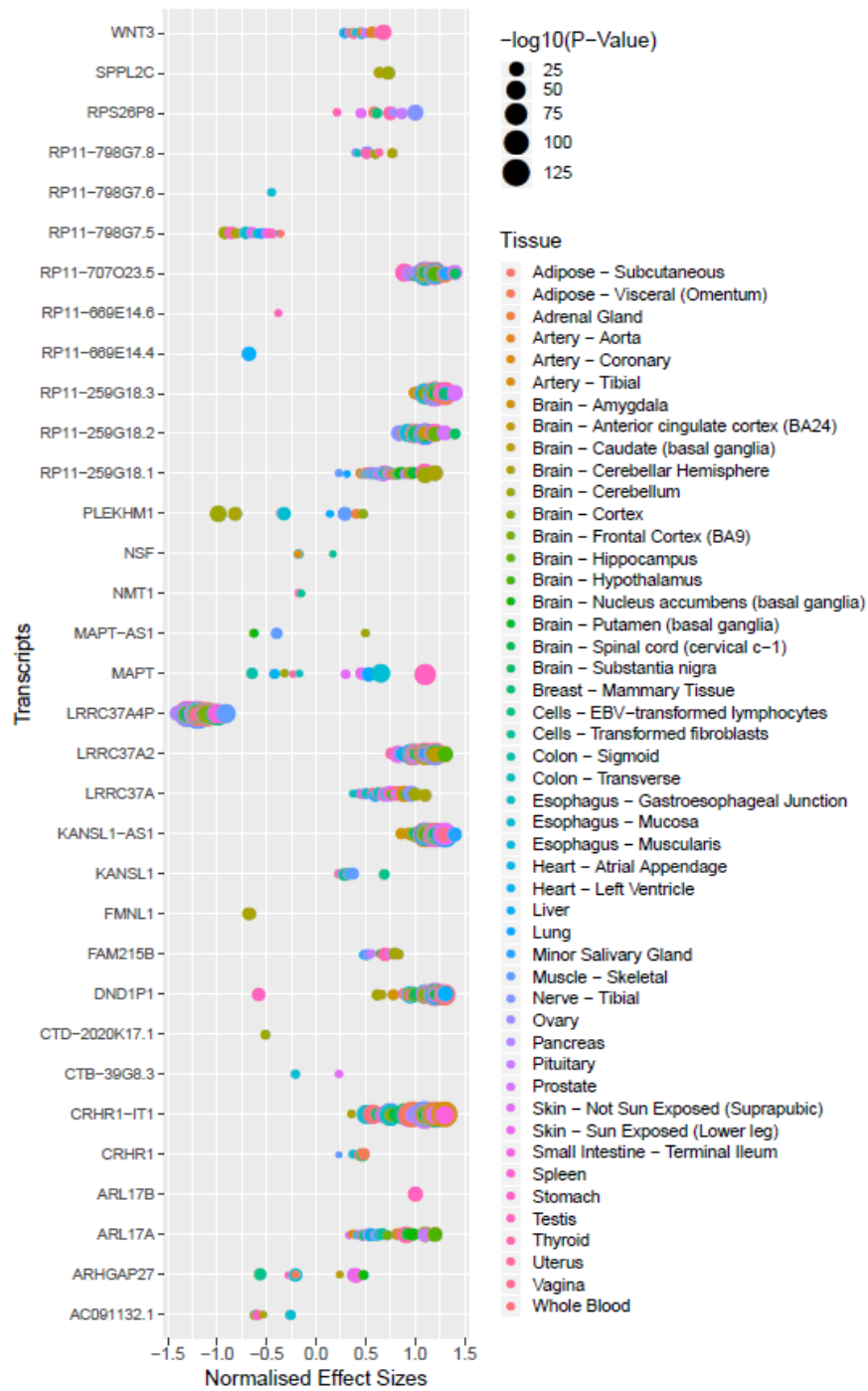




cis-eQTLs effects in different tissues  
rs1991556

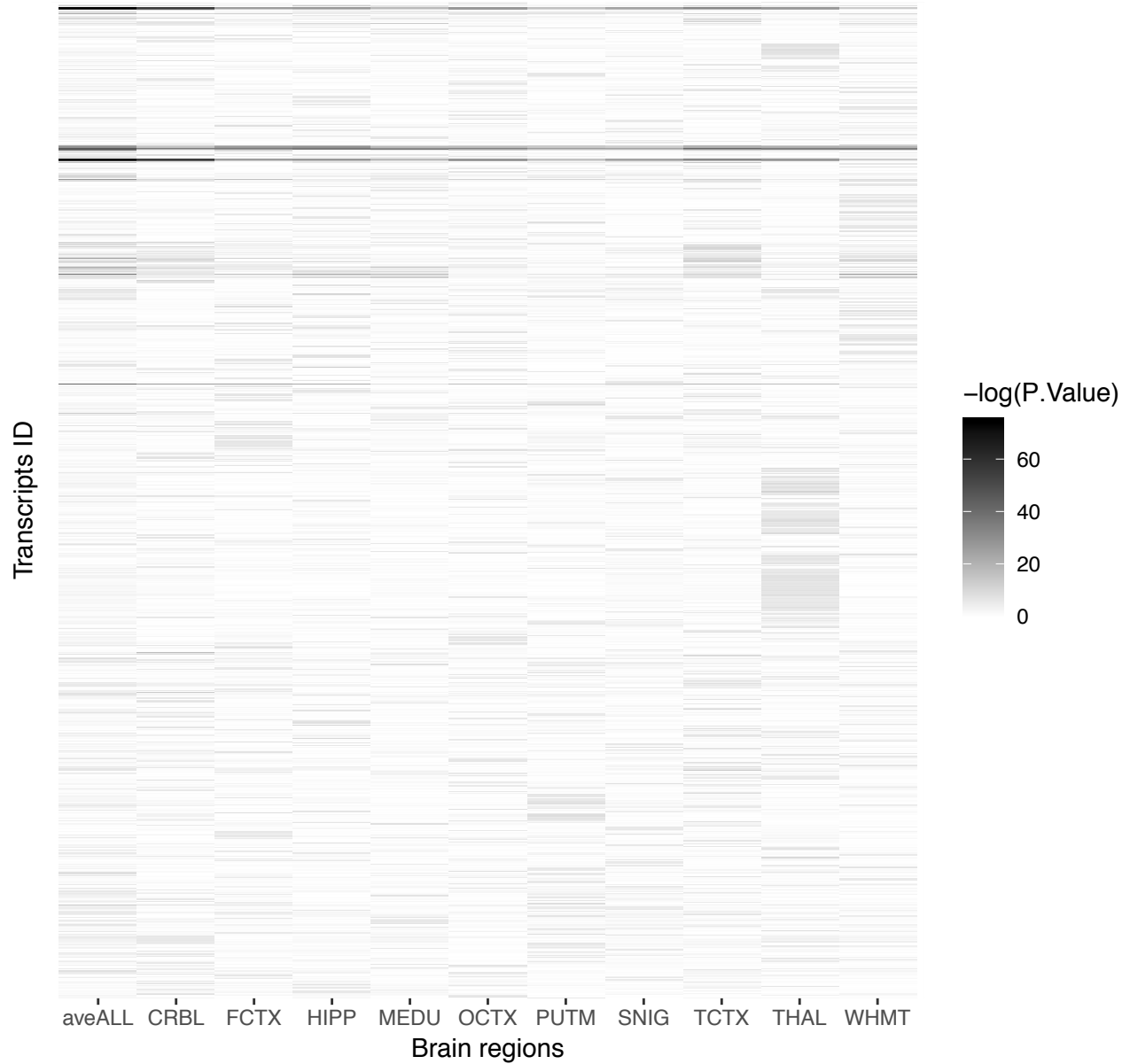


Supplementary Figure 2

cis-eQTL effect of rs9901937 on expression of neighboring genes in 48 tissues (GTEx dataset).

The y-axis represents affected transcripts whereas the x-axis represent eQTL effect sizes. Expression in each tissue is colour-coded, while the significance of transcript-SNP associations is represented by the size of each bubble which is proportional to the  $P$ -value

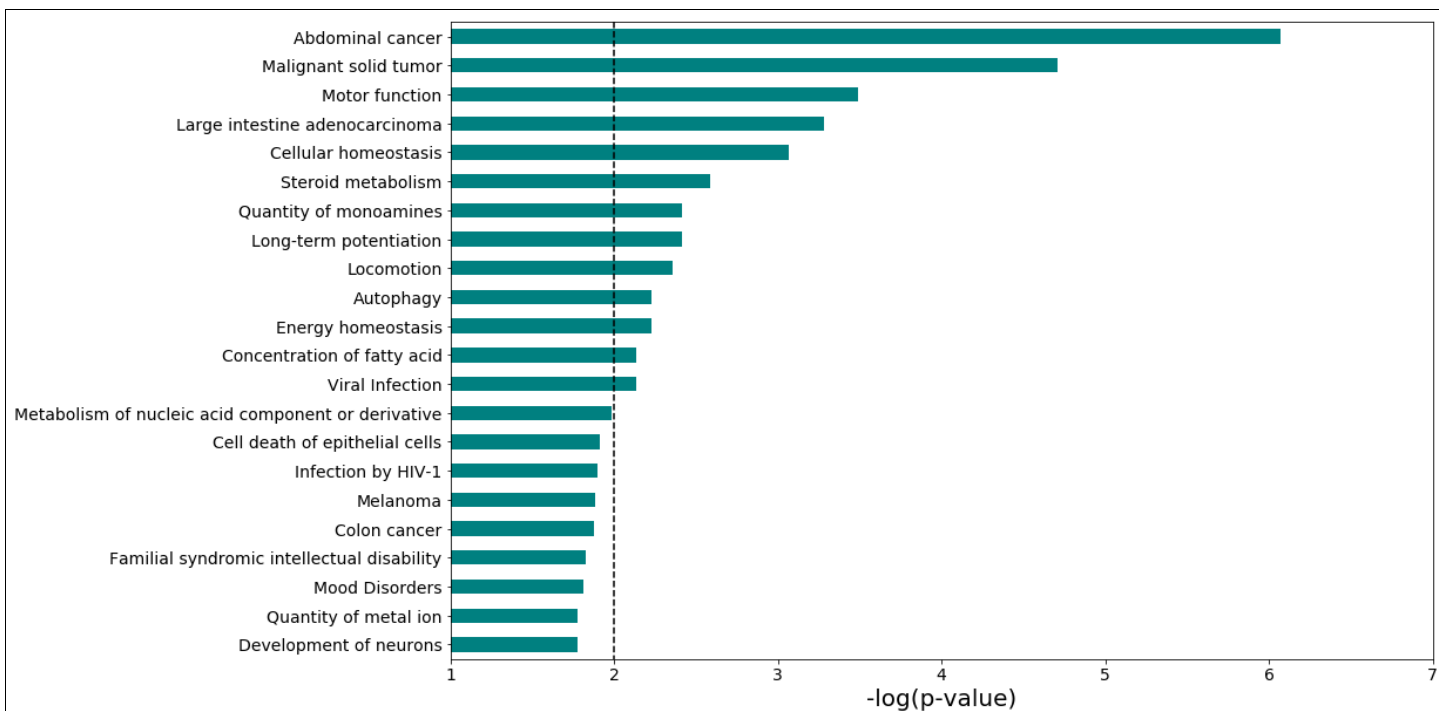
cis-eQTLs effects in the brain  
(all SNPs)



**Supplementary Figure 3**

**cis-eQTL effect of all SNPs on expression of different genes in 10 brain regions.**

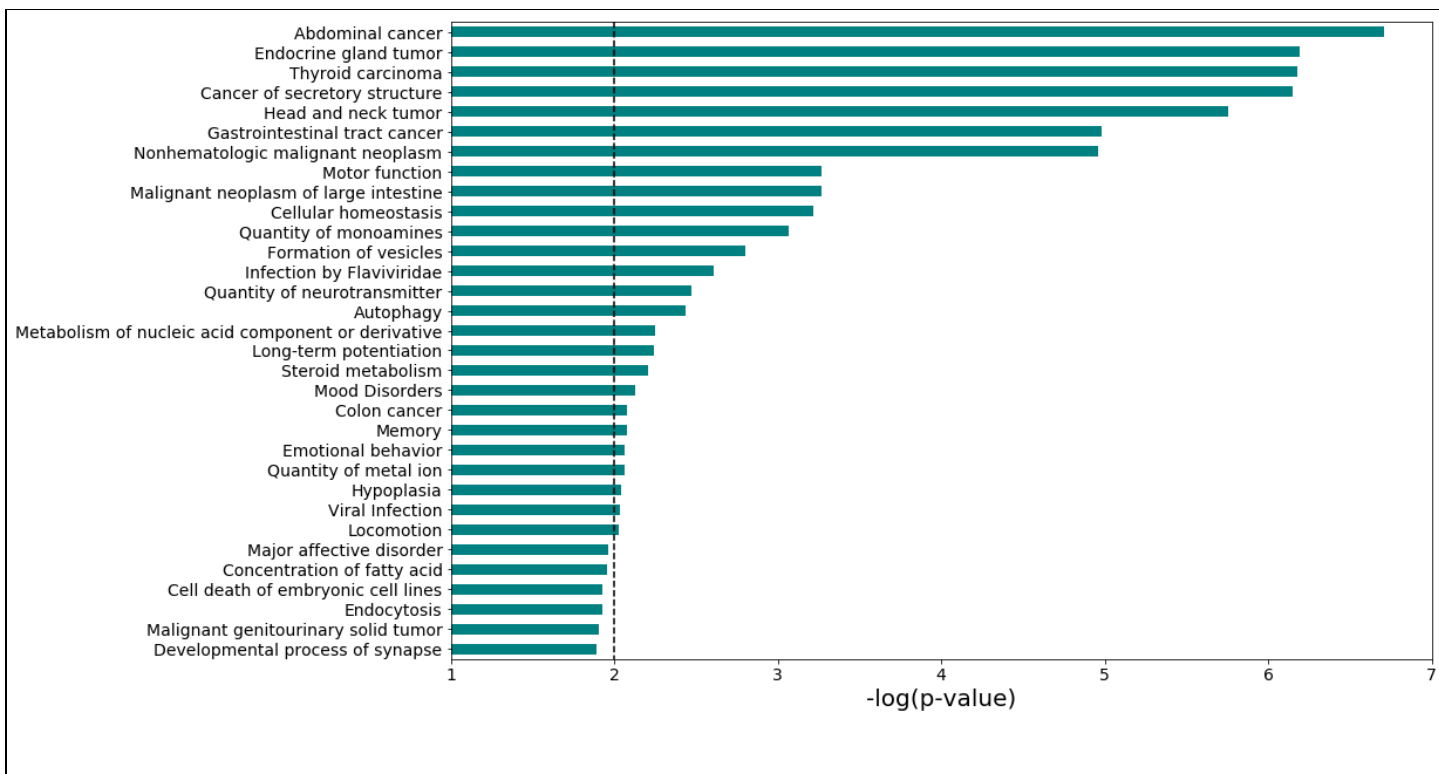
Transcripts-SNP pairs with eQTL  $P$ -values  $< 0.0045$  in at least one brain tissue are included in this plot. We have removed the transcript ID of the y-axis for simplicity. Details for this figure, including transcripts ID can be found in Supplementary Table 14.



#### Supplementary Figure 4

#### Gene over-representation enrichment analysis using IPA.

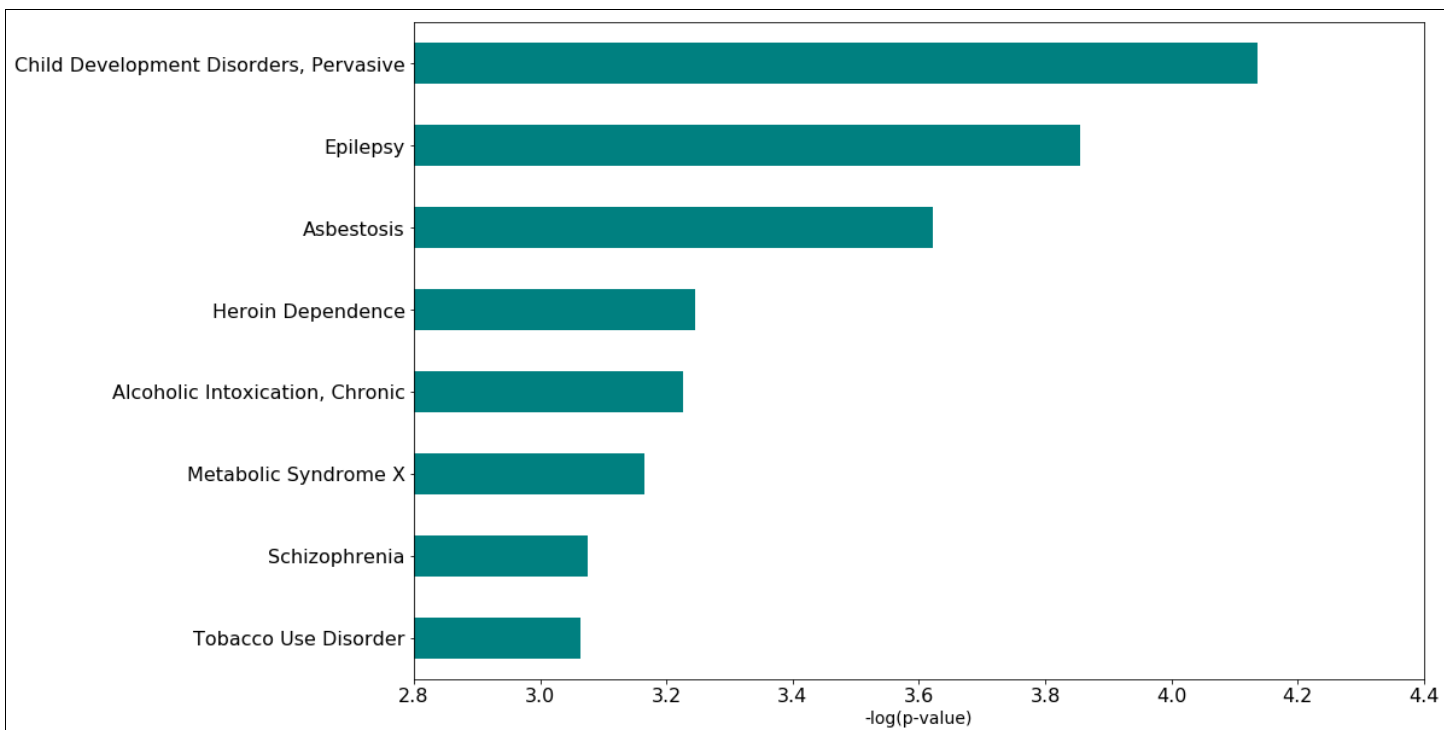
Enriched disease and biological function terms within the list of 146 GTEx eQTL genes are shown ranked according to their  $P$ -value. Only terms having at least 5 gene matches to the list were used for the analysis. Dashed line marks the significance threshold ( $P = 0.01$ )



### Supplementary Figure 5

#### Gene over-representation enrichment analysis using IPA.

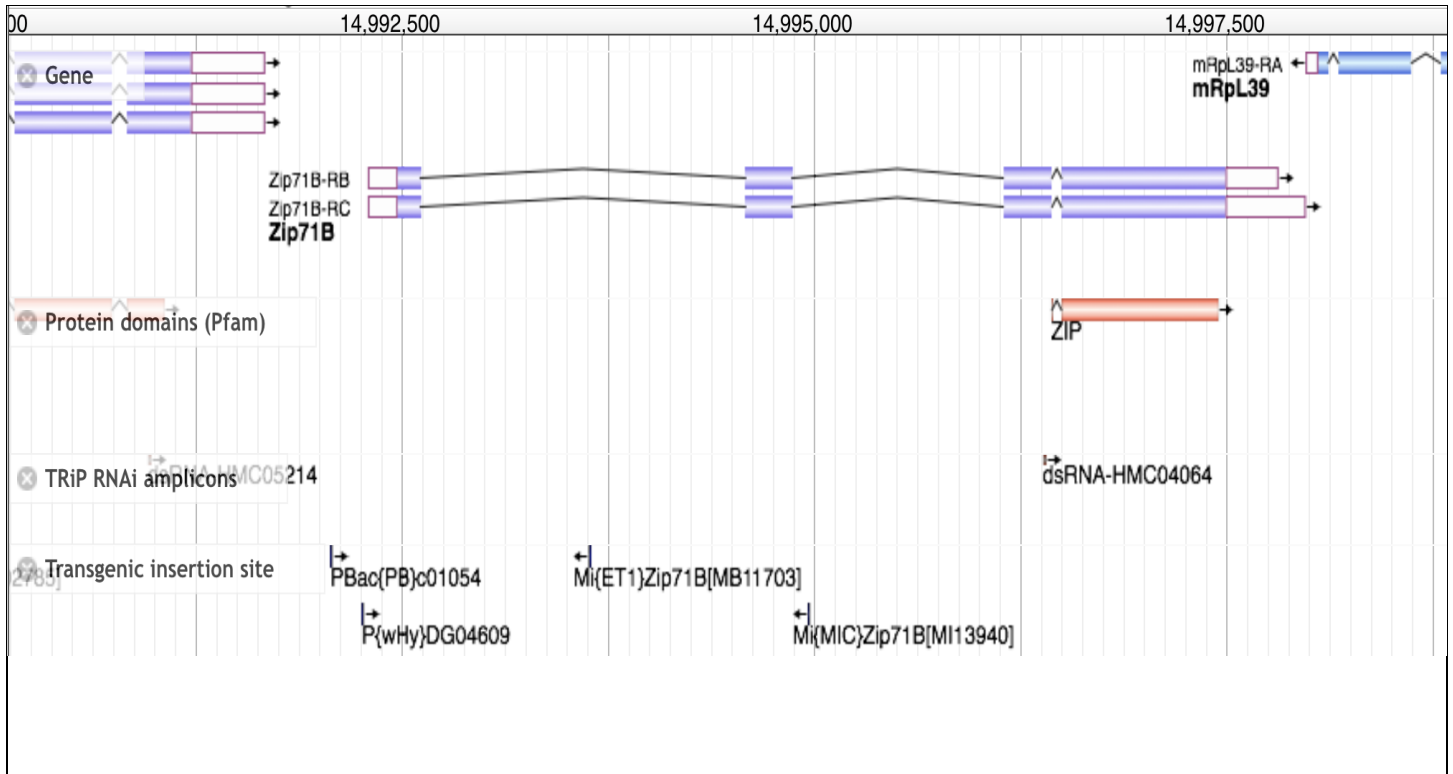
Enriched disease and biological function terms within the list of 160 GTEx eQTL genes are shown ranked according to their  $P$ -value. Only terms having at least 5 gene matches to the list were used for the analysis. Dashed line marks the significance threshold ( $P = 0.01$ )



**Supplementary Figure 6**

**Gene over-representation analysis using WebGestalt.**

Novel and known variants are significantly enriched in several diseases and traits



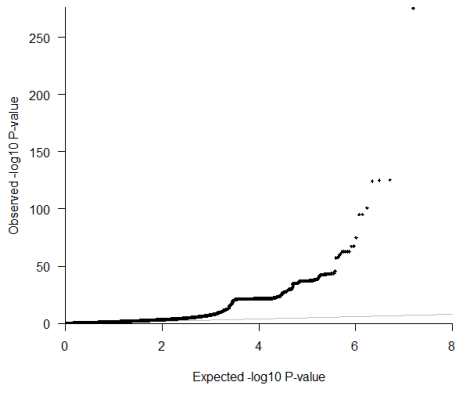
### Supplementary Figure 7

#### *dZip71B* gene structure.

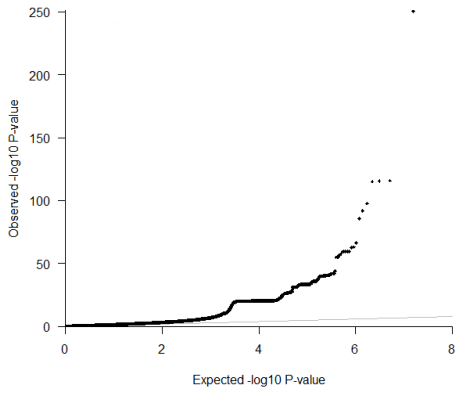
*Drosophila* genome browser screen shot. The top track shows the gene structure, with exons indicated by boxes, and the open reading frame shaded purple. The second track shows the location of the conserved transporter channel domain (red). Track three indicates the location of the short hairpin RNAi target used to knock down *dZip71B*. The bottom track displays the location of various transposon insertions in the *dZip71B* gene. We used transheterozygous flies carrying one allele each of the *MB11703* and *M113940* insertions, which are both located in the middle of the gene, in introns flanked by coding exons. The scale atop is in base pairs.

**Supplementary Figure 8. Quantile-quantile (QQ) plots.** The figure shows QQ plots for a) meta-analysis summary level data b) UK-Biobank only and c) AlcGen and Charge+ only.

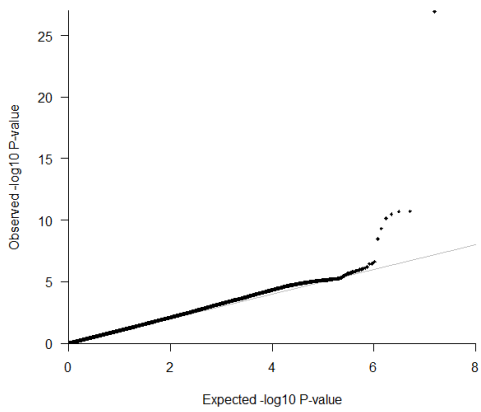
**a.**



**b.**

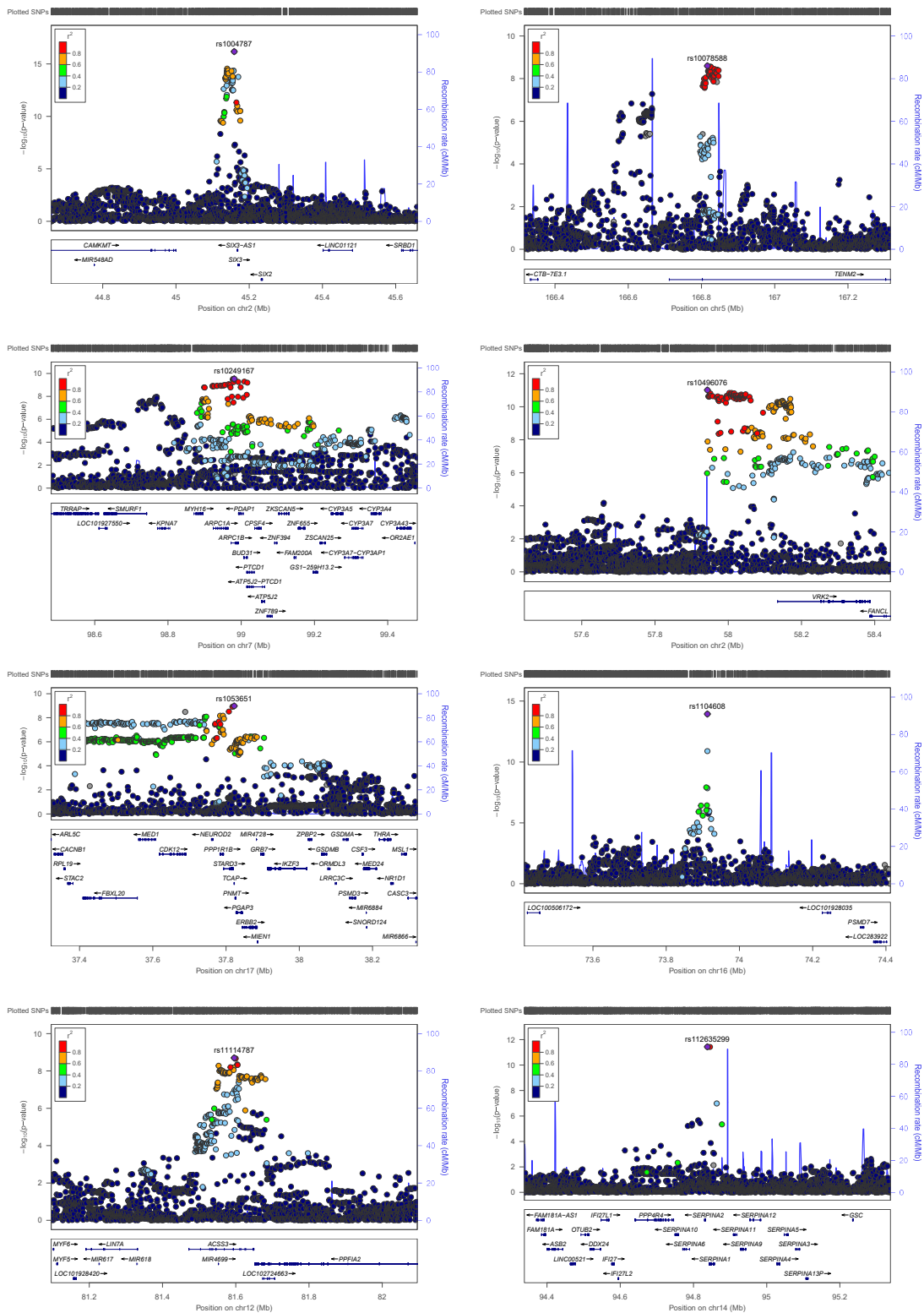


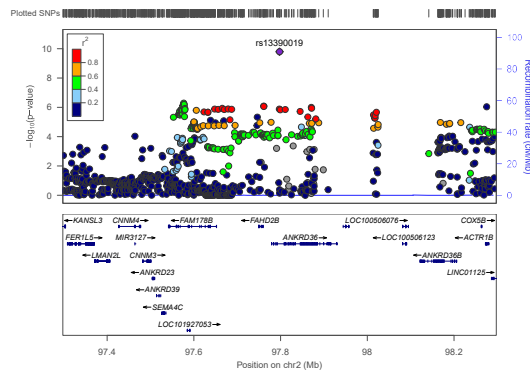
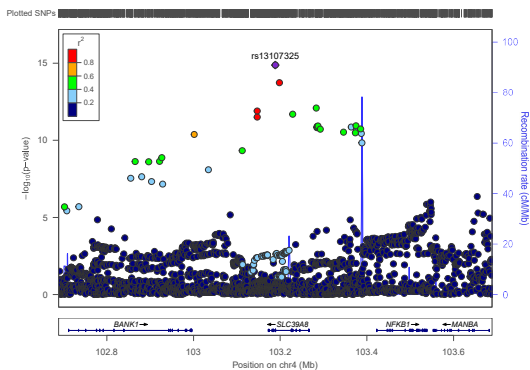
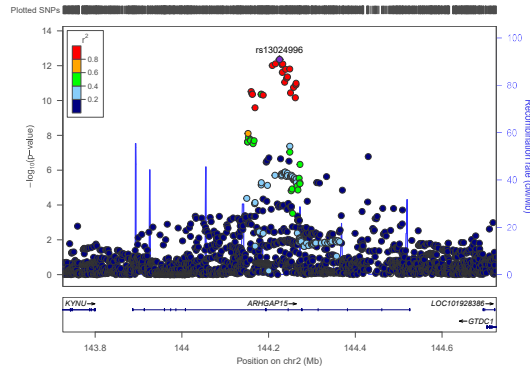
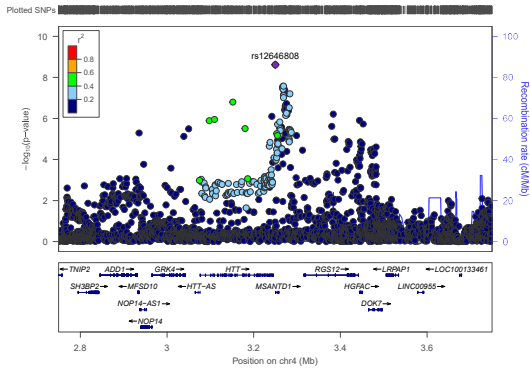
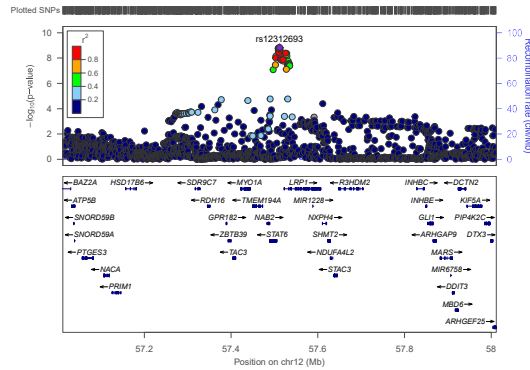
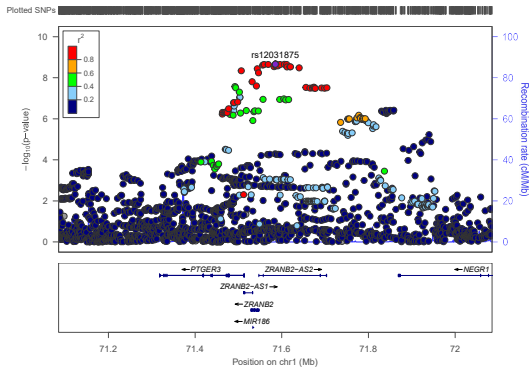
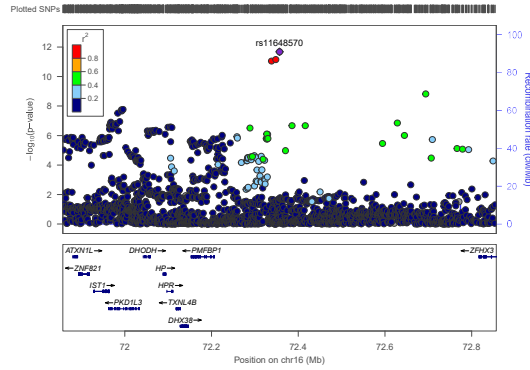
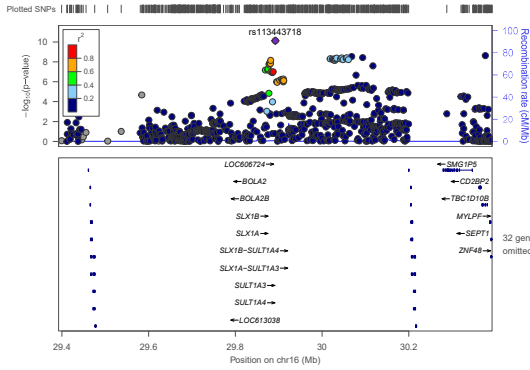
**c.**

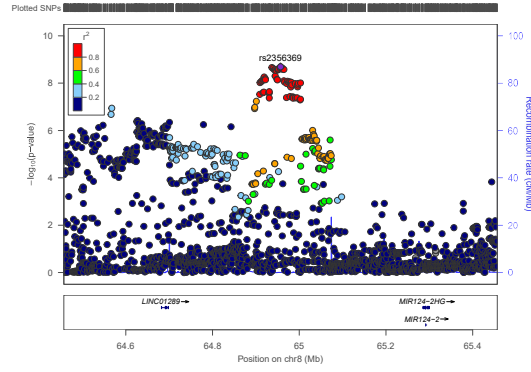
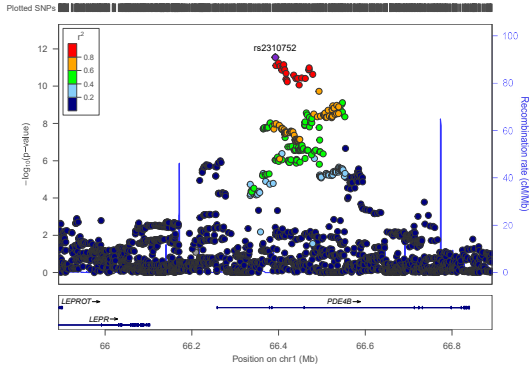
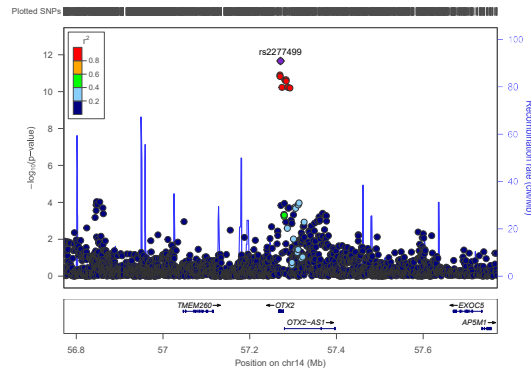
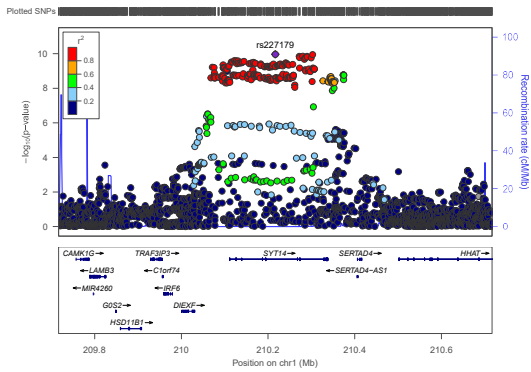
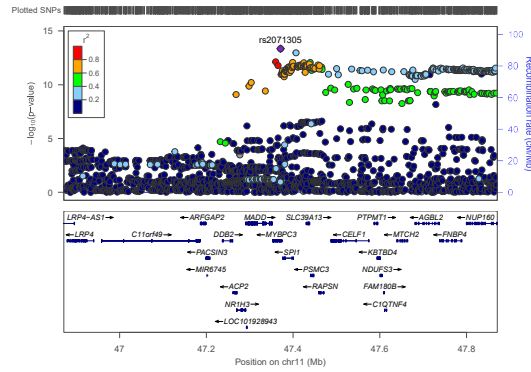
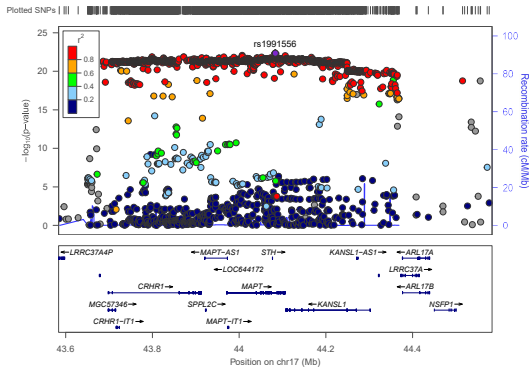
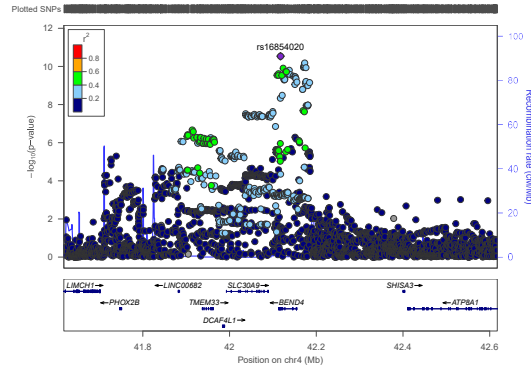
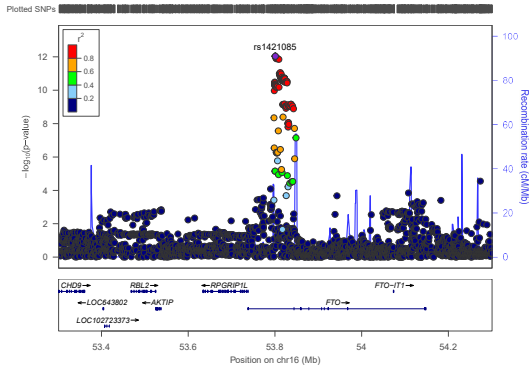


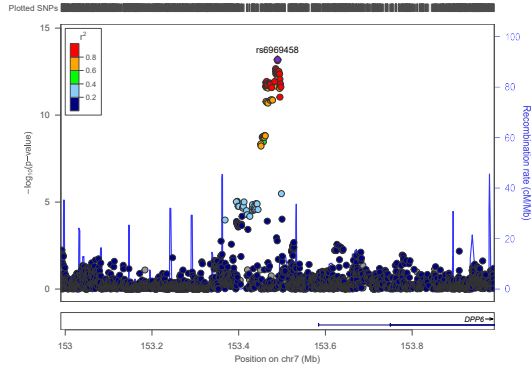
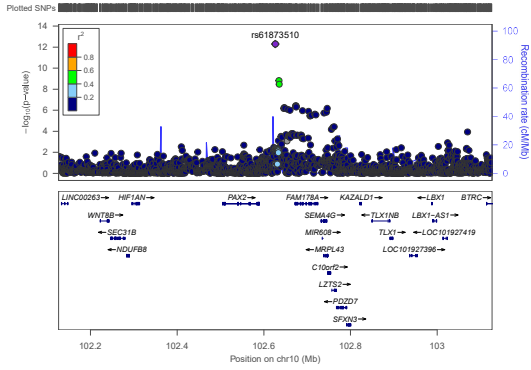
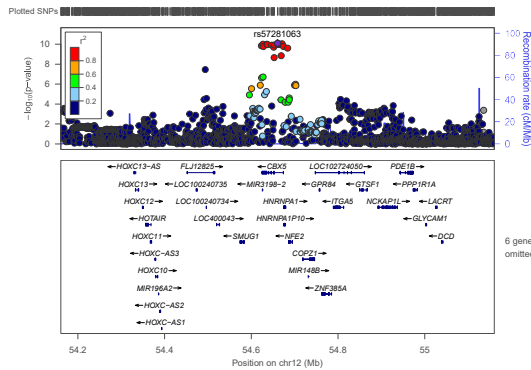
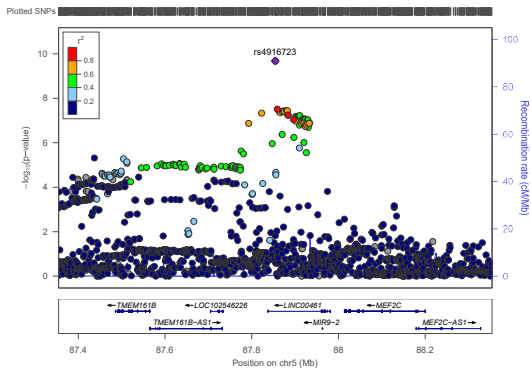
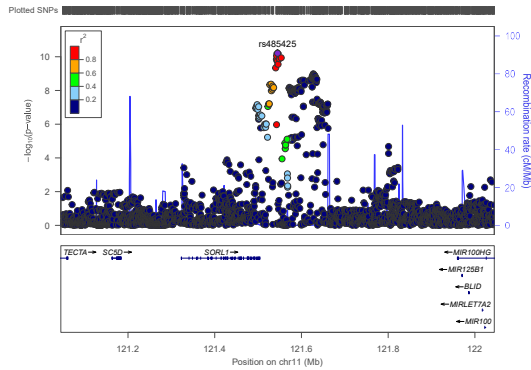
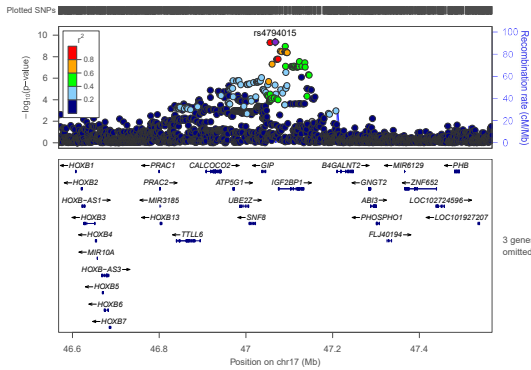
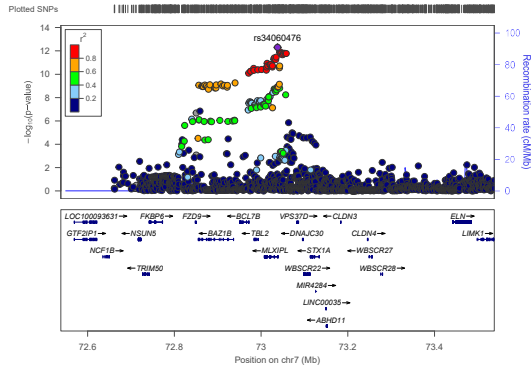
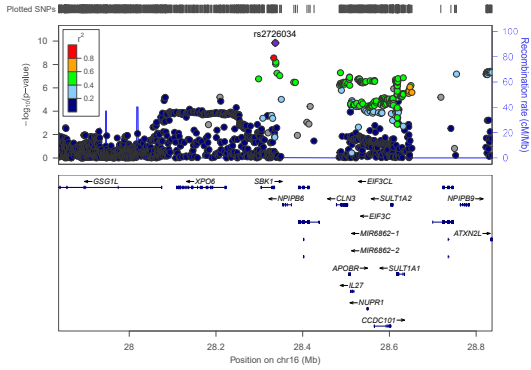


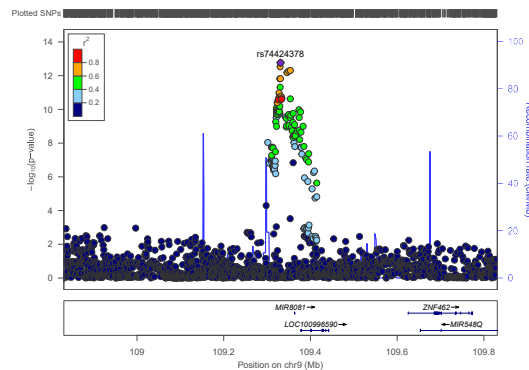
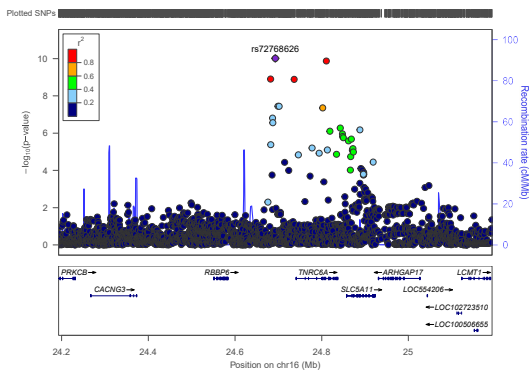
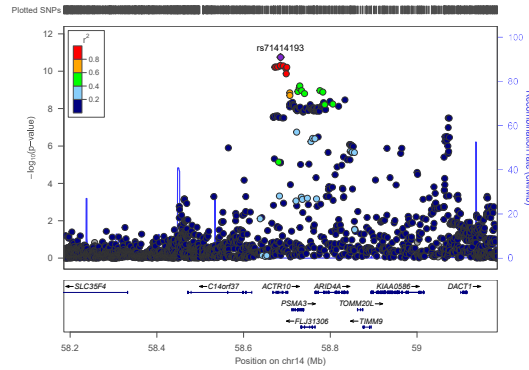
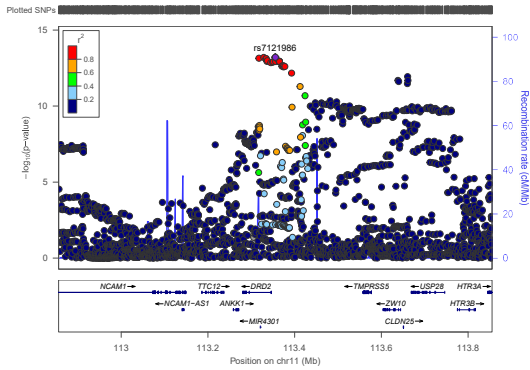
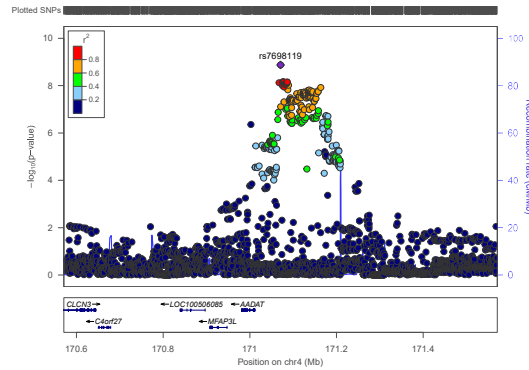
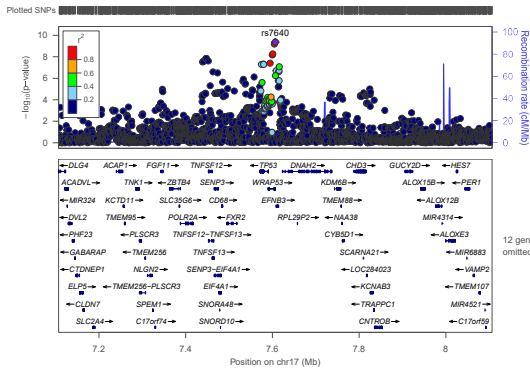
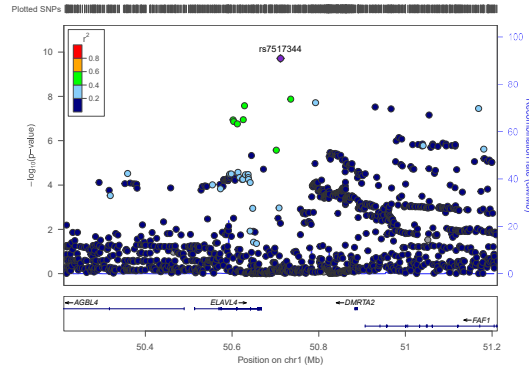
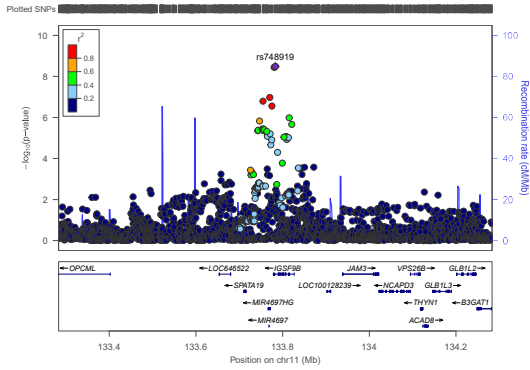
**Supplementary Figure 9. Regional plots for all novel SNPs.** For each plot the  $-\log_{10} P$  values of the SNPs are shown according to their chromosomal positions (x axis). The lead SNPs are labeled by their rs ID (blue) and the  $r^2$  values of the rest of the SNPs with are indicated by different colors.

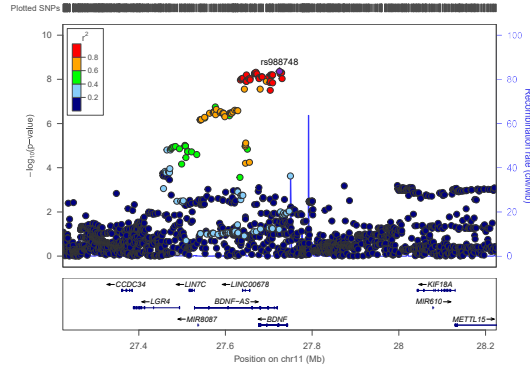
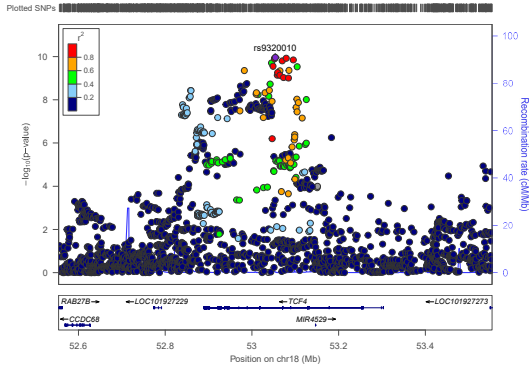
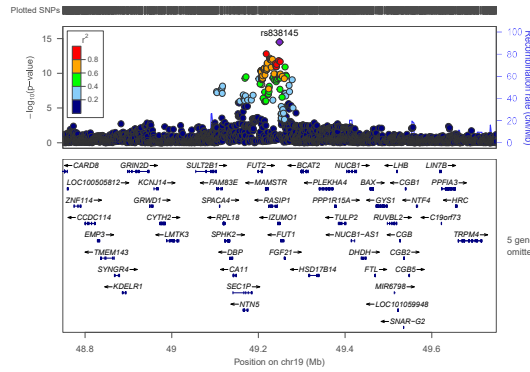
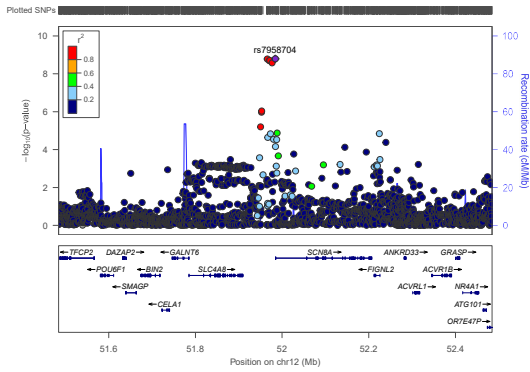
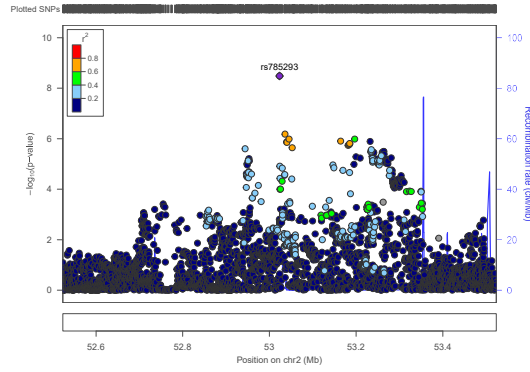
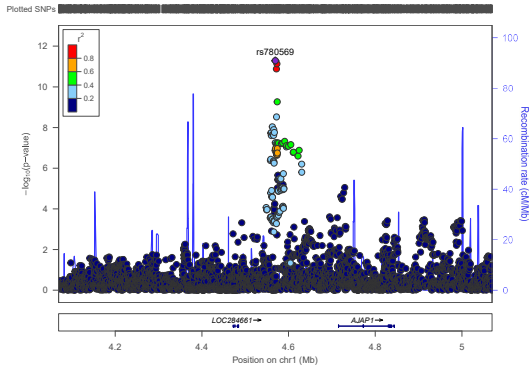












## Supplementary Note

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The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health."

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GAPP: The GAPP study was supported by the Liechtenstein Government, the Swiss Heart Foundation, the Swiss Society of Hypertension, the University of Basel, the University Hospital Basel, the Hanel Foundation, the Mach-Gaensslen Foundation, Schiller AG, and Novartis.

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