

Figure. 1. Manhattan plot of the general factor of ASD and ADHD using Genomic SEM. Genome-wide significant SPNs ($p < 5e-8$) are indicated.

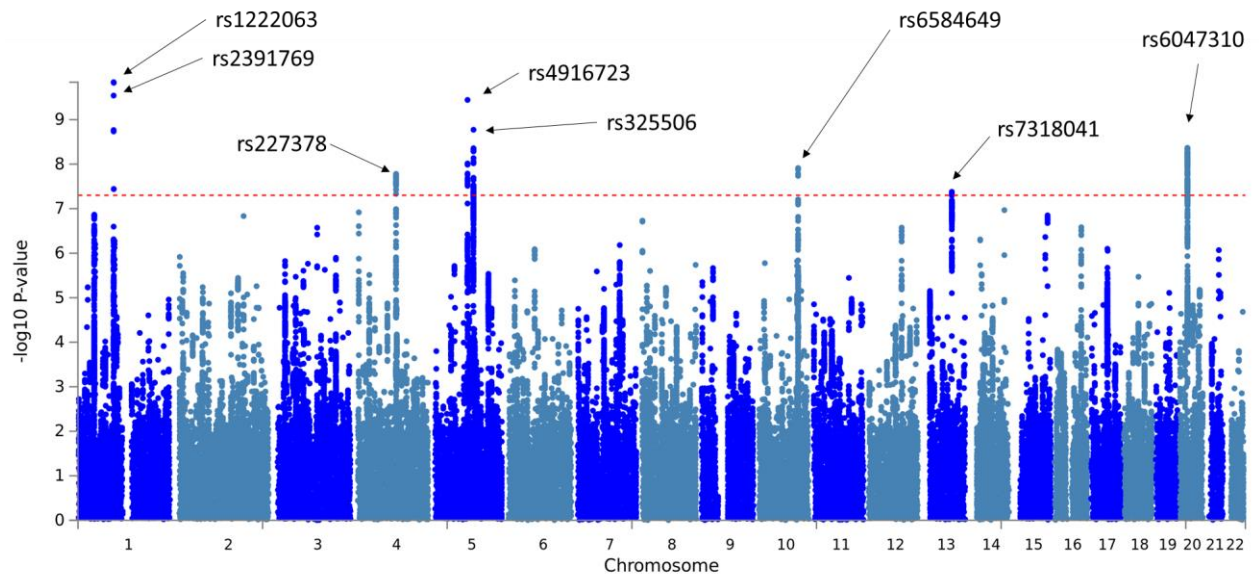


Figure. 2. Region around rs227378 (250kb around the SNP) in ADHD (upper figure) and ASD (lower figure) GWAS (chr = 4). FUMA SNP2GENE prioritized *MANBA* in region 4q24 around rs227378 (framed in yellow).

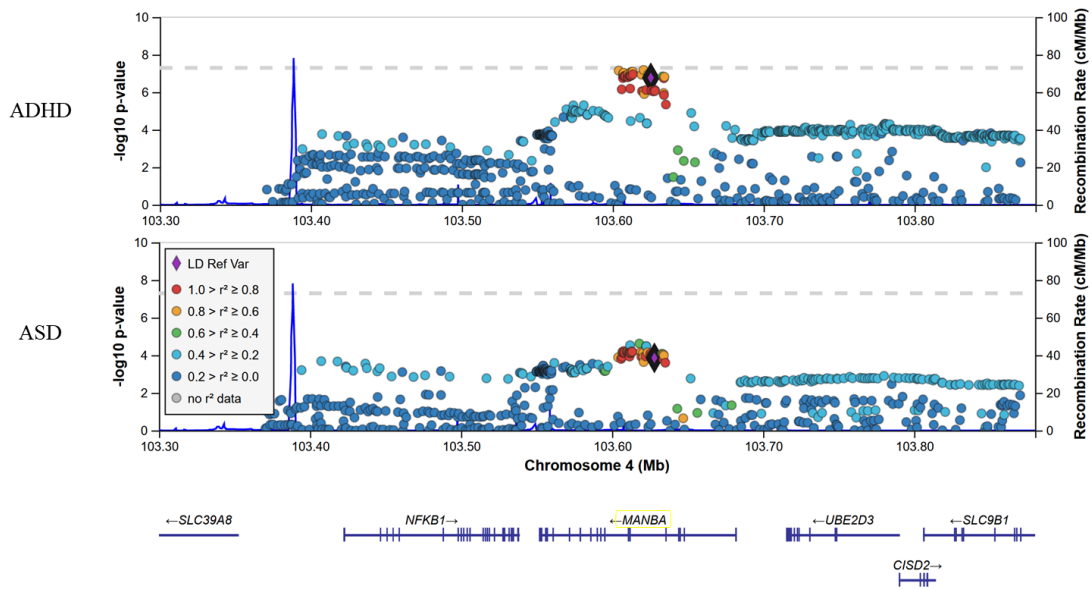


Figure 3. Tissue specific expression patterns (average expression per label (log2 transformed p -values for the enrichment of Differentially Expressed Gene (DEG)) using GTEx v6 RNA-seq data (FUMA GENE2FUNC - gene expression heatmap) of genes mapped SNPs that are (A) shared by ASD and ADHD and those that are specific to (B) ASD and (C) ADHD.

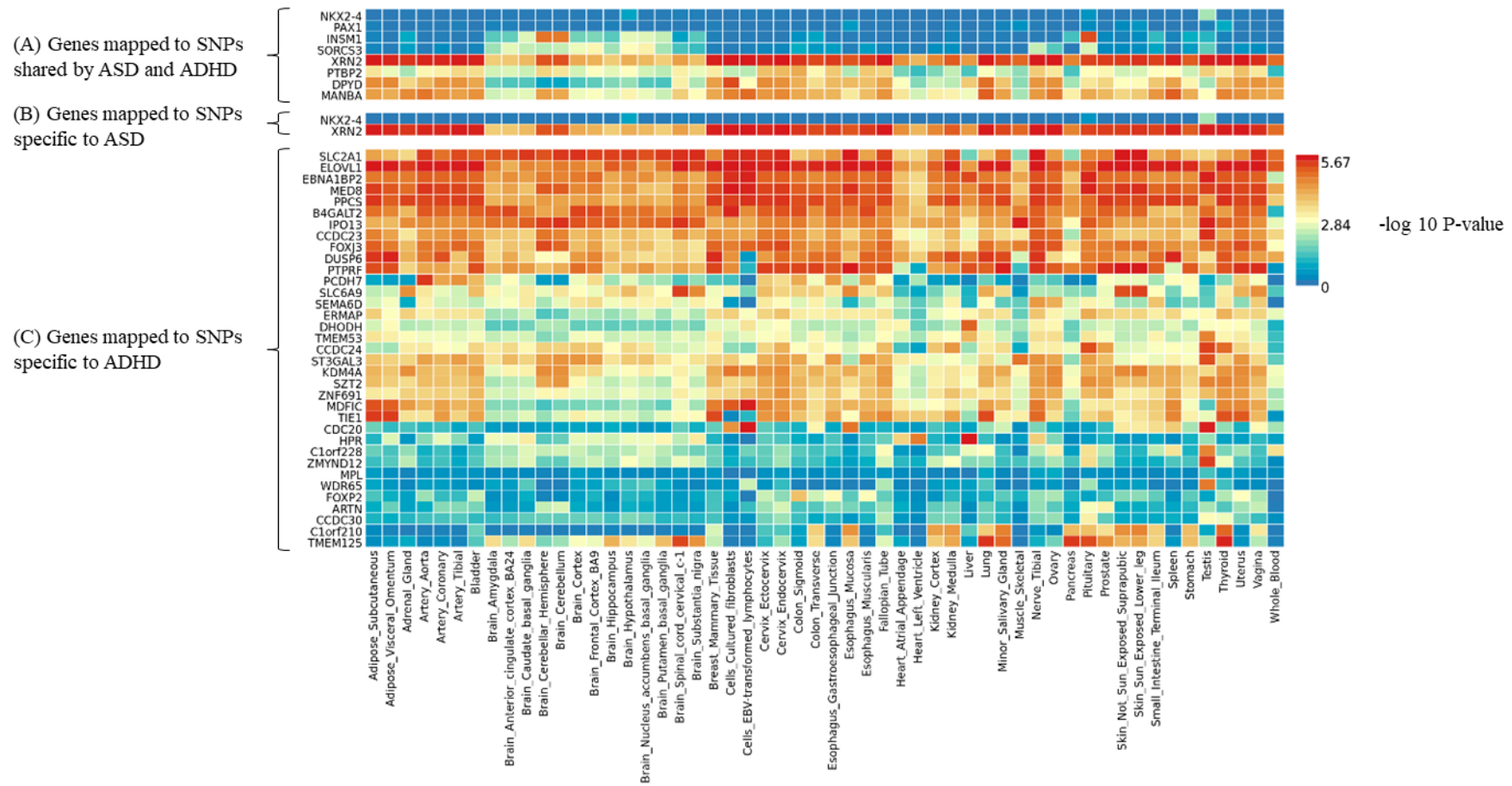


Figure 4. Bidirectional MR using multiple MR methods. **Panel A:** Multi-method MR estimation of the effect of ASD on ADHD. SNP-ADHD effects are regressed on SNP-exposure effects, i.e. instruments indexing ASD (p -value at $1e-6$). **Panel B:** Similar to A in the direction from ADHD to ASD. **Panel C:** Results from the multiple MR methods to evaluate the association between the genetic instruments indexing ASD and ADHD as the outcome. Point estimates and 95% confidence intervals are represented for each MR method. **Panel D:** Similar to C in the direction from ADHD to ASD. **Panel E:** Forest plot corresponding to MR analyses shown in Panel A. Each black dot reflects the ratio estimate per SNP and 95% confidence intervals. **Panel F:** Forest plot corresponding to MR analyses shown in Panel B.

