



Supplemental Figure S9: P_{CT} scores of Z-W pairs across 4 and 14 birds. (A,C) P_{CT} score distributions of all gene-miRNA interactions (A) Z-W pairs including predictions from three additional birds with male and female genome sequence ($n = 2,187$ interactions from 78 genes) and other ancestral Z genes ($n = 15,357$ interactions from 607 genes), or (C) Z-W pairs including read depth-based predictions from 10 additional birds with only female genome sequence ($n = 4,458$ interactions from 157 genes) and other ancestral Z genes ($n = 13,086$ interactions from 528 genes) *** $p < 0.001$, two-sided Kolmogorov-Smirnov test. (B,D) Gene-level mean P_{CT} scores. *** $p < 0.01$, two-sided Wilcoxon rank-sum test.