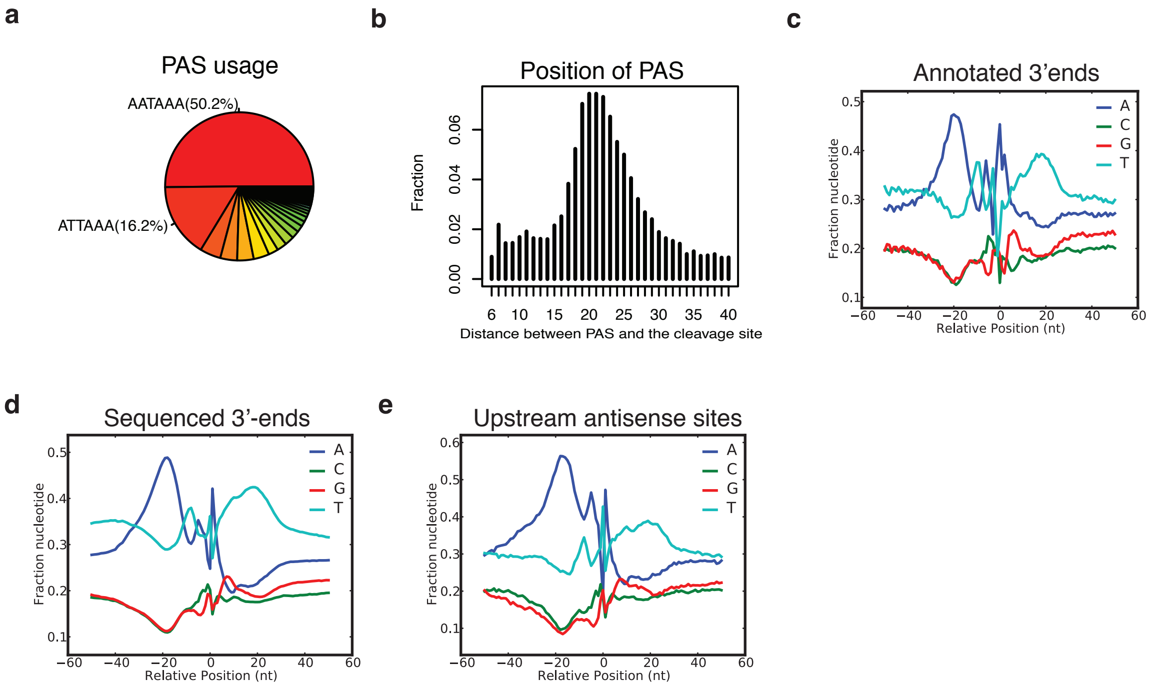

Supplementary Figure 5. Upstream antisense cleavage sites resemble annotated gene TES. (a) Pie chart displaying the usage of each PAS among unique cleavage sites in the upstream antisense region. (b) Histogram showing the distance of the PAS 5' end relative to the cleavage site indicated as position zero. For (a-b), figures include all 36 PAS hexamers with the percentage of all PAS hexamers in (a) described in Supplementary Table 4b. (c-e) The nucleotide frequency flanking cleavage sites (position 0): annotated end of genes (c), cleavage sites detected from our 3' end sequencing -- sites within 2 kb of annotated gene ends (d), and upstream antisense sites (e).