Supplemental Figure S4: $P_C T$ score comparisons with consistent and variable escape genes separated. (A) $P_C T$ 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 $P_C T$ 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 $P_C T$ score at least as large as the true difference.