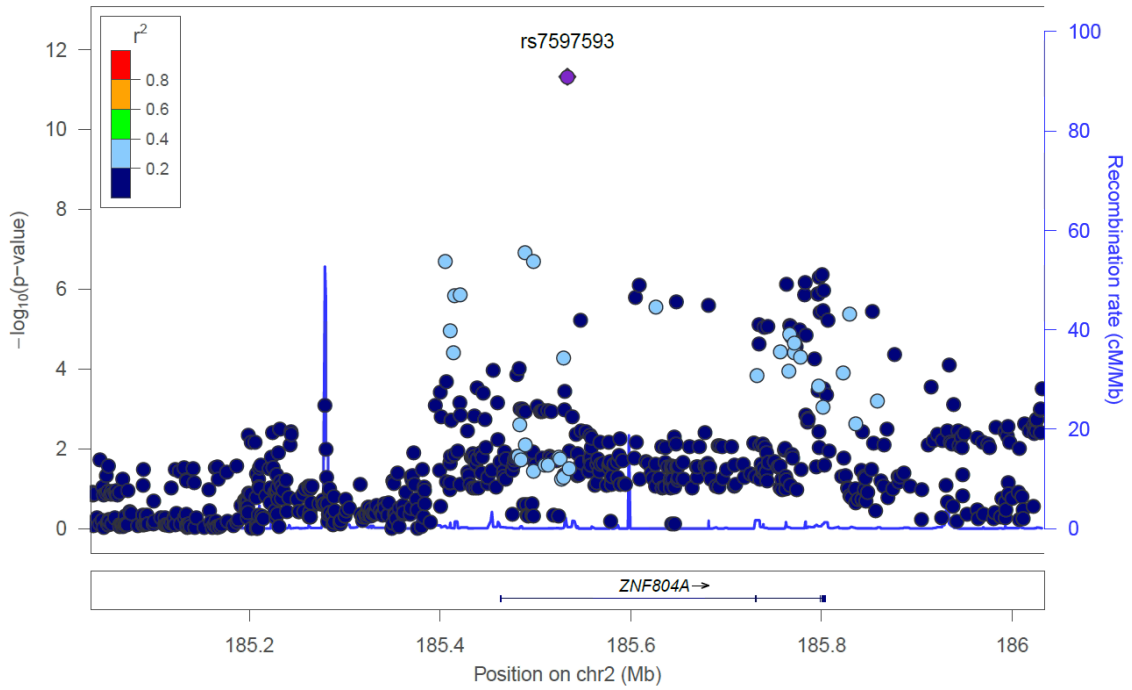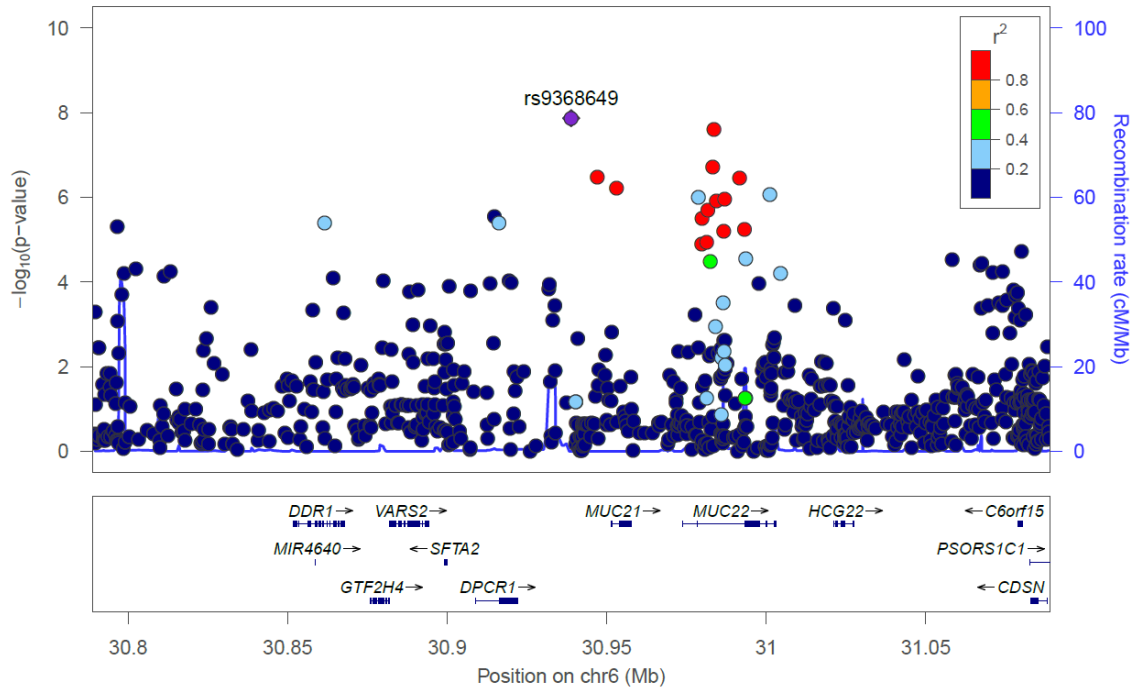Depression_SCZ2014_rs7597593

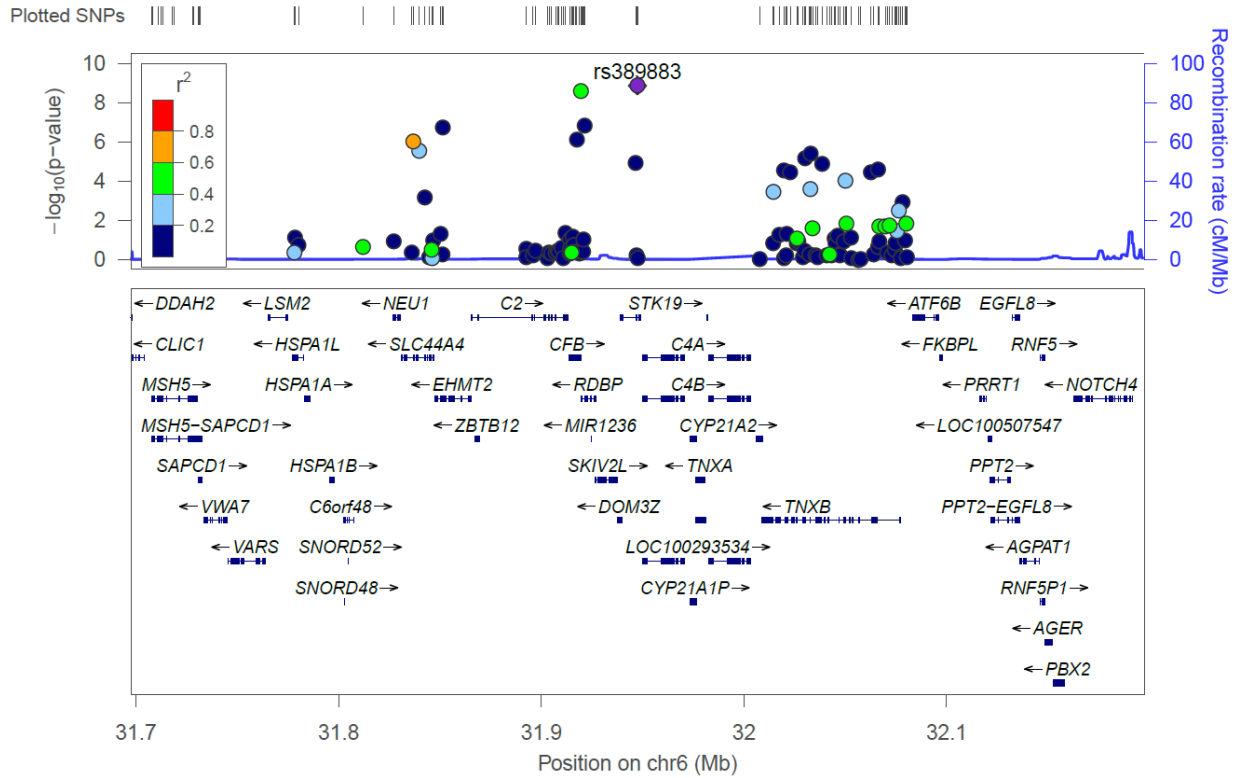MDD23andme_depression_joint_analysis_rs9368649
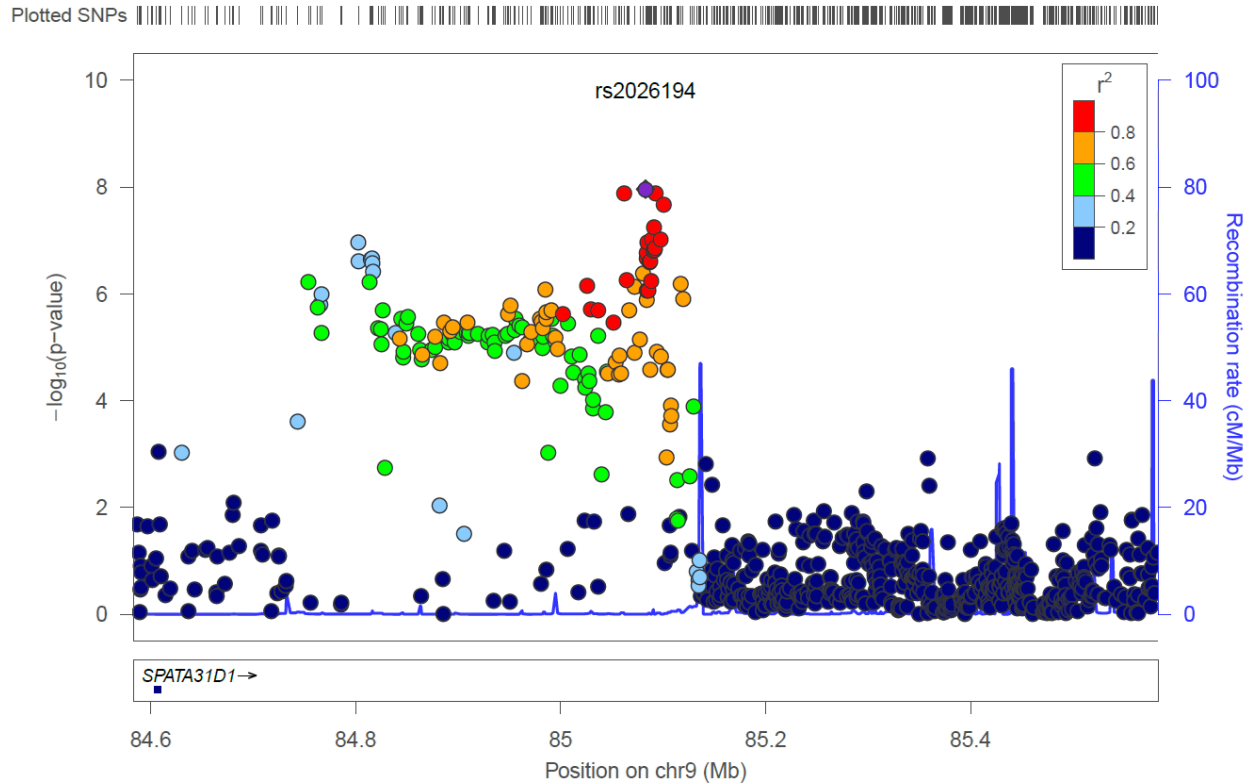
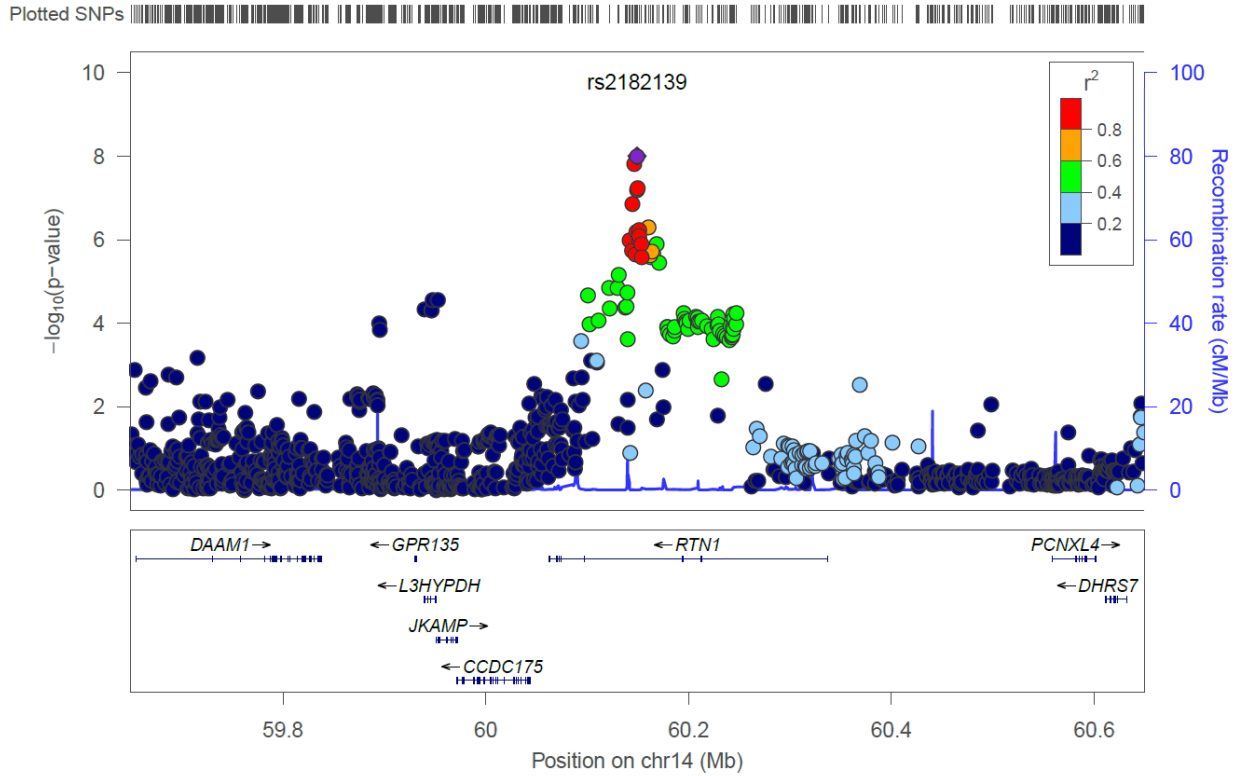Depression_SCZ2014_rs911186

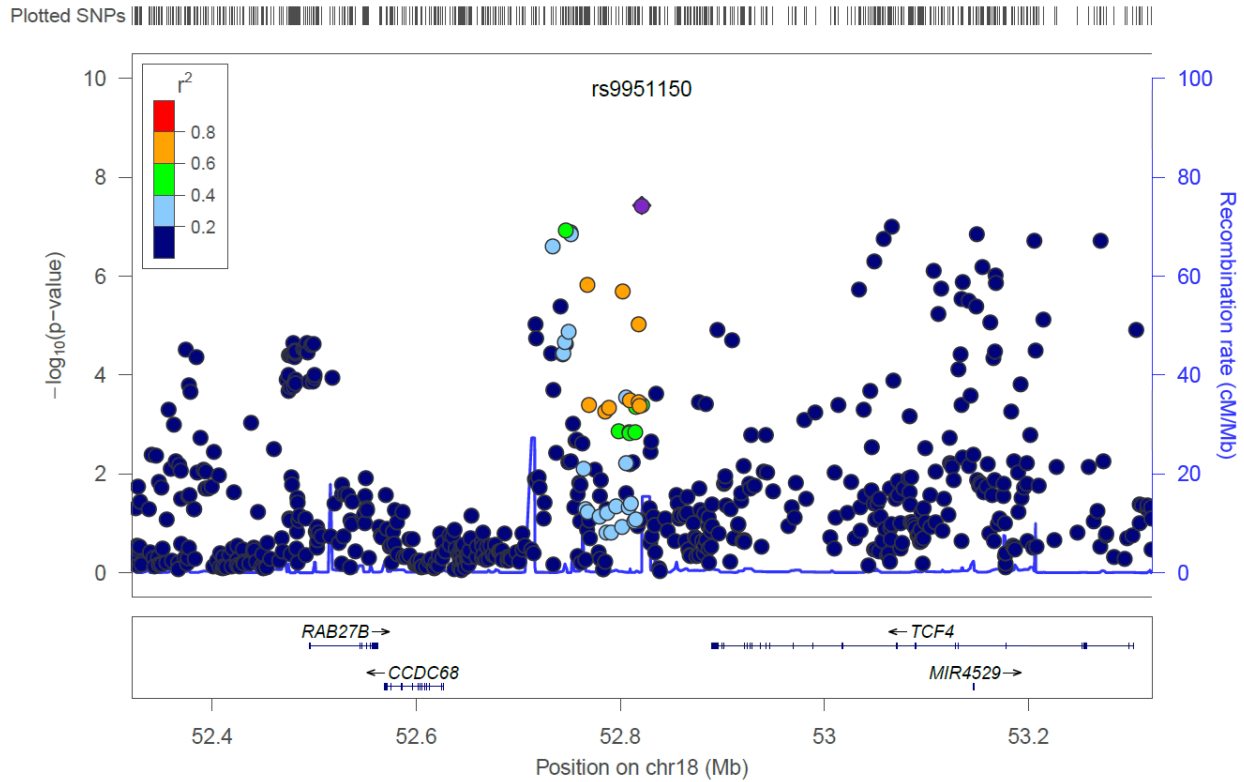Depression_SCZ2014_rs1265099

Depression_SCZ2014_rs389883

Depression_SCZ2014_rs2026194

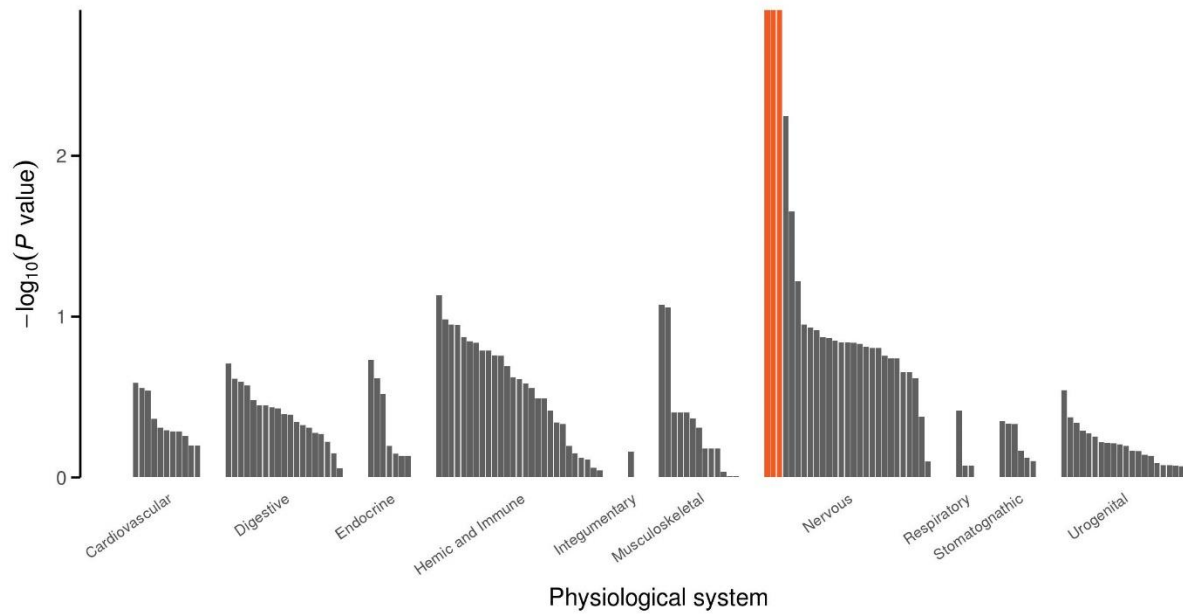# Depression_SCZ2014_rs2182139

Depression_SCZ2014_rs9951150

Supplementary Figure 1: Regional association plots of the eight genetic loci novel for depression from the 13 replicated gSNPs
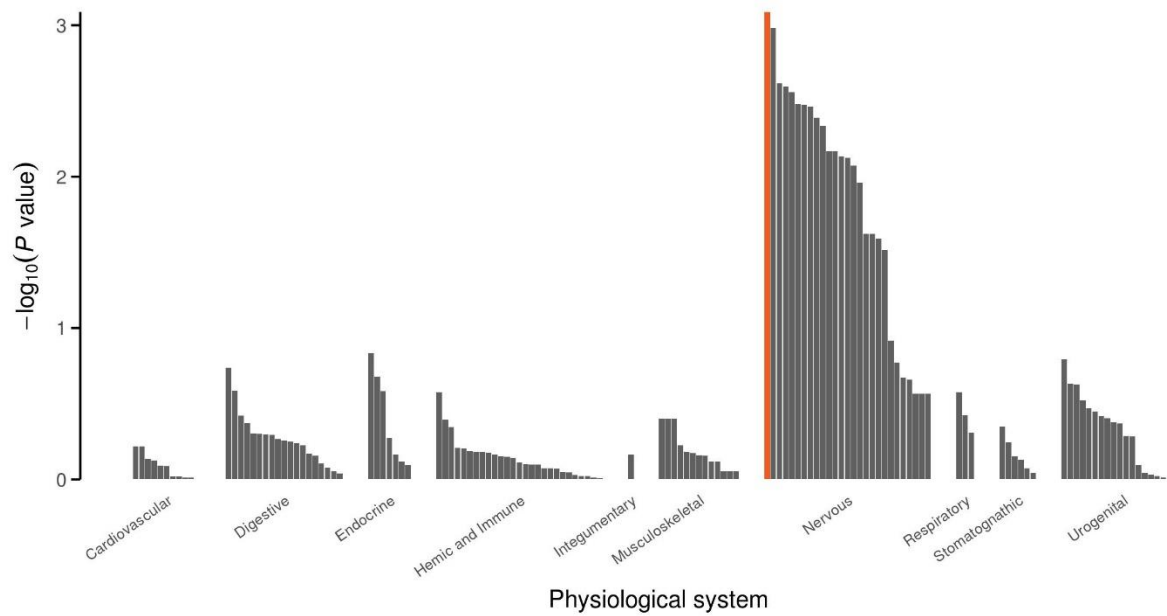
NOTE: The lead SNP and the psychiatric traits are indicated in the top line. In the plots rs-numbers of the lead SNPs are given. Color coding reflects the LD (r^2) of the SNP with this lead SNP according to the legend. The left y-axis represents -log10(p-value) of association; the right y-axis indicates recombination rate. The x-axis depicts the position on the chromosome (Mb) and lists known genes near the locus.

Abbreviations: SCZ2014: Schizophrenia 2014 GWAS study, MDD23andme: self-reported MDD from 23andme GWAS study.

a)

b)

Supplementary Figure 2: DEPICT results of tissue/cell type enrichment analysis using bivariate GWAS analyses of the broad depression phenotype with **a)** schizophrenia, and; **b)** self-reported MDD. The red bars are significant (FDR<0.05).