



Figure S10. 3'UTR association with the non-redundant planarian transcriptome. **A)** The barplot represents the number of clusters obtained from CD-HIT using different % sequence identity thresholds. **B)** The distribution of derived gene clusters across different transcript association categories. **C)** The number of transcripts (gene clusters) associated with different polyadenylation sites. Around 40% of transcripts associate with more than one polyadenylation sites. **D)** Number of gene clusters that could be extended further based upon the 3P-Peaks associated with them. **E)** Genomic distance of nearest polyadenylation site found from the known transcript models are binned. Around 48% of gene models are associated with polyadenylation/cleavage site within 2kb downstream.