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 log2-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).