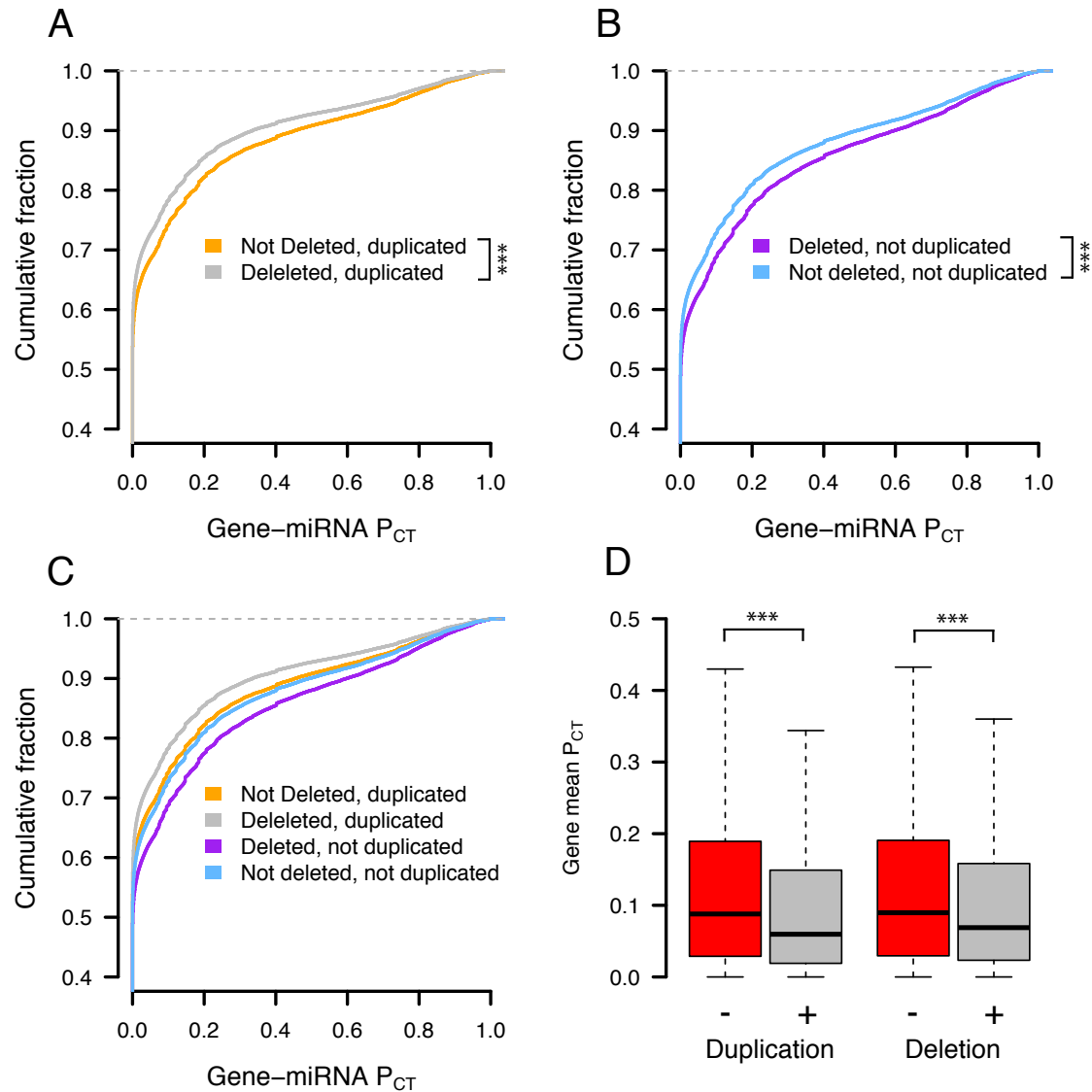




**Supplemental Figure S1: Effect of deletion status on autosomal  $P_{CT}$  scores.** Probabilities of conserved targeting ( $P_{CT}$ ) of all gene-miRNA interactions involving non-deleted and deleted genes, further stratified as (A) duplicated (grey,  $n = 69,339$  interactions from 4,118 genes; orange,  $n = 51,514$  interactions from 2,916 genes) or (B) not duplicated (purple,  $n = 72,826$  interactions from 3,510 genes; blue,  $n = 80,290$  interactions from 3,976 genes). \*\*\*  $p < 0.001$ , two-sided Kolmogorov-Smirnov test. (C)  $P_{CT}$  scores for all gene sets in (A) and (B) superimposed on one plot. (D) Mean gene-level  $P_{CT}$  scores when aggregating sets of duplicated/not duplicated (left) or deleted/not deleted (right) genes. \*\*\*  $p < 0.0001$ , two-sided Wilcoxon rank-sum test.