







Figure S1. AREScore distribution in comparison to randomized controls. The AREScore was calculated for all annotated 3'UTRs ≥ 10 nt in length in the transcriptomes of 14 metazoan species. The AREScore distribution was compared to fully adjusted, randomized control sets of sequences whose lengths and A/T/G/C-content were identical to the 3'UTRs of the respective transcriptome. Percentage of transcripts were depicted on a logarithmic scale for the following species: (A) *Homo sapiens*, man; (B) *Mus musculus*, common house mouse; (C) *Gallus gallus*, chicken; (D) *Xenopus laevis*, African clawed frog; (E) *Danio rerio*, zebrafish; (F) *Branchiostoma floridae*, Florida lancelet; (G) *Ciona intestinalis*, vase tunicate; (H) *Strongylocentrotus purpuratus*, purple sea urchin; (I) *Drosophila melanogaster*, fruit fly; (J) *Ixodes scapularis*, deer tick; (K) *Caenorhabditis elegans*, roundworm; (L) *Aplysia californica*, California sea hare; (M) *Hydra magnipapillata*, freshwater polyp; (N) *Amphimedon queenslandica*, demosponge.