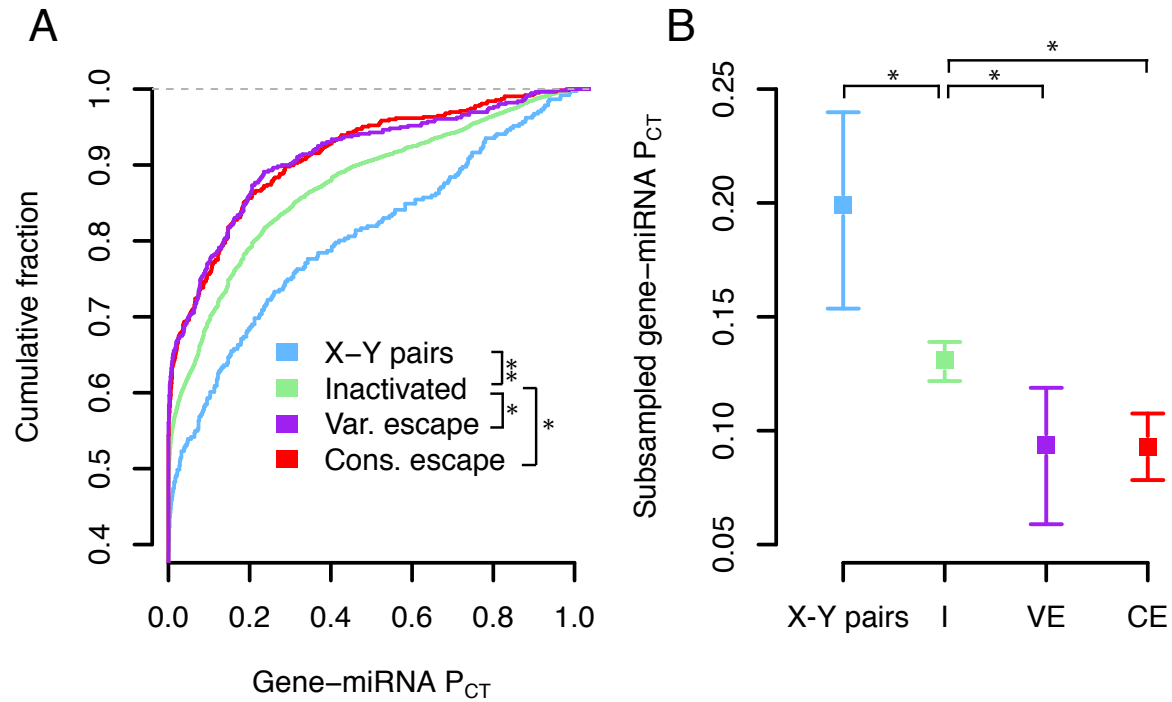




**Supplemental Figure S4:  $P_{CT}$  score comparisons with consistent and variable escape genes**

**separated.** (A)  $P_{CT}$  score distributions of all gene-miRNA interactions involving X-Y pairs ( $n = 371$  interactions from 16 genes), X-inactivated genes ( $n = 6743$  interactions from 329 genes), consistent escape genes ( $n = 567$  interactions from 30 genes), or variable escape genes ( $n = 470$  interactions from 26 genes) as defined by Balaton et al (Balaton et al., 2015). \*  $p < 0.05$ , \*\*  $p < 0.01$ , two-sided Kolmogorov-Smirnov test. (B) Resampled gene-miRNA  $P_{CT}$  scores of gene classes from (A). Points and error bars represent the median and 95% confidence intervals from 1,000 gene samplings with replacement. \*  $p < 0.05$ , empirical p-value computed as the fraction of random non-overlapping gene sets with a median difference in  $P_{CT}$  score at least as large as the true difference.