

**Supplemental Table II. Molecular network components of genotype-independent stress response.** Synonyms, function, subcellular localization and potential interaction was derived from the databases TAIR (<https://www.arabidopsis.org/>), MapMan (<https://mapman.gabipd.org/>), SUBA4 (<http://suba.live/>), and String (<https://string-db.org/>). Code for subcellular localization: *italic*: SUBAcon (consensus, SUBA4), bolt: confirmation with FP (SUBA4), underlined: TAIR.

AGI	Synonym	Function	Subcellular localization	(Potential) Interaction	Processes involved in
AT5G52310	COR78 LTI78 LTI140 RD29A	Low-temperature-induced 78	<u>Nucleus</u>	KIN1 COR15B At1g16850 P5CS2 ADH1	MM: Stress, abiotic, cold has cis-acting regulatory elements that can impart cold-regulated gene expression INVOLVED in: circadian rhythm, hyperosmotic salinity response, leaf senescence, regulation of root development, response to abscisic acid, response to cold, response to desiccation, response to mannitol, response to osmotic stress, response to reactive oxygen species, response to salt, response to salt stress, response to symbiotic bacterium, response to water deprivation, response to wounding
AT2G42530	COR15B	cold regulated 15b	<u>Chloroplast</u>	COR78 KIN1 AT1g16850	MM: Stress, abiotic, cold protects chloroplast membranes during freezing INVOLVED in: cold acclimation, defense response to fungus, leaf senescence, response to abscisic acid, response to cold
AT5G15960	KIN1	stress-induced protein (KIN1)	<u>Cytosol</u>	COR78 COR15B	MM: hormone metabolism, ABA cold and ABA inducible protein kin1, possibly functions as an anti-freeze protein. Transcript level of this gene is induced by cold, ABA, dehydration and osmoticum (mannitol). Protein activity of GUS fused to the promoter of this gene is inhibited by cold treatment, suggesting an inhibition of the protein by increased transcript level. INVOLVED in: cold acclimation, red or far-red light signaling pathway, response to abscisic acid, response to cold, response to osmotic stress, response to water deprivation
AT1G16850	-	Unknown protein transmembrane protein	<u>Endoplasmic reticulum</u> <u>Extracellular region</u>	COR15B COR78	MM: not assigned INVOLVED in: response to salt stress
AT3G55610	P5CS2	delta 1-pyrroline-5-carboxylate synthase 2	<u>Cytosol</u> <u>Chloroplast</u> <u>Mitochondria</u> <u>Plasmodesma</u>	COR78 mtHsc70-1 CLPB3 PAL2 ADH1 PAL1	MM: amino acid metabolism, synthesis, glutamate, proline Gene expression is induced by dehydration, high salt and ABA FUNCTIONS in: oxidoreductase activity, glutamate-5-semialdehyde dehydrogenase activity, catalytic activity, glutamate 5-kinase activity; INVOLVED in: L-proline biosynthetic process, embryo development ending in seed dormancy, hyperosmotic salinity response, oxidation-reduction process, phosphorylation, pollen development, proline biosynthetic process, response to abscisic acid CONTAINS InterPro DOMAIN/s: Glutamate 5-kinase, Aspartate/glutamate/uridylyl kinase, Glutamate 5-kinase, conserved site, Aldehyde dehydrogenase, N-terminal, Gamma-glutamyl phosphate reductase GPR, conserved site, Aldehyde dehydrogenase, C-terminal, Delta 1-pyrroline-5-carboxylate synthetase, Gamma-glutamyl phosphate reductase GPR, Aldehyde/histidinol dehydrogenase, Glutamate 5-kinase, ProB-related
AT4G37910	mtHsc70-1	mitochondrial heat shock protein 70-1	<u>Mitochondrion</u> <u>Cell wall</u> <u>Vacuolar membrane</u>	CLPB3 P5CS2	MM: stress, abiotic, heat mitochondrial heat shock protein FUNCTIONS in: zinc ion binding, ATP binding; INVOLVED in: protein folding, response to cadmium ion, response to salt stress, response to cytokinin CONTAINS InterPro DOMAIN/s: Heat shock protein 70, conserved site, Chaperone DnaK, Heat shock protein Hsp70, Heat shock protein 70
AT5G15450	CLPB3 CLPB-P APG6 ATCLPB3	casein lytic proteinase B3	<u>Chloroplast (Stroma)</u> Cyttoplasm	mtHsc70-1 P5CS2	MM: stress, abiotic, heat Functions as a molecular chaperone involved in plastid differentiation mediating internal thylakoid membrane formation and conferring thermotolerance to chloroplasts during heat stress Expression is upregulated in response to heat shock in various organs, but not in response to other abiotic stresses. FUNCTIONS in: nucleoside-triphosphatase activity, ATPase activity, nucleotide binding, ATP binding; INVOLVED in: chloroplast organization, response to heat, protein metabolic process, protein refolding CONTAINS InterPro DOMAIN/s: Clp ATPase, C-terminal, ATPase, AAA+ type, core, ATPase, AAA-2, ATPase, AAA-type, core, Chaperonin clpA/B, Chaperonin ClpB, Chaperonin ClpA/B, conserved site, Clp, N-terminal
AT1G77120	ADH1	alcohol dehydrogenase 1	<u>Cytosol</u> <u>Nucleus</u> <u>Plasma membrane</u>	F3H COR78 P5CS2 SUS1 TT4 TT5	Cellular respiration, oxidation-reduction process, positive regulation of cellular response to hypoxia, response to abscisic acid, response to cadmium ion, response to caffeine, response to cold, response to estradiol, response to flooding, response to hydrogen peroxide, response to hypoxia, response to osmotic stress, response to salt stress, response to sucrose, response to water deprivation
AT2G37040	PAL1 ATPAL1 PHE Ammonia Lyase 1	phenylalanine ammonia-lyase 1	<u>Cytosol</u>	F3H P5CS2 PAL2 TT4 TT5	L-phenylalanine catabolic process/cinnamic acid biosynthetic process/defense response/drought recovery/lignin catabolic process/phenylpropanoid biosynthetic process/pollen development/response to UV-B/response to karrikin/response to oxidative stress/response to wounding/salicylic acid catabolic

					process
AT3G53260	PAL2 ATPAL2	phenylalanine ammonia-lyase 2	<u>Cytosol</u> <u>Cytoplasm</u>	P5CS2 F3H TT4 PAL1	MM: secondary metabolism, phenylpropanoids, lignin synthesis FUNCTIONS in: phenylalanine ammonia-lyase activity; protein binding, INVOLVED in: response to oxidative stress, response to karrikin, phenylpropanoid biosynthetic process, response to wounding, defense response, L-phenylalanine catabolic process, cinnamic acid biosynthetic process, defense response CONTAINS InterPro DOMAIN/s: Phenylalanine/histidine ammonia-lyase, Phenylalanine/histidine ammonia-lyases, active site, L-Aspartase-like, Phenylalanine ammonia-lyase;
AT3G51240	F3H TT6	flavanone 3-hydroxylase	<u>Cytosol</u> <u>Cytoplasm</u>	TT4 TT5 PAL2 RHM1 ADH1 PAL1	MM: Secondary Metabolism, flavonoids, dihydroflavonols Regulates flavonoid biosynthesis, oxidation-reduction process, response to UV-B Has ATP binding, L-ascorbic acid binding, metal ion binding, naringenin 3-dioxygenase activity, oxidoreductase activity INVOLVED in: flavonoid biosynthetic process, oxidation-reduction process, response to UV-B CONTAINS InterPro DOMAIN/s: Oxoglutarate/iron-dependent oxygenase;
AT5G13930	TT4 CHS ATCHS	Chalcone and stilbene synthase family protein	<u>Endoplasmic reticulum</u> <u>Nucleus</u> <u>Cytoplasm</u>	F3H PAL2 TT5 RHM1 ADH1 PAL1	MM: secondary metabolism, flavonoids, chalcones; naringenin-chalcone synthase Encodes chalcone synthase (CHS), a key enzyme involved in the biosynthesis of flavonoids. Required for the accumulation of purple anthocyanins in leaves and stems. Also involved in the regulation of auxin transport and the modulation of root gravitropism. FUNCTIONS in: naringenin-chalcone synthase activity INVOLVED in: auxin polar transport, chalcone biosynthetic process, flavonoid biosynthetic process, regulation of anthocyanin biosynthetic process, response to UV-B, response to auxin, response to gravity, response to jasmonic acid, response to oxidative stress, response to wounding CONTAINS InterPro DOMAIN/s: Chalcone/stilbene synthase, N-terminal, Thiolase-like (InterPro:IPR016039), Polyketide synthase, type III, Chalcone/stilbene synthase, active site, Chalcone/stilbene synthase, C-terminal, Thiolase-like, subgroup;
AT3G55120	TT5 A11 CFI CHI ATCHI	Chalcone-flavanone isomerase family protein	<u>Endoplasmic reticulum</u> <u>Nucleus</u> <u>Chloroplast</u> (ohne Isoform: ER, Nuc, Vacuole Membrane)	TT4 F3H ADH1 PAL1	MM: secondary metabolism, flavonoids, chalcones; Catalyzes the conversion of chalcones into flavanones. Required for the accumulation of purple anthocyanins in leaves and stems. Co-expressed with CHS. FUNCTIONS in: chalcone isomerase activity; INVOLVED in: response to UV, response to UV-B, response to karrikin, response to sucrose stimulus, flavonoid biosynthetic process; response to auxin CONTAINS InterPro DOMAIN/s: Chalcone isomerase, subgroup, Chalcone isomerase, 3-layer sandwich, Chalcone isomerase
AT1G78570	RHM1 ROL1 ATRHM1	rhamnose biosynthesis 1	<u>Cytosol</u> <u>Chloroplast</u> <u>Plasmodesma</u>	F3H TT4 SUS1	MM: cell wall, precursor synthesis, UDP-glucose 4,6-dehydratase Encodes a UDP-L-Rhamnose synthase involved in the biosynthesis of rhamnose, a major monosaccharide component of pectin. Catalyzes the conversion of UDP-D-Glc to UDP-L-Rha. The dehydrogenase domain of RHM1 was shown to catalyze the conversion of UDP-D-Glc to the reaction intermediate UDP-4-keto-6-deoxy-D-Glc using recombinant protein assay but the activity of the full-length protein was not determined as it could not be expressed in E. coli INVOLVED in: UDP-rhamnose biosynthetic process, auxin efflux, cell differentiation, cell wall organization, flavonol biosynthetic process, nucleotide-sugar metabolic process, oxidation-reduction process, regulation of cell proliferation CONTAINS InterPro DOMAIN/s: NAD-dependent epimerase/dehydratase, NAD(P)-binding domain, dTDP-4-dehydrorhamnose reductase
AT5G20830	SUS1 ASUS1 atsus1	sucrose synthase 1	<u>Cytosol</u>	RHM1 MIPS1 ADH1	MM: major CHO metabolism, degradation, sucrose, Susy FUNCTIONS in: UDP-glycosyltransferase activity, sucrose synthase activity; INVOLVED in: response to cadmium ion, response to cold, response to flooding, response to glucose, response to hypoxia, response to mannitol, response to osmotic stress, response to sorbitol, response to sucrose, response to water deprivation, sucrose biosynthetic process, sucrose metabolic process CONTAINS InterPro DOMAIN/s: Sucrose synthase, plant/cyanobacteria, Sucrose synthase, Glycosyl transferase, group 1
AT4G39800	MIPS1 ATMIPS1 ATIPS1 MI-1-P SYNTHAS E	myo-inositol-1-phosphate synthase 1  myo-inositol-3-phosphate synthase 1	<u>Cytosol</u> <u>Cytoplasm</u>	SUS1	MM: minor CHO metabolism, myo-inositol, InsP Synthases INVOLVED in: embryo development ending in seed dormancy, inositol biosynthetic process, myo-inositol hexakisphosphate biosynthetic process, phosphatidylserine biosynthetic process, phospholipid biosynthetic process, post-embryonic development CONTAINS InterPro DOMAIN/s: Myo-inositol-1-phosphate synthase, Myo-inositol-1-phosphate synthase, GAPDH-like, NAD(P)-binding domain
AT3G53460	CP29	chloroplast RNA-binding protein 29	<u>Chloroplast</u>	AT2G37220	MM: RNA, regulation of transcription/RNA binding, Encodes a nuclear gene with a consensus RNA-binding domain that is localized to the chloroplast FUNCTIONS in: RNA binding, mRNA binding, poly(U) RNA binding INVOLVED in: RNA processing, RNA splicing, RNA stabilization, cold acclimation, mRNA processing, response to cold CONTAINS InterPro DOMAIN/s: RNA recognition motif RNP-1, Nucleotide-binding alpha-beta plait;
AT2G37220	-	RNA-binding (RRM/RBD/RNP motifs) family protein	<u>Chloroplast</u>	CP29	MM: RNA, RNA binding, Encodes a chloroplast RNA binding protein. A substrate of the type III effector HopU1 (mono-ADP-ribosyltransferase). Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds FUNCTIONS in: RNA binding, poly(U) RNA binding;

					INVOLVED in: response to cold, response to abscisic acid, innate immune response; mRNA processing CONTAINS InterPro DOMAIN/s: RNA recognition motif RNP-1; Nucleotide-binding alpha-beta plait
<b>AT3G23830</b>	<b>GRP4</b> RBGA4	glycine-rich RNA-binding protein 4	<u>Mitochondria</u>	-	Response to cold/response to osmotic stress/ response to salt stress/response to water deprivation
<b>AT2G21660</b>	<b>CCR2</b> ATGRP7 GR-RBP7 GRP7 RBGA3	cold, circadian rhythm, and RNA binding 2	<u>Nucleus</u> <u>Cytosol</u> <u>Peroxisome</u> <u>Chloroplast</u>	-	MM: RNA binding, TAIR: Encodes a small glycine-rich RNA binding protein that is part of a negative-feedback loop through which ATGRP7 regulates the circadian oscillations of its own transcript. Gene expression is induced by cold. GRP7 appears to promote stomatal opening and reduce tolerance under salt and dehydration stress conditions, but, promotes stomatal closing and thereby increases stress tolerance under conditions of cold tolerance. Loss of function mutations have increased susceptibility to pathogens suggesting a role in mediating innate immune response. Mutants are also late flowering in a non-photoperiodic manner and are responsive to vernalization suggesting an interaction with the autonomous flowering pathway. There is a reduction of mRNA export from the nucleus in grp7 mutants. GRP7:GFP fusion proteins can be found in the cytosol and nucleus. A substrate of the type III effector HopU1 (mono-ADP-ribosyltransferase). cold, circadian rhythm, and rna binding 2 (CCR2); FUNCTIONS in: double-stranded DNA binding, mRNA binding, single-stranded DNA binding; INVOLVED in: DNA duplex unwinding, RNA secondary structure unwinding, alternative mRNA splicing, via spliceosome, circadian rhythm, innate immune response, mRNA export from nucleus, regulation of stomatal movement, response to cadmium ion, response to cold, response to cytokinin, response to osmotic stress, response to salt stress, response to water deprivation, response to zinc ion, vegetative to reproductive phase transition of meristem CONTAINS InterPro DOMAIN/s: RNA recognition motif, glycine rich protein, RNA recognition motif, RNP-1, Nucleotide-binding, alpha-beta plait;
<b>AT4G04020</b>	<b>FIB1A</b> FIB PGL35	Fibrillin precursor protein	<u>Chloroplast/Stroma</u>	-	MM: cell, organisation Fibrillin precursor protein. The fibrillin preprotein, but not the mature protein interacts with ABI2. Regulated by abscisic acid response regulators. Involved in abscisic acid-mediated photoprotection. The mRNA is cell-to-cell mobile. FUNCTIONS in: structural molecule activity; INVOLVED in: photoinhibition, response to cold, response to abscisic acid CONTAINS InterPro DOMAIN/s: Plastid lipid-associated protein/fibrillin
<b>AT5G01600</b>	<b>FER1</b> ATFER1	Ferritin 1	<u>Chloroplast</u>	-	MM: metal handling, binding, chelation and storage Ferric iron, iron binding Encodes a ferritin protein that is targeted to the chloroplast. Member of a Ferritin gene family. Gene expression is induced in response to iron overload and by nitric oxide. Expression of the gene is downregulated in the presence of paraquat, an inducer of photoxidative stress. FUNCTIONS in: ferric iron binding, iron ion binding; INVOLVED in: cellular iron ion homeostasis, flower development, intracellular sequestering of iron ion, iron ion homeostasis, iron ion transport, leaf development, oxidation-reduction process, photosynthesis, response to bacterium, response to cold, response to cytokinin, response to hydrogen peroxide, response to iron ion, response to reactive oxygen species, response to zinc ion CONTAINS InterPro DOMAIN/s: Ferritin, N-terminal, Ferritin-related, Ferritin-like, Ferritin, conserved site, Ferritin/ribonucleotide reductase-like, Ferritin/Dps protein
<b>AT5G13650</b>	<b>SVR3</b>	elongation factor family protein / suppressor of variegation	<u>Chloroplast</u> <u>Plasma Membrane</u>	-	MM: Protein synthesis, elongation Encodes SVR3, a putative chloroplast TypA translation elongation GTPase. Loss of SVR3 suppresses variegation mediated by var2. SVR3 is essential for plants? ability to develop functional chloroplasts under chilling stress (8C), but not at normal temperature (22C). elongation factor family protein; FUNCTIONS in: GTP binding, translation elongation factor activity, GTPase activity; INVOLVED in: chloroplast RNA processing, regulation of gene expression, response to reactive oxygen species CONTAINS InterPro DOMAIN/s: Small GTP-binding protein, Translation elongation factor EFTu/EF1A, domain 2, Translation elongation factor EFG/EF2, C-terminal, GTP-binding protein TypA, Protein synthesis factor, GTP-binding, Elongation factor G/III/V, Translation elongation/initiation factor/Ribosomal, beta-barrel