



Figure S5. Identification of polyadenylation/cleavage sites from *SmedSxl.V3.1* genome.

A) The computational pipeline to obtain 3P tags from 3P-seq reads. The workflow explains all the pre-processing steps to obtain 3P-tags. **B)** Density distribution of reads per locus indicating the genomic coverage of 3P-tags. The x-axis denotes the genomic coverage in normal (below) & log scale (above), whereas the y-axis represents the density of number of locus. **C)** Binned histogram representing the length of 3P-peaks. Majority of the 3P-Peaks are 45-60nts in length. **D)** Violin plot representing the length distribution of identified cleavage/polyadenylation peaks (3P-Peaks) from our computational pipeline. The mean and median of the distribution is 50 nts & 55nts respectively. As expected, identified cleavage sites are AT rich suggesting that these are from 3' end of the transcript.