



Figure S6. Identification of conserved PolyA signal (PAS). **A)** Schematic describing the computational pipeline to identify PAS signal. Identification of major and minor/secondary signal by fisher's exact test & directed PAS search. **B)** Alternate pipeline used to identify PAS from identified cleavage site based on peak height. **C)** Association of PAS to identified cleavage sites. Venn diagram depicting the percentage of identified cleavage sites that have AAUAAA or single nucleotide variant of AAUAAA at 10-40nt upstream of cleavage sites. **D)** Overlap of the identified PAS from *Schmidtea* with PolyA signal database.