



Fig S5. Overrepresented functions in transcripts with extremely short or long poly(A) tails.

We performed a Gene Ontology (GO) term enrichment with the genes showing the shortest (decile 1) and longest (decile 10) poly(A) tails. Poly(A) tail was computed as the average poly(A) tail of all the reads with poly(A) tail length information mapping to that gene. Purple bars indicate significant over-representation of genes compared to the background and gray bars under-representation.