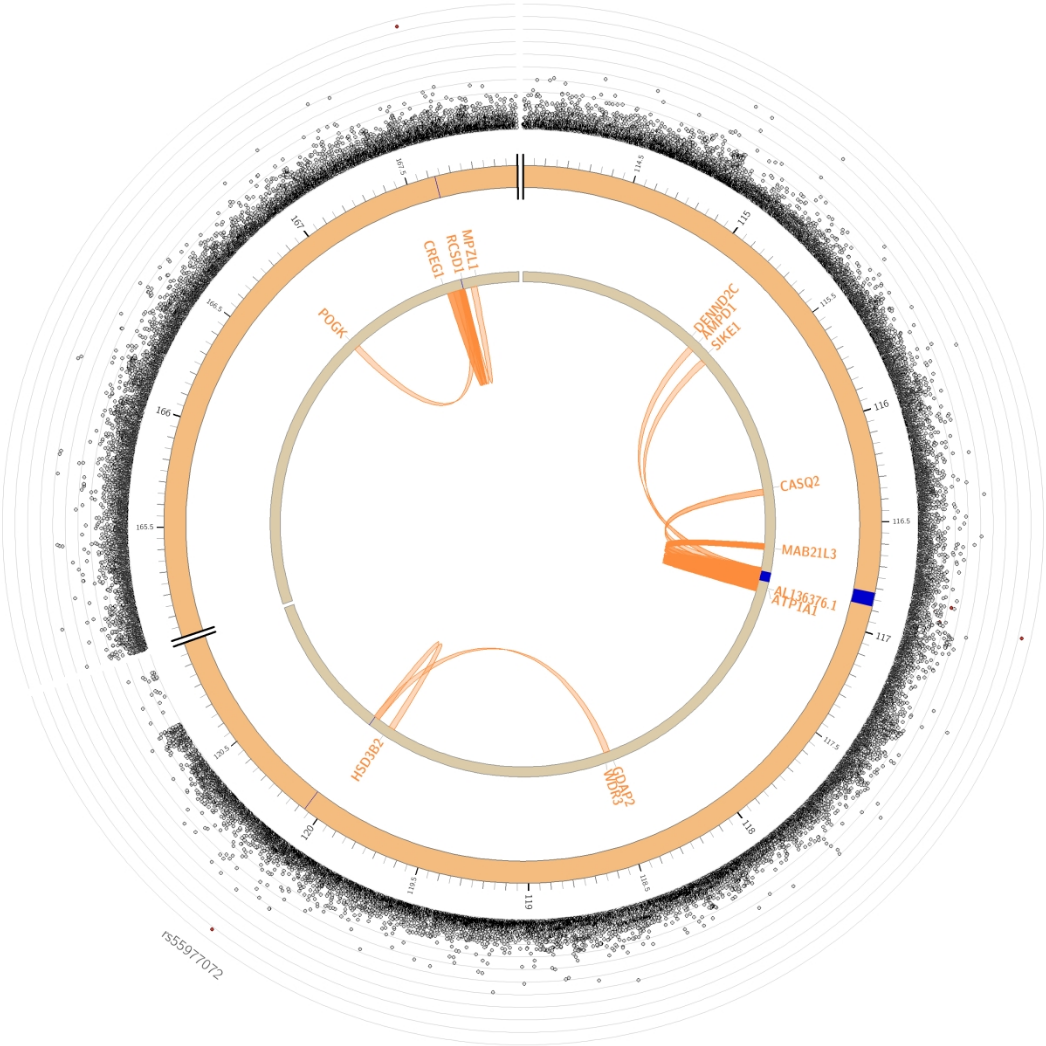
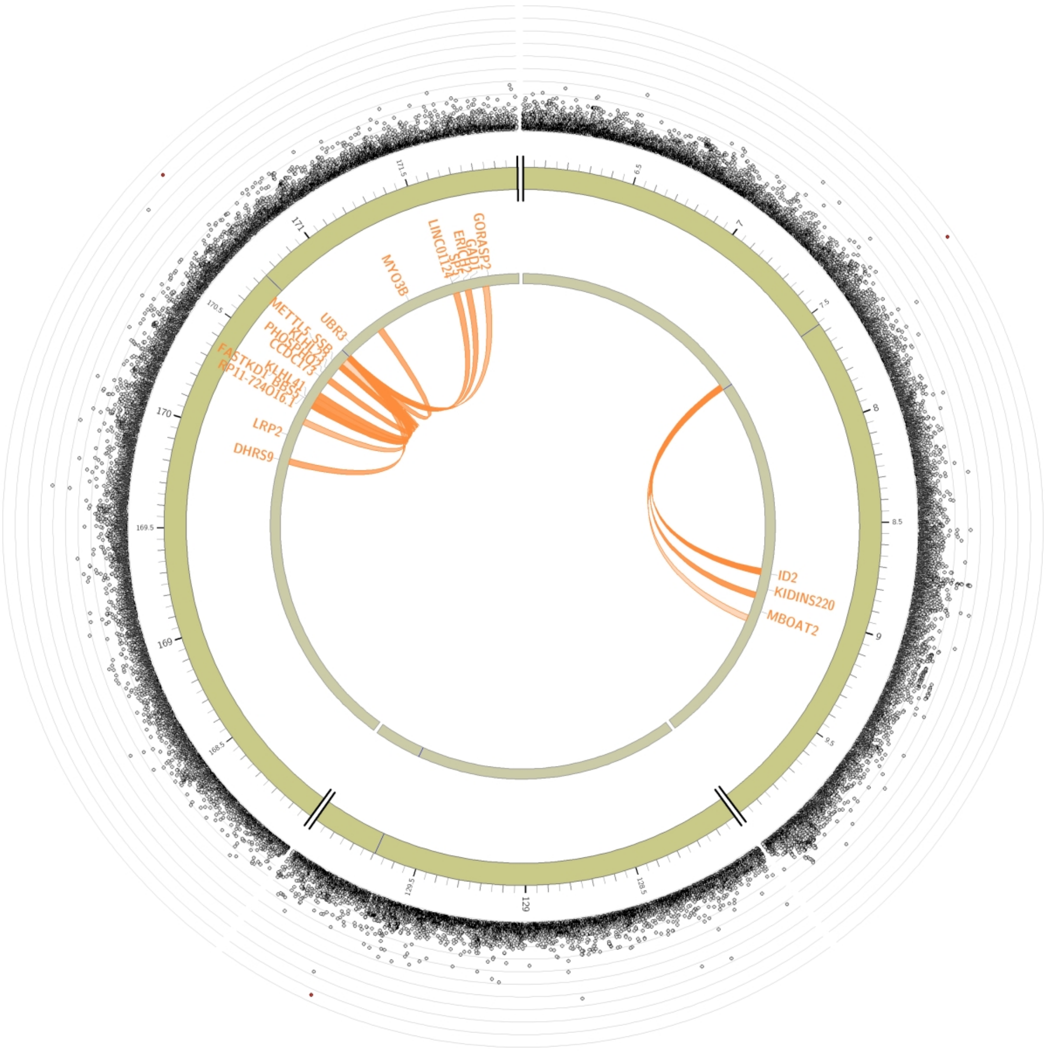
Supplementary Data 2

Circos plots of chromatin interactions and eQTLs for each chromosome harboring VD risk loci based on the Cross-ancestry meta-analysis (Stage 2). Outer-most layer: Manhattan plot displaying lead SNPs, where additional independent significant SNPs in loci are colored according to linkage disequilibrium (r^2; red [$r^2>0.8$], orange [$r^2>0.6$], green [$r^2>0.4$], blue [$r^2>0.2$], grey [$r^2\leq0.2$]); -$\log_{10}$ *P*-values for meta-analysis effect estimates for each SNP is indicated on the y-axis. Second layer: chromosome ring with coordinates and genomic risk loci highlighted in blue. Third layer: chromosome ring showing genes mapped by chromatin interactions (orange), eQTL (green), or both (red).

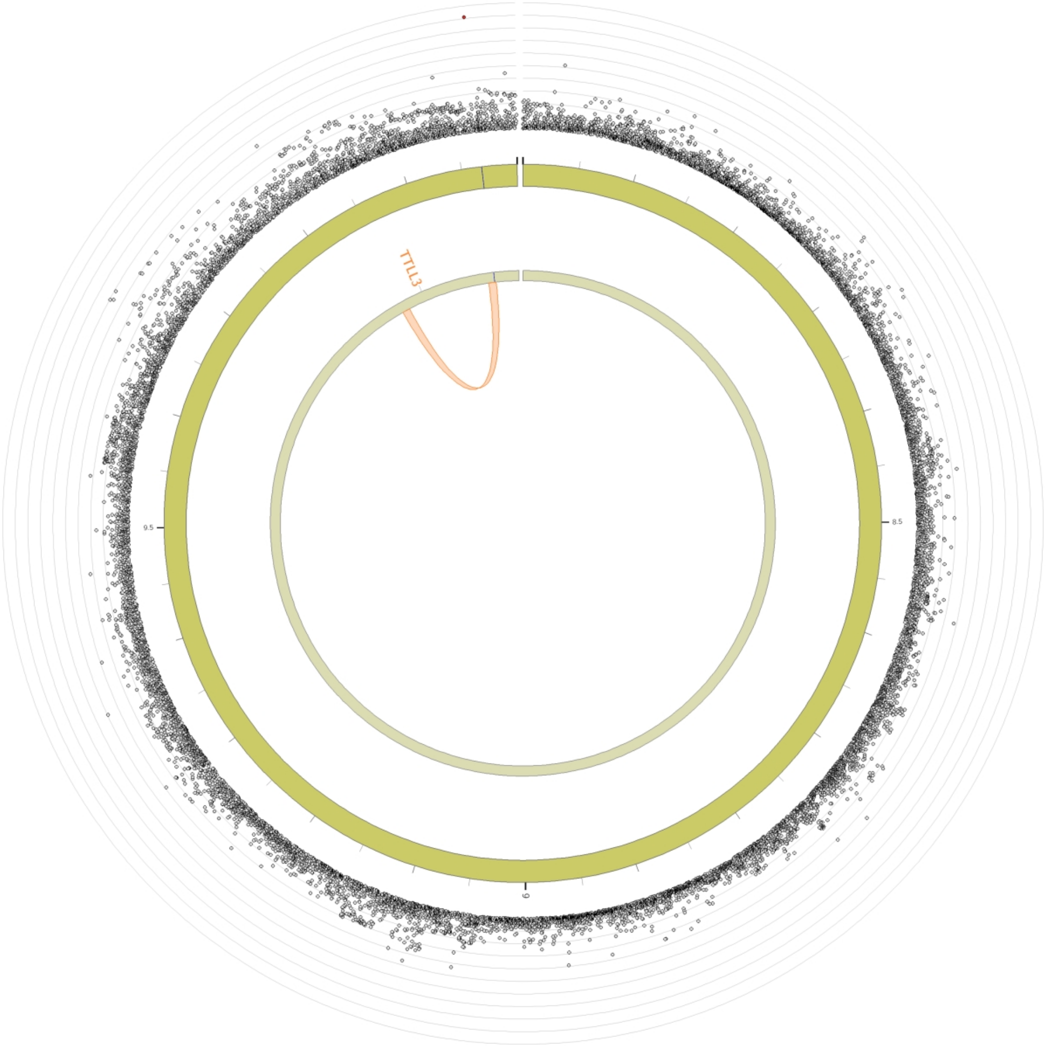
Chromosome 1



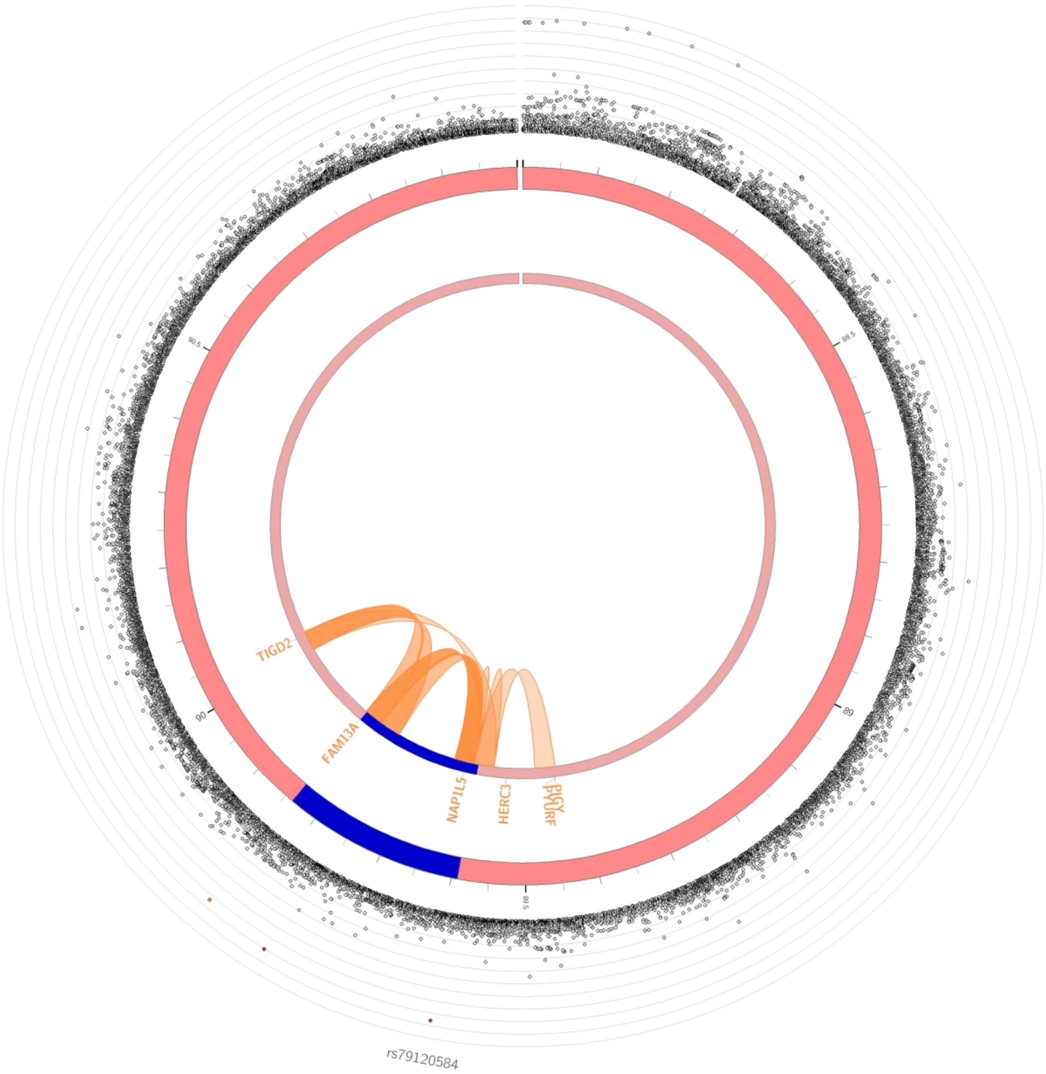
Chromosome 2



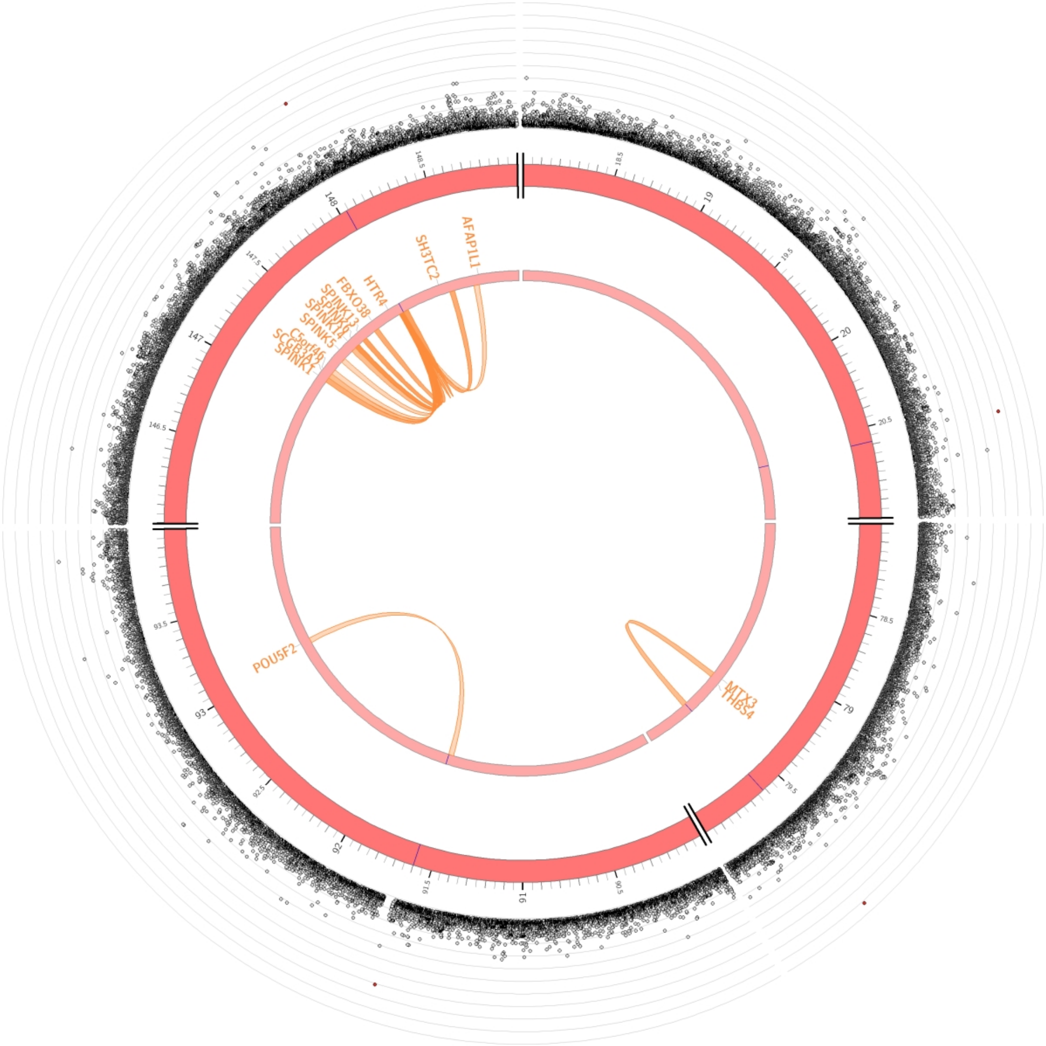
Chromosome 3



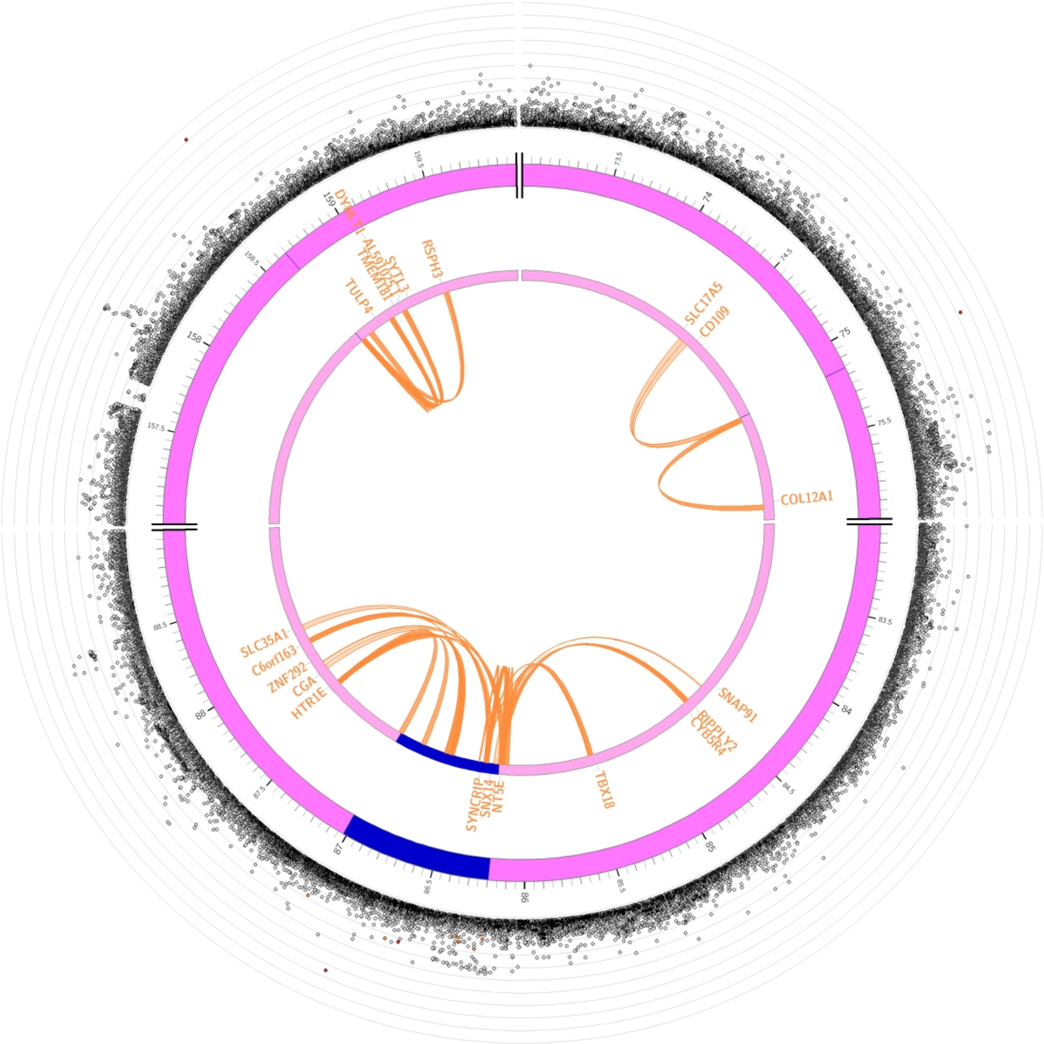
Chromosome 4



Chromosome 5



Chromosome 6



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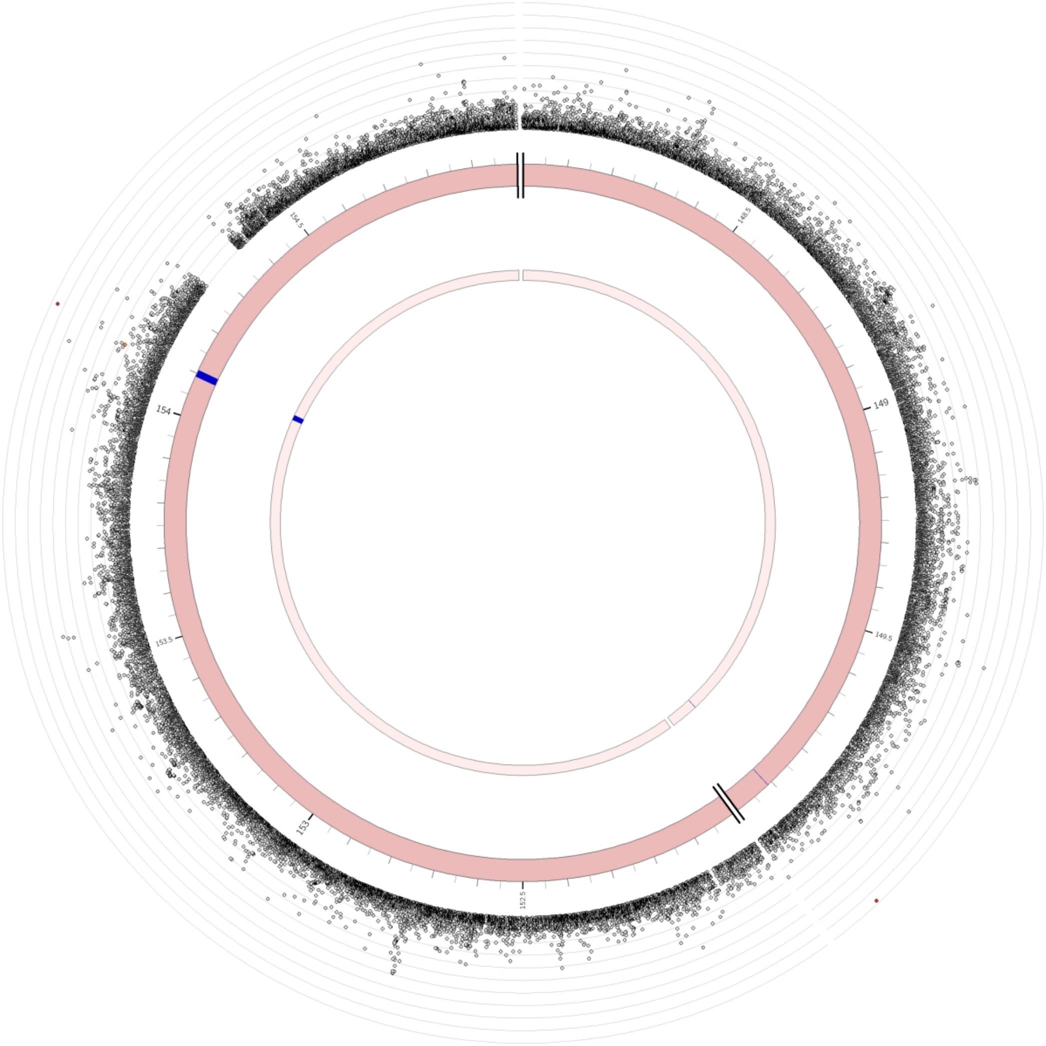
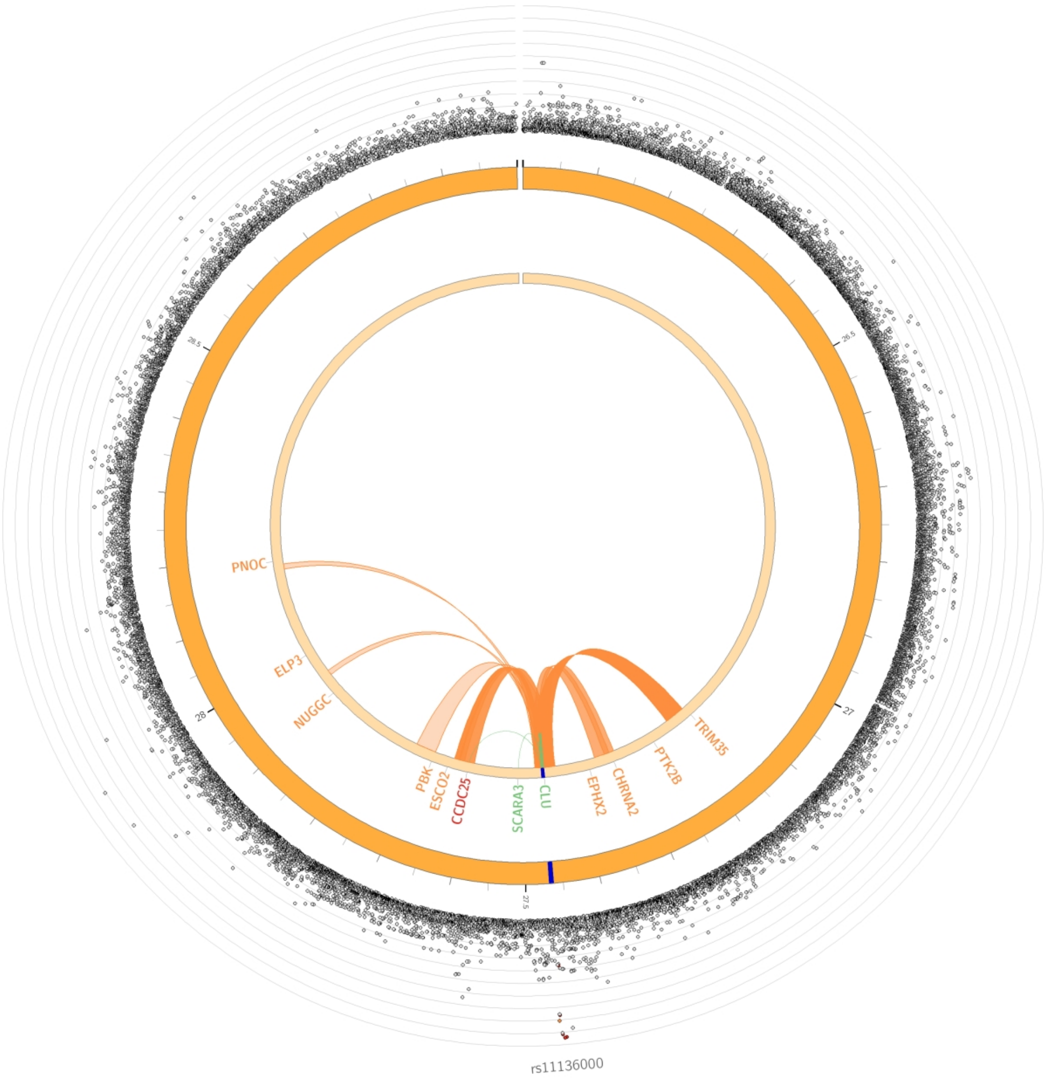
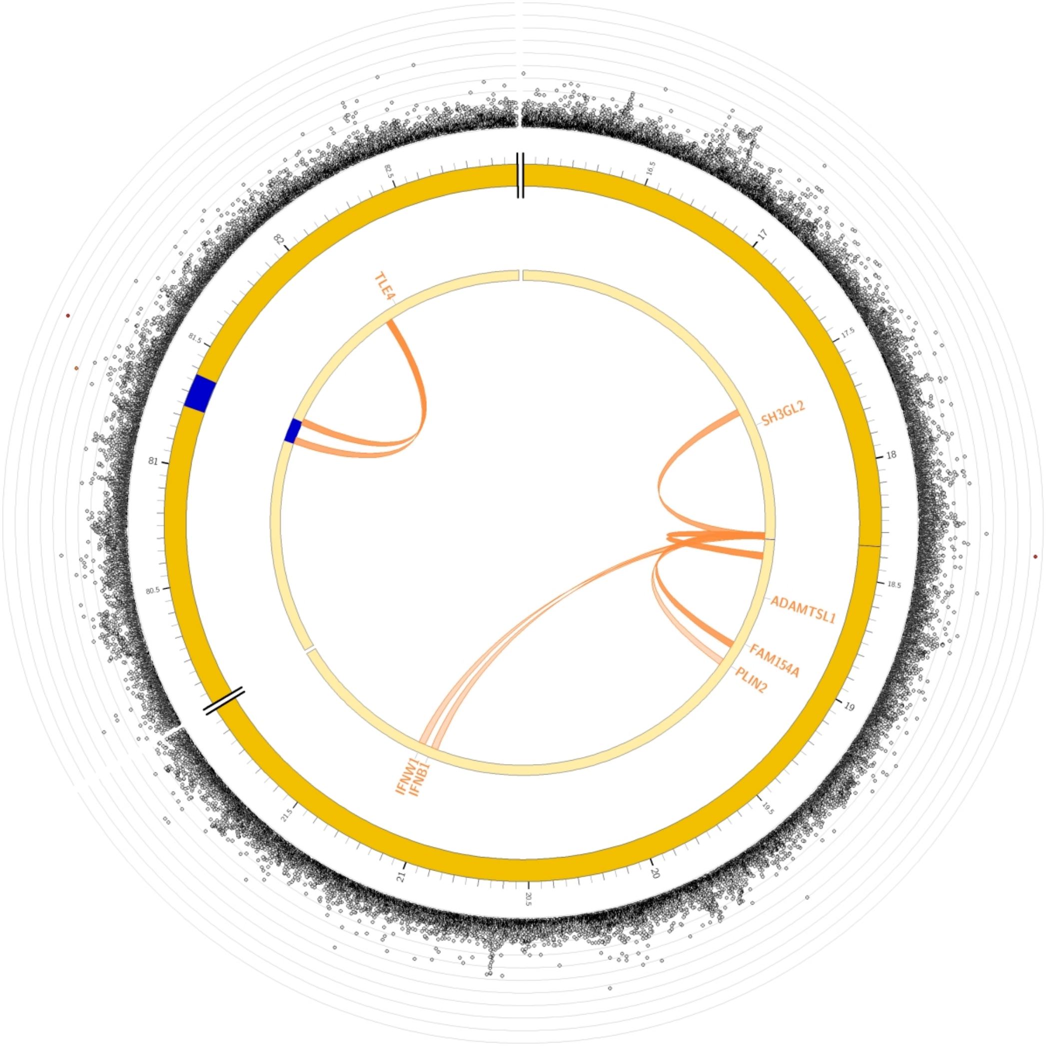


Chromosome 8

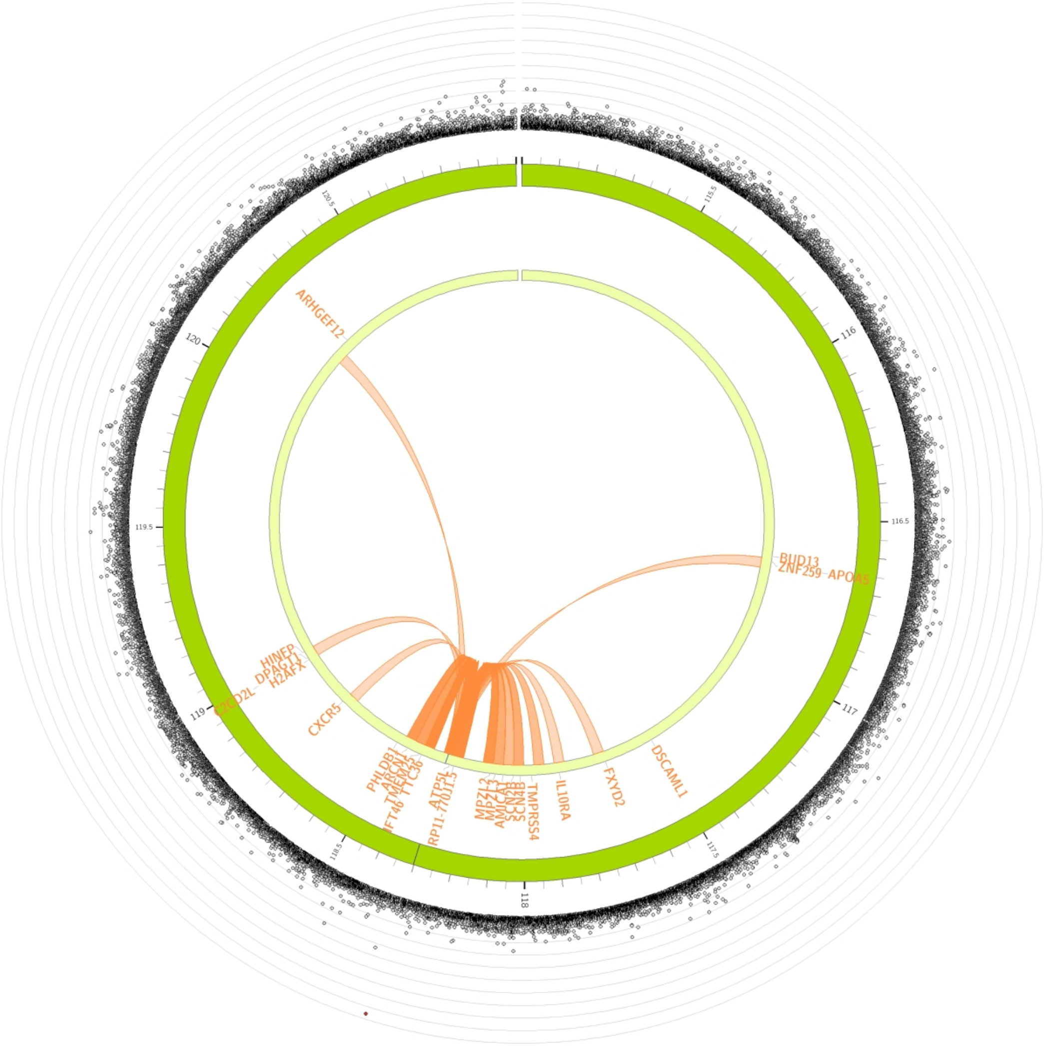


Chromosome 9

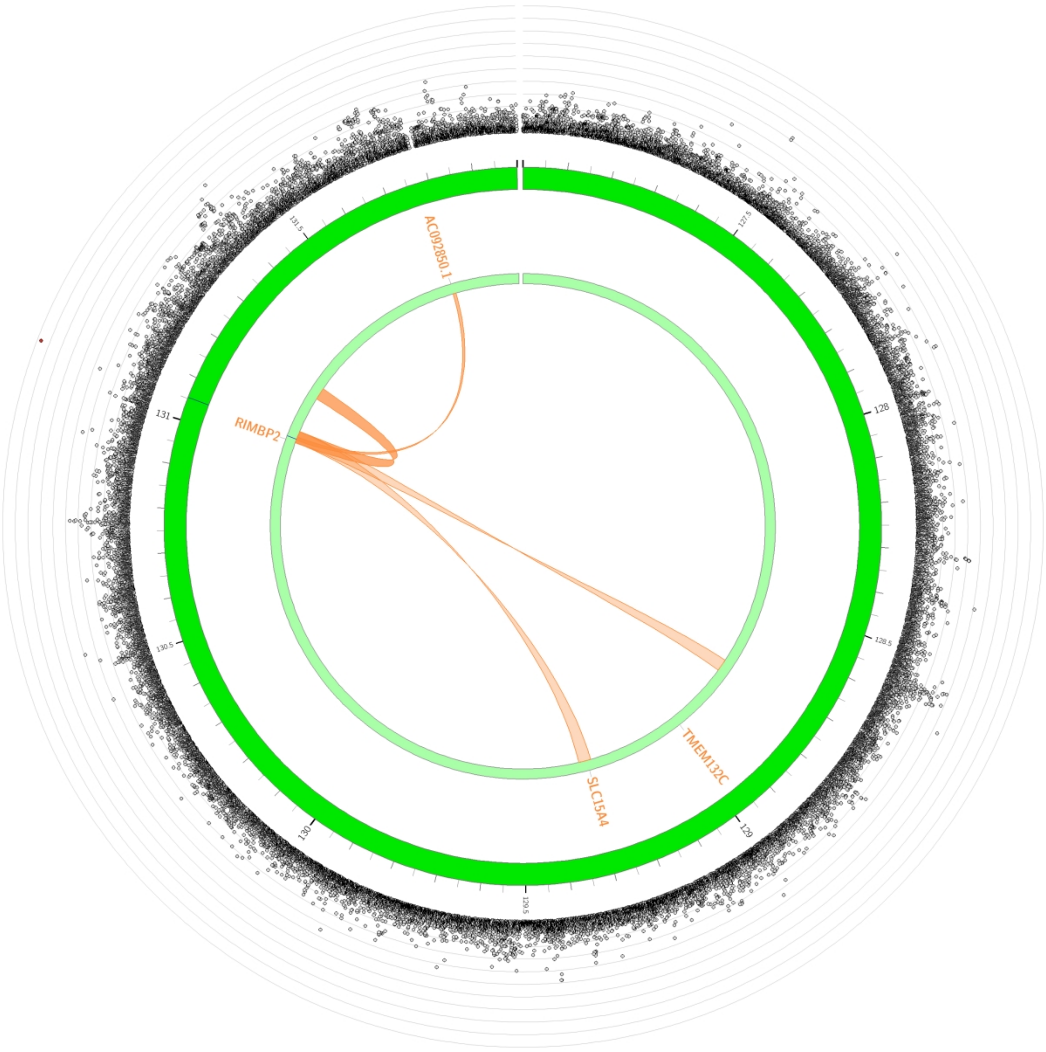


Chromosome 10

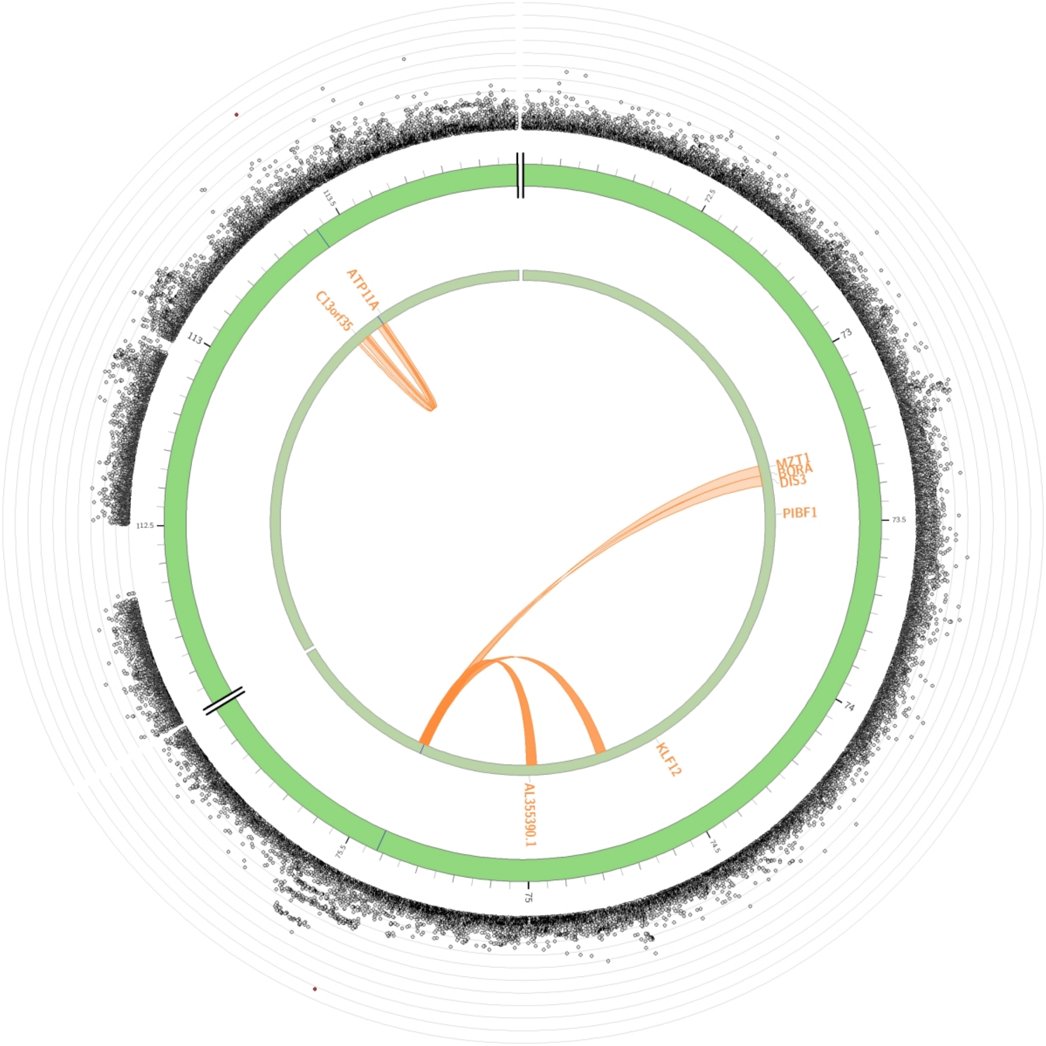
Chromosome 11



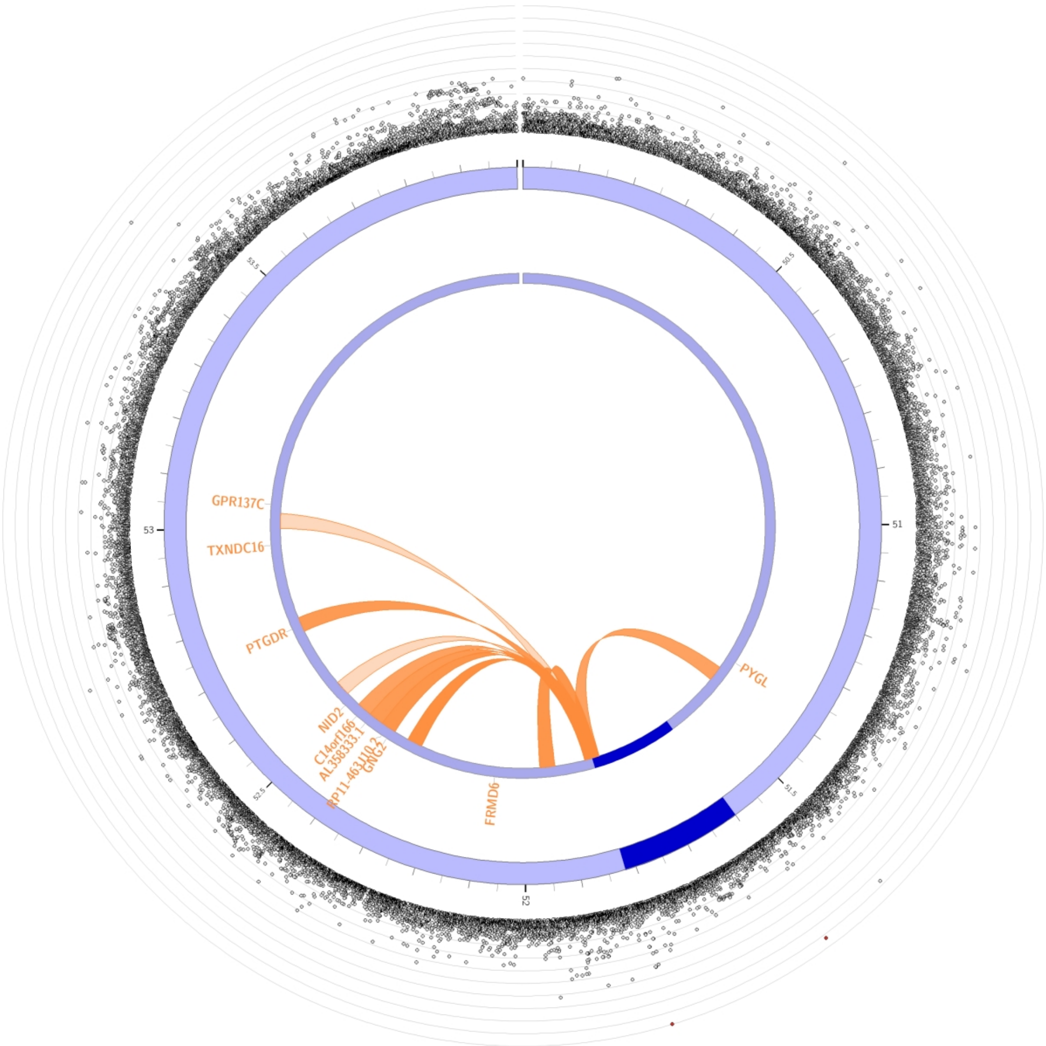
Chromosome 12



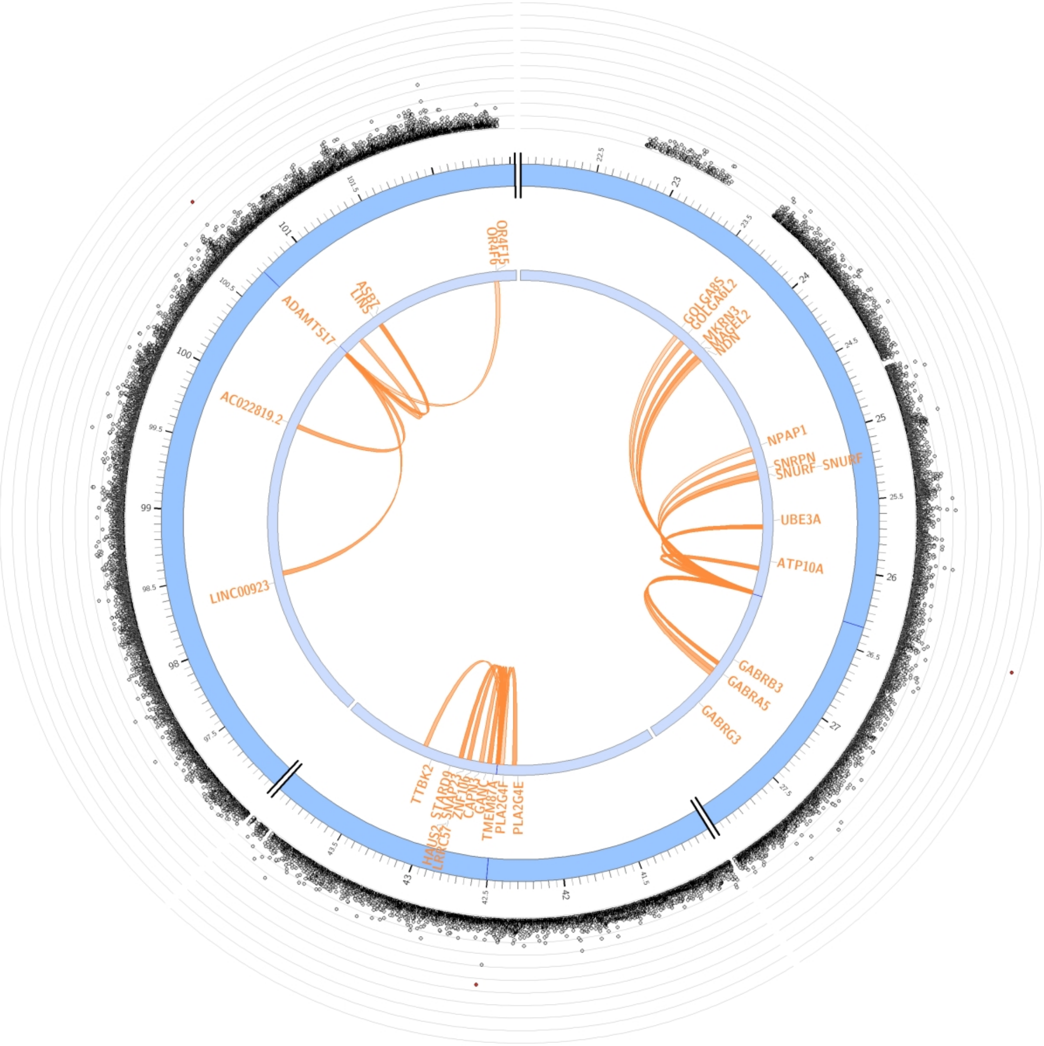
Chromosome 13



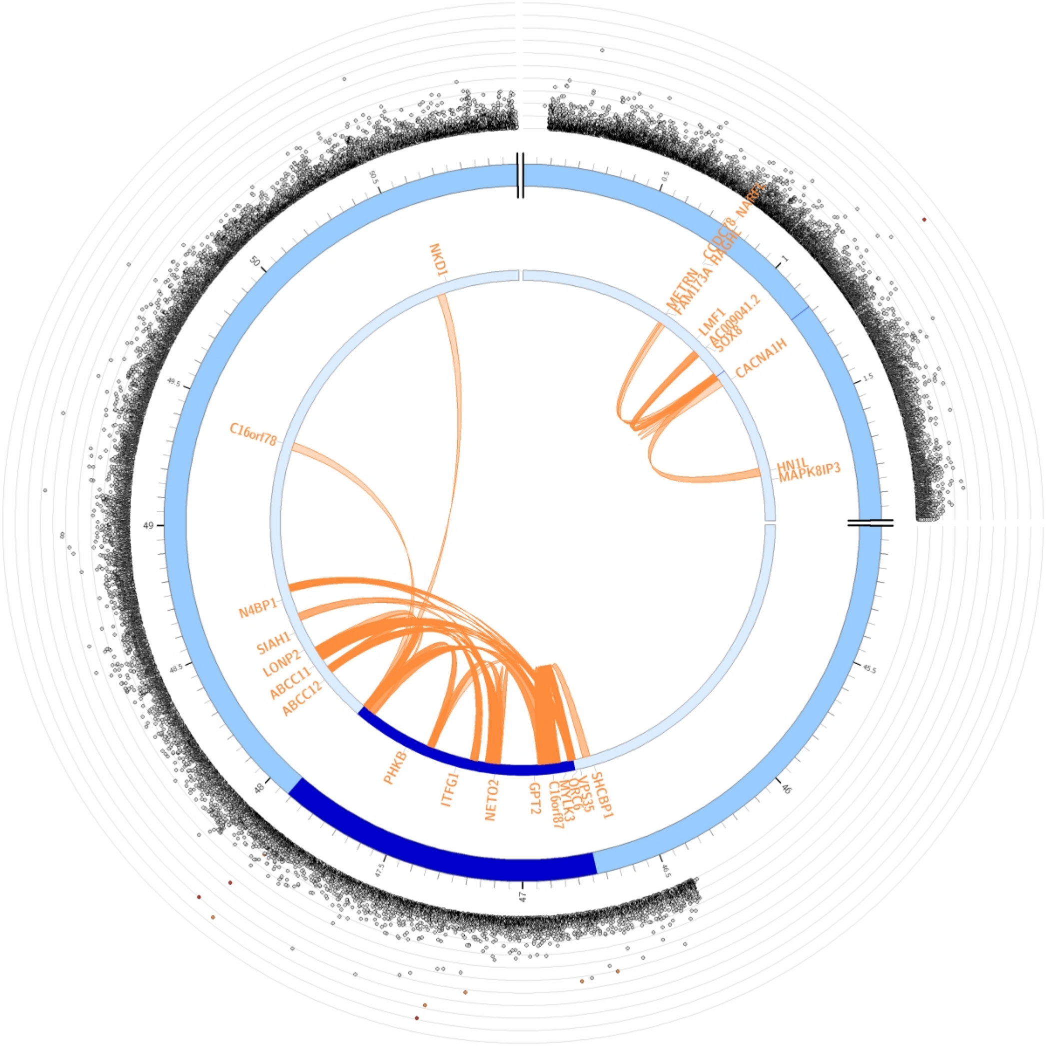
Chromosome 14



Chromosome 15



Chromosome 16



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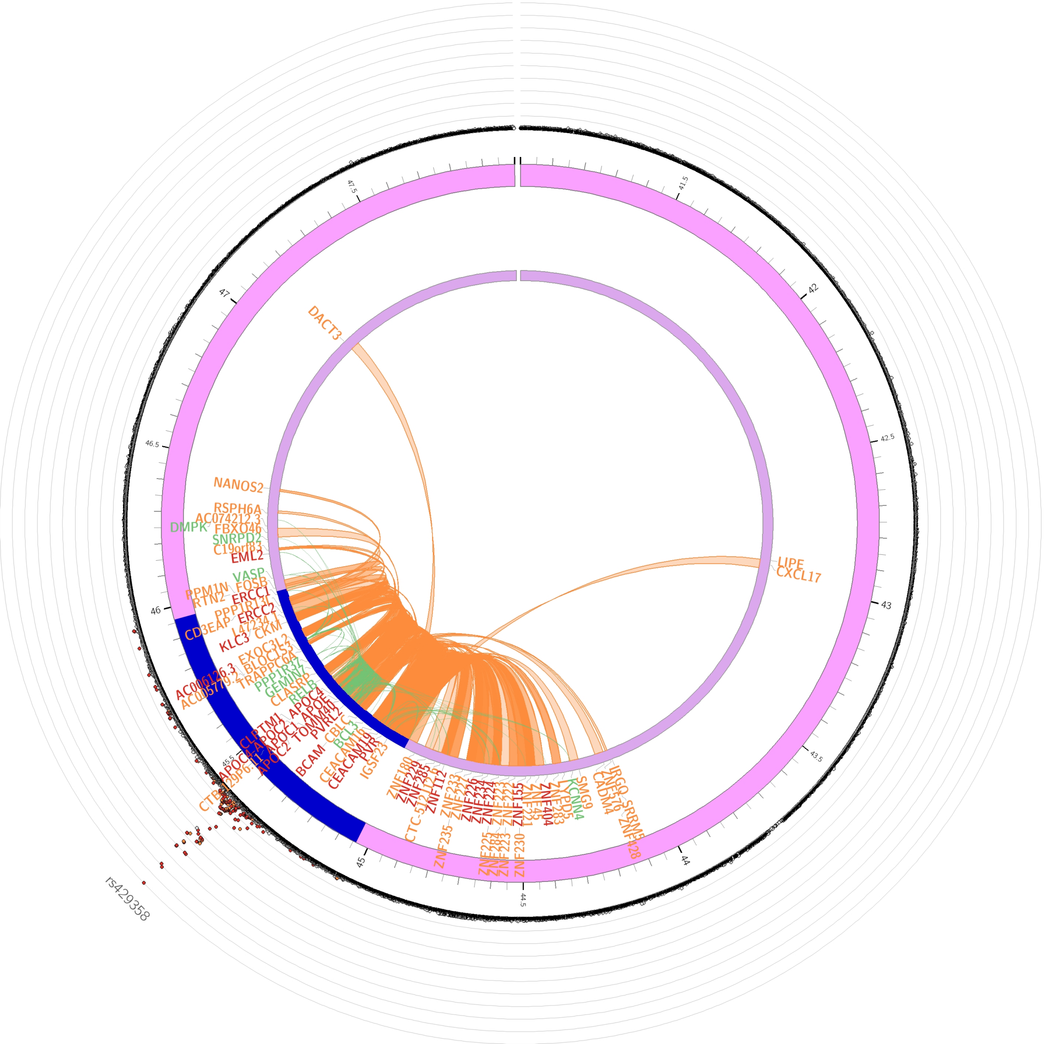
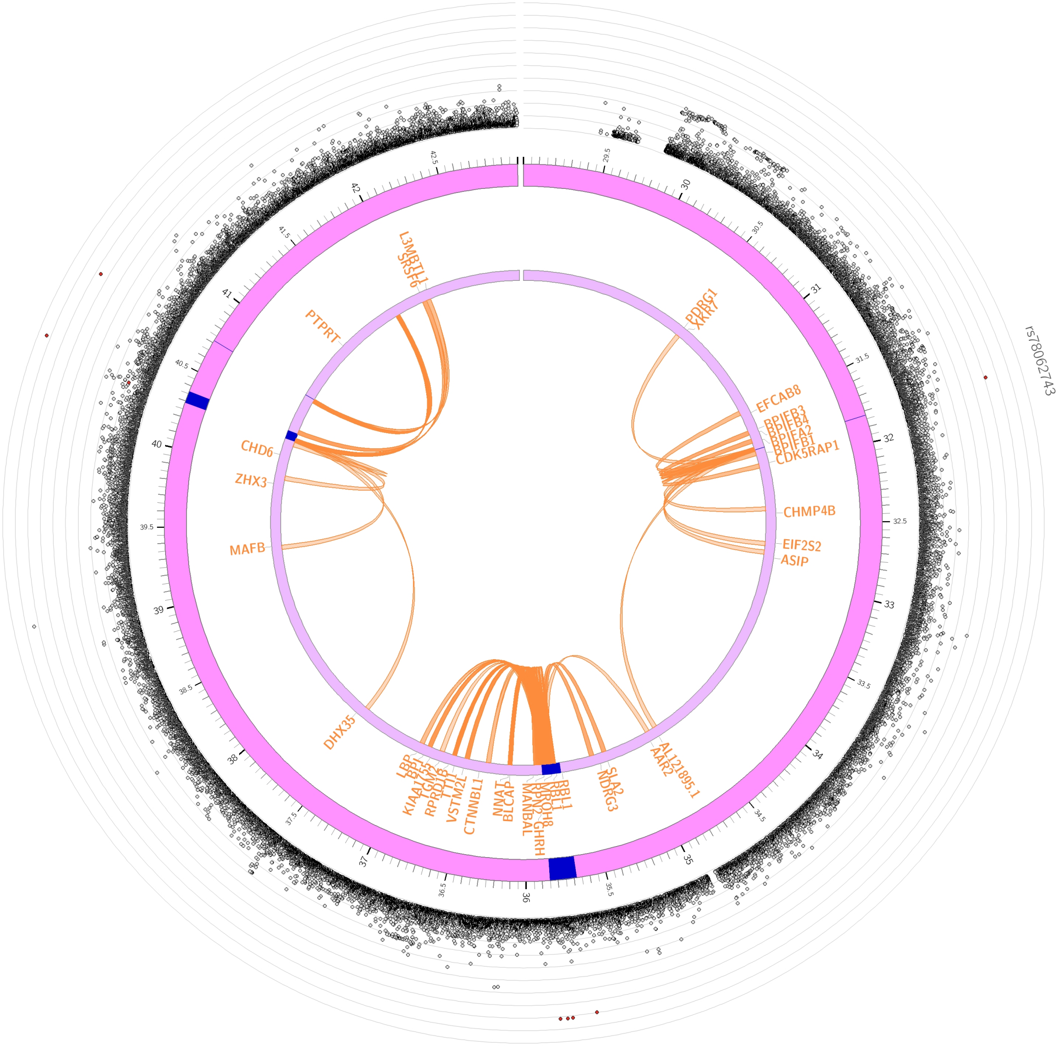


Chromosome 20



Chromosome 22