



## GeBP/GPL Transcription Factors Regulate a Subset of CPR5-Dependent Processes.

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Daniel Perazza, Frédéric Laporte, Claudine Balagué, Florian Chevalier, Shanterika Remo, et al.. GeBP/GPL Transcription Factors Regulate a Subset of CPR5-Dependent Processes.. Plant Physiology, 2011, 157 (3), pp.1232-42. 10.1104/pp.111.179804 . hal-00636599

**HAL Id: hal-00636599**

**<https://hal.science/hal-00636599>**

Submitted on 28 May 2020

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|           |                |                                                                   | Misregulated genes in <i>gebp gpl1,2,3</i> quadruple mutant                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                               |                                                                       |                                                                    |  |
|-----------|----------------|-------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------|-----------------------------------------------------------------------|--------------------------------------------------------------------|--|
| Name      | CATMA R factor | Name/Function                                                     | Description                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Biological process                                            | Molecular function                                                    | Cellular component                                                 |  |
| AT1G02205 | 1,17           | CER1 (ECERIFERUM 1)                                               | Encodes the CER1 gene associated with production of stem epicuticular wax and pollen fertility. Biochemical studies showed that cer1 mutants are blocked in the conversion of stem wax C30 aldehydes to C29 alkanes, and they also lack the secondary alcohols and ketones. These suggested the CER1 protein is a aldehyde decarbonylase. Members of the CER family are also involved in HR response.                                                                                                  | (GO:0042335) cuticle development [IMP]                        | (GO:0010025) wax biosynthetic process [IMP]                           | (GO:0009924) octadecanal decarbonylase activity [IMP]              |  |
| AT1G03090 | -1,36          | MCCA                                                              | MCCA is the biotinylated subunit of the dimer MCCase, which is involved in leucine degradation. Both subunits are nuclear coded and the active enzyme is located in the mitochondrion.                                                                                                                                                                                                                                                                                                                 | (GO:0006552) leucine catabolic process [IDA]                  | (GO:0004485) methylcrotonoyl-CoA carboxylase activity [IDA]           | (GO:0005739) mitochondrion [IDA]                                   |  |
| AT1G08630 | -1,00          | aldehyde-lyase                                                    | Encodes a threonine aldolase, involved in threonine degradation to glycine. Primarily expressed in seeds and seedlings.                                                                                                                                                                                                                                                                                                                                                                                | (GO:0006567) threonine catabolic process [IMP]                | (GO:0004793) threonine aldolase activity [IDA]                        | (GO:0016832) aldehyde-lyase activity [ISS]                         |  |
| AT1G10070 | -1,84          | branched-chain-amino-acid transaminase/ catalytic unknown protein | Encodes a chloroplast branched-chain amino acid aminotransferase. Complements the yeast leu/iso-leu/val auxotrophy mutant.                                                                                                                                                                                                                                                                                                                                                                             | (GO:0008152) metabolic process [IEA]                          | (GO:0009081) branched chain family amino acid metabolic process [IEA] | (GO:0004084) branched-chain-amino-acid transaminase activity [IGI] |  |
| AT1G18710 | 1,07           | DNA binding / transcription factor                                | Member of the R2R3 factor gene family.                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | (GO:0006355) regulation of transcription, DNA-dependent [ISS] | (GO:0009651) response to salt stress [IEP]                            | (GO:0009753) response to jasmonic acid stimulus [IEP]              |  |
| AT1G48750 | 1,09           | lipid binding clathrin binding                                    | storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] (TAIR:AT3G18280.1); similar to TED4 [Zinnia elegans] (GB:BAA06462.1); contains InterPro domain Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor (InterPro:IPR003612); contains InterPro domain Bifunctional inhibitor/plant lipid transfer protein/seed storage (InterPro:IPR016140); contains InterPro domain Plant lipid transfer protein and hydrophobic protein, helical; (InterPro:IPR013770) | (GO:0006869) lipid transport [ISS]                            | (GO:0008289) lipid binding [ISS]                                      | (GO:0012505) endomembrane system [IEA]                             |  |

|           |       |                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                               |                                                   |                                                     |  |
|-----------|-------|--------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------|---------------------------------------------------|-----------------------------------------------------|--|
| AT1G49470 | 0.68  | unknown protein                | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G55230.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN63047.1); contains InterPro domain Protein of unknown function DUF716 (InterPro:IPR006904)                                                                                                                                                                                                                                                                                                                                      | (GO:0008150) biological_process [ND]          | (GO:0003674) molecular_function [ND]              | (GO:0012505) endomembrane system [IEA]              |  |
| AT1G52990 | 1.23  | electron transporter           | [Arabidopsis thaliana] (TAIR:AT3G23320.1); similar to 52O08_2 [Brassica rapa subsp. pekinensis] (GB:AAZ67547.1); contains InterPro domain Polynucleotidyl transferase, Ribonuclease H fold; (InterPro:IPR012337); contains InterPro domain Thioredoxin family (InterPro:IPR015467); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Thioredoxin fold (InterPro:IPR012335); contains InterPro domain Thioredoxin-related; (InterPro:IPR006662); contains InterPro domain Thioredoxin domain (InterPro:IPR013766) | No annotation for biological_process          | (GO:0003676) nucleic acid binding [IEA]           | (GO:0012505) endomembrane system [IEA]              |  |
| AT1G55360 | 0.92  | unknown protein                | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G56530.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13510.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22094.1); similar to unknown [Populus trichocarpa] (GB:ABK93966.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN72570.1); contains InterPro domain Protein of unknown function DUF239, plant (InterPro:IPR004314)                                                                                                                          | (GO:0008150) biological_process [ND]          | (GO:0003674) molecular_function [ISS]             | (GO:0012505) endomembrane system [IEA]              |  |
| AT1G58290 | -0.87 | HEMA1; glutamyl-tRNA reductase | Encodes a protein with glutamyl-tRNA reductase (GluTR) activity, catalyzing the NADPH-dependent reduction of Glu-tRNA(Glu) to glutamate 1-semialdehyde (GSA) with the release of free tRNA(Glu). It is involved in the early steps of chlorophyll biosynthesis.                                                                                                                                                                                                                                                                                               | (GO:0009416) response to light stimulus [IEP] | (GO:0006779) porphyrin biosynthetic process [TAS] | (GO:0015995) chlorophyll biosynthetic process [IMP] |  |

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|-----------|-------|------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------|-------------------------------------------|-------------------------------------------|--|
| AT1G66100 | -0,99 | toxin receptor binding | [Contains: Probable thionin-2.4; Acidic protein] [Arabidopsis thaliana] (GB:Q9C8D6); similar to TH12.2 (THIONIN 2.2), toxin receptor binding [Arabidopsis thaliana] (TAIR:AT5G36910.1); similar to crambin precursor=thionin variant Thi2Ca2 [Crambe abyssinica, seeds, Peptide Partial, 134 aa] (GB:AAB33004.1); contains InterPro domain Thionin; (InterPro:IPR001010)                                                                                                                                                                                                                                                                                                                   | (GO:0006952) defense response [ISS]  | (GO:0003674) molecular_function [ISS]     | (GO:0050827) toxin receptor binding [ISS] |  |
| AT1G67750 | 1,23  | pectate lyase          | Identical to Probable pectate lyase 5 precursor [Arabidopsis thaliana] (GB:Q9FXD8;GB:Q8L8V9;GB:Q8W116); similar to pectate lyase family protein [Arabidopsis thaliana] (TAIR:AT4G24780.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42465.1); similar to pectate lyase [Salix gilgiana] (GB:BAB59066.1); similar to unknown [Populus trichocarpa] (GB:ABK94358.1); contains InterPro domain Pectin lyase fold (InterPro:IPR012334); contains InterPro domain Pectate lyase/Amb allergen (InterPro:IPR002022); contains InterPro domain Parallel beta-helix repeat (InterPro:IPR006626); contains InterPro domain Pectin lyase fold/virulence factor (InterPro:IPR011050) | (GO:0008150) biological_process [ND] | (GO:0030570) pectate lyase activity [ISS] | (GO:0012505) endomembrane system [IEA]    |  |
| AT1G68340 | 1,30  | unknown protein        | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G25370.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68084.1); contains InterPro domain Protein of unknown function DUF1639 (InterPro:IPR012438)                                                                                                                                                                                                                                                                                                                                                                                                                                                               | (GO:0008150) biological_process [ND] | (GO:0003674) molecular_function [ND]      | (GO:0005575) cellular_component [ND]      |  |

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| AT1G73600 | 0,74  | S-adenosylmethionine-dependent methyltransferase/ methyltransferase/ phosphoethanolamine N-methyltransferase | Thaliana] (GB:Q9C6B9;GB:Q9C9V1); similar to NMT1 (N-METHYLTRANSFERASE 1), phosphoethanolamine N-methyltransferase [Arabidopsis thaliana] (TAIR:AT3G18000.1); similar to phosphoethanolamine N-methyltransferase 2, putative (NMT2) [Arabidopsis thaliana] (TAIR:AT1G48600.1); similar to phosphoethanolamine N-methyltransferase 2, putative (NMT2) [Arabidopsis thaliana] (TAIR:AT1G48600.2); similar to hypothetical protein [Vitis vinifera] (GB:CAN64744.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68187.1); similar to phosphoethanolamine N-methyltransferase [Brassica napus] (GB:AAP83582.1); contains InterPro domain Methyltransferase type 11; (InterPro:IPR013216) | (GO:0008152) metabolic process [IEA]                          | (GO:0000234) phosphoethanolamine N-methyltransferase activity [ISS] | No annotation for cellular_component    |  |
| AT1G78320 | 0,70  | ATGSTU23; glutathione transferase                                                                            | Encodes glutathione transferase belonging to the tau class of GSTs. Naming convention according to Wagner et al. (2002).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | (GO:0009407) toxin catabolic process [TAS]                    | (GO:0004364) glutathione transferase activity [ISS]                 | (GO:0005737) cytoplasm [NAS]            |  |
| AT1G78620 | 1,70  | unknown protein                                                                                              | similar to unknown [Picea sitchensis] (GB:ABK22124.1); similar to Os01g0729100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001044132.1); contains InterPro domain Protein of unknown function DUF92, transmembrane (InterPro:IPR002794)                                                                                                                                                                                                                                                                                                                                                                                                                                                         | No annotation for biological_process                          | No annotation for molecular_function                                | (GO:0009941) chloroplast envelope [IDA] |  |
| AT2G02470 | -0,79 | DNA binding / protein binding / zinc ion binding                                                             | similar to PHD finger family protein [Arabidopsis thaliana] (TAIR:AT1G14510.1); similar to PHD5 [Glycine max] (GB:ABI97244.1); contains InterPro domain Zinc finger, RING/FYVE/PHD-type (InterPro:IPR013083); contains InterPro domain Zinc finger, PHD-type; (InterPro:IPR001965); contains InterPro domain Zinc finger, FYVE/PHD-type; (InterPro:IPR011011)                                                                                                                                                                                                                                                                                                                                       | (GO:0006355) regulation of transcription, DNA-dependent [ISS] | (GO:0003677) DNA binding [ISS]                                      | (GO:0005575) cellular_component [ND]    |  |

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|-----------|-------|------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------|-----------------------------------------------------------------------|-------------------------------------------------|--|
| AT2G07675 | 0.99  | structural constituent of ribosome | similar to ribosomal protein S12 [Brassica napus] (GB:BAA02857.1); contains InterPro domain Ribosomal protein S12, bacterial-type; (InterPro:IPR005679); contains InterPro domain Ribosomal protein S12/S23; (InterPro:IPR006032); contains InterPro domain Nucleic acid-binding, OB-fold (InterPro:IPR012340); contains InterPro domain Nucleic acid-binding, OB-fold-like (InterPro:IPR016027)                                                                           | (GO:0006412) translation [ISS]                      | (GO:0003735) structural constituent of ribosome [ISS]                 | (GO:0005840) ribosome [ISS]                     |  |
| AT2G18420 | -1.31 | unknown protein                    | Encodes a Gibberellin-regulated GASA/GAST/Snakin family protein                                                                                                                                                                                                                                                                                                                                                                                                            | (GO:0009739) response to gibberellin stimulus [ISS] | (GO:0003674) molecular_function [ND]                                  | (GO:0012505) endomembrane system [IEA]          |  |
| AT2G20875 | -0.94 | unknown protein                    | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G34245.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24097.1)                                                                                                                                                                                                                                                                                                                                  | (GO:0010375) stomatal complex patterning [IMP]      | (GO:0003674) molecular_function [ND]                                  | No annotation for cellular_component            |  |
| AT2G25450 | -3.93 | unknown protein                    | encodes a protein whose sequence is similar to ACC oxidase                                                                                                                                                                                                                                                                                                                                                                                                                 | (GO:0008150) biological_process [ND]                | (GO:0009815) 1-aminocyclopropane-1-carboxylate oxidase activity [ISS] | (GO:0005575) cellular_component [ND]            |  |
| AT2G28120 | -0.89 | unknown protein                    | [Arabidopsis thaliana] (TAIR:AT2G39210.1); similar to unknown [Populus trichocarpa] (GB:ABK95139.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO16759.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN82898.1); contains InterPro domain Major facilitator superfamily MFS-1 (InterPro:IPR011701); contains InterPro domain MFS general substrate transporter (InterPro:IPR016196); contains InterPro domain Nodulin-like (InterPro:IPR010658) | No annotation for biological_process                | No annotation for molecular_function                                  | (GO:0005886) plasma membrane [IDA]              |  |
| AT2G31660 | -2.96 | protein transporter                | drought 2) encodes an importin beta-domain family protein likely to be involved in nuclear transport in ABA signaling. Subcellular localization of GFP-tagged SAD2 showed a predominantly nuclear localization, consistent with a role for SAD2 in nuclear transport. Mutation of SAD2 in Arabidopsis alters abscisic acid sensitivity. SAD2 was ubiquitously expressed at low levels in all tissues except flowers. SAD2 expression was not induced by ABA or stress.     | (GO:0006606) protein import into nucleus [IDA]      | (GO:0000059) protein import into nucleus, docking [ISS]               | (GO:0008565) protein transporter activity [ISS] |  |

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|-----------|-------|-------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------|---------------------------------------|-----------------------------------------------------|--|
| AT2G31810 | -1,20 | acetolactate synthase/ amino acid binding | similar to acetolactate synthase small subunit, putative [Arabidopsis thaliana] (TAIR:AT5G16290.2); similar to acetolactate synthase small subunit, putative [Arabidopsis thaliana] (TAIR:AT5G16290.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN61470.1); contains InterPro domain Amino acid-binding ACT; (InterPro:IPR002912); contains InterPro domain Acetolactate synthase, small subunit; (InterPro:IPR004789)                                                             | (GO:0009082) branched chain family amino acid biosynthetic process [TAS] | (GO:0016597) amino acid binding [IEA] | (GO:0003984) acetolactate synthase activity [IEA]   |  |
| AT2G36340 | 1,85  | transcription regulator                   | similar to DNA-binding storekeeper protein-related [Arabidopsis thaliana] (TAIR:AT2G25650.1); similar to hypothetical protein PFE0440w [Plasmodium falciparum 3D7] (GB:XP_001351647.1); contains InterPro domain Protein of unknown function DUF573 (InterPro:IPR007592)                                                                                                                                                                                                                         | No annotation for biological_process                                     | (GO:0003674) molecular_function [ISS] | (GO:0030528) transcription regulator activity [TAS] |  |
| AT2G37130 | -0,88 | peroxidase                                | <b>Identical to Peroxidase 21 precursor (PER21) [Arabidopsis Thaliana] (GB:Q42580;GB:Q43733;GB:Q93YM9); similar to PRXR1 (peroxidase 42), peroxidase [Arabidopsis thaliana] (TAIR:AT4G21960.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO18132.1); contains InterPro domain Plant peroxidase; (InterPro:IPR000823); contains InterPro domain Haem peroxidase; (InterPro:IPR010255); contains InterPro domain Haem peroxidase, plant/fungal/bacterial; (InterPro:IPR002016)</b> | (GO:0050832) defense response to fungus [IMP]                            | (GO:0003674) molecular_function [TAS] | (GO:0004601) peroxidase activity [ISS]              |  |
| AT2G39570 | -0,88 | amino acid binding                        | similar to ACT domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G36840.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69235.1); contains InterPro domain Amino acid-binding ACT; (InterPro:IPR002912)                                                                                                                                                                                                                                                                   | (GO:0008152) metabolic process [IEA]                                     | (GO:0016597) amino acid binding [IEA] | No annotation for cellular_component                |  |

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|-----------|-------|-----------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------|------------------------------------------------|---------------------------------------------------|--|
| AT2G41240 | 2,25  | DNA binding / transcription factor            | similar to BHLH039/ORG3 (OBP3-RESPONSIVE GENE 3), DNA binding / transcription factor [Arabidopsis thaliana] (TAIR:AT3G56980.1); similar to basic helix-loop-helix family protein [Thlaspi caerulescens] (GB:ABD37969.1); contains InterPro domain Achaete-scute transcription factor related (InterPro:IPR015660); contains InterPro domain Basic helix-loop-helix dimerisation region bHLH; (InterPro:IPR001092); contains InterPro domain Helix-loop-helix DNA-binding; (InterPro:IPR011598) | (GO:0009414) response to water deprivation [IEP] | (GO:0045449) regulation of transcription [TAS] | (GO:0003677) DNA binding [ISS]                    |  |
| AT3G21190 | -0,72 | EUGENE prediction                             | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G51630.1); similar to Os09g0498800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063569.1); similar to unknown [Flaveria brownii] (GB:AAW56451.1); contains InterPro domain Protein of unknown function DUF246, plant; (InterPro:IPR004348)                                                                                                                                                                                    |                                                  |                                                |                                                   |  |
| AT3G01290 | -1,16 | unknown protein                               | <b>[Arabidopsis thaliana] (TAIR:AT5G62740.1); similar to hypersensitive-induced response protein [Carica papaya] (GB:ABS01349.1); contains InterPro domain Stomatin; (InterPro:IPR001972); contains InterPro domain Band 7 protein (InterPro:IPR001107)</b>                                                                                                                                                                                                                                    | No annotation for biological_process             | No annotation for molecular_function           | (GO:0016020) membrane [IDA]                       |  |
| AT3G15630 | -1,12 | unknown protein                               | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G52720.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46032.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN71657.1)                                                                                                                                                                                                                                                                                    | (GO:0008150) biological_process [ND]             | (GO:0003674) molecular_function [ND]           | (GO:0009507) chloroplast [IEA]                    |  |
| AT3G20340 | -0,86 | unknown protein                               | Expression of the gene is downregulated in the presence of paraquat, an inducer of photooxidative stress.                                                                                                                                                                                                                                                                                                                                                                                      | (GO:0006979) response to oxidative stress [IMP]  | (GO:0003674) molecular_function [ND]           | (GO:0005575) cellular_component [ND]              |  |
| AT3G30775 | -2,06 | ERD5 (PROLINE OXIDASE); proline dehydrogenase | Encodes a proline oxidase that is predicted to localize to the inner mitochondrial membrane, its mRNA expression induced by high levels of AI and by osmotic stress. The promoter contains an L-proline-inducible element.                                                                                                                                                                                                                                                                     | (GO:0006979) response to oxidative stress [IEP]  | (GO:0006562) proline catabolic process [IGI]   | (GO:0006537) glutamate biosynthetic process [ISS] |  |

|           |       |                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                            |                                                                                          |                                                   |  |
|-----------|-------|----------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------|------------------------------------------------------------------------------------------|---------------------------------------------------|--|
| AT3G47340 | -1,67 | ASN1 (DARK INDUCIBLE 6)                      | <p>encodes a glutamine-dependent asparagine synthetase, the predicted ASN1 peptide contains a purF-type glutamine-binding domain, and is expressed predominantly in shoot tissues, where light has a negative effect on its mRNA accumulation. Expression is induced within 3 hours of dark treatment, in senescing leaves and treatment with exogenous photosynthesis inhibitor. Induction of gene expression was suppressed in excised leaves supplied with sugar. The authors suggest that the gene's expression pattern is responding to the level of sugar in the cell.</p> | (GO:0043617) cellular response to sucrose starvation [IEP] | (GO:0009063) amino acid catabolic process [TAS]                                          | (GO:0009646) response to absence of light [TAS]   |  |
| AT3G54880 | -1,07 | unknown protein                              | <p>similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25360.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68874.1)</p>                                                                                                                                                                                                                                                                                                                                                                                                                                 | (GO:0008150) biological_process [ND]                       | (GO:0003674) molecular_function [ND]                                                     | (GO:0005575) cellular_component [ND]              |  |
| AT3G55500 | 1,81  | ATEXPA16 (ARABIDOPSIS THALIANA EXPANSIN A16) | <p>expansin-like protein. Naming convention from the Expansin Working Group (Kende et al, 2004. Plant Mol Bio). Involved in the formation of nematode-induced syncytia in roots of Arabidopsis thaliana.</p>                                                                                                                                                                                                                                                                                                                                                                     | (GO:0009826) unidimensional cell growth [NAS]              | (GO:0009831) plant-type cell wall modification during multidimensional cell growth [ISS] | (GO:0009828) plant-type cell wall loosening [NAS] |  |
| AT3G56980 | 1,34  | ORG3; DNA binding / transcription factor     | <p>similar to BHLH038/ORG2 (OBP3-RESPONSIVE GENE 2), DNA binding / transcription factor [Arabidopsis thaliana] (TAIR:AT3G56970.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN64266.1); contains InterPro domain Achaete-scute transcription factor related (InterPro:IPR015660); contains InterPro domain Basic helix-loop-helix dimerisation region bHLH; (InterPro:IPR001092); contains InterPro domain Helix-loop-helix DNA-binding; (InterPro:IPR011598)</p>                                                                                                   | (GO:0045449) regulation of transcription [TAS]             | (GO:0003677) DNA binding [ISS]                                                           | (GO:0003700) transcription factor activity [ISS]  |  |

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|-----------|-------|-------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------------------|-----------------------------------------------------------------|--|
| AT4G00970 | 1.47  | ATP binding / protein kinase/ protein-serine/threonine kinase/ protein-tyrosine kinase    | Identical to Cysteine-rich receptor-like protein kinase 41 precursor (CRK41) [Arabidopsis thaliana] (GB:O23081); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:AT4G21410.1); similar to receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris] (GB:AAD21872.1); contains InterPro domain Protein of unknown function DUF26 (InterPro:IPR002902); contains InterPro domain Protein kinase, core; (InterPro:IPR000719); contains InterPro domain Protein kinase-like (InterPro:IPR011009); contains InterPro domain Serine/threonine protein kinase, active site; (InterPro:IPR008271) | (GO:0006468) protein amino acid phosphorylation [IEA]            | (GO:0004672) protein kinase activity [ISS]             | (GO:0012505) endomembrane system [IEA]                          |  |
| AT4G03510 | -1.21 | RMA1; protein binding / ubiquitin-protein ligase/ zinc ion binding                        | RMA1 encodes a novel 28 kDa protein with a RING finger motif and a C-terminal membrane-anchoring domain that is involved in the secretory pathway.                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | (GO:0006511) ubiquitin-dependent protein catabolic process [IDA] | (GO:0032940) secretion by cell [IGI]                   | (GO:0005515) protein binding [ISS]                              |  |
| AT4G16745 | 1.29  | unknown protein                                                                           | similar to exostosin family protein [Arabidopsis thaliana] (TAIR:AT5G19670.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO16155.1); contains InterPro domain Exostosin-like; (InterPro:IPR004263)                                                                                                                                                                                                                                                                                                                                                                                                      | (GO:0008150) biological_process [ND]                             | (GO:0003674) molecular_function [ND]                   | (GO:0016020) membrane [ISS]                                     |  |
| AT4G24230 | -0.86 | acyl-CoA binding                                                                          | acyl-CoA-binding protein ACBP3. Localized extracellularly in transiently expressed tobacco BY-2 cells and onion epidermal cells. Binds arachidonyl-CoA with high affinity.                                                                                                                                                                                                                                                                                                                                                                                                                                             | (GO:0015908) fatty acid transport [TAS]                          | (GO:0000062) acyl-CoA binding [IDA]                    | (GO:0005576) extracellular region [IDA]                         |  |
| AT4G24880 | 0.92  | unknown protein                                                                           | similar to P0402A09.9 [Oryza sativa (japonica cultivar-group)] (GB:BAB62626.1); similar to Os01g0101300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001041742.1); contains domain FAMILY NOT NAMED (PTHR13403); contains domain no description (G3D.2.90.10.10); contains domain SUBFAMILY NOT NAMED (PTHR13403:SF3); contains domain DNA ligase/mRNA capping enzyme, catalytic domain (SSF56091)                                                                                                                                                                                                                  |                                                                  |                                                        |                                                                 |  |
| AT4G30270 | -1.39 | MERI5B; hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds | encodes a protein similar to endo xyloglucan transferase in sequence. It is also very similar to BRU1 in soybean, which is involved in brassinosteroid response.                                                                                                                                                                                                                                                                                                                                                                                                                                                       | (GO:0007568) aging [IEP]                                         | (GO:0009740) gibberellic acid mediated signaling [TAS] | (GO:0016762) xyloglucan:xyloglucosyl transferase activity [IDA] |  |

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|-----------|-------|--------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------|--------------------------------------------------------------------|--|
| AT4G36670 | -1,76 | carbohydrate transporter/ sugar porter           | Identical to Probable polyol transporter 6 (PLT6) [Arabidopsis thaliana] (GB:Q8GXR2;GB:O23213); similar to mannitol transporter, putative [Arabidopsis thaliana] (TAIR:AT2G18480.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN68316.1); contains InterPro domain General substrate transporter; (InterPro:IPR005828); contains InterPro domain Major facilitator superfamily; (InterPro:IPR007114); contains InterPro domain Sugar transporter, conserved site; (InterPro:IPR005829); contains InterPro domain MFS general substrate transporter (InterPro:IPR016196); contains InterPro domain Sugar transporter; (InterPro:IPR003663) | (GO:0006810) transport [IEA]                                     | (GO:0008643) carbohydrate transport [IEA]  | (GO:0015144) carbohydrate transmembrane transporter activity [ISS] |  |
| AT5G01200 | 1,39  | DNA binding / transcription factor               | [Arabidopsis thaliana] (TAIR:AT2G38090.1); similar to MYB transcription factor [Hevea brasiliensis] (GB:AAU06309.1); contains InterPro domain Molecular chaperone, heat shock protein, Hsp40, DnaJ (InterPro:IPR015609); contains InterPro domain SANT, DNA-binding; (InterPro:IPR001005); contains InterPro domain Homeodomain-like (InterPro:IPR009057); contains InterPro domain Myb, DNA-binding (InterPro:IPR014778); contains InterPro domain Myb-like DNA-binding region, SHAQKYF class (InterPro:IPR006447)                                                                                                                                    | (GO:0006355) regulation of transcription, DNA-dependent [ISS]    | (GO:0003677) DNA binding [ISS]             | (GO:0003700) transcription factor activity [ISS]                   |  |
| AT5G01730 | 1,51  | wave3                                            | putative WAVE homolog                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | (GO:0051127) positive regulation of actin nucleation [IMP]       | (GO:0003674) molecular_function [ND]       | (GO:0031209) SCAR complex [TAS]                                    |  |
| AT5G03545 | 1,14  | unknown protein                                  | No description                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | (GO:0008150) biological_process [ND]                             | (GO:0003674) molecular_function [ND]       | (GO:0005575) cellular_component [ND]                               |  |
| AT5G05780 | -1,62 | ATHMOV34                                         | Encodes a putative 26S proteasome subunit RPN8a. The function of RPN8a and other 26S subunits may be required for specifying leaf adaxial identity.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | (GO:0006511) ubiquitin-dependent protein catabolic process [TAS] | (GO:0009965) leaf morphogenesis [IMP]      | (GO:0003674) molecular_function [ND]                               |  |
| AT5G07440 | -1,85 | GDH2 (GLUTAMATE DEHYDROGENASE 2); oxidoreductase | Encodes the alpha-subunit of the glutamate dehydrogenase. The enzyme is almost exclusively found in the mitochondria of stem and leaf companion cells.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | (GO:0046686) response to cadmium ion [IEP]                       | (GO:0009651) response to salt stress [IEP] | (GO:0004353) glutamate dehydrogenase [NAD(P)+] activity [IDA]      |  |

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|-----------|-------|---------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------|--|
| AT5G14280 | -1,04 | transcription regulator                                                                           | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G27270.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14611.1); contains InterPro domain TRAM, LAG1 and CLN8 homology; (InterPro:IPR006634); contains InterPro domain Protein of unknown function DUF573 (InterPro:IPR007592)                                                                        | (GO:0008150) biological_process [ND]            | (GO:0003674) molecular_function [ISS]                                   | (GO:0030528) transcription regulator activity [TAS] |  |
| AT5G15500 | 0,99  | protein binding                                                                                   | similar to ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:AT4G10720.1); similar to Ankyrin [Medicago truncatula] (GB:ABO82122.1); contains InterPro domain Ankyrin (InterPro:IPR002110)                                                                                                                                                                             | (GO:0008150) biological_process [ND]            | (GO:0005515) protein binding [ISS]                                      | (GO:0012505) endomembrane system [IEA]              |  |
| AT5G20230 | -0,96 | <b>ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron transporter</b> | <b>Al-stress-induced gene</b>                                                                                                                                                                                                                                                                                                                                                   | (GO:0006979) response to oxidative stress [TAS] | (GO:0009611) response to wounding [IEP]                                 | (GO:0009646) response to absence of light [IEP]     |  |
| AT5G20250 | -1,07 | DIN10 (DARK INDUCIBLE 10); hydrolase, hydrolyzing O-glycosyl compounds                            | encodes a member of glycosyl hydrolase family 36. Expression is induced within 3 hours of dark treatment, in senescing leaves and treatment with exogenous photosynthesis inhibitor. Induction of gene expression was suppressed in excised leaves supplied with sugar. The authors suggest that the gene's expression pattern is responding to the level of sugar in the cell. | No annotation for biological_process            | (GO:0004553) hydrolase activity, hydrolyzing O-glycosyl compounds [ISS] | (GO:0009507) chloroplast [IDA]                      |  |
| AT5G22920 | -0,92 | ubiquitin-protein ligase/ zinc ion binding                                                        | similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:AT5G25560.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO16747.1); contains InterPro domain Zinc finger, CHY-type; (InterPro:IPR008913); contains InterPro domain Zinc finger, RING-type; (InterPro:IPR001841)                                                      | No annotation for biological_process            | (GO:0008270) zinc ion binding [ISS]                                     | No annotation for cellular_component                |  |
| AT5G27845 | 2,09  | unknown protein                                                                                   | transposable element gene; non-LTR retrotransposon family (LINE), has a 6.6e-32 P-value blast match to GB:AAA39398 ORF2 (Mus musculus) (LINE-element)                                                                                                                                                                                                                           |                                                 |                                                                         |                                                     |  |
| AT5G28910 | 1,07  | unknown protein                                                                                   | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G28960.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO44656.1)                                                                                                                                                                                                                                       | (GO:0008150) biological_process [ND]            | No annotation for molecular_function                                    | (GO:0005739) mitochondrion [IEA]                    |  |
| AT5G28920 | -1,17 | unknown protein                                                                                   | No description                                                                                                                                                                                                                                                                                                                                                                  | (GO:0008150) biological_process [ND]            | (GO:0003674) molecular_function [ND]                                    | (GO:0005575) cellular_component [ND]                |  |

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| AT5G33320 | 2.00  | CUE1 (CAB UNDEREXPRESSED 1); antiporter/ triose-phosphate transporter | Encodes a plastid inner envelope protein PPT (phosphoenolpyruvate/phosphate translocator) that catalyzes the transport of phosphoenolpyruvate and phosphate across the inner envelope membrane of plastids.                                                                                                                                                                                                                                                                                                                                                                                             | (GO:0015717) triose phosphate transport [ISS] | (GO:0009670) triose-phosphate transmembrane transporter activity [ISS] | (GO:0015297) antiporter activity [ISS]                      |
| AT5G35935 | -0.80 | unknown protein                                                       | transposable element gene; copia-like retrotransposon family, has a 2.0e-232 P-value blast match to GB:CAA72989 open reading frame 1 (Ty1_Copia-element) (Brassica oleracea)                                                                                                                                                                                                                                                                                                                                                                                                                            |                                               |                                                                        |                                                             |
| AT5G36930 | -0.83 | ATP binding / transmembrane receptor                                  | [Arabidopsis thaliana] (TAIR:AT5G17680.1); similar to TIR-NBS type disease resistance protein [Populus trichocarpa] (GB:ABF81459.1); similar to TIR-NBS disease resistance-like protein [Populus trichocarpa] (GB:ABB82027.1); similar to TIR-NBS disease resistance-like protein [Populus trichocarpa] (GB:ABB82031.1); contains InterPro domain Disease resistance protein; (InterPro:IPR000767); contains InterPro domain Toll-Interleukin receptor; (InterPro:IPR000157); contains InterPro domain NB-ARC; (InterPro:IPR002182); contains InterPro domain Leucine-rich repeat; (InterPro:IPR001611) | (GO:0006952) defense response [ISS]           | (GO:0005524) ATP binding [IEA]                                         | (GO:0005515) protein binding [IEA]                          |
| AT5G37350 | -0.83 | unknown protein                                                       | similar to RIO1 family protein [Arabidopsis thaliana] (TAIR:AT2G24990.1); similar to RIO kinase [Nicotiana tabacum] (GB:BAD12556.1); contains InterPro domain Protein kinase-like (InterPro:IPR011009); contains InterPro domain RIO kinase; (InterPro:IPR000687)                                                                                                                                                                                                                                                                                                                                       | No annotation for biological_process          | (GO:0005524) ATP binding [IEA]                                         | (GO:0004674) protein serine/threonine kinase activity [IEA] |
| AT5G39580 | -1.01 | peroxidase                                                            | (PER62) [Arabidopsis Thaliana] (GB:Q9FKA4;GB:P93724); similar to peroxidase, putative [Arabidopsis thaliana] (TAIR:AT5G64120.1); similar to Cationic peroxidase 2 precursor (PNPC2) (GB:P22196); contains InterPro domain Plant peroxidase; (InterPro:IPR000823); contains InterPro domain Haem peroxidase; (InterPro:IPR010255); contains InterPro domain Haem peroxidase, plant/fungal/bacterial; (InterPro:IPR002016)                                                                                                                                                                                | (GO:0050832) defense response to fungus [IMP] | (GO:0004601) peroxidase activity [ISS]                                 | (GO:0012505) endomembrane system [IEA]                      |

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| AT5G40370 | 1.00  | arsenate reductase (glutaredoxin)/<br>electron transporter/ thiol-disulfide<br>exchange intermediate | Identical to Glutaredoxin-C2 (GRXC2)<br>[Arabidopsis thaliana] (GB:Q9FNE2);<br>similar to glutaredoxin, putative<br>[Arabidopsis thaliana]<br>(TAIR:AT5G63030.1); similar to<br>glutaredoxin [Tilia platyphyllos]<br>(GB:AAL04507.1); contains InterPro<br>domain Thioredoxin-like fold<br>(InterPro:IPR012336); contains InterPro<br>domain Glutaredoxin, eukaryotic and<br>viruses; (InterPro:IPR011899); contains<br>InterPro domain Thioredoxin fold<br>(InterPro:IPR012335); contains InterPro<br>domain Glutaredoxin;<br>(InterPro:IPR002109); contains InterPro<br>domain Glutaredoxin subgroup<br>(InterPro:IPR014025)                                                                                                       | No annotation for<br>biological_process             | (GO:0008794) arsenate reductase<br>(glutaredoxin) activity [ISS]          | (GO:0005886) plasma<br>membrane [IDA]                 |  |
| AT5G41080 | -1.56 | glycerophosphodiester<br>phosphodiesterase                                                           | similar to SRG3 (SENESCENCE-<br>RELATED GENE 3),<br>glycerophosphodiester<br>phosphodiesterase [Arabidopsis thaliana]<br>(TAIR:AT3G02040.1); similar to unnamed<br>protein product [Vitis vinifera]<br>(GB:CAO49062.1); similar to hypothetical<br>protein [Vitis vinifera] (GB:CAN71478.1);<br>contains InterPro domain<br>Glycerophosphoryl diester<br>phosphodiesterase; (InterPro:IPR004129)                                                                                                                                                                                                                                                                                                                                     | (GO:0006071)<br>glycerol metabolic<br>process [ISS] | (GO:0008889)<br>glycerophosphodiester<br>phosphodiesterase activity [ISS] | No annotation for<br>cellular_component               |  |
| AT5G41370 | -0.81 | XPB1; ATP binding / ATP-<br>dependent helicase/ DNA binding /<br>helicase/ nucleic acid binding      | Encodes XPB1, a DNA repair protein and<br>transcription factor. Arabidopsis thaliana<br>has duplicated XPB gene (AtXPB1 and<br>AtXPB2, with high similarity to each<br>other). XPB proteins are involved in both<br>DNA repair and transcription, they are<br>component of the transcription factor IIH<br>(TFIIH) and are responsible for DNA<br>helicase activity during nucleotide (nt)<br>excision repair (NER). Complementation<br>assays in yeast rad25 mutant strains<br>suggest the involvement of AtXPB2 in<br>DNA repair. Although both genes are<br>expressed in a constitutive manner during<br>the plant life cycle, Northern blot analyses<br>suggest that light modulates the<br>expression level of both XPB copies. | (GO:0009411)<br>response to UV [IEP]                | (GO:0009636) response to toxin<br>[IMP]                                   | (GO:0008026) ATP-dependent<br>helicase activity [ISS] |  |

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| AT5G42390 | -0.79 | metalloendopeptidase | similar to peptidase M16 family protein / insulinase family protein [Arabidopsis thaliana] (TAIR:AT5G56730.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO66322.1); similar to metalloendopeptidase (GB:AAA81472.1); similar to hypothetical protein OsJ_021174 [Oryza sativa (japonica cultivar-group)] (GB:EAZ37691.1); contains InterPro domain Peptidase M16, N-terminal; (InterPro:IPR011765); contains InterPro domain Peptidase M16, C-terminal; (InterPro:IPR007863); contains InterPro domain Metalloenzyme, LuxS/M16 peptidase-like, metal-binding; (InterPro:IPR011249); contains InterPro domain Peptidase M16, core; (InterPro:IPR011237) | (GO:0006508) proteolysis [ISS]            | (GO:0004222) metalloendopeptidase activity [ISS] | (GO:0005739) mitochondrion [IDA]     |  |
| AT5G42850 | 0.74  | electron transporter | similar to unnamed protein product [Vitis vinifera] (GB:CAO15096.1); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Thioredoxin fold (InterPro:IPR012335); contains InterPro domain Thioredoxin-related; (InterPro:IPR006662); contains InterPro domain Protein of unknown function DUF953, thioredoxin-like (InterPro:IPR010357)                                                                                                                                                                                                                                                                                       | (GO:0045454) cell redox homeostasis [ISS] | No annotation for molecular_function             | (GO:0005575) cellular_component [ND] |  |
| AT5G43050 | -0.82 | unknown protein      | similar to hypothetical protein Osl_015859 [Oryza sativa (indica cultivar-group)] (GB:EAY94626.1); similar to Os04g0488600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001053153.1); contains InterPro domain Protein of unknown function DUF565 (InterPro:IPR007572)                                                                                                                                                                                                                                                                                                                                                                                              | (GO:0008150) biological_process [ND]      | (GO:0003674) molecular_function [ND]             | (GO:0009507) chloroplast [IEA]       |  |
| AT5G43210 | 1.40  | nuclease             | similar to endo/excinuclease amino terminal domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G30350.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO40743.1); contains InterPro domain Excinuclease ABC, C subunit, N-terminal; (InterPro:IPR000305)                                                                                                                                                                                                                                                                                                                                                                                           | (GO:0006281) DNA repair [ISS]             | (GO:0004518) nuclease activity [ISS]             | (GO:0005622) intracellular [ISS]     |  |

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| AT5G44090 | 0.80  | calcium ion binding                                                                            | protein [Arabidopsis thaliana] (TAIR:AT1G03960.1); similar to calcium-binding EF-hand family protein [Arabidopsis thaliana] (TAIR:AT1G54450.1); similar to calcium-binding EF hand family protein [Arabidopsis thaliana] (TAIR:AT5G28850.2); similar to putative protein phosphatase 2A regulatory subunit [Oryza sativa (japonica cultivar-group)] (GB:AAK13162.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40604.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65086.1); contains InterPro domain EF-Hand type; (InterPro:IPR011992); contains InterPro domain Calcium-binding EF-hand; (InterPro:IPR002048) | (GO:0008150) biological_process [ND]                  | (GO:0005509) calcium ion binding [ISS] | (GO:0005739) mitochondrion [IDA]     |
| AT5G45430 | -1.45 | ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase | similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:AT4G19110.2); similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:AT4G19110.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO66722.1); contains InterPro domain Serine/threonine protein kinase; (InterPro:IPR002290); contains InterPro domain Protein kinase, core; (InterPro:IPR000719); contains InterPro domain Protein kinase-like (InterPro:IPR011009); contains InterPro domain Serine/threonine protein kinase, active site; (InterPro:IPR008271)                                                                                             | (GO:0006468) protein amino acid phosphorylation [IEA] | (GO:0016301) kinase activity [ISS]     | (GO:0005575) cellular_component [ND] |
| AT5G45490 | -2.56 | ATP binding                                                                                    | Identical to Probable disease resistance protein At5g45490 [Arabidopsis Thaliana] (GB:Q9FHI7); similar to disease resistance protein-related [Arabidopsis thaliana] (TAIR:AT5G45440.1); similar to blight resistance protein RGA3-like [Oryza sativa (japonica cultivar-group)] (GB:BAB92410.1); contains InterPro domain NB-ARC; (InterPro:IPR002182)                                                                                                                                                                                                                                                                                             | (GO:0006915) apoptosis [IEA]                          | (GO:0005524) ATP binding [IEA]         | (GO:0005575) cellular_component [ND] |

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| AT5G45500 | -1,32 | unknown protein | [ <i>Arabidopsis thaliana</i> ] (TAIR:AT5G45520.1); similar to unnamed protein product [ <i>Vitis vinifera</i> ] (GB:CAO43141.1); similar to Os01g0799000 [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:NP_001044526.1); contains domain SSF52047 (SSF52047); contains domain G3DSA:3.80.10.10 (G3DSA:3.80.10.10)                                                                                                                                                                                     | (GO:0008150) biological_process [ND] | (GO:0003674) molecular_function [ND] | (GO:0005575) cellular_component [ND]   |  |
| AT5G45510 | -0,96 | unknown protein | [ <i>Arabidopsis thaliana</i> ] (GB:Q8VZC7;GB:Q9FHI5); similar to mob1/phocein family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:AT4G19050.1); similar to predicted protein [ <i>Physcomitrella patens</i> subsp. <i>patens</i> ] (GB:EDQ65894.1); contains InterPro domain Disease resistance protein; (InterPro:IPR000767); contains InterPro domain Leucine-rich repeat; (InterPro:IPR001611)                                                                                                          | (GO:0006952) defense response [IEA]  | (GO:0005515) protein binding [IEA]   | (GO:0005575) cellular_component [ND]   |  |
| AT5G47250 | 1,07  | ATP binding     | Identical to Probable disease resistance protein At5g47250 [ <i>Arabidopsis thaliana</i> ] (GB:Q9LVT4;GB:Q0WVJ2); similar to disease resistance protein (CC-NBS-LRR class), putative [ <i>Arabidopsis thaliana</i> ] (TAIR:AT1G12280.1); similar to RFL1 [ <i>Arabidopsis lyrata</i> ] (GB:AAL65637.1); contains InterPro domain Disease resistance protein; (InterPro:IPR000767); contains InterPro domain NB-ARC; (InterPro:IPR002182); contains InterPro domain Leucine-rich repeat; (InterPro:IPR001611) | (GO:0006952) defense response [ISS]  | (GO:0005524) ATP binding [IEA]       | (GO:0005515) protein binding [IEA]     |  |
| AT5G48335 | -1,02 | unknown protein | similar to unknown protein [ <i>Arabidopsis thaliana</i> ] (TAIR:AT3G07580.1); similar to unnamed protein product [ <i>Vitis vinifera</i> ] (GB:CAO44467.1)                                                                                                                                                                                                                                                                                                                                                  | (GO:0008150) biological_process [ND] | (GO:0003674) molecular_function [ND] | (GO:0009507) chloroplast [IEA]         |  |
| AT5G48490 | 0,94  | lipid binding   | INDUCED RESISTANCE 1), lipid binding [ <i>Arabidopsis thaliana</i> ] (TAIR:AT5G48485.1); similar to unnamed protein product [ <i>Vitis vinifera</i> ] (GB:CAO15596.1); contains InterPro domain Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor (InterPro:IPR003612); contains InterPro domain Bifunctional inhibitor/plant lipid transfer protein/seed storage (InterPro:IPR016140)                                                                                               | (GO:0006869) lipid transport [ISS]   | (GO:0008289) lipid binding [ISS]     | (GO:0012505) endomembrane system [IEA] |  |

similar to WD-40 repeat family protein /

|           |       |                          |                                                                                                                                                                                                                                                                                                                                                   |                                                           |                                                                                                                           |                                                     |  |
|-----------|-------|--------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------|--|
| AT5G50650 | -0.90 | nucleotide binding       | St12p protein, putative [Arabidopsis thaliana] (TAIR:AT5G50550.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42285.1); contains InterPro domain WD40 repeat-like (InterPro:IPR011046); contains InterPro domain WD40/YVTN repeat-like (InterPro:IPR015943); contains InterPro domain WD40 repeat (InterPro:IPR001680)            | (GO:0008150) biological_process [ND]                      | (GO:0000166) nucleotide binding [ISS]                                                                                     | (GO:0005575) cellular_component [ND]                |  |
| AT5G51820 | -0.87 | PGM (PHOSPHOGLUCOMUTASE) | Encodes a plastid isoform of the enzyme phosphoglucomutase involved in controlling photosynthetic carbon flow. Effective petiole movement against the direction of the gravity requires functional PGM activity that is required for full development of amyloplasts.                                                                             | (GO:0019252) starch biosynthetic process [IMP]            | (GO:0009590) detection of gravity [IMP]                                                                                   | (GO:0009409) response to cold [IEP]                 |  |
| AT5G52470 | -0.97 | FIB1 (FIBRILLARIN 1)     | encodes a fibrillarlin, a key nucleolar protein in eukaryotes which associates with box C/D small nucleolar RNAs (snoRNAs) directing 2'-O-ribose methylation of the rRNA. This gene also encodes a novel box C/D snoRNA, U60.1f in its fifth intron that accumulates in seedlings and that their targeted residue on the 25 S rRNA is methylated. | (GO:0001510) RNA methylation [IGI]                        | (GO:0006364) rRNA processing [IGI]                                                                                        | (GO:0030515) snoRNA binding [ISS]                   |  |
| AT5G64090 | 1.06  | unknown protein          | similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G21050.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO43471.1)                                                                                                                                                                                                         | (GO:0008150) biological_process [ND]                      | (GO:0003674) molecular_function [ND]                                                                                      | (GO:0005886) plasma membrane [IDA]                  |  |
| ATCG00200 | 1.05  | tRNA-Cys                 | a chloroplast-encoded tRNA for cysteine                                                                                                                                                                                                                                                                                                           | (GO:0006414) translational elongation [TAS]               | (GO:0030533) triplet codon-amino acid adaptor activity [TAS]                                                              | (GO:0009507) chloroplast [TAS]                      |  |
| ATCG00210 | 1.35  | YCF6                     | hypothetical protein                                                                                                                                                                                                                                                                                                                              | (GO:0017004) cytochrome complex assembly [IEA]            | (GO:0045158) electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II activity [IEA] | (GO:0012505) endomembrane system [IEA]              |  |
| ATCG00380 | 5.22  | RPS4                     | Chloroplast encoded ribosomal protein S4                                                                                                                                                                                                                                                                                                          | (GO:0006412) translation [TAS]                            | (GO:0003735) structural constituent of ribosome [TAS]                                                                     | (GO:0016020) membrane [IDA]                         |  |
| ATCG00380 | 5.37  | RPS4                     | Chloroplast encoded ribosomal protein S4                                                                                                                                                                                                                                                                                                          | (GO:0006412) translation [TAS]                            | (GO:0003735) structural constituent of ribosome [TAS]                                                                     | (GO:0016020) membrane [IDA]                         |  |
| ATCG00430 | 1.06  | PSBG NDHC                | thought to be part of photosystem II but its wheat homolog was later shown to encode for subunit K of NADH dehydrogenase.                                                                                                                                                                                                                         | (GO:0008120) electron transport, NADH to ubiquinone [IEA] | (GO:0016651) oxidoreductase activity, acting on NADH or NADPH [IEA]                                                       | (GO:0051539) 4 iron, 4 sulfur cluster binding [IEA] |  |
| ATCG01040 | -1.10 | YCF5                     | hypothetical protein                                                                                                                                                                                                                                                                                                                              | (GO:0008535) respiratory chain complex IV assembly [IEA]  | (GO:0006461) protein complex assembly [IEA]                                                                               | No annotation for molecular_function                |  |

|                                                                                                                             |       |        |                      |  |  |  |  |
|-----------------------------------------------------------------------------------------------------------------------------|-------|--------|----------------------|--|--|--|--|
| ATMG01090                                                                                                                   | -1,06 | ORF262 | hypothetical protein |  |  |  |  |
| Notes:                                                                                                                      |       |        |                      |  |  |  |  |
|                                                                                                                             |       |        |                      |  |  |  |  |
| For meaning of evidence codes (IDA, ISS, IEA, ...) please refer to evidence code guide on Gene Ontology Consortium website. |       |        |                      |  |  |  |  |
| Grey lines indicate cell wall-related entries                                                                               |       |        |                      |  |  |  |  |