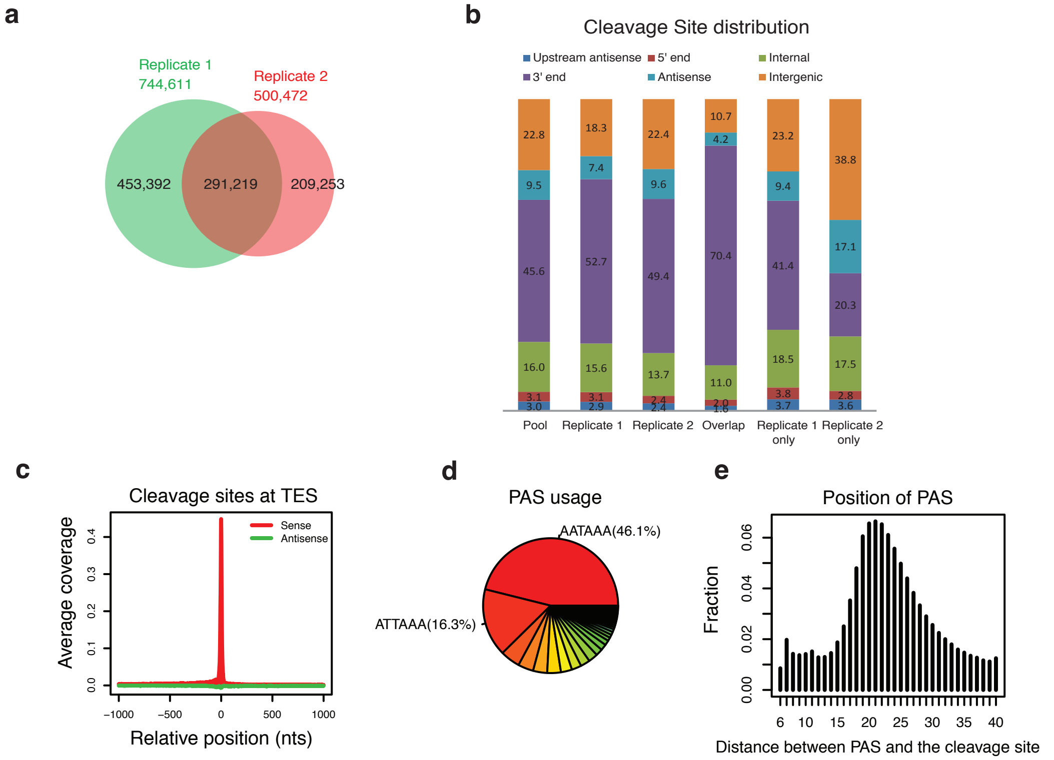

Supplementary Figure 1. Mapping the 3’ ends of polyadenylated RNAs by deep sequencing in mESCs. (a) Venn diagram depicts the overlap of unique cleavage sites between two 3’-end libraries that were constructed and denoted as library replicate 1 and replicate 2. (b) The fraction of cleavage sites in six non-overlapping categories including: 2 kb flanking 3’ end of the gene (3’ end), 5 kb downstream the TSS in the gene (5’ end), internal of the gene (Internal, not 5’ end or 3’ end), upstream antisense of the TSS within 5 kb (Upstream antisense), antisense to the gene (Antisense), and other intergenic regions (Intergenic) in pool (combining replicate 1 and 2), replicate 1, replicate 2, overlap (only common to replicate 1 and 2), and sites unique to replicate 1 or replicate 2. (c) Density of unique cleavage sites at annotated 3’ ends of genes with sense and antisense sites shown in red and green, respectively. Position zero denotes the annotated TES. Average coverage equals the number of unique cleavage sites per nucleotide per gene. (d) Pie chart displaying the usage of each PAS (all percentages shown in Supplementary Table 4a) among all unique cleavage sites. (e) Histogram showing the distance of the PAS (all 36 hexamers) 5’ end relative to the cleavage site (indicated as position zero on the x-axis) and fraction of all cleavage sites that have a PAS at each position is shown on the y-axis.