Expanded View Figures

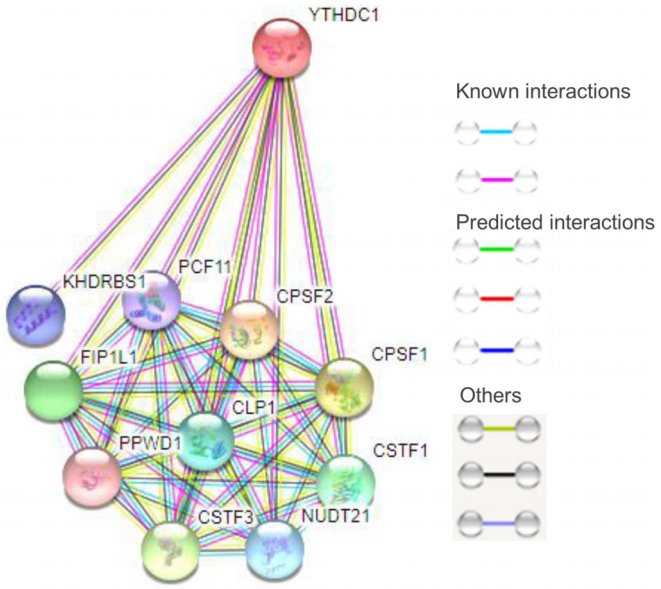

Figure EV1. The putative interaction between YTHDC1 and 3′ end processing factors analyzed with STRING protein–protein interaction database.

There are several 3′end processing factors (including CPSF, CFIm, CFIIm, CSTF) that may interact with YTHDC1, suggesting YTHDC1 as a potential candidate linking m^6A to APA.

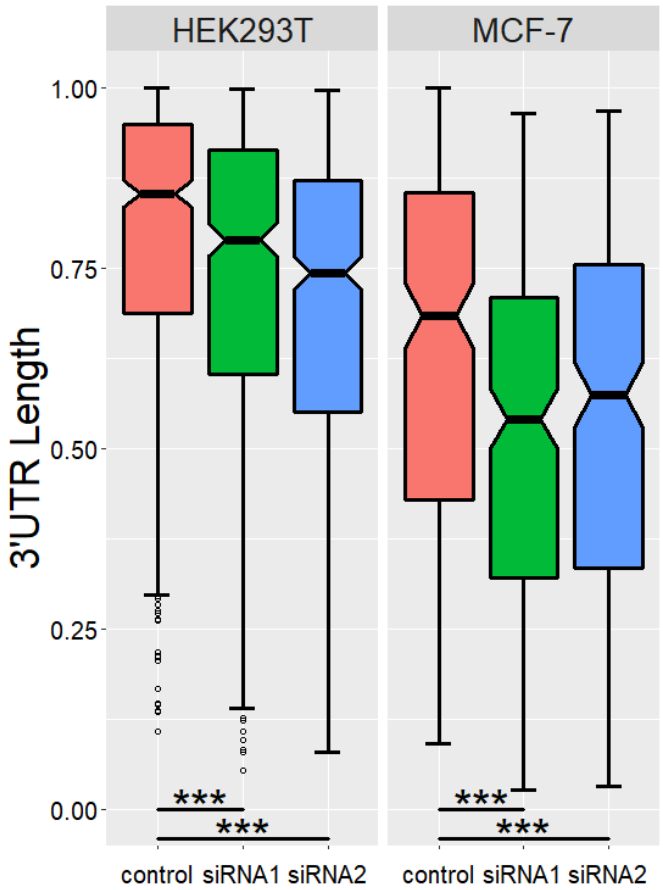

Figure EV2. Notched boxplot of weighted mean of 3′ UTR length.

For each gene that undergoes 3′ UTR shortening, the length of each 3′ UTR isoform was normalized to the longest 3′UTR, and the weighted mean of 3′ UTR length was calculated. ***$P < 3.18 \times 10^{-39}$, P values were obtained with paired t-test.

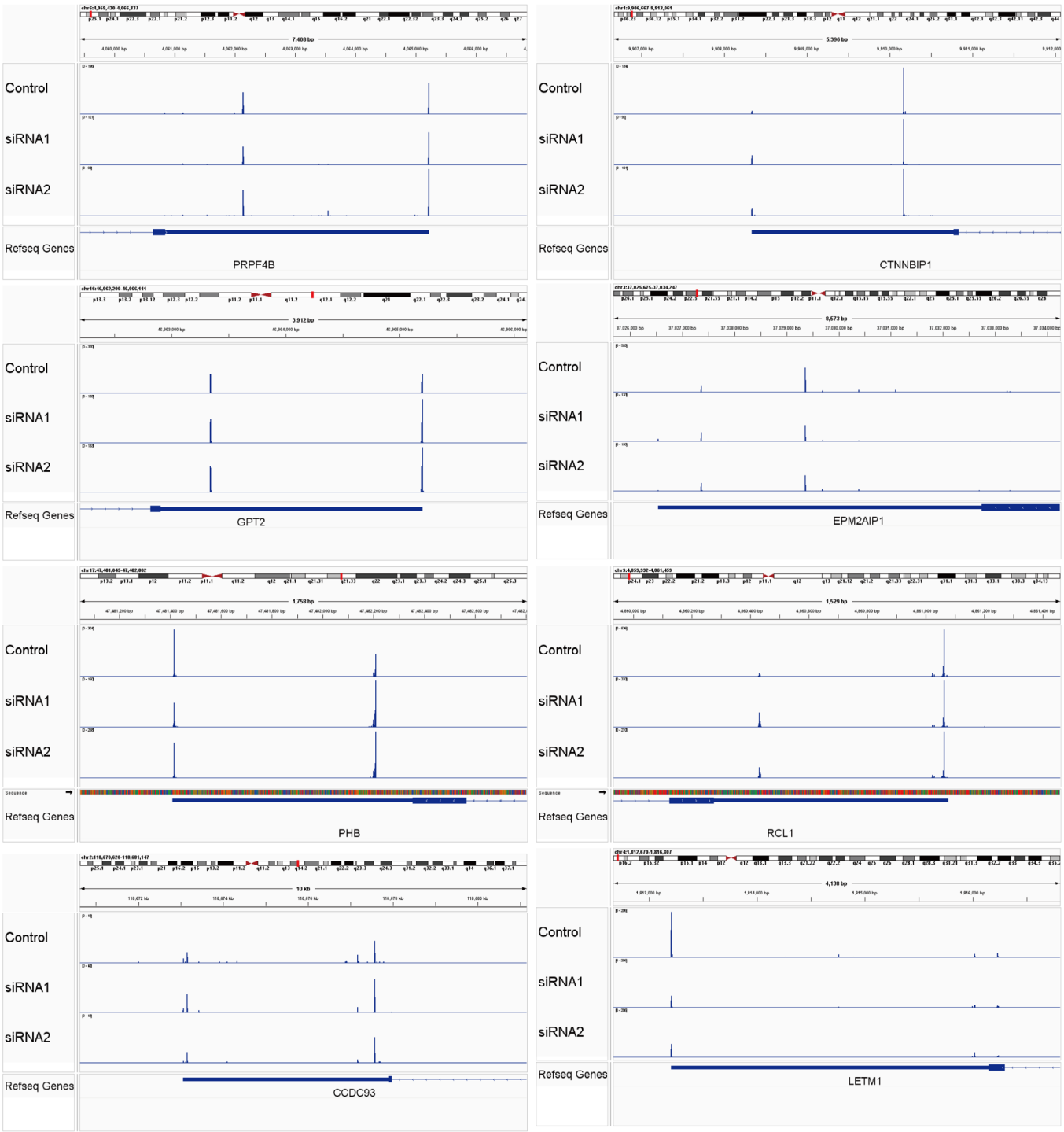

Figure EV3. IVT-SAPAS sequencing reads distribution for genes validated with qRT-PCR, related to Fig 1E.

The *x* and *y* axes denote genome position of APA sites and sequencing reads number, respectively. The different rows represent the treatment.

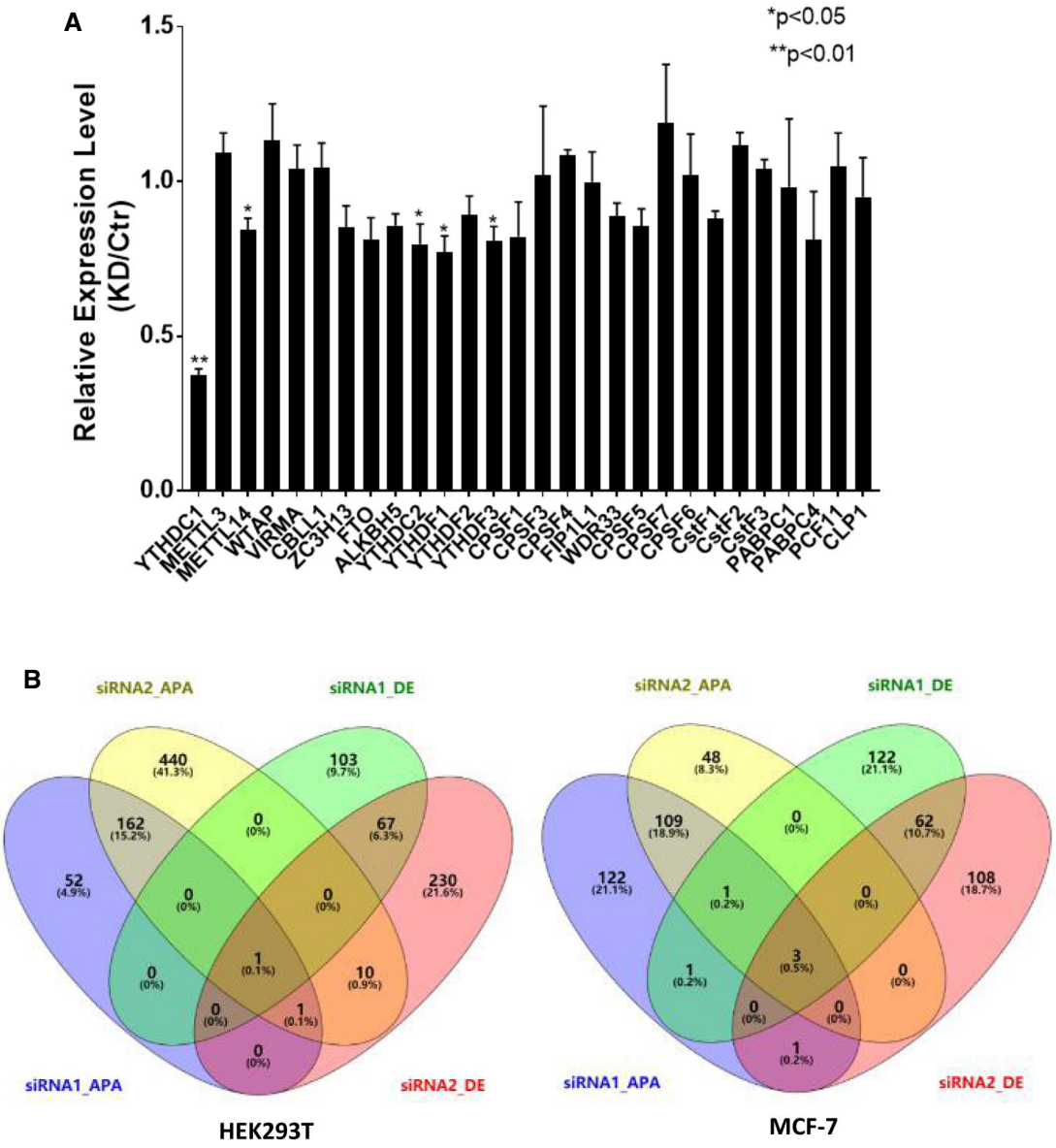

Figure EV4. The effects of YTHDC1 knockdown on APA is a direct regulation from YTHDC1.

A qRT-PCR analysis of m^{6}A related factors and 3′ end processing factors after knockdown of YTHDC1 in HEK293T cells. Knockdown of YTHDC1 has little effect on mRNA expression of those factors, which may mediate indirect effect on APA. Data are presented as mean ± SEM of three biological replicates. *$P < 0.05$, **$P < 0.01$, the P values were obtained from unpaired two-tailed Student's t-test.

B Venn diagram of genes with differential expression levels and genes with APA sites switching after knockdown of YTHDC1 in HEK293T (left) and MCF7 (right). The siRNA-APA denotes APA switching genes, siRNA-DE denotes differential expression genes, and number denotes different siRNA. There are few intersections between genes with APA sites switching and genes with differential expression level, indicating that change of 3′UTR length was not caused by RNA degradation.

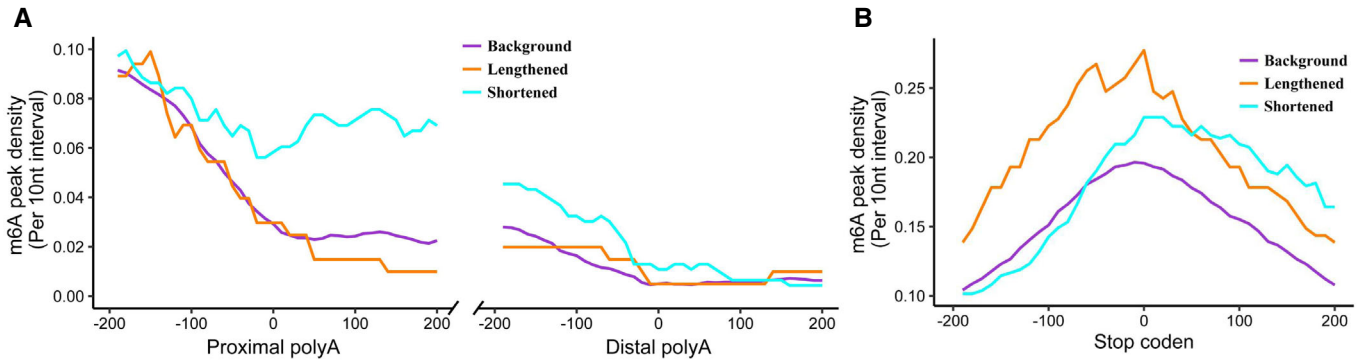

Figure EV5. Higher m^{6}A levels in the proximal poly(A) sites correlates with genes with more proximal poly(A) sites usage after knockdown of YTHDC1.

A, B m^{6}A peak density near APA sites and stop codon in (A and B), respectively. Genes with shortened 3′ UTR show a higher m^{6}A modification near of the proximal APA sites compared with genes with lengthened 3′ UTR or background. But shortened 3′ UTR near of the stop codon did not show enriched m^{6}A modification than mRNA with lengthened 3′ UTR or background. The density of m^{6}A peak was calculated as the number of peak in a 10-nt interval divided by the total number of mRNAs that contained this position.