



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.