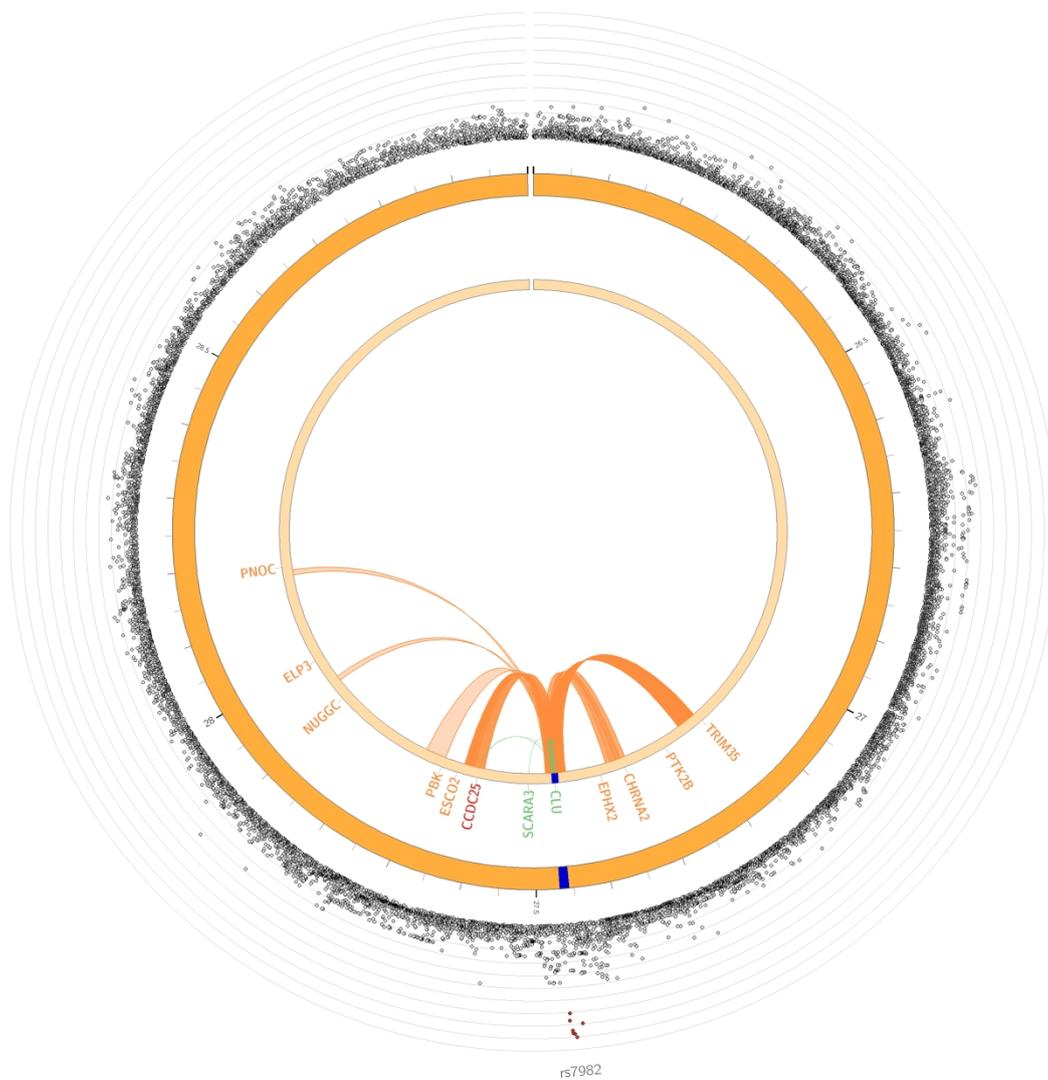


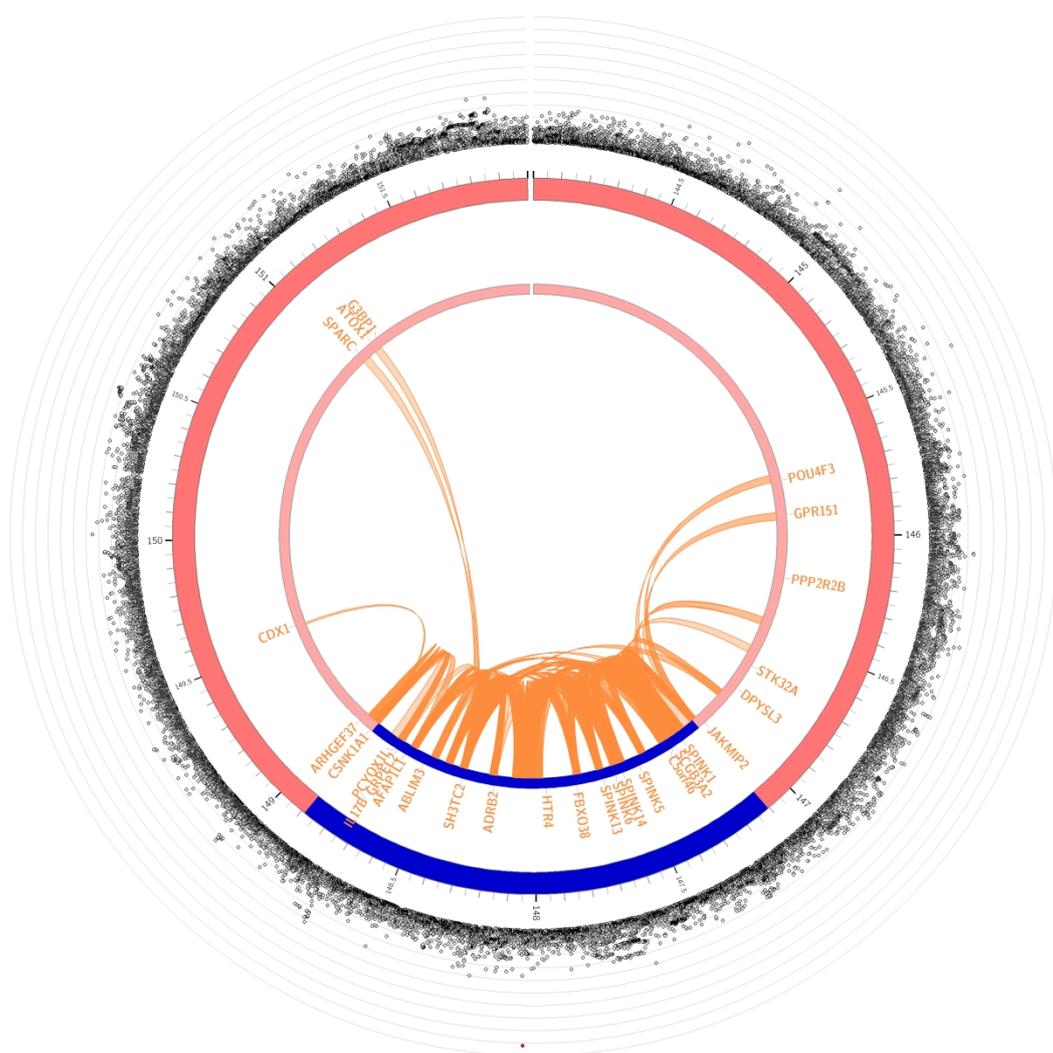
## Supplementary Data 1

**Circos plots of chromatin interactions and eQTLs for each chromosome harboring VD risk loci based on the European-specific meta-analysis (Stage 1).** 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 [ $r^2 \leq 0.2$ ]);  $-\log_{10} P$ -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

