



### Supplementary Figure 3

#### Ancestrally broad expression of Z–W pairs.

Violin plots marked with the median (black circle) and interquartile range (black bar) comparing the annotations of the human orthologs of ancestral Z–W gene pairs identified in chicken (dark pink); 4 species (chicken, collared flycatcher, crested ibis, and emu) (medium pink); and all 14 published female avian genomes (light pink) versus the human orthologs of the remainder of ancestral Z genes (light yellow). *P* values obtained using one-tailed Mann–Whitney *U* tests are reported with the associated test statistic, *U*. **(a)** The human orthologs of ancestral Z–W pairs are more broadly expressed in adult human tissues than other ancestral Z genes. Chicken Z–W pairs  $n = 26$ , other ancestral Z genes  $n = 516$ ,  $P < 1.6 \times 10^{-3}$ ,  $U = 9,012$ ; 4 species Z–W pairs  $n = 70$ , other ancestral Z genes  $n = 472$ ,  $P < 0.047$ ,  $U = 18,563$ ; 14 species Z–W pairs  $n = 133$ , other ancestral Z genes  $n = 409$ ,  $P < 0.13$ ,  $U = 28,960$ . **(b)** The human orthologs of ancestral Z–W pairs are more highly expressed in human blastocysts than other ancestral Z genes. Chicken Z–W pairs  $n = 26$ , other ancestral Z genes  $n = 495$ ,  $P < 5.4 \times 10^{-5}$ ,  $U = 9,333$ ; 4 species Z–W pairs  $n = 68$ , other ancestral Z genes  $n = 453$ ,  $P < 0.087$ ,  $U = 18,156$ ; 14 species Z–W pairs  $n = 129$ , other ancestral Z genes  $n = 392$ ,  $P < 0.011$ ,  $U = 28,720$ .