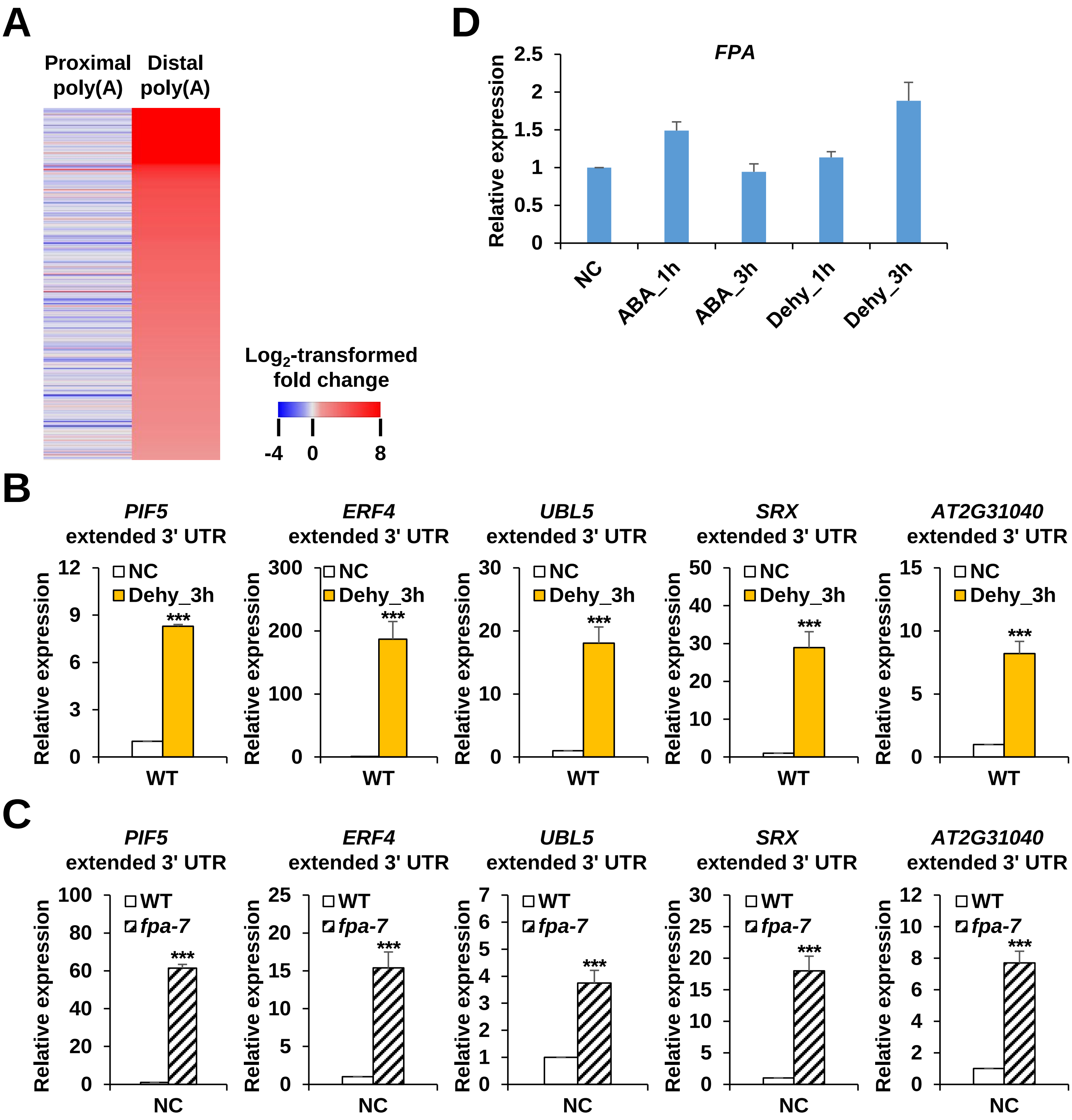
Supplemental Figure 10



Supplemental Figure 10. FPA partially regulates biogenesis of 3' UTR extensions.
(A) Heatmap showing fold changes of DRS reads at proximal and distal poly(A) sites. A total of 420 transcripts with enhanced distal polyadenylation in *fpa* mutant compared to WT were used for this plot. Blue and red represent log$_2$-transformed fold changes < 0 and > 0, respectively. **(B)** Real-time PCR analysis showing expression levels of extended 3' UTR of *PIF5*, *ERF4*, *UBL5*, *SRX* and *AT2G31040* in WT. The expression level of each gene in WT plants grown in normal condition (NC) was set to 1. **(C)** Real-time PCR analysis showing expression levels of extended 3' UTR in WT and *fpa-7* mutant. **(D)** Real-time PCR analysis of expression levels of *FPA*. The expression level in normal condition (NC) was set to 1. Transcript levels were normalized to *ACT2* expression. The expression level of each gene in WT plants grown in normal condition (NC) was set to 1. Data are shown as mean ± s.d. (n = 3) of one representative result of three independent biological replicates. Asterisks indicate statistically significant differences compared with WT (* $P < 0.05$, ** $P < 0.01$; *** $P < 0.001$; *t* test).