

Genome-wide cross-trait analysis of vascular dementia and Alzheimer's disease highlights novel loci and lung-brain axis

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Supplementary Figures

Supplementary Figure 1. Quantile-quantile (Q-Q) plots for the GWAS meta-analysis of vascular dementia.

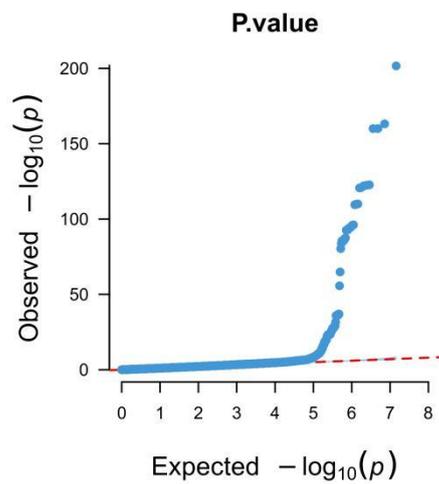
Supplementary Figure 2. Regional association plots for three significant locus from the European-specific GWAS meta-analysis of vascular dementia (Stage 1).

Supplementary Figure 3. Regional association plots for three significant locus from the Cross-ancestry GWAS meta-analysis of vascular dementia (Stage 2).

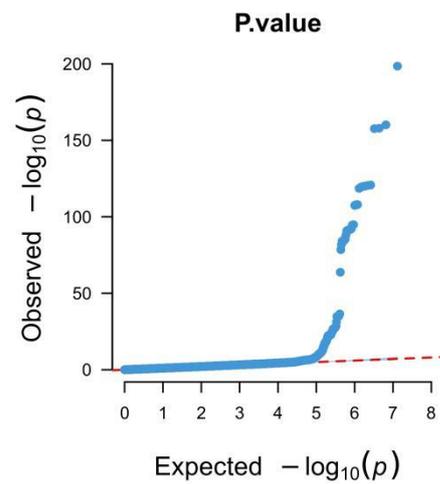
Supplementary Figure 4. Box plot of genes from differential expression analysis using GSE282111.

Supplementary Figure 1. Quantile-quantile (Q-Q) plots for the GWAS meta-analysis of vascular dementia. A) Q-Q plot for association with vascular dementia in Stage 1, Genomic inflation factor (λ_{GC}) = 1.0754, B) Q-Q plot for association with vascular dementia in Stage 2, λ_{GC} = 1.0742. The horizontal axis shows $-\log_{10} p$ values expected under the null distribution. The vertical axis shows observed $-\log_{10} p$ values. The blue framed line shows the 95% confidence interval.

A.



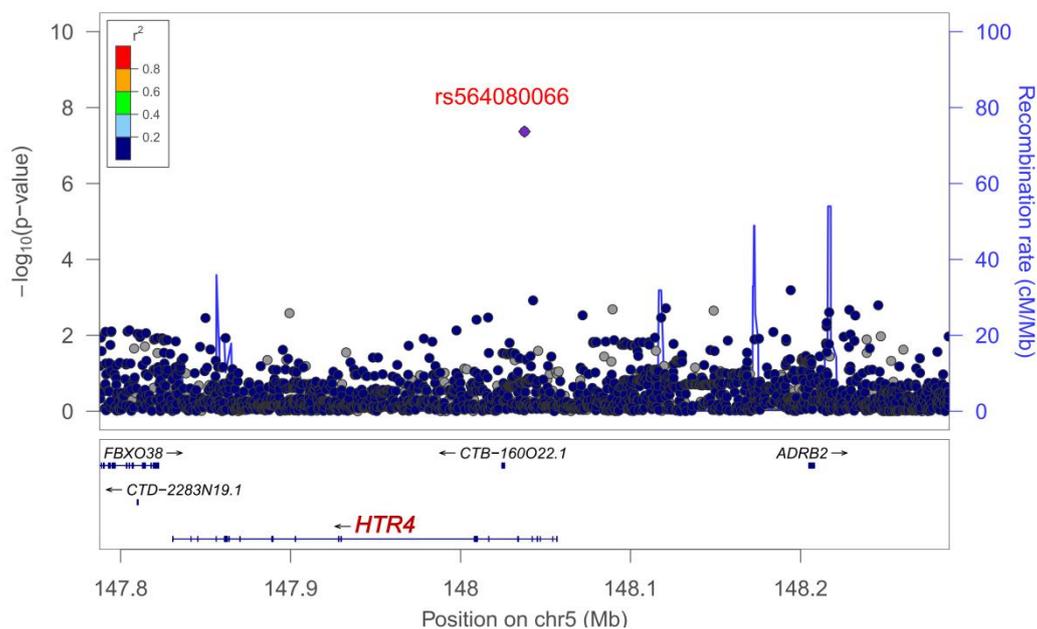
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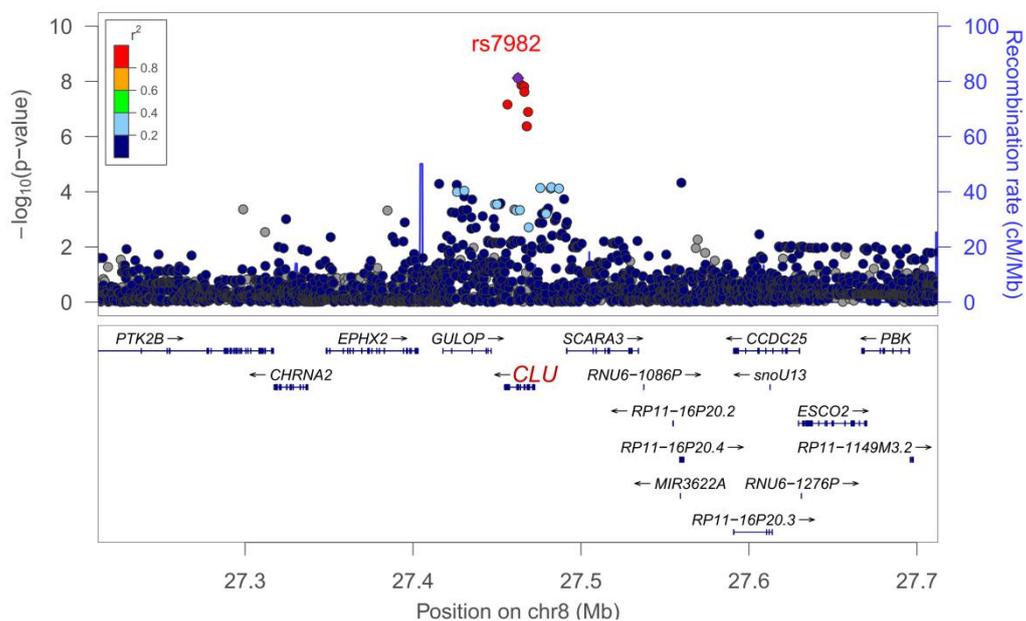
Supplementary Figure 2. Regional association plots for three significant locus from the European-specific GWAS meta-analysis of vascular dementia (Stage 1).

A) rs564080066 is located on *HTR4*, B) rs7982 is located on *CLU*, C) rs429358 is located on *APOE*. The x-axis represents the shows the chromosomal position of SNPs (hg19). The y-axis represents $-\log_{10}$ p-values from two-sided z-tests for meta-analysis effect estimates. LD estimates of surrounding SNPs with the labeled index SNP (LD r^2 values estimated based on the 1000 Genomes Phase 3 European panel) is indicated by color (color bar on side of plot indicates color coding of r^2). Local estimates of recombination rate are indicated in light blue (legend on vertical axis at right). Gene names, strands, and boundaries are shown in the box below the regional plot.

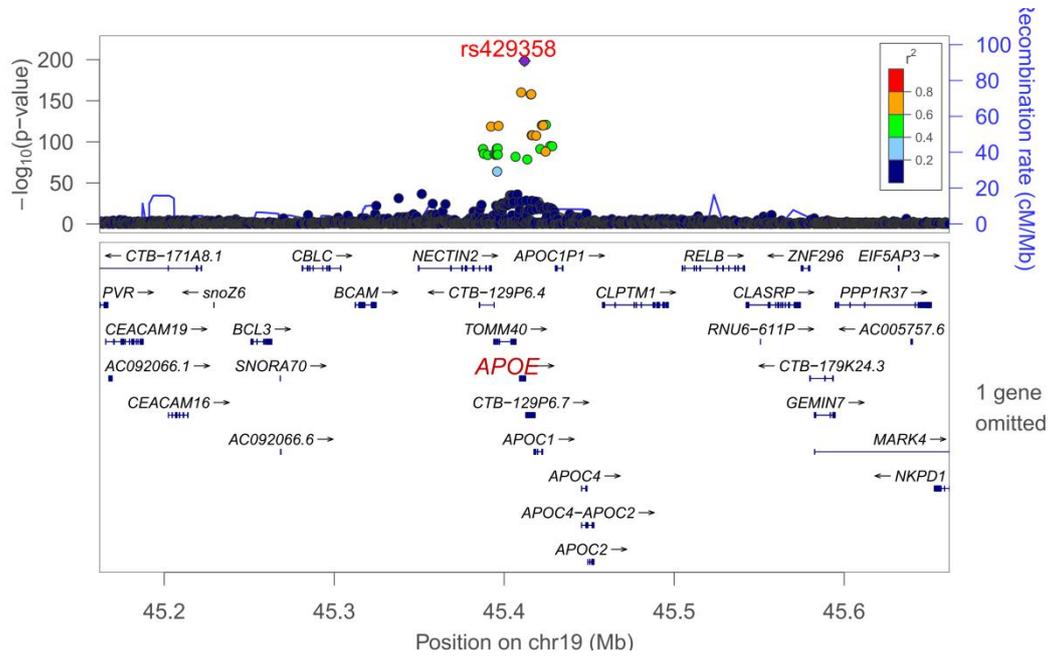
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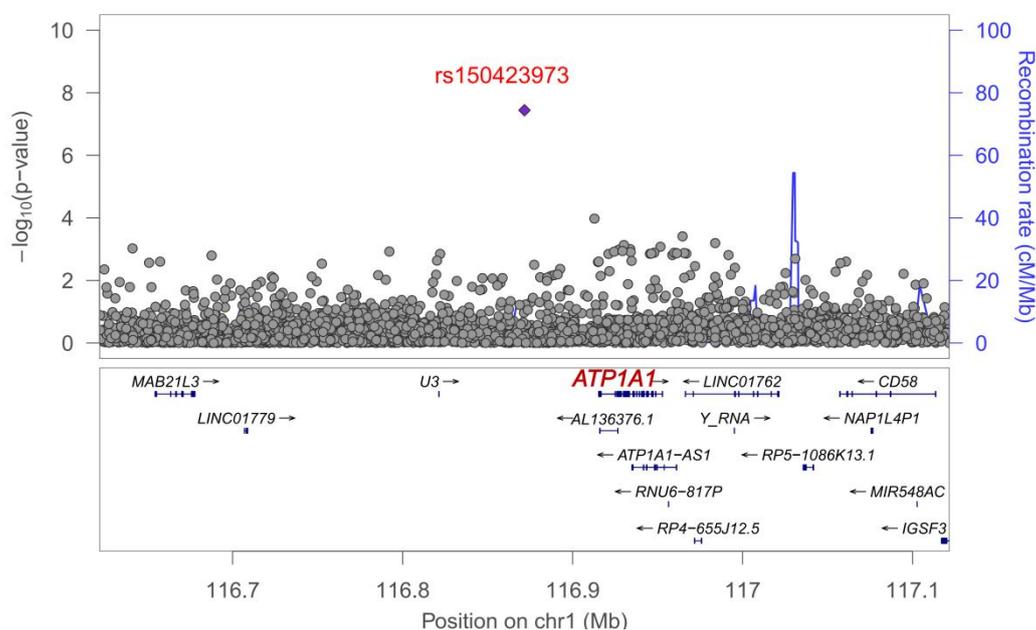


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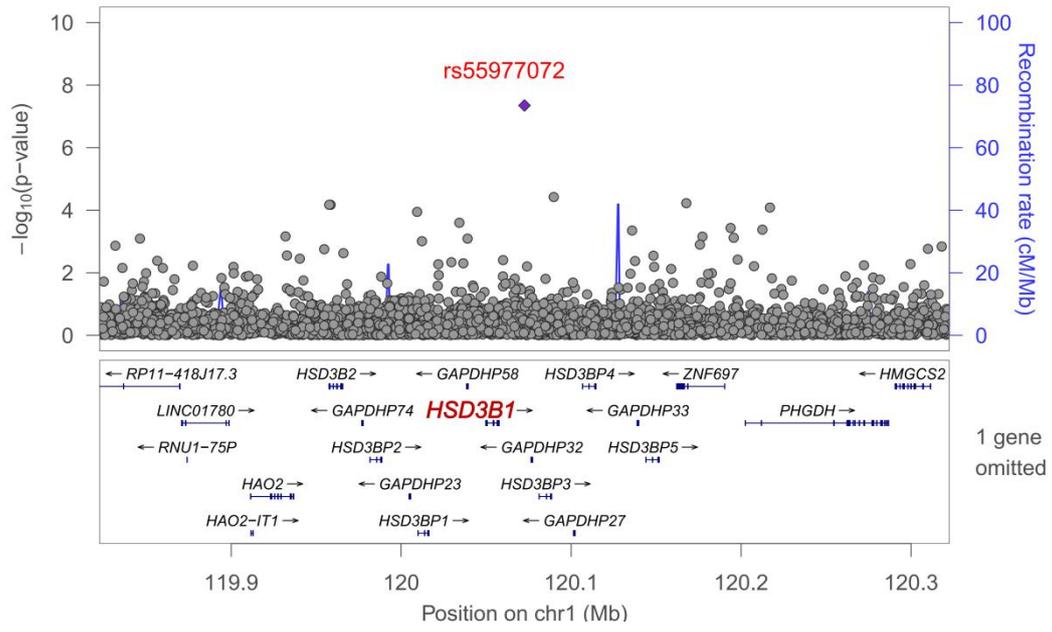


Supplementary Figure 3. Regional association plots for thirty-seven significant locus from the Cross-ancestry GWAS meta-analysis of vascular dementia (Stage 2). A) rs150423973 is located on *ATP1A1*, B) rs55977072 is located on *HSD3B1*, C) rs555863053 is located on *RCS1D1*, D) rs543737714 is located on *RSAD2*, E) rs571573246 is located on *HS6ST1*, F) rs138654898 is located on *UBR3*, G) rs536931879 is located on *CRELD1*, H) rs79120584 is located on *HERC3*, I) rs534723021 is located on *CDH18*, J) rs200249535 is located on *SPZ1*, K) rs563370505 is located on *ADGRV1*, L) rs564080066 is located on *HTR4*, M) rs202007547 is located on *COL12A1*, N) rs542806512 is located on *NT5E*, O) rs576730428 is located on *GTF2H5*, P) rs561189374 is located on *ACTR3C*, Q) rs138507927 is located on *DPP6*, R) rs11136000 is located on *CLU*, S) rs192554851 is located on *ADAMTSL1*, T) rs570028361 is located on *PSAT1*, U) rs546018638 is located on *HPSE2*, V) rs535202922 is located on *ATP5L*, W) rs184836761 is located on *PIWIL1*, X) rs533330090 is located on *TBC1D4*, Y) rs576381927 is located on *ATP11A*, Z) rs527795127 is located on *TMX1*, AA) rs547455871 is located on *ATP10A*, AB) rs183472759 is located on *TMEM87A*, AC) rs146972069 is located on *ADAMTSL7*, AD) rs564332482 is located on *CACNA1H*, AE) rs529505148 is located on *ITFG1*, AF) rs429358 is located on *APOE*, AG) rs78062743 is located on *BPIFA3*, AH) rs573127339 is located on *MROH8*, AI) rs569752694 is located on *CHD6*, AJ) rs575233877 is located on *PTPRT*, AK) rs529401448 is located on *TBC1D22A*.

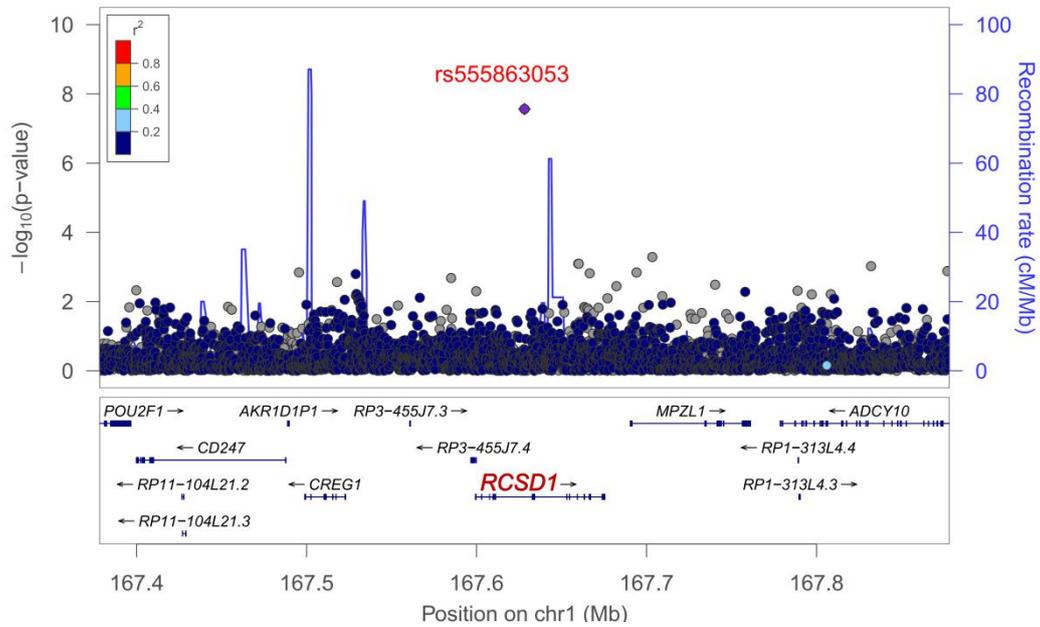
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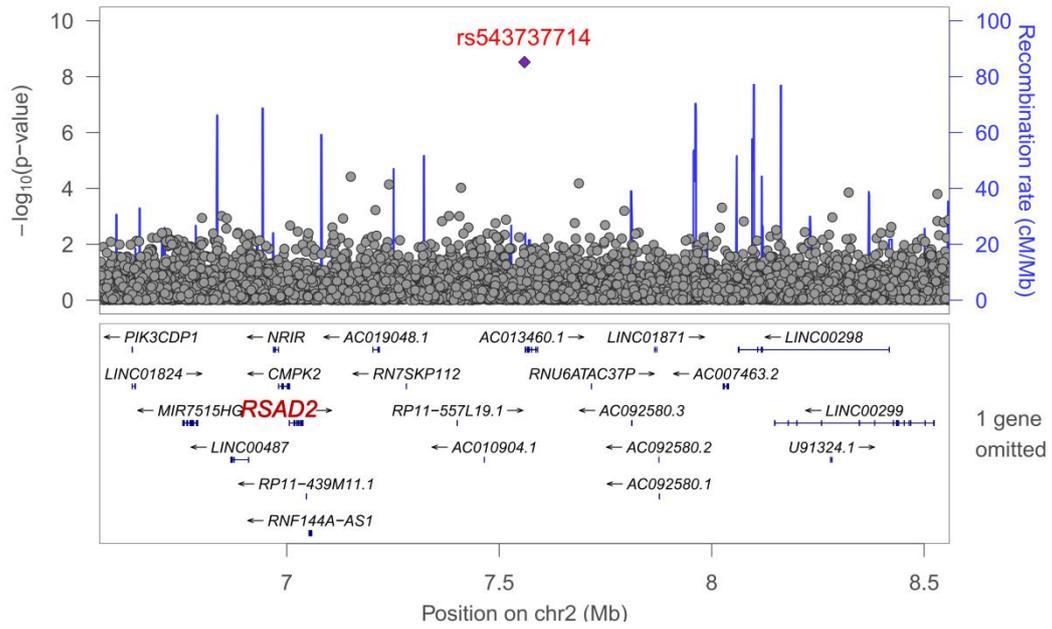
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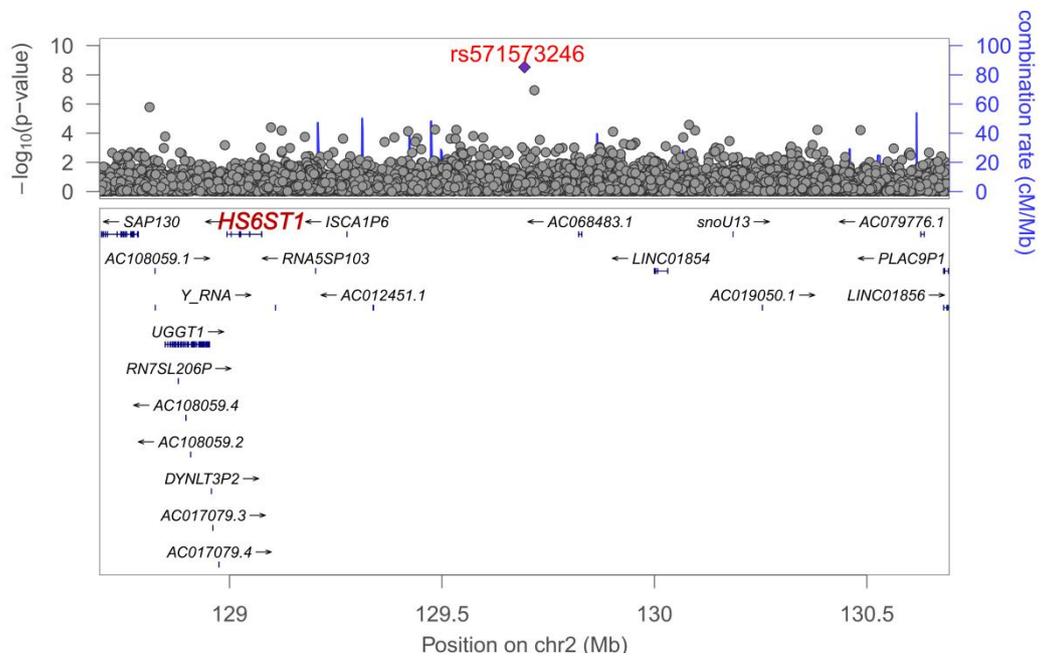
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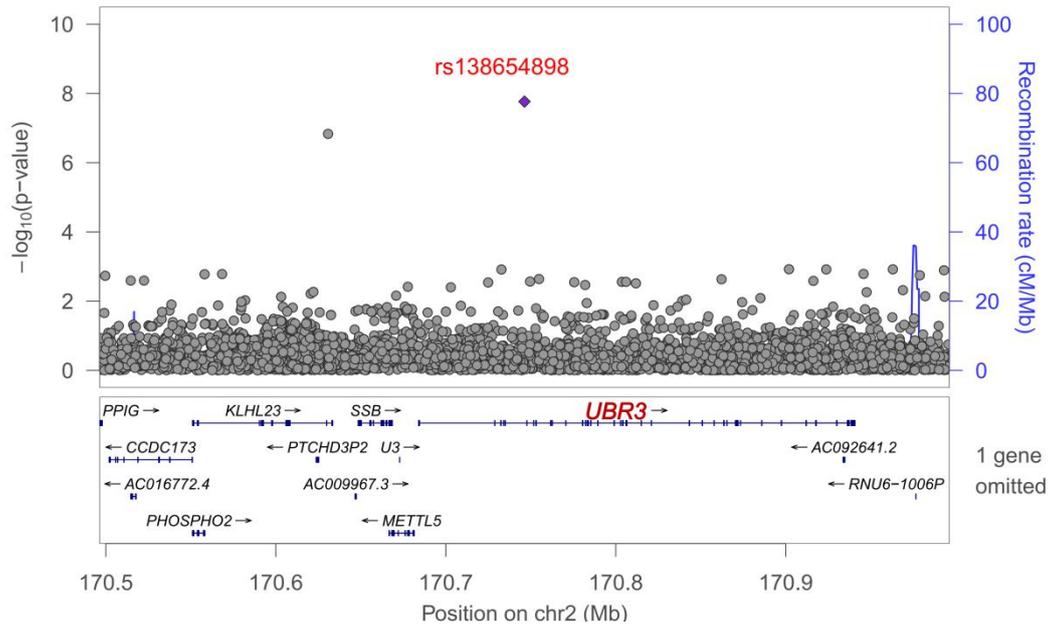
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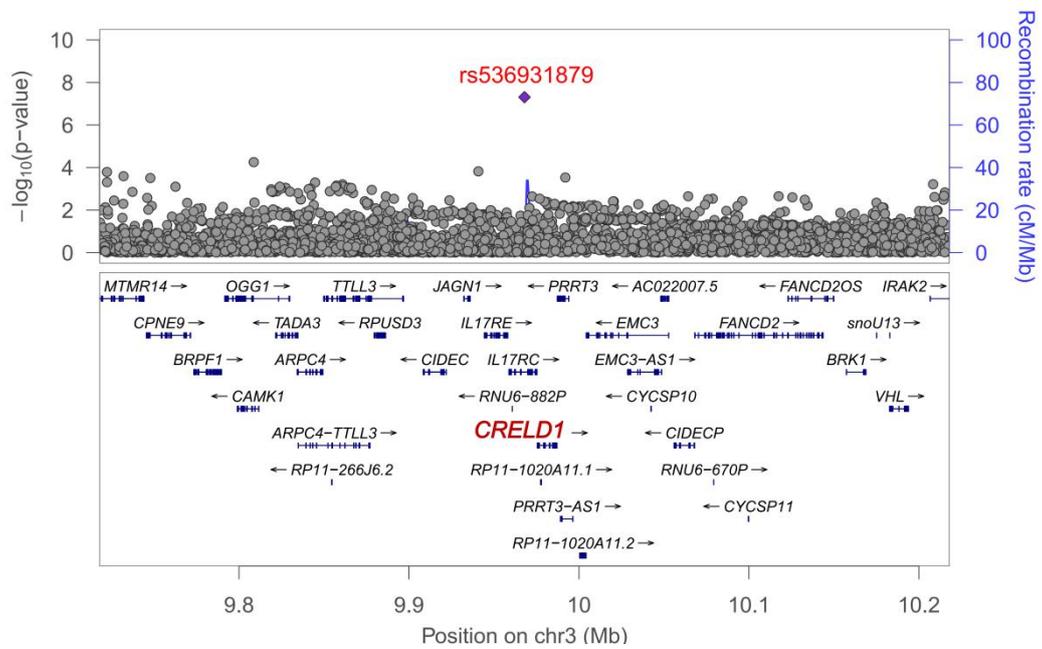
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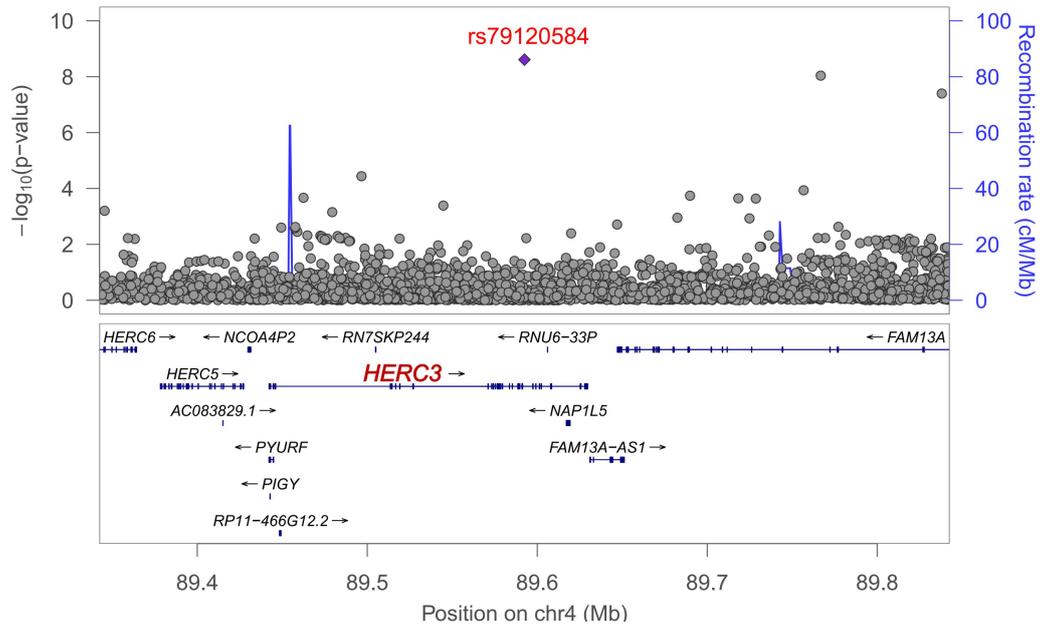
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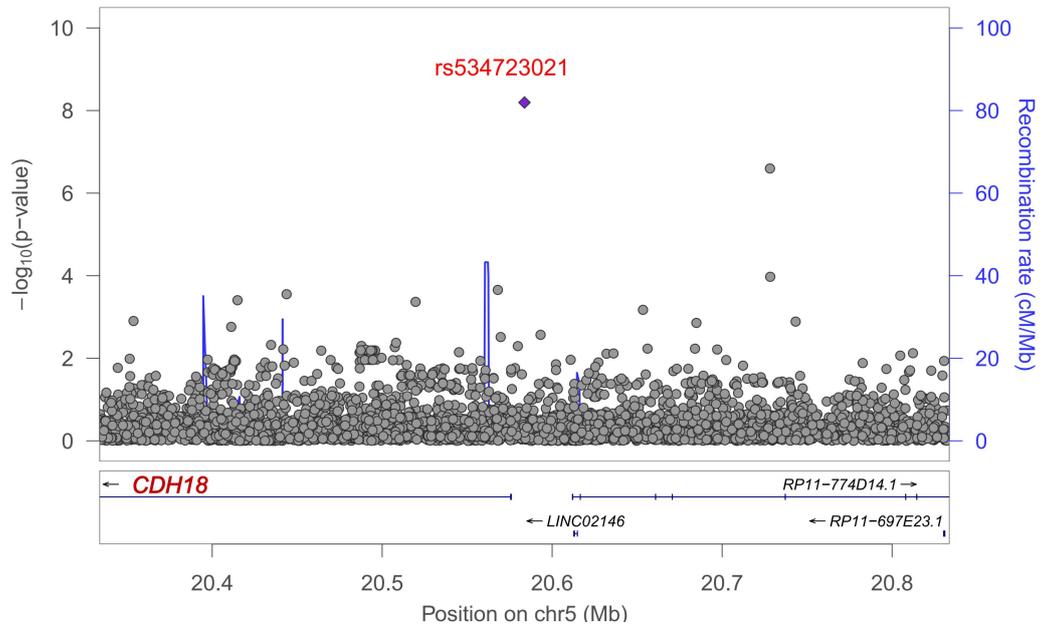
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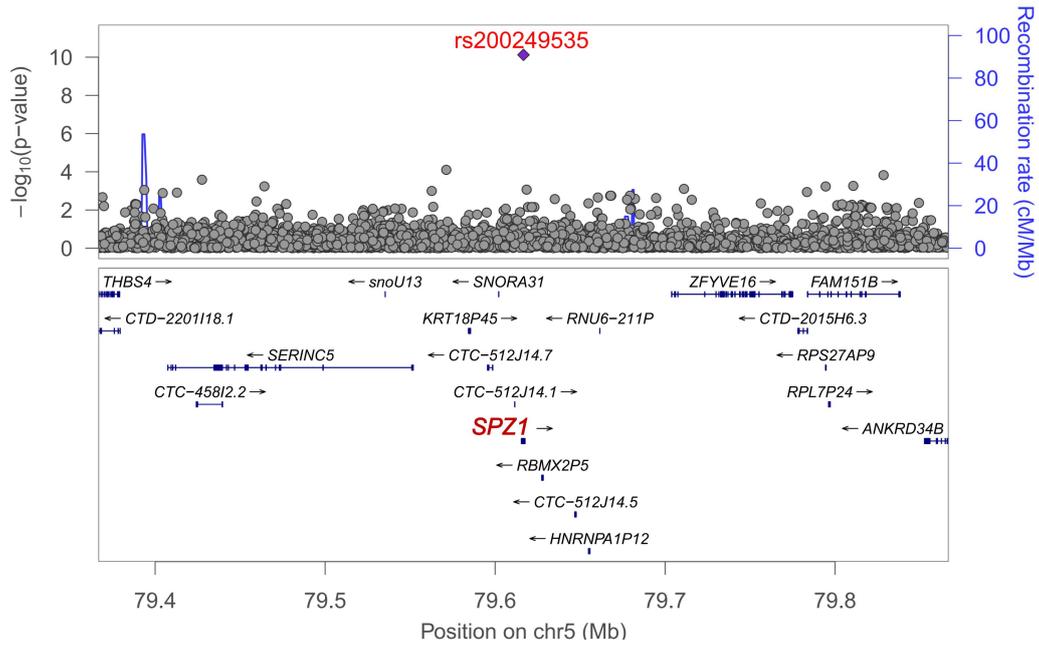
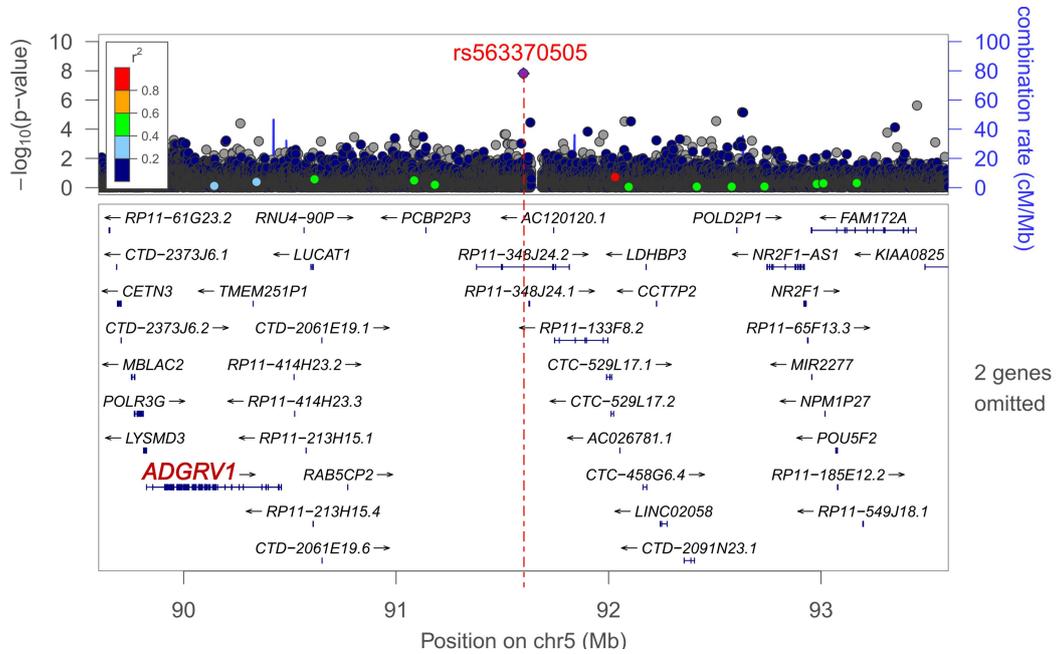


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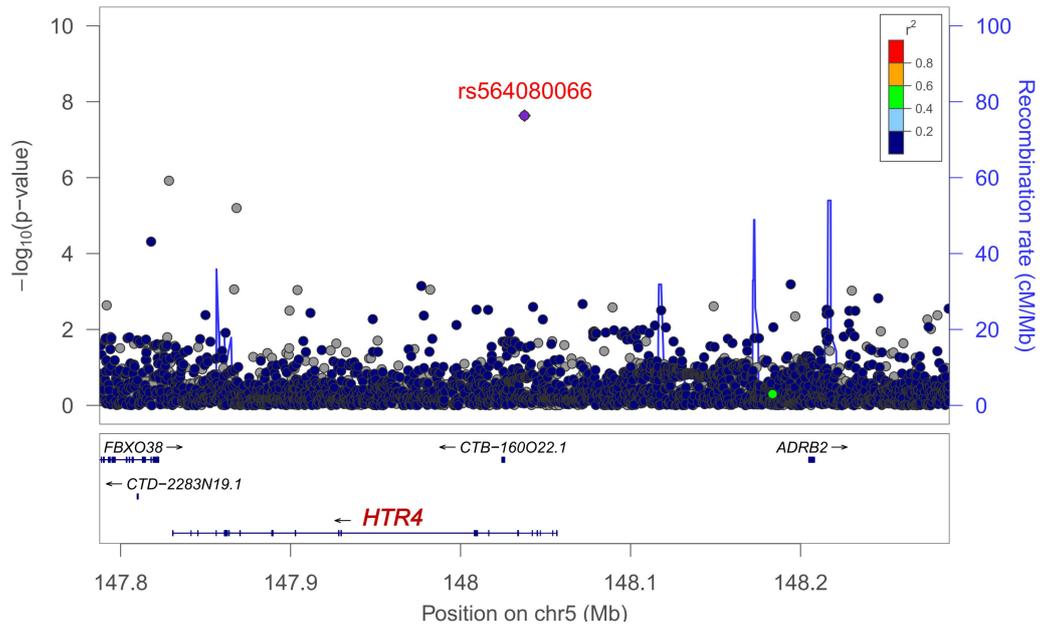


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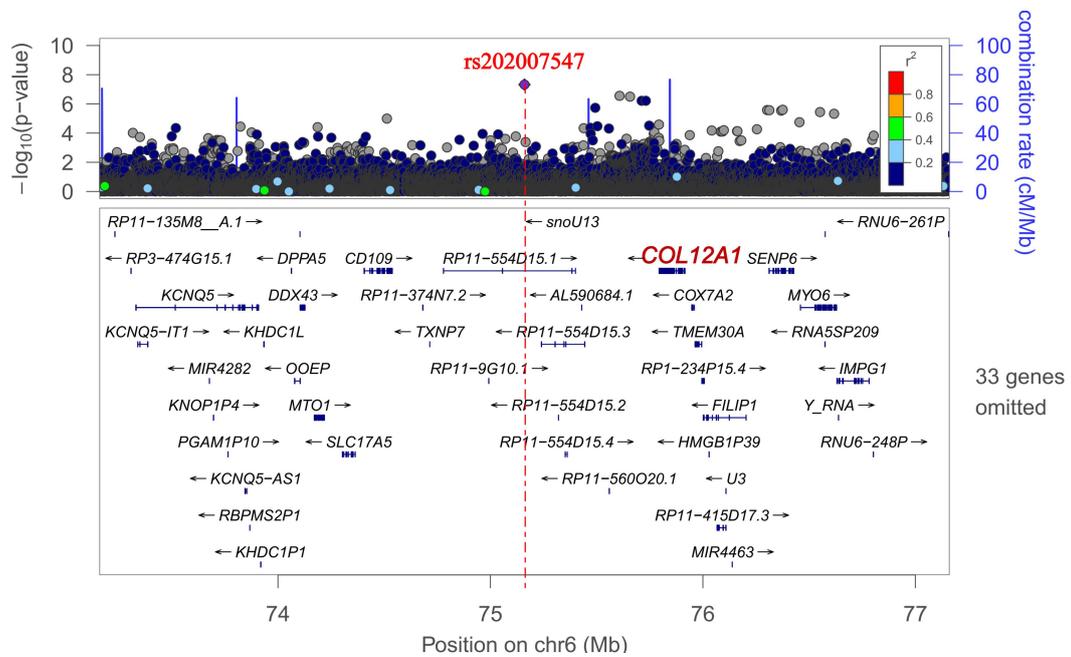


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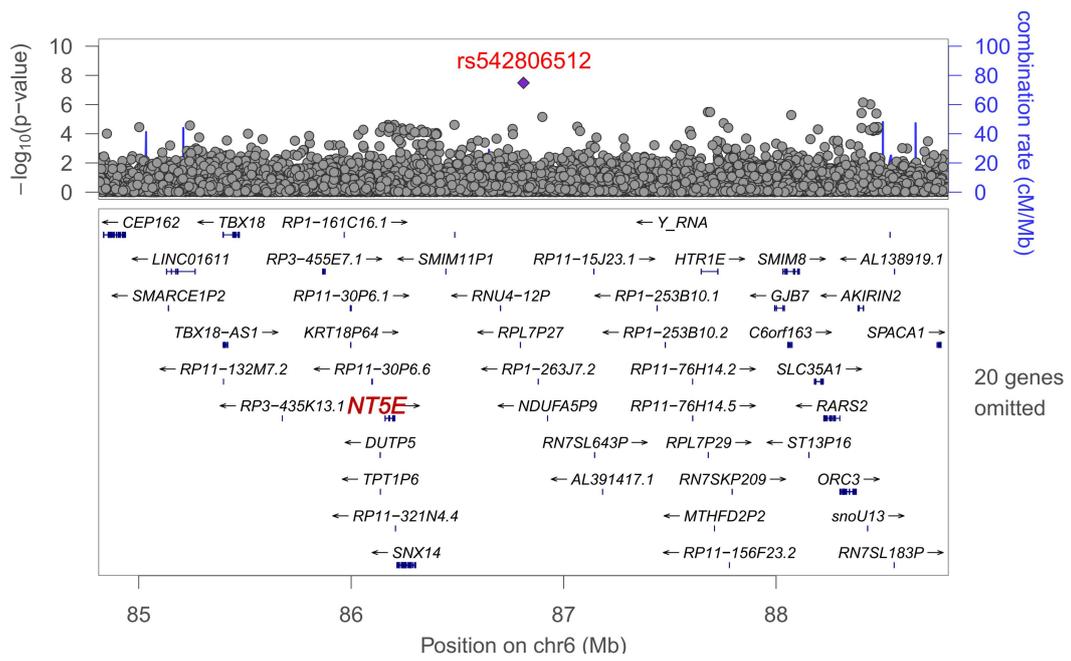
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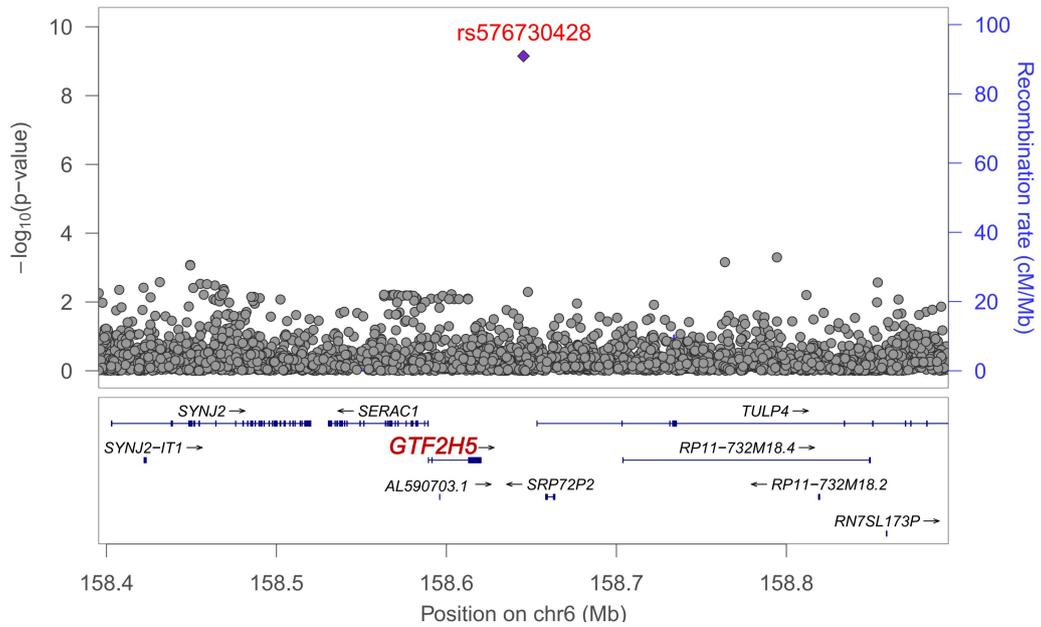
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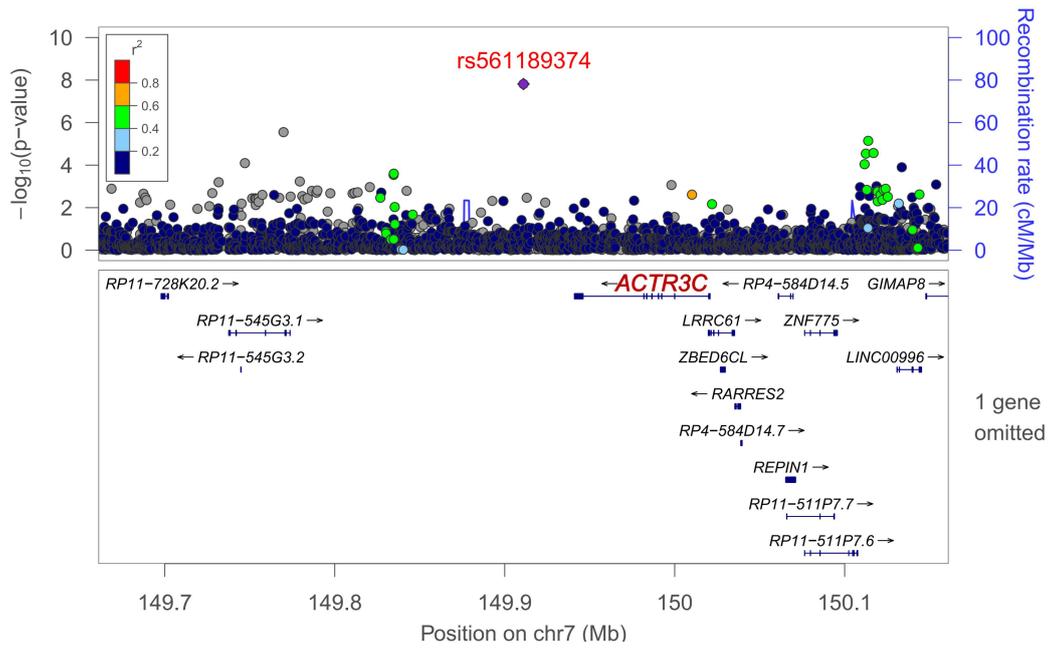
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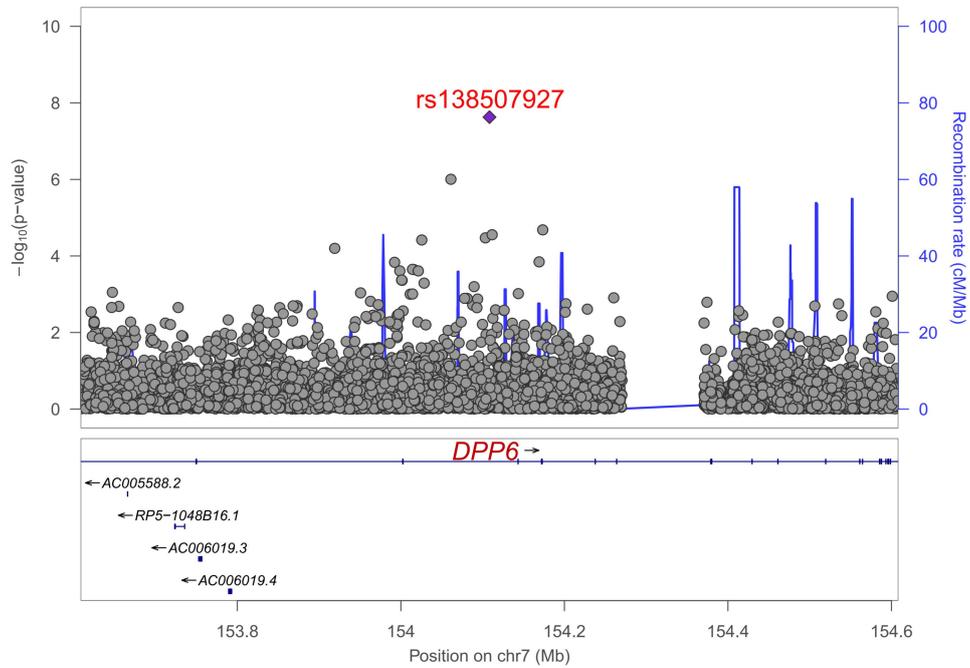
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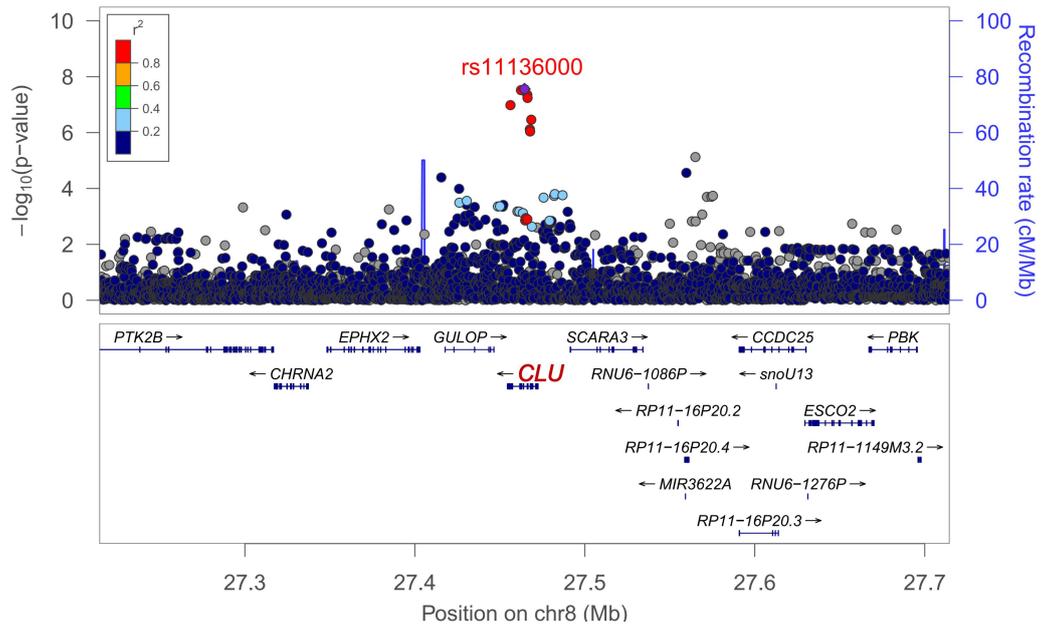
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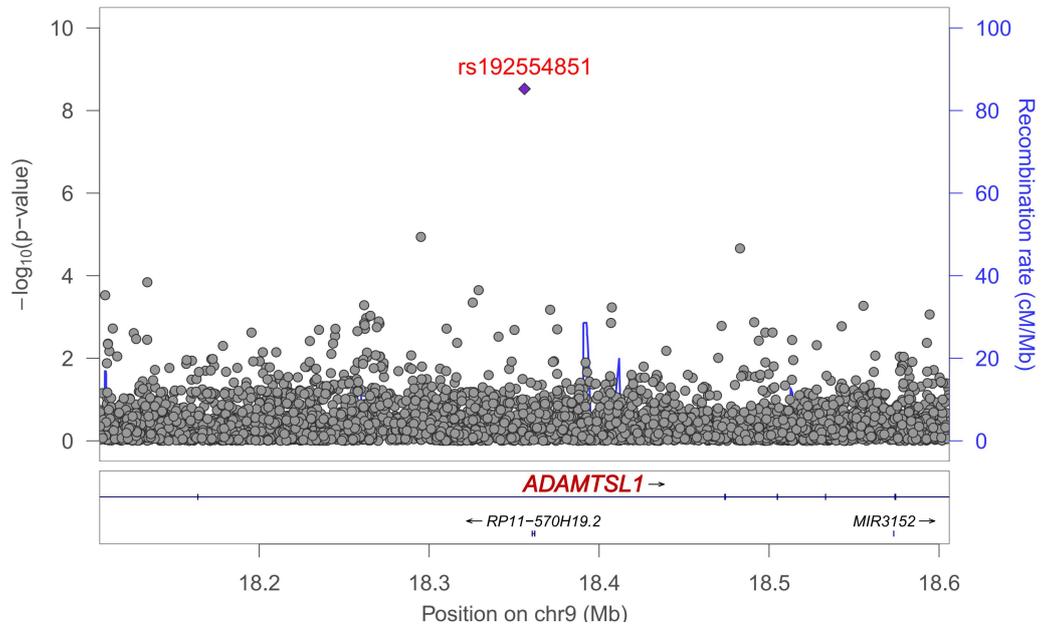
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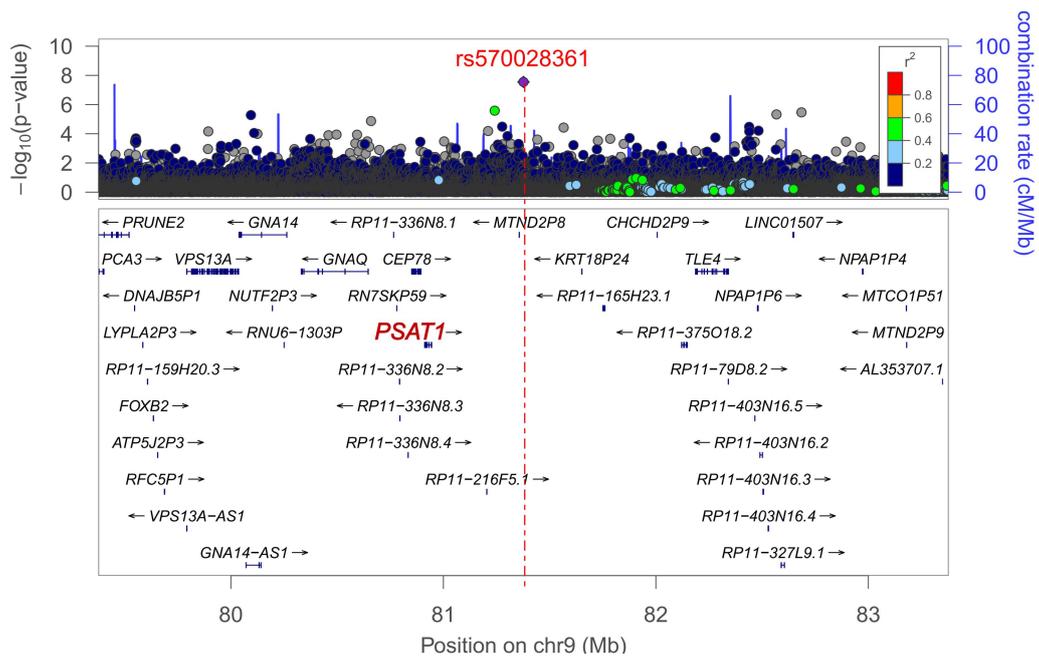
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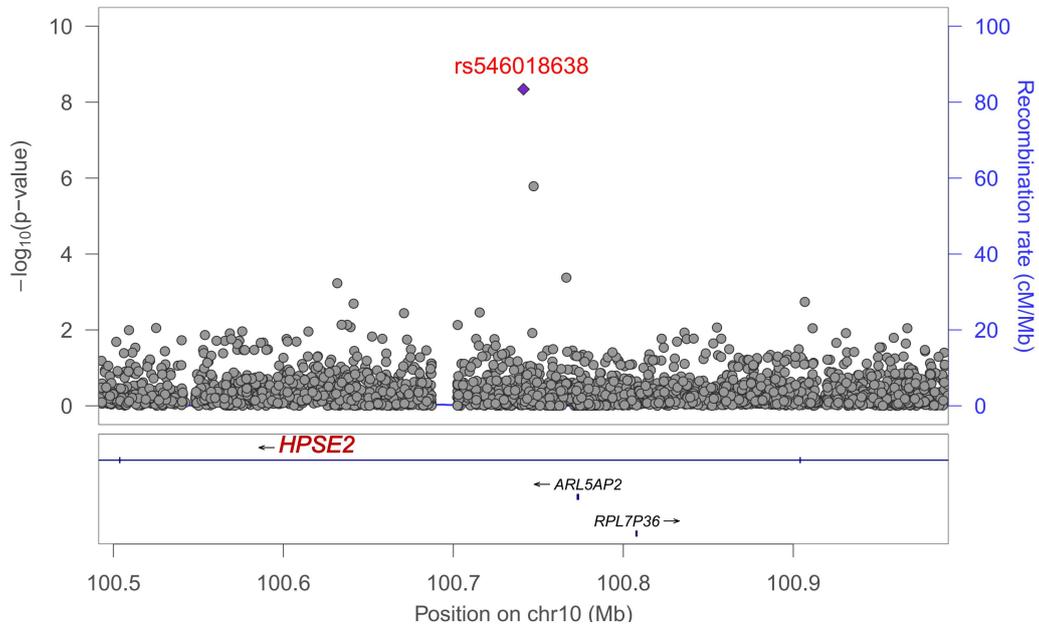
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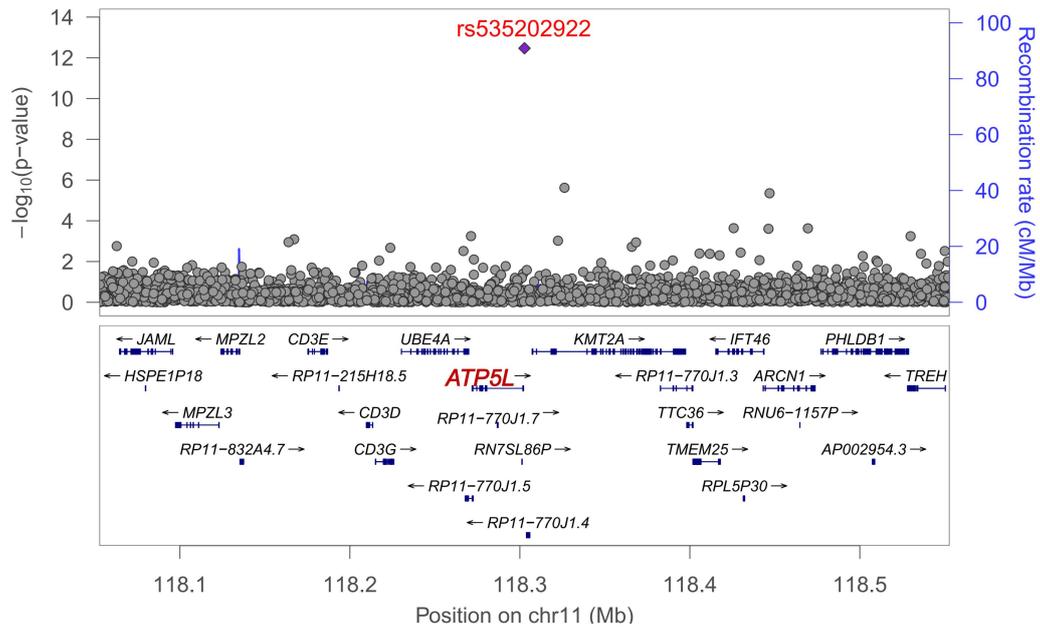
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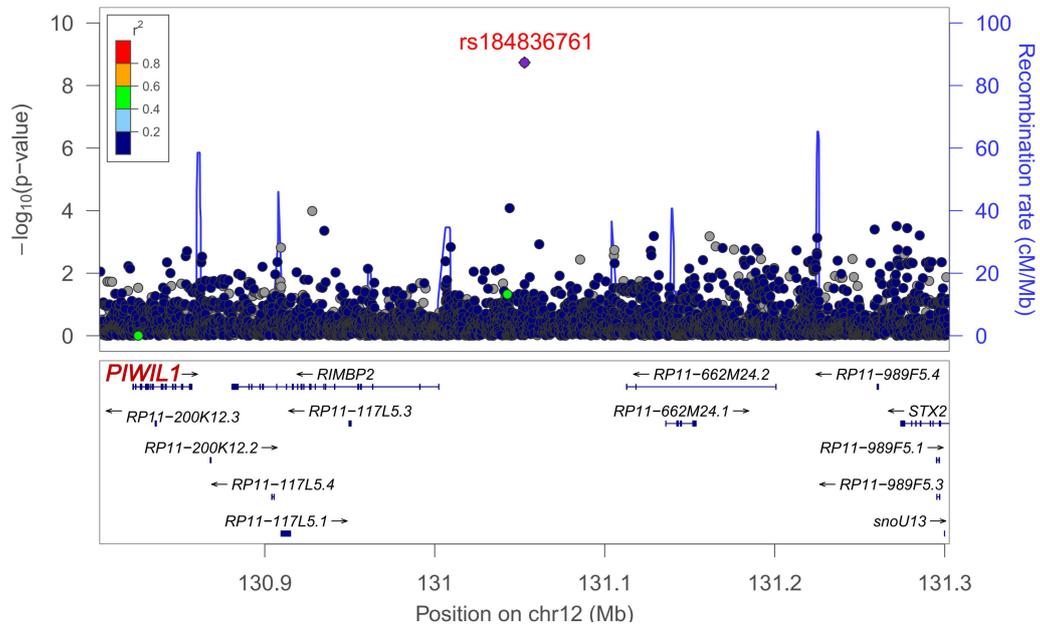
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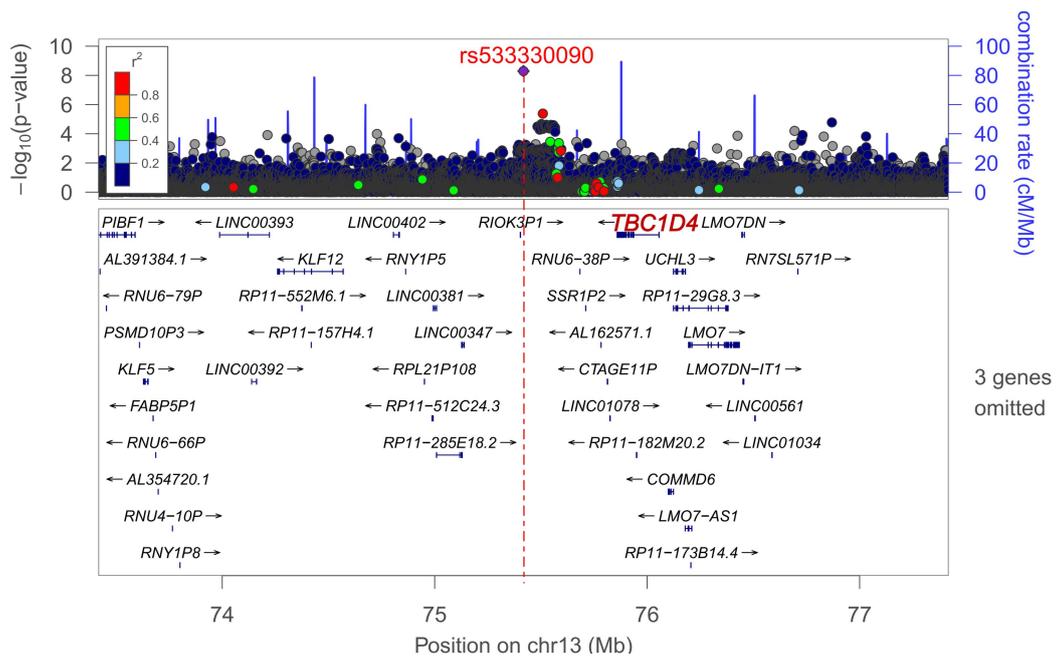
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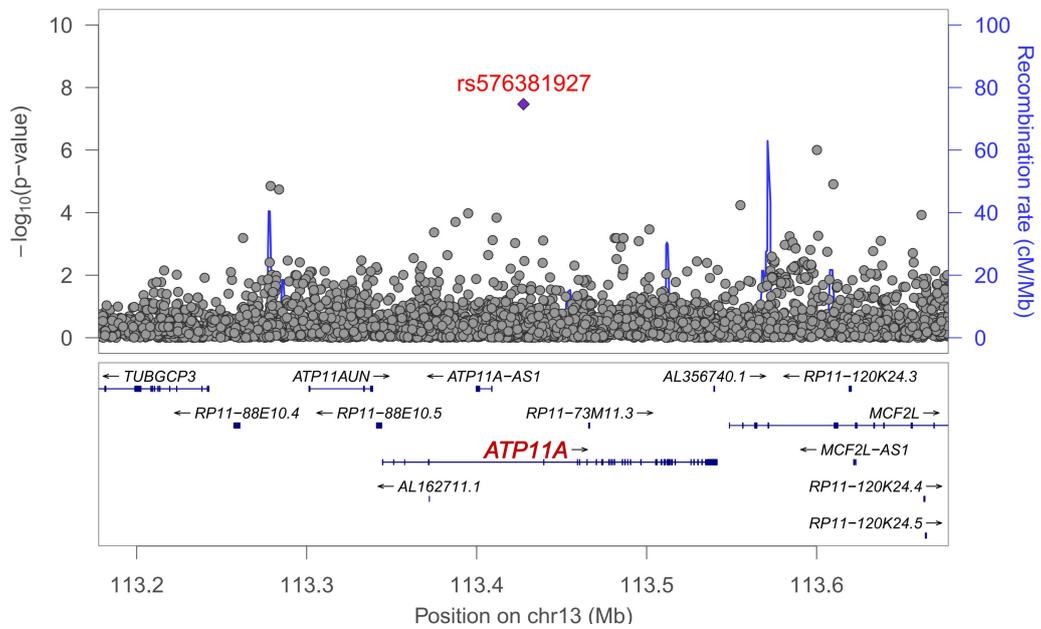
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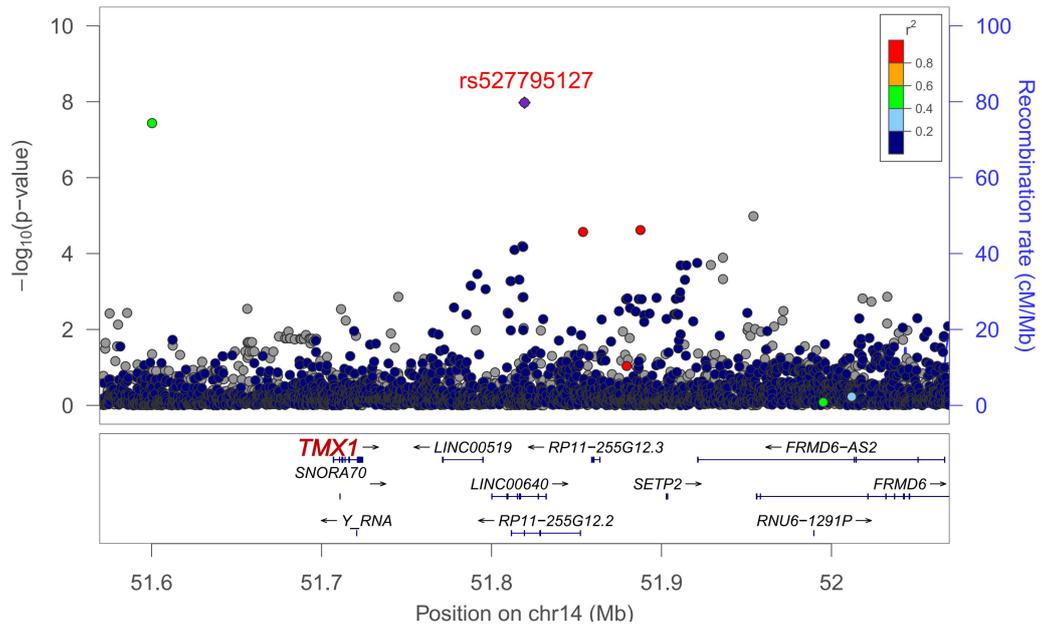
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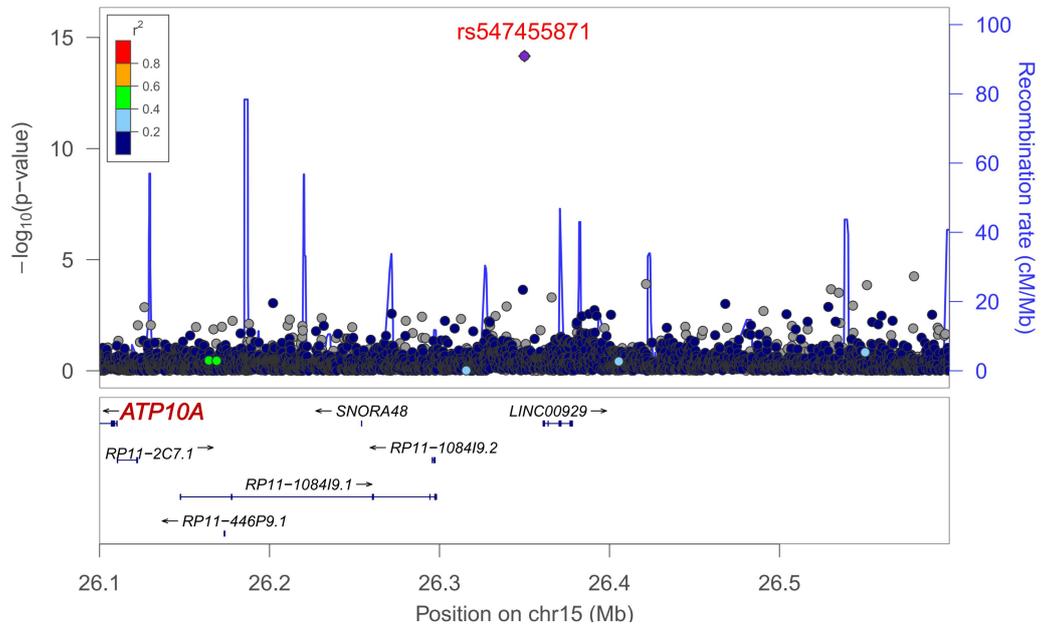
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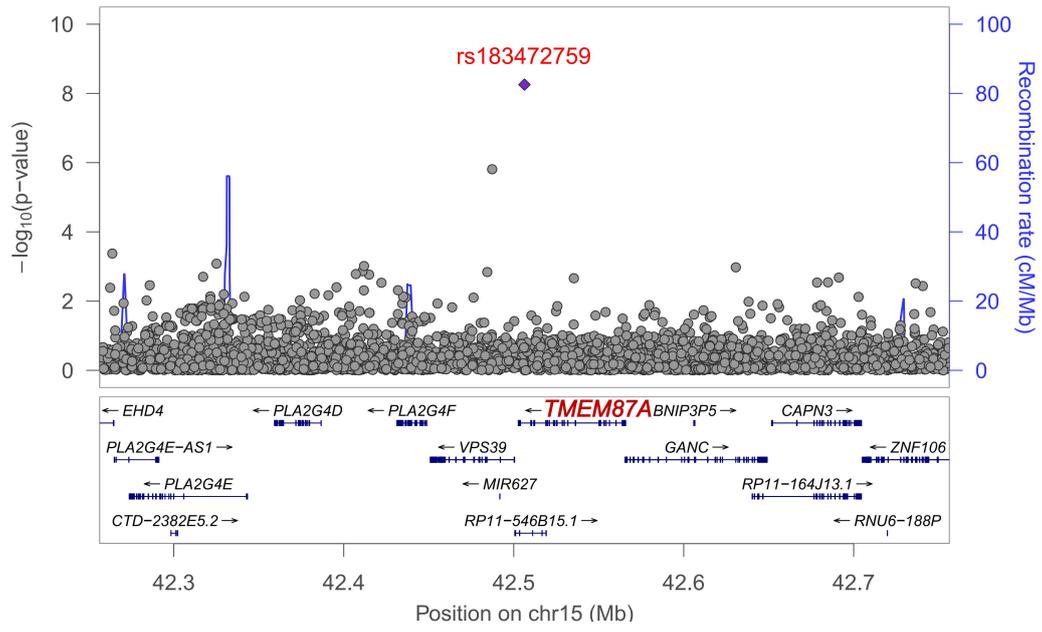
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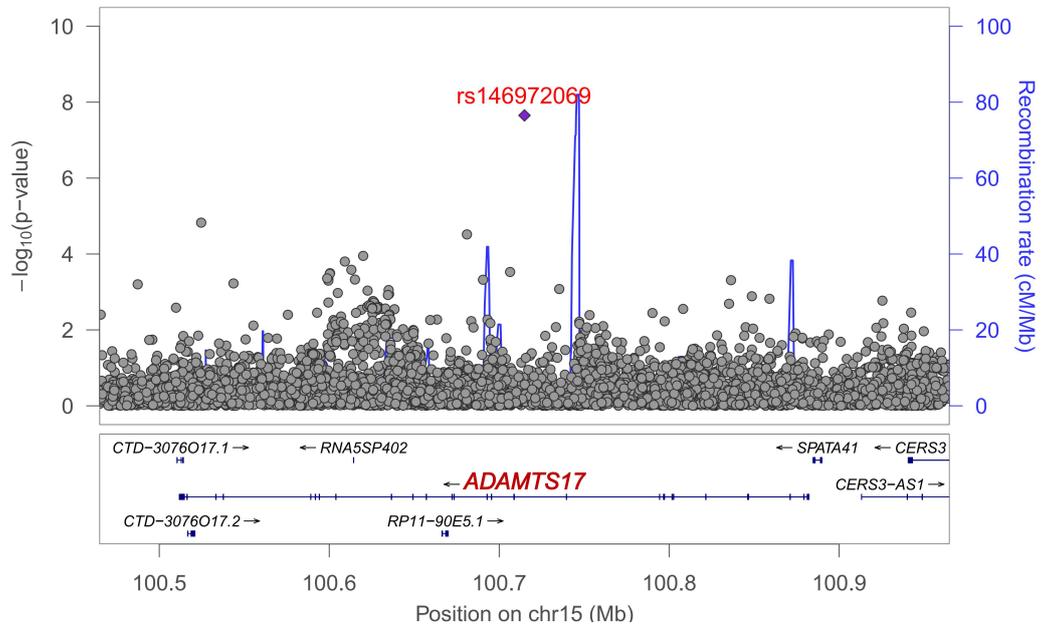
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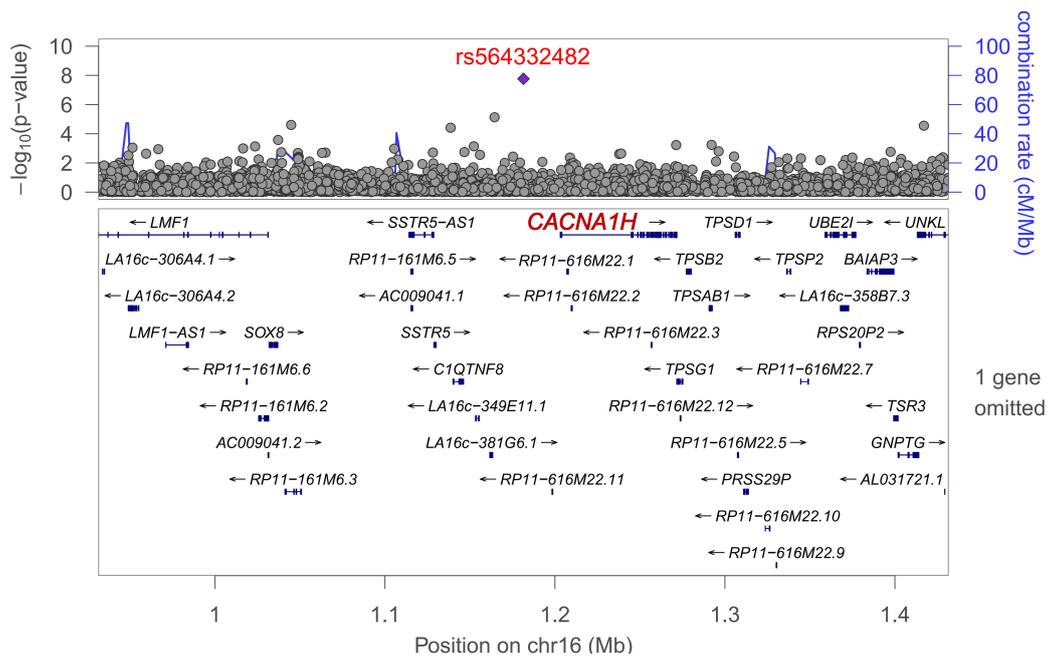
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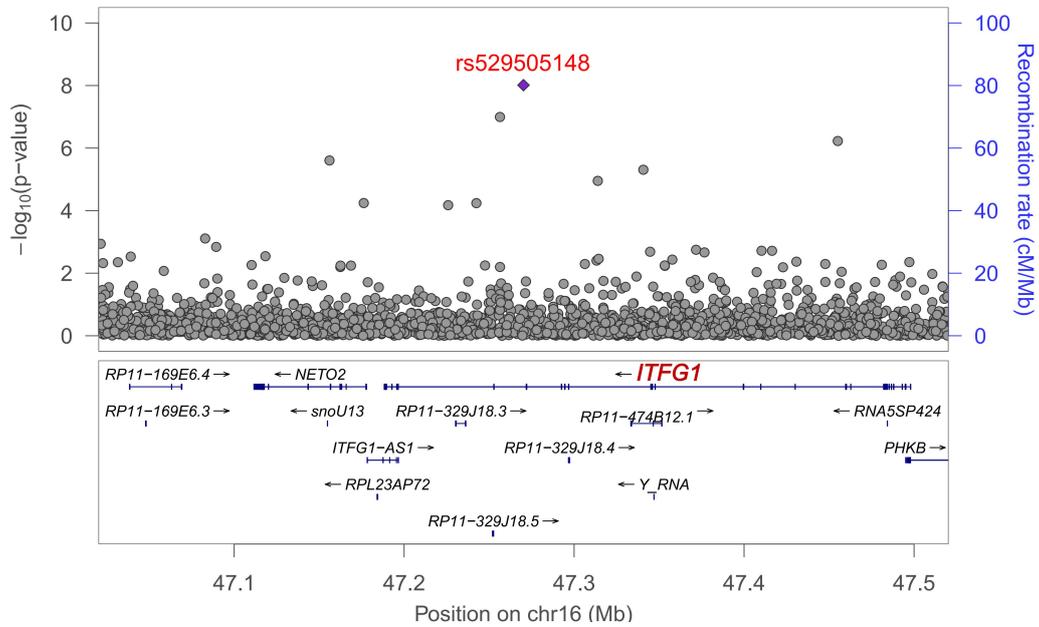
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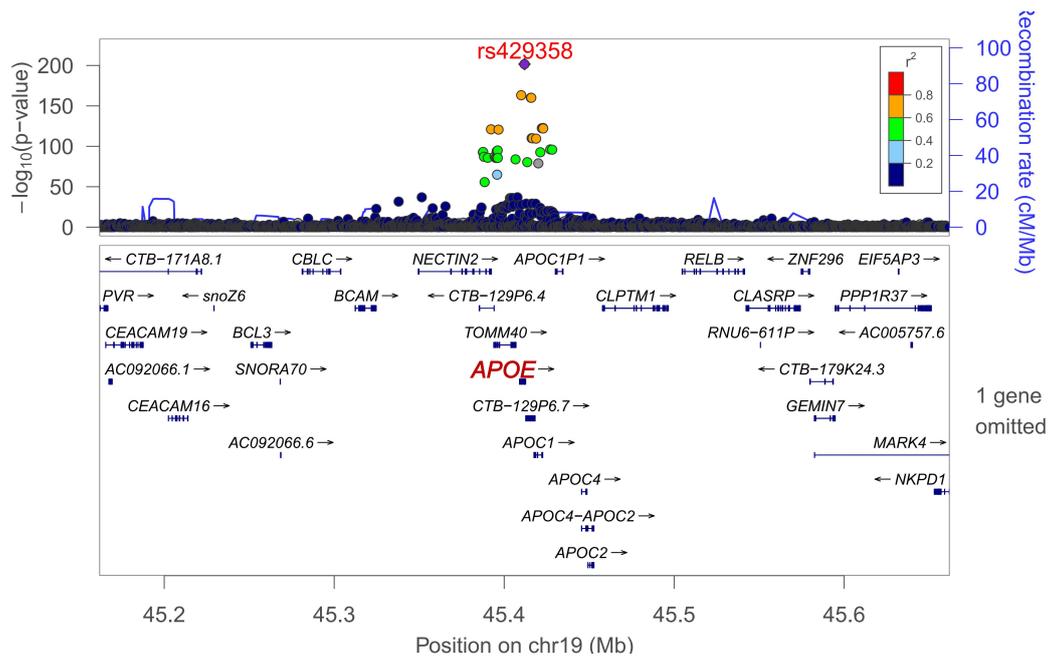
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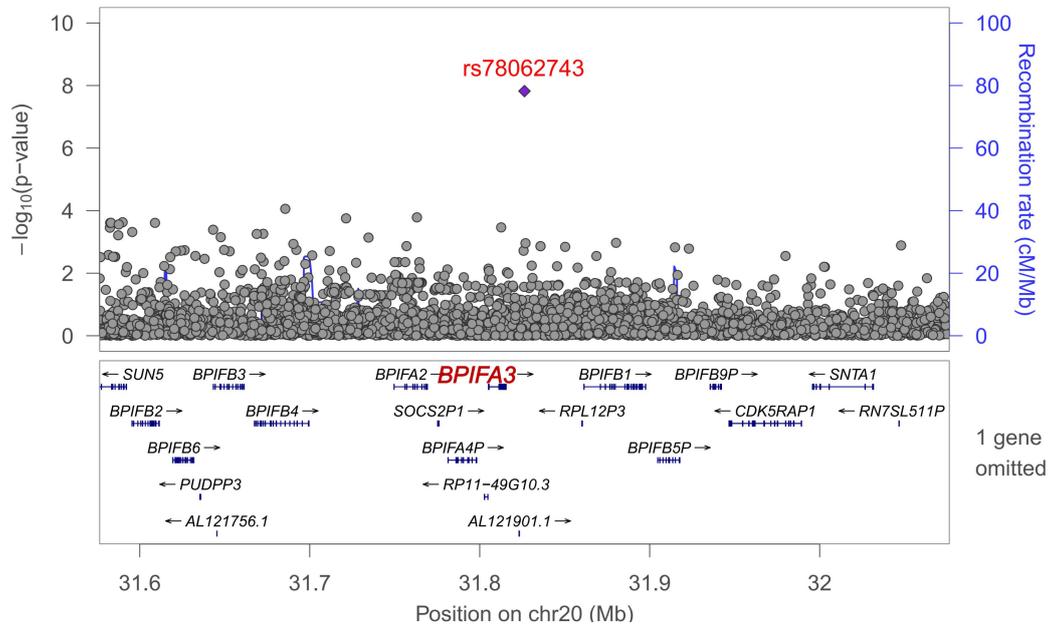
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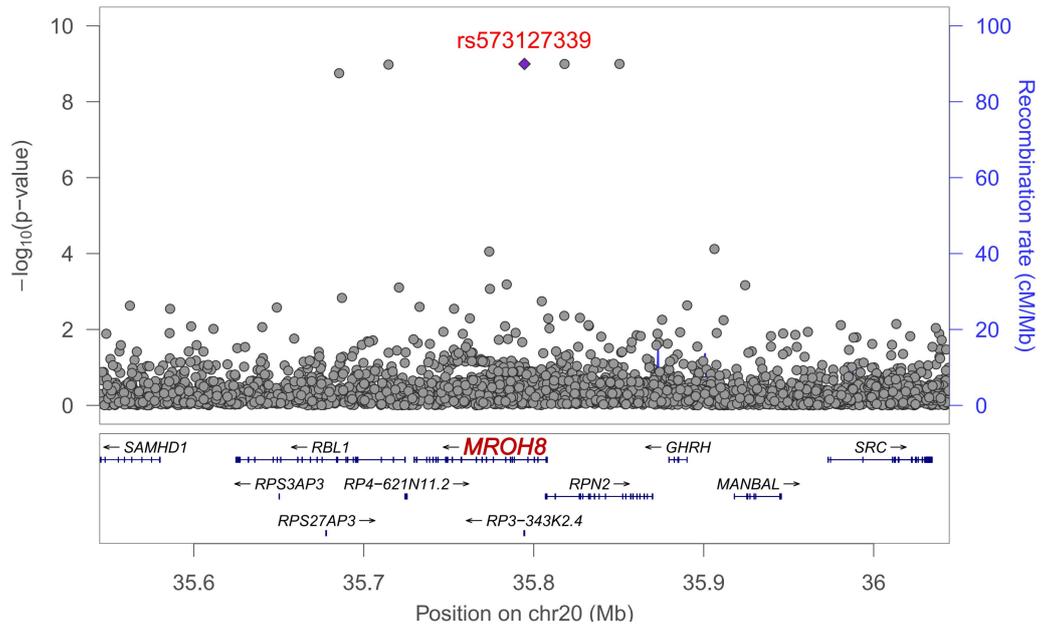
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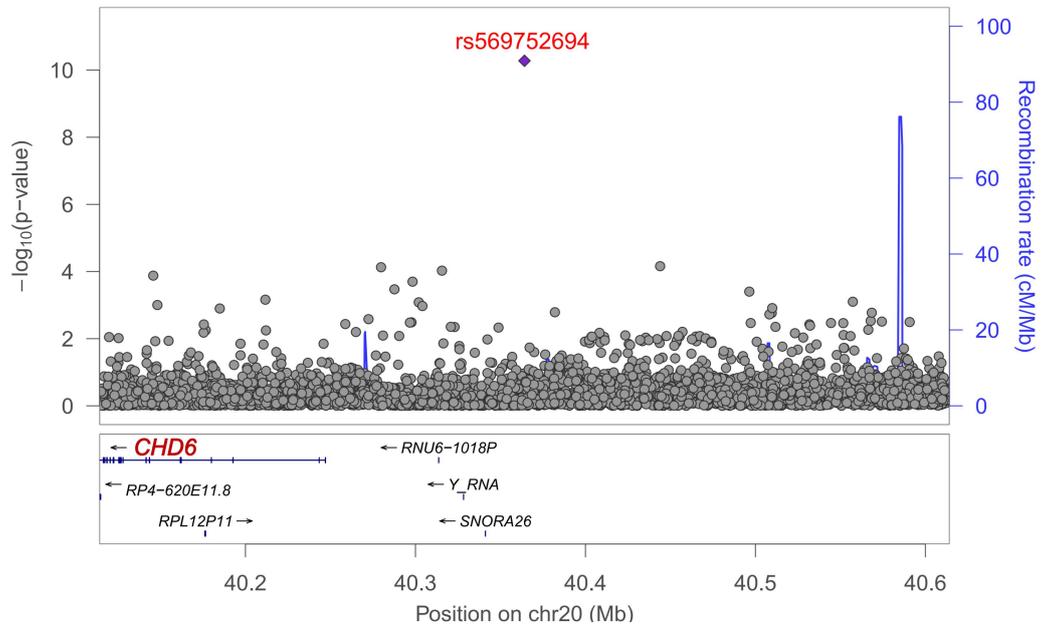
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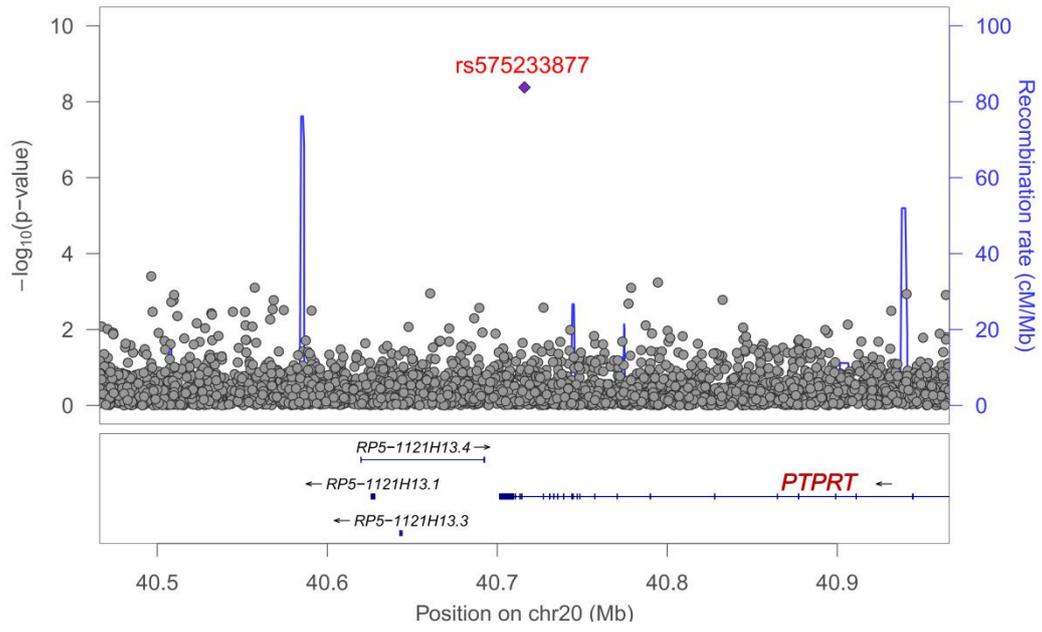
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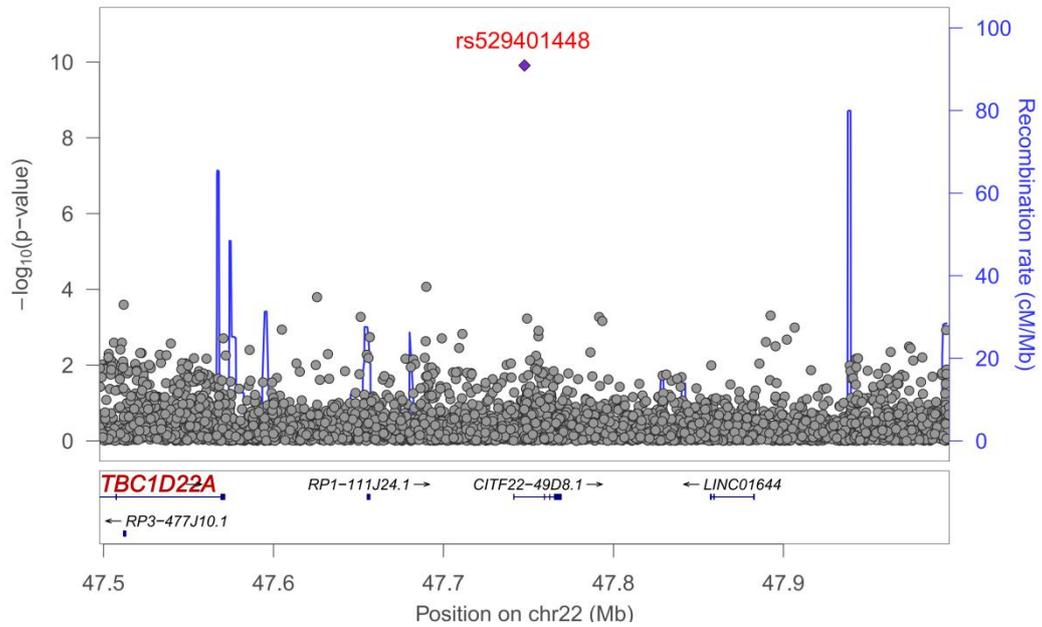
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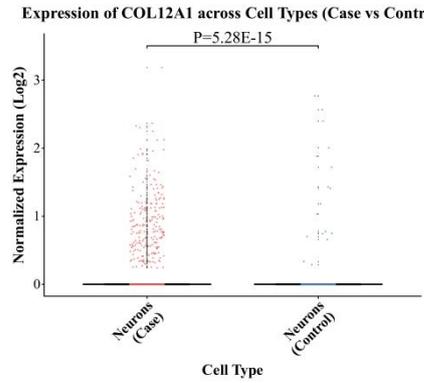


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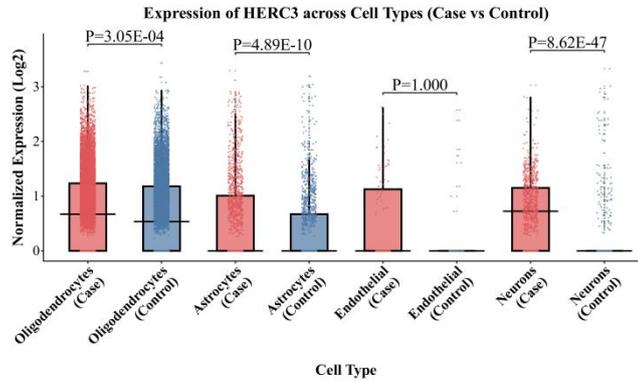


Supplementary Figure 4. Box plot of genes from differential expression analysis using GSE282111.

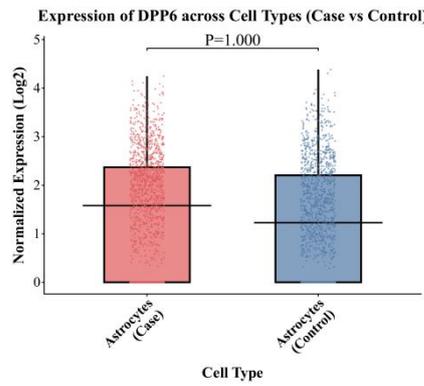
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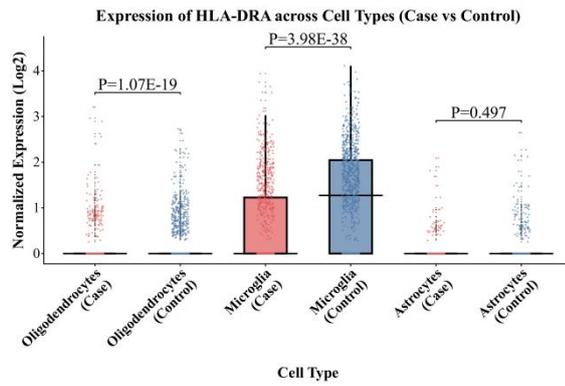
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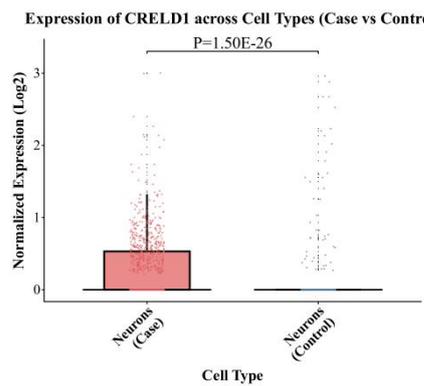
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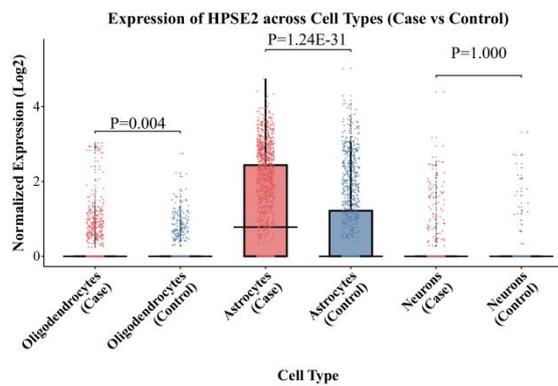
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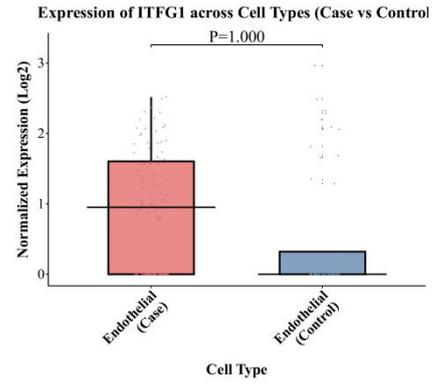
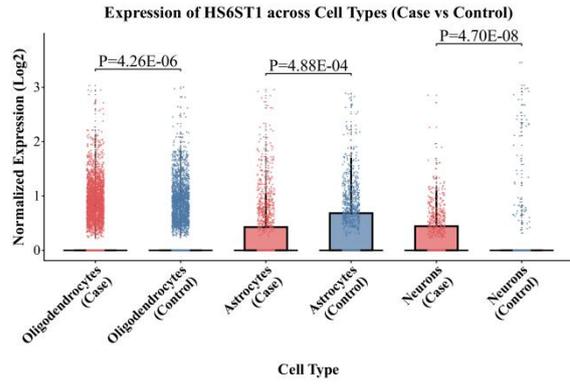


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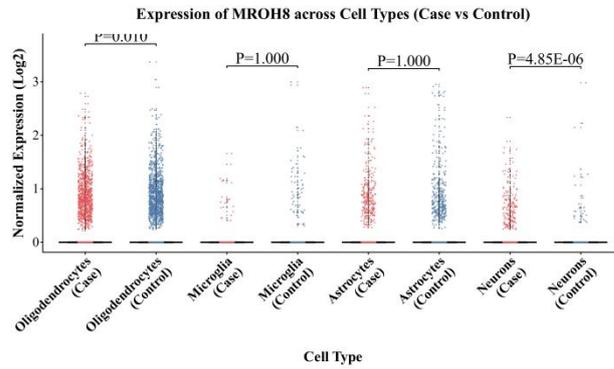


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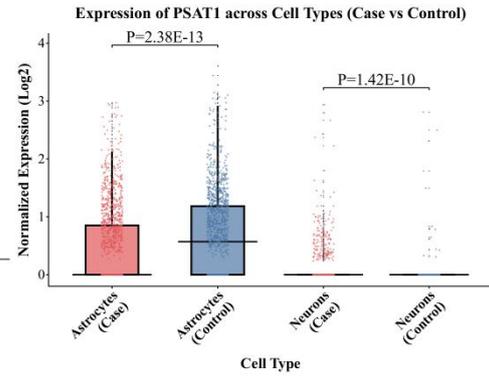
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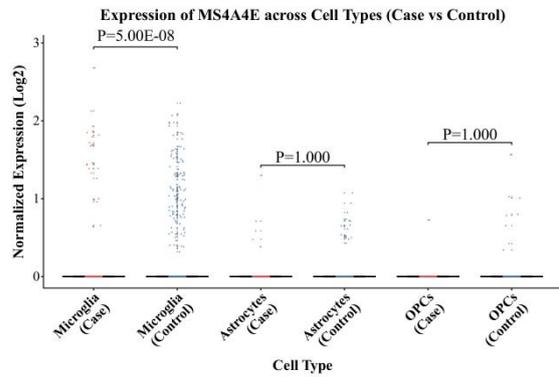
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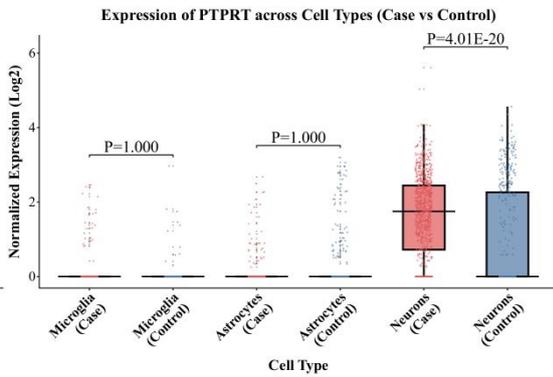
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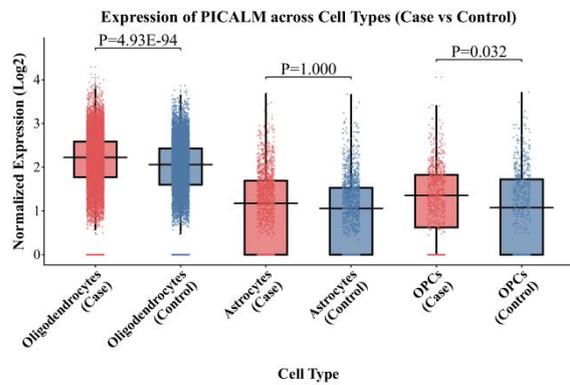
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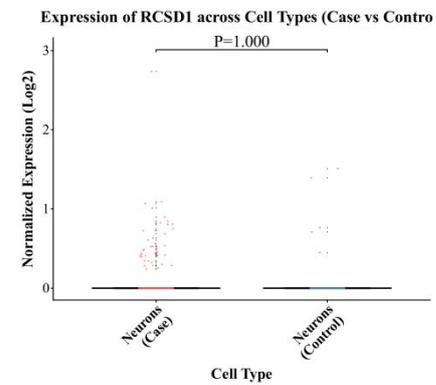
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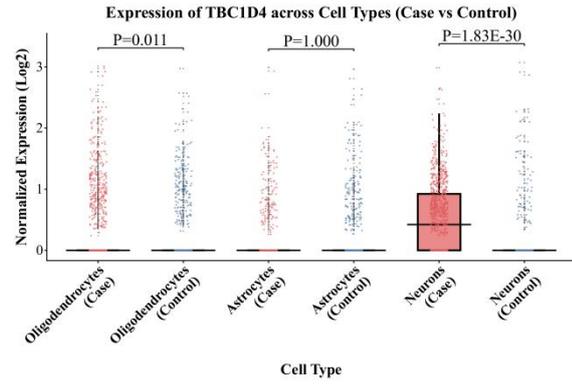
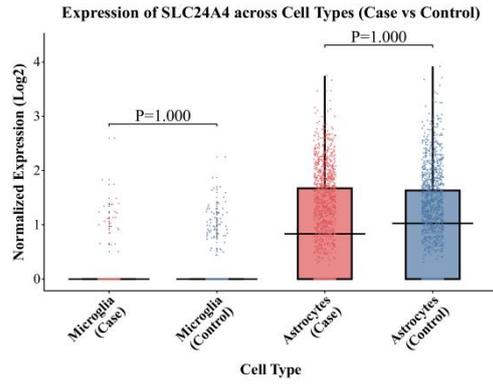


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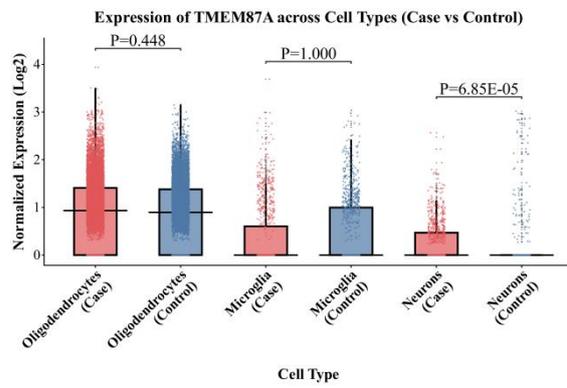


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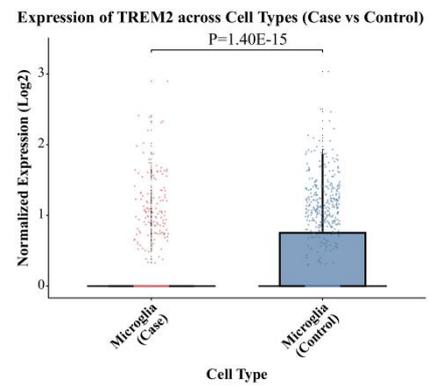
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R.



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