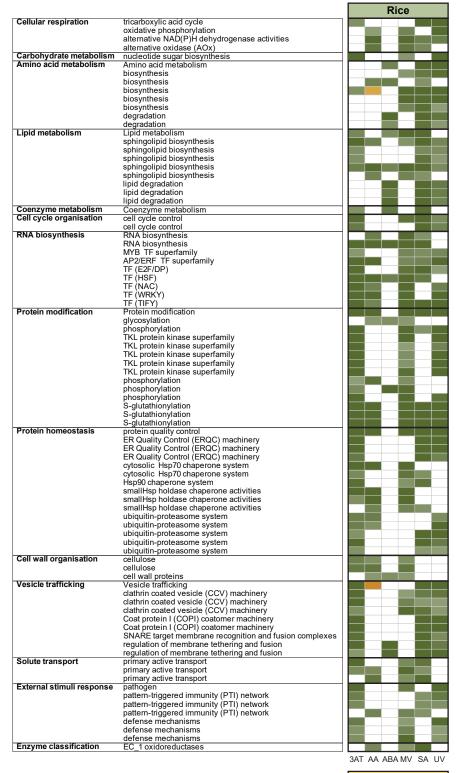


3AT AA ABA MV SA UV



Barley Cellular respiration oxidative phosphorylation trehalose metabolism lipid bodies-associated activities Carbohydrate metabolism Lipid metabolism Secondary metabolism indole alkaloid biosynthesis Phytohormone action RNA biosynthesis jasmonic acid transcriptional regulation AP2/ERF TF superfamily AP2/ERF TF superfamily AP2/ERF TF superfamily TF (HSF) TF (C2H2-ZF) TF (MCC) TF (WRKY) TF (TIFY) Protein modification TKL protein kinase superfamily TKL protein kinase superfamily TKL protein kinase superfamily CAMK protein kinase superfamily S-glutathionylation
S-glutathionylation
S-glutathionylation
S-glutathionylation
protein quality control
smallHsp holdase chaperone activities Protein homeostasis smallHsp holdase chaperone activities ubiquitin-fold protein conjugation ubiquitin-fold protein conjugation Solute transport primary active transport ABC superfamily ABC superfamily ABC superfamily APC superfamily anion channel (SLAC) sulfur assimilation Nutrient uptake sulfur assimilation Enzyme classification EC_1 oxidoreductases EC_1 oxidoreductases EC_2 transferases EC_2 transferases 3AT AA ABAMV SA UV

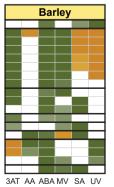
> z-score -3 0 3 under-repr. over-repr.

Supplemental Figure 1a. Functional categories of up-regulated genes in response to stress across species. Full PageMan (Usadel et al., 2006) output showing over- and under-represented (PageMan - Fisher's test) functional categories in all species for all differentially expressed genes that are upregulated. AA = antimycin A, ABA = abscisic acid, MV = methyl viologen, SA = salicylic acid, UV = ultraviolet radiation.

| | | Arabidopsis |
|----------------------|--|-------------|
| Photosynthesis | photophosphorylation | |
| Nucleotide | purines | |
| Secondary metabolism | punnes | |
| Secondary metabolism | nitrogen-containing secondary compounds | |
| | nitrogen-containing secondary compounds | |
| | nitrogen-containing secondary compounds | |
| Phytohormones | auxin | |
| Phytonormones | auxin | |
| | auxin | |
| | signalling peptides | |
| Cell cycle | interphase | |
| Cell cycle | mitosis and meiosis | |
| | organelle machineries | |
| RNA biosynthesis | organene macimenes | |
| INA biosynthesis | transcriptional activation | |
| | C2C2 superfamily | |
| | GATA transcription factor | |
| | HB (Homeobox) superfamily | |
| | zf-HD transcription factor | |
| | bHLH transcription factor | |
| | OFP transcription factor | |
| | organelle machineries | |
| | RNA polymerase activities | |
| | transcription | |
| | mTERF transcription factor | |
| RNA processing | III ERF transcription factor | |
| KNA processing | RNA splicing | |
| | RNA splicing | |
| | RNA modification | |
| | RNA modification | |
| | RNA modification | |
| | | |
| | organelle machineries | |
| | RNA splicing | |
| | plastidial RNA splicing | |
| | RNA editing | |
| Protein modification | plastidial RNA editing | |
| | phosphorylation | |
| Drotoin dogradation | phosphorylation peptidase families | |
| Protein degradation | peptidase families peptidase families | |
| | | |
| | peptidase families | |
| Cell wall | peptidase families | |
| Cell Wall | hemicellulose | |
| | | |
| | hemicellulose | |
| | pectin | |
| | pectin | |
| | pectin | |
| | cell wall proteins | |
| | hydroxyproline-rich glycoproteins | |
| | expansins | |
| | expansins | |
| | expansins | |
| | cutin and suberin | |
| | cuticular lipid formation | |
| | cuticular lipid formation | |
| | cutin polyester synthesis | |
| Solute transport | MIP family | |
| | MIP family | |

Rice Photosynthesis photophosphorylation photosystem II photosystem II photosystem II photosystem II photosystem I photosystem I photosystem I chlororespiration chlororespiration chlororespiration chlororespiration calvin cycle calvin cycle ribulose-1,5-bisphosphat carboxylase/oxygenase (RuBisCo) activity ribulose-1,5-bisphosphat carboxylase/oxygenase (RuBisCo) activity ribulose-1,5-bisphosphat carboxylase/oxygenase (RuBisCo) activity Coenzyme metabolism tetrapyrrol biosynthesis chlorophyll metabolism Secondary metabolism terpenoids gibberellin organelle machinery RNA polymerase activities RNA polymerase activities organelle machinery RNA stability RNA editing RNA editing Phytohormone action RNA biosynthesis RNA processing RNA editing Protein biosynthesis ribosome biogenesis large ribosomal subunit (LSU) large ribosomal subunit (LSU) large ribosomal subunit (LSU) large ribosomal subunit (LSU) small ribosomal subunit (SSU) small ribosomal subunit (SSU) small ribosomal subunit (SSU) small ribosomal subunit (SSU) organelle machinery plastidial ribosome plastidial ribosome Solute transport carrier-mediated transport MFS superfamily MFS superfamily MFS superfamily APC superfamily channels light External stimuli response red/far red light
SnRK1-kinase regulatory system Multi-process regulation SnRK1-kinase regulatory system Enzyme classification EC_1 oxidoreductases EC_1 oxidoreductases EC_2 transferases EC_2 transferases EC_3 hydrolases

| Photosynthesis | photophosphorylation | |
|------------------------|-------------------------------------|--|
| Protein biosynthesis | Blank | |
| | ribosome biogenesis | |
| | large ribosomal subunit (LSU) | |
| | large ribosomal subunit (LSU) | |
| | small ribosomal subunit (SSÚ) | |
| | small ribosomal subunit (SSU) | |
| | small ribosomal subunit (SSU) | |
| Protein modification | N-linked glycosylation | |
| | TKL protein kinase superfamily | |
| | TKL protein kinase superfamily | |
| Protein homeostasis | ER Quality Control (ERQC) machinery | |
| | on alpha-beta-Tubulin heterodimer | |
| Cell wall organisation | Blank | |
| Solute transport | Blank | |
| | carrier-mediated transport | |
| | MFS superfamily | |
| Enzyme classification | EC_2 transferases | |
| | | |

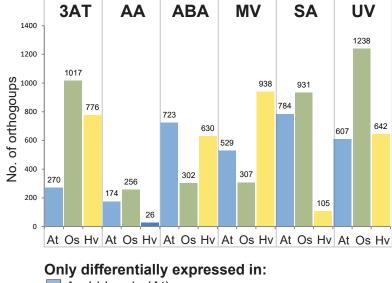


3AT AA ABAMV SA UV

z-score -3 0 3 under-repr. over-repr.

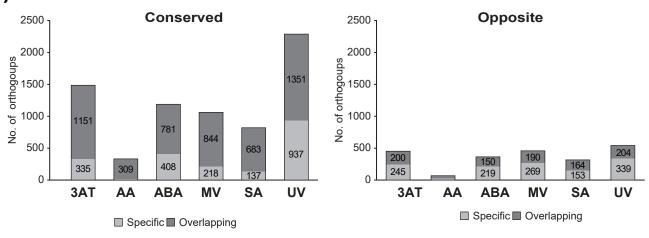
Supplemental Figure 1b. Functional categories of down-regulated genes in response to stress across species. Full PageMan (Usadel et al., 2006) output showing over- and under-represented (PageMan - Fisher's test) functional categories in all species for all differentially expressed genes that are upregulated. AA = antimycin A, ABA = abscisic acid, MV = methyl viologen, SA = salicylic acid, UV = ultraviolet radiation.





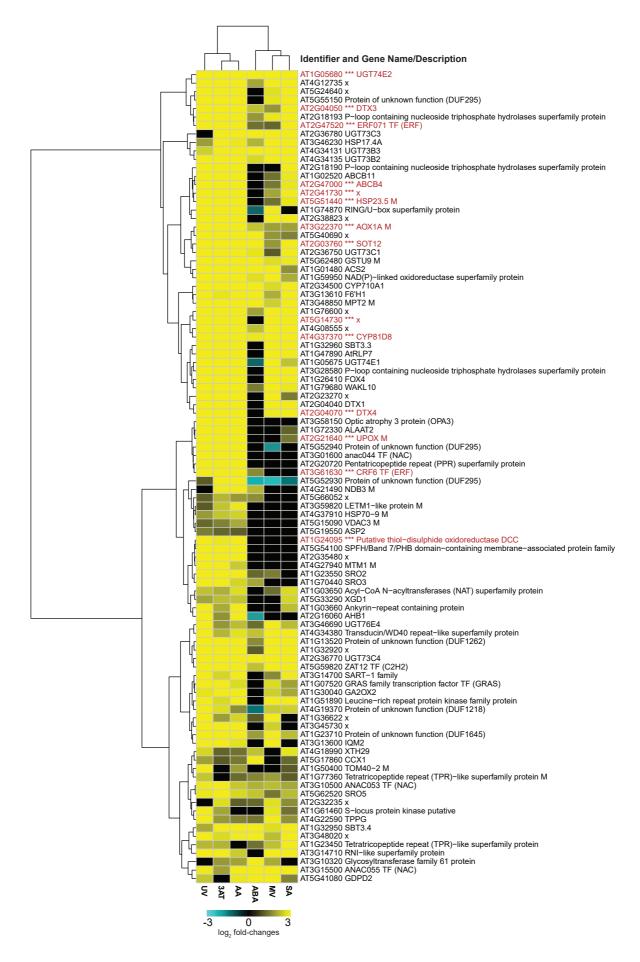
Arabidopsis (At)
Rice (Os)
Barley (Hv)





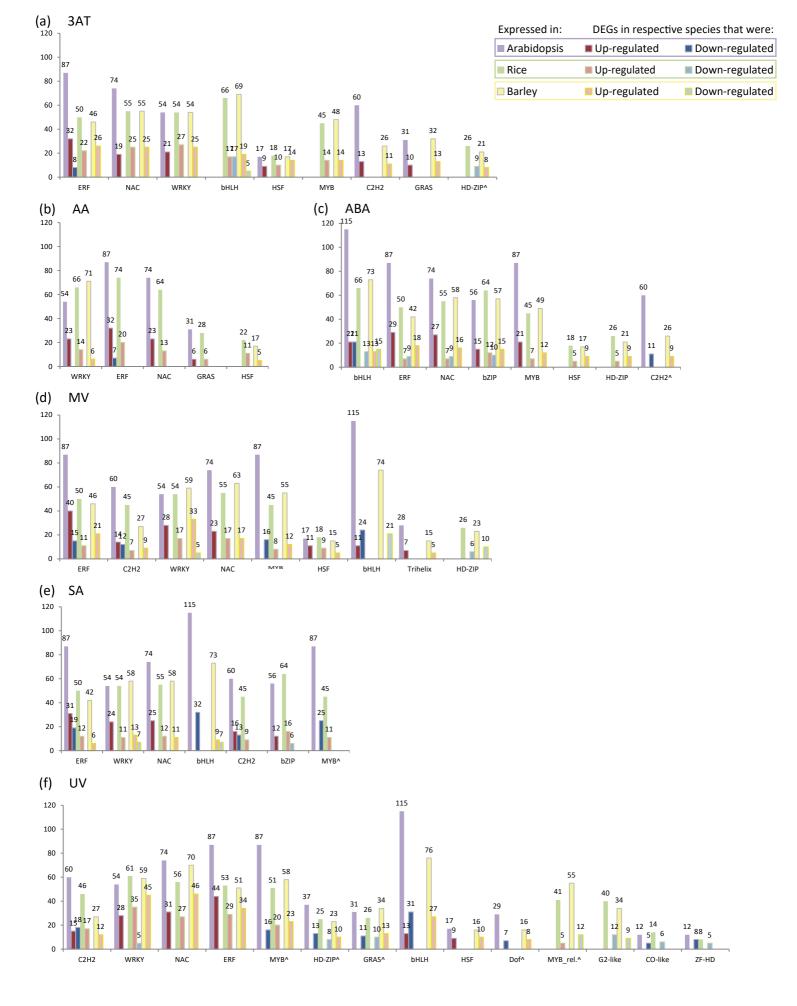
Supplemental Figure 2. Differentially expressed genes within orthogroups from Arabidopsis, rice and barley.

a) The number of DEGs that were within orthogroups in which significant differntial expression was only observed in one species, while the ortholgous genes in the other species within that orthogroup remain unchanging in expression. b) Conserved and distinct stress responses in Arabidopsis, rice and barley. The total number of conserved and opposite OGs for each stress with the numbers that were treatment specific (light grey) and overlapping (dark grey) indicated. 3AT = 3-amino-1,2,4-triazole; AA = antimycin A; ABA = abscisic acid; MV = methyl viologen; SA = salicylic acid; UV = ultraviolet radiation; At = Arabidopsis; Os =Rice; Hv = Barley.



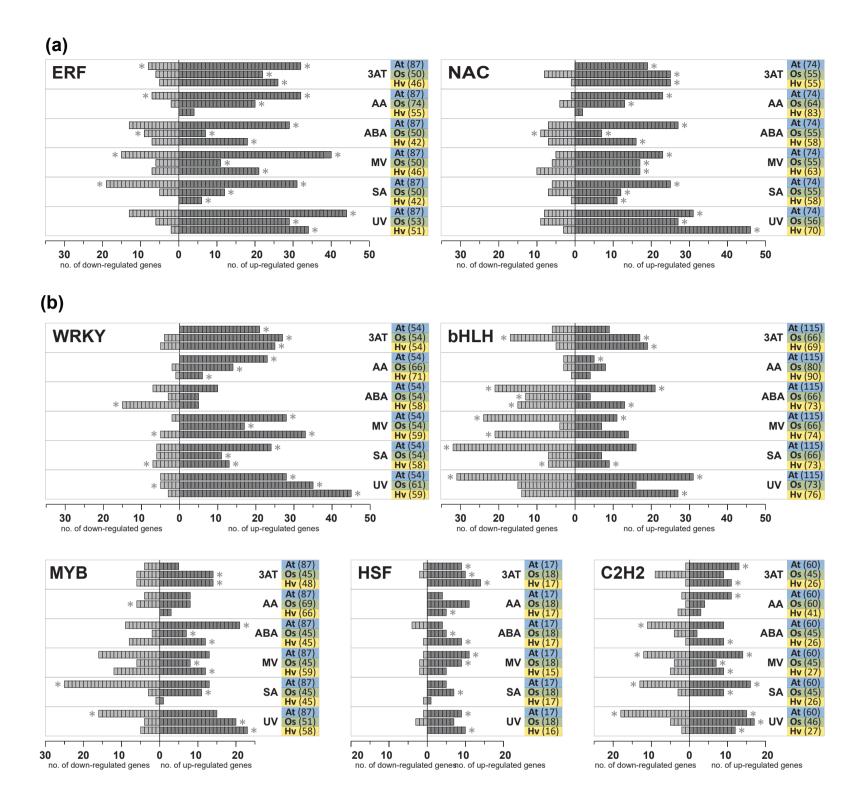
Supplemental Figure 3. Heatmap of MDS candidate genes in Arabidopsis.

Hierarchically clustered heatmap of expression values from all ANAC017 gene regulatory network (GRN) genes (Meng et al., 2019) that containing the stringent MDM in their promotor region, are highly stress responsive to AA and or 3AT and differentially expressed in at least 3 out of 6 treatments. Previously characterised MDS genes (De Clercq et al., 2013) are highlighted in red. AA = antimycin A, ABA = abscisic acid, MV = methyl viologen, SA = salicylic acid, UV = ultraviolet radiation.



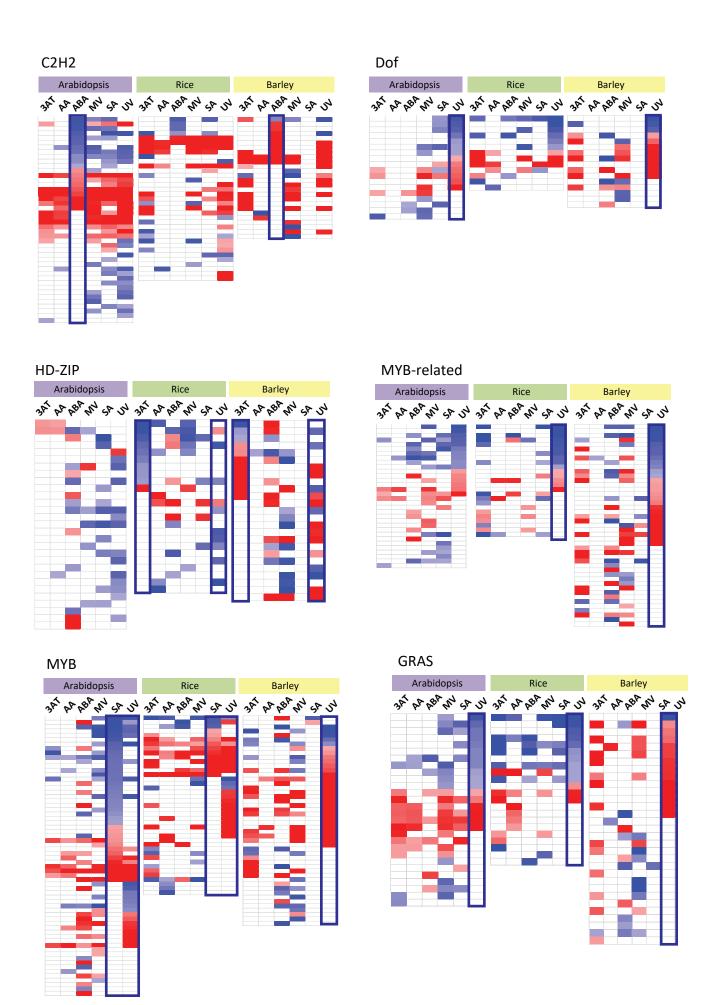
Supplemental Figure 4. Expression of genes encoding transcription factors in Arabidopsis, rice and barley in response to different stress treatments.

Numbers of transcription factors (TFs) expressed in the TF families in Arabidopsis (purple), Rice (green) and Barley (yellow) are shown, next to columns indicating the number that were up-regulated (red/pink) or down-regulated (blue/light blue) for that family. (a) 3AT = 3-amino-1,2,4-triazole, (b) AA = antimycin A, (c) ABA = abscisic acid, (d) MV = methyl viologen, (e) SA = salicylic acid, (f) UV = ultraviolet radiation. The number of TFs expressed in the families that were enriched in at least two species across at least two stresses. Note ^ indicates families that are over-represented in oppositely responsive sub-sets.



Supplemental Figure 5. Enrichment of transcription factor families in response to stress across species.

Expression of genes encoding transcription factors (TFs) in Arabidopsis (At), rice (Os) and barley (Hv) in response to different stress treatments. a) Number of differentially expressed (up-regulation = dark grey; down-regulation = light grey) TFs with families that were enriched (hypergeometric distribution; p-value< 0.05; Supplemental Table 11) in at least two species across all six stresses. ERF and NAC TF families are visualized. The total number of TFs identified for each family in each species (http://planttfdb.cbi.pku.edu.cn/) is shown in brackets b) Number of differentially expressed TFs with families that were enriched in at least two species across five stresses. WRKY, bHLH, MYB, HSF and C2H2 TF families are visualized. 3AT = 3-amino-1,2,4-triazole, AA = antimycin A, ABA = abscisic acid, MV = methyl viologen, SA = salicylic acid, UV = ultraviolet radiation.



Supp Fig 6. Transcription factor families that were enriched in oppositely responsive gene-sets (up/down-regulated). Heatmaps showing gene expression of different transcription factor families that show opposite responses to some treatments in Arabidopsis, rice and barley. 3AT = 3-amino-1,2,4-triazole, AA = antimycin A, ABA = abscisic acid, MV = methyl viologen, SA = salicylic acid, UV = ultraviolet radiation.