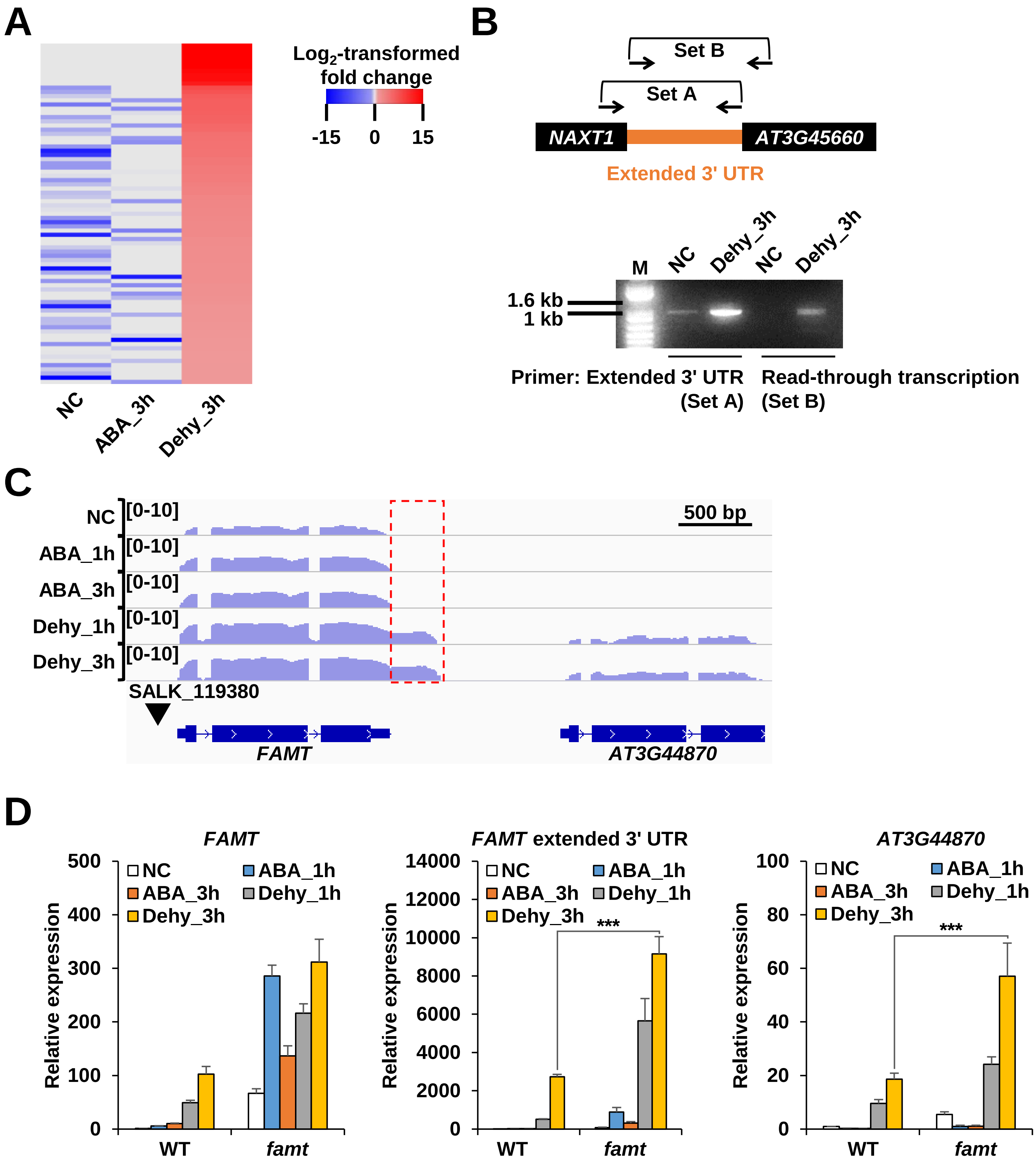
Supplemental Figure 7



Supplemental Figure 7. Activation or read-through transcription of downstream genes by 3' UTR extensions. **(A)** Heatmap showing fold changes (relative to 2nd highest expression level) of 81 downstream genes that are upregulated in dehydration stress compared to both normal condition (Dehy_3h/NC ≥ 2) and ABA treatment (Dehy_3h/ABA_3h ≥ 2). Blue and red represent log$_2$-transformed fold changes < 0 and > 0, respectively. **(B)** Validation of *NAXT1-AT3G45660* read-through transcription using RT-PCR. **(C)** Genome browser view showing *FAMT* and *AT3G44870*. Blue color represents read abundance of forward strand. Extended 3' UTRs is depicted by a red rectangle. T-DNA insertion site is indicated by a black inverted triangle. **(D)** Real-time PCR analysis of expression levels of *FAMT* (left), *FAMT* extended 3' UTR (middle) and *AT3G44870* (right) in WT and *famt* mutant. 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 (* P < 0.05, ** P < 0.01; *** P < 0.001; *t* test).