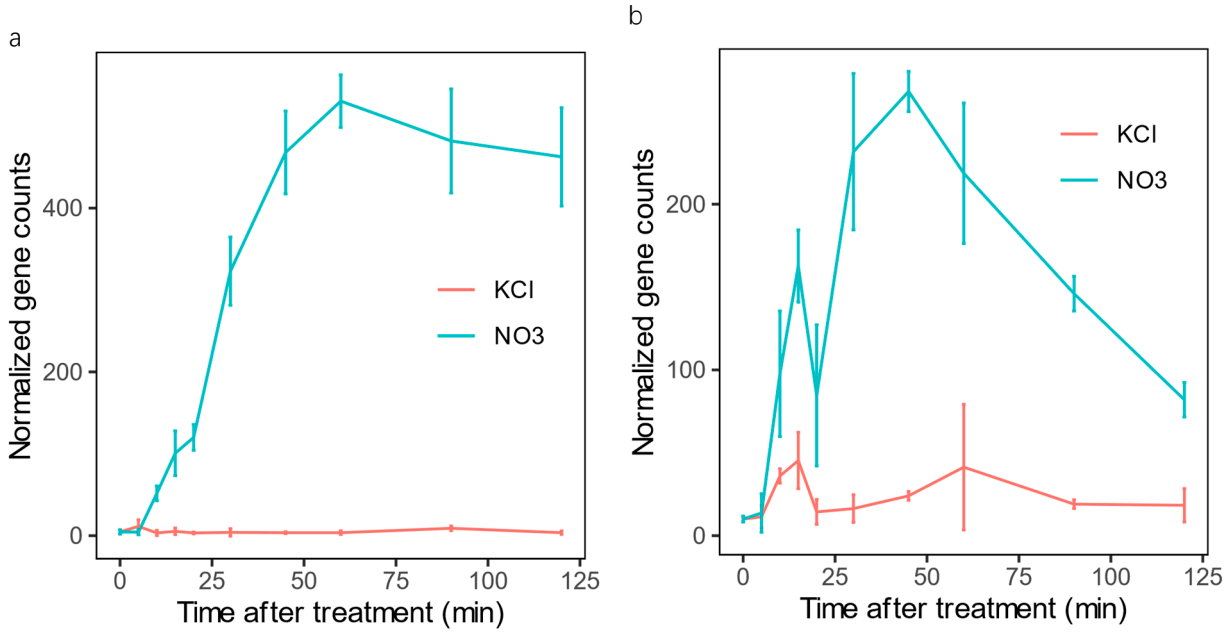


Figure S1. Dynamical mRNA level of *ERF56* in response to NO_3^-. (a) gene counts in shoots of *Arabidopsis*. (b) gene counts in roots of *Arabidopsis*. Data are means ± SD. mRNA level were detected with transcriptome analysis by Varala *et al*. (2018).

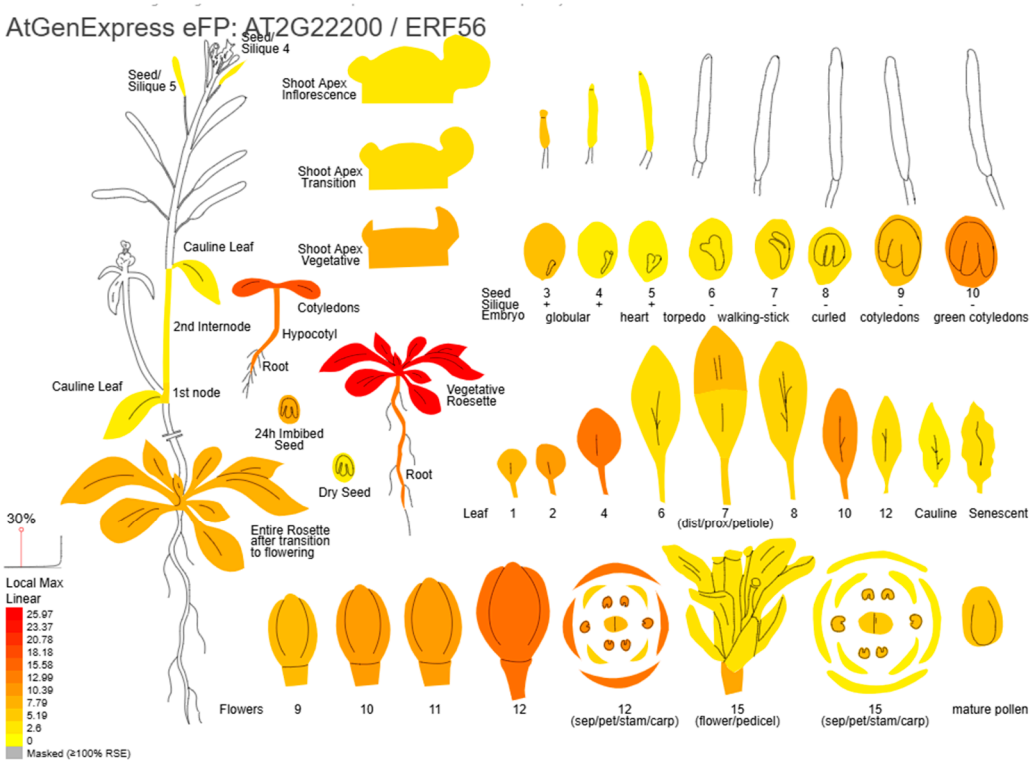


Figure S2. mRNA levels of *ERF56* in different tissues. Data were obtained from https://bar.utoronto.ca/eplant.

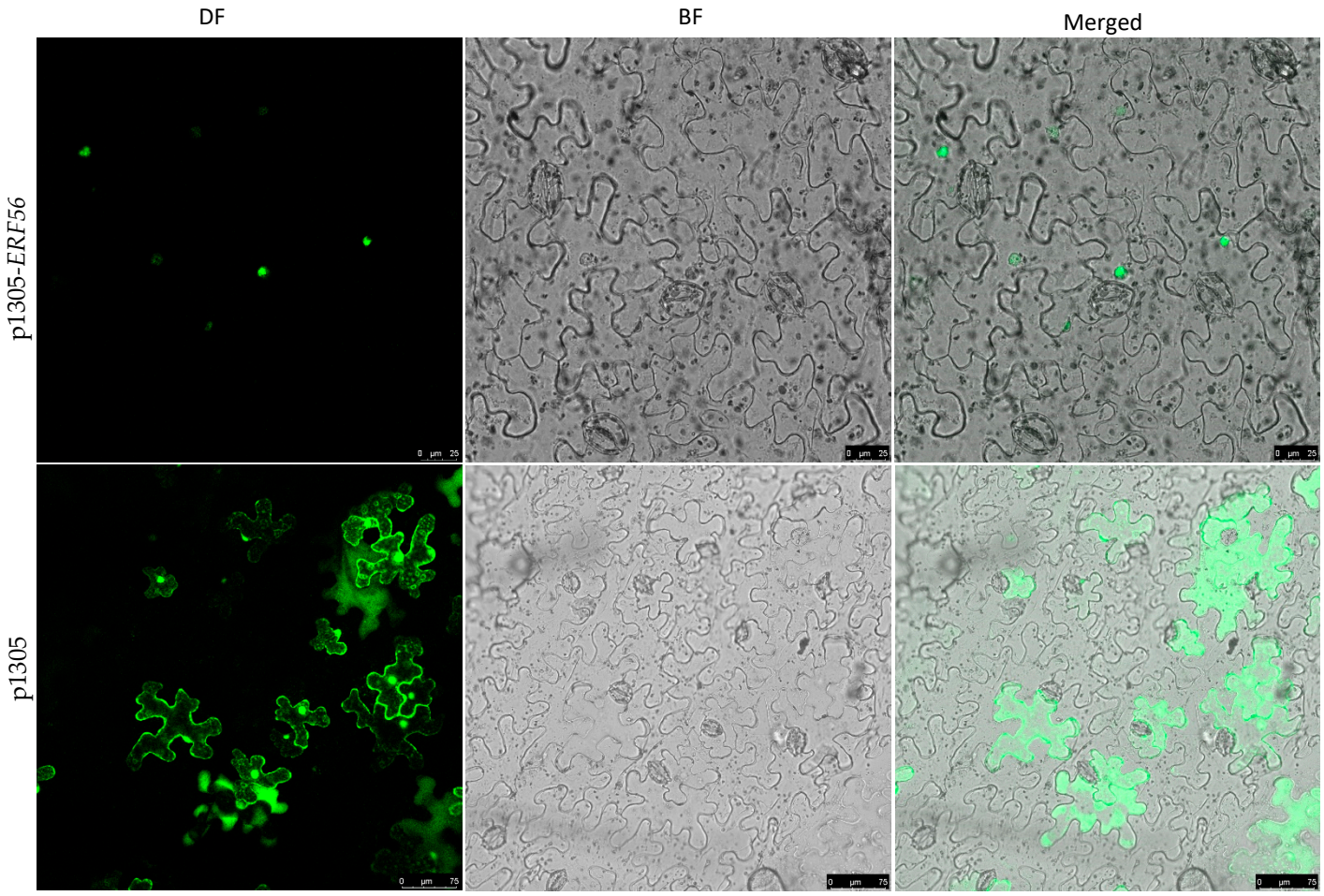


Figure S3. ERF56 is a nucleu-localized protein. Confocal imaging epidermal cells of leaves of *Nicotiana benthamiana* which were infiltrated with *Agrobacteria* containing the plastid carrying *ERF56* (p1305-*ERF56*) or the empty control plastid (p1305). In the plasmid carrying *ERF56*, the CDS of *ERF56* was cloned into the NcoI site of a modified version of the vector pCAMBIA1305 (p1305) with its C-terminal being fused in frame with *GFP* in the vector. DF, the dark field image with laser-aided confocal laser scanning. BF, the bright field image with transmitted light.

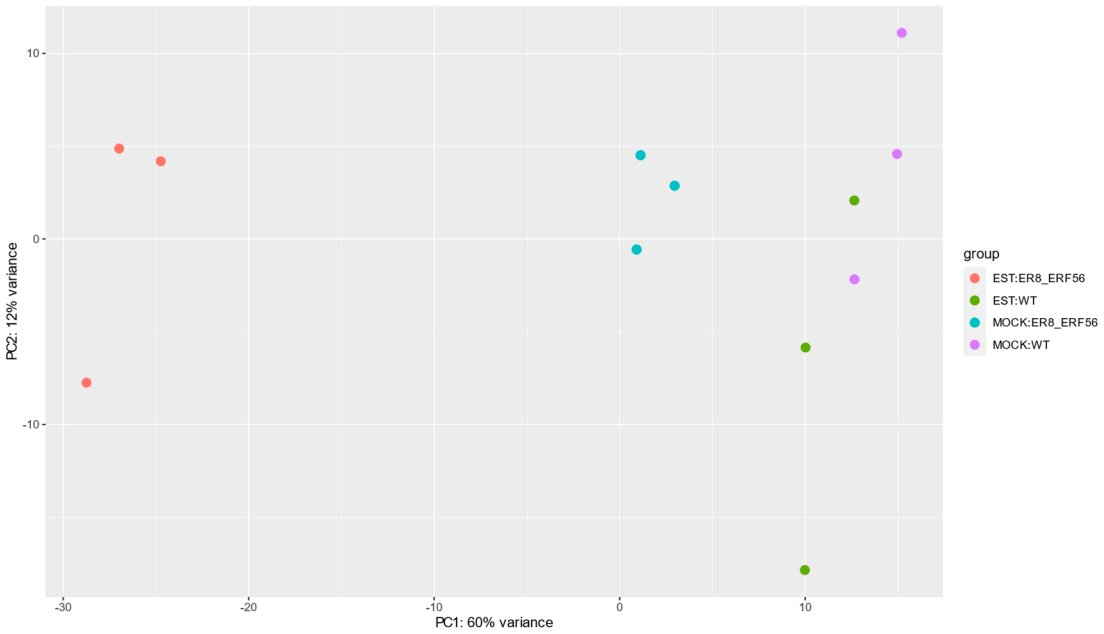


Figure S4. Clustering samples of transcriptome analysis by principal component analysis of gene counts data. For transcriptome assays, 10-day-old *ER8-ERF56-1* plants deficient for nitrate were transferred to fresh nitrate-free medium containing 2-uM 17-ß-estradiol (EST) or not, as mock treatment (MOCK), for 3 hours. Each sample had 20 plants. *ER8-ERF56:* an inducible *ERF56* over-expressor. Normalized gene counts with a variance stabilizing transformation in the software DESeq2 were used in the analysis.