



Figure S5. Gene Ontology categories of m⁶A modified transcripts recovered by MeRIP-seq analysis. Genes that were recovered in the MeRIP-seq analysis were used to identify GO categories using the shinyGO program. Categories are enlisted according to the fold enrichment and the false discovery rate (FDR, in $-\log^{10}$) is shown in a color scale as indicated in the figure. Number of genes included in each GO category are represented by the size of the circle.