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A catalog of genetic loci associated with kidney function from analyses of a million individuals

Chronic kidney disease (CKD) is responsible for a public health burden with multi-systemic complications. Through trans-ancestry meta-analysis of genome-wide association studies of estimated glomerular filtration rate (eGFR) and independent replication ($n = 1{,}046{,}070$), we identified 264 associated loci (166 new). Of these, 147 were likely to be relevant for kidney function on the basis of associations with the alternative kidney function marker blood urea nitrogen ($n = 416{,}178$). Pathway and enrichment analyses, including mouse models with renal phenotypes, support the kidney as the main target organ. A genetic risk score for lower eGFR was associated with clinically diagnosed CKD in 452,264 independent individuals. Colocalization analyses of associations with eGFR among 783,978 European-ancestry individuals and gene expression across 46 human tissues, including tubulo-interstitial and glomerular kidney compartments, identified 17 genes differentially expressed in kidney. Fine-mapping highlighted missense driver variants in 11 genes and kidney-specific regulatory variants. These results provide a comprehensive priority list of molecular targets for translational research.

CKD is a major public health issue, with increasing incidence and prevalence worldwide[1]. Its associated burden of disease encompasses metabolic disturbances, end-stage kidney disease and multi-systemic complications such as cardiovascular disease[1–4]. CKD is a leading cause of death[5] and has shown one of the highest increases in disease-attributable mortality over the last decade[2]. Nevertheless, public and clinical awareness remain low[3]. Moreover, clinical trials in nephrology are still under-represented[6], which has resulted in a scarcity of therapeutic options to alter disease progression and high costs for health systems[7]. A major barrier to developing new therapeutics is the limited understanding of the mechanisms underlying kidney function in health and disease, with the consequent lack of therapeutic targets.

Genome-wide association studies (GWAS) and exome-chip studies of the glomerular filtration rate estimated from serum creatinine (eGFR), the main biomarker to quantify kidney function and define CKD, have identified nearly 100 eGFR-associated genetic loci[8] in samples of European[9–15], Asian[16–19] and multiple[20] ancestry. However, similarly to other complex traits and diseases, identifying causal genes and molecular mechanisms implicated by genetic associations is challenging and has only been successful for a few kidney-function-associated loci[21,22]. Advanced statistical fine-mapping approaches and newly emerging multi-tissue gene expression data provide new opportunities for prioritizing putative causal variants, effector genes and target tissues from the results of large-scale GWAS meta-analyses.

We therefore conducted a trans-ancestry GWAS meta-analysis in the CKD Genetics (CKDGen) Consortium ($n = 765{,}348$) and replicated findings in the Million Veteran Program (MVP; $n = 280{,}722$)[23], for a combined sample size of greater than 1 million participants. The first aim of this study was to identify new globally important loci for kidney function through maximizing statistical power (Supplementary Fig. 1). Results from GWAS of the complementary kidney function marker blood urea nitrogen (BUN; $n = 416{,}178$) were used to prioritize the eGFR-associated loci on the basis of those most likely to be relevant for kidney function. A genetic risk score (GRS) for low eGFR was used to test relevance for clinically diagnosed CKD among 452,264 independent individuals. The second aim was to characterize replicated eGFR-associated loci through complementary computational approaches, including various enrichment and network analyses, fine-mapping, and colocalization with gene expression in 46 tissues and protein levels (Supplementary Fig. 1). We focused this aim on European-ancestry individuals, as fine-mapping based on summary statistics requires linkage disequilibrium (LD) reference panels whose sample size scales with that of the GWAS[24]. The resulting list of prioritized variants and genes provides a rich resource of potential therapeutic targets to improve CKD treatment and prevention.

Results

Discovery trans-ancestry meta-analysis. We performed 121 GWAS encompassing 765,348 individuals of European ($n = 567{,}460$), East Asian ($n = 165{,}726$), African-American ($n = 13{,}842$), South Asian ($n = 13{,}359$) and Hispanic ($n = 4{,}961$) ancestry (median age, 54 years; 50% female; Supplementary Table 1). The median of the study-specific mean eGFR values was 89 ml min^{-1} per 1.73 m^2 (interquartile range, IQR: 81, 94). GWAS were based on genotypes imputed from Haplotype Reference Consortium[25] or 1000 Genomes Project[26] reference panels (Methods and Supplementary Table 2). Following study-specific variant filtering and quality-control procedures, we performed a fixed-effects inverse-variance-weighted meta-analysis, finding no evidence of unmodeled population structure (LD score regression intercept = 1.04; genomic control factor $\lambda_{GC} = 1.05$). After variant filtering, 8,221,591 SNPs were used for downstream analysis (Methods).

We discovered 308 loci containing at least one eGFR-associated SNP at genome-wide significance (Methods), of which 200 were new and 108 contained an index SNP reported by previous GWAS of eGFR (Fig. 1 and Supplementary Table 3). Regional association plots are shown in Supplementary Fig. 2. The minor alleles across index SNPs showed both decreasing and increasing effects on eGFR, with larger effects observed for lower-frequency SNPs (Fig. 1, inset). The 308 index SNPs explained 7.1% of the eGFR variance, nearly doubling recent GWAS-based estimates[9], and 19.6% of eGFR genetic heritability ($h^2 = 39\%$, 95% credible interval = 32%, 47%), estimated in a participating general-population-based pedigree study (Methods and Supplementary Fig. 3). The effects of index SNPs were largely homogeneous across studies (Fig. 2a and

A full list of members and affiliations appears at the end of the paper.

Supplementary Table 3) and ancestry groups (Supplementary Table 4 and Supplementary Note 1).

Replication and meta-analysis of more than 1 million individuals. We assessed replication in an independent trans-ancestry GWAS meta-analysis of eGFR performed among 280,722 MVP participants[23]. Effect estimates, available for 305 of the 308 SNPs, showed almost perfect directional consistency (302/305 SNPs, 99%) and very strong correlation with the discovery results (Fig. 2b). For these 305 SNPs, we performed a meta-analysis of the 1,046,070 discovery and replication samples. Replication was met by 262 SNPs (Fig. 1, Methods and Supplementary Table 3). Of the three SNPs not available in MVP, the index SNPs at *SHROOM3* ($P=3.5\times10^{-120}$) and *SH3YL1* ($P=1.2\times10^{-11}$) were also considered to be replicated on the basis of previous evidence[15,27], resulting in a total of 264 replicated SNPs (166 new). Of these, 74 SNPs were genome-wide significant in MVP alone (Supplementary Table 3).

Association of eGFR loci with BUN and CKD. To evaluate whether associations with creatinine-based eGFR were probably related to kidney function or potentially to creatinine metabolism, we assessed the association of the 264 eGFR-associated index SNPs with BUN, an alternative marker of kidney function that is inversely correlated with eGFR. Trans-ancestry meta-analysis of 65 GWAS for BUN ($n=416{,}178$; Supplementary Table 1) showed no evidence of unmodeled population structure ($\lambda_{GC}=1.03$; LD score regression intercept = 0.98) and yielded 111 genome-wide-significant loci (15 known, 96 new; Supplementary Fig. 4 and Supplementary Table 5).

Of the 264 replicated eGFR index SNPs, 34 and 146 showed genome-wide-significant and nominally significant ($P<0.05$) association with BUN, respectively (Supplementary Table 6). SNP effects were inversely correlated ($r=-0.65$; Fig. 2c). Relevance to kidney function was classified as 'likely' for 147 eGFR index SNPs with inverse, significant associations with BUN (one-sided $P<0.05$); 'inconclusive' for 102 eGFR index SNPs not associated with BUN ($P\geq0.05$); and 'unlikely' for 15 eGFR index SNPs showing concordant, significant association with BUN (one-sided $P<0.05$; Supplementary Table 6). This comparative analysis of complementary biomarkers supports the idea that signals at the majority of eGFR-associated loci probably reflect kidney function.

Next, we investigated the effects of the eGFR index SNPs on CKD in CKDGen studies ($n=625{,}219$, including 64,164 CKD cases; Methods). GWAS meta-analysis of CKD identified 23 genome-wide-significant loci, including 17 likely relevant for kidney function (*SDCCAG8*, *LARP4B*, *DCDC1*, *WDR72*, *UMOD–PDILT*, *MYO19*, *AQP4*, *NFATC1*, *PSD4*, *HOXD8*, *NRIP1*, *SHROOM3*, *FGF5*, *SLC34A1*, *DAB2*, *UNCX* and *PRKAG2*; Supplementary Table 6). The majority of replicated eGFR index SNPs (224 of 264) were associated with CKD (one-sided $P<0.05$; Fig. 1, inset), including 130 likely relevant for kidney function (Supplementary Table 6).

Finally, we tested whether a GRS based on the combined effect of the 147 eGFR index SNPs likely relevant for kidney function was associated with clinically diagnosed CKD and CKD-related outcomes in the UK Biobank ($n=452{,}264$; Methods). A lower GRS, reflecting genetically lower eGFR, was associated with higher odds ratios (ORs) of chronic renal failure, glomerular diseases, acute renal failure and hypertensive diseases (Fig. 2d and Supplementary Fig. 5). The OR of chronic renal failure per 10% lower GRS-predicted eGFR was 2.13 (95% CI = 1.90, 2.39; $P=8.1\times10^{-38}$). A significant protective association with urolithiasis may reflect a reduced ability to concentrate urine at lower eGFR.

Genetic correlations of eGFR and BUN with other phenotypes. We assessed genome-wide genetic correlations (r_g) of eGFR associations with each of 748 complex traits and diseases (Methods)[28]. We observed 37 significant correlations ($P<6.7\times10^{-5}=0.05/748$; Supplementary Fig. 6 and Supplementary Table 7). After serum creatinine, the largest negative correlations were observed between eGFR and serum citrate ($r_g=-0.27$) and urate ($r_g=-0.23$), followed by anthropometric traits including lean mass and physical fitness (for example, $r_g=-0.20$ for left hand grip strength). While the inverse correlation with muscle-mass-related traits probably reflects higher creatinine generation leading to lower creatinine-based eGFR, the correlations with citrate and urate levels probably reflect reduced filtration function, as does the positive correlation with GFR estimated from cystatin C ($r_g=0.53$).

A very similar pattern of genetic correlations was observed for BUN (Supplementary Table 7), but the genetic correlations with muscle-mass-related traits were generally lower than for eGFR. The largest genetic correlation for BUN was observed with CKD ($r_g=0.47$), as compared to creatinine-based ($r_g=-0.29$) and cystatin C-based ($r_g=-0.26$) eGFR.

In summary, significant genetic correlations with eGFR reflect the two biological components that govern serum creatinine concentrations: its excretion via the kidney and its generation in muscle. The fact that genetic correlations between BUN and muscle-mass-related traits are generally lower than was observed for eGFR underscores the value of using genetic associations with BUN to help prioritize eGFR-associated loci most likely to be relevant for kidney function.

Functional enrichment and pathway analyses. To identify molecular mechanisms and tissues of importance for kidney function, we assessed the enrichment of the eGFR and BUN genetic associations by using tissue-specific gene expression, regulatory annotations, and gene sets and pathways (Methods). First, we used eGFR-associated SNPs ($P<5\times10^{-8}$) to explore enriched pathways, tissues and cell types on the basis of gene expression data with DEPICT[29]. We identified 16 significantly enriched physiological systems, cell types and tissues highlighting several aspects of kidney function, physiology and disease. The strongest enrichment was observed for urogenital and renal physiological systems and tissues (kidney, kidney cortex and urinary tract; false-discovery rate (FDR) < 0.05; Supplementary Fig. 7a,b). Pathway and gene set enrichment analysis identified three highly correlated and strongly associated meta gene sets ($P<1\times10^{-6}$, FDR < 0.05), including some relevant to the kidney such as polyuria, dilated renal tubules and expanded mesangial matrix, as well as signaling and transcription, and energy metabolism (Supplementary Fig. 7c). Tissue and cell-type enrichment analysis of BUN-associated SNPs associated at $P<5\times10^{-8}$ highlighted a very similar pattern (Supplementary Fig. 8) but without enrichment for muscle tissues, further supporting the use of BUN to prioritize the loci most likely to be related to kidney function.

Second, we used stratified LD score regression[30] on the genome-wide eGFR and BUN summary statistics to identify cell-type groups with enriched heritability on the basis of data from diverse cell-type-specific functional genomic elements. The strongest enrichment for eGFR was observed for the kidney (13.2-fold), followed by the liver (7.3-fold) and adrenal/pancreas (5.7-fold enrichment; Supplementary Table 8). The kidney was also the most enriched cell-type group for BUN (11.5-fold enrichment; Supplementary Table 8).

Finally, by using a complementary approach, we assessed enrichment of eGFR-associated variants in genes in which disruption results in kidney phenotypes in genetically manipulated mice[31]. From the Mouse Genome Informatics (MGI) database, we selected all genes for which disruption causes abnormal GFR ($n=24$), abnormal kidney physiology ($n=453$) or abnormal kidney morphology ($n=764$) and interrogated their human orthologs in the eGFR summary statistics (Methods). We identified significant associations in ten genes linked to abnormal GFR in mice (enrichment $P=8.9\times10^{-4}$), 55 linked to abnormal kidney physiology

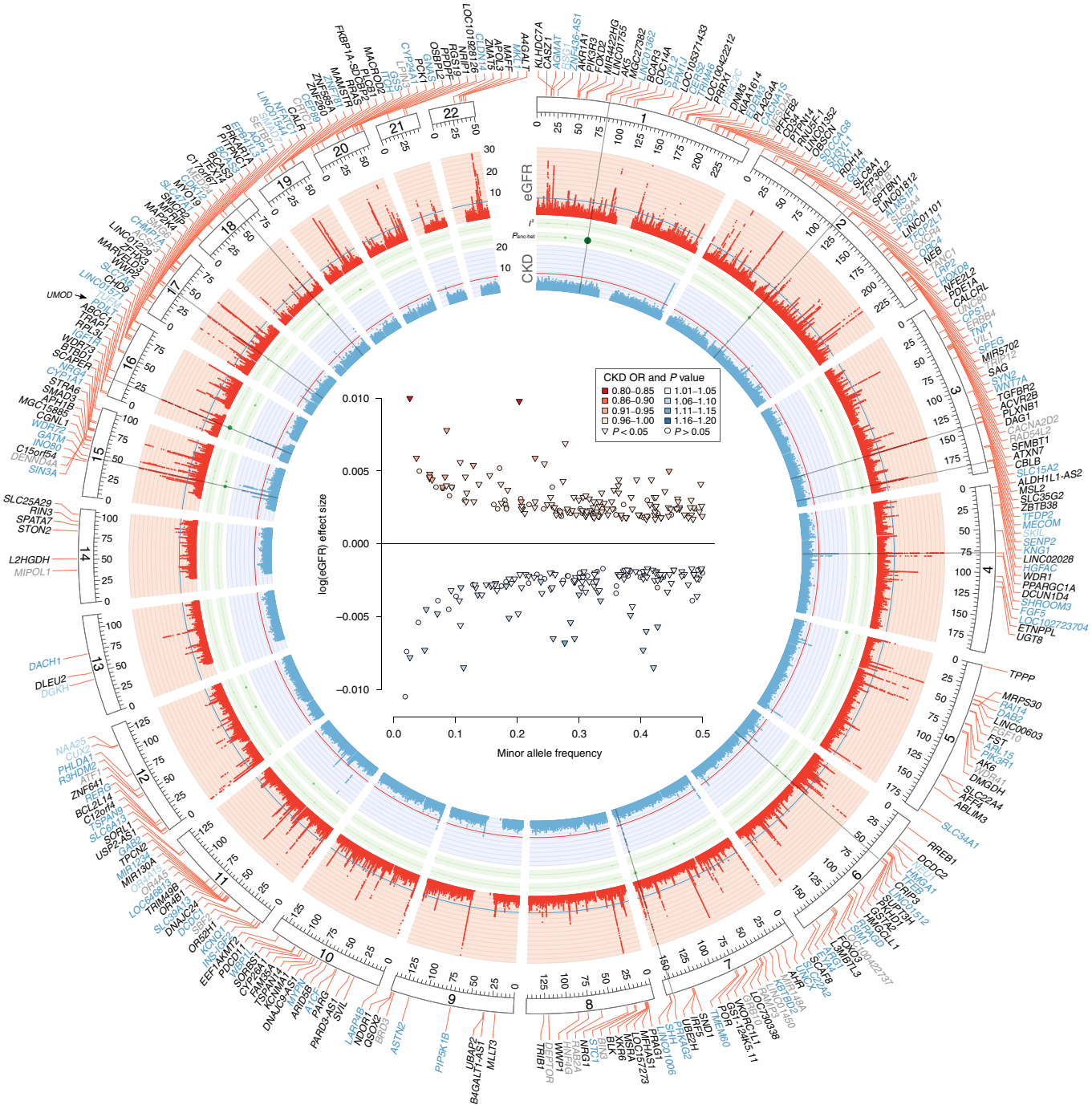

Fig. 1 | Trans-ancestry GWAS meta-analysis identifies 308 loci associated with eGFR. Circos plot. The red band corresponds to $-\log_{10}(P)$ for association with eGFR (*y* axis truncated at 30), by chromosomal position. The blue line indicates genome-wide significance ($P = 5 \times 10^{-8}$). Black gene labels indicate new loci, while blue labels indicate known loci. Non-replicating loci are colored in gray (new) or light blue (known). The green band corresponds to measures of heterogeneity related to the index SNPs associated with eGFR. Dot sizes are proportional to I^2 or ancestry-related heterogeneity ($P_{anc\text{-}het}$). The blue band corresponds to $-\log_{10}(P)$ for association with CKD (*y* axis truncated at 20), by chromosomal position. The red line indicates genome-wide significance ($P = 5 \times 10^{-8}$). Radial lines mark regions with $P_{anc\text{-}het} < 1.6 \times 10^{-4} = 0.05/308$ or $I^2 > 25\%$. Inset, effects of all 308 index SNPs on log(eGFR) by minor allele frequency, colored by the associated OR for CKD (red scale for OR ≤ 1, blue scale for OR > 1). The largest effects on CKD were observed for rs77924615 at *UMOD–PDILT* (OR = 0.81, 95% confidence interval (CI) = 0.80, 0.83), rs187355703 at *HOXD8* (OR = 0.82, 95% CI = 0.77, 0.87) and rs10254101 at *PRKAG2* (OR = 1.11, 95% CI = 1.09, 1.11). Triangles highlight SNPs that were associated with CKD (one-sided $P < 0.05$).

(enrichment $P = 1.1 \times 10^{-4}$) and 96 linked to abnormal kidney morphology (enrichment $P = 1.8 \times 10^{-5}$; Fig. 3 and Methods). Of these, 25 genes represent new eGFR candidate genes in humans; that is, they have not previously been reported to contain genome-wide-significant eGFR-associated SNPs or map near known loci (Supplementary Table 9). The existing mouse models may pave the way for experimental confirmation of these findings.

Fine-mapping and secondary signal analysis in European-ancestry individuals. Conditional and fine-mapping analyses were

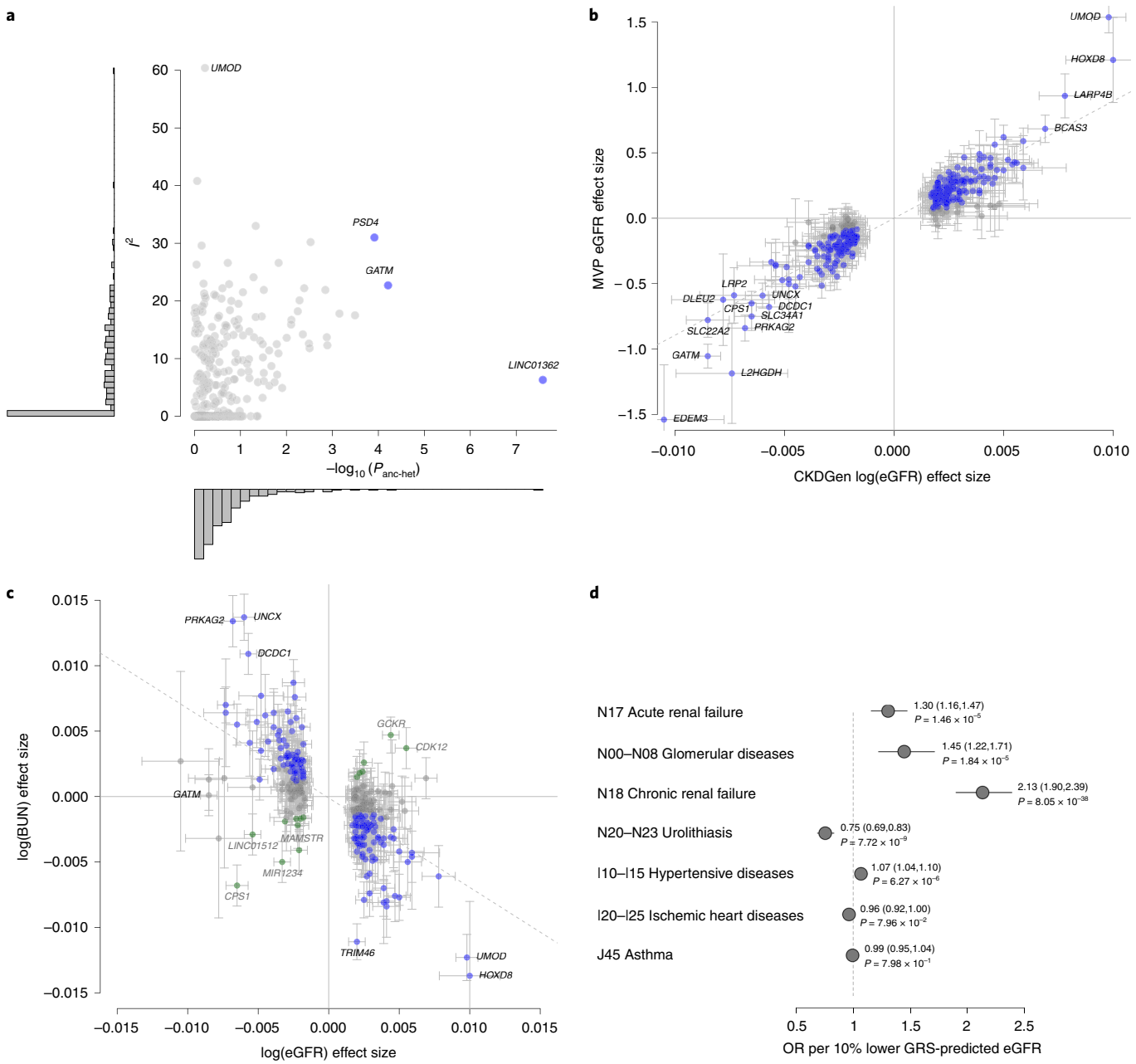

Fig. 2 | Generalizability with respect to other populations and other kidney function markers. a, Measures of heterogeneity for the 308 eGFR-associated index SNPs. Each variant's heterogeneity quantified as I^2 from the trans-ancestry meta-analysis (*y* axis) is compared to the ancestry-related heterogeneity from meta-regression ($-\log_{10}(P_{anc\text{-}het})$; *x* axis). Histograms summarize the distribution of the heterogeneity measures on both axes. SNPs with ancestry-related heterogeneity ($P_{anc\text{-}het} < 1.6 \times 10^{-4} = 0.05/308$) are marked in blue and labeled; SNPs with $I^2 > 50\%$ are labeled. **b**, Comparison of genetic effect estimates between CKDGen Consortium discovery (*x* axis) and MVP replication (*y* axis). Blue font indicates one-sided $P < 0.05$ in the MVP. Error bars correspond to 95% CIs. The dashed line corresponds to the line of best fit. Pearson's correlation coefficient $r = 0.92$ (95% CI = 0.90, 0.94). **c**, The magnitude of genetic effects on eGFR (*x* axis) as compared to BUN (*y* axis) for the 264 replicated eGFR-associated index SNPs. Color coding reflects evidence of kidney function relevance (Methods), which is coded as 'likely' (blue), 'inconclusive' (gray) or 'unlikely' (green). Error bars correspond to 95% CIs. The dashed line corresponds to the line of best fit. Pearson's correlation coefficient $r = -0.65$ (95% CI = −0.72, −0.58). **d**, Association of lower genetically predicted eGFR based on a GRS of 147 SNPs likely to be most relevant for kidney function with ICD-10-based clinical diagnoses for 452,264 individuals from the UK Biobank. Asthma was included as a negative control. Results are displayed as the OR and 95% CI per 10% lower GRS-predicted eGFR (Methods).

restricted to European-ancestry participants, for whom data to construct a large enough LD reference panel were publicly available (Methods). Meta-analysis of 85 European-ancestry CKDGen GWAS identified 256 genome-wide-significant loci (Supplementary Table 10). Replication among 216,518 European-ancestry MVP participants confirmed 228 SNPs, including 227 index SNPs that met replication criteria and the *SHROOM3* index SNP (Methods and Supplementary Table 10). Of these 228 SNPs, 221 mapped to one of the 264 replicated loci from the trans-ancestry analysis (≤500 kb up- or downstream of the trans-ancestry index SNP), and

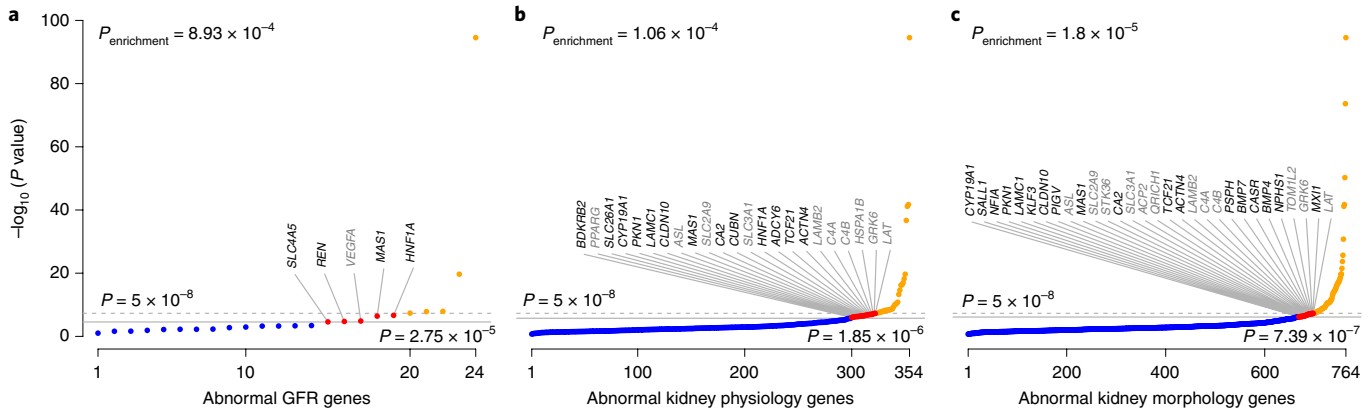

Fig. 3 | Human orthologs of genes with renal phenotypes in genetically manipulated mice are enriched for association signals with eGFR. a–c, Signals in candidate genes identified on the basis of the mouse phenotypes of abnormal GFR (**a**), abnormal kidney physiology (**b**) and abnormal kidney morphology (**c**). The *y* axis shows $-\log_{10}$ (*P*) for association with eGFR in the trans-ancestry meta-analysis for the variant with the lowest *P* value in each candidate gene. The dashed line corresponds to genome-wide significance ($P = 5 \times 10^{-8}$), and the solid gray line corresponds to the experiment-wide significance threshold for each nested candidate gene analysis. Orange, genome-wide significance; red, experiment-wide but not genome-wide significance; blue, no significantly associated SNPs. Genes are labeled if they reached experiment- but not genome-wide significance; black font indicates genes not mapping to loci reported in the main analysis. Enrichment *P* values correspond to the observed number of genes with association signals below the experiment-wide threshold against the number expected on the basis of the complementary cumulative binomial distribution (Methods).

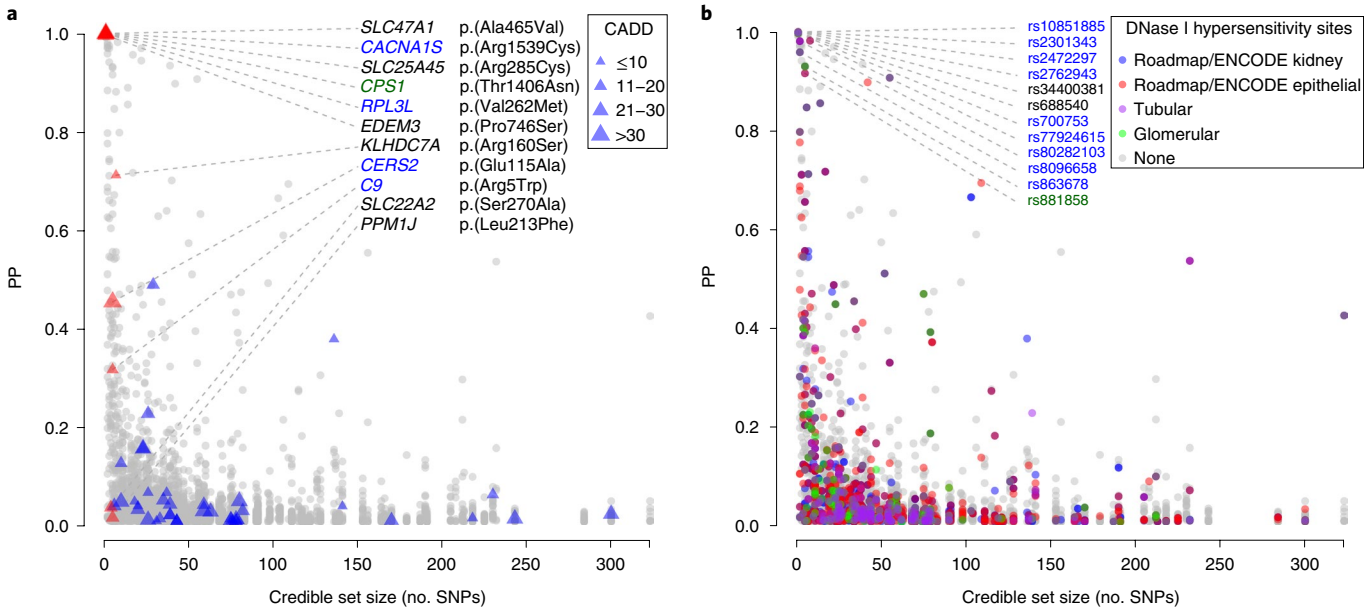

Fig. 4 | Credible set size plotted against variant posterior probability for 3,655 SNPs in 253 99% credible sets according to variant annotation. a, Exonic variants. SNPs are marked by triangles, with triangle size proportional to CADD score. Red triangles indicate missense SNPs mapping to small credible sets (≤5 SNPs) or to sets containing SNPs with high individual PP of driving the association signal (>50%). **b**, SNPs with regulatory potential. Symbol color corresponds to regulatory potential as derived from DNase I hypersensitivity analysis in target tissues (Methods). Annotation was restricted to variants with PP > 1%; SNPs with PP ≥ 90% contained in credible sets with ≤10 SNPs are labeled. Data are plotted as credible set size (*x* axis) against variant PP (*y* axis). Blue and green color coding for gene and SNP labels refers to kidney-function relevance and has the same meaning as in Fig. 2.

the remaining 7 showed $P \leq 3.3 \times 10^{-6}$ in the trans-ancestry discovery analysis. BUN GWAS meta-analysis of CKDGen European-ancestry studies ($n = 243{,}029$) allowed us to classify 122 SNPs as likely relevant for kidney function, 90 as inconclusive and 16 as unlikely (Supplementary Table 10).

To conduct statistical fine-mapping of the 228 eGFR loci, we first performed summary-statistics-based conditional analysis and identified 253 independent genome-wide-significant SNPs (Supplementary Table 11) mapping to 189 regions (Methods). For each independent variant, we computed a 99% credible set[32], with a median set size of 26 SNPs (IQR: 6, 60). We observed 58 small credible sets (≤5 SNPs), including 20 single-SNP sets: *EDEM3*, *CACNA1S*, *HOXD11*, *CPS1*, *DAB2*, *SLC34A1*, *LINC01512*, *LARP4B*, *DCDC1*, *SLC25A45*, *SLC6A13*, *GATM*, *CGNL1*, *CYP1A1*, *NRG4*, *RPL3L*, *UMOD–PDILT*, *SLC47A1* and two independent sets at *BCL2L14* (Fig. 4 and Supplementary Table 11). Of the 58 small credible sets, 33 were likely relevant for kidney function and contain genes and SNPs that can now be prioritized for further study (Supplementary Table 11).

Table 1 | Genes implicated as causal via identification of missense SNPs with high probability of driving the eGFR association signal

Gene	SNP[a]	Credible set size	SNP PP	Functional consequence	CADD score	DHSs, tissue	Brief summary of the gene's function and relevant literature
CACNA1S	**rs3850625**	1	1.00	p.(Arg1539Cys) (NP_000060.2)	34.0	–	Encodes a subunit of the slowly inactivating L-type voltage-dependent calcium channel in skeletal muscle. Reports of altered expression in kidney cancer[48] and after indoxyl sulfate treatment[49]. Rare variants can cause autosomal dominant hypokalemic periodic paralysis, type 1 (MIM 170400) or malignant hyperthermia susceptibility (MIM 601887). Common variation at this locus has been reported as associated with eGFR in previous GWAS[10,50].
CPS1	rs1047891	1	1.00	p.(Thr1406Asn) (NP_001866.2)	22.1	–	Encodes a key mitochondrial enzyme of the urea cycle that catalyzes the synthesis of carbamoyl phosphate from ammonia and bicarbonate to remove excess urea. Rare mutations cause autosomal recessive carbamoyl phosphate synthetase I deficiency (MIM 237300). GWAS locus for eGFR[13], serum metabolites[51] and urinary glycine[52], as well as for many other quantitative biomarkers. This variant has been reported to associate with hyperammonemia after valproate therapy[53].
EDEM3	rs78444298	1	1.00	p.(Pro746Ser) (NP_079467.3)	24.6	–	The gene product accelerates proteasome-mediated ER-associated degradation of glycoproteins by catalyzing mannose trimming from $Man_8GlcNAc_2$ to yield $Man_7GlcNAc_2$ on *N*-glycans. This variant has been identified by a previous exome chip association study with eGFR[27].
KLHDC7A	rs11261022	7	0.71	p.(Arg160Ser) (NP_689588.2)	1.1	Roadmap + ENCODE, kidney	This gene encodes the Kelch-domain-containing 7A protein and is a paralog of *KBTBD11*. No specific entry in relation to kidney disease in PubMed.
RPL3L	**rs113956264**	1	1.00	p.(Val262Met) (NP_005052.1)	27.2	–	The gene product has sequence similarity with ribosomal protein L3. It has a tissue-specific expression pattern, with the highest levels in skeletal muscle and heart.
SLC25A45	rs34400381	1	1.00	p.(Arg285Cys) (NP_001070709.2)	26.0	ENCODE, kidney	The encoded protein belongs to the SLC25 family of mitochondrial carrier proteins and is an orphan transporter. This variant has already been identified in a GWAS of symmetric dimethylarginine levels[54] and in a whole-genome-sequencing analysis of serum creatinine[55]. *SLC25A45* may have a role in biosynthesis of arginine, which is involved in the synthesis of creatine.
SLC47A1	rs111653425	1	1.00	p.(Ala465Val) (NP_060712.2)	24.6	–	Encodes a multidrug and toxin extrusion protein (MATE1), a transport protein responsible for the secretion of cationic drugs and creatinine across brush border membranes. This variant has already been identified in a whole-genome-sequencing analysis of serum creatinine from Iceland[55]. Rare and common variants in the locus have been identified in exome chip studies[27] and GWAS[13] of eGFR, respectively. *Slc47a1*-knockout mice show higher levels of serum creatinine and BUN[34], arguing against a sole effect on creatinine transport and supporting an effect on kidney function.
PPM1J	rs34611728	5	0.02	p.(Leu213Phe) (NP_005158.5)	13.1	ENCODE, kidney	This gene encodes a serine/threonine protein phosphatase. The variant has been reported in association with eGFR in an exome chip association study[27].

Continued

Table 1 | Genes implicated as causal via identification of missense SNPs with high probability of driving the eGFR association signal (Continued)

Gene	SNP[a]	Credible set size	SNP PP	Functional consequence	CADD score	DHSs, tissue	Brief summary of the gene's function and relevant literature
CERS2	**rs267738**	5	0.46	p.(Glu115Ala) (NP_071358.1)	32.0/28.2	-	Encodes ceramide synthase 2, which may be involved in sphingolipid synthesis. Changes in ceramide levels were reported as essential in renal Madin–Darby canine kidney (MDCK) cell differentiation[56]. *Cers2*-knockout mice show strongly reduced ceramide levels in the kidney and develop renal parenchyma abnormalities[57]. This variant has been reported as associated with the rate of albuminuria increase in individuals with diabetes[58].
C9	**rs700233**	5	0.32	p.(Arg5Trp) (NP_001728.1)	6.6	-	Encodes a constituent of the membrane attack complex that has a key role in the innate and adaptive immune responses. Rare mutations can cause C9 deficiency (MIM 613825). *C9* is mentioned in several kidney disease case reports, including for patients with congenital factor 9 deficiency showing IgA nephropathy[59].
SLC22A2	rs316019	4	0.04	p.(Ser270Ala) (NP_003049.2)	12.7	-	Encodes the polyspecific organic cation transporter (OCT2) that is primarily expressed in the kidney, where it mediates tubular uptake of organic compounds including creatinine from the circulation. Many publications relate *SLC22A2* to kidney function. rs316019 is a known pharmacogenomics variant associated with response to metformin and other drugs such as cisplatin. Carriers of the risk allele have a higher risk of cisplatin-induced nephrotoxicity[43], indicating that this transporter is essential in excreting toxins. The locus has been reported in previous GWAS of eGFR[13].

Genes are included if they contain a missense SNP with a PP of association of >50% or map to a small credible set (≤5 SNPs). PP, posterior probability; CADD score, combined annotation-dependent depletion (CADD) Phred-like score (Methods); DHSs, DNase I-hypersensitive sites. [a]Boldface indicates the SNPs most likely to be relevant for kidney function on the basis of combined effects on eGFR and BUN.

Credible set SNPs were annotated with respect to their functional consequence and regulatory potential. Missense SNPs with >50% posterior probability (PP) of driving the association and/or mapping to a small credible set are of particular interest because they directly implicate the affected gene. Such missense SNPs were identified in 11 genes (*SLC47A1*, *RPL3L*, *SLC25A45*, *CACNA1S*, *EDEM3*, *CPS1*, *KLHDC7A*, *PPM1J*, *CERS2*, *C9* and *SLC22A2*; Supplementary Table 12), of which *CACNA1S*, *RPL3L*, *CERS2* and *C9* were likely relevant for kidney function (Fig. 4a). The majority of the 11 variants had a combined annotation-dependent depletion (CADD) score greater than 15, indicating potential deleteriousness[33]. Several identified genes are plausible biological candidates for driving the association signal (Table 1). For example, the missense p.(Ala465Val) SNP in *SLC47A1* (PP > 99%) alters the encoded multidrug and toxin extrusion protein (MATE1), a transport protein responsible for the secretion of cationic drugs, toxins and internal metabolites including creatinine across brush border membranes, including kidney-proximal tubules. The fact that *Slc47a1*-knockout mice have higher blood levels of both creatinine and BUN[34] argues against a sole effect on creatinine transport.

To evaluate the regulatory potential of SNPs from small credible sets in the kidney, we annotated them to open chromatin regions identified from primary human tubular and glomerular cell cultures[35], as well as from publicly available kidney cell types (Methods). We identified 72 SNPs mapping to one of these annotations, which may thus represent causal regulatory variants (Supplementary Table 12). A particularly interesting finding was the intronic rs77924615 SNP in *PDILT*, which showed PP > 99% of driving the association at the *UMOD* locus and mapped to open chromatin in all evaluated resources (native kidney cells, ENCODE and Roadmap kidney cell types; Fig. 4b).

Gene prioritization: colocalization with gene expression. We performed colocalization analyses for each eGFR-associated locus with gene expression in *cis* across 46 tissues, including kidney glomerular and tubulo-interstitial compartments (Methods). PP > 80% of colocalization in at least one kidney tissue was observed for 17 transcripts mapping to 16 of the 228 replicated loci (Fig. 5), pointing toward a shared underlying SNP associated with both eGFR and gene expression and implicating the gene encoding the colocalized transcript as the effector gene for the locus.

New insights emerged on several levels: first, *UMOD* is a well-established causal gene for CKD and can therefore be used to evaluate our workflow. In the tubulo-interstitial compartment, we observed a shared underlying variant associated with higher *UMOD* gene expression and lower eGFR (Fig. 5), in agreement with previous GWAS of urinary uromodulin concentration, in which alleles associated with lower eGFR at *UMOD*[15] were associated with higher urinary uromodulin concentrations[36]. The lead SNP at this locus was rs77924615, highlighted above as the candidate causal regulatory variant mapping to an intron of *PDILT* (upstream of *UMOD*). The association with differential *UMOD* but not *PDILT* gene expression supports *UMOD* as the causal gene and rs77924615 as a regulatory SNP.

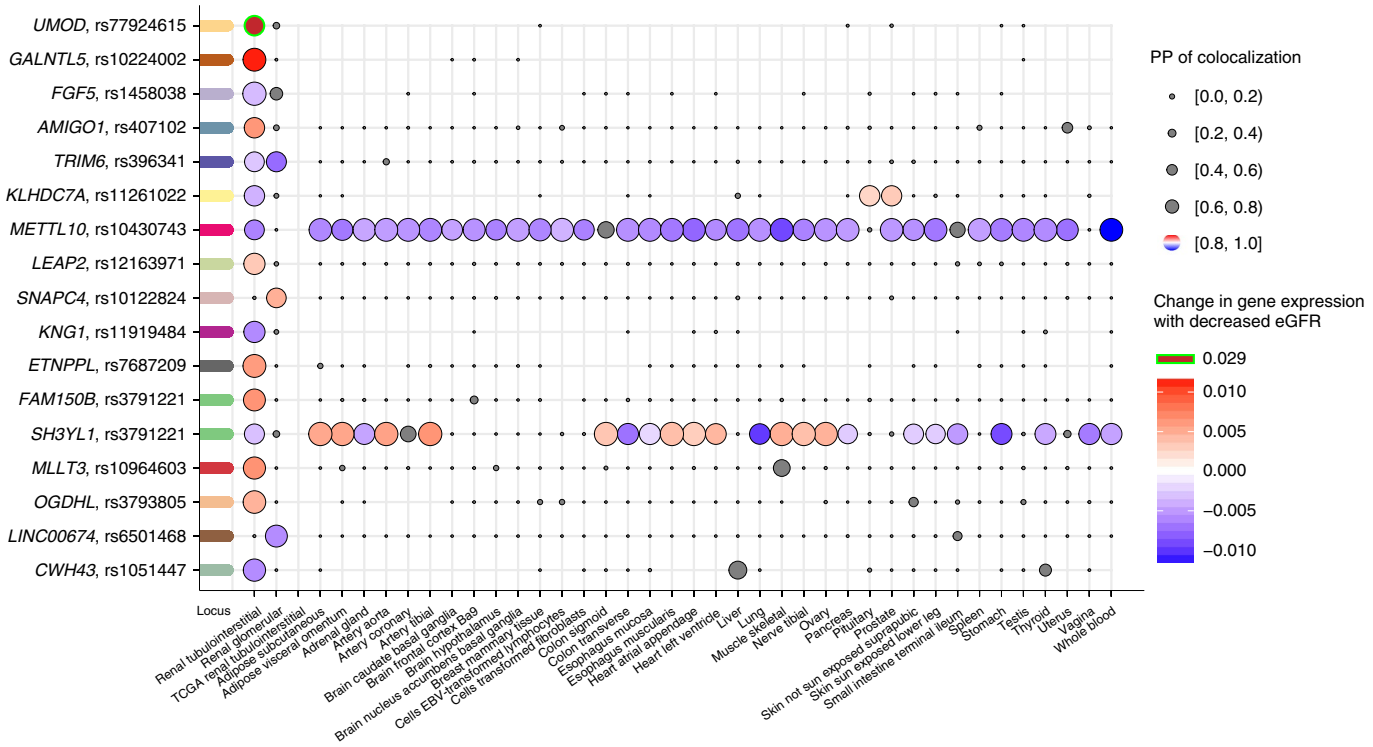

Fig. 5 | Colocalization of eGFR association signals with gene expression in kidney tissues. All eGFR loci were tested for colocalization with all eQTLs where the eQTL *cis* window overlapped (±100 kb) the sentinel genetic variant. Genes with at least one positive colocalization (PP of one common causal variant (H_4) ≥ 80%) in a kidney tissue are shown with the respective sentinel SNP (*y* axis). Colocalizations across all tissues (*x* axis) are illustrated as dots, where dot size corresponds to the PP of colocalization. Negative colocalizations (PP for H_4 < 80%) are gray, while positive colocalizations are colored according to the predicted change in expression relative to the allele associated with lower eGFR.

Second, new biologically plausible candidates emerged. For example, our results suggest *KNG1* and *FGF5* as effector genes in the respective eGFR-associated loci (Fig. 5 and Supplementary Table 13). *KNG1* encodes the high-molecular-weight kininogen, which is cleaved to bradykinin. Bradykinin influences blood pressure, natriuresis and diuresis and can be linked to kidney function via the renin–angiotensin–aldosterone system[37]. *FGF5* encodes fibroblast growth factor 5, and the index SNPs for eGFR or highly correlated SNPs ($r^2 > 0.9$) have been identified in multiple GWAS of blood pressure, atrial fibrillation, coronary artery disease, hematocrit and multiple kidney-function-related traits (Supplementary Table 13). The eGFR index SNP rs1458038 (PP > 50%, CADD score = 14.8; Supplementary Table 13) colocalized with the eGFR signal only in the tubulo-interstitial kidney portion (Fig. 5), supporting its regulatory potential in controlling the expression levels of *FGF5* in this compartment. Both *KNG1* and *FGF5* index SNPs were associated with BUN and CKD and are thus probably related to kidney function.

Third, for loci that showed colocalization of eGFR signals with gene expression in kidney and multiple other tissues, in some cases the allelic effect direction on gene expression was concordant across all tissues (for example, *METTL10*), whereas in other cases it differed by tissue (for example, *SH3YL1*; Fig. 5). These observations were also reflected broadly across all transcripts with evidence of colocalization in any tissue (Supplementary Fig. 9) and highlight tissue-shared and tissue-specific signals[38,39].

Finally, *trans* expression quantitative trait locus (*trans*-eQTL) annotation of the index SNPs in whole and peripheral blood identified a reproducible link of rs10774625 (12q24.11) with several transcripts (Methods, Supplementary Tables 14 and 15, and Supplementary Note 2).

Colocalization with uromodulin protein levels in urine. The *UMOD* locus is of particular clinical interest for CKD research[21]: rare *UMOD* mutations cause autosomal dominant tubulo-interstitial kidney disease[40], and common variants at *UMOD* give rise to the strongest eGFR and CKD GWAS signals[15]. We therefore performed conditional analyses based on European-ancestry-specific summary statistics and found two independent variants: rs77924615, mapping upstream of *PDILT*, and rs34882080, mapping to an intron of *UMOD* (Fig. 6a). SNP association with the urinary uromodulin-to-creatinine ratio (UUCR) in one participating cohort (Fig. 6b) matched the eGFR association pattern. Colocalization of the conditional eGFR and UUCR associations was evaluated separately for rs34882080 (Fig. 6c) and rs77924615 (Fig. 6d). Both regions showed high probability of a shared underlying variant driving the respective associations with eGFR and UUCR levels (PP = 97% and 96%, respectively), further supporting rs77924615 as a causal regulatory variant and *UMOD* as its effector gene.

A summary of the various gene characterization results for replicated loci from the European-ancestry analysis is shown in Supplementary Table 16, to facilitate selection of the most promising candidates for further experimental studies.

Discussion

This trans-ancestry study is fivefold larger than previous GWAS meta-analyses for eGFR and identified 264 replicated loci, 166 of which are reported here for the first time. By also analyzing BUN, an established complementary marker of kidney function, we highlight eGFR-associated loci that are likely to be important for kidney function as opposed to creatinine metabolism and provide a comprehensive annotation resource. Clinical relevance is supported by associations of a GRS for low eGFR with higher odds of

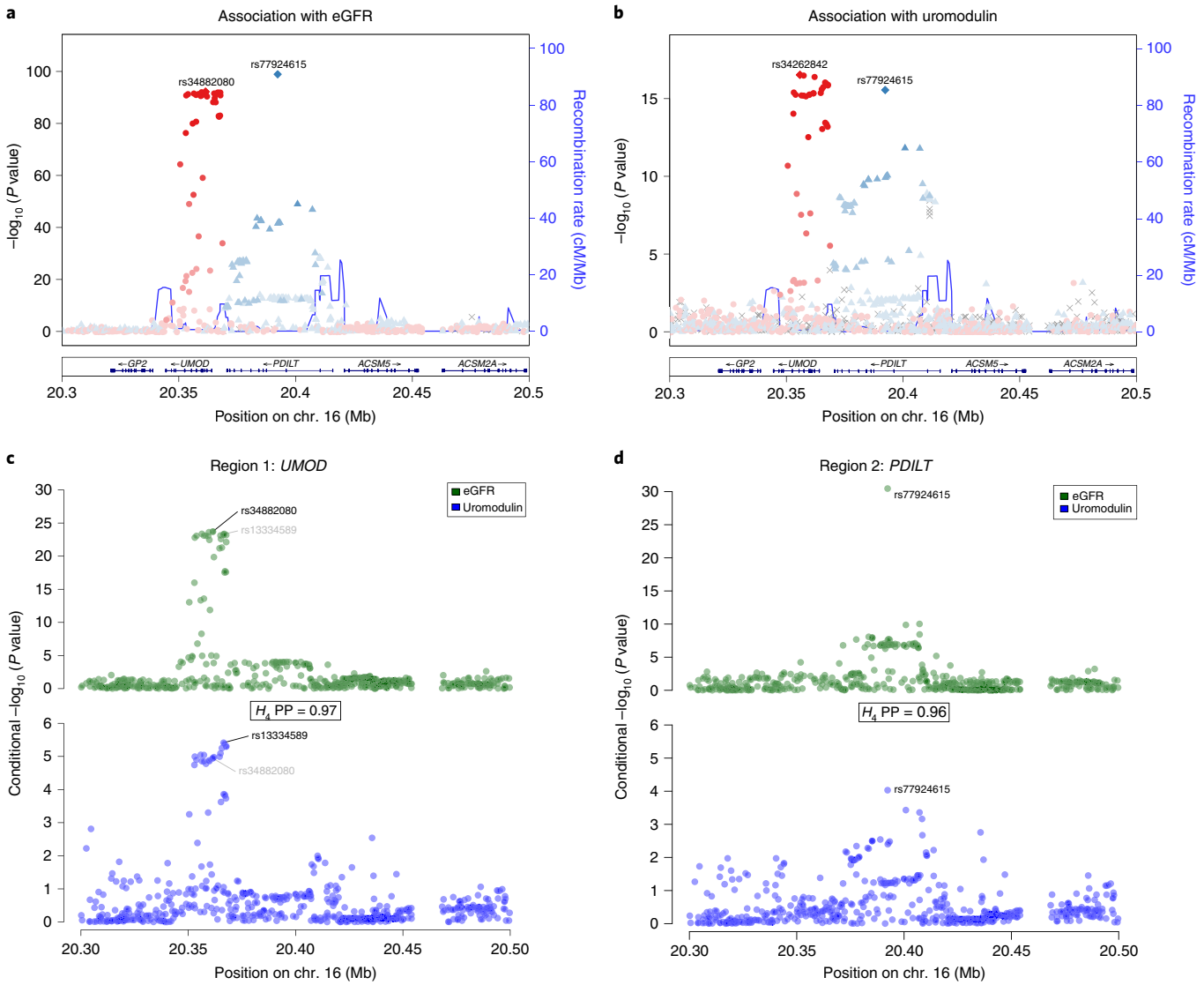

Fig. 6 | Colocalization of independent eGFR association signals at the *UMOD–PDILT* locus with urinary uromodulin concentrations (UUCR) supports *UMOD* as the effector gene. Association plots show association $-\log_{10}$(*P* value) (*y* axis) plotted against chromosomal position (*x* axis). **a**, Approximate conditional analyses among European-ancestry individuals support the presence of two independent eGFR-associated signals. **b**, The association signal for uromodulin (UUCR) levels is similar; $r^2 = 0.93$ between rs34882080 and rs34262842. **c**,**d**, Colocalization of association with eGFR (top) and uromodulin (UUCR) levels (bottom) for the independent regions centered on *UMOD* (**c**) and *PDILT* (**d**) supports a shared underlying variant in both regions with high PP.

clinically diagnosed CKD, CKD-related phenotypes and hypertension. Enrichment analyses confirm the kidney as the main target organ. Colocalization of associations with eGFR and gene expression in the kidney implicates specific target genes for follow-up. Conditional analyses, fine-mapping and functional annotation at 228 replicated eGFR-associated loci among European-ancestry participants implicate single potentially causal variants at 20 loci.

Most previous GWAS meta-analyses for eGFR have been limited to a single ancestry group[8] and did not prioritize causal variants or effector genes in associated loci. Although underpowered to uncover new loci, one previous trans-ancestry study used fine-mapping, resolving one signal to a single variant[20], rs77924615 at *UMOD–PDILT*, which is also identified in our study. At this locus, we further characterized the relationship between the causal variant, *UMOD* expression in the target tissue and uromodulin protein levels. This increase in resolution—from a locus to a single potentially causal variant with its effector gene, protein and target tissue—represents a critical advance over 10 years of eGFR GWAS[15] and is a prerequisite for translational research.

The complementary multi-tissue approaches, including enrichment analyses based on gene expression, regulatory annotations, and gene sets and pathways, highlight the kidney as the most important target organ. However, relatively few kidney-specific experimental datasets are publicly available. For example, the kidney is not well represented in the Genotype-Tissue Expression (GTEx) Project and is not included in its tissue-specific eQTL datasets[38], emphasizing the value of open-access resources and in-depth characterization of uncommon tissues and cell types. We were able to specifically investigate the kidney by using a recently published eQTL dataset from glomerular and tubulo-interstitial portions of microdissected human kidney biopsies[41], kidney-specific regulatory information from the ENCODE and Roadmap Epigenomics resources, and by obtaining regulatory information from primary cultures of human glomerular and tubulo-interstitial cells[35].

Functional follow-up studies of potentially causal variants should benefit from prioritized loci that show clear evidence supporting one or a few SNPs driving the association signal. The fine-mapping workflow allowed us to prioritize several SNPs at single-SNP

resolution or at a resolution of ≤5 SNPs, some of which may have broader clinical relevance. For example, the OCT2 protein encoded by *SLC22A2* transports several cationic drugs such as metoprolol, cisplatin, metformin and cimetidine across the basolateral membrane of renal tubular cells[42]. The prioritized missense SNP encodes p.(Ser270Ala), a known pharmacogenomic variant that alters the transport of these drugs and their side effects, such as cisplatin-induced nephrotoxicity[43]. Along the same lines, the prioritized SNP encoding the p.(Ala465Val) substitution in the transporter MATE1 encoded by *SLC47A1* may affect the ability to secrete drugs and other toxins from proximal tubular cells into the urine[44] and hence alter CKD risk.

Strengths of this project include the large sample size with dense genotype imputation, standardized and automated phenotype generation and quality control, and independent replication, as well as the advanced and comprehensive downstream bioinformatics analyses. Further strengths are the use of BUN to prioritize eGFR-associated loci likely relevant for kidney function and to provide genome-wide BUN summary statistics as an annotation resource for other studies of eGFR. Moreover, we evaluated a GRS for eGFR for association with clinically diagnosed CKD in a large independent study. Among the limitations, non-European populations are still under-represented in our study, as in many other genomic efforts[45]. Statistical fine-mapping using trans-ancestry data with different LD structures can potentially narrow association signals. However, a sufficiently large reference dataset to compute ancestry-matched LD structure for summary-statistics-based fine-mapping was only available for European ancestry, highlighting the potential of future large-scale efforts with trans-ancestry fine-mapping and the need to generate data from non-European-ancestry populations, thereby enabling such endeavors. Finally, several SNPs had small effective sample sizes in some subpopulations, which might have affected the ability to assess between-ancestry heterogeneity and potentially underestimated true heterogeneity.

We estimated GFR from serum creatinine, as done in clinical practice and observational studies, because direct measurement of kidney function is invasive, time-consuming and burdensome. Under the assumption that genetic associations supported by multiple markers are less likely to reflect marker metabolism, we used BUN to prioritize eGFR-associated loci likely to be relevant to kidney function. Blood creatinine, urea and cystatin C concentrations are influenced not only by glomerular filtration but also by the synthesis, active secretion and reabsorption of these molecules, as illustrated by loci detected in our study: for example, the *GATM* locus was associated with eGFR but not with BUN, in agreement with the function of the encoded protein as a rate-limiting enzyme in creatine synthesis[46]. Conversely, the *SLC14A2* locus was associated with BUN but not with eGFR, in line with the function of the encoded protein as a urea transporter[47]. Even so, lack of association for a SNP with one kidney function marker based on a combination of *P* value and effect direction may not necessarily mean that the locus is not relevant to kidney function. Our categorization of the eGFR loci into three classes on the basis of direction of effect and significance of BUN association should be interpreted with caution, with 'likely' and 'unlikely' reflecting uncertainty of the assignment. Factors complicating the comparison of eGFR and BUN associations at the locus level are differential statistical power, differential ancestry distribution and potential allelic heterogeneity. Further large-scale studies with multiple kidney function markers measured in the same individuals are therefore warranted.

To identify broadly representative and generalizable association signals, we focused on SNPs that were present in the majority of the participating studies. This choice might have limited our ability to uncover new variants or to fine-map low-frequency or population-specific variants, which represents a complementary avenue of research. Moreover, even with well-powered fine-mapping approaches, potentially causal SNPs need to be confirmed as functional variants in experimental studies. Although colocalization with gene expression can help prioritize effector genes, these associations are based on measures from a single time point and hence cannot answer whether changes in gene expression precede or follow changes in kidney function.

In summary, we have identified and characterized a large number of loci associated with eGFR and prioritized potential effector genes, driver variants and target tissues. These findings will help direct functional studies and advance the understanding of kidney function biology, a prerequisite to develop novel therapies to reduce the burden of CKD.

Online content

Any methods, additional references, Nature Research reporting summaries, source data, statements of code and data availability and associated accession codes are available at https://doi.org/10.1038/s41588-019-0407-x.

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Author contributions

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Methods

Overview. We set up a collaborative meta-analysis based on a distributive data model and quality-control procedures. To maximize phenotype standardization across studies, an analysis plan and a command line script (https://github.com/genepi-freiburg/ckdgen-pheno) were created centrally and provided to all participating studies (mostly population-based studies; Supplementary Table 1). Data processing, analysis and troubleshooting instructions were distributed to all studies via a wiki system (https://ckdgen.eurac.edu/mediawiki/index.php/CKDGen_Round_4_EPACTS_analysis_plan). Automatically generated summary files were checked centrally. Upon phenotype approval, studies ran their GWAS and uploaded results and imputation quality (IQ) information to a common calculation server. GWAS quality control was performed with GWAtoolbox[60] and custom scripts to assess ancestry-matched allele frequencies and variant positions. All studies had their own research protocols approved by the respective local ethics committees. All participants in all studies provided written informed consent.

Phenotype definition. Each study measured serum creatinine and BUN concentrations as described in Supplementary Table 1. Creatinine values obtained with a Jaffé assay before 2009 were calibrated by multiplying by 0.95 (ref. [61]). Studies on adults (>18 years of age) estimated GFR with the Chronic Kidney Disease Epidemiology Collaboration (CKD-EPI) equation[62], by using the R package nephro[63]. Studies on individuals who were 18 years old or younger used the Schwartz formula[64]. eGFR was winsorized at 15 and 200 ml min^{-1} per 1.73 m^2. CKD was defined as an eGFR below 60 ml min^{-1} per 1.73 m^2. In studies reporting blood urea measurements, BUN was derived as blood urea × 2.8, with units expressed as mg dl^{-1}.

Genotyping and genotype imputation. Genotypes were imputed on the basis of the Haplotype Reference Consortium v1.1 or 1000 Genomes Project phase 3 v5 (1000Gp3v5) ALL or phase 1 v3 (1000Gp1v3) ALL panel. Imputed variants were coded as allelic dosages accompanied by the corresponding IQ scores (IMPUTE2 info score, MACH/minimac RSQ or as applicable) and annotated on the NCBI b37 (hg19) reference build (see Supplementary Table 2 for study-specific genotyping arrays, haplotype phasing and genotype imputation methods).

Genome-wide association studies. Each study fitted sex- and age-adjusted linear regression models to log(eGFR) and BUN. Regression residuals were regressed on SNP dosage, assuming an additive genetic model. Study site, genetic principal components, relatedness and other study-specific features were accounted for in the study-specific models as appropriate (Supplementary Table 2). Logistic regression models were fitted for CKD.

Trans-ancestry GWAS meta-analysis. Studies contributed 121 GWAS summary statistics files for eGFR (total post-quality-control $n = 765{,}348$), 60 GWAS files for CKD (total post-quality-control $n = 625{,}219$, including 64,164 CKD cases) and 65 GWAS files for BUN (total post-quality-control $n = 416{,}178$). Ancestry-specific details for eGFR, CKD and BUN are given in Supplementary Table 1.

Before meta-analysis, study-specific GWAS files were filtered to retain only variants with IQ score > 0.6 and minor allele count (MAC) > 10, and genomic control (GC) correction was applied in the case where GC factor $\lambda_{GC} > 1$. Fixed-effects inverse-variance-weighted meta-analysis was performed with METAL[65], which was adapted to increase the precision of effect estimates and their standard errors (seven decimal places instead of four).

After meta-analysis of 43,994,957 SNPs, only SNPs present in ≥50% of the GWAS files and with total MAC ≥ 400 were retained. Across ancestry groups, this yielded 8,221,591 variants for eGFR (8,834,748 in European ancestry), 8,176,554 variants for BUN (8,358,347 in European ancestry) and 9,585,923 variants for CKD. Post-meta-analysis GC correction was not applied (LD score regression intercept ≈ 1 in all analyses of eGFR, BUN and CKD)[66]. The genome-wide significance level was set at 5×10^{-8}. Between-study heterogeneity was assessed with the I^2 statistic[67]. For CKD, variants with $I^2 \geq 95\%$ were removed to moderate the influence of single large studies. Variants were assigned to loci by selecting the SNP with the lowest P value across the genome as the index SNP, defining the corresponding locus as the 1-Mb segment centered on the index SNP, and repeating the procedure until no further genome-wide-significant SNPs remained. The extended major histocompatibility complex (MHC) region was considered as a single locus. A locus was considered to be new if not containing any variant identified by previous GWAS of eGFR.

Meta-regression analysis of trans-ancestry GWAS. For eGFR, we evaluated ancestry-related heterogeneity by using the software Meta-Regression of Multi-Ethnic Genetic Association (MR-MEGA, v0.1.2)[68] with study-specific GWAS results. Meta-regression models included three axes of genetic variation. Genomic control correction was applied to the meta-regression results. The 308 genome-wide-significant index SNPs from the trans-ancestry GWAS meta-analysis were tested for ancestry-related heterogeneity of the allelic effects at a significance level of $0.05/308 = 1.6 \times 10^{-4}$ (referring to the corresponding P value as $P_{anc\text{-}het}$).

Variance explained and genetic heritability. The proportion of phenotypic variance explained by the index SNPs was estimated as $\beta^2\left(\frac{2p(1-p)}{\text{var}}\right)$, with β being the SNP effect, p the effect allele frequency and var the variance of the sex- and age-adjusted log(eGFR) residuals (assumed to be 0.016 on the basis of data from 11,827 European-ancestry participants of the population-based ARIC study)[9]. Genetic heritability for age- and sex-adjusted log(eGFR) was estimated with the R package MCMCglmm[69] on the Cooperative Health Research in South Tyrol (CHRIS) study[70], a participating pedigree-based study with 186 pedigrees of up to five generations ($n = 4{,}373$)[71]. We fitted two models with and without inclusion of the identified index SNPs (304/308), running 1 million MCMC iterations (burn-in = 500,000)[71].

Comparison with and replication of results in the MVP. The eGFR-associated SNPs identified in the discovery GWAS meta-analyses were tested for replication in a GWAS from the MVP[23], an independent trans-ancestry study with participants recruited across 63 US Veterans Administration (VA) medical facilities. Written informed consent was obtained and all documents and protocols were approved by the VA Central Institutional Review Board. After genotyping and quality control, genotypes were phased and imputed on the 1000Gp3v5 reference panel. Serum creatinine was assessed up to 1 year before MVP enrollment by isotope dilution mass spectrometry. GFR was estimated by using the CKD-EPI equation[62] after excluding subjects on dialysis, transplant patients, amputees, individuals on HIV medications and those with creatinine values of <0.4 mg dl^{-1}. GWAS of eGFR on SNP dosage were performed by fitting linear regression models adjusted for age at creatinine measurement, age^2, sex, body-mass index and the first ten genetic principal components, by using SNPTEST v2.5.4-beta[72]. All GWAS were stratified by self-reported ancestry (79.6% white non-Hispanic, 20.4% black non-Hispanic), diabetes and hypertension status. Results were combined across strata by fixed-effects inverse-variance-weighted meta-analysis in METAL[65]. This analysis encompassed a total of 280,722 individuals across all strata, of whom 216,518 were non-Hispanic whites (European ancestry). The MVP is described more extensively in the Supplementary Note 3.

Of the 308 eGFR index SNPs identified in the CKDGen trans-ancestry analysis, 305 variants or their good proxies were available in the MVP GWAS (proxies were required to have $r^2 \geq 0.8$ with the index SNP and were selected by maximum r^2 followed by minimum distance in the case of ties). Replication testing of the 256 European-ancestry-specific index SNPs was restricted to the MVP European-ancestry GWAS. CKDGen and MVP meta-analysis results were pooled via sample-size-weighted meta-analysis of z scores with METAL[65]. In both the trans-ancestry and European-ancestry-specific analyses, replication was defined by one-sided $P < 0.05$ in the MVP and genome-wide significance of the CKDGen and MVP meta-analysis result.

Assessment of relevance to kidney function with BUN. We used genetic associations with BUN to assess replicated eGFR-associated SNPs with respect to their potential relevance to kidney function. Support for kidney function relevance was categorized as 'likely' for all eGFR index SNPs with an inverse, significant (one-sided $P < 0.05$) association with BUN for a given reference allele, 'inconclusive' for eGFR index SNPs whose effect on BUN was not different from 0 ($P \geq 0.05$) and 'unlikely' for all eGFR index SNPs with a concordant, significant (one-sided $P < 0.05$) association with BUN for a given reference allele.

Genetic risk score analysis in the UK Biobank dataset. To test the combined effect of eGFR-associated SNPs on outcomes related to clinically diagnosed CKD, a GRS-based association analysis was conducted on the basis of summary GWAS results, as described previously[73,74]. Genetic association results with diseases were obtained for 452,264 UK Biobank participants available in the GeneAtlas[75] database for glomerular diseases (ICD-10 codes N00–N08; 2,289 cases); acute renal failure (N17; 4,913 cases); chronic renal failure (N18; 4,905 cases); urolithiasis (N20–N23; 7,053 cases); hypertensive diseases (I10–I15; 84,910 cases); and ischemic heart diseases (I20–I25; 33,387 cases). Asthma (J45; 28,628 cases) was included as a negative control. The log(estimated OR) value provided by the GeneAtlas PheWAS interface was used as the effect size, and its standard error was calculated from the corresponding effect size and P value. When OR = 1, the standard error was imputed by the median value of the remaining associations of the trait. Of the 147 eGFR index SNPs from the trans-ancestry GWAS meta-analysis that were replicated and showed likely relevance to kidney function, 144 were available in the UK Biobank dataset, and 259 of all 264 replicated trans-ancestry GWAS meta-analysis SNPs were available. The effect of the GRS association (β) corresponds to the OR for the disease depending on the relative change in eGFR, for example, $OR = 1.10^{\beta}$ for a 10% change in eGFR. Alternatively, $\exp(\beta)$ can be interpreted as the OR for the disease per unit change in log(eGFR).

Genetic correlations with other complex traits and diseases. Genome-wide genetic correlation analysis was performed to investigate evidence of co-regulation or shared genetic basis between eGFR and BUN concentrations and other complex traits and diseases, both known and not known to correlate with eGFR and BUN. We estimated pairwise genetic correlation coefficients (r_g) between the results of our trans-ancestry meta-analyses of eGFR and BUN and each of 748 precomputed and publicly available GWAS summary statistics for complex traits and diseases available through LD Hub v1.9.0 by using LD score regression[28]. An overview of

the sources of these summary statistics and their corresponding sample sizes is available at http://ldsc.broadinstitute.org/. Statistical significance was assessed at the Bonferroni-corrected level of $0.05/748 = 6.7 \times 10^{-5}$.

Pathway and tissue enrichment analysis. We used DEPICT v1 release 194 to perform DEPICT analysis[29], including pathway/gene set enrichment and tissue/cell-type analyses as described previously[9,10]. All 14,461 gene sets were reconstituted by identifying genes that were transcriptionally co-regulated with other genes in a panel of 77,840 gene expression microarrays[76], from mouse knockout studies, and molecular pathways from protein–protein interaction screening. In the tissue and cell-type enrichment analysis, we tested whether genes in associated regions were highly expressed in 209 MeSH annotation categories for 37,427 microarrays (Affymetrix U133 Plus 2.0 array platform). For both eGFR and BUN, we included all variants associated with the trait at $P < 5 \times 10^{-8}$ in the trans-ancestry meta-analysis. Independent variant clumping was performed by using PLINK 1.9 (ref. [77]) with 500-kb flanking regions and $r^2 > 0.01$ in the 1000Gp1v3 dataset. After excluding the MHC region, DEPICT was run with 500 repetitions to estimate the FDR and 5,000 permutations to compute *P* values adjusted for gene length by using 500 null GWAS. All significant gene sets were merged into meta gene sets by running an affinity propagation algorithm[78] implemented in the Python scikit-learn package (http://scikit-learn.org/). The resulting network was visualized with Cytoscape (http://cytoscape.org/).

Enrichment of heritability by cell-type group. We used stratified LD score regression to investigate important tissues and cell types on the basis of the trans-ancestry eGFR and BUN meta-analysis results. Heritability enrichment in ten cell-type groups was assessed by using the default options of stratified LD score regression described previously[30]. The ten cell-type groups were collapsed from 220 cell-type-specific regulatory annotations for the four histone marks H3K4me1, H3K4me3, H3K9ac and H3K27ac. Enrichment in a cell-type category was defined as the proportion of SNP heritability in that group divided by the proportion of SNPs in the same cell-type group.

Analysis of genes causing kidney phenotypes in mice. A nested candidate gene analysis was performed with GenToS[79] to identify additional genetic associations that were not genome-wide significant. Candidate genes that when manipulated cause kidney phenotypes in mice were selected with the comprehensive MGI phenotype ontology in September 2017 (abnormal renal glomerular filtration rate (MP:0002847); abnormal kidney morphology (MP:0002135); abnormal kidney physiology (MP:0002136)). The human orthologs of these genes were obtained, when available, with the Human–Mouse: Disease Connection webtool (http://www.informatics.jax.org/humanDisease.html). Statistical significance was defined as Bonferroni correction of a type I error level of 0.05 for the number of independent common SNPs across all genes in each of the three candidate gene lists plus their flanking regions, derived from an ancestry-matched reference population. The GWAS meta-analysis summary statistics for eGFR were queried for significantly associated SNPs mapping to the selected candidate genes. Enrichment of significant genetic associations in genes within each candidate list was computed from the complementary cumulative binomial distribution[79]. GenToS was used with default parameters on each of the three candidate gene lists, with the 1000 Genomes phase 3 release 2 ALL dataset as reference.

Independent variant identification in the European-ancestry meta-analysis. To identify additional independent eGFR-associated variants within the European-ancestry-specific and replicated loci, approximate conditional analyses were performed on the basis of genome-wide discovery summary statistics that incorporated LD information from an ancestry-matched reference population. These analyses were restricted to participants of European ancestry because an LD reference sample scaled to the size of our meta-analysis could only be constructed from publicly available data for European-ancestry individuals[24], for which we randomly selected 15,000 UK Biobank participants (dataset ID 8974). Individuals who withdrew consent and those not meeting data cleaning requirements were excluded, keeping only those who passed a sex-consistency check, had a ≥95% call rate and did not represent outliers with respect to SNP heterozygosity. For each pair of individuals, the proportion of variants shared identical by descent (IBD) was computed with PLINK[80]. Only one member of each pair with an IBD coefficient ≥0.1875 was retained. Individuals were restricted to those of European ancestry by excluding outliers along the first two principal components from a principal-component analysis seeded with the HapMap phase 3 release 2 populations as reference. The final dataset to estimate LD included 13,558 European-ancestry individuals and 16,969,363 SNPs.

The basis for statistical fine-mapping was the 228 1-Mb genome-wide-significant loci identified in the European-ancestry meta-analysis, clipping at chromosome borders. Overlapping loci as well as pairs of loci whose respective index SNPs were correlated ($r^2 > 0.1$ in the UK Biobank LD dataset described above) were merged. A single SNP was chosen to represent the MHC region, resulting in a final list of 189 regions before fine-mapping. Within each region, the GCTA COJO Slct algorithm[81] was applied to identify independent variants by using a stepwise forward selection approach. We used the default collinearity cutoff of 0.9 (sensitivity analyses showed no major influence of alternative cutoff values; data not shown). We deemed an additional SNP as independently genome-wide significant if the SNP's *P* value conditional on all previously identified SNPs in the same region was $<5 \times 10^{-8}$.

Fine-mapping and credible sets in the European-ancestry meta-analysis. For each region containing multiple independent SNPs and for each independent SNP in such regions, approximate conditional analyses were conducted with the GCTA COJO-Cond algorithm to generate approximate conditional association statistics conditioned on the other independent SNPs in the region. By using Wakefield's formula implemented in the R package gtx[82], we derived approximate Bayes factors (ABFs) from conditional estimates in regions with multiple independent SNPs and from the original estimates for regions with a single independent SNP. Given that 95% of the SNP effects on log(eGFR) fell within the range −0.01 to 0.01, the standard deviation prior was chosen as 0.0051 on the basis of formula (8) in the original publication[32]. Sensitivity analyses showed that results were robust when higher values were used for the standard deviation prior (data not shown). For each variant within an evaluated region, the ABF obtained from the association β values and their standard errors for the marginal (single-signal regions) or conditional (multi-signal regions) estimates was used to calculate the PP for a SNP of driving the association signal ('causal variant'). We derived 99% credible sets, representing the SNP sets containing the variant(s) driving the association signal with 99% probability, by ranking variants by their PPs and adding them to the set until cumulative PP > 99% was reached in each region.

Variant annotation. Functional annotation of SNPs mapping to credible sets was performed with SNiPA v3.2 (March 2017)[83], on the basis of the 1000Gp3v5 and Ensembl v87 datasets. SNiPA was also used to derive the CADD Phred-like score[84], on the basis of CADD v1.3. The Ensembl VEP tool[85] was used for prediction of the primary effects of SNPs.

Colocalization of eGFR signal and gene expression in *cis*. As the great majority of gene expression datasets are generated on the basis of European-ancestry samples, colocalization analysis was based on genetic associations with eGFR in the European-ancestry sample and with gene expression (eQTLs) quantified from microdissected human glomerular and tubulo-interstitial kidney portions from 187 individuals from the NEPTUNE study[41], as well as the 44 tissues included in the GTEx Project v6p release[38]. The eQTL and GWAS effect alleles were harmonized. For each locus, we identified tissue gene pairs with reported eQTL data within ±100 kb of each GWAS index SNP. The region for each colocalization test was the eQTL *cis* window defined in the underlying GTEx and NephQTL studies. We used the coloc.fast function, with the default setting, from the R package gtx (https://github.com/tobyjohnson/gtx), which is an adaptation of Giambartolomei's colocalization method[86]. The gtx package was also used to estimate the direction of effect over the credible sets as the ratio of the average PP-weighted GWAS effects over the PP-weighted eQTL effects.

***Trans*-eQTL analysis.** We performed *trans*-eQTL annotation through LD mapping on the basis of the 1000Gp3v5 European reference panel (r^2 cutoff of >0.8). We limited annotation to replicated index SNPs with fine-mapping PP ≥ 1%. Owing to expected small effect sizes, only genome-wide *trans*-eQTL studies of either peripheral blood mononuclear cells or whole blood with $n \geq 1{,}000$ individuals were considered, resulting in five non-overlapping studies[87–91] (Supplementary Table 14). For one study[91], we had access to an update with larger sample size ($n = 6{,}645$) obtained by combining two non-overlapping studies (LIFE-Heart[92] and LIFE-Adult[93]). To improve the stringency of results, we focused the analysis on interchromosomal *trans*-eQTLs with $P < 5 \times 10^{-8}$ in ≥2 studies.

Colocalization with urinary uromodulin concentrations. Association of genetic variants with UUCR at the *UMOD–PDILT* locus was evaluated in the German Chronic Kidney Disease (GCKD) study[94]. Uromodulin concentrations were measured from frozen stored urine by an established ELISA with excellent performance[36]. Concentrations were indexed to creatinine to account for urine dilution. Genetic associations were assessed with the same software and settings as for eGFR association (Supplementary Table 2). Colocalization analyses were performed with identical software and settings as described above for the association with gene expression.

Reporting Summary. Further information on research design is available in the Nature Research Reporting Summary linked to this article.

Data availability

Genome-wide summary statistics for this study have been made publicly available at http://ckdgen.imbi.uni-freiburg.de.

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n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
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☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☐	☒	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	To maximize phenotype standardization across studies, an analysis plan and a command line script (https://github.com/genepi-freiburg/ckdgen-pheno) were created centrally and provided to all participating studies. Data processing, analysis and troubleshooting instructions were distributed to all studies via a Wiki system (https://ckdgen.eurac.edu/mediawiki/index.php/CKDGen_Round_4_EPACTS_analysis_plan). Automatically generated summary files were checked centrally. Upon phenotype approval, studies run their GWAS and uploaded results and imputation quality (IQ) information to a common calculation server. GWAS QC was performed using GWAtoolbox and custom (R, Bash) scripts to assess ancestry-matched allele frequencies and variant positions.
Data analysis	See Supplementary Table 2 for study-specific genotyping arrays, haplotype phasing and genotype imputation methods. Fixed effects inverse-variance weighted meta-analysis was performed using METAL (version 2011-03-25), which was adapted to increase the precision of effect estimates and their standard errors (SE; seven decimal places instead of four). We evaluated ancestry-related heterogeneity using the software Meta-Regression of Multi-Ethnic Genetic Association (MR-MEGA v0.1.2). Genetic heritability was estimated using the R package 'MCMCglmm'. We estimated pairwise genetic correlation coefficients through LD Hub v1.9.0 using LD Score regression. We used DEPICT v1 release 194 to perform Data-Driven Expression Prioritized Integration for Complex Traits analysis. A nested candidate gene analysis was performed using GenToS (https://github.com/genepi-freiburg/GenToS). Approximate conditional analyses were conducted using the GCTA v1.91.6beta COJO-Cond and -Slct algorithms. Using the Wakefield's formula implemented in the R package 'gtx', we derived approximate Bayes factors (ABF). Functional annotation of SNPs mapping into credible sets was performed with SNiPA v3.2 (March 2017), based on the 1000Gp3v5 and Ensembl v87 datasets. SNiPA was also used to derive the Combined Annotation Dependent Depletion (CADD) PHRED-like score, based on CADD v1.3. The Ensembl VEP tool was used for SNP's primary effect prediction. For co-localization analyses, we used the 'coloc.fast' function from the R package 'gtx' (https://github.com/tobyjohnson/gtx), which is an adaption of Giambartolomei's co-localization method.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Genome-wide summary statistics for this study are made publicly available through dbGaP accession number phs000930.v7.p1 and at http://ckdgen.imbi.uni-freiburg.de.

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Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Studies contributed 121 GWAS summary statistics files for eGFR (total post-QC n=765,348), 60 GWAS files for CKD (total post-QC n=625,219, including 64,164 CKD cases), and 65 GWAS files for BUN (total post-QC n=416,178).
Data exclusions	Before meta-analysis, study-specific GWAS files were filtered to retain only variants with IQ score>0.6 and minor allele count (MAC)>10. After meta-analysis of 43,994,957 SNPs, only SNPs present in ≥50% of the GWAS files and with total MAC≥400 were retained. Across ancestries, this yielded 8,221,591 variants for eGFR (8,834,748 in EA), 8,176,554 for BUN (8,358,347 in EA), and 9,585,923 for CKD.
Replication	The eGFR-associated SNPs identified in the discovery GWAS meta-analyses were tested for replication in a GWAS from the MVP, an independent trans-ethnic study with participants recruited across 63 U.S. Veteran's Administration (VA) medical facilities.
Randomization	This does not apply to our study. All samples were analyzed together.
Blinding	This does not apply to our study. No group allocation was necessary.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Human research participants

Policy information about studies involving human research participants

Population characteristics	See Supplementary Table 1 for population characteristics and phenotype distributions of all participating studies, including covariates such as age and sex.
Recruitment	See Supplementary Table 1 for a description of all participating studies and their study design.
Ethics oversight	All studies had their own research protocols approved by the respective local ethics committees. Participants provided written informed consent.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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SUPPLEMENTARY INFORMATION

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A catalog of genetic loci associated with kidney function from analyses of a million individuals

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A catalogue of genetic loci associated with kidney function from analyses of a million individuals

Supplementary Materials

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Supplementary Tables are provided separately as a spreadsheet.

Supplementary Note 1: Between-study heterogeneity and ancestry-related heterogeneity in the discovery meta-analysis

Before seeking replication, we evaluated results from the discovery meta-analysis for heterogeneity by design and heterogeneity related to ancestry. Most of the 308 SNPs showed homogeneous effects across studies (median I^2=5%, interquartile range: 0-13%; **Supplementary Table 3**; **Figure 2A**). Only one index SNP had I^2>50% (*UMOD-PDILT* locus, I^2=60%), where previously described heterogeneity[1,2] is suspected to be age-related.[3] We then investigated the heterogeneity of genetic effects that was correlated with ancestry using meta-regression[4] (Methods) and identified three index SNPs with significant ancestry-related heterogeneity at the *LINC01362*, *GATM*, and *PSD4* loci (ancestry heterogeneity p-value (p-anc-het) <0.05/308; **Figure 2A**, **Supplementary Table 3**). The index SNP at *UMOD-PDILT* did not show evidence for ancestry-related heterogeneity (p-anc-het=0.59). These results do not support large differences in estimated effects across ancestries for the majority of the identified SNPs. Ancestry-specific results for all 308 index SNPs are reported in **Supplementary Table 4**.

Supplementary Note 2: *Trans*-eQTL analysis

Trans-eQTL annotation of the index SNPs was only performed using whole blood and peripheral blood mononuclear cells, for which eQTL datasets with large sample size were available (Methods). Based on the analysis of 5 non-overlapping EA genome-wide eQTL studies (sample size range 1469 - 6645, **Supplementary Table 14**), we identified, among others, a reproducible link of rs10774625 (12q24.11) with several transcripts, including one for the calcium-binding protein gene *S100A10* (1q21.3) and *STAT1* (2q32.2). *S100A10* encodes a subunit of annexin A2, which co-localizes with *PLA2R* at the cell surface and in extracellular vesicles from podocytes.[5] Inhibition of *STAT1* has been reported to protect from glomerular mesangial cell senescence[6] and to ameliorate renal oxidative stress[7] (**Supplementary Table 15**).

Suppplementary Note 3: Details on the replication study: the Million Veteran's Program (MVP)

Study definition. The MVP[8] is an independent trans-ethnic study whose participants were recruited across 63 U.S. Veteran's Administration (VA) medical facilities. Written informed consent was obtained and all documents and protocols were approved by the VA Central Institutional Review Board.

Genotypes. DNA was genotyped using a customized Affymetrix Axiom Biobank Array chip with additional content added to provide coverage of African and Hispanic haplotypes, as well as markers for common diseases in the VA population. After QC, genotypes were pre-phased using EAGLE v2[9] and imputed based on the 1000Gp3v5 reference panel using minimac3.[10] Genotype PCs were estimated using FlashPCA.[11]

Phenotype. Serum creatinine was assessed up to one year prior to MVP enrollment using isotope dilution mass spectrometry. GFR was estimated using the CKD-EPI equation[12] after excluding subjects on dialysis, transplant patients, amputees, individuals on HIV medications, and those with creatinine values of <0.4 mg/dl.

Additional epidemiological information. Diabetes was defined as use of anti-diabetic medications or by assignment of an International Classification of Diseases 9 (ICD-9) code for diabetes during the baseline period. Hypertension was defined as having an ICD-9 code for hypertension, being on antihypertensive drug or having ≥2 measures of systolic or diastolic blood pressure >140 mmHg or >90 mmHg, respectively.

Genome-wide association study. GWAS of eGFR on SNP dosage levels were performed by fitting linear regression models adjusted for age at creatinine measurement, age^2, sex, body mass index, and the first 10 genetic PCs, using SNPTEST v2.5.4-beta.[13] All GWAS were stratified by self-reported ethnicity (79.6% White non-Hispanic; 20.4% Black non-Hispanic), diabetes, and hypertension status. Results were combined across strata using fixed effects inverse-variance weighted meta-analysis in METAL.[14] This analysis encompassed 280,722 individuals across all strata, of whom 216,518 were non-Hispanic Whites (EA).

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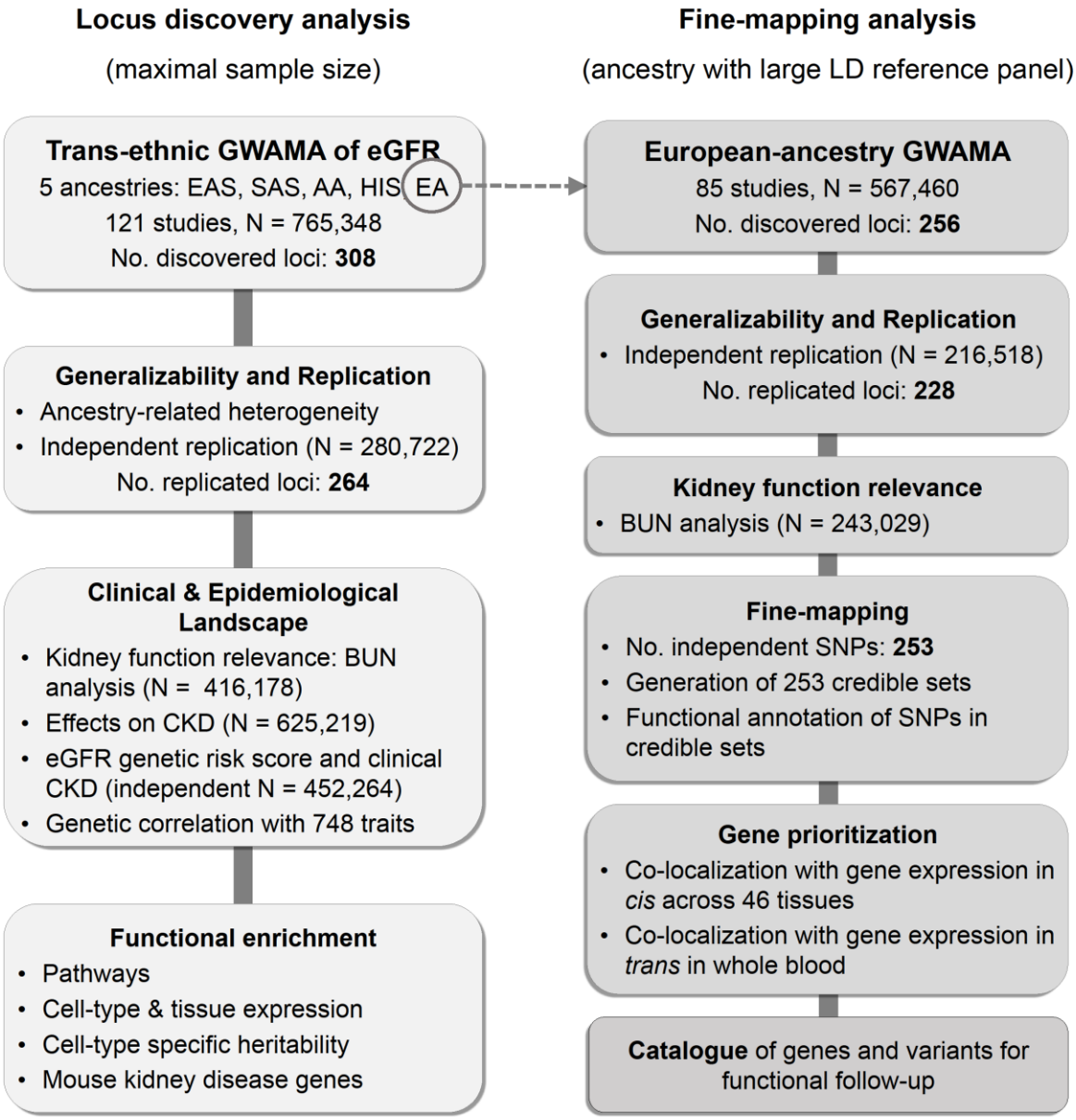
Supplementary Figure 1: Analysis Flowchart

Locus discovery analysis in the trans-ethnic sample and fine-mapping analysis in EA participants.



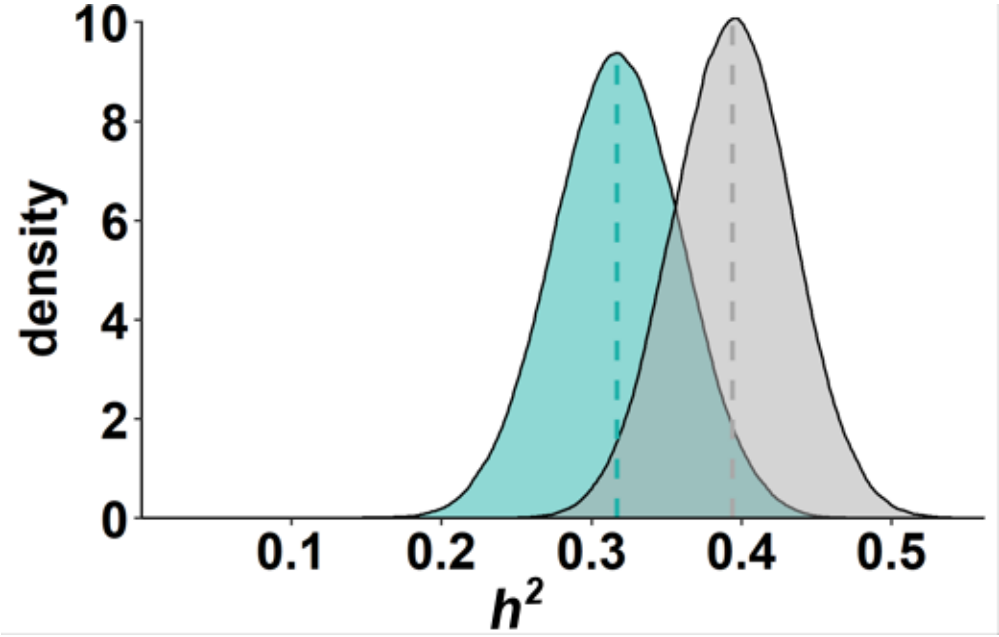
Supplementary Figure 2: Regional Association Plots

Regional Association Plot Booklet for all 308 loci identified in association with eGFR through trans-ethnic meta-analyses.

The PDF booklet is available online as a separate download with the Supplementary Information.

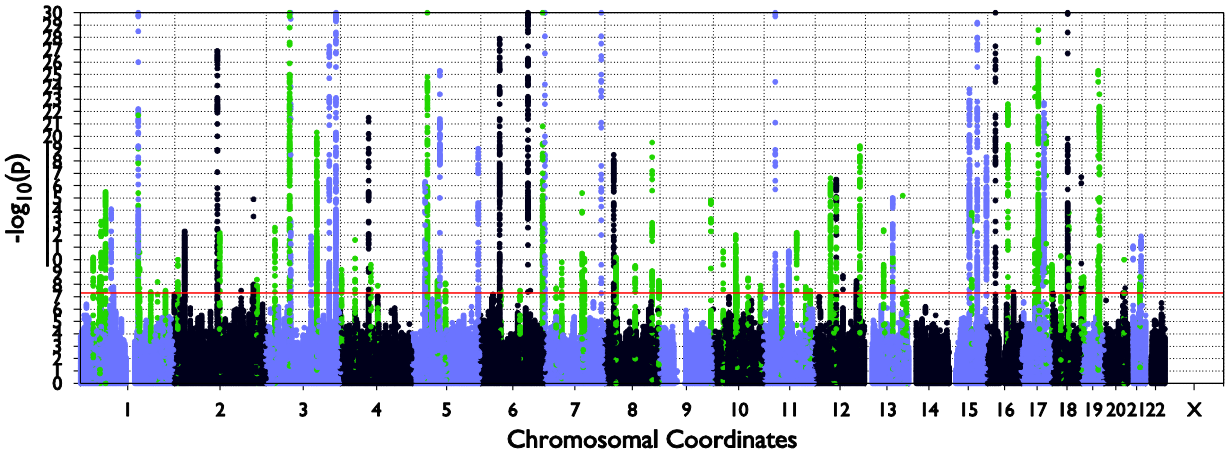
Supplementary Figure 3: Genetic Heritability

Distribution of the genetic heritability (h^2) estimates of age- and sex-adjusted log(eGFR) residuals in the Cooperative Health Research In South Tyrol (CHRIS) study, for index SNPs from the trans-ethnic GWAS. h^2 distribution is shown before (gray) and after (green) inclusion of the index SNPs into the model, with the shift representing the amount of h^2 explained by the index SNPs.



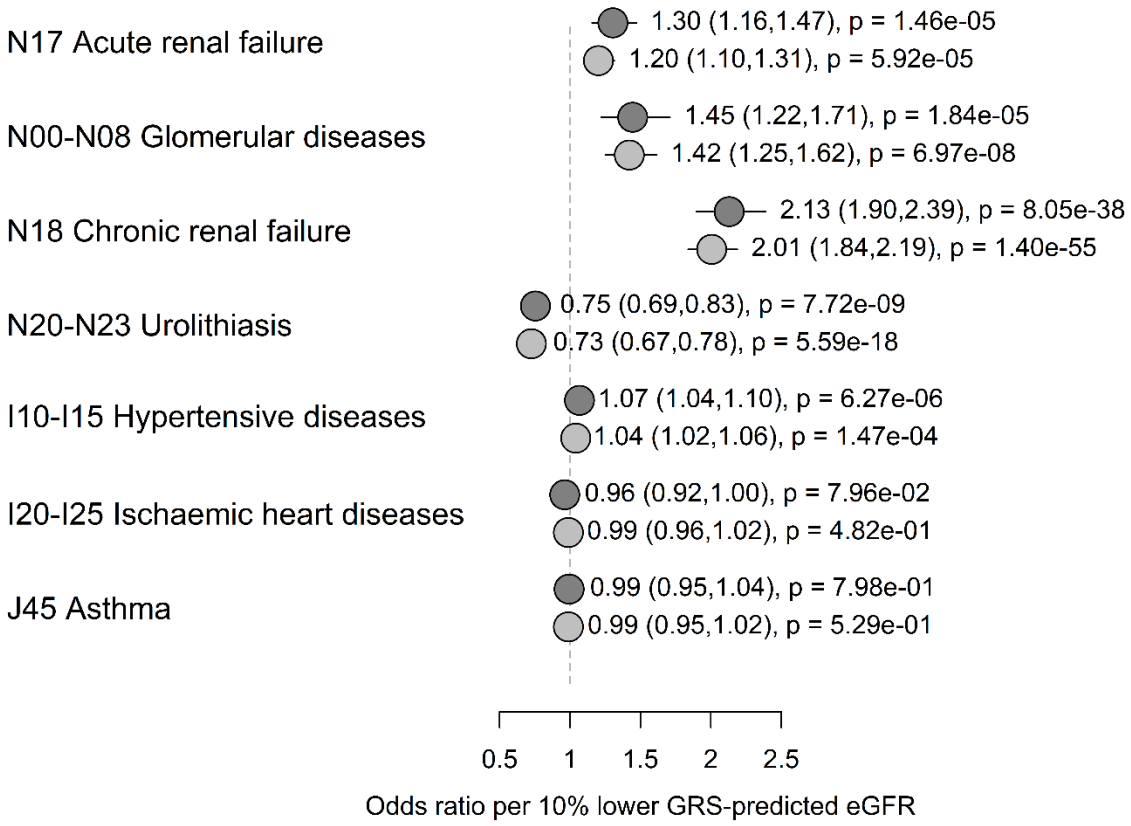
Supplementary Figure 4: BUN Manhattan plot

Manhattan plot of results from the GWAS meta-analysis of blood urea nitrogen (BUN).



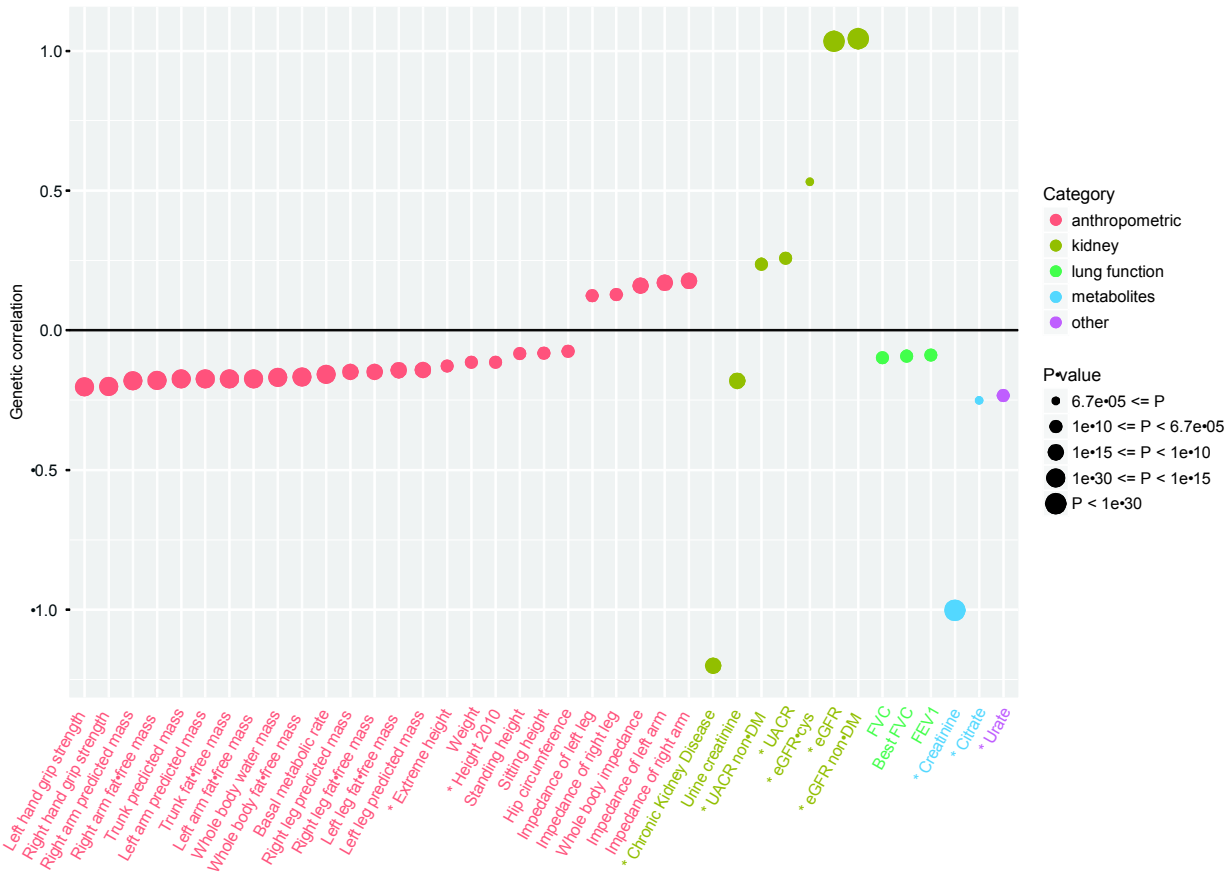
Supplementary Figure 5: Genetic Risk Score analysis

Association between lower genetically-predicted eGFR based on a genetic risk score (GRS) and ICD-10 based clinical diagnoses from 452,264 individuals from the UK Biobank. Asthma is included as a negative control. The GRS was derived as described in the Methods. Displayed are odds ratios and their 95% CIs per 10% lower GRS-predicted eGFR. Dark gray is used for results from the 147 SNPs likely to be most relevant for kidney function (same as in **Figure 2D**), light gray is used for results from all 264 replicated eGFR-associated index SNPs.



Supplementary Figure 6: Genetic correlation plot for eGFR

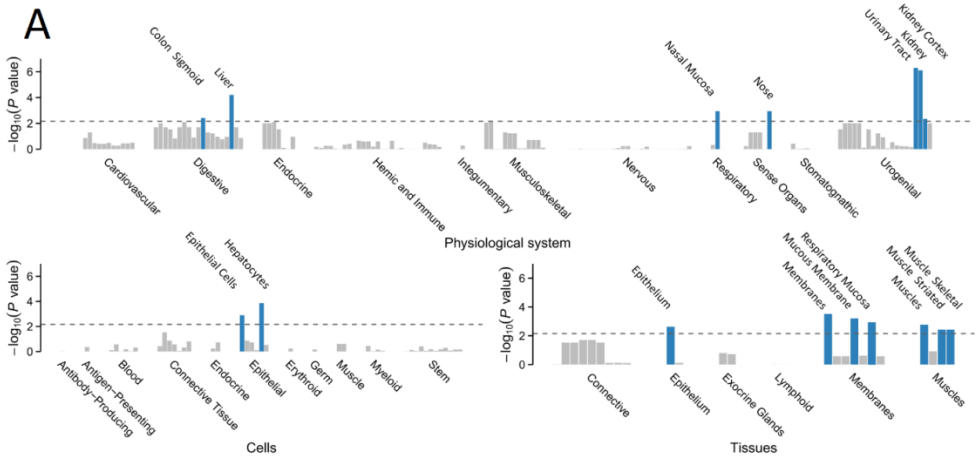
Genetic correlation plot based on the summary statistics from the trans-ethnic GWAS meta-analysis of eGFR and 748 other complex traits and diseases available through LD Hub.



The genetic correlations with citrate and cystatin C were not significant (P=6.0×10^{-4} and 4.0×10^{-4}, respectively, **Supplementary Table 7**), because these traits were measured in a limited number of studies, resulting in smaller GWAS sample sizes.

Supplementary Figure 7: Pathway and tissue enrichment analysis with DEPICT (eGFR)

Shown is the barplot of the results of the tissue and cell type enrichment analysis in **Panel A**. Cells, tissues and physiological systems are highlighted in blue if the association false discovery rate (FDR) was <0.05 and are summarized in the table in **Panel B**. The strongest enrichment was observed for urogenital and renal physiological systems and tissues: kidney, kidney cortex, and urinary tract. We additionally found significant enrichment for mucous membrane, respiratory mucosa, nasal mucosa, and nose (enrichment p-values from 3.1×10^{-4} to 1.2×10^{-3}), possibly reflecting epithelial cell processes including transport mechanisms shared with the kidney. **Panel C** illustrates the highly correlated and strongly associated meta gene sets (P <$1.x10^{-6}$, FDR<0.05) from the pathway and gene-set enrichment analysis clustered according to their biological relevance for kidney function, energy metabolism and signaling and transcription.

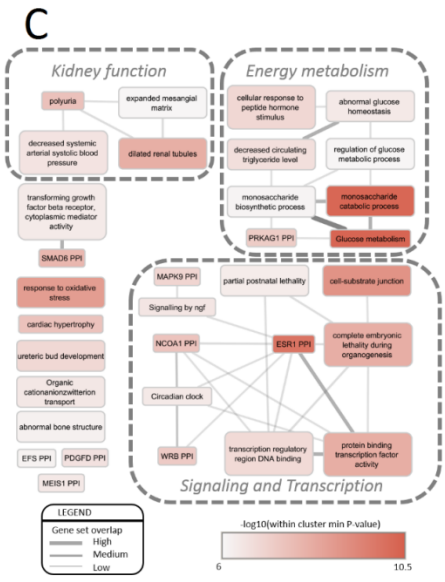


B

Enriched tissues and cell types identified by DEPICT. Shown are the tissues and cell types significantly (FDR<0.05) enriched in the meta-analysis results of subjects from all ethnicities.

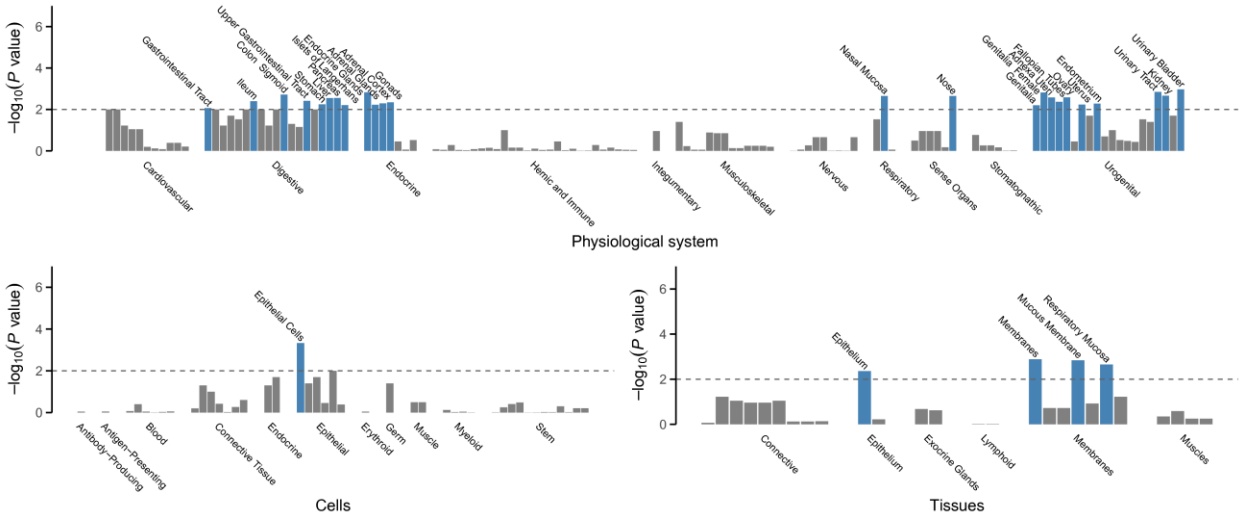
MeSH term	Name	MeSH 1st level term	MeSH 2nd level term	Nominal P-value
A05.810	Urinary Tract	Urogenital System	Urinary Tract	4.99×10^{-7}*
A05.810.453	Kidney	Urogenital System	Urinary Tract	7.84×10^{-7}*
A03.620	Liver	Digestive System	Liver	6.46×10^{-5}*
A11.436.348	Hepatocytes	Cells	Epithelial Cells	1.38×10^{-4}*
A10.615	Membranes	Tissues	Membranes	3.14×10^{-4}*
A10.615.550	Mucous Membrane	Tissues	Membranes	6.30×10^{-4}*
A10.615.550.760	Respiratory Mucosa	Tissues	Membranes	1.15×10^{-3}
A04.531.520	Nasal Mucosa	Respiratory System	Nose	1.15×10^{-3}
A09.531	Nose	Sense Organs	Nose	1.15×10^{-3}
A11.436	Epithelial Cells	Cells	Epithelial Cells	1.28×10^{-3}
A10.690	Muscles	Tissues	Muscles	1.72×10^{-3}
A10.272	Epithelium	Tissues	Epithelium	2.42×10^{-3}
A10.690.552	Muscle Striated	Tissues	Muscles	3.78×10^{-3}
A10.690.552.500	Muscle Skeletal	Tissues	Muscles	3.78×10^{-3}
A03.556.249.249.356.668	Colon Sigmoid	Digestive System	Gastrointestinal Tract	3.90×10^{-3}
A05.810.453.324	Kidney Cortex	Urogenital System	Urinary Tract	4.64×10^{-3}

MeSH = Medical Subject Heading, MeSH 1st level term is given as Cells, Tissues or as the respective annotation in the Physiological system, Nominal P-values with * indicate a False Discovery Rate < 0.01



Supplementary Figure 8: Pathway and tissue enrichment analysis with DEPICT (BUN)

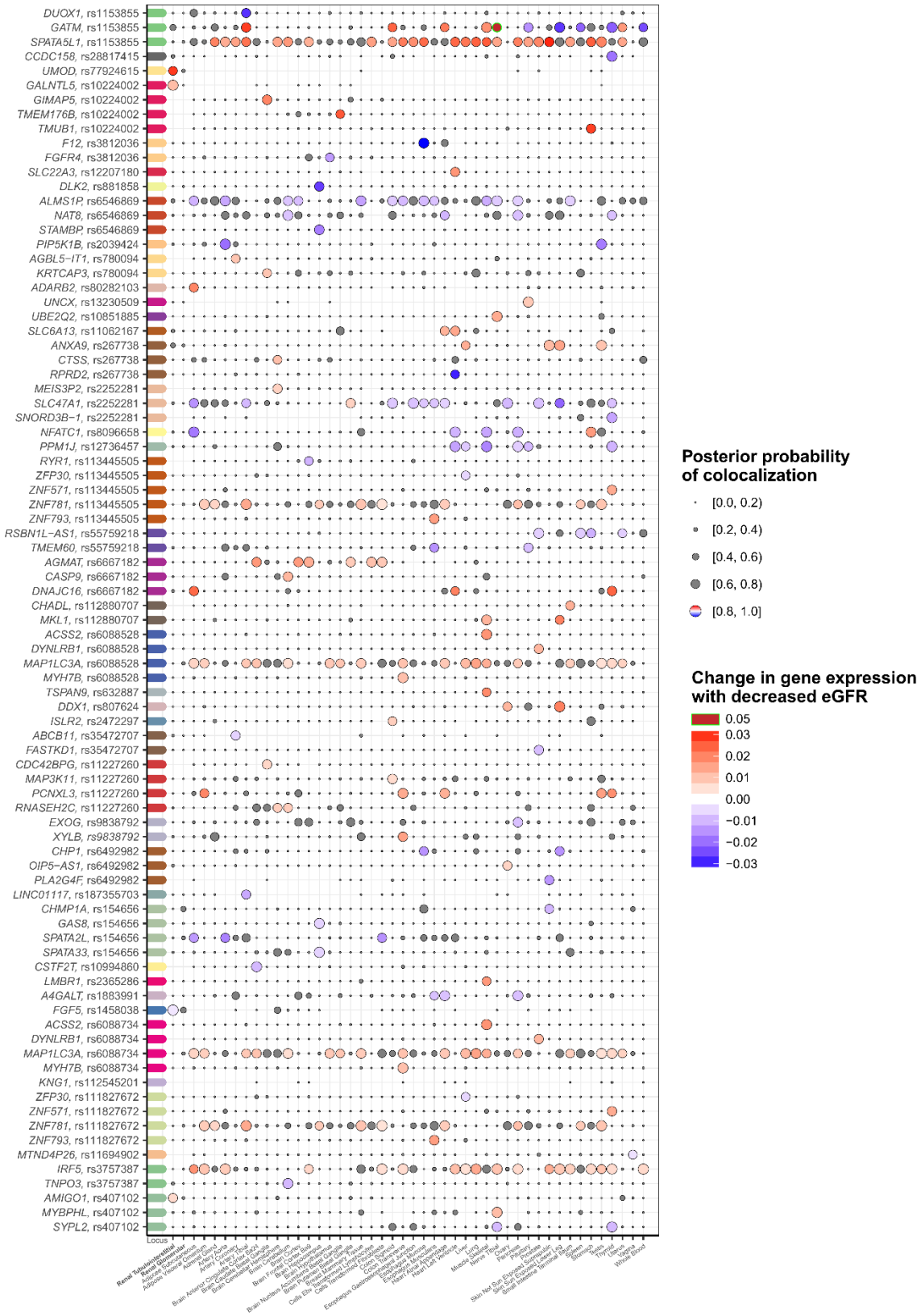
Shown is the barplot of the results of the tissue and cell type enrichment analysis. Cells, tissues and physiological systems are highlighted in blue if the association FDR was <0.05. Tissue and cell-type enrichment analysis of BUN-associated SNPs with $P<5\times10^{-8}$ highlighted a very similar pattern to the one observed for eGFR: the strongest enrichment was observed for urogenital and renal physiological systems and tissues, and significant enrichment was also observed for mucous membrane, respiratory mucosa, nasal mucosa, nose, epithelial cells and the epithelium.



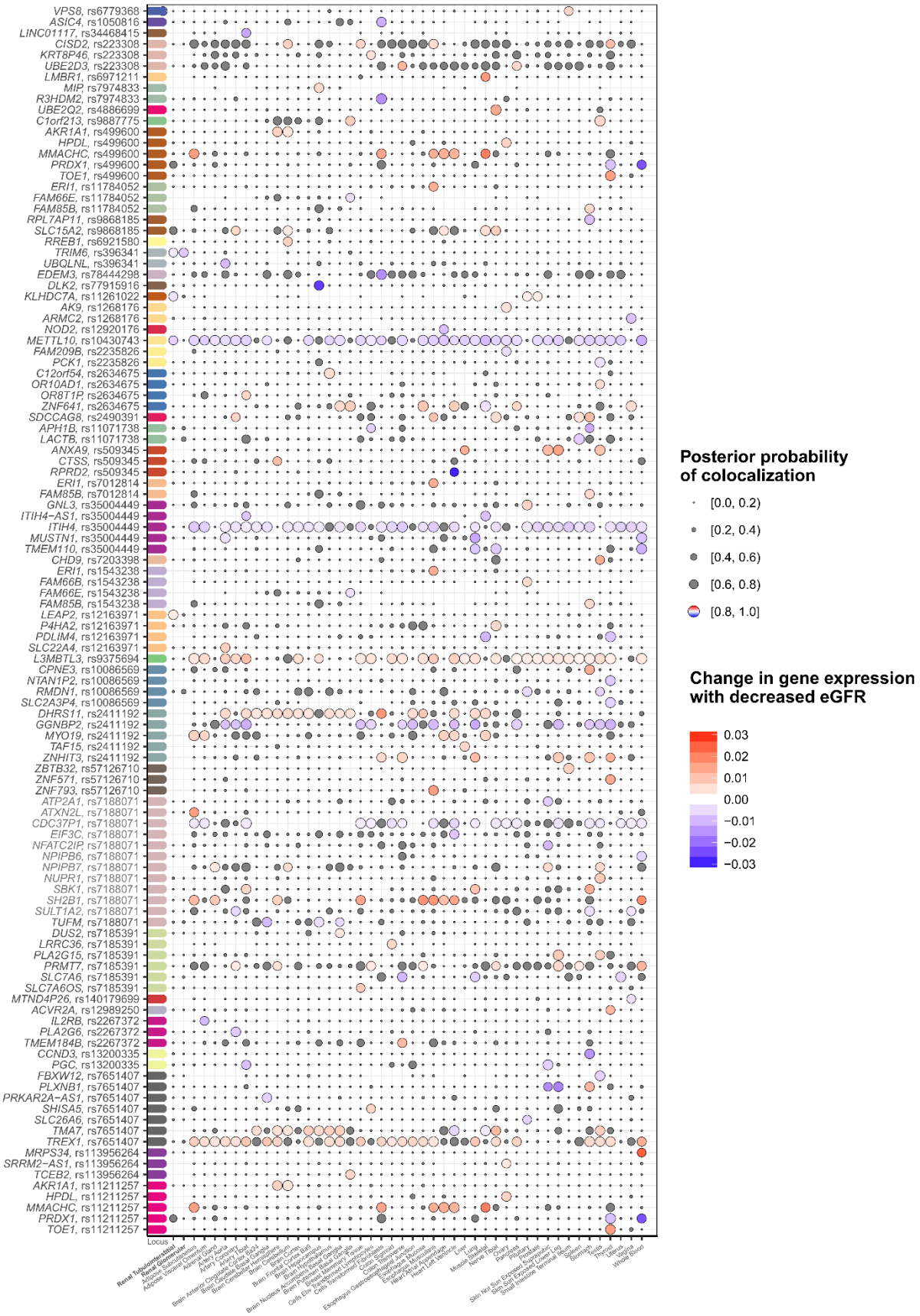
Supplementary Figure 9: Co-localization of eGFR-association signals with gene expression across 44 GTEx tissues and two kidney tissues

All eGFR loci were tested for co-localization with all eQTLs where the eQTL cis-window overlapped (±100 kb) the sentinel genetic variants. Genes with at least one positive co-localization (posterior probability of one common causal variant, H4, ≥0.80) in any of the 44 tissues for which eQTL data was released by the GTEx Project or in two renal tissue are illustrated with the respective sentinel variants (Y-axis). Co-localizations across all tissues (X-axis) are illustrated as dots, where the size of the dots indicates the posterior probability of the co-localization. Negative co-localizations (posterior probability of H4 <0.80) are grey, while the positive co-localizations are color-coded based on the predicted change in expression relative to the allele associated with lower eGFR.

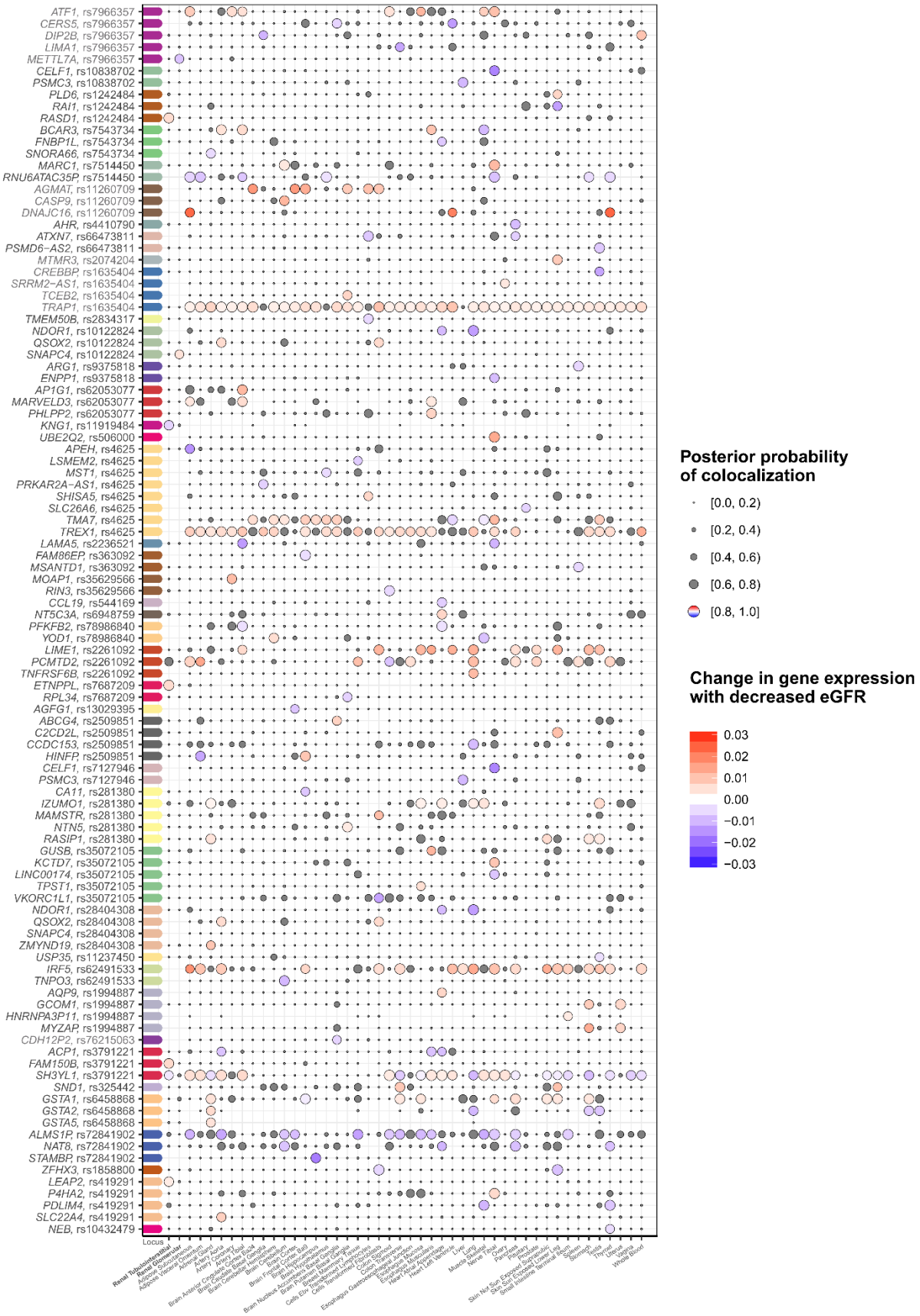
Supplementary Figure 9 – continued (1/4)



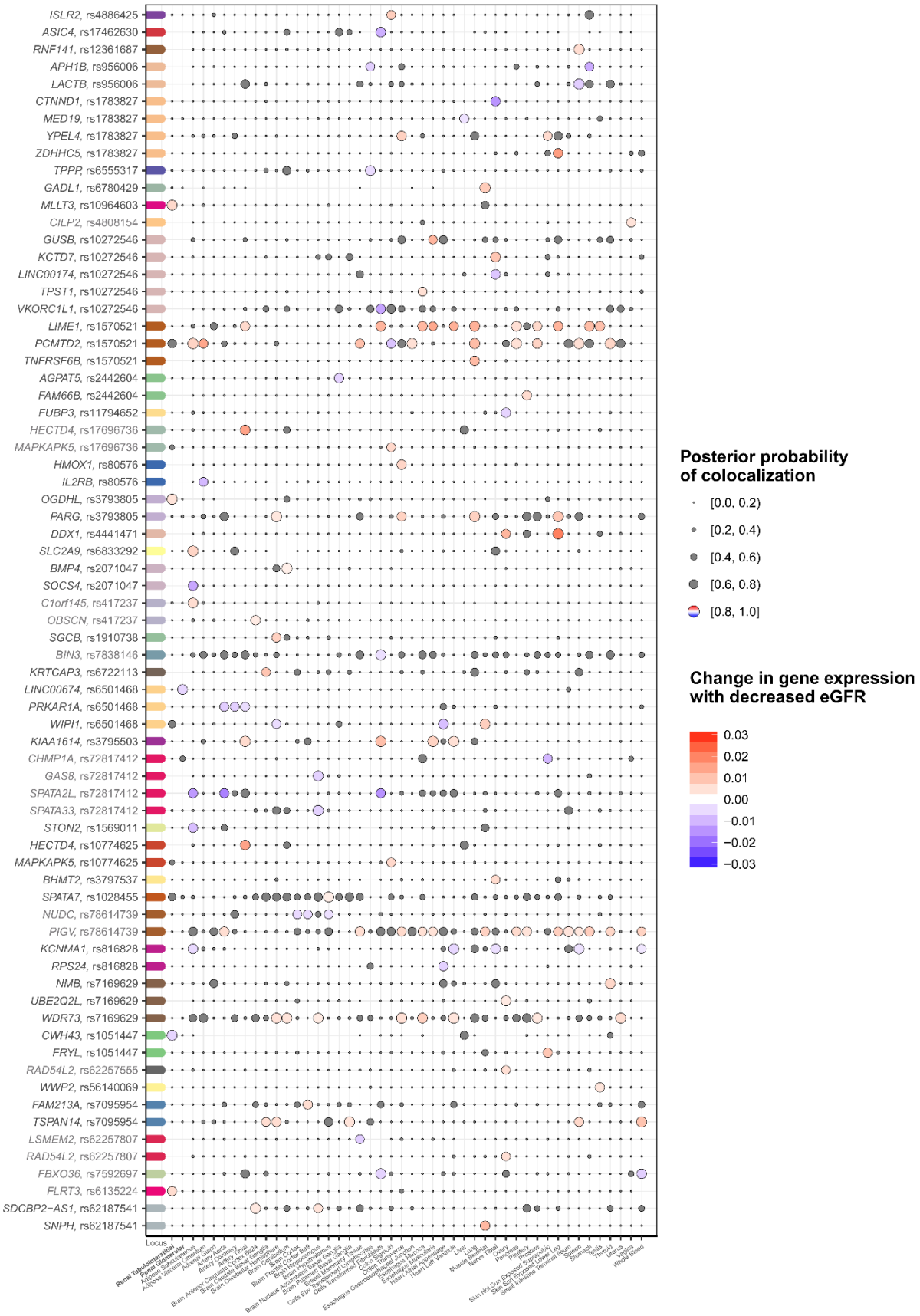
Supplementary Figure 9 – continued (2/4)



Supplementary Figure 9 – continued (3/4)



Supplementary Figure 9 – continued (4/4)



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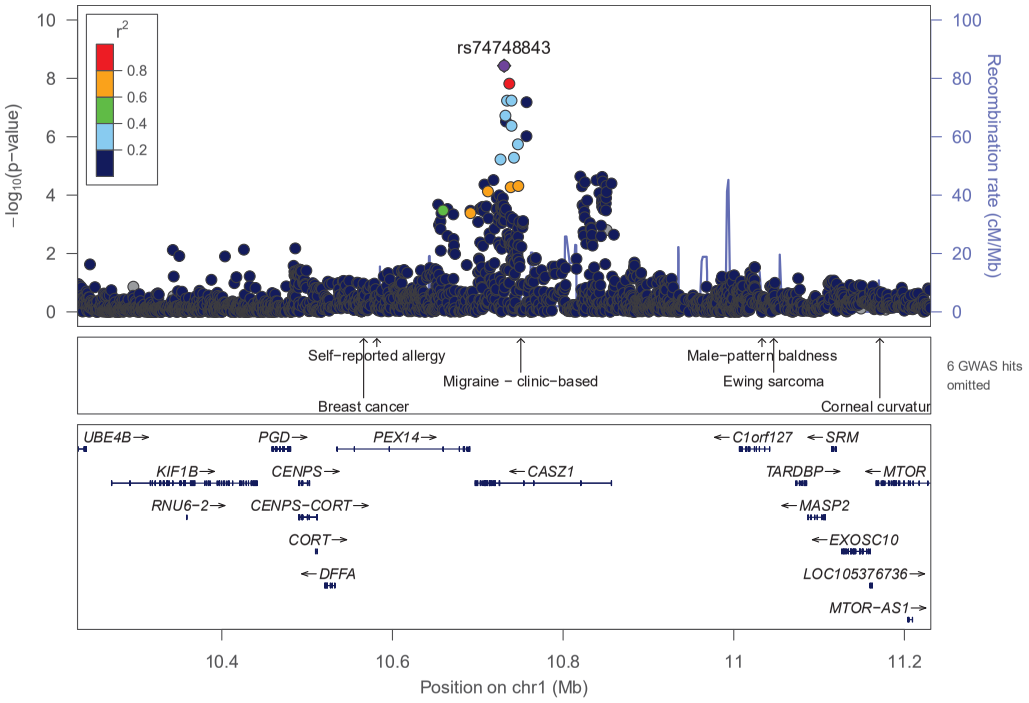
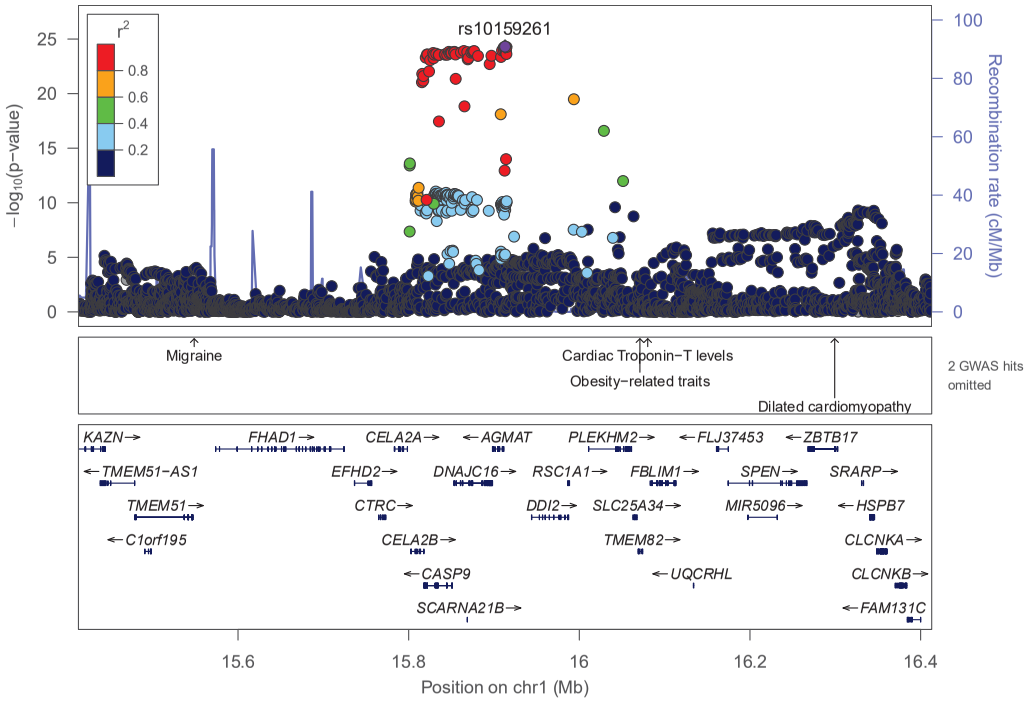
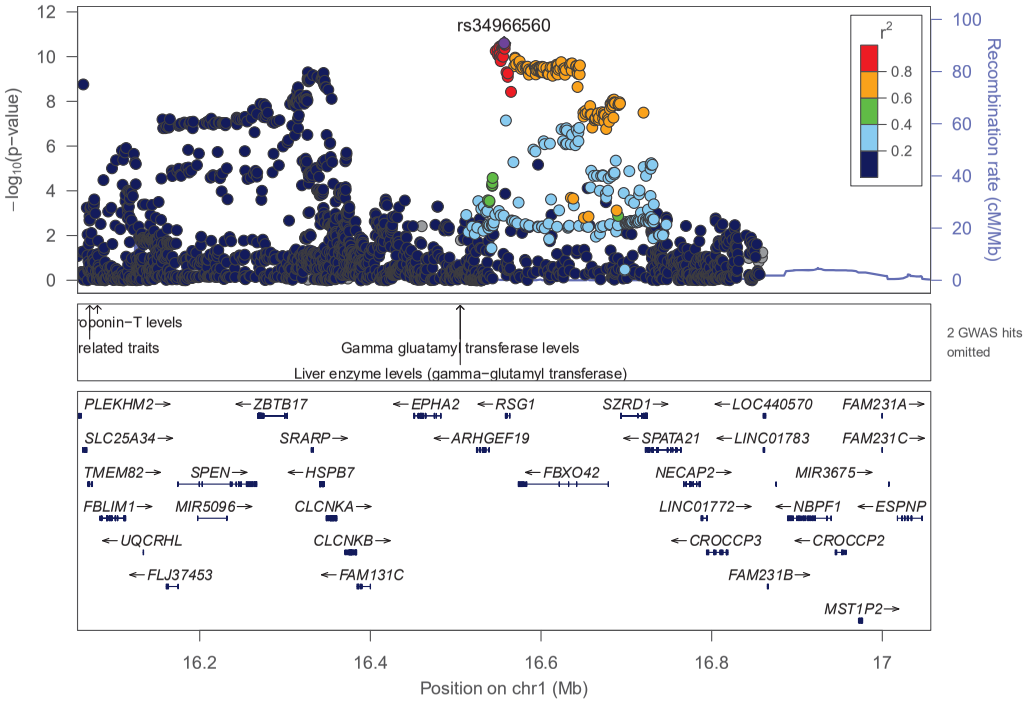
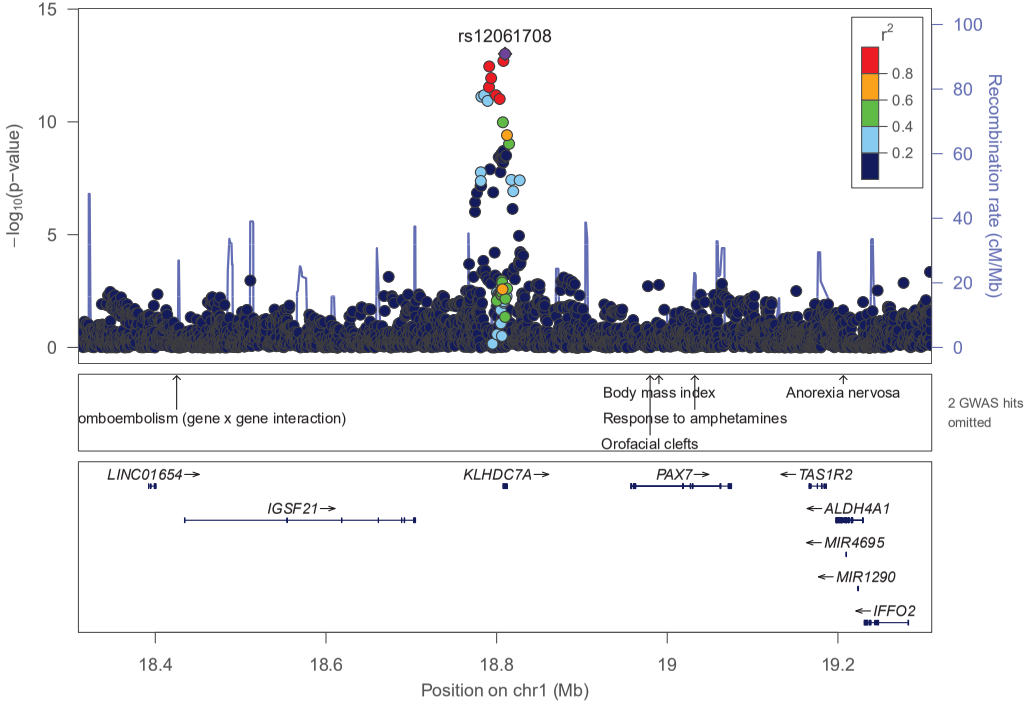
- VA Eastern Kansas Health Care System (Mary Oehlert)
- VA Greater Los Angeles Health Care System (Agnes Wallbom)
- VA Loma Linda Healthcare System (Ronald Fernando)
- VA Long Beach Healthcare System (Timothy Morgan)
- VA Maine Healthcare System (Todd Stapley)

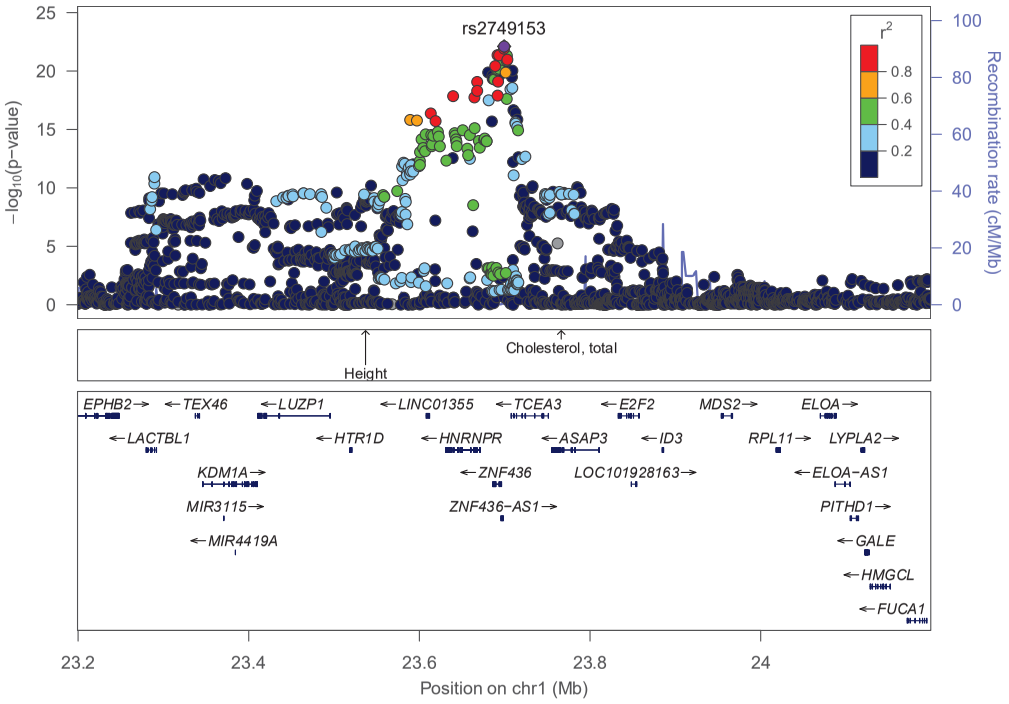
- VA New York Harbor Healthcare System (Scott Sherman)
- VA Pacific Islands Health Care System (Gwenevere Anderson)
- VA Palo Alto Health Care System (Philip Tsao)
- VA Pittsburgh Health Care System (Elif Sonel)
- VA Puget Sound Health Care System (Edward Boyko)
- VA Salt Lake City Health Care System (Laurence Meyer)
- VA San Diego Healthcare System (Samir Gupta)
- VA Southern Nevada Healthcare System (Joseph Fayad)
- VA Tennessee Valley Healthcare System (Adriana Hung)
- Washington DC VA Medical Center (Jack Lichy)
- W.G. (Bill) Hefner VA Medical Center (Robin Hurley)
- White River Junction VA Medical Center (Brooks Robey)
- William S. Middleton Memorial Veterans Hospital (Robert Striker)

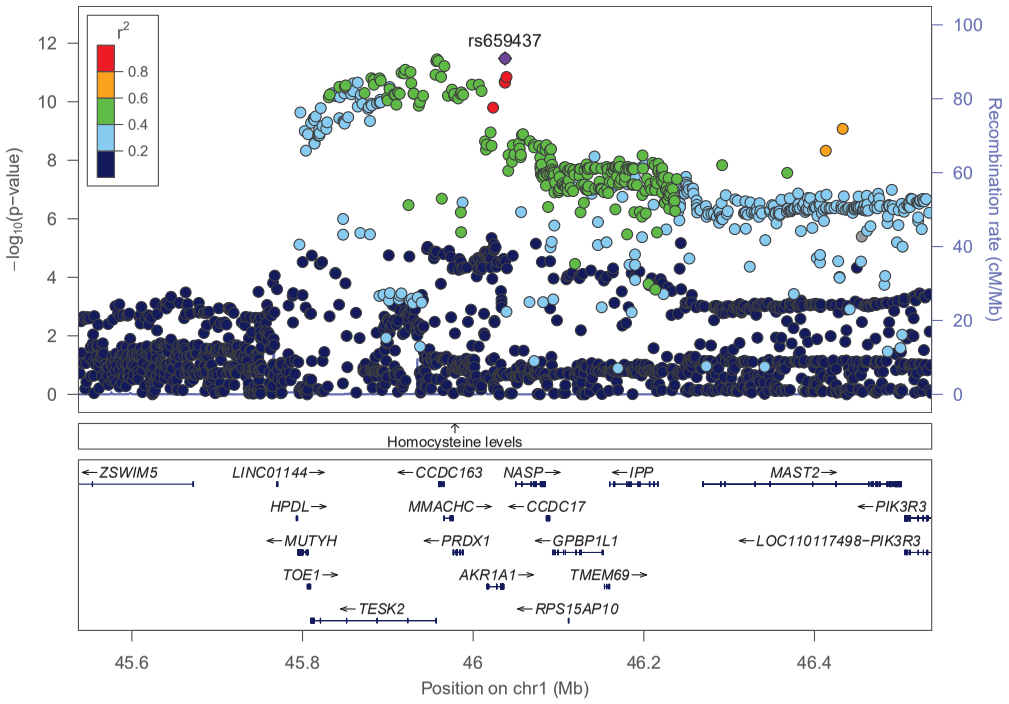

rs74748843
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Self−reported allergy
Migraine − clinic−based
Male−pattern baldness
Ewing sarcoma
Breast cancer
Corneal curvatur
6 GWAS hits omitted
UBE4B→
PGD→
PEX14→
←C1orf127
←SRM
KIF1B→
CENPS→
←CASZ1
TARDBP→
←MTOR
RNU6−2→
CENPS−CORT→
←MASP2
CORT→
←EXOSC10
←DFFA
LOC105376736→
MTOR−AS1→
Position on chr1 (Mb)

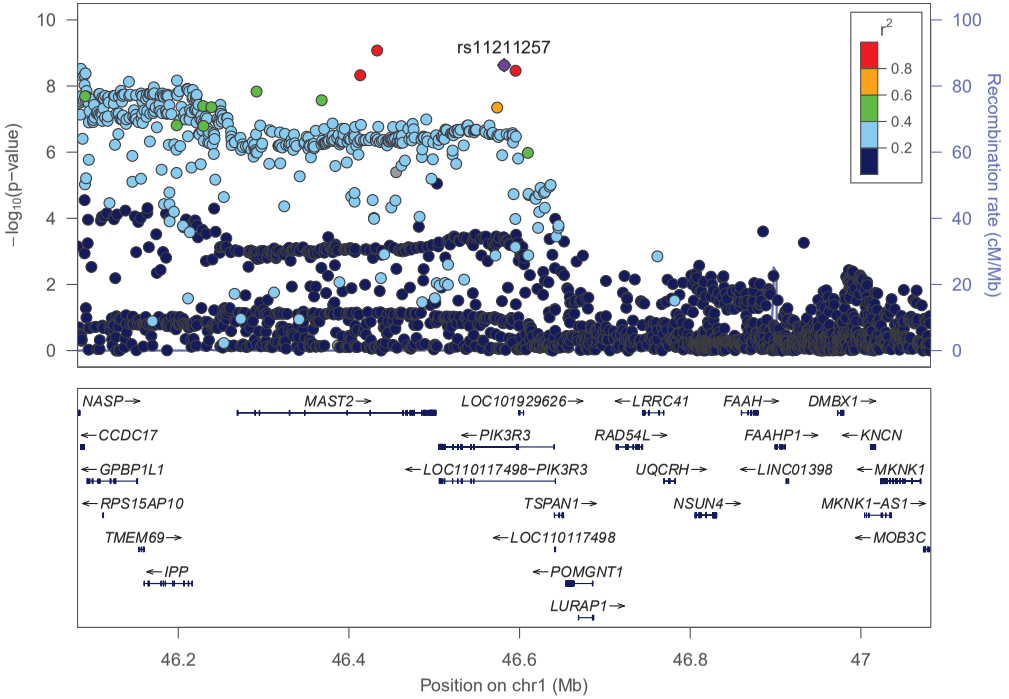

rs10159261
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Migraine
Cardiac Troponin−T levels
Obesity−related traits
Dilated cardiomyopathy
2 GWAS hits omitted
KAZN→
FHAD1→
CELA2A→
←AGMAT
PLEKHM2→
←FLJ37453
←ZBTB17
←TMEM51−AS1
EFHD2→
DNAJC16→
RSC1A1→
FBLIM1→
SPEN→
SRARP→
TMEM51→
CTRC→
DDI2→
SLC25A34→
MIR5096→
←HSPB7
←C1orf195
CELA2B→
TMEM82→
CLCNKA→
←CASP9
←UQCRHL
CLCNKB→
SCARNA21B→
←FAM131C
Position on chr1 (Mb)

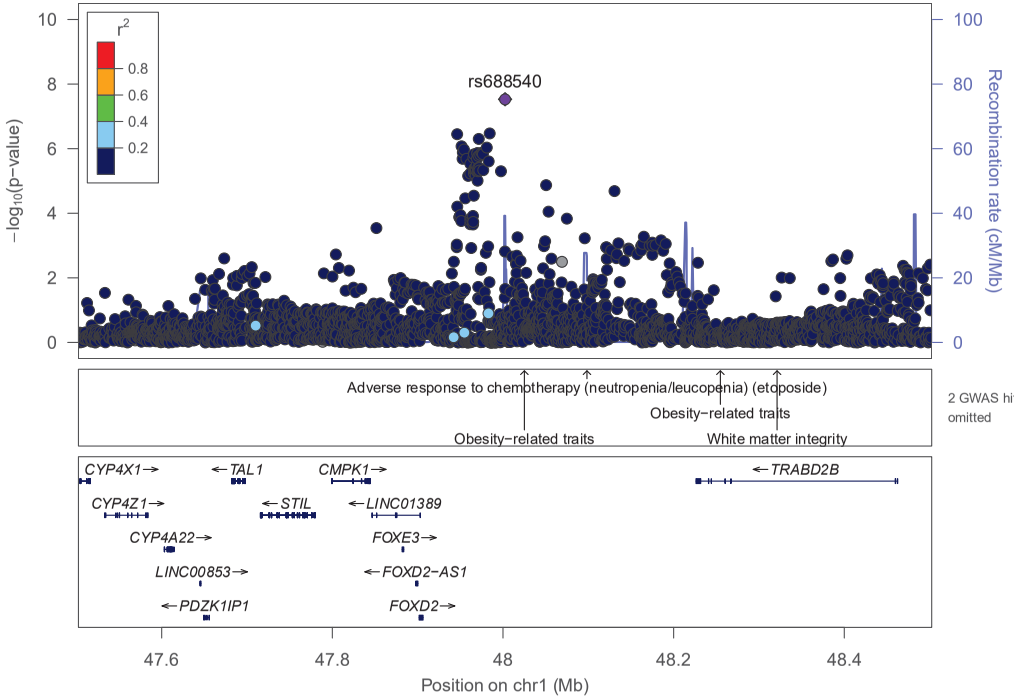

rs34966560
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
oponin−T levels
related traits
Gamma gluatamyl transferase levels
Liver enzyme levels (gamma−glutamyl transferase)
2 GWAS hits omitted
PLEKHM2→
←ZBTB17
←EPHA2
←RSG1
SZRD1→
←LOC440570
FAM231A→
SLC25A34→
SRARP→
←ARHGEF19
←SPATA21
←LINC01783
FAM231C→
TMEM82→
SPEN→
←HSPB7
←FBXO42
NECAP2→
MIR3675→
FBLIM1→
MIR5096→
CLCNKA→
LINC01772→
←NBPF1
←ESPNP
←UQCRHL
CLCNKB→
←CROCCP3
←CROCCP2
←FLJ37453
←FAM131C
FAM231B→
MST1P2→
Position on chr1 (Mb)

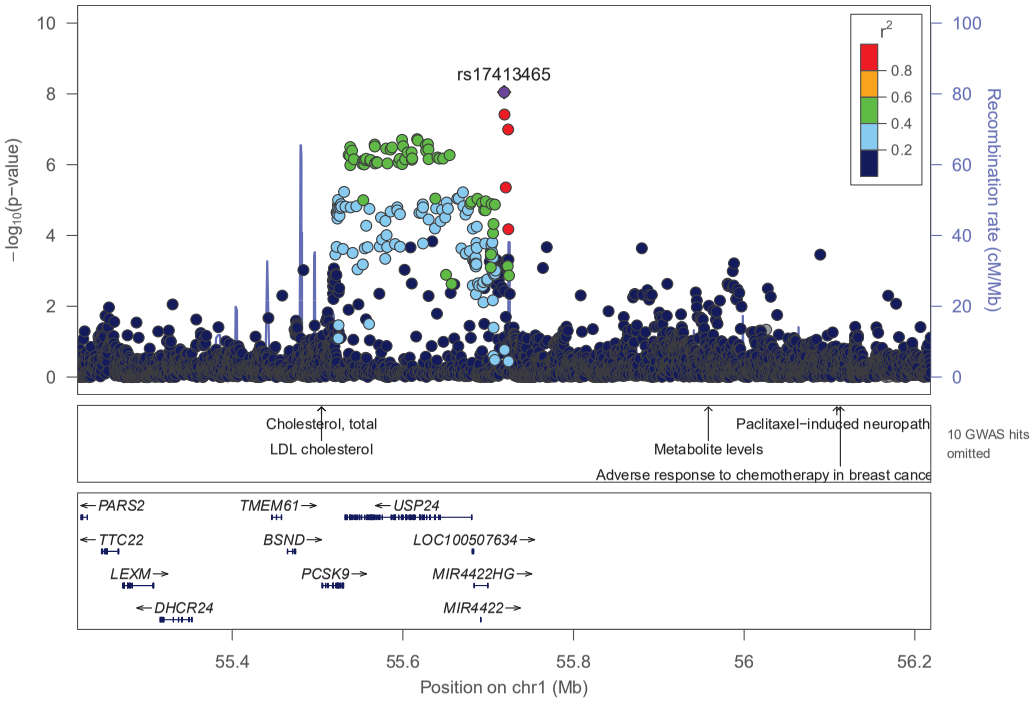

rs12061708
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
omboembolism (gene x gene interaction)
Body mass index
Response to amphetamines
Orofacial clefts
Anorexia nervosa
2 GWAS hits omitted
LINC01654→
KLHDC7A→
PAX7→
←TAS1R2
IGSF21→
←ALDH4A1
←MIR4695
←MIR1290
←IFFO2
Position on chr1 (Mb)

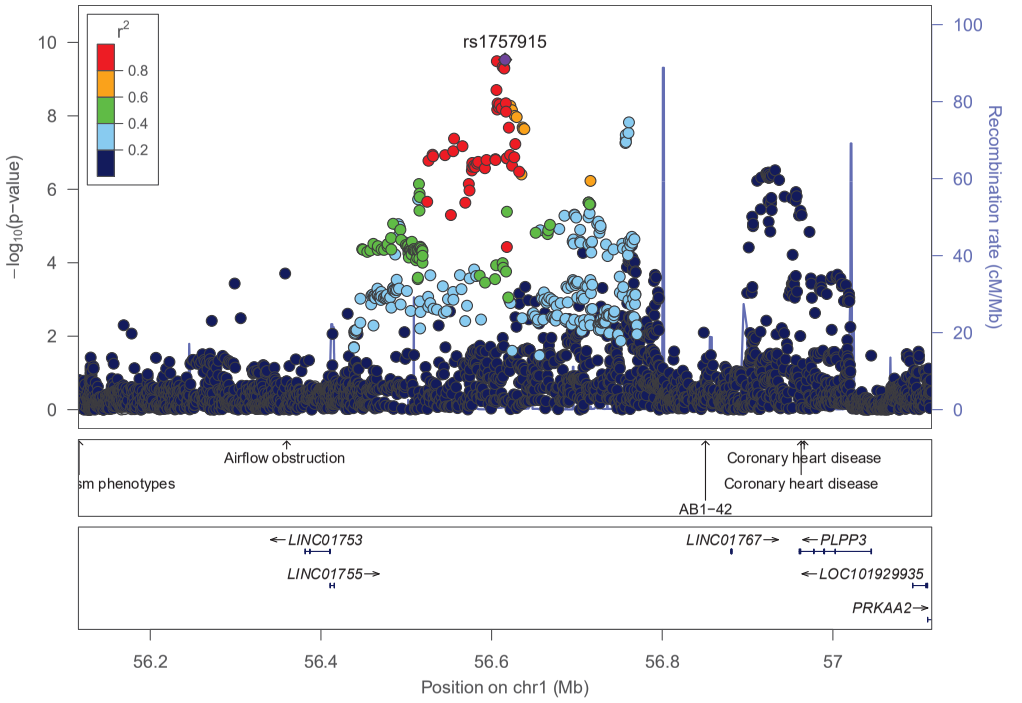

rs2749153
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Height
Cholesterol, total
EPHB2→ ←TEX46 ←LUZP1 ←LINC01355 ←TCEA3 ←E2F2 MDS2→ ELOA→
←LACTBL1 ←HTR1D ←HNRNPR ←ASAP3 ←ID3 RPL11→ LYPLA2→
KDM1A→ ←ZNF436 LOC101928163→ ←ELOA−AS1
MIR3115→ ZNF436−AS1→ PITHD1→
←MIR4419A ←GALE
←HMGCL
←FUCA1
Position on chr1 (Mb)

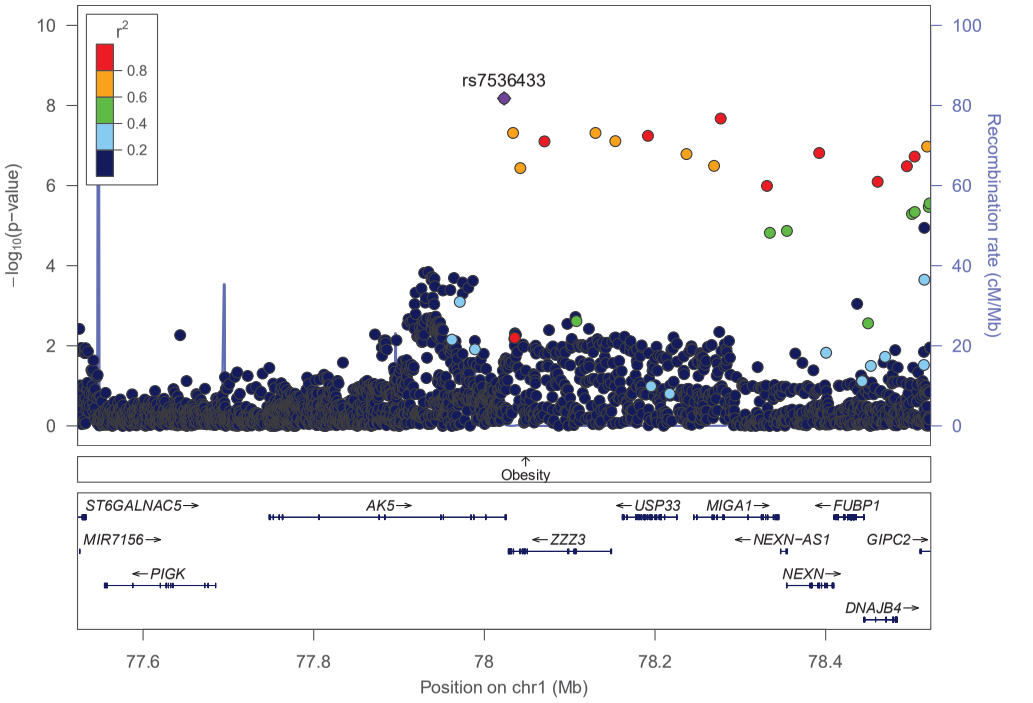

rs659437
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Homocysteine levels
←ZSWIM5 LINC01144→ ←CCDC163 NASP→ ←IPP MAST2→
HPDL→ MMACHC→ ←CCDC17 ←PIK3R3
←MUTYH ←PRDX1 ←GPBP1L1 ←LOC110117498−PIK3R3
TOE1→ AKR1A1→ TMEM69→
←TESK2 ←RPS15AP10
Position on chr1 (Mb)

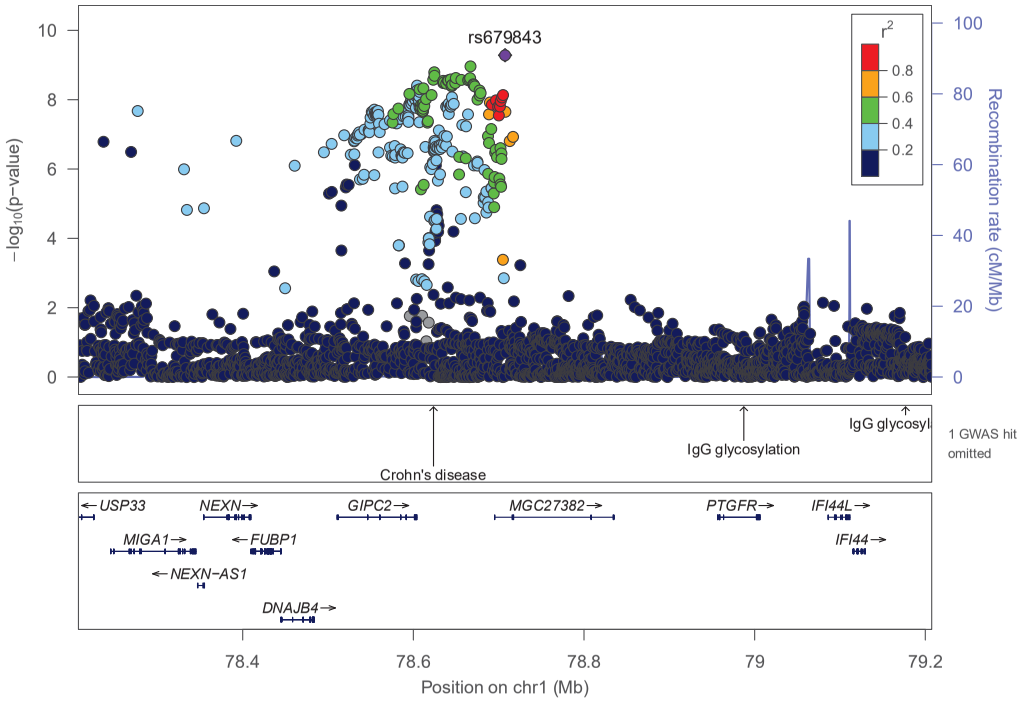

rs11211257
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
NASP→ MAST2→ LOC101929626→ ←LRRC41 FAAH→ DMBX1→
←CCDC17 ←PIK3R3 RAD54L→ FAAHP1→ ←KNCN
←GPBP1L1 ←LOC110117498−PIK3R3 UQCRH→ ←LINC01398 ←MKNK1
←RPS15AP10 TSPAN1→ NSUN4→ MKNK1−AS1→
TMEM69→ ←LOC110117498 ←MOB3C
←IPP ←POMGNT1
LURAP1→
Position on chr1 (Mb)

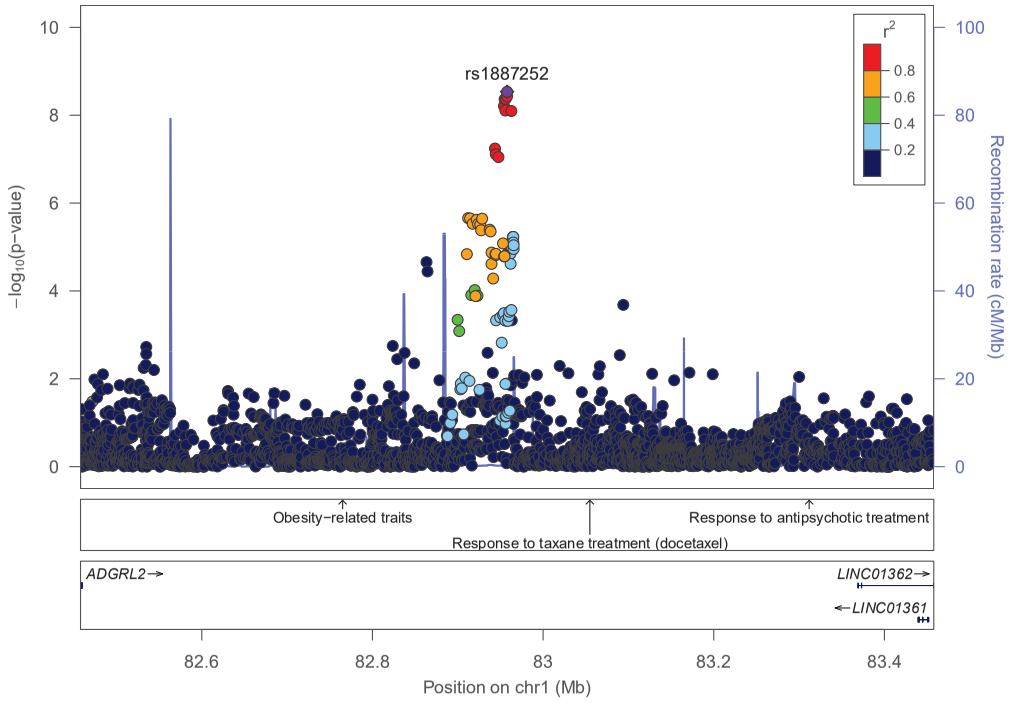

rs688540
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Adverse response to chemotherapy (neutropenia/leucopenia) (etoposide)
Obesity−related traits
Obesity−related traits
White matter integrity
2 GWAS hits omitted
CYP4X1→ ←TAL1 CMPK1→ ←TRABD2B
CYP4Z1→ ←STIL ←LINC01389
CYP4A22→ FOXE3→
LINC00853→ ←FOXD2−AS1
←PDZK1IP1 FOXD2→
Position on chr1 (Mb)

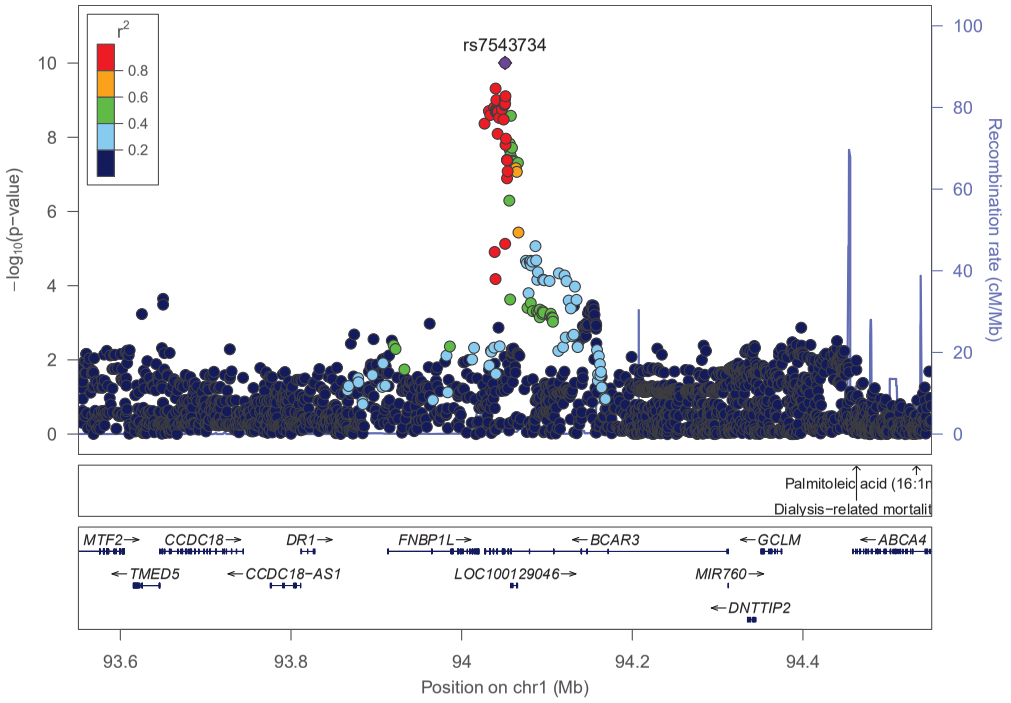

rs17413465
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
LDL cholesterol
Metabolite levels
Paclitaxel−induced neuropath
Adverse response to chemotherapy in breast cance
10 GWAS hits omitted
PARS2
TMEM61
USP24
TTC22
BSND
LOC100507634
LEXM
PCSK9
MIR4422HG
DHCR24
MIR4422
55.4
55.6
55.8
56
56.2
Position on chr1 (Mb)

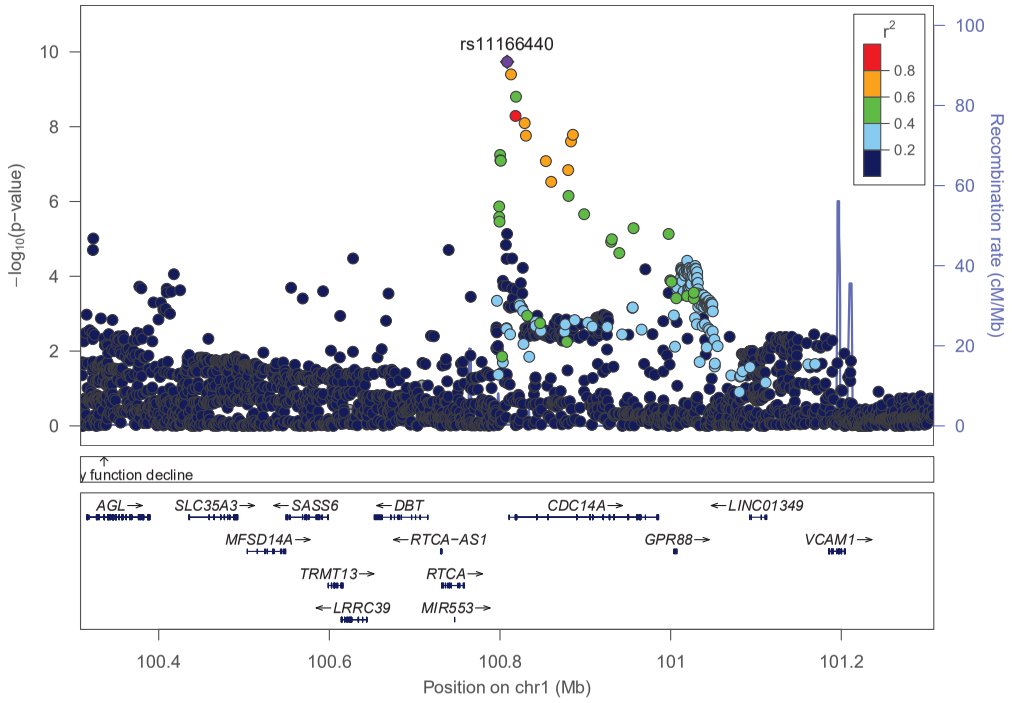

rs1757915
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Airflow obstruction
Coronary heart disease
Coronary heart disease
AB1−42
LINC01753
LINC01755
LINC01767
PLPP3
LOC101929935
PRKAA2
56.2
56.4
56.6
56.8
57
Position on chr1 (Mb)

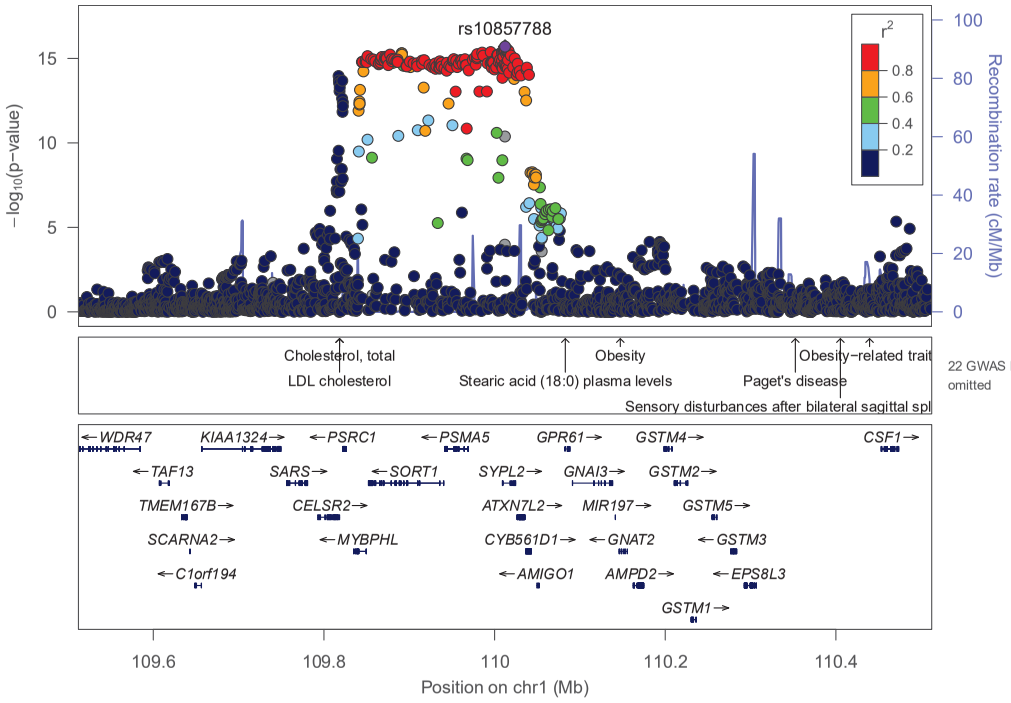

rs7536433
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity
ST6GALNAC5
AK5
USP33
MIGA1
FUBP1
MIR7156
ZZZ3
NEXN−AS1
GIPC2
PIGK
NEXN
DNAJB4
77.6
77.8
78
78.2
78.4
Position on chr1 (Mb)

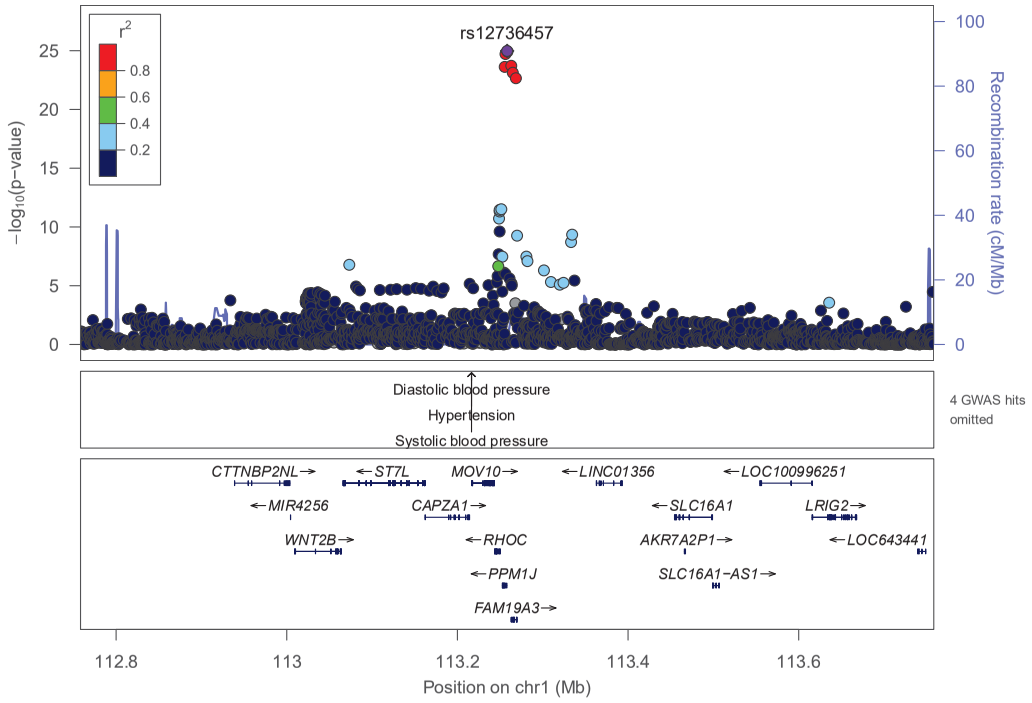

rs679843
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Crohn's disease
IgG glycosylation
IgG glycosyl
1 GWAS hit omitted
USP33
NEXN
GIPC2
MGC27382
PTGFR
IFI44L
MIGA1
FUBP1
IFI44
NEXN−AS1
DNAJB4
78.4
78.6
78.8
79
79.2
Position on chr1 (Mb)

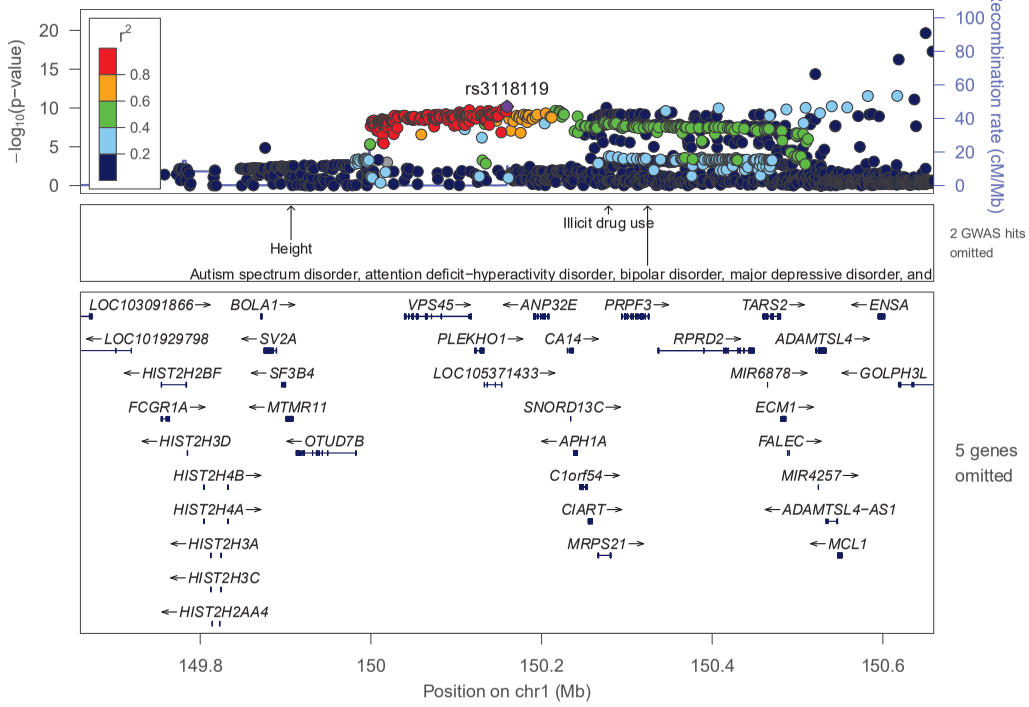

rs1887252
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Response to taxane treatment (docetaxel)
Response to antipsychotic treatment
ADGRL2→
LINC01362→
←LINC01361
82.6
82.8
83
83.2
83.4
Position on chr1 (Mb)

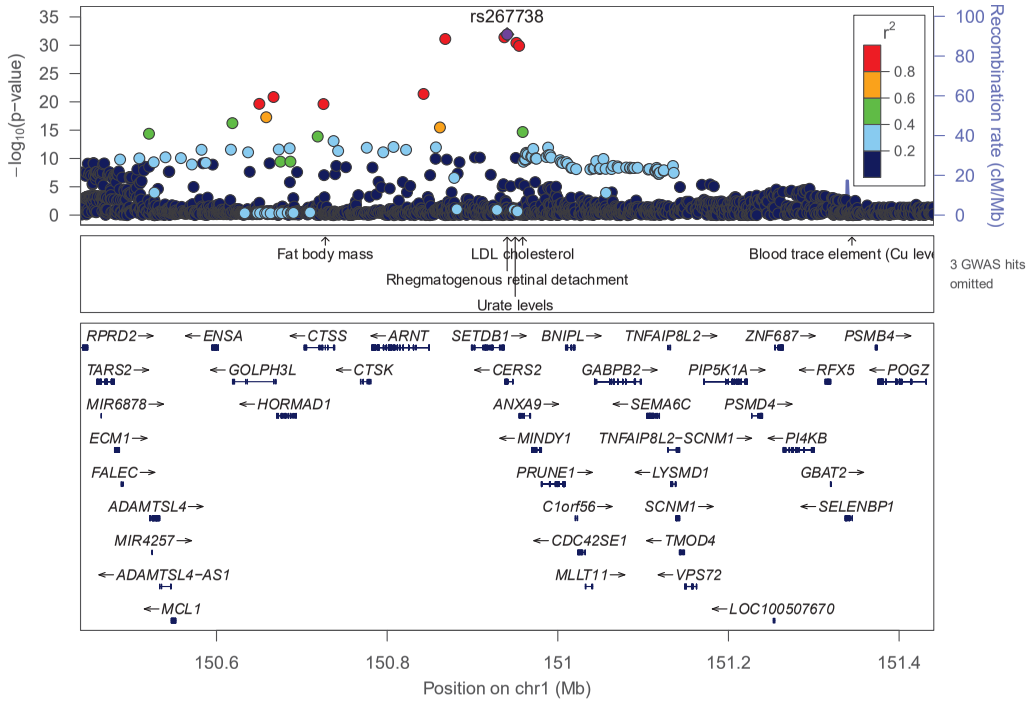

rs7543734
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Palmitoleic acid (16:1n
Dialysis−related mortalit
MTF2→
CCDC18→
DR1→
FNBP1L→
←BCAR3
←GCLM
←ABCA4
←TMED5
←CCDC18−AS1
LOC100129046→
MIR760→
←DNTTIP2
93.6
93.8
94
94.2
94.4
Position on chr1 (Mb)

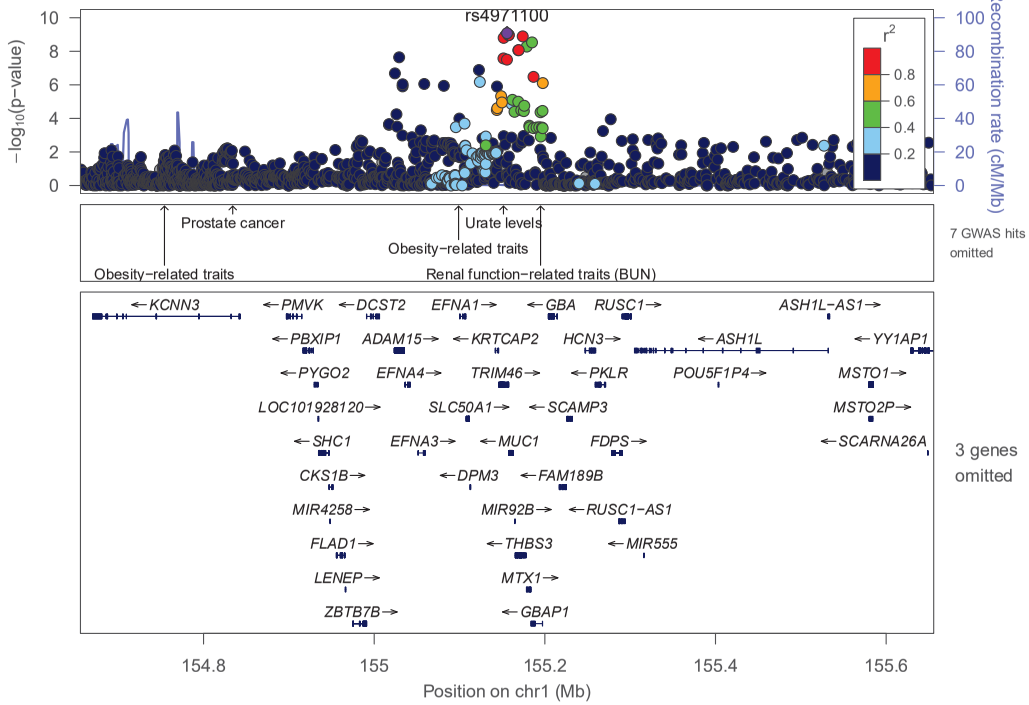

rs11166440
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
v function decline
AGL→
SLC35A3→
←SASS6
←DBT
CDC14A→
←LINC01349
MFSD14A→
←RTCA−AS1
GPR88→
VCAM1→
TRMT13→
RTCA→
←LRRC39
MIR553→
100.4
100.6
100.8
101
101.2
Position on chr1 (Mb)

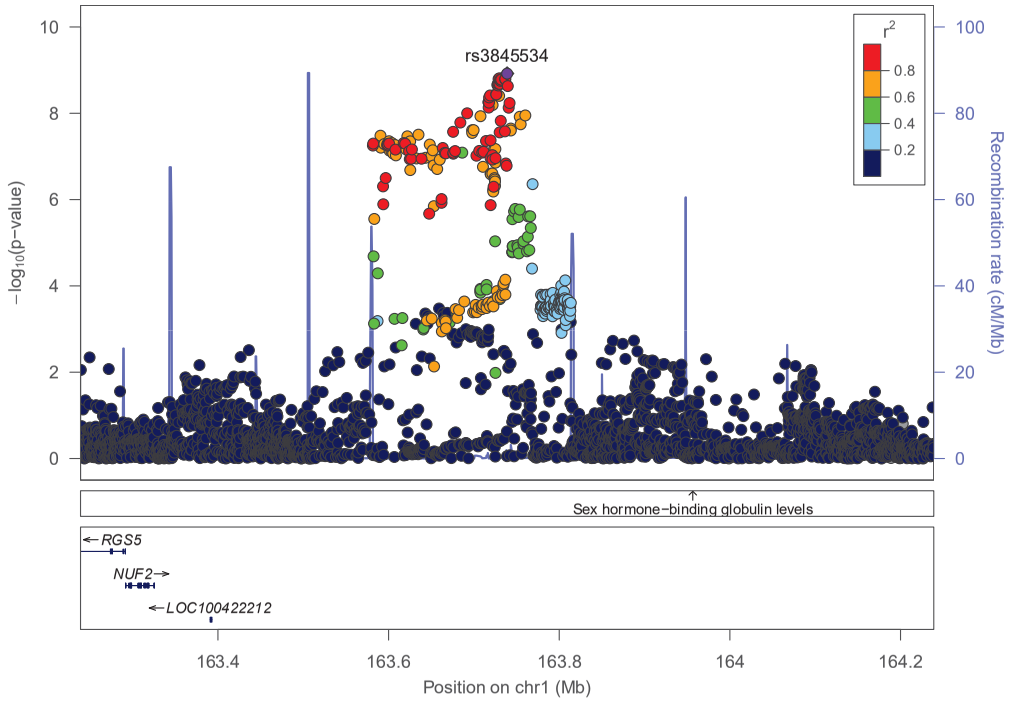

rs10857788
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
LDL cholesterol
Obesity
Stearic acid (18:0) plasma levels
Paget's disease
Obesity−related trait
Sensory disturbances after bilateral sagittal spl
22 GWAS hits
omitted
←WDR47
KIAA1324→
←PSRC1
←PSMA5
GPR61→
GSTM4→
CSF1→
←TAF13
SARS→
←SORT1
SYPL2→
GNAI3→
GSTM2→
TMEM167B→
CELSR2→
ATXN7L2→
MIR197→
GSTM5→
SCARNA2→
←MYBPHL
CYB561D1→
←GNAT2
←GSTM3
←C1orf194
←AMIGO1
AMPD2→
←EPS8L3
GSTM1→
109.6
109.8
110
110.2
110.4
Position on chr1 (Mb)

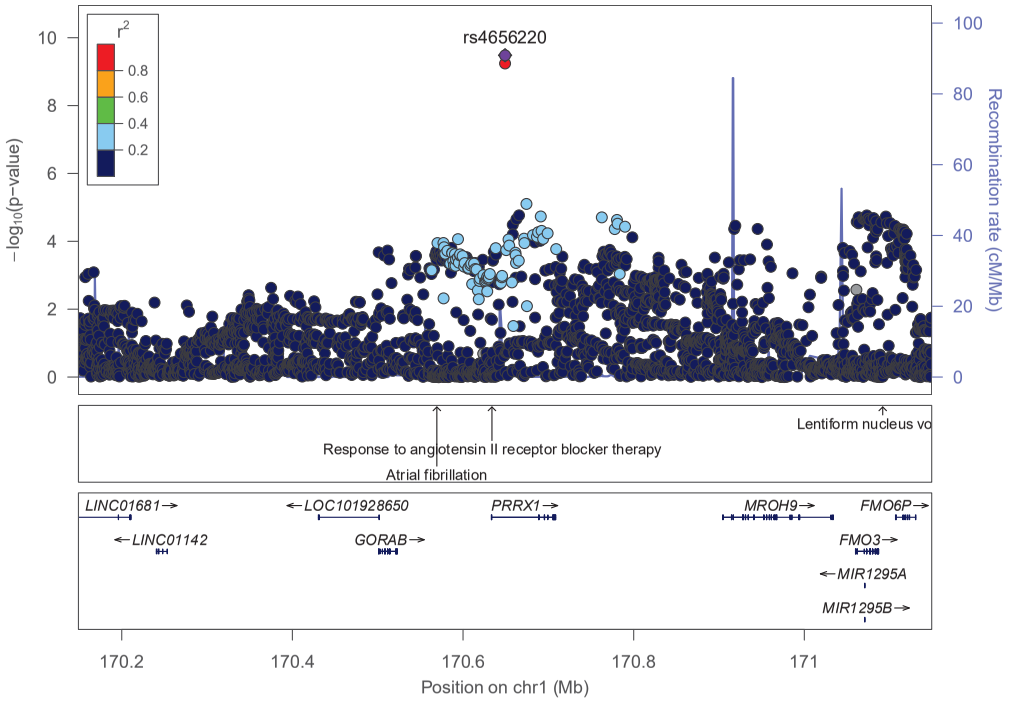

rs12736457
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Diastolic blood pressure
Hypertension
Systolic blood pressure
4 GWAS hits omitted
CTTNBP2NL→ ←ST7L MOV10→ ←LINC01356 ←LOC100996251
←MIR4256 CAPZA1→ ←SLC16A1 LRIG2→
WNT2B→ ←RHOC AKR7A2P1→ ←LOC643441
←PPM1J SLC16A1−AS1→
FAM19A3→
112.8 113 113.2 113.4 113.6
Position on chr1 (Mb)

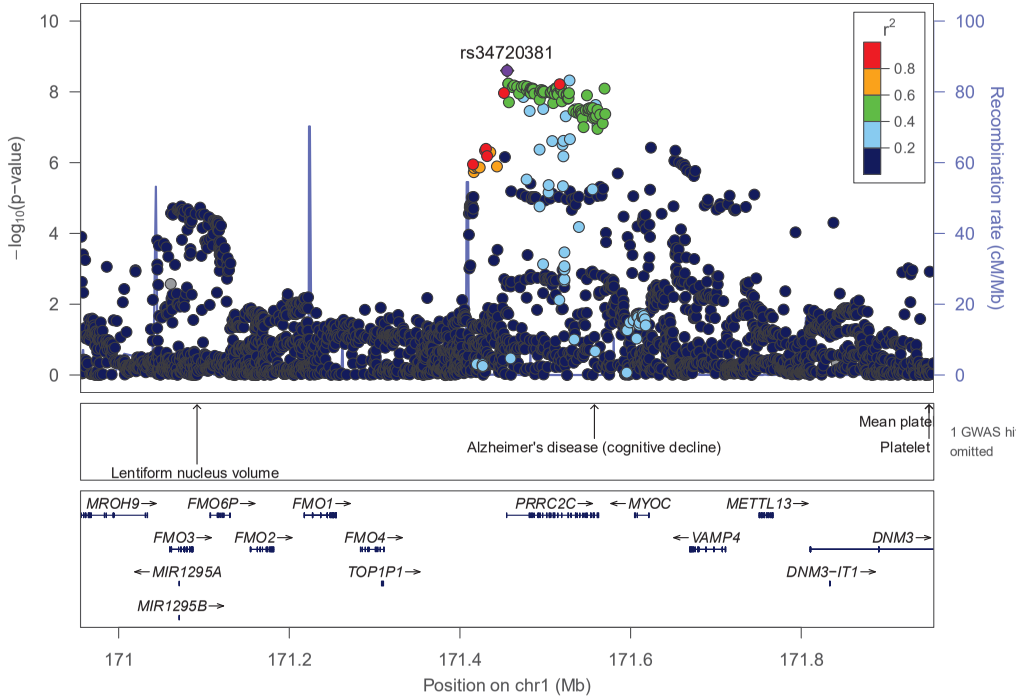

rs3118119
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Height
Illicit drug use
Autism spectrum disorder, attention deficit−hyperactivity disorder, bipolar disorder, major depressive disorder, and
2 GWAS hits omitted
LOC103091866→ BOLA1→ VPS45→ ←ANP32E PRPF3→ TARS2→ ←ENSA
←LOC101929798 ←SV2A PLEKHO1→ CA14→ RPRD2→ ADAMTSL4→
←HIST2H2BF ←SF3B4 LOC105371433→ MIR6878→ ←GOLPH3L
FCGR1A→ ←MTMR11 SNORD13C→ ECM1→
←HIST2H3D ←OTUD7B ←APH1A FALEC→
HIST2H4B→ C1orf54→ MIR4257→
HIST2H4A→ CIART→ ←ADAMTSL4−AS1
←HIST2H3A MRPS21→ ←MCL1
←HIST2H3C
←HIST2H2AA4
5 genes omitted
149.8 150 150.2 150.4 150.6
Position on chr1 (Mb)

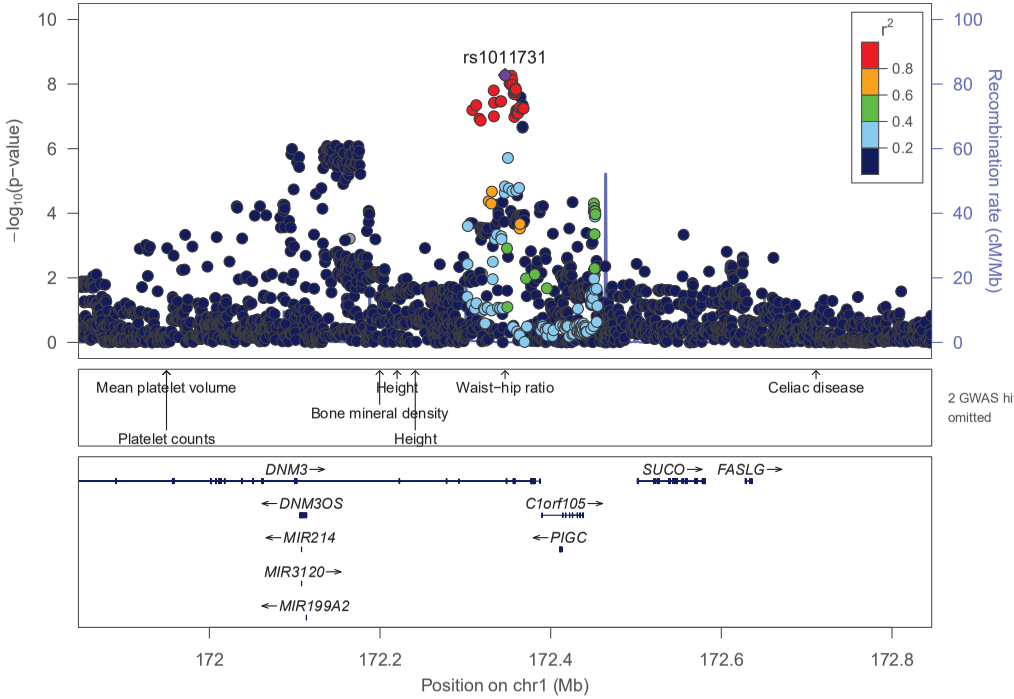

rs267738
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Fat body mass
LDL cholesterol
Rhegmatogenous retinal detachment
Urate levels
Blood trace element (Cu lev
3 GWAS hits omitted
RPRD2→ ←ENSA ←CTSS ←ARNT SETDB1→ BNIPL→ TNFAIP8L2→ ZNF687→ PSMB4→
TARS2→ ←GOLPH3L ←CTSK ←CERS2 GABPB2→ PIP5K1A→ ←RFX5 ←POGZ
MIR6878→ ←HORMAD1 ANXA9→ ←SEMA6C PSMD4→
ECM1→ ←MINDY1 TNFAIP8L2−SCNM1→ ←PI4KB
FALEC→ PRUNE1→ ←LYSMD1 GBAT2→
ADAMTSL4→ C1orf56→ SCNM1→ ←SELENBP1
MIR4257→ ←CDC42SE1 ←TMOD4
←ADAMTSL4−AS1 MLLT11→ ←VPS72
←MCL1 ←LOC100507670
150.6 150.8 151 151.2 151.4
Position on chr1 (Mb)

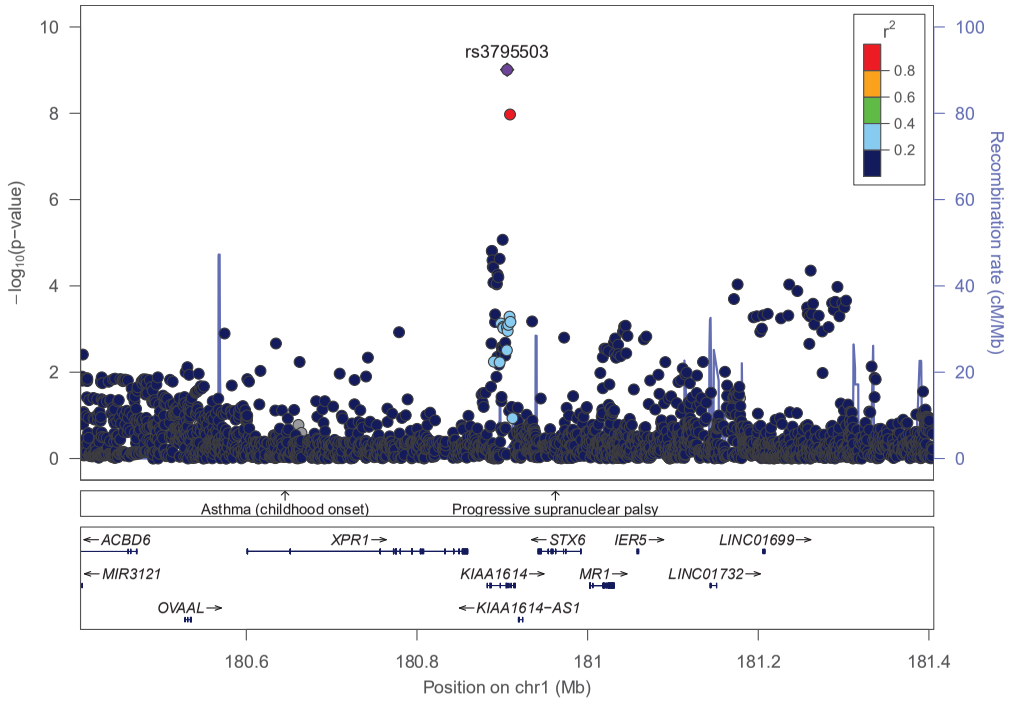

rs4971100
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Prostate cancer
Urate levels
Obesity−related traits
Obesity−related traits
Renal function−related traits (BUN)
7 GWAS hits omitted
←KCNN3 ←PMVK ←DCST2 EFNA1→ ←GBA RUSC1→ ASH1L−AS1→
←PBXIP1 ADAM15→ ←KRTCAP2 HCN3→ ←ASH1L ←YY1AP1
←PYGO2 EFNA4→ TRIM46→ ←PKLR POU5F1P4→ MSTO1→
LOC101928120→ SLC50A1→ ←SCAMP3 MSTO2P→
←SHC1 EFNA3→ ←MUC1 FDPS→ ←SCARNA26A
CKS1B→ ←DPM3 ←FAM189B
MIR4258→ MIR92B→ ←RUSC1−AS1
FLAD1→ ←THBS3 ←MIR555
LENEP→ MTX1→
ZBTB7B→ ←GBAP1
3 genes omitted
154.8 155 155.2 155.4 155.6
Position on chr1 (Mb)

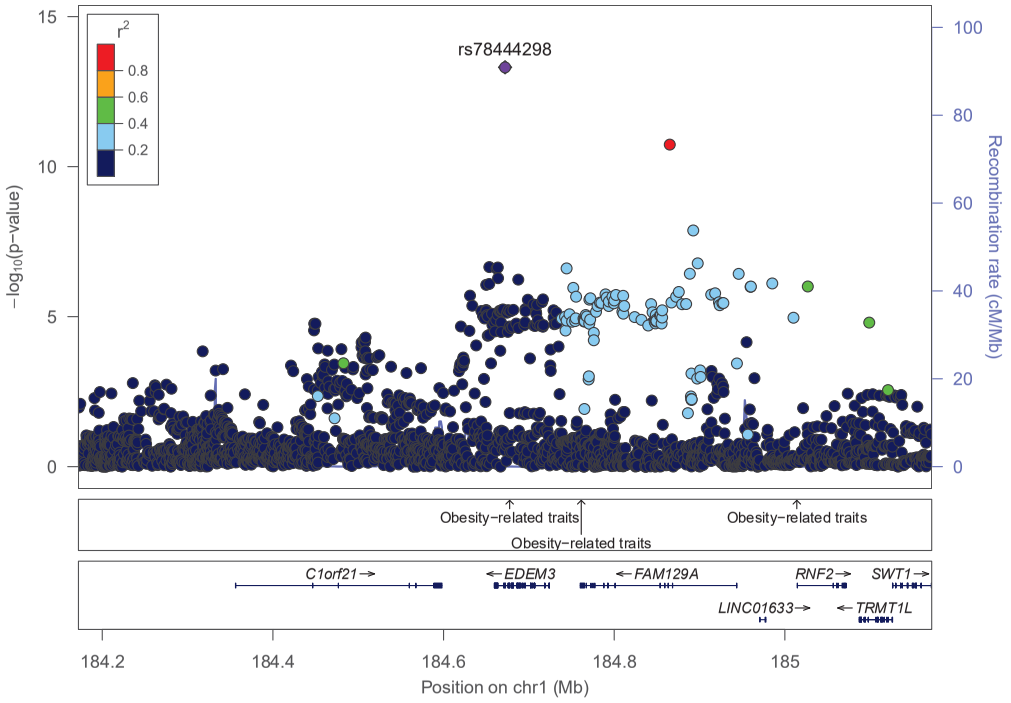

rs3845534
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Sex hormone−binding globulin levels
RGS5
NUF2
LOC100422212
Position on chr1 (Mb)

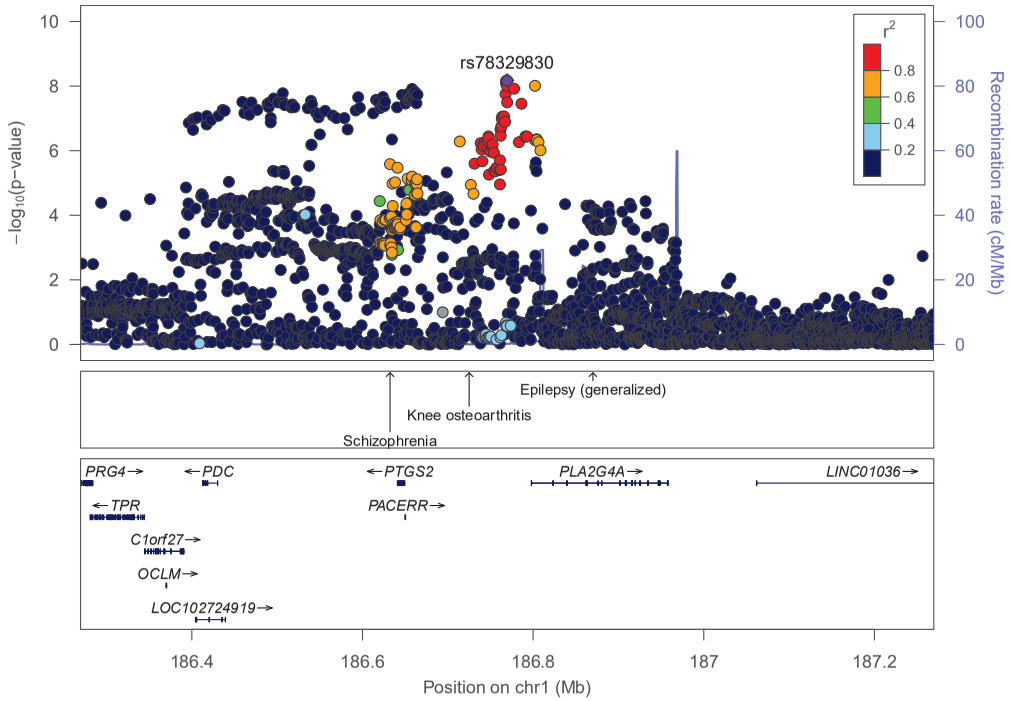

rs4656220
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Lentiform nucleus vo
Response to angiotensin II receptor blocker therapy
Atrial fibrillation
LINC01681
LINC01142
LOC101928650
GORAB
PRRX1
MROH9
FMO6P
FMO3
MIR1295A
MIR1295B
Position on chr1 (Mb)

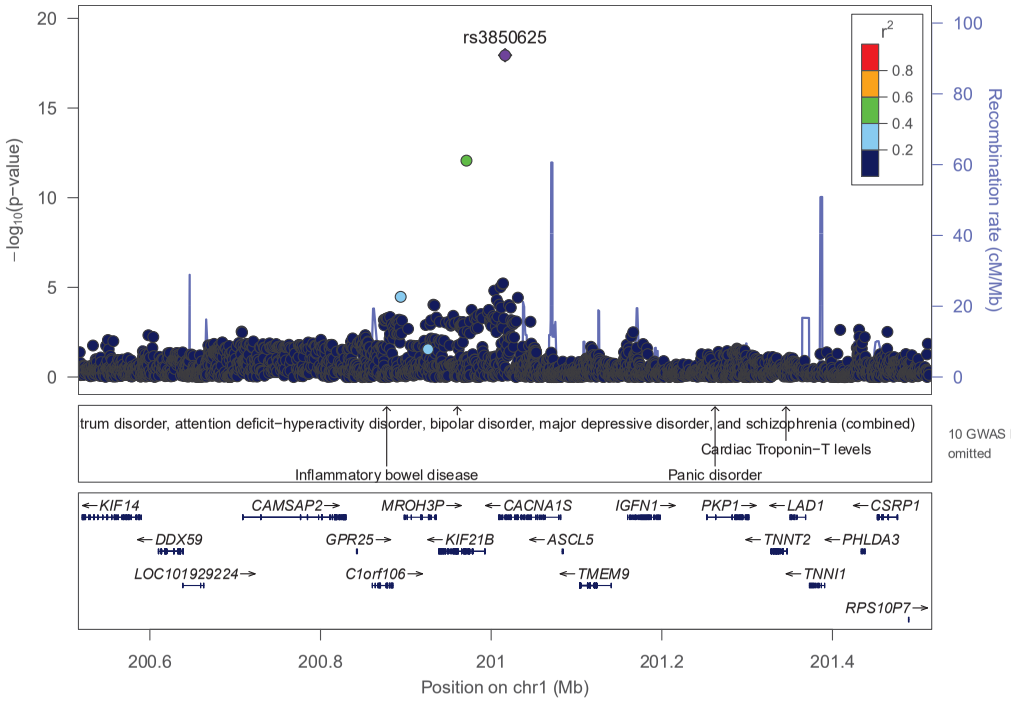

rs34720381
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Lentiform nucleus volume
Alzheimer's disease (cognitive decline)
Mean plate
Platelet
1 GWAS hit
omitted
MROH9
FMO6P
FMO1
PRRC2C
MYOC
METTL13
FMO3
FMO2
FMO4
VAMP4
DNM3
MIR1295A
TOP1P1
DNM3−IT1
MIR1295B
Position on chr1 (Mb)

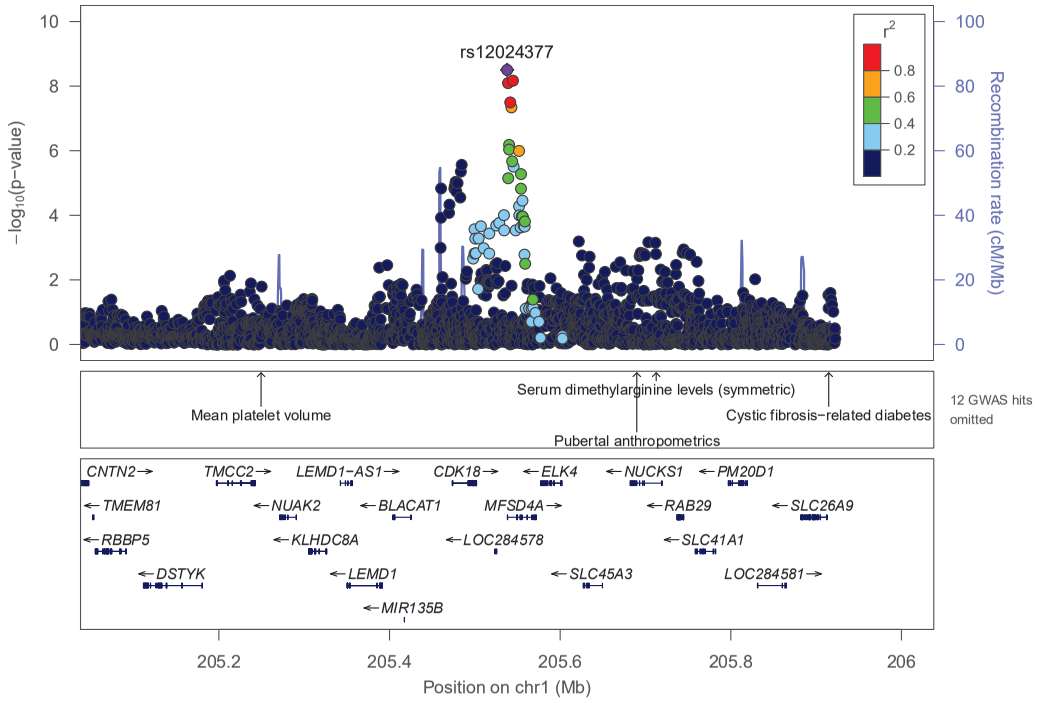

rs1011731
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Mean platelet volume
Platelet counts
Height
Bone mineral density
Height
Waist−hip ratio
Celiac disease
2 GWAS hits
omitted
DNM3
SUCO
FASLG
DNM3OS
C1orf105
MIR214
PIGC
MIR3120
MIR199A2
Position on chr1 (Mb)

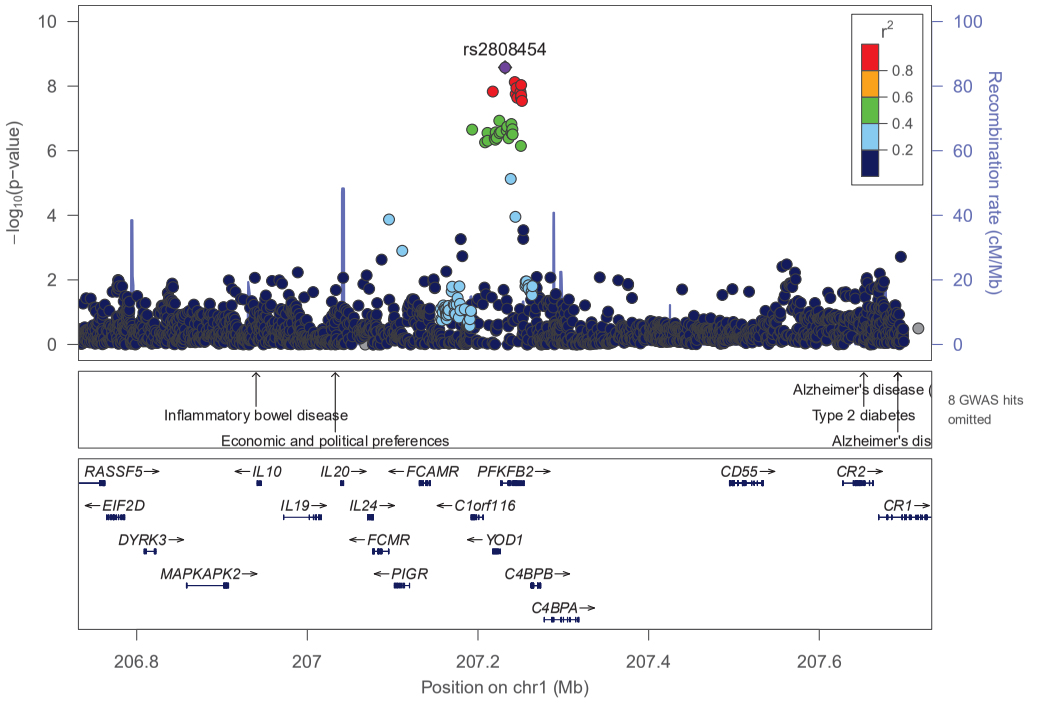

rs3795503
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Asthma (childhood onset)
Progressive supranuclear palsy
ACBD6
XPR1
STX6
IER5
LINC01699
MIR3121
KIAA1614
MR1
LINC01732
OVAAL
KIAA1614−AS1
Position on chr1 (Mb)

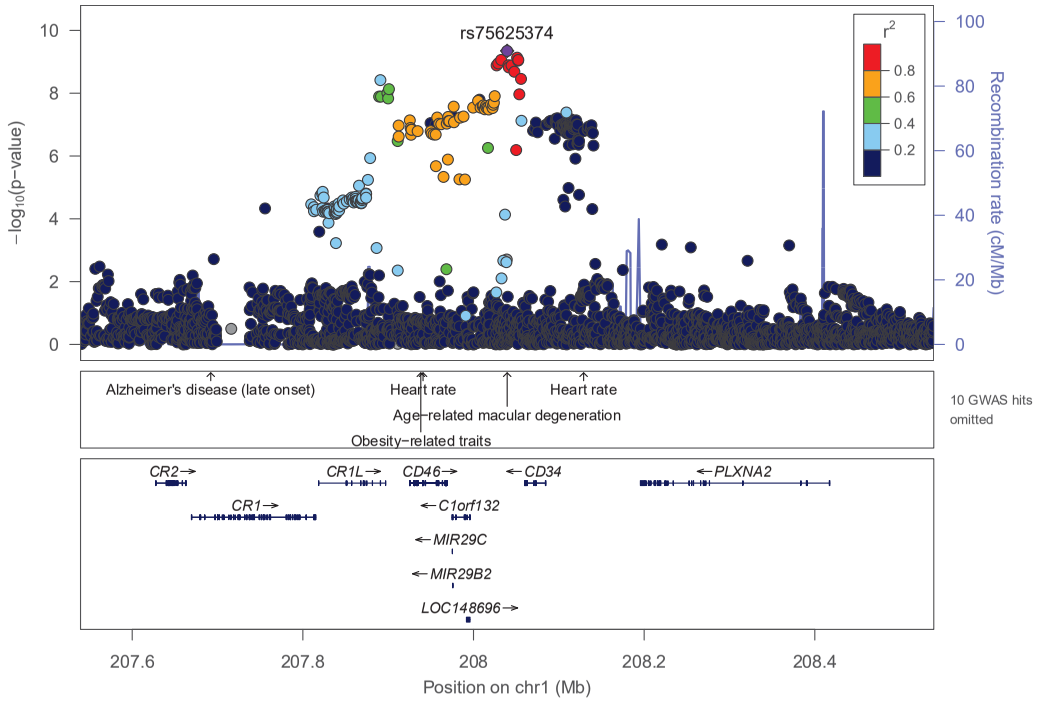

rs78444298
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Obesity−related traits
Obesity−related traits
C1orf21
EDEM3
FAM129A
RNF2
SWT1
LINC01633
TRMT1L
Position on chr1 (Mb)

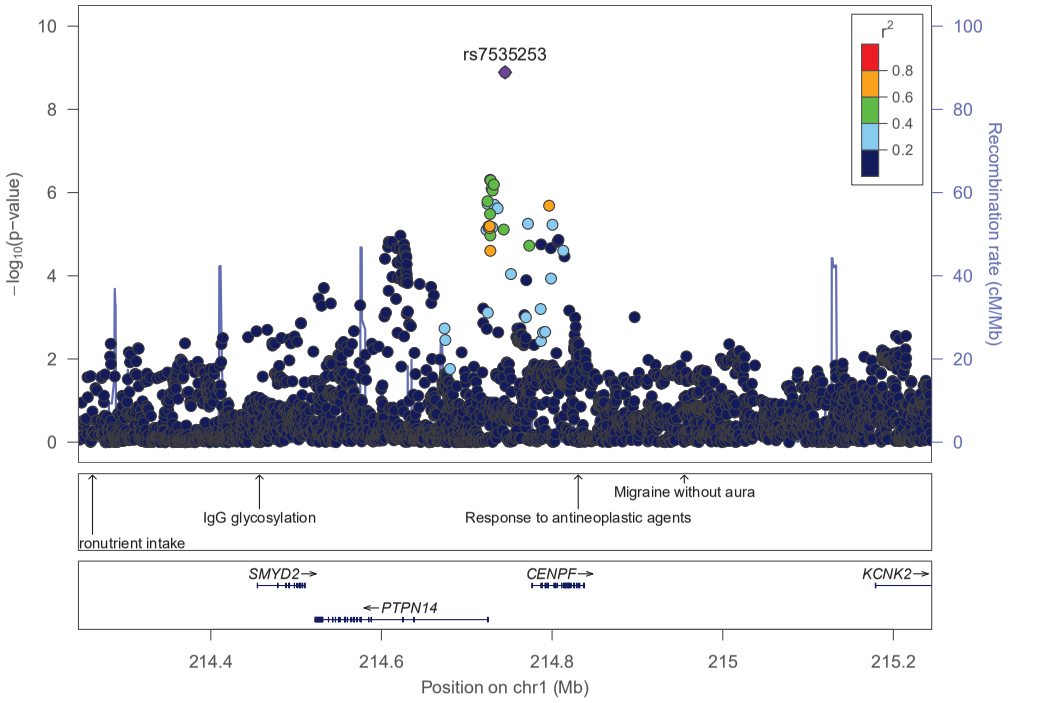

rs78329830
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Epilepsy (generalized)
Knee osteoarthritis
Schizophrenia
PRG4
PDC
PTGS2
PLA2G4A
LINC01036
TPR
PACERR
C1orf27
OCLM
LOC102724919
Position on chr1 (Mb)

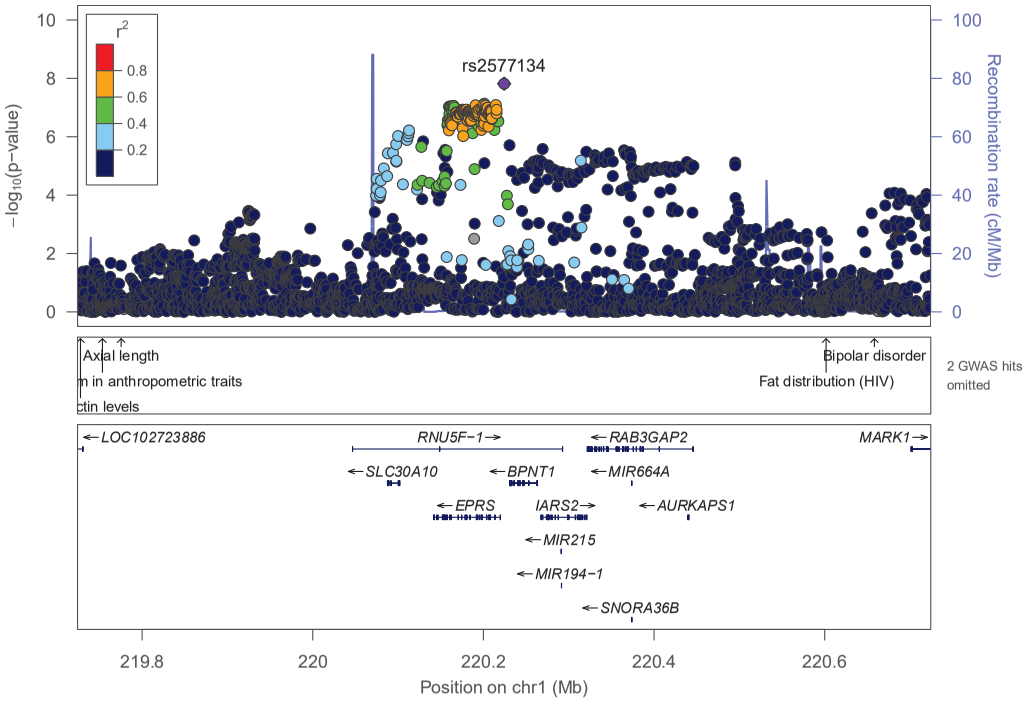

rs3850625
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
trum disorder, attention deficit−hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined)
Cardiac Troponin−T levels
Inflammatory bowel disease
Panic disorder
10 GWAS hits omitted
KIF14
CAMSAP2
MROH3P
CACNA1S
IGFN1
PKP1
LAD1
CSRP1
DDX59
GPR25
KIF21B
ASCL5
TNNT2
PHLDA3
LOC101929224
C1orf106
TMEM9
TNNI1
RPS10P7
Position on chr1 (Mb)

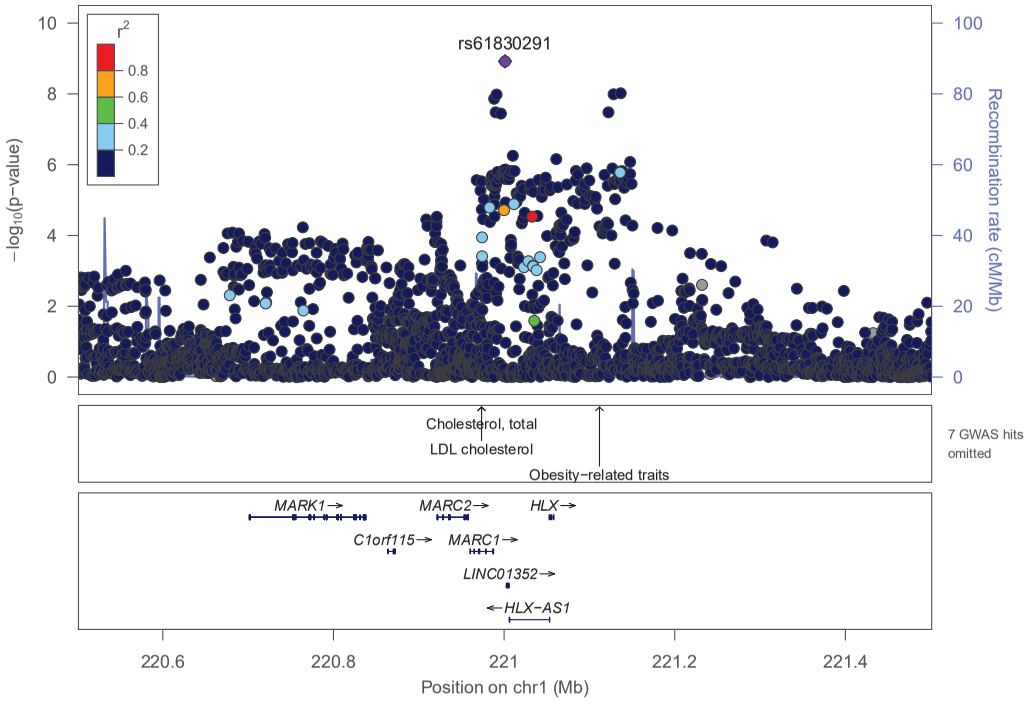

rs12024377
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Mean platelet volume
Serum dimethylarginine levels (symmetric)
Pubertal anthropometrics
Cystic fibrosis−related diabetes
12 GWAS hits omitted
CNTN2 TMCC2 LEMD1−AS1 CDK18 ELK4 NUCKS1 PM20D1
TMEM81 NUAK2 BLACAT1 MFSD4A RAB29 SLC26A9
RBBP5 KLHDC8A LOC284578 SLC41A1
DSTYK LEMD1 SLC45A3 LOC284581
MIR135B
205.2 205.4 205.6 205.8 206
Position on chr1 (Mb)

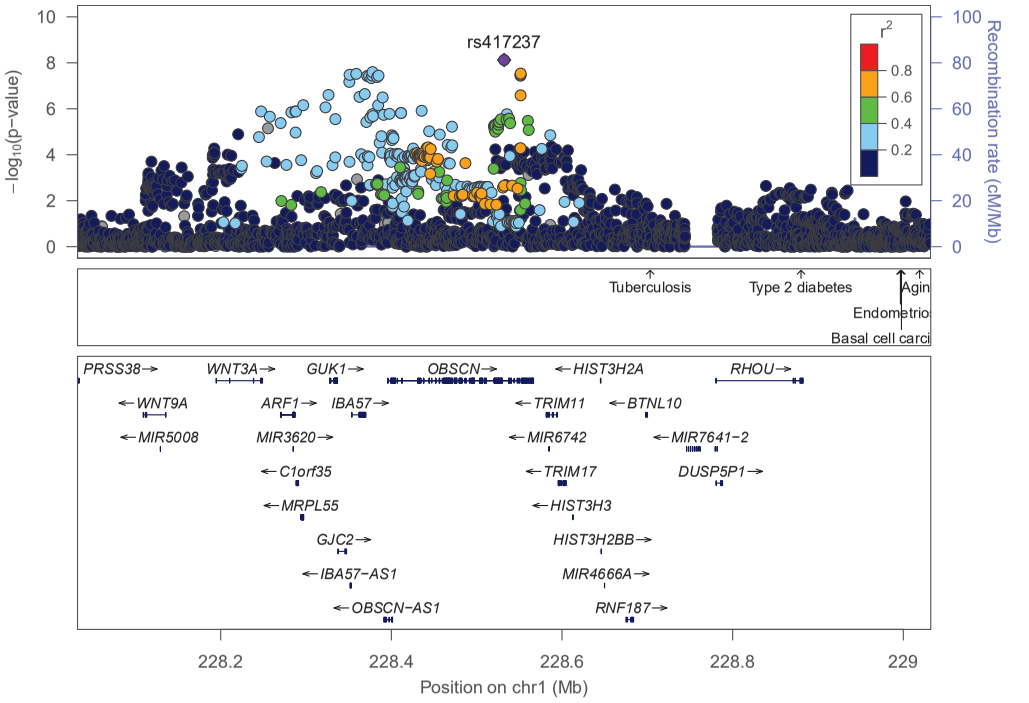

rs2808454
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Inflammatory bowel disease
Economic and political preferences
Alzheimer's disease
Type 2 diabetes
8 GWAS hits omitted
RASSF5 IL10 IL20 FCAMR PFKFB2 CD55 CR2
EIF2D IL19 IL24 C1orf116 CR1
DYRK3 FCMR YOD1
MAPKAPK2 PIGR C4BPB
C4BPA
206.8 207 207.2 207.4 207.6
Position on chr1 (Mb)

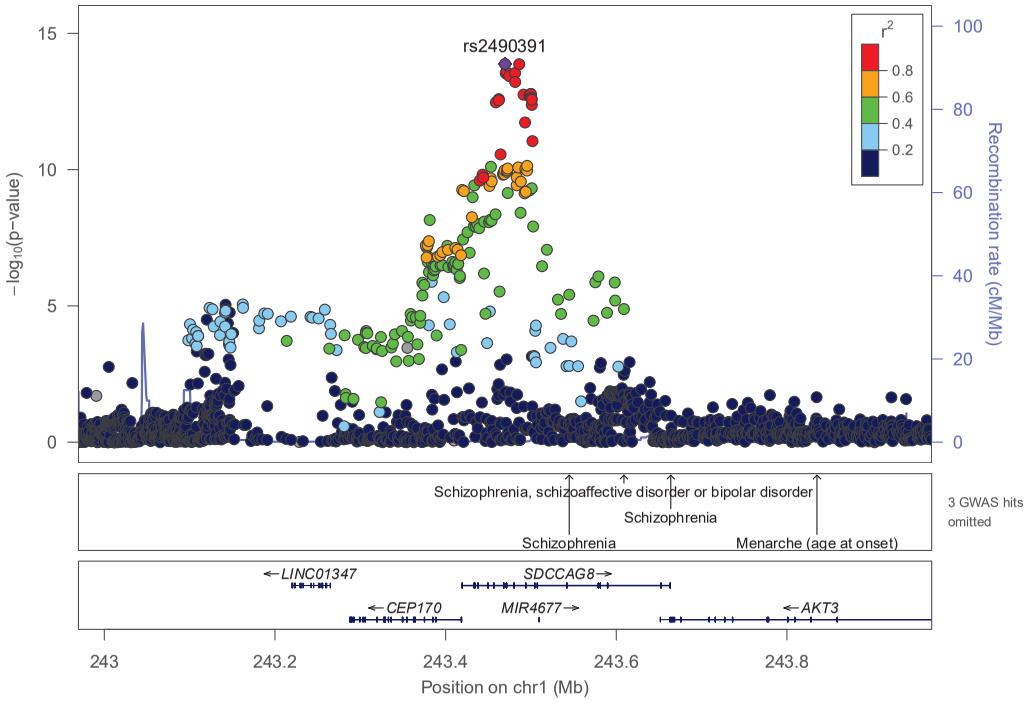

rs75625374
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Alzheimer's disease (late onset)
Heart rate
Heart rate
Age−related macular degeneration
Obesity−related traits
10 GWAS hits omitted
CR2 CR1L CD46 CD34 PLXNA2
CR1 C1orf132
MIR29C
MIR29B2
LOC148696
207.6 207.8 208 208.2 208.4
Position on chr1 (Mb)

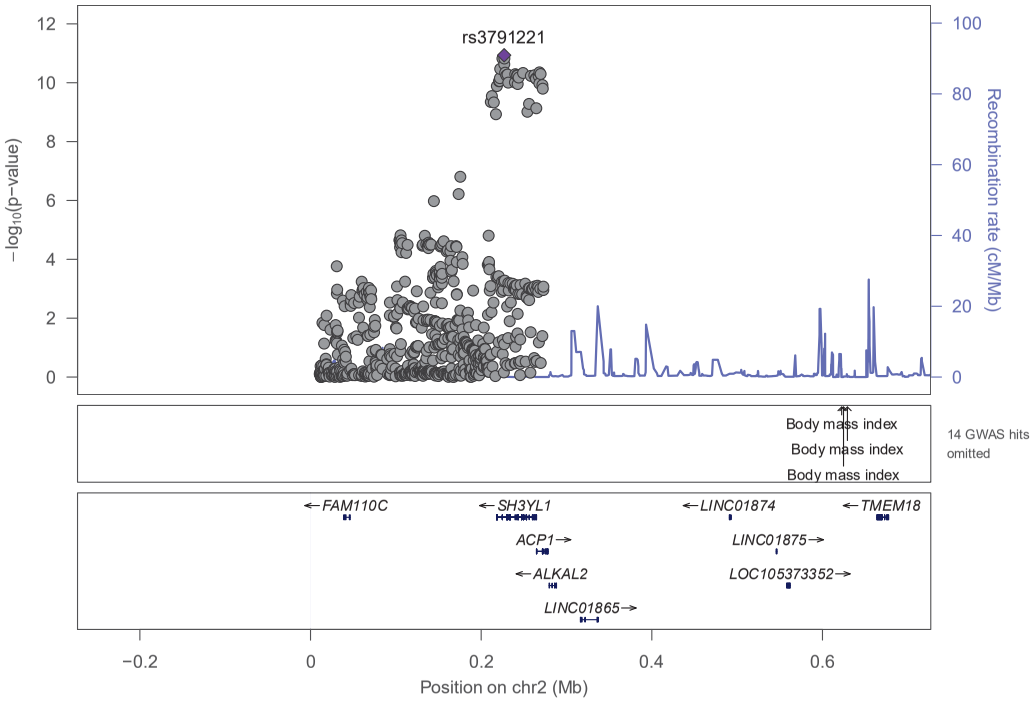

rs7535253
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
IgG glycosylation
Response to antineoplastic agents
Migraine without aura
ronutrient intake
SMYD2 CENPF KCNK2
PTPN14
214.4 214.6 214.8 215 215.2
Position on chr1 (Mb)

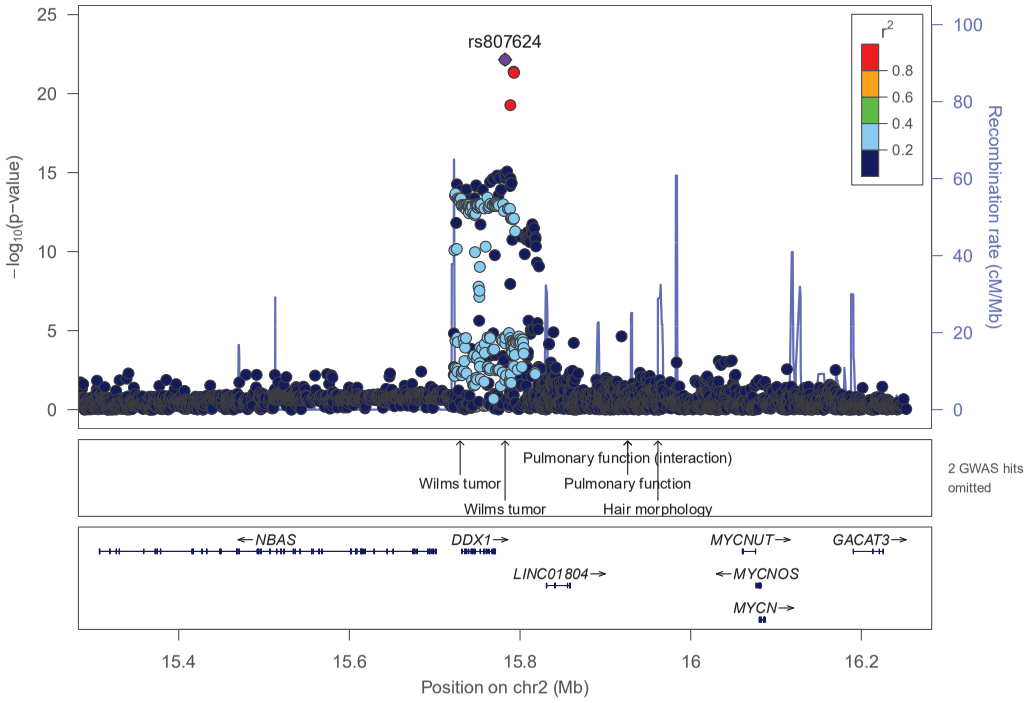

rs2577134
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Axial length
n in anthropometric traits
ctin levels
Bipolar disorder
Fat distribution (HIV)
2 GWAS hits omitted
LOC102723886
RNU5F−1
RAB3GAP2
MARK1
SLC30A10
BPNT1
MIR664A
EPRS
IARS2
AURKAPS1
MIR215
MIR194−1
SNORA36B
219.8
220
220.2
220.4
220.6
Position on chr1 (Mb)

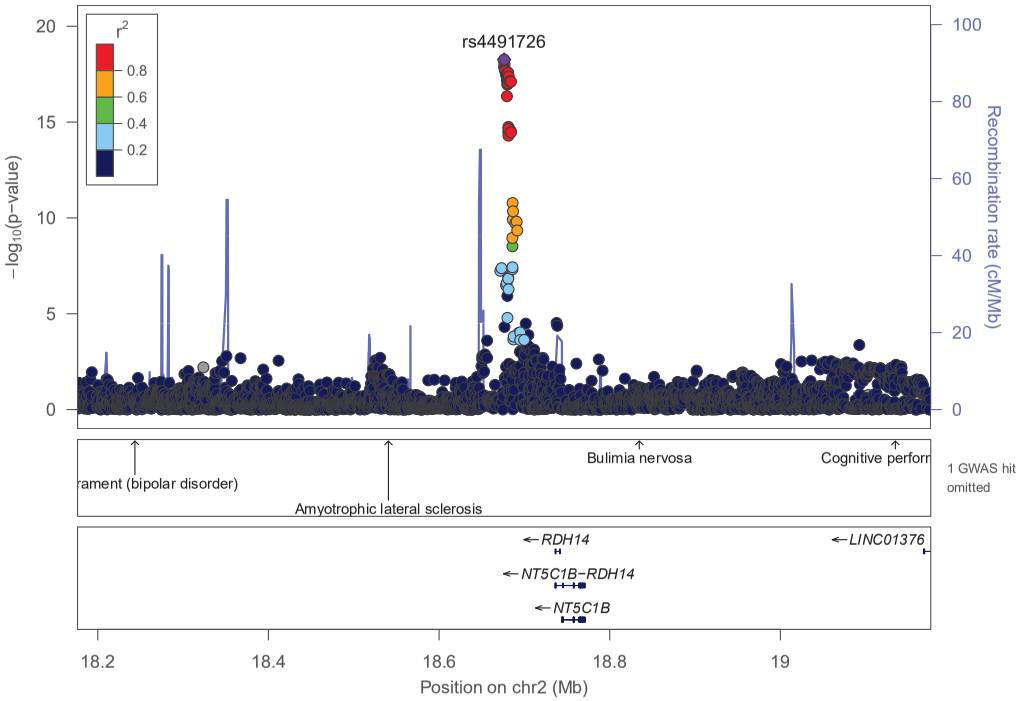

rs61830291
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
LDL cholesterol
Obesity−related traits
7 GWAS hits omitted
MARK1
MARC2
HLX
C1orf115
MARC1
LINC01352
HLX−AS1
220.6
220.8
221
221.2
221.4
Position on chr1 (Mb)

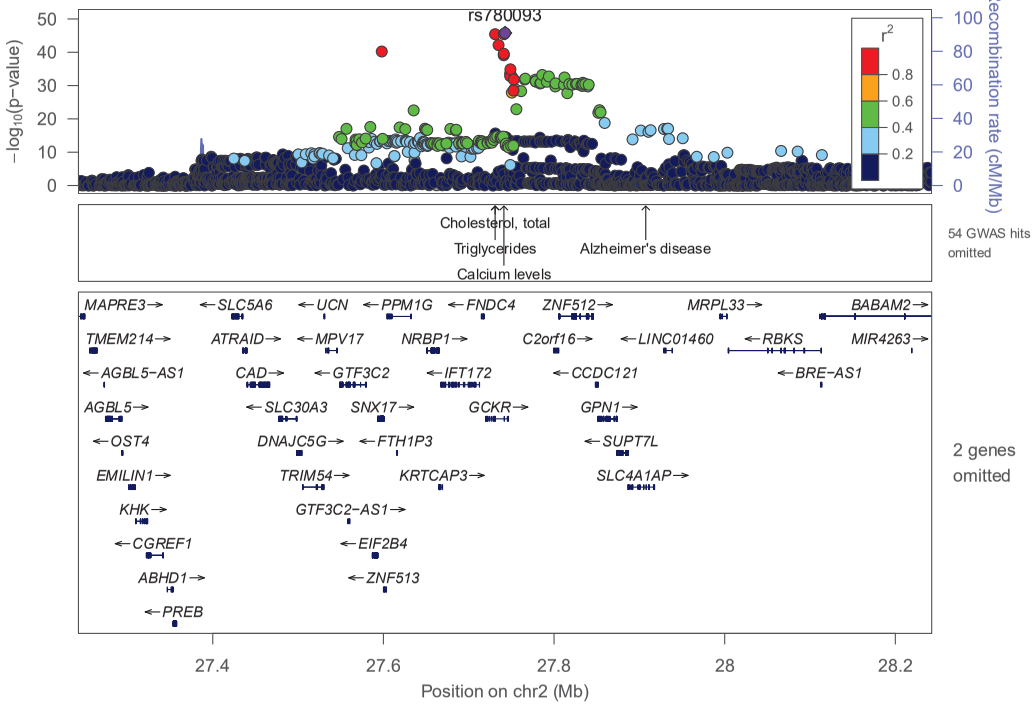

rs417237
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Tuberculosis
Type 2 diabetes
Agin
Endometrio
Basal cell carci
PRSS38
WNT3A
GUK1
OBSCN
HIST3H2A
RHOU
WNT9A
ARF1
IBA57
TRIM11
BTNL10
MIR5008
MIR3620
MIR6742
MIR7641−2
C1orf35
TRIM17
DUSP5P1
MRPL55
HIST3H3
GJC2
HIST3H2BB
IBA57−AS1
MIR4666A
OBSCN−AS1
RNF187
228.2
228.4
228.6
228.8
229
Position on chr1 (Mb)

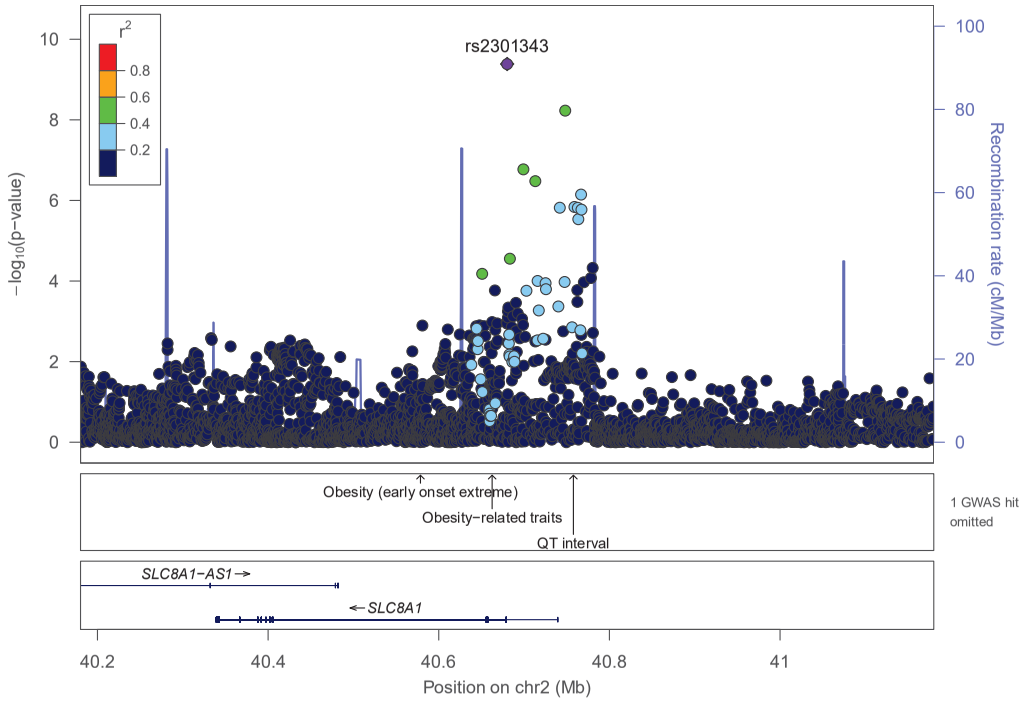

rs2490391
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Schizophrenia, schizoaffective disorder or bipolar disorder
Schizophrenia
Schizophrenia
Menarche (age at onset)
3 GWAS hits omitted
LINC01347
SDCCAG8
CEP170
MIR4677
AKT3
243
243.2
243.4
243.6
243.8
Position on chr1 (Mb)

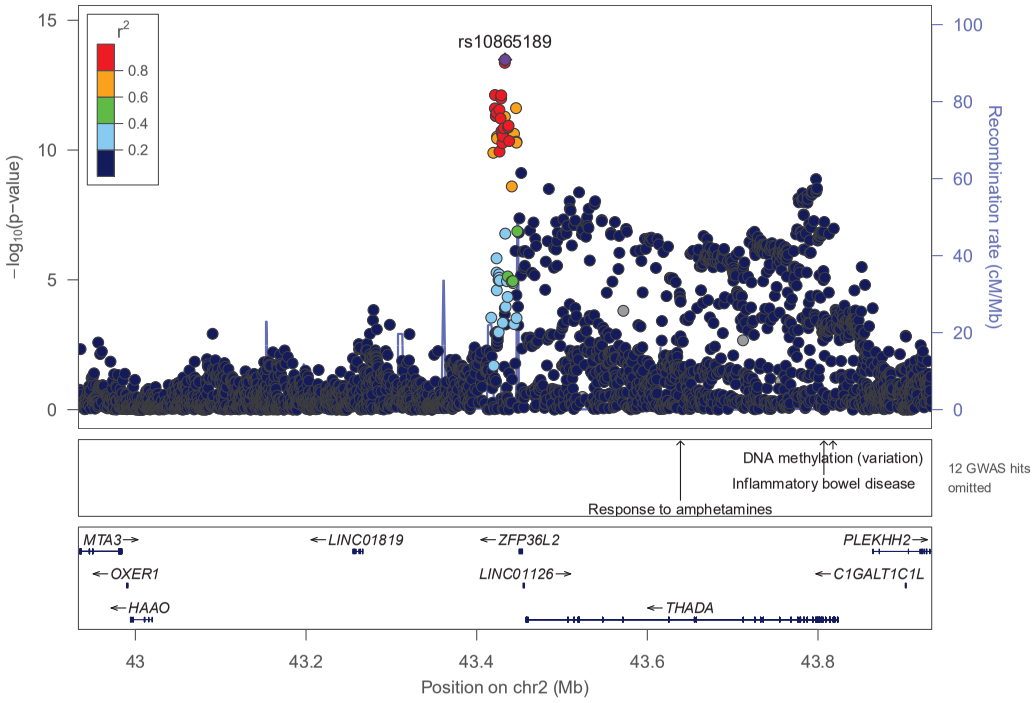

rs3791221
−log10(p−value)
Recombination rate (cM/Mb)
Body mass index
Body mass index
Body mass index
14 GWAS hits omitted
←FAM110C
←SH3YL1
←LINC01874
←TMEM18
ACP1→
LINC01875→
←ALKAL2
LOC105373352→
LINC01865→
Position on chr2 (Mb)

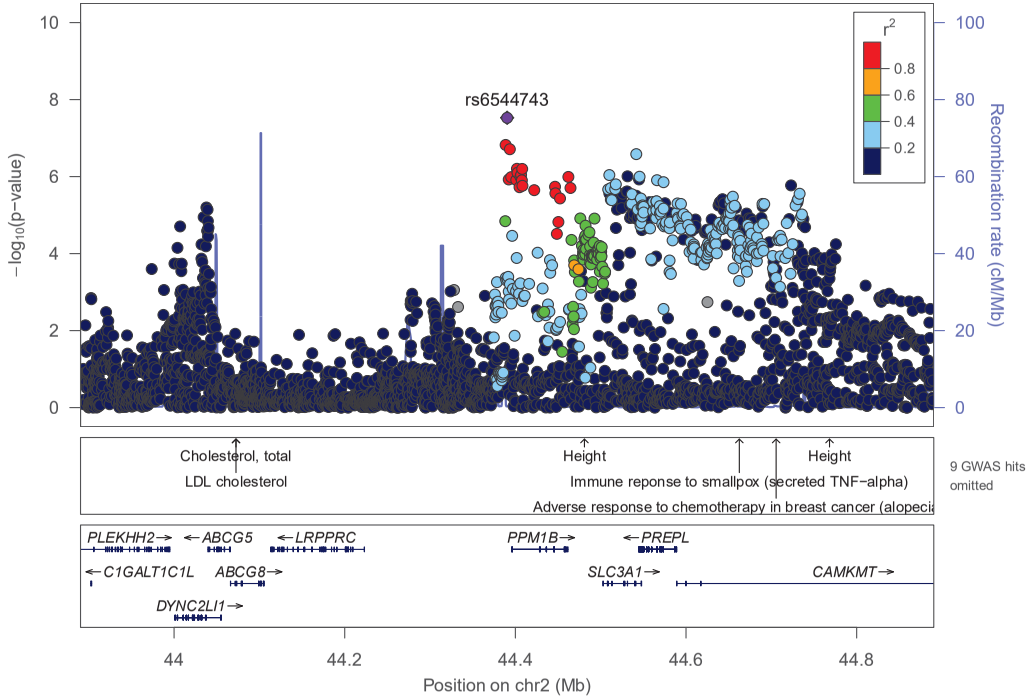

rs807624
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Wilms tumor
Wilms tumor
Pulmonary function (interaction)
Pulmonary function
Hair morphology
2 GWAS hits omitted
←NBAS
DDX1→
MYCNUT→
GACAT3→
LINC01804→
←MYCNOS
MYCN→
Position on chr2 (Mb)

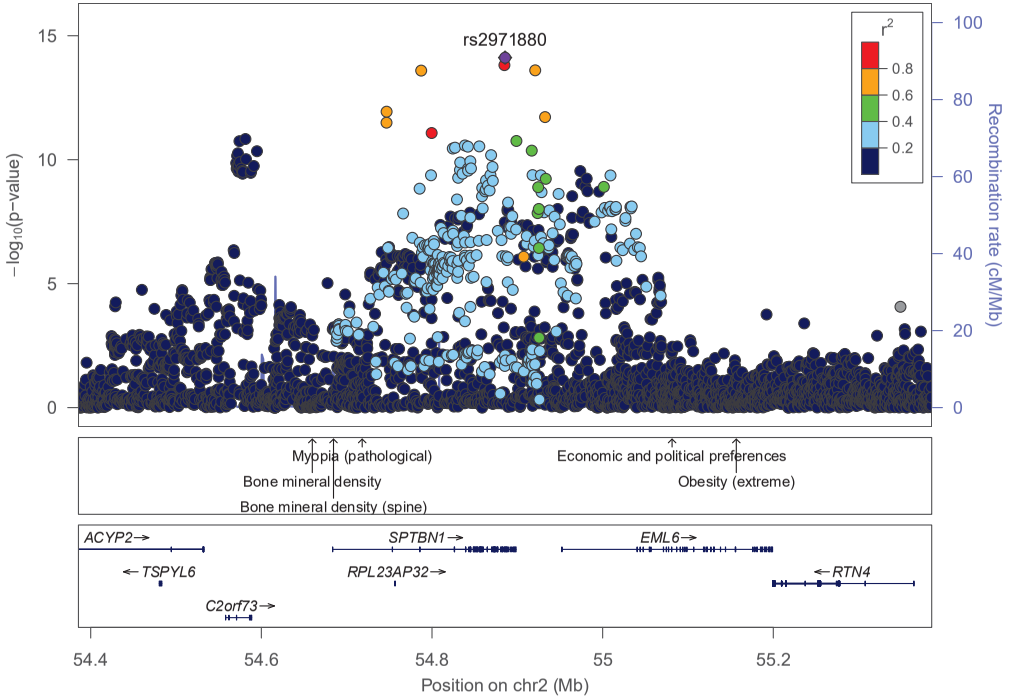

rs4491726
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
rament (bipolar disorder)
Amyotrophic lateral sclerosis
Bulimia nervosa
Cognitive perforr
1 GWAS hit omitted
←RDH14
←LINC01376
←NT5C1B−RDH14
←NT5C1B
Position on chr2 (Mb)

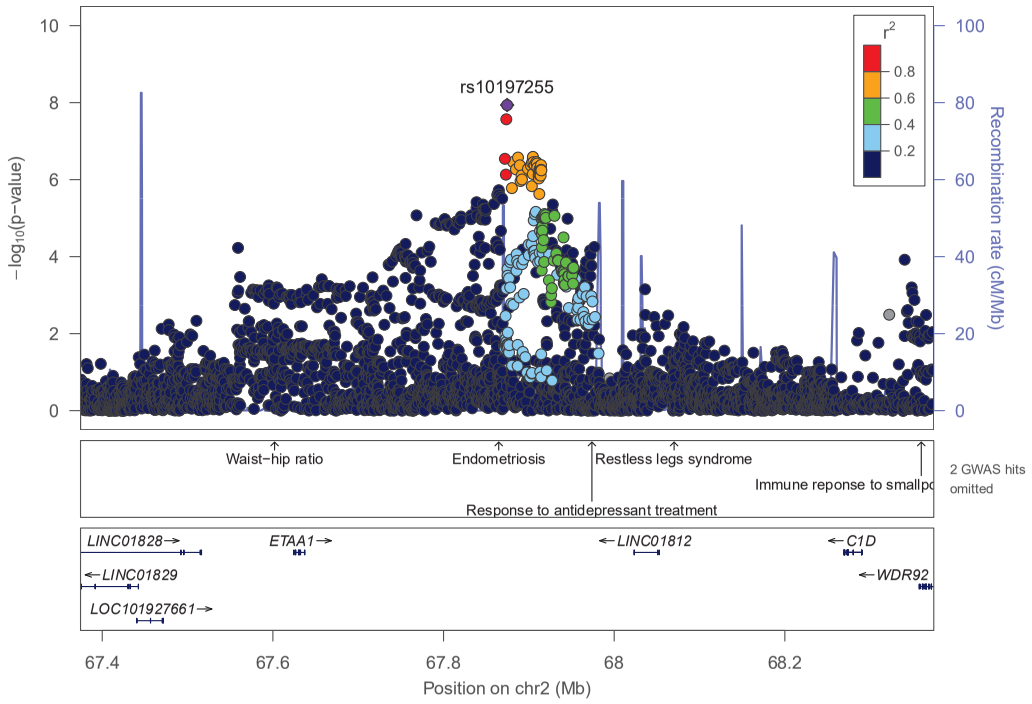

rs780093
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
Triglycerides
Calcium levels
Alzheimer's disease
54 GWAS hits omitted
MAPRE3→
←SLC5A6
←UCN
←PPM1G
←FNDC4
ZNF512→
MRPL33→
BABAM2→
TMEM214→
ATRAID→
←MPV17
NRBP1→
C2orf16→
←LINC01460
←RBKS
MIR4263→
←AGBL5−AS1
CAD→
←GTF3C2
←IFT172
←CCDC121
←BRE−AS1
AGBL5→
←SLC30A3
SNX17→
GCKR→
GPN1→
←OST4
DNAJC5G→
←FTH1P3
←SUPT7L
EMILIN1→
TRIM54→
KRTCAP3→
SLC4A1AP→
KHK→
GTF3C2−AS1→
←CGREF1
←EIF2B4
ABHD1→
←ZNF513
←PREB
2 genes omitted
Position on chr2 (Mb)

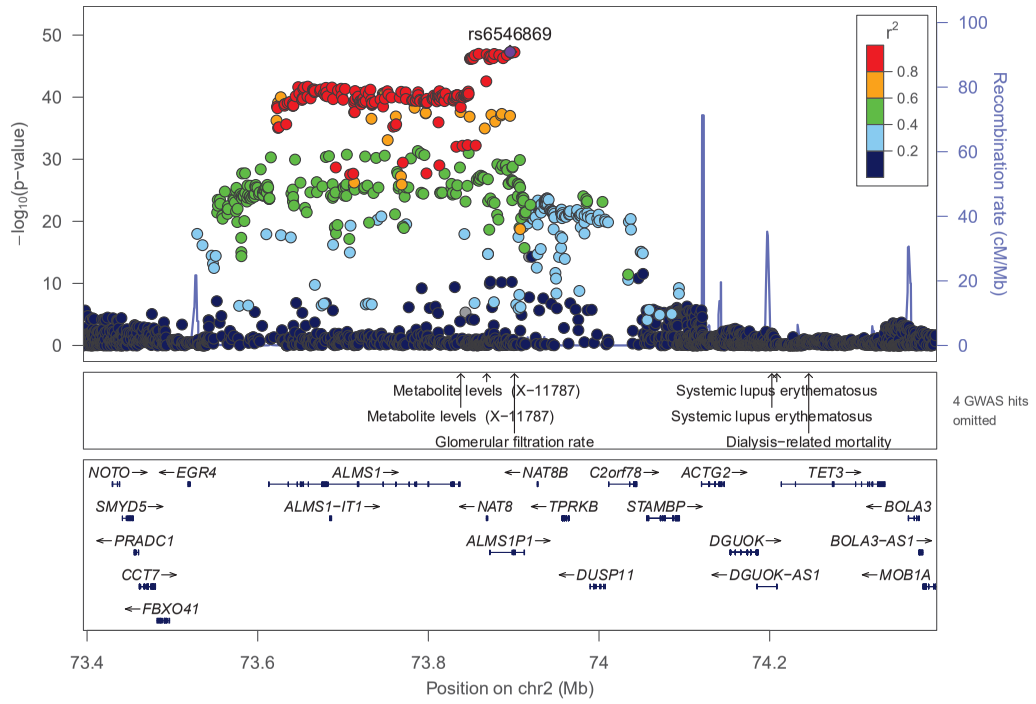

rs2301343
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity (early onset extreme)
Obesity−related traits
QT interval
1 GWAS hit omitted
SLC8A1−AS1→
←SLC8A1
Position on chr2 (Mb)

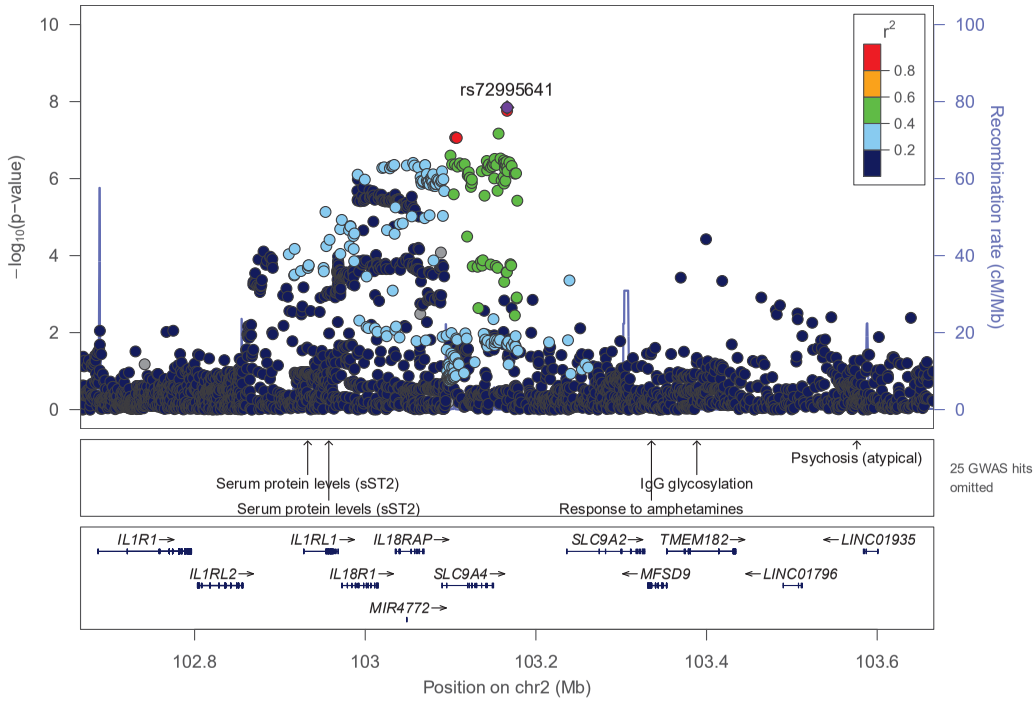

rs10865189
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
DNA methylation (variation)
Inflammatory bowel disease
Response to amphetamines
12 GWAS hits omitted
MTA3→
←LINC01819
←ZFP36L2
PLEKHH2→
←OXER1
LINC01126→
←C1GALT1C1L
←HAAO
←THADA
Position on chr2 (Mb)

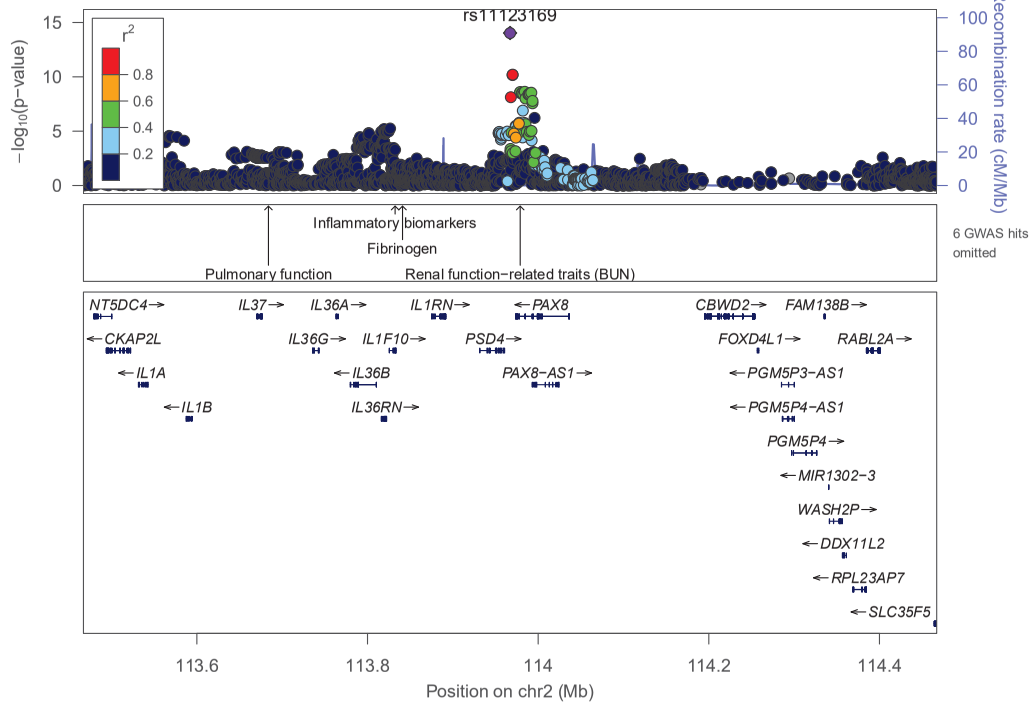

rs6544743
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
LDL cholesterol
Height
Immune reponse to smallpox (secreted TNF−alpha)
Height
Adverse response to chemotherapy in breast cancer (alopeci
9 GWAS hits omitted
PLEKHH2→
←ABCG5
←LRPPRC
PPM1B→
←PREPL
←C1GALT1C1L
ABCG8→
SLC3A1→
CAMKMT→
DYNC2LI1→
Position on chr2 (Mb)

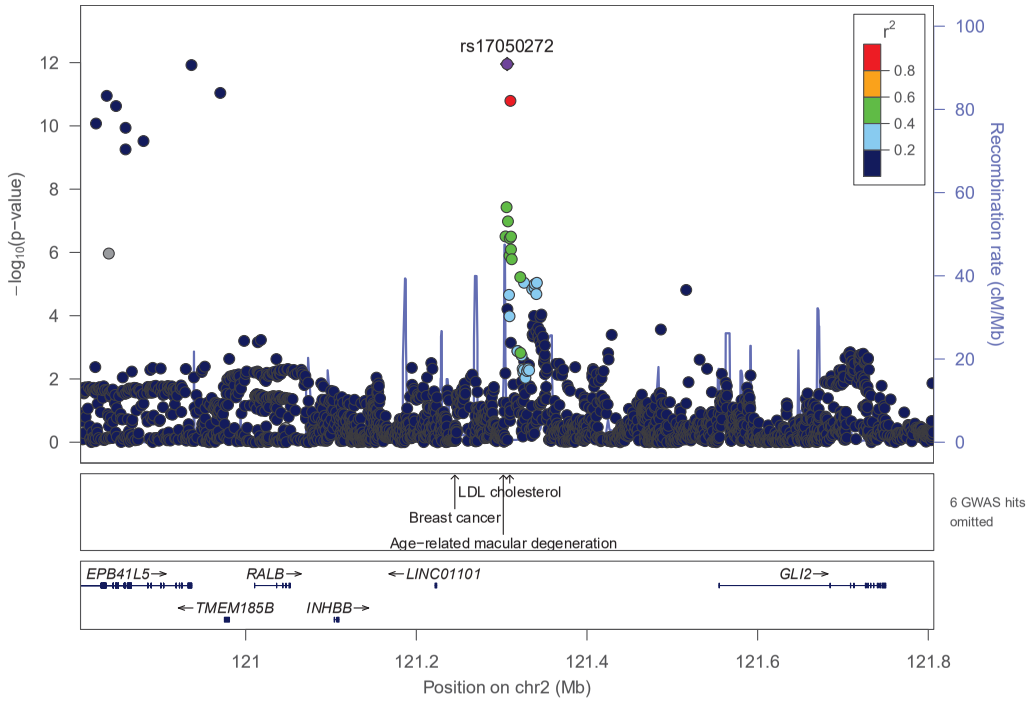

rs2971880
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Myopia (pathological)
Bone mineral density
Bone mineral density (spine)
Economic and political preferences
Obesity (extreme)
ACYP2→
SPTBN1→
EML6→
←TSPYL6
RPL23AP32→
←RTN4
C2orf73→
Position on chr2 (Mb)

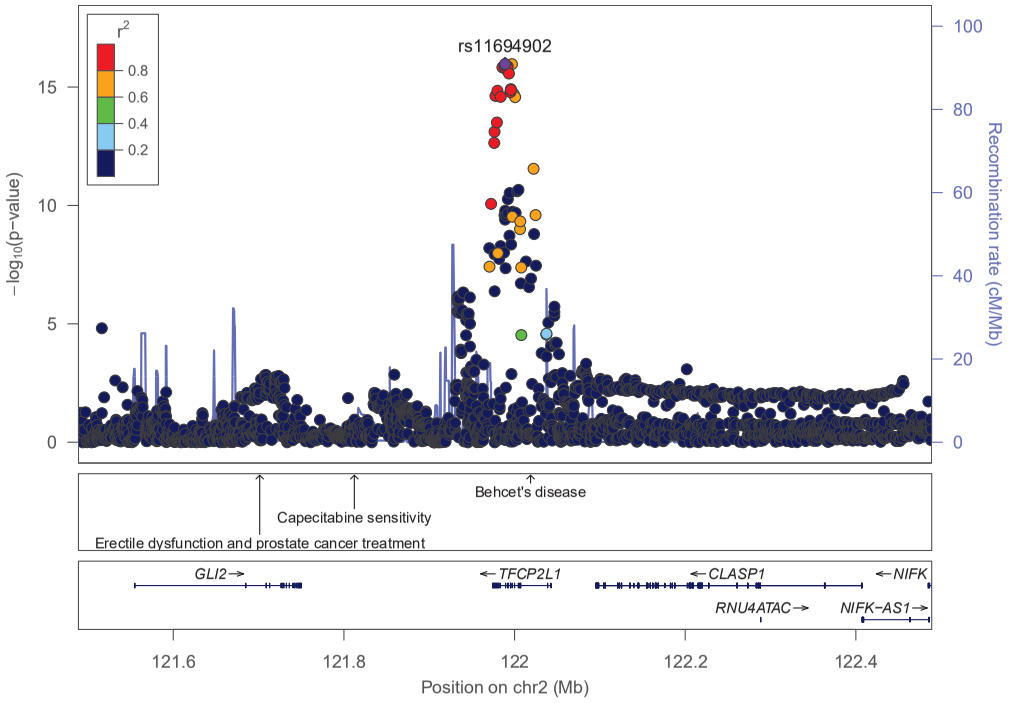

rs10197255
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Waist−hip ratio
Endometriosis
Restless legs syndrome
Immune reponse to smallpo
Response to antidepressant treatment
2 GWAS hits omitted
LINC01828→
ETAA1→
←LINC01812
←C1D
←LINC01829
←WDR92
LOC101927661→
67.4
67.6
67.8
68
68.2
Position on chr2 (Mb)

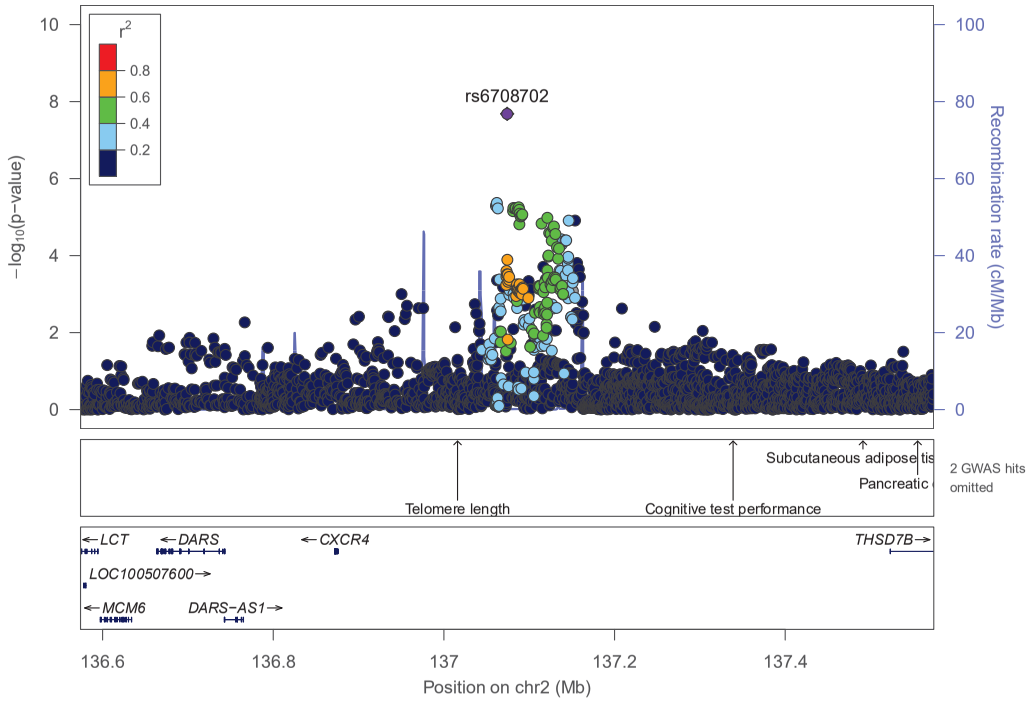

rs6546869
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Metabolite levels (X−11787)
Metabolite levels (X−11787)
Glomerular filtration rate
Systemic lupus erythematosus
Systemic lupus erythematosus
Dialysis−related mortality
4 GWAS hits omitted
NOTO→
←EGR4
ALMS1→
←NAT8B
C2orf78→
ACTG2→
TET3→
SMYD5→
ALMS1−IT1→
←NAT8
←TPRKB
STAMBP→
←BOLA3
←PRADC1
ALMS1P1→
DGUOK→
BOLA3−AS1→
CCT7→
←DUSP11
←DGUOK−AS1
←MOB1A
←FBXO41
73.4
73.6
73.8
74
74.2
Position on chr2 (Mb)

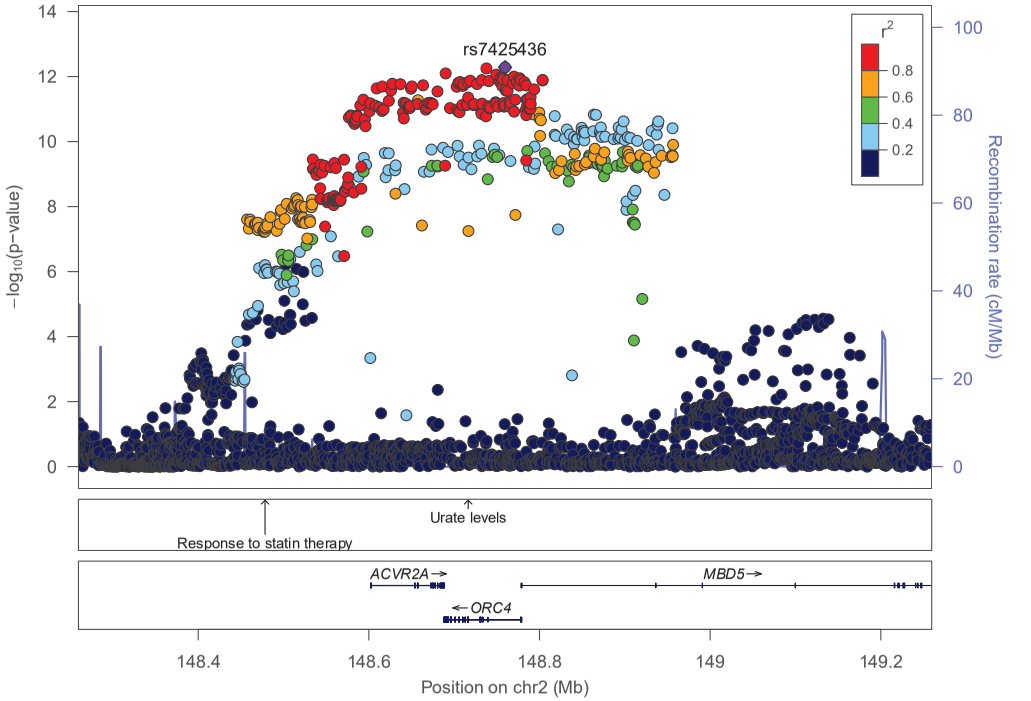

rs72995641
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Serum protein levels (sST2)
Serum protein levels (sST2)
IgG glycosylation
Response to amphetamines
Psychosis (atypical)
25 GWAS hits omitted
IL1R1→
IL1RL1→
IL18RAP→
SLC9A2→
TMEM182→
←LINC01935
IL1RL2→
IL18R1→
SLC9A4→
←MFSD9
←LINC01796
MIR4772→
102.8
103
103.2
103.4
103.6
Position on chr2 (Mb)

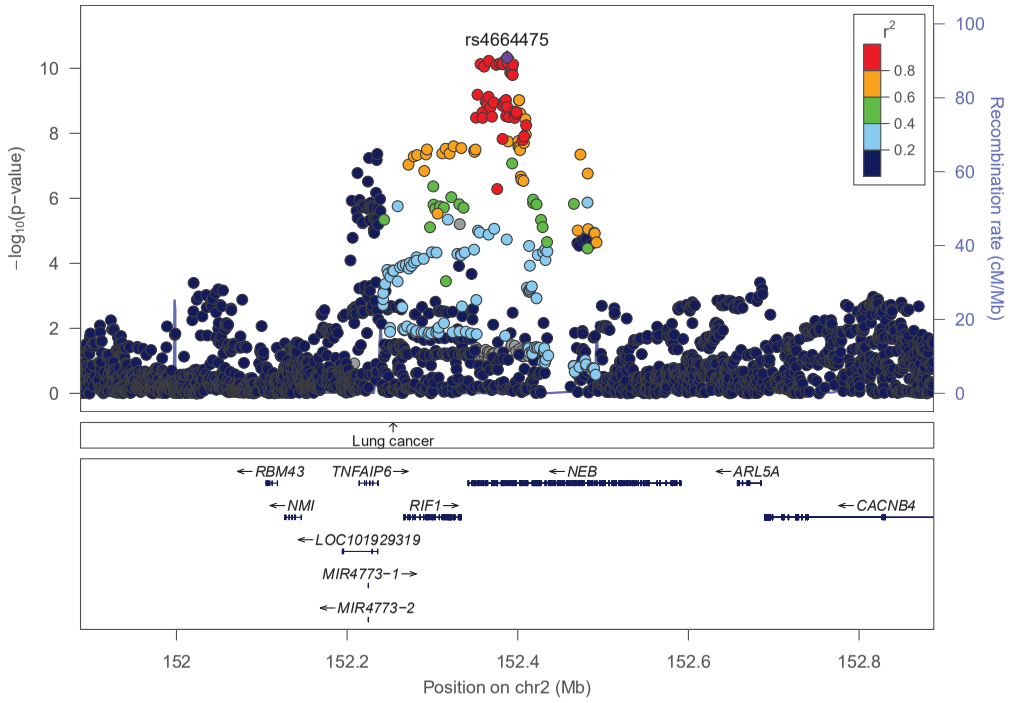

rs11123169
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Inflammatory biomarkers
Fibrinogen
Pulmonary function
Renal function−related traits (BUN)
6 GWAS hits omitted
NT5DC4→
IL37→
IL36A→
IL1RN→
←PAX8
CBWD2→
FAM138B→
←CKAP2L
IL36G→
IL1F10→
PSD4→
FOXD4L1→
RABL2A→
←IL1A
←IL36B
PAX8−AS1→
←PGM5P3−AS1
←IL1B
IL36RN→
←PGM5P4−AS1
PGM5P4→
←MIR1302−3
WASH2P→
←DDX11L2
←RPL23AP7
←SLC35F5
113.6
113.8
114
114.2
114.4
Position on chr2 (Mb)

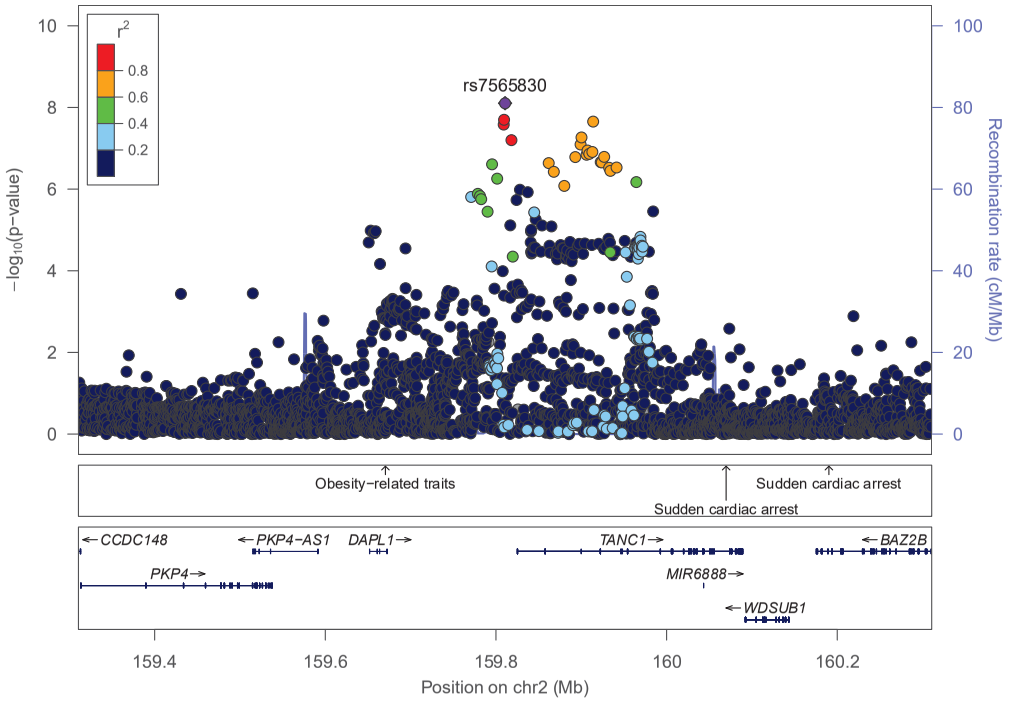

rs17050272
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
LDL cholesterol
Breast cancer
Age−related macular degeneration
6 GWAS hits omitted
EPB41L5→
RALB→
←LINC01101
GLI2→
←TMEM185B
INHBB→
Position on chr2 (Mb)

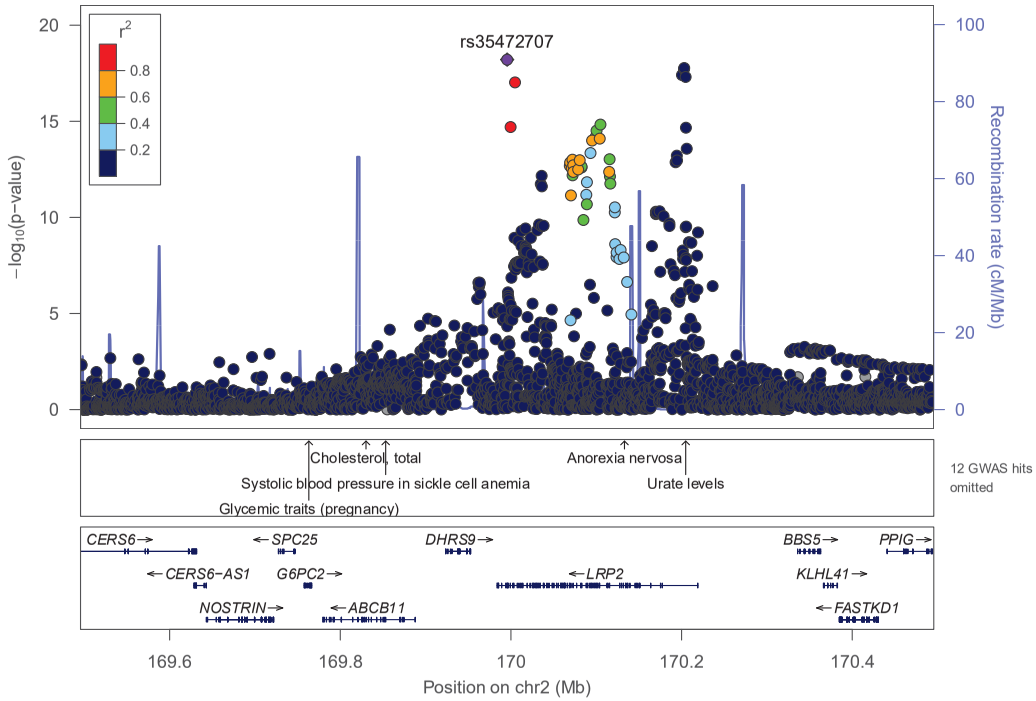

rs11694902
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Capecitabine sensitivity
Behcet's disease
Erectile dysfunction and prostate cancer treatment
GLI2→
←TFCP2L1
←CLASP1
←NIFK
RNU4ATAC→
NIFK−AS1→
Position on chr2 (Mb)

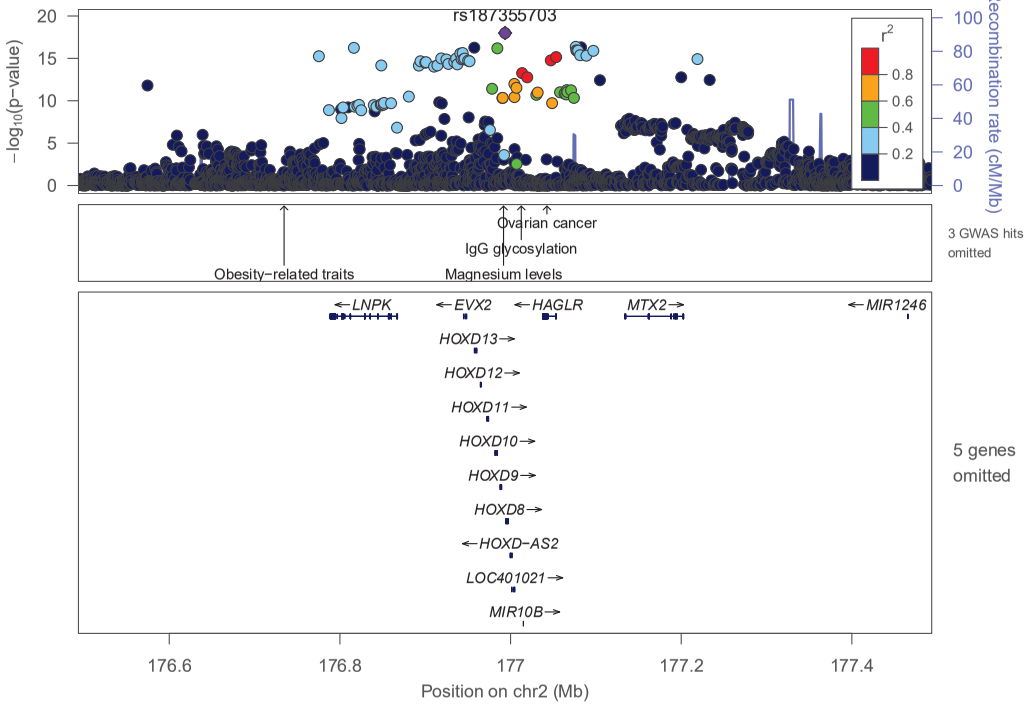

rs6708702
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Telomere length
Cognitive test performance
Subcutaneous adipose tis
Pancreatic
2 GWAS hits omitted
←LCT
←DARS
←CXCR4
THSD7B→
LOC100507600→
←MCM6
DARS−AS1→
Position on chr2 (Mb)

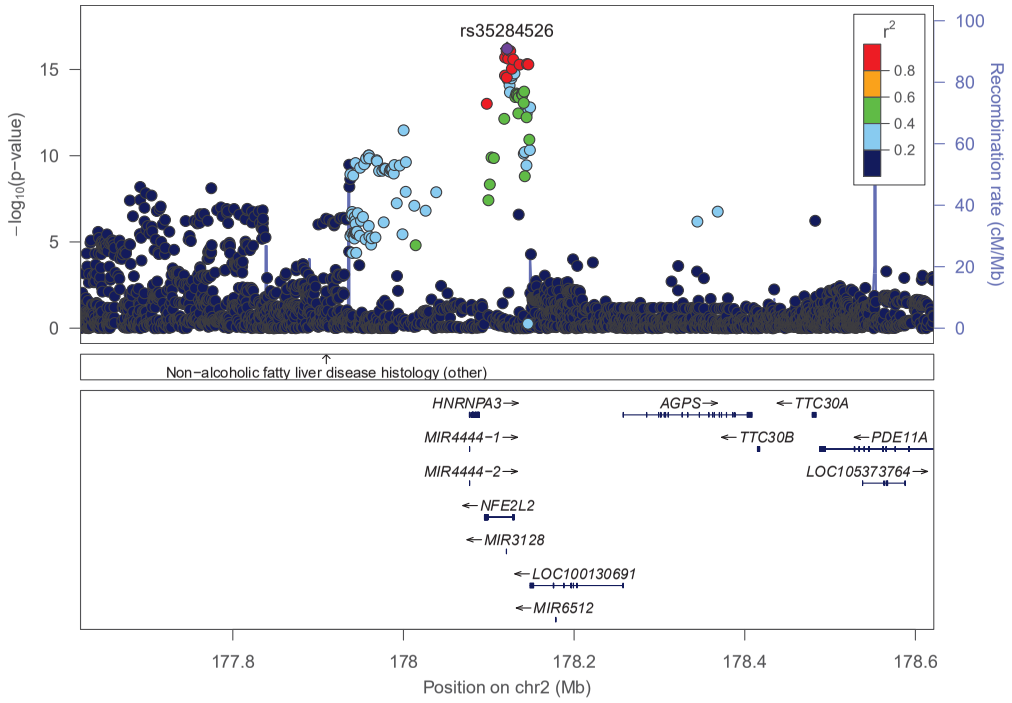

rs7425436
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Response to statin therapy
Urate levels
ACVR2A→
MBD5→
←ORC4
Position on chr2 (Mb)

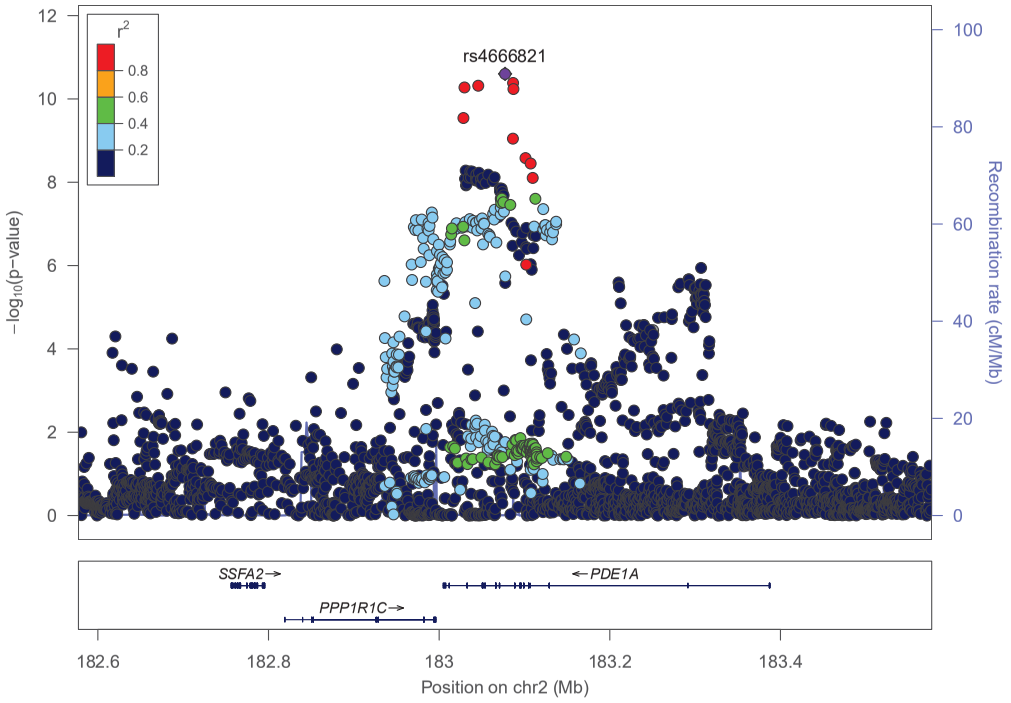

rs4664475
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Lung cancer
RBM43
TNFAIP6
NEB
ARL5A
NMI
RIF1
CACNB4
LOC101929319
MIR4773−1
MIR4773−2
Position on chr2 (Mb)

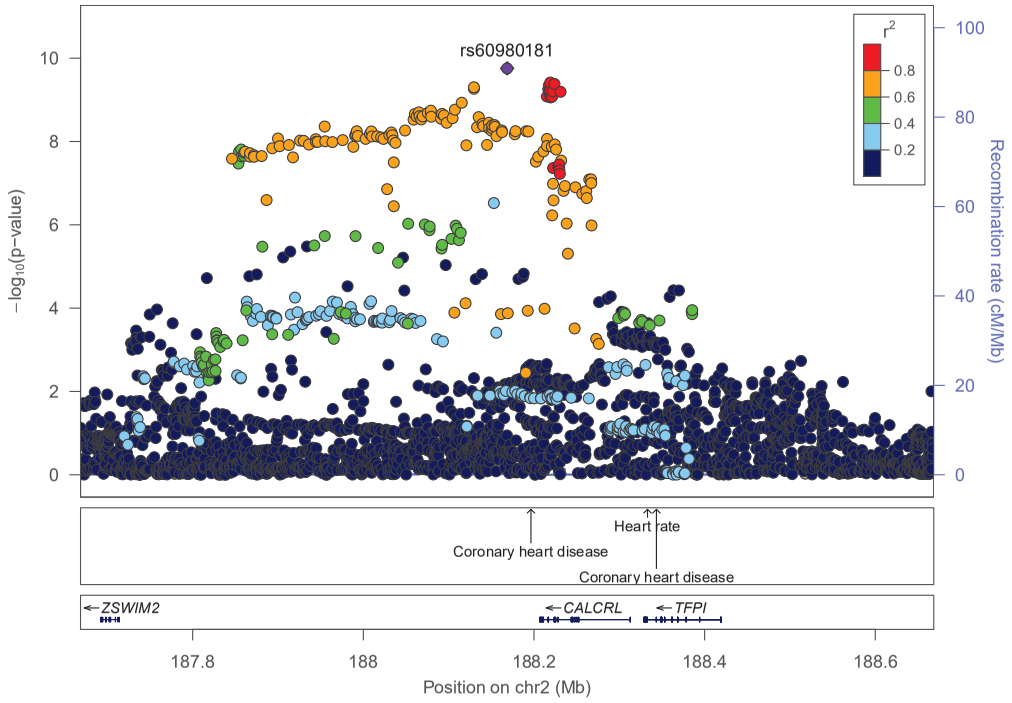

rs7565830
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Sudden cardiac arrest
Sudden cardiac arrest
CCDC148
PKP4−AS1
DAPL1
TANC1
BAZ2B
PKP4
MIR6888
WDSUB1
Position on chr2 (Mb)

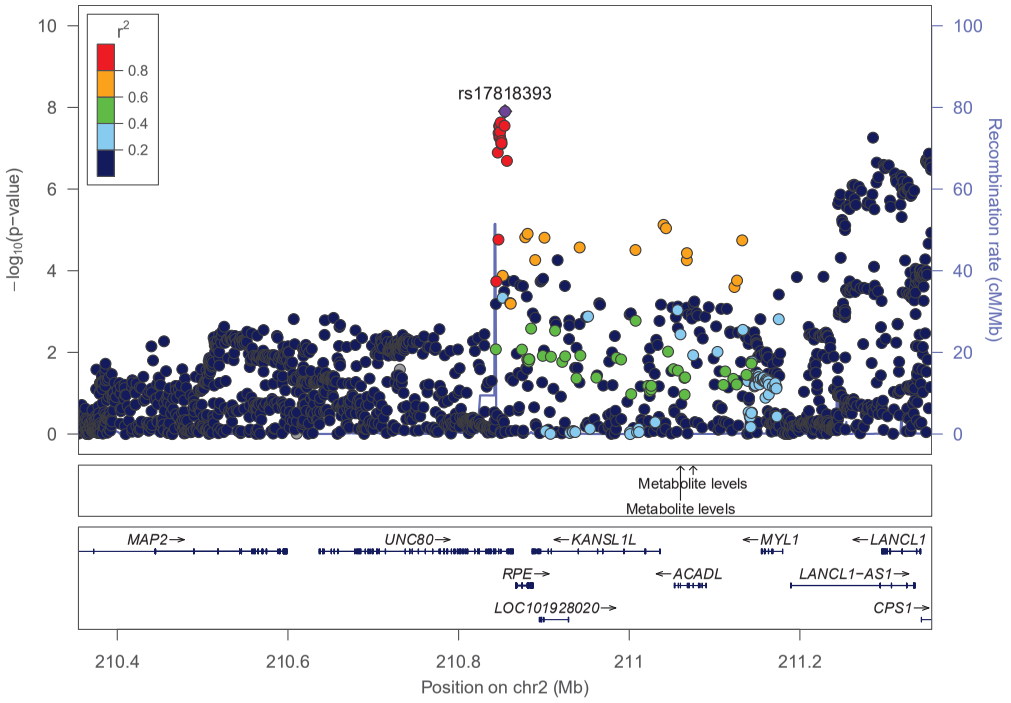

rs35472707
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
Systolic blood pressure in sickle cell anemia
Glycemic traits (pregnancy)
Anorexia nervosa
Urate levels
12 GWAS hits
omitted
CERS6
SPC25
DHRS9
BBS5
PPIG
CERS6−AS1
G6PC2
LRP2
KLHL41
NOSTRIN
ABCB11
FASTKD1
Position on chr2 (Mb)

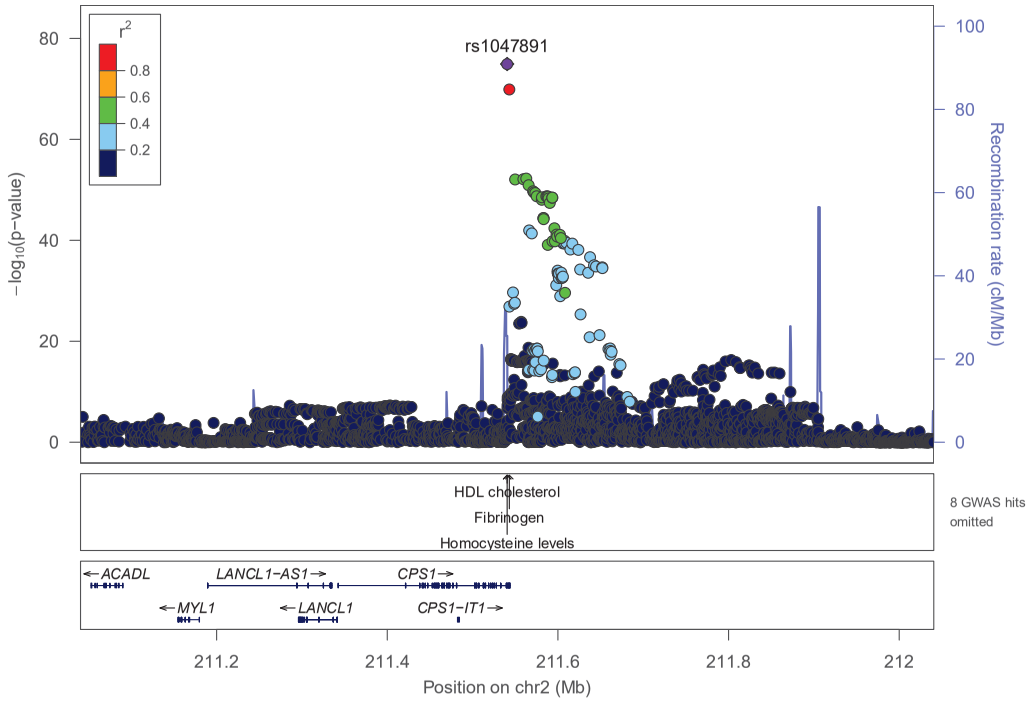

rs187355703
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Ovarian cancer
IgG glycosylation
Magnesium levels
3 GWAS hits
omitted
LNPK
EVX2
HAGLR
MTX2
MIR1246
HOXD13
HOXD12
HOXD11
HOXD10
HOXD9
HOXD8
HOXD−AS2
LOC401021
MIR10B
5 genes
omitted
Position on chr2 (Mb)

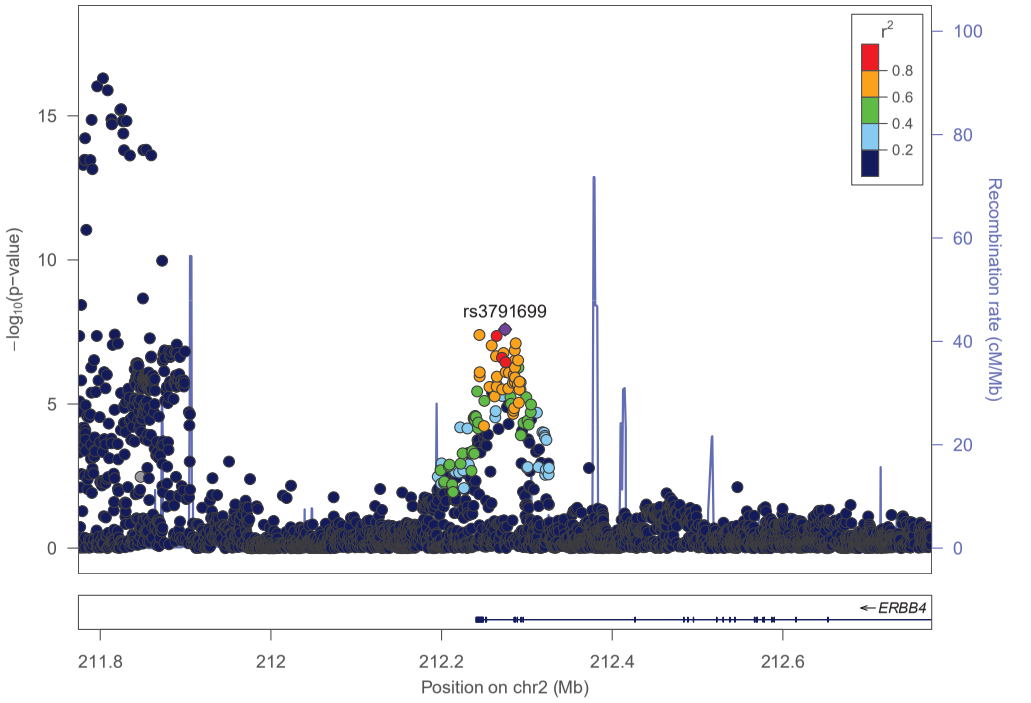

rs35284526
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Non−alcoholic fatty liver disease histology (other)
HNRNPA3→
AGPS→
←TTC30A
MIR4444−1→
←TTC30B
←PDE11A
MIR4444−2→
LOC105373764→
←NFE2L2
←MIR3128
←LOC100130691
←MIR6512
Position on chr2 (Mb)

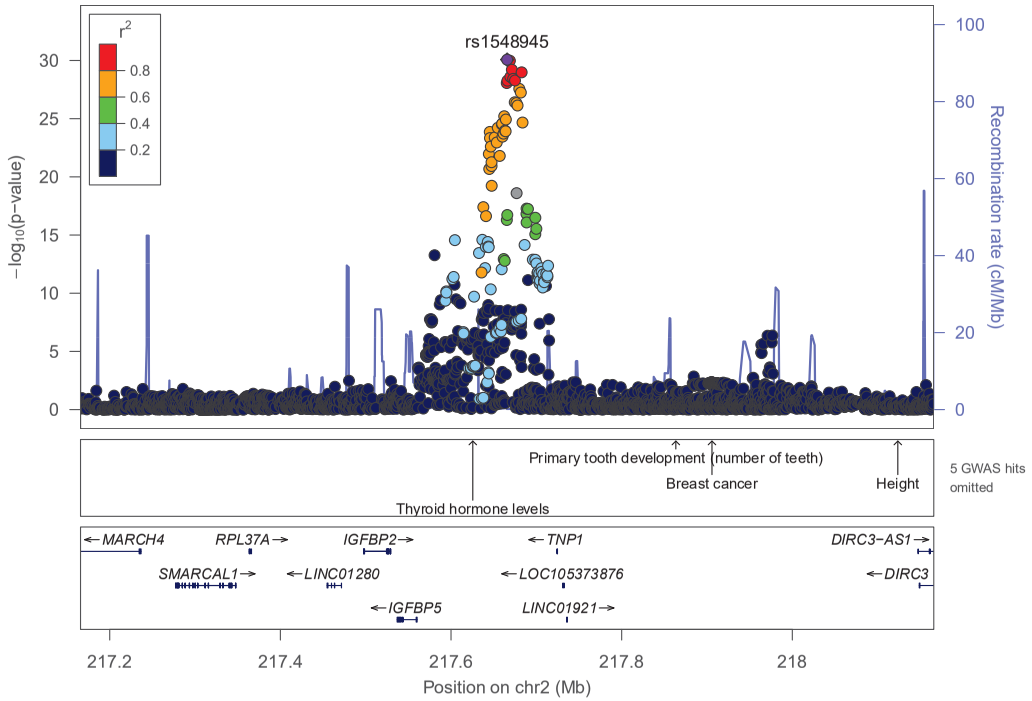

rs4666821
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
SSFA2→
←PDE1A
PPP1R1C→
Position on chr2 (Mb)

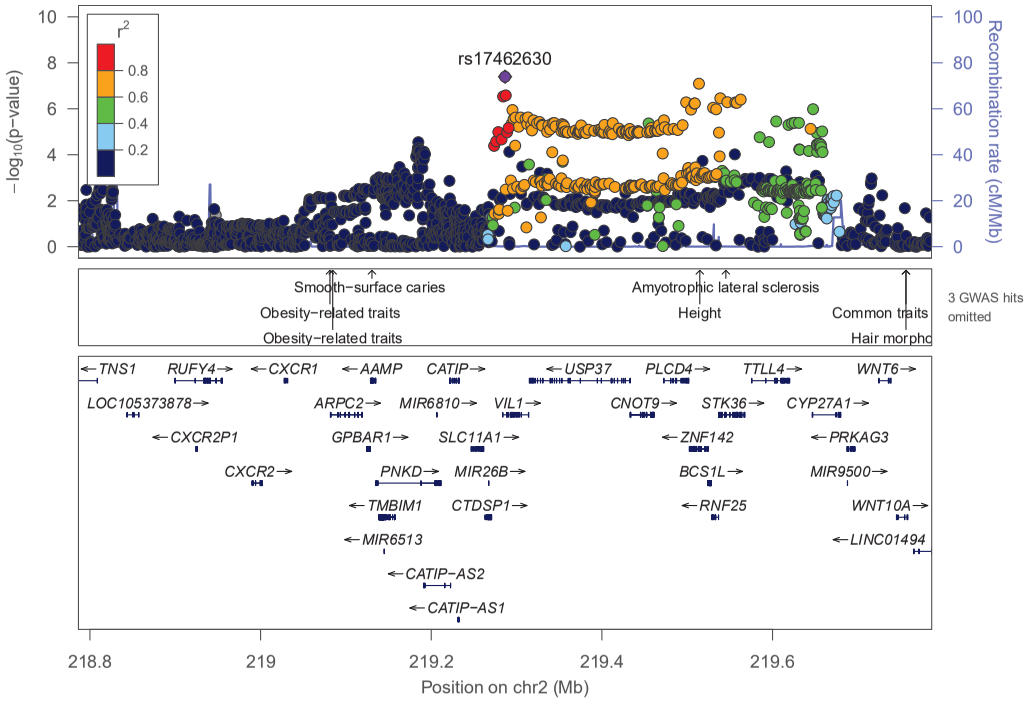

rs60980181
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Coronary heart disease
Heart rate
Coronary heart disease
←ZSWIM2
←CALCRL
←TFPI
Position on chr2 (Mb)

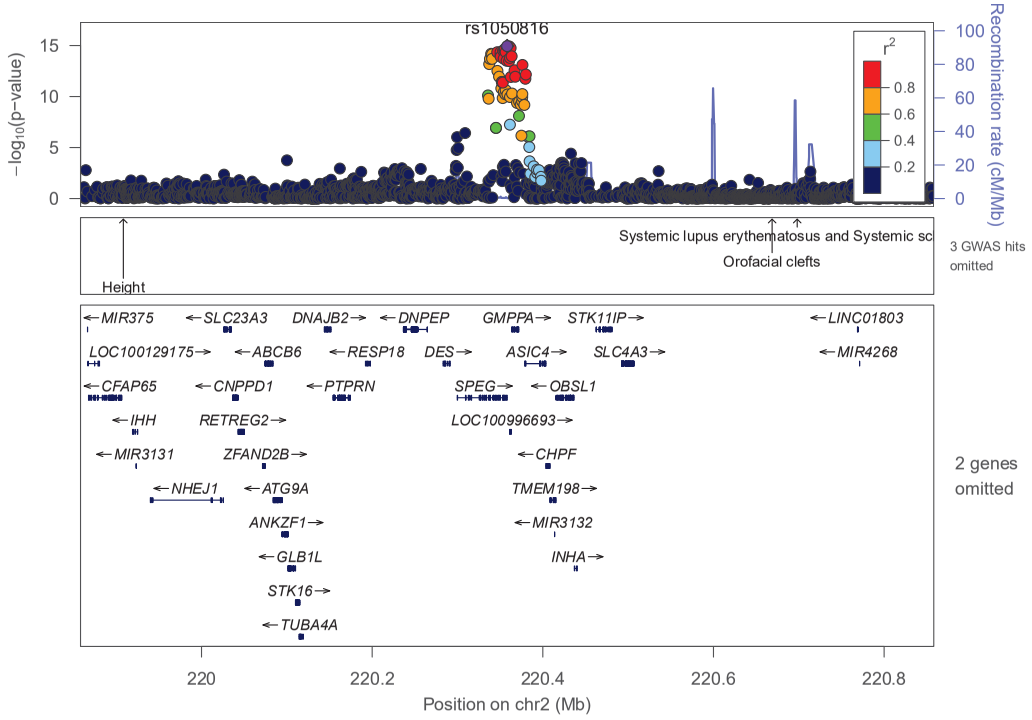

rs17818393
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Metabolite levels
Metabolite levels
MAP2→
UNC80→
←KANSL1L
←MYL1
←LANCL1
RPE→
←ACADL
LANCL1−AS1→
LOC101928020→
CPS1→
Position on chr2 (Mb)

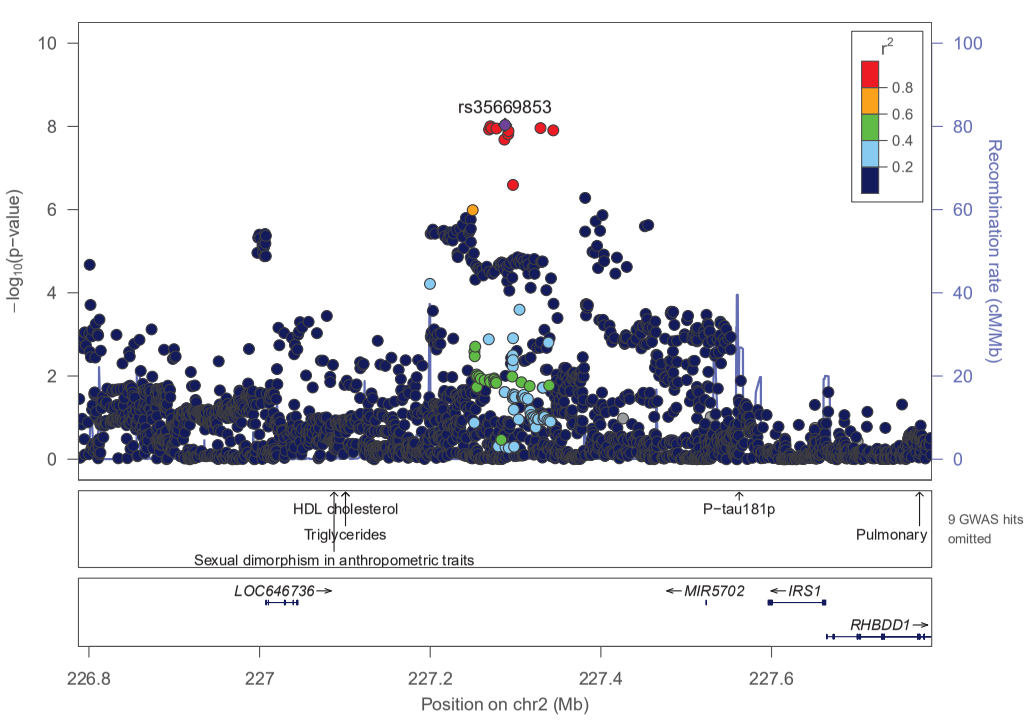

rs1047891
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
HDL cholesterol
Fibrinogen
Homocysteine levels
8 GWAS hits omitted
←ACADL
LANCL1−AS1→
CPS1→
←MYL1
←LANCL1
CPS1−IT1→
211.2
211.4
211.6
211.8
212
Position on chr2 (Mb)

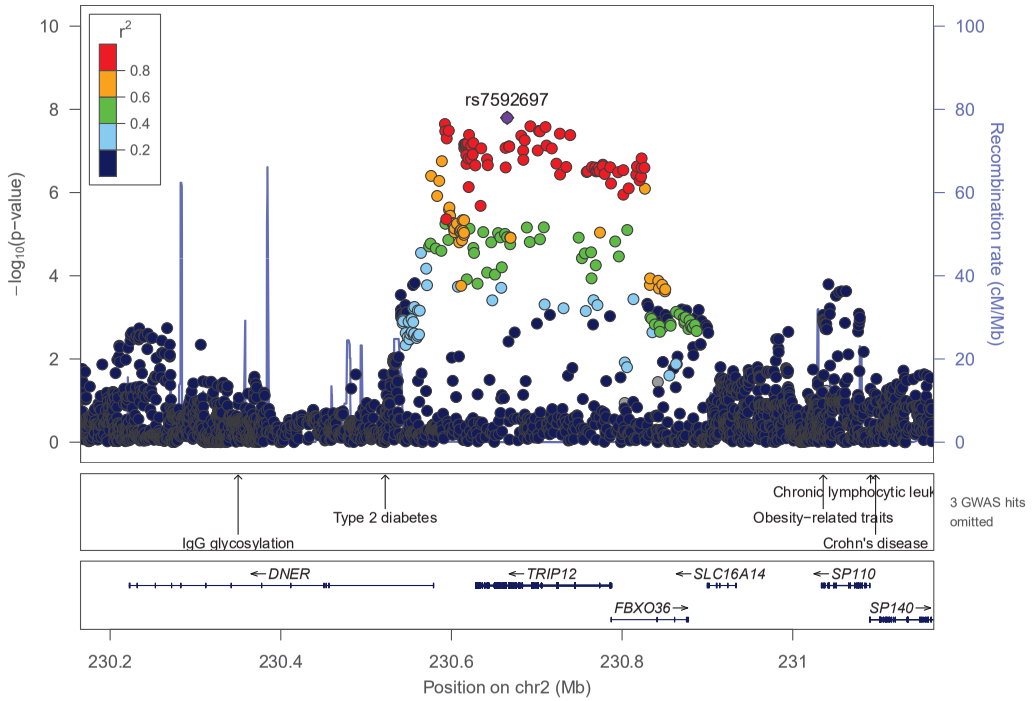

rs3791699
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
←ERBB4
211.8
212
212.2
212.4
212.6
Position on chr2 (Mb)

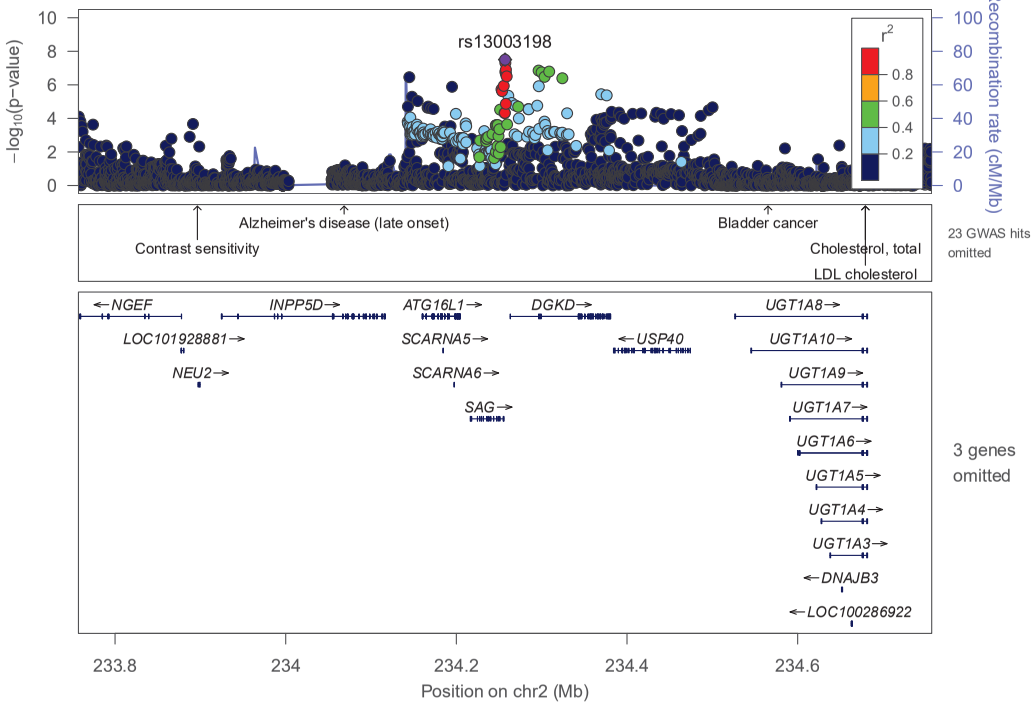

rs1548945
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Primary tooth development (number of teeth)
Breast cancer
Height
Thyroid hormone levels
5 GWAS hits omitted
←MARCH4
RPL37A→
IGFBP2→
←TNP1
DIRC3−AS1→
SMARCAL1→
←LINC01280
←LOC105373876
←DIRC3
←IGFBP5
LINC01921→
217.2
217.4
217.6
217.8
218
Position on chr2 (Mb)

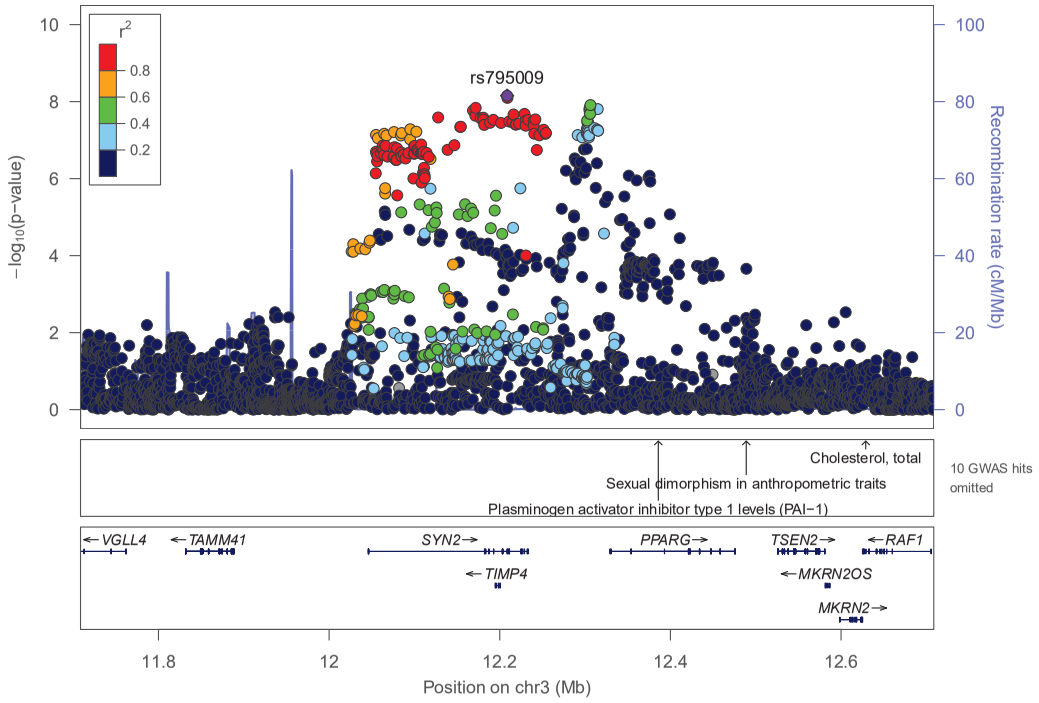

rs17462630
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Smooth−surface caries
Obesity−related traits
Obesity−related traits
Amyotrophic lateral sclerosis
Height
Common traits
Hair morpho
3 GWAS hits omitted
←TNS1
RUFY4→
←CXCR1
←AAMP
CATIP→
←USP37
PLCD4→
TTLL4→
WNT6→
LOC105373878→
ARPC2→
MIR6810→
VIL1→
CNOT9→
STK36→
CYP27A1→
←CXCR2P1
GPBAR1→
SLC11A1→
←ZNF142
←PRKAG3
CXCR2→
PNKD→
MIR26B→
BCS1L→
MIR9500→
←TMBIM1
CTDSP1→
←RNF25
WNT10A→
←MIR6513
←LINC01494
←CATIP−AS2
←CATIP−AS1
218.8
219
219.2
219.4
219.6
Position on chr2 (Mb)

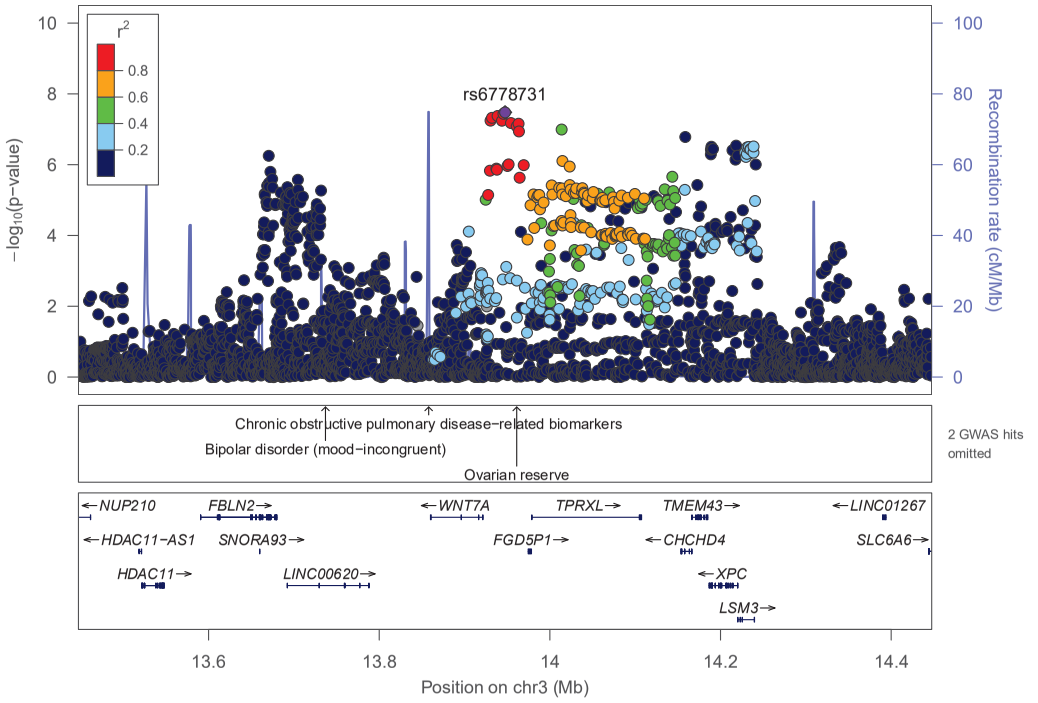

rs1050816
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Systemic lupus erythematosus and Systemic sc
Orofacial clefts
Height
3 GWAS hits omitted
MIR375
SLC23A3
DNAJB2
DNPEP
GMPPA
STK11IP
LINC01803
LOC100129175
ABCB6
RESP18
DES
ASIC4
SLC4A3
MIR4268
CFAP65
CNPPD1
PTPRN
SPEG
OBSL1
IHH
RETREG2
LOC100996693
MIR3131
ZFAND2B
CHPF
NHEJ1
ATG9A
TMEM198
ANKZF1
MIR3132
GLB1L
INHA
STK16
TUBA4A
2 genes omitted
Position on chr2 (Mb)

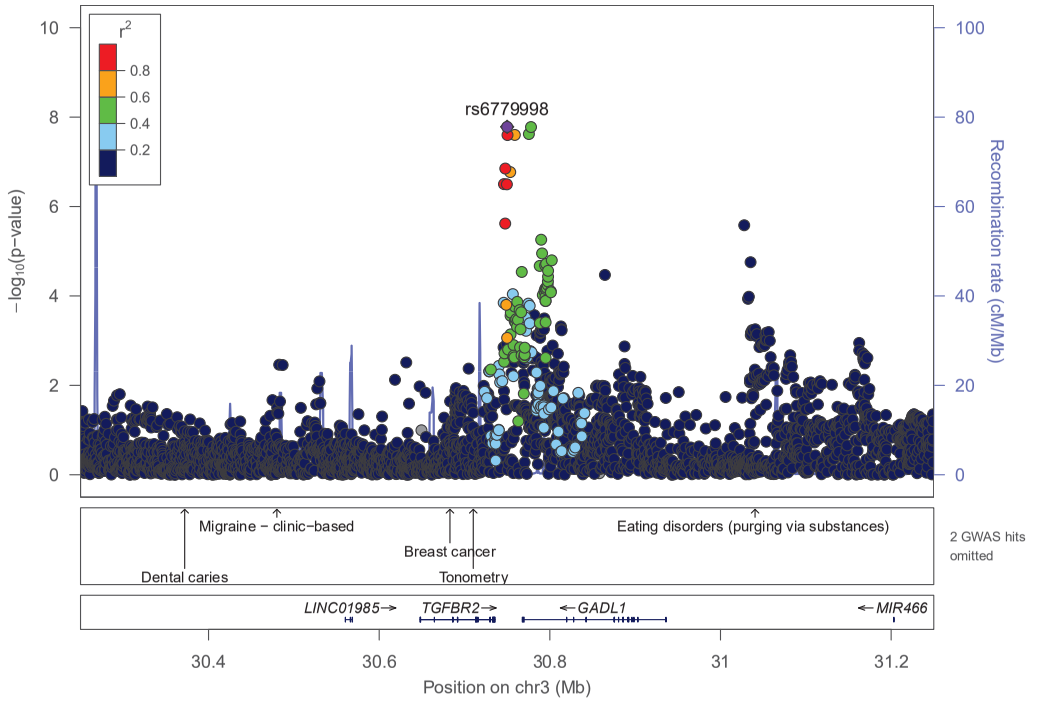

rs35669853
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
HDL cholesterol
Triglycerides
Sexual dimorphism in anthropometric traits
P−tau181p
Pulmonary
9 GWAS hits omitted
LOC646736
MIR5702
IRS1
RHBDD1
Position on chr2 (Mb)

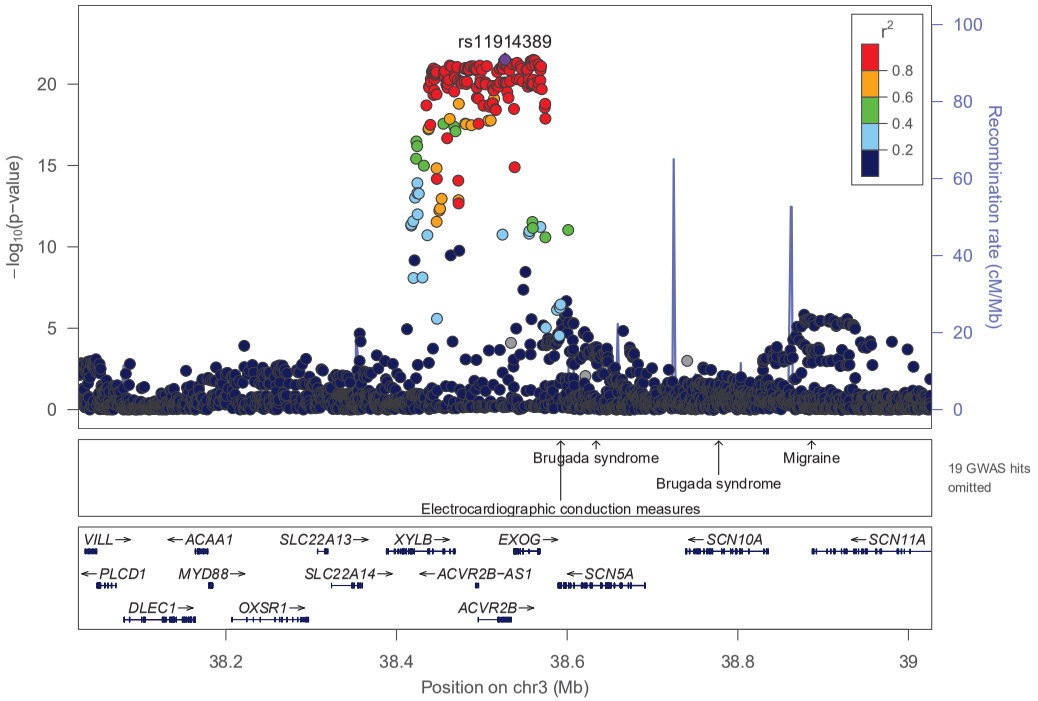

rs7592697
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
IgG glycosylation
Type 2 diabetes
Chronic lymphocytic leuk
Obesity−related traits
Crohn's disease
3 GWAS hits omitted
DNER
TRIP12
SLC16A14
SP110
FBXO36
SP140
Position on chr2 (Mb)

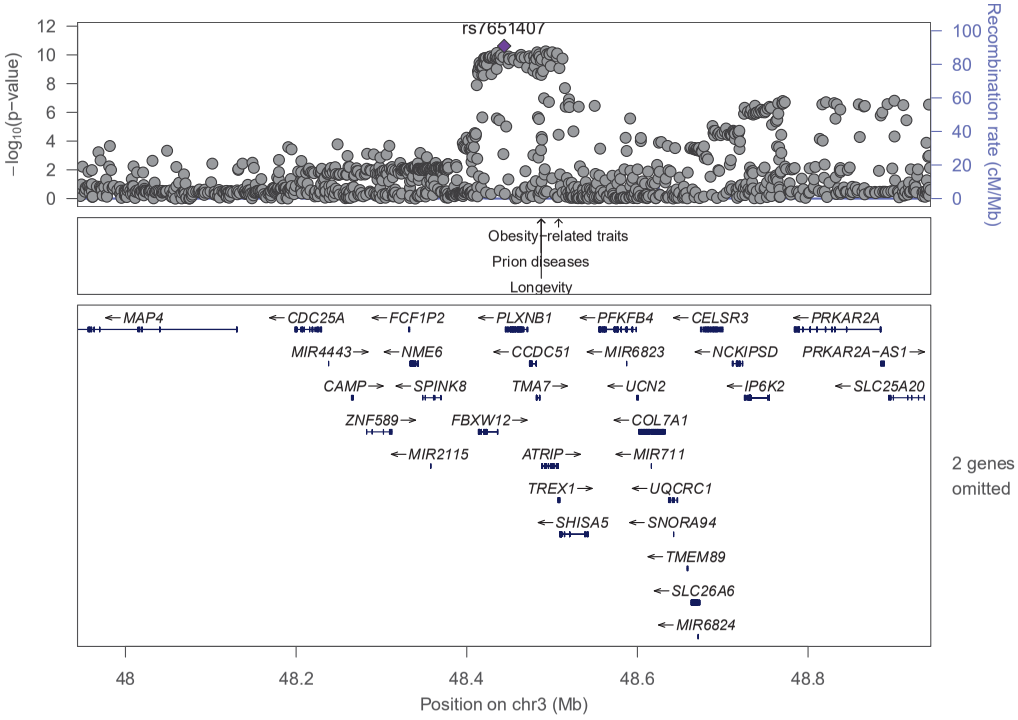

rs13003198
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Contrast sensitivity
Alzheimer's disease (late onset)
Bladder cancer
Cholesterol, total
LDL cholesterol
23 GWAS hits omitted
NGEF
INPP5D
ATG16L1
DGKD
UGT1A8
LOC101928881
SCARNA5
USP40
UGT1A10
NEU2
SCARNA6
UGT1A9
SAG
UGT1A7
UGT1A6
UGT1A5
UGT1A4
UGT1A3
DNAJB3
LOC100286922
3 genes omitted
Position on chr2 (Mb)

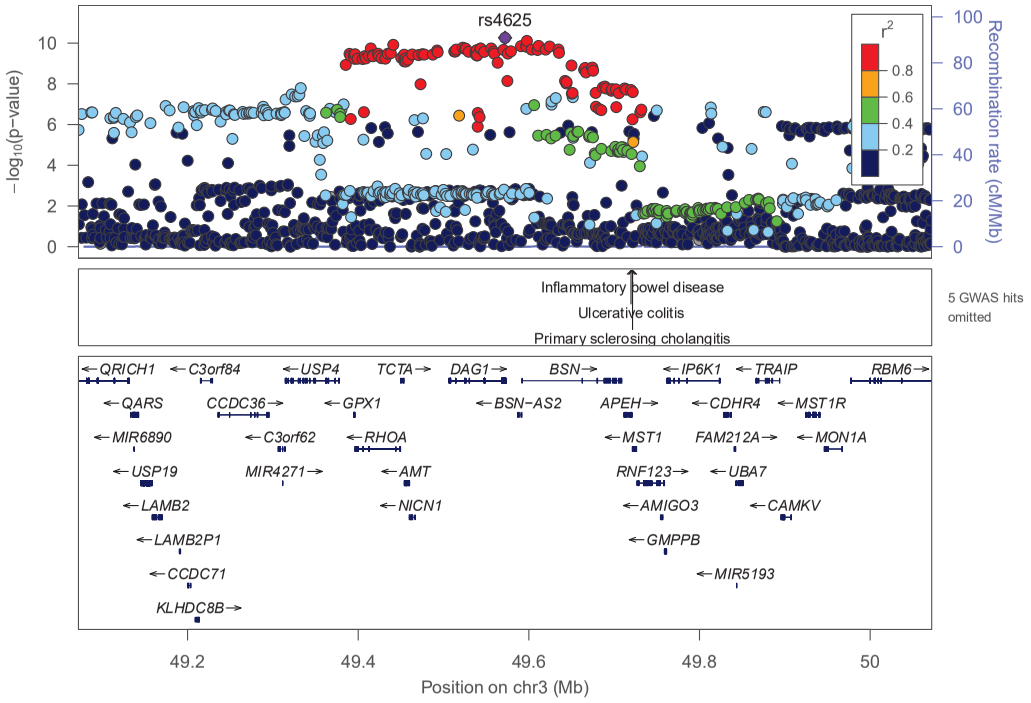

rs795009
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
Sexual dimorphism in anthropometric traits
Plasminogen activator inhibitor type 1 levels (PAI−1)
10 GWAS hits omitted
VGLL4
TAMM41
SYN2
TIMP4
PPARG
TSEN2
MKRN2OS
RAF1
MKRN2
Position on chr3 (Mb)

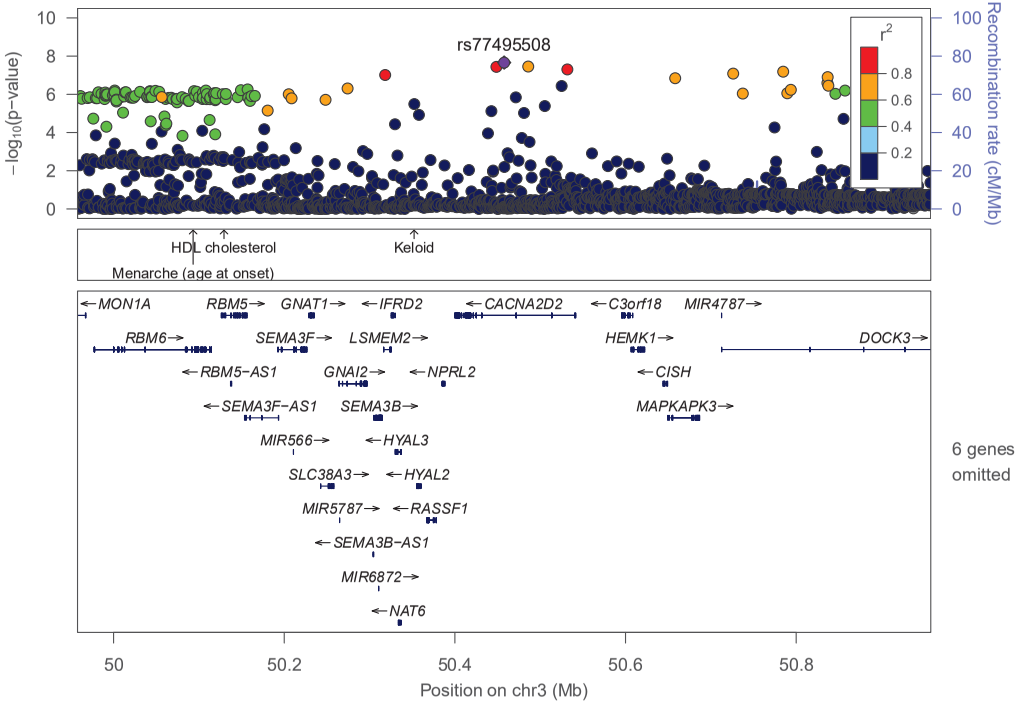

rs6778731
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Chronic obstructive pulmonary disease−related biomarkers
Bipolar disorder (mood−incongruent)
Ovarian reserve
2 GWAS hits omitted
NUP210
FBLN2
WNT7A
TPRXL
TMEM43
LINC01267
HDAC11−AS1
SNORA93
FGD5P1
CHCHD4
SLC6A6
HDAC11
LINC00620
XPC
LSM3
Position on chr3 (Mb)

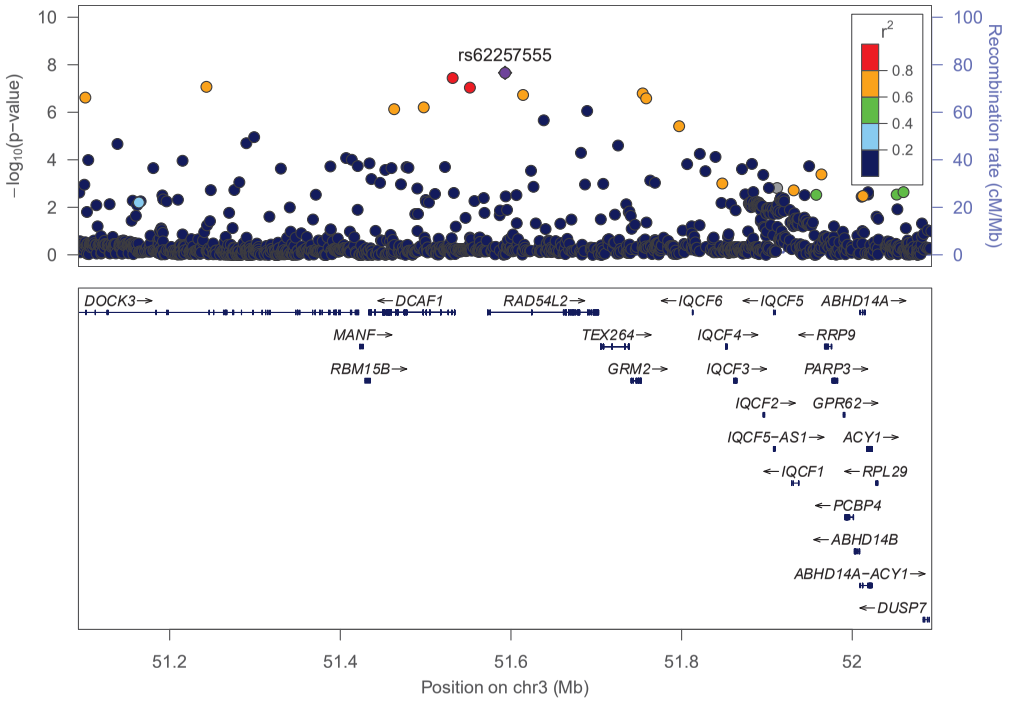

rs6779998
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Migraine − clinic−based
Dental caries
Breast cancer
Tonometry
Eating disorders (purging via substances)
2 GWAS hits omitted
LINC01985
TGFBR2
GADL1
MIR466
Position on chr3 (Mb)

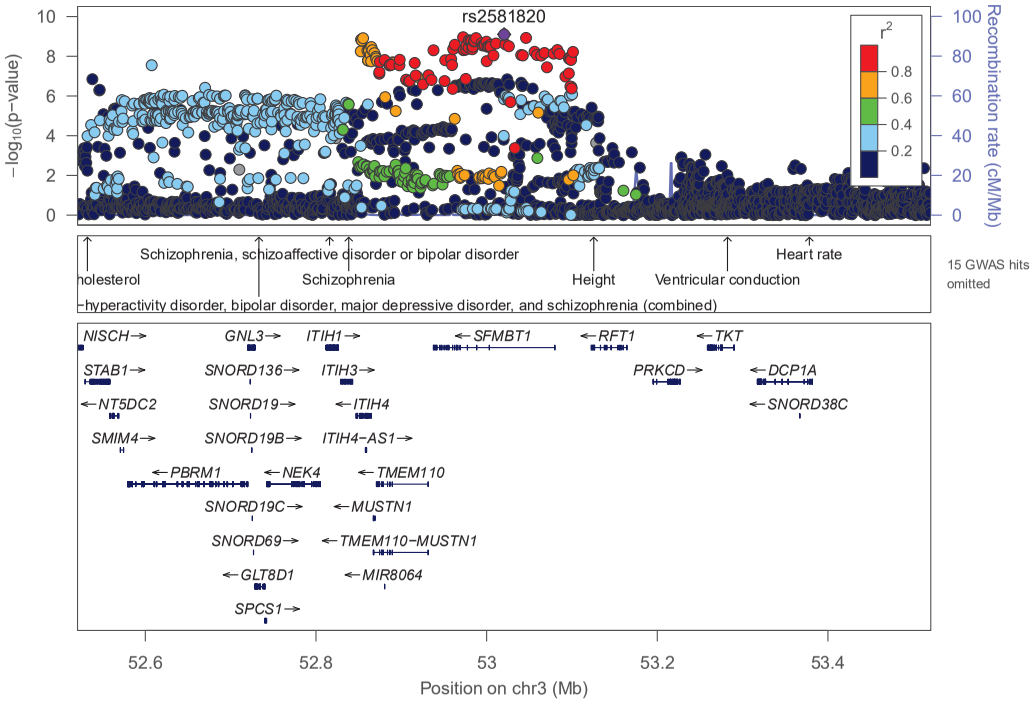

rs11914389
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Brugada syndrome
Brugada syndrome
Migraine
Electrocardiographic conduction measures
19 GWAS hits omitted
VILL
ACAA1
SLC22A13
XYLB
EXOG
SCN10A
SCN11A
PLCD1
MYD88
SLC22A14
ACVR2B−AS1
SCN5A
DLEC1
OXSR1
ACVR2B
Position on chr3 (Mb)

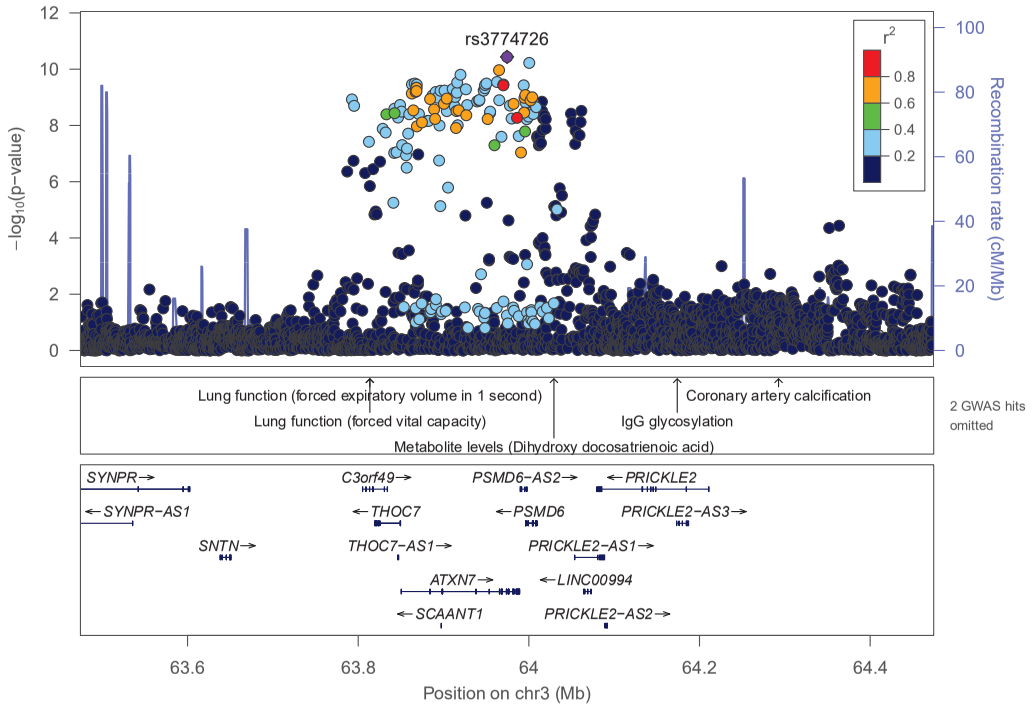

rs7651407
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Prion diseases
Longevity
2 genes omitted
Position on chr3 (Mb)

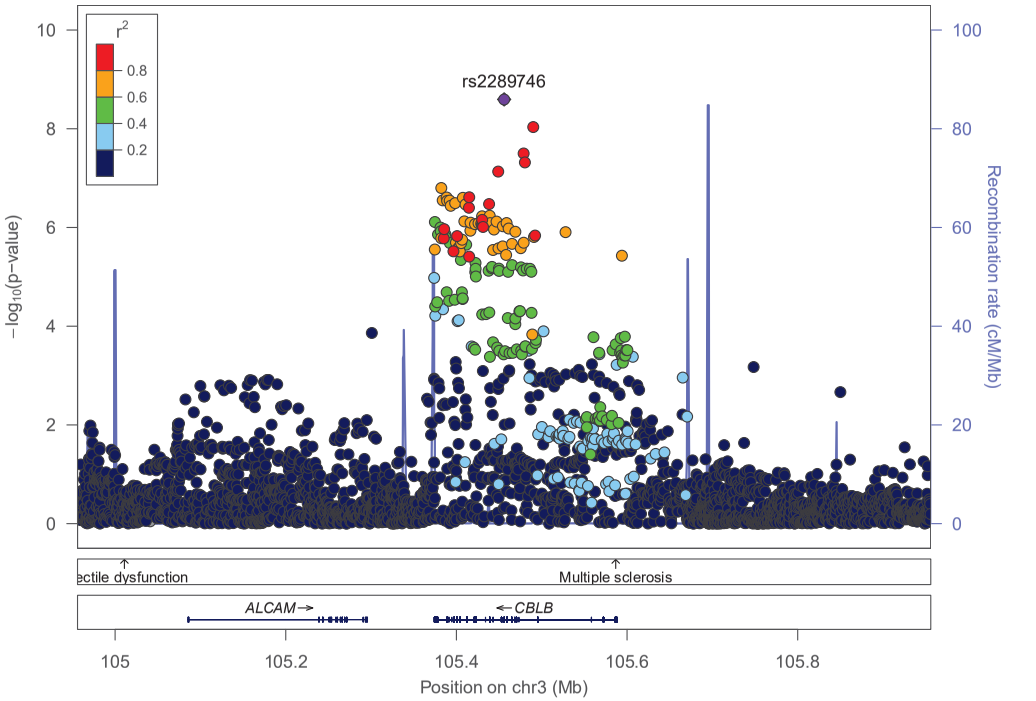

rs4625
r2
−log10(p−value)
Recombination rate (cM/Mb)
Inflammatory bowel disease
Ulcerative colitis
Primary sclerosing cholangitis
5 GWAS hits omitted
Position on chr3 (Mb)

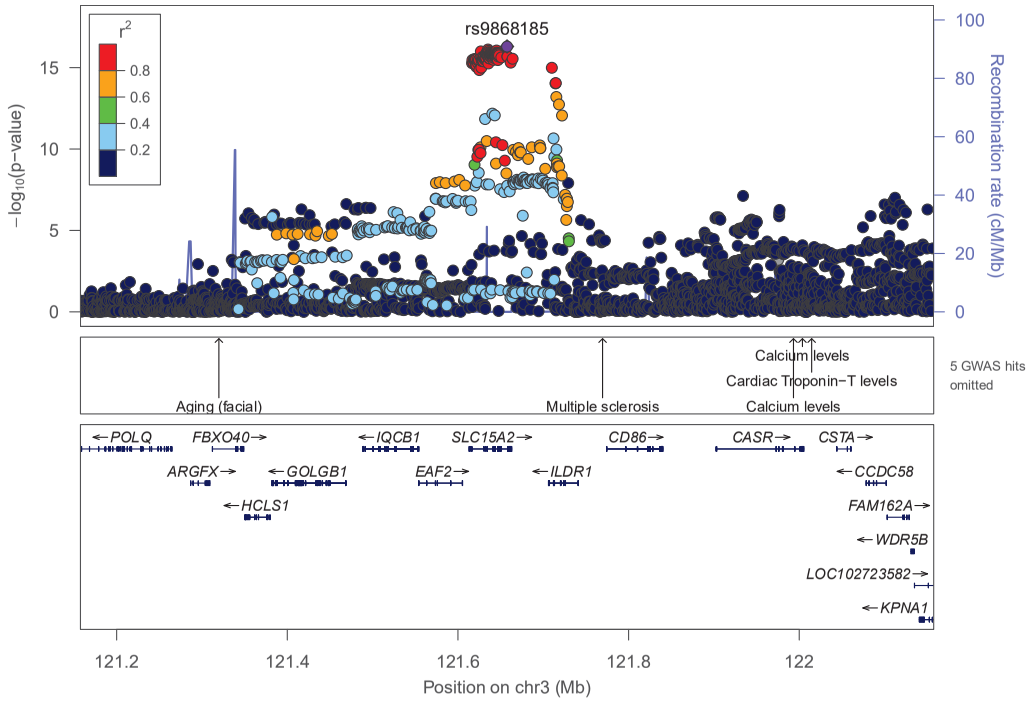

rs77495508
r2
−log10(p−value)
Recombination rate (cM/Mb)
HDL cholesterol
Menarche (age at onset)
Keloid
6 genes omitted
Position on chr3 (Mb)

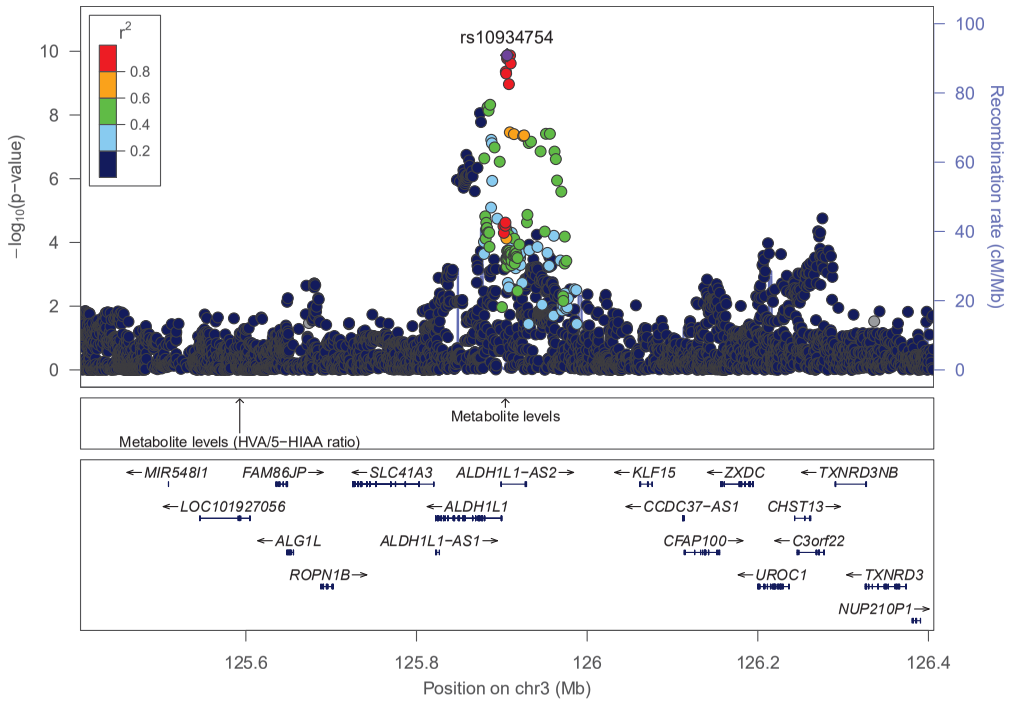

rs62257555
r2
−log10(p−value)
Recombination rate (cM/Mb)
Position on chr3 (Mb)

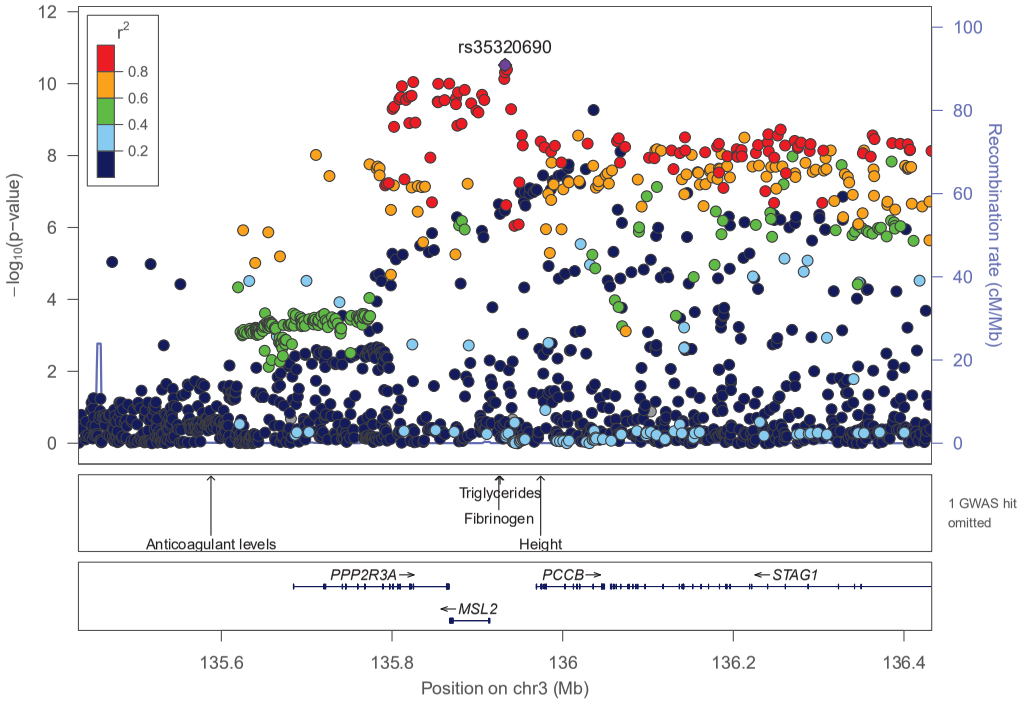

rs2581820
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
holesterol
Schizophrenia, schizoaffective disorder or bipolar disorder
Schizophrenia
Height
Ventricular conduction
Heart rate
-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined)
15 GWAS hits omitted
NISCH→ GNL3→ ITIH1→ ←SFMBT1 ←RFT1 ←TKT
STAB1→ SNORD136→ ITIH3→ PRKCD→ ←DCP1A
←NT5DC2 SNORD19→ ←ITIH4 ←SNORD38C
SMIM4→ SNORD19B→ ITIH4−AS1→
←PBRM1 ←NEK4 ←TMEM110
SNORD19C→ ←MUSTN1
SNORD69→ ←TMEM110−MUSTN1
←GLT8D1 ←MIR8064
SPCS1→
52.6 52.8 53 53.2 53.4
Position on chr3 (Mb)

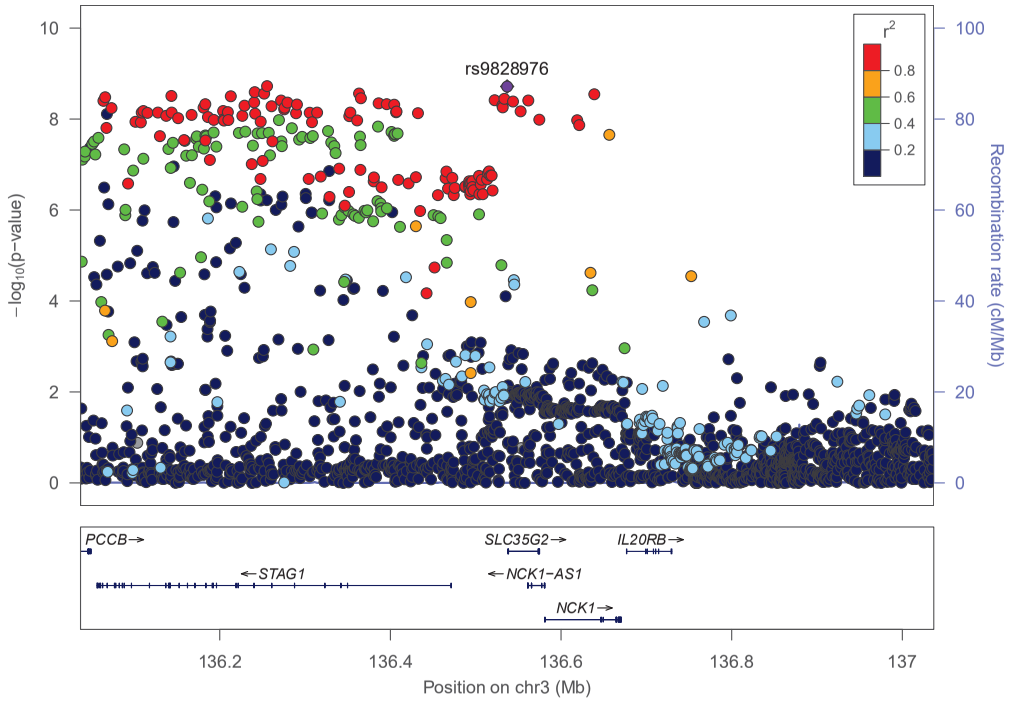

rs3774726
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Lung function (forced expiratory volume in 1 second)
Lung function (forced vital capacity)
Metabolite levels (Dihydroxy docosatrienoic acid)
IgG glycosylation
Coronary artery calcification
2 GWAS hits omitted
SYNPR→ C3orf49→ PSMD6−AS2→ ←PRICKLE2
←SYNPR−AS1 ←THOC7 ←PSMD6 PRICKLE2−AS3→
SNTN→ THOC7−AS1→ PRICKLE2−AS1→
ATXN7→ ←LINC00994
←SCAANT1 PRICKLE2−AS2→
63.6 63.8 64 64.2 64.4
Position on chr3 (Mb)

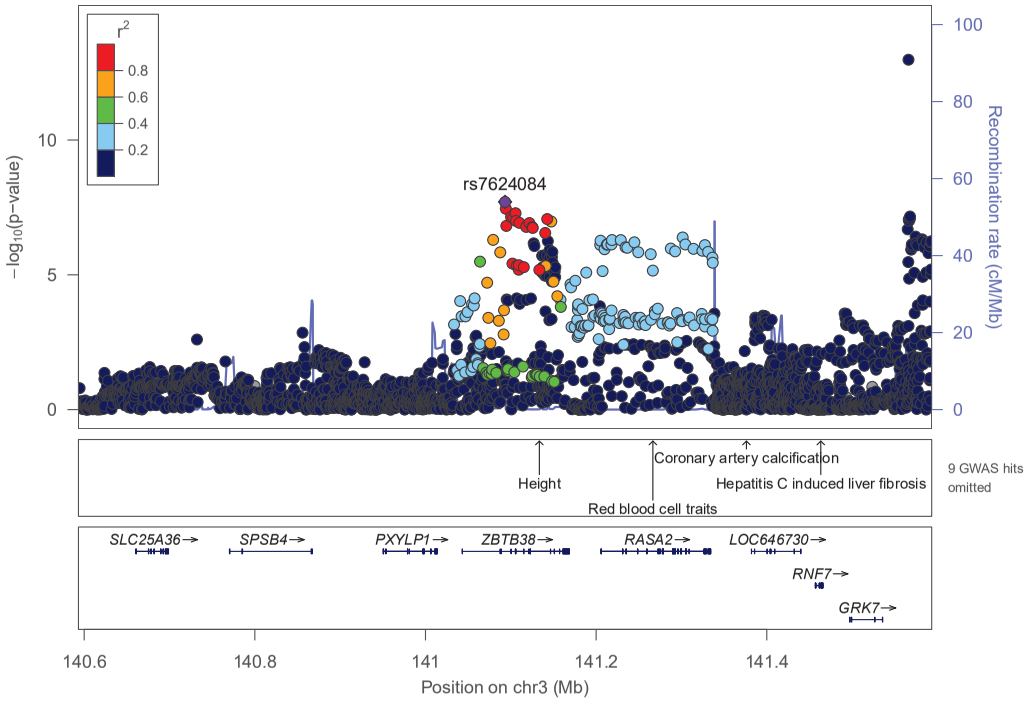

rs2289746
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ectile dysfunction
Multiple sclerosis
ALCAM→ ←CBLB
105 105.2 105.4 105.6 105.8
Position on chr3 (Mb)

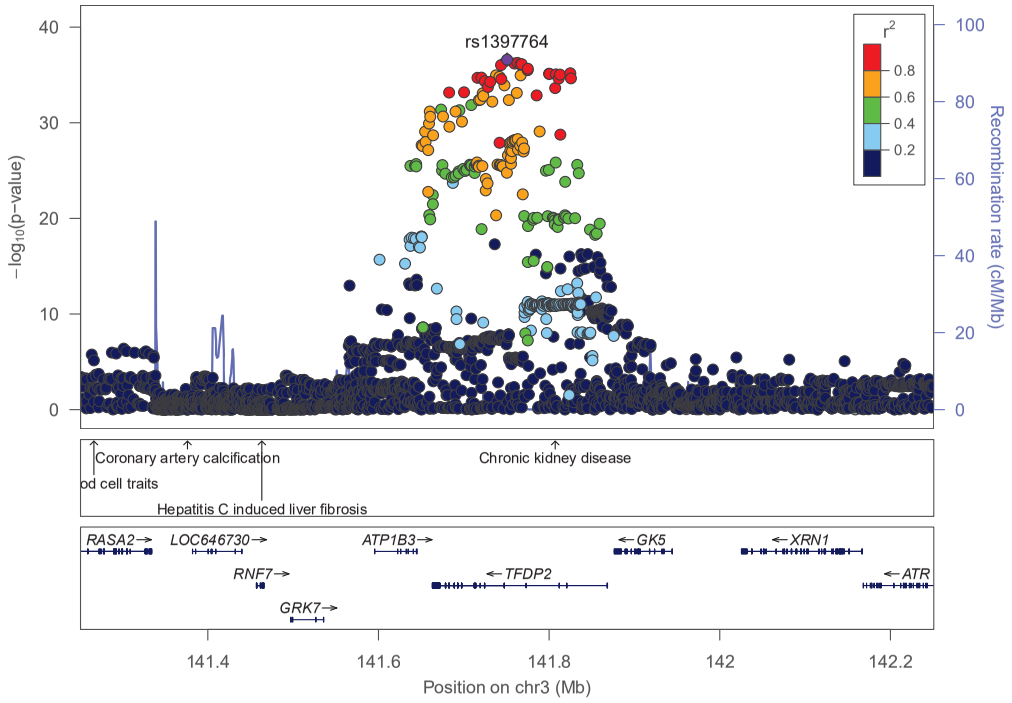

rs9868185
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Aging (facial)
Multiple sclerosis
Calcium levels
Cardiac Troponin−T levels
Calcium levels
5 GWAS hits omitted
←POLQ FBXO40→ ←IQCB1 SLC15A2→ CD86→ CASR→ CSTA→
ARGFX→ ←GOLGB1 EAF2→ ←ILDR1 ←CCDC58
←HCLS1 FAM162A→
←WDR5B
LOC102723582→
←KPNA1
121.2 121.4 121.6 121.8 122
Position on chr3 (Mb)

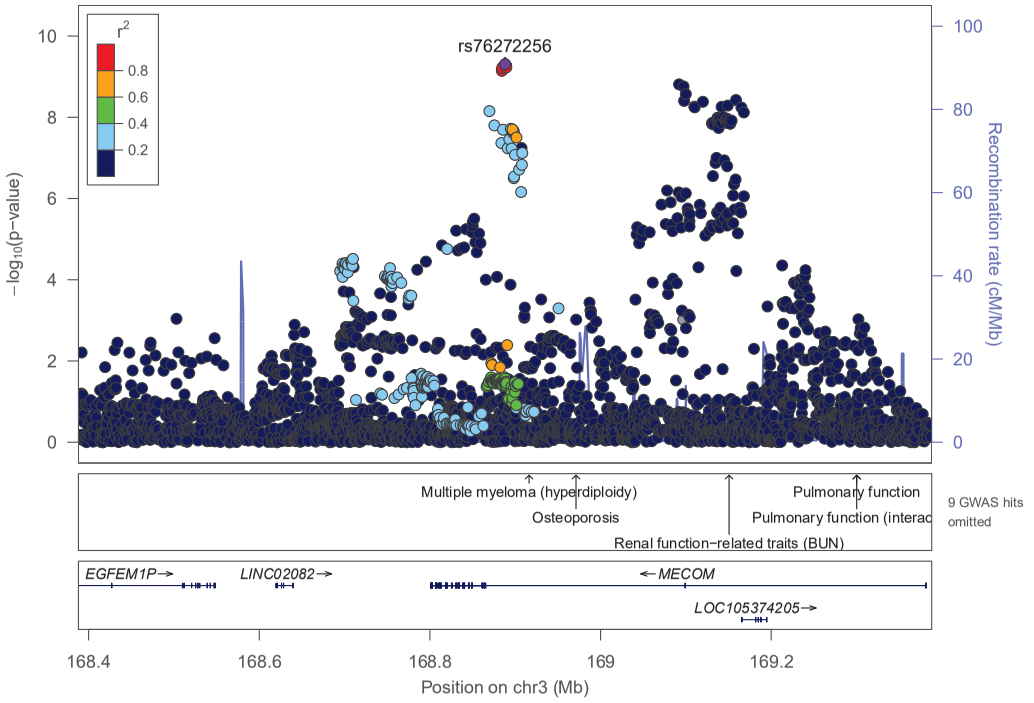

rs10934754
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Metabolite levels (HVA/5−HIAA ratio)
Metabolite levels
MIR548I1
FAM86JP
SLC41A3
ALDH1L1−AS2
KLF15
ZXDC
TXNRD3NB
LOC101927056
ALDH1L1
CCDC37−AS1
CHST13
ALG1L
ALDH1L1−AS1
CFAP100
C3orf22
ROPN1B
UROC1
TXNRD3
NUP210P1
Position on chr3 (Mb)

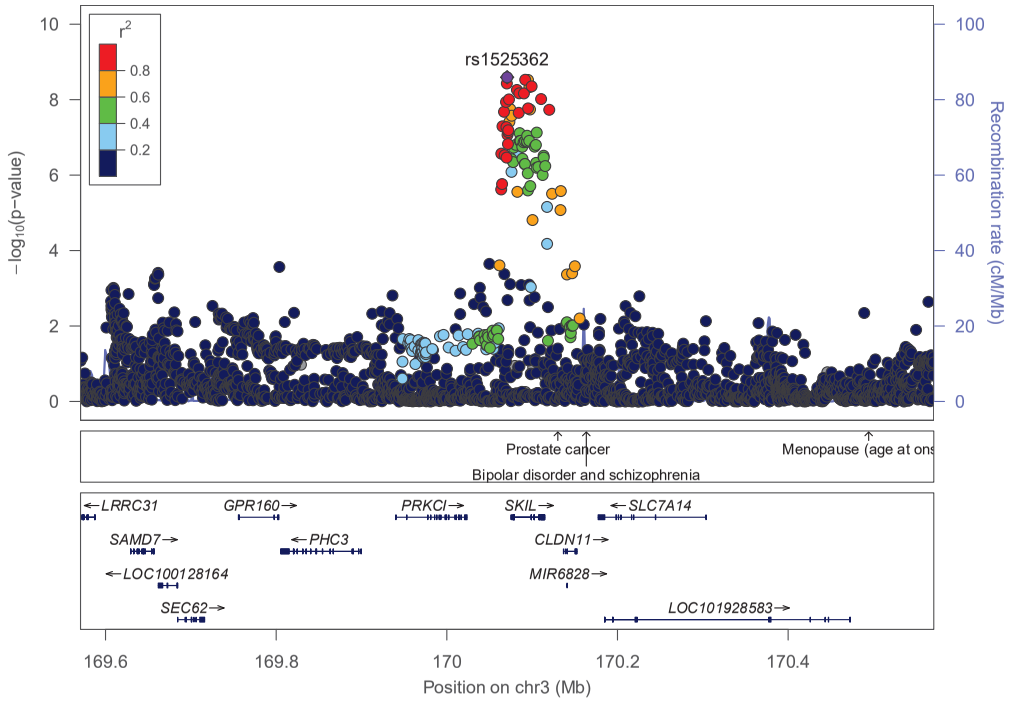

rs35320690
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Anticoagulant levels
Triglycerides
Fibrinogen
Height
1 GWAS hit omitted
PPP2R3A
PCCB
STAG1
MSL2
Position on chr3 (Mb)

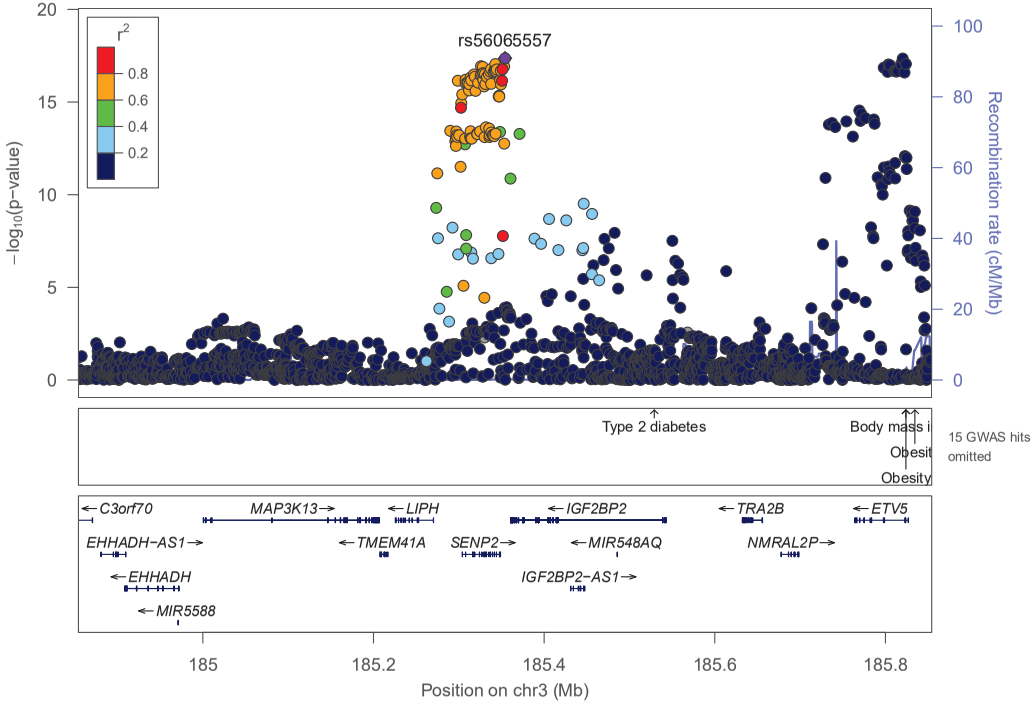

rs9828976
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
PCCB
SLC35G2
IL20RB
STAG1
NCK1−AS1
NCK1
Position on chr3 (Mb)

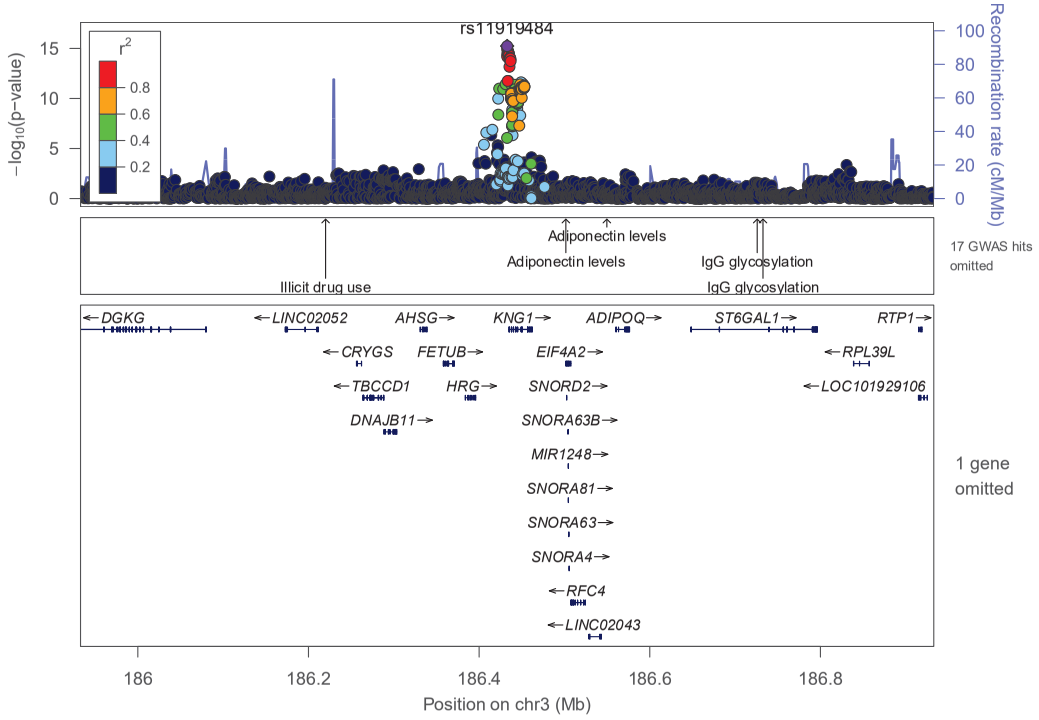

rs7624084
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Height
Coronary artery calcification
Hepatitis C induced liver fibrosis
Red blood cell traits
9 GWAS hits omitted
SLC25A36
SPSB4
PXYLP1
ZBTB38
RASA2
LOC646730
RNF7
GRK7
Position on chr3 (Mb)

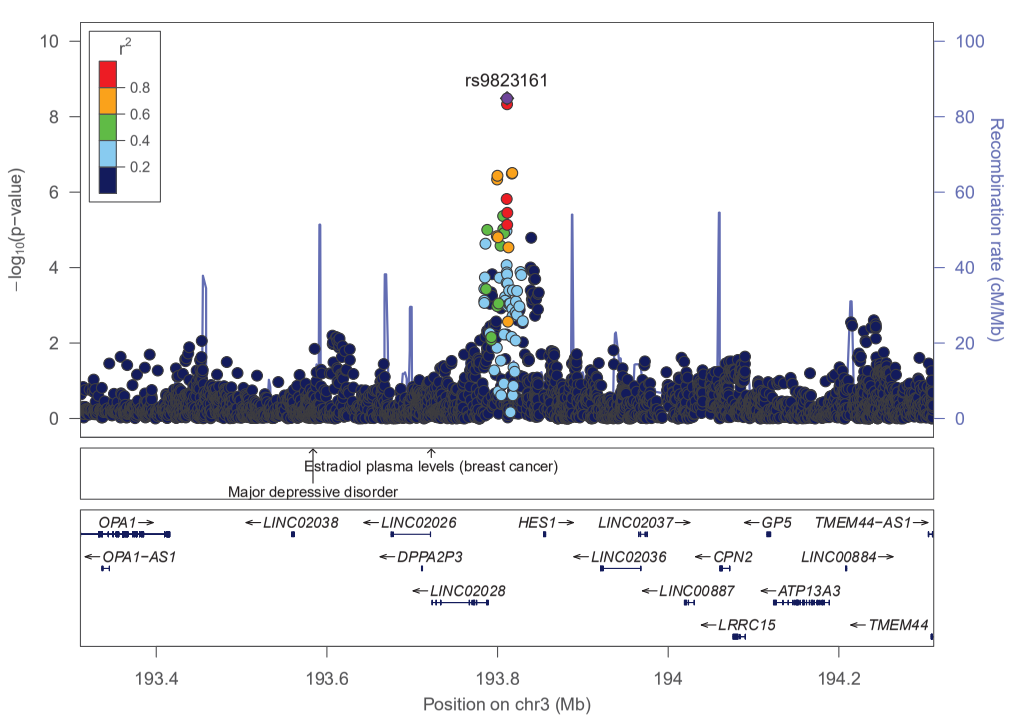

rs1397764
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Coronary artery calcification
od cell traits
Hepatitis C induced liver fibrosis
Chronic kidney disease
RASA2→
LOC646730→
ATP1B3→
←GK5
←XRN1
RNF7→
←TFDP2
←ATR
GRK7→
Position on chr3 (Mb)

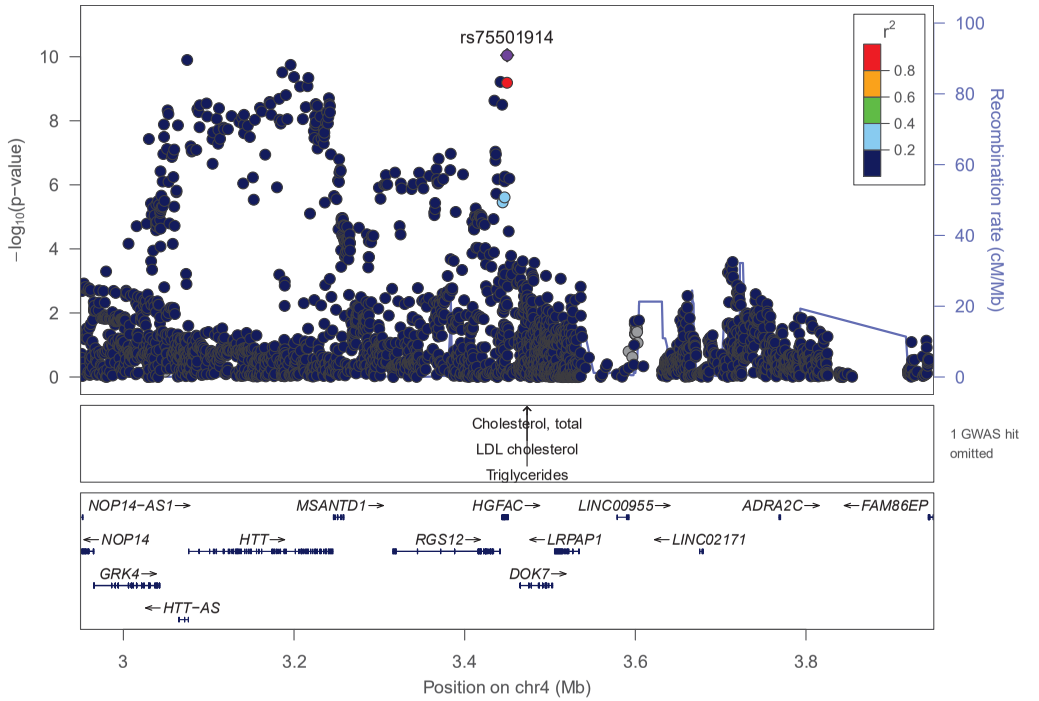

rs76272256
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Multiple myeloma (hyperdiploidy)
Osteoporosis
Renal function−related traits (BUN)
Pulmonary function
Pulmonary function (interac
9 GWAS hits
omitted
EGFEM1P→
LINC02082→
←MECOM
LOC105374205→
Position on chr3 (Mb)

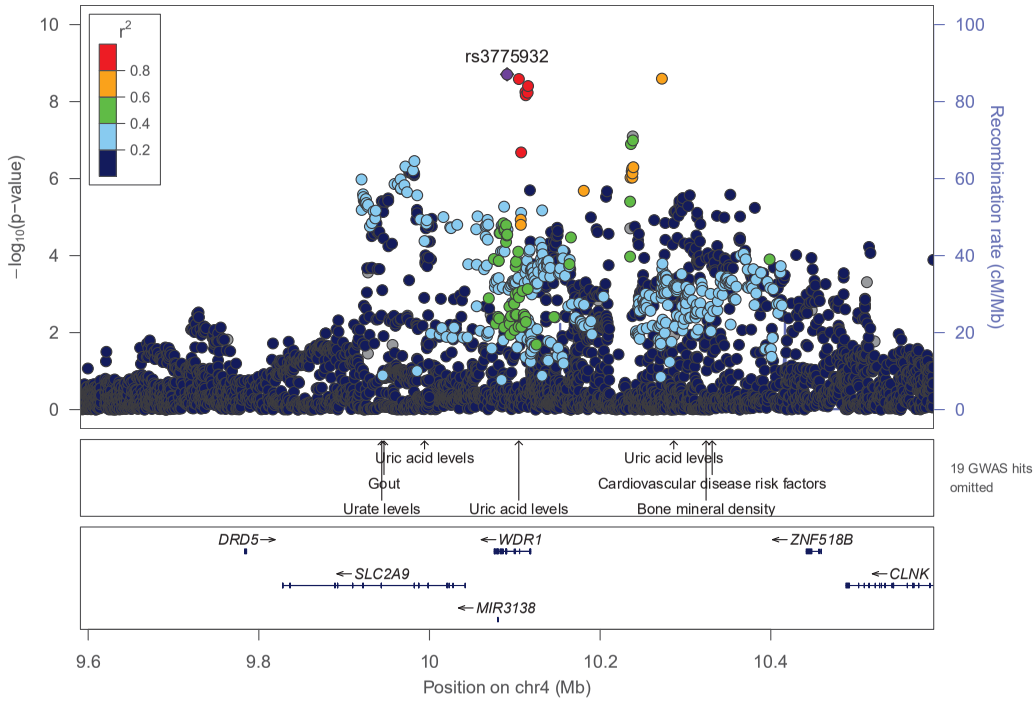

rs1525362
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Prostate cancer
Bipolar disorder and schizophrenia
Menopause (age at ons
←LRRC31
GPR160→
PRKCI→
SKIL→
←SLC7A14
SAMD7→
←PHC3
CLDN11→
←LOC100128164
MIR6828→
SEC62→
LOC101928583→
Position on chr3 (Mb)

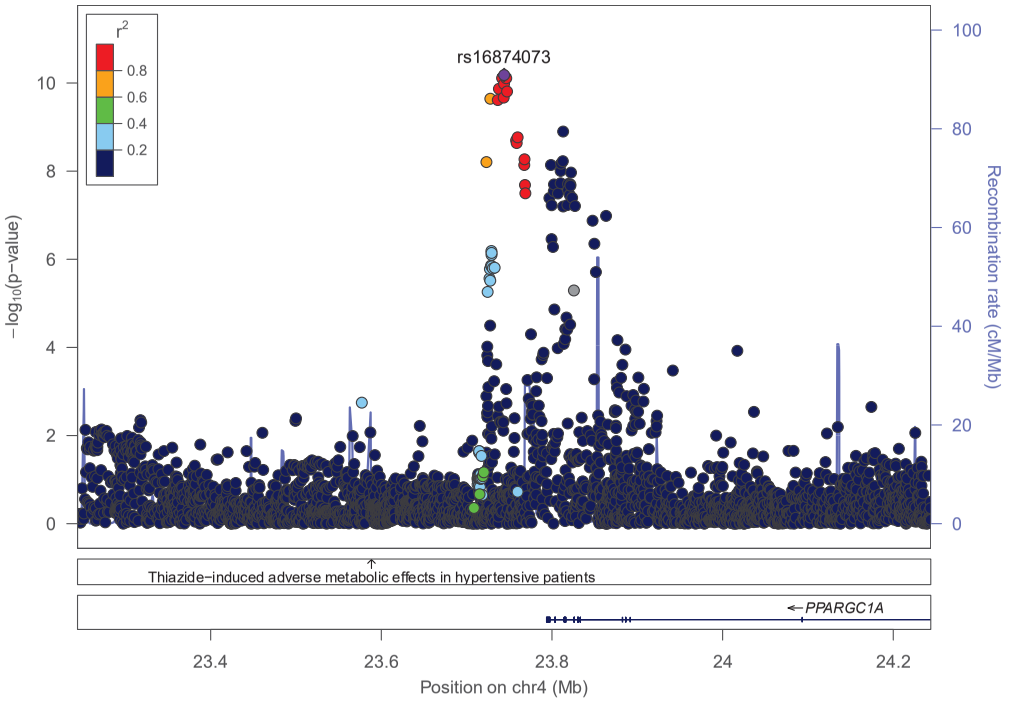

rs56065557
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Type 2 diabetes
Body mass i
Obesit
Obesity
15 GWAS hits
omitted
←C3orf70
MAP3K13→
←LIPH
←IGF2BP2
←TRA2B
←ETV5
EHHADH−AS1→
←TMEM41A
SENP2→
←MIR548AQ
NMRAL2P→
←EHHADH
IGF2BP2−AS1→
←MIR5588
Position on chr3 (Mb)

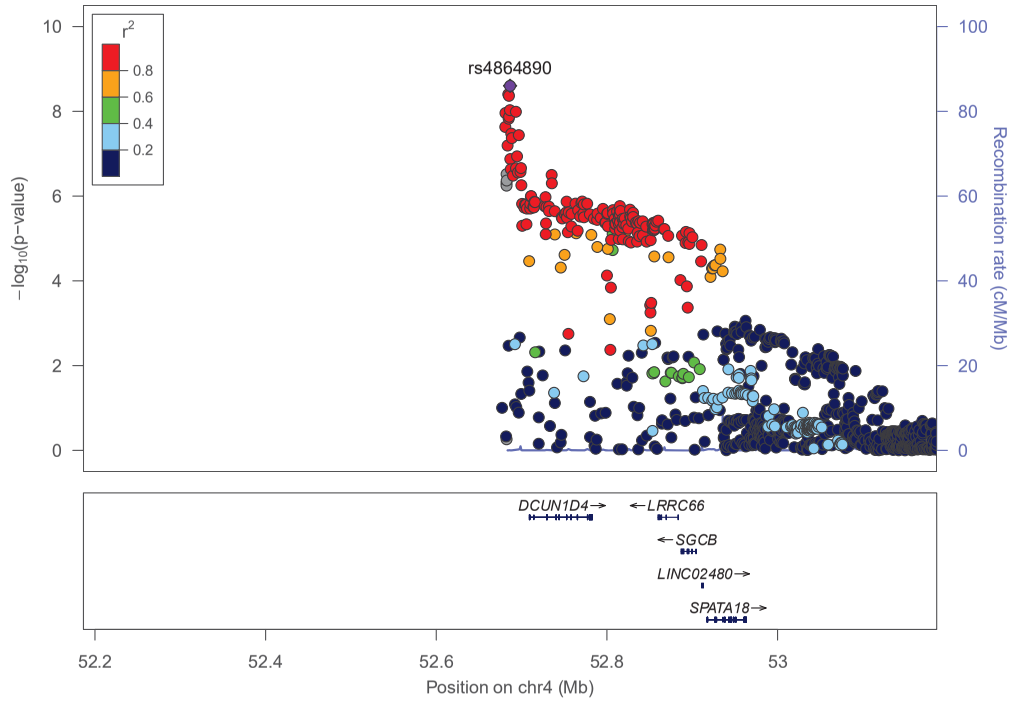

rs11919484
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Illicit drug use
Adiponectin levels
Adiponectin levels
IgG glycosylation
IgG glycosylation
17 GWAS hits omitted
DGKG
LINC02052
AHSG
KNG1
ADIPOQ
ST6GAL1
RTP1
CRYGS
FETUB
EIF4A2
RPL39L
TBCCD1
HRG
SNORD2
LOC101929106
DNAJB11
SNORA63B
MIR1248
SNORA81
SNORA63
SNORA4
RFC4
LINC02043
1 gene omitted
186
186.2
186.4
186.6
186.8
Position on chr3 (Mb)

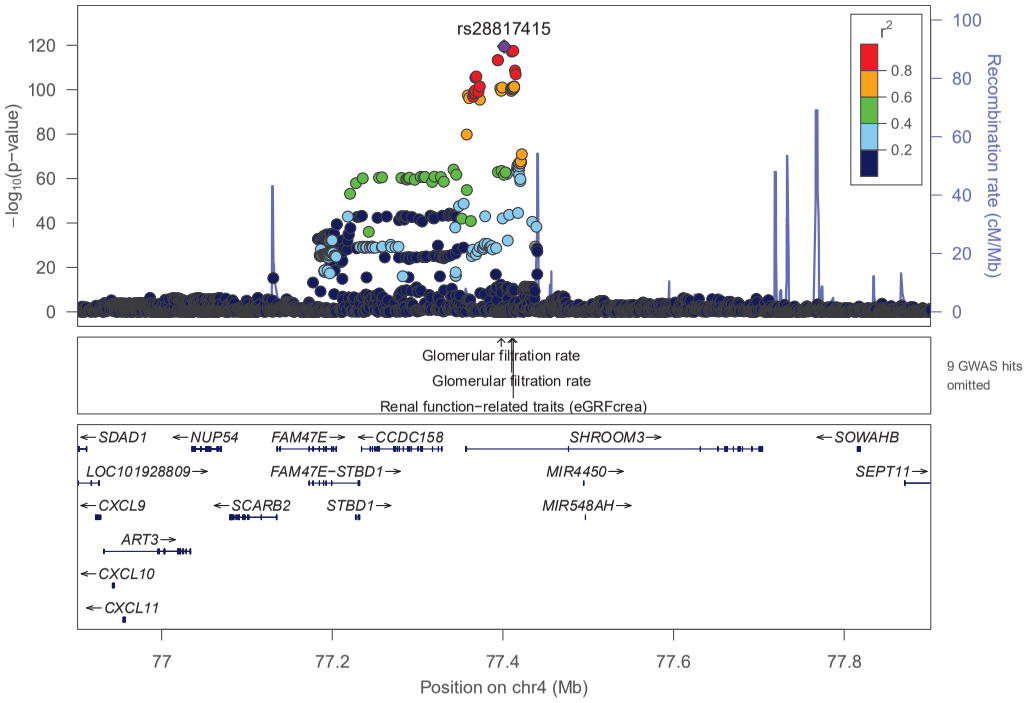

rs9823161
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Estradiol plasma levels (breast cancer)
Major depressive disorder
OPA1
LINC02038
LINC02026
HES1
LINC02037
GP5
TMEM44−AS1
OPA1−AS1
DPPA2P3
LINC02036
CPN2
LINC00884
LINC02028
LINC00887
ATP13A3
LRRC15
TMEM44
193.4
193.6
193.8
194
194.2
Position on chr3 (Mb)

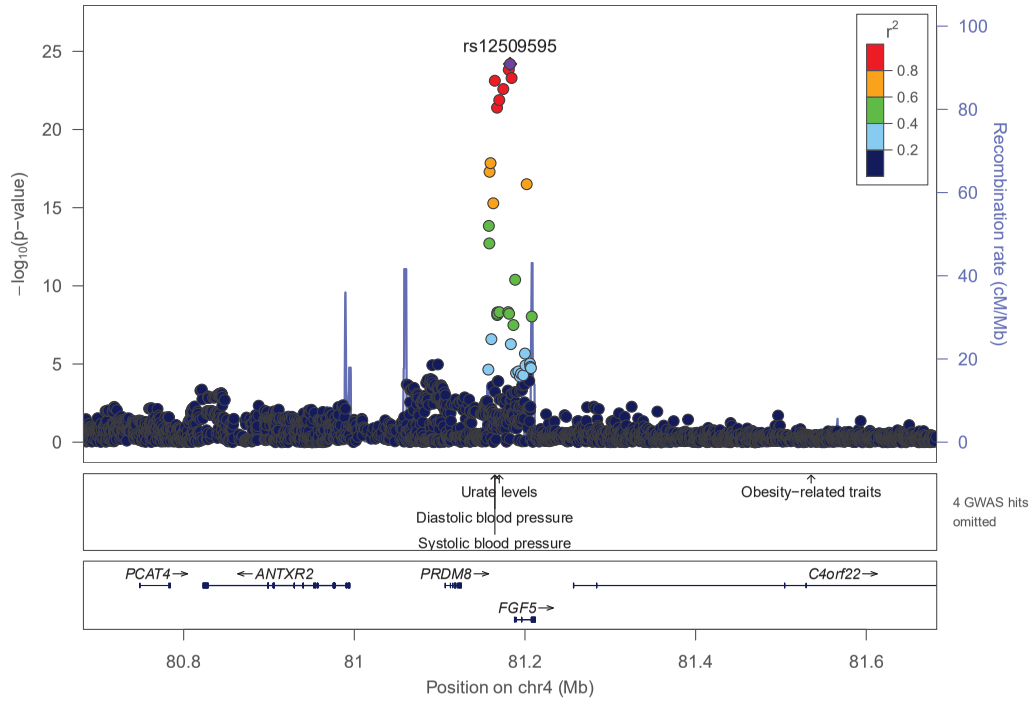

rs75501914
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
LDL cholesterol
Triglycerides
1 GWAS hit omitted
NOP14−AS1
MSANTD1
HGFAC
LINC00955
ADRA2C
FAM86EP
NOP14
HTT
RGS12
LRPAP1
LINC02171
GRK4
DOK7
HTT−AS
3
3.2
3.4
3.6
3.8
Position on chr4 (Mb)

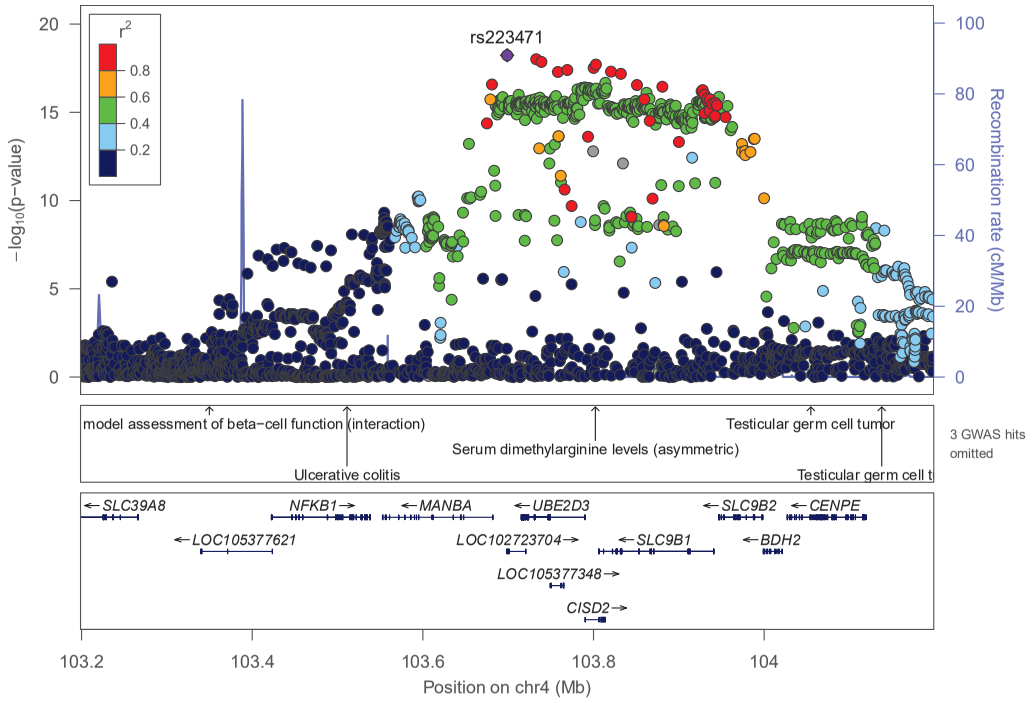

rs3775932
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Uric acid levels
Gout
Urate levels
Uric acid levels
Uric acid levels
Cardiovascular disease risk factors
Bone mineral density
19 GWAS hits omitted
DRD5
WDR1
ZNF518B
SLC2A9
CLNK
MIR3138
9.6
9.8
10
10.2
10.4
Position on chr4 (Mb)

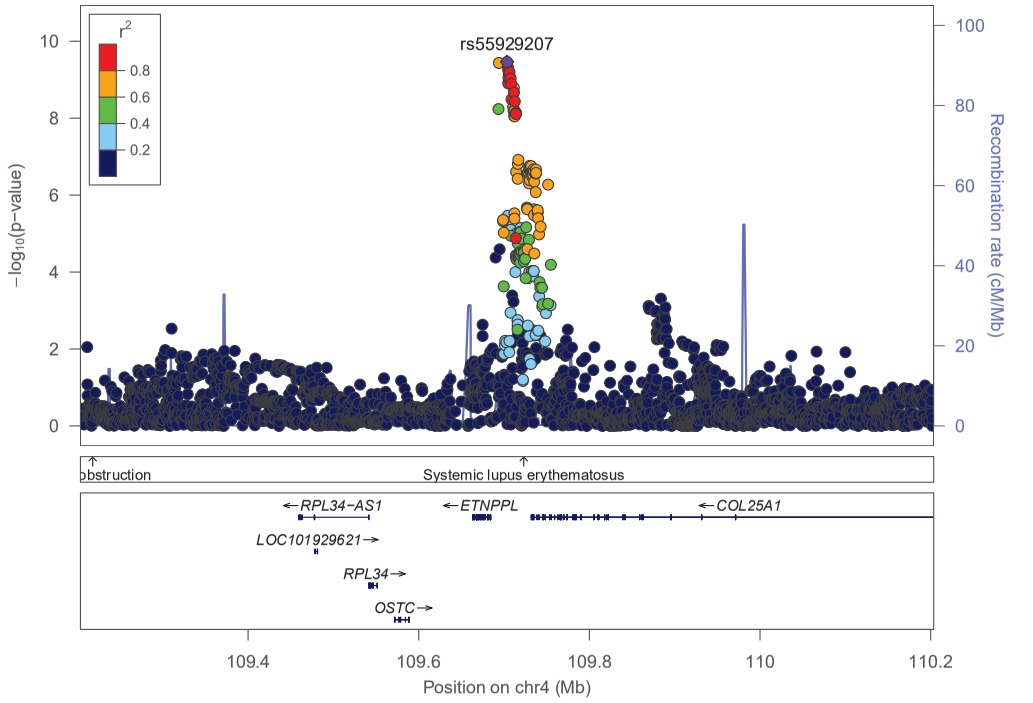

rs16874073
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Thiazide−induced adverse metabolic effects in hypertensive patients
←PPARGC1A
Position on chr4 (Mb)

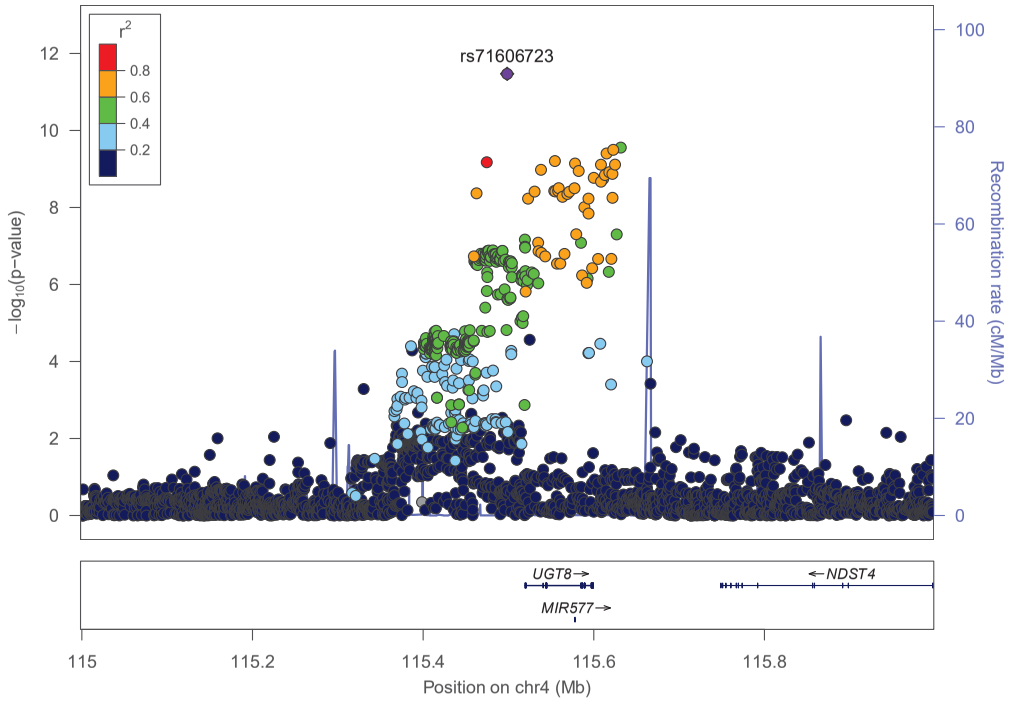

rs4864890
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
DCUN1D4→
←LRRC66
←SGCB
LINC02480→
SPATA18→
Position on chr4 (Mb)

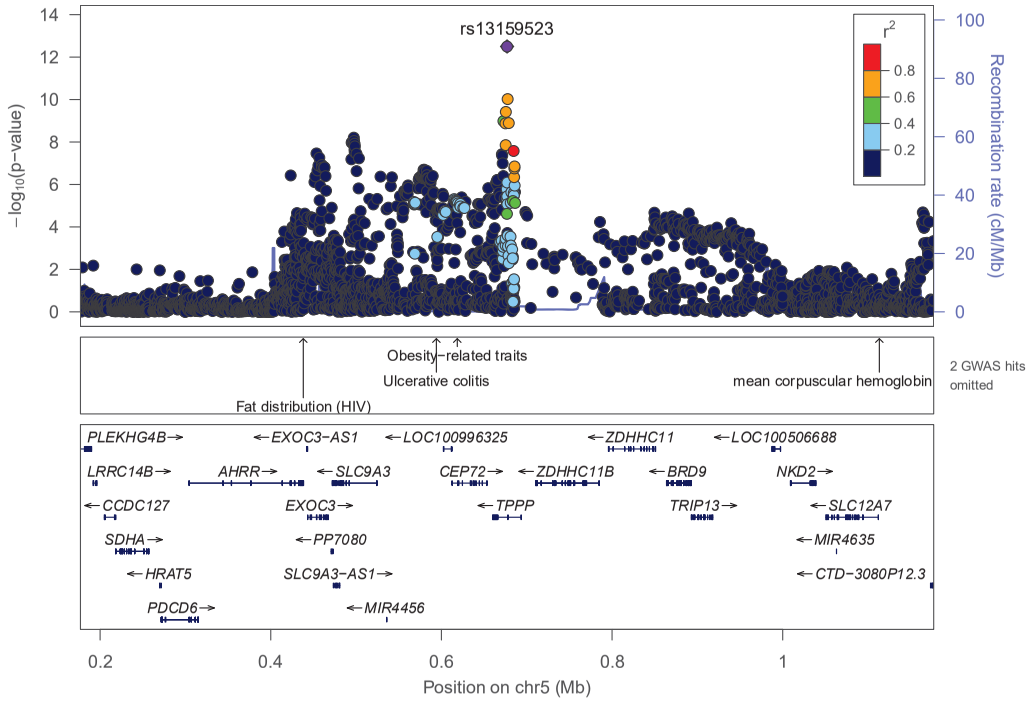

rs28817415
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Glomerular filtration rate
Glomerular filtration rate
Renal function−related traits (eGRFcrea)
9 GWAS hits omitted
←SDAD1
←NUP54
FAM47E→
←CCDC158
SHROOM3→
←SOWAHB
LOC101928809→
FAM47E−STBD1→
MIR4450→
SEPT11→
←CXCL9
←SCARB2
STBD1→
MIR548AH→
ART3→
←CXCL10
←CXCL11
Position on chr4 (Mb)

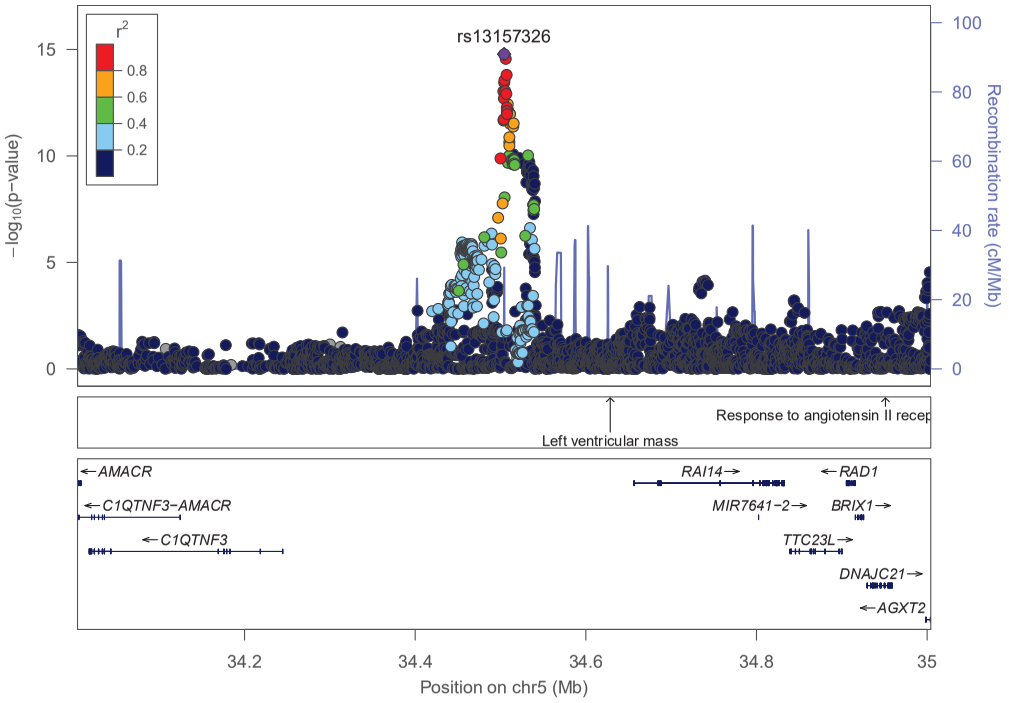

rs12509595
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Urate levels
Diastolic blood pressure
Systolic blood pressure
Obesity−related traits
4 GWAS hits omitted
PCAT4→
←ANTXR2
PRDM8→
C4orf22→
FGF5→
Position on chr4 (Mb)

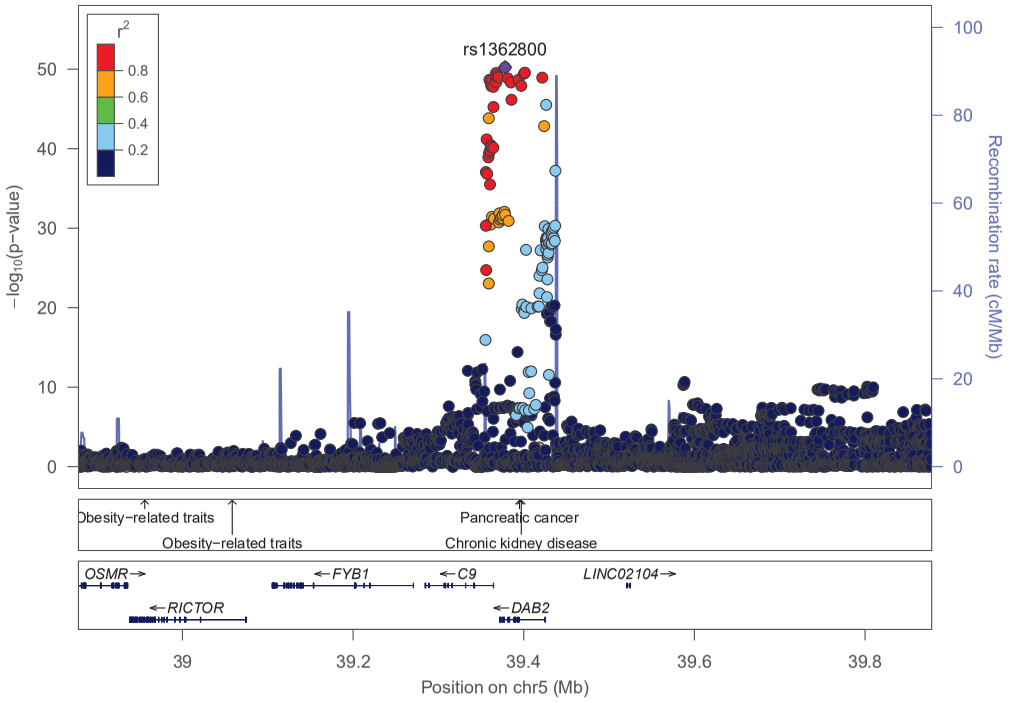

rs223471
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
model assessment of beta−cell function (interaction)
Ulcerative colitis
Serum dimethylarginine levels (asymmetric)
Testicular germ cell tumor
Testicular germ cell t
3 GWAS hits omitted
SLC39A8
NFKB1
MANBA
UBE2D3
SLC9B2
CENPE
LOC105377621
LOC102723704
SLC9B1
BDH2
LOC105377348
CISD2
Position on chr4 (Mb)

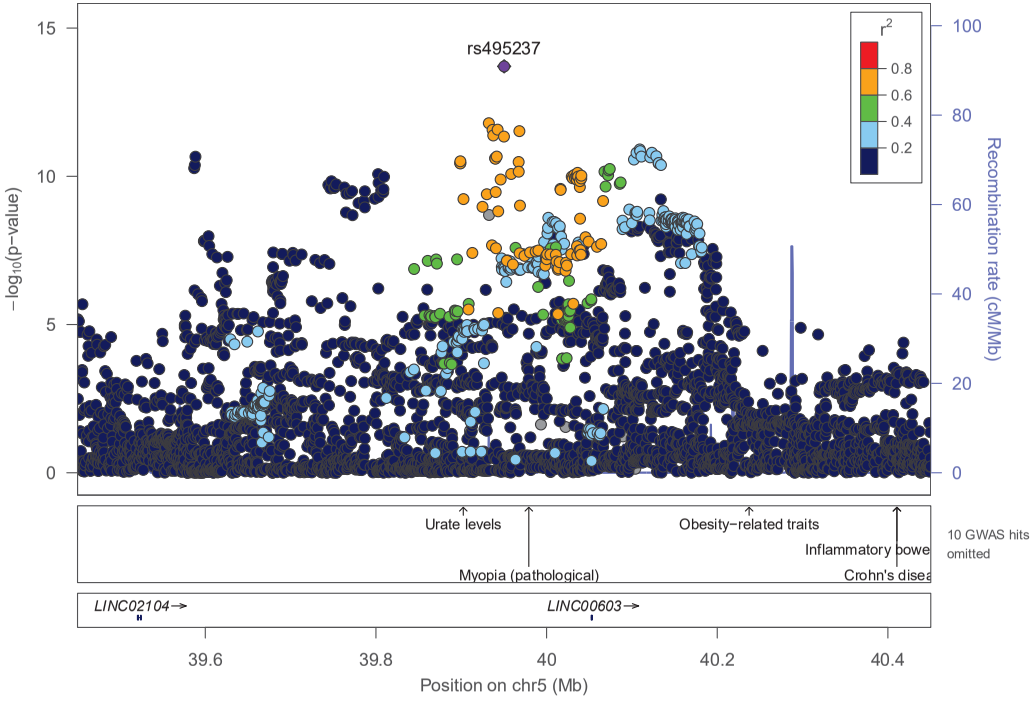

rs55929207
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
obstruction
Systemic lupus erythematosus
RPL34−AS1
ETNPPL
COL25A1
LOC101929621
RPL34
OSTC
Position on chr4 (Mb)

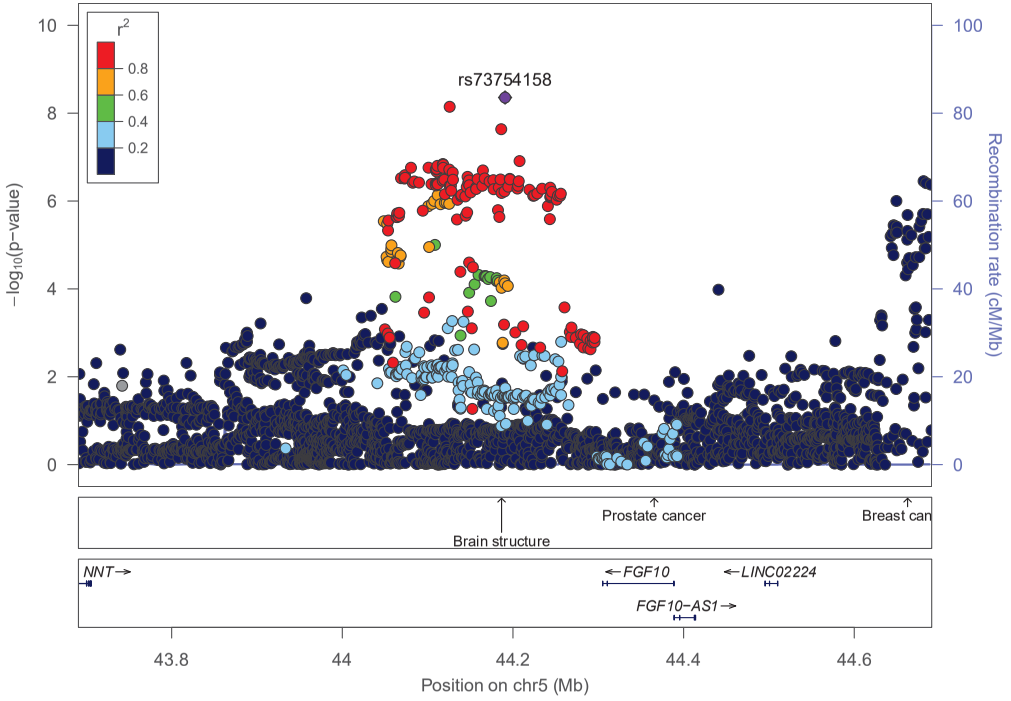

rs71606723
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
UGT8
NDST4
MIR577
Position on chr4 (Mb)

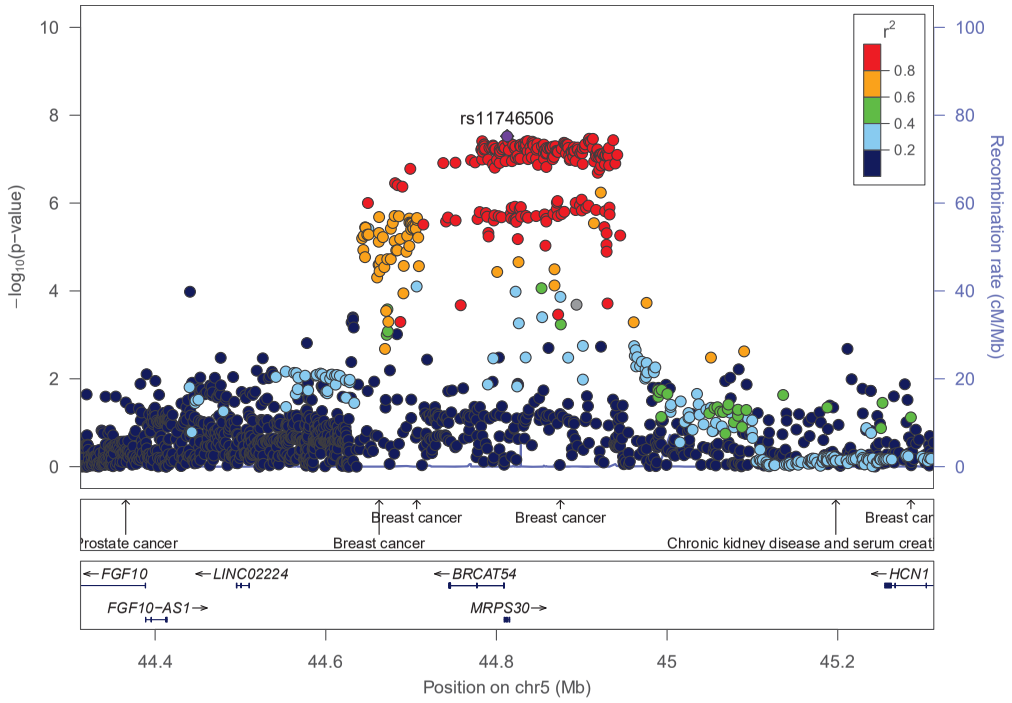

rs13159523
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Fat distribution (HIV)
Obesity−related traits
Ulcerative colitis
mean corpuscular hemoglobin
2 GWAS hits omitted
PLEKHG4B
EXOC3−AS1
LOC100996325
ZDHHC11
LOC100506688
LRRC14B
AHRR
SLC9A3
CEP72
ZDHHC11B
BRD9
NKD2
CCDC127
EXOC3
TPPP
TRIP13
SLC12A7
SDHA
PP7080
MIR4635
HRAT5
SLC9A3−AS1
CTD−3080P12.3
PDCD6
MIR4456
Position on chr5 (Mb)

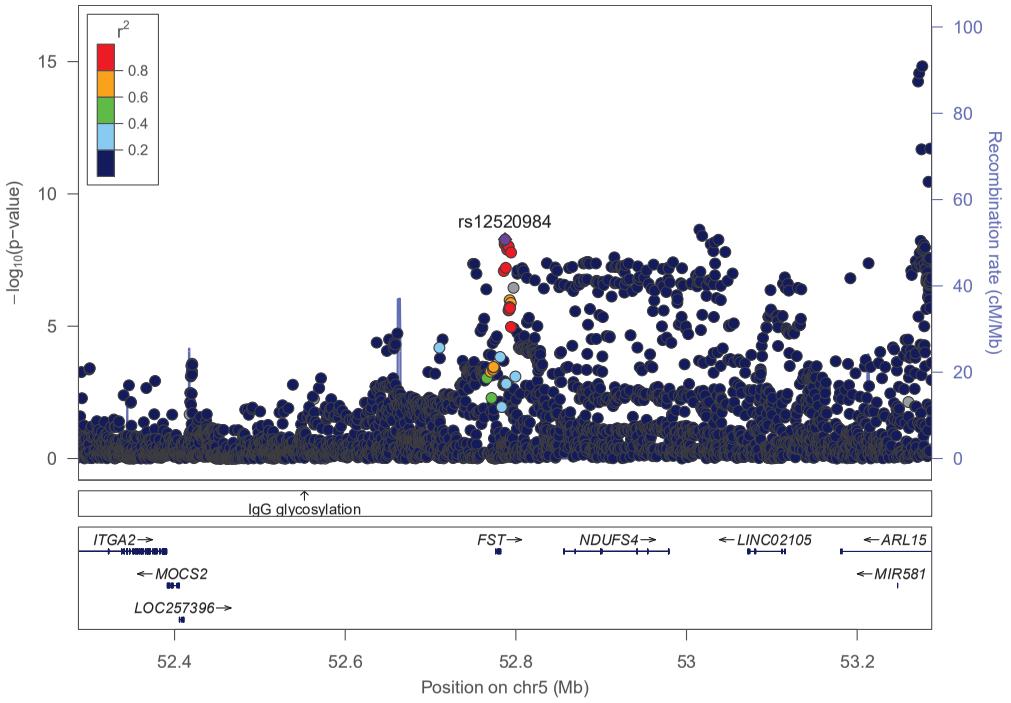

rs13157326
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Left ventricular mass
Response to angiotensin II recep
←AMACR
←C1QTNF3−AMACR
←C1QTNF3
RAI14→
←RAD1
MIR7641−2→
BRIX1→
TTC23L→
DNAJC21→
←AGXT2
Position on chr5 (Mb)

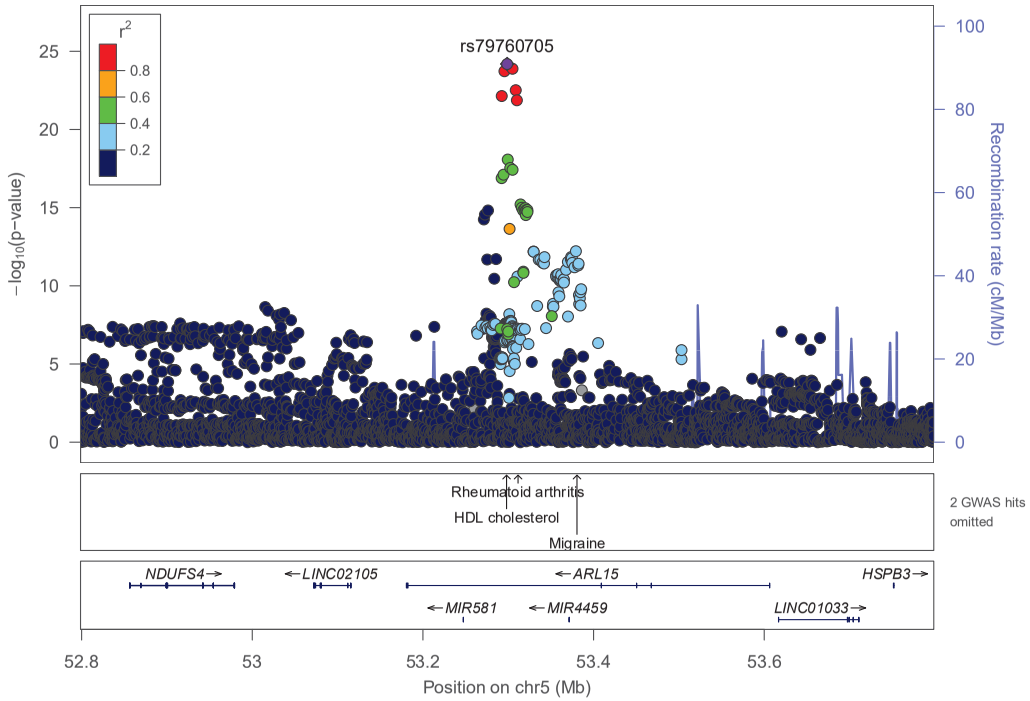

rs1362800
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Obesity−related traits
Pancreatic cancer
Chronic kidney disease
OSMR→
←FYB1
←C9
LINC02104→
←RICTOR
←DAB2
Position on chr5 (Mb)

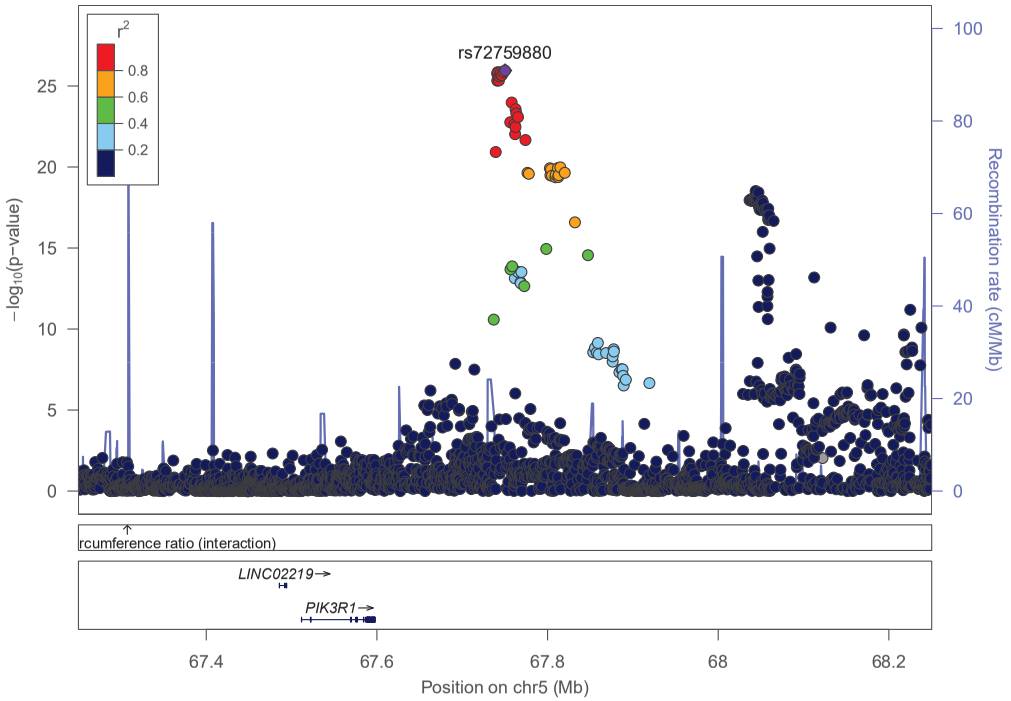

rs495237
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Urate levels
Myopia (pathological)
Obesity−related traits
Inflammatory bowe
Crohn's disea
10 GWAS hits
omitted
LINC02104→
LINC00603→
Position on chr5 (Mb)

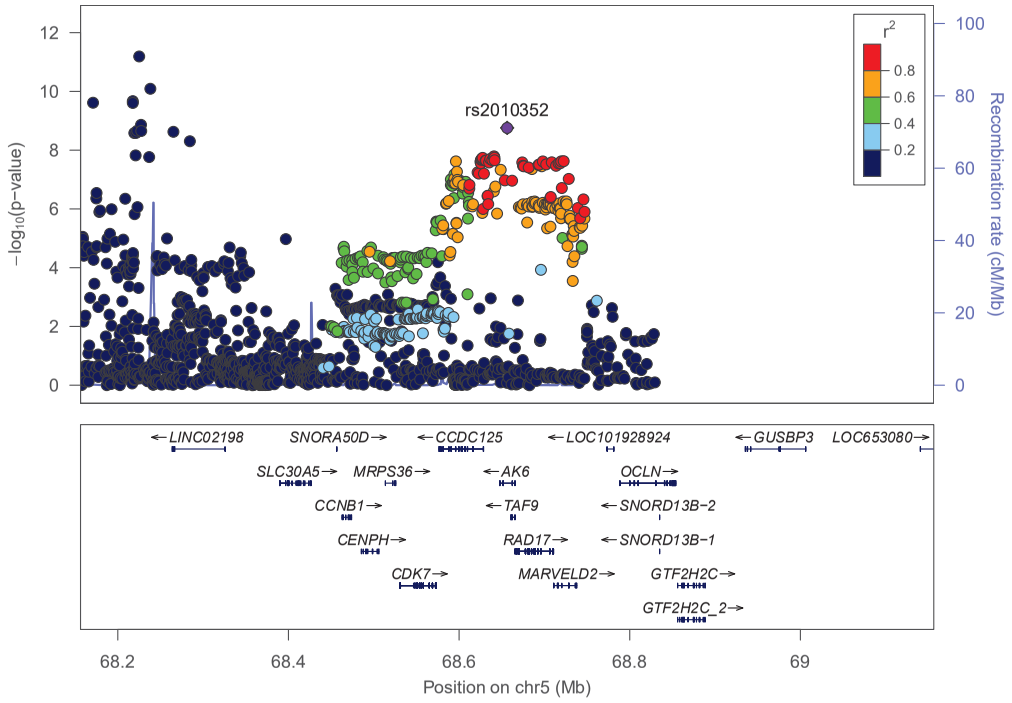

rs73754158
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Brain structure
Prostate cancer
Breast can
NNT→
←FGF10
←LINC02224
FGF10−AS1→
Position on chr5 (Mb)

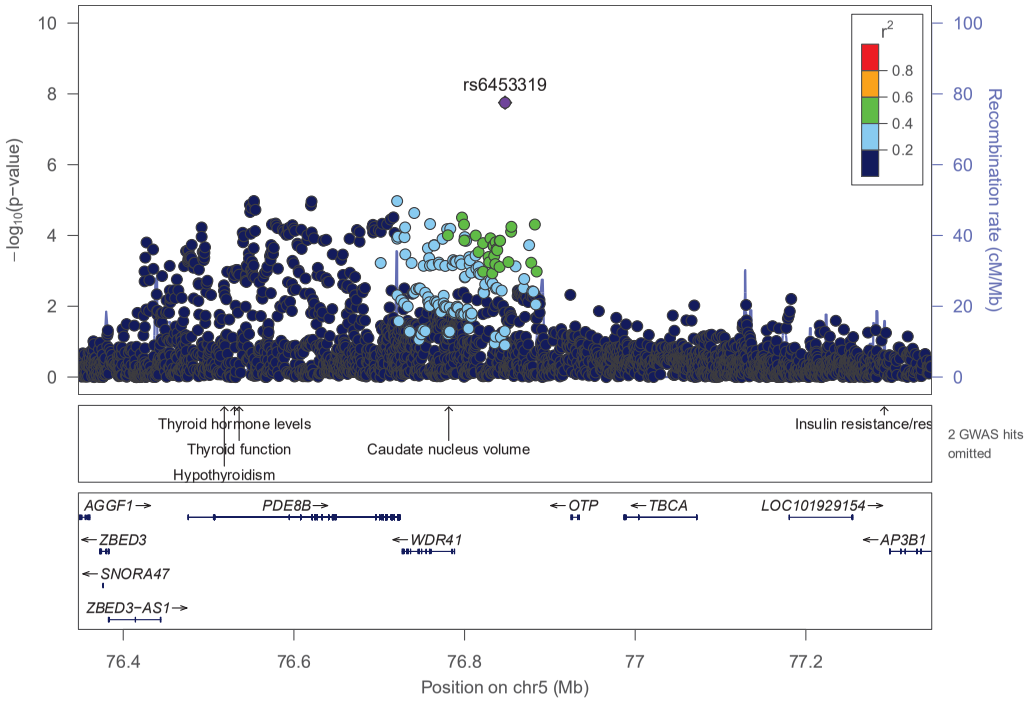

rs11746506
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Breast cancer
Breast cancer
Breast cancer
Chronic kidney disease and serum creat
Breast car
FGF10
LINC02224
BRCAT54
HCN1
FGF10−AS1
MRPS30
Position on chr5 (Mb)

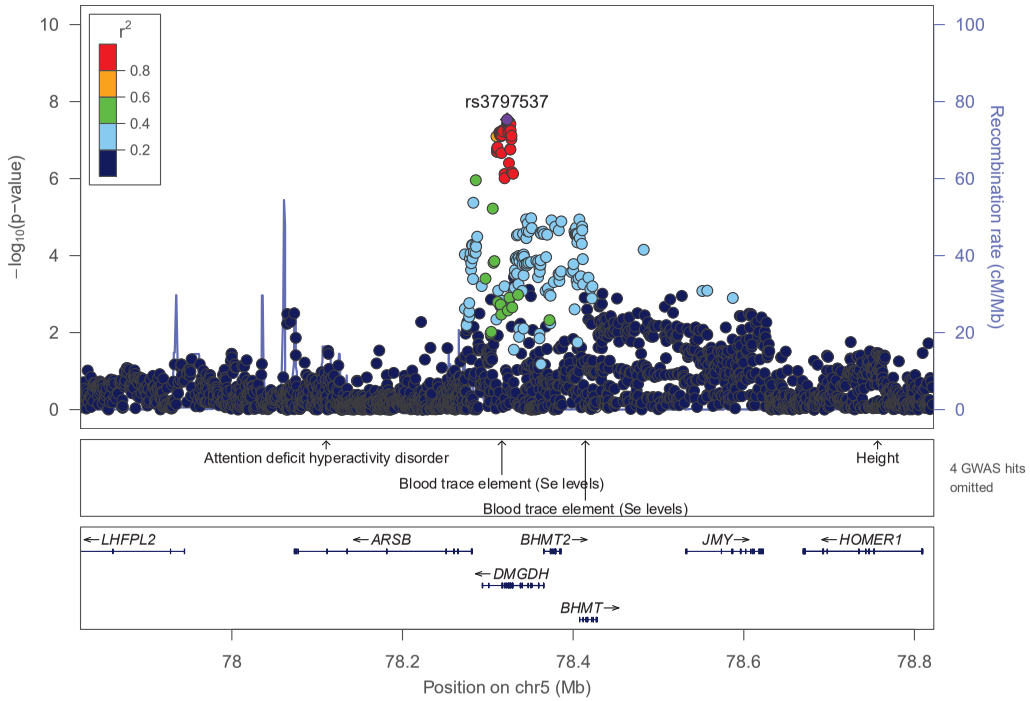

rs12520984
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
IgG glycosylation
ITGA2
FST
NDUFS4
LINC02105
ARL15
MOCS2
MIR581
LOC257396
Position on chr5 (Mb)

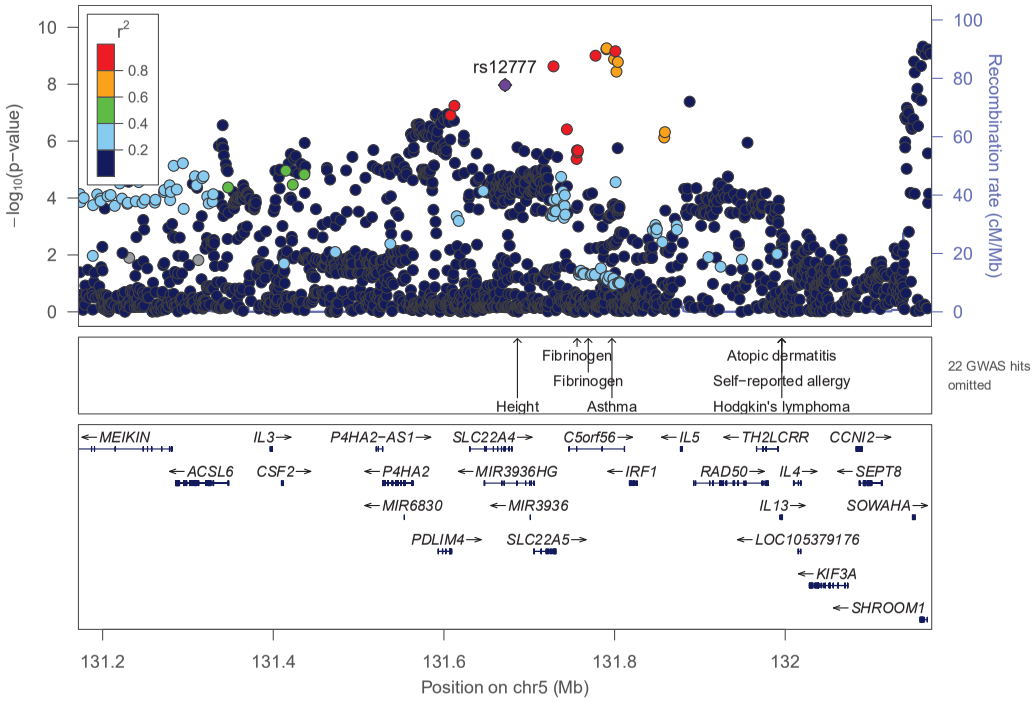

rs79760705
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Rheumatoid arthritis
HDL cholesterol
Migraine
2 GWAS hits
omitted
NDUFS4
LINC02105
ARL15
HSPB3
MIR581
MIR4459
LINC01033
Position on chr5 (Mb)

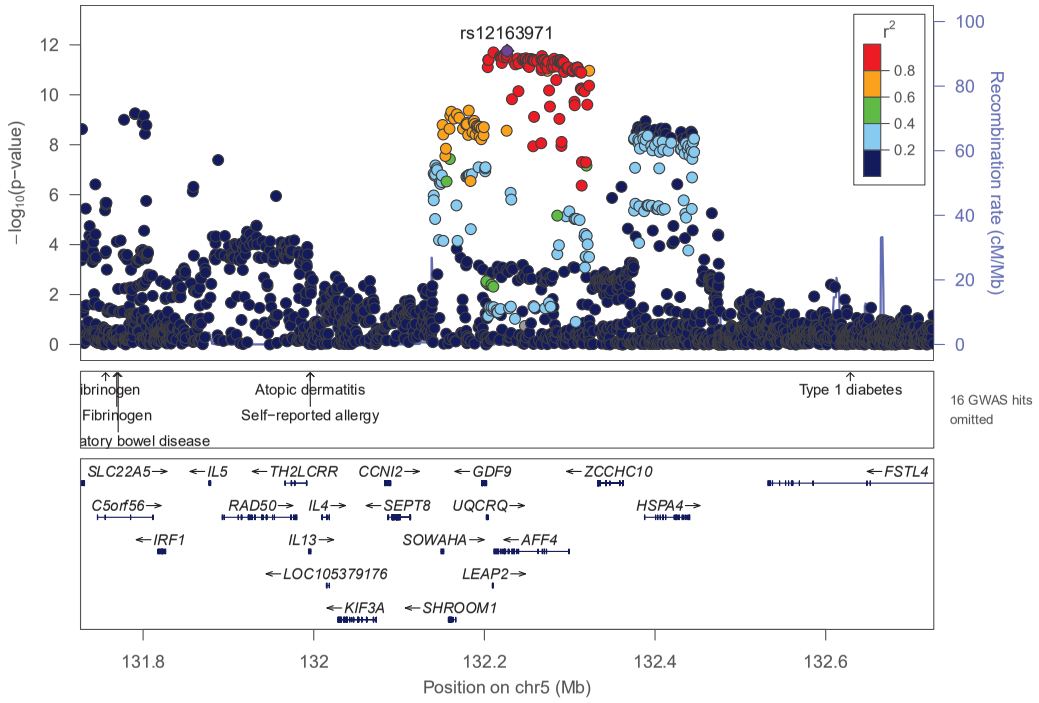

rs72759880
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
rcumference ratio (interaction)
LINC02219
PIK3R1
Position on chr5 (Mb)

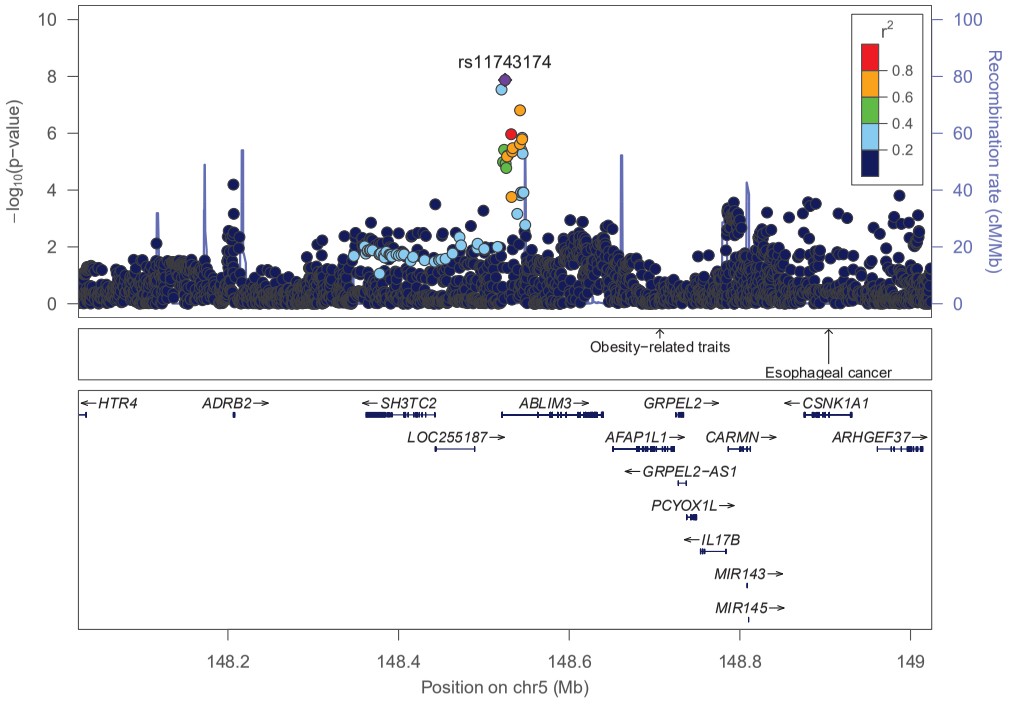

rs2010352
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
LINC02198
SNORA50D
CCDC125
LOC101928924
GUSBP3
LOC653080
SLC30A5
MRPS36
AK6
OCLN
CCNB1
TAF9
SNORD13B−2
CENPH
RAD17
SNORD13B−1
CDK7
MARVELD2
GTF2H2C
GTF2H2C_2
Position on chr5 (Mb)

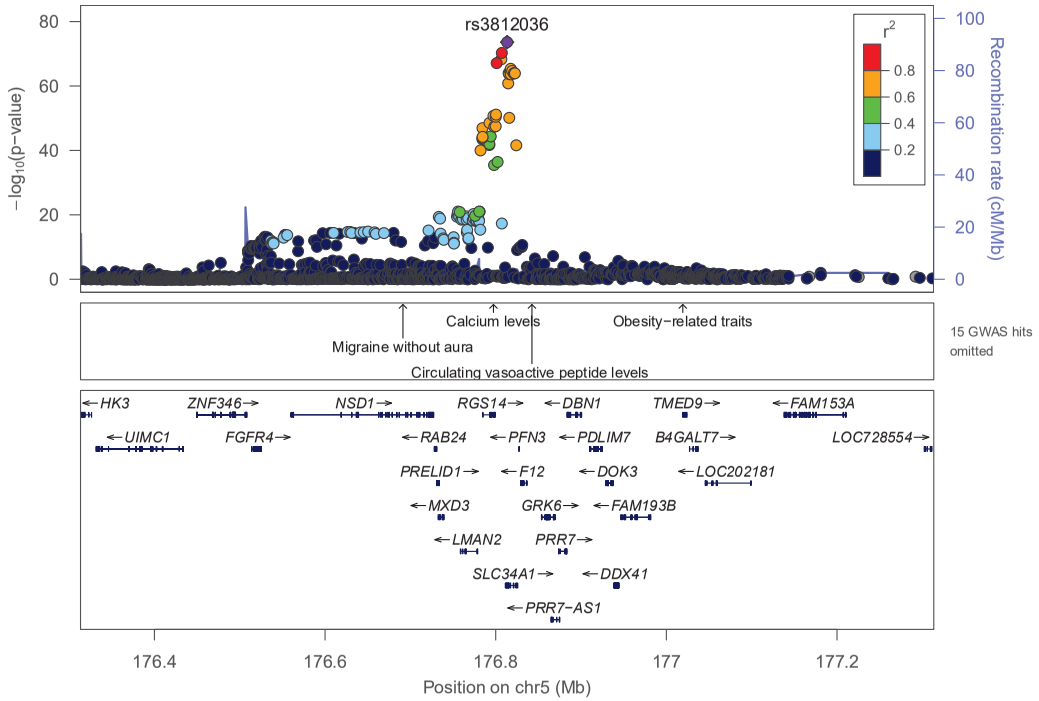

rs6453319
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Thyroid hormone levels
Thyroid function
Hypothyroidism
Caudate nucleus volume
Insulin resistance/res
2 GWAS hits omitted
AGGF1
PDE8B
OTP
TBCA
LOC101929154
ZBED3
WDR41
AP3B1
SNORA47
ZBED3−AS1
Position on chr5 (Mb)

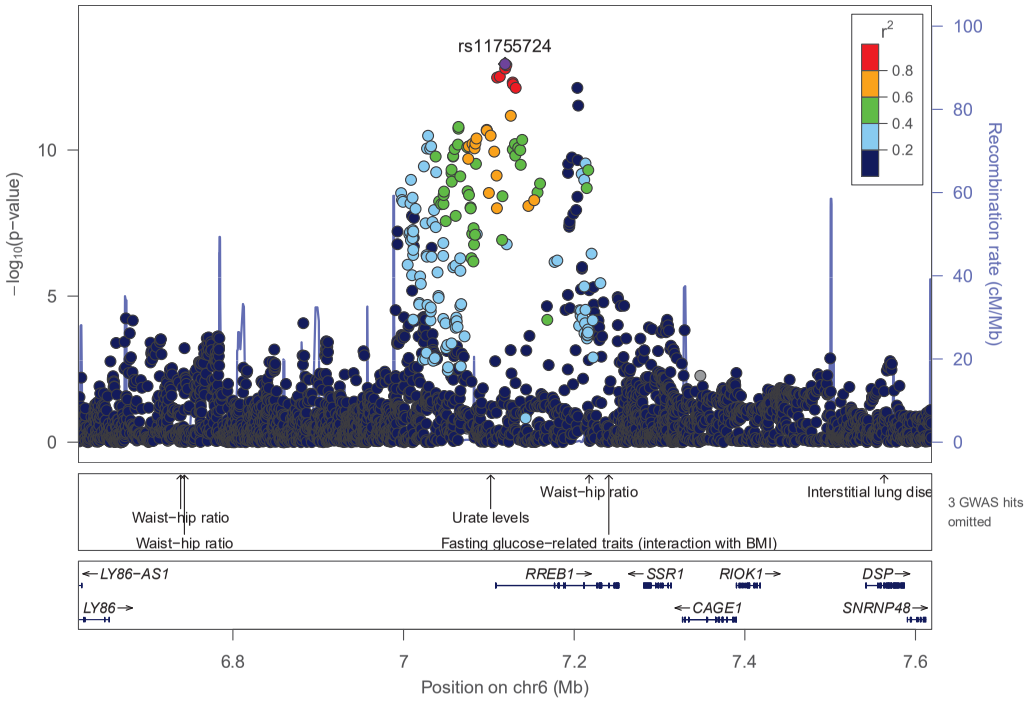

rs3797537
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Attention deficit hyperactivity disorder
Blood trace element (Se levels)
Blood trace element (Se levels)
Height
4 GWAS hits omitted
LHFPL2
ARSB
BHMT2
JMY
HOMER1
DMGDH
BHMT
Position on chr5 (Mb)

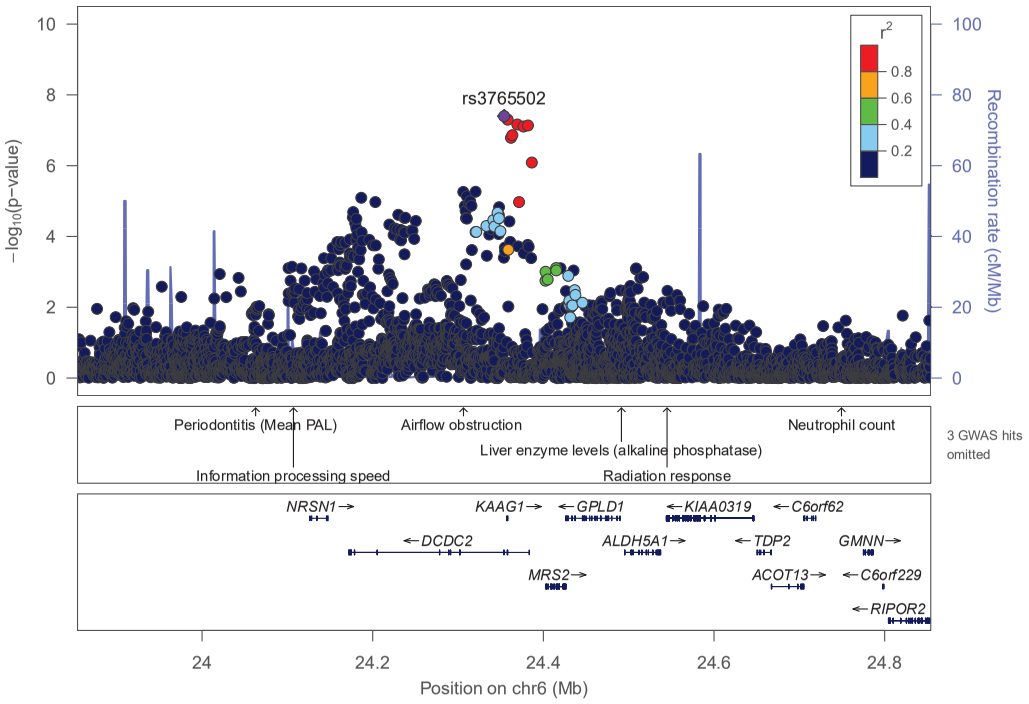

rs12777
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Height
Fibrinogen
Fibrinogen
Asthma
Atopic dermatitis
Self−reported allergy
Hodgkin's lymphoma
22 GWAS hits omitted
MEIKIN
IL3
P4HA2−AS1
SLC22A4
C5orf56
IL5
TH2LCRR
CCNI2
ACSL6
CSF2
P4HA2
MIR3936HG
IRF1
RAD50
IL4
SEPT8
MIR6830
MIR3936
IL13
SOWAHA
PDLIM4
SLC22A5
LOC105379176
KIF3A
SHROOM1
Position on chr5 (Mb)

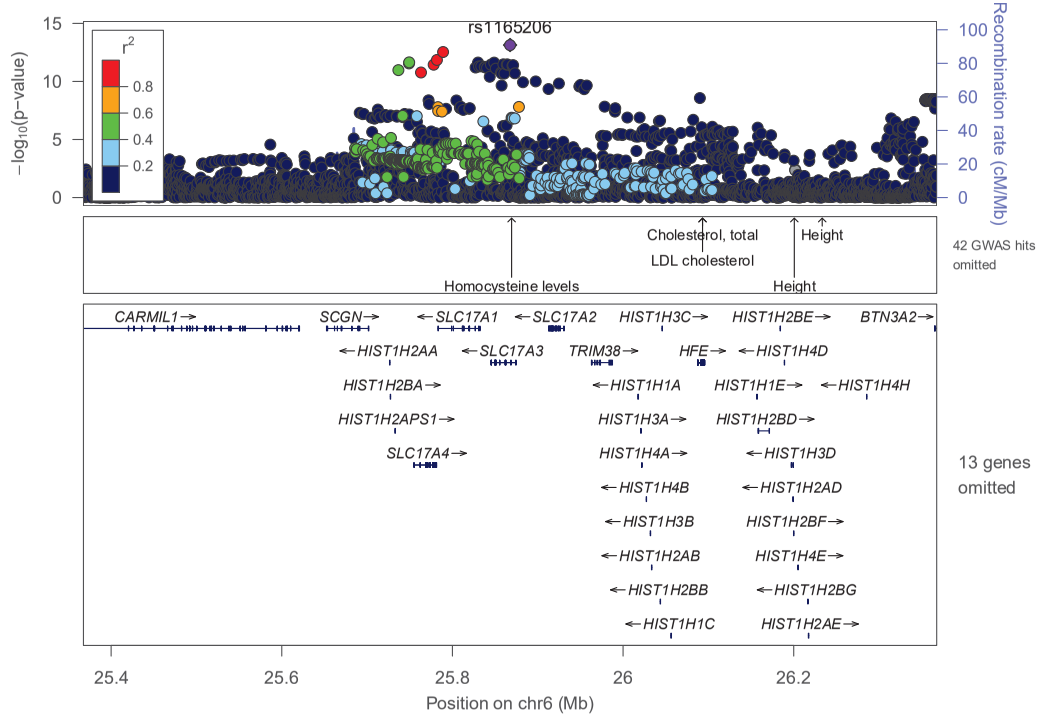

rs12163971
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ibrinogen
Fibrinogen
atory bowel disease
Atopic dermatitis
Self−reported allergy
Type 1 diabetes
16 GWAS hits omitted
SLC22A5→ ←IL5 ←TH2LCRR CCNI2→ ←GDF9 ←ZCCHC10 ←FSTL4
C5orf56→ RAD50→ IL4→ ←SEPT8 UQCRQ→ HSPA4→
←IRF1 IL13→ SOWAHA→ ←AFF4
←LOC105379176 LEAP2→
←KIF3A ←SHROOM1
131.8
132
132.2
132.4
132.6
Position on chr5 (Mb)

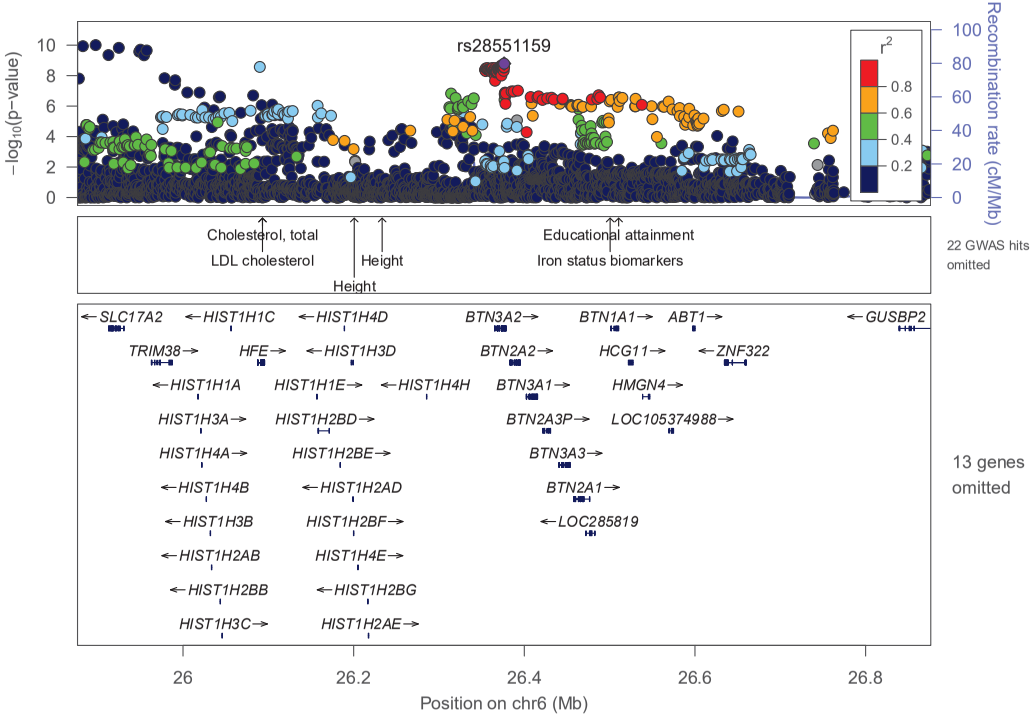

rs11743174
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Esophageal cancer
←HTR4 ADRB2→ ←SH3TC2 ABLIM3→ GRPEL2→ ←CSNK1A1
LOC255187→ AFAP1L1→ CARMN→ ARHGEF37→
←GRPEL2−AS1
PCYOX1L→
←IL17B
MIR143→
MIR145→
148.2
148.4
148.6
148.8
149
Position on chr5 (Mb)

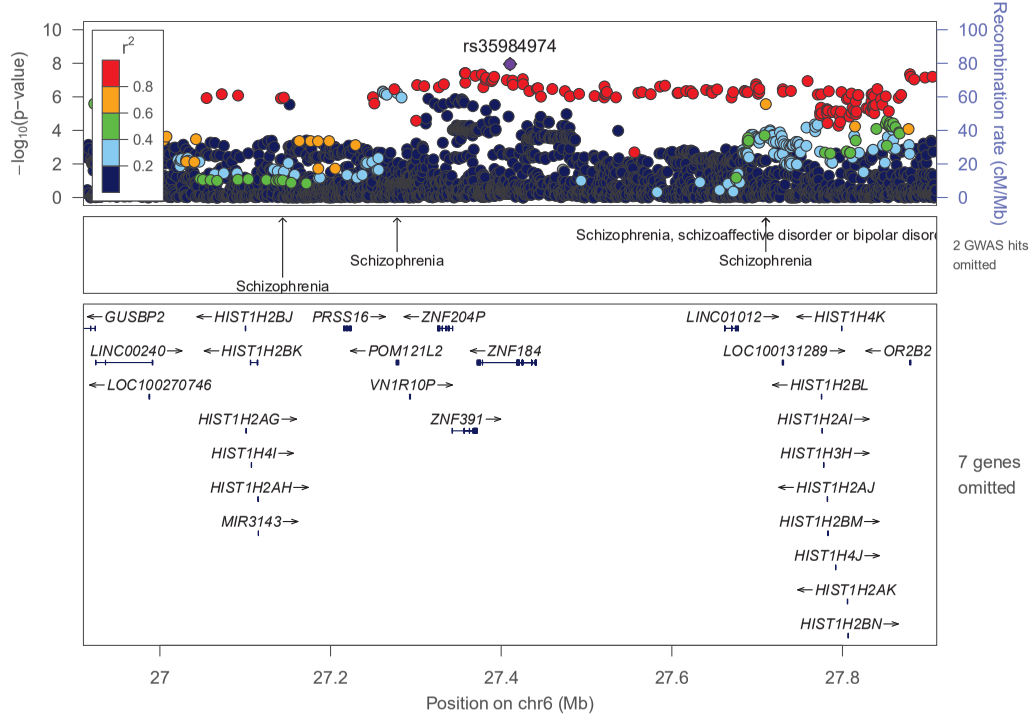

rs3812036
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Migraine without aura
Calcium levels
Circulating vasoactive peptide levels
Obesity−related traits
15 GWAS hits omitted
←HK3 ZNF346→ NSD1→ RGS14→ ←DBN1 TMED9→ ←FAM153A
←UIMC1 FGFR4→ ←RAB24 ←PFN3 ←PDLIM7 B4GALT7→ LOC728554→
PRELID1→ ←F12 ←DOK3 ←LOC202181
←MXD3 GRK6→ ←FAM193B
←LMAN2 PRR7→
SLC34A1→ ←DDX41
←PRR7−AS1
176.4
176.6
176.8
177
177.2
Position on chr5 (Mb)

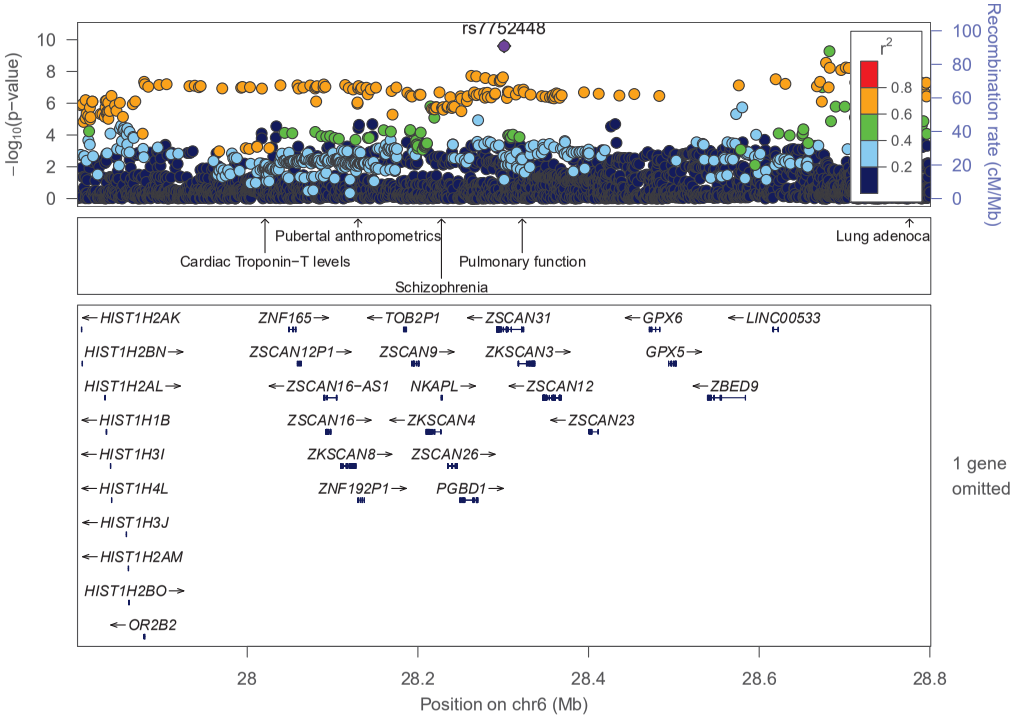

rs11755724
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Waist−hip ratio
Waist−hip ratio
Urate levels
Fasting glucose−related traits (interaction with BMI)
Waist−hip ratio
Interstitial lung dise
3 GWAS hits omitted
←LY86−AS1
LY86→
RREB1→ ←SSR1 RIOK1→ DSP→
←CAGE1 SNRNP48→
6.8
7
7.2
7.4
7.6
Position on chr6 (Mb)

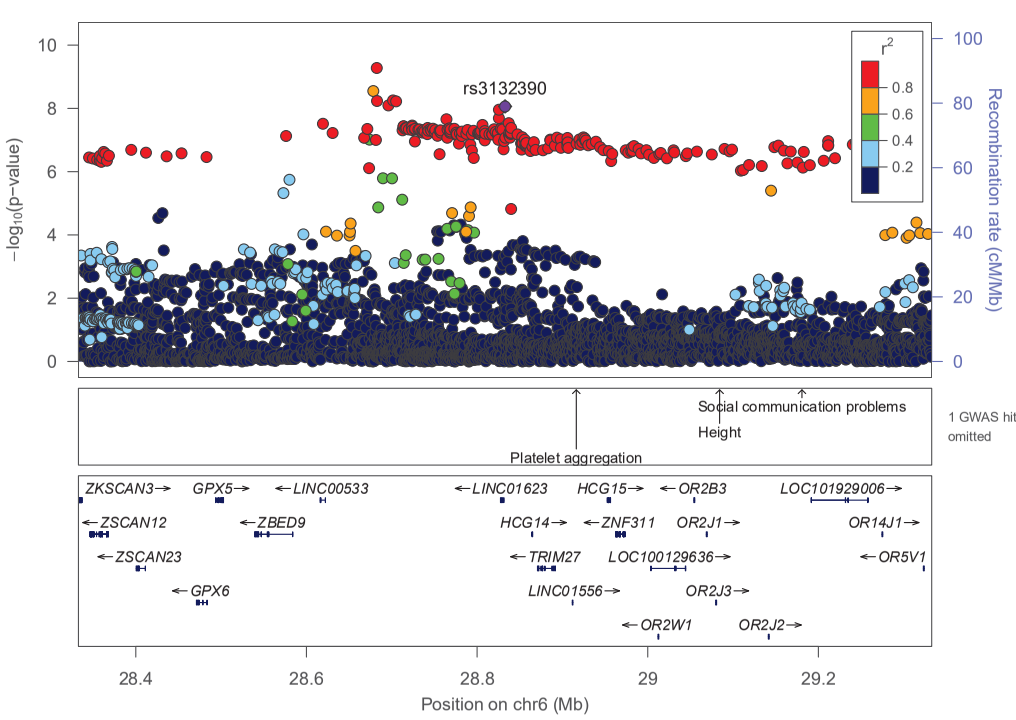

rs3765502
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Periodontitis (Mean PAL)
Airflow obstruction
Neutrophil count
Liver enzyme levels (alkaline phosphatase)
Information processing speed
Radiation response
3 GWAS hits omitted
NRSN1
KAAG1
GPLD1
KIAA0319
C6orf62
DCDC2
ALDH5A1
TDP2
GMNN
MRS2
ACOT13
C6orf229
RIPOR2
Position on chr6 (Mb)

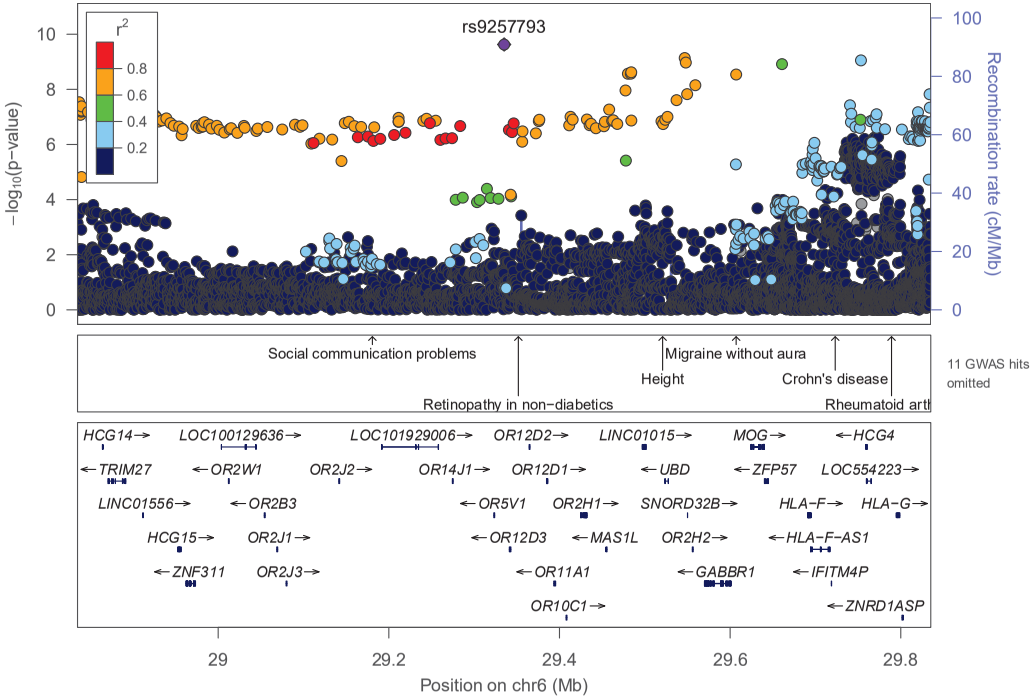

rs1165206
−log10(p−value)
Recombination rate (cM/Mb)
r2
Cholesterol, total
LDL cholesterol
Height
Homocysteine levels
Height
42 GWAS hits omitted
CARMIL1
SCGN
SLC17A1
SLC17A2
HIST1H3C
HIST1H2BE
BTN3A2
HIST1H2AA
SLC17A3
TRIM38
HFE
HIST1H4D
HIST1H2BA
HIST1H1A
HIST1H1E
HIST1H4H
HIST1H2APS1
HIST1H3A
HIST1H2BD
SLC17A4
HIST1H4A
HIST1H3D
HIST1H4B
HIST1H2AD
HIST1H3B
HIST1H2BF
HIST1H2AB
HIST1H4E
HIST1H2BB
HIST1H2BG
HIST1H1C
HIST1H2AE
13 genes omitted
Position on chr6 (Mb)

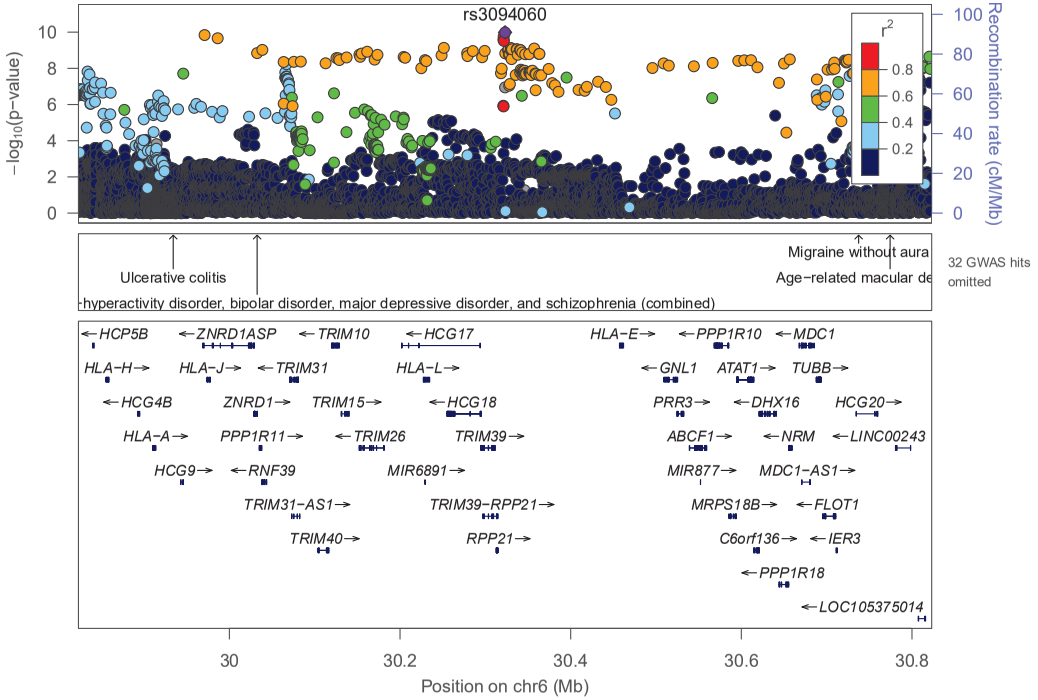

rs28551159
−log10(p−value)
Recombination rate (cM/Mb)
r2
Cholesterol, total
LDL cholesterol
Height
Height
Educational attainment
Iron status biomarkers
22 GWAS hits omitted
SLC17A2
HIST1H1C
HIST1H4D
BTN3A2
BTN1A1
ABT1
GUSBP2
TRIM38
HFE
HIST1H3D
BTN2A2
HCG11
ZNF322
HIST1H1A
HIST1H1E
HIST1H4H
BTN3A1
HMGN4
HIST1H3A
HIST1H2BD
BTN2A3P
LOC105374988
HIST1H4A
HIST1H2BE
BTN3A3
HIST1H4B
HIST1H2AD
BTN2A1
HIST1H3B
HIST1H2BF
LOC285819
HIST1H2AB
HIST1H4E
HIST1H2BB
HIST1H2BG
HIST1H3C
HIST1H2AE
13 genes omitted
Position on chr6 (Mb)

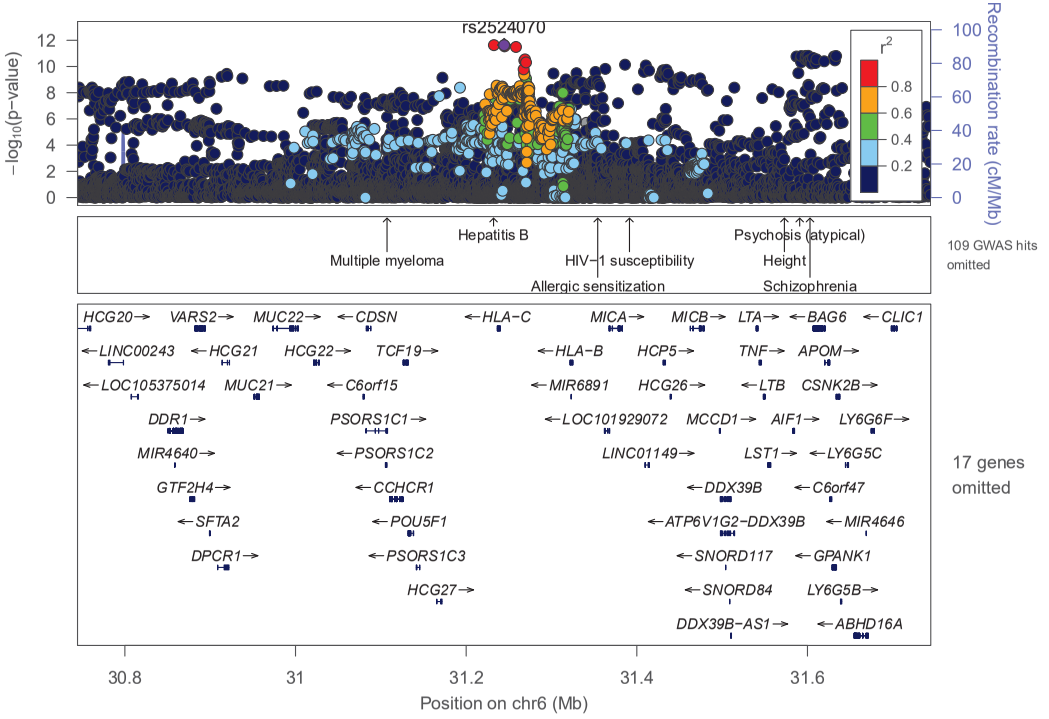

rs35984974
−log10(p−value)
Recombination rate (cM/Mb)
r2
Schizophrenia
Schizophrenia
Schizophrenia, schizoaffective disorder or bipolar disor
Schizophrenia
2 GWAS hits omitted
GUSBP2
HIST1H2BJ
PRSS16
ZNF204P
LINC01012
HIST1H4K
LINC00240
HIST1H2BK
POM121L2
ZNF184
LOC100131289
OR2B2
LOC100270746
VN1R10P
HIST1H2BL
HIST1H2AG
ZNF391
HIST1H2AI
HIST1H4I
HIST1H3H
HIST1H2AH
HIST1H2AJ
MIR3143
HIST1H2BM
HIST1H4J
HIST1H2AK
HIST1H2BN
7 genes omitted
Position on chr6 (Mb)

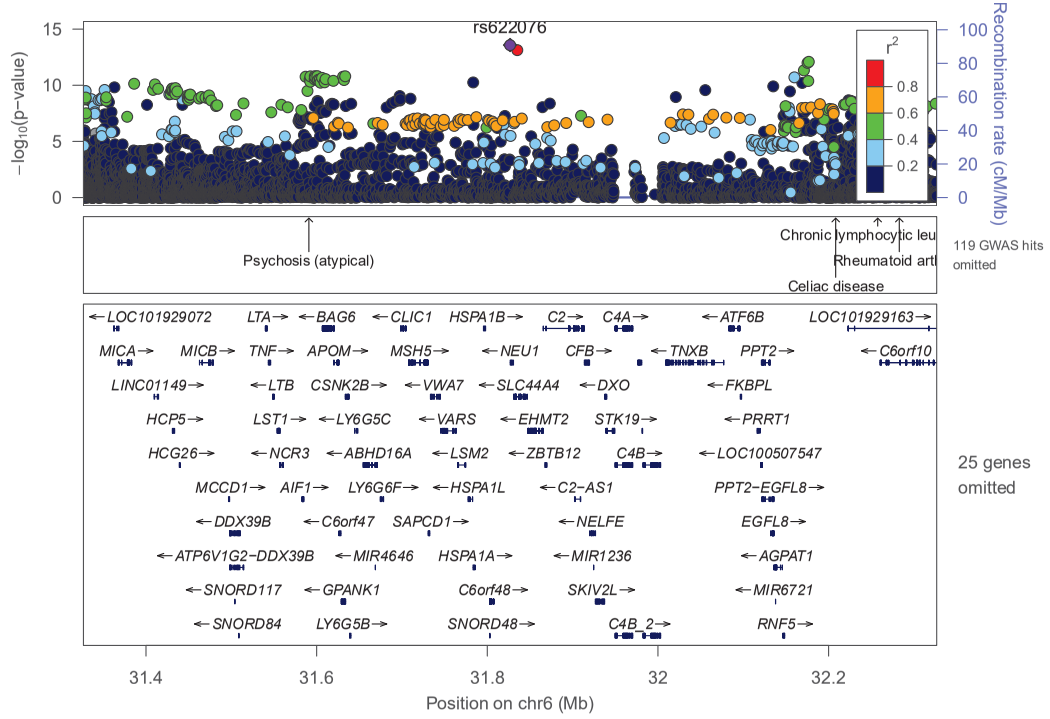

rs7752448
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Pubertal anthropometrics
Cardiac Troponin−T levels
Schizophrenia
Pulmonary function
Lung adenoca
HIST1H2AK
ZNF165
TOB2P1
ZSCAN31
GPX6
LINC00533
HIST1H2BN
ZSCAN12P1
ZSCAN9
ZKSCAN3
GPX5
HIST1H2AL
ZSCAN16−AS1
NKAPL
ZSCAN12
ZBED9
HIST1H1B
ZSCAN16
ZKSCAN4
ZSCAN23
HIST1H3I
ZKSCAN8
ZSCAN26
HIST1H4L
ZNF192P1
PGBD1
HIST1H3J
HIST1H2AM
HIST1H2BO
OR2B2
1 gene
omitted
Position on chr6 (Mb)

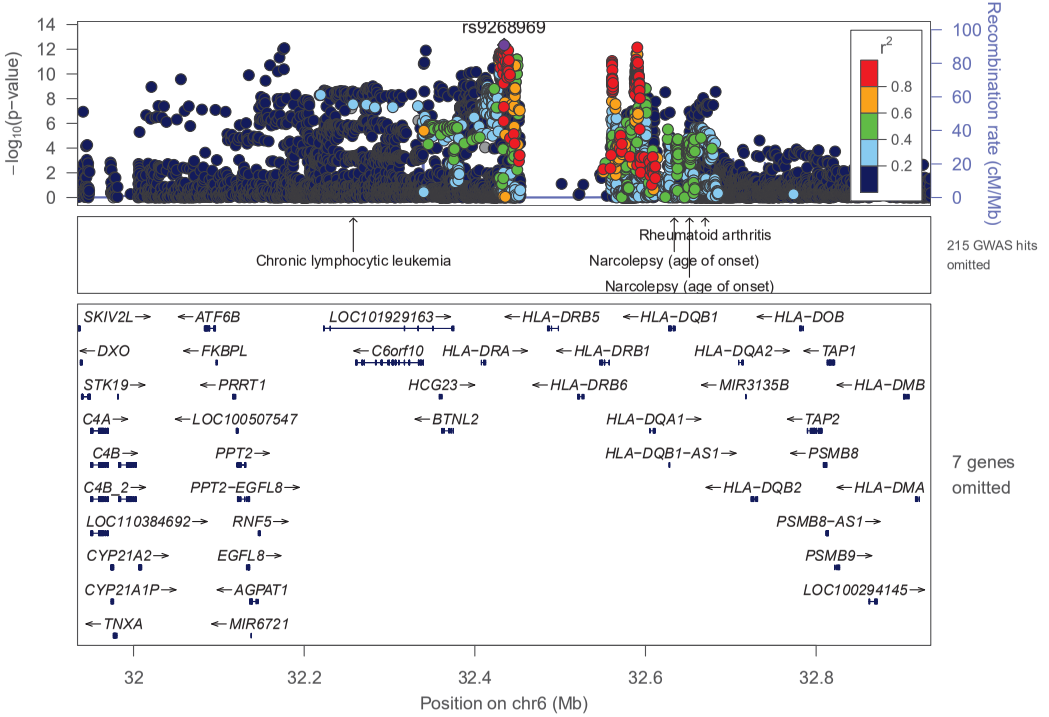

rs3132390
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Platelet aggregation
Social communication problems
Height
1 GWAS hit
omitted
ZKSCAN3
GPX5
LINC00533
LINC01623
HCG15
OR2B3
LOC101929006
ZSCAN12
ZBED9
HCG14
ZNF311
OR2J1
OR14J1
ZSCAN23
TRIM27
LOC100129636
OR5V1
GPX6
LINC01556
OR2J3
OR2W1
OR2J2
Position on chr6 (Mb)

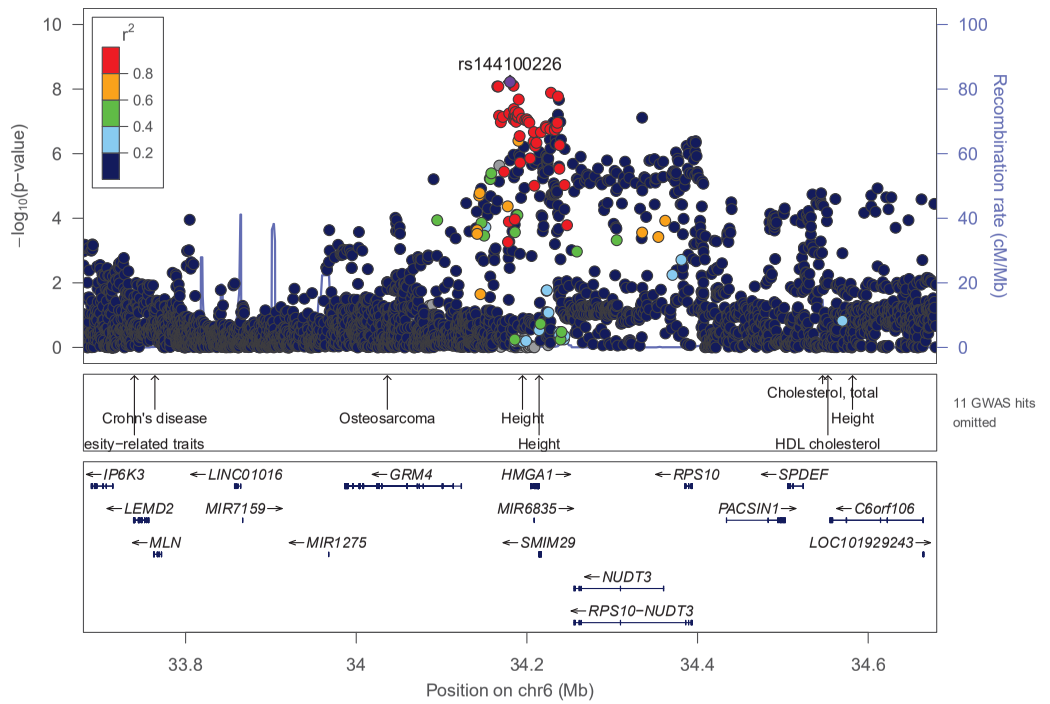

rs9257793
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Social communication problems
Retinopathy in non−diabetics
Migraine without aura
Height
Crohn's disease
Rheumatoid arth
11 GWAS hits
omitted
HCG14
LOC100129636
LOC101929006
OR12D2
LINC01015
MOG
HCG4
TRIM27
OR2W1
OR2J2
OR14J1
OR12D1
UBD
ZFP57
LOC554223
LINC01556
OR2B3
OR5V1
OR2H1
SNORD32B
HLA−F
HLA−G
HCG15
OR2J1
OR12D3
MAS1L
OR2H2
HLA−F−AS1
ZNF311
OR2J3
OR11A1
GABBR1
IFITM4P
OR10C1
ZNRD1ASP
Position on chr6 (Mb)

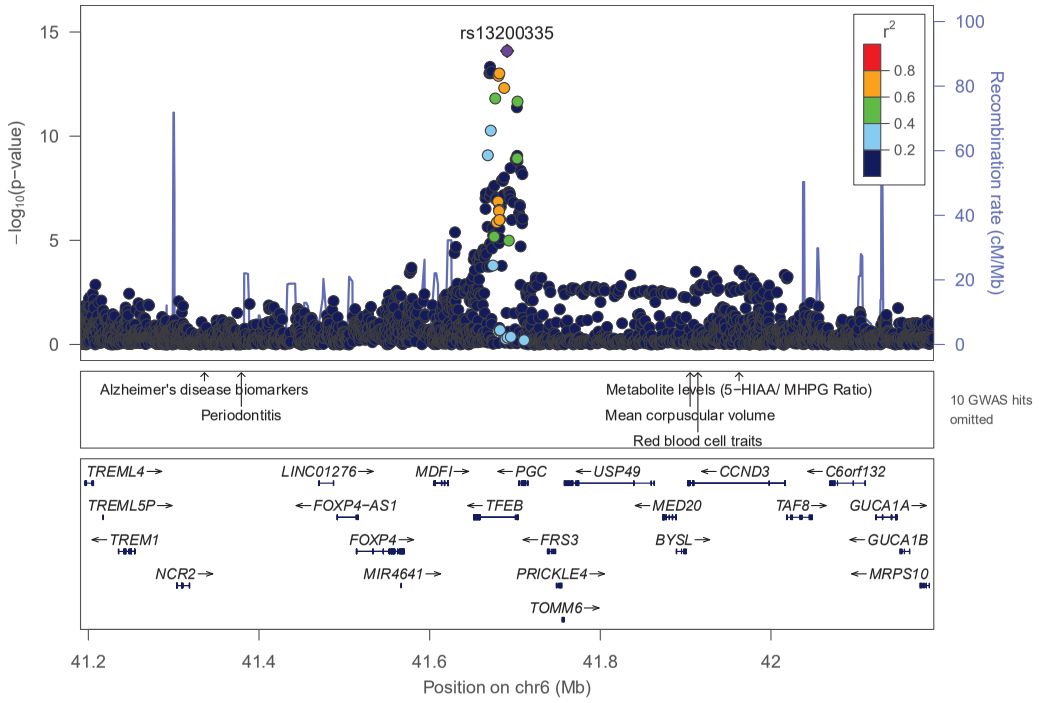

rs3094060
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Ulcerative colitis
hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined)
Migraine without aura
Age−related macular de
32 GWAS hits
omitted
HCP5B
ZNRD1ASP
TRIM10
HCG17
HLA−E
PPP1R10
MDC1
HLA−H
HLA−J
TRIM31
HLA−L
GNL1
ATAT1
TUBB
HCG4B
ZNRD1
TRIM15
HCG18
PRR3
DHX16
HCG20
HLA−A
PPP1R11
TRIM26
TRIM39
ABCF1
NRM
LINC00243
HCG9
RNF39
MIR6891
MIR877
MDC1−AS1
TRIM31−AS1
TRIM39−RPP21
MRPS18B
FLOT1
TRIM40
RPP21
C6orf136
IER3
PPP1R18
LOC105375014
Position on chr6 (Mb)

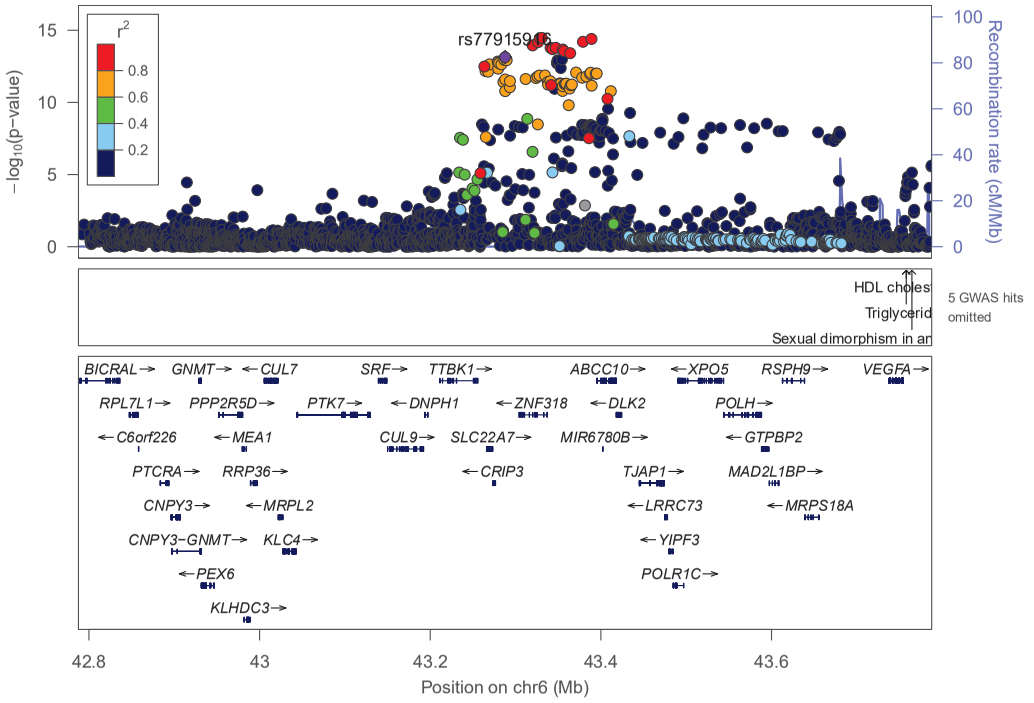

rs2524070
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Multiple myeloma
Hepatitis B
HIV−1 susceptibility
Allergic sensitization
Psychosis (atypical)
Height
Schizophrenia
109 GWAS hits omitted
17 genes omitted
Position on chr6 (Mb)

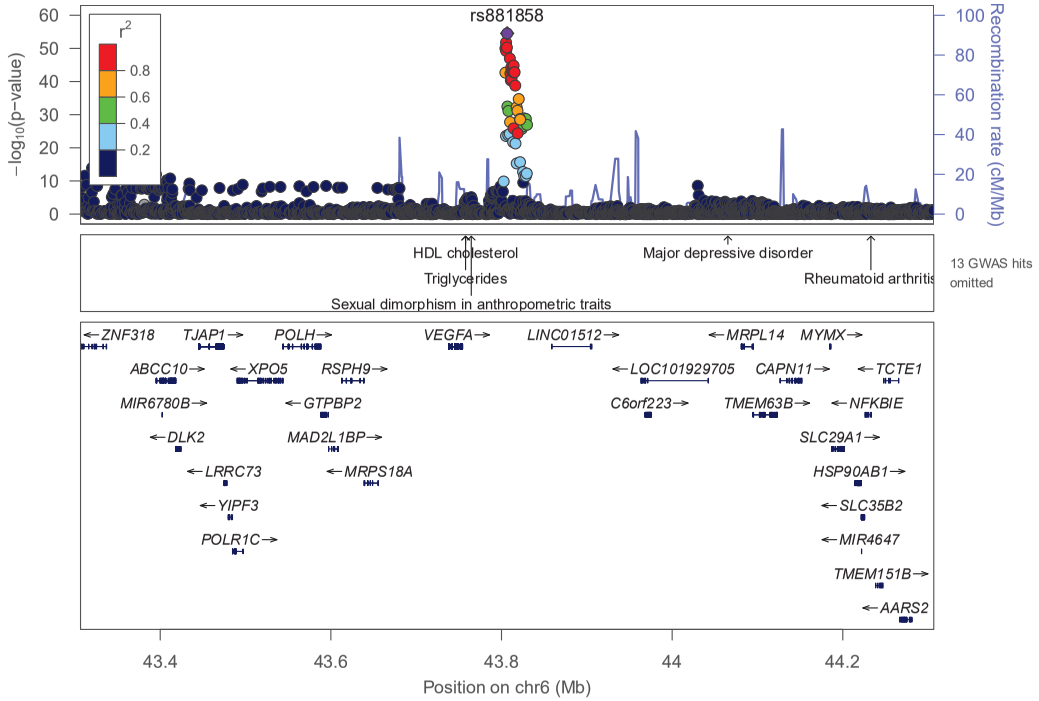

rs622076
−log10(p−value)
Recombination rate (cM/Mb)
r2
Psychosis (atypical)
Chronic lymphocytic leu
Rheumatoid arth
Celiac disease
119 GWAS hits omitted
25 genes omitted
Position on chr6 (Mb)

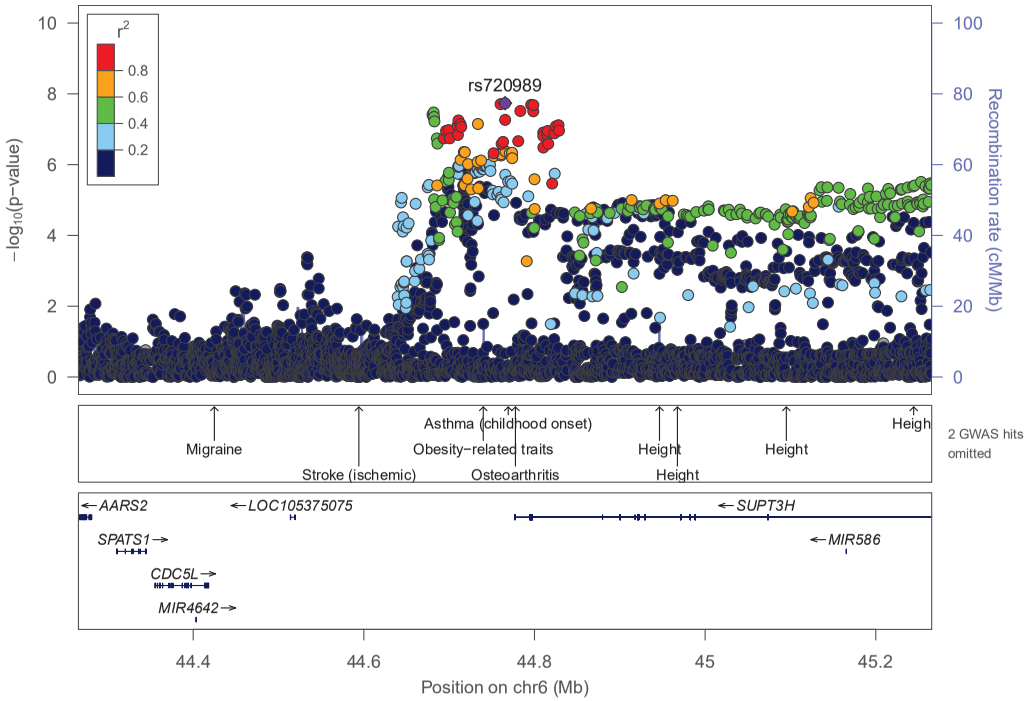

rs9268969
−log10(p−value)
Recombination rate (cM/Mb)
r2
Chronic lymphocytic leukemia
Rheumatoid arthritis
Narcolepsy (age of onset)
Narcolepsy (age of onset)
215 GWAS hits omitted
7 genes omitted
Position on chr6 (Mb)

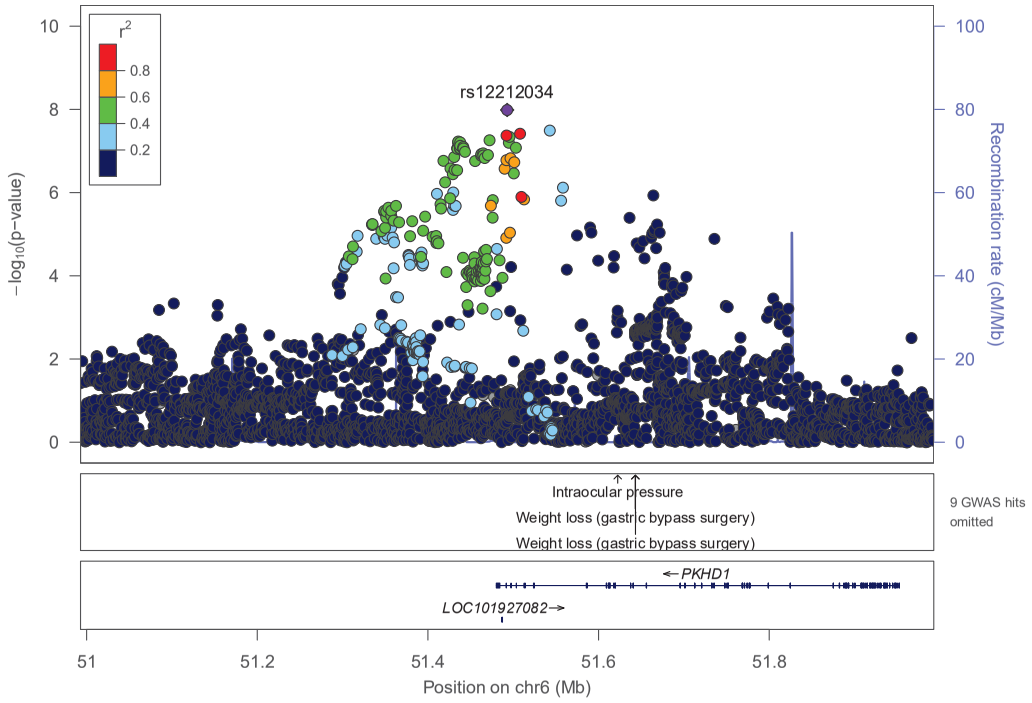

rs144100226
−log10(p−value)
Recombination rate (cM/Mb)
r2
Crohn's disease
esity−related traits
Osteosarcoma
Height
Height
Cholesterol, total
Height
HDL cholesterol
11 GWAS hits omitted
Position on chr6 (Mb)

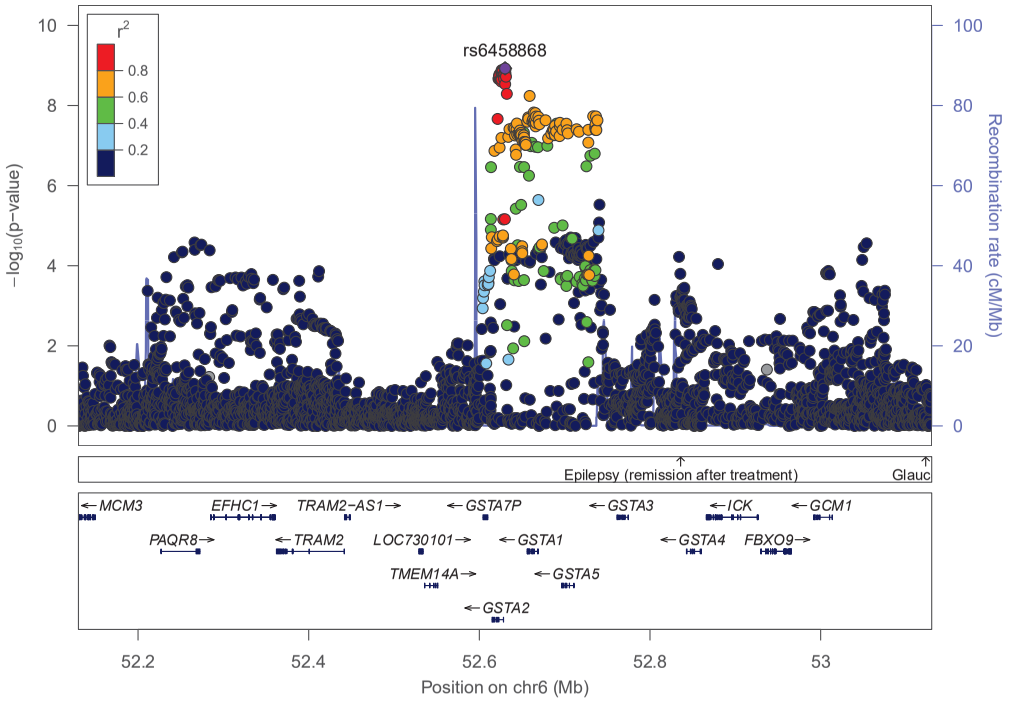

rs13200335
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Alzheimer's disease biomarkers
Periodontitis
Metabolite levels (5−HIAA/ MHPG Ratio)
Mean corpuscular volume
Red blood cell traits
10 GWAS hits omitted
TREML4→ LINC01276→ MDFI→ ←PGC ←USP49 ←CCND3 ←C6orf132
TREML5P→ ←FOXP4−AS1 ←TFEB ←MED20 TAF8→ GUCA1A→
←TREM1 FOXP4→ ←FRS3 BYSL→ ←GUCA1B
NCR2→ MIR4641→ PRICKLE4→ ←MRPS10
TOMM6→
41.2 41.4 41.6 41.8 42
Position on chr6 (Mb)

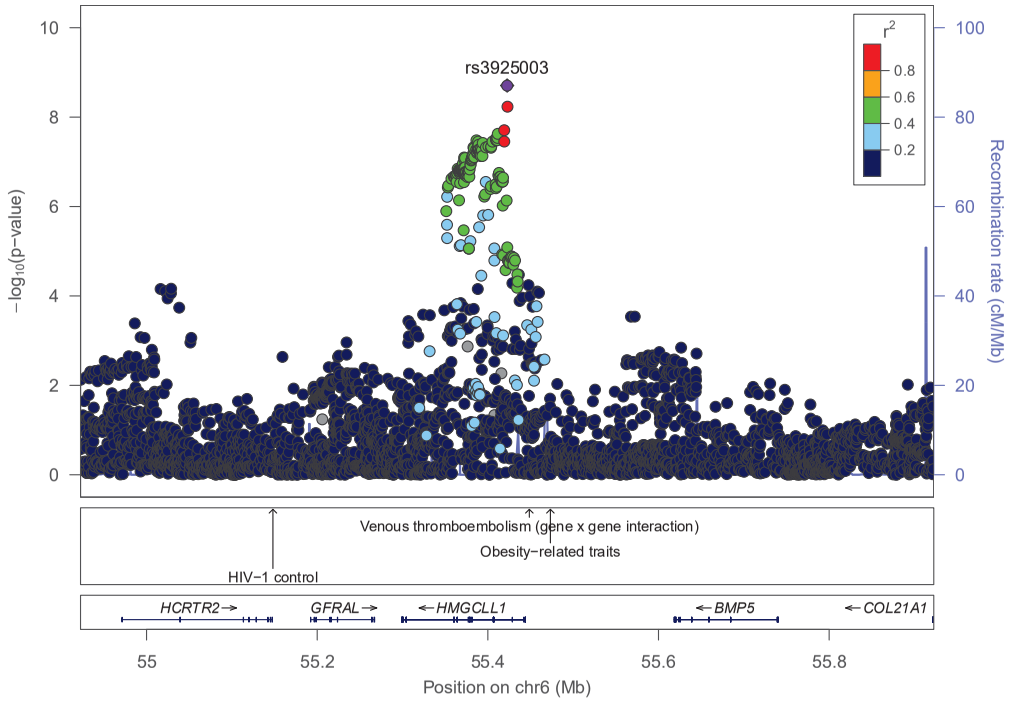

rs77915946
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
HDL choles
Triglycerid
Sexual dimorphism in an
5 GWAS hits omitted
BICRAL→ GNMT→ ←CUL7 SRF→ TTBK1→ ABCC10→ ←XPO5 RSPH9→ VEGFA→
RPL7L1→ PPP2R5D→ PTK7→ ←DNPH1 ←ZNF318 ←DLK2 POLH→
←C6orf226 ←MEA1 CUL9→ SLC22A7→ MIR6780B→ ←GTPBP2
PTCRA→ RRP36→ ←CRIP3 TJAP1→ MAD2L1BP→
CNPY3→ ←MRPL2 ←LRRC73 ←MRPS18A
CNPY3−GNMT→ KLC4→ ←YIPF3
←PEX6 POLR1C→
KLHDC3→
42.8 43 43.2 43.4 43.6
Position on chr6 (Mb)

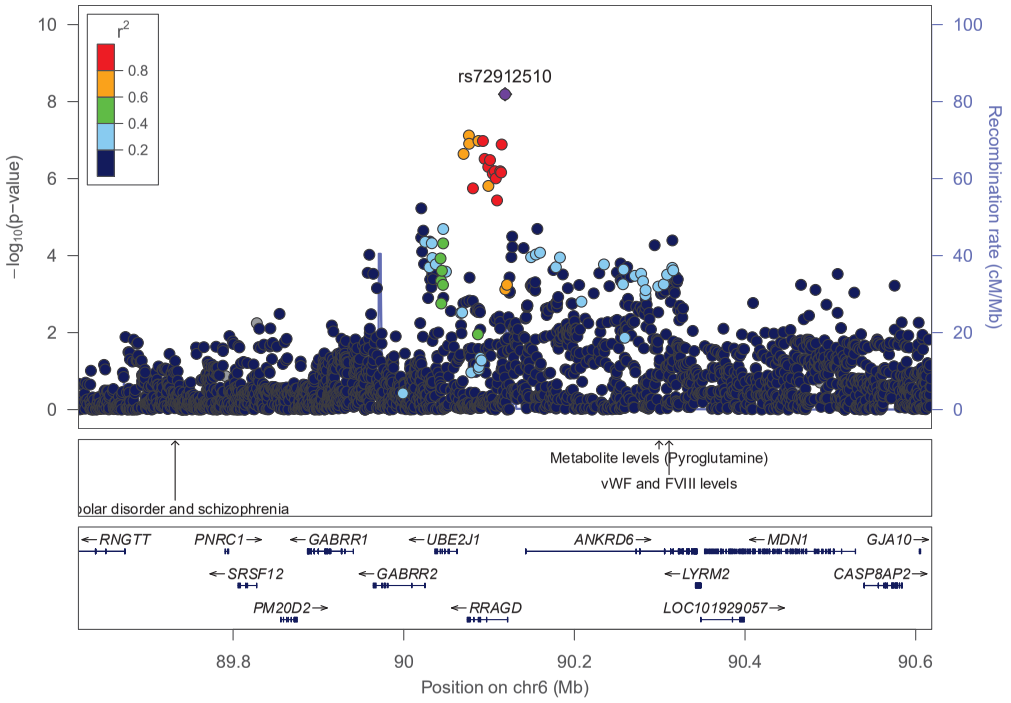

rs881858
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
HDL cholesterol
Triglycerides
Sexual dimorphism in anthropometric traits
Major depressive disorder
Rheumatoid arthritis
13 GWAS hits omitted
←ZNF318 TJAP1→ POLH→ VEGFA→ LINC01512→ ←MRPL14 MYMX→
ABCC10→ ←XPO5 RSPH9→ ←LOC101929705 CAPN11→ ←TCTE1
MIR6780B→ ←GTPBP2 C6orf223→ TMEM63B→ ←NFKBIE
←DLK2 MAD2L1BP→ SLC29A1→
←LRRC73 ←MRPS18A HSP90AB1→
←YIPF3 ←SLC35B2
POLR1C→ ←MIR4647
TMEM151B→
←AARS2
43.4 43.6 43.8 44 44.2
Position on chr6 (Mb)

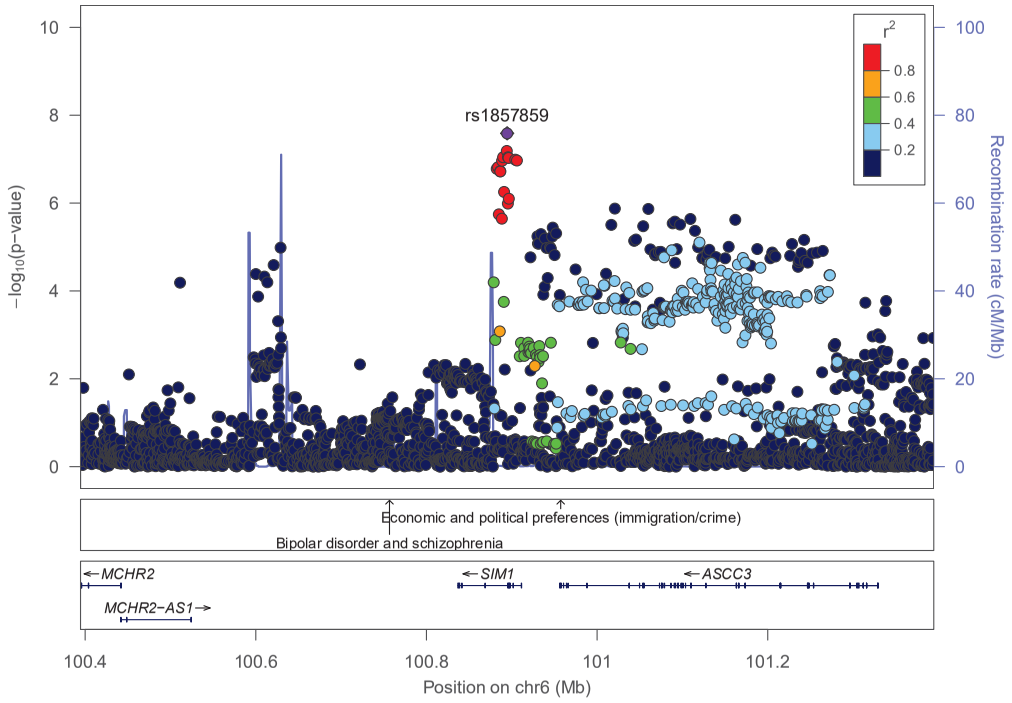

rs720989
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Migraine
Stroke (ischemic)
Asthma (childhood onset)
Obesity−related traits
Osteoarthritis
Height
Height
Height
Height
2 GWAS hits omitted
←AARS2 ←LOC105375075 ←SUPT3H
SPATS1→ ←MIR586
CDC5L→
MIR4642→
44.4 44.6 44.8 45 45.2
Position on chr6 (Mb)

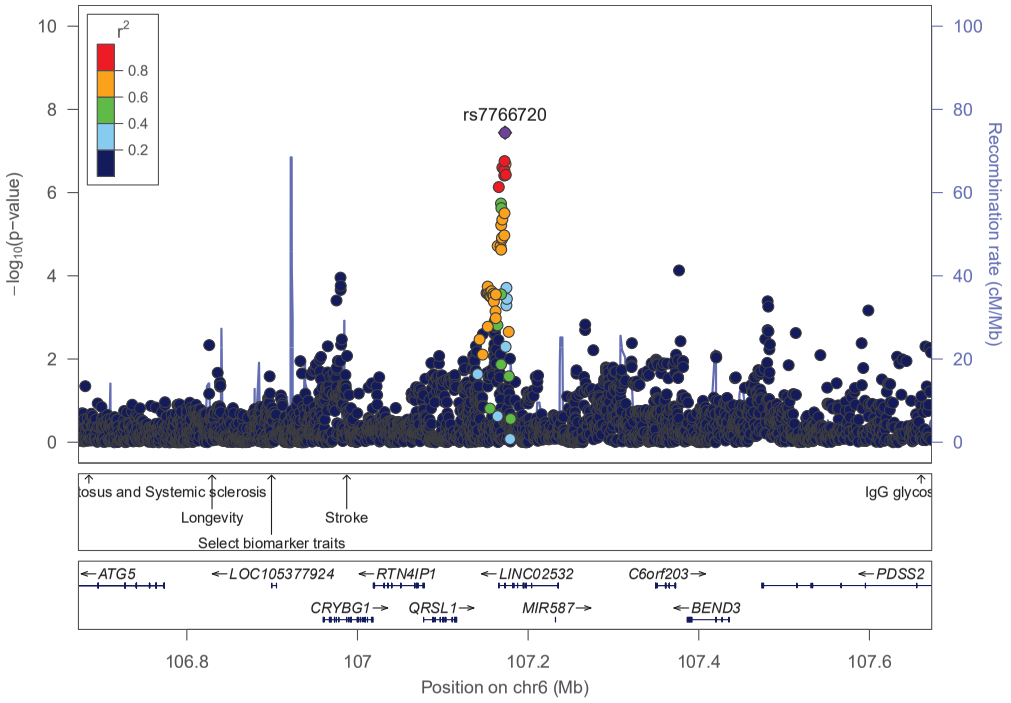

rs12212034
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Intraocular pressure
Weight loss (gastric bypass surgery)
Weight loss (gastric bypass surgery)
9 GWAS hits omitted
PKHD1
LOC101927082
Position on chr6 (Mb)

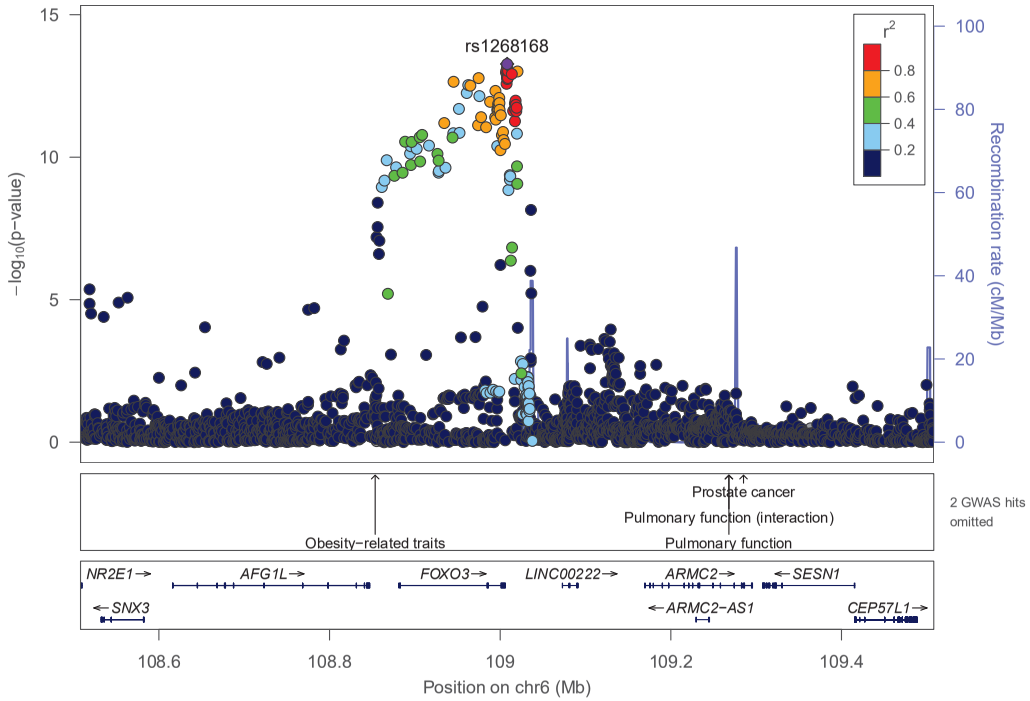

rs6458868
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Epilepsy (remission after treatment)
Glauc
MCM3
EFHC1
TRAM2−AS1
GSTA7P
GSTA3
ICK
GCM1
PAQR8
TRAM2
LOC730101
GSTA1
GSTA4
FBXO9
TMEM14A
GSTA5
GSTA2
Position on chr6 (Mb)

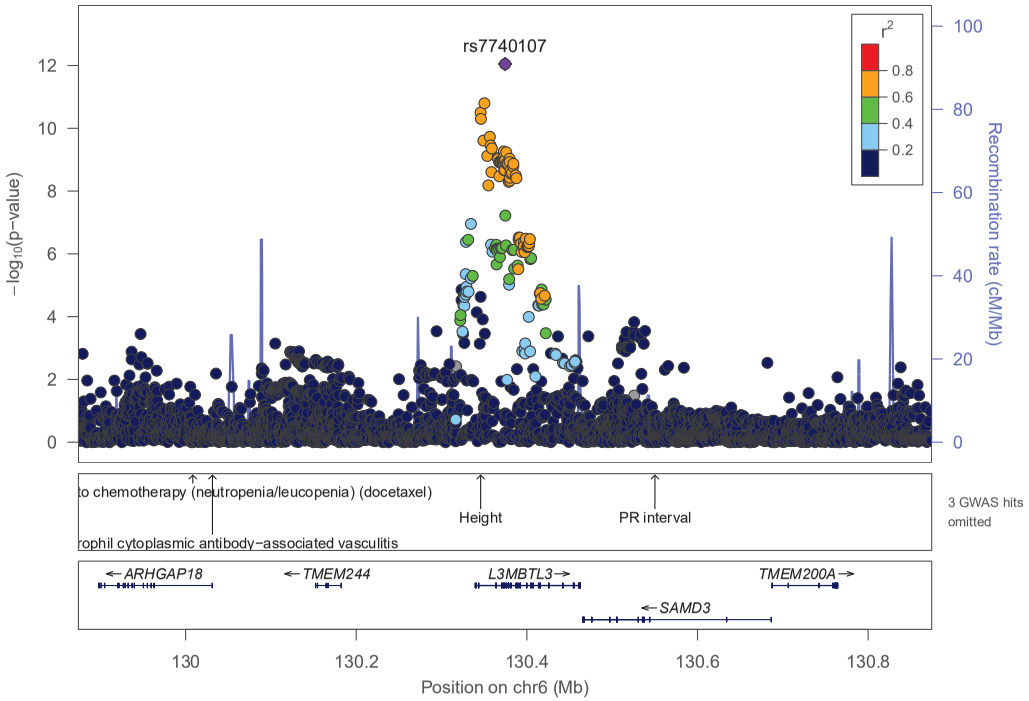

rs3925003
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Venous thromboembolism (gene x gene interaction)
Obesity−related traits
HIV−1 control
HCRTR2
GFRAL
HMGCLL1
BMP5
COL21A1
Position on chr6 (Mb)

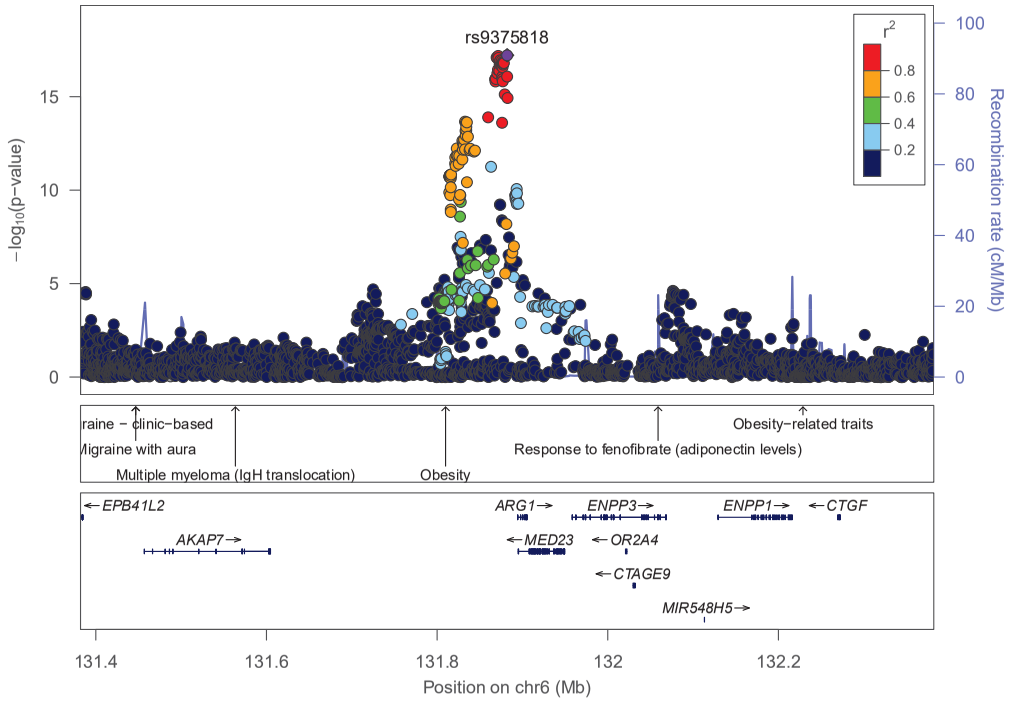

rs72912510
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Metabolite levels (Pyroglutamine)
vWF and FVIII levels
olar disorder and schizophrenia
RNGTT
PNRC1
GABRR1
UBE2J1
ANKRD6
MDN1
GJA10
SRSF12
GABRR2
LYRM2
CASP8AP2
PM20D2
RRAGD
LOC101929057
Position on chr6 (Mb)

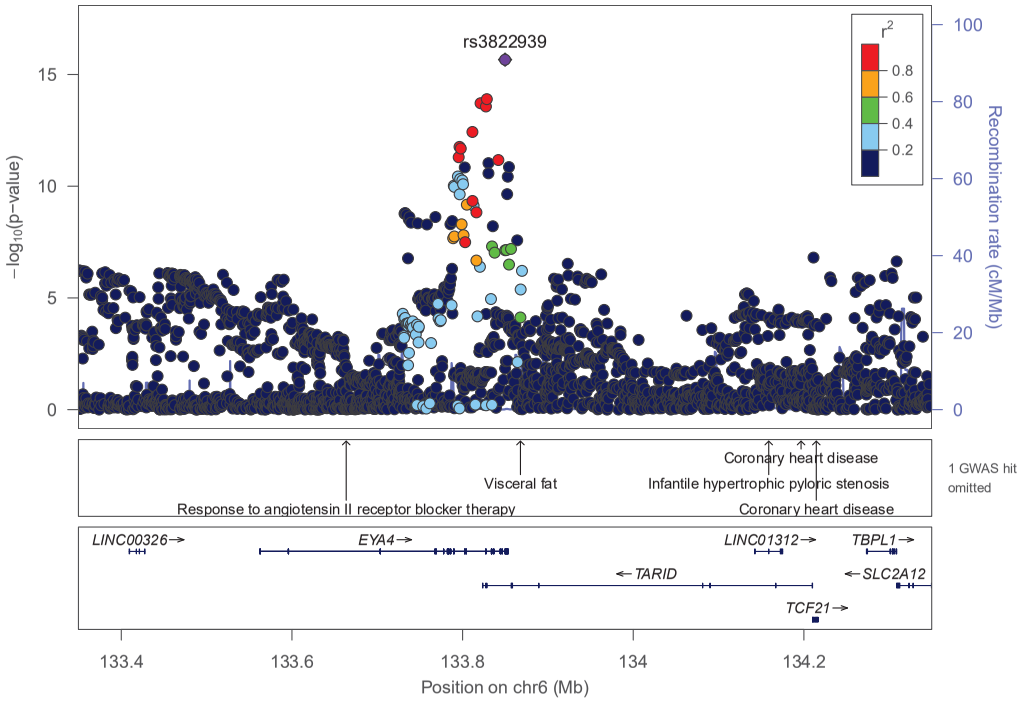

rs1857859
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Economic and political preferences (immigration/crime)
Bipolar disorder and schizophrenia
MCHR2
SIM1
ASCC3
MCHR2−AS1
100.4
100.6
100.8
101
101.2
Position on chr6 (Mb)

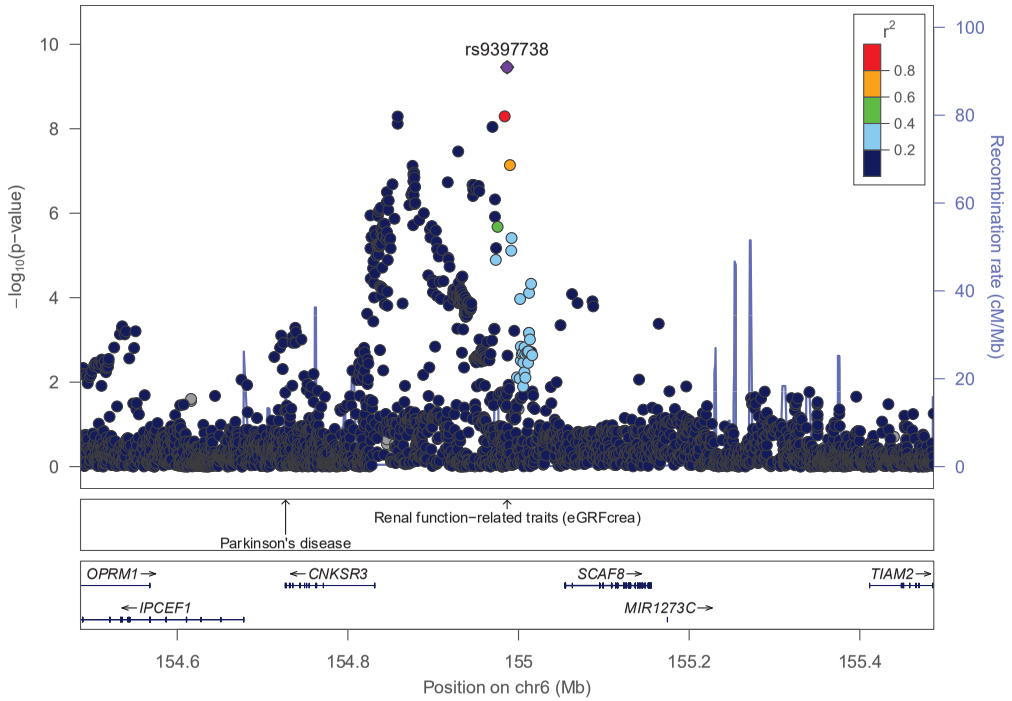

rs7766720
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
tosus and Systemic sclerosis
Longevity
Stroke
Select biomarker traits
IgG glycos
ATG5
LOC105377924
RTN4IP1
LINC02532
C6orf203
PDSS2
CRYBG1
QRSL1
MIR587
BEND3
106.8
107
107.2
107.4
107.6
Position on chr6 (Mb)

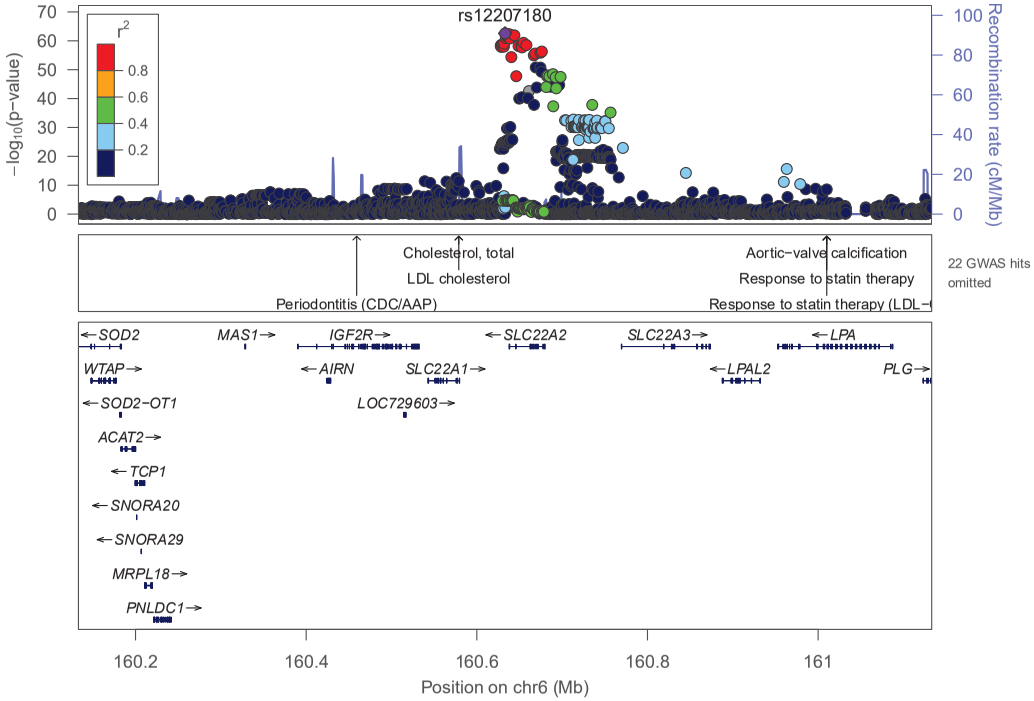

rs1268168
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Prostate cancer
Pulmonary function (interaction)
Pulmonary function
Obesity−related traits
2 GWAS hits
omitted
NR2E1
AFG1L
FOXO3
LINC00222
ARMC2
SESN1
SNX3
ARMC2−AS1
CEP57L1
108.6
108.8
109
109.2
109.4
Position on chr6 (Mb)

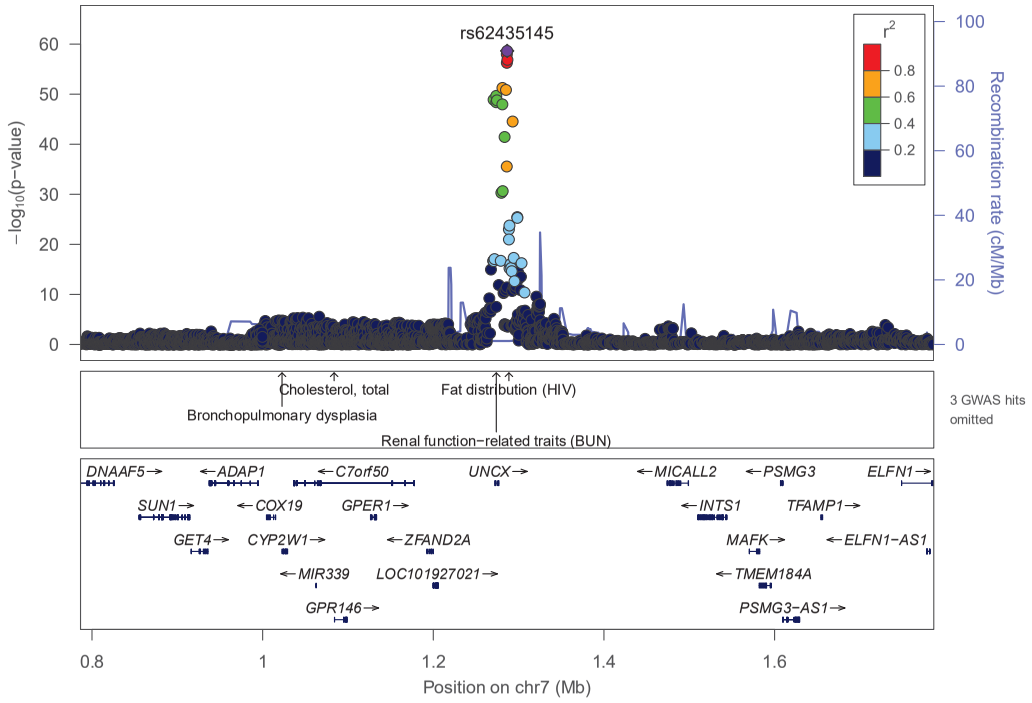

rs7740107
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
o chemotherapy (neutropenia/leucopenia) (docetaxel)
rophil cytoplasmic antibody−associated vasculitis
Height
PR interval
3 GWAS hits
omitted
ARHGAP18
TMEM244
L3MBTL3
TMEM200A
SAMD3
130
130.2
130.4
130.6
130.8
Position on chr6 (Mb)

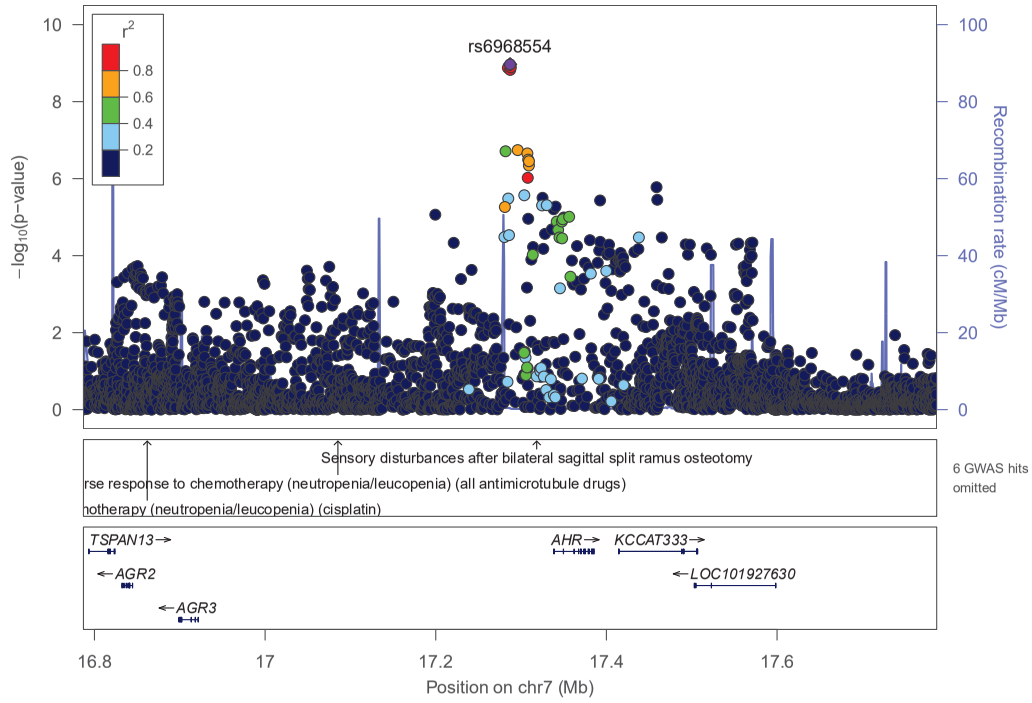

rs9375818
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
raine − clinic−based
Migraine with aura
Multiple myeloma (IgH translocation)
Obesity
Response to fenofibrate (adiponectin levels)
Obesity−related traits
EPB41L2
AKAP7
ARG1
ENPP3
MED23
OR2A4
CTAGE9
MIR548H5
ENPP1
CTGF
131.4
131.6
131.8
132
132.2
Position on chr6 (Mb)

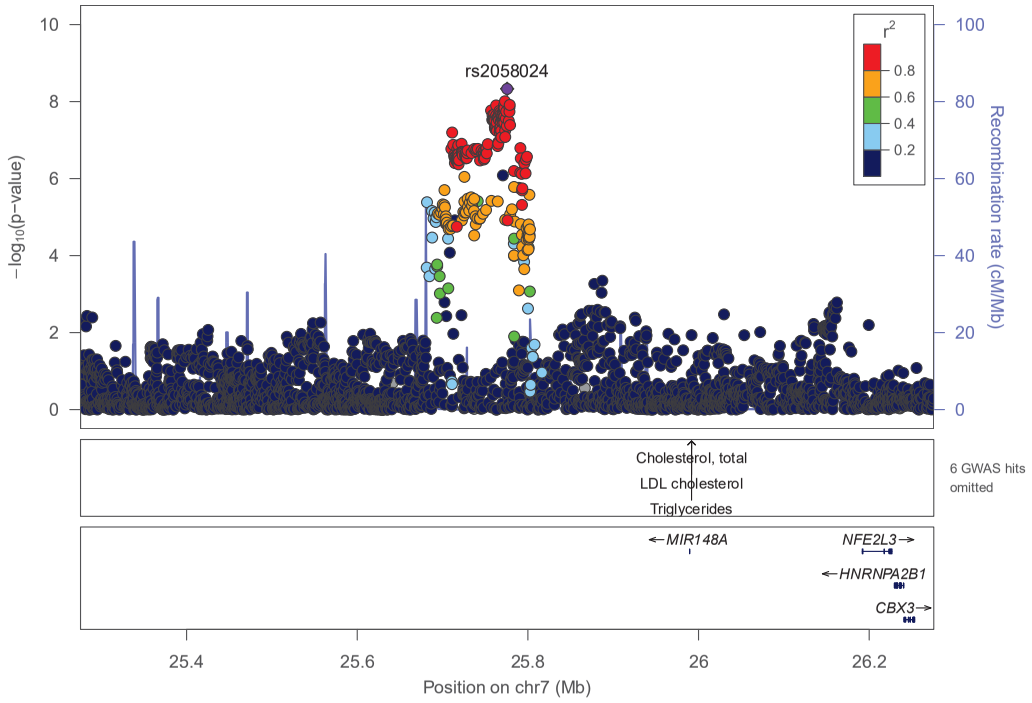

rs3822939
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Response to angiotensin II receptor blocker therapy
Visceral fat
Coronary heart disease
Infantile hypertrophic pyloric stenosis
Coronary heart disease
1 GWAS hit omitted
LINC00326
EYA4
TARID
LINC01312
TBPL1
SLC2A12
TCF21
133.4
133.6
133.8
134
134.2
Position on chr6 (Mb)

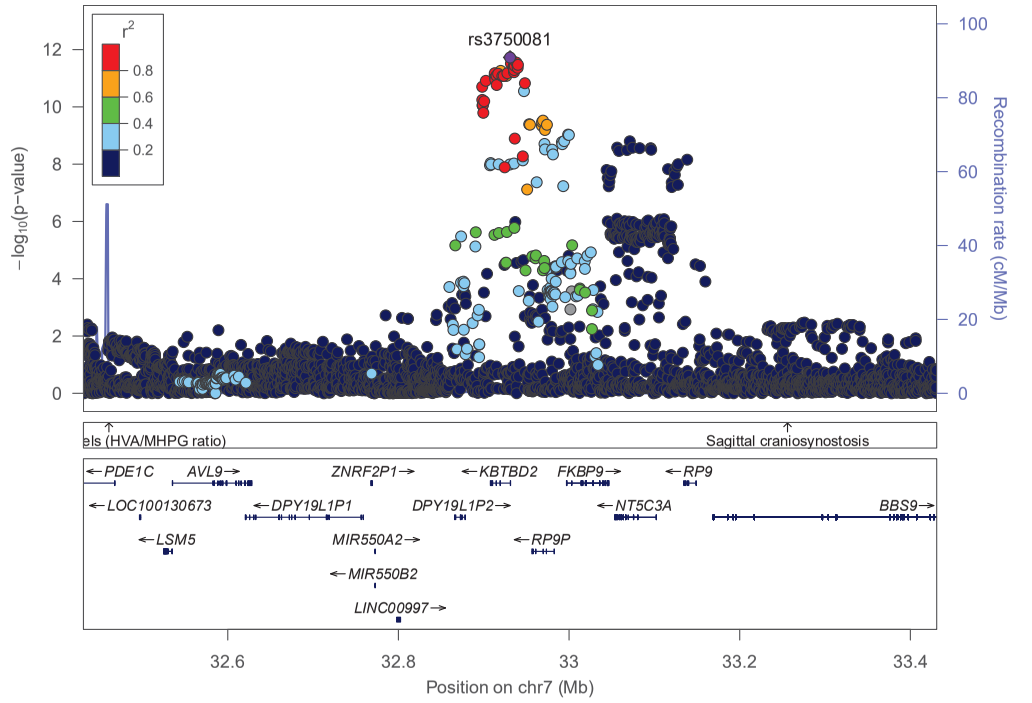

rs9397738
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Parkinson's disease
Renal function−related traits (eGRFcrea)
OPRM1
IPCEF1
CNKSR3
SCAF8
MIR1273C
TIAM2
154.6
154.8
155
155.2
155.4
Position on chr6 (Mb)

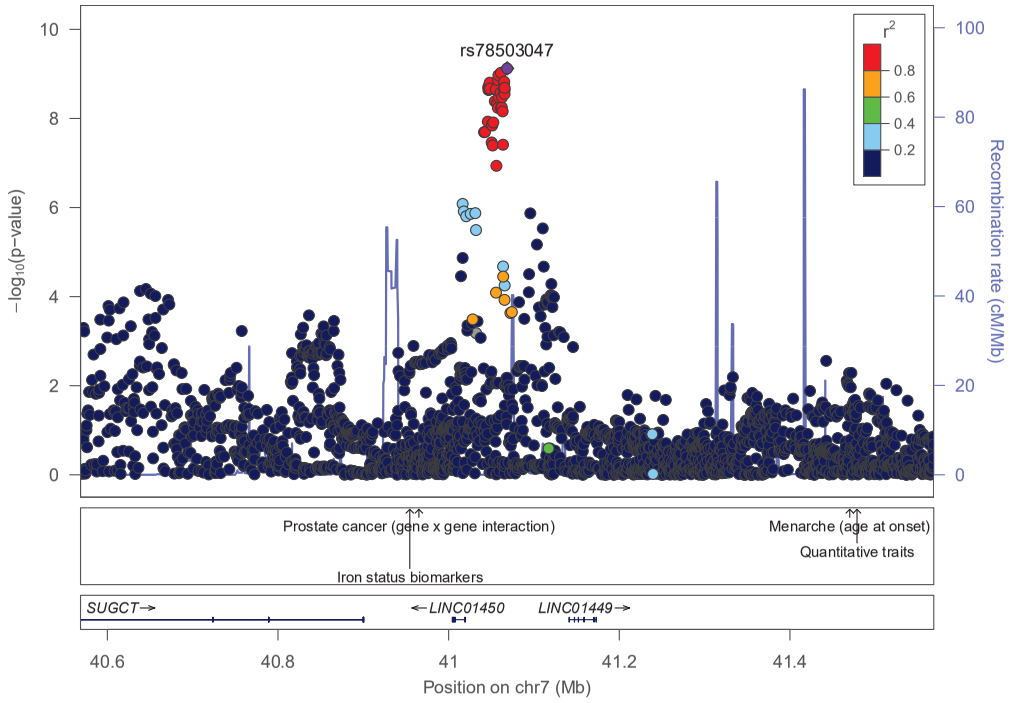

rs12207180
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Periodontitis (CDC/AAP)
Cholesterol, total
LDL cholesterol
Aortic−valve calcification
Response to statin therapy
Response to statin therapy (LDL−
22 GWAS hits omitted
SOD2
WTAP
SOD2−OT1
ACAT2
TCP1
SNORA20
SNORA29
MRPL18
PNLDC1
MAS1
AIRN
IGF2R
SLC22A1
LOC729603
SLC22A2
SLC22A3
LPAL2
LPA
PLG
160.2
160.4
160.6
160.8
161
Position on chr6 (Mb)

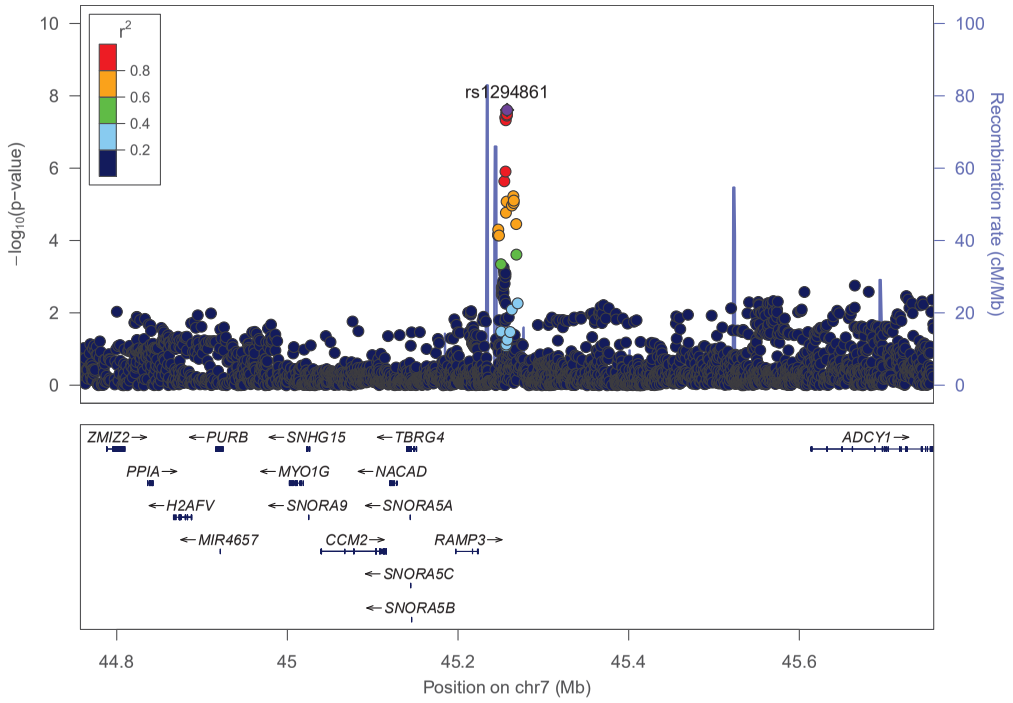

rs62435145
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
Fat distribution (HIV)
Bronchopulmonary dysplasia
Renal function−related traits (BUN)
3 GWAS hits omitted
DNAAF5→ ←ADAP1 ←C7orf50 UNCX→ ←MICALL2 ←PSMG3 ELFN1→
SUN1→ ←COX19 GPER1→ ←INTS1 TFAMP1→
GET4→ CYP2W1→ ←ZFAND2A MAFK→ ←ELFN1−AS1
←MIR339 LOC101927021→ ←TMEM184A
GPR146→ PSMG3−AS1→
Position on chr7 (Mb)

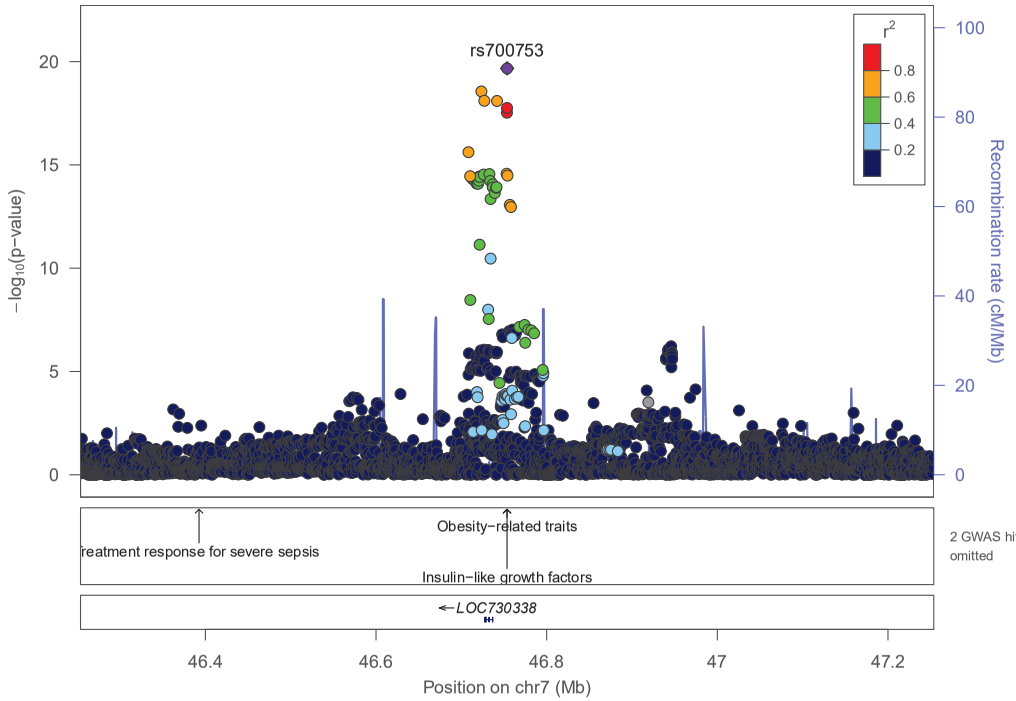

rs6968554
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Sensory disturbances after bilateral sagittal split ramus osteotomy
rse response to chemotherapy (neutropenia/leucopenia) (all antimicrotubule drugs)
notherapy (neutropenia/leucopenia) (cisplatin)
6 GWAS hits omitted
TSPAN13→ AHR→ KCCAT333→
←AGR2 ←LOC101927630
←AGR3
Position on chr7 (Mb)

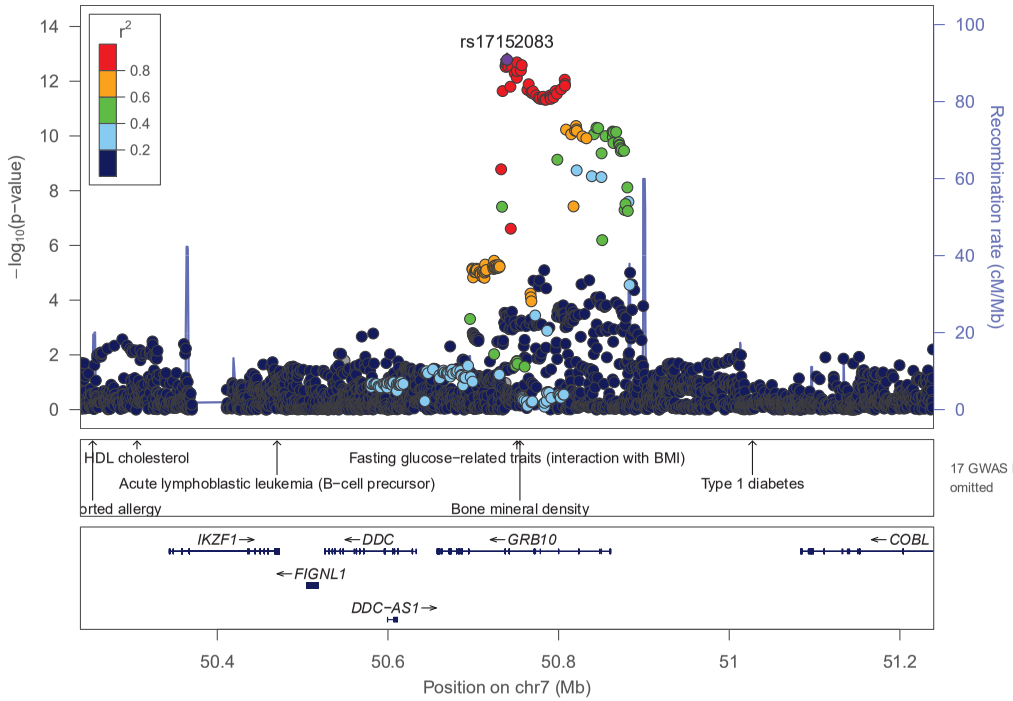

rs2058024
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
LDL cholesterol
Triglycerides
6 GWAS hits omitted
←MIR148A NFE2L3→
←HNRNPA2B1
CBX3→
Position on chr7 (Mb)

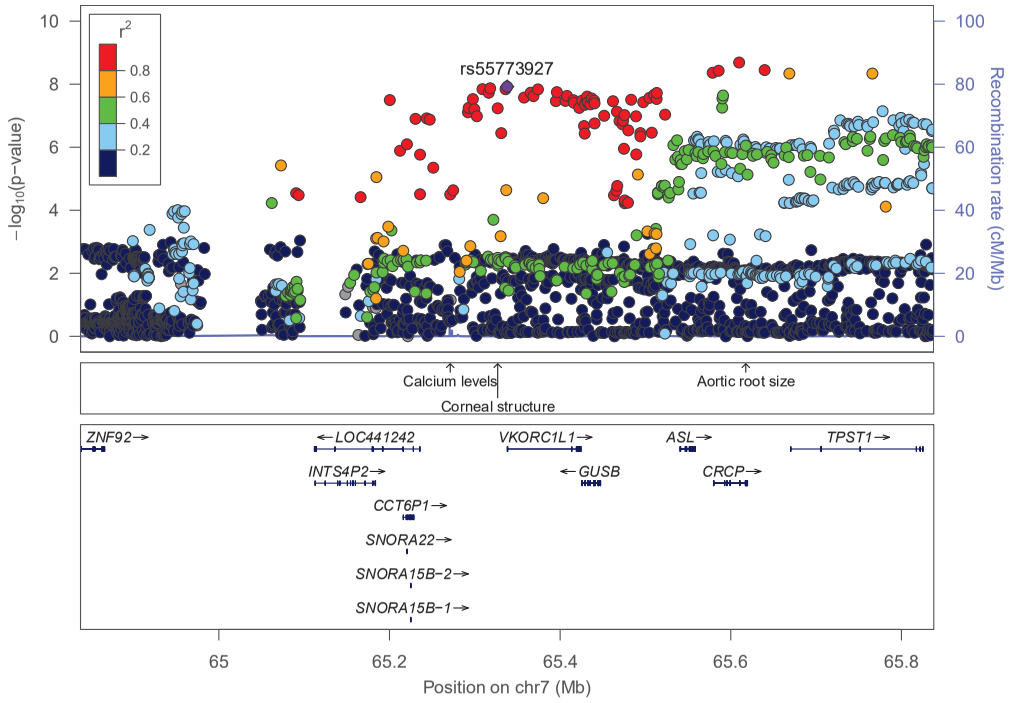

rs3750081
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
els (HVA/MHPG ratio)
Sagittal craniosynostosis
←PDE1C AVL9→ ZNRF2P1→ ←KBTBD2 FKBP9→ ←RP9
←LOC100130673 ←DPY19L1P1 DPY19L1P2→ ←NT5C3A BBS9→
←LSM5 MIR550A2→ ←RP9P
←MIR550B2
LINC00997→
Position on chr7 (Mb)

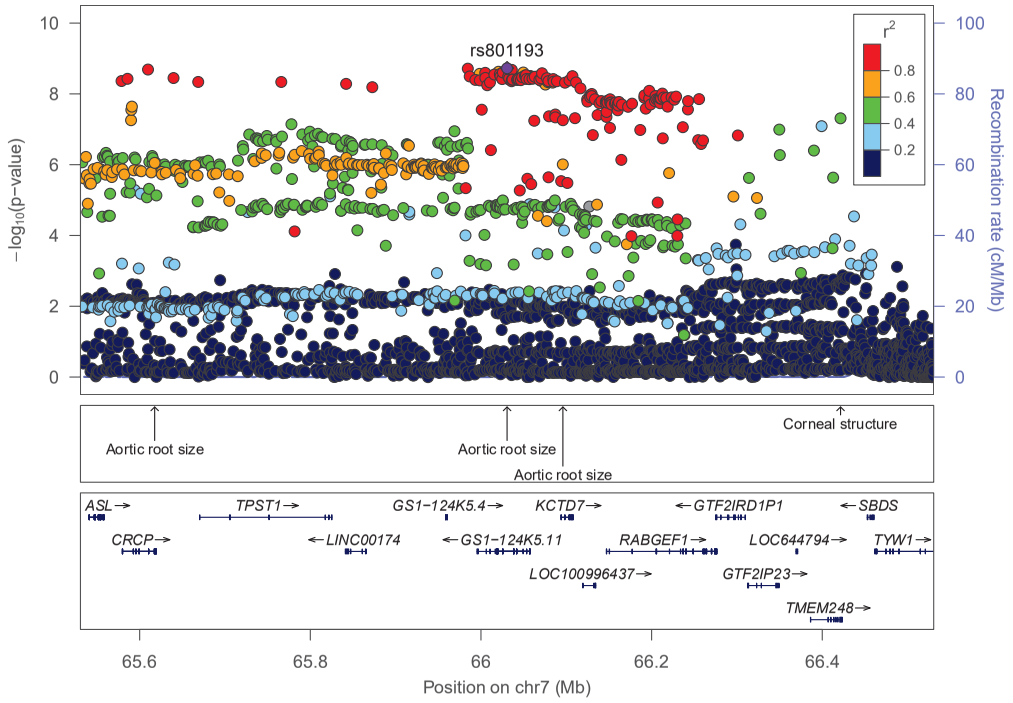

rs78503047
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Prostate cancer (gene x gene interaction)
Iron status biomarkers
Menarche (age at onset)
Quantitative traits
SUGCT→
←LINC01450
LINC01449→
40.6
40.8
41
41.2
41.4
Position on chr7 (Mb)

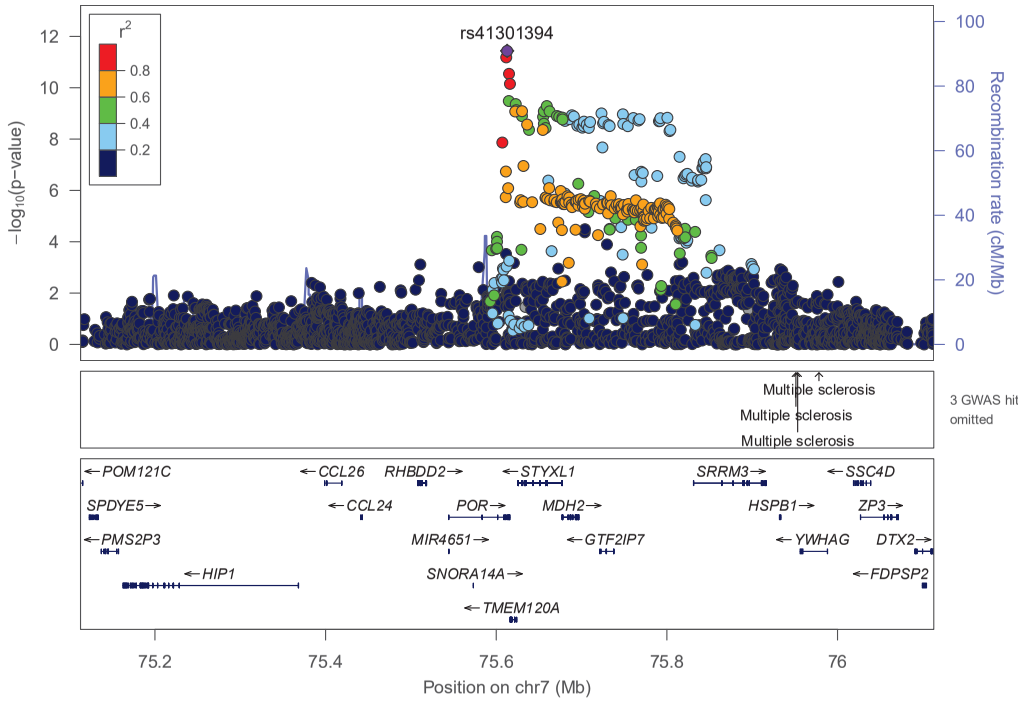

rs1294861
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ZMIZ2→
←PURB
←SNHG15
←TBRG4
ADCY1→
PPIA→
←MYO1G
←NACAD
←H2AFV
←SNORA9
←SNORA5A
←MIR4657
CCM2→
RAMP3→
←SNORA5C
←SNORA5B
44.8
45
45.2
45.4
45.6
Position on chr7 (Mb)

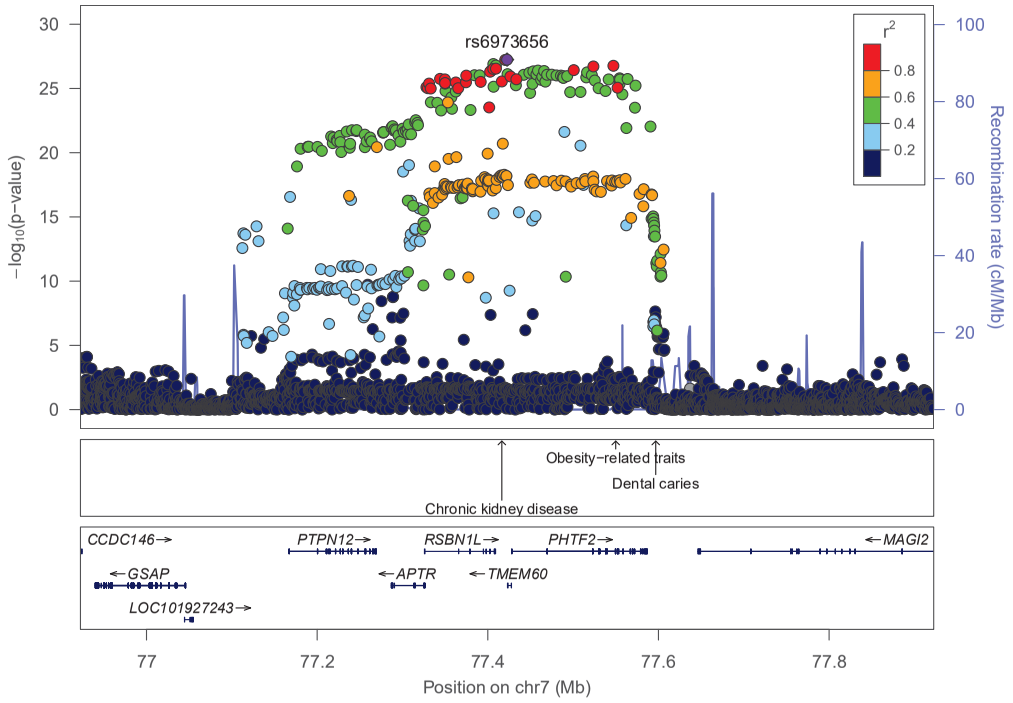

rs700753
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
reatment response for severe sepsis
Obesity−related traits
Insulin−like growth factors
2 GWAS hits
omitted
←LOC730338
46.4
46.6
46.8
47
47.2
Position on chr7 (Mb)

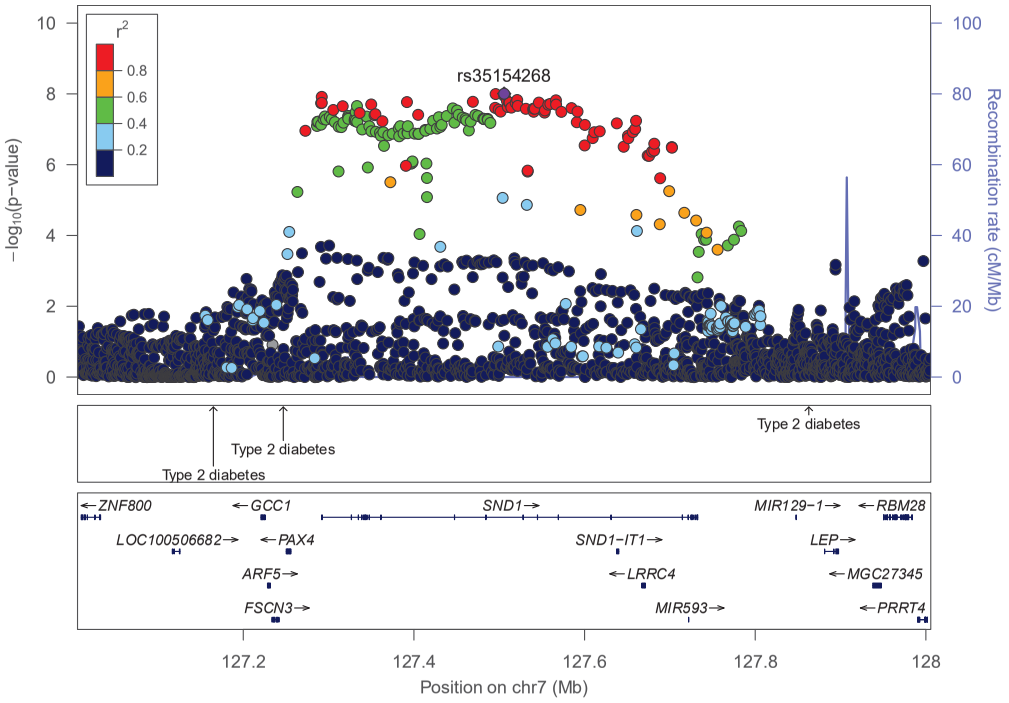

rs17152083
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
HDL cholesterol
Acute lymphoblastic leukemia (B−cell precursor)
Fasting glucose−related traits (interaction with BMI)
Type 1 diabetes
orted allergy
Bone mineral density
17 GWAS hits
omitted
IKZF1→
←DDC
←GRB10
←COBL
←FIGNL1
DDC−AS1→
50.4
50.6
50.8
51
51.2
Position on chr7 (Mb)

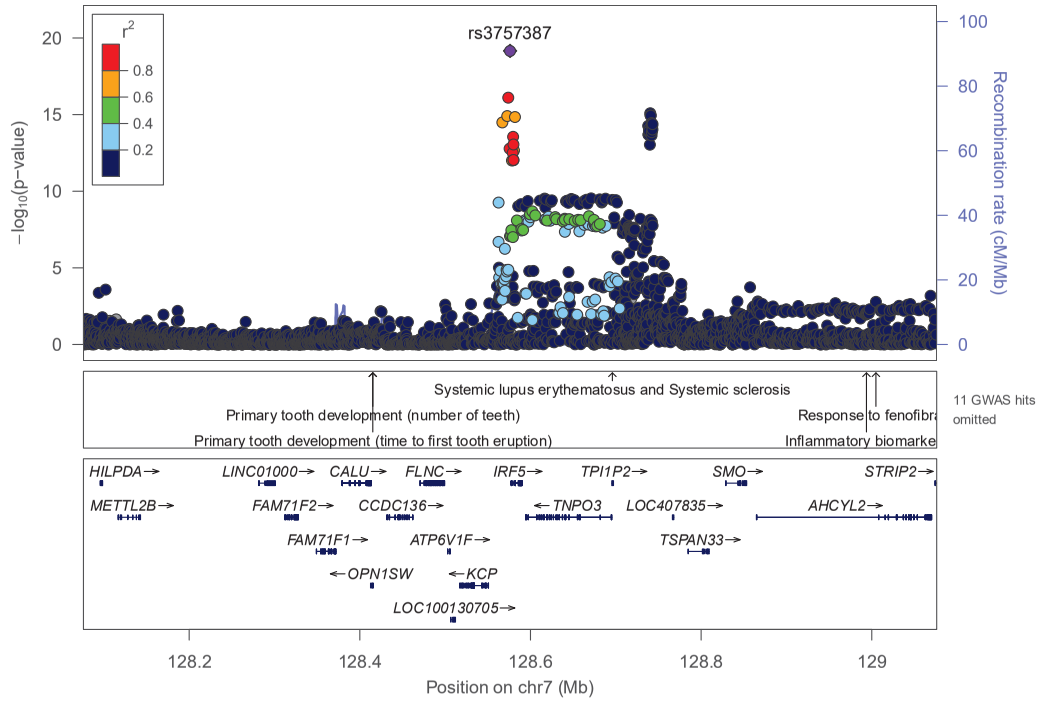

rs55773927
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Calcium levels
Corneal structure
Aortic root size
ZNF92→
←LOC441242
VKORC1L1→
ASL→
TPST1→
INTS4P2→
←GUSB
CRCP→
CCT6P1→
SNORA22→
SNORA15B−2→
SNORA15B−1→
Position on chr7 (Mb)

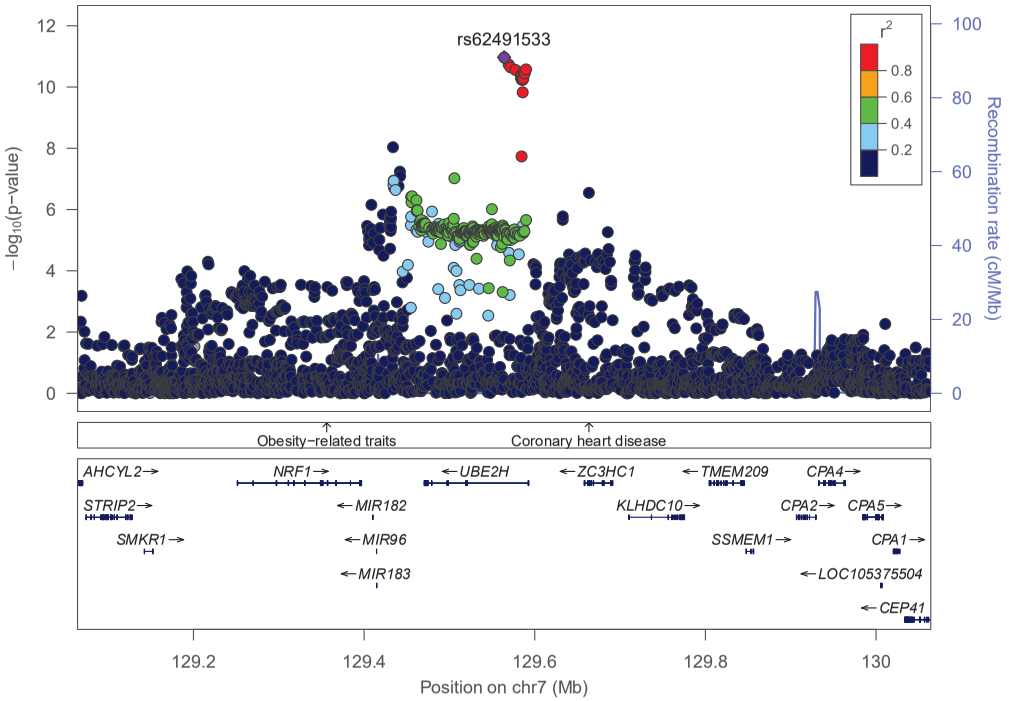

rs801193
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Aortic root size
Aortic root size
Aortic root size
Corneal structure
ASL→
TPST1→
GS1−124K5.4→
KCTD7→
←GTF2IRD1P1
←SBDS
CRCP→
←LINC00174
←GS1−124K5.11
RABGEF1→
LOC644794→
TYW1→
LOC100996437→
GTF2IP23→
TMEM248→
Position on chr7 (Mb)

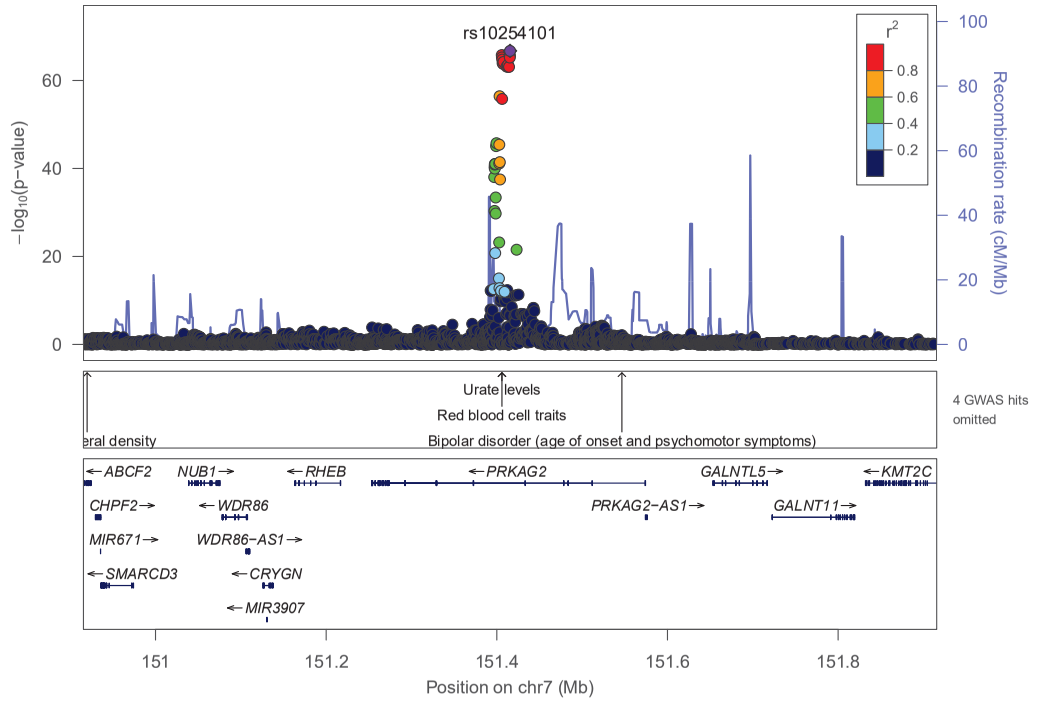

rs41301394
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Multiple sclerosis
Multiple sclerosis
Multiple sclerosis
3 GWAS hits omitted
←POM121C
←CCL26
RHBDD2→
←STYXL1
SRRM3→
←SSC4D
SPDYE5→
←CCL24
POR→
MDH2→
HSPB1→
ZP3→
←PMS2P3
MIR4651→
←GTF2IP7
←YWHAG
DTX2→
←HIP1
SNORA14A→
←FDPSP2
←TMEM120A
Position on chr7 (Mb)

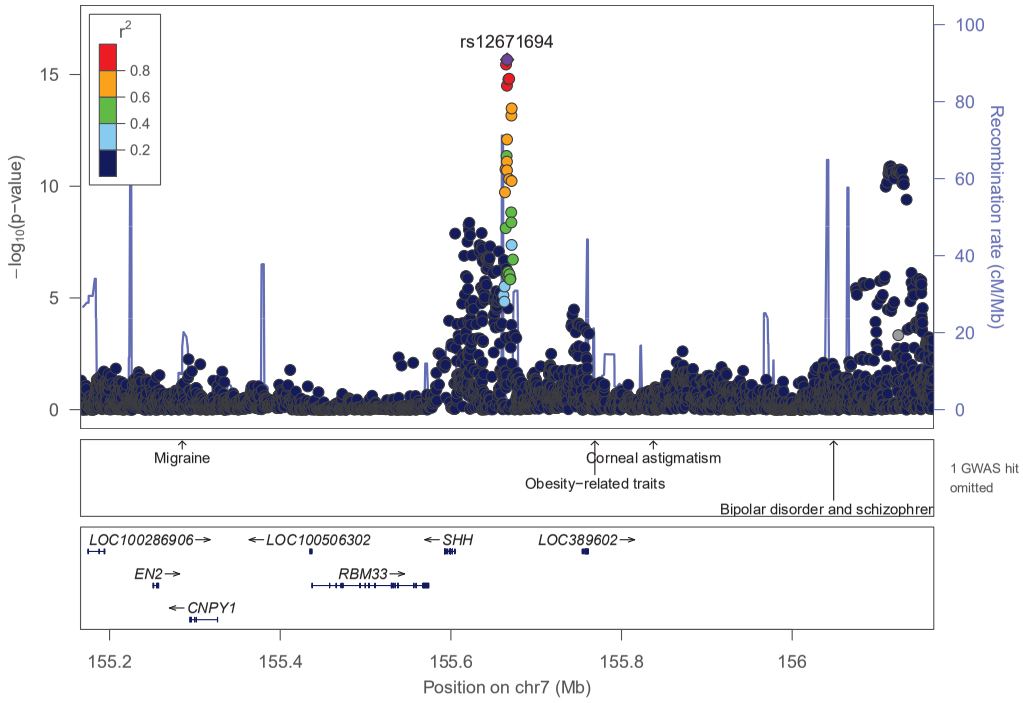

rs6973656
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Dental caries
Chronic kidney disease
CCDC146→
PTPN12→
RSBN1L→
PHTF2→
←MAGI2
←GSAP
←APTR
←TMEM60
LOC101927243→
Position on chr7 (Mb)

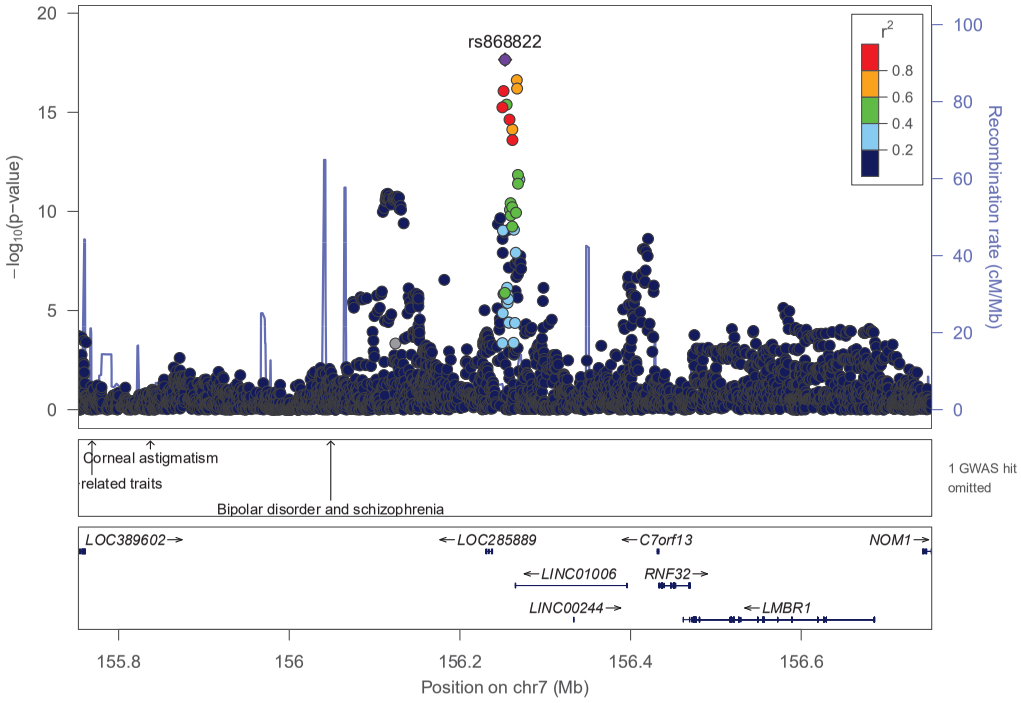

rs35154268
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Type 2 diabetes
Type 2 diabetes
Type 2 diabetes
ZNF800
GCC1
SND1
MIR129−1
RBM28
LOC100506682
PAX4
SND1−IT1
LEP
ARF5
LRRC4
MGC27345
FSCN3
MIR593
PRRT4
127.2
127.4
127.6
127.8
128
Position on chr7 (Mb)

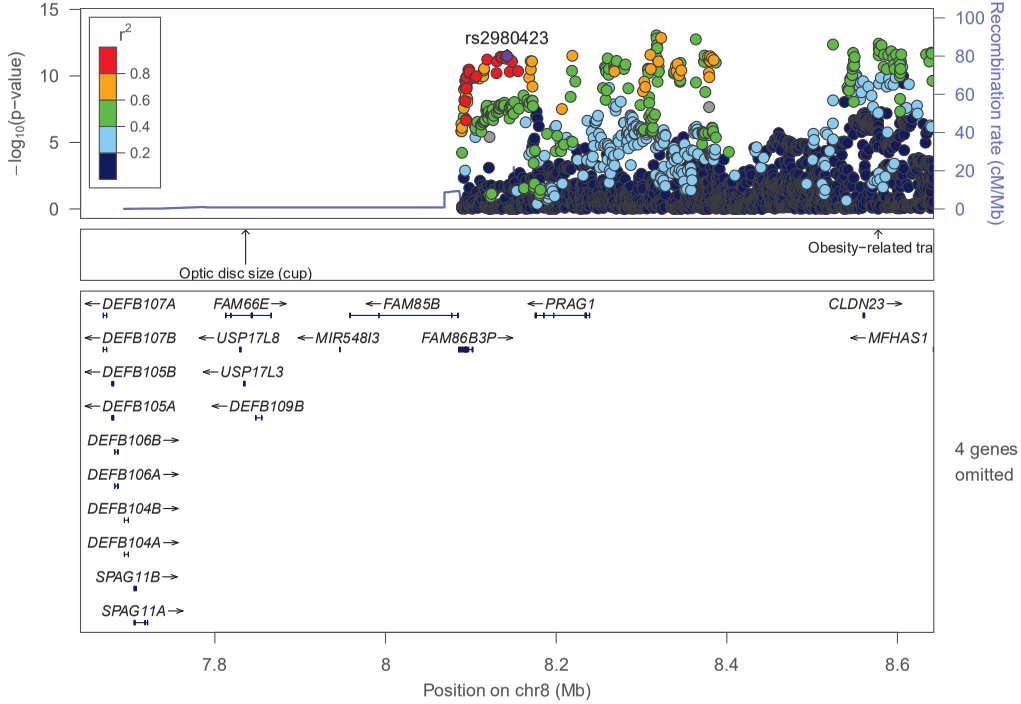

rs3757387
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Systemic lupus erythematosus and Systemic sclerosis
Primary tooth development (number of teeth)
Primary tooth development (time to first tooth eruption)
Response to fenofibra
Inflammatory biomarke
11 GWAS hits omitted
HILPDA
LINC01000
CALU
FLNC
IRF5
TPI1P2
SMO
STRIP2
METTL2B
FAM71F2
CCDC136
TNPO3
LOC407835
AHCYL2
FAM71F1
ATP6V1F
TSPAN33
OPN1SW
KCP
LOC100130705
128.2
128.4
128.6
128.8
129
Position on chr7 (Mb)

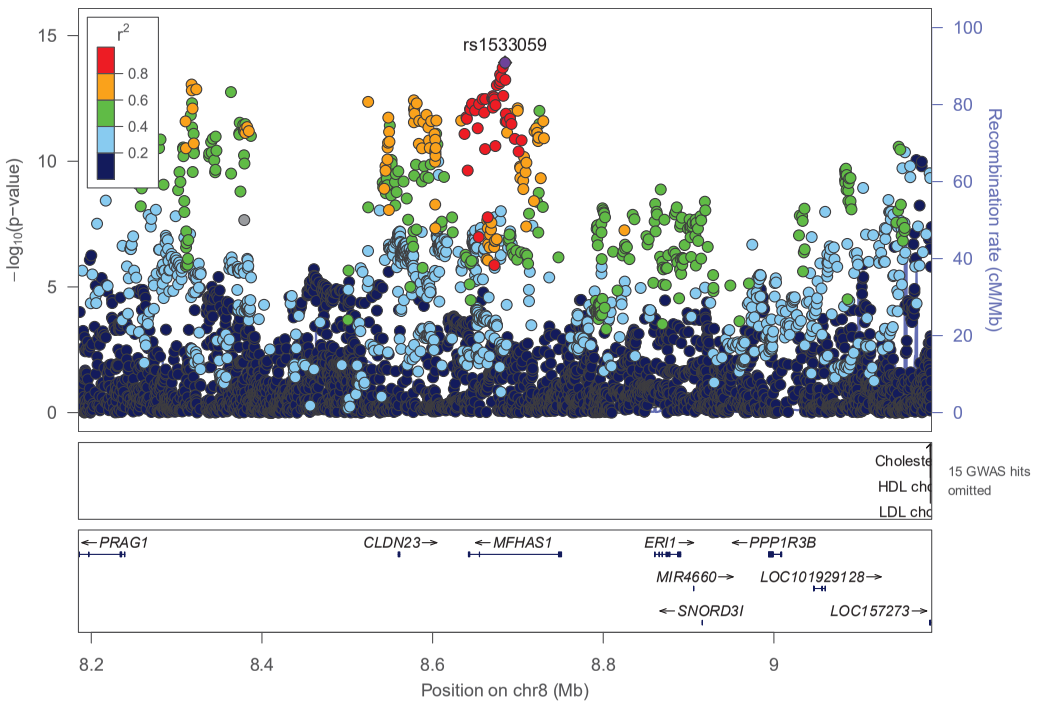

rs62491533
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Coronary heart disease
AHCYL2
NRF1
UBE2H
ZC3HC1
TMEM209
CPA4
STRIP2
MIR182
KLHDC10
CPA2
CPA5
SMKR1
MIR96
SSMEM1
CPA1
MIR183
LOC105375504
CEP41
129.2
129.4
129.6
129.8
130
Position on chr7 (Mb)

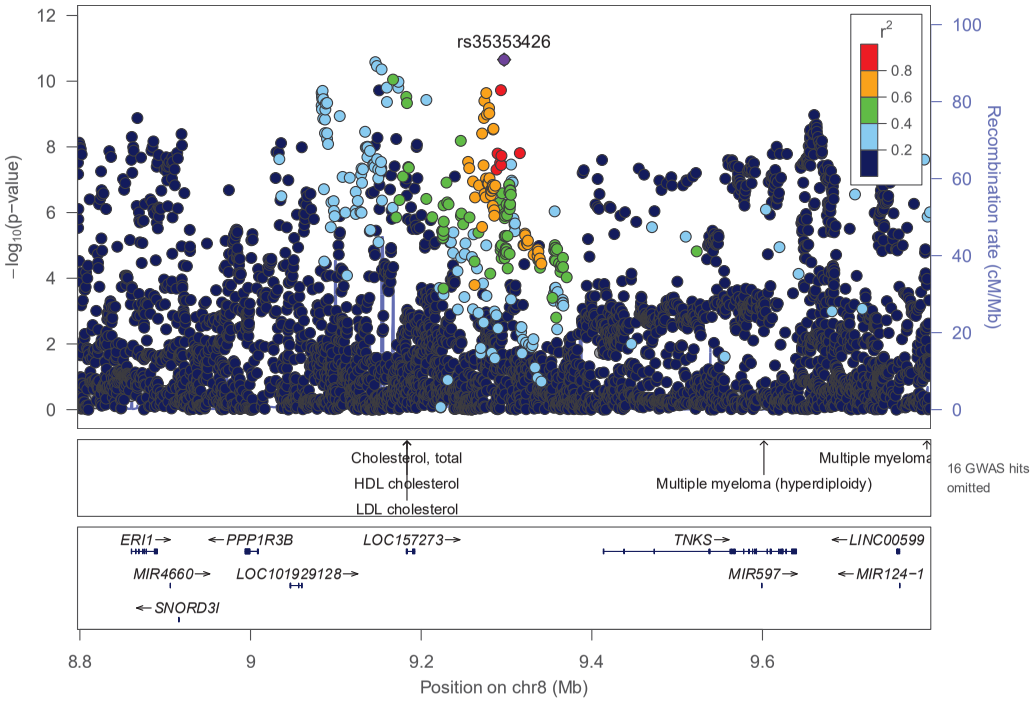

rs10254101
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Urate levels
Red blood cell traits
eral density
Bipolar disorder (age of onset and psychomotor symptoms)
4 GWAS hits omitted
ABCF2
NUB1
RHEB
PRKAG2
GALNTL5
KMT2C
CHPF2
WDR86
PRKAG2−AS1
GALNT11
MIR671
WDR86−AS1
SMARCD3
CRYGN
MIR3907
151
151.2
151.4
151.6
151.8
Position on chr7 (Mb)

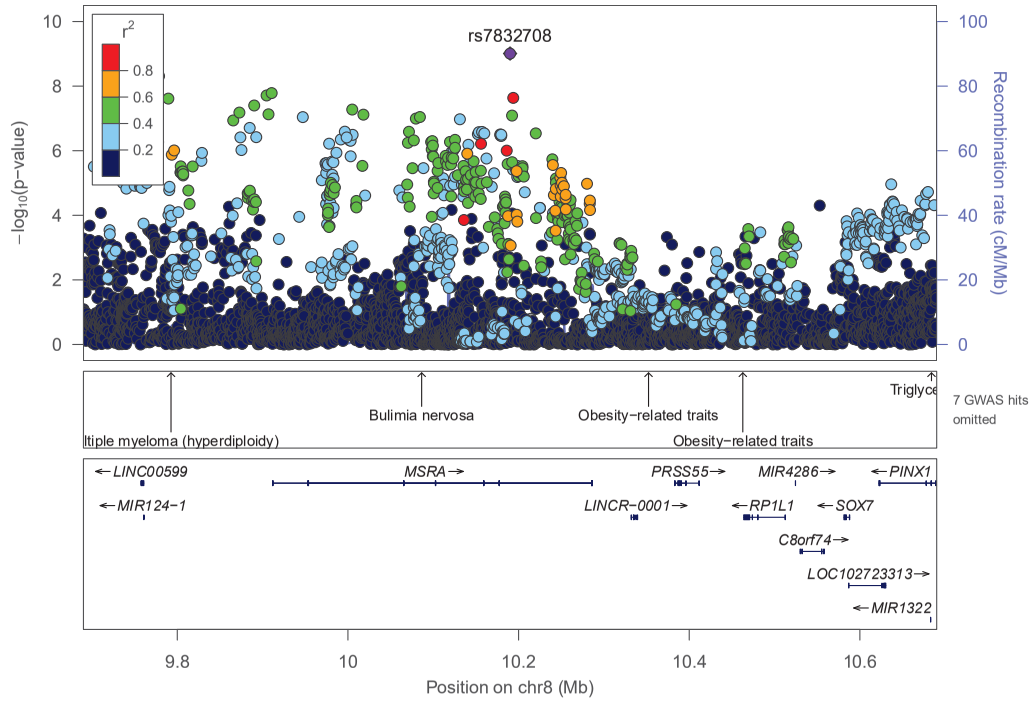

rs12671694
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Migraine
Corneal astigmatism
Obesity−related traits
Bipolar disorder and schizophrer
1 GWAS hit omitted
LOC100286906
LOC100506302
SHH
LOC389602
EN2
RBM33
CNPY1
155.2
155.4
155.6
155.8
156
Position on chr7 (Mb)

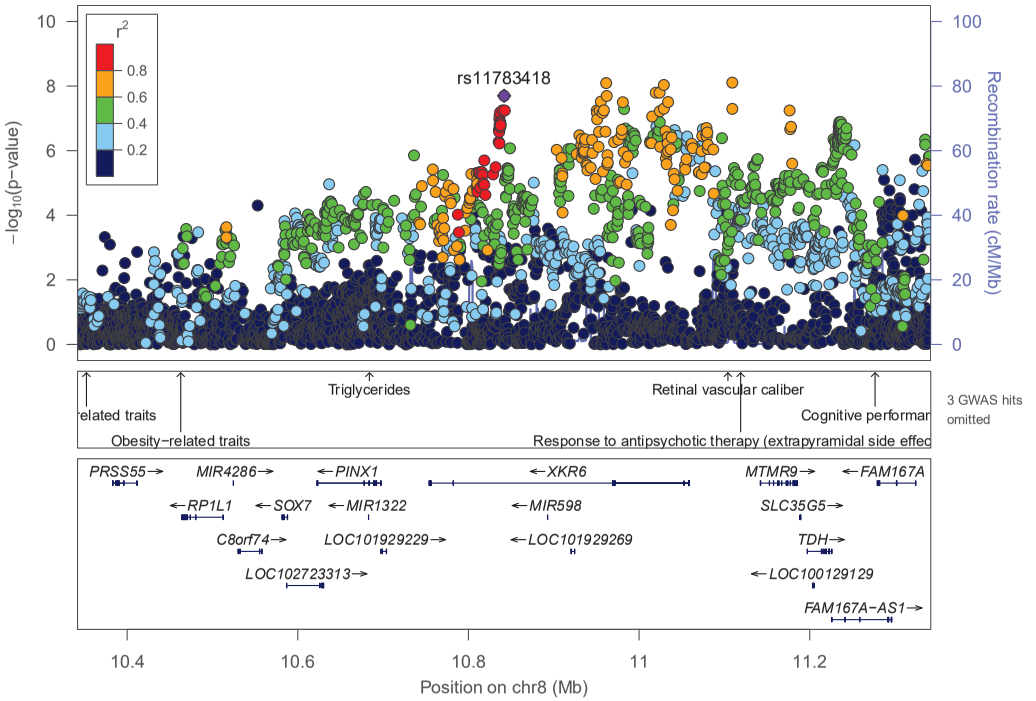

rs868822
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Corneal astigmatism
related traits
Bipolar disorder and schizophrenia
1 GWAS hit omitted
LOC389602
LOC285889
C7orf13
NOM1
LINC01006
RNF32
LINC00244
LMBR1
155.8
156
156.2
156.4
156.6
Position on chr7 (Mb)

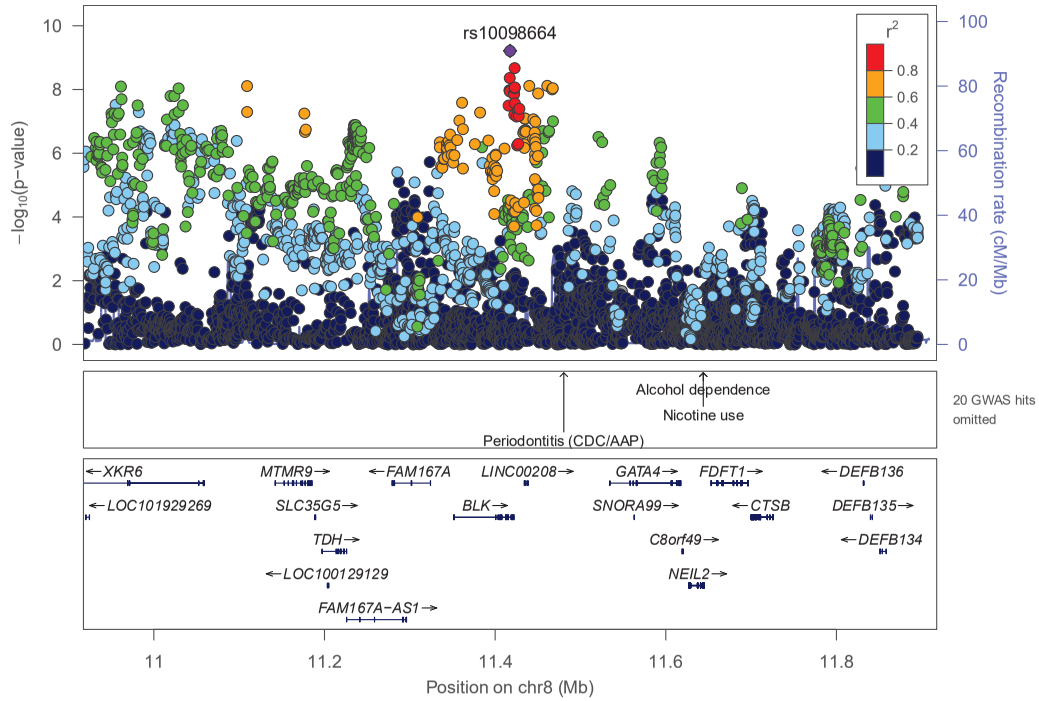

rs2980423
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Optic disc size (cup)
Obesity−related tra
DEFB107A
FAM66E
FAM85B
PRAG1
CLDN23
DEFB107B
USP17L8
MIR548I3
FAM86B3P
MFHAS1
DEFB105B
USP17L3
DEFB105A
DEFB109B
DEFB106B
DEFB106A
DEFB104B
DEFB104A
SPAG11B
SPAG11A
4 genes omitted
7.8
8
8.2
8.4
8.6
Position on chr8 (Mb)

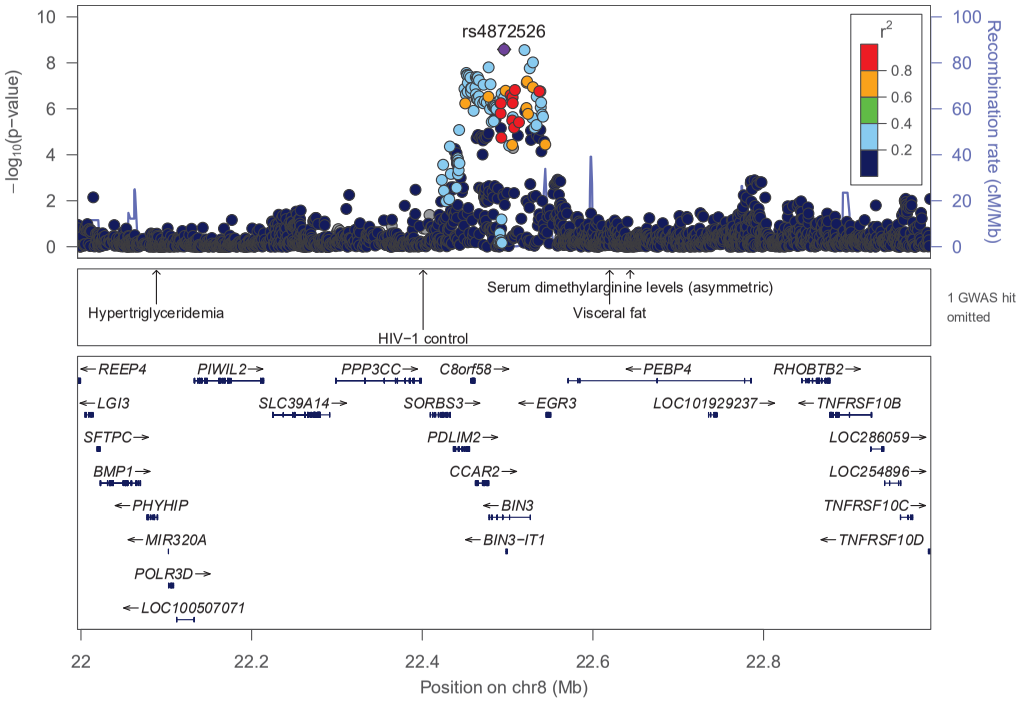

rs1533059
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholest
HDL cho
LDL cho
15 GWAS hits omitted
PRAG1
CLDN23
MFHAS1
ERI1
PPP1R3B
MIR4660
LOC101929128
SNORD3I
LOC157273
8.2
8.4
8.6
8.8
9
Position on chr8 (Mb)

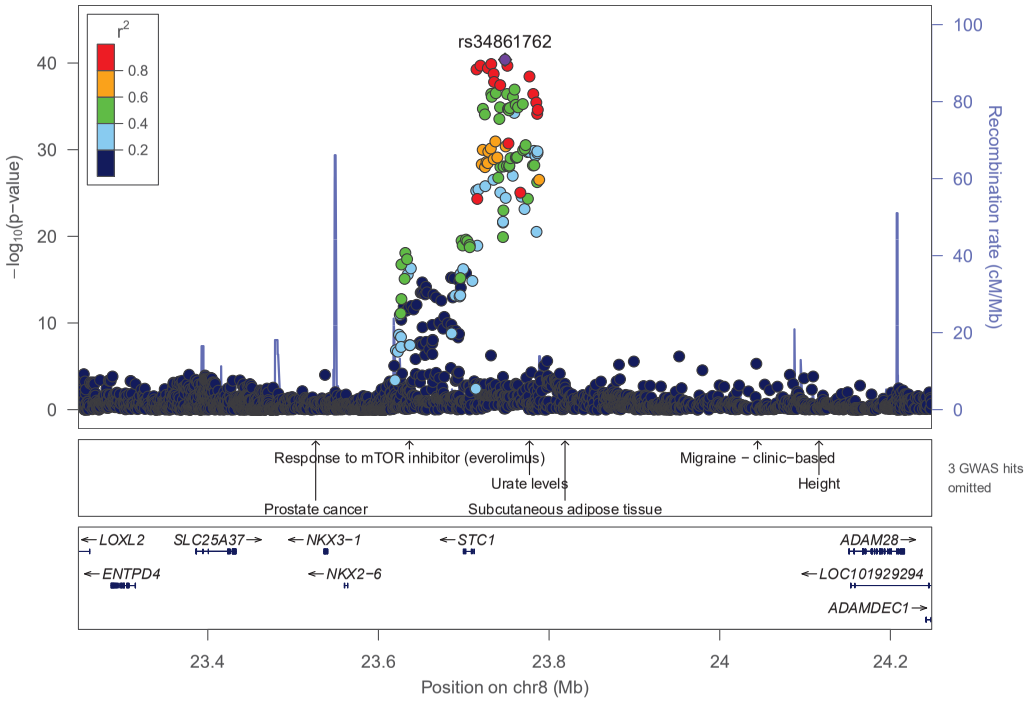

rs35353426
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
HDL cholesterol
LDL cholesterol
Multiple myeloma (hyperdiploidy)
Multiple myeloma
16 GWAS hits omitted
ERI1→
←PPP1R3B
LOC157273→
TNKS→
←LINC00599
MIR4660→
LOC101929128→
MIR597→
←MIR124−1
←SNORD3I
Position on chr8 (Mb)

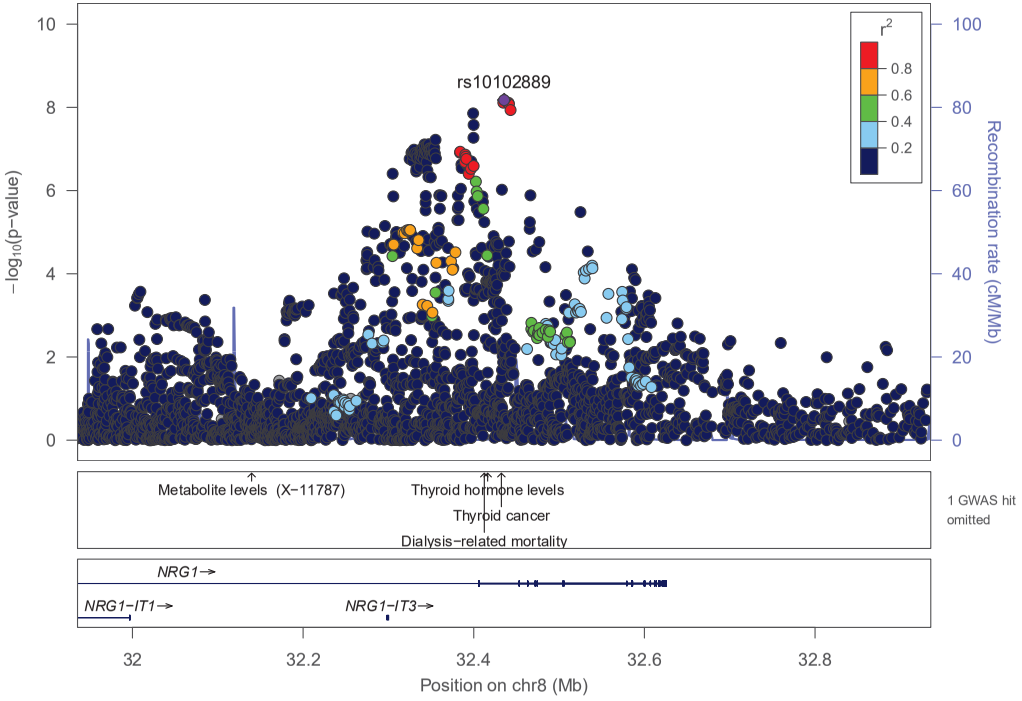

rs7832708
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Bulimia nervosa
Obesity−related traits
Obesity−related traits
7 GWAS hits omitted
←LINC00599
MSRA→
PRSS55→
MIR4286→
←PINX1
←MIR124−1
LINCR−0001→
←RP1L1
←SOX7
C8orf74→
LOC102723313→
←MIR1322
Position on chr8 (Mb)

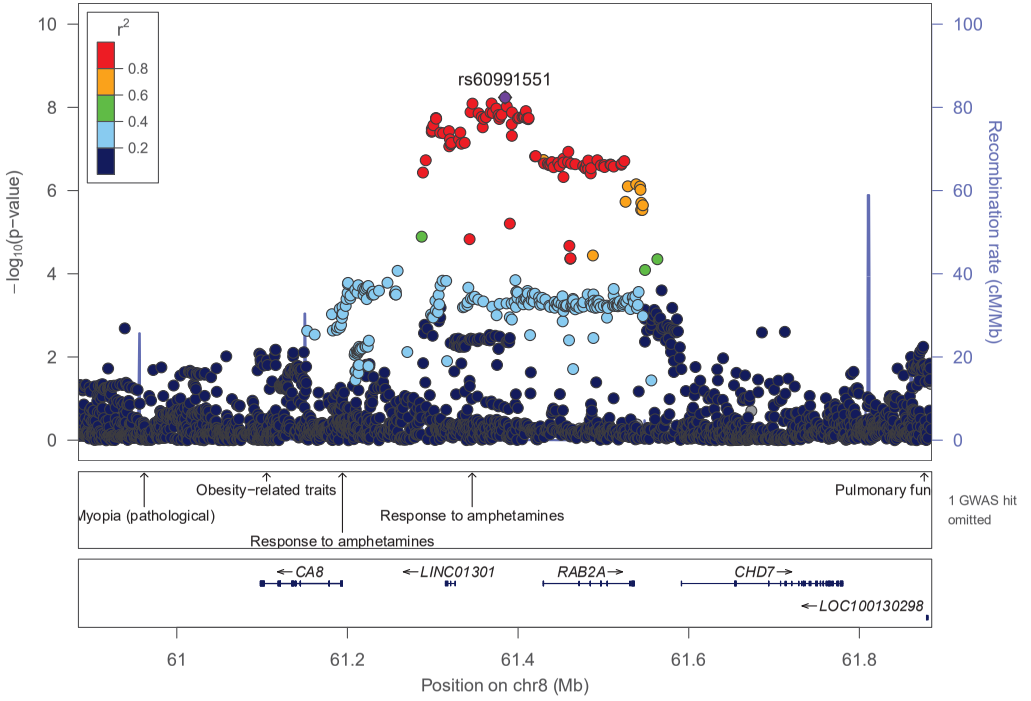

rs11783418
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Triglycerides
Retinal vascular caliber
Cognitive performar
Obesity−related traits
Response to antipsychotic therapy (extrapyramidal side effec
3 GWAS hits omitted
PRSS55→
MIR4286→
←PINX1
←XKR6
MTMR9→
←FAM167A
←RP1L1
←SOX7
←MIR1322
←MIR598
SLC35G5→
C8orf74→
LOC101929229→
←LOC101929269
TDH→
LOC102723313→
←LOC100129129
FAM167A−AS1→
Position on chr8 (Mb)

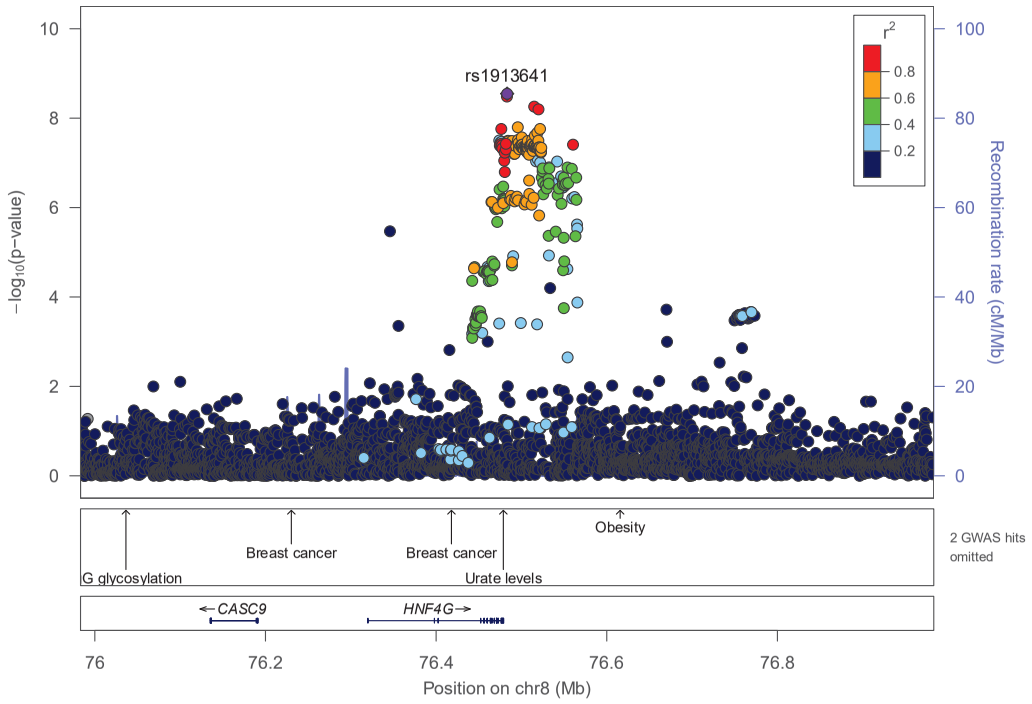

rs10098664
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Alcohol dependence
Nicotine use
Periodontitis (CDC/AAP)
20 GWAS hits omitted
←XKR6
MTMR9→
←FAM167A
LINC00208→
GATA4→
FDFT1→
←DEFB136
←LOC101929269
SLC35G5→
BLK→
SNORA99→
←CTSB
DEFB135→
TDH→
C8orf49→
←DEFB134
←LOC100129129
NEIL2→
FAM167A−AS1→
Position on chr8 (Mb)

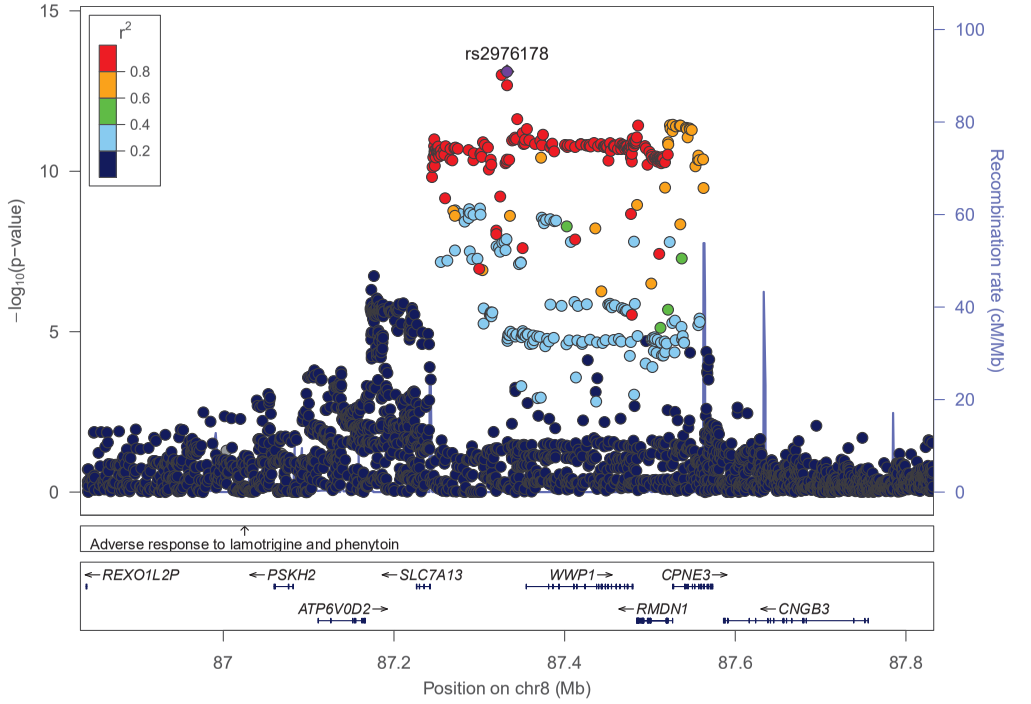

rs4872526
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Hypertriglyceridemia
HIV−1 control
Serum dimethylarginine levels (asymmetric)
Visceral fat
1 GWAS hit omitted
REEP4
PIWIL2
PPP3CC
C8orf58
PEBP4
RHOBTB2
LGI3
SLC39A14
SORBS3
EGR3
LOC101929237
TNFRSF10B
SFTPC
PDLIM2
LOC286059
BMP1
CCAR2
LOC254896
PHYHIP
BIN3
TNFRSF10C
MIR320A
BIN3−IT1
TNFRSF10D
POLR3D
LOC100507071
Position on chr8 (Mb)

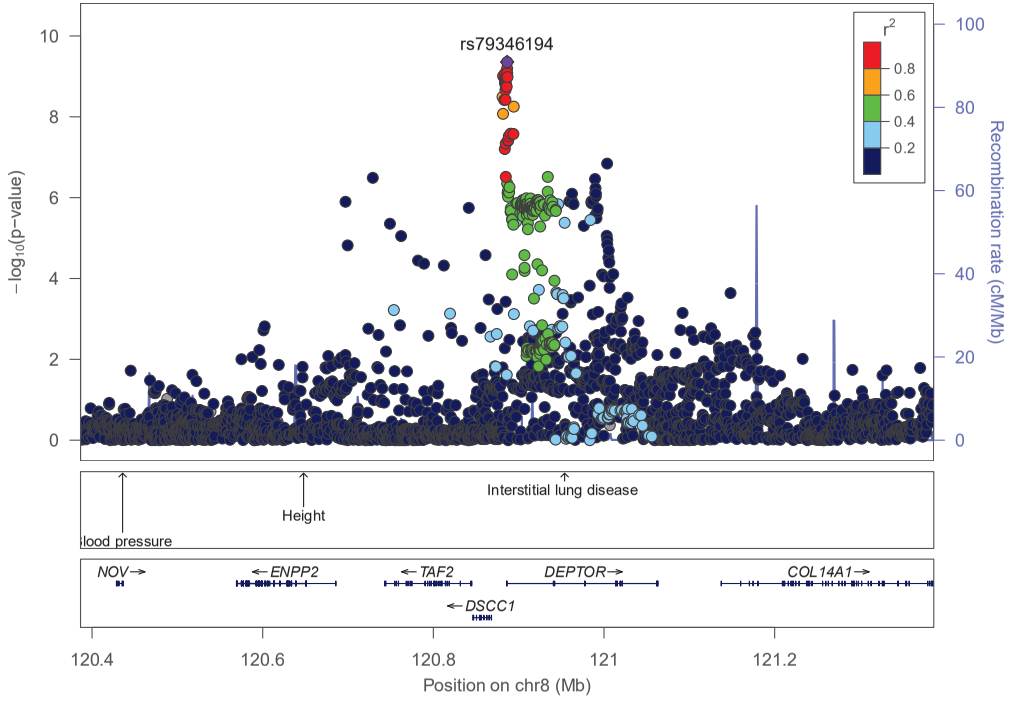

rs34861762
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Response to mTOR inhibitor (everolimus)
Prostate cancer
Urate levels
Subcutaneous adipose tissue
Migraine − clinic−based
Height
3 GWAS hits omitted
LOXL2
SLC25A37
NKX3−1
STC1
ADAM28
ENTPD4
NKX2−6
LOC101929294
ADAMDEC1
Position on chr8 (Mb)

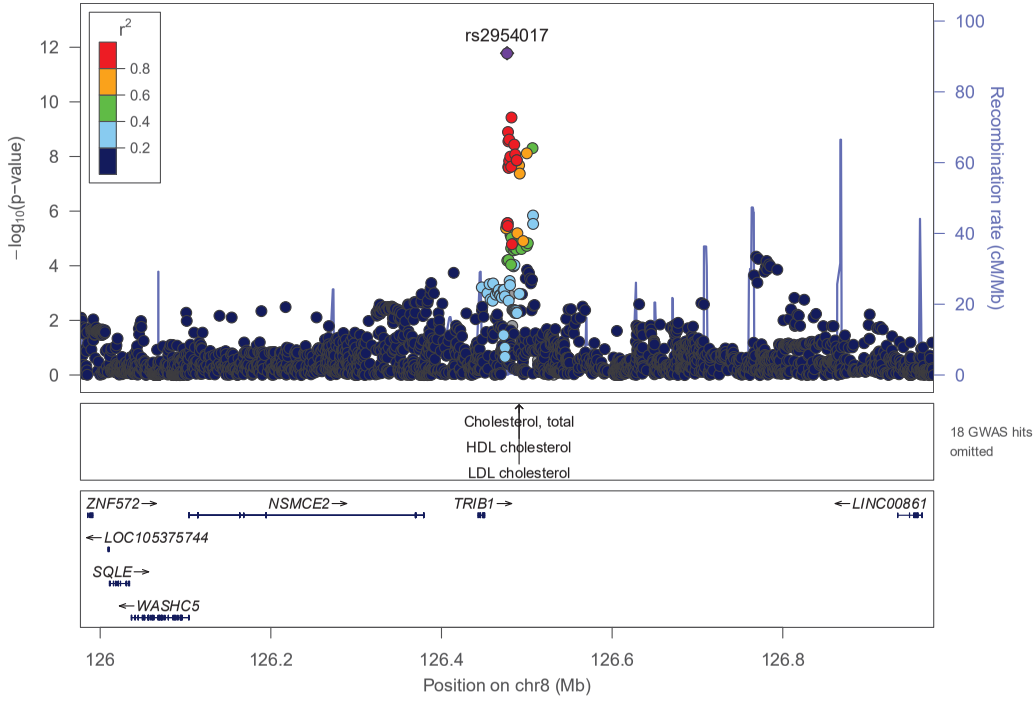

rs10102889
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Metabolite levels (X−11787)
Thyroid hormone levels
Thyroid cancer
Dialysis−related mortality
1 GWAS hit omitted
NRG1
NRG1−IT1
NRG1−IT3
Position on chr8 (Mb)

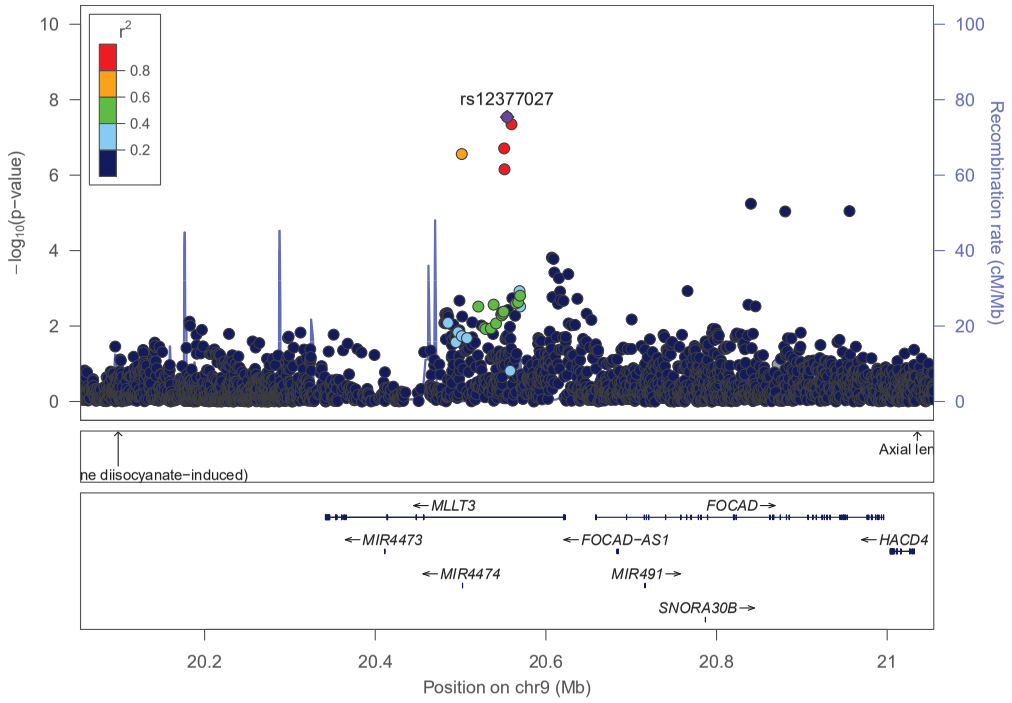

rs60991551
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Myopia (pathological)
Obesity−related traits
Response to amphetamines
Response to amphetamines
Pulmonary fun
1 GWAS hit omitted
CA8
LINC01301
RAB2A
CHD7
LOC100130298
Position on chr8 (Mb)

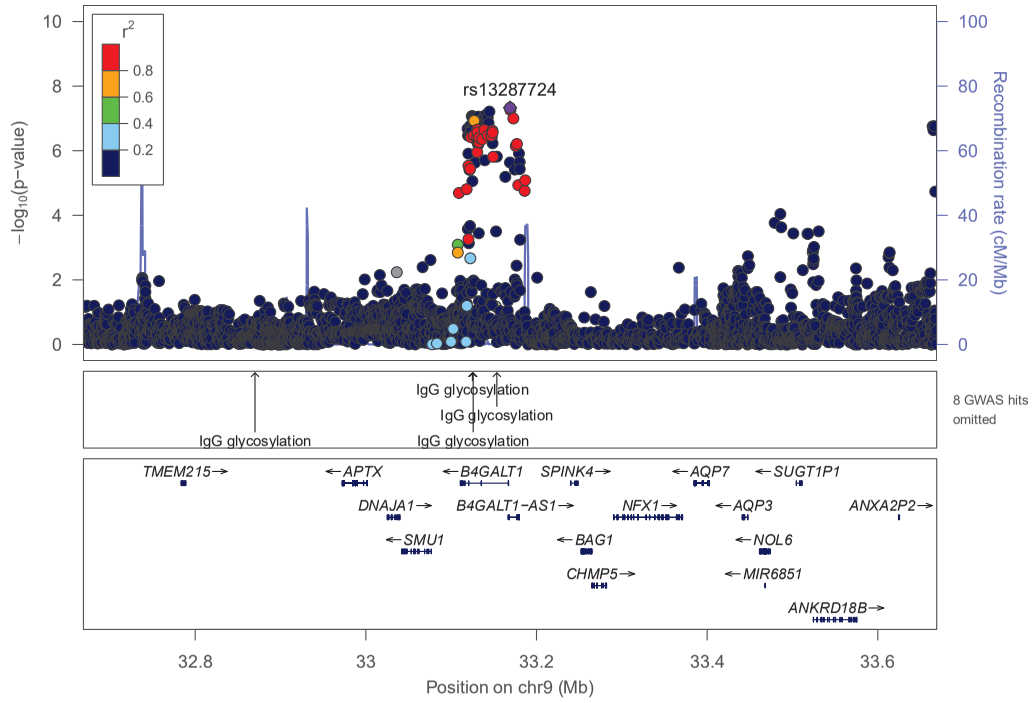

rs1913641
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Breast cancer
Breast cancer
Obesity
G glycosylation
Urate levels
2 GWAS hits
omitted
CASC9
HNF4G
Position on chr8 (Mb)

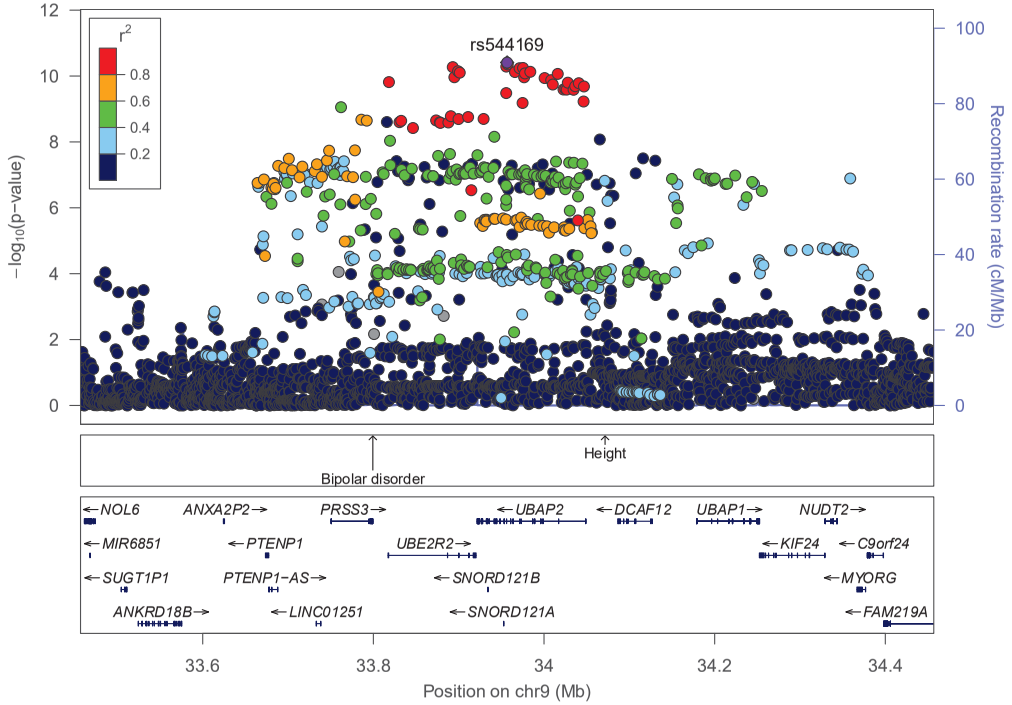

rs2976178
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Adverse response to lamotrigine and phenytoin
REXO1L2P
PSKH2
SLC7A13
WWP1
CPNE3
ATP6V0D2
RMDN1
CNGB3
Position on chr8 (Mb)

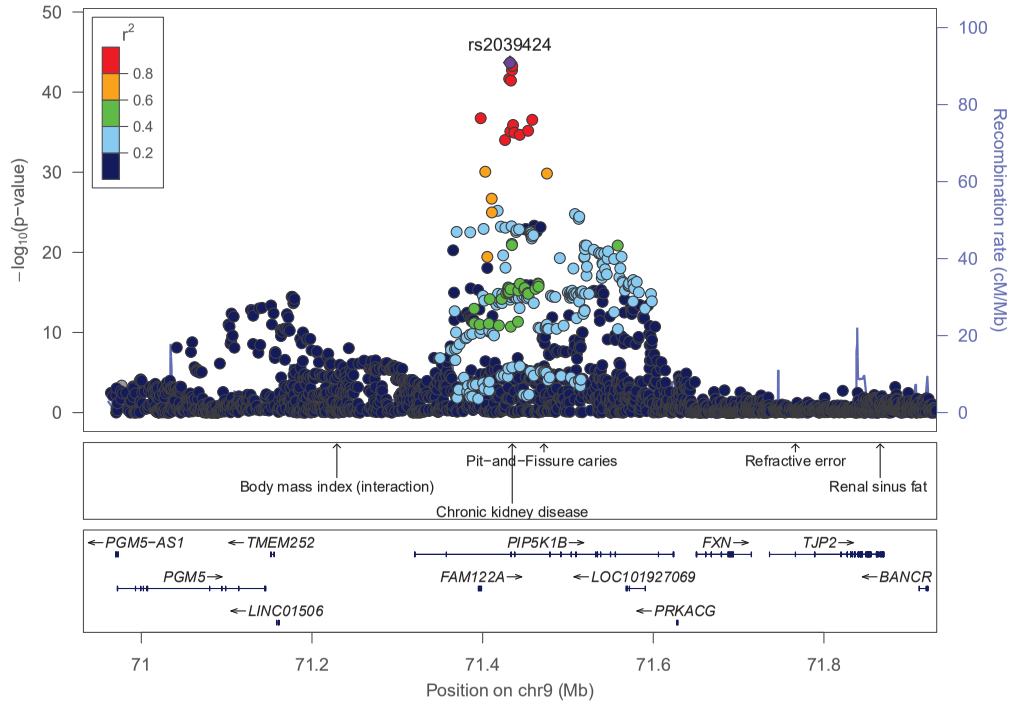

rs79346194
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Height
Interstitial lung disease
NOV
ENPP2
TAF2
DEPTOR
COL14A1
DSCC1
Position on chr8 (Mb)

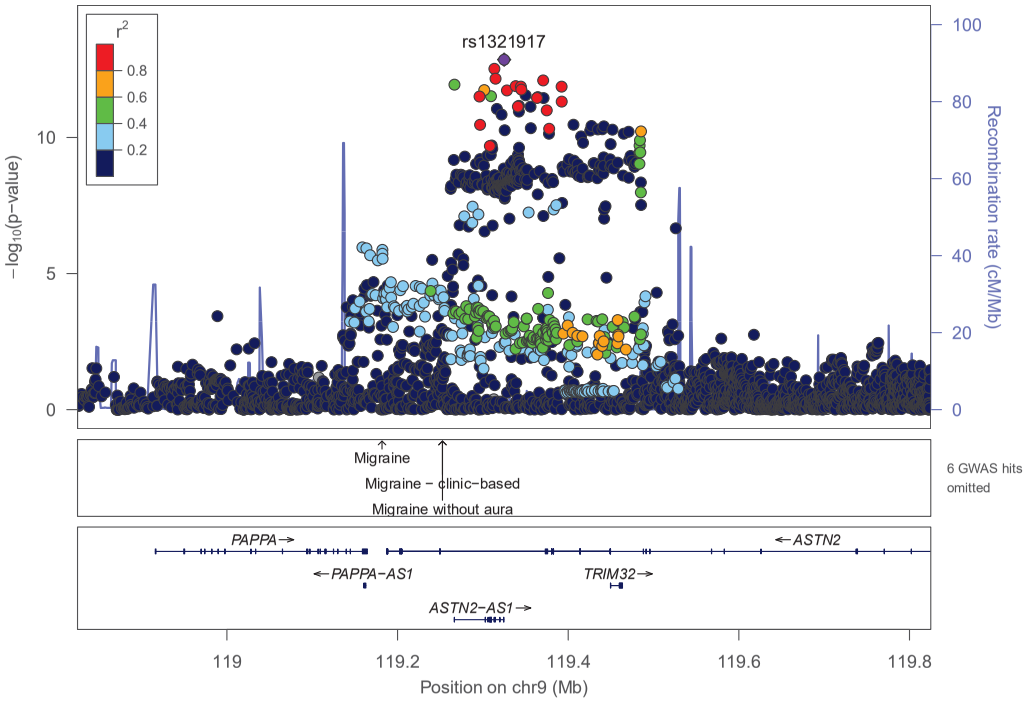

rs2954017
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
HDL cholesterol
LDL cholesterol
18 GWAS hits
omitted
ZNF572
NSMCE2
TRIB1
LINC00861
LOC105375744
SQLE
WASHC5
Position on chr8 (Mb)

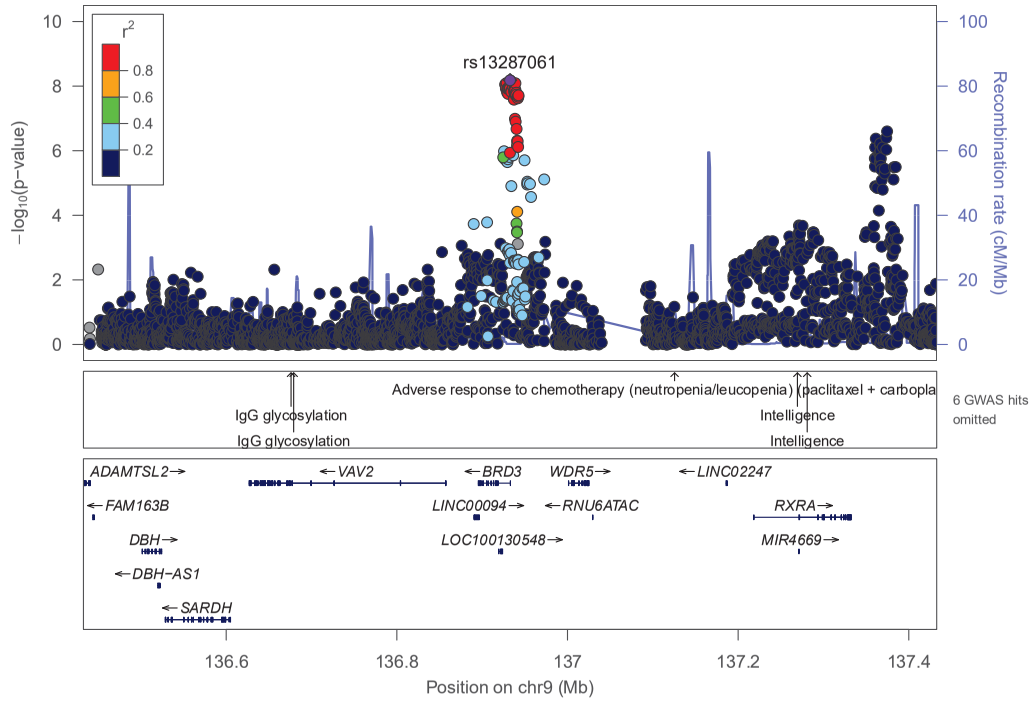

rs12377027
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
he diisocyanate−induced)
Axial len
MLLT3
FOCAD
MIR4473
FOCAD−AS1
HACD4
MIR4474
MIR491
SNORA30B
Position on chr9 (Mb)

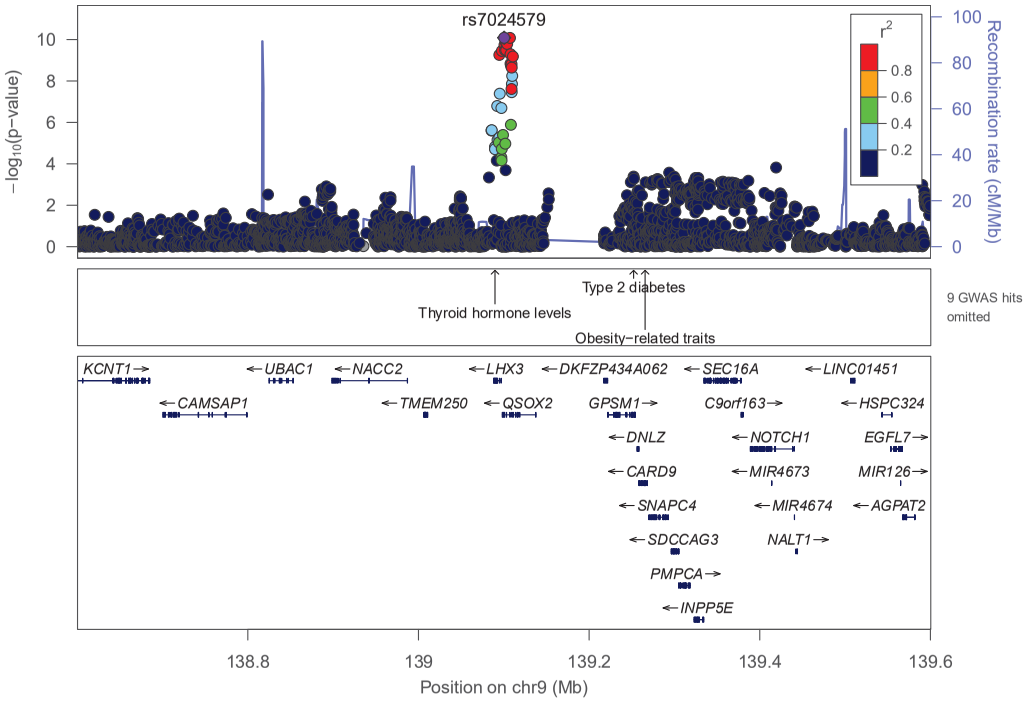

rs13287724
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
IgG glycosylation
IgG glycosylation
IgG glycosylation
IgG glycosylation
8 GWAS hits
omitted
TMEM215
APTX
B4GALT1
SPINK4
AQP7
SUGT1P1
DNAJA1
B4GALT1−AS1
NFX1
AQP3
ANXA2P2
SMU1
BAG1
NOL6
CHMP5
MIR6851
ANKRD18B
Position on chr9 (Mb)

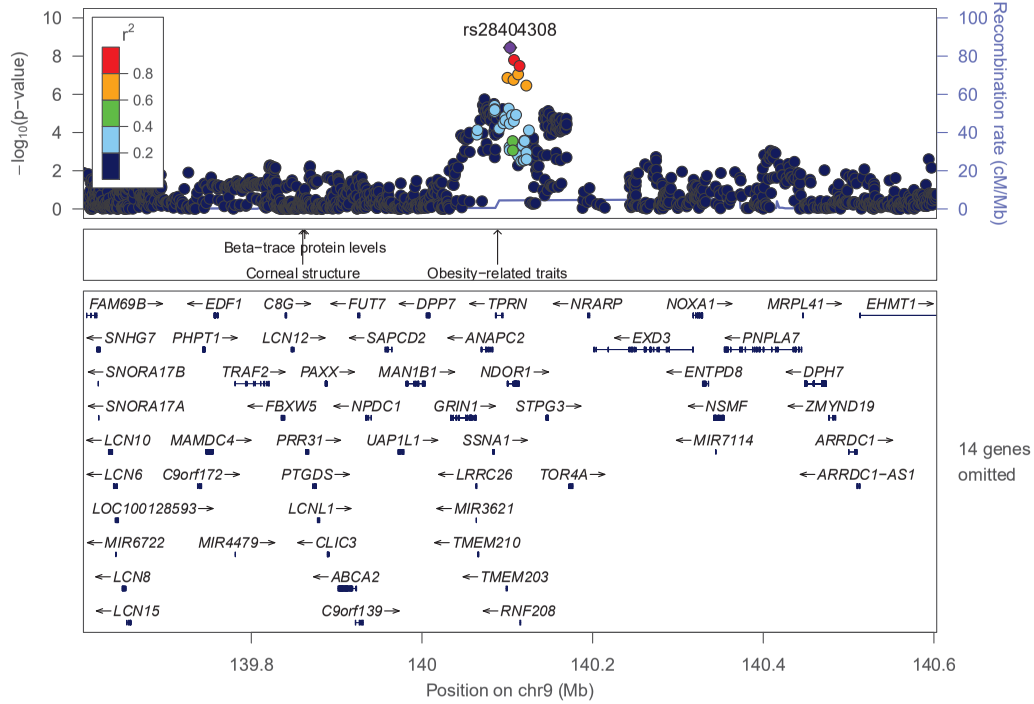

rs544169
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Bipolar disorder
Height
NOL6
ANXA2P2
PRSS3
UBAP2
DCAF12
UBAP1
NUDT2
MIR6851
PTENP1
UBE2R2
KIF24
C9orf24
SUGT1P1
PTENP1−AS
SNORD121B
MYORG
ANKRD18B
LINC01251
SNORD121A
FAM219A
Position on chr9 (Mb)

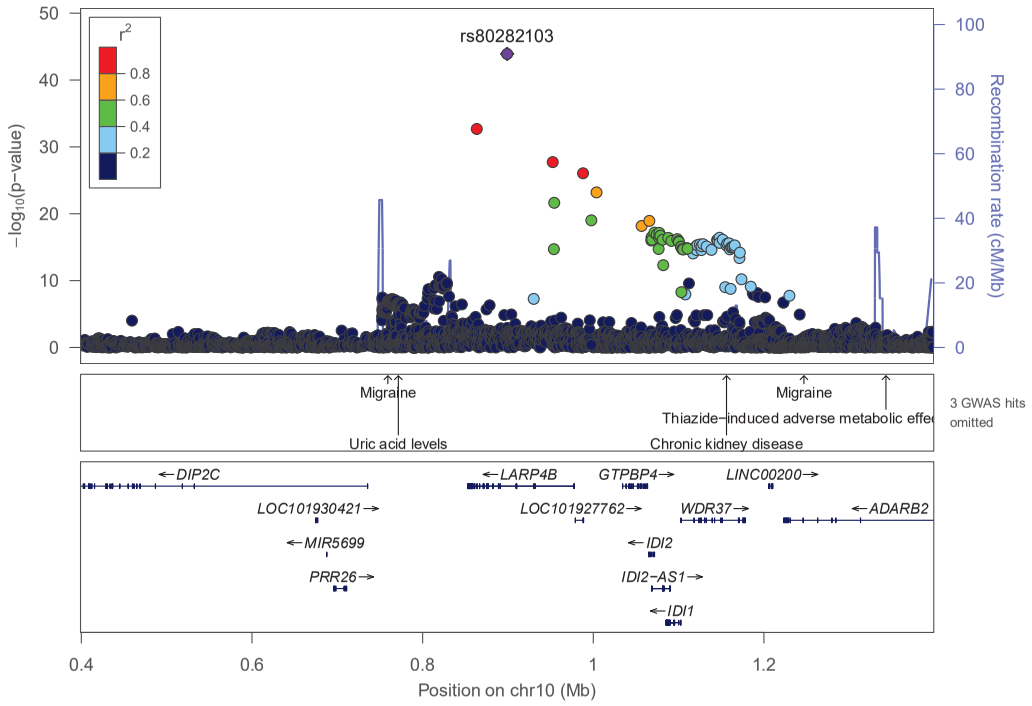

rs2039424
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Body mass index (interaction)
Pit−and−Fissure caries
Chronic kidney disease
Refractive error
Renal sinus fat
PGM5−AS1
TMEM252
PIP5K1B
FXN
TJP2
PGM5
FAM122A
LOC101927069
BANCR
LINC01506
PRKACG
Position on chr9 (Mb)

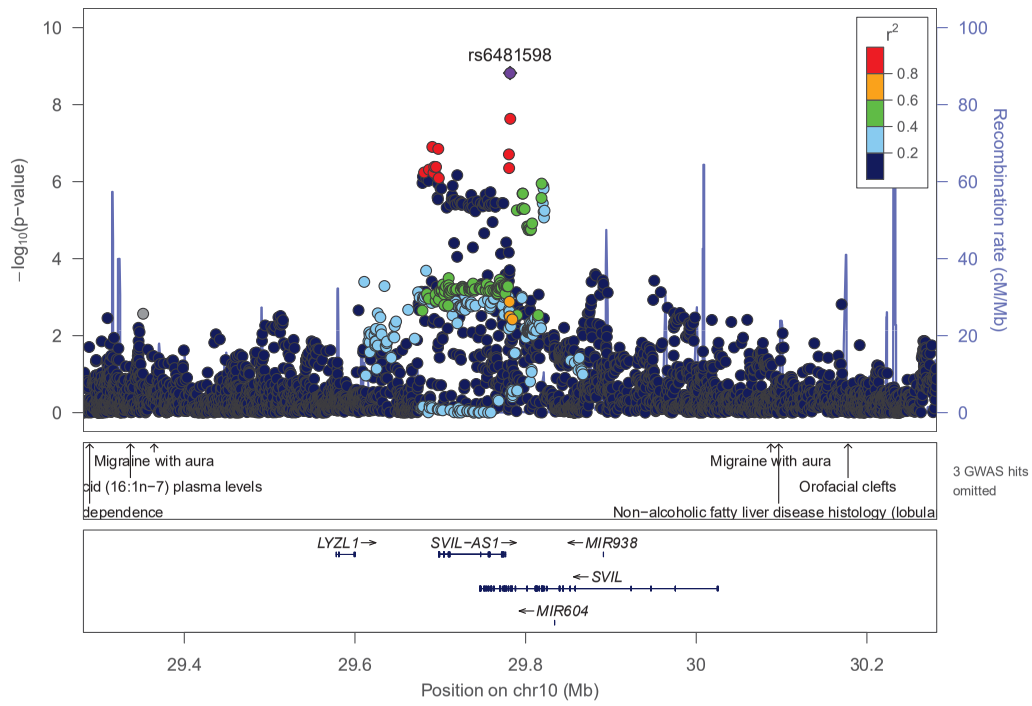

rs1321917
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Migraine
Migraine − clinic−based
Migraine without aura
6 GWAS hits omitted
PAPPA→
←ASTN2
←PAPPA−AS1
TRIM32→
ASTN2−AS1→
119
119.2
119.4
119.6
119.8
Position on chr9 (Mb)

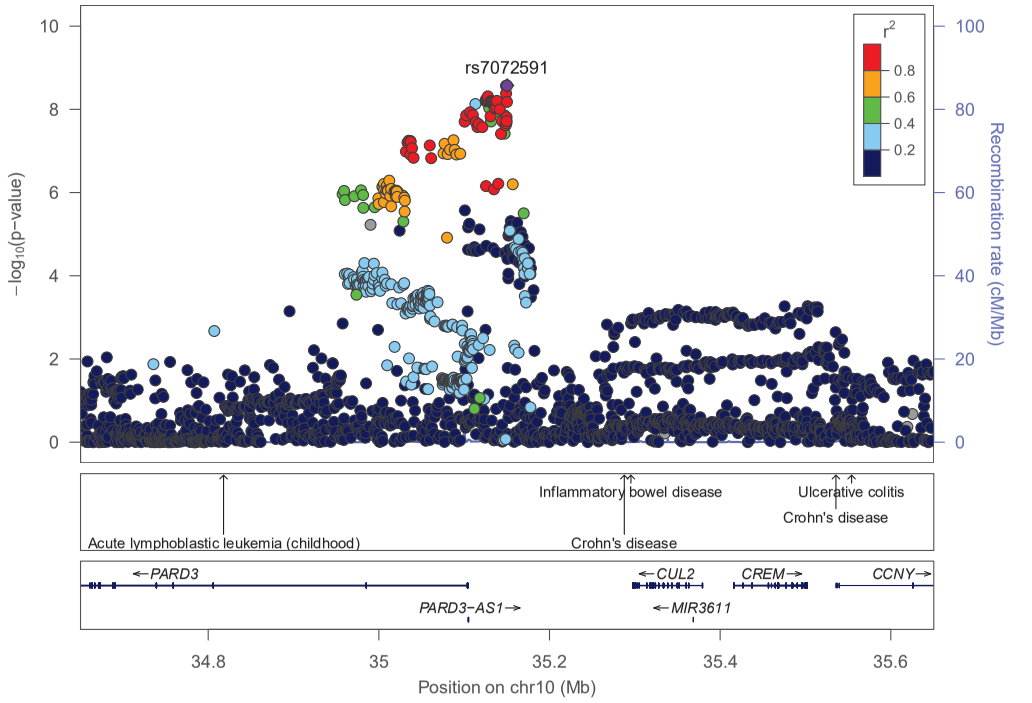

rs13287061
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
IgG glycosylation
IgG glycosylation
Adverse response to chemotherapy (neutropenia/leucopenia) (paclitaxel + carbopla
Intelligence
Intelligence
6 GWAS hits omitted
ADAMTSL2→
←VAV2
←BRD3
WDR5→
←LINC02247
←FAM163B
LINC00094→
←RNU6ATAC
RXRA→
DBH→
LOC100130548→
MIR4669→
←DBH−AS1
←SARDH
136.6
136.8
137
137.2
137.4
Position on chr9 (Mb)

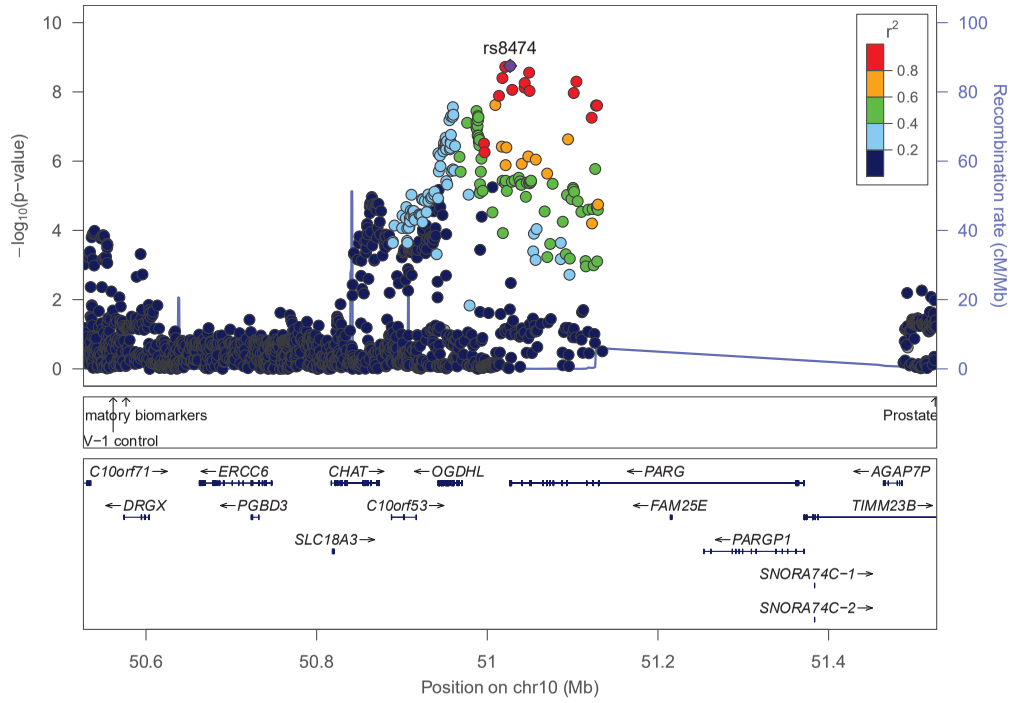

rs7024579
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Thyroid hormone levels
Type 2 diabetes
Obesity−related traits
9 GWAS hits omitted
KCNT1→
←UBAC1
←NACC2
←LHX3
←DKFZP434A062
←SEC16A
←LINC01451
←CAMSAP1
←TMEM250
←QSOX2
GPSM1→
C9orf163→
←HSPC324
←DNLZ
←NOTCH1
EGFL7→
←CARD9
←MIR4673
MIR126→
←SNAPC4
←MIR4674
←AGPAT2
←SDCCAG3
NALT1→
PMPCA→
←INPP5E
138.8
139
139.2
139.4
139.6
Position on chr9 (Mb)

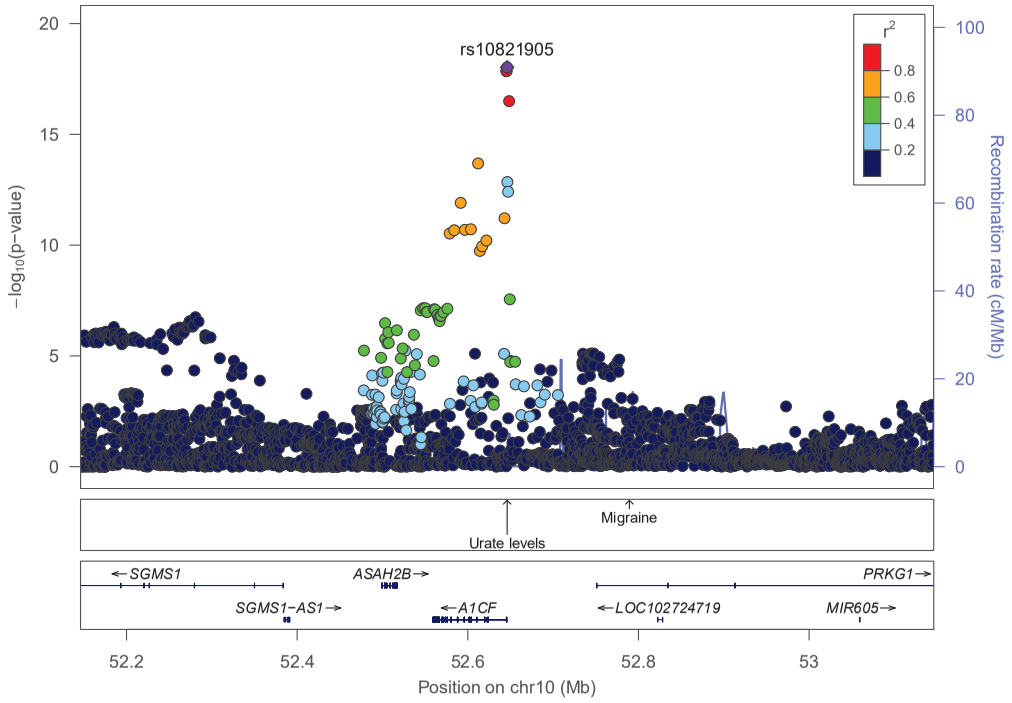

rs28404308
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Beta−trace protein levels
Corneal structure
Obesity−related traits
14 genes omitted
FAM69B→
←EDF1
C8G→
←FUT7
←DPP7
←TPRN
←NRARP
NOXA1→
MRPL41→
EHMT1→
←SNHG7
PHPT1→
LCN12→
←SAPCD2
←ANAPC2
←EXD3
←PNPLA7
←SNORA17B
TRAF2→
PAXX→
MAN1B1→
NDOR1→
←ENTPD8
←DPH7
←SNORA17A
←FBXW5
←NPDC1
GRIN1→
STPG3→
←NSMF
←ZMYND19
←LCN10
MAMDC4→
PRR31→
UAP1L1→
SSNA1→
←MIR7114
ARRDC1→
←LCN6
C9orf172→
PTGDS→
←LRRC26
TOR4A→
←ARRDC1−AS1
LOC100128593→
LCNL1→
←MIR3621
←MIR6722
MIR4479→
←CLIC3
←TMEM210
←LCN8
←ABCA2
←TMEM203
←LCN15
C9orf139→
←RNF208
139.8
140
140.2
140.4
140.6
Position on chr9 (Mb)

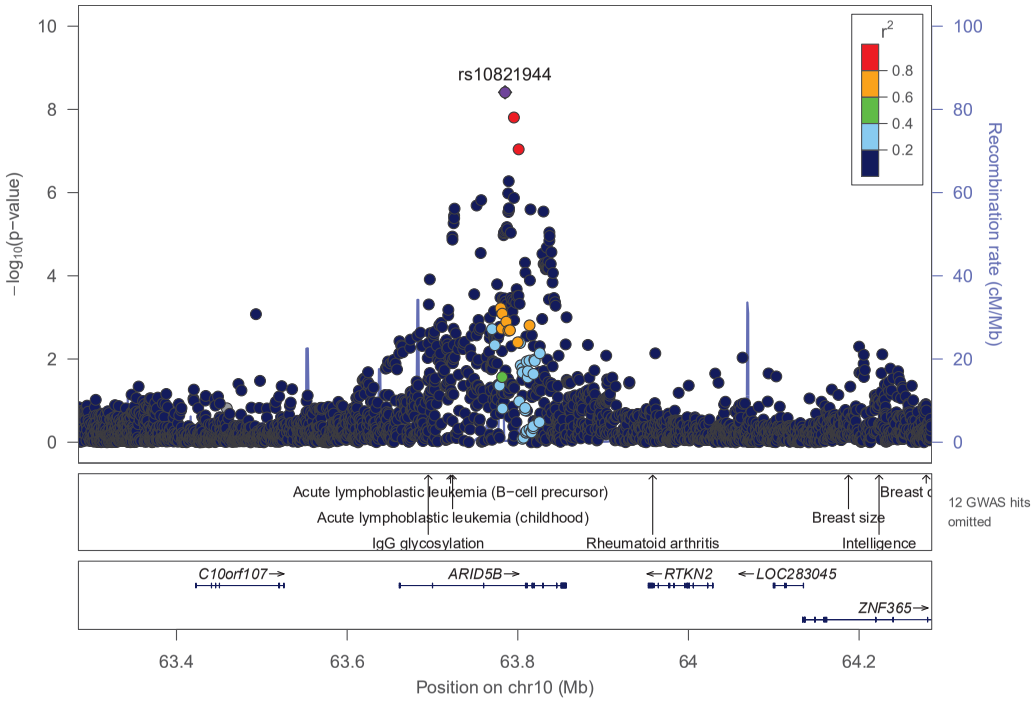

rs80282103
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Migraine
Uric acid levels
Migraine
Thiazide−induced adverse metabolic effe
Chronic kidney disease
3 GWAS hits omitted
DIP2C
LARP4B
GTPBP4
LINC00200
LOC101930421
LOC101927762
WDR37
ADARB2
MIR5699
IDI2
PRR26
IDI2−AS1
IDI1
Position on chr10 (Mb)

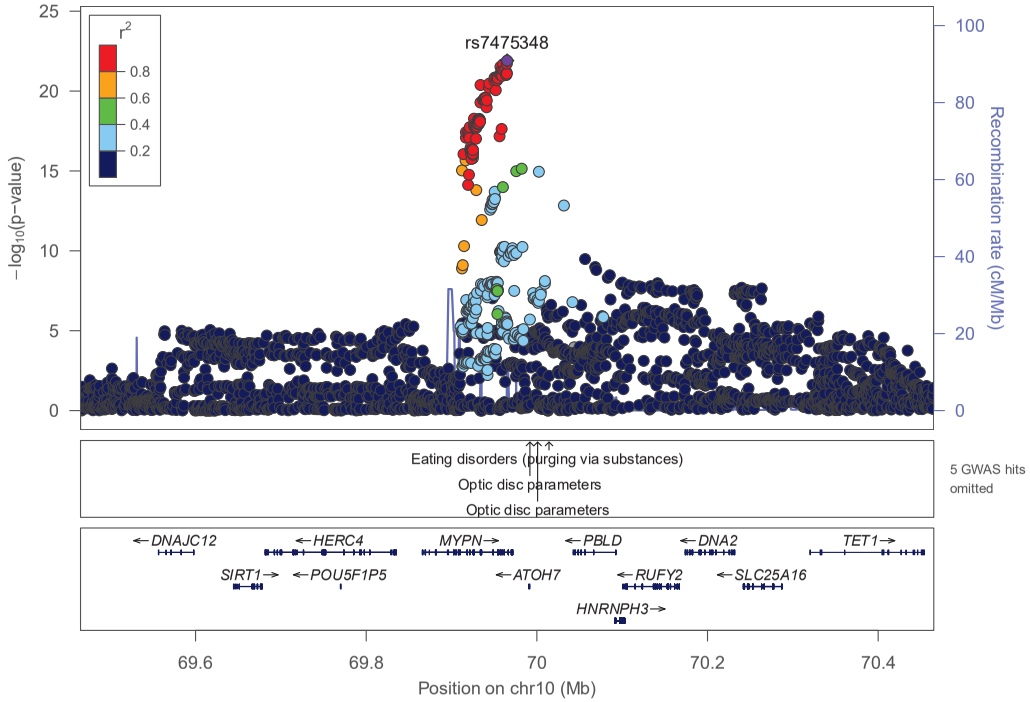

rs6481598
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Migraine with aura
id (16:1n−7) plasma levels
dependence
Migraine with aura
Orofacial clefts
Non−alcoholic fatty liver disease histology (lobula
3 GWAS hits omitted
LYZL1
SVIL−AS1
MIR938
SVIL
MIR604
Position on chr10 (Mb)

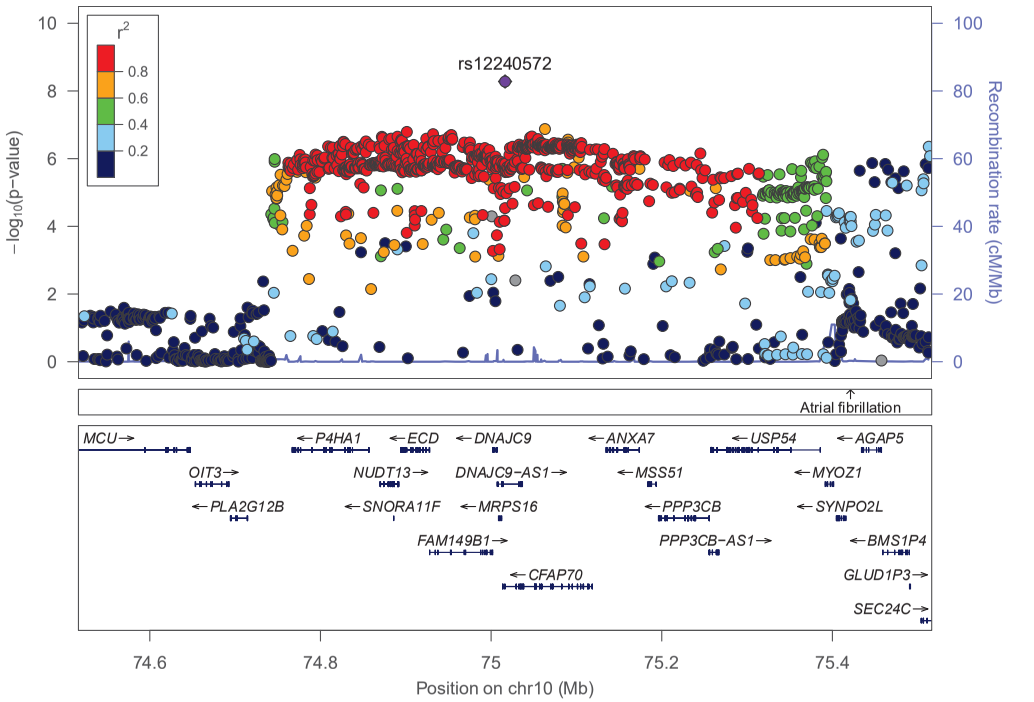

rs7072591
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Inflammatory bowel disease
Ulcerative colitis
Crohn's disease
Acute lymphoblastic leukemia (childhood)
Crohn's disease
PARD3
CUL2
CREM
CCNY
PARD3−AS1
MIR3611
Position on chr10 (Mb)

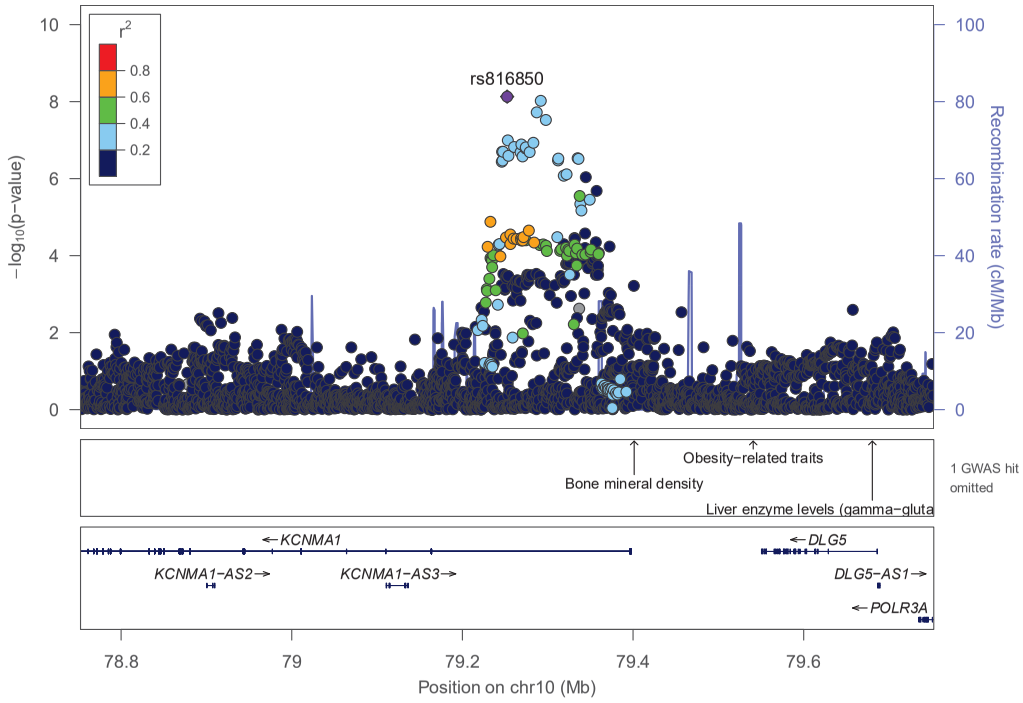

rs8474
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
matory biomarkers
V−1 control
Prostate
C10orf71
ERCC6
CHAT
OGDHL
PARG
AGAP7P
DRGX
PGBD3
C10orf53
FAM25E
TIMM23B
SLC18A3
PARGP1
SNORA74C−1
SNORA74C−2
Position on chr10 (Mb)

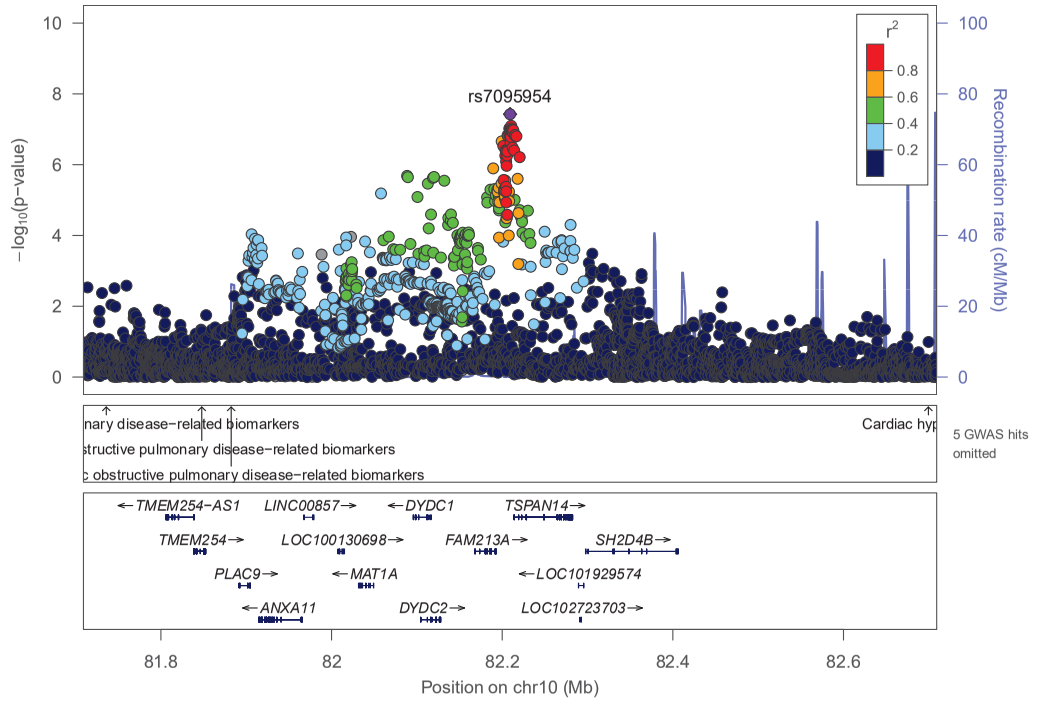

rs10821905
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Urate levels
Migraine
SGMS1
ASAH2B
PRKG1
SGMS1−AS1
A1CF
LOC102724719
MIR605
Position on chr10 (Mb)

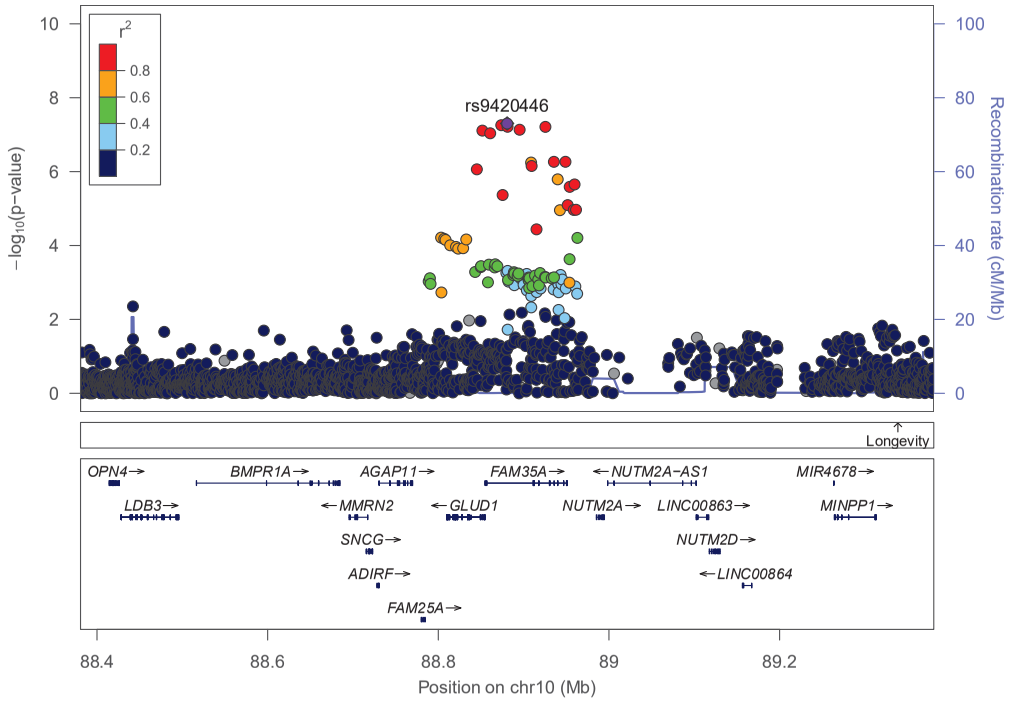

rs10821944
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Acute lymphoblastic leukemia (B−cell precursor)
Acute lymphoblastic leukemia (childhood)
IgG glycosylation
Rheumatoid arthritis
Breast size
Intelligence
12 GWAS hits omitted
C10orf107
ARID5B
RTKN2
LOC283045
ZNF365
Position on chr10 (Mb)

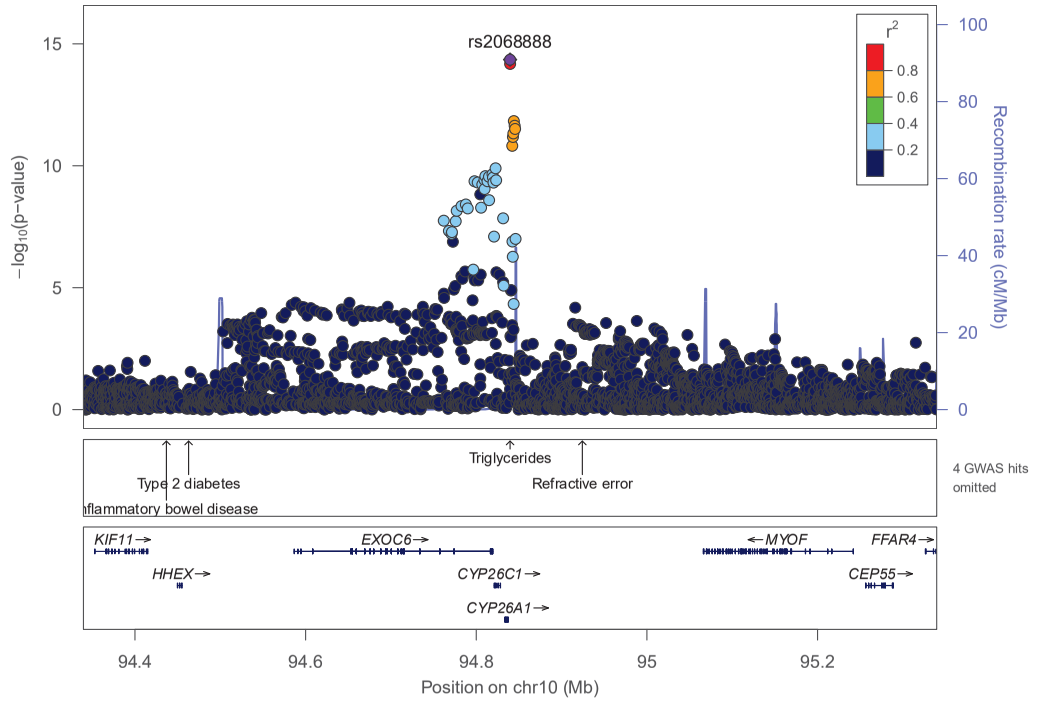

rs7475348
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Eating disorders (purging via substances)
Optic disc parameters
Optic disc parameters
5 GWAS hits omitted
DNAJC12
HERC4
MYPN
PBLD
DNA2
TET1
SIRT1
POU5F1P5
ATOH7
RUFY2
SLC25A16
HNRNPH3
Position on chr10 (Mb)

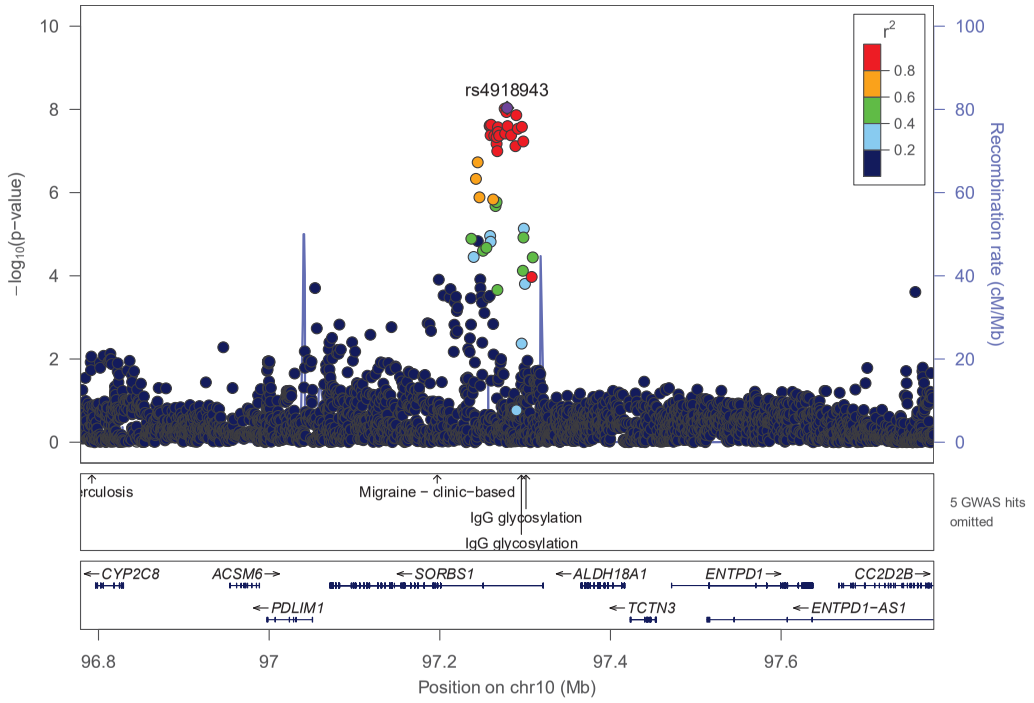

rs12240572
r2
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Atrial fibrillation
MCU
P4HA1
ECD
DNAJC9
ANXA7
USP54
AGAP5
OIT3
NUDT13
DNAJC9−AS1
MSS51
MYOZ1
PLA2G12B
SNORA11F
MRPS16
PPP3CB
SYNPO2L
FAM149B1
PPP3CB−AS1
BMS1P4
CFAP70
GLUD1P3
SEC24C
Position on chr10 (Mb)

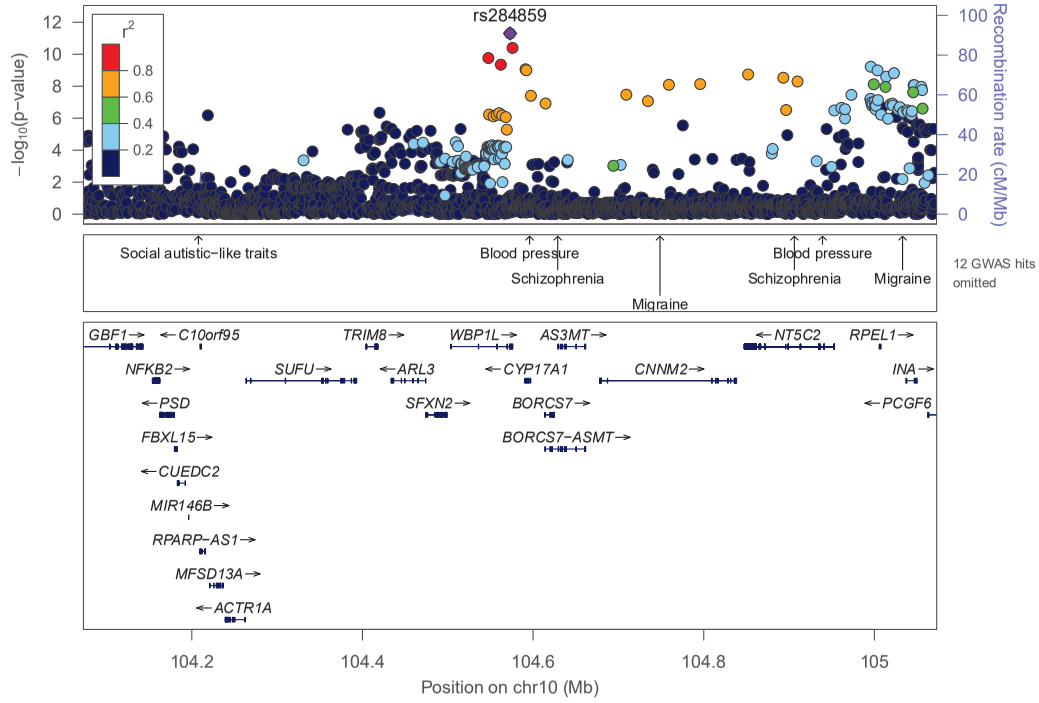

rs816850
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Bone mineral density
Obesity−related traits
Liver enzyme levels (gamma−gluta
1 GWAS hit omitted
KCNMA1
DLG5
KCNMA1−AS2
KCNMA1−AS3
DLG5−AS1
POLR3A
Position on chr10 (Mb)

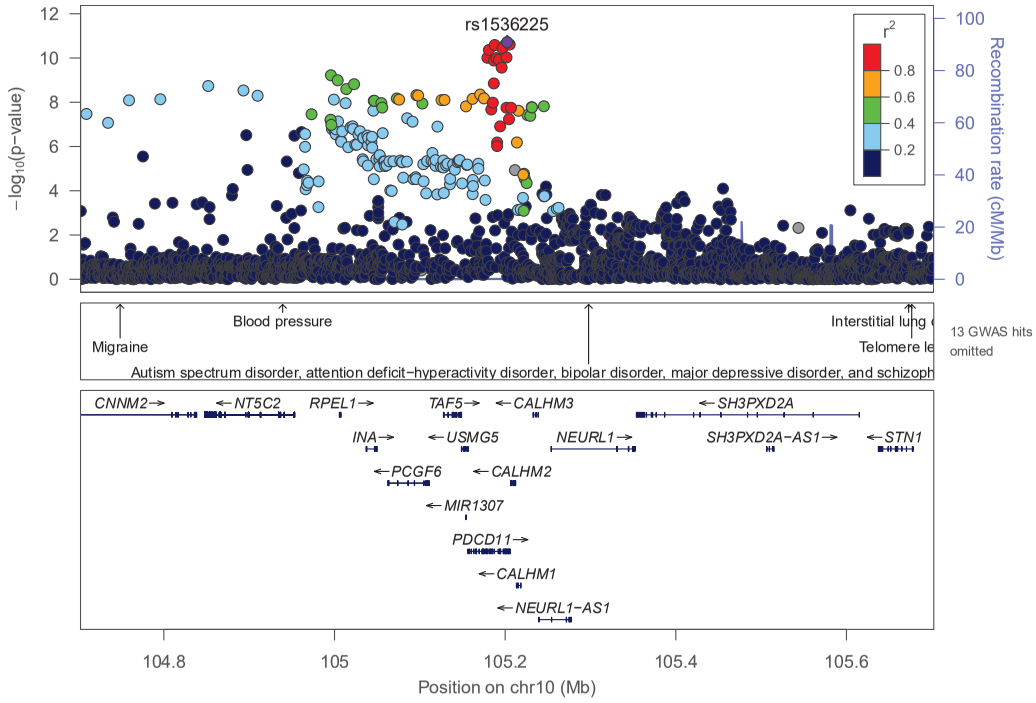

rs7095954
r²
−log10(p−value)
Recombination rate (cM/Mb)
nary disease−related biomarkers
structive pulmonary disease−related biomarkers
obstructive pulmonary disease−related biomarkers
Cardiac hyp
5 GWAS hits omitted
TMEM254−AS1
LINC00857
DYDC1
TSPAN14
TMEM254
LOC100130698
FAM213A
SH2D4B
PLAC9
MAT1A
LOC101929574
ANXA11
DYDC2
LOC102723703
Position on chr10 (Mb)

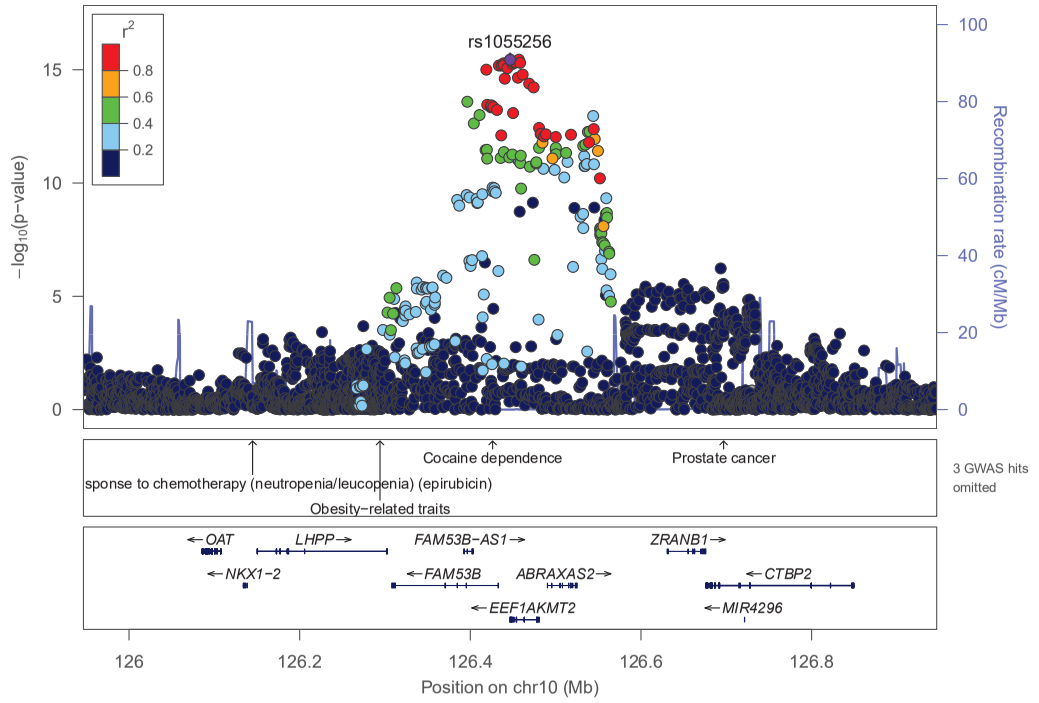

rs9420446
r²
−log10(p−value)
Recombination rate (cM/Mb)
Longevity
OPN4
BMPR1A
AGAP11
FAM35A
NUTM2A−AS1
MIR4678
LDB3
MMRN2
GLUD1
NUTM2A
LINC00863
MINPP1
SNCG
NUTM2D
ADIRF
LINC00864
FAM25A
Position on chr10 (Mb)

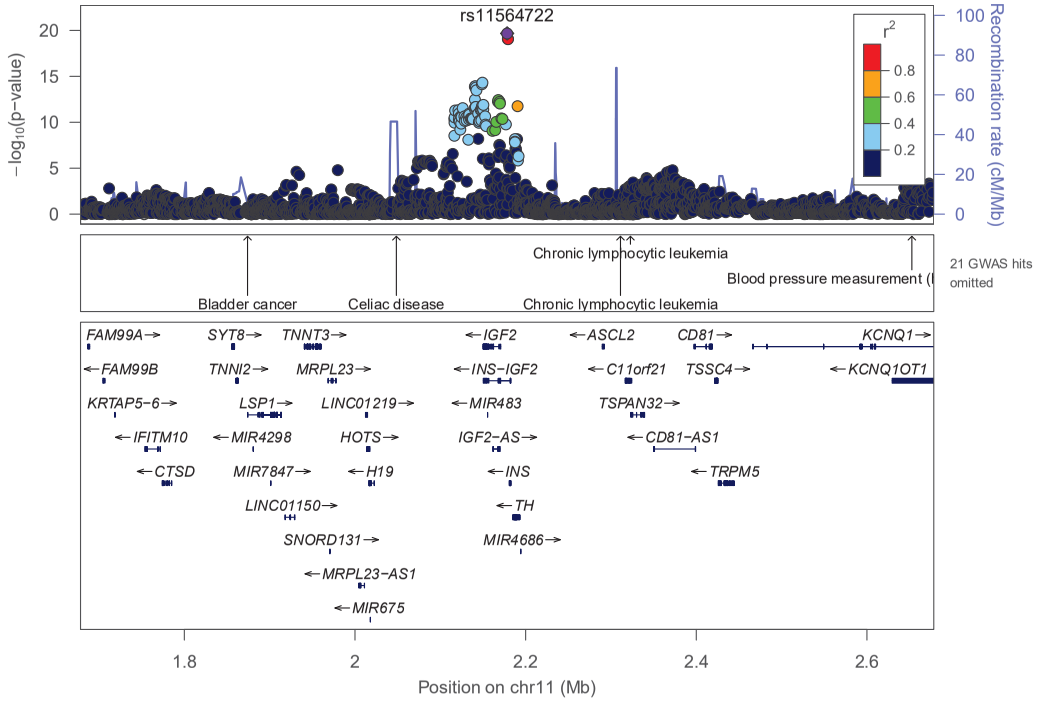

rs2068888
r²
−log10(p−value)
Recombination rate (cM/Mb)
Triglycerides
Type 2 diabetes
Refractive error
flammatory bowel disease
4 GWAS hits omitted
KIF11
EXOC6
MYOF
FFAR4
HHEX
CYP26C1
CEP55
CYP26A1
Position on chr10 (Mb)

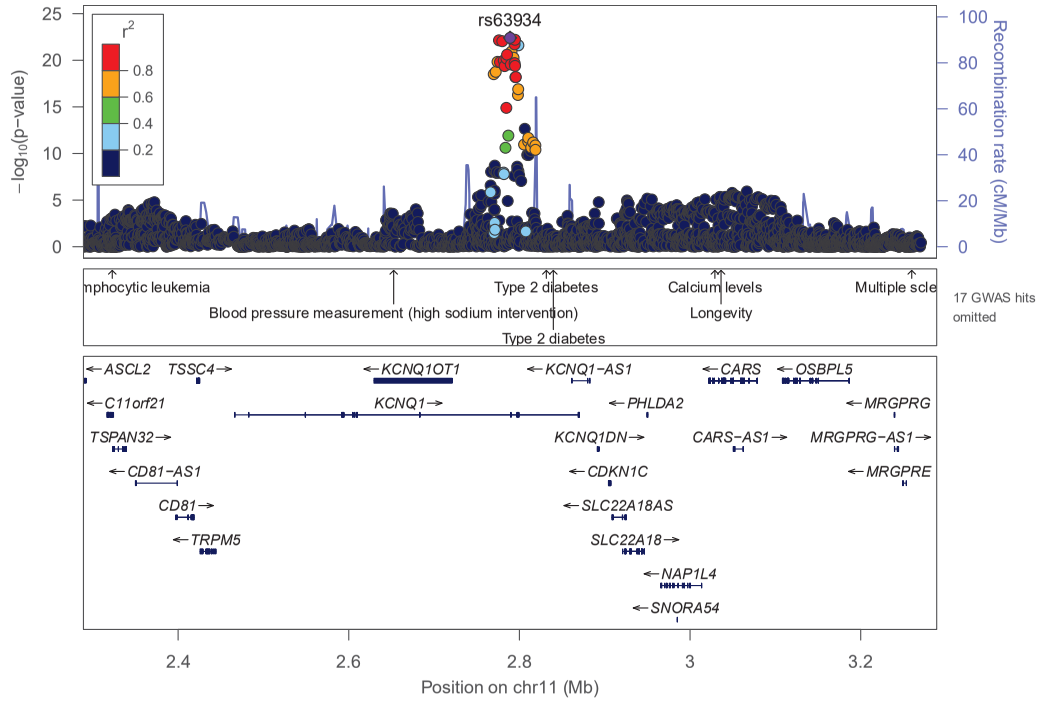

rs4918943
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
rculosis
Migraine − clinic−based
IgG glycosylation
IgG glycosylation
5 GWAS hits omitted
CYP2C8
ACSM6
SORBS1
ALDH18A1
ENTPD1
CC2D2B
PDLIM1
TCTN3
ENTPD1−AS1
Position on chr10 (Mb)

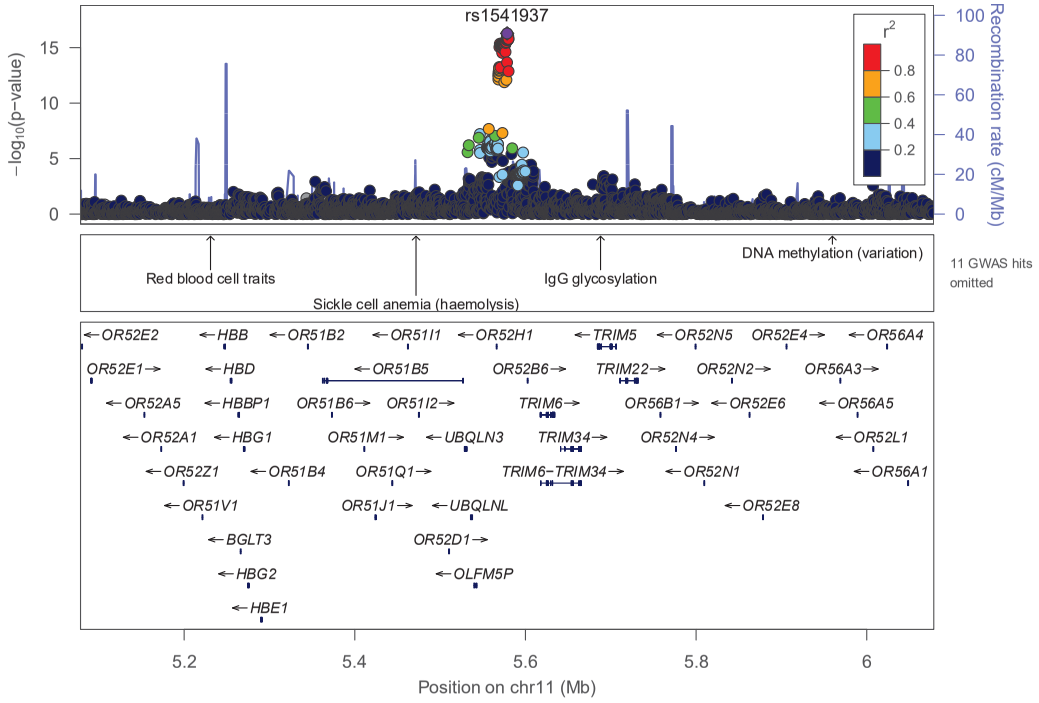

rs284859
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Social autistic−like traits
Blood pressure
Schizophrenia
Migraine
Blood pressure
Schizophrenia
Migraine
12 GWAS hits omitted
GBF1
C10orf95
TRIM8
WBP1L
AS3MT
NT5C2
RPEL1
NFKB2
SUFU
ARL3
CYP17A1
CNNM2
INA
PSD
SFXN2
BORCS7
PCGF6
FBXL15
BORCS7−ASMT
CUEDC2
MIR146B
RPARP−AS1
MFSD13A
ACTR1A
Position on chr10 (Mb)

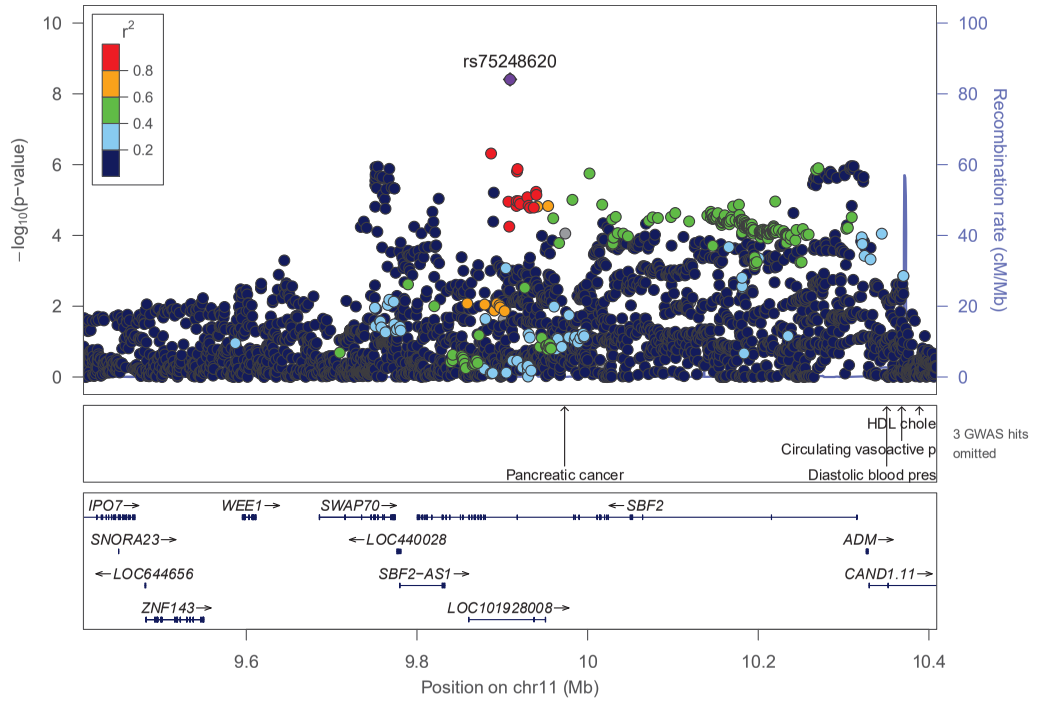

rs1536225
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Migraine
Blood pressure
Interstitial lung
Telomere le
13 GWAS hits omitted
Autism spectrum disorder, attention deficit−hyperactivity disorder, bipolar disorder, major depressive disorder, and schizoph
CNNM2
NT5C2
RPEL1
TAF5
CALHM3
SH3PXD2A
INA
USMG5
NEURL1
SH3PXD2A−AS1
STN1
PCGF6
CALHM2
MIR1307
PDCD11
CALHM1
NEURL1−AS1
Position on chr10 (Mb)

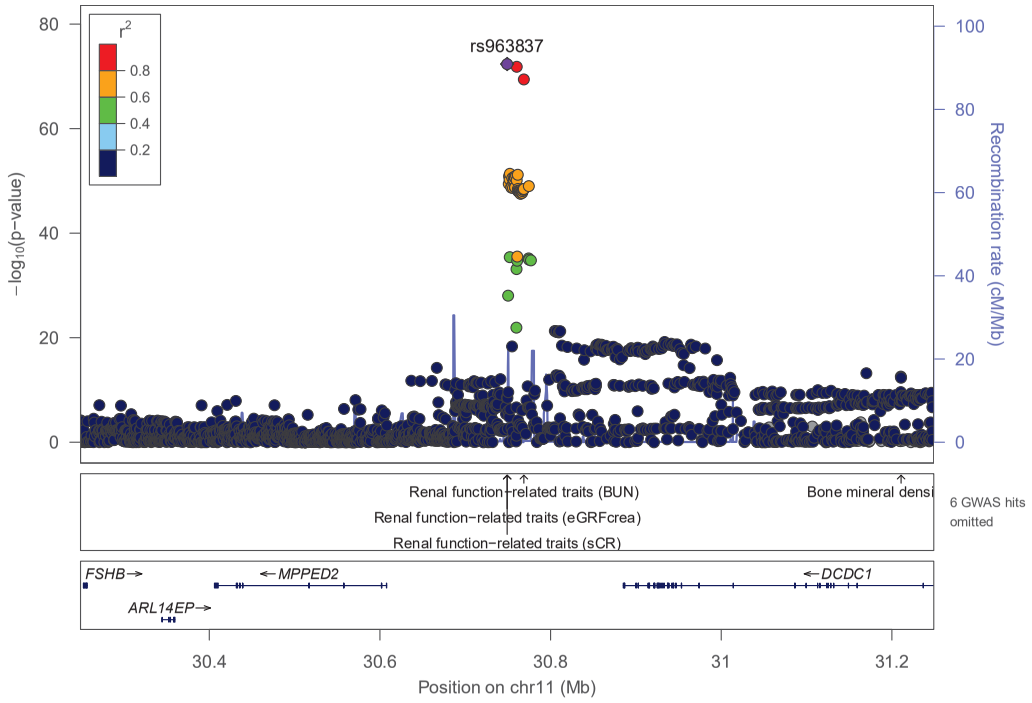

rs1055256
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cocaine dependence
Prostate cancer
sponse to chemotherapy (neutropenia/leucopenia) (epirubicin)
Obesity−related traits
3 GWAS hits omitted
OAT
LHPP
FAM53B−AS1
ZRANB1
NKX1−2
FAM53B
ABRAXAS2
CTBP2
EEF1AKMT2
MIR4296
Position on chr10 (Mb)

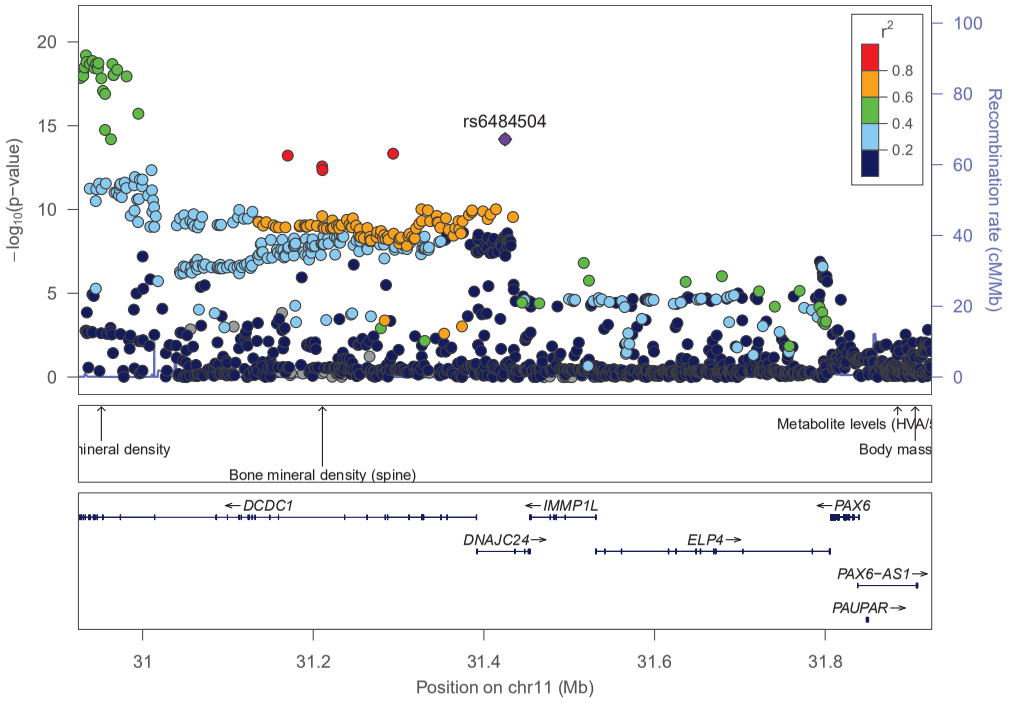

rs11564722
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Bladder cancer
Celiac disease
Chronic lymphocytic leukemia
Chronic lymphocytic leukemia
Blood pressure measurement (
21 GWAS hits omitted
FAM99A→ SYT8→ TNNT3→ ←IGF2 ←ASCL2 CD81→ KCNQ1→
←FAM99B TNNI2→ MRPL23→ ←INS−IGF2 ←C11orf21 TSSC4→ ←KCNQ1OT1
KRTAP5−6→ LSP1→ LINC01219→ ←MIR483 TSPAN32→
←IFITM10 ←MIR4298 HOTS→ IGF2−AS→ ←CD81−AS1
←CTSD MIR7847→ ←H19 ←INS ←TRPM5
LINC01150→ ←TH
SNORD131→ MIR4686→
←MRPL23−AS1
←MIR675
1.8
2
2.2
2.4
2.6
Position on chr11 (Mb)

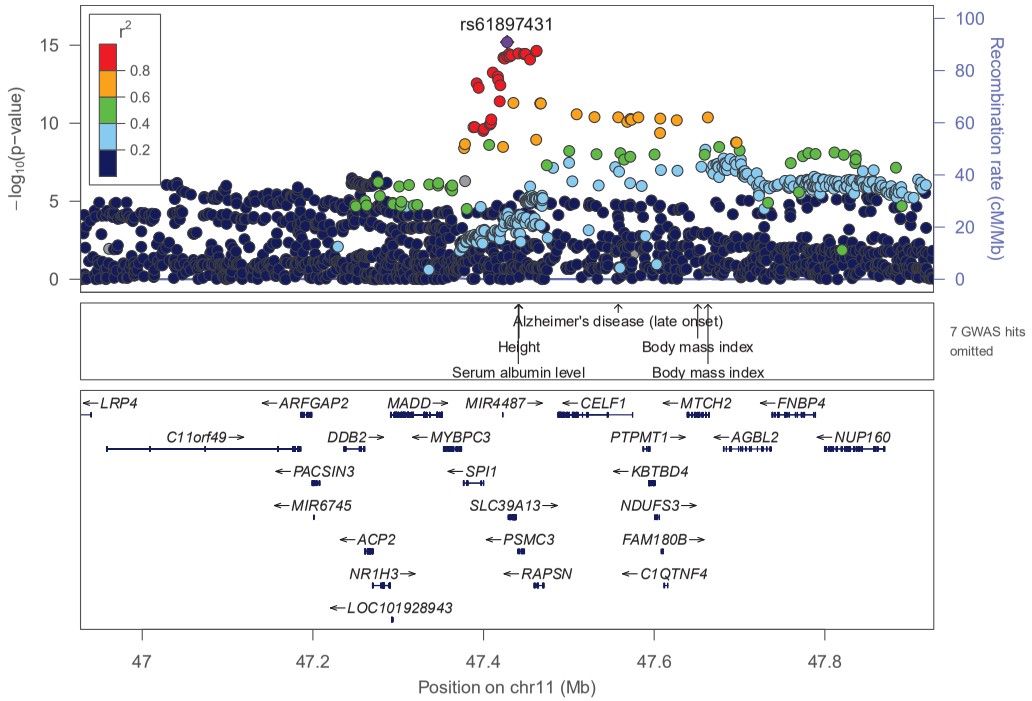

rs63934
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
nphocytic leukemia
Blood pressure measurement (high sodium intervention)
Type 2 diabetes
Type 2 diabetes
Calcium levels
Longevity
Multiple scle
17 GWAS hits omitted
←ASCL2 TSSC4→ ←KCNQ1OT1 ←KCNQ1−AS1 ←CARS ←OSBPL5
←C11orf21 KCNQ1→ ←PHLDA2 ←MRGPRG
TSPAN32→ KCNQ1DN→ CARS−AS1→ MRGPRG−AS1→
←CD81−AS1 ←CDKN1C ←MRGPRE
CD81→ ←SLC22A18AS
←TRPM5 SLC22A18→
←NAP1L4
←SNORA54
2.4
2.6
2.8
3
3.2
Position on chr11 (Mb)

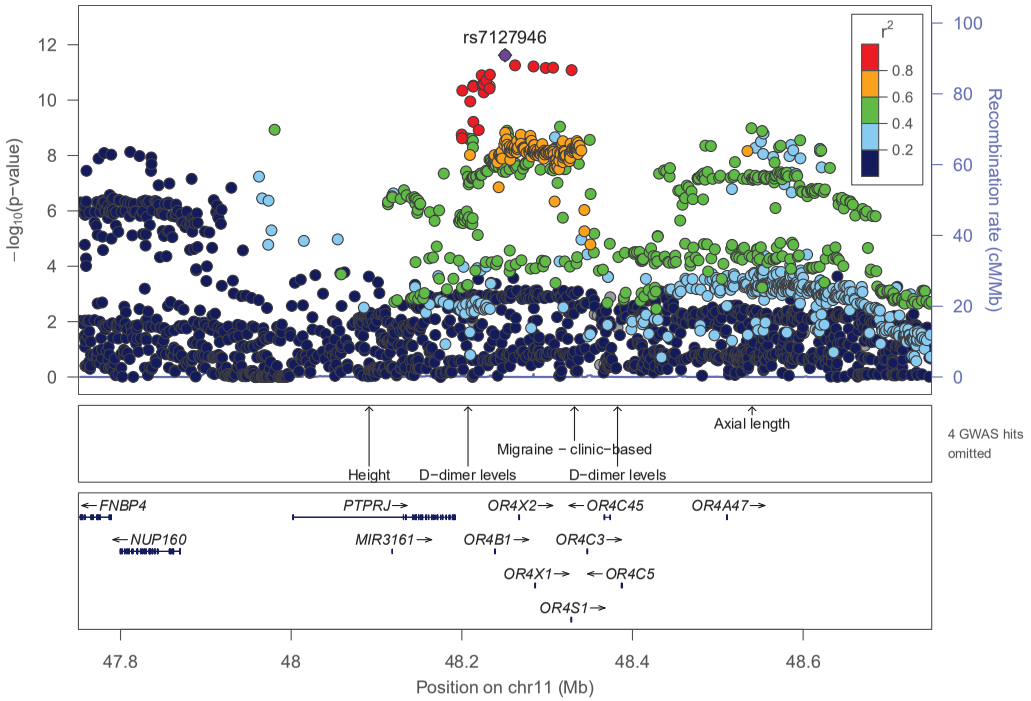

rs1541937
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Red blood cell traits
Sickle cell anemia (haemolysis)
IgG glycosylation
DNA methylation (variation)
11 GWAS hits omitted
←OR52E2 ←HBB ←OR51B2 ←OR51I1 ←OR52H1 ←TRIM5 ←OR52N5 OR52E4→ ←OR56A4
OR52E1→ ←HBD ←OR51B5 OR52B6→ TRIM22→ OR52N2→ OR56A3→
←OR52A5 ←HBBP1 OR51B6→ OR51I2→ TRIM6→ OR56B1→ ←OR52E6 ←OR56A5
←OR52A1 ←HBG1 OR51M1→ ←UBQLN3 TRIM34→ OR52N4→ ←OR52L1
←OR52Z1 ←OR51B4 OR51Q1→ TRIM6−TRIM34→ ←OR52N1 ←OR56A1
←OR51V1 OR51J1→ ←UBQLNL ←OR52E8
←BGLT3 OR52D1→
←HBG2 ←OLFM5P
←HBE1
5.2
5.4
5.6
5.8
6
Position on chr11 (Mb)

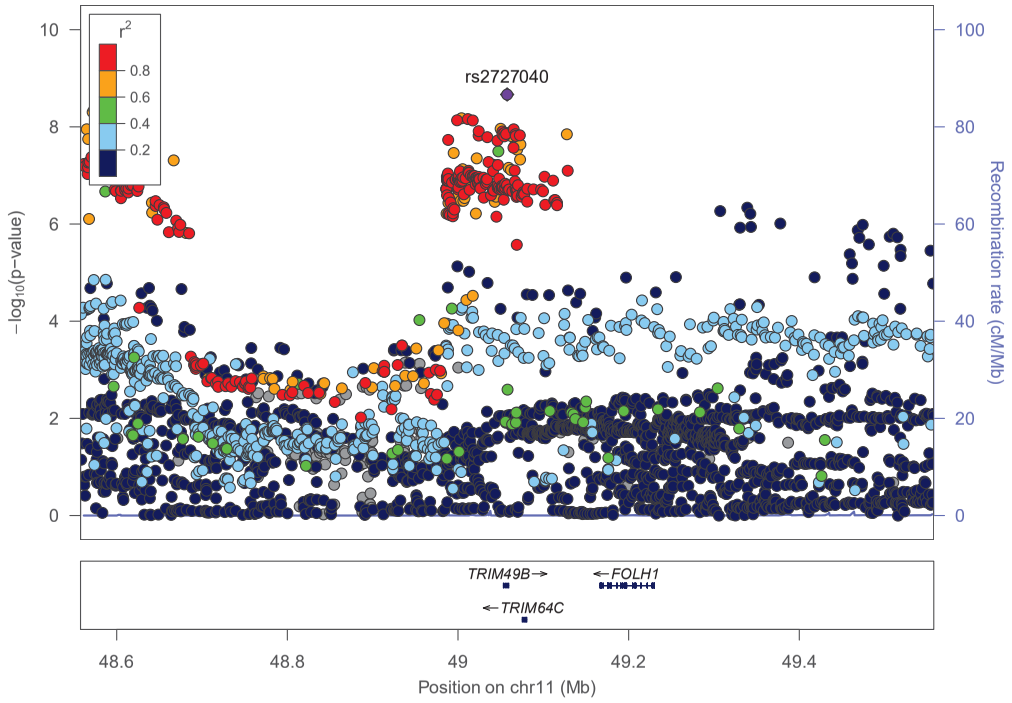

rs75248620
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Pancreatic cancer
HDL chole
Circulating vasoactive p
Diastolic blood pres
3 GWAS hits omitted
IPO7→ WEE1→ SWAP70→ ←SBF2
SNORA23→ ←LOC440028 ADM→
←LOC644656 SBF2−AS1→ CAND1.11→
ZNF143→ LOC101928008→
9.6
9.8
10
10.2
10.4
Position on chr11 (Mb)

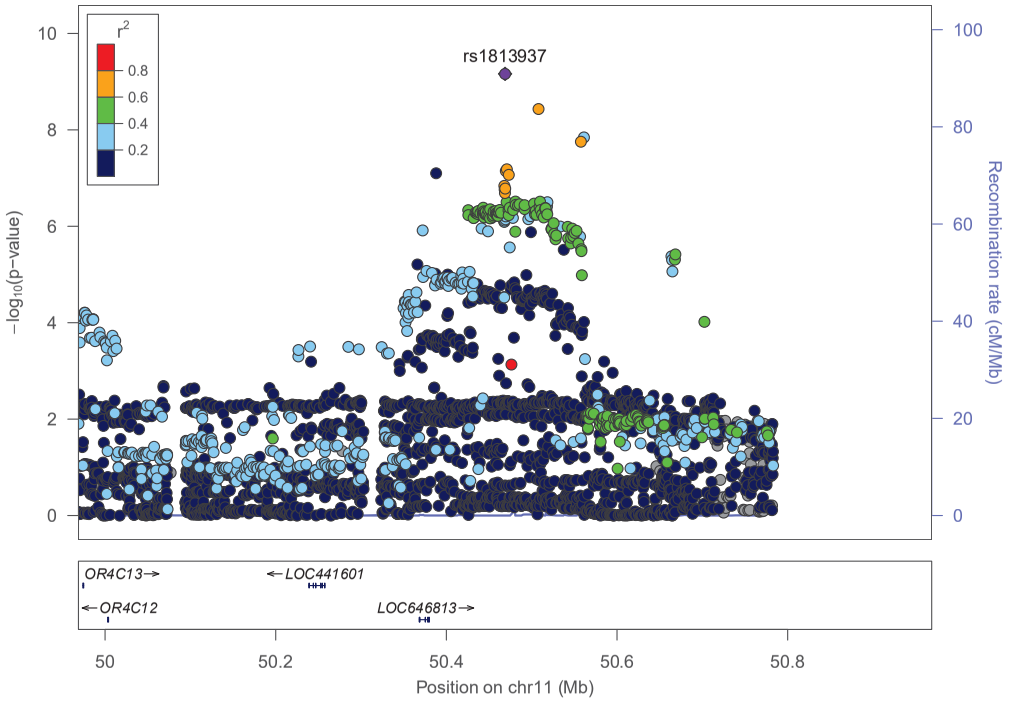

rs963837
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Renal function−related traits (BUN)
Renal function−related traits (eGRFcrea)
Renal function−related traits (sCR)
Bone mineral densi
6 GWAS hits omitted
FSHB→
←MPPED2
←DCDC1
ARL14EP→
Position on chr11 (Mb)

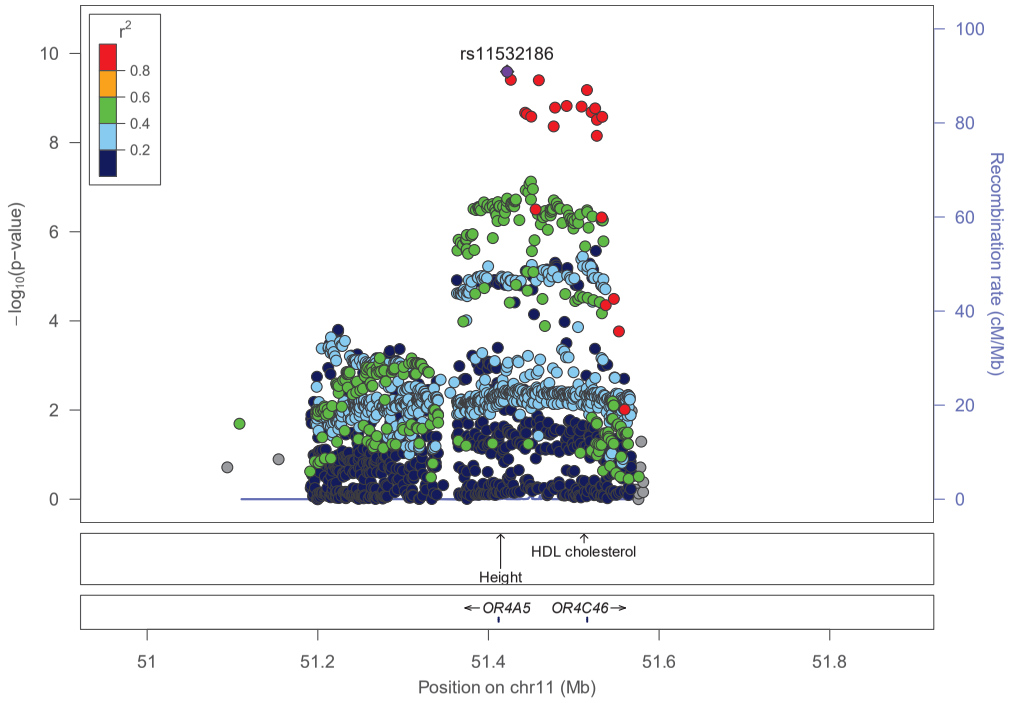

rs6484504
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ineral density
Bone mineral density (spine)
Metabolite levels (HVA/
Body mass
←DCDC1
←IMMP1L
←PAX6
DNAJC24→
ELP4→
PAX6−AS1→
PAUPAR→
Position on chr11 (Mb)

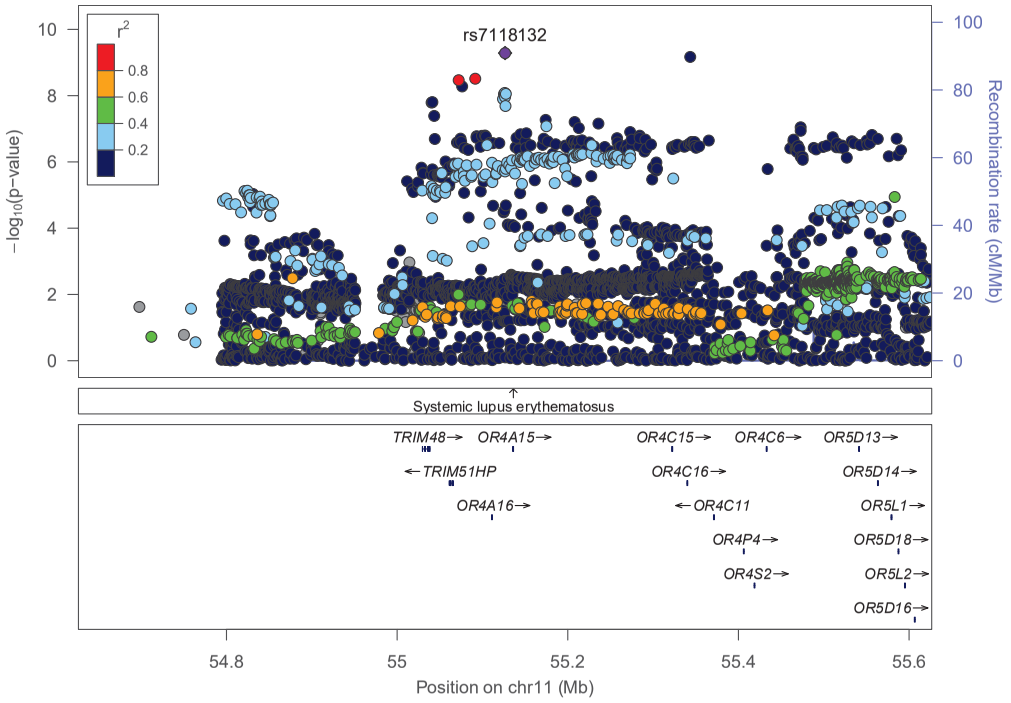

rs61897431
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Alzheimer's disease (late onset)
Height
Body mass index
Serum albumin level
Body mass index
7 GWAS hits omitted
←LRP4
←ARFGAP2
MADD→
MIR4487→
←CELF1
←MTCH2
←FNBP4
C11orf49→
DDB2→
←MYBPC3
PTPMT1→
←AGBL2
←NUP160
←PACSIN3
←SPI1
←KBTBD4
←MIR6745
SLC39A13→
NDUFS3→
←ACP2
←PSMC3
FAM180B→
NR1H3→
←RAPSN
←C1QTNF4
←LOC101928943
Position on chr11 (Mb)

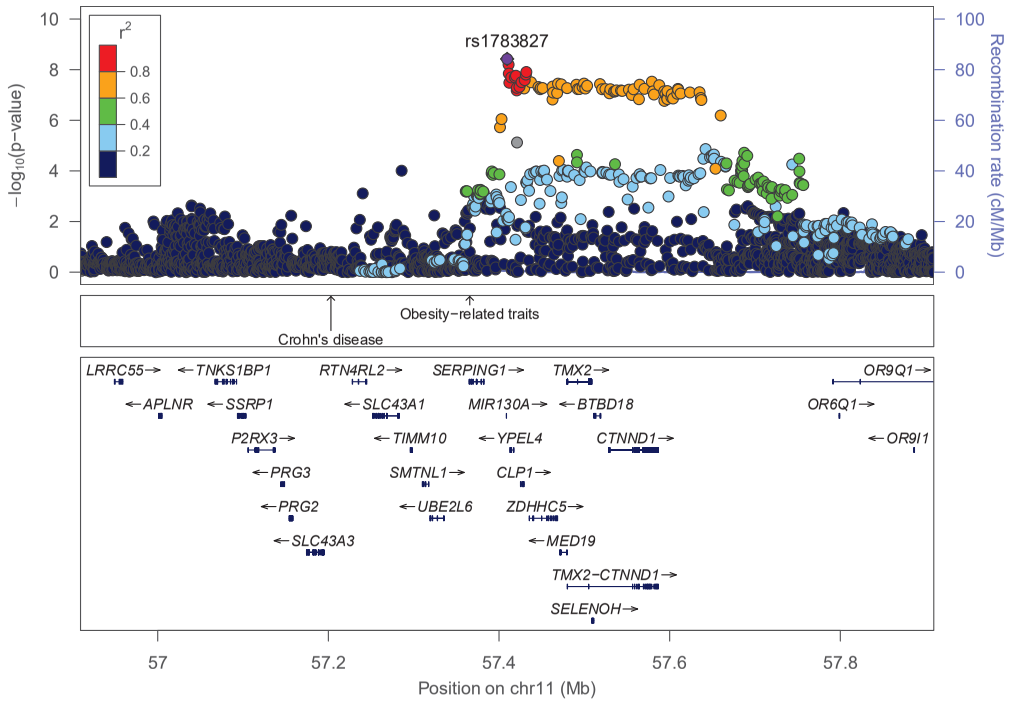

rs7127946
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Height
D−dimer levels
Migraine − clinic−based
D−dimer levels
Axial length
4 GWAS hits omitted
←FNBP4
PTPRJ→
OR4X2→
←OR4C45
OR4A47→
←NUP160
MIR3161→
OR4B1→
OR4C3→
OR4X1→
←OR4C5
OR4S1→
Position on chr11 (Mb)

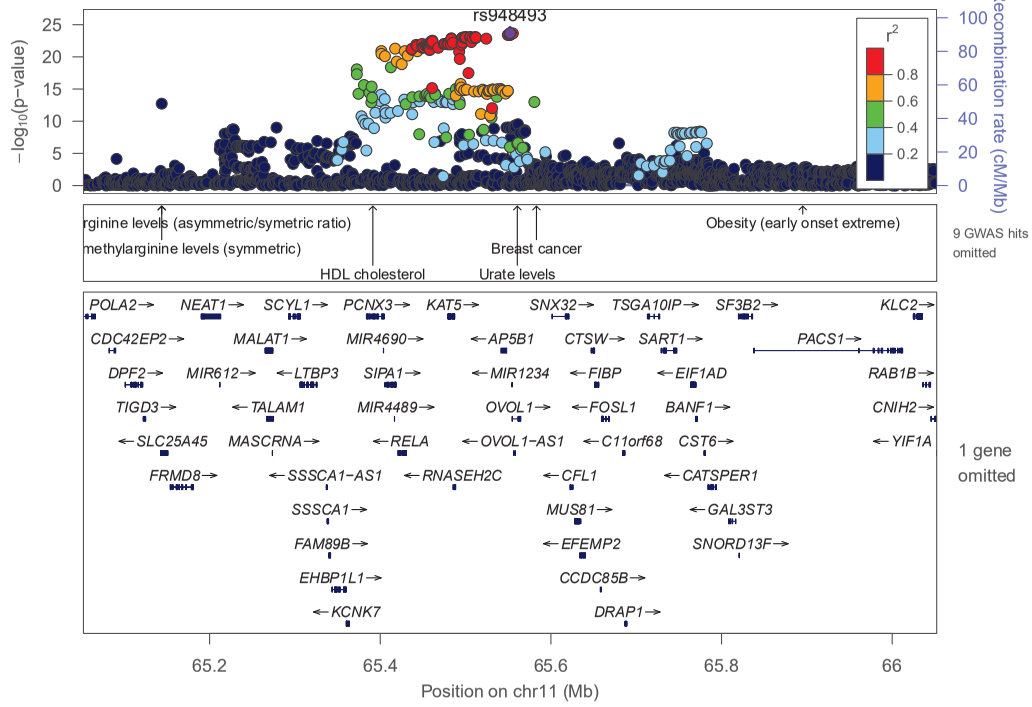

rs2727040
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
TRIM49B→
←FOLH1
←TRIM64C
48.6
48.8
49
49.2
49.4
Position on chr11 (Mb)

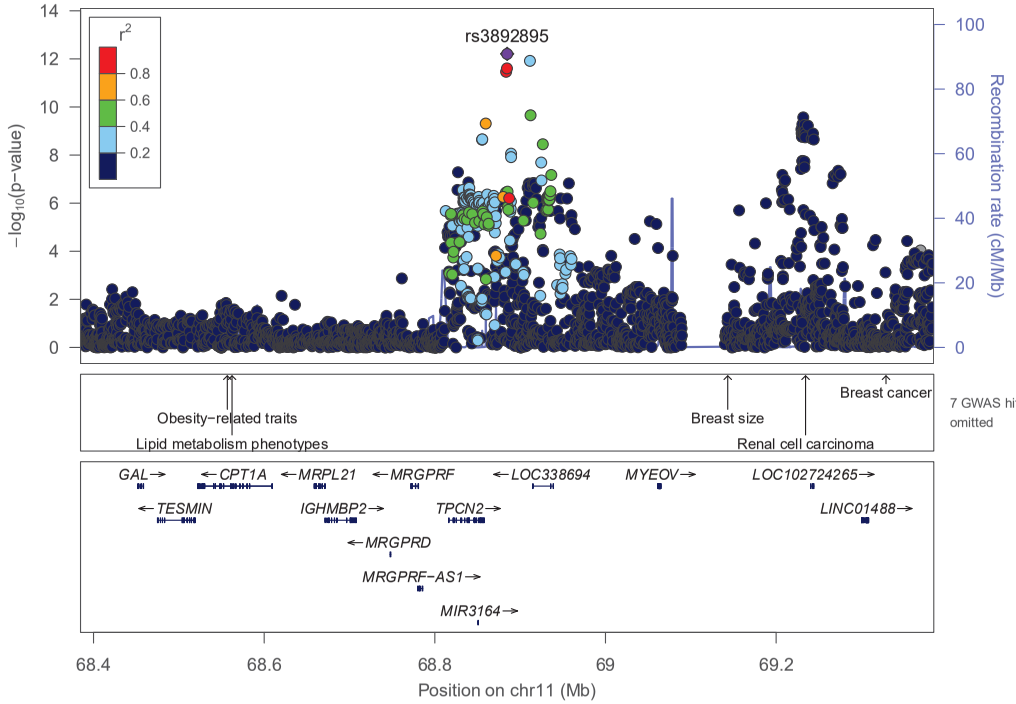

rs1813937
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
OR4C13→
←LOC441601
←OR4C12
LOC646813→
50
50.2
50.4
50.6
50.8
Position on chr11 (Mb)

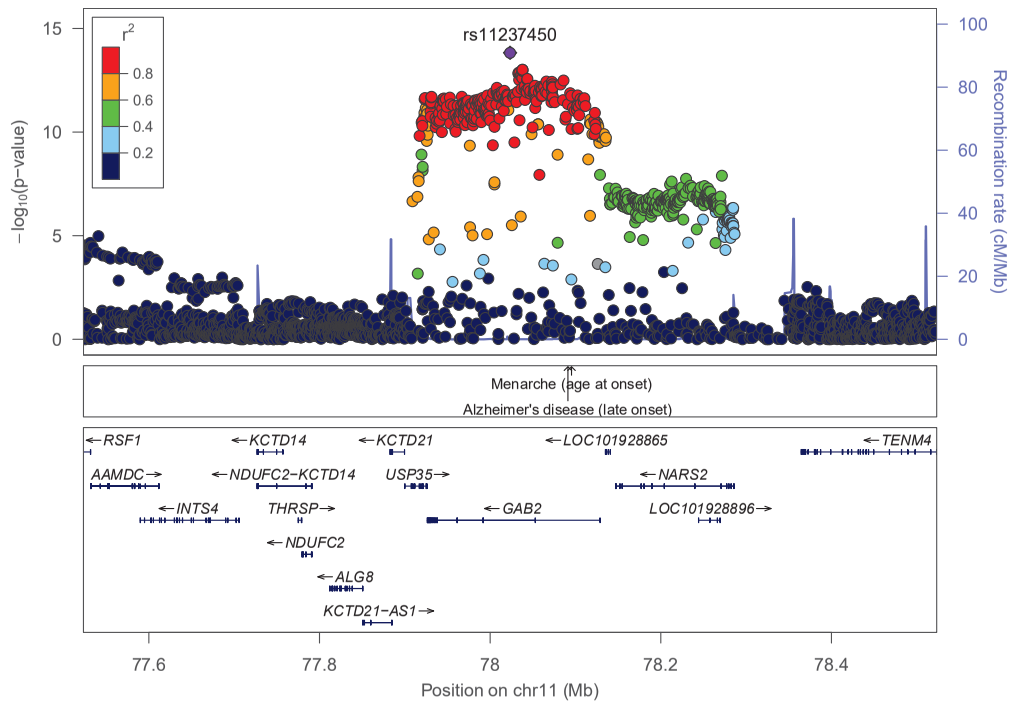

rs11532186
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
HDL cholesterol
Height
←OR4A5
OR4C46→
51
51.2
51.4
51.6
51.8
Position on chr11 (Mb)

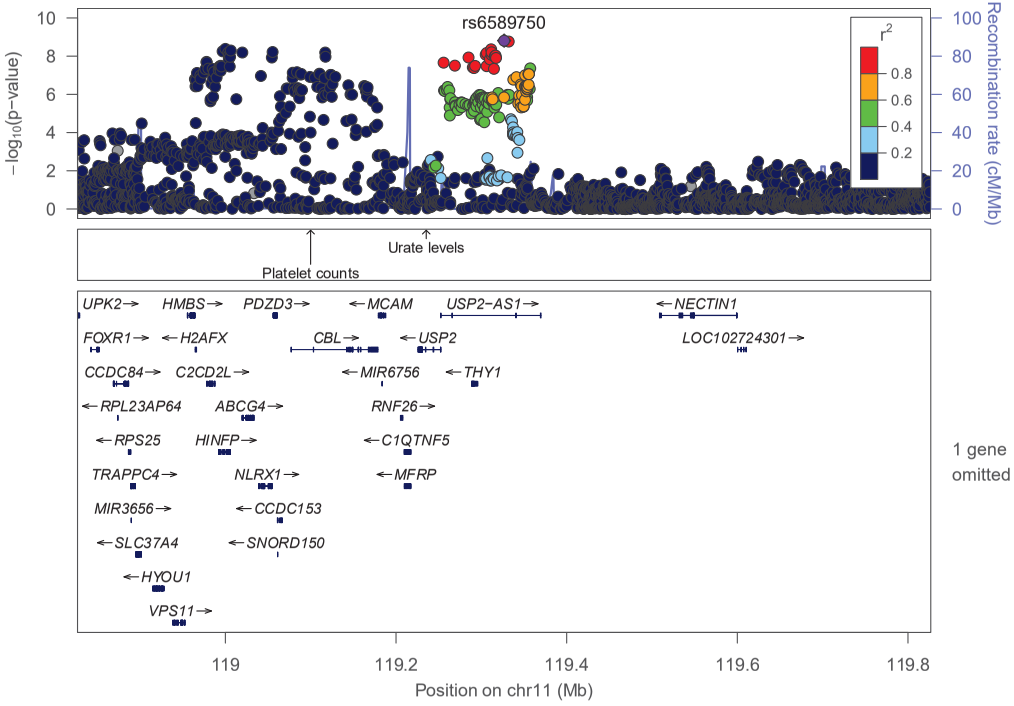

rs7118132
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Systemic lupus erythematosus
TRIM48→
OR4A15→
←TRIM51HP
OR4A16→
OR4C15→
OR4C6→
OR5D13→
OR4C16→
OR5D14→
←OR4C11
OR5L1→
OR4P4→
OR5D18→
OR4S2→
OR5L2→
OR5D16→
54.8
55
55.2
55.4
55.6
Position on chr11 (Mb)

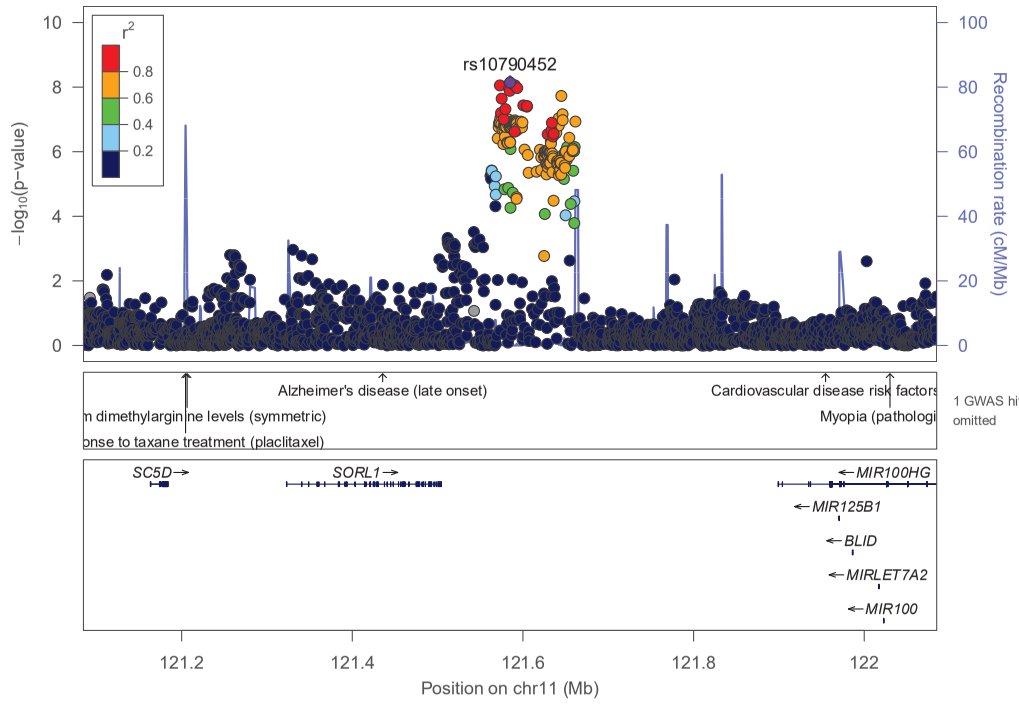

rs1783827
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Crohn's disease
LRRC55→ ←TNKS1BP1 RTN4RL2→ SERPING1→ TMX2→ OR9Q1→
←APLNR ←SSRP1 ←SLC43A1 MIR130A→ ←BTBD18 OR6Q1→
P2RX3→ ←TIMM10 ←YPEL4 CTNND1→ ←OR9I1
←PRG3 SMTNL1→ CLP1→
←PRG2 ←UBE2L6 ZDHHC5→
←SLC43A3 ←MED19
TMX2−CTNND1→
SELENOH→
57 57.2 57.4 57.6 57.8
Position on chr11 (Mb)

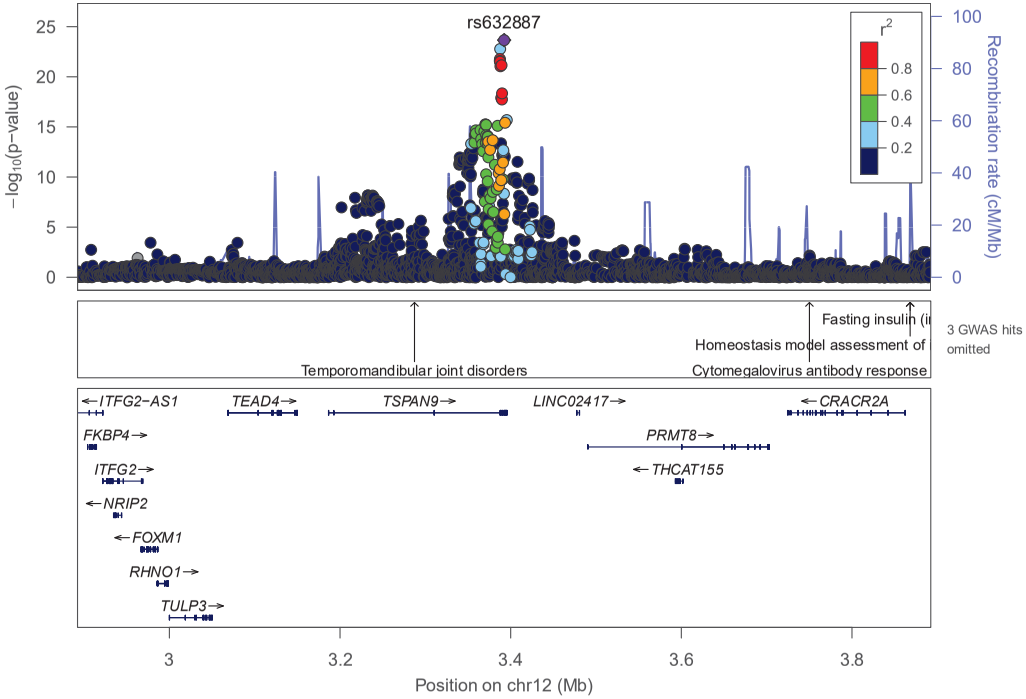

rs948493
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
rginine levels (asymmetric/symetric ratio)
methylarginine levels (symmetric)
HDL cholesterol
Breast cancer
Urate levels
Obesity (early onset extreme)
9 GWAS hits omitted
POLA2→ NEAT1→ SCYL1→ PCNX3→ KAT5→ SNX32→ TSGA10IP→ SF3B2→ KLC2→
CDC42EP2→ MALAT1→ MIR4690→ ←AP5B1 CTSW→ SART1→ PACS1→
DPF2→ MIR612→ ←LTBP3 SIPA1→ ←MIR1234 ←FIBP ←EIF1AD RAB1B→
TIGD3→ ←TALAM1 MIR4489→ OVOL1→ ←FOSL1 BANF1→ CNIH2→
←SLC25A45 MASCRNA→ ←RELA ←OVOL1−AS1 ←C11orf68 CST6→ ←YIF1A
FRMD8→ ←SSSCA1−AS1 ←RNASEH2C ←CFL1 ←CATSPER1
SSSCA1→ MUS81→ ←GAL3ST3
FAM89B→ ←EFEMP2 SNORD13F→
EHBP1L1→ CCDC85B→
←KCNK7 DRAP1→
1 gene omitted
65.2 65.4 65.6 65.8 66
Position on chr11 (Mb)

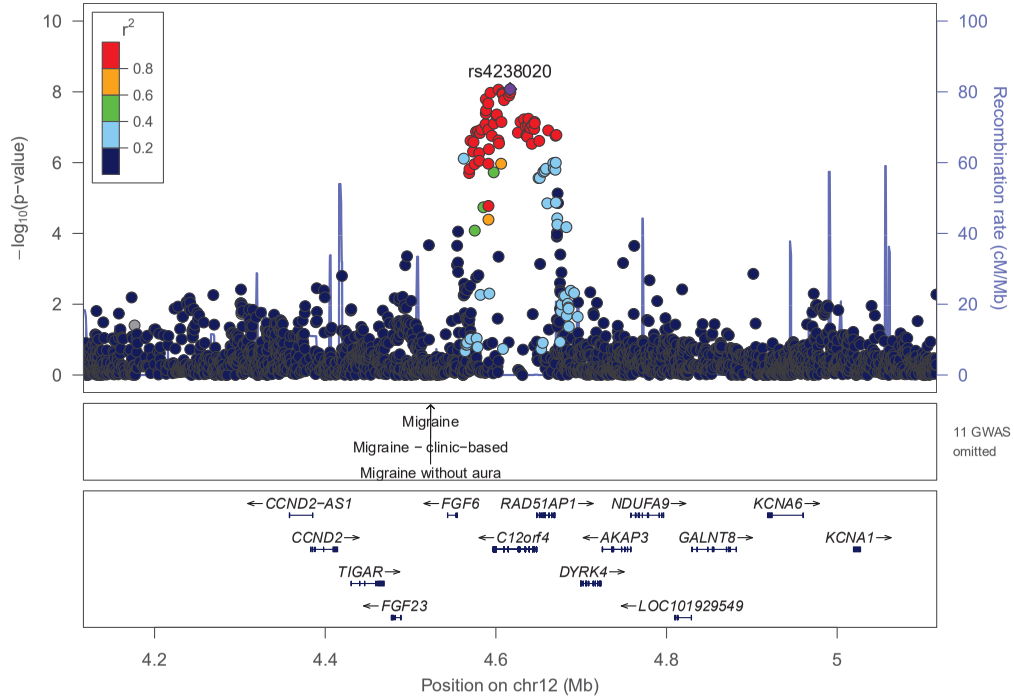

rs3892895
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Lipid metabolism phenotypes
Breast size
Renal cell carcinoma
Breast cancer
7 GWAS hits omitted
GAL→ ←CPT1A ←MRPL21 ←MRGPRF ←LOC338694 MYEOV→ LOC102724265→
←TESMIN IGHMBP2→ TPCN2→ LINC01488→
←MRGPRD
MRGPRF−AS1→
MIR3164→
68.4 68.6 68.8 69 69.2
Position on chr11 (Mb)

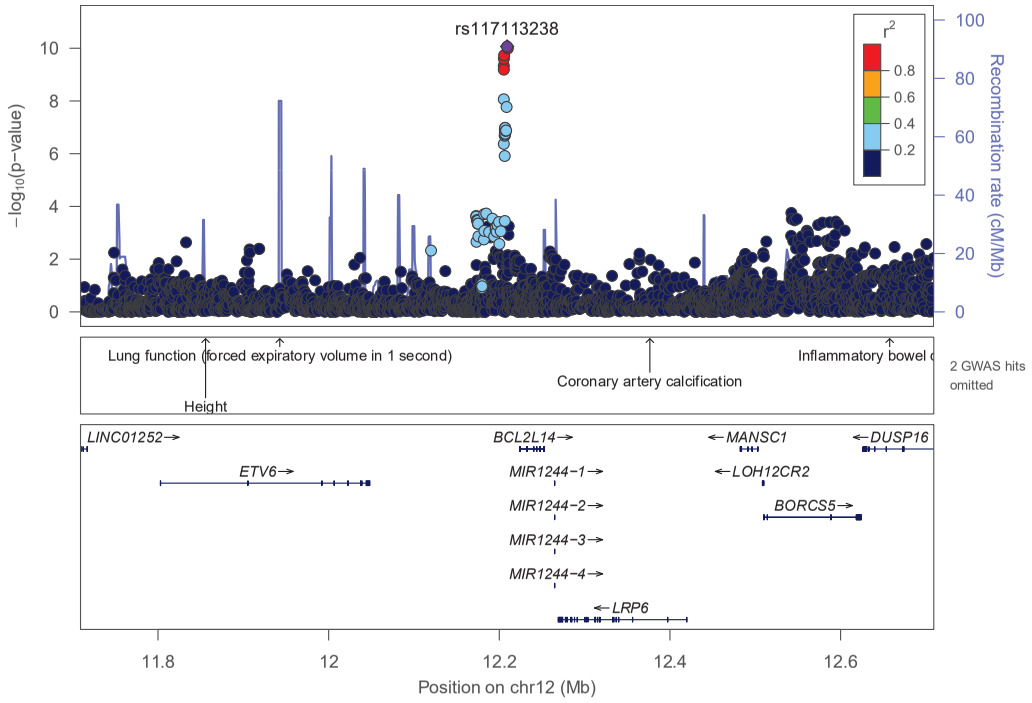

rs11237450
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Menarche (age at onset)
Alzheimer's disease (late onset)
←RSF1 ←KCTD14 ←KCTD21 ←LOC101928865 ←TENM4
AAMDC→ ←NDUFC2−KCTD14 USP35→ ←NARS2
←INTS4 THRSP→ ←GAB2 LOC101928896→
←NDUFC2
←ALG8
KCTD21−AS1→
77.6 77.8 78 78.2 78.4
Position on chr11 (Mb)

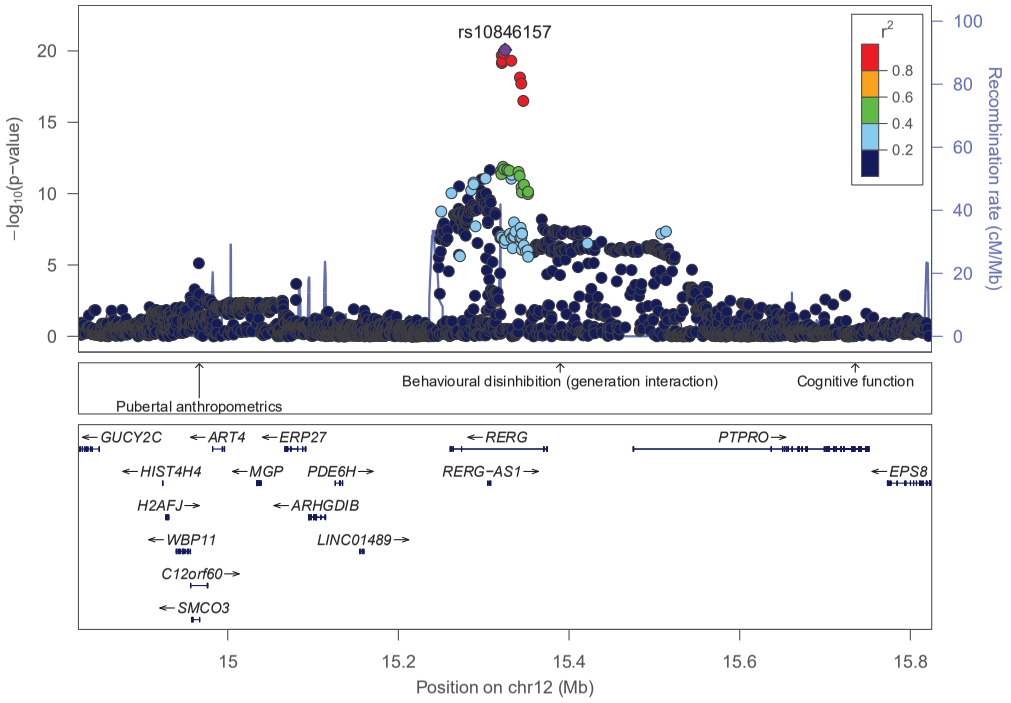

rs6589750
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Platelet counts
Urate levels
1 gene omitted
UPK2→ HMBS→ PDZD3→ ←MCAM USP2−AS1→ ←NECTIN1
FOXR1→ ←H2AFX ←CBL ←USP2 LOC102724301→
CCDC84→ C2CD2L→ ←MIR6756 ←THY1
←RPL23AP64 ABCG4→ RNF26→
←RPS25 HINFP→ ←C1QTNF5
TRAPPC4→ NLRX1→ ←MFRP
MIR3656→ ←CCDC153
←SLC37A4 ←SNORD150
←HYOU1
VPS11→
Position on chr11 (Mb)

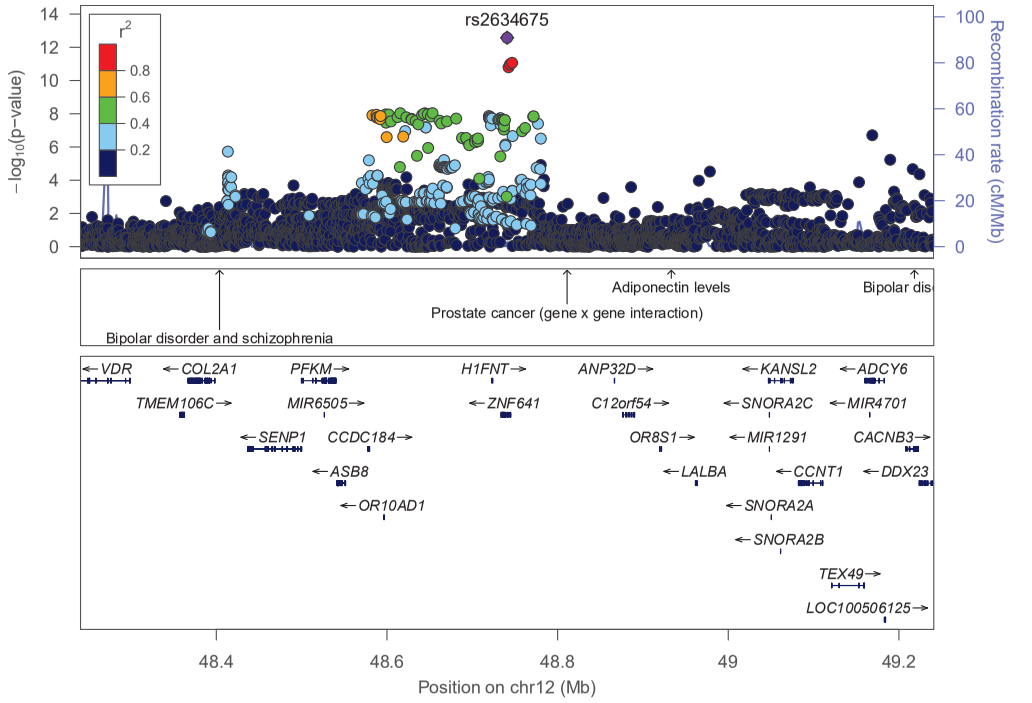

rs10790452
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Alzheimer's disease (late onset)
Cardiovascular disease risk factors
Myopia (pathologi
1 GWAS hit omitted
SC5D→ SORL1→ ←MIR100HG
←MIR125B1
←BLID
←MIRLET7A2
←MIR100
Position on chr11 (Mb)

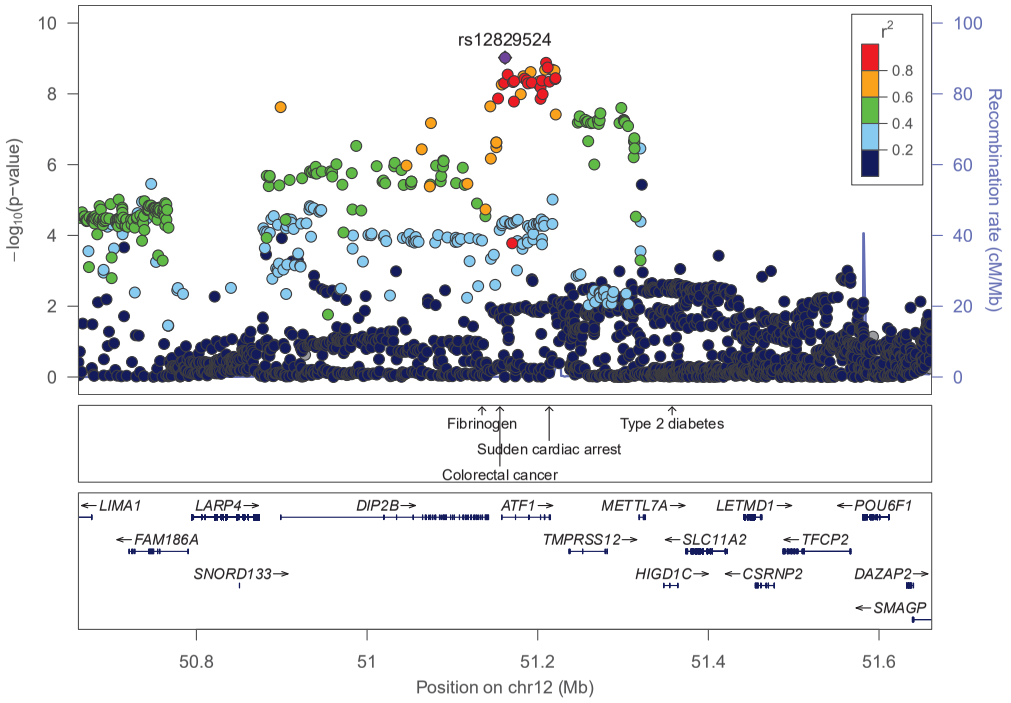

rs632887
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Temporomandibular joint disorders
Homeostasis model assessment of
Cytomegalovirus antibody response
3 GWAS hits omitted
←ITFG2−AS1 TEAD4→ TSPAN9→ LINC02417→ ←CRACR2A
FKBP4→ PRMT8→
ITFG2→ ←THCAT155
←NRIP2
←FOXM1
RHNO1→
TULP3→
Position on chr12 (Mb)

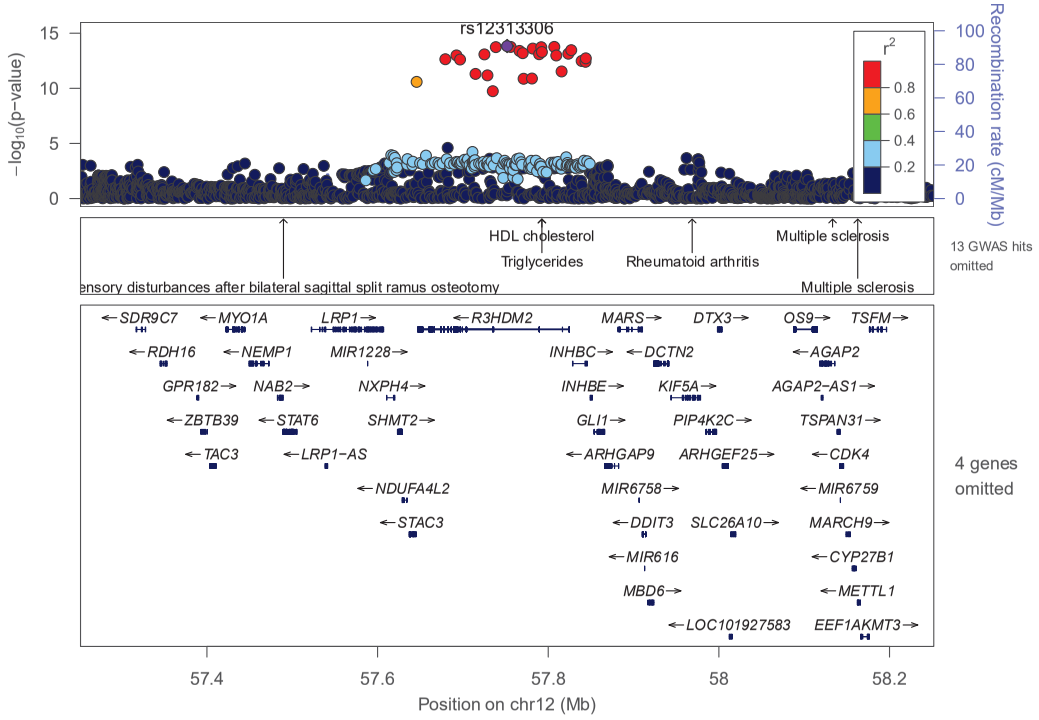

rs4238020
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Migraine
Migraine − clinic−based
Migraine without aura
11 GWAS hits omitted
←CCND2−AS1 ←FGF6 RAD51AP1→ NDUFA9→ KCNA6→
CCND2→ ←C12orf4 ←AKAP3 GALNT8→ KCNA1→
TIGAR→ DYRK4→
←FGF23 ←LOC101929549
Position on chr12 (Mb)

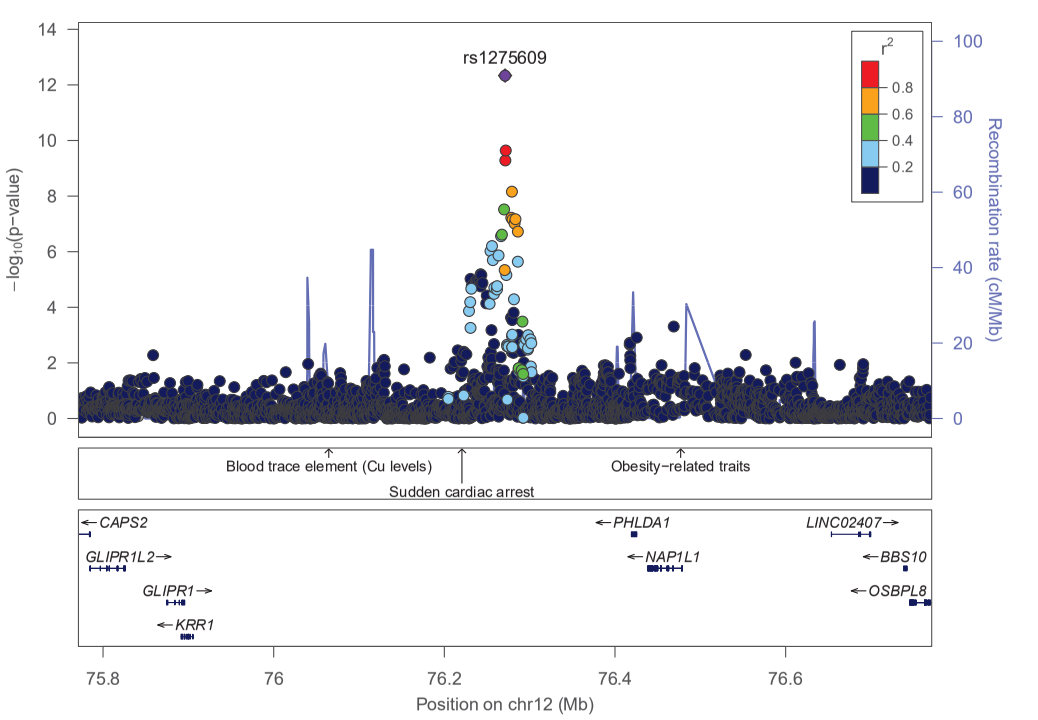

rs117113238
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Lung function (forced expiratory volume in 1 second)
Height
Coronary artery calcification
Inflammatory bowel
2 GWAS hits omitted
LINC01252→
BCL2L14→
←MANSC1
←DUSP16
ETV6→
MIR1244−1→
←LOH12CR2
MIR1244−2→
BORCS5→
MIR1244−3→
MIR1244−4→
←LRP6
11.8
12
12.2
12.4
12.6
Position on chr12 (Mb)

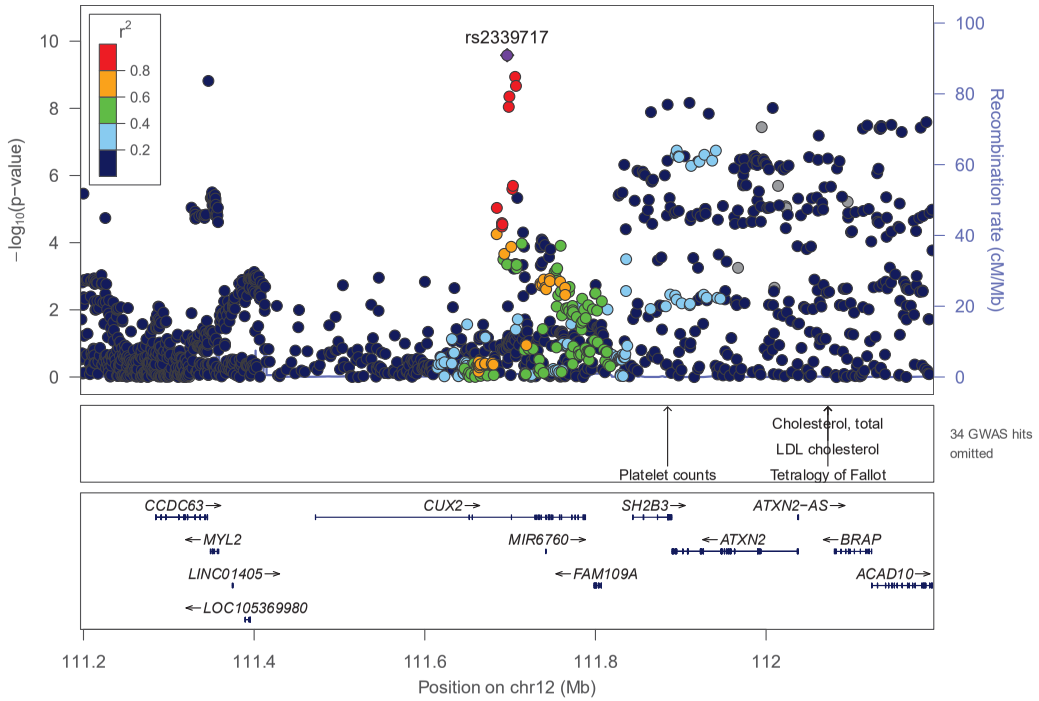

rs10846157
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Pubertal anthropometrics
Behavioural disinhibition (generation interaction)
Cognitive function
←GUCY2C
←ART4
←ERP27
←RERG
PTPRO→
←HIST4H4
←MGP
PDE6H→
RERG−AS1→
←EPS8
H2AFJ→
←ARHGDIB
←WBP11
LINC01489→
C12orf60→
←SMCO3
15
15.2
15.4
15.6
15.8
Position on chr12 (Mb)

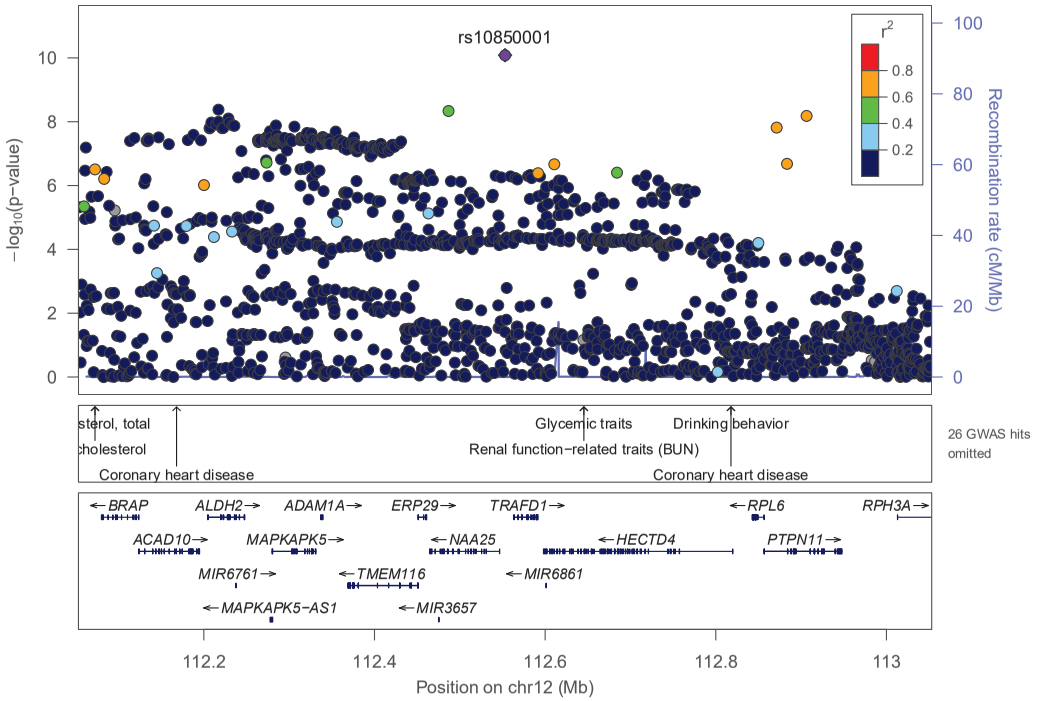

rs2634675
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Bipolar disorder and schizophrenia
Prostate cancer (gene x gene interaction)
Adiponectin levels
Bipolar dis
←VDR
←COL2A1
PFKM→
H1FNT→
ANP32D→
←KANSL2
←ADCY6
TMEM106C→
MIR6505→
←ZNF641
C12orf54→
←SNORA2C
←MIR4701
←SENP1
CCDC184→
OR8S1→
←MIR1291
CACNB3→
←ASB8
←LALBA
←CCNT1
←DDX23
←OR10AD1
←SNORA2A
←SNORA2B
TEX49→
LOC100506125→
48.4
48.6
48.8
49
49.2
Position on chr12 (Mb)

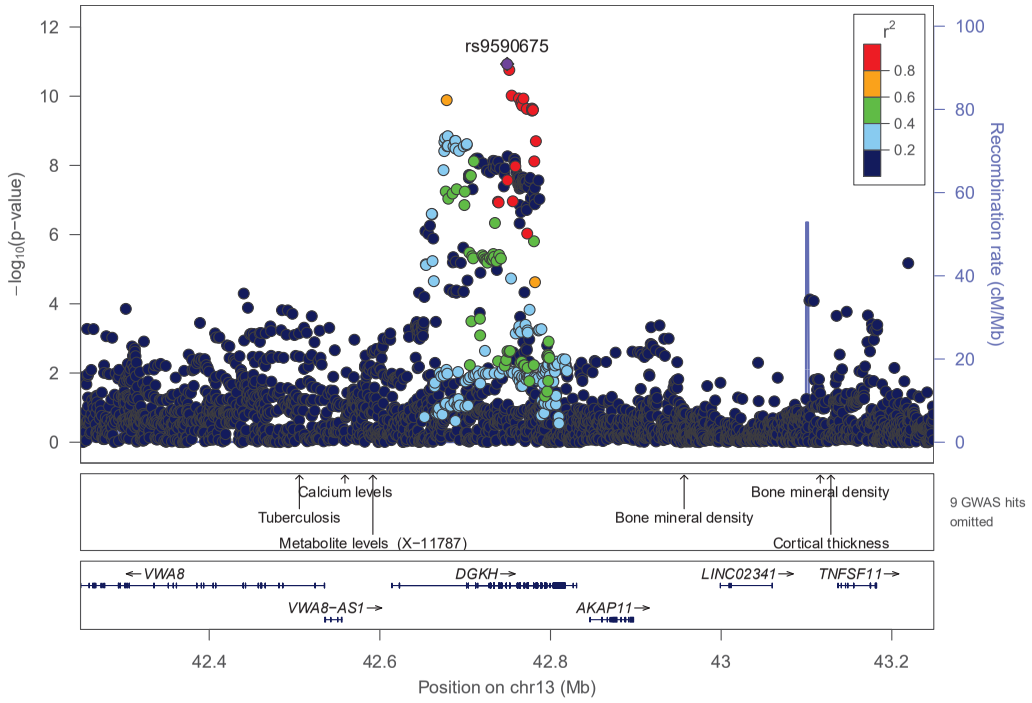

rs12829524
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Fibrinogen
Sudden cardiac arrest
Colorectal cancer
Type 2 diabetes
←LIMA1
LARP4→
DIP2B→
ATF1→
METTL7A→
LETMD1→
←POU6F1
←FAM186A
TMPRSS12→
←SLC11A2
←TFCP2
SNORD133→
HIGD1C→
←CSRNP2
DAZAP2→
←SMAGP
50.8
51
51.2
51.4
51.6
Position on chr12 (Mb)

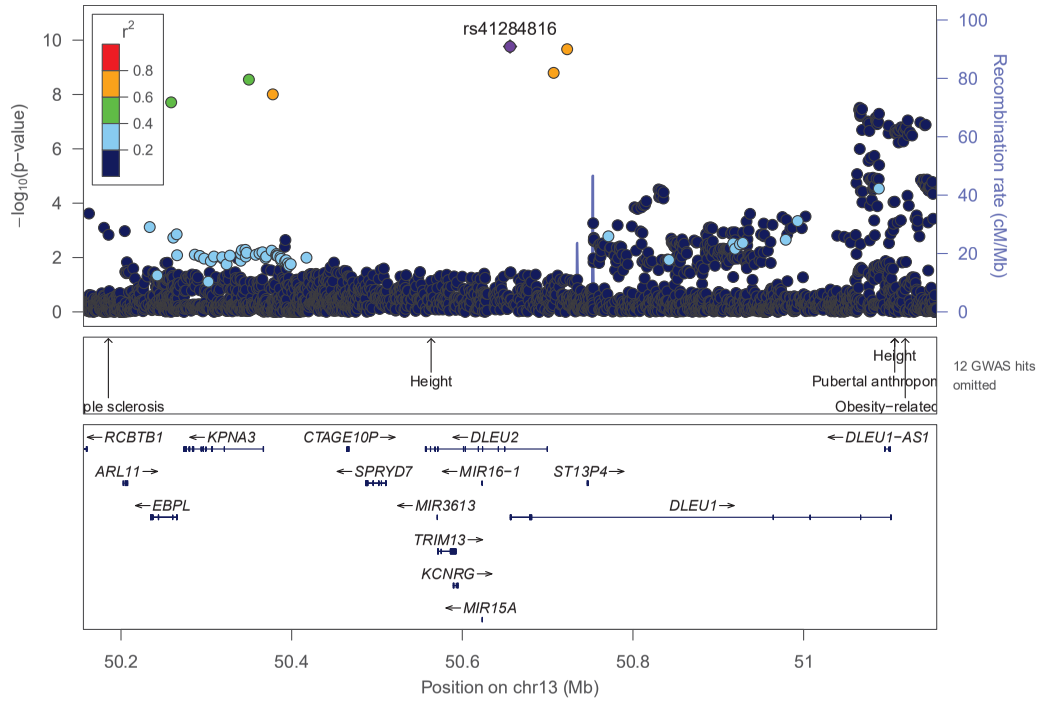

rs12313306
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
HDL cholesterol
Triglycerides
Rheumatoid arthritis
Multiple sclerosis
Multiple sclerosis
ensory disturbances after bilateral sagittal split ramus osteotomy
13 GWAS hits omitted
SDR9C7
MYO1A
LRP1
R3HDM2
MARS
DTX3
OS9
TSFM
RDH16
NEMP1
MIR1228
INHBC
DCTN2
AGAP2
GPR182
NAB2
NXPH4
INHBE
KIF5A
AGAP2−AS1
ZBTB39
STAT6
SHMT2
GLI1
PIP4K2C
TSPAN31
TAC3
LRP1−AS
ARHGAP9
ARHGEF25
CDK4
NDUFA4L2
MIR6758
MIR6759
STAC3
DDIT3
SLC26A10
MARCH9
MIR616
CYP27B1
MBD6
METTL1
LOC101927583
EEF1AKMT3
4 genes omitted
57.4
57.6
57.8
58
58.2
Position on chr12 (Mb)

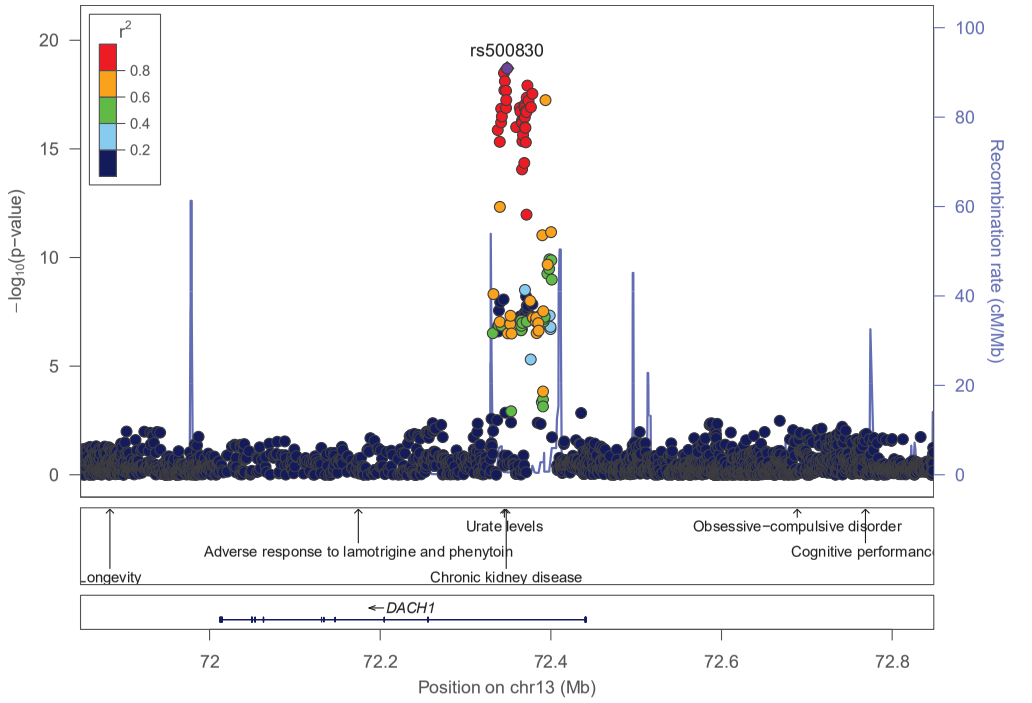

rs1275609
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Blood trace element (Cu levels)
Sudden cardiac arrest
Obesity−related traits
CAPS2
PHLDA1
LINC02407
GLIPR1L2
NAP1L1
BBS10
GLIPR1
OSBPL8
KRR1
75.8
76
76.2
76.4
76.6
Position on chr12 (Mb)

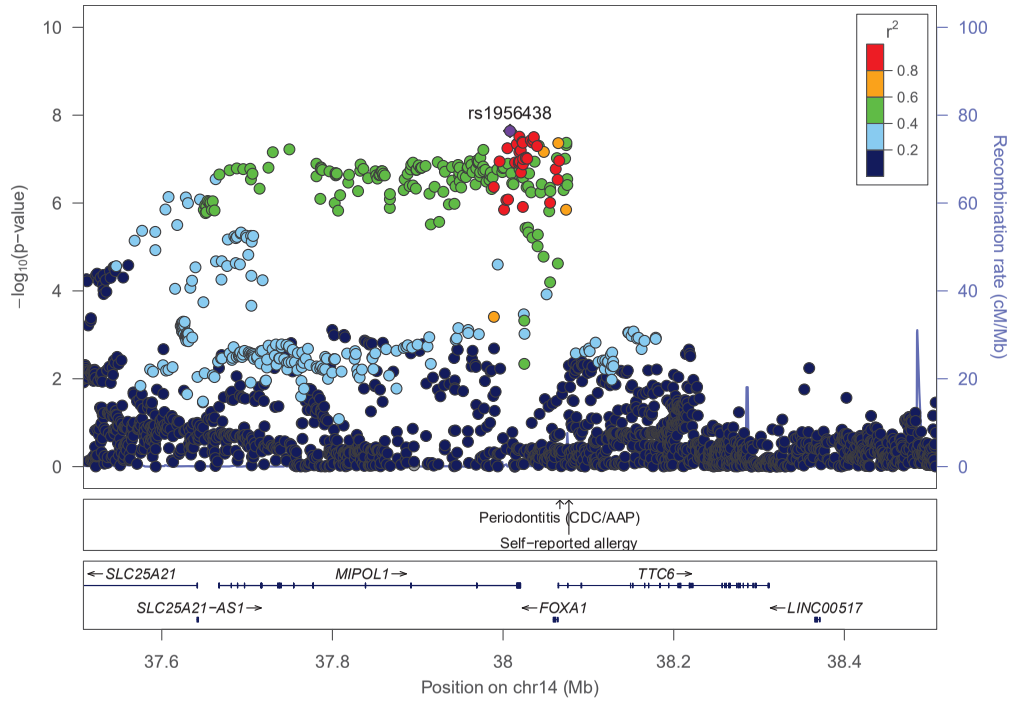

rs2339717
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
Platelet counts
Cholesterol, total
LDL cholesterol
Tetralogy of Fallot
34 GWAS hits omitted
CCDC63
CUX2
SH2B3
ATXN2−AS
MYL2
MIR6760
ATXN2
BRAP
LINC01405
FAM109A
ACAD10
LOC105369980
111.2
111.4
111.6
111.8
112
Position on chr12 (Mb)

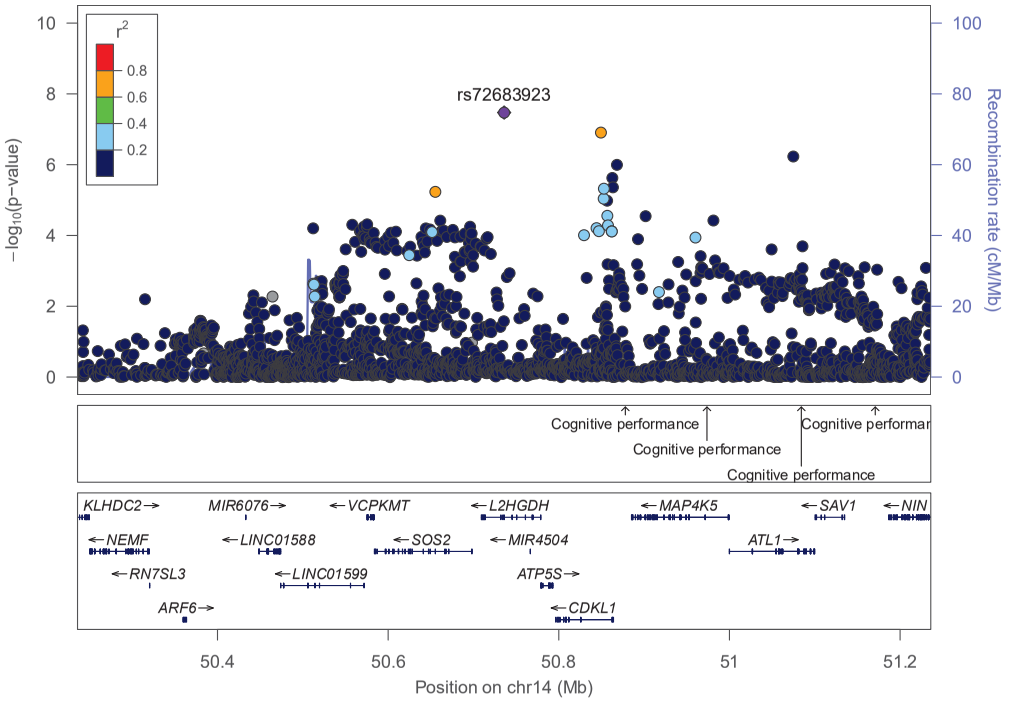

rs10850001
−log10(p−value)
Recombination rate (cM/Mb)
r2
0.8
0.6
0.4
0.2
sterol, total
cholesterol
Coronary heart disease
Glycemic traits
Renal function−related traits (BUN)
Drinking behavior
Coronary heart disease
26 GWAS hits omitted
BRAP
ALDH2
ADAM1A
ERP29
TRAFD1
RPL6
RPH3A
ACAD10
MAPKAPK5
NAA25
HECTD4
PTPN11
MIR6761
TMEM116
MIR6861
MAPKAPK5−AS1
MIR3657
112.2
112.4
112.6
112.8
113
Position on chr12 (Mb)

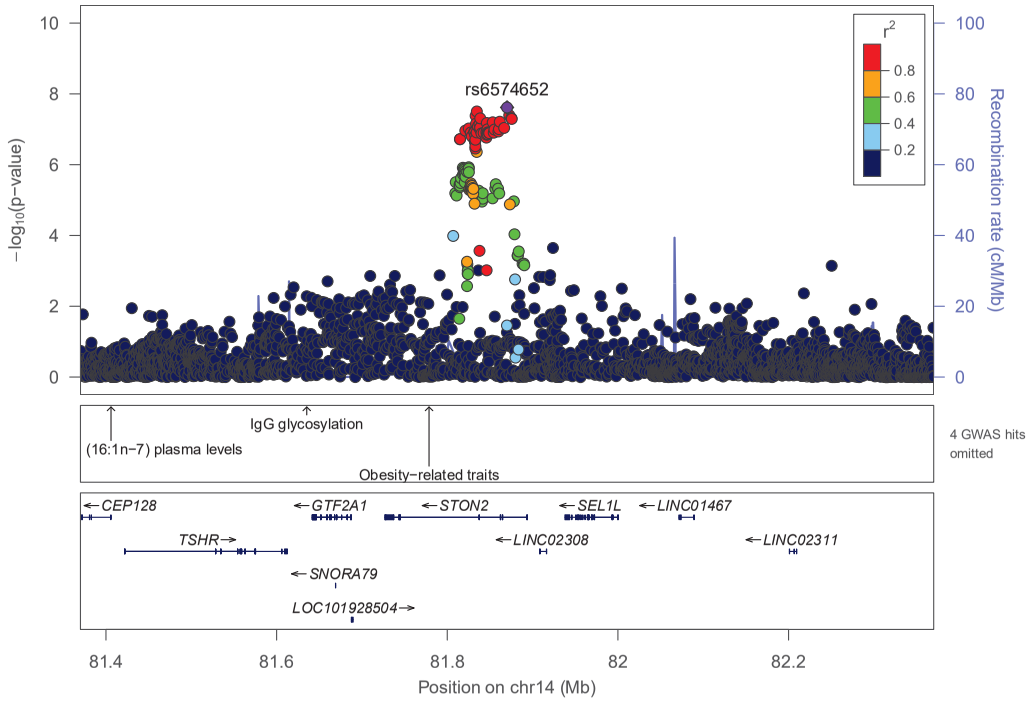

rs9590675
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Calcium levels
Tuberculosis
Metabolite levels (X−11787)
Bone mineral density
Bone mineral density
Cortical thickness
9 GWAS hits omitted
VWA8
DGKH
LINC02341
TNFSF11
VWA8−AS1
AKAP11
Position on chr13 (Mb)

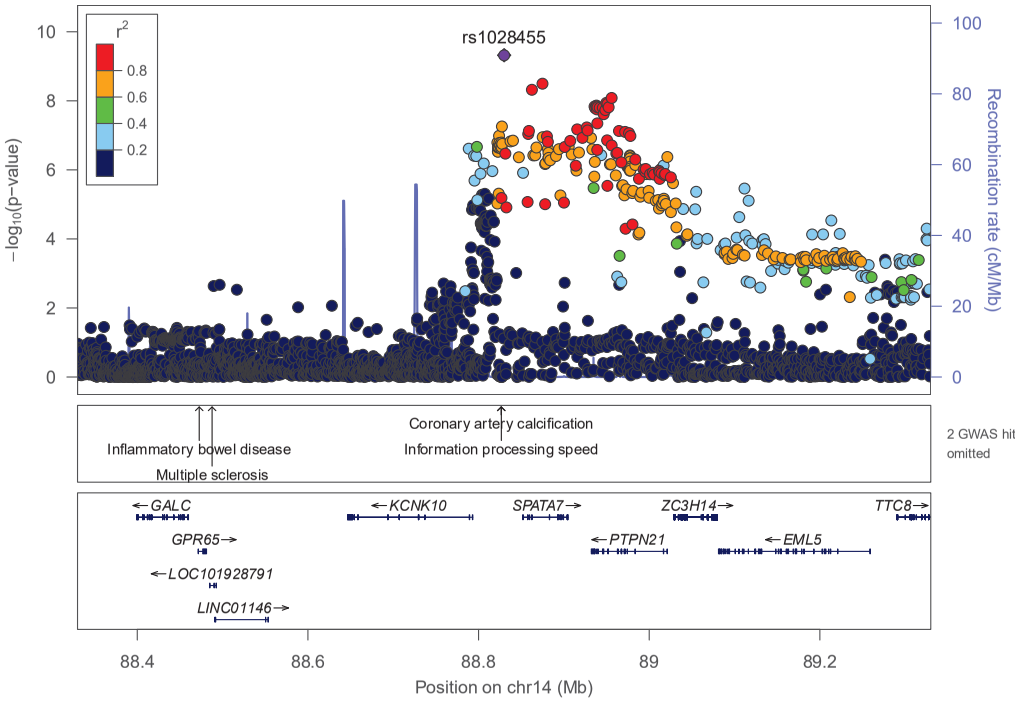

rs41284816
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Height
Height
Pubertal anthropon
Obesity−related
12 GWAS hits omitted
RCBTB1
KPNA3
CTAGE10P
DLEU2
DLEU1−AS1
ARL11
SPRYD7
MIR16−1
ST13P4
EBPL
MIR3613
DLEU1
TRIM13
KCNRG
MIR15A
Position on chr13 (Mb)

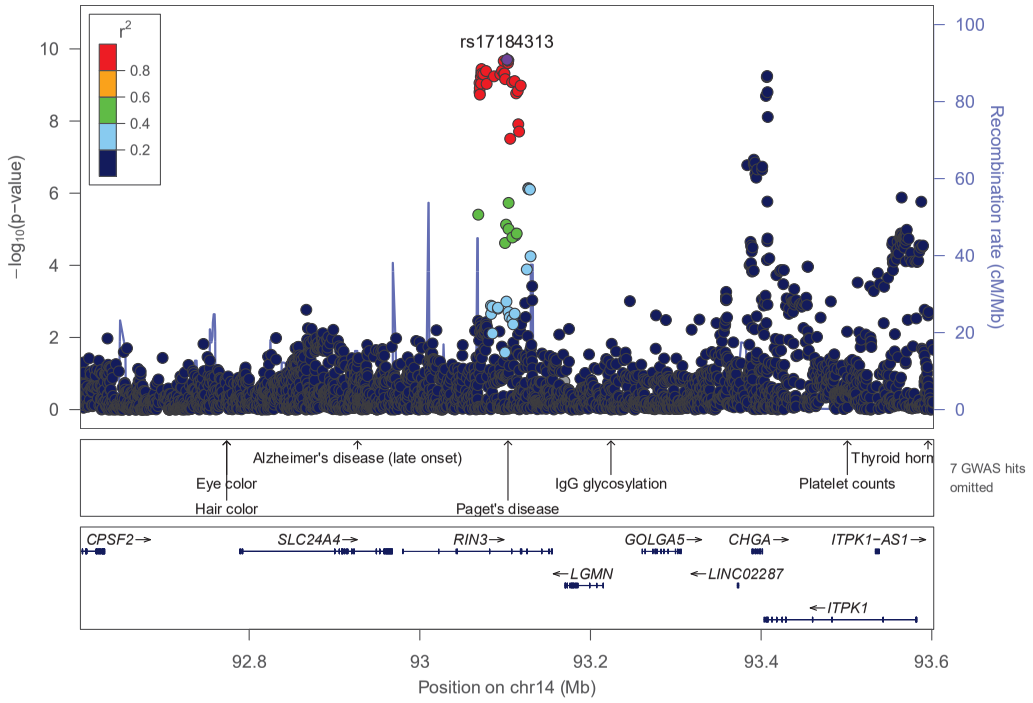

rs500830
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Urate levels
Obsessive−compulsive disorder
Adverse response to lamotrigine and phenytoin
Cognitive performanc
Longevity
Chronic kidney disease
DACH1
Position on chr13 (Mb)

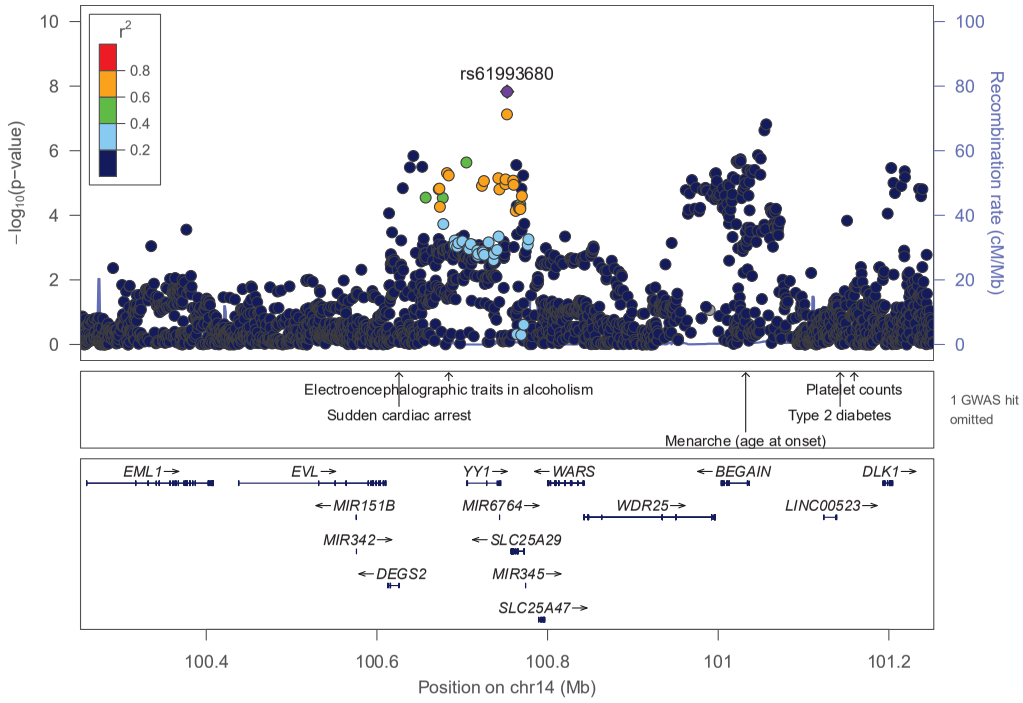

rs1956438
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Periodontitis (CDC/AAP)
Self−reported allergy
SLC25A21
MIPOL1
TTC6
SLC25A21−AS1
FOXA1
LINC00517
Position on chr14 (Mb)

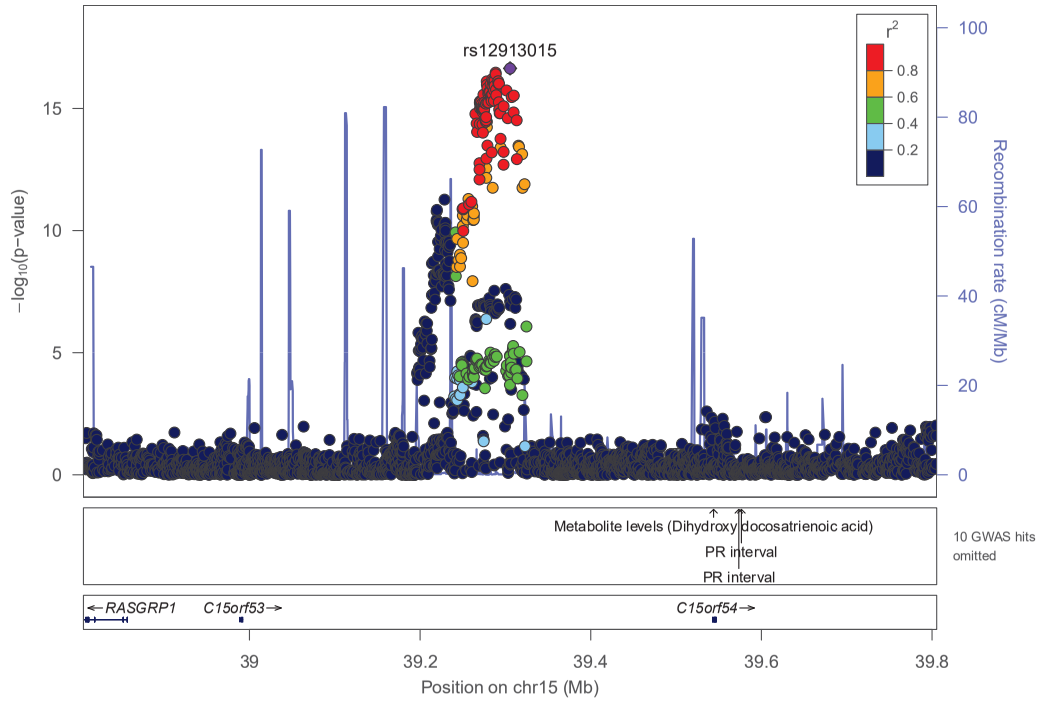

rs72683923
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cognitive performance
Cognitive performance
Cognitive performance
Cognitive performar
KLHDC2→
MIR6076→
←VCPKMT
←L2HGDH
←MAP4K5
←SAV1
←NIN
←NEMF
←LINC01588
←SOS2
←MIR4504
ATL1→
←RN7SL3
←LINC01599
ATP5S→
ARF6→
←CDKL1
Position on chr14 (Mb)

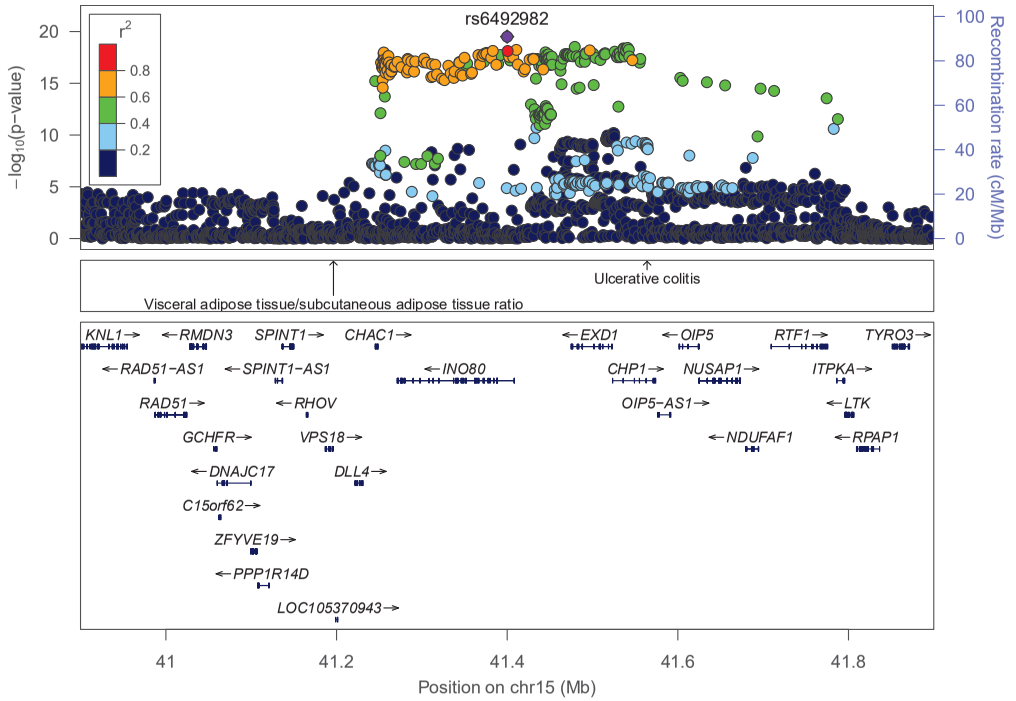

rs6574652
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
IgG glycosylation
(16:1n−7) plasma levels
Obesity−related traits
4 GWAS hits omitted
←CEP128
←GTF2A1
←STON2
←SEL1L
←LINC01467
TSHR→
←LINC02308
←LINC02311
←SNORA79
LOC101928504→
Position on chr14 (Mb)

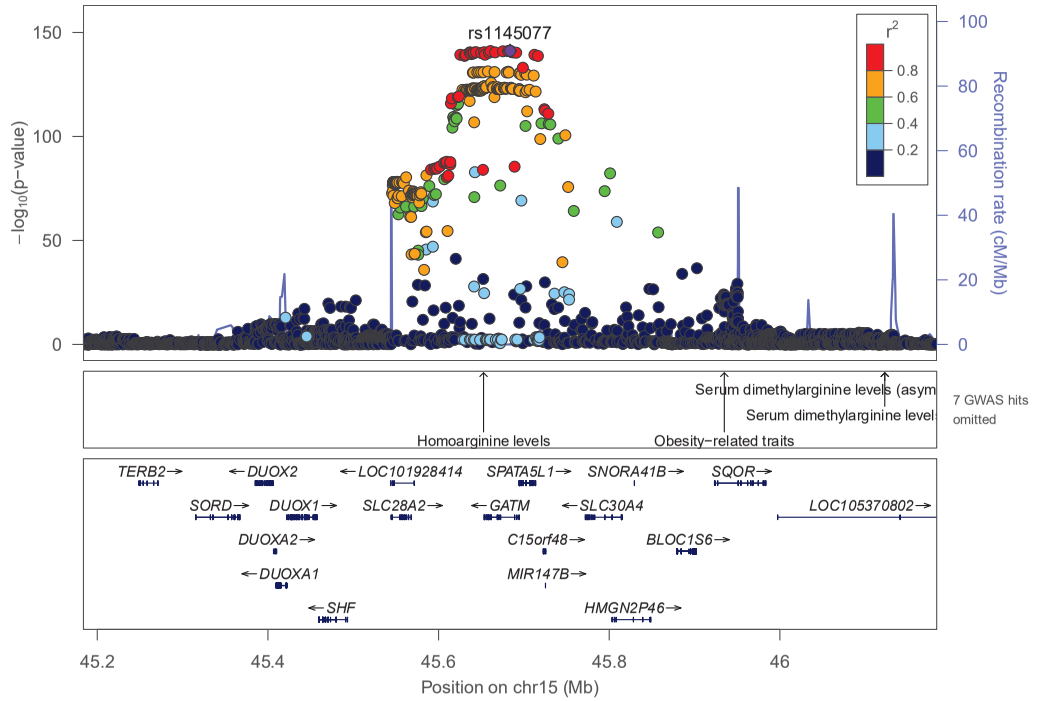

rs1028455
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Coronary artery calcification
Inflammatory bowel disease
Information processing speed
Multiple sclerosis
2 GWAS hits omitted
←GALC
←KCNK10
SPATA7→
ZC3H14→
TTC8→
GPR65→
←PTPN21
←EML5
←LOC101928791
LINC01146→
Position on chr14 (Mb)

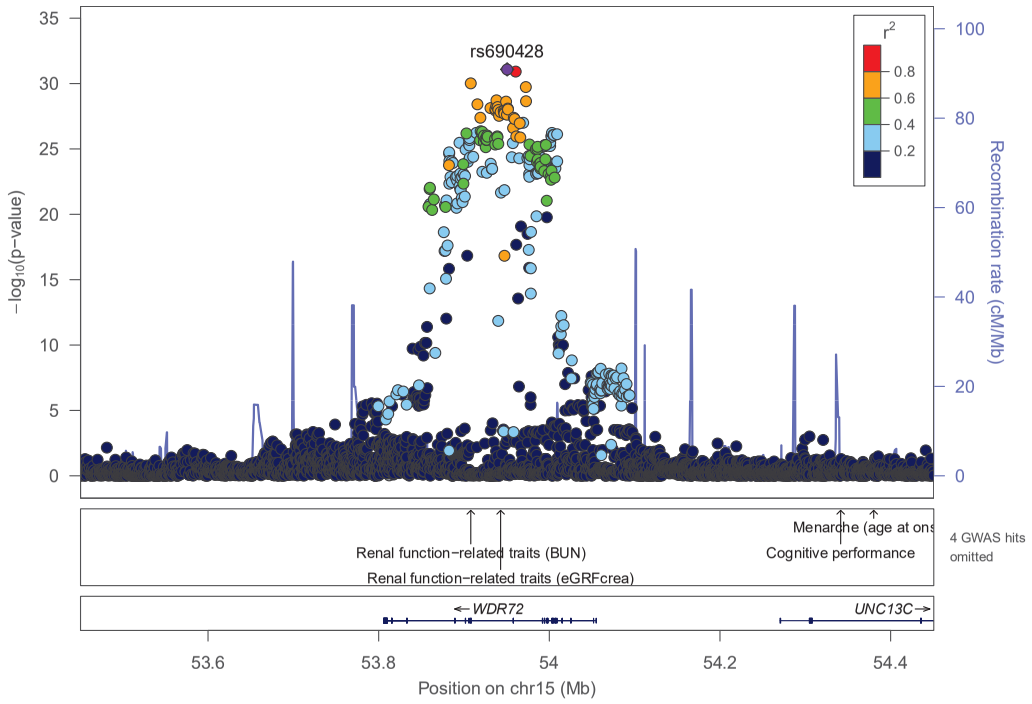

rs17184313
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Alzheimer's disease (late onset)
Eye color
Hair color
Paget's disease
IgG glycosylation
Thyroid horn
Platelet counts
7 GWAS hits omitted
CPSF2→
SLC24A4→
RIN3→
GOLGA5→
CHGA→
ITPK1−AS1→
←LGMN
←LINC02287
←ITPK1
Position on chr14 (Mb)

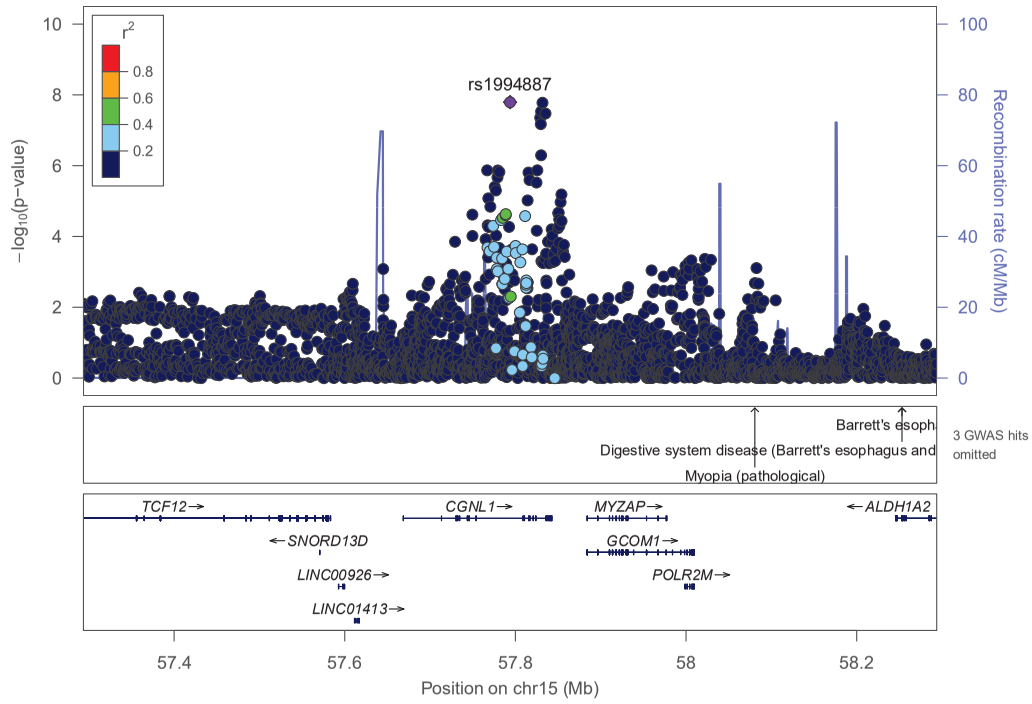

rs61993680
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Electroencephalographic traits in alcoholism
Sudden cardiac arrest
Menarche (age at onset)
Platelet counts
Type 2 diabetes
1 GWAS hit omitted
EML1→
EVL→
YY1→
←WARS
←BEGAIN
DLK1→
←MIR151B
MIR6764→
WDR25→
LINC00523→
MIR342→
←SLC25A29
←DEGS2
MIR345→
SLC25A47→
100.4
100.6
100.8
101
101.2
Position on chr14 (Mb)

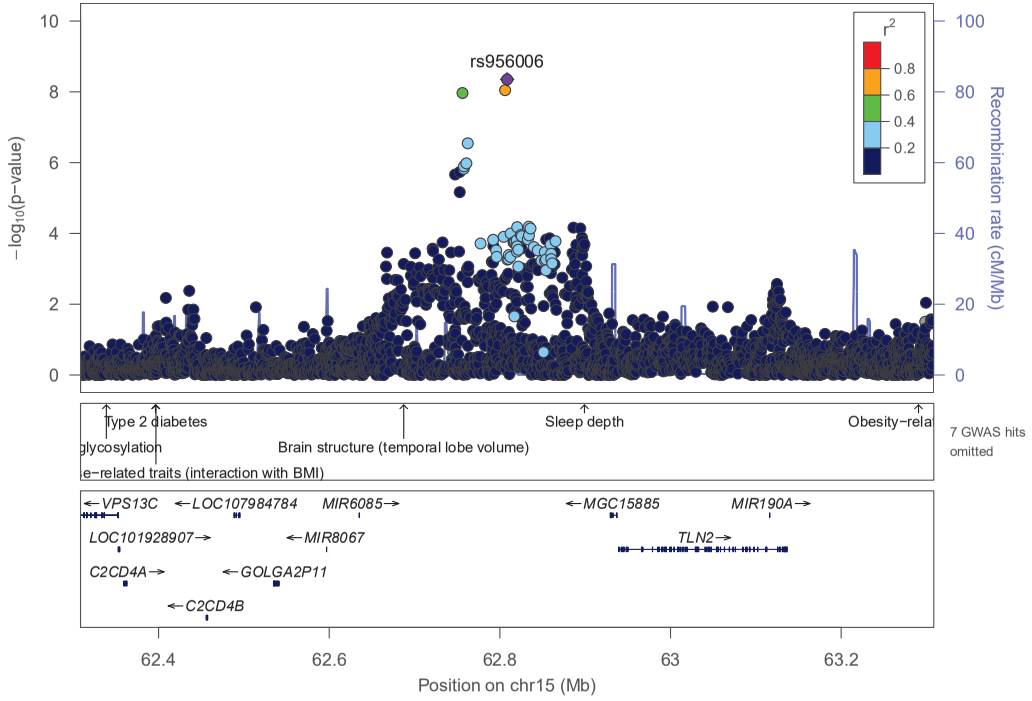

rs12913015
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Metabolite levels (Dihydroxy docosatrienoic acid)
PR interval
PR interval
10 GWAS hits omitted
←RASGRP1
C15orf53→
C15orf54→
39
39.2
39.4
39.6
39.8
Position on chr15 (Mb)

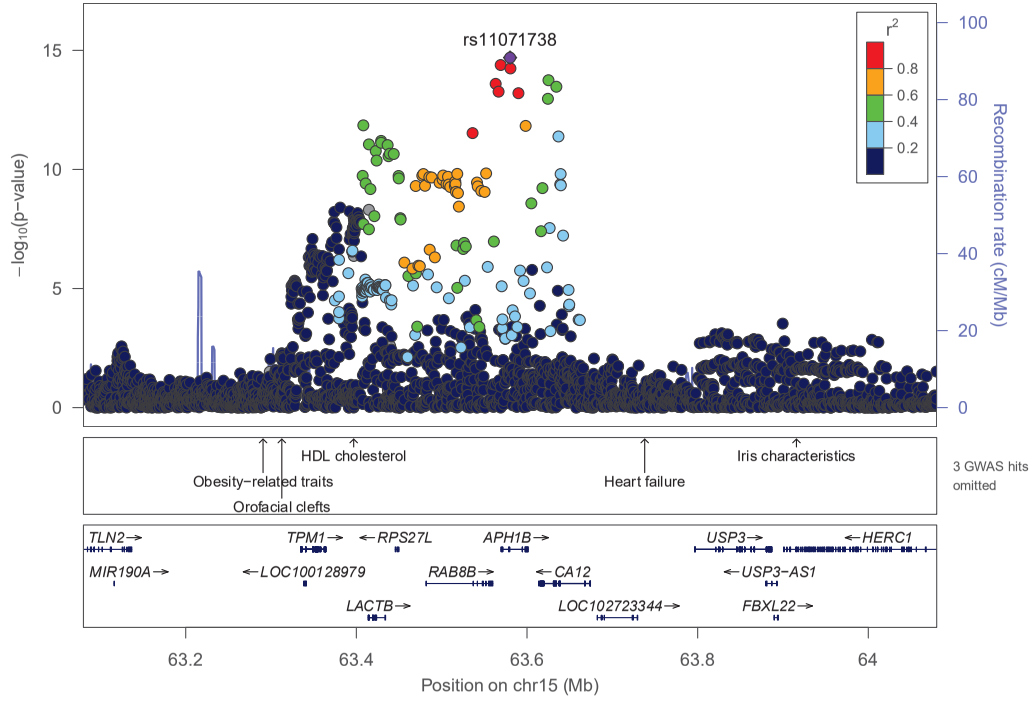

rs6492982
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Visceral adipose tissue/subcutaneous adipose tissue ratio
Ulcerative colitis
KNL1→
←RMDN3
SPINT1→
CHAC1→
←EXD1
←OIP5
RTF1→
TYRO3→
←RAD51−AS1
←SPINT1−AS1
←INO80
CHP1→
NUSAP1→
ITPKA→
RAD51→
←RHOV
OIP5−AS1→
←LTK
GCHFR→
VPS18→
←NDUFAF1
←RPAP1
←DNAJC17
DLL4→
C15orf62→
ZFYVE19→
←PPP1R14D
LOC105370943→
41
41.2
41.4
41.6
41.8
Position on chr15 (Mb)

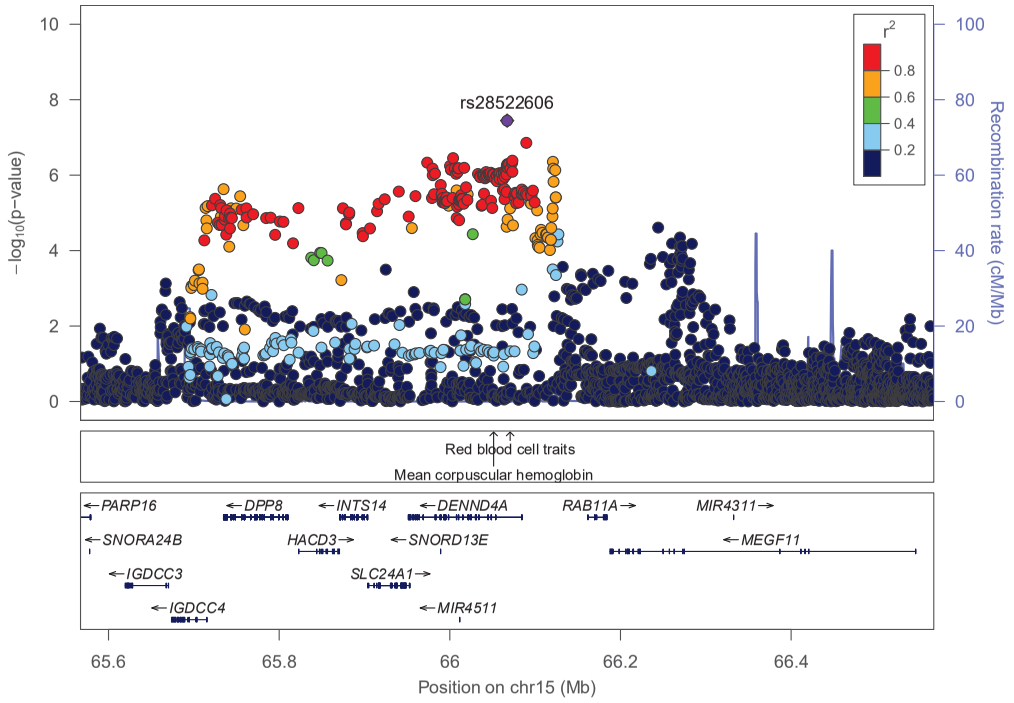

rs1145077
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Homoarginine levels
Obesity−related traits
Serum dimethylarginine levels (asym
Serum dimethylarginine level
7 GWAS hits omitted
TERB2→
←DUOX2
←LOC101928414
SPATA5L1→
SNORA41B→
SQOR→
SORD→
DUOX1→
SLC28A2→
←GATM
←SLC30A4
LOC105370802→
DUOXA2→
C15orf48→
BLOC1S6→
←DUOXA1
MIR147B→
←SHF
HMGN2P46→
45.2
45.4
45.6
45.8
46
Position on chr15 (Mb)

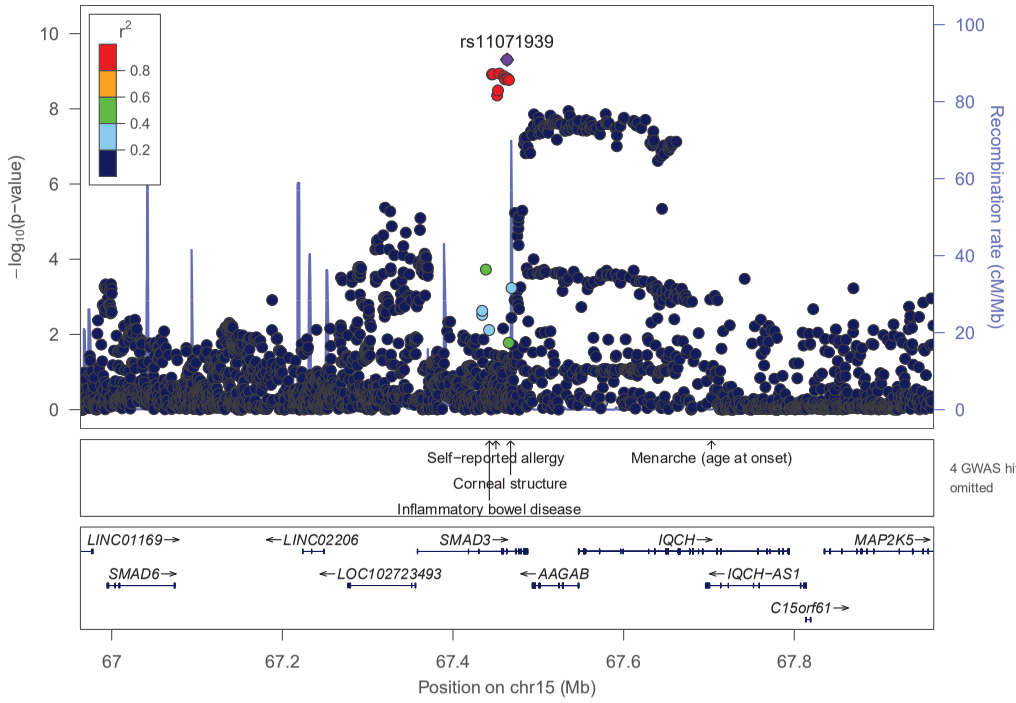

rs690428
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Renal function−related traits (BUN)
Renal function−related traits (eGRFcrea)
Menarche (age at ons
Cognitive performance
4 GWAS hits omitted
WDR72
UNC13C
Position on chr15 (Mb)

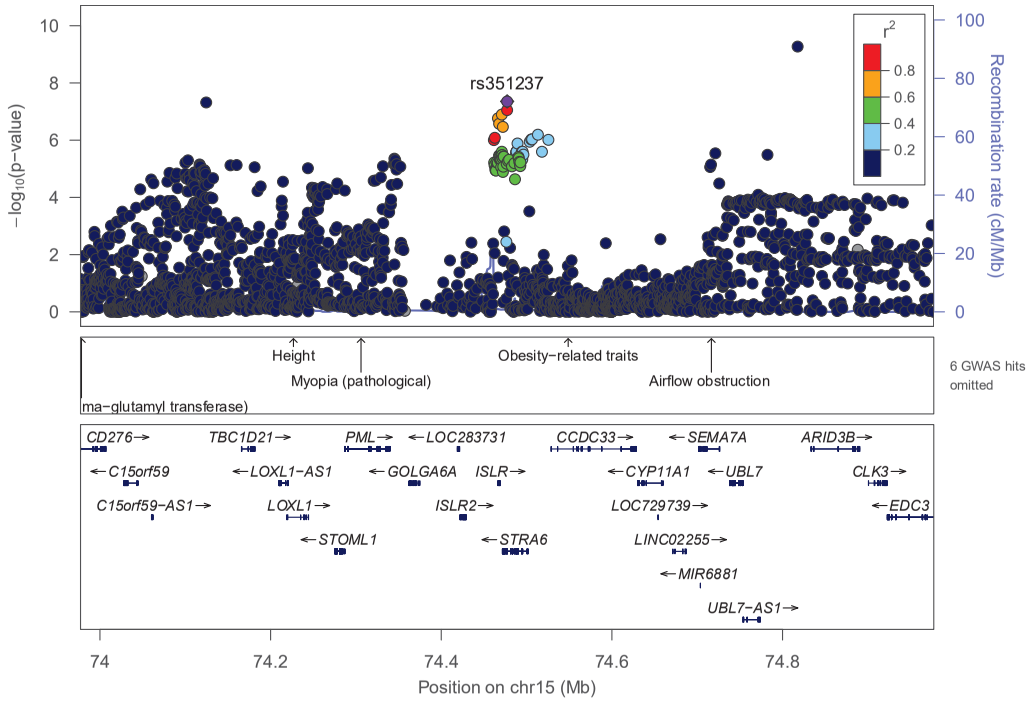

rs1994887
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Barrett's esoph
Digestive system disease (Barrett's esophagus and
Myopia (pathological)
3 GWAS hits omitted
TCF12
CGNL1
MYZAP
ALDH1A2
SNORD13D
GCOM1
LINC00926
POLR2M
LINC01413
Position on chr15 (Mb)

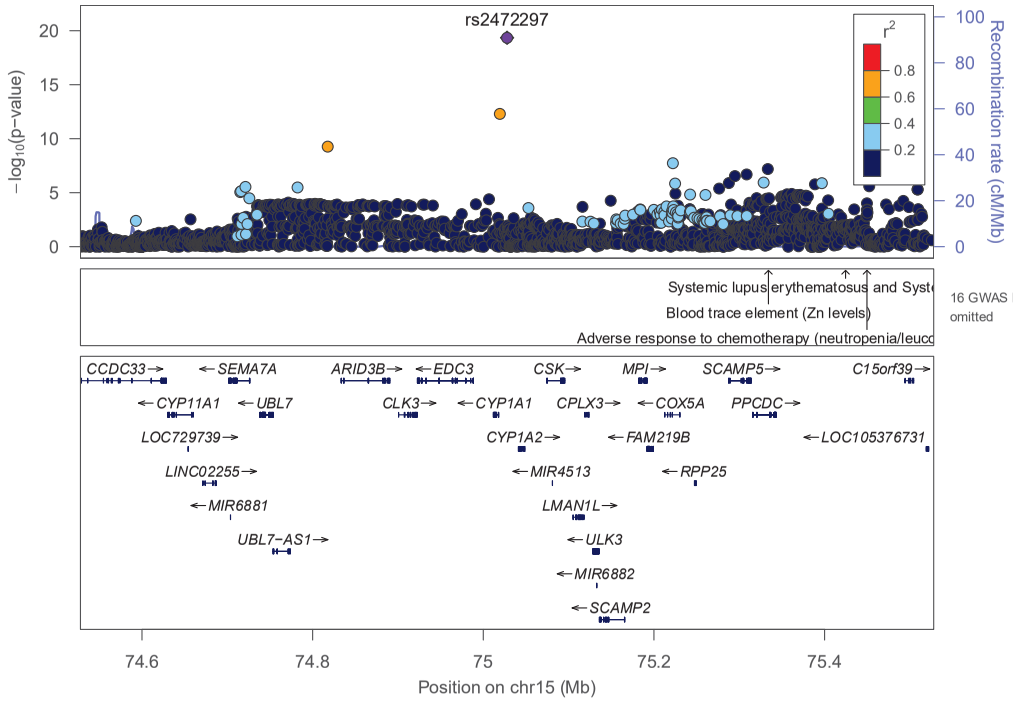

rs956006
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Type 2 diabetes
glycosylation
e−related traits (interaction with BMI)
Brain structure (temporal lobe volume)
Sleep depth
Obesity−rela
7 GWAS hits omitted
VPS13C
LOC107984784
MIR6085
MGC15885
MIR190A
LOC101928907
MIR8067
TLN2
C2CD4A
GOLGA2P11
C2CD4B
Position on chr15 (Mb)

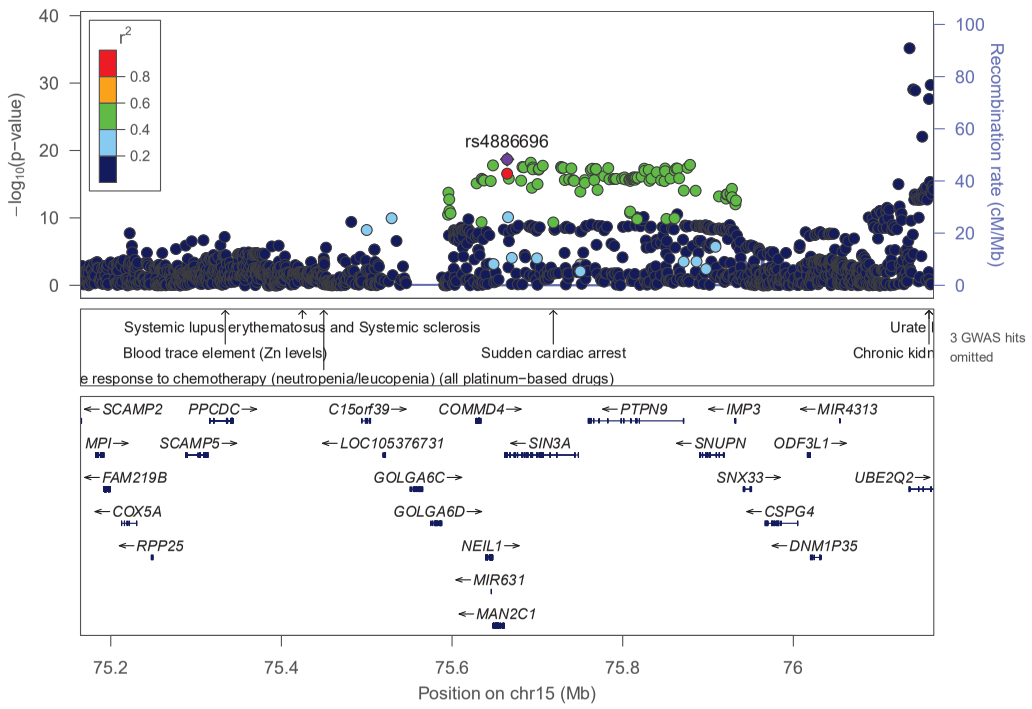

rs11071738
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Orofacial clefts
HDL cholesterol
Heart failure
Iris characteristics
3 GWAS hits omitted
TLN2
TPM1
RPS27L
APH1B
USP3
HERC1
MIR190A
LOC100128979
RAB8B
CA12
USP3−AS1
LACTB
LOC102723344
FBXL22
Position on chr15 (Mb)

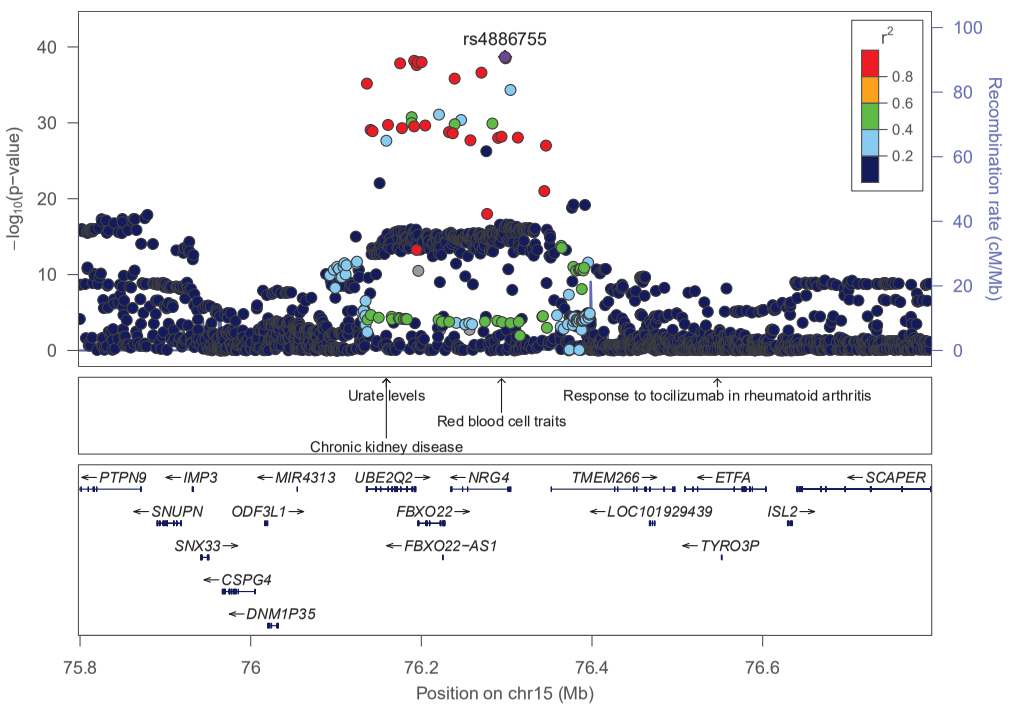

rs28522606
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Red blood cell traits
Mean corpuscular hemoglobin
←PARP16
←DPP8
←INTS14
←DENND4A
RAB11A→
MIR4311→
←SNORA24B
HACD3→
←SNORD13E
←MEGF11
←IGDCC3
SLC24A1→
←IGDCC4
←MIR4511
Position on chr15 (Mb)

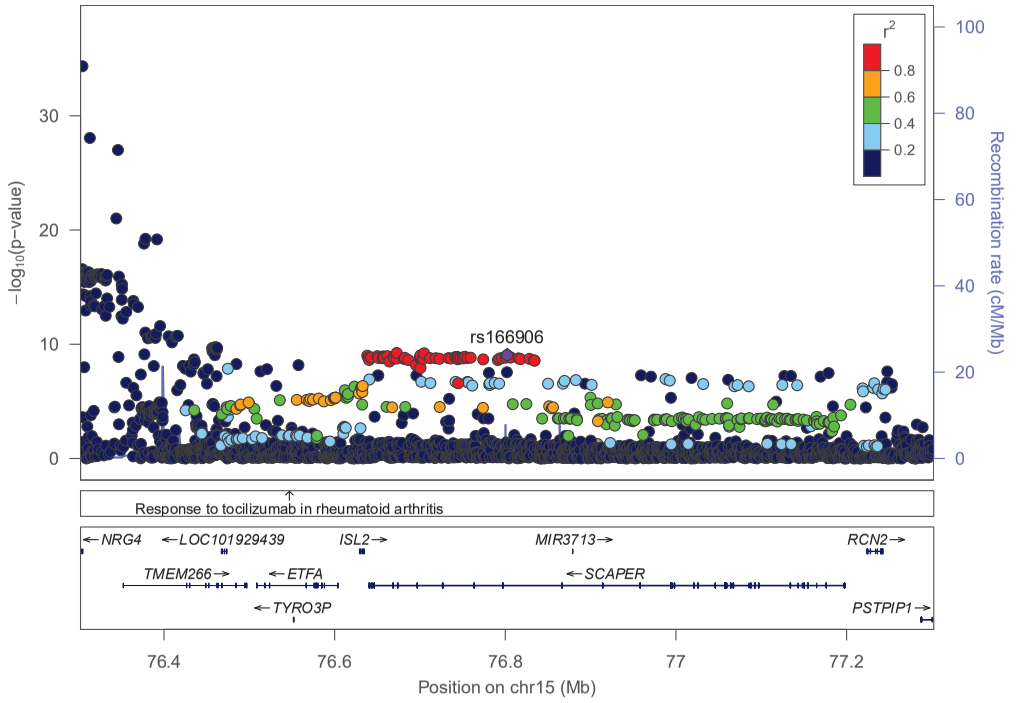

rs11071939
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Self−reported allergy
Corneal structure
Inflammatory bowel disease
Menarche (age at onset)
4 GWAS hits omitted
LINC01169→
←LINC02206
SMAD3→
IQCH→
MAP2K5→
SMAD6→
←LOC102723493
←AAGAB
←IQCH−AS1
C15orf61→
Position on chr15 (Mb)

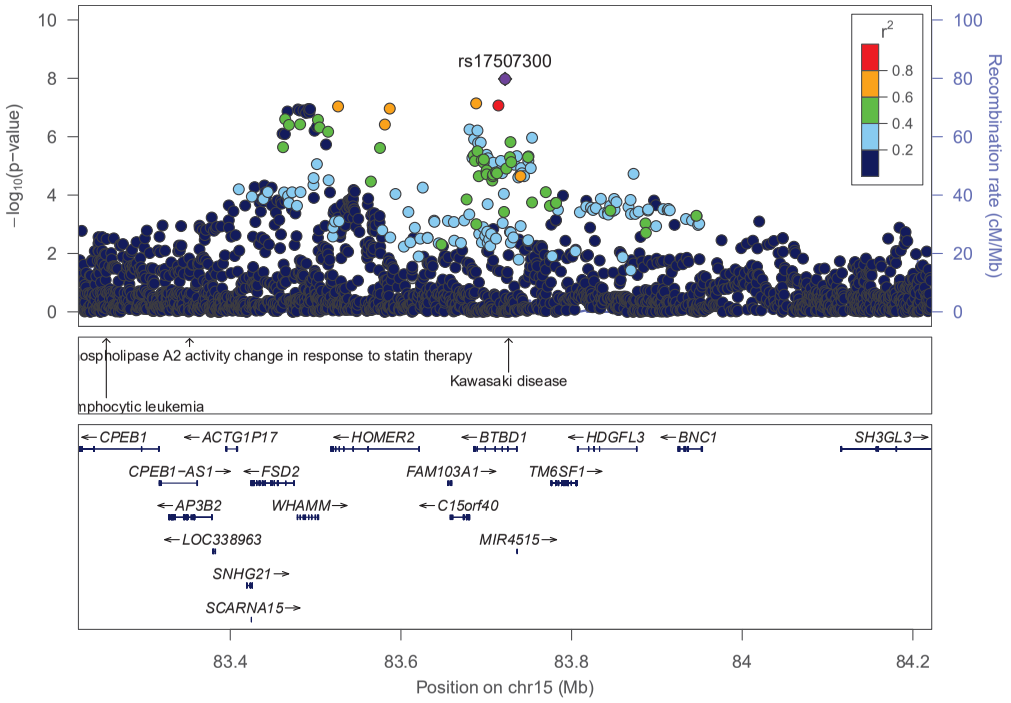

rs351237
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Height
Myopia (pathological)
Obesity−related traits
Airflow obstruction
6 GWAS hits omitted
ma−glutamyl transferase)
CD276→
TBC1D21→
PML→
←LOC283731
CCDC33→
←SEMA7A
ARID3B→
←C15orf59
←LOXL1−AS1
←GOLGA6A
ISLR→
←CYP11A1
←UBL7
CLK3→
C15orf59−AS1→
LOXL1→
ISLR2→
LOC729739→
←EDC3
←STOML1
STRA6→
LINC02255→
←MIR6881
UBL7−AS1→
Position on chr15 (Mb)

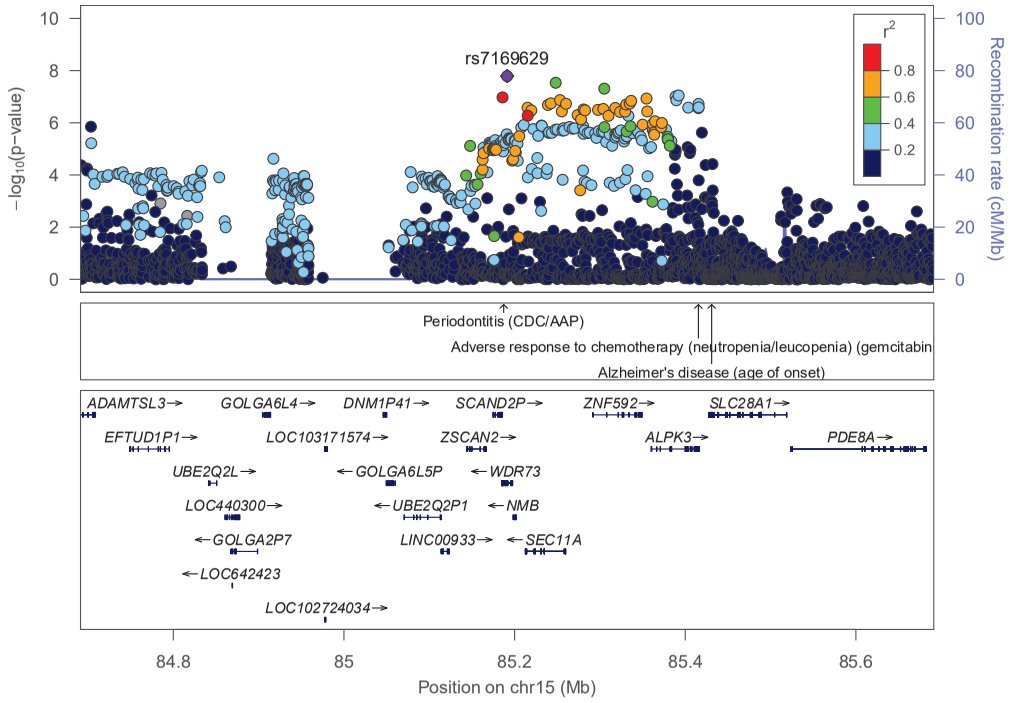

rs2472297
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Systemic lupus erythematosus and Syst
Blood trace element (Zn levels)
Adverse response to chemotherapy (neutropenia/leuco
16 GWAS hits omitted
CCDC33→
←SEMA7A
ARID3B→
←EDC3
CSK→
MPI→
SCAMP5→
C15orf39→
←CYP11A1
←UBL7
CLK3→
←CYP1A1
CPLX3→
←COX5A
PPCDC→
LOC729739→
CYP1A2→
←FAM219B
←LOC105376731
LINC02255→
←MIR4513
←RPP25
←MIR6881
LMAN1L→
UBL7−AS1→
←ULK3
←MIR6882
←SCAMP2
Position on chr15 (Mb)

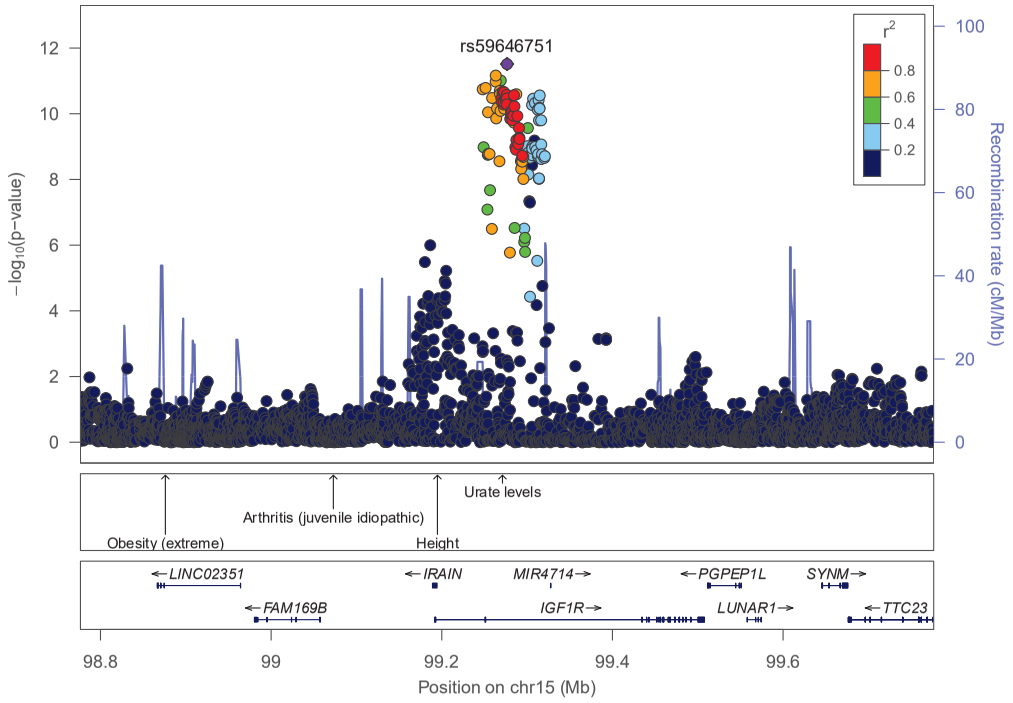

rs4886696
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Systemic lupus erythematosus and Systemic sclerosis
Blood trace element (Zn levels)
Sudden cardiac arrest
Urate
Chronic kidn
3 GWAS hits omitted
e response to chemotherapy (neutropenia/leucopenia) (all platinum−based drugs)
SCAMP2 PPCDC C15orf39 COMMD4 PTPN9 IMP3 MIR4313
MPI SCAMP5 LOC105376731 SIN3A SNUPN ODF3L1
FAM219B GOLGA6C SNX33 UBE2Q2
COX5A GOLGA6D CSPG4
RPP25 NEIL1 DNM1P35
MIR631
MAN2C1
75.2 75.4 75.6 75.8 76
Position on chr15 (Mb)

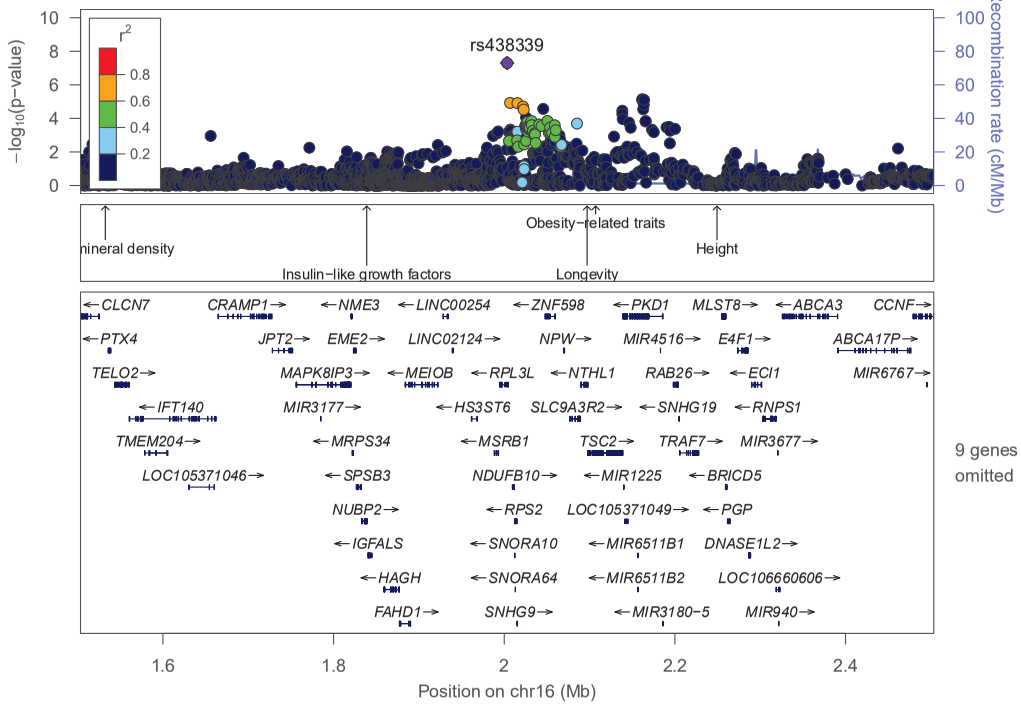

rs4886755
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Urate levels
Red blood cell traits
Response to tocilizumab in rheumatoid arthritis
Chronic kidney disease
PTPN9 IMP3 MIR4313 UBE2Q2 NRG4 TMEM266 ETFA SCAPER
SNUPN ODF3L1 FBXO22 LOC101929439 ISL2
SNX33 FBXO22−AS1 TYRO3P
CSPG4
DNM1P35
75.8 76 76.2 76.4 76.6
Position on chr15 (Mb)

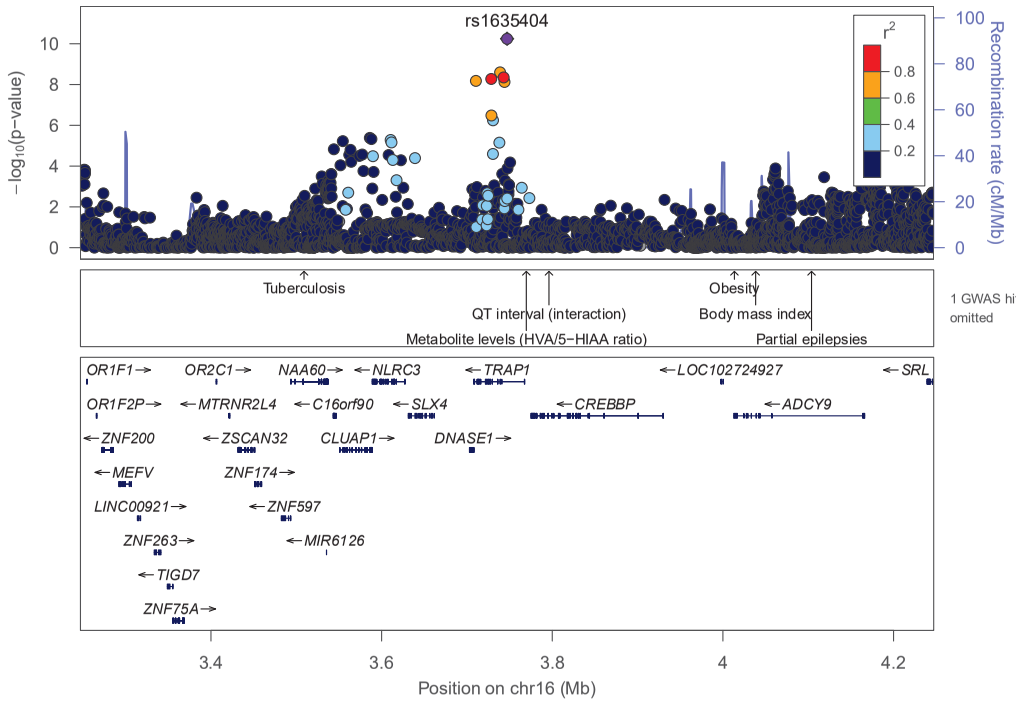

rs166906
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Response to tocilizumab in rheumatoid arthritis
NRG4 LOC101929439 ISL2 MIR3713 RCN2
TMEM266 ETFA SCAPER
TYRO3P PSTPIP1
76.4 76.6 76.8 77 77.2
Position on chr15 (Mb)

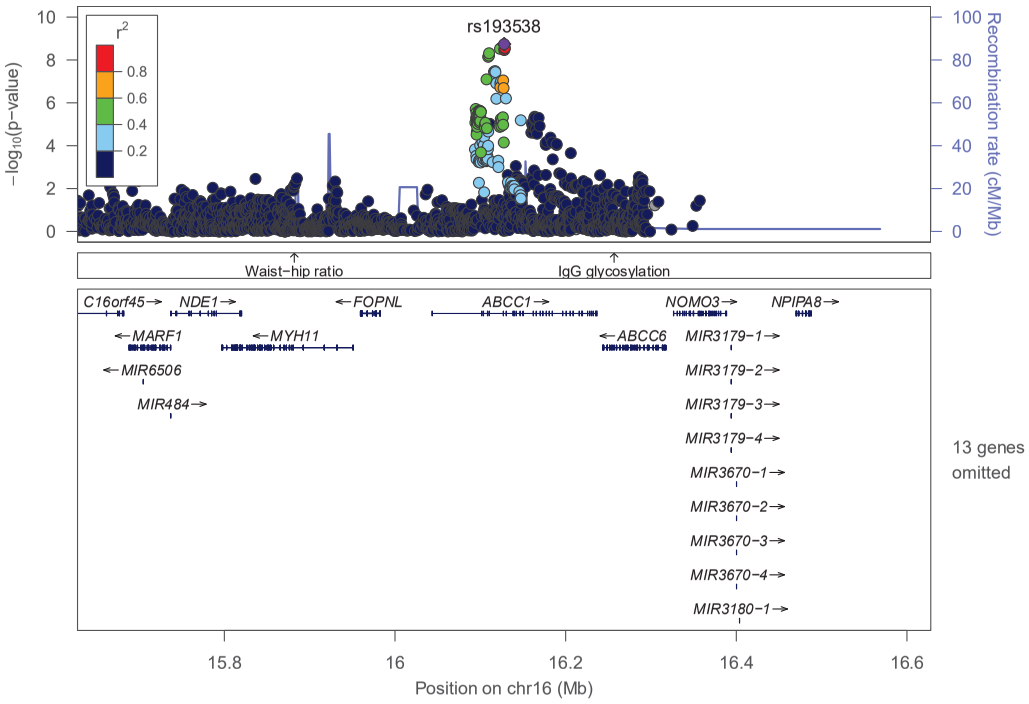

rs17507300
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ospholipase A2 activity change in response to statin therapy
Kawasaki disease
nphocytic leukemia
CPEB1 ACTG1P17 HOMER2 BTBD1 HDGFL3 BNC1 SH3GL3
CPEB1−AS1 FSD2 FAM103A1 TM6SF1
AP3B2 WHAMM C15orf40
LOC338963 MIR4515
SNHG21
SCARNA15
83.4 83.6 83.8 84 84.2
Position on chr15 (Mb)

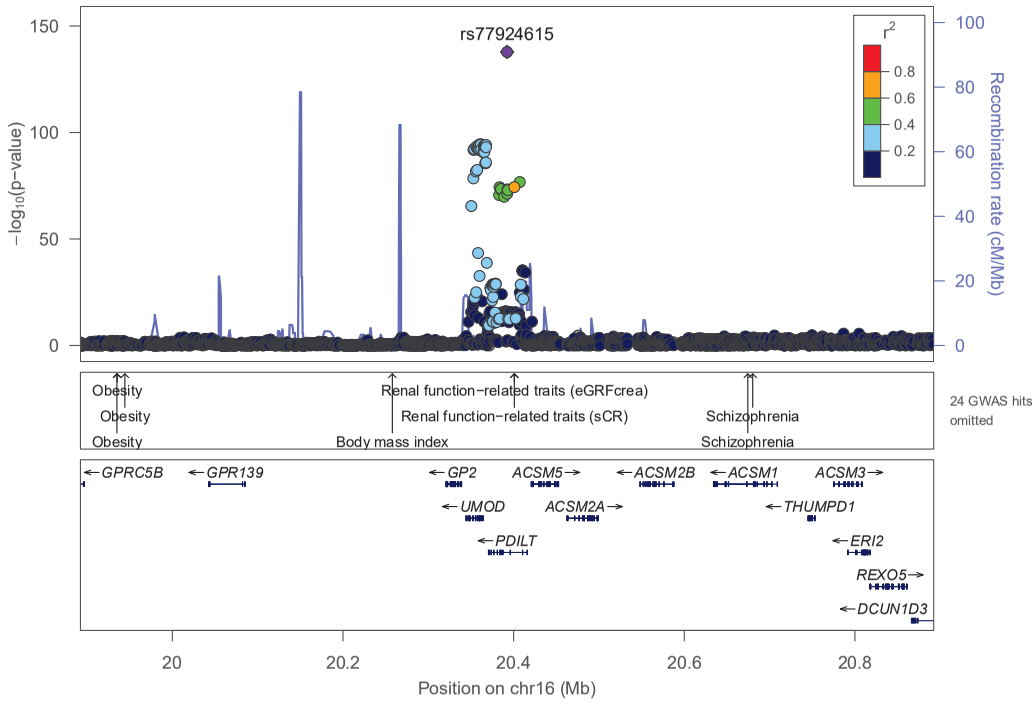

rs7169629
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Periodontitis (CDC/AAP)
Adverse response to chemotherapy (neutropenia/leucopenia) (gemcitabin
Alzheimer's disease (age of onset)
ADAMTSL3→ GOLGA6L4→ DNM1P41→ SCAND2P→ ZNF592→ SLC28A1→
EFTUD1P1→ LOC103171574→ ZSCAN2→ ALPK3→ PDE8A→
UBE2Q2L→ ←GOLGA6L5P ←WDR73
LOC440300→ ←UBE2Q2P1 ←NMB
←GOLGA2P7 LINC00933→ ←SEC11A
←LOC642423
LOC102724034→
84.8
85
85.2
85.4
85.6
Position on chr15 (Mb)

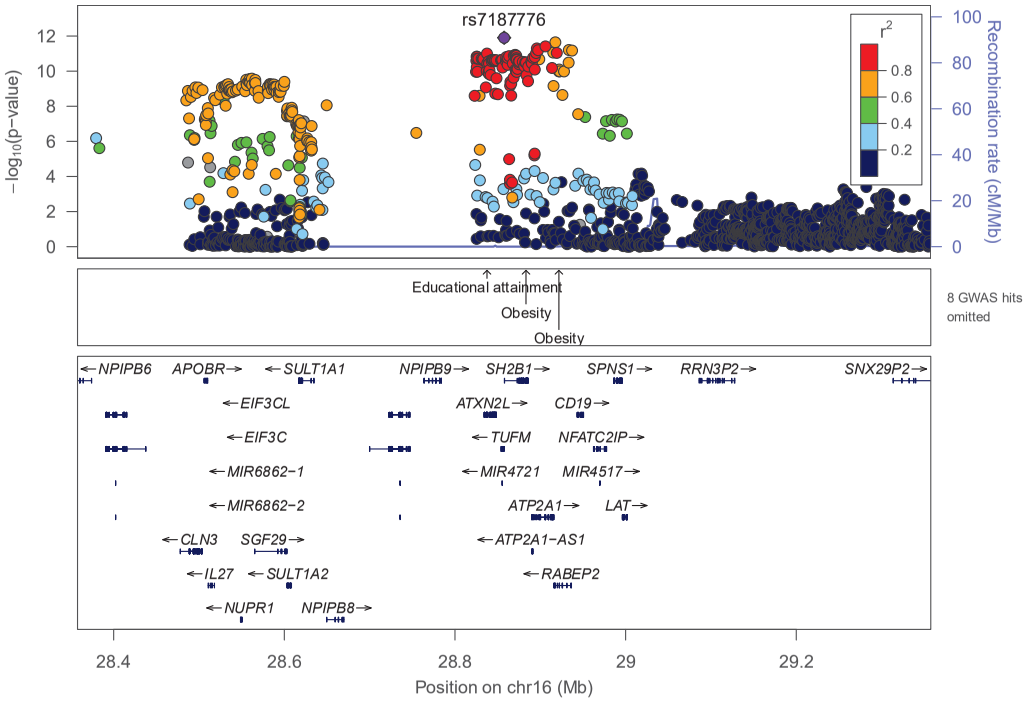

rs59646751
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity (extreme)
Arthritis (juvenile idiopathic)
Height
Urate levels
←LINC02351 ←IRAIN MIR4714→ ←PGPEP1L SYNM→
←FAM169B IGF1R→ LUNAR1→ ←TTC23
98.8
99
99.2
99.4
99.6
Position on chr15 (Mb)

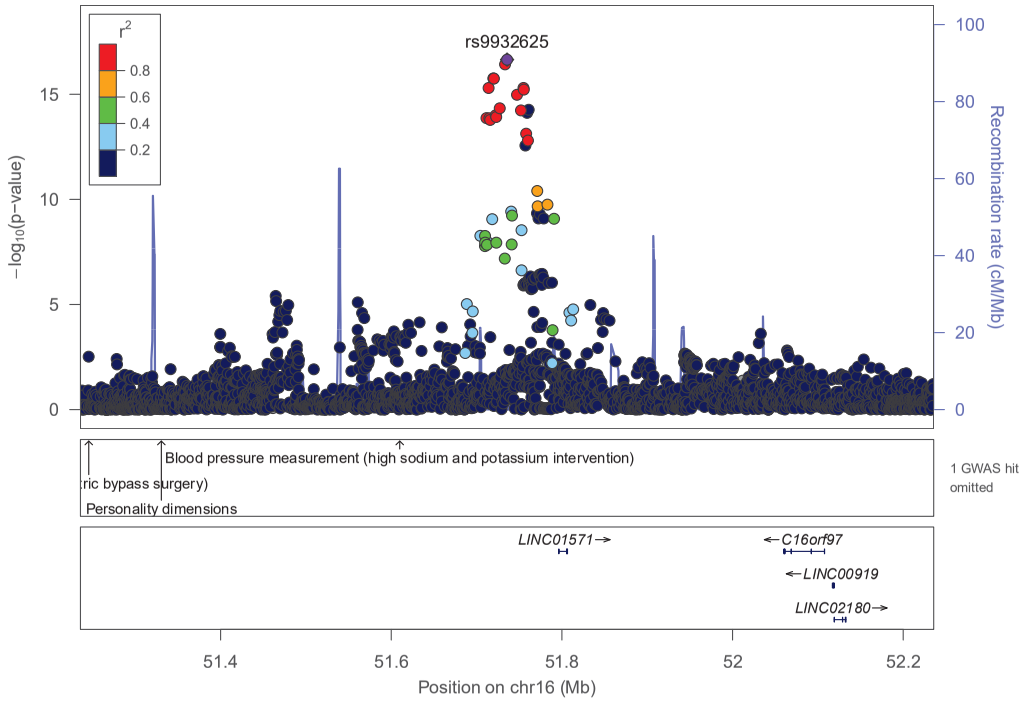

rs438339
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
nineral density
Insulin−like growth factors
Longevity
Obesity−related traits
Height
←CLCN7 CRAMP1→ ←NME3 ←LINC00254 ←ZNF598 ←PKD1 MLST8→ ←ABCA3 CCNF→
←PTX4 JPT2→ EME2→ LINC02124→ NPW→ MIR4516→ E4F1→ ABCA17P→
TELO2→ MAPK8IP3→ ←MEIOB ←RPL3L ←NTHL1 RAB26→ ←ECI1 MIR6767→
←IFT140 MIR3177→ ←HS3ST6 SLC9A3R2→ ←SNHG19 ←RNPS1
TMEM204→ ←MRPS34 ←MSRB1 TSC2→ TRAF7→ MIR3677→
LOC105371046→ ←SPSB3 NDUFB10→ ←MIR1225 ←BRICD5
NUBP2→ ←RPS2 LOC105371049→ ←PGP
←IGFALS ←SNORA10 ←MIR6511B1 DNASE1L2→
←HAGH ←SNORA64 ←MIR6511B2 LOC106660606→
FAHD1→ SNHG9→ ←MIR3180−5 MIR940→
9 genes omitted
1.6
1.8
2
2.2
2.4
Position on chr16 (Mb)

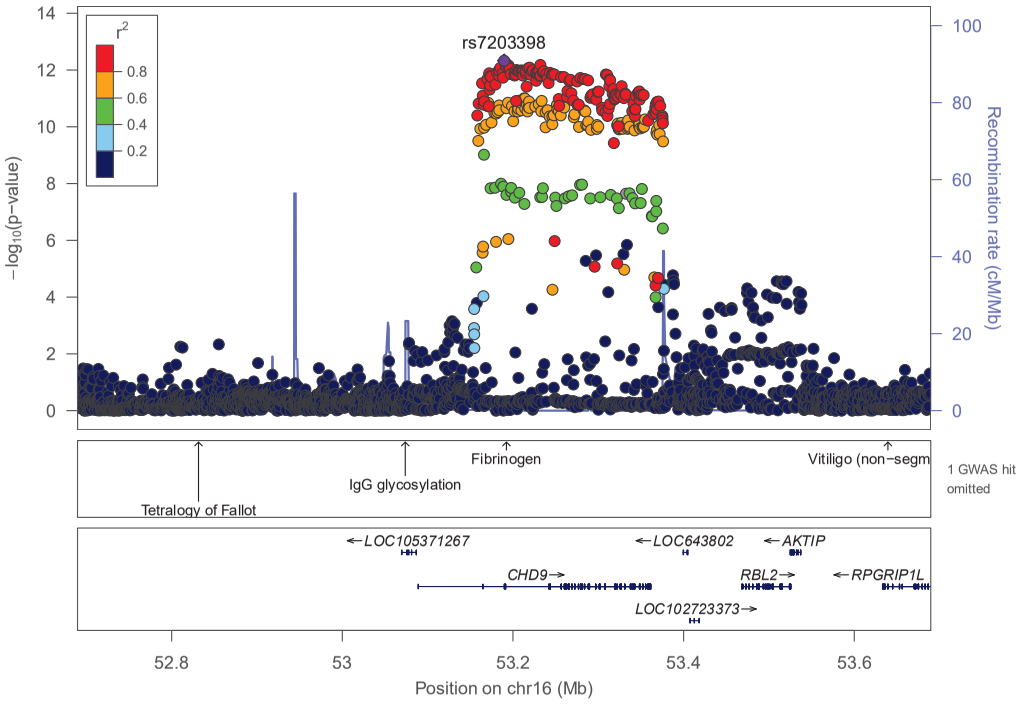

rs1635404
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Tuberculosis
QT interval (interaction)
Metabolite levels (HVA/5−HIAA ratio)
Obesity
Body mass index
Partial epilepsies
1 GWAS hit omitted
OR1F1→ OR2C1→ NAA60→ ←NLRC3 ←TRAP1 ←LOC102724927 ←SRL
OR1F2P→ ←MTRNR2L4 ←C16orf90 ←SLX4 ←CREBBP ←ADCY9
←ZNF200 ←ZSCAN32 CLUAP1→ DNASE1→
←MEFV ZNF174→
LINC00921→ ←ZNF597
ZNF263→ ←MIR6126
←TIGD7
ZNF75A→
3.4
3.6
3.8
4
4.2
Position on chr16 (Mb)

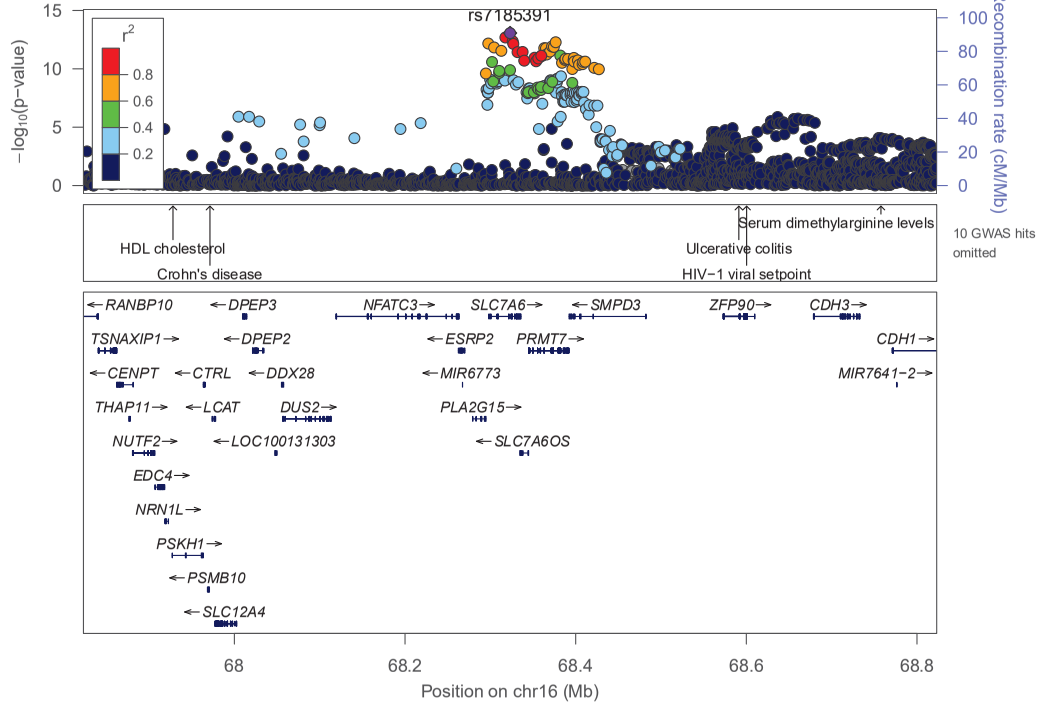

rs193538
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Waist−hip ratio
IgG glycosylation
C16orf45→
NDE1→
←FOPNL
ABCC1→
NOMO3→
NPIPA8→
←MARF1
←MYH11
←ABCC6
MIR3179−1→
MIR3179−2→
MIR3179−3→
MIR3179−4→
←MIR6506
MIR484→
MIR3670−1→
MIR3670−2→
MIR3670−3→
MIR3670−4→
MIR3180−1→
13 genes omitted
15.8
16
16.2
16.4
16.6
Position on chr16 (Mb)

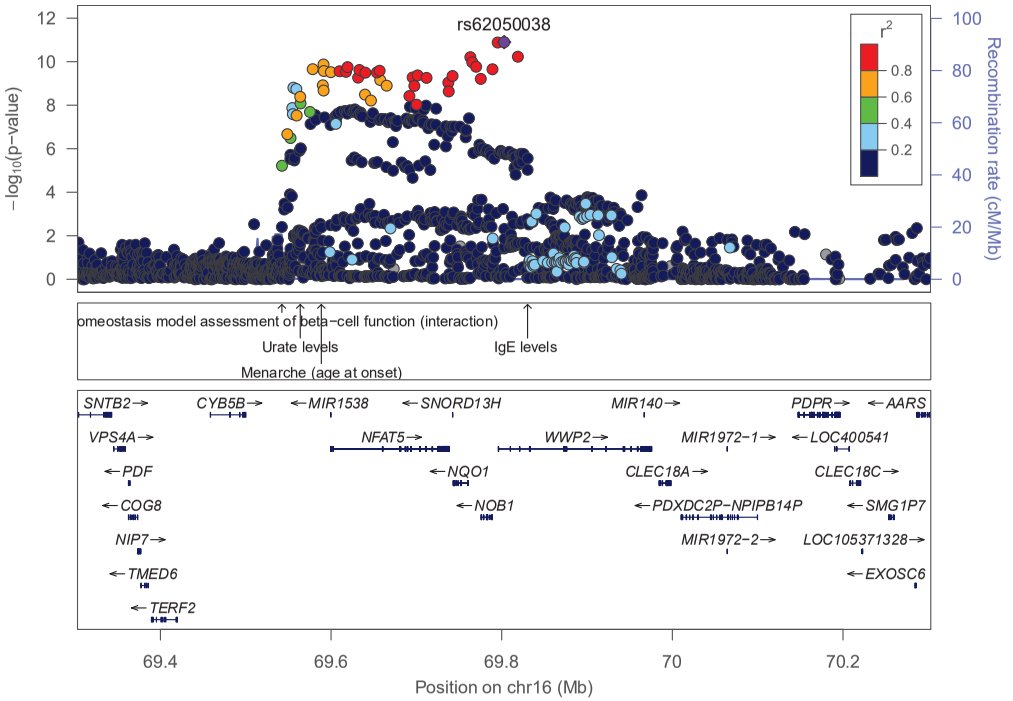

rs77924615
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity
Obesity
Obesity
Renal function−related traits (eGRFcrea)
Renal function−related traits (sCR)
Body mass index
Schizophrenia
Schizophrenia
24 GWAS hits omitted
←GPRC5B
←GPR139
←GP2
ACSM5→
←ACSM2B
←ACSM1
ACSM3→
←UMOD
ACSM2A→
←THUMPD1
←PDILT
←ERI2
REXO5→
←DCUN1D3
20
20.2
20.4
20.6
20.8
Position on chr16 (Mb)

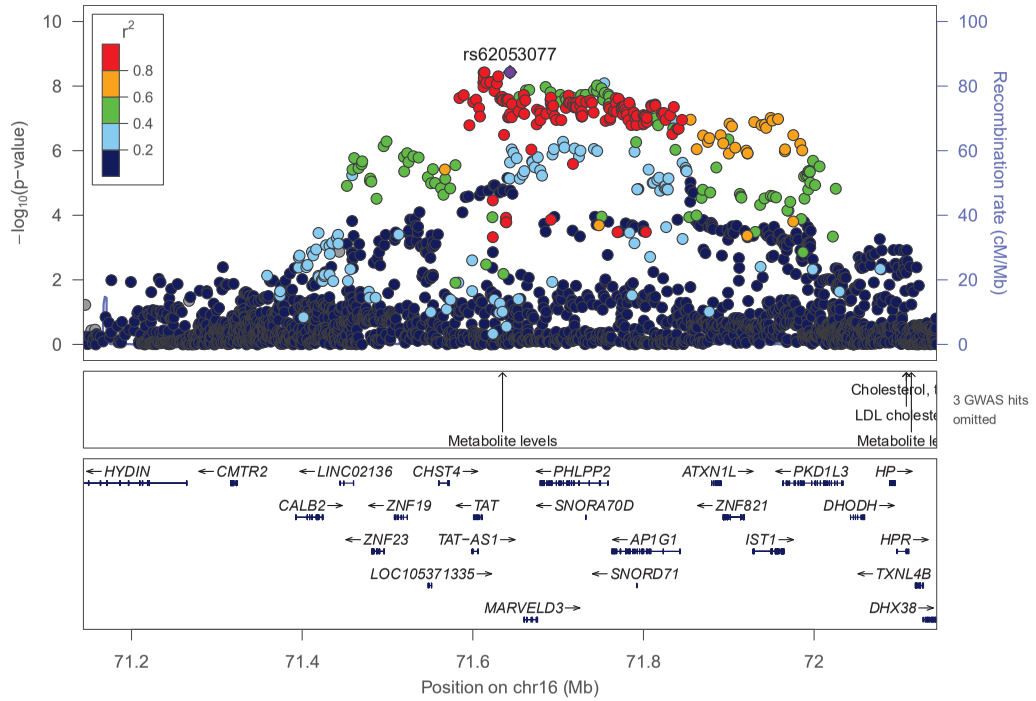

rs7187776
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Educational attainment
Obesity
Obesity
8 GWAS hits omitted
←NPIPB6
APOBR→
←SULT1A1
NPIPB9→
SH2B1→
SPNS1→
RRN3P2→
SNX29P2→
←EIF3CL
ATXN2L→
CD19→
←EIF3C
←TUFM
NFATC2IP→
←MIR6862−1
←MIR4721
MIR4517→
←MIR6862−2
ATP2A1→
LAT→
←CLN3
SGF29→
←ATP2A1−AS1
←IL27
←SULT1A2
←RABEP2
←NUPR1
NPIPB8→
28.4
28.6
28.8
29
29.2
Position on chr16 (Mb)

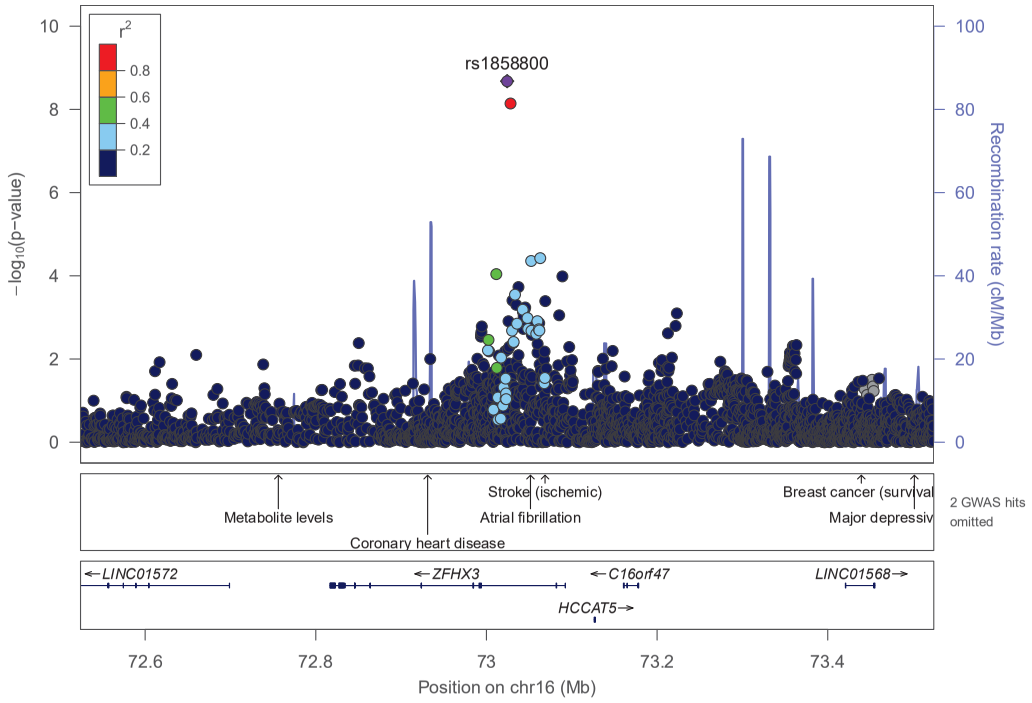

rs9932625
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ric bypass surgery)
Blood pressure measurement (high sodium and potassium intervention)
Personality dimensions
1 GWAS hit omitted
LINC01571→
←C16orf97
←LINC00919
LINC02180→
51.4
51.6
51.8
52
52.2
Position on chr16 (Mb)

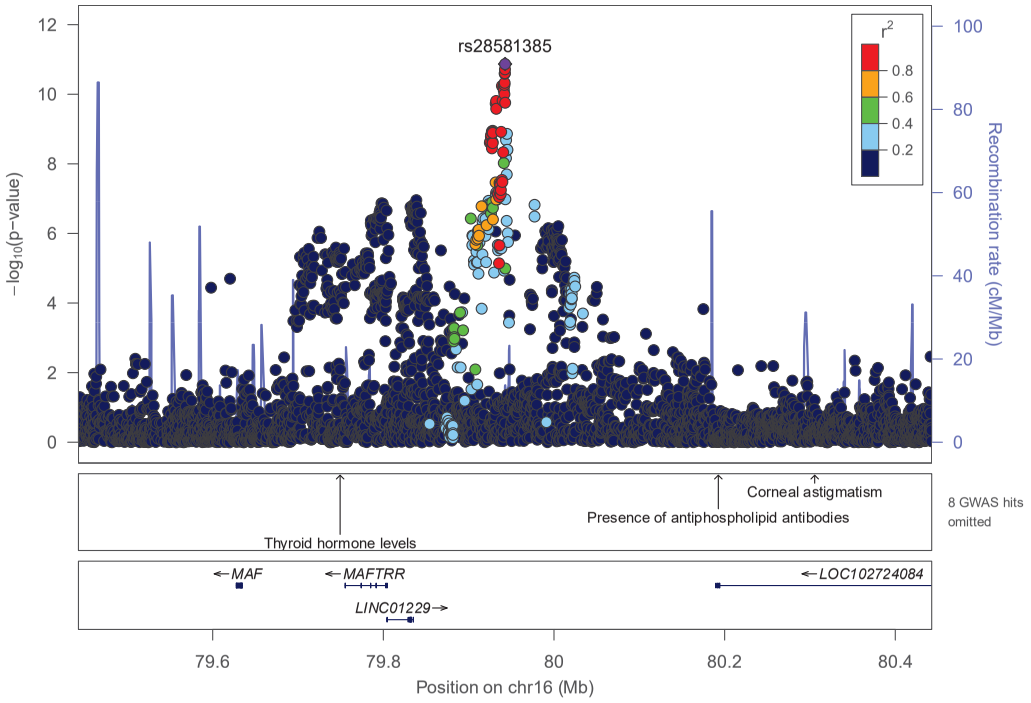

rs7203398
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Tetralogy of Fallot
IgG glycosylation
Fibrinogen
Vitiligo (non−segm
1 GWAS hit omitted
LOC105371267
LOC643802
AKTIP
CHD9
RBL2
RPGRIP1L
LOC102723373
Position on chr16 (Mb)

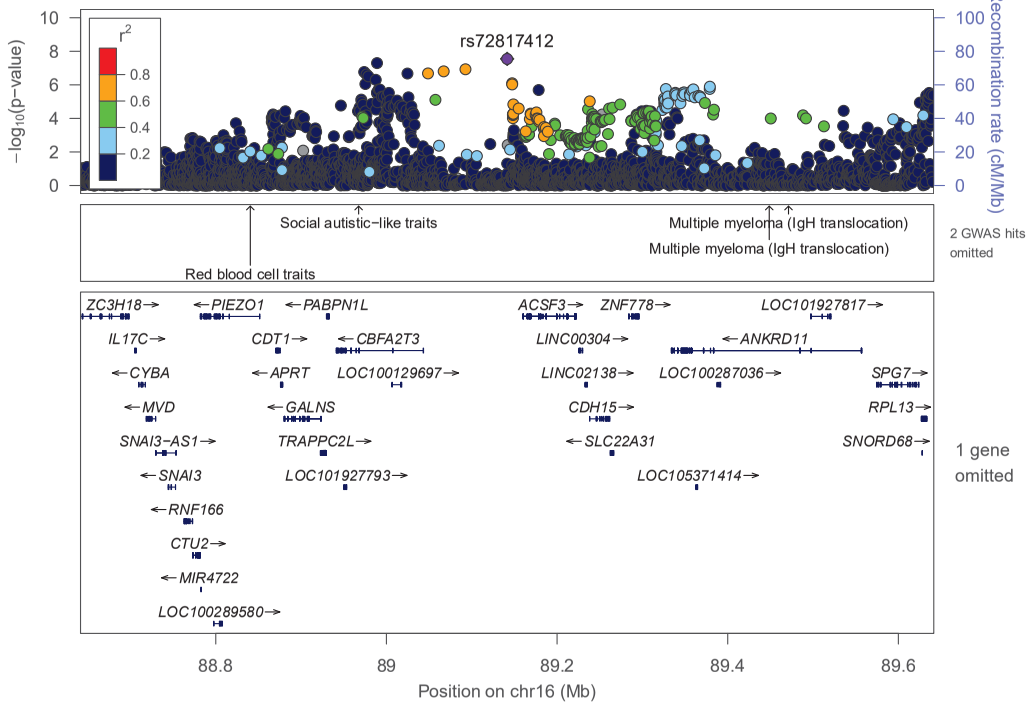

rs7185391
r²
−log10(p−value)
Recombination rate (cM/Mb)
HDL cholesterol
Crohn's disease
Serum dimethylarginine levels
Ulcerative colitis
HIV−1 viral setpoint
10 GWAS hits omitted
RANBP10
DPEP3
NFATC3
SLC7A6
SMPD3
ZFP90
CDH3
TSNAXIP1
DPEP2
ESRP2
PRMT7
CDH1
CENPT
CTRL
DDX28
MIR6773
MIR7641−2
THAP11
LCAT
DUS2
PLA2G15
NUTF2
LOC100131303
SLC7A6OS
EDC4
NRN1L
PSKH1
PSMB10
SLC12A4
Position on chr16 (Mb)

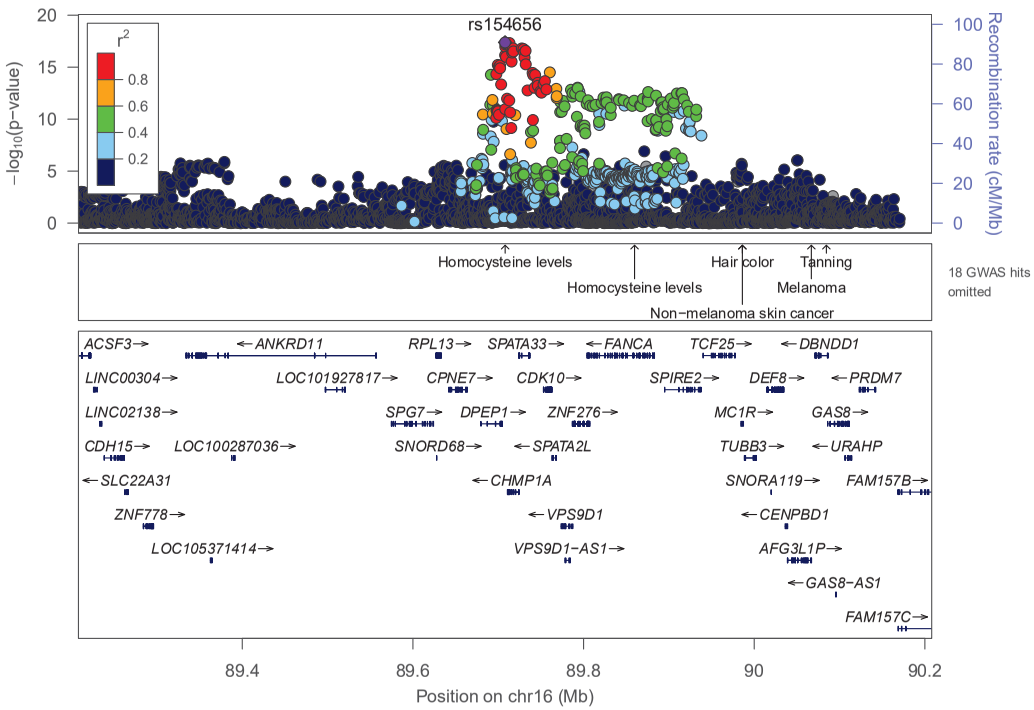

rs62050038
r²
−log10(p−value)
Recombination rate (cM/Mb)
omeostasis model assessment of beta−cell function (interaction)
Urate levels
Menarche (age at onset)
IgE levels
SNTB2
CYB5B
MIR1538
SNORD13H
MIR140
PDPR
AARS
VPS4A
NFAT5
WWP2
MIR1972−1
LOC400541
PDF
NQO1
CLEC18A
CLEC18C
COG8
NOB1
PDXDC2P−NPIPB14P
SMG1P7
NIP7
MIR1972−2
LOC105371328
TMED6
EXOSC6
TERF2
Position on chr16 (Mb)

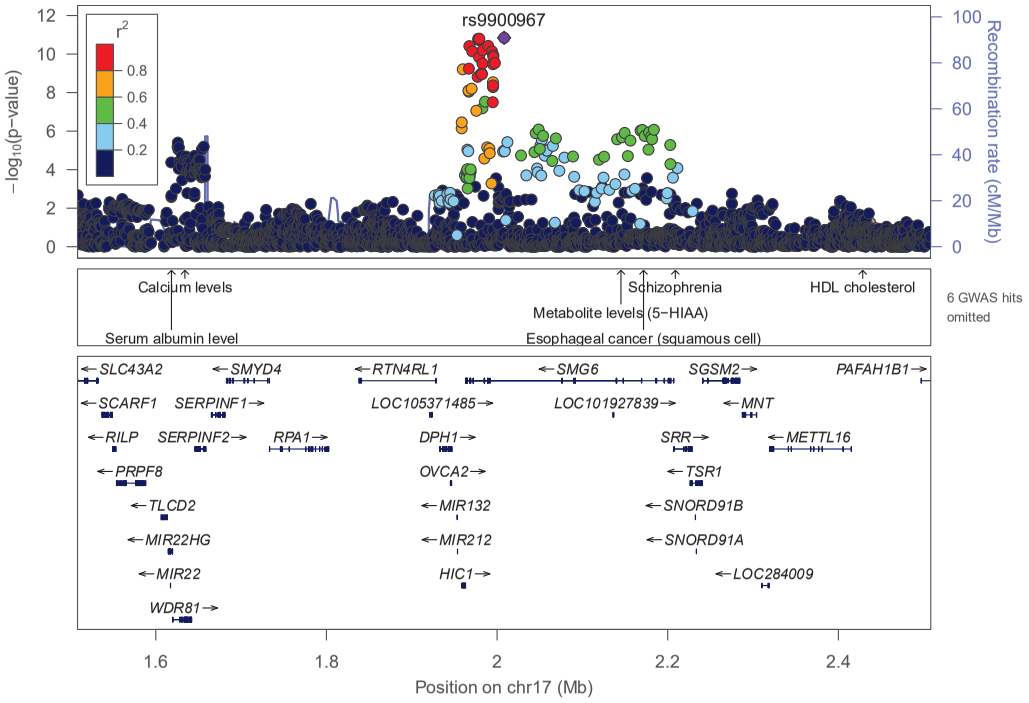

rs62053077
r²
−log10(p−value)
Recombination rate (cM/Mb)
Metabolite levels
3 GWAS hits omitted
HYDIN
CMTR2
LINC02136
CHST4
PHLPP2
ATXN1L
PKD1L3
HP
CALB2
ZNF19
TAT
SNORA70D
ZNF821
DHODH
ZNF23
TAT−AS1
AP1G1
IST1
HPR
LOC105371335
SNORD71
TXNL4B
MARVELD3
DHX38
Position on chr16 (Mb)

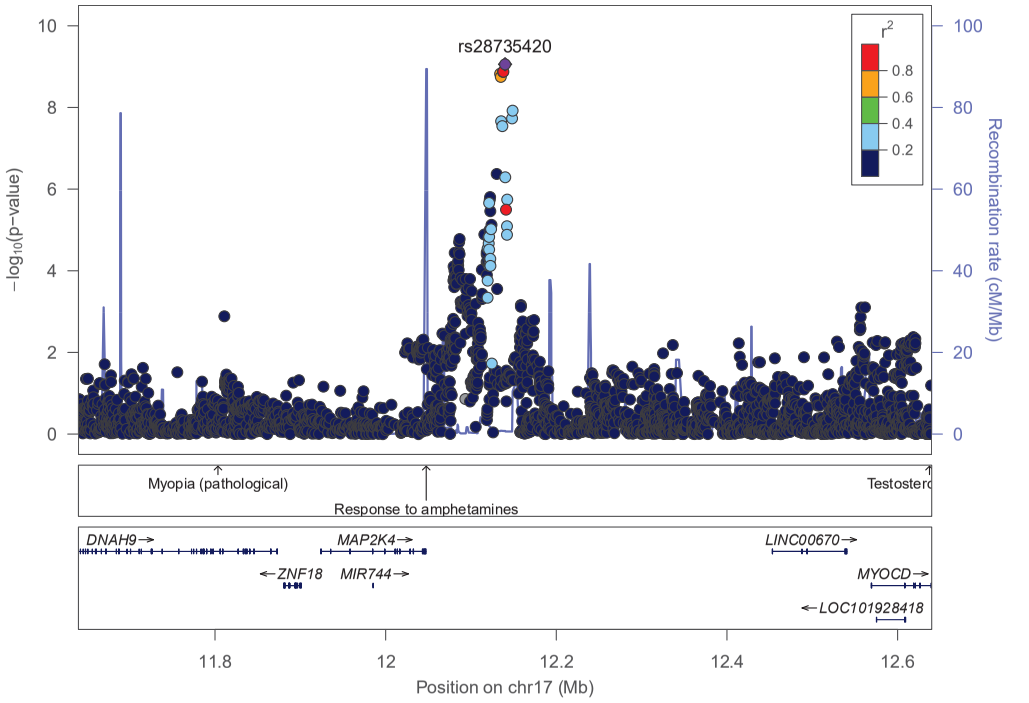

rs1858800
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Metabolite levels
Coronary heart disease
Stroke (ischemic)
Atrial fibrillation
Breast cancer (survival
Major depressiv
2 GWAS hits omitted
LINC01572
ZFHX3
C16orf47
LINC01568
HCCAT5
Position on chr16 (Mb)

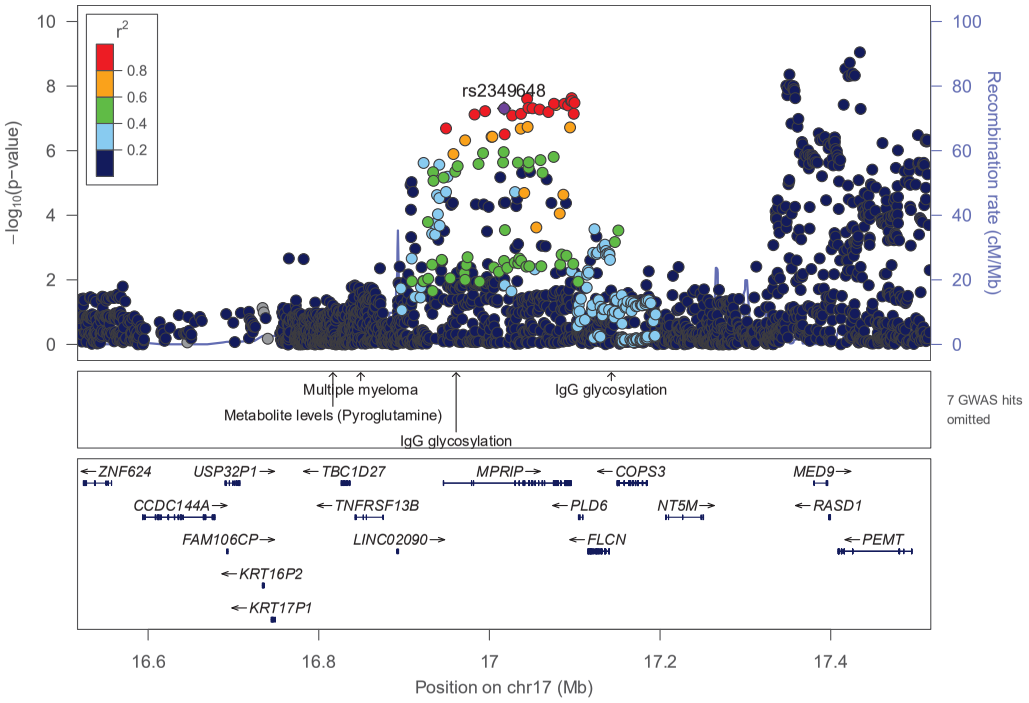

rs28581385
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Thyroid hormone levels
Presence of antiphospholipid antibodies
Corneal astigmatism
8 GWAS hits omitted
MAF
MAFTRR
LOC102724084
LINC01229
Position on chr16 (Mb)

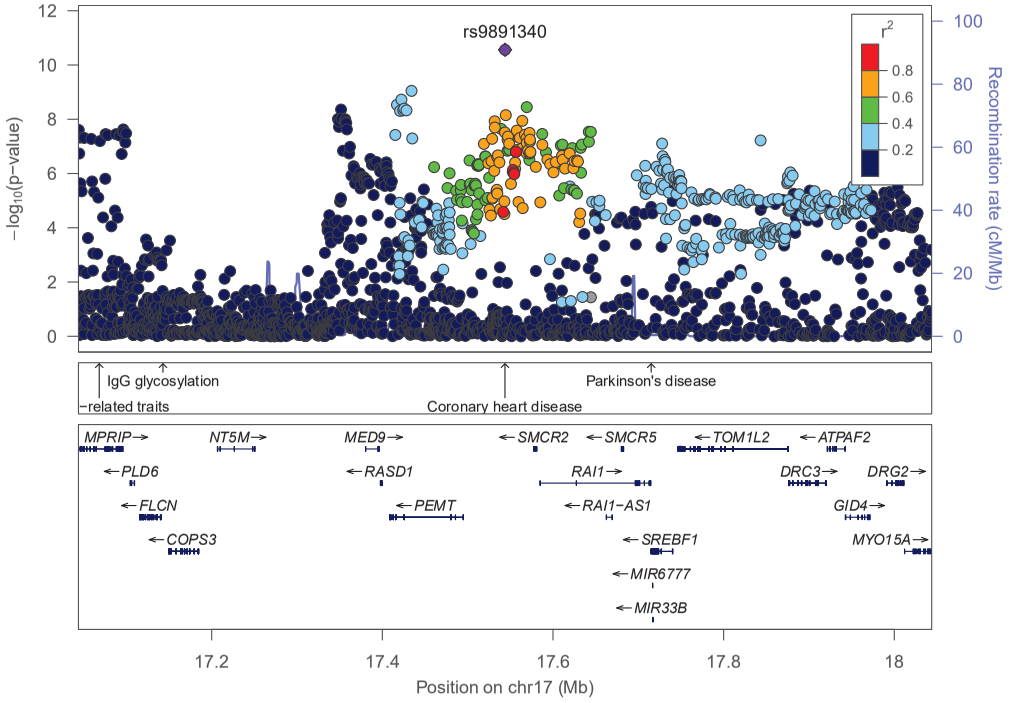

rs72817412
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Red blood cell traits
Social autistic−like traits
Multiple myeloma (IgH translocation)
Multiple myeloma (IgH translocation)
2 GWAS hits omitted
ZC3H18
PIEZO1
PABPN1L
ACSF3
ZNF778
LOC101927817
IL17C
CDT1
CBFA2T3
LINC00304
ANKRD11
CYBA
APRT
LOC100129697
LINC02138
LOC100287036
SPG7
MVD
GALNS
CDH15
RPL13
SNAI3−AS1
TRAPPC2L
SLC22A31
SNORD68
SNAI3
LOC101927793
LOC105371414
RNF166
CTU2
MIR4722
LOC100289580
1 gene omitted
Position on chr16 (Mb)

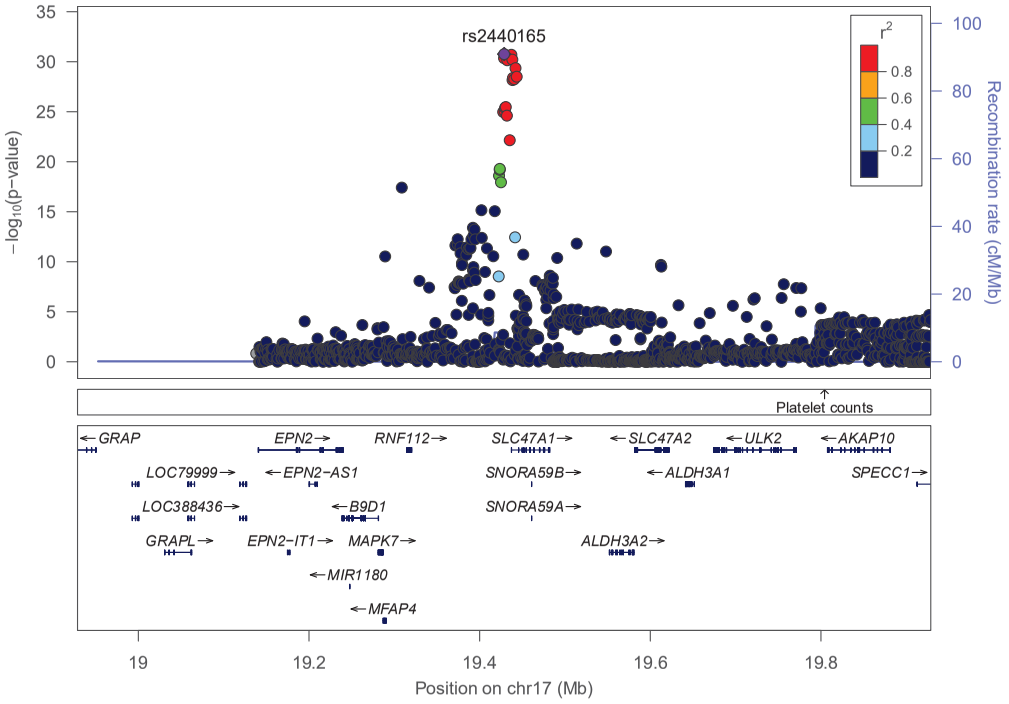

rs154656
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Homocysteine levels
Homocysteine levels
Hair color
Tanning
Melanoma
Non−melanoma skin cancer
18 GWAS hits omitted
ACSF3
ANKRD11
RPL13
SPATA33
FANCA
TCF25
DBNDD1
LINC00304
LOC101927817
CPNE7
CDK10
SPIRE2
DEF8
PRDM7
LINC02138
SPG7
DPEP1
ZNF276
MC1R
GAS8
CDH15
LOC100287036
SNORD68
SPATA2L
TUBB3
URAHP
SLC22A31
CHMP1A
SNORA119
FAM157B
ZNF778
VPS9D1
CENPBD1
LOC105371414
VPS9D1−AS1
AFG3L1P
GAS8−AS1
FAM157C
Position on chr16 (Mb)

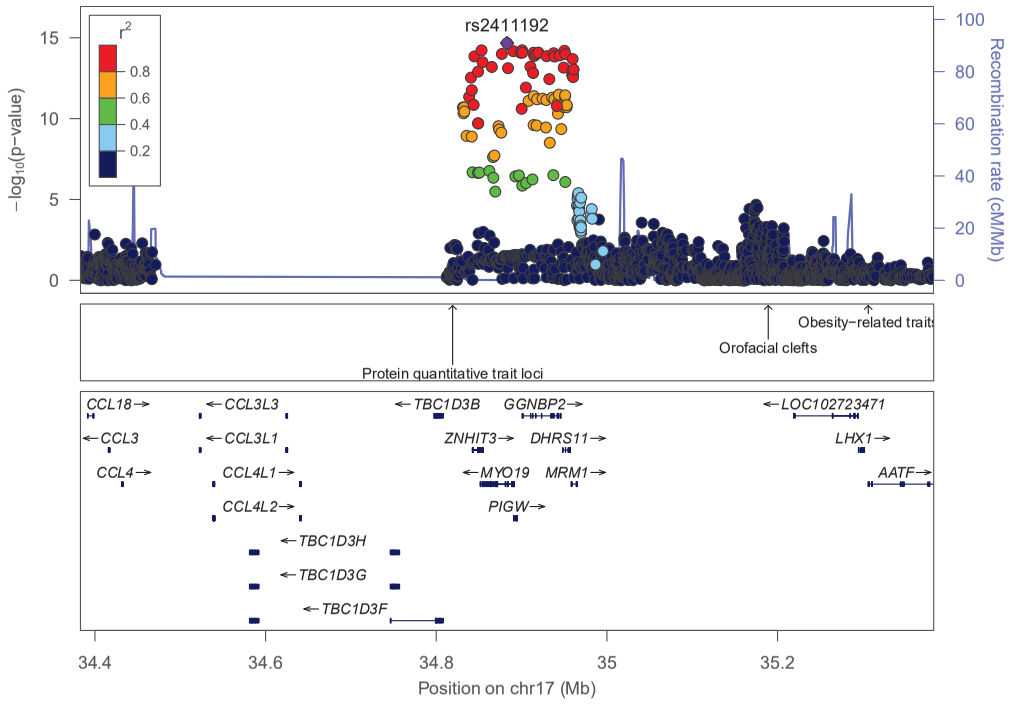

rs9900967
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Calcium levels
Serum albumin level
Schizophrenia
Metabolite levels (5−HIAA)
Esophageal cancer (squamous cell)
HDL cholesterol
6 GWAS hits omitted
SLC43A2
SMYD4
RTN4RL1
SMG6
SGSM2
PAFAH1B1
SCARF1
SERPINF1
LOC105371485
LOC101927839
MNT
RILP
SERPINF2
RPA1
DPH1
SRR
METTL16
PRPF8
OVCA2
TSR1
TLCD2
MIR132
SNORD91B
MIR22HG
MIR212
SNORD91A
MIR22
HIC1
LOC284009
WDR81
Position on chr17 (Mb)

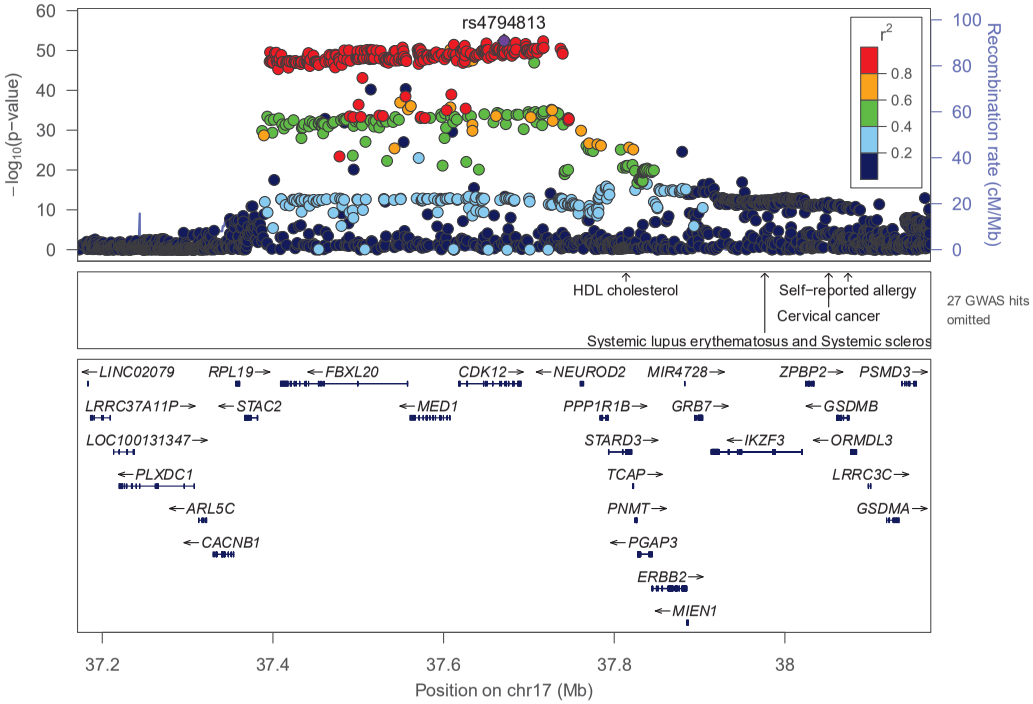

rs28735420
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Myopia (pathological)
Response to amphetamines
Testosterc
DNAH9
MAP2K4
LINC00670
ZNF18
MIR744
MYOCD
LOC101928418
Position on chr17 (Mb)

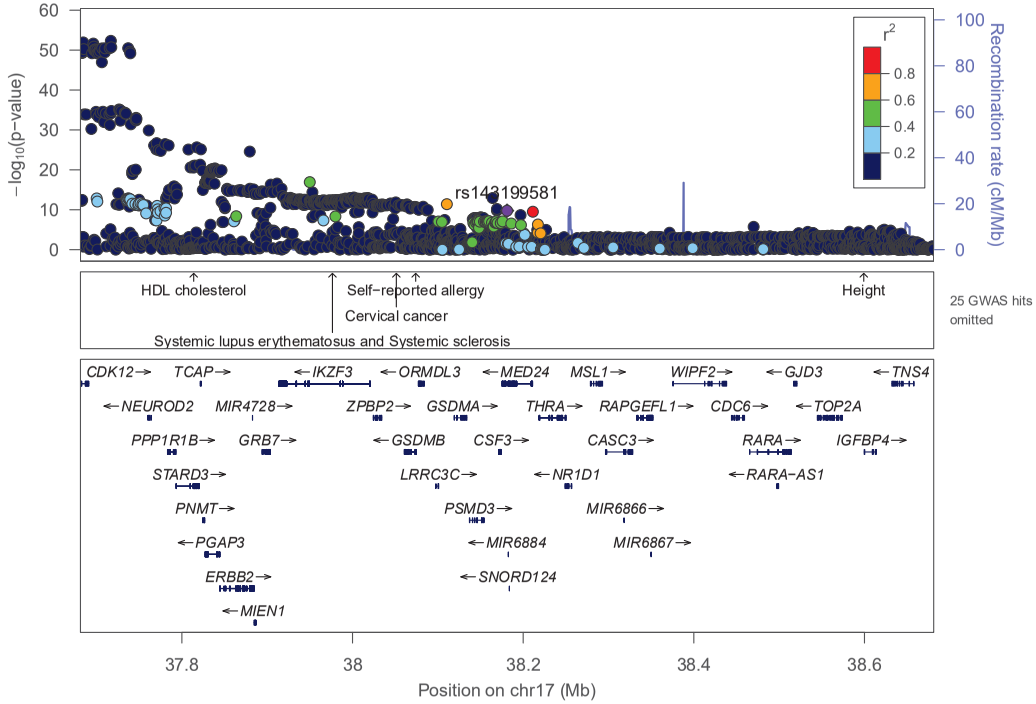

rs2349648
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Multiple myeloma
Metabolite levels (Pyroglutamine)
IgG glycosylation
IgG glycosylation
7 GWAS hits omitted
ZNF624
USP32P1
TBC1D27
MPRIP
COPS3
MED9
CCDC144A
TNFRSF13B
PLD6
NT5M
RASD1
FAM106CP
LINC02090
FLCN
PEMT
KRT16P2
KRT17P1
Position on chr17 (Mb)

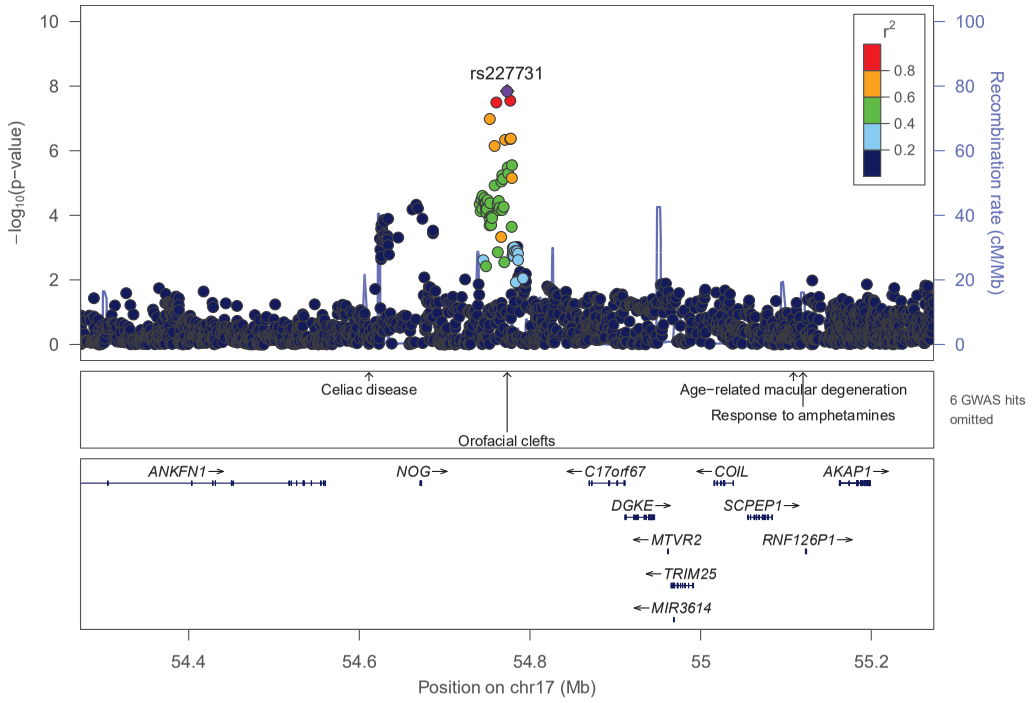

rs9891340
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
IgG glycosylation
−related traits
Coronary heart disease
Parkinson's disease
MPRIP
NT5M
MED9
SMCR2
SMCR5
TOM1L2
ATPAF2
PLD6
RASD1
RAI1
DRC3
DRG2
FLCN
PEMT
RAI1−AS1
GID4
COPS3
SREBF1
MYO15A
MIR6777
MIR33B
Position on chr17 (Mb)

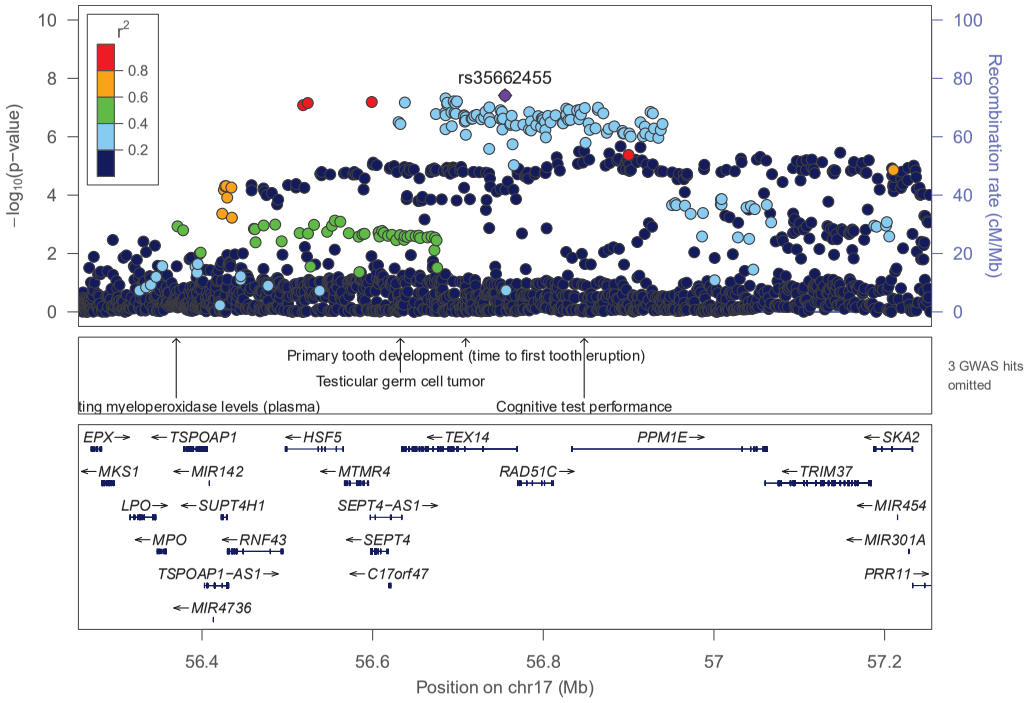

rs2440165
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Platelet counts
GRAP
EPN2
RNF112
SLC47A1
SLC47A2
ULK2
AKAP10
LOC79999
EPN2−AS1
SNORA59B
ALDH3A1
SPECC1
LOC388436
B9D1
SNORA59A
GRAPL
EPN2−IT1
MAPK7
ALDH3A2
MIR1180
MFAP4
Position on chr17 (Mb)

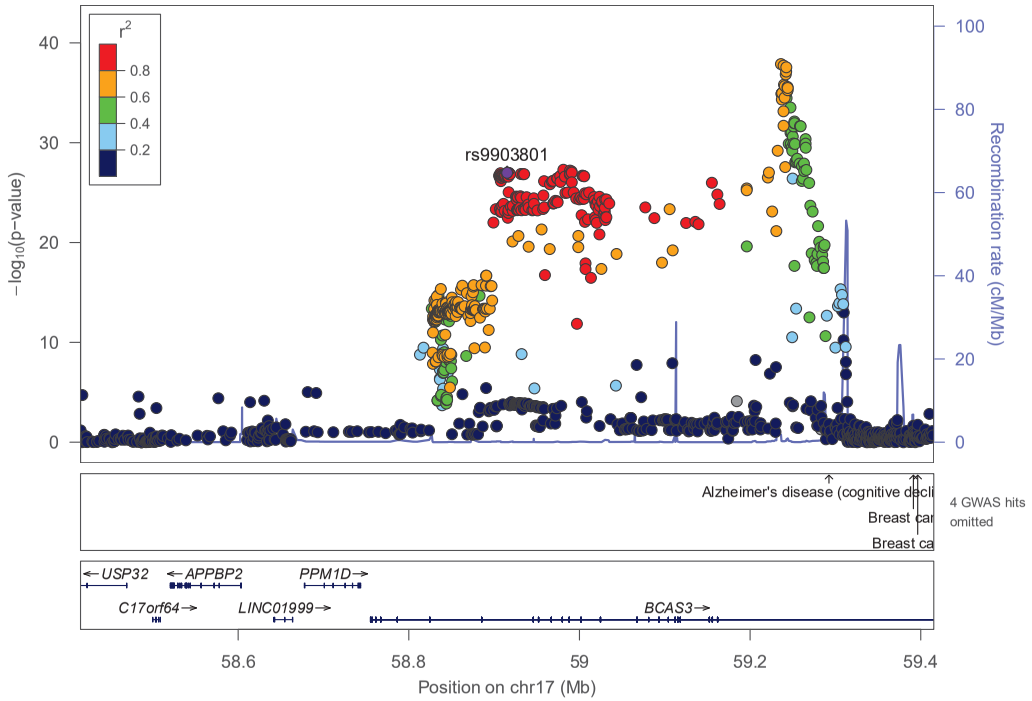

rs2411192
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Protein quantitative trait loci
Orofacial clefts
Obesity−related traits
CCL18
CCL3L3
TBC1D3B
GGNBP2
LOC102723471
CCL3
CCL3L1
ZNHIT3
DHRS11
LHX1
CCL4
CCL4L1
MYO19
MRM1
AATF
CCL4L2
PIGW
TBC1D3H
TBC1D3G
TBC1D3F
Position on chr17 (Mb)

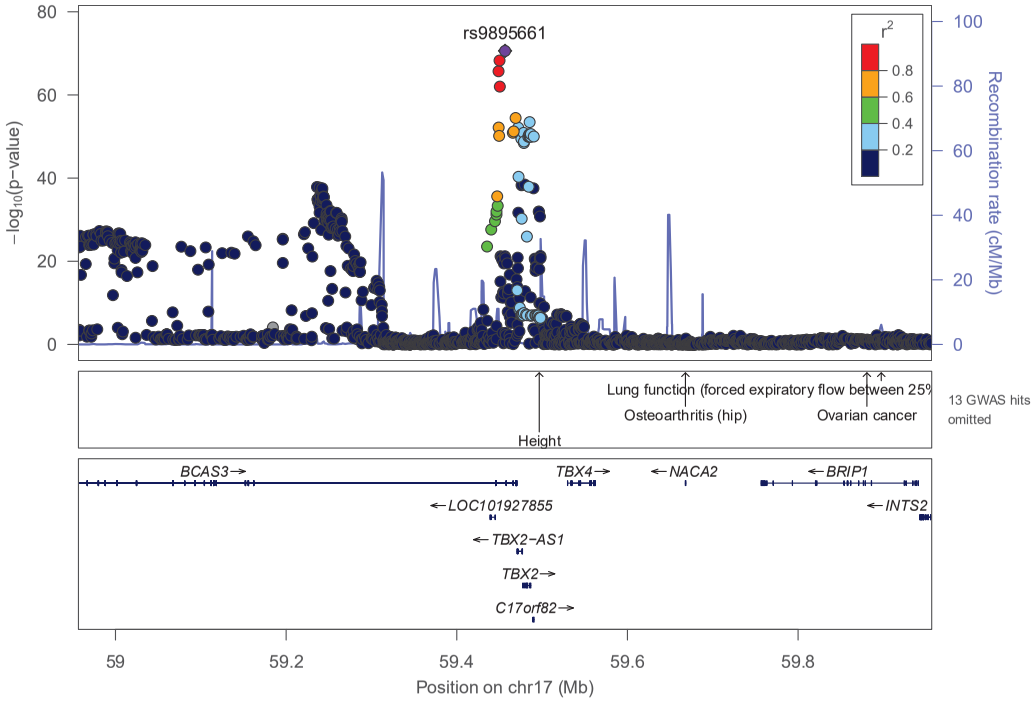

rs4794813
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
HDL cholesterol
Self−reported allergy
Cervical cancer
Systemic lupus erythematosus and Systemic sclerosis
27 GWAS hits omitted
LINC02079
RPL19
FBXL20
CDK12
NEUROD2
MIR4728
ZPBP2
PSMD3
LRRC37A11P
STAC2
MED1
PPP1R1B
GRB7
GSDMB
LOC100131347
STARD3
IKZF3
ORMDL3
PLXDC1
TCAP
LRRC3C
ARL5C
PNMT
GSDMA
CACNB1
PGAP3
ERBB2
MIEN1
Position on chr17 (Mb)

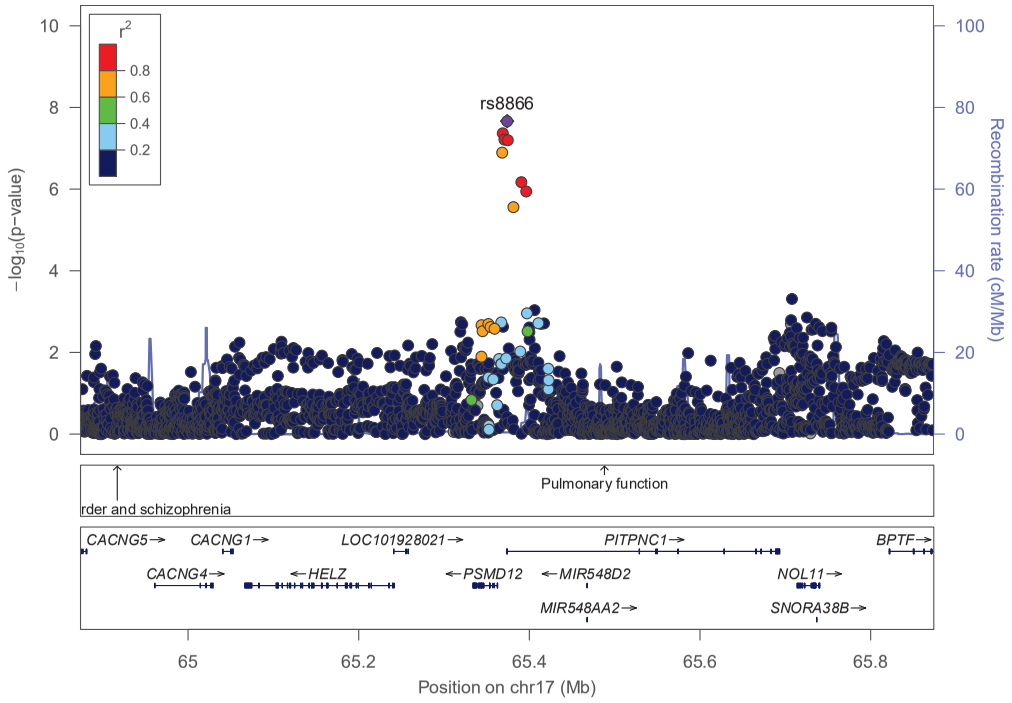

rs143199581
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
HDL cholesterol
Self−reported allergy
Cervical cancer
Systemic lupus erythematosus and Systemic sclerosis
Height
25 GWAS hits omitted
CDK12
TCAP
IKZF3
ORMDL3
MED24
MSL1
WIPF2
GJD3
TNS4
NEUROD2
MIR4728
ZPBP2
GSDMA
THRA
RAPGEFL1
CDC6
TOP2A
PPP1R1B
GRB7
GSDMB
CSF3
CASC3
RARA
IGFBP4
STARD3
LRRC3C
NR1D1
RARA−AS1
PNMT
PSMD3
MIR6866
PGAP3
MIR6884
MIR6867
ERBB2
SNORD124
MIEN1
Position on chr17 (Mb)

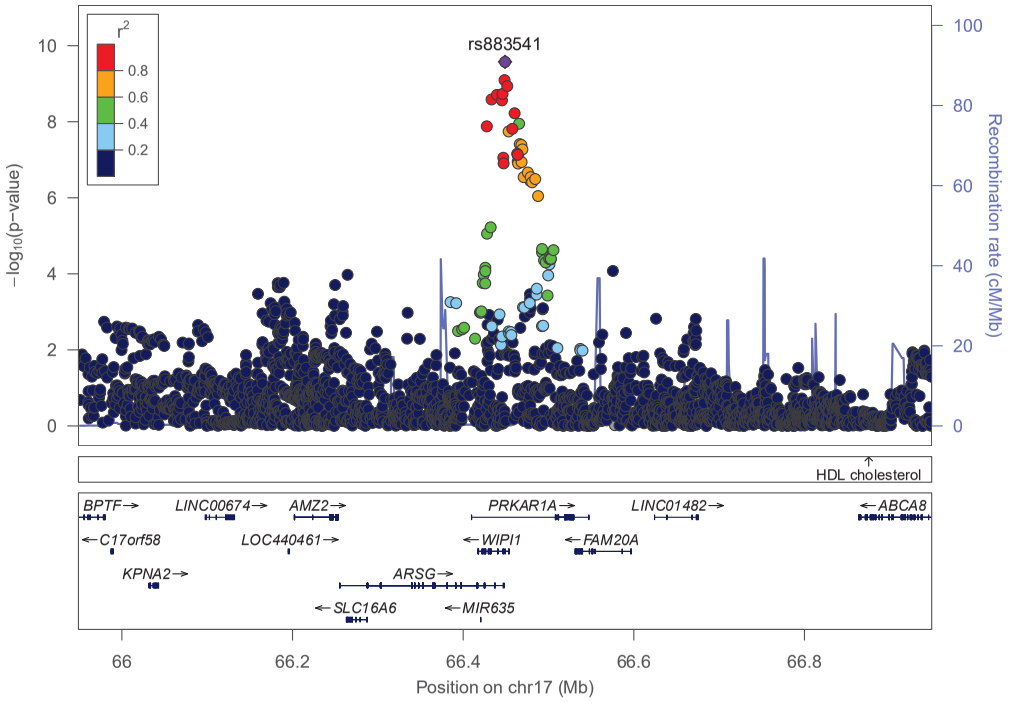

rs227731
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Celiac disease
Orofacial clefts
Age−related macular degeneration
Response to amphetamines
6 GWAS hits omitted
ANKFN1→
NOG→
←C17orf67
←COIL
AKAP1→
DGKE→
SCPEP1→
←MTVR2
RNF126P1→
←TRIM25
←MIR3614
Position on chr17 (Mb)

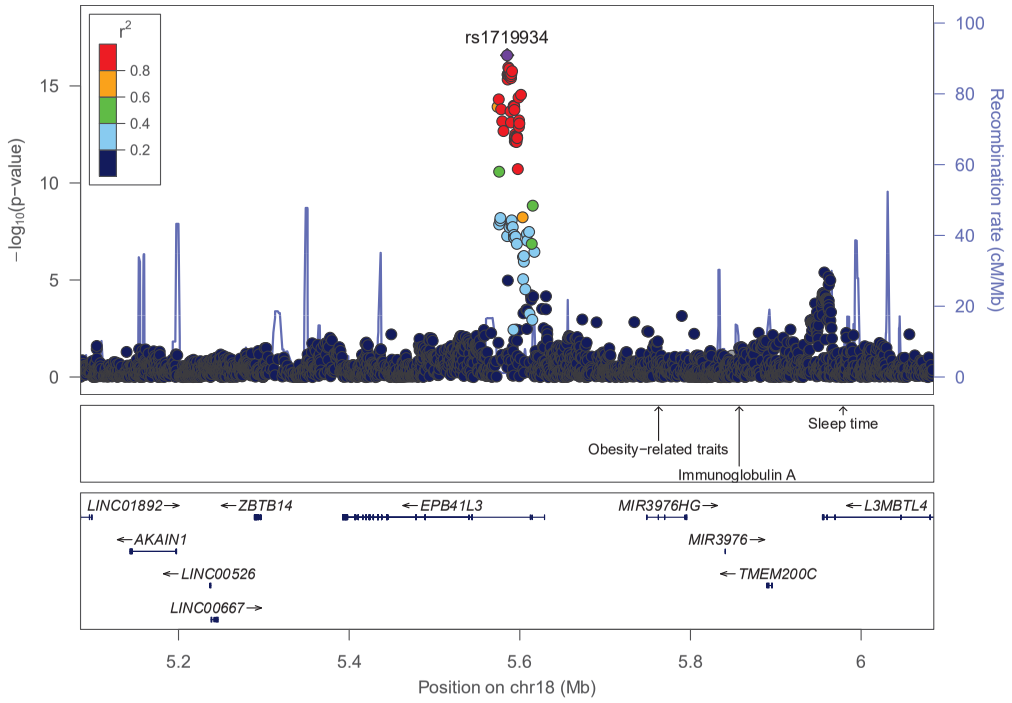

rs35662455
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Primary tooth development (time to first tooth eruption)
Testicular germ cell tumor
ting myeloperoxidase levels (plasma)
Cognitive test performance
3 GWAS hits omitted
EPX→
←TSPOAP1
←HSF5
←TEX14
PPM1E→
←SKA2
←MKS1
←MIR142
←MTMR4
RAD51C→
←TRIM37
LPO→
←SUPT4H1
SEPT4−AS1→
←MIR454
←MPO
←RNF43
←SEPT4
←MIR301A
TSPOAP1−AS1→
←C17orf47
PRR11→
←MIR4736
Position on chr17 (Mb)

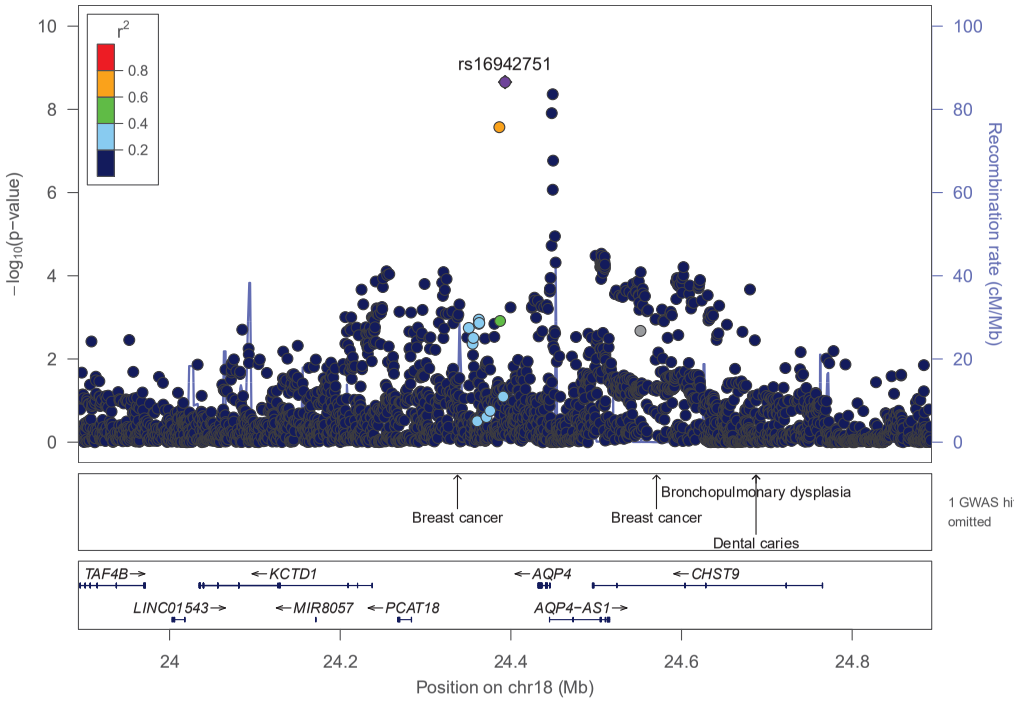

rs9903801
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Alzheimer's disease (cognitive decli
Breast can
Breast ca
4 GWAS hits omitted
←USP32
←APPBP2
PPM1D→
C17orf64→
LINC01999→
BCAS3→
Position on chr17 (Mb)

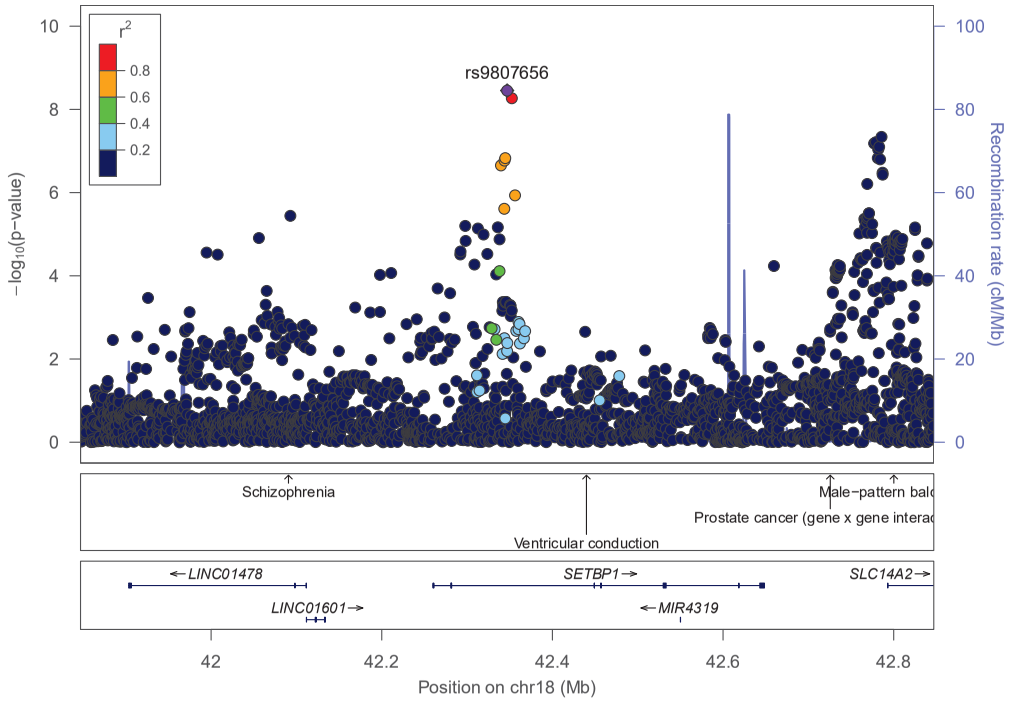

rs9895661
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Lung function (forced expiratory flow between 25%
Osteoarthritis (hip)
Ovarian cancer
Height
13 GWAS hits omitted
BCAS3→
TBX4→
←NACA2
←BRIP1
←LOC101927855
←INTS2
←TBX2−AS1
TBX2→
C17orf82→
Position on chr17 (Mb)

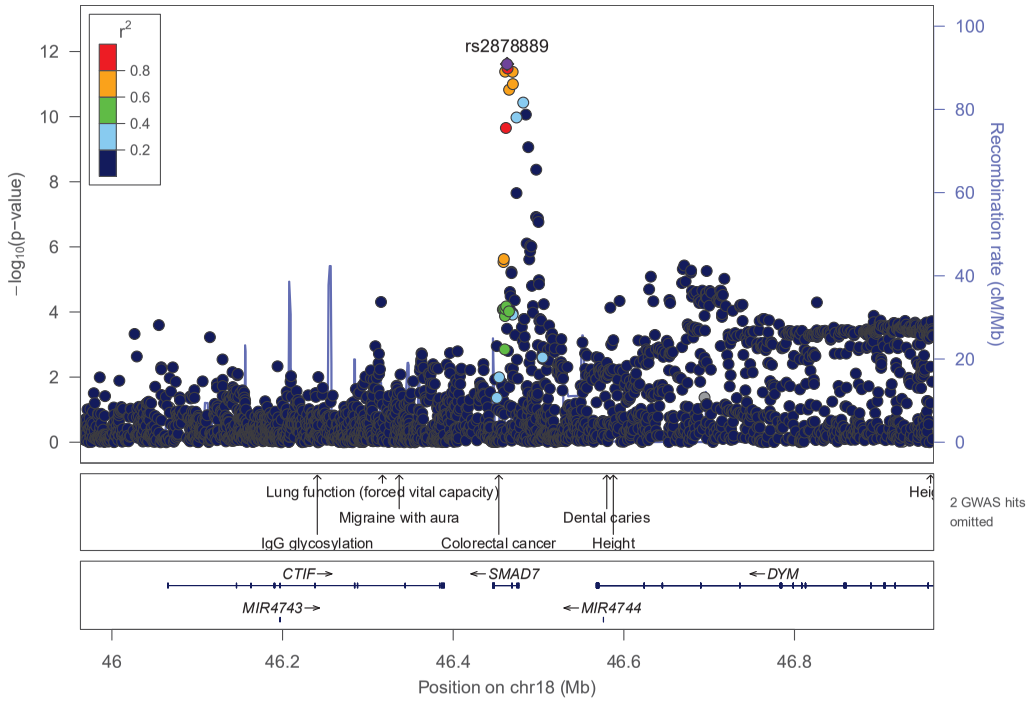

rs8866
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
rder and schizophrenia
Pulmonary function
CACNG5→
CACNG1→
LOC101928021→
PITPNC1→
BPTF→
CACNG4→
←HELZ
←PSMD12
←MIR548D2
NOL11→
MIR548AA2→
SNORA38B→
Position on chr17 (Mb)

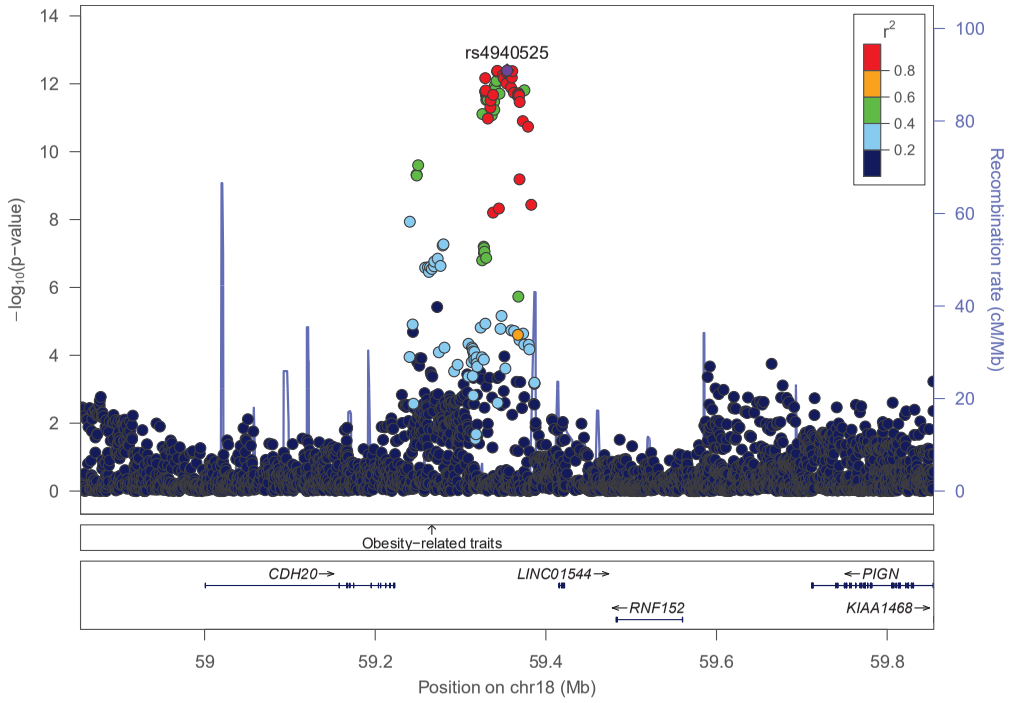

rs883541
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
HDL cholesterol
BPTF→
LINC00674→
AMZ2→
PRKAR1A→
LINC01482→
←ABCA8
←C17orf58
LOC440461→
←WIPI1
←FAM20A
KPNA2→
ARSG→
←SLC16A6
←MIR635
Position on chr17 (Mb)

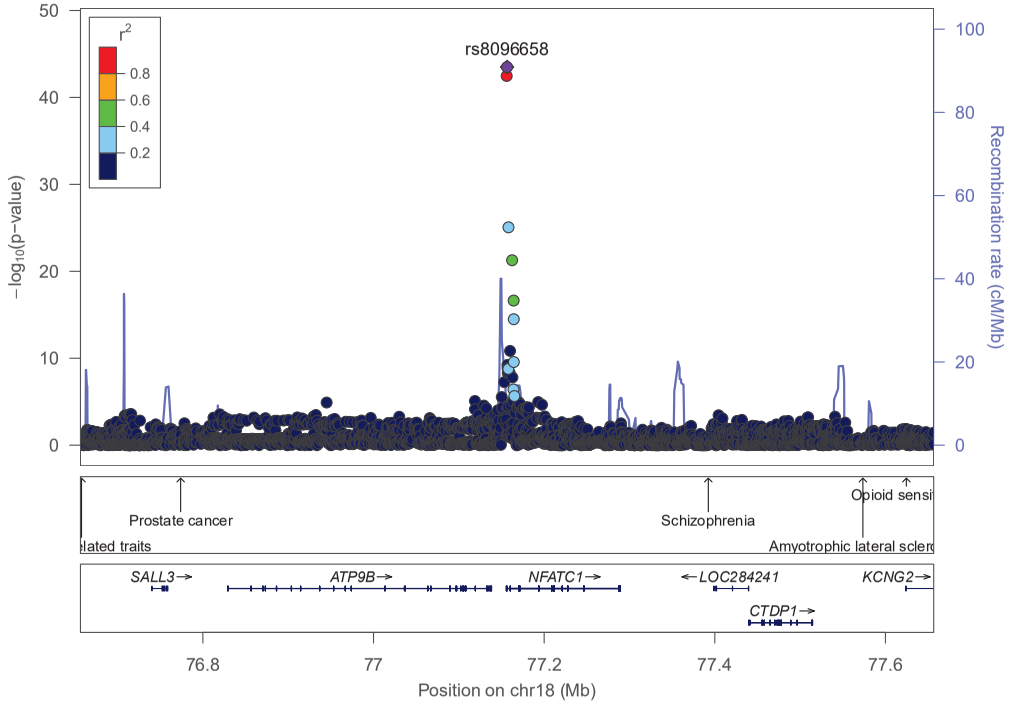

rs1719934
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
Immunoglobulin A
Sleep time
LINC01892→
←ZBTB14
←EPB41L3
MIR3976HG→
←L3MBTL4
←AKAIN1
MIR3976→
←LINC00526
←TMEM200C
LINC00667→
Position on chr18 (Mb)

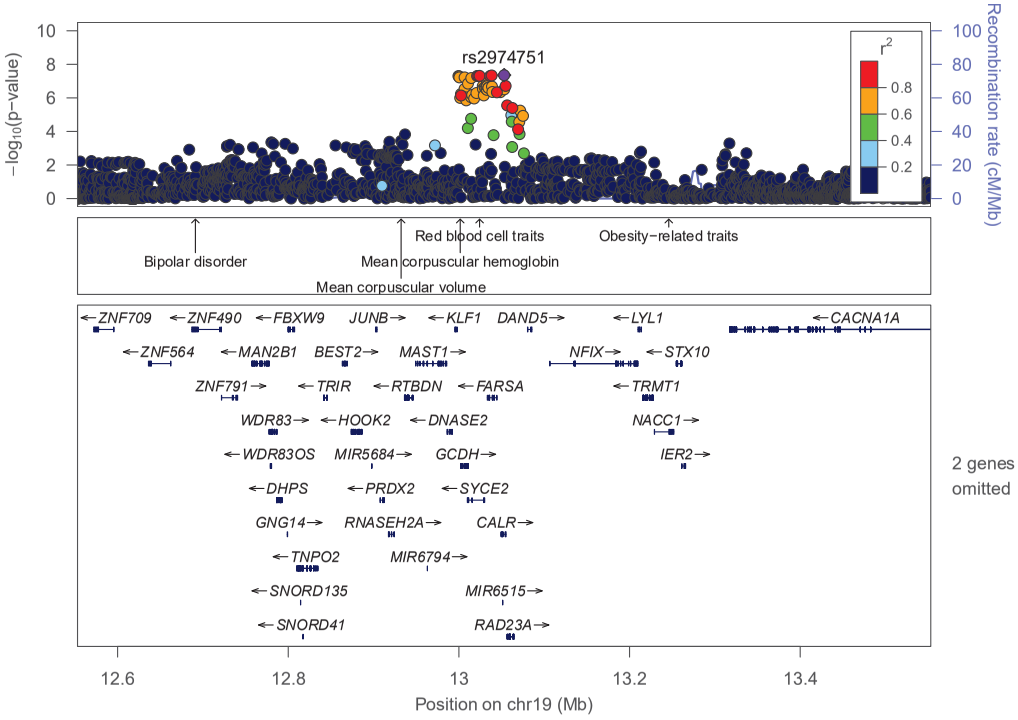

rs16942751
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Breast cancer
Breast cancer
Bronchopulmonary dysplasia
Dental caries
1 GWAS hit
omitted
TAF4B→
←KCTD1
←AQP4
←CHST9
LINC01543→
←MIR8057
←PCAT18
AQP4−AS1→
Position on chr18 (Mb)

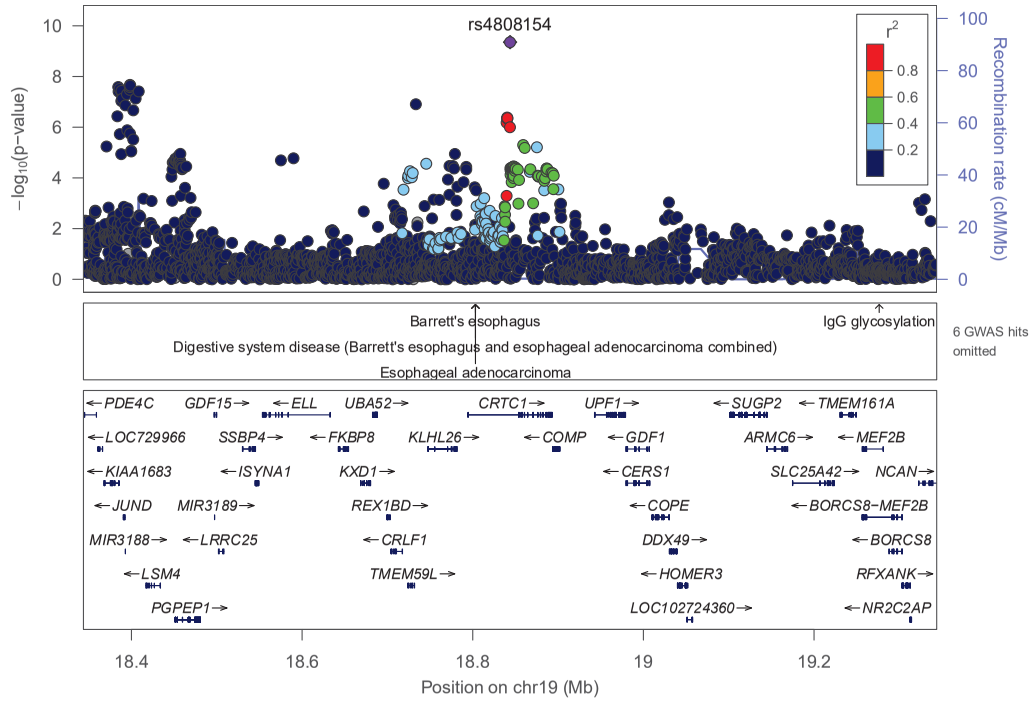

rs9807656
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Schizophrenia
Ventricular conduction
Male−pattern bald
Prostate cancer (gene x gene interac
LINC01478
SETBP1
SLC14A2
LINC01601
MIR4319
Position on chr18 (Mb)

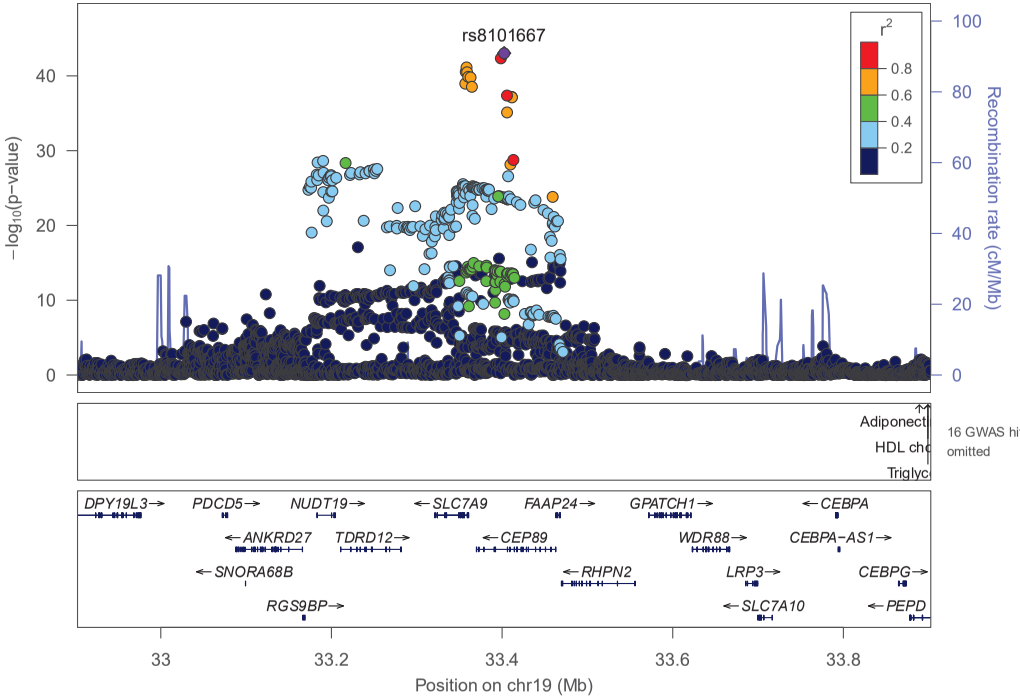

rs2878889
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Lung function (forced vital capacity)
Migraine with aura
IgG glycosylation
Colorectal cancer
Dental caries
Height
2 GWAS hits omitted
CTIF
SMAD7
DYM
MIR4743
MIR4744
Position on chr18 (Mb)

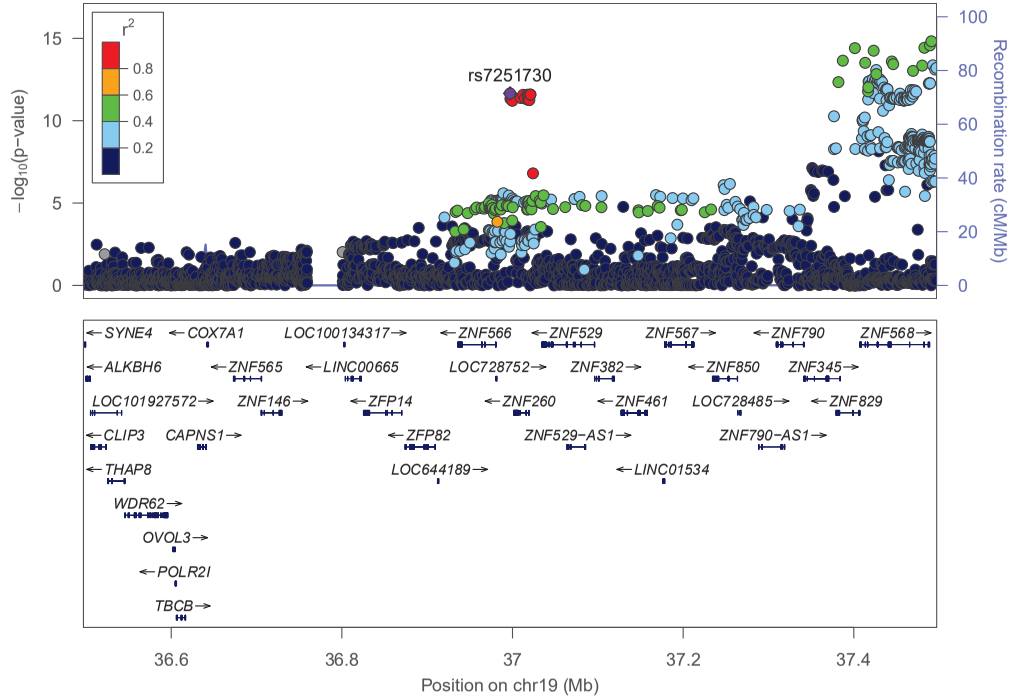

rs4940525
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Obesity−related traits
CDH20
LINC01544
PIGN
RNF152
KIAA1468
Position on chr18 (Mb)

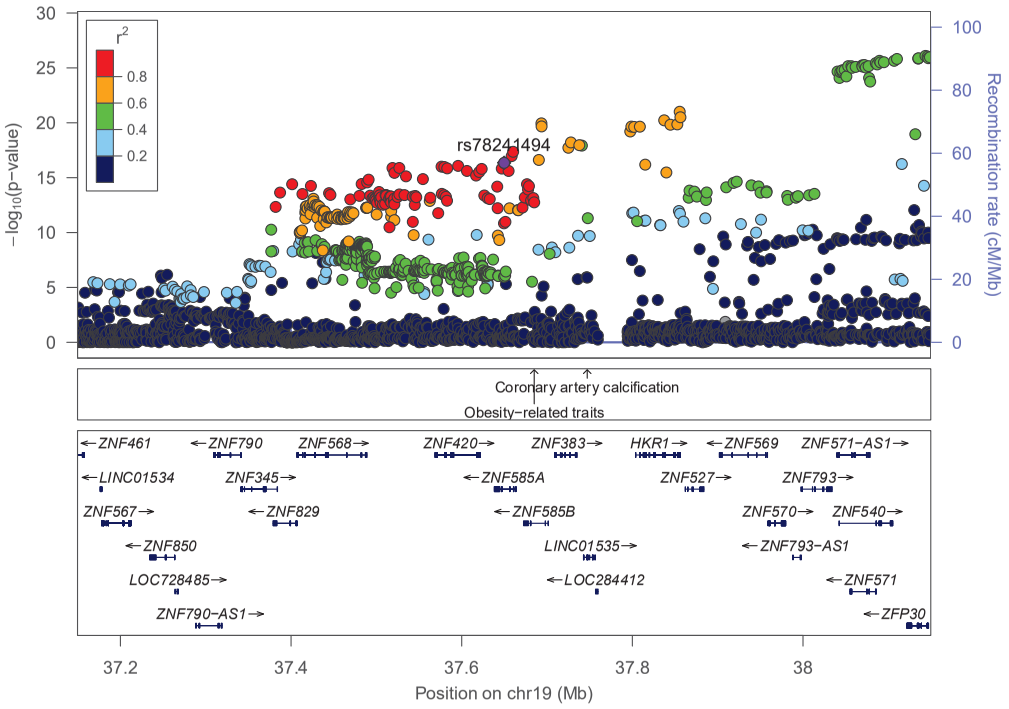

rs8096658
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Prostate cancer
Schizophrenia
Amyotrophic lateral sclero
SALL3
ATP9B
NFATC1
LOC284241
KCNG2
CTDP1
Position on chr18 (Mb)

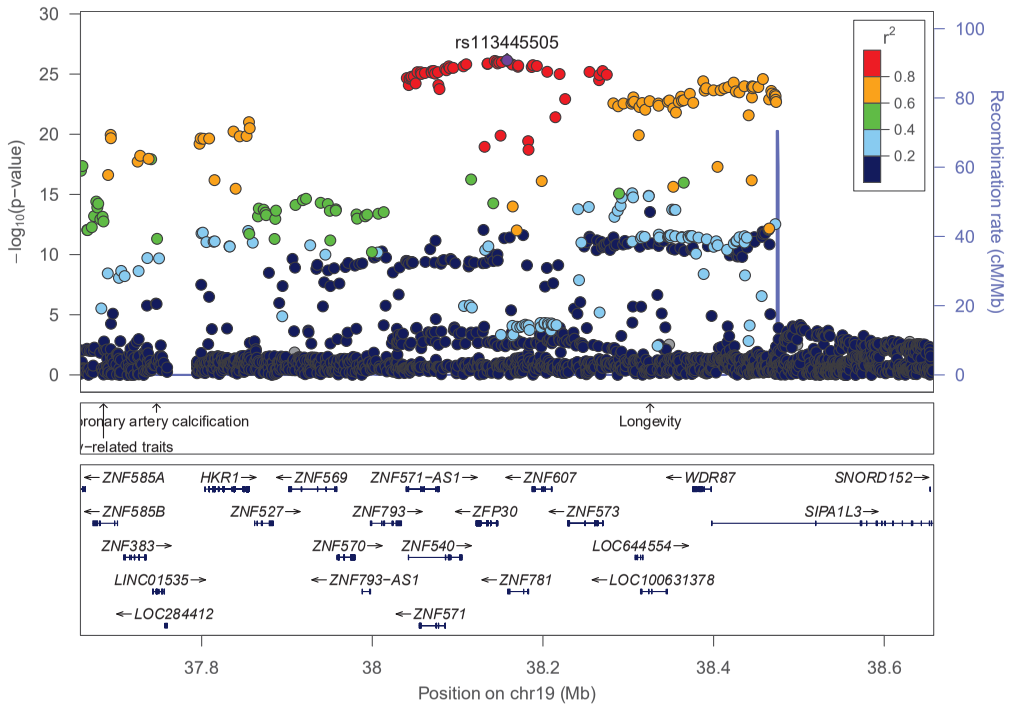

rs2974751
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Bipolar disorder
Mean corpuscular volume
Mean corpuscular hemoglobin
Red blood cell traits
Obesity−related traits
2 genes omitted
Position on chr19 (Mb)

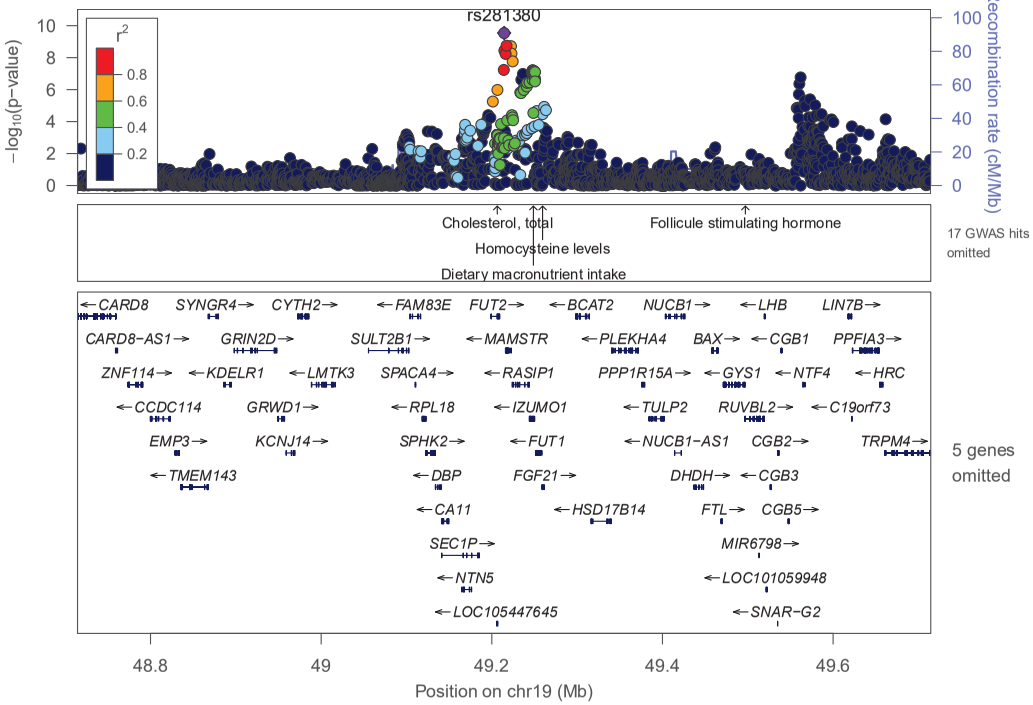

rs4808154
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Barrett's esophagus
Digestive system disease (Barrett's esophagus and esophageal adenocarcinoma combined)
Esophageal adenocarcinoma
IgG glycosylation
6 GWAS hits omitted
Position on chr19 (Mb)

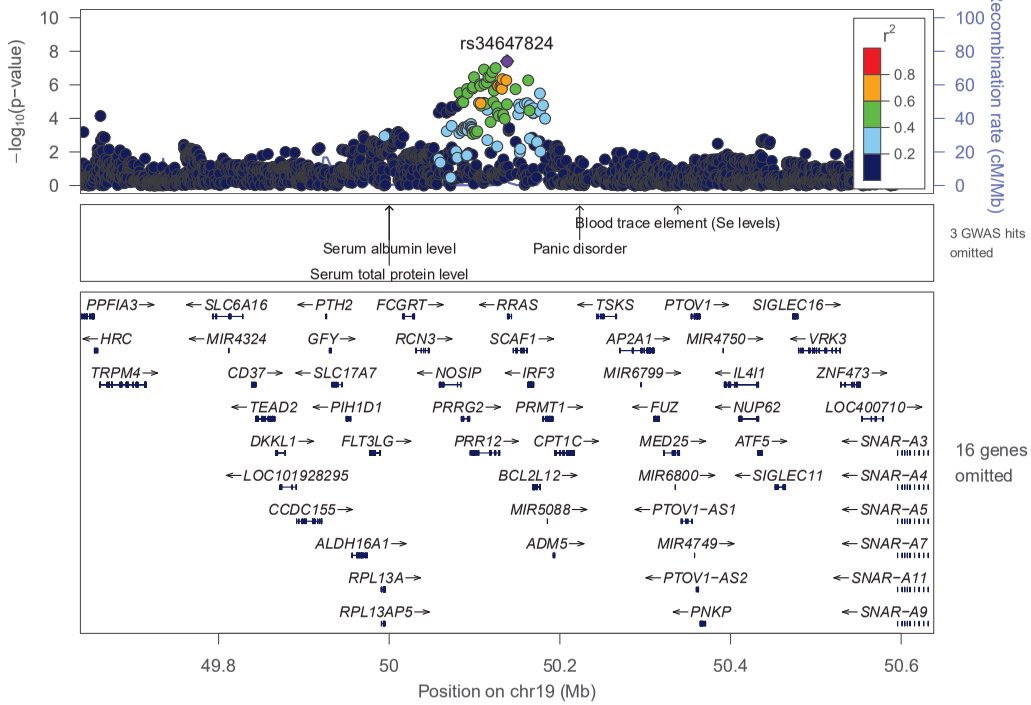

rs8101667
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
16 GWAS hits omitted
Position on chr19 (Mb)

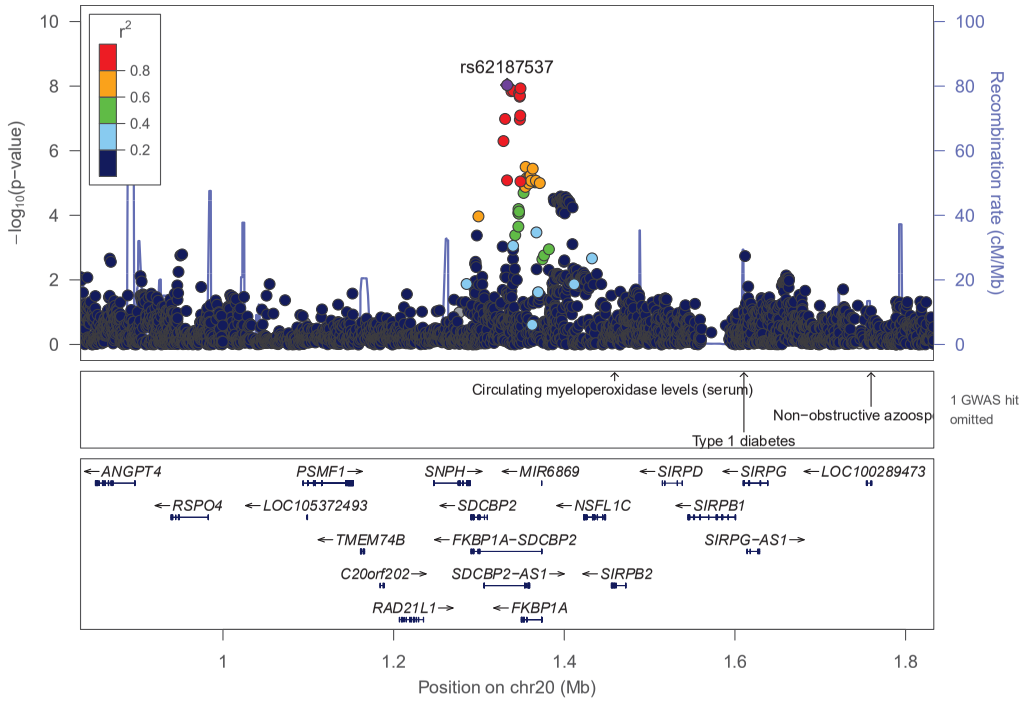

rs7251730
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Position on chr19 (Mb)

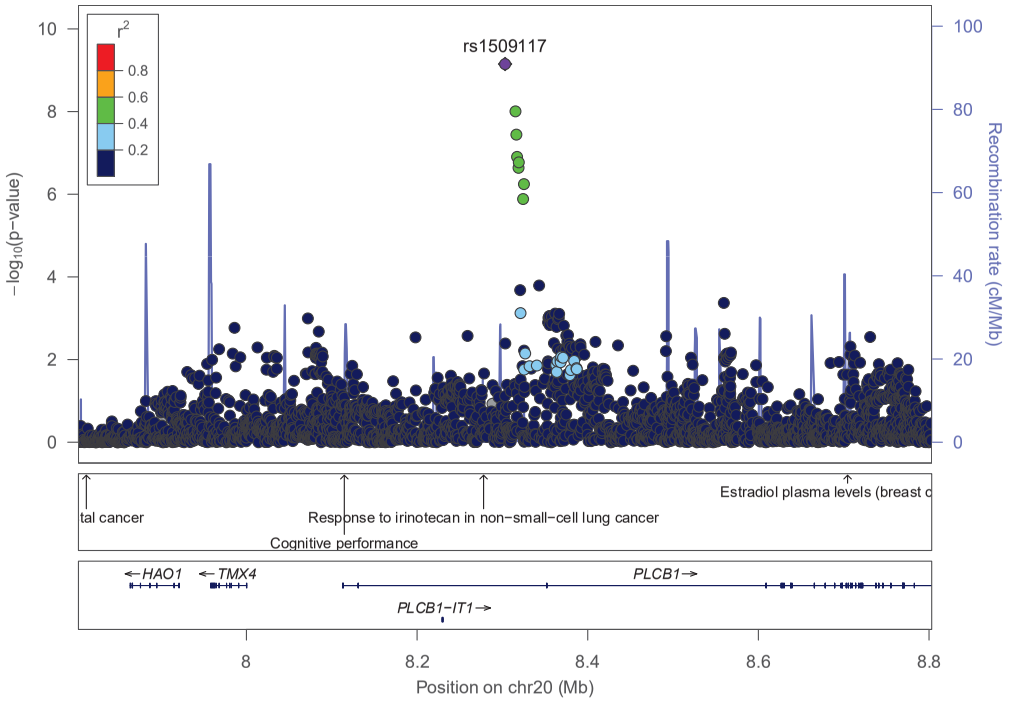

rs78241494
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Coronary artery calcification
Obesity−related traits
ZNF461 ZNF790 ZNF568 ZNF420 ZNF383 HKR1 ZNF569 ZNF571−AS1
LINC01534 ZNF345 ZNF585A ZNF527 ZNF793
ZNF567 ZNF829 ZNF585B ZNF570 ZNF540
ZNF850 LINC01535 ZNF793−AS1
LOC728485 LOC284412 ZNF571
ZNF790−AS1 ZFP30
37.2 37.4 37.6 37.8 38
Position on chr19 (Mb)

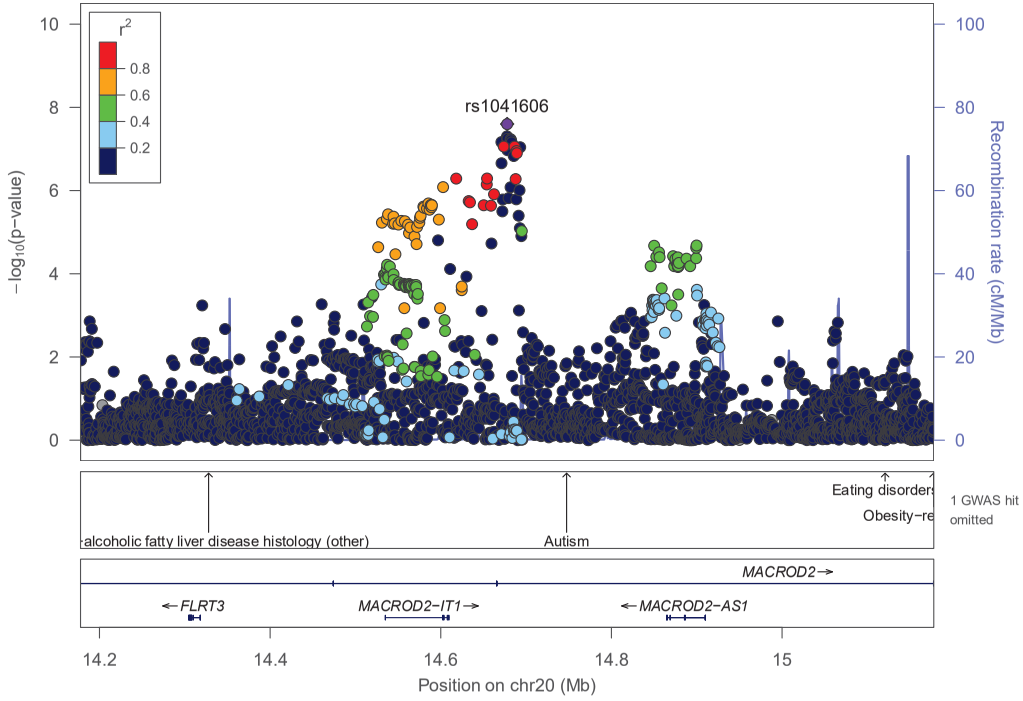

rs113445505
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ronary artery calcification
−related traits
Longevity
ZNF585A HKR1 ZNF569 ZNF571−AS1 ZNF607 WDR87 SNORD152
ZNF585B ZNF527 ZNF793 ZFP30 ZNF573 SIPA1L3
ZNF383 ZNF570 ZNF540 LOC644554
LINC01535 ZNF793−AS1 ZNF781 LOC100631378
LOC284412 ZNF571
37.8 38 38.2 38.4 38.6
Position on chr19 (Mb)

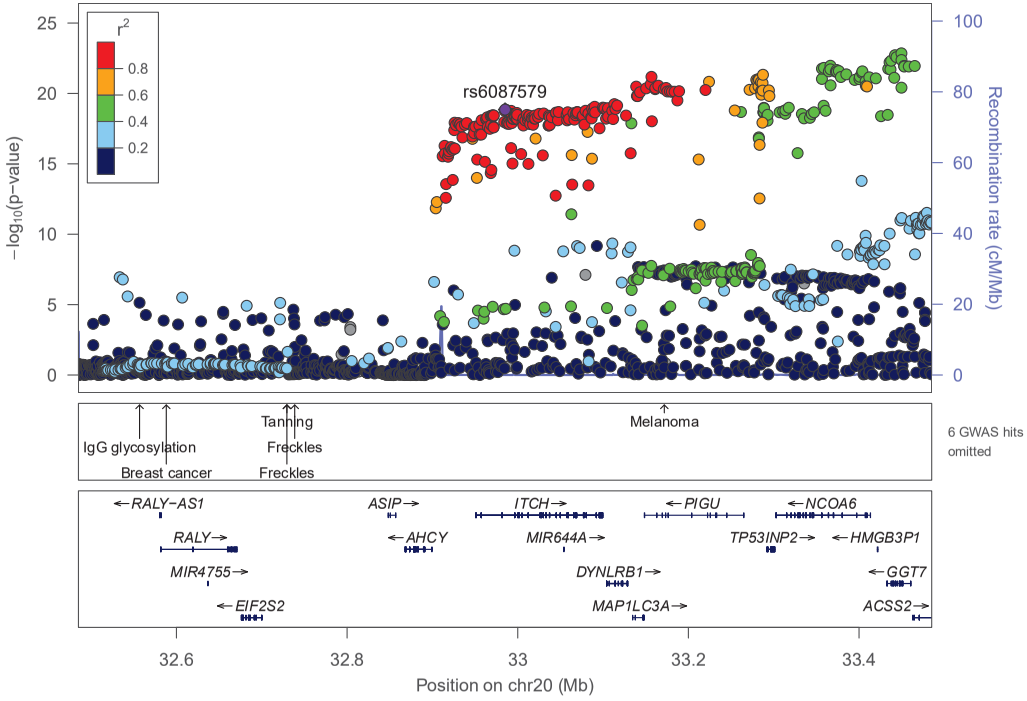

rs281380
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
Homocysteine levels
Dietary macronutrient intake
Follicule stimulating hormone
17 GWAS hits omitted
CARD8 SYNGR4 CYTH2 FAM83E FUT2 BCAT2 NUCB1 LHB LIN7B
CARD8−AS1 GRIN2D SULT2B1 MAMSTR PLEKHA4 BAX CGB1 PPFIA3
ZNF114 KDELR1 LMTK3 SPACA4 RASIP1 PPP1R15A GYS1 NTF4 HRC
CCDC114 GRWD1 RPL18 IZUMO1 TULP2 RUVBL2 C19orf73
EMP3 KCNJ14 SPHK2 FUT1 NUCB1−AS1 CGB2 TRPM4
TMEM143 DBP FGF21 DHDH CGB3
CA11 HSD17B14 FTL CGB5
SEC1P MIR6798
NTN5 LOC101059948
LOC105447645 SNAR−G2
5 genes omitted
48.8 49 49.2 49.4 49.6
Position on chr19 (Mb)

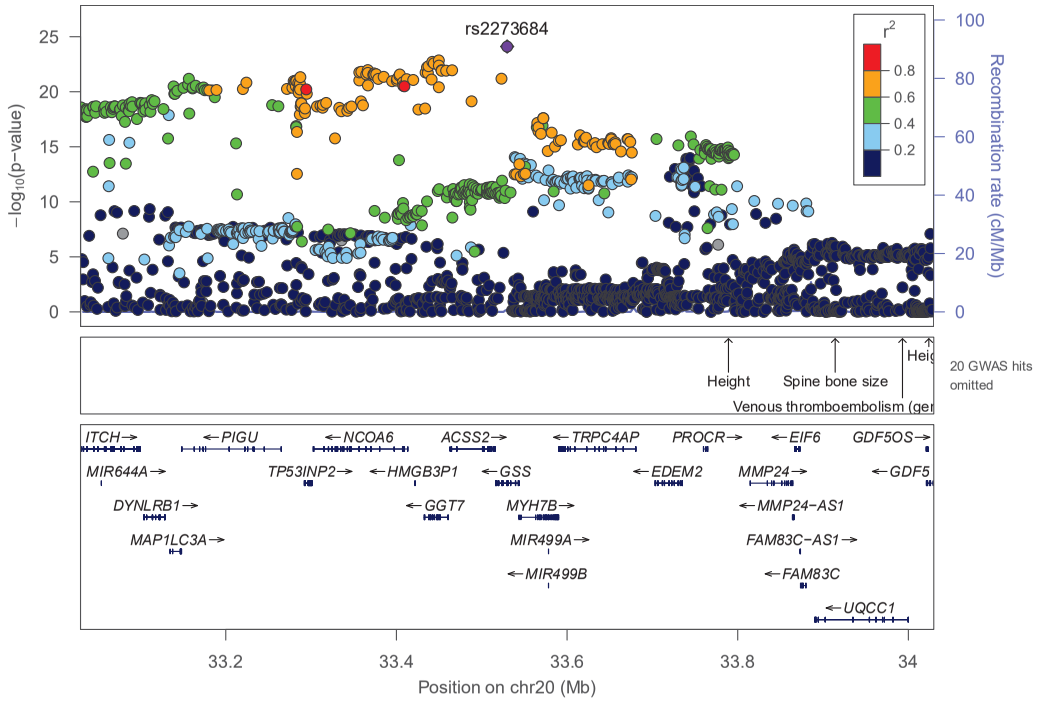

rs34647824
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Serum albumin level
Serum total protein level
Blood trace element (Se levels)
Panic disorder
3 GWAS hits omitted
PPFIA3 SLC6A16 PTH2 FCGRT RRAS TSKS PTOV1 SIGLEC16
HRC MIR4324 GFY RCN3 SCAF1 AP2A1 MIR4750 VRK3
TRPM4 CD37 SLC17A7 NOSIP IRF3 MIR6799 IL4I1 ZNF473
TEAD2 PIH1D1 PRRG2 PRMT1 FUZ NUP62 LOC400710
DKKL1 FLT3LG PRR12 CPT1C MED25 ATF5 SNAR−A3
LOC101928295 BCL2L12 MIR6800 SIGLEC11 SNAR−A4
CCDC155 MIR5088 PTOV1−AS1 SNAR−A5
ALDH16A1 ADM5 MIR4749 SNAR−A7
RPL13A PTOV1−AS2 SNAR−A11
RPL13AP5 PNKP SNAR−A9
16 genes omitted
49.8 50 50.2 50.4 50.6
Position on chr19 (Mb)

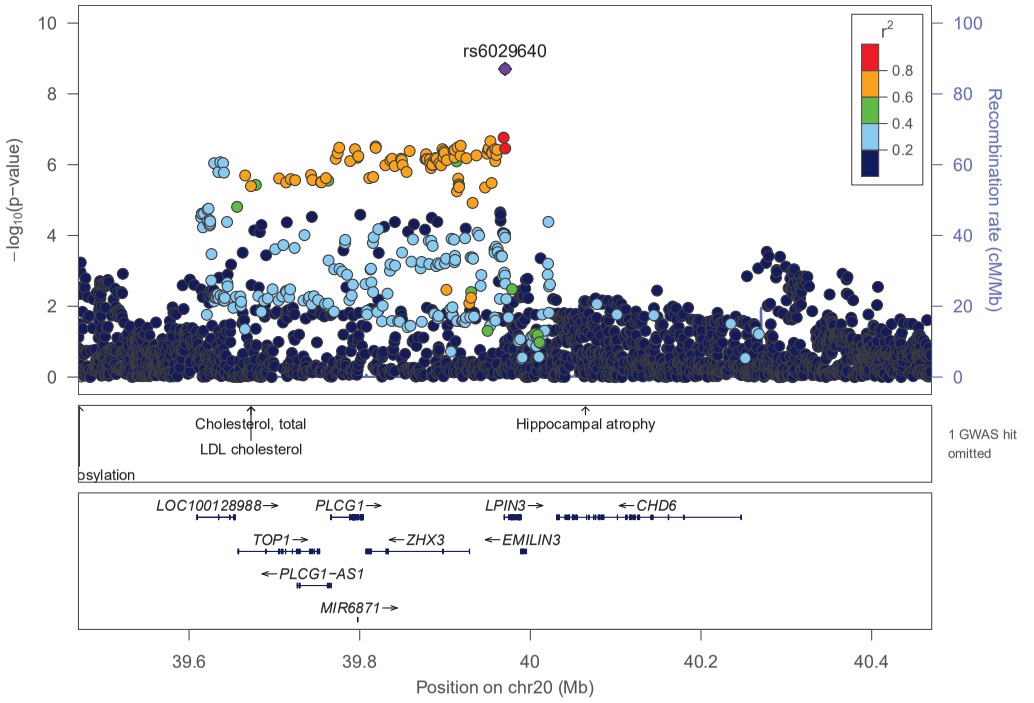

rs62187537
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Circulating myeloperoxidase levels (serum)
Type 1 diabetes
Non−obstructive azoosp
1 GWAS hit omitted
ANGPT4
PSMF1
SNPH
MIR6869
SIRPD
SIRPG
LOC100289473
RSPO4
LOC105372493
SDCBP2
NSFL1C
SIRPB1
TMEM74B
FKBP1A−SDCBP2
SIRPG−AS1
C20orf202
SDCBP2−AS1
SIRPB2
RAD21L1
FKBP1A
Position on chr20 (Mb)

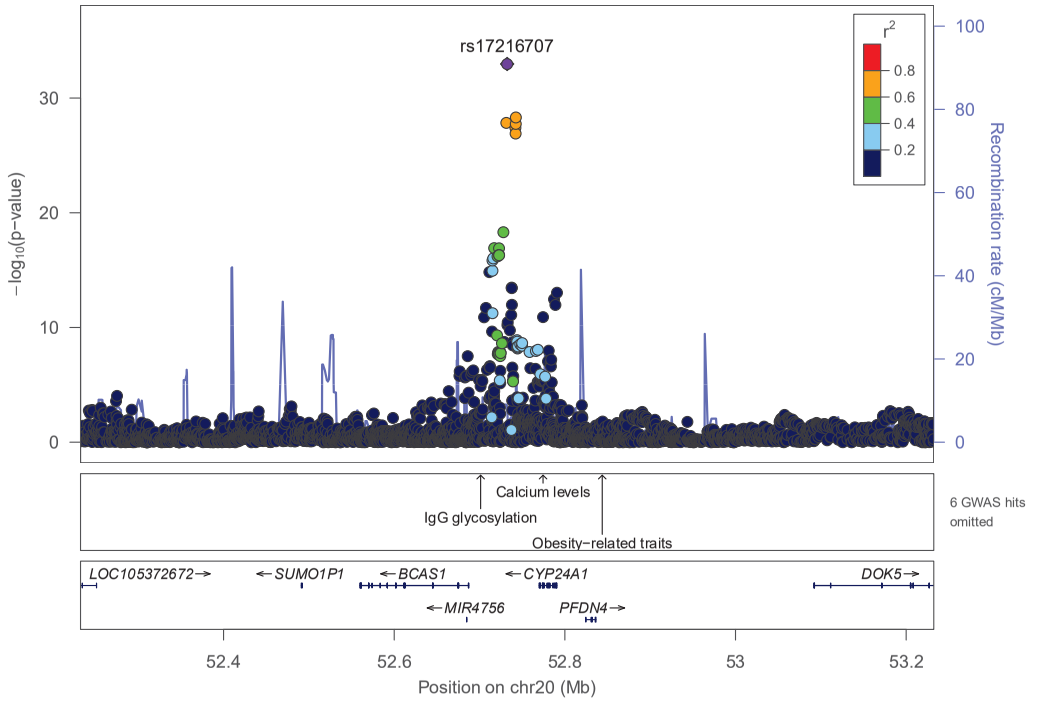

rs1509117
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
tal cancer
Response to irinotecan in non−small−cell lung cancer
Cognitive performance
Estradiol plasma levels (breast c
HAO1
TMX4
PLCB1
PLCB1−IT1
Position on chr20 (Mb)

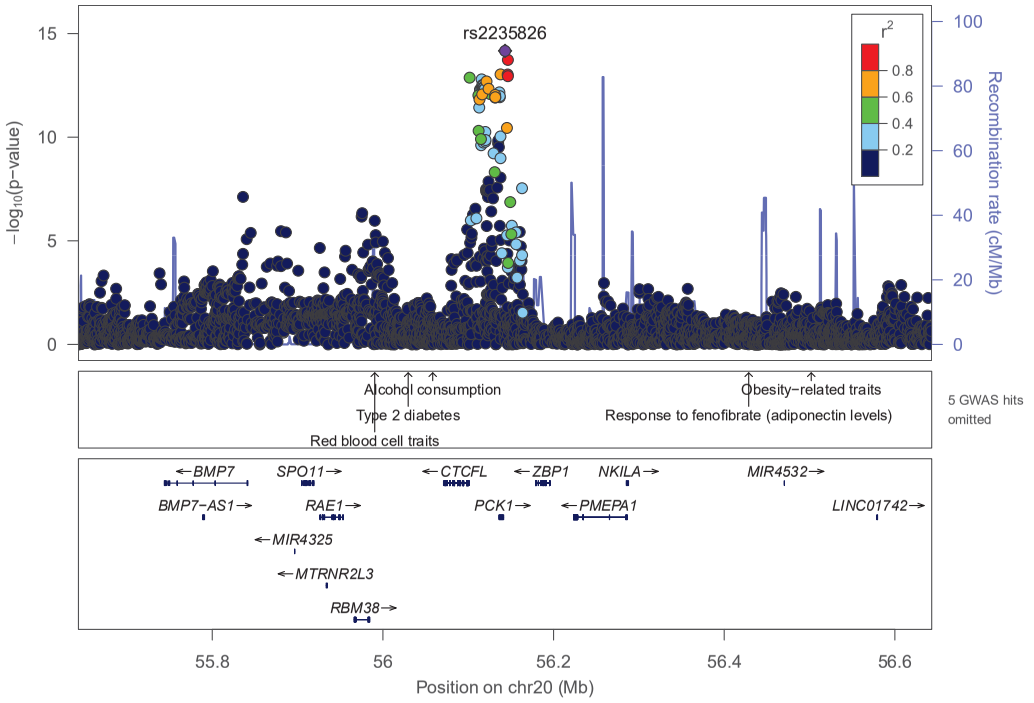

rs1041606
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
alcoholic fatty liver disease histology (other)
Autism
Eating disorders
Obesity−re
1 GWAS hit omitted
MACROD2
FLRT3
MACROD2−IT1
MACROD2−AS1
Position on chr20 (Mb)

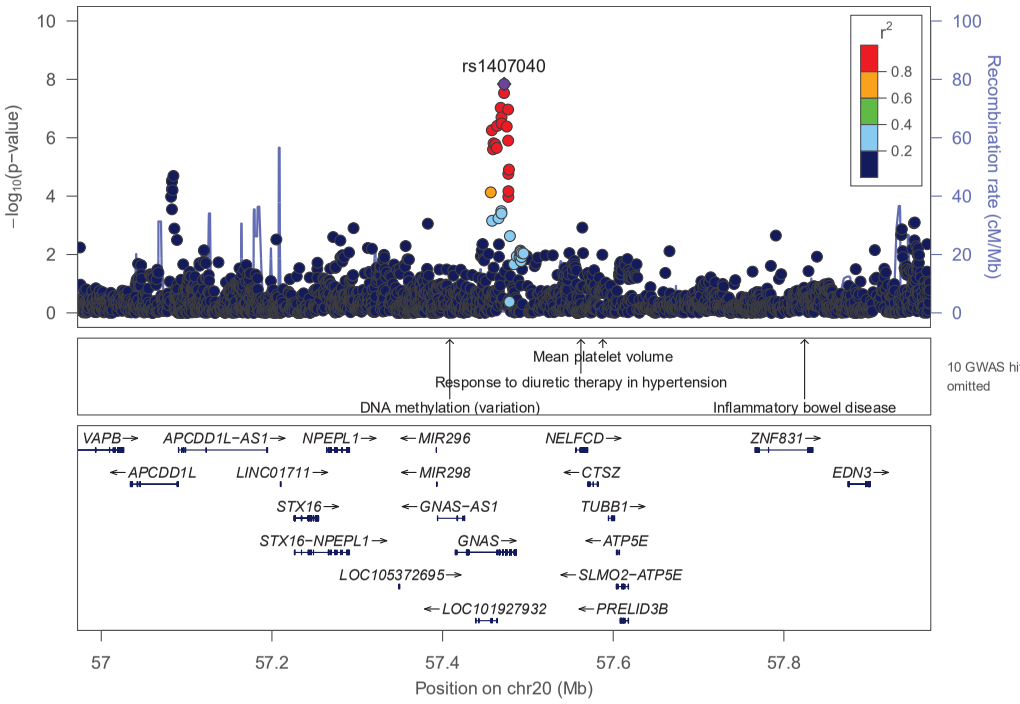

rs6087579
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
IgG glycosylation
Breast cancer
Tanning
Freckles
Freckles
Melanoma
6 GWAS hits omitted
RALY−AS1
ASIP
ITCH
PIGU
NCOA6
RALY
AHCY
MIR644A
TP53INP2
HMGB3P1
MIR4755
DYNLRB1
GGT7
EIF2S2
MAP1LC3A
ACSS2
Position on chr20 (Mb)

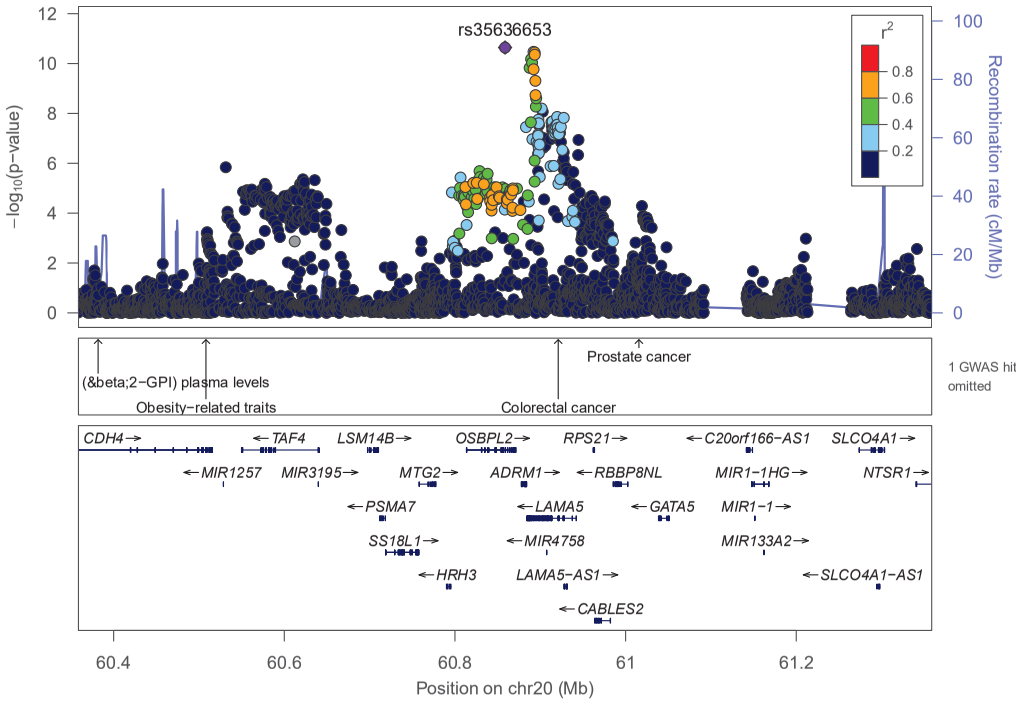

rs2273684
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Height
Spine bone size
Venous thromboembolism
20 GWAS hits omitted
ITCH→ ←PIGU ←NCOA6 ACSS2→ ←TRPC4AP PROCR→ ←EIF6 GDF5OS→
MIR644A→ TP53INP2→ ←HMGB3P1 ←GSS ←EDEM2 MMP24→ ←GDF5
DYNLRB1→ ←GGT7 MYH7B→ ←MMP24−AS1
MAP1LC3A→ MIR499A→ FAM83C−AS1→
←MIR499B ←FAM83C
←UQCC1
Position on chr20 (Mb)

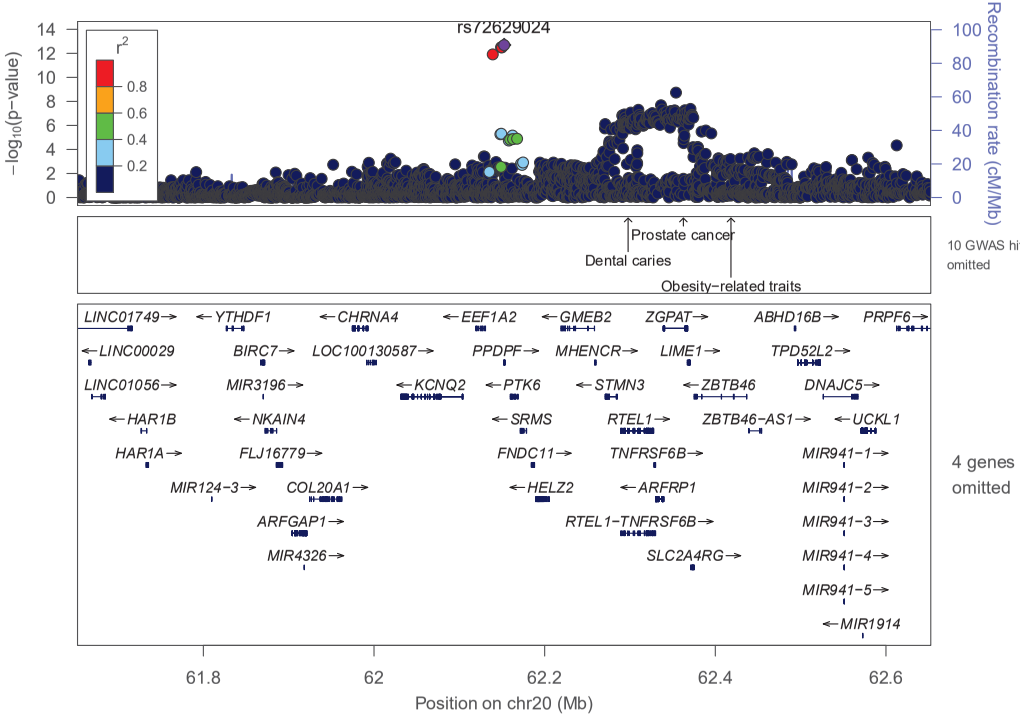

rs6029640
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Cholesterol, total
LDL cholesterol
Hippocampal atrophy
1 GWAS hit omitted
LOC100128988→ PLCG1→ LPIN3→ ←CHD6
TOP1→ ←ZHX3 ←EMILIN3
←PLCG1−AS1
MIR6871→
Position on chr20 (Mb)

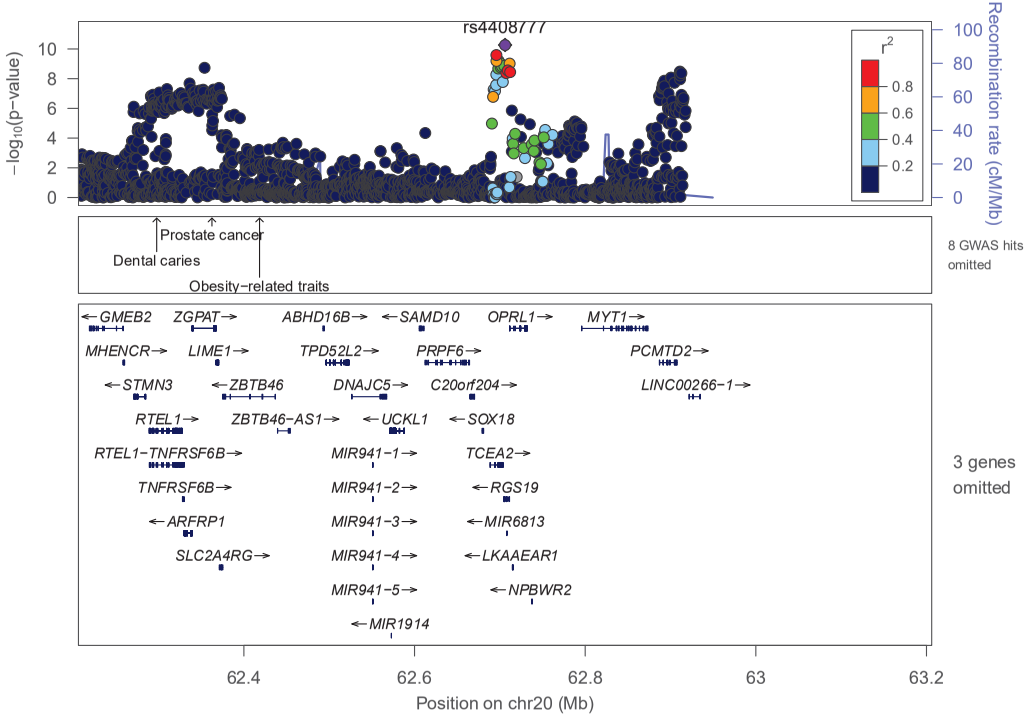

rs17216707
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Calcium levels
IgG glycosylation
Obesity−related traits
6 GWAS hits omitted
LOC105372672→ ←SUMO1P1 ←BCAS1 ←CYP24A1 DOK5→
←MIR4756 PFDN4→
Position on chr20 (Mb)

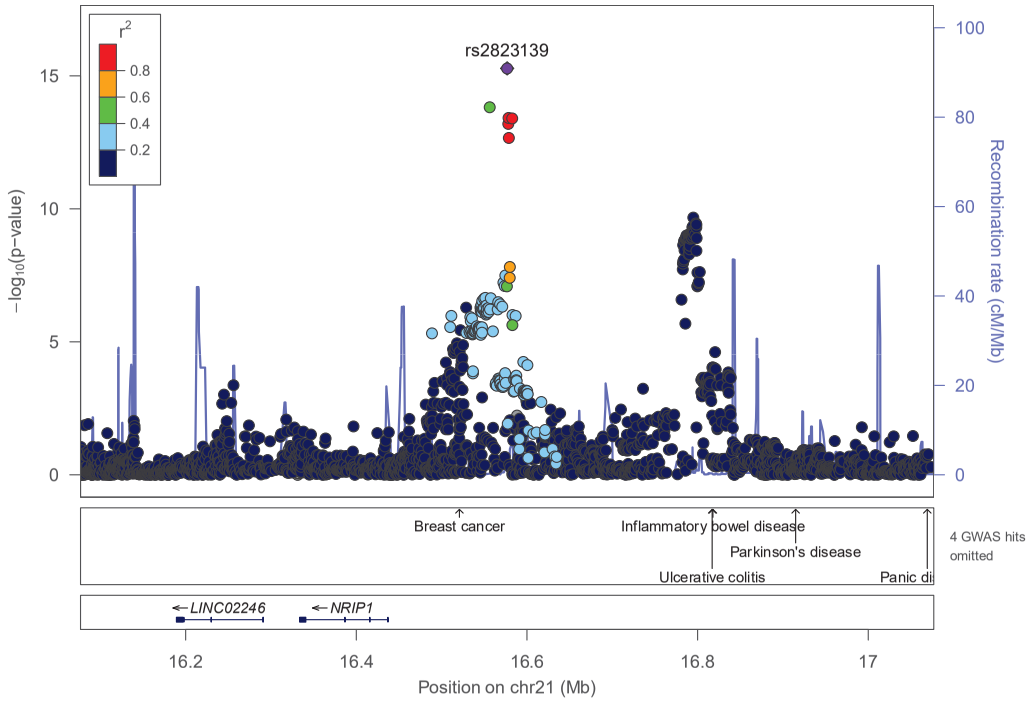

rs2235826
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Alcohol consumption
Type 2 diabetes
Red blood cell traits
Obesity−related traits
Response to fenofibrate (adiponectin levels)
5 GWAS hits omitted
←BMP7 SPO11→ ←CTCFL ←ZBP1 NKILA→ MIR4532→
BMP7−AS1→ RAE1→ PCK1→ ←PMEPA1 LINC01742→
←MIR4325
←MTRNR2L3
RBM38→
Position on chr20 (Mb)

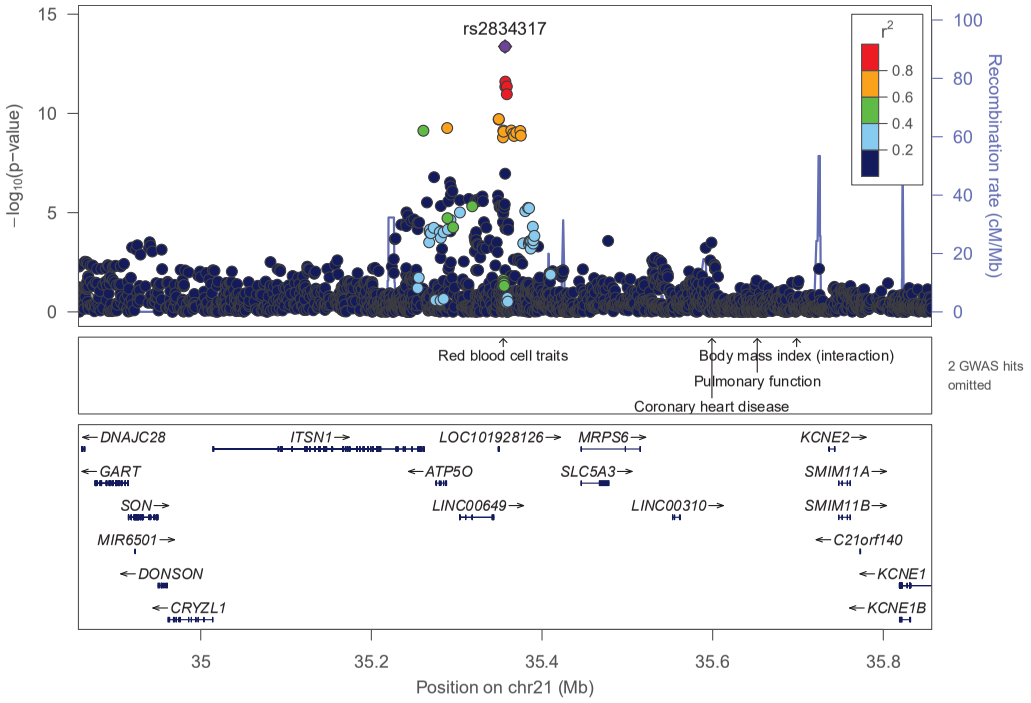

rs1407040
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Mean platelet volume
Response to diuretic therapy in hypertension
DNA methylation (variation)
Inflammatory bowel disease
10 GWAS hits omitted
VAPB→ APCDD1L−AS1→ NPEPL1→ ←MIR296 NELFCD→ ZNF831→
←APCDD1L LINC01711→ ←MIR298 ←CTSZ EDN3→
STX16→ ←GNAS−AS1 TUBB1→
STX16−NPEPL1→ GNAS→ ←ATP5E
LOC105372695→ ←SLMO2−ATP5E
←LOC101927932 ←PRELID3B
57 57.2 57.4 57.6 57.8
Position on chr20 (Mb)

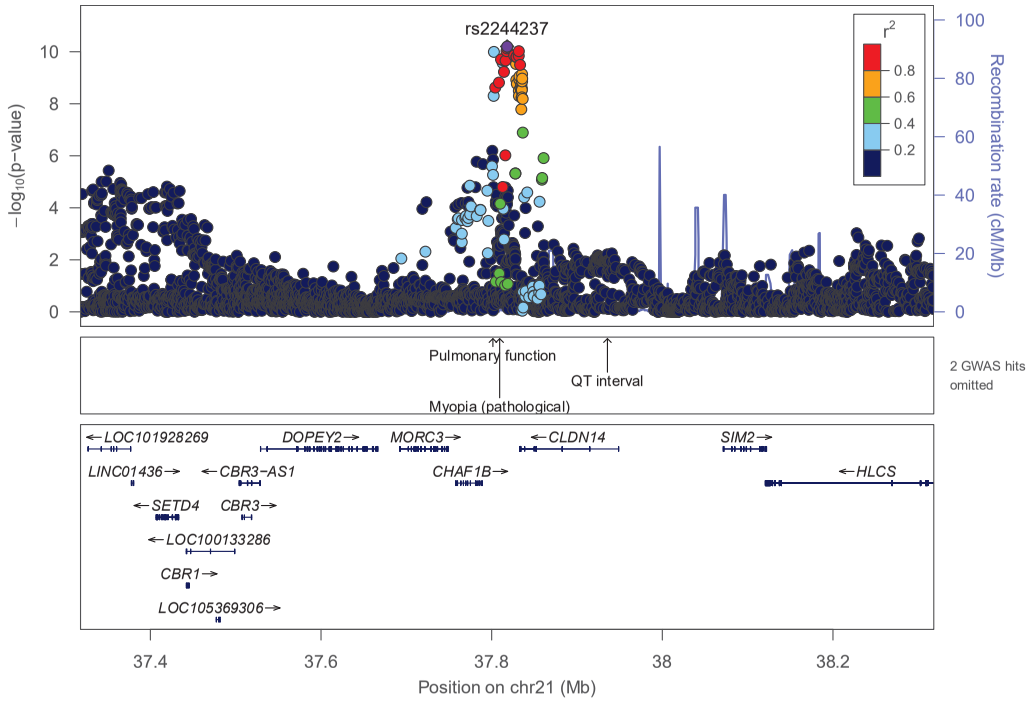

rs35636653
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
(β2−GPI) plasma levels
Obesity−related traits
Prostate cancer
Colorectal cancer
1 GWAS hit omitted
CDH4→ ←TAF4 LSM14B→ OSBPL2→ RPS21→ ←C20orf166−AS1 SLCO4A1→
←MIR1257 MIR3195→ MTG2→ ADRM1→ ←RBBP8NL MIR1−1HG→ NTSR1→
←PSMA7 ←LAMA5 ←GATA5 MIR1−1→
SS18L1→ ←MIR4758 MIR133A2→
←HRH3 LAMA5−AS1→ ←SLCO4A1−AS1
←CABLES2
60.4 60.6 60.8 61 61.2
Position on chr20 (Mb)

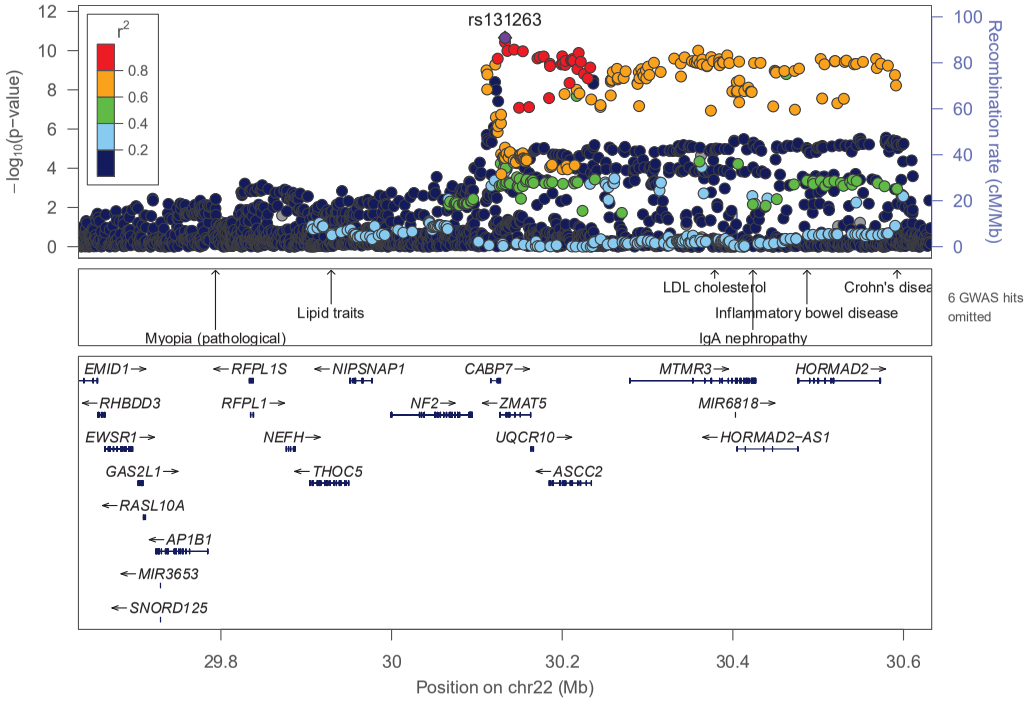

rs72629024
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Prostate cancer
Dental caries
Obesity−related traits
10 GWAS hits omitted
LINC01749→ ←YTHDF1 ←CHRNA4 ←EEF1A2 ←GMEB2 ZGPAT→ ABHD16B→ PRPF6→
←LINC00029 BIRC7→ LOC100130587→ PPDPF→ MHENCR→ LIME1→ TPD52L2→
LINC01056→ MIR3196→ ←KCNQ2 ←PTK6 ←STMN3 ←ZBTB46 DNAJC5→
←HAR1B ←NKAIN4 ←SRMS RTEL1→ ZBTB46−AS1→ ←UCKL1
HAR1A→ FLJ16779→ FNDC11→ TNFRSF6B→ MIR941−1→
MIR124−3→ COL20A1→ ←HELZ2 ←ARFRP1 MIR941−2→
ARFGAP1→ RTEL1−TNFRSF6B→ MIR941−3→
MIR4326→ SLC2A4RG→ MIR941−4→
MIR941−5→
←MIR1914
4 genes omitted
61.8 62 62.2 62.4 62.6
Position on chr20 (Mb)

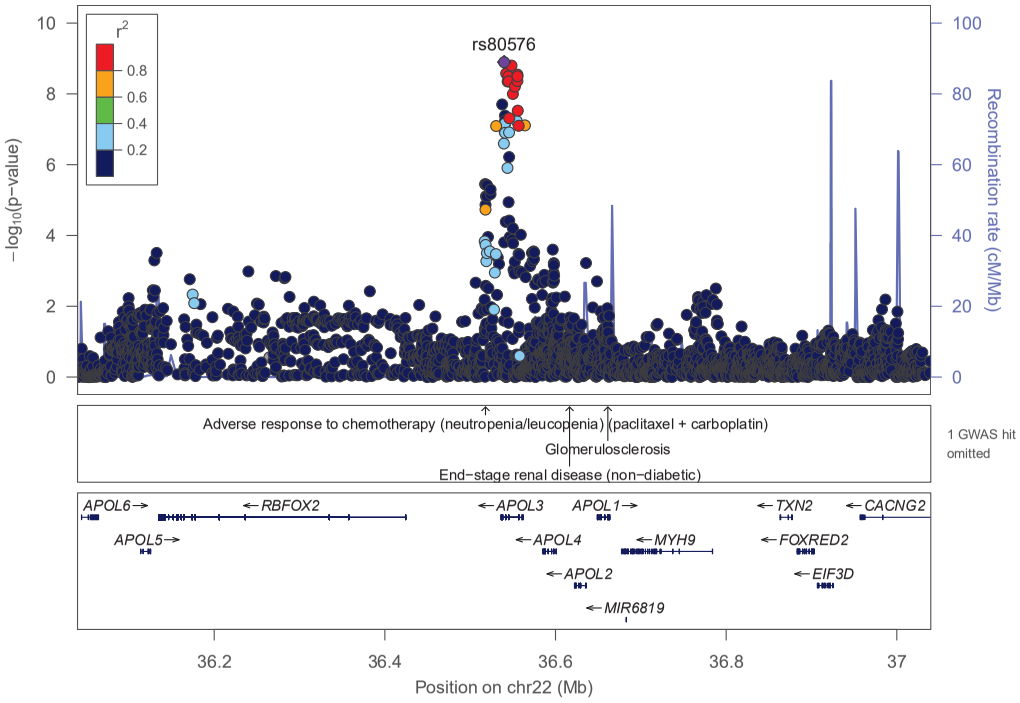

rs4408777
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Prostate cancer
Dental caries
Obesity−related traits
8 GWAS hits omitted
←GMEB2 ZGPAT→ ABHD16B→ ←SAMD10 OPRL1→ MYT1→
MHENCR→ LIME1→ TPD52L2→ PRPF6→ PCMTD2→
←STMN3 ←ZBTB46 DNAJC5→ C20orf204→ LINC00266−1→
RTEL1→ ZBTB46−AS1→ ←UCKL1 ←SOX18
RTEL1−TNFRSF6B→ MIR941−1→ TCEA2→
TNFRSF6B→ MIR941−2→ ←RGS19
←ARFRP1 MIR941−3→ ←MIR6813
SLC2A4RG→ MIR941−4→ ←LKAAEAR1
MIR941−5→ ←NPBWR2
←MIR1914
3 genes omitted
62.4 62.6 62.8 63 63.2
Position on chr20 (Mb)

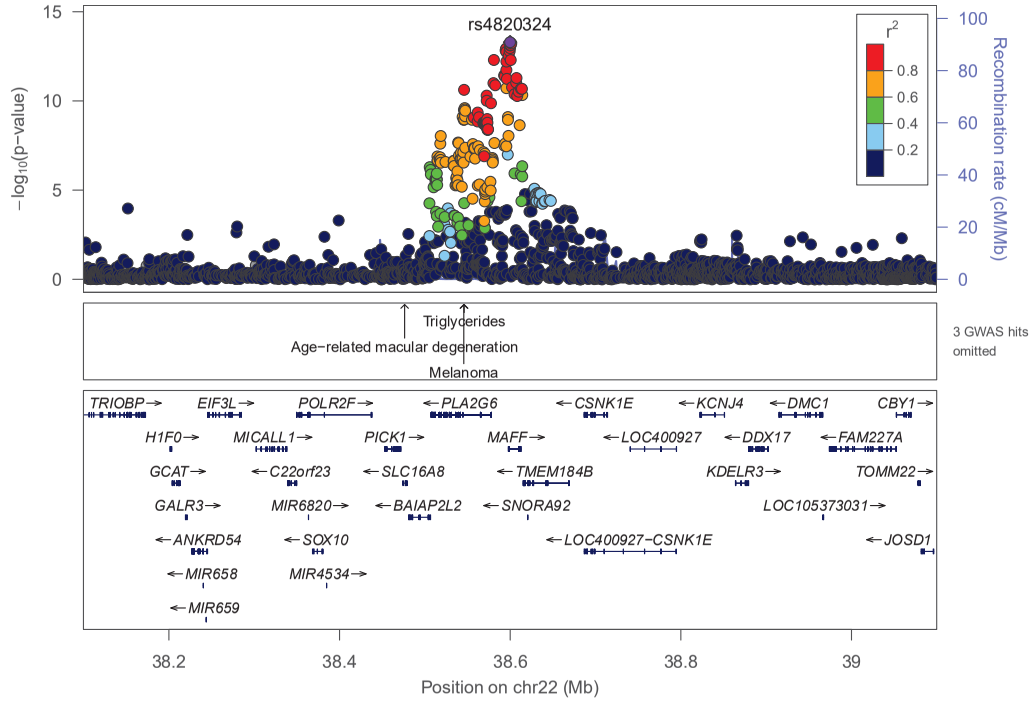

rs2823139
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Breast cancer
Inflammatory bowel disease
Parkinson's disease
Ulcerative colitis
Panic di
4 GWAS hits omitted
LINC02246
NRIP1
16.2
16.4
16.6
16.8
17
Position on chr21 (Mb)

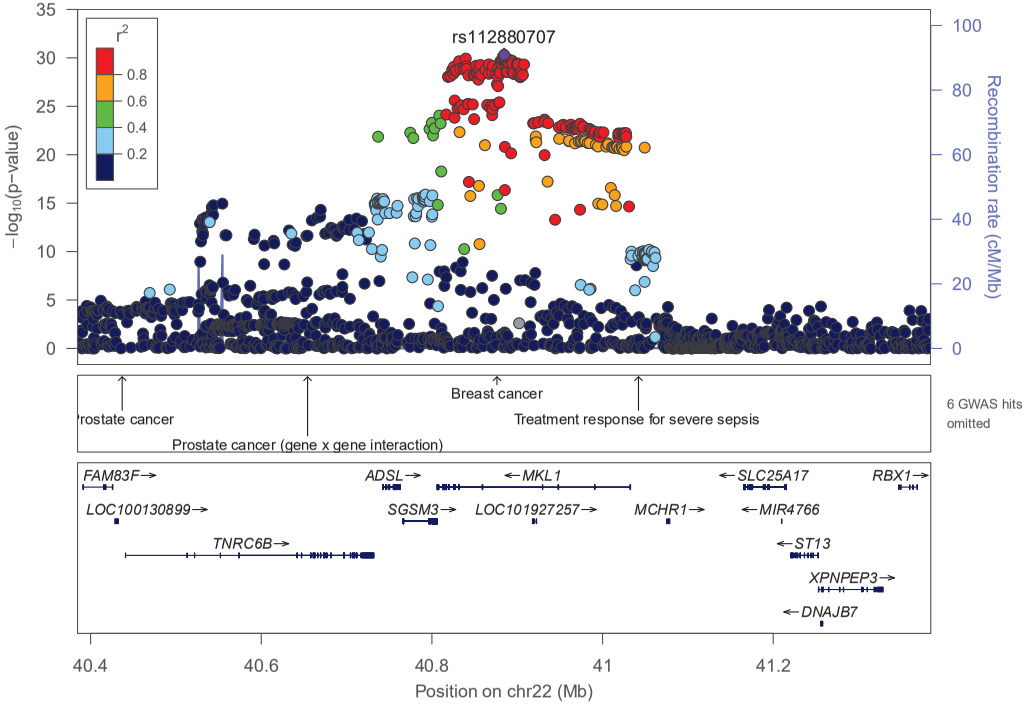

rs2834317
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Red blood cell traits
Body mass index (interaction)
Pulmonary function
Coronary heart disease
2 GWAS hits omitted
DNAJC28
ITSN1
LOC101928126
MRPS6
KCNE2
GART
ATP5O
SLC5A3
SMIM11A
SON
LINC00649
LINC00310
SMIM11B
MIR6501
C21orf140
DONSON
KCNE1
CRYZL1
KCNE1B
35
35.2
35.4
35.6
35.8
Position on chr21 (Mb)

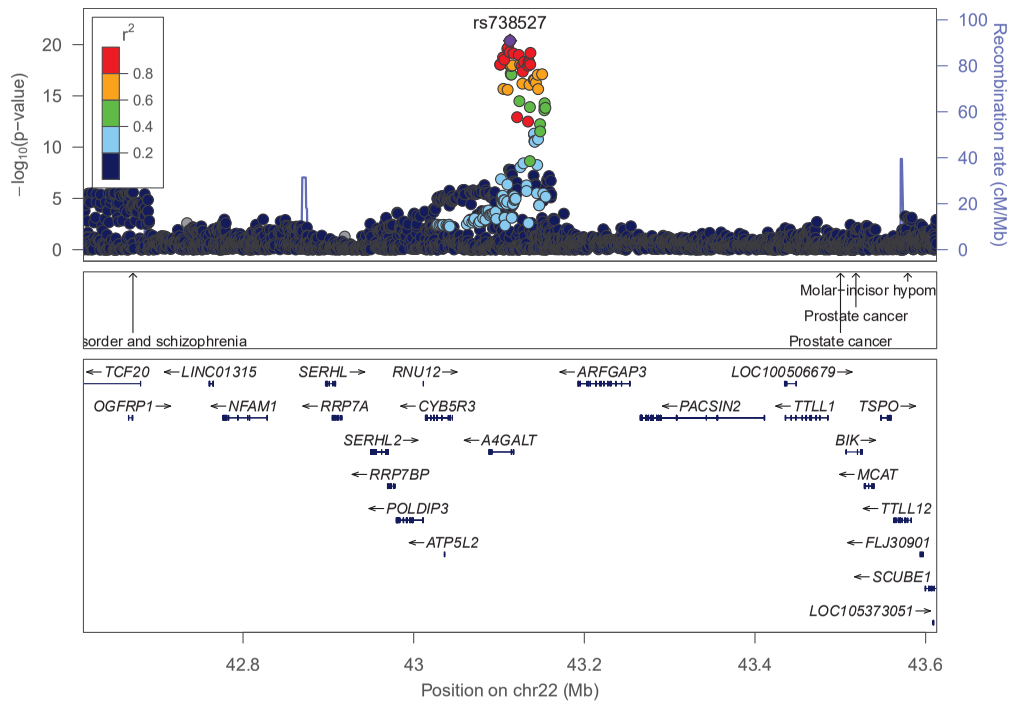

rs2244237
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Pulmonary function
QT interval
Myopia (pathological)
2 GWAS hits omitted
LOC101928269
DOPEY2
MORC3
CLDN14
SIM2
LINC01436
CBR3−AS1
CHAF1B
HLCS
SETD4
CBR3
LOC100133286
CBR1
LOC105369306
37.4
37.6
37.8
38
38.2
Position on chr21 (Mb)


rs131263
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Myopia (pathological)
Lipid traits
LDL cholesterol
Inflammatory bowel disease
IgA nephropathy
Crohn's disea
6 GWAS hits omitted
EMID1
RFPL1S
NIPSNAP1
CABP7
MTMR3
HORMAD2
RHBDD3
RFPL1
NF2
ZMAT5
MIR6818
EWSR1
NEFH
UQCR10
HORMAD2−AS1
GAS2L1
THOC5
ASCC2
RASL10A
AP1B1
MIR3653
SNORD125
29.8
30
30.2
30.4
30.6
Position on chr22 (Mb)


rs80576
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Adverse response to chemotherapy (neutropenia/leucopenia) (paclitaxel + carboplatin)
Glomerulosclerosis
End−stage renal disease (non−diabetic)
1 GWAS hit omitted
APOL6→ ←RBFOX2 ←APOL3 APOL1→ ←TXN2 ←CACNG2
APOL5→ ←APOL4 ←MYH9 ←FOXRED2
←APOL2 ←EIF3D
←MIR6819
36.2
36.4
36.6
36.8
37
Position on chr22 (Mb)


rs4820324
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Triglycerides
Age−related macular degeneration
Melanoma
3 GWAS hits omitted
TRIOBP→ ←EIF3L→ ←POLR2F→ ←PLA2G6 ←CSNK1E ←KCNJ4 ←DMC1 CBY1→
H1F0→ ←MICALL1→ ←PICK1→ ←MAFF→ ←LOC400927 ←DDX17 ←FAM227A
GCAT→ ←C22orf23 ←SLC16A8 ←TMEM184B KDELR3→ TOMM22→
GALR3→ ←MIR6820→ ←BAIAP2L2 ←SNORA92 LOC105373031→
←ANKRD54 ←SOX10 ←LOC400927−CSNK1E ←JOSD1
←MIR658 ←MIR4534→
←MIR659
38.2
38.4
38.6
38.8
39
Position on chr22 (Mb)


rs112880707
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Breast cancer
rostate cancer
Treatment response for severe sepsis
Prostate cancer (gene x gene interaction)
6 GWAS hits omitted
FAM83F→ ←ADSL→ ←MKL1 ←SLC25A17 RBX1→
LOC100130899→ SGSM3→ ←LOC101927257→ MCHR1→ ←MIR4766
←TNRC6B→ ←ST13
←XPNPEP3→
←DNAJB7
40.4
40.6
40.8
41
41.2
Position on chr22 (Mb)


rs738527
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
order and schizophrenia
Molar−incisor hypom
Prostate cancer
Prostate cancer
←TCF20 ←LINC01315 SERHL→ RNU12→ ←ARFGAP3 LOC100506679→
OGFRP1→ ←NFAM1 ←RRP7A ←CYB5R3 ←PACSIN2 ←TTLL1 TSPO→
SERHL2→ ←A4GALT BIK→
←RRP7BP ←MCAT
←POLDIP3 ←TTLL12
←ATP5L2 ←FLJ30901
←SCUBE1
LOC105373051→
42.8
43
43.2
43.4
43.6
Position on chr22 (Mb)