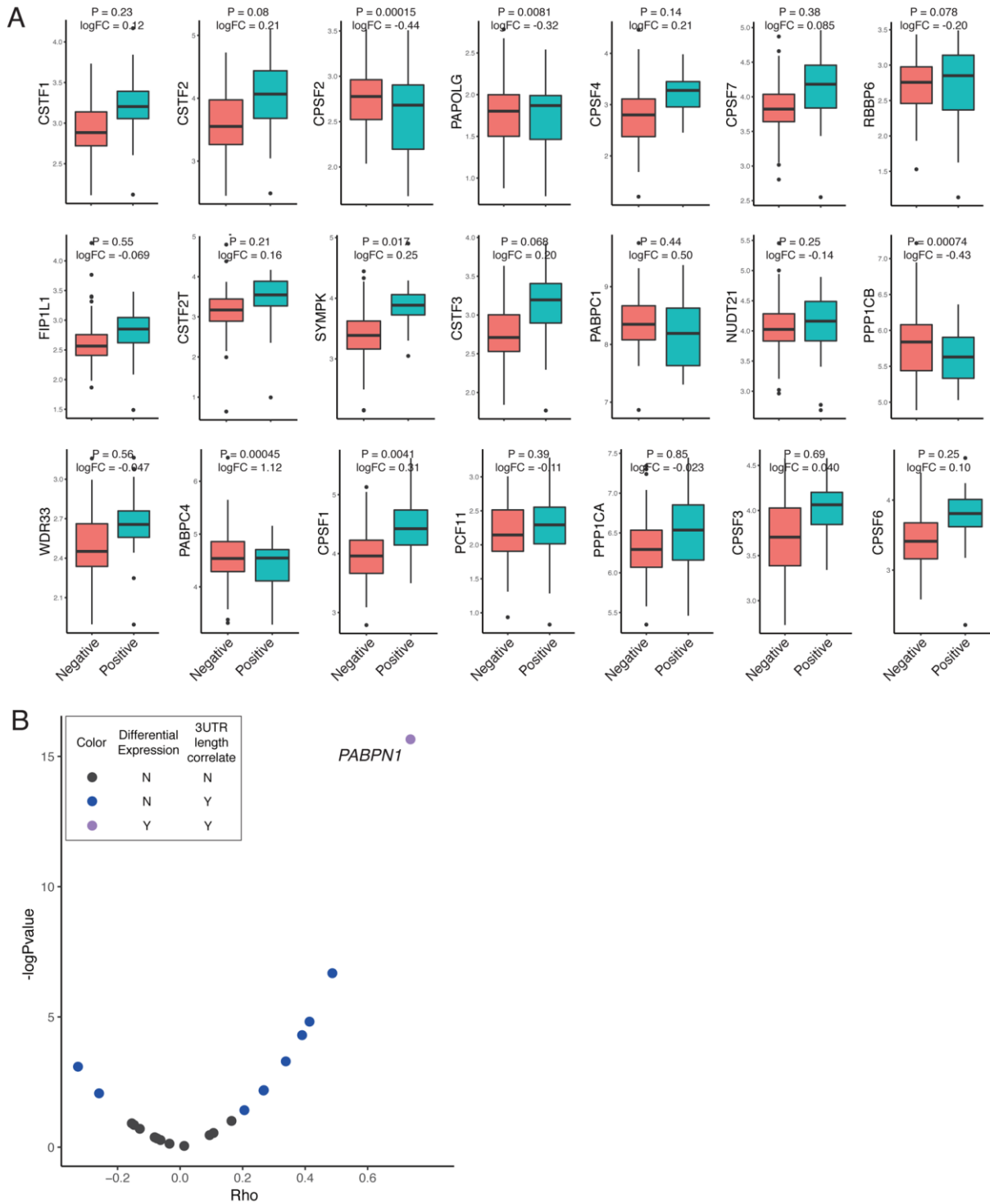
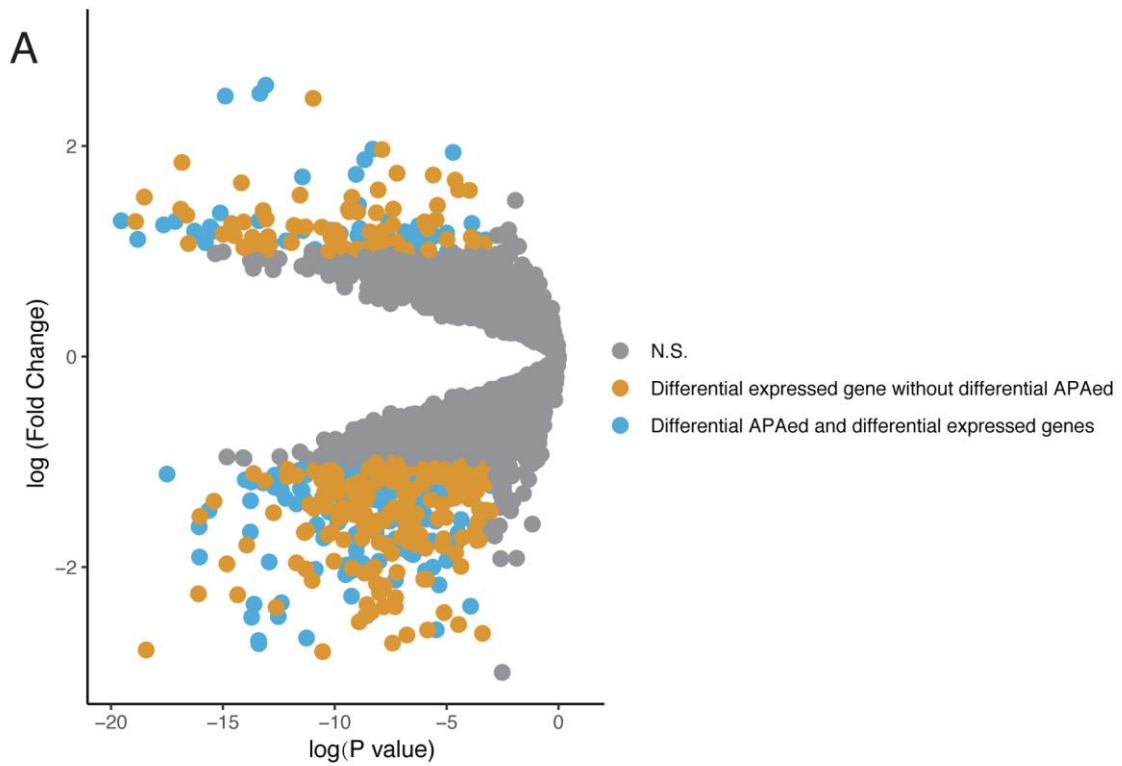


SUPPLEMENTARY FIGURES



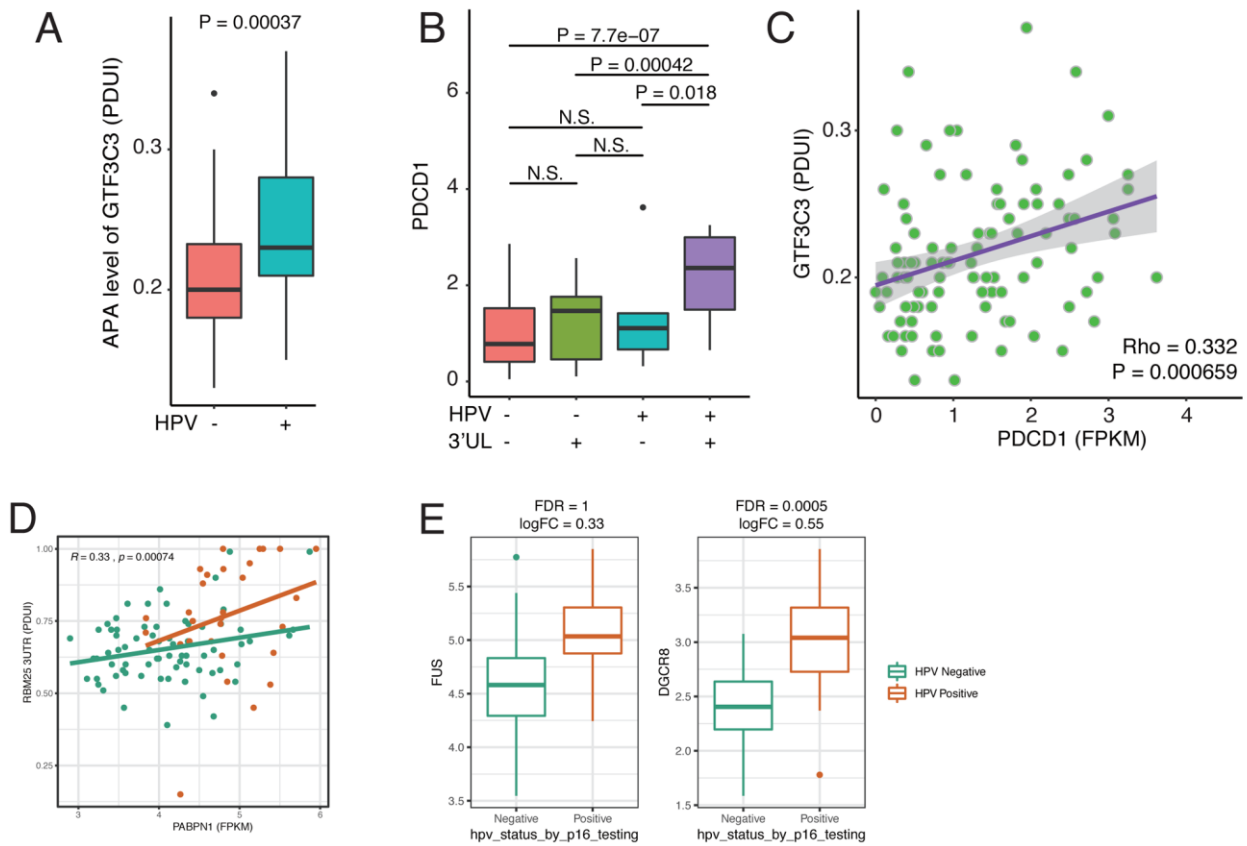
**Supplementary Figure 1. The expression profile of key APA regulation components. (A)** The list of regulators was fetched from the literature (Ref. 20). The Y-axis refers to the FPKM value of each mRNA. **(B)** Scatter plot of all components shows PABPN1 plays key roles in HPV-mediated APA. Each dot represents each known APA regulators, colored according to whether this regulator is differentially expressed in HPV+ samples or whether the expression is correlated with the median 3'UTR length of all APA events ( $|\text{Spearman Rho}| > 0.3$  and  $P\text{-value} < 0.05$ ).



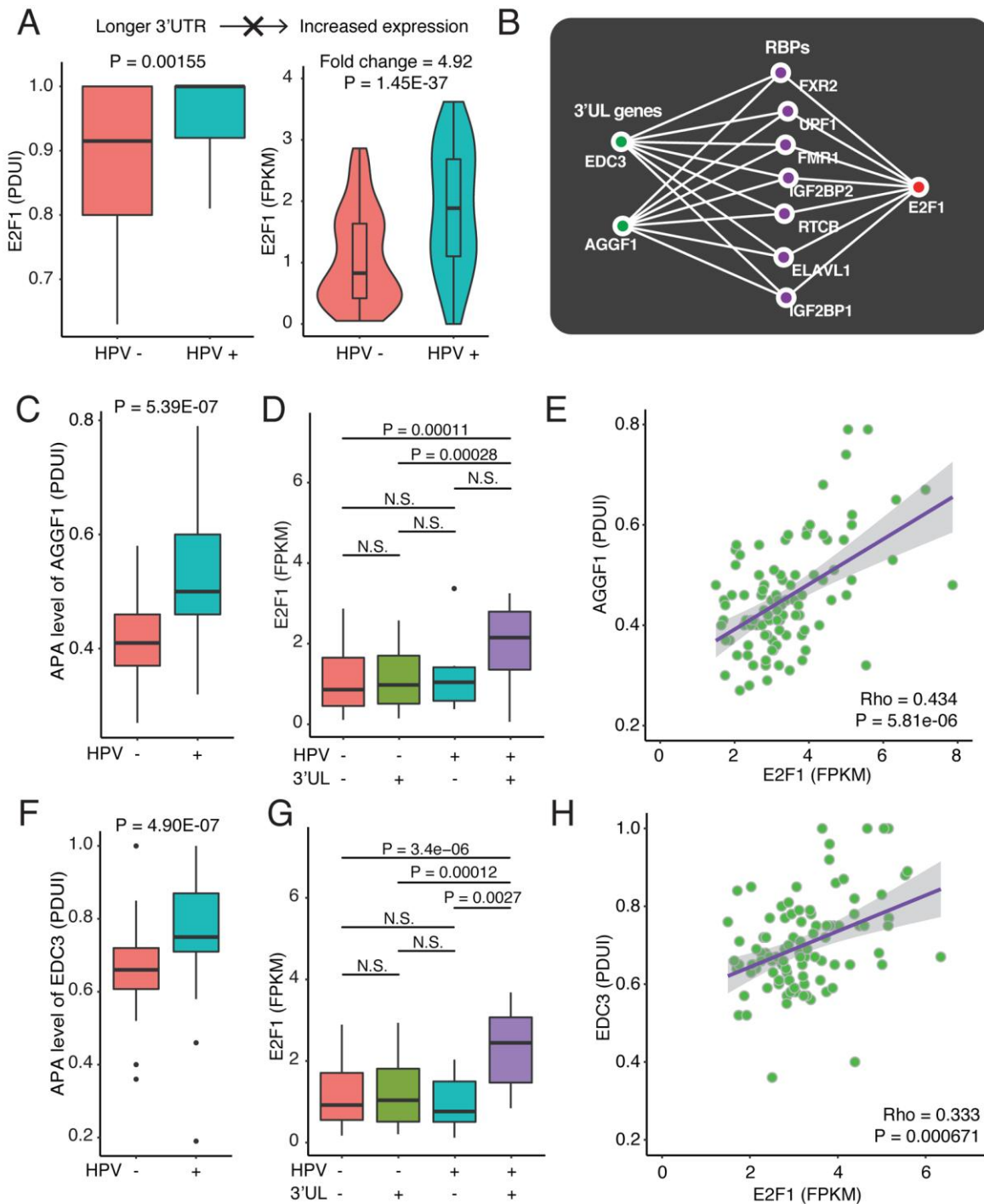
**B**

Gene sets	P value (hypergeometric test)	Significance
Tumor suppressor (Uniprot)	0.4992319	N.S.
Oncogene (Uniprot)	0.7815282	N.S.
Tumor suppressor (TSGD)	0.9227407	N.S.
Oncogene (NCG)	0.998491	N.S.
Immune genes (Bindea 2013)	0.7493049	N.S.
HPV changed genes (MSigDB)	0.7229499	N.S.

**Supplementary Figure 2. 3'UTR-longer genes cannot explain the differential expression and are not enriched in cancer-associated pathways.** (A) Differentially APA genes are not enriched in differentially expressed genes. (B) 3'UL genes with direct down-regulated gene expression were not associated with cancer and immunity. All 6 signature shows no significant results (hypergeometric test).



**Supplementary Figure 3. HPV upregulates PD-1 via impacting RBPs.** (A) 3'UTR level of GTF3C3 is significantly longer in HPV+ samples (Wilcoxon test). (B) 3'UL+ and HPV+ group shows the highest PDCD1 expression (FPKM). (C) 3'UTR length of GTF3C3 is positively correlated with PDCD1 expression. (D) Correlation between 3'UTR length of RBM25 and PABPN1 RNA expression. (E) The expression difference of FUS and DGCR8 between HPV positive and negative samples.



**Supplementary Figure 4. HPV-mediated longer 3'UTR of AGGF1, EDC3 upregulates E2F1 via RBPs.** (A) HPV+ samples show a longer 3'UTR length of E2F1. However, E2F1 is upregulated in HPV+ samples. The down-regulated expression of E2F1 may not be caused by 3'UL in cis. The right plot means PDCD1 is upregulated in the HPV+ samples. Fold change and P-value were computed through EdgeR. The right plot means. (B) Based on CLIP-seq, the 3'UL—RBP—E2F1 network was computed. (C) 3'UTR level of AGGF1 is significantly longer in HPV+ samples (Wilcoxon test). (D) 3'UL+ and HPV+ group shows the highest E2F1 expression (FPKM). (E) 3'UTR length of AGGF1 is positively correlated with E2F1 expression. (F) 3'UTR level of EDC3 is significantly longer in HPV+ samples (Wilcoxon test). (G) 3'UL+ and HPV+ group shows the highest E2F1 expression (FPKM). (H) 3'UTR length of EDC3 is positively correlated with E2F1 expression.