



Figure S13. GO enrichment for two-3P peak & coding region polyadenylation (crApA) candidates. **A)** Scatterplot derived from REVIGO analysis depicting the clusters of GO terms (Biological Process) associated with the transcripts having multiple polyadenylation sites. Each circle represents a GO-term, the color reflects the significance of enrichment and the size denotes the abundance of that particular GO-term in the background uniprot dataset. **B)**

Scatterplot derived from REVIGO analysis depicting the clusters of GO terms associated with polyadenylation event that could lead to putative loss of protein domains.