



**Figure S9. Completing gene models for planarian transcriptomes.** **A)** The pie chart depicts the percentage distribution of polyadenylation sites across different exons. **B)** 3P-peaks that were present on the genomic contigs with no transcript annotation (Category 6). Number of polyadenylation sites that are in opposite orientation to the transcript (Category 7) & polyadenylation sites that cannot be associated with specific transcripts (Category 8). **C)** The schematic explains the computational workflow used to stitch the annotated 3'UTR to known transcripts. **D)** The density distribution of number of amino acids extended after stitching the known transcript model. **E)** The number of transcripts that had additional protein domain in the extended region of the transcript.