Supplemental Figure S13: Ancestral miRNA targeting of Z-W pairs across 4 birds. (A)

Distributions of sites conserved between 3` UTRs of human and chicken orthologs (top) or
comparisons to background expectation (bottom, see Methods) for Z-W pairs across chicken and
three additional birds with male and female genome sequence (4 birds, n = 73) and other
ancestral Z genes (n = 532). (D) Statistics as in (C), but using sites conserved between human
and anolis 3` UTRs; Z-W pairs across 4 birds (n = 73), other ancestral Z genes (n = 527). *** p <
0.001, two-sided Fisher’s exact test.