

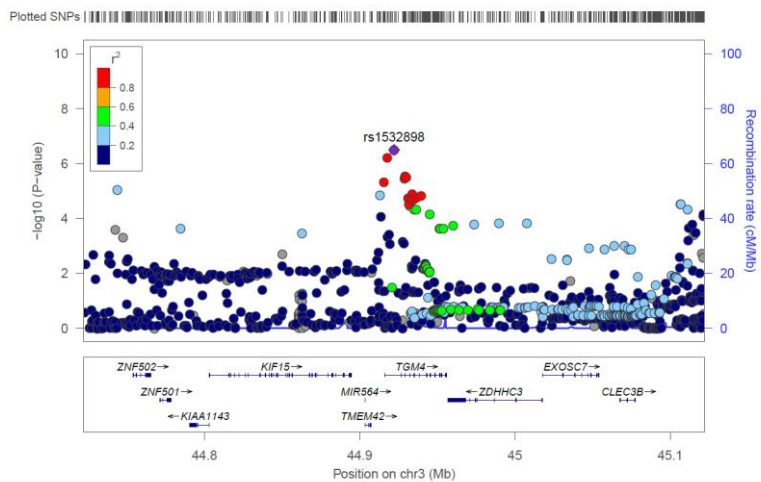
Genome-wide association study suggests that variation at the RCOR1 locus is associated with tinnitus in UK Biobank.

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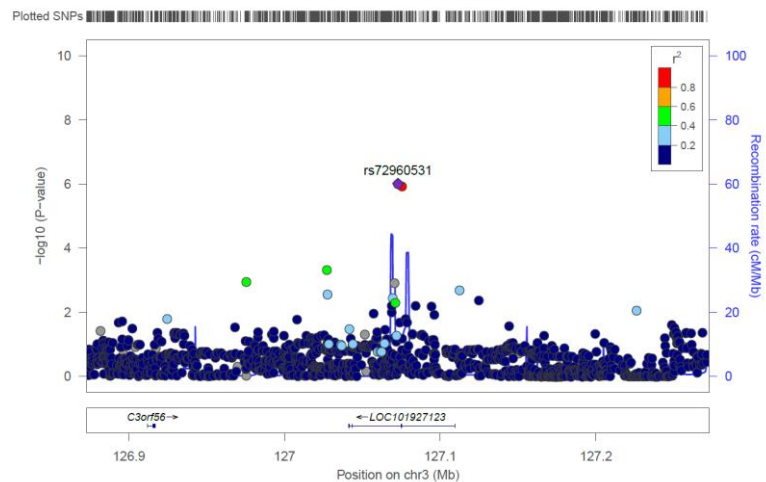
Supplementary Figure 1. Locus plots for each of the 11 suggestive loci.

Supplementary Figure 2. Manhattan plot for genetic association analysis with severest tinnitus subgroup only

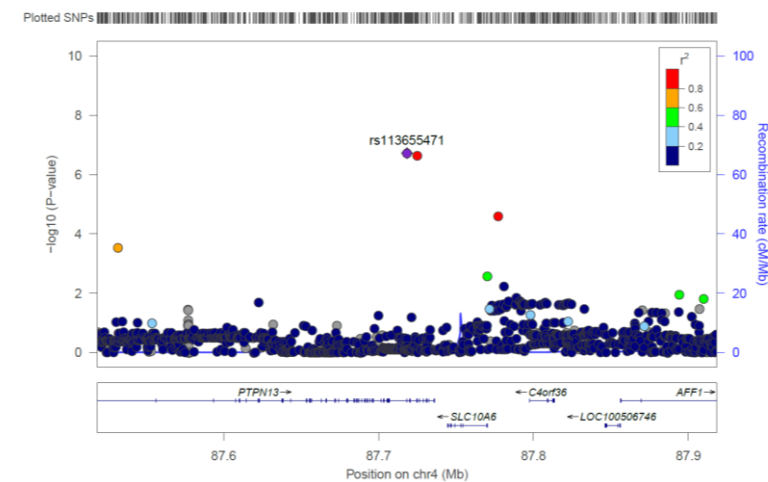
rs1532898 tinnitus



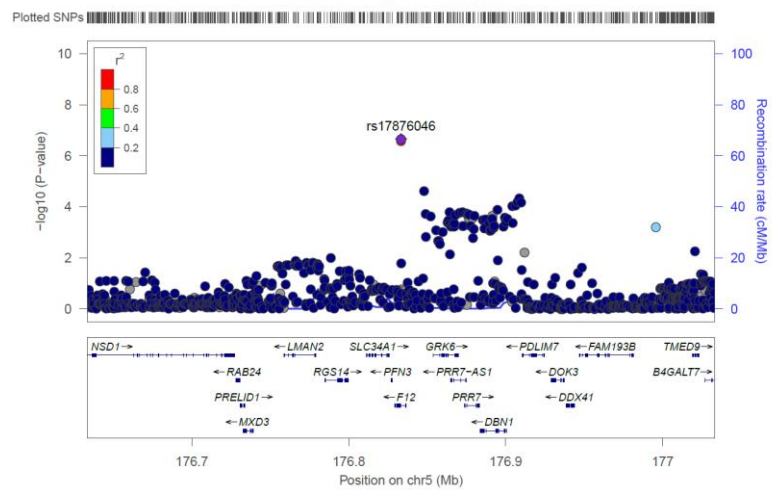
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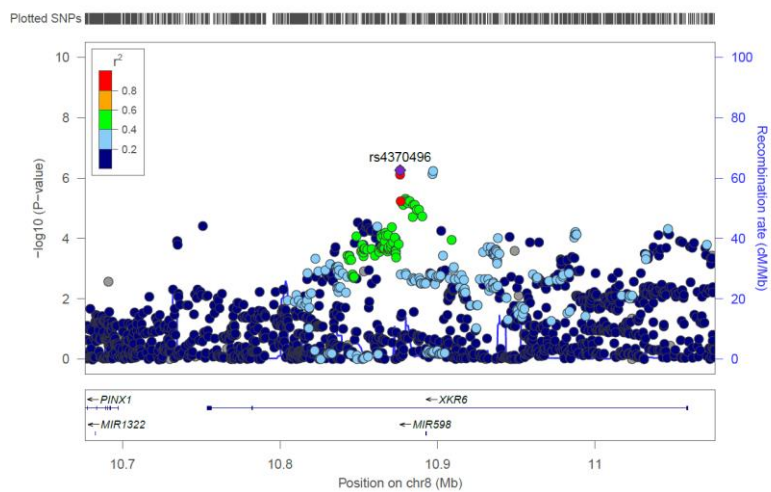
rs113655471 tinnitus



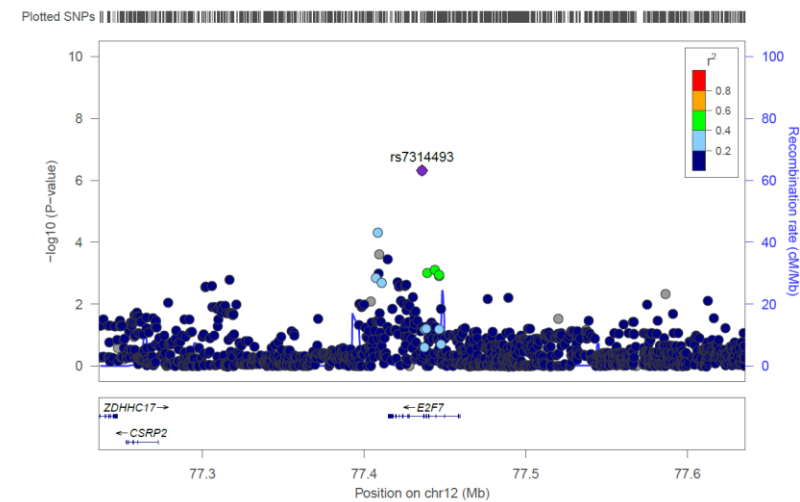
rs17876046 tinnitus

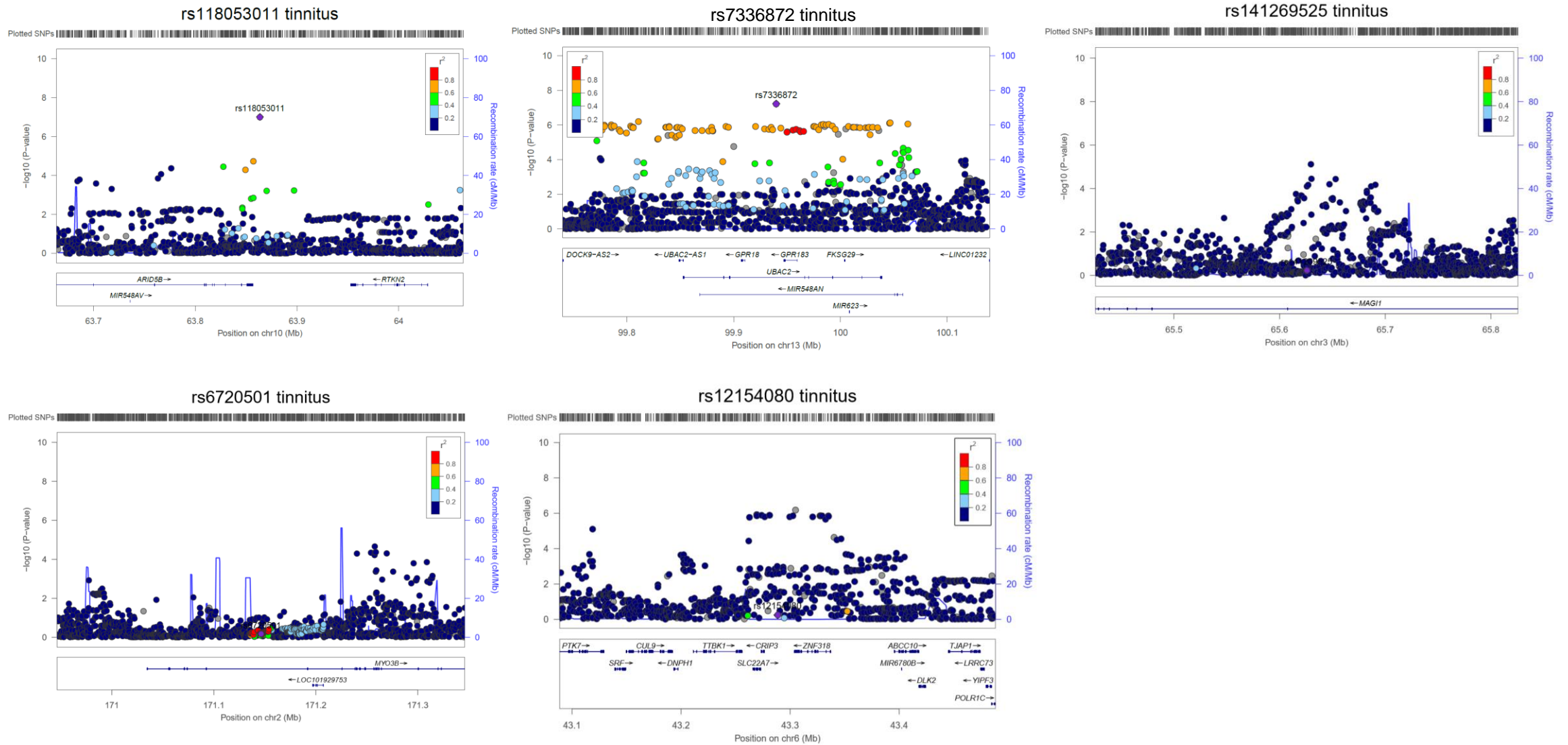


rs4370496 tinnitus



rs7314493 tinnitus





Supplementary Figure 1. Locus Plots for 11 loci at suggestive level associations with tinnitus in UKBB. Purple indicates lead independent SNP generated from GCTA-COJO conditional analysis. The colouring of remaining SNPs is based on the linkage disequilibrium (r^2) with the leads. Where LD information is not available, SNPs are coloured grey. The genes within the region are annotated and the direction of transcription is indicated by arrows. Plots were generated using LD Zoom and for 3 loci the lead SNPs were not available and for these the region around the closest available SNP in LD Zoom was plotted [rs6720501 for 2:171146084_CTT_C; rs1215408 for rs553448379; rs141269525 for rs557511691].

Supplementary Figure 2. Manhattan plot for genetic association analysis with severest tinnitus subgroup only
The red dotted line marks the genome-wide significance threshold of $P < 5E-08$.

