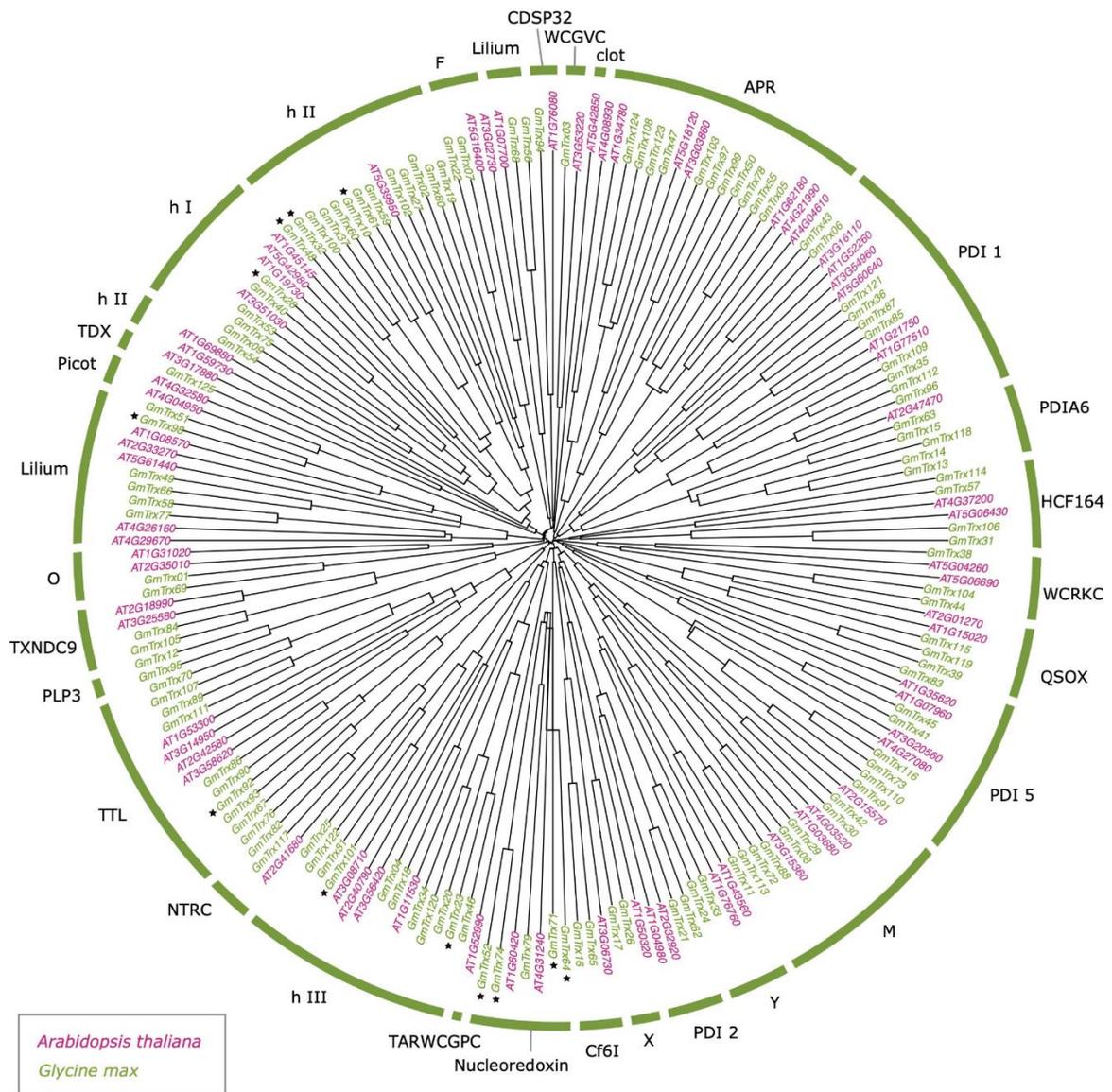
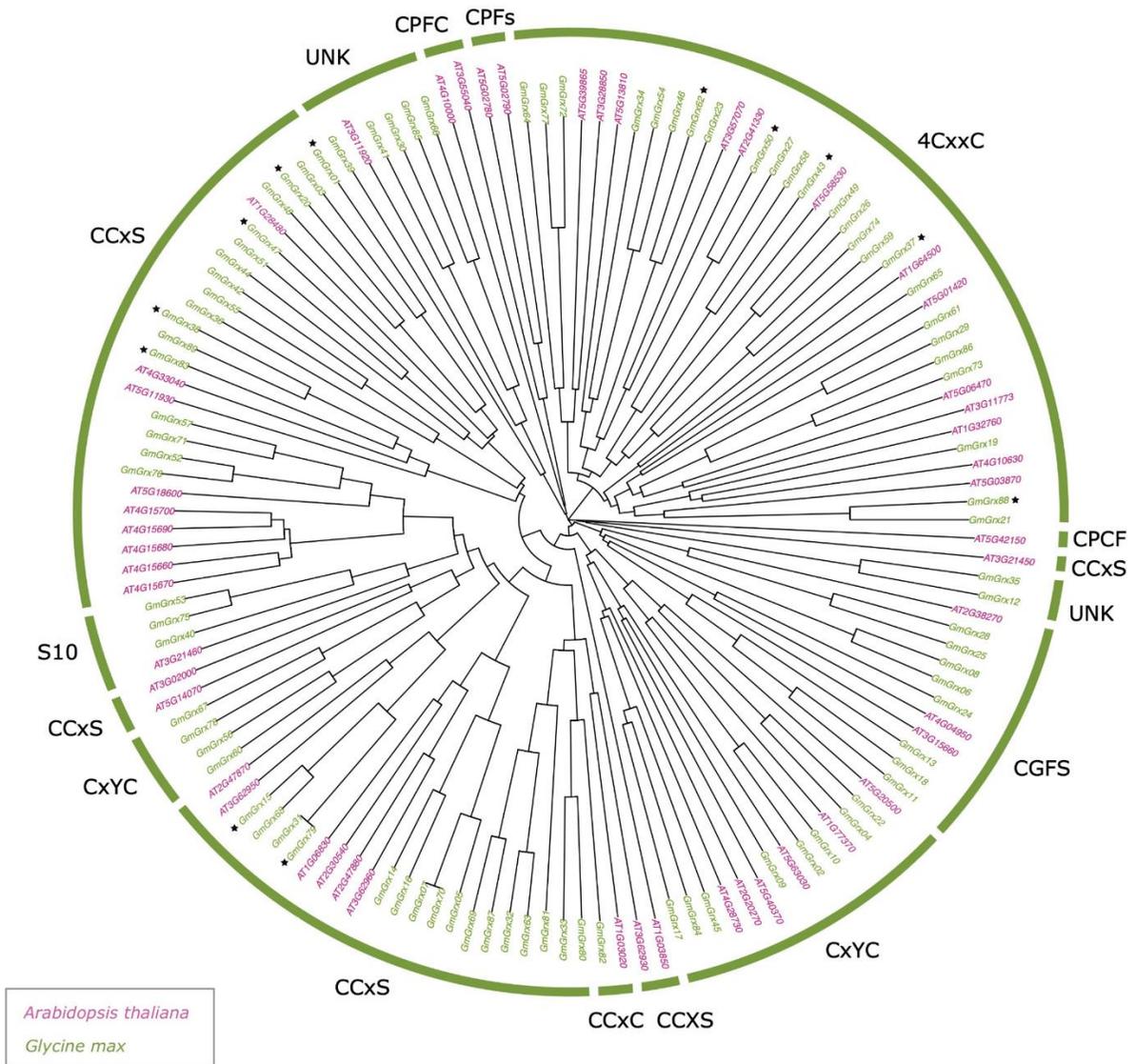


**Figure S1. Substrate water retention curves from plants comprising the four combined treatments during the water deficit period (5 to 7 days).** WW: well-watered plants; WR: water-restricted plants; N: nodulated plants; NN: non-nodulated plants. HP (%): amount of water in the substrate (sand:vermiculite, 1:1) expressed as a % of its dry weight. The dotted line indicates the HP (%) at which the substrate is at its field capacity (40% in the case of the substrate used in this assay).



**Figure S2. Thioredoxin Gene Family of *Glycine max*.** *G. max* and *A. thaliana* amino acid sequences were aligned using ClustalW, as implemented in the R package msa [29]. The phylogenetic relationship of thioredoxins (Trxs) shown in the unrooted tree was estimated using multiple sequence alignment as input in phangorn [30] to construct the neighbor-joining phylogenetic trees. Active site signatures are indicated with a line outside the tree.



**Figure S3. Glutaredoxin Gene Family of *Glycine max*.** *G. max* and *A. thaliana* amino acid sequences were aligned using ClustalW, as implemented in the R package msa [29]. The phylogenetic relationship of glutaredoxins (Grxs) shown in the unrooted tree was estimated using multiple sequence alignment as input in phangorn [30] to construct the neighbor-joining phylogenetic trees. Active site signatures are indicated with a line outside the tree.



