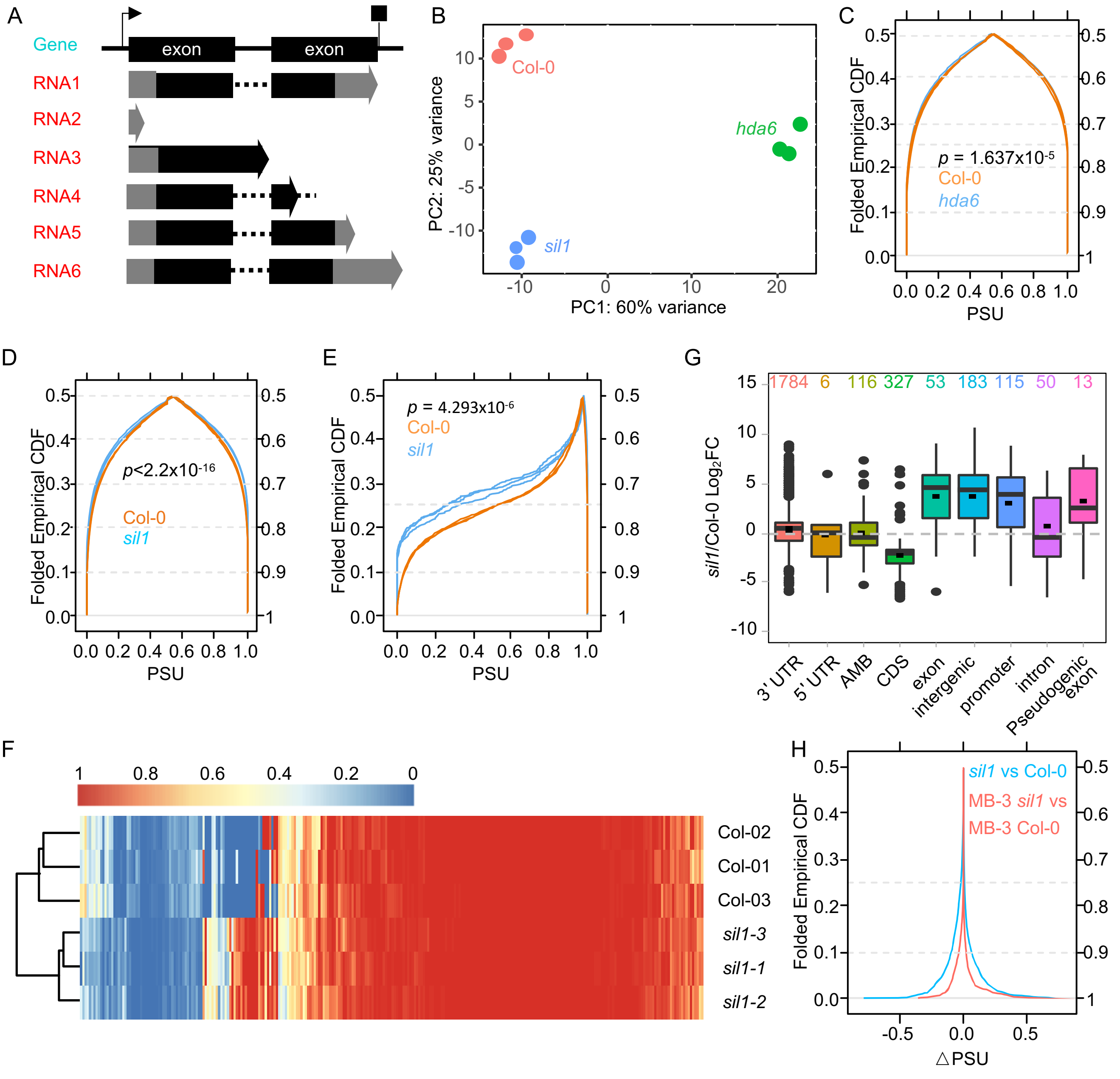

Supplemental Fig S2. Mutation of HDA6 affects polyadenylation. A, A schematic diagram shows that APA results in varied lengths of RNAs from the same gene. RNA1 is a normal full length transcript. RNA2 ~ 6 represent poly(A) sites located in 5' UTR, intron, exon, 3' UTR and intergenic region, respectively. Black rectangles indicate exons. Gray rectangles indicate UTRs. Black lines indicate introns or intergenic regions of DNA. Dash lines represent spliced introns. B, A principle component analysis shows good repeatability of PAT-seq results. C and D, Folded cumulative distribution frequency (CDF) of genome wide PSUs of allele mutants (*hda6* and *sil1*, respectively) and Col-0, respectively. E and F, Folded CDF and heatmap of PSUs of DE poly(A) sites between *sil1* and Col-0. G, Distribution of DE poly(A) sites of *sil1*. H, MB-3 treatment reduces the difference of PSUs between *sil1* and Col-0. △PSU represents the difference of PSU of a poly(A) site in *sil1* and Col-0.