

Comparative functional genomic analyses of abiotic stress responsive genes in *Arabidopsis thaliana*: Insights from functional enrichment, biological pathways and phenotypes - Supplementary Material (Supplementary_File_1.doc):

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GO ID~GO Term (Biological Process category)	P-value⁺
GO:0009628~response to abiotic stimulus	8.30E-24
GO:0042214~terpene metabolic process	1.50E-15
GO:0009415~response to water	2.10E-14
GO:0009414~response to water deprivation	1.70E-13
GO:0009687~abscisic acid metabolic process	7.60E-13
GO:0043288~apocarotenoid metabolic process	7.60E-13
GO:0043289~apocarotenoid biosynthetic process	1.70E-12
GO:0009688~abscisic acid biosynthetic process	1.70E-12
GO:0045116~protein neddylation	1.70E-12
GO:0006970~response to osmotic stress	6.40E-12
GO:0009737~response to abscisic acid stimulus	1.80E-11
GO:0051761~sesquiterpene metabolic process	1.60E-11
GO:0006714~sesquiterpenoid metabolic process	1.60E-11
GO:0009719~response to endogenous stimulus	3.00E-11
GO:0010033~response to organic substance	5.30E-11
GO:0009725~response to hormone stimulus	1.10E-10
GO:0016106~sesquiterpenoid biosynthetic process	1.10E-10
GO:0051762~sesquiterpene biosynthetic process	1.10E-10
GO:0009651~response to salt stress	1.90E-10
GO:0009738~abscisic acid mediated signaling	7.20E-10
GO:0046246~terpene biosynthetic process	1.90E-09
GO:0046686~response to cadmium ion	4.30E-08
GO:0009266~response to temperature stimulus	1.10E-07
GO:0006721~terpenoid metabolic process	1.00E-07
GO:0009416~response to light stimulus	2.80E-07
GO:0010038~response to metal ion	2.70E-07
GO:0010224~response to UV-B	3.70E-07
GO:0019748~secondary metabolic process	3.90E-07
GO:0006720~isoprenoid metabolic process	6.30E-07
GO:0009314~response to radiation	6.10E-07
GO:0009787~regulation of abscisic acid mediated signaling	7.40E-07
GO:0016053~organic acid biosynthetic process	1.10E-06
GO:0046394~carboxylic acid biosynthetic process	1.10E-06
GO:0010035~response to inorganic substance	5.50E-06
GO:0009788~negative regulation of abscisic acid mediated signaling	5.90E-06
GO:0016114~terpenoid biosynthetic process	2.50E-05
GO:0009409~response to cold	4.20E-05
GO:0009611~response to wounding	5.10E-05
GO:0009968~negative regulation of signal transduction	5.00E-05
GO:0010648~negative regulation of cell communication	5.00E-05
GO:0009411~response to UV	5.20E-05
GO:0008299~isoprenoid biosynthetic process	9.50E-05

GO:0009617~response to bacterium	2.70E-04
GO:0042742~defense response to bacterium	3.40E-04
GO:0008610~lipid biosynthetic process	5.50E-04
GO:0016119~carotene metabolic process	7.10E-04
GO:0016122~xanthophyll metabolic process	1.20E-03
GO:0046165~alcohol biosynthetic process	1.20E-03
GO:0009408~response to heat	1.50E-03
GO:0009850~auxin metabolic process	1.70E-03
GO:0006511~ubiquitin-dependent protein catabolic process	2.00E-03
GO:0048585~negative regulation of response to stimulus	3.50E-03
GO:0009226~nucleotide-sugar biosynthetic process	4.80E-03
GO:0016054~organic acid catabolic process	4.70E-03
GO:0046395~carboxylic acid catabolic process	4.70E-03
GO:0044242~cellular lipid catabolic process	4.60E-03
GO:0032870~cellular response to hormone stimulus	5.10E-03
GO:0009755~hormone-mediated signaling	5.10E-03
GO:0010119~regulation of stomatal movement	5.10E-03
GO:0055114~oxidation reduction	5.30E-03
GO:0030163~protein catabolic process	5.30E-03
GO:0007242~intracellular signaling cascade	5.70E-03
GO:0009225~nucleotide-sugar metabolic process	5.90E-03
GO:0006631~fatty acid metabolic process	5.90E-03
GO:0019438~aromatic compound biosynthetic process	6.20E-03
GO:0006979~response to oxidative stress	6.10E-03
GO:0009751~response to salicylic acid stimulus	6.90E-03
GO:0019319~hexose biosynthetic process	7.10E-03
GO:0009269~response to desiccation	7.10E-03
GO:0044271~nitrogen compound biosynthetic process	7.00E-03
GO:0044265~cellular macromolecule catabolic process	7.10E-03
GO:0042787~protein ubiquitination during ubiquitin-dependent protein catabolic process	8.60E-03
GO:0046247~terpene catabolic process	8.60E-03
GO:0046364~monosaccharide biosynthetic process	8.70E-03
GO:0009057~macromolecule catabolic process	8.80E-03
GO:0044257~cellular protein catabolic process	1.00E-02
GO:0016567~protein ubiquitination	1.00E-02
GO:0034220~ion transmembrane transport	1.00E-02
GO:0009851~auxin biosynthetic process	1.30E-02
GO:0016108~tetraterpenoid metabolic process	1.50E-02
GO:0016116~carotenoid metabolic process	1.50E-02
GO:0051603~proteolysis involved in cellular protein catabolic process	1.60E-02
GO:0009063~cellular amino acid catabolic process	1.50E-02
GO:0070647~protein modification by small protein conjugation or	1.60E-02

removal	
GO:0032446~protein modification by small protein conjugation	1.70E-02
GO:0005996~monosaccharide metabolic process	1.70E-02
GO:0009733~response to auxin stimulus	1.90E-02
GO:0015986~ATP synthesis coupled proton transport	1.90E-02
GO:0015985~energy coupled proton transport, down electrochemical gradient	1.90E-02
GO:0009642~response to light intensity	1.80E-02
GO:0010817~regulation of hormone levels	1.80E-02
GO:0034637~cellular carbohydrate biosynthetic process	2.00E-02
GO:0009310~amine catabolic process	2.00E-02
GO:0048573~photoperiodism, flowering	2.80E-02
GO:0055085~transmembrane transport	2.80E-02
GO:0006508~proteolysis	3.20E-02
GO:0015992~proton transport	3.20E-02
GO:0006818~hydrogen transport	3.20E-02
GO:0009743~response to carbohydrate stimulus	3.20E-02
GO:0010182~sugar mediated signaling	3.50E-02
GO:0009756~carbohydrate mediated signaling	3.50E-02
GO:0009615~response to virus	3.40E-02
GO:0043632~modification-dependent macromolecule catabolic process	3.80E-02
GO:0019941~modification-dependent protein catabolic process	3.80E-02
GO:0009648~photoperiodism	3.80E-02
GO:0016137~glycoside metabolic process	4.20E-02
GO:0006560~proline metabolic process	4.40E-02
GO:0006790~sulfur metabolic process	4.60E-02
GO:0016110~tetraterpenoid catabolic process	4.90E-02
GO:0016118~carotenoid catabolic process	4.90E-02
GO:0016124~xanthophyll catabolic process	4.90E-02
GO:0016121~carotene catabolic process	4.90E-02

Table S1: Significantly enriched GO terms (biological process category) terms associated with ABA responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

GO ID~GO Term (Biological Process category)	P-value⁺
GO:0009628~response to abiotic stimulus	9.50E-62
GO:0009266~response to temperature stimulus	4.90E-32
GO:0009409~response to cold	5.70E-32
GO:0010033~response to organic substance	3.50E-28
GO:0006970~response to osmotic stress	3.50E-28
GO:0010035~response to inorganic substance	4.60E-25
GO:0009651~response to salt stress	2.10E-24
GO:0009719~response to endogenous stimulus	9.90E-23
GO:0009725~response to hormone stimulus	1.10E-21
GO:0009414~response to water deprivation	3.00E-21
GO:0009415~response to water	3.30E-20
GO:0009416~response to light stimulus	6.90E-18
GO:0009314~response to radiation	5.20E-17
GO:0009737~response to abscisic acid stimulus	6.20E-17
GO:0046686~response to cadmium ion	1.60E-16
GO:0010038~response to metal ion	1.70E-16
GO:0010224~response to UV-B	5.90E-14
GO:0006979~response to oxidative stress	2.50E-12
GO:0009411~response to UV	2.90E-12
GO:0045116~protein neddylation	7.20E-11
GO:0009631~cold acclimation	1.60E-10
GO:0000302~response to reactive oxygen species	1.70E-09
GO:0009743~response to carbohydrate stimulus	4.70E-09
GO:0042542~response to hydrogen peroxide	1.10E-08
GO:0010200~response to chitin	1.50E-08
GO:0009723~response to ethylene stimulus	1.60E-07
GO:0009751~response to salicylic acid stimulus	7.30E-07
GO:0009755~hormone-mediated signaling	6.50E-06
GO:0032870~cellular response to hormone stimulus	6.50E-06
GO:0009611~response to wounding	6.90E-06
GO:0010114~response to red light	1.20E-05
GO:0009642~response to light intensity	1.70E-05
GO:0015979~photosynthesis	6.10E-05
GO:0009753~response to jasmonic acid stimulus	7.00E-05
GO:0009408~response to heat	7.50E-05
GO:0009738~abscisic acid mediated signaling	9.30E-05
GO:0009644~response to high light intensity	1.30E-04
GO:0010218~response to far red light	1.30E-04
GO:0007242~intracellular signaling cascade	1.50E-04
GO:0009733~response to auxin stimulus	1.90E-04
GO:0009617~response to bacterium	2.10E-04
GO:0009639~response to red or far red light	2.80E-04
GO:0042742~defense response to bacterium	3.80E-04

GO:0016053~organic acid biosynthetic process	6.90E-04
GO:0046394~carboxylic acid biosynthetic process	6.90E-04
GO:0009873~ethylene mediated signaling pathway	7.90E-04
GO:0009269~response to desiccation	9.10E-04
GO:0006800~oxygen and reactive oxygen species metabolic process	9.30E-04
GO:0000160~two-component signal transduction system (phosphorelay)	9.60E-04
GO:0006972~hyperosmotic response	1.80E-03
GO:0042744~hydrogen peroxide catabolic process	1.80E-03
GO:0070301~cellular response to hydrogen peroxide	1.80E-03
GO:0042538~hyperosmotic salinity response	2.20E-03
GO:0016051~carbohydrate biosynthetic process	2.30E-03
GO:0042743~hydrogen peroxide metabolic process	2.50E-03
GO:0006073~cellular glucan metabolic process	4.50E-03
GO:0042398~cellular amino acid derivative biosynthetic process	5.30E-03
GO:0006790~sulfur metabolic process	5.40E-03
GO:0007623~circadian rhythm	5.60E-03
GO:0034614~cellular response to reactive oxygen species	5.60E-03
GO:0034599~cellular response to oxidative stress	6.20E-03
GO:0044042~glucan metabolic process	6.40E-03
GO:0055114~oxidation reduction	7.00E-03
GO:0044264~cellular polysaccharide metabolic process	8.10E-03
GO:0009853~photorespiration	9.10E-03
GO:0006091~generation of precursor metabolites and energy	1.30E-02
GO:0009833~primary cell wall biogenesis	1.40E-02
GO:0044271~nitrogen compound biosynthetic process	1.60E-02
GO:0019684~photosynthesis, light reaction	1.70E-02
GO:0009814~defense response, incompatible interaction	1.70E-02
GO:0005976~polysaccharide metabolic process	2.40E-02
GO:0048511~rhythmic process	2.60E-02
GO:0009612~response to mechanical stimulus	2.60E-02
GO:0042787~protein ubiquitination during ubiquitin-dependent protein catabolic process	2.90E-02
GO:0016567~protein ubiquitination	2.90E-02
GO:0009765~photosynthesis, light harvesting	2.90E-02
GO:0070647~protein modification by small protein conjugation or removal	2.90E-02
GO:0007047~cell wall organization	3.10E-02
GO:0006955~immune response	3.50E-02
GO:0009699~phenylpropanoid biosynthetic process	3.50E-02
GO:0009309~amine biosynthetic process	4.00E-02
GO:0044272~sulfur compound biosynthetic process	4.10E-02
GO:0000096~sulfur amino acid metabolic process	4.20E-02

GO:0019748~secondary metabolic process	4.30E-02
GO:0009063~cellular amino acid catabolic process	4.30E-02
GO:0032446~protein modification by small protein conjugation	4.80E-02

Table S2: Significantly enriched GO terms (biological process category) terms associated with COLD responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

GO ID~GO Term (Biological Process category)	P-value ⁺
GO:0009628~response to abiotic stimulus	1.20E-26
GO:0009409~response to cold	1.80E-23
GO:0009266~response to temperature stimulus	2.90E-23
GO:0009737~response to abscisic acid stimulus	4.90E-17
GO:0009414~response to water deprivation	2.70E-12
GO:0009631~cold acclimation	3.50E-12
GO:0009415~response to water	3.60E-12
GO:0006970~response to osmotic stress	8.60E-11
GO:0009725~response to hormone stimulus	4.20E-09
GO:0009719~response to endogenous stimulus	1.10E-08
GO:0010033~response to organic substance	2.10E-08
GO:0009738~abscisic acid mediated signaling	1.50E-06
GO:0009651~response to salt stress	1.40E-06
GO:0007242~intracellular signaling cascade	1.20E-03
GO:0006560~proline metabolic process	5.90E-03
GO:0050826~response to freezing	8.30E-03
GO:0010286~heat acclimation	1.70E-02
GO:0009269~response to desiccation	2.00E-02
GO:0006979~response to oxidative stress	2.10E-02
GO:0032870~cellular response to hormone stimulus	2.00E-02
GO:0009755~hormone-mediated signaling	2.00E-02
GO:0009084~glutamine family amino acid biosynthetic process	3.60E-02

Table S3: Significantly enriched GO terms (biological process category) terms associated with COLD-DROUGHT-SALT responsive genes in *Arabidopsis thaliana*.

⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Biological Process category)	<i>P</i>-value⁺
GO:0015992~proton transport	1.60E-02
GO:0006818~hydrogen transport	1.60E-02
GO:0015672~monovalent inorganic cation transport	2.20E-02

Table S4: Significantly enriched GO terms (biological process category) terms associated with DEHYDRATION responsive genes in *Arabidopsis thaliana*.

⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Biological Process category)	P-value⁺
GO:0009628~response to abiotic stimulus	2.00E-65
GO:0009409~response to cold	3.60E-42
GO:0009266~response to temperature stimulus	1.30E-39
GO:0009414~response to water deprivation	4.70E-38
GO:0009415~response to water	8.30E-38
GO:0009737~response to abscisic acid stimulus	1.40E-28
GO:0010033~response to organic substance	1.50E-27
GO:0006970~response to osmotic stress	1.70E-27
GO:0009611~response to wounding	2.60E-24
GO:0009651~response to salt stress	8.10E-23
GO:0009719~response to endogenous stimulus	7.40E-21
GO:0009617~response to bacterium	1.40E-20
GO:0009725~response to hormone stimulus	5.60E-17
GO:0042742~defense response to bacterium	4.60E-14
GO:0006979~response to oxidative stress	4.50E-13
GO:0009416~response to light stimulus	6.80E-12
GO:0009314~response to radiation	2.70E-11
GO:0019748~secondary metabolic process	2.30E-10
GO:0009743~response to carbohydrate stimulus	3.40E-10
GO:0009738~abscisic acid mediated signaling	5.50E-10
GO:0009269~response to desiccation	6.70E-10
GO:0006952~defense response	2.60E-09
GO:0016054~organic acid catabolic process	4.70E-09
GO:0046395~carboxylic acid catabolic process	4.70E-09
GO:0019438~aromatic compound biosynthetic process	1.00E-08
GO:0019253~reductive pentose-phosphate cycle	2.40E-08
GO:0015979~photosynthesis	2.40E-08
GO:0009753~response to jasmonic acid stimulus	3.90E-08
GO:0019685~photosynthesis, dark reaction	5.10E-08
GO:0009631~cold acclimation	6.30E-08
GO:0010035~response to inorganic substance	1.10E-07
GO:0006631~fatty acid metabolic process	1.30E-07
GO:0010200~response to chitin	3.20E-07
GO:0009063~cellular amino acid catabolic process	4.50E-07
GO:0055114~oxidation reduction	8.20E-07
GO:0042398~cellular amino acid derivative biosynthetic process	8.10E-07
GO:0009310~amine catabolic process	1.00E-06
GO:0015977~carbon utilization by fixation of carbon dioxide	1.10E-06
GO:0046686~response to cadmium ion	6.00E-06
GO:0009642~response to light intensity	6.10E-06
GO:0046394~carboxylic acid biosynthetic process	8.10E-06
GO:0016053~organic acid biosynthetic process	8.10E-06
GO:0010038~response to metal ion	1.30E-05

GO:0006575~cellular amino acid derivative metabolic process	1.30E-05
GO:0042434~indole derivative metabolic process	1.80E-05
GO:0042430~indole and derivative metabolic process	1.80E-05
GO:0032870~cellular response to hormone stimulus	3.30E-05
GO:0009755~hormone-mediated signaling	3.30E-05
GO:0009809~lignin biosynthetic process	3.60E-05
GO:0042435~indole derivative biosynthetic process	4.00E-05
GO:0009698~phenylpropanoid metabolic process	1.00E-04
GO:0009699~phenylpropanoid biosynthetic process	1.10E-04
GO:0009694~jasmonic acid metabolic process	1.50E-04
GO:0031407~oxylipin metabolic process	1.50E-04
GO:0009867~jasmonic acid mediated signaling pathway	1.90E-04
GO:0009408~response to heat	3.60E-04
GO:0007242~intracellular signaling cascade	4.50E-04
GO:0009695~jasmonic acid biosynthetic process	5.50E-04
GO:0009723~response to ethylene stimulus	1.10E-03
GO:0009787~regulation of abscisic acid mediated signaling	1.10E-03
GO:0000302~response to reactive oxygen species	1.20E-03
GO:0009808~lignin metabolic process	1.20E-03
GO:0009644~response to high light intensity	1.20E-03
GO:0016051~carbohydrate biosynthetic process	2.40E-03
GO:0009072~aromatic amino acid family metabolic process	2.40E-03
GO:0006972~hyperosmotic response	2.70E-03
GO:0007623~circadian rhythm	2.80E-03
GO:0016137~glycoside metabolic process	2.70E-03
GO:0031408~oxylipin biosynthetic process	3.00E-03
GO:0044271~nitrogen compound biosynthetic process	4.10E-03
GO:0042538~hyperosmotic salinity response	4.50E-03
GO:0006633~fatty acid biosynthetic process	4.80E-03
GO:0042542~response to hydrogen peroxide	5.10E-03
GO:0010114~response to red light	6.80E-03
GO:0009744~response to sucrose stimulus	9.00E-03
GO:0006091~generation of precursor metabolites and energy	9.70E-03
GO:0009639~response to red or far red light	9.70E-03
GO:0006790~sulfur metabolic process	1.00E-02
GO:0034285~response to disaccharide stimulus	1.00E-02
GO:0009309~amine biosynthetic process	1.10E-02
GO:0048511~rhythmic process	1.20E-02
GO:0009788~negative regulation of abscisic acid mediated signaling	1.20E-02
GO:0006955~immune response	1.50E-02
GO:0046219~indolalkylamine biosynthetic process	1.50E-02
GO:0000162~tryptophan biosynthetic process	1.50E-02
GO:0042401~biogenic amine biosynthetic process	1.50E-02

GO:0009968~negative regulation of signal transduction	1.80E-02
GO:0010648~negative regulation of cell communication	1.80E-02
GO:0009864~induced systemic resistance, jasmonic acid mediated signaling pathway	1.70E-02
GO:0008652~cellular amino acid biosynthetic process	2.00E-02
GO:0031328~positive regulation of cellular biosynthetic process	2.40E-02
GO:0009891~positive regulation of biosynthetic process	2.40E-02
GO:0009073~aromatic amino acid family biosynthetic process	2.60E-02
GO:0046417~chorismate metabolic process	2.60E-02
GO:0006568~tryptophan metabolic process	2.70E-02
GO:0006586~indolalkylamine metabolic process	2.70E-02
GO:0009626~plant-type hypersensitive response	2.80E-02
GO:0019684~photosynthesis, light reaction	3.10E-02
GO:0009407~toxin catabolic process	3.20E-02
GO:0009404~toxin metabolic process	3.20E-02
GO:0034050~host programmed cell death induced by symbiont	3.20E-02
GO:0006576~biogenic amine metabolic process	3.30E-02
GO:0007568~aging	3.60E-02
GO:0010120~camalexin biosynthetic process	4.00E-02
GO:0052317~camalexin metabolic process	4.00E-02
GO:0009682~induced systemic resistance	4.00E-02
GO:0016138~glycoside biosynthetic process	4.40E-02
GO:0010557~positive regulation of macromolecule biosynthetic process	4.80E-02
GO:0009312~oligosaccharide biosynthetic process	4.90E-02
GO:0009620~response to fungus	4.90E-02

Table S5: Significantly enriched GO terms (biological process category) terms associated with DROUGHT responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

GO ID~GO Term (Biological Process category)	<i>P</i>-value⁺
GO:0016053~organic acid biosynthetic process	2.60E-02
GO:0046394~carboxylic acid biosynthetic process	2.60E-02
GO:0006790~sulfur metabolic process	2.90E-02
GO:0044272~sulfur compound biosynthetic process	4.60E-02
GO:0000097~sulfur amino acid biosynthetic process	4.80E-02

Table S6: Significantly enriched GO terms (biological process category) terms associated with IRON responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Biological Process category)	P-value⁺
GO:0045116~protein neddylation	2.40E-12
GO:0009628~response to abiotic stimulus	3.00E-10
GO:0010033~response to organic substance	1.50E-09
GO:0010224~response to UV-B	3.30E-08
GO:0010038~response to metal ion	4.80E-07
GO:0009411~response to UV	1.10E-06
GO:0010035~response to inorganic substance	1.90E-06
GO:0009719~response to endogenous stimulus	3.80E-06
GO:0046686~response to cadmium ion	8.10E-06
GO:0006979~response to oxidative stress	6.00E-05
GO:0009725~response to hormone stimulus	1.70E-04
GO:0010200~response to chitin	2.50E-04
GO:0009416~response to light stimulus	5.70E-04
GO:0006970~response to osmotic stress	1.00E-03
GO:0009314~response to radiation	1.00E-03
GO:0009611~response to wounding	1.30E-03
GO:0009651~response to salt stress	1.30E-03
GO:0009743~response to carbohydrate stimulus	1.30E-03
GO:0006511~ubiquitin-dependent protein catabolic process	1.80E-03
GO:0019748~secondary metabolic process	2.10E-03
GO:0016567~protein ubiquitination	2.30E-03
GO:0009409~response to cold	2.90E-03
GO:0009266~response to temperature stimulus	3.40E-03
GO:0009751~response to salicylic acid stimulus	3.70E-03
GO:0070647~protein modification by small protein conjugation or removal	3.70E-03
GO:0032446~protein modification by small protein conjugation	3.80E-03
GO:0009617~response to bacterium	4.50E-03
GO:0030163~protein catabolic process	8.20E-03
GO:0042742~defense response to bacterium	1.00E-02
GO:0042787~protein ubiquitination during ubiquitin-dependent protein catabolic process	1.00E-02
GO:0044257~cellular protein catabolic process	1.90E-02
GO:0044265~cellular macromolecule catabolic process	2.20E-02
GO:0009699~phenylpropanoid biosynthetic process	2.50E-02
GO:0019941~modification-dependent protein catabolic process	2.60E-02
GO:0043632~modification-dependent macromolecule catabolic process	2.60E-02
GO:0051603~proteolysis involved in cellular protein catabolic process	2.90E-02
GO:0009057~macromolecule catabolic process	3.60E-02

Table S7: Significantly enriched GO terms (biological process category) terms associated with LIGHT responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

GO ID~GO Term (Biological Process category)	P-value⁺
GO:0009628~response to abiotic stimulus	1.90E-57
GO:0006970~response to osmotic stress	1.90E-29
GO:0009415~response to water	1.90E-27
GO:0009414~response to water deprivation	5.40E-26
GO:0009651~response to salt stress	1.10E-25
GO:0009737~response to abscisic acid stimulus	7.40E-25
GO:0009719~response to endogenous stimulus	2.70E-24
GO:0010033~response to organic substance	3.70E-23
GO:0009725~response to hormone stimulus	4.00E-23
GO:0009409~response to cold	1.50E-17
GO:0009266~response to temperature stimulus	2.00E-17
GO:0010035~response to inorganic substance	5.90E-17
GO:0009416~response to light stimulus	3.40E-15
GO:0009314~response to radiation	1.00E-14
GO:0009611~response to wounding	4.80E-14
GO:0009753~response to jasmonic acid stimulus	5.40E-14
GO:0009751~response to salicylic acid stimulus	6.70E-14
GO:0010038~response to metal ion	2.60E-13
GO:0045116~protein neddylation	3.10E-13
GO:0046686~response to cadmium ion	4.80E-13
GO:0015979~photosynthesis	1.10E-11
GO:0009617~response to bacterium	7.00E-08
GO:0009765~photosynthesis, light harvesting	1.40E-07
GO:0009642~response to light intensity	2.00E-07
GO:0009269~response to desiccation	2.10E-07
GO:0009723~response to ethylene stimulus	2.30E-07
GO:0009733~response to auxin stimulus	2.60E-07
GO:0042742~defense response to bacterium	2.80E-07
GO:0010224~response to UV-B	3.40E-07
GO:0055114~oxidation reduction	3.70E-07
GO:0006979~response to oxidative stress	1.50E-06
GO:0009411~response to UV	4.70E-06
GO:0006091~generation of precursor metabolites and energy	7.10E-06
GO:0009739~response to gibberellin stimulus	7.10E-06
GO:0009631~cold acclimation	9.90E-06
GO:0019684~photosynthesis, light reaction	1.00E-05
GO:0009637~response to blue light	2.00E-05
GO:0010218~response to far red light	5.60E-05
GO:0010114~response to red light	1.50E-04
GO:0016054~organic acid catabolic process	7.00E-04
GO:0046395~carboxylic acid catabolic process	7.00E-04
GO:0009738~abscisic acid mediated signaling	7.40E-04
GO:0019253~reductive pentose-phosphate cycle	1.30E-03

GO:0019748~secondary metabolic process	1.30E-03
GO:0018298~protein-chromophore linkage	1.40E-03
GO:0009644~response to high light intensity	1.90E-03
GO:0019685~photosynthesis, dark reaction	1.90E-03
GO:0009639~response to red or far red light	2.00E-03
GO:0009743~response to carbohydrate stimulus	2.90E-03
GO:0006833~water transport	5.90E-03
GO:0042044~fluid transport	5.90E-03
GO:0000302~response to reactive oxygen species	8.90E-03
GO:0007568~aging	9.00E-03
GO:0015977~carbon utilization by fixation of carbon dioxide	1.00E-02
GO:0006790~sulfur metabolic process	1.40E-02
GO:0019438~aromatic compound biosynthetic process	2.00E-02
GO:0009408~response to heat	2.10E-02
GO:0016137~glycoside metabolic process	2.90E-02
GO:0042538~hyperosmotic salinity response	2.90E-02
GO:0042787~protein ubiquitination during ubiquitin-dependent protein catabolic process	2.90E-02
GO:0010119~regulation of stomatal movement	3.20E-02
GO:0009787~regulation of abscisic acid mediated signaling	3.30E-02
GO:0031407~oxylipin metabolic process	3.30E-02
GO:0009063~cellular amino acid catabolic process	3.60E-02
GO:0009404~toxin metabolic process	4.80E-02
GO:0009407~toxin catabolic process	4.80E-02

Table S8: Significantly enriched GO terms (biological process category) terms associated with NaCl responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

GO ID~GO Term (Biological Process category)	P-value⁺
GO:0006979~response to oxidative stress	1.10E-36
GO:0006800~oxygen and reactive oxygen species metabolic process	1.10E-29
GO:0000302~response to reactive oxygen species	1.20E-27
GO:0055114~oxidation reduction	4.40E-27
GO:0034614~cellular response to reactive oxygen species	8.10E-27
GO:0034599~cellular response to oxidative stress	8.20E-27
GO:0033554~cellular response to stress	1.30E-18
GO:0010035~response to inorganic substance	3.30E-18
GO:0006801~superoxide metabolic process	4.80E-17
GO:0042542~response to hydrogen peroxide	1.90E-15
GO:0000303~response to superoxide	1.10E-14
GO:0000305~response to oxygen radical	1.10E-14
GO:0042744~hydrogen peroxide catabolic process	1.30E-13
GO:0070301~cellular response to hydrogen peroxide	1.30E-13
GO:0042743~hydrogen peroxide metabolic process	1.70E-13
GO:0019430~removal of superoxide radicals	1.10E-12
GO:0009628~response to abiotic stimulus	1.60E-03
GO:0006995~cellular response to nitrogen starvation	1.90E-03
GO:0009617~response to bacterium	3.80E-03
GO:0009970~cellular response to sulfate starvation	3.80E-03
GO:0010038~response to metal ion	3.80E-03
GO:0043562~cellular response to nitrogen levels	4.30E-03
GO:0046688~response to copper ion	7.90E-03
GO:0042742~defense response to bacterium	9.60E-03
GO:0010193~response to ozone	1.40E-02
GO:0009651~response to salt stress	1.70E-02
GO:0006970~response to osmotic stress	2.30E-02
GO:0016036~cellular response to phosphate starvation	2.70E-02
GO:0009753~response to jasmonic acid stimulus	4.70E-02

Table S9: Significantly enriched GO terms (biological process category) terms associated with OXIDATIVE-STRESS responsive genes in *Arabidopsis thaliana*.
⁺Bonferroni adjusted P-values.

GO ID~GO Term (Biological Process category)	P-value ⁺
GO:0010200~response to chitin	1.00E-09
GO:0010033~response to organic substance	4.90E-09
GO:0009743~response to carbohydrate stimulus	6.50E-08
GO:0009719~response to endogenous stimulus	1.00E-03
GO:0009611~response to wounding	8.20E-03
GO:0006952~defense response	4.60E-02

Table S10: Significantly enriched GO terms (biological process category) terms associated with UV-B responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted P-values.

GO ID~GO Term (Cellular Component category)	P-value ⁺
GO:0005886~plasma membrane	1.10E-18
GO:0005773~vacuole	1.70E-17
GO:0043233~organelle lumen	1.80E-04
GO:0070013~intracellular organelle lumen	1.80E-04
GO:0031974~membrane-enclosed lumen	1.90E-04
GO:0005759~mitochondrial matrix	8.10E-04
GO:0031980~mitochondrial lumen	8.10E-04
GO:0033176~proton-transporting V-type ATPase complex	1.40E-03
GO:0044429~mitochondrial part	1.90E-03
GO:0005829~cytosol	2.00E-03
GO:0005730~nucleolus	4.00E-03
GO:0031090~organelle membrane	6.00E-03
GO:0000502~proteasome complex	1.10E-02
GO:0031981~nuclear lumen	1.10E-02
GO:0022627~cytosolic small ribosomal subunit	1.40E-02
GO:0031967~organelle envelope	1.40E-02
GO:0031975~envelope	1.40E-02
GO:0016469~proton-transporting two-sector ATPase complex	1.50E-02
GO:0019866~organelle inner membrane	2.00E-02
GO:0044434~chloroplast part	2.20E-02
GO:0000267~cell fraction	2.50E-02
GO:0005783~endoplasmic reticulum	2.50E-02
GO:0044435~plastid part	3.40E-02
GO:0015935~small ribosomal subunit	3.50E-02
GO:0005618~cell wall	3.80E-02
GO:0022625~cytosolic large ribosomal subunit	4.10E-02
GO:0030312~external encapsulating structure	4.10E-02
GO:0033179~proton-transporting V-type ATPase, V0 domain	4.10E-02

Table S11: Significantly enriched GO terms (cellular component category) associated with ABA responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted P-values.

GO ID~GO Term (Cellular Component category)	P-value⁺
GO:0005886~plasma membrane	6.70E-28
GO:0005618~cell wall	3.30E-16
GO:0030312~external encapsulating structure	3.80E-16
GO:0005773~vacuole	2.20E-14
GO:0048046~apoplast	3.00E-11
GO:0044434~chloroplast part	7.80E-11
GO:0044435~plastid part	1.90E-10
GO:0005829~cytosol	5.00E-10
GO:0009526~plastid envelope	3.30E-08
GO:0009941~chloroplast envelope	1.10E-07
GO:0031967~organelle envelope	3.10E-07
GO:0031975~envelope	4.00E-07
GO:0022626~cytosolic ribosome	1.50E-06
GO:0043233~organelle lumen	2.20E-06
GO:0070013~intracellular organelle lumen	2.20E-06
GO:0031974~membrane-enclosed lumen	3.10E-06
GO:0009532~plastid stroma	3.50E-06
GO:0009570~chloroplast stroma	4.30E-06
GO:0022627~cytosolic small ribosomal subunit	6.00E-06
GO:0005730~nucleolus	2.60E-05
GO:0015935~small ribosomal subunit	6.90E-05
GO:0044445~cytosolic part	7.10E-05
GO:0031090~organelle membrane	1.10E-04
GO:0042651~thylakoid membrane	1.20E-04
GO:0005840~ribosome	1.60E-04
GO:0031984~organelle subcompartment	1.60E-04
GO:0031981~nuclear lumen	1.70E-04
GO:0009521~photosystem	1.80E-04
GO:0009535~chloroplast thylakoid membrane	2.10E-04
GO:0055035~plastid thylakoid membrane	2.10E-04
GO:0034357~photosynthetic membrane	2.20E-04
GO:0009534~chloroplast thylakoid	2.70E-04
GO:0031976~plastid thylakoid	2.70E-04
GO:0009505~plant-type cell wall	2.80E-04
GO:0044436~thylakoid part	3.90E-04
GO:0010287~plastoglobule	4.30E-04
GO:0009536~plastid	6.20E-04
GO:0009507~chloroplast	6.50E-04
GO:0009579~thylakoid	6.70E-04
GO:0022625~cytosolic large ribosomal subunit	7.50E-04
GO:0033279~ribosomal subunit	1.10E-03
GO:0030529~ribonucleoprotein complex	1.30E-03
GO:0005576~extracellular region	1.50E-03

GO:0043228~non-membrane-bounded organelle	1.50E-03
GO:0043232~intracellular non-membrane-bounded organelle	1.50E-03
GO:0044459~plasma membrane part	1.50E-03
GO:0015934~large ribosomal subunit	1.70E-03
GO:0031226~intrinsic to plasma membrane	1.80E-03
GO:0009522~photosystem I	3.50E-03
GO:0005783~endoplasmic reticulum	1.20E-02
GO:0046658~anchored to plasma membrane	1.20E-02
GO:0016021~integral to membrane	1.70E-02
GO:0000325~plant-type vacuole	2.00E-02
GO:0009523~photosystem II	2.80E-02
GO:0031224~intrinsic to membrane	3.10E-02
GO:0008287~protein serine/threonine phosphatase complex	3.30E-02
GO:0010319~stromule	3.30E-02
GO:0005774~vacuolar membrane	4.30E-02

Table S12: Significantly enriched GO terms (cellular component category) associated with COLD responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

GO ID~GO Term (Cellular Component category)	P-value ⁺
GO:0031975~envelope	7.50E-03
GO:0031967~organelle envelope	1.40E-02

Table S13: Significantly enriched GO terms (cellular component category) associated with COLD-DROUGHT-SALT responsive genes in *Arabidopsis thaliana*.

⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Cellular Component category)	P-value ⁺
GO:0005829~cytosol	3.10E-05
GO:0005886~plasma membrane	5.60E-05
GO:0030312~external encapsulating structure	1.30E-03
GO:0005618~cell wall	1.60E-03
GO:0033176~proton-transporting V-type ATPase complex	3.10E-03
GO:0044445~cytosolic part	6.90E-03
GO:0033179~proton-transporting V-type ATPase, V0 domain	1.90E-02
GO:0022627~cytosolic small ribosomal subunit	3.30E-02
GO:0016469~proton-transporting two-sector ATPase complex	3.70E-02
GO:0015935~small ribosomal subunit	3.80E-02
GO:0022626~cytosolic ribosome	4.00E-02
GO:0033279~ribosomal subunit	4.00E-02
GO:0043228~non-membrane-bounded organelle	4.10E-02
GO:0043232~intracellular non-membrane-bounded organelle	4.10E-02

Table S14: Significantly enriched GO terms (cellular component category) associated with DEHYDRATION responsive genes in *Arabidopsis thaliana*.

⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Cellular Component category)	P-value⁺
GO:0044435~plastid part	3.90E-18
GO:0044434~chloroplast part	9.60E-18
GO:0009526~plastid envelope	2.70E-15
GO:0009570~chloroplast stroma	6.20E-14
GO:0048046~apoplast	8.90E-14
GO:0009532~plastid stroma	8.60E-14
GO:0031967~organelle envelope	2.00E-13
GO:0009941~chloroplast envelope	2.30E-13
GO:0031975~envelope	2.30E-13
GO:0009579~thylakoid	1.10E-12
GO:0009535~chloroplast thylakoid membrane	1.60E-12
GO:0055035~plastid thylakoid membrane	1.60E-12
GO:0044436~thylakoid part	3.50E-12
GO:0031976~plastid thylakoid	6.70E-12
GO:0009534~chloroplast thylakoid	6.70E-12
GO:0042651~thylakoid membrane	6.80E-12
GO:0031984~organelle subcompartment	7.10E-12
GO:0010319~stromule	2.00E-11
GO:0034357~photosynthetic membrane	7.20E-11
GO:0009536~plastid	2.80E-09
GO:0009507~chloroplast	3.20E-09
GO:0031090~organelle membrane	1.70E-08
GO:0005773~vacuole	5.00E-08
GO:0005886~plasma membrane	8.00E-08
GO:0005618~cell wall	1.10E-06
GO:0030312~external encapsulating structure	1.70E-06
GO:0009521~photosystem	9.30E-06
GO:0010287~plastoglobule	3.30E-04
GO:0009505~plant-type cell wall	6.20E-04
GO:0005576~extracellular region	1.10E-03
GO:0042579~microbody	1.20E-03
GO:0005777~peroxisome	1.20E-03
GO:0048492~ribulose biphosphate carboxylase complex	1.20E-03
GO:0009573~chloroplast ribulose biphosphate carboxylase complex	1.20E-03
GO:0031977~thylakoid lumen	2.10E-03
GO:0009523~photosystem II	2.80E-03
GO:0005783~endoplasmic reticulum	6.60E-03
GO:0009522~photosystem I	2.00E-02
GO:0030095~chloroplast photosystem II	1.90E-02
GO:0030093~chloroplast photosystem I	2.20E-02
GO:0009543~chloroplast thylakoid lumen	3.10E-02
GO:0031978~plastid thylakoid lumen	3.10E-02

GO:0044437~vacuolar part	4.80E-02
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Table S15: Significantly enriched GO terms (cellular component category) associated with DROUGHT responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

GO ID~GO Term (Cellular Component category)	P-value ⁺
GO:0016021~integral to membrane	1.60E-02
GO:0031224~intrinsic to membrane	1.00E-02

Table S16: Significantly enriched GO terms (cellular component category) associated with IRON responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Cellular Component category)	P-value⁺
GO:0005773~vacuole	2.20E-14
GO:0022626~cytosolic ribosome	1.80E-10
GO:0044434~chloroplast part	2.10E-10
GO:0044435~plastid part	2.40E-10
GO:0009507~chloroplast	1.10E-09
GO:0009536~plastid	1.20E-09
GO:0044445~cytosolic part	1.30E-09
GO:0005840~ribosome	2.30E-09
GO:0005829~cytosol	2.40E-09
GO:0022625~cytosolic large ribosomal subunit	3.30E-09
GO:0022627~cytosolic small ribosomal subunit	3.60E-09
GO:0033279~ribosomal subunit	6.10E-09
GO:0015935~small ribosomal subunit	8.10E-09
GO:0031967~organelle envelope	8.00E-08
GO:0031975~envelope	9.90E-08
GO:0015934~large ribosomal subunit	1.60E-07
GO:0043233~organelle lumen	1.80E-07
GO:0070013~intracellular organelle lumen	1.80E-07
GO:0031974~membrane-enclosed lumen	2.50E-07
GO:0031090~organelle membrane	2.90E-07
GO:0005886~plasma membrane	3.00E-07
GO:0009526~plastid envelope	1.80E-06
GO:0030529~ribonucleoprotein complex	1.80E-06
GO:0005730~nucleolus	2.80E-06
GO:0043228~non-membrane-bounded organelle	4.50E-06
GO:0043232~intracellular non-membrane-bounded organelle	4.50E-06
GO:0009941~chloroplast envelope	1.30E-05
GO:0031981~nuclear lumen	1.40E-04
GO:0009570~chloroplast stroma	2.50E-04
GO:0005783~endoplasmic reticulum	2.80E-04
GO:0042651~thylakoid membrane	4.00E-04
GO:0009535~chloroplast thylakoid membrane	5.10E-04
GO:0055035~plastid thylakoid membrane	5.10E-04
GO:0009532~plastid stroma	5.40E-04
GO:0048046~apoplast	6.80E-04
GO:0019866~organelle inner membrane	7.00E-04
GO:0034357~photosynthetic membrane	1.10E-03
GO:0044429~mitochondrial part	1.20E-03
GO:0005788~endoplasmic reticulum lumen	2.90E-03
GO:0044436~thylakoid part	2.90E-03
GO:0005618~cell wall	4.90E-03
GO:0005739~mitochondrion	4.90E-03
GO:0009534~chloroplast thylakoid	4.90E-03

GO:0031976~plastid thylakoid	4.90E-03
GO:0031984~organelle subcompartment	4.90E-03
GO:0030312~external encapsulating structure	6.00E-03
GO:0033178~proton-transporting two-sector ATPase complex, catalytic domain	6.50E-03
GO:0005740~mitochondrial envelope	1.30E-02
GO:0005774~vacuolar membrane	1.30E-02
GO:0009528~plastid inner membrane	1.40E-02
GO:0044437~vacuolar part	1.60E-02
GO:0009579~thylakoid	1.80E-02
GO:0009706~chloroplast inner membrane	2.00E-02
GO:0005777~peroxisome	3.10E-02
GO:0042579~microbody	3.10E-02
GO:0005743~mitochondrial inner membrane	4.60E-02

Table S17: Significantly enriched GO terms (cellular component category) associated with LIGHT responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

GO ID~GO Term (Cellular Component category)	P-value⁺
GO:0009579~thylakoid	1.20E-15
GO:0005773~vacuole	2.20E-15
GO:0042651~thylakoid membrane	7.40E-15
GO:0009535~chloroplast thylakoid membrane	9.90E-15
GO:0055035~plastid thylakoid membrane	9.90E-15
GO:0048046~apoplast	3.00E-14
GO:0031984~organelle subcompartment	3.40E-14
GO:0009534~chloroplast thylakoid	3.60E-14
GO:0031976~plastid thylakoid	3.60E-14
GO:0034357~photosynthetic membrane	4.40E-14
GO:0044436~thylakoid part	4.60E-14
GO:0005886~plasma membrane	1.10E-13
GO:0044434~chloroplast part	6.10E-13
GO:0044435~plastid part	1.50E-12
GO:0031090~organelle membrane	3.70E-12
GO:0010287~plastoglobule	1.20E-11
GO:0009521~photosystem	5.40E-11
GO:0009522~photosystem I	7.80E-11
GO:0031967~organelle envelope	3.80E-10
GO:0031975~envelope	5.20E-10
GO:0009526~plastid envelope	3.30E-09
GO:0009941~chloroplast envelope	5.20E-09
GO:0009570~chloroplast stroma	1.70E-06
GO:0030076~light-harvesting complex	2.30E-06
GO:0005777~peroxisome	3.80E-06
GO:0042579~microbody	3.80E-06
GO:0005618~cell wall	6.10E-06
GO:0009532~plastid stroma	6.20E-06
GO:0030312~external encapsulating structure	9.30E-06
GO:0010319~stromule	1.10E-05
GO:0009523~photosystem II	2.20E-05
GO:0009536~plastid	2.30E-05
GO:0043233~organelle lumen	2.40E-05
GO:0070013~intracellular organelle lumen	2.40E-05
GO:0009507~chloroplast	2.90E-05
GO:0031974~membrane-enclosed lumen	3.40E-05
GO:0009538~photosystem I reaction center	1.60E-04
GO:0009505~plant-type cell wall	6.40E-04
GO:0005730~nucleolus	1.60E-03
GO:0009573~chloroplast ribulose biphosphate carboxylase complex	2.60E-03
GO:0048492~ribulose biphosphate carboxylase complex	2.60E-03
GO:0005576~extracellular region	4.00E-03

GO:0031977~thylakoid lumen	1.50E-02
GO:0005635~nuclear envelope	1.80E-02
GO:0031981~nuclear lumen	2.90E-02
GO:0022627~cytosolic small ribosomal subunit	3.20E-02

Table S18: Significantly enriched GO terms (cellular component category) associated with NaCl responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

GO ID~GO Term (Cellular Component category)	P-value ⁺
GO:0005777~peroxisome	3.60E-04
GO:0042579~microbody	3.60E-04
GO:0044435~plastid part	6.30E-04
GO:0044434~chloroplast part	2.00E-03
GO:0009536~plastid	4.50E-03
GO:0009532~plastid stroma	8.20E-03
GO:0009507~chloroplast	8.30E-03
GO:0009570~chloroplast stroma	8.70E-03
GO:0005739~mitochondrion	1.20E-02
GO:0009526~plastid envelope	4.80E-02

Table S19: Significantly enriched GO terms (cellular component category) associated with OXIDATIVE-STRESS responsive genes in *Arabidopsis thaliana*.
⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Molecular Function category)	P-value ⁺
GO:0010436~carotenoid dioxygenase activity	6.30E-06
GO:0045549~9-cis-epoxycarotenoid dioxygenase activity	6.30E-06
GO:0016702~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	1.50E-02
GO:0016836~hydro-lyase activity	2.10E-02
GO:0016701~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	2.40E-02
GO:0048037~cofactor binding	2.70E-02
GO:0004031~aldehyde oxidase activity	2.80E-02
GO:0050662~coenzyme binding	2.80E-02
GO:0016887~ATPase activity	3.00E-02
GO:0030151~molybdenum ion binding	3.10E-02

Table S20: Significantly enriched GO terms (molecular function category) associated with ABA responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Molecular Function category)	P-value ⁺
GO:0005372~water transporter activity	1.70E-05
GO:0015250~water channel activity	1.70E-05
GO:0016762~xyloglucan:xyloglucosyl transferase activity	1.10E-03
GO:0005509~calcium ion binding	1.50E-03
GO:0016563~transcription activator activity	3.50E-02
GO:0015267~channel activity	3.90E-02
GO:0022803~passive transmembrane transporter activity	3.90E-02
GO:0022838~substrate specific channel activity	4.20E-02

Table S21: Significantly enriched GO terms (molecular function category) associated with COLD responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Molecular Function category)	P-value ⁺
GO:0016563~transcription activator activity	2.70E-03

Table S22: Significantly enriched GO terms (molecular function category) associated with COLD-DROUGHT-SALT responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Molecular Function category)	P-value ⁺
GO:0016563~transcription activator activity	3.70E-05
GO:0016620~oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	2.20E-04
GO:0016165~lipoxygenase activity	2.10E-02
GO:0004364~glutathione transferase activity	4.20E-02
GO:0043295~glutathione binding	4.40E-02
GO:0048037~cofactor binding	4.50E-02
GO:0005507~copper ion binding	4.80E-02

Table S23: Significantly enriched GO terms (molecular function category) associated with DROUGHT responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Molecular Function category)	<i>P</i> -value ⁺
GO:0003735~structural constituent of ribosome	1.80E-06
GO:0005198~structural molecule activity	1.10E-04

Table S24: Significantly enriched GO terms (molecular function category) associated with LIGHT responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Molecular Function category)	P-value ⁺
GO:0016168~chlorophyll binding	4.20E-05
GO:0005372~water transporter activity	3.60E-04
GO:0015250~water channel activity	3.60E-04
GO:0009815~1-aminocyclopropane-1-carboxylate oxidase activity	3.90E-02
GO:0048037~cofactor binding	3.90E-02

Table S25: Significantly enriched GO terms (molecular function category) associated with NaCl responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

GO ID~GO Term (Molecular Function category)	P-value ⁺
GO:0016209~antioxidant activity	2.30E-47
GO:0004601~peroxidase activity	2.10E-24
GO:0016684~oxidoreductase activity, acting on peroxide as acceptor	2.10E-24
GO:0004784~superoxide dismutase activity	2.60E-19
GO:0016721~oxidoreductase activity, acting on superoxide radicals as acceptor	2.60E-19
GO:0016688~L-ascorbate peroxidase activity	3.60E-16
GO:0004602~glutathione peroxidase activity	3.00E-13
GO:0005507~copper ion binding	6.60E-09
GO:0046872~metal ion binding	1.10E-08
GO:0020037~heme binding	2.00E-08
GO:0043167~ion binding	2.70E-08
GO:0046914~transition metal ion binding	2.70E-08
GO:0043169~cation binding	2.80E-08
GO:0046906~tetrapyrrole binding	2.90E-08
GO:0005506~iron ion binding	1.30E-07
GO:0030955~potassium ion binding	2.80E-06
GO:0031420~alkali metal ion binding	7.40E-06
GO:0004096~catalase activity	1.00E-04
GO:0005509~calcium ion binding	1.90E-02
GO:0047066~phospholipid-hydroperoxide glutathione peroxidase activity	2.30E-02
GO:0008447~L-ascorbate oxidase activity	3.30E-02
GO:0016672~oxidoreductase activity, acting on sulfur group of donors, quinone or similar compound as acceptor	4.20E-02
GO:0045174~glutathione dehydrogenase (ascorbate) activity	4.20E-02

Table S26: Significantly enriched GO terms (molecular function category) associated with OXIDATIVE-STRESS responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

Pfam Accession: Pfam ID	Pfam domain description	<i>P</i>-value⁺
PF00240:Ubiquitin	Ubiquitin family	2.9E-13
PF01020:Ribosomal_L40e	Ribosomal L40e family	2.9E-13
PF01599:Ribosomal_S27	Ribosomal protein S27a	2.9E-13
PF03055:RPE65	Carotenoid oxygenase	3.3E-09
PF00941:FAD_binding_5	FAD binding domain in molybdopterin dehydrogenase	2.4E-03
PF01315:Ald_Xan_dh_C	Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain	2.4E-03
PF01799:Fer2_2	[2Fe-2S] binding domain	2.4E-03
PF03450:CO_deh_flav_C	CO dehydrogenase flavoprotein C-terminal domain	2.4E-03
PF02738:Ald_Xan_dh_C2	Molybdopterin-binding domain of aldehyde dehydrogenase	2.5E-02
PF00111:Fer2	Ferredoxin	2.9E-02
PF01370:Epimerase	NAD dependent epimerase/dehydratase family	3.1E-02

Table S27: Significantly enriched protein domains associated with ABA responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

Pfam Accession: Pfam ID	Pfam domain description	P-value*
PF00240:Ubiquitin	Ubiquitin family	3.6E-11
PF01020:Ribosomal_L40e	Ribosomal L40e family	3.6E-11
PF01599:Ribosomal_S27	Ribosomal protein S27a	3.6E-11
PF00847:AP2	AP2 domain	1.8E-06
PF00230:MIP	Major intrinsic proteins	2.3E-06
PF00643:zf-B_box	B-box zinc finger	6.5E-05
PF00722:Glyco_hydro_16	Glycosyl hydrolases family 16	3.2E-04
PF06955:XET_C	Xyloglucan endo-transglycosylase (XET) C-terminus	3.2E-04
PF00141:peroxidase	Peroxidase	8.4E-04
PF03822:NAF	NAF domain	1.7E-02

Table S28: Significantly enriched protein domains associated with COLD responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

Pfam Accession: Pfam ID	Pfam domain description	<i>P</i>-value⁺
PF00257:Dehydrin	Dehydrin	9.8E-08
PF00847:AP2 domain	AP2 domain	3.6E-05
PF03822:NAF	NAF domain	1.3E-02

Table S29: Significantly enriched protein domains associated with COLD-DROUGHT-SALT responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

Pfam Accession: Pfam ID	Pfam domain description	<i>P</i>-value⁺
PF00137:ATP-synt_C	ATP synthase subunit C	1.1E-02
PF00333:Ribosomal_S5	Ribosomal protein S5, N-terminal domain	4.8E-02
PF03719:Ribosomal_S5_C	Ribosomal protein S5, C-terminal domain	4.8E-02

Table S30: Significantly enriched protein domains associated with DEHYDRATION responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

Pfam Accession: Pfam ID	Pfam domain description	<i>P</i>-value*
PF00257:Dehydrin	Dehydrin	9.8E-03
PF03822:NAF	NAF domain	3.9E-02
PF00847:AP2	AP2 domain	4.2E-02
PF02798:GST_N	Glutathione S-transferase, N-terminal domain	4.8E-02

Table S31: Significantly enriched protein domains associated with DROUGHT responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

Pfam Accession: Pfam ID	Pfam domain description	<i>P</i>-value⁺
PF01020:Ribosomal_L40e	Ribosomal L40e family	9.6E-14
PF01599:Ribosomal_S27	Ribosomal protein S27a	9.6E-14
PF00240:ubiquitin	Ubiquitin family	1.8E-05
PF03143:GTP_EFTU_D3	GTP-binding elongation factor family, EF-Tu/EF-1A subfamily	1.6E-02

Table S32: Significantly enriched protein domains associated with LIGHT responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

Pfam Accession: Pfam ID	Pfam domain description	<i>P</i>-value⁺
PF00240:ubiquitin	Ubiquitin family	2.6E-11
PF01020:Ribosomal_L40e	Ribosomal L40e family	2.6E-11
PF01599:Ribosomal_S27	Ribosomal protein S27a	2.6E-11
PF00504:Chloroa_b-bind	Chlorophyll A-B binding protein	2.9E-08
PF00249:Myb_DNA-binding	Myb-like DNA-binding domain	1.7E-06
PF00230:MIP	Major intrinsic proteins	4.7E-04
PF00257:Dehydrin	Dehydrin	6.3E-03
PF00101:RuBisCO_small	Ribulose biphosphate carboxylase, small chain	4.8E-02

Table S33: Significantly enriched protein domains associated with NaCl responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

Pfam Accession: Pfam ID	Pfam domain description	<i>P</i>-value⁺
PF00255:GSHPx	Glutathione peroxidase	3.7E-14
PF00081:Sod_Fe_N	Iron/manganese superoxide dismutases, alpha-hairpin domain	1.2E-09
PF02777:Sod_Fe_C	Iron/manganese superoxide dismutases, C-terminal domain	1.2E-09
PF00141:peroxidase	Peroxidase	2.4E-09
PF00080:Sod_Cu	Copper/zinc superoxide dismutase (SODC)	2.8E-07
PF00199:Catalase	Catalase	9.6E-05
PF06628:Catalase-rel	Catalase-related immune-responsive	9.6E-05
PF00394:Cu-oxidase	Multicopper oxidase	4.1E-04
PF07731:Cu-oxidase_2	Multicopper oxidase	4.1E-04
PF07732:Cu-oxidase_3	Multicopper oxidase	4.4E-04

Table S34: Significantly enriched protein domains associated with OXIDATIVE-STRESS responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

Pfam Accession: Pfam ID	Pfam domain description	<i>P</i>-value*
PF05678:VQ	VQ motif	4.5E-2

Table S35: Significantly enriched protein domains associated with WOUNDING responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value⁺
PO:0020030	cotyledon	8.9E-31
PO:0025281	pollen	1.3E-27
PO:0025280	microgametophyte	1.3E-27
PO:0025277	pollen sac	1.4E-27
PO:0025202	microsporangium	2.9E-27
PO:0025094	sporangium	3.6E-27
PO:0009007	portion of plant tissue	6.9E-26
PO:0009002	plant cell	1.5E-25
PO:0020038	petiole	2.0E-22
PO:0025066	stalk	3.9E-22
PO:0025139	phyllome apex	9.3E-22
PO:0020137	leaf apex	9.3E-22
PO:0008019	leaf lamina base	2.1E-21
PO:0000230	inflorescence meristem	2.3E-21
PO:0020039	leaf lamina	2.5E-21
PO:0025060	lamina	2.5E-21
PO:0000293	guard cell	8.3E-21
PO:0000013	cauline leaf	9.3E-21
PO:0009013	meristem	1.0E-20
PO:0002000	stomatal complex	3.4E-20
PO:0025165	shoot epidermal cell	6.1E-20
PO:0000005	cultured plant cell	1.1E-18
PO:0000004	in vitro plant structure	1.2E-18
PO:0006035	shoot epidermis	1.7E-18
PO:0009061	androecium	9.2E-18
PO:0009029	stamen	9.2E-18
PO:0009025	vascular leaf	2.2E-17
PO:0004013	epidermal cell	3.2E-17
PO:0025034	leaf	4.7E-17
PO:0009027	megasporophyll	6.6E-16
PO:0009030	carpel	6.6E-16
PO:0025195	pollen tube cell	7.1E-16
PO:0005679	epidermis	1.3E-15
PO:0005005	shoot internode	1.8E-15
PO:0020142	stem internode	1.8E-15
PO:0020100	hypocotyl	1.8E-15
PO:0009062	gynoecium	8.1E-14
PO:0009001	fruit	1.5E-13
PO:0009028	microsporophyll	2.3E-13
PO:0009081	inflorescence branch	1.4E-11
PO:0009052	pedicel	1.4E-11
PO:0020122	inflorescence axis	1.8E-11
PO:0009010	seed	2.4E-11

PO:0000037	shoot apex	2.9E-11
PO:0025001	cardinal organ part	3.1E-10
PO:0009026	sporophyll	1.4E-09
PO:0005052	plant callus	1.7E-09
PO:0009009	plant embryo	2.2E-09
PO:0009005	root	3.4E-09
PO:0025025	root system	6.0E-09
PO:0009047	stem	9.4E-09
PO:0009049	inflorescence	1.3E-08
PO:0009059	corolla	1.5E-08
PO:0009032	petal	1.5E-08
PO:0009060	calyx	1.1E-07
PO:0009031	sepal	1.1E-07
PO:0000084	plant sperm cell	7.3E-07
PO:0025006	gamete	3.9E-06
PO:0009058	perianth	1.0E-05
PO:0025022	collective leaf structure	1.1E-05
PO:0000003	whole plant	1.1E-05
PO:0006001	phyllome	2.0E-05
PO:0000025	root tip	1.3E-04
PO:0025029	shoot axis	9.2E-04
PO:0025023	collective phyllome structure	2.4E-02

Table S36: Significantly enriched PO (anatomy / plant anatomical entity) terms associated with ABA responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value⁺
PO:0020030	cotyledon	4.8E-37
PO:0009025	vascular leaf	3.6E-27
PO:0025034	leaf	2.0E-26
PO:0000005	cultured plant cell	1.5E-24
PO:0000004	in vitro plant structure	1.8E-24
PO:0002000	stomatal complex	2.5E-24
PO:0000293	guard cell	2.9E-24
PO:0025165	shoot epidermal cell	5.6E-24
PO:0025139	phyllome apex	3.4E-23
PO:0020137	leaf apex	3.4E-23
PO:0006035	shoot epidermis	4.7E-22
PO:0004013	epidermal cell	5.8E-21
PO:0025066	stalk	8.2E-21
PO:0020038	petiole	8.8E-21
PO:0009007	portion of plant tissue	9.8E-21
PO:0005679	epidermis	4.5E-20
PO:0000230	inflorescence meristem	5.5E-20
PO:0009013	meristem	1.1E-19
PO:0000013	cauline leaf	8.1E-18
PO:0009061	androecium	2.5E-17
PO:0009029	stamen	2.5E-17
PO:0006339	juvenile vascular leaf	6.4E-17
PO:0008019	leaf lamina base	7.6E-17
PO:0020039	leaf lamina	9.3E-17
PO:0025060	lamina	9.3E-17
PO:0005005	shoot internode	1.2E-16
PO:0020142	stem internode	1.2E-16
PO:0020100	hypocotyl	1.2E-16
PO:0025281	pollen	1.9E-16
PO:0025280	microgametophyte	1.9E-16
PO:0025277	pollen sac	2.0E-16
PO:0025202	microsporangium	2.4E-16
PO:0025094	sporangium	2.9E-16
PO:0009028	microsporophyll	5.6E-13
PO:0009027	megasporophyll	6.4E-13
PO:0009030	carpel	6.4E-13
PO:0009047	stem	2.3E-11
PO:0025001	cardinal organ part	9.9E-11
PO:0009062	gynoecium	2.2E-10
PO:0009026	sporophyll	2.1E-09
PO:0009049	inflorescence	5.0E-09
PO:0000037	shoot apex	7.1E-09
PO:0009005	root	5.3E-08

PO:0025025	root system	8.8E-08
PO:0009059	corolla	1.8E-07
PO:0009032	petal	1.8E-07
PO:0006001	phyllome	2.0E-07
PO:0009081	inflorescence branch	3.4E-07
PO:0009052	pedicel	3.4E-07
PO:0020122	inflorescence axis	4.5E-07
PO:0009060	calyx	4.9E-07
PO:0009031	sepal	4.9E-07
PO:0009001	fruit	5.3E-07
PO:0005052	plant callus	1.6E-06
PO:0009010	seed	1.9E-05
PO:0000025	root tip	6.4E-05
PO:0025029	shoot axis	6.9E-05
PO:0009058	perianth	1.1E-04
PO:0025022	collective leaf structure	2.3E-04
PO:0009002	plant cell	2.8E-04
PO:0009009	plant embryo	5.8E-04
PO:0000282	trichome	1.2E-03
PO:0025004	plant axis	1.5E-03
PO:0005020	vascular bundle	3.2E-03
PO:0005421	parenchyma	4.9E-03
PO:0025195	pollen tube cell	8.9E-03
PO:0005426	chlorenchyma	1.5E-02
PO:0006070	mesophyll	1.5E-02
PO:0000034	vascular system	4.6E-02
PO:0000003	whole plant	4.7E-02

Table S37: Significantly enriched PO (anatomy / plant anatomical entity) terms associated with COLD responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values

PO ID	PO Term	P-value ⁺
PO:0000293	guard cell	1.5E-02
PO:0002000	stomatal complex	1.8E-02
PO:0025165	shoot epidermal cell	1.9E-02
PO:0006035	shoot epidermis	3.2E-02
PO:0009061	androecium	3.5E-02
PO:0009029	stamen	3.5E-02
PO:0005679	epidermis	4.9E-02

Table S38: Significantly enriched PO (anatomy / plant anatomical entity) terms associated with COLD-DROUGHT-SALT responsive genes in *Arabidopsis thaliana*.

⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0000005	cultured plant cell	1.6E-07
PO:0000004	in vitro plant structure	1.7E-07
PO:0025281	pollen	8.7E-06
PO:0025280	microgametophyte	8.7E-06
PO:0025277	pollen sac	8.8E-06
PO:0025202	microsporangium	9.9E-06
PO:0025094	sporangium	1.0E-05
PO:0008019	leaf lamina base	1.8E-04
PO:0020039	leaf lamina	1.9E-04
PO:0025060	lamina	1.9E-04
PO:0020030	cotyledon	3.4E-04
PO:0025139	phyllome apex	1.4E-03
PO:0020137	leaf apex	1.4E-03
PO:0020038	petiole	2.3E-03
PO:0000013	cauline leaf	2.3E-03
PO:0025066	stalk	2.9E-03
PO:0009002	plant cell	4.8E-03
PO:0009027	megasporophyll	1.2E-02
PO:0009030	carpel	1.2E-02
PO:0006075	primary phloem	1.3E-02
PO:0000293	guard cell	1.4E-02
PO:0009062	gynoecium	1.5E-02
PO:0009025	vascular leaf	1.7E-02
PO:0002000	stomatal complex	1.7E-02
PO:0025165	shoot epidermal cell	1.8E-02
PO:0025034	leaf	2.8E-02
PO:0006035	shoot epidermis	3.9E-02
PO:0000230	inflorescence meristem	4.2E-02
PO:0009061	androecium	4.6E-02
PO:0009029	stamen	4.6E-02

Table S39: Significantly enriched PO (anatomy / plant anatomical entity) terms associated with DEHYDRATION responsive genes in *Arabidopsis thaliana*.

⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value⁺
PO:0020030	cotyledon	4.5E-37
PO:0009061	androecium	2.3E-33
PO:0009029	stamen	2.3E-33
PO:0025202	microsporangium	6.5E-33
PO:0025281	pollen	6.8E-33
PO:0025280	microgametophyte	6.8E-33
PO:0025277	pollen sac	7.3E-33
PO:0025094	sporangium	8.3E-33
PO:0009028	microsporophyll	4.8E-26
PO:0009025	vascular leaf	2.4E-24
PO:0009027	megasporophyll	2.0E-23
PO:0009030	carpel	2.0E-23
PO:0025034	leaf	2.5E-23
PO:0009007	portion of plant tissue	4.5E-22
PO:0006339	juvenile vascular leaf	8.1E-22
PO:0009047	stem	1.2E-21
PO:0025139	phyllome apex	2.2E-21
PO:0020137	leaf apex	2.2E-21
PO:0009062	gynoecium	1.4E-20
PO:0009026	sporophyll	1.8E-19
PO:0000013	cauline leaf	2.8E-19
PO:0000230	inflorescence meristem	8.6E-19
PO:0025066	stalk	1.9E-18
PO:0020038	petiole	3.4E-18
PO:0000293	guard cell	1.9E-17
PO:0009013	meristem	2.1E-17
PO:0008019	leaf lamina base	2.2E-17
PO:0020039	leaf lamina	2.7E-17
PO:0025060	lamina	2.7E-17
PO:0002000	stomatal complex	7.4E-17
PO:0025165	shoot epidermal cell	1.3E-16
PO:0005005	shoot internode	2.7E-15
PO:0020142	stem internode	2.7E-15
PO:0020100	hypocotyl	2.7E-15
PO:0006035	shoot epidermis	3.9E-15
PO:0004013	epidermal cell	4.4E-14
PO:0009060	calyx	4.5E-14
PO:0009031	sepal	4.5E-14
PO:0025195	pollen tube cell	2.2E-13
PO:0025001	cardinal organ part	3.6E-13
PO:0009059	corolla	4.1E-13
PO:0009032	petal	4.1E-13
PO:0006001	phyllome	3.4E-12

PO:0025029	shoot axis	8.5E-12
PO:0009058	perianth	9.2E-12
PO:0005679	epidermis	2.9E-11
PO:0009081	inflorescence branch	3.2E-11
PO:0009052	pedicel	3.2E-11
PO:0020122	inflorescence axis	4.3E-11
PO:0025022	collective leaf structure	5.7E-11
PO:0009049	inflorescence	8.4E-11
PO:0025023	collective phyllome structure	4.3E-10
PO:0009002	plant cell	4.5E-10
PO:0025004	plant axis	1.4E-09
PO:0009009	plant embryo	7.1E-09
PO:0000003	whole plant	2.7E-08
PO:0009005	root	5.6E-08
PO:0025025	root system	1.8E-07
PO:0000037	shoot apex	1.3E-06
PO:0000034	vascular system	5.2E-06
PO:0000005	cultured plant cell	3.6E-05
PO:0000004	in vitro plant structure	3.9E-05
PO:0009046	flower	7.9E-05
PO:0009015	portion of vascular tissue	1.1E-04
PO:0025082	reproductive shoot system	1.9E-04
PO:0009001	fruit	3.4E-04
PO:0009006	shoot system	5.5E-04
PO:0009010	seed	6.2E-04
PO:0005052	plant callus	1.6E-03
PO:0009008	plant organ	2.5E-03
PO:0000016	lateral root primordium	5.0E-02

Table S40: Significantly enriched PO (anatomy / plant anatomical entity) terms associated with DROUGHT responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0025025	root system	3.00E-04
PO:0005005	shoot internode	5.20E-04
PO:0020142	stem internode	5.20E-04
PO:0020100	hypocotyl	5.20E-04
PO:0009005	root	5.40E-04
PO:0009047	stem	4.30E-03
PO:0005052	plant callus	3.50E-02

Table S41: Significantly enriched PO (anatomy / plant anatomical entity) terms associated with IRON responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value⁺
PO:0020030	cotyledon	8.2E-24
PO:0025139	phyllome apex	2.9E-18
PO:0020137	leaf apex	2.9E-18
PO:0025281	pollen	7.0E-18
PO:0025280	microgametophyte	7.0E-18
PO:0025277	pollen sac	7.3E-18
PO:0025202	microsporangium	1.3E-17
PO:0025094	sporangium	1.5E-17
PO:0020038	petiole	4.1E-17
PO:0025066	stalk	1.5E-16
PO:0008019	leaf lamina base	4.3E-14
PO:0020039	leaf lamina	4.9E-14
PO:0025060	lamina	4.9E-14
PO:0009007	portion of plant tissue	1.4E-13
PO:0009025	vascular leaf	1.7E-13
PO:0025034	leaf	3.2E-13
PO:0000013	cauline leaf	1.9E-12
PO:0009013	meristem	1.9E-12
PO:0000230	inflorescence meristem	2.3E-12
PO:0000293	guard cell	5.5E-12
PO:0025165	shoot epidermal cell	9.5E-12
PO:0009061	androecium	1.5E-11
PO:0009029	stamen	1.5E-11
PO:0002000	stomatal complex	1.5E-11
PO:0006035	shoot epidermis	9.2E-11
PO:0000005	cultured plant cell	1.1E-09
PO:0000004	in vitro plant structure	1.2E-09
PO:0004013	epidermal cell	2.6E-09
PO:0009028	microsporophyll	7.8E-09
PO:0005005	shoot internode	3.4E-08
PO:0020142	stem internode	3.4E-08
PO:0020100	hypocotyl	3.4E-08
PO:0009027	megasporophyll	4.8E-08
PO:0009030	carpel	4.8E-08
PO:0005679	epidermis	1.8E-07
PO:0000037	shoot apex	4.6E-07
PO:0009062	gynoecium	9.1E-07
PO:0005052	plant callus	2.6E-06
PO:0009081	inflorescence branch	3.6E-06
PO:0009052	pedicel	3.6E-06
PO:0020122	inflorescence axis	4.4E-06
PO:0009026	sporophyll	1.5E-05
PO:0009001	fruit	1.6E-05

PO:0009002	plant cell	3.4E-05
PO:0009047	stem	4.0E-05
PO:0009049	inflorescence	5.5E-05
PO:0025001	cardinal organ part	2.0E-04
PO:0009010	seed	2.7E-04
PO:0009005	root	6.6E-04
PO:0009059	corolla	8.2E-04
PO:0009032	petal	8.2E-04
PO:0025025	root system	9.8E-04
PO:0006001	phyllome	1.5E-03
PO:0009060	calyx	1.0E-02
PO:0009031	sepal	1.0E-02
PO:0009009	plant embryo	1.5E-02
PO:0025022	collective leaf structure	1.8E-02

Table S42: Significantly enriched PO (anatomy / plant anatomical entity) terms associated with LIGHT responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value⁺
PO:0020030	cotyledon	8.2E-24
PO:0025139	phyllome apex	2.9E-18
PO:0020137	leaf apex	2.9E-18
PO:0025281	pollen	7.0E-18
PO:0025280	microgametophyte	7.0E-18
PO:0025277	pollen sac	7.3E-18
PO:0025202	microsporangium	1.3E-17
PO:0025094	sporangium	1.5E-17
PO:0020038	petiole	4.1E-17
PO:0025066	stalk	1.5E-16
PO:0008019	leaf lamina base	4.3E-14
PO:0020039	leaf lamina	4.9E-14
PO:0025060	lamina	4.9E-14
PO:0009007	portion of plant tissue	1.4E-13
PO:0009025	vascular leaf	1.7E-13
PO:0025034	leaf	3.2E-13
PO:0000013	cauline leaf	1.9E-12
PO:0009013	meristem	1.9E-12
PO:0000230	inflorescence meristem	2.3E-12
PO:0000293	guard cell	5.5E-12
PO:0025165	shoot epidermal cell	9.5E-12
PO:0009061	androecium	1.5E-11
PO:0009029	stamen	1.5E-11
PO:0002000	stomatal complex	1.5E-11
PO:0006035	shoot epidermis	9.2E-11
PO:0000005	cultured plant cell	1.1E-09
PO:0000004	in vitro plant structure	1.2E-09
PO:0004013	epidermal cell	2.6E-09
PO:0009028	microsporophyll	7.8E-09
PO:0005005	shoot internode	3.4E-08
PO:0020142	stem internode	3.4E-08
PO:0020100	hypocotyl	3.4E-08
PO:0009027	megasporophyll	4.8E-08
PO:0009030	carpel	4.8E-08
PO:0005679	epidermis	1.8E-07
PO:0000037	shoot apex	4.6E-07
PO:0009062	gynoecium	9.1E-07
PO:0005052	plant callus	2.6E-06
PO:0009081	inflorescence branch	3.6E-06
PO:0009052	pedicel	3.6E-06
PO:0020122	inflorescence axis	4.4E-06
PO:0009026	sporophyll	1.5E-05
PO:0009001	fruit	1.6E-05

PO:0009002	plant cell	3.4E-05
PO:0009047	stem	4.0E-05
PO:0009049	inflorescence	5.5E-05
PO:0025001	cardinal organ part	2.0E-04
PO:0009010	seed	2.7E-04
PO:0009005	root	6.6E-04
PO:0009059	corolla	8.2E-04
PO:0009032	petal	8.2E-04
PO:0025025	root system	9.8E-04
PO:0006001	phyllome	1.5E-03
PO:0009060	calyx	1.0E-02
PO:0009031	sepal	1.0E-02
PO:0009009	plant embryo	1.5E-02
PO:0025022	collective leaf structure	1.8E-02

Table S43: Significantly enriched PO (anatomy / plant anatomical entity) terms associated with NaCl responsive genes in *Arabidopsis thaliana*. *Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0000293	guard cell	9.0E-03
PO:0002000	stomatal complex	1.0E-02
PO:0025165	shoot epidermal cell	1.1E-02
PO:0006035	shoot epidermis	1.9E-02
PO:0020030	cotyledon	2.1E-02
PO:0008019	leaf lamina base	2.7E-02
PO:0020039	leaf lamina	2.7E-02
PO:0025060	lamina	2.7E-02
PO:0005020	vascular bundle	2.9E-02
PO:0009061	androecium	3.7E-02
PO:0009029	stamen	3.7E-02
PO:0004013	epidermal cell	4.2E-02

Table S44: Significantly enriched PO (anatomy / plant anatomical entity) terms associated with OXIDATIVE-STRESS responsive genes in *Arabidopsis thaliana*.

⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value⁺
PO:0020030	cotyledon	1.20E-05
PO:0009047	stem	8.10E-04
PO:0009061	androecium	1.70E-03
PO:0009029	stamen	1.70E-03
PO:0025004	plant axis	2.20E-03
PO:0025029	shoot axis	8.40E-03
PO:0009025	vascular leaf	2.30E-02
PO:0025034	leaf	4.10E-02
PO:0009028	microsporophyll	4.50E-02

Table S45: Significantly enriched PO (anatomy / plant anatomical entity) terms associated with UV-B responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0007095	LP.08 eight leaves visible	6.9E-17
PO:0007123	LP.06 six leaves visible	2.0E-15
PO:0007064	LP.12 twelve leaves visible	3.3E-14
PO:0007103	LP.10 ten leaves visible	7.8E-13
PO:0007098	LP.02 two leaves visible	2.8E-12
PO:0001017	M germinated pollen stage	5.2E-12
PO:0001054	4 leaf senescence stage	4.1E-11
PO:0001050	leaf development stages	4.8E-11
PO:0007131	seedling development stage	5.9E-11
PO:0001007	pollen developmental stages	9.3E-11
PO:0007605	androecium developmental stages	9.7E-11
PO:0007134	A vegetative growth	7.5E-10
PO:0007033	whole plant growth stage	9.2E-10
PO:0001016	L mature pollen stage	1.9E-09
PO:0007115	LP.04 four leaves visible	2.9E-08
PO:0007133	leaf production	3.6E-06
PO:0007112	1 main shoot growth	3.8E-06
PO:0001185	C globular stage	5.2E-04
PO:0001081	F mature embryo stage	1.8E-03
PO:0004507	D bilateral stage	5.5E-03

Table S46: Significantly enriched PO (temporal/plant structure development stage) terms associated with ABA responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0007131	seedling development stage	2.7E-30
PO:0007095	LP.08 eight leaves visible	3.4E-17
PO:0007123	LP.06 six leaves visible	4.2E-14
PO:0007064	LP.12 twelve leaves visible	6.1E-13
PO:0007134	A vegetative growth	1.9E-10
PO:0007103	LP.10 ten leaves visible	2.3E-10
PO:0007098	LP.02 two leaves visible	2.5E-10
PO:0007033	whole plant growth stage	2.5E-10
PO:0007115	LP.04 four leaves visible	1.5E-06
PO:0001054	4 leaf senescence stage	2.2E-05
PO:0001050	leaf development stages	2.6E-05
PO:0007133	leaf production	2.2E-04
PO:0007112	1 main shoot growth	2.3E-04

Table S47: Significantly enriched PO (temporal/plant structure development stage) terms associated with COLD responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0007123	LP.06 six leaves visible	2.0E-04
PO:0007098	LP.02 two leaves visible	7.1E-04
PO:0007064	LP.12 twelve leaves visible	1.1E-03
PO:0007095	LP.08 eight leaves visible	1.2E-03
PO:0001054	4 leaf senescence stage	2.8E-03
PO:0001050	leaf development stages	2.9E-03
PO:0007103	LP.10 ten leaves visible	3.0E-03
PO:0007134	A vegetative growth	6.4E-03
PO:0007033	whole plant growth stage	6.6E-03
PO:0007115	LP.04 four leaves visible	9.3E-03
PO:0007131	seedling development stage	1.8E-02
PO:0007133	leaf production	4.6E-02
PO:0007112	1 main shoot growth	4.6E-02

Table S48: Significantly enriched PO (temporal/plant structure development stage) terms associated with DEHYDRATION responsive genes in *Arabidopsis thaliana*.

⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0007131	seedling development stage	6.9E-20
PO:0007123	LP.06 six leaves visible	1.9E-16
PO:0007095	LP.08 eight leaves visible	4.6E-13
PO:0007115	LP.04 four leaves visible	5.0E-11
PO:0007134	A vegetative growth	5.0E-11
PO:0007033	whole plant growth stage	6.3E-11
PO:0007133	leaf production	2.9E-09
PO:0007112	1 main shoot growth	3.1E-09
PO:0007103	LP.10 ten leaves visible	7.9E-09
PO:0007064	LP.12 twelve leaves visible	2.2E-08
PO:0007098	LP.02 two leaves visible	3.3E-07
PO:0001017	M germinated pollen stage	1.7E-06
PO:0007605	androecium developmental stages	3.2E-06
PO:0001007	pollen developmental stages	4.6E-06
PO:0001054	4 leaf senescence stage	1.6E-04
PO:0001050	leaf development stages	1.7E-04
PO:0001040	dry seed stage	3.5E-04
PO:0001016	L mature pollen stage	1.2E-03

Table S49: Significantly enriched PO (temporal/plant structure development stage) terms associated with DROUGHT responsive genes in *Arabidopsis thaliana*.

⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0007095	LP.08 eight leaves visible	2.2E-02
PO:0007131	seedling development stage	3.0E-02

Table S50: Significantly enriched PO (temporal/plant structure development stage) terms associated with IRON responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0007095	LP.08 eight leaves visible	3.2E-16
PO:0007123	LP.06 six leaves visible	6.6E-15
PO:0007064	LP.12 twelve leaves visible	1.7E-14
PO:0007103	LP.10 ten leaves visible	4.7E-12
PO:0007098	LP.02 two leaves visible	1.1E-11
PO:0007131	seedling development stage	1.2E-10
PO:0007134	A vegetative growth	9.4E-10
PO:0007033	whole plant growth stage	1.1E-09
PO:0007115	LP.04 four leaves visible	4.1E-07
PO:0001054	4 leaf senescence stage	1.2E-06
PO:0001050	leaf development stages	1.3E-06
PO:0007133	leaf production	3.1E-05
PO:0007112	1 main shoot growth	3.2E-05

Table S51: Significantly enriched PO (temporal/plant structure development stage) terms associated with LIGHT responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0007131	seedling development stage	4.4E-22
PO:0007095	LP.08 eight leaves visible	2.6E-14
PO:0007123	LP.06 six leaves visible	2.6E-14
PO:0007103	LP.10 ten leaves visible	3.3E-08
PO:0007134	A vegetative growth	1.2E-07
PO:0007064	LP.12 twelve leaves visible	1.3E-07
PO:0007033	whole plant growth stage	1.4E-07
PO:0007098	LP.02 two leaves visible	3.6E-07
PO:0007115	LP.04 four leaves visible	1.9E-06
PO:0001054	4 leaf senescence stage	3.8E-06
PO:0001050	leaf development stages	4.4E-06
PO:0001017	M germinated pollen stage	5.0E-05
PO:0007133	leaf production	6.8E-05
PO:0007112	1 main shoot growth	7.3E-05
PO:0007605	androecium developmental stages	2.8E-03
PO:0001007	pollen developmental stages	3.6E-03
PO:0001016	L mature pollen stage	8.7E-03
PO:0001040	dry seed stage	1.5E-02

Table S52: Significantly enriched PO (temporal/plant structure development stage) terms associated with NaCl responsive genes in *Arabidopsis thaliana*. ⁺Bonferroni adjusted *P*-values.

PO ID	PO Term	P-value ⁺
PO:0007131	seedling development stage	8.2E-05

Table S53: Significantly enriched PO (temporal/plant structure development stage) terms associated with OXIDATIVE-STRESS responsive genes in *Arabidopsis thaliana*.
⁺Bonferroni adjusted *P*-values.

Gene ID	PASS2 - PSI- BLAST ¹	PASS2- HMMER ²	GENTHREAD R ³	PHYRE ⁴	Pcons ⁵	Pfam ⁶	CDD ⁷
AT1G68440	D1ux5a 13/35 (37%) E-value= 9.1	BH2638-like; E-value=0.1	1wxrA; (Low confidence)	Protein binding/si gnaling protein (c2kwuA) (Confidenc e: 37.3)	PDB: 4AG5, E-value: 0.062	RNA polymeras e I specific transcripti on initiation factor RRN3 Evalue: 0.47	Glutamate -cysteine ligase family 2 E-value: 0.01
AT1G59590	d1dysa- 12/28 (42%) E-value =7.2	Multiheme cytochrome; E-value=1	1gqfA (Low confidence)	Transport protein (c2k58B_) (Confidenc e: 30.1)	PDB: 2YFA, E-value: 1.2	Baculovira l E56 protein, specific to ODV envelope E value: 0.076	Phage shock protein C (PspC) that is thought to be a transcripti onal regulator. E-value: 0.01
AT5G58770	d1ueha 91/224 (40%) E-value = 4e-42	Undecaprenyl diphosphate synthase E- value=0.001	2vg3A (Certain confidence)	Transferas e (c2vg2C_) (Confidenc e: 100)	PDB: 2YFA, E-value: 1e-106	Undecapr enyl diphospha te synthase E-Value: 4.7e-80	undecapre nyl diphospha te synthase E-value: 3.67e-92
AT1G49450	d2ovrb2 71/229 (31%) E-value = 6e-12	WD40 repeat-like; E-value =0.001	2hesX (Certain confidence)	Sugar binding protein / Signaling protein(c3 dm0A) (Confidenc e: 100)	PDB: 2OVR, E-value: 2e-41	WD domain, E-value: 0.0088	WD40 domain E-value: 1.88e-29
AT3G53110	d1ux5a- 72/212 (33%) E-value: 2e- 22	Phosphoenol pyruvate/pyr uvate domain E-value= 0.1	3fhtA (Certain confidence)	Hydrolase (c3pexA_) (Confidenc e: 100)	PDB: 2JOS, E-value: 1e-125	DEAD/DE AH box helicase E-value: 2.4e-32	DEAD-box helicases E-value: 1.69e-28

Table S54: Structure-function prediction of genes responsive to multiple stress signals

¹ PASS2-PSIBLAST search is used for fold search. Results are SCOP folds with E-values of the top hit

² PASS2-HMMER search is used to find structural homolog using sequence data. Top

SCOP domain hit with homologous residues, sequence identity and E-values are provided for each gene. Both tools are accessed from the URL:

<http://caps.ncbs.res.in/pass2/tools/tools-landing.php>

³ GENTHREADER (URL: <http://bioinf.cs.ucl.ac.uk/psipred/?program=genthreader>) was queried using sequence data for fold recognition. Top- hits (SCOP/CATH identifiers) and confidence levels are provided.

⁴ PHYRE2 (URL: <http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index>) was queried using sequence data for fold recognition. Top- hits with PDB classification, PHYRE2 Fold library identifiers and confidence levels are provided.

⁵ Pcons (URL: <http://pcons.net>) was queried using sequence data for fold recognition. Top- hits with PDB identifier, Pcons protein fold identifiers and E-values are provided.

⁶ Pfam (URL: <http://pfam.sanger.ac.uk/>) was queried using sequence data for function prediction and functional domains name and E-values are provided.

⁷ CDD (URL: http://www.ncbi.nlm.nih.gov/Structure/cdd/docs/cdd_search.html) was queried using sequence data for conserved domain prediction. Top hits and E-values are provided.