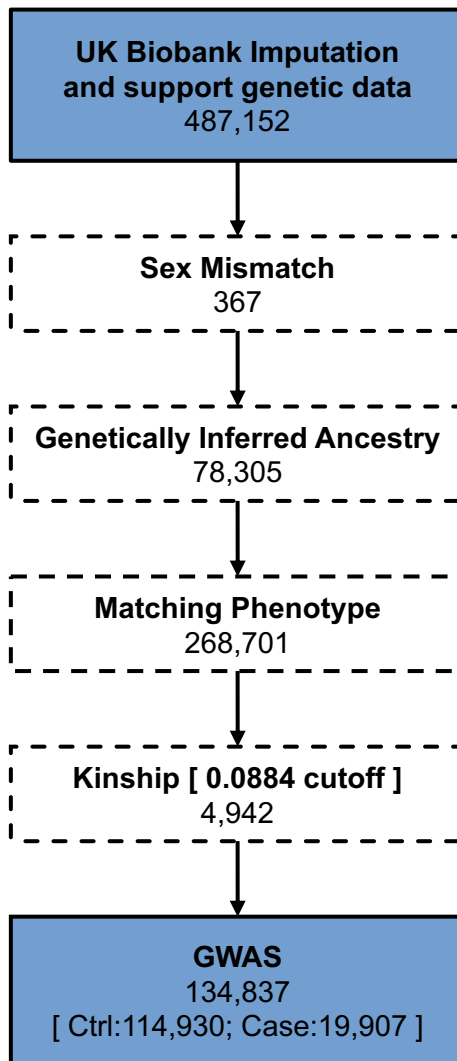**Supplemental Figures**

Comparison of GWAS results between *de novo* tinnitus and cancer treatment-related tinnitus suggests distinctive roles for genetic risk factors

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Supplemental Figure 1. Outline of sample preparation for genome wide association analysis in UK Biobank.
Dashed boxes designate filtration steps with number of removed subjects.
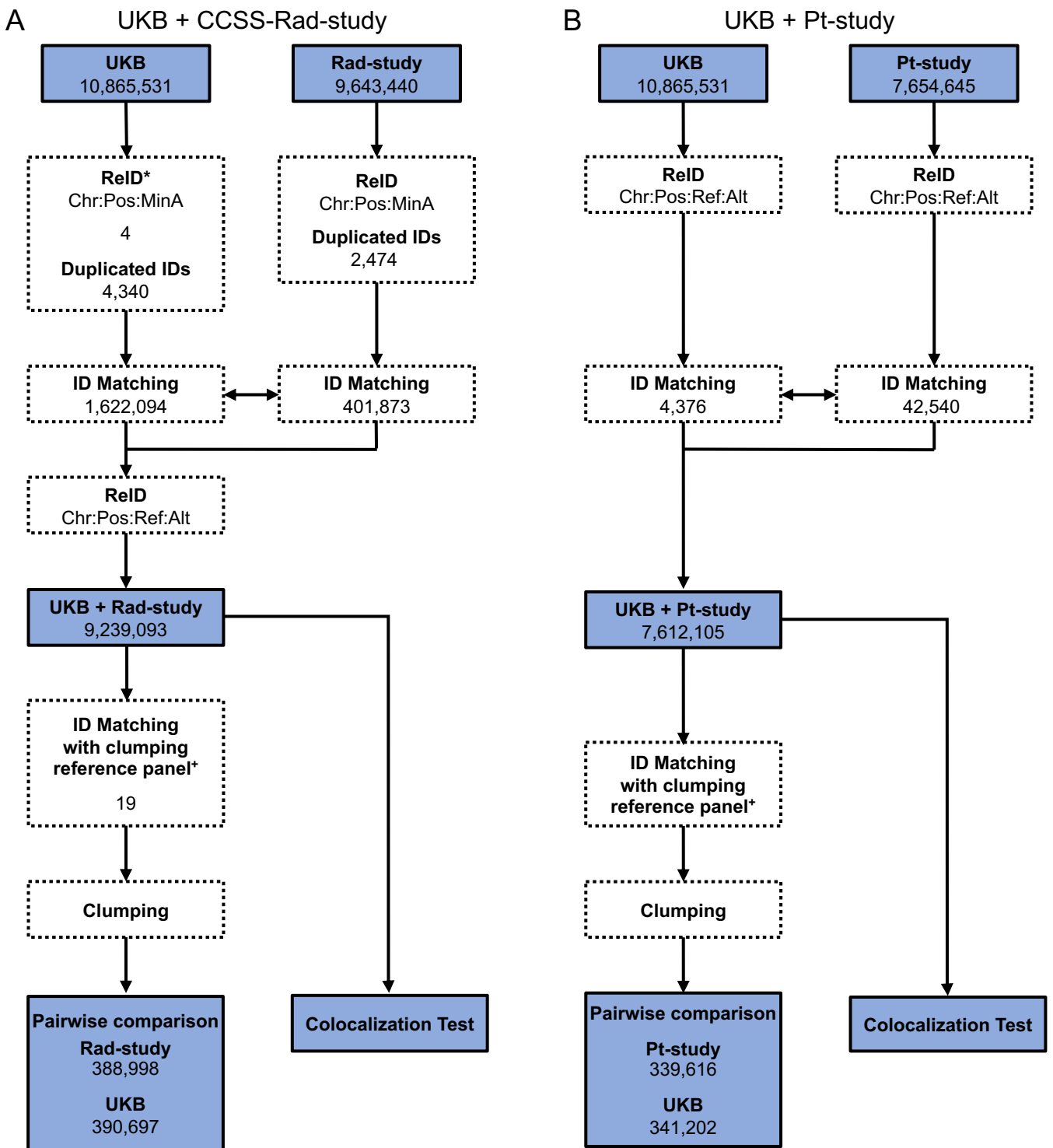
Supplemental Figure 2. Preparation of GWAS summary statistics for pairwise comparison and colocalization analyses. (A) Alignment and clumping of variants shared between the UK Biobank and the CCSS-Rad-study datasets. After variant ID matching, reference and alternative allele information from the UK Biobank dataset were applied to CCSS-Rad-study. **(B)** Alignment and clumping of variants shared between the UK Biobank and the Pt-study datasets. Blue boxes designate input and output data. Dashed boxes show action steps and variants excluded. Solid boxes show the intermediate data and number of their variants. *Removed 4 variants with equal allele frequencies in UK Biobank. + Reference matching performed by PLINK prior to clumping. Rad-study: CCSS-Rad-study.
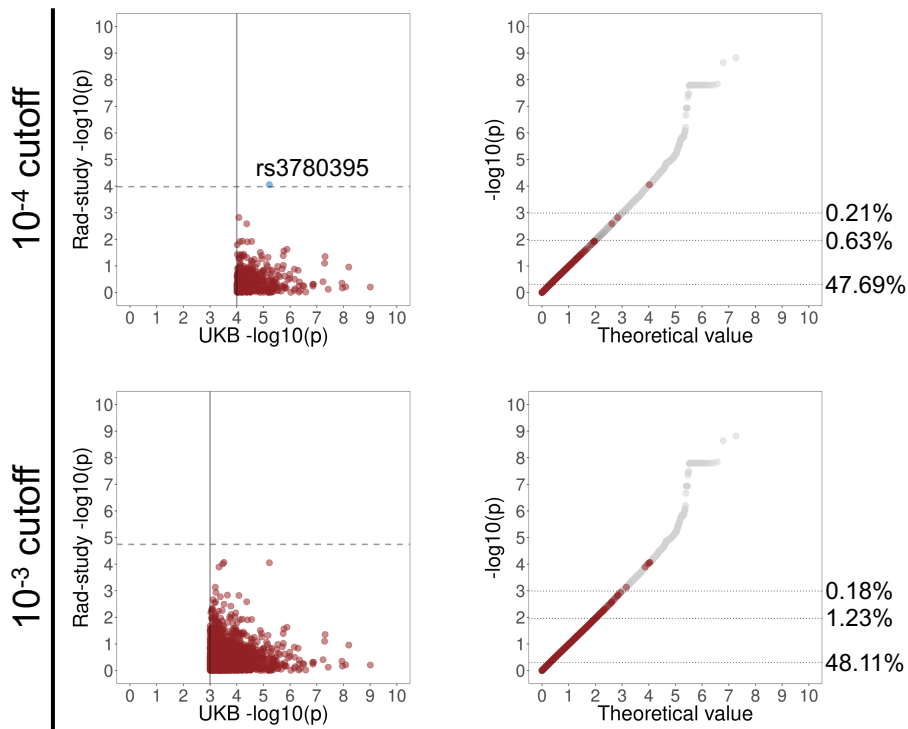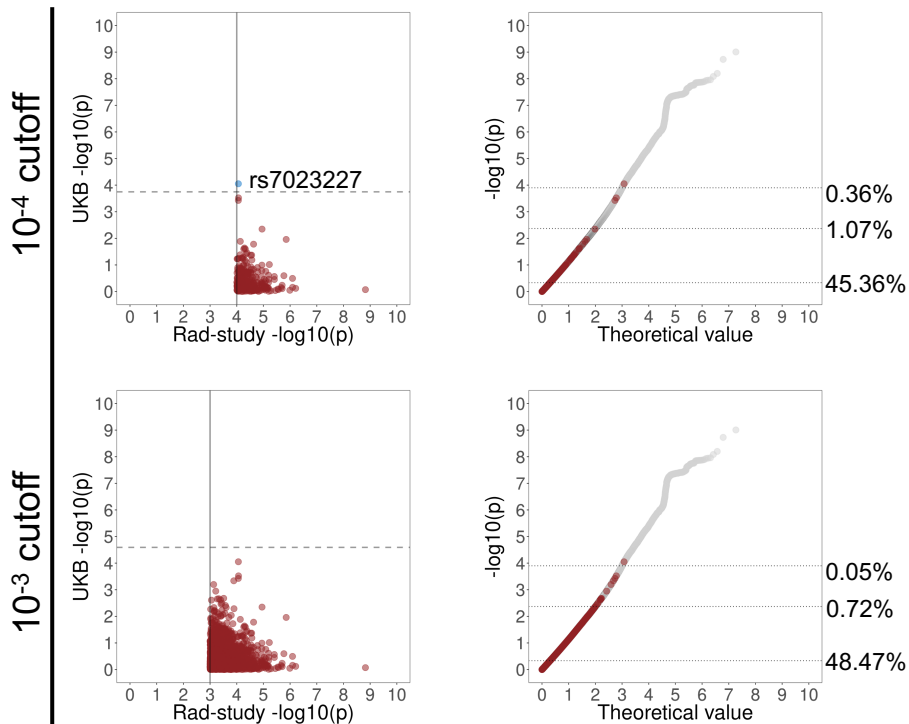
Supplemental Figure 3. Pairwise comparison of lead variants associated with tinnitus across UK Biobank and CCSS-Rad-study using cutoffs of 10^{-4} and 10^{-3}. (A) Distribution of the UK Biobank lead variants in the CCSS-Rad-study results. Left panel shows -log10(p) of the UK Biobank lead variants across both GWA sets. Blue color indicates matching direction of effect size in the significant variants. Right panel shows the position of the UK Biobank lead variants (red) in the QQ plot of the CCSS-Rad-study GWA results (grey). **(B)** Distribution of the CCSS-Rad-study lead variants in the UK Biobank results. Left panel shows the -log10(p) of the CCSS-Rad-study lead variants across both GWA sets. Right panel shows the position of the CCSS-Rad-study lead variants (red) in the QQ plot of the UK Biobank results (grey). Dotted lines show the 50th, 99th and 99.9th percentiles of the base dataset and values next to them show percent of the lead variants of the target dataset above each line. Solid line: cutoff; dashed line: the Bonferroni corrected replication cutoff. Rad-study: CCSS-Rad-study.
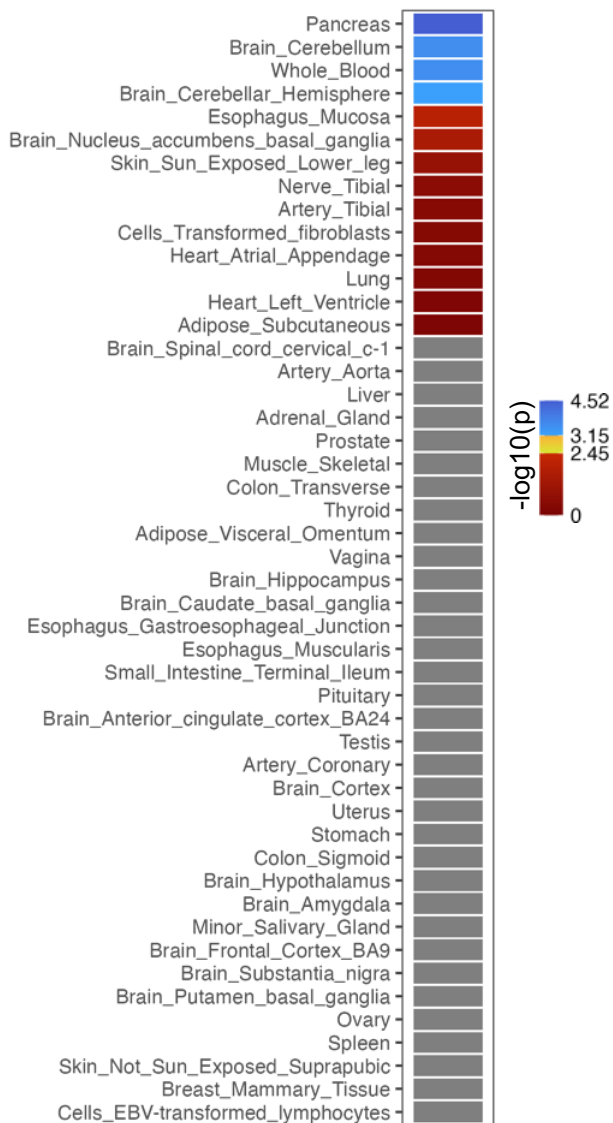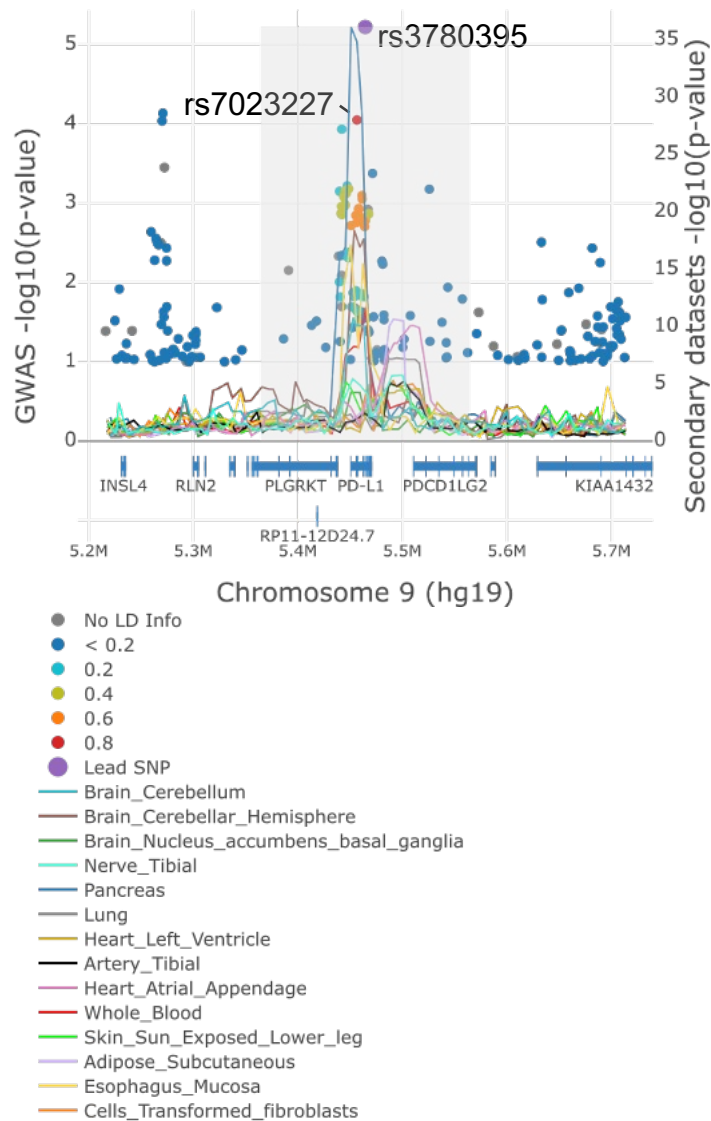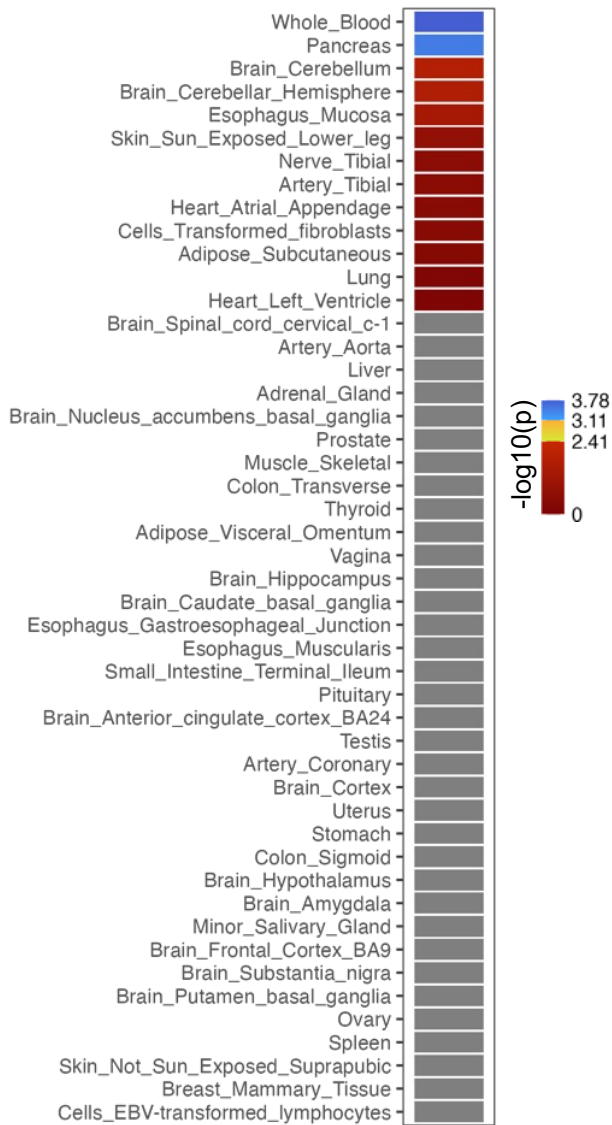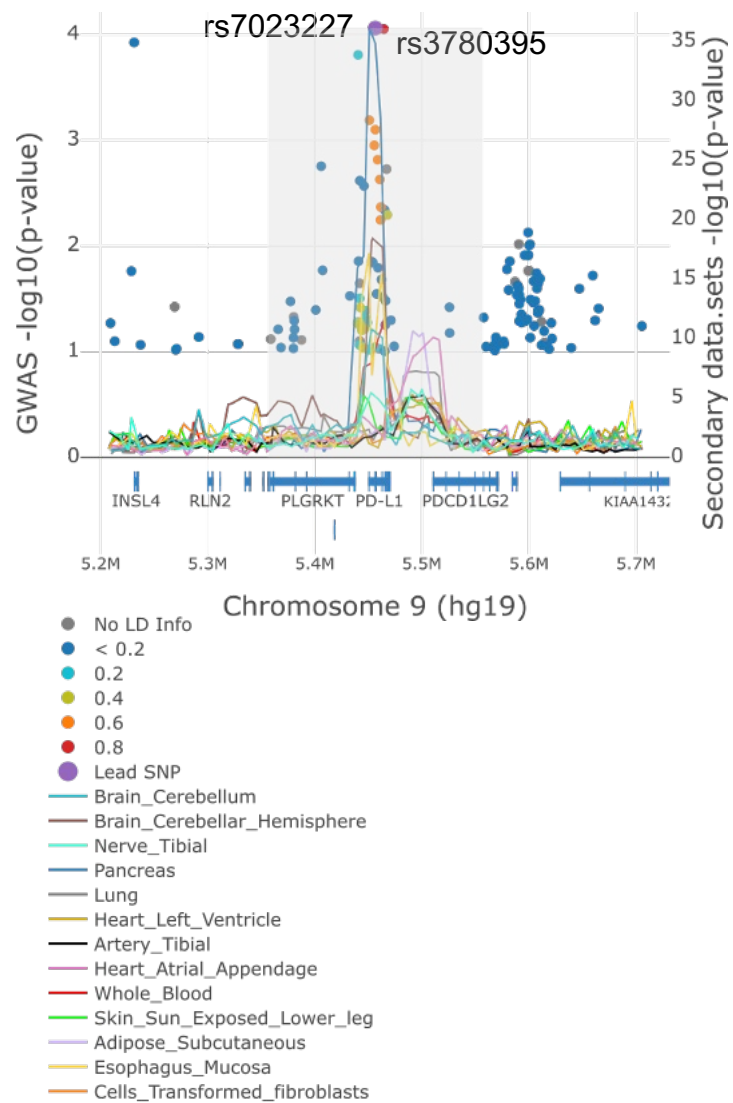
Supplemental Figure 4. LocusFocus colocalization of the UK Biobank GWAS results and eQTL associations for CD274 expression. A. Heatmap of the Simple Sum p-values for colocalization across 48 tissues. Gray boxes were excluded during first stage filtration. 2.45 and 3.15 represent converted p-value cutoffs of 0.05 and 0.01 respectively, after the Bonferroni correction. **B.** A Manhattan plot of the UK Biobank GWAS results at rs3780395 with trendlines following variant associations with expression of CD274 in the tissues tested for colocalization. Gray region shows the 100 kb distance from the lead GWAS variant (rs3780395), used for colocalization analyses.

Supplemental Figure 5. LocusFocus colocalization of the CCSS-Rad-study GWAS results and eQTL associations for CD274 expression. A. Heatmap of the Simple Sum p-values for colocalization across 48 tissues. Gray boxes were excluded during first stage filtration. 2.41 and 3.11 represent converted p-value cutoffs of 0.05 and 0.01 respectively, after the Bonferroni correction. **B.** A Manhattan plot of the CCSS-Rad-study GWAS results around rs7023227 with trendlines following variant associations with expression of CD274 in the tissues tested for colocalization. Gray region shows the 100 kb distance from the lead GWAS variant, used for colocalization analyses.
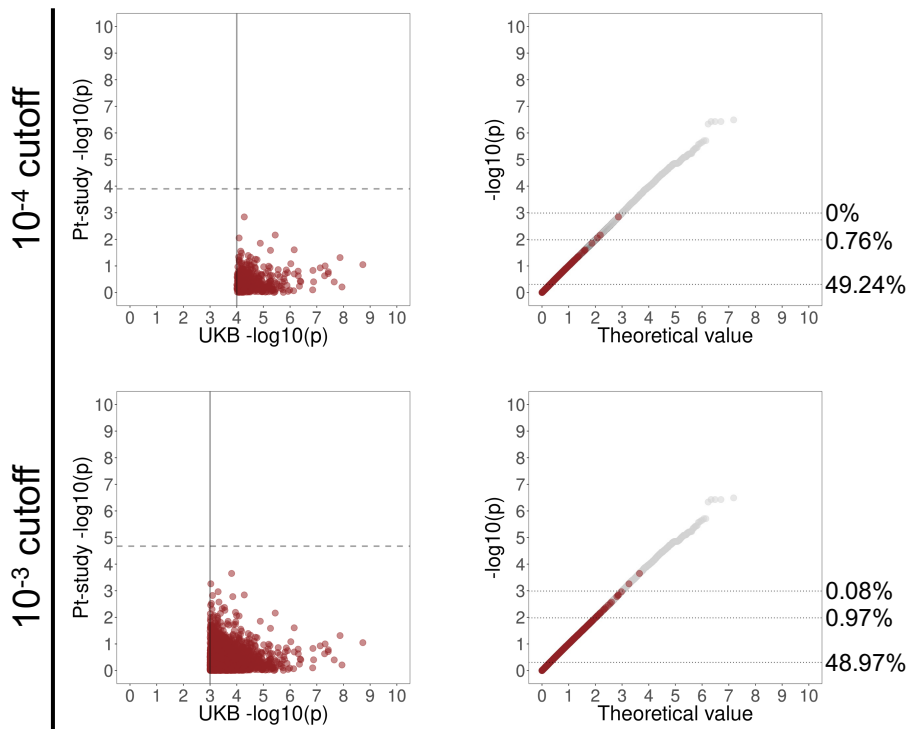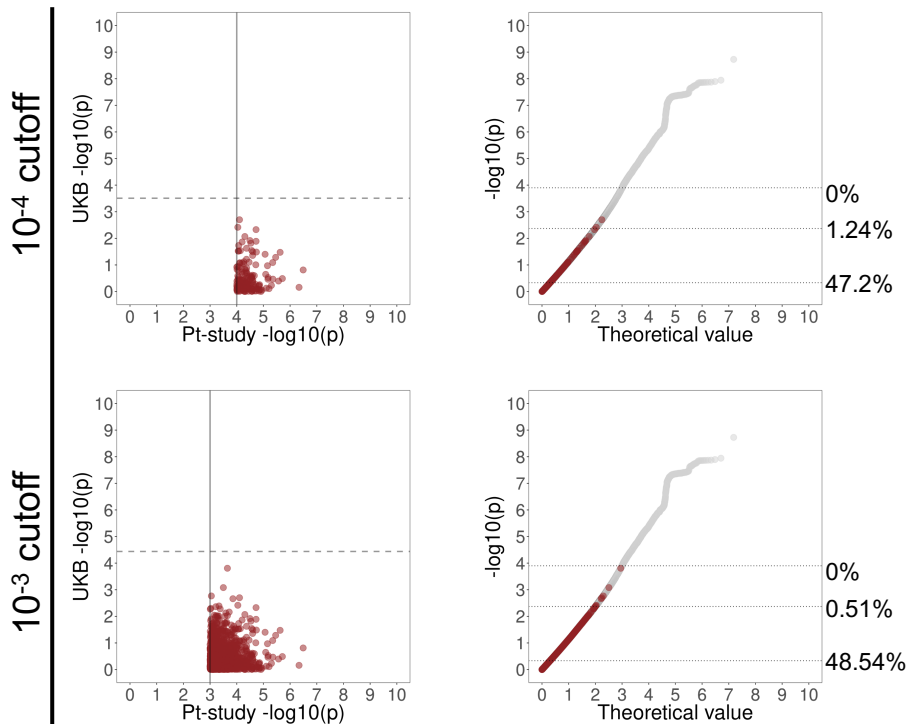
Supplemental Figure 6. Pairwise comparison of lead variants associated with tinnitus across UK Biobank and Pt-study using cutoffs of 10^{-4} and 10^{-3}. (A) Distribution of the UK Biobank lead variants in the Pt-study results. Left panel shows -log10(p) of the UK Biobank lead variants across both GWA sets. Right panel shows the position of the UK Biobank lead variants (red) in the QQ plot of the Pt-study GWA results (grey). **(B)** Distribution of the Pt-study lead variants in the UK Biobank results. Left panel shows the -log10(p) of the Pt-study lead variants across both GWA sets. Right panel shows the position of the Pt-study lead variants (red) in the QQ plot of the UK Biobank results (grey). Dotted lines show the 50th, 99th and 99.9th percentiles of the base dataset and values next to them show percent of the lead variants of the target dataset above each line. Solid line: cutoff; dashed line: the Bonferroni corrected replication cutoff.