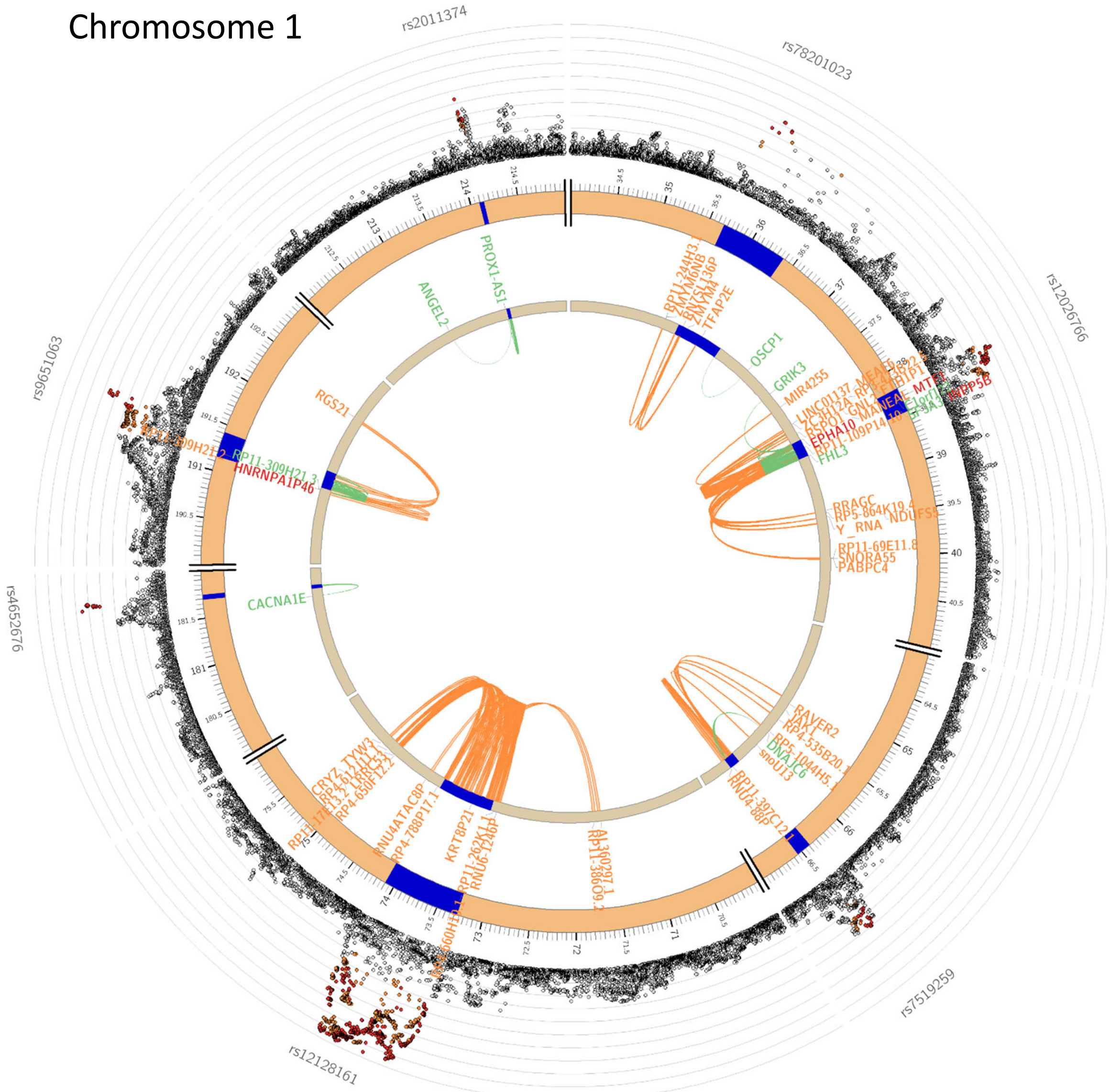
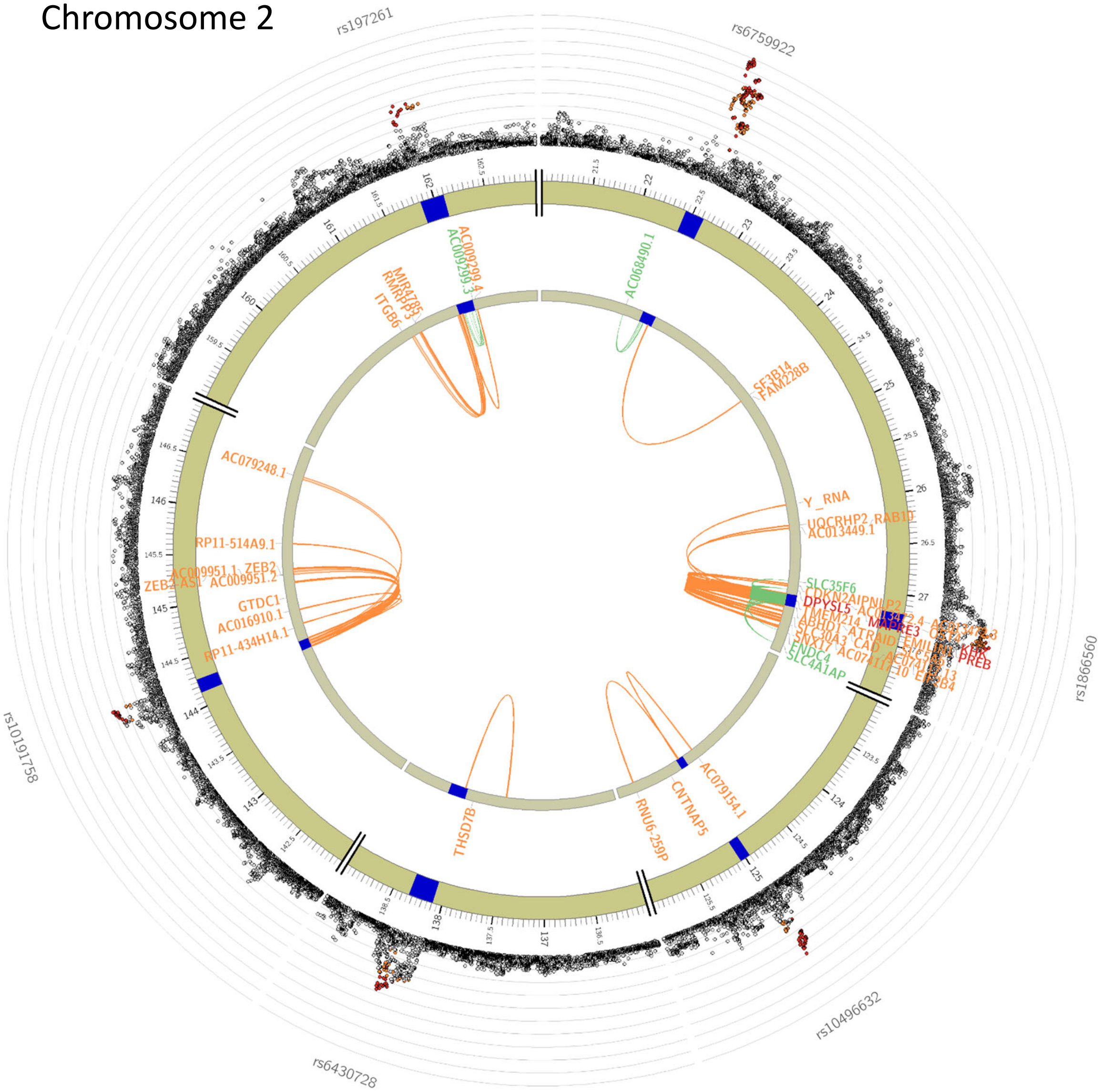
Supplementary Data 3

Circos Plot of Chromatin Interactions and eQTLs for each chromosome harboring PTSD risk loci based on the EA Meta-Analysis. 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 [$r^2 \leq 0.2$]); -log10 *P*-values 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). Links (orange for chromatin interactions and green for eQTL) are based on all brain tissues available in FUMA v 1.4.1.

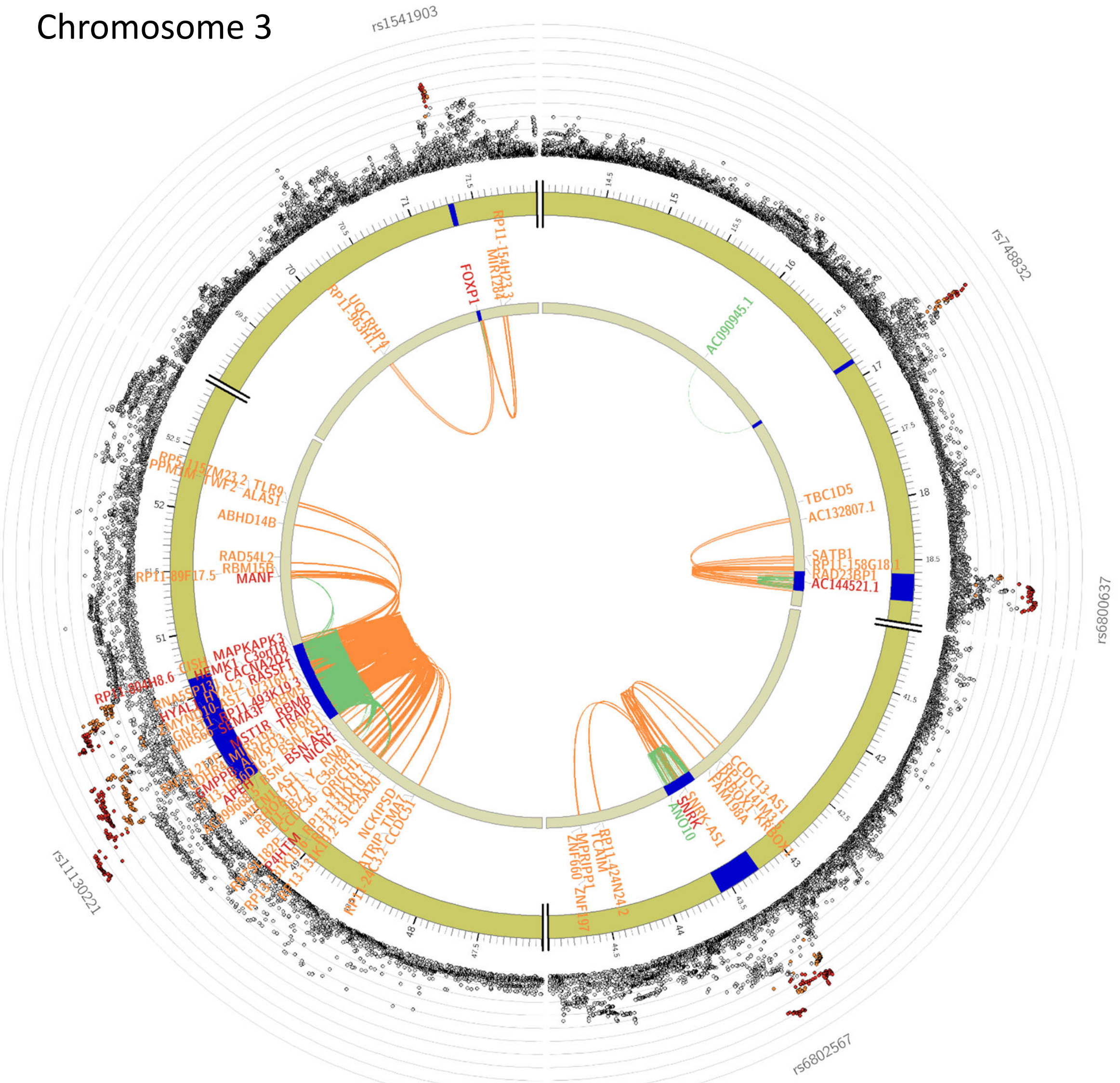
Chromosome 1



Chromosome 2

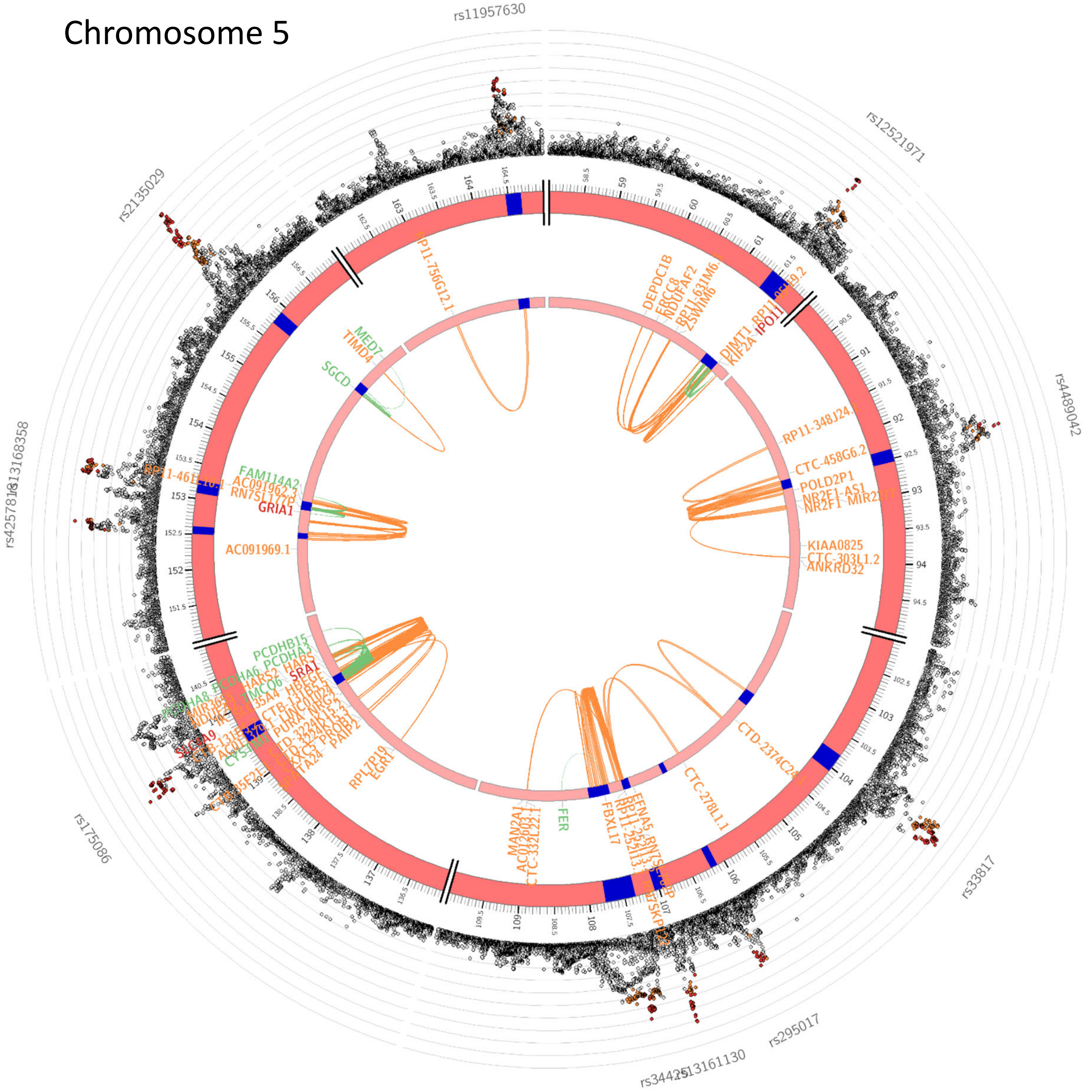


Chromosome 3



Chromosome 4

Chromosome 5



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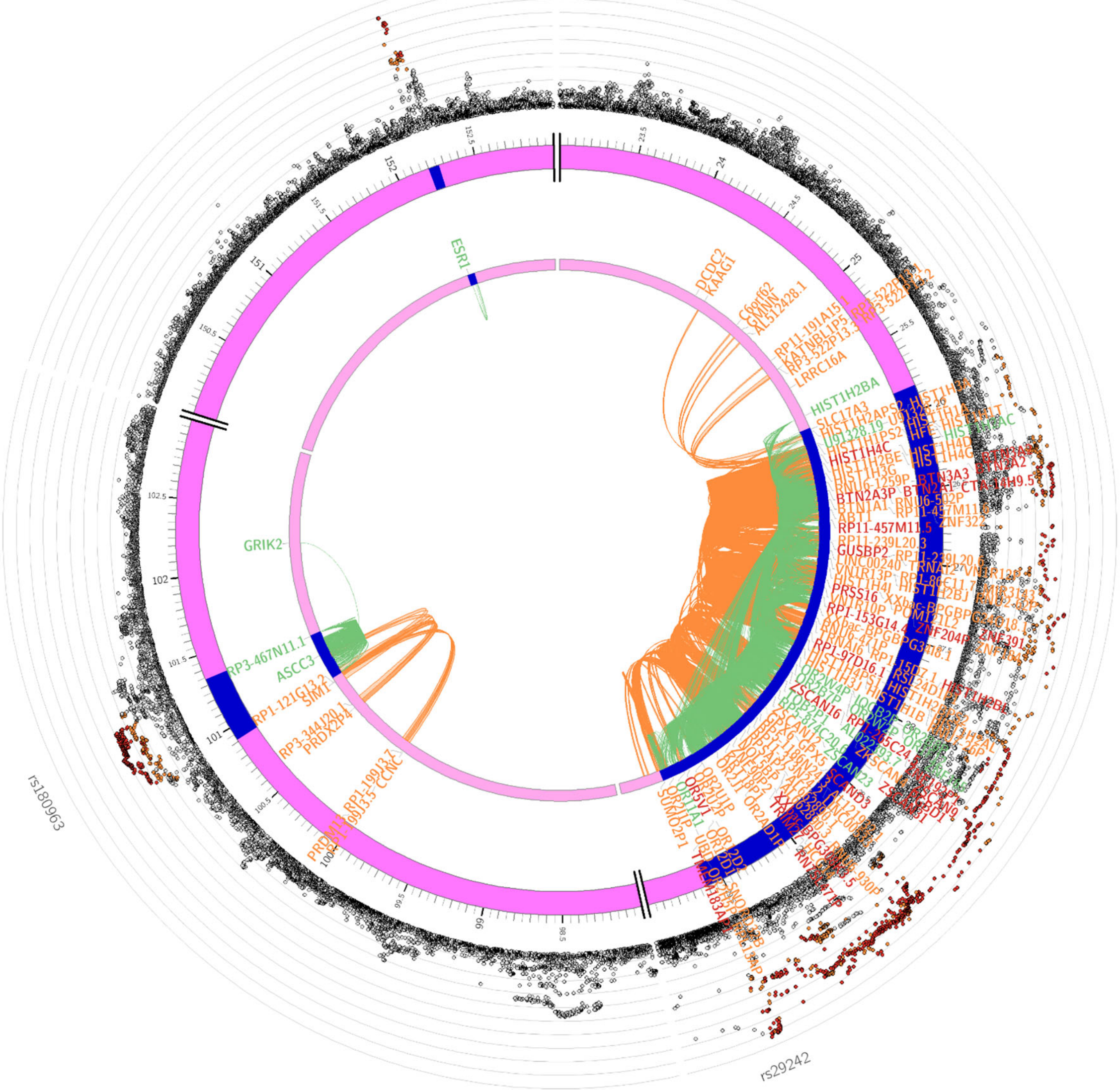

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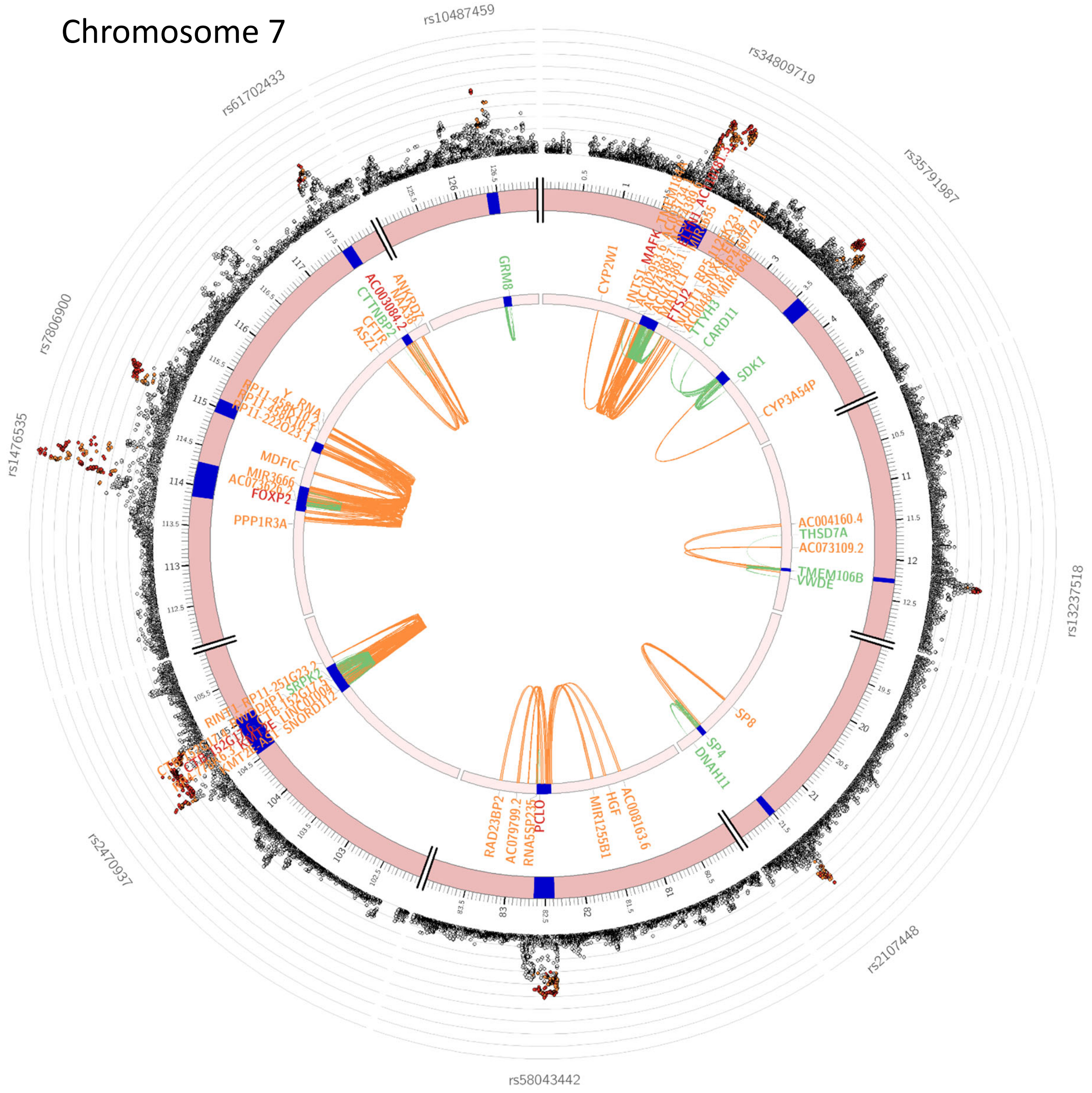

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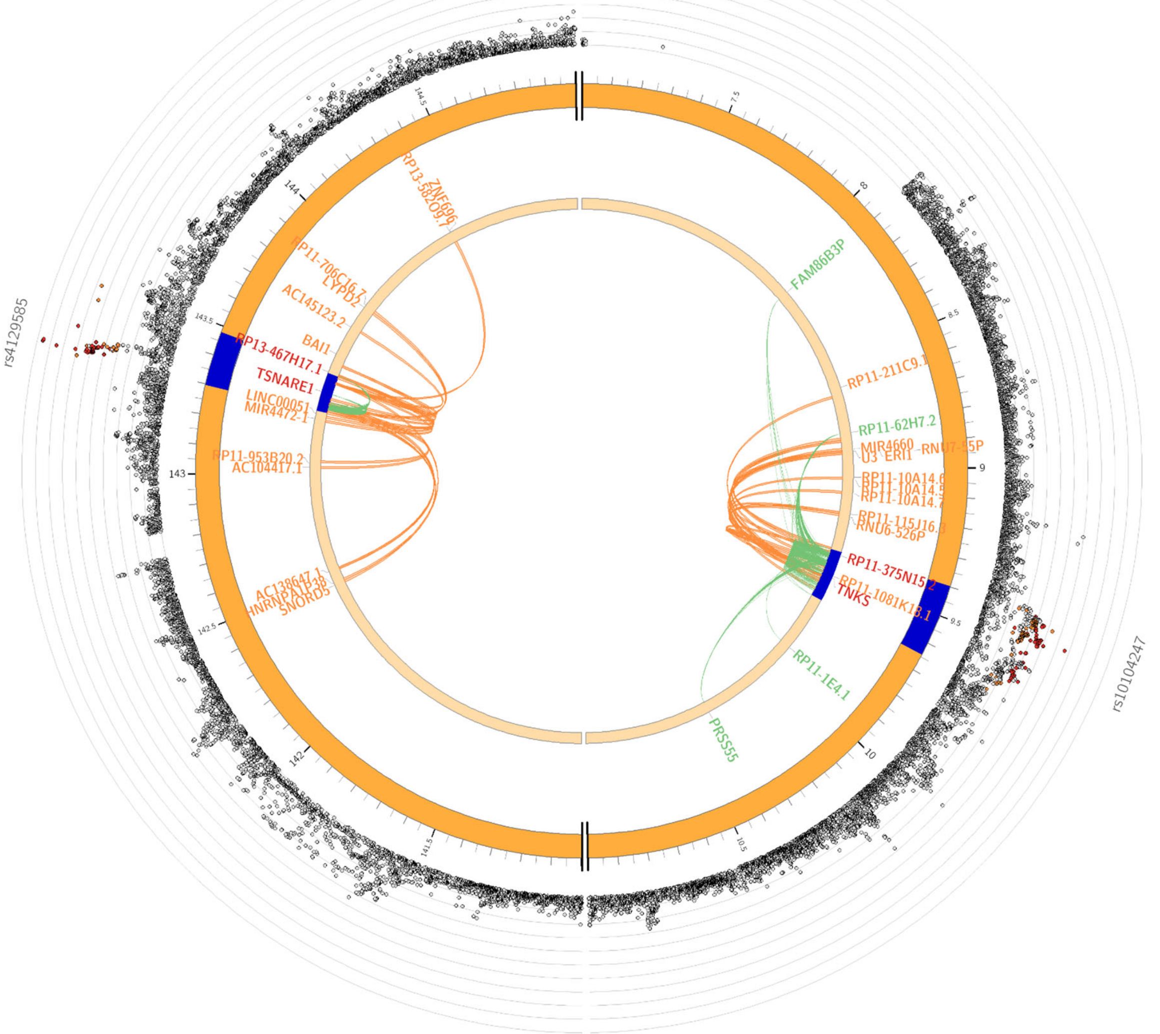
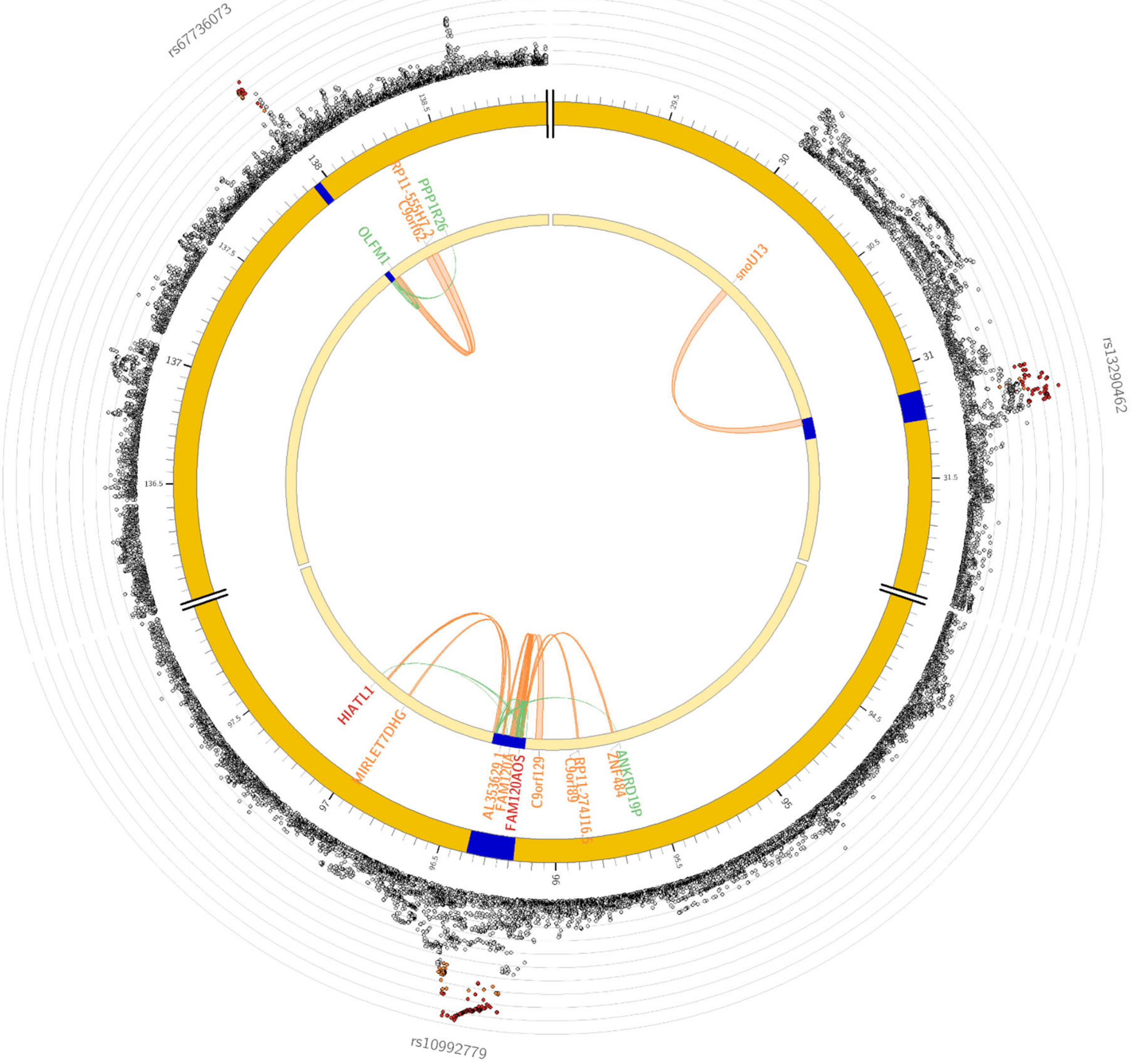
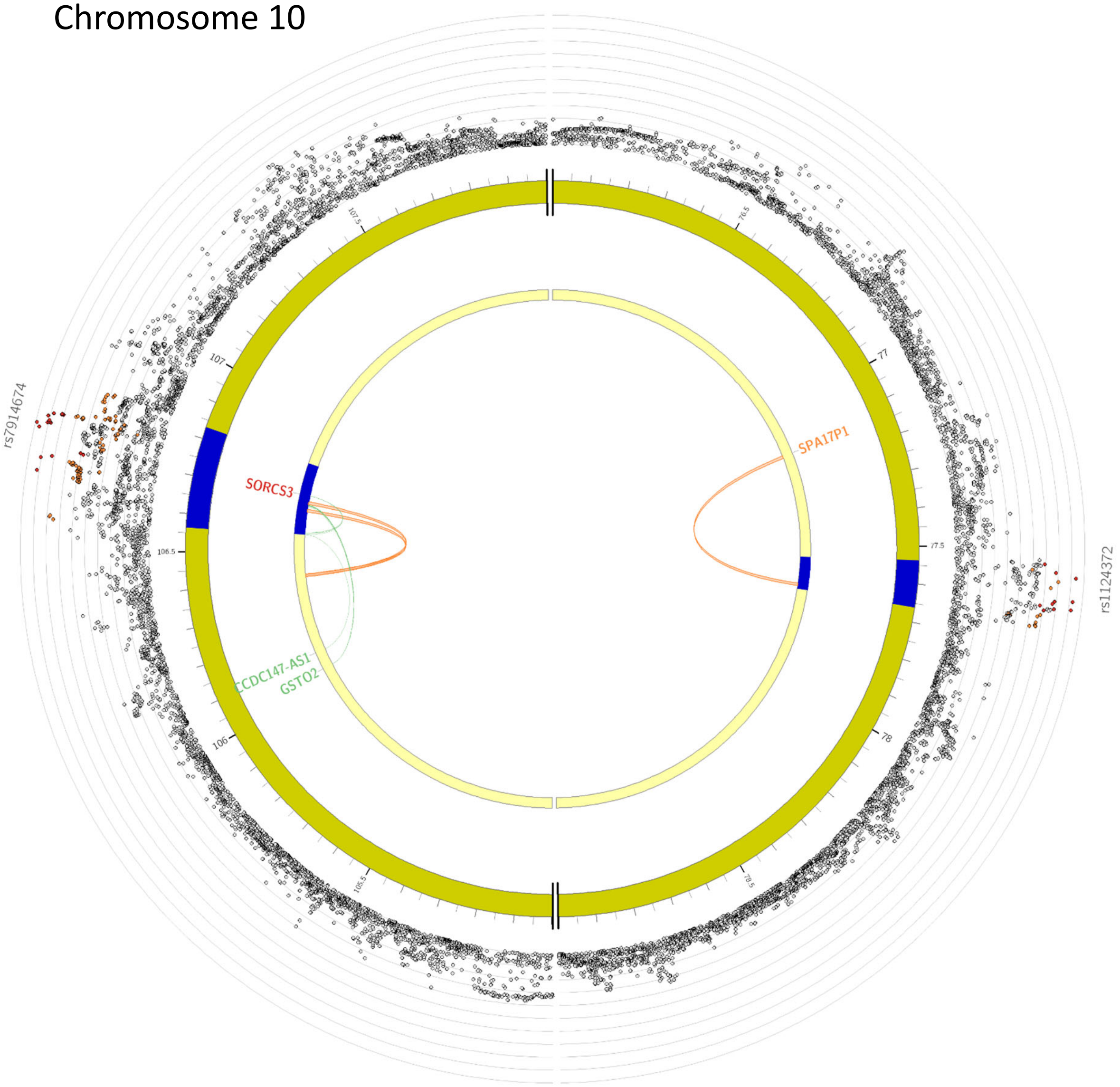


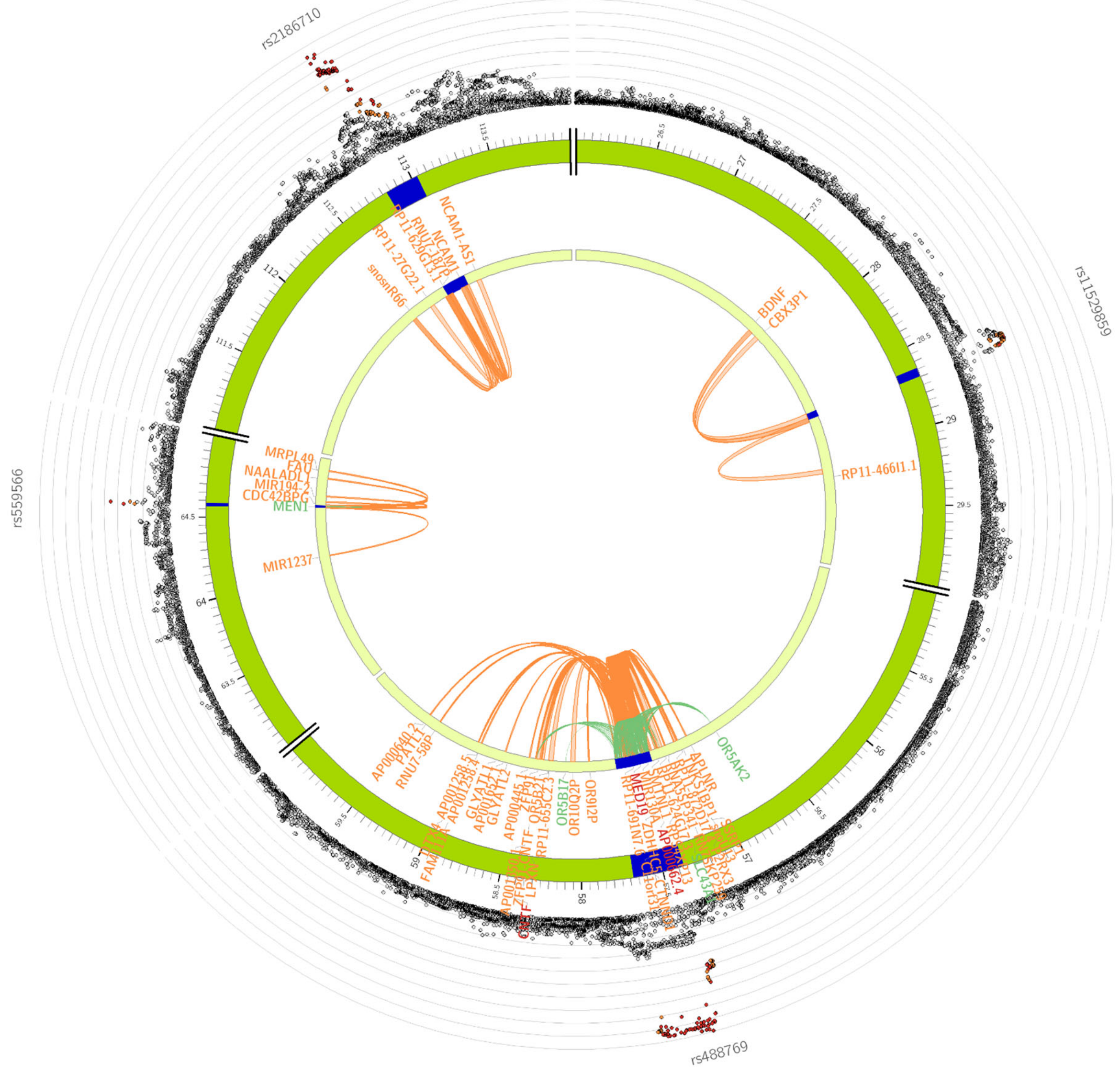
Chromosome 9



Chromosome 10



Chromosome 11



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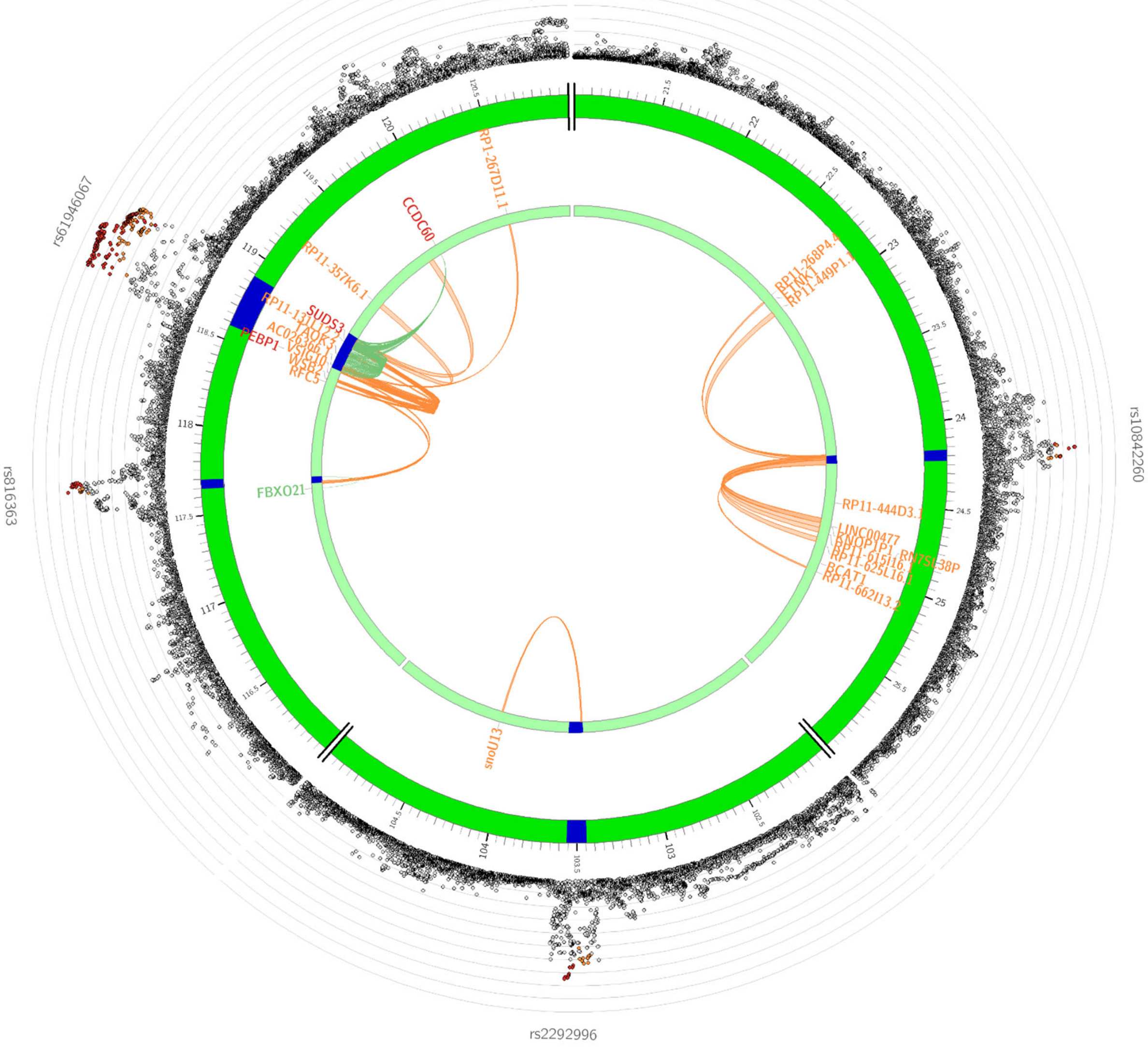

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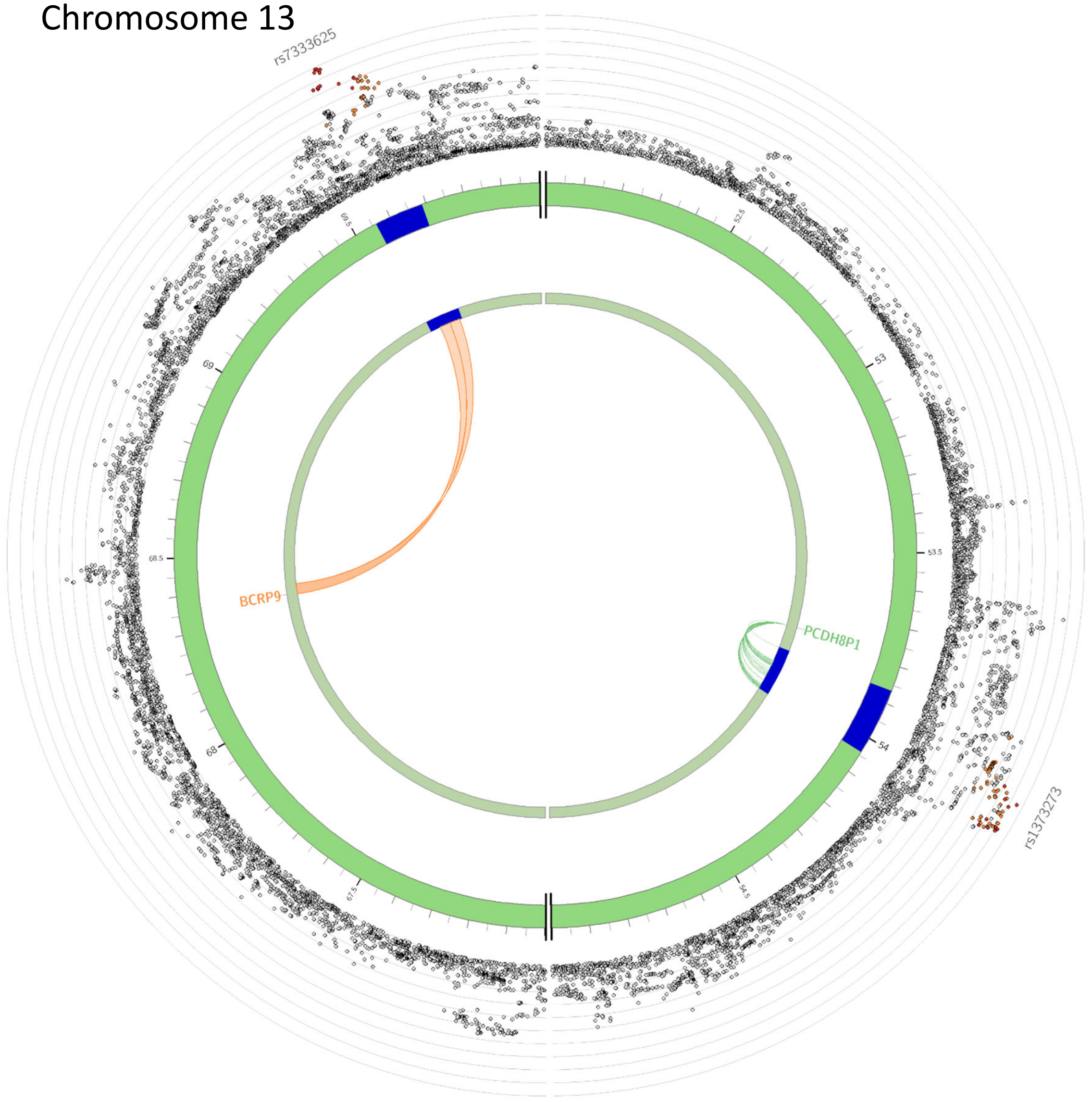
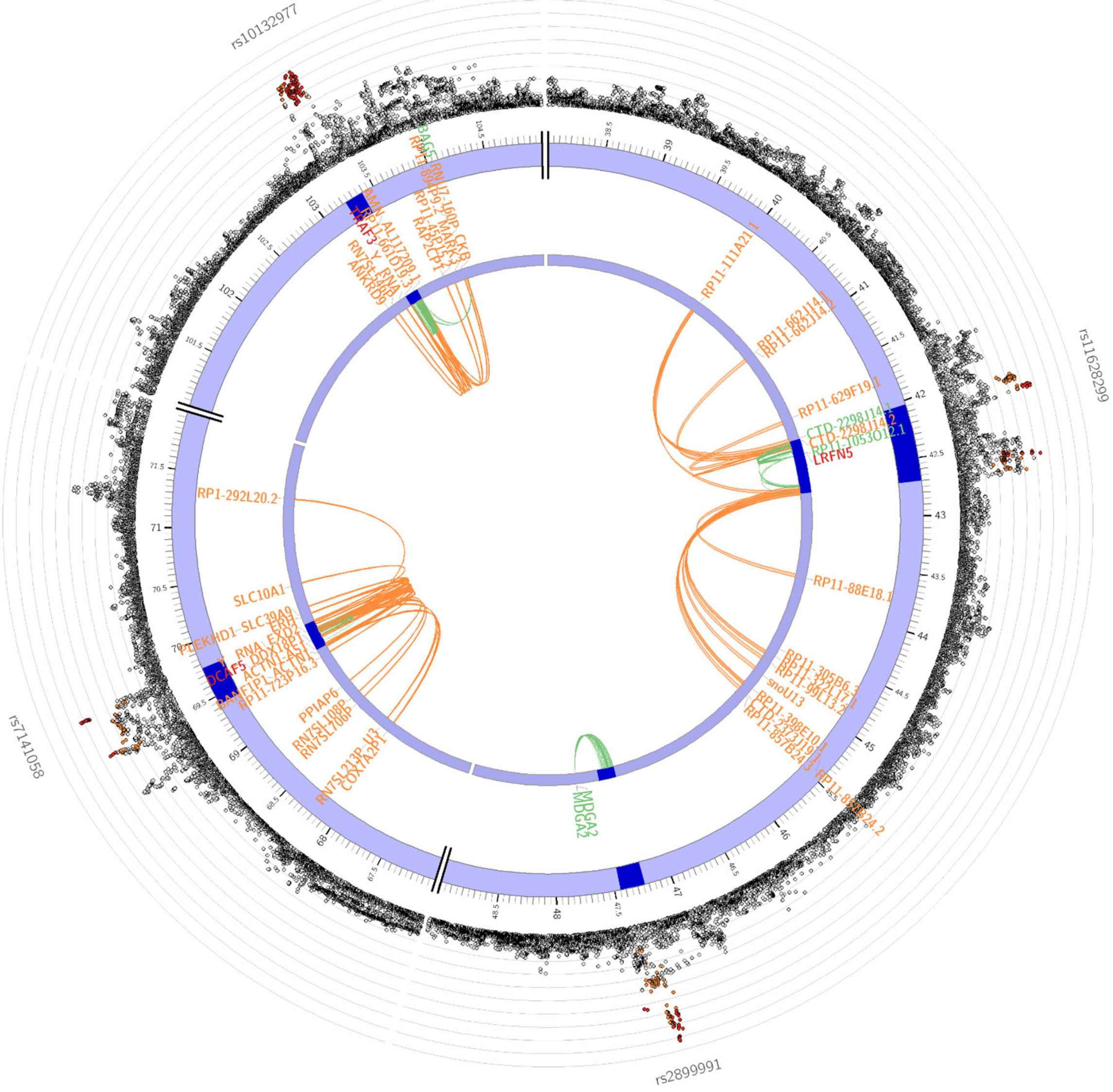
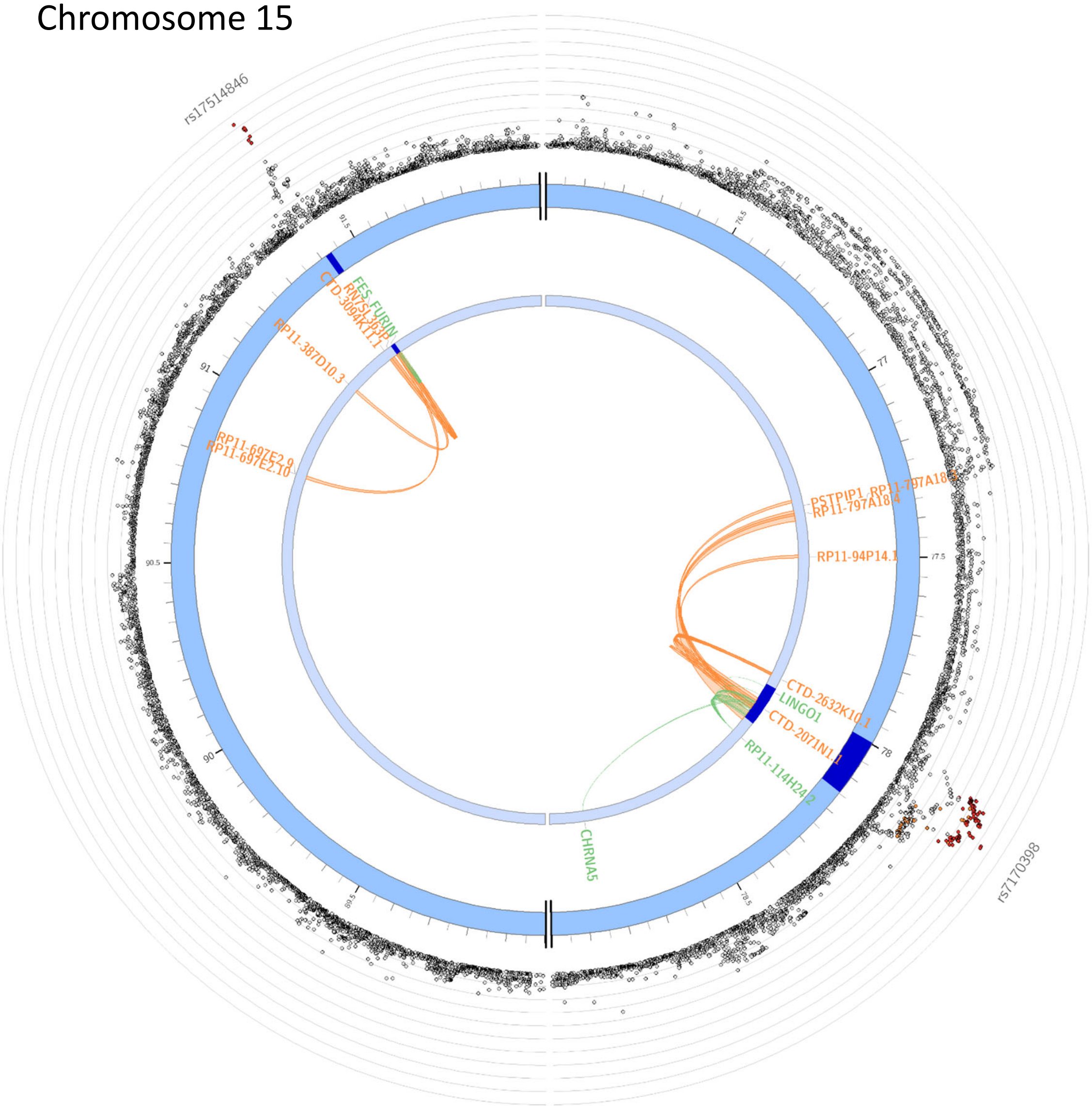


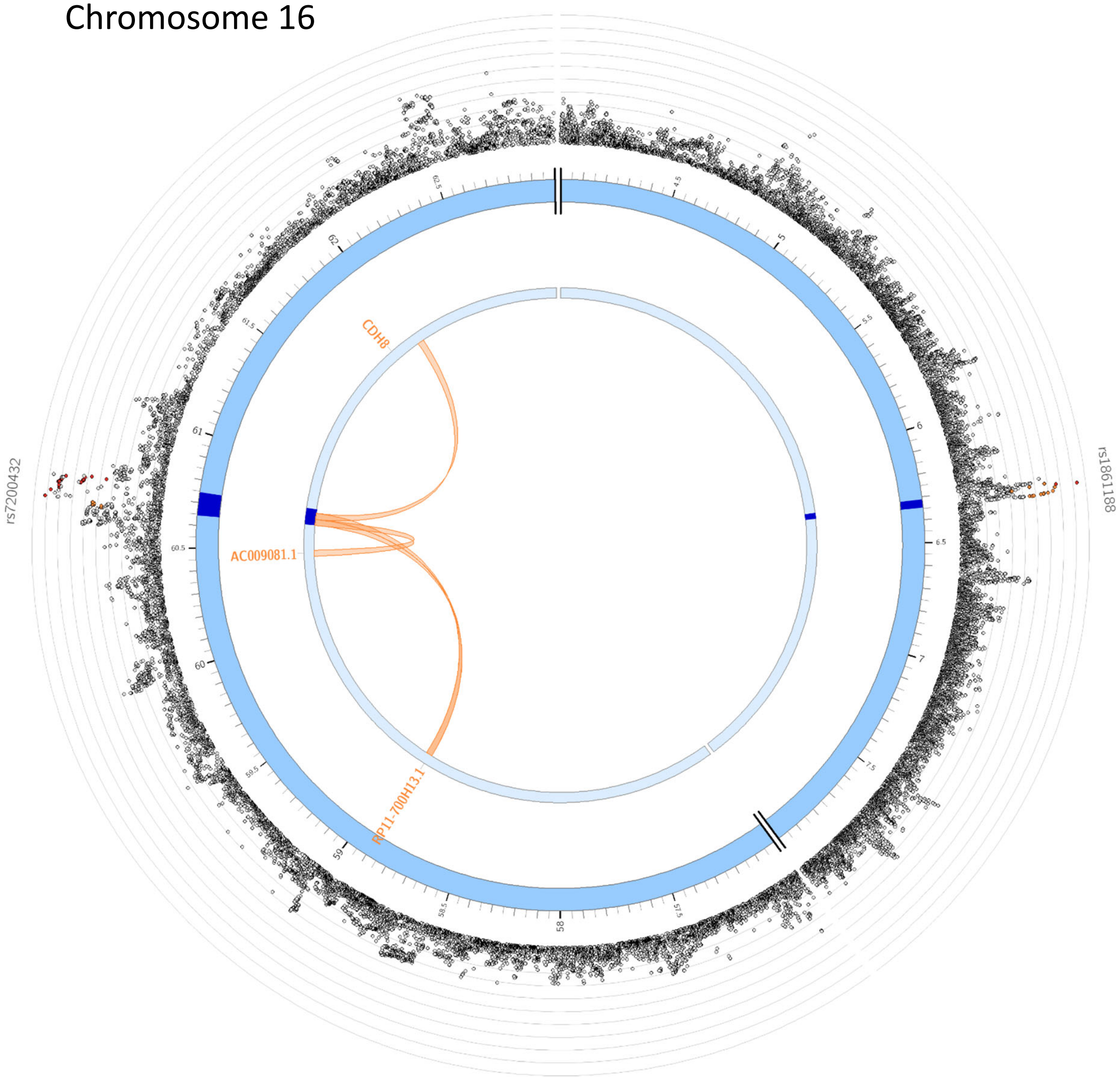
Chromosome 14



Chromosome 15



Chromosome 16



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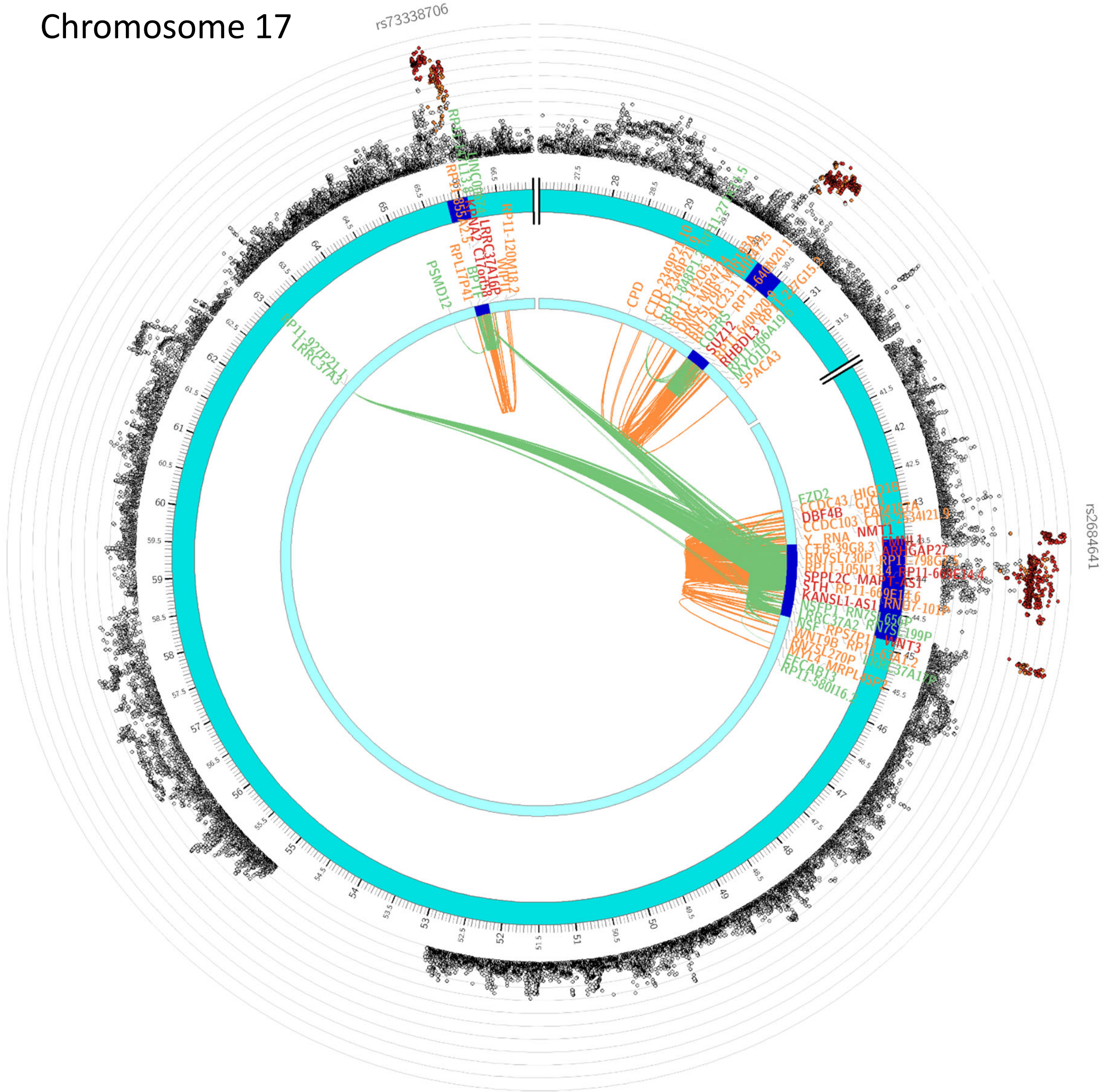

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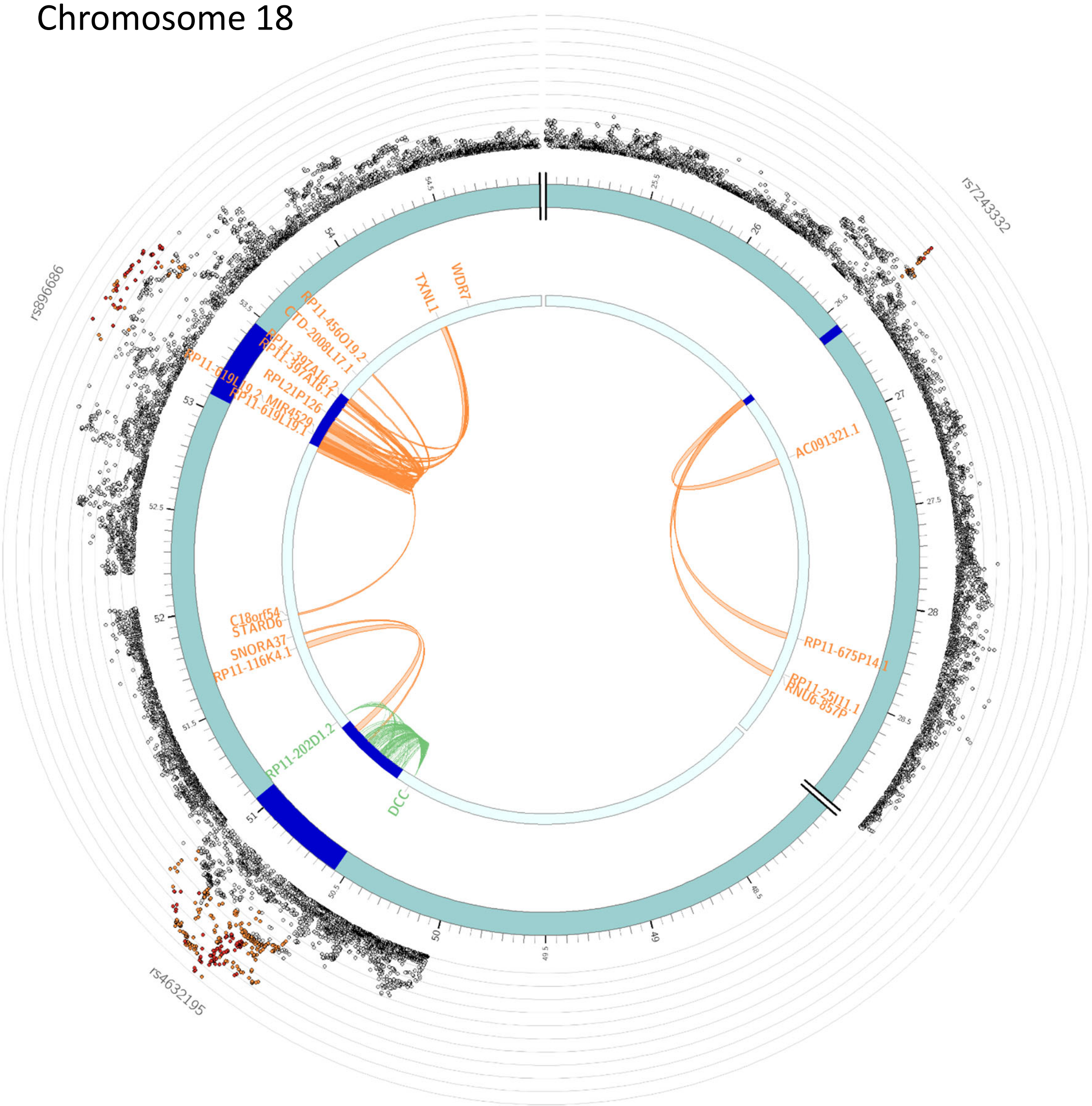

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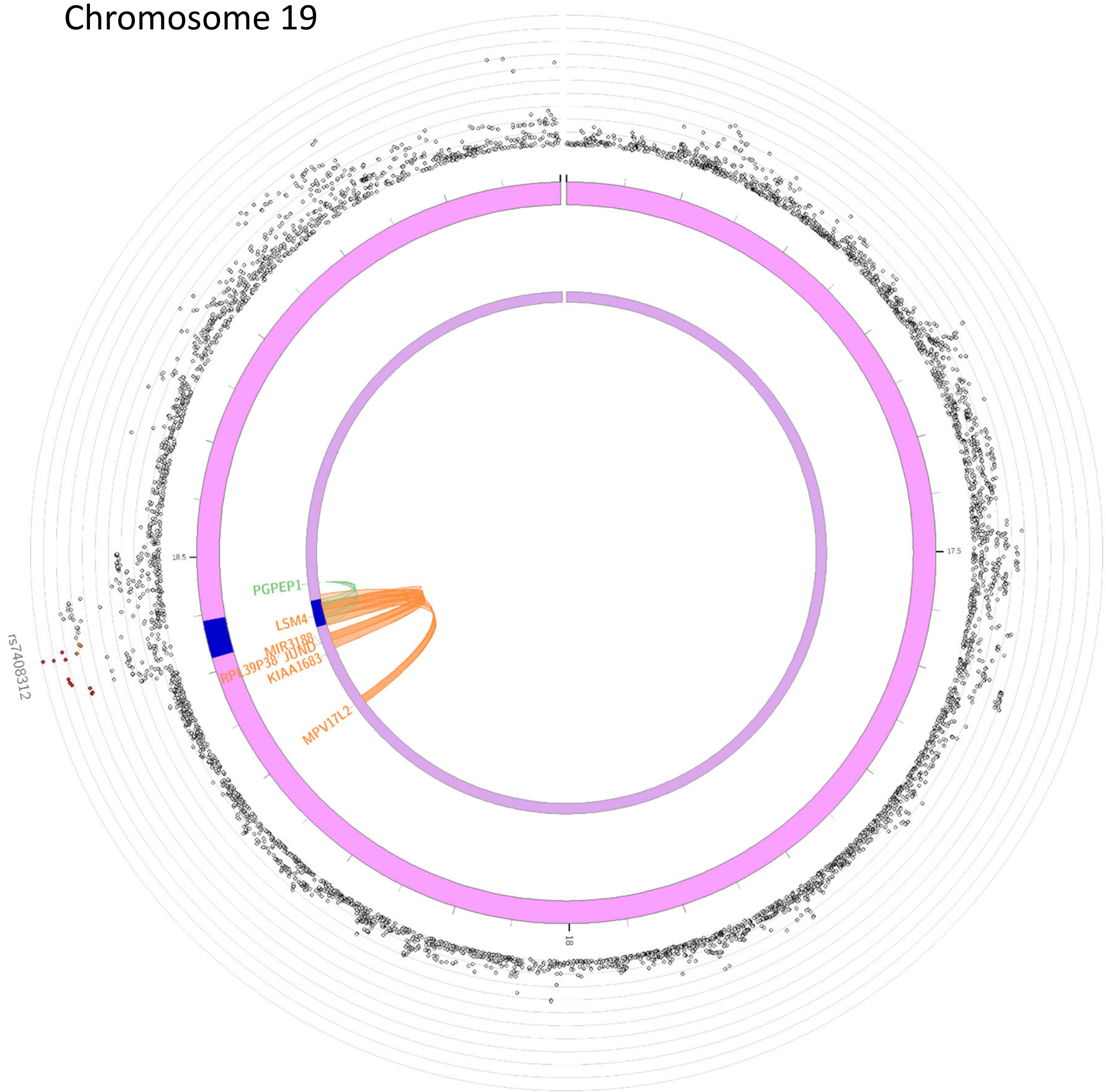
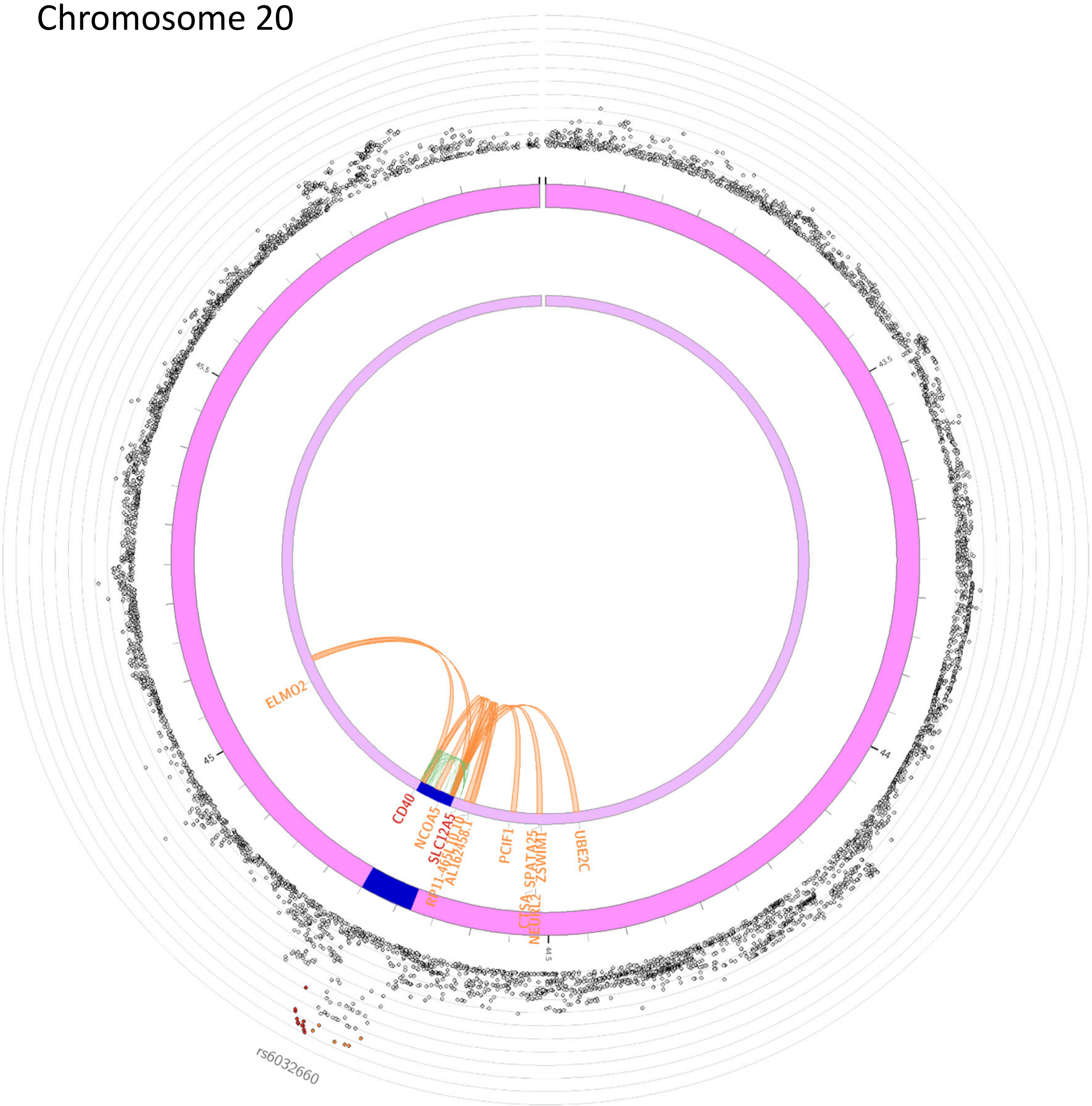


Chromosome 20



Chromosome X