

Supplementary Materials

Morphological, physiological and molecular markers for salt-stressed plants

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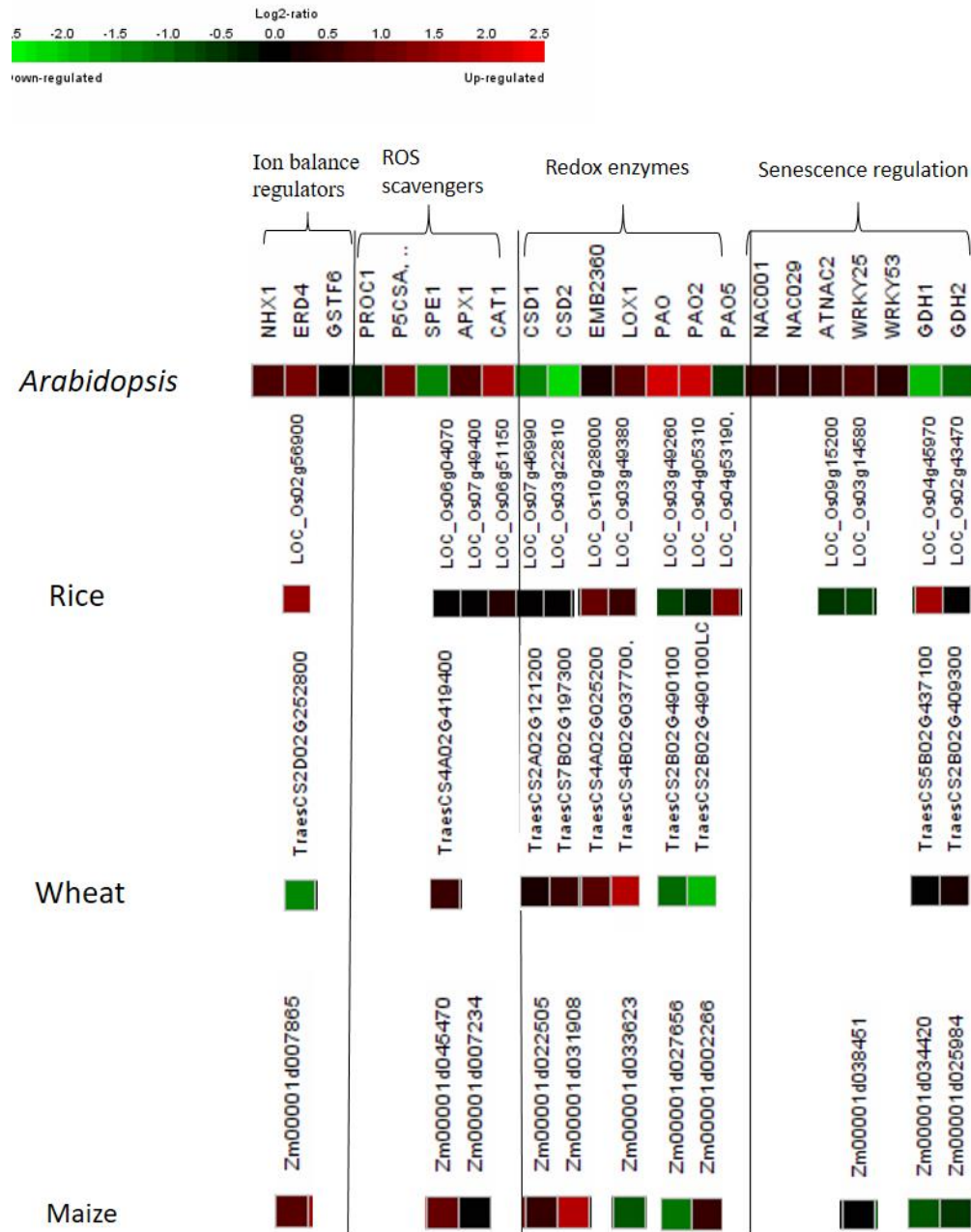


Figure S1. Change in expression of genes in *Arabidopsis*, wheat, rice and maize triggered by salt stress. Inspection of the transcripts responses was performed in published microarray collections (GENEVESTIGATOR; <https://www.genevestigator.ethz.ch>). The analysis is presented in Log2 view (fold change in expression relative to control treatment), and the results are presented as a heat map. The transcript analysis done with genes involved in ion balance regulation, ROS scavengers, Redox enzymes and senescence regulatory genes (list of genes was collected from Table 4) in shoots part of *Arabidopsis* and rice plants after 3 hours and wheat (Chinese Spring) and maize after 24h of NaCl applications. The functional orthologs of *Arabidopsis* genes were retrieved from maize, wheat and rice using the GENEVESTIGATOR Ortholog Search Tool.