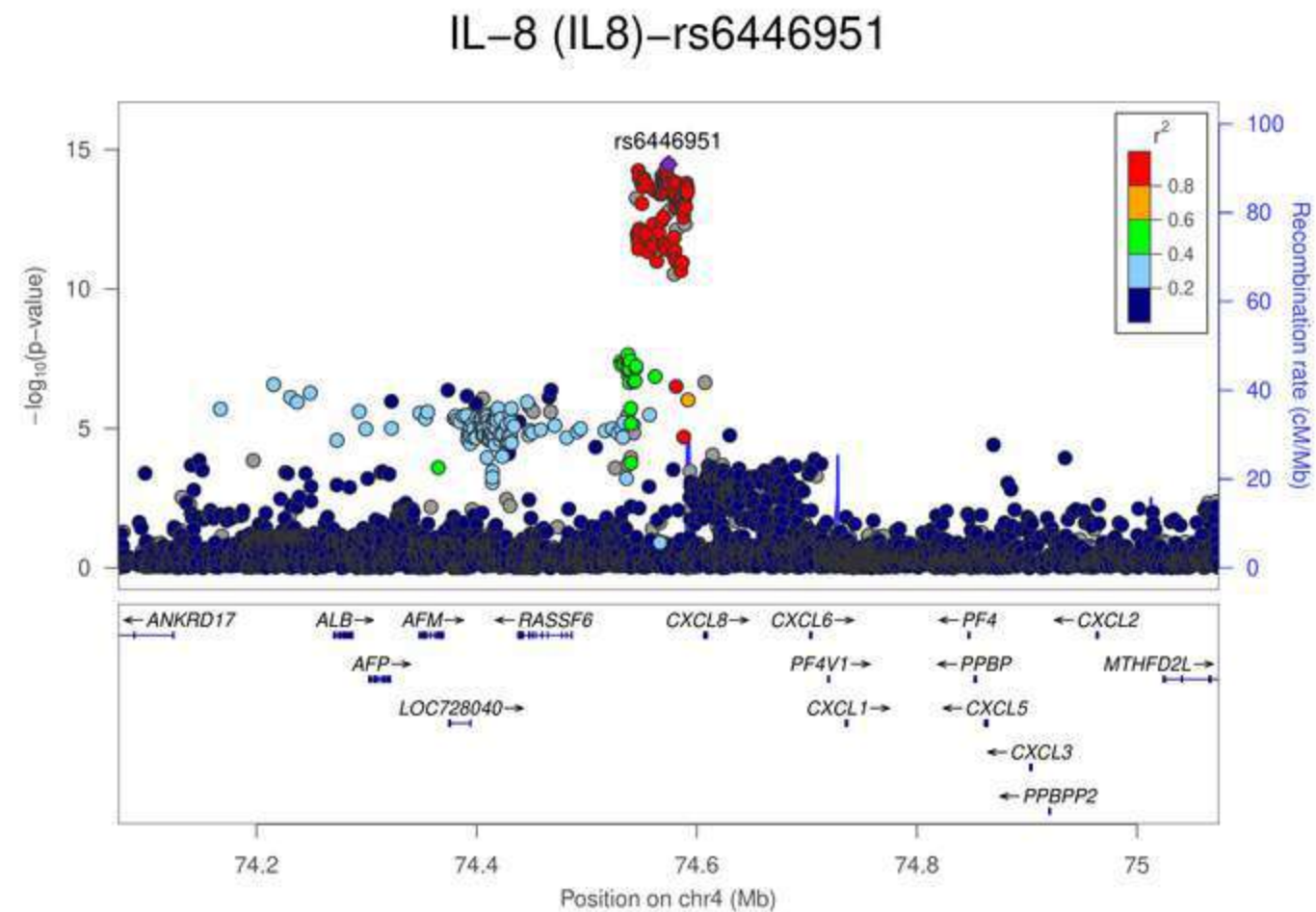
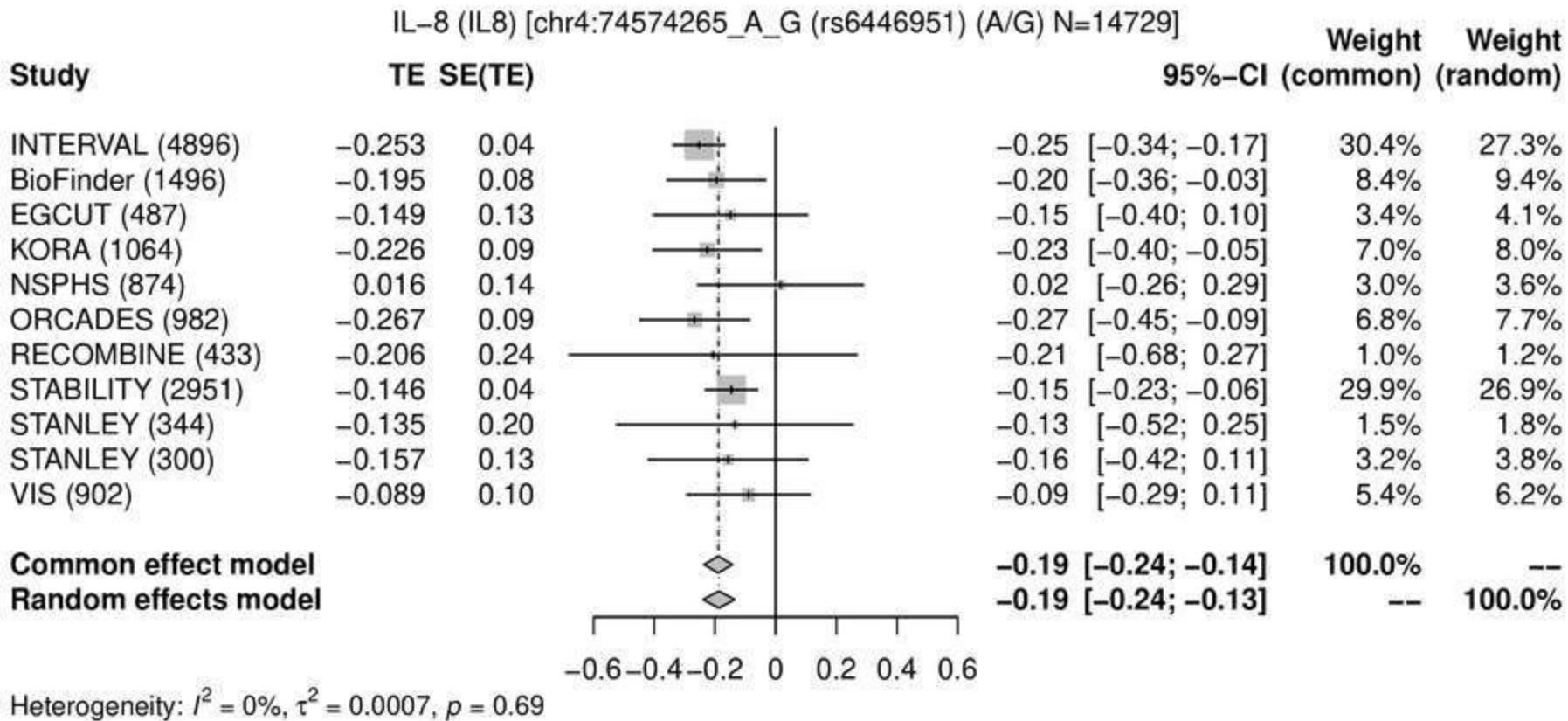
Study	TE	SE(TE)		95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.220	0.03		0.22 [0.15; 0.29]	44.5%	26.6%
BioFinder (1496)	0.105	0.06		0.11 [-0.02; 0.23]	12.9%	19.4%
EGCUT (487)	0.265	0.10		0.27 [0.08; 0.46]	5.4%	12.7%
KORA (1064)	0.283	0.07		0.28 [0.14; 0.43]	9.3%	16.9%
STABILITY (2951)	0.060	0.04		0.06 [-0.02; 0.14]	27.8%	24.4%
Common effect model				0.17 [0.13; 0.21]	100.0%	--
Random effects model				0.18 [0.09; 0.26]	--	100.0%

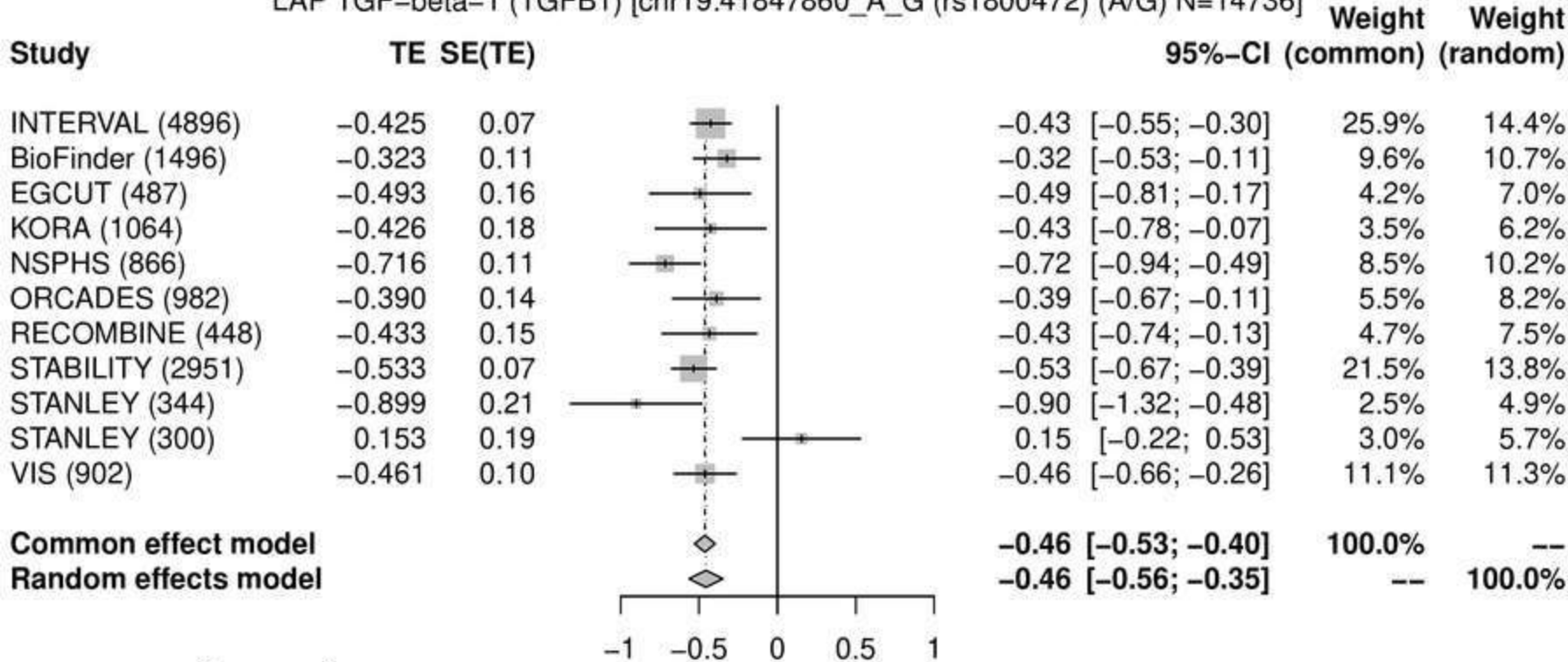


Heterogeneity: $I^2 = 70\%$, $\tau^2 = 0.0064$, $p = 0.01$

IL-7 (IL7)-rs112359206

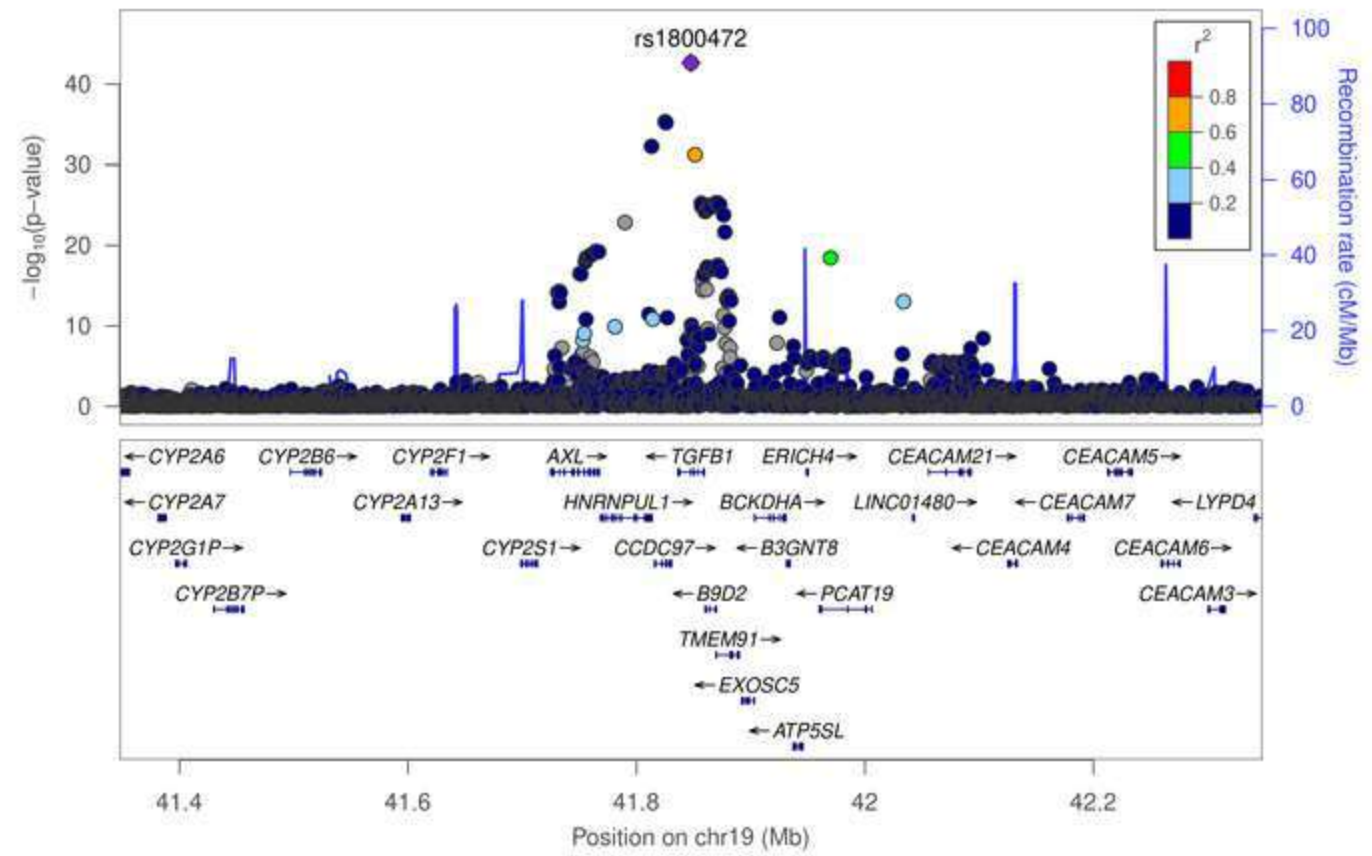




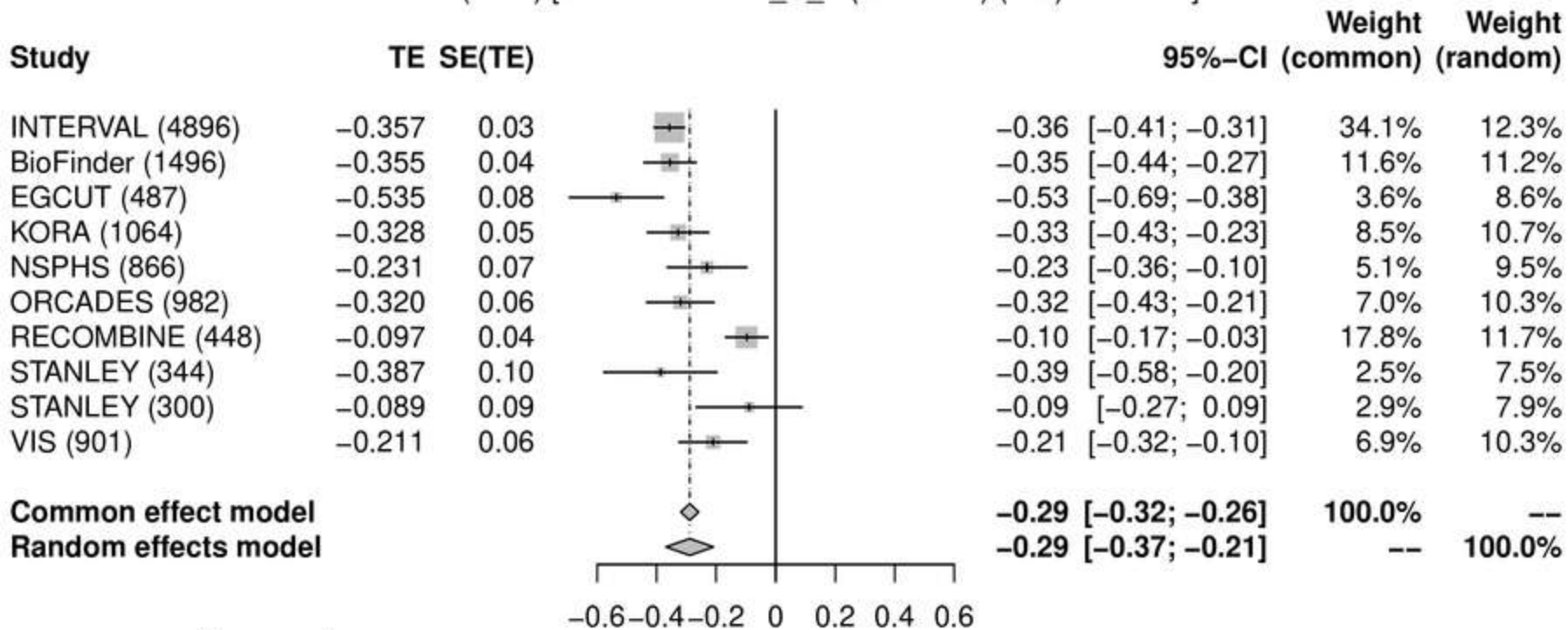


Heterogeneity: $I^2 = 56\%$, $\tau^2 = 0.0170$, $p = 0.01$

LAP (TGF-beta-1)-rs1800472

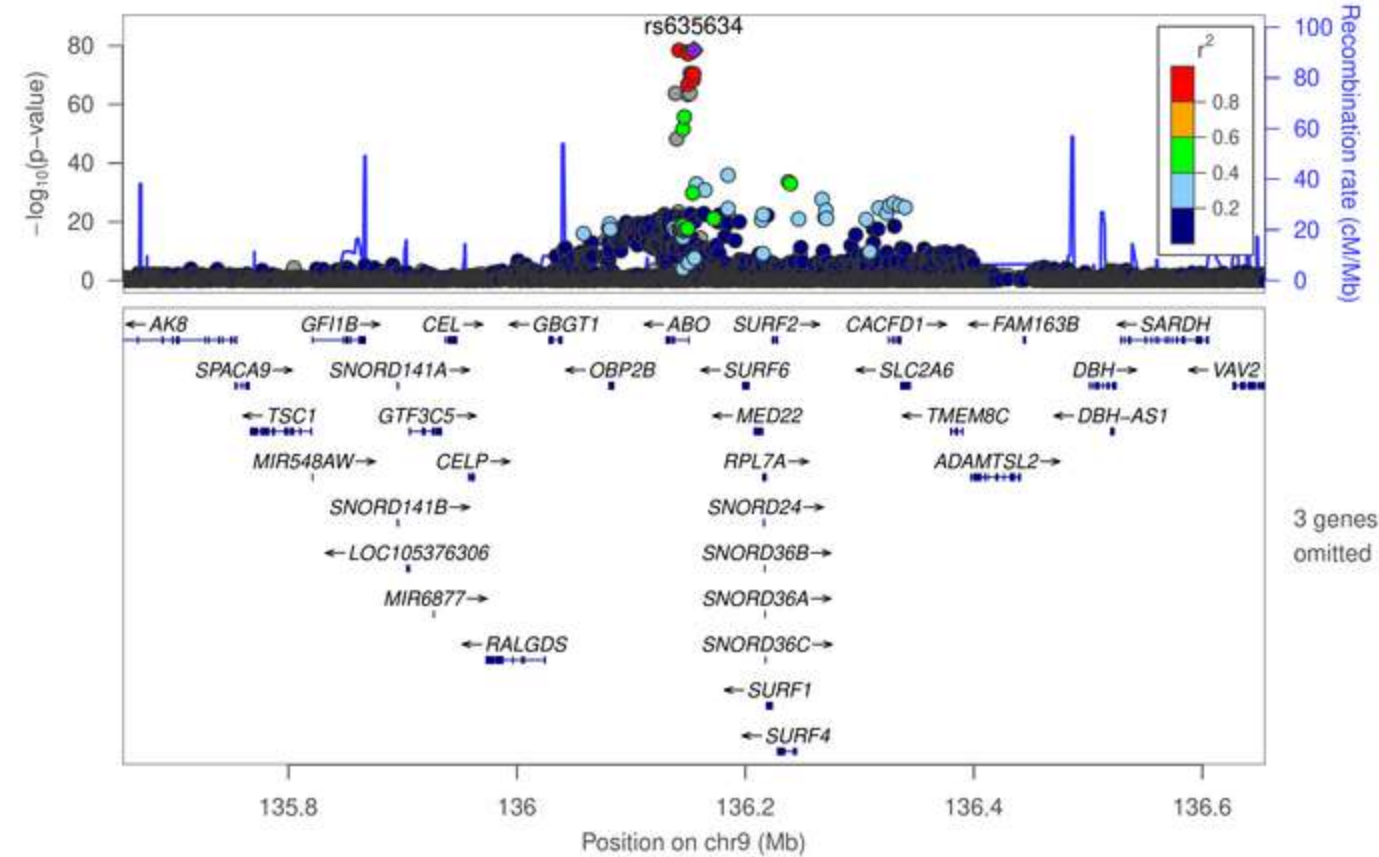


LIF-R (LIFR) [chr9:136155000_C_T (rs635634) (T/C) N=11784]



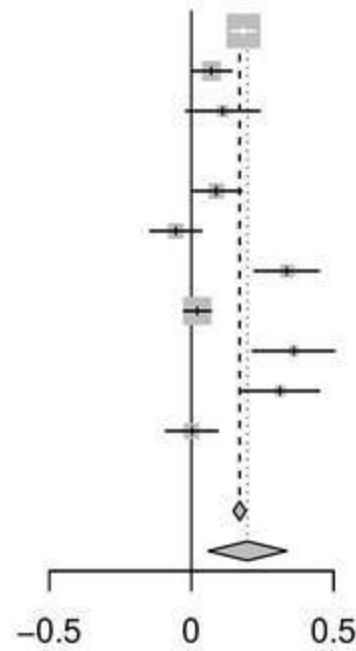
Heterogeneity: $I^2 = 84\%$, $\tau^2 = 0.0130$, $p < 0.01$

LIF-R (LIFR)-rs635634



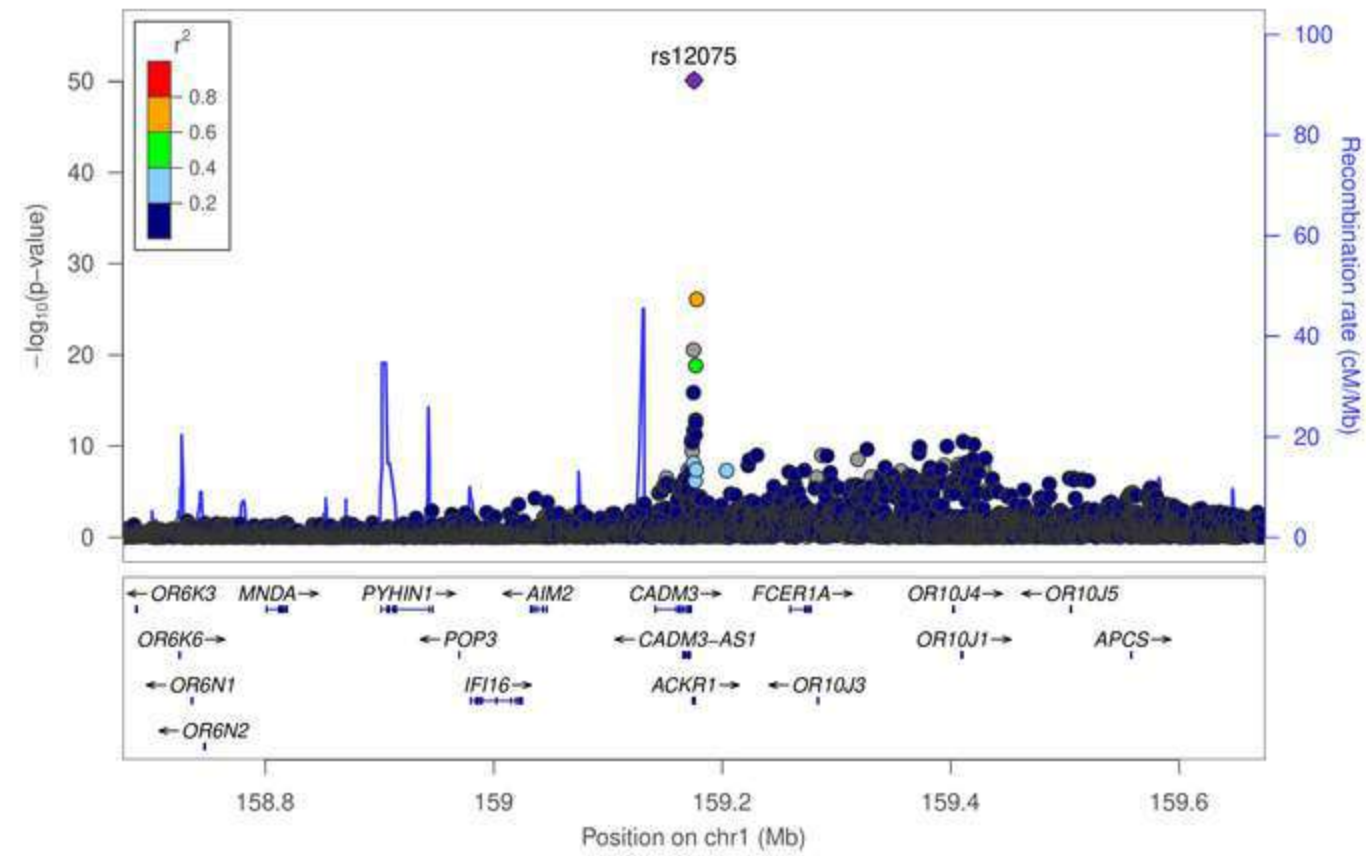
MCP-1 (CCL2) [chr1:159175354_A_G (rs12075) (A/G) N=14730]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight Weight (random)
INTERVAL (4896)	0.182	0.02	0.18 [0.14; 0.22]	31.0%
BioFinder (1496)	0.070	0.04	0.07 [-0.00; 0.14]	9.4%
EGCUT (487)	0.110	0.07	0.11 [-0.02; 0.24]	2.9%
KORA (1064)	0.756	0.04	0.76 [0.68; 0.83]	8.9%
NSPHS (866)	0.087	0.05	0.09 [-0.00; 0.18]	6.2%
ORCADES (981)	-0.055	0.05	-0.05 [-0.15; 0.04]	5.9%
RECOMBINE (445)	0.335	0.06	0.33 [0.22; 0.45]	3.8%
STABILITY (2951)	0.021	0.02	0.02 [-0.03; 0.07]	21.2%
STANLEY (344)	0.360	0.07	0.36 [0.22; 0.50]	2.4%
STANLEY (300)	0.311	0.07	0.31 [0.17; 0.45]	2.5%
VIS (900)	0.001	0.05	0.00 [-0.09; 0.09]	5.8%
Common effect model			0.17 [0.15; 0.19]	100.0%
Random effects model			0.20 [0.06; 0.34]	-- 100.0%



Heterogeneity: $I^2 = 97\%$, $\tau^2 = 0.0528$, $p < 0.01$

MCP-1 (CCL2)-rs12075



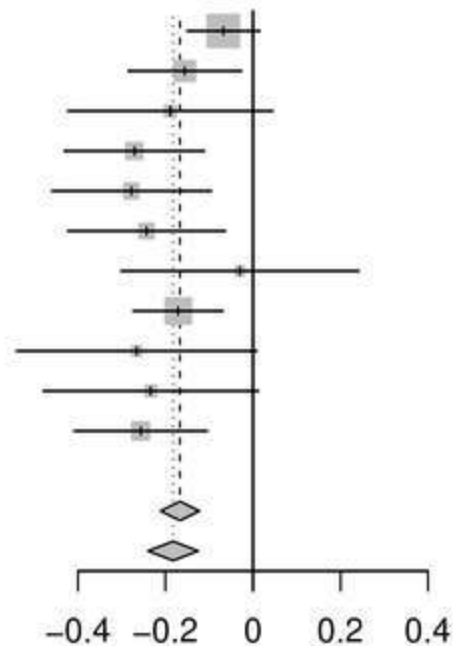
Study

INTERVAL (4896)
 BioFinder (1496)
 EGCUT (487)
 KORA (1064)
 NSPHS (866)
 ORCADES (981)
 RECOMBINE (447)
 STABILITY (2951)
 STANLEY (344)
 STANLEY (300)
 VIS (900)

MCP-1 (CCL2) [chr3:42906116_C_T (rs2228467) (T/C) N=14732]

TE SE(TE)

-0.067 0.04
 -0.156 0.07
 -0.189 0.12
 -0.271 0.08
 -0.278 0.09
 -0.243 0.09
 -0.030 0.14
 -0.171 0.05
 -0.266 0.14
 -0.233 0.13
 -0.257 0.08



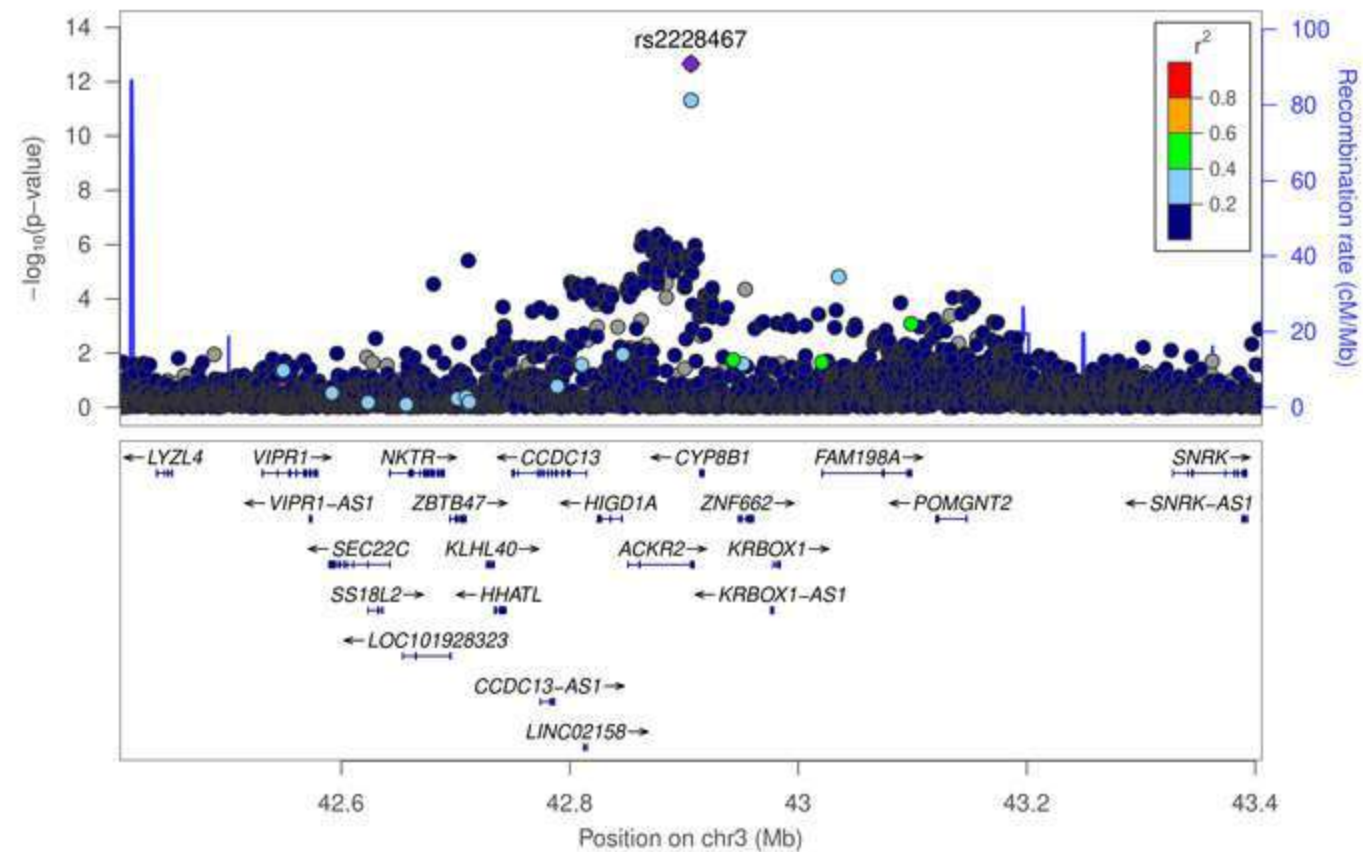
Common effect model
 Random effects model

Heterogeneity: $I^2 = 19\%$, $\tau^2 = 0.0026$, $p = 0.26$

Weight Weight
 95%-CI (common) (random)

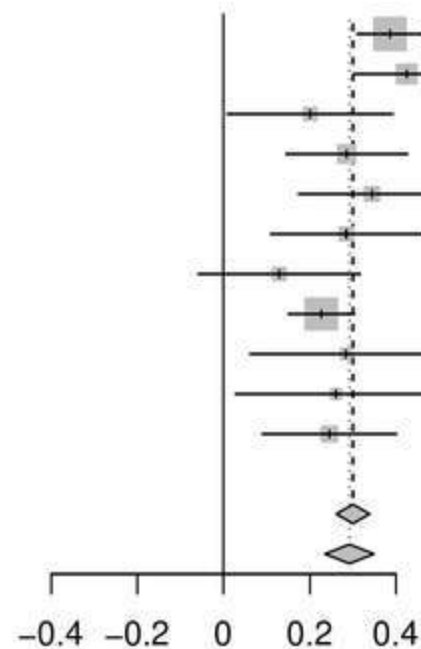
-0.07 [-0.15; 0.02] 28.7% 19.4%
 -0.16 [-0.29; -0.03] 11.8% 12.3%
 -0.19 [-0.42; 0.05] 3.6% 5.1%
 -0.27 [-0.43; -0.11] 7.7% 9.3%
 -0.28 [-0.46; -0.10] 6.0% 7.7%
 -0.24 [-0.42; -0.06] 6.1% 7.8%
 -0.03 [-0.30; 0.24] 2.7% 3.9%
 -0.17 [-0.27; -0.07] 18.8% 16.0%
 -0.27 [-0.54; 0.01] 2.6% 3.9%
 -0.23 [-0.48; 0.01] 3.3% 4.7%
 -0.26 [-0.41; -0.10] 8.6% 9.9%
 -0.17 [-0.21; -0.12] 100.0% --
 -0.18 [-0.24; -0.13] -- 100.0%

MCP-1 (CCL2)-rs2228467



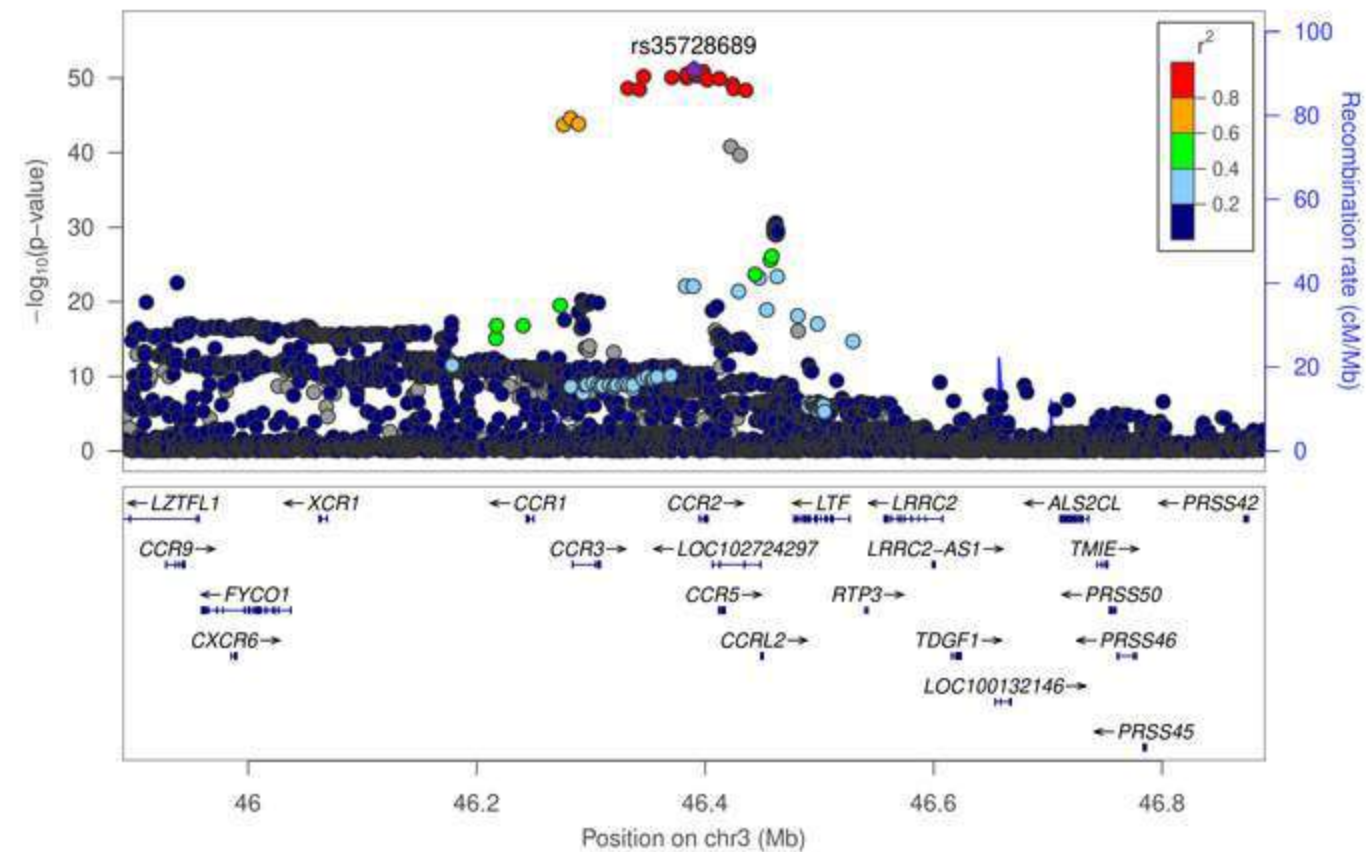
MCP-1 (CCL2) [chr3:46390228_A_G (rs35728689) (A/G) N=14732]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.386	0.04	0.39 [0.31; 0.46]	26.1%
BioFinder (1496)	0.425	0.06	0.43 [0.30; 0.55]	10.0%
EGCUT (487)	0.201	0.10	0.20 [0.01; 0.39]	4.1%
KORA (1064)	0.286	0.07	0.29 [0.15; 0.43]	7.6%
NSPHS (866)	0.345	0.09	0.34 [0.17; 0.51]	5.2%
ORCADES (981)	0.285	0.09	0.28 [0.11; 0.46]	4.9%
RECOMBINE (447)	0.129	0.10	0.13 [-0.06; 0.32]	4.3%
STABILITY (2951)	0.227	0.04	0.23 [0.15; 0.30]	25.7%
STANLEY (344)	0.284	0.11	0.28 [0.06; 0.51]	3.0%
STANLEY (300)	0.261	0.12	0.26 [0.03; 0.50]	2.8%
VIS (900)	0.245	0.08	0.25 [0.09; 0.40]	6.3%
Common effect model			0.30 [0.26; 0.34]	100.0%
Random effects model			0.29 [0.24; 0.35]	100.0%



Heterogeneity: $I^2 = 43\%$, $\tau^2 = 0.0037$, $p = 0.06$

MCP-1 (CCL2)-rs35728689



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (445)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 71\%$, $\tau^2 = 0.0049$, $p < 0.01$

MCP-2 (CCL8) [chr1:159175354_A_G (rs12075) (A/G) N=14733]

TE SE(TE)

-0.131 0.02

-0.035 0.04

-0.130 0.07

-0.086 0.04

0.123 0.05

-0.196 0.05

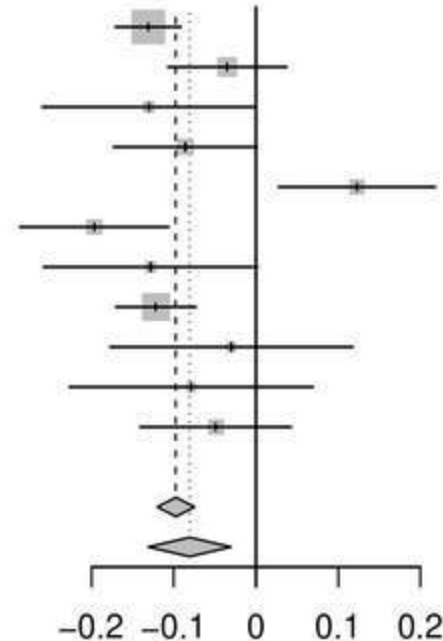
-0.128 0.07

-0.122 0.02

-0.030 0.08

-0.079 0.08

-0.049 0.05

Weight
95%-CI (common) (random)

-0.13 [-0.17; -0.09] 32.4% 12.6%

-0.03 [-0.11; 0.04] 9.9% 10.7%

-0.13 [-0.26; -0.00] 3.1% 7.2%

-0.09 [-0.17; 0.00] 6.8% 9.7%

0.12 [0.03; 0.22] 5.7% 9.2%

-0.20 [-0.29; -0.11] 6.3% 9.5%

-0.13 [-0.26; 0.00] 3.1% 7.2%

-0.12 [-0.17; -0.07] 21.9% 12.1%

-0.03 [-0.18; 0.12] 2.4% 6.3%

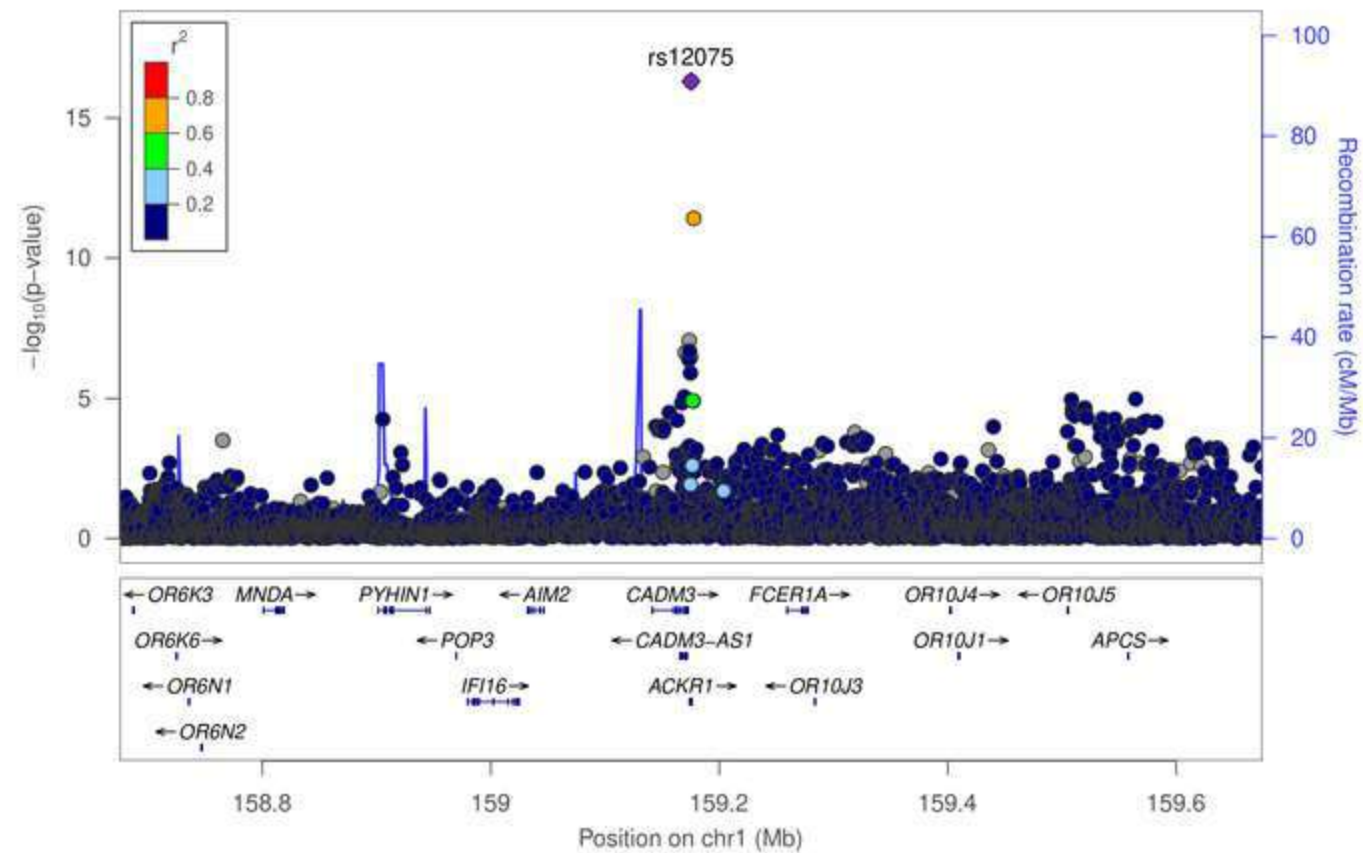
-0.08 [-0.23; 0.07] 2.4% 6.3%

-0.05 [-0.14; 0.04] 6.1% 9.4%

-0.10 [-0.12; -0.07] 100.0% --

-0.08 [-0.13; -0.03] -- 100.0%

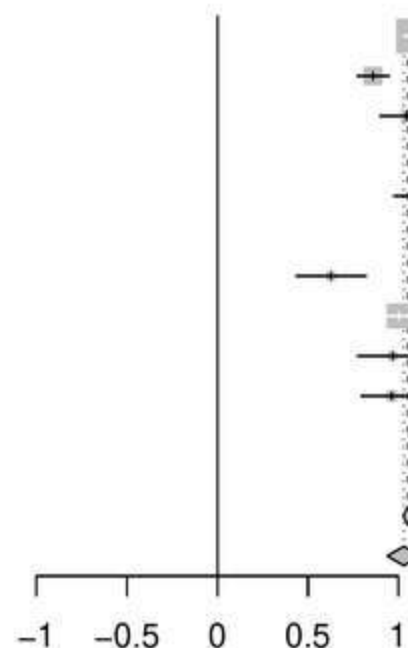
MCP-2 (CCL8)-rs12075



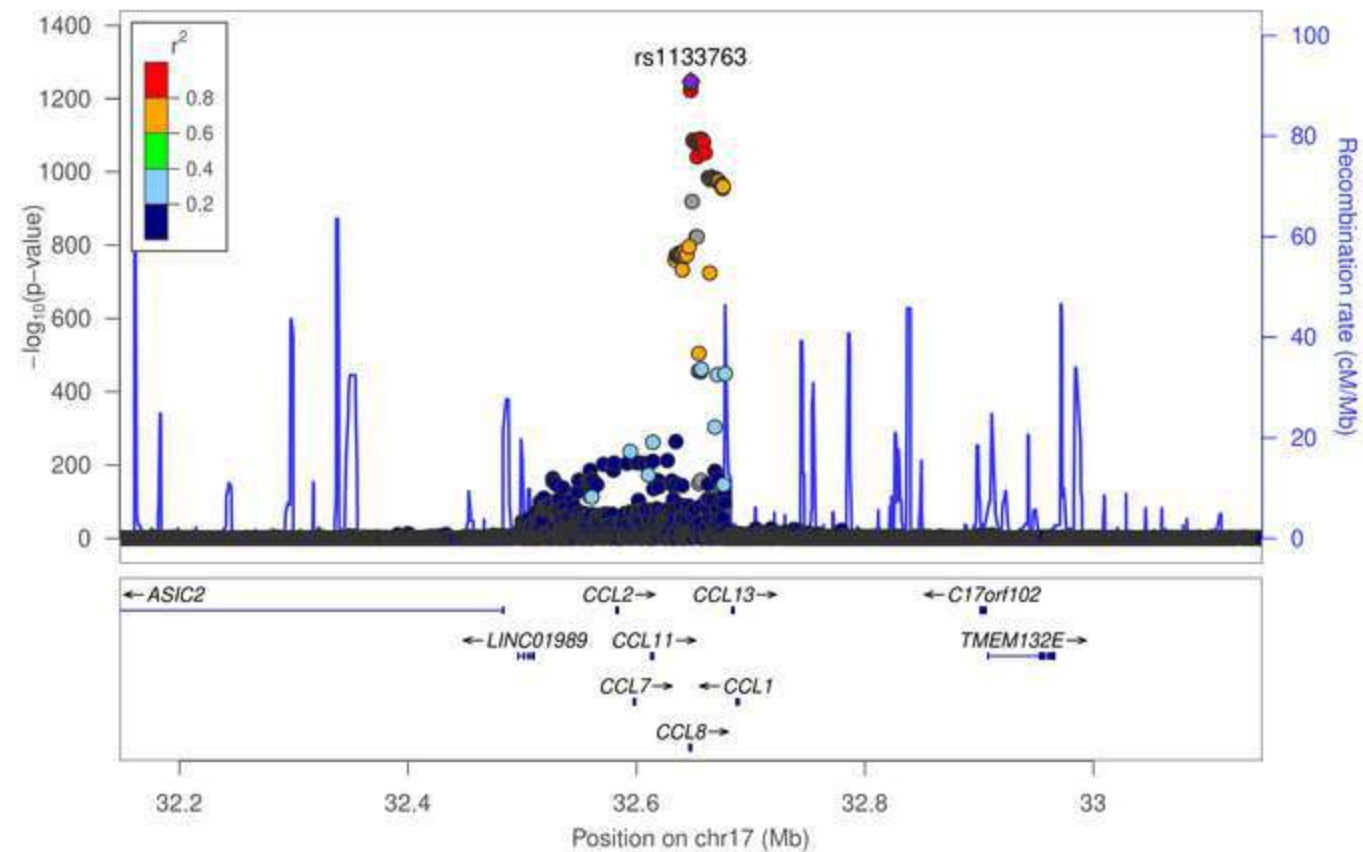
MCP-2 (CCL8) [chr17:32647831_A_C (rs1133763) (A/C) N=14716]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	1.079	0.02	1.08 [1.03; 1.13]	34.7%	10.7%
BioFinder (1496)	0.860	0.04	0.86 [0.77; 0.95]	9.7%	10.0%
EGCUT (487)	1.045	0.07	1.05 [0.90; 1.19]	3.5%	8.6%
KORA (1064)	1.213	0.05	1.21 [1.12; 1.31]	8.8%	9.9%
NSPHS (866)	1.131	0.08	1.13 [0.98; 1.29]	3.1%	8.3%
ORCADES (982)	1.173	0.06	1.17 [1.06; 1.28]	6.3%	9.5%
RECOMBINE (428)	0.628	0.10	0.63 [0.44; 0.82]	2.0%	7.4%
STABILITY (2951)	1.004	0.03	1.00 [0.94; 1.07]	18.8%	10.4%
STANLEY (344)	0.971	0.10	0.97 [0.78; 1.17]	2.0%	7.3%
STANLEY (300)	0.964	0.09	0.96 [0.79; 1.13]	2.6%	8.0%
VIS (902)	1.152	0.05	1.15 [1.06; 1.25]	8.6%	9.9%
Common effect model			1.05 [1.03; 1.08]	100.0%	--
Random effects model			1.03 [0.94; 1.12]	--	100.0%

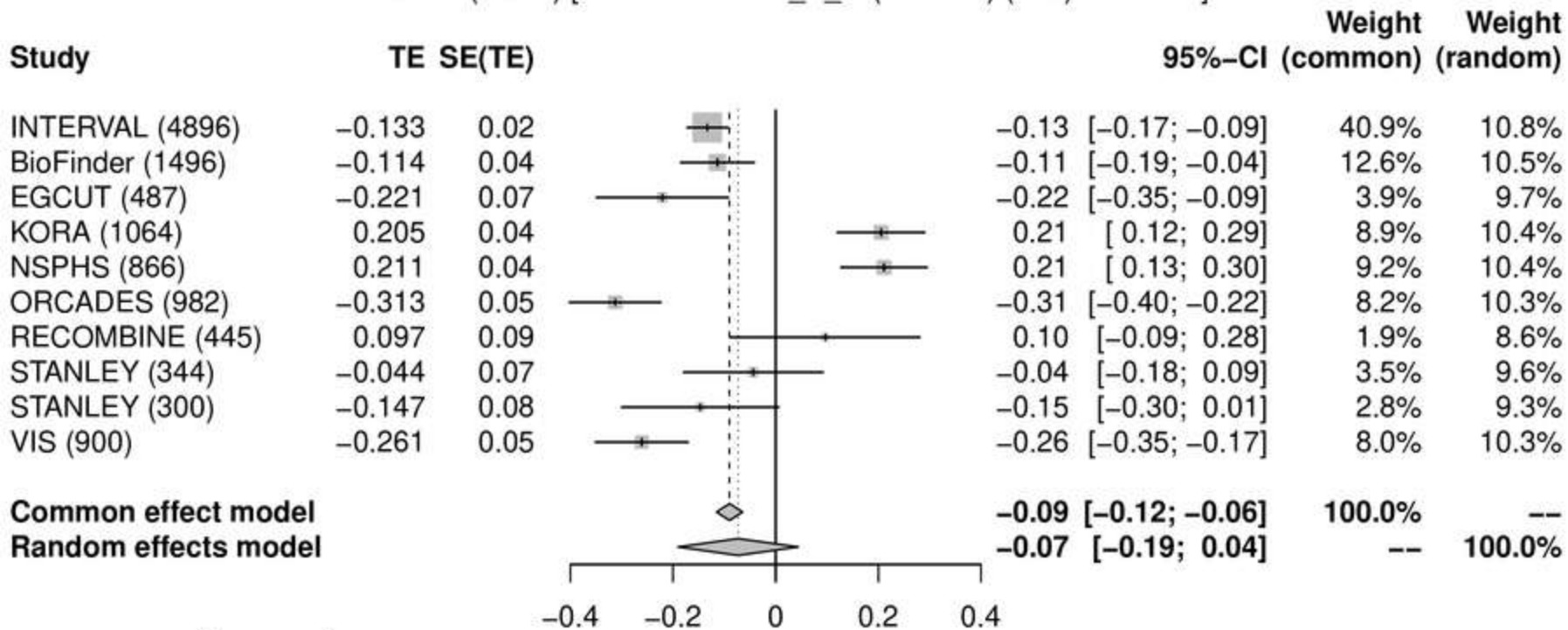
Heterogeneity: $I^2 = 84\%$, $\tau^2 = 0.0199$, $p < 0.01$



MCP-2 (CCL8)-rs1133763

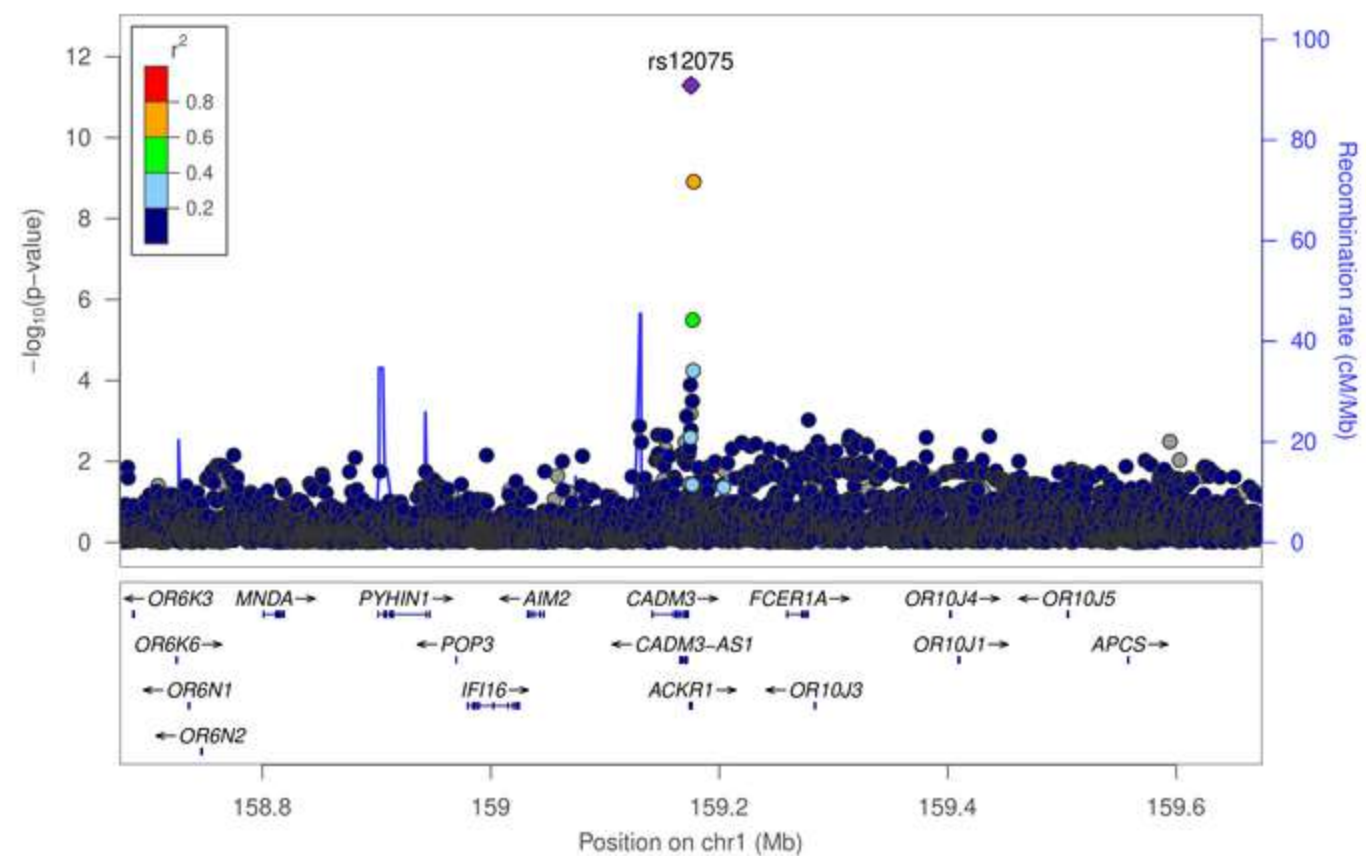


MCP-3 (CCL7) [chr1:159175354_A_G (rs12075) (A/G) N=11780]

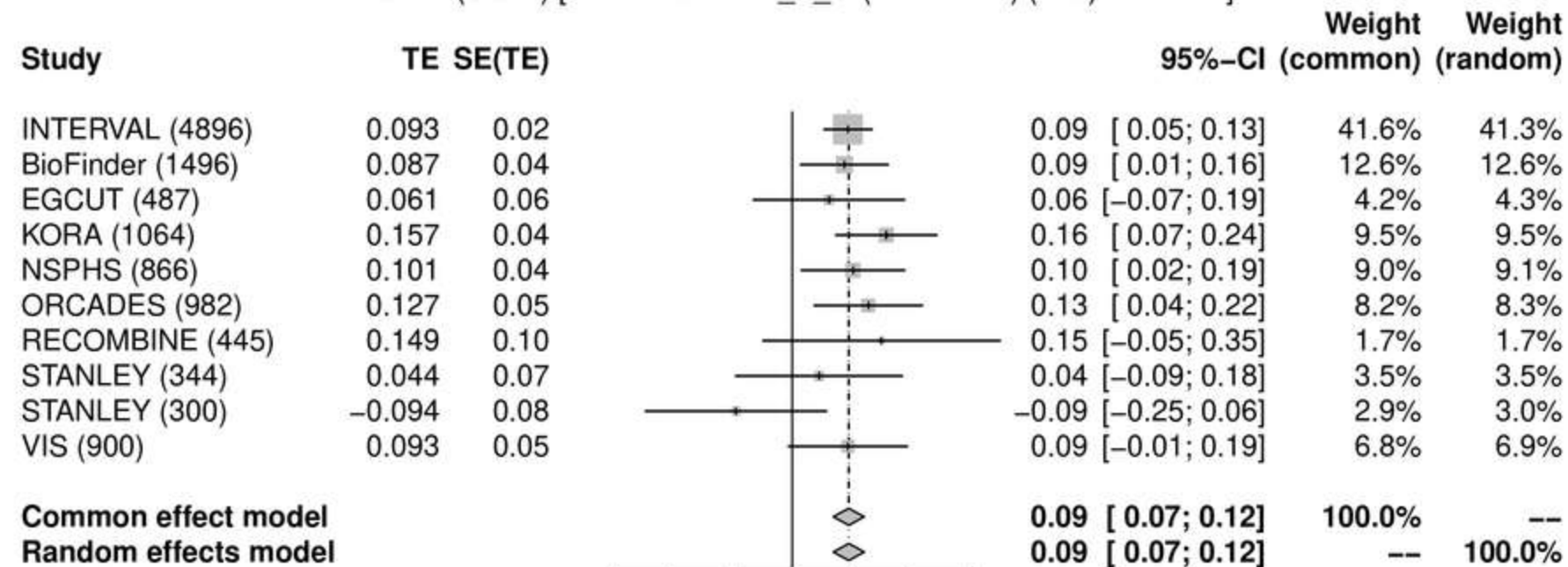


Heterogeneity: $I^2 = 94\%$, $\tau^2 = 0.0327$, $p < 0.01$

MCP-3 (CCL7)-rs12075

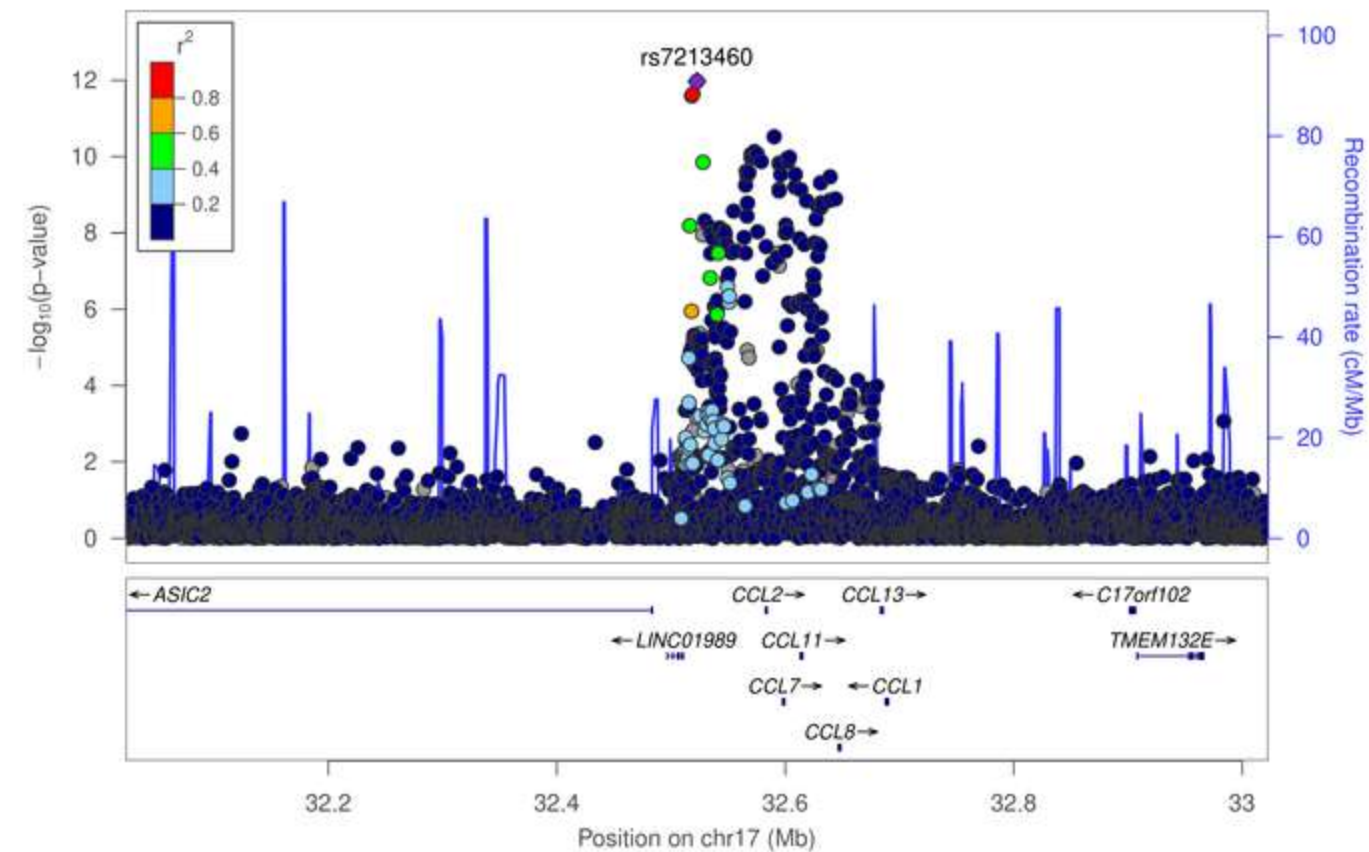


MCP-3 (CCL7) [chr17:32522613_A_G (rs7213460) (A/G) N=11780]

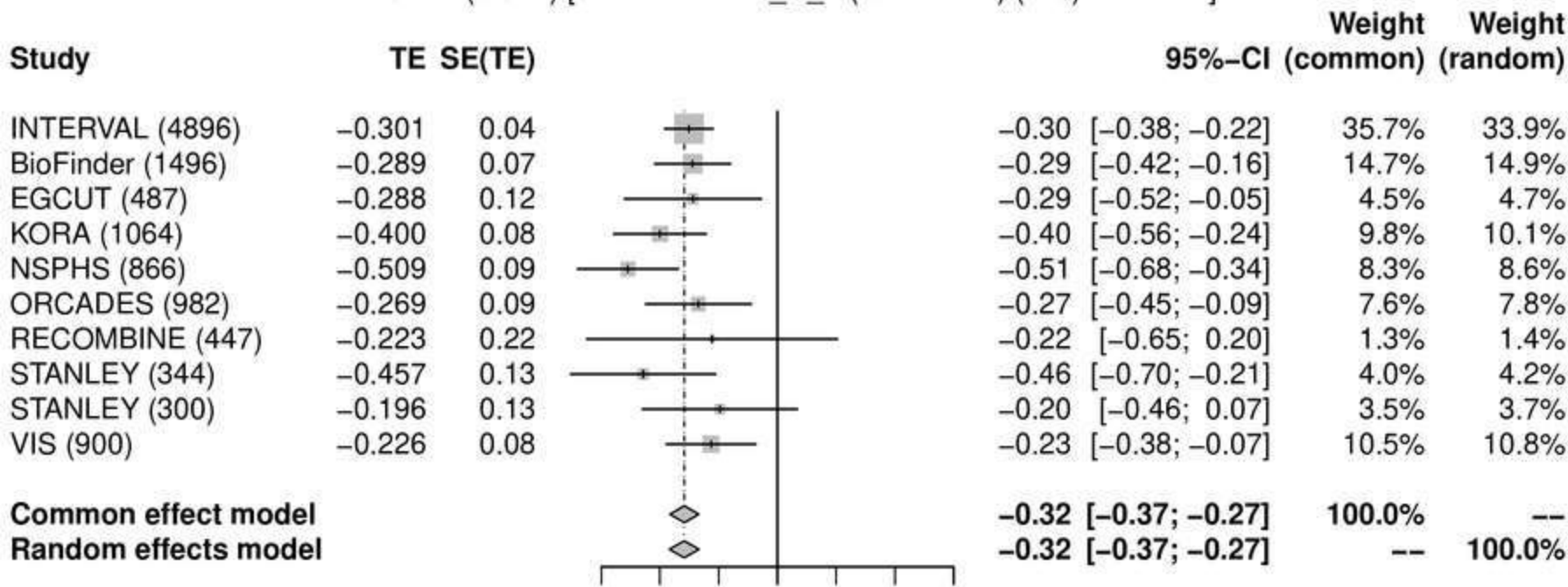


Heterogeneity: $I^2 = 7\%$, $\tau^2 < 0.0001$, $p = 0.38$

MCP-3 (CCL7)-rs7213460

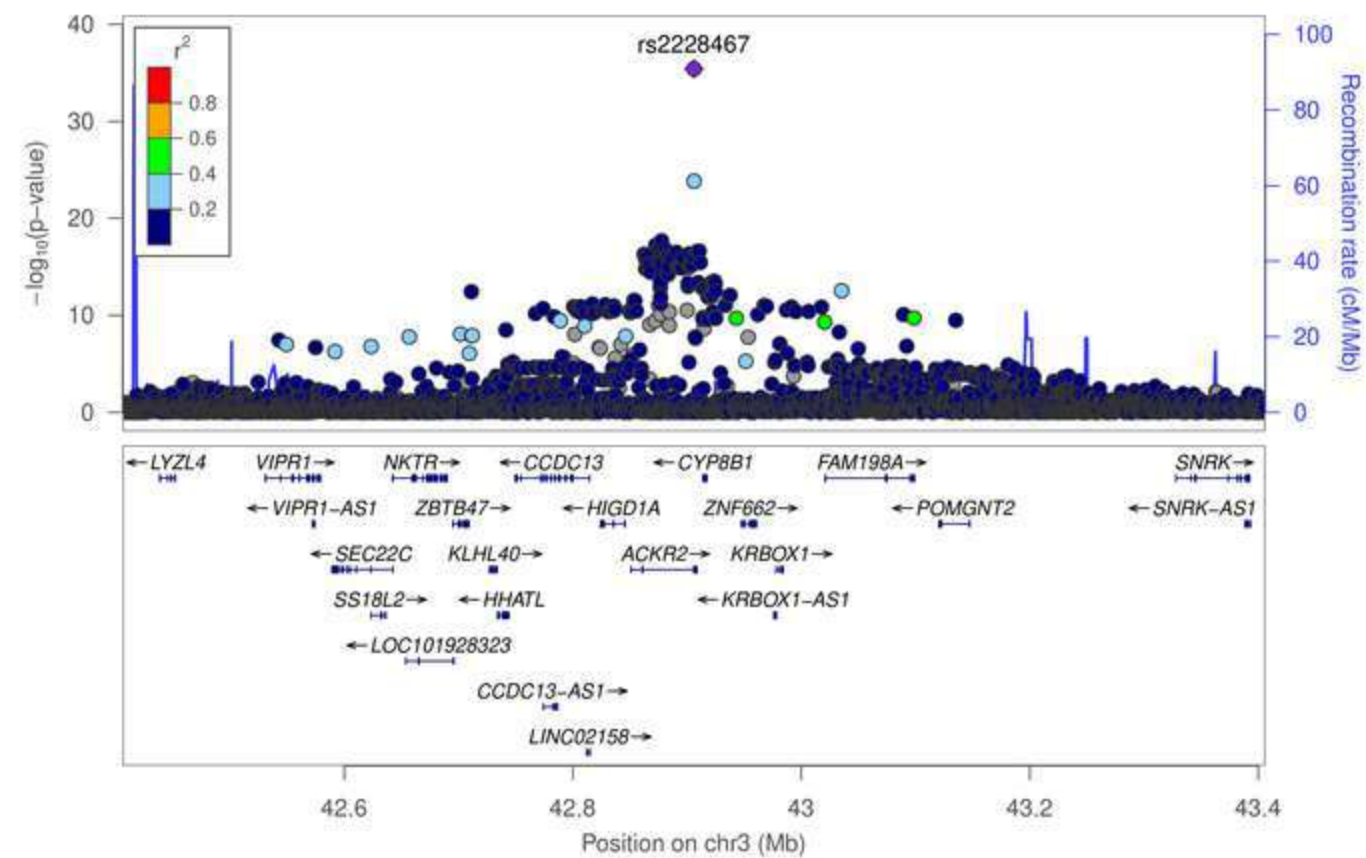


MCP-3 (CCL7) [chr3:42906116_C_T (rs2228467) (T/C) N=11782]



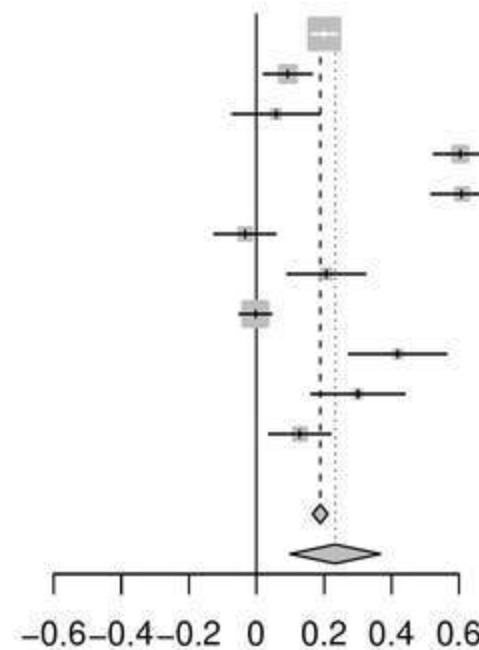
Heterogeneity: $I^2 = 11\%$, $\tau^2 = 0.0002$, $p = 0.34$

MCP-3 (CCL7)-rs2228467



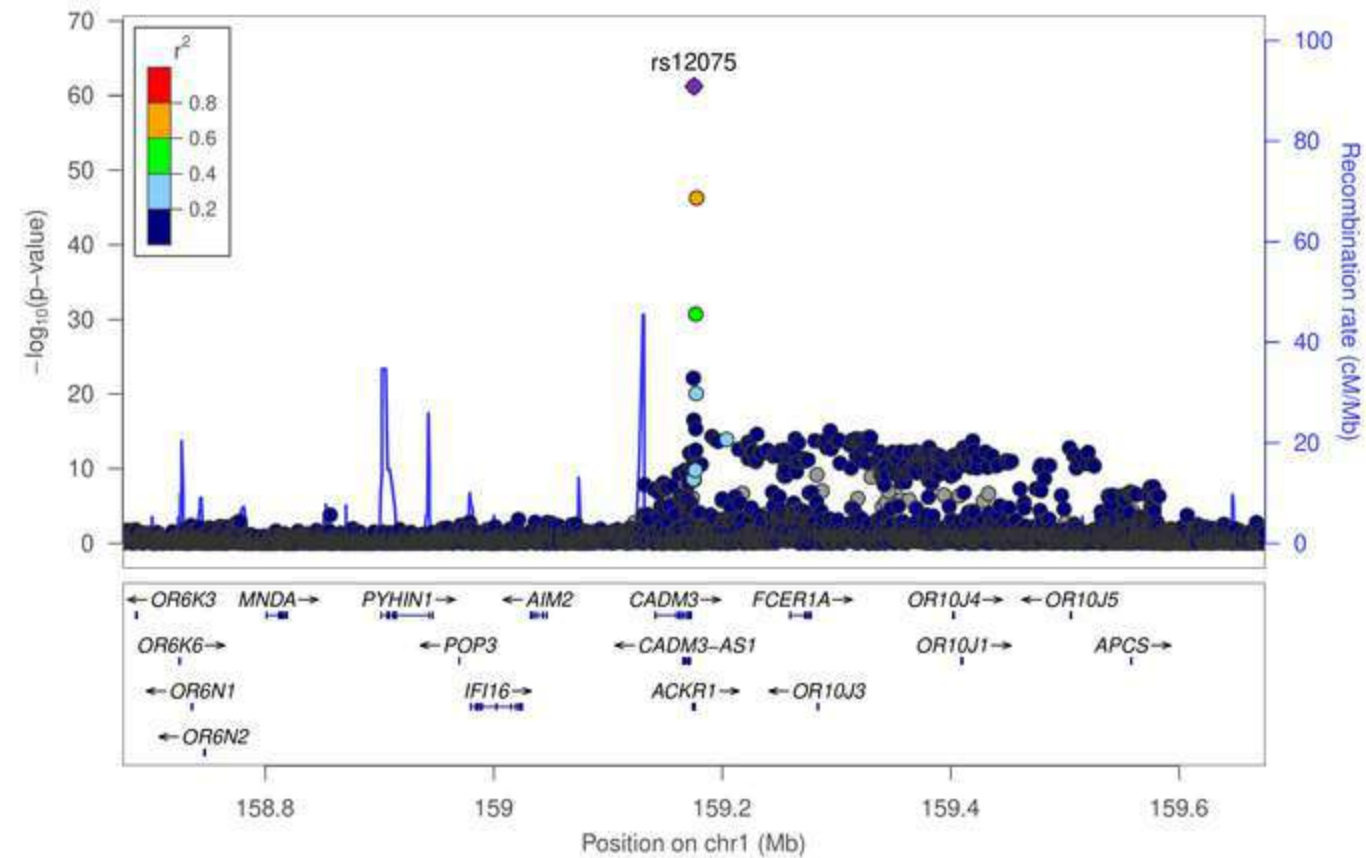
MCP-4 (CCL13) [chr1:159175354_A_G (rs12075) (A/G) N=14733]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight Weight (random)
INTERVAL (4896)	0.201	0.02	0.20 [0.16; 0.24]	31.6%
BioFinder (1496)	0.093	0.04	0.09 [0.02; 0.16]	9.6%
EGCUT (487)	0.058	0.07	0.06 [-0.07; 0.19]	2.9%
KORA (1064)	0.603	0.04	0.60 [0.52; 0.68]	8.0%
NSPHS (866)	0.608	0.05	0.61 [0.52; 0.70]	5.9%
ORCADES (982)	-0.034	0.05	-0.03 [-0.13; 0.06]	6.0%
RECOMBINE (445)	0.207	0.06	0.21 [0.09; 0.32]	3.7%
STABILITY (2951)	-0.003	0.02	-0.00 [-0.05; 0.04]	21.4%
STANLEY (344)	0.418	0.07	0.42 [0.27; 0.56]	2.4%
STANLEY (300)	0.300	0.07	0.30 [0.16; 0.44]	2.6%
VIS (902)	0.128	0.05	0.13 [0.04; 0.22]	5.9%
Common effect model			0.19 [0.17; 0.21]	100.0%
Random effects model			0.23 [0.10; 0.37]	-- 100.0%



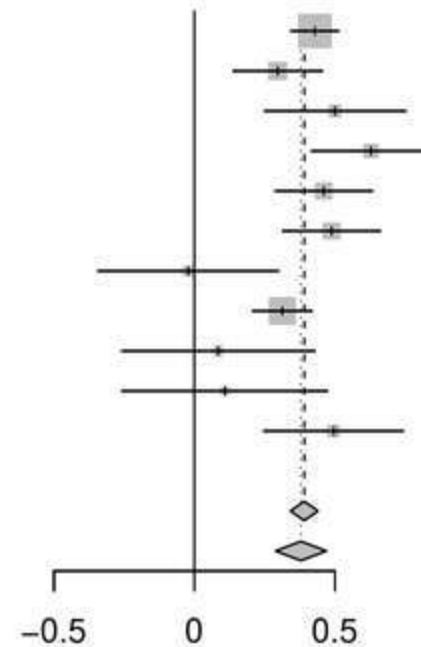
Heterogeneity: $I^2 = 97\%$, $\tau^2 = 0.0489$, $p < 0.01$

MCP-4 (CCL13)-rs12075



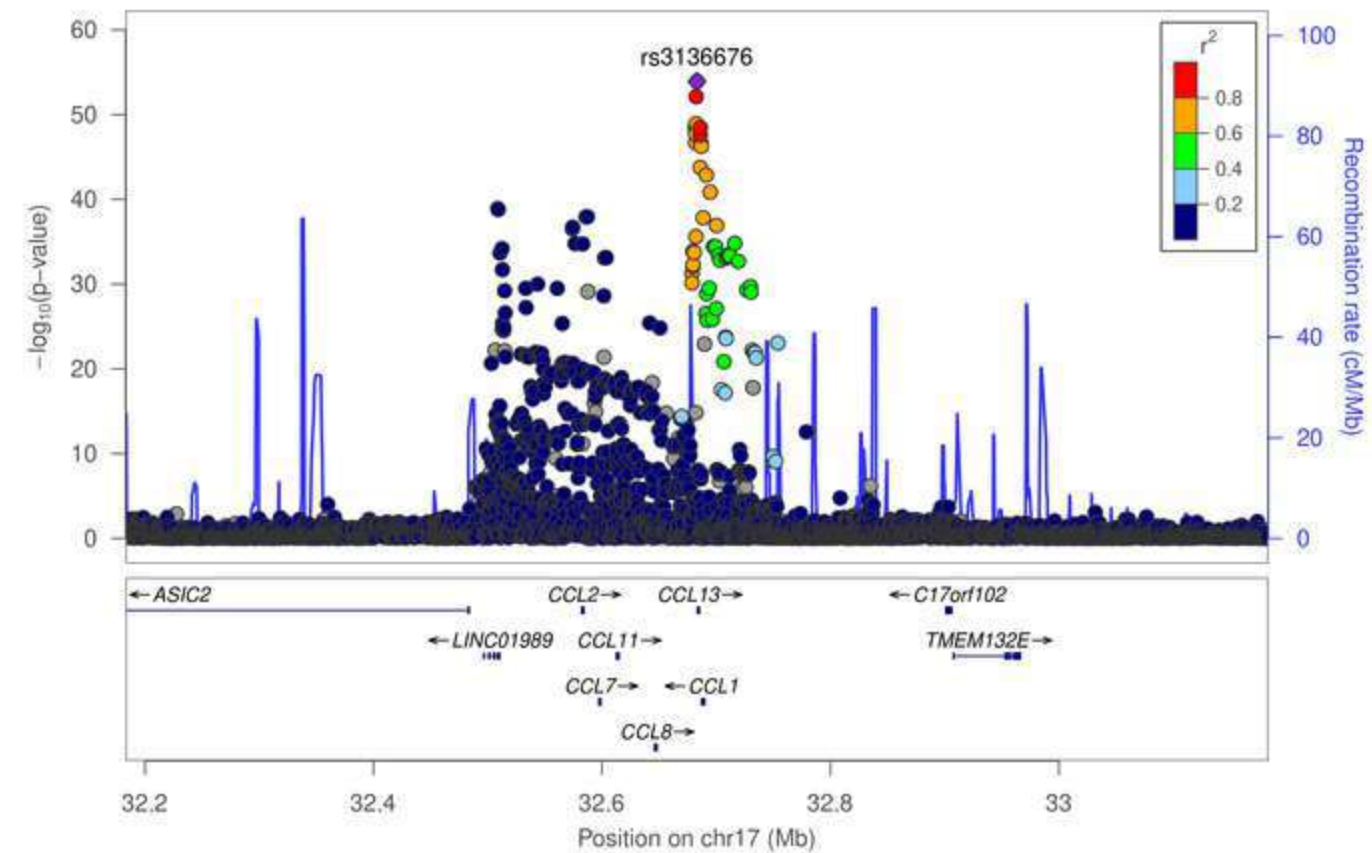
MCP-4 (CCL13) [chr17:32683289_A_G (rs3136676) (A/G) N=14728]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.428	0.04	0.43 [0.34; 0.51]	33.3%
BioFinder (1496)	0.296	0.08	0.30 [0.14; 0.46]	9.6%
EGCUT (487)	0.500	0.13	0.50 [0.25; 0.75]	3.8%
KORA (1064)	0.628	0.11	0.63 [0.42; 0.84]	5.4%
NSPHS (866)	0.460	0.09	0.46 [0.29; 0.63]	8.1%
ORCADES (982)	0.487	0.09	0.49 [0.31; 0.66]	8.0%
RECOMBINE (440)	-0.022	0.16	-0.02 [-0.34; 0.30]	2.3%
STABILITY (2951)	0.312	0.05	0.31 [0.21; 0.42]	21.7%
STANLEY (344)	0.085	0.18	0.08 [-0.26; 0.43]	2.1%
STANLEY (300)	0.108	0.19	0.11 [-0.26; 0.47]	1.8%
VIS (902)	0.495	0.13	0.50 [0.25; 0.74]	3.9%
Common effect model			0.39 [0.34; 0.44]	100.0%
Random effects model			0.38 [0.29; 0.47]	100.0%

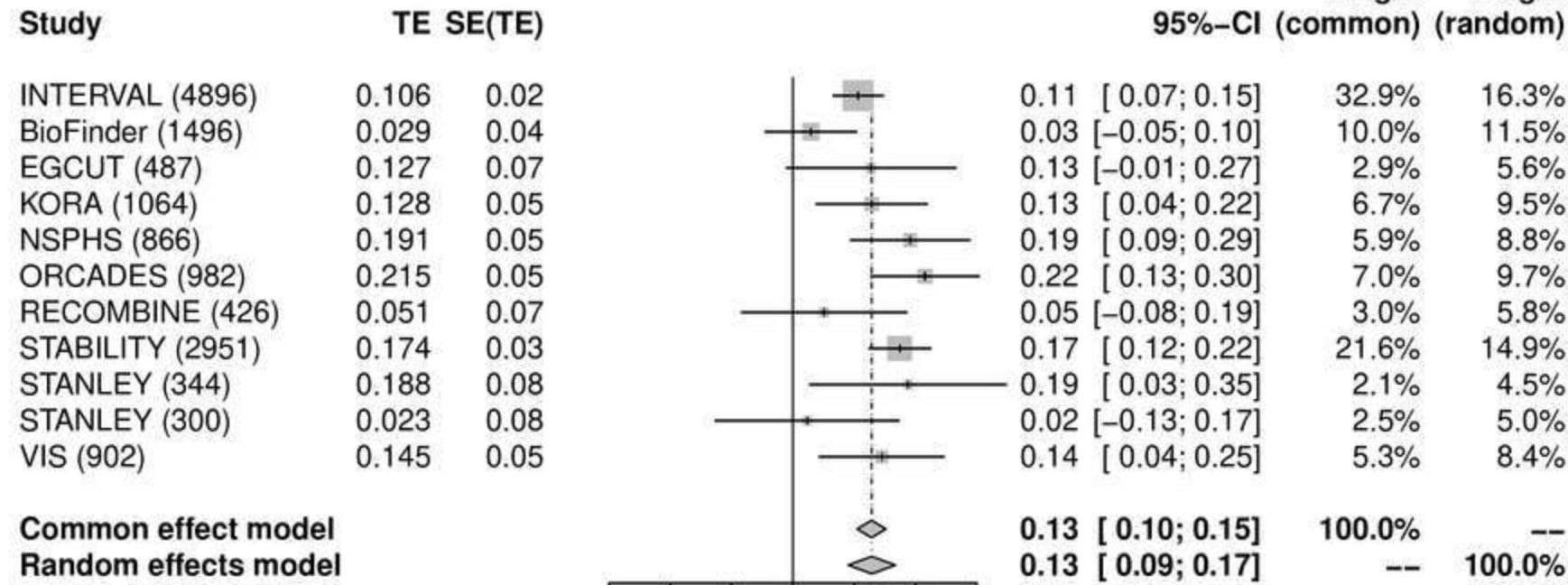


Heterogeneity: $I^2 = 58\%$, $\tau^2 = 0.0124$, $p < 0.01$

MCP-4 (CCL13)-rs3136676

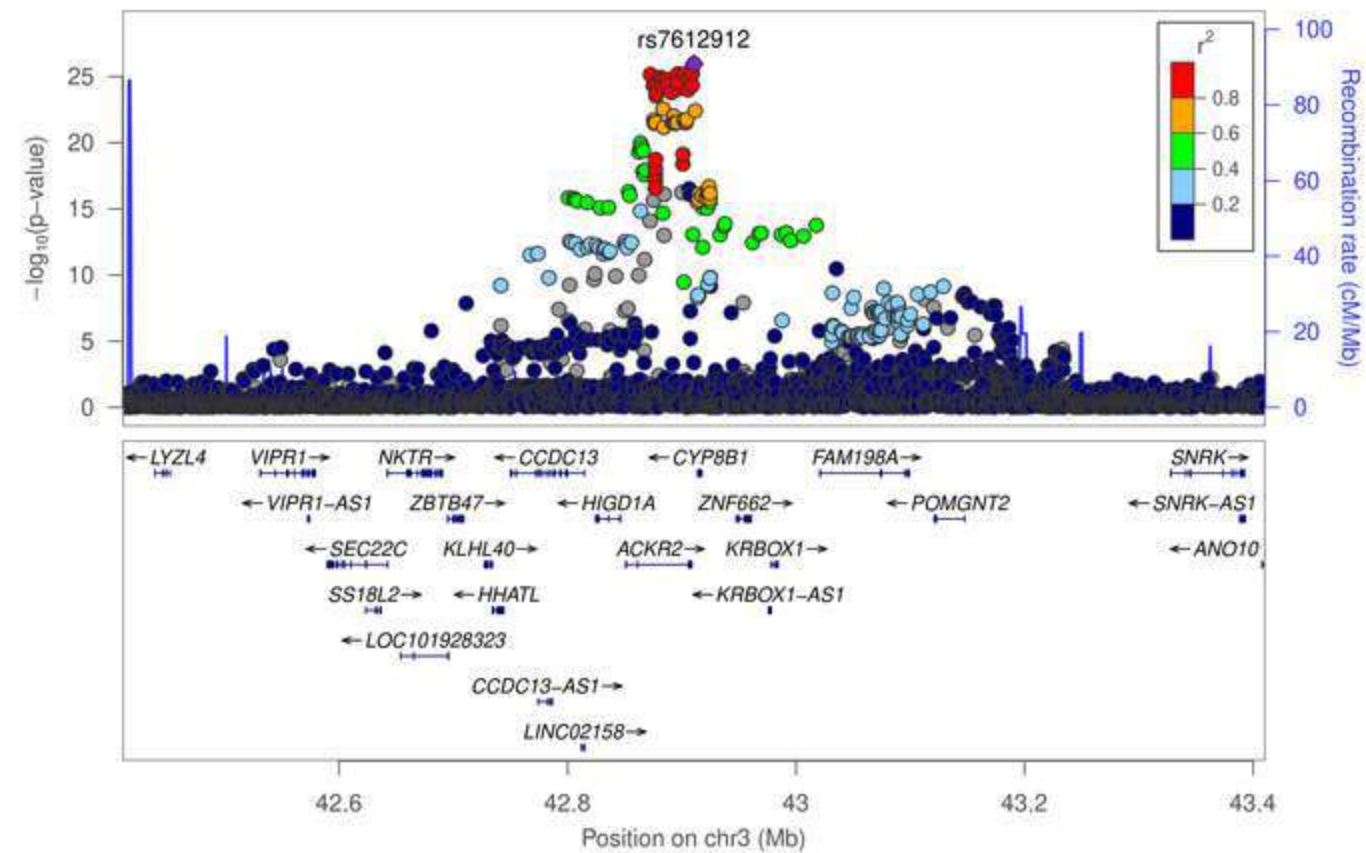


MCP-4 (CCL13) [chr3:42910621_C_T (rs7612912) (T/C) N=14714]



Heterogeneity: $I^2 = 51\%$, $\tau^2 = 0.0020$, $p = 0.03$

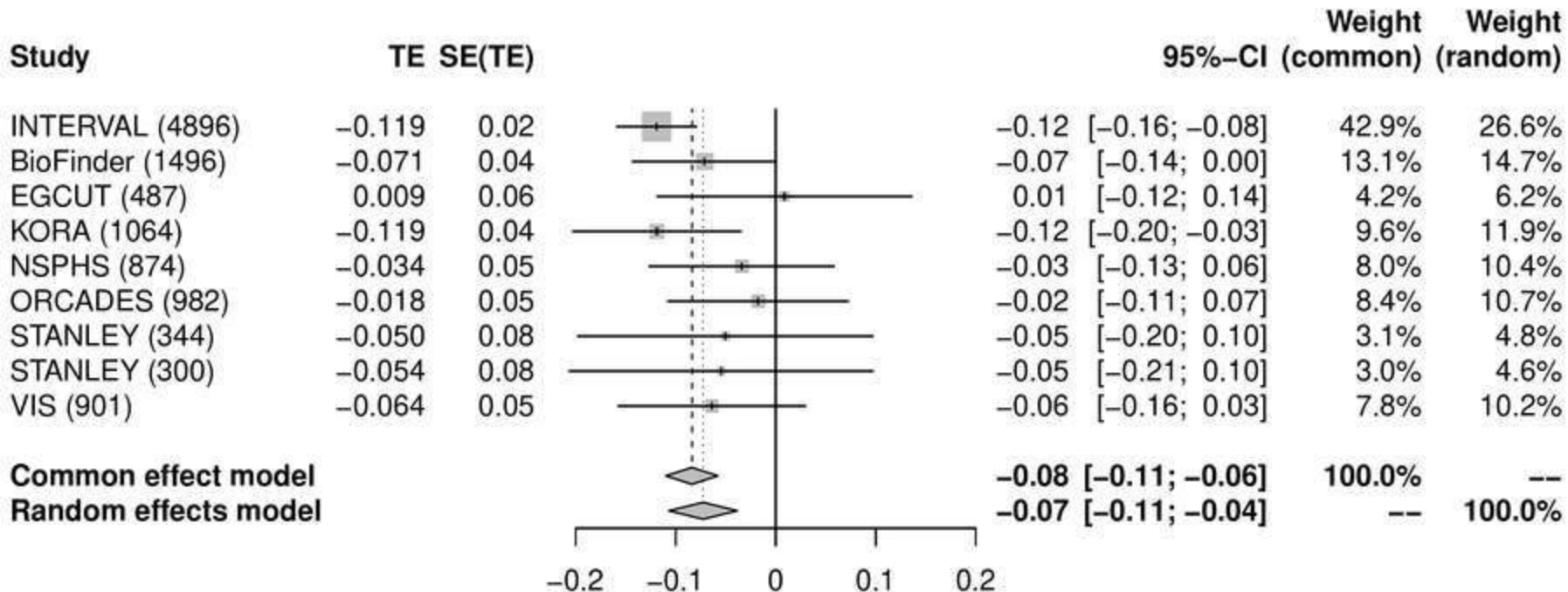
MCP-4 (CCL13)-rs7612912



MCP-4 (CCL13)-rs2721961

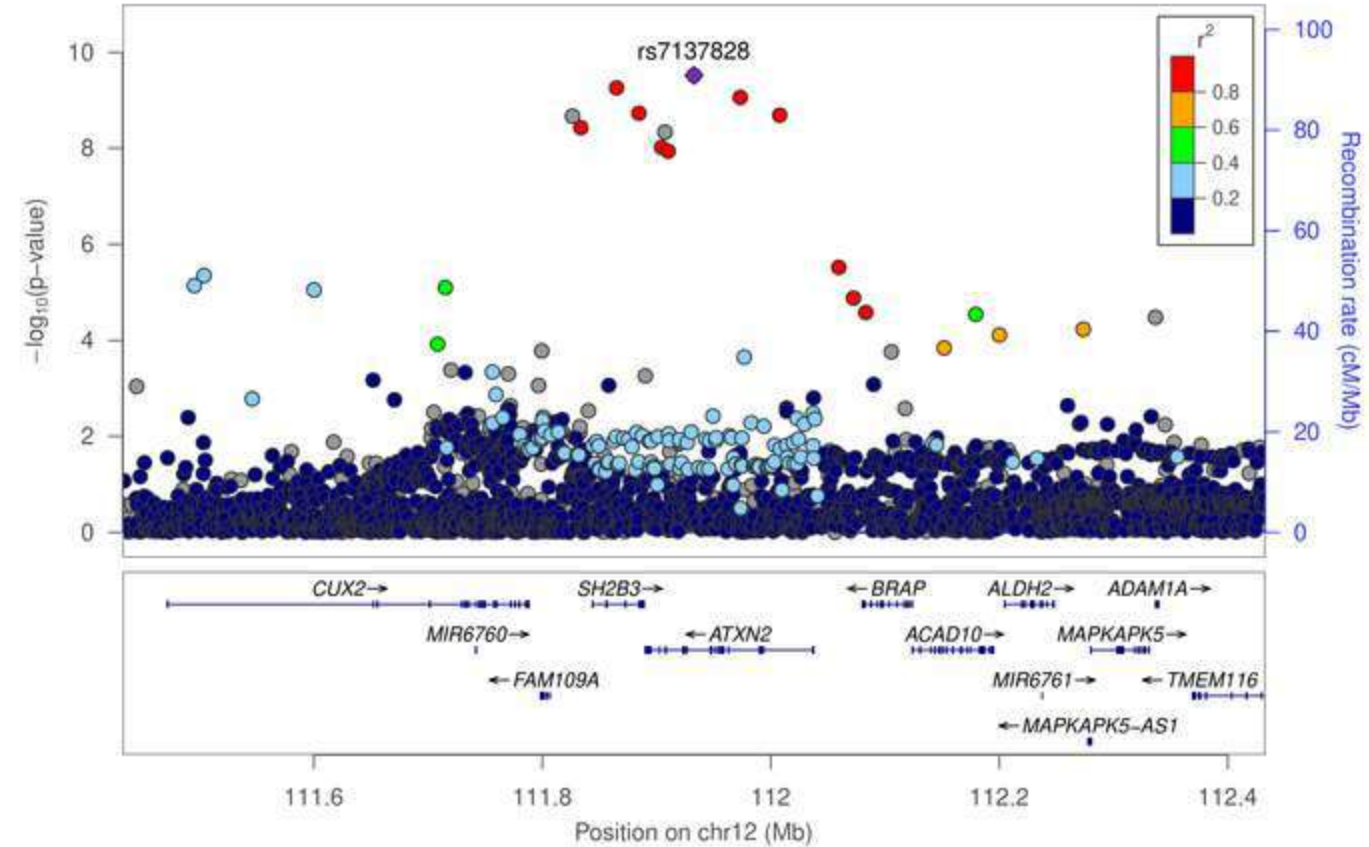
Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.88$

MIP-1 alpha (CCL3) [chr12:111932800_C_T (rs7137828) (T/C) N=11344]

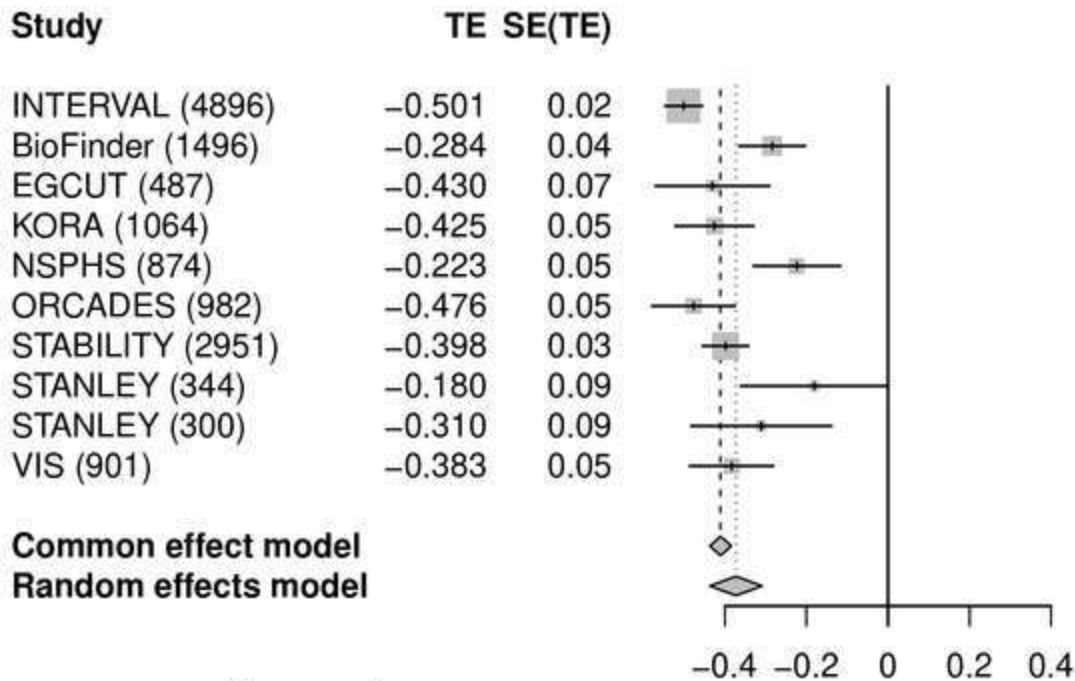


Heterogeneity: $I^2 = 16\%$, $\tau^2 = 0.0007$, $p = 0.30$

MIP-1 (alpha)-rs7137828



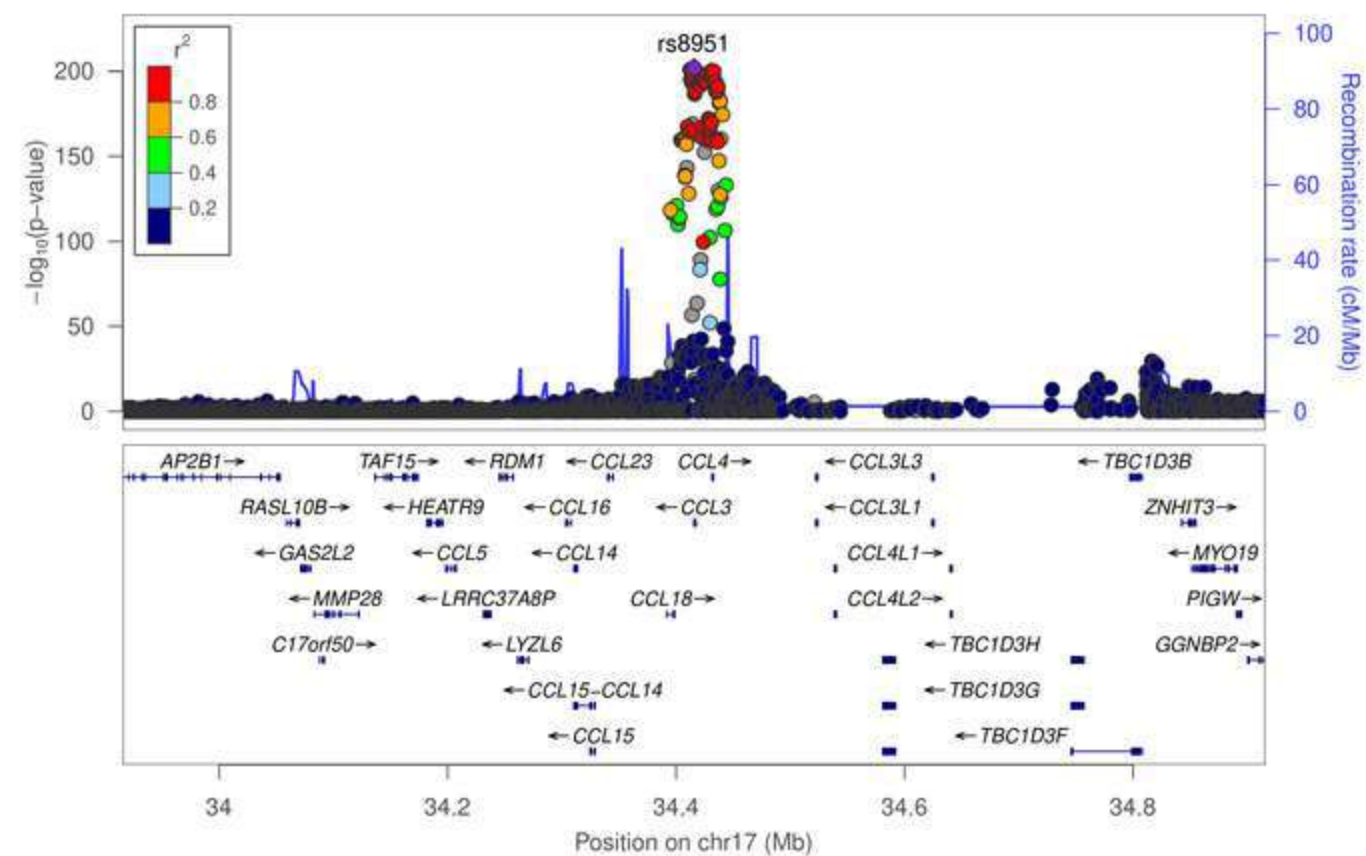
MIP-1 alpha (CCL3) [chr17:34415720_C_T (rs8951) (T/C) N=14295]



Heterogeneity: $I^2 = 80\%$, $\tau^2 = 0.0078$, $p < 0.01$

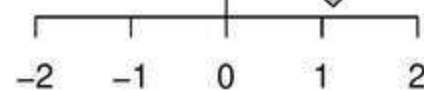
	Weight	Weight
95%-CI (common)	(common)	(random)
-0.50 [-0.55; -0.46]	33.1%	13.0%
-0.28 [-0.37; -0.20]	10.5%	11.4%
-0.43 [-0.57; -0.29]	3.6%	8.4%
-0.43 [-0.52; -0.33]	7.4%	10.6%
-0.22 [-0.33; -0.12]	6.1%	10.1%
-0.48 [-0.58; -0.37]	6.7%	10.3%
-0.40 [-0.45; -0.34]	21.5%	12.5%
-0.18 [-0.36; 0.00]	2.1%	6.6%
-0.31 [-0.48; -0.14]	2.3%	6.9%
-0.38 [-0.49; -0.28]	6.6%	10.2%
-0.41 [-0.44; -0.38]	100.0%	--
-0.37 [-0.44; -0.31]	--	100.0%

MIP-1 (alpha)-rs8951



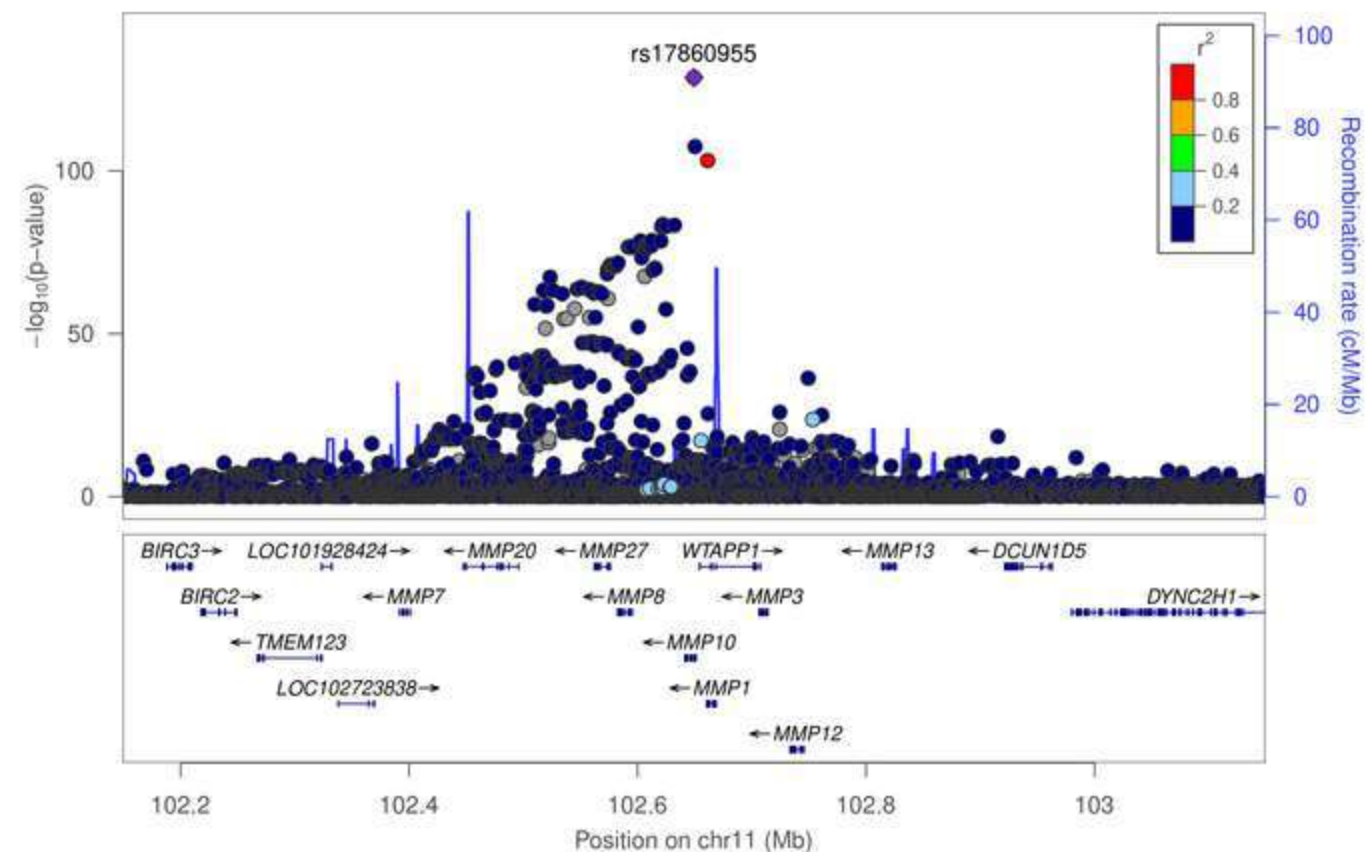
MMP-10 (MMP10) [chr11:102649482_C_T (rs17860955) (T/C) N=14256]

Study	TE	SE(TE)		95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	1.224	0.07		1.22 [1.08; 1.37]	41.4%	31.7%
BioFinder (1496)	1.258	0.16		1.26 [0.94; 1.58]	8.3%	9.9%
KORA (1064)	0.967	0.16		0.97 [0.66; 1.28]	8.8%	10.4%
NSPHS (874)	0.994	0.18		0.99 [0.65; 1.34]	7.2%	8.8%
ORCADES (982)	0.911	0.22		0.91 [0.48; 1.34]	4.7%	6.0%
RECOMBINE (447)	-0.105	0.40		-0.10 [-0.90; 0.69]	1.4%	1.8%
STABILITY (2951)	1.175	0.11		1.18 [0.96; 1.39]	18.7%	19.0%
STANLEY (344)	1.092	0.26		1.09 [0.57; 1.61]	3.2%	4.1%
STANLEY (300)	1.570	0.46		1.57 [0.67; 2.47]	1.0%	1.4%
VIS (902)	1.072	0.20		1.07 [0.67; 1.47]	5.4%	6.8%
Common effect model				1.14 [1.04; 1.23]	100.0%	--
Random effects model				1.12 [1.01; 1.23]	--	100.0%



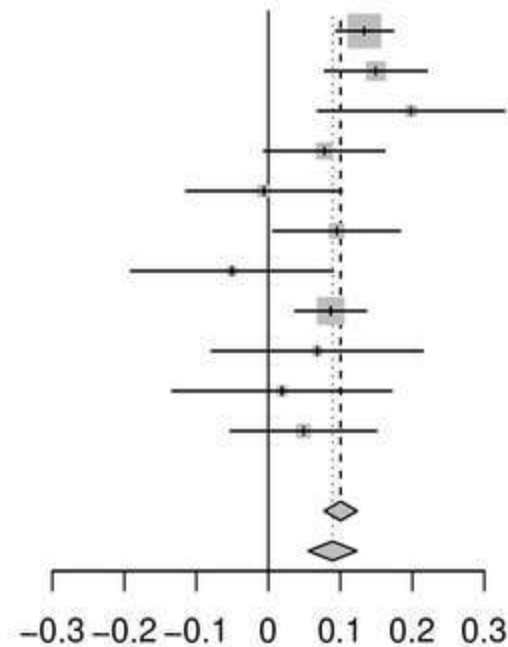
Heterogeneity: $I^2 = 42\%$, $\tau^2 = 0.0043$, $p = 0.08$

MMP-10 (MMP10)-rs17860955



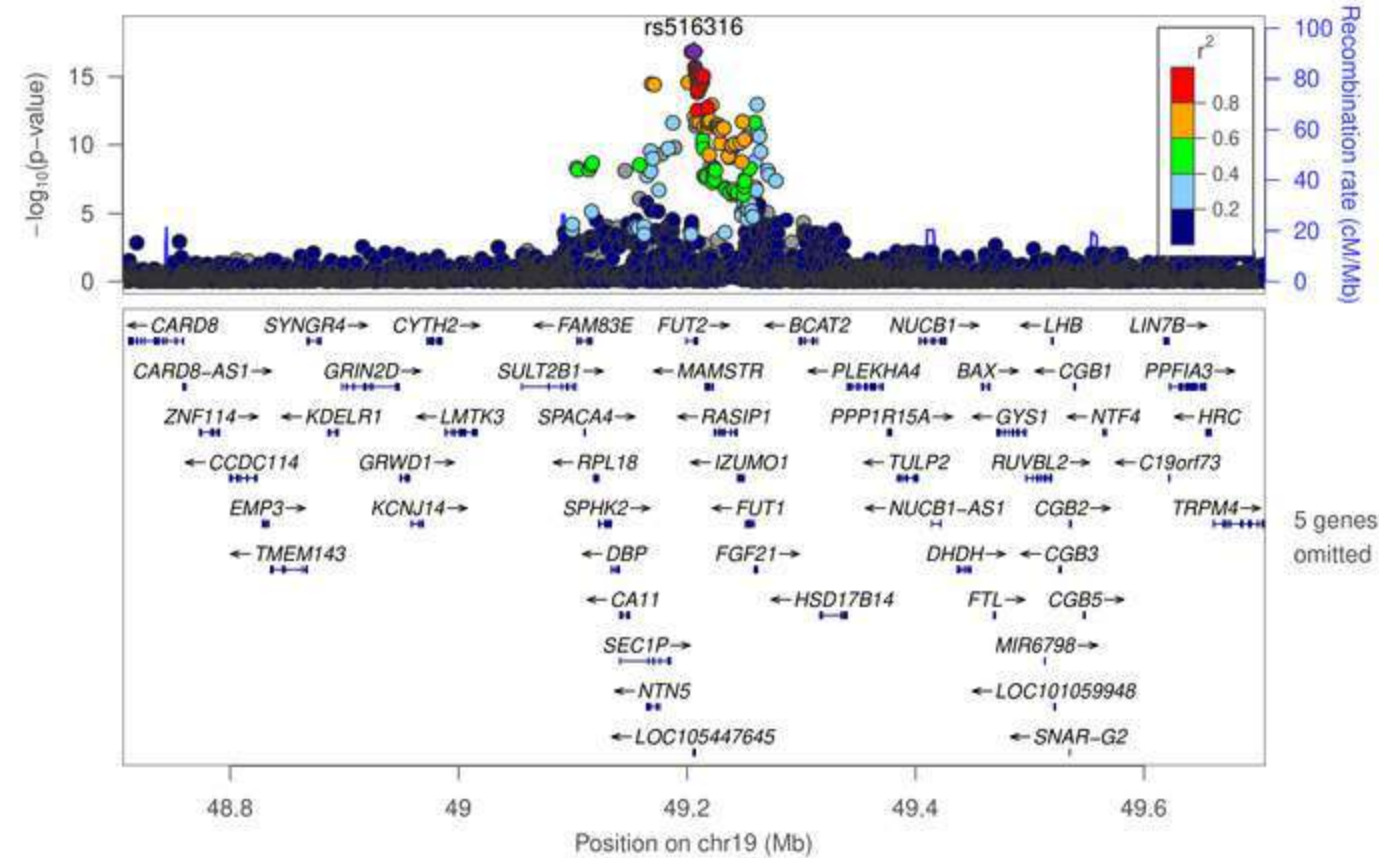
MMP-10 (MMP10) [chr19:49206145_C_G (rs516316) (C/G) N=14742]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.133	0.02	0.13 [0.09; 0.17]	33.4%	18.8%
BioFinder (1496)	0.149	0.04	0.15 [0.08; 0.22]	10.5%	12.0%
EGCUT (487)	0.198	0.07	0.20 [0.07; 0.33]	3.1%	5.4%
KORA (1064)	0.078	0.04	0.08 [-0.01; 0.16]	7.5%	9.9%
NSPHS (874)	-0.006	0.06	-0.01 [-0.11; 0.10]	4.5%	7.1%
ORCADES (982)	0.095	0.05	0.09 [0.01; 0.18]	6.8%	9.3%
RECOMBINE (446)	-0.051	0.07	-0.05 [-0.19; 0.09]	2.7%	4.7%
STABILITY (2951)	0.086	0.03	0.09 [0.04; 0.14]	21.6%	16.5%
STANLEY (344)	0.068	0.07	0.07 [-0.08; 0.21]	2.5%	4.4%
STANLEY (300)	0.019	0.08	0.02 [-0.13; 0.17]	2.3%	4.1%
VIS (902)	0.049	0.05	0.05 [-0.05; 0.15]	5.1%	7.7%
Common effect model			0.10 [0.08; 0.12]	100.0%	--
Random effects model			0.09 [0.06; 0.12]	--	100.0%



Heterogeneity: $I^2 = 43\%$, $\tau^2 = 0.0012$, $p = 0.06$

MMP-10 (MMP10)-rs516316



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (874)

ORCADES (982)

RECOMBINE (433)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 77\%$, $\tau^2 = 0.0062$, $p < 0.01$

MMP-1 (MMP1) [chr11:102697731_A_G (rs471994) (A/G) N=14729]

TE SE(TE)

-0.390 0.02

-0.304 0.04

-0.374 0.07

-0.457 0.04

-0.445 0.05

-0.370 0.04

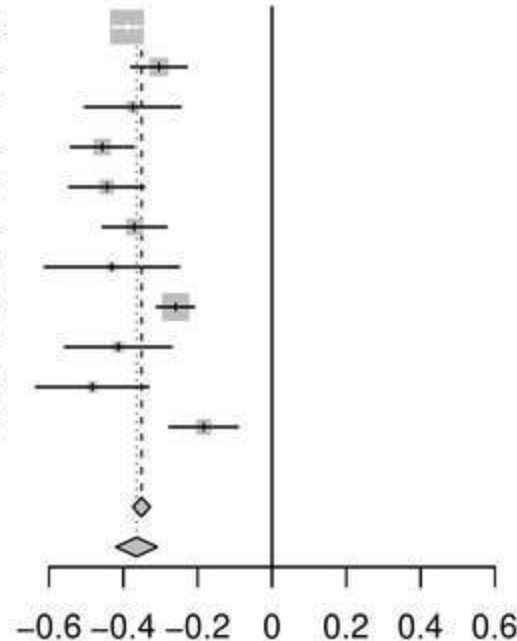
-0.431 0.09

-0.260 0.03

-0.414 0.07

-0.483 0.08

-0.184 0.05

Weight
95%-CI (common) (random)

-0.39 [-0.43; -0.35] 33.4% 12.2%

-0.30 [-0.38; -0.23] 9.5% 10.5%

-0.37 [-0.50; -0.24] 3.2% 7.6%

-0.46 [-0.54; -0.37] 7.5% 10.0%

-0.44 [-0.55; -0.34] 5.3% 9.1%

-0.37 [-0.46; -0.28] 7.2% 9.9%

-0.43 [-0.61; -0.25] 1.6% 5.5%

-0.26 [-0.31; -0.21] 20.9% 11.8%

-0.41 [-0.56; -0.27] 2.6% 7.0%

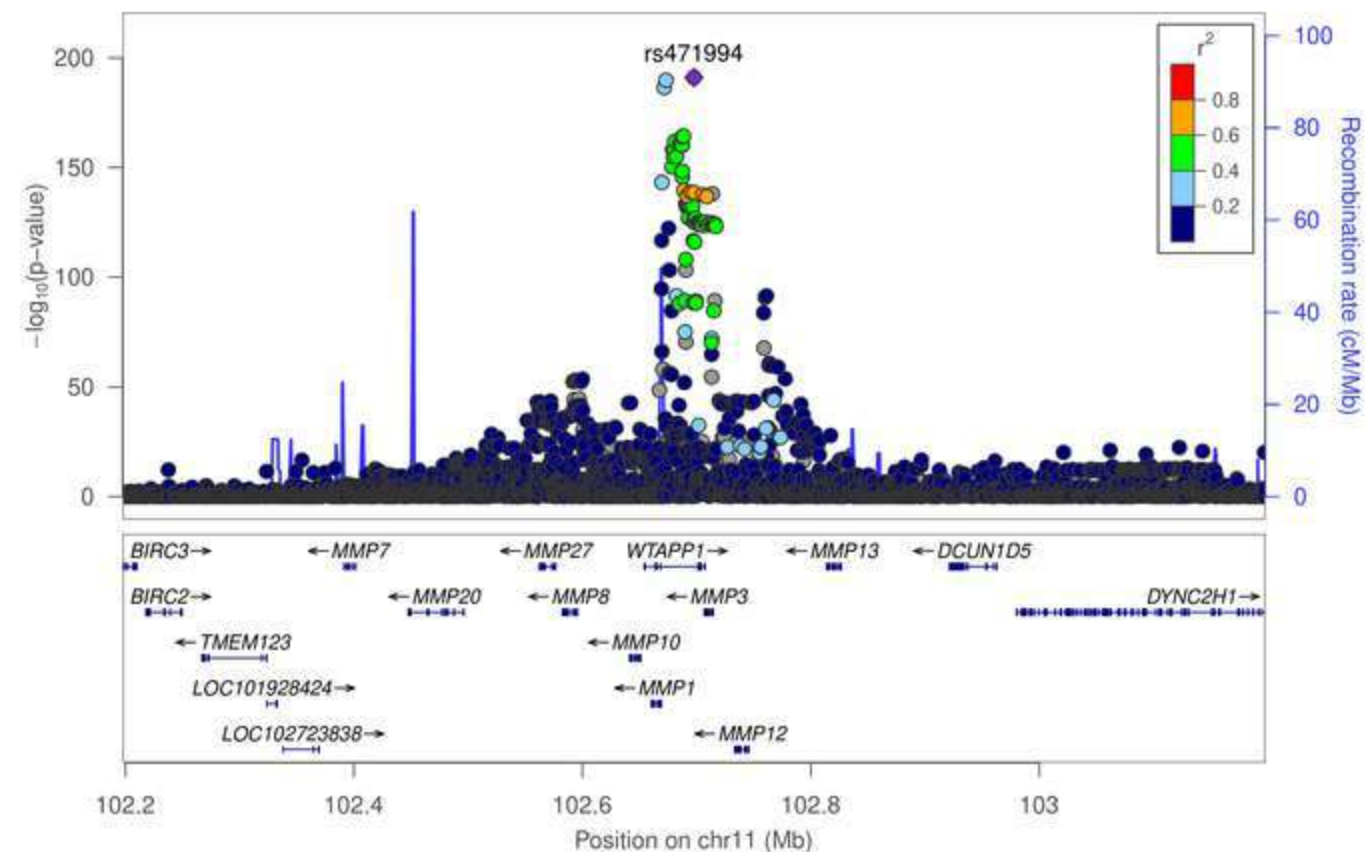
-0.48 [-0.64; -0.33] 2.3% 6.6%

-0.18 [-0.28; -0.09] 6.3% 9.6%

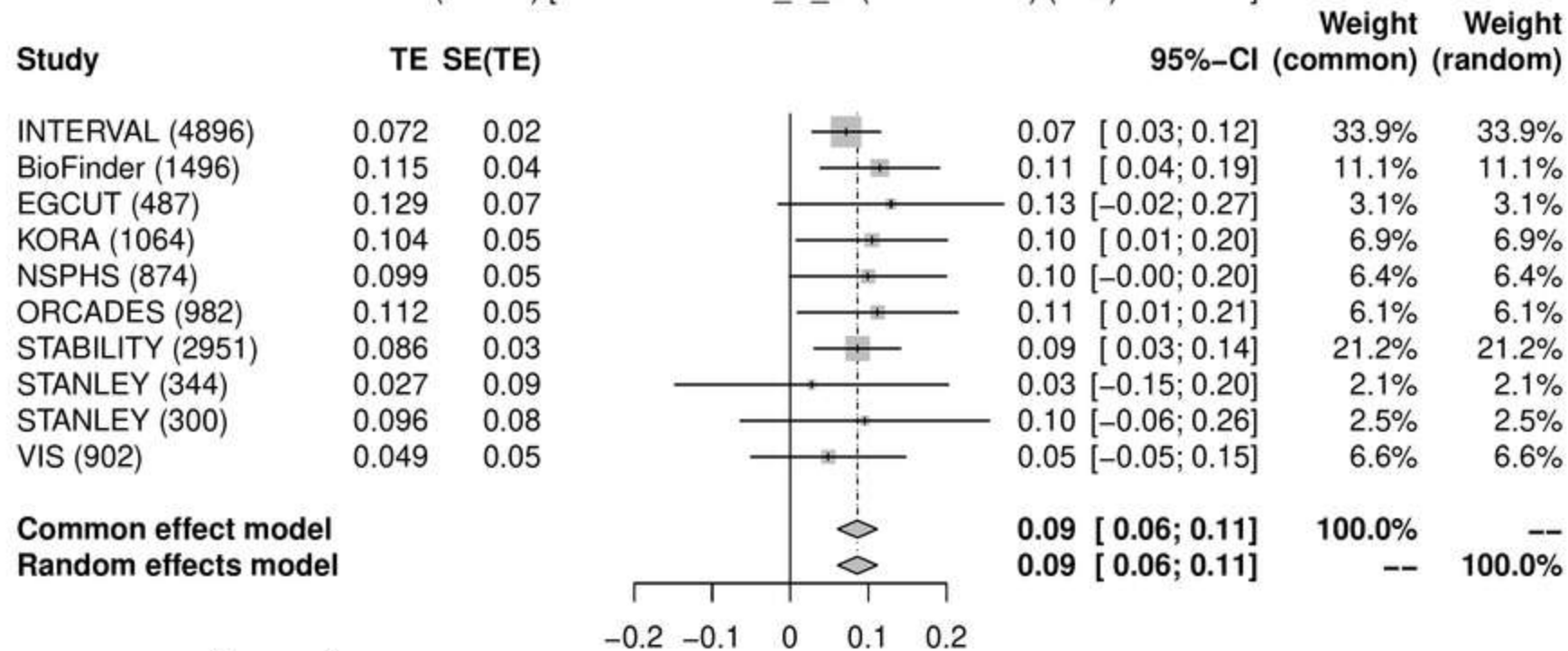
-0.35 [-0.37; -0.33] 100.0% --

-0.36 [-0.42; -0.31] -- 100.0%

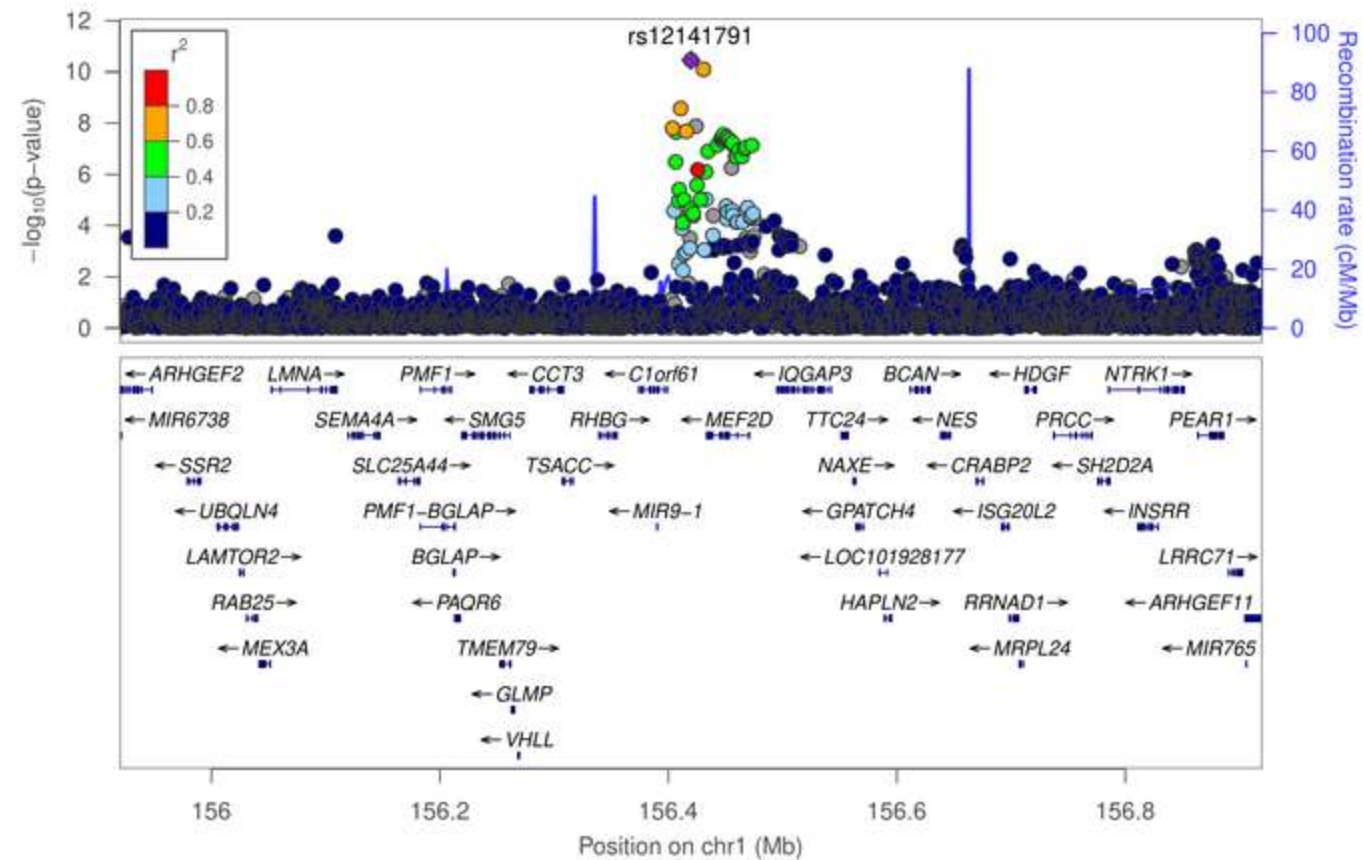
MMP-1 (MMP1)-rs471994



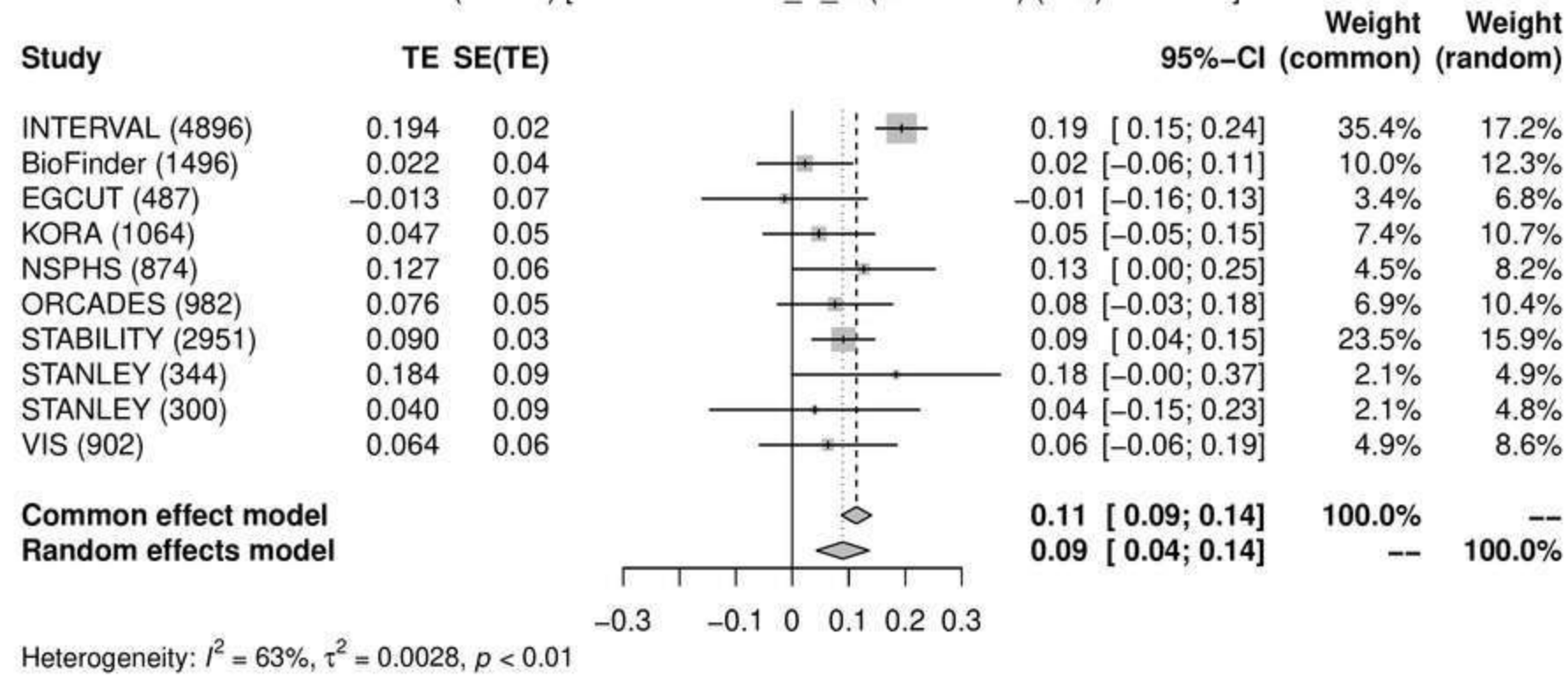
MMP-1 (MMP1) [chr1:156419786_A_G (rs12141791) (A/G) N=14296]



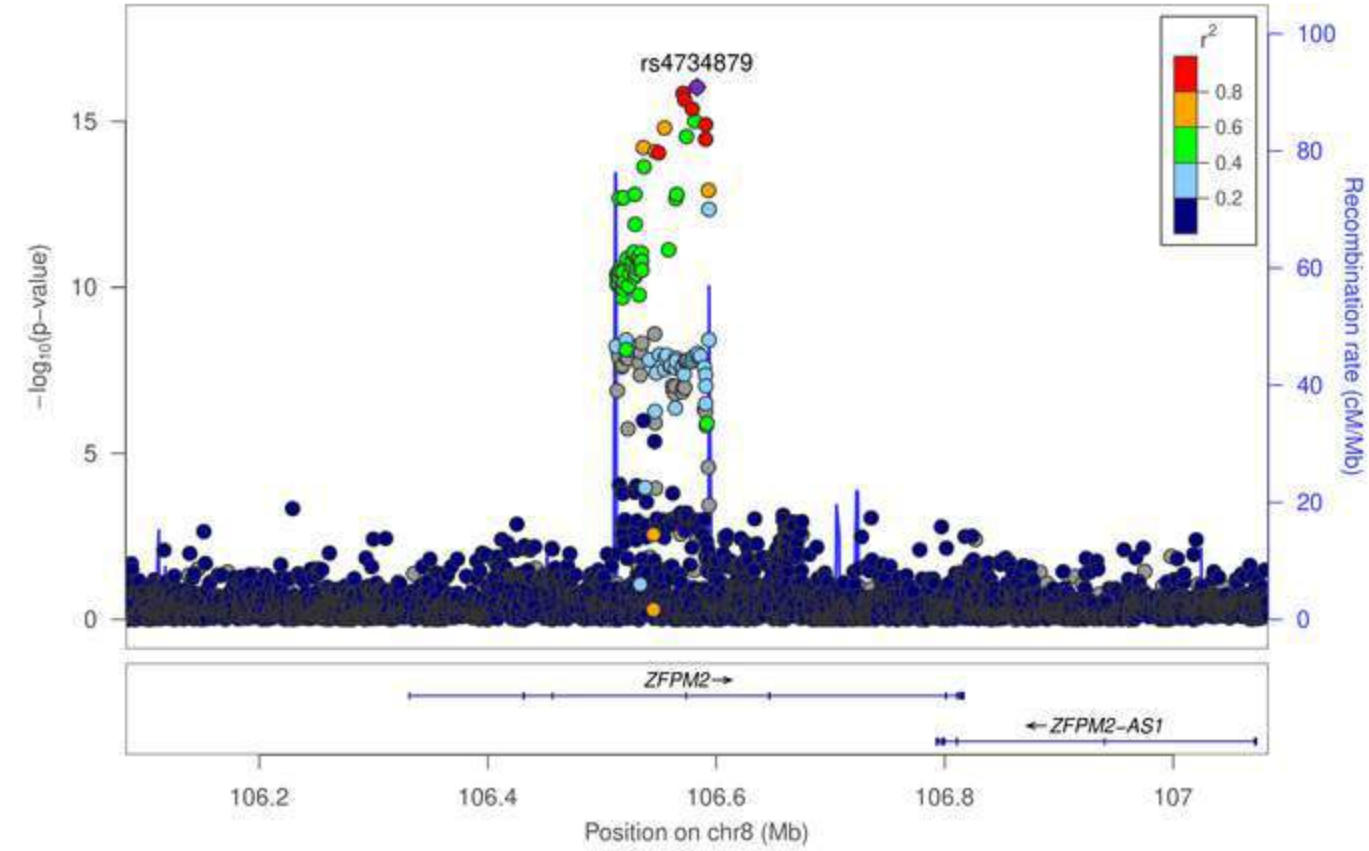
MMP-1 (MMP1)-rs12141791



MMP-1 (MMP1) [chr8:106583124_A_G (rs4734879) (A/G) N=14296]



MMP-1 (MMP1)-rs4734879



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (874)

ORCADES (982)

RECOMBINE (441)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 5\%$, $\tau^2 < 0.0001$, $p = 0.40$

NT-3 (NTF3) [chr15:88514855_C_G (rs28735437) (C/G) N=14737]

TE SE(TE)

-0.113 0.03

-0.074 0.05

-0.025 0.09

-0.212 0.06

-0.078 0.09

-0.171 0.06

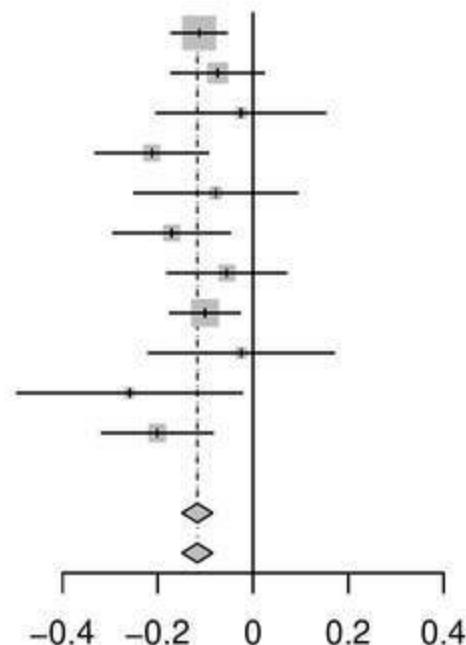
-0.055 0.06

-0.101 0.04

-0.025 0.10

-0.259 0.12

-0.201 0.06

Weight
95%-CI (common) (random)

-0.11 [-0.17; -0.05] 30.3% 30.3%

-0.07 [-0.17; 0.02] 10.9% 10.9%

-0.03 [-0.20; 0.15] 3.3% 3.3%

-0.21 [-0.33; -0.09] 7.3% 7.3%

-0.08 [-0.25; 0.09] 3.5% 3.5%

-0.17 [-0.29; -0.05] 6.9% 6.9%

-0.05 [-0.18; 0.07] 6.6% 6.6%

-0.10 [-0.17; -0.03] 19.1% 19.1%

-0.02 [-0.22; 0.17] 2.7% 2.7%

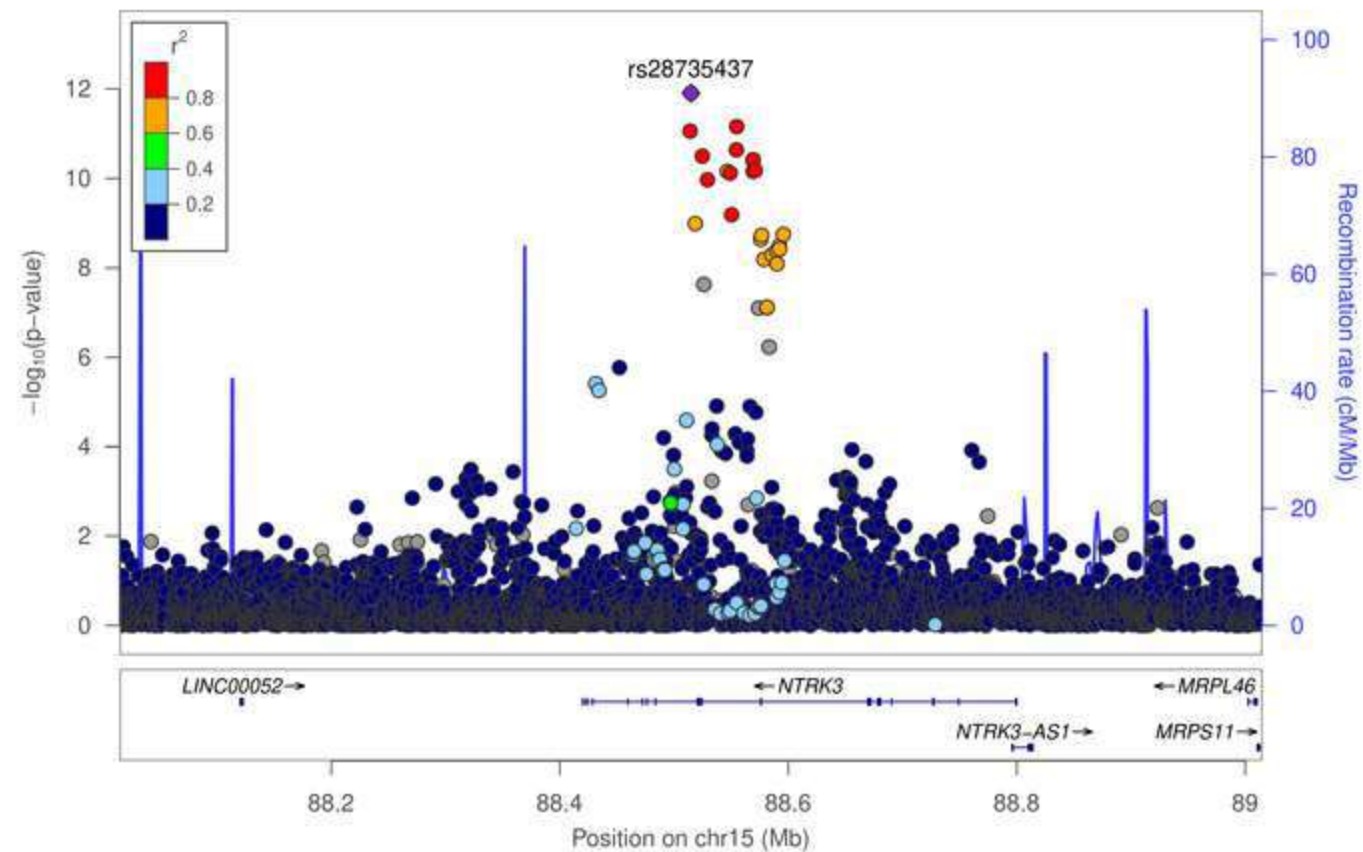
-0.26 [-0.50; -0.02] 1.9% 1.9%

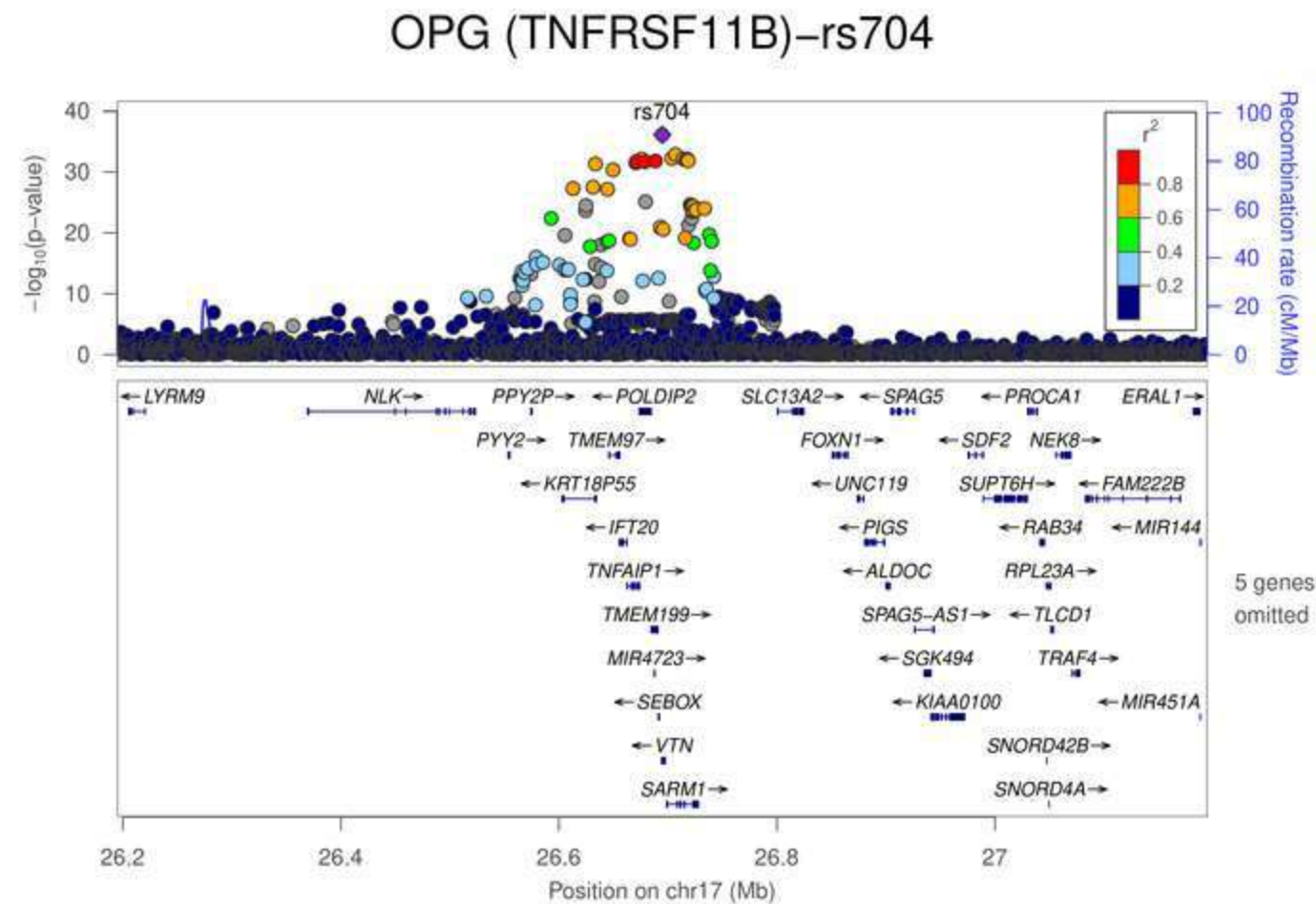
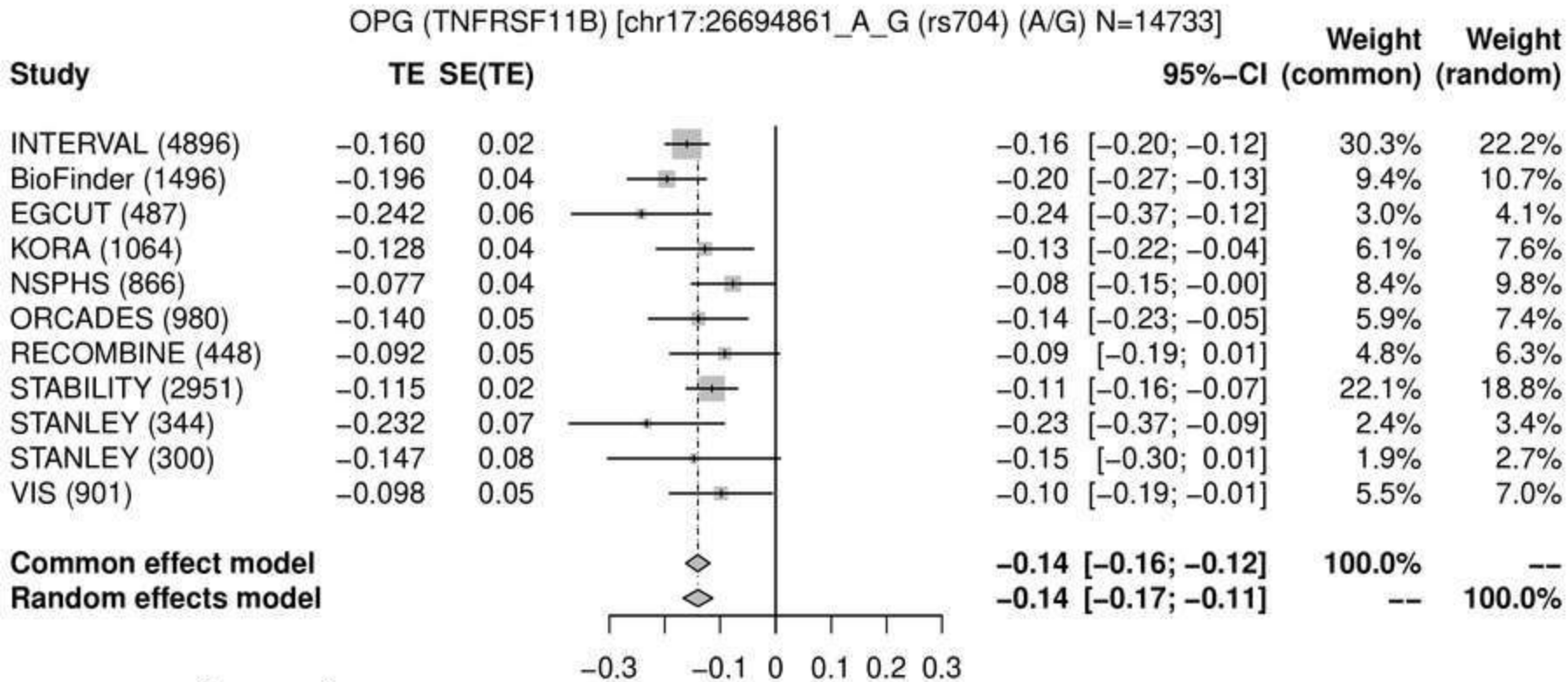
-0.20 [-0.32; -0.08] 7.6% 7.6%

-0.12 [-0.15; -0.08] 100.0% --

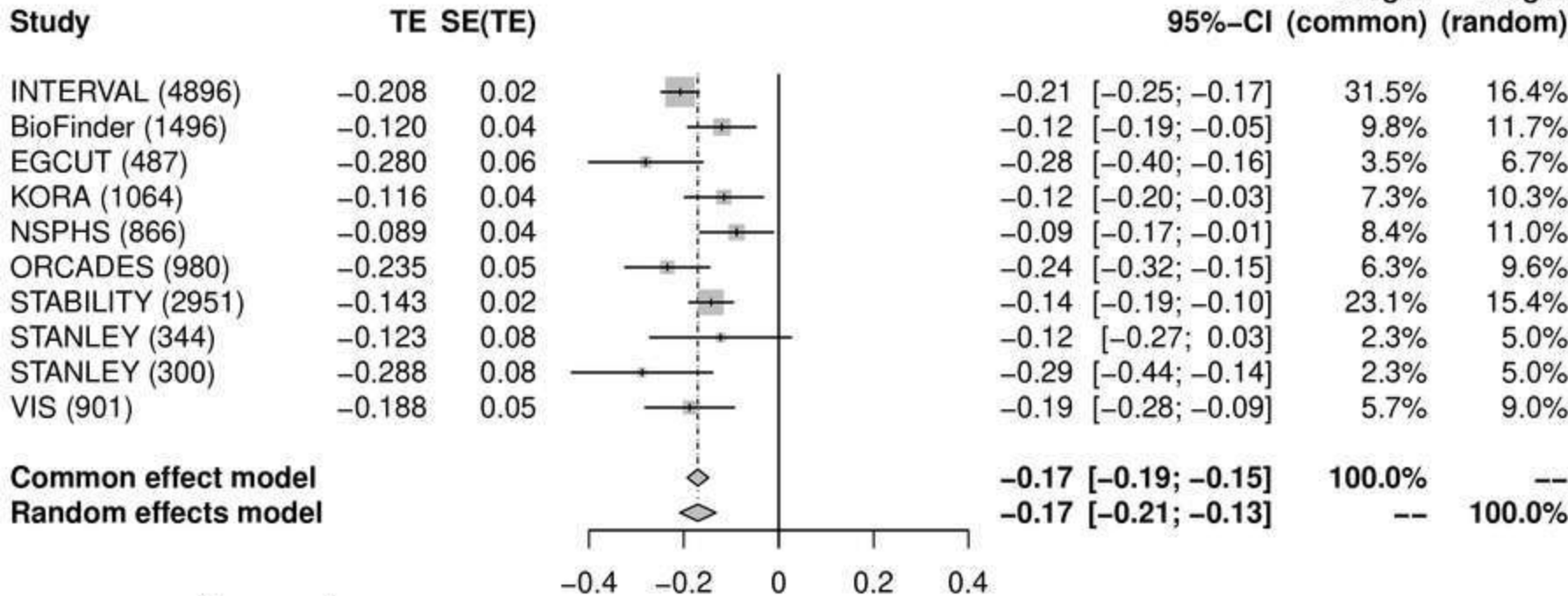
-0.12 [-0.15; -0.08] -- 100.0%

NT-3 (NTF3)-rs28735437



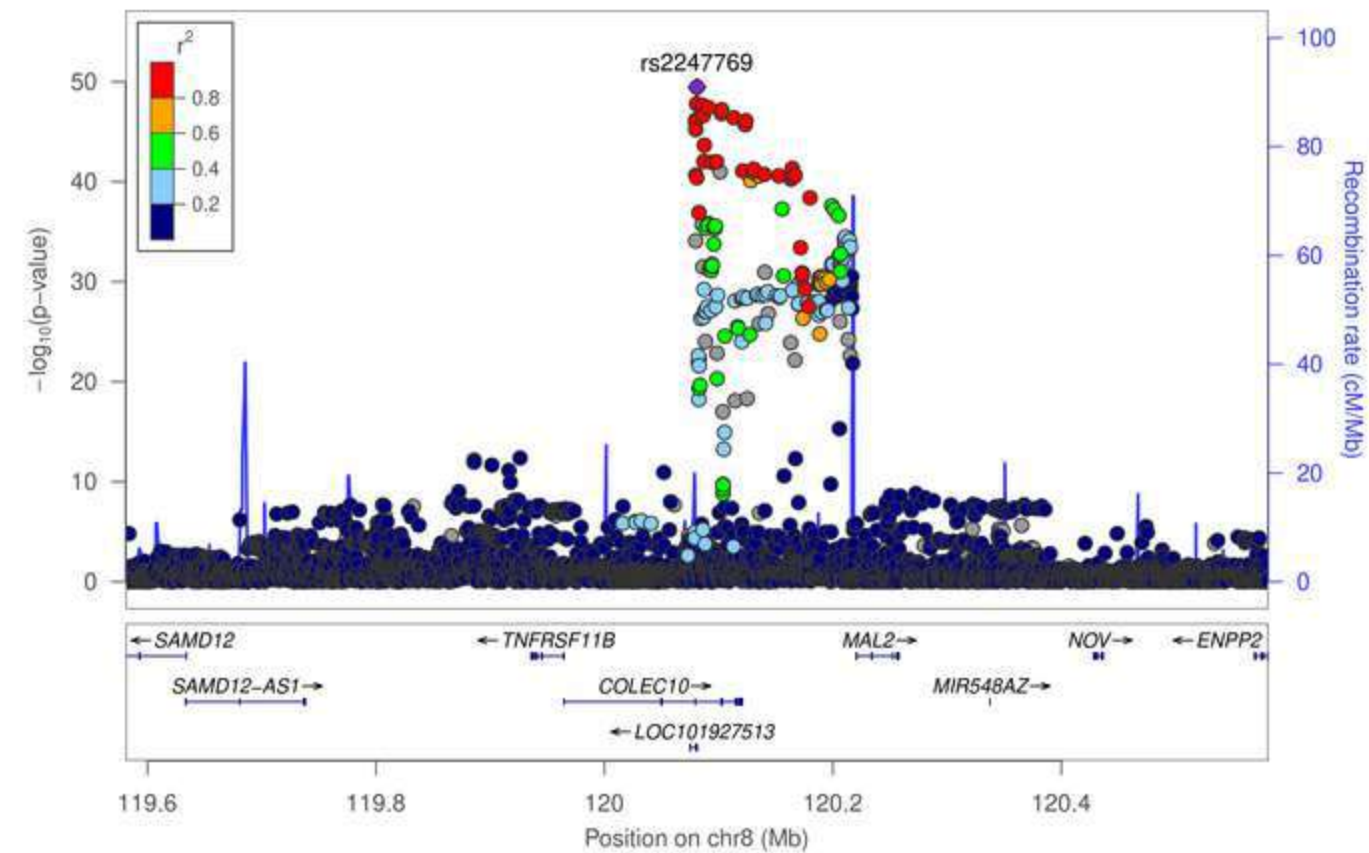


OPG (TNFRSF11B) [chr8:120081031_C_T (rs2247769) (T/C) N=14285]

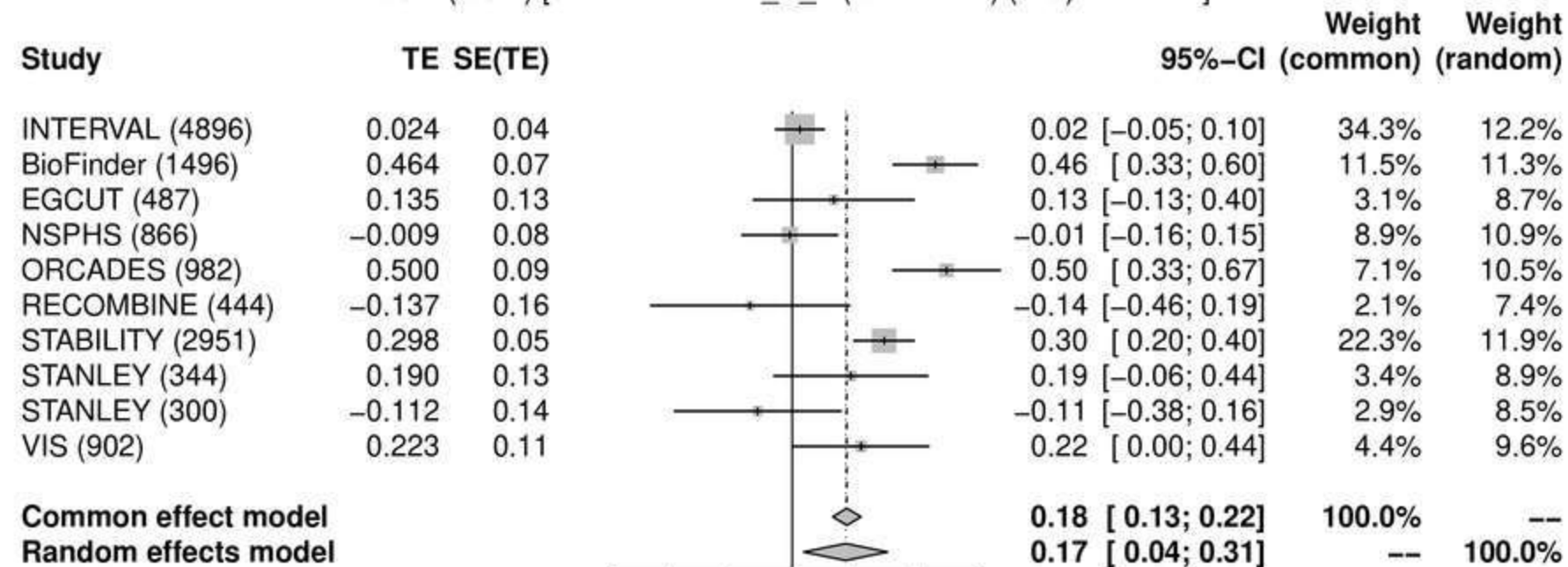


Heterogeneity: $I^2 = 57\%$, $\tau^2 = 0.0019$, $p = 0.01$

OPG (TNFRSF11B)-rs2247769

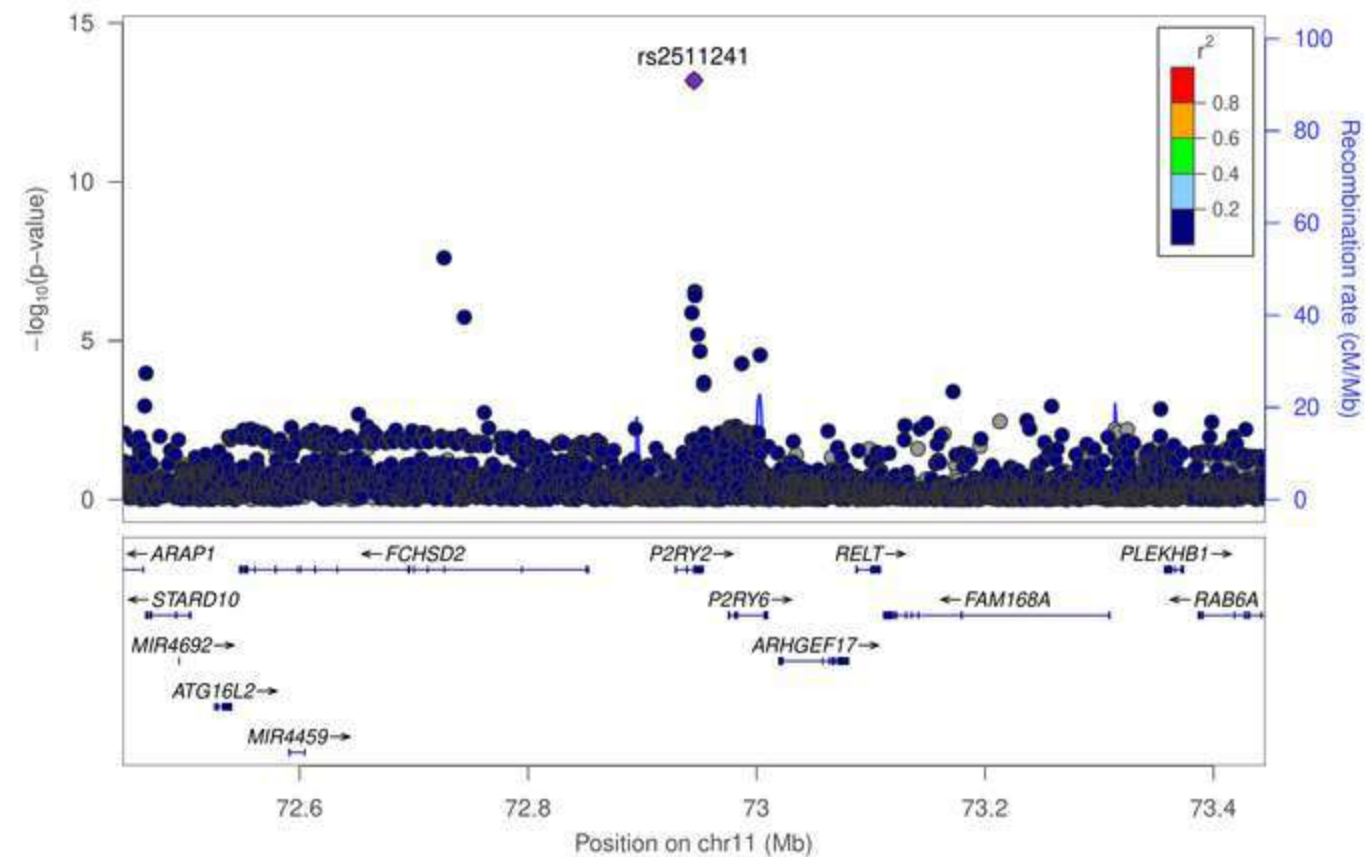


OSM (OSM) [chr11:72945341_C_T (rs2511241) (T/C) N=13668]



Heterogeneity: $I^2 = 86\%$, $\tau^2 = 0.0383$, $p < 0.01$

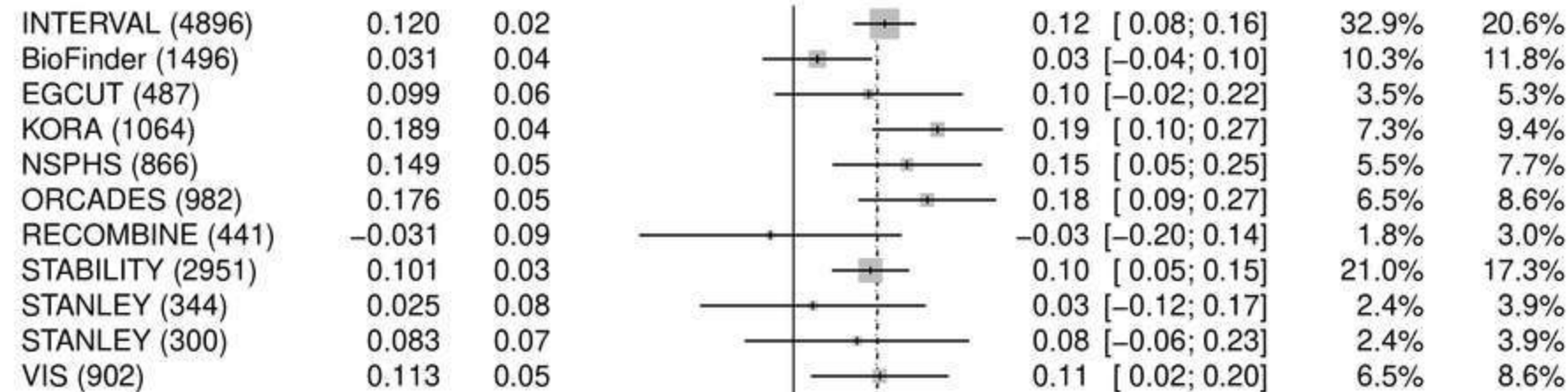
OSM (OSM)-rs2511241



Study

OSM (OSM) [chr17:38137033_A_G (rs3859189) (A/G) N=14729]

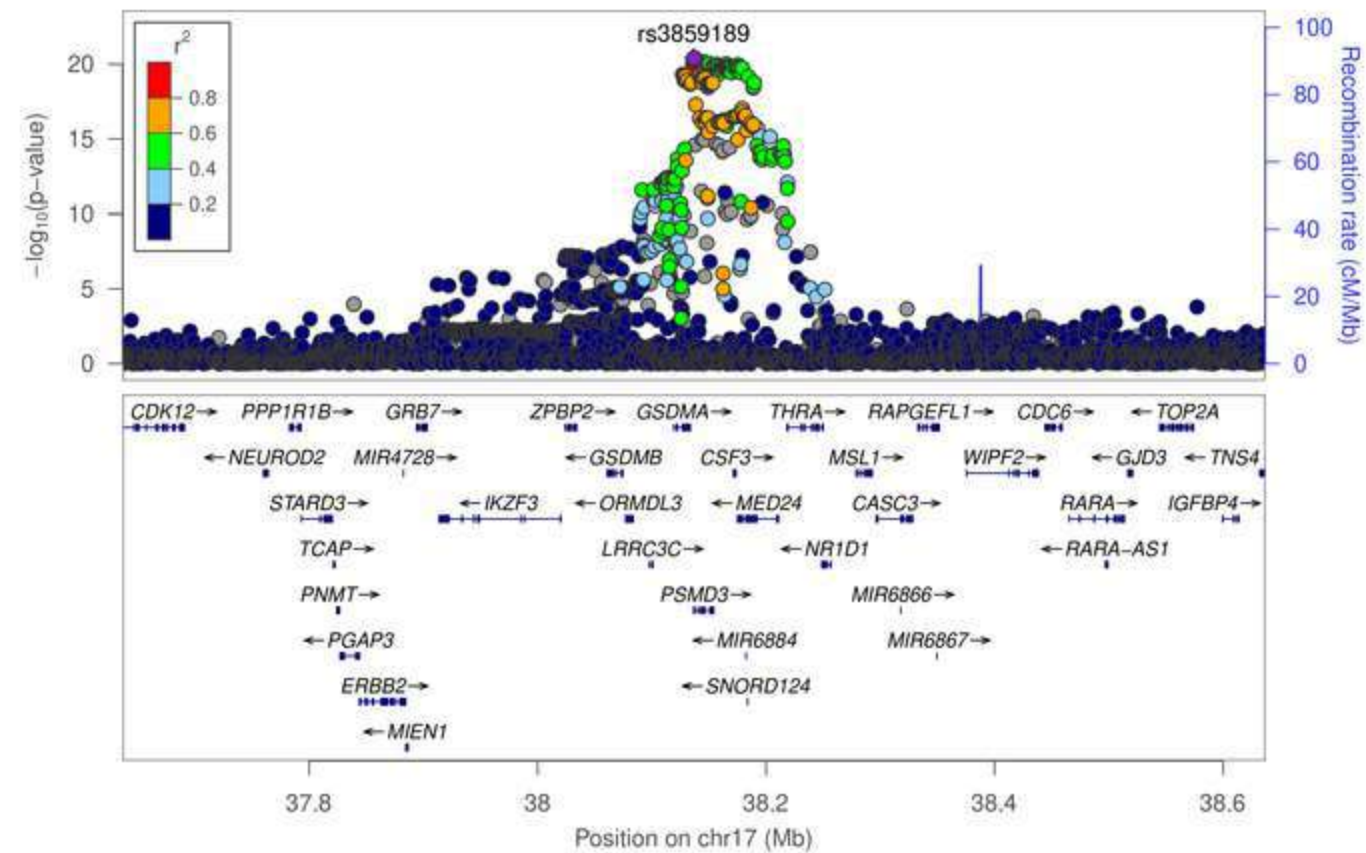
TE SE(TE)

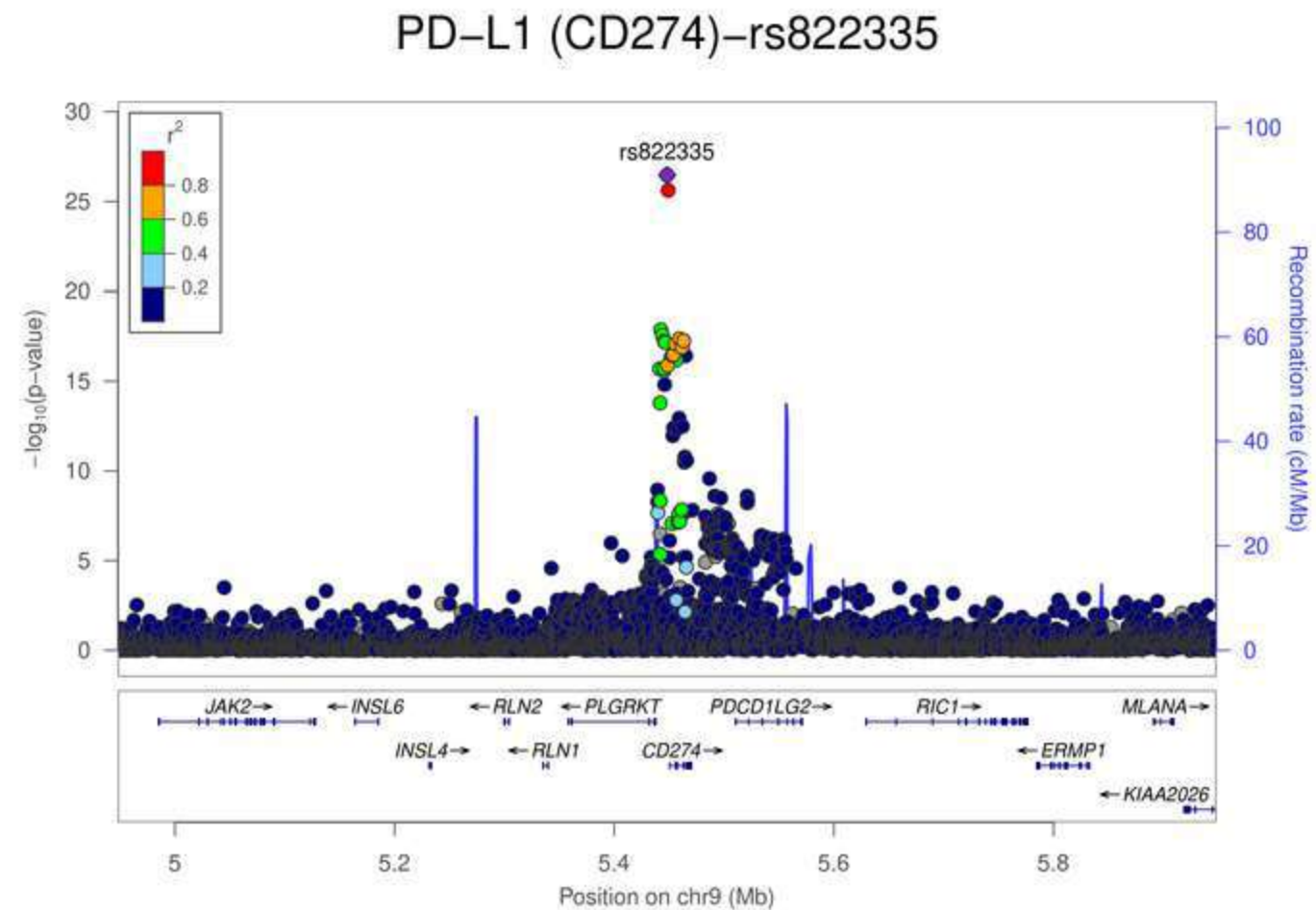
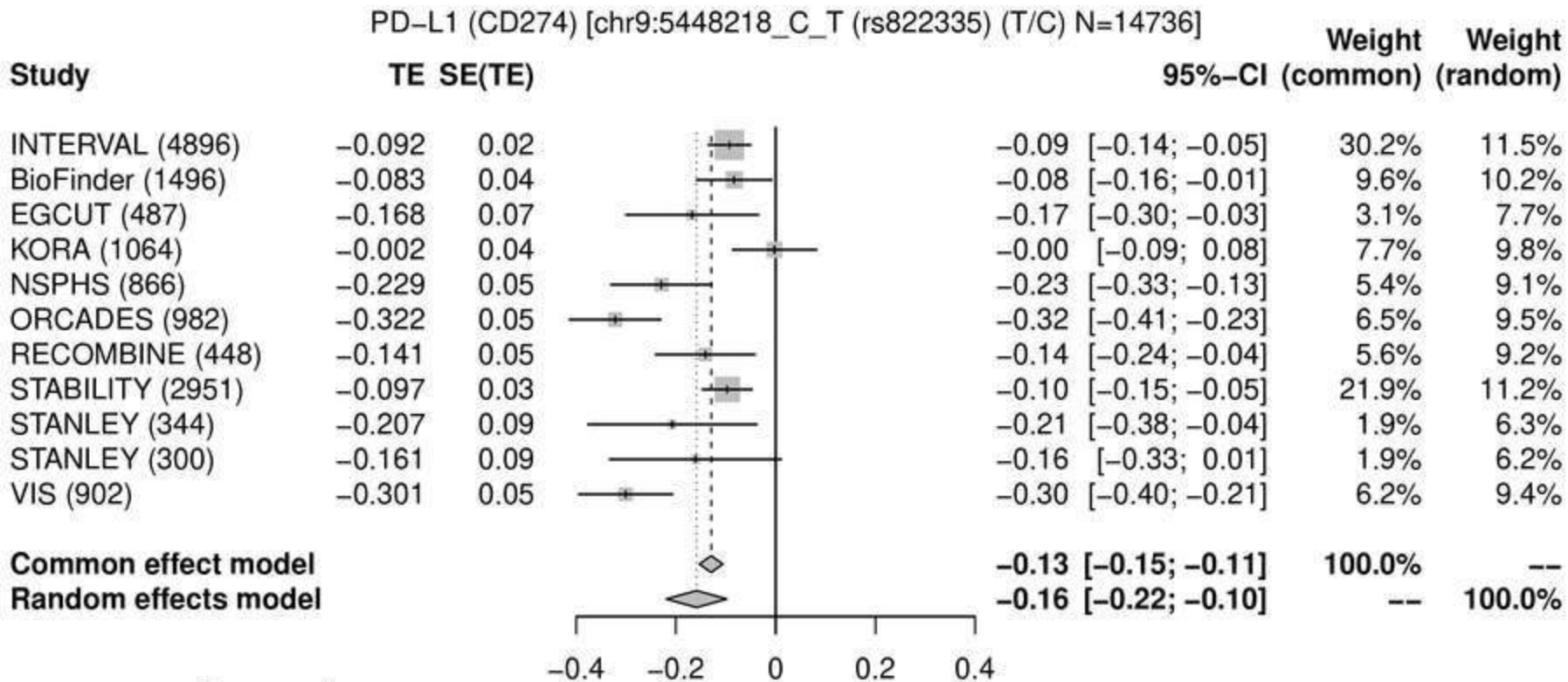
Weight
95%-CI (common) Weight
(random)

Common effect model
Random effects model

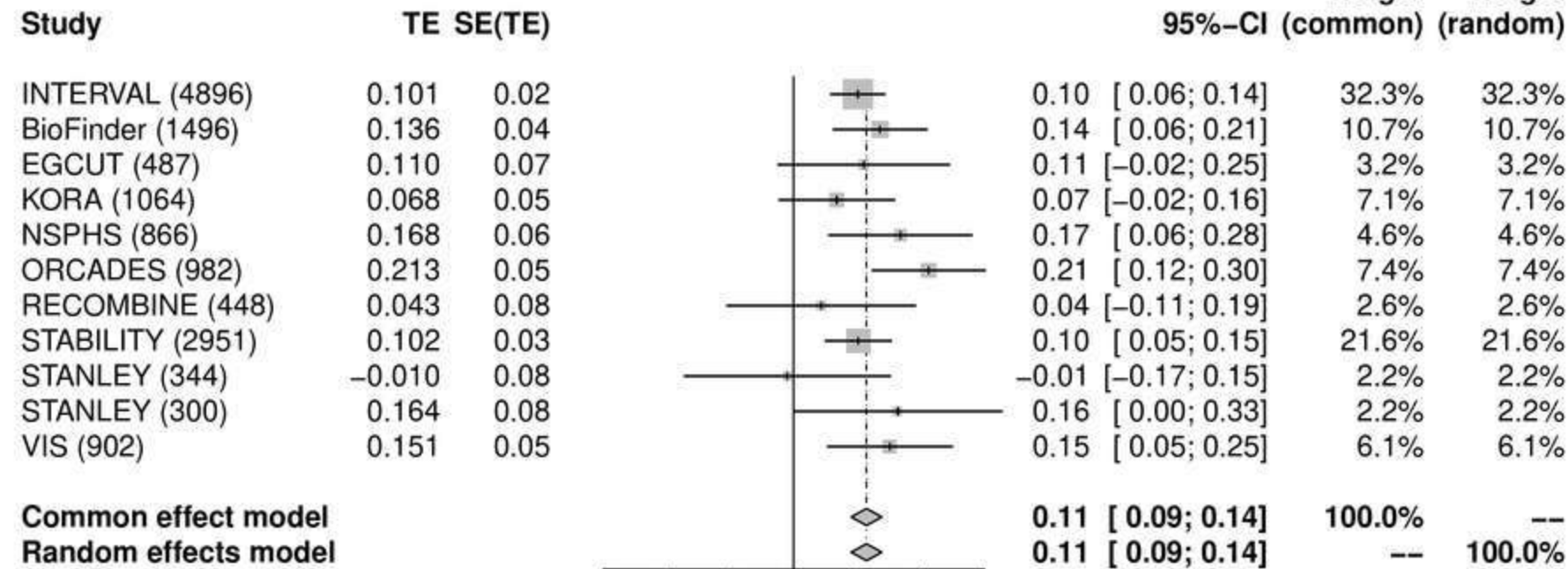
Heterogeneity: $I^2 = 34\%$, $\tau^2 = 0.0008$, $p = 0.13$

OSM (OSM)-rs3859189



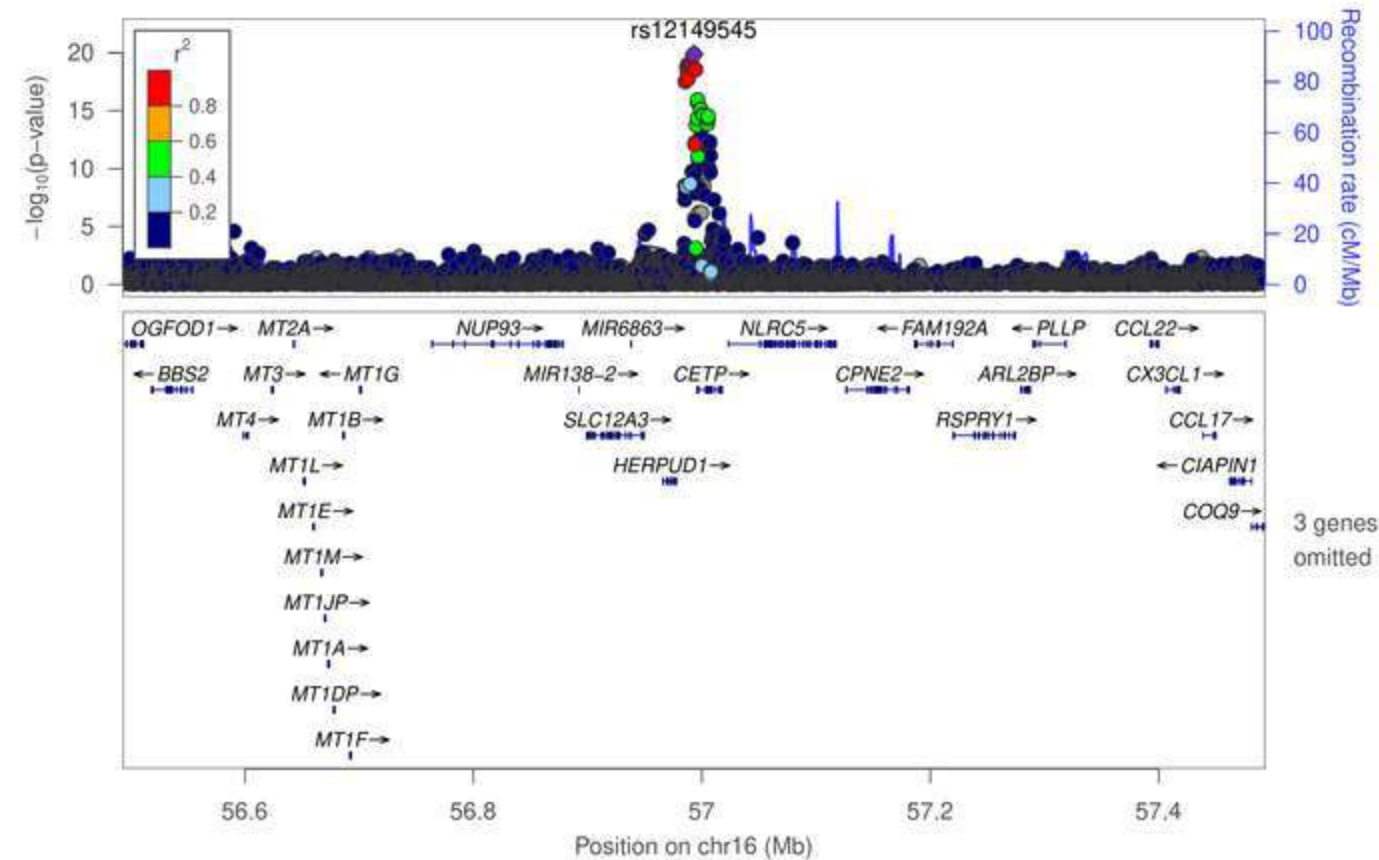


SCF (KITLG) [chr16:56993161_A_G (rs12149545) (A/G) N=14736]



Heterogeneity: $I^2 = 13\%$, $\tau^2 < 0.0001$, $p = 0.32$

SCF (KITLG)-rs12149545



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (448)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 1\%$, $\tau^2 = 0.0007$, $p = 0.43$

SCF (KITLG) [chr16:67940350_A_G (rs55781197) (A/G) N=14736]

TE SE(TE)

-0.157

0.03

-0.287

0.05

-0.152

0.09

-0.226

0.06

-0.120

0.07

-0.144

0.06

-0.164

0.10

-0.115

0.04

-0.147

0.11

-0.314

0.12

-0.173

0.07

Weight
95%-CI (common) (random)

-0.16 [-0.22; -0.09]

29.2%

23.1%

-0.29 [-0.39; -0.18]

9.8%

10.9%

-0.15 [-0.32; 0.02]

3.9%

4.9%

-0.23 [-0.35; -0.10]

7.7%

8.9%

-0.12 [-0.25; 0.01]

6.4%

7.6%

-0.14 [-0.27; -0.02]

7.2%

8.4%

-0.16 [-0.37; 0.04]

2.7%

3.5%

-0.12 [-0.19; -0.05]

22.8%

19.9%

-0.15 [-0.36; 0.06]

2.6%

3.3%

-0.31 [-0.55; -0.08]

2.1%

2.8%

-0.17 [-0.32; -0.03]

5.6%

6.8%

-0.17 [-0.20; -0.13]

100.0%

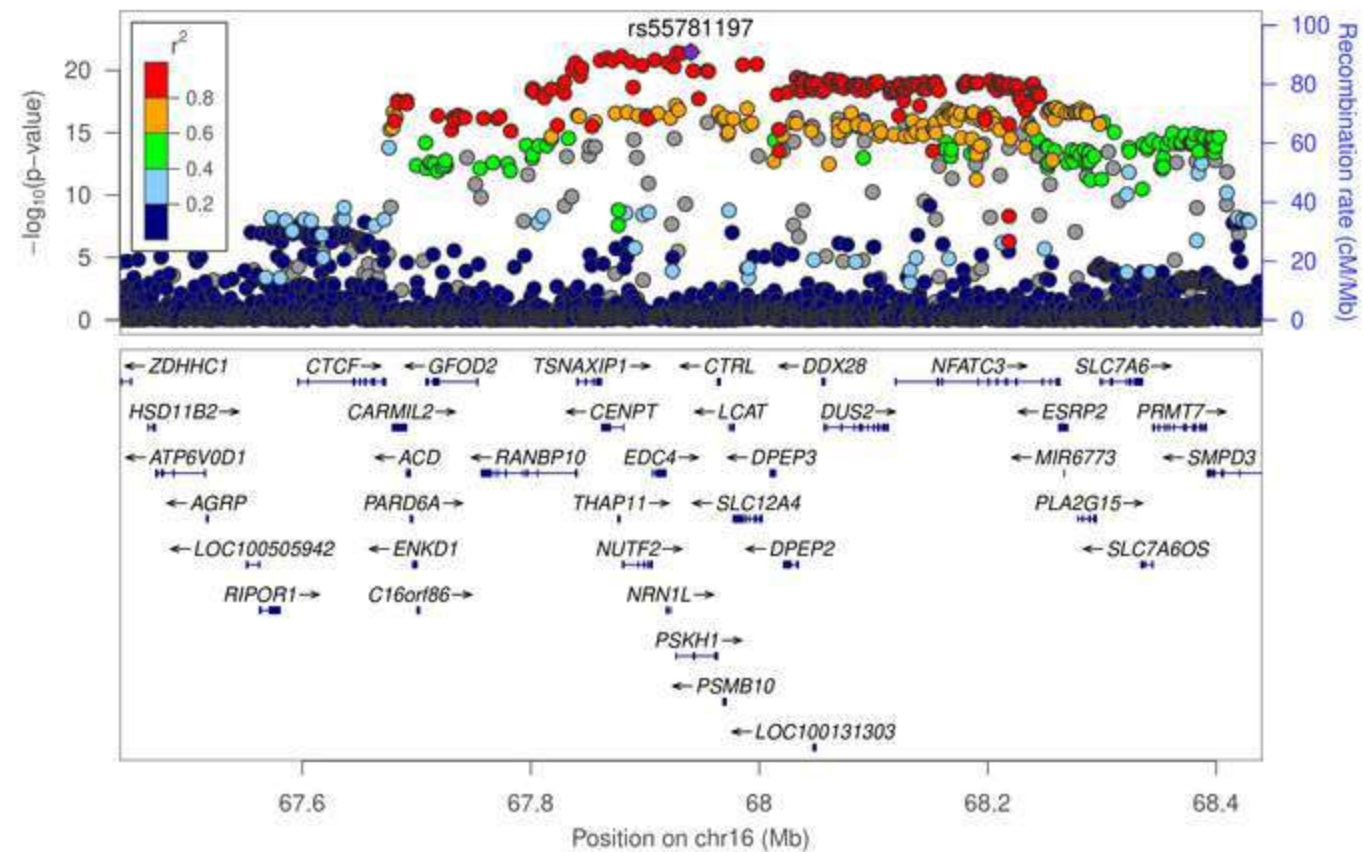
--

-0.17 [-0.21; -0.13]

--

100.0%

SCF (KITLG)-rs55781197



Study

SCF (KITLG) [chr19:54793830_C_G (rs798893) (C/G) N=14725]

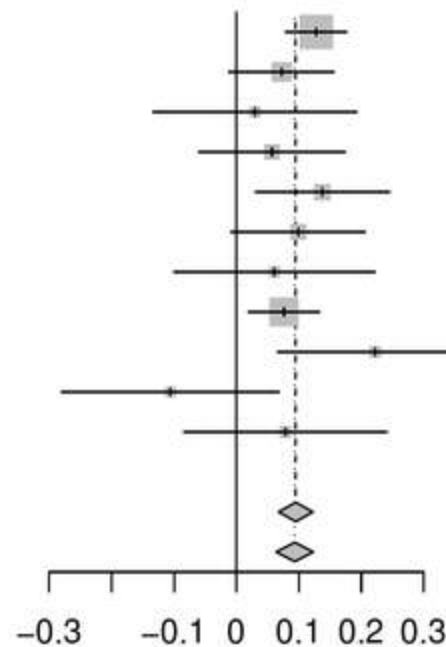
TE SE(TE)

Weight
95%-CI (common) Weight
(random)

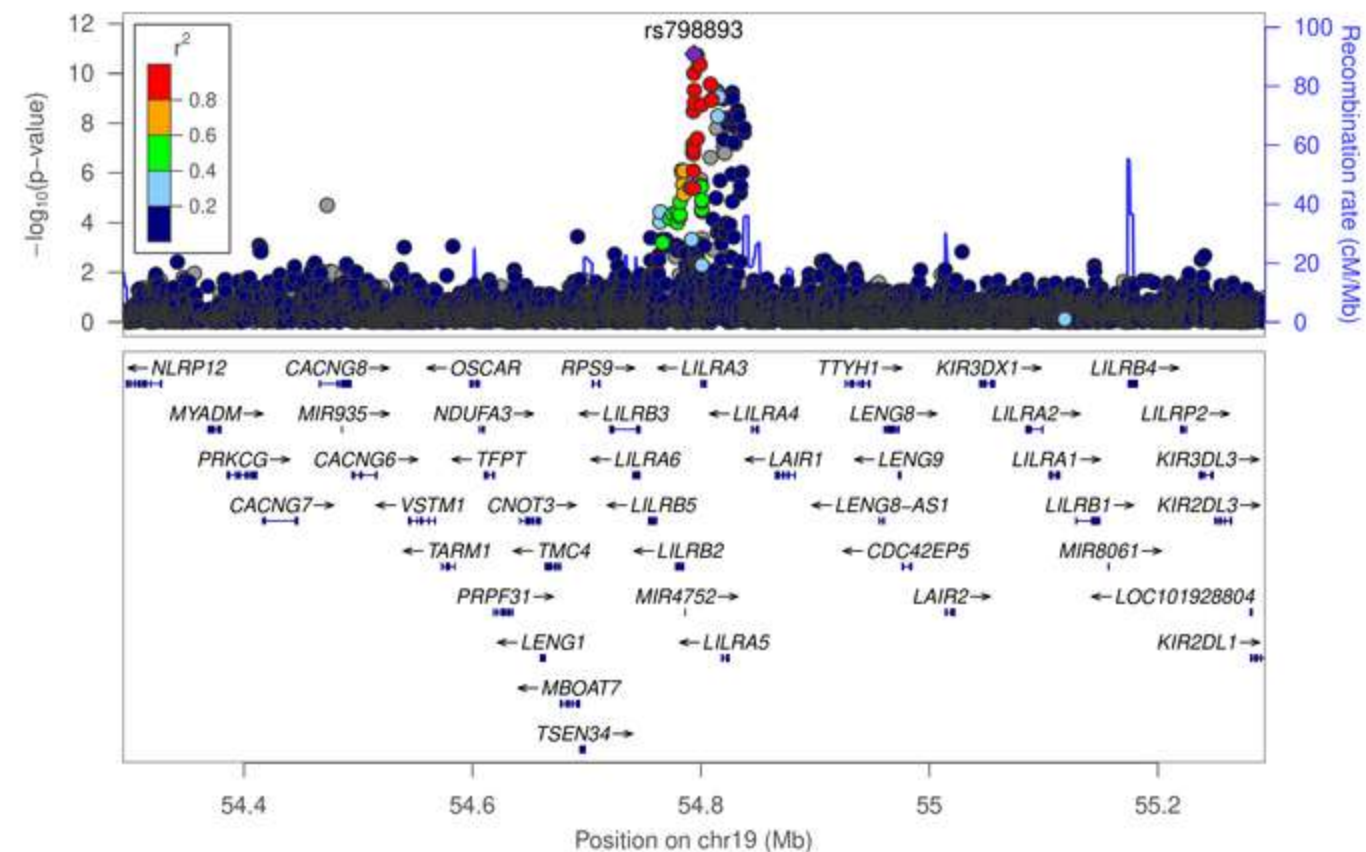
INTERVAL (4896)	0.128	0.02		0.13	[0.08; 0.18]	32.2%	28.8%
BioFinder (1496)	0.072	0.04		0.07	[-0.01; 0.16]	10.8%	11.5%
EGCUT (487)	0.030	0.08		0.03	[-0.13; 0.19]	2.9%	3.3%
KORA (1064)	0.057	0.06		0.06	[-0.06; 0.17]	5.6%	6.2%
NSPHS (866)	0.138	0.05		0.14	[0.03; 0.25]	6.7%	7.3%
ORCADES (982)	0.099	0.05		0.10	[-0.01; 0.21]	6.6%	7.3%
RECOMBINE (437)	0.061	0.08		0.06	[-0.10; 0.22]	3.0%	3.3%
STABILITY (2951)	0.076	0.03		0.08	[0.02; 0.13]	23.8%	22.6%
STANLEY (344)	0.222	0.08		0.22	[0.07; 0.38]	3.1%	3.6%
STANLEY (300)	-0.106	0.09		-0.11	[-0.28; 0.07]	2.5%	2.9%
VIS (902)	0.078	0.08		0.08	[-0.08; 0.24]	2.9%	3.3%

Common effect model

Random effects model

Heterogeneity: $I^2 = 16\%$, $\tau^2 = 0.0002$, $p = 0.29$

SCF (KITLG)-rs798893



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (442)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 69\%$, $\tau^2 = 0.0044$, $p < 0.01$

SCF (KITLG) [chr20:44551855_C_T (rs6073958) (T/C) N=14730]

TE SE(TE)

-0.364

0.02

-0.196

0.04

-0.333

0.07

-0.376

0.05

-0.376

0.06

-0.243

0.06

-0.271

0.09

-0.183

0.03

-0.200

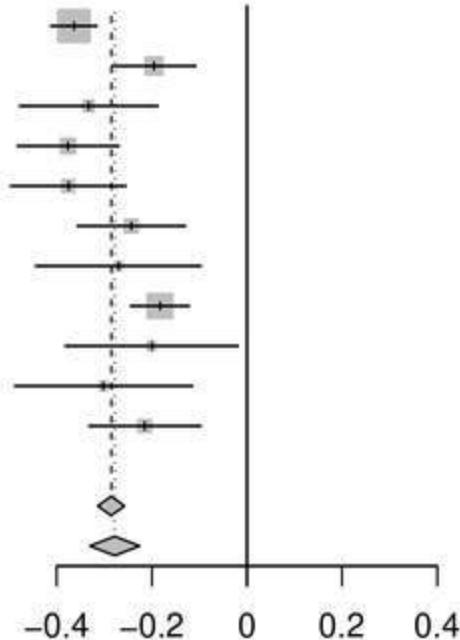
0.09

-0.302

0.10

-0.215

0.06

Weight
95%-CI (common) (random)

-0.36 [-0.41; -0.32]

33.6%

14.4%

-0.20 [-0.28; -0.11]

10.2%

11.2%

-0.33 [-0.48; -0.19]

3.7%

7.3%

-0.38 [-0.48; -0.27]

7.0%

9.8%

-0.38 [-0.50; -0.25]

5.4%

8.8%

-0.24 [-0.36; -0.13]

6.2%

9.3%

-0.27 [-0.44; -0.10]

2.6%

5.9%

-0.18 [-0.25; -0.12]

20.8%

13.4%

-0.20 [-0.38; -0.02]

2.4%

5.5%

-0.30 [-0.49; -0.11]

2.3%

5.3%

-0.21 [-0.33; -0.10]

5.7%

9.0%

-0.29 [-0.31; -0.26]

100.0%

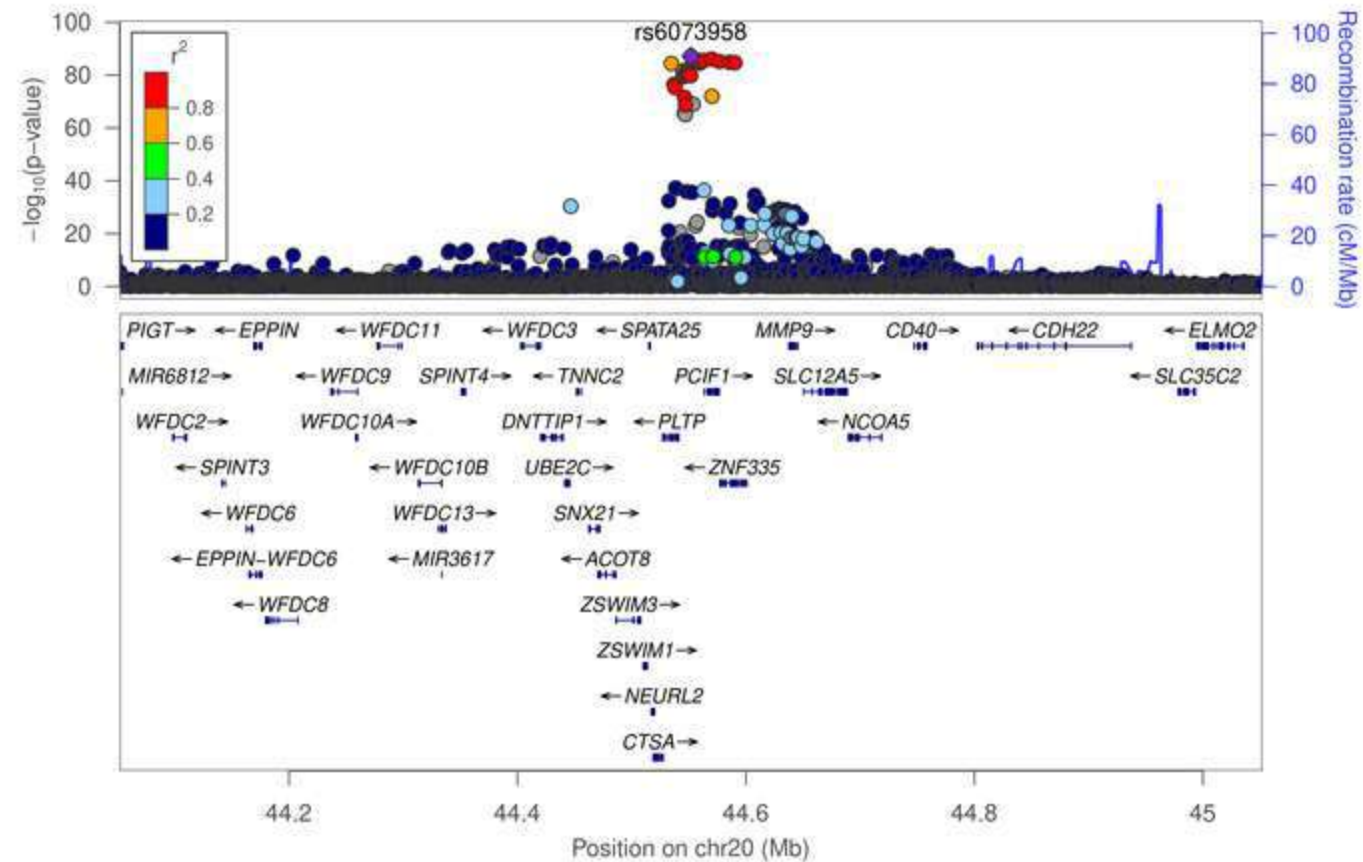
--

-0.28 [-0.33; -0.23]

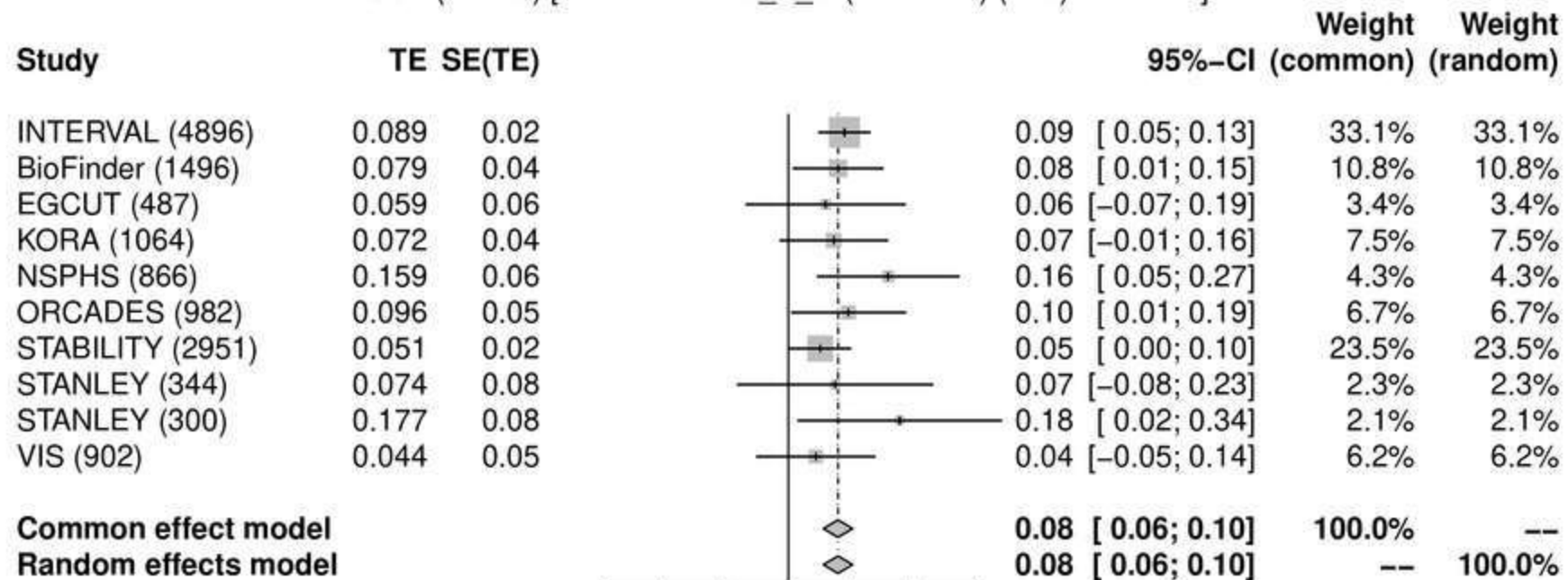
--

100.0%

SCF (KITLG)-rs6073958

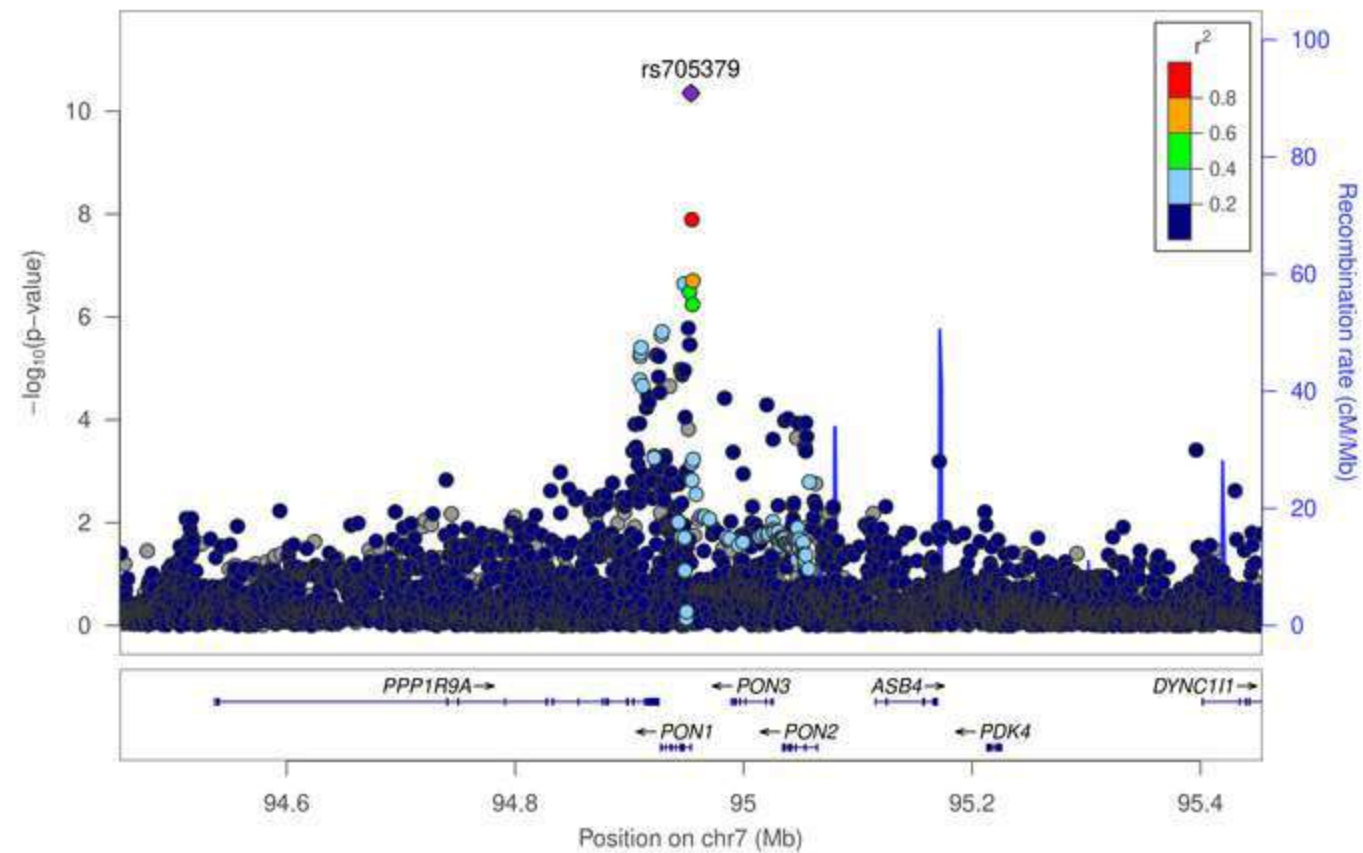


SCF (KITLG) [chr7:94953895_A_G (rs705379) (A/G) N=14288]



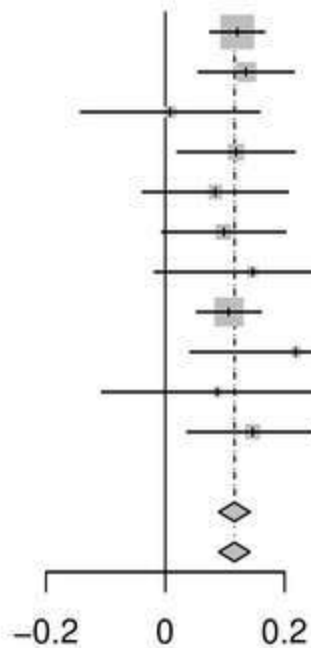
Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.77$

SCF (KITLG)-rs705379



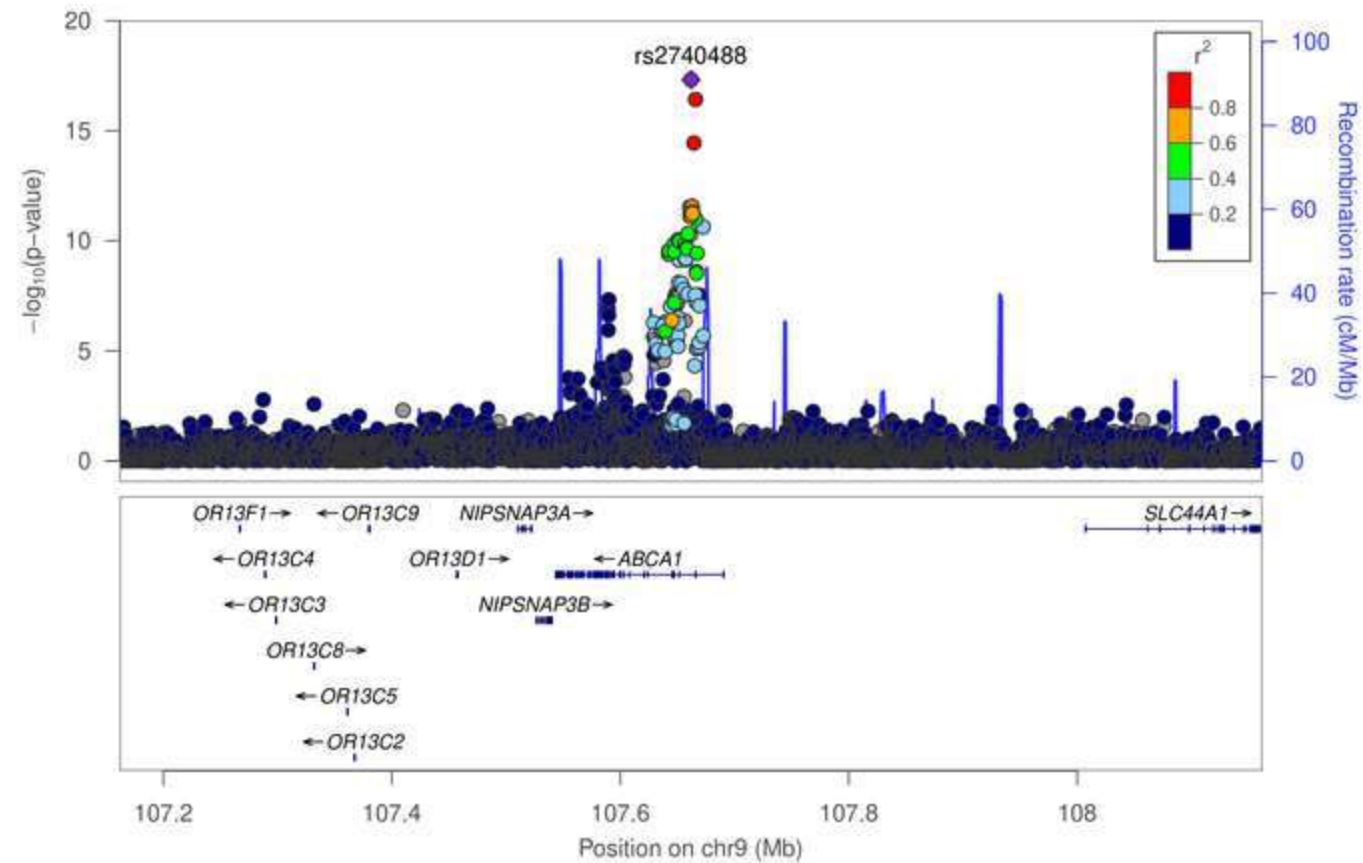
SCF (KITLG) [chr9:107661742_A_C (rs2740488) (A/C) N=14732]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.120	0.02	0.12 [0.07; 0.17]	32.7%	32.7%
BioFinder (1496)	0.135	0.04	0.14 [0.06; 0.22]	10.6%	10.6%
EGCUT (487)	0.008	0.08	0.01 [-0.14; 0.16]	3.0%	3.0%
KORA (1064)	0.118	0.05	0.12 [0.02; 0.22]	7.0%	7.0%
NSPHS (866)	0.084	0.06	0.08 [-0.04; 0.21]	4.6%	4.6%
ORCADES (982)	0.098	0.05	0.10 [-0.01; 0.20]	6.3%	6.3%
RECOMBINE (444)	0.146	0.08	0.15 [-0.02; 0.31]	2.5%	2.5%
STABILITY (2951)	0.106	0.03	0.11 [0.05; 0.16]	23.6%	23.6%
STANLEY (344)	0.219	0.09	0.22 [0.04; 0.40]	2.2%	2.2%
STANLEY (300)	0.087	0.10	0.09 [-0.11; 0.28]	1.8%	1.8%
VIS (902)	0.146	0.06	0.15 [0.04; 0.26]	5.6%	5.6%
Common effect model			0.12 [0.09; 0.14]	100.0%	--
Random effects model			0.12 [0.09; 0.14]	--	100.0%



Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.92$

SCF (KITLG)-rs2740488



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (448)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.73$

SCF (KITLG) [chr9:128807910_C_T (rs138854302) (T/C) N=14736]

TE SE(TE)

-0.137

0.04

-0.170

0.06

-0.173

0.11

-0.185

0.07

-0.284

0.11

-0.101

0.09

-0.255

0.13

-0.078

0.04

-0.267

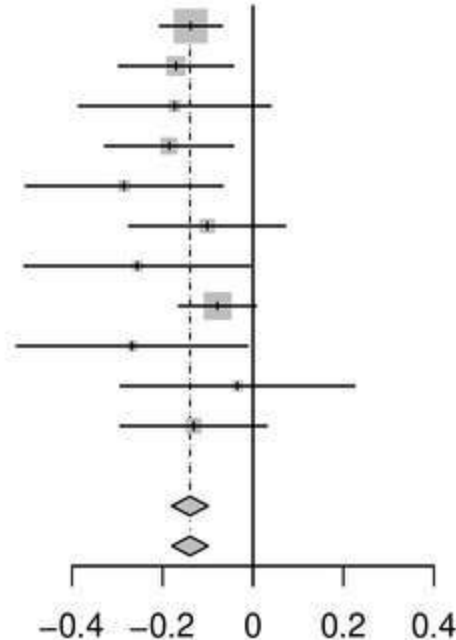
0.13

-0.034

0.13

-0.131

0.08

Weight
95%-CI (common) (random)

-0.14 [-0.21; -0.07]

33.9%

33.9%

-0.17 [-0.30; -0.04]

10.1%

10.1%

-0.17 [-0.38; 0.04]

3.6%

3.6%

-0.19 [-0.33; -0.04]

8.0%

8.0%

-0.28 [-0.50; -0.07]

3.4%

3.4%

-0.10 [-0.27; 0.07]

5.4%

5.4%

-0.26 [-0.51; -0.01]

2.6%

2.6%

-0.08 [-0.16; 0.01]

22.0%

22.0%

-0.27 [-0.52; -0.01]

2.5%

2.5%

-0.03 [-0.29; 0.22]

2.4%

2.4%

-0.13 [-0.29; 0.03]

6.2%

6.2%

-0.14 [-0.18; -0.10]

100.0%

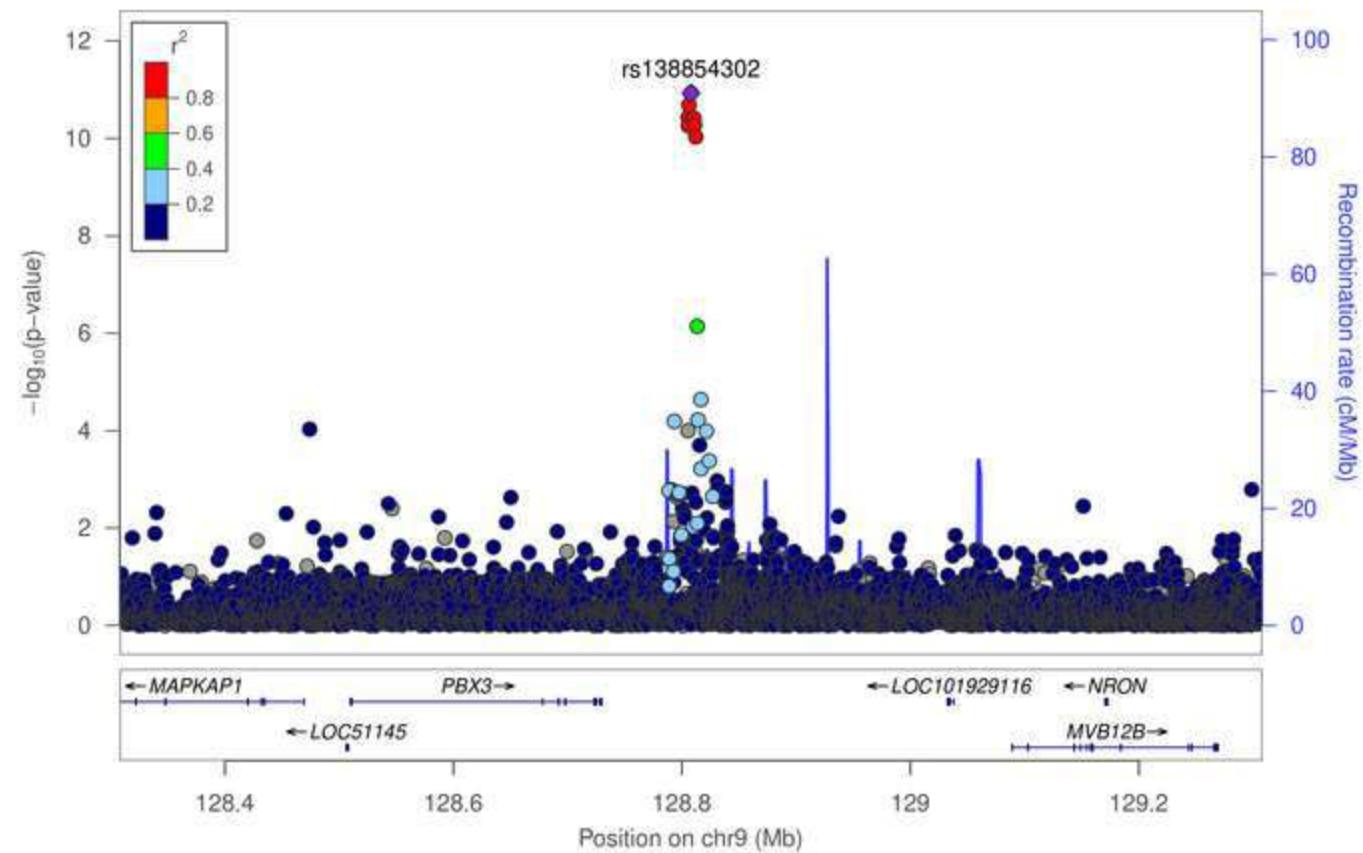
--

-0.14 [-0.18; -0.10]

--

100.0%

SCF (KITLG)-rs138854302



Study

SIRT2 (SIRT2) [chr19:39379770_C_T (rs144373891) (T/C) N=14736]

TE SE(TE)

Weight
95%-CI (common) Weight
(random)

INTERVAL (4896)

-0.591 0.09

BioFinder (1496)

-0.400 0.13

EGCUT (487)

-1.339 0.31

KORA (1064)

-1.702 0.33

NSPHS (866)

-0.642 0.32

ORCADES (982)

-1.251 0.40

RECOMBINE (448)

-0.267 0.26

STABILITY (2951)

-0.510 0.11

STANLEY (344)

-0.801 0.29

STANLEY (300)

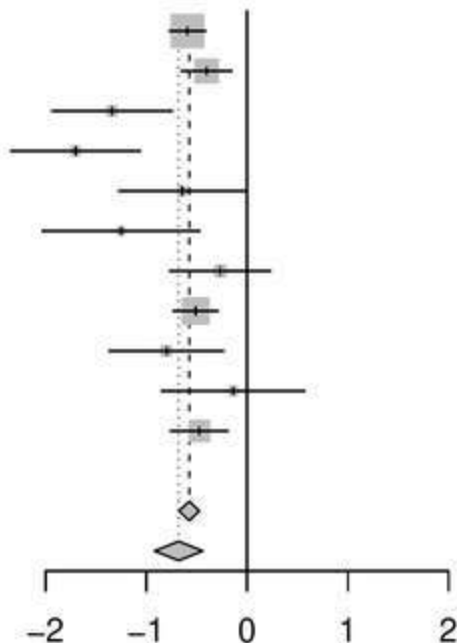
-0.138 0.36

VIS (902)

-0.474 0.14

Common effect model

Random effects model

Heterogeneity: $I^2 = 63\%$, $\tau^2 = 0.1065$, $p < 0.01$ 

-0.59 [-0.77; -0.41] 31.9% 13.1%

-0.40 [-0.65; -0.15] 16.2% 12.2%

-1.34 [-1.94; -0.74] 2.8% 7.5%

-1.70 [-2.35; -1.06] 2.5% 7.0%

-0.64 [-1.27; -0.01] 2.6% 7.2%

-1.25 [-2.03; -0.47] 1.7% 5.6%

-0.27 [-0.77; 0.23] 4.1% 8.7%

-0.51 [-0.73; -0.29] 20.5% 12.6%

-0.80 [-1.37; -0.23] 3.2% 7.9%

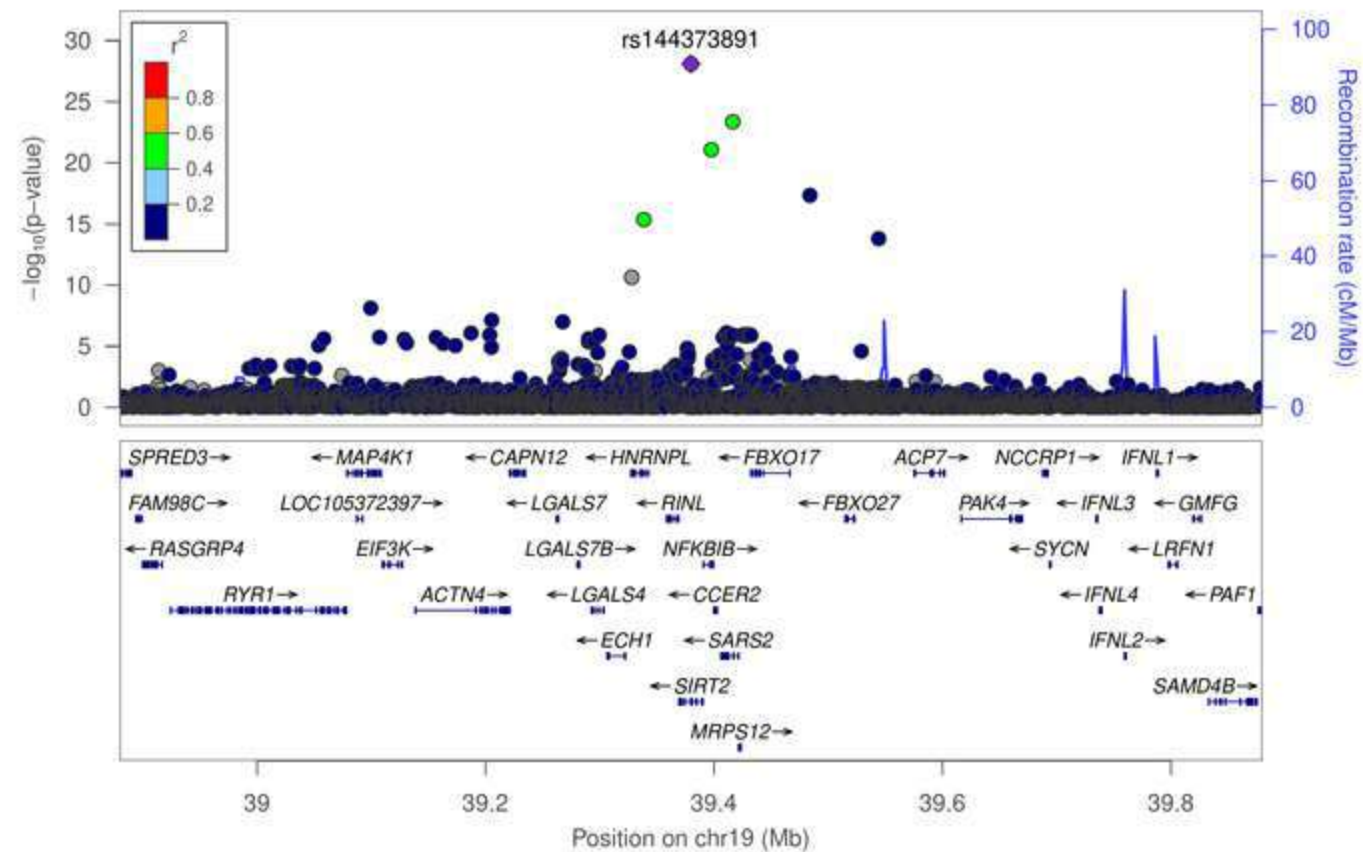
-0.14 [-0.85; 0.57] 2.0% 6.3%

-0.47 [-0.76; -0.19] 12.6% 11.8%

-0.57 [-0.67; -0.47] 100.0% --

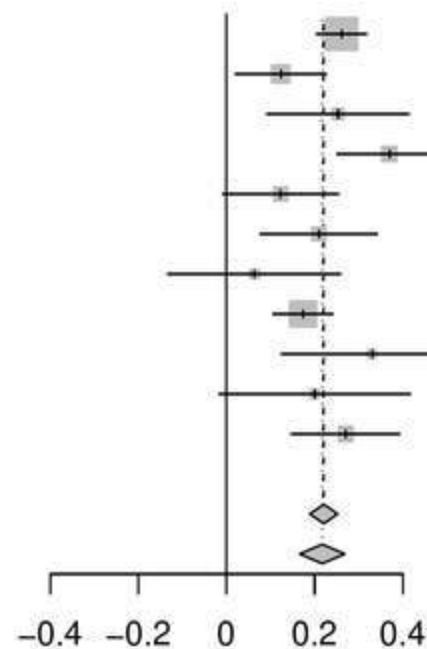
-0.68 [-0.92; -0.44] -- 100.0%

SIRT2 (SIRT2)-rs144373891



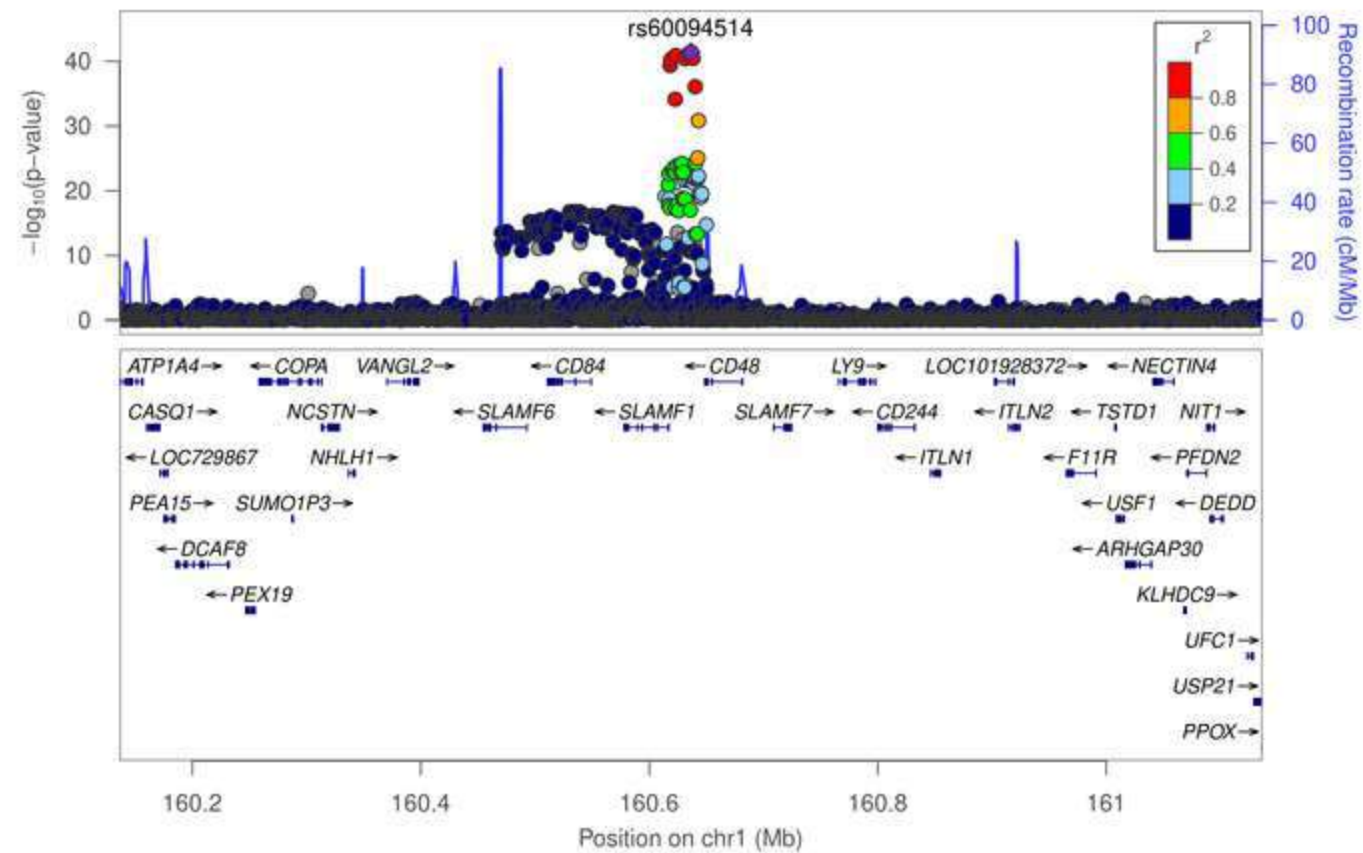
SLAMF1 (SLAMF1) [chr1:160636559_C_T (rs60094514) (T/C) N=14733]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.261	0.03	0.26 [0.21; 0.32]	31.9%	16.3%
BioFinder (1496)	0.123	0.05	0.12 [0.02; 0.23]	9.6%	11.2%
EGCUT (487)	0.253	0.08	0.25 [0.09; 0.41]	3.9%	6.8%
KORA (1064)	0.370	0.06	0.37 [0.25; 0.49]	7.1%	9.7%
NSPHS (866)	0.123	0.07	0.12 [-0.01; 0.25]	5.9%	8.7%
ORCADES (982)	0.209	0.07	0.21 [0.08; 0.34]	5.8%	8.6%
RECOMBINE (447)	0.063	0.10	0.06 [-0.13; 0.26]	2.6%	5.1%
STABILITY (2951)	0.173	0.03	0.17 [0.11; 0.24]	21.9%	14.9%
STANLEY (344)	0.331	0.10	0.33 [0.13; 0.54]	2.4%	4.8%
STANLEY (300)	0.200	0.11	0.20 [-0.02; 0.42]	2.2%	4.4%
VIS (900)	0.270	0.06	0.27 [0.15; 0.39]	6.7%	9.4%
Common effect model			0.22 [0.19; 0.25]	100.0%	--
Random effects model			0.22 [0.17; 0.27]	--	100.0%

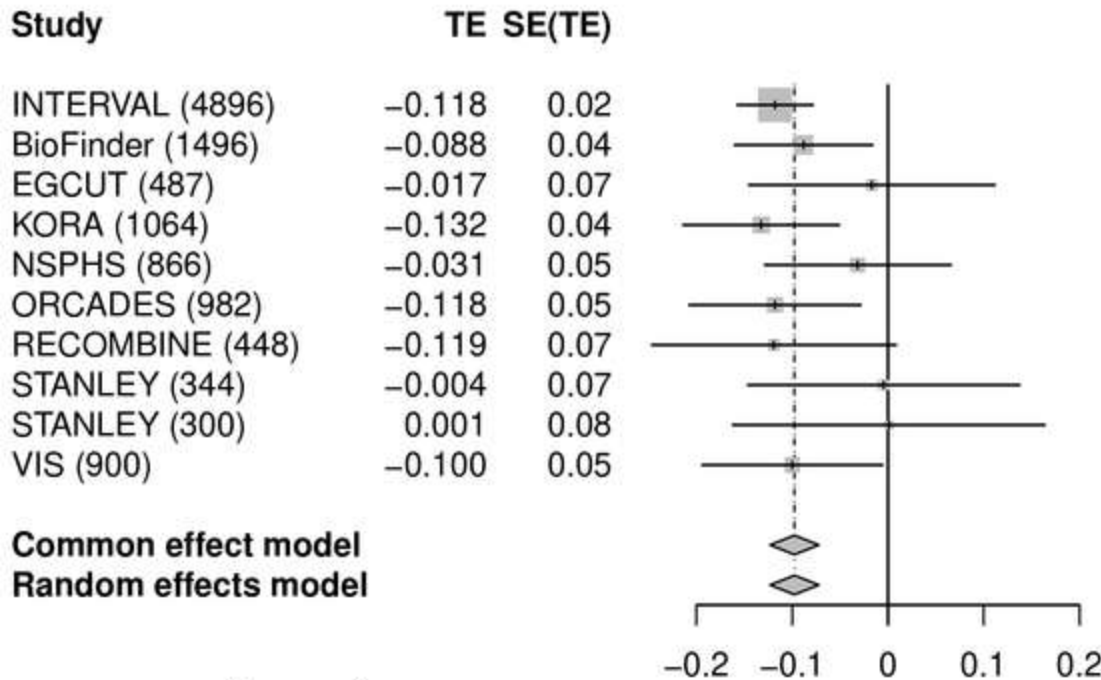


Heterogeneity: $I^2 = 50\%$, $\tau^2 = 0.0034$, $p = 0.03$

SLAMF1 (SLAMF1)-rs60094514

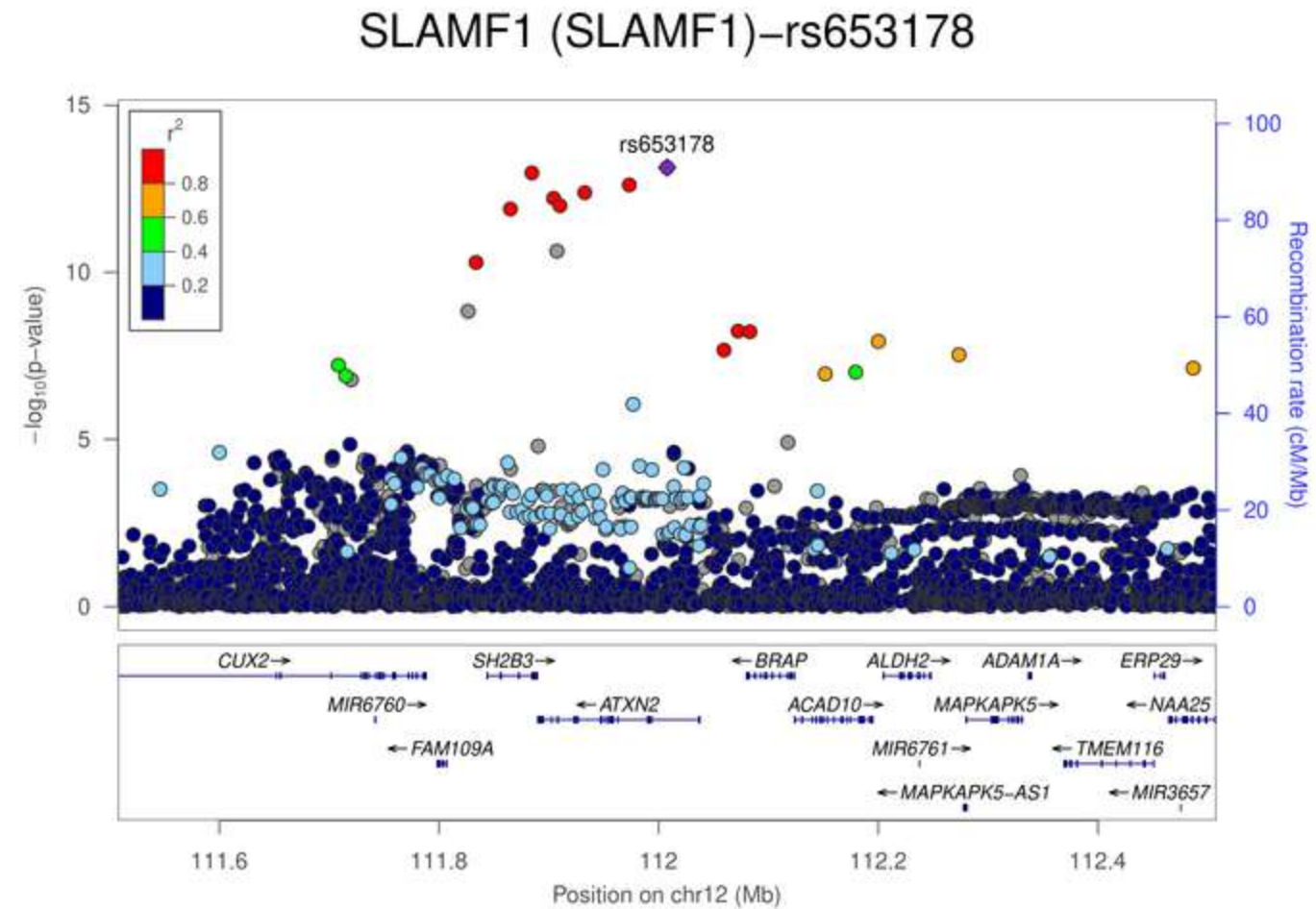


SLAMF1 (SLAMF1) [chr12:112007756_C_T (rs653178) (T/C) N=11783]

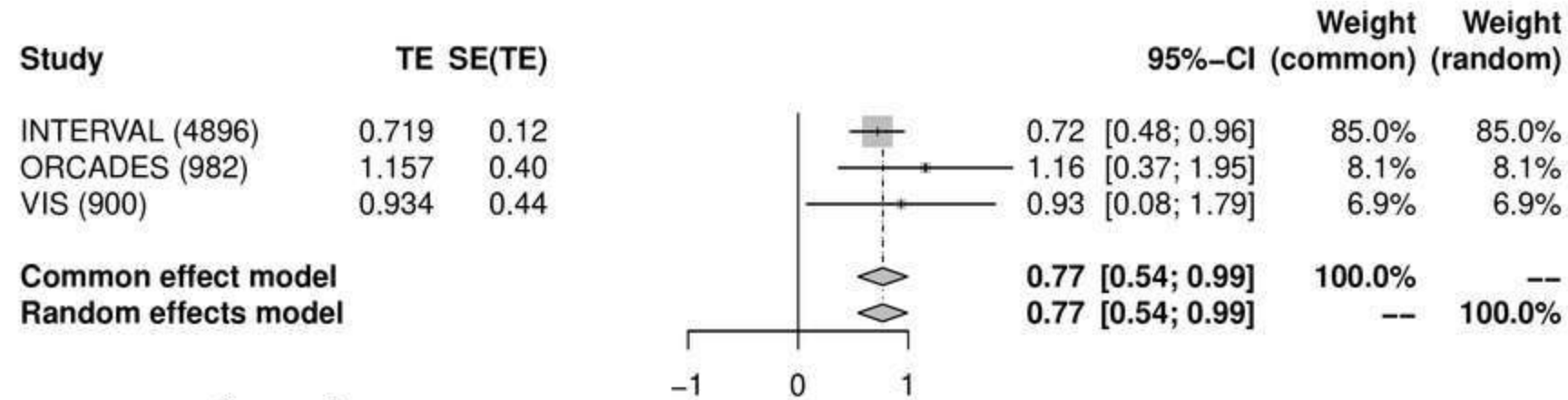


Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.49$

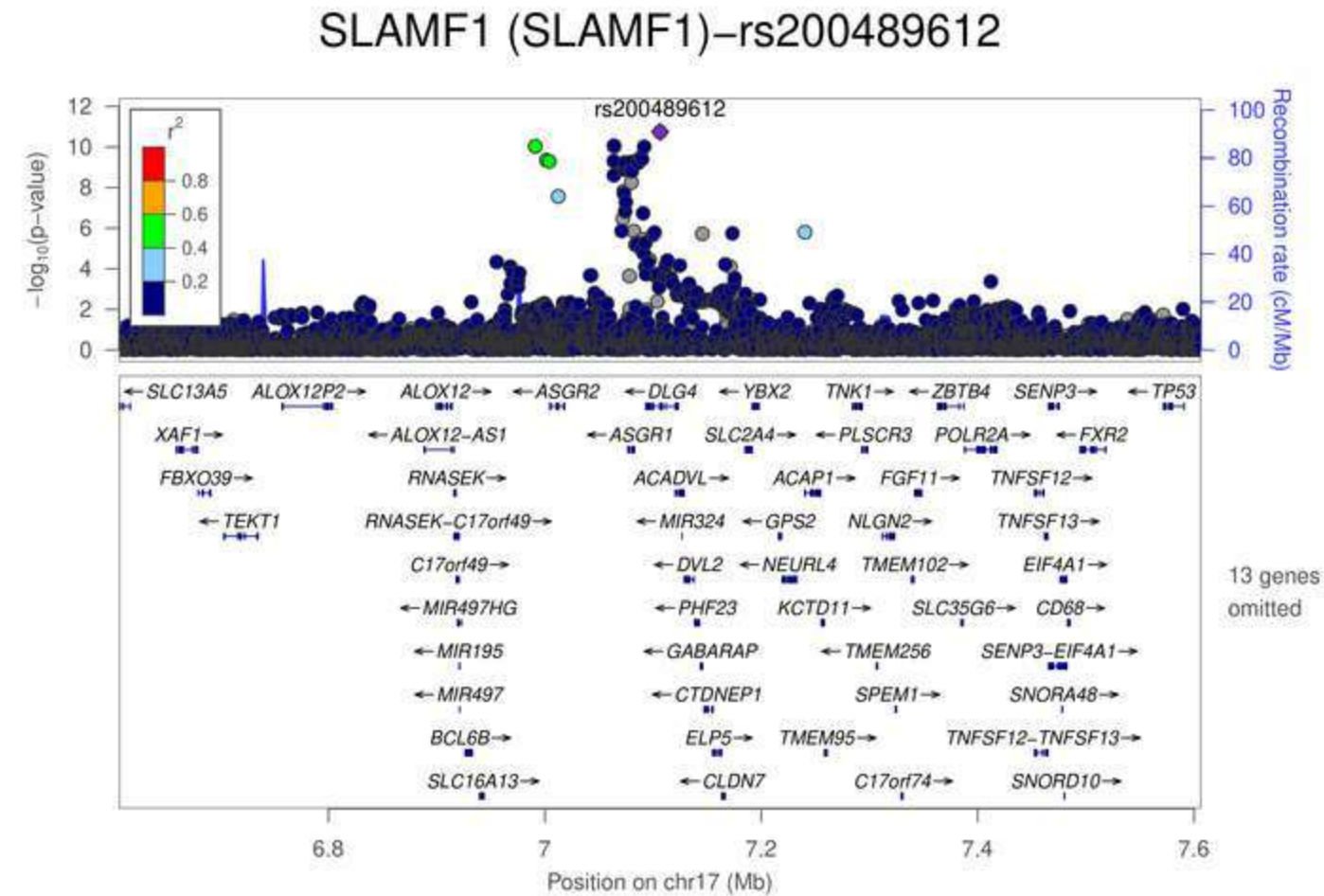
	Weight	Weight
95%-CI (common)	(common)	(random)
-0.12 [-0.16; -0.08]	41.5%	41.5%
-0.09 [-0.16; -0.02]	12.6%	12.6%
-0.02 [-0.15; 0.11]	4.0%	4.0%
-0.13 [-0.21; -0.05]	9.8%	9.8%
-0.03 [-0.13; 0.07]	6.9%	6.9%
-0.12 [-0.21; -0.03]	8.1%	8.1%
-0.12 [-0.25; 0.01]	4.0%	4.0%
-0.00 [-0.15; 0.14]	3.3%	3.3%
0.00 [-0.16; 0.16]	2.5%	2.5%
-0.10 [-0.19; -0.01]	7.4%	7.4%
-0.10 [-0.12; -0.07]	100.0%	--
-0.10 [-0.12; -0.07]	--	100.0%



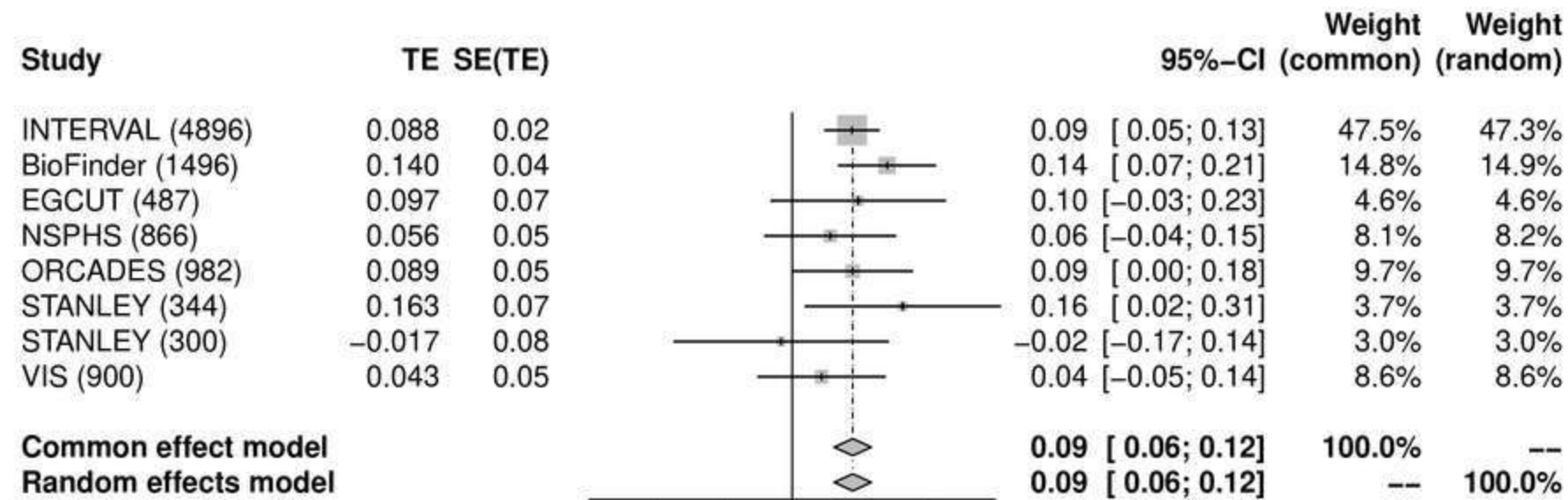
SLAMF1 (SLAMF1) [chr17:7106378_A_G (rs200489612) (A/G) N=6778]



Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.54$

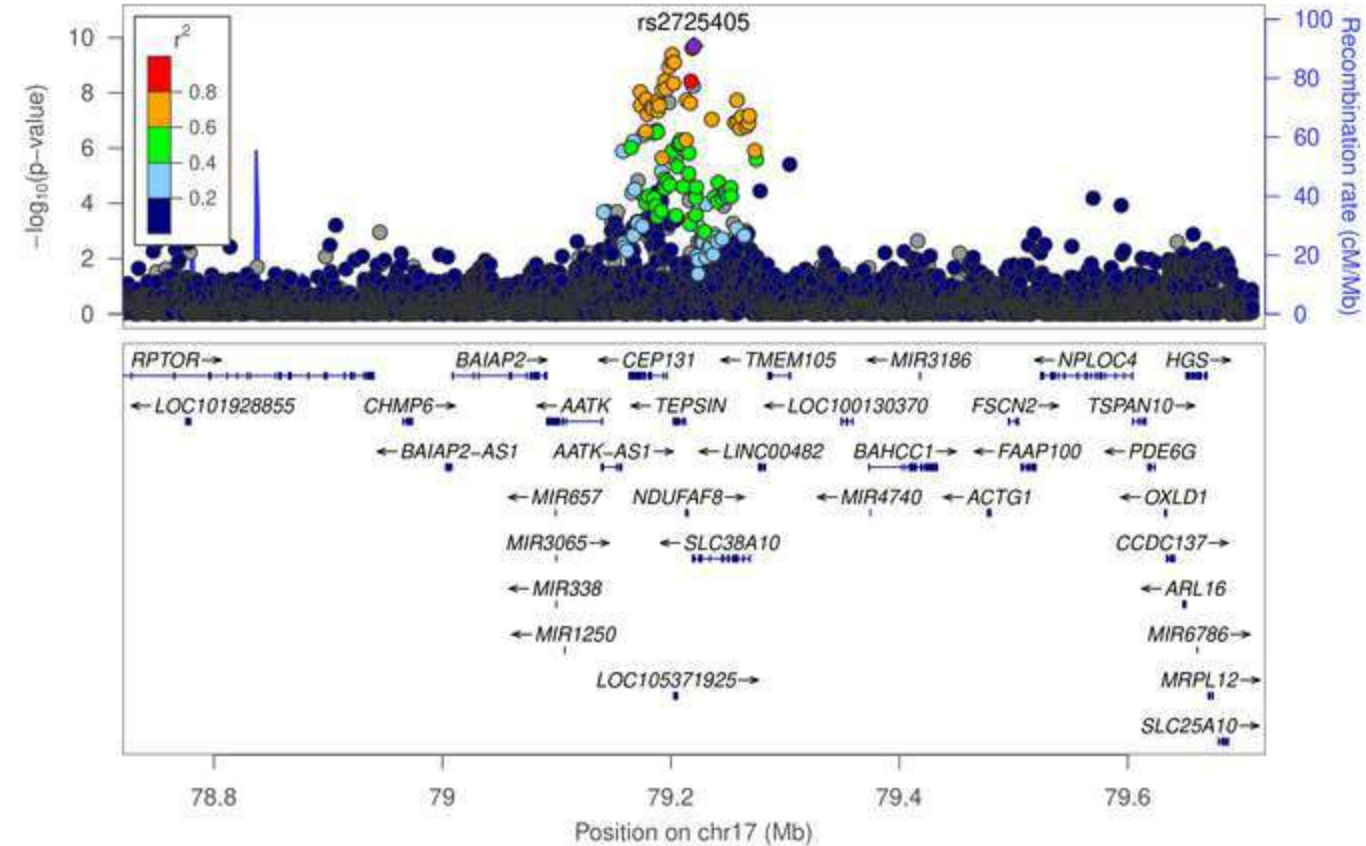


SLAMF1 (SLAMF1) [chr17:79220224_C_G (rs2725405) (C/G) N=10271]



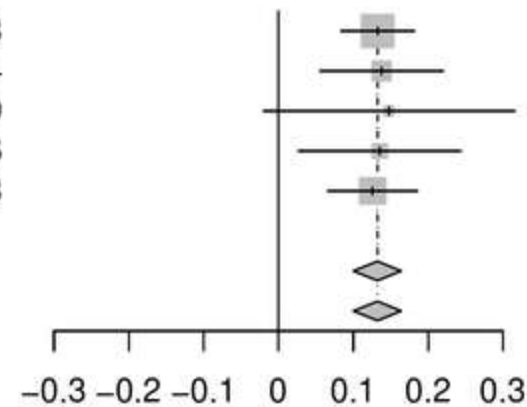
Heterogeneity: $I^2 = 0\%$, $\tau^2 < 0.0001$, $p = 0.53$

SLAMF1 (SLAMF1)-rs2725405



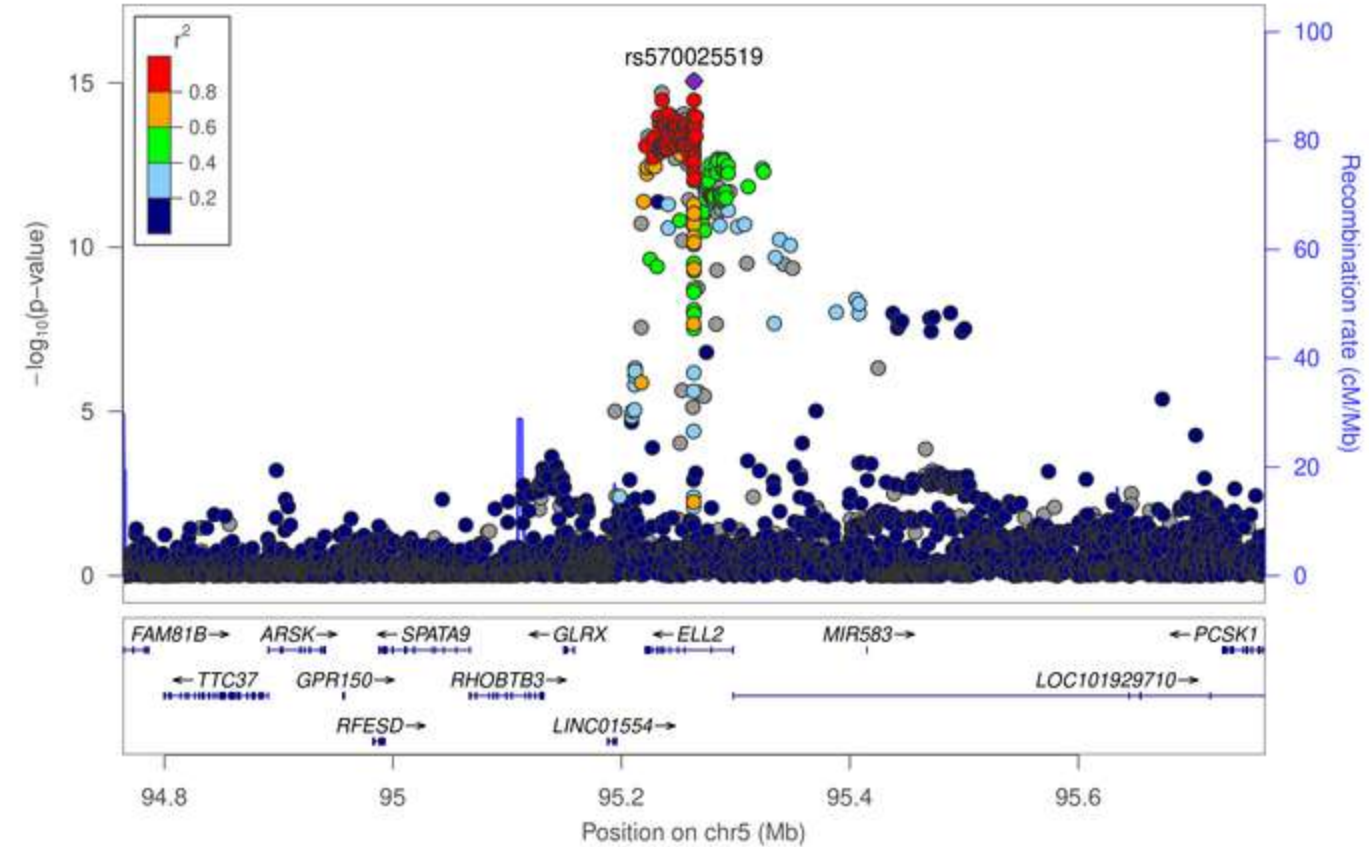
SLAMF1 (SLAMF1) [chr5:95263427_A_G (rs570025519) (A/G) N=10894]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.132	0.03	0.13 [0.08; 0.18]	43.1%	43.1%
BioFinder (1496)	0.138	0.04	0.14 [0.06; 0.22]	15.4%	15.4%
EGCUT (487)	0.148	0.09	0.15 [-0.02; 0.32]	3.7%	3.7%
KORA (1064)	0.135	0.06	0.14 [0.03; 0.24]	8.8%	8.8%
STABILITY (2951)	0.126	0.03	0.13 [0.07; 0.19]	29.0%	29.0%
Common effect model			0.13 [0.10; 0.16]	100.0%	--
Random effects model			0.13 [0.10; 0.16]	--	100.0%

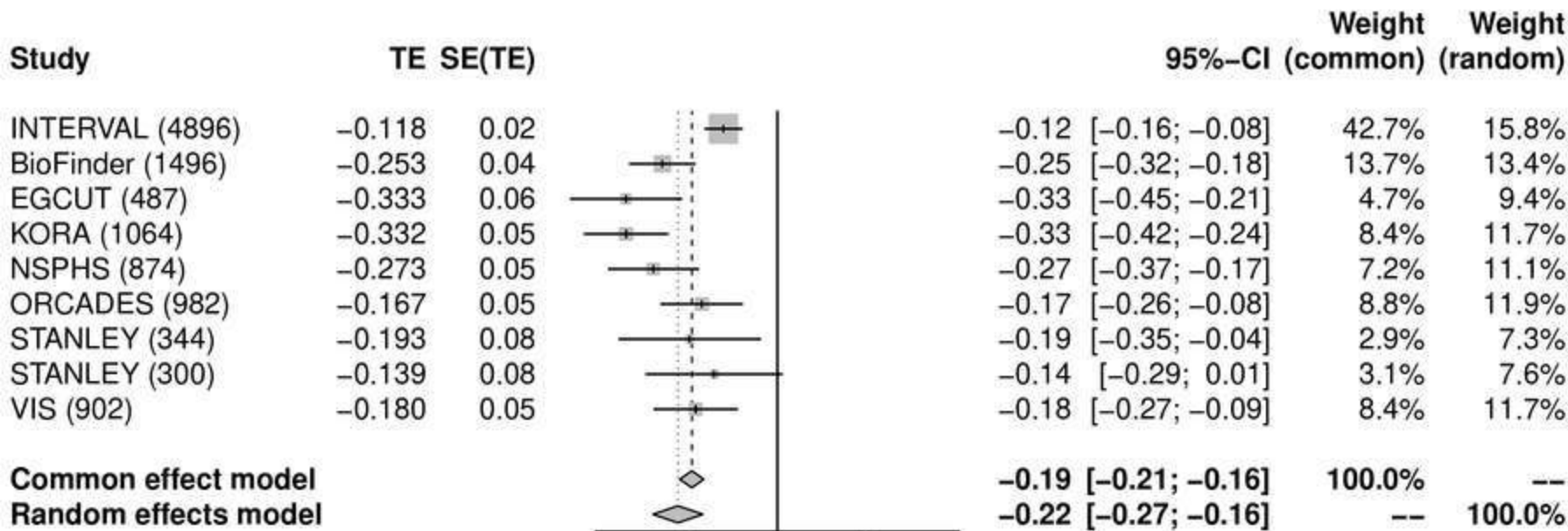


Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 1.00$

SLAMF1 (SLAMF1)-rs570025519

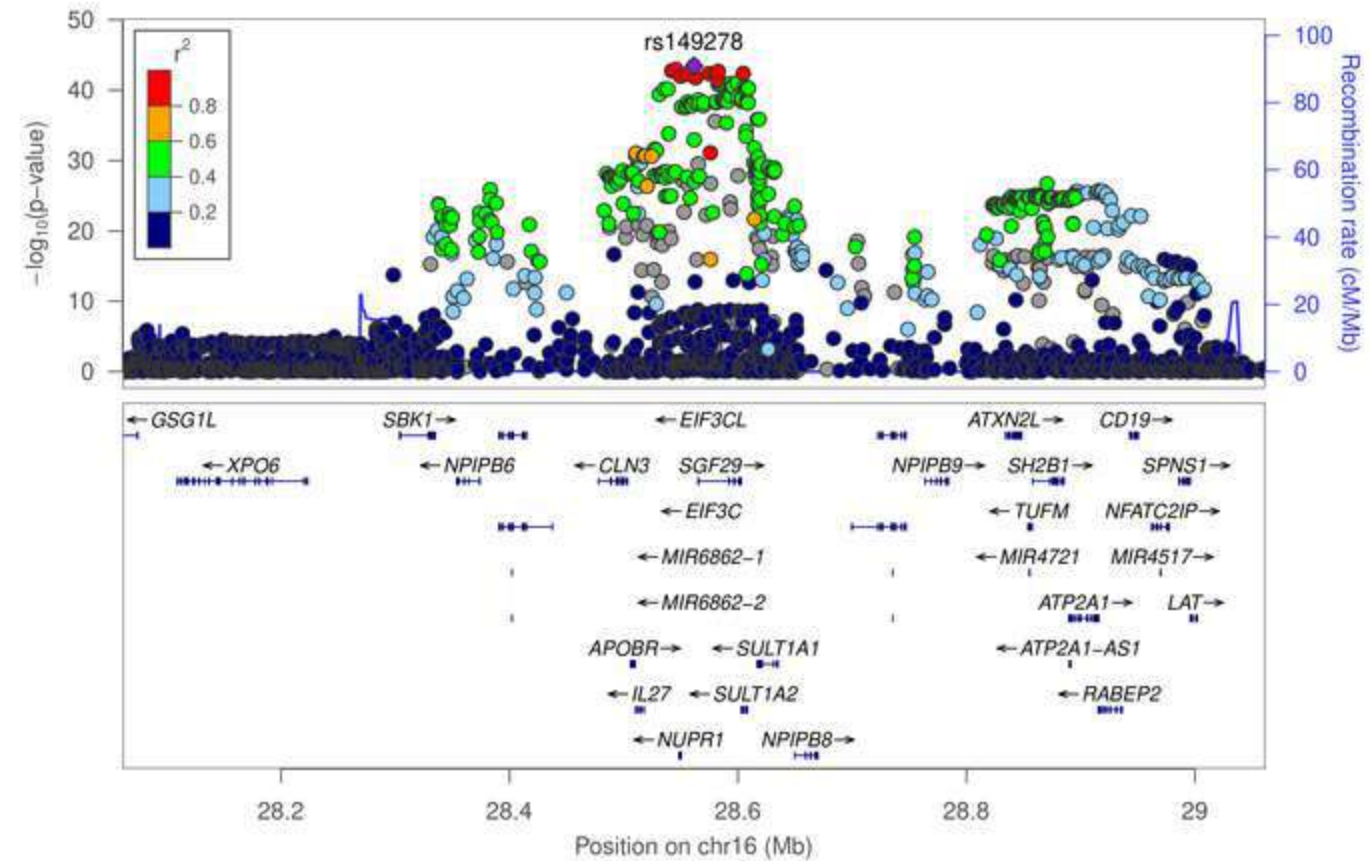


ST1A1 (SULT1A1) [chr16:28561581_C_T (rs149278) (T/C) N=11345]

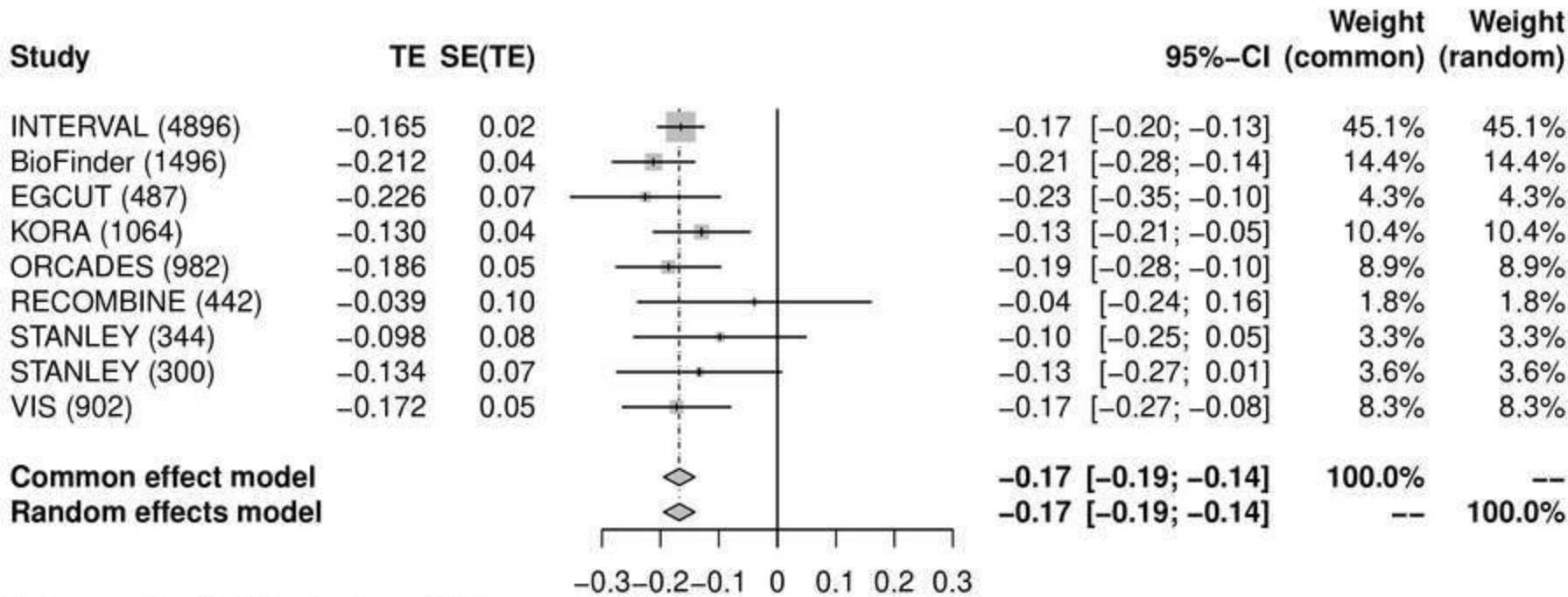


Heterogeneity: $I^2 = 76\%$, $\tau^2 = 0.0046$, $p < 0.01$

ST1A1 (SULT1A1)-rs149278

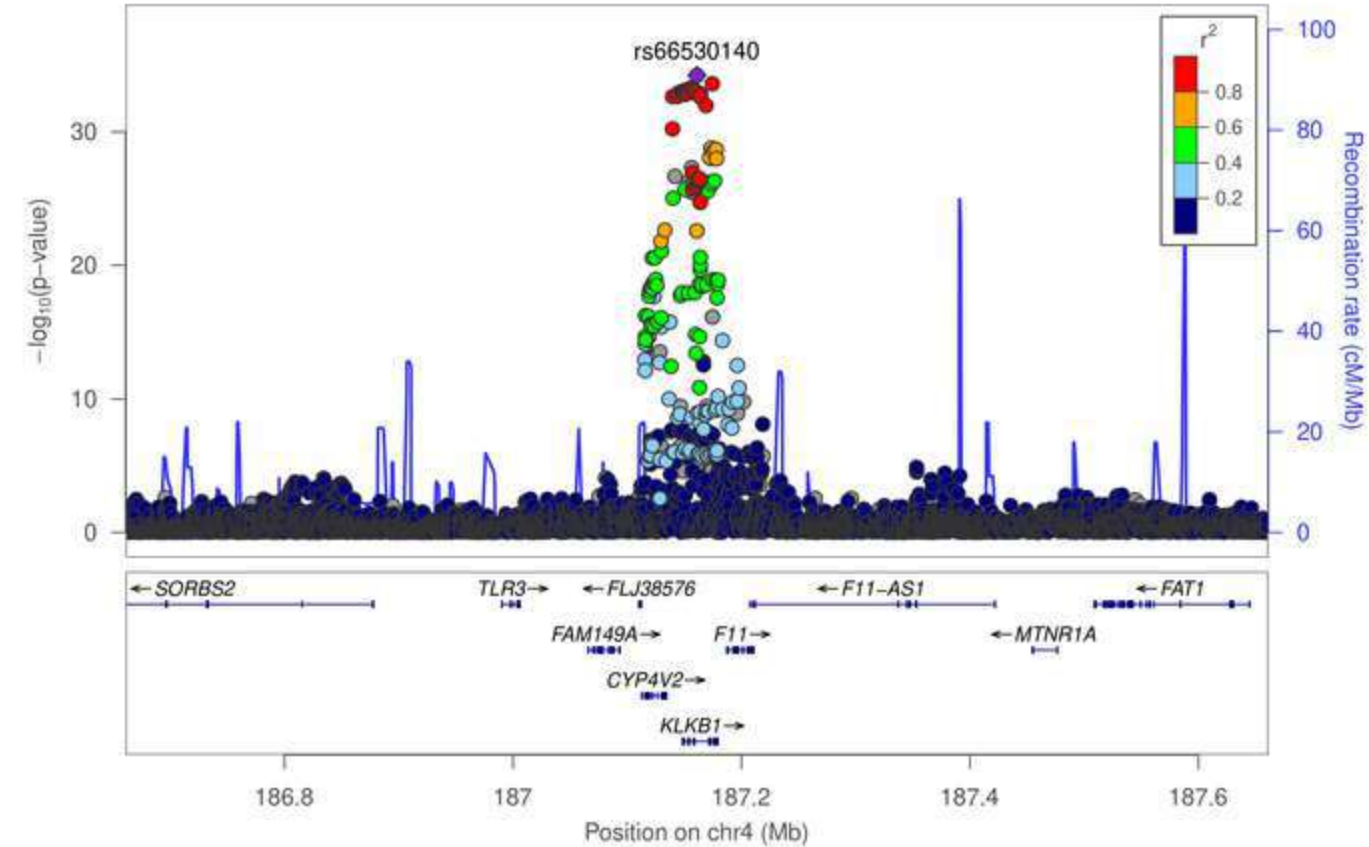


ST1A1 (SULT1A1) [chr4:187161211_C_T (rs66530140) (T/C) N=10913]



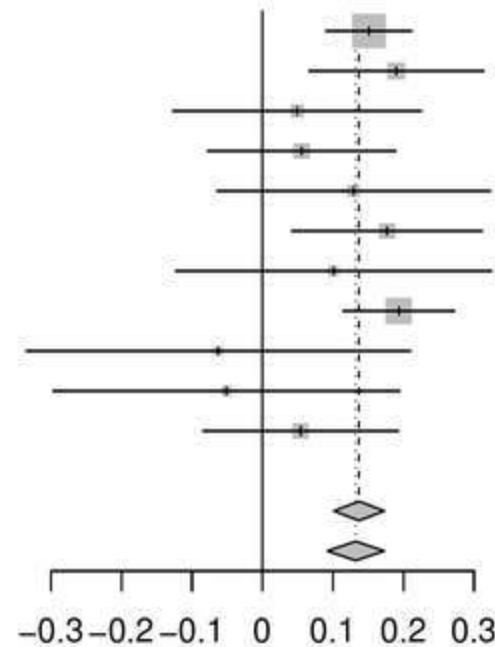
Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.65$

ST1A1 (SULT1A1)-rs66530140



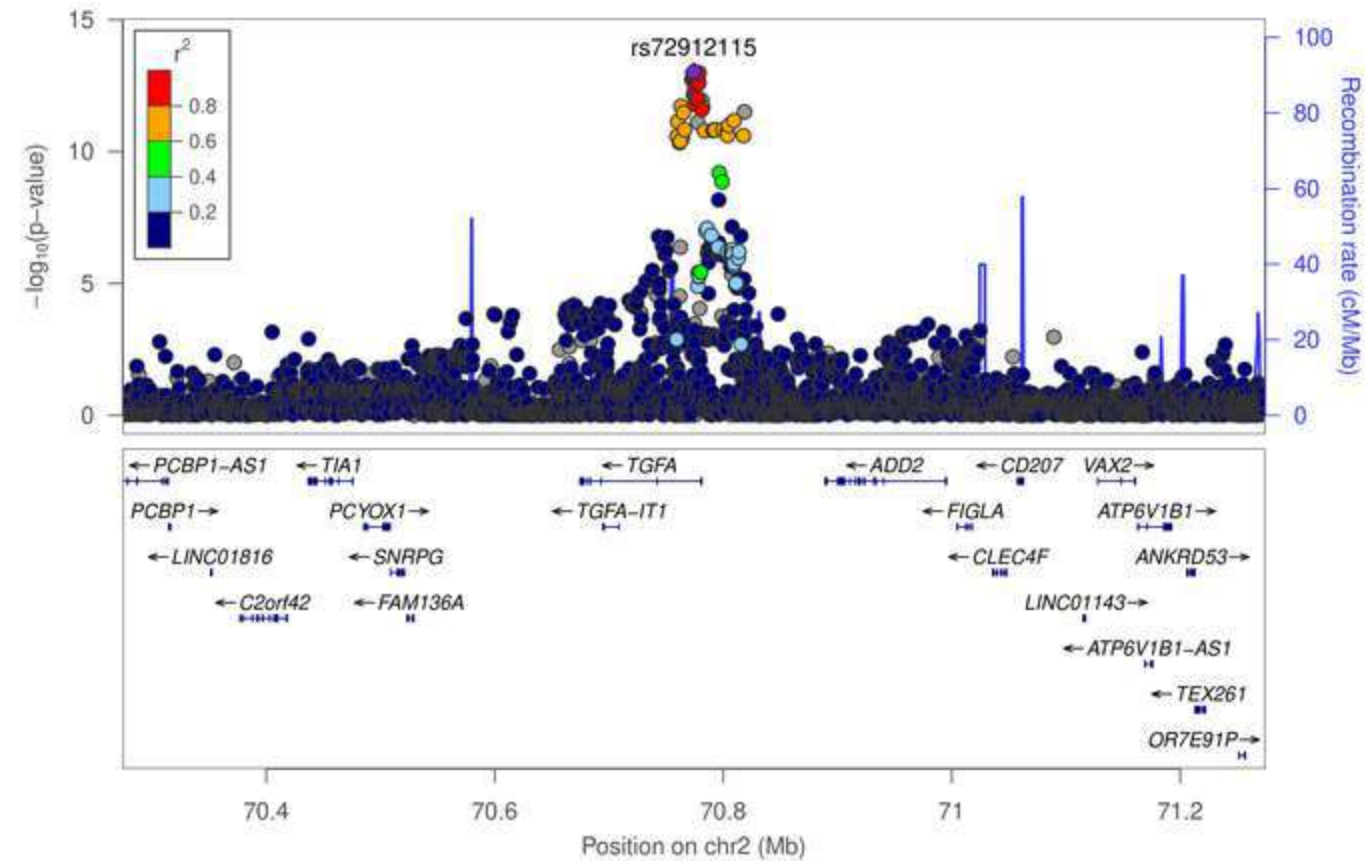
TGF-alpha (TGFA) [chr2:70774295_A_T (rs72912115) (A/T) N=14728]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.151	0.03	0.15 [0.09; 0.21]	35.3%
BioFinder (1496)	0.190	0.06	0.19 [0.07; 0.31]	8.5%
EGCUT (487)	0.049	0.09	0.05 [-0.13; 0.23]	4.2%
KORA (1064)	0.056	0.07	0.06 [-0.08; 0.19]	7.3%
NSPHS (866)	0.129	0.10	0.13 [-0.06; 0.32]	3.5%
ORCADES (979)	0.177	0.07	0.18 [0.04; 0.31]	7.1%
RECOMBINE (443)	0.101	0.11	0.10 [-0.12; 0.32]	2.6%
STABILITY (2951)	0.193	0.04	0.19 [0.11; 0.27]	20.9%
STANLEY (344)	-0.063	0.14	-0.06 [-0.34; 0.21]	1.8%
STANLEY (300)	-0.051	0.13	-0.05 [-0.30; 0.19]	2.2%
VIS (902)	0.054	0.07	0.05 [-0.08; 0.19]	6.8%
Common effect model			0.14 [0.10; 0.17]	100.0%
Random effects model			0.13 [0.09; 0.17]	100.0%



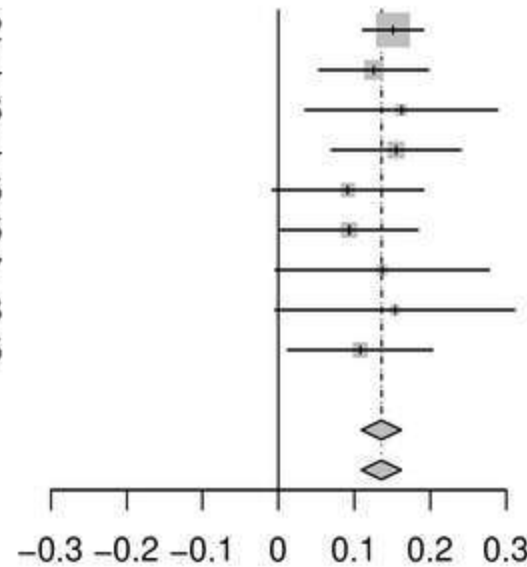
Heterogeneity: $I^2 = 12\%$, $\tau^2 = 0.0005$, $p = 0.33$

TGF-alpha (TGFA)-rs72912115



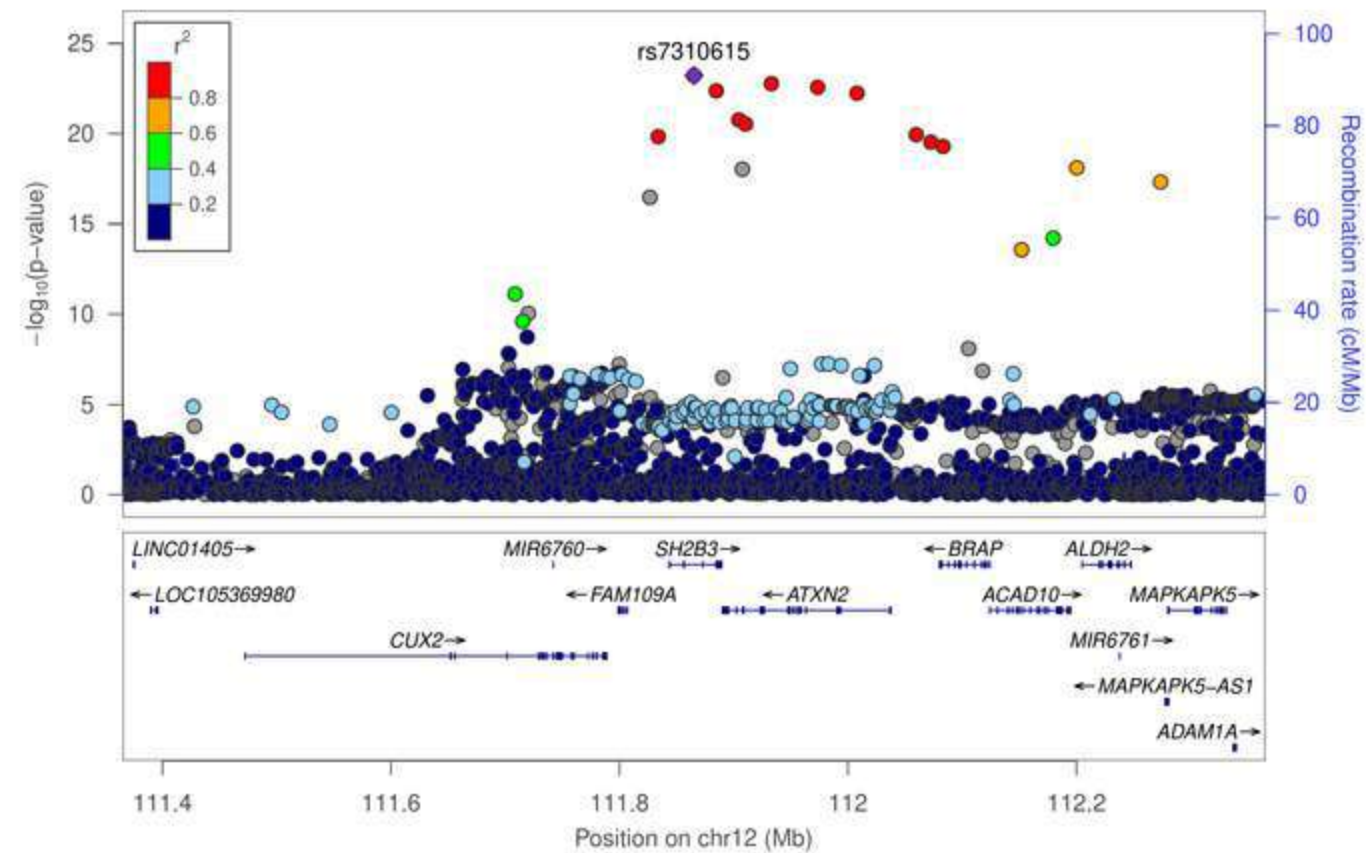
TNFB (LTA) [chr12:111865049_C_G (rs7310615) (C/G) N=11344]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.151	0.02	0.15 [0.11; 0.19]	43.4%
BioFinder (1496)	0.125	0.04	0.13 [0.05; 0.20]	13.4%
EGCUT (487)	0.162	0.06	0.16 [0.04; 0.29]	4.3%
KORA (1064)	0.155	0.04	0.16 [0.07; 0.24]	9.5%
NSPHS (874)	0.091	0.05	0.09 [-0.01; 0.19]	7.0%
ORCADES (981)	0.093	0.05	0.09 [0.00; 0.18]	8.5%
STANLEY (344)	0.137	0.07	0.14 [-0.00; 0.28]	3.5%
STANLEY (300)	0.153	0.08	0.15 [-0.00; 0.31]	2.8%
VIS (902)	0.108	0.05	0.11 [0.01; 0.20]	7.6%
Common effect model			0.14 [0.11; 0.16]	100.0%
Random effects model			0.14 [0.11; 0.16]	-- 100.0%



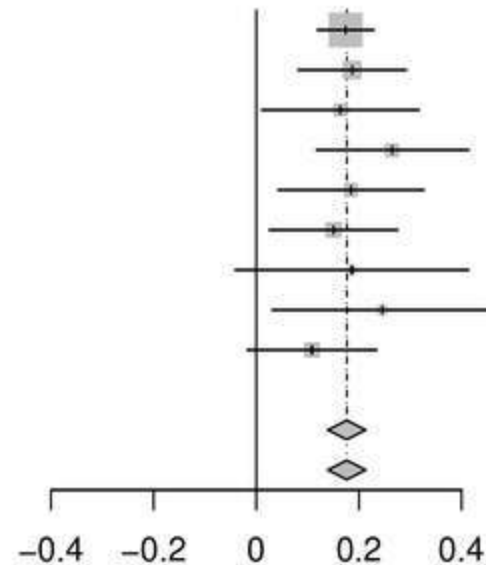
Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.94$

TNFB (LTA)-rs7310615



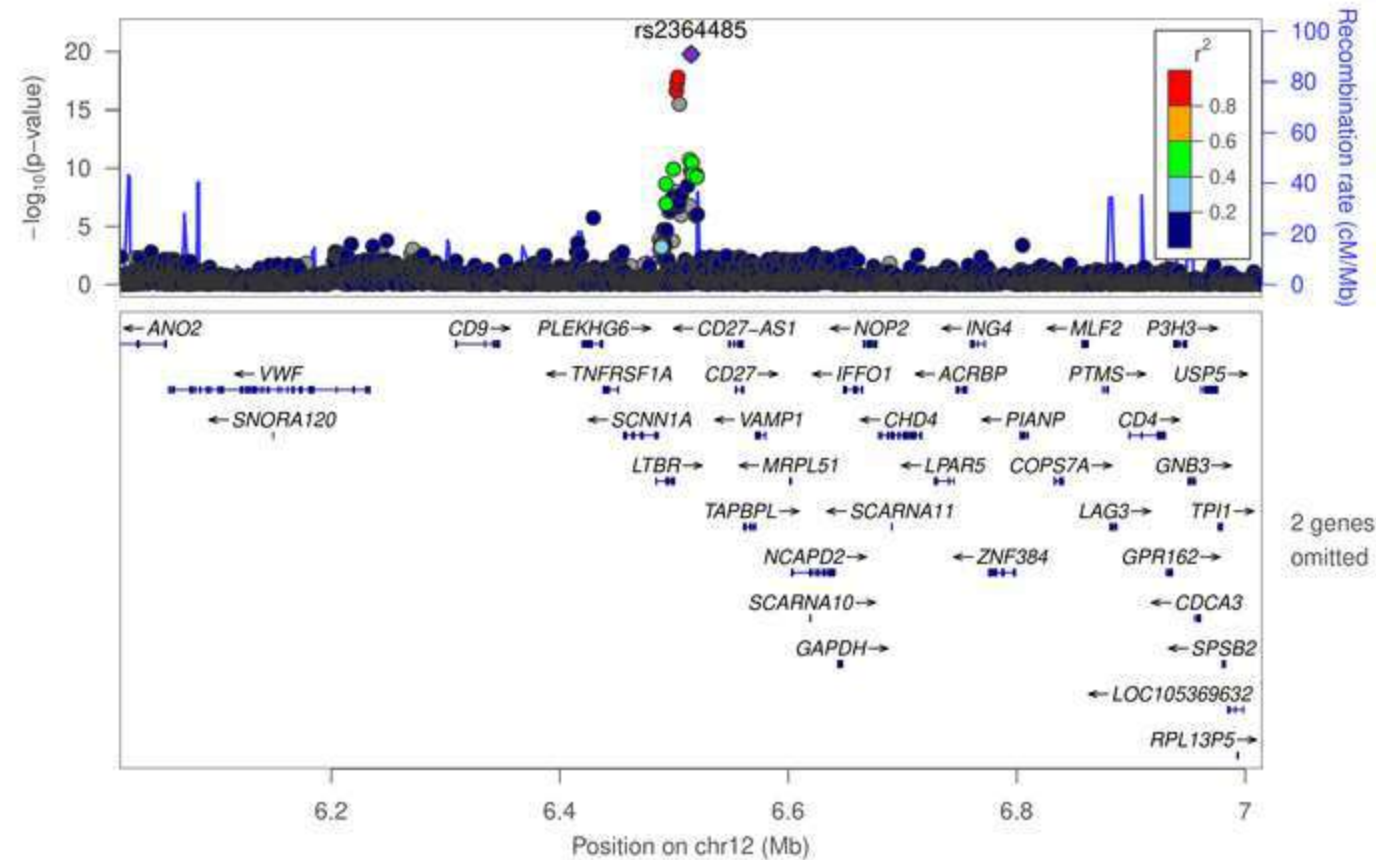
TNFB (LTA) [chr12:6514963_A_C (rs2364485) (A/C) N=11344]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.174	0.03	0.17 [0.12; 0.23]	45.4%
BioFinder (1496)	0.187	0.05	0.19 [0.08; 0.29]	12.4%
EGCUT (487)	0.164	0.08	0.16 [0.01; 0.32]	5.9%
KORA (1064)	0.265	0.08	0.27 [0.12; 0.41]	6.3%
NSPHS (874)	0.184	0.07	0.18 [0.04; 0.33]	6.8%
ORCADES (981)	0.150	0.06	0.15 [0.03; 0.28]	8.8%
STANLEY (344)	0.186	0.12	0.19 [-0.04; 0.41]	2.7%
STANLEY (300)	0.245	0.11	0.25 [0.03; 0.46]	3.0%
VIS (902)	0.108	0.06	0.11 [-0.02; 0.23]	8.7%
Common effect model			0.18 [0.14; 0.21]	100.0%
Random effects model			0.18 [0.14; 0.21]	100.0%



Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.92$

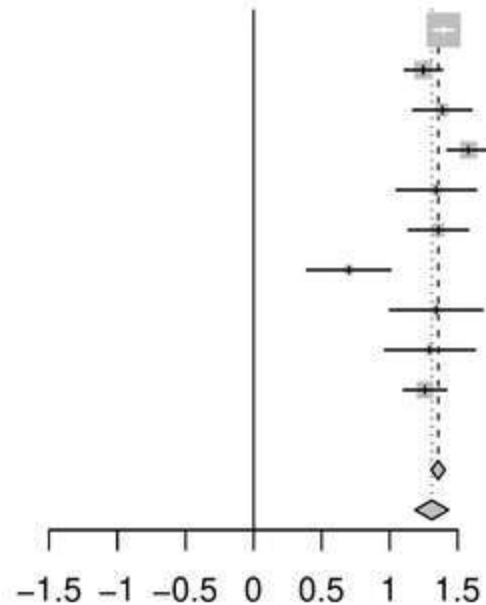
TNFB (LTA)–rs2364485



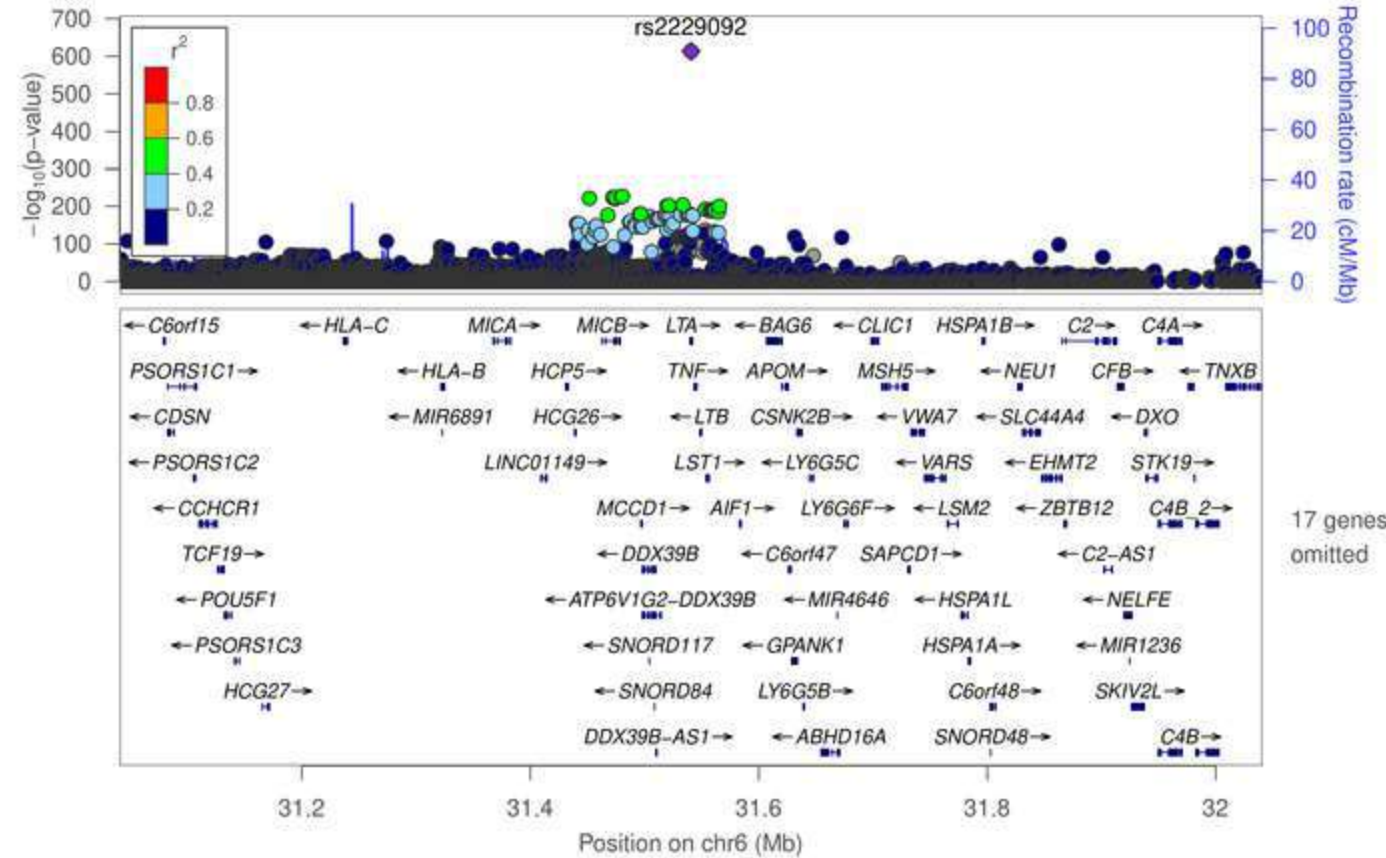
TNFB (LTA) [chr6:31540757_A_C (rs2229092) (A/C) N=11792]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	1.397	0.04	1.40 [1.32; 1.47]	46.1%	14.0%
BioFinder (1496)	1.248	0.07	1.25 [1.11; 1.39]	13.0%	12.4%
EGCUT (487)	1.387	0.11	1.39 [1.17; 1.60]	5.3%	10.1%
KORA (1064)	1.579	0.08	1.58 [1.42; 1.73]	10.3%	11.9%
NSPHS (874)	1.343	0.15	1.34 [1.05; 1.64]	2.9%	8.0%
ORCADES (981)	1.358	0.11	1.36 [1.14; 1.58]	5.2%	10.0%
RECOMBINE (448)	0.700	0.16	0.70 [0.39; 1.01]	2.6%	7.7%
STANLEY (344)	1.342	0.17	1.34 [1.00; 1.68]	2.2%	6.9%
STANLEY (300)	1.296	0.17	1.30 [0.96; 1.63]	2.3%	7.1%
VIS (902)	1.260	0.08	1.26 [1.10; 1.42]	10.1%	11.9%
Common effect model			1.36 [1.31; 1.41]	100.0%	--
Random effects model			1.31 [1.19; 1.43]	--	100.0%

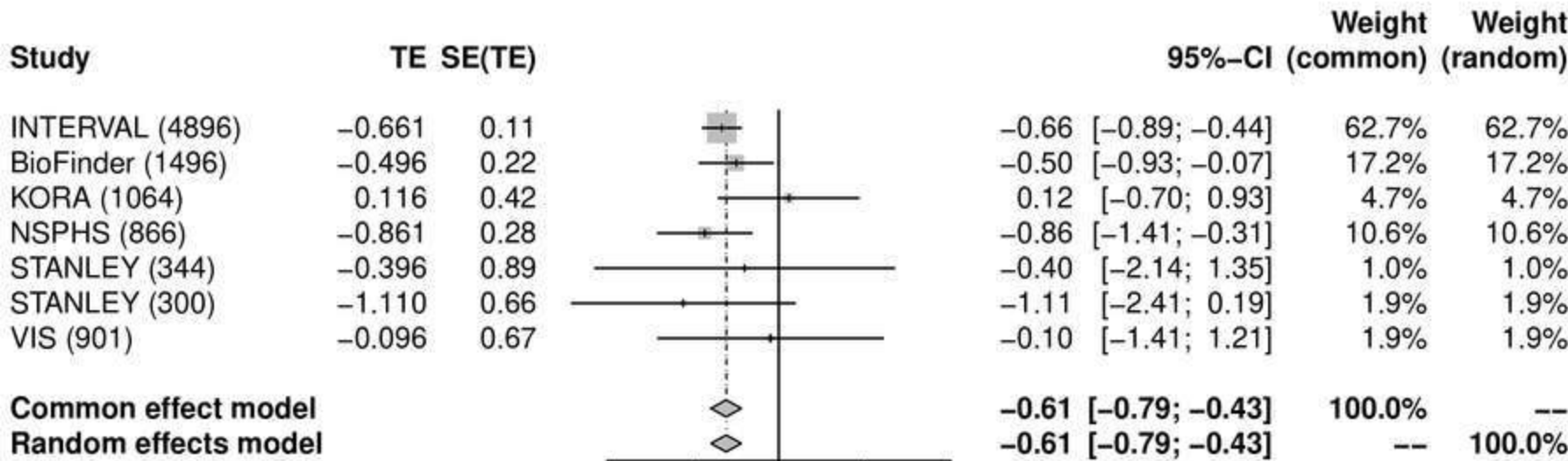
Heterogeneity: $I^2 = 70\%$, $\tau^2 = 0.0271$, $p < 0.01$



TNFB (LTA)-rs2229092

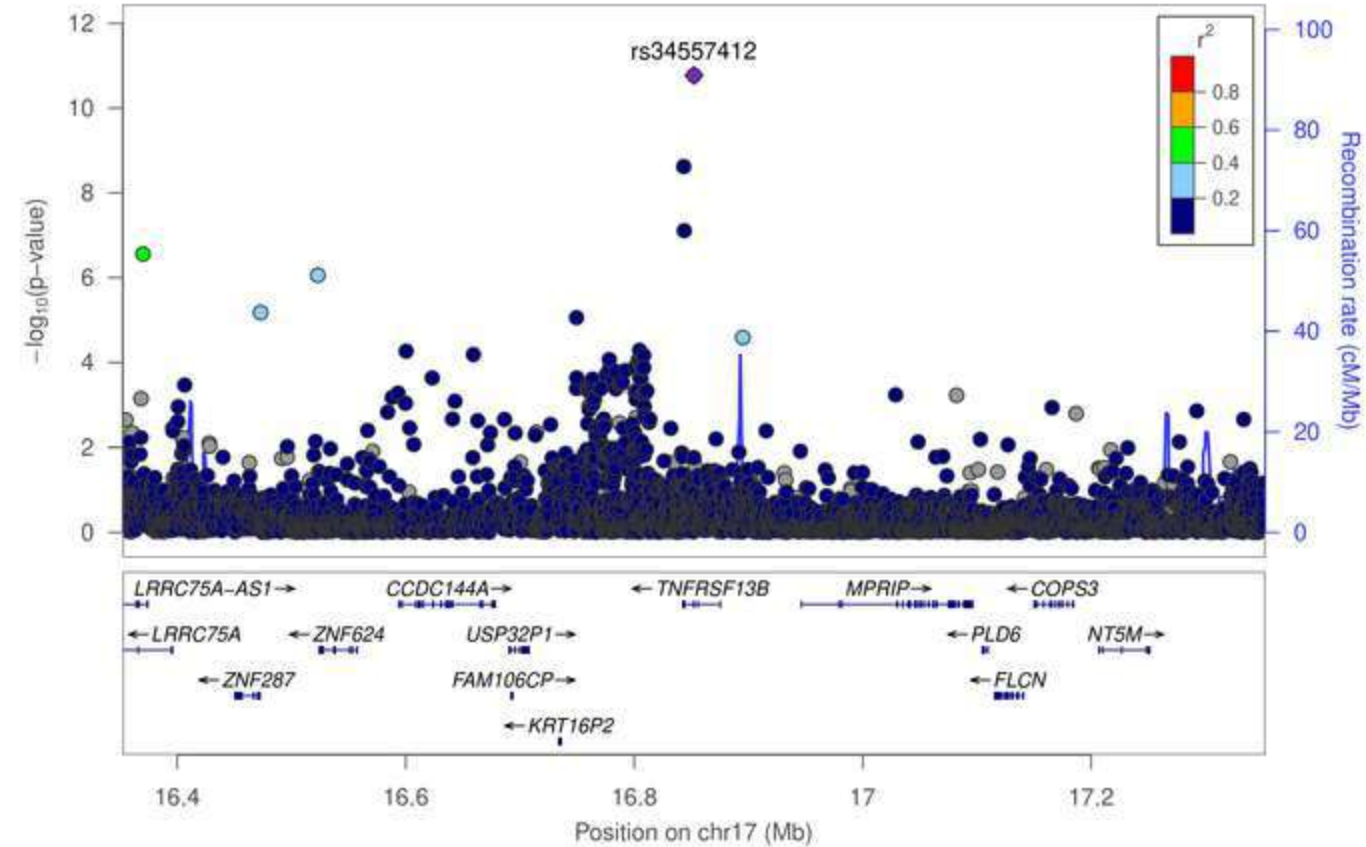


TNFRSF9 (TNFRSF9) [chr17:16852187_A_G (rs34557412) (A/G) N=9867]

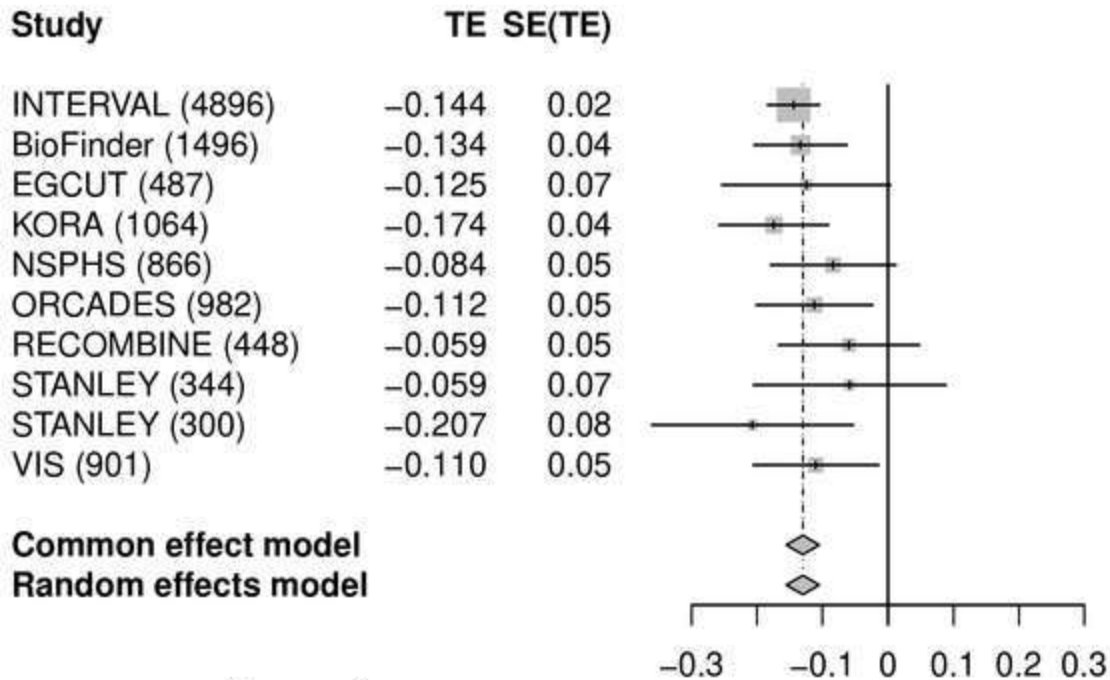


Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.48$

TNFRSF9 (TNFRSF9)-rs34557412



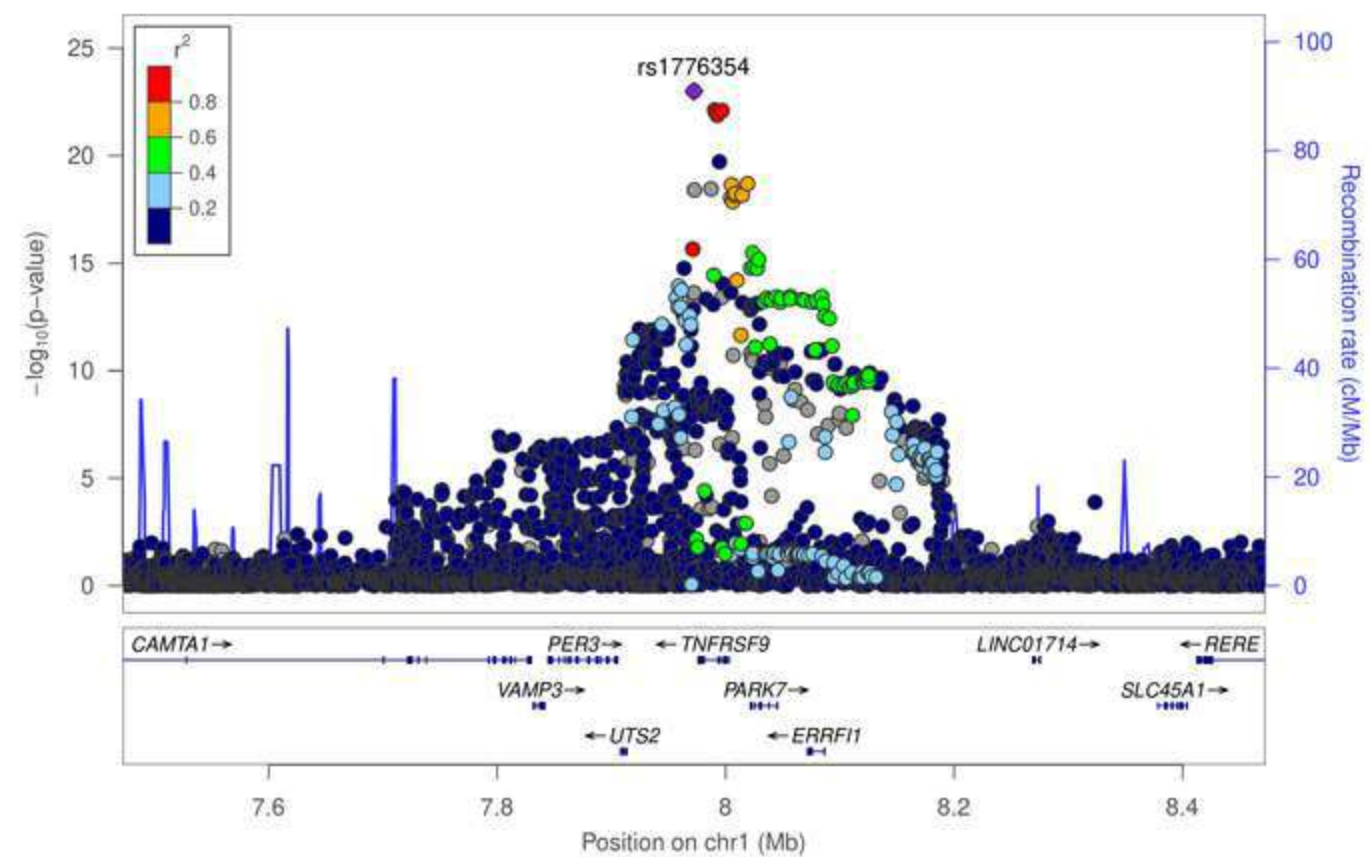
TNFRSF9 (TNFRSF9) [chr1:7972201_A_G (rs1776354) (A/G) N=11784]



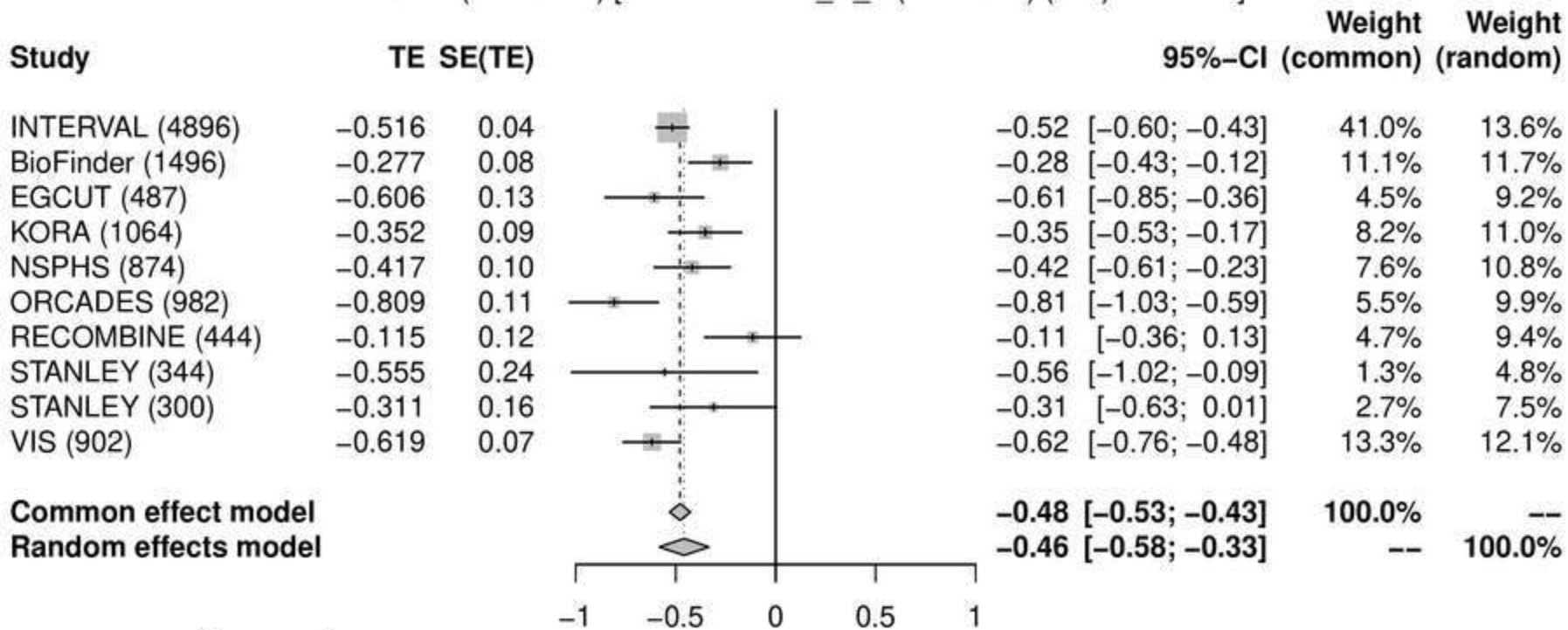
Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.71$

	Weight	Weight
95%-CI (common)	(common)	(random)
-0.14 [-0.18; -0.10]	40.7%	40.7%
-0.13 [-0.20; -0.06]	12.8%	12.8%
-0.12 [-0.25; 0.00]	3.9%	3.9%
-0.17 [-0.26; -0.09]	9.2%	9.2%
-0.08 [-0.18; 0.01]	7.0%	7.0%
-0.11 [-0.20; -0.02]	8.2%	8.2%
-0.06 [-0.17; 0.05]	5.6%	5.6%
-0.06 [-0.21; 0.09]	3.0%	3.0%
-0.21 [-0.36; -0.05]	2.7%	2.7%
-0.11 [-0.21; -0.01]	7.0%	7.0%
-0.13 [-0.16; -0.10]	100.0%	--
-0.13 [-0.16; -0.10]	--	100.0%

TNFRSF9 (TNFRSF9)-rs1776354

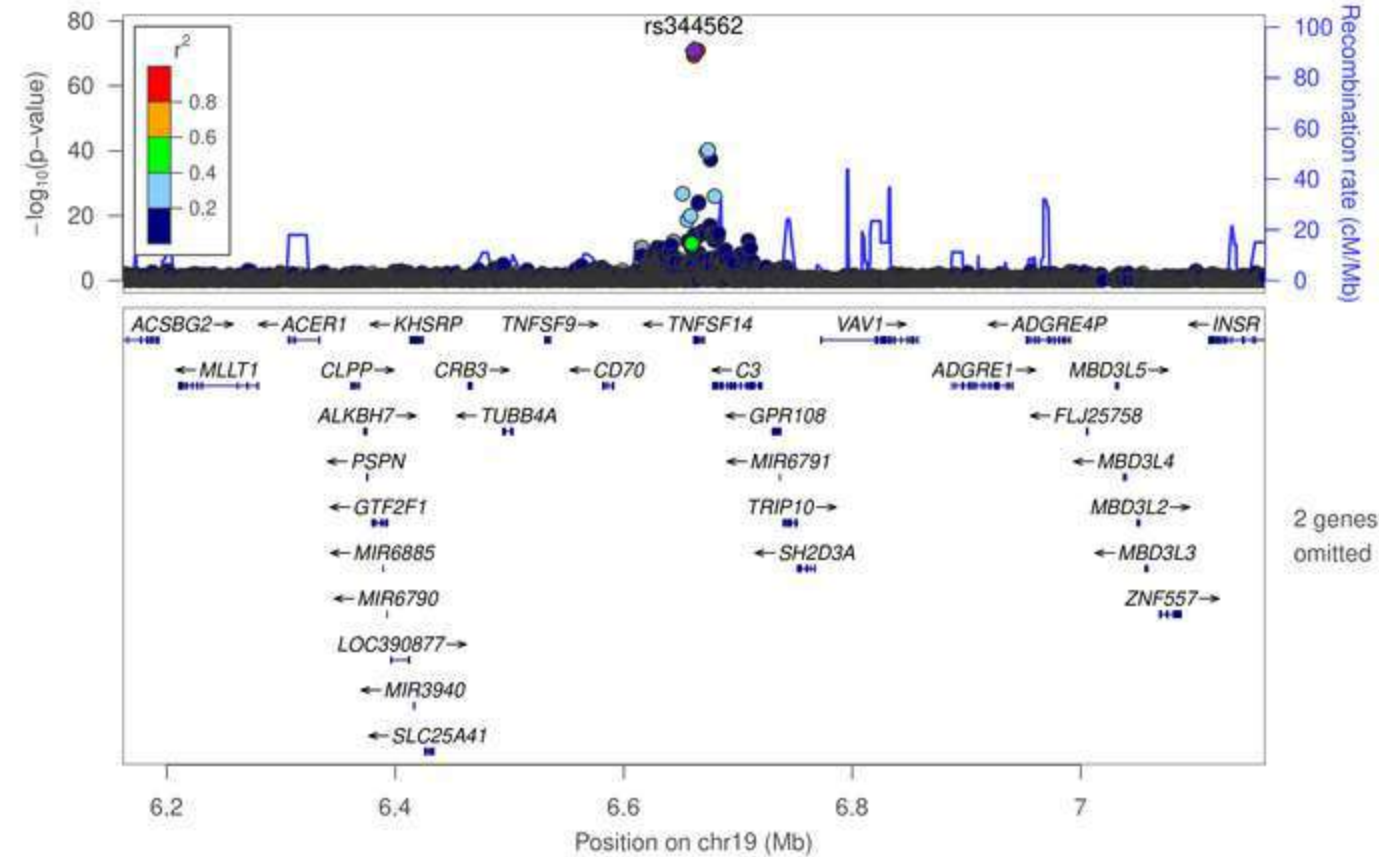


TNFSF14 (TNFSF14) [chr19:6661549_C_T (rs344562) (T/C) N=11789]

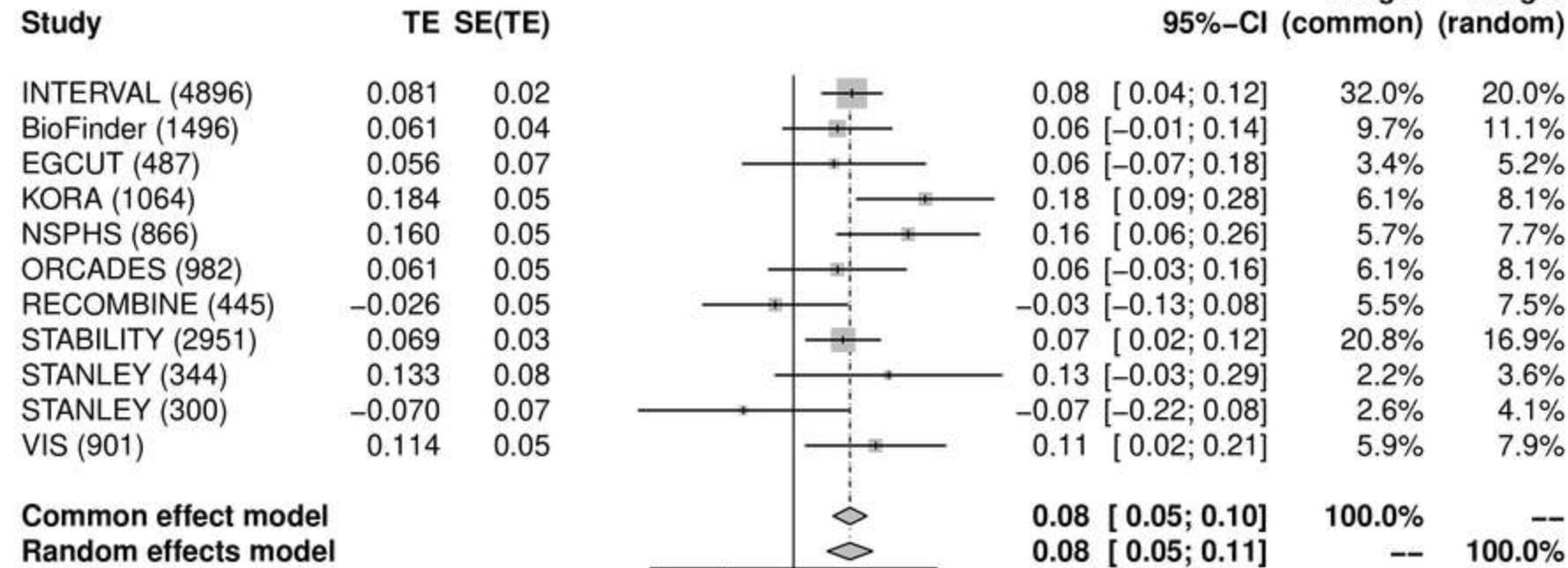


Heterogeneity: $I^2 = 72\%$, $\tau^2 = 0.0280$, $p < 0.01$

TNFSF14 (TNFSF14)-rs344562

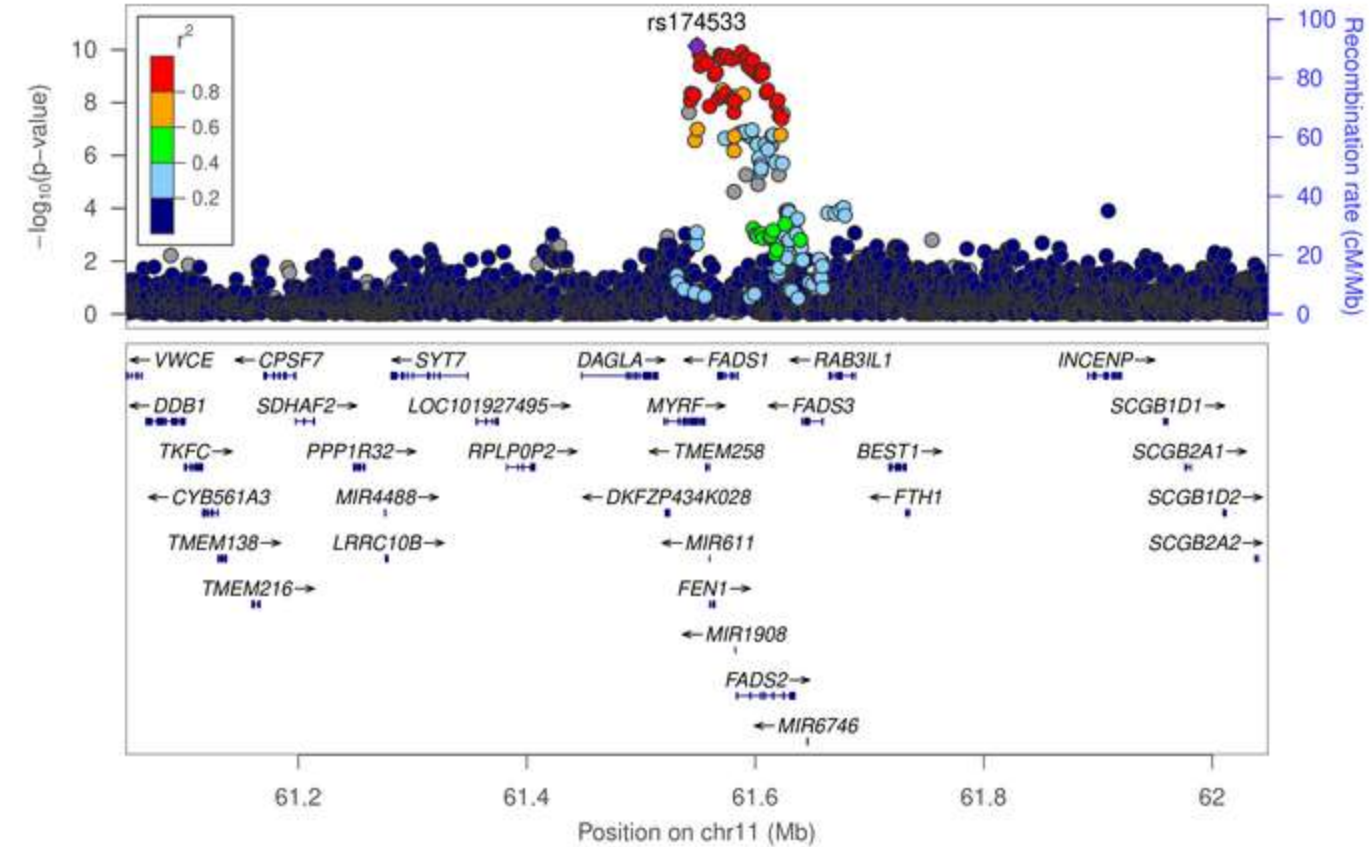


TRAIL (TNFSF10) [chr11:61549025_A_G (rs174533) (A/G) N=14732]



Heterogeneity: $I^2 = 41\%$, $\tau^2 = 0.0009$, $p = 0.08$

TRAIL (TNFSF10)-rs174533



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (438)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.99$

TRAIL (TNFSF10) [chr1:196710916_C_T (rs16840522) (T/C) N=14725]

TE SE(TE)

-0.141 0.03

-0.080 0.05

-0.114 0.08

-0.119 0.06

-0.098 0.08

-0.088 0.06

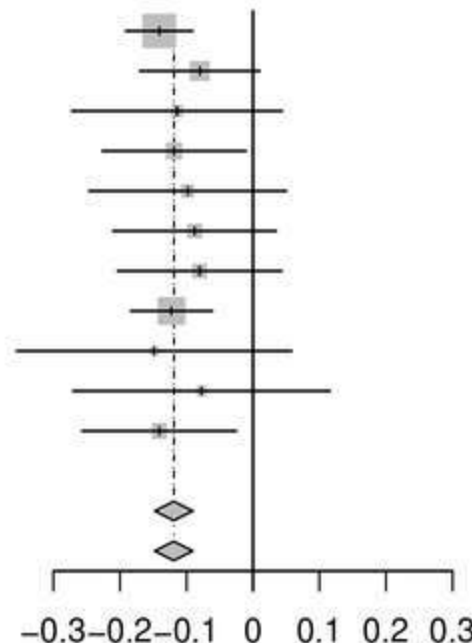
-0.080 0.06

-0.122 0.03

-0.148 0.11

-0.077 0.10

-0.141 0.06

Weight
95%-CI (common) (random)

-0.14 [-0.19; -0.09] 32.5% 32.5%

-0.08 [-0.17; 0.01] 10.1% 10.1%

-0.11 [-0.27; 0.04] 3.3% 3.3%

-0.12 [-0.23; -0.01] 7.1% 7.1%

-0.10 [-0.25; 0.05] 3.8% 3.8%

-0.09 [-0.21; 0.03] 5.5% 5.5%

-0.08 [-0.20; 0.04] 5.4% 5.4%

-0.12 [-0.18; -0.06] 22.0% 22.0%

-0.15 [-0.35; 0.06] 1.9% 1.9%

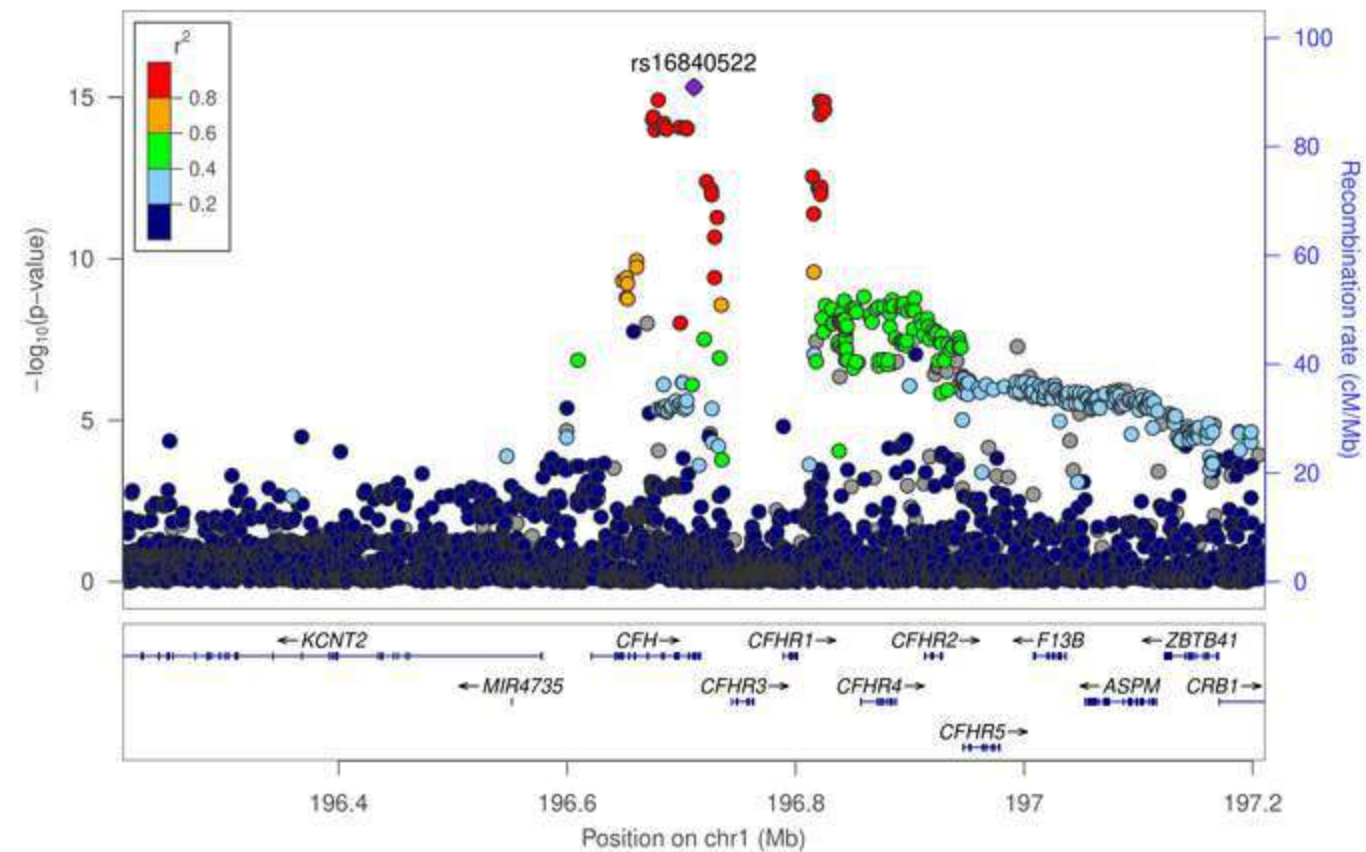
-0.08 [-0.27; 0.12] 2.2% 2.2%

-0.14 [-0.26; -0.02] 6.1% 6.1%

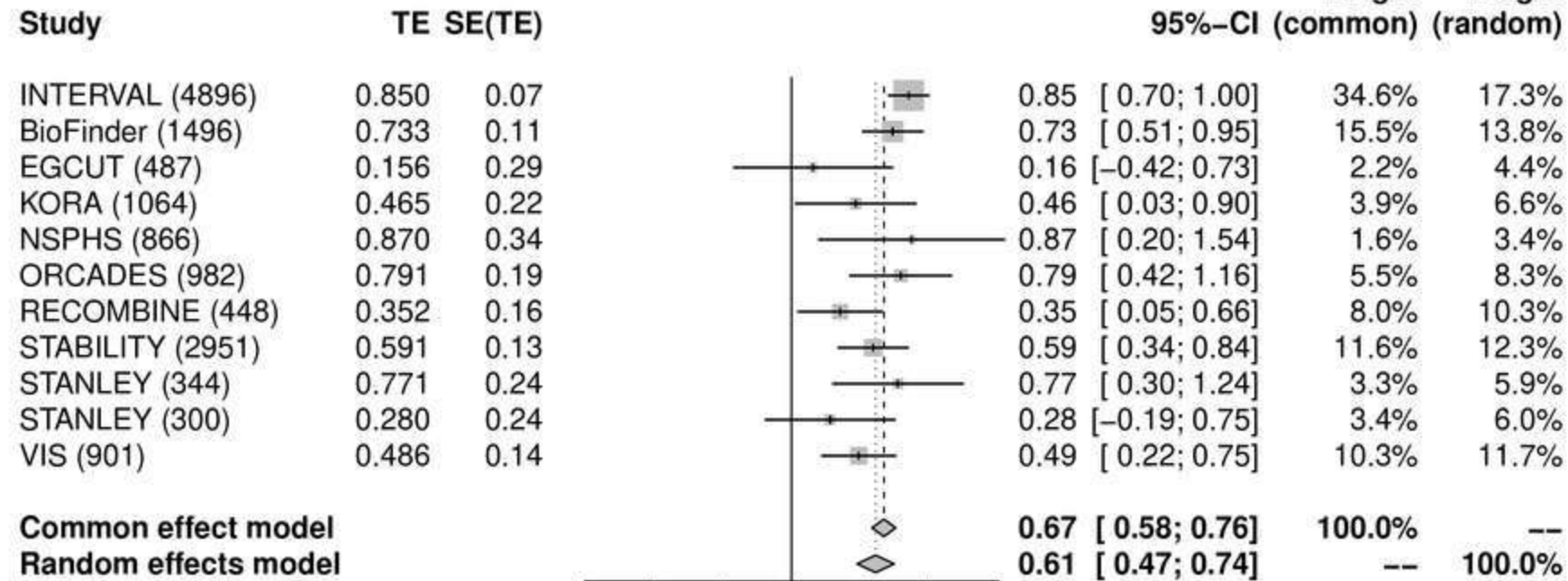
-0.12 [-0.15; -0.09] 100.0% --

-0.12 [-0.15; -0.09] -- 100.0%

TRAIL (TNFSF10)-rs16840522

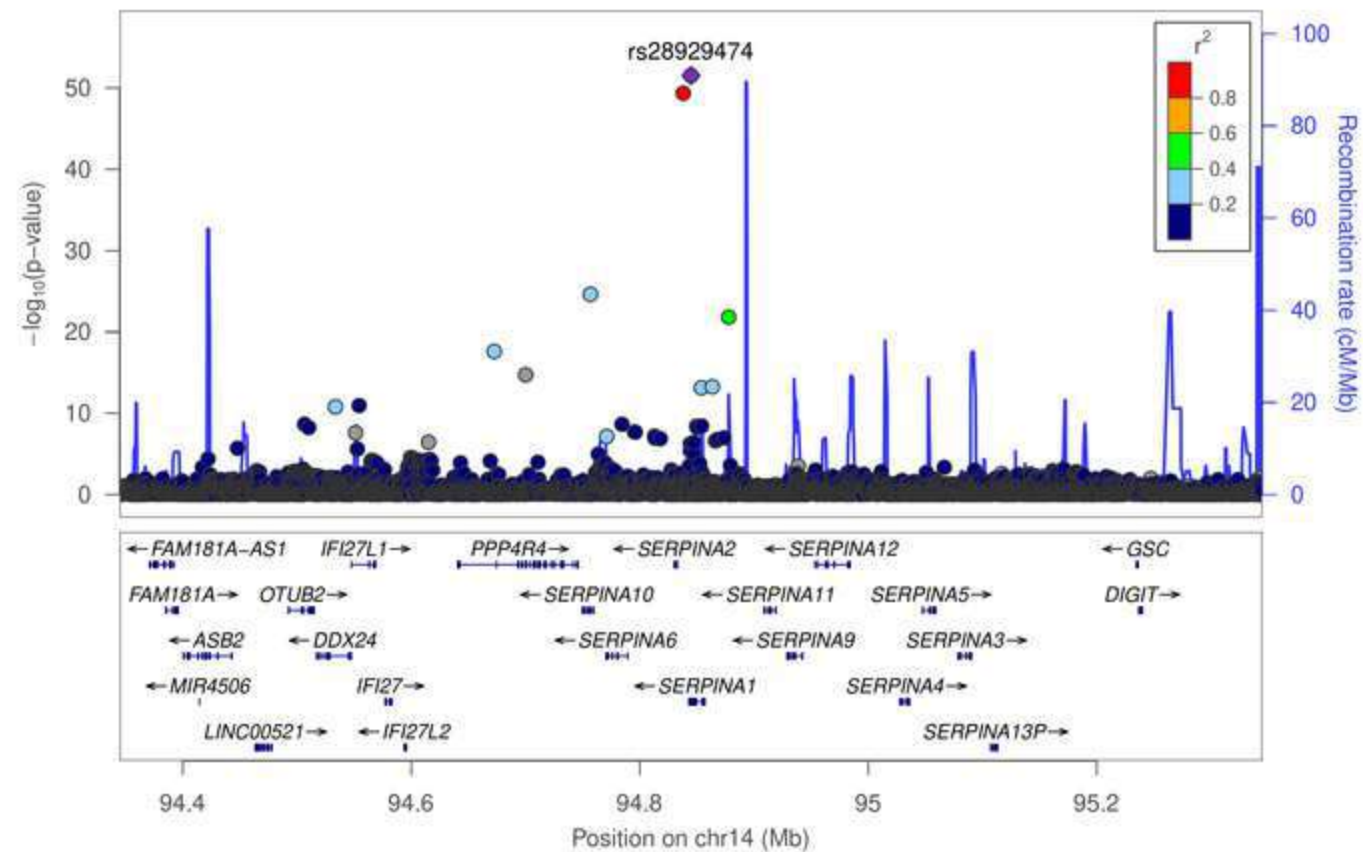


TRAIL (TNFSF10) [chr14:94844947_C_T (rs28929474) (T/C) N=14735]



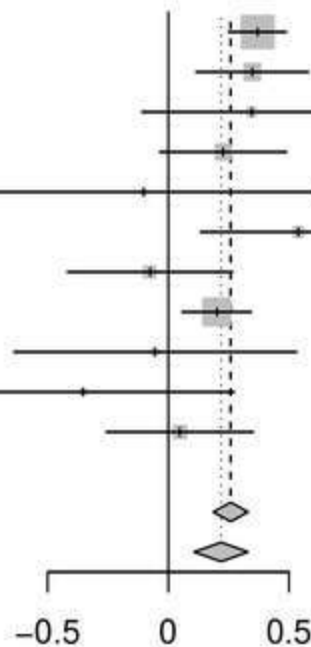
Heterogeneity: $I^2 = 50\%$, $\tau^2 = 0.0218$, $p = 0.03$

TRAIL (TNFSF10)-rs28929474



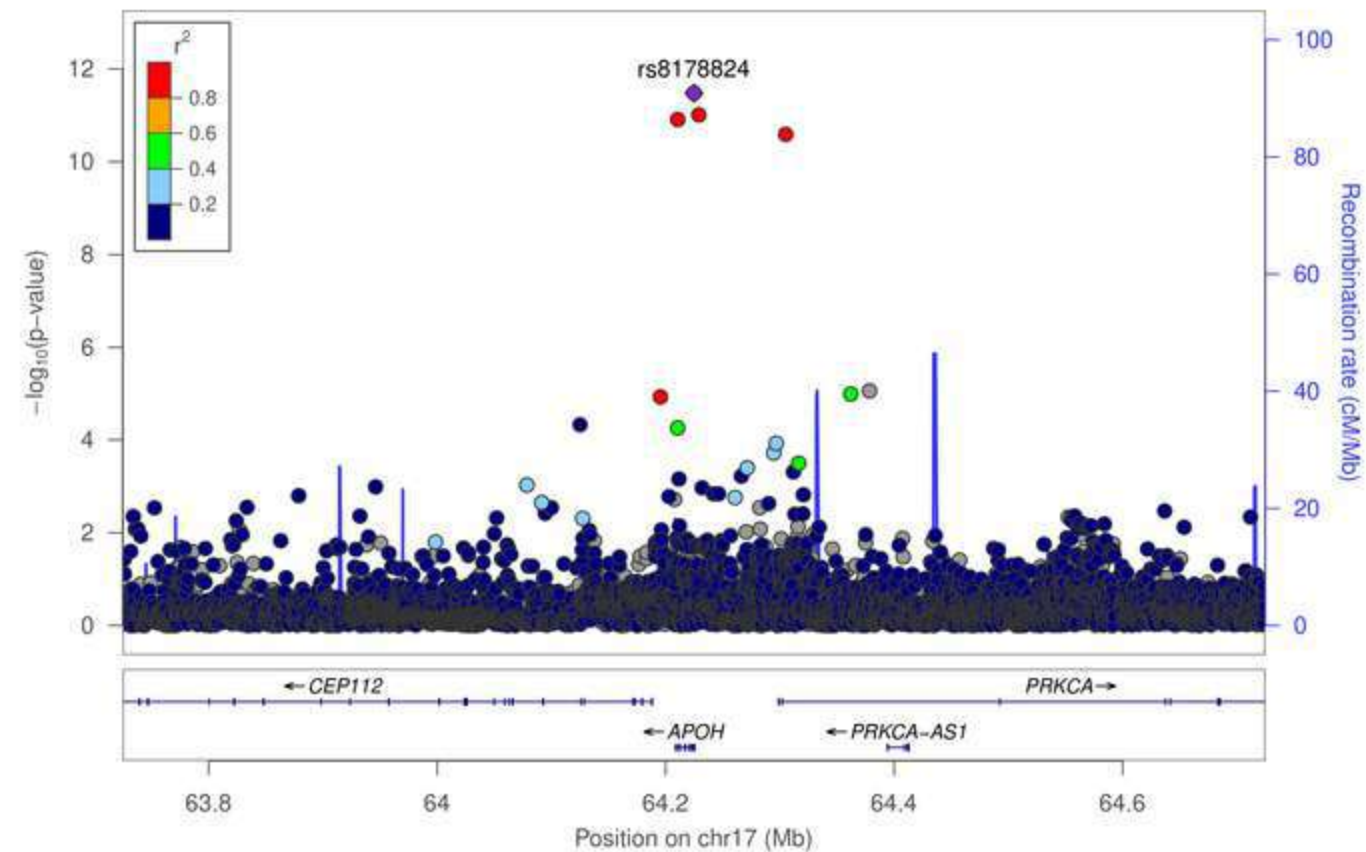
TRAIL (TNFSF10) [chr17:64224775_C_T (rs8178824) (T/C) N=14735]

Study	TE	SE(TE)		Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.369	0.06		0.37 [0.25; 0.49]	37.0%
BioFinder (1496)	0.347	0.12		0.35 [0.11; 0.58]	9.7%
EGCUT (487)	0.344	0.23		0.34 [-0.11; 0.80]	2.5%
KORA (1064)	0.226	0.13		0.23 [-0.04; 0.49]	7.7%
NSPHS (866)	-0.104	0.37		-0.10 [-0.84; 0.63]	1.0%
ORCADES (982)	0.537	0.21		0.54 [0.13; 0.94]	3.2%
RECOMBINE (448)	-0.076	0.17		-0.08 [-0.42; 0.27]	4.5%
STABILITY (2951)	0.200	0.07		0.20 [0.06; 0.34]	25.9%
STANLEY (344)	-0.055	0.30		-0.06 [-0.64; 0.53]	1.5%
STANLEY (300)	-0.353	0.32		-0.35 [-0.98; 0.27]	1.3%
VIS (901)	0.047	0.15		0.05 [-0.26; 0.35]	5.7%
Common effect model				0.26 [0.18; 0.33]	100.0%
Random effects model				0.22 [0.11; 0.33]	-- 100.0%



Heterogeneity: $I^2 = 44\%$, $\tau^2 = 0.0120$, $p = 0.06$

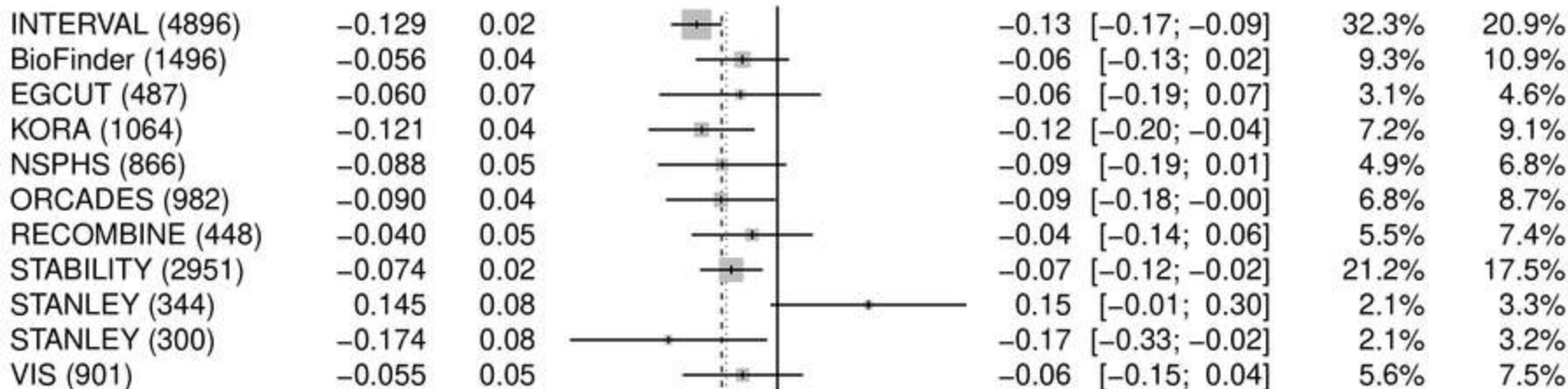
TRAIL (TNFSF10)-rs8178824



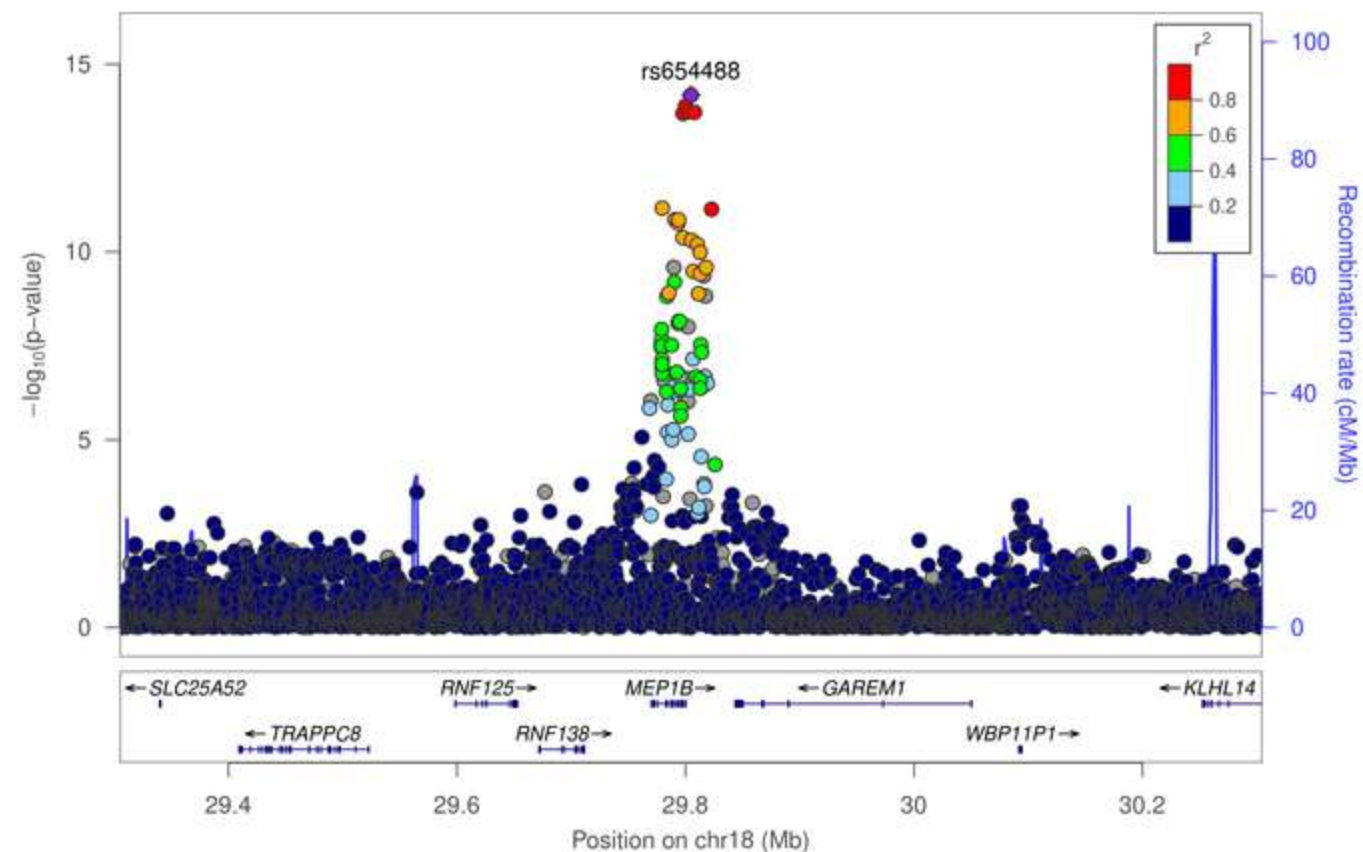
Study

TRAIL (TNFSF10) [chr18:29804863_A_T (rs654488) (A/T) N=14735]

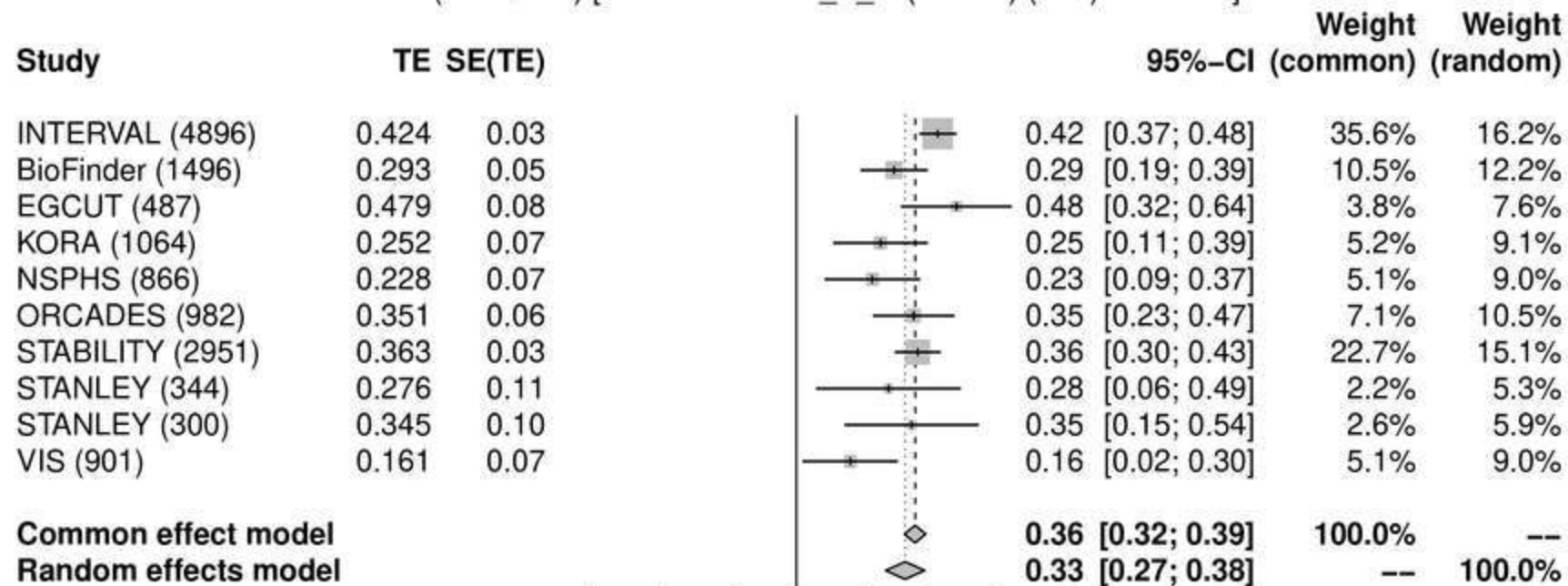
TE SE(TE)

Weight
95%-CI (common) (random)Common effect model
Random effects modelHeterogeneity: $I^2 = 42\%$, $\tau^2 = 0.0007$, $p = 0.07$

TRAIL (TNFSF10)-rs654488

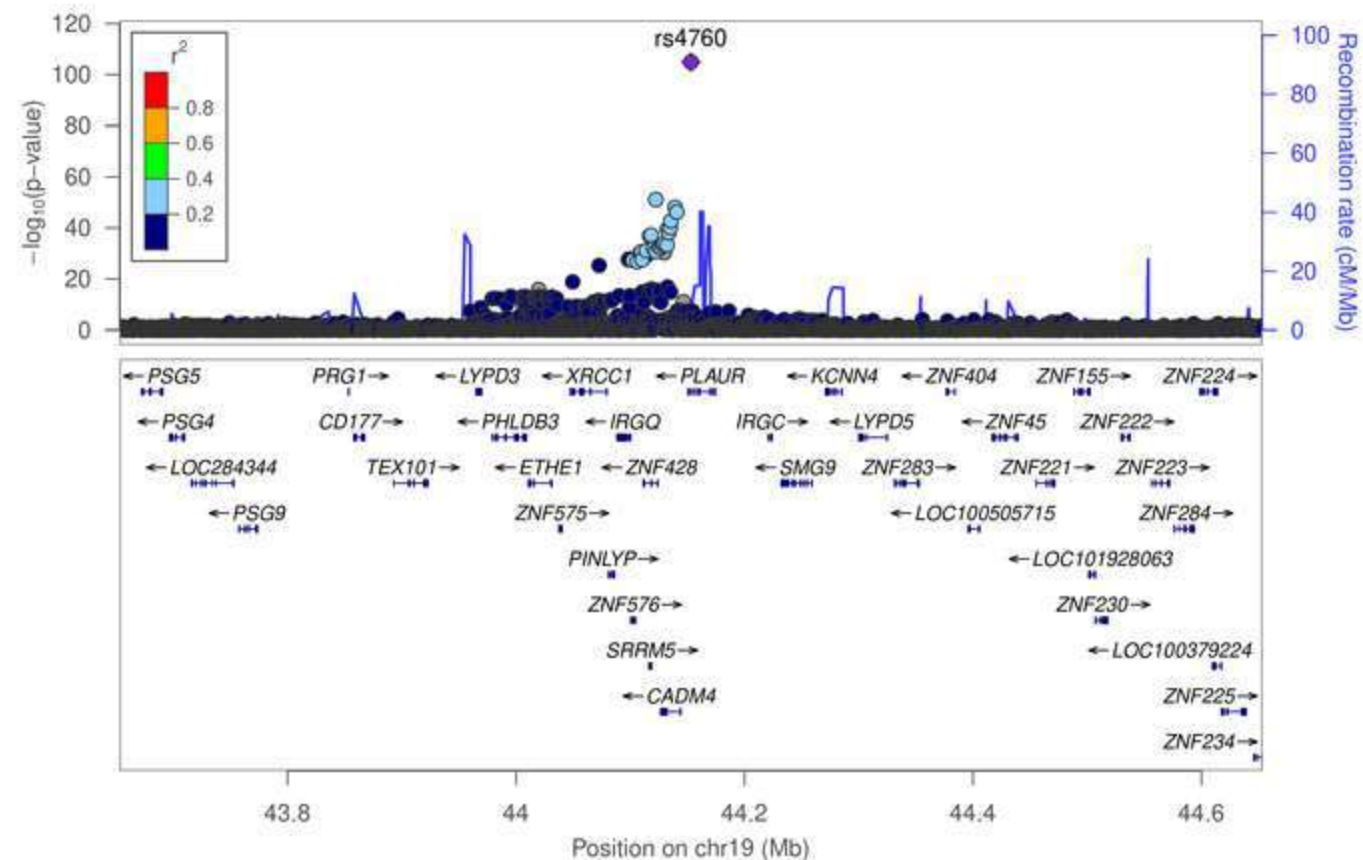


TRAIL (TNFSF10) [chr19:44153100_A_G (rs4760) (A/G) N=14287]

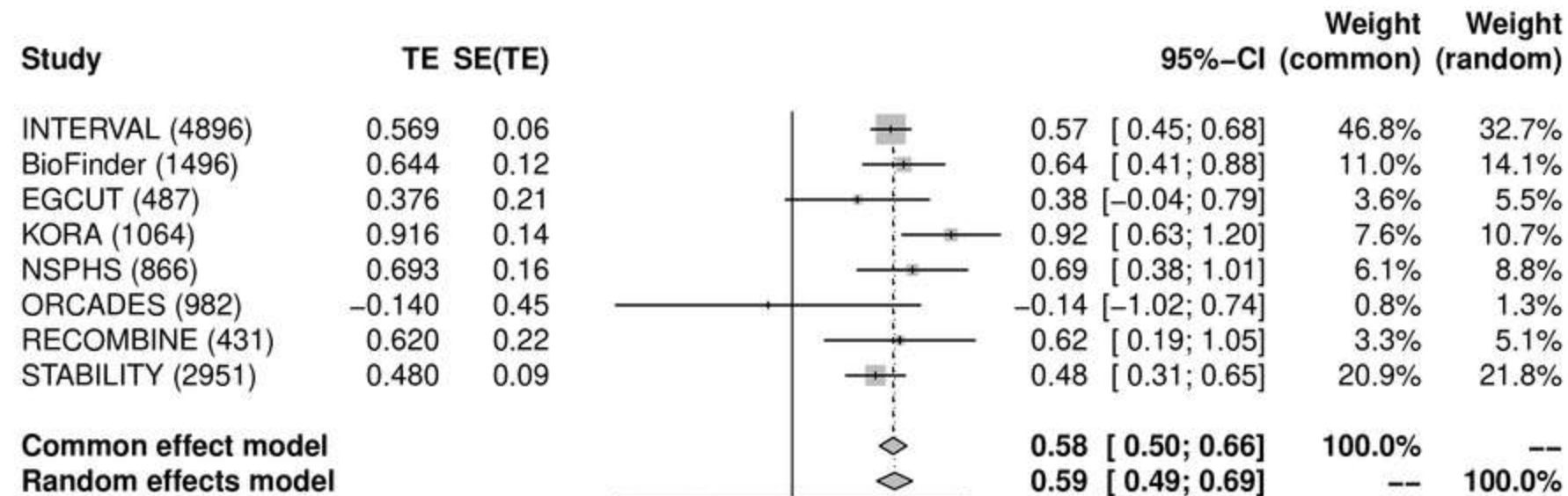


Heterogeneity: $I^2 = 61\%$, $\tau^2 = 0.0048$, $p < 0.01$

TRAIL (TNFSF10)-rs4760

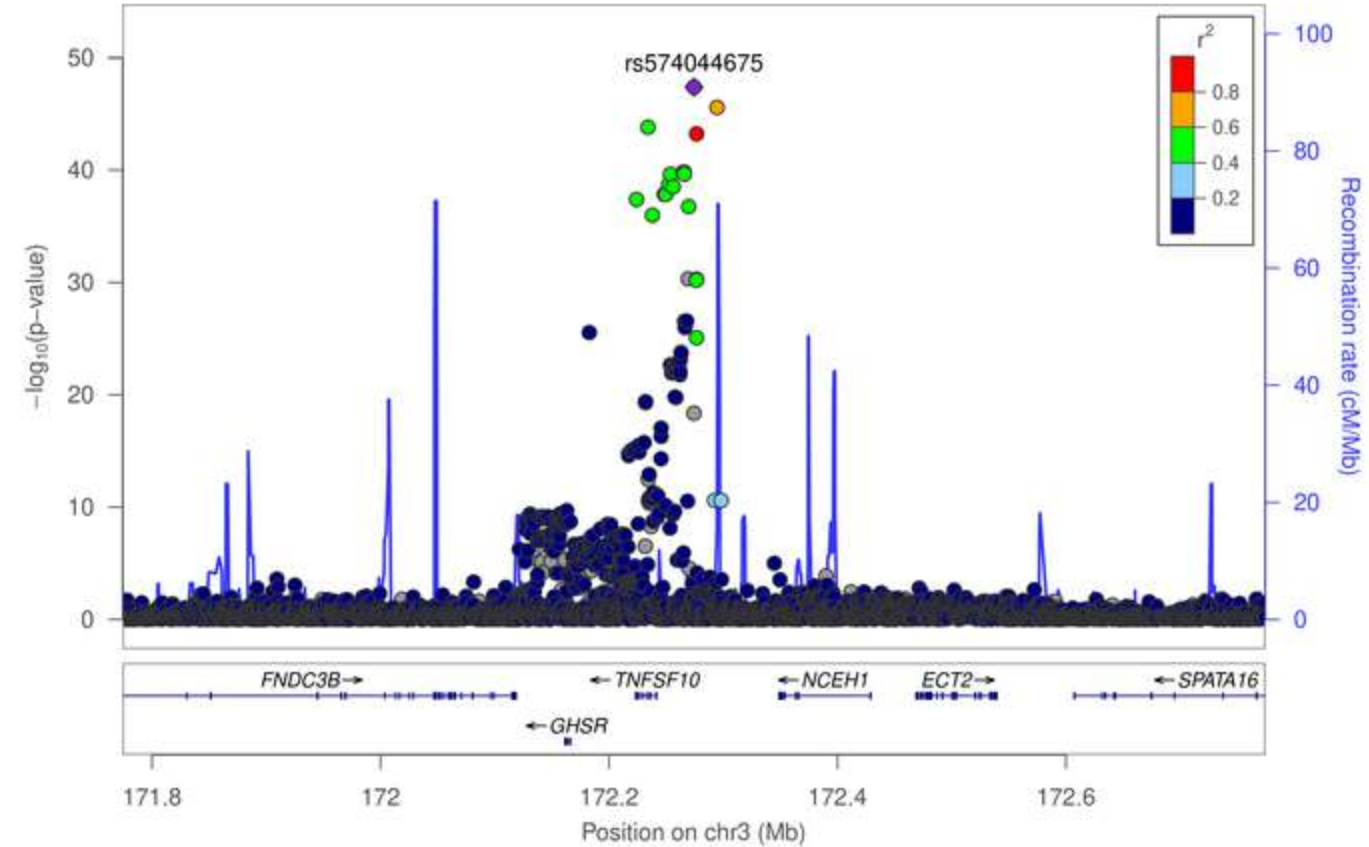


TRAIL (TNFSF10) [chr3:172274232_A_C (rs574044675) (A/C) N=13173]



Heterogeneity: $I^2 = 37\%$, $\tau^2 = 0.0050$, $p = 0.14$

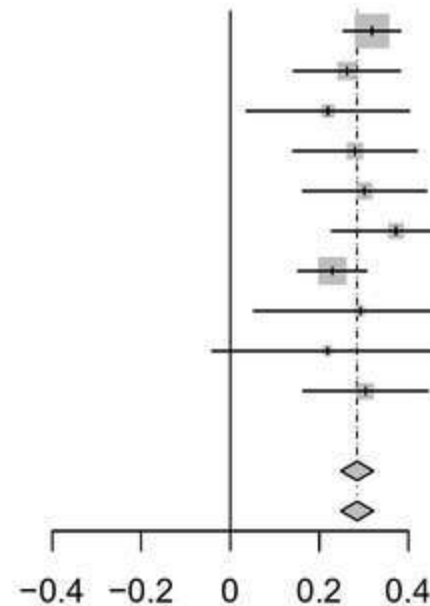
TRAIL (TNFSF10)-rs574044675



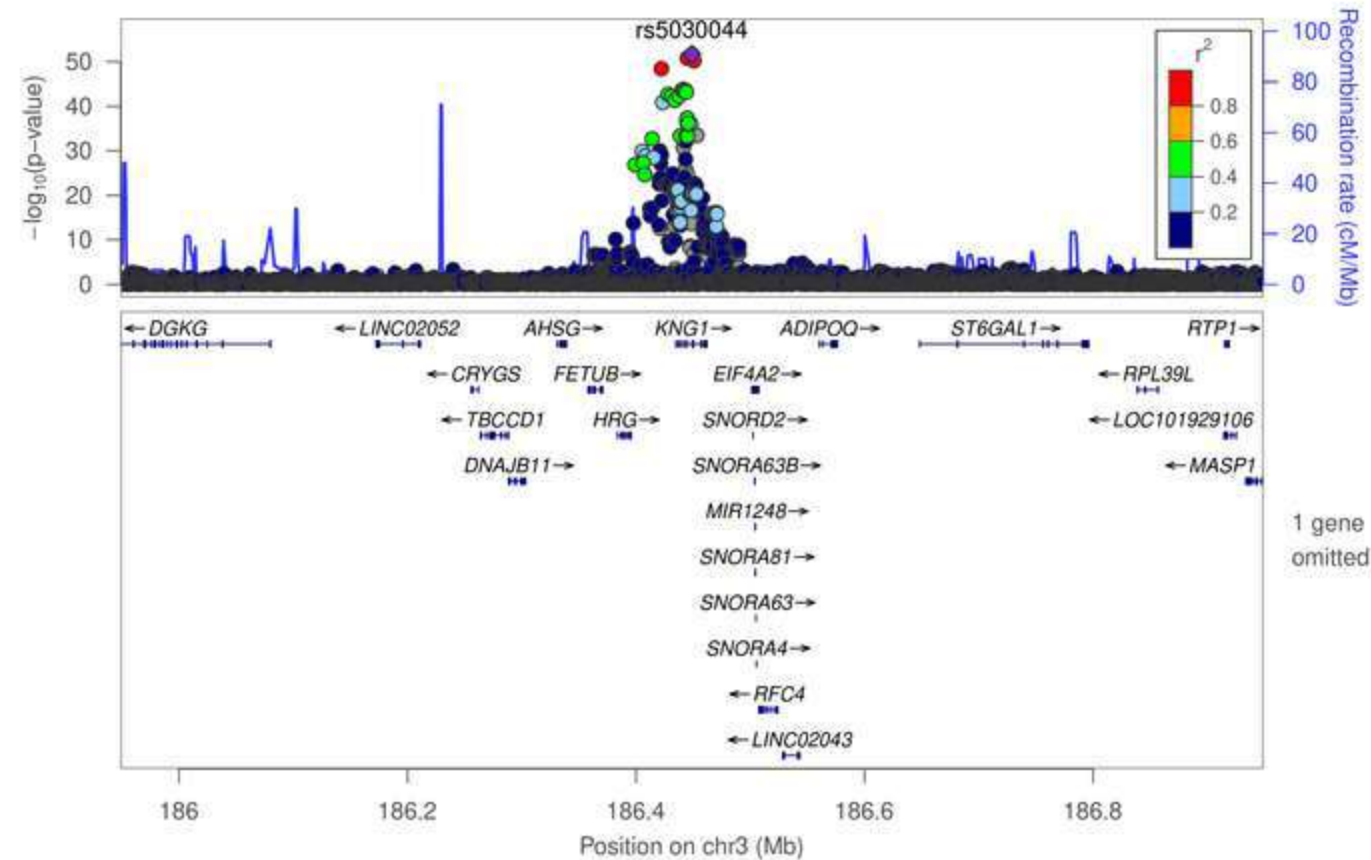
TRAIL (TNFSF10) [chr3:186449122_A_G (rs5030044) (A/G) N=14287]

Study	TE	seTE	95%-CI	Weight (fixed)	Weight (random)
INTERVAL (4896)	0.32	0.0327	0.32 [0.25; 0.38]	32.7%	32.7%
BioFinder (1496)	0.26	0.0611	0.26 [0.14; 0.38]	9.4%	9.4%
EGCUT (487)	0.22	0.0935	0.22 [0.04; 0.40]	4.0%	4.0%
KORA (1064)	0.28	0.0711	0.28 [0.14; 0.42]	6.9%	6.9%
NSPHS (866)	0.30	0.0710	0.30 [0.16; 0.44]	6.9%	6.9%
ORCADES (982)	0.37	0.0738	0.37 [0.23; 0.52]	6.4%	6.4%
STABILITY (2951)	0.23	0.0394	0.23 [0.15; 0.31]	22.5%	22.5%
STANLEY (344)	0.29	0.1219	0.29 [0.05; 0.53]	2.4%	2.4%
STANLEY (300)	0.22	0.1322	0.22 [-0.04; 0.48]	2.0%	2.0%
VIS (901)	0.30	0.0717	0.30 [0.16; 0.44]	6.8%	6.8%
Fixed effect model			0.29 [0.25; 0.32]	100.0%	--
Random effects model			0.29 [0.25; 0.32]	--	100.0%

Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.79$

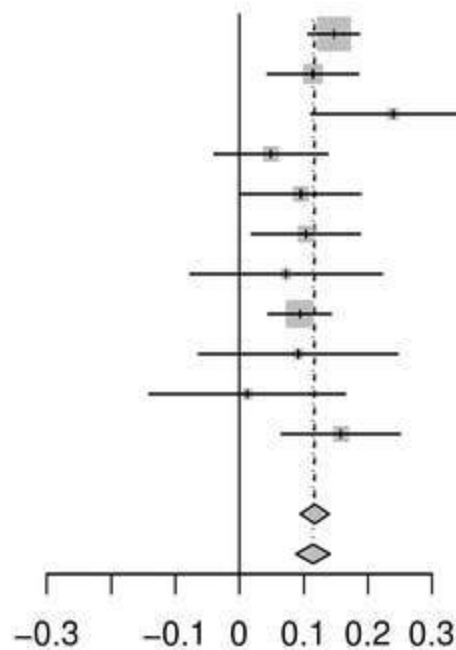


TRAIL (TNFSF10)-rs5030044



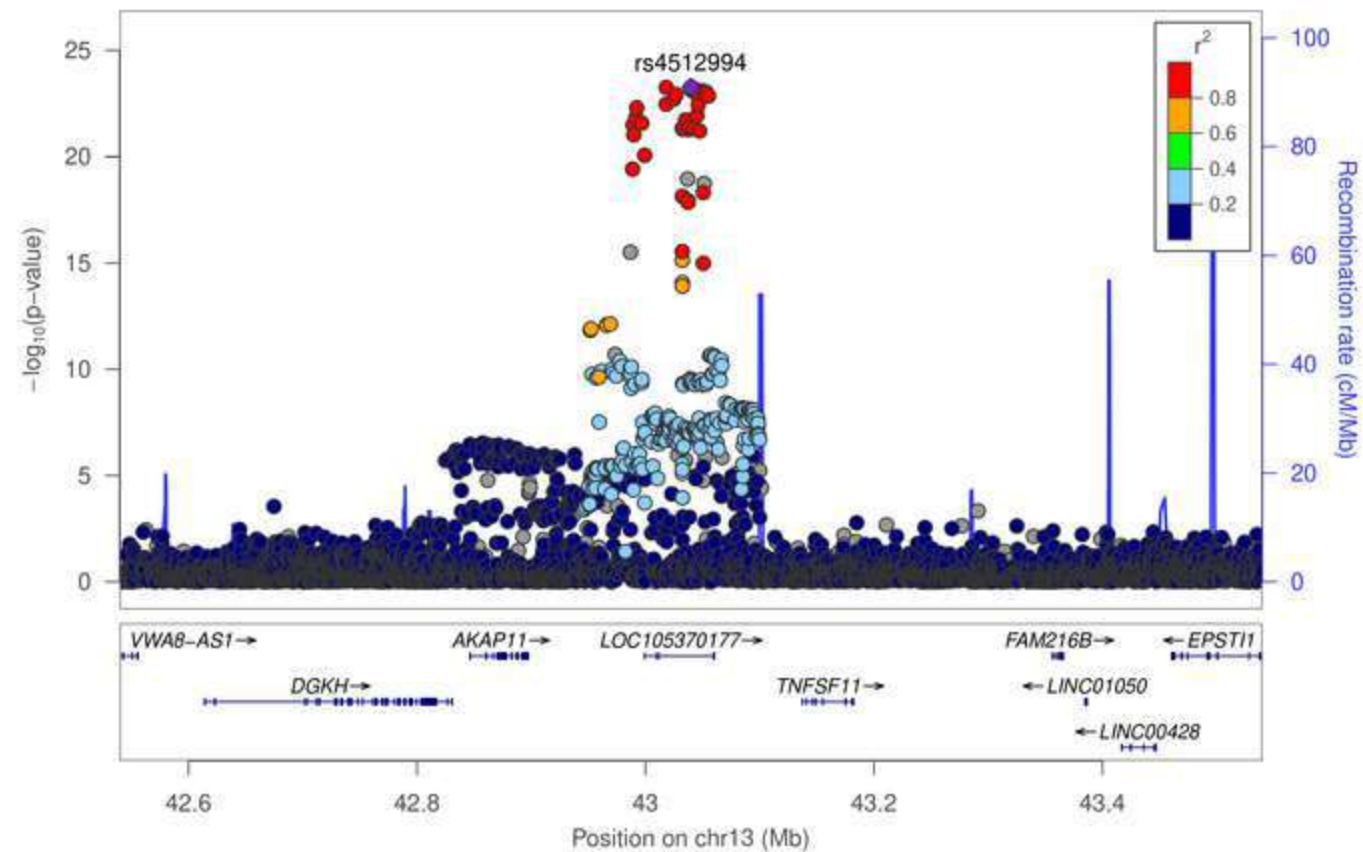
TRANCE (TNFSF11) [chr13:43039673_A_C (rs4512994) (A/C) N=14736]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.147	0.02	0.15 [0.11; 0.19]	32.7%	25.3%
BioFinder (1496)	0.114	0.04	0.11 [0.04; 0.19]	10.3%	11.4%
EGCUT (487)	0.239	0.07	0.24 [0.11; 0.37]	3.1%	4.0%
KORA (1064)	0.049	0.05	0.05 [-0.04; 0.14]	6.6%	7.9%
NSPHS (866)	0.096	0.05	0.10 [0.00; 0.19]	5.9%	7.2%
ORCADES (982)	0.103	0.04	0.10 [0.02; 0.19]	7.2%	8.5%
RECOMBINE (448)	0.073	0.08	0.07 [-0.08; 0.22]	2.3%	3.0%
STABILITY (2951)	0.094	0.03	0.09 [0.04; 0.14]	21.4%	19.6%
STANLEY (344)	0.092	0.08	0.09 [-0.06; 0.25]	2.2%	2.8%
STANLEY (300)	0.012	0.08	0.01 [-0.14; 0.16]	2.2%	2.9%
VIS (902)	0.158	0.05	0.16 [0.07; 0.25]	6.1%	7.3%
Common effect model			0.12 [0.09; 0.14]	100.0%	--
Random effects model			0.11 [0.09; 0.14]	--	100.0%



Heterogeneity: $I^2 = 17\%$, $\tau^2 = 0.0003$, $p = 0.28$

TRANCE (TNFSF11)–rs4512994



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (448)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 61\%$, $\tau^2 = 0.0032$, $p < 0.01$

TRANCE (TNFSF11) [chr17:26694861_A_G (rs704) (A/G) N=14736]

TE SE(TE)

-0.102 0.02

-0.138 0.04

0.068 0.06

-0.116 0.05

-0.063 0.05

-0.095 0.05

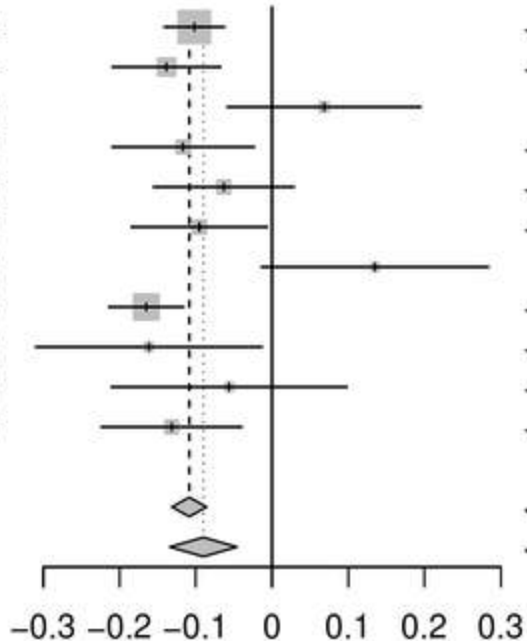
0.135 0.08

-0.165 0.03

-0.162 0.08

-0.056 0.08

-0.132 0.05

Weight
95%-CI (common) (random)

-0.10 [-0.14; -0.06] 33.4% 14.1%

-0.14 [-0.21; -0.07] 10.3% 11.2%

0.07 [-0.06; 0.20] 3.2% 6.9%

-0.12 [-0.21; -0.02] 6.0% 9.3%

-0.06 [-0.16; 0.03] 6.1% 9.4%

-0.10 [-0.18; -0.01] 6.5% 9.6%

0.14 [-0.01; 0.28] 2.3% 5.7%

-0.16 [-0.21; -0.12] 21.5% 13.3%

-0.16 [-0.31; -0.01] 2.4% 5.7%

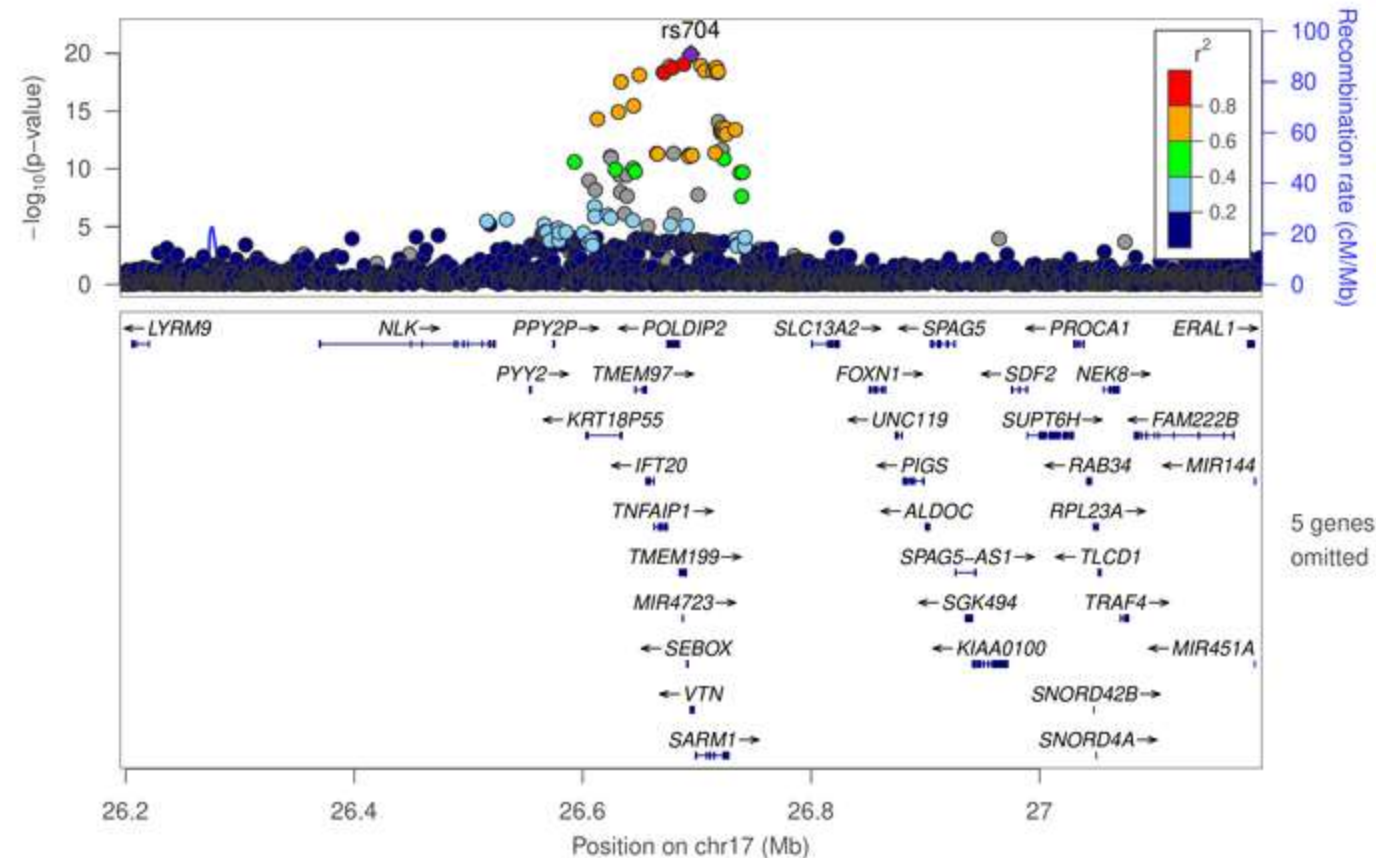
-0.06 [-0.21; 0.10] 2.2% 5.4%

-0.13 [-0.22; -0.04] 6.1% 9.4%

-0.11 [-0.13; -0.09] 100.0% --

-0.09 [-0.13; -0.05] -- 100.0%

TRANCE (TNFSF11)-rs704



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (982)

RECOMBINE (431)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 54\%$, $\tau^2 = 0.0191$, $p = 0.02$

TRANCE (TNFSF11) [chr3:172294500_A_G (rs79287178) (A/G) N=14719]

TE SE(TE)

-0.552 0.05

-0.495 0.11

-0.511 0.18

-0.905 0.15

-0.419 0.14

-0.706 0.13

-0.001 0.28

-0.321 0.08

-0.676 0.29

-0.278 0.28

-0.325 0.13

Weight
95%-CI (common) (random)

-0.55 [-0.66; -0.45] 39.7% 16.7%

-0.49 [-0.71; -0.28] 10.0% 11.9%

-0.51 [-0.85; -0.17] 3.8% 7.4%

-0.90 [-1.20; -0.61] 5.2% 8.8%

-0.42 [-0.69; -0.15] 6.3% 9.7%

-0.71 [-0.97; -0.44] 6.6% 10.0%

-0.00 [-0.54; 0.54] 1.5% 3.8%

-0.32 [-0.48; -0.16] 17.3% 14.2%

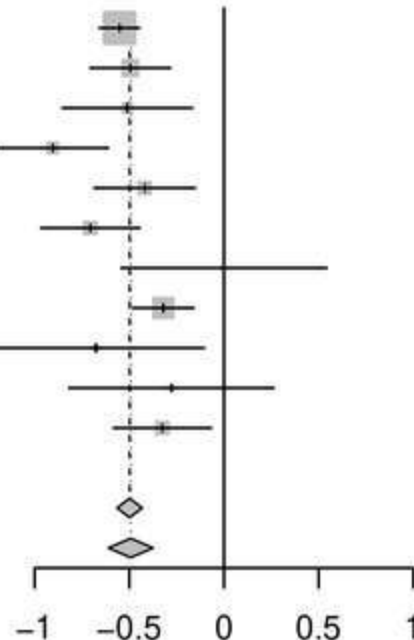
-0.68 [-1.25; -0.11] 1.4% 3.5%

-0.28 [-0.82; 0.26] 1.5% 3.8%

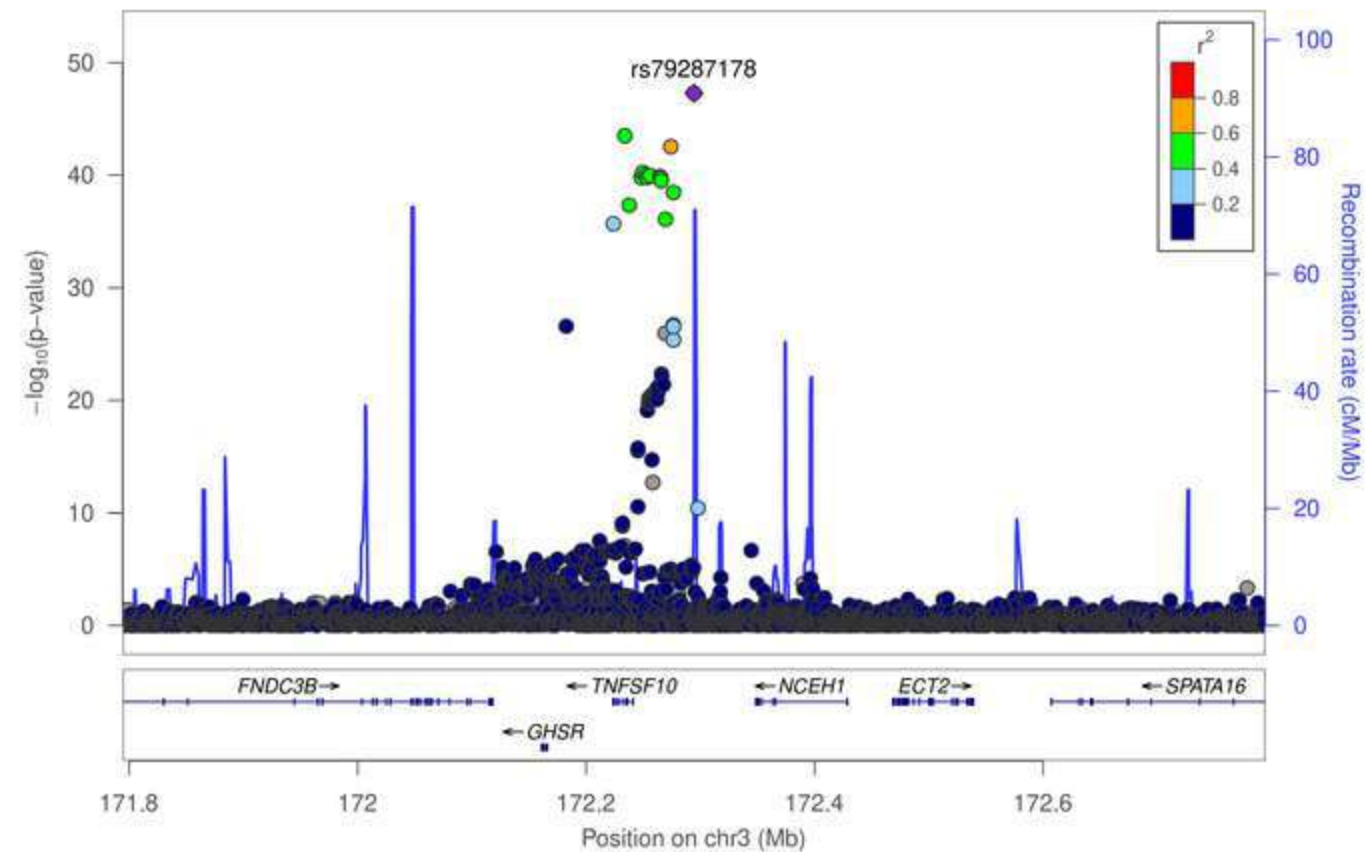
-0.32 [-0.58; -0.07] 6.7% 10.1%

-0.50 [-0.57; -0.43] 100.0% --

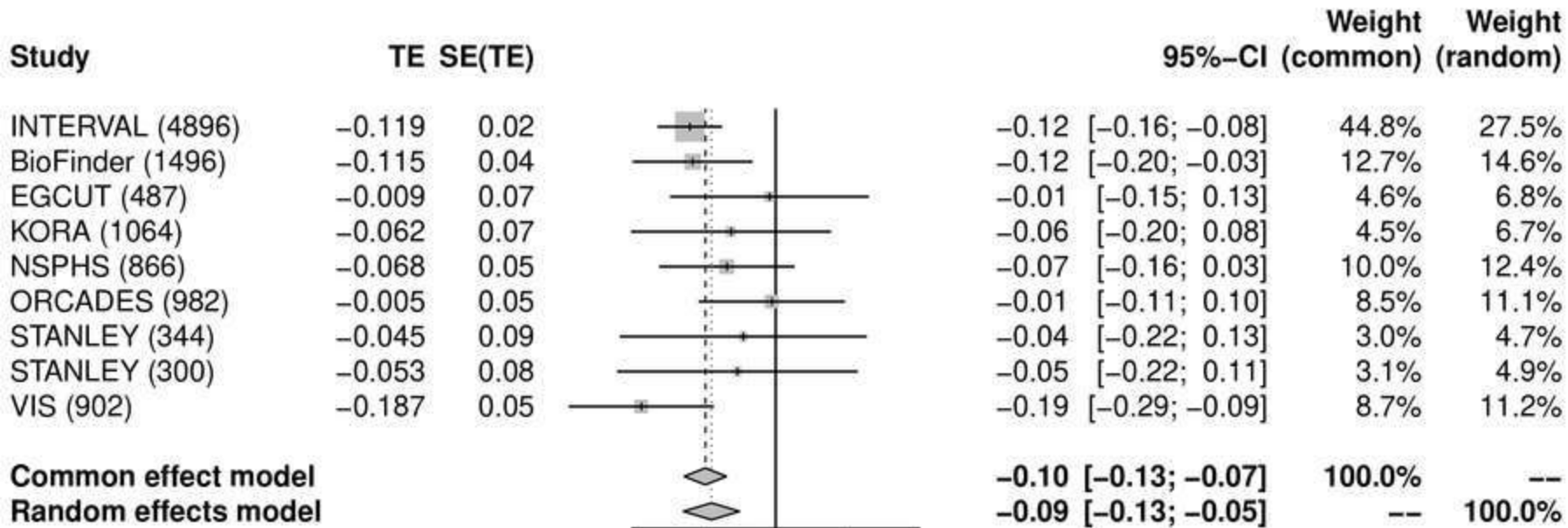
-0.49 [-0.61; -0.37] -- 100.0%



TRANCE (TNFSF11)-rs79287178

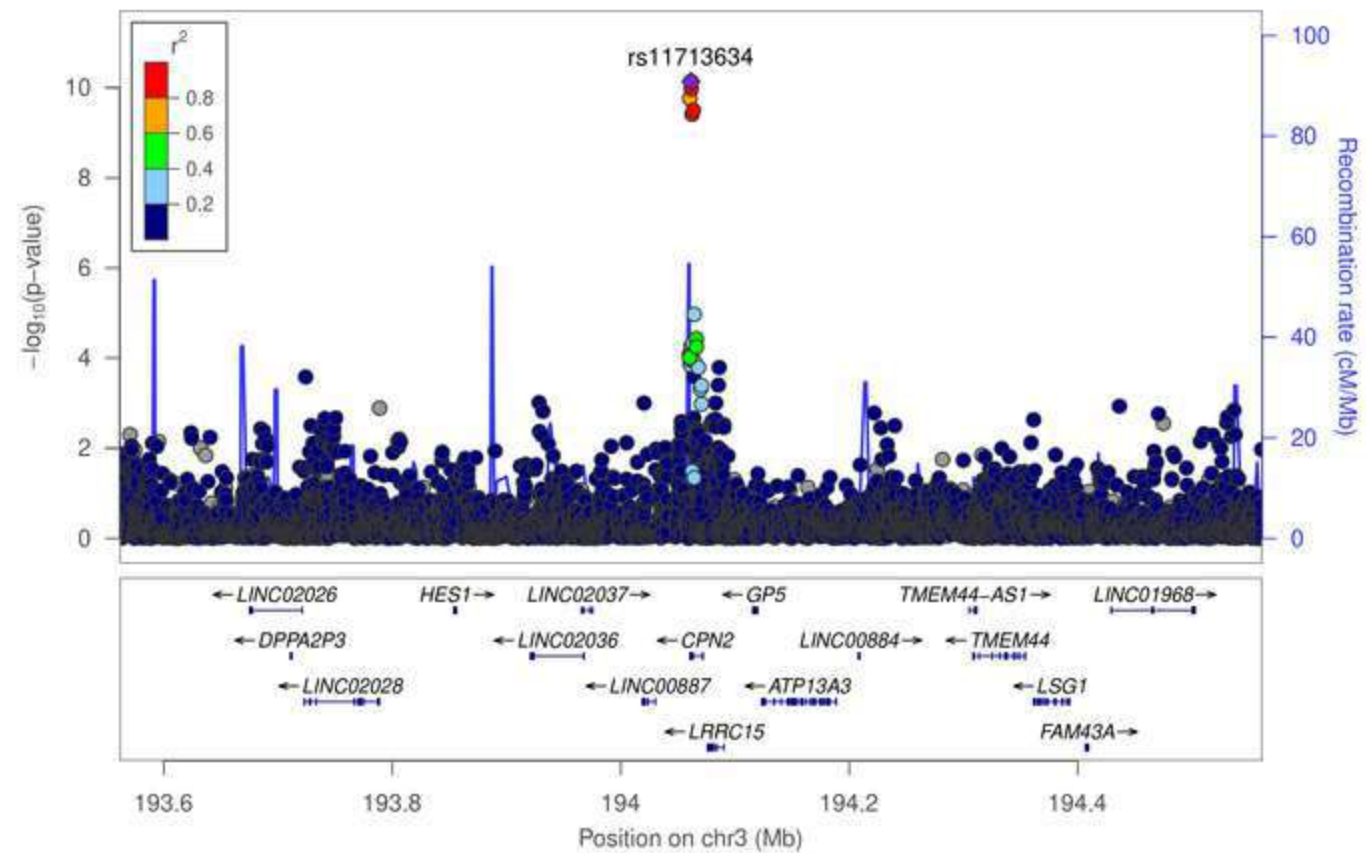


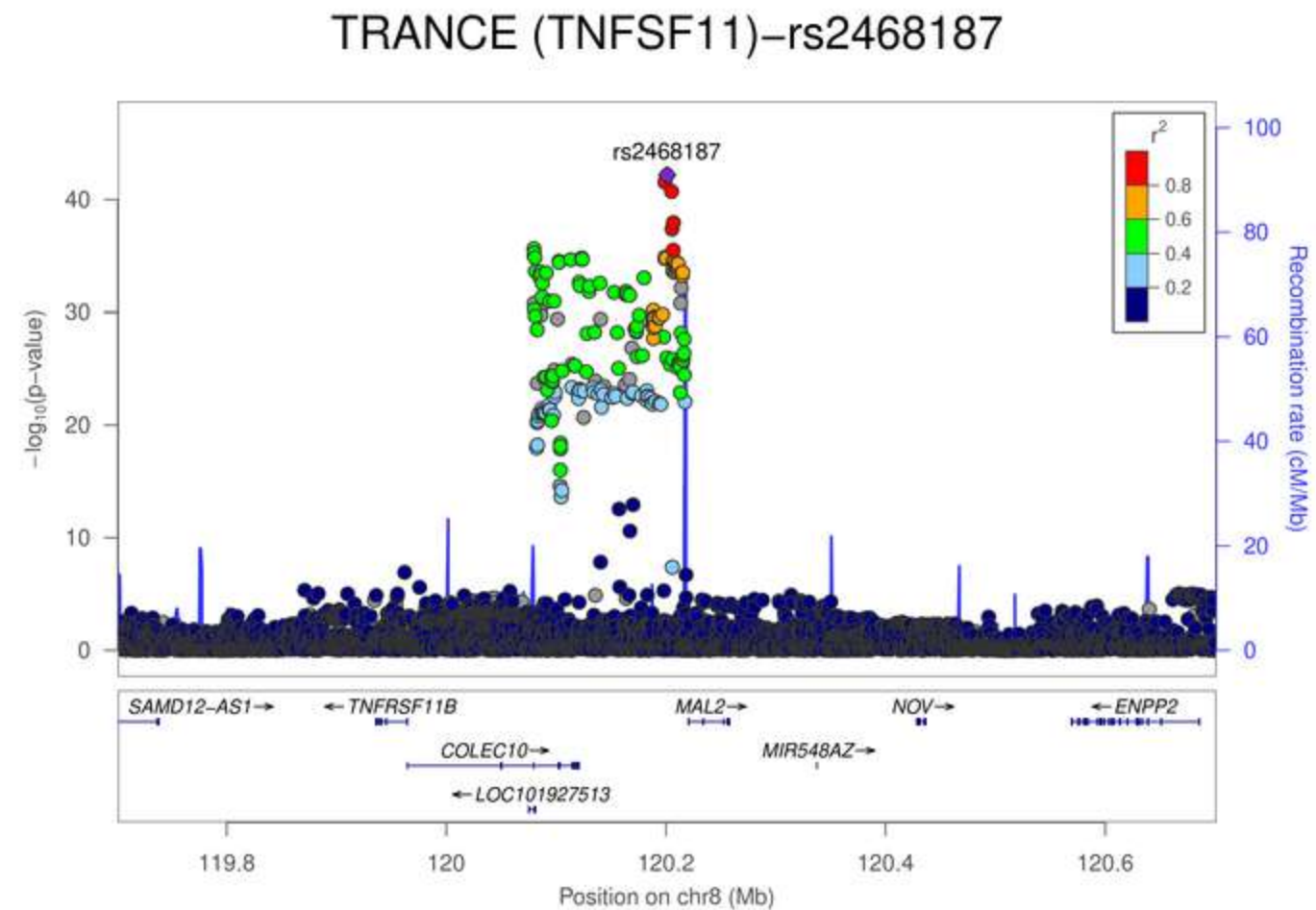
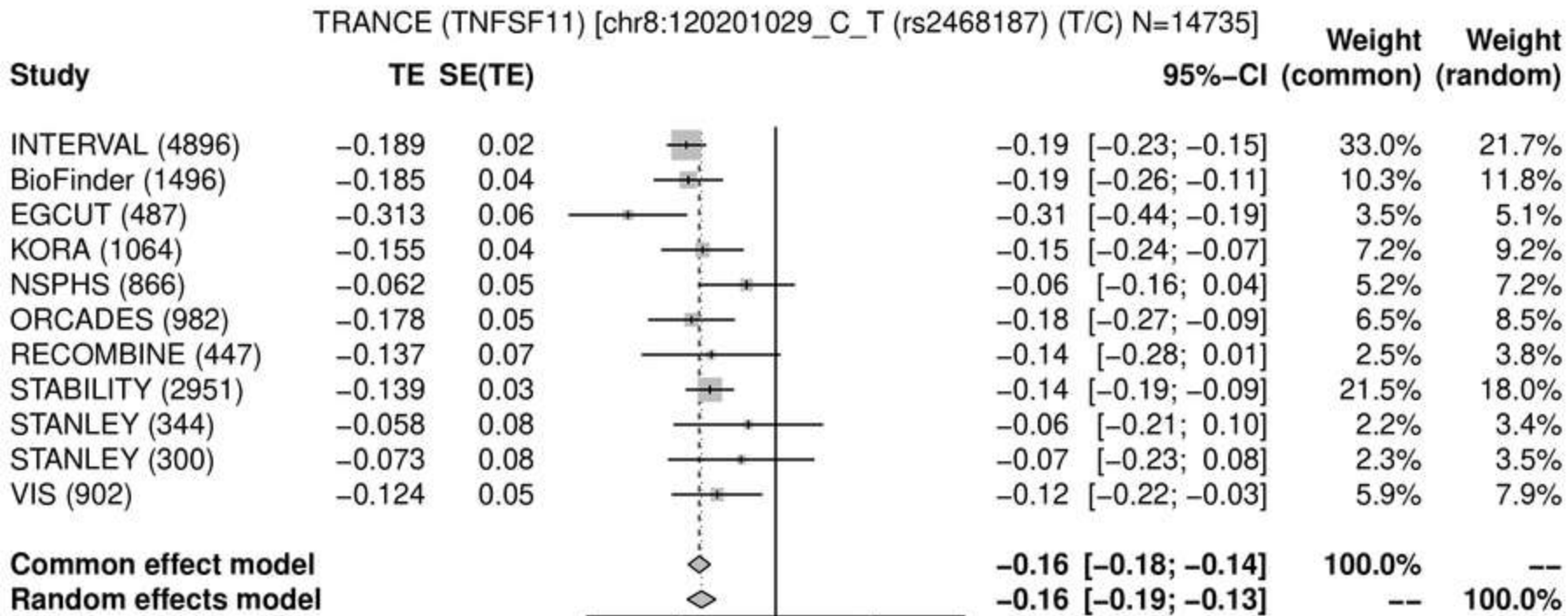
TRANCE (TNFSF11) [chr3:194061578_A_G (rs11713634) (A/G) N=11337]



Heterogeneity: $I^2 = 22\%$, $\tau^2 = 0.0009$, $p = 0.24$

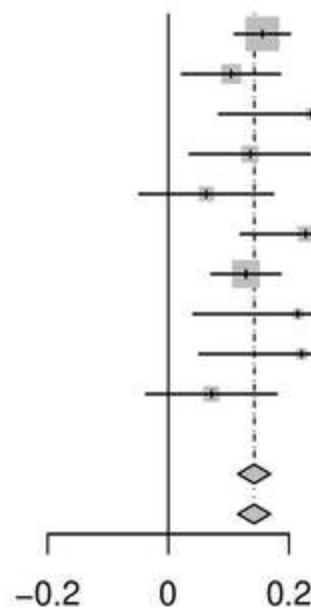
TRANCE (TNFSF11)-rs11713634





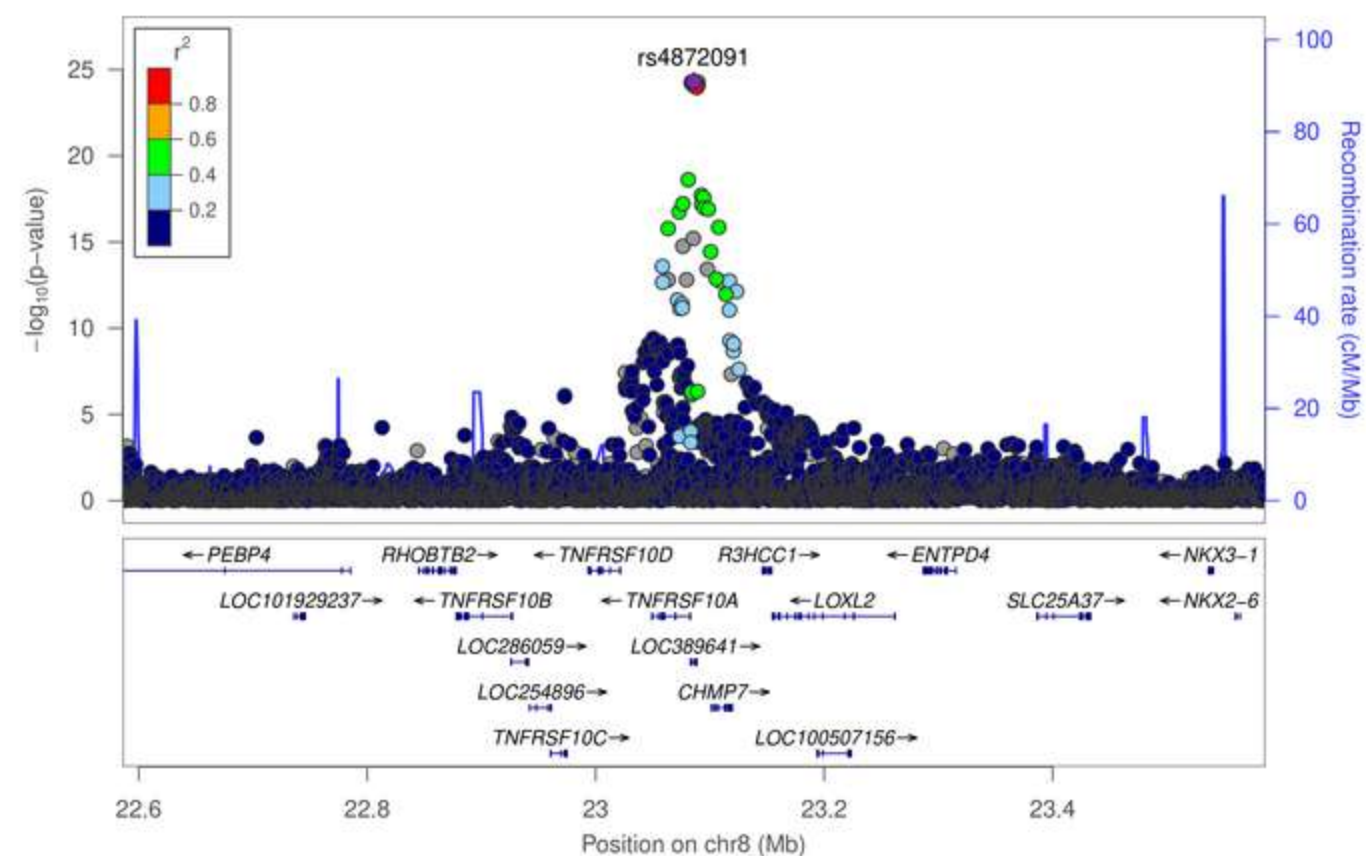
TRANCE (TNFSF11) [chr8:23085868_A_G (rs4872091) (A/G) N=14288]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.155	0.02	0.16 [0.11; 0.20]	34.1% 34.0%
BioFinder (1496)	0.104	0.04	0.10 [0.02; 0.19]	10.8% 10.9%
EGCUT (487)	0.237	0.08	0.24 [0.08; 0.39]	3.0% 3.1%
KORA (1064)	0.135	0.05	0.14 [0.03; 0.24]	7.2% 7.2%
NSPHS (866)	0.062	0.06	0.06 [-0.05; 0.17]	5.8% 5.9%
ORCADES (982)	0.227	0.05	0.23 [0.12; 0.33]	6.2% 6.3%
STABILITY (2951)	0.128	0.03	0.13 [0.07; 0.19]	21.7% 21.7%
STANLEY (344)	0.214	0.09	0.21 [0.04; 0.39]	2.4% 2.4%
STANLEY (300)	0.221	0.09	0.22 [0.05; 0.39]	2.5% 2.5%
VIS (902)	0.071	0.06	0.07 [-0.04; 0.18]	6.1% 6.2%
Common effect model			0.14 [0.11; 0.17]	100.0% --
Random effects model			0.14 [0.11; 0.17]	-- 100.0%



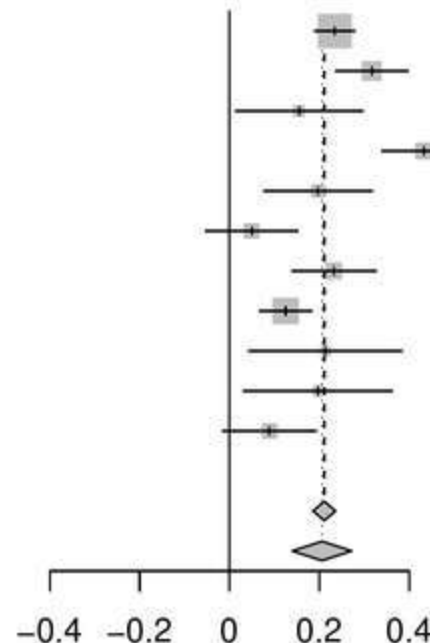
Heterogeneity: $I^2 = 13\%$, $\tau^2 < 0.0001$, $p = 0.32$

TRANCE (TNFSF11)-rs4872091



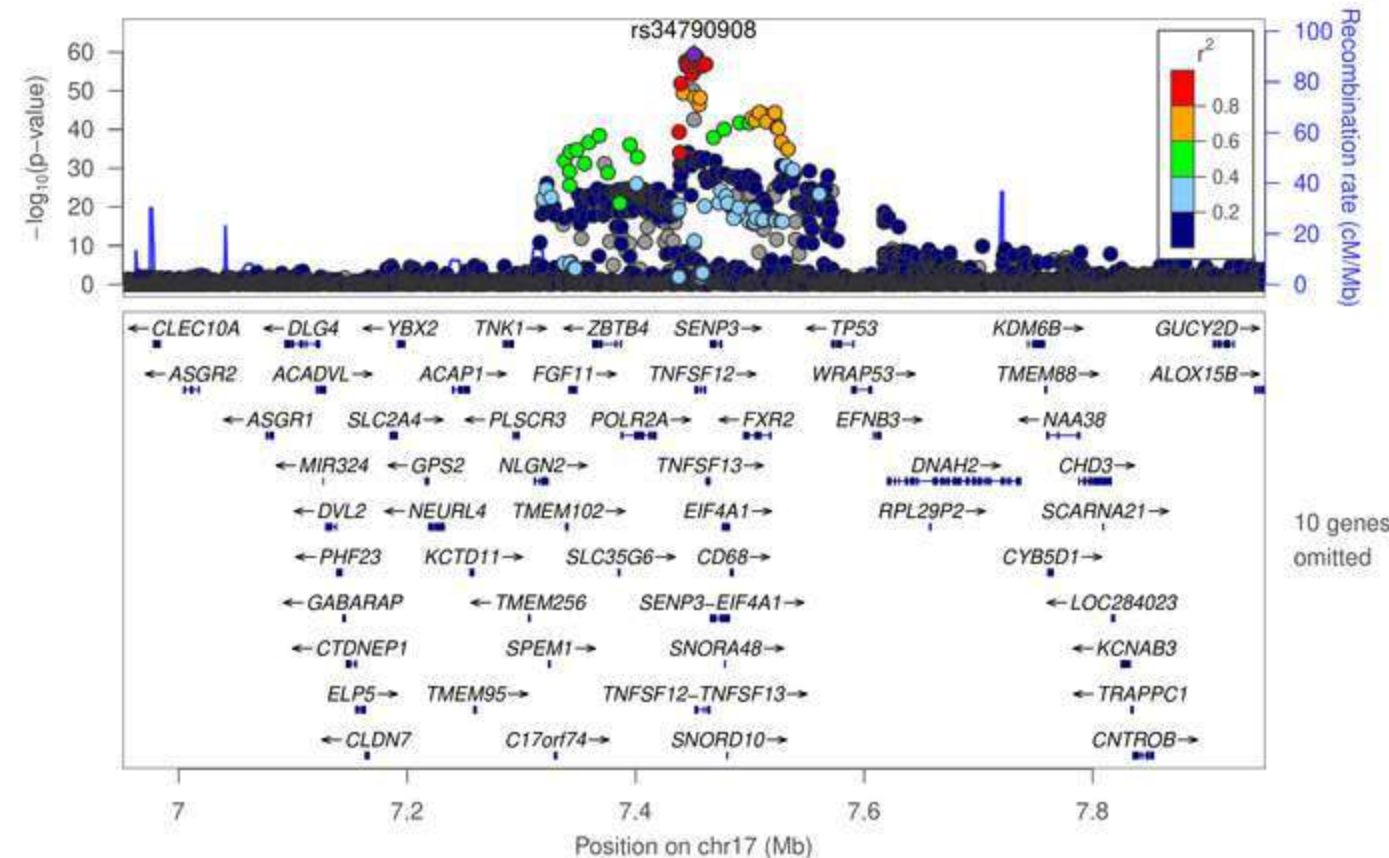
TWEAK (TNFSF12) [chr17:7451110_C_T (rs34790908) (T/C) N=14732]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.234	0.02	0.23 [0.19; 0.28]	32.4%
BioFinder (1496)	0.317	0.04	0.32 [0.24; 0.40]	9.9%
EGCUT (487)	0.155	0.07	0.16 [0.01; 0.30]	3.2%
KORA (1064)	0.433	0.05	0.43 [0.34; 0.53]	7.4%
NSPHS (866)	0.198	0.06	0.20 [0.08; 0.32]	4.4%
ORCADES (982)	0.050	0.05	0.05 [-0.05; 0.15]	6.1%
RECOMBINE (444)	0.233	0.05	0.23 [0.14; 0.33]	7.3%
STABILITY (2951)	0.125	0.03	0.13 [0.07; 0.18]	19.0%
STANLEY (344)	0.214	0.09	0.21 [0.04; 0.38]	2.2%
STANLEY (300)	0.196	0.08	0.20 [0.03; 0.36]	2.3%
VIS (902)	0.089	0.05	0.09 [-0.01; 0.19]	5.9%
Common effect model			0.21 [0.19; 0.24]	100.0%
Random effects model			0.21 [0.14; 0.27]	-- 100.0%



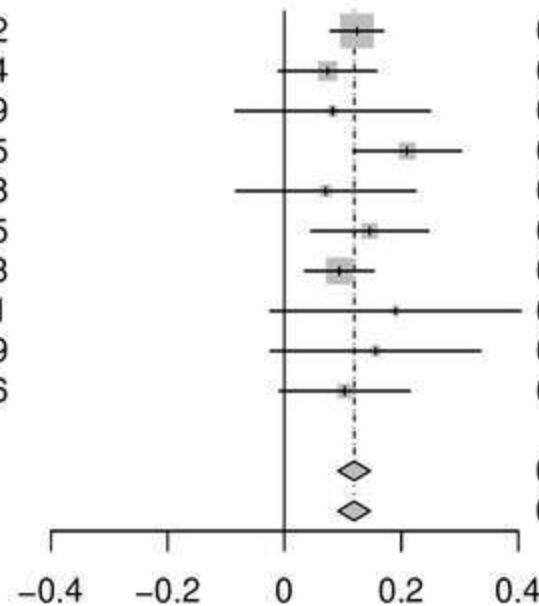
Heterogeneity: $I^2 = 81\%$, $\tau^2 = 0.0097$, $p < 0.01$

TWEAK (TNFSF12)-rs34790908



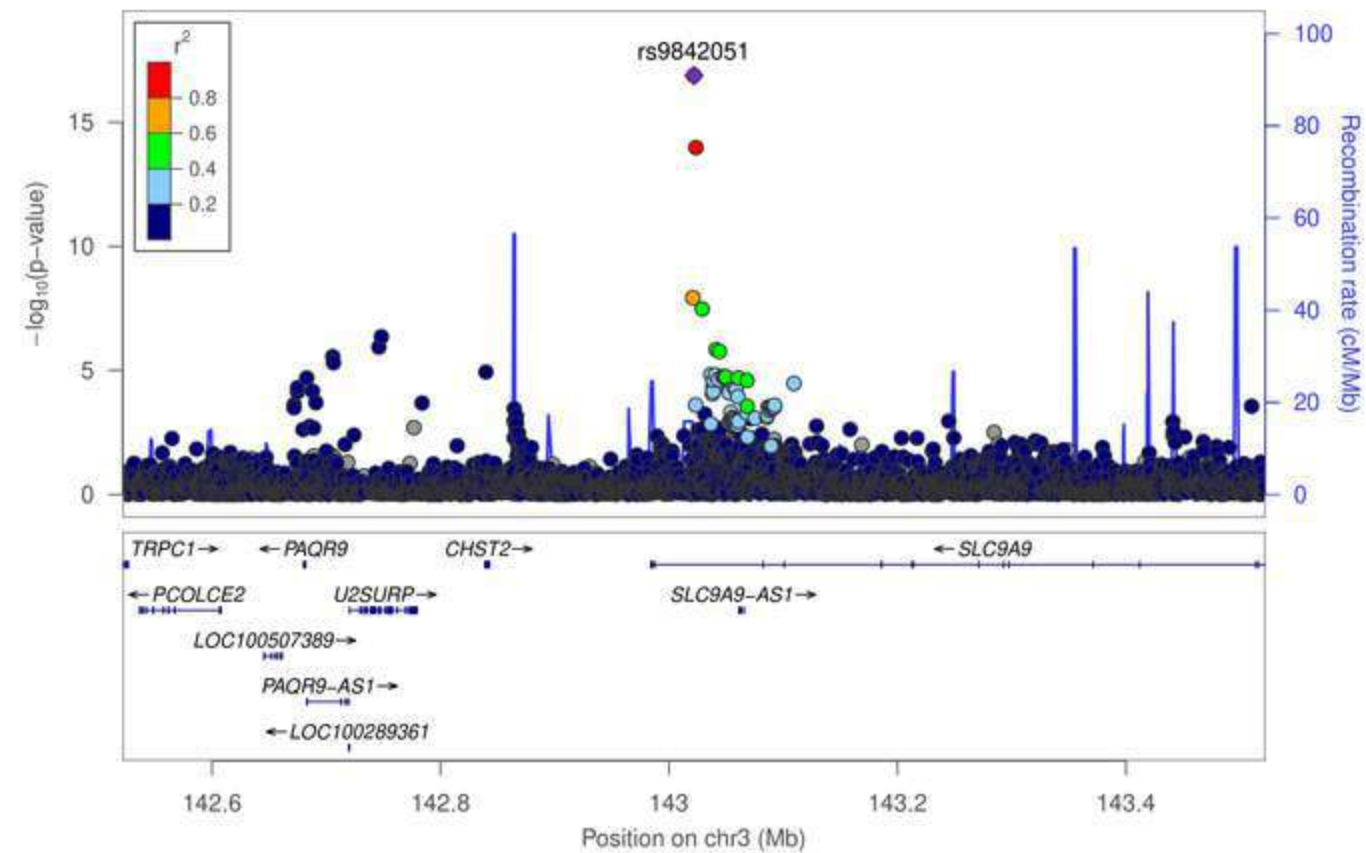
TWEAK (TNFSF12) [chr3:143021856_C_G (rs9842051) (C/G) N=14288]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.124	0.02	0.12 [0.08; 0.17]	36.2%	36.2%
BioFinder (1496)	0.074	0.04	0.07 [-0.01; 0.16]	10.6%	10.6%
EGCUT (487)	0.082	0.09	0.08 [-0.08; 0.25]	2.7%	2.7%
KORA (1064)	0.210	0.05	0.21 [0.12; 0.30]	8.8%	8.8%
NSPHS (866)	0.071	0.08	0.07 [-0.08; 0.22]	3.2%	3.2%
ORCADES (982)	0.146	0.05	0.15 [0.05; 0.25]	7.4%	7.4%
STABILITY (2951)	0.094	0.03	0.09 [0.03; 0.15]	21.3%	21.3%
STANLEY (344)	0.190	0.11	0.19 [-0.02; 0.40]	1.6%	1.6%
STANLEY (300)	0.156	0.09	0.16 [-0.02; 0.34]	2.3%	2.3%
VIS (902)	0.103	0.06	0.10 [-0.01; 0.21]	6.0%	6.0%
Common effect model			0.12 [0.09; 0.15]	100.0%	--
Random effects model			0.12 [0.09; 0.15]	--	100.0%

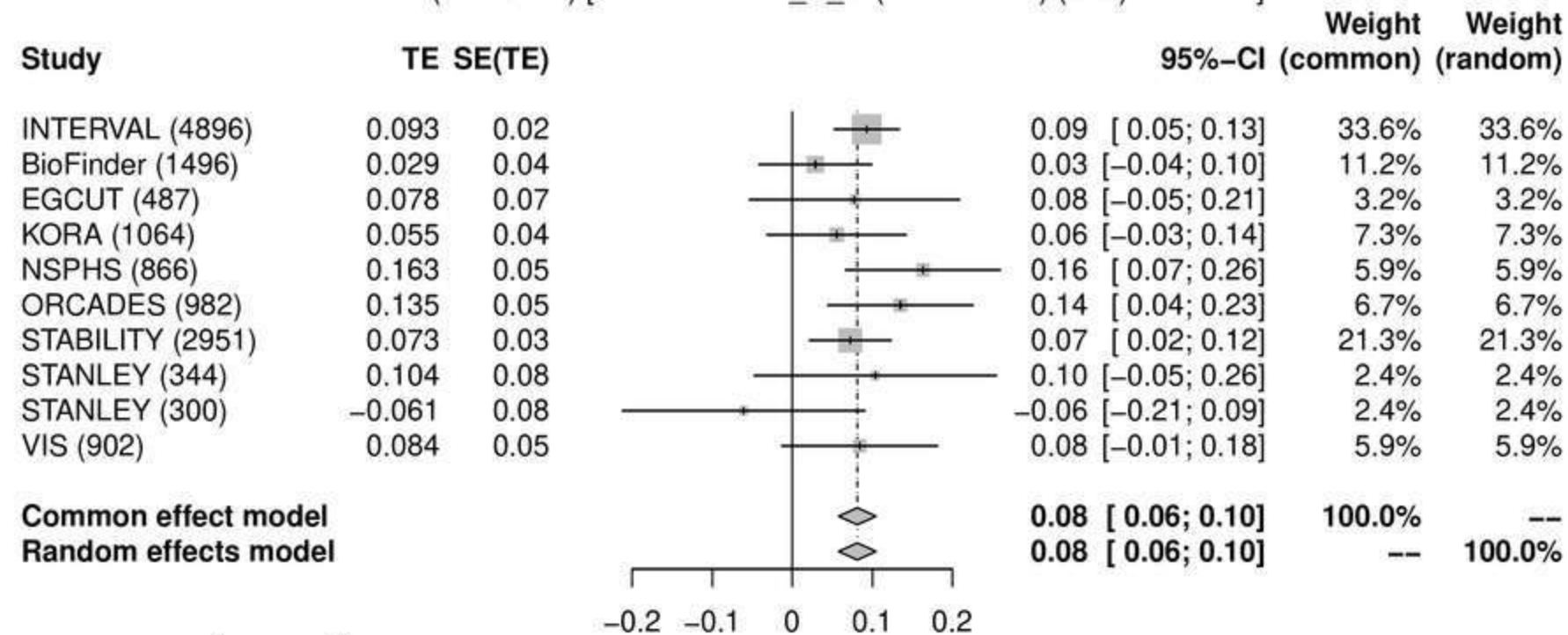


Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.63$

TWEAK (TNFSF12)-rs9842051

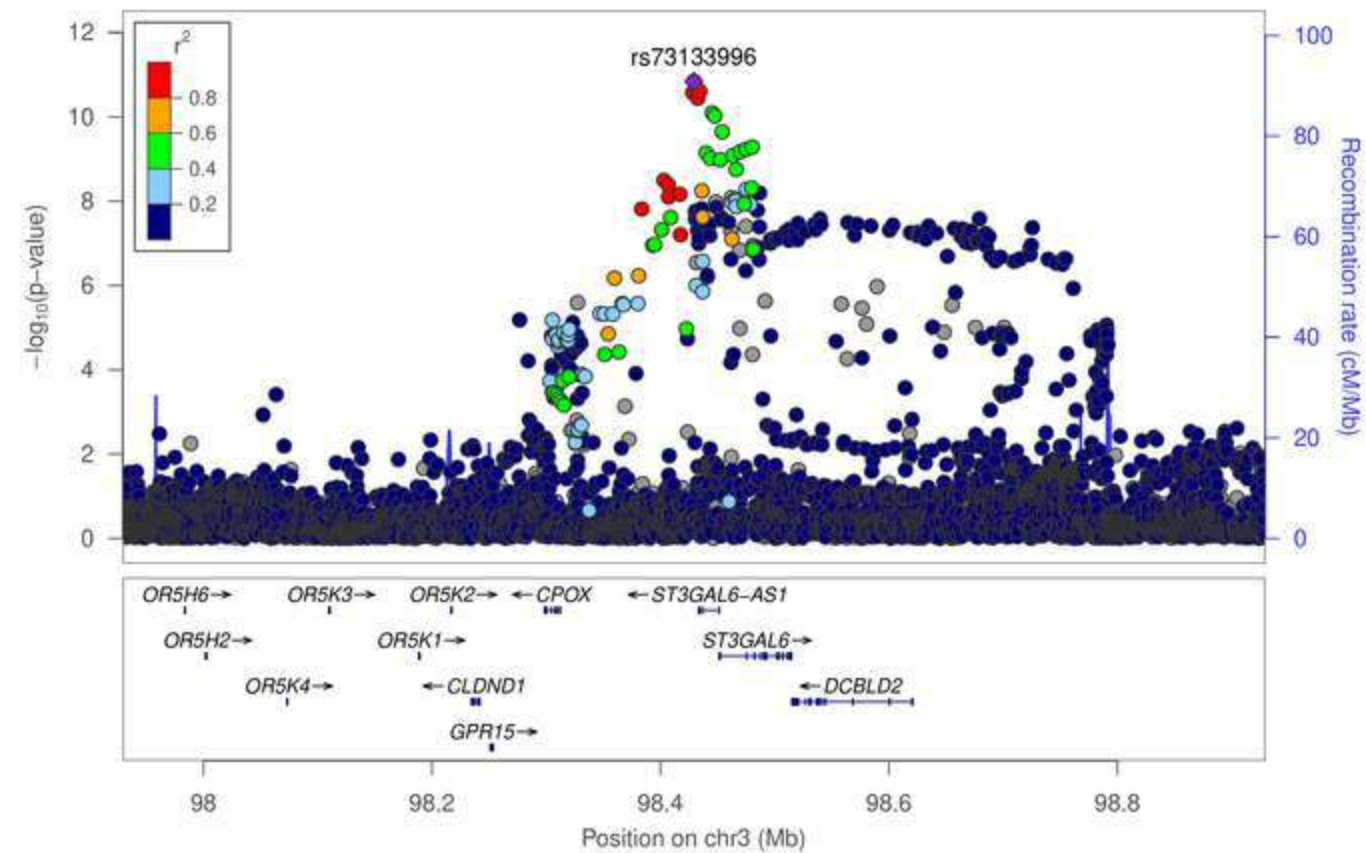


TWEAK (TNFSF12) [chr3:98429219_C_G (rs73133996) (C/G) N=14288]



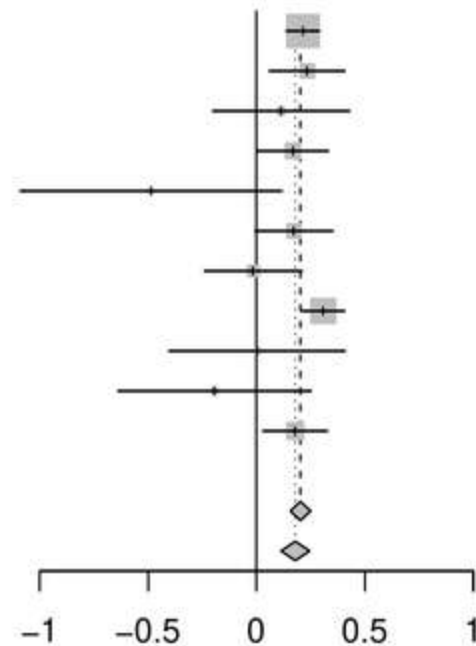
Heterogeneity: $I^2 = 14\%$, $\tau^2 < 0.0001$, $p = 0.31$

TWEAK (TNFSF12)-rs73133996



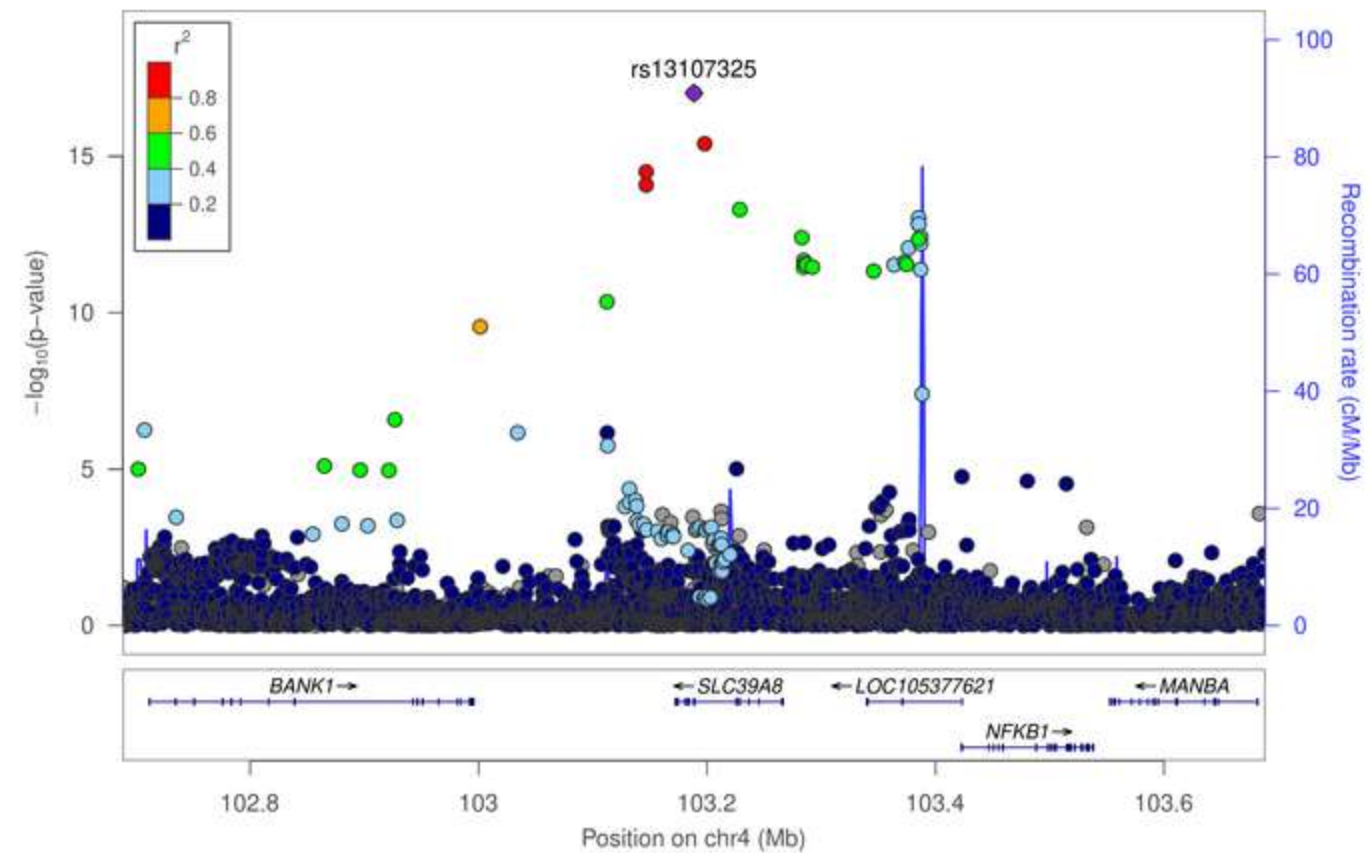
TWEAK (TNFSF12) [chr4:103188709_C_T (rs13107325) (T/C) N=14733]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight Weight (random)
INTERVAL (4896)	0.214	0.04	0.21 [0.14; 0.29]	37.1% 22.4%
BioFinder (1496)	0.233	0.09	0.23 [0.06; 0.41]	7.1% 10.0%
EGCUT (487)	0.114	0.16	0.11 [-0.20; 0.43]	2.2% 3.9%
KORA (1064)	0.168	0.08	0.17 [0.01; 0.33]	8.1% 10.8%
NSPHS (866)	-0.487	0.31	-0.49 [-1.09; 0.12]	0.6% 1.2%
ORCADES (982)	0.173	0.09	0.17 [-0.01; 0.35]	6.7% 9.5%
RECOMBINE (445)	-0.015	0.11	-0.01 [-0.24; 0.21]	4.3% 6.8%
STABILITY (2951)	0.307	0.05	0.31 [0.21; 0.41]	21.9% 18.6%
STANLEY (344)	0.003	0.21	0.00 [-0.40; 0.41]	1.3% 2.4%
STANLEY (300)	-0.193	0.23	-0.19 [-0.64; 0.25]	1.1% 2.1%
VIS (902)	0.179	0.08	0.18 [0.03; 0.33]	9.8% 12.3%
Common effect model			0.20 [0.16; 0.25]	100.0%
Random effects model			0.18 [0.11; 0.25]	-- 100.0%

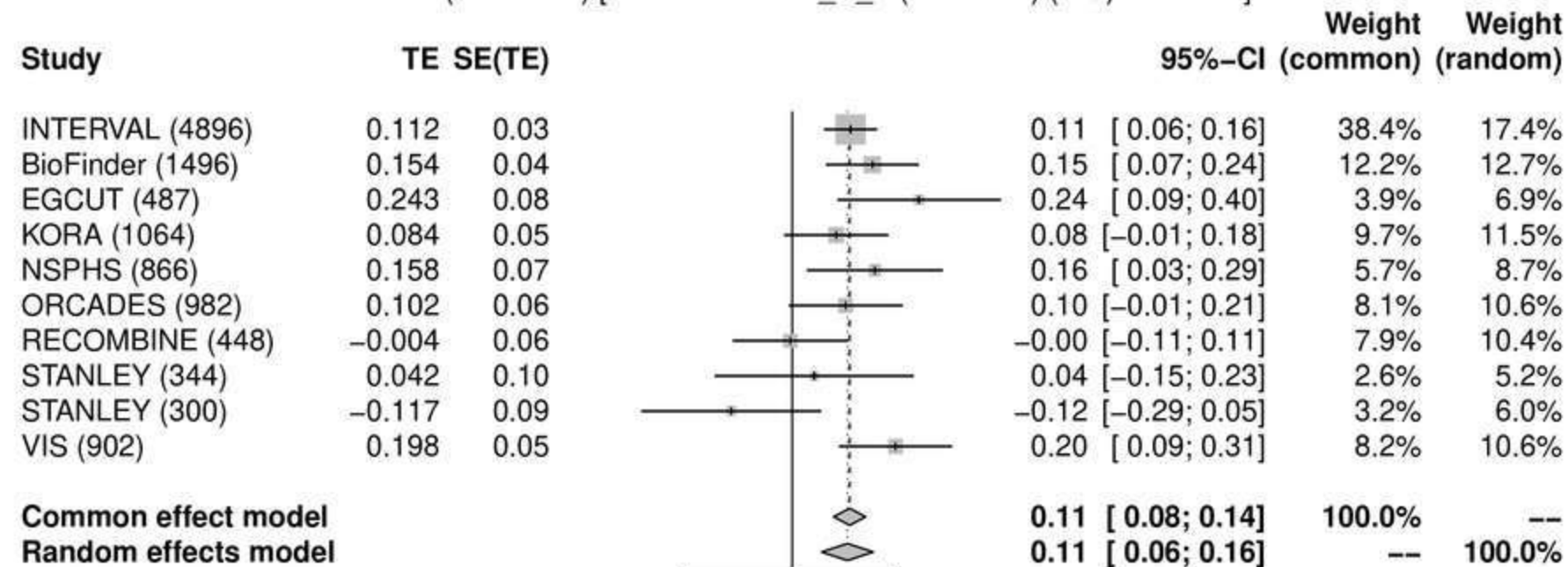


Heterogeneity: $I^2 = 44\%$, $\tau^2 = 0.0036$, $p = 0.06$

TWEAK (TNFSF12)-rs13107325

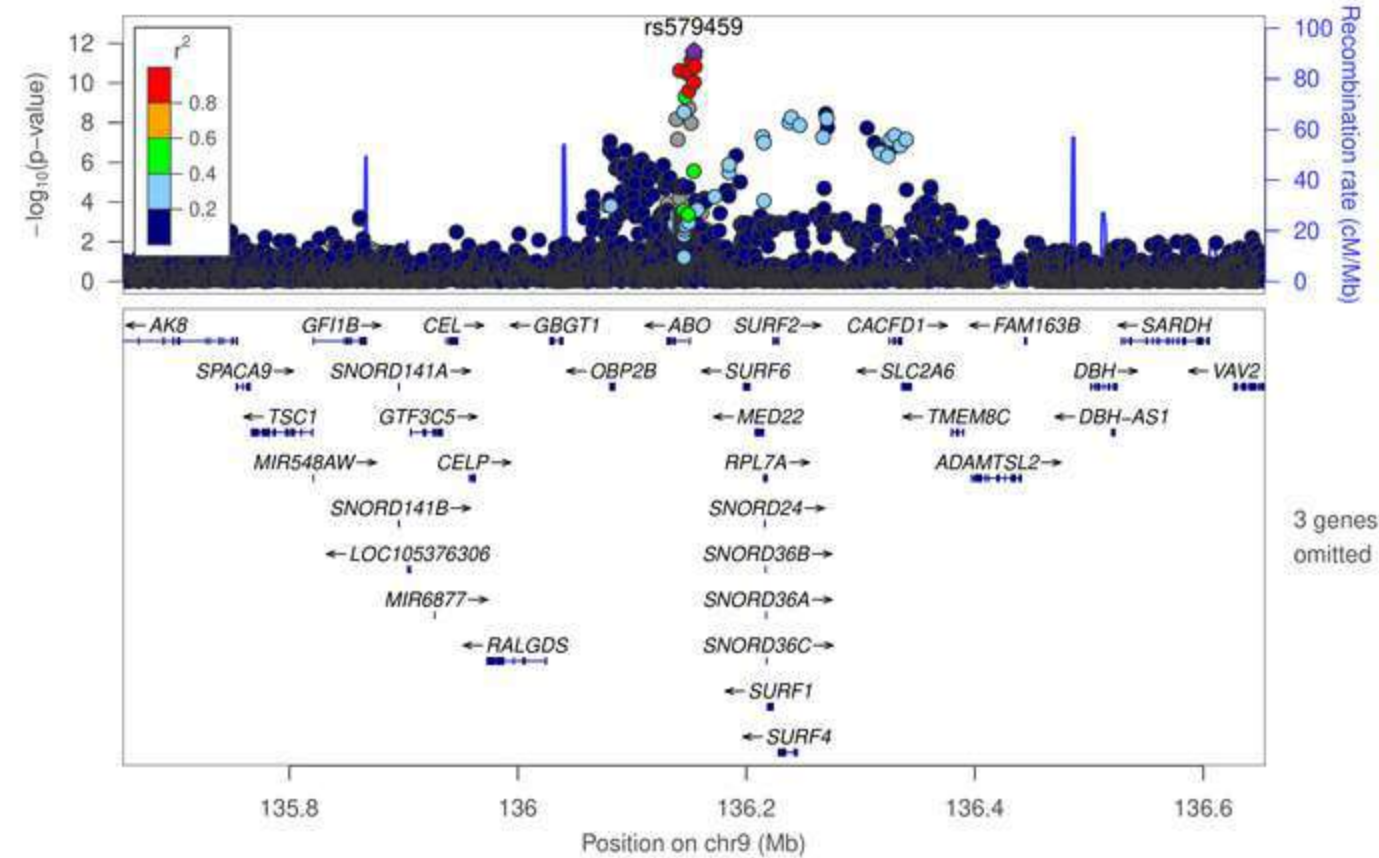


TWEAK (TNFSF12) [chr9:136154168_C_T (rs579459) (T/C) N=11785]

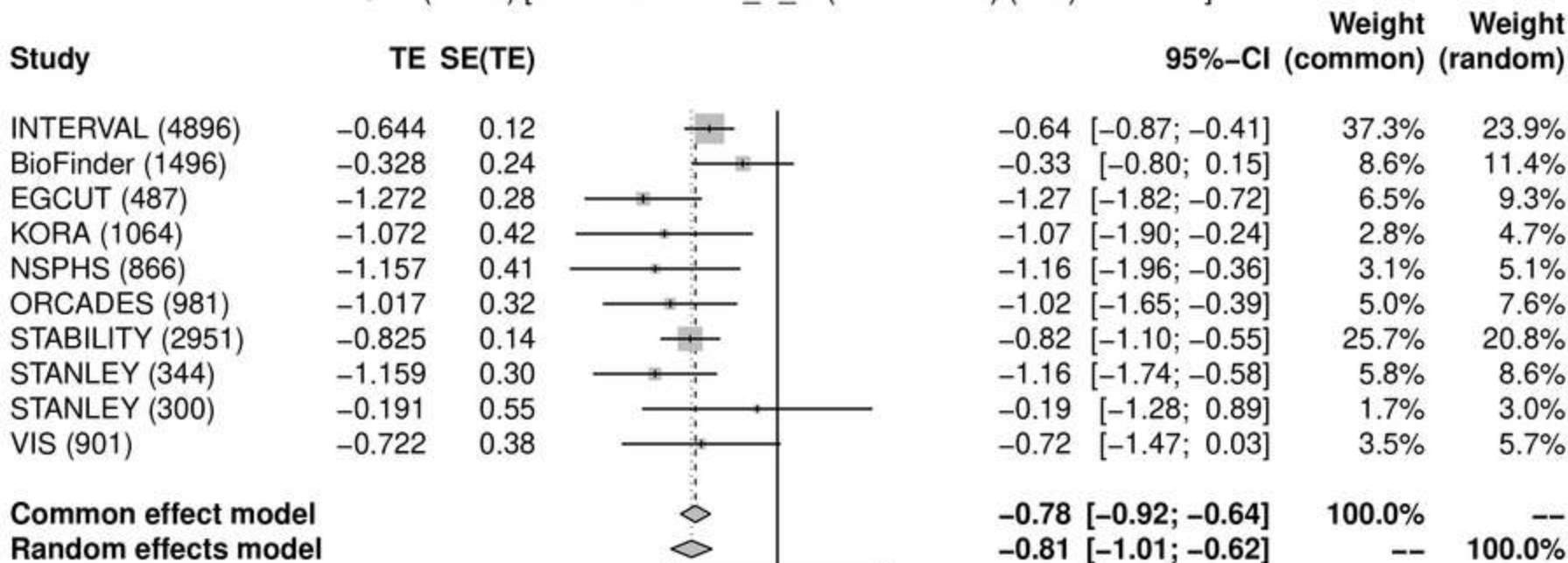


Heterogeneity: $I^2 = 52\%$, $\tau^2 = 0.0031$, $p = 0.03$

TWEAK (TNFSF12)-rs579459

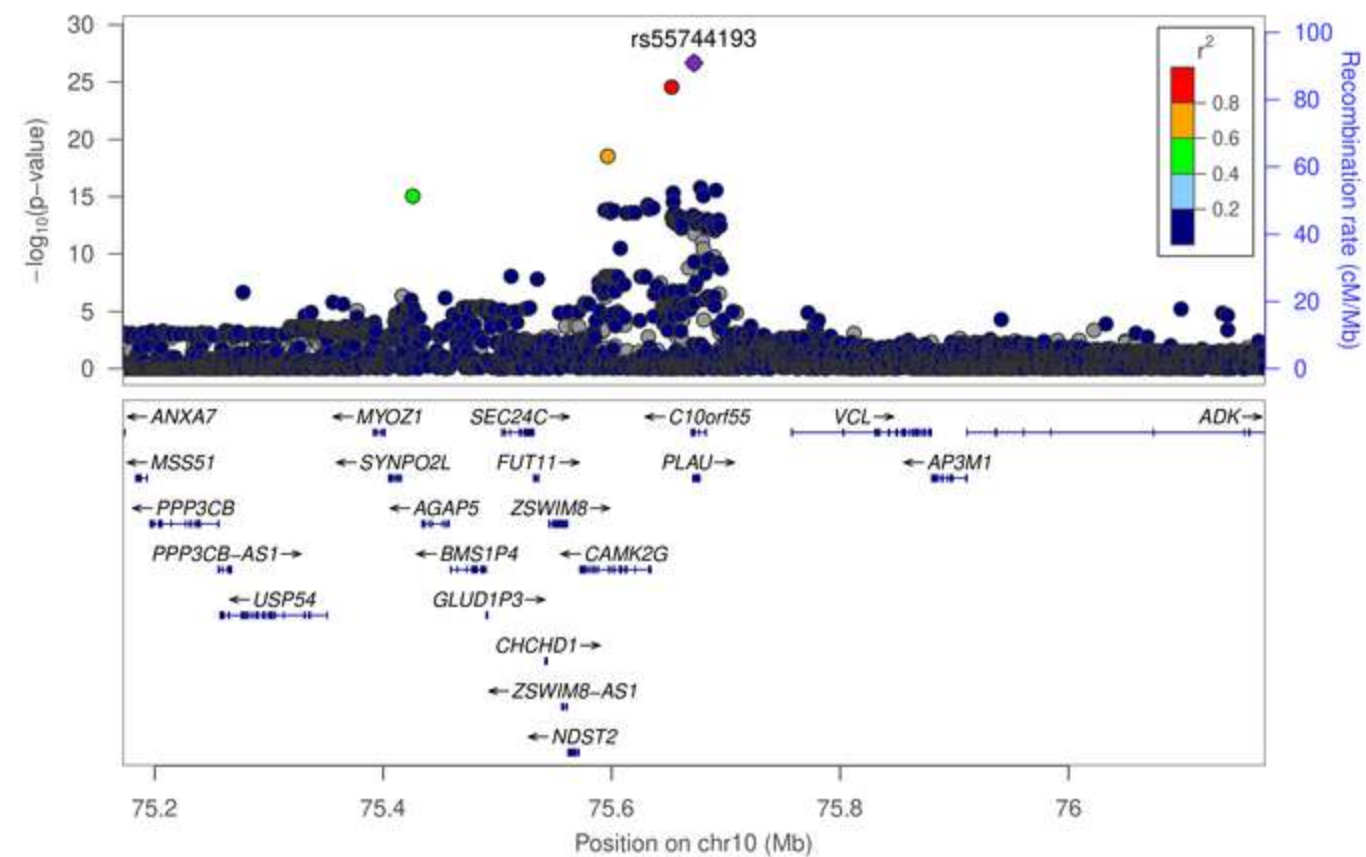


uPA (PLAU) [chr10:75672059_A_G (rs55744193) (A/G) N=14286]



Heterogeneity: $I^2 = 29\%$, $\tau^2 = 0.0276$, $p = 0.18$

uPA (PLAU)-rs55744193



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (981)

RECOMBINE (445)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 0\%$, $\tau^2 = 0$, $p = 0.84$

uPA (PLAU) [chr11:126243952_A_G (rs11220462) (A/G) N=14731]

TE SE(TE)

-0.123

0.03

-0.083

0.05

-0.162

0.08

-0.112

0.07

-0.034

0.05

-0.071

0.07

-0.103

0.06

-0.075

0.04

-0.145

0.10

-0.124

0.11

-0.206

0.07

Weight 95%-CI (common)

-0.12 [-0.18; -0.06]

-0.08 [-0.18; 0.02]

-0.16 [-0.32; -0.01]

-0.11 [-0.24; 0.02]

-0.03 [-0.14; 0.07]

-0.07 [-0.20; 0.06]

-0.10 [-0.22; 0.02]

-0.07 [-0.14; -0.00]

-0.15 [-0.35; 0.06]

-0.12 [-0.34; 0.09]

-0.21 [-0.35; -0.06]

Weight (random)

28.7%

9.6%

4.1%

6.0%

8.7%

6.1%

7.1%

20.5%

2.5%

2.1%

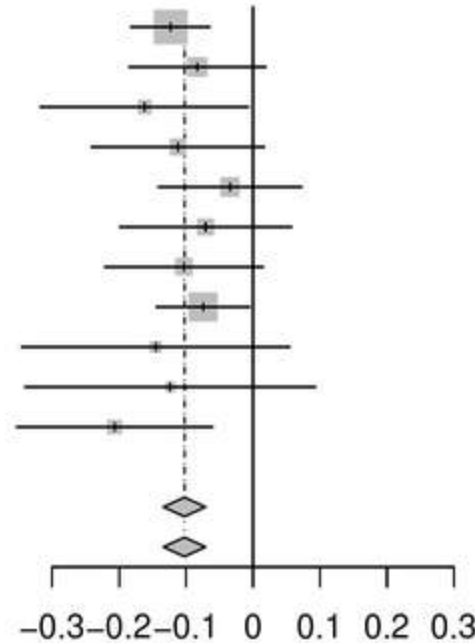
4.7%

-0.10 [-0.13; -0.07]

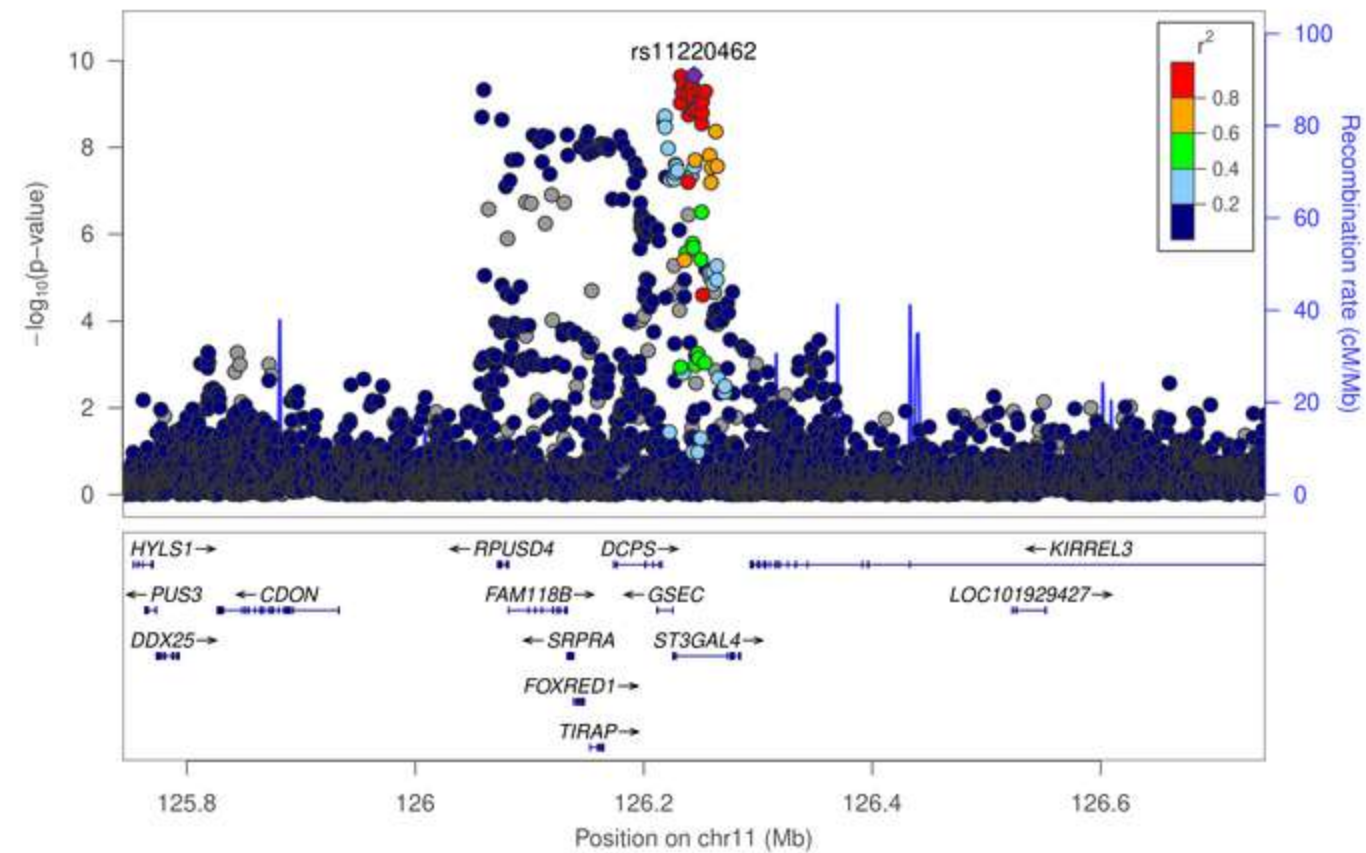
100.0%

-0.10 [-0.13; -0.07]

-- 100.0%



uPA (PLAU)-rs11220462



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (981)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 19\%$, $\tau^2 = 0.0001$, $p = 0.27$

uPA (PLAU) [chr17:7063667_C_T (rs7406661) (T/C) N=14286]

TE SE(TE)

-0.129 0.03

-0.098 0.04

-0.129 0.08

-0.271 0.07

0.003 0.06

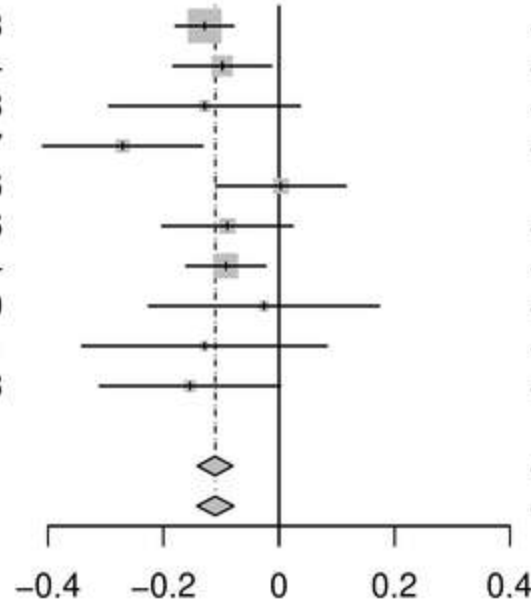
-0.089 0.06

-0.092 0.04

-0.026 0.10

-0.129 0.11

-0.154 0.08

Weight
95%-CI (common) (random)

-0.13 [-0.18; -0.08] 36.6% 34.0%

-0.10 [-0.18; -0.01] 12.8% 13.2%

-0.13 [-0.29; 0.04] 3.4% 3.7%

-0.27 [-0.41; -0.13] 4.9% 5.2%

0.00 [-0.11; 0.12] 7.4% 7.8%

-0.09 [-0.20; 0.02] 7.2% 7.7%

-0.09 [-0.16; -0.02] 19.5% 19.5%

-0.03 [-0.23; 0.17] 2.3% 2.5%

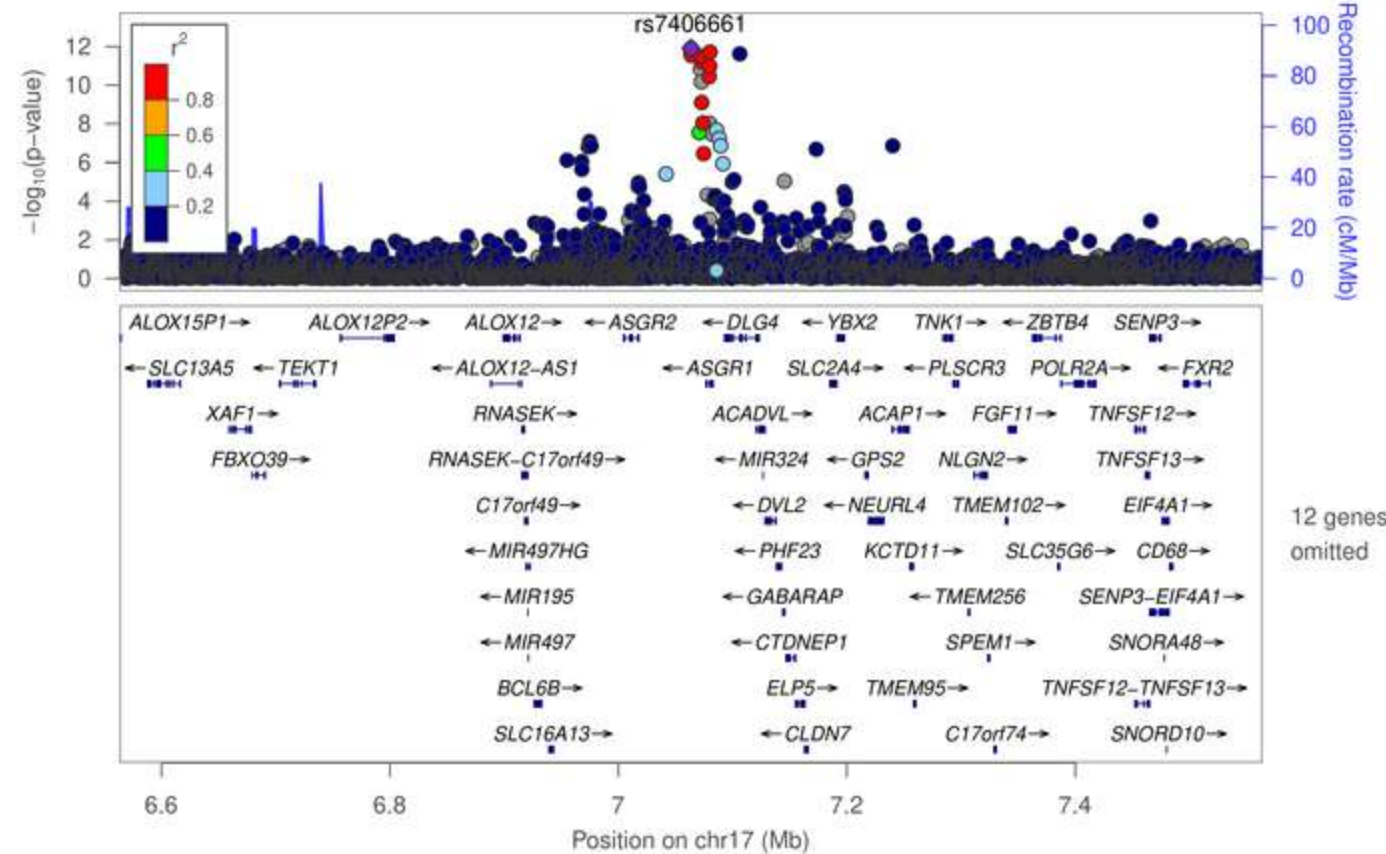
-0.13 [-0.34; 0.08] 2.1% 2.2%

-0.15 [-0.31; 0.00] 3.8% 4.1%

-0.11 [-0.14; -0.08] 100.0% --

-0.11 [-0.14; -0.08] -- 100.0%

uPA (PLAU)-rs7406661



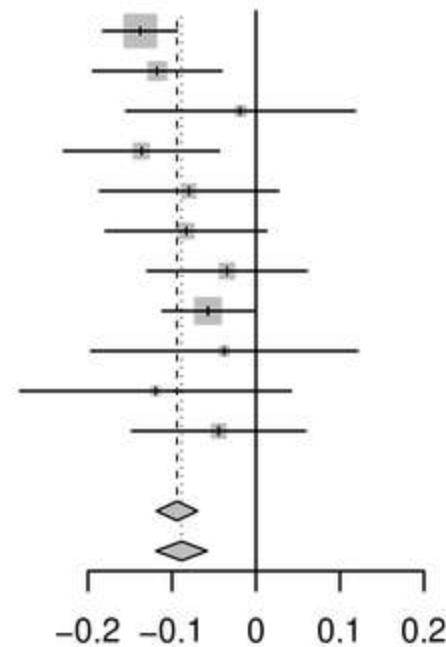
Study

uPA (PLAU) [chr18:24686365_C_T (rs4800787) (T/C) N=14730]

TE SE(TE)

INTERVAL (4896)	-0.138	0.02
BioFinder (1496)	-0.118	0.04
EGCUT (487)	-0.018	0.07
KORA (1064)	-0.136	0.05
NSPHS (866)	-0.080	0.05
ORCADES (981)	-0.083	0.05
RECOMBINE (444)	-0.034	0.05
STABILITY (2951)	-0.057	0.03
STANLEY (344)	-0.038	0.08
STANLEY (300)	-0.120	0.08
VIS (901)	-0.044	0.05

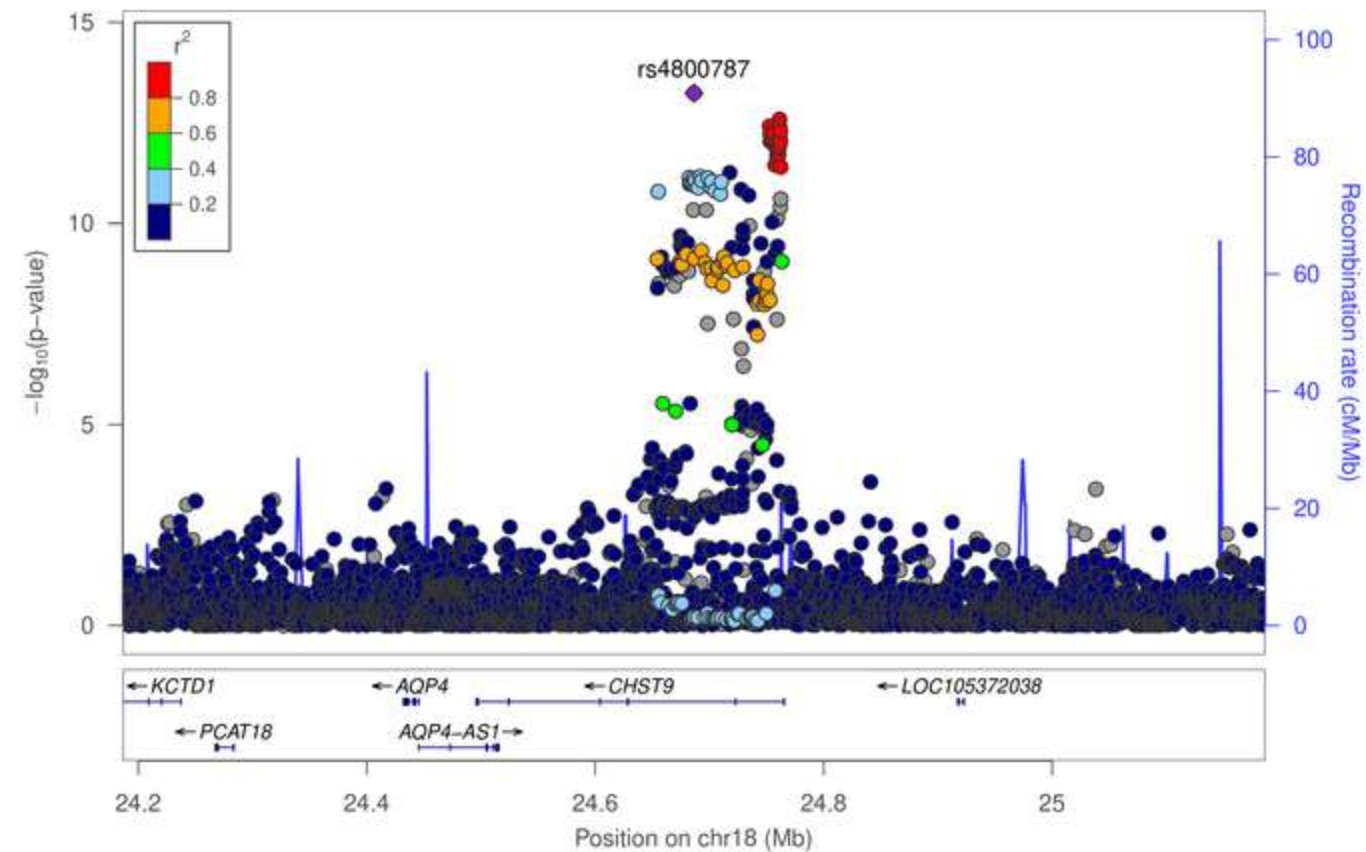
Common effect model
Random effects model

Heterogeneity: $I^2 = 9\%$, $\tau^2 = 0.0006$, $p = 0.36$ 

Weight
95%-CI (common) (random)

-0.14	[-0.18; -0.09]	30.6%	21.4%
-0.12	[-0.19; -0.04]	10.2%	11.3%
-0.02	[-0.16; 0.12]	3.2%	4.5%
-0.14	[-0.23; -0.04]	7.0%	8.5%
-0.08	[-0.19; 0.03]	5.3%	6.8%
-0.08	[-0.18; 0.01]	6.5%	8.0%
-0.03	[-0.13; 0.06]	6.6%	8.2%
-0.06	[-0.11; -0.00]	20.3%	17.5%
-0.04	[-0.20; 0.12]	2.4%	3.4%
-0.12	[-0.28; 0.04]	2.3%	3.3%
-0.04	[-0.15; 0.06]	5.6%	7.1%
-0.09	[-0.12; -0.07]	100.0%	--
-0.09	[-0.12; -0.06]	--	100.0%

uPA (PLAU)-rs4800787



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (981)

RECOMBINE (448)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 15\%$, $\tau^2 = 0.0033$, $p = 0.30$

uPA (PLAU) [chr19:44174441_C_T (rs4251805) (T/C) N=14734]

TE SE(TE)

-0.486

0.06

-0.381

0.08

-0.389

0.17

-0.519

0.13

-0.658

0.18

-0.473

0.16

-0.228

0.10

-0.488

0.08

-0.427

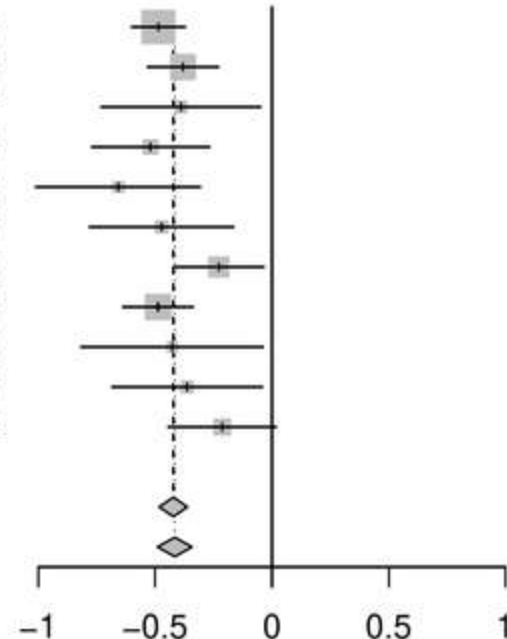
0.20

-0.363

0.16

-0.213

0.12



95%-CI (common)

Weight

Weight

(random)

-0.49 [-0.60; -0.37]

28.5%

21.3%

-0.38 [-0.53; -0.23]

16.1%

15.3%

-0.39 [-0.73; -0.05]

3.2%

4.2%

-0.52 [-0.77; -0.27]

5.8%

7.2%

-0.66 [-1.01; -0.31]

3.0%

4.0%

-0.47 [-0.78; -0.16]

3.9%

5.1%

-0.23 [-0.42; -0.03]

10.0%

11.0%

-0.49 [-0.64; -0.34]

16.4%

15.5%

-0.43 [-0.82; -0.04]

2.5%

3.3%

-0.36 [-0.68; -0.04]

3.6%

4.7%

-0.21 [-0.44; 0.02]

7.0%

8.3%

-0.42 [-0.48; -0.36]

100.0%

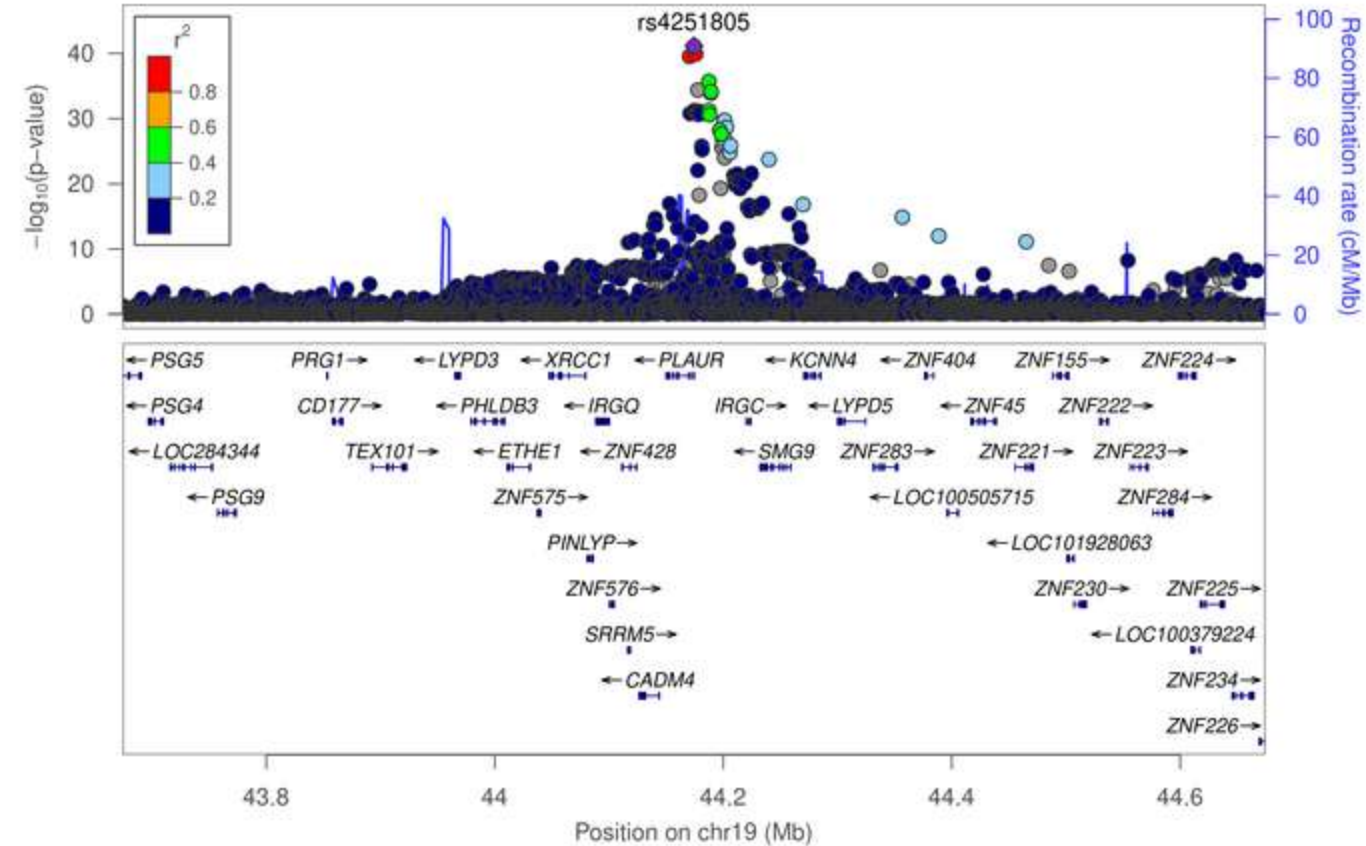
--

-0.42 [-0.49; -0.34]

--

100.0%

uPA (PLAU)-rs4251805



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (866)

ORCADES (981)

RECOMBINE (443)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (901)

Common effect model

Random effects model

Heterogeneity: $I^2 = 18\%$, $\tau^2 = 0.0005$, $p = 0.27$

uPA (PLAU) [chr2:160726868_A_G (rs7564243) (A/G) N=14729]

TE SE(TE)

-0.108

0.02

-0.079

0.04

-0.111

0.07

-0.156

0.04

-0.069

0.06

-0.096

0.05

-0.096

0.04

-0.048

0.02

-0.056

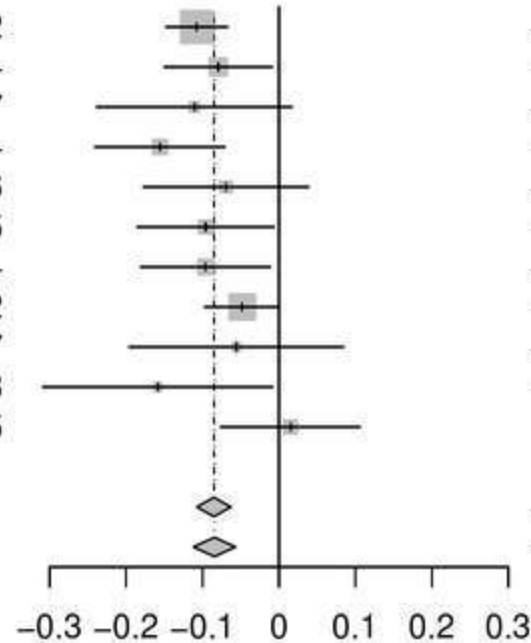
0.07

-0.159

0.08

0.015

0.05

Weight
95%-CI (common) (random)

-0.11 [-0.15; -0.07]

31.1%

22.3%

-0.08 [-0.15; -0.01]

10.0%

11.2%

-0.11 [-0.24; 0.02]

3.1%

4.2%

-0.16 [-0.24; -0.07]

6.9%

8.4%

-0.07 [-0.18; 0.04]

4.3%

5.6%

-0.10 [-0.19; -0.01]

6.2%

7.7%

-0.10 [-0.18; -0.01]

6.9%

8.4%

-0.05 [-0.10; 0.00]

20.8%

18.1%

-0.06 [-0.20; 0.08]

2.5%

3.5%

-0.16 [-0.31; -0.01]

2.2%

3.1%

0.01 [-0.08; 0.11]

6.0%

7.5%

-0.09 [-0.11; -0.06]

100.0%

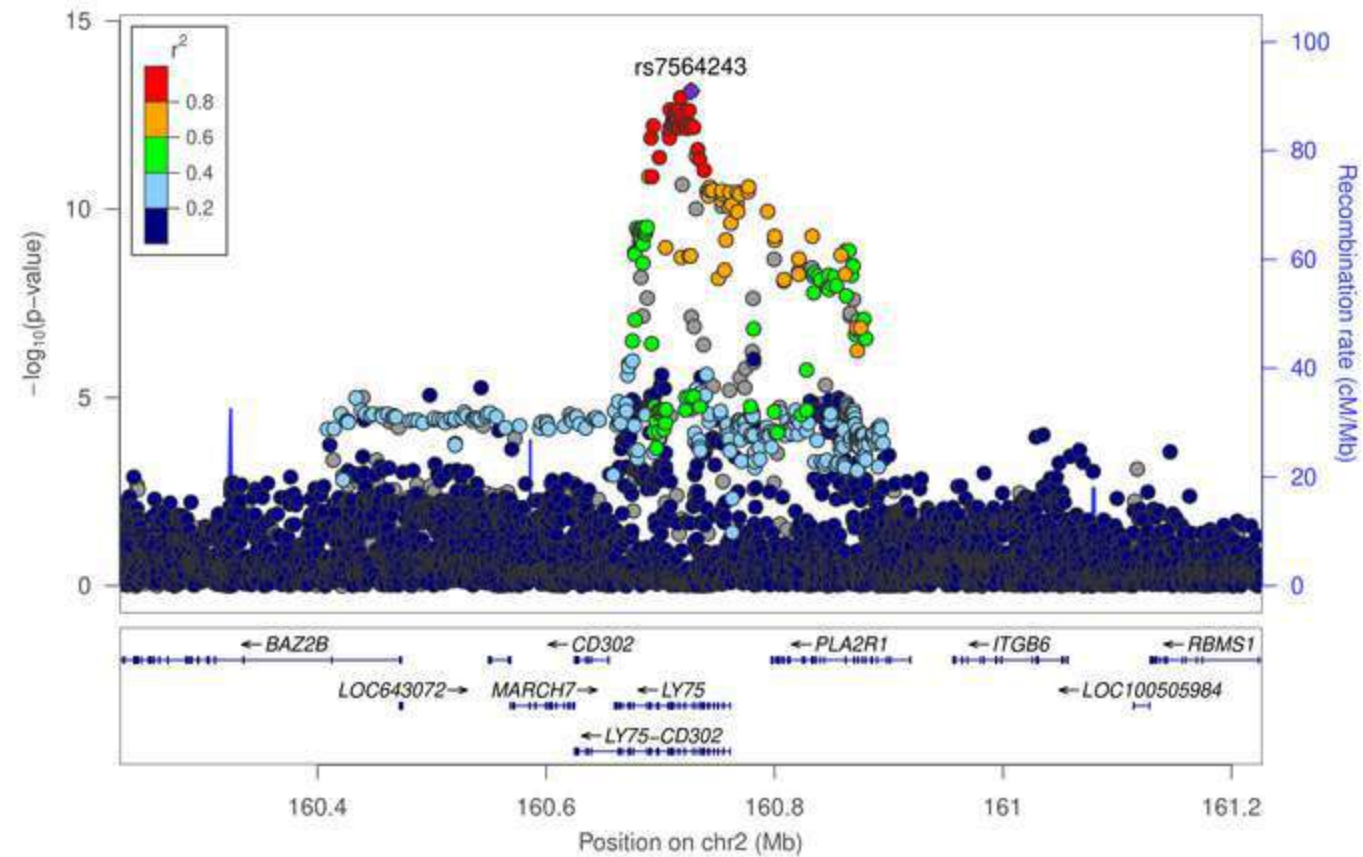
--

-0.08 [-0.11; -0.06]

--

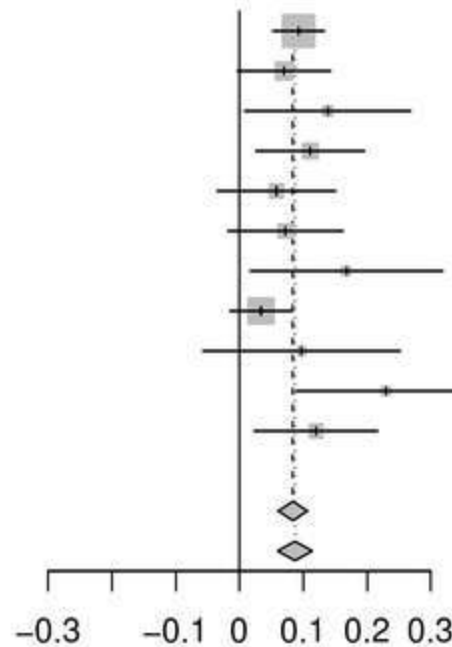
100.0%

uPA (PLAU)-rs7564243



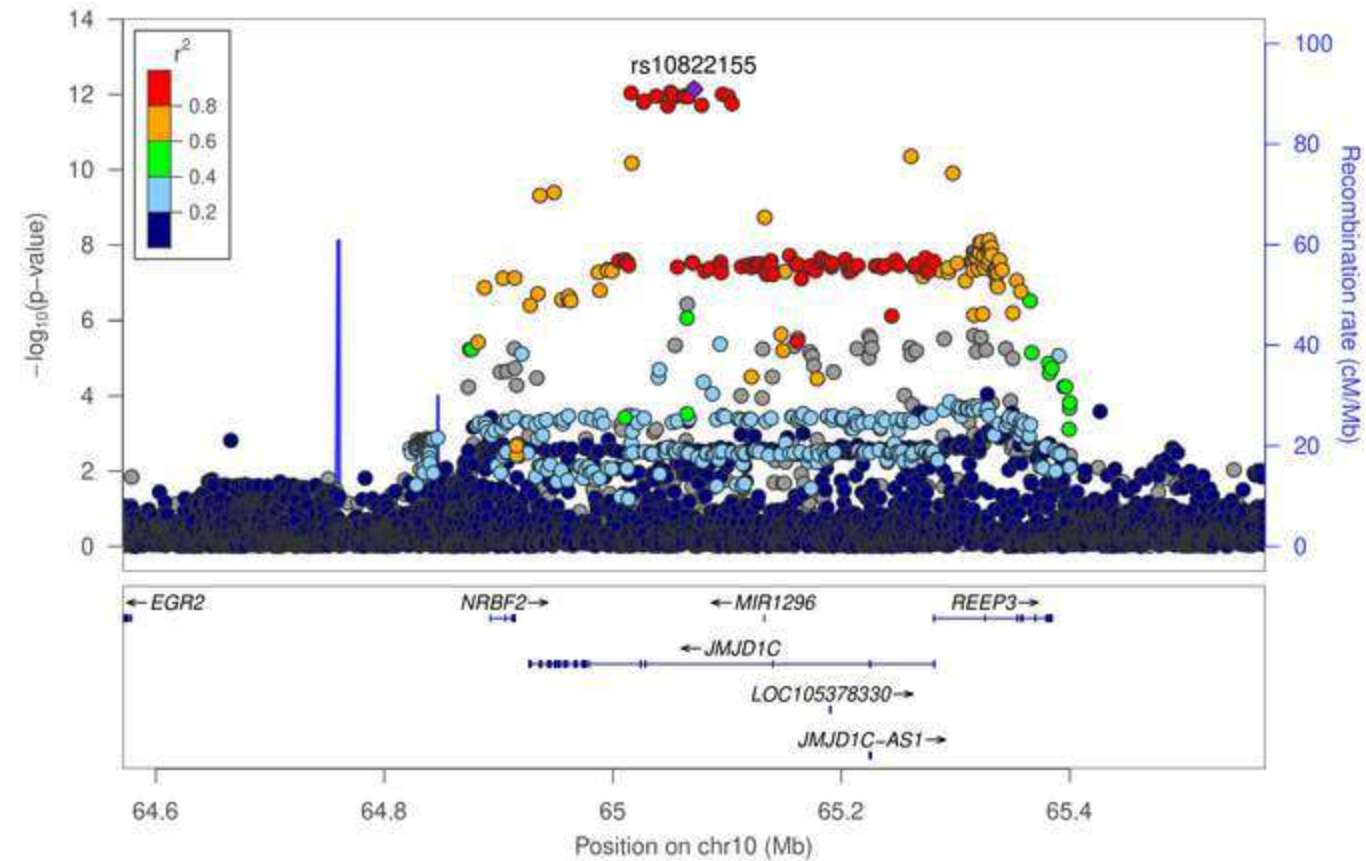
VEGF_A (VEGFA) [chr10:65071215_A_C (rs10822155) (A/C) N=14744]

Study	TE	SE(TE)	Weight 95%-CI (common)	Weight (random)
INTERVAL (4896)	0.093	0.02	0.09 [0.05; 0.13]	32.5%
BioFinder (1496)	0.070	0.04	0.07 [-0.00; 0.14]	9.9%
EGCUT (487)	0.138	0.07	0.14 [0.01; 0.27]	3.1%
KORA (1064)	0.111	0.04	0.11 [0.03; 0.20]	7.2%
NSPHS (874)	0.058	0.05	0.06 [-0.03; 0.15]	6.1%
ORCADES (982)	0.072	0.05	0.07 [-0.02; 0.16]	6.5%
RECOMBINE (448)	0.168	0.08	0.17 [0.02; 0.32]	2.3%
STABILITY (2951)	0.034	0.02	0.03 [-0.02; 0.08]	21.9%
STANLEY (344)	0.097	0.08	0.10 [-0.06; 0.25]	2.2%
STANLEY (300)	0.230	0.07	0.23 [0.09; 0.37]	2.6%
VIS (902)	0.120	0.05	0.12 [0.02; 0.22]	5.6%
Common effect model			0.08 [0.06; 0.11]	100.0%
Random effects model			0.09 [0.06; 0.11]	-- 100.0%



Heterogeneity: $I^2 = 14\%$, $\tau^2 = 0.0004$, $p = 0.31$

VEGF_A (VEGFA)-rs10822155



Study

INTERVAL (4896)

BioFinder (1496)

EGCUT (487)

KORA (1064)

NSPHS (874)

ORCADES (982)

RECOMBINE (437)

STABILITY (2951)

STANLEY (344)

STANLEY (300)

VIS (902)

Common effect model

Random effects model

Heterogeneity: $I^2 = 95\%$, $\tau^2 = 0.0252$, $p < 0.01$

VEGF_A (VEGFA) [chr6:43925607_A_G (rs6921438) (A/G) N=14733]

TE SE(TE)

-0.480 0.02

-0.615 0.03

-0.510 0.06

-0.797 0.05

-0.397 0.05

-0.283 0.04

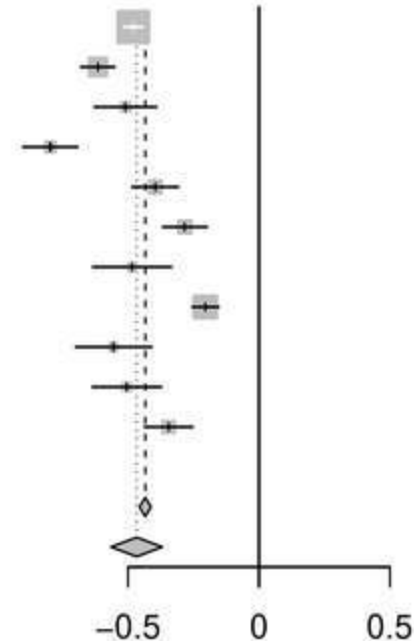
-0.484 0.08

-0.204 0.03

-0.555 0.07

-0.504 0.07

-0.345 0.05

Weight
95%-CI (common) (random)

-0.48 [-0.52; -0.44] 34.9% 9.9%

-0.62 [-0.68; -0.55] 11.8% 9.6%

-0.51 [-0.63; -0.39] 3.5% 8.8%

-0.80 [-0.90; -0.69] 4.5% 9.0%

-0.40 [-0.49; -0.31] 6.2% 9.3%

-0.28 [-0.37; -0.20] 6.8% 9.4%

-0.48 [-0.63; -0.33] 2.2% 8.1%

-0.20 [-0.26; -0.15] 19.2% 9.8%

-0.55 [-0.70; -0.41] 2.3% 8.2%

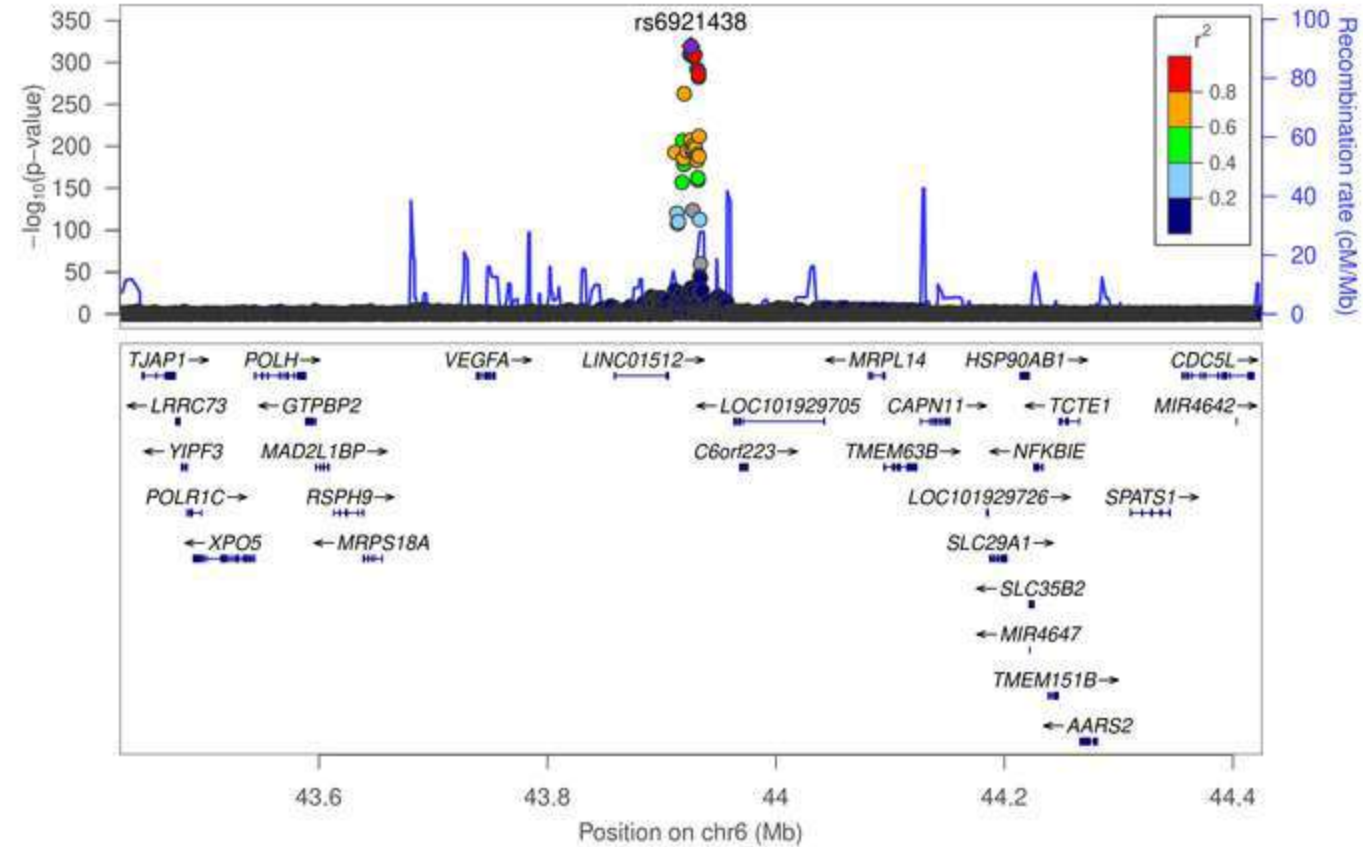
-0.50 [-0.64; -0.37] 2.8% 8.5%

-0.34 [-0.44; -0.25] 5.8% 9.2%

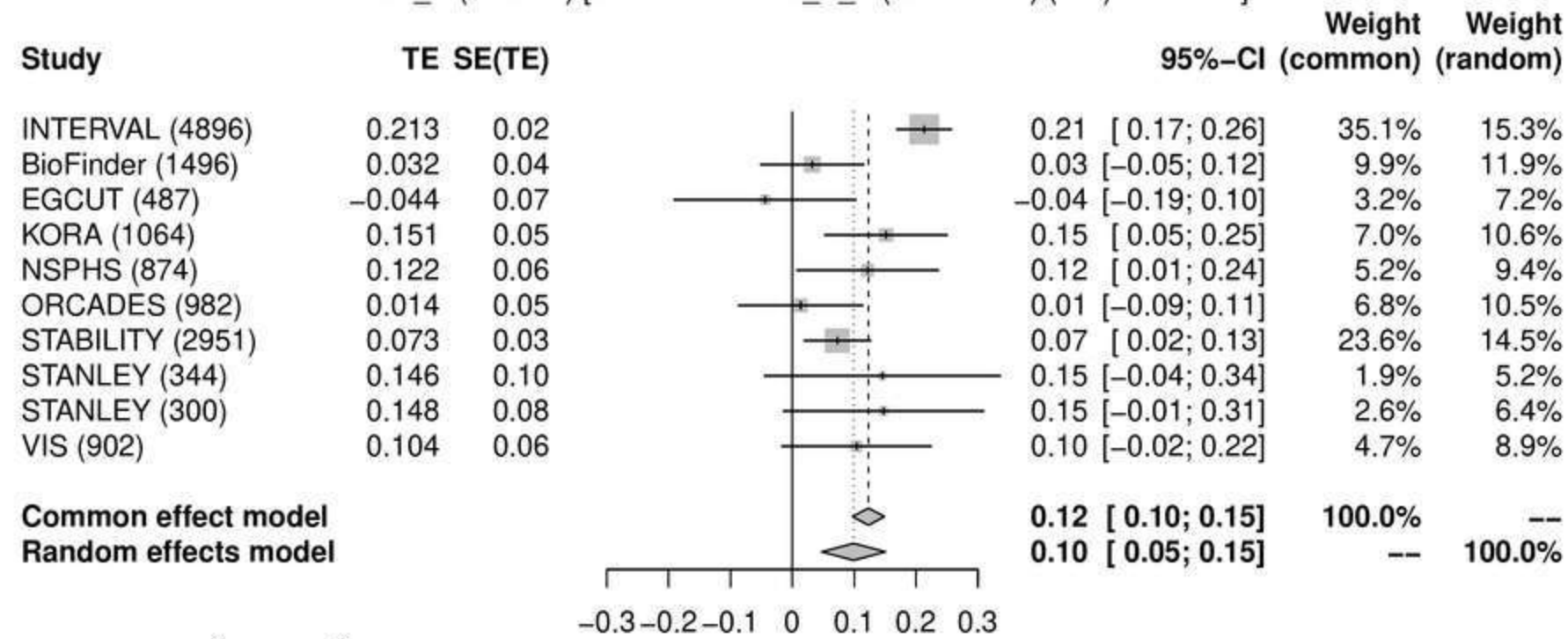
-0.43 [-0.46; -0.41] 100.0% --

-0.47 [-0.57; -0.37] -- 100.0%

VEGF_A (VEGFA)-rs6921438

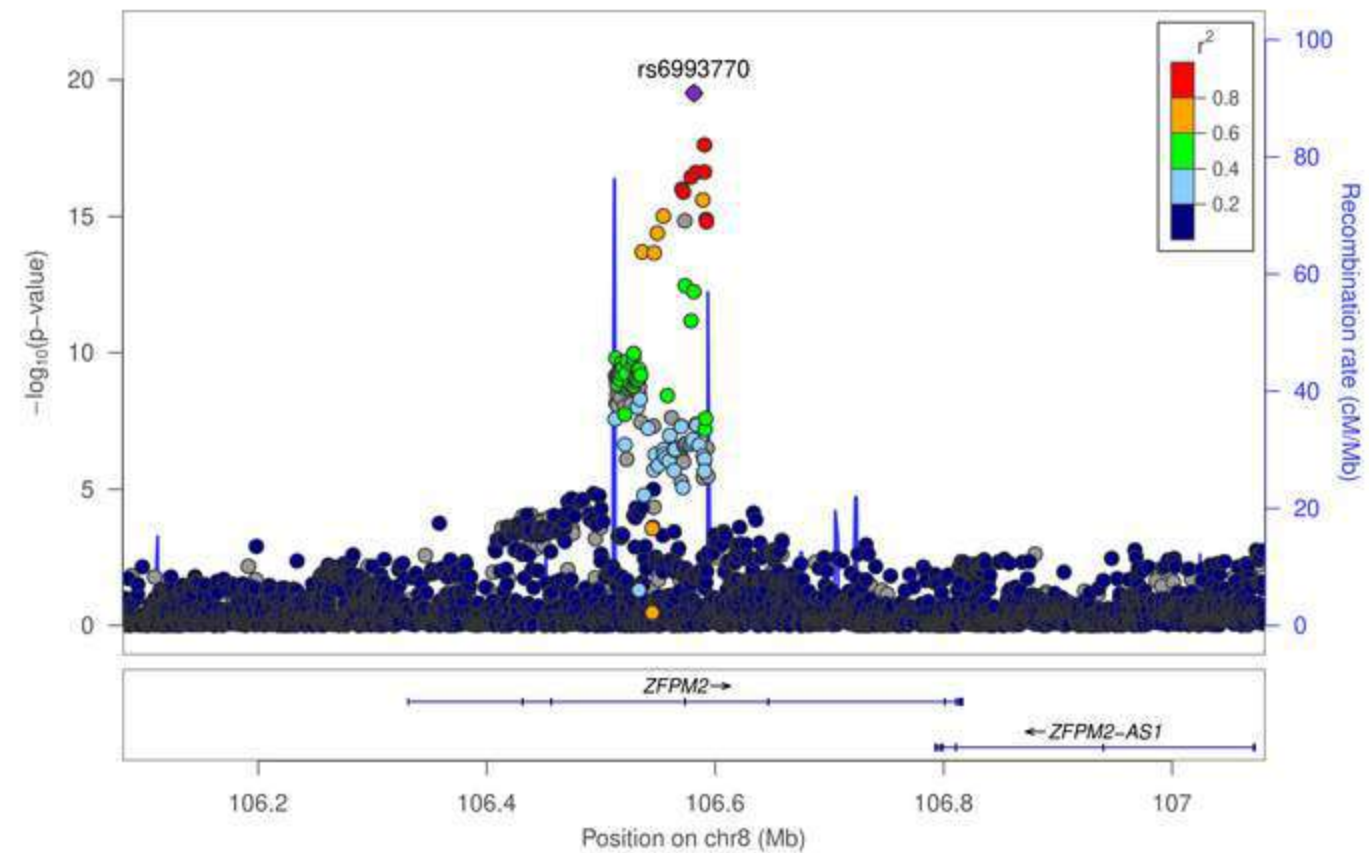


VEGF_A (VEGFA) [chr8:106581528_A_T (rs6993770) (A/T) N=14296]



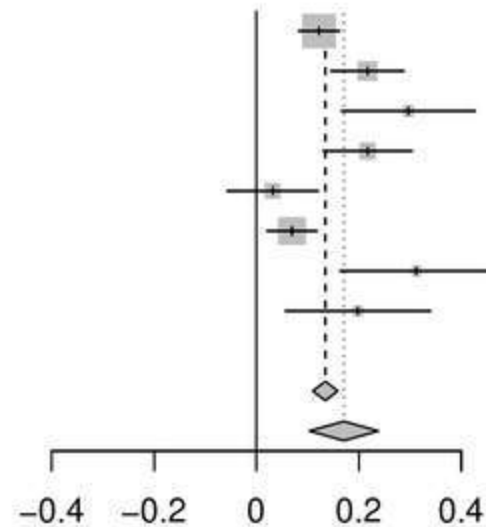
Heterogeneity: $I^2 = 73\%$, $\tau^2 = 0.0040$, $p < 0.01$

VEGF_A (VEGFA)-rs6993770



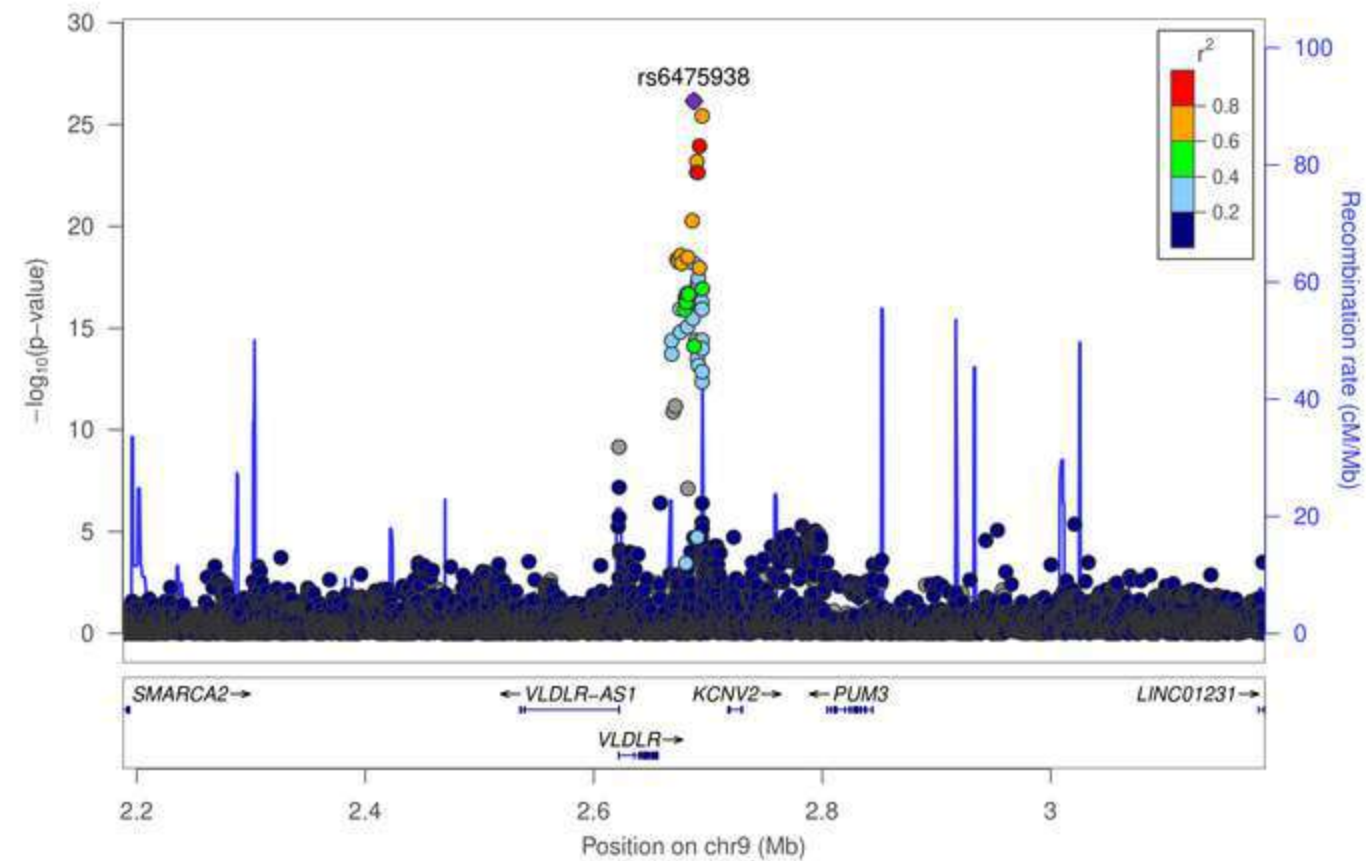
VEGF_A (VEGFA) [chr9:2687795_A_T (rs6475938) (A/T) N=12412]

Study	TE	SE(TE)	95%-CI	Weight (common)	Weight (random)
INTERVAL (4896)	0.122	0.02	0.12 [0.08; 0.16]	37.9%	15.7%
BioFinder (1496)	0.217	0.04	0.22 [0.15; 0.29]	11.9%	14.0%
EGCUT (487)	0.296	0.07	0.30 [0.17; 0.43]	3.5%	10.3%
KORA (1064)	0.217	0.04	0.22 [0.13; 0.30]	8.0%	13.0%
NSPHS (874)	0.032	0.05	0.03 [-0.06; 0.12]	7.7%	12.9%
STABILITY (2951)	0.069	0.02	0.07 [0.02; 0.12]	25.3%	15.3%
STANLEY (344)	0.312	0.08	0.31 [0.16; 0.46]	2.7%	9.2%
STANLEY (300)	0.198	0.07	0.20 [0.06; 0.34]	3.0%	9.6%
Common effect model			0.13 [0.11; 0.16]	100.0%	--
Random effects model			0.17 [0.10; 0.24]	--	100.0%



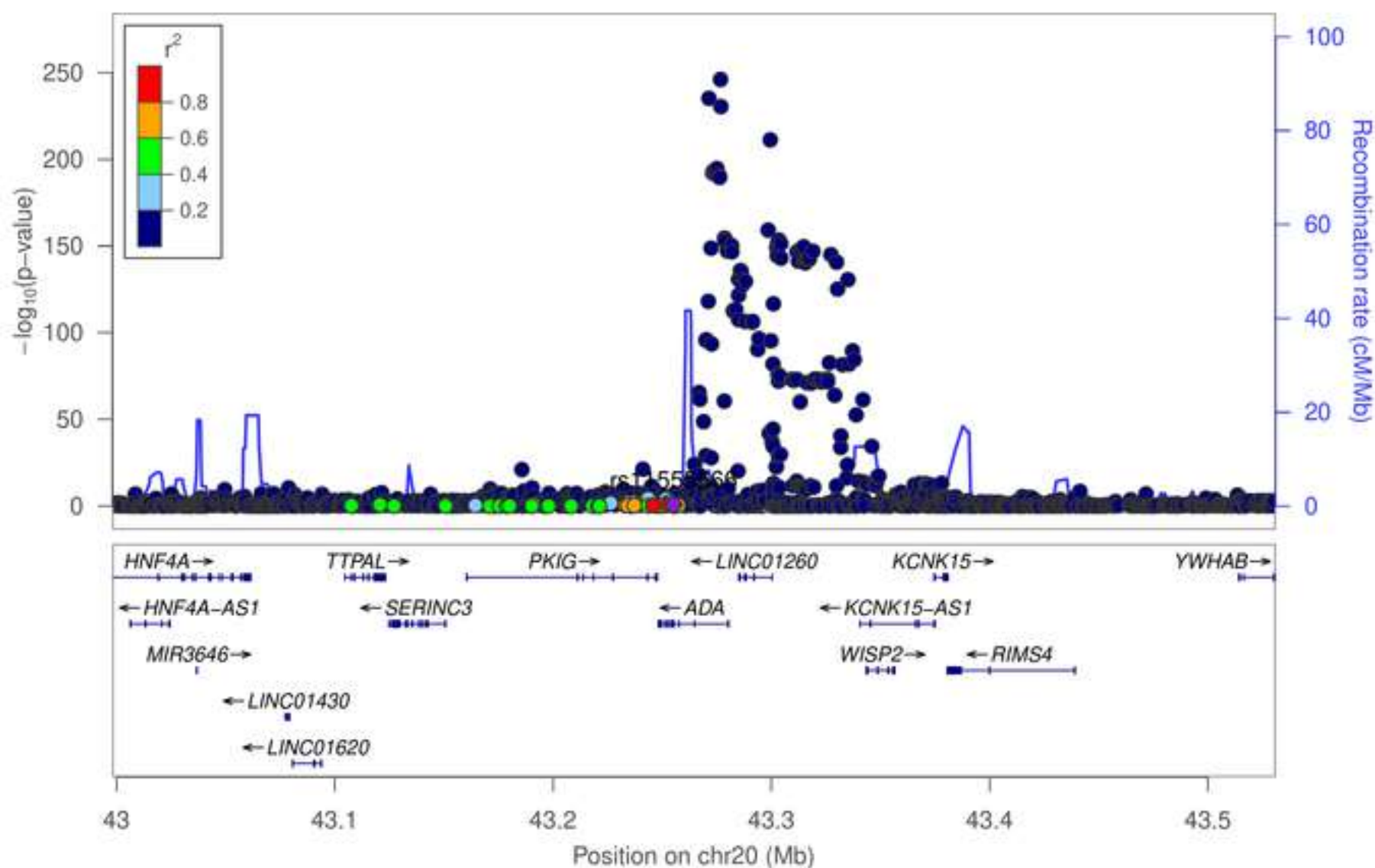
Heterogeneity: $I^2 = 79\%$, $\tau^2 = 0.0072$, $p < 0.01$

VEGF_A (VEGFA)-rs6475938

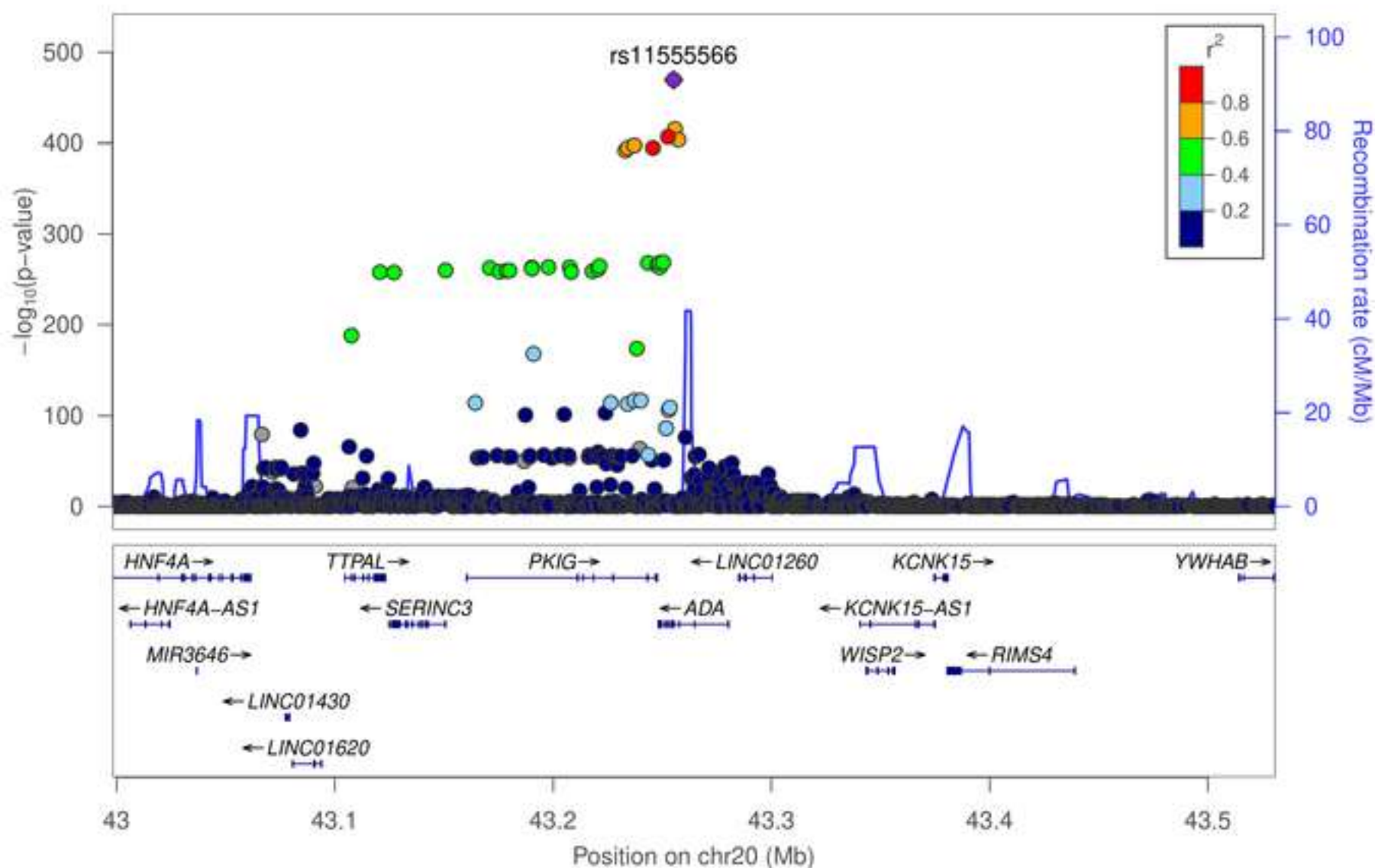


Supplementary Figure 3. Regional association plots comparing plasma *cis*-pQTLs and blood *cis*-eQTLs for the gene encoding the corresponding protein. 'LocusZoom' regional association plots comparing the plasma *cis*-pQTL signals (lower panel) with the eQTL signals for the encoding gene in whole blood from the eQTLGen data (upper panel). The sentinel variant for the pQTL is coloured in purple. LD (r^2) to the sentinel pQTL is indicated by the colour key. Two-sided P -values are from meta-analysis of linear regression estimates.

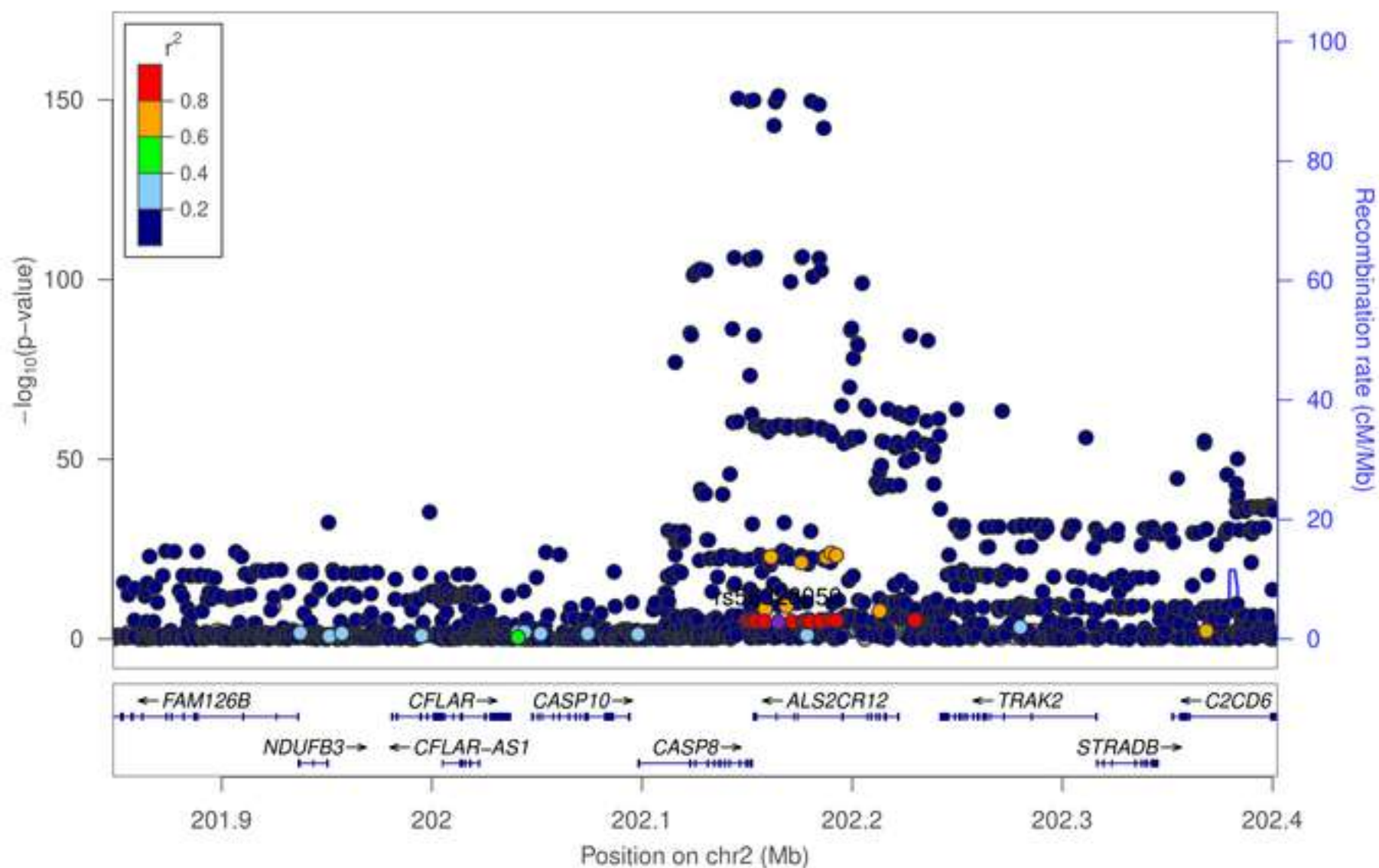
eQTLGen: ADA (ADA)-rs11555566



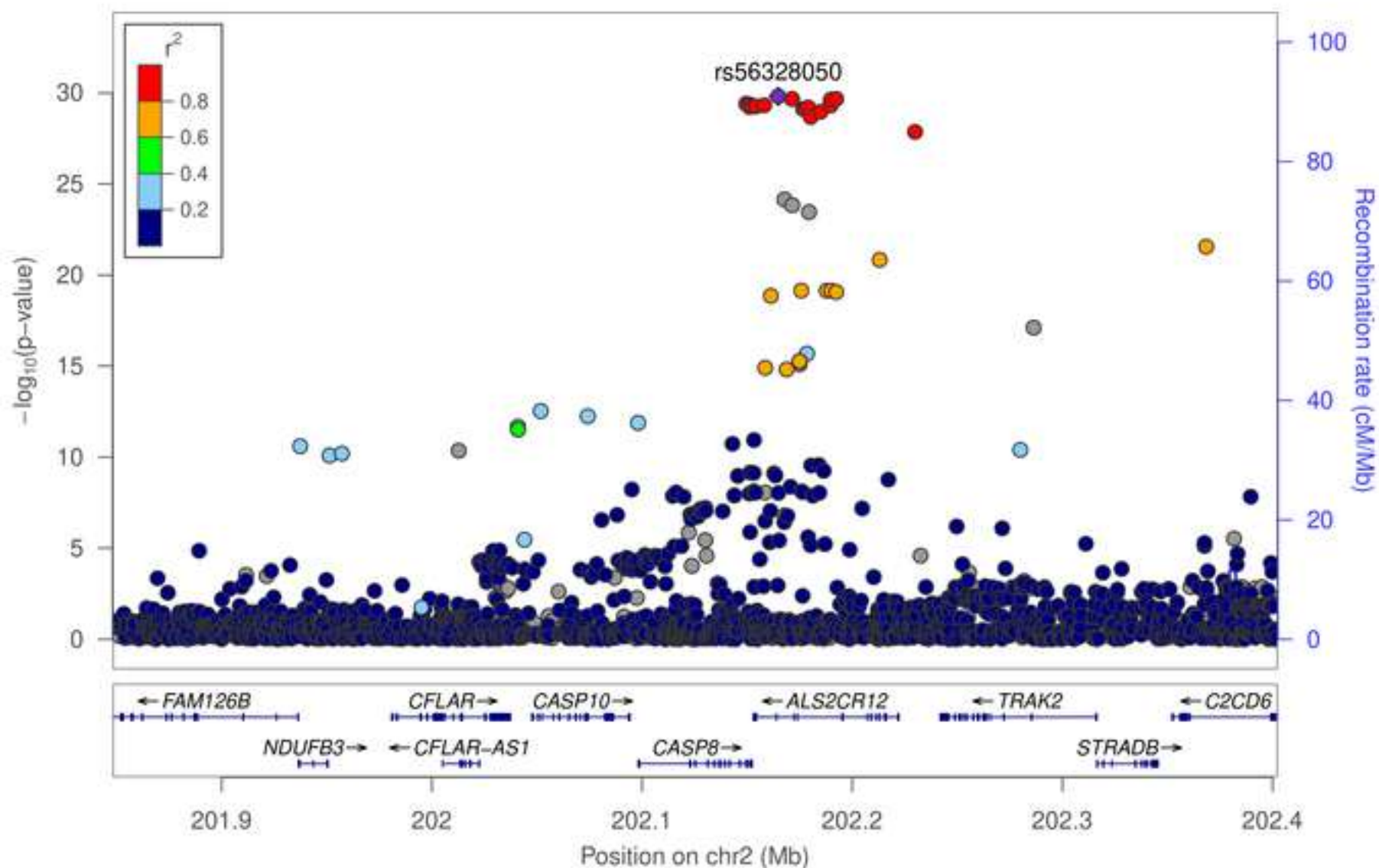
SCALLOP: ADA (ADA)-rs11555566



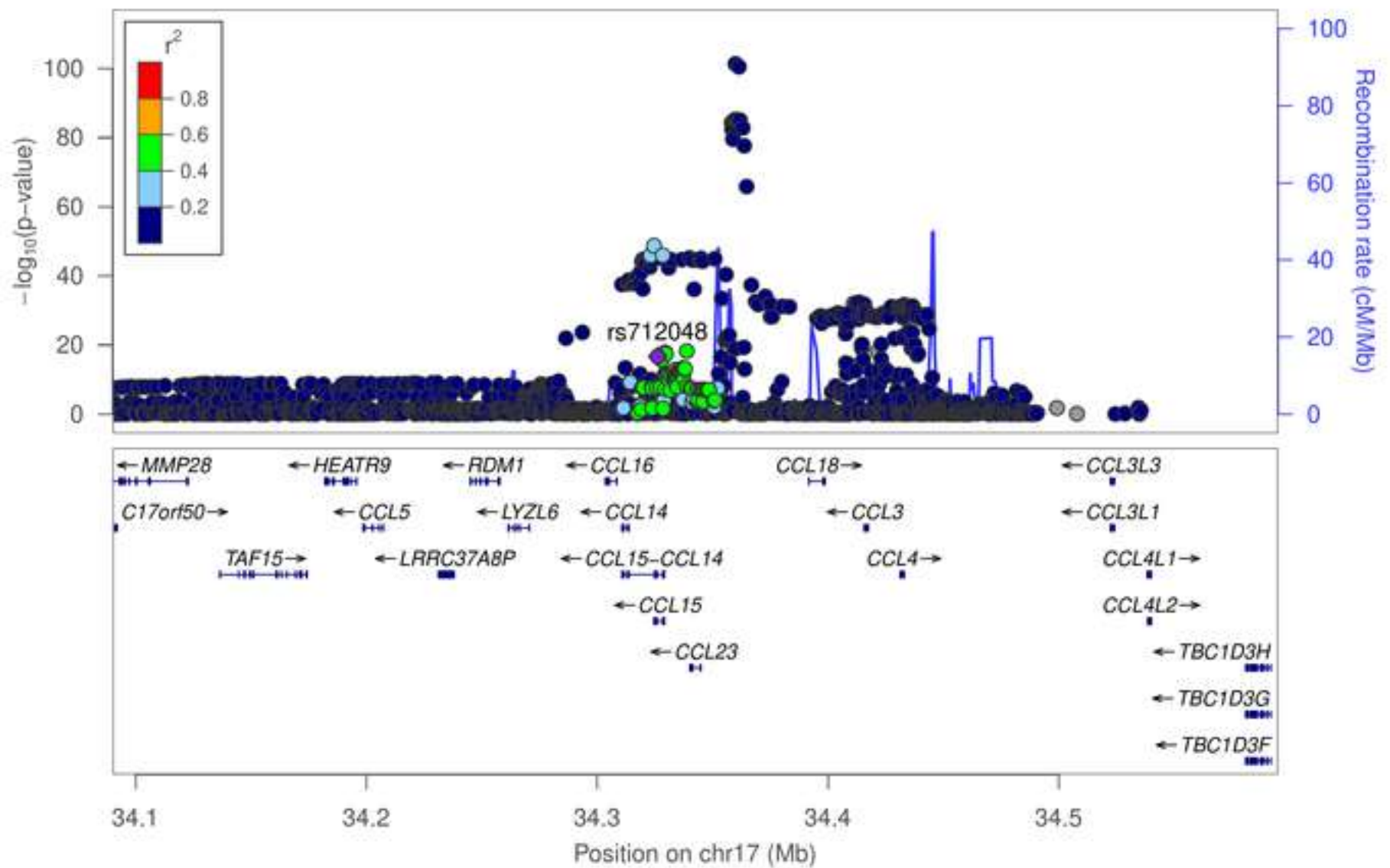
eQTLGen: CASP-8 (CASP8)-rs56328050



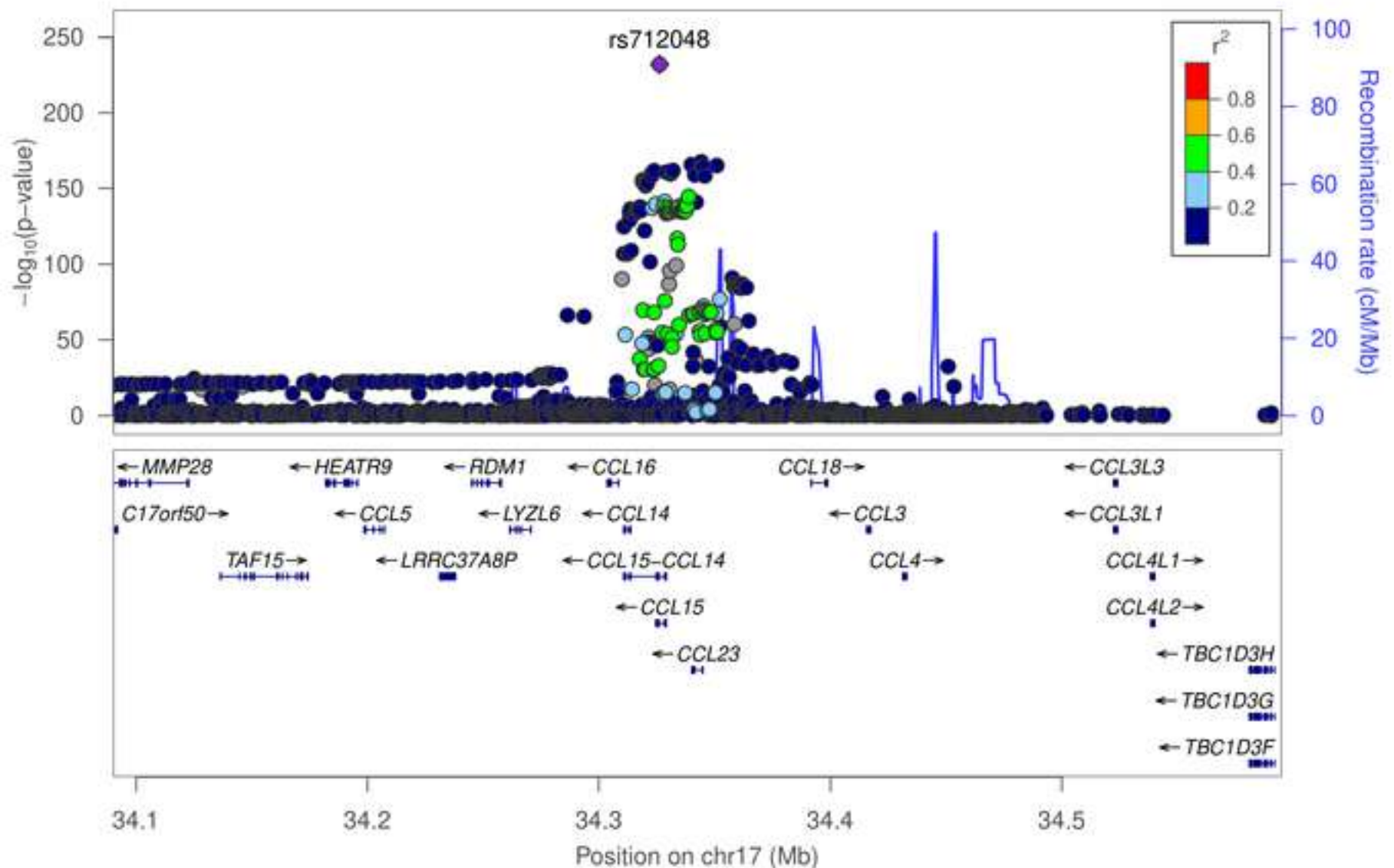
SCALLOP: CASP-8 (CASP8)-rs56328050



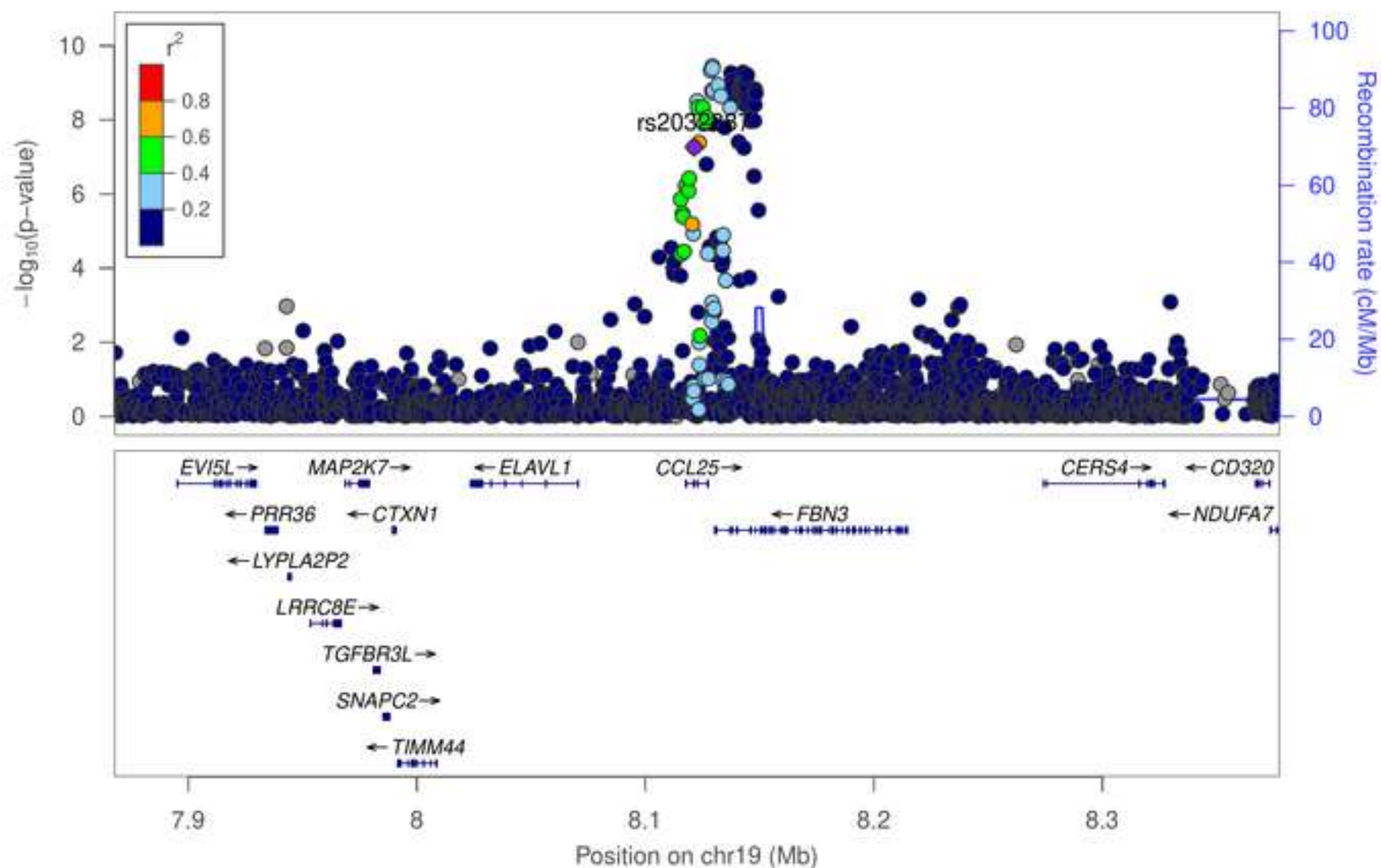
eQTLGen: CCL23 (CCL23)-rs712048



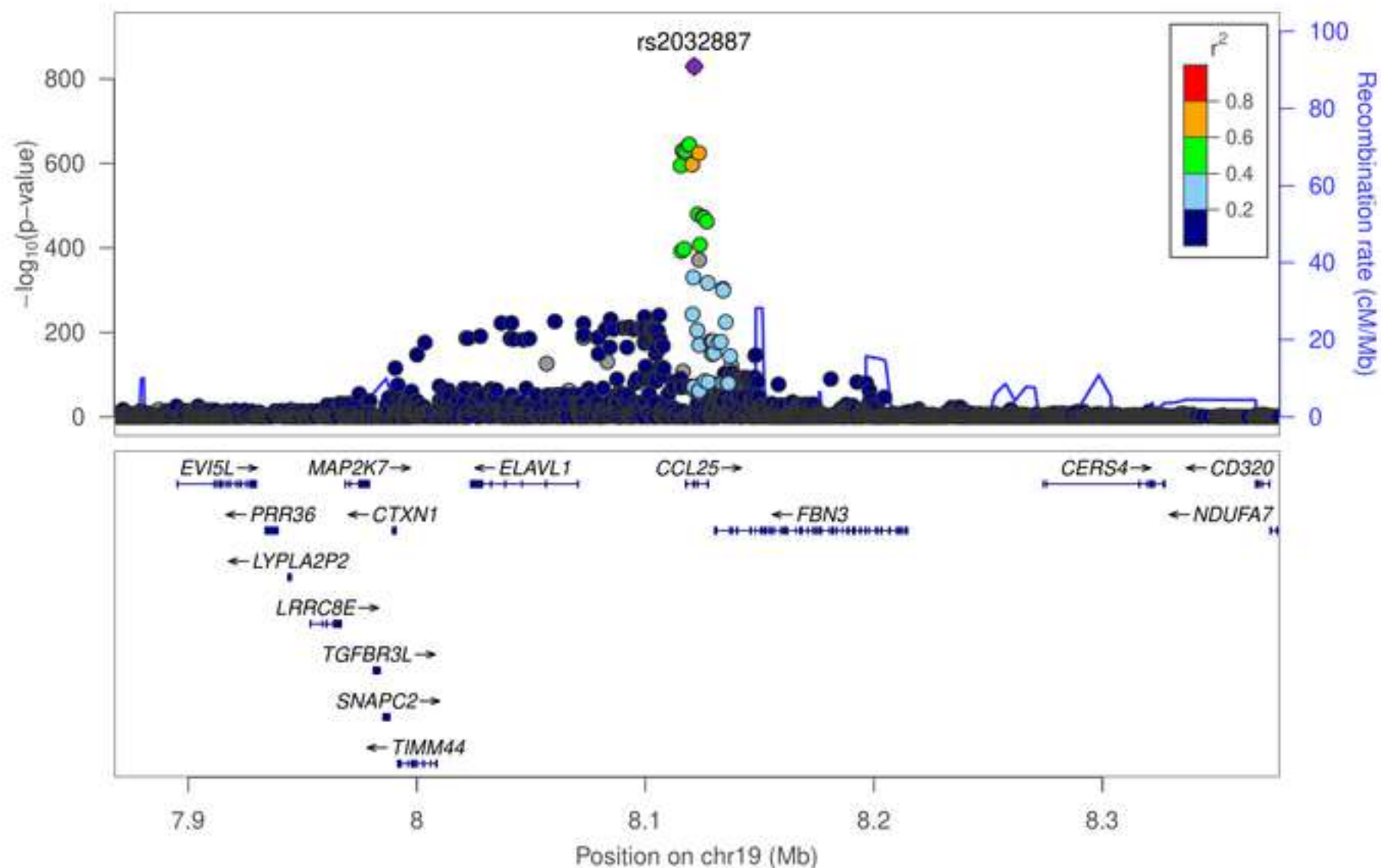
SCALLOP: CCL23 (CCL23)-rs712048



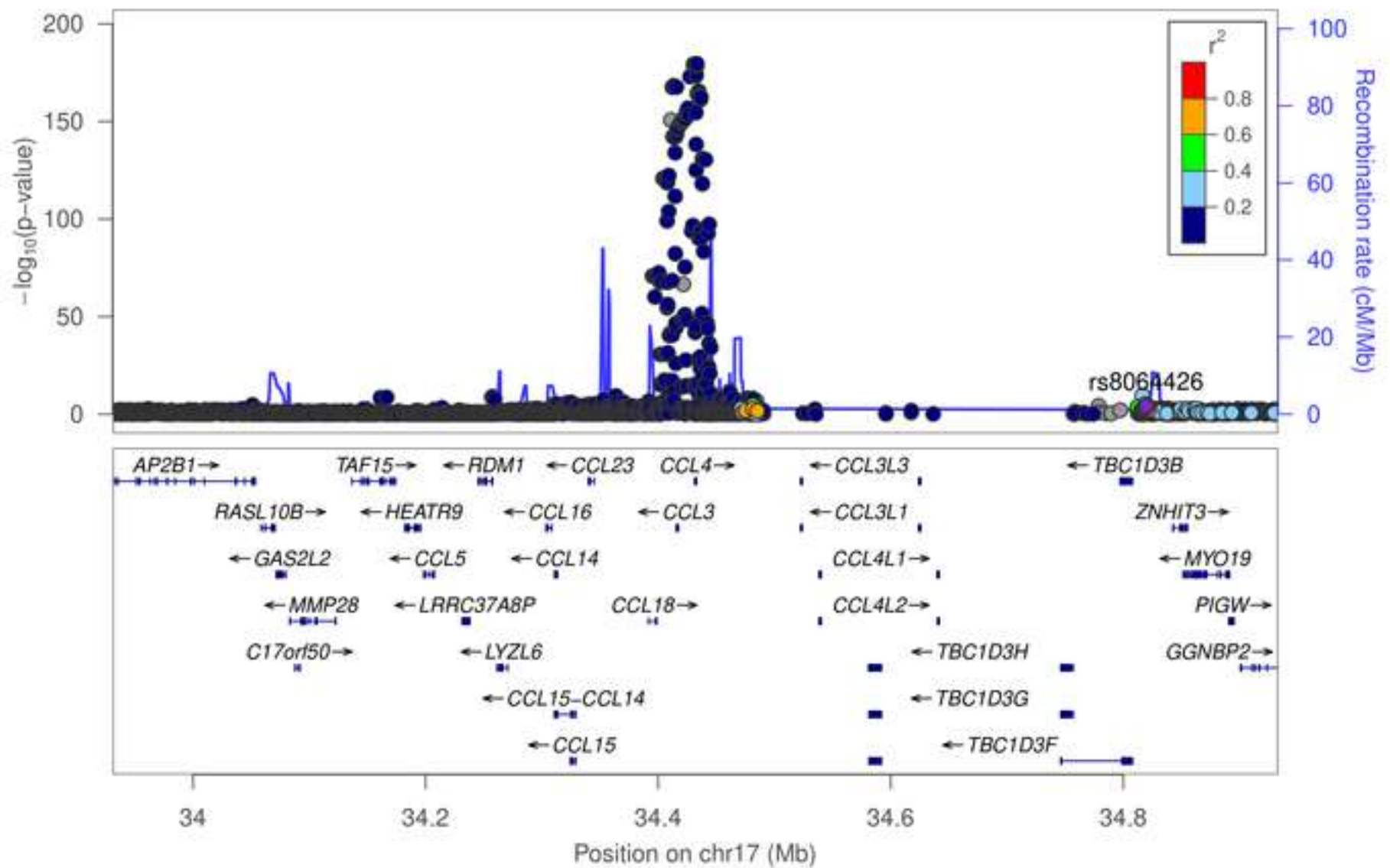
eQTLGen: CCL25 (CCL25)-rs2032887



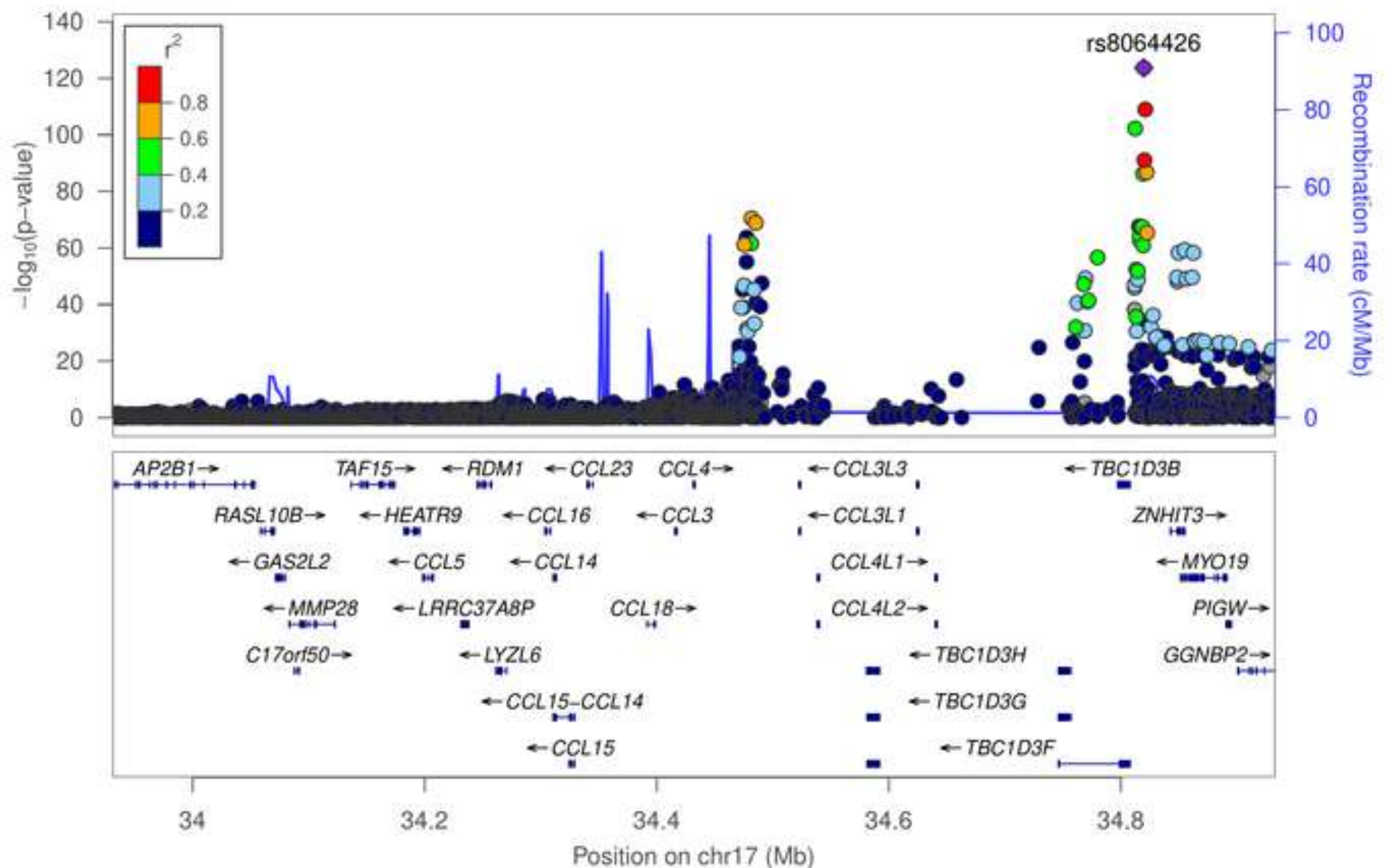
SCALLOP: CCL25 (CCL25)-rs2032887



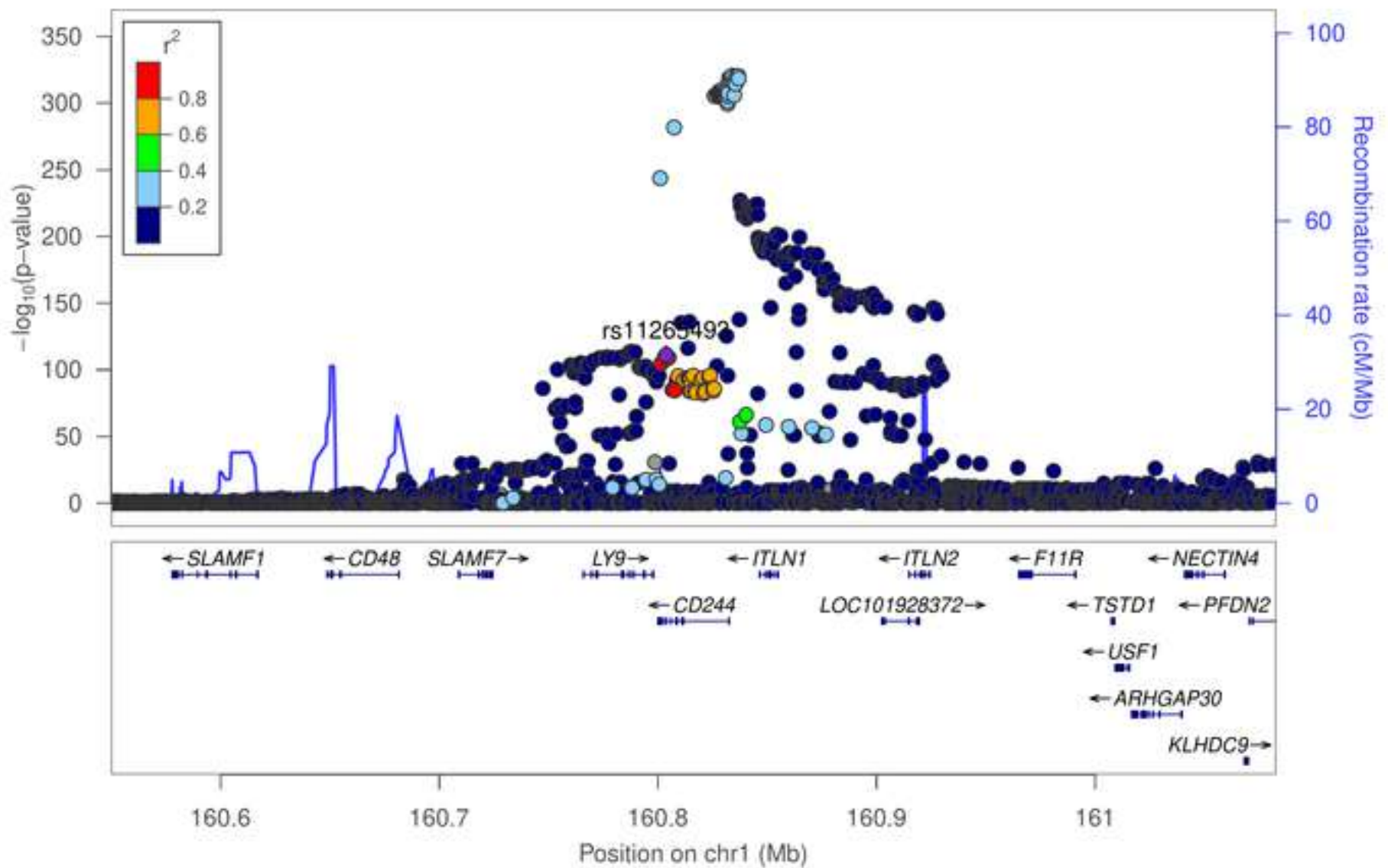
eQTLGen: CCL4 (CCL4)-rs8064426



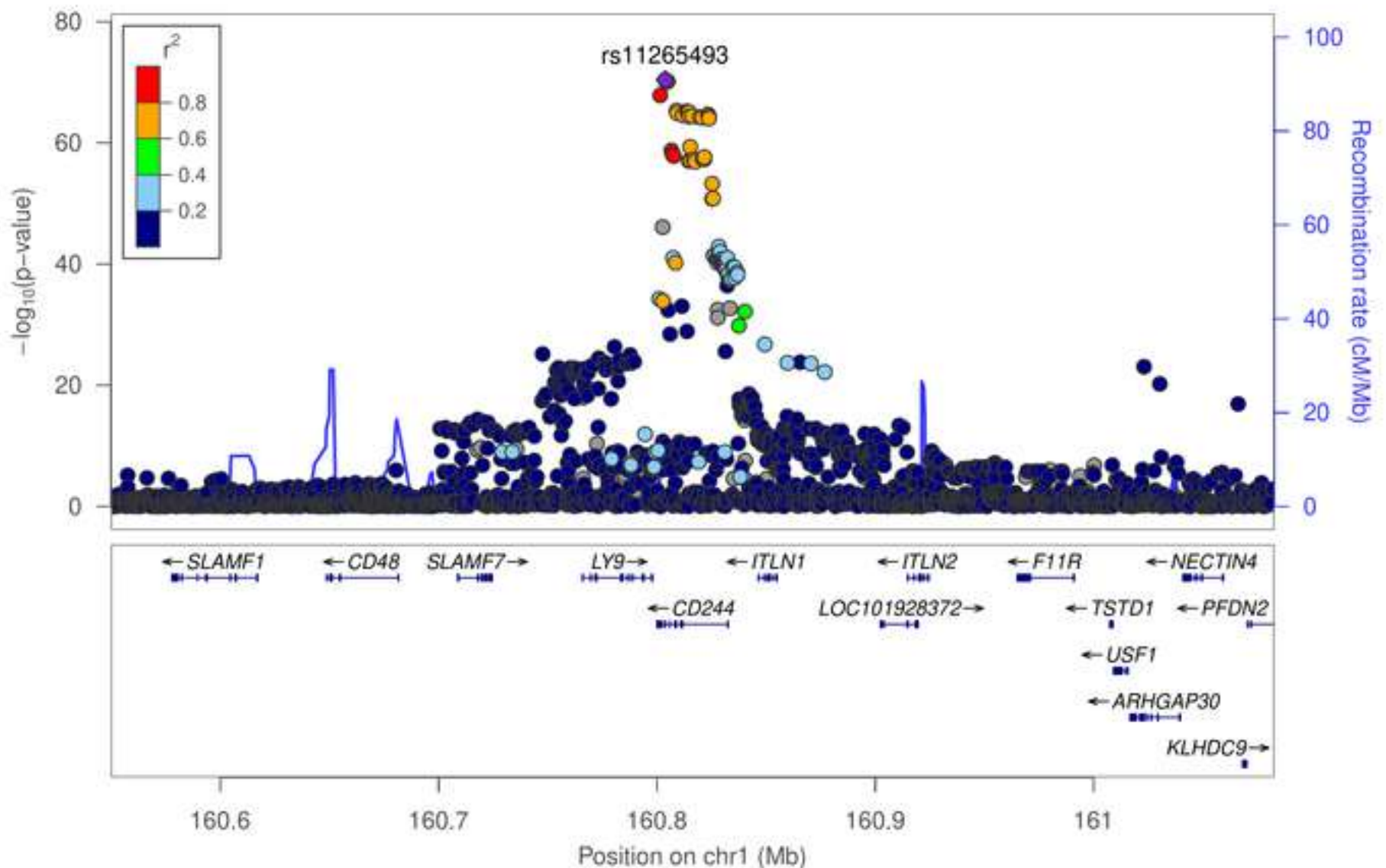
SCALLOP: CCL4 (CCL4)-rs8064426



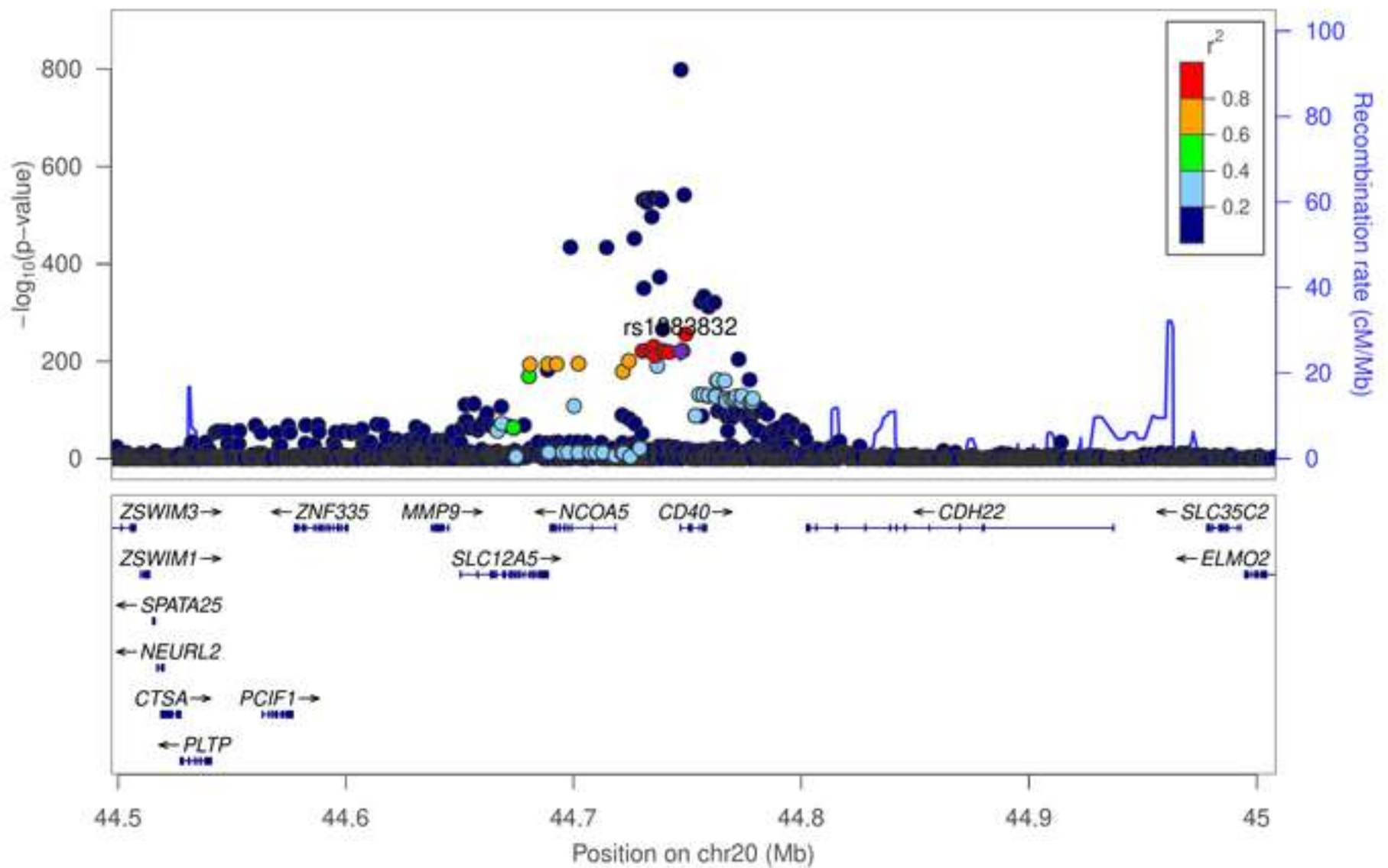
eQTLGen: CD244 (CD244)–rs11265493



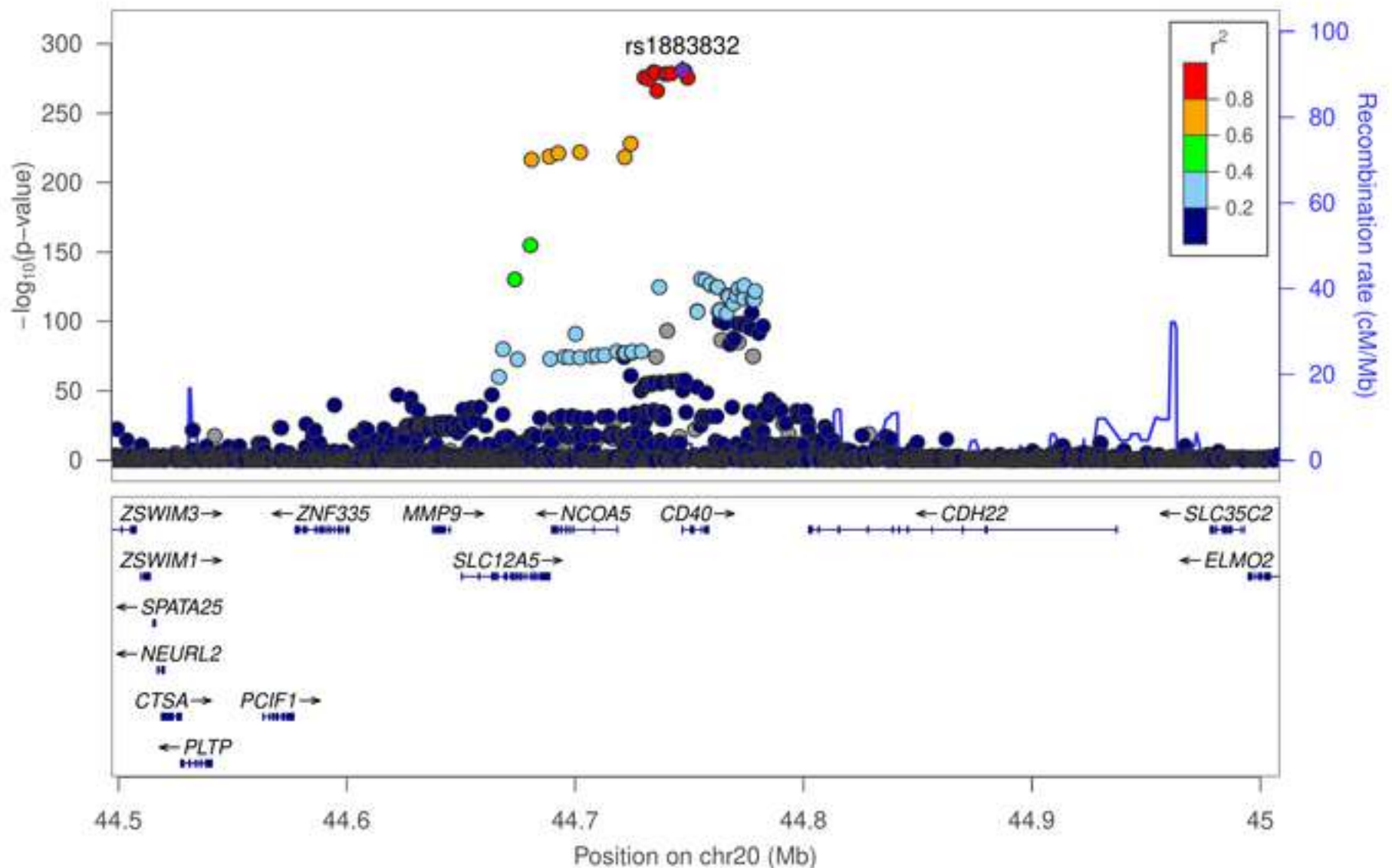
SCALLOP: CD244 (CD244)–rs11265493



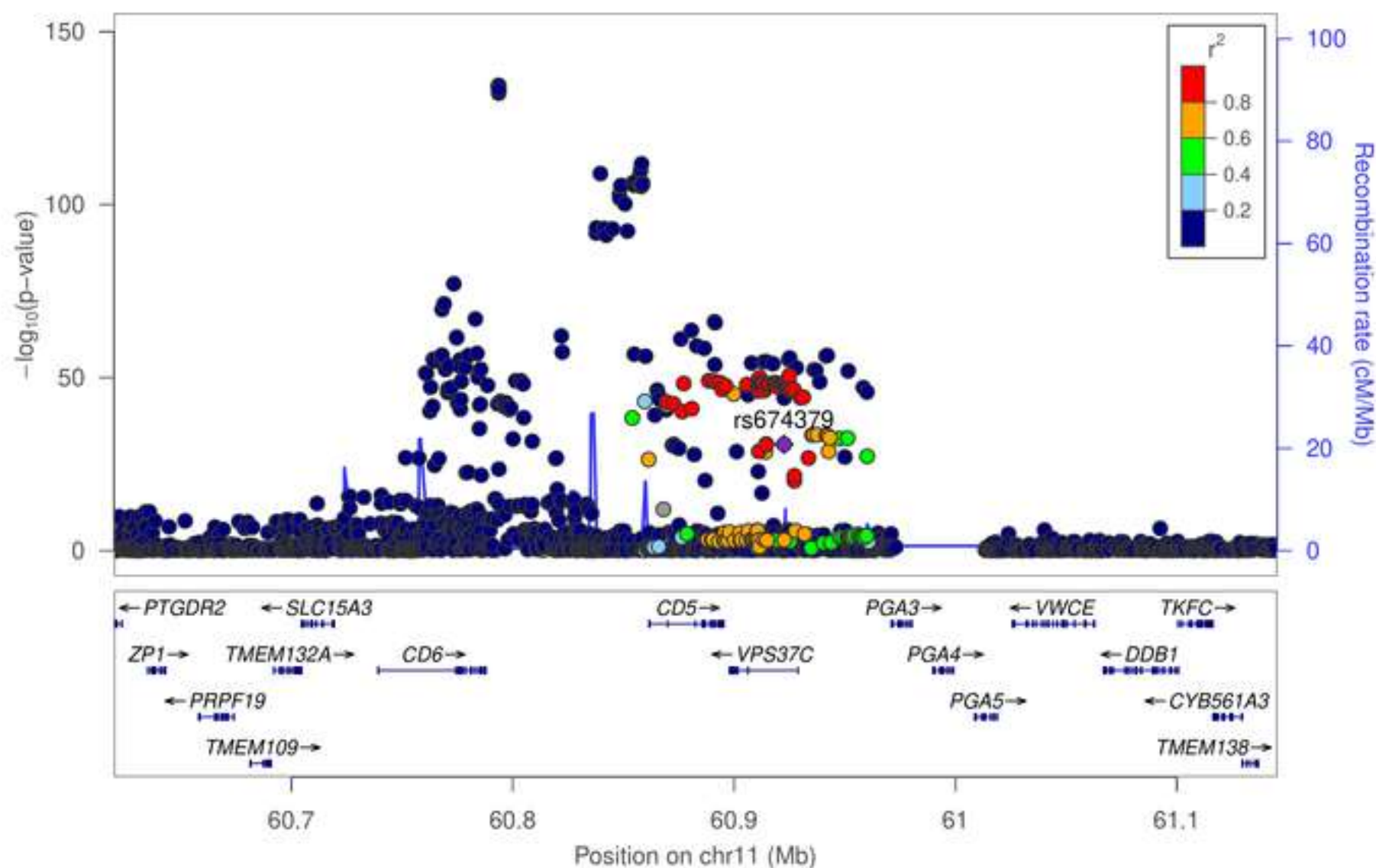
eQTLGen: CD40 (CD40)-rs1883832



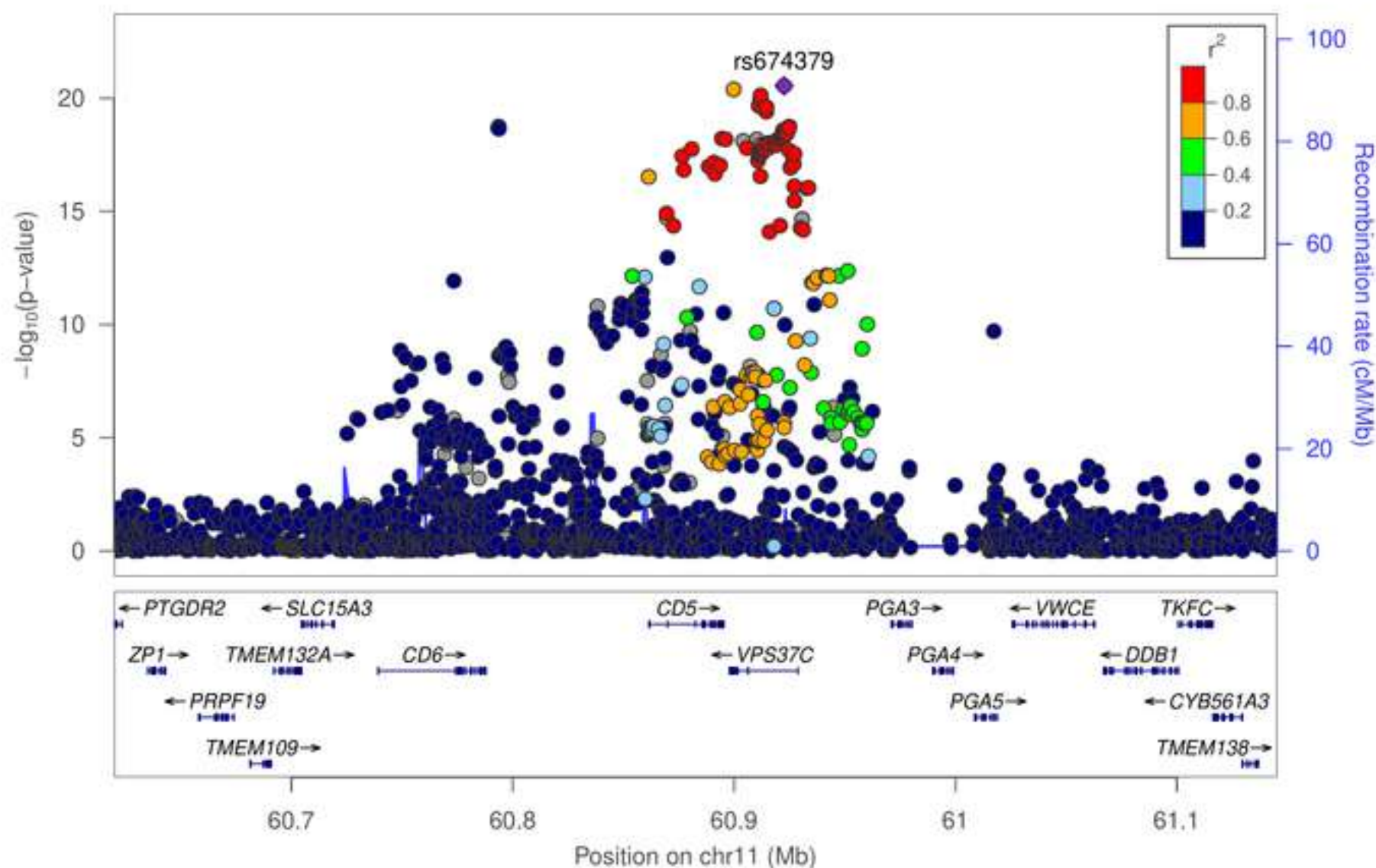
SCALLOP: CD40 (CD40)-rs1883832



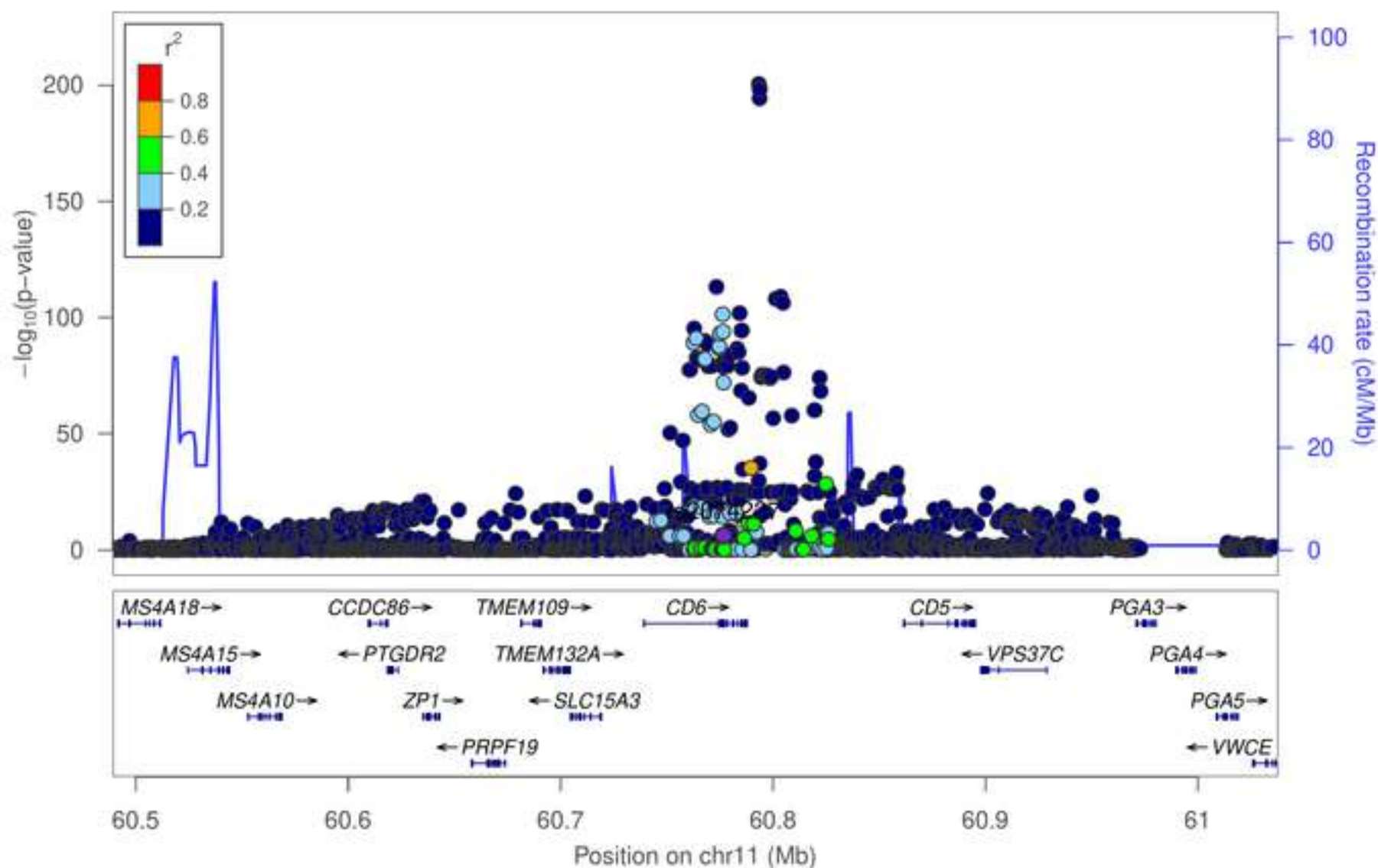
eQTLGen: CD5 (CD5)-rs674379



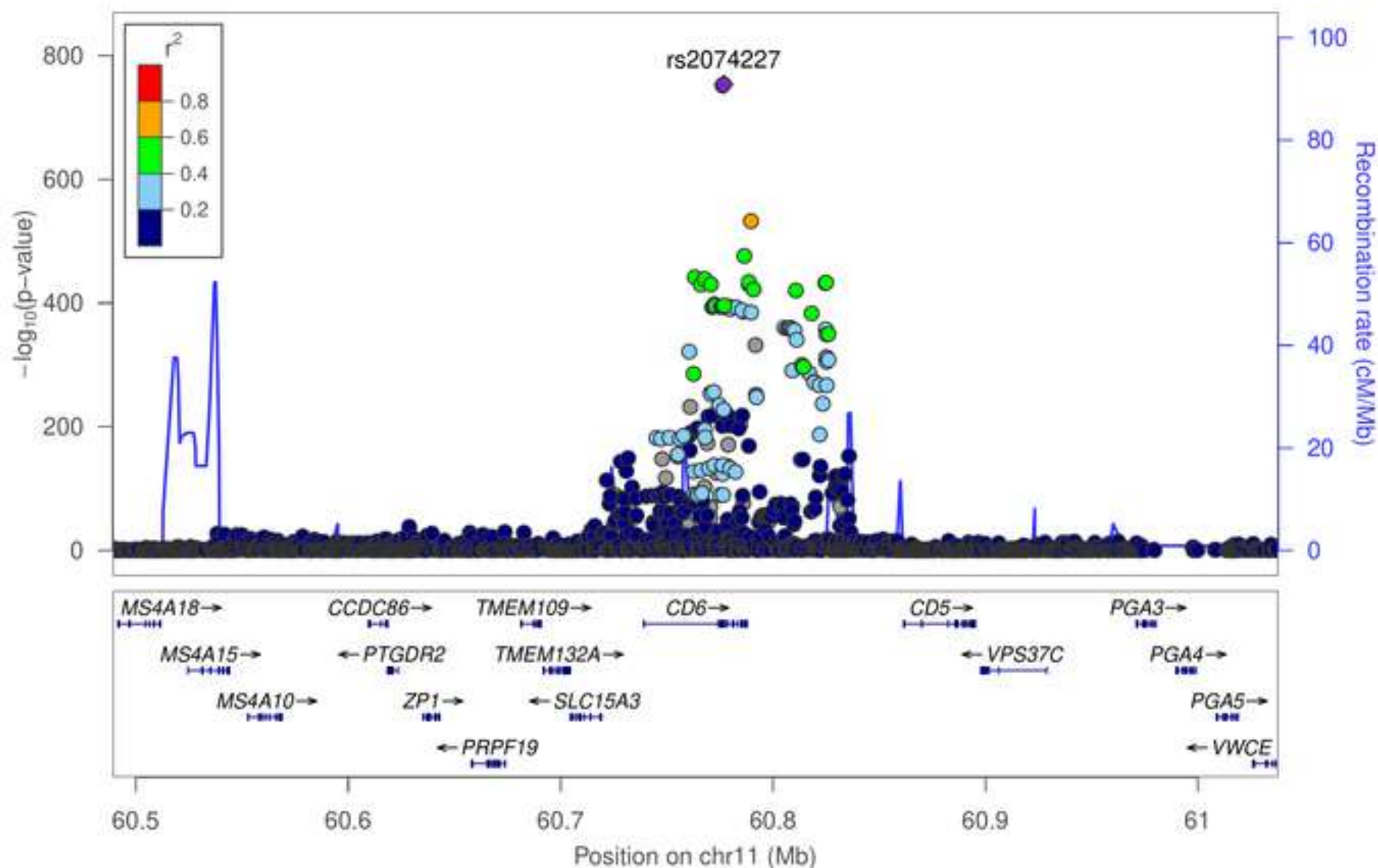
SCALLOP: CD5 (CD5)-rs674379



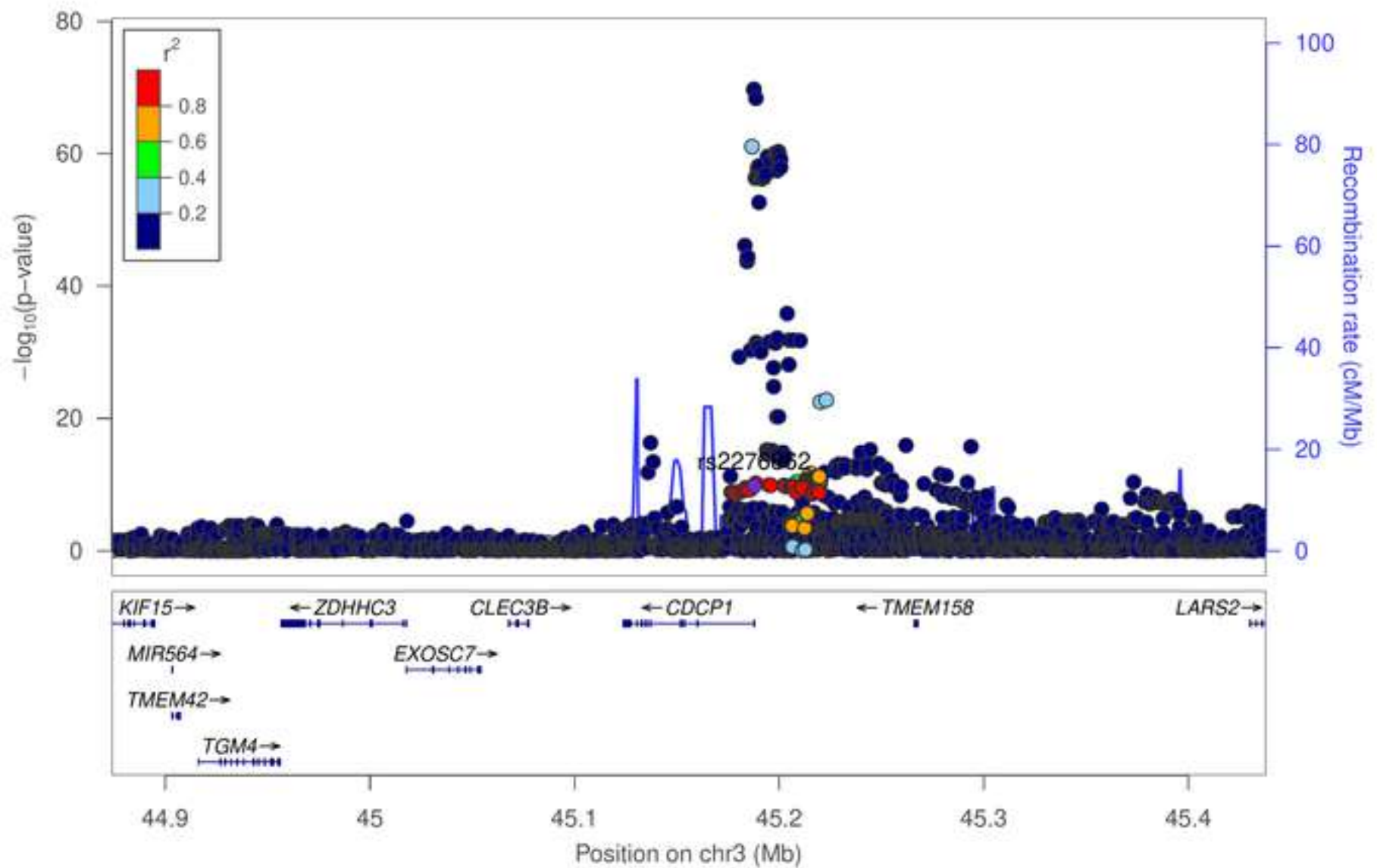
eQTLGen: CD6 (CD6)-rs2074227



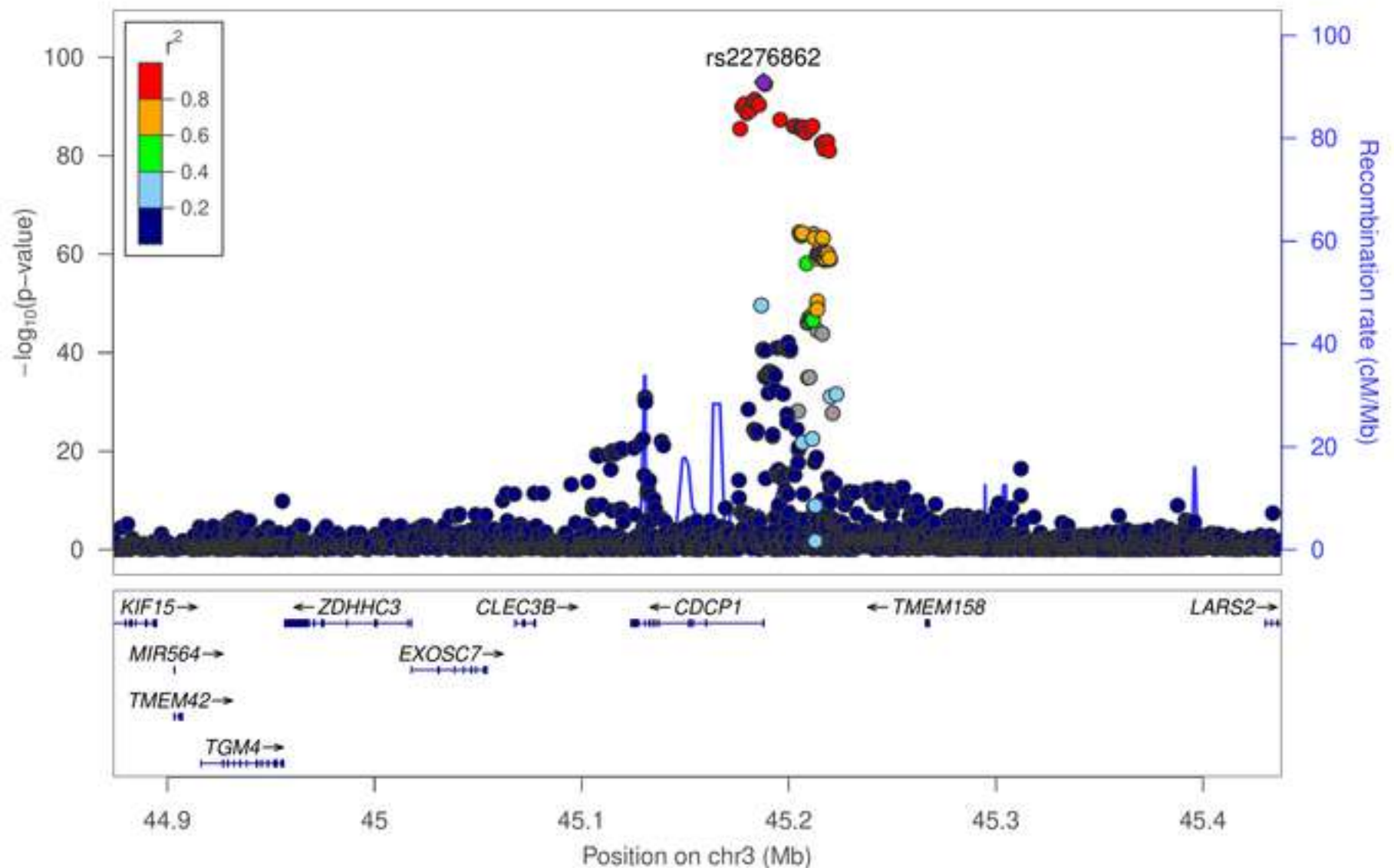
SCALLOP: CD6 (CD6)-rs2074227



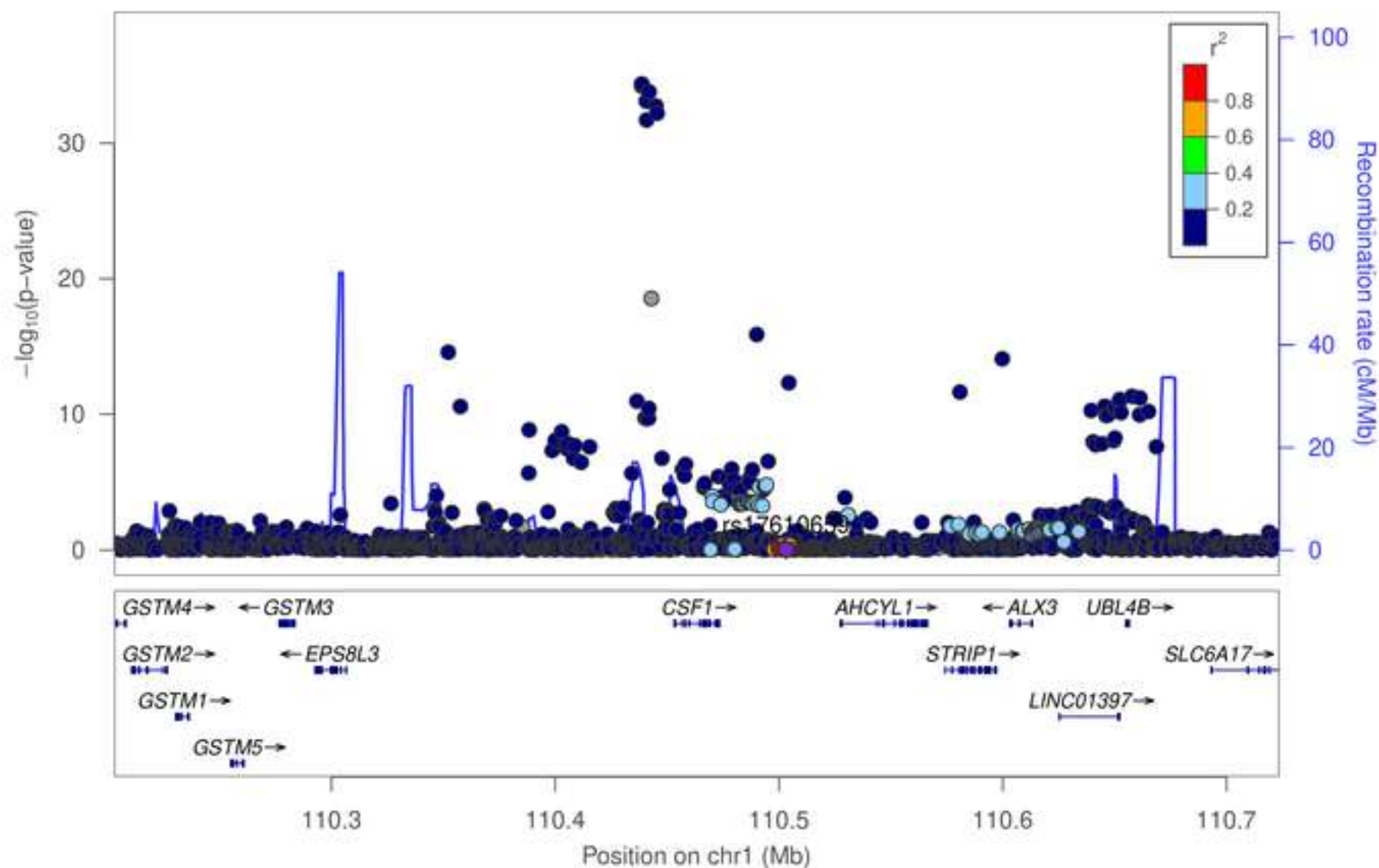
eQTLGen: CDCP1 (CDCP1)-rs2276862



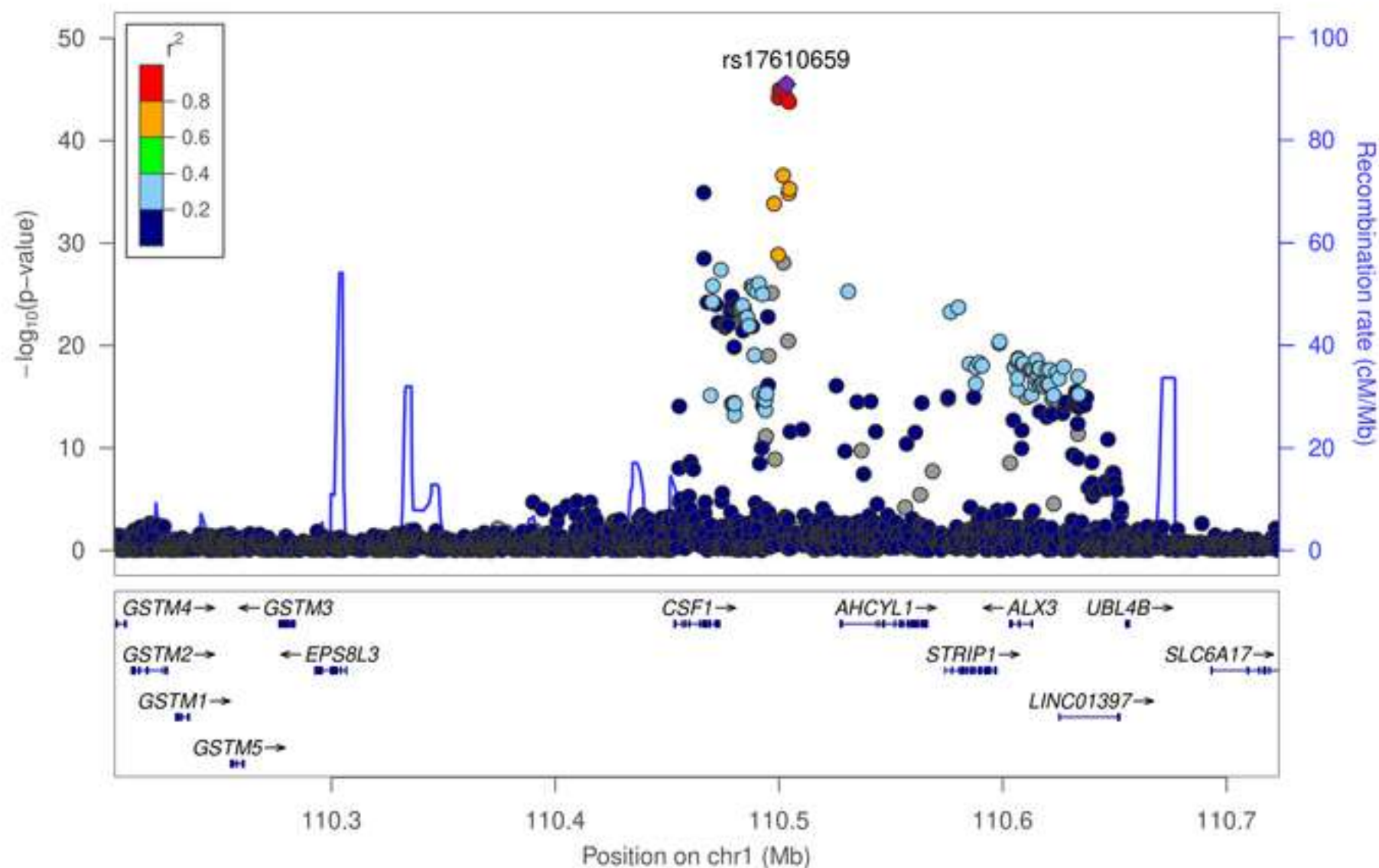
SCALLOP: CDCP1 (CDCP1)-rs2276862



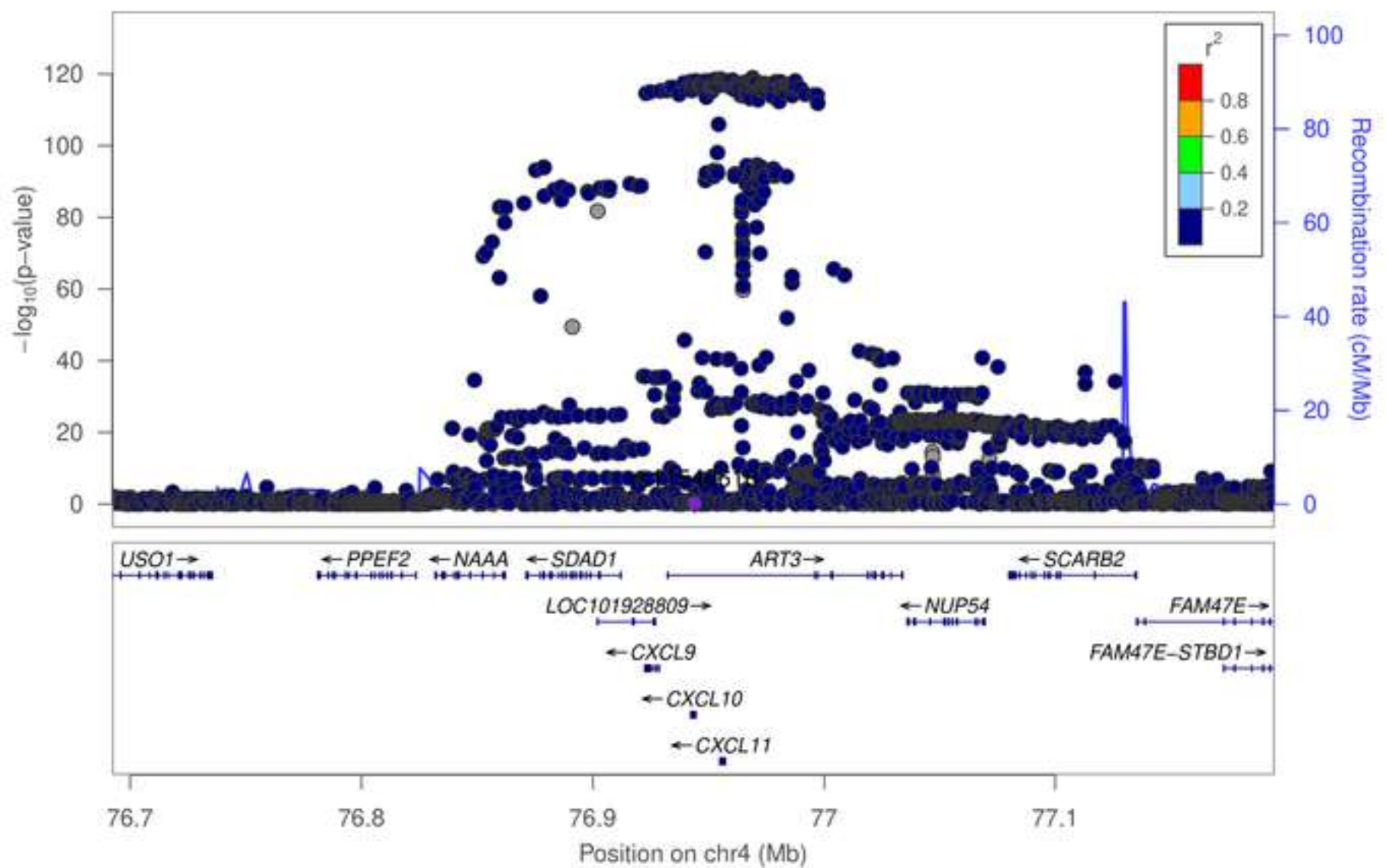
eQTLGen: CSF-1 (CSF1)-rs17610659



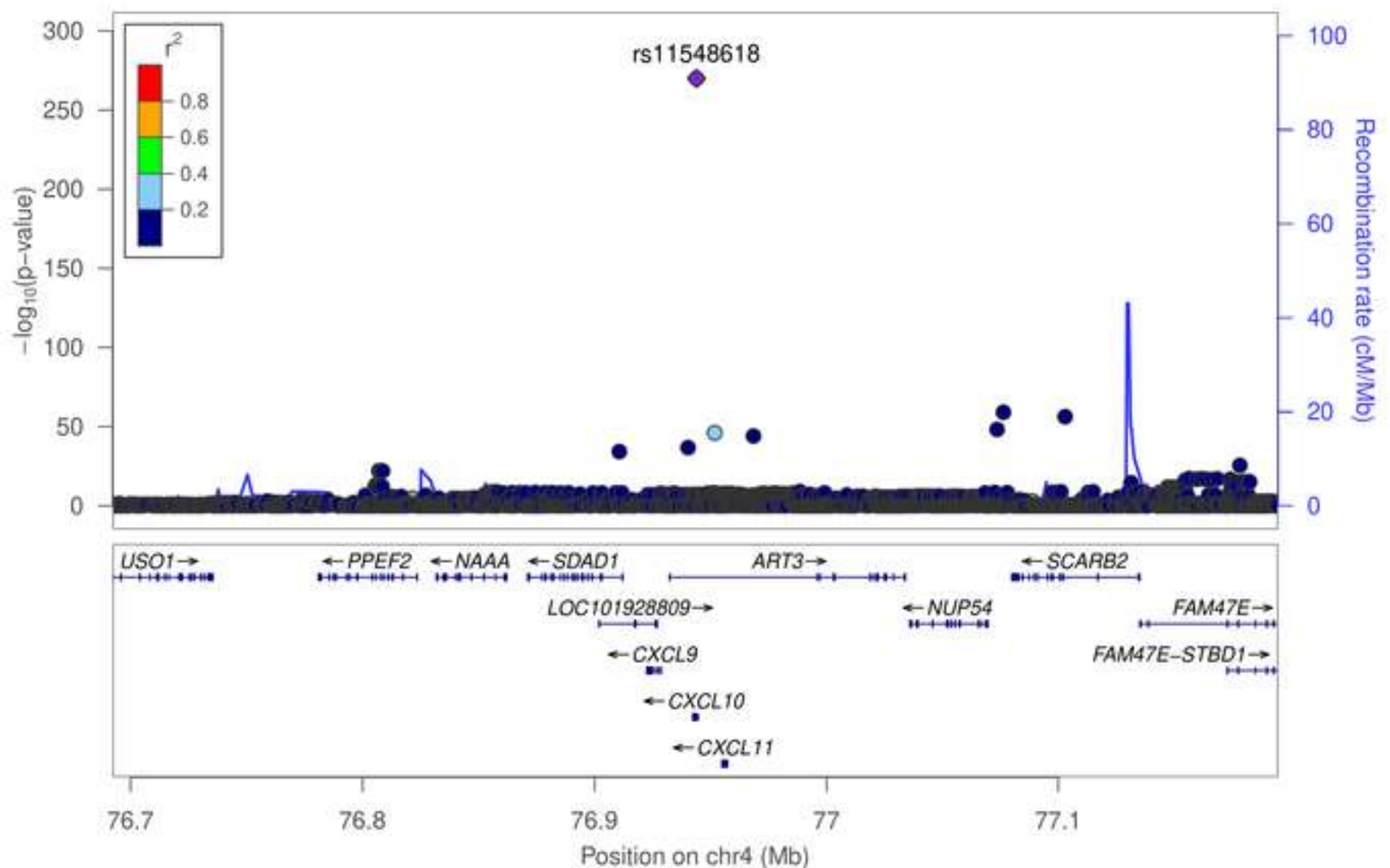
SCALLOP: CSF-1 (CSF1)-rs17610659



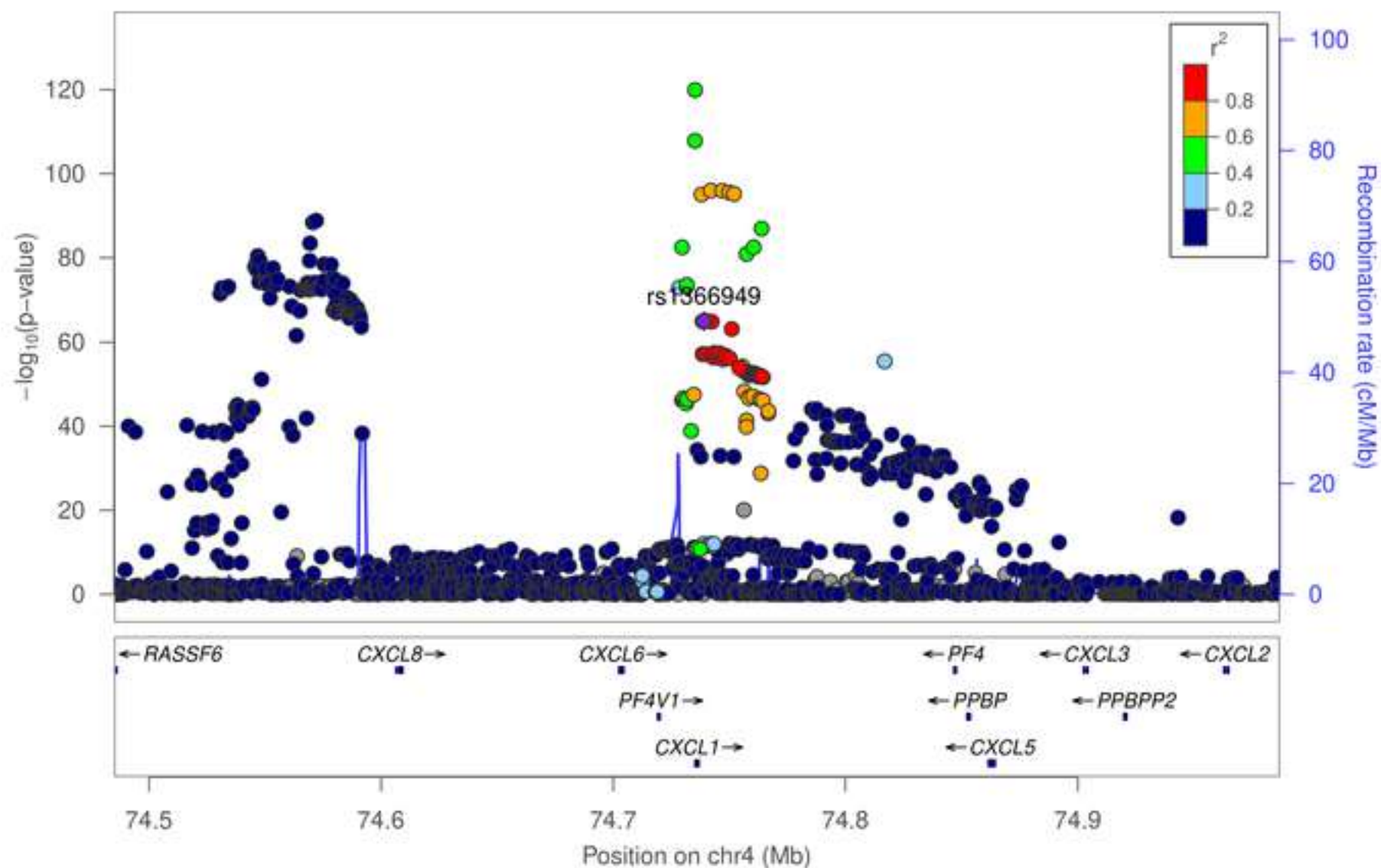
eQTLGen: CXCL10 (CXCL10)-rs11548618



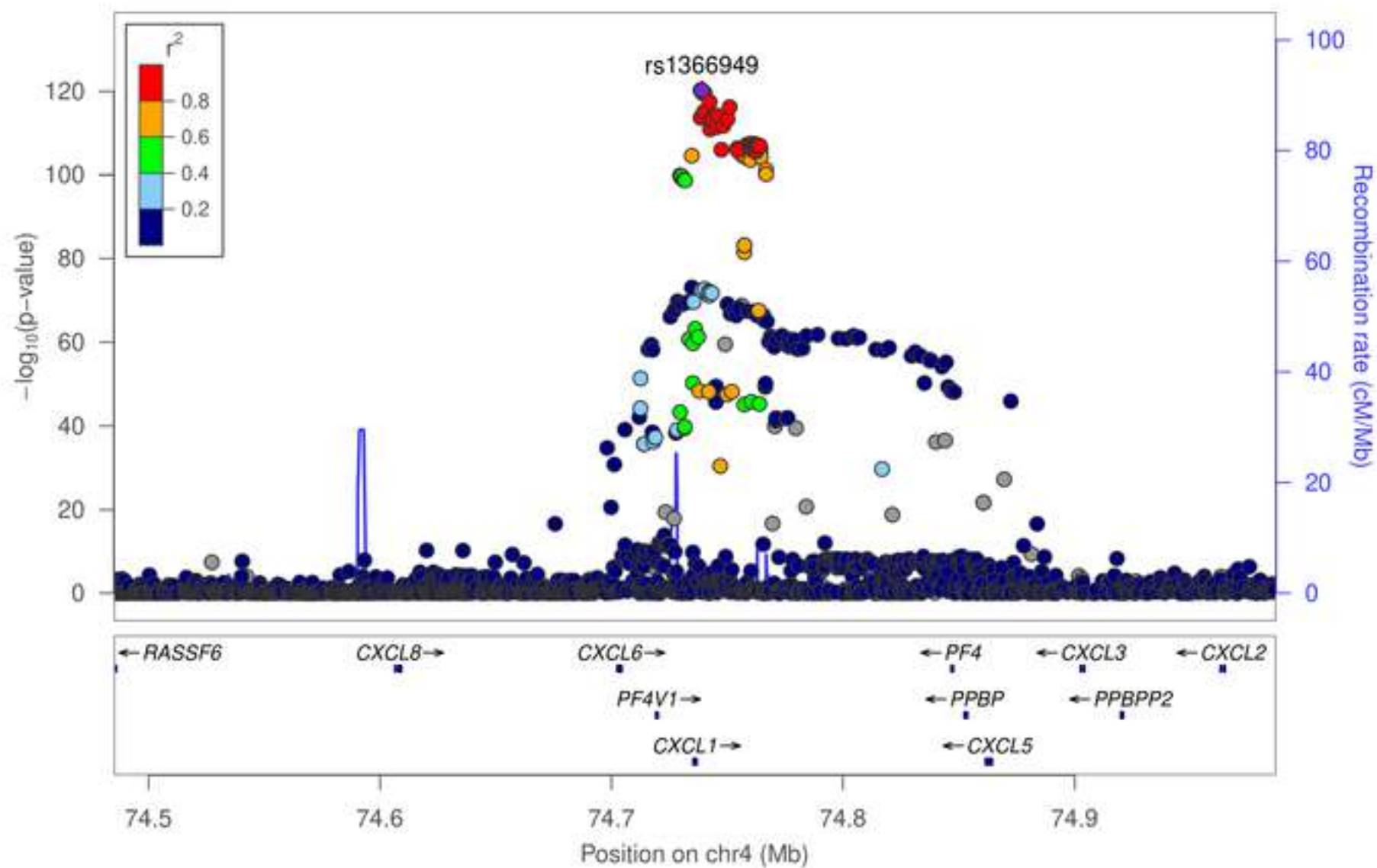
SCALLOP: CXCL10 (CXCL10)-rs11548618



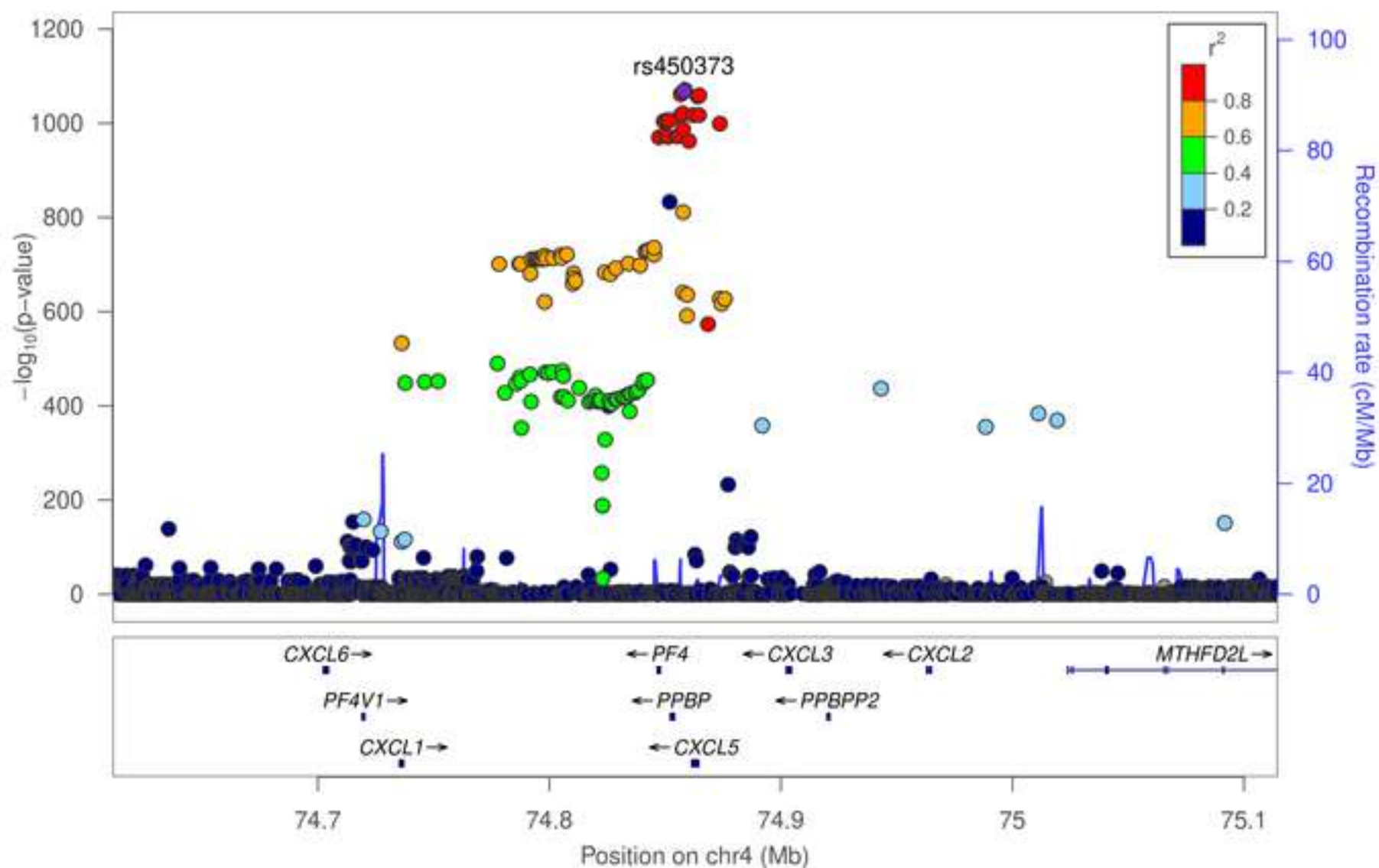
eQTLGen: CXCL1 (CXCL1)-rs1366949



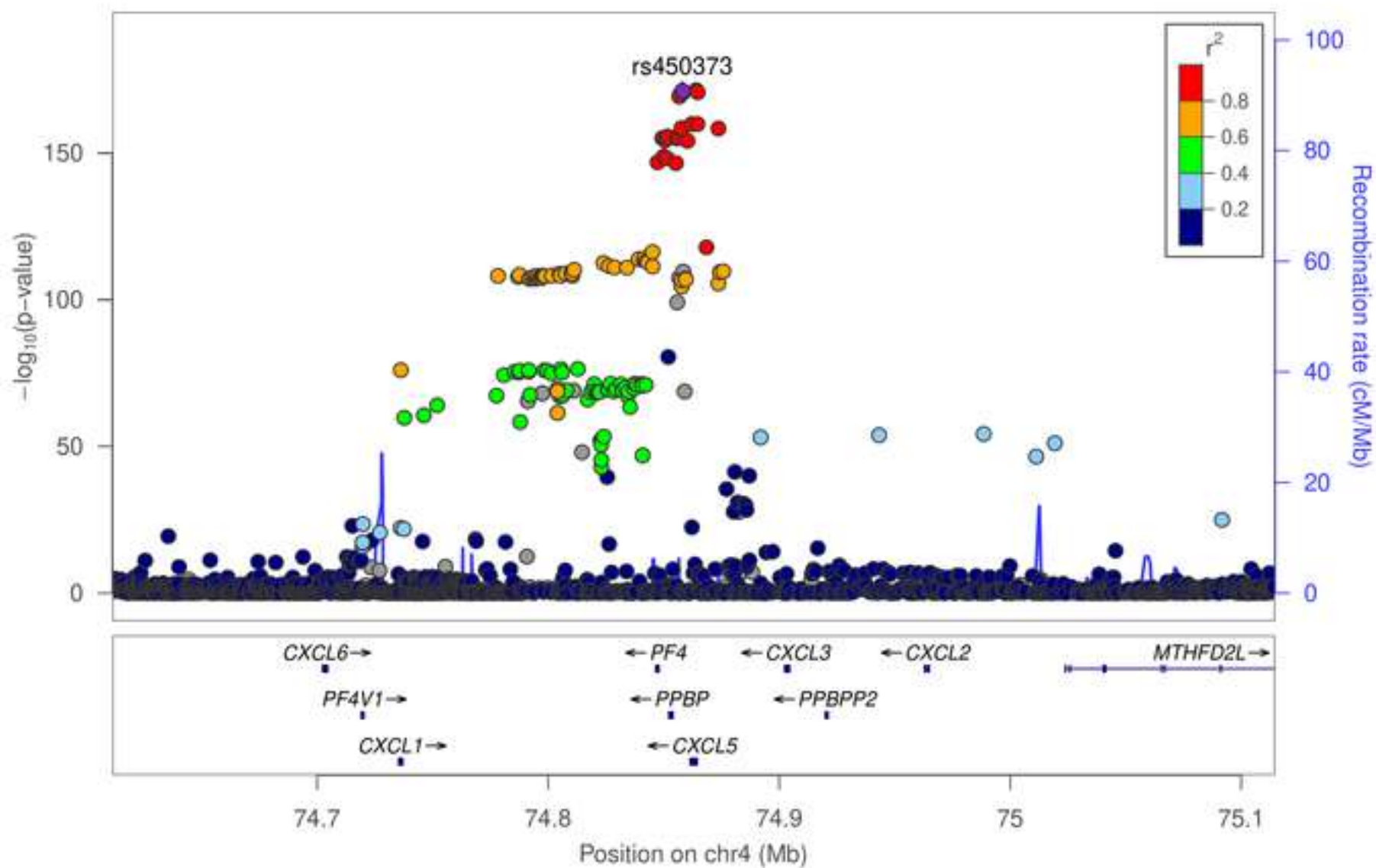
SCALLOP: CXCL1 (CXCL1)-rs1366949



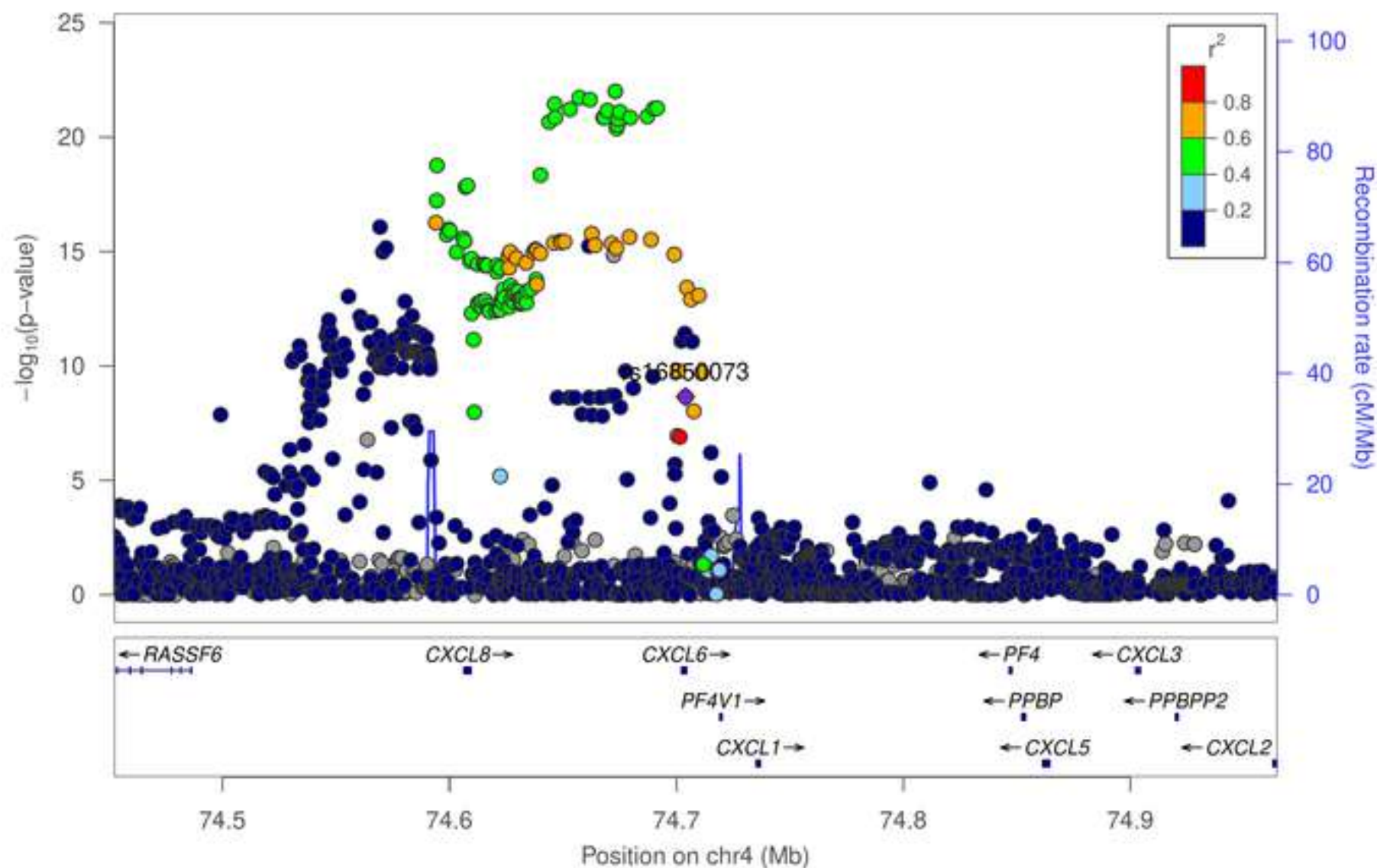
eQTLGen: CXCL5 (CXCL5)-rs450373



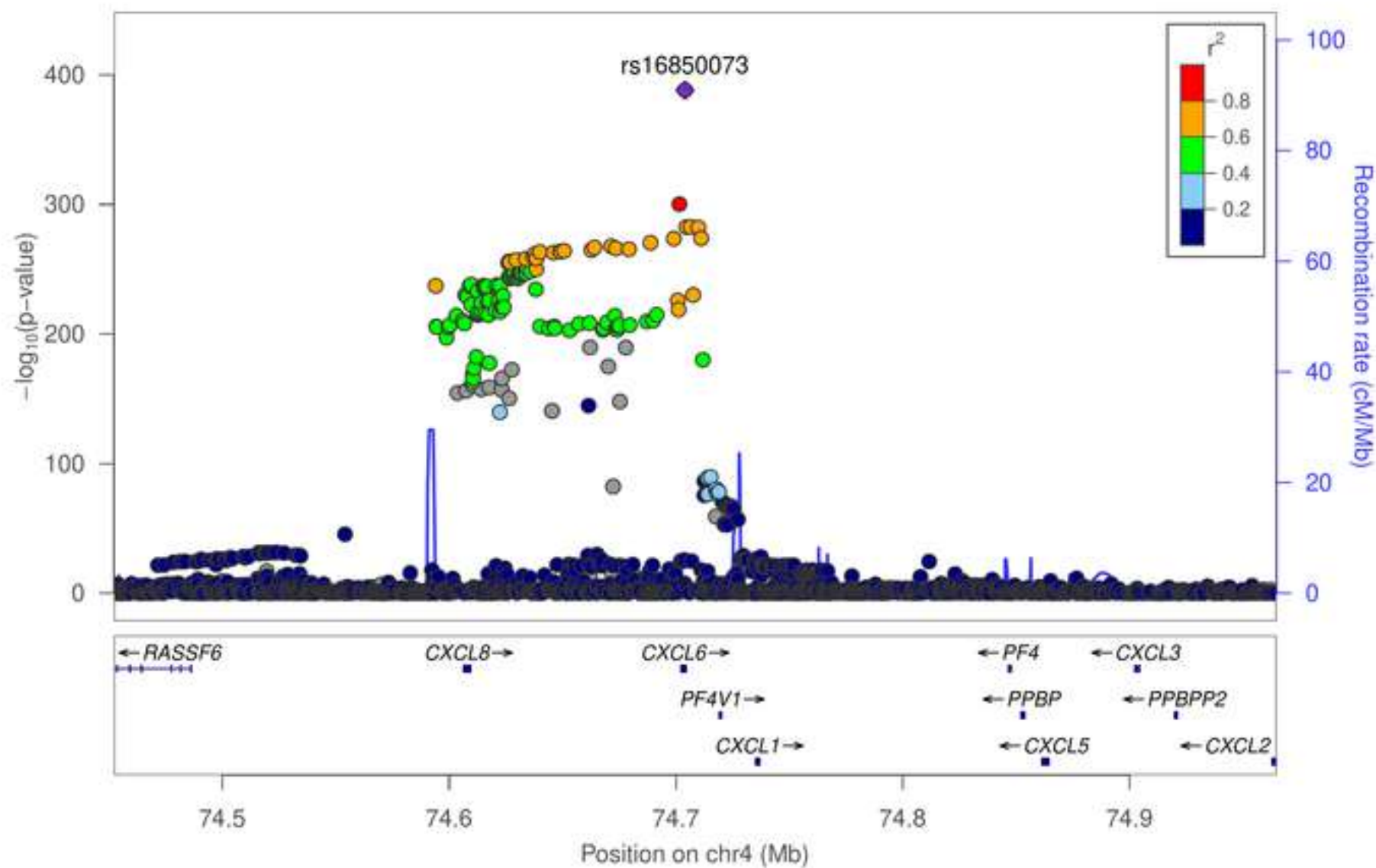
SCALLOP: CXCL5 (CXCL5)-rs450373



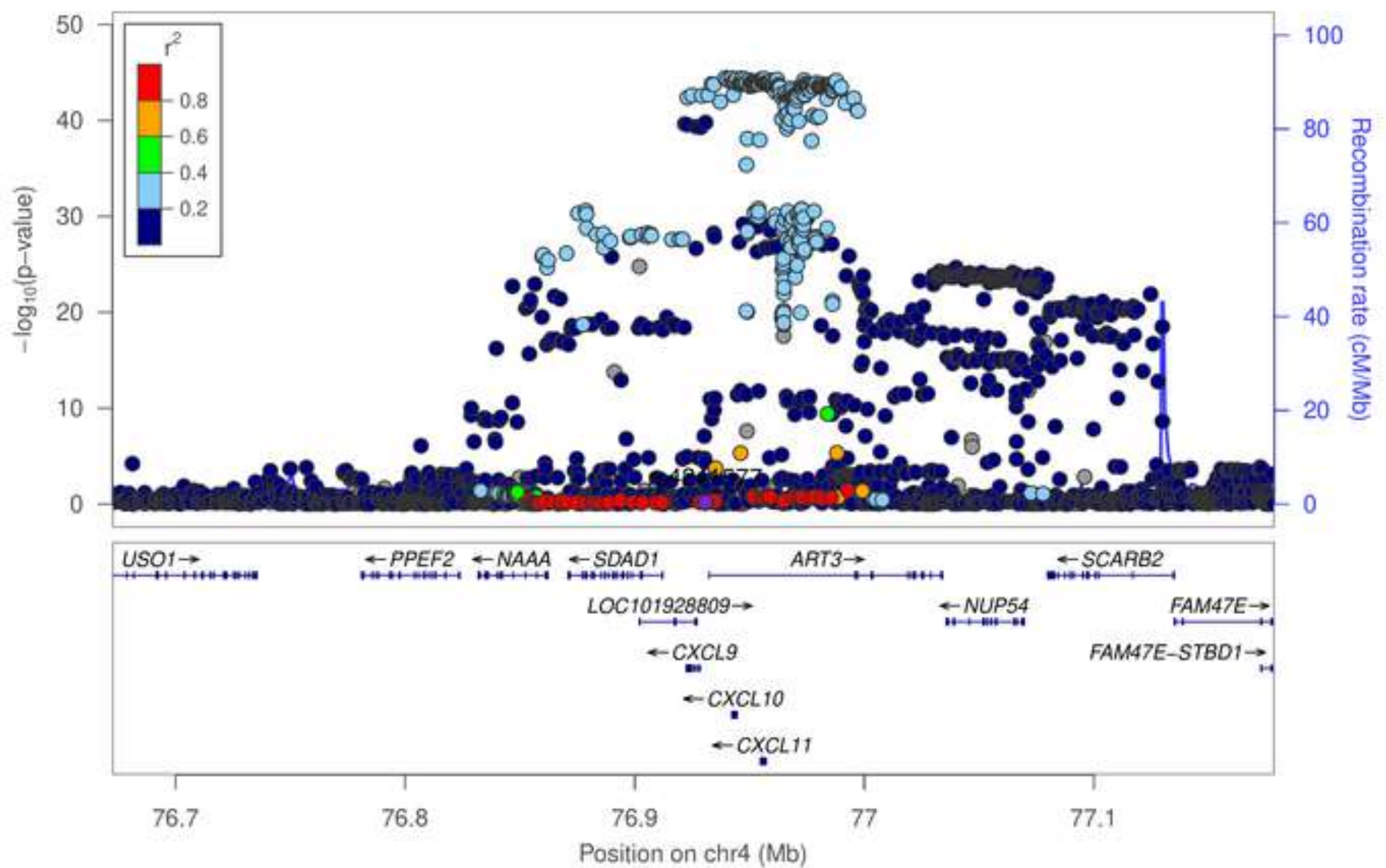
eQTLGen: CXCL6 (CXCL6)–rs16850073



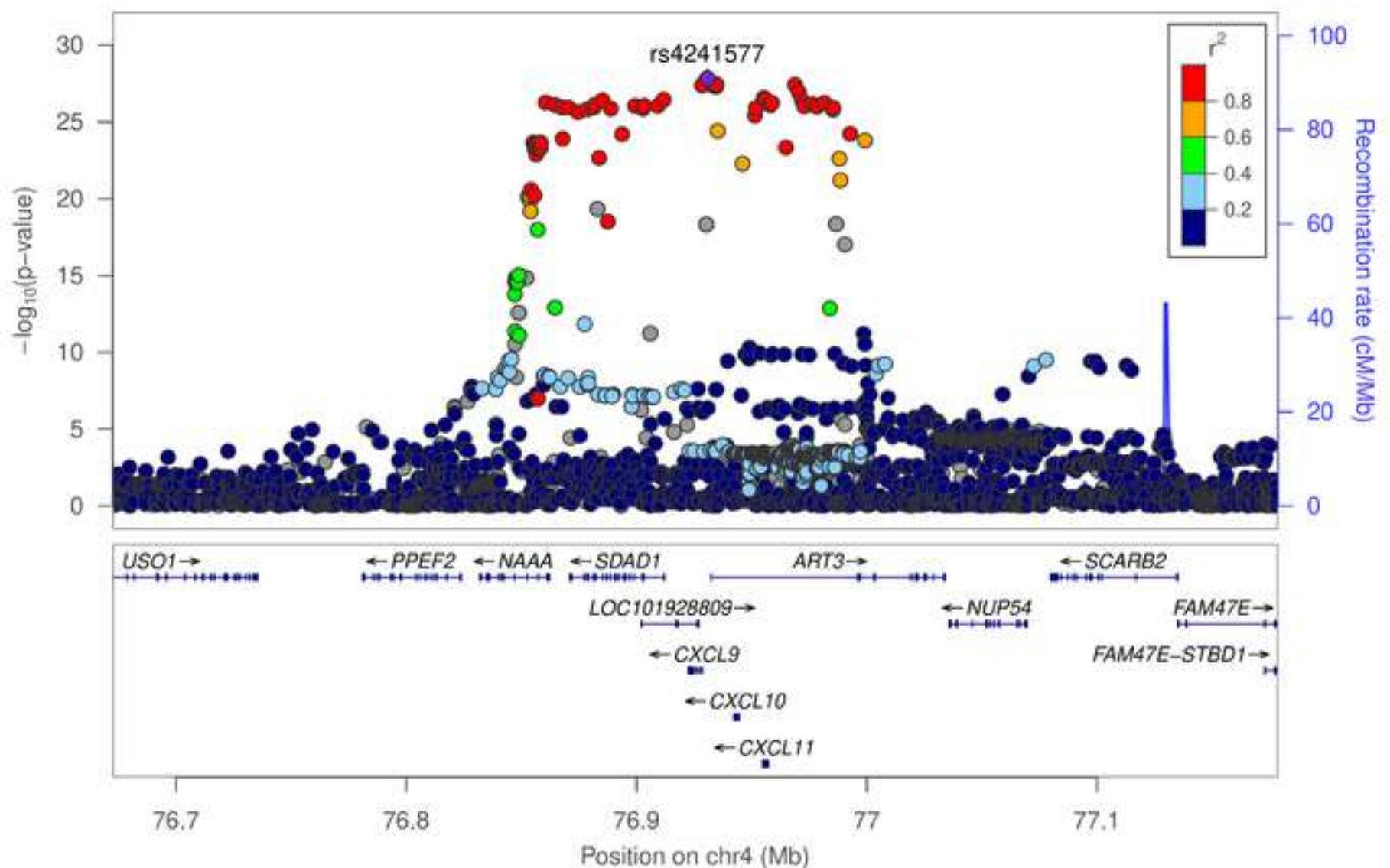
SCALLOP: CXCL6 (CXCL6)–rs16850073



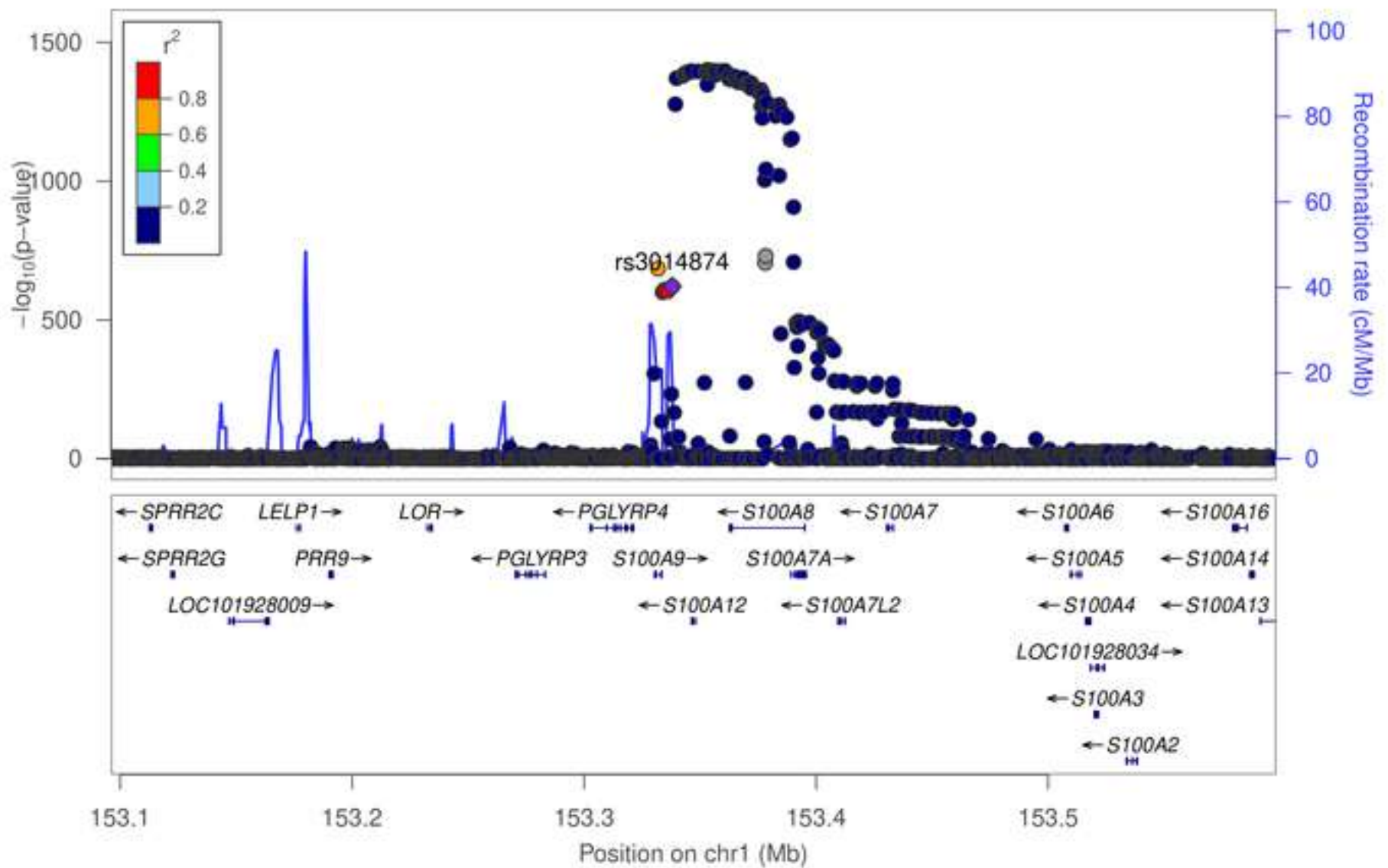
eQTLGen: CXCL9 (CXCL9)-rs4241577



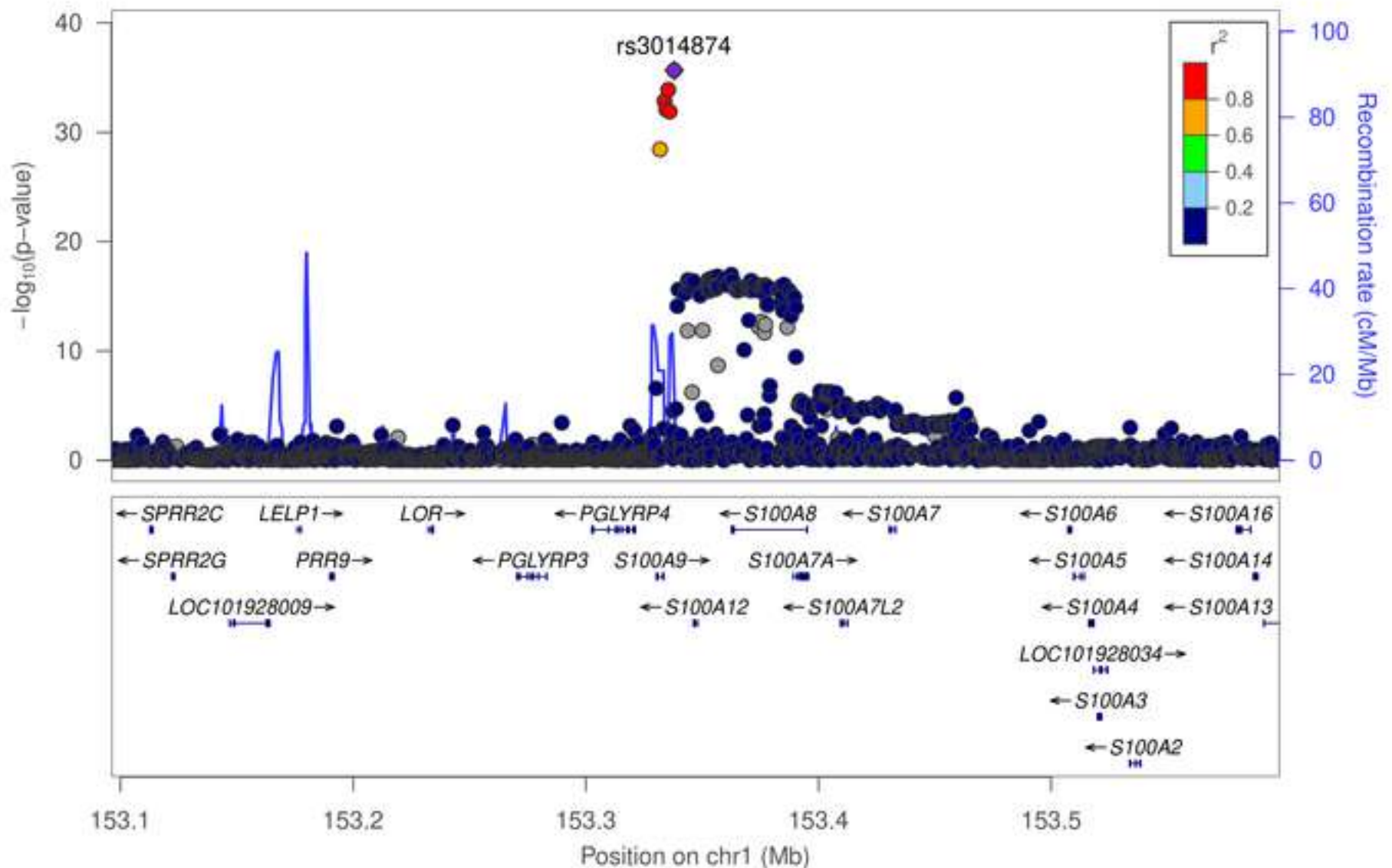
SCALLOP: CXCL9 (CXCL9)-rs4241577



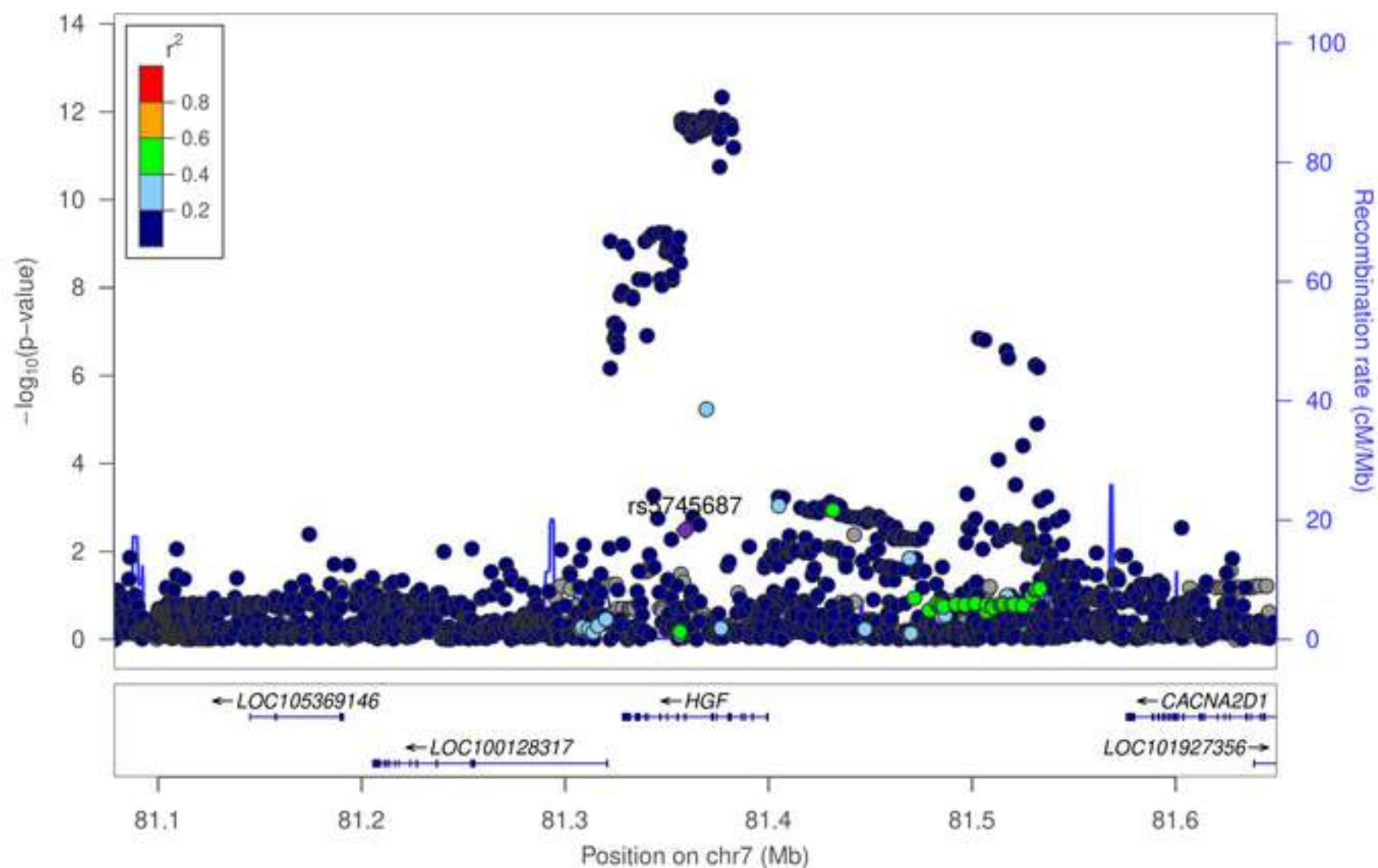
eQTLGen: EN-RAGE (S100A12)-rs3014874



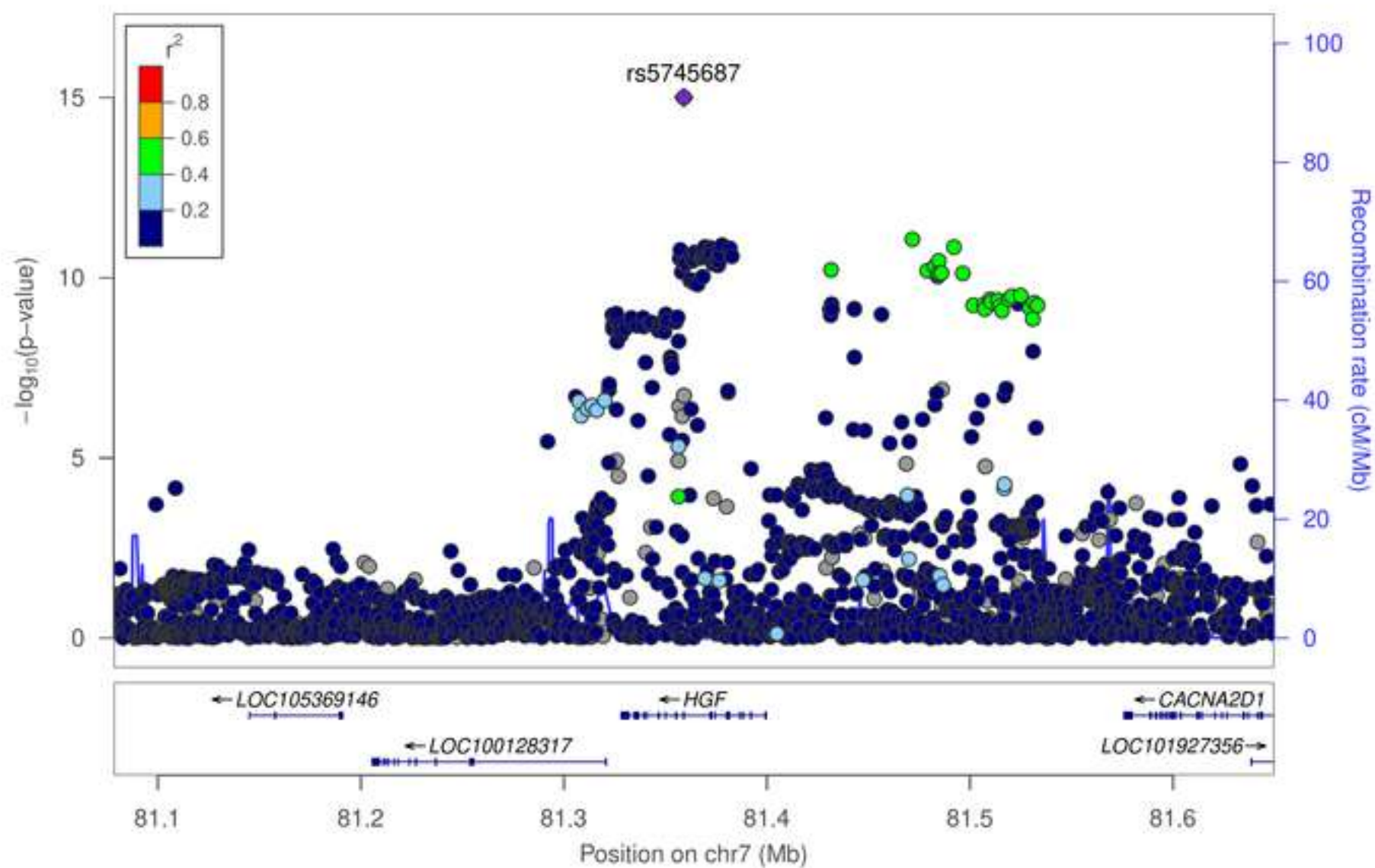
SCALLOP: EN-RAGE (S100A12)-rs3014874



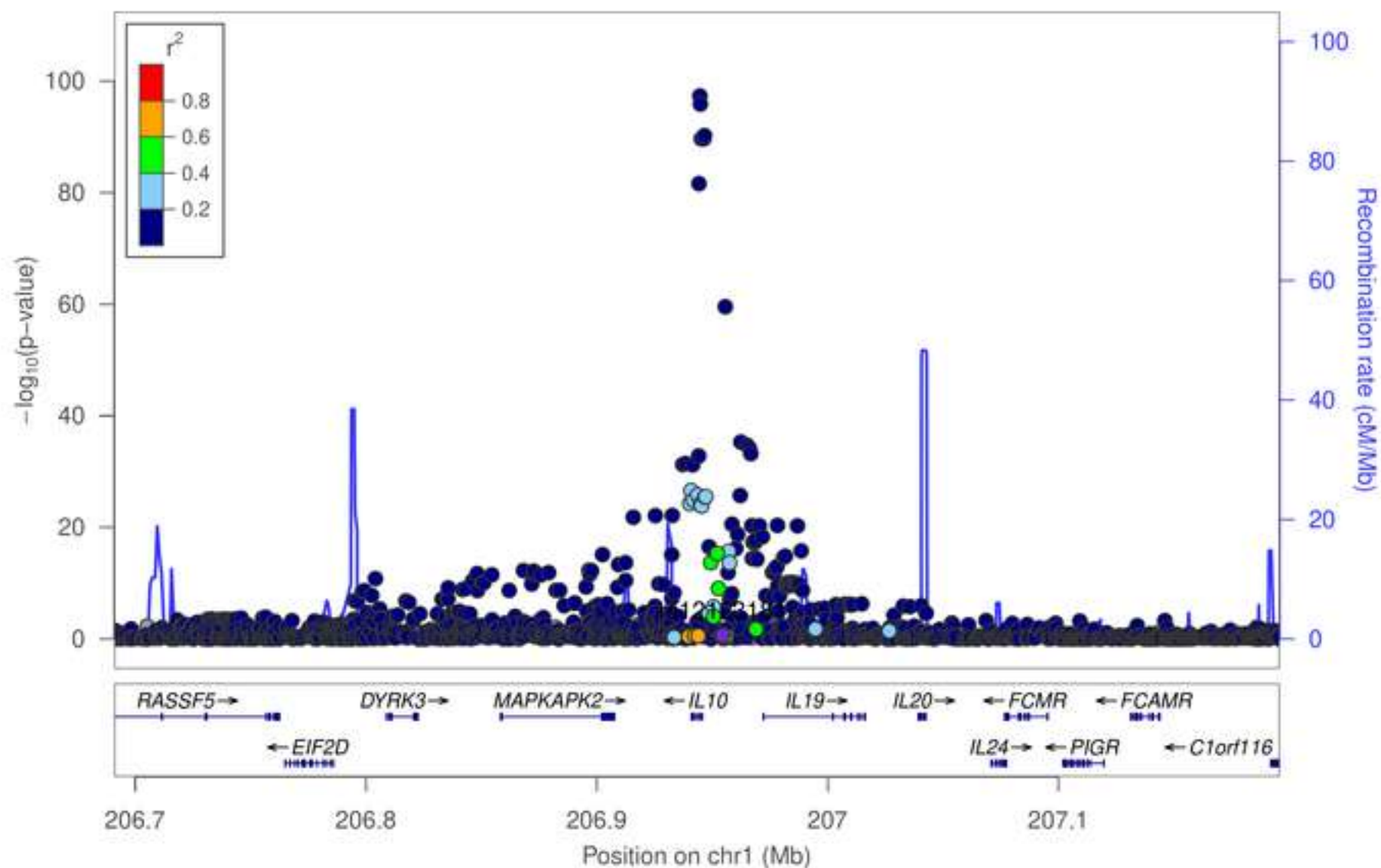
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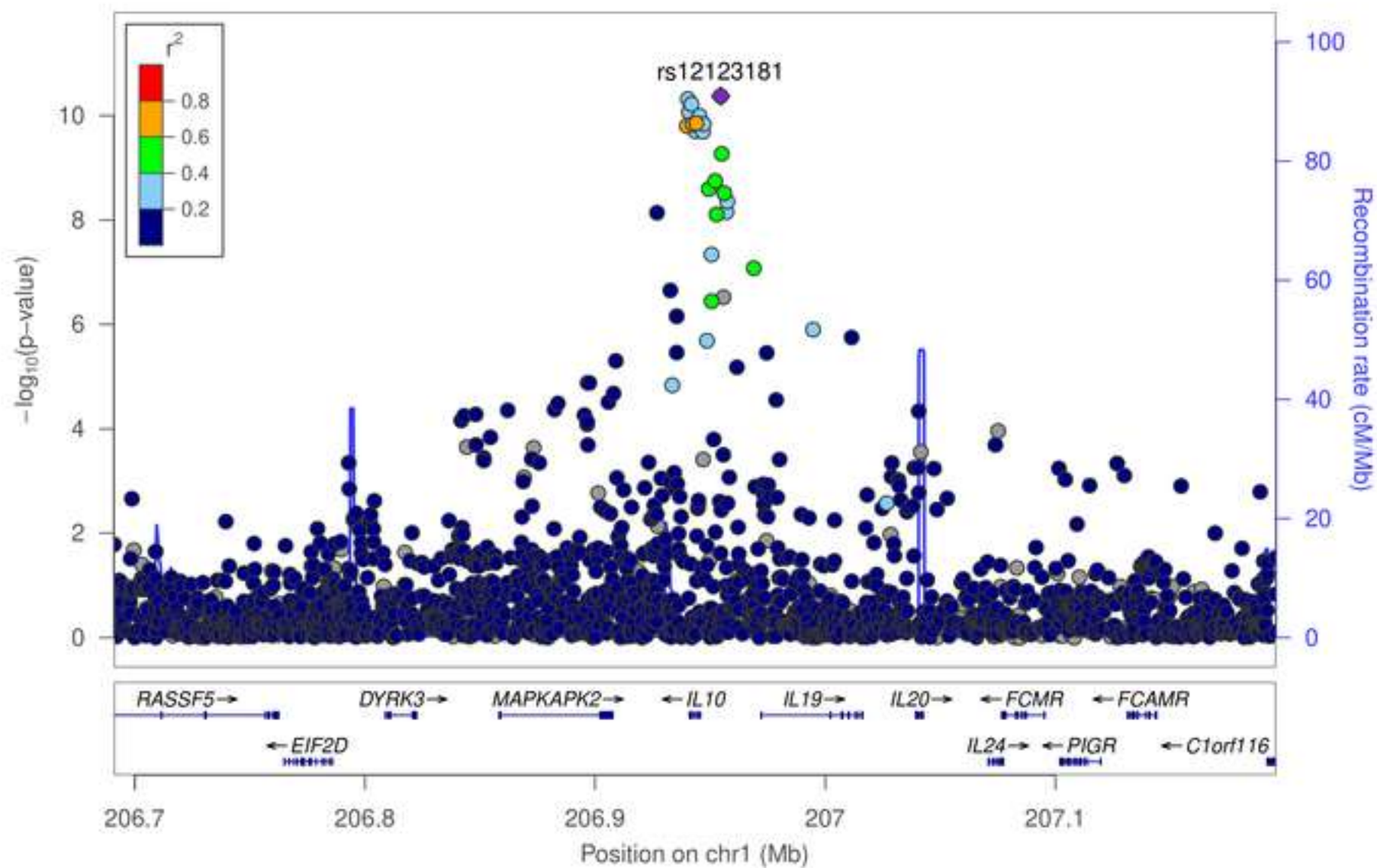
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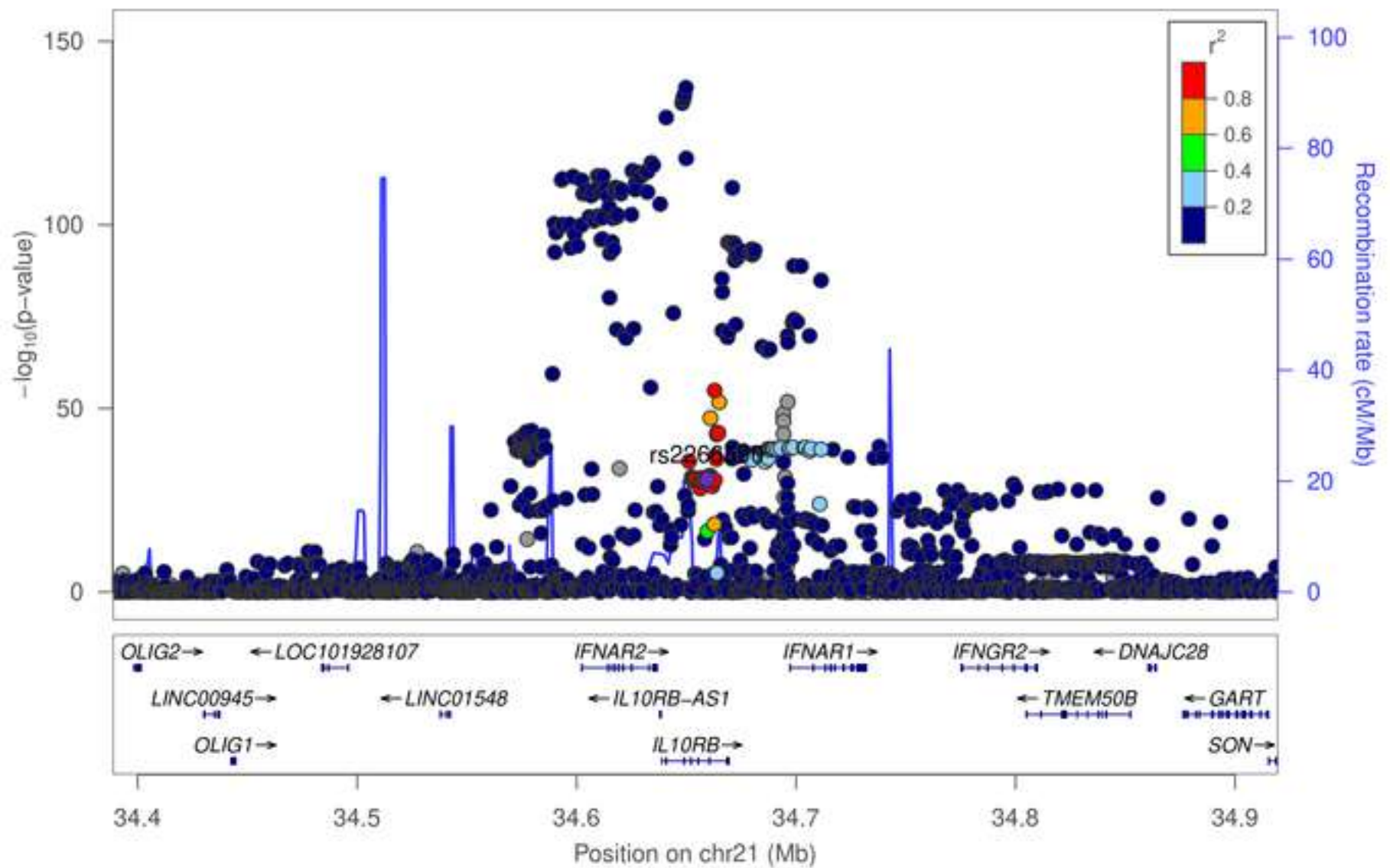
eQTLGen: IL-10 (IL10)-rs12123181



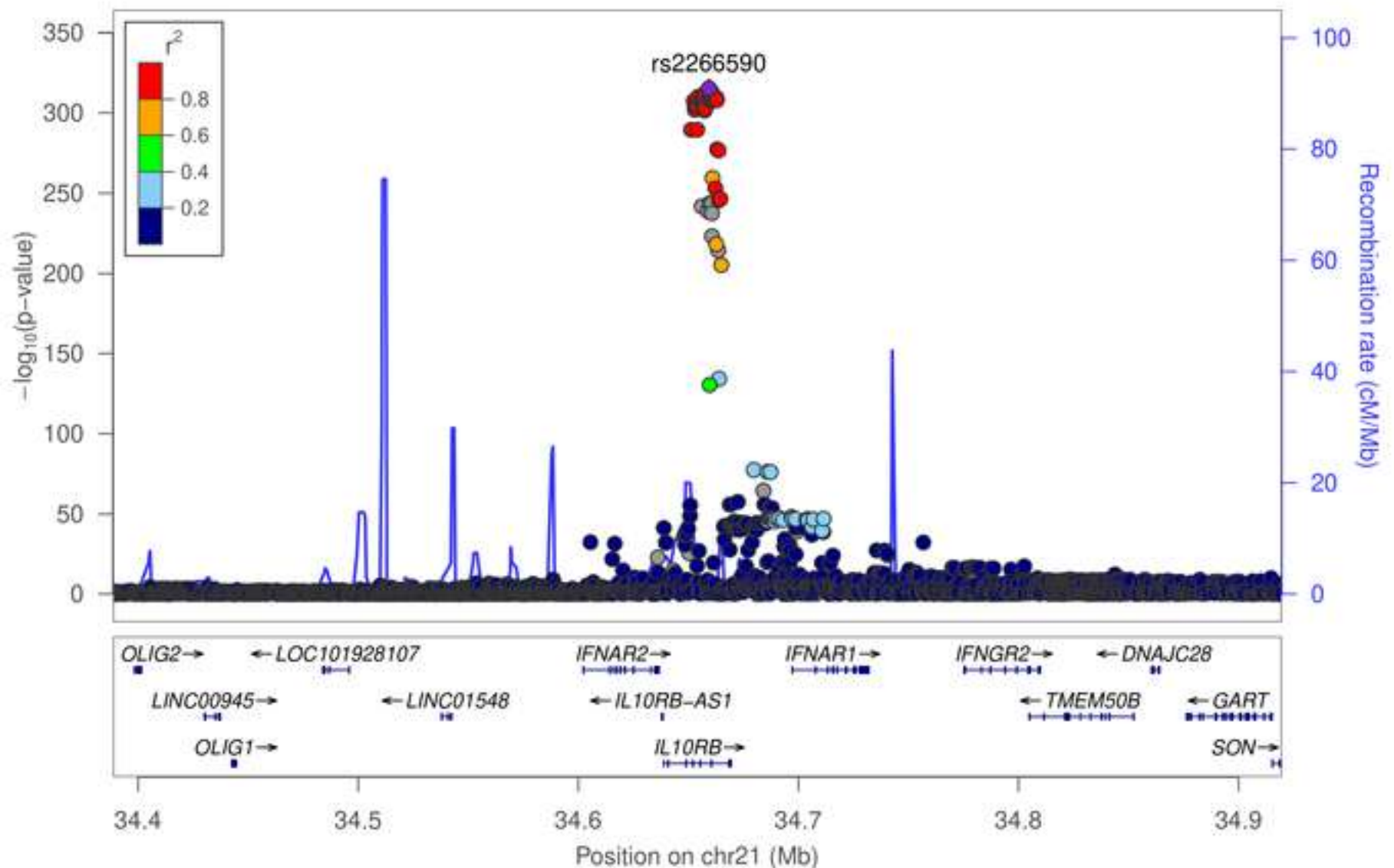
SCALLOP: IL-10 (IL10)-rs12123181



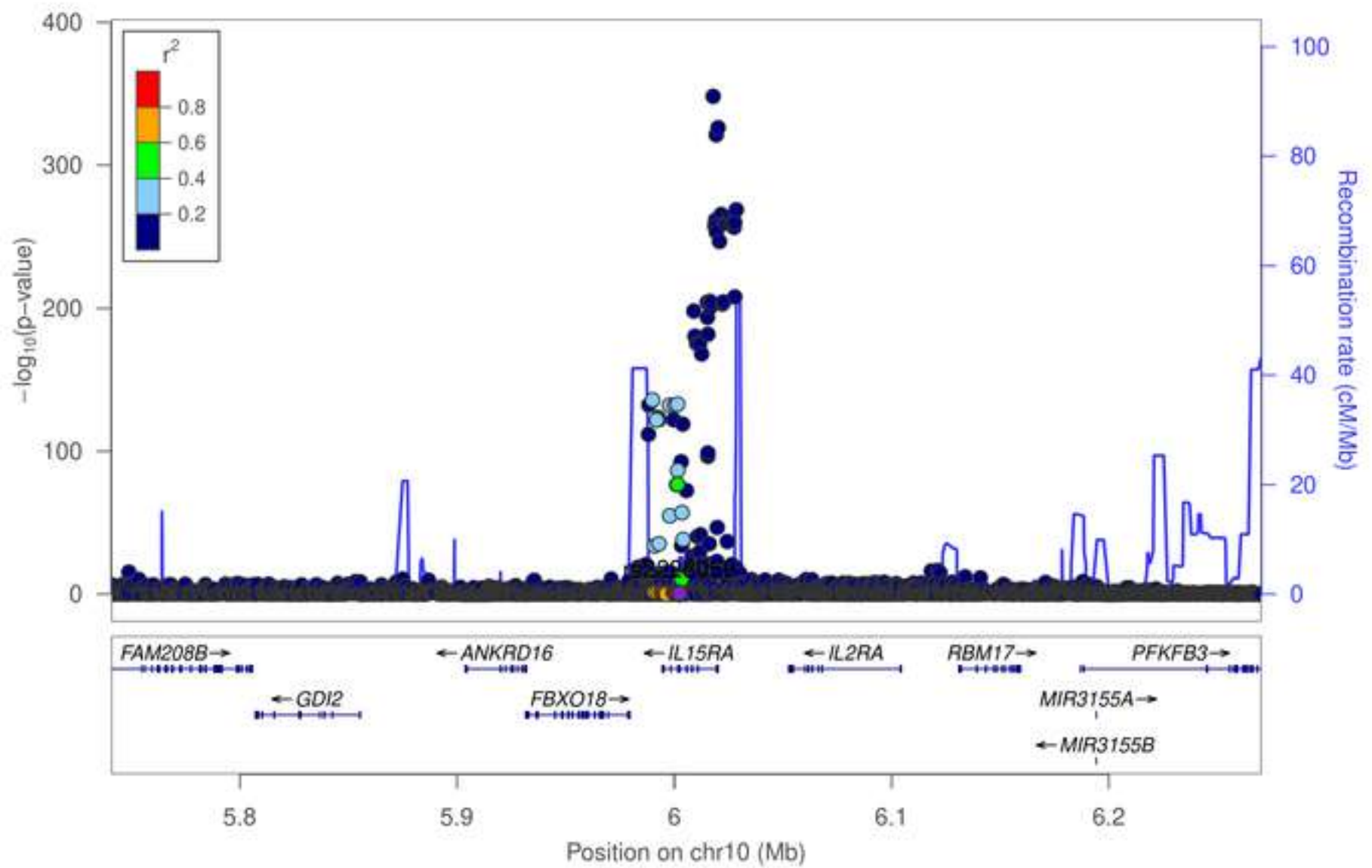
eQTLGen: IL10RB (IL10RB)-rs2266590



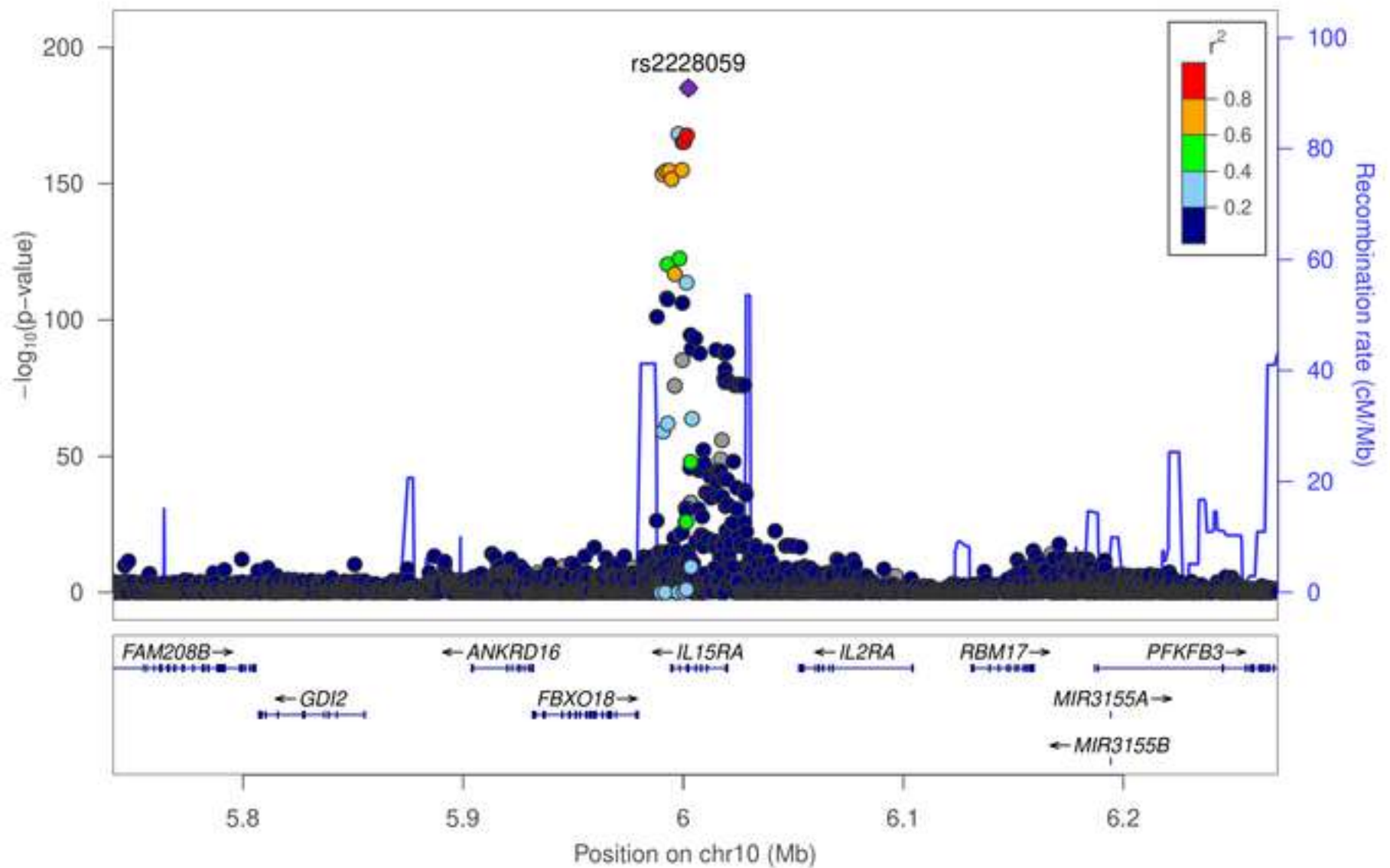
SCALLOP: IL10RB (IL10RB)-rs2266590



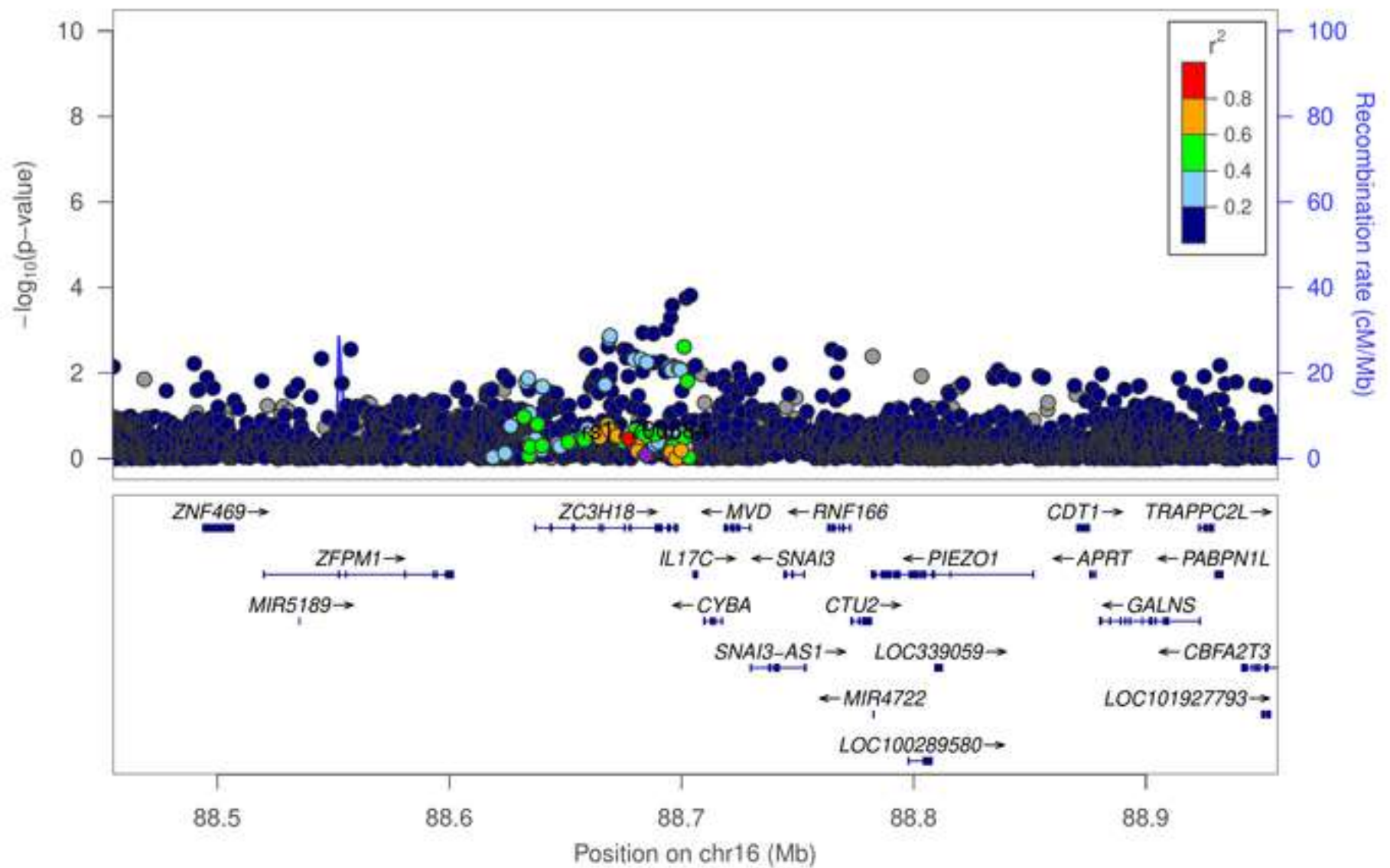
eQTLGen: IL-15RA (IL15RA)-rs2228059



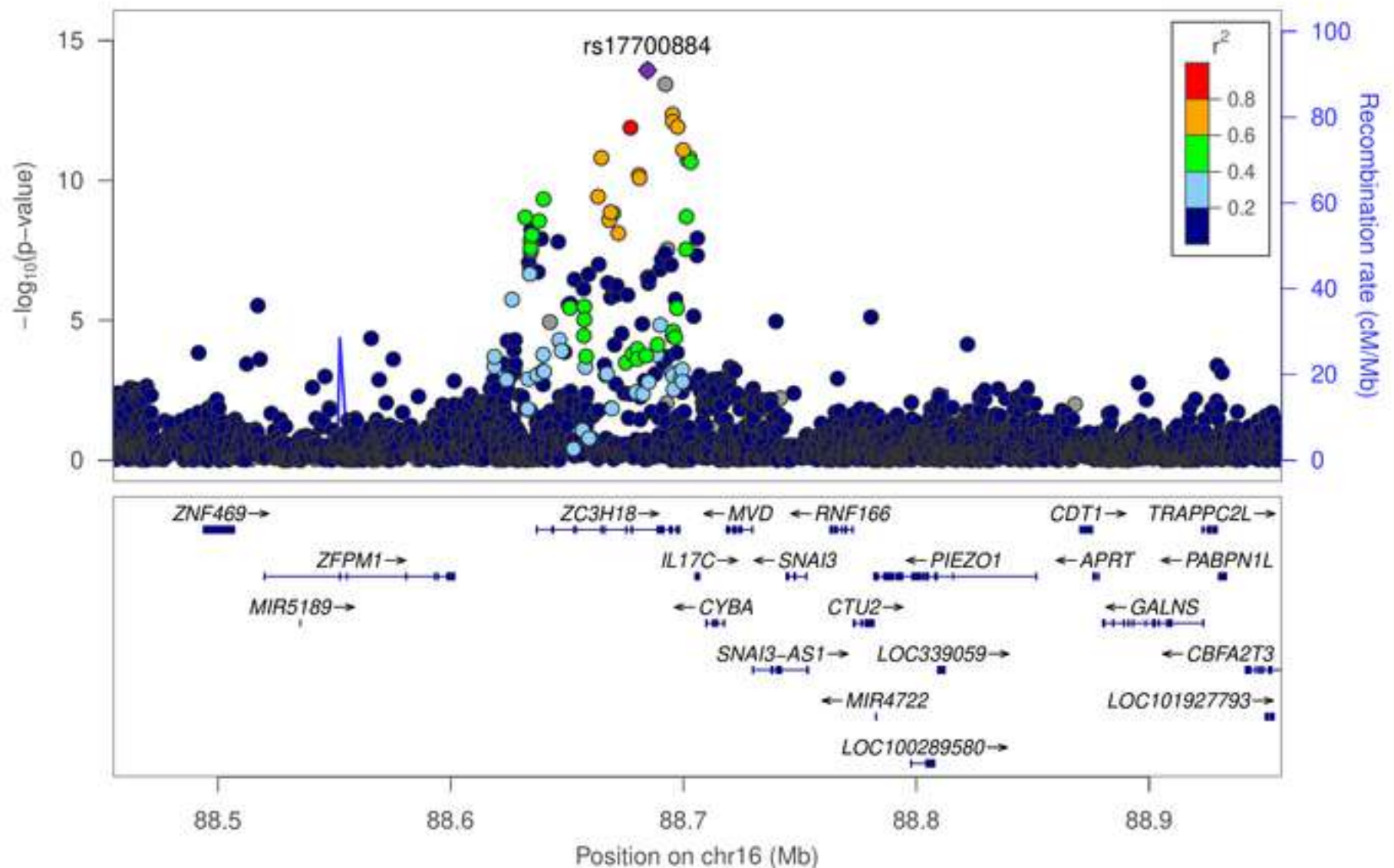
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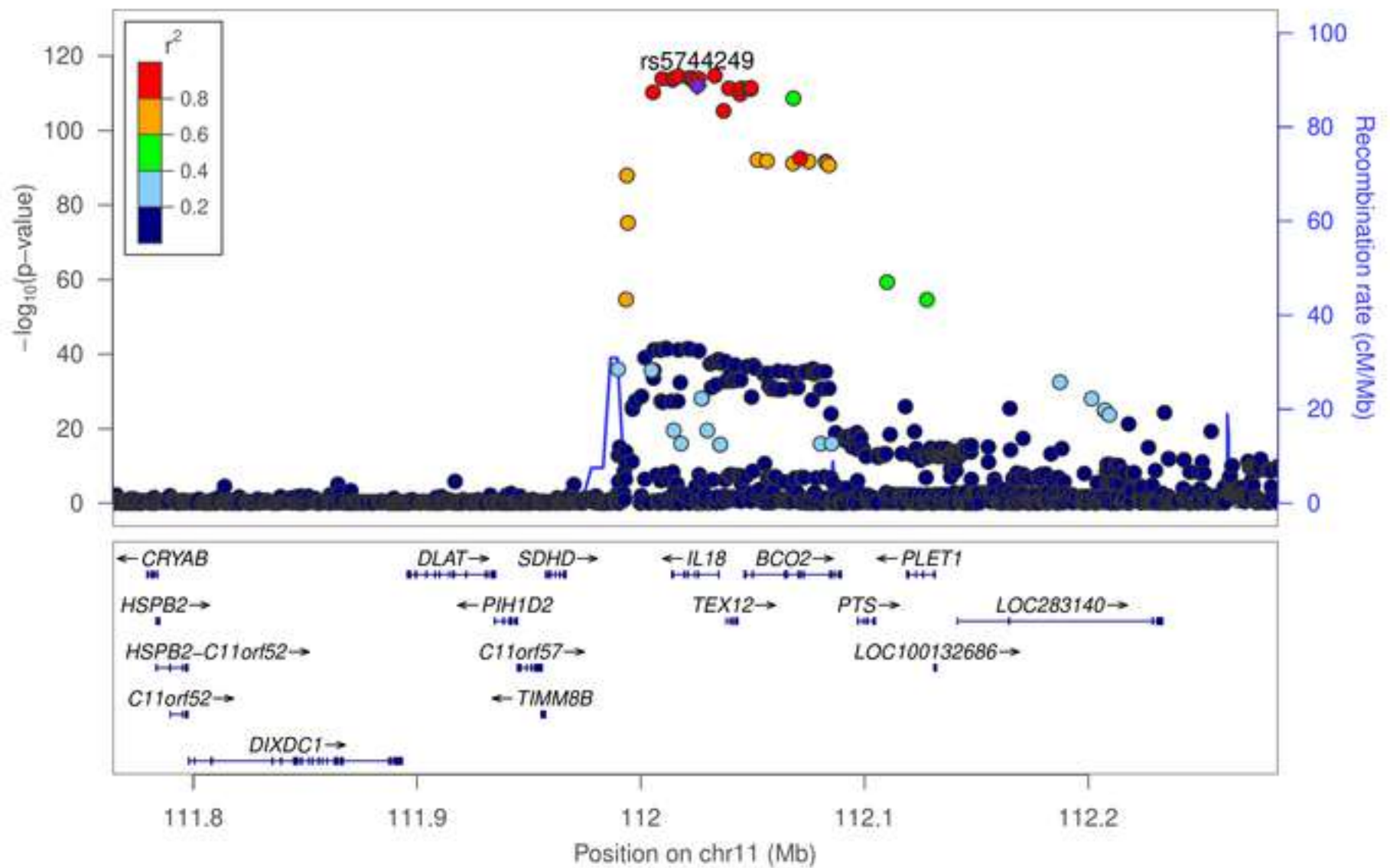
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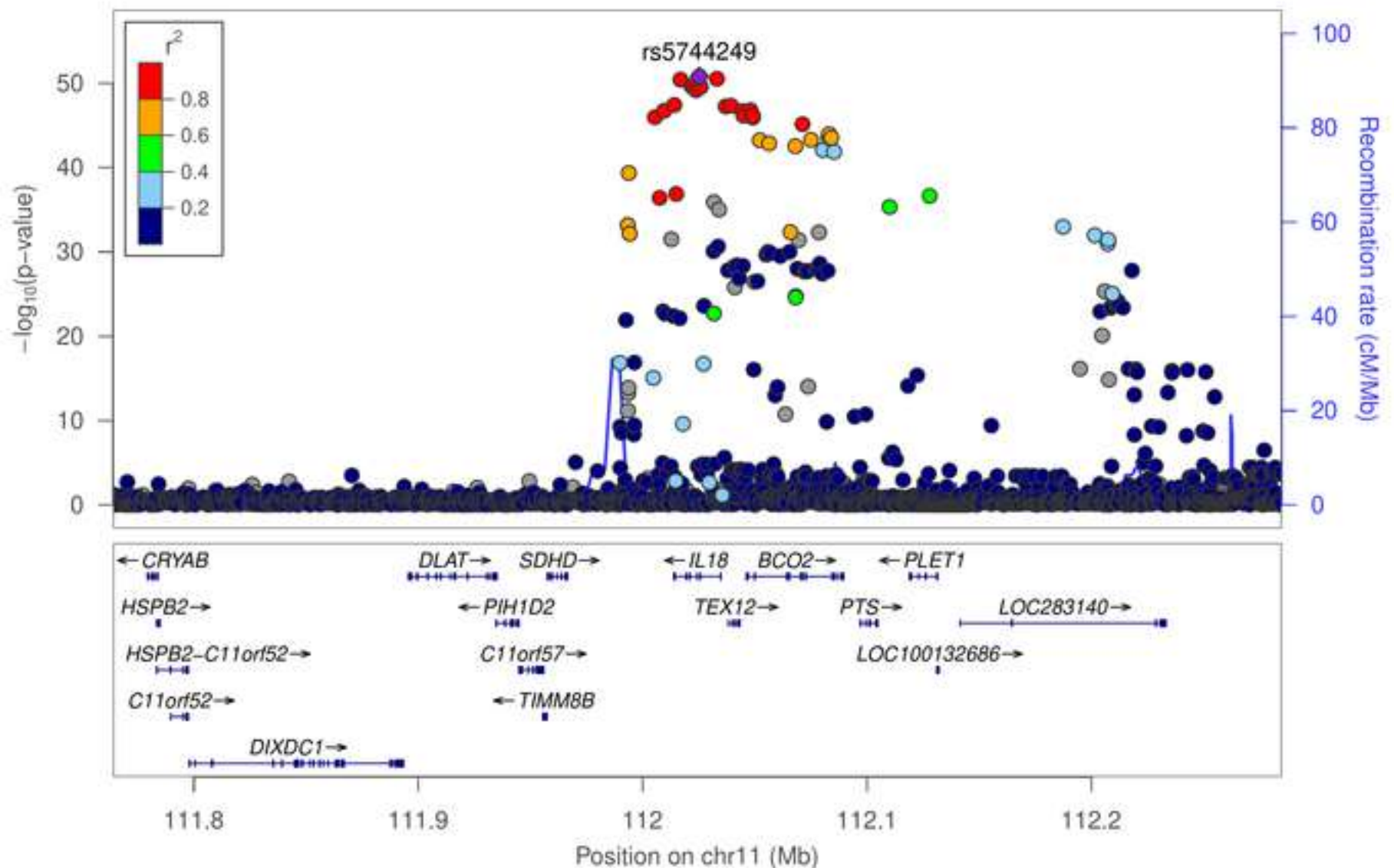
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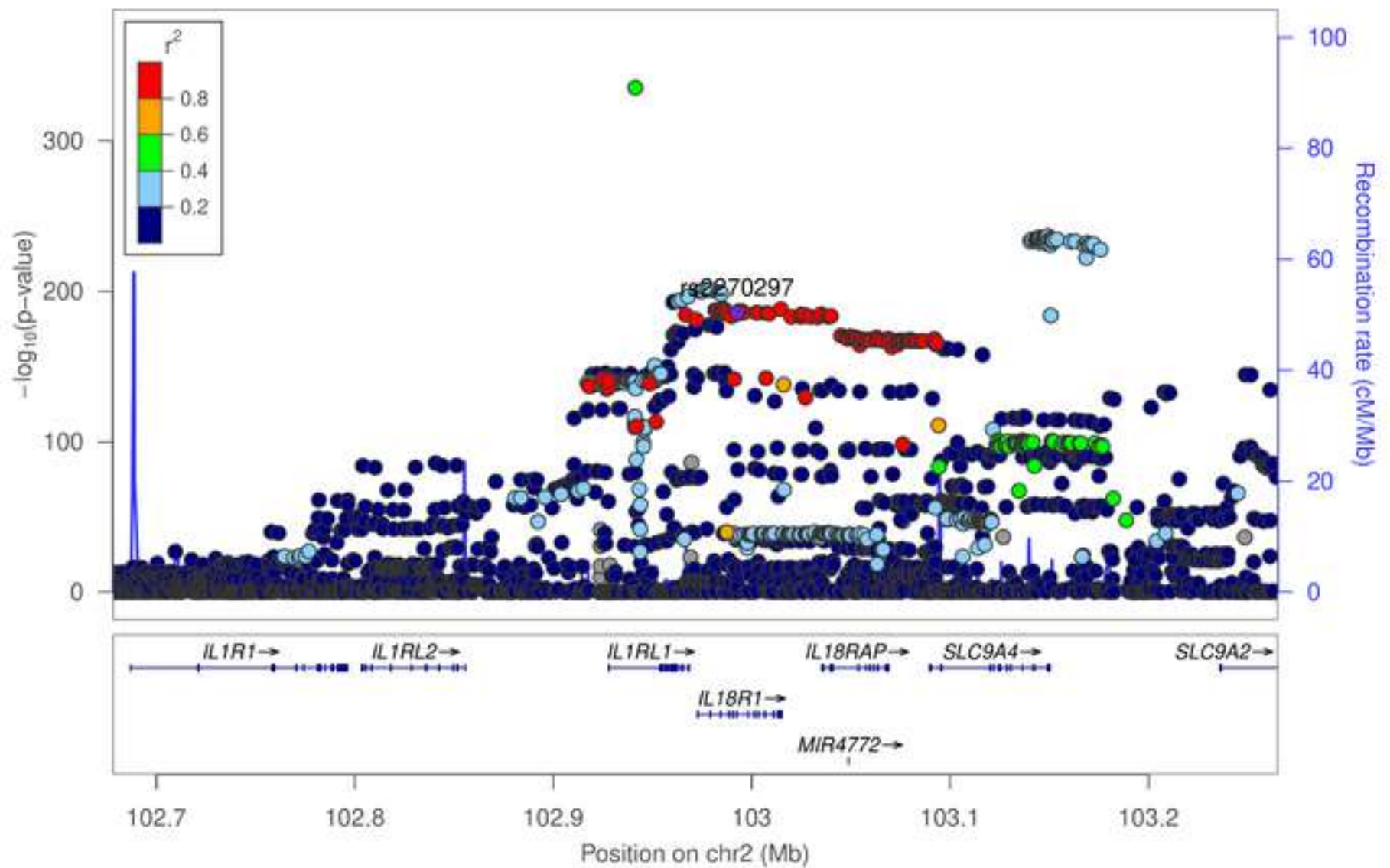
eQTLGen: IL-18 (IL18)-rs5744249



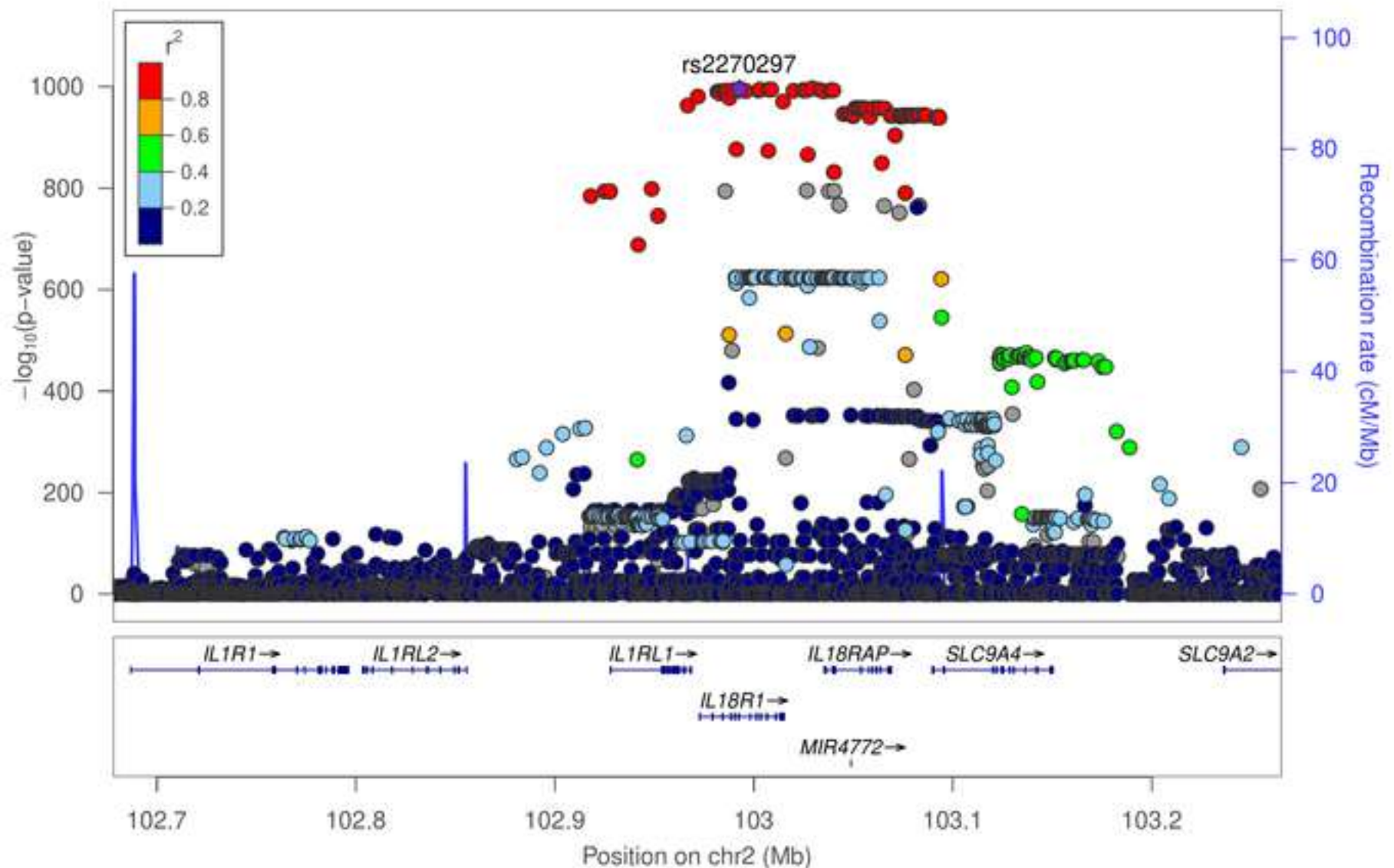
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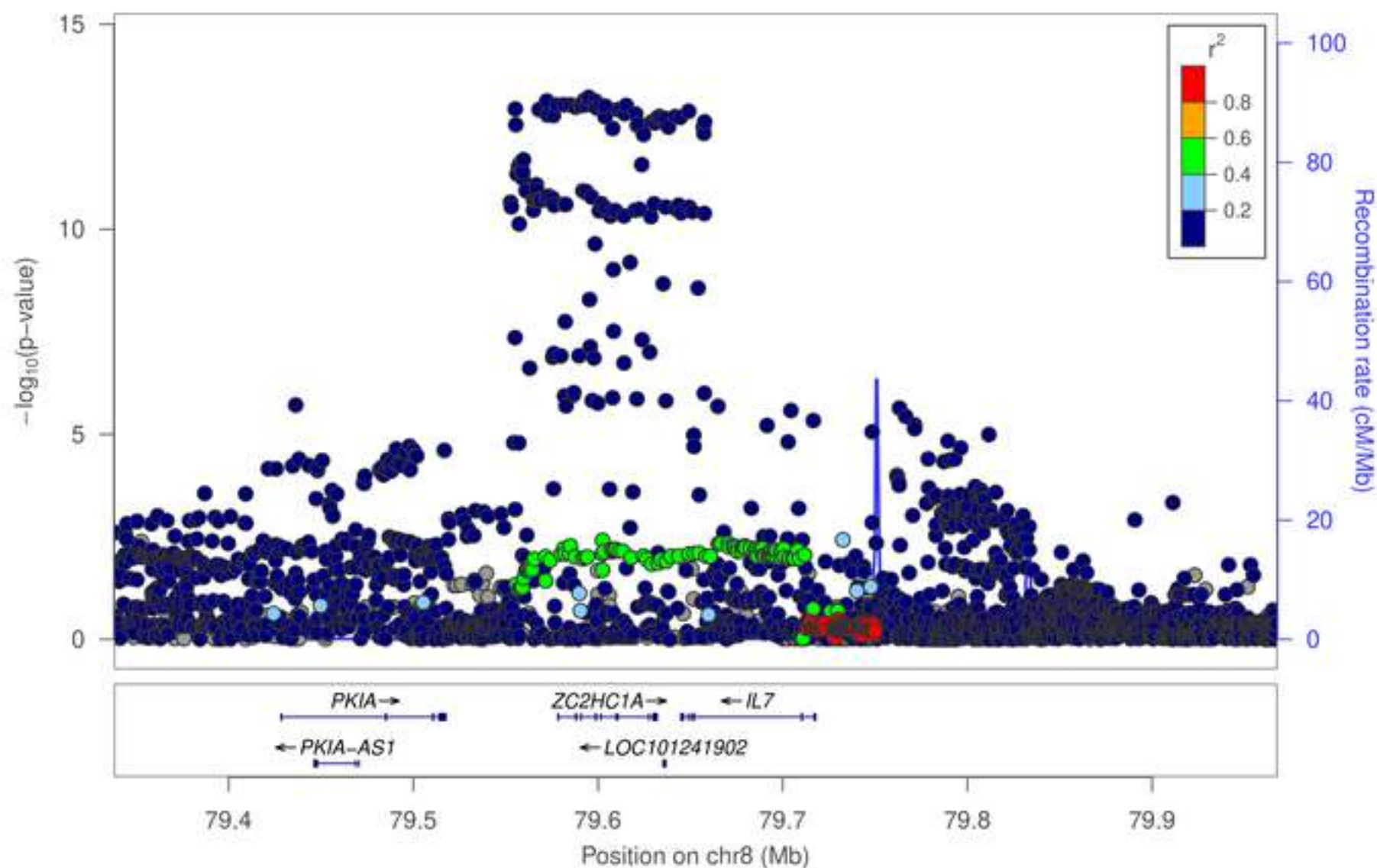
eQTLGen: IL-18R1 (IL18R1)-rs2270297



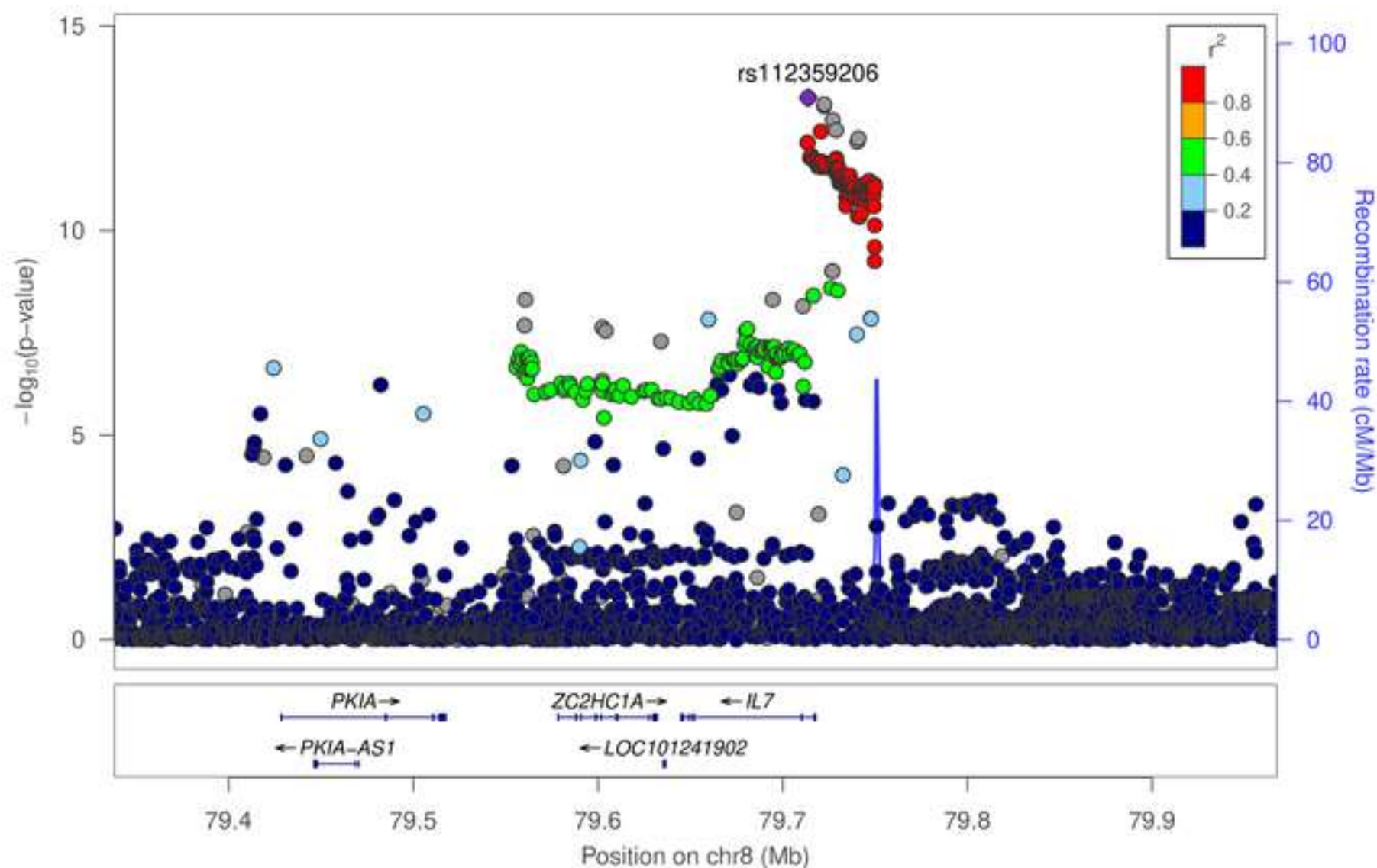
SCALLOP: IL-18R1 (IL18R1)-rs2270297



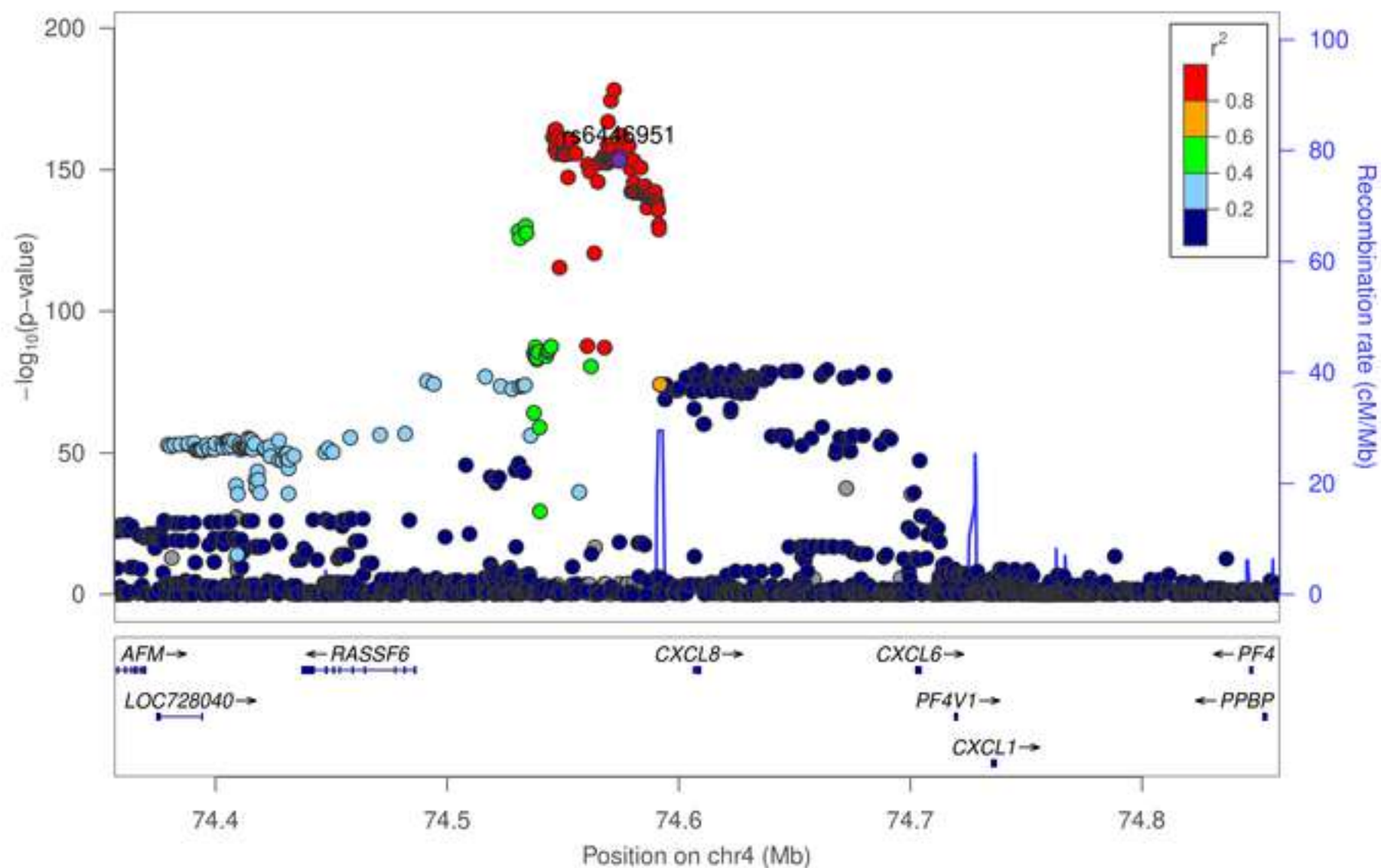
eQTLGen: IL-7 (IL7)-rs112359206



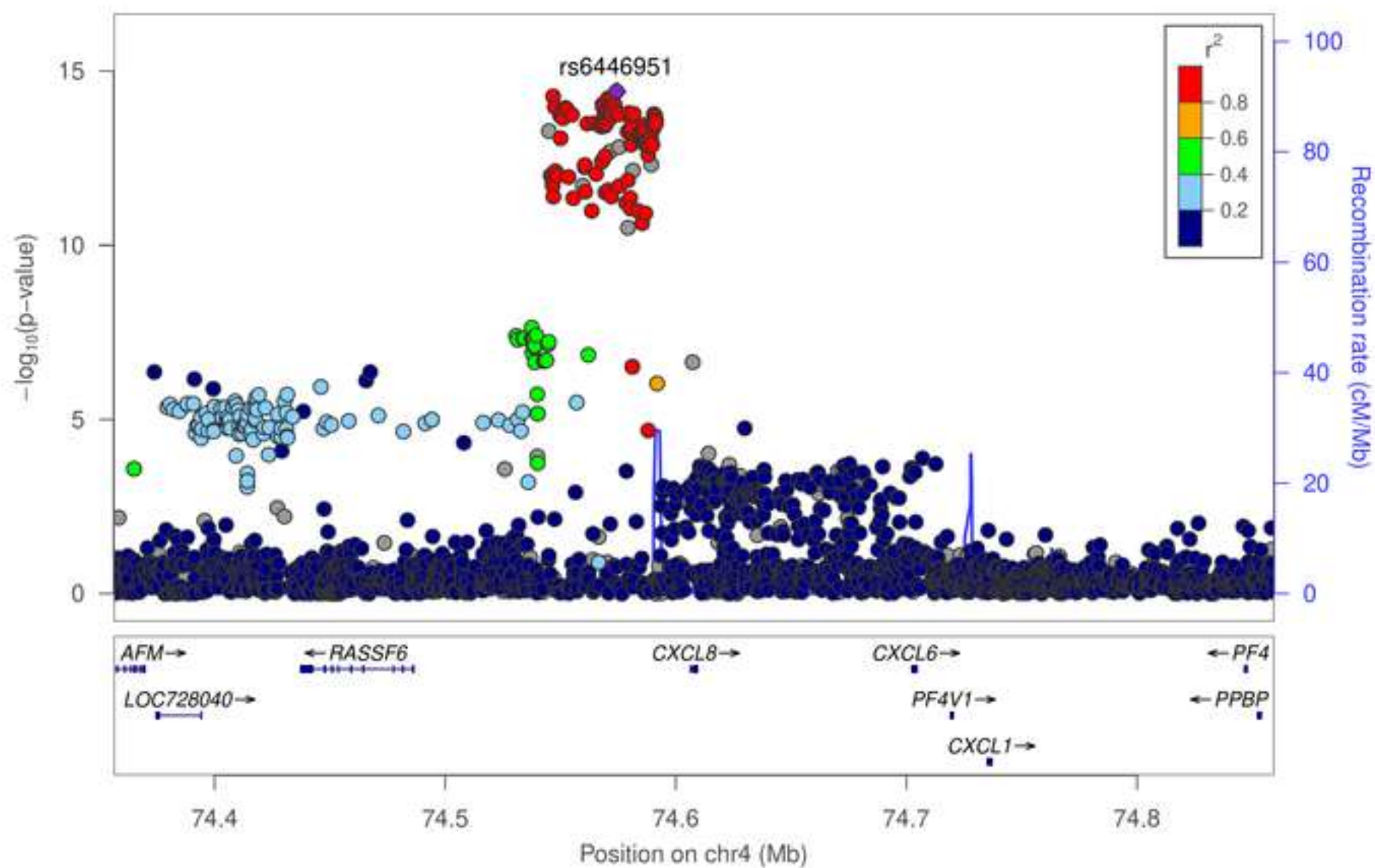
SCALLOP: IL-7 (IL7)-rs112359206



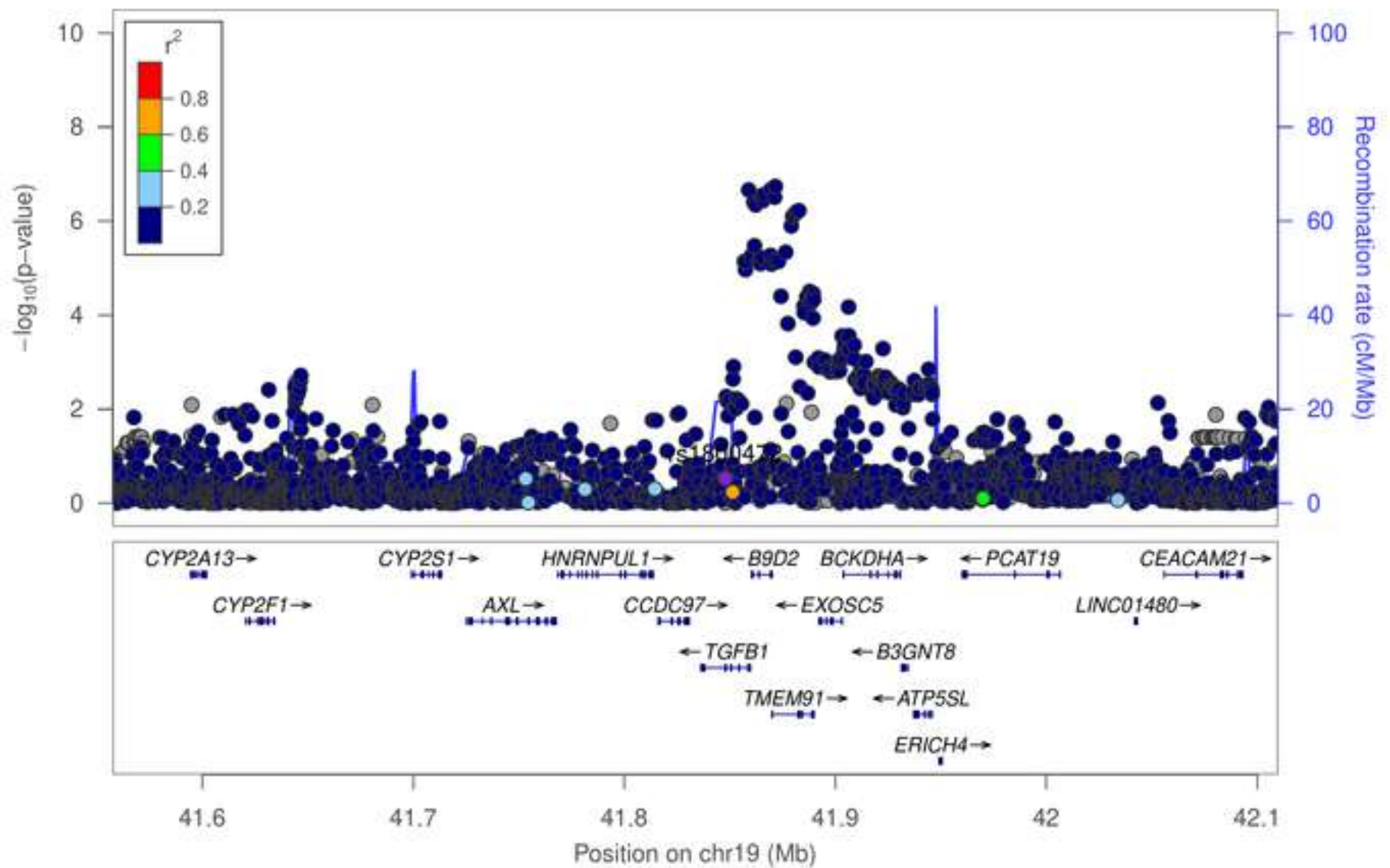
eQTLGen: IL-8 (IL8)-rs6446951



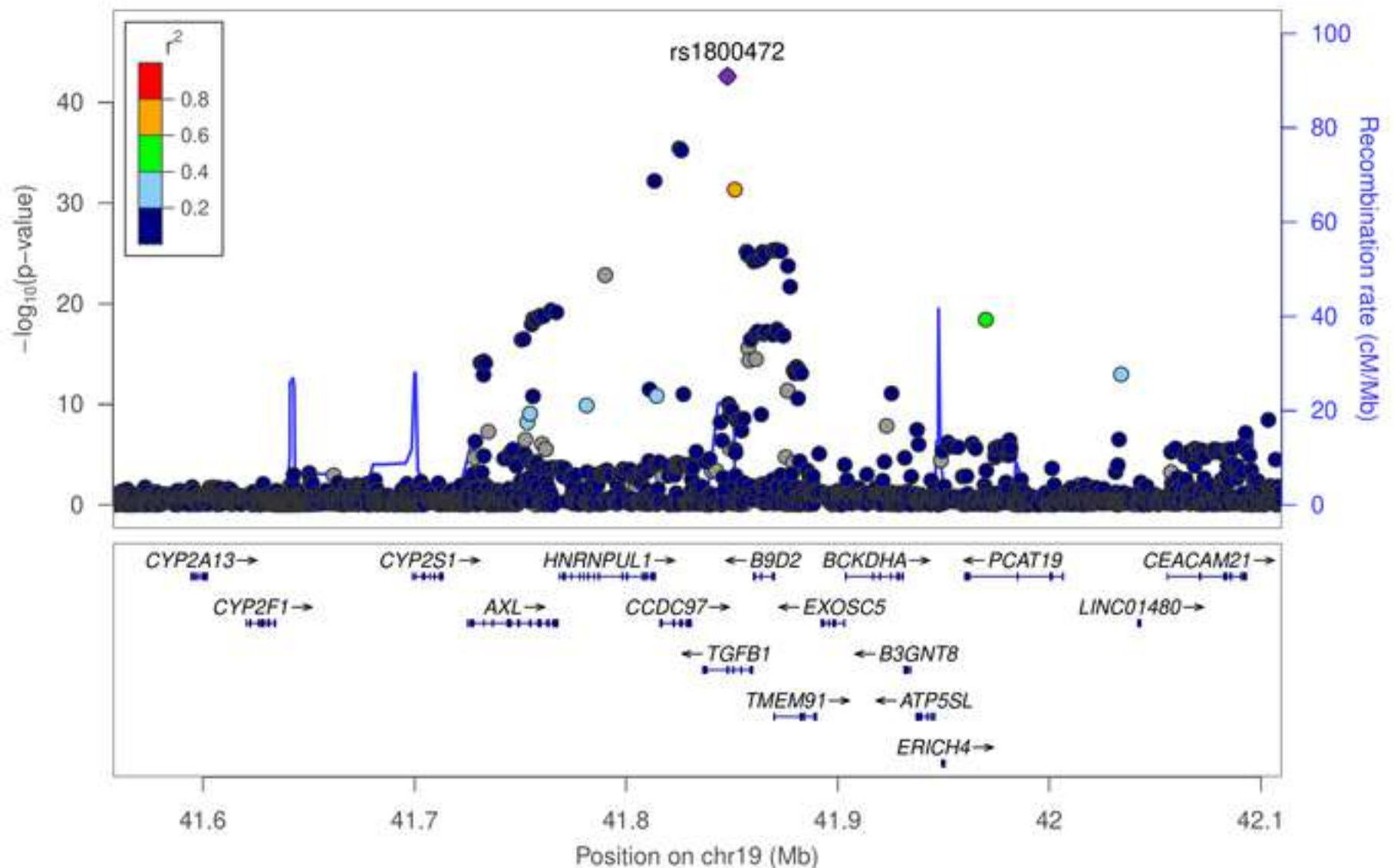
SCALLOP: IL-8 (IL8)-rs6446951



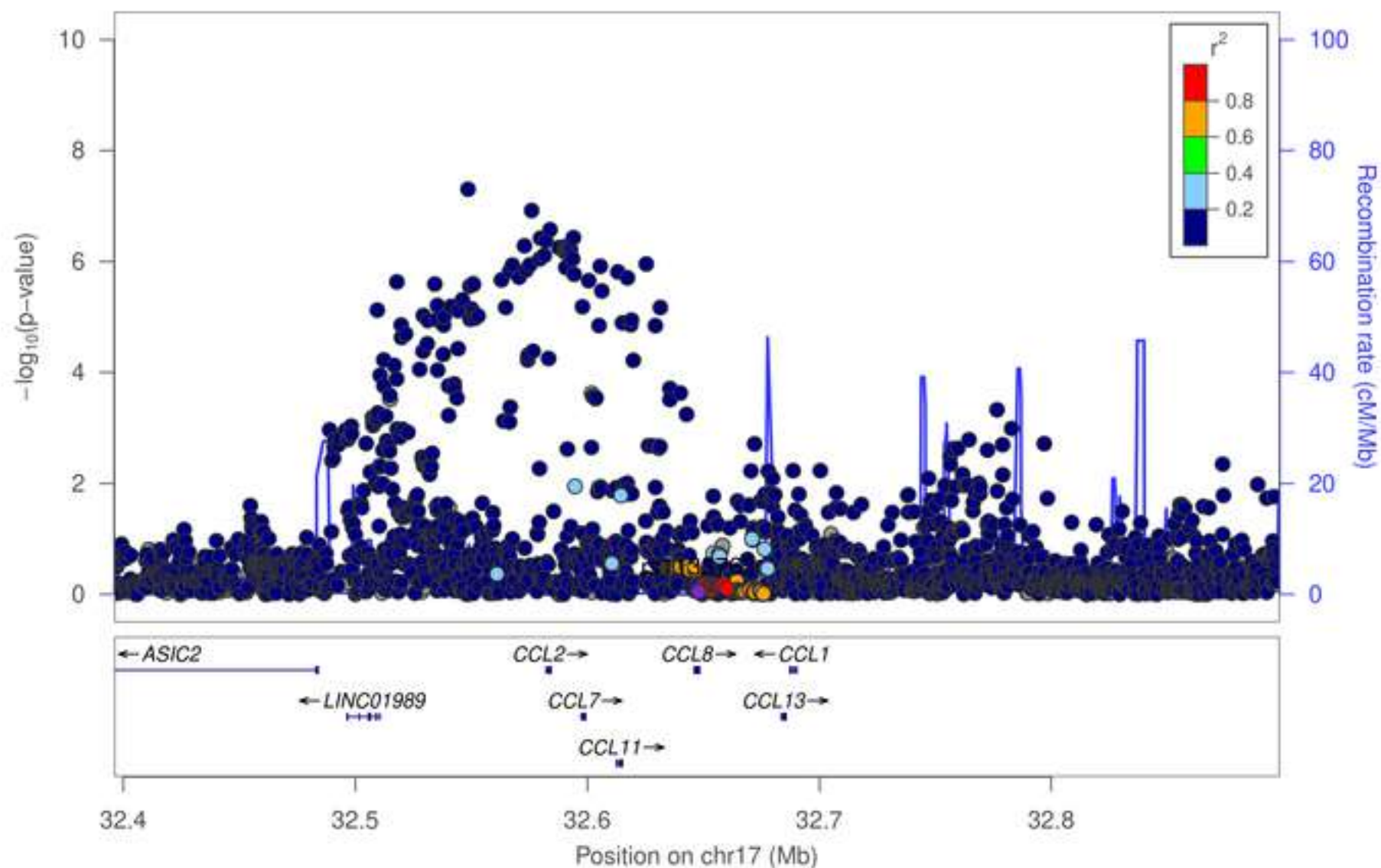
eQTLGen: LAP (TGFB1)–rs1800472



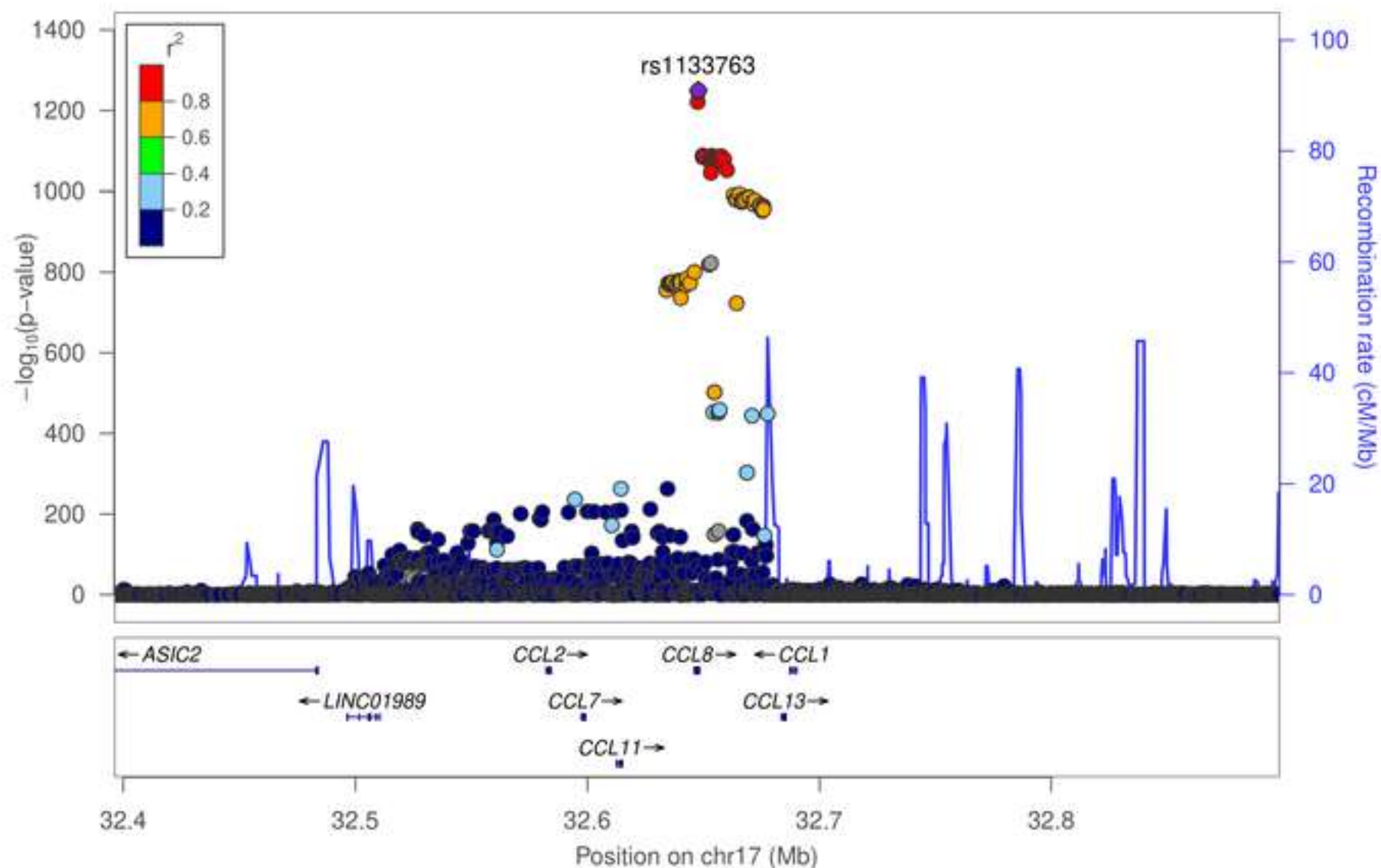
SCALLOP: LAP (TGFB1)–rs1800472



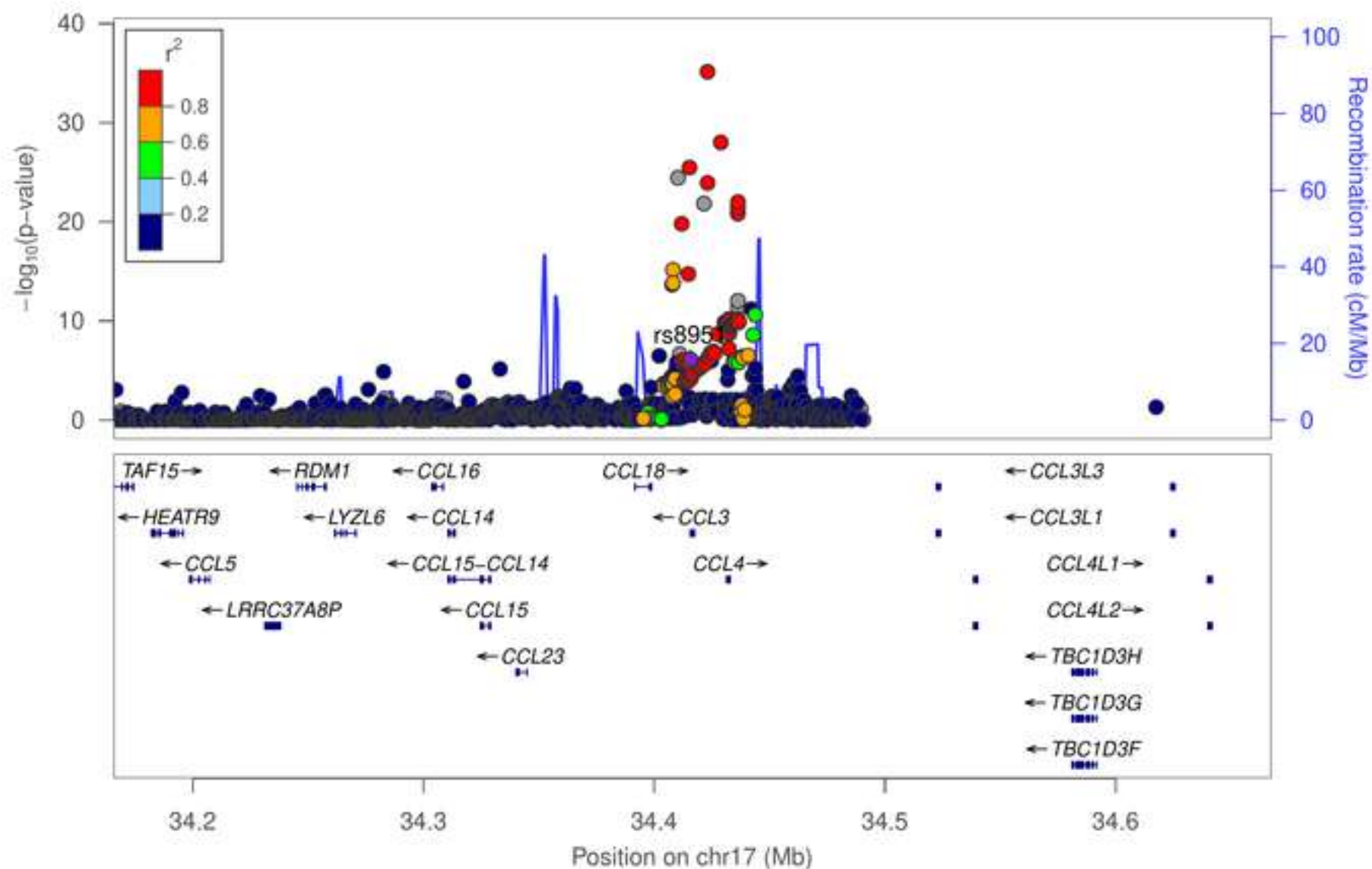
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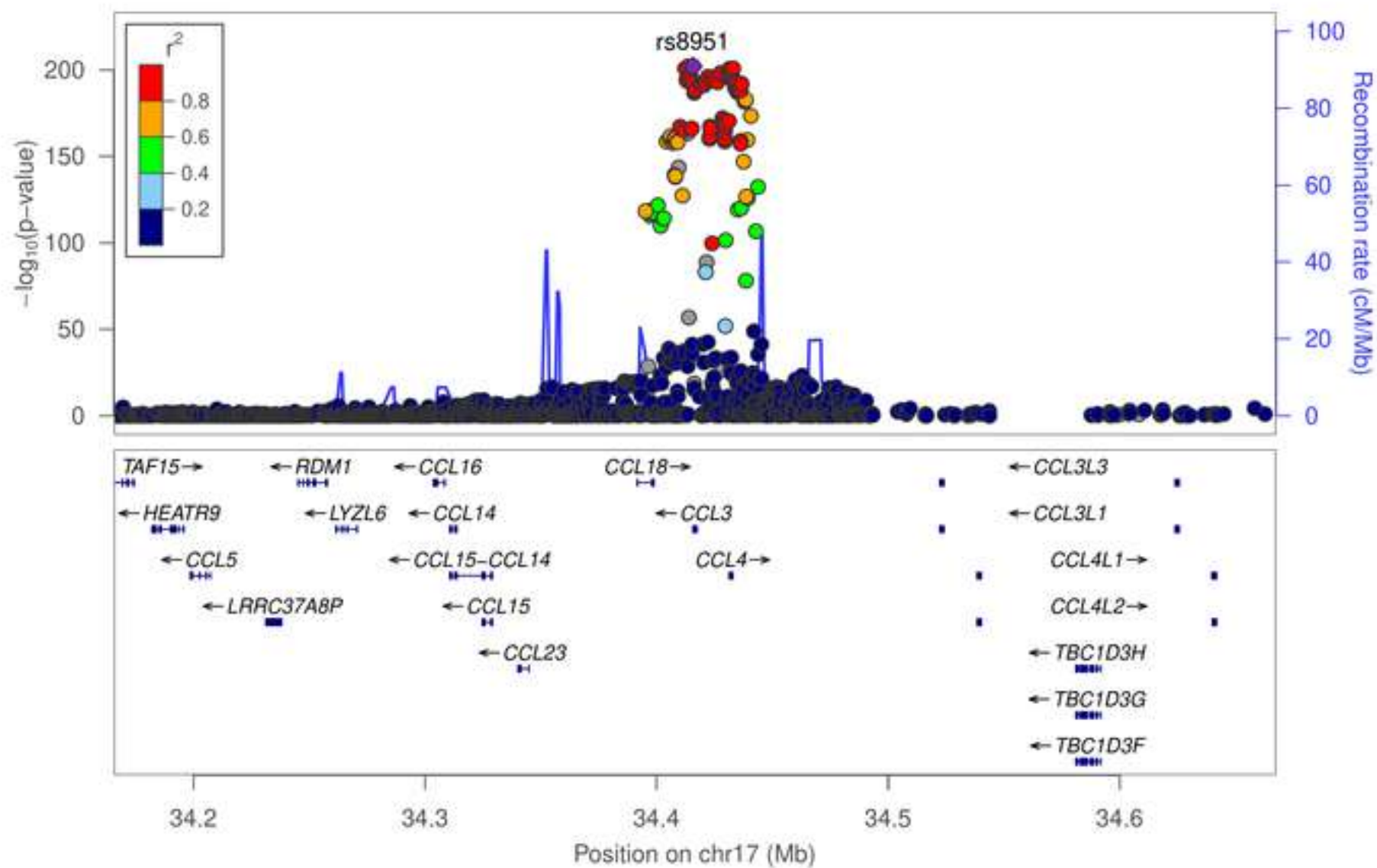
SCALLOP: MCP-2 (CCL8)-rs1133763



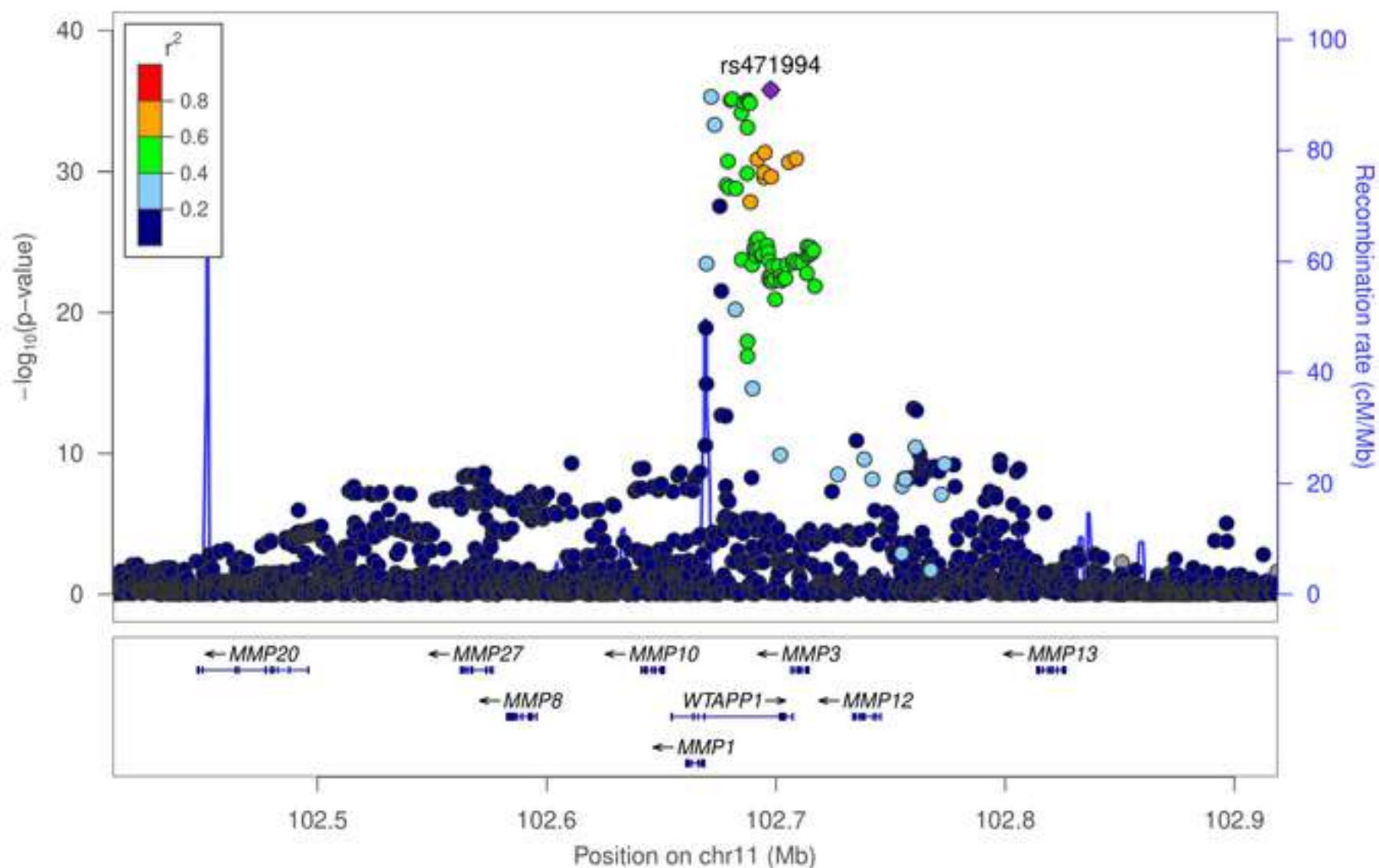
eQTLGen: MIP-1 (CCL3)-rs8951



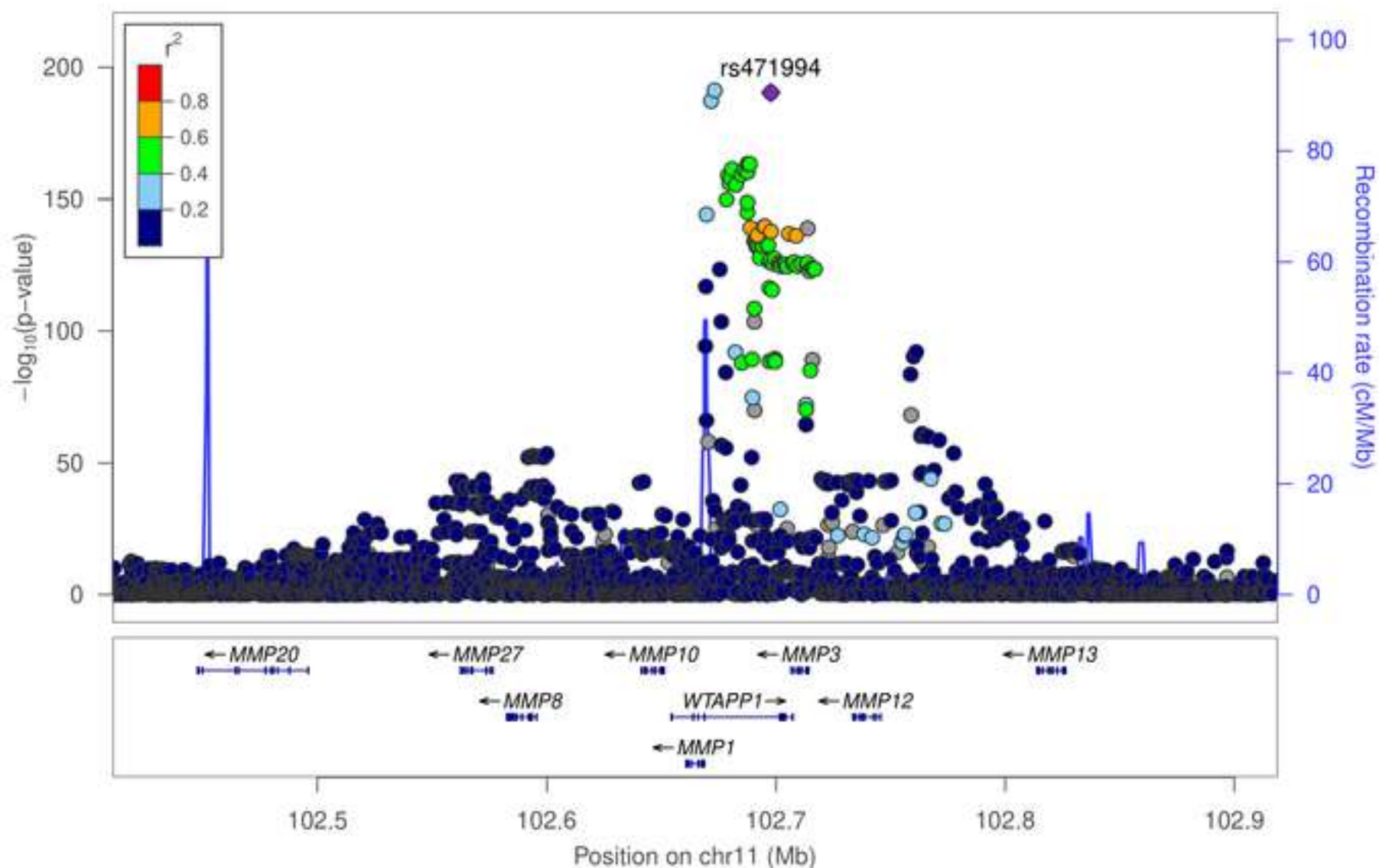
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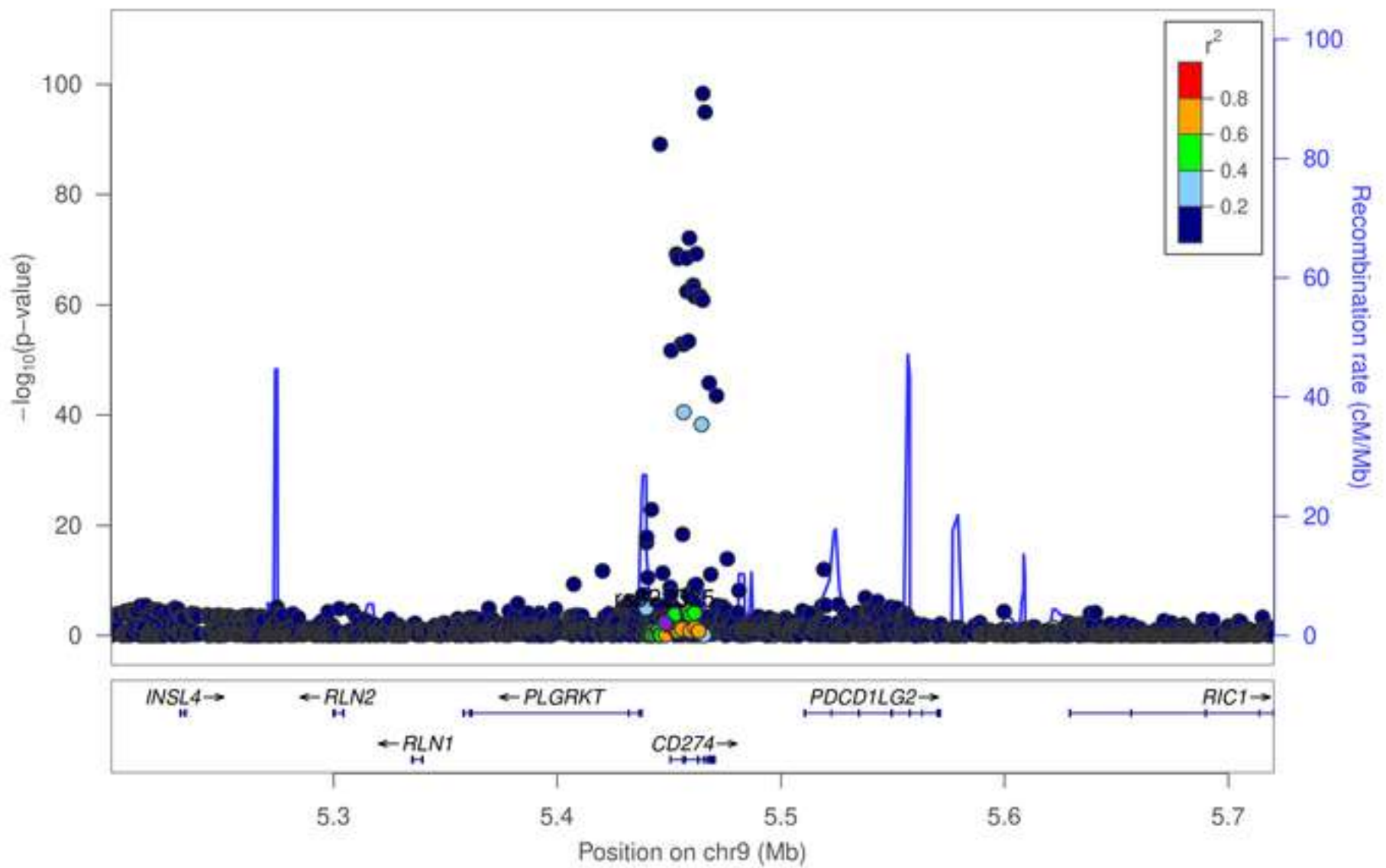
eQTLGen: MMP-1 (MMP1)-rs471994



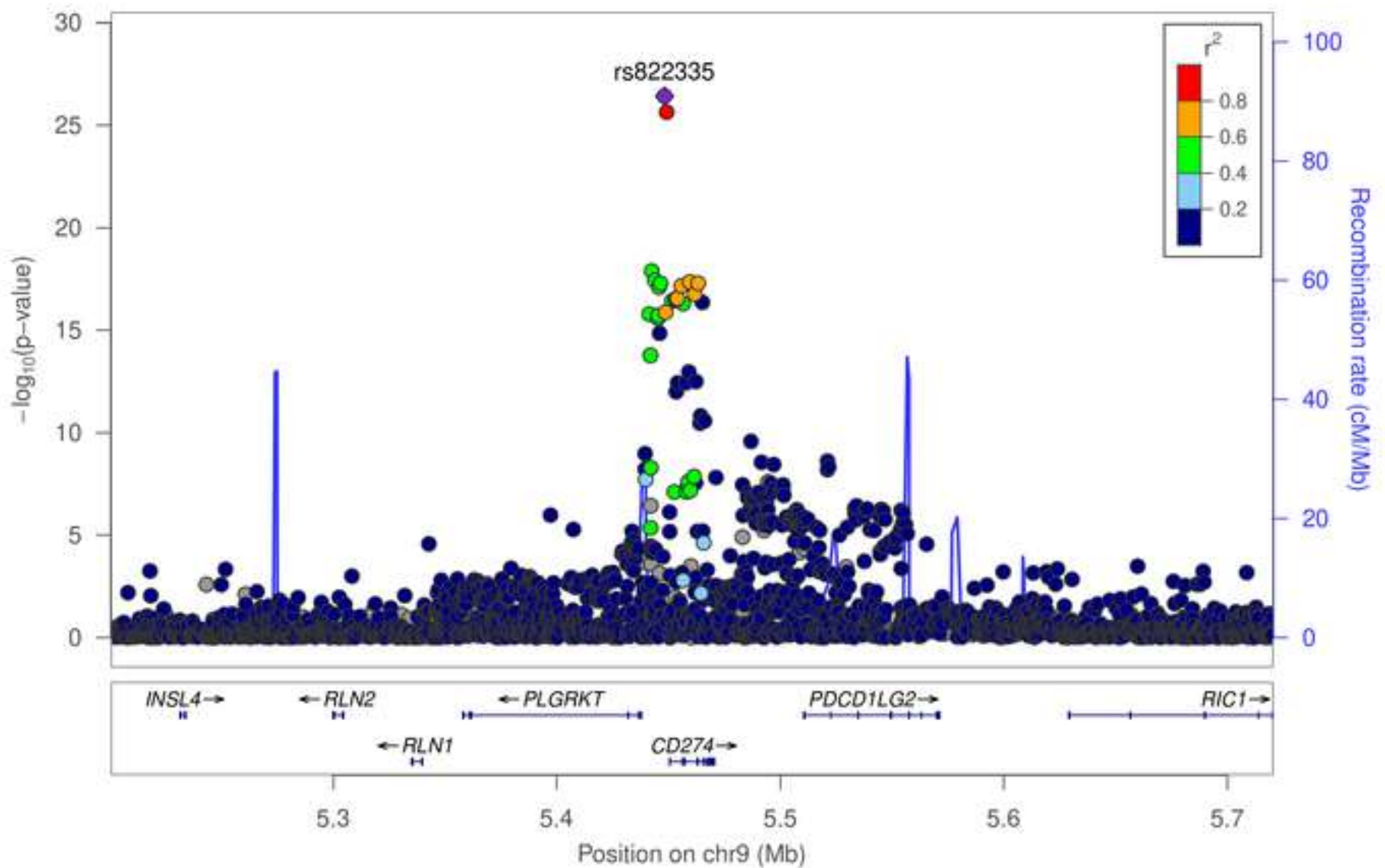
SCALLOP: MMP-1 (MMP1)-rs471994



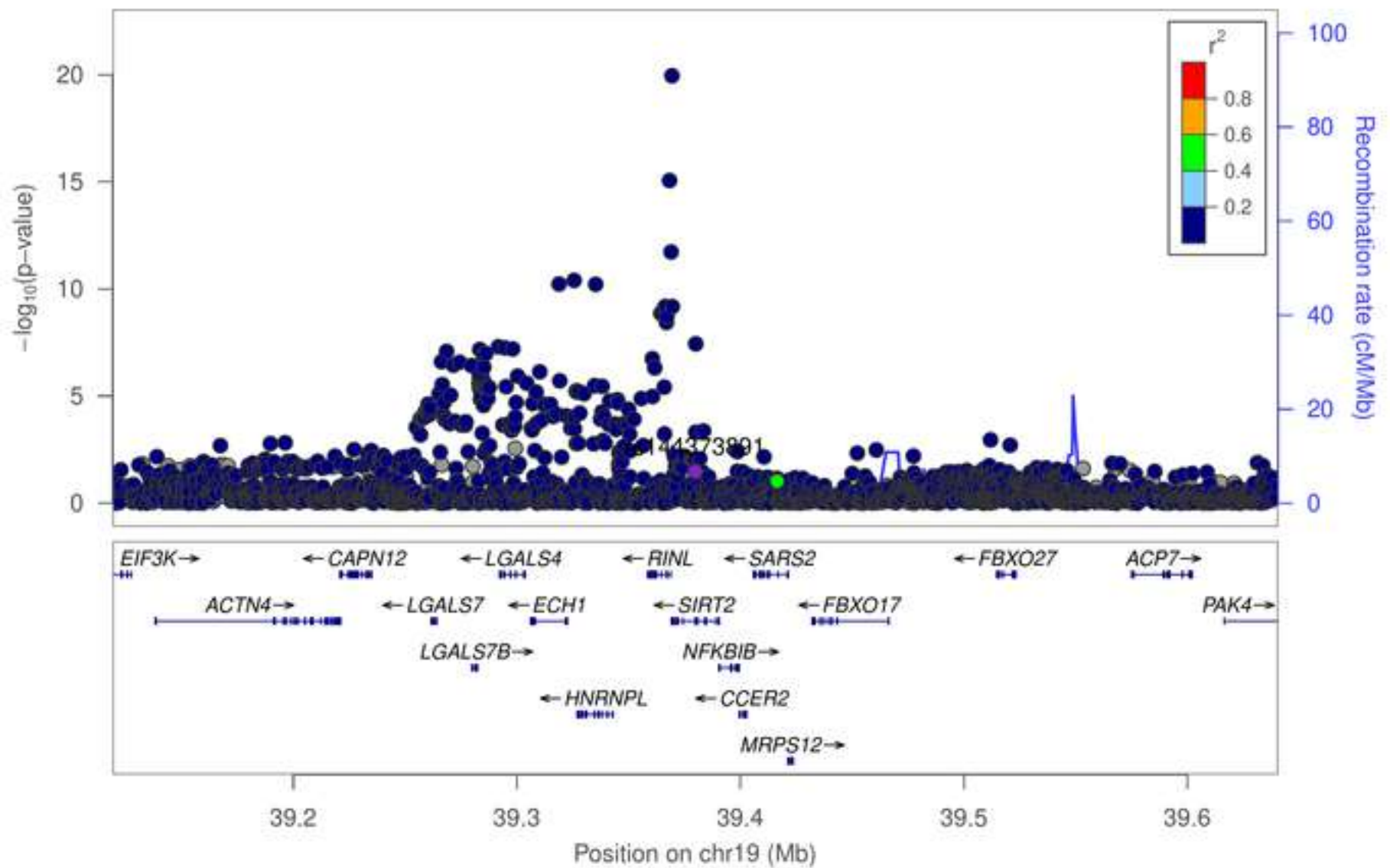
eQTLGen: PD-L1 (CD274)-rs822335



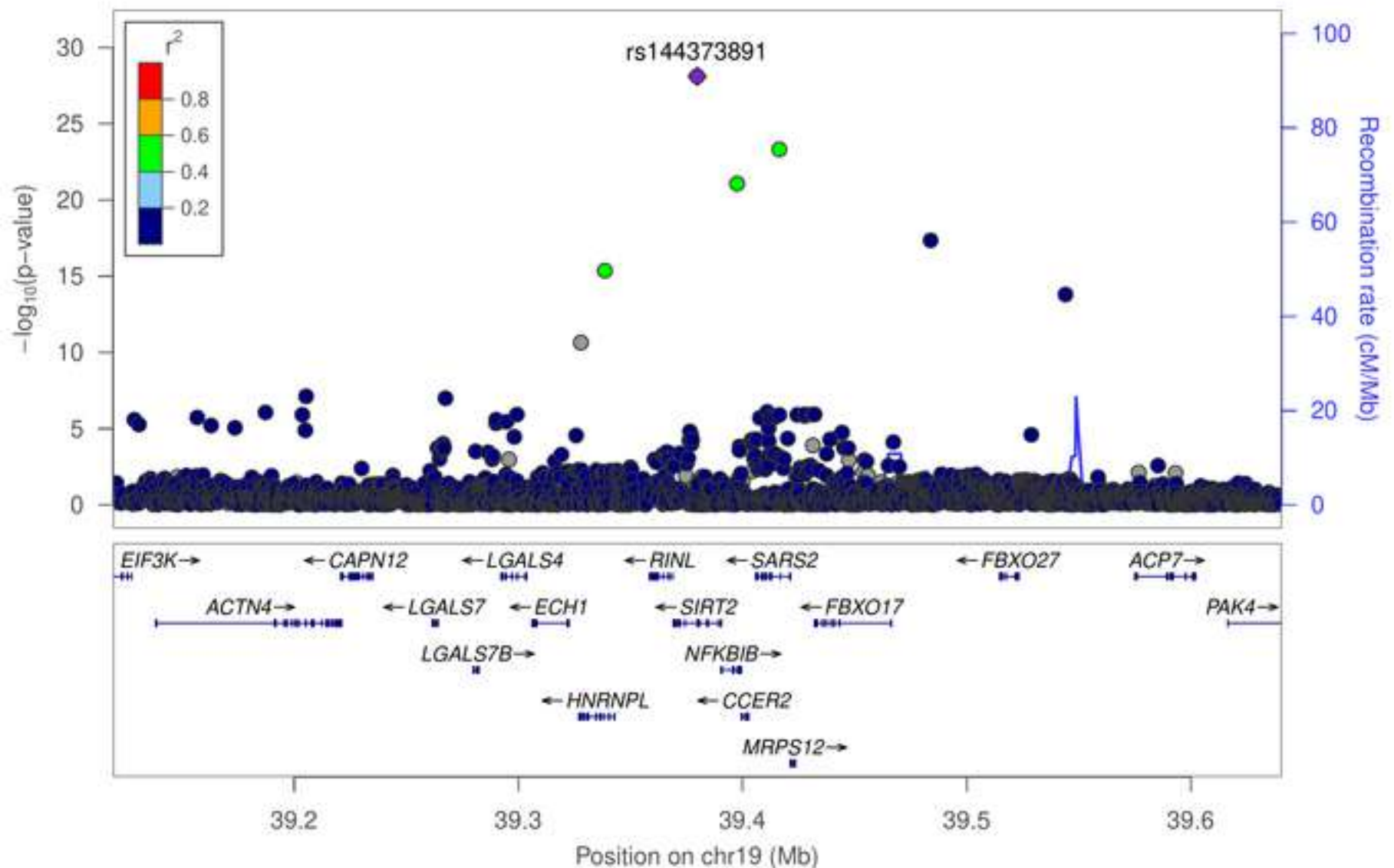
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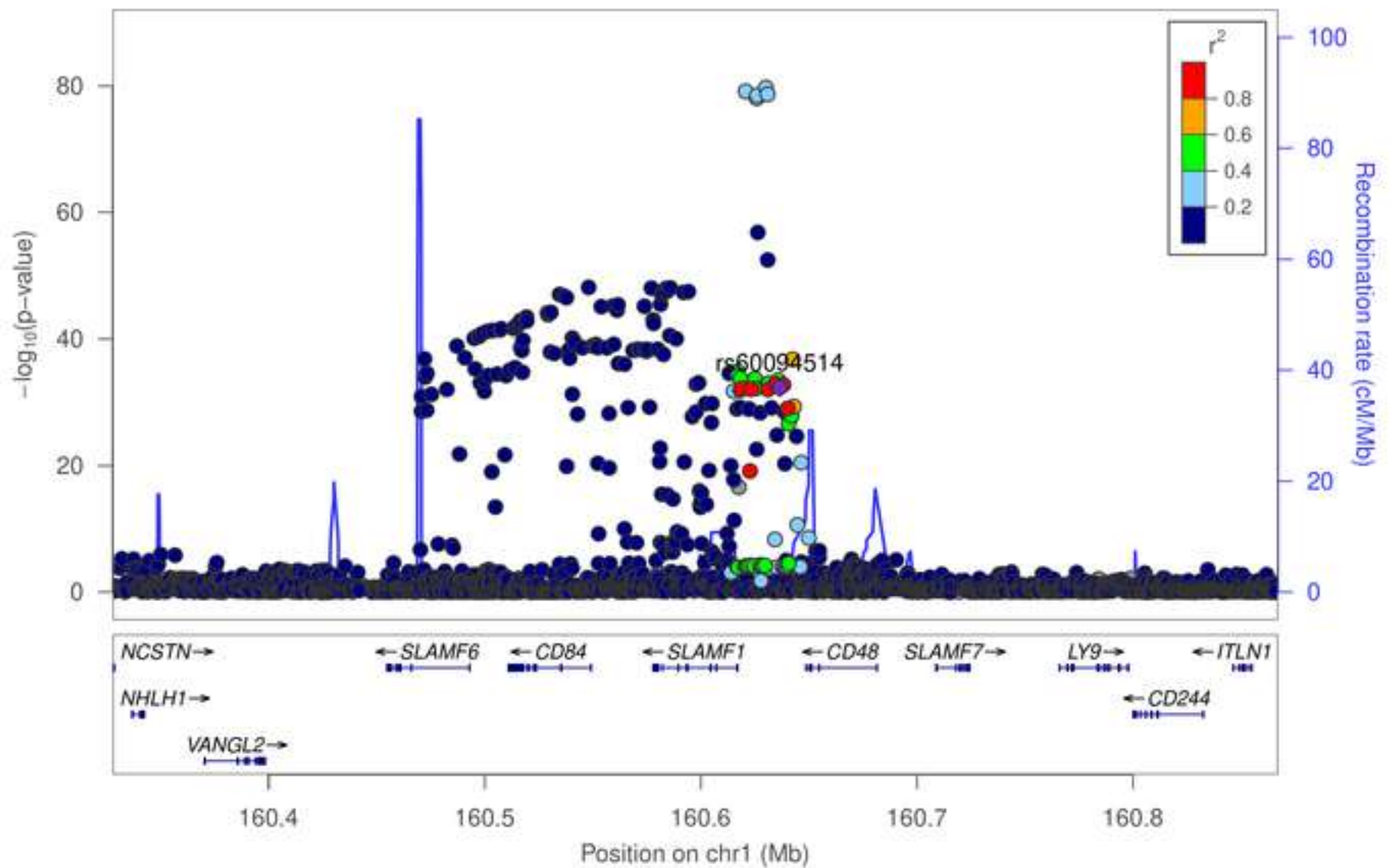
eQTLGen: SIRT2 (SIRT2)-rs144373891



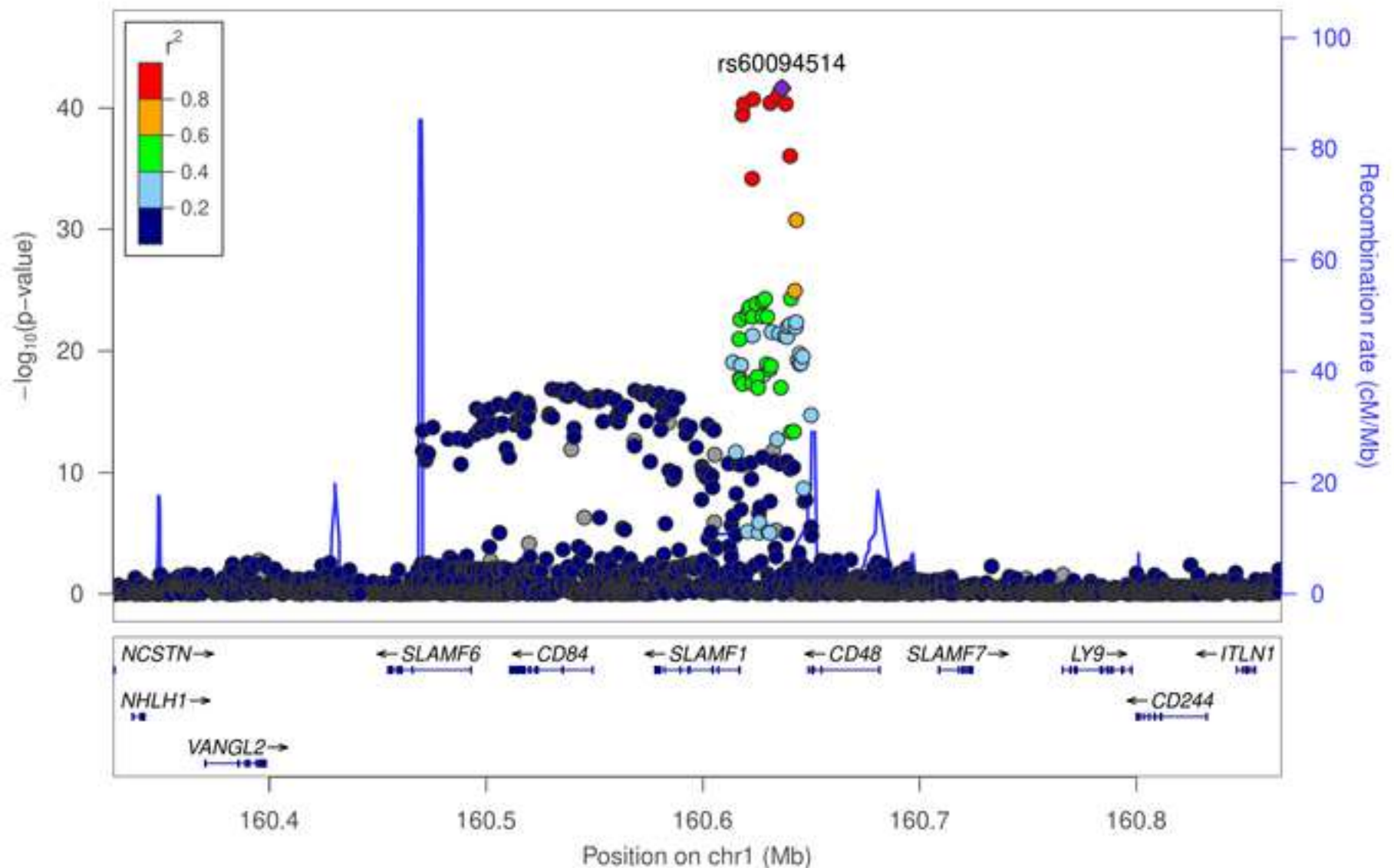
SCALLOP: SIRT2 (SIRT2)-rs144373891



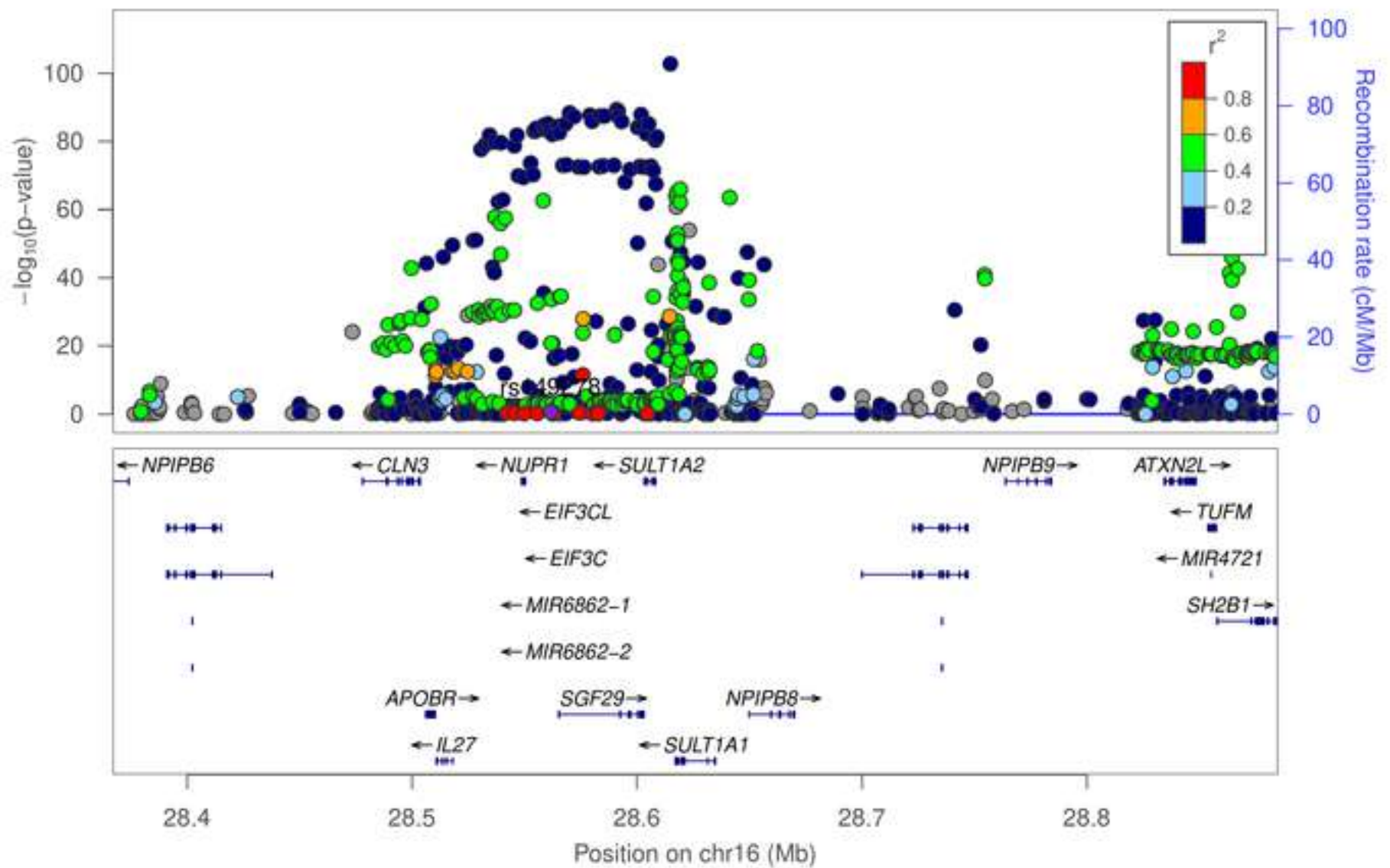
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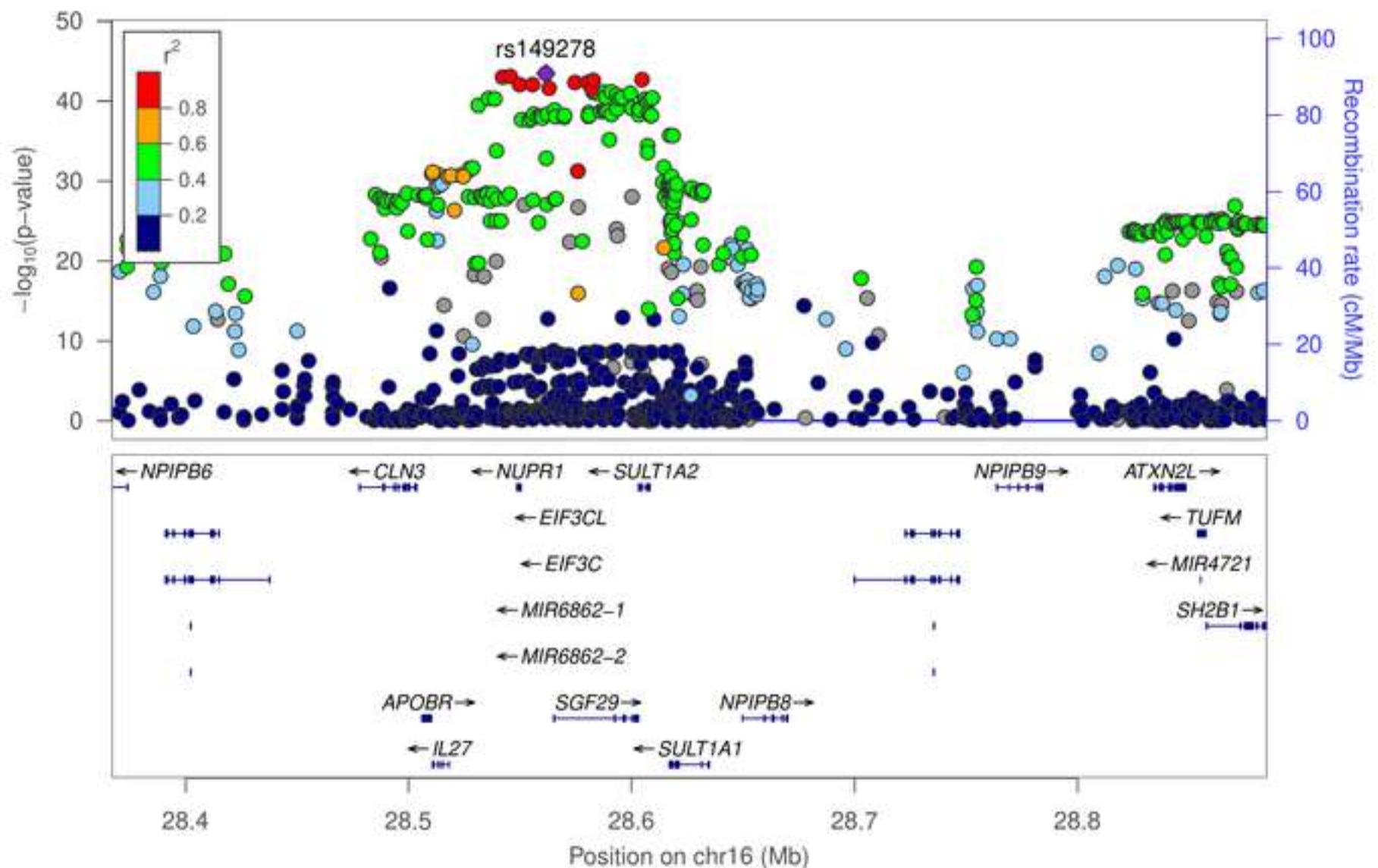
SCALLOP: SLAMF1 (SLAMF1)–rs60094514



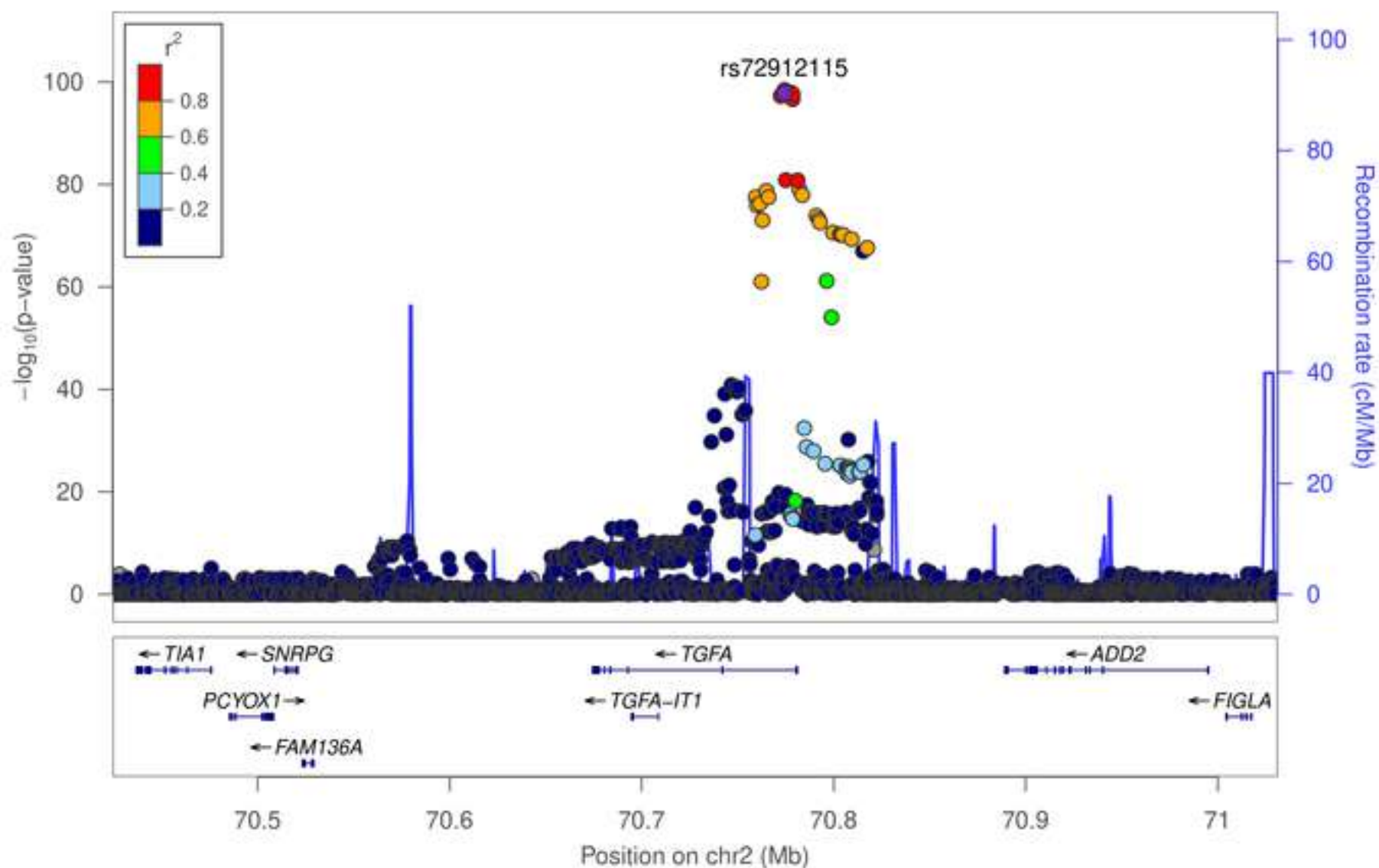
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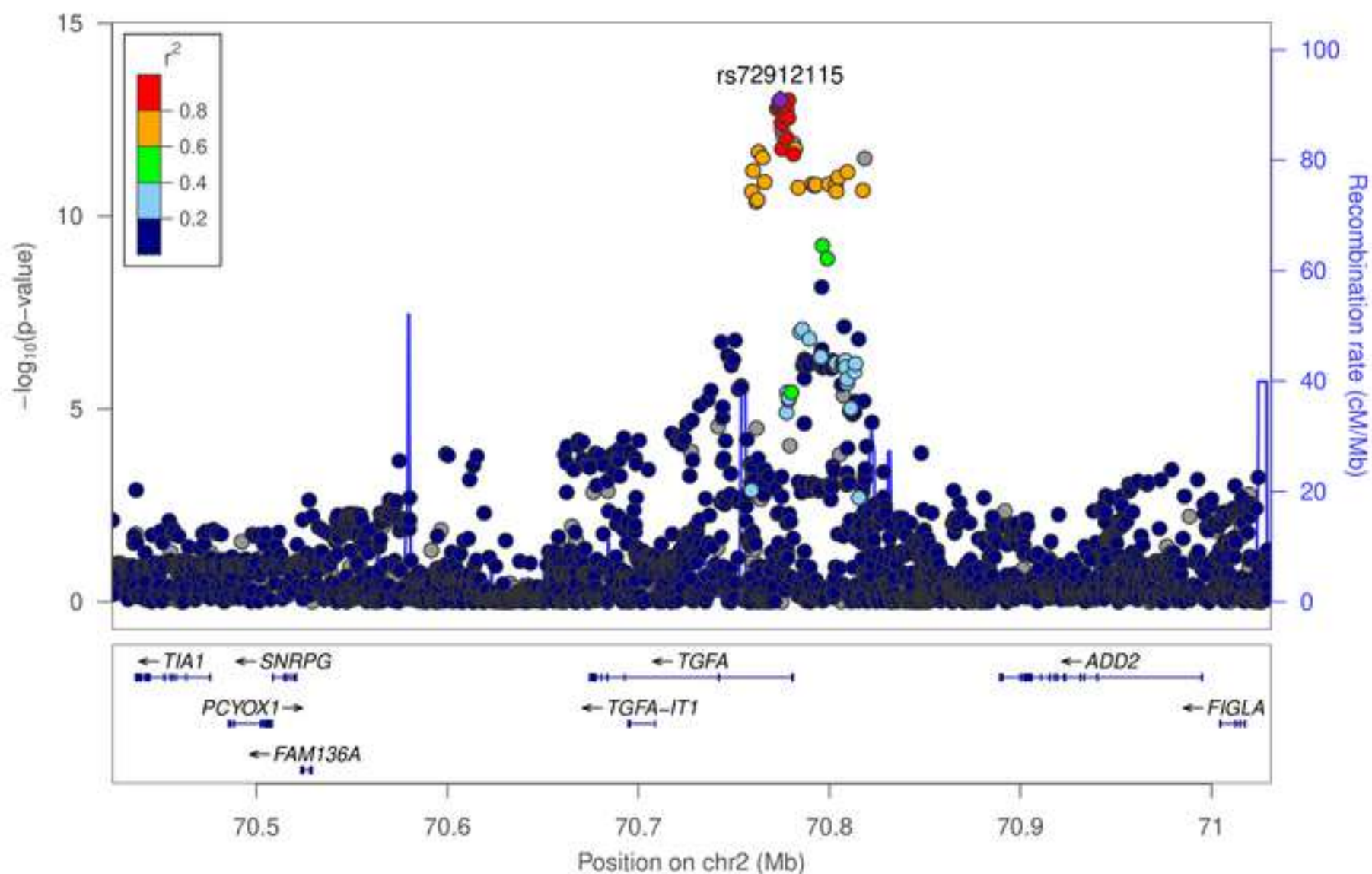
SCALLOP: ST1A1 (SULT1A1)-rs149278



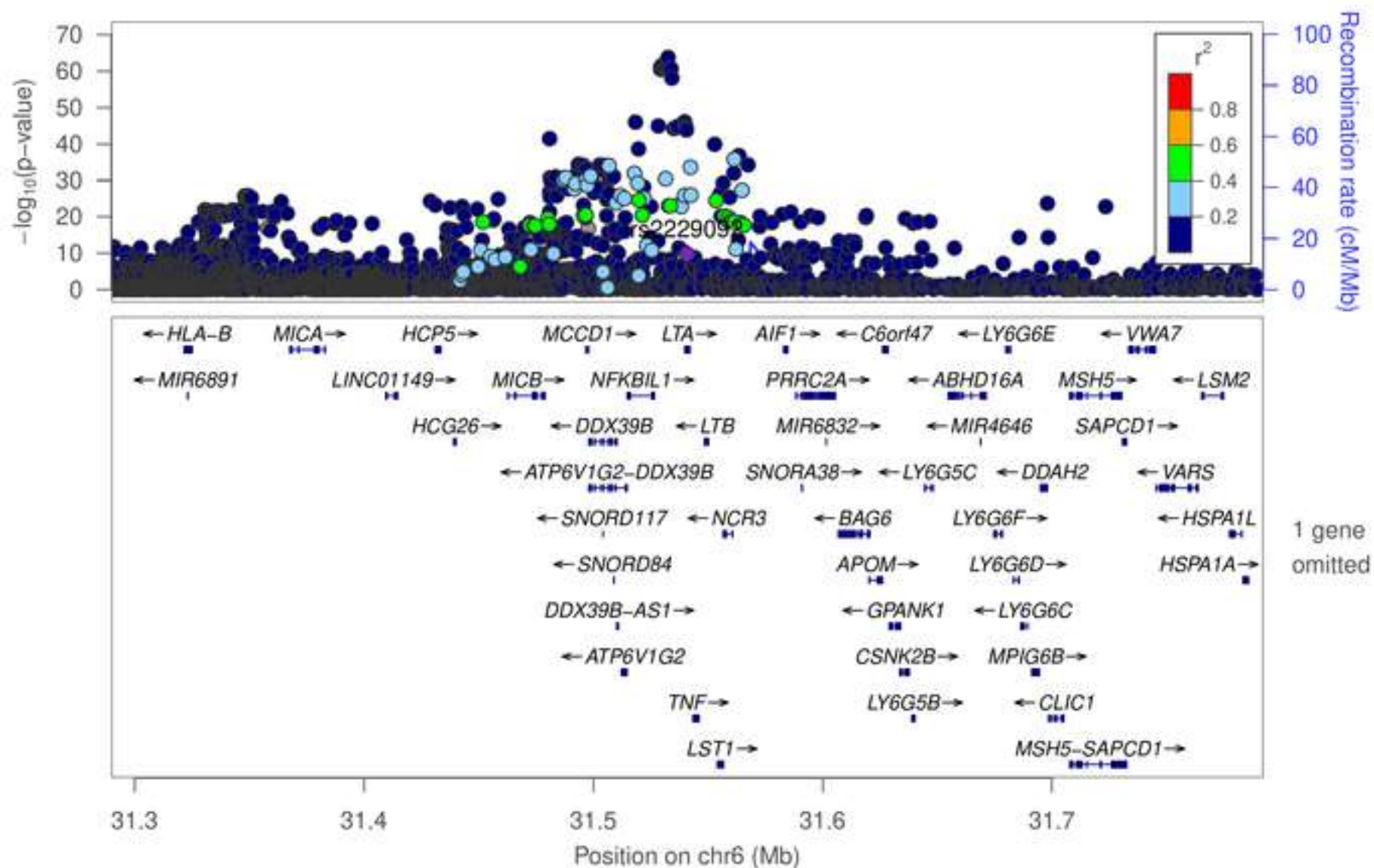
eQTLGen: TGF- α (TGFA)-rs72912115



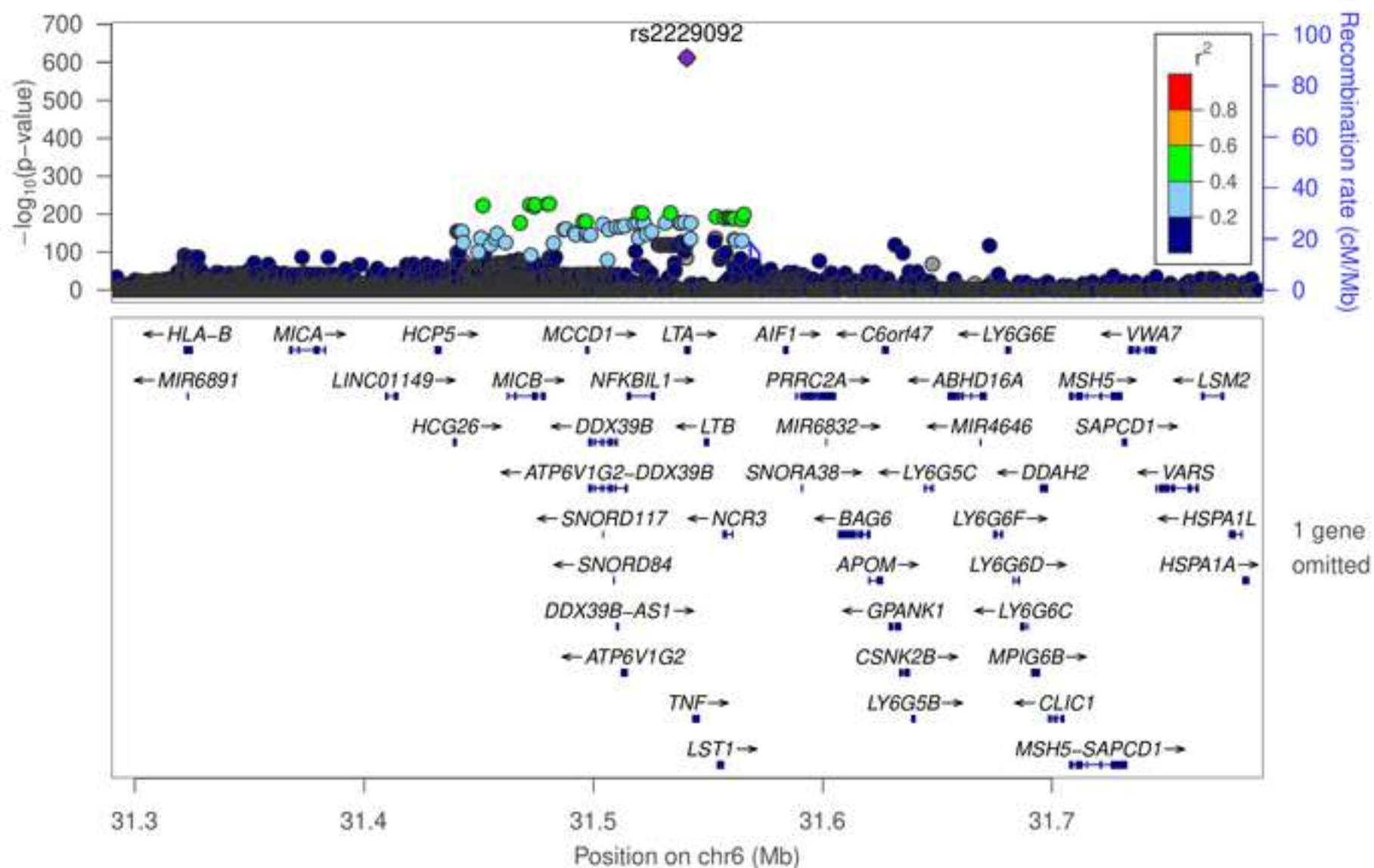
SCALLOP: TGF- α (TGFA)-rs72912115



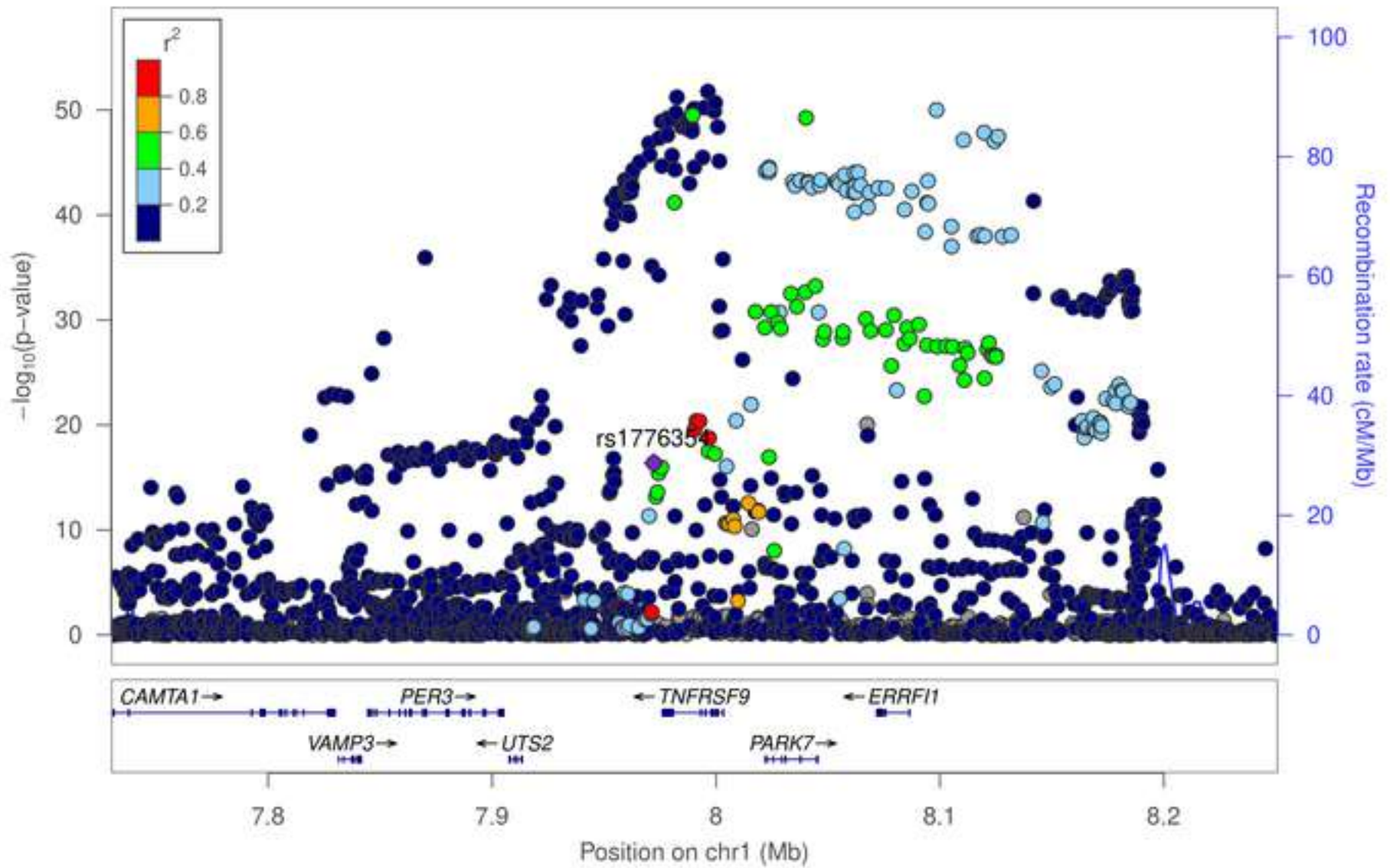
eQTLGen: TNFB (LTA)–rs2229092



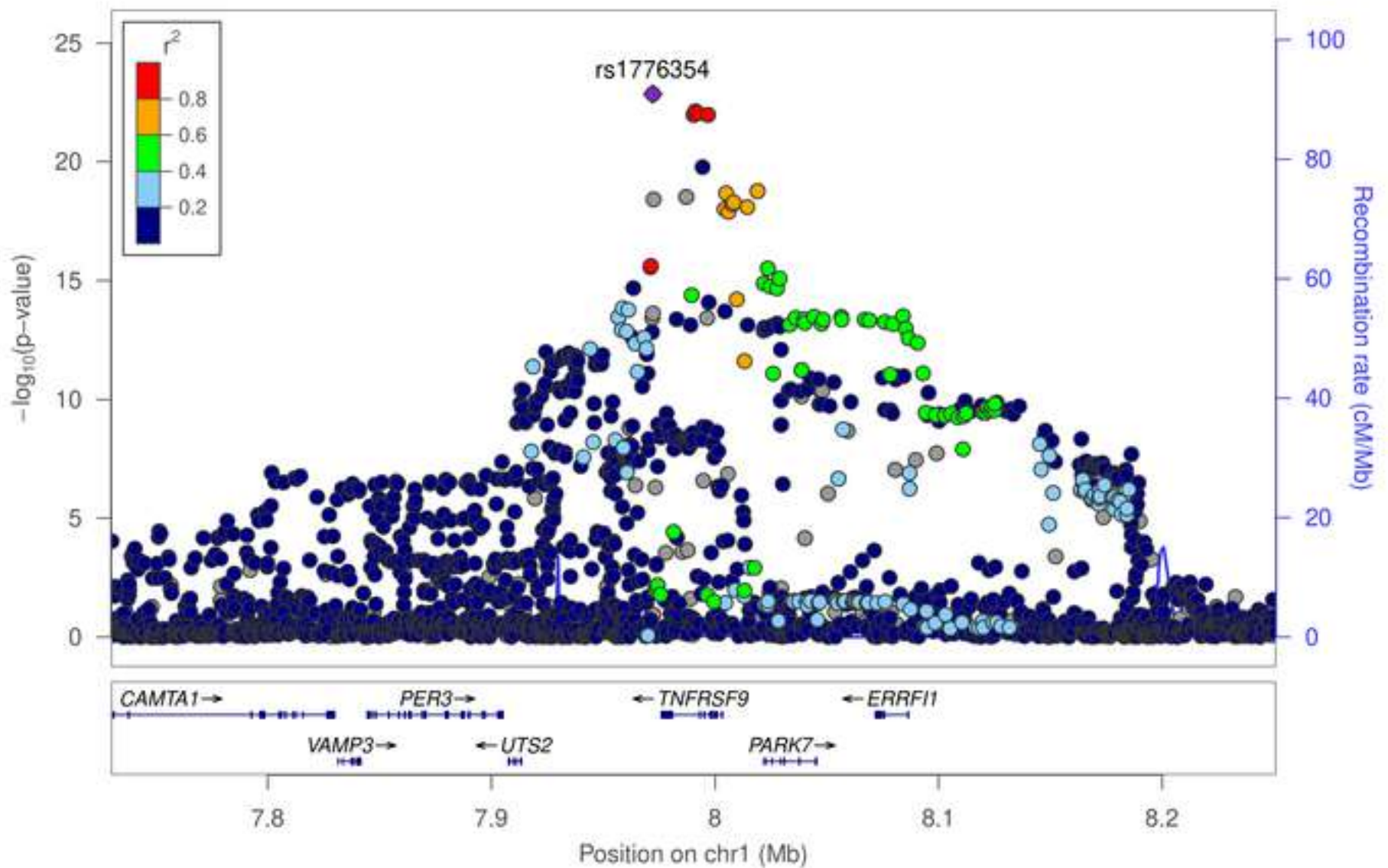
SCALLOP: TNFB (LTA)–rs2229092



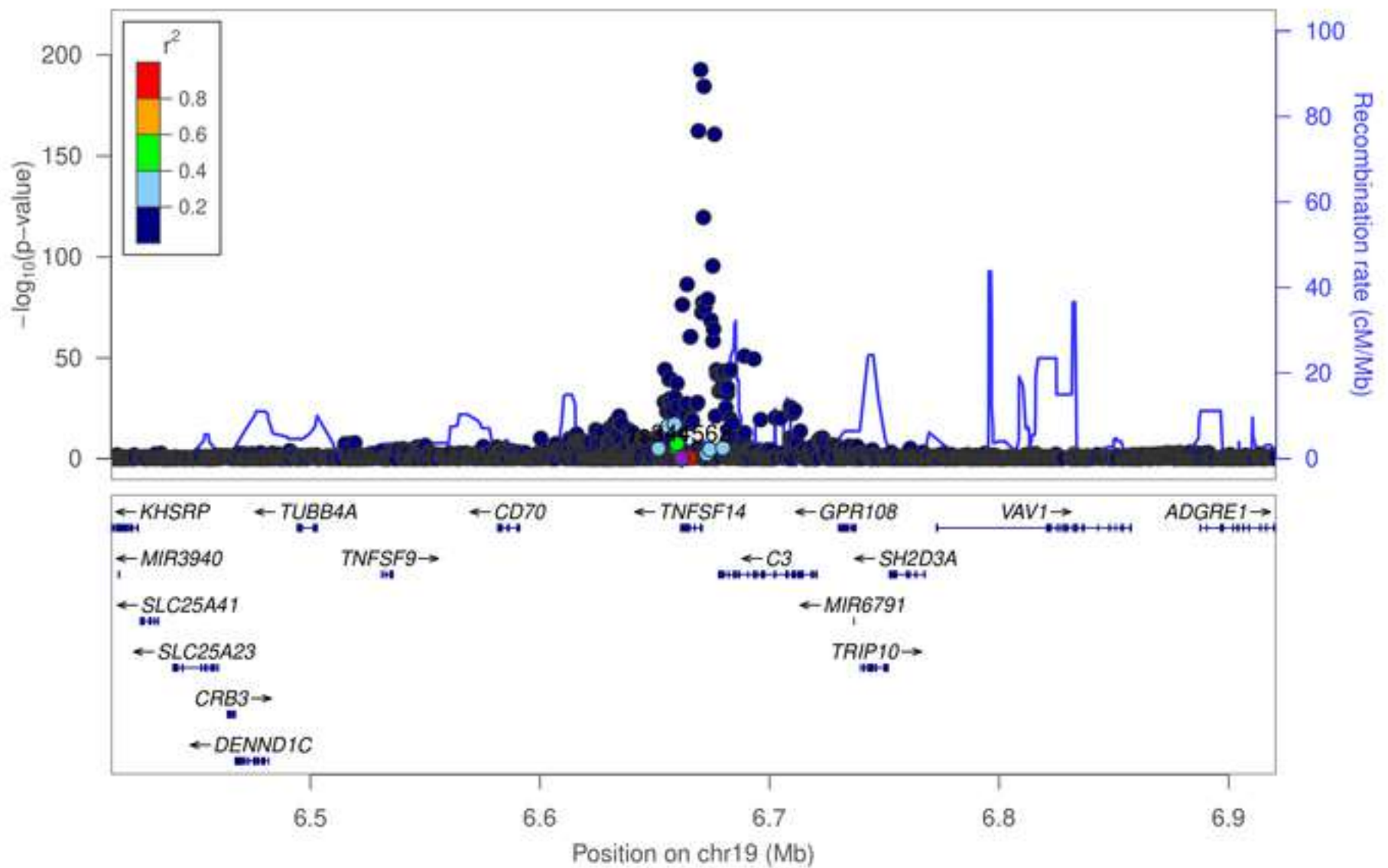
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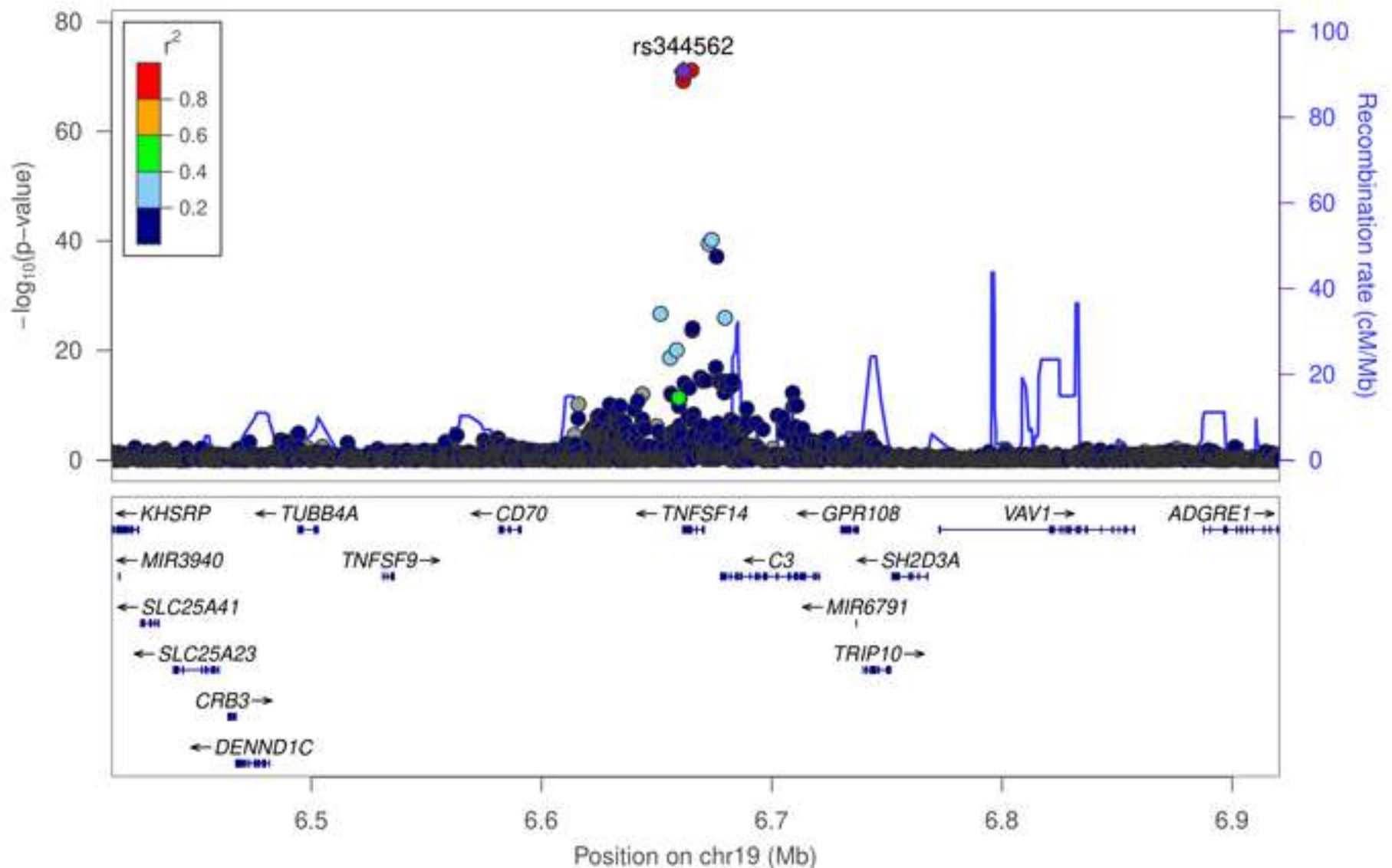
SCALLOP: TNFRSF9 (TNFRSF9)-rs1776354



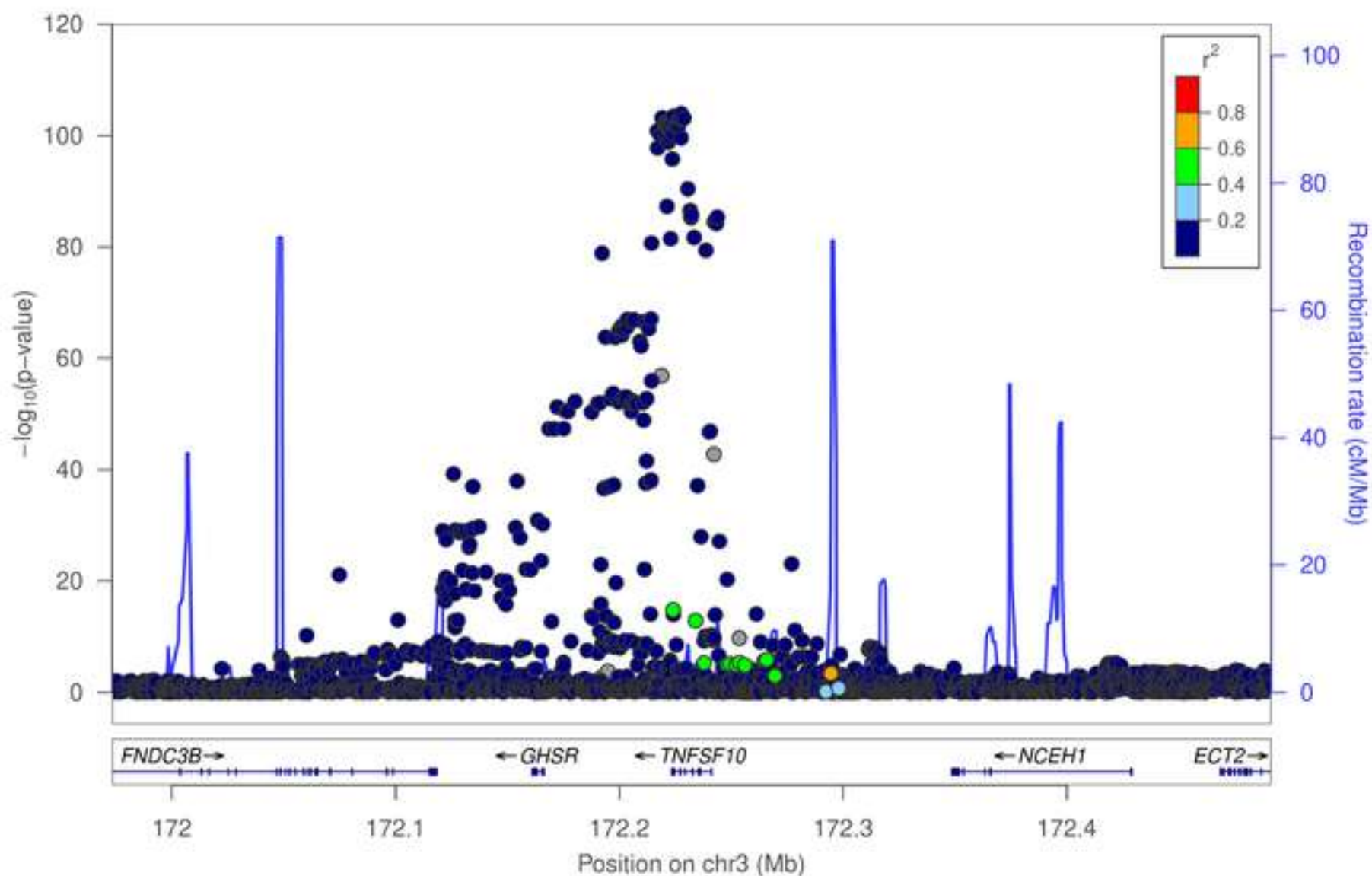
eQTLGen: TNFSF14 (TNFSF14)-rs344562



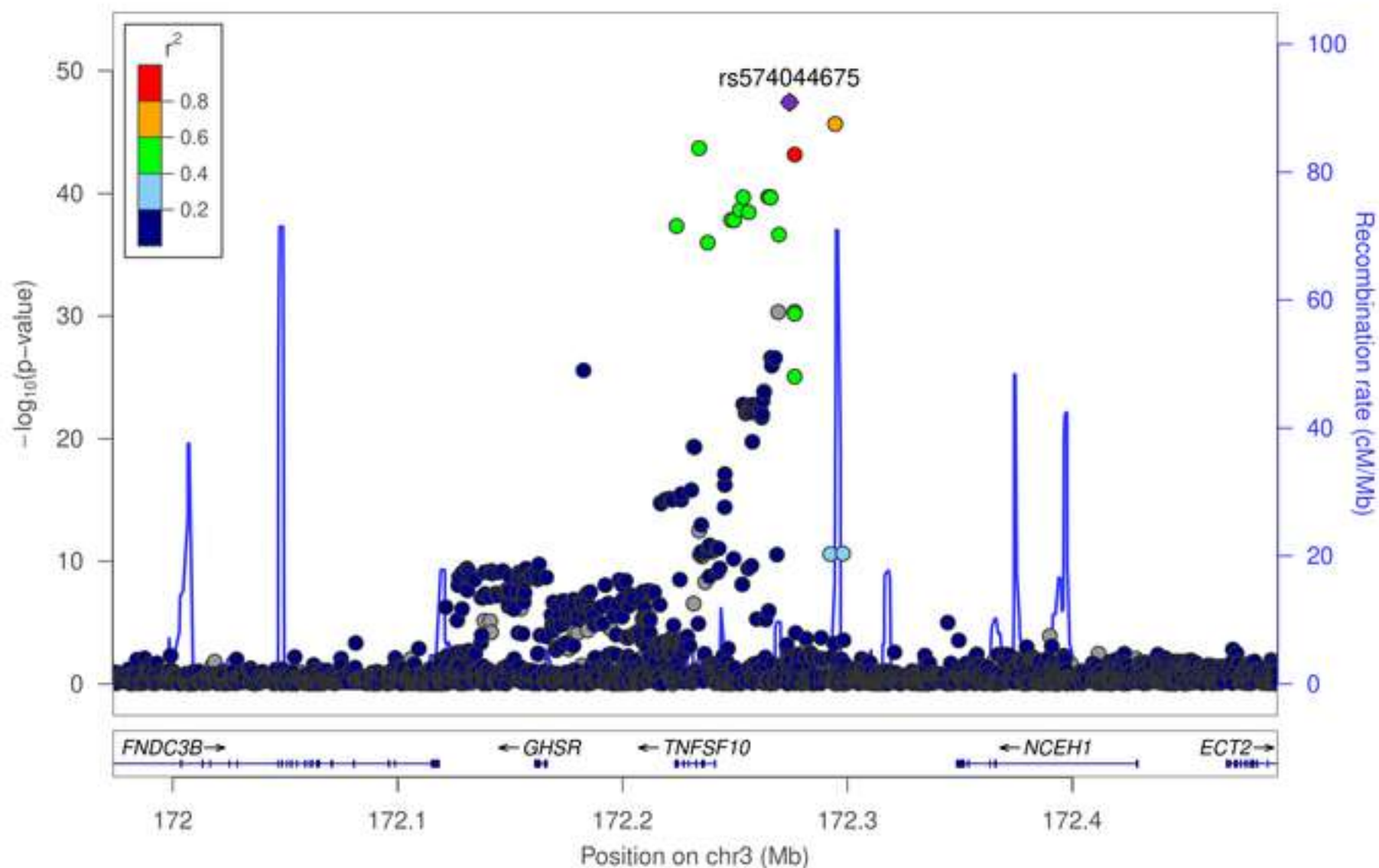
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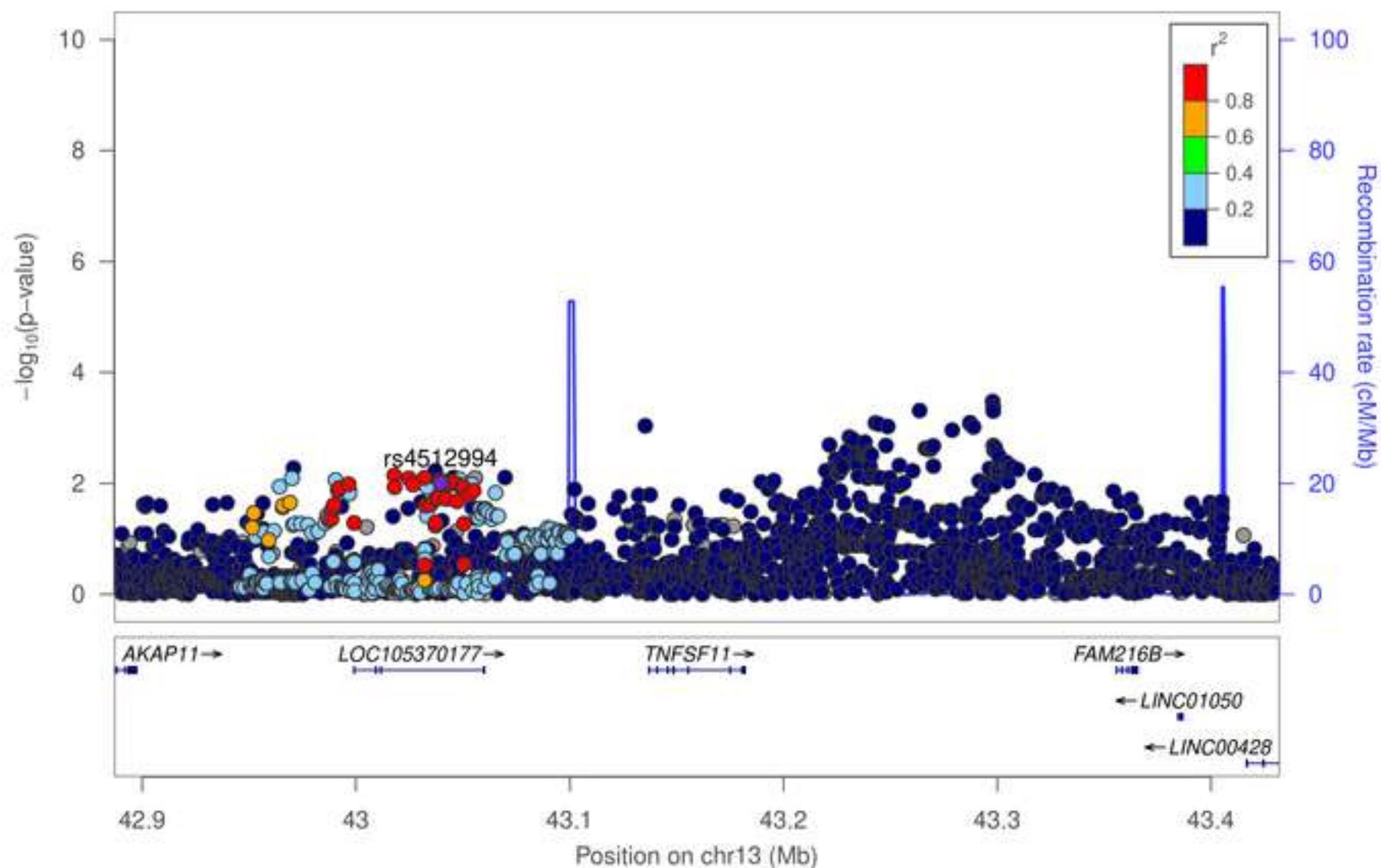
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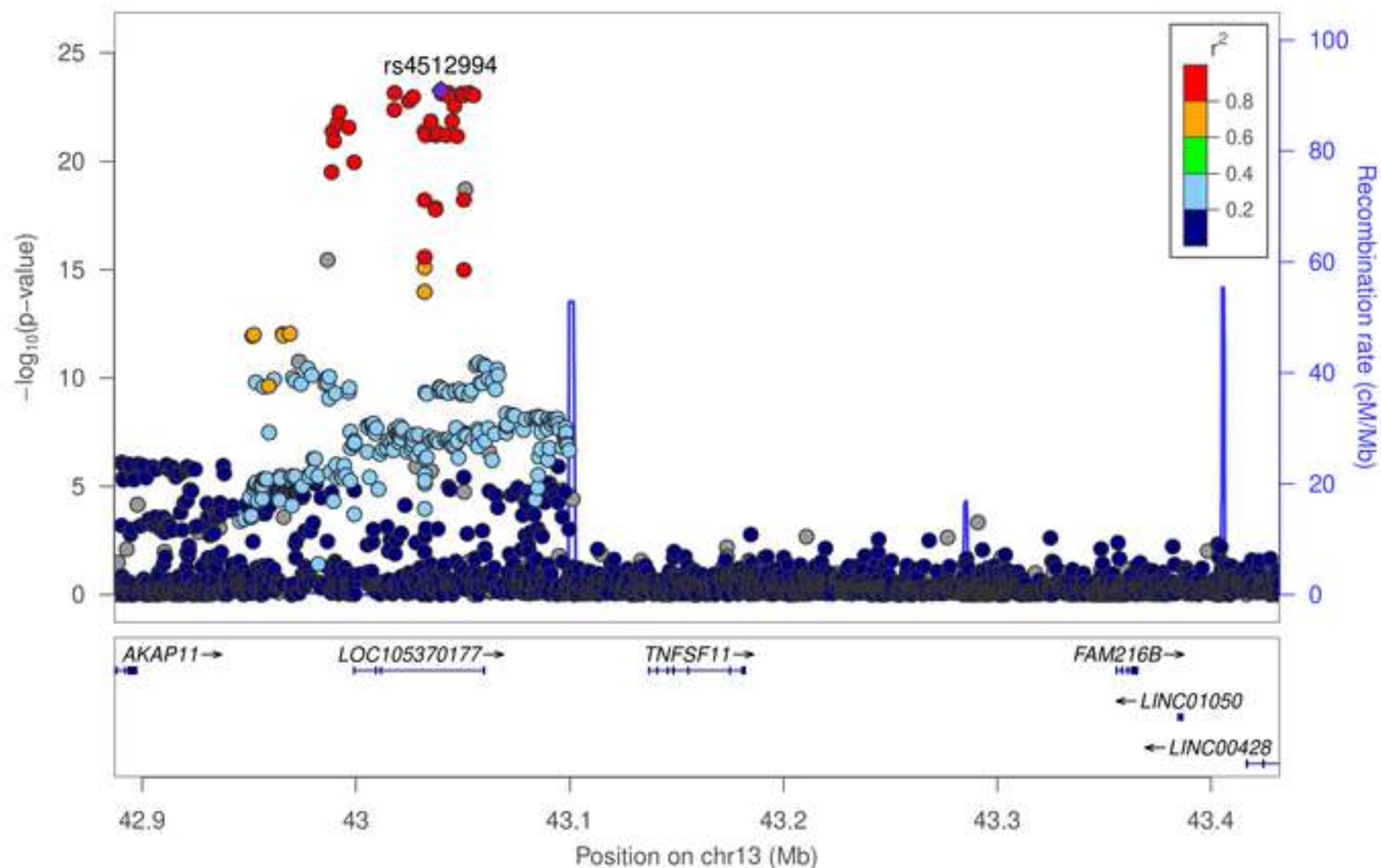
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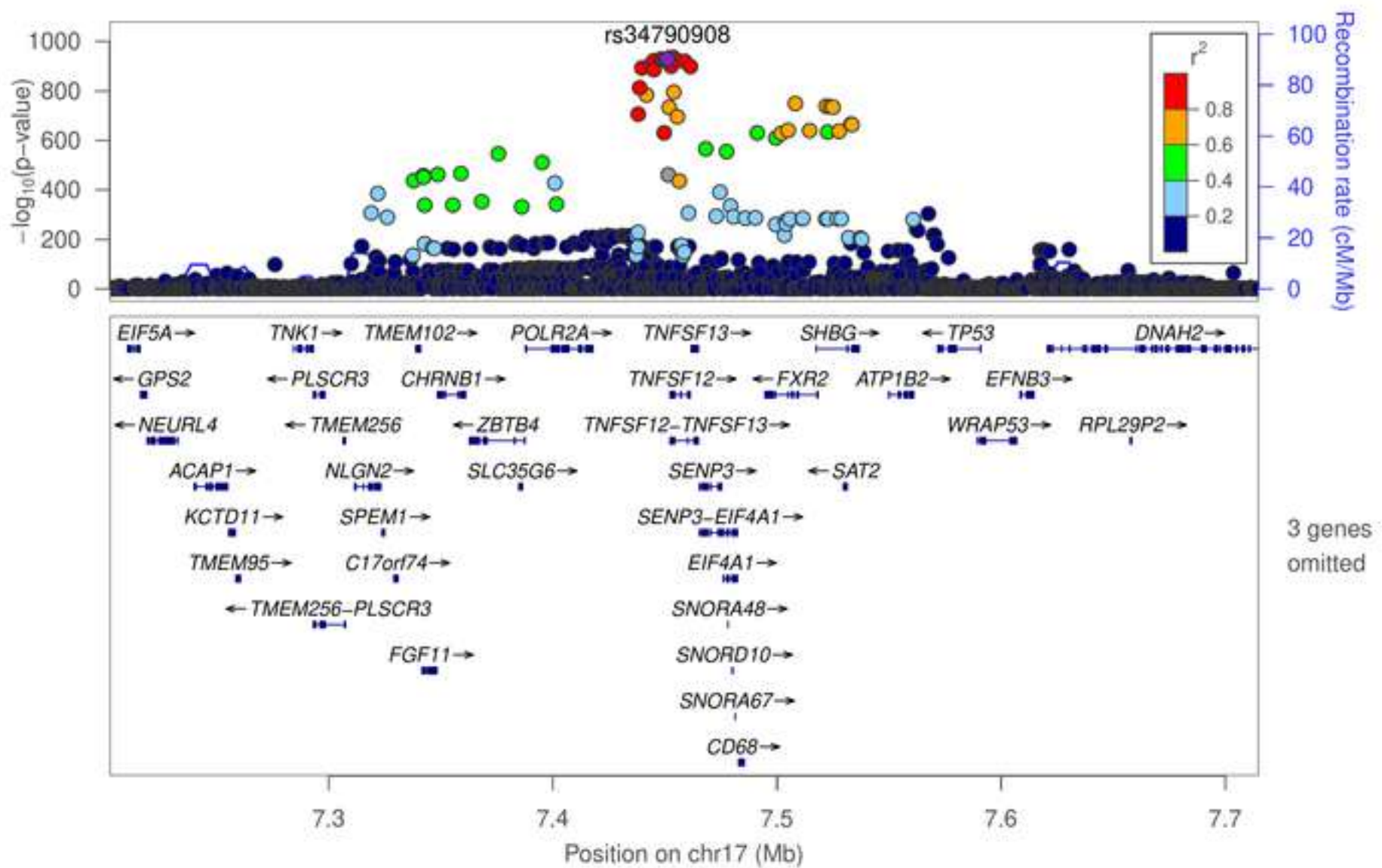
eQTLGen: TRANCE (TNFSF11)–rs4512994



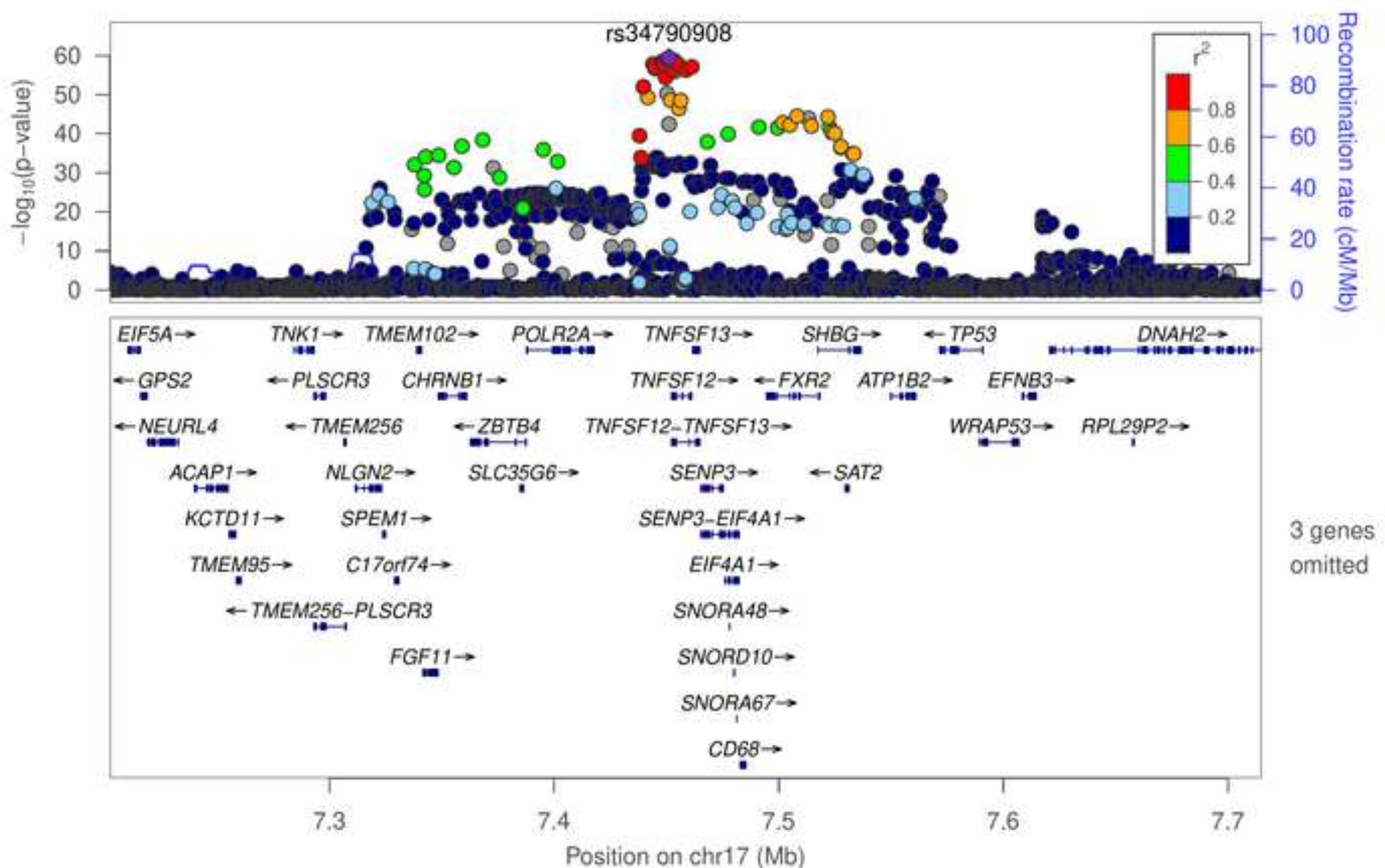
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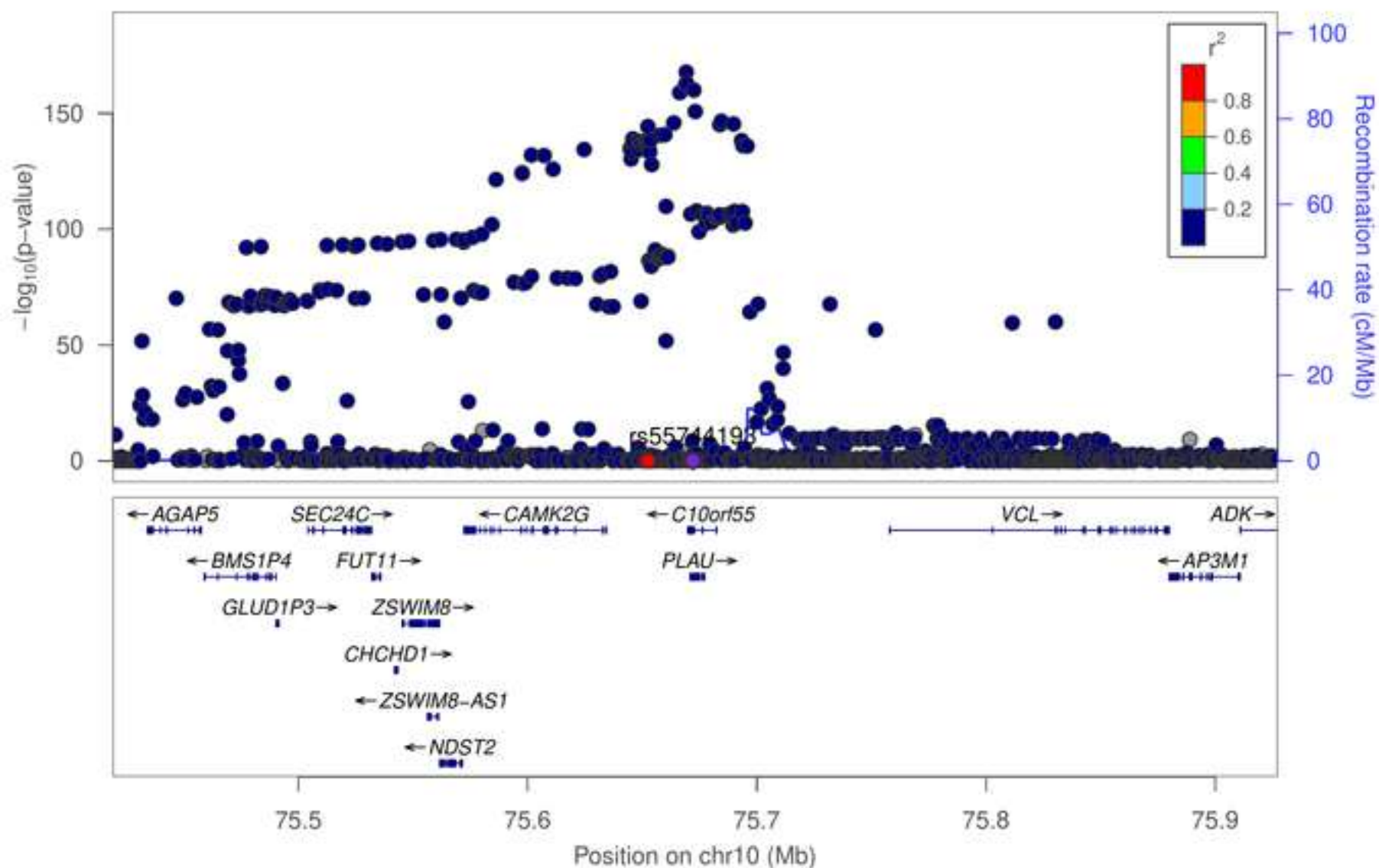
eQTLGen: TWEAK (TNFSF12)–rs34790908



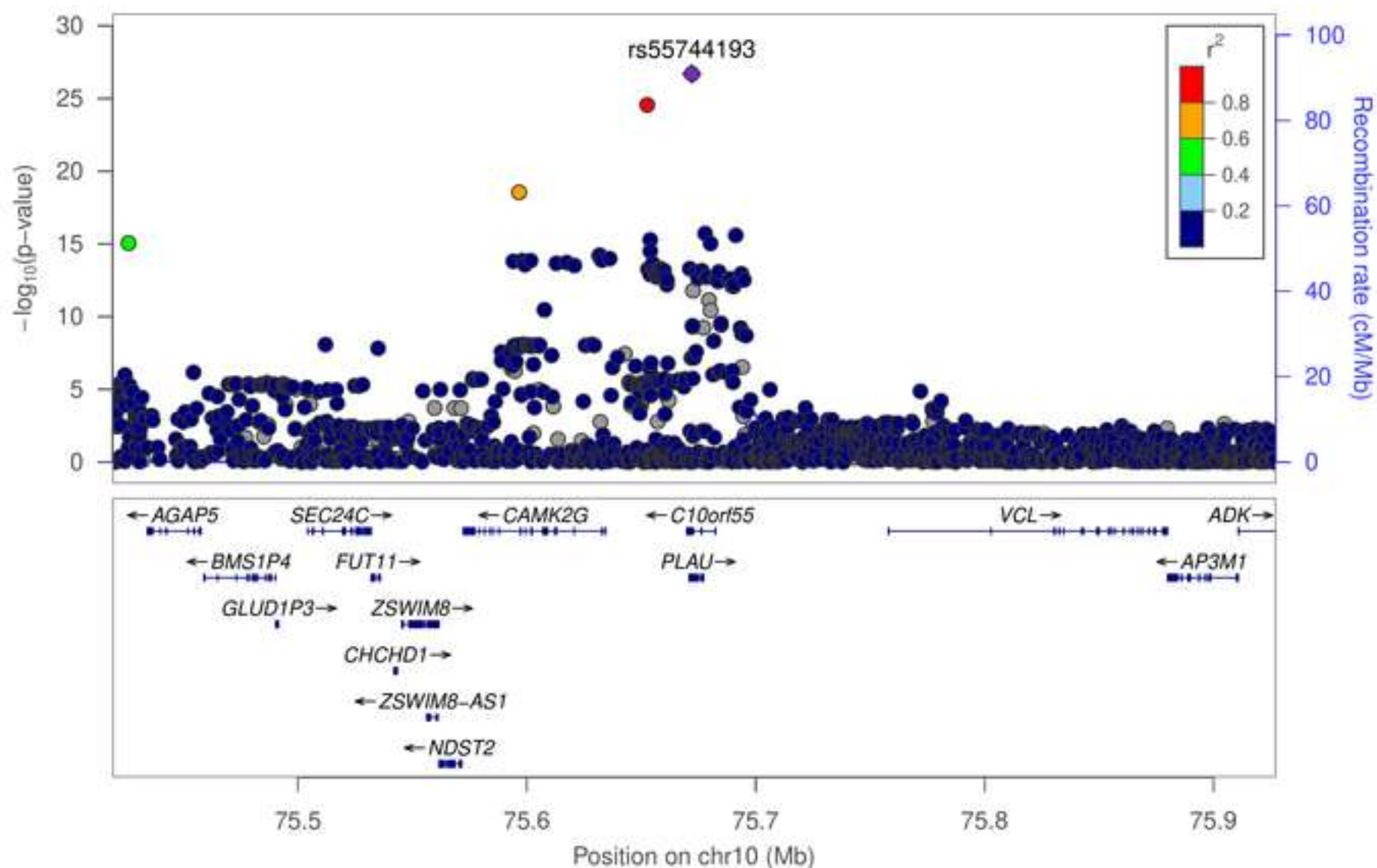
SCALLOP: TWEAK (TNFSF12)–rs34790908



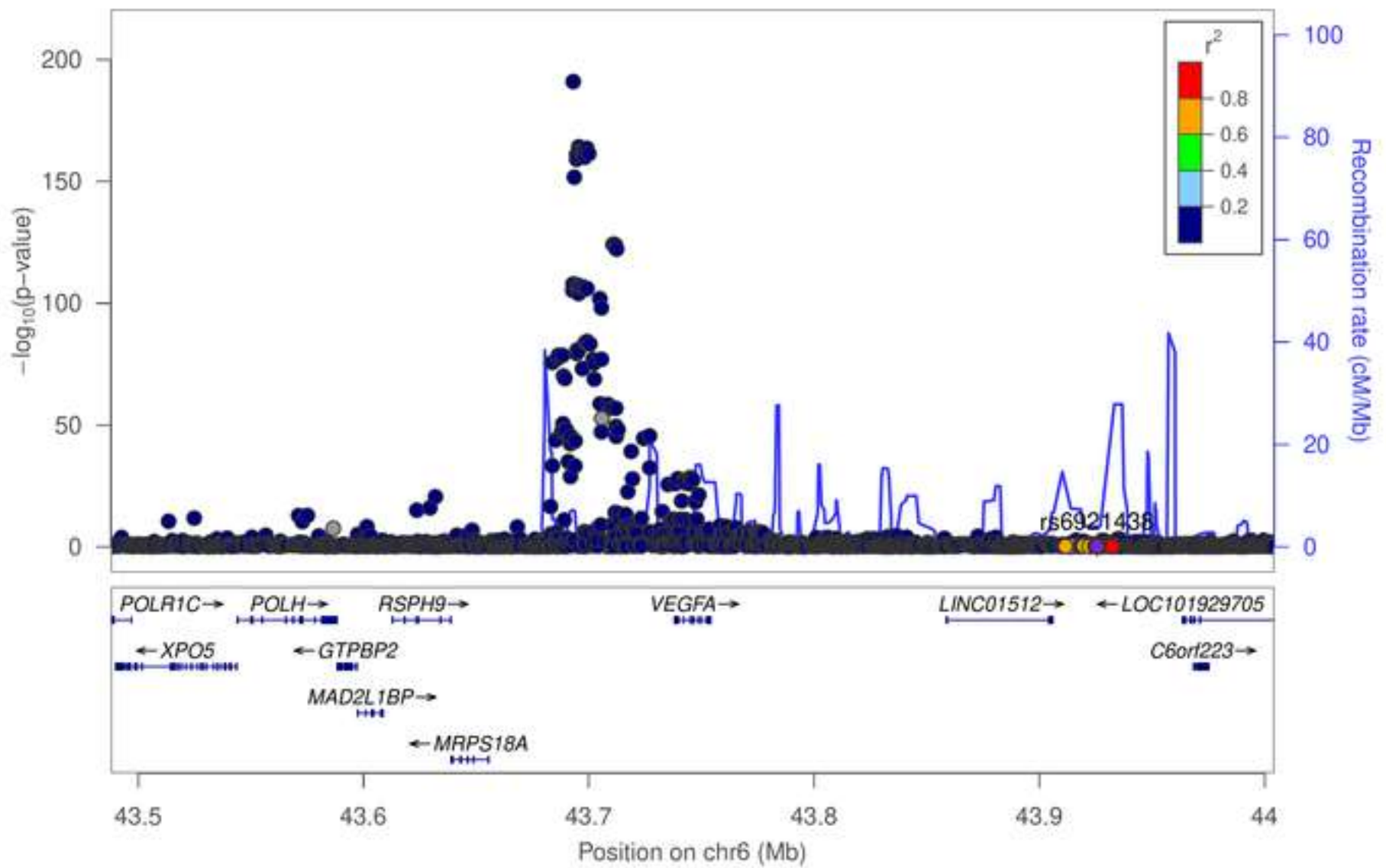
eQTLGen: uPA (PLAU)–rs55744193



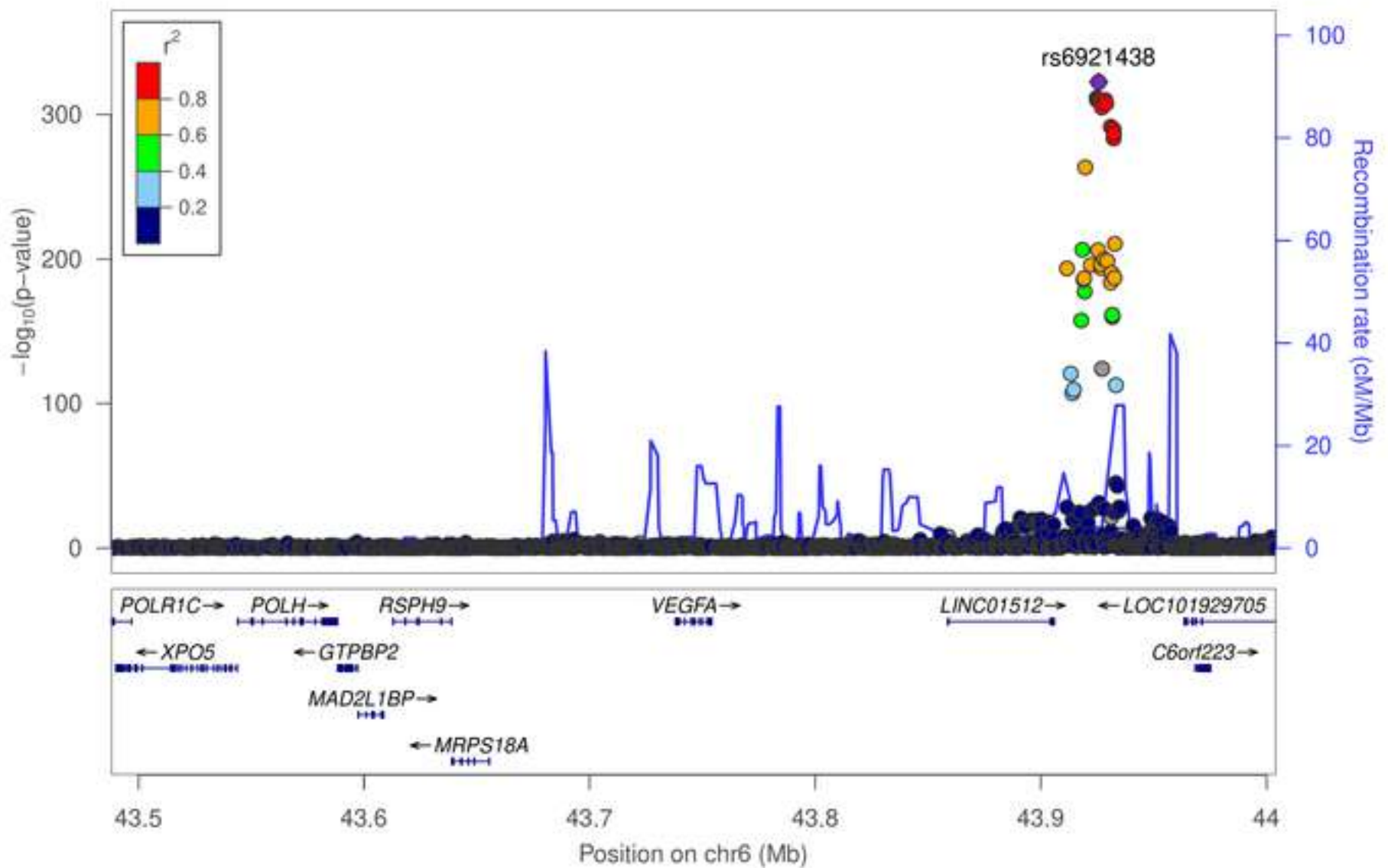
SCALLOP: uPA (PLAU)–rs55744193



eQTLGen: VEGF_A (VEGFA)–rs6921438

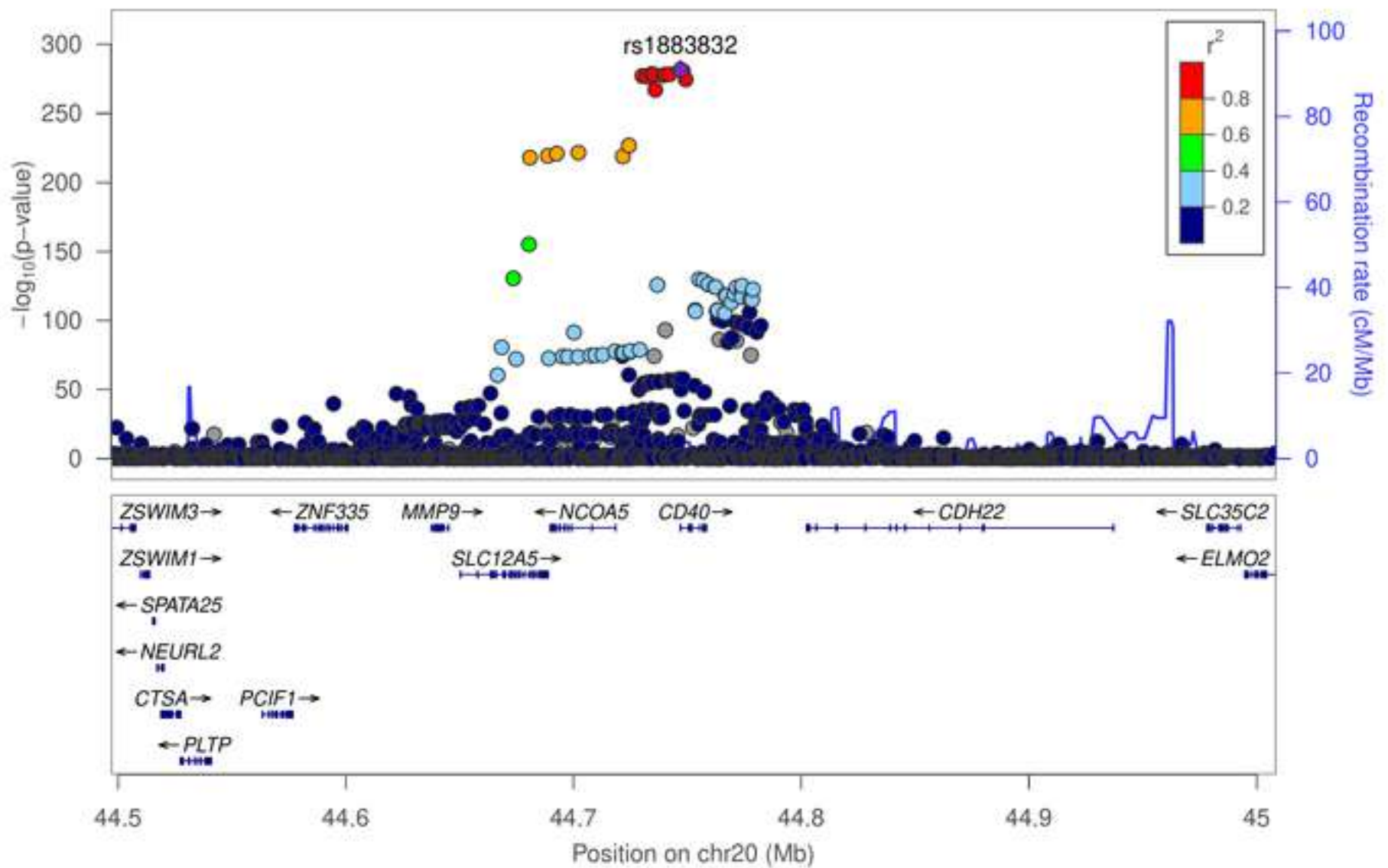


SCALLOP: VEGF_A (VEGFA)–rs6921438

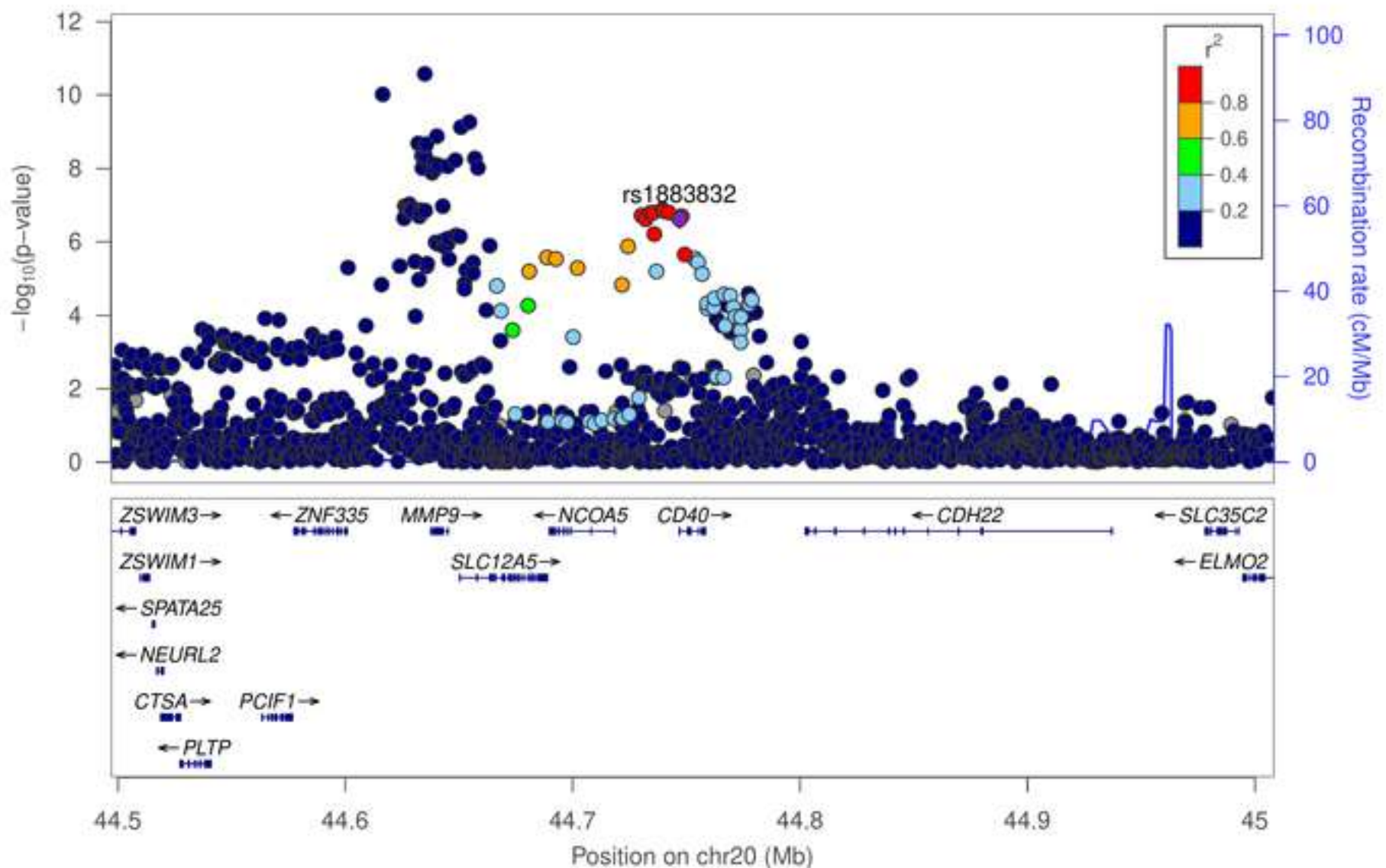


Supplementary Figure 4. Regional association plots comparing plasma *cis*-pQTLs and disease associations. 'LocusZoom' regional association plots comparing the plasma *cis*-pQTL signals (upper panel) with the relevant disease signals (lower panel) for the 12 protein-disease pairs with significant GSMR results following our initial filters prior to colocalisation testing (see Methods). The sentinel variant for the pQTL is coloured in purple. LD (r^2) to the sentinel pQTL is indicated by the colour key. For pQTLs, two-sided P -values are from meta-analysis of linear regression estimates. For diseases, P -values are from logistic regression.

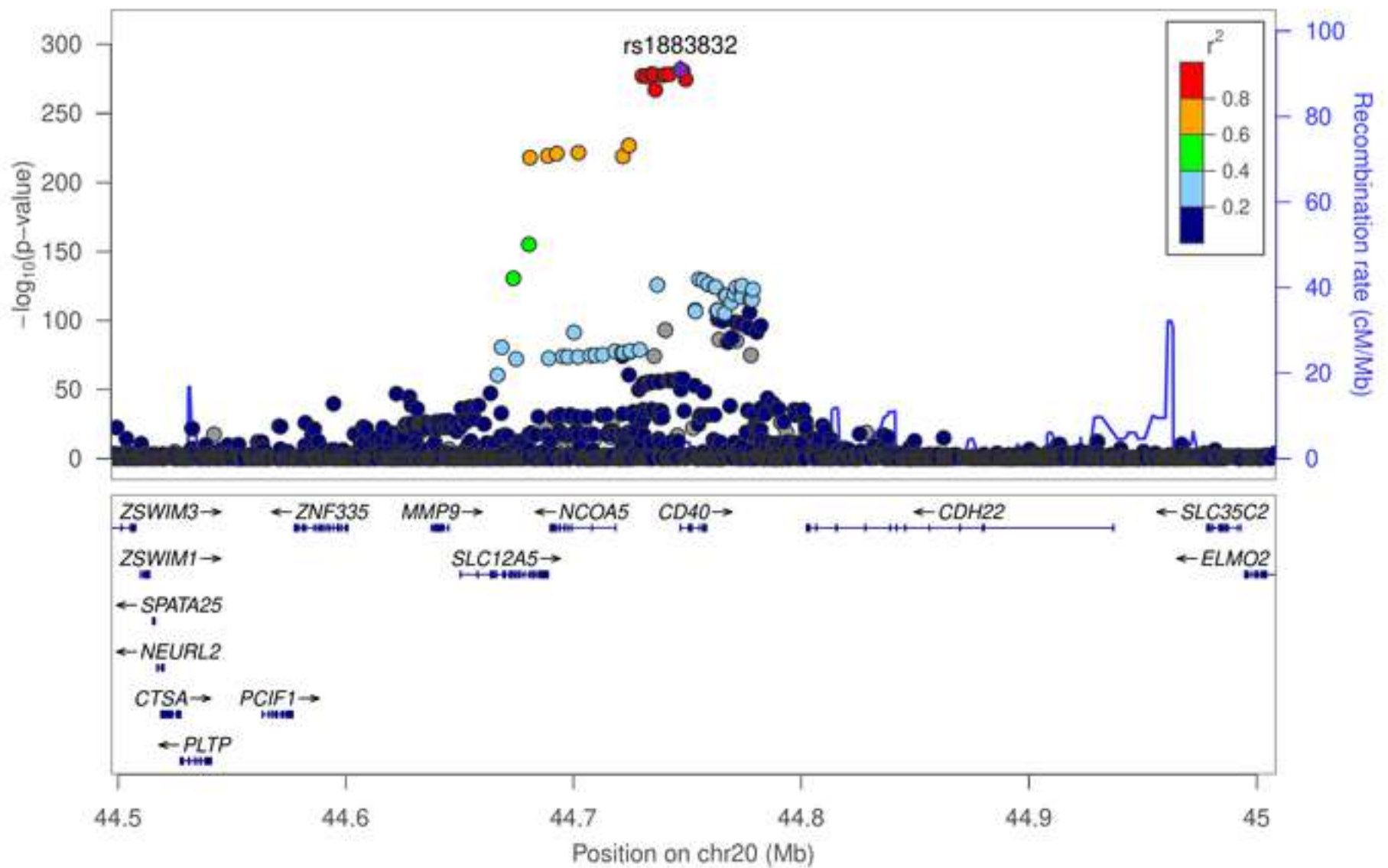
SCALLOP: CD40-rs1883832



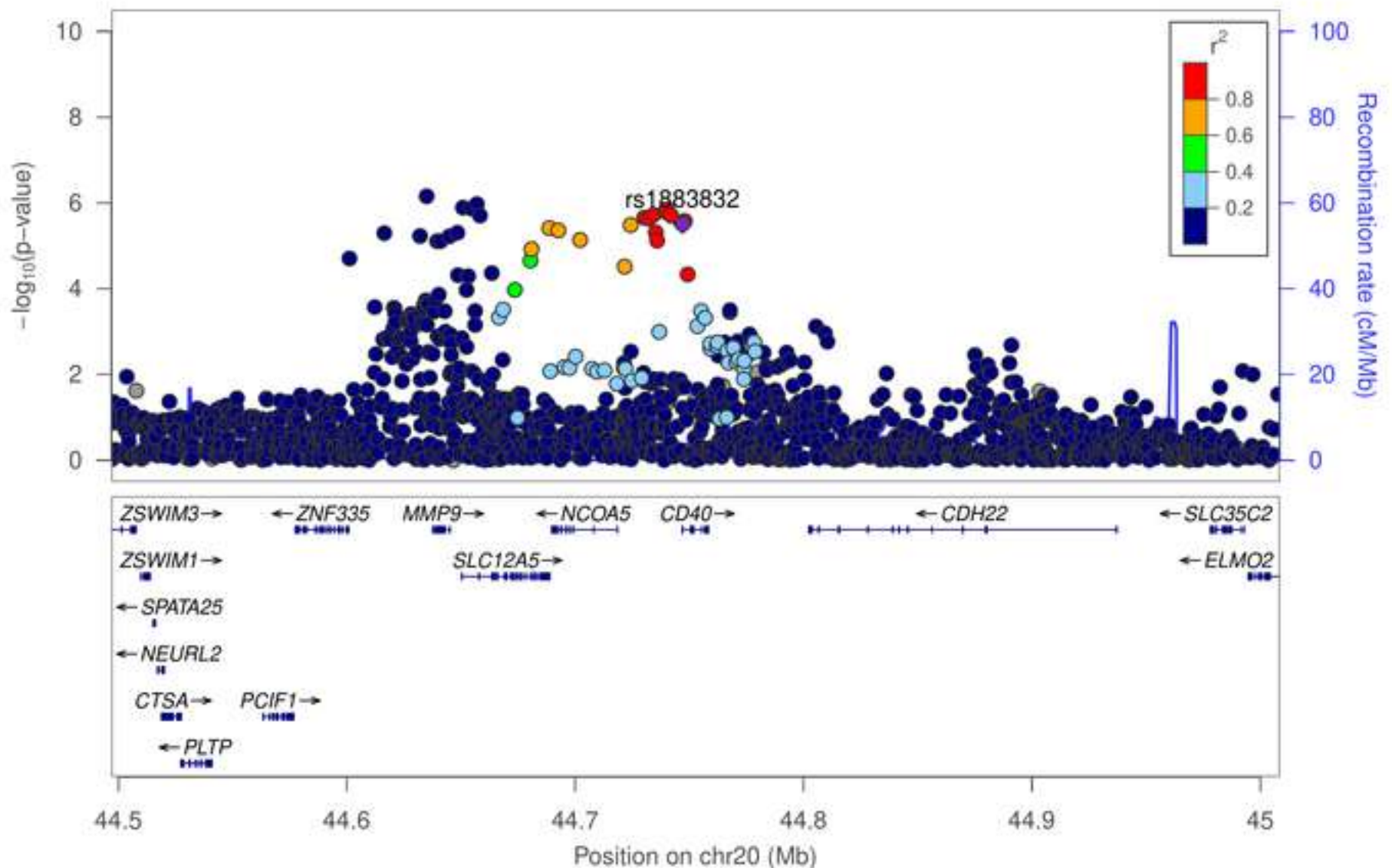
'Crohns disease'(ebi-a-GCST004132)-rs1883832



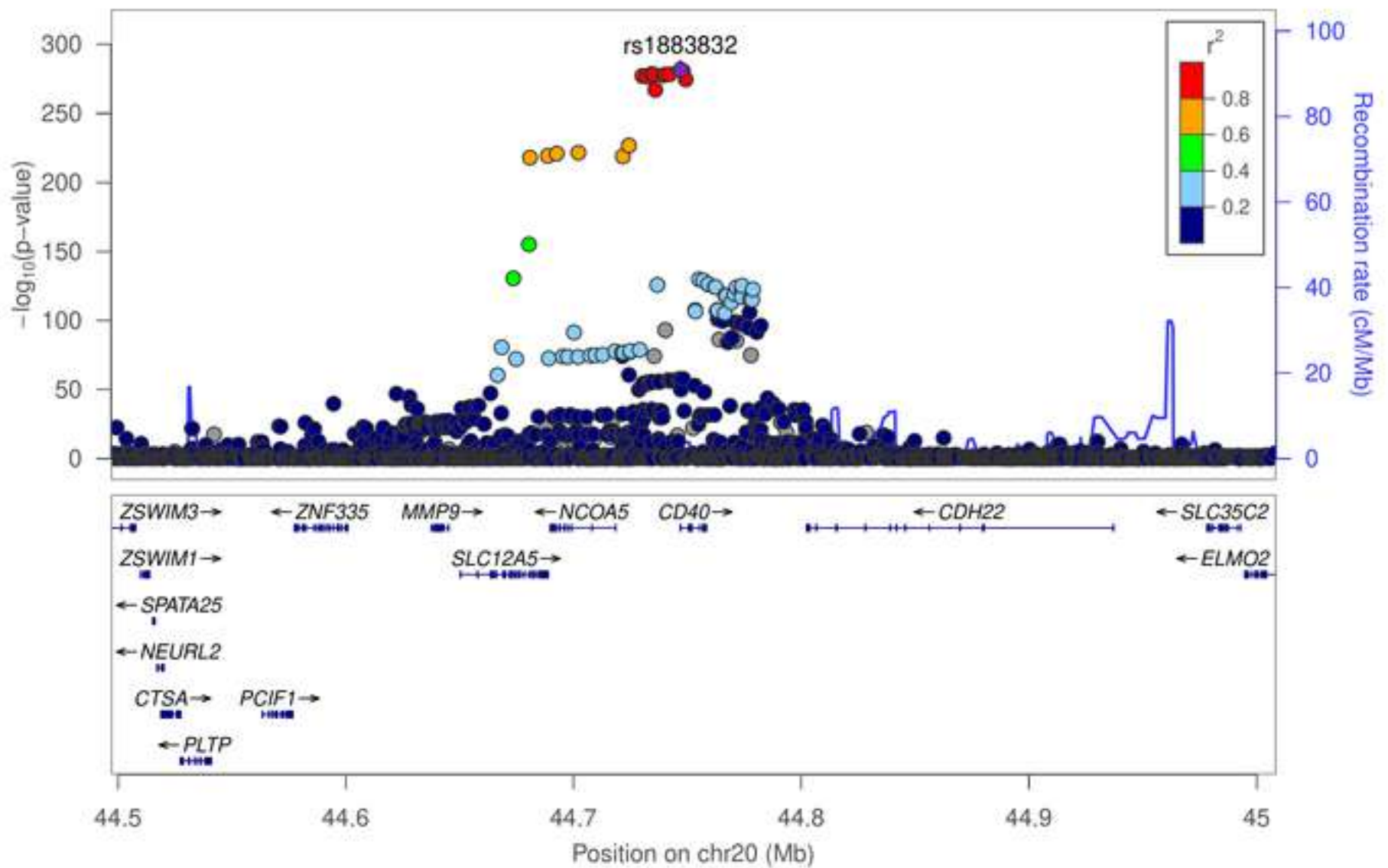
SCALLOP: CD40-rs1883832



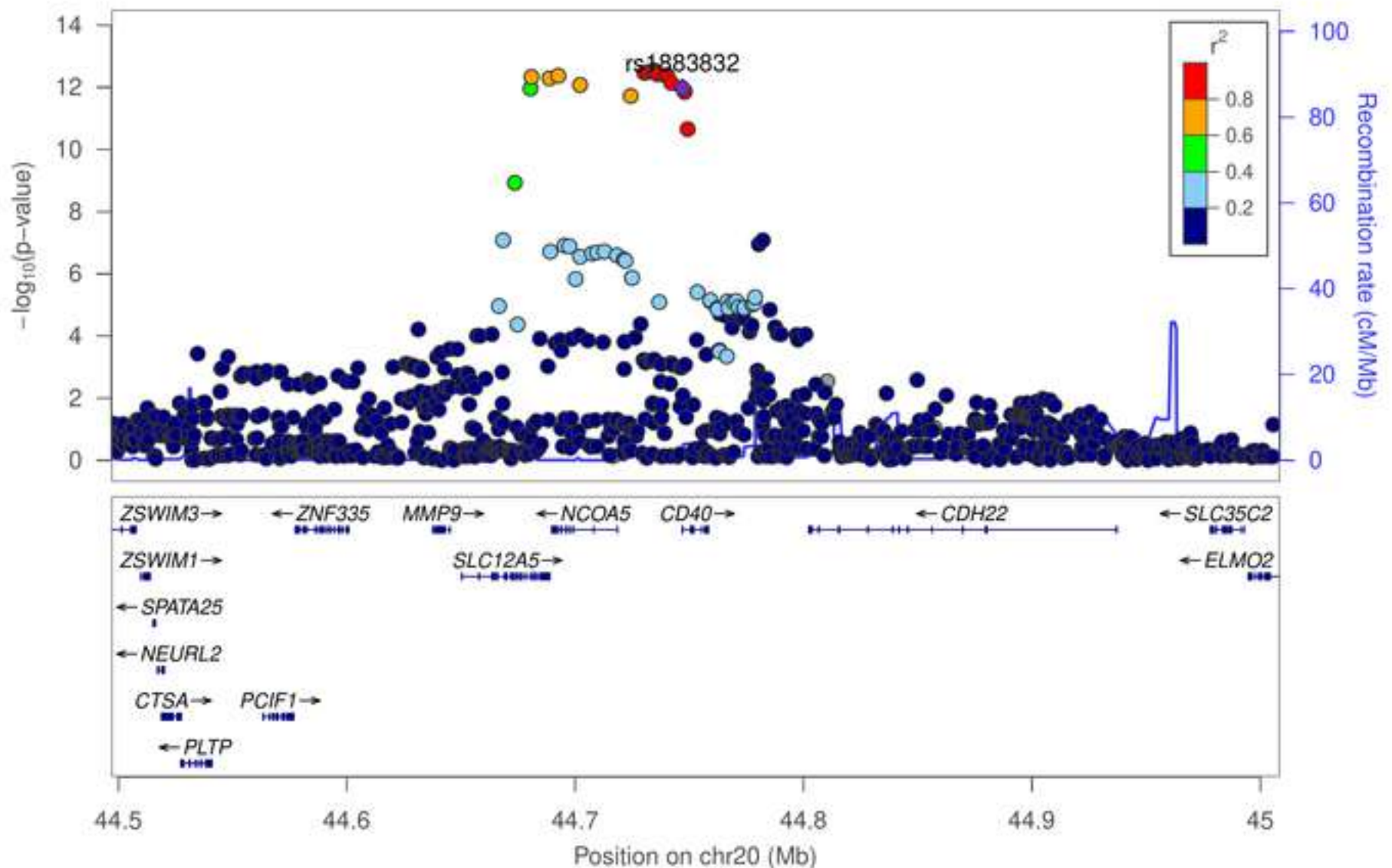
'Inflammatory bowel disease'(ebi-a-GCST004131)-rs1883832



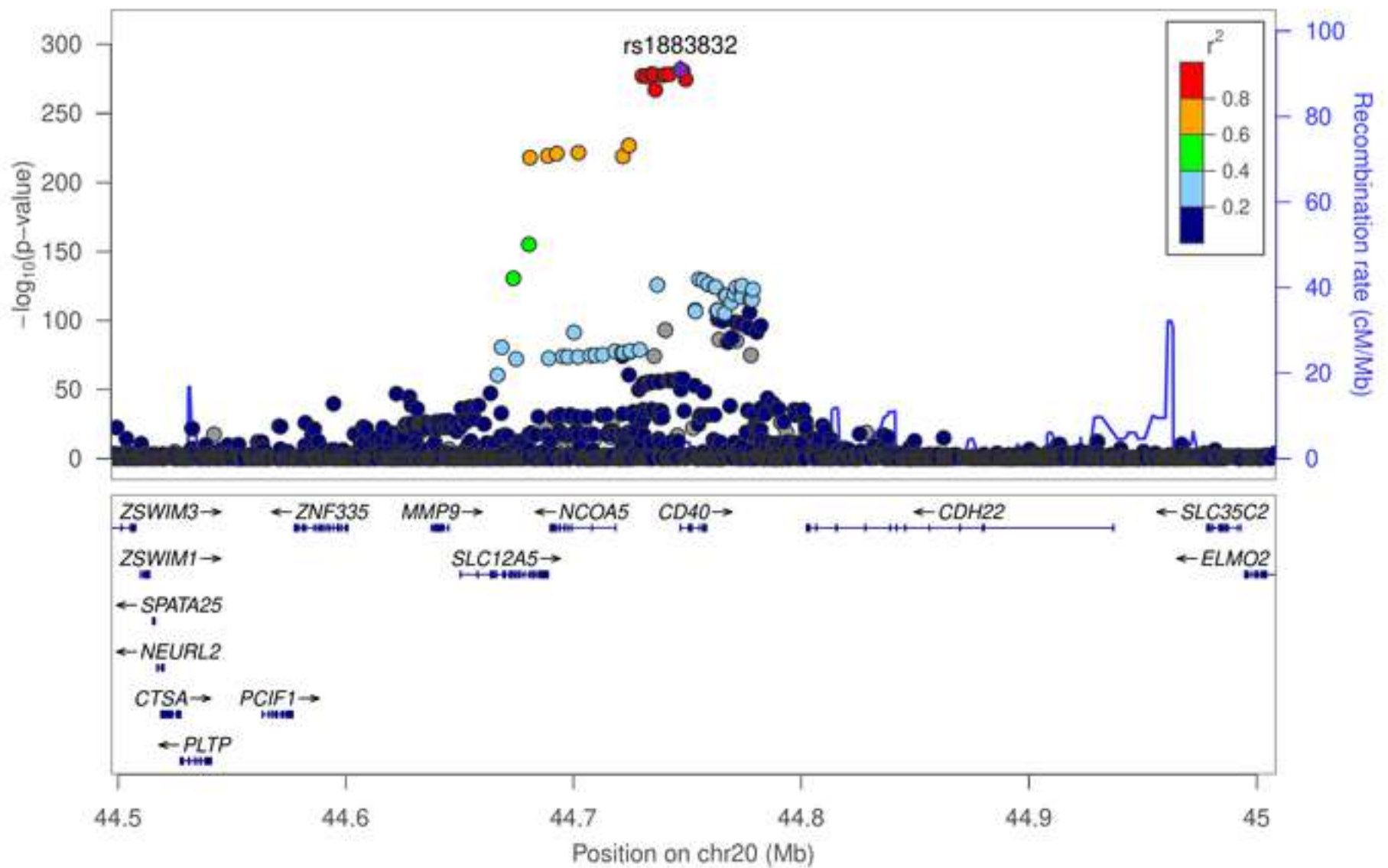
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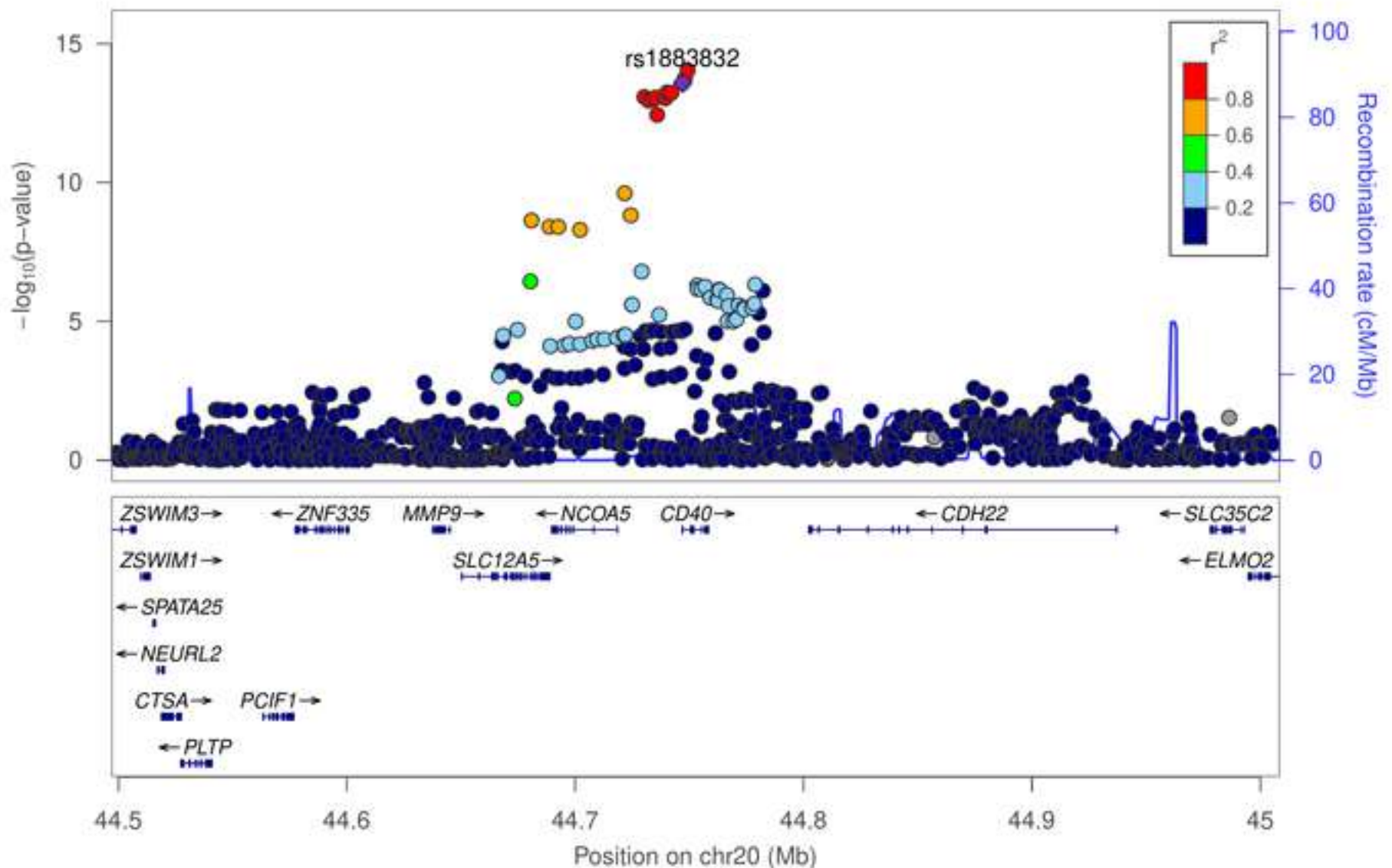
'Multiple sclerosis'(ieu-b-18)-rs1883832



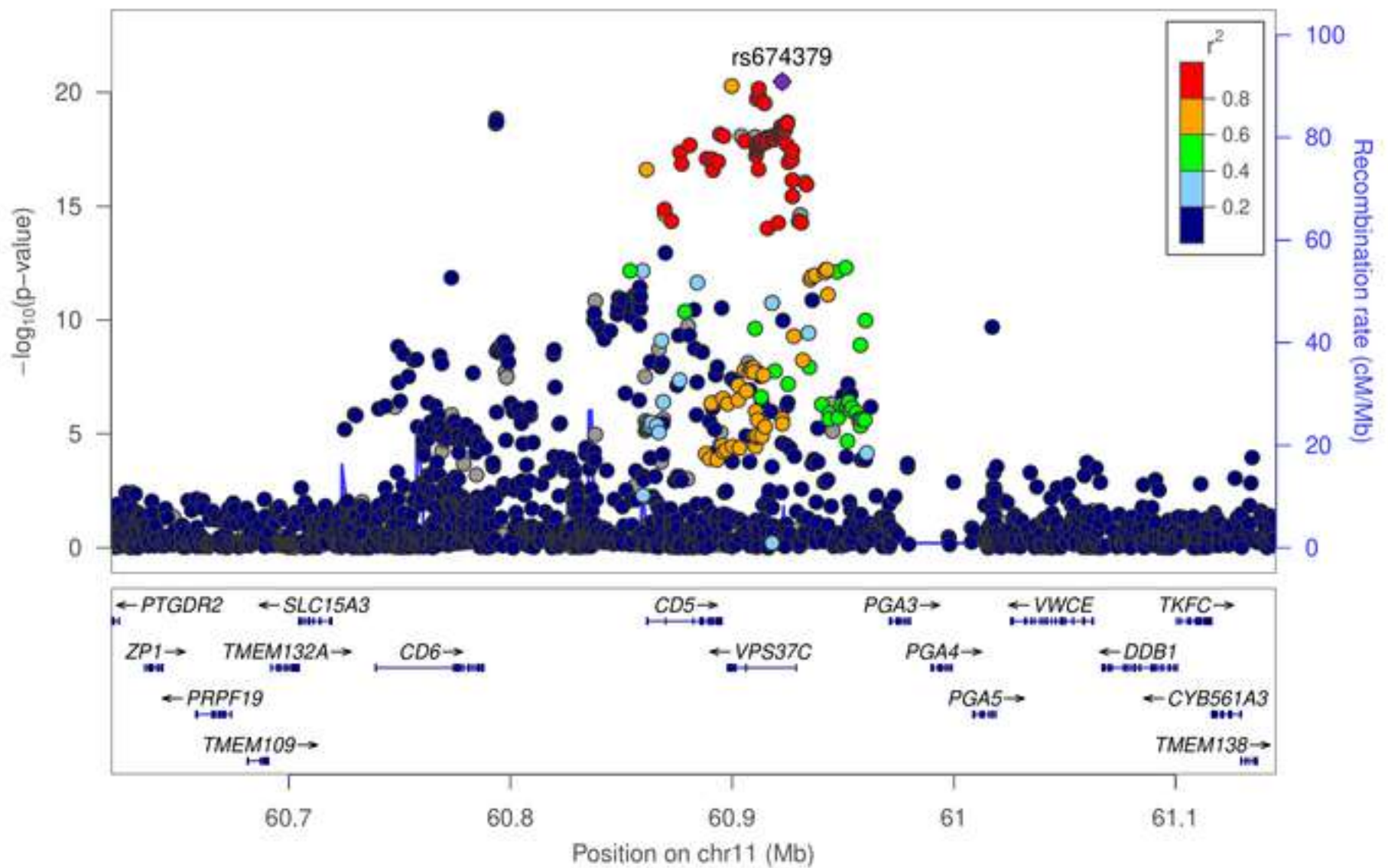
SCALLOP: CD40-rs1883832



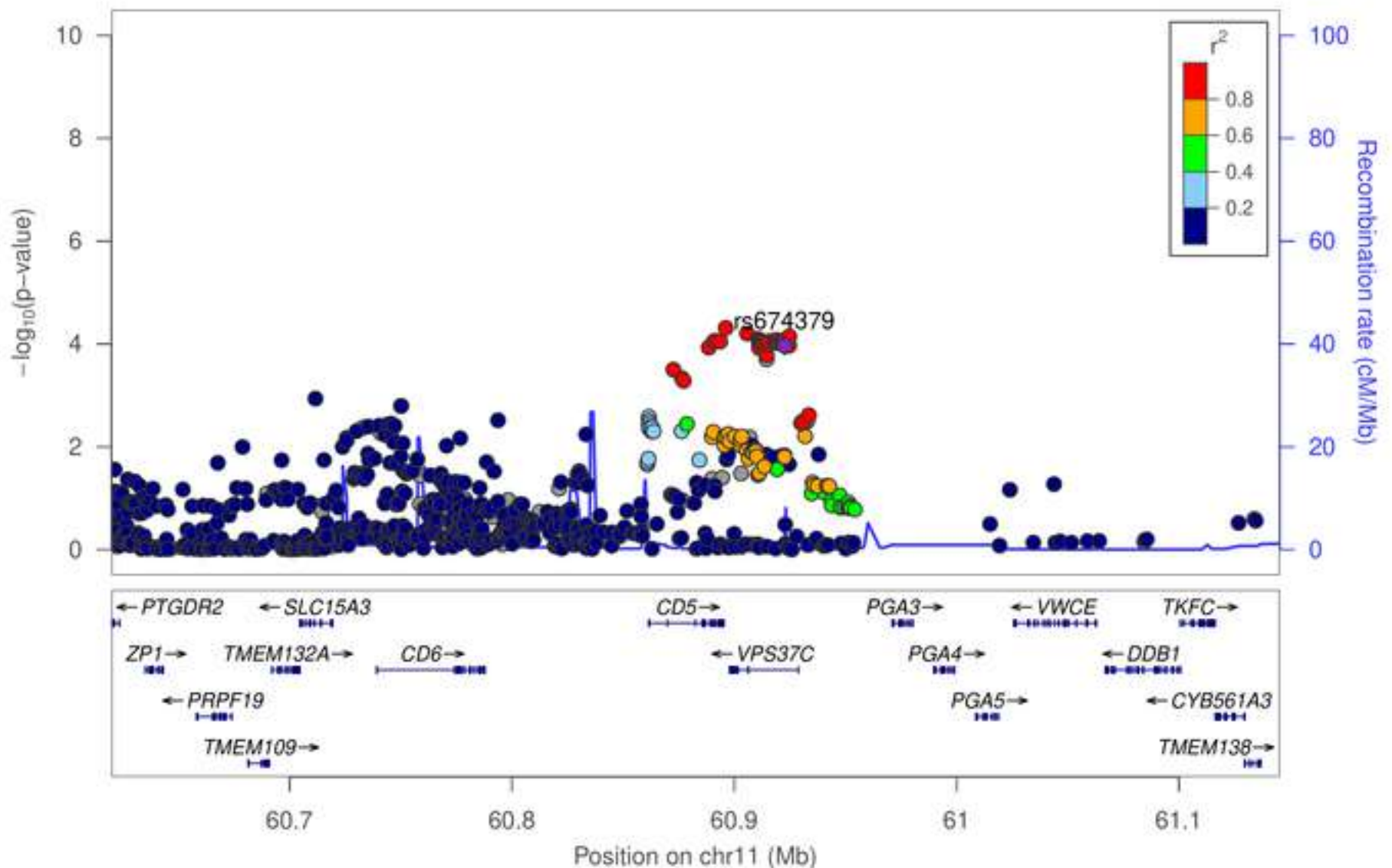
'Rheumatoid arthritis'(ieu-a-833)-rs1883832



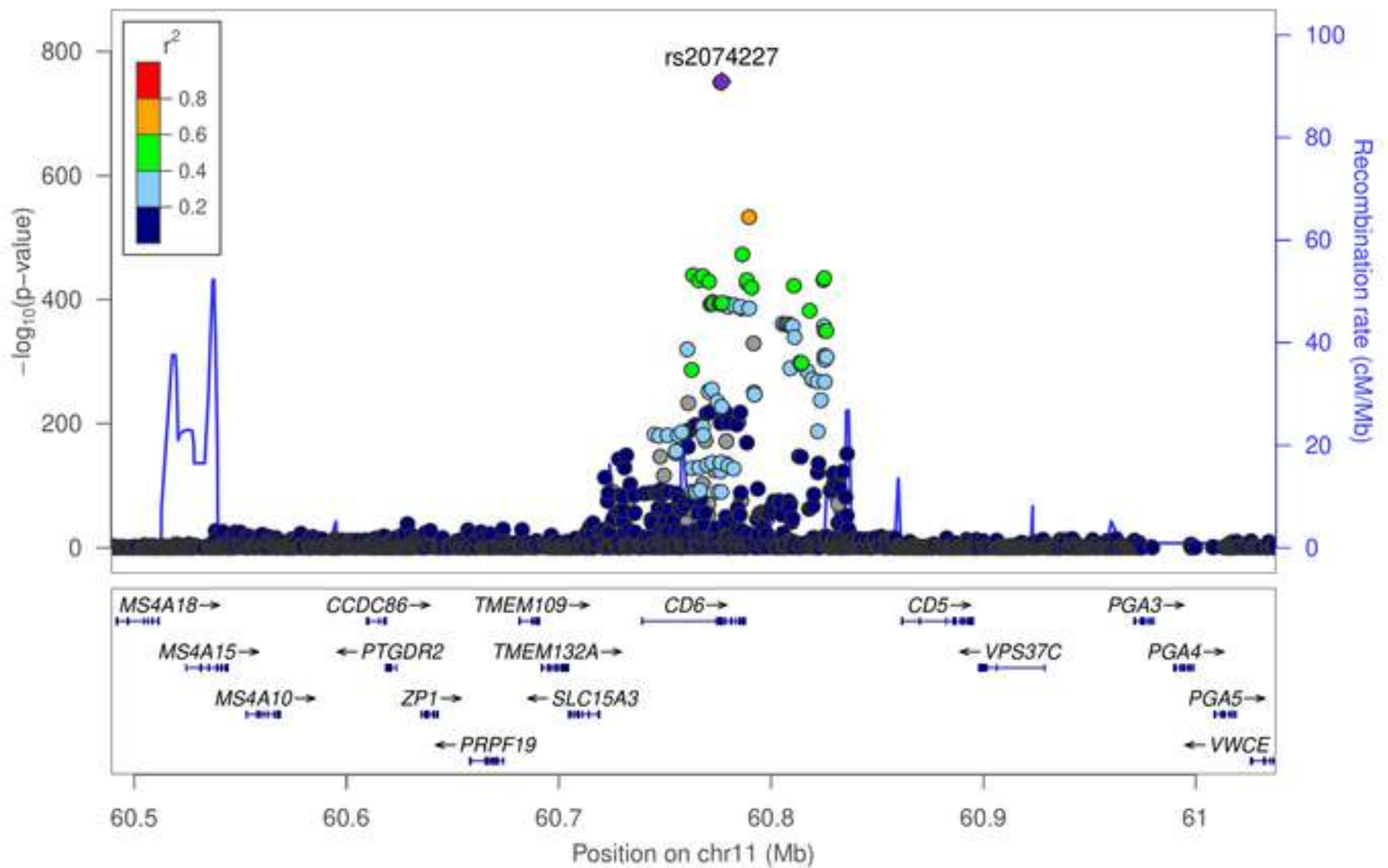
SCALLOP: CD5-rs674379



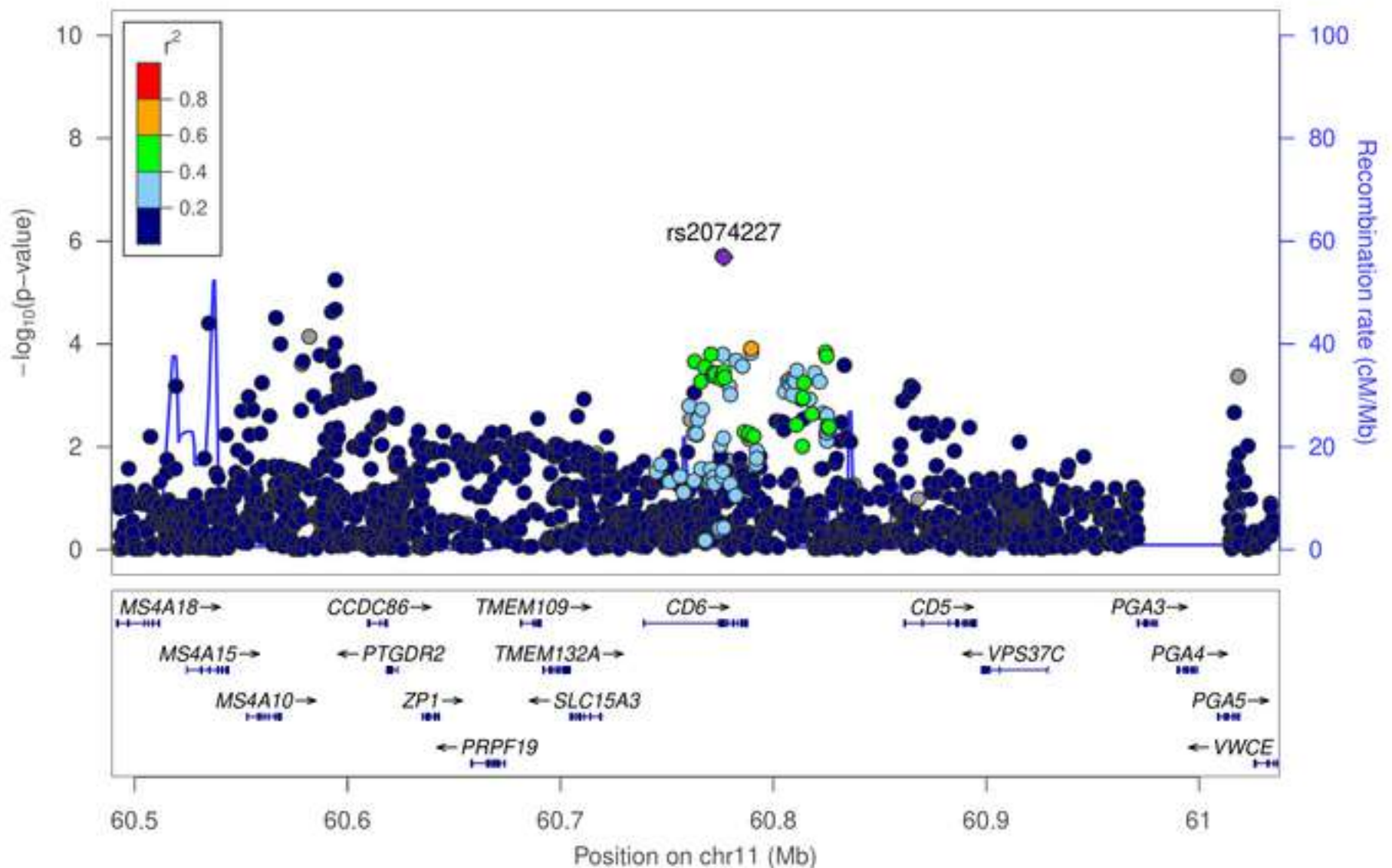
'Primary sclerosing cholangitis'(ieu-a-1112)-rs674379



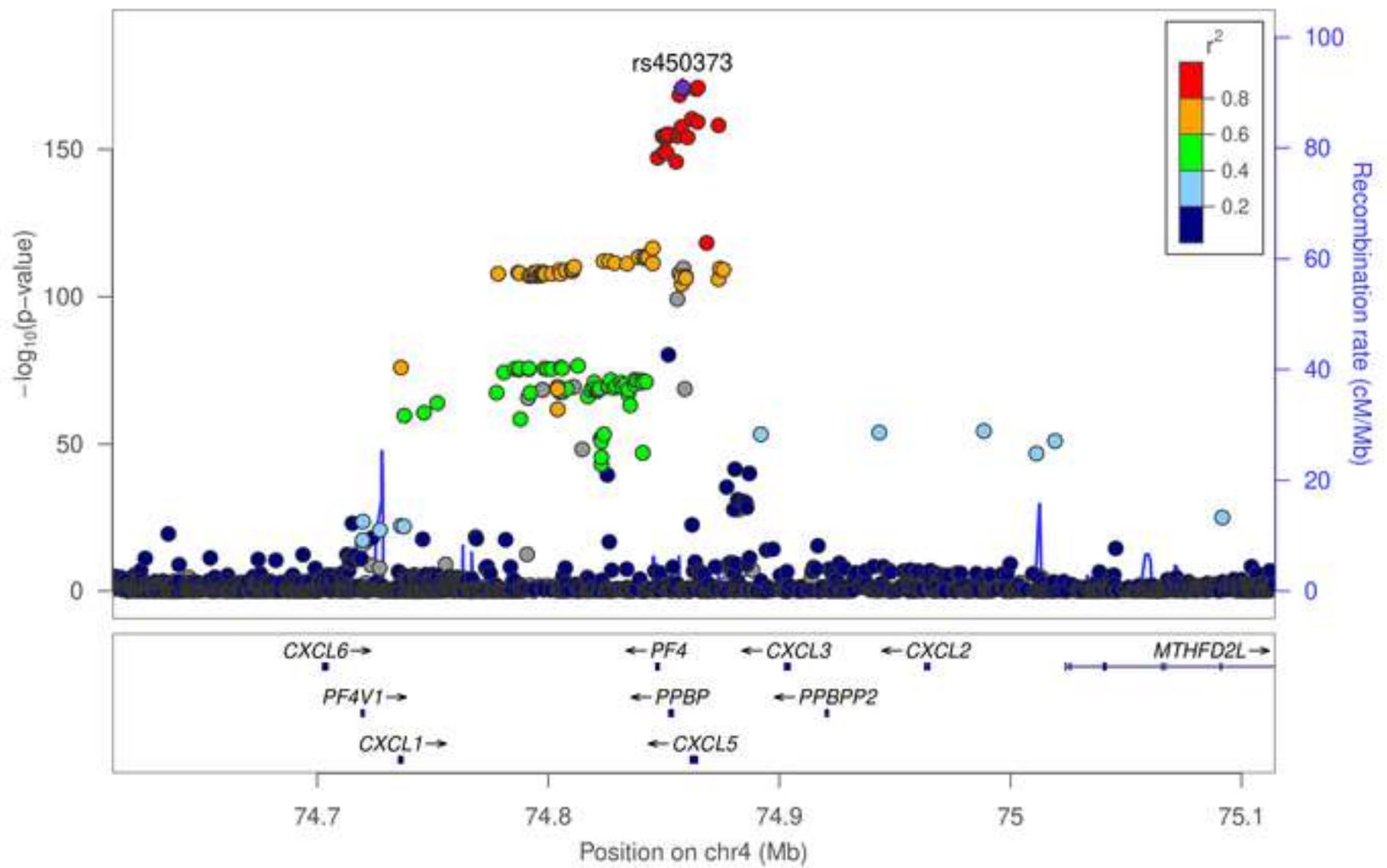
SCALLOP: CD6-rs2074227



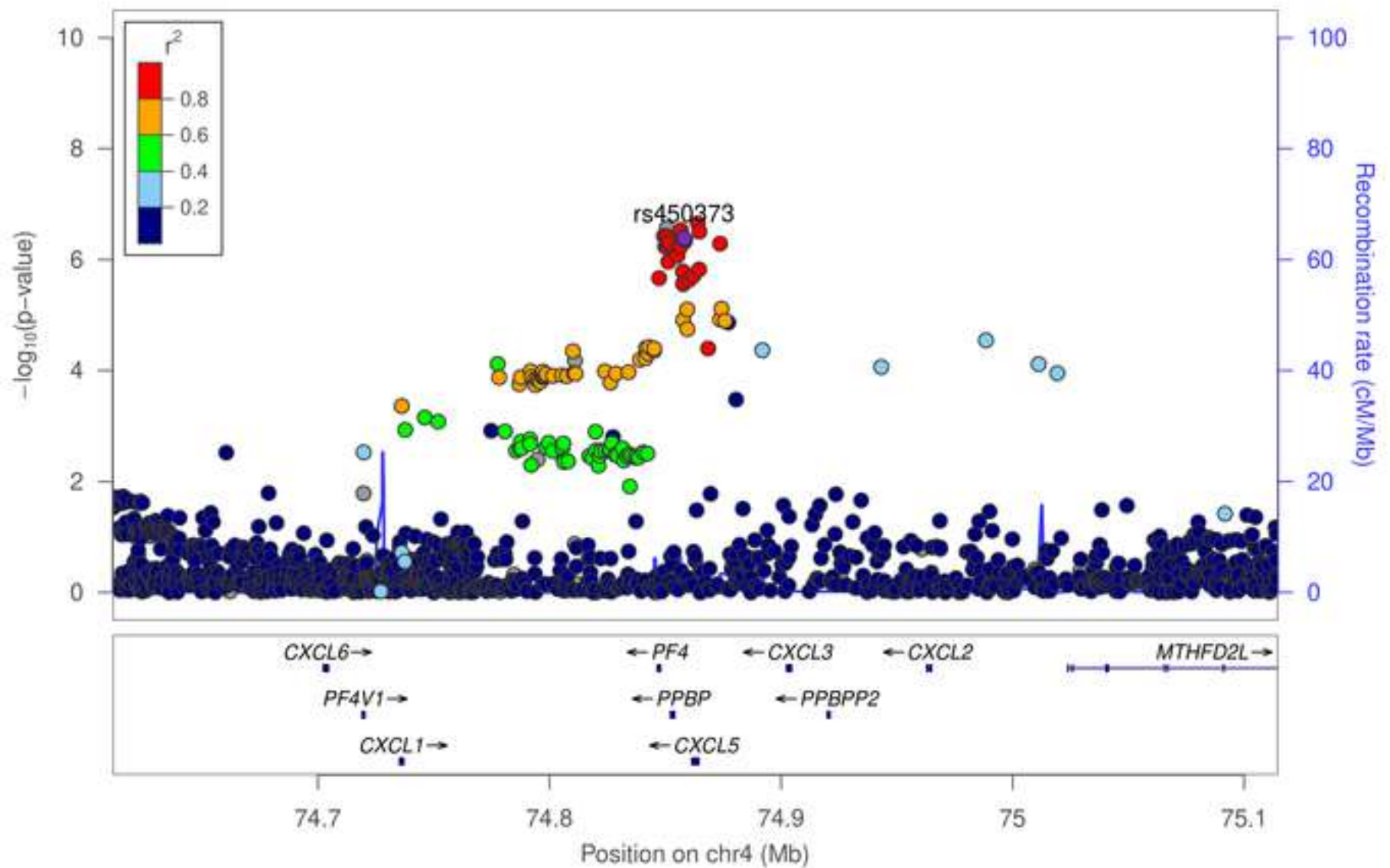
'Inflammatory bowel disease'(ebi-a-GCST004131)-rs2074227



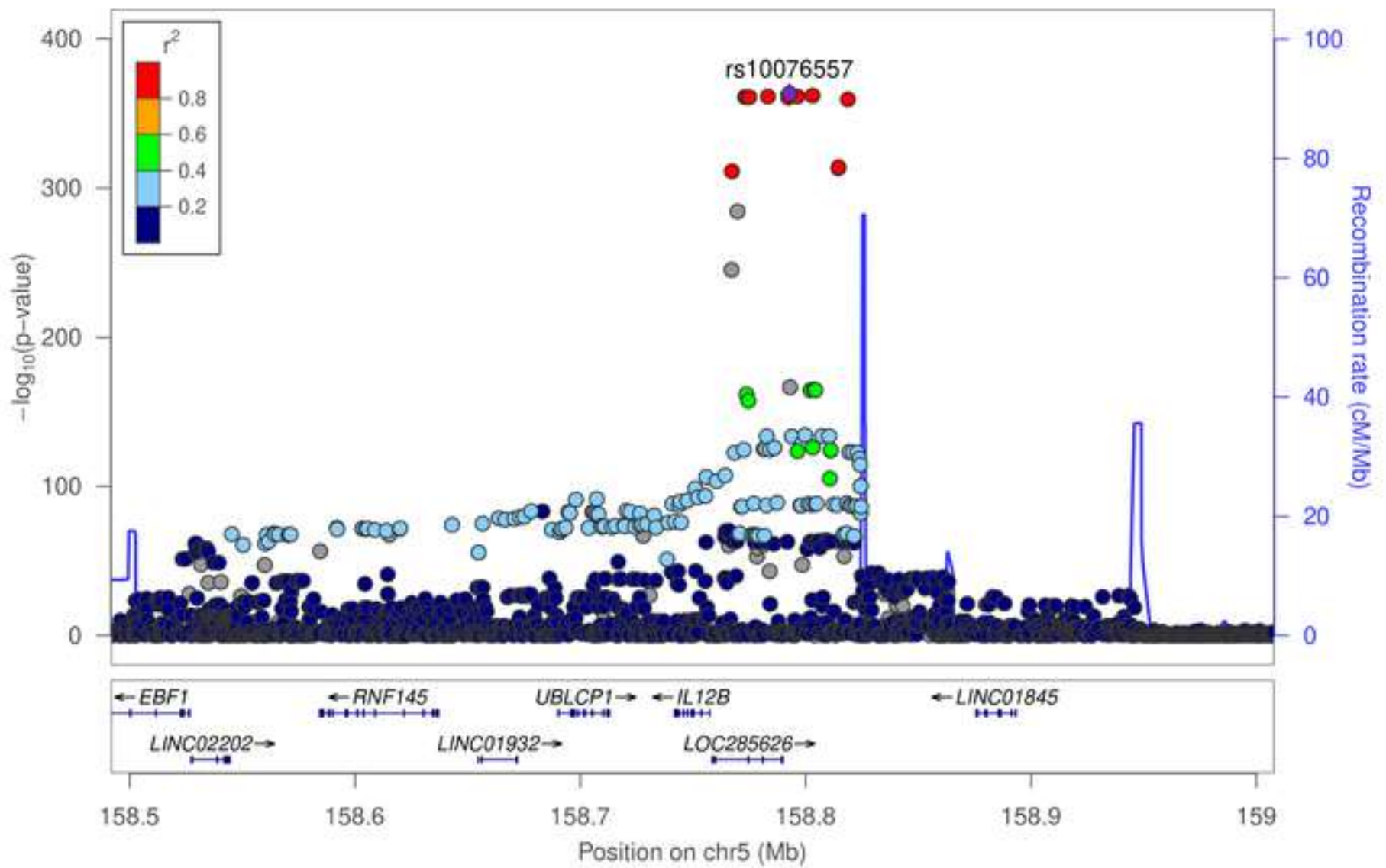
SCALLOP: CXCL5-rs450373



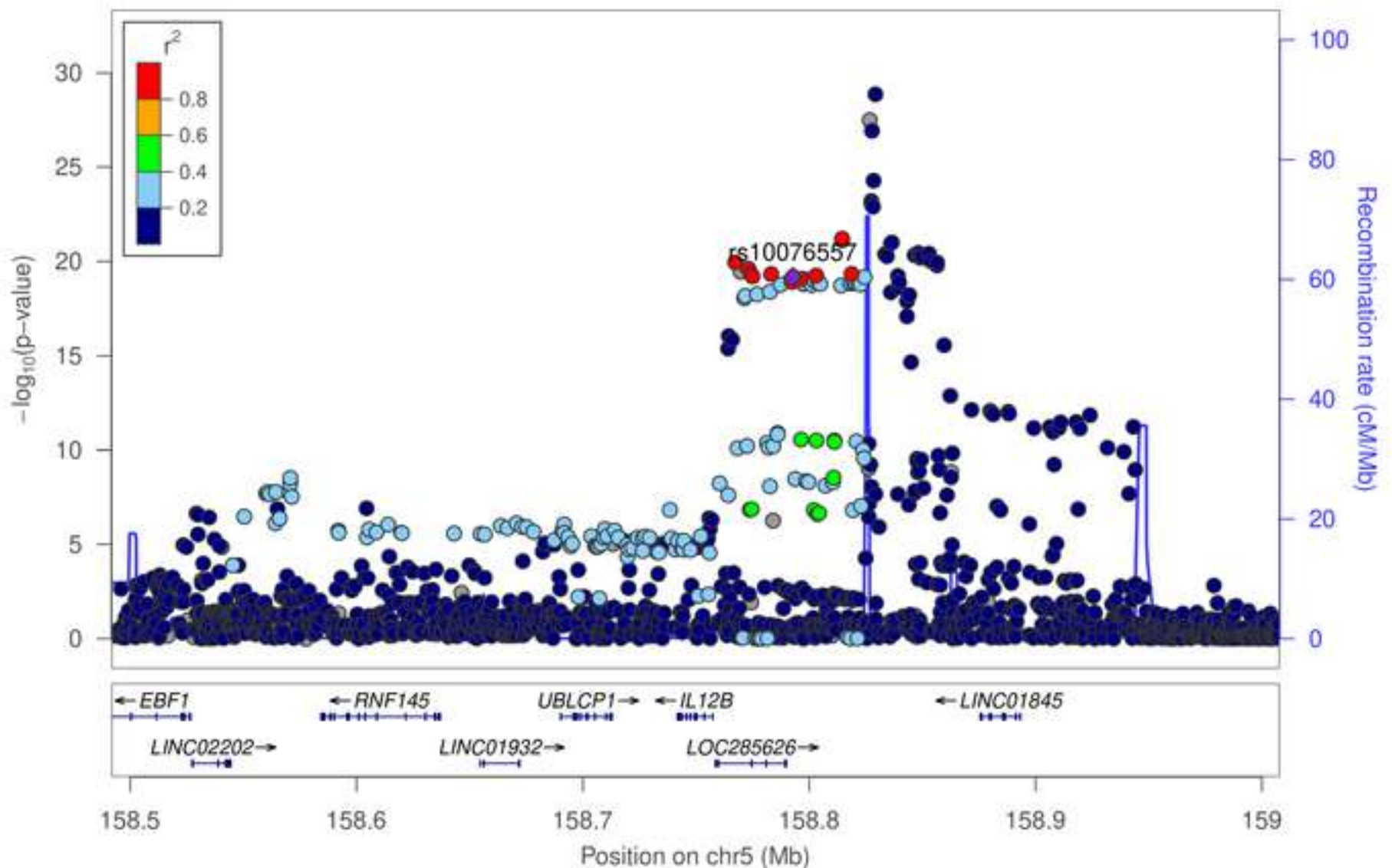
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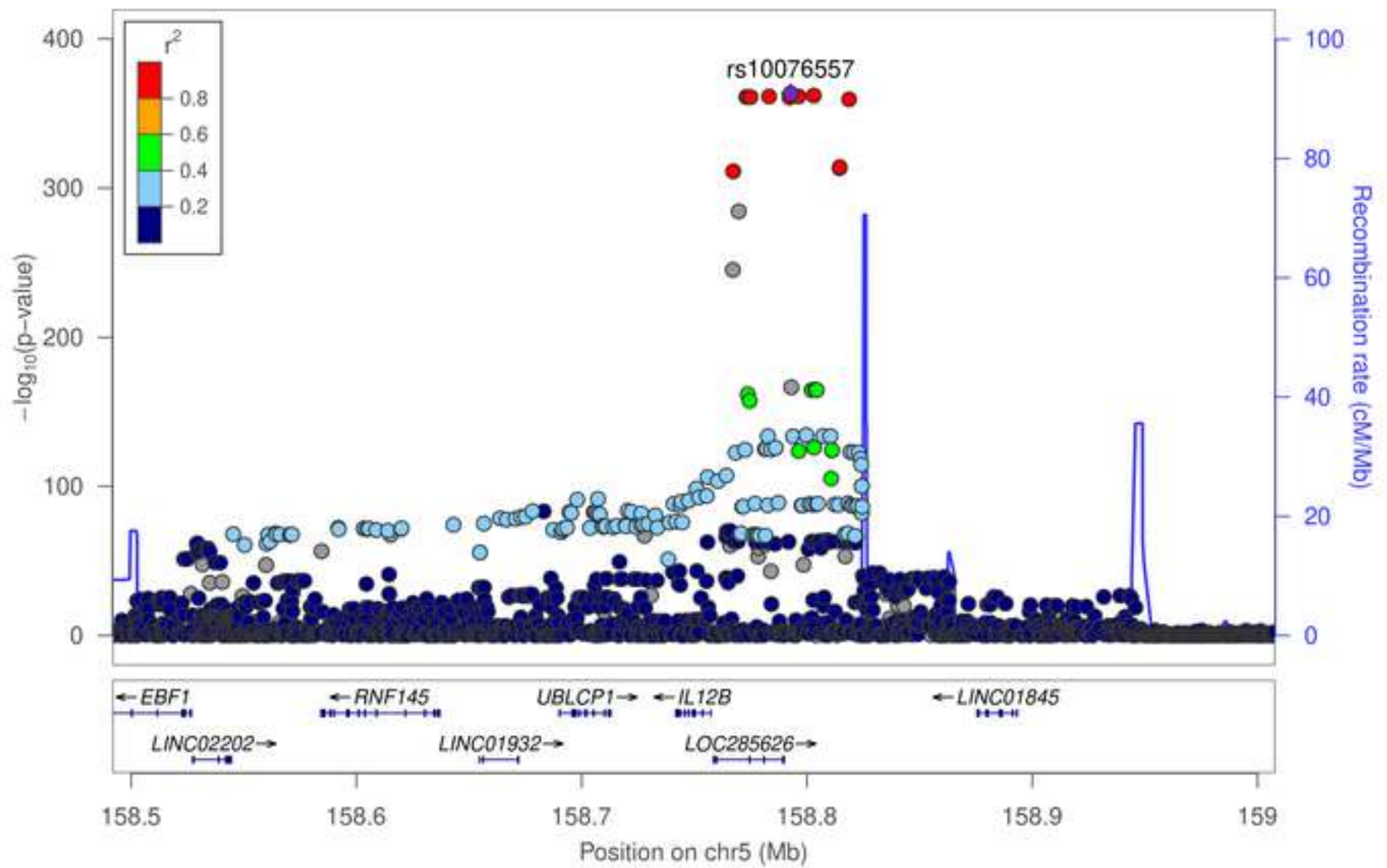
SCALLOP: IL12B-rs10076557



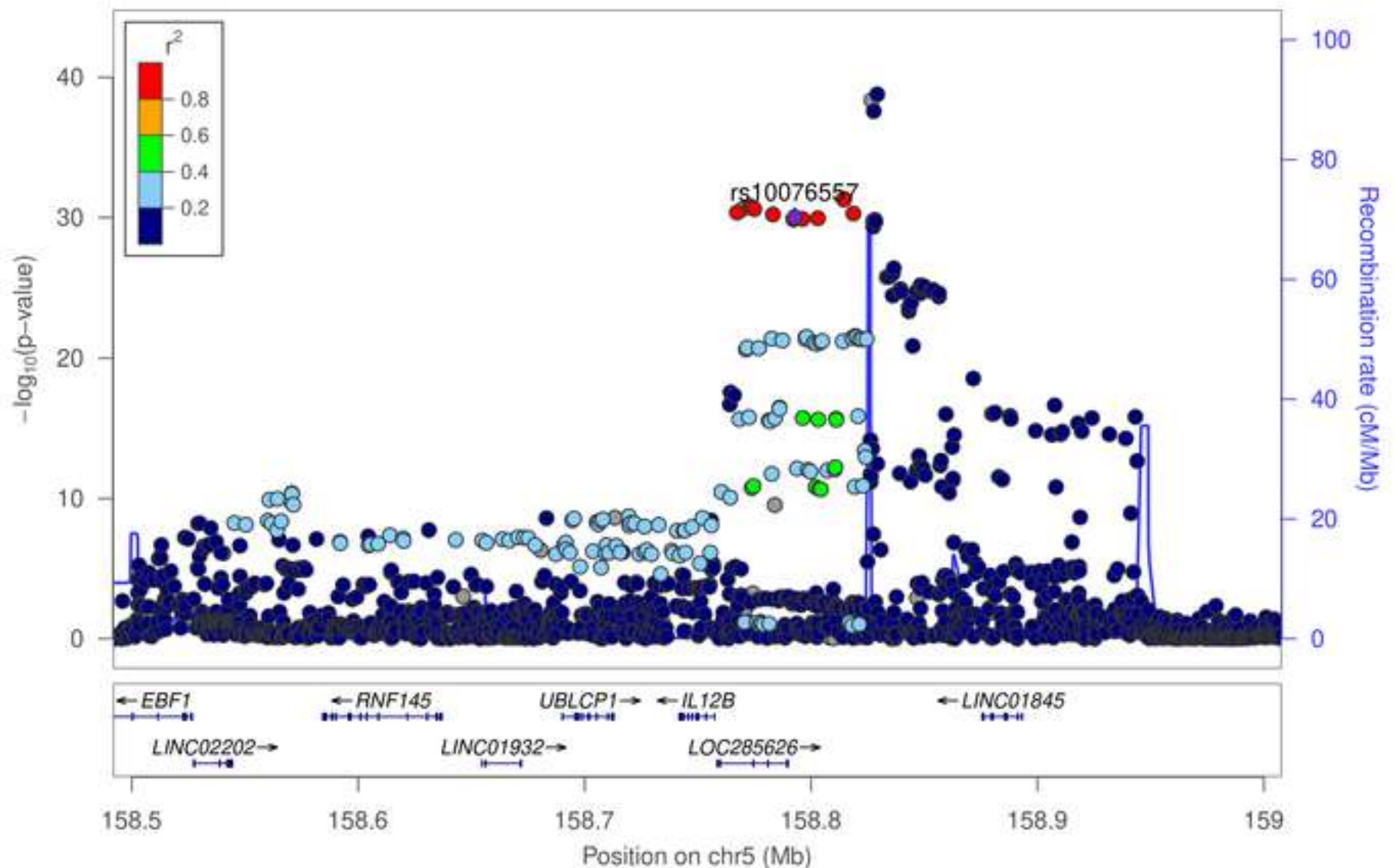
'Crohns disease'(ebi-a-GCST004132)-rs10076557



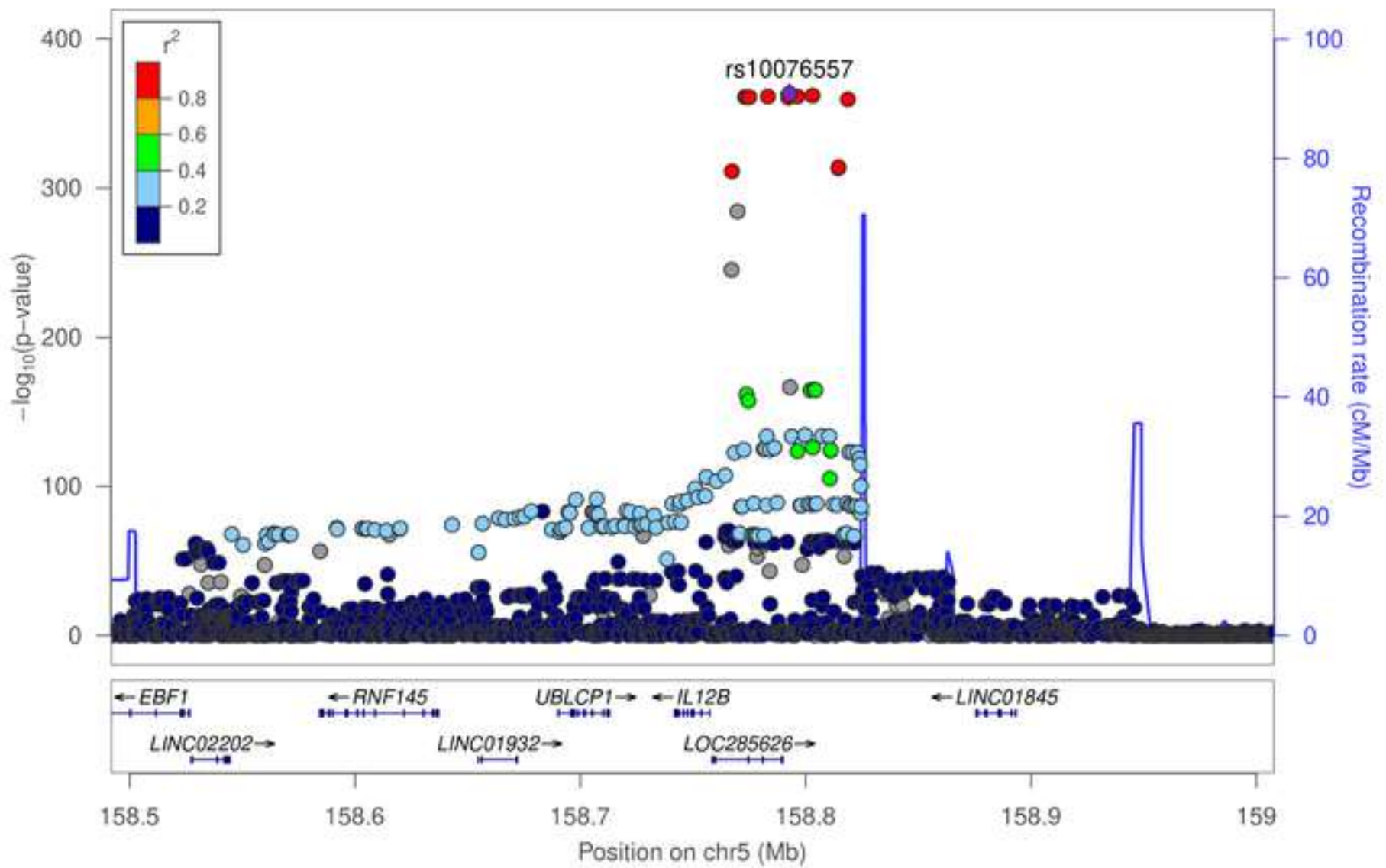
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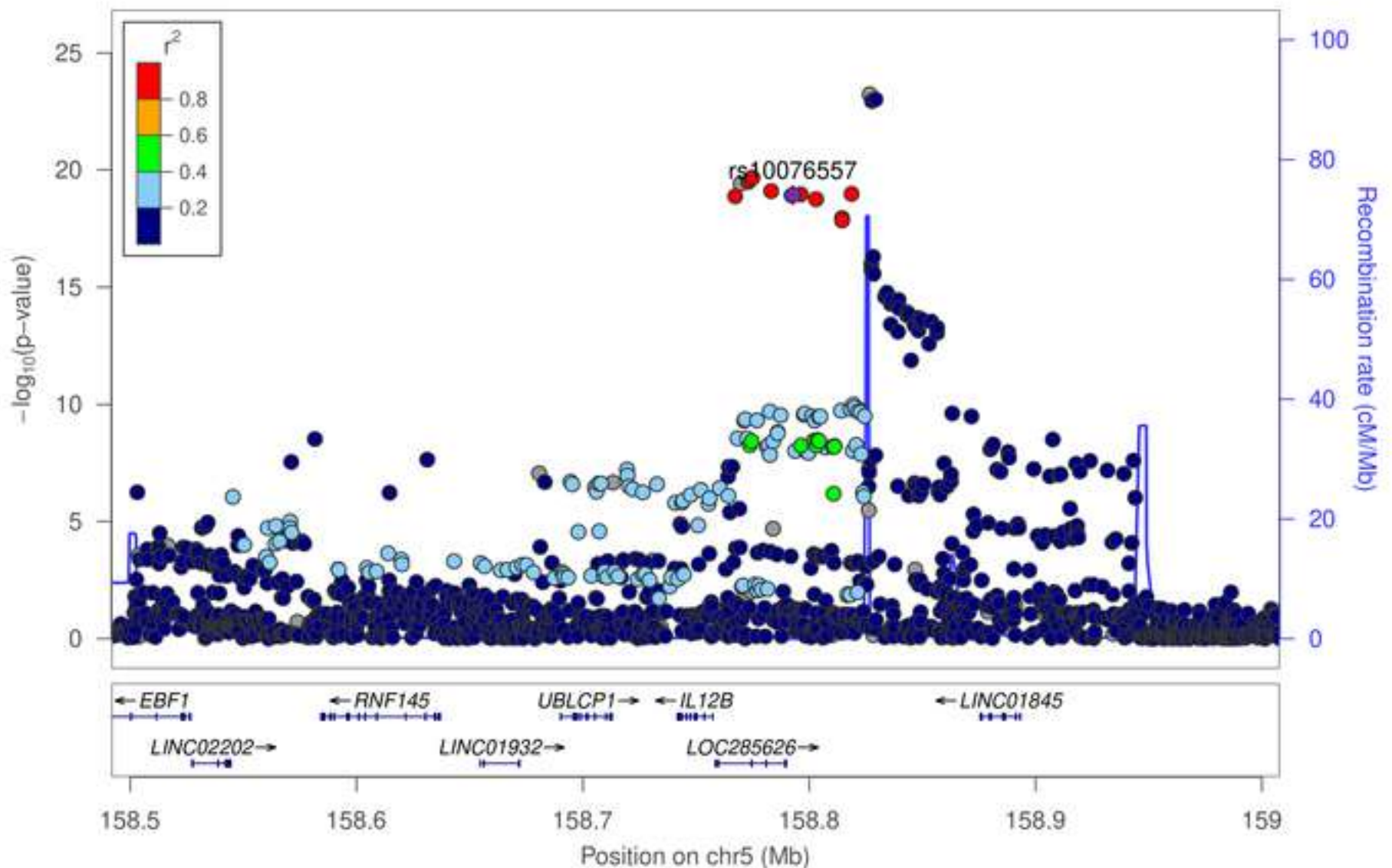
'Inflammatory bowel disease'(ebi-a-GCST004131)-rs10076557



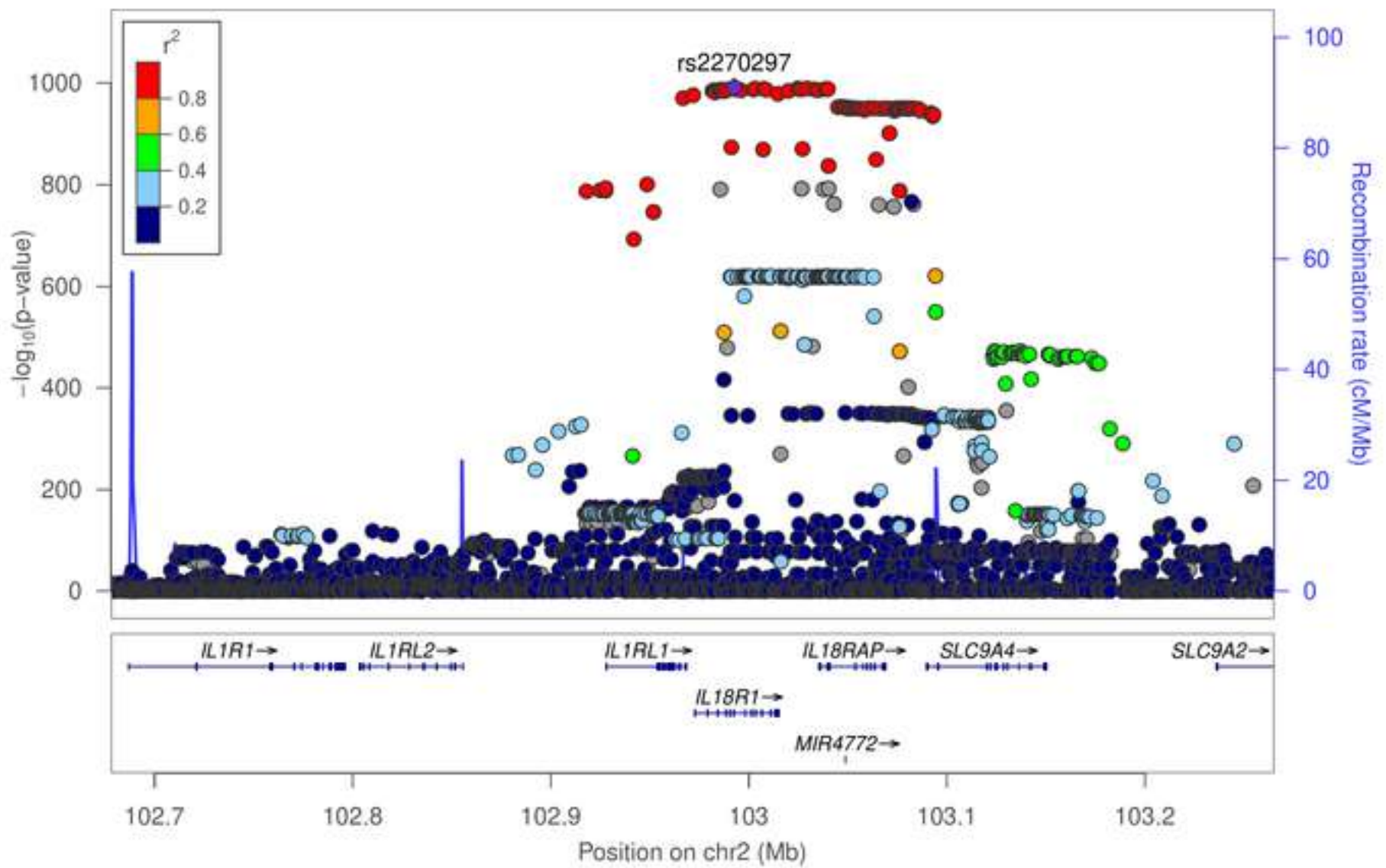
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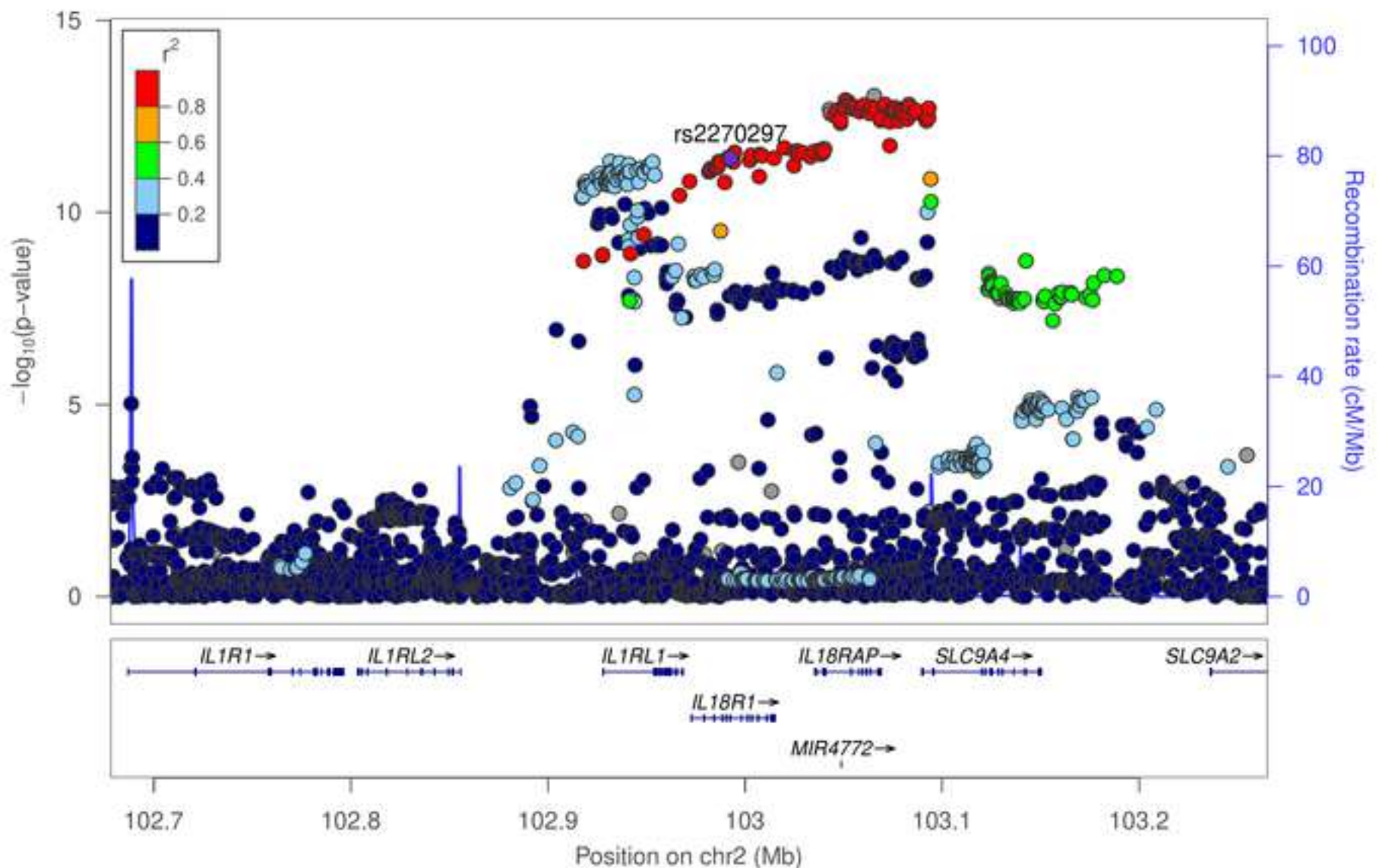
'Ulcerative colitis'(ebi-a-GCST004133)-rs10076557



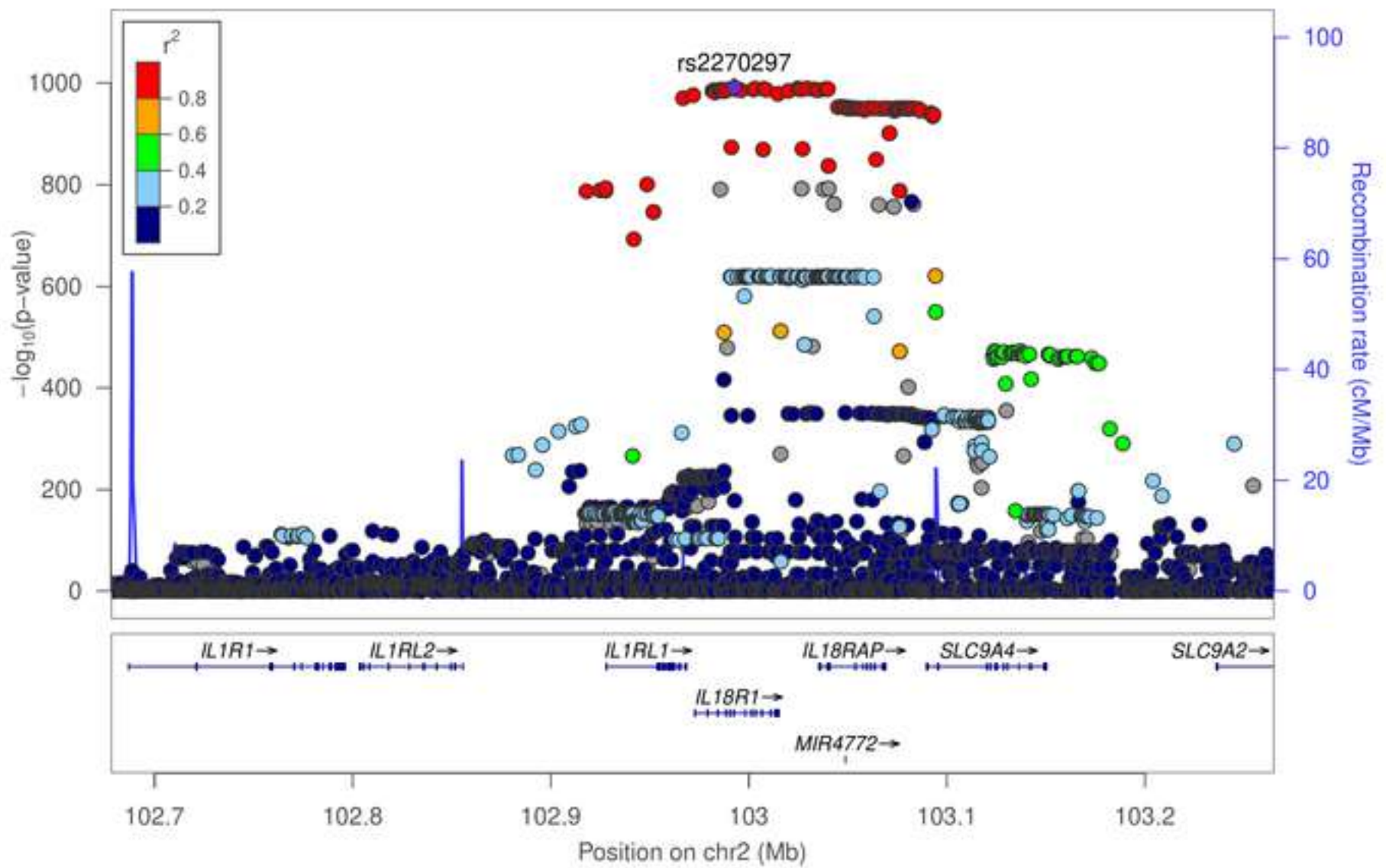
SCALLOP: IL18R1-rs2270297



'Crohns disease'(ebi-a-GCST004132)-rs2270297



SCALLOP: IL18R1-rs2270297



Eczema(ieu-a-996)-rs2270297

