Supplementary Figure 1

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

The eQTL effects are stratified by SNP. The y-axis represents affected transcripts whereas the x-axis represents 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-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 *MI13940* 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.

![QQ plot for meta-analysis summary level data](image1)

b.

![QQ plot for UK-Biobank only](image2)

c.

![QQ plot for AlcGen and Charge+](image3)
**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 are indicated by different colors.
RNAm:\n\[\text{rs748919} \quad 0.2 \quad 0.4 \quad 0.6 \quad 0.8 \quad r^2\]
\[\text{OPCML} \quad \text{LOC646522} \quad \text{SPATA19} \quad \text{MIR4697HG} \quad \text{MIR4697} \quad \text{IGSF9B} \quad \text{LOC100128239} \quad \text{JAM3} \quad \text{NCAPD3} \quad \text{VPS26B} \quad \text{THYN1} \quad \text{ACAD8} \quad \text{GLB1L3} \quad \text{GLB1L2} \quad \text{B3GAT1} \quad 133.4 \quad 133.6 \quad 133.8 \quad 134 \quad 134.2 \quad \text{Position on chr11 (Mb)} \quad \text{Plotted SNPs}\\
\[\text{rs7517344} \quad 0.2 \quad 0.4 \quad 0.6 \quad 0.8 \quad r^2\]
\[\text{AGBL4} \quad \text{ELAVL4} \quad \text{DMRTA2} \quad \text{FAF1} \quad 50.4 \quad 50.6 \quad 50.8 \quad 51 \quad 51.2 \quad \text{Position on chr1 (Mb)} \quad \text{Plotted SNPs}\\
\[\text{rs7640} \quad 0.2 \quad 0.4 \quad 0.6 \quad 0.8 \quad r^2\]
\[\text{DLG4} \quad \text{ACADVL} \quad \text{MIR324} \quad \text{DVL2} \quad \text{PHF23} \quad \text{GABARAP} \quad \text{CTDNEP1} \quad \text{ELP5} \quad \text{CLDN7} \quad \text{SLC2A4} \quad \text{ACAP1} \quad \text{KCTD11} \quad \text{TMEM95} \quad \text{TNK1} \quad \text{PLSCR3} \quad \text{TMEM256−PLSCR3} \quad \text{TMEM256} \quad \text{NLGN2} \quad \text{SPEM1} \quad \text{C17orf74} \quad \text{FGF11} \quad \text{ZBTB4} \quad \text{SLC35G6} \quad \text{POLR2A} \quad \text{TNFSF12} \quad \text{TNFSF12−TNFSF13} \quad \text{TNFSF13} \quad \text{SENP3} \quad \text{SENP3−EIF4A1} \quad \text{EIF4A1} \quad \text{SNORA48} \quad \text{SNORD10} \quad \text{CD68} \quad \text{FXR2} \quad \text{TP53} \quad \text{WRAP53} \quad \text{EFNB3} \quad \text{DNAH2} \quad \text{RPL29P2} \quad \text{KDM6B} \quad \text{TMEM88} \quad \text{NAA38} \quad \text{CYB5D1} \quad \text{CHD3} \quad \text{SCARNA21} \quad \text{LOC284023} \quad \text{KCNAB3} \quad \text{TRAPPC1} \quad \text{CNTROB} \quad \text{GUCY2D} \quad \text{ALOX15B} \quad \text{ALOX12B} \quad \text{MIR4314} \quad \text{ALOXE3} \quad \text{HES7} \quad \text{PER1} \quad \text{MIR6883} \quad \text{VAMP2} \quad \text{TMEM107} \quad \text{MIR4521} \quad \text{C17orf59} \quad 7.2 \quad 7.4 \quad 7.6 \quad 7.8 \quad 8 \quad \text{Position on chr17 (Mb)} \quad \text{Plotted SNPs}\\
\[\text{rs7121986} \quad 0.2 \quad 0.4 \quad 0.6 \quad 0.8 \quad r^2\]
\[\text{NCAM1} \quad \text{NCAM1−AS1} \quad \text{TTC12} \quad \text{ANKK1} \quad \text{DRD2} \quad \text{MIR4301} \quad \text{TMPRSS5} \quad \text{ZW10} \quad \text{CLDN25} \quad \text{USP28} \quad \text{HTR3B} \quad \text{HTR3A} \quad 113 \quad 113.2 \quad 113.4 \quad 113.6 \quad 113.8 \quad \text{Position on chr11 (Mb)} \quad \text{Plotted SNPs}\\
\[\text{rs71414193} \quad 0.2 \quad 0.4 \quad 0.6 \quad 0.8 \quad r^2\]
\[\text{SLC35F4} \quad \text{C14orf37} \quad \text{ACTR10} \quad \text{PSMA3} \quad \text{FLJ31306} \quad \text{ARID4A} \quad \text{TOMM20L} \quad \text{TIMM9} \quad \text{KIAA0586} \quad \text{DACT1} \quad 58.2 \quad 58.4 \quad 58.6 \quad 58.8 \quad 59 \quad \text{Position on chr14 (Mb)} \quad \text{Plotted SNPs}\\
\[\text{rs72768626} \quad 0.2 \quad 0.4 \quad 0.6 \quad 0.8 \quad r^2\]
\[\text{PRKCB} \quad \text{CACNG3} \quad \text{RBBP6} \quad \text{TNRC6A} \quad \text{SLC5A11} \quad \text{ARHGAP17} \quad \text{LOC554206} \quad \text{LOC102723510} \quad \text{LCMT1} \quad \text{LOC100506655} \quad 24.2 \quad 24.4 \quad 24.6 \quad 24.8 \quad 25 \quad \text{Position on chr16 (Mb)} \quad \text{Plotted SNPs}\\
\[\text{rs74424378} \quad 0.2 \quad 0.4 \quad 0.6 \quad 0.8 \quad r^2\]
\[\text{MIR8081} \quad \text{LOC100996590} \quad \text{ZNF462} \quad \text{MIR548Q} \quad 109 \quad 109.2 \quad 109.4 \quad 109.6 \quad 109.8 \quad \text{Position on chr9 (Mb)} \quad \text{Plotted SNPs}\\

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