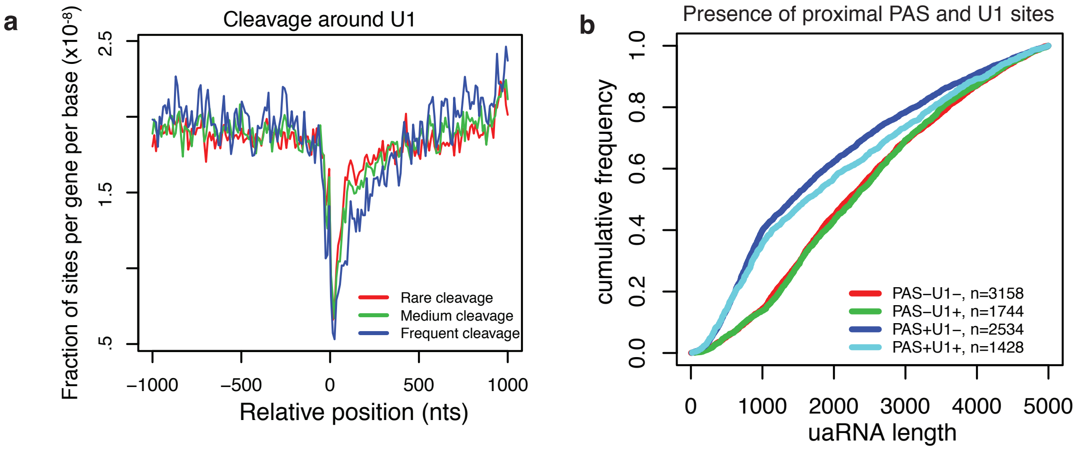

Supplementary Figure 7. Proximal U1 sites are associated with uaRNA length. (a) Distribution of cleavage sites flanking strong U1 sites (position 0). Cleavage sites are classified as rare, medium, and frequent sites based on the number of reads supporting each cleavage site (rare: 1 read, medium: 2-9 reads, frequent: >9 reads). Y-axis is shown as the fraction of sites per gene per base. (b) CDF plot comparing the length of uaRNAs grouped by the presence/absence of promoter proximal PAS and U1 sites. PAS+/- (U1+/-) indicates the presence/absence of PAS or U1 sites in the first 1 kb of uaRNA region. The length of uaRNAs is estimated using the distance from cleavage sites to coding gene TSS.