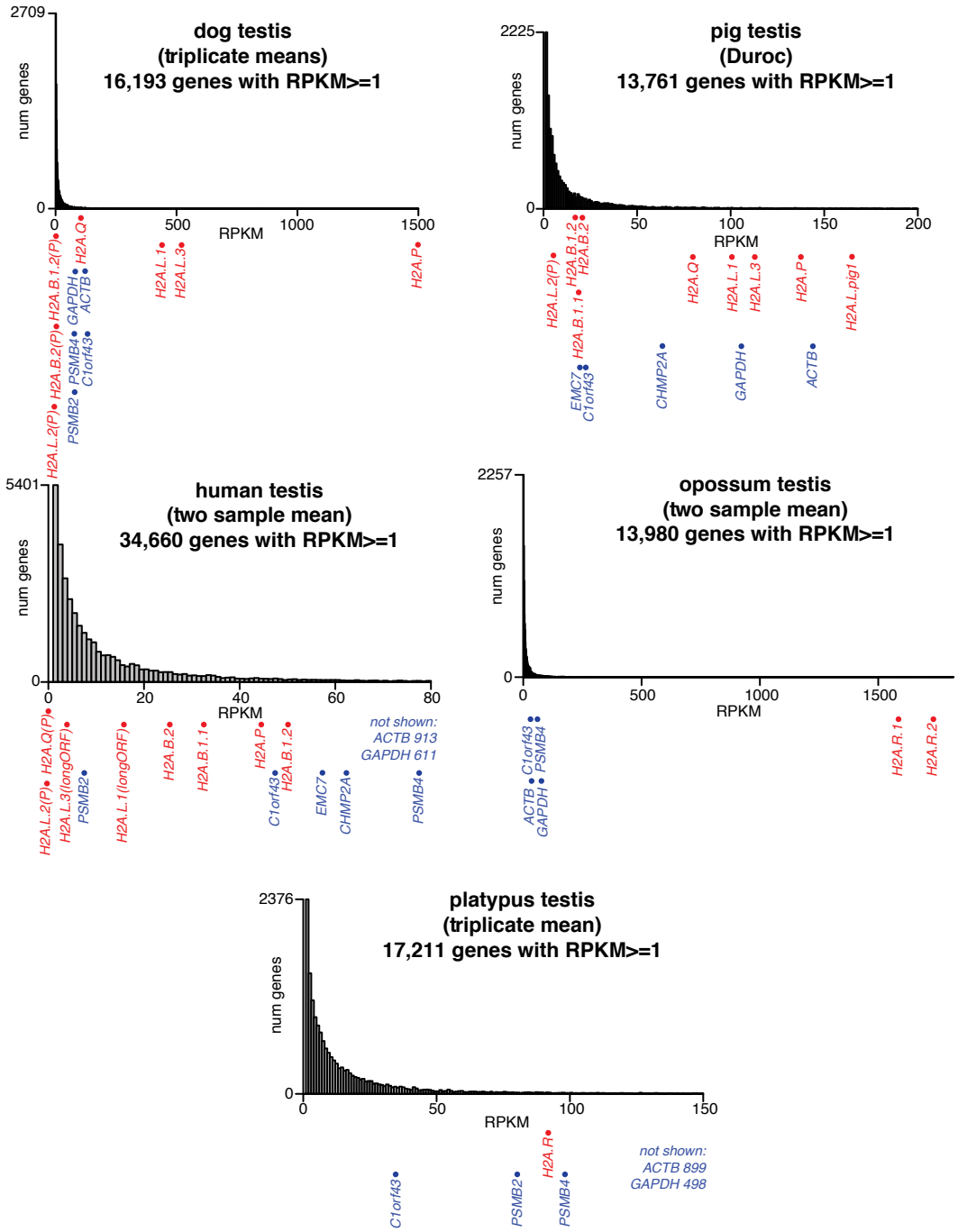

Supplemental Fig S3: Ranking of short *H2A* and *H2A.R* expression levels in testis transcriptome. We obtained RPKM values representing expression levels in testis RNA-seq samples from five species, for short *H2As* and *H2A.R* genes, as well as for all other genes (see Methods). In each panel we depict a histogram of RPKM values for any gene with RPKM >= 1. Below the x-axis, we show RPKM values for individual short *H2A/H2A.R* genes (red) and for selected housekeeping genes (blue), using the same x-axis scale as the histogram. X-axes are scaled differently for each plot, with a maximum chosen so that most genes of interest are visible (dog and opossum x-axis maxima are so high that the histograms are very compressed). These data show that expression levels for intact short *H2As* and *H2A.Rs* are greater than those of most other genes in the genome, and comparable to those of housekeeping genes. In contrast, expression levels of short H2A pseudogenes are low or undetectable. For platypus and human, *GAPDH* and beta-actin (*ACTB*) have much higher RPKM values than the other genes of interest, and values are listed in text boxes rather than plotted as data points. Note that *GAPDH* and beta-actin (*ACTB*) are shown for reference, but are not considered good "housekeeping" controls in RNA-seq analysis because many genomes contain processed pseudogenes that are similar to the parental genes: RPKM values shown for these genes are probably inaccurate.

Supplemental Fig S3
Molaro et al.