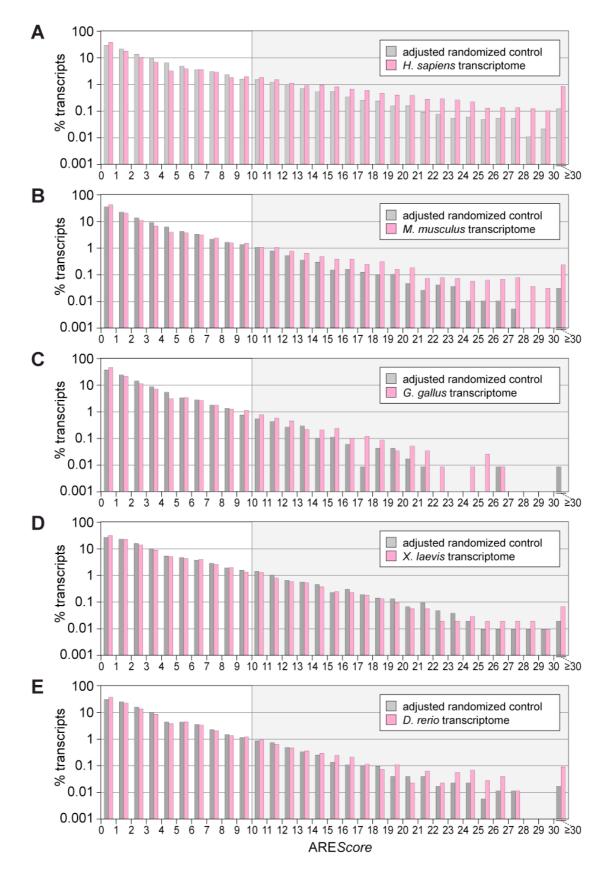
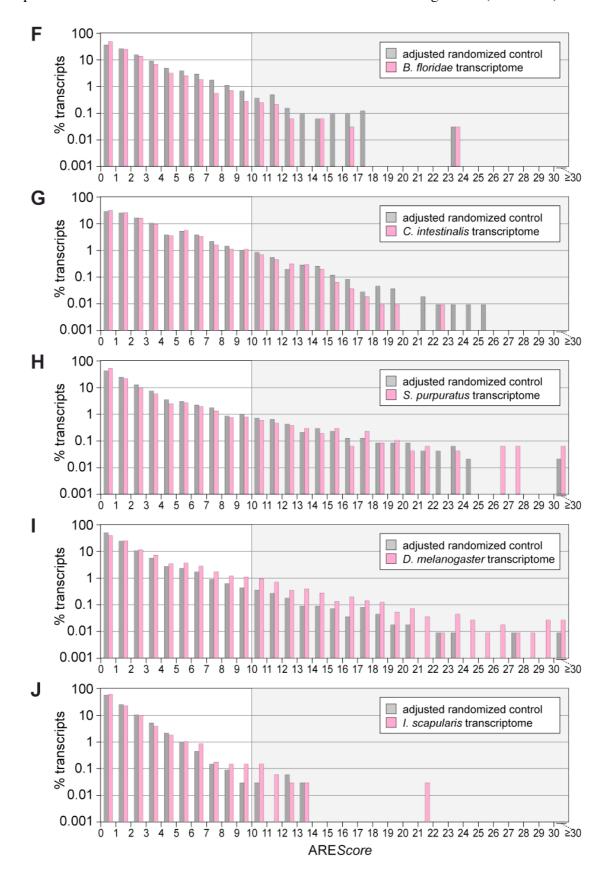
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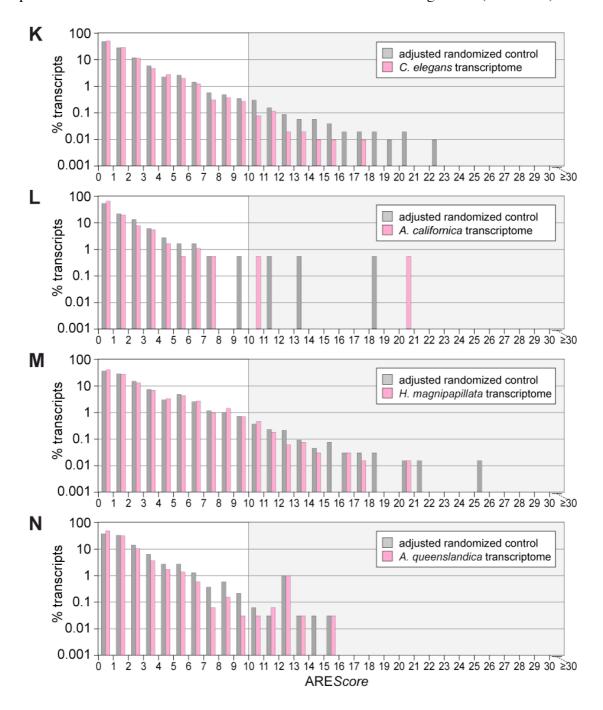


Figure S1. AREScore distribution in comparison to randomized controls. The AREScore was calculated for all annotated 3'UTRs ≥10 nt in legth in the transcriptomes of 14 metazoan species. The AREScore distribution was compared to fully adjusted, randomized control sets of sequences whose lengths and A/T/G/C-content 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.