



Figure S15. Lift over of polyadenylation site coordinates from SmedSxl_V3.1 to SmedSxl_V4.0. **A)** The 3P reads derived from this study are individually aligned to SxIV4 & AsxIV1 genome and the same computational pipeline described earlier was used to identify polyadenylation sites. We identified 29836 & 11998 peaks from SxIV4 & AsxIV1 genome respectively. More than 45% of identified cleavage sites have AAUAAA as their PAS signal. **B)** Venn diagram depicting the overlap of identified major & minor/secondary signals from SxIV3.1, SxIV4 and AsxIV1 genome assemblies. 14 PAS are conserved across polyadenylation sites derived from three genome assemblies. **C)** The distribution of 3P-Peak lengths derived from three different genome assemblies. Polyadenylation site identified from SxIV3.1 & SxIV4 shows similar distribution. **D)** Schematic explaining methodology used to identify correspondence of polyadenylation peaks from SxIV3.1 to SxIV4 genome. We used reverse blast to identify genomic coordinates & then used bedtools (intersectbed) to calculate the overlap. **E)** Table highlighting the corresponding polyadenylation sites from SxIV3.1 and SxIV4 genome. Around 79% of the 3P-peaks determined from SmedSxIV4 genome overlapped with previously derived 3P-peak using SmedSxIV3.1 genome (with $\geq 85\%$ coverage overlap between cleavage sites).