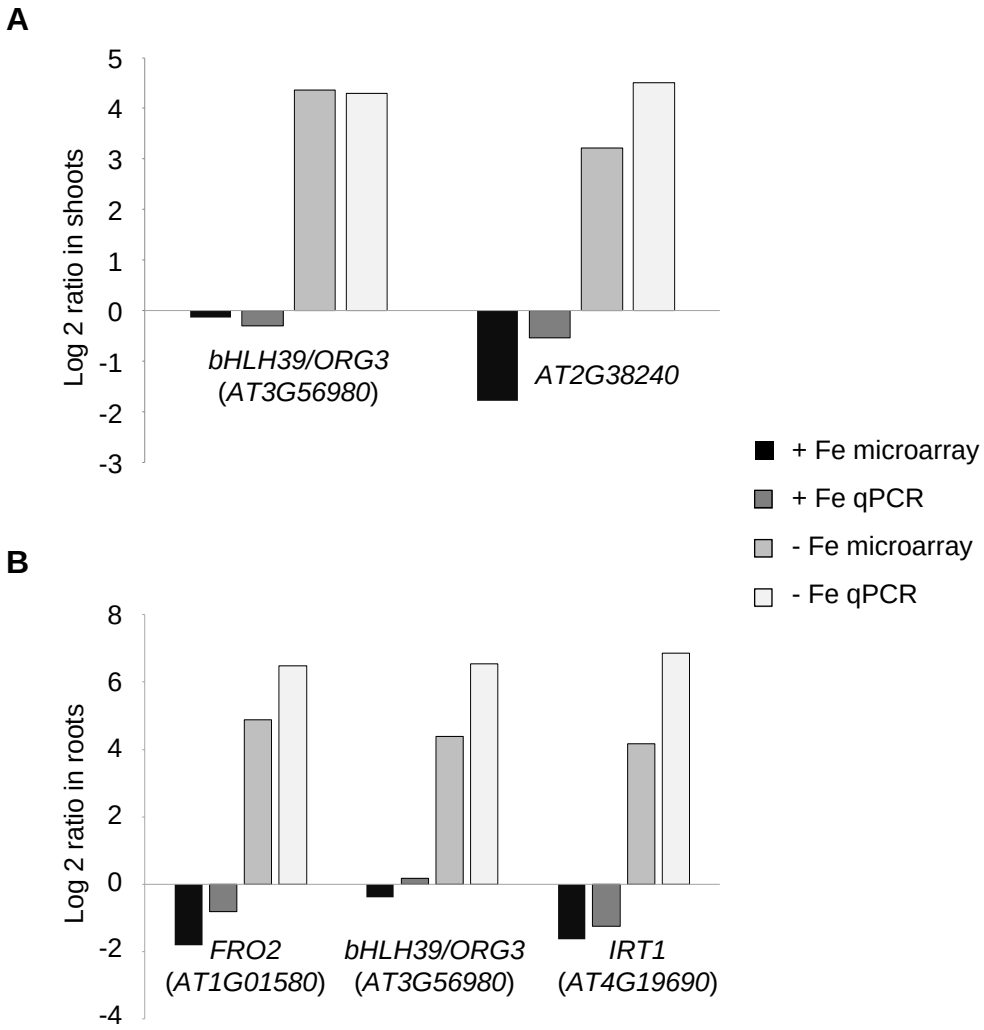

Figure S1. RT-qPCR validation of the results obtained in the microarray analysis.
Plants were treated as described in Fig. 1 and RNAs were extracted from shoots or roots 3 days after apo-pyo treatment.
A. Expression of *bHLH39/ORG3* and *AT2G38240* in shoots
B. Expression of *FRO2*, *bHLH39/ORG3* and *IRT1* in roots
Gene expression was normalized against transcript levels of the housekeeping genes *AT5G08290* and *AT4G26410* and was expressed in log 2 ratio to enable simple comparison with the CATMA transcriptomic data.

+ Fe: Fe 25 apo-pyo *versus* Fe 25; - Fe: Fe 25 apo-pyo *versus* Fe 25.

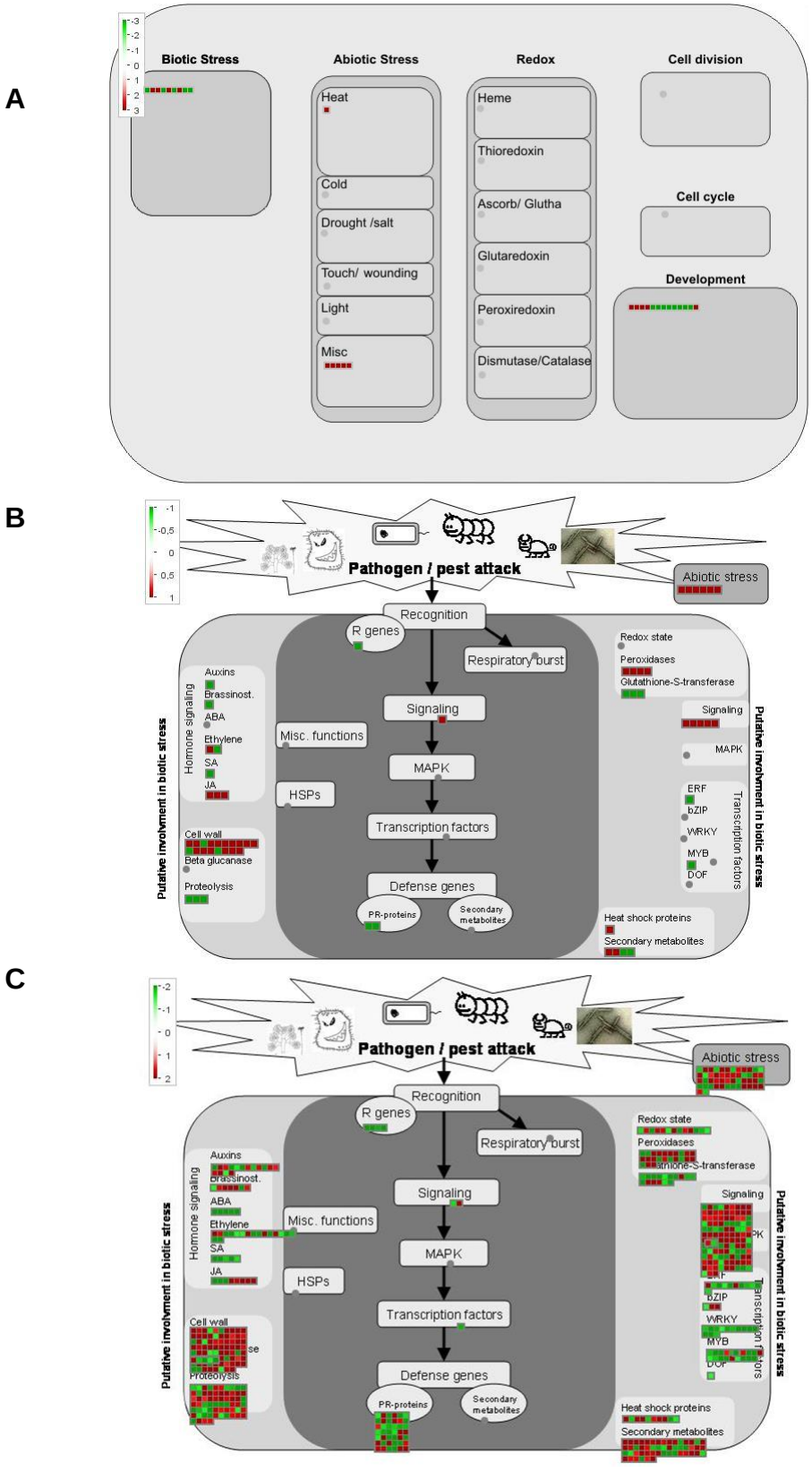

Figure S2. Mapman analysis of genes modulated by apo-pyo in the roots of plants facing iron deficiency.
A. General classification based on cellular responses (log 2 ratio ≥ + 3 or ≤ - 3; p-value ≤ 0.05).
B. Focus on the genes involved in biotic stress responses with log 2 ratio ≥ + 3 or ≤ - 3 (p-value ≤ 0.05).
C. Focus on the genes involved in biotic stress responses with log 2 ratio ≥ + 1.5 or ≤ - 1.5 (p-value ≤ 0.05).

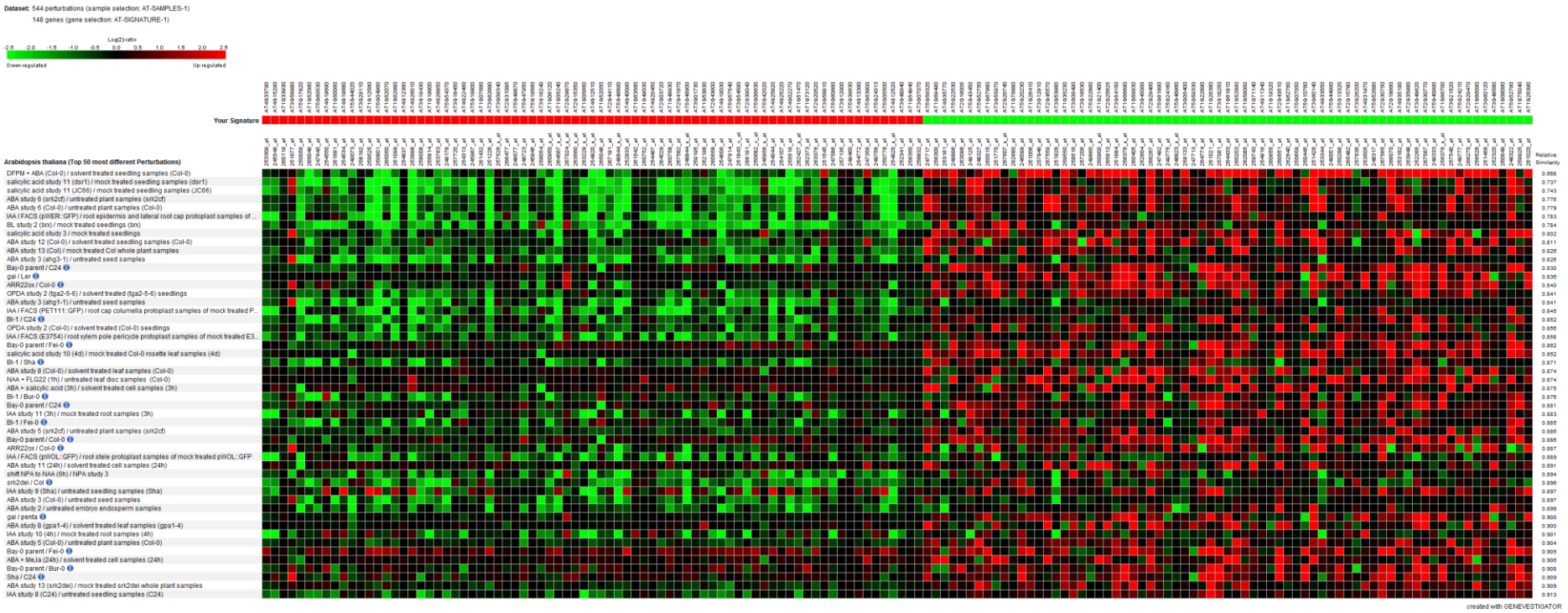

Figure S3. Comparison between the profile of expression of the most induced and repressed genes by apo-pyo in the roots in iron-deficiency medium (log 2 ratio ≥ + 3 or ≤ - 3) to the profiles of other transcriptomic data (most different perturbations). The results were generated using the tool “signature” of Genevestigator with the particular condition "hormones".

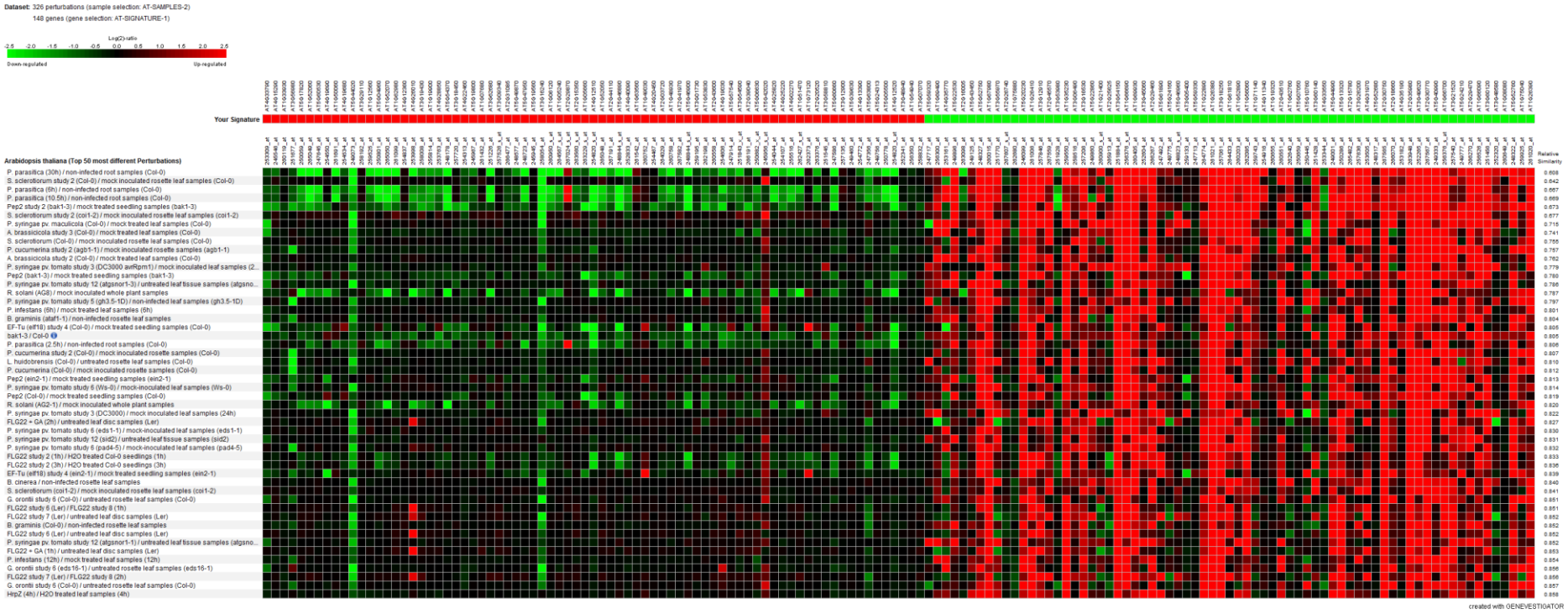

Figure S4. Comparison between the profile of expression of the most induced and repressed genes by apo-pyo in the roots in iron-deficiency medium (log 2 ratio ≥ + 3 or ≤ - 3) to the profiles of other transcriptomic data (most different perturbations). The results were generated using the tool “signature” of Genevestigator with the particular conditions "elicitor" and "biotic".

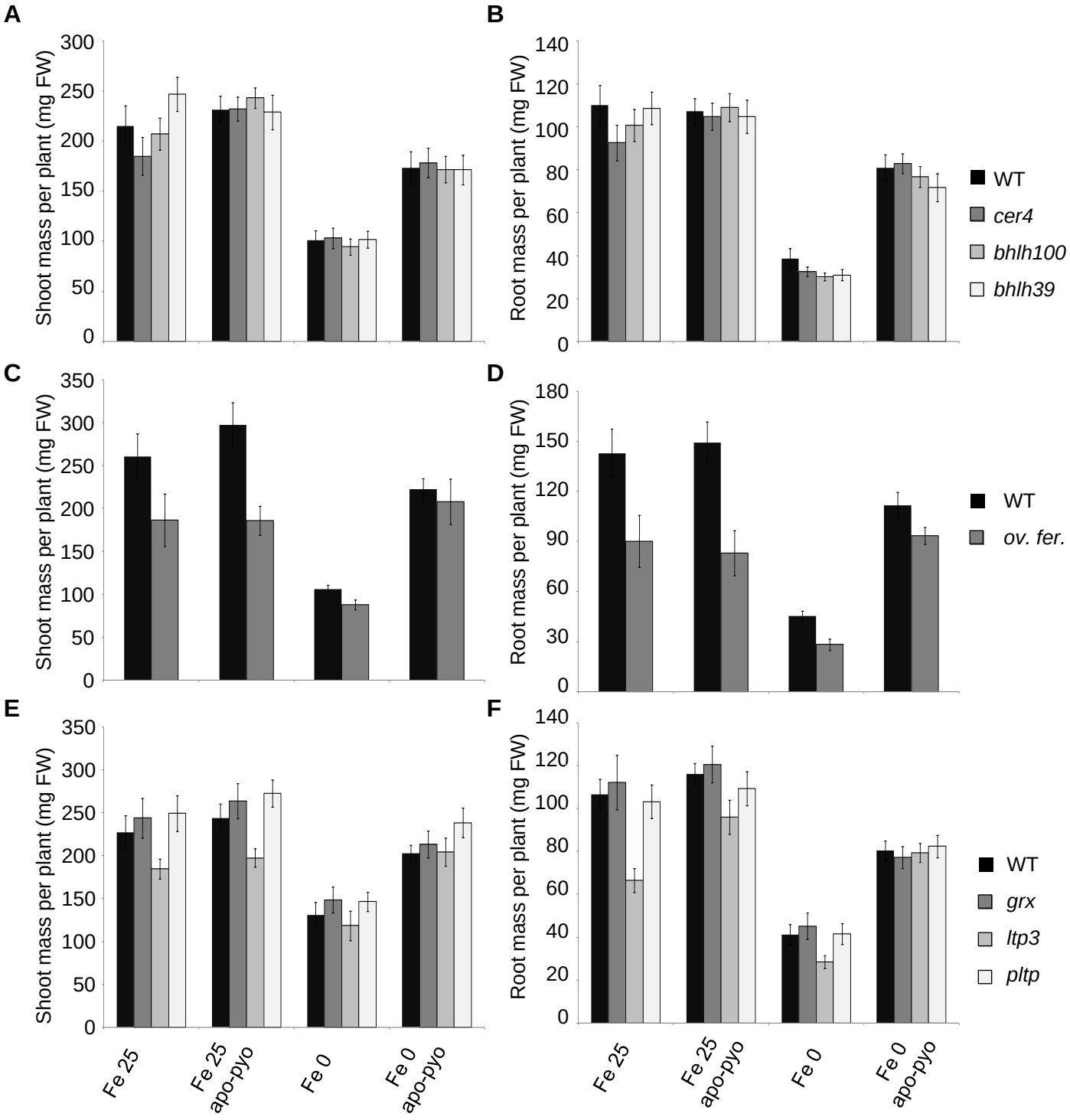

Figure S5. Growth phenotypes of mutants overexpressing or impaired in genes involved in iron homeostasis (*bhlh100*, *bhlh39*, *ov. fer.*) or defense responses or/and growth (*cer4*, *grx*, *ltp3* and *pltp*) in response to apo-pyo in iron sufficient or in iron deficient medium.

Plants were treated as described in Fig. 2.

A,B. Fresh shoot and root masses measured in WT, *cer4*, *bhlh100* and *bhlh39*.

C,D. Fresh shoot and root masses measured in WT and *ov. fer.*

E,F. Fresh shoot and root masses measured in WT, *grx*, *ltp3* and *pltp*.

Each value represents the mean ± SE of almost 12 measurements from almost 3 independent biological experiments. Two-way ANOVA followed by Tukey's HSD revealed no significant difference between the shoot and root masses of WT and of the mutants in response to apo-pyoverdine or iron deficiency ($P < 0.05$).

FW: fresh weight.

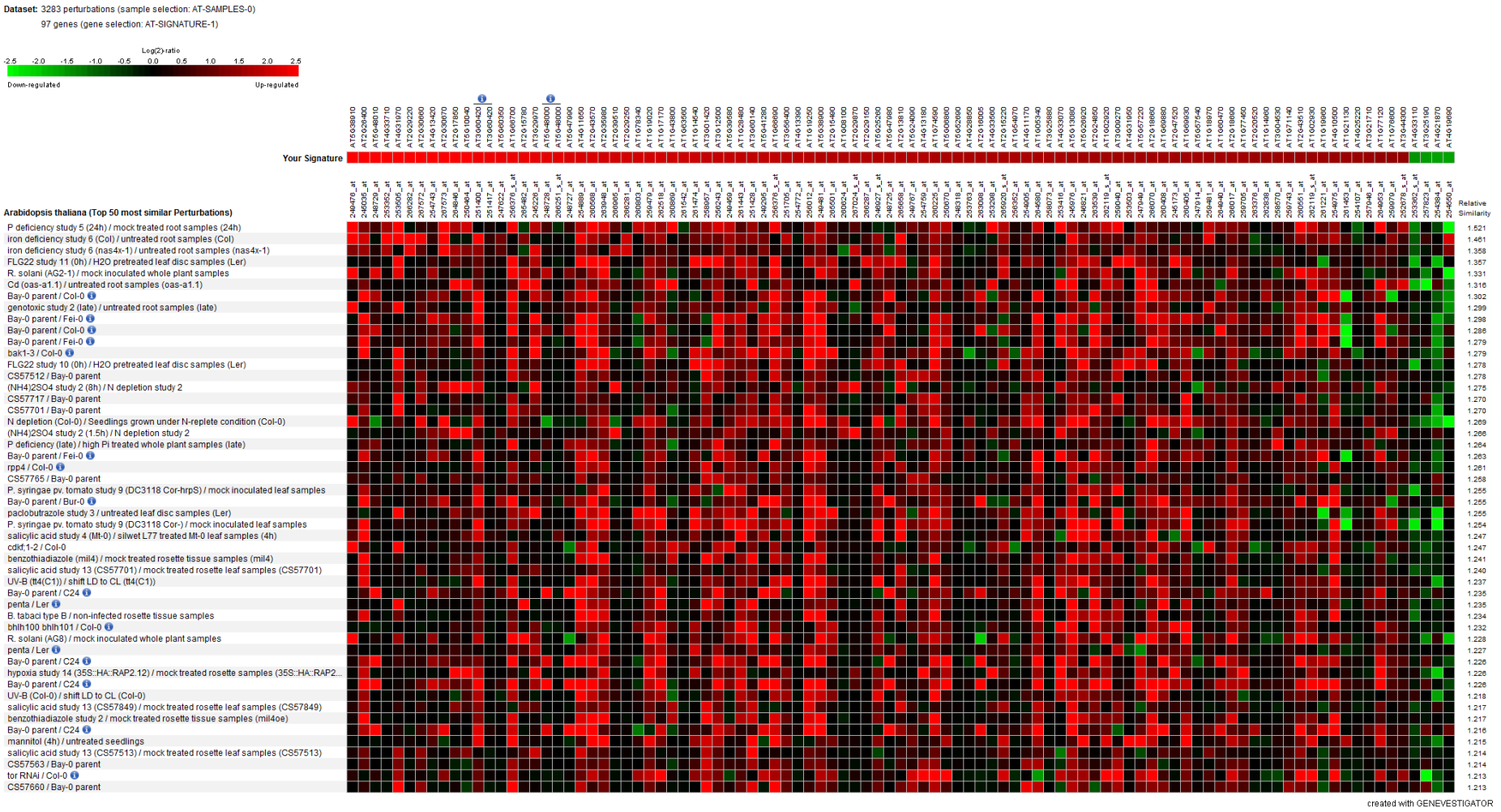

Figure S6. Comparison between the profile of expression of the genes modulated by apo-pyo in the roots in iron-containing medium (log 2 ratio ≥ + 1.5 or ≤ - 1.5) to the profiles of other transcriptomic data (most similar perturbations).
The results were generated using the tool “signature” of Genevestigator.

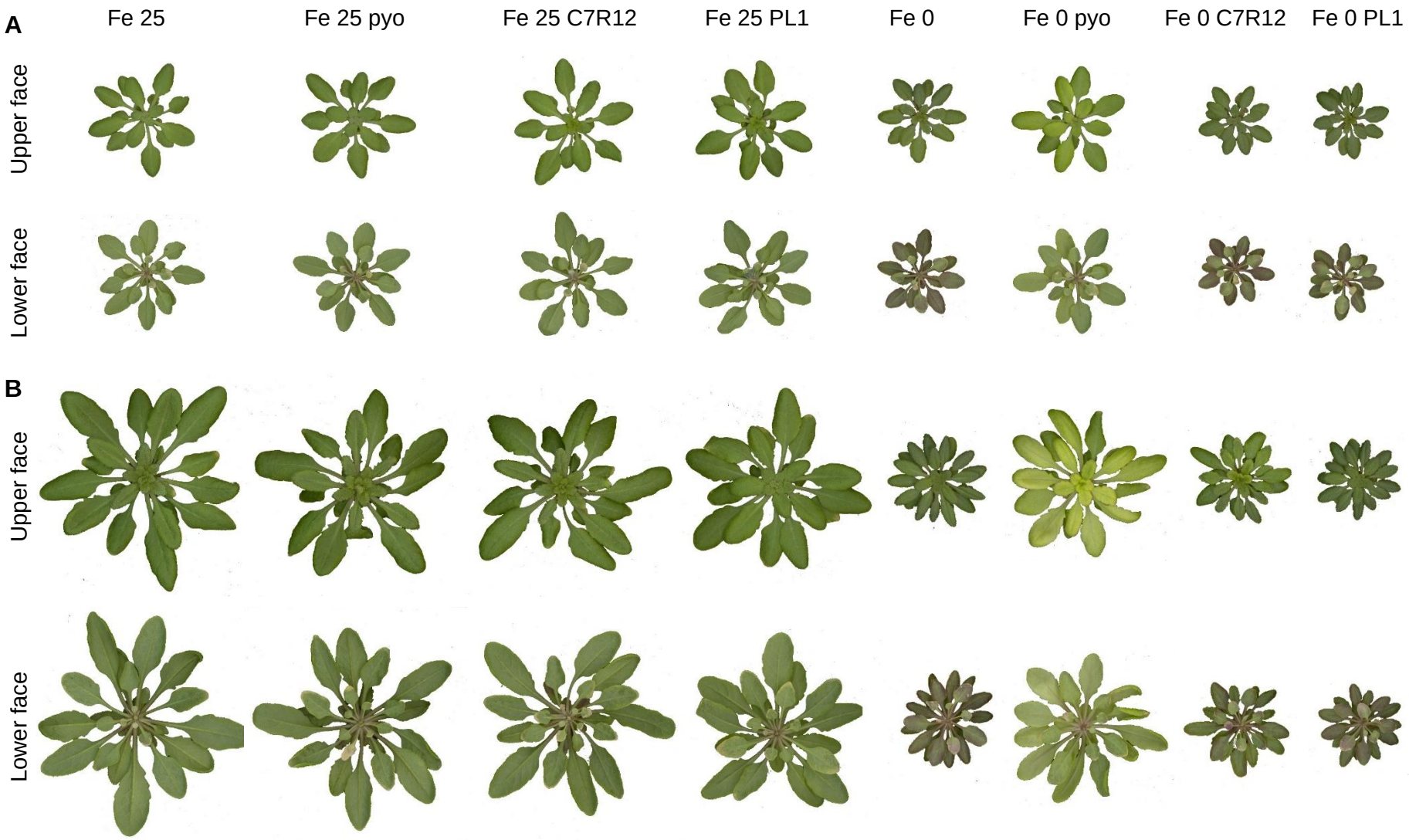

Figure S7. Rosette macroscopic phenotype of *A. thaliana* plantlets exposed to apo-pyo or inoculated with the C7R12 or PL1 strains in iron-sufficient or iron-deficient conditions.

Plants were cultivated and treated by apo-pyo as indicated in Fig. 1 or by C7R12 or PL1 bacteria as described in the Materials and Methods section.

A. Phenotypes were observed 7 days after the addition of apo-pyo, C7R12 or PL1 bacteria.

B. Phenotypes were observed 14 days after the addition of apo-pyo, C7R12 or PL1 bacteria.

Results are representative of 3 experiments.