



**Supplemental Figure S7: Background human-chicken 3' UTR conservation among classes of X-linked genes.** Mean number of human-chicken conserved sites found using shuffled miRNA seed sequences for (A) human X-Y pairs ( $n = 15$  genes), X-inactivated genes ( $n = 329$  genes) and X escape genes ( $n = 56$  genes), and (B) X-Y pairs across eight mammals ( $n = 32$  genes) and genes with no Y homolog in any of eight mammals ( $n = 457$  genes). \*\*\*  $p < 0.001$ , two-sided Wilcoxon rank-sum test.