## Supplementary Table 11. Function of *L. maritima* specific genes with homolog in Swiss-prot database.

| Gene ID   | Swiss-Prot Annotation | Gene Function                                                                                                                                 |
|-----------|-----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|
| Lma12953.t1 | ACFR1_ARATH           | Two-heme-containing cytochrome. Catalyzes ascorbate-dependent trans-membrane ferric-chelate reduction. Able to use dihydrolipoic acid (DHLA) as an alternative substrate to ascorbate. |
| Lma16848.t1 | RLF4_ARATH            | Cell signaling peptide that may regulate plant stress, growth, and development. Mediates a rapid alkalization of extracellular space by mediating a transient increase in the cytoplasmic Ca(2+) concentration leading to a calcium-dependent signaling events through a cell surface receptor and a concomitant activation of some intracellular mitogen-activated protein kinases (By similarity). |
| Lma17380.t1 | ALEU_ARATH            | May play a role in proteolysis leading to mobilization of nitrogen during senescence and starvation.                                           |
| Lma22861.t1 | DNJ10_ARATH           | Have a continuous role in plant development probably in the structural organization of compartments.                                         |
| Lma00592.t1 | ASY2_ARATH            | Required for normal meiosis.                                                                                                                  |
| Lma10446.t1 | ASY2_ARATH            | Required for normal meiosis.                                                                                                                  |
| Lma25849.t1 | ASY2_ARATH            | Required for normal meiosis.                                                                                                                  |
| Lma14963.t1 | RFA1B_ARATH           | Component of the replication protein A complex (RPA) required for DNA recombination, repair and replication. The activity of RPA is mediated by single-stranded DNA binding and protein interactions (By similarity). Probably involved in repair of double-strand DNA breaks (DSBs) induced by genotoxic stresses (By similarity). |
| Lma17596.t1 | RFA1B_ARATH           | Component of the replication protein A complex (RPA) required for DNA recombination, repair and replication. The activity of RPA is mediated by single-stranded DNA binding and protein interactions (By similarity). Probably involved in repair of double-strand DNA breaks (DSBs) induced by genotoxic stresses (By similarity). |
E3 ubiquitin-protein ligase that mediates ubiquitination and subsequent proteasomal degradation of target proteins. E3 ubiquitin ligases accept ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates. It probably triggers the ubiquitin-mediated degradation of different substrates.
Lma10414.t1  PMTT_ARATH  May be involved in the synthesis of homogalacturonan. Required for normal cell adhesion and plant development.
Lma10861.t1  PMTT_ARATH  May be involved in the synthesis of homogalacturonan. Required for normal cell adhesion and plant development.
Lma12584.t1  PMTT_ARATH  May be involved in the synthesis of homogalacturonan. Required for normal cell adhesion and plant development.
Lma25957.t1  PMTT_ARATH  May be involved in the synthesis of homogalacturonan. Required for normal cell adhesion and plant development.
Lma03871.t1  EA6_ARATH  Probable beta-1,3-glucanase that may be involved in the degradation of callose walls around the microspore tetrad during pollen development (Probable). May be required for pollen exine formation.
Lma06492.t1  EA6_ARATH  Probable beta-1,3-glucanase that may be involved in the degradation of callose walls around the microspore tetrad during pollen development (Probable). May be required for pollen exine formation.
Lma09994.t1  EA6_ARATH  Probable beta-1,3-glucanase that may be involved in the degradation of callose walls around the microspore tetrad during pollen development (Probable). May be required for pollen exine formation.
Lma12299.t1  EA6_ARATH  Probable beta-1,3-glucanase that may be involved in the degradation of callose walls around the microspore tetrad during pollen development (Probable). May be required for pollen exine formation.
Lma25457.t1  EA6_ARATH  Probable beta-1,3-glucanase that may be involved in the degradation of callose walls around the microspore tetrad during pollen development (Probable). May be required for pollen exine formation.
Lma10690.t1  XCP2_ARATH  Participates in micro autolysis within the intact central vacuole before mega autolysis is initiated by tonoplast implosion involved in susceptibility to the bacterial plant pathogen Ralstonia solanacearum. Cysteine protease involved in xylem tracheary element (TE) autolysis during xylogenesis in roots.
Lma14957.t1  XCP2_ARATH  Participates in micro autolysis within the intact central vacuole before mega autolysis is initiated by tonoplast implosion involved in susceptibility to the bacterial plant pathogen Ralstonia solanacearum. Cysteine protease involved in xylem tracheary element (TE) autolysis during xylogenesis in roots.
Lma14986.t1  XCP2_ARATH  Participates in micro autolysis within the intact central vacuole before mega autolysis is initiated by tonoplast implosion involved in susceptibility to the bacterial plant pathogen Ralstonia solanacearum.
Lma18192.t1  TF2B2_ARATH  General factor that plays a major role in the activation of eukaryotic genes transcribed by RNA polymerase II.
Lma20293.t1 TF2B_SOYBN General factor that plays a major role in the activation of eukaryotic genes transcribed by RNA polymerase II.

Lma20294.t1 TF2B1_ARATH General factor that plays a major role in the activation of eukaryotic genes transcribed by RNA polymerase II (By similarity). Interacts with TBP2 and is required for activated transcription and possibly basal transcription. Plays important roles in pollen tube growth, guidance, and reception as well as endosperm development. Is partially functionally different from TFIIB2 and PBRP2.

Lma20295.t1 TF2B1_ARATH General factor that plays a major role in the activation of eukaryotic genes transcribed by RNA polymerase II (By similarity). Interacts with TBP2 and is required for activated transcription and possibly basal transcription. Plays important roles in pollen tube growth, guidance, and reception as well as endosperm development. Is partially functionally different from TFIIB2 and PBRP2.

Lma20296.t1 TF2B1_ARATH General factor that plays a major role in the activation of eukaryotic genes transcribed by RNA polymerase II (By similarity). Interacts with TBP2 and is required for activated transcription and possibly basal transcription. Plays important roles in pollen tube growth, guidance, and reception as well as endosperm development. Is partially functionally different from TFIIB2 and PBRP2.

Lma00469.t1 RPS6R_ARATH Disease resistance (R) protein that specifically recognizes the hopA1 type III effector avirulence protein from Pseudomonas syringae. Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth.

Lma17365.t1 RPS6C_ARATH Disease resistance protein of the TIR-NB-LRR-type. Part of the RPS6 locus that contains a cluster of several paralogous disease resistance (R) genes. Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. (By similarity). Required for [5-(3,4-dichlorophenyl)furan-2-yl]-piperidine-1-ylmethanethione- (DFPM-) induced root growth arrest due to reduced number of meristem cells in the division zone of the primary root and inhibition of abscisic acid- (ABA-) induced stomatal closing.
Disease resistance protein of the TIR-NB-LRR-type. Part of the RPS6 locus that contains a cluster of several paralogous disease resistance (R) genes. Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth (By similarity). Required for \([5-(3,4\text{-dichlorophenyl})\text{furan-2-yl}]\text{-piperidine-1-ylmethanethione-} (\text{DFPM})\) induced root growth arrest due to reduced number of meristem cells in the division zone of the primary root and inhibition of abscisic acid- (ABA-) induced stomatal closing.

Disease resistance protein of the TIR-NB-LRR-type. Part of the RPS6 locus that contains a cluster of several paralogous disease resistance (R) genes. Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth (By similarity). Required for \([5-(3,4\text{-dichlorophenyl})\text{furan-2-yl}]\text{-piperidine-1-ylmethanethione-} (\text{DFPM})\) induced root growth arrest due to reduced number of meristem cells in the division zone of the primary root and inhibition of abscisic acid- (ABA-) induced stomatal closing.

Accepts the ubiquitin from the E1 complex and catalyzes its covalent attachment to other proteins. Mediates the selective degradation of short-lived and abnormal proteins.

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Accepts the ubiquitin from the E1 complex and catalyzes its covalent attachment to other proteins. Mediates the selective degradation of short-lived and abnormal proteins.

Required for normal meiosis.

Required for normal meiosis.

Specific inhibitor of cysteine proteinases. Probably involved in the regulation of endogenous processes and in defense against pests and pathogens (By similarity).

Specific inhibitor of cysteine proteinases. Probably involved in the regulation of endogenous processes and in defense against pests and pathogens (By similarity).
Lma08619.t1  CYT4_ARATH  Specific inhibitor of cysteine proteinases. Probably involved in the regulation of endogenous processes and in defense against pests and pathogens (By similarity).

Lma24225.t1  CYT4_ARATH  Specific inhibitor of cysteine proteinases. Probably involved in the regulation of endogenous processes and in defense against pests and pathogens (By similarity).

Lma03430.t1  3AT1_ARATH  Involved in the acylation of the 6" position of the 3- O-glucose residue of anthocyanin. Also able to use flavonol 3- glucosides as the acyl acceptor.

Lma05002.t1  3AT1_ARATH  Involved in the acylation of the 6" position of the 3- O-glucose residue of anthocyanin. Also able to use flavonol 3- glucosides as the acyl acceptor.

Lma06935.t1  3AT1_ARATH  Involved in the acylation of the 6" position of the 3- O-glucose residue of anthocyanin. Also able to use flavonol 3- glucosides as the acyl acceptor.

Lma26149.t1  3AT1_ARATH  Involved in the acylation of the 6" position of the 3- O-glucose residue of anthocyanin. Also able to use flavonol 3- glucosides as the acyl acceptor.

Lma00172.t1  MIA40_ARATH  Required for the import and folding of small cysteine-containing proteins in the mitochondrial intermembrane space (Probable). Involved in the mitochondrial oxidative folding of the copper-zinc superoxide dismutase CSD1, the copper chaperone for superoxide dismutase CCS, and subunits of the mitochondrial membrane respiratory chain NADH dehydrogenase (Complex I). Involved in the peroxisomal oxidative folding of the copper-zinc superoxide dismutase CSD3, and the fatty acid beta-oxidation multifunctional protein AIM1.

Lma00191.t1  MIA40_ARATH  Required for the import and folding of small cysteine-containing proteins in the mitochondrial intermembrane space (Probable). Involved in the mitochondrial oxidative folding of the copper-zinc superoxide dismutase CSD1, the copper chaperone for superoxide dismutase CCS, and subunits of the mitochondrial membrane respiratory chain NADH dehydrogenase (Complex I). Involved in the peroxisomal oxidative folding of the copper-zinc superoxide dismutase CSD3, and the fatty acid beta-oxidation multifunctional protein AIM1.

Lma14406.t1  MIA40_ARATH  Required for the import and folding of small cysteine-containing proteins in the mitochondrial intermembrane space (Probable). Involved in the mitochondrial oxidative folding of the copper-zinc superoxide dismutase CSD1, the copper chaperone for superoxide dismutase CCS, and subunits of the mitochondrial membrane respiratory chain NADH dehydrogenase (Complex I). Involved in the peroxisomal oxidative folding of the copper-zinc superoxide dismutase CSD3, and the fatty acid beta-oxidation multifunctional protein AIM1.
**Lma19027.t1 MIA40_ARATH**
Required for the import and folding of small cysteine-containing proteins in the mitochondrial intermembrane space (Probable). Involved in the mitochondrial oxidative folding of the copper-zinc superoxide dismutase CSD1, the copper chaperone for superoxide dismutase CCS, and subunits of the mitochondrial membrane respiratory chain NADH dehydrogenase (Complex I). Involved in the peroxisomal oxidative folding of the copper-zinc superoxide dismutase CSD3, and the fatty acid beta-oxidation multifunctional protein AIM1.

**Lma05267.t1 RTNLA_ARATH**
Plays a role in the Agrobacterium-mediated plant transformation via its interaction with VirB2, the major component of the T-pilus.

**Lma11002.t1 RTNLA_ARATH**
Plays a role in the Agrobacterium-mediated plant transformation via its interaction with VirB2, the major component of the T-pilus.

**Lma19575.t1 RTNLA_ARATH**
Plays a role in the Agrobacterium-mediated plant transformation via its interaction with VirB2, the major component of the T-pilus.

**Lma22096.t1 RTNLA_ARATH**
Plays a role in the Agrobacterium-mediated plant transformation via its interaction with VirB2, the major component of the T-pilus.

**Lma06374.t1 B3GT2_ARATH**
Beta-1,3-galactosyltransferase that transfers galactose from UDP-galactose to substrates with a terminal glycosyl residue.

**Lma10752.t1 B3GT2_ARATH**
Beta-1,3-galactosyltransferase that transfers galactose from UDP-galactose to substrates with a terminal glycosyl residue.

**Lma04667.t1 SMD1A_ARATH**
Involved in splicing regulation. Facilitates post-transcriptional gene silencing (PTGS) by limiting the degradation of transgene aberrant RNAs by the RNA quality control (RQC) machinery, thus favoring their entry into cytoplasmic siRNA bodies where they can trigger PTGS. Does not participate in the production of small RNAs.

**Lma10175.t1 SMD1A_ARATH**
Involved in splicing regulation. Facilitates post-transcriptional gene silencing (PTGS) by limiting the degradation of transgene aberrant RNAs by the RNA quality control (RQC) machinery, thus favoring their entry into cytoplasmic siRNA bodies where they can trigger PTGS. Does not participate in the production of small RNAs.

**Lma26191.t1 SMD1A_ARATH**
Involved in splicing regulation. Facilitates post-transcriptional gene silencing (PTGS) by limiting the degradation of transgene aberrant RNAs by the RNA quality control (RQC) machinery, thus favoring their entry into cytoplasmic siRNA bodies where they can trigger PTGS. Does not participate in the production of small RNAs.
Component of the COP9 signalosome complex (CSN), a complex involved in various cellular and developmental processes such as photomorphogenesis and auxin and jasmonate responses. The CSN complex is an essential regulator of the ubiquitin (Ubl) conjugation pathway by mediating the deneddylation of the cullin subunits of SCF-type E3 ligase complexes, leading to decrease the Ubl ligase activity of SCF. It is involved in repression of photomorphogenesis in darkness by regulating the activity of COP1-containing Ubl ligase complexes. The complex is also required for degradation of PSIAA6 by regulating the activity of the Ubl ligase SCF-TIR complex. Essential for the structural integrity of the CSN holocomplex.

Might act as an E3 ubiquitin-protein ligase, or as part of E3 complex, which accepts ubiquitin from specific E2 ubiquitin-conjugating enzymes and then transfers it to substrates.

Involved in morphogenesis and proliferation of mitochondria. Does not act redundantly with PMD1. Is not involved in peroxisomal proliferation.

Reduced transferring electrons from NADH to cytochrome b5. Required for the NADH-dependent electron transfer involved in the desaturation and hydroxylation of fatty acids and in the desaturation of sterol precursors. No activity with NADPH as electron donor.
Reductase transferring electrons from NADH to cytochrome b5. Required for the NADH-dependent
electron transfer involved in the desaturation and hydroxylation of fatty acids and in the desaturation of
sterol precursors. No activity with NADPH as electron donor.

Plays a central role in integrating RNA silencing and chromatin signals in 21 nt siRNA-dependent DNA
methylation on cytosine pathway leading to transcriptional gene silencing of specific sequences. Involved
in a chromatin-based RNA silencing pathway that encompasses both post-transcriptional gene silencing
(PTGS) (e.g. RDR1, RDR6 and AGO2) and transcriptional gene silencing (TGS) (e.g. siRNA-dependent
DNA methylation and histone H3) components. Mediates siRNA accumulation at specific chromatin loci.
Binds H3K4me0 through its PHD to enforce low levels of H3K4 methylation and gene silencing at a
subset of genomic loci.

Probable carboxypeptidase.

Disease resistance protein. Resistance proteins guard the plant against pathogens that contain an
appropriate avirulence protein via a direct or indirect interaction with this avirulence protein. That triggers
da defense system including the hypersensitive response, which restricts the pathogen growth.

Disease resistance protein. Resistance proteins guard the plant against pathogens that contain an
appropriate avirulence protein via a direct or indirect interaction with this avirulence protein. That triggers
da defense system including the hypersensitive response, which restricts the pathogen growth (By
similarity).

Transcription activator that recognizes and binds to the DNA consensus sequence 5'-CACGCGC-3'.
Activates the expression of FHY1 and FHL involved in light responses. When associated with PHYA,
protects it from being recognized and degraded by the COP1/SPA complex. Positive regulator of
chlorophyll biosynthesis via the activation of HEMB1 gene expression.

Transcription activator that recognizes and binds to the DNA consensus sequence 5'-CACGCGC-3'.
Activates the expression of FHY1 and FHL involved in light responses. When associated with PHYA,
protects it from being recognized and degraded by the COP1/SPA complex. Positive regulator of
chlorophyll biosynthesis via the activation of HEMB1 gene expression.
Lma25607.t1  FRS5_ARATH  Putative transcription activator involved in regulating light control of development.
Lma03847.t1  ASY2_ARATH  Required for normal meiosis.
Lma13315.t1  ASY2_ARATH  Required for normal meiosis.
Lma10801.t1  OEP80_ARATH  Plays an essential role during early stages of plastid development.
Lma15057.t1  OEP80_ARATH  Plays an essential role during early stages of plastid development.
Lma19432.t1  OEP80_ARATH  Plays an essential role during early stages of plastid development.

Kinase that can phosphorylate various inositol polyphosphate such as Ins(3,4,5,6)P4 or Ins(1,3,4)P3. Phosphorylates Ins(3,4,5,6)P4 to form InsP5. This reaction is thought to have regulatory importance, since Ins(3,4,5,6)P4 is an inhibitor of plasma membrane Ca(2+)-activated Cl(-) channels, while Ins(1,3,4,5,6)P5 is not (By similarity). Also phosphorylates Ins(1,3,4)P3 or a racemic mixture of Ins(1,4,6)P3 and Ins(3,4,6)P3 to form InsP4Ins(1,3,4,6)P4 is an essential molecule in the hexakisphosphate (InsP6) pathway (By similarity). Plays a role in seed coat development and lipid polyester barrier formation.

Lma05131.t1  ITPK2_ARATH  Kinase that can phosphorylate various inositol polyphosphate such as Ins(3,4,5,6)P4 or Ins(1,3,4)P3. Phosphorylates Ins(3,4,5,6)P4 to form InsP5. This reaction is thought to have regulatory importance, since Ins(3,4,5,6)P4 is an inhibitor of plasma membrane Ca(2+)-activated Cl(-) channels, while Ins(1,3,4,5,6)P5 is not (By similarity). Also phosphorylates Ins(1,3,4)P3 or a racemic mixture of Ins(1,4,6)P3 and Ins(3,4,6)P3 to form InsP4Ins(1,3,4,6)P4 is an essential molecule in the hexakisphosphate (InsP6) pathway (By similarity). Plays a role in seed coat development and lipid polyester barrier formation.

Lma14754.t1  THAH_ARATH  Hydroxylates thalianol into thalian-diol.

Lma13064.t1  BI1_ARATH  Suppressor of apoptosis. Modulator of endoplasmic reticulum stress-mediated programmed cell death. Involved in methyl jasmonate-induced leaf senescence through regulating cytoplasmic calcium level.

Lma22957.t1  RPP1_ARATH  TIR-NB-LRR receptor-like protein that confers resistance to the pathogen Hyaloperonospora arabidopsis.
Lma22958.t1  RPP1_ARATH  TIR-NB-LRR receptor-like protein that confers resistance to the pathogen Hyaloperonospora arabidopsis.

Lma00736.t1  CDPKD_ARATH  May play a role in signal transduction pathways that involve calcium as a second messenger.
Lma15146.t1  CDPKD_ARATH  May play a role in signal transduction pathways that involve calcium as a second messenger.
Lma24053.t1  CDPKD_ARATH  May play a role in signal transduction pathways that involve calcium as a second messenger.
Lma00575.t2  SWET8_ARATH  Mediates both low-affinity uptake and efflux of sugar across the plasma membrane. Required, in pollen, for microspore cell integrity and primexine pattern formation.
Lma14978.t2  SWET8_ARATH  Mediates both low-affinity uptake and efflux of sugar across the plasma membrane. Required, in pollen, for microspore cell integrity and primexine pattern formation.
Lma15042.t2  SWET8_ARATH  Mediates both low-affinity uptake and efflux of sugar across the plasma membrane. Required, in pollen, for microspore cell integrity and primexine pattern formation.
Lma07325.t1  LBD6_MAIZE
Promotes the switch from proliferation to differentiation in the embryo sac. Negative regulator of cell proliferation in the adaxial side of leaves. Regulates the formation of a symmetric lamina and the establishment of venation. Interacts directly with RS2 (rough sheath 2) to repress some knox homeobox genes.
Component of the peroxisomal and mitochondrial division machineries. Plays a role in promoting the fission of mitochondria and peroxisomes. In association with PEX11C, PEX11D, PEX11E and DRP3A, is involved in cell cycle-associated constitutive self-replication of preexisting peroxisomes.

Lma11770.t5  FIS1B_ARATH
Component of the peroxisomal and mitochondrial division machineries. Plays a role in promoting the fission of mitochondria and peroxisomes. In association with PEX11C, PEX11D, PEX11E and DRP3A, is involved in cell cycle-associated constitutive self-replication of preexisting peroxisomes.

Lma17635.t1  FIS1B_ARATH
Component of the peroxisomal and mitochondrial division machineries. Plays a role in promoting the fission of mitochondria and peroxisomes. In association with PEX11C, PEX11D, PEX11E and DRP3A, is involved in cell cycle-associated constitutive self-replication of preexisting peroxisomes.

Lma25970.t5  FIS1B_ARATH
Component of the peroxisomal and mitochondrial division machineries. Plays a role in promoting the fission of mitochondria and peroxisomes. In association with PEX11C, PEX11D, PEX11E and DRP3A, is involved in cell cycle-associated constitutive self-replication of preexisting peroxisomes.

Lma04858.t1  TBCC_ARATH
Essential tubulin-folding protein involved in the final step of the tubulin folding pathway. Required for continuous microtubule cytoskeleton organization, mitotic division, cytokinesis, and to couple cell cycle progression to cell division in embryos and endosperms. Not essential for cell viability. Binds probably to the multimeric supercomplex, stimulating GTP hydrolysis by the bound beta-tubulin and the release of the alpha-/beta-tubulin heterodimer.
Essential tubulin-folding protein involved in the final step of the tubulin folding pathway. Required for continuous microtubule cytoskeleton organization, mitotic division, cytokinesis, and to couple cell cycle progression to cell division in embryos and endosperms. Not essential for cell viability. Binds probably to the multimeric supercomplex, stimulating GTP hydrolysis by the bound beta-tubulin and the release of the alpha-/beta-tubulin heterodimer.

Lma05962.t1  TBCC_ARATH
Essential tubulin-folding protein involved in the final step of the tubulin folding pathway. Required for continuous microtubule cytoskeleton organization, mitotic division, cytokinesis, and to couple cell cycle progression to cell division in embryos and endosperms. Not essential for cell viability. Binds probably to the multimeric supercomplex, stimulating GTP hydrolysis by the bound beta-tubulin and the release of the alpha-/beta-tubulin heterodimer.

Lma12386.t1  TBCC_ARATH
Essential tubulin-folding protein involved in the final step of the tubulin folding pathway. Required for continuous microtubule cytoskeleton organization, mitotic division, cytokinesis, and to couple cell cycle progression to cell division in embryos and endosperms. Not essential for cell viability. Binds probably to the multimeric supercomplex, stimulating GTP hydrolysis by the bound beta-tubulin and the release of the alpha-/beta-tubulin heterodimer.
Associates in vitro with the adrenodoxin-like protein MFDX1 to form an efficient low potential electron transfer chain that is able to reduce cytochrome C (, ). Functions as accessory mitochondrial protein involved with BIO2 in the plant biotin synthase reaction.
Associates in vitro with the adrenodoxin-like protein MFDX1 to form an efficient low potential electron transfer chain that is able to reduce cytochrome C. Functions as accessory mitochondrial protein involved with BIO2 in the plant biotin synthase reaction.

Disease resistance (R) protein that specifically recognizes the hopA1 type III effector avirulence protein from Pseudomonas syringae. Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth.

Probable aspartic protease activated by the transcription factor MYB80. May participate in the regulation of the timing of tapetal programmed cell death (PCD) which is critical for pollen development.

Part of a translocon most abundantly expressed in etiolated plants and involved in the protochlorophyllide-dependent import of the precursor NADPH:protochlorophyllide oxidoreductase A (pPORA).

Putative transcriptional activator that binds specifically to the DNA sequence 5'-[AG]GATT-3'. Functions as response regulator involved in His-to-Asp phosphorelay signal transduction system. Phosphorylation of the Asp residue in the receiver domain activates the ability of the protein to promote the transcription of target genes. Could directly activate some type-A response regulators in response to cytokinins (By similarity).
Putative transcriptional activator that binds specifically to the DNA sequence 5'-[AG]GATT-3'. Functions as response regulator involved in His-to-Asp phosphorelay signal transduction system. Phosphorylation of the Asp residue in the receiver domain activates the ability of the protein to promote the transcription of target genes. Could directly activate some type-A response regulators in response to cytokinins (By similarity).

Plays a role in protein import into the endoplasmic reticulum (ER). May function as chaperone docking protein during post-translational protein translocation into the ER. Chaperone receptor mediating Hsp70-dependent protein targeting to chloroplasts. Interacts specifically with some chloroplast precursors, but not with mitochondrial precursors. Able to select precursors for delivery to the chloroplast translocase independently of Hsp70.

Plays a role in protein import into the endoplasmic reticulum (ER). May function as chaperone docking protein during post-translational protein translocation into the ER. Chaperone receptor mediating Hsp70-dependent protein targeting to chloroplasts. Interacts specifically with some chloroplast precursors, but not with mitochondrial precursors. Able to select precursors for delivery to the chloroplast translocase independently of Hsp70.

Vesicle trafficking protein that functions in the secretory pathway.

Serine/threonine protein kinase involved in autophagy in a nutritional condition-dependent manner. The ATG1-ATG13 protein kinase complex regulates downstream events required for autophagosome enclosure and/or vacuolar delivery. Becomes a target of autophagy under nutrient starvation. Connects autophagy to plant nutritional status.

Serine/threonine protein kinase involved in autophagy in a nutritional condition-dependent manner. The ATG1-ATG13 protein kinase complex regulates downstream events required for autophagosome enclosure and/or vacuolar delivery. Becomes a target of autophagy under nutrient starvation. Connects autophagy to plant nutritional status.

Probable cyclic nucleotide-gated ion channel.

Probable cyclic nucleotide-gated ion channel.

The 26S proteasome is involved in the ATP-dependent degradation of ubiquitinated proteins. The regulatory (or ATPase) complex confers ATP dependency and substrate specificity to the 26S complex.
The 26S proteasome is involved in the ATP-dependent degradation of ubiquitinated proteins. The regulatory (or ATPase) complex confers ATP dependency and substrate specificity to the 26S complex.

Probable transcription factor that forms heterodimers with the MADS-box proteins AGL66 and AGL104 and is involved in the regulation of pollen maturation at the late stages of pollen development and pollen tube growth.

Implicated in mitochondrial protein import and macromolecular assembly. May facilitate the correct folding of imported proteins. May also prevent misfolding and promote the refolding and proper assembly of unfolded polypeptides generated under stress conditions in the mitochondrial matrix (By similarity).

Transcription regulator that probably binds to the GCC-box pathogenesis-related promoter element. Binds also to the S-box (5'–CACTTCCA-3') photosynthesis-associated nuclear genes-related (PhANGs-related) promoter element, and thus acts as a transcription inhibitor. Involved in the regulation of gene expression by stress factors and by components of stress signal transduction pathways. May have a function in the deetiolation process. Confers sensitivity to abscisic acid (ABA), and regulates the ABA signaling pathway during seed germination, upon nitrate-mediated lateral root inhibition, in hexokinase-dependent sugar responses (including feed-back regulation of photosynthesis and mobilization of storage lipid during germination), and in response to osmotic stress mediated by NaCl, KCl or mannitol. Plays a role in sucrose sensing or signaling, especially at low fluence far red light. Also involved in plant response to glucose treatment, especially at low concentration and in young seedlings. Required for the trehalose-mediated root inhibition and starch accumulation in cotyledons, probably by inhibiting starch breakdown. However, seems to not be involved in sugar-mediated senescence. Required for the ABA-dependent beta-amino-butryic acid (BABA) signaling pathway. BABA primes ABA synthesis and promotes resistance to drought and salt, and leads to a prime callose accumulation that confers resistance against necrotrophic pathogens such as A.brassicicola and P.cucumerina. Seems to be involved in resistance to S.sclerotiorum probably by regulating the ABA-mediated stomatal closure apparently by antagonistic interaction with oxalate. Negative regulator of low water potential-induced Pro accumulation whose effect is decreased by high levels of sugar.
Transcription regulator that probably binds to the GCC-box pathogenesis-related promoter element. Binds also to the S-box (5'-CACTTCCA-3') photosynthesis-associated nuclear genes-related (PhANGs-related) promoter element, and thus acts as a transcription inhibitor. Involved in the regulation of gene expression by stress factors and by components of stress signal transduction pathways. May have a function in the deetiolation process. Confers sensitivity to abscisic acid (ABA), and regulates the ABA signaling pathway during seed germination, upon nitrate-mediated lateral root inhibition, in hexokinase-dependent sugar responses (including feed-back regulation of photosynthesis and mobilization of storage lipid during germination), and in response to osmotic stress mediated by NaCl, KCl or mannitol. Plays a role in sucrose sensing or signaling, especially at low fluence far red light. Also involved in plant response to glucose treatment, especially at low concentration and in young seedlings. Required for the trehalose-mediated root inhibition and starch accumulation in cotyledons, probably by inhibiting starch breakdown. However, seems to not be involved in sugar-mediated senescence. Required for the ABA-dependent beta-amino-butyric acid (BABA) signaling pathway. BABA primes ABA synthesis and promotes resistance to drought and salt, and leads to a prime callose accumulation that confers resistance against necrotrophic pathogens such as A. brassicicola and P. cucumerina. Seems to be involved in resistance to S. sclerotiorum probably by regulating the ABA-mediated stomatal closure apparently by antagonistic interaction with oxalate. Negative regulator of low water potential-induced Pro accumulation whose effect is decreased by high levels of sugar.

Required for correct initiation of floral organ primordia and for proper development of organ primordia. Phosphorylates in vitro ASF1B/SGA1, the C-terminal part of TK11 and histone H3.

Together with GSO2, receptor-like serine/threonine-kinase required during the development of the epidermal surface in embryos and cotyledons. In coordination with GSO2, regulates root growth through control of cell division and cell fate specification. Controls seedling root growth by modulating sucrose response after germination. Receptor of the peptide hormones CIF1 and CIF2 required for contiguous Caspian strip diffusion barrier formation in roots. Required for localizing CASP proteins into the Caspian strip following an uninterrupted, ring-like domain, to trigger endodermal differentiation and thus regulate potassium ion (K) homeostasis. Involved in the maintenance of water transport and root pressure. May also be involved in the regulation of suberin accumulation in the endodermis.
Lma12882.t1  DR100_ARATH
This protein is able to complement bacterial recA mutations, but its native function in the plant is not known.

Lma14373.t1  ERD15_ARATH
Central component of stress responses that interacts with poly(A)-binding proteins. Negative regulator of abscisic acid (ABA) responses, including resistance to drought and freezing as well as stomatal closure regulation. Mediates resistance to the bacterial necrotroph pathogen Erwinia carotovora subsp. carotovora and promotes the induction of marker genes for systemic acquired resistance (SAR).

Lma26266.t1  ERD15_ARATH
Central component of stress responses that interacts with poly(A)-binding proteins. Negative regulator of abscisic acid (ABA) responses, including resistance to drought and freezing as well as stomatal closure regulation. Mediates resistance to the bacterial necrotroph pathogen Erwinia carotovora subsp. carotovora and promotes the induction of marker genes for systemic acquired resistance (SAR).

Lma13658.t1  ASNA1_CHLRE
ATPase required for the post-translational delivery of tail-anchored (TA) proteins to the chloroplast. Required for the accumulation of TOC34, an essential component of the outer chloroplast membrane translocon (TOC) complex. Recognizes and selectively binds the transmembrane domain of TA proteins in the cytosol. This complex then targets to chloroplast, where the tail-anchored protein is released for insertion. This process is regulated by ATP binding and hydrolysis.

Lma21263.t1  XTH24_ARATH
Catalyzes xyloglucan endohydrolysis (XEH) and/or endotransglycosylation (XET). Cleaves and religates xyloglucan polymers, an essential constituent of the primary cell wall, and thereby participates in cell wall construction of growing tissues. May be required during development to modify the walls of cells under mechanical stress.

Lma22972.t1  MSL6_ARATH
Mechanosensitive channel that opens in response to stretch forces in the membrane lipid bilayer.

Lma20766.t1  GAUT3_ARATH
May be involved in pectin and/or xylans biosynthesis in cell walls.

Lma20768.t1  GAUT3_ARATH
May be involved in pectin and/or xylans biosynthesis in cell walls.

Lma21540.t1  CDPKM_ARATH
May play a role in signal transduction pathways that involve calcium as a second messenger.

Lma21541.t1  CDPKM_ARATH
May play a role in signal transduction pathways that involve calcium as a second messenger.

Lma10785.t1  MSL6_ARATH
Mechanosensitive channel that opens in response to stretch forces in the membrane lipid bilayer.
| Lma05615.t1    | SNL4_ARATH    | Acts as a transcriptional repressor. Plays roles in regulating gene expression and genome stability (By similarity). |
| Lma22448.t1    | SNL4_ARATH    | Acts as a transcriptional repressor. Plays roles in regulating gene expression and genome stability (By similarity). |
| Lma22179.t1    | ATX4_ARATH    | Histone methyltransferase. |
| Lma24547.t1    | ATX5_ARATH    | Histone methyltransferase. |
| Lma10784.t1    | PRB1_ARATH    | Probably involved in the defense reaction of plants against pathogens. |
| Lma21102.t1    | PRB1_ARATH    | Probably involved in the defense reaction of plants against pathogens. Produces CoA thioesters of a variety of hydroxy- and methoxy-substituted cinnamic acids, which are used to synthesize several phenylpropanoid-derived compounds, including anthocyanins, flavonoids, isoflavonoids, coumarins, lignin, suberin and wall-bound phenolics. |
| Lma00244.t1    | 4CL2_ARATH    | Produces CoA thioesters of a variety of hydroxy- and methoxy-substituted cinnamic acids, which are used to synthesize several phenylpropanoid-derived compounds, including anthocyanins, flavonoids, isoflavonoids, coumarins, lignin, suberin and wall-bound phenolics. |
| Lma15368.t1    | 4CL4_ARATH    | Produces CoA thioesters of a variety of hydroxy- and methoxy-substituted cinnamic acids, which are used to synthesize several phenylpropanoid-derived compounds, including anthocyanins, flavonoids, isoflavonoids, coumarins, lignin, suberin and wall-bound phenolics. |
| Lma00102.t1    | PME2_ARATH    | Acts in the modification of cell walls via demethylesterification of cell wall pectin. Catalytic subunit of cellulose synthase terminal complexes ('rosettes'), required for beta-1,4-glucan microfibril crystallization, a major mechanism of the cell wall formation. Involved in the secondary cell wall formation. Required for the xylem cell wall thickening. Catalytic subunit of cellulose synthase terminal complexes ('rosettes'), required for beta-1,4-glucan microfibril crystallization, a major mechanism of the cell wall formation. Involved in the secondary cell wall formation. Required for the xylem cell wall thickening. Catalytic subunit of cellulose synthase terminal complexes ('rosettes'), required for beta-1,4-glucan microfibril crystallization, a major mechanism of the cell wall formation. Involved in the secondary cell wall formation. Required for the xylem cell wall thickening. Catalytic subunit of cellulose synthase terminal complexes ('rosettes'), required for beta-1,4-glucan microfibril crystallization, a major mechanism of the cell wall formation. Involved in the secondary cell wall formation. Required for the xylem cell wall thickening. Catalytic subunit of cellulose synthase terminal complexes ('rosettes'), required for beta-1,4-glucan microfibril crystallization, a major mechanism of the cell wall formation. Involved in the secondary cell wall formation. Required for the xylem cell wall thickening. Catalytic subunit of cellulose synthase terminal complexes ('rosettes'), required for beta-1,4-glucan microfibril crystallization, a major mechanism of the cell wall formation. Involved in the secondary cell wall formation. Required for the xylem cell wall thickening. |
| Lma15231.t1    | CESA4_ARATH   | Probable ubiquitin-protein ligase which is mainly involved pre-mRNA splicing and DNA repair (By similarity). Component of the MAC complex that probably regulates defense responses through transcriptional control and thereby is essential for plant innate immunity. |
| Lma17690.t1    | VP241_ARATH   | Component of the ESCRT-III complex, which is required for multivesicular bodies (MVBs) formation and sorting of endosomal cargo proteins into MVBs. The ESCRT-III complex is probably involved in the concentration of MVB cargo (By similarity). |
| Lma07599.t1    | HR2_ARATH     | Probable disease resistance (R) protein. |
| Lma07600.t1    | HR2_ARATH     | Probable disease resistance (R) protein. |
| Lma15105.t1    | PR19B_ARATH   | Component of the ESCRT-III complex, which is required for multivesicular bodies (MVBs) formation and sorting of endosomal cargo proteins into MVBs. The ESCRT-III complex is probably involved in the concentration of MVB cargo (By similarity). |
| Lma15105.t1    | PR19B_ARATH   | Component of the ESCRT-III complex, which is required for multivesicular bodies (MVBs) formation and sorting of endosomal cargo proteins into MVBs. The ESCRT-III complex is probably involved in the concentration of MVB cargo (By similarity). |
| Gene ID     | Accession   | Description                                                                                           |
|------------|-------------|-------------------------------------------------------------------------------------------------------|
| Lma07921.t1| ARR9_ARATH  | Functions as response regulator involved in His-to-Asp phosphorelay signal transduction system.       |
|            |             | Phosphorylation of the Asp residue in the receiver domain activates the ability of the protein to promote |
|            |             | the transcription of target genes. Type-A response regulators seem to act as negative regulators of the   |
|            |             | cytokinin signaling.                                                                                 |
|            | Lma24339.t1| ARR9_ARATH                                                                                           |
|            |             | Functions as response regulator involved in His-to-Asp phosphorelay signal transduction system.       |
|            |             | Phosphorylation of the Asp residue in the receiver domain activates the ability of the protein to promote |
|            |             | the transcription of target genes. Type-A response regulators seem to act as negative regulators of the   |
|            |             | cytokinin signaling.                                                                                 |
| Lma06261.t1| RFS4_ARATH  | Transglycosidase operating by a ping-pong reaction mechanism. Involved in the synthesis of raffinose, a |
|            |             | major soluble carbohydrate in seeds, roots and tubers (By similarity).                                |
| Lma10737.t1| RFS4_ARATH  | Transglycosidase operating by a ping-pong reaction mechanism. Involved in the synthesis of raffinose, a |
|            |             | major soluble carbohydrate in seeds, roots and tubers (By similarity).                                |
| Lma17915.t1| RK3B_ARATH  | One of the primary rRNA binding proteins, it binds directly near the 3'-end of the 23S rRNA, where it    |
|            |             | nucleates assembly of the 50S subunit.                                                                |
| Lma25041.t1| RK3B_ARATH  | One of the primary rRNA binding proteins, it binds directly near the 3'-end of the 23S rRNA, where it    |
|            |             | nucleates assembly of the 50S subunit.                                                                |
| Lma12130.t2| RFI2_ARATH  | Mediates phytochrome (phyA and phyB)-controlled seedling deetiolation responses such as hypocotyl       |
|            |             | elongation in response to red and far-red light (, ). Required for light-induced expression of LHCb3 and |
|            |             | CHALCONE SYNTHASE (CHS)Regulates negatively CONSTANS (CO) and FLOWERING LOCUS T (FT) expression and     |
|            |             | photoperiodic flowering                                                                               |
| Lma11554.t1| CHR7_ARATH  | Chromatin remodeling factor that represses the expression of embryonic trait genes upon and after seed  |
|            |             | germination and thus enables the developmental switch to post-germinative growth.                      |
| Lma11671.t1| ALFL1_ARATH | Histone-binding component that specifically recognizes H3 tails trimethylated on 'Lys-4' (H3K4me3),     |
|            |             | which mark transcription start sites of virtually all active genes.                                   |
| Lma11672.t1| ALFL1_ORYSJ | Histone-binding component that specifically recognizes H3 tails trimethylated on 'Lys-4' (H3K4me3),     |
|            |             | which mark transcription start sites of virtually all active genes.                                   |
| Lma10862.t1| SOT7_ARATH  | Sulfortransferase that utilizes 3'-phospho-5'-adenylyl sulfate (PAPS) as sulfonate donor.              |
| Lma10863.t1| SOT7_ARATH  | Sulfortransferase that utilizes 3'-phospho-5'-adenylyl sulfate (PAPS) as sulfonate donor.              |
| Lma01051.t1| ZAT7_ARATH  | Probable transcription factor involved in oxidative stress response.                                  |
| Lma01052.t1| ZAT9_ARATH  | Probable transcription factor that may be involved in stress responses.                               |
Lma00566.t1 MTM1_ARATH
Involved in the mitochondrial activation of MSD1 by specifically facilitating insertion of the essential manganese cofactor. Has the ability to activate iron regulon in an iron-dependent manner.

Lma24291.t1 MTM1_ARATH
Involved in the mitochondrial activation of MSD1 by specifically facilitating insertion of the essential manganese cofactor. Has the ability to activate iron regulon in an iron-dependent manner.

Lma24858.t1 TIL_ARATH
Involved in basal (BT) and acquired thermotolerance (AT), probably by preventing plasma membrane lipids peroxidation induced by severe heat-shock (HS) (, ). Lipocalin that confers protection against oxidative stress caused by heat, freezing, paraquat and light (, ). Confers resistance to high salt (NaCl) levels, probably by protecting chloroplasts from ion toxicity via ion homeostasis maintenance (, ). Required for seed longevity by insuring polyunsaturated lipids integrity.

Lma24859.t1 TIL_ARATH
Involved in basal (BT) and acquired thermotolerance (AT), probably by preventing plasma membrane lipids peroxidation induced by severe heat-shock (HS) (, ). Lipocalin that confers protection against oxidative stress caused by heat, freezing, paraquat and light (, ). Confers resistance to high salt (NaCl) levels, probably by protecting chloroplasts from ion toxicity via ion homeostasis maintenance (, ). Required for seed longevity by insuring polyunsaturated lipids integrity.

Lma04613.t1 CDPKF_ARATH
May play a role in signal transduction pathways that involve calcium as a second messenger.

Lma04614.t1 CDPKF_ARATH
May play a role in signal transduction pathways that involve calcium as a second messenger.

Lma04080.t1 VQ11_ARATH
May modulate WRKY transcription factor activities.

Lma05255.t1 VQ11_ARATH
May modulate WRKY transcription factor activities.

Lma25903.t1 RDR5_ARATH
Probably involved in the RNA silencing pathway and required for the generation of small interfering RNAs (siRNAs).

Lma26713.t1 PILR1_ARATH
Reductase involved in lignan biosynthesis. Unlike conventional pinoresinol reductases that can reduce both pinoresinol and lariciresinol, PRR1 shows a strict substrate preference toward pinoresinol. Active on both (+) and (-)-pinoresinol. Abstracts the 4R-hydride from the NADPH cofactor during catalysis.

Lma08747.t1 SPL5_ARATH
Trans-acting factor that binds specifically to the consensus nucleotide sequence 5'-TNCGTACAA-3' of AP1 promoter. Promotes both vegetative phase change and flowering.

Lma10561.t1 PSK3_ARATH
Promotes plant cell differentiation, organogenesis and somatic embryogenesis as well as cell proliferation.

Lma10265.t1 MORF9_ARATH
Involved in organellar RNA editing. Required for the processing of multiple editing sites in plastids.
Lma09902.t2  PAE5_ARATH  Hydrolyzes acetyl esters in homogalacturonan regions of pectin. In type I primary cell wall, galacturonic acid residues of pectin can be acetylated at the O-2 and O-3 positions. Decreasing the degree of acetylation of pectin gels in vitro alters their physical properties.

Lma09353.t7  ERD2B_ARATH  Determines the specificity of the luminal endoplasmic reticulum protein retention system. Required for the retro-transport of calreticulin-3 (CRT3) from the Golgi to the ER. Specifically required for elongation factor Tu receptor (EFR) function in response to the pathogen-associated molecular pattern (PAMP) elf18.

Lma10586.t1  LEUC_ARATH  Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate.

Lma10383.t1  ACA1_ARATH  This magnesium-dependent enzyme catalyzes the hydrolysis of ATP coupled with the translocation of calcium from the cytosol out of the cell or into organelles.

Lma10120.t1  RNS1_ARATH  May remobilize phosphate, particularly when cells senesce or when phosphate becomes limiting.

Lma09467.t2  IAA14_ARATH  Aux/IAA proteins are short-lived transcriptional factors that function as repressors of early auxin response genes at low auxin concentrations. Repression is thought to result from the interaction with auxin response factors (ARFs), proteins that bind to the auxin-responsive promoter element (AuxRE). Formation of heterodimers with ARF proteins may alter their ability to modulate early auxin response genes expression.

Lma08678.t1  VRN2_ARATH  Polycomb group (PcG) protein. Plays a central role in vernalization by maintaining repressed the homeotic gene FLC, a floral repressor, after a cold treatment. PcG proteins act by forming multiprotein complexes, which are required to maintain the transcriptionally repressive state of homeotic genes throughout development. PcG proteins are not required to initiate repression, but to maintain it during later stages of development. They probably act via the methylation of histones, rendering chromatin heritably changed in its expressibility. Associates constitutively along the whole FLC locus.

Lma08633.t1  PER41_ARATH  Removal of H(2)O(2), oxidation of toxic reductants, biosynthesis and degradation of lignin, suberization, auxin catabolism, response to environmental stresses such as wounding, pathogen attack and oxidative stress. These functions might be dependent on each isozyme/isoform in each plant tissue.

Lma09045.t1  LUP2_ARATH  Multifunctional enzyme that converts oxidosqualene to nine different triterpenes, mainly lupeol, beta-amyrin and alpha-amyrin in a 15:50:30 ratio.
Component of the eukaryotic translation initiation factor 3 (eIF-3) complex, which is involved in protein synthesis of a specialized repertoire of mRNAs and, together with other initiation factors, stimulates binding of mRNA and methionyl-tRNAi to the 40S ribosome. The eIF-3 complex specifically targets and initiates translation of a subset of mRNAs involved in cell proliferation.

Prohibitin probably acts as a holdase/unfoldase for the stabilization of newly synthesized mitochondrial proteins.

Aspartic proteinase that can use azocasein as substrate and regulates endogenous sugar levels (e.g. sucrose, glucose and fructose) by modulating starch accumulation and remobilization. Involved in the maintenance of the shoot apical meristem (SAM). Influences general morphology and development.

This is a component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is part of the mitochondrial respiratory chain. This protein may mediate formation of the complex between cytochromes c and c1.

Component of the PAM complex, a complex required for the translocation of transit peptide-containing proteins from the inner membrane into the mitochondrial matrix in an ATP-dependent manner.

Probable lipid transfer protein (LTP). May improve freezing survival. Seems to control the flowering process and lignin synthesis. Confers resistance to Botrytis cinerea.

Catalytic subunit of the error prone DNA polymerase zeta. Involved in damage-tolerance mechanisms through translesion DNA synthesis.

Sulfotransferase that utilizes 3'-phospho-5'-adenylyl sulfate (PAPS) as sulfonate donor to catalyze the sulfate conjugation of desulfo-glucosinolates (dsGSs), the final step in the biosynthesis of the glucosinolate core structure. Substrate preference is desulfo-benzyl glucosinolate > desulfo-6-methylthiohexyl glucosinolate. Increased specific activity with increasing chain length of desulfo-glucosinolate derived from methionine. Preferred substrate is desulfo-8-methylthiooctyl glucosinolate. May play a role in meristem function, and may be involved in maintaining cells in an undifferentiated, meristematic state, and its expression disappears at the same time the shoot apex undergoes the transition from vegetative to reproductive development. Positive regulator of LATERAL ORGAN BOUNDARIES (LOB) Probably binds to the DNA sequence 5’-TGAC-3’ Able to traffic from the L1 to the L2/L3 layers of the meristem, presumably through plasmodesmata
ATP-dependent 3'-5' DNA helicase, component of the general transcription and DNA repair factor IIH (TFIIH) core complex, which is involved in general and transcription-coupled nucleotide excision repair (NER) of damaged DNA and, when complexed to CAK, in RNA transcription by RNA polymerase II. In NER, TFIIH acts by opening DNA around the lesion to allow the excision of the damaged oligonucleotide and its replacement by a new DNA fragment. The ATPase activity of XPB, but not its helicase activity, is required for DNA opening. In transcription, TFIIH has an essential role in transcription initiation. When the pre-initiation complex (PIC) has been established, TFIIH is required for promoter opening and promoter escape. The ATP-dependent helicase activity of XPB is required for promoter opening and promoter escape. Phosphorylation of the C-terminal tail (CTD) of the largest subunit of RNA polymerase II by the kinase module CAK controls the initiation of transcription (By similarity). Required during the early stages of development, including seed germination.

Component of the ribosome, a large ribonucleoprotein complex responsible for the synthesis of proteins in the cell. The small ribosomal subunit (SSU) binds messenger RNAs (mRNAs) and translates the encoded message by selecting cognate aminoacyl-transfer RNA (tRNA) molecules. The large subunit (LSU) contains the ribosomal catalytic site termed the peptidyl transferase center (PTC), which catalyzes the formation of peptide bonds, thereby polymerizing the amino acids delivered by tRNAs into a polypeptide chain. The nascent polypeptides leave the ribosome through a tunnel in the LSU and interact with protein factors that function in enzymatic processing, targeting, and the membrane insertion of nascent chains at the exit of the ribosomal tunnel.

Transcriptional activator that binds specifically to the DNA sequence 5'-[AG]GATT-3'. Functions as a response regulator involved in His-to-Asp phosphorelay signal transduction system. Phosphorylation of the Asp residue in the receiver domain activates the ability of the protein to promote the transcription of target genes. Could directly activate some type-A response regulators in response to cytokinins. Regulates SHY2 by binding to its promoter. Involved in the root-meristem size determination through the regulation of cell differentiation.

Transcriptional regulator that specifically binds 5'-GATA-3' or 5'-GAT-3' motifs within gene promoters.

Prohibitin probably acts as a holdase/unfoldase for the stabilization of newly synthesized mitochondrial proteins.
RNA-binding component of the eukaryotic translation initiation factor 3 (eIF-3) complex, which is involved in protein synthesis of a specialized repertoire of mRNAs and, together with other initiation factors, stimulates binding of mRNA and methionyl-tRNAi to the 40S ribosome. The eIF-3 complex specifically targets and initiates translation of a subset of mRNAs involved in cell proliferation.

Proteoglycan that seems to be implicated in diverse developmental roles such as differentiation, cell-cell recognition, embryogenesis and programmed cell death.

Probably not redundant with AED1 and not involved in restriction of salicylic acid (SA) or systemic acquired resistance (SAR) signaling.

Transcription factor that specifically binds AT-rich DNA sequences related to the nuclear matrix attachment regions (MARs).

Contributes to pathogen-associated molecular pattern (PAMP)-triggered immunity (PTI) signaling and defense responses downstream of FLS2. Acts additively with BIK1 in PTI defenses. Seems not required for flg22-induced MAPK activation (Probable). Required for Pep1-induced defenses. Pep1 is an endogenous elicitor that potentiates PAMP-inducible plant responses.

Probable transcription factor that may be involved in stress responses.

Involved in ubiquitination and subsequent proteasomal degradation of target proteins. Together with CUL1, RBX1 and a F-box protein, it forms a SCF E3 ubiquitin ligase complex. The functional specificity of this complex depends on the type of F-box protein. In the SCF complex, it serves as an adapter that links the F-box protein to CUL1 (By similarity).

Myosin heavy chain that is required for the cell cycle-regulated transport of various organelles and proteins for their segregation. Functions by binding with its tail domain to receptor proteins on organelles and exerting force with its N-terminal motor domain against actin filaments, thereby transporting its cargo along polarized actin cables (By similarity).

Necessary for protein translocation in the endoplasmic reticulum.

Cytokinin-activating enzyme working in the direct activation pathway. Phosphoribohydrolase that converts inactive cytokinin nucleotides to the biologically active free-base forms (By similarity).

Required for the promotion of megasporogenesis, or promotion of germ cell formation from somatic precursor cells. Acts redundantly with WIH1. Functions in a genetic pathway downstream of SPL/NZZ and WUS and together with TRN2 in promoting megasporogenesis.

Membrane-anchored myosin receptors that define a distinct, plant-specific transport vesicle compartment.
| Gene ID   | Description                                                                                                                                                                                                 |
|----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Lma19797.t1 HUMS_ARATH | Involved in sesquiterpene (C15) biosynthesis. The major products are beta-caryophyllene and alpha-humulene. Does not convert geranyl diphosphate (GPP) to any monoterpenes. |
| Lma19892.t1 FIP37_ARATH | Probable regulatory subunit of the N6-methyltransferase complex, a multiprotein complex that mediates N6-methyladenosine (m6A) methylation at the 5'-[AG]GAC-3' consensus sites of some mRNAs. Associates with MTA, MTB, VIR and HAKAI to form the m6A writer complex which is essential for adenosine methylation at specific mRNA sequences. N6-methyladenosine (m6A) plays a role in mRNA stability, processing, translation efficiency and editing. Essential protein required during endosperm development and embryogenesis. Involved in endoreduplication, especially in trichomes. May play a role in splicing events. |
| Lma18681.t1 NACA1_ARATH | May promote appropriate targeting of ribosome-nascent polypeptide complexes. Plays a role in RNA transcription or processing during stress. Binds RNAs and DNAs sequence with a preference to single-stranded nucleic acids. Displays strong affinity to poly(U) and poly(G) sequence. Involved in mRNA alternative splicing of numerous targets by modulating splice site selection. Negatively regulates the circadian oscillations of its own transcript as well as RBG8 transcript. Forms an interlocked post-transcriptional negative feedback loop with the RBG8 autoregulatory circuit. Both proteins negatively autoregulate and reciprocally crossregulate by binding to their pre-mRNAs and promoting unproductive splicing coupled to degradation via the NMD pathway. Involved in the regulation of abscisic acid and stress responses. Affects the growth and stress tolerance under high salt and dehydration stress conditions, and also confers freezing tolerance, particularly via the regulation of stomatal opening and closing in the guard cells. Exhibits RNA chaperone activity during the cold adaptation process. Involved in the export of mRNAs from the nucleus to the cytoplasm under cold stress conditions. Target of the Pseudomonas syringae type III effector HopU1, which could probably be involved in plant innate immunity. Component of the flowering autonomous pathway which promotes floral transition, at least partly by down-regulating FLC. |
| Lma20712.t1 RBG7_ARATH | Collaborates with REM4.2 to positively regulate the BCTV and BSCTV susceptibility. |
Lma20595.t1  XXT1_ARATH  Xylosyltransferase specific to UDP-D-xylose that accepts both cellopentaose and cellohexaose as substrates, with a better use of cellohexaose, to produce xyloglucan. Adds preferentially the first xylosyl residue to the fourth glucosyl residue from the reducing end of both acceptors. Transfer one xylose mainly to the second glucose residue from the non-reducing end. The acceptor should have a minimum of four glucose residues.

Lma19641.t1  TGT1_ARATH  Probable transcription factor that binds specifically to the core DNA sequence 5′-GGTTAA-3′. May act as a molecular switch in response to light signals.

Molecular chaperone (, , ). May act as a suppressor of FtsH-mediated thylakoid membrane biogenesis and may enhance photoinhibitionSeems not involved in chloroplastic protein importProbable component of the TIC-associated stromal import motor involved in inner membrane translocationHas an ATPase activity, but no ADPase activityInteracts with transit peptides with a positional preference (, ).

Localization of the signal sequence at the N-terminal end of a protein seems mandatory for interaction to take place

Lma20637.t1  LFG2_ARATH  Regulates the brassinosteroid (BR) signaling pathway that mediates cell elongation and organ morphogenesis

Lma20637.t1  LFG2_ARATH  (Microbial infection) May prevent cell death upon A.alternata f.sp. lycopersici (AAL) toxin treatment.

Lma20315.t1  AGP23_ARATH  Proteoglycan that seems to be implicated in diverse developmental roles such as differentiation, cell-cell recognition, embryogenesis and programmed cell death.

Lma19275.t1  HIP6_ARATH  Heavy-metal-binding protein. Involved in the maintenance of heavy metal homeostasis and/or in detoxification.

Lma18790.t1  BIG1D_ARATH  Involved in auxin transport. Regulator of the auxin signaling pathway.

Extracellular signal peptide secreted by differentiated root cells that regulates root cell fate. Acts with ACR4 as a ligand-receptor pair in a signal transduction pathway, coordinating movement of the root tip and organization of cell divisions in the root meristem. Promotes cell differentiation in the distal root meristem in a dose-dependent manner, especially the transition from columella stem cells (CSC) daughters into columella cells (CCs). Induces ACR4 expression in root quiescent center (QC). Involved in WUX5 QC-specific expression pattern regulation.

May be required for accurate chromosome segregation. Required for proper maturation of seed storage proteins. Forms a complex with MAG2, MIP2 and MIP3 on the endoplasmic reticulum that may be responsible for efficient transport of seed storage proteins.
Lma13269.t1  PME1_ARATH  Acts in the modification of cell walls via demethylesterification of cell wall pectin (By similarity). Demethylates protein phosphatase 2A (PP2A) that have been reversibly carboxymethylated by LCMT1. Acts as negative regulators of genes involved in salt stress response.

Lma14343.t2  SCAB2_ARATH  Probable plant-specific actin binding protein that bundles and stabilizes microfilaments (MFs).

Lma14396.t1  ZED1_ARATH  Probable non-functional pseudokinase required for recognition of the Pseudomonas syringae type III effector HopZ1a by ZAR1. May function as a decoy to trap HopZ1a in the ZAR1 complex for recognition by the plant immune system. Required for the promotion of megasporogenesis, or promotion of germ cell formation from somatic precursor cells. Acts redundantly with WIH1. Functions in a genetic pathway downstream of SPL/NZZ and WUS and together with TRN2 in promoting megasporogenesis.

Lma14372.t1  WIH2_ARATH  Required for the promotion of megasporogenesis, or promotion of germ cell formation from somatic precursor cells. Acts redundantly with WIH1. Functions in a genetic pathway downstream of SPL/NZZ and WUS and together with TRN2 in promoting megasporogenesis.

Lma14137.t1  PUB2_ARATH  Functions as an E3 ubiquitin ligase.

Lma12479.t1  FRO3_ARATH  Ferric chelate reductase involved in iron reduction in roots. May participate in the transport of electrons to a Fe(3+) ion via FAD and heme intermediates.

Lma14074.t1  PABN2_ARATH  Involved in the 3'-end formation of mRNA precursors (pre-mRNA) by the addition of a poly(A) tail of 200-250 nt to the upstream cleavage product. Stimulates poly(A) polymerase (PAPOLA) conferring processivity on the poly(A) tail elongation reaction and controls the poly(A) tail length. Increases the affinity of poly(A) polymerase for RNA. Binds to poly(A) and to poly(G) with high affinity. May protect the poly(A) tail from degradation.

Lma13458.t1  RPK1_ARATH  Involved in the main abscisic acid-mediated (ABA) signaling pathway and in early ABA perception. Together with RPK2, required for pattern formation along the radial axis (e.g. the apical embryonic domain cell types that generate cotyledon primordia), and the apical-basal axis (e.g. differentiation of the basal pole during early embryogenesis).

Lma13193.t1  MCES1_ARATH  mRNA-capping methyltransferase that methylates the N7 position of the added guanosine to the 5'-cap structure of mRNAs. Binds RNA containing 5'-terminal GpppC (By similarity).
Lma14148.t1  ERF10_ARATH
Probably acts as a transcriptional activator. Binds to the GCC-box pathogenesis-related promoter element. May be involved in the regulation of gene expression by stress factors and by components of stress signal transduction pathways (By similarity).

Lma13276.t1  P2C56_ARATH
Key component and repressor of the abscisic acid (ABA) signaling pathway that regulates numerous ABA responses, such as stomatal closure, osmotic water permeability of the plasma membrane (Pos), drought-induced resistance and rhizogenesis, response to glucose, high light stress, seed germination and inhibition of vegetative growth. During the stomatal closure regulation, modulates the inward calcium-channel permeability as well as the actin reorganization in guard cells in response to ABA. Involved in the resistance to the bacterial pathogen Pseudomonas syringae pv. tomato. Controls negatively fibrillin expression that is involved in mediating ABA-induced photoprotection. May be involved in ABA content regulation. Plays a role in the Pro accumulation in response to reduced water availability (low water potential). Required for the ABA negative regulation of the ethylene-induced hyponastic growth. Involved in acquired thermostolerance of root growth and seedling survival. Activates/represses SRK2E/OST1 in response to ABA-dependent stimuli, especially in stomata closure regulation involving SLAC1. Represses MAPK18 activity and promotes MAPK18 degradation by the proteosome pathway upon abscisic acid (ABA) treatment Represses KIN10 activity by the specific dephosphorylation of its T-loop Thr-198, leading to a poststress inactivation of SnRK1 signaling

Lma13793.t1  VIP4_ARATH
Component of the PAF1 complex (PAF1C) which is involved in histone modifications such as methylation on histone H3 'Lys-4' (H3K4me3) Involved in regulation of flowering time. Required for the expression of the flowering repressor and MADS box gene FLC Involved in the control of seed dormancy and germination Binds and presumably selects ubiquitin-conjugates for destruction. Prefers multiubiquitin chains rather than single ubiquitins, with a binding affinity for 'Lys-48'-linked ubiquitin chains. Acts as a ubiquitin receptor that associates with the 26S proteasomal docking subunit RPN10 for the indirect recognition of ubiquitinated substrates of ubiquitin/26S proteasome-mediated proteolysis (UPP).

Lma13646.t1  DSK2A_ARATH

Lma14376.t1  ATS3A_ARATH
May play a role during embryo development.
Transcription activator involved in the activation of cuticular wax biosynthesis under drought stress. Binds directly to DNA consensus sequences found in the promoters of genes encoding very-long-chain fatty acid-condensing enzymes involved in cuticular wax biosynthesis. Functions together with MYB94 in the activation of cuticular wax biosynthesis. Involved in drought stress response through abscisic acid (ABA) signaling. Mediates ABA signals that enhance plant resistance to drought by reducing stomatal opening. Mediates ABA-auxin cross-talk to regulate lateral root growth under drought stress conditions. Involved in the regulation of ABA biosynthesis and ABA-dependent seed dormancy state. Binds to the promoters of NCED2 and NCED6, which are enzymes catalyzing the first step of ABA biosynthesis. Regulates seed germination by controlling the expression of ABI4, a repressor of lipid breakdown during seed germination. Binds to the promoter of LTP3 and transactivates LTP3 gene in response to drought stress and freezing. Involved in cold stress response. Binds directly to the promoters of heptahelical protein (HHP) genes in response to cold stress. HHPs modulate the expression of SCRM/ICE1, SCRM2/ICE2 and CAMTA3, which are upstream regulators of cold-responsive C-repeat-binding factors (CBFs). Involved in defense responses against the bacterial pathogen Pseudomonas syringae. May act as a molecular link that mediates cross-talks between ABA and salicylate. Involved in a crosstalk between the circadian clock and ABA signaling. Binds directly to the promoter of APRR1/TOC1 to activate its expression.

Plays a role in protein import into the endoplasmic reticulum (ER). May function as chaperone docking protein during post-translational protein translocation into the ER. Chaperone receptor mediating Hsp70-dependent protein targeting to chloroplasts. Interacts specifically with some chloroplast precursors, but not with mitochondrial precursors. Able to select precursors for delivery to the chloroplast translocase independently of Hsp70.

Prohibitin probably acts as a holdase/unfoldase for the stabilization of newly synthesized mitochondrial proteins.

Oxidizes N-terminal cysteine residues, thus preparing the protein for N-end rule pathway-mediated proteasomal degradation.

Probable carboxypeptidase.

May play an important role in maintaining the flux of carbon towards starch formation in endosperm. May also be involved in a sugar-sensing pathway.
| GenBank ID | Accession | Description |
|-----------|-----------|-------------|
| Lma13067.t1 | RAN4_ARATH | GTP-binding protein involved in nucleocytoplasmic transport. Required for the import of protein into the nucleus and also for RNA export. Involved in chromatin condensation and control of cell cycle (By similarity). |
| Lma13332.t1 | RA51D_ARATH | Involved in the homologous recombination repair (HRR) pathway of double-stranded DNA breaks arising during DNA replication or induced by DNA-damaging agents. |
| Lma14053.t1 | HIT4_ARATH | Essential protein required for basal thermotolerance, especially during heat-induced chromocentre decondensation, thus regulating transcriptional gene silencing (TGS). |
| Lma13548.t1 | CYP59_ARATH | PPIases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides. Influences somehow regulation of RNA pol II (CTD) phosphorylation. Binds RNA with preferences for GC-rich sequences. Probably involved in activities connecting transcription and pre-mRNA processing. Involved in brassinostroid response. |
| Lma13325.t1 | CD27B_ARATH | Component of the anaphase promoting complex/cyclosome (APC/C), a cell cycle-regulated E3 ubiquitin-protein ligase complex that controls progression through mitosis and the G1 phase of the cell cycle. The APC/C complex controls several key steps in the cell cycle by mediating ubiquitination and subsequent degradation of target proteins such as cyclins. The APC/C complex is required for the female gametophyte development and is involved in several aspect of development by controlling cell division and cell elongation. Involved in the control of endoreduplication. Functionally redundant with CDC27A in the control of gametophyte development. |
| Lma25648.t1 | COV1_ARATH | Involved in the regulation of vascular patterning in the stem, probably by negatively regulating the differentiation of vascular tissue. |
| Lma22741.t1 | TI10B_ARATH | Repressor of jasmonate responses. Jasmonoyl-isoleucine (JA-Ile) specifically promotes COII-TIFY10B/JAZ2 interaction. Activated by MYC2, MYC3 and MYC4 transcription factors. |
| Lma22377.t1 | AHL8_ARATH | Transcription factor that specifically binds AT-rich DNA sequences related to the nuclear matrix attachment regions (MARs). |
| Lma22154.t1 | DNJ10_ARATH | Have a continuous role in plant development probably in the structural organization of compartments. |
| Lma20981.t1 | CDPKI_ARATH | May play a role in signal transduction pathways that involve calcium as a second messenger. Maybe involved in both the vernalization and photoperiod pathways by regulating gene expression. Binds preferentially to dimethylated histone H3 'Lys-9' (H3K9me2). Promotes flowering in non-inductive photoperiods (e.g. short days) through the maintenance of the epigenetically repressed state of MAF5 via H3K9me2 and plant homeodomain / polycomb repressive complex 2 (PHD-PRC2)-dependent H3K27me3. |
Involved in the spatial control of cell division, patterning and differentiation of Arabidopsis root epidermal cells. Could be part of a complex that negatively modulates GLABRA2 and CAPRICE expression via the maintenance of a repressor histone H3 epigenetics status of the GL2 and CPC promoters.

Transports methylammonium or ammonium in yeast cells, preferentially at high medium pH. May participate in vacuolar compartmentation and detoxification of ammonium.

Peptide hormone required for contiguous Casparian strip diffusion barrier formation in roots via the regulation of CASPs protein expression and distribution in a GSO1-GSO2 signaling pathway. The Casparian strip is required for ion homeostasis (e.g. iron and potassium ions).

Probable plus end-directed motor protein that functions in the NACK-PQR (ANP3-MKK6-MPK4) MAP kinase signaling pathway, which is essential for somatic cell cytokinesis, especially for the cell-plate formation and its expansion. May regulate the activity and the localization of ANP3, probably by association through the non-catalytic region of the kinase. Functionally redundant with NACK1 and essential to promote the progression of cytokinesis and for cellularization (formation of the cell plate) during microgametogenesis and megagametogenesis.

Required for normal spindle orientation at male meiosis II and normal formation of tetrad of microspores. Not involved in female meiosis.

Involved in indole glucosinolate biosynthesis. Catalyzes hydroxylation reactions of the glucosinolate indole ring. Converts indol-3-yl-methylglucosinolate (I3M) to 4-hydroxy-indol-3-yl- methylglucosinolate (4OH-I3M) and/or 1-hydroxy-indol-3-yl- methylglucosinolate (1OH-I3M) intermediates. These hydroxy intermediates are converted to 4-methoxy-indol-3-yl- methylglucosinolate (4MO-I3M) and 1-methoxy-indol-3-yl- methylglucosinolate (1MO-I3M) by indole glucosinolate methyltransferase 1 and 2 (IGMT1 and IGMT2).

Molecular chaperone; assists the folding of proteins upon ATP hydrolysis. Known to play a role, in vitro, in the folding of actin and tubulin.

Required for transport of secretory proteins from the Golgi complex (By similarity). Catalyzes the transfer of phosphatidylinositol and phosphatidylcholine between membranes in vitro. Plays a role in root hair tip elongation as a key regulator of polarized membrane trafficking. May promote the PtdIns(4,5)P2 synthesis and organization in root hair membrane.
Disease resistance (R) protein that specifically recognizes the avrPphB type III effector avirulence protein from Pseudomonas syringae. Also confers resistance against Hyaloperonospora parasitica (downy mildew). Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. Requires PBS1 to trigger the defense reaction against avrPphB. In case of infection by Pseudomonas syringae, AvrPphB triggers RPS5-mediated defense mechanism via the cleavage of PBS1, suggesting that the cleavage of PBS1 could trigger an exchange of ADP for ATP, thereby activating RPS5. May function as a fine-tuned sensor of alterations in the structure of the effector target PBS1.

Transcription factor. Interacts specifically with the W box (5'- (T)TGAC[CT]-3'), a frequently occurring elicitor-responsive cis-acting element (By similarity).

Possesses antifungal activity sensitive to inorganic cations.

May act as an acid--thiol ligase that activates carboxylic acids by forming acyl-CoAs.

Myosin heavy chain that is required for the cell cycle-regulated transport of various organelles and proteins for their segregation. Functions by binding with its tail domain to receptor proteins on organelles and exerting force with its N-terminal motor domain against actin filaments, thereby transporting its cargo along polarized actin cables.

Probable cyclin-dependent protein kinase (CDK) inhibitor that functions as a repressor of mitosis in the endoreduplication cell cycle (By similarity). May inhibit CDKA-1/CYCD complexes during S-phase, preventing the re-initiation of DNA replication.

Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated proteins.

Has phosphatase activity toward Ins(1,4,5)P3 and Ins(1,3,4,5)P4, but not toward Ins(1,4)P2, Ins(1)PSeems to be involved in the abscisic acid (ABA) signaling pathway. Could also be able to hydrolyze PtdIns(4,5)P2 and PtdIns(3,4,5)P3.

Possibly has a role in RNA transcription or processing during stress (By similarity). Binds RNAs and DNAs sequence with a preference to single-stranded nucleic acids. Displays strong affinity to poly(U) sequence. Involved in C-to-U editing of mitochondrial RNA. Functions as major mitochondrial editing factor. Controls 44 percent of the mitochondrial editing sites.
Removal of H(2)O(2), oxidation of toxic reductants, biosynthesis and degradation of lignin, suberization, auxin catabolism, response to environmental stresses such as wounding, pathogen attack and oxidative stress. These functions might be dependent on each isozyme/isoform in each plant tissue.

May be involved in the biosynthesis of ascorbic acid.

Pectin methylesterase (PME) inhibitor involved in the maintenance of cell wall integrity in response to necrotrophic pathogens. Modulates PME activity and pectin methylesterification during infection by Botrytis cinerea and contributes to resistance against the pathogen.

Component of the protein complex eIF4F, which is involved in the recognition of the mRNA cap, ATP-dependent unwinding of 5'-terminal secondary structure and recruitment of mRNA to the ribosome. Plays a role in the accumulation of some potyvirus during viral infection. Required for the accumulation of cucumber mosaic virus 3a protein and turnip crinkle virus p28 replication protein during viral infection. These proteins are necessary for cell-to-cell movement of the virus.

Might be involved in the organization and polarity of the actin cytoskeleton. Interacts with the barbed end of actin filaments and nucleates actin-filament polymerization in vitro.

Binds to the ABA-responsive element (ABRE). Mediates stress-responsive ABA signaling. Sulotransferase that utilizes 3'-phospho-5'-adenyl sulfate (PAPS) as sulfonate donor to catalyze the sulfate conjugation of desulfo-glucosinolates (dsGSs), the final step in the biosynthesis of the glucosinolate core structure. Preferred substrate are the long-chain desulfo-glucosinolates, 7-methylthioheptyl and 8-methylthiooctyl, derived from methionine. Substrate preference is desulfo-benzyl glucosinolate > desulfo-4- methylthiobutyl glucosinolate > desulfo-6-methylthiohexyl glucosinolate > desulfo-3-methylthiopropyl glucosinolate > desulfo-indol-3-yl methyl glucosinolate > desulfo-singrin > desulfo-3-butenyl glucosinolate.

PPIases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides (By similarity).

Probable GTPase-activating protein.

Involved in copper import into the cell. May play a role in copper detoxification in roots.
E3 ubiquitin-protein ligase. Participates in CpG methylation-dependent transcriptional regulation and epigenetic transcriptional silencing. Mediates ubiquitination with the E2 ubiquitin-conjugating enzyme UBC11. Promotes methylation-mediated gene silencing leading, for example, to early flowering. Associates with methylated DNA, and can bind to CpG, CpNpG, and CpNpN DNA motifs, with a strong preference for methylated forms, and with highest affinity for CpG substrate. Probably acts at the DNA methylation\-histone interface to maintain centromeric heterochromatin.

Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated proteins.

Lea proteins are late embryonic proteins abundant in higher plant seed embryos.

Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron donor and to act on fatty acids esterified to galactolipids, sulfolipids and phosphatidylglycerol. Morning-phased transcription factor integrating the circadian clock and auxin pathways. Binds to the evening element (EE) of promoters. Does not act within the central clock, but regulates free auxin levels in a time-of-day specific manner. Positively regulates the expression of YUC8 during the day, but has no effect during the night. Negative regulator of freezing tolerance.

May play a role in signaling. May be not involved in abscisic acid (ABA) signaling. Catalyzes the conversion of the C20 (E,E)- geranyllinalool to the volatile C16-homoterpene 4,8,12-trimethyltrideca-1,3,7,11-tetraene (TMTT) that is produced upon insect herbivore attack. Catalyzes the conversion of the C15 (E)- nerolidol to the volatile C11-homoterpene (E)-4,8-dimethyl-1,3,7-nonatriene (DMNT).

Serine protease. Has a substrate preference for the hydrophobic residues Phe and Ala and the basic residue Asp in the P1 position, and for Asp, Leu or Ala in the P1' position. Essential for mucilage release from seed coats. Triggers the accumulation and/or activation of cell wall modifying enzymes necessary either for the loosening of the outer primary cell wall, or to facilitate swelling of the mucilage.

Nuclear-encoded DNA-dependent RNA polymerase that catalyzes the transcription of DNA into RNA in chloroplasts using the four ribonucleoside triphosphates as substrates (Probable). Required for chloroplast development and leaf mesophyll cell proliferation.

General splicing factor. Can promote splice site selection in vitro presumably by antagonizing the effects of the A1 heterogeneous nuclear ribonucleoprotein. May have an essential function during early plant development.
Lma15410.t1  GRP5_ARATH  Involved in organ growth by promoting cell elongation processes.
Lma14793.t1  AAE2_ARATH  May act as an acid–thiol ligase that activates carboxylic acids by forming acyl-CoAs. Ubiquitin-like protein involved in cytoplasm to vacuole transport (Cvt) and autophagy vesicles formation. Conjugation with ATG5 through a ubiquitin-like conjugating system involving also ATG7 as an E1-like activating enzyme and ATG10 as an E2-like conjugating enzyme, is essential for its function. ATG12/ATG5 conjugate has an essential role in plant nutrient recycling.
Lma15788.t2  AT12B_ARATH  Ubiquitin-like protein involved in cytoplasm to vacuole transport (Cvt) and autophagy vesicles formation. Conjugation with ATG5 through a ubiquitin-like conjugating system involving also ATG7 as an E1-like activating enzyme and ATG10 as an E2-like conjugating enzyme, is essential for its function. ATG12/ATG5 conjugate has an essential role in plant nutrient recycling.
Lma15837.t4  HMG10_ARATH  Binds preferentially DNA with A/T-rich content.
Lma16268.t1  HIP43_ARATH  Heavy-metal-binding protein. Hydrolyzes acetyl esters in homogalacturonan regions of pectin. In type I primary cell wall, galacturonic acid residues of pectin can be acetylated at the O-2 and O-3 positions. Decreasing the degree of acetylation of pectin gels in vitro alters their physical properties. Functions as downstream effector of Rho-related GTP binding proteins of the "Rho of Plants" (ROPs) family. Participates in the propagation of ROP GTPase signals in specific cellular responses. Is involved in pollen tube growth regulation through its interaction with ARAC11/ROP1.
Lma16079.t1  PAE5_ARATH  Hydrolyzes acetyl esters in homogalacturonan regions of pectin. In type I primary cell wall, galacturonic acid residues of pectin can be acetylated at the O-2 and O-3 positions. Decreasing the degree of acetylation of pectin gels in vitro alters their physical properties. Functions as downstream effector of Rho-related GTP binding proteins of the "Rho of Plants" (ROPs) family. Participates in the propagation of ROP GTPase signals in specific cellular responses. Is involved in pollen tube growth regulation through its interaction with ARAC11/ROP1.
Lma14621.t1  RIC6_ARATH  Functions as downstream effector of Rho-related GTP binding proteins of the "Rho of Plants" (ROPs) family. Participates in the propagation of ROP GTPase signals in specific cellular responses. Is involved in pollen tube growth regulation through its interaction with ARAC11/ROP1.
Lma14716.t1  DSC2_ARATH  TIR-NB-LRR receptor-like protein involved in plant defense. Acts as a trigger of hypersensitive response (HR). Functions as guard of CAMTA3, a negative regulator of immunity, during pathogen infection.
Lma16309.t1  ATL6_ARATH  E3 ubiquitin-protein ligase able to catalyze polyubiquitination with ubiquitin-conjugating enzyme E2 UBC8 in vitro. May be involved in the plant C/N response and the early steps of the plant defense signaling pathway. Involved in the regulation of gravitropic response and basipetal auxin transport in roots. Involved in salt stress tolerance. May facilitate membrane trafficking and asymmetric cell elongation via SYT1. Binds stigmasterol and dipalmitoyl phosphoethanolamine (DPPE) in vitro. Probable transcription regulator that acts as a developmental regulator by promoting cell growth in response to light.
Lma15651.t1  ROSY1_ARATH  Probable transcription regulator that acts as a developmental regulator by promoting cell growth in response to light.
Lma16355.t1  LSH2_ARATH  Involved in auxin transport. Regulator of the auxin signaling pathway.
Lma15770.t1  GDL21_ARATH  Involved in organization of the endomembrane system and is required for endoplasmic reticulum morphology and organelle distribution. May act by inhibiting the formation of PYK10 complex by binding to GLL23 and exporting it from the ER. Required for proper subcellular localization of myrosinase TGG2. Has no lipase or esterase activity.
Lma15900.t1  LNK3_ARATH  Probable transcriptional coactivator.
Lma07210.t2 ARF1_SOLTU GTP-binding protein involved in protein trafficking; may modulate vesicle budding and uncoating within the Golgi apparatus.

Lma08161.t1 CPC_ARATH Transcription factor. Determines the fate of epidermal cell differentiation. Represses trichome development by lateral inhibition. Together with GL3 or BHLH2, promotes the formation of hair developing cells (H position) in root epidermis, probably by inhibiting non-hair cell formation. Represses the expression of GL2 and WER in H cells. Positively regulates stomatal formation in the hypocotyl

Lma07201.t1 NAC86_ARATH Transcription factor directing sieve element enucleation and cytosol degradation. Not required for formation of lytic vacuoles. Regulates, with NAC045, the transcription of NEN1, NEN2, NEN3, NEN4, RTM1, RTM2, UBP16, PLDZETA, ABCB10 and At1g26450.

Lma06390.t1 ATL45_ARATH Probable E3 ubiquitin-protein ligase that may possess E3 ubiquitin ligase activity in vitro (By similarity). May be involved in the early steps of the plant defense signaling pathway (Probable). May be involved in cooperative interactions with calmodulins or calmodulin-like proteins. May associate with nucleic acids and regulate gene expression at the transcriptional or post-transcriptional level (By similarity).

Lma08067.t1 IQD14_ARATH Catalyzes conversion of folates to polyglutamate derivatives allowing concentration of folate compounds in the cell and the intracellular retention of these cofactors, which are important substrates for most of the folate-dependent enzymes that are involved in one-carbon transfer reactions involved in purine, pyrimidine and amino acid synthesis. Essential for organellar and whole-plant folate homeostasis.

Lma07847.t1 FPGS3_ARATH Glycosyltransferase involved in the formation of rhamnogalacturonan I (RG-I) oligosaccharides in the seed coat mucilage, which is a specialized cell wall with abundant RG-I Transfers the rhamnose residue from UDP-beta-L-rhamnose to RG-I oligosaccharidesPrefers RG-I oligosaccharides with a degree of polymerization of 5 or larger than 5Does not act on oligosaccharides with a degree of polymerization of 4 or smaller than 4Does not require metal ions for its activity

Lma07283.t1 RRT1_ARATH
**Lma07362.t1  DRM2_ARATH**
Involved in de novo DNA methylation. Controls asymmetric and CpNpG methylation. Required for FWA gene silencing but not for the maintenance of SUP gene silencing. Functionally redundant to CMT3 to maintain non-CpG methylation. Involved in RNA-directed DNA methylation (RdDM) (, ). Acts as major DNA methyltransferase in the RdDM pathway, and is essential for RNA-directed de novo DNA methylation of cytosines in all sequence contexts (, ). Associates with long non-coding RNA (lncRNA) produced by RNA polymerase V (Pol V). This association is dependent on AGO4 and IDN2, and results in DNA methylation of RdDM target loci.

**Lma07669.t1  HFA7A_ARATH**
Transcriptional activator that specifically binds DNA sequence 5'-AGAAnnTTCT-3' known as heat shock promoter elements (HSE).

**Lma06514.t1  PLRX4_ARATH**
Modulates cell morphogenesis by regulating cell wall formation and assembly, and/or growth polarization.

**Lma07290.t1  SP1L4_ARATH**
Acts redundantly with SPR1 in maintaining the cortical microtubules organization essential for anisotropic cell growth.

**Lma07060.t1  DRE1C_ARATH**
Transcriptional activator that binds specifically to the DNA sequence 5'-[AG]CCGAC-3'. Binding to the C-repeat/DRE element mediates cold-inducible transcription. CBF/DREB1 factors play a key role in freezing tolerance and cold acclimation.

**Lma07365.t1  AGP6_ARATH**
Proteoglycan that seems to be implicated in diverse developmental roles such as differentiation, cell-cell recognition, embryogenesis and programmed cell death (By similarity). Plays an important role during the formation of the nexine layer of the pollen wall.

**Lma07583.t1  SBT17_ARATH**
Serine protease. Has a substrate preference for the hydrophobic residues Phe and Ala and the basic residue Asp in the P1 position, and for Asp, Leu or Ala in the P1' position. Essential for mucilage release from seed coats. Triggers the accumulation and/or activation of cell wall modifying enzymes necessary either for the loosening of the outer primary cell wall, or to facilitate swelling of the mucilage.

**Lma06686.t1  GDU1_ARATH**
Probable subunit of an amino acid transporter involved in the regulation of the amino acid metabolism. Stimulates amino acid export by activating nonselective amino acid facilitators. Required the interaction with the RING-type E3 ubiquitin-protein ligase LOG2 to fulfill its function. Plays a role in the Gln export at hydathodes, at xylem parenchyma into xylem sap and from mesophyll into leaf apoplasm. Acts upstream genes involved in the salicylic acid (SA) pathway and in the geminivirus-host interaction.

**Lma06448.t1  DRL27_ARATH**
Disease resistance protein.
Removal of H(2)O(2), oxidation of toxic reductants, biosynthesis and degradation of lignin, suberization, auxin catabolism, response to environmental stresses such as wounding, pathogen attack and oxidative stress. These functions might be dependent on each isozyme/isoform in each plant tissue.

Involved in peroxisomal proliferation. Promotes peroxisomal duplication, aggregation or elongation without fission.

Microtubule-associated protein that stabilize microtubules (MT). Involved in the regulation of MT organization and dynamics. Confers MT resistance to the drug propyzamide and cold conditions.

Aquaporins facilitate the transport of water and small neutral solutes across cell membranes.

Stimulates the GTPase/ATPase activities of Obg-like ATPases (By similarity). Mediates the transient calcium-dependent interaction of PYR/PYL/RCAR abscisic acid (ABA) receptors with the plasma membrane and thus regulates ABA sensitivity. Binds liposomes in the absence of exogenous Ca(2+), but this activity is enhanced in the presence of Ca(2+) and generates membrane curvature (By similarity).

Adapter-like transcriptional repressor recruiting TPL/TPR corepressors to inhibit TCP transcription factors (By similarity). May be involved in leaf development.

Involved in light signaling, probably by mediating the transport and correct distribution of protoporphyrin IX, a chlorophyll precursor, in response to far-red light.

Involved in trafficking to the vacuole. Required for cell proliferation and cell expansion, but not for cell differentiation. Acts in low affinity electroneutral exchange of protons for cations such as Na(+) or K(+) across membranes. May also exchange Li(+) and Cs(+) with a lower affinity.

Transcriptional activator involved in the regulation of plant development and tolerance to abiotic stresses. Involved in salt and osmotic stress response pathways. May be regulated by the stress-related genes RD29A, RD22, DREB1A or P5CS during stress response. Binds to the GCC-box pathogenesis-related promoter element. May be involved in the regulation of gene expression by stress factors and by components of stress signal transduction pathways (By similarity).

Functions as positive effectors of cell expansion through modulation of auxin transport.

Transcription elongation factor that enhances the transcription elongation by RNA polymerase II (RNAPII).

In the regulation of gene expression by stress factors and by components of stress signal transduction pathways. Transcription factor that binds to the GCC-box pathogenesis-related promoter element. Acts as a transcriptional inhibitor and may regulate other AtERFs (By similarity).
Pleiotropic regulator of glucose, stress and hormone responses. Also regulates cytochrome P450 CYP90A1/CPD. Coordinates the expression of hormone- and stress-related genes and genes related to cell wall modification and growth, leading to altered sugar-dependent growth and developmental responses. Component of the MAC complex that probably regulates defense responses through transcriptional control and thereby is essential for plant innate immunity. By suppressing the expression of several (1)O(2)-responsive genes, PRL1 seems to play a major role in modulating responses of plants to environmental changes by interconnecting (1)O(2)-mediated retrograde signaling with other signaling pathways. Acts as negative regulator of SNF1-related protein kinases AKIN10 and AKIN11 via the inhibition of their interaction with SKP1/ASK1. Component of the CUL4-RBX1-DDB1-PRL1 E3 ubiquitin-protein ligase complex, PRL1 may function as the substrate recognition module within this complex, leading to the AKIN10 degradation.

Lma16544.t1 SH3P2_ARATH Regulator for autophagosomal formation and/or maturation (, Ref.9). Binds phosphatidylinositol 3-phosphate.

Lma17230.t1 NLTP_VIGUN Potential lipid transfer protein.

Lma17970.t1 EXTN3_ARATH Structural component which strengthens the primary cell wall. Forms dendritic structures indicating a propensity for self-assembly through tyrosine cross-linking (, ). Forms intermolecular cross-links exclusively by pulcherosine (three Tyr) Scaffold formation requires an unobstructed C-terminus of EXT3. Required for the correct positioning of the cell plate during cytokinesis in cells of the developing embryo. Extensins contain a characteristic repeat of the pentapeptide Ser-Pro(4). For this particular extensin, a typical repeat of Ser-Pro(3) is found.

Lma18089.t1 TAR1_ARATH Probably involved in auxin production. TAA1, TAR1 and TAR2 are required for proper embryo patterning.

Lma17676.t1 GAOX4_ARATH Key oxidase enzyme in the biosynthesis of gibberellin that catalyzes the conversion of GA12 and GA53 to GA9 and GA20 respectively, via a three-step oxidation at C-20 of the GA skeleton.

Lma18026.t1 DEF02_ARATH Confers broad-spectrum resistance to pathogens.

Lma16800.t1 KRP4_ARATH Binds and inhibits CYCD2-1/CDKA-1 complex kinase activity. May target specifically CDKA-1.
Ubiquitin exists either covalently attached to another protein, or free (unanchored). When covalently bound, it is conjugated to target proteins via an isopeptide bond either as a monomer (monoubiquitin), a polymer linked via different Lys residues of the ubiquitin (polyubiquitin chains) or a linear polymer linked via the initiator Met of the ubiquitin (linear polyubiquitin chains). Polyubiquitin chains, when attached to a target protein, have different functions depending on the Lys residue of the ubiquitin that is linked: Lys-11-linked is involved in ERAD (endoplasmic reticulum-associated degradation) and in cell-cycle regulation; Lys-29-linked is involved in lysosomal degradation; Lys-33-linked is involved in kinase modification; Lys-48-linked is involved in protein degradation via the proteasome; Lys-63-linked is involved in endocytosis, and DNA-damage responses. Linear polymer chains formed via attachment by the initiator Met lead to cell signaling. Ubiquitin is usually conjugated to Lys residues of target proteins, however, in rare cases, conjugation to Cys or Ser residues has been observed. When polyubiquitin is free (unanchored-polyubiquitin), it also has distinct roles, such as in activation of protein kinases, and in signaling (By similarity).

Transcriptional activator that binds to the G-box motif (5'-CACGTG-3') and other cis-acting elements with 5'-ACGT-3' core, such as Hex, C-box and as-1 motifs. Possesses high binding affinity to G-box, much lower affinity to Hex and C-box, and little affinity to as-1 elementG-box and G-box-like motifs are cis-acting elements defined in promoters of certain plant genes which are regulated by such diverse stimuli as light-induction or hormone control (Probable). Binds to the G-box motif 5'-CACGTG-3' of LHCB2.4 (At3g27690) promoter. May act as transcriptional repressor in light-regulated expression of LHCB2.4. Binds DNA as monomer. DNA-binding activity is redox-dependent

TIR-NB-LRR receptor-like protein involved in plant defense. Acts as a trigger of hypersensitive response (HR). Functions as guard of CAMTA3, a negative regulator of immunity, during pathogen infection.

Proton-conducting pore forming subunit of the membrane integral V0 complex of vacuolar ATPase. V-ATPase is responsible for acidifying a variety of intracellular compartments in eukaryotic cells. Involved in trafficking to the vacuole. Required for cell proliferation and cell expansion, but not for cell differentiation. Acts in low affinity electroneutral exchange of protons for cations such as Na(+) or K(+) across membranes. May also exchange Li(+) and Cs(+) with a lower affinity.
Involved in the detoxification of reactive carbonyls (, ). Acts on lipid peroxide-derived reactive aldehydes. Specific to a double bond activated by an adjacent carbonyl group. Can use both quinones and diamide as substrates, but not menadione, ferricyanide or phylloquinone. Can use 4-hydroxy-(2E)-nonenal (HNE), 4-hydroxy-(2E)-hexenal (HHE), (2E)-nonenal, (2E)-hexenal, (2E)-pentenal, propenal (acrolein), 3-buten-2-one and 3-penten-2-one, but not (R)-(-)-carvone, n-nonanal, n-hexanal, (3Z)-hexanal, cyclohex-2-en-1-one or 12-oxo phytyadienoic acid (OPDA) as electron acceptors. Catalyzes the reduction of the alpha,beta-unsaturated bond of 2-alkenals, of lipid peroxide-derived oxenes 9-oxo-10(E),12(Z)-octadecadienoic acid (9-KODE) and 13-oxo-9(Z),11(E)-octadecadienoic acid (13-KODE), as well as 4-oxo-(2E)-nonenal and 4-hydroxynonenal. Can use 12-oxo-10(E) dodecanol (traumatin), trans-1,3 diphenyl-2-propenone, trans-1,4-diphenyl-2-butene-1,4-dione, 9-oxo-12,13-epoxy-(10E)-octadecenoic acid (trans-EKODE-1b) and 9,13-dihydroxy-10-oxo-11-octadecenoic acid as substrates. Catalyzes the reduction of the 7-8 double bond of phenylpropanol substrates, such as p-coumaryl aldehyde and coniferyl aldehyde (in vitro). Has activity towards toxic substrates, such as 4-hydroxy-(2E)-nonenal (in vitro). May play a distinct role in plant antioxidant defense and is possibly involved in NAD(P)/NAD(P)H homeostasis.

Located at the top of the head of the 40S subunit, it contacts several helices of the 18S rRNA.

May be involved in the sloughing (cell-cell separation) of the root cap cells from root tip.

Involved in pyrimidine breakdown rather than in pyrimidine salvage. Unable to use cytidine as a substrate.

Specific inhibitor of cysteine proteinases. Probably involved in the regulation of endogenous processes and in defense against pests and pathogens (By similarity).

Involved in the trafficking of vacuolar proteins. May function as a sorting receptor for protein trafficking to the protein storage vacuole (PSV) (By similarity). Thioredoxin reductase (TR) that exhibits both TR and thioredoxin (Trx) activities. Contains a C-terminal functional Trx domain. Functions as an electron donor for plastidial 2-Cys peroxiredoxins and participates in a NADPH-dependent hydrogen peroxide scavenging system in chloroplasts in the dark. Required for chlorophyll biosynthesis and biogenesis of the photosynthetic apparatus. Activates aerobic cyclase which converts Mg-protoporphyrin monomethyl ester into protochlorophyllide. Involved in a light-dependent regulation of starch biosynthesis by redox activation of the ADP-glucose pyrophosphorylase (AGPase), a central enzyme of starch synthesis.

Sugar transporter.
| Accession | Description | Function |
|-----------|-------------|----------|
| Lma11826.t1 | SG1_ARATH | Required for the early stage of chloroplast development. May be involved in chloroplast protein biosynthesis and/or degradation. Catalyzes the reduction of the 7-8 double bond of phenylpropanal substrates, such as p-coumaryl aldehyde and coniferyl aldehyde (in vitro). Has activity towards toxic substrates, such as 4-hydroxy-(2E)-nonenal (in vitro) (By similarity). May play a distinct role in plant antioxidant defense and is possibly involved in NAD(P)/NAD(P)h homeostasis. Hydrolyzes glycerol-phospholipids at the terminal phosphodiesteric bond to generate phosphatidic acids (PA). Phosphatidylcholine-selective. Regulates vesicle trafficking and auxin responses. Required for the normal cycling of PIN-2 containing vesicles. Contributes to the supply of inorganic phosphorus for cell metabolism and diacylglycerol moieties for galactolipid synthesis in phosphorus-starved roots (, ). Involved in root elongation during phosphate limitation. |
| Lma12004.t1 | P2_ARATH | Catalyzes the reduction of the 7-8 double bond of phenylpropanal substrates, such as p-coumaryl aldehyde and coniferyl aldehyde (in vitro). Has activity towards toxic substrates, such as 4-hydroxy-(2E)-nonenal (in vitro) (By similarity). May play a distinct role in plant antioxidant defense and is possibly involved in NAD(P)/NAD(P)h homeostasis. Hydrolyzes glycerol-phospholipids at the terminal phosphodiesteric bond to generate phosphatidic acids (PA). Phosphatidylcholine-selective. Regulates vesicle trafficking and auxin responses. Required for the normal cycling of PIN-2 containing vesicles. Contributes to the supply of inorganic phosphorus for cell metabolism and diacylglycerol moieties for galactolipid synthesis in phosphorus-starved roots (, ). Involved in root elongation during phosphate limitation. |
| Lma10837.t2 | PLDZ2_ARATH | Hydrolyzes glycerol-phospholipids at the terminal phosphodiesteric bond to generate phosphatidic acids (PA). Phosphatidylcholine-selective. Regulates vesicle trafficking and auxin responses. Required for the normal cycling of PIN-2 containing vesicles. Contributes to the supply of inorganic phosphorus for cell metabolism and diacylglycerol moieties for galactolipid synthesis in phosphorus-starved roots (, ). Involved in root elongation during phosphate limitation. |
| Lma10915.t1 | CATIN_ARATH | Required for embryogenesis. May be involved with the spliceosome. Involves in callose synthesis at the forming cell plate during cytokinesis. During plant growth and development, callose is found as a transitory component of the cell plate in dividing cells, is a major component of pollen mother cell walls and pollen tubes, and is found as a structural component of plasmodesmatal canals (By similarity). |
| Lma1167.t1 | OHP2_ARATH | May play a photoprotective role within PSI in response to light stress. Involves in callose synthesis at the forming cell plate during cytokinesis. During plant growth and development, callose is found as a transitory component of the cell plate in dividing cells, is a major component of pollen mother cell walls and pollen tubes, and is found as a structural component of plasmodesmatal canals (By similarity). |
| Lma10991.t1 | CALS3_ARATH | Involved in callose synthesis at the forming cell plate during cytokinesis. During plant growth and development, callose is found as a transitory component of the cell plate in dividing cells, is a major component of pollen mother cell walls and pollen tubes, and is found as a structural component of plasmodesmatal canals (By similarity). |
| Lma10934.t1 | PLT3_ARATH | Plasma membrane sugar-proton symporter. |
| Lma11436.t1 | AGP7_ARATH | Proteoglycan that seems to be implicated in diverse developmental roles such as differentiation, cell-cell recognition, embryogenesis and programmed cell death. Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP). Is a limiting enzyme for plastidic isoprenoid biosynthesis and essential for chloroplast development. |
| Lma10781.t3 | DXS_ARATH | Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP). Is a limiting enzyme for plastidic isoprenoid biosynthesis and essential for chloroplast development. |
| Lma11781.t1 | ZAT5_ARATH | Probable transcription factor that may be involved in stress responses. |
| Lma11896.t1 | PBL8_ARATH | May be involved in plant defense signaling. |
| Lma12275.t1 | PTR33_ARATH | Low-affinity nitrate transporter. |
| Lma11648.t1 | GPAT7_ARATH | Esterifies acyl-group from acyl-ACP to the sn-1 position of glycerol-3-phosphate, an essential step in glycerolipid biosynthesis. |
| Lma12101.t1 | DAW1_CHLRE | Functions as a cargo-specific adapter between intraflagellar transport (IFT) particles and outer row dynein. Required for efficient dynein-mediated transport into the flagellar compartment. |
| Lma11829.t1 | TIC32_ARATH | Involved in protein precursor import into chloroplasts. Part of the redox regulon consisting of TIC32, TIC55 and TIC62. Involved in the regulation of gravitropic response and basipetal auxin transport in roots. Involved in salt stress tolerance. May facilitate membrane trafficking and asymmetric cell elongation via SYT1. Binds stigmasterol and dipalmitoyl phosphoethanolamine (DPPE) in vitro. |
| Lma11854.t1 | ROSY1_ARATH | PPIases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides. Required for the light-induced increase of thiol accumulation. Assists the folding or assembly of SAT1 enzyme to form the cysteine synthase complex. Links light and redox signals to the regulation of cysteine biosynthesis in response to stress. |
| Lma10821.t1 | CP20C_ARATH | Transcriptional repressor that associates with ribosomal protein promoters. |
| Lma11664.t1 | LIMYB_ARATH | Probable sphingolipid transporter. Fatty acid desaturase involved in the first desaturation step leading to the formation of hexadeca 7,10,13-trienoic acid (16:3(7Z,10Z,13Z)), the major functional components of thylakoid membranes, (, , ). |
| Lma10939.t1 | SPNS3_ARATH | RNS3_ARATH | May remobilize phosphate, particularly when cells senesce or when phosphate becomes limiting. Guanine-nucleotide exchange factor (GEF) that acts as an activator of Rop (Rho of plants) GTPases by promoting the exchange of GDP for GTP. Functions as a light-signaling switch that functions in root growth and development through the activation of Rop in a phytochrome-dependent manner. May act as a negative regulator of phytochrome-mediated primary root development. Required during abscisic acid (ABA)-mediated activation of Ca(2+) channels. Regulates ABA signaling pathways. Modulates the expression of genes related to cell elongation and ABA signaling during root growth. Stimulates the transcription of various genes by recognizing and binding to a CCAAT motif in promoters (By similarity). Involved in the blue light (BL) and abscisic acid (ABA) signaling pathways. |
| Lma12155.t1 | GL17_ARATH | SPNS3_ARATH | ADD3_ARATH | Probable sphingolipid transporter. |
Ubiquitin exists either covalently attached to another protein, or free (unanchored). When covalently bound, it is conjugated to target proteins via an isopeptide bond either as a monomer (monoubiquitin), a polymer linked via different Lys residues of the ubiquitin (polyubiquitin chains) or a linear polymer linked via the initiator Met of the ubiquitin (linear polyubiquitin chains). Polyubiquitin chains, when attached to a target protein, have different functions depending on the Lys residue of the ubiquitin that is linked: Lys-6-linked may be involved in DNA repair; Lys-11-linked is involved in ERAD (endoplasmic reticulum-associated degradation) and in cell-cycle regulation; Lys-29-linked is involved in lysosomal degradation; Lys-33-linked is involved in kinase modification; Lys-48-linked is involved in protein degradation via the proteasome; Lys-63-linked is involved in endocytosis, DNA-damage responses as well as in signaling processes leading to activation of the transcription factor NF-kappa-B. Linear polymer chains formed via attachment by the initiator Met lead to cell signaling. Ubiquitin is usually conjugated to Lys residues of target proteins, however, in rare cases, conjugation to Cys or Ser residues has been observed. When polyubiquitin is free (unanchored-polyubiquitin), it also has distinct roles, such as in activation of protein kinases, and in signaling (By similarity).

Inhibits bovine beta-trypsin and alpha-chymotrypsin on a 1:1 molar basis. Transcription factor involved in RNA polymerase II (RNAPII) transcription regulation. Involved in transcription elongation. May function at post-recruitment and elongation steps of transcription. May be recruited by BZR2/BES1 to target genes and promote their expression during transcription elongation process. Required for brassinosteroid (BR)-induced gene expression. Required for regulation of numerous nitrogen-responsive genes in roots. Acts in roots to repress NRT2.1 transcription in response to high nitrogen supply. This repression is associated with an IWS1-dependent increase of trimethylation on 'Lys-27' H3K27me3 at the NRT2.1 locus.

Acetyltransferase enzyme. Acetylates histones, giving a specific tag for transcriptional activation. Acts as a co-chaperone for HSP90. Controls root development through the modulation of auxin distribution in the root meristem.

Catalyzes the final step of sucrose synthesis. Displays a dual function. As a soluble protein, exhibits glutathione-dependent thiol transferase and dehydroascorbate (DHA) reductase activities. Exhibits glutathione-dependent thiol transferase and dehydroascorbate (DHA) reductase activities. Key component of the ascorbate recycling system. Involved in the redox homeostasis, especially in scavenging of ROS under oxidative stresses. Plays a role in ozone tolerance.
JASON_ARATH

Required for normal spindle orientation at male meiosis II and normal formation of tetrad of microspores. Acts as positive regulator of PS1 in male sporogenesis. Not involved in female meiosis.

C86B1_ARATH

Involves in very long chain fatty acids (VLCFA) omega- hydroxylation. Required for the synthesis of saturated VLCFA alpha, omega-bifunctional suberin monomers.

CML7_ARATH

Potential calcium sensor.

BAM5_ARATH

Beta-amylase activity. Major cytosolic beta-amylase isoform in rosette leaves and inflorescences stems.

RGAP5_ARATH

Acts as a GTPase activator for the Rac-type GTPase by converting it to an inactive GDP-bound state.

GT14A_ARATH

Beta-glucuronosyltransferase involved in the biosynthesis of type II arabinogalactan (AG). Modifies both the beta-1,6-linked galactan and beta-1,3-linked galactan present in type II AG. Transfers glucuronate to beta-1,6- galactooligosaccharides with degrees of polymerization ranging from 3 to 11. Transfers glucuronate to beta-1,3- galactooligosaccharides with degrees of polymerization ranging from 5 to 7. The addition of glucuronate at the O6 position may terminate galactose chain extension. Required for cell elongation during seedling growth.

T2FA_ARATH

TFIIF is a general transcription initiation factor that binds to RNA polymerase II and helps to recruit it to the initiation complex in collaboration with TFIIB. It promotes transcription elongation (By similarity).

MPPA1_ARATH

Cleaves presequences (transit peptides) from mitochondrial protein precursors.

PUM8_ARATH

Sequence-specific RNA-binding protein that regulates translation and mRNA stability by binding the 3'-UTR of target mRNAs.

BRE1B_ARATH

E3 ubiquitin-protein ligase that monoubiquitinates H2B to form H2BK143ub1. H2BK143ub1 gives a specific tag for epigenetic transcriptional activation and is also prerequisite for H3K4me and maybe H3K79me. It thereby plays a central role in histone code and gene regulation. Forms a ubiquitin ligase complex in cooperation with the E2 enzyme UBC2/RAD6.

DIR20_ARATH

Dirigent proteins impart stereoselectivity on the phenoxy radical-coupling reaction, yielding optically active lignans from two molecules of coniferyl alcohol in the biosynthesis of lignans, flavonolignans, and alkaloids and thus plays a central role in plant secondary metabolism.
Lma02086.t1  AGDP1_ARATH  Heterochromatin-binding protein that preferentially occupies long transposons and specifically recognizes the histone H3 'Lys-9' methylation (H3K9me) marks, with a stronger affinity for dimethylated H3K9 (H3K9me2) (, ). Required for transcriptional silencing, non-CG DNA methylation (e.g. CHG and CHH regions), and H3K9 dimethylation (H3K9me2) at some loci (, ). Mediates heterochromatin phase separation and chromocenter formation.

Lma00101.t1  PME2_ARATH  Acts in the modification of cell walls via demethylesterification of cell wall pectin.

Lma01225.t1  NSRB_ARATH  Alternative splicing (AS) regulator that binds to specific mRNAs and modulates auxin effects on the transcriptome. Displaced from its targets upon binding to AS competitor long non-coding RNA (ASCO-RNA).

Lma00832.t1  CIN2_ARATH  Involved in monoterpene (C10) biosynthesis. The major product is 1,8-cineole (52%) followed by minor amounts of sabinene (14.5%), myrcene (13.3%), (-)-(1S)-beta-pinene (7.8%), (-)-(4S)-limonene (4.0%), (E)-beta-ocimene (2.7%), alpha-terpineol (2.4%), (-)-(1S)-alpha-pinene (1.9%), terpinolene (0.8%), and (+)-alpha-thujene (0.6%).

Lma00451.t1  REHY_ARATH  Thiol-specific peroxidase that catalyzes the reduction of hydrogen peroxide and organic hydroperoxides to water and alcohols, respectively (By similarity). Seems to contribute to the inhibition of germination during stress.

Lma00610.t2  IF413_TOBAC  ATP-dependent RNA helicase which is a subunit of the eIF4F complex involved in cap recognition and is required for mRNA binding to ribosome. In the current model of translation initiation, eIF4A unwinds RNA secondary structures in the 5'-UTR of mRNAs which is necessary to allow efficient binding of the small ribosomal subunit, and subsequent scanning for the initiator codon (By similarity).

Lma00809.t1  CSP1_ARATH  Chaperone that binds to RNA, single- (ssDNA) and double- stranded (dsDNA) DNA, and unwinds nucleic acid duplex. Exhibits a DNA melting activity. May be involved in cold resistance. Prevents seed germination under dehydration or salt stress conditions.

Lma00552.t1  PSBS_ARATH  Plays an important role in non-photochemical quenching, a process maintains the balance between dissipation and utilization of light energy to minimize generation of oxidizing molecules, thereby protecting the plant against photo-oxidative damage. Is not necessary for efficient light harvesting and photosynthesis.
Lma03645.t1  GSH1_ARATH

Seems to play an important role in controlling the expression of resistance responses like the regulation of salicylic acid (SA) and phytoalexin (camalexin) production. Involved in resistance to fungal and bacterial pathogens. Required for the regulation of cell proliferation in root apical meristems through the GSH-dependent developmental pathway. Also participates in the detoxification process, the antioxidant response and is essential for embryo development and proper seed maturation.

Lma03960.t1  PME20_ARATH

Acts in the modification of cell walls via demethylesterification of cell wall pectin. Regulates prospindle assembly during late prophase and at the onset of mitosis, before nuclear envelope breakdown (NEB). Is exported from the nucleus shortly before NEB and organized into two polar crescents. After NEB, is progressively associated with the forming spindle. Probably mediates AUR1 activation and localization to spindle microtubules. Has a microtubule binding capability and is able to trigger microtubule assembly induced by RanGTP in a heterologous system. Not involved in phragmoplast assembly, nuclear envelope reformation, and cortical microtubule assembly at the onset of G1. Involved in the formation of specific nuclear and perinuclear microtubular arrays in the nuclei of acentrosomal plant cells. Fungi and plants have acentrosomal microtubule arrays because they lack centrosomes. They use other microtubule organizing center (MTOC) structures to organize their microtubules. May function through interaction with importin.

Lma02547.t1  TPX2_ARATH

Required for ribosome biogenesis. Part of a complex which catalyzes pseudouridylation of rRNA. This involves the isomerization of uridine such that the ribose is subsequently attached to C5, instead of the normal N1. Pseudouridine ("psi") residues may serve to stabilize the conformation of rRNAs (By similarity).

Lma03828.t1  NHP2_ARATH

Phosphorylates the second messenger diacylglycerol (DAG) to generate phosphatidic acid (PA), another important signaling molecule. PA is required for plant development and responses to abiotic stress and pathogen attack. May be involved in the accumulation of PA during cold stress.

Lma03102.t1  DGK6_ARATH

Transcriptional regulator of sporocyte development Acts as an adapter-like transcriptional repressor recruiting TPL/TPR corepressors to inhibit TCP transcription factors. Required for nucellus and embryo sac development. Plays a central role in patterning both the proximal-distal and the adaxial-abaxial axes during ovule development. Involved in establishing the prospective chalaza of the ovule and in controlling the cell number and the length of the funiculus, and is required for the development of the integuments. Required, with BEL1, for cytokinin-induced PIN1 expression in ovules. Involved in controlling stamen identity. May also regulate the morphology of lateral organs by repressing auxin production.
| Gene ID       | Gene Symbol | Description                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|---------------|-------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Lma03025.t1   | AGP10_ARATH | Proteoglycan that seems to be implicated in diverse developmental roles such as differentiation, cell-cell recognition, embryogenesis and programmed cell death.                                                                                                                                                                                                                                                                                                                                 |
| Lma02837.t1   | SCL34_ARATH | Probable transcription factor involved in plant development.                                                                                                                                                                                                                                                                                                                                                                                                                |
| Lma03216.t1   | PUM6_ARATH  | Sequence-specific RNA-binding protein that regulates translation and mRNA stability by binding the 3'-UTR of target mRNAs. Binds the APUM-binding elements (APBEs) in the 3'-UTR mRNA sequence of CLV1, PNH, WUS and FAS2. Small heat shock protein required for the establishment of auxin gradients and for patterning of the apical domain of the embryo. Involved in the specification of the cotyledon primordia. Also required for normal inflorescence and floral meristem function, normal developmental patterning and thermotolerance. Acts as a molecular chaperone (By similarity).  May have a structural role to stabilize the lipid body during desiccation of the seed by preventing coalescence of the oil. Probably interacts with both lipid and phospholipid moieties of lipid bodies. May also provide recognition signals for specific lipase anchorage in lipolysis during seedling growth. Catalyzes the transfer of D-xylose from UDP-alpha-D-xylose onto L-fucose. Probably involved in the biosynthesis of rhamnomgalacturonan II (RG-II) through xylosylation of the internal fucose moiety of the A-chain of RG-II, a structurally complex pectic polysaccharide of the primary cell wall. RG-II is essential for the cell wall integrity of rapidly growing tissues such as roots and pollen tube growth and elongation. Myosin heavy chain that is required for the cell cycle-regulated transport of various organelles and proteins for their segregation. Functions by binding with its tail domain to receptor proteins on organelles and exerting force with its N-terminal motor domain against actin filaments, thereby transporting its cargo along polarized actin cables (By similarity). Involved in endocytosis via its action in endosomal trafficking. P5CS plays a key role in proline biosynthesis, leading to osmoregulation in plants. Involved in the regulation of the onset of mitosis. Involved in a pathway that coordinates cell proliferation and differentiation. Implicated in spindle pole body (SPD) duplication (By similarity). May be a downstream regulator of auxin signaling in the formation of secondary roots (Probable). Together with HP30-1 and HP30-2, triggers the import and insertion of transit sequence-less multi-pass transmembrane proteins (e.g. CEQORH) into the chloroplastic inner membrane. Involved in the targeting and/or fusion of transport vesicles to their target membrane.       |
Involved in chlorophyll biosynthesis. Catalyzes the insertion of magnesium ion into protoporphyrin IX to yield Mg- protoporphyrin IX. The magnesium-chelatase is a complex of three subunits, CHL1, CHLD and CHLH. The reaction takes place in two steps, with an ATP-dependent activation followed by an ATP-dependent chelation step. Possesses high affinity for ATP and may play a major role in chlorophyll biosynthesis. Does not bind abscisic acid (ABA), but is a positive regulator of ABA signaling.

The PI(3,5)P2 regulatory complex regulates both the synthesis and turnover of phosphatidylinositol 3,5-bisphosphate (PtdIns(3,5)P2). Required for autophagy (By similarity).

Transcription factor required for normal cell differentiation. Positively regulates LATERAL ORGAN BOUNDARIES (LOB) within the shoot apex, and the class III HD-ZIP genes REV, PHB, and PHV. Interacts directly with ASYMMETRIC LEAVES 2 (LBD6/AS2) to repress the knox homeobox genes BP/KNAT1, KNAT2, and KNAT6 and the abaxial determinants ARF3/ETT, KAN2 and YAB5. May act in parallel with the RDR6-SGS3-AGO7 pathway, an endogenous RNA silencing pathway, to regulate the leaf morphogenesis (, , , , , , , ). Binds directly to KNAT1, KNAT2, and KNATM chromatin, regulating leaf developmentLBD6 is required for this bindingPositive regulator of flowering that binds to the promoter of FTRegulates FT expression by forming a functional complex with COInvolved in leaf polarity establishment by functioning cooperatively with NUCL1 to repress abaxial genes ARF3, ARF4, KAN1, KAN2, YAB1 and YAB5, and the knox homeobox genes KNAT1, KNAT2, KNAT6, and STM to promote adaxial development in leaf primordia at shoot apical meristems at high temperatures

May be involved in iron transport and iron homeostasis.
Catalyzes the irreversible hydrolysis of pyrophosphate (PPI) to phosphate. The MgPPi(2-) complex binds to the enzyme only after a free Mg(2+) ion has bound (Ref.9). No activity with glycerol-3-phosphate, glucose-6-phosphate, p-nitrophenylphosphate, ADP, NADP(+), NAD(+),NADH, NADPH or phosphoribosyl pyrophosphate as substrates (Ref.9). Controls the equilibrium of gluconeogenic reactions in the heterotrophic growth phase of early seedling establishment. Determinates the rate of cytosolic glycolysis, providing carbon for seed storage lipid accumulation.
Component of the Mediator complex, a coactivator involved in the regulated transcription of nearly all RNA polymerase II-dependent genes. Mediator functions as a bridge to convey information from gene-specific regulatory proteins to the basal RNA polymerase II transcription machinery. The Mediator complex, having a compact conformation in its free form, is recruited to promoters by direct interactions with regulatory proteins and serves for the assembly of a functional preinitiation complex with RNA polymerase II and the general transcription factors (By similarity).

Auxin response factors (ARFs) are transcriptional factors that bind specifically to the DNA sequence 5'-TGTCTC-3' found in the auxin-responsive promoter elements (AuxREs). Could act as transcriptional activator or repressor. Formation of heterodimers with Aux/IAA proteins may alter their ability to modulate early auxin response genes expression.

CPSF plays a key role in pre-mRNA 3'-end formation, recognizing the AAUAAA signal sequence and interacting with poly(A)polymerase and other factors to bring about cleavage and poly(A) addition (By similarity). Required for antisense-RNA- mediated gene silencing.

Voltage-dependent peptide-sensitive high conductance rectifying cation channel with a strong affinity for TIC32 that is imported into the chloroplast. Conductance is pH-dependent decreasing with decreasing pH values.

Links the histone deacetylase complex to transcriptional repressors bound to chromatin. Involved in the tethering of the SIN3 complex to core histone proteins.

Probable subunit of an amino acid transporter involved in the regulation of the amino acid metabolism. Stimulates amino acid export by activating nonselective amino acid facilitators.

Required for specific RNA editing events in chloroplasts and stabilizes specific chloroplast mRNAs (By similarity).

Thiol-disulfide oxidoreductase that may participate in various redox reactions. Possesses insulin disulfide bonds reducing activity. Reduced by thioredoxin reductases NTRA and NTRB.

Transcription activation factor positively regulating trichomes development Has a function nearly equivalent to that of GL1 and can complement gl1 mutants.

Proteoglycan that seems to be implicated in diverse developmental roles such as differentiation, cell-cell recognition, embryogenesis and programmed cell death.

E3 ubiquitin-protein ligase that is required for the plant C/N response during seedling growth transition. May be involved in the early steps of the plant defense signaling pathway.

Cytokinin-activating enzyme working in the direct activation pathway. Phosphoribohydrolase that converts inactive cytokinin nucleotides to the biologically active free-base forms.
Lma25212.t1  HIP33_ARATH  Heavy-metal-binding protein. Required for the promotion of megasporogenesis, or promotion of germ cell formation from somatic precursor cells. Acts redundantly with WIH1. Functions in a genetic pathway downstream of SPL/NZZ and WUS and together with TRN2 in promoting megasporogenesis.

Lma23965.t1  WIH2_ARATH  Transcriptional repressor that may regulate multiple aspects of plant growth and development through the regulation of BEL1-LIKE (BLH) and KNOX TALE (KNAT) homeodomain transcription factors.

Lma25087.t1  OFP10_ARATH  Transcriptional repressor that may regulate multiple aspects of plant growth and development through the regulation of BEL1-LIKE (BLH) and KNOX TALE (KNAT) homeodomain transcription factors.

Lma24680.t1  EDM2_ARATH  Cellular antisilencing factor and regulator of genome DNA methylation patterns involved in the regulation of chromatin states. Together with SUVH4, monitors repressive epigenetic marks H3K27me1, H3K9me2, and prevents DNA-methylation at CHG sites, affecting especially the expression of transposons and developmentally important genes (, , ). Regulates alternative RNA processing such as distal 3' polyadenylation by intrinsic heterochromatin transcription factor that binds DNA and contributes to transcriptional transposable element (TE) silencing by modulating levels of the repressive post-translational histone modifications (PHM) H3K9me2In cv. Columbia, required for RPP7-dependent disease resistance against the Hyaloperonospora arabidopsidis isolate Hiks1, by promoting levels of RPP7 via alternative polyadenylation (APA), resulting from cooption of epigenetic information at the TE insertion locus COPIA-R7 (, , ). Regulates development processes such as the formation of leaf pavement cells, leaf expansion, fertility and flowering (, , ). Prevents FLC accumulation to control flowering

Lma24656.t1  ODO2A_ARATH  The 2-oxoglutarate dehydrogenase complex catalyzes the overall conversion of 2-oxoglutarate to succinyl-CoA and CO(2). It contains multiple copies of three enzymatic components: 2- oxoglutarate dehydrogenase (E1), dihydrolipoamide succinyltransferase (E2) and lipoamide dehydrogenase (E3) (By similarity).

Lma24673.t1  WAXS5_ARATH  Catalyzes the final step in the synthesis of long-chain linear esters (waxes).

Lma23269.t1  FLA3_ARATH  May be a cell surface adhesion protein. Myosin heavy chain that is required for the cell cycle- regulated transport of various organelles and proteins for their segregation. Functions by binding with its tail domain to receptor proteins on organelles and exerting force with its N-terminal motor domain against actin filaments, thereby transporting its cargo along polarized actin cables (By similarity). Involved in endocytosis via its action in endosomal trafficking.

Lma23900.t1  THAH_ARATH  Hydroxylates thalianol into thalian-diol.
May be involved in the regulation of ethylene receptor signaling. Promotes cell expansion and plant growth.

Involved in RNA editing event in chloroplasts. Required for the editing of a single site in ndhD transcript, which is a plastid-encoded subunit of the chloroplast NAD(P)H dehydrogenase (NDH) complex. Not essential for the activity of the NDH complex of the photosynthetic electron transport chain.

Forms multiple COMPASS-like complexes involved in histone methylation by interacting with different histone H3 'Lys-4' methyltransferases such as ATX1, SDG14 or SDG16Binds to target loci chromatin, increasing H3K4 trimethylation and causing activation of the geneUpregulates FLC and MAF4 expression to delay flowering

May act as a substrate-specific adapter of an E3 ubiquitin-protein ligase complex (CUL3-RBX1-BTB) which mediates the ubiquitination and subsequent proteasomal degradation of target proteins.

Transcription factor.

May act as an adapter to facilitate the interaction of SnRK1 complex with effector proteins, conferring tissue- and stimulus-type specific differences in the SnRK1 regulation pathway. Transcriptional coactivator necessary for expression of the clock genes PRR5 and TOC1 (,). Antagonizes REV8 function in the regulation of anthocyanin accumulationInvolved in red light input to the clockActivates clock-controlled genes with afternoon peakMediates light inhibition of hypocotyl elongation

Probable transcription factor involved in phosphate signaling in roots.

Required for red (R) and far red (FR) light-induced and phytochrome-mediated deregulation of negative gravitropism leading to randomization of hypocotyl growth orientation.

Single-stranded DNA-binding protein that functions in both chloroplasts and nucleus. In chloroplasts, maintains plastid genome stability by preventing break-induced and short homology-dependent illegitimate recombinations. In the nucleus, is recruited to a distal element upstream of the kinesin KP1 to mediate the transcriptional repression of KP1. Can bind double-stranded DNA in vivo.

Required for the promotion of meigasporogenesis, or promotion of germ cell formation from somatic precursor cells. Acts redundantly with WIH2. Functions in a genetic pathway downstream of SPL/NZZ and WUS and together with TRN2 in promoting meigasporogenesis.
Lma05286.t1 VP52A_ARATH Acts as component of the GARP complex that is involved in retrograde transport from early and late endosomes to the trans-Golgi network (TGN). The GARP complex facilitates tethering as well as SNARE complex assembly at the Golgi (By similarity). Required for pollen tube elongation and other polar growth.

Lma05202.t1 RPK1_ARATH Involved in the main abscisic acid-mediated (ABA) signaling pathway and in early ABA perception. Together with RPK2, required for pattern formation along the radial axis (e.g. the apical embryonic domain cell types that generate cotyledon primordia), and the apical-basal axis (e.g. differentiation of the basal pole during early embryogenesis).

Lma06194.t1 PUB2_ARATH Functions as an E3 ubiquitin ligase.

Lma04304.t1 BBX21_ARATH Transcription activator that acts as positive regulator of seedling photomorphogenesisActs downstream of COP1 and play an important role in early and long-term adjustment of the shade avoidance syndrome (SAS) responses in natural environments

Lma06105.t1 WRK19_ARATH Transcription factor. Interacts specifically with the W box (5'-(T)TGAC[CT]-3'), a frequently occurring elicitor- responsive cis-acting element. May act also as a disease resistance protein with a serine/threonine-protein kinase activity (By similarity).

Lma05310.t1 EMS1_ARATH Receptor with a serine/threonine-protein kinase activity required for the specification of the correct number of male archesporial initials and for the subsequent specification of tapetal and middle cell layer identities. In seeds, required for enhancing cell size and the rate of embryonic development.

Lma06002.t2 SUD1_ARATH Probable E3 ubiquitin ligase acting as a positive post- transcriptional regulator of 3-hydroxy-3-methylglutaryl-coenzyme A reductase activity. Might be involved in the quality control that degrades misfolded proteins (By similarity).

Lma05056.t1 KPYC_ARATH Key regulatory enzyme of the glycolytic pathway that catalyzes the final step of glycolysis, converting ADP and phosphoenolpyruvate (PEP) to ATP and pyruvate by essentially irreversible transphosphorylation.

Lma06020.t1 PEX14_ARATH Controls intracellular transport of both PTS1- and PTS2- containing proteins. Required for the proper targeting of PEX7 to the peroxisome.

Lma05279.t1 IMDH1_ARATH Catalyzes the conversion of inosine 5'-phosphate (IMP) to xanthosine 5'-phosphate (XMP), the first committed and rate-limiting step in the de novo synthesis of guanine nucleotides, and therefore plays an important role in the regulation of cell growth.

Lma06087.t1 AGP1_ARATH Proteoglycan that seems to be implicated in diverse developmental roles such as differentiation, cell-cell recognition, embryogenesis and programmed cell death.
| Lma04147.t2  | BRG2_ARATH | Probable E3 ubiquitin-protein ligase. Has no effect on the stability of the DELLA proteins. |
|-------------|------------|------------------------------------------------------------------------------------------|
| Lma04261.t1  | CST_ARATH  | Acts as a spatial inhibitor of signaling that modulates abscission zone cell adhesion and expansion. Acts both directly and indirectly by physically interacting with RLK5/HAE and SOBIR1/EVR at the cell surface. |
| Lma04495.t1  | PUB10_ARATH | Functions as an E3 ubiquitin ligase.                                                      |
| Lma05455.t1  | PLCD4_ARATH | The production of the second messenger molecules diacylglycerol (DAG) and inositol 1,4,5-trisphosphate (IP3) is mediated by activated phosphatidylinositol-specific phospholipase C enzymes. Catalytic subunit of cellulose synthase terminal complexes ('rosettes'), required for beta-1,4-glucan microfibril crystallization, a major mechanism of the cell wall formation. Involved in the primary cell wall formation. The presence of each protein CESA1 and CESA6 is critical for cell expansion. The hypocotyl elongation is based on a CESA6-dependent cell elongation in dark and a CESA6-independent cell elongation in light. The transition between these two mechanisms requires photosynthesis and PHYB, but not CRY1. The CESA6-dependent cell elongation seems to be independent of gibberellic acid, auxin and ethylene. May be involved in sensitivity to isoxaben. Associates with and moves along cortical microtubules for the process of cellulose deposition. |
| Lma04668.t1  | CESA6_ARATH | Synthesizes nicotianamine, a polyamine which serves as a sensor for the physiological iron status within the plant, and/or might be involved in the transport of iron. |
| Lma05314.t1  | NAS2_ARATH  |                                                                                          |