

Figure S1. Intersection analysis between drought and recovery time points. Upset plot of (A) up- and (B) down-regulated genes, (C) PCA plot recovery specific genes (D-E) Single gene expression examples of (D) drought responsive, (E) recovery specific, and (F) drought-invariable, recovery down-regulated genes.

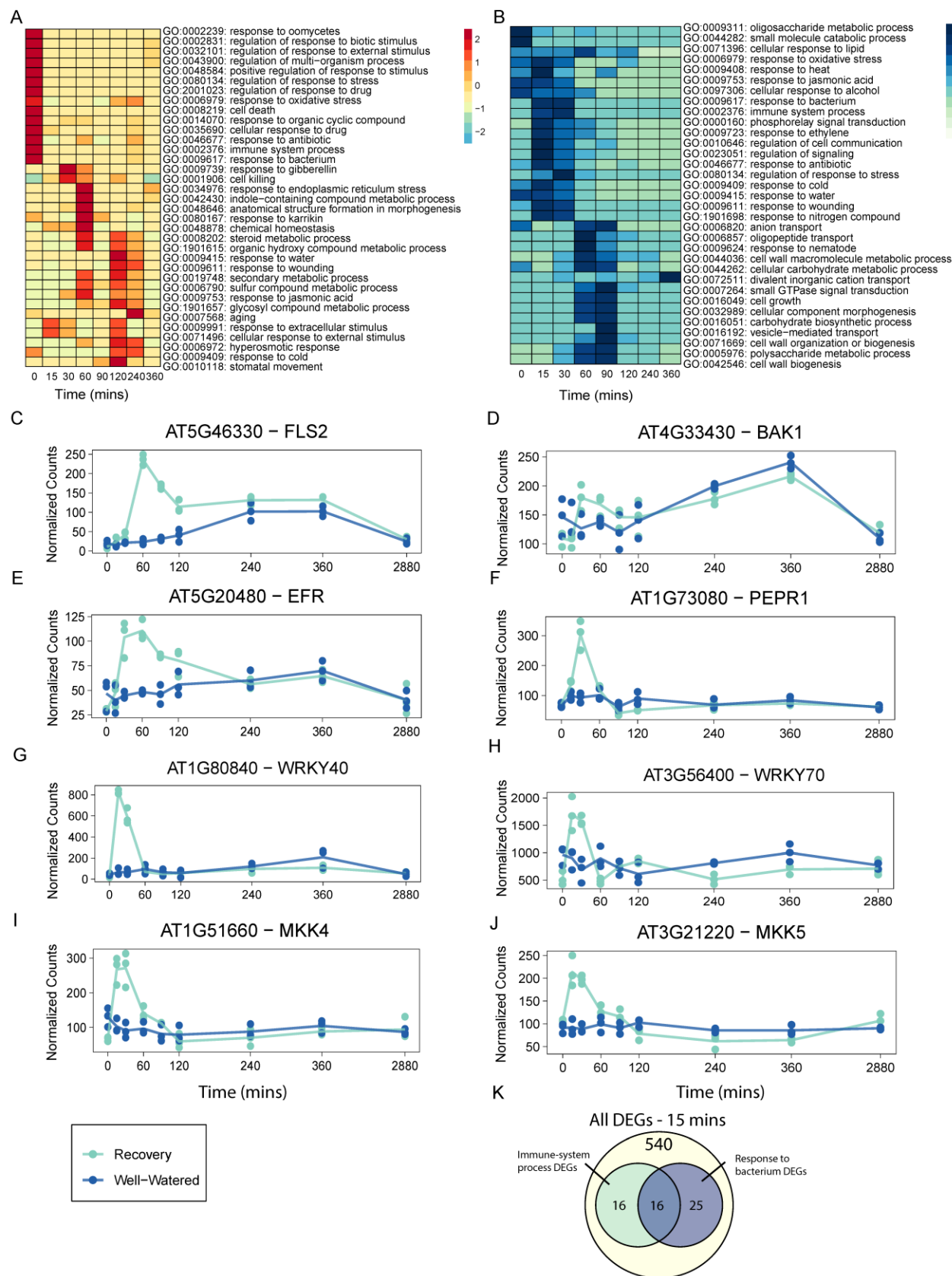


Figure S2. GO term enrichment analysis of all DE genes. (A) Down-regulated genes (B) Up-regulated genes (C-J) single immune-related genes expression (C) FLS2 (D) BAK1 (E) EFR (F) PEPR1 (G) WRKY40 (H) WRKY70 (I) MKK4 and (J) MKK5 (K) Overlap of immune-related genes with all DEGs after 15 minutes of rehydration.

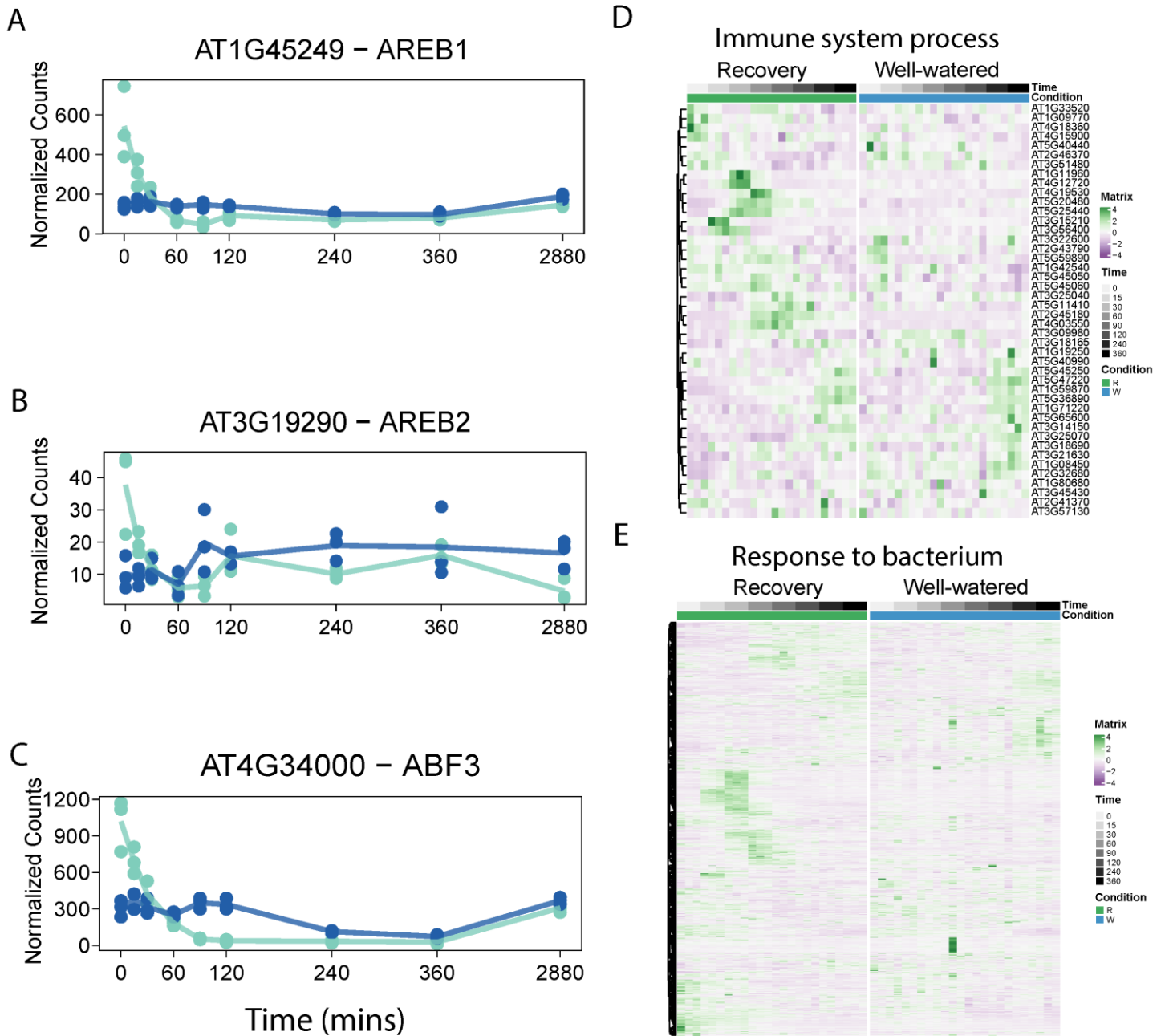


Figure S3. (A-C) ‘ABA triggered immune suppression genes’ identified in our dataset (A) AREB1 (B) AREB2 and (C) ABF3. (D-E) Robust and transient immune transcription response upon drought recovery (heatmaps of the genes from the two GO terms (D and E) separately).

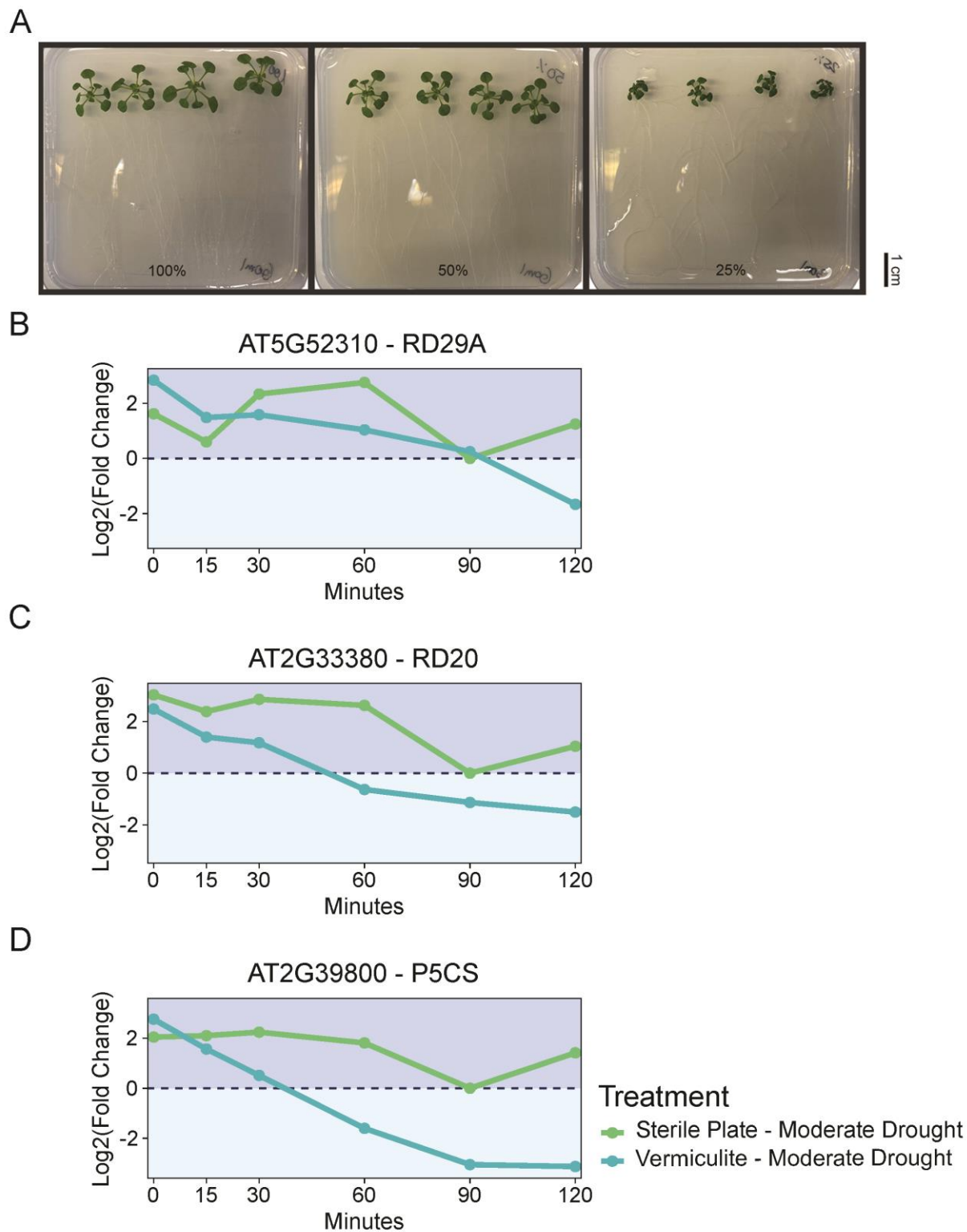


Figure S4. LW plate system for simulating drought stress on plates. (A) plant image on plates. Marker gene plot: **(B)** RD29A, **(C)** RD20, **(D)** P5CS.

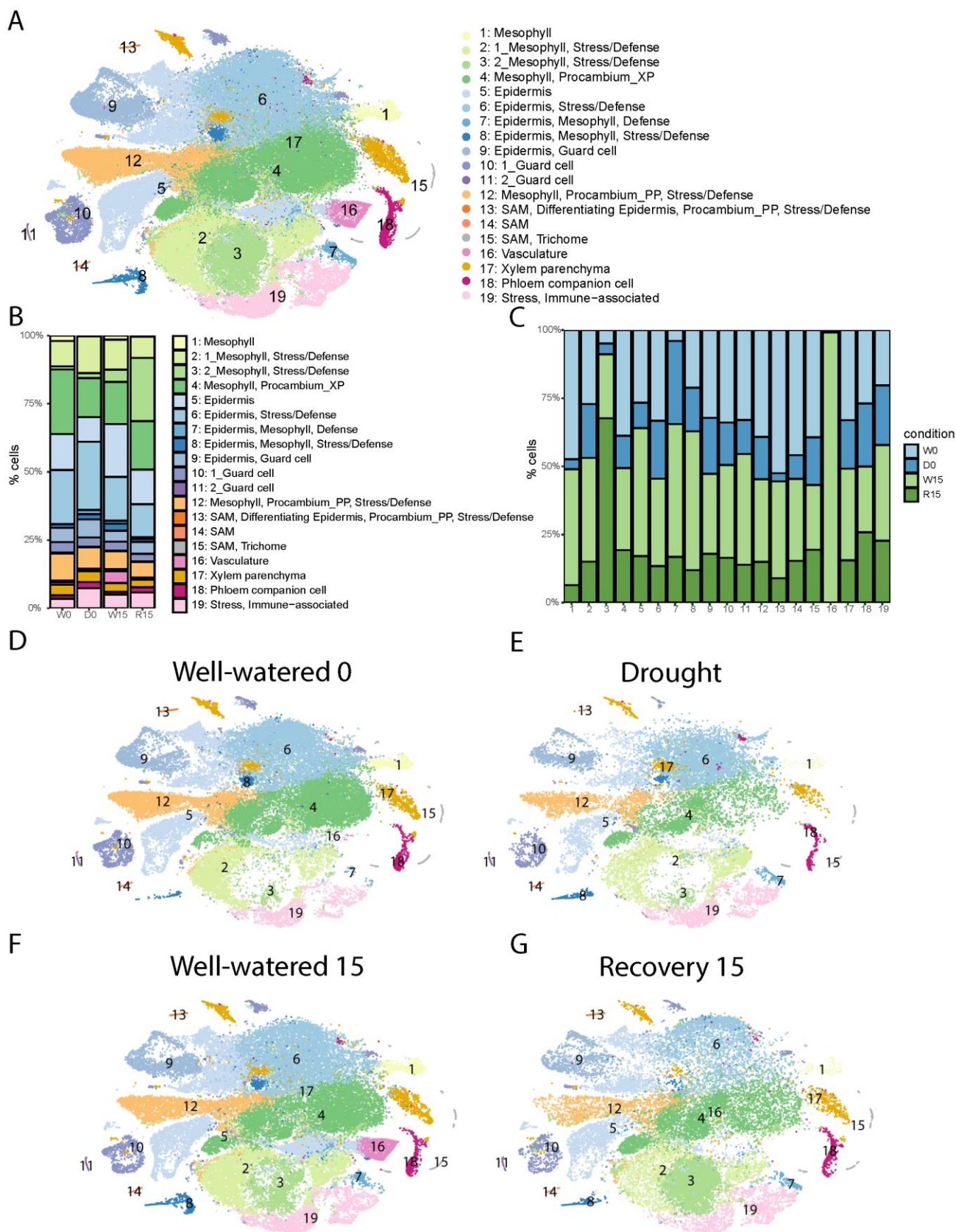


Figure S6. Unsupervised clustering on well-watered, drought and 15 min rehydration reveals 19 distinct cell populations. (A) tSNE of integrated data. **(B)** percentage of cells by condition. **(C)** percentage of condition cells in each cluster. **(D-G)** tSNE of cells from each treatment; **(D)** Well watered time 0 **(E)** Drought **(F)** well-watered time 15 and **(G)** Drought recovery time 15.

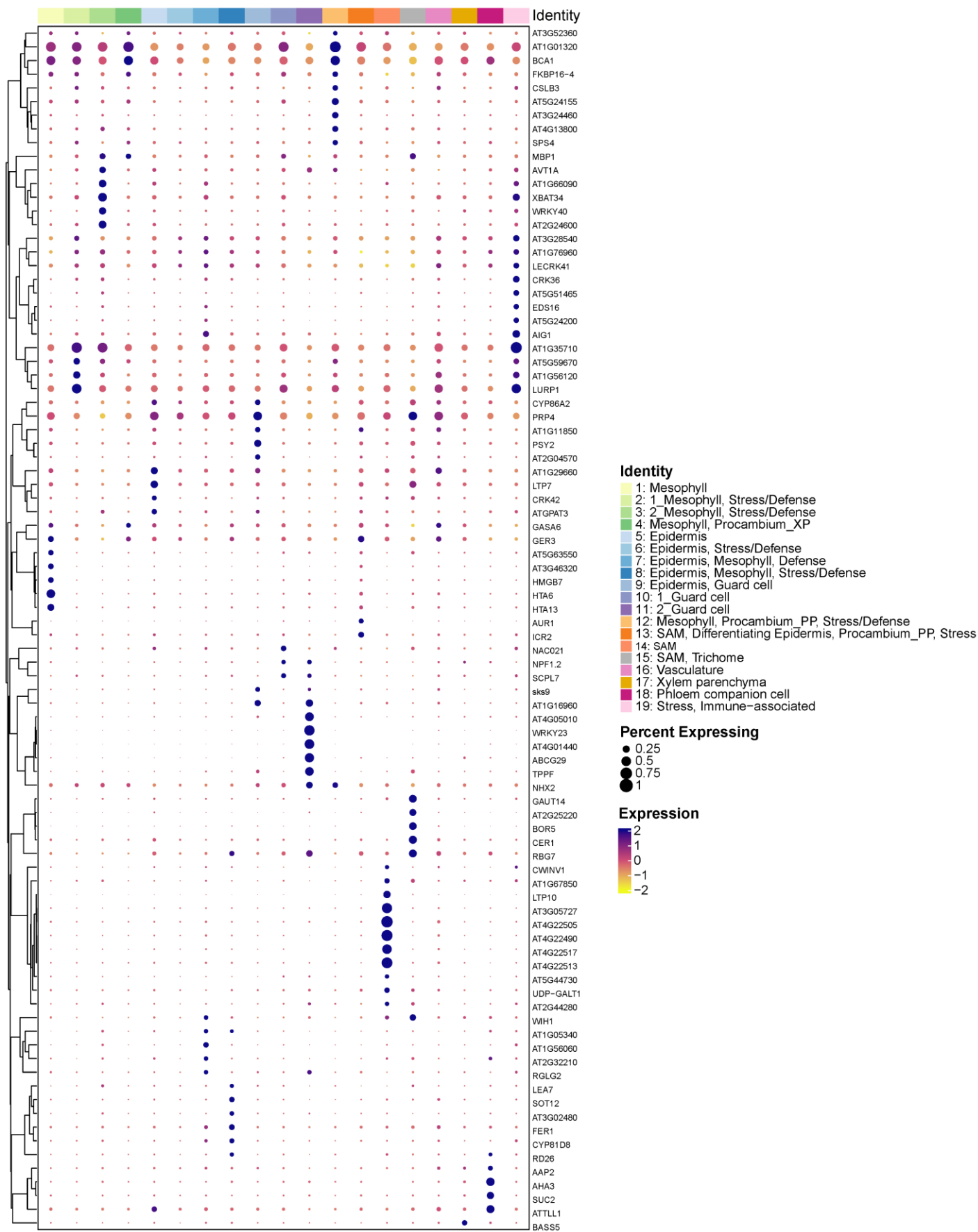


Figure S7. Selected marker genes for clusters 1-19, filtered with FDR<0.05 and average log₂(FC).

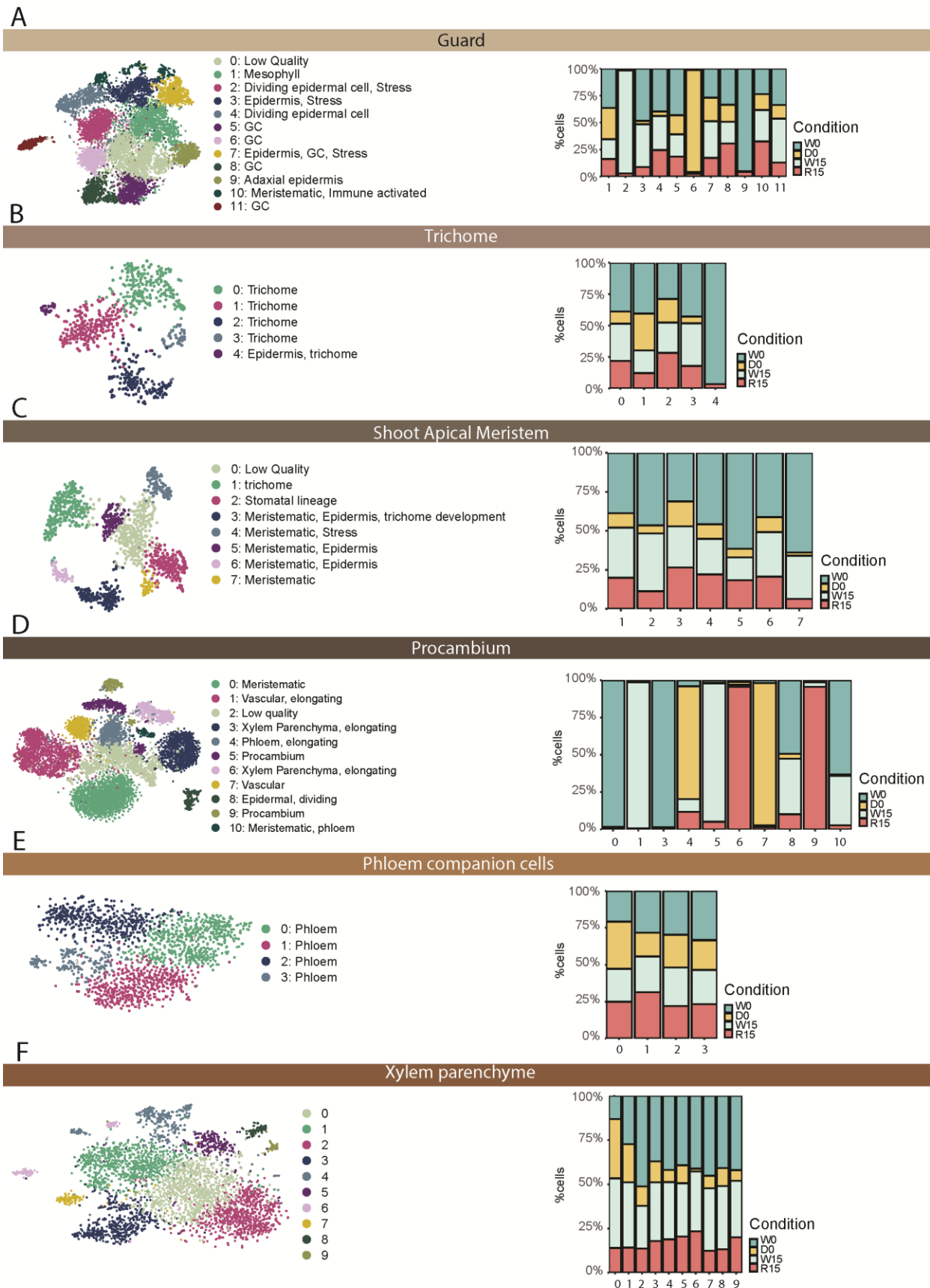


Figure S8. Figure 5. Recovery from drought stress enhanced pathogen resistance. (A) Overlap of bulk RNA-seq recovery specific up-regulated genes and Bjornson et al., (2021) genes up-regulated by different biotic elicitors. (B) plants grown on LW sterile plates after submergence in *Pto* DC3000 ($OD_{600}=0.005$) or mock. Bacterial growth was measured at 2 days post-inoculation. (ns = $P > 0.05$,

* = $P \leq 0.05$, ** = $P \leq 0.01$, *** = $P \leq 0.001$, **** = $P \leq 0.0001$, we merged two independent experiments, total n=12 per treatment. Significance values for log₁₀(CFU) on the plates were calculated with a two-way ANOVA of treatment and batch followed by a Tukey test. P-values are FDR-corrected) **(C)** Representative plants images four days post-inoculation. **(D)** Soil-grown plants spraying or mock after Pto DC3000 (OD₆₀₀=0.05). Bacterial growth was measured 4 hours and 24 hours post-inoculation. (ns = $P > 0.05$, * = $P \leq 0.05$, ** = $P \leq 0.01$, *** = $P \leq 0.001$, **** = $P \leq 0.0001$, two-way student's t-test) **(E)** representative plants images 14 days post-inoculation.

(A) Guard **(B)** Trichome **(C)** SAM **(D)** Procambium **(E)** Phloem companion cells **(F)** Xylem parenchyma.