Supplemental Figure S11: Variation in within-UTR conservation cannot account for observed differences in P_{CT} score among classes of Z-linked genes. (A) Boxplots of within-UTR conservation bias (see Methods) for all gene-miRNA interactions involving chicken Z-W pairs or other ancestral X genes. Numbers of interactions and genes as in Figure 4A. ** $p < 0.01$, two-side Wilcoxon rank-sum test. (B) Comparisons of P_{CT} scores normalized by within-UTR bias. *** $p < 0.001$, two-sided Kolmogorov-Smirnov test.