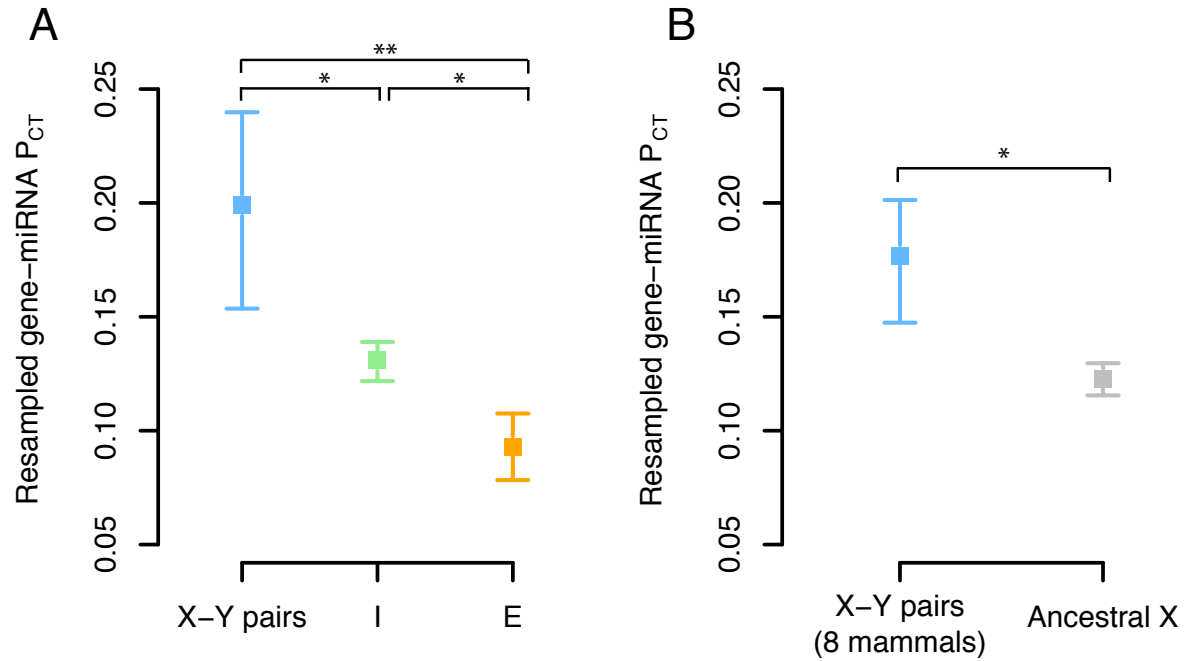




Supplemental Figure S3: Resampled mean P_{CT} scores of X-linked genes. (A) Resampled gene-miRNA P_{CT} scores for human X-Y pairs ($n = 15$ genes), X-inactivated genes ($n = 329$ genes) and X escape genes ($n = 56$ genes). (B) Resampled gene-miRNA P_{CT} scores for X-Y pairs across eight mammals ($n = 32$ genes) and genes with no Y homolog in any of eight mammals ($n = 457$ genes). Points and error bars represent the median and 95% confidence intervals from 1,000 gene samplings with replacement. * $p < 0.05$, ** $p < 0.01$, 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.