**Table S3** Functional annotation with Blast2GO predicted for the new loci, DEGs and DEGs under high impact predicted effects (HIPE).

| Cufflinks ID | Major Transcript | Sequence Description | GO Terms | Enzymes | Kegg Maps |
|---|---|---|---|---|---|
| **NEW LOCI** | | | | | |
| XLOC_000084 | TCONS_00000157 | dna-directed rna polymerases i and iii subunit rpac2 | DNA-directed RNA polymerase III complex;DNA binding;DNA-directed RNA polymerase activity;protein dimerization activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_000219 | TCONS_00000420 | aspartate aminotransferase mitochondrial | L-aspartate:2-oxoglutarate aminotransferase activity;pyridoxal phosphate binding;L-phenylalanine:2-oxoglutarate aminotransferase activity;cellular amino acid metabolic process;biosynthetic process | ec:2.6.1.57-transaminase;ec:2.6.1.9-transaminase;ec:2.6.1.5-transaminase;ec:2.6.1.1-transaminase | Lysine biosynthesis;Phenylalanine metabolism;Tropane, piperidine and pyridine alkaloid biosynthesis;Tyrosine metabolism;Biosynthesis of antibiotics;Isoquinoline alkaloid biosynthesis;Cysteine and methionine metabolism;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesisPhenylalanine metabolism;Tropane, piperidine and pyridine alkaloid biosynthesis;Tyrosine metabolism;Biosynthesis of antibiotics;Histidine metabolism;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesisPhenylalanine metabolism;Ubiquinone and other terpenoid-quinone biosynthesis;Tropane, piperidine and pyridine alkaloid biosynthesis;Tyrosine metabolism;Biosynthesis of antibiotics;Isoquinoline alkaloid biosynthesis;Cysteine and methionine metabolism;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesisArginine and proline metabolism;Phenylalanine metabolism;Carbon fixation in photosynthetic organisms;Tropane, piperidine and pyridine alkaloid biosynthesis;Tyrosine metabolism;Arginine biosynthesis;Alanine, aspartate and glutamate metabolism;Biosynthesis of antibiotics;Isoquinoline alkaloid biosynthesis;Cysteine and methionine metabolism;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesis |
| XLOC_000316 | TCONS_00000626 | tom1-like protein 2 | intracellular;intracellular protein transport | | |
| XLOC_000351 | TCONS_00000697 | peroxisomal -dienoyl-reductase-like | | | |
| XLOC_000434 | TCONS_00000869 | cysteine-rich and transmembrane domain-containing protein a-like | | | |
| XLOC_000483 | TCONS_00000970 | k(+) efflux antiporter 4 isoform x1 | | | |
| XLOC_000484 | TCONS_00000973 | hypothetical protein PHAVU_001G118000g | | | |
| XLOC_000516 | TCONS_00001026 | regulation of nuclear pre-mrna domain-containing protein 1b-like | | | |
| XLOC_000534 | TCONS_00001052 | transcription factor iiib 90 kda subunit-like isoform x2 | transcription factor TFIIIB complex;zinc ion binding;TBP-class protein binding;regulation of transcription, DNA-templated;transcription | | |

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| | | | initiation from RNA polymerase III promoter | | |
| XLOC_000535 | TCONS_00001053 | transcription factor iiib 90 kda subunit-like isoform x2 | transcription factor TFIIIB complex;zinc ion binding;TBP-class protein binding;regulation of transcription, DNA-templated;transcription initiation from RNA polymerase III promoter | | |
| XLOC_000574 | TCONS_00001132 | histone deacetylase | nucleus;metal ion binding;cellular process | | |
| XLOC_000576 | TCONS_00001136 | hypothetical protein PHAVU_L006100g | | | |
| XLOC_000666 | TCONS_00001297 | abc transporter g family member 15-like | plasmodesma;membrane;ATP binding;organic phosphonate transmembrane-transporting ATPase activity;metabolic process;response to salt stress;organic phosphonate transport;organophosphate ester transport;cutin transport;petal epidermis patterning | ec:3.6.3.28;ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_000683 | TCONS_00001315 | disease resistance protein rga4 | phosphoprotein phosphatase activity;ADP binding;protein dephosphorylation | ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| XLOC_000774 | TCONS_00001487 | pre-mrna-splicing factor 18 | spliceosomal complex;RNA splicing | | |
| XLOC_000790 | TCONS_00001518 | protein clec16a like | | | |
| XLOC_000814 | TCONS_00001558 | hypothetical protein LR48_Vigan05g011100 | | | |
| XLOC_000895 | TCONS_00001723 | syntaxin of plants protein | endoplasmic reticulum;plasma membrane;plasmodesma;SNAP receptor activity;protein transporter activity;protein targeting to membrane;membrane fusion | | |
| XLOC_001428 | TCONS_00002742 | hypothetical protein VIGAN_03280800 | | | |
| XLOC_001558 | TCONS_00002992 | myosin-j heavy chain | myosin complex;motor activity;DNA topoisomerase type I activity;ATP binding;actin filament binding;metabolic process | ec:5.99.1.2;ec:3.6.1.15-phosphatase;ec:3.6.1;ec:5.99.1 | Purine metabolism;Thiamine metabolism |
| XLOC_001581 | TCONS_00003037 | hypothetical protein VIGAN_03245500 | | | |
| XLOC_001720 | TCONS_00003349 | peroxisomal -dienoyl-reductase-like | vacuolar membrane;peroxisome;kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;2,4-dienoyl-CoA reductase (NADPH) activity;microtubule-based movement;oxidation-reduction process | ec:3.6.1.15-phosphatase;ec:1.3.1.34;ec:3.6.1 | Purine metabolism;Thiamine metabolism |

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| XLOC_001761 | TCONS_00003426 | peptidyl-prolyl cis-trans isomerase fkbp62-like | nucleus;cytosol;cell periphery;peptidyl-prolyl cis-trans isomerase activity;phosphatidylinositol-3-phosphate binding;phosphatidylinositol-3,5-bisphosphate binding;protein peptidyl-prolyl isomerization;protein folding;response to osmotic stress;response to heat;response to cytokinin;seed germination | ec:5.2.1.8 | |
| XLOC_001777 | TCONS_00003464 | glycerophosphodiester phosphodiesterase gdpd6 | vacuole;glycerophosphodiester phosphodiesterase activity;glycerol metabolic process;lipid metabolic process | ec:3.1.4.46-phosphodiesterase;ec:3.1 | Glycerophospholipid metabolism |
| XLOC_001781 | TCONS_00003471 | brefeldin a-inhibited guanine nucleotide-exchange protein 5 | ARF guanyl-nucleotide exchange factor activity;regulation of ARF protein signal transduction;positive regulation of GTPase activity | | |
| XLOC_001821 | TCONS_00003544 | ribonuclease h protein at1g65750 | | | |
| XLOC_001840 | TCONS_00003575 | squalene synthase 1 | integral component of membrane;farnesyl-diphosphate farnesyltransferase activity;squalene synthase activity;lipid biosynthetic process | ec:2.5.1.29-diphosphate synthase;ec:2.5.1.21-synthase;ec:2.5.1 | Terpenoid backbone biosynthesis;Biosynthesis of antibioticsSesquiterpenoid and triterpenoid biosynthesis;Steroid biosynthesis;Biosynthesis of antibiotics |
| XLOC_001867 | TCONS_00003614 | transcription-repair-coupling factor | nucleic acid binding;helicase activity;ATP binding;DNA repair;heme biosynthetic process | ec:3.6.1.15-phosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolism |
| XLOC_001912 | TCONS_00003688 | hypothetical protein VIGAN_04253900 | | | |
| XLOC_002065 | TCONS_00004007 | fact complex subunit ssrp1-like | nucleus;DNA binding;2-alkenal reductase [NAD(P)] activity;oxidation-reduction process | ec:1.3.1.74 | |
| XLOC_002066 | TCONS_00004009 | wrky transcription factor 12 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| XLOC_002145 | TCONS_00004159 | nuclease harbi1 | | | |
| XLOC_002282 | TCONS_00004444 | transporter mch1 | integral component of membrane;transmembrane transport | | |
| XLOC_002305 | TCONS_00004479 | histone deacetylase hdt1 | nucleic acid binding;metal ion binding | | |
| XLOC_002484 | TCONS_00004819 | transcription factor pif3 isoform x1 | nucleus;transcription factor activity, sequence-specific DNA binding;protein dimerization activity;regulation of transcription, DNA-templated | | |
| XLOC_002563 | TCONS_00004976 | glutamate--cysteine chloroplastic | chloroplast stroma;glutamate-cysteine ligase activity;ATP binding;defense response to insect;glucose catabolic process;gluconeogenesis;glycolytic process;glutathione biosynthetic process;response to | ec:6.3.2.2-ligase | Glutathione metabolism;Cysteine and methionine metabolism |

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|  |  |  | heat;response to salt stress;indole phytoalexin biosynthetic process;defense response to bacterium, incompatible interaction;flower development;cysteine biosynthetic process;glucosinolate biosynthetic process;cellulose biosynthetic process;defense response to fungus;defense response by callose deposition in cell wall |  |  |
| XLOC_002741 | TCONS_00005314 | atp synthase cf1 alpha partial | mitochondrion;chloroplast thylakoid membrane;proton-transporting ATP synthase complex, catalytic core F(1);ATP binding;proton-transporting ATP synthase activity, rotational mechanism;proton-transporting ATPase activity, rotational mechanism;ATP synthesis coupled proton transport;ATP hydrolysis coupled proton transport | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_002747 | TCONS_00005320 | nuclease harbi1 | vacuolar membrane;plasma membrane;chloroplast |  |  |
| XLOC_002748 | TCONS_00005321 | hypothetical protein PHAVU_011G176000g | organic cyclic compound binding;heterocyclic compound binding |  |  |
| XLOC_002749 | TCONS_00005322 | hypothetical protein PHAVU_001G154000g, partial |  |  |  |
| XLOC_002752 | TCONS_00005325 | hypothetical protein PHAVU_001G048900g | protein serine/threonine kinase activity;ATP binding;polysaccharide binding;protein phosphorylation | ec:2.7.11 |  |
| XLOC_002753 | TCONS_00005326 | transmembrane amino acid transporter family protein | membrane |  |  |
| XLOC_002756 | TCONS_00005329 | plasma membrane atpase 1 |  |  |  |
| XLOC_002762 | TCONS_00005335 | hypothetical protein (mitochondrion) |  |  |  |
| XLOC_002763 | TCONS_00005336 | hypothetical protein glysoja_046184 |  |  |  |
| XLOC_002769 | TCONS_00005342 | hypothetical protein PHAVU_004G040400g, partial |  |  |  |
| XLOC_002771 | TCONS_00005344 | catalytic region zinc cchc-type peptidase catalytic | metal ion binding |  |  |
| XLOC_002776 | TCONS_00005349 | rna-directed dna polymerase (reverse transcriptase) chromo zinc cchc-type peptidase active site | binding;transferase activity;DNA metabolic process |  |  |

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| | | polynucleotidyl ribonuclease h fold | | | |
| XLOC_002777 | TCONS_00005350 | hypothetical protein ARALYDRAFT_893970 | | | |
| XLOC_002778 | TCONS_00005351 | ethylene-insensitive protein 2 | intracellular;membrane;transporter activity;establishment of planar polarity;response to molecule of bacterial origin;lipid transport;intra-Golgi vesicle-mediated transport;response to heat;response to salt stress;positive regulation of abscisic acid-activated signaling pathway;jasmonic acid and ethylene-dependent systemic resistance, ethylene mediated signaling pathway;auxin polar transport;regulation of stomatal movement;leaf senescence;sugar mediated signaling pathway;lithium ion transport;protein import into peroxisome matrix;negative regulation of defense response;defense response to bacterium;root hair cell differentiation;cotyledon development;defense response to fungus;defense response by callose deposition in cell wall | | |
| XLOC_002779 | TCONS_00005352 | hypothetical protein PHAVU_006G007700g | | | |
| XLOC_002780 | TCONS_00005353 | disease resistance protein (cc-nbs-lrr class) family protein | ATP binding;ADP binding | | |
| XLOC_002781 | TCONS_00005354 | hypothetical protein PHAVU_006G024500g | | | |
| XLOC_002783 | TCONS_00005356 | esterase lipase thioesterase family protein | transferase activity, transferring acyl groups other than amino-acyl groups;metabolic process | | |
| XLOC_002788 | TCONS_00005361 | rna-directed dna polymerase (reverse transcriptase) chromo zinc cchc-type peptidase active site polynucleotidyl ribonuclease h fold | | | |
| XLOC_002791 | TCONS_00005364 | hypothetical protein LR48_Vigan08g047200 | | | |
| XLOC_002793 | TCONS_00005366 | hypothetical protein PHAVU_010G070700g | | | |

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| XLOC_002794 | TCONS_00005367 | hypothetical protein PHAVU_004G102000g | | | |
| XLOC_002796 | TCONS_00005369 | hypothetical protein PHAVU_001G068700g | | | |
| XLOC_002797 | TCONS_00005370 | integrase core domain containing protein | | | |
| XLOC_002800 | TCONS_00005373 | serine protease chloroplastic-like | integral component of membrane;chloroplast part;peptidase activity;signal peptide processing | | |
| XLOC_002801 | TCONS_00005374 | probable acyl-dehydrogenase ibr3 isoform x2 | | | |
| XLOC_002803 | TCONS_00005376 | hypothetical protein PHAVU_001G035000g | | | |
| XLOC_002805 | TCONS_00005378 | hypothetical protein PHAVU_011G0958002g, partial | | | |
| XLOC_002806 | TCONS_00005379 | glycine-rich protein 2-like | DNA binding;zinc ion binding;regulation of transcription, DNA-templated | | |
| XLOC_002808 | TCONS_00005381 | topless-related protein 4-like | regulation of transcription, DNA-templated | | |
| XLOC_002809 | TCONS_00005382 | abc transporter family protein | nucleotide binding;ATPase activity, coupled to transmembrane movement of substances;single-organism transport;organic substance transport;nitrogen compound transport | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_002810 | TCONS_00005383 | hypothetical protein PHAVU_001G126500g | | | |
| XLOC_002811 | TCONS_00005384 | disease resistance protein rga4 | phosphoprotein phosphatase activity;ADP binding;protein dephosphorylation | ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| XLOC_002812 | TCONS_00005385 | photosystem ii d2 protein | chloroplast;electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity;photosynthetic electron transport in photosystem II | | |
| XLOC_002813 | TCONS_00005386 | pre-mrna-splicing factor 18 | spliceosomal complex;RNA splicing | | |
| XLOC_002822 | TCONS_00005395 | photosystem i p700 apoprotein a1 | plastid;photosynthetic membrane;binding;metabolic process | | |
| XLOC_002836 | TCONS_00005409 | glycine-rich cell wall structural isoform x3 | | | |
| XLOC_002840 | TCONS_00005413 | ribosomal protein s7 | chloroplast;small ribosomal subunit;structural constituent of ribosome;rRNA binding;translation | | |

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| XLOC_003010 | TCONS_00005733 | hypothetical protein glysoja_003246 | | | |
| XLOC_003011 | TCONS_00005734 | guanylate-binding protein 1-like | | | |
| XLOC_003305 | TCONS_00006370 | udp-n-acetylglucosamine transferase subunit alg14 like | N-acetylglucosaminyldiphosphodolichol N-acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1.141-N-acetylglucosaminyltransferase;ec:2.4.1 | Various types of N-glycan biosynthesis;N-Glycan biosynthesis |
| XLOC_003348 | TCONS_00006442 | pre-mrna-processing-splicing factor 8 | spliceosomal complex;U6 snRNA binding;U5 snRNA binding;mRNA splicing, via spliceosome | | |
| XLOC_003388 | TCONS_00006518 | alpha beta fold hydrolase | acylglycerol lipase activity;metabolic process | ec:3.1.1.23-lipase;ec:3.1.1.1-ali-esterase;ec:3.1.1 | Glycerolipid metabolismDrug metabolism - other enzymes |
| XLOC_003500 | TCONS_00006753 | hypothetical protein PHAVU_002G130100g | ADP binding | | |
| XLOC_003618 | TCONS_00006959 | copper transporter -like | | | |
| XLOC_003707 | TCONS_00007106 | hypothetical protein PHAVU_009G238900g | | | |
| XLOC_003713 | TCONS_00007116 | probable dna primase large subunit | primosome complex;DNA binding;DNA primase activity;metal ion binding;4 iron, 4 sulfur cluster binding;DNA replication, synthesis of RNA primer | ec:2.7.7.6-RNA polymerase; ec:2.7.7 | Purine metabolism;Pyrimidine metabolism |
| XLOC_003731 | TCONS_00007151 | glyceraldehyde-3-phosphate dehydrogenase | | | |
| XLOC_004204 | TCONS_00008106 | hypothetical protein VIGAN_01070900 | | | |
| XLOC_004473 | TCONS_00008651 | vacuolar protein sorting-associated | | | |
| XLOC_004843 | TCONS_00009426 | receptor-like serine threonine-protein kinase ale2 | plasma membrane;protein serine/threonine kinase activity;ATP binding;protoderm histogenesis;cuticle development;protein autophosphorylation;organ formation | ec:2.7.11 | |
| XLOC_004855 | TCONS_00009462 | peroxisomal acyl-coenzyme a oxidase-like protein | peroxisome;acyl-CoA dehydrogenase activity;acyl-CoA oxidase activity;flavin adenine dinucleotide binding;fatty acid beta-oxidation | ec:1.3.99.3;ec:1.3.3.6-oxidase | Fatty acid degradation;Biosynthesis of unsaturated fatty acids;alpha-Linolenic acid metabolism |
| XLOC_004920 | TCONS_00009575 | glycoside hydrolase family 79 amino-terminal domain protein | membrane;hydrolase activity, acting on glycosyl bonds;carbohydrate metabolic process | | |
| XLOC_004975 | TCONS_00009700 | hypothetical protein | | | |

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| | | VIGAN_01263100 | | | |
| XLOC_004981 | TCONS_00009708 | probable polygalacturonase at3g15720 | extracellular region;polygalacturonase activity;carbohydrate metabolic process;cell wall organization | ec:3.2.1.15-pectin depolymerase | Pentose and glucuronate interconversions;Starch and sucrose metabolism |
| XLOC_005087 | TCONS_00009916 | hypothetical protein LR48_Vigan05g133500 | | | |
| XLOC_005128 | TCONS_00010004 | serine threonine-protein kinase afc3 | protein kinase activity;ATP binding;protein phosphorylation | | |
| XLOC_005207 | TCONS_00010158 | glycogen synthase | starch synthase activity;metabolic process | ec:2.4.1.21-synthase (glycosyl-transferring);ec:2.4.1 | Starch and sucrose metabolism |
| XLOC_005217 | TCONS_00010176 | PREDICTED: uncharacterized protein LOC106764048 isoform X2 | | | |
| XLOC_005229 | TCONS_00010196 | zinc c3hc4 type (ring finger) protein | zinc ion binding | | |
| XLOC_005273 | TCONS_00010287 | cpd photolyase | | | |
| XLOC_005354 | TCONS_00010469 | asparagine synthase | mitochondrion;double-stranded DNA binding;asparagine synthase (glutamine-hydrolyzing) activity;regulation of transcription, DNA-templated;asparagine biosynthetic process | ec:6.3.5.4-synthase (glutamine-hydrolysing) | Alanine, aspartate and glutamate metabolism |
| XLOC_005373 | TCONS_00010513 | transcription factor gte1 | | | |
| XLOC_005471 | TCONS_00010729 | myo-inositol oxygenase | cytoplasm;iron ion binding;inositol oxygenase activity;inositol catabolic process;oxidation-reduction process | ec:1.13.99.1-oxygenase | Ascorbate and aldarate metabolism;Inositol phosphate metabolism |
| XLOC_005480 | TCONS_00010750 | inter-alpha-trypsin inhibitor heavy chain-like protein | transferase activity | | |
| XLOC_005481 | TCONS_00010751 | inter-alpha-trypsin inhibitor heavy chain-like protein | NAD+ ADP-ribosyltransferase activity;glycogen phosphorylase activity;pyridoxal phosphate binding;carbohydrate metabolic process | ec:2.4.1.1-phosphorylase;ec:2.4.2.30 | Starch and sucrose metabolism |
| XLOC_005513 | TCONS_00010809 | two-pore potassium channel 3-like | vacuolar membrane;integral component of membrane;voltage-gated potassium channel activity;cellular potassium ion homeostasis;potassium ion transmembrane transport | | |
| XLOC_005582 | TCONS_00010929 | hypothetical protein PHAVU_002G108200g | | | |
| XLOC_005706 | TCONS_00011167 | hypothetical protein LR48_Vigan609s002200 | | | |
| XLOC_005748 | TCONS_00011255 | hypothetical protein | | | |

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| | | VIGAN_01106500, partial | | | |
| XLOC_005913 | TCONS_00011593 | hypothetical protein VIGAN_01068200 | | | |
| XLOC_006068 | TCONS_00011895 | atp-dependent zinc metalloprotease ftsh mitochondrial | integral component of membrane;metalloendopeptidase activity;ATP binding;proteolysis;iron ion transport;zinc II ion transport;magnesium ion transport;transmembrane transport | ec:3.4.24 | |
| XLOC_006181 | TCONS_00012152 | luminal-binding protein 5 | ATP binding;2-alkenal reductase [NAD(P)] activity;oxidation-reduction process | ec:1.3.1.74 | |
| XLOC_006206 | TCONS_00012196 | hypothetical protein VIGAN_03201500 | | | |
| XLOC_006208 | TCONS_00012198 | hypothetical protein PHAVU_005G0985002g, partial | | | |
| XLOC_006213 | TCONS_00012203 | ppr containing plant-like protein | | | |
| XLOC_006214 | TCONS_00012204 | hypothetical protein LR48_Vigan11g162500 | | | |
| XLOC_006215 | TCONS_00012205 | hypothetical protein VIGAN_10206100 | | | |
| XLOC_006223 | TCONS_00012213 | PREDICTED: uncharacterized protein LOC101488260, partial | | | |
| XLOC_006231 | TCONS_00012221 | lob domain-containing protein 4-like | carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity;metabolic process;determination of bilateral symmetry;polarity specification of adaxial/abaxial axis;meristem initiation;regulation of meristem growth | ec:6.3.5.5-synthase (glutamine-hydrolysing) | Alanine, aspartate and glutamate metabolism;Pyrimidine metabolism |
| XLOC_006232 | TCONS_00012222 | l-ascorbate oxidase | extracellular region;copper ion binding;L-ascorbate oxidase activity;systemic acquired resistance;salicylic acid biosynthetic process;sterol biosynthetic process;sphingoid biosynthetic process;oxidation-reduction process | ec:1.10.3;ec:1.10.3.3-oxidase | Ascorbate and aldarate metabolism |
| XLOC_006233 | TCONS_00012223 | hypothetical protein PHAVU_011G146800g | | | |
| XLOC_006235 | TCONS_00012225 | rna polymerase beta subunit | chloroplast;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_006236 | TCONS_00012226 | hypothetical chloroplast rf15 | mitochondrion;chloroplast | | |

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| XLOC_006238 | TCONS_00012228 | trna(adenine ) chloroplastic-like isoform x1 | zinc ion binding;hydrolase activity;metabolic process | | |
| XLOC_006244 | TCONS_00012234 | photosystem ii phosphoprotein | photosystem II;chloroplast thylakoid membrane;integral component of membrane;phosphate ion binding;photosynthesis;protein stabilization | | |
| XLOC_006246 | TCONS_00012236 | ring u-box protein | zinc ion binding | | |
| XLOC_006255 | TCONS_00012245 | aldo keto reductase family oxidoreductase | oxidoreductase activity;oxidation-reduction process | | |
| XLOC_006256 | TCONS_00012246 | ribosomal protein l14 | chloroplast;large ribosomal subunit;structural constituent of ribosome;rRNA binding;translation | | |
| XLOC_006260 | TCONS_00012250 | uncharacterized mitochondrial protein g00810-like | nucleic acid binding;zinc ion binding | | |
| XLOC_006262 | TCONS_00012252 | hypothetical protein VIGAN_01185400, partial | | | |
| XLOC_006263 | TCONS_00012253 | abc transporter c family member 2-like isoform x1 | | | |
| XLOC_006265 | TCONS_00012255 | hypothetical protein PHAVU_L006100g | | | |
| XLOC_006266 | TCONS_00012256 | hypothetical protein LR48_Vigan205s006200 | | | |
| XLOC_006269 | TCONS_00012259 | hypothetical protein PHAVU_008G128800g | organic cyclic compound binding;heterocyclic compound binding | | |
| XLOC_006270 | TCONS_00012260 | ribosomal protein s14 | mitochondrion;chloroplast;small ribosomal subunit;structural constituent of ribosome;rRNA binding;translation | | |
| XLOC_006272 | TCONS_00012262 | hypothetical protein PHAVU_002G212100g | | | |
| XLOC_006276 | TCONS_00012266 | rna polymerase beta partial | chloroplast;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_006278 | TCONS_00012268 | transmembrane protein, putative | | | |
| XLOC_006279 | TCONS_00012269 | ycf68 protein | | | |
| XLOC_006280 | TCONS_00012270 | probable dolichyl pyrophosphate man9 c2 alpha- -glucosyltransferase isoform x1 | endoplasmic reticulum membrane;transferase activity, transferring hexosyl groups;metabolic process | | |

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| XLOC_006281 | TCONS_00012271 | wrky transcription factor 22-like | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| XLOC_006282 | TCONS_00012272 | hypothetical protein glysoja_010825 | | | |
| XLOC_006284 | TCONS_00012274 | reverse partial | nucleus;nucleic acid binding;aspartic-type endopeptidase activity;zinc ion binding;proteolysis;DNA integration | ec:3.4.23 | |
| XLOC_006293 | TCONS_00012283 | hypothetical protein glysoja_002809, partial | | | |
| XLOC_006296 | TCONS_00012286 | aspartate-semialdehyde dehydrogenase | mitochondrion;chloroplast stroma;N-acetyl-gamma-glutamyl-phosphate reductase activity;aspartate-semialdehyde dehydrogenase activity;protein dimerization activity;NADP binding;NAD binding;purine nucleotide biosynthetic process;methionine biosynthetic process;threonine biosynthetic process;lysine biosynthetic process via diaminopimelate;isoleucine biosynthetic process;oxidation-reduction process | ec:1.2.1.38-reductase;ec:1.2.1.11-dehydrogenase | Arginine biosynthesis;Biosynthesis of antibioticsLysine biosynthesis;Monobactam biosynthesis;Glycine, serine and threonine metabolism;Biosynthesis of antibiotics;Cysteine and methionine metabolism |
| XLOC_006298 | TCONS_00012288 | hypothetical protein glysoja_023492 | | | |
| XLOC_006468 | TCONS_00012620 | peroxisomal -dienoyl-reductase | vacuolar membrane;peroxisome;2,4-dienoyl-CoA reductase (NADPH) activity;oxidation-reduction process | ec:1.3.1.34 | |
| XLOC_006482 | TCONS_00012647 | ribonuclease h protein | catalytic activity;cellular macromolecule metabolic process;nucleic acid metabolic process | | |
| XLOC_006612 | TCONS_00012897 | e3 ubiquitin-protein ligase herc1 | ligase activity;metal ion binding;metabolic process | | |
| XLOC_006730 | TCONS_00013148 | protein transport protein sec24-like at3g07100-like isoform x1 | COPII vesicle coat;zinc ion binding;intracellular protein transport;ER to Golgi vesicle-mediated transport | | |
| XLOC_006744 | TCONS_00013176 | fruit weight protein | | | |
| XLOC_006807 | TCONS_00013301 | pleiotropic drug resistance protein 1 | integral component of membrane;ATP binding;ATPase activity;transport;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_006949 | TCONS_00013526 | t-complex protein 1 subunit alpha | cellular protein metabolic process;single-organism process | | |
| XLOC_006966 | TCONS_00013564 | pre-mrna-processing-splicing factor 8-like | spliceosomal complex;U6 snRNA binding;U5 snRNA binding;mRNA splicing, via spliceosome | | |

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| XLOC_007105 | TCONS_00013857 | hypothetical protein HQ43_09450 | | | |
| XLOC_007105 | TCONS_00013857 | hypothetical protein HQ43_09450 | | | |
| XLOC_007172 | TCONS_00013999 | pleiotropic drug resistance protein 1-like | integral component of membrane;ATP binding;ATPase activity;transport;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_007185 | TCONS_00014025 | protein enhanced disease resistance 2-like isoform x1 | lipid binding | | |
| XLOC_007186 | TCONS_00014026 | pleckstrin-like and lipid-binding start domain protein | plasma membrane;lipid binding;cysteine biosynthetic process | | |
| XLOC_007278 | TCONS_00014224 | pentatricopeptide repeat-containing protein at1g74750-like | | | |
| XLOC_007384 | TCONS_00014450 | agamous-like mads-box protein agl19 | | | |
| XLOC_007414 | TCONS_00014513 | leukocyte receptor cluster member 1 homolog | | | |
| XLOC_007421 | TCONS_00014529 | dwnn a cchc-type zinc finger protein | nucleus;nucleic acid binding;zinc ion binding | | |
| XLOC_007535 | TCONS_00014761 | frigida-like protein 3 | | | |
| XLOC_007575 | TCONS_00014830 | lrr and nb-arc domain disease resistance protein | | | |
| XLOC_007745 | TCONS_00015144 | pentatricopeptide repeat-containing protein chloroplastic | | | |
| XLOC_007764 | TCONS_00015198 | asc1-like protein | endoplasmic reticulum membrane;integral component of membrane;sphingosine N-acyltransferase activity;lipid metabolic process | ec:2.3.1;ec:2.3.1.24-N-acyltransferase | Sphingolipid metabolism |
| XLOC_007862 | TCONS_00015399 | tetratricopeptide repeat protein 7b | | | |
| XLOC_007864 | TCONS_00015402 | ubx domain-containing protein 1 | metal ion binding | | |
| XLOC_007865 | TCONS_00015404 | hypothetical protein PHAVU_009G043500g | tRNA binding | | |
| XLOC_008029 | TCONS_00015793 | h aca ribonucleoprotein complex subunit 1-like protein 1 | | | |
| XLOC_008064 | TCONS_00015856 | ribonuclease h protein | | | |
| XLOC_008065 | TCONS_00015857 | ribonuclease h protein | catalytic activity;cellular macromolecule metabolic | | |

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|---|---|---|---|---|---|
| | | | process;nucleic acid metabolic process | | |
| XLOC_008118 | TCONS_00015985 | probable cadmium zinc-transporting atpase chloroplastic | chloroplast envelope;integral component of membrane;calcium-transporting ATPase activity;ATP binding;cadmium-exporting ATPase activity;cadmium-transporting ATPase activity;zinc transporting ATPase activity;metal ion binding;cellular copper ion homeostasis;metabolic process;response to toxic substance;response to light intensity;zinc ion homeostasis;cadmium ion transmembrane transport;calcium ion transmembrane transport;zinc II ion transmembrane transport | ec:3.6.1.15-phosphatase;ec:3.6.3.8;ec:3.6.3.3;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.3.46 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_008150 | TCONS_00016046 | hypothetical protein PHAVU_003G053500g | | | |
| XLOC_008186 | TCONS_00016112 | cysteine chloroplastic chromoplastic | cysteine synthase activity;transferase activity;cysteine biosynthetic process from serine | ec:2.5.1.47-synthase | Sulfur metabolism;Biosynthesis of antibiotics;Cysteine and methionine metabolism |
| XLOC_008327 | TCONS_00016389 | glyceraldehyde-3-phosphate dehydrogenase | chloroplast;glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity;NADP binding;NAD binding;glucose metabolic process;glycolytic process;oxidation-reduction process | ec:1.2.1.59-dehydrogenase (NAD(P)+) (phosphorylating);ec:1.2.1.12-dehydrogenase (phosphorylating) | Glycolysis / Gluconeogenesis;Carbon fixation in photosynthetic organisms;Biosynthesis of antibioticsGlycolysis / Gluconeogenesis;Carbon fixation in photosynthetic organisms;Biosynthesis of antibiotics |
| XLOC_008370 | TCONS_00016484 | hypothetical protein PHAVU_005G102300g | | | |
| XLOC_008379 | TCONS_00016499 | pyrimidine-specific ribonucleoside hydrolase riha | xanthine dehydrogenase activity;hydrolase activity;oxidation-reduction process | ec:1.17.1;ec:1.17.1.4-dehydrogenase | Purine metabolism |
| XLOC_008395 | TCONS_00016521 | myosin-j heavy chain | myosin complex;motor activity;ATP binding;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolism |
| XLOC_008417 | TCONS_00016574 | respiratory burst oxidase-like protein | calcium ion binding | | |
| XLOC_008533 | TCONS_00016803 | hypothetical protein GLYMA_13G109900 | | | |
| XLOC_008645 | TCONS_00017029 | dna-directed rna polymerase chloroplastic | mitochondrion;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_008646 | TCONS_00017030 | dna-directed rna polymerase chloroplastic | DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_008647 | TCONS_00017031 | dna-directed rna polymerase chloroplastic | mitochondrion;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_008664 | TCONS_00017066 | PREDICTED: uncharacterize | | | |

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| | | d protein LOC106767492 isoform X1 | | | |
| XLOC_008968 | TCONS_00017704 | neurofilament heavy partial | | | |
| XLOC_009024 | TCONS_00017824 | dna-binding protein escarola | response to hormone;floral organ development;floral whorl development;phyllome development | | |
| XLOC_009070 | TCONS_00017923 | cbs domain-containing protein chloroplastic | | | |
| XLOC_009096 | TCONS_00017981 | peptidyl-prolyl cis-trans isomerase-like 3 | peptidyl-prolyl cis-trans isomerase activity;protein peptidyl-prolyl isomerization;protein folding | ec:5.2.1.8 | |
| XLOC_009245 | TCONS_00018294 | pentatricopeptide repeat-containing protein mitochondrial | mitochondrion;response to oxidative stress;response to salt stress;response to abscisic acid;mitochondrial ATP synthesis coupled electron transport | | |
| XLOC_009305 | TCONS_00018446 | plastocyanin-like domain protein | electron carrier activity | | |
| XLOC_009311 | TCONS_00018452 | nuclease harbi1 | | | |
| XLOC_009312 | TCONS_00018453 | probable nucleoredoxin 1 isoform x6 | | | |
| XLOC_009314 | TCONS_00018455 | hypothetical protein PHAVU_007G108600g | | | |
| XLOC_009315 | TCONS_00018456 | ribonuclease h protein at1g65750 | nucleic acid binding;RNA-DNA hybrid ribonuclease activity;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1;ec:3.1.30;ec:3.1.26;ec:3.1.26.4 | |
| XLOC_009317 | TCONS_00018458 | maturase k | | | |
| XLOC_009318 | TCONS_00018459 | isoflavone synthase 1 | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;isomerase activity;heme binding;oxidation-reduction process | | |
| XLOC_009319 | TCONS_00018460 | hypothetical protein PHAVU_003G053500g | | | |
| XLOC_009323 | TCONS_00018464 | hypothetical protein LR48_Vigan01g112400 | | | |
| XLOC_009326 | TCONS_00018467 | gag-pol polyprotein | nucleic acid binding;zinc ion binding;DNA integration | | |
| XLOC_009328 | TCONS_00018469 | hypothetical protein PHAVU_011G164600g | | | |
| XLOC_009332 | TCONS_00018473 | hypothetical protein PHAVU_001G104900g, partial | | | |
| XLOC_009333 | TCONS_00018474 | a subunit of nadh dehydrogenase | chloroplast thylakoid membrane;integral component of membrane;NADH dehydrogenase (ubiquinone) | ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:1.6.5.3-reductase | Oxidative phosphorylationOxidative phosphorylation |

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| | | | activity;quinone binding;transport;ATP synthesis coupled electron transport | (H+-translocating) | |
| XLOC_009335 | TCONS_00018476 | hypothetical protein PHAVU_005G070100g | | | |
| XLOC_009336 | TCONS_00018477 | copia partial | nucleic acid binding;zinc ion binding | | |
| XLOC_009338 | TCONS_00018479 | lysine-specific demethylase jmj16 | nucleus;transcription factor activity, sequence-specific DNA binding;methyltransferase activity;oxidoreductase activity;protein glycosylation;gravitropism;vegetative to reproductive phase transition of meristem;glucuronoxylan metabolic process;protein desumoylation;methylation;post-translational protein modification;xylan biosynthetic process;positive regulation of transcription, DNA-templated;hydrogen peroxide biosynthetic process;oxidation-reduction process | | |
| XLOC_009340 | TCONS_00018481 | PREDICTED: uncharacterized protein LOC105778352 | | | |
| XLOC_009345 | TCONS_00018486 | copia partial | binding;transferase activity, transferring alkyl or aryl (other than methyl) groups;metabolic process | | |
| XLOC_009347 | TCONS_00018488 | hypothetical protein PHAVU_002G097600g, partial | | | |
| XLOC_009348 | TCONS_00018489 | photosystem i p700 chlorophyll a partial | ribosome;chloroplast;photosystem I;integral component of membrane;structural constituent of ribosome;ATP binding;translation;photosynthesis | | |
| XLOC_009349 | TCONS_00018490 | hypothetical protein B456_001G165700 | | | |
| XLOC_009353 | TCONS_00018494 | probable prefoldin subunit 3 | | | |
| XLOC_009354 | TCONS_00018495 | lysine-specific demethylase jmj16 | nucleus;transcription factor activity, sequence-specific DNA binding;methyltransferase activity;oxidoreductase activity;protein glycosylation;gravitropism;vegetative to reproductive phase transition of meristem;glucuronoxylan metabolic process;protein desumoylation;methylation;post-translational protein modification;xylan biosynthetic process;positive regulation of transcription, DNA-templated;hydrogen peroxide biosynthetic process;oxidation-reduction process | | |

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| XLOC_009355 | TCONS_00018496 | myb transcription factor | DNA binding | | |
| XLOC_009356 | TCONS_00018497 | maturase k | chloroplast;RNA binding;mRNA processing;tRNA processing;RNA splicing | | |
| XLOC_009360 | TCONS_00018501 | mannose-1-phosphate guanylyltransferase 1-like | mannose-1-phosphate guanylyltransferase (GDP) activity;biosynthetic process | ec:2.7.7.22-guanylyltransferase (GDP);ec:2.7.7 | Amino sugar and nucleotide sugar metabolism;Fructose and mannose metabolism |
| XLOC_009361 | TCONS_00018502 | nad h-quinone oxidoreductase subunit 2 chloroplastic isoform x2 | chloroplast | | |
| XLOC_009362 | TCONS_00018503 | nuclease harbi1 | | | |
| XLOC_009363 | TCONS_00018504 | hypothetical protein PHAVU_011G004100g | | | |
| XLOC_009365 | TCONS_00018506 | hypothetical protein PHAVU_008G101400g | nucleotide binding;nucleic acid binding | | |
| XLOC_009367 | TCONS_00018508 | k(+) efflux antiporter 4 isoform x1 | | | |
| XLOC_009370 | TCONS_00018511 | pathogenesis-related protein pr-1 | extracellular region | | |
| XLOC_009372 | TCONS_00018513 | hypothetical protein PHAVU_011G148300g | | | |
| XLOC_009374 | TCONS_00018515 | hypothetical protein VIGAN_01410200 | | | |
| XLOC_009376 | TCONS_00018517 | PREDICTED: uncharacterized protein LOC103931614 | | | |
| XLOC_009378 | TCONS_00018519 | upf0057 membrane protein at4g30660-like | | | |
| XLOC_009379 | TCONS_00018520 | serine carboxypeptidase 24-like | carboxypeptidase activity | | |
| XLOC_009395 | TCONS_00018536 | werner syndrome-like exonuclease | nucleic acid binding;3'-5' exonuclease activity;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| XLOC_009397 | TCONS_00018538 | ribonuclease h protein at1g65750 | | | |
| XLOC_009400 | TCONS_00018541 | PREDICTED: uncharacterized protein LOC103501196 | | | |
| XLOC_009401 | TCONS_00018542 | photosystem i p700 apoprotein a1 | photosystem I;chloroplast thylakoid membrane;integral component of membrane;magnesium ion binding;electron carrier activity;chlorophyll binding;oxidoreductase activity;4 iron, 4 sulfur cluster binding;photosynthesis;prot | | |

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| | | | ein-chromophore linkage;oxidation-reduction process | | |
| XLOC_009407 | TCONS_00018548 | gag polyprotein | | | |
| XLOC_009413 | TCONS_00018554 | rna polymerase beta subunit | chloroplast;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_009417 | TCONS_00018558 | hypothetical protein PHAVU_003G107200g | | | |
| XLOC_009421 | TCONS_00018562 | photosystem ii p680 chlorophyll a partial | chloroplast;photosystem;integral component of membrane;chlorophyll binding;photosynthetic electron transport chain;protein-chromophore linkage | | |
| XLOC_009572 | TCONS_00018843 | zeitlupe partial | | | |
| XLOC_009795 | TCONS_00019241 | ccr4-not transcription complex subunit 3 | nucleus;regulation of transcription, DNA-templated | | |
| XLOC_009806 | TCONS_00019258 | pentatricopeptide repeat-containing protein mitochondrial-like | | | |
| XLOC_009813 | TCONS_00019271 | leucine-rich repeat receptor-like tyrosine-protein kinase at2g41820-like | protein kinase activity;ATP binding;protein phosphorylation | | |
| XLOC_009814 | TCONS_00019272 | lrr receptor-like kinase family protein | membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| XLOC_009829 | TCONS_00019290 | beta-galactosidase 17 | beta-galactosidase activity;protein kinase activity;ATP binding;protein phosphorylation;vegetative to reproductive phase transition of meristem;glucuronoxylan metabolic process;protein desumoylation;xylan biosynthetic process;hydrogen peroxide biosynthetic process | ec:3.2.1.23-lactase (ambiguous);<br>ec:3.2.1 | Other glycan degradation;Glycosphingolipid biosynthesis - ganglio series;Sphingolipid metabolism;Galactose metabolism;Glycosaminoglycan degradation |
| XLOC_009853 | TCONS_00019336 | hypothetical protein PHAVU_005G084700g | | | |
| XLOC_009855 | TCONS_00019339 | hypothetical protein PHAVU_003G046100g | | | |
| XLOC_009875 | TCONS_00019375 | transcription initiation factor tfiid subunit 10 | | | |
| XLOC_009889 | TCONS_00019395 | protein lurp-one-related 6 | | | |
| XLOC_009934 | TCONS_00019460 | probable wrky transcription factor 12 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |

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| XLOC_009935 | TCONS_00019462 | fact complex subunit ssrp1 | nuclear euchromatin;FACT complex;DNA binding;2-alkenal reductase [NAD(P)] activity;polar nucleus fusion;vegetative to reproductive phase transition of meristem;oxidation-reduction process | ec:1.3.1.74 |  |
| XLOC_010310 | TCONS_00020188 | PREDICTED: uncharacterized protein LOC104810178 |  |  |  |
| XLOC_010322 | TCONS_00020213 | hypothetical protein PHAVU_L009500g |  |  |  |
| XLOC_010328 | TCONS_00020220 | hypothetical protein PHAVU_004G0078002g, partial |  |  |  |
| XLOC_010340 | TCONS_00020245 | nbs-lrr type disease resistance protein cnl-j9 | ADP binding |  |  |
| XLOC_010438 | TCONS_00020452 | abc transporter b family member 25-like isoform x2 |  |  |  |
| XLOC_010568 | TCONS_00020646 | pentatricopeptide repeat-containing protein at2g15690 | microtubule-severing ATPase activity;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.4.3;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_010633 | TCONS_00020763 | chaperone protein dnaj 10-like |  |  |  |
| XLOC_010649 | TCONS_00020793 | gdt1-like protein 2 |  |  |  |
| XLOC_010653 | TCONS_00020802 | bifunctional epoxide hydrolase 2-like | peroxisome;epoxide hydrolase activity;cis-stilbene-oxide hydrolase activity;metabolic process | ec:3.3.2.10-epoxide hydrolase;ec:3.3.2.9-epoxide hydrolase | Chloroalkane and chloroalkene degradation;Arachidonic acid metabolismMetabolism of xenobiotics by cytochrome P450 |
| XLOC_010687 | TCONS_00020869 | p23 co-chaperone protein |  |  |  |
| XLOC_010703 | TCONS_00020896 | nuclear pore complex protein nup107 isoform x2 |  |  |  |
| XLOC_010718 | TCONS_00020916 | t-complex protein 1 subunit theta-like | cytoplasm;ATP binding;unfolded protein binding;protein folding |  |  |
| XLOC_010758 | TCONS_00020992 | PREDICTED: uncharacterized protein LOC102665818 |  |  |  |
| XLOC_010839 | TCONS_00021136 | dna replication complex gins protein psf2 | nucleus;DNA replication |  |  |
| XLOC_010897 | TCONS_00021237 | short-chain dehydrogenase tic chloroplastic | oxidoreductase activity;oxidation-reduction process |  |  |

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| XLOC_010898 | TCONS_00021238 | short-chain dehydrogenase tic chloroplastic | chloroplast inner membrane;calmodulin binding;oxidoreductase activity;protein transport;oxidation-reduction process | | |
| XLOC_010936 | TCONS_00021319 | hypothetical protein LR48_Vigan10g088200 | | | |
| XLOC_010963 | TCONS_00021361 | hypothetical protein PHAVU_001G035000g | | | |
| XLOC_011009 | TCONS_00021428 | nuclease harbi1 | kinase activity;phosphorylation | | |
| XLOC_011095 | TCONS_00021580 | nuclease harbi1 | | | |
| XLOC_011121 | TCONS_00021630 | mechanosensitive ion channel protein chloroplastic-like isoform x1 | plasma membrane;integral component of membrane;chloroplast membrane;ion channel activity;response to osmotic stress;jasmonic acid metabolic process;response to jasmonic acid;chloroplast fission;ion transmembrane transport | | |
| XLOC_011259 | TCONS_00021849 | hypothetical protein PHAVU_008G145700g, partial | | | |
| XLOC_011260 | TCONS_00021850 | phospholipid-transporting atpase 8 | integral component of membrane;magnesium ion binding;phospholipid-translocating ATPase activity;ATP binding;metabolic process;phospholipid translocation | ec:3.6.1.15-phosphatase;ec:3.6.3.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_011262 | TCONS_00021852 | disease resistance protein cyr1 | ADP binding | | |
| XLOC_011263 | TCONS_00021853 | senescence-associated protein | | | |
| XLOC_011264 | TCONS_00021854 | metalloendoproteinase 1 | | | |
| XLOC_011271 | TCONS_00021861 | chaperone protein 1 | ATP binding;protein metabolic process | | |
| XLOC_011272 | TCONS_00021862 | hypothetical protein glysoja_045364, partial | | | |
| XLOC_011277 | TCONS_00021867 | oligopeptide transporter 7 | methyltransferase activity;methylation;transmembrane transport | | |
| XLOC_011282 | TCONS_00021872 | neoxanthin synthase | PSII associated light-harvesting complex II;chloroplast envelope;abscisic acid biosynthetic process;photoprotection;xanthophyll metabolic process;regulation of superoxide anion generation;hydrogen peroxide catabolic process | | |
| XLOC_011283 | TCONS_00021873 | gag- partial | | | |
| XLOC_011284 | TCONS_00021874 | PREDICTED: uncharacterized protein LOC102668698 | | | |

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| XLOC_011286 | TCONS_00021876 | transcription factor scream2-like | DNA binding;protein dimerization activity | | |
| XLOC_011289 | TCONS_00021879 | mitochondrial phosphate carrier protein mitochondrial-like | integral component of membrane;glutathione transferase activity;transport;metabolic process;response to salt stress;response to ethylene | ec:2.5.1.18-transferase | Glutathione metabolism;Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450 |
| XLOC_011290 | TCONS_00021880 | hypothetical protein LR48_Vigan406s007800 | | | |
| XLOC_011294 | TCONS_00021884 | hypothetical protein PHAVU_008G035300g | | | |
| XLOC_011298 | TCONS_00021888 | PREDICTED: uncharacterized protein LOC102664980 | | | |
| XLOC_011303 | TCONS_00021893 | PREDICTED: uncharacterized protein LOC106779432 | | | |
| XLOC_011307 | TCONS_00021897 | hypothetical protein VIGAN_03201500 | | | |
| XLOC_011308 | TCONS_00021898 | gag-pol poly | nucleic acid binding;ion binding;metabolic process | | |
| XLOC_011309 | TCONS_00021899 | glycine--trna mitochondrial 1 | | | |
| XLOC_011313 | TCONS_00021903 | hypothetical protein PHAVU_009G156200g | | | |
| XLOC_011314 | TCONS_00021904 | protein involved in de novo 2-like | gene silencing by RNA | | |
| XLOC_011315 | TCONS_00021905 | pollen protein ole e i-like protein | structural constituent of cell wall;plant-type cell wall organization | | |
| XLOC_011317 | TCONS_00021907 | hypothetical protein PHAVU_009G162400g | | | |
| XLOC_011321 | TCONS_00021911 | lrr receptor-like serine threonine-protein kinase gso2-like | | | |
| XLOC_011323 | TCONS_00021913 | nadh-plastoquinone oxidoreductase subunit 6 | chloroplast thylakoid membrane;integral component of membrane;NADH dehydrogenase (ubiquinone) activity;quinone binding;transport;oxidation-reduction process | ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:1.6.5.3-reductase (H+-translocating) | Oxidative phosphorylationOxidative phosphorylation |
| XLOC_011324 | TCONS_00021914 | extensin-2 isoform x3 | | | |
| XLOC_011326 | TCONS_00021916 | rna-binding protein with multiple splicing | nucleotide binding;snRNA binding;mRNA splicing, via spliceosome | | |
| XLOC_011331 | TCONS_00021921 | hypothetical protein M569_00246 | | | |
| XLOC_011335 | TCONS_00021925 | hypothetical protein | | | |

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| | | PHAVU_002G163900g | | | |
| XLOC_011337 | TCONS_00021927 | wrky family transcription factor | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| XLOC_011341 | TCONS_00021931 | lrr receptor-like serine threonine-protein kinase gso2-like | | | |
| XLOC_011343 | TCONS_00021933 | PREDICTED: uncharacterized protein LOC106766088 | | | |
| XLOC_011344 | TCONS_00021934 | ribosomal protein s11 | ribosome;chloroplast;structural constituent of ribosome;rRNA binding;translation | | |
| XLOC_011346 | TCONS_00021936 | hypothetical protein PHAVU_L006100g | metal ion binding | | |
| XLOC_011348 | TCONS_00021938 | rna polymerase beta subunit | mitochondrion;chloroplast;DNA binding;DNA-directed RNA polymerase activity;ribonucleoside binding;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_011349 | TCONS_00021939 | udp-glycosyltransferase 90a1-like | transferase activity | | |
| XLOC_011350 | TCONS_00021940 | nadh-plastoquinone oxidoreductase subunit 7 | | | |
| XLOC_011352 | TCONS_00021942 | udp-glucosyl transferase isoform 1 | coniferyl-alcohol glucosyltransferase activity;hydroquinone glucosyltransferase activity;metabolic process | ec:2.4.1.218; ec:2.4.1.111-glucosyltransferase;ec:2.4.1 | Phenylpropanoid biosynthesis |
| XLOC_011355 | TCONS_00021945 | photosystem ii d2 partial | chloroplast;photosystem II;integral component of membrane;electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity;metal ion binding;photosynthetic electron transport in photosystem II | | |
| XLOC_011446 | TCONS_00022106 | hypothetical protein PHAVU_002G108200g | | | |
| XLOC_011500 | TCONS_00022219 | 1-o-acylglucose:anthocyanin acyltransferase | integral component of membrane;serine-type carboxypeptidase activity;ATP binding;transferase activity, transferring acyl groups;ATPase activity, coupled to transmembrane movement of substances;proteolysis;transmembrane transport | ec:3.4.16;ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1;ec:3.4.21 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_011602 | TCONS_00022423 | peroxisomal -2-hydroxy-acid oxidase isoform x1 | FMN binding;very-long-chain-(S)-2-hydroxy-acid oxidase activity;long-chain-(S)-2-hydroxy-long-chain-acid oxidase activity;medium-chain-(S)-2- | ec:1.1.3.15-oxidase | Biosynthesis of antibiotics;Glyoxylate and dicarboxylate metabolism |

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| | | | hydroxy-acid oxidase activity;oxidation-reduction process | | |
| XLOC_011666 | TCONS_00022546 | dna polymerase epsilon catalytic subunit a | epsilon DNA polymerase complex;nucleotide binding;DNA binding;DNA-directed DNA polymerase activity;zinc ion binding;3'-5' exonuclease activity;DNA replication;DNA repair;DNA biosynthetic process;nucleic acid phosphodiester bond hydrolysis | ec:3.1;ec:2.7.7.7-DNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_011667 | TCONS_00022547 | PREDICTED: uncharacterized protein LOC105954144 | binding | | |
| XLOC_011689 | TCONS_00022593 | nuclear pore complex protein nup98-nup96 | nuclear pore;transport | | |
| XLOC_011715 | TCONS_00022648 | protein yippee-like at5g53940 | nucleus | | |
| XLOC_011720 | TCONS_00022655 | dna polymerase delta small subunit | DNA binding;DNA-directed DNA polymerase activity;metal ion binding;DNA-dependent DNA replication;DNA methylation;methylation-dependent chromatin silencing;microtubule nucleation;cell proliferation;embryo sac egg cell differentiation;regulation of flower development;chromatin silencing by small RNA;floral organ formation;histone H3-K9 methylation;DNA biosynthetic process | ec:2.7.7.7-DNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_011742 | TCONS_00022706 | choline transporter-like protein 2 | trans-Golgi network;plasma membrane;plasmodesma;phragmoplast;integral component of membrane;sieve plate;choline transmembrane transporter activity;xylem and phloem pattern formation;phloem development;choline transport;root development;sieve element differentiation | | |
| XLOC_011743 | TCONS_00022707 | choline transporter-like protein 2 | trans-Golgi network;plasma membrane;plasmodesma;phragmoplast;integral component of membrane;sieve plate;choline transmembrane transporter activity;xylem and phloem pattern formation;phloem development;choline transport;root development;sieve element differentiation | | |
| XLOC_011757 | TCONS_00022736 | transcription factor gte1 | | | |
| XLOC_011759 | TCONS_00022742 | trafficking protein particle complex ii-specific | trans-Golgi network;cell plate assembly | | |

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| | | subunit 130 homolog | | | |
| XLOC_011869 | TCONS_00022953 | inter-alpha-trypsin inhibitor heavy chain-like protein | NAD+ ADP-ribosyltransferase activity;metabolic process | ec:2.4.2.30 | |
| XLOC_011898 | TCONS_00023010 | hypothetical protein LR48_Vigan05g161300 | | | |
| XLOC_011997 | TCONS_00023212 | solanesyl diphosphate synthase | heptaprenyl diphosphate synthase activity;trans-octaprenyltranstransferase activity;all-trans-nonaprenyl-diphosphate synthase (geranyl-diphosphate specific) activity;isoprenoid biosynthetic process;photosynthesis | ec:2.5.1.30-diphosphate synthase;ec:2.5.1.85-diphosphate synthase [geranylgeranyl-diphosphate specific];ec:2.5.1.84-synthase [geranyl-diphosphate specific] | Terpenoid backbone biosynthesisTerpenoid backbone biosynthesisTerpenoid backbone biosynthesis |
| XLOC_012032 | TCONS_00023285 | nuclease harbi1 | ATP binding;sequence-specific DNA binding;DNA replication initiation;regulation of DNA replication | | |
| XLOC_012070 | TCONS_00023355 | extensin-2-like isoform x1 | | | |
| XLOC_012138 | TCONS_00023499 | leucine-rich repeat receptor-like protein kinase | chloroplast;protein serine/threonine kinase activity;ATP binding;acyl-[acyl-carrier-protein] desaturase activity;protein phosphorylation;fatty acid biosynthetic process;oxidation-reduction process | ec:2.7.11;ec:1.14.19;ec:1.14.19.2-9-desaturase | Fatty acid biosynthesis;Biosynthesis of unsaturated fatty acids |
| XLOC_012375 | TCONS_00024011 | mlp-like protein 31 | defense response;response to biotic stimulus | | |
| XLOC_012376 | TCONS_00024012 | mlp-like protein 28 | defense response;response to biotic stimulus | | |
| XLOC_012504 | TCONS_00024255 | amino-terminal domain cyclin | protein kinase binding;regulation of cyclin-dependent protein serine/threonine kinase activity;regulation of transcription, DNA-templated | | |
| XLOC_012532 | TCONS_00024315 | peroxisomal -2-hydroxy-acid oxidase | FMN binding;very-long-chain-(S)-2-hydroxy-acid oxidase activity;long-chain-(S)-2-hydroxy-long-chain-acid oxidase activity;medium-chain-(S)-2-hydroxy-acid oxidase activity;oxidation-reduction process | ec:1.1.3.15-oxidase | Biosynthesis of antibiotics;Glyoxylate and dicarboxylate metabolism |
| XLOC_012624 | TCONS_00024473 | dna ligase 1 | nucleotide binding;DNA ligase activity;DNA repair;cellular macromolecule biosynthetic process | ec:6.5.1 | |
| XLOC_012674 | TCONS_00024585 | lrr receptor-like kinase | protein kinase activity;protein phosphorylation | | |
| XLOC_012679 | TCONS_00024596 | probable leucine-rich repeat receptor-like serine threonine- | transferase activity | | |

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| | | protein kinase at3g14840 | | | |
| XLOC_012682 | TCONS_00024604 | probable leucine-rich repeat receptor-like serine threonine-protein kinase at3g14840 | protein kinase activity;ATP binding;protein phosphorylation | | |
| XLOC_012683 | TCONS_00024605 | lrr receptor-like kinase | protein kinase activity;ATP binding;protein phosphorylation | | |
| XLOC_012699 | TCONS_00024631 | lysine-specific demethylase jmj16 | nucleus;transcription factor activity, sequence-specific DNA binding;methyltransferase activity;oxidoreductase activity;protein glycosylation;gravitropism;vegetative to reproductive phase transition of meristem;glucuronoxylan metabolic process;protein desumoylation;methylation;post-translational protein modification;xylan biosynthetic process;positive regulation of transcription, DNA-templated;hydrogen peroxide biosynthetic process;oxidation-reduction process | | |
| XLOC_012706 | TCONS_00024646 | histone acetyltransferase hac1-like isoform x1 | nucleus;transcription cofactor activity;histone acetyltransferase activity;zinc ion binding;regulation of transcription, DNA-templated;histone acetylation | ec:2.3.1.48;ec:2.3.1 | |
| XLOC_012721 | TCONS_00024689 | hypothetical protein PHAVU_003G116000g, partial | nucleic acid binding;zinc ion binding | | |
| XLOC_012735 | TCONS_00024721 | hypothetical protein PHAVU_005G084700g | | | |
| XLOC_012966 | TCONS_00025137 | beta- -galactosyltransferase 2 | Golgi apparatus;integral component of membrane;galactosylxylosyl protein 3-beta-galactosyltransferase activity;protein glycosylation | ec:2.4.1.134-3-beta-galactosyltransferase;ec:2.4.1 | Glycosaminoglycan biosynthesis - heparan sulfate / heparin;Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate |
| XLOC_012967 | TCONS_00025142 | beta- -galactosyltransferase 2 | Golgi apparatus;integral component of membrane;galactosylxylosyl protein 3-beta-galactosyltransferase activity;protein glycosylation | ec:2.4.1.134-3-beta-galactosyltransferase;ec:2.4.1 | Glycosaminoglycan biosynthesis - heparan sulfate / heparin;Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate |
| XLOC_013129 | TCONS_00025478 | leucine-rich repeat receptor-like protein kinase | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| XLOC_013244 | TCONS_00025686 | zinc finger protein zpr1-like | nucleus;cytosol;zinc ion binding | | |
| XLOC_013247 | TCONS_00025689 | reverse partial | transferase activity, transferring alkyl or aryl (other than methyl) groups;metabolic process | | |
| XLOC_013252 | TCONS_00025694 | transmembrane | | | |
| XLOC_013255 | TCONS_00025697 | copia partial | nucleic acid binding;zinc ion binding | | |

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| XLOC_013256 | TCONS_00025698 | e3 ubiquitin-protein ligase rglg2-like | zinc ion binding | | |
| XLOC_013258 | TCONS_00025700 | hypothetical protein LR48_Vigan01g134000 | | | |
| XLOC_013261 | TCONS_00025703 | protein pat1 like 1 | isomerase activity;metabolic process | | |
| XLOC_013267 | TCONS_00025709 | ribonuclease h partial | oxidoreductase activity | | |
| XLOC_013268 | TCONS_00025710 | PREDICTED: uncharacterized protein LOC105954144 | nucleic acid binding | | |
| XLOC_013269 | TCONS_00025711 | clavata3 esr gene family member | | | |
| XLOC_013275 | TCONS_00025717 | disease resistance protein (tir-nbs-lrr class) | ADP binding;signal transduction | | |
| XLOC_013277 | TCONS_00025719 | hypothetical protein PHAVU_009G162400g | | | |
| XLOC_013278 | TCONS_00025720 | photosystem i p700 apoprotein a2 | photosystem I;chloroplast thylakoid membrane;integral component of membrane;magnesium ion binding;electron carrier activity;chlorophyll binding;oxidoreductase activity;4 iron, 4 sulfur cluster binding;photosynthesis;protein-chromophore linkage;oxidation-reduction process | | |
| XLOC_013280 | TCONS_00025722 | hypothetical protein PHAVU_005G079800g | | | |
| XLOC_013281 | TCONS_00025723 | ethylene-responsive transcription factor rap2-7-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;multicellular organismal development | | |
| XLOC_013283 | TCONS_00025725 | hypothetical protein PHAVU_001G081900g, partial | | | |
| XLOC_013288 | TCONS_00025730 | hypothetical chloroplast rf2 | chloroplast stroma;ATP binding | | |
| XLOC_013290 | TCONS_00025732 | pentatricopeptide repeat-containing mitochondrial | | | |
| XLOC_013296 | TCONS_00025738 | hydroxcinnamoyl- quinate shikimate partial | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| XLOC_013297 | TCONS_00025739 | glutamyl-trna reductase chloroplastic-like | chloroplast;glutamyl-tRNA reductase activity;NADP binding;protoporphyrinogen IX biosynthetic process;chlorophyll biosynthetic process;oxidation-reduction process | ec:1.2.1.70-reductase | Porphyrin and chlorophyll metabolism |

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| XLOC_013301 | TCONS_00025743 | hypothetical protein PHAVU_001G067100g | | | |
| XLOC_013302 | TCONS_00025744 | shikimate o-hydroxycinnamoyltransferase-like | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| XLOC_013303 | TCONS_00025745 | pentatricopeptide repeat-containing protein at1g06270 | plastid membrane | | |
| XLOC_013306 | TCONS_00025748 | probable indole-3-acetic acid-amido synthetase | jasmonate-amino synthetase activity;response to wounding;jasmonic acid metabolic process;induced systemic resistance, jasmonic acid mediated signaling pathway | | |
| XLOC_013307 | TCONS_00025749 | hypothetical protein PHAVU_002G085800g | | | |
| XLOC_013308 | TCONS_00025750 | probable serine threonine-protein kinase fhke-like | | | |
| XLOC_013309 | TCONS_00025751 | hypothetical protein LR48_Vigan05g172500 | nucleic acid binding;protein dimerization activity | | |
| XLOC_013314 | TCONS_00025756 | hypothetical protein Poptr_cp015 | | | |
| XLOC_013320 | TCONS_00025762 | nadh-plastoquinone oxidoreductase subunit 2 | plasma membrane;chloroplast thylakoid membrane;integral component of membrane;NADH dehydrogenase (ubiquinone) activity;quinone binding;transport;photosynthesis, light reaction;ATP synthesis coupled electron transport | ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:1.6.5.3-reductase (H+-translocating) | Oxidative phosphorylationOxidative phosphorylation |
| XLOC_013322 | TCONS_00025764 | hypothetical protein PHAVU_001G0336001g, partial | DNA binding | | |
| XLOC_013342 | TCONS_00025801 | transcriptional adapter ada2a | nucleus;DNA binding;zinc ion binding;regulation of transcription from RNA polymerase II promoter;histone acetylation | | |
| XLOC_013365 | TCONS_00025862 | pleiotropic drug resistance subfamily g protein | plasmodesma;integral component of membrane;ATP binding;ATPase activity;transport;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_013397 | TCONS_00025929 | telomeric repeat-binding factor 1-like | metal ion binding | | |
| XLOC_013398 | TCONS_00025931 | transposon tf2-1 polyprotein isoform x1 | | | |
| XLOC_013426 | TCONS_00025981 | hypothetical protein PHAVU_003G274300g | | | |

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| XLOC_013473 | TCONS_00026077 | 6-phosphofructo-2-kinase fructose- -bisphosphatase-like | binding;organic substance metabolic process | | |
| XLOC_013495 | TCONS_00026111 | hypothetical protein | | | |
| XLOC_013496 | TCONS_00026113 | hypothetical protein | | | |
| XLOC_013503 | TCONS_00026131 | lysine-specific demethylase jmj16 | metal ion binding;primary metabolic process;cellular macromolecule metabolic process | | |
| XLOC_013569 | TCONS_00026229 | protein zinc induced facilitator-like 1 | integral component of membrane;transporter activity;transmembrane transport | | |
| XLOC_013575 | TCONS_00026238 | disease resistance gene nbs-lrr family protein | | | |
| XLOC_013597 | TCONS_00026284 | glyceraldehyde-3-phosphate dehydrogenase a | oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;NADP binding;NAD binding;glucose metabolic process;oxidation-reduction process | | |
| XLOC_013645 | TCONS_00026376 | histone-lysine n- h3 lysine-9 specific suvh5-like | intracellular organelle;binding;methyltransferase activity;methylation | | |
| XLOC_013968 | TCONS_00026979 | rab proteins geranylgeranyltransferase component a-like | cytoplasm;transferase activity;metabolic process | | |
| XLOC_014473 | TCONS_00027964 | abc transporter c family member 13 | integral component of membrane;ATP binding;zinc ion binding;oxidoreductase activity;ATPase activity, coupled to transmembrane movement of substances;transmembrane transport;oxidation-reduction process | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_014537 | TCONS_00028095 | protein transport protein sec24-like at3g07100-like isoform x2 | COPII vesicle coat;zinc ion binding;intracellular protein transport;ER to Golgi vesicle-mediated transport | | |
| XLOC_014550 | TCONS_00028115 | probable apyrase 6 | | | |
| XLOC_014554 | TCONS_00028121 | myosin-j heavy chain | myosin complex;motor activity;ATP binding;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolism |
| XLOC_014571 | TCONS_00028146 | rna-binding protein ylmh | RNA binding;anatomical structure morphogenesis;cellular component organization;cell development;plant epidermis development | | |
| XLOC_014604 | TCONS_00028198 | hypothetical protein | | | |
| XLOC_014614 | TCONS_00028221 | ring u-box superfamily protein isoform 1 | zinc ion binding | | |
| XLOC_014668 | TCONS_00028326 | hypothetical protein PHAVU_001G035000g | | | |

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| XLOC_014752 | TCONS_00028478 | dna-directed rna polymerases i and iii subunit rpac1 | DNA binding;DNA-directed RNA polymerase activity;protein dimerization activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_014782 | TCONS_00028534 | hypothetical protein LR48_Vigan09g116500 | | | |
| XLOC_015084 | TCONS_00029103 | pseudo histidine-containing phosphotransfer protein 6-like | | | |
| XLOC_015315 | TCONS_00029533 | ankyrin repeat protein | | | |
| XLOC_015334 | TCONS_00029569 | leucine--trna cytoplasmic-like isoform x1 | cytosol;plasmodesma;chloroplast;aminoacyl-tRNA editing activity;leucine-tRNA ligase activity;ATP binding;leucyl-tRNA aminoacylation;regulation of translational fidelity | ec:6.1.1.4-ligase;ec:6.1.1;ec:3.1.1.1-ali-esterase | Aminoacyl-tRNA biosynthesisDrug metabolism - other enzymes |
| XLOC_015560 | TCONS_00030012 | transcriptional adapter ada2 | nucleus;DNA binding;zinc ion binding;regulation of transcription from RNA polymerase II promoter;histone acetylation | | |
| XLOC_015561 | TCONS_00030013 | long chain acyl-synthetase 8 | endoplasmic reticulum;Golgi apparatus;chloroplast envelope;long-chain fatty acid-CoA ligase activity;long-chain fatty acid metabolic process | ec:6.2.1;ec:6.2.1.3-ligase | Fatty acid degradation;Fatty acid biosynthesis |
| XLOC_015568 | TCONS_00030020 | golgin candidate 4-like | | | |
| XLOC_015572 | TCONS_00030024 | hypothetical protein PHAVU_001G197200g | cysteine-type peptidase activity;ubiquitinyl hydrolase activity;ubiquitin-dependent protein catabolic process | ec:3.4 | |
| XLOC_015576 | TCONS_00030028 | spermidine hydroxycinnamoyl transferase-like | shikimate O-hydroxycinnamoyltransferase activity;anthranilate N-benzoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.144;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| XLOC_015579 | TCONS_00030031 | hypothetical protein LR48_Vigan09g091200 | | | |
| XLOC_015580 | TCONS_00030032 | transcription factor bhlh086 | hydrolase activity;protein dimerization activity;metabolic process | | |
| XLOC_015581 | TCONS_00030033 | hypothetical protein LR48_Vigan09g091200 | | | |
| XLOC_015584 | TCONS_00030036 | hypothetical chloroplast rf68 | chloroplast | | |
| XLOC_015585 | TCONS_00030037 | squalene monooxygenase | plastid;integral component of membrane;cytoplasmic membrane-bounded vesicle;squalene monooxygenase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.14.13;ec:1.14.13.132 | |
| XLOC_015586 | TCONS_00030038 | squalene monooxygenase | integral component of membrane;squalene monooxygenase | ec:1.14.13;ec:1.14.13.132 | |

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| | | | activity;flavin adenine dinucleotide binding;oxidation-reduction process | | |
| XLOC_015591 | TCONS_00030043 | histone-lysine n- h3 lysine-9 specific suvh6 | nucleus;chromosome;zinc ion binding;histone-lysine N-methyltransferase activity;histone binding;histone lysine methylation | ec:2.1.1;ec:2.1.1.43-N-methyltransferase | Lysine degradation |
| XLOC_015592 | TCONS_00030044 | PREDICTED: uncharacterized protein LOC106753175 | | | |
| XLOC_015593 | TCONS_00030045 | phd finger protein partial | binding | | |
| XLOC_015594 | TCONS_00030046 | hypothetical protein PHAVU_003G093300g | | | |
| XLOC_015598 | TCONS_00030050 | jq0280 hypothetical 12k protein (trna intron) - rice chloroplast | chloroplast | | |
| XLOC_015605 | TCONS_00030057 | ubiquitin-conjugating enzyme e2-17 kda | | | |
| XLOC_015613 | TCONS_00030065 | hypothetical protein glysoja_001754 | | | |
| XLOC_015615 | TCONS_00030067 | atp-citrate synthase beta chain protein 1-like | | | |
| XLOC_015620 | TCONS_00030072 | hypothetical protein | | | |
| XLOC_015623 | TCONS_00030075 | wall associated kinase-like protein | kinase activity;polysaccharide binding;phosphorylation | | |
| XLOC_015624 | TCONS_00030076 | wrky transcription factor 22-like | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| XLOC_015628 | TCONS_00030080 | PREDICTED: uncharacterized protein LOC102666466 | | | |
| XLOC_015629 | TCONS_00030081 | dvl family protein | | | |
| XLOC_015631 | TCONS_00030083 | hypothetical protein PHAVU_010G021000g | | | |
| XLOC_015632 | TCONS_00030084 | at4g21420p-like protein | nucleic acid binding;RNA-DNA hybrid ribonuclease activity;transferase activity;transport;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1;ec:3.1.30;ec:3.1.26;ec:3.1.26.4 | |
| XLOC_015697 | TCONS_00030224 | nuclease harbi1 | | | |
| XLOC_015830 | TCONS_00030453 | hypothetical protein LR48_Vigan694s000300 | | | |

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| XLOC_015899 | TCONS_00030569 | transcription regulatory protein snf2 | helicase activity;ATP binding;histone binding;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolism |
| XLOC_016025 | TCONS_00030844 | u1 small nuclear ribonucleoprotein a-like | | | |
| XLOC_016038 | TCONS_00030872 | hypothetical protein PHAVU_007G081200g | | | |
| XLOC_016042 | TCONS_00030879 | hypothetical protein LR48_Vigan02g201600 | | | |
| XLOC_016043 | TCONS_00030880 | hypothetical protein LR48_Vigan02g201600 | | | |
| XLOC_016045 | TCONS_00030883 | hypothetical protein PHAVU_007G0816001g | | | |
| XLOC_016155 | TCONS_00031111 | exosome complex exonuclease rrp46 homolog isoform x1 | kinesin complex;microtubule;microtubule motor activity;exonuclease activity;ATP binding;microtubule binding;mRNA splicing, via spliceosome;RNA methylation;protein targeting to mitochondrion;microtubule-based movement;protein maturation;nucleic acid phosphodiester bond hydrolysis | ec:3.1;ec:3.6.1.15-phosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolism |
| XLOC_016161 | TCONS_00031125 | transcriptional activator demeter-like | catalytic activity;DNA metabolic process;single-organism process | | |
| XLOC_016234 | TCONS_00031263 | hypothetical protein LR48_Vigan03g138500 | | | |
| XLOC_016248 | TCONS_00031288 | serine threonine protein phosphatase 2a regulatory subunit b beta-like | calcium ion binding | | |
| XLOC_016390 | TCONS_00031555 | hypothetical protein glysoja_007957 | | | |
| XLOC_016665 | TCONS_00032118 | hypothetical protein PHAVU_006G036900g, partial | | | |
| XLOC_016701 | TCONS_00032178 | polyketide cyclase dehydrase and lipid transporter | | | |
| XLOC_016713 | TCONS_00032194 | hypothetical protein LR48_Vigan02g146700 | | | |
| XLOC_016754 | TCONS_00032274 | fk506-binding protein 5-like | | | |
| XLOC_017074 | TCONS_00032863 | dna mismatch repair protein | nuclear chromatin;mismatch repair complex;ATP binding;mismatched DNA binding;mitotic cell | | |

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| | | | cycle;double-strand break repair via homologous recombination;DNA-dependent DNA replication;regulation of DNA replication;mismatch repair;DNA methylation;mitotic recombination;sister chromatid cohesion;synapsis;pollen development;embryo sac egg cell differentiation;response to abscisic acid;seed germination;seed dormancy process;regulation of cell cycle process;somatic cell DNA recombination;chromatin modification;gene silencing by RNA;meiotic DNA double-strand break formation;cotyledon development | | |
| XLOC_017187 | TCONS_00033109 | cysteine-rich receptor-kinase-like protein | protein serine/threonine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| XLOC_017321 | TCONS_00033359 | cysteine-rich receptor-like protein kinase 29 | protein serine/threonine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| XLOC_017342 | TCONS_00033413 | exosome complex exonuclease rrp46 homolog isoform x1 | exonuclease activity;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| XLOC_017343 | TCONS_00033415 | cysteine-rich receptor-kinase-like protein | nucleotide binding;protein kinase activity;protein phosphorylation | | |
| XLOC_017516 | TCONS_00033752 | pentatricopeptide repeat-containing protein mitochondrial | zinc ion binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.4.3;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_017565 | TCONS_00033852 | zinc c3hc4 type (ring finger) protein | zinc ion binding | | |
| XLOC_017569 | TCONS_00033859 | abc transporter g family member 24-like | plasma membrane;ATP binding;xenobiotic-transporting ATPase activity;drug transmembrane transport;metabolic process;xenobiotic transport | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.3.44 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_017620 | TCONS_00033960 | hypothetical protein PHAVU_003G046100g | | | |
| XLOC_017637 | TCONS_00033992 | magnesium transporter mrs2-2-like | integral component of membrane;magnesium ion transmembrane transporter activity;magnesium ion transport;transmembrane transport | | |
| XLOC_017674 | TCONS_00034049 | ftsh extracellular | plasmodesma;chloroplast envelope;metalloendopeptidase activity;ATP | ec:3.4.24 | |

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| | | protease family protein | binding;proteolysis;regulation of apoptotic process | | |
| XLOC_017794 | TCONS_00034309 | signal recognition particle 43 kda chloroplastic | chloroplast thylakoid membrane;chloroplast envelope;signal recognition particle, chloroplast targeting;identical protein binding;response to blue light;response to sucrose;response to red light;regulation of proton transport;response to far red light;cysteine biosynthetic process;protein import into chloroplast thylakoid membrane;protein autophosphorylation | | |
| XLOC_017843 | TCONS_00034409 | nad -binding rossmann-fold protein | tropine dehydrogenase activity;oxidation-reduction process | ec:1.1.1.206-reductase I | Tropane, piperidine and pyridine alkaloid biosynthesis |
| XLOC_017913 | TCONS_00034541 | mitogen-activated protein kinase homolog mmk2-like | intracellular;MAP kinase activity;ATP binding;MAPK cascade | ec:2.7.11;ec:2.7.11.24-protein kinase | mTOR signaling pathway |
| XLOC_018020 | TCONS_00034803 | protein mon2 homolog isoform x2 | protein transport | | |
| XLOC_018037 | TCONS_00034850 | auxin-responsive protein iaa16-like partial | | | |
| XLOC_018176 | TCONS_00035138 | myb-like protein p | | | |
| XLOC_018187 | TCONS_00035163 | acylphosphatase family isoform 1 | acylphosphatase activity;metabolic process | ec:3.6.1.7-acetylphosphatase | Aminobenzoate degradation;Pyruvate metabolism |
| XLOC_018249 | TCONS_00035272 | PREDICTED: uncharacterized protein LOC100789825 isoform X2 | chloroplast;hydrolase activity;lipid metabolic process | | |
| XLOC_018489 | TCONS_00035755 | hypothetical protein PHAVU_004G124900g | | | |
| XLOC_018494 | TCONS_00035760 | hypothetical protein glysoja_015948 | | | |
| XLOC_018498 | TCONS_00035764 | hypothetical protein PHAVU_007G081200g | | | |
| XLOC_018501 | TCONS_00035767 | hypothetical protein M569_00483, partial | | | |
| XLOC_018507 | TCONS_00035773 | atp synthase cf0 subunit i | plasma membrane;chloroplast thylakoid membrane;integral component of membrane;proton-transporting ATP synthase complex, coupling factor F(o);ATP binding;proton-transporting ATP synthase activity, rotational mechanism;ATP synthesis coupled proton transport | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_018510 | TCONS_00035776 | hypothetical chloroplast rf1 | chloroplast inner membrane;integral component of membrane;protein transport | | |

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|---|---|---|---|---|---|
| XLOC_018516 | TCONS_00035782 | endonuclease exonuclease phosphatase family protein | | | |
| XLOC_018517 | TCONS_00035783 | hypothetical protein PHAVU_002G227000g | | | |
| XLOC_018521 | TCONS_00035787 | hypothetical protein PHAVU_001G121300g | | | |
| XLOC_018523 | TCONS_00035789 | histone deacetylase 6 | oxidoreductase activity;hydrolase activity;cellular protein metabolic process;single-organism metabolic process | | |
| XLOC_018527 | TCONS_00035793 | hypothetical protein PHAVU_006G007700g | | | |
| XLOC_018528 | TCONS_00035794 | nadh-plastoquinone oxidoreductase subunit 2 | chloroplast thylakoid membrane;integral component of membrane;NADH dehydrogenase (ubiquinone) activity;quinone binding;transport;photosynthesis, light reaction;ATP synthesis coupled electron transport | ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:1.6.5.3-reductase (H+-translocating) | Oxidative phosphorylationOxidative phosphorylation |
| XLOC_018529 | TCONS_00035795 | maturase | mitochondrion;chloroplast;RNA binding;mRNA processing;tRNA processing;RNA splicing | | |
| XLOC_018532 | TCONS_00035798 | PREDICTED: uncharacterized protein LOC102660158 | | | |
| XLOC_018533 | TCONS_00035799 | hypothetical protein PHAVU_003G069400g | | | |
| XLOC_018543 | TCONS_00035809 | dead-box atp-dependent rna helicase 7 | nucleus;RNA binding;helicase activity;ATP binding;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolism |
| XLOC_018545 | TCONS_00035811 | uncharacterized mitochondrial protein g00810-like | catalytic activity | | |
| XLOC_018550 | TCONS_00035816 | transmembrane protein, putative | | | |
| XLOC_018554 | TCONS_00035820 | PREDICTED: uncharacterized protein LOC102664214 | nucleic acid binding;protein dimerization activity | | |
| XLOC_018555 | TCONS_00035821 | hypothetical protein PHAVU_004G0453000g, partial | DNA binding | | |
| XLOC_018561 | TCONS_00035827 | photosystem ii d1 partial | chloroplast;photosystem II;integral component of membrane;oxidoreductase activity;electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity;metal ion binding;photosynthetic electron transport in photosystem II | | |

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| XLOC_018563 | TCONS_00035829 | PREDICTED: uncharacterized protein LOC105036210 |  |  |  |
| XLOC_018564 | TCONS_00035830 | calmodulin-binding family protein |  |  |  |
| XLOC_018707 | TCONS_00036123 | serine-threonine kinase | protein kinase activity;ATP binding;protein phosphorylation |  |  |
| XLOC_018947 | TCONS_00036541 | agamous-like 20 isoform partial | nucleus;cytoplasm;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription factor binding;protein dimerization activity;protein import into nucleus, translocation;transcription, DNA-templated;regulation of transcription, DNA-templated;positive regulation of flower development;maintenance of inflorescence meristem identity |  |  |
| XLOC_018960 | TCONS_00036570 | hypothetical protein PHAVU_008G075700g |  |  |  |
| XLOC_018973 | TCONS_00036607 | probable lrr receptor-like serine threonine-protein kinase rfk1 isoform x2 | protein kinase activity;phosphorylation |  |  |
| XLOC_019070 | TCONS_00036784 | aaa-type atpase family protein | intracellular;ATP binding;microtubule-severing ATPase activity;fatty acid beta-oxidation;protein import into peroxisome matrix | ec:3.6.1.15-phosphatase;ec:3.6.4.3;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_019116 | TCONS_00036870 | hypothetical protein PHAVU_001G133800g |  |  |  |
| XLOC_019216 | TCONS_00037034 | hypothetical protein PHAVU_L006100g | DNA binding;zinc ion binding |  |  |
| XLOC_019264 | TCONS_00037126 | wound-induced basic protein | cytosol;response to cytokinin |  |  |
| XLOC_019320 | TCONS_00037227 | unnamed protein product | ATP-dependent DNA helicase activity;ATP binding;DNA repair;chromatin remodeling;DNA duplex unwinding | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_019344 | TCONS_00037265 | gata transcription factor 7-like | binding |  |  |
| XLOC_019362 | TCONS_00037292 | glutamate receptor 2 | integral component of membrane;ionotropic glutamate receptor activity;ion transport;ionotropic glutamate receptor signaling pathway |  |  |
| XLOC_019386 | TCONS_00037333 | iron-sulfur cluster biosynthesis family protein | chloroplast envelope |  |  |

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| XLOC_019388 | TCONS_00037335 | nucleic acid-ob-fold-like protein | | | |
| XLOC_019446 | TCONS_00037436 | hypothetical protein VIGAN_03165800, partial | | | |
| XLOC_019472 | TCONS_00037481 | sugar transporter | integral component of membrane;substrate-specific transmembrane transporter activity;2-alkenal reductase [NAD(P)] activity;carbohydrate transport;transmembrane transport;oxidation-reduction process | ec:1.3.1.74 | |
| XLOC_019541 | TCONS_00037605 | hypothetical protein PHAVU_005G084700g | | | |
| XLOC_019643 | TCONS_00037802 | hypothetical protein LR48_Vigan05g133500 | | | |
| XLOC_020164 | TCONS_00038830 | ankyrin repeat and sam domain-containing protein 3-like | | | |
| XLOC_020297 | TCONS_00039100 | protein transport protein sec24-1 | COPII vesicle coat;zinc ion binding;intracellular protein transport;ER to Golgi vesicle-mediated transport | | |
| XLOC_020421 | TCONS_00039396 | phytochrome a-associated f-box protein | organic cyclic compound binding;heterocyclic compound binding;cellular protein metabolic process;system development;regulation of biological process | | |
| XLOC_020515 | TCONS_00039576 | hypothetical protein PHAVU_003G177200g | | | |
| XLOC_020535 | TCONS_00039627 | acyl-coenzyme a oxidase peroxisomal | oxidoreductase activity | | |
| XLOC_020664 | TCONS_00039870 | hedgehog isoform 2 | plasma membrane;plasmodesma;integral component of membrane;hedgehog receptor activity;signal transduction;cholesterol transport | | |
| XLOC_020667 | TCONS_00039876 | transcription factor hy5-like | | | |
| XLOC_020674 | TCONS_00039893 | g-type lectin s-receptor-like serine threonine-kinase | protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation;recognition of pollen | ec:2.7.11 | |
| XLOC_020681 | TCONS_00039909 | dna-directed rna polymerase iii subunit rpc3 | DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_020748 | TCONS_00040036 | protein transport protein sec24 | COPII vesicle coat;zinc ion binding;intracellular protein transport;ER to Golgi vesicle-mediated transport | | |
| XLOC_020761 | TCONS_00040054 | u6 snrna phosphodiesterase isoform x3 | nucleus;nuclease activity;mRNA processing;RNA splicing;U6 snRNA 3'-end processing;nucleic acid | ec:3.1 | |

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|---|---|---|---|---|---|
|  |  |  | phosphodiester bond hydrolysis |  |  |
| XLOC_020771 | TCONS_00040067 | hypothetical protein PHAVU_002G203500g |  |  |  |
| XLOC_020794 | TCONS_00040116 | u4 u6 small nuclear ribonucleoprotein prp31 | viral nucleocapsid;U4/U6 x U5 tri-snRNP complex;spliceosomal tri-snRNP complex assembly |  |  |
| XLOC_020796 | TCONS_00040120 | actin-related protein 2 | Arp2/3 protein complex;ATP binding;multidimensional cell growth;trichome morphogenesis;Arp2/3 complex-mediated actin nucleation |  |  |
| XLOC_020797 | TCONS_00040123 | serine hydroxymethyltransferase | transferase activity, transferring one-carbon groups;organic cyclic compound binding;heterocyclic compound binding;one-carbon metabolic process;serine family amino acid metabolic process |  |  |
| XLOC_020802 | TCONS_00040133 | glutamate receptor 2 | integral component of membrane;ionotropic glutamate receptor activity;ion transport;ionotropic glutamate receptor signaling pathway |  |  |
| XLOC_020820 | TCONS_00040168 | trehalose-phosphate phosphatase | trehalose-phosphatase activity;trehalose biosynthetic process;protein dephosphorylation | ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1;ec:3.1.3.12-trehalose 6-phosphatase | Aminobenzoate degradationStarch and sucrose metabolism |
| XLOC_020838 | TCONS_00040209 | translation elongation factor ef protein | intracellular;translation elongation factor activity;GTPase activity;GTP binding;translational elongation | ec:3.6.1.15-phosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolism |
| XLOC_020857 | TCONS_00040237 | btb poz domain-containing protein at1g21780-like | cytoplasm;Cul3-RING ubiquitin ligase complex;protein binding;fatty acid beta-oxidation;intra-Golgi vesicle-mediated transport;proximal/distal pattern formation;floral organ abscission;protein import into peroxisome matrix;protein ubiquitination;flower morphogenesis |  |  |
| XLOC_020863 | TCONS_00040257 | mads-box transcription factor 50 | nucleus;DNA binding;metal ion binding;protein dimerization activity;transcription, DNA-templated;regulation of transcription, DNA-templated |  |  |
| XLOC_020934 | TCONS_00040382 | hypothetical protein LR48_Vigan46s000800 |  |  |  |
| XLOC_021014 | TCONS_00040540 | ribonuclease e | RNA binding;ribonuclease activity;starch binding;RNA processing;RNA phosphodiester bond hydrolysis | ec:3.1 |  |
| XLOC_021047 | TCONS_00040620 | disease resistance | ADP binding;signal transduction |  |  |

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| | | protein (tir-nbs-lrr class) | | | |
| XLOC_021310 | TCONS_00041124 | two-component response regulator arr2-like protein | intracellular;DNA binding;phosphorelay signal transduction system | | |
| XLOC_021548 | TCONS_00041550 | rna polymerase beta subunit | plastid;nucleotidyltransferase activity | | |
| XLOC_021549 | TCONS_00041551 | spfh domain band 7 family protein | nucleic acid binding;zinc ion binding;DNA integration | | |
| XLOC_021551 | TCONS_00041553 | hypothetical protein PHAVU_004G108700g | | | |
| XLOC_021554 | TCONS_00041556 | 40s ribosomal protein s2-4-like | small ribosomal subunit;RNA binding;structural constituent of ribosome;translation | | |
| XLOC_021561 | TCONS_00041563 | downstream target of agl15-4 | protein kinase activity;ATP binding;protein phosphorylation | | |
| XLOC_021562 | TCONS_00041564 | protein lurp-one-related 15 | | | |
| XLOC_021565 | TCONS_00041567 | hypothetical protein PHAVU_011G106500g | | | |
| XLOC_021566 | TCONS_00041568 | protein lurp-one-related 15-like | | | |
| XLOC_021567 | TCONS_00041569 | hypothetical protein LR48_Vigan04g240900 | | | |
| XLOC_021572 | TCONS_00041574 | hypothetical protein VITISV_008145 | | | |
| XLOC_021574 | TCONS_00041576 | hypothetical protein PHAVU_L006100g | | | |
| XLOC_021575 | TCONS_00041577 | hypothetical protein PHAVU_004G088700g | | | |
| XLOC_021578 | TCONS_00041580 | rna polymerase beta partial | chloroplast;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_021579 | TCONS_00041581 | gdsl esterase lipase cprd49 | hydrolase activity, acting on ester bonds;vegetative to reproductive phase transition of meristem;protein desumoylation;hydrogen peroxide biosynthetic process | | |
| XLOC_021580 | TCONS_00041582 | atp synthase cf1 alpha partial | mitochondrial inner membrane;plasma membrane;chloroplast thylakoid membrane;proton-transporting ATP synthase complex, catalytic core F(1);ATP binding;proton-transporting ATP synthase activity, rotational mechanism;proton-transporting ATPase activity, rotational mechanism;ATP synthesis coupled proton | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |

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| | | | transport;ATP hydrolysis coupled proton transport | | |
| XLOC_021582 | TCONS_00041584 | hypothetical protein LR48_Vigan03g146600 | | | |
| XLOC_021584 | TCONS_00041586 | ribosomal protein l16 | mitochondrion;ribosome;chloroplast;structural constituent of ribosome;rRNA binding;translation | | |
| XLOC_021585 | TCONS_00041587 | beta-glucosidase 11 | beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1.21-gentiobiase; ec:3.2.1 | Cyanoamino acid metabolism;Phenylpropanoid biosynthesis;Starch and sucrose metabolism |
| XLOC_021586 | TCONS_00041588 | hypothetical protein LR48_Vigan583s003200 | | | |
| XLOC_021588 | TCONS_00041590 | cytochrome p450 family protein | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| XLOC_021592 | TCONS_00041594 | ribulose- -bisphosphate carboxylase oxygenase large partial | chloroplast;magnesium ion binding;monooxygenase activity;ribulose-bisphosphate carboxylase activity;reductive pentose-phosphate cycle;oxidation-reduction process | ec:4.1.1.39-carboxylase | Carbon fixation in photosynthetic organisms;Biosynthesis of antibiotics;Glyoxylate and dicarboxylate metabolism |
| XLOC_021593 | TCONS_00041595 | hypothetical protein PHAVU_010G029600g | ATP binding;ADP binding;signal transduction | | |
| XLOC_021595 | TCONS_00041597 | hypothetical protein Csa_2G055570 | mitochondrion;chloroplast | | |
| XLOC_021596 | TCONS_00041598 | hypothetical protein PHAVU_001G0336001g, partial | DNA binding | | |
| XLOC_021597 | TCONS_00041599 | integrase core domain containing protein | | | |
| XLOC_021598 | TCONS_00041600 | hypothetical protein PHAVU_009G162400g | | | |
| XLOC_021599 | TCONS_00041601 | rna polymerase beta subunit | chloroplast;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_021601 | TCONS_00041603 | cysteine-rich rlk (receptor-like protein kinase) 8 | binding | | |
| XLOC_021603 | TCONS_00041605 | plant t8m16-150 | | | |
| XLOC_021607 | TCONS_00041609 | pentatricopeptide repeat-containing protein at2g06000 | microtubule-severing ATPase activity;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.4.3;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_021608 | TCONS_00041610 | hypothetical protein LR48_Vigan97s002000 | | | |

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| XLOC_021609 | TCONS_00041611 | hypothetical protein PHAVU_011G140600g | DNA binding | | |
| XLOC_021612 | TCONS_00041614 | photosystem ii protein partial | chloroplast;electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity;photosynthetic electron transport in photosystem II | | |
| XLOC_021618 | TCONS_00041620 | ubiquitin ligase sinat3 | nucleus;ubiquitin-protein transferase activity;zinc ion binding;ligase activity;ubiquitin-dependent protein catabolic process;multicellular organismal development;protein ubiquitination | | |
| XLOC_021619 | TCONS_00041621 | integrase core domain containing protein | | | |
| XLOC_021624 | TCONS_00041626 | exocyst complex component exo70b1-like | exocyst;exocytosis | | |
| XLOC_021625 | TCONS_00041627 | exocyst complex component exo70b1-like | exocyst;exocytosis | | |
| XLOC_021627 | TCONS_00041629 | hypothetical protein LR48_Vigan07g170500 | | | |
| XLOC_021628 | TCONS_00041630 | cytochrome f | chloroplast thylakoid membrane;integral component of thylakoid membrane;iron ion binding;electron carrier activity;heme binding;photosynthesis;oxidation-reduction process | | |
| XLOC_021633 | TCONS_00041635 | atp synthase cf0 subunit i | plasma membrane;chloroplast thylakoid membrane;integral component of membrane;proton-transporting ATP synthase complex, coupling factor F(o);ATP binding;proton-transporting ATP synthase activity, rotational mechanism;ATP synthesis coupled proton transport | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_021634 | TCONS_00041636 | endonuclease exonuclease phosphatase family protein | catalytic activity;cellular metabolic process | | |
| XLOC_021636 | TCONS_00041638 | rna polymerase beta subunit | chloroplast;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_021642 | TCONS_00041644 | gag-pol polyprotein | | | |
| XLOC_021645 | TCONS_00041647 | hypothetical protein GLYMA_06G042000 | | | |
| XLOC_021647 | TCONS_00041649 | atp synthase cf1 alpha subunit | | | |

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| XLOC_021649 | TCONS_00041651 | hypothetical protein VIGAN_03082100 | | | |
| XLOC_021664 | TCONS_00041666 | multidrug resistance protein abc transporter family protein | integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_021724 | TCONS_00041758 | folate transporter carrier-like protein | | | |
| XLOC_021753 | TCONS_00041810 | guanine nucleotide-binding protein subunit beta-like protein 1 homolog | nucleus;cytoplasm;Cul4-RING E3 ubiquitin ligase complex;regulation of DNA repair;cellular response to DNA damage stimulus;pollen development;plasmodesma organization;embryo development ending in seed dormancy;response to aluminum ion;plasmodesmata-mediated intercellular transport;DNA integrity checkpoint;ovule development;acquisition of desiccation tolerance in seed;positive regulation of cell cycle arrest;response to cisplatin;regulation of root development | | |
| XLOC_021797 | TCONS_00041911 | duf241 domain protein | | | |
| XLOC_022009 | TCONS_00042380 | cell wall invertase 2 isoform 2 | sucrose alpha-glucosidase activity;carbohydrate metabolic process | ec:3.2.1.48-alpha-glucosidase;ec:3.2.1.26-invertase;ec:3.2.1 | Starch and sucrose metabolismGalactose metabolism;Starch and sucrose metabolism |
| XLOC_022070 | TCONS_00042500 | ferrochelatase - chloroplastic | plastid;ferrochelatase activity;heme biosynthetic process;response to stress;macromolecule localization;regulation of programmed cell death | ec:4.99.1.1-ferro-protoporphyrin chelatase | Porphyrin and chlorophyll metabolism |
| XLOC_022312 | TCONS_00043004 | pentatricopeptide repeat-containing protein at4g17915 | | | |
| XLOC_022425 | TCONS_00043219 | zinc finger (c3hc4-type ring finger) family protein | plasma membrane;zinc ion binding | | |
| XLOC_022543 | TCONS_00043496 | 4-coumarate--ligase-like 9 | ligase activity;Photinus-luciferin 4-monooxygenase (ATP-hydrolyzing) activity;oxidation-reduction process | ec:1.13.12;ec:1.13.12.7 | |
| XLOC_022572 | TCONS_00043545 | c2 and gram domain-containing protein at1g03370-like | lyase activity;metabolic process | | |
| XLOC_022666 | TCONS_00043755 | mlo-like protein 10 | integral component of membrane;calmodulin binding;defense response;response to biotic stimulus | | |

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| XLOC_022719 | TCONS_00043846 | lipase rog1 isoform x3 | | | |
| XLOC_022735 | TCONS_00043870 | pentatricopeptide repeat-containing protein at5g55840 | microtubule-severing ATPase activity;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.4.3;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_023069 | TCONS_00044551 | pentatricopeptide repeat-containing protein at2g13600-like isoform x1 | microtubule-severing ATPase activity;metabolic process | ec:3.6.1.15-phosphatase;ec:3.6.4.3;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_023127 | TCONS_00044665 | duf241 domain protein | | | |
| XLOC_023140 | TCONS_00044682 | protein transport protein sec24-1 | COPII vesicle coat;zinc ion binding;intracellular protein transport;ER to Golgi vesicle-mediated transport | | |
| XLOC_023375 | TCONS_00045188 | chromosome region maintenance protein 1 exportin | intracellular;Ran GTPase binding;intracellular protein transport | | |
| XLOC_023440 | TCONS_00045306 | hypothetical protein VIGAN_02068400 | | | |
| XLOC_023474 | TCONS_00045372 | protein topless-like isoform x1 | regulation of transcription, DNA-templated | | |
| XLOC_023475 | TCONS_00045373 | topless-like protein | regulation of transcription, DNA-templated | | |
| XLOC_023610 | TCONS_00045657 | protein far1-related sequence 2 | zinc ion binding;regulation of transcription, DNA-templated | | |
| XLOC_023611 | TCONS_00045659 | protein far1-related sequence 2 | zinc ion binding;regulation of transcription, DNA-templated | | |
| XLOC_023648 | TCONS_00045724 | hypothetical protein PHAVU_009G125600g | | | |
| XLOC_023693 | TCONS_00045812 | hat transposon superfamily isoform 2 | DNA binding;protein dimerization activity | | |
| XLOC_023694 | TCONS_00045813 | myosin id heavy chain-like protein | | | |
| XLOC_023743 | TCONS_00045924 | hypothetical protein PHAVU_009G156200g | | | |
| XLOC_023868 | TCONS_00046178 | protein dehydration-induced 19 homolog 6-like isoform x2 | | | |
| XLOC_023878 | TCONS_00046192 | c2 and gram domain-containing protein | phosphatidylserine decarboxylase activity;protein kinase C activity;ligase activity;protein phosphorylation | ec:2.7.11;ec:4.1.1.65-decarboxylase;ec:2.7.11.13-kinase C | Glycerophospholipid metabolismPhosphatidylinositol signaling system |
| XLOC_023887 | TCONS_00046208 | serine threonine protein phosphatase 2a 55 kda regulatory | regulation of cellular process | | |

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| | | subunit b beta isoform-like isoform x2 | | | |
| XLOC_023896 | TCONS_00046231 | peroxisomal membrane protein pex14 | peroxisomal membrane;protein import into peroxisome matrix, docking | | |
| XLOC_024006 | TCONS_00046452 | protein lurp-one-related 6-like | | | |
| XLOC_024211 | TCONS_00046876 | upf0047 protein | chloroplast | | |
| XLOC_024320 | TCONS_00047063 | photosystem i p700 apoprotein a2 | photosystem I;chloroplast thylakoid membrane;integral component of membrane;magnesium ion binding;electron carrier activity;chlorophyll binding;oxidoreductase activity;4 iron, 4 sulfur cluster binding;photosynthesis;protein-chromophore linkage;oxidation-reduction process | | |
| XLOC_024322 | TCONS_00047065 | ribosomal protein s15 | ribosome;chloroplast;structural constituent of ribosome;translation | | |
| XLOC_024323 | TCONS_00047066 | nadh-plastoquinone oxidoreductase subunit i | plasma membrane;chloroplast thylakoid membrane;iron ion binding;NADH dehydrogenase (ubiquinone) activity;quinone binding;4 iron, 4 sulfur cluster binding;photosynthesis, light reaction;oxidation-reduction process | ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:1.6.5.3-reductase (H+-translocating) | Oxidative phosphorylationOxidative phosphorylation |
| XLOC_024324 | TCONS_00047067 | rna polymerase beta subunit | chloroplast;DNA binding;DNA-directed RNA polymerase activity;ribonucleoside binding;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_024325 | TCONS_00047068 | hypothetical protein MTR_3g073490 | | | |
| XLOC_024332 | TCONS_00047075 | calmodulin-binding transcription activator 2-like | nucleus;DNA binding;response to cold;leaf senescence;defense response to bacterium;defense response to fungus | | |
| XLOC_024334 | TCONS_00047077 | nadh-plastoquinone oxidoreductase subunit 4 | chloroplast thylakoid membrane;integral component of membrane;NADH dehydrogenase (ubiquinone) activity;quinone binding;ATP synthesis coupled electron transport | ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:1.6.5.3-reductase (H+-translocating) | Oxidative phosphorylationOxidative phosphorylation |
| XLOC_024338 | TCONS_00047081 | pentatricopeptide repeat-containing protein at5g14080 | | | |
| XLOC_024346 | TCONS_00047089 | hypothetical protein VITISV_005281 | | | |
| XLOC_024348 | TCONS_00047091 | atp synthase mitochondrial f1 complex assembly factor 2 | proton-transporting ATP synthase complex assembly | | |

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| XLOC_024351 | TCONS_00047094 | hypothetical protein LR48_Vigan561s006800 | | | |
| XLOC_024359 | TCONS_00047102 | hypothetical protein PHAVU_005G103000g, partial | nucleotide binding;nucleic acid binding | | |
| XLOC_024360 | TCONS_00047103 | hypothetical protein PHAVU_008G1333001g, partial | | | |
| XLOC_024363 | TCONS_00047106 | nad-dependent epimerase dehydratase family protein | mitochondrion;chloroplast thylakoid;translation initiation factor activity;rRNA processing;translational initiation;response to blue light;response to red light;photosystem II assembly;response to far red light;carotenoid biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | | |
| XLOC_024367 | TCONS_00047110 | replication factor c subunit 4 | DNA replication factor C complex;nucleolus;DNA clamp loader activity;DNA-directed DNA polymerase activity;ATP binding;RNA methylation;DNA-dependent DNA replication;pyrimidine ribonucleotide biosynthetic process;embryo development ending in seed dormancy;regulation of flower development;histone modification;floral organ formation;DNA biosynthetic process | ec:3.6.1.15-phosphatase;ec:2.7.7.7-DNA polymerase; ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism;Pyrimidine metabolismPurine metabolism |
| XLOC_024370 | TCONS_00047113 | hypothetical protein glysoja_046184 | | | |
| XLOC_024377 | TCONS_00047120 | atp synthase cf0 subunit i | plasma membrane;chloroplast thylakoid membrane;integral component of membrane;proton-transporting ATP synthase complex, coupling factor F(o);ATP binding;proton-transporting ATP synthase activity, rotational mechanism;ATP synthesis coupled proton transport | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_024379 | TCONS_00047122 | 2-oxoisovalerate dehydrogenase subunit alpha mitochondrial-like | 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity;oxidation-reduction process | ec:1.2.4.4-dehydrogenase (2-methylpropanoyl-transferring) | Propanoate metabolism;Valine, leucine and isoleucine degradation;Biosynthesis of antibiotics |
| XLOC_024380 | TCONS_00047123 | magnesium transporter nipa2 | integral component of membrane;magnesium ion transmembrane transporter activity;magnesium ion transport | | |
| XLOC_024385 | TCONS_00047128 | photosystem ii cp43 chlorophyll partial | photosystem II;chloroplast thylakoid membrane;integral component of membrane;chlorophyll binding;electron transporter, transferring electrons within the cyclic electron transport | | |

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| | | | pathway of photosynthesis activity;metal ion binding;photosynthetic electron transport in photosystem II;protein-chromophore linkage | | |
| XLOC_024386 | TCONS_00047129 | hypothetical protein PHAVU_003G200800g | | | |
| XLOC_024392 | TCONS_00047135 | double-stranded rna-binding motif protein | double-stranded RNA binding | | |
| XLOC_024394 | TCONS_00047137 | protein chloroplastic | | | |
| XLOC_024396 | TCONS_00047139 | envelope membrane protein | chloroplast inner membrane;integral component of membrane;hydrogen ion transmembrane transporter activity;hydrogen ion transmembrane transport | | |
| XLOC_024398 | TCONS_00047141 | protein dennd6a | | | |
| XLOC_024400 | TCONS_00047143 | atp synthase cf1 alpha subunit | mitochondrial inner membrane;plasma membrane;chloroplast thylakoid membrane;proton-transporting ATP synthase complex, catalytic core F(1);ATP binding;proton-transporting ATP synthase activity, rotational mechanism;proton-transporting ATPase activity, rotational mechanism;ATP synthesis coupled proton transport;ATP hydrolysis coupled proton transport | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_024402 | TCONS_00047145 | hypothetical protein LR48_Vigan01g305800 | | | |
| XLOC_024405 | TCONS_00047148 | endonuclease exonuclease phosphatase family protein | | | |
| XLOC_024409 | TCONS_00047152 | nuclease harbi1 | | | |
| XLOC_024413 | TCONS_00047156 | cysteine-rich rlk (receptor-like protein kinase) 8 | cytoskeleton;protein complex;kinase activity;purine ribonucleoside binding;purine ribonucleotide binding;purine ribonucleoside triphosphate binding;phosphorylation;primary metabolic process;cellular macromolecule metabolic process | | |
| XLOC_024416 | TCONS_00047159 | hypothetical protein PHAVU_006G105700g | nucleic acid binding | | |
| XLOC_024418 | TCONS_00047161 | hypothetical protein PHAVU_005G063000g | | | |
| XLOC_024425 | TCONS_00047178 | vacuolar cation proton exchanger 3 | membrane;cation transmembrane transporter activity;calcium ion transport;cation transmembrane transport | | |

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| XLOC_024477 | TCONS_00047261 | ribonuclease chloroplastic mitochondrial | mitochondrion;chloroplast;3'-5'-exoribonuclease activity;exoribonuclease II activity;rRNA processing;tRNA metabolic process;chloroplast relocation;thylakoid membrane organization;RNA phosphodiester bond hydrolysis, exonucleolytic | ec:3.1.15;ec:3.1.13;ec:3.1;ec:3.1.13.1 | |
| XLOC_024497 | TCONS_00047288 | unknown | | | |
| XLOC_024539 | TCONS_00047350 | nbs-lrr protein | ADP binding | | |
| XLOC_024553 | TCONS_00047373 | tmv resistance protein n-like isoform x1 | ADP binding;signal transduction | | |
| XLOC_024557 | TCONS_00047384 | hypothetical protein PHAVU_010G025500g | ATP binding;ADP binding;signal transduction | | |
| XLOC_024765 | TCONS_00047744 | alpha beta fold hydrolase | chloroplast;hydrolase activity;metabolic process | | |
| XLOC_024793 | TCONS_00047785 | serine acetyltransferase 5-like | cytosol;magnesium ion binding;serine O-acetyltransferase activity;terpene synthase activity;cysteine biosynthetic process from serine;protein targeting to membrane;response to wounding;response to fungus;jasmonic acid biosynthetic process;salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;regulation of plant-type hypersensitive response | ec:2.3.1;ec:2.3.1.30-O-acetyltransferase | Sulfur metabolism;Biosynthesis of antibiotics;Cysteine and methionine metabolism |
| XLOC_024795 | TCONS_00047791 | condensin complex subunit 1 | mitotic nuclear division;chromosome condensation | | |
| XLOC_024823 | TCONS_00047830 | hypothetical protein PHAVU_006G010500g, partial | | | |
| XLOC_024833 | TCONS_00047843 | mate efflux family protein | integral component of membrane;serine-type endopeptidase activity;drug transmembrane transporter activity;antiporter activity;proteolysis;drug transmembrane transport | ec:3.4.21 | |
| XLOC_024853 | TCONS_00047897 | hypothetical protein PHAVU_006G035700g | zinc ion binding | | |
| XLOC_024866 | TCONS_00047929 | acyl-activating enzyme 19 | ligase activity;cell-cell signaling;virus induced gene silencing;production of ta-siRNAs involved in RNA interference;production of miRNAs involved in gene silencing by miRNA | | |
| XLOC_024896 | TCONS_00047978 | phosphoprotein phosphatase | ADP binding | | |
| XLOC_024922 | TCONS_00048028 | probable lrr receptor-like serine threonine-protein kinase rfk1 isoform x2 | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| XLOC_024949 | TCONS_00048081 | actin family protein | ATP binding | | |

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| XLOC_024966 | TCONS_00048111 | pleiotropic drug resistance protein 1-like | integral component of membrane;ATP binding;heme-transporting ATPase activity;metabolic process;heme transport | ec:3.6.3.41;ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_025065 | TCONS_00048297 | protein lhy | DNA binding | | |
| XLOC_025316 | TCONS_00048789 | protein far1-related sequence partial | methylmalonate-semialdehyde dehydrogenase (acylating) activity;hydrolase activity, acting on glycosyl bonds;regulation of transcription, DNA-templated;oxidation-reduction process | ec:1.2.1.27-dehydrogenase (CoA-acylating) | Propanoate metabolism;Valine, leucine and isoleucine degradation |
| XLOC_025408 | TCONS_00048984 | hypothetical protein PHAVU_010G019200g, partial | | | |
| XLOC_025463 | TCONS_00049099 | hypothetical protein PHAVU_010G0291001g, partial | ATP binding;ADP binding;signal transduction | | |
| XLOC_025544 | TCONS_00049247 | patatin group a-3 | lipid metabolic process | | |
| XLOC_025545 | TCONS_00049248 | patatin-like protein 2 | hydrolase activity;lipid catabolic process | | |
| XLOC_025618 | TCONS_00049386 | alpha-l-fucosidase 2 | apoplast;1,2-alpha-L-fucosidase activity;metabolic process | ec:3.2.1.51-alpha-fucosidase;ec:3.2.1;ec:3.2.1.63 | Other glycan degradation |
| XLOC_025660 | TCONS_00049465 | nucleotidyltransferase family protein isoform 4 | nucleotidyltransferase activity;metabolic process | | |
| XLOC_025687 | TCONS_00049517 | acyl- oxidase | acyl-CoA dehydrogenase activity;acyl-CoA oxidase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.3.99.3;ec:1.3.3.6-oxidase | Fatty acid degradation;Biosynthesis of unsaturated fatty acids;alpha-Linolenic acid metabolism |
| XLOC_025693 | TCONS_00049524 | 4-coumarate--ligase-like 10 | plasmodesma;chloroplast stroma;apoplast;o-succinylbenzoate-CoA ligase activity;oxalate-CoA ligase activity;positive regulation of seed germination;response to nitrate;seed coat development;nitrate transport;oxalate catabolic process;para-aminobenzoic acid metabolic process;defense response to fungus | ec:6.2.1.8-ligase;ec:6.2.1.26-ligase | Glyoxylate and dicarboxylate metabolismUbiquinone and other terpenoid-quinone biosynthesis |
| XLOC_025694 | TCONS_00049525 | histone-lysine n-methyltransferase eza1-like isoform x1 | PcG protein complex;histone-lysine N-methyltransferase activity;histone lysine methylation | ec:2.1.1;ec:2.1.1.43-N-methyltransferase | Lysine degradation |
| XLOC_025714 | TCONS_00049559 | mate efflux family protein | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| XLOC_025729 | TCONS_00049586 | exocyst complex component sec6-like | exocyst;extracellular region;cell wall;cytosol;cytoskeleton;plasma membrane;plasmodesma;phragmoplast;SNARE | | |

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| | | | binding;exocytosis;pollen germination;pollen tube growth;exocyst localization | | |
| XLOC_025787 | TCONS_00049690 | pentatricopeptide repeat-containing protein at2g17140 | | | |
| XLOC_025825 | TCONS_00049782 | probable polygalacturonase | extracellular region;polygalacturonase activity;carbohydrate metabolic process;cell wall organization | ec:3.2.1.15-pectin depolymerase | Pentose and glucuronate interconversions;Starch and sucrose metabolism |
| XLOC_025855 | TCONS_00049833 | hypothetical protein PHAVU_003G068600g | | | |
| XLOC_025931 | TCONS_00049965 | autophagy-related protein 18b isoform x3 | | | |
| XLOC_025972 | TCONS_00050043 | disease resistance protein (tir-nbs-lrr class) | signal transduction | | |
| XLOC_025978 | TCONS_00050060 | disease resistance protein (tir-nbs-lrr class) | ADP binding;signal transduction | | |
| XLOC_026078 | TCONS_00050258 | mediator of rna polymerase ii transcription subunit 15a-like | transcription cofactor activity;protein kinase activity;ATP binding;regulation of transcription, DNA-templated;protein phosphorylation | | |
| XLOC_026125 | TCONS_00050332 | gag-pol partial | binding;macromolecule metabolic process;primary metabolic process | | |
| XLOC_026127 | TCONS_00050334 | hypothetical protein PHAVU_010G084700g | | | |
| XLOC_026128 | TCONS_00050335 | hypothetical protein PHAVU_010G071400g | | | |
| XLOC_026132 | TCONS_00050339 | hypothetical protein LR48_Vigan845s005400 | | | |
| XLOC_026133 | TCONS_00050340 | hypothetical protein PHAVU_011G131100g | | | |
| XLOC_026135 | TCONS_00050342 | hypothetical protein PHAVU_010G025200g | ATP binding;ADP binding;signal transduction | | |
| XLOC_026136 | TCONS_00050343 | hypothetical protein PHAVU_010G025400g | ATP binding;ADP binding;signal transduction | | |
| XLOC_026137 | TCONS_00050344 | hypothetical protein | | | |
| XLOC_026138 | TCONS_00050345 | disease resistance protein (tir-nbs-lrr class) | ADP binding;signal transduction | | |
| XLOC_026144 | TCONS_00050351 | rna polymerase beta subunit | chloroplast;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |

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| XLOC_026146 | TCONS_00050353 | hypothetical protein GLYMA_01G137800 | | | |
| XLOC_026147 | TCONS_00050354 | rna-directed dna polymerase | RNA-directed DNA polymerase activity;RNA-dependent DNA replication;mRNA processing | ec:2.7.7.49 | |
| XLOC_026149 | TCONS_00050356 | probable l-type lectin-domain containing receptor kinase | protein kinase activity;binding;phosphorylation | | |
| XLOC_026153 | TCONS_00050360 | solute carrier family 40 protein | integral component of membrane;iron ion transmembrane transporter activity;iron ion transmembrane transport | | |
| XLOC_026154 | TCONS_00050361 | hypothetical protein PHAVU_011G131100g | binding;metabolic process | | |
| XLOC_026159 | TCONS_00050366 | nadh-plastoquinone oxidoreductase subunit 3 | plasma membrane;chloroplast thylakoid membrane;integral component of membrane;mitochondrial membrane;proton-transporting ATP synthase complex, catalytic core F(1);respiratory chain;NADH dehydrogenase (ubiquinone) activity;proton-transporting ATP synthase activity, rotational mechanism;proton-transporting ATPase activity, rotational mechanism;quinone binding;ATP synthesis coupled proton transport;photosynthesis, light reaction;oxidation-reduction process | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:1.6.5.3-reductase (H+-translocating) | Purine metabolism;Thiamine metabolismPurine metabolismOxidative phosphorylationOxidative phosphorylation |
| XLOC_026160 | TCONS_00050367 | hypothetical protein LR48_Vigan03g139700 | | | |
| XLOC_026161 | TCONS_00050368 | photosystem i assembly protein ycf3 | chloroplast thylakoid membrane;photosynthesis | | |
| XLOC_026165 | TCONS_00050372 | rna polymerase beta subunit | chloroplast;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_026166 | TCONS_00050373 | hypothetical protein PHAVU_011G120700g | | | |
| XLOC_026173 | TCONS_00050380 | hypothetical protein PHAVU_011G184000g | | | |
| XLOC_026175 | TCONS_00050382 | hypothetical protein PHAVU_010G087400g | organic cyclic compound binding;heterocyclic compound binding | | |
| XLOC_026179 | TCONS_00050386 | disease resistance protein | nucleotide binding | | |
| XLOC_026183 | TCONS_00050390 | hypothetical protein PHAVU_007G108600g | | | |

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| XLOC_026184 | TCONS_00050391 | PREDICTED: uncharacterized protein LOC105953446 | | | |
| XLOC_026185 | TCONS_00050392 | uncharacterized mitochondrial protein g00810-like | nucleic acid binding;zinc ion binding | | |
| XLOC_026189 | TCONS_00050396 | hypothetical protein CICLE_v10023190mg | | | |
| XLOC_026194 | TCONS_00050401 | disease resistance protein (tir-nbs-lrr class) | ADP binding;signal transduction | | |
| XLOC_026197 | TCONS_00050404 | hypothetical protein PhapfoPp088 | chloroplast;catalytic activity;metal ion binding;metabolic process | | |
| XLOC_026199 | TCONS_00050406 | abc transporter-like family-protein | integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_026202 | TCONS_00050409 | protein far-red impaired response 1 | regulation of transcription, DNA-templated | | |
| XLOC_026246 | TCONS_00050499 | hypothetical protein PHAVU_011G007700g | | | |
| XLOC_026270 | TCONS_00050555 | hypothetical protein PHAVU_007G129600g | | | |
| XLOC_026341 | TCONS_00050691 | PREDICTED: uncharacterized protein LOC100527898 | | | |
| XLOC_026345 | TCONS_00050695 | tudor pwwp mbt domain-containing isoform 2 | 3-hydroxyisobutyrate dehydrogenase activity;oxidation-reduction process | ec:1.1.1.31-dehydrogenase | Valine, leucine and isoleucine degradation |
| XLOC_026591 | TCONS_00051207 | hypothetical protein PHAVU_011G075800g | | | |
| XLOC_026612 | TCONS_00051256 | adrenodoxin-like protein mitochondrial | electron carrier activity;metal ion binding;2 iron, 2 sulfur cluster binding | | |
| XLOC_026696 | TCONS_00051403 | serine acetyltransferase 5-like | cytosol;magnesium ion binding;serine O-acetyltransferase activity;terpene synthase activity;cysteine biosynthetic process from serine;protein targeting to membrane;response to wounding;response to fungus;jasmonic acid biosynthetic process;salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;regulation of plant-type hypersensitive response | ec:2.3.1;ec:2.3.1.30-O-acetyltransferase | Sulfur metabolism;Biosynthesis of antibiotics;Cysteine and methionine metabolism |
| XLOC_026772 | TCONS_00051517 | hypothetical protein LR48_Vigan08g111800 | photorespiration | | |

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| XLOC_026788 | TCONS_00051538 | transmembrane e3 ubiquitin-protein ligase 1-like | integral component of membrane;zinc ion binding;ligase activity;metabolic process | | |
| XLOC_026865 | TCONS_00051656 | hypothetical protein PHAVU_011G131100g | | | |
| XLOC_026949 | TCONS_00051774 | scarecrow-like protein 21 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| XLOC_027015 | TCONS_00051893 | wd repeat-containing protein 25 | Cul4-RING E3 ubiquitin ligase complex;photoperiodism, flowering | | |
| XLOC_027091 | TCONS_00052034 | pentatricopeptide repeat-containing protein at1g53330 | embryo development;fruit development;root development;shoot system development | | |
| XLOC_027135 | TCONS_00052113 | glucan endo- -beta-glucosidase | glucan exo-1,3-beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1.58-1,3-beta-glucosidase; ec:3.2.1.21-gentiobiase; ec:3.2.1 | Starch and sucrose metabolismCyanoamino acid metabolism;Phenylpropanoid biosynthesis;Starch and sucrose metabolism |
| XLOC_027242 | TCONS_00052297 | hypothetical protein PHAVU_011G194800g | | | |
| XLOC_027588 | TCONS_00052954 | specific tissue protein | | | |
| XLOC_027643 | TCONS_00053076 | suppressor of rps4-rld 1 | intracellular part;regulation of transcription, DNA-templated;response to stress;negative regulation of gene expression;single-organism cellular process | | |
| XLOC_027767 | TCONS_00053359 | zinc c3hc4 type (ring finger) protein | anaphase-promoting complex;protein kinase activity;ubiquitin-protein transferase activity;ATP binding;zinc ion binding;protein phosphorylation;protein ubiquitination | | |
| XLOC_027885 | TCONS_00053593 | hypothetical protein glysoja_006702 | | | |
| XLOC_027916 | TCONS_00053639 | lysine-specific demethylase jmj16 | nucleus;transcription factor activity, sequence-specific DNA binding;protein glycosylation;gravitropism;vegetative to reproductive phase transition of meristem;glucuronoxylan metabolic process;protein desumoylation;post-translational protein modification;xylan biosynthetic process;positive regulation of transcription, DNA-templated;hydrogen peroxide biosynthetic process | | |
| XLOC_027985 | TCONS_00053754 | hypothetical protein PHAVU_010G070700g | | | |
| XLOC_028007 | TCONS_00053786 | probable inactive serine threonine-protein kinase lvsg | Cul4-RING E3 ubiquitin ligase complex;protein kinase activity;ATP binding;protein phosphorylation;protein N-linked glycosylation;protein targeting to vacuole;defense | | |

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| | | | response to bacterium, incompatible interaction | | |
| XLOC_028058 | TCONS_00053862 | protein lurp-one-related 6-like | | | |
| XLOC_028126 | TCONS_00053979 | protein spa1-related 3 | protein kinase activity;ATP binding;ligase activity;2-alkenal reductase [NAD(P)] activity;protein phosphorylation;oxidation-reduction process | ec:1.3.1.74 | |
| XLOC_028139 | TCONS_00054008 | hypothetical protein LR48_Vigan07g230300 | | | |
| XLOC_028191 | TCONS_00054108 | lrr receptor-like | catalytic activity;metabolic process | | |
| XLOC_028193 | TCONS_00054111 | lrr receptor-like | protein kinase activity;ATP binding;protein phosphorylation;regulation of cellular process | | |
| XLOC_028205 | TCONS_00054130 | chaperone protein dnaj 49 | | | |
| XLOC_028213 | TCONS_00054151 | aldehyde dehydrogenase 22a1 | cytosol;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;nitronate monooxygenase activity;para-aminobenzoic acid metabolic process;oxidation-reduction process | ec:1.13.12.16-monooxygenase;ec:1.13.12 | Nitrogen metabolism |
| XLOC_028322 | TCONS_00054362 | serine carboxypeptidase-like protein | serine-type carboxypeptidase activity;proteolysis | ec:3.4.16;ec:3.4.21 | |
| XLOC_028393 | TCONS_00054500 | e3 ubiquitin-protein ligase orthrus 2 | zinc ion binding;histone binding | | |
| XLOC_028396 | TCONS_00054503 | disease resistance rpp13-like protein 1 | | | |
| XLOC_028397 | TCONS_00054504 | lrr and nb-arc domain disease resistance protein | | | |
| XLOC_028405 | TCONS_00054512 | abc transporter g family member 15-like isoform x1 | | | |
| XLOC_028410 | TCONS_00054517 | maturase k | chloroplast;RNA binding;mRNA processing;tRNA processing;RNA splicing | | |
| XLOC_028412 | TCONS_00054519 | hypothetical protein B456_003G094200 | | | |
| XLOC_028414 | TCONS_00054521 | maturase k | chloroplast;RNA binding;mRNA processing;tRNA processing;RNA splicing | | |
| XLOC_028415 | TCONS_00054522 | hypothetical protein PHAVU_006G0250000g, partial | DNA binding | | |
| XLOC_028417 | TCONS_00054524 | probable serine threonine- | protein kinase activity;ATP binding;protein phosphorylation | | |

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| | | protein kinase gcn2 isoform x1 | | | |
| XLOC_028418 | TCONS_00054525 | hypothetical protein PHAVU_005G070100g | | | |
| XLOC_028419 | TCONS_00054526 | hypothetical protein VIGAN_06199800, partial | | | |
| XLOC_028421 | TCONS_00054528 | hypothetical protein LR48_Vigan238s000200 | | | |
| XLOC_028427 | TCONS_00054534 | hypothetical protein VIGAN_06177900 | | | |
| XLOC_028430 | TCONS_00054537 | hypothetical protein PHAVU_010G034700g | | | |
| XLOC_028431 | TCONS_00054538 | hypothetical protein glysoja_008166 | | | |
| XLOC_028435 | TCONS_00054542 | metal transporter nramp6 | membrane;transporter activity;transport | | |
| XLOC_028436 | TCONS_00054543 | disease resistance-dirigent domain protein | | | |
| XLOC_028441 | TCONS_00054548 | hypothetical chloroplast rf68 | chloroplast | | |
| XLOC_028445 | TCONS_00054552 | PREDICTED: uncharacterized protein LOC106302390 | | | |
| XLOC_028449 | TCONS_00054556 | ctp:phosphorylcholine cytidylyltransferase | choline-phosphate cytidylyltransferase activity;phosphatidylcholine biosynthetic process | ec:2.7.7.15-cytidylyltransferase | Phosphonate and phosphinate metabolism;Glycerophospholipid metabolism |
| XLOC_028450 | TCONS_00054557 | hypothetical protein GLYMA_09G051300 | | | |
| XLOC_028452 | TCONS_00054559 | hypothetical protein PHAVU_002G055500g | | | |
| XLOC_028453 | TCONS_00054560 | hypothetical protein PHAVU_011G121500g | | | |
| XLOC_028454 | TCONS_00054561 | hypothetical protein PHAVU_011G1212001g | | | |
| XLOC_028457 | TCONS_00054564 | cyclic nucleotide-gated ion channel 4-like | integral component of membrane;ion channel activity;ion transmembrane transport | | |
| XLOC_028459 | TCONS_00054566 | photosystem i p700 chlorophyll a apoprotein a2 | photosystem I;chloroplast thylakoid membrane;integral component of membrane;magnesium ion binding;electron carrier activity;chlorophyll binding;oxidoreductase activity;4 iron, 4 sulfur | | |

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| | | | cluster binding;photosynthesis;protein-chromophore linkage;oxidation-reduction process | | |
| XLOC_028461 | TCONS_00054568 | hypothetical protein LR48_Vigan09g073700 | | | |
| XLOC_028466 | TCONS_00054573 | rna-binding protein 28 | nucleus;nucleotide binding;RNA binding | | |
| XLOC_028468 | TCONS_00054575 | pap-specific phosphatase hal2-like | inositol-1,4-bisphosphate 1-phosphatase activity;3'(2'),5'-bisphosphate nucleotidase activity;phosphotransferase activity, alcohol group as acceptor;protein dephosphorylation;sulfur compound metabolic process;phosphatidylinositol phosphorylation | ec:3.1.3.57-1-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1;ec:3.1.3.31;ec:3.1.3.7-nucleotidase;ec:3.1.3 | Phosphatidylinositol signaling system;Inositol phosphate metabolismAminobenzoate degradationSulfur metabolism |
| XLOC_028471 | TCONS_00054578 | cysteine-rich rlk (receptor-like protein kinase) 8 | nucleic acid binding;cellular metabolic process | | |
| XLOC_028472 | TCONS_00054579 | ubiquitin-conjugating enzyme e2 26 | ligase activity;metabolic process | | |
| XLOC_028473 | TCONS_00054580 | hypothetical protein PHAVU_011G163800g | | | |
| XLOC_028474 | TCONS_00054581 | glucan endo- -beta-glucosidase 14 | nucleus;anchored component of plasma membrane;hydrolase activity, hydrolyzing O-glycosyl compounds;carbohydrate metabolic process;protein targeting to membrane;salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;regulation of plant-type hypersensitive response | | |
| XLOC_028477 | TCONS_00054584 | hypothetical protein PHAVU_008G173400g | | | |
| XLOC_028480 | TCONS_00054587 | photosystem i p700 chlorophyll a apoprotein a2 | photosystem I;chloroplast thylakoid membrane;integral component of membrane;magnesium ion binding;electron carrier activity;chlorophyll binding;oxidoreductase activity;4 iron, 4 sulfur cluster binding;photosynthesis;protein-chromophore linkage;oxidation-reduction process | | |
| XLOC_028484 | TCONS_00054591 | photosystem ii phosphoprotein | photosystem II;chloroplast thylakoid membrane;integral component of membrane;phosphate ion binding;photosynthesis;protein stabilization | | |
| XLOC_028487 | TCONS_00054594 | disease resistance protein | ADP binding | | |
| XLOC_028491 | TCONS_00054598 | PREDICTED: uncharacterized protein | | | |

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| | | LOC102668362, partial | | | |
| XLOC_028492 | TCONS_00054599 | nbs-lrr-like protein cd8 | ADP binding | | |
| XLOC_028494 | TCONS_00054601 | hypothetical protein PHAVU_011G201800g | | | |
| XLOC_028495 | TCONS_00054602 | disease resistance rpp13-like protein 1 | | | |
| XLOC_028496 | TCONS_00054603 | nadh-plastoquinone oxidoreductase subunit partial | chloroplast thylakoid membrane;integral component of membrane;NADH dehydrogenase (ubiquinone) activity;quinone binding;transport;photosynthesis, light reaction;ATP synthesis coupled electron transport | ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:1.6.5.3-reductase (H+-translocating) | Oxidative phosphorylationOxidative phosphorylation |
| XLOC_028497 | TCONS_00054604 | dis3-exonuclease-like protein | exonuclease activity;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| XLOC_028498 | TCONS_00054605 | hypothetical chloroplast rf1 | chloroplast inner membrane;integral component of membrane;protein transport | | |
| XLOC_028510 | TCONS_00054623 | serine threonine-protein kinase sapk7-like isoform x2 | DNA binding;protein kinase activity;ATP binding;protein dimerization activity;protein phosphorylation | | |
| XLOC_028545 | TCONS_00054686 | nadh dehydrogenase subunit 1 | plasma membrane;chloroplast thylakoid membrane;integral component of membrane;oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor;quinone binding;photosynthesis, light reaction;oxidation-reduction process | | |
| XLOC_028551 | TCONS_00054693 | atp synthase alpha partial | mitochondrial inner membrane;chloroplast thylakoid membrane;proton-transporting ATP synthase complex, catalytic core F(1);ATP binding;proton-transporting ATP synthase activity, rotational mechanism;proton-transporting ATPase activity, rotational mechanism;ATP synthesis coupled proton transport;ATP hydrolysis coupled proton transport | ec:3.6.1.15-phosphatase;ec:3.6.1.3-adenylpyrophosphatase; ec:3.6.1 | Purine metabolism;Thiamine metabolismPurine metabolism |
| XLOC_028552 | TCONS_00054694 | hypothetical protein GLYMA_07G099300 | | | |
| XLOC_028558 | TCONS_00054702 | protein rst1 isoform x3 | cellular protein modification process;response to abiotic stimulus;embryo development ending in seed dormancy;meristem structural organization;seed maturation;cellular macromolecule biosynthetic process;single-organism biosynthetic process;single-organism carbohydrate metabolic process;single- | | |

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| | | | organism cellular process;xylan metabolic process;leaf development;regulation of developmental process;regulation of cellular process;cellular component organization or biogenesis | | |
| XLOC_028561 | TCONS_00054706 | potassium transporter 12 | | | |
| XLOC_028572 | TCONS_00054719 | glycerophosphodiester phosphodiesterase gdpdl4-like isoform x2 | | | |
| XLOC_028573 | TCONS_00054720 | nbs-lrr type disease resistance protein cnl-b19 | ADP binding | | |
| XLOC_028574 | TCONS_00054722 | cellular apoptosis susceptibility protein importin-alpha re- isoform 1 | nuclear pore;cytosol;plasmodesma;chloroplast;membrane;Ran GTPase binding;protein transporter activity;protein import into nucleus, docking;gluconeogenesis;cytoskeleton organization;response to wounding;response to fungus;jasmonic acid biosynthetic process;response to jasmonic acid;proteasomal protein catabolic process | | |
| XLOC_028588 | TCONS_00054740 | sister chromatid cohesion pds5-like protein | | | |
| XLOC_028600 | TCONS_00054753 | protein rst1 isoform x1 | protein glycosylation;cuticle hydrocarbon biosynthetic process;sister chromatid cohesion;photomorphogenesis;seed germination;embryonic pattern specification;regulation of flower development;primary shoot apical meristem specification;seed dormancy process;sugar mediated signaling pathway;vegetative to reproductive phase transition of meristem;glucuronoxylan metabolic process;regulation of cell cycle process;protein ubiquitination;lipid storage;xylan biosynthetic process;regulation of cell differentiation;cotyledon development;response to freezing;cell division | | |
| XLOC_028601 | TCONS_00054755 | lysosomal alpha-mannosidase | vacuolar membrane;plant-type cell wall;apoplast;alpha-mannosidase activity;zinc ion binding;carbohydrate binding;mannose metabolic process;microtubule nucleation;cysteine biosynthetic process | ec:3.2.1.24-alpha-D-mannosidase;ec:3.2.1 | Other glycan degradation |
| XLOC_028606 | TCONS_00054761 | cytochrome b6 | chloroplast thylakoid membrane;integral component of membrane;iron ion | | |

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| | | | binding;oxidoreductase activity;heme binding;electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II activity;photosynthesis;respiratory electron transport chain | | |
| XLOC_028615 | TCONS_00054771 | plant invertase pectin methylesterase inhibitor | enzyme inhibitor activity;pectinesterase activity;metabolic process;negative regulation of catalytic activity | ec:3.1.1.1-ali-esterase;ec:3.1.1.11-pectin demethoxylase | Drug metabolism - other enzymesPentose and glucuronate interconversions;Starch and sucrose metabolism |
| XLOC_028625 | TCONS_00054787 | casp poptrdraft-like protein | plasma membrane;integral component of membrane | | |
| XLOC_028639 | TCONS_00054806 | cytochrome b6 f complex subunit iv | chloroplast thylakoid membrane;integral component of membrane;oxidoreductase activity;electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity;electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II activity;photosynthetic electron transport chain | | |

| SeqName | Sequence Description | GO Terms | Enzymes | Kegg Maps |
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| **DEG** | | | | |
| Phvul.001G005800 | hypothetical protein PHAVU_001G005800g | | | |
| Phvul.001G016600 | pathogenesis-related protein 5-like | | | |
| Phvul.001G017200 | type i inositol -trisphosphate 5-phosphatase 11-like | phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity;nuclease activity;phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase activity;phosphatidylinositol-3,5-bisphosphate 5-phosphatase activity;protein dephosphorylation;phosphatidylinositol-3-phosphate biosynthetic process;phosphatidylinositol dephosphorylation | ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1;ec:3.1.3.36-5-phosphatase;ec:3.1.3 | Aminobenzoate degradationInositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.001G018300 | probable transcription factor kan4 | DNA binding;oxidoreductase activity;single-organism process | | |
| Phvul.001G020300 | patatin-like phospholipase | hydrolase activity;lipid catabolic process | | |
| Phvul.001G024400 | serine threonine plant-type | kinase activity;phosphorylation | | |
| Phvul.001G025300 | hypothetical protein PHAVU_001G025300g | | | |
| Phvul.001G029100 | hypothetical protein PHAVU_001G029100g | | | |
| Phvul.001G029200 | phytosulfokines 3-like | extracellular region;growth factor activity;cell proliferation | | |
| Phvul.001G029500 | basic leucine zipper 1-like | intracellular;transcription factor activity, sequence-specific DNA binding;MAP kinase activity;sequence-specific DNA binding;MAPK cascade;regulation of transcription, DNA-templated | ec:2.7.11.24-protein kinase;ec:2.7.11 | mTOR signaling pathway |
| Phvul.001G037100 | cytochrome p450 711a1-like | iron ion binding;heme binding;aromatase activity;auxin polar transport;regulation of meristem structural organization;secondary shoot formation;oxidation-reduction process | ec:1.14.14;ec:1.14.14.1-monooxygenase | Linoleic acid metabolism;Arachidonic acid metabolism;Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Caffeine metabolism;Aminobenzoate degradation;Tryptophan metabolism;Fatty acid degradation;Retinol metabolism;Steroid hormone biosynthesis |
| Phvul.001G038500 | hypothetical protein PHAVU_001G038500g | | | |
| Phvul.001G039600 | solute carrier family 25 member 44 | integral component of membrane;transmembrane transport | | |
| Phvul.001G039700 | kda class ii heat shock protein | cytoplasm | | |
| Phvul.001G039800 | kda class ii heat shock protein | cytoplasm | | |
| Phvul.001G040600 | l-type lectin-domain containing receptor kinase -like | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;carbohydrate binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.001G040800 | l-type lectin-domain containing | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |

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| | receptor kinase -like | kinase activity;ATP binding;carbohydrate binding;peptidyl-tyrosine phosphorylation | | |
| Phvul.001G042200 | wrky family transcription factor | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.001G043500 | protein glutamine dumper 3-like | | | |
| Phvul.001G050400 | hypothetical protein PHAVU_001G050400g | | | |
| Phvul.001G051000 | hypothetical protein PHAVU_001G051000g | | | |
| Phvul.001G052100 | cytochrome p450 family 71 protein | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.001G054500 | pleiotropic drug resistance protein 1-like | integral component of membrane;ATP binding;organic phosphonate transmembrane-transporting ATPase activity;polyamine-transporting ATPase activity;metabolic process;organic phosphonate transport;organophosphate ester transport;polyamine transmembrane transport | ec:3.6.3.31;ec:3.6.3.28;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G055000 | gibberellin 3-beta-dioxygenase 1-like | iron ion binding;gibberellin 3-beta-dioxygenase activity;oxidation-reduction process | ec:1.14.11.15-3beta-dioxygenase;ec:1.14.11 | Diterpenoid biosynthesis |
| Phvul.001G059600 | hypothetical protein PHAVU_001G059600g | | | |
| Phvul.001G064000 | alcohol dehydrogenase 1 | cytoplasm;alcohol dehydrogenase (NAD) activity;zinc ion binding;S-(hydroxymethyl)glutathione dehydrogenase activity;oxidation-reduction process | ec:1.1.1.284-dehydrogenase;ec:1.1.1.1-dehydrogenase | Methane metabolismalpha-Linolenic acid metabolism;Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Naphthalene degradation;Chloroalkane and chloroalkene degradation;Biosynthesis of antibiotics;Glycolysis / Gluconeogenesis;Fatty acid degradation;Glycine, serine and threonine metabolism;Tyrosine metabolism;Retinol metabolism |
| Phvul.001G067400 | ef hand calcium-binding family protein | calcium ion binding | | |
| Phvul.001G071200 | probable receptor-like protein kinase at1g11050 | transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.001G074200 | ultraviolet-b receptor uvr8 | ligase activity;metabolic process | | |
| Phvul.001G075400 | probable protein phosphatase 2c 51 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | ec:3.1.3.16-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | T cell receptor signaling pathwayAminobenzoate degradation |
| Phvul.001G076000 | peroxidase 5-like | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |

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| Phvul.001G076700 | beta-glucosidase 12-like | beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.001G077000 | amino acid permease 6 | plasma membrane;integral component of membrane;acidic amino acid transmembrane transporter activity;neutral amino acid transmembrane transporter activity;neutral amino acid transport;aspartate transport;tryptophan transport | | |
| Phvul.001G081000 | aluminum-activated malate transporter 10-like | malate transport | | |
| Phvul.001G085900 | transmembrane protein 45b | integral component of membrane | | |
| Phvul.001G088200 | probable wrky transcription factor 75 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.001G091600 | 2-isopropylmalate synthase | 2-isopropylmalate synthase activity;leucine biosynthetic process | ec:2.3.3.13-synthase | Valine, leucine and isoleucine biosynthesis;Pyruvate metabolism |
| Phvul.001G103600 | protein transparent testa 12 | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.001G108300 | protein transparent testa 12 | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.001G112400 | spermidine hydroxycinnamoyltransferase-like | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.001G112500 | spermidine hydroxycinnamoyltransferase-like | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.001G124700 | s-adenosylmethionine-dependent methyltransferase | mitochondrion;methyltransferase activity;methylation | | |
| Phvul.001G124800 | s-adenosylmethionine-dependent methyltransferase | mitochondrion;methyltransferase activity;methylation | | |
| Phvul.001G127700 | gibberellin induced protein | | | |
| Phvul.001G128500 | glucan endo- -beta- basic isoform-like | vacuole;glucan endo-1,3-beta-D-glucosidase activity;carbohydrate metabolic process;defense response | ec:3.2.1;ec:3.2.1.39-endo-1,3-beta-D-glucosidase;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolismStarch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.001G131000 | heat stress transcription factor b-3 | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated;toxin catabolic process;response to heat | | |
| Phvul.001G135200 | probable galactinol--sucrose galactosyltransferase 2 | plasmodesma;galactinol-raffinose galactosyltransferase activity;raffinose alpha-galactosidase activity;raffinose catabolic process | ec:3.2.1;ec:2.4.1;ec:2.4.1.67-galactosyltransferase;ec:3.2.1.22-melibiase | Galactose metabolismGlycosphingolipid biosynthesis - globo series;Sphingolipid metabolism;Glycerolipid metabolism;Galactose metabolism |
| Phvul.001G139400 | -dihydroxypterocarpan 6a-monooxygenase | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |

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| Phvul.001G140000 | polygalacturonase inhibiting protein | transferase activity;metabolic process | | |
| Phvul.001G142000 | seed maturation protein lea 4 | embryo development | | |
| Phvul.001G143100 | seed maturation protein lea 4 | embryo development | | |
| Phvul.001G143500 | homeobox-leucine zipper protein hox11-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.001G145600 | disease resistance response protein | | | |
| Phvul.001G145700 | disease resistance response protein 206 | | | |
| Phvul.001G148000 | hypothetical protein PHAVU_001G148000g | | | |
| Phvul.001G148100 | hypothetical protein PHAVU_001G148100g | | | |
| Phvul.001G151900 | copalyldiphosphate synthase | magnesium ion binding;ent-copalyl diphosphate synthase activity;terpene synthase activity;metabolic process | ec:5.5.1.13-diphosphate synthase | Diterpenoid biosynthesis |
| Phvul.001G152100 | copalyldiphosphate synthase | chloroplast;magnesium ion binding;ent-copalyl diphosphate synthase activity;terpene synthase activity;gibberellin biosynthetic process | ec:5.5.1.13-diphosphate synthase | Diterpenoid biosynthesis |
| Phvul.001G154200 | sulfate transporter -like | chloroplast;integral component of membrane;secondary active sulfate transmembrane transporter activity;sulfate transmembrane transport | | |
| Phvul.001G154500 | bi1-like protein | integral component of membrane;protein folding;response to heat;response to high light intensity;response to hydrogen peroxide | | |
| Phvul.001G156500 | auxin-induced protein 22e-like | nucleus;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |
| Phvul.001G156900 | phospholipase a1-chloroplastic-like | hydrolase activity;lipid metabolic process | | |
| Phvul.001G158100 | cytochrome p450 94a1-like | endoplasmic reticulum membrane;integral component of membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.001G160100 | ap2 domain class transcription factor | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;ethylene-activated signaling pathway | | |
| Phvul.001G160200 | ethylene-responsive transcription factor 1b | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.001G161000 | myb-related protein myb4-like | DNA binding;response to acid chemical;response to stress;hormone-mediated signaling pathway;response to oxygen-containing compound | | |
| Phvul.001G162800 | long-chain-alcohol oxidase fao2-like | integral component of membrane;long-chain-alcohol oxidase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.1.3.20 | |
| Phvul.001G163400 | peptide transporter | membrane;transporter activity;transport | | |
| Phvul.001G165200 | photosystem ii reaction center psb28 chloroplastic | photosystem II oxygen evolving complex;photosynthesis | | |
| Phvul.001G165700 | drug resistance transporter-like abc domain protein | integral component of membrane;ATP binding;ATPase activity;transport;metabolic process | ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G166000 | drug resistance transporter-like abc domain protein | integral component of membrane;ATP binding;organic phosphonate transmembrane-transporting ATPase activity;metabolic process;organic phosphonate transport;organophosphate ester transport | ec:3.6.3.28;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec | Purine metabolismPurine metabolism;Thiamine metabolism |

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| | | | :3.6.1.15-phosphatase | |
| Phvul.001G166700 | two-component response regulator arr22-like | intracellular;kinase activity;phosphorelay signal transduction system;phosphorylation | | |
| Phvul.001G169300 | cation h(+) antiporter 20 | endoplasmic reticulum;integral component of membrane;solute:proton antiporter activity;protein targeting to vacuole;regulation of pH;response to stress;cellular potassium ion homeostasis;water homeostasis;hydrogen ion transmembrane transport | | |
| Phvul.001G173300 | glutathione s-transferase l3 | cytoplasm;glutathione transferase activity;metabolic process | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolism |
| Phvul.001G174200 | transcription factor asg4 | DNA binding | | |
| Phvul.001G177100 | hypothetical protein PHAVU_001G177100g | | | |
| Phvul.001G180500 | transporter mch1 | integral component of membrane;transmembrane transport | | |
| Phvul.001G182300 | udp-glucosyltransferase family protein | transferase activity, transferring hexosyl groups;metabolic process | | |
| Phvul.001G183300 | leucoanthocyanidin dioxygenase-like protein | monooxygenase activity;iron ion binding;methyltransferase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;heme binding;methylation;oxidation-reduction process | ec:1.14.11 | |
| Phvul.001G184600 | embryonic protein dc-8-like | | | |
| Phvul.001G185700 | plant t22k18-16 | response to oxidative stress | | |
| Phvul.001G187800 | drug resistance transporter-like abc domain protein | integral component of membrane;ATP binding;organic phosphonate transmembrane-transporting ATPase activity;metabolic process;organic phosphonate transport;organophosphate ester transport | ec:3.6.3.28;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G194800 | protein yls9-like | | | |
| Phvul.001G201300 | peroxidase 3-like | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.001G201500 | probable atp-dependent rna helicase ddx56 | | | |
| Phvul.001G205900 | translocator protein homolog | Golgi stack;integral component of membrane;heme binding;porphyrin-containing compound metabolic process | | |
| Phvul.001G206000 | xyloglucan 6-xylosyltransferase 2 | Golgi apparatus;integral component of membrane;GTP binding;xyloglucan 6-xylosyltransferase activity;metabolic process | ec:2.4.2.39 | |
| Phvul.001G206700 | abc transporter c family member 4 | integral component of membrane;ATP binding;2-alkenal reductase [NAD(P)] activity;ATPase activity, coupled to transmembrane movement of substances;transmembrane transport;oxidation-reduction process | ec:1.3.1.74;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G207500 | caffeoylshikimate esterase-like | plasma membrane;acylglycerol lipase activity;lipid metabolic process | ec:3.1.1.23-lipase;ec:3.1.1.1-ali-esterase;ec:3.1.1 | Glycerolipid metabolismDrug metabolism - other enzymes |
| Phvul.001G209200 | pectinesterase pectinesterase inhibitor | cell wall;enzyme inhibitor activity;pectinesterase activity;aspartyl esterase activity;cell wall modification;negative regulation of catalytic activity;pectin catabolic process | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug |

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| | | | | metabolism - other enzymes |
| Phvul.001G211200 | mitochondrial carrier family protein | | | |
| Phvul.001G211300 | hypothetical protein PHAVU_001G211300g | protein folding;response to heat;response to high light intensity;terpenoid biosynthetic process;response to hydrogen peroxide;positive regulation of transcription, DNA-templated | | |
| Phvul.001G211900 | alpha beta-hydrolases superfamily protein | proteasome complex;hydrolase activity;lipid metabolic process;cellular macromolecule metabolic process | | |
| Phvul.001G215700 | boron transporter 1-like | integral component of membrane;inorganic anion exchanger activity;anion transmembrane transport | | |
| Phvul.001G215900 | polygalacturonase glycoside hydrolase family protein | extracellular region;polygalacturonase activity;galacturan 1,4-alpha-galacturonidase activity;carbohydrate metabolic process;cell wall organization | ec:3.2.1.67-1,4-alpha-galacturonidase;ec:3.2.1.15-pectin depolymerase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsStarch and sucrose metabolism;Pentose and glucuronate interconversions |
| Phvul.001G219300 | suppressor of disruption of tfiis | hydrolase activity;metabolic process;response to nitrate;nitrate transport | | |
| Phvul.001G220800 | hypothetical protein PHAVU_001G220800g | | | |
| Phvul.001G223700 | galactinol synthase | inositol 3-alpha-galactosyltransferase activity;galactose metabolic process | ec:2.4.1.123-3-alpha-galactosyltransferase;ec:2.4.1 | Galactose metabolism |
| Phvul.001G226300 | heat shock protein binding | | | |
| Phvul.001G231900 | little protein 1 | | | |
| Phvul.001G235000 | transcriptional regulator superman protein | metal ion binding | | |
| Phvul.001G246500 | cation h(+) antiporter 15-like | integral component of membrane;monovalent cation:proton antiporter activity;potassium ion transport;sodium ion transport;hydrogen ion transmembrane transport | | |
| Phvul.001G247300 | cation h(+) antiporter 15-like | integral component of membrane;monovalent cation:proton antiporter activity;potassium ion transport;sodium ion transport;hydrogen ion transmembrane transport | | |
| Phvul.001G249600 | e3 ubiquitin-protein ligase rha2a | zinc ion binding | | |
| Phvul.001G250900 | duf581 family protein | | | |
| Phvul.001G255200 | probable e3 ubiquitin-protein ligase xerico | catalytic activity;zinc ion binding | | |
| Phvul.001G258900 | hypothetical protein PHAVU_001G258900g | peroxisome | | |
| Phvul.001G263200 | hypothetical protein LR48_Vigan102s009700 | integral component of membrane | | |
| Phvul.001G263900 | hypothetical protein PHAVU_001G263900g | | | |
| Phvul.001G264400 | cysteine proteinase inhibitor b | cysteine-type endopeptidase inhibitor activity;negative regulation of endopeptidase activity | | |
| Phvul.001G265800 | pentatricopeptide repeat-containing protein mitochondrial | membrane;microtubule-severing ATPase activity;metabolic process | ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec | Purine metabolismPurine metabolism;Thiamine metabolism |

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| | | | :3.6.4.3;ec:3.6.1.15-phosphatase | |
| Phvul.002G002000 | protein tify 10a-like | | | |
| Phvul.002G004100 | expansin-like b1 | extracellular region | | |
| Phvul.002G007500 | basic helix loop helix dna-binding family protein | protein dimerization activity | | |
| Phvul.002G008300 | epidermal patterning factor-like protein 2 | | | |
| Phvul.002G009700 | vq motif protein | | | |
| Phvul.002G014700 | isoflavone 2 -hydroxylase | membrane;iron ion binding;heme binding;aromatase activity;oxidation-reduction process | ec:1.14.14;ec:1.14.14.1-monooxygenase | Linoleic acid metabolism;Arachidonic acid metabolism;Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Caffeine metabolism;Aminobenzoate degradation;Tryptophan metabolism;Fatty acid degradation;Retinol metabolism;Steroid hormone biosynthesis |
| Phvul.002G017500 | caffeoyl- o-methyltransferase | caffeoyl-CoA O-methyltransferase activity;metal ion binding;lignin biosynthetic process;methylation | ec:2.1.1;ec:2.1.1.104-O-methyltransferase | Phenylalanine metabolism;Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.002G018100 | map3k-like kinase | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.002G019100 | heat shock factor protein hsf24-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;response to acid chemical;regulation of transcription, DNA-templated;signal transduction;response to heat;response to organic substance;response to endoplasmic reticulum stress;cellular metabolic process;single-organism metabolic process;response to oxygen-containing compound | | |
| Phvul.002G021800 | reticulon-like protein b13 | endoplasmic reticulum membrane;integral component of membrane | | |
| Phvul.002G027900 | vicilin-like antimicrobial peptides 2-2 | nutrient reservoir activity | | |
| Phvul.002G029900 | plant mud21-2 protein | | | |
| Phvul.002G031100 | late embryogenesis abundant domain protein lea domain | | | |
| Phvul.002G033100 | isoflavone reductase | 2'-hydroxyisoflavone reductase activity;oxidation-reduction process | ec:1.3.1.45-reductase | Isoflavonoid biosynthesis |
| Phvul.002G035800 | nuclear transport factor 2 family protein | chloroplast thylakoid membrane;peptidyl-prolyl cis-trans isomerase activity;protein peptidyl-prolyl isomerization;protein folding;transport;chlorophyll catabolic process | ec:5.2.1.8 | |
| Phvul.002G035900 | ethylene-responsive transcription factor erf021-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.002G043000 | 12-oxophytodienoate reductase 2 | FMN binding;12-oxophytodienoate reductase activity;oxidation-reduction process | ec:1.3.1.42-reductase | alpha-Linolenic acid metabolism |
| Phvul.002G046800 | sugar transport protein 13 | plasma membrane;plasmodesma;integral component of membrane;high-affinity hydrogen:glucose symporter | ec:1.3.1.74 | |

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| | | activity;2-alkenal reductase [NAD(P)] activity;glucose transport;hexose transmembrane transport;amino acid import;oxidation-reduction process | | |
| Phvul.002G048100 | tryptophan synthase beta chain 1-like | tryptophan synthase activity;2-alkenal reductase [NAD(P)] activity;tryptophan biosynthetic process;oxidation-reduction process | ec:1.3.1.74;ec:4.2.1.20-synthase | Biosynthesis of antibiotics;Phenylalanine, tyrosine and tryptophan biosynthesis;Glycine, serine and threonine metabolism |
| Phvul.002G049000 | gibberellin 2-beta-dioxygenase 8-like | gibberellin 3-beta-dioxygenase activity;metal ion binding;oxidation-reduction process | ec:1.14.11.15-3beta-dioxygenase;ec:1.14.11 | Diterpenoid biosynthesis |
| Phvul.002G050700 | probable zinc metallopeptidase chloroplastic isoform x1 | aminopeptidase activity;protein folding;proteolysis | ec:3.4.11 | |
| Phvul.002G055600 | g-type lectin s-receptor-like serine threonine-protein kinase rlk1-like | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;carbohydrate binding;peptidyl-tyrosine phosphorylation;recognition of pollen | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.002G061200 | acid beta-fructofuranosidase | vacuole;sucrose alpha-glucosidase activity;sucrose metabolic process | ec:3.2.1;ec:3.2.1.48-alpha-glucosidase;ec:3.2.1.26-invertase | Starch and sucrose metabolismStarch and sucrose metabolism;Galactose metabolism |
| Phvul.002G061900 | peptide nitrate transporter | plasma membrane;integral component of membrane;nitrate transmembrane transporter activity;oligopeptide transport;response to water deprivation;response to nitrate;nitrate transport;sterol biosynthetic process;glucosinolate biosynthetic process;plant-type cell wall cellulose metabolic process;cell wall pectin metabolic process | | |
| Phvul.002G063500 | polygalacturonase at1g48100 | extracellular region;polygalacturonase activity;galacturan 1,4-alpha-galacturonidase activity;carbohydrate metabolic process;cell wall organization | ec:3.2.1.67-1,4-alpha-galacturonidase;ec:3.2.1.15-pectin depolymerase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsStarch and sucrose metabolism;Pentose and glucuronate interconversions |
| Phvul.002G070300 | dna (cytosine-5)-methyltransferase drm2-like isoform x1 | DNA binding;transferase activity;DNA methylation | | |
| Phvul.002G072000 | u-box domain-containing protein 19 | ubiquitin-protein transferase activity;zinc ion binding;ligase activity;protein ubiquitination | | |
| Phvul.002G075200 | udp-glycosyltransferase 74b1-like | indole-3-acetate beta-glucosyltransferase activity;thiohydroximate beta-D-glucosyltransferase activity;tryptophan catabolic process;indoleacetic acid biosynthetic process;glucosinolate biosynthetic process;defense response to bacterium;root hair elongation;defense response by callose deposition in cell wall | ec:2.4.1.121;ec:2.4.1;ec:2.4.1.195-S-beta-glucosyltransferase | Tryptophan metabolism;Glucosinolate biosynthesis |
| Phvul.002G076700 | metalloendoproteinase 1-like | extracellular matrix;metalloendopeptidase activity;zinc ion binding;proteolysis | ec:3.4.24 | |
| Phvul.002G081400 | clavata3 esr -related protein 9-like | extracellular region | | |
| Phvul.002G083800 | myb transcription factor | DNA binding | | |
| Phvul.002G085000 | phd finger protein male sterility 1 | zinc ion binding;pollen germination;pollen wall assembly;positive regulation of transcription, DNA-templated;anther wall tapetum morphogenesis;microgametogenesis | | |
| Phvul.002G089700 | probable wrky transcription factor 72-like | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.002G093000 | chaperone -domain superfamily | nucleus;cytoplasm;protein folding;response to heat;response to high light intensity;response to hydrogen peroxide | | |

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| Phvul.002G096600 | glycoside hydrolase family 17 protein | hydrolase activity, hydrolyzing O-glycosyl compounds;carbohydrate metabolic process | | |
| Phvul.002G099700 | probable zinc transporter 10 | integral component of membrane;zinc ion transmembrane transporter activity;iron ion transport;water transport;cellular response to iron ion starvation;zinc II ion transmembrane transport | | |
| Phvul.002G103300 | hypothetical protein PHAVU_002G103300g | | | |
| Phvul.002G105700 | protein fd-like | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.002G108200 | hypothetical protein PHAVU_002G108200g | | | |
| Phvul.002G112600 | thiosulfate sulfurtransferase chloroplastic-like | thiosulfate sulfurtransferase activity;metabolic process | ec:2.8.1.1-sulfurtransferase | Sulfur metabolism |
| Phvul.002G117700 | auxin efflux carrier family protein | integral component of membrane;transmembrane transport | | |
| Phvul.002G123500 | lrr receptor-like kinase | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.002G124100 | hypothetical protein PHAVU_002G124100g | | | |
| Phvul.002G134700 | sn1-specific diacylglycerol lipase alpha | hydrolase activity;lipid metabolic process | | |
| Phvul.002G140000 | tpr repeat protein | | | |
| Phvul.002G141600 | plant mza15-19 | | | |
| Phvul.002G141900 | abscisic acid receptor pyr1-like | | | |
| Phvul.002G148700 | 6-phosphofructokinase chloroplastic-like | chloroplast;6-phosphofructokinase activity;ATP binding;metal ion binding;fructose 6-phosphate metabolic process;glycolytic process;carbohydrate phosphorylation | ec:2.7.1;ec:2.7.1.11-phosphohexokinase | Biosynthesis of antibiotics;Pentose phosphate pathway;Methane metabolism;Glycolysis / Gluconeogenesis;Galactose metabolism;Fructose and mannose metabolism |
| Phvul.002G154900 | protein iq-domain 14 | | | |
| Phvul.002G155400 | protein p21-like | | | |
| Phvul.002G156100 | tubby c 2 protein | | | |
| Phvul.002G159800 | 1-aminocyclopropane-1-carboxylate synthase | 1-aminocyclopropane-1-carboxylate synthase activity;pyridoxal phosphate binding;identical protein binding;ethylene biosynthetic process;response to ethylene;response to abscisic acid;fruit ripening;response to chitin;1-aminocyclopropane-1-carboxylate biosynthetic process | ec:4.4.1.14-synthase | Cysteine and methionine metabolism |
| Phvul.002G160100 | wrky transcription factor 22 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.002G160600 | protein lurp-one-related 17 | | | |
| Phvul.002G163900 | probable protein phosphatase 2c 8 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | ec:3.1.3.16-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | T cell receptor signaling pathwayAminobenzoate degradation |

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| Phvul.002G166600 | probable methyltransferase pmt27 | endomembrane system;intracellular membrane-bounded organelle;cytoplasmic part;methyltransferase activity;methylation | | |
| Phvul.002G170200 | nac domain-containing protein 29 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.002G170800 | ribonuclease 1 | extracellular region;cell wall;plasma membrane;RNA binding;ribonuclease T2 activity;anthocyanin-containing compound biosynthetic process;proline transport;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1.31;ec:3.1.27.1;ec:3.1.27;ec:3.1 | |
| Phvul.002G180900 | bon1-associated-like protein | | | |
| Phvul.002G181200 | type i inositol- -trisphosphate 5-phosphatase cvp2 | phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity;protein dephosphorylation;glucuronoxylan metabolic process;xylan biosynthetic process;phosphatidylinositol dephosphorylation | ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1;ec:3.1.3.36-5-phosphatase | Aminobenzoate degradationInositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.002G184600 | transcription factor myb108-like | DNA binding | | |
| Phvul.002G185800 | glutamate decarboxylase 1 | glutamate decarboxylase activity;pyridoxal phosphate binding;glutamate metabolic process | ec:4.1.1.15-decarboxylase | Taurine and hypotaurine metabolism;beta-Alanine metabolism;Butanoate metabolism;Alanine, aspartate and glutamate metabolism |
| Phvul.002G186000 | glutamate decarboxylase 1 | glutamate decarboxylase activity;pyridoxal phosphate binding;glutamate metabolic process | ec:4.1.1.15-decarboxylase | Taurine and hypotaurine metabolism;beta-Alanine metabolism;Butanoate metabolism;Alanine, aspartate and glutamate metabolism |
| Phvul.002G186600 | map3k-like kinase | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.002G187800 | cytochrome p450 family 81 protein | endoplasmic reticulum membrane;integral component of membrane;iron ion binding;heme binding;isoflavone 2'-hydroxylase activity;4'-methoxyisoflavone 2'-hydroxylase activity;aromatase activity;oxidation-reduction process | ec:1.14.13.53;ec:1.14.14;ec:1.14.13;ec:1.14.13.89-2'-hydroxylase;ec:1.14.14.1-monooxygenase | Isoflavonoid biosynthesisLinoleic acid metabolism;Arachidonic acid metabolism;Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Caffeine metabolism;Aminobenzoate degradation;Tryptophan metabolism;Fatty acid degradation;Retinol metabolism;Steroid hormone biosynthesis |
| Phvul.002G197800 | stress up-regulated nod 19 protein | | | |
| Phvul.002G199000 | fad-binding berberine family protein | UDP-N-acetylmuramate dehydrogenase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.1.1.158 | |
| Phvul.002G199700 | cannabidiolic acid synthase-like 2-like | UDP-N-acetylmuramate dehydrogenase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.1.1.158 | |
| Phvul.002G200600 | cannabidiolic acid synthase-like 2-like | UDP-N-acetylmuramate dehydrogenase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.1.1.158 | |
| Phvul.002G204900 | histidine decarboxylase | cell part;histidine decarboxylase activity;pyridoxal phosphate binding;phenylalanine decarboxylase activity;carboxylic acid metabolic process | ec:4.1.1.53-decarboxylase;ec:4.1.1.22-decarboxylase | Phenylalanine metabolismHistidine metabolism |

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| Phvul.002G208900 | hypothetical protein PHAVU_002G208900g |  |  |  |
| Phvul.002G209400 | stress-induced protein sam22 | defense response;response to biotic stimulus |  |  |
| Phvul.002G209500 | stress-induced protein sam22 | defense response;response to biotic stimulus |  |  |
| Phvul.002G209900 | ice-like protease p20 domain protein | cysteine-type endopeptidase activity;proteolysis | ec:3.4.22;ec:3.4 |  |
| Phvul.002G210400 | abc transporter g family member 11 | membrane;ATP binding;organic phosphonate transmembrane-transporting ATPase activity;metabolic process;organic phosphonate transport;organophosphate ester transport | ec:3.6.3.28;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G210500 | abc transporter g family member 11 | membrane;ATP binding;ATPase activity;metabolic process;single-organism transport;organic substance transport | ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G215100 | serine-threonine protein plant- | integral component of membrane;protein serine/threonine kinase activity;ATP binding;oxidoreductase activity;protein phosphorylation | ec:2.7.11 |  |
| Phvul.002G218300 | phosphosulfolactate synthase | catalytic activity;protein folding;response to high light intensity;heat acclimation;posttranscriptional regulation of gene expression;coenzyme M biosynthetic process;response to hydrogen peroxide |  |  |
| Phvul.002G219100 | ( )-nerolidol synthase 1-like | plastid;magnesium ion binding;terpene synthase activity;metabolic process |  |  |
| Phvul.002G220300 | hydrolyzing o-glycosyl compounds hydrolase | hydrolase activity, hydrolyzing O-glycosyl compounds;carbohydrate binding;carbohydrate metabolic process |  |  |
| Phvul.002G223400 | internal alternative nad h-ubiquinone oxidoreductase mitochondrial-like | NADH dehydrogenase (ubiquinone) activity;oxidation-reduction process | ec:1.6.5.3-reductase (H+-translocating);ec:1.6.99.5;ec:1.6.99.3-dehydrogenase | Oxidative phosphorylationOxidative phosphorylation |
| Phvul.002G228400 | heat stress transcription factor b-2a-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated;response to heat |  |  |
| Phvul.002G228700 | linoleate 13s-lipoxygenase 3-chloroplastic-like | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;metal ion binding;oxylipin biosynthetic process;oxidation-reduction process | ec:1.13.11 |  |
| Phvul.002G231400 | kda class i heat shock protein | cytoplasm |  |  |
| Phvul.002G231500 | kda class i heat shock protein | cytoplasm |  |  |
| Phvul.002G231600 | kda class i heat shock protein | cytoplasm |  |  |
| Phvul.002G231700 | kda class i heat shock protein | cytoplasm |  |  |
| Phvul.002G231800 | kda class i heat shock protein | cytoplasm |  |  |
| Phvul.002G232800 | protein srg1 | gibberellin 3-beta-dioxygenase activity;flavonol synthase activity;metal ion binding;flavonol biosynthetic process;oxidation-reduction process | ec:1.14.11.15-3beta-dioxygenase;ec:1.14.11;ec:1.14.11.23-synthase | Diterpenoid biosynthesisFlavonoid biosynthesis |
| Phvul.002G235100 | duf761 domain protein |  |  |  |
| Phvul.002G239300 | papain family cysteine protease | cysteine-type peptidase activity;proteolysis | ec:3.4 |  |
| Phvul.002G240100 | leucine-rich repeat family protein | kinase activity;phosphorylation |  |  |
| Phvul.002G241400 | tau class glutathione s-transferase | glutathione transferase activity;metabolic process | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome |

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| | | | | P450;Glutathione metabolism |
| Phvul.002G244900 | sulfite exporter family protein | integral component of membrane | | |
| Phvul.002G249300 | serine threonine-protein kinase srk2a | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.002G256900 | zinc finger protein stop1 homolog | nucleic acid binding;metal ion binding | | |
| Phvul.002G270900 | probable pectinesterase pectinesterase inhibitor 51 | cell wall;enzyme inhibitor activity;pectinesterase activity;aspartyl esterase activity;cell wall modification;negative regulation of catalytic activity;pectin catabolic process | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.002G271900 | coiled-coil domain-containing protein isoform partial | | | |
| Phvul.002G274900 | hypothetical protein PHAVU_002G274900g | integral component of membrane | | |
| Phvul.002G280400 | nfu1 iron-sulfur mitochondrial | protein folding;response to heat;response to high light intensity;response to hydrogen peroxide | | |
| Phvul.002G284700 | saur-like auxin-responsive family protein | response to auxin | | |
| Phvul.002G285800 | probable wrky transcription factor 75 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;response to ethylene;cellular response to phosphate starvation;galactolipid biosynthetic process;regulation of response to nutrient levels;cellular response to water deprivation;regulation of DNA-templated transcription in response to stress;lateral root development | | |
| Phvul.002G287300 | clavata3 esr gene family member | | | |
| Phvul.002G306400 | inositol oxygenase 2-like | cytoplasm;iron ion binding;inositol oxygenase activity;inositol catabolic process;oxidation-reduction process | ec:1.13.99.1-oxygenase | Inositol phosphate metabolism;Ascorbate and aldarate metabolism |
| Phvul.002G306800 | 6-phosphofructokinase 3 | cytoplasm;6-phosphofructokinase activity;ATP binding;metal ion binding;fructose 6-phosphate metabolic process;glycolytic process;carbohydrate phosphorylation | ec:2.7.1;ec:2.7.1.11-phosphohexokinase | Biosynthesis of antibiotics;Pentose phosphate pathway;Methane metabolism;Glycolysis / Gluconeogenesis;Galactose metabolism;Fructose and mannose metabolism |
| Phvul.002G308000 | pectinesterase 53 | cell wall;cytoplasm;lyase activity;pectinesterase activity;aspartyl esterase activity;response to UV;flavonoid biosynthetic process;cell wall modification | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.002G309100 | protein phosphatase 2c 56-like | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | ec:3.1.3.16-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | T cell receptor signaling pathwayAminobenzoate degradation |
| Phvul.002G314600 | heavy metal transport detoxification superfamily protein | metal ion binding;metal ion transport | | |
| Phvul.002G316100 | zinc finger protein constans-like 16 | intracellular;zinc ion binding | | |
| Phvul.002G316900 | transcription factor bee 1-like | nucleus;transcription factor activity, sequence-specific DNA binding;protein dimerization activity;regulation of transcription, DNA-templated | | |

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| Phvul.002G317000 | transcription factor myb21 | DNA binding | | |
| Phvul.002G319000 | protein plant cadmium resistance 2-like | | | |
| Phvul.002G319200 | protein plant cadmium resistance 2-like | | | |
| Phvul.002G320400 | protein xap5 circadian timekeeper isoform x2 | nucleus;response to blue light;ethylene-activated signaling pathway;regulation of photomorphogenesis;response to red light;regulation of circadian rhythm | | |
| Phvul.002G320600 | hypothetical protein PHAVU_002G320600g | | | |
| Phvul.002G322300 | two-component response regulator arr2 | intracellular;DNA binding;phosphorelay signal transduction system | | |
| Phvul.002G324400 | clathrin assembly protein at2g25430 | clathrin-coated vesicle;1-phosphatidylinositol binding;oxidoreductase activity;clathrin binding;clathrin coat assembly | | |
| Phvul.002G325400 | disease resistance-dirigent domain protein | | | |
| Phvul.002G326600 | 1-aminocyclopropane-1-carboxylate oxidase | 1-aminocyclopropane-1-carboxylate oxidase activity;L-ascorbic acid binding;naringenin 3-dioxygenase activity;metal ion binding;ethylene biosynthetic process;fruit ripening;oxidation-reduction process | ec:1.14.11;ec:1.14.17.4-oxidase;ec:1.14.11.9-3-dioxygenase | Cysteine and methionine metabolismFlavonoid biosynthesis |
| Phvul.002G326700 | mate efflux family protein | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.002G331800 | u-box domain-containing protein 21-like | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.002G332300 | monoglyceride lipase-like | acylglycerol lipase activity;metabolic process | ec:3.1.1.23-lipase;ec:3.1.1.1-ali-esterase;ec:3.1.1 | Glycerolipid metabolismDrug metabolism - other enzymes |
| Phvul.003G002500 | hypothetical protein PHAVU_003G002500g | ADP binding | | |
| Phvul.003G002800 | hypothetical protein PHAVU_003G002800g | ADP binding | | |
| Phvul.003G007200 | dishevelled egl-10 leckstrin domain protein | intracellular;electron carrier activity;protein disulfide oxidoreductase activity;intracellular signal transduction;cell redox homeostasis;oxidation-reduction process | | |
| Phvul.003G007300 | phototropic-responsive nph3 family protein | | | |
| Phvul.003G012600 | plastocyanin-like domain protein | electron carrier activity | | |
| Phvul.003G015600 | probable pectinesterase 29 | cell wall;pectinesterase activity;aspartyl esterase activity;metabolic process;cell wall modification | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.003G016400 | probable s-adenosylmethionine-dependent methyltransferase at5g38100 | methyltransferase activity;methylation | | |
| Phvul.003G024700 | abc transporter g family member 21 | membrane;ATP binding;organic phosphonate transmembrane-transporting ATPase activity;metabolic process;organic phosphonate transport;organophosphate ester transport | ec:3.6.3.28;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |

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| Phvul.003G027000 | pectinesterase-like protein | cell wall;pectinesterase activity;aspartyl esterase activity;metabolic process;cell wall modification | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.003G029400 | hypothetical protein PHAVU_003G029400g | integral component of membrane | | |
| Phvul.003G030500 | s1 p1 nuclease family protein | nucleic acid binding;endonuclease activity;DNA catabolic process;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.003G031300 | 3-ketoacyl-synthase 6 | membrane;transferase activity, transferring acyl groups other than amino-acyl groups;fatty acid biosynthetic process | | |
| Phvul.003G034200 | duf1262 family protein | | | |
| Phvul.003G036600 | long chain acyl-synthetase 2 | endoplasmic reticulum;plasmodesma;long-chain fatty acid-CoA ligase activity;very long-chain fatty acid-CoA ligase activity;long-chain fatty acid metabolic process;cutin biosynthetic process;lateral root formation;defense response to fungus | ec:6.2.1.3-ligase;ec:6.2.1 | Fatty acid degradation;Fatty acid biosynthesis |
| Phvul.003G041200 | cytochrome p450 78a5-like | endoplasmic reticulum;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;positive regulation of cell proliferation;regulation of meristem growth;leaf formation;organ growth;regulation of growth rate;positive regulation of organ growth;floral organ development;oxidation-reduction process | | |
| Phvul.003G044600 | formiminotransferase-cyclodeaminase-like protein | folic acid binding;glutamate formimidoyltransferase activity;metabolic process | ec:2.1.2;ec:2.1.2.5-formimidoyltransferase | One carbon pool by folate;Histidine metabolism |
| Phvul.003G048700 | transcription termination factor family protein | mitochondrion;double-stranded DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.003G049800 | phytochrome kinase substrate | kinase activity;lyase activity;phosphorylation | | |
| Phvul.003G051700 | isoflavone synthase 1 | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;isomerase activity;heme binding;oxidation-reduction process | | |
| Phvul.003G051800 | isoflavone synthase 1 | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;isomerase activity;heme binding;oxidation-reduction process | | |
| Phvul.003G051900 | plastocyanin-like domain protein | electron carrier activity | | |
| Phvul.003G055500 | gibberellin-regulated family protein | | | |
| Phvul.003G057900 | cle1 protein | | | |
| Phvul.003G058700 | u-box domain-containing protein 7-like | | | |
| Phvul.003G064300 | protein transparent testa 12-like | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.003G064500 | 70 kda peptidyl-prolyl isomerase-like | peptidyl-prolyl cis-trans isomerase activity;protein peptidyl-prolyl isomerization;protein folding | ec:5.2.1.8 | |
| Phvul.003G071000 | pentatricopeptide repeat-containing protein mitochondrial | chloroplast;endonuclease activity;mRNA modification;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.003G074000 | isoflavone synthase 1 | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;isomerase activity;heme binding;oxidation-reduction process | | |

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| Phvul.003G077800 | hypothetical protein PHAVU_003G077800g | DNA binding | | |
| Phvul.003G078100 | hypothetical protein PHAVU_003G078100g | | | |
| Phvul.003G079800 | 5 -adenylylsulfate reductase chloroplastic-like | cell;adenylyl-sulfate reductase (glutathione) activity;sulfate reduction;cell redox homeostasis | ec:1.8.4.9-reductase (glutathione) | Sulfur metabolism |
| Phvul.003G087500 | probable adp-ribosylation factor gtpase-activating protein agd13 | vacuole;plasma membrane;phosphatidylserine decarboxylase activity;phospholipase A2 activity;metabolic process | ec:4.1.1.65-decarboxylase;ec:3.1.1.4-A2;ec:3.1.1.1-ali-esterase;ec:3.1.1 | Glycerophospholipid metabolismalpha-Linolenic acid metabolism;Linoleic acid metabolism;Arachidonic acid metabolism;Ether lipid metabolism;Glycerophospholipid metabolismDrug metabolism - other enzymes |
| Phvul.003G087700 | web family protein at1g12150-like | | | |
| Phvul.003G089500 | transmembrane protein 64 | | | |
| Phvul.003G092100 | basic 7s globulin | aspartic-type endopeptidase activity;proteolysis | ec:3.4.23 | |
| Phvul.003G093100 | adenylate isopentenyltransferase | AMP dimethylallyltransferase activity;tRNA processing | ec:2.5.1.27-dimethylallyltransferase | Zeatin biosynthesis |
| Phvul.003G096700 | late embryogenesis abundant protein lea5 | response to stress | | |
| Phvul.003G098600 | tryptophan aminotransferase-related protein 4 | carbon-sulfur lyase activity;metabolic process | | |
| Phvul.003G099100 | inosine-uridine preferring nucleoside hydrolase | xanthine dehydrogenase activity;hydrolase activity;oxidation-reduction process | ec:1.17.1.4-dehydrogenase;ec:1.17.1 | Purine metabolism |
| Phvul.003G108400 | mono di-acylglycerol amino-terminal | hydrolase activity;lipid catabolic process | | |
| Phvul.003G109000 | pathogenesis-related protein bet v i family protein | defense response;response to biotic stimulus | | |
| Phvul.003G109200 | stress-induced protein sam22 | defense response;response to biotic stimulus | | |
| Phvul.003G109600 | stress-induced protein sam22 | defense response;response to biotic stimulus | | |
| Phvul.003G109800 | stress-induced protein sam22 | defense response;response to biotic stimulus | | |
| Phvul.003G118300 | gibberellin 2-beta-dioxygenase 2-like | iron ion binding;gibberellin 2-beta-dioxygenase activity;oxidation-reduction process;organic substance metabolic process | ec:1.14.11.13-2beta-dioxygenase;ec:1.14.11 | Diterpenoid biosynthesis |
| Phvul.003G118400 | alkaline neutral invertase cinv2-like | mitochondrion;chloroplast;sucrose alpha-glucosidase activity;glycopeptide alpha-N-acetylgalactosaminidase activity;ethylene biosynthetic process;regulation of seed germination;regulation of timing of transition from vegetative to reproductive phase | ec:3.2.1.97;ec:3.2.1;ec:3.2.1.48-alpha-glucosidase;ec:3.2.1.26-invertase | Starch and sucrose metabolismStarch and sucrose metabolism;Galactose metabolism |
| Phvul.003G120100 | double clp-n motif p-loop nucleoside triphosphate hydrolase superfamily protein | | | |
| Phvul.003G120900 | hypothetical protein | nucleus | | |

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|  | PHAVU_003G120900g |  |  |  |
| Phvul.003G121900 | group 3 lea protein |  |  |  |
| Phvul.003G122700 | abc transporter b family protein | integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G124100 | cytidine deoxycytidylate deaminase family protein | cytosine deaminase activity;zinc ion binding;metabolic process | ec:3.5.4.1-deaminase | Arginine and proline metabolism;Pyrimidine metabolism |
| Phvul.003G124300 | hypothetical protein PHAVU_003G124300g | binding |  |  |
| Phvul.003G126300 | lysine-ketoglutarate reductase saccharopine dehydrogenase | cytosol;saccharopine dehydrogenase (NADP+, L-glutamate-forming) activity;saccharopine dehydrogenase (NADP+, L-lysine-forming) activity;response to sucrose;response to fructose;vegetative to reproductive phase transition of meristem;protein desumoylation;L-lysine catabolic process;hydrogen peroxide biosynthetic process;oxidation-reduction process | ec:1.5.1.10-dehydrogenase (NADP+, L-glutamate-forming);ec:1.5.1;ec:1.5.1.8-dehydrogenase (NADP+, L-lysine-forming) | Biosynthesis of antibiotics;Lysine degradation;Lysine biosynthesisBiosynthesis of antibiotics;Lysine degradation |
| Phvul.003G126600 | pectinesterase pectinesterase inhibitor | cell wall;enzyme inhibitor activity;pectinesterase activity;aspartyl esterase activity;cell wall modification;negative regulation of catalytic activity;pectin catabolic process | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.003G128400 | hypothetical protein PHAVU_003G128400g |  |  |  |
| Phvul.003G129200 | protein tify 10a-like |  |  |  |
| Phvul.003G131400 | auxin-binding protein abp19a | nucleus;plant-type cell wall;extracellular matrix;apoplast;manganese ion binding;nutrient reservoir activity;auxin-activated signaling pathway;stomatal complex morphogenesis;photosynthesis, light reaction;cellular cation homeostasis;defense response to bacterium;divalent metal ion transport |  |  |
| Phvul.003G131500 | 12-oxophytodienoate reductase 3 | peroxisome;FMN binding;12-oxophytodienoate reductase activity;tryptophan catabolic process;response to water deprivation;response to wounding;indoleacetic acid biosynthetic process;jasmonic acid biosynthetic process;response to ethylene;response to auxin;abscisic acid-activated signaling pathway;jasmonic acid mediated signaling pathway;hyperosmotic salinity response;oxidation-reduction process | ec:1.3.1.42-reductase | alpha-Linolenic acid metabolism |
| Phvul.003G133400 | membrane protein |  |  |  |
| Phvul.003G135400 | heat stress transcription factor a-2-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated;response to heat |  |  |
| Phvul.003G135700 | transcription factor bhlh041 | protein dimerization activity |  |  |
| Phvul.003G138800 | thioredoxin superfamily protein isoform 1 |  |  |  |
| Phvul.003G138900 | mitochondrial ribosomal protein l37 isoform 1 | ribosome |  |  |
| Phvul.003G140800 | transcription factor bhlh35 | DNA binding;amino acid binding;protein dimerization activity;metabolic process |  |  |
| Phvul.003G146700 | probable beta- -galactosyltransferase 16 | Golgi apparatus;integral component of membrane;galactosyltransferase activity;protein glycosylation | ec:2.4.1 |  |
| Phvul.003G147100 | zinc finger protein 2 | nucleic acid binding;metal ion binding |  |  |

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| Phvul.003G148600 | cbl-interacting serine threonine-protein kinase 21 isoform x1 | protein serine/threonine kinase activity;ATP binding;protein phosphorylation;signal transduction | ec:2.7.11 | |
| Phvul.003G148900 | 1-deoxy-d-xylulose-5-phosphate synthase | 1-deoxy-D-xylulose-5-phosphate synthase activity;terpenoid biosynthetic process | ec:2.2.1.7-synthase | Biosynthesis of antibiotics;Terpenoid backbone biosynthesis;Thiamine metabolism |
| Phvul.003G154800 | heat shock 70 kda protein | cell wall;plasma membrane;chloroplast;ATP binding;2-alkenal reductase [NAD(P)] activity;protein folding;response to high light intensity;heat acclimation;response to endoplasmic reticulum stress;response to hydrogen peroxide;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.003G160900 | plant msj11-3 | | | |
| Phvul.003G163400 | lactoylglutathione lyase glyoxalase i family protein | transferase activity;lyase activity;metabolic process | | |
| Phvul.003G164000 | protein nrt1 ptr family | cell;integral component of membrane;transporter activity;oligopeptide transport;cellular cation homeostasis;divalent metal ion transport | | |
| Phvul.003G167700 | auxin-responsive protein iaa29-like | nucleus;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |
| Phvul.003G173600 | hypothetical protein PHAVU_003G173600g | | | |
| Phvul.003G176800 | transcription factor divaricata | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;regulation of transcription, DNA-templated;mRNA modification | | |
| Phvul.003G177800 | oleosin 1-like | monolayer-surrounded lipid storage body;integral component of membrane | | |
| Phvul.003G178300 | adenine nucleotide alpha hydrolases-like superfamily protein isoform 2 | response to stress | | |
| Phvul.003G181300 | serine threonine-protein kinase rio2-like isoform x1 | | | |
| Phvul.003G182600 | adenine nucleotide alpha hydrolase superfamily protein | hydrolase activity;response to stress;metabolic process | | |
| Phvul.003G184200 | ninja-family protein afp3-like isoform x3 | | | |
| Phvul.003G187200 | probable lrr receptor-like serine threonine-protein kinase at1g74360 | mitochondrion;integral component of membrane;MAP kinase kinase kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity;peptidyl-tyrosine phosphorylation | ec:2.7.10.1;ec:2.7.11.25;ec:2.7.11;ec:2.7.10 | |
| Phvul.003G190400 | r2r3-myb transcription factor | DNA binding | | |
| Phvul.003G192800 | protein nrt1 ptr family | membrane;transporter activity;transport | | |
| Phvul.003G193400 | peptide nitrate transporter | membrane;transporter activity;transport | | |
| Phvul.003G199200 | u-box domain-containing protein 19-like | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.003G207000 | myosin heavy chain kinase b | transferase activity | | |
| Phvul.003G209000 | hypothetical protein PHAVU_003G209000g | | | |
| Phvul.003G209100 | malate glyoxysomal | glyoxysome;malate synthase activity;glyoxylate cycle;tricarboxylic acid cycle | ec:2.3.3.9-synthase | Pyruvate metabolism;Glyoxylate |

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| | | | | and dicarboxylate metabolism |
| Phvul.003G 212600 | mate efflux family protein 5-like | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.003G 212900 | protein gar2-like | | | |
| Phvul.003G 217200 | 21 kda protein | enzyme inhibitor activity;pectinesterase activity;metabolic process;negative regulation of catalytic activity | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.003G 225700 | cationic amino acid transporter chloroplastic-like | integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.003G 227500 | invertase inhibitor | enzyme inhibitor activity;pectinesterase activity;metabolic process;negative regulation of catalytic activity | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.003G 228000 | expansin-like b1 | extracellular region | | |
| Phvul.003G 228700 | type i inositol- -trisphosphate 5-phosphatase 2 | phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity;inositol-polyphosphate 5-phosphatase activity;protein dephosphorylation;response to abscisic acid;seed germination;inositol trisphosphate metabolic process;inositol phosphate dephosphorylation;phosphatidylinositol dephosphorylation | ec:3.1.3.56-5-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1;ec:3.1.3.36-5-phosphatase;ec:3.1.3 | Inositol phosphate metabolism;Phosphatidylinositol signaling systemAminobenzoate degradationInositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.003G 230300 | seed maturation protein | embryo development | | |
| Phvul.003G 233400 | phytosulfokines 3-like | extracellular region;growth factor activity;cell proliferation | | |
| Phvul.003G 235800 | probable n-acetyltransferase hls1 | N-acetyltransferase activity;metabolic process | ec:2.3.1 | |
| Phvul.003G 236200 | lateral organ boundaries domain protein | | | |
| Phvul.003G 238700 | indole-3-acetic acid-amido synthetase | | | |
| Phvul.003G 239800 | hypothetical protein PHAVU_003G239800g | | | |
| Phvul.003G 243400 | triacylglycerol lipase-like protein | feruloyl esterase activity;lipid metabolic process | ec:3.1.1.73;ec:3.1.1.1-ali-esterase | Drug metabolism - other enzymes |
| Phvul.003G 247100 | disease resistance protein | | | |
| Phvul.003G 247400 | disease resistance protein | ADP binding | | |
| Phvul.003G 252500 | probable polyol transporter 6 | integral component of membrane;substrate-specific transmembrane transporter activity;transmembrane transport | | |
| Phvul.003G 259200 | cytochrome p450 84a1-like | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.003G 264600 | histidine kinase 1 | intracellular;membrane;phosphorelay sensor kinase activity;osmosensor activity;histidine phosphotransfer kinase activity;phosphorelay signal transduction system;response to osmotic stress;response to water deprivation;stomatal complex patterning;seed maturation;peptidyl-histidine phosphorylation;signal transduction by protein phosphorylation | ec:2.7.3;ec:2.7.13.3 | |
| Phvul.003G 267000 | receptor-like protein kinase theseus 1 | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |

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| Phvul.003G 268500 | chitinase (class ib) hevein | chitinase activity;chitin binding;carbohydrate metabolic process;chitin catabolic process;cell wall macromolecule catabolic process | ec:3.2.1.14-chitodextrinase | Amino sugar and nucleotide sugar metabolism |
| Phvul.003G 268600 | chitinase (class ib) hevein | chitinase activity;chitin binding;polysaccharide catabolic process;chitin catabolic process;defense response;cell wall macromolecule catabolic process | ec:3.2.1.14-chitodextrinase | Amino sugar and nucleotide sugar metabolism |
| Phvul.003G 269500 | dirigent protein 19-like | | | |
| Phvul.003G 277900 | late embryogenesis abundant protein | | | |
| Phvul.003G 278400 | cytochrome p450 family aba 8 -hydroxylase | iron ion binding;(+)-abscisic acid 8'-hydroxylase activity;heme binding;oxidation-reduction process | ec:1.14.13;ec:1.14.13.93-acid 8'-hydroxylase | Carotenoid biosynthesis |
| Phvul.003G 281200 | protein strictosidine synthase-like 10-like | strictosidine synthase activity;biosynthetic process | ec:4.3.3.2-synthase | Indole alkaloid biosynthesis |
| Phvul.003G 283100 | transcription factor jumonji family protein | catalytic activity;metabolic process | | |
| Phvul.003G 287400 | probable mannitol dehydrogenase | zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.003G 287500 | probable mannitol dehydrogenase | zinc ion binding;cinnamyl-alcohol dehydrogenase activity;sinapyl alcohol dehydrogenase activity;oxidation-reduction process | ec:1.1.1.195-dehydrogenase | Phenylpropanoid biosynthesis |
| Phvul.004G 005400 | cytochrome p450 86b1-like | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.004G 008900 | nbs-lrr type disease resistance protein cnl-j9 | ADP binding | | |
| Phvul.004G 009000 | nbs-lrr type disease resistance protein cnl-j3 | ADP binding | | |
| Phvul.004G 012800 | nbs-lrr type disease resistance protein cnl-b18 | ADP binding | | |
| Phvul.004G 013400 | hypothetical protein | | | |
| Phvul.004G 014600 | formate dehydrogenase | mitochondrion;chloroplast;thylakoid;formate dehydrogenase (NAD+) activity;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;NAD binding;oxidation-reduction process | ec:1.2.1.2-dehydrogenase | Methane metabolism;Glyoxylate and dicarboxylate metabolism |
| Phvul.004G 014700 | formate dehydrogenase | mitochondrion;chloroplast;thylakoid;formate dehydrogenase (NAD+) activity;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;NAD binding;oxidation-reduction process | ec:1.2.1.2-dehydrogenase | Methane metabolism;Glyoxylate and dicarboxylate metabolism |
| Phvul.004G 015500 | cyclin-like f-box | | | |
| Phvul.004G 018900 | alpha-dioxygenase 1-like | peroxidase activity;heme binding;dioxygenase activity;response to oxidative stress;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.004G 021200 | cytochrome p450 family 82 protein | membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.004G 021300 | cytochrome p450 82a4-like | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.004G 021400 | cytochrome p450 82a4-like | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.004G 030500 | expansin a10 | extracellular region;cell wall;membrane;plant-type cell wall organization;unidimensional cell growth;primary root development | | |
| Phvul.004G 037700 | transcription factor tcp13 | | | |
| Phvul.004G 041700 | cytochrome p450 85a | integral component of membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of | | |

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| | | molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.004G044800 | lrr receptor-like kinase family protein | | | |
| Phvul.004G045800 | ocs element-binding factor 1 | intracellular;transcription factor activity, sequence-specific DNA binding;MAP kinase activity;sequence-specific DNA binding;MAPK cascade;regulation of transcription, DNA-templated | ec:2.7.11.24-protein kinase;ec:2.7.11 | mTOR signaling pathway |
| Phvul.004G046200 | calcium-transporting atpase plasma membrane-type | cell;integral component of membrane;calcium-transporting ATPase activity;ATP binding;metal ion binding;cellular zinc ion homeostasis;metabolic process;response to nematode;calcium ion transmembrane transport | ec:3.6.3.8;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.004G049900 | protein pns1-like | integral component of membrane | | |
| Phvul.004G054800 | triacylglycerol lipase 2 | lipase activity;defense response to insect;fatty acid beta-oxidation | ec:3.1.1 | |
| Phvul.004G054900 | triacylglycerol lipase-like protein | hydrolase activity;lipid catabolic process | | |
| Phvul.004G055200 | calcium-binding protein cml38 | intracellular;calcium ion binding;MAPK cascade;respiratory burst involved in defense response;protein targeting to membrane;ethylene biosynthetic process;salicylic acid biosynthetic process;systemic acquired resistance, salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;response to chitin;regulation of hydrogen peroxide metabolic process;regulation of plant-type hypersensitive response;endoplasmic reticulum unfolded protein response;negative regulation of defense response;defense response to bacterium;defense response to fungus | | |
| Phvul.004G056700 | lysine histidine transporter 1-like | plasma membrane;integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport;amino acid import | | |
| Phvul.004G058400 | cystinosin homolog | membrane | | |
| Phvul.004G058500 | retrovirus-related pol polyprotein from transposon tnt 1- partial | metal ion binding;metabolic process | | |
| Phvul.004G061400 | mads-box transcription factor pheres 2 | | | |
| Phvul.004G068400 | cytochrome p450 81e8-like | integral component of membrane;iron ion binding;heme binding;isoflavone 2'-hydroxylase activity;oxidation-reduction process | ec:1.14.13;ec:1.14.13.89-2'-hydroxylase | Isoflavonoid biosynthesis |
| Phvul.004G070500 | mitochondrial phosphate carrier protein mitochondrial-like | integral component of membrane;glutathione transferase activity;transport;metabolic process;response to salt stress;response to ethylene | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolism |
| Phvul.004G071700 | mlo-like protein 12 | integral component of membrane;calmodulin binding;defense response;response to biotic stimulus | | |
| Phvul.004G072900 | upf0481 protein at3g47200-like | | | |
| Phvul.004G076400 | calmodulin | cytosol;phosphorylase kinase activity;calcium ion binding;protein binding;2-alkenal reductase [NAD(P)] activity;detection of calcium ion;acetyl-CoA metabolic process;protein phosphorylation;response to mechanical stimulus;regulation of photomorphogenesis;calcium-mediated signaling;oxidation-reduction process | ec:1.3.1.74;ec:2.7.11.19;ec:2.7.11.17;ec:2.7.11 | |
| Phvul.004G077400 | nac domain-containing protein 29 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;single-organism process | | |
| Phvul.004G080200 | glutamate dehydrogenase 1 | oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor;cellular amino acid metabolic process;oxidation-reduction process | | |
| Phvul.004G085100 | sucrose transport protein suc8-like | integral component of plasma membrane;sucrose transmembrane transporter activity;sucrose transport | | |

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| Phvul.004G088400 | tryptophan aminotransferase-related protein 4 | transaminase activity;alliin lyase activity;metabolic process | ec:4.4.1.4 | |
| Phvul.004G090200 | methionine gamma-lyase-like | cytosol;cystathionine gamma-synthase activity;methionine gamma-lyase activity;pyridoxal phosphate binding;metabolic process;protein homotetramerization | ec:2.5.1.48-gamma-synthase;ec:4.4.1.11-gamma-lyase | Sulfur metabolism;Biosynthesis of antibiotics;Cysteine and methionine metabolism;Selenocompound metabolismCysteine and methionine metabolism;Selenocompound metabolism |
| Phvul.004G090300 | transcription factor myc2-like | protein dimerization activity | | |
| Phvul.004G092100 | ethylene-responsive transcription factor abr1-like isoform x1 | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.004G099100 | lrr receptor-like serine threonine-protein kinase gso2-like | kinase activity;phosphorylation | | |
| Phvul.004G101500 | acidic endochitinase-like | extracellular space;chitinase activity;polysaccharide catabolic process;chitin catabolic process | ec:3.2.1.14-chitodextrinase | Amino sugar and nucleotide sugar metabolism |
| Phvul.004G103900 | isoflavone 7-o-glucosyltransferase 1-like | hydroquinone glucosyltransferase activity;metabolic process | ec:2.4.1;ec:2.4.1.218 | |
| Phvul.004G106500 | f-box fbd lrr-repeat protein at1g78750-like | | | |
| Phvul.004G107700 | heat shock protein 83 | ATP binding;unfolded protein binding;protein folding;response to stress | | |
| Phvul.004G108900 | beta-carotene hydroxylase | integral component of membrane;iron ion binding;oxidoreductase activity;fatty acid biosynthetic process;oxidation-reduction process | | |
| Phvul.004G111600 | transporter arsb | integral component of membrane;arsenite transmembrane transporter activity;arsenite transport;transmembrane transport | | |
| Phvul.004G111900 | transporter arsb | integral component of membrane;arsenite transmembrane transporter activity;arsenite transport;transmembrane transport | | |
| Phvul.004G114300 | cytochrome p450 family 72 protein | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.004G114600 | oxalate-- ligase | plasmodesma;chloroplast stroma;apoplast;o-succinylbenzoate-CoA ligase activity;4-coumarate-CoA ligase activity;oxalate-CoA ligase activity;positive regulation of seed germination;response to nitrate;seed coat development;nitrate transport;oxalate catabolic process;para-aminobenzoic acid metabolic process;defense response to fungus | ec:6.2.1.8-ligase;ec:6.2.1.26-ligase;ec:6.2.1.12-ligase | Glyoxylate and dicarboxylate metabolismUbiquinone and other terpenoid-quinone biosynthesisUbiquinone and other terpenoid-quinone biosynthesis;Phenylalanine metabolism;Phenylpropanoid biosynthesis |
| Phvul.004G115300 | lrr receptor-like serine threonine-protein kinase gso2-like | | | |
| Phvul.004G116600 | lrr receptor-like serine threonine-protein kinase gso2-like | | | |
| Phvul.004G117100 | low-temperature-induced 65 kda | | | |
| Phvul.004G118200 | e3 ubiquitin-protein ligase atl31-like | zinc ion binding | | |

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| Phvul.004G119400 | hypothetical protein PHAVU_004G119400g | | | |
| Phvul.004G123600 | gibberellin 20-oxidase | iron ion binding;gibberellin 3-beta-dioxygenase activity;gibberellin-44 dioxygenase activity;oxidation-reduction process | ec:1.14.11.15-3beta-dioxygenase;ec:1.14.11.12-dioxygenase;ec:1.14.11 | Diterpenoid biosynthesisDiterpenoid biosynthesis |
| Phvul.004G124200 | transcription factor | DNA binding;protein kinase activity;ATP binding;protein dimerization activity;protein phosphorylation | | |
| Phvul.004G129400 | kda class iv heat shock protein | | | |
| Phvul.004G131400 | clathrin assembly protein at1g33340 | clathrin-coated vesicle;1-phosphatidylinositol binding;clathrin binding;clathrin coat assembly | | |
| Phvul.004G134400 | uncharacterized oxidoreductase at4g09670-like | trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity;oxidation-reduction process | ec:1.3.1.20-dehydrogenase | Metabolism of xenobiotics by cytochrome P450 |
| Phvul.004G134800 | upf0481 protein at3g02645 | | | |
| Phvul.004G138500 | kunitz type trypsin inhibitor miraculin | endopeptidase inhibitor activity;negative regulation of endopeptidase activity | | |
| Phvul.004G138600 | gram domain protein aba-responsive-like protein | | | |
| Phvul.004G141300 | blue copper | electron carrier activity;root hair cell differentiation | | |
| Phvul.004G142000 | organic cation carnitine transporter 1 | integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.004G142400 | lrr receptor-like serine threonine-protein kinase gso1 | | | |
| Phvul.004G142500 | lrr receptor-like serine threonine-protein kinase gso1 | | | |
| Phvul.004G142600 | lrr receptor-like serine threonine-protein kinase gso1 | transferase activity | | |
| Phvul.004G142700 | lrr receptor-like serine threonine-protein kinase gso1 | transferase activity | | |
| Phvul.004G143600 | beta-amylase chloroplastic | beta-amylase activity;polysaccharide catabolic process | ec:3.2.1;ec:3.2.1.2-saccharogen amylase | Starch and sucrose metabolism |
| Phvul.004G148400 | uncharacterized protein LOC100527740 | | | |
| Phvul.004G150400 | pentatricopeptide repeat-containing protein mitochondrial-like | | | |
| Phvul.004G152900 | ctd small phosphatase-like protein 2 | phosphoprotein phosphatase activity;protein dephosphorylation | ec:3.1.3.16-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | T cell receptor signaling pathwayAminobenzoate degradation |
| Phvul.004G155000 | receptor-like kinase | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;polysaccharide binding;2-alkenal reductase [NAD(P)] activity;peptidyl-tyrosine phosphorylation;oxidation-reduction process | ec:1.3.1.74;ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.004G155200 | receptor-like kinase | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;polysaccharide binding;2-alkenal reductase [NAD(P)] activity;peptidyl-tyrosine phosphorylation;oxidation-reduction process | ec:1.3.1.74;ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |

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| Phvul.004G158800 | maturation-associated protein | response to stress;response to water | | |
| Phvul.004G160300 | atp-dependent clp protease adapter protein | peptidase activity;proteolysis;protein catabolic process | | |
| Phvul.004G162100 | multiprotein-bridging factor 1c | nucleolus;cytoplasm;transcription factor activity, sequence-specific DNA binding;transcription coactivator activity;sequence-specific DNA binding;transcription, DNA-templated;protein folding;response to heat;response to water deprivation;response to high light intensity;response to abscisic acid;ethylene-activated signaling pathway;response to endoplasmic reticulum stress;response to hydrogen peroxide;positive regulation of transcription, DNA-templated | | |
| Phvul.004G168400 | seed linoleate 9s-lipoxygenase | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;metal ion binding;oxylipin biosynthetic process;oxidation-reduction process | ec:1.13.11 | |
| Phvul.004G173400 | vacuolar protein sorting-associated protein 32 homolog 2-like | intracellular;vacuolar transport | | |
| Phvul.004G175200 | probable pectinesterase 53 | cell wall;cytoplasm;lyase activity;pectinesterase activity;aspartyl esterase activity;response to UV;flavonoid biosynthetic process;cell wall modification | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.005G004400 | fad-linked oxidoreductase | UDP-N-acetylmuramate dehydrogenase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.1.1.158 | |
| Phvul.005G005400 | anthocyanidin -o-glucosyltransferase | transferase activity, transferring hexosyl groups;metabolic process | | |
| Phvul.005G005500 | anthocyanidin -o-glucosyltransferase | transferase activity, transferring hexosyl groups;metabolic process | | |
| Phvul.005G012000 | pectinesterase pectinesterase inhibitor 24 | cell wall;enzyme inhibitor activity;pectinesterase activity;aspartyl esterase activity;cell wall modification;negative regulation of catalytic activity;pectin catabolic process | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.005G014000 | disease resistance rpp13-like protein 1 | hydrolase activity;ADP binding;metabolic process | | |
| Phvul.005G014600 | ubiquitin-associated ts-n domain | | | |
| Phvul.005G014900 | cysteine-rich receptor-kinase-like protein | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.005G015900 | wat1-related protein at5g07050-like | integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.005G016400 | probable carboxylesterase 15 | carboxylic ester hydrolase activity;metabolic process | ec:3.1.1.1-ali-esterase | Drug metabolism - other enzymes |
| Phvul.005G018500 | protein radialis-like 1-like | nucleus;DNA binding | | |
| Phvul.005G021600 | mlp-like protein 31 | defense response;response to biotic stimulus | | |
| Phvul.005G021900 | mate efflux family protein | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.005G022500 | polygalacturonase-like | extracellular region;polygalacturonase activity;carbohydrate metabolic process;cell wall organization | ec:3.2.1.15-pectin depolymerase | Starch and sucrose metabolism;Pentose and glucuronate interconversions |
| Phvul.005G029700 | dna-directed rna polymerase v subunit 5c-like | nucleus;DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |

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| Phvul.005G032000 | subtilisin inhibitor 1 | serine-type endopeptidase inhibitor activity;response to wounding;negative regulation of endopeptidase activity | | |
| Phvul.005G034000 | cytokinin dehydrogenase 6 | UDP-N-acetylmuramate dehydrogenase activity;cytokinin dehydrogenase activity;flavin adenine dinucleotide binding;cytokinin metabolic process;oxidation-reduction process | ec:1.5.99.12-dehydrogenase;ec:1.1.1.158 | Zeatin biosynthesis |
| Phvul.005G035800 | late embryogenesis abundant protein d-34-like | | | |
| Phvul.005G044200 | seed maturation protein pm41 | cytoplasm | | |
| Phvul.005G046200 | zinc finger protein zat11-like | nucleic acid binding;metal ion binding | | |
| Phvul.005G047200 | ankyrin repeat-containing protein at3g12360 | | | |
| Phvul.005G049000 | plant f3o9-12 protein | | | |
| Phvul.005G051600 | 9-cis-epoxycarotenoid dioxygenase | chloroplast thylakoid membrane;9-cis-epoxycarotenoid dioxygenase activity;metal ion binding;abscisic acid biosynthetic process;oxidation-reduction process | ec:1.13.11;ec:1.13.11.51-dioxygenase | Carotenoid biosynthesis |
| Phvul.005G053000 | pentatricopeptide repeat-containing protein at1g20230-like | microtubule-severing ATPase activity;metabolic process | ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.005G053400 | cytochrome p450 87a3 | iron ion binding;heme binding;taxane 10-beta-hydroxylase activity;oxidation-reduction process | ec:1.14.13.76-10beta-hydroxylase;ec:1.14.13 | Diterpenoid biosynthesis |
| Phvul.005G053600 | cytochrome p450 87a3-like | iron ion binding;heme binding;taxane 10-beta-hydroxylase activity;oxidation-reduction process | ec:1.14.13.76-10beta-hydroxylase;ec:1.14.13 | Diterpenoid biosynthesis |
| Phvul.005G053900 | glutathione s-amino-terminal domain protein | glutathione transferase activity;lactoylglutathione lyase activity;metabolic process | ec:2.5.1.18-transferase;ec:4.4.1.5-lyase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolismPyruvate metabolism |
| Phvul.005G054000 | glutathione s-transferase | glutathione transferase activity;metabolic process | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolism |
| Phvul.005G054100 | glutathione s-transferase | glutathione transferase activity;metabolic process | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolism |
| Phvul.005G054200 | glutathione s-transferase | glutathione transferase activity;metabolic process | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolism |
| Phvul.005G055000 | serine threonine-protein kinase | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation;protein autophosphorylation | ec:2.7.10.2-protein-tyrosine kinase;ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | T cell receptor signaling pathway |
| Phvul.005G058900 | nitrile-specifier protein 5 | | | |
| Phvul.005G059100 | feruloyl ortho-hydroxylase 1 | iron ion binding;flavonol synthase activity;naringenin 3-dioxygenase activity;flavonol biosynthetic process;oxidation-reduction process | ec:1.14.11;ec:1.14.11.9-3- | Flavonoid biosynthesisFlavonoid biosynthesis |

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| | | | dioxygenase;ec:1.14.11.23-synthase | |
| Phvul.005G065100 | f-box fbd lrr-repeat protein at3g14710-like | | | |
| Phvul.005G075400 | protein srg1 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;metal ion binding;oxidation-reduction process | ec:1.14.11 | |
| Phvul.005G075500 | protein srg1-like | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;metal ion binding;oxidation-reduction process | ec:1.14.11 | |
| Phvul.005G077000 | pgr5-like protein chloroplastic | | | |
| Phvul.005G078100 | lrr receptor-like kinase | transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.005G078400 | probable leucine-rich repeat receptor-like serine threonine-protein kinase at3g14840 | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.005G080600 | gamma-glutamyl hydrolase 2-like | extracellular space;cell wall;gamma-glutamyl-peptidase activity;proteolysis;glutamine metabolic process | ec:3.4.19.9-hydrolase;ec:3.4.19 | Folate biosynthesis |
| Phvul.005G084500 | nac transcription factor-like protein | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.005G084700 | callose synthase 10-like | | | |
| Phvul.005G096300 | seed biotin-containing protein sbp65 | | | |
| Phvul.005G097000 | nitrogen-induced cle 1 | | | |
| Phvul.005G097200 | transcription factor tcp4-like | signal transduction;post-embryonic development;cellular component organization;regulation of cellular metabolic process;reproductive structure development;phyllome development | | |
| Phvul.005G099500 | fasciclin-like arabinogalactan protein 13 | | | |
| Phvul.005G106500 | indole-3-acetic acid-amido synthetase | chloroplast;jasmonate-amino synthetase activity;response to wounding;response to salt stress;jasmonic acid metabolic process;response to abscisic acid;induced systemic resistance, jasmonic acid mediated signaling pathway | | |
| Phvul.005G108100 | wound-induced protein | | | |
| Phvul.005G108800 | anthocyanin 5-aromatic acyltransferase | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.005G109000 | malonyl-coenzyme a:anthocyanin 3-o-glucoside-6 -o-malonyltransferase | shikimate O-hydroxycinnamoyltransferase activity;anthranilate N-benzoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.144;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.005G109700 | myb-related protein myb4-like | DNA binding | | |
| Phvul.005G111100 | hypothetical protein PHAVU_005G111100g | | | |
| Phvul.005G111400 | sesquiterpene synthase | magnesium ion binding;isoprene synthase activity;metabolic process | ec:4.2.3.27-synthase | Terpenoid backbone biosynthesis |
| Phvul.005G111500 | sesquiterpene synthase | magnesium ion binding;isoprene synthase activity;metabolic process | ec:4.2.3.27-synthase | Terpenoid backbone biosynthesis |

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| Phvul.005G 111700 | sesquiterpene synthase | magnesium ion binding;isoprene synthase activity;metabolic process | ec:4.2.3.27-synthase | Terpenoid backbone biosynthesis |
| Phvul.005G 112700 | cysteine-rich repeat secretory protein 38-like | | | |
| Phvul.005G 116500 | cellulose synthase-like protein h1 | integral component of membrane;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.005G 116600 | plant t7a14-6 protein | | | |
| Phvul.005G 118900 | protein faf-chloroplastic | | | |
| Phvul.005G 121600 | hypothetical protein PHAVU_005G121600g | response to karrikin | | |
| Phvul.005G 138400 | hypothetical protein PHAVU_005G138400g | | | |
| Phvul.005G 141500 | zinc finger protein zat12 | metal ion binding | | |
| Phvul.005G 145600 | hypothetical protein PHAVU_005G145600g | | | |
| Phvul.005G 147600 | aldehyde dehydrogenase family 3 member f1 | aldehyde dehydrogenase [NAD(P)+] activity;cellular aldehyde metabolic process;oxidation-reduction process | ec:1.2.1.5-dehydrogenase [NAD(P)+] | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;beta-Alanine metabolism;Glycolysis / Gluconeogenesis;Phenylalanine metabolism;Tyrosine metabolism;Histidine metabolism |
| Phvul.005G 151600 | glycoside hydrolase family 1 protein | beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.005G 155800 | endochitinase pr4-like | chitinase activity;chitin binding;polysaccharide catabolic process;chitin catabolic process;defense response;cell wall macromolecule catabolic process | ec:3.2.1.14-chitodextrinase | Amino sugar and nucleotide sugar metabolism |
| Phvul.005G 156700 | seed linoleate 9s-lipoxygenase-2 | cytoplasm;linoleate 13S-lipoxygenase activity;metal ion binding;oxylipin biosynthetic process;oxidation-reduction process | ec:1.13.11.12-13S-lipoxygenase;ec:1.13.11 | alpha-Linolenic acid metabolism;Linoleic acid metabolism |
| Phvul.005G 158500 | cell-wall invertase | sucrose alpha-glucosidase activity;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.48-alpha-glucosidase;ec:3.2.1.26-invertase | Starch and sucrose metabolismStarch and sucrose metabolism;Galactose metabolism |
| Phvul.005G 163100 | leucine-rich repeat receptor-like protein kinase | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.005G 166800 | duf1677 family protein | | | |
| Phvul.005G 167800 | mitochondrial carnitine acylcarnitine carrier protein cacl | mitochondrion;integral component of membrane;L-ornithine transmembrane transporter activity;L-histidine transmembrane transporter activity;arginine transmembrane transporter activity;L-lysine transmembrane transporter activity;proline biosynthetic process;L-arginine import;L-histidine transmembrane transport;L-ornithine transmembrane transport;L-lysine transmembrane transport;arginine transmembrane transport | | |
| Phvul.005G 171900 | coatomer subunit beta -1-like | | | |
| Phvul.005G 173000 | auxin-responsive protein iaa1 | nucleus;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |

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| Phvul.005G173500 | gibberellin 3-beta-dioxygenase 1-like | iron ion binding;gibberellin 3-beta-dioxygenase activity;gibberellin biosynthetic process;oxidation-reduction process | ec:1.14.11.15-3beta-dioxygenase;ec:1.14.11 | Diterpenoid biosynthesis |
| Phvul.005G173600 | drug resistance transporter-like abc domain protein | integral component of membrane;ATP binding;ATPase activity;transport;metabolic process | ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.005G174400 | boron transporter 4 | integral component of membrane;inorganic anion exchanger activity;anion transmembrane transport | | |
| Phvul.005G174800 | late embryogenesis abundant protein group 3 protein | | | |
| Phvul.005G181300 | helix loop helix dna-binding domain protein | protein dimerization activity | | |
| Phvul.005G181700 | ds12 from 2d-page of leaf | amino acid binding;metabolic process | | |
| Phvul.006G001900 | protein tify 5a-like | | | |
| Phvul.006G004800 | duf868 family protein | | | |
| Phvul.006G005100 | probable e3 ubiquitin-protein ligase xerico | zinc ion binding;hydrolase activity;ligase activity;abscisic acid metabolic process | | |
| Phvul.006G007700 | hypothetical protein PHAVU_006G007700g | | | |
| Phvul.006G011600 | l-ascorbate oxidase | extracellular region;copper ion binding;L-ascorbate oxidase activity;oxidation-reduction process | ec:1.10.3;ec:1.10.3.3-oxidase | Ascorbate and aldarate metabolism |
| Phvul.006G014000 | hyp o-arabinosyltransferase homolog | transferase activity;metabolic process | | |
| Phvul.006G016900 | linoleate 13s-lipoxygenase 2-chloroplastic-like | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;metal ion binding;oxylipin biosynthetic process;oxidation-reduction process | ec:1.13.11 | |
| Phvul.006G023100 | nac domain-containing protein 42 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;response to stress;single-organism biosynthetic process;single-organism cellular process;organonitrogen compound biosynthetic process | | |
| Phvul.006G023900 | hxxxd-type acyl-transferase family protein | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.006G028700 | protein transparent testa 12-like | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.006G033000 | probable alpha-mannosidase i mns5 isoform x1 | membrane;mannosyl-oligosaccharide 1,2-alpha-mannosidase activity;calcium ion binding;regulation of mitotic cell cycle;metabolic process | ec:3.2.1;ec:3.2.1.24-alpha-D-mannosidase;ec:3.2.1.113-1,2-alpha-mannosidase | Other glycan degradationVarious types of N-glycan biosynthesis;N-Glycan biosynthesis |
| Phvul.006G033300 | g-type lectin s-receptor-like serine threonine-protein kinase rlk1 | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;carbohydrate binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.006G043100 | duf4228 domain protein | | | |
| Phvul.006G045800 | gdsl-like lipase acylhydrolase | hydrolase activity, acting on ester bonds;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-dicis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.006G046000 | small heat shock chloroplastic-like | | | |

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| Phvul.006G054200 | cytochrome p450 family 71 protein | iron ion binding;heme binding;flavonoid 3',5'-hydroxylase activity;oxidation-reduction process | ec:1.14.13;ec:1.14.13.88-3',5'-hydroxylase | Flavone and flavonol biosynthesis;Flavonoid biosynthesis |
| Phvul.006G054500 | cytochrome p450 family 71 protein | iron ion binding;heme binding;flavonoid 3',5'-hydroxylase activity;oxidation-reduction process | ec:1.14.13;ec:1.14.13.88-3',5'-hydroxylase | Flavone and flavonol biosynthesis;Flavonoid biosynthesis |
| Phvul.006G056300 | retrotransposon-like protein 1 | | | |
| Phvul.006G058600 | cellulose synthase-like protein e1 | plasma membrane;integral component of membrane;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process;para-aminobenzoic acid metabolic process | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.006G060700 | chaperone protein dnaj chloroplastic-like | | | |
| Phvul.006G068600 | microsomal omega-3 fatty acid desaturase | endoplasmic reticulum membrane;integral component of membrane;oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water;unsaturated fatty acid biosynthetic process;oxidation-reduction process | ec:1.14.19 | |
| Phvul.006G069300 | asparagine synthetase | asparagine synthase (glutamine-hydrolyzing) activity;ATP binding;glutamine metabolic process;L-asparagine biosynthetic process | ec:6.3.5.4-synthase (glutamine-hydrolysing) | Alanine, aspartate and glutamate metabolism |
| Phvul.006G075600 | cationic peroxidase 1-like | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.006G075900 | peroxidase 4-like | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.006G078800 | cytochrome p450 partial | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.006G078900 | cytochrome p450 partial | endoplasmic reticulum;integral component of membrane;organelle membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;cyanogenic glycoside biosynthetic process;oxidation-reduction process | | |
| Phvul.006G079100 | cytochrome p450 partial | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.006G079500 | oxalate-- ligase-like | plasmodesma;chloroplast stroma;apoplast;o-succinylbenzoate-CoA ligase activity;4-coumarate-CoA ligase activity;oxalate-CoA ligase activity;positive regulation of seed germination;response to nitrate;seed coat development;nitrate transport;oxalate catabolic process;para-aminobenzoic acid metabolic process;defense response to fungus | ec:6.2.1.8-ligase;ec:6.2.1.26-ligase;ec:6.2.1.12-ligase | Glyoxylate and dicarboxylate metabolismUbiquinone and other terpenoid-quinone biosynthesisUbiquinone and other terpenoid-quinone biosynthesis;Phenylalanine metabolism;Phenylpropanoid biosynthesis |
| Phvul.006G079600 | probable glutathione s-transferase para | glutathione transferase activity;glutathione metabolic process;auxin-activated signaling pathway | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolism |
| Phvul.006G080600 | 60s ribosomal protein l10 | ribosome;structural constituent of ribosome;translation | | |
| Phvul.006G080700 | metal tolerance protein 4 isoform 1 | integral component of membrane;cation transmembrane transporter activity;cation transmembrane transport | | |
| Phvul.006G083700 | protein root primordium defective 1-like | | | |

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| Phvul.006G083800 | probable metal-nicotianamine transporter ysl7 | plasma membrane;integral component of membrane;oligopeptide transporter activity;oligopeptide transport;amino acid transport;transmembrane transport | | |
| Phvul.006G084300 | psbq-like protein chloroplastic | photosystem II oxygen evolving complex;extrinsic component of membrane;calcium ion binding;photosynthesis | | |
| Phvul.006G084600 | cysteine-rich receptor-like protein kinase 2-like | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.006G084900 | cysteine-rich receptor-like protein kinase 2 | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.006G096200 | protein bonzai 3 | calcium-dependent phospholipid binding;negative regulation of cell death | | |
| Phvul.006G100700 | b3 domain-containing protein at5g66980 isoform x1 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.006G102300 | pathogenesis-related protein pr-4-like | chitin binding;defense response to bacterium;defense response to fungus | | |
| Phvul.006G109000 | acidic endochitinase-like | chitinase activity;carbohydrate metabolic process | ec:3.2.1.14-chitodextrinase | Amino sugar and nucleotide sugar metabolism |
| Phvul.006G112300 | non-specific lipid-transfer protein a-like | lipid binding;lipid transport | | |
| Phvul.006G116000 | homeobox-leucine zipper protein athb-12-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.006G116500 | permease transmembrane protein | membrane | | |
| Phvul.006G117300 | nicotianamine synthase | nicotianamine synthase activity;nicotianamine biosynthetic process | ec:2.5.1.43 | |
| Phvul.006G127500 | probable 3-hydroxyisobutyrate mitochondrial isoform x1 | phosphogluconate dehydrogenase (decarboxylating) activity;3-hydroxyisobutyrate dehydrogenase activity;NAD binding;valine catabolic process;oxidation-reduction process | ec:1.1.1.44-dehydrogenase (NADP+-dependent, decarboxylating);ec:1.1.1.31-dehydrogenase | Biosynthesis of antibiotics;Pentose phosphate pathway;Glutathione metabolismValine, leucine and isoleucine degradation |
| Phvul.006G129500 | peroxidase 15 | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.006G133600 | ferric reduction oxidase chloroplastic-like | integral component of membrane;NAD(P)H oxidase activity;oxidation-reduction process | ec:1.6.3.1 | |
| Phvul.006G136800 | web family protein at1g12150-like | | | |
| Phvul.006G137300 | wall associated kinase-like protein | protein kinase activity;ATP binding;polysaccharide binding;protein phosphorylation | | |
| Phvul.006G139100 | 14 kda proline-rich | | | |
| Phvul.006G143300 | tnfr cd27 30 40 95 cysteine-rich region | | | |
| Phvul.006G146900 | plant t7a14-6 protein | | | |
| Phvul.006G148400 | f-box plant-like | | | |
| Phvul.006G150900 | serine threonine-protein kinase pbs1-like | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.006G153100 | extracellular dermal glycoprotein | aspartic-type endopeptidase activity;transferase activity;proteolysis | ec:3.4.23 | |
| Phvul.006G156100 | beta-amyrin synthase | cycloartenol synthase activity;metabolic process | ec:5.4.99.8-synthase | Steroid biosynthesis |

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| Phvul.006G166000 | hypothetical protein PHAVU_006G166000g | | | |
| Phvul.006G168000 | btb poz domain-containing protein at5g03250-like | | | |
| Phvul.006G168600 | duf584 protein | | | |
| Phvul.006G171000 | major intrinsic protein family transporter | integral component of membrane;transporter activity;transport | | |
| Phvul.006G173000 | b-cell lymphoma 6 | | | |
| Phvul.006G173600 | wat1-related protein at3g30340-like | integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.006G176500 | olee1-like protein | extracellular space | | |
| Phvul.006G178300 | 3 -n-debenzoyl-2 -deoxytaxol n-benzoyltransferase | cytoplasm;transferase activity, transferring acyl groups other than amino-acyl groups;response to wounding;systemic acquired resistance;coumarin biosynthetic process;positive regulation of flavonoid biosynthetic process;response to endoplasmic reticulum stress | | |
| Phvul.006G187500 | asparagine synthetase | asparagine synthase (glutamine-hydrolyzing) activity;metabolic process | ec:6.3.5.4-synthase (glutamine-hydrolysing) | Alanine, aspartate and glutamate metabolism |
| Phvul.006G188500 | polyphenol oxidase chloroplastic | catechol oxidase activity;metal ion binding;pigment biosynthetic process;oxidation-reduction process | ec:1.10.3;ec:1.10.3.1-oxidase | Isoquinoline alkaloid biosynthesis;Tyrosine metabolism |
| Phvul.006G188900 | nac transcription factor 25-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.006G189100 | serine carboxypeptidase-like 31 | serine-type carboxypeptidase activity;proteolysis | ec:3.4.21;ec:3.4.16 | |
| Phvul.006G190400 | pap-specific phosphatase hal2-like | 3'(2'),5'-bisphosphate nucleotidase activity;protein dephosphorylation;sulfur compound metabolic process;phosphatidylinositol phosphorylation | ec:3.1.3.7-nucleotidase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1;ec:3.1.3.31 | Sulfur metabolismAminobenzoate degradation |
| Phvul.006G191200 | cfe protein | | | |
| Phvul.006G194200 | beta-amyrin synthase | cycloartenol synthase activity;metabolic process | ec:5.4.99.8-synthase | Steroid biosynthesis |
| Phvul.006G194600 | receptor-like serine threonine-protein kinase sd1-8 | protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation;recognition of pollen | ec:2.7.11 | |
| Phvul.006G197200 | basic form of pathogenesis-related protein 1-like | extracellular region | | |
| Phvul.006G205300 | protein exordium-like 2 | | | |
| Phvul.006G209000 | clathrin assembly protein at1g03050 | clathrin-coated vesicle;1-phosphatidylinositol binding;oxidoreductase activity;clathrin binding;clathrin coat assembly | | |
| Phvul.006G209500 | cytochrome p450 family 71 protein | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.006G210300 | wat1-related protein at1g68170-like | integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.006G215400 | like subfamily b member 13 | unfolded protein binding;protein folding | | |
| Phvul.006G215700 | potassium channel akt2 3 | plasmodesma;integral component of membrane;voltage-gated potassium channel activity;identical protein binding;myo-inositol hexakisphosphate biosynthetic process;regulation of | | |

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| | | membrane potential;potassium ion transmembrane transport | | |
| Phvul.006G216700 | ferredoxin-chloroplastic | electron carrier activity;metal ion binding;2 iron, 2 sulfur cluster binding;electron transport chain | | |
| Phvul.007G013000 | ---NA--- | | | |
| Phvul.007G018700 | zeaxanthin chloroplastic-like | zeaxanthin epoxidase [overall] activity;salicylate 1-monooxygenase activity;zeaxanthin epoxidase activity;antheraxanthin epoxidase activity;oxidation-reduction process | ec:1.14.13;ec:1.14.13.1-1-monooxygenase;ec:1.14.13.90-epoxidase | Naphthalene degradation;Polycyclic aromatic hydrocarbon degradation;Dioxin degradationCarotenoid biosynthesis |
| Phvul.007G021100 | pentatricopeptide repeat-containing protein at2g35130 | | | |
| Phvul.007G025700 | probable carboxylesterase 6 | hydrolase activity;metabolic process | | |
| Phvul.007G031000 | wall associated kinase-like protein | protein serine/threonine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.2-protein-tyrosine kinase;ec:2.7.11;ec:2.7.10 | T cell receptor signaling pathway |
| Phvul.007G032200 | auxin-responsive protein iaa32 | nucleus;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |
| Phvul.007G032800 | amino-acid permease bat1 homolog isoform x1 | integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.007G034500 | mate efflux family protein | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.007G036600 | hypothetical protein PHAVU_007G036600g | | | |
| Phvul.007G036900 | hypothetical protein PHAVU_007G036600g | integral component of membrane | | |
| Phvul.007G044500 | zinc finger protein zat10-like | metal ion binding | | |
| Phvul.007G045400 | glycosyl hydrolase family 10 protein | endo-1,4-beta-xylanase activity;xylan catabolic process | ec:3.2.1.8 | |
| Phvul.007G046200 | hypothetical protein PHAVU_007G046200g | | | |
| Phvul.007G048500 | cysteine-rich receptor-kinase-like protein | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.007G048800 | cysteine-rich receptor-like protein kinase 29-like | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.007G049600 | cysteine-rich receptor-like protein kinase 29 | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.007G050300 | cysteine-rich receptor-kinase-like protein | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.007G050400 | cysteine-rich receptor-kinase-like protein | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.007G056000 | haloacid dehalogenase-like hydrolase | hydrolase activity;metabolic process | | |
| Phvul.007G057900 | late embryogenesis abundant protein d-34-like | | | |
| Phvul.007G058500 | lipid transfer protein | lipid binding;lipid transport | | |

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| Phvul.007G061800 | heat stress transcription factor a-6b-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated;response to heat | | |
| Phvul.007G062500 | meiotic recombination protein dmc1 homolog | nucleus;DNA binding;ATP binding;DNA-dependent ATPase activity;DNA repair;reciprocal meiotic recombination | ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G066200 | protein hothead-like | oxidoreductase activity, acting on CH-OH group of donors;mandelonitrile lyase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:4.1.2.10-lyase | Cyanoamino acid metabolism |
| Phvul.007G067700 | leucine-rich repeat receptor protein kinase exs | intracellular;integral component of membrane;MAP kinase kinase kinase activity;transmembrane receptor protein tyrosine kinase activity;phosphoprotein phosphatase activity;ATP binding;2-alkenal reductase [NAD(P)] activity;MAPK cascade;activation of MAPKK activity;response to molecule of bacterial origin;protein dephosphorylation;microsporogenesis;stomatal complex morphogenesis;anther wall tapetum cell fate specification;peptidyl-tyrosine phosphorylation;oxidation-reduction process | ec:1.3.1.74;ec:3.1.3.16-phosphatase;ec:2.7.10.1;ec:2.7.11.25;ec:2.7.11;ec:2.7.10;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | T cell receptor signaling pathwayAminobenzoate degradation |
| Phvul.007G069800 | low-temperature-induced 65 kda | | | |
| Phvul.007G070000 | copper transport protein family | metal ion binding;metal ion transport | | |
| Phvul.007G071500 | cytochrome p450 family 72 protein | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.007G077300 | g-type lectin s-receptor-like serine threonine-protein kinase at5g24080 | protein serine/threonine kinase activity;calmodulin binding;ATP binding;carbohydrate binding;protein phosphorylation;recognition of pollen | ec:2.7.11 | |
| Phvul.007G082000 | ethylene-responsive transcription factor erf110-like isoform x1 | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G091000 | isoliquiritigenin 2 -o-methyltransferase | licodione 2'-O-methyltransferase activity;quercetin 3-O-methyltransferase activity;isoliquiritigenin 2'-O-methyltransferase activity;protein dimerization activity;caffeate O-methyltransferase activity;methylation | ec:2.1.1.154;ec:2.1.1;ec:2.1.1.76-3-O-methyltransferase;ec:2.1.1.68-O-methyltransferase;ec:2.1.1.65 | Flavone and flavonol biosynthesisPhenylpropanoid biosynthesis |
| Phvul.007G092400 | hypothetical protein PHAVU_007G092400g | | | |
| Phvul.007G096100 | phenylalanine ammonia lyase | cytoplasm;phenylalanine ammonia-lyase activity;L-phenylalanine catabolic process;cinnamic acid biosynthetic process | ec:4.3.1.25-ammonia-lyase;ec:4.3.1.24-ammonia-lyase | Phenylalanine metabolism;Phenylpropanoid biosynthesisPhenylalanine metabolism;Phenylpropanoid biosynthesis |
| Phvul.007G100700 | aba induced plasma membrane protein | | | |
| Phvul.007G109000 | basic 7s globulin-like | aspartic-type endopeptidase activity;transferase activity;proteolysis | ec:3.4.23 | |
| Phvul.007G113300 | reticuline oxidase-like | UDP-N-acetylmuramate dehydrogenase activity;reticuline oxidase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.21.3;ec:1.21.3.3-oxidase;ec:1.1.1.158 | Isoquinoline alkaloid biosynthesis |
| Phvul.007G113700 | kda class iv heat shock protein | endoplasmic reticulum | | |
| Phvul.007G114200 | peroxidase 47 | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.007G116300 | leucine-rich repeat receptor- | integral component of membrane;protein serine/threonine kinase activity;ATP | ec:2.7.11 | |

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| | like protein kinase pxl1 | binding;vasculature development;response to molecule of bacterial origin;protein phosphorylation;signal transduction;procambium histogenesis;stomatal complex morphogenesis;stamen development | | |
| Phvul.007G118300 | probable tyrosine-protein phosphatase at1g05000 | protein tyrosine phosphatase activity;peptidyl-tyrosine dephosphorylation | ec:3.1.3.16-phosphatase;ec:3.1.3.48;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | T cell receptor signaling pathwayAminobenzoate degradation |
| Phvul.007G120200 | ammonium transporter 1 member 2-like | plasma membrane;integral component of membrane;ammonium transmembrane transporter activity;myo-inositol hexakisphosphate biosynthetic process;methylammonium transport;ammonium transmembrane transport | | |
| Phvul.007G120600 | #NOME? | | | |
| Phvul.007G127200 | phosphoenolpyruvate carboxylase kinase 1-like | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.007G127800 | ethylene-responsive transcription factor 1b | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;response to stimulus | | |
| Phvul.007G128100 | ethylene-responsive transcription factor erf098-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G132300 | myb transcription factor | DNA binding | | |
| Phvul.007G133600 | hypothetical protein PHAVU_007G1336002g, partial | | | |
| Phvul.007G135600 | 1-aminocyclopropane-1-carboxylate oxidase | 1-aminocyclopropane-1-carboxylate oxidase activity;naringenin 3-dioxygenase activity;metal ion binding;oxidation-reduction process | ec:1.14.11;ec:1.14.17.4-oxidase;ec:1.14.11.9-3-dioxygenase | Cysteine and methionine metabolismFlavonoid biosynthesis |
| Phvul.007G137600 | ring-h2 finger protein atl70-like | zinc ion binding;ligase activity;metabolic process | | |
| Phvul.007G138300 | oleosin 1 | monolayer-surrounded lipid storage body;integral component of membrane | | |
| Phvul.007G149000 | auxin response factor 18-like isoform x2 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |
| Phvul.007G158600 | wat1-related protein at2g37460-like | integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.007G160000 | exocyst complex component exo70a1-like | exocyst;exocytosis | | |
| Phvul.007G164400 | beta- -xylosyltransferase irx9 | membrane;galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase activity;glucuronoxylan metabolic process;cell wall biogenesis | ec:2.4.1.17-1-naphthol glucuronyltransferase;ec:2.4.1.135-3-beta-glucuronosyltransferase | Drug metabolism - other enzymes;Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Porphyrin and chlorophyll metabolism;Starch and sucrose metabolism;Ascorbate and aldarate metabolism;Retinol metabolism;Steroid hormone biosynthesis;Pentose and glucuronate interconversionsOther types of O-glycan biosynthesis;Glycosaminoglycan biosynthesis - heparan sulfate / heparin;Glycosaminogl |

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| | | | | ycan biosynthesis - chondroitin sulfate / dermatan sulfate |
| Phvul.007G167000 | probable atp-dependent rna helicase ddx56 | | | |
| Phvul.007G170900 | basic 7s globulin | aspartic-type endopeptidase activity;proteolysis | ec:3.4.23 | |
| Phvul.007G181100 | root phototropism protein 3-like | protein ubiquitination | | |
| Phvul.007G183300 | viral a-type inclusion | intracellular membrane-bounded organelle | | |
| Phvul.007G184800 | late embryogenesis abundant protein d-34-like | pollen tube growth | | |
| Phvul.007G185700 | trna(adenine ) chloroplastic | zinc ion binding;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines;deaminase activity;metabolic process | | |
| Phvul.007G192700 | patellin-4-like | phosphatase activity;protein dephosphorylation | ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | Aminobenzoate degradation |
| Phvul.007G192800 | glycinin | intracellular membrane-bounded organelle;cytoplasmic part;nutrient reservoir activity | | |
| Phvul.007G193700 | ethylene-responsive transcription factor 1b | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G193800 | ethylene-responsive transcription factor 1b | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G193900 | ethylene-responsive transcription factor erf098-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G195100 | lob domain-containing protein 16-like | nucleus;viral capsid;structural molecule activity;lateral root formation | | |
| Phvul.007G197500 | hypoxia-responsive family protein | integral component of membrane;transferase activity;metabolic process | | |
| Phvul.007G198700 | probable protein phosphatase 2c 73-like isoform x1 | protein serine/threonine phosphatase activity;protein dephosphorylation | ec:3.1.3.16-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | T cell receptor signaling pathwayAminobenzoate degradation |
| Phvul.007G201100 | hypothetical protein PHAVU_007G201100g | | | |
| Phvul.007G203400 | galactinol synthase | inositol 3-alpha-galactosyltransferase activity;galactose metabolic process | ec:2.4.1.123-3-alpha-galactosyltransferase;ec:2.4.1 | Galactose metabolism |
| Phvul.007G208800 | auxin-responsive aux iaa family protein | nucleus;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |
| Phvul.007G208900 | chitinase 10 | chitinase activity;carbohydrate metabolic process;chitin catabolic process;cell wall macromolecule catabolic process | ec:3.2.1.14-chitodextrinase | Amino sugar and nucleotide sugar metabolism |
| Phvul.007G210400 | pectinesterase pectinesterase inhibitor | cell wall;enzyme inhibitor activity;pectinesterase activity;aspartyl esterase activity;cell wall modification;negative regulation of catalytic activity;pectin catabolic process | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.007G211400 | polygalacturonase glycoside hydrolase family protein | extracellular region;polygalacturonase activity;galacturan 1,4-alpha-galacturonidase activity;carbohydrate metabolic process;cell wall organization | ec:3.2.1.67-1,4-alpha-galacturonidase;ec:3.2.1.15-pectin depolymerase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsStarch and sucrose |

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| Phvul.007G 211900 | myb-related protein 305 | DNA binding | | |
| Phvul.007G 220200 | ubiquitin carboxyl-terminal hydrolase 34-like | | | |
| Phvul.007G 220500 | hypothetical protein PHAVU_007G220 500g | | | |
| Phvul.007G 222400 | hypothetical protein PHAVU_007G222 400g | | | |
| Phvul.007G 222500 | dehydration-responsive element-binding protein 1b-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G 222900 | fructose-bisphosphate cytoplasmic isozyme | fructose-bisphosphate aldolase activity;glycolytic process | ec:4.1.2.13-aldolase | Biosynthesis of antibiotics;Pentose phosphate pathway;Methane metabolism;Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis;Fructose and mannose metabolism |
| Phvul.007G 223100 | phytosulfokine precursor protein | extracellular region;growth factor activity;cell proliferation | | |
| Phvul.007G 225200 | late embryogenesis abundant partial | | | |
| Phvul.007G 228200 | glycinol 4-dimethylallyltransferase-like | integral component of membrane;prenyltransferase activity;metabolic process | ec:2.5.1 | |
| Phvul.007G 228300 | glycinol 4-dimethylallyltransferase-like | integral component of membrane;prenyltransferase activity;metabolic process | ec:2.5.1 | |
| Phvul.007G 228500 | glycinol 4-dimethylallyltransferase-like | integral component of membrane;prenyltransferase activity;metabolic process | ec:2.5.1 | |
| Phvul.007G 230600 | protein trichome birefringence-like 8 | | | |
| Phvul.007G 231800 | transcription factor myb48 | DNA binding | | |
| Phvul.007G 239800 | lectin precursor | carbohydrate binding | | |
| Phvul.007G 242000 | mitogen-activated protein kinase kinase kinase | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.007G 246700 | probable pectinesterase pectinesterase inhibitor 7 | cell wall;enzyme inhibitor activity;pectinesterase activity;aspartyl esterase activity;cell wall modification;negative regulation of catalytic activity;pectin catabolic process | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.007G 248500 | gibberellin 20 oxidase 1 | gibberellin 3-beta-dioxygenase activity;gibberellin-44 dioxygenase activity;oxidation-reduction process | ec:1.14.11.15-3beta-dioxygenase;ec:1.14.11.12-dioxygenase;ec:1.14.11 | Diterpenoid biosynthesisDiterpenoid biosynthesis |
| Phvul.007G 248700 | gibberellin 20 oxidase 1 | metal ion binding;gibberellin-44 dioxygenase activity;oxidation-reduction process | ec:1.14.11.12-dioxygenase;ec:1.14.11 | Diterpenoid biosynthesis |
| Phvul.007G 257300 | cytochrome p450 93a3-like | iron ion binding;flavonoid 3'-monooxygenase activity;heme binding;oxidation-reduction process | ec:1.14.13.21-3'-monooxygenase;ec:1.14.13 | Flavone and flavonol biosynthesis;Flavonoid biosynthesis |
| Phvul.007G 258900 | duf761 domain protein | | | |

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| Phvul.007G259400 | seed maturation protein lea 4 | embryo development | | |
| Phvul.007G259500 | omega-6 fatty acid endoplasmic reticulum isozyme 2 | oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water;delta12-fatty acid dehydrogenase activity;lipid metabolic process;oxidation-reduction process | ec:1.14.99.33;ec:1.14.19 | |
| Phvul.007G269400 | cytokinin riboside 5 -monophosphate phosphoribohydrolase log7 | nucleus;cytosol;hydrolase activity;metabolic process | | |
| Phvul.007G273000 | ethylene-responsive transcription factor 1b | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;response to stimulus | | |
| Phvul.007G275700 | mung bean seed albumin | metal ion binding | | |
| Phvul.007G276100 | achain crystal structure of hemopexin fold protein cp4 from cow pea | metal ion binding | | |
| Phvul.007G276200 | achain crystal structure of hemopexin fold protein cp4 from cow pea | metal ion binding | | |
| Phvul.007G276400 | albumin-2 protein | metal ion binding | | |
| Phvul.007G276500 | albumin-2 protein | metal ion binding | | |
| Phvul.007G276600 | albumin-2 protein | metal ion binding | | |
| Phvul.007G276700 | achain crystal structure of hemopexin fold protein cp4 from cow pea | metal ion binding | | |
| Phvul.007G276900 | phosphatase 2c family protein | protein serine/threonine phosphatase activity;protein dephosphorylation | ec:3.1.3.16-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | T cell receptor signaling pathwayAminobenzoate degradation |
| Phvul.007G277000 | achain crystal structure of hemopexin fold protein cp4 from cow pea | metal ion binding | | |
| Phvul.007G278800 | dentin sialophospho | | | |
| Phvul.007G278900 | calmodulin-like protein 11 | calcium ion binding | | |
| Phvul.007G280700 | transcription factor bhlh92-like | protein dimerization activity | | |
| Phvul.008G005200 | ist1-like protein | response to stress;single-organism cellular process;regulation of biological process | | |
| Phvul.008G007900 | probable serine threonine-protein kinase at1g18390 isoform x1 | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.008G008000 | probable receptor-like protein kinase at1g67000 | binding;kinase activity;phosphorylation | | |
| Phvul.008G008100 | glutamine amidotransferase | GMP synthase (glutamine-hydrolyzing) activity;transferase activity;hydrolase activity;glutamine metabolic process | ec:6.3.5.2-synthase (glutamine-hydrolysing) | Drug metabolism - other enzymes;Purine metabolism |
| Phvul.008G008400 | protein plastid movement impaired 15-like | | | |
| Phvul.008G008800 | hypothetical protein | | | |

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| | PHAVU_008G008800g | | | |
| Phvul.008G012600 | probable mediator of rna polymerase ii transcription subunit 37e | ATP binding;2-alkenal reductase [NAD(P)] activity;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.008G016200 | triphosphate tunel metalloenzyme 3-like | | | |
| Phvul.008G016500 | bag domain protein | chaperone binding | | |
| Phvul.008G016600 | bag domain protein | chaperone binding | | |
| Phvul.008G017100 | wrky transcription factor-like protein | | | |
| Phvul.008G019600 | ethylene response factor | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.008G020100 | family transcriptional | DNA binding;DNA-directed RNA polymerase activity;protein dimerization activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| Phvul.008G023600 | hypothetical protein LR48_Vigan03g004300 | | | |
| Phvul.008G024200 | upf0481 plant-like protein | | | |
| Phvul.008G028000 | transcription factor myb59 | DNA binding | | |
| Phvul.008G028400 | serine-threonine kinase | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G029600 | serine-threonine kinase | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G030300 | hypothetical protein PHAVU_008G030300g | | | |
| Phvul.008G031900 | anthocyanin 5-aromatic acyltransferase | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.008G032200 | anthocyanin 5-aromatic acyltransferase | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.008G032400 | anthocyanin 5-aromatic acyltransferase | malonyltransferase activity;shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.008G036500 | duf679 domain membrane protein | | | |
| Phvul.008G040500 | nitrate transporter -like | membrane;nitrate transmembrane transporter activity;nitrate transport | | |
| Phvul.008G041800 | transcription factor bhlh135 | protein dimerization activity | | |
| Phvul.008G042300 | o-acyltransferase wsd1-like protein | diacylglycerol O-acyltransferase activity;glycerolipid biosynthetic process | ec:2.3.1;ec:2.3.1.20-O-acyltransferase | Cutin, suberine and wax biosynthesis;Glycerolipid metabolism |
| Phvul.008G043400 | lrr receptor-like kinase | transferase activity;2-alkenal reductase [NAD(P)] activity;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.008G044900 | p-loop nucleoside triphosphate hydrolase superfamily protein | ATP binding;hydrolase activity;metabolic process | | |

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| Phvul.008G045100 | homeobox-leucine zipper protein hat3 | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.008G046500 | ethylene-responsive transcription factor 1-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.008G048400 | pentatricopeptide repeat-containing protein chloroplastic | microtubule-severing ATPase activity;metabolic process | ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G050900 | helix loop helix dna-binding domain protein | 2-alkenal reductase [NAD(P)] activity;protein dimerization activity;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.008G055200 | auxin efflux carrier component 8 | endoplasmic reticulum;integral component of membrane;auxin transmembrane transporter activity;pollen development;auxin homeostasis;transmembrane transport;intracellular auxin transport | | |
| Phvul.008G056800 | type receptor kinase | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.008G058400 | 1-aminocyclopropane-1-carboxylate synthase 1-like | 1-aminocyclopropane-1-carboxylate synthase activity;pyridoxal phosphate binding;1-aminocyclopropane-1-carboxylate biosynthetic process | ec:4.4.1.14-synthase | Cysteine and methionine metabolism |
| Phvul.008G062700 | gibberellin 3-beta-dioxygenase 4 | iron ion binding;gibberellin-44 dioxygenase activity;oxidation-reduction process | ec:1.14.11.12-dioxygenase;ec:1.14.11 | Diterpenoid biosynthesis |
| Phvul.008G065500 | duf3245 family protein | | | |
| Phvul.008G065800 | trypsin inhibitor | extracellular region;serine-type endopeptidase inhibitor activity;peptidase activity;proteolysis;negative regulation of endopeptidase activity | | |
| Phvul.008G068300 | (+)-neomenthol dehydrogenase | carbonyl reductase (NADPH) activity;oxidation-reduction process | ec:1.1.1.184-reductase (NADPH) | Arachidonic acid metabolism;Metabolism of xenobiotics by cytochrome P450 |
| Phvul.008G069400 | spx domain-containing membrane protein at4g22990-like | integral component of membrane;transmembrane transport | | |
| Phvul.008G069500 | peptidoglycan-binding domain protein | | | |
| Phvul.008G073200 | polyphenol oxidase chloroplastic | catechol oxidase activity;metal ion binding;pigment biosynthetic process;oxidation-reduction process | ec:1.10.3;ec:1.10.3.1-oxidase | Isoquinoline alkaloid biosynthesis;Tyrosine metabolism |
| Phvul.008G077500 | cysteine-rich receptor-kinase-like protein | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G079700 | receptor-like protein 12 | transferase activity;metabolic process | | |
| Phvul.008G087500 | golgin subfamily a member 5-like | | | |
| Phvul.008G087600 | alanine--glyoxylate aminotransferase 2 homolog mitochondrial-like | alanine-glyoxylate transaminase activity;pyridoxal phosphate binding;metabolic process | ec:2.6.1.44-transaminase | Cysteine and methionine metabolism;Glycine, serine and threonine metabolism;Alanine, aspartate and glutamate metabolism |
| Phvul.008G089400 | tubby c 2 protein | | | |
| Phvul.008G089900 | short-chain dehydrogenase reductase 2a-like | 3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity;xanthoxin dehydrogenase activity;oxidation-reduction process | ec:1.1.1.288-dehydrogenase;ec:2.3.1.85-synthase;ec:1.1.1.100-reductase;ec:1.1.1.1-dehydrogenase | Carotenoid biosynthesisFatty acid biosynthesisBiosynthesis of unsaturated fatty acids;Biotin metabolism;Fatty acid biosynthesisalpha-Linolenic acid metabolism;Drug |

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| | | | | metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Naphthalene degradation;Chloroalkane and chloroalkene degradation;Biosynthesis of antibiotics;Glycolysis / Gluconeogenesis;Fatty acid degradation;Glycine, serine and threonine metabolism;Tyrosine metabolism;Retinol metabolism |
| Phvul.008G093200 | lrr receptor-like kinase | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.008G094400 | nodulation-signaling pathway 2 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.008G098200 | alc-interacting protein | | | |
| Phvul.008G098500 | leucoanthocyanidin dioxygenase-like | iron ion binding;leucocyanidin oxygenase activity;oxidation-reduction process | ec:1.14.11.19-oxygenase;ec:1.14.11 | Flavonoid biosynthesis |
| Phvul.008G103500 | gdsl esterase lipase cprd49-like | hydrolase activity, acting on ester bonds;vegetative to reproductive phase transition of meristem;protein desumoylation;hydrogen peroxide biosynthetic process | | |
| Phvul.008G103600 | gdsl esterase lipase cprd49 | hydrolase activity, acting on ester bonds;vegetative to reproductive phase transition of meristem;protein desumoylation;hydrogen peroxide biosynthetic process | | |
| Phvul.008G104600 | probable envelope carrier chloroplastic | integral component of membrane;transmembrane transport | | |
| Phvul.008G105800 | hypothetical protein PHAVU_008G105800g | | | |
| Phvul.008G106500 | lrr receptor-like kinase family protein | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G108900 | mitochondrial uncoupling protein 1-like | integral component of membrane;mitochondrial membrane;mitochondrial transport | | |
| Phvul.008G109000 | lrr receptor-like serine threonine-protein kinase gso1 | | | |
| Phvul.008G109100 | lrr receptor-like serine threonine-protein kinase gso1 | transferase activity | | |
| Phvul.008G109300 | lrr receptor-like serine threonine-protein kinase gso1 | transferase activity | | |
| Phvul.008G109600 | lrr receptor-like serine threonine-protein kinase gso1 | transferase activity | | |
| Phvul.008G111000 | ppr superfamily protein | | | |
| Phvul.008G113700 | tau class glutathione s-transferase | glutathione transferase activity;metabolic process | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolism |
| Phvul.008G121000 | hypothetical protein | | | |

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| | PHAVU_008G121000g, partial | | | |
| Phvul.008G123300 | hypothetical protein PHAVU_008G123300g | | | |
| Phvul.008G127000 | g-type lectin s-receptor-like serine threonine-kinase | protein kinase activity;ATP binding;carbohydrate binding;protein phosphorylation;recognition of pollen | | |
| Phvul.008G127400 | 2og-fe oxygenase family oxidoreductase | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;metal ion binding;oxidation-reduction process | ec:1.14.11 | |
| Phvul.008G134100 | gibberellin 20 oxidase 1 | iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidation-reduction process | ec:1.14.11 | |
| Phvul.008G134800 | serine threonine-protein kinase oxi1-like | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.008G140000 | hypothetical protein PHAVU_008G140000g | | | |
| Phvul.008G146400 | hypothetical protein PHAVU_008G146400g, partial | | | |
| Phvul.008G155000 | cytochrome p450 family 71 protein | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.008G160400 | transcription factor bhlh086-like | hydrolase activity;protein dimerization activity;metabolic process | | |
| Phvul.008G164100 | wat1-related protein at4g08290-like | integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.008G169600 | aminotransferase ald1-like | L,L-diaminopimelate aminotransferase activity;pyridoxal phosphate binding;lysine biosynthetic process via diaminopimelate | ec:2.6.1.83-aminotransferase | Biosynthesis of antibiotics;Lysine biosynthesis |
| Phvul.008G174800 | hypothetical protein PHAVU_008G174800g | | | |
| Phvul.008G175500 | udp-glucosyltransferase family protein | transferase activity, transferring hexosyl groups;metabolic process | | |
| Phvul.008G176100 | protein exordium-like 2 | | | |
| Phvul.008G176900 | zinc finger cchc domain-containing protein 10-like | | | |
| Phvul.008G183400 | hypothetical protein PHAVU_008G183400g | plasma membrane | | |
| Phvul.008G186200 | voltage-dependent t-type calcium channel subunit alpha- | | | |
| Phvul.008G186800 | probable inorganic phosphate transporter 1-3 | integral component of membrane;inorganic phosphate transmembrane transporter activity;phosphate ion transport;transmembrane transport | | |
| Phvul.008G188100 | hypothetical protein PHAVU_008G188100g | | | |

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| Phvul.008G188200 | ribonuclease p family protein rpp14 family protein isoform 1 | vacuole;ribonuclease P activity;tRNA processing;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1.26.5;ec:3.1.30;ec:3.1.26;ec:3.1 | |
| Phvul.008G191600 | glycerol-3-phosphate acyltransferase 1 | mitochondrion;membrane;glycerol-3-phosphate O-acyltransferase activity;glycerol-3-phosphate 2-O-acyltransferase activity;phosphatidylglycerol biosynthetic process;pollen sperm cell differentiation | ec:2.3.1;ec:2.3.1.15-1-O-acyltransferase | Glycerophospholipid metabolism;Glycerolipid metabolism |
| Phvul.008G194600 | nac domain-containing protein 42 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;response to stress;single-organism biosynthetic process;single-organism cellular process;organonitrogen compound biosynthetic process | | |
| Phvul.008G207900 | zinc-binding alcohol dehydrogenase family protein | zinc ion binding;S-(hydroxymethyl)glutathione dehydrogenase activity;oxidation-reduction process | ec:1.1.1.284-dehydrogenase | Methane metabolism |
| Phvul.008G213800 | 1-aminocyclopropane-1-carboxylate oxidase | 1-aminocyclopropane-1-carboxylate oxidase activity;naringenin 3-dioxygenase activity;metal ion binding;oxidation-reduction process | ec:1.14.11;ec:1.14.17.4-oxidase;ec:1.14.11.9-3-dioxygenase | Cysteine and methionine metabolismFlavonoid biosynthesis |
| Phvul.008G213900 | 1-aminocyclopropane-1-carboxylate oxidase | 1-aminocyclopropane-1-carboxylate oxidase activity;naringenin 3-dioxygenase activity;metal ion binding;oxidation-reduction process | ec:1.14.11;ec:1.14.17.4-oxidase;ec:1.14.11.9-3-dioxygenase | Cysteine and methionine metabolismFlavonoid biosynthesis |
| Phvul.008G214200 | 1-aminocyclopropane-1-carboxylate oxidase | 1-aminocyclopropane-1-carboxylate oxidase activity;L-ascorbic acid binding;naringenin 3-dioxygenase activity;metal ion binding;ethylene biosynthetic process;fruit ripening;oxidation-reduction process | ec:1.14.11;ec:1.14.17.4-oxidase;ec:1.14.11.9-3-dioxygenase | Cysteine and methionine metabolismFlavonoid biosynthesis |
| Phvul.008G219800 | neuronal pas domain-containing protein 4 | | | |
| Phvul.008G220400 | dehydration-responsive element-binding protein 2c | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.008G223500 | leucoanthocyanidin dioxygenase-like protein | iron ion binding;methyltransferase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;methylation;oxidation-reduction process | ec:1.14.11 | |
| Phvul.008G224100 | phosphoinositide phospholipase c 6 | intracellular;phosphatidylinositol phospholipase C activity;signal transducer activity;lipid catabolic process;intracellular signal transduction | ec:3.1.4.11-phospholipase C;ec:3.1;ec:3.1.1 | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.008G225600 | hypothetical protein PHAVU_008G225600g | | | |
| Phvul.008G226200 | uncharacterized acetyltransferase at3g50280 | shikimate O-hydroxycinnamoyltransferase activity;anthranilate N-benzoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.144;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.008G227100 | glucan endo- -beta-glucosidase 12 | hydrolase activity, hydrolyzing O-glycosyl compounds;carbohydrate metabolic process | | |
| Phvul.008G228000 | kda class i heat shock | | | |
| Phvul.008G228100 | kda class i heat shock | | | |
| Phvul.008G228900 | cucumisin-like isoform x1 | serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.008G229100 | cucumisin-like isoform x1 | serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.008G238200 | hypothetical protein PHAVU_008G238200g | | | |
| Phvul.008G242900 | protein yls9 | | | |

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| Phvul.008G249500 | peroxidase 4 | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.008G249900 | cationic peroxidase 1-like | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.008G251000 | wound-induced-like protein | | | |
| Phvul.008G251400 | cation h(+) antiporter 15-like | integral component of membrane;monovalent cation:proton antiporter activity;potassium ion transport;sodium ion transport;hydrogen ion transmembrane transport | | |
| Phvul.008G251500 | duf4228 domain protein | | | |
| Phvul.008G251700 | exocyst subunit exo70 family protein | Golgi apparatus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.008G252000 | achain crystal structure of hemopexin fold protein cp4 from cow pea | metal ion binding | | |
| Phvul.008G256600 | udp-glycosyltransferase 87a1-like | indole-3-acetate beta-glucosyltransferase activity;limonoid glucosyltransferase activity;metabolic process | ec:2.4.1.121;ec:2.4.1;ec:2.4.1.210 | |
| Phvul.008G259700 | mitogen-activated protein kinase kinase kinase npk1-like | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.008G261200 | protein early flowering 4-like | nucleus;protein homodimerization activity;positive regulation of circadian rhythm | | |
| Phvul.008G264000 | duf868 family protein | | | |
| Phvul.008G268200 | geranyl-diphosphate synthase | | | |
| Phvul.008G270500 | probable wrky transcription factor 31 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.008G273800 | receptor-like protein | | | |
| Phvul.008G275400 | nucleic acid binding | | | |
| Phvul.008G279600 | cellulose synthase-like protein e1 | integral component of membrane;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.008G279800 | cellulose synthase-like protein e6 | integral component of membrane;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.008G282200 | heavy metal transport detoxification superfamily protein | metal ion binding;single-organism process | | |
| Phvul.008G282600 | probable galactinol--sucrose galactosyltransferase 1 | galactinol-raffinose galactosyltransferase activity;metabolic process | ec:2.4.1;ec:2.4.1.67-galactosyltransferase | Galactose metabolism |
| Phvul.008G285200 | hypothetical protein PHAVU_008G285200g | | | |
| Phvul.008G287200 | polyketide reductase | alcohol dehydrogenase (NADP+) activity;6'-deoxychalcone synthase activity;flavonoid biosynthetic process;oxidation-reduction process | ec:2.3.1.170-synthase;ec:1.1.1;ec:1.1.1.2-dehydrogenase (NADP+) | Flavonoid biosynthesisBiosynthesis of antibiotics;Glycolysis / Gluconeogenesis;Glycerolipid metabolism;Caprolactam degradation;Pentose and glucuronate interconversions |

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| Phvul.008G290700 | vq motif-containing protein 22-like | | | |
| Phvul.009G005300 | late embryogenesis abundant | response to stress;response to water | | |
| Phvul.009G012700 | beta-galactosidase 5 | beta-galactosidase activity;carbohydrate binding;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.23-lactase (ambiguous) | Other glycan degradation;Glycosphingolipid biosynthesis - ganglio series;Sphingolipid metabolism;Galactose metabolism;Glycosaminoglycan degradation |
| Phvul.009G017700 | pathogenesis-related thaumatin family protein | | | |
| Phvul.009G018300 | gdsl esterase lipase exl3 | lipase activity;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase;ec:3.1.1 | Carotenoid biosynthesis |
| Phvul.009G024300 | specific tissue protein | | | |
| Phvul.009G027700 | lob domain-containing protein 36-like | carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity;regulation of transcription, DNA-templated;metabolic process;proximal/distal pattern formation;leaf morphogenesis;petal development | ec:6.3.5.5-synthase (glutamine-hydrolysing) | Alanine, aspartate and glutamate metabolism;Pyrimidine metabolism |
| Phvul.009G042800 | voltage-dependent t-type calcium channel subunit alpha- | chloroplast | | |
| Phvul.009G043200 | wrky transcription factor 55 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.009G046500 | small heat shock chloroplastic | chloroplast;protein folding;heat acclimation | | |
| Phvul.009G054300 | hypothetical protein PHAVU_009G054300g, partial | nucleotidyltransferase activity;metabolic process | | |
| Phvul.009G054400 | probable trehalose-phosphate phosphatase c isoform x1 | trehalose-phosphatase activity;transferase activity, transferring glycosyl groups;trehalose biosynthetic process;protein dephosphorylation | ec:3.1.3.12-trehalose 6-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | Starch and sucrose metabolismAminobenzoate degradation |
| Phvul.009G057300 | aldehyde dehydrogenase | | | |
| Phvul.009G059900 | hypothetical protein PHAVU_009G059900g | | | |
| Phvul.009G061600 | cytochrome p450 82c4-like | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.009G062600 | early nodulin-55-2-like | electron carrier activity | | |
| Phvul.009G064900 | chlorophyll a-b binding protein chloroplastic | photosystem II;chloroplast thylakoid membrane;photosystem I antenna complex;integral component of membrane;chlorophyll binding;pigment binding;metal ion binding;rRNA processing;photosynthesis, light harvesting in photosystem I;thylakoid membrane organization;photosystem II assembly;protein-chromophore linkage | | |
| Phvul.009G066300 | uncharacterized acetyltransferase at3g50280-like | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |

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| Phvul.009G066900 | uncharacterized acetyltransferase at3g50280-like | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.009G067900 | probable carbohydrate esterase at4g34215 | | | |
| Phvul.009G068000 | transcription factor myb44-like | DNA binding | | |
| Phvul.009G075100 | branched-chain amino acid aminotransferase | L-leucine transaminase activity;L-valine transaminase activity;L-isoleucine transaminase activity;branched-chain amino acid metabolic process;toxin catabolic process | ec:2.6.1.42-transaminase | Valine, leucine and isoleucine biosynthesis;Biosynthesis of antibiotics;Valine, leucine and isoleucine degradation;Pantothenate and CoA biosynthesis;Glucosinolate biosynthesis;Cysteine and methionine metabolism |
| Phvul.009G075500 | zinc finger ccch domain-containing protein 23-like | metal ion binding | | |
| Phvul.009G078300 | heat shock factor protein hsf30 isoform x1 | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;transcription regulatory region DNA binding;response to hypoxia;heat acclimation;cellular response to unfolded protein;cellular metabolic process;positive regulation of transcription, DNA-templated | | |
| Phvul.009G080200 | kda class ii heat shock protein | | | |
| Phvul.009G087700 | hypothetical protein PHAVU_009G087700g | | | |
| Phvul.009G094000 | eg45-like domain containing protein 2 | | | |
| Phvul.009G094600 | upf0481 protein | | | |
| Phvul.009G100300 | flowering-promoting factor 1-like | | | |
| Phvul.009G104200 | ef hand calcium-binding family protein | calcium ion binding | | |
| Phvul.009G108300 | bark storage protein a-like | catalytic activity;nucleoside metabolic process | | |
| Phvul.009G108700 | probable lactoylglutathione chloroplast | chloroplast stroma;stromule;thylakoid lumen;lactoylglutathione lyase activity;metal ion binding;dioxygenase activity;oxidation-reduction process | ec:4.4.1.5-lyase | Pyruvate metabolism |
| Phvul.009G109100 | carotenoid (9 )-cleavage dioxygenase 1-like | dioxygenase activity;oxidation-reduction process | | |
| Phvul.009G111500 | nadp-dependent malic enzyme | cytoplasm;malate dehydrogenase (decarboxylating) (NAD+) activity;malate dehydrogenase (decarboxylating) (NADP+) activity;oxaloacetate decarboxylase activity;metal ion binding;NAD binding;malate metabolic process;oxidation-reduction process | ec:1.1.1.40-dehydrogenase (oxaloacetate-decarboxylating) (NADP+);ec:4.1.1.3-decarboxylase;ec:1.1.1.39-dehydrogenase (decarboxylating);ec:1.1.1.38-dehydrogenase (oxaloacetate-decarboxylating) | Pyruvate metabolism;Carbon fixation in photosynthetic organismsPyruvate metabolismPyruvate metabolism;Carbon fixation in photosynthetic organismsPyruvate metabolism |

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| Phvul.009G116800 | hypothetical protein PHAVU_009G116800g | | | |
| Phvul.009G118800 | plant phospholipase-like protein | | | |
| Phvul.009G120400 | nodulin family protein | | | |
| Phvul.009G120500 | probable endo- - beta-xylanase c | endo-1,4-beta-xylanase activity;xylan catabolic process | ec:3.2.1.8 | |
| Phvul.009G121000 | nitrate reductase | nitrate reductase (NADH) activity;heme binding;molybdenum ion binding;molybdopterin cofactor binding;nitrate reductase (NADPH) activity;nitric oxide biosynthetic process;nitrate assimilation;oxidation-reduction process | ec:1.7.1.3-reductase (NADPH);ec:1.7.1.1-reductase (NADH);ec:1.7.99.4-reductase | Nitrogen metabolismNitrogen metabolismNitrogen metabolism |
| Phvul.009G125100 | photosystem ii 22 kda chloroplastic | PSII associated light-harvesting complex II;chlorophyll binding;xanthophyll binding;maltose metabolic process;rRNA processing;thylakoid membrane organization;stomatal complex morphogenesis;nonphotochemical quenching;photosystem II assembly;starch biosynthetic process;cysteine biosynthetic process;positive regulation of catalytic activity | | |
| Phvul.009G125900 | nac domain-containing protein 2 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.009G127900 | metal transporter nramp5-like | membrane;transporter activity;transport | | |
| Phvul.009G131000 | chalcone synthase | nucleus;endoplasmic reticulum;plant-type vacuole membrane;naringenin-chalcone synthase activity;response to gravity;anthocyanin-containing compound biosynthetic process;response to sucrose;auxin polar transport;response to UV-B | ec:2.3.1.74-synthase | Flavonoid biosynthesis |
| Phvul.009G132900 | 2-oxoisovalerate dehydrogenase subunit alpha mitochondrial-like | 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity;oxidation-reduction process | ec:1.2.4.4-dehydrogenase (2-methylpropanoyl-transferring) | Biosynthesis of antibiotics;Valine, leucine and isoleucine degradation;Propanoate metabolism |
| Phvul.009G135300 | wat1-related protein at1g70260-like | integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.009G136000 | glycolipid transfer protein family protein | cytoplasm;glycolipid transporter activity;glycolipid binding;glycolipid transport | | |
| Phvul.009G137900 | ethylene-responsive transcription factor erf114 | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.009G140700 | peroxidase 4-like | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.009G142500 | potassium transporter 2 | nucleus;integral component of membrane;DNA binding;zinc ion binding;potassium ion transmembrane transporter activity;chloroplast organization;myo-inositol hexakisphosphate biosynthetic process;positive regulation of transcription, DNA-templated;potassium ion transmembrane transport | | |
| Phvul.009G143700 | rho gtpase-activating protein ren1-like isoform x2 | GTPase activator activity;signal transduction;positive regulation of GTPase activity | | |
| Phvul.009G152400 | kda class i heat shock protein | cytoplasm | | |
| Phvul.009G152500 | kda class i heat shock protein | cytoplasm | | |
| Phvul.009G153300 | hypothetical protein PHAVU_009G153300g | integral component of membrane | | |
| Phvul.009G155800 | pentatricopeptide repeat-containing protein | microtubule-severing ATPase activity;metabolic process | ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec | Purine metabolismPurine |

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| | | | :3.6.4.3;ec:3.6.1.15-phosphatase | metabolism;Thiamine metabolism |
| Phvul.009G156500 | cation h(+) antiporter 15 | integral component of membrane;monovalent cation:proton antiporter activity;potassium ion transport;sodium ion transport;regulation of pH;plant-type cell wall modification;pollen tube growth;hydrogen ion transmembrane transport | | |
| Phvul.009G158100 | scorpion toxin-like knottin superfamily protein | defense response | | |
| Phvul.009G160300 | hypothetical protein PHAVU_009G160300g | | | |
| Phvul.009G161000 | ethylene-responsive transcription factor erf114-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.009G162000 | transcription factor ice1-like | 2-alkenal reductase [NAD(P)] activity;protein dimerization activity;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.009G168000 | hypothetical protein PHAVU_009G168000g | | | |
| Phvul.009G173900 | hypothetical protein PHAVU_009G173900g | | | |
| Phvul.009G176400 | lrr receptor-like serine threonine-protein kinase gso1 | integral component of membrane;kinase activity;2-alkenal reductase [NAD(P)] activity;phosphorylation;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.009G179600 | transcription factor bhlh36 | DNA binding;protein dimerization activity | | |
| Phvul.009G182300 | betaine aldehyde dehydrogenase | nucleotide binding;betaine-aldehyde dehydrogenase activity;aminobutyraldehyde dehydrogenase activity;1-pyrroline dehydrogenase activity;oxidation-reduction process | ec:1.2.1.19-dehydrogenase;ec:1.2.1.8-dehydrogenase;ec:1.2.1.3-dehydrogenase (NAD+) | Arginine and proline metabolism;beta-Alanine metabolismGlycine, serine and threonine metabolismArginine and proline metabolism;Chloroalkane and chloroalkene degradation;Pyruvate metabolism;Biosynthesis of antibiotics;Tryptophan metabolism;Valine, leucine and isoleucine degradation;Limonene and pinene degradation;beta-Alanine metabolism;Lysine degradation;Glycolysis / Gluconeogenesis;Fatty acid degradation;Glycerolipid metabolism;Ascorbate and aldarate metabolism;Histidine metabolism;Pentose and glucuronate interconversions |
| Phvul.009G186700 | disulfide bond formation protein b | | | |
| Phvul.009G196200 | zein-binding protein | | | |
| Phvul.009G197000 | ids4-like protein | cellular response to phosphate starvation | | |
| Phvul.009G207800 | non-functional nadph-dependent | oxidoreductase activity;transferase activity, transferring acyl groups;oxidation-reduction process | | |

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| | codeinone reductase 2-like | | | |
| Phvul.009G210900 | auxin efflux carrier component 2 | integral component of membrane;transmembrane transport | | |
| Phvul.009G211200 | uncharacterized protein CPUR_03533 | | | |
| Phvul.009G224300 | hypothetical protein PHAVU_009G224300g | | | |
| Phvul.009G239700 | g-type lectin s-receptor-like serine threonine-protein kinase | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;carbohydrate binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.009G239900 | g-type lectin s-receptor-like serine threonine-protein kinase | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;carbohydrate binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.009G240500 | upf0481 protein at3g47200-like | | | |
| Phvul.009G240600 | glycoside hydrolase family 18 protein | hydrolase activity, hydrolyzing O-glycosyl compounds;carbohydrate metabolic process | | |
| Phvul.009G244000 | isoflavone 2 -hydroxylase-like | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.009G259600 | homeodomain-like superfamily protein isoform 2 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;circadian rhythm;response to cold;response to red or far red light;myo-inositol hexakisphosphate biosynthetic process;negative regulation of circadian rhythm;regulation of protein homodimerization activity;negative regulation of transcription, DNA-templated;positive regulation of transcription, DNA-templated;long-day photoperiodism, flowering | | |
| Phvul.009G261400 | ring-h2 finger protein atl3 | zinc ion binding | | |
| Phvul.010G000300 | leucoanthocyanidin dioxygenase-like | iron ion binding;leucocyanidin oxygenase activity;oxidation-reduction process | ec:1.14.11.19-oxygenase;ec:1.14.11 | Flavonoid biosynthesis |
| Phvul.010G003400 | hypothetical protein PHAVU_010G003400g | | | |
| Phvul.010G004000 | protein nrt1 ptr family -like | membrane;transporter activity;transport | | |
| Phvul.010G004300 | protein nrt1 ptr family -like | membrane;transporter activity;transport | | |
| Phvul.010G004900 | disease resistance rpp13-like protein 1 | hydrolase activity;ADP binding;metabolic process | | |
| Phvul.010G005600 | plant t7h20-70 protein | | | |
| Phvul.010G008800 | glycinol 4-dimethylallyltransferase-like | plastid;integral component of membrane;prenyltransferase activity;cellular amino acid metabolic process;fatty acid metabolic process;cellular aromatic compound metabolic process;coenzyme metabolic process;sulfur compound metabolic process;lipid biosynthetic process;heterocycle metabolic process;regulation of biological process;monocarboxylic acid biosynthetic process;organic cyclic compound metabolic process | ec:2.5.1 | |
| Phvul.010G009400 | protein nrt1 ptr family -like | integral component of membrane;transporter activity;oligopeptide transport | | |
| Phvul.010G012300 | type 2 metallothionein | hydrolase activity;metal ion binding;metabolic process | | |
| Phvul.010G012900 | cytochrome p450 | integral component of membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |

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| Phvul.010G013000 | cytochrome p450 | integral component of membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.010G013100 | isoflavone 2 -hydroxylase | integral component of membrane;iron ion binding;heme binding;isoflavone 2'-hydroxylase activity;oxidation-reduction process | ec:1.14.13;ec:1.14.13.89-2'-hydroxylase | Isoflavonoid biosynthesis |
| Phvul.010G013700 | verticillium wilt disease resistance protein | transferase activity;metabolic process | | |
| Phvul.010G014100 | vinorine synthase-like | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.010G016300 | transcriptional regulator rabbit ears | metal ion binding | | |
| Phvul.010G019000 | hypothetical protein PHAVU_010G019000g, partial | | | |
| Phvul.010G019300 | hypothetical protein PHAVU_010G019300g | | | |
| Phvul.010G021000 | gdsl esterase lipase 1 | hydrolase activity, acting on ester bonds;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.010G022000 | ninja-family protein afp2-like | | | |
| Phvul.010G031900 | cysteine-rich rlk (receptor-like kinase) protein | protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.010G036100 | feruloyl ortho-hydroxylase 1-like | iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidation-reduction process | ec:1.14.11 | |
| Phvul.010G050500 | ethylene-responsive transcription factor 13-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;response to stress;response to abiotic stimulus;response to abscisic acid;response to jasmonic acid;ethylene-activated signaling pathway;response to chitin;regulation of programmed cell death;cellular response to acid chemical;cellular response to oxygen-containing compound | | |
| Phvul.010G050700 | ap2-domain dna-binding protein | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.010G051100 | uncharacterized transporter ybr287w-like | integral component of membrane;transmembrane transport | | |
| Phvul.010G054200 | tmv resistance protein n | ADP binding;signal transduction | | |
| Phvul.010G054400 | tmv resistance protein n-like | ADP binding;signal transduction | | |
| Phvul.010G056200 | squamosa promoter-binding-like protein 7 | nucleus;DNA binding | | |
| Phvul.010G057900 | wrky transcription factor | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.010G063800 | disease resistance response protein 206 | | | |
| Phvul.010G073500 | phosphatidylethanolamine-binding protein | seed dormancy process;myo-inositol hexakisphosphate biosynthetic process;positive regulation of transcription, DNA-templated | | |

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| Phvul.010G073900 | hypothetical protein PHAVU_010G073900g | | | |
| Phvul.010G077200 | cytochrome p450 family 71 protein | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.010G083700 | myeloid leukemia factor 1 | | | |
| Phvul.010G093500 | bon1-associated-like protein | | | |
| Phvul.010G096900 | f-box lrr-repeat protein at5g41630-like | | | |
| Phvul.010G097800 | math domain protein | | | |
| Phvul.010G101500 | oxidoreductase ferric-chelate reductase | integral component of membrane;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.010G103900 | 1-aminocyclopropane-1-carboxylate synthase 1-like | 1-aminocyclopropane-1-carboxylate synthase activity;pyridoxal phosphate binding;1-aminocyclopropane-1-carboxylate biosynthetic process | ec:4.4.1.14-synthase | Cysteine and methionine metabolism |
| Phvul.010G107400 | bag family molecular chaperone regulator 6 | chaperone binding | | |
| Phvul.010G111000 | mitogen-activated protein kinase kinase kinase 7-like | intracellular;MAP kinase kinase kinase activity;protein serine/threonine/tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity | ec:2.7.12.1;ec:2.7.11.25;ec:2.7.11 | |
| Phvul.010G111200 | protein suppressor of phya-105 1 | protein kinase activity;ATP binding;ligase activity;2-alkenal reductase [NAD(P)] activity;protein phosphorylation;multicellular organism development;response to light stimulus;regulation of biological process;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.010G117200 | homeobox-leucine zipper protein athb-12-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.010G120200 | caffeic acid o-methyltransferase | O-methyltransferase activity;quercetin 3-O-methyltransferase activity;protein dimerization activity;methylation | ec:2.1.1;ec:2.1.1.76-3-O-methyltransferase | Flavone and flavonol biosynthesis |
| Phvul.010G122500 | ring-h2 finger protein atl60 | zinc ion binding;ligase activity;metabolic process | | |
| Phvul.010G124000 | duf581 family protein | linoleate 13S-lipoxygenase activity;metal ion binding;oxidation-reduction process | ec:1.13.11.12-13S-lipoxygenase;ec:1.13.11 | alpha-Linolenic acid metabolism;Linoleic acid metabolism |
| Phvul.010G124800 | gdsl esterase lipase 5-like | lipase activity;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;proline transport;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase;ec:3.1.1 | Carotenoid biosynthesis |
| Phvul.010G125300 | kda class iii heat shock protein | protein folding | | |
| Phvul.010G127500 | probable inactive leucine-rich repeat receptor-like protein kinase at5g20690 | intracellular;integral component of membrane;MAP kinase kinase kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity;peptidyl-tyrosine phosphorylation | ec:2.7.10.1;ec:2.7.11.25;ec:2.7.11;ec:2.7.10 | |
| Phvul.010G129900 | auxin-binding protein abp19a | extracellular region;cell;extracellular matrix;manganese ion binding;nutrient reservoir activity;stomatal complex morphogenesis;cellular cation homeostasis;divalent metal ion transport | | |
| Phvul.010G135800 | seed linoleate 9s-lipoxygenase | cytoplasm;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;metal ion binding;oxylipin biosynthetic process;oxidation-reduction process | ec:1.13.11 | |
| Phvul.010G136700 | disease resistance protein (tir-nbs-lrr class) | ADP binding;signal transduction | | |

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| Phvul.010G137300 | calmodulin-binding family protein | | | |
| Phvul.010G139800 | phospholipase d epsilon | membrane;phospholipase D activity;calcium ion binding;N-acylphosphatidylethanolamine-specific phospholipase D activity;lipid catabolic process;phosphatidylcholine metabolic process | ec:3.1.4.4-D;ec:3.1;ec:3.1.1 | Ether lipid metabolism;Glycerophospholipid metabolism |
| Phvul.010G140800 | inorganic pyrophosphatase 2 | pyridoxal phosphatase activity;protein dephosphorylation | ec:3.1.3.74-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | Vitamin B6 metabolismAminobenzoate degradation |
| Phvul.010G144200 | stem 28 kda glycoprotein | acid phosphatase activity;protein dephosphorylation | ec:3.1.3.2-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | Aminobenzoate degradationAminobenzoate degradation |
| Phvul.010G144600 | stem 28 kda glycoprotein | acid phosphatase activity;protein dephosphorylation | ec:3.1.3.2-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | Aminobenzoate degradationAminobenzoate degradation |
| Phvul.010G152300 | probable 2-oxoglutarate-dependent dioxygenase aop1 | iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidation-reduction process | ec:1.14.11 | |
| Phvul.010G152400 | probable 2-oxoglutarate-dependent dioxygenase aop1 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;metal ion binding;oxidation-reduction process | ec:1.14.11 | |
| Phvul.010G152800 | root phototropism protein 3-like | | | |
| Phvul.010G154300 | duf761 domain protein | | | |
| Phvul.010G154400 | lactoylglutathione lyase glyoxalase i family protein | transferase activity;lyase activity;metabolic process | | |
| Phvul.010G155300 | kda heat shock mitochondrial | | | |
| Phvul.010G156200 | palmitoyl-monogalactosyldiacylglycerol delta-7 chloroplastic | integral component of membrane;stearoyl-CoA 9-desaturase activity;fatty acid biosynthetic process;oxidation-reduction process | ec:1.14.19;ec:1.14.19.1-9-desaturase | Biosynthesis of unsaturated fatty acids |
| Phvul.010G158400 | helix loop helix dna-binding domain protein | 2-alkenal reductase [NAD(P)] activity;protein dimerization activity;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.010G160700 | bifunctional dihydroflavonol 4-reductase flavanone 4-reductase | cinnamoyl-CoA reductase activity;dihydrokaempferol 4-reductase activity;coenzyme binding;oxidation-reduction process | ec:1.1.1.219-4-reductase;ec:1.2.1.44-reductase | Flavonoid biosynthesisPhenylpropanoid biosynthesis |
| Phvul.010G160900 | cbl-interacting kinase | protein serine/threonine kinase activity;ATP binding;protein phosphorylation;signal transduction | ec:2.7.11 | |
| Phvul.010G161100 | wrky transcription factor 40 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.010G161300 | photosynthetic ndh subunit of subcomplex b chloroplastic | chloroplast thylakoid membrane;NAD(P)H dehydrogenase complex (plastoquinone);transferase activity, transferring glycosyl groups;pentose-phosphate shunt;photosynthetic electron transport in photosystem I;photosystem II assembly;carotenoid biosynthetic process | | |
| Phvul.010G162900 | #NOME? | oxidoreductase activity, acting on CH-OH group of donors;mandelonitrile lyase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:4.1.2.10-lyase | Cyanoamino acid metabolism |
| Phvul.010G163600 | hypothetical protein PHAVU_010G163600g | | | |

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| Phvul.011G008100 | lrr receptor-like kinase family protein | integral component of membrane;protein kinase activity;ATP binding;oxidoreductase activity;protein phosphorylation;single-organism metabolic process;regulation of cellular process | | |
| Phvul.011G008600 | pp890_soybn ame: full=protein propep890 short=890 contains: ame: full=peptide ep890 flags: precursor | | | |
| Phvul.011G012600 | duf642 family protein | | | |
| Phvul.011G014000 | cytokinin dehydrogenase 6-like | UDP-N-acetylmuramate dehydrogenase activity;cytokinin dehydrogenase activity;flavin adenine dinucleotide binding;cytokinin metabolic process;oxidation-reduction process | ec:1.5.99.12-dehydrogenase;ec:1.1.1.158 | Zeatin biosynthesis |
| Phvul.011G015000 | scarecrow-like protein 3 isoform x1 | nucleus;transcription factor activity, transcription factor binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.011G015400 | hypothetical protein PHAVU_011G015400g | | | |
| Phvul.011G016100 | small heat shock protein | mitochondrion | | |
| Phvul.011G016200 | small heat shock protein | | | |
| Phvul.011G022300 | cinnamyl-alcohol dehydrogenase family protein | cinnamoyl-CoA reductase activity;coenzyme binding;oxidation-reduction process | ec:1.2.1.44-reductase | Phenylpropanoid biosynthesis |
| Phvul.011G025800 | aquaporin tip1-2-like | integral component of membrane;transporter activity;transport | | |
| Phvul.011G026200 | hypothetical protein PHAVU_011G026200g | | | |
| Phvul.011G026700 | proline-rich protein 4-like | | | |
| Phvul.011G029200 | hypothetical protein PHAVU_011G029200g | | | |
| Phvul.011G030200 | lignin-forming anionic peroxidase | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.011G033800 | chaperone protein dnaj chloroplastic-like | | | |
| Phvul.011G037900 | auxin-induced protein 15a-like | response to auxin | | |
| Phvul.011G044700 | allergenic isoflavone reductase-like protein bet protein | oxidoreductase activity;oxidation-reduction process | | |
| Phvul.011G047800 | cytochrome c biogenesis protein chloroplastic | maltose metabolic process;phosphatidylglycerol biosynthetic process;leaf morphogenesis;thylakoid membrane organization;carotenoid biosynthetic process;mRNA modification;starch biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;cell differentiation;positive regulation of catalytic activity | | |
| Phvul.011G049900 | myosin heavy chain kinase c | | | |
| Phvul.011G051300 | orn lys arg decarboxylase major region protein | lysine decarboxylase activity;metabolic process | ec:4.1.1.18-decarboxylase | Lysine degradation;Tropane, piperidine and pyridine alkaloid biosynthesis |
| Phvul.011G055900 | beta-glucosidase 12-like | beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |

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|---|---|---|---|---|
| Phvul.011G056100 | beta-glucosidase 12-like | beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.011G060400 | copper transporter 6-like | integral component of membrane;copper ion transmembrane transporter activity;copper ion transmembrane transport | | |
| Phvul.011G060500 | copper transporter 6-like | integral component of membrane;copper ion transmembrane transporter activity;copper ion transmembrane transport | | |
| Phvul.011G062900 | haloacid dehalogenase-like hydrolase | hydrolase activity;metabolic process | | |
| Phvul.011G066800 | zinc finger protein zat11-like | metal ion binding | | |
| Phvul.011G067200 | tonoplast intrinsic protein | integral component of membrane;urea transmembrane transporter activity;water channel activity;water transport;urea transmembrane transport | | |
| Phvul.011G070400 | hypothetical protein PHAVU_011G070400g | | | |
| Phvul.011G072200 | lob domain-containing protein 1-like | carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity;metabolic process | ec:6.3.5.5-synthase (glutamine-hydrolysing) | Alanine, aspartate and glutamate metabolism;Pyrimidine metabolism |
| Phvul.011G076400 | bud13 homolog | nucleus;cytosol | | |
| Phvul.011G077600 | beta-galactosidase 8 isoform 1 | cell wall;beta-galactosidase activity;carbohydrate binding;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.23-lactase (ambiguous) | Other glycan degradation;Glycosphingolipid biosynthesis - ganglio series;Sphingolipid metabolism;Galactose metabolism;Glycosaminoglycan degradation |
| Phvul.011G081800 | lysm domain receptor-like kinase 4 | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.011G083500 | high affinity nitrate transporter | integral component of membrane;transmembrane transport | | |
| Phvul.011G084300 | 4-coumarate: ligase-like protein | peroxisome;fatty-acyl-CoA synthase activity;4-coumarate-CoA ligase activity;Photinus-luciferin 4-monooxygenase (ATP-hydrolyzing) activity;jasmonic acid biosynthetic process;oxidation-reduction process | ec:2.3.1;ec:1.13.12;ec:2.3.1.86-synthase;ec:1.13.12.7;ec:6.2.1.12-ligase | Fatty acid biosynthesisUbiquinone and other terpenoid-quinone biosynthesis;Phenylalanine metabolism;Phenylpropanoid biosynthesis |
| Phvul.011G089600 | gaba transporter 1-like | plasma membrane;integral component of membrane;gamma-aminobutyric acid transmembrane transporter activity;gamma-aminobutyric acid transport | | |
| Phvul.011G089800 | gaba transporter 1-like | plasma membrane;integral component of membrane;gamma-aminobutyric acid transmembrane transporter activity;gamma-aminobutyric acid transport | | |
| Phvul.011G091300 | stress responsive a b barrel domain protein | chloroplast | | |
| Phvul.011G097100 | momilactone a synthase | ubiquitin-protein transferase activity;oxidoreductase activity;ligase activity;protein ubiquitination;oxidation-reduction process | | |
| Phvul.011G099300 | e3 ubiquitin-protein ligase pub24-like | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.011G102700 | aquaporin sip1-1-like | integral component of membrane;transporter activity;transport | | |
| Phvul.011G106300 | zinc finger protein constans-like 14 | intracellular;zinc ion binding | | |
| Phvul.011G109700 | myb-related transcription factor | DNA binding | | |

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|---|---|---|---|---|
| Phvul.011G119500 | helix loop helix dna-binding domain protein | DNA binding;protein dimerization activity | | |
| Phvul.011G120100 | protein longifolia 1-like | | | |
| Phvul.011G125300 | zinc finger ccch domain-containing protein 2-like | metal ion binding | | |
| Phvul.011G127100 | kdel-tailed cysteine endopeptidase cep1-like | cysteine-type peptidase activity;2-alkenal reductase [NAD(P)] activity;proteolysis;oxidation-reduction process | ec:1.3.1.74;ec:3.4 | |
| Phvul.011G128200 | peroxidase p7-like | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.011G135600 | seed biotin-containing protein sbp65 | | | |
| Phvul.011G136600 | fatty alcohol oxidase 3 isoform 1 | integral component of membrane;intracellular membrane-bounded organelle;long-chain-alcohol oxidase activity;flavin adenine dinucleotide binding;alcohol metabolic process;response to cold;oxidation-reduction process | ec:1.1.3.20 | |
| Phvul.011G142300 | scarecrow-like protein 21 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.011G142600 | (-)-germacrene d synthase-like isoform x3 | magnesium ion binding;casbene synthase activity;metabolic process | ec:4.2.3.8-synthase | Diterpenoid biosynthesis |
| Phvul.011G147100 | g-type lectin s-receptor-like serine threonine-protein kinase | protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation;recognition of pollen | ec:2.7.11 | |
| Phvul.011G147800 | nac domain-containing protein 72 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.011G148500 | hypothetical protein PHAVU_011G148500g | | | |
| Phvul.011G150400 | g-type lectin s-receptor-like serine threonine-protein kinase | protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;zinc ion binding;carbohydrate binding;peptidyl-tyrosine phosphorylation;recognition of pollen | ec:2.7.10.1;ec:2.7.11;ec:2.7.10 | |
| Phvul.011G152700 | g-type lectin s-receptor-like serine threonine-protein kinase at4g27290-like | protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation;recognition of pollen | ec:2.7.11 | |
| Phvul.011G160600 | clavata3 esr gene family member | | | |
| Phvul.011G160700 | clavata3 esr gene family member | | | |
| Phvul.011G163800 | ankyrin repeat protein | | | |
| Phvul.011G167000 | acidic endochitinase | hydrolase activity, hydrolyzing O-glycosyl compounds;carbohydrate metabolic process | | |
| Phvul.011G169500 | cell division control protein 2 homolog | cyclin-dependent protein serine/threonine kinase activity;ATP binding;protein phosphorylation;cell division;regulation of cell cycle | ec:2.7.11.22;ec:2.7.11 | |
| Phvul.011G182900 | mlp-like protein 43 | defense response;response to biotic stimulus | | |
| Phvul.011G183000 | mlp-like protein 43 | defense response;response to biotic stimulus | | |
| Phvul.011G183300 | mlp-like protein 43 | defense response;response to biotic stimulus | | |
| Phvul.011G183600 | mlp-like protein 43 | defense response;response to biotic stimulus | | |
| Phvul.011G183800 | mlp-like protein 43 | defense response;response to biotic stimulus | | |
| Phvul.011G183900 | mlp-like protein 43 | defense response;response to biotic stimulus | | |

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|---|---|---|---|---|
| Phvul.011G184200 | pathogenesis-related protein bet v i family protein | defense response;response to biotic stimulus |  |  |
| Phvul.011G184600 | udp-glycosyltransferase 74e1-like | transferase activity, transferring hexosyl groups;metabolic process |  |  |
| Phvul.011G189200 | 12-oxophytodienoate reductase 11 | FMN binding;12-oxophytodienoate reductase activity;oxidation-reduction process | ec:1.3.1.42-reductase | alpha-Linolenic acid metabolism |
| Phvul.011G189300 | 12-oxophytodienoate reductase 11 | FMN binding;12-oxophytodienoate reductase activity;oxidation-reduction process | ec:1.3.1.42-reductase | alpha-Linolenic acid metabolism |
| Phvul.011G189900 | protein zinc induced facilitator-like 1 | integral component of membrane;transporter activity;transmembrane transport |  |  |
| Phvul.011G191400 | hypothetical protein PHAVU_011G191400g | ADP binding |  |  |
| Phvul.011G191900 | proline-rich receptor-like protein kinase perk12 | protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.10 |  |
| Phvul.011G192400 | hypothetical protein PHAVU_011G192400g | ADP binding |  |  |
| Phvul.011G193600 | hypothetical protein PHAVU_011G193600g | ADP binding |  |  |
| Phvul.011G193800 | hypothetical protein PHAVU_011G193800g | ADP binding |  |  |
| Phvul.011G193900 | cysteine-rich receptor-kinase-like protein | protein kinase activity;ATP binding;protein phosphorylation |  |  |
| Phvul.011G194100 | hypothetical protein PHAVU_011G194000g | ADP binding |  |  |
| Phvul.011G194400 | cysteine-rich receptor-like protein kinase 10-like | protein serine/threonine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.2-protein-tyrosine kinase;ec:2.7.11;ec:2.7.10 | T cell receptor signaling pathway |
| Phvul.011G197000 | probable carboxylesterase 15 | carboxylic ester hydrolase activity;metabolic process | ec:3.1.1.1-ali-esterase | Drug metabolism - other enzymes |
| Phvul.011G198800 | nb-lrr receptor | ADP binding |  |  |
| Phvul.011G201000 | nbs-lrr type disease resistance protein rpg1-b | ADP binding |  |  |
| Phvul.011G201700 | glycoside hydrolase family 1 protein | beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.011G208300 | zinc finger protein 512b |  |  |  |
| Phvul.011G211600 | hypothetical protein PHAVU_011G211600g |  |  |  |
| Phvul.011G215300 | myb-like hth transcriptional regulator family | DNA binding |  |  |
| Phvul.L002700 | probable zinc transporter 10 | integral component of membrane;zinc ion transmembrane transporter activity;zinc II ion transmembrane transport |  |  |
| Phvul.L003000 | adipose-regulatory protein |  |  |  |

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|---|---|---|---|---|
| Phvul.L005900 | two-pore potassium channel 3-like | vacuolar membrane;integral component of membrane;voltage-gated potassium channel activity;polysaccharide catabolic process;cellular potassium ion homeostasis;potassium ion transmembrane transport | | |
| Phvul.L006800 | nbs-lrr type disease resistance protein cnl-j9 | ADP binding | | |
| Phvul.L006900 | triacylglycerol lipase 2-like | lipase activity;defense response to insect;fatty acid beta-oxidation | ec:3.1.1 | |
| Phvul.L008100 | vq motif protein | | | |
| Phvul.L009500 | hypothetical protein PHAVU_L009500g | | | |
| Phvul.L011500 | pentatricopeptide repeat-containing protein at1g20230-like | microtubule-severing ATPase activity;metabolic process | ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| XLOC_000483 | ---NA--- | | | |
| XLOC_000683 | disease resistance protein rga4 | phosphoprotein phosphatase activity;ADP binding;protein dephosphorylation | ec:3.1.3.16-phosphatase;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1 | T cell receptor signaling pathwayAminobenzoate degradation |
| XLOC_000689 | ---NA--- | | | |
| XLOC_002282 | transporter mch1 | integral component of membrane;transmembrane transport | | |
| XLOC_002350 | ---NA--- | | | |
| XLOC_002627 | ---NA--- | | | |
| XLOC_002736 | ---NA--- | | | |
| XLOC_002758 | ---NA--- | | | |
| XLOC_002766 | ---NA--- | | | |
| XLOC_002785 | ---NA--- | | | |
| XLOC_002793 | hypothetical protein PHAVU_010G070700g | | | |
| XLOC_002805 | hypothetical protein PHAVU_011G0958002g, partial | | | |
| XLOC_002817 | ---NA--- | | | |
| XLOC_002827 | ---NA--- | | | |
| XLOC_002839 | ---NA--- | | | |
| XLOC_003618 | copper transporter -like | | | |
| XLOC_003707 | hypothetical protein PHAVU_009G238900g | | | |
| XLOC_003885 | ---NA--- | | | |
| XLOC_005217 | ---NA--- | | | |
| XLOC_005373 | transcription factor gte1 | | | |
| XLOC_006160 | ---NA--- | | | |
| XLOC_006229 | ---NA--- | | | |

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|---|---|---|---|---|
| XLOC_006239 | ---NA--- |  |  |  |
| XLOC_006245 | ---NA--- |  |  |  |
| XLOC_006252 | ---NA--- |  |  |  |
| XLOC_006267 | ---NA--- |  |  |  |
| XLOC_006277 | ---NA--- |  |  |  |
| XLOC_006286 | ---NA--- |  |  |  |
| XLOC_006298 | hypothetical protein glysoja_023492 |  |  |  |
| XLOC_006748 | ---NA--- |  |  |  |
| XLOC_006966 | pre-mrna-processing-splicing factor 8-like | spliceosomal complex;U6 snRNA binding;U5 snRNA binding;mRNA splicing, via spliceosome |  |  |
| XLOC_007575 | lrr and nb-arc domain disease resistance protein |  |  |  |
| XLOC_007780 | ---NA--- |  |  |  |
| XLOC_007865 | hypothetical protein PHAVU_009G043500g | tRNA binding |  |  |
| XLOC_008029 | h aca ribonucleoprotein complex subunit 1-like protein 1 |  |  |  |
| XLOC_008379 | pyrimidine-specific ribonucleoside hydrolase riha | xanthine dehydrogenase activity;hydrolase activity;oxidation-reduction process | ec:1.17.1.4-dehydrogenase;ec:1.17.1 | Purine metabolism |
| XLOC_008533 | ---NA--- |  |  |  |
| XLOC_009318 | isoflavone synthase 1 | monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;isomerase activity;heme binding;oxidation-reduction process |  |  |
| XLOC_009320 | ---NA--- |  |  |  |
| XLOC_009321 | ---NA--- |  |  |  |
| XLOC_009332 | hypothetical protein PHAVU_001G104900g, partial |  |  |  |
| XLOC_009335 | hypothetical protein PHAVU_005G070100g |  |  |  |
| XLOC_009338 | ---NA--- |  |  |  |
| XLOC_009355 | myb transcription factor | DNA binding |  |  |
| XLOC_009372 | hypothetical protein PHAVU_011G148300g |  |  |  |
| XLOC_009383 | ---NA--- |  |  |  |
| XLOC_009385 | ---NA--- |  |  |  |
| XLOC_009395 | werner syndrome-like exonuclease | nucleic acid binding;3'-5' exonuclease activity;nucleic acid phosphodiester bond hydrolysis | ec:3.1 |  |
| XLOC_009404 | ---NA--- |  |  |  |
| XLOC_009407 | ---NA--- |  |  |  |

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|---|---|---|---|---|
| XLOC_009410 | ---NA--- | | | |
| XLOC_009423 | ---NA--- | | | |
| XLOC_009463 | ---NA--- | | | |
| XLOC_009875 | transcription initiation factor tfiid subunit 10 | | | |
| XLOC_010325 | ---NA--- | | | |
| XLOC_010340 | nbs-lrr type disease resistance protein cnl-j9 | ADP binding | | |
| XLOC_010758 | PREDICTED: uncharacterized protein LOC102665818 | | | |
| XLOC_011258 | ---NA--- | | | |
| XLOC_011259 | hypothetical protein PHAVU_008G145700g, partial | | | |
| XLOC_011273 | ---NA--- | | | |
| XLOC_011298 | PREDICTED: uncharacterized protein LOC102664980 | | | |
| XLOC_011299 | ---NA--- | | | |
| XLOC_011309 | ---NA--- | | | |
| XLOC_011313 | hypothetical protein PHAVU_009G156200g | | | |
| XLOC_011335 | hypothetical protein PHAVU_002G163900g | | | |
| XLOC_011339 | ---NA--- | | | |
| XLOC_011342 | ---NA--- | | | |
| XLOC_011343 | ---NA--- | | | |
| XLOC_011346 | hypothetical protein PHAVU_L006100g | metal ion binding | | |
| XLOC_011347 | ---NA--- | | | |
| XLOC_011353 | ---NA--- | | | |
| XLOC_011356 | ---NA--- | | | |
| XLOC_011689 | nuclear pore complex protein nup98-nup96 | nuclear pore;transport | | |
| XLOC_011757 | transcription factor gte1 | | | |
| XLOC_011869 | inter-alpha-trypsin inhibitor heavy chain-like protein | NAD+ ADP-ribosyltransferase activity;metabolic process | ec:2.4.2.30 | |
| XLOC_012375 | mlp-like protein 31 | defense response;response to biotic stimulus | | |
| XLOC_012682 | probable leucine-rich repeat receptor-like serine threonine-protein kinase at3g14840 | protein kinase activity;ATP binding;protein phosphorylation | | |

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|---|---|---|---|---|
| XLOC_012683 | lrr receptor-like kinase | protein kinase activity;ATP binding;protein phosphorylation | | |
| XLOC_012735 | hypothetical protein PHAVU_005G084700g | | | |
| XLOC_012777 | ---NA--- | | | |
| XLOC_013251 | retrotransposon polyprotein | catalytic activity;metabolic process | | |
| XLOC_013252 | ---NA--- | | | |
| XLOC_013260 | ---NA--- | | | |
| XLOC_013266 | ---NA--- | | | |
| XLOC_013267 | ribonuclease h partial | oxidoreductase activity | | |
| XLOC_013284 | ---NA--- | | | |
| XLOC_013316 | ---NA--- | | | |
| XLOC_013644 | retrotransposon expressed | macromolecule metabolic process;primary metabolic process | | |
| XLOC_013645 | histone-lysine n-h3 lysine-9 specific suvh5-like | intracellular organelle;binding;methyltransferase activity;methylation | | |
| XLOC_013810 | ---NA--- | | | |
| XLOC_015572 | hypothetical protein PHAVU_001G197200g | cysteine-type peptidase activity;thiol-dependent ubiquitinyl hydrolase activity;ubiquitin-dependent protein catabolic process | ec:3.4.19.12;ec:3.4 | |
| XLOC_015573 | ---NA--- | | | |
| XLOC_015575 | ---NA--- | | | |
| XLOC_015577 | ---NA--- | | | |
| XLOC_015620 | hypothetical protein | | | |
| XLOC_015623 | wall associated kinase-like protein | kinase activity;polysaccharide binding;phosphorylation | | |
| XLOC_015625 | ---NA--- | | | |
| XLOC_016045 | hypothetical protein PHAVU_007G0816001g | | | |
| XLOC_016155 | exosome complex exonuclease rrp46 homolog isoform x1 | kinesin complex;microtubule;microtubule motor activity;exonuclease activity;ATP binding;microtubule binding;mRNA splicing, via spliceosome;RNA methylation;protein targeting to mitochondrion;microtubule-based movement;protein maturation;nucleic acid phosphodiester bond hydrolysis | ec:3.6.1;ec:3.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| XLOC_017321 | cysteine-rich receptor-like protein kinase 29 | protein serine/threonine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.10.2-protein-tyrosine kinase;ec:2.7.11;ec:2.7.10 | T cell receptor signaling pathway |
| XLOC_017342 | exosome complex exonuclease rrp46 homolog isoform x1 | exonuclease activity;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| XLOC_017343 | cysteine-rich receptor-kinase-like protein | nucleotide binding;protein kinase activity;protein phosphorylation | | |
| XLOC_018503 | ---NA--- | | | |
| XLOC_018504 | ---NA--- | | | |
| XLOC_018505 | ---NA--- | | | |
| XLOC_018527 | hypothetical protein | | | |

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|---|---|---|---|---|
| | PHAVU_006G007700g | | | |
| XLOC_018539 | ---NA--- | | | |
| XLOC_018563 | ---NA--- | | | |
| XLOC_018564 | calmodulin-binding family protein | | | |
| XLOC_018567 | ---NA--- | | | |
| XLOC_020674 | g-type lectin s-receptor-like serine threonine-kinase | protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation;recognition of pollen | ec:2.7.11 | |
| XLOC_020681 | dna-directed rna polymerase iii subunit rpc3 | DNA binding;DNA-directed RNA polymerase activity;transcription, DNA-templated | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| XLOC_020682 | ---NA--- | | | |
| XLOC_020771 | hypothetical protein PHAVU_002G203500g | | | |
| XLOC_020934 | hypothetical protein LR48_Vigan46s000800 | | | |
| XLOC_021551 | hypothetical protein PHAVU_004G108700g | | | |
| XLOC_021560 | ---NA--- | | | |
| XLOC_021563 | ---NA--- | | | |
| XLOC_021564 | ---NA--- | | | |
| XLOC_021565 | hypothetical protein PHAVU_011G106500g | | | |
| XLOC_021571 | ---NA--- | | | |
| XLOC_021572 | hypothetical protein VITISV_008145 | | | |
| XLOC_021576 | ---NA--- | | | |
| XLOC_021586 | hypothetical protein LR48_Vigan583s003200 | | | |
| XLOC_021600 | ---NA--- | | | |
| XLOC_021642 | gag-pol polyprotein | | | |
| XLOC_021644 | ---NA--- | | | |
| XLOC_021652 | ---NA--- | | | |
| XLOC_021653 | ---NA--- | | | |
| XLOC_021905 | ---NA--- | | | |
| XLOC_021926 | ---NA--- | | | |
| XLOC_024008 | ---NA--- | | | |
| XLOC_024208 | ---NA--- | | | |
| XLOC_024325 | hypothetical protein MTR_3g073490 | | | |

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|---|---|---|---|---|
| XLOC_024326 | ---NA--- | | | |
| XLOC_024327 | ---NA--- | | | |
| XLOC_024340 | ---NA--- | | | |
| XLOC_024342 | ---NA--- | | | |
| XLOC_024356 | ---NA--- | | | |
| XLOC_024362 | ---NA--- | | | |
| XLOC_024378 | ---NA--- | | | |
| XLOC_024387 | ---NA--- | | | |
| XLOC_024388 | ---NA--- | | | |
| XLOC_024404 | ---NA--- | | | |
| XLOC_024405 | endonuclease exonuclease phosphatase family protein | | | |
| XLOC_024557 | hypothetical protein PHAVU_010G025500g | ATP binding;ADP binding;signal transduction | | |
| XLOC_024793 | serine acetyltransferase 5-like | cytosol;magnesium ion binding;serine O-acetyltransferase activity;terpene synthase activity;cysteine biosynthetic process from serine;protein targeting to membrane;response to wounding;response to fungus;jasmonic acid biosynthetic process;salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;regulation of plant-type hypersensitive response | ec:2.3.1;ec:2.3.1.30-O-acetyltransferase | Sulfur metabolism;Biosynthesis of antibiotics;Cysteine and methionine metabolism |
| XLOC_025114 | ---NA--- | | | |
| XLOC_025625 | ---NA--- | | | |
| XLOC_025627 | ---NA--- | | | |
| XLOC_025787 | pentatricopeptide repeat-containing protein at2g17140 | | | |
| XLOC_025825 | probable polygalacturonase | extracellular region;polygalacturonase activity;carbohydrate metabolic process;cell wall organization | ec:3.2.1.15-pectin depolymerase | Starch and sucrose metabolism;Pentose and glucuronate interconversions |
| XLOC_026121 | ---NA--- | | | |
| XLOC_026123 | ---NA--- | | | |
| XLOC_026129 | ---NA--- | | | |
| XLOC_026139 | ---NA--- | | | |
| XLOC_026160 | hypothetical protein LR48_Vigan03g139700 | | | |
| XLOC_026172 | ---NA--- | | | |
| XLOC_026190 | ---NA--- | | | |
| XLOC_026270 | ---NA--- | | | |
| XLOC_026888 | ---NA--- | | | |
| XLOC_026955 | ---NA--- | | | |
| XLOC_027632 | ---NA--- | | | |

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|---|---|---|---|---|
| XLOC_027916 | lysine-specific demethylase jmj16 | nucleus;transcription factor activity, sequence-specific DNA binding;protein glycosylation;gravitropism;vegetative to reproductive phase transition of meristem;glucuronoxylan metabolic process;protein desumoylation;post-translational protein modification;xylan biosynthetic process;positive regulation of transcription, DNA-templated;hydrogen peroxide biosynthetic process | | |
| XLOC_027985 | ---NA--- | | | |
| XLOC_028038 | ---NA--- | | | |
| XLOC_028432 | ---NA--- | | | |
| XLOC_028436 | disease resistance-dirigent domain protein | | | |
| XLOC_028457 | cyclic nucleotide-gated ion channel 4-like | integral component of membrane;ion channel activity;ion transmembrane transport | | |
| XLOC_028476 | ---NA--- | | | |
| XLOC_028488 | ---NA--- | | | |
| XLOC_028495 | disease resistance rpp13-like protein 1 | | | |
| XLOC_028589 | ---NA--- | | | |
| XLOC_028640 | ---NA--- | | | |

| Transcript ID | Sequence Description | GO Terms | Enzymes | Kegg Maps |
|---|---|---|---|---|
| **DEGs under high impact predicted effects (HIPE)** | | | | |
| Phvul.001G000600.1 | Fanconi anemia group J homolog isoform X1 | DNA binding;ATP-dependent DNA helicase activity;ATP binding;nucleobase-containing compound metabolic process;DNA duplex unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G000600.2 | Fanconi anemia group J homolog isoform X1 | DNA binding;ATP-dependent DNA helicase activity;ATP binding;nucleobase-containing compound metabolic process;DNA duplex unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G000800.1 | 12-oxophytodienoate reductase 11 | intracellular;NADPH dehydrogenase activity;FMN binding;12-oxophytodienoate reductase activity;oxidation-reduction process | ec:1.3.1.42-reductase;ec:1.6.99.1 | alpha-Linolenic acid metabolism |
| Phvul.001G000800.2 | 12-oxophytodienoate reductase 11 | intracellular;NADPH dehydrogenase activity;FMN binding;12-oxophytodienoate reductase activity;oxidation-reduction process | ec:1.3.1.42-reductase;ec:1.6.99.1 | alpha-Linolenic acid metabolism |
| Phvul.001G001000.1 | catalase | glyoxysome;catalase activity;heme binding;metal ion binding;response to hydrogen peroxide;hydrogen peroxide catabolic process;oxidation-reduction process;cellular oxidant detoxification | ec:1.11.1.7-lactoperoxidase;ec:1.11.1.6-equilase | Phenylpropanoid biosynthesisBiosynthesis of antibiotics;Tryptophan metabolism;Glyoxylate and dicarboxylate metabolism |
| Phvul.001G001300.1 | 4-coumarate--ligase-like 5 | integral component of membrane;ligase activity;Photinus-luciferin 4-monooxygenase (ATP-hydrolyzing) activity;oxidation-reduction process | ec:1.13.12;ec:1.13.12.7 | |
| Phvul.001G001500.1 | L-ascorbate oxidase homolog | plant-type cell wall;plasmodesma;integral component of membrane;copper ion binding;L-ascorbate oxidase activity;oxidoreductase activity, oxidizing metal ions;oxidation-reduction process | ec:1.10.3.3-oxidase;ec:1.10.3 | Ascorbate and aldarate metabolism |
| Phvul.001G001800.1 | hypothetical protein PHAVU_001G001800g | | | |
| Phvul.001G002800.1 | Calcium-dependent kinase 29 | nucleus;cytoplasm;plasma membrane;calmodulin-dependent protein kinase activity;calcium ion binding;calmodulin binding;ATP binding;calcium-dependent protein serine/threonine kinase activity;systemic acquired resistance;salicylic acid biosynthetic process;abscisic acid-activated signaling pathway;peptidyl-serine phosphorylation;intracellular signal transduction;protein autophosphorylation | ec:2.7.11;ec:2.7.11.17 | |
| Phvul.001G003900.1 | UPF0496 At1g20180-like | integral component of membrane | | |
| Phvul.001G005400.1 | transcription elongation factor (TFIIS) family , | elongin complex;DNA binding;transcription elongation from RNA polymerase II promoter | | |
| Phvul.001G006000.1 | vacuolar sorting-associated 35B-like | late endosome;retromer complex;protein transporter activity;intracellular protein transport;retrograde transport, endosome to Golgi | | |
| Phvul.001G008000.1 | Filament-like plant 4 | | | |
| Phvul.001G009000.1 | transcription factor RF2a-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.001G009000.2 | transcription factor RF2a-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.001G009000.3 | transcription factor RF2a-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.001G009300.1 | lysine-specific histone demethylase 1 homolog 3-like isoform X1 | nucleus;integral component of membrane;DNA binding;methyltransferase activity;oxidoreductase activity;transcription, DNA-templated;methylation;oxidation-reduction process | | |

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| Phvul.001G009500.1 | ACCUMULATION AND REPLICATION OF CHLOROPLASTS 6, chloroplastic | integral component of chloroplast inner membrane;protein self-association;chloroplast fission;photosystem II assembly | | |
| Phvul.001G010000.1 | ROOT PRIMORDIUM DEFECTIVE 1 | hydrolase activity;metabolic process;negative regulation of cell proliferation;lateral root morphogenesis | | |
| Phvul.001G011900.1 | Peptide upstream open reading frame 5 | integral component of membrane | | |
| Phvul.001G012200.1 | Inositol-pentakisphosphate 2-kinase | ATP binding;inositol pentakisphosphate 2-kinase activity;phosphorylation | ec:2.7.1.158-2-kinase | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.001G012200.2 | Inositol-pentakisphosphate 2-kinase | ATP binding;inositol pentakisphosphate 2-kinase activity;phosphorylation | ec:2.7.1.158-2-kinase | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.001G014000.1 | sugar transporter ERD6-like 6 | integral component of plasma membrane;sugar:proton symporter activity;glucose transmembrane transporter activity;2-alkenal reductase [NAD(P)] activity;proton transport;glucose import;oxidation-reduction process;glucose transmembrane transport | ec:1.3.1.74 | |
| Phvul.001G014400.1 | probable LRR receptor-like serine threonine- kinase At2g16250 | integral component of membrane;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.001G014500.1 | probable methyltransferase PMT28 | endosome;trans-Golgi network;integral component of membrane;iron ion binding;methyltransferase activity;FMN binding;iron-sulfur cluster binding;methylation;oxidation-reduction process | | |
| Phvul.001G014700.1 | hypothetical protein PHAVU_001G014700g | cytosol;integral component of membrane;hydroxypyruvate reductase activity;glyoxylate reductase (NADP) activity | ec:1.1.1.81-reductase;ec:1.1.1.79-reductase (NADP+) | Glycine, serine and threonine metabolism;Glyoxylate and dicarboxylate metabolismPyruvate metabolism;Glyoxylate and dicarboxylate metabolism |
| Phvul.001G015400.1 | uncharacterized membrane At1g75140 | integral component of membrane | | |
| Phvul.001G015600.1 | lysophospholipid acyltransferase LPEAT1-like isoform X2 | nucleus;integral component of membrane;1-acylglycerophosphocholine O-acyltransferase activity;phosphatidylglycerol biosynthetic process | ec:2.3.1.23-O-acyltransferase;ec:2.3.1 | Glycerophospholipid metabolism |
| Phvul.001G015600.2 | lysophospholipid acyltransferase LPEAT1-like isoform X1 | nucleus;integral component of membrane;1-acylglycerophosphocholine O-acyltransferase activity;phosphatidylglycerol biosynthetic process | ec:2.3.1.23-O-acyltransferase;ec:2.3.1 | Glycerophospholipid metabolism |
| Phvul.001G015600.3 | lysophospholipid acyltransferase LPEAT1-like isoform X1 | nucleus;integral component of membrane;1-acylglycerophosphocholine O-acyltransferase activity;phosphatidylglycerol biosynthetic process | ec:2.3.1.23-O-acyltransferase;ec:2.3.1 | Glycerophospholipid metabolism |
| Phvul.001G017600.1 | plant MJB21-3 | integral component of membrane;DNA-directed RNA polymerase activity;RNA biosynthetic process | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| Phvul.001G018700.1 | nucleobase-ascorbate transporter 3 | plasma membrane;plasmodesma;integral component of membrane;transporter activity;transmembrane transport | | |
| Phvul.001G019900.1 | probable inactive heme oxygenase 2, chloroplastic | chloroplast;heme oxygenase (decyclizing) activity;heme oxidation;phytochromobilin biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | ec:1.14.99.3 | |
| Phvul.001G020200.1 | patatin 2 | cytoplasm;membrane;phospholipase activity;acylglycerol lipase activity;lipid catabolic process | ec:3.1.1.23-lipase;ec:3.1.1;ec:3.1.1.1-ali-esterase | Glycerolipid metabolismDrug metabolism - other enzymes |

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| Phvul.001G021200.1 | probable phosphatase 2C 12 isoform X1 | cytosol;protein serine/threonine phosphatase activity;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.001G023100.1 | probable BOI-related E3 ubiquitin- ligase 2 | nucleus;ubiquitin-protein transferase activity;zinc ion binding;hormone-mediated signaling pathway;protein ubiquitination;regulation of defense response;photoperiodism, flowering | | |
| Phvul.001G023800.1 | aceous RNase P 1, chloroplastic mitochondrial | | | |
| Phvul.001G024200.1 | kinesin FRA1 isoform X1 | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G025100.1 | probable carbohydrate esterase At4g34215 | | | |
| Phvul.001G026300.1 | transcription initiation factor TFIID subunit 4b isoform X1 | transcription factor TFIID complex;translation initiation factor activity;protein heterodimerization activity;DNA-templated transcription, initiation;translational initiation | | |
| Phvul.001G026300.2 | transcription initiation factor TFIID subunit 4b isoform X1 | transcription factor TFIID complex;translation initiation factor activity;protein heterodimerization activity;DNA-templated transcription, initiation;translational initiation | | |
| Phvul.001G028600.1 | hypothetical protein PHAVU_001G028600g, partial | | | |
| Phvul.001G029000.2 | FKBP-type peptidyl-prolyl cis-trans isomerase | endoplasmic reticulum membrane;peptidyl-prolyl cis-trans isomerase activity;FK506 binding;protein peptidyl-prolyl isomerization;chaperone-mediated protein folding | ec:5.2.1.8 | |
| Phvul.001G030200.1 | PAX3- and PAX7-binding 1 | U2-type post-mRNA release spliceosomal complex;RNA polymerase II core promoter proximal region sequence-specific DNA binding;transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding;negative regulation of transcription from RNA polymerase II promoter;spliceosomal complex disassembly | | |
| Phvul.001G032900.1 | EARLY FLOWERING 3 | | | |
| Phvul.001G032900.2 | EARLY FLOWERING 3 | | | |
| Phvul.001G034600.1 | calcineurin B 10 | plant-type vacuole membrane;integral component of membrane;catalytic activity;calcium ion binding;polysaccharide biosynthetic process;multidimensional cell growth;cell tip growth;regulation of hormone levels;calcium-mediated signaling;hyperosmotic salinity response;regulation of potassium ion transport;anthocyanin accumulation in tissues in response to UV light;root hair elongation;cell wall organization;regulation of ion homeostasis | | |
| Phvul.001G034600.2 | calcineurin B 10 | cytoplasm;membrane;calcium ion binding;metabolic process;response to abiotic stimulus;cellular component organization;cell growth;single-multicellular organism process;cellular developmental process;regulation of biological process;developmental growth involved in morphogenesis;regulation of biological quality | | |
| Phvul.001G035000.1 | DUF1230 family | chloroplast;integral component of membrane;chlorophyll catabolic process | | |
| Phvul.001G035000.2 | DUF1230 family | chloroplast;integral component of membrane;chlorophyll catabolic process | | |
| Phvul.001G035000.3 | DUF1230 family | chloroplast;integral component of membrane;chlorophyll catabolic process | | |
| Phvul.001G035300.1 | BPS1, chloroplastic | | | |

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| Phvul.001G035500.1 | glycine dehydrogenase (decarboxylating), mitochondrial | mitochondrion;cytosol;glycine cleavage complex;glycine dehydrogenase (decarboxylating) activity;glycine binding;glycine decarboxylation via glycine cleavage system;oxidation-reduction process | ec:1.4.4.2-dehydrogenase (aminomethyl-transferring) | Glycine, serine and threonine metabolism |
| Phvul.001G036300.1 | BAAT acyl- thioester hydrolase carboxy-terminal | peroxisome;hydrolase activity;metabolic process | | |
| Phvul.001G037500.1 | probable magnesium transporter NIPA9 isoform X1 | integral component of membrane;magnesium ion transmembrane transporter activity;magnesium ion transport;magnesium ion transmembrane transport | | |
| Phvul.001G038700.1 | F-box LRR-repeat 15-like | | | |
| Phvul.001G040200.2 | hypothetical protein PHAVU_001G040200g | | | |
| Phvul.001G043000.1 | LRR receptor-like serine threonine-kinase GSO1 | integral component of membrane | | |
| Phvul.001G043800.1 | F-box only 13-like | | | |
| Phvul.001G045100.1 | adenine nucleotide alpha hydrolase-like domain kinase | protein kinase activity;ATP binding;protein phosphorylation;response to stress | | |
| Phvul.001G045100.2 | adenine nucleotide alpha hydrolase-like domain kinase | protein kinase activity;ATP binding;protein phosphorylation;response to stress | | |
| Phvul.001G045500.1 | probable folate-biopterin transporter 2 | integral component of membrane;transport | | |
| Phvul.001G045900.1 | U-box domain-containing 13 | | | |
| Phvul.001G045900.2 | U-box domain-containing 13 | | | |
| Phvul.001G047000.1 | aspartate aminotransferase | mitochondrial matrix;chloroplast stroma;chloroplast envelope;stromule;apoplast;L-aspartate:2-oxoglutarate aminotransferase activity;pyridoxal phosphate binding;identical protein binding;L-phenylalanine:2-oxoglutarate aminotransferase activity;2-oxoglutarate metabolic process;aspartate metabolic process;glutamate metabolic process;ethylene biosynthetic process | ec:2.6.1.57-transaminase;ec:2.6.1.9-transaminase;ec:2.6.1.5-transaminase;ec:2.6.1.1-transaminase | Biosynthesis of antibiotics;Tropane, piperidine and pyridine alkaloid biosynthesis;Cysteine and methionine metabolism;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesis;Isoquinoline alkaloid biosynthesis;Lysine biosynthesis;Phenylalanine metabolism;Tyrosine metabolismBiosynthesis of antibiotics;Tropane, piperidine and pyridine alkaloid biosynthesis;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesis;Phenylalanine metabolism;Tyrosine metabolism;Histidine metabolismUbiquinone and other terpenoid-quinone biosynthesis;Biosynthesis of antibiotics;Tropane, piperidine and pyridine alkaloid biosynthesis;Cysteine and methionine |

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| | | | | metabolism;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesis;Isoquinoline alkaloid biosynthesis;Phenylalanine metabolism;Tyrosine metabolismArginine and proline metabolism;Biosynthesis of antibiotics;Arginine biosynthesis;Carbon fixation in photosynthetic organisms;Tropane, piperidine and pyridine alkaloid biosynthesis;Cysteine and methionine metabolism;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesis;Isoquinoline alkaloid biosynthesis;Phenylalanine metabolism;Tyrosine metabolism;Alanine, aspartate and glutamate metabolism |
| Phvul.001G048800.2 | glycerophosphodiester phosphodiesterase kinase domain-containing GDPDL2-like | integral component of membrane;protein serine/threonine kinase activity;ATP binding;polysaccharide binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.001G050000.1 | uncharacterized vacuolar membrane YML018C-like isoform X1 | integral component of membrane | | |
| Phvul.001G052800.1 | peptidyl-prolyl cis-trans isomerase CYP95-like isoform X1 | peptidyl-prolyl cis-trans isomerase activity;protein peptidyl-prolyl isomerization;protein folding | ec:5.2.1.8 | |
| Phvul.001G053400.1 | carbon catabolite repressor 4 homolog 6 isoform X1 | | | |
| Phvul.001G055000.1 | gibberellin 3-beta-dioxygenase 1-like | iron ion binding;gibberellin 3-beta-dioxygenase activity;oxidation-reduction process | ec:1.14.11.15-3beta-dioxygenase;ec:1.14.11 | Diterpenoid biosynthesis |
| Phvul.001G055100.1 | tify 8 , partial | nucleus;transcription corepressor activity;response to wounding;regulation of defense response;negative regulation of nucleic acid-templated transcription;regulation of jasmonic acid mediated signaling pathway | | |
| Phvul.001G055200.1 | pentatricopeptide repeat-containing At5g11310, mitochondrial | | | |
| Phvul.001G055600.1 | E3 ubiquitin- ligase At1g63170 | plasma membrane;integral component of membrane;zinc ion binding;hydrolase activity;ligase activity;metabolic process | | |
| Phvul.001G056400.1 | glucan endo-1,3-beta-glucosidase 4-like | hydrolase activity, hydrolyzing O-glycosyl compounds;protein histidine kinase activity;carbohydrate metabolic process;peptidyl-histidine phosphorylation | ec:2.7.13.3 | |
| Phvul.001G057900.1 | RNA methyltransferase At5g10620 | cytoplasm;methyltransferase activity;rRNA processing;methylation | | |

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| Phvul.001G058100.1 | core-2 I-branching enzyme | integral component of membrane;acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1 | |
| Phvul.001G058100.2 | core-2 I-branching enzyme | integral component of membrane;acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1 | |
| Phvul.001G058100.3 | core-2 I-branching enzyme | integral component of membrane;acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1 | |
| Phvul.001G058900.1 | plasma membrane ATPase 4 | integral component of plasma membrane;intracellular membrane-bounded organelle;ATP binding;hydrogen-exporting ATPase activity, phosphorylative mechanism;metal ion binding;ATP biosynthetic process;regulation of intracellular pH;hydrogen ion transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.6.3.6-ATPase | Purine metabolismPurine metabolism;Thiamine metabolismOxidative phosphorylation |
| Phvul.001G059500.1 | pentatricopeptide repeat-containing At5g10690 | cytosol;catalytic activity;mRNA modification;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | | |
| Phvul.001G059700.1 | DNA ligase 1-like | integral component of membrane | | |
| Phvul.001G060000.1 | two-on-two hemoglobin-3 | oxygen binding;heme binding | | |
| Phvul.001G060700.1 | dihydrofolate synthetase | tetrahydrofolylpolyglutamate synthase activity;ATP binding;dihydrofolate synthase activity;one-carbon metabolic process;dihydrofolate biosynthetic process;embryo development ending in seed dormancy;tetrahydrofolylpolyglutamate biosynthetic process | ec:6.3.2.17-synthase;ec:6.3.2.12-synthase | Folate biosynthesisFolate biosynthesis |
| Phvul.001G060700.2 | tetrahydrofolylpolyglutamate synthase | tetrahydrofolylpolyglutamate synthase activity;ATP binding;dihydrofolate synthase activity;one-carbon metabolic process;dihydrofolate biosynthetic process;embryo development ending in seed dormancy;tetrahydrofolylpolyglutamate biosynthetic process | ec:6.3.2.17-synthase;ec:6.3.2.12-synthase | Folate biosynthesisFolate biosynthesis |
| Phvul.001G060700.3 | tetrahydrofolylpolyglutamate synthase | tetrahydrofolylpolyglutamate synthase activity;ATP binding;dihydrofolate synthase activity;dihydrofolate biosynthetic process;tetrahydrofolylpolyglutamate biosynthetic process | ec:6.3.2.17-synthase;ec:6.3.2.12-synthase | Folate biosynthesisFolate biosynthesis |
| Phvul.001G060700.4 | dihydrofolate synthetase | tetrahydrofolylpolyglutamate synthase activity;ATP binding;dihydrofolate synthase activity;one-carbon metabolic process;dihydrofolate biosynthetic process;embryo development ending in seed dormancy;tetrahydrofolylpolyglutamate biosynthetic process | ec:6.3.2.17-synthase;ec:6.3.2.12-synthase | Folate biosynthesisFolate biosynthesis |
| Phvul.001G060700.5 | tetrahydrofolylpolyglutamate synthase | tetrahydrofolylpolyglutamate synthase activity;ATP binding;dihydrofolate synthase activity;dihydrofolate biosynthetic process;tetrahydrofolylpolyglutamate biosynthetic process | ec:6.3.2.17-synthase;ec:6.3.2.12-synthase | Folate biosynthesisFolate biosynthesis |
| Phvul.001G060700.6 | tetrahydrofolylpolyglutamate synthase | tetrahydrofolylpolyglutamate synthase activity;ATP binding;dihydrofolate synthase activity;one-carbon metabolic process;dihydrofolate biosynthetic process;embryo development ending in seed dormancy;tetrahydrofolylpolyglutamate biosynthetic process | ec:6.3.2.17-synthase;ec:6.3.2.12-synthase | Folate biosynthesisFolate biosynthesis |
| Phvul.001G061400.1 | RNA polymerase sigma factor sigE, chloroplastic mitochondrial-like | chloroplast;plastid sigma factor activity;DNA binding;transcription factor activity, sequence-specific DNA binding;DNA-templated transcription, initiation;response to blue light;chloroplast organization;photosystem II assembly;myo-inositol hexakisphosphate biosynthetic process;positive regulation of transcription, DNA-templated | | |
| Phvul.001G064800.1 | ras-related RABC1 | intracellular;membrane;GTPase activity;GTP binding;intracellular protein transport;nucleocytoplasmic transport;small GTPase mediated signal transduction;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |

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| Phvul.001G066400.1 | wall-associated receptor kinase-like 16 isoform X2 | integral component of membrane;protein serine/threonine kinase activity;calcium ion binding;ATP binding;polysaccharide binding;protein phosphorylation | ec:2.7.11 |  |
| Phvul.001G067200.1 | probable methyltransferase PMT10 | integral component of membrane;S-adenosylmethionine-dependent methyltransferase activity;methylation |  |  |
| Phvul.001G068400.1 | pentatricopeptide repeat-containing At2g35030, mitochondrial | zinc ion binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G071400.1 | probable receptor kinase At1g11050 | plasma membrane;integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 |  |
| Phvul.001G072300.1 | U-box domain-containing 13 |  |  |  |
| Phvul.001G073100.1 | UDP-glucuronate:xylan alpha-glucuronosyltransferase 3 | endosome;trans-Golgi network;integral component of membrane;glucuronosyltransferase activity;plant-type secondary cell wall biogenesis;xylan biosynthetic process | ec:2.4.1.17-1-naphthol glucuronyltransferase | Drug metabolism - other enzymes;Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Porphyrin and chlorophyll metabolism;Starch and sucrose metabolism;Ascorbate and aldarate metabolism;Retinol metabolism;Steroid hormone biosynthesis;Pentose and glucuronate interconversions |
| Phvul.001G074000.1 | nuclear pore complex NUP85 | nuclear pore outer ring;structural constituent of nuclear pore;mRNA export from nucleus;protein import into nucleus;photomorphogenesis;embryo development ending in seed dormancy;seed germination;regulation of flower development;meristem structural organization;vernalization response;maintenance of meristem identity;seed dormancy process;sugar mediated signaling pathway;vegetative to reproductive phase transition of meristem;cullin deneddylation;protein ubiquitination;histone methylation;protein deubiquitination;lipid storage;positive regulation of transcription, DNA-templated;response to freezing |  |  |
| Phvul.001G074100.1 | nuclear pore complex NUP85 | nuclear pore outer ring;structural constituent of nuclear pore;mRNA export from nucleus;protein import into nucleus;photomorphogenesis;embryo development ending in seed dormancy;seed germination;regulation of flower development;meristem structural organization;vernalization response;maintenance of meristem identity;seed dormancy process;sugar mediated signaling pathway;vegetative to reproductive phase transition of meristem;cullin deneddylation;protein ubiquitination;histone methylation;protein deubiquitination;lipid storage;positive regulation of transcription, DNA-templated;response to freezing |  |  |
| Phvul.001G074600.1 | early nodulin-93-like | mitochondrion;integral component of membrane;response to ethylene |  |  |
| Phvul.001G075000.1 | aminoacrylate hydrolase | integral component of membrane;hydrolase activity;metabolic process |  |  |

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| Phvul.001G075200.1 | ATPase family AAA domain-containing 1-like | integral component of membrane;ATP binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G075700.1 | carbon catabolite repressor | integral component of membrane | | |
| Phvul.001G076100.1 | stress-induced receptor-like kinase | integral component of membrane;protein serine/threonine kinase activity;ATP binding;polysaccharide binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.001G076800.1 | TATA-box-binding | nucleus;DNA binding;DNA-templated transcription, initiation | | |
| Phvul.001G078300.1 | haloacid dehalogenase-like hydrolase | chloroplast;metalloendopeptidase activity;trehalose-phosphatase activity;rRNA processing;proteolysis;dephosphorylation;small molecule biosynthetic process | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.12-trehalose 6-phosphatase;ec:3.4.24 | Aminobenzoate degradationStarch and sucrose metabolism |
| Phvul.001G078500.1 | sulfite exporter family | integral component of membrane | | |
| Phvul.001G080200.1 | Testis-expressed sequence 2 | integral component of membrane | | |
| Phvul.001G081400.1 | early nodulin 3 | integral component of membrane;anchored component of plasma membrane;electron carrier activity | | |
| Phvul.001G082200.1 | RING FYVE PHD zinc finger , | zinc ion binding | | |
| Phvul.001G082300.1 | Ubiquitin-specific protease 9 isoform 1 | thiol-dependent ubiquitin-specific protease activity;zinc ion binding;ubiquitin-dependent protein catabolic process;protein deubiquitination | ec:3.4;ec:3.4.19.12 | |
| Phvul.001G083800.1 | Brain 44 | mitochondrial inner membrane;integral component of membrane;mitochondrial pyruvate transport | | |
| Phvul.001G083800.2 | Brain 44 | mitochondrial inner membrane;integral component of membrane;mitochondrial pyruvate transport | | |
| Phvul.001G084700.1 | alpha-mannosidase-like isoform X1 | vacuolar membrane;plant-type cell wall;apoplast;alpha-mannosidase activity;zinc ion binding;carbohydrate binding;mannose metabolic process;protein deglycosylation;microtubule nucleation;cysteine biosynthetic process | ec:3.2.1;ec:3.2.1.24-alpha-D-mannosidase | Other glycan degradation |
| Phvul.001G085900.1 | transmembrane 45B | integral component of membrane | | |
| Phvul.001G087700.1 | acyltransferase At3g26840, chloroplastic | plastoglobule;integral component of membrane;diacylglycerol O-acyltransferase activity;phytol metabolic process | ec:2.3.1.20-O-acyltransferase;ec:2.3.1 | Cutin, suberine and wax biosynthesis;Glycerolipid metabolism |
| Phvul.001G090700.1 | probable S-acyltransferase 7 | integral component of membrane;zinc ion binding;oxidoreductase activity;protein-cysteine S-palmitoyltransferase activity;oxidation-reduction process | ec:2.3.1.225;ec:2.3.1 | |
| Phvul.001G093500.1 | yrdC domain-containing , mitochondrial | double-stranded RNA binding | | |
| Phvul.001G095300.1 | hypothetical protein LR48_Vigan03g181500 | | | |
| Phvul.001G096900.1 | apyrase 2-like | integral component of membrane;hydrolase activity;metabolic process | | |
| Phvul.001G097700.1 | Eukaryotic peptide chain release factor subunit 1-3 | cytoplasm;translation release factor activity, codon specific;translational termination | | |
| Phvul.001G099000.1 | DNA cross-link repair | nuclear chromosome, telomeric region;damaged DNA binding;benzoate 4-monooxygenase activity;5'-3' exodeoxyribonuclease activity;double-strand break repair via nonhomologous end joining;protection from non-homologous end joining at telomere;interstrand cross-link repair;oxidation-reduction process;nucleic acid phosphodiester bond hydrolysis | ec:3.1.15;ec:3.1.11;ec:3.1;ec:1.14.13;ec:1.14.13.12-4-monooxygenase | Aminobenzoate degradation;Benzoate degradation |

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| Phvul.001G101800.1 | transmembrane , | integral component of membrane | | |
| Phvul.001G102200.1 | COP9 signalosome complex subunit 2 | proteasome complex;cytosol;photomorphogenesis;cullin deneddylation;protein catabolic process | | |
| Phvul.001G104000.1 | probable 2-isopropylmalate synthase | 2-isopropylmalate synthase activity;leucine biosynthetic process;nitrogen fixation;nodulation | ec:2.3.3.13-synthase | Valine, leucine and isoleucine biosynthesis;Pyruvate metabolism |
| Phvul.001G105100.1 | polyribonucleotide nucleotidyltransferase | chloroplast stroma;3'-5'-exoribonuclease activity;RNA binding;polyribonucleotide nucleotidyltransferase activity;mRNA catabolic process;negative regulation of isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;chlorophyll biosynthetic process;cellular response to phosphate starvation;carotene biosynthetic process;xanthophyll biosynthetic process;chloroplast RNA processing;RNA phosphodiester bond hydrolysis, exonucleolytic | ec:3.1.15;ec:3.1.13;ec:3.1;ec:2.7.7.8-nucleotidyltransferase | Purine metabolism;Pyrimidine metabolism |
| Phvul.001G105500.1 | cation calcium exchanger 2-like | integral component of membrane;transmembrane transport | | |
| Phvul.001G108000.1 | co-chaperone family | mitochondrial matrix;chloroplast stroma;thylakoid;adenyl-nucleotide exchange factor activity;copper ion binding;protein homodimerization activity;chaperone binding;protein folding;regulation of catalytic activity | | |
| Phvul.001G109100.1 | PHYTOCHROME KINASE SUBSTRATE 4-like | kinase activity;phosphorylation | | |
| Phvul.001G109600.1 | HNH endonuclease domain | nucleic acid binding;endonuclease activity;response to desiccation;response to cold;response to salt stress;response to abscisic acid;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.001G110000.1 | ARM repeat | | | |
| Phvul.001G110000.2 | ARM repeat | | | |
| Phvul.001G111900.1 | importin-5-like | cytoplasm;nuclear membrane;nuclear periphery;nuclear localization sequence binding;Ran GTPase binding;protein transporter activity;protein import into nucleus, docking;protein import into nucleus, translocation;NLS-bearing protein import into nucleus;ribosomal protein import into nucleus | | |
| Phvul.001G113200.1 | Inhibitor of Bruton tyrosine kinase | kinase activity;phosphorylation | | |
| Phvul.001G113200.2 | Inhibitor of Bruton tyrosine kinase | kinase activity;phosphorylation | | |
| Phvul.001G113700.1 | Nucleolar MIF4G domain-containing 1 | nucleolus;integral component of membrane;RNA binding;mitotic recombination;embryo sac egg cell differentiation;ribosomal small subunit biogenesis | | |
| Phvul.001G114700.3 | DNA replication complex GINS PSF2 | GINS complex;replication fork protection complex;3'-5' DNA helicase activity;double-strand break repair via break-induced replication;DNA duplex unwinding;mitotic DNA replication initiation | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.001G114900.1 | diphthine--ammonia ligase | | | |
| Phvul.001G117600.1 | cytochrome f (chloroplast) | chloroplast thylakoid membrane;integral component of thylakoid membrane;iron ion binding;electron carrier activity;heme binding;photosynthesis;oxidation-reduction process | | |
| Phvul.001G120700.1 | serine carboxypeptidase-like 45 | serine-type carboxypeptidase activity;transferase activity, transferring acyl groups other than amino-acyl groups;secondary metabolic process;proteolysis involved in cellular protein catabolic process | ec:3.4.21;ec:3.4.16 | |

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| Phvul.001G122400.1 | exocyst complex component EXO70B1-like | exocyst;integral component of membrane;exocytosis |  |  |
| Phvul.001G123200.1 | microtubule-associated 70-2-like | integral component of membrane;microtubule binding;cytoskeleton organization |  |  |
| Phvul.001G123900.1 | ferredoxin-dependent glutamate synthase, chloroplastic | glutamate synthase (ferredoxin) activity;glutamate biosynthetic process;ammonia assimilation cycle;oxidation-reduction process | ec:1.4;ec:1.4.7.1-synthase (ferredoxin) | Nitrogen metabolism;Glyoxylate and dicarboxylate metabolism |
| Phvul.001G126800.1 | triacylglycerol lipase SDP1 | phospholipase A2 activity;sterol esterase activity;triglyceride lipase activity;lipid metabolic process | ec:3.1.1.13-esterase;ec:3.1.1;ec:3.1.1.4-A2;ec:3.1.1.3-lipase;ec:3.1.1.1-ali-esterase | Steroid biosynthesisalpha-Linolenic acid metabolism;Linoleic acid metabolism;Arachidonic acid metabolism;Ether lipid metabolism;Glycerophospholipid metabolismGlycerolipid metabolismDrug metabolism - other enzymes |
| Phvul.001G128200.1 | disease resistance (TIR-NBS-LRR class), | nucleic acid binding;RNA-DNA hybrid ribonuclease activity;ADP binding;signal transduction;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1.30;ec:3.1.26;ec:3.1;ec:3.1.26.4 |  |
| Phvul.001G129200.1 | DNA helicase INO80 | DNA binding;helicase activity;ATP binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.001G129300.1 | glycerol-3-phosphate dehydrogenase [NAD(+)] GPDHC1, cytosolic | glycerol-3-phosphate dehydrogenase complex;glycerol-3-phosphate dehydrogenase [NAD+] activity;NAD binding;carbohydrate metabolic process;glycerol-3-phosphate catabolic process;oxidation-reduction process | ec:1.1.1.8-dehydrogenase (NAD+);ec:1.1.1.94-dehydrogenase [NAD(P)+] | Glycerophospholipid metabolismGlycerophospholipid metabolism |
| Phvul.001G129400.1 | hypothetical protein PHAVU_001G129400g | DNA-templated transcription, termination |  |  |
| Phvul.001G129400.2 | hypothetical protein PHAVU_001G129400g | DNA-templated transcription, termination |  |  |
| Phvul.001G129800.2 | tRNA-splicing endonuclease subunit Sen54 | tRNA-intron endonuclease complex;tRNA-intron endonuclease activity;tRNA-type intron splice site recognition and cleavage;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1.31;ec:3.1.27;ec:3.1.27.9;ec:3.1 |  |
| Phvul.001G130300.1 | kinesin KP1 | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;chromatin organization;microtubule-based movement;metabolic process;single-organism organelle organization | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.001G131100.1 | ABC transporter family | vacuolar membrane;integral component of membrane;ATP binding;polyamine-transporting ATPase activity;heme-transporting ATPase activity;protein N-linked glycosylation;lipid transport;heme transport;polyamine transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.6.3.41;ec:3.6.3.31 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G131300.1 | AP2-like ethylene-responsive transcription factor At2g41710 isoform X1 | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;multicellular organismal development |  |  |
| Phvul.001G131700.1 | villin-3-like isoform X1 | actin filament binding;actin filament bundle assembly |  |  |
| Phvul.001G131700.2 | villin-3-like isoform X1 | actin filament binding;actin filament bundle assembly |  |  |
| Phvul.001G133600.1 | disease resistance RGA1 | ADP binding;defense response |  |  |
| Phvul.001G134300.1 | disease resistance RGA1 | phosphoprotein phosphatase activity;ADP binding;protein dephosphorylation;defense response | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |

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| Phvul.001G135900.1 | armadillo beta-catenin-like repeat |  |  |  |
| Phvul.001G136300.1 | oligopeptide transporter OPT family | integral component of membrane;transmembrane transport |  |  |
| Phvul.001G136300.2 | oligopeptide transporter OPT family | integral component of membrane;transmembrane transport |  |  |
| Phvul.001G137300.1 | probably inactive leucine-rich repeat receptor kinase At5g06940 | integral component of membrane;protein kinase activity;ATP binding;2-alkenal reductase [NAD(P)] activity;protein phosphorylation;oxidation-reduction process | ec:1.3.1.74 |  |
| Phvul.001G137800.2 | ribosomal RNA processing brix domain | nucleolus;RNA binding;ribosomal large subunit assembly |  |  |
| Phvul.001G137800.4 | ribosomal RNA processing brix domain | nucleolus;RNA binding;ribosomal large subunit assembly |  |  |
| Phvul.001G138100.1 | tRNA-splicing endonuclease subunit Sen2-1-like | tRNA-intron endonuclease complex;tRNA-intron endonuclease activity;nucleic acid binding;lyase activity;tRNA-type intron splice site recognition and cleavage;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1.31;ec:3.1.27;ec:3.1.27.9;ec:3.1 |  |
| Phvul.001G140300.1 | TBCC domain-containing 1-like | integral component of membrane;cell morphogenesis |  |  |
| Phvul.001G142700.1 | nudix hydrolase 23, chloroplastic | hydrolase activity;flavin-containing compound metabolic process |  |  |
| Phvul.001G143000.1 | WRC | nucleus;transcription, DNA-templated;developmental process |  |  |
| Phvul.001G143000.2 | WRC | nucleus;transcription, DNA-templated;developmental process |  |  |
| Phvul.001G144100.1 | E3 ubiquitin- ligase SINAT2 | nucleus;cytoplasm;zinc ion binding;ligase activity;ubiquitin protein ligase activity;apoptotic process;multicellular organismal development;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;proteasome-mediated ubiquitin-dependent protein catabolic process |  |  |
| Phvul.001G144400.1 | DNA-directed RNA polymerase subunit beta | chloroplast |  |  |
| Phvul.001G144700.1 | colon cancer-associated Mic1 |  |  |  |
| Phvul.001G146800.1 | receptor-like cytosolic serine threonine- kinase RBK2 | protein serine/threonine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.001G146900.1 | probable LRR receptor-like serine threonine- kinase RKF3 | plasma membrane;integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 |  |
| Phvul.001G150700.1 | Rho GTPase | integral component of mitochondrial outer membrane;GTPase activity;calcium ion binding;GTP binding;mitochondrion organization;small GTPase mediated signal transduction;metabolic process;protein transport | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.001G151200.1 | Ribosome biogenesis GTPase A | cell;GTPase activity;GTP binding;maltose metabolic process;phosphatidylglycerol biosynthetic process;chloroplast relocation;thylakoid membrane organization;starch biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;ncRNA metabolic process;ribosome biogenesis | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.001G151300.1 | ARM REPEAT PROTEIN INTERACTING WITH ABF2-like |  |  |  |
| Phvul.001G152000.1 | fatty-acid-binding 1 | mitochondrion;chloroplast envelope;fatty acid binding;intramolecular lyase activity;fatty acid metabolic process |  |  |

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| Phvul.001G152600.1 | plant T24G3-80 | | | |
| Phvul.001G154100.1 | NETWORKED 1D-like | | | |
| Phvul.001G154300.1 | serine threonine-kinase Nek4-like | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.001G154300.2 | serine threonine-kinase Nek4-like | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.001G154300.3 | serine threonine-kinase Nek4-like | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.001G155100.1 | hypothetical protein PHAVU_001G155100g | | | |
| Phvul.001G155300.3 | hypothetical protein PHAVU_001G155300g | plastid | | |
| Phvul.001G160900.1 | DUF4283 domain | nucleic acid binding;zinc ion binding | | |
| Phvul.001G162600.1 | glutathione gamma-glutamylcysteinyltransferase 1 | glutathione gamma-glutamylcysteinyltransferase activity;metal ion binding;response to metal ion;phytochelatin biosynthetic process | ec:2.3.2.15 | |
| Phvul.001G162700.1 | glutathione gamma-glutamylcysteinyltransferase 3-like | glutathione gamma-glutamylcysteinyltransferase activity;metal ion binding;response to metal ion;phytochelatin biosynthetic process | ec:2.3.2.15 | |
| Phvul.001G162800.1 | long-chain-alcohol oxidase FAO2-like | integral component of membrane;long-chain-alcohol oxidase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.1.3.20 | |
| Phvul.001G163300.1 | BREAST CANCER SUSCEPTIBILITY 1 homolog | plasma membrane;integral component of membrane;BRCA1-BARD1 complex;BRCA1-A complex;ubiquitin-protein transferase activity;zinc ion binding;ligase activity;double-strand break repair via homologous recombination;DNA replication;protein ubiquitination;chromatin modification;positive regulation of histone acetylation;negative regulation of histone acetylation;regulation of cell proliferation;macromolecule methylation;negative regulation of fatty acid biosynthetic process;positive regulation of transcription from RNA polymerase II promoter;leaf development;positive regulation of cell cycle arrest | | |
| Phvul.001G163300.2 | BREAST CANCER SUSCEPTIBILITY 1 like | plasma membrane;integral component of membrane;BRCA1-BARD1 complex;BRCA1-A complex;ubiquitin-protein transferase activity;zinc ion binding;ligase activity;double-strand break repair via homologous recombination;DNA replication;protein ubiquitination;chromatin modification;positive regulation of histone acetylation;negative regulation of histone acetylation;regulation of cell proliferation;macromolecule methylation;negative regulation of fatty acid biosynthetic process;positive regulation of transcription from RNA polymerase II promoter;leaf development;positive regulation of cell cycle arrest | | |
| Phvul.001G163800.1 | probable LRR receptor-like serine threonine- kinase At4g08850 | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.001G165300.1 | Subtilisin-like protease SDD1 | cell wall;external side of plasma membrane;integral component of membrane;serine-type endopeptidase activity;2-alkenal reductase [NAD(P)] activity;proteolysis;stomatal complex morphogenesis;regulation of cell proliferation;oxidation-reduction process | ec:1.3.1.74;ec:3.4.21 | |

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| Phvul.001G165500.1 | ABC transporter C family member 5-like | plant-type vacuole;vacuolar membrane;integral component of membrane;ATP binding;sulfonylurea receptor activity;ATPase activity, coupled to transmembrane movement of substances;microtubule cytoskeleton organization;cytokinesis by cell plate formation;ER to Golgi vesicle-mediated transport;signal transduction;metabolic process;response to salt stress;cellular potassium ion homeostasis;amino acid import;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G165700.1 | drug resistance transporter-like ABC domain | plasma membrane;integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G168700.1 | transcription factor | protein dimerization activity | | |
| Phvul.001G168700.2 | transcription factor | protein dimerization activity | | |
| Phvul.001G169200.1 | Histone H4 | nucleosome;nucleolus;vacuolar membrane;Golgi apparatus;cytosol;plasma membrane;plasmodesma;chloroplast;thylakoid;DNA binding;protein heterodimerization activity;nucleosome assembly;response to water deprivation | | |
| Phvul.001G169300.1 | cation H(+) antiporter 20 | endoplasmic reticulum;integral component of membrane;monovalent cation:proton antiporter activity;protein targeting to vacuole;regulation of pH;response to stress;cellular potassium ion homeostasis;water homeostasis;hydrogen ion transmembrane transport | | |
| Phvul.001G170700.1 | ACCELERATED CELL DEATH 6-like | integral component of membrane;regulation of defense response;cellular response to salicylic acid stimulus;regulation of salicylic acid mediated signaling pathway | | |
| Phvul.001G170700.2 | ACCELERATED CELL DEATH 6-like | integral component of membrane;regulation of defense response;cellular response to salicylic acid stimulus;regulation of salicylic acid mediated signaling pathway | | |
| Phvul.001G171500.1 | exocyst complex component EXO70A1-like | exocyst;exocytosis | | |
| Phvul.001G172600.1 | serine arginine-rich splicing factor RS2Z32-like isoform X1 | nucleotide binding;nucleic acid binding;zinc ion binding | | |
| Phvul.001G172600.2 | serine arginine-rich splicing factor RS2Z32 isoform X1 | nucleotide binding;nucleic acid binding;zinc ion binding | | |
| Phvul.001G173000.1 | dirigent 17-like | | | |
| Phvul.001G174800.1 | flocculation FLO11-like isoform X1 | | | |
| Phvul.001G182700.1 | UDP-glycosyltransferase 73C6-like | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |
| Phvul.001G184000.1 | cactus-binding carboxy-terminal, cactin | | | |
| Phvul.001G185600.1 | plant T32M21-140 | membrane | | |
| Phvul.001G185600.2 | plant T32M21-140 | membrane | | |
| Phvul.001G186800.1 | PAN domain-containing At5g03700 | Golgi apparatus;integral component of membrane;recognition of pollen | | |
| Phvul.001G187200.1 | UPF0481 At3g47200-like | integral component of membrane;response to brassinosteroid | | |
| Phvul.001G188100.1 | serine threonine-kinase D6PKL1-like | cytoplasm;plasma membrane;protein serine/threonine kinase activity;ATP | ec:2.7.11 | |

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| | | binding;protein phosphorylation;intracellular signal transduction | | |
| Phvul.001G188100.2 | serine threonine-kinase D6PKL1-like | cytoplasm;plasma membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;intracellular signal transduction | ec:2.7.11 | |
| Phvul.001G188100.3 | serine threonine-kinase D6PKL1-like | cytoplasm;plasma membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;intracellular signal transduction | ec:2.7.11 | |
| Phvul.001G189900.1 | plant F3C22-140 , | | | |
| Phvul.001G190400.1 | heme-binding At3g10130, chloroplastic | chloroplast thylakoid membrane | | |
| Phvul.001G190400.2 | heme-binding At3g10130, chloroplastic | chloroplast thylakoid membrane | | |
| Phvul.001G193000.1 | embryo defective 2735 | | | |
| Phvul.001G193000.2 | embryo defective 2735 | | | |
| Phvul.001G193000.3 | embryo defective 2735 | | | |
| Phvul.001G193000.4 | embryo defective 2735 | | | |
| Phvul.001G193100.1 | B3 domain-containing At2g36080-like | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.001G194400.1 | cytokinin riboside 5 -monophosphate phosphoribohydrolase LOG7 | nucleus;cytosol;hydrolase activity, hydrolyzing N-glycosyl compounds;cytokinin biosynthetic process | | |
| Phvul.001G194700.1 | syringolide-induced B13-1-9 | plasmodesma;integral component of membrane;anchored component of plasma membrane;signal transducer activity;defense response;signal transduction | | |
| Phvul.001G196100.1 | dof zinc finger -like | DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.001G196200.1 | trafficking particle complex subunit 8 | pre-autophagosomal structure;cytoplasmic vesicle;TRAPPIII protein complex;autophagosome assembly;ER to Golgi vesicle-mediated transport;pexophagy;CVT pathway;protein localization to pre-autophagosomal structure;nucleophagy | | |
| Phvul.001G197900.1 | fasciclin-like arabinogalactan 16 | | | |
| Phvul.001G198500.1 | downstream neighbor of Son | | | |
| Phvul.001G198700.1 | F-box At5g06550 | nucleus;core promoter proximal region sequence-specific DNA binding;transferase activity;histone demethylase activity (H3-K36 specific);regulation of transcription, DNA-templated;protein targeting to mitochondrion;regulation of flower development;positive regulation of seed germination;histone H4-R3 methylation;oxidation-reduction process;histone H3-K36 demethylation | ec:1.14.11.27;ec:1.14.11 | |
| Phvul.001G198800.1 | myosin-binding 7-like | integral component of membrane | | |
| Phvul.001G204000.1 | Spermatogenesis-associated 20 | chloroplast;thymidylate kinase activity;nucleotide phosphorylation | ec:2.7.4.9-kinase | Pyrimidine metabolism |
| Phvul.001G204500.1 | CW-type zinc-finger | zinc ion binding | | |
| Phvul.001G208500.1 | histone-lysine N-methyltransferase ATX3 | nucleus;zinc ion binding;histone-lysine N-methyltransferase activity;histone lysine methylation | ec:2.1.1;ec:2.1.1.43-N-methyltransferase | Lysine degradation |
| Phvul.001G209200.1 | pectinesterase pectinesterase inhibitor | cell wall;pectinesterase activity;aspartyl esterase activity;pectinesterase inhibitor activity;cell wall modification;negative regulation of catalytic activity;pectin catabolic process | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |

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| Phvul.001G209800.3 | choline ethanolaminephosphotransferase 1 | integral component of membrane;phosphotransferase activity, for other substituted phosphate groups;phospholipid biosynthetic process | | |
| Phvul.001G210400.1 | Heat shock binding | | | |
| Phvul.001G210500.1 | P-loop nucleoside triphosphate hydrolase superfamily | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G211000.1 | cellulose synthase D5 | integral component of membrane;cellulose synthase (UDP-forming) activity;1,4-beta-D-xylan synthase activity;mannan synthase activity;microtubule cytoskeleton organization;double-strand break repair via homologous recombination;cytokinesis by cell plate formation;response to water deprivation;response to salt stress;leaf morphogenesis;response to cyclopentenone;cellulose biosynthetic process;regulation of cell proliferation;cell wall biogenesis;cell wall organization;mannosylation | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.2.24-synthase;ec:2.4.1 | Starch and sucrose metabolismAmino sugar and nucleotide sugar metabolism;Starch and sucrose metabolism |
| Phvul.001G212600.1 | DNA replication licensing factor MCM7 | nucleus;cytoplasm;MCM complex;DNA binding;DNA helicase activity;ATP binding;DNA unwinding involved in DNA replication;DNA replication initiation;DNA methylation;chromatin silencing;cell proliferation;sugar mediated signaling pathway;histone H3-K9 methylation | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.001G213200.1 | trichome birefringence-like 6 | Golgi apparatus;integral component of membrane;O-acetyltransferase activity;cell wall organization or biogenesis | ec:2.3.1 | |
| Phvul.001G213800.1 | HIT zinc finger,PAPA-1-like conserved region isoform 1 | Ino80 complex;chromatin remodeling;regulation of transcription, DNA-templated | | |
| Phvul.001G213800.2 | HIT zinc finger,PAPA-1-like conserved region isoform 1 | Ino80 complex;chromatin remodeling;regulation of transcription, DNA-templated | | |
| Phvul.001G214100.1 | DEAD-box ATP-dependent RNA helicase 24 | nucleic acid binding;ATP-dependent RNA helicase activity;ATP binding;RNA secondary structure unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G216500.1 | WD repeat-containing 6 | Cul4-RING E3 ubiquitin ligase complex | | |
| Phvul.001G217700.1 | pentatricopeptide repeat-containing At4g02750-like | microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G218500.1 | probable WRKY transcription factor 47 isoform X1 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.001G218800.1 | transcription factor PIF3-like | protein dimerization activity | | |
| Phvul.001G219300.1 | Haloacid dehalogenase-like hydrolase superfamily | hydrolase activity;metabolic process;response to nitrate;nitrate transport | | |
| Phvul.001G219500.1 | phosphatase 2C 32 | intracellular;plasma membrane;protein serine/threonine phosphatase activity;[pyruvate dehydrogenase (lipoamide)] phosphatase activity;phospholipid binding;microtubule cytoskeleton organization;cytokinesis by cell plate formation;mRNA export from nucleus;protein dephosphorylation;cell adhesion;regulation of flower development;regulation of meristem structural organization;maintenance of meristem identity;trichome morphogenesis;post-translational protein modification;actin nucleation;positive regulation of transcription, DNA-templated;root hair cell differentiation;cell wall organization | ec:3.1;ec:3.1.3.43;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |

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| Phvul.001G223300.1 | glucose-6-phosphate 1-dehydrogenase 4, chloroplastic | glucose-6-phosphate dehydrogenase activity;NADP binding;glucose metabolic process;pentose-phosphate shunt;oxidation-reduction process | ec:1.1.1.49-dehydrogenase (NADP+) | Biosynthesis of antibiotics;Pentose phosphate pathway;Glutathione metabolism |
| Phvul.001G223800.1 | chloroplast stem-loop binding of 41 kDa b, chloroplastic | vacuole;peroxisome;ribosome;plasmodesma;chloroplast stroma;chloroplast envelope;stromule;membrane;apoplast;catalytic activity;heteropolysaccharide binding;coenzyme binding;MAPK cascade;monosaccharide metabolic process;pentose-phosphate shunt;protein targeting to membrane;unsaturated fatty acid biosynthetic process;detection of biotic stimulus;response to blue light;salicylic acid biosynthetic process;photorespiration;systemic acquired resistance, salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;chloroplast relocation;leaf morphogenesis;thylakoid membrane organization;response to red light;response to chitin;photosystem II assembly;response to far red light;regulation of hydrogen peroxide metabolic process;regulation of plant-type hypersensitive response;chlorophyll biosynthetic process;carotenoid biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;cell differentiation;negative regulation of defense response;plastid translation;ncRNA metabolic process;regulation of protein dephosphorylation;transcription from plastid promoter;positive regulation of catalytic activity;regulation of multi-organism process;positive regulation of translation;positive regulation of transcription, DNA-templated;defense response to fungus | | |
| Phvul.001G224800.1 | Rab9 effector with kelch motifs | | | |
| Phvul.001G224800.2 | Rab9 effector with kelch motifs | | | |
| Phvul.001G224900.1 | Homeobox knotted-1-like 1 | nucleus;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.001G225100.1 | hypothetical protein PHAVU_001G225100g | | | |
| Phvul.001G226000.1 | calmodulin-binding 60 G-like | calmodulin binding;single-organism cellular process;innate immune response;regulation of cellular process;defense response to other organism | | |
| Phvul.001G226200.1 | Calmodulin-binding, isoform 2, partial | calmodulin binding;signal transduction;defense response, incompatible interaction;regulation of cellular metabolic process;cellular metabolic process;regulation of innate immune response;cellular response to acid chemical;cellular response to organic substance;cellular response to oxygen-containing compound | | |
| Phvul.001G227600.1 | Serine threonine kinases,ATP binding,catalytics isoform 1 | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.001G229700.1 | nudix hydrolase 18, mitochondrial-like | hydrolase activity;metabolic process | | |
| Phvul.001G232200.1 | pyridoxal kinase | cytosol;pyridoxal kinase activity;pyridoxine biosynthetic process;pyridoxal 5'-phosphate salvage;trichoblast differentiation;phosphorylation;hyperosmotic salinity response | ec:2.7.1.35-kinase | Vitamin B6 metabolism |
| Phvul.001G233800.1 | anaphase promoting complex subunit 2 | anaphase-promoting complex;spindle;ubiquitin protein ligase binding;ubiquitin protein ligase activity;cell-cell signaling;gamete generation;megagametogenesis;virus induced gene silencing;production of ta-siRNAs involved | | |

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| | | in RNA interference;regulation of DNA endoreduplication;production of miRNAs involved in gene silencing by miRNA;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of cell division;regulation of unidimensional cell growth | | |
| Phvul.001G233800.2 | anaphase promoting complex subunit 2 | anaphase-promoting complex;spindle;ubiquitin protein ligase binding;ubiquitin protein ligase activity;cell-cell signaling;gamete generation;megagametogenesis;virus induced gene silencing;production of ta-siRNAs involved in RNA interference;regulation of DNA endoreduplication;production of miRNAs involved in gene silencing by miRNA;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of cell division;regulation of unidimensional cell growth | | |
| Phvul.001G236700.1 | stellacyanin-like | anchored component of plasma membrane;electron carrier activity | | |
| Phvul.001G237000.2 | integral membrane Yip1 family | integral component of membrane | | |
| Phvul.001G238900.1 | UDP-glycosyltransferase 76F1-like | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |
| Phvul.001G239800.3 | Trafficking particle complex subunit 5 | intracellular;ligase activity;cellulose biosynthetic process;Golgi vesicle transport | | |
| Phvul.001G240000.1 | Myb SANT-like DNA-binding domain | | | |
| Phvul.001G240900.1 | 26S proteasome non-ATPase regulatory subunit 7 homolog A | proteasome complex;integral component of membrane;proteasome-mediated ubiquitin-dependent protein catabolic process | | |
| Phvul.001G241300.1 | nematode resistance -like HSPRO2 | defense response | | |
| Phvul.001G241900.1 | Arginyl-tRNA--transferase 1 | cytoplasm;arginyltransferase activity;arginine-tRNA ligase activity;ATP binding;arginyl-tRNA aminoacylation;protein arginylation | ec:6.1.1;ec:2.3.2.8;ec:6.1.1.19-ligase | Aminoacyl-tRNA biosynthesis |
| Phvul.001G242800.1 | DNA replication complex GINS PSF3-like | nucleus;DNA replication | | |
| Phvul.001G243100.1 | phosphoinositide-specific phospholipase C family | intracellular;phosphatidylinositol phospholipase C activity;signal transducer activity;lipid catabolic process;intracellular signal transduction | ec:3.1.1;ec:3.1;ec:3.1.4.11-phospholipase C | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.001G243800.1 | serine threonine-kinase CCR3 | intracellular;integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein homodimerization activity;protein phosphorylation;protein targeting to membrane;response to ethylene;abscisic acid-activated signaling pathway;regulation of plant-type hypersensitive response;intracellular signal transduction;negative regulation of programmed cell death | ec:2.7.11 | |
| Phvul.001G244100.1 | N-(5-phosphoribosyl)anthranilate isomerase | phosphoribosylanthranilate isomerase activity;tryptophan biosynthetic process | ec:5.3.1.24-isomerase | Biosynthesis of antibiotics;Phenylalanine, tyrosine and tryptophan biosynthesis |
| Phvul.001G244100.2 | N-(5-phosphoribosyl)anthranilate isomerase | phosphoribosylanthranilate isomerase activity;tryptophan biosynthetic process | ec:5.3.1.24-isomerase | Biosynthesis of antibiotics;Phenylalanine, tyrosine and tryptophan biosynthesis |
| Phvul.001G244900.1 | UDP-glucose pyrophosphorylase | cytosol;UDP-N-acetylglucosamine diphosphorylase activity;UDP-N-acetylglucosamine biosynthetic process;cellular response to phosphate starvation;galactolipid biosynthetic process | ec:2.7.7.23-diphosphorylase | Biosynthesis of antibiotics;Amino sugar and nucleotide sugar metabolism |

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| Phvul.001G245100.1 | probable inactive serine threonine-kinase bub1 | kinase activity;mitotic spindle assembly checkpoint;phosphorylation | | |
| Phvul.001G246000.1 | DEAD-box ATP-dependent RNA helicase 18 | RNA binding;ATP-dependent RNA helicase activity;ATP binding;RNA secondary structure unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G247500.1 | Sel1 repeat | metal ion binding;metal ion transport | | |
| Phvul.001G247800.1 | PLAC8 family | integral component of membrane | | |
| Phvul.001G250100.1 | cellulose synthase-interactive | | | |
| Phvul.001G250100.2 | cellulose synthase-interactive | | | |
| Phvul.001G252900.1 | chaperone -like | ATP binding;heat shock protein binding;metal ion binding;unfolded protein binding;protein folding;response to heat | | |
| Phvul.001G254100.1 | helicase, IBR and zinc finger | integral component of membrane;ATP-dependent RNA helicase activity;ATP binding;zinc ion binding;poly(A) RNA binding;RNA processing | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G254200.1 | transmembrane , | integral component of membrane | | |
| Phvul.001G254400.1 | probable glucan 1,3-beta-glucosidase A | integral component of membrane;glucan exo-1,3-beta-glucosidase activity;protein binding, bridging;actin filament binding;carbohydrate metabolic process;actin filament organization | ec:3.2.1.58-1,3-beta-glucosidase;ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolismStarch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.001G256000.1 | GLE1 isoform X1 | nuclear pore;membrane;mitotic recombination;embryo sac egg cell differentiation;poly(A)+ mRNA export from nucleus;seed development | | |
| Phvul.001G259600.1 | flocculation FLO11-like | | | |
| Phvul.001G260000.1 | urease | urease activity;nickel cation binding;urea catabolic process | ec:3.5.1.5-ec:3.5.1.5 | urease |
| Phvul.001G260800.1 | ribosome biogenesis GTPase | GTPase activity;GTP binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.001G262100.1 | alpha-ketoglutarate-dependent dioxygenase alkB | dioxygenase activity;DNA repair;oxidation-reduction process | | |
| Phvul.001G263600.1 | 15-cis-zeta-carotene isomerase, chloroplastic | integral component of membrane;9,15,9'-tri-cis-zeta-carotene isomerase activity;carotene biosynthetic process | | |
| Phvul.001G264300.1 | DNA topoisomerase 3-beta isoform X1 | DNA binding;DNA topoisomerase type I activity;DNA topological change;photoperiodism, flowering | ec:5.99.1.2;ec:5.99.1 | |
| Phvul.001G264500.1 | phragmoplast-associated kinesin-related | kinesin complex;microtubule;ATP binding;microtubule binding;ATP-dependent microtubule motor activity, plus-end-directed;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.4;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.001G264600.1 | C2H2 type zinc finger | mitochondrion;nucleic acid binding;transcription factor activity, sequence-specific DNA binding;metal ion binding;regulation of transcription, DNA-templated | | |
| Phvul.002G002200.1 | serine threonine-kinase SAPK3-like | cytoplasm;plasma membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;intracellular signal transduction | ec:2.7.11 | |
| Phvul.002G002200.2 | serine threonine-kinase SAPK3-like | cytoplasm;plasma membrane;protein serine/threonine kinase activity;ATP | ec:2.7.11 | |

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| | | binding;protein phosphorylation;intracellular signal transduction | | |
| Phvul.002G003300.1 | regulator of nonsense transcripts 1 homolog | cytosol;plasma membrane;plasmodesma;integral component of membrane;DNA binding;helicase activity;ATP binding;zinc ion binding;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;response to wounding;response to sucrose;salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;sugar mediated signaling pathway;RNA interference;defense response to bacterium;long-day photoperiodism;cotyledon development | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.002G003300.2 | regulator of nonsense transcripts 1 homolog | cytosol;plasma membrane;plasmodesma;integral component of membrane;DNA binding;helicase activity;ATP binding;zinc ion binding;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;response to wounding;response to sucrose;salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;sugar mediated signaling pathway;RNA interference;defense response to bacterium;long-day photoperiodism;cotyledon development | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.002G004400.1 | pentatricopeptide repeat-containing At1g32415, mitochondrial-like | microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G007900.1 | Tubulin alpha-2 chain | cytoplasm;microtubule;GTPase activity;structural constituent of cytoskeleton;GTP binding;microtubule-based process;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.002G009800.1 | Histone-lysine N-methyltransferase NSD3, | | | |
| Phvul.002G009900.1 | galactomannan galactosyltransferase 1-like | Golgi membrane;integral component of membrane;xyloglucan 6-xylosyltransferase activity;metabolic process;cell wall organization | ec:2.4.2.39 | |
| Phvul.002G010100.1 | transmembrane , | integral component of membrane | | |
| Phvul.002G010800.1 | peptidyl-prolyl cis-trans isomerase CYP65 | nucleus;peptidyl-prolyl cis-trans isomerase activity;ligase activity;ubiquitin-ubiquitin ligase activity;protein polyubiquitination;protein peptidyl-prolyl isomerization;protein folding | ec:5.2.1.8 | |
| Phvul.002G011100.1 | 60S ribosomal L26-1 | cytosolic large ribosomal subunit;structural constituent of ribosome;cytoplasmic translation;ribosomal large subunit biogenesis | | |
| Phvul.002G011500.1 | condensin-2 complex subunit G2, | nucleus;mitochondrion | | |
| Phvul.002G012000.1 | probable N-acetyltransferase HLS1 | protein acetyltransferase complex;peptide alpha-N-acetyltransferase activity;N-terminal protein amino acid acetylation | ec:2.3.1.88;ec:2.3.1 | |
| Phvul.002G012300.1 | Peroxidase 51 | extracellular region;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;hydrogen peroxide catabolic process;oxidation-reduction process;cellular oxidant detoxification | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.002G012600.1 | Ribonuclease 3 | nucleus;double-stranded RNA binding;ribonuclease III activity;thylakoid membrane organization;production of ta-siRNAs involved in RNA interference;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;primary miRNA processing;pre-miRNA processing;defense response to virus;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1.30;ec:3.1.26;ec:3.1;ec:3.1.26.3 | |
| Phvul.002G013900.1 | suppressor of RPS4-RLD 1-like | nucleus;perinuclear region of cytoplasm;protein complex scaffold;mitotic cell cycle;methylation-dependent chromatin silencing;RNA processing;defense response to bacterium, incompatible interaction;vernalization response;RNA | | |

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| | | interference;negative regulation of defense response;post-translational protein modification;positive regulation of transcription, DNA-templated | | |
| Phvul.002G014400.1 | probable indole-3-acetic acid-amido synthetase | | | |
| Phvul.002G014800.1 | cytochrome P450 81E8-like | integral component of membrane;iron ion binding;heme binding;aromatase activity;oxidation-reduction process | ec:1.14.14.1-monooxygenase;ec:1.14.14 | Linoleic acid metabolism;Arachidonic acid metabolism;Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Caffeine metabolism;Aminobenzoate degradation;Tryptophan metabolism;Fatty acid degradation;Retinol metabolism;Steroid hormone biosynthesis |
| Phvul.002G017000.1 | filament-like plant 7 | | | |
| Phvul.002G017400.1 | F-box At5g67140 | ligase activity;metabolic process | | |
| Phvul.002G018100.1 | MAP3K-like kinase | cytoplasm;protein serine/threonine kinase activity;ATP binding;regulation of mitotic cell cycle;signal transduction by protein phosphorylation;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process | ec:2.7.11 | |
| Phvul.002G018900.1 | CLK4-associating serine arginine rich | | | |
| Phvul.002G021600.1 | Kinase superfamily isoform 2 | nucleus;cytosol;ATP binding;calcium-dependent protein serine/threonine kinase activity;protein phosphatase binding;sucrose metabolic process;protein phosphorylation;unsaturated fatty acid biosynthetic process;response to water deprivation;response to salt stress;response to abscisic acid;stomatal movement;regulation of stomatal movement;regulation of anion channel activity;triglyceride biosynthetic process;intracellular signal transduction;growth;defense response to bacterium;hydrogen peroxide catabolic process;leaf development;regulation of reactive oxygen species metabolic process | ec:2.7.11 | |
| Phvul.002G022500.1 | nuclear pore complex NUP58 isoform X1 | nuclear pore;peroxidase activity;nucleocytoplasmic transport;cellular oxidant detoxification | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.002G022800.1 | cytochrome P450 CYP82D47-like | iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.002G024200.1 | DUF4228 domain | | | |
| Phvul.002G026600.1 | Major facilitator superfamily isoform 1 | integral component of membrane;transmembrane transport | | |
| Phvul.002G027000.1 | probable Xaa-Pro aminopeptidase P | cytosol;plasma membrane;aminopeptidase activity;N-1-naphthylphthalamic acid binding;metal ion binding;protein N-linked glycosylation;proteolysis;lipid transport;intra-Golgi vesicle-mediated transport;auxin polar transport;lithium ion transport;protein import into peroxisome matrix | ec:3.4.11 | |
| Phvul.002G029800.1 | succinate dehydrogenase [ubiquinone] flavo subunit 1, mitochondrial | mitochondrial respiratory chain complex II, succinate dehydrogenase complex (ubiquinone);succinate dehydrogenase (ubiquinone) activity;flavin adenine dinucleotide binding;tricarboxylic acid | ec:1.3.99.1;ec:1.3.5.1-dehydrogenase | Carbon fixation pathways in prokaryotes;Oxidative phosphorylation;Biosynthesis of antibiotics;Citrate cycle |

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| | | cycle;mitochondrial electron transport, succinate to ubiquinone | | (TCA cycle);Butanoate metabolism |
| Phvul.002G031200.1 | ATPase family AAA domain-containing 3 | ATP binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G031600.1 | laccase-11-like | apoplast;copper ion binding;oxidoreductase activity, oxidizing metal ions;hydroquinone:oxygen oxidoreductase activity;lignin biosynthetic process;lignin catabolic process;oxidation-reduction process | ec:1.10.3.2;ec:1.10.3 | |
| Phvul.002G032000.1 | pentatricopeptide repeat-containing At5g66520 | chloroplast;microtubule-severing ATPase activity;cytidine to uridine editing;mRNA modification;chloroplast RNA modification | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G033000.1 | Isoflavone reductase | oxidoreductase activity;oxidation-reduction process | | |
| Phvul.002G033200.1 | isoflavone reductase | integral component of membrane;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.002G033200.2 | isoflavone reductase | integral component of membrane;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.002G034200.1 | heat shock with TPR , | cellular component organization;single-organism cellular process;single-organism developmental process;anatomical structure development | | |
| Phvul.002G034300.1 | zinc finger CCCH domain-containing 55-like | integral component of membrane;nucleotide binding;RNA binding;metal ion binding | | |
| Phvul.002G035300.1 | DUF506 family | | | |
| Phvul.002G035500.1 | abhydrolase domain-containing | hydrolase activity;metabolic process | | |
| Phvul.002G035700.1 | peptidyl-prolyl cis-trans isomerase FKBP53 | endoplasmic reticulum membrane;peptidyl-prolyl cis-trans isomerase activity;FK506 binding;protein peptidyl-prolyl isomerization;transport;chaperone-mediated protein folding | ec:5.2.1.8 | |
| Phvul.002G035800.1 | nuclear transport factor 2 (NTF2) family | chloroplast thylakoid membrane;peptidyl-prolyl cis-trans isomerase activity;protein peptidyl-prolyl isomerization;protein folding;transport;chlorophyll catabolic process | ec:5.2.1.8 | |
| Phvul.002G036500.1 | pentatricopeptide repeat-containing At3g18110, chloroplastic | microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G037400.1 | transferring glycosyl group transferase | integral component of membrane;transferase activity;metabolic process | | |
| Phvul.002G037800.1 | tudor PWWP MBT superfamily | | | |
| Phvul.002G039600.1 | SMG9 | | | |
| Phvul.002G040200.1 | Cellulose synthase D3 | integral component of membrane;cellulose synthase (UDP-forming) activity;1,4-beta-D-xylan synthase activity;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.2.24-synthase;ec:2.4.1 | Starch and sucrose metabolismAmino sugar and nucleotide sugar metabolism;Starch and sucrose metabolism |
| Phvul.002G040500.1 | heat stress transcription factor A-1e-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.002G041400.1 | PLATZ transcription factor family | | | |
| Phvul.002G041700.1 | RING FYVE PHD zinc finger , | nucleic acid binding;zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.002G043800.1 | NETWORKED 1A-like | transferase activity | | |
| Phvul.002G045700.1 | Chromodomain-helicase-DNA-binding 4 | DNA binding;helicase activity;zinc ion binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |

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| Phvul.002G047800.1 | glyco membrane precursor GPI-anchored | integral component of membrane | | |
| Phvul.002G048900.1 | tyrosyl-DNA phosphodiesterase 1 isoform X1 | nucleus;3'-tyrosyl-DNA phosphodiesterase activity;DNA repair;virus induced gene silencing;vegetative phase change | ec:3.1 | |
| Phvul.002G049200.1 | probable UDP-3-O-acylglucosamine N-acyltransferase 2, mitochondrial | N-acyltransferase activity;lipid A biosynthetic process | ec:2.3.1 | |
| Phvul.002G049300.1 | cysteine-rich receptor kinase 10 | plasma membrane;plasmodesma;integral component of membrane;nucleic acid binding;protein serine/threonine kinase activity;ATP binding;methyltransferase activity;protein phosphorylation;defense response;methylation | ec:2.7.11 | |
| Phvul.002G049700.1 | DUF1005 family | | | |
| Phvul.002G050000.1 | cytochrome c heme attachment (chloroplast) | plastid;thylakoid;integral component of membrane;heme binding;cytochrome complex assembly | | |
| Phvul.002G050100.1 | NADH-plastoquinone oxidoreductase subunit 4 (chloroplast) | chloroplast thylakoid membrane;integral component of membrane;NADH dehydrogenase (ubiquinone) activity;quinone binding;ATP synthesis coupled electron transport | ec:1.6.5.3-reductase (H+-translocating);ec:1.6.99.5;ec:1.6.99.3-dehydrogenase | Oxidative phosphorylationOxidative phosphorylation |
| Phvul.002G052200.1 | 40S ribosomal S29 | integral component of membrane;cytosolic small ribosomal subunit;RNA binding;structural constituent of ribosome;zinc ion binding;translation | | |
| Phvul.002G052400.1 | probable polyamine transporter At3g19553 | integral component of membrane;L-amino acid transmembrane transporter activity;polyamine transmembrane transporter activity;antiporter activity;hydrolase activity;amino acid transmembrane transport;chlorophyll catabolic process;polyamine transmembrane transport | | |
| Phvul.002G053800.1 | dnaJ homolog subfamily C member 21-like | nucleus;nucleic acid binding;zinc ion binding;protein folding | | |
| Phvul.002G054300.1 | CHROMATIN REMODELING 25 | ATP binding;transferase activity;hydrolase activity;synapsis;reciprocal meiotic recombination;male meiosis;response to ionizing radiation;vegetative to reproductive phase transition of meristem;somatic cell DNA recombination;regulation of telomere maintenance;telomere maintenance in response to DNA damage;post-translational protein modification;double-strand break repair via synthesis-dependent strand annealing;positive regulation of transcription, DNA-templated | | |
| Phvul.002G054400.1 | presequence protease 1, chloroplastic mitochondrial-like | metalloendopeptidase activity;zinc ion binding;protein processing | ec:3.4.24 | |
| Phvul.002G054700.1 | Histone deacetylase 19 | nucleus;NAD-dependent histone deacetylase activity (H3-K14 specific);transcription, DNA-templated;regulation of transcription, DNA-templated;histone H3 deacetylation | ec:3.5.1.98 | |
| Phvul.002G054700.2 | Histone deacetylase 19 | nucleus;NAD-dependent histone deacetylase activity (H3-K14 specific);transcription, DNA-templated;regulation of transcription, DNA-templated;histone H3 deacetylation | ec:3.5.1.98 | |
| Phvul.002G055700.1 | ethylene-responsive transcription factor 1A | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.002G057100.1 | DNA mismatch repair MSH4 isoform X3 | synaptonemal complex;plasmodesma;germ cell nucleus;damaged DNA binding;ATP binding;mismatched DNA binding;cytokinesis by cell plate formation;double-strand break repair;mitotic recombination;sister chromatid cohesion;mitotic nuclear division;synapsis;response to gamma | | |

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|  |  | radiation;regulation of cell cycle process;meiotic mismatch repair involved in reciprocal meiotic recombination;regulation of telomere maintenance;multicellular organism reproduction;meiotic DNA double-strand break formation;telomere maintenance in response to DNA damage |  |  |
| Phvul.002G057800.1 | agenet domain |  |  |  |
| Phvul.002G057800.2 | agenet domain |  |  |  |
| Phvul.002G058500.1 | pentatricopeptide repeat-containing At1g09820 |  |  |  |
| Phvul.002G058500.2 | pentatricopeptide repeat-containing At1g09820 |  |  |  |
| Phvul.002G058500.3 | pentatricopeptide repeat-containing At1g09820 |  |  |  |
| Phvul.002G058700.1 | AP-5 complex subunit beta-1-like |  |  |  |
| Phvul.002G060400.1 | HAT transposon superfamily | DNA binding;protein dimerization activity |  |  |
| Phvul.002G061100.1 | thylakoid lumenal | chloroplast thylakoid membrane |  |  |
| Phvul.002G061400.1 | pentatricopeptide repeat-containing At4g18975, chloroplastic | nutrient reservoir activity;mitotic cell cycle;RNA processing |  |  |
| Phvul.002G061800.1 | oxysterol-binding -related 2A-like isoform X1 |  |  |  |
| Phvul.002G062500.1 | phosphatidylinositol phosphatidylcholine transfer SFH11-like isoform X1 | intracellular;transporter activity;transport |  |  |
| Phvul.002G063500.1 | polygalacturonase At1g48100 | extracellular region;integral component of membrane;polygalacturonase activity;galacturan 1,4-alpha-galacturonidase activity;carbohydrate metabolic process;cell wall organization | ec:3.2.1.15-pectin depolymerase;ec:3.2.1.67-1,4-alpha-galacturonidase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsStarch and sucrose metabolism;Pentose and glucuronate interconversions |
| Phvul.002G063700.1 | cysteine-rich receptor kinase 2 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein folding;oligopeptide transport;defense response;response to heat;response to high light intensity;response to endoplasmic reticulum stress;response to hydrogen peroxide;protein autophosphorylation | ec:2.7.11 |  |
| Phvul.002G063700.2 | cysteine-rich receptor kinase 2 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein folding;oligopeptide transport;defense response;response to heat;response to high light intensity;response to endoplasmic reticulum stress;response to hydrogen peroxide;protein autophosphorylation | ec:2.7.11 |  |
| Phvul.002G064400.1 | NSP-INTERACTING KINASE 3 | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;microtubule nucleation;regulation of meristem growth;peptidyl-tyrosine phosphorylation;anther development | ec:2.7.11;ec:2.7.10;ec:2.7.10.2-protein-tyrosine kinase;ec:2.7.10.1 | T cell receptor signaling pathway |
| Phvul.002G066000.1 | transcription initiation factor IIB-2-like | nucleus;TFIIB-class transcription factor binding;double-stranded DNA binding;translation initiation factor activity;zinc ion binding;RNA polymerase binding;DNA- |  |  |

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| | | templated transcription, initiation;regulation of transcription, DNA-templated;translational initiation;embryo development ending in seed dormancy;pollen germination;stomatal lineage progression | | |
| Phvul.002G066300.1 | plant T7N9-9 | | | |
| Phvul.002G067200.1 | homeobox-leucine zipper HAT5 | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.002G069000.1 | hypothetical protein PHAVU_002G069000g | maltose metabolic process;stomatal complex morphogenesis;starch biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;positive regulation of transcription, DNA-templated | | |
| Phvul.002G070100.1 | phosphatidylinositol 3-kinase, root isoform | pre-autophagosomal structure;endosome;peroxisome;phosphatidylinositol 3-kinase complex, class III, type I;phosphatidylinositol 3-kinase complex, class III, type II;ATP binding;1-phosphatidylinositol-3-kinase activity;autophagosome assembly;protein phosphorylation;protein N-linked glycosylation;endocytosis;response to salt stress;vegetative to reproductive phase transition of meristem;endosomal transport;protein desumoylation;pexophagy;inositol trisphosphate metabolic process;phosphatidylinositol-3-phosphate biosynthetic process;phosphatidylinositol phosphorylation;inositol phosphate dephosphorylation;phosphatidylinositol-mediated signaling;hydrogen peroxide biosynthetic process;microgametogenesis | ec:2.7.1;ec:2.7.1.137-3-kinase | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.002G071800.1 | DUF936 family | | | |
| Phvul.002G072100.1 | aldehyde dehydrogenase family 2 member B7, mitochondrial-like | aldehyde dehydrogenase (NAD) activity;vegetative to reproductive phase transition of meristem;protein desumoylation;hydrogen peroxide biosynthetic process;oxidation-reduction process | ec:1.2.1.3-dehydrogenase (NAD+) | Arginine and proline metabolism;Chloroalkane and chloroalkene degradation;Pyruvate metabolism;Biosynthesis of antibiotics;Tryptophan metabolism;Valine, leucine and isoleucine degradation;Limonene and pinene degradation;beta-Alanine metabolism;Lysine degradation;Glycolysis / Gluconeogenesis;Fatty acid degradation;Glycerolipid metabolism;Ascorbate and aldarate metabolism;Histidine metabolism;Pentose and glucuronate interconversions |
| Phvul.002G076100.1 | hypothetical protein PHAVU_002G076100g | | | |
| Phvul.002G076700.1 | metalloendo ase 1-like | membrane;extracellular matrix;metalloendopeptidase activity;zinc ion binding;proteolysis | ec:3.4.24 | |
| Phvul.002G077100.1 | formin 8 | integral component of membrane | | |

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| Phvul.002G077800.1 | paired amphipathic helix Sin3-like 4 isoform X1 | histone deacetylase complex;chromatin;RNA polymerase II transcription corepressor activity;histone deacetylase activity;negative regulation of transcription from RNA polymerase II promoter;histone deacetylation | ec:3.5.1.98 | |
| Phvul.002G077800.2 | paired amphipathic helix Sin3-like 4 isoform X1 | histone deacetylase complex;chromatin;RNA polymerase II transcription corepressor activity;histone deacetylase activity;negative regulation of transcription from RNA polymerase II promoter;histone deacetylation | ec:3.5.1.98 | |
| Phvul.002G078200.1 | DNA topoisomerase 2-binding 1-A isoform X1 | isomerase activity;metabolic process | | |
| Phvul.002G078200.2 | DNA topoisomerase 2-binding 1-A isoform X1 | isomerase activity;metabolic process | | |
| Phvul.002G078200.3 | DNA topoisomerase 2-binding 1-A isoform X1 | isomerase activity;metabolic process | | |
| Phvul.002G078200.4 | DNA topoisomerase 2-binding 1-A isoform X1 | isomerase activity;metabolic process | | |
| Phvul.002G078300.1 | UPF0392 RCOM_0530710 | Golgi apparatus;integral component of membrane | | |
| Phvul.002G079600.1 | plant F14N23-31 | | | |
| Phvul.002G079600.2 | plant F14N23-31 | | | |
| Phvul.002G081300.1 | probable leucine-rich repeat receptor kinase At1g35710 | integral component of membrane;kinase activity;phosphorylation | | |
| Phvul.002G082500.1 | transmembrane , | integral component of membrane;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | | |
| Phvul.002G085500.1 | myb X | integral component of membrane;cytosolic large ribosomal subunit;RNA binding;structural constituent of ribosome;translation;ribosome biogenesis | | |
| Phvul.002G085900.1 | probable methyltransferase PMT2 | integral component of membrane;S-adenosylmethionine-dependent methyltransferase activity;methylation | | |
| Phvul.002G086200.1 | haloacid dehalogenase-like hydrolase domain | hydrolase activity;metabolic process | | |
| Phvul.002G086200.2 | haloacid dehalogenase-like hydrolase domain | hydrolase activity;metabolic process | | |
| Phvul.002G089600.1 | SNF1-related kinase regulatory subunit gamma-1-like | integral component of membrane;transcription factor activity, sequence-specific DNA binding;kinase activity;sequence-specific DNA binding;regulation of transcription, DNA-templated;phosphorylation | | |
| Phvul.002G090200.1 | Sporulation RMD1 | mitochondrion;embryo sac egg cell differentiation;regulation of root meristem growth;regulation of DNA endoreduplication;regulation of cell division | | |
| Phvul.002G090200.2 | Sporulation RMD1 | mitochondrion;embryo sac egg cell differentiation;regulation of root meristem growth;regulation of DNA endoreduplication;regulation of cell division | | |
| Phvul.002G090200.3 | Sporulation RMD1 | mitochondrion;embryo sac egg cell differentiation;regulation of root meristem growth;regulation of DNA endoreduplication;regulation of cell division | | |
| Phvul.002G090900.1 | Eukaryotic translation initiation factor 5A | translation initiation factor activity;translation elongation factor activity;ribosome binding;translational initiation;translational frameshifting;positive regulation of translational elongation;positive regulation of translational termination | | |
| Phvul.002G091300.1 | DUF1336 family | regulation of anion channel activity | | |
| Phvul.002G091400.1 | probable S-acyltransferase 22 | integral component of membrane;zinc ion binding;protein-cysteine S-palmitoyltransferase activity;microtubule nucleation;metabolic | ec:2.3.1.225;ec:2.3.1 | |

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| | | process;plant-type cell wall organization;plant-type cell wall biogenesis;regulation of meristem growth | | |
| Phvul.002G091700.1 | O-fucosyltransferase family | cytoplasm;integral component of membrane;calcium ion binding;transferase activity, transferring glycosyl groups;metabolic process | | |
| Phvul.002G095700.1 | phytanoyl-dioxygenase domain | plasma membrane;integral component of membrane;beta-galactosidase activity;phytanoyl-CoA dioxygenase activity;oxidation-reduction process | ec:3.2.1;ec:3.2.1.23-lactase (ambiguous);ec:1.14.11.18;ec:1.14.11 | Other glycan degradation;Glycosphingolipid biosynthesis - ganglio series;Sphingolipid metabolism;Galactose metabolism;Glycosaminoglycan degradation |
| Phvul.002G097900.1 | DCD (development and cell death) domain | | | |
| Phvul.002G098200.1 | TMV resistance N-like isoform X1 | ADP binding;signal transduction | | |
| Phvul.002G098200.2 | TMV resistance N-like isoform X1 | ADP binding;signal transduction | | |
| Phvul.002G098500.1 | trypsin family | peptidase activity;proteolysis | | |
| Phvul.002G099000.1 | probable inorganic phosphate transporter 1-9 | integral component of plasma membrane;substrate-specific transmembrane transporter activity;transmembrane transport | | |
| Phvul.002G099000.2 | probable inorganic phosphate transporter 1-9 | integral component of plasma membrane;substrate-specific transmembrane transporter activity;transmembrane transport | | |
| Phvul.002G101300.1 | pyruvate kinase, cytosolic isozyme | magnesium ion binding;pyruvate kinase activity;kinase activity;potassium ion binding;glycolytic process | ec:2.7.1.40-kinase | Purine metabolism;Pyruvate metabolism;Biosynthesis of antibiotics;Glycolysis / Gluconeogenesis |
| Phvul.002G103300.1 | transmembrane , | integral component of membrane | | |
| Phvul.002G103300.2 | transmembrane , | integral component of membrane | | |
| Phvul.002G104500.1 | DNA-directed RNA polymerase II subunit 1 | DNA-directed RNA polymerase II, core complex;RNA polymerase II activity;DNA binding;transcription from RNA polymerase II promoter | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| Phvul.002G104700.1 | L-ascorbate peroxidase 3, peroxisomal | integral component of membrane;peroxidase activity;heme binding;response to oxidative stress;oxidation-reduction process;cellular oxidant detoxification | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.002G106200.1 | MID1-COMPLEMENTING ACTIVITY 1-like | | | |
| Phvul.002G106200.2 | MID1-COMPLEMENTING ACTIVITY 1-like | | | |
| Phvul.002G106200.3 | MID1-COMPLEMENTING ACTIVITY 1-like | | | |
| Phvul.002G106200.4 | MID1-COMPLEMENTING ACTIVITY 1-like | | | |
| Phvul.002G106900.1 | DUF630 family | | | |
| Phvul.002G107400.1 | FKBP12-interacting of 37 kDa | nucleus;regulation of alternative mRNA splicing, via spliceosome;mRNA methylation | | |
| Phvul.002G108000.1 | ferredoxin--NADP reductase, leaf isozyme, chloroplastic | chloroplast thylakoid membrane;chloroplast stroma;chloroplast envelope;thylakoid lumen;apoplast;nucleotide binding;ferredoxin-NADP+ reductase activity;protein binding;poly(U) RNA binding;electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity;electron transporter, transferring electrons within the noncyclic electron transport pathway of photosynthesis activity;MAPK cascade;pentose-phosphate | ec:1.18.1.2-reductase;ec:1.18.1 | Photosynthesis |

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| | | shunt;rRNA processing;protein targeting to membrane;response to cold;detection of biotic stimulus;plastid organization;salicylic acid biosynthetic process;photosynthetic electron transport in photosystem I;systemic acquired resistance, salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;response to chitin;photosystem II assembly;regulation of hydrogen peroxide metabolic process;regulation of plant-type hypersensitive response;glucosinolate biosynthetic process;negative regulation of defense response;positive regulation of catalytic activity;regulation of multi-organism process;defense response to fungus | | |
| Phvul.002G109100.1 | transcription initiation factor TFIID subunit 14b | integral component of membrane;regulation of transcription, DNA-templated | | |
| Phvul.002G110800.1 | histone H1 | nucleosome;nucleus;nucleosomal DNA binding;nucleosome assembly | | |
| Phvul.002G111600.1 | zinc finger CCCH domain-containing 44 | nucleus;DNA binding;zinc ion binding;DNA-templated transcription, initiation;histone modification | | |
| Phvul.002G113100.1 | general transcription factor 3C | | | |
| Phvul.002G114800.1 | GRIP | synaptonemal complex;trans-Golgi network;protein targeting to Golgi;mitotic cell cycle;RNA processing;reciprocal meiotic recombination;gravitropism;cellulose biosynthetic process | | |
| Phvul.002G115200.1 | tRNA nucleotidyltransferase poly(A) polymerase | RNA binding;hydrolase activity;CTP:tRNA cytidylyltransferase activity;CTP:3'-cytidine-tRNA cytidylyltransferase activity;ATP:3'-cytidine-cytidine-tRNA adenylyltransferase activity;tRNA 3'-terminal CCA addition | ec:2.7.7.25;ec:2.7.7.72 | |
| Phvul.002G117100.1 | Serine threonine- kinase SRPK | protein serine/threonine kinase activity;protein serine/threonine/tyrosine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11;ec:2.7.12.1 | |
| Phvul.002G117500.1 | glutamate receptor | integral component of membrane;G-protein coupled receptor activity;ionotropic glutamate receptor activity;ion transport;G-protein coupled receptor signaling pathway;ionotropic glutamate receptor signaling pathway | | |
| Phvul.002G117500.2 | glutamate receptor | integral component of membrane;G-protein coupled receptor activity;ionotropic glutamate receptor activity;ion transport;G-protein coupled receptor signaling pathway;ionotropic glutamate receptor signaling pathway | | |
| Phvul.002G117500.3 | glutamate receptor | integral component of membrane;G-protein coupled receptor activity;ionotropic glutamate receptor activity;ion transport;G-protein coupled receptor signaling pathway;ionotropic glutamate receptor signaling pathway | | |
| Phvul.002G121700.1 | ---NA--- | | | |
| Phvul.002G122000.1 | arabinosyltransferase XEG113-like | endosome;trans-Golgi network;integral component of membrane;microtubule-severing ATPase activity;arabinosyltransferase activity;protein glycosylation;cell wall pectin biosynthetic process;root hair cell development | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G122600.1 | long-chain-alcohol oxidase FAO4A-like | integral component of membrane;long-chain-alcohol oxidase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.1.3.20 | |
| Phvul.002G123100.1 | hypothetical protein PHAVU_002G123100g | | | |
| Phvul.002G123500.1 | probable LRR receptor-like serine threonine- kinase At3g47570 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |

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| Phvul.002G127000.1 | neutral alpha-glucosidase | chloroplast;integral component of membrane;alpha-1,4-glucosidase activity;carbohydrate binding;maltose alpha-glucosidase activity;maltose metabolic process | ec:3.2.1;ec:3.2.1.20-maltase | Starch and sucrose metabolism;Galactose metabolism |
| Phvul.002G129100.1 | probable methyltransferase PMT20 | endosome;trans-Golgi network;integral component of membrane;S-adenosylmethionine-dependent methyltransferase activity;methylation | | |
| Phvul.002G129100.2 | probable methyltransferase PMT20 | endosome;trans-Golgi network;integral component of membrane;S-adenosylmethionine-dependent methyltransferase activity;methylation | | |
| Phvul.002G129600.1 | disease resistance RGA4 | ADP binding;defense response | | |
| Phvul.002G129700.1 | disease resistance RGA4 | ADP binding;defense response | | |
| Phvul.002G130600.1 | disease resistance RGA4 | ADP binding;defense response | | |
| Phvul.002G133000.1 | CSC1 At1g32090 | Golgi apparatus;plasma membrane;plasmodesma;integral component of membrane;4-alpha-glucanotransferase activity;glycogen metabolic process | ec:2.4.1.25-disproportionating enzyme | Starch and sucrose metabolism |
| Phvul.002G133400.1 | disease resistance RPM1-like | ADP binding;defense response | | |
| Phvul.002G134200.1 | extra-large guanine nucleotide-binding 3 isoform X1 | GTPase activity;signal transducer activity;GTP binding;G-protein beta/gamma-subunit complex binding;G-protein coupled receptor signaling pathway;metabolic process;gravitropism;thigmotropism;response to ethylene;response to abscisic acid;response to sucrose;response to glucose;response to fructose;response to mannitol;root development;regulation of root morphogenesis | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.002G134200.2 | extra-large guanine nucleotide-binding 3 isoform X1 | GTPase activity;signal transducer activity;GTP binding;G-protein beta/gamma-subunit complex binding;G-protein coupled receptor signaling pathway;metabolic process;gravitropism;thigmotropism;response to ethylene;response to abscisic acid;response to sucrose;response to glucose;response to fructose;response to mannitol;root development;regulation of root morphogenesis | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.002G134200.3 | extra-large guanine nucleotide-binding 3 isoform X1 | GTPase activity;signal transducer activity;GTP binding;G-protein beta/gamma-subunit complex binding;G-protein coupled receptor signaling pathway;metabolic process;gravitropism;thigmotropism;response to ethylene;response to abscisic acid;response to sucrose;response to glucose;response to fructose;response to mannitol;root development;regulation of root morphogenesis | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.002G135100.1 | disease resistance RGA2-like | ADP binding;defense response | | |
| Phvul.002G135300.1 | plant F3C3-6 | chloroplast stroma;leaf morphogenesis;regulation of proton transport;cell differentiation;protein autophosphorylation | | |
| Phvul.002G135800.1 | ankyrin repeat | integral component of membrane | | |
| Phvul.002G136400.1 | alpha beta hydrolase domain-containing 17B | plasma membrane;hydrolase activity;metabolic process;determination of bilateral symmetry;polarity specification of adaxial/abaxial axis;meristem initiation;regulation of meristem growth | | |
| Phvul.002G136400.2 | alpha beta superfamily hydrolase | plasma membrane;hydrolase activity;metabolic process;determination of bilateral symmetry;polarity specification of adaxial/abaxial axis;meristem initiation;regulation of meristem growth | | |
| Phvul.002G137000.1 | Homeobox-leucine zipper ROC3 | nucleus;lipid binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.002G138500.1 | heat shock factor HSF8 | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA | | |

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| | | binding;regulation of transcription, DNA-templated;toxin catabolic process | | |
| Phvul.002G142800.1 | Transcription factor bHLH93 | 2-alkenal reductase [NAD(P)] activity;protein dimerization activity;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.002G142800.2 | Transcription factor bHLH93 | 2-alkenal reductase [NAD(P)] activity;protein dimerization activity;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.002G142900.1 | probable beta-D-xylosidase 6 | vacuolar membrane;plant-type cell wall;beta-glucosidase activity;xylan 1,4-beta-xylosidase activity;alpha-L-arabinofuranosidase activity;arabinan catabolic process;xylan catabolic process | ec:3.2.1.55-end alpha-L-arabinofuranosidase;ec:3.2.1.37-1,4-beta-xylosidase;ec:3.2.1;ec:3.2.1.21-gentiobiase | Amino sugar and nucleotide sugar metabolismAmino sugar and nucleotide sugar metabolism;Starch and sucrose metabolismStarch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.002G143600.1 | probable cytosolic oligopeptidase A | chloroplast;metalloendopeptidase activity;metal ion binding;proteolysis;peptide metabolic process | ec:3.4.24 | |
| Phvul.002G146600.1 | U-box domain-containing 50 | intracellular;MAP kinase kinase kinase activity;ubiquitin-protein transferase activity;ATP binding;ligase activity;MAPK cascade;activation of MAPKK activity;protein ubiquitination | ec:2.7.11;ec:2.7.11.25 | |
| Phvul.002G146700.1 | nucleobase-ascorbate transporter 11-like | integral component of membrane;transporter activity;transmembrane transport | | |
| Phvul.002G147900.1 | GPI ethanolamine phosphate transferase 2 | integral component of endoplasmic reticulum membrane;CP2 mannose-ethanolamine phosphotransferase activity;GPI anchor biosynthetic process | | |
| Phvul.002G148400.1 | exocyst subunit exo70 family | integral component of membrane | | |
| Phvul.002G149600.1 | flavonol synthase flavanone 3-hydroxylase-like | oxidoreductase activity;metal ion binding;oxidation-reduction process | | |
| Phvul.002G149600.2 | flavonol synthase flavanone 3-hydroxylase-like | oxidoreductase activity;metal ion binding;oxidation-reduction process | | |
| Phvul.002G149600.3 | flavonol synthase flavanone 3-hydroxylase-like | oxidoreductase activity;metal ion binding;oxidation-reduction process | | |
| Phvul.002G151500.1 | MATE efflux family DTX1 | plasma membrane;integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport;regulation of stomatal opening | | |
| Phvul.002G151700.1 | Armadillo repeat-containing kinesin 3 | kinesin complex;microtubule;ATP binding;microtubule binding;ATP-dependent microtubule motor activity, plus-end-directed;microtubule-based movement;protein localization;metabolic process;cytoskeleton-dependent intracellular transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.4;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G153400.1 | phospholipase D beta 1-like | membrane;phospholipase D activity;calcium ion binding;N-acylphosphatidylethanolamine-specific phospholipase D activity;lipid catabolic process;phosphatidylcholine metabolic process | ec:3.1.1;ec:3.1;ec:3.1.4.4-D | Ether lipid metabolism;Glycerophospholipid metabolism |
| Phvul.002G155900.1 | myosin heavy chain | | | |
| Phvul.002G156500.1 | vacuolar amino acid transporter 1-like | integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.002G157400.1 | pre-16S rRNA nuclease isoform X1 | nucleus;membrane;DNA binding;methyltransferase activity;zinc ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;rRNA processing;methylation;oxidation-reduction process | ec:1.14.11 | |

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| Phvul.002G157400.2 | pre-16S rRNA nuclease isoform X1 | nucleus;membrane;DNA binding;methyltransferase activity;zinc ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;rRNA processing;methylation;oxidation-reduction process | ec:1.14.11 | |
| Phvul.002G157500.1 | transcription factor jumonji ( ) domain | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;methyltransferase activity;zinc ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;mitotic cell cycle;regulation of transcription, DNA-templated;rRNA processing;vegetative to reproductive phase transition of meristem;glucuronoxylan metabolic process;protein desumoylation;methylation;xylan biosynthetic process;hydrogen peroxide biosynthetic process;oxidation-reduction process | ec:1.14.11 | |
| Phvul.002G157700.1 | RNase P Rpr2 Rpp21 subunit domain | | | |
| Phvul.002G157700.2 | RNase P Rpr2 Rpp21 subunit domain | | | |
| Phvul.002G157700.3 | RNase P Rpr2 Rpp21 subunit domain | | | |
| Phvul.002G157700.4 | RNase P Rpr2 Rpp21 subunit domain | | | |
| Phvul.002G160700.1 | respiratory burst oxidase homolog A | integral component of membrane;peroxidase activity;calcium ion binding;NAD(P)H oxidase activity;oxidation-reduction process;cellular oxidant detoxification | ec:1.6.3.1;ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.002G161000.1 | AAA domain-containing | ATP binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G161400.1 | WRKY transcription factor 19 | | | |
| Phvul.002G164900.1 | GDSL esterase lipase At4g10955-like | integral component of membrane;hydrolase activity;lipid metabolic process | | |
| Phvul.002G164900.2 | GDSL esterase lipase At4g10955-like | integral component of membrane;hydrolase activity;lipid metabolic process | | |
| Phvul.002G167200.1 | beta-galactosidase 3-like | cell wall;beta-galactosidase activity;carbohydrate binding;carbohydrate metabolic process;polyamine catabolic process;plant-type cell wall organization;phenylpropanoid metabolic process;plant-type cell wall biogenesis;regulation of meristem growth;cellular modified amino acid biosynthetic process | ec:3.2.1;ec:3.2.1.23-lactase (ambiguous) | Other glycan degradation;Glycosphingolipid biosynthesis - ganglio series;Sphingolipid metabolism;Galactose metabolism;Glycosaminoglycan degradation |
| Phvul.002G169000.1 | transmembrane , | integral component of membrane | | |
| Phvul.002G169900.1 | hypothetical protein PHAVU_002G169900g | | | |
| Phvul.002G171400.1 | disease resistance (TIR-NBS-LRR class) | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.002G175000.1 | U-box domain-containing 45-like | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.002G175400.1 | pre-mRNA-splicing factor ATP-dependent RNA | spliceosomal complex;ATP-dependent RNA helicase activity;ATP binding;poly(A) RNA binding;RNA processing;sister chromatid | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphata | Purine metabolismPurine |

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| | helicase PRP1 isoform X1 | cohesion;reciprocal meiotic recombination;response to gamma radiation;glucuronoxylan metabolic process;regulation of telomere maintenance;meiotic DNA double-strand break formation;telomere maintenance in response to DNA damage;meiotic chromosome segregation;xylan biosynthetic process | se;ec:3.6.1.15-phosphatase;ec:2.7.7 | metabolism;Thiamine metabolism |
| Phvul.002G175800.1 | carboxy-terminal region remorin | | | |
| Phvul.002G176300.1 | probable zinc transporter DDB_G0291141 | integral component of membrane;cation transmembrane transporter activity;cation transmembrane transport | | |
| Phvul.002G176700.1 | type II-like restriction endonuclease, | DNA binding;endonuclease activity;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.002G176700.2 | type II-like restriction endonuclease, | DNA binding;endonuclease activity;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.002G177300.1 | RING finger 141 | zinc ion binding;ligase activity;metabolic process | | |
| Phvul.002G177800.1 | carboxy-terminal region remorin | plasma membrane | | |
| Phvul.002G180400.1 | ornithine aminotransferase | cytoplasm;ornithine-oxo-acid transaminase activity;zinc ion binding;pyridoxal phosphate binding;identical protein binding;proline biosynthetic process;ornithine catabolic process;fatty acid beta-oxidation;peroxisome organization;plant-type hypersensitive response;arginine catabolic process to proline via ornithine;organ senescence;arginine catabolic process to glutamate;hyperosmotic salinity response | ec:2.6.1.13-aminotransferase | Arginine and proline metabolism;Biosynthesis of antibiotics |
| Phvul.002G181300.2 | Purple acid phosphatase 3 | acid phosphatase activity;dephosphorylation | ec:3.1.3.2-phosphatase;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase | Aminobenzoate degradationAminobenzoate degradation |
| Phvul.002G183300.1 | Transmembrane 214 | integral component of membrane | | |
| Phvul.002G183800.1 | pentatricopeptide repeat-containing At4g33170-like | integral component of membrane;zinc ion binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G184800.1 | serine threonine-kinase BRI1-like 2 | intracellular;integral component of membrane;transmembrane receptor protein serine/threonine kinase activity;MAP kinase kinase kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity;response to molecule of bacterial origin;transmembrane receptor protein serine/threonine kinase signaling pathway;auxin-activated signaling pathway;brassinosteroid mediated signaling pathway;regulation of meristem growth;stomatal complex morphogenesis;phloem transport;leaf vascular tissue pattern formation;peptidyl-tyrosine phosphorylation;stamen development | ec:2.7.11;ec:2.7.10;ec:2.7.11.25;ec:2.7.10.1 | |
| Phvul.002G186300.1 | zinc finger CCCH domain-containing 17 | metal ion binding;protein modification by small protein conjugation or removal | | |
| Phvul.002G186600.1 | MAP3K-like kinase | cytoplasm;protein serine/threonine kinase activity;ATP binding;regulation of mitotic cell cycle;signal transduction by protein phosphorylation;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process | ec:2.7.11 | |
| Phvul.002G188100.2 | translocator assembly and maintenance | | | |
| Phvul.002G188100.4 | translocator assembly and maintenance | | | |

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| Phvul.002G188400.1 | NAD(P)-binding rossmann-fold , | | | |
| Phvul.002G189100.1 | inositol oxygenase 2-like | cytoplasm;iron ion binding;inositol oxygenase activity;inositol catabolic process;oxidation-reduction process | ec:1.13.99.1-oxygenase | Inositol phosphate metabolism;Ascorbate and aldarate metabolism |
| Phvul.002G189700.1 | E3 ubiquitin- ligase UPL1-like isoform X1 | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination involved in ubiquitin-dependent protein catabolic process | | |
| Phvul.002G190300.1 | RNA-binding pno1-like | nucleolus;RNA binding | | |
| Phvul.002G190900.1 | ATP-dependent zinc metalloprotease FTSH 2, chloroplastic | mitochondrion;chloroplast thylakoid membrane;chloroplast envelope;integral component of membrane;ATP-dependent peptidase activity;metalloendopeptidase activity;ATP binding;zinc ion binding;proteolysis;thylakoid membrane organization;photoinhibition;photosystem II repair;PSII associated light-harvesting complex II catabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.4.24 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G193700.1 | eukaryotic cytochrome b561 | integral component of membrane;oxidation-reduction process | | |
| Phvul.002G195100.1 | hypothetical protein PHAVU_002G195100g | | | |
| Phvul.002G201500.1 | alpha N-terminal methyltransferase 1 | cytoplasm;methyltransferase activity;dolichyldiphosphatase activity;N-terminal protein amino acid methylation | ec:3.6.1;ec:3.6.1.43-dolichol diphosphatase | N-Glycan biosynthesis |
| Phvul.002G204200.1 | agenet domain | | | |
| Phvul.002G204400.1 | Auxin-induced 5NG4 | plasma membrane;integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.002G204400.2 | nodulin 21 -like transporter family | plasma membrane;integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.002G204400.3 | nodulin 21 -like transporter family | plasma membrane;integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.002G204400.4 | Auxin-induced 5NG4 | plasma membrane;integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.002G205600.1 | tRNA (guanine(10)-N2)-methyltransferase homolog | intracellular;nucleic acid binding;methyltransferase activity;tRNA modification;protein targeting to mitochondrion;methylation;2-methylguanosine metabolic process | | |
| Phvul.002G206200.1 | mitochondrial arginine transporter BAC2 | integral component of membrane;structural constituent of ribosome;translation;transmembrane transport | | |
| Phvul.002G206700.1 | WRKY transcription factor 19 | | | |
| Phvul.002G206900.1 | BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.002G209800.1 | outer envelope 64, mitochondrial-like | cytoplasm;integral component of membrane;carbon-nitrogen ligase activity, with glutamine as amido-N-donor;protein targeting to membrane;protein targeting to mitochondrion;nucleotide transport;ER to Golgi vesicle-mediated transport;metabolic process;regulation of plant-type hypersensitive response;ammonium transport;basic amino acid transport;negative regulation of programmed cell death;amino acid import;regulation of ion transport | | |
| Phvul.002G209900.1 | metacaspase-1-like isoform X1 | cysteine-type endopeptidase activity;proteolysis | ec:3.4;ec:3.4.22 | |
| Phvul.002G211500.1 | probable 2-oxoglutarate Fe(II)-dependent dioxygenase | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of | ec:1.14.11 | |

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| | | oxygen into both donors;metal ion binding;oxidation-reduction process | | |
| Phvul.002G211700.1 | 5-oxoprolinase | cytosol;plasmodesma;5-oxoprolinase (ATP-hydrolyzing) activity;glutathione catabolic process | ec:3.5.2.9-(ATP-hydrolysing) | Glutathione metabolism |
| Phvul.002G211700.2 | 5-oxoprolinase | cytosol;plasmodesma;5-oxoprolinase (ATP-hydrolyzing) activity;glutathione catabolic process | ec:3.5.2.9-(ATP-hydrolysing) | Glutathione metabolism |
| Phvul.002G211700.3 | 5-oxoprolinase | cytosol;plasmodesma;5-oxoprolinase (ATP-hydrolyzing) activity;glutathione catabolic process | ec:3.5.2.9-(ATP-hydrolysing) | Glutathione metabolism |
| Phvul.002G212300.1 | chaperone -domain | | | |
| Phvul.002G212700.1 | ycf20 | chloroplast;integral component of membrane;nonphotochemical quenching | | |
| Phvul.002G215600.1 | Heat shock 70 kDa , mitochondrial | ATP binding;unfolded protein binding;protein folding | | |
| Phvul.002G217900.1 | probably inactive leucine-rich repeat receptor kinase At5g48380 | intracellular;integral component of membrane;MAP kinase kinase kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.11.25;ec:2.7.10.1 | |
| Phvul.002G218100.1 | kinesin motor catalytic domain | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G218100.2 | kinesin motor catalytic domain | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G218400.1 | hypothetical protein PHAVU_002G218400g | integral component of membrane | | |
| Phvul.002G218400.2 | hypothetical protein PHAVU_002G218400g | integral component of membrane | | |
| Phvul.002G219400.1 | pentatricopeptide repeat-containing At1g55890, mitochondrial-like | | | |
| Phvul.002G219600.1 | transcription factor bHLH112-like | nucleus;core promoter sequence-specific DNA binding;transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding;protein dimerization activity;transcription from RNA polymerase II promoter;positive regulation of transcription from RNA polymerase II promoter | | |
| Phvul.002G221000.1 | Transcription factor MYB39 | DNA binding;response to stress;metabolic process;response to abiotic stimulus;hormone-mediated signaling pathway;cellular response to acid chemical;cellular response to oxygen-containing compound | | |
| Phvul.002G222500.1 | anaphase-promoting complex subunit 4 | anaphase-promoting complex;embryo development;regulation of mitotic metaphase/anaphase transition;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;plant ovule development | | |
| Phvul.002G223300.1 | GDSL esterase lipase At5g14450-like | plant-type cell wall;plasmodesma;hydrolase activity, acting on ester bonds;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.002G223700.1 | secretory carrier-associated membrane | integral component of membrane;protein serine/threonine/tyrosine kinase activity;protein phosphorylation;protein transport | ec:2.7.12.1 | |
| Phvul.002G223900.1 | POLLEN DEFECTIVE IN GUIDANCE 1-like | integral component of membrane;multicellular organismal process;single-organism process;anatomical structure development | | |

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| Phvul.002G223900.2 | POLLEN DEFECTIVE IN GUIDANCE 1-like isoform X1 | integral component of membrane |  |  |
| Phvul.002G224000.1 | Bromodomain 4, |  |  |  |
| Phvul.002G225200.1 | hypothetical protein PHAVU_002G225200g |  |  |  |
| Phvul.002G226200.1 | splicing factor 3B subunit 2 | spliceosomal complex |  |  |
| Phvul.002G226900.1 | RNA polymerase II C-terminal domain phosphatase-like 1 | DNA-directed RNA polymerase II, holoenzyme;CTD phosphatase activity;dephosphorylation of RNA polymerase II C-terminal domain | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.002G227400.1 | bifunctional 3-dehydroquinate dehydratase shikimate dehydrogenase, chloroplastic-like isoform X1 | 3-dehydroquinate dehydratase activity;shikimate 3-dehydrogenase (NADP+) activity;NADP binding;shikimate metabolic process;oxidation-reduction process | ec:4.2.1.10-dehydratase;ec:1.1.1.282-dehydrogenase;ec:1.1.1.25-dehydrogenase | Biosynthesis of antibiotics;Phenylalanine, tyrosine and tryptophan biosynthesisBiosynthesis of antibiotics;Phenylalanine, tyrosine and tryptophan biosynthesisBiosynthesis of antibiotics;Phenylalanine, tyrosine and tryptophan biosynthesis |
| Phvul.002G228300.1 | monothiol glutaredoxin-S17 | cytosol;electron carrier activity;protein disulfide oxidoreductase activity;nuclear division;nucleolus organization;response to heat;auxin polar transport;cell redox homeostasis;oxidation-reduction process;reactive oxygen species metabolic process |  |  |
| Phvul.002G228500.1 | vesicle-fusing ATPase | vacuole;Golgi stack;plasma membrane;plasmodesma;ATP binding;ATPase activity;intra-Golgi vesicle-mediated transport;metabolic process;Golgi to plasma membrane protein transport;Golgi vesicle docking | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G231100.1 | haloacid dehalogenase superfamily |  |  |  |
| Phvul.002G232200.1 | homeobox domain | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated |  |  |
| Phvul.002G232200.2 | homeobox domain | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated |  |  |
| Phvul.002G232500.1 | DUF4283 domain | nucleic acid binding;zinc ion binding |  |  |
| Phvul.002G233100.1 | 1-O-acylglucose:anthocyanin acyltransferase | integral component of membrane;serine-type carboxypeptidase activity;ATP binding;transferase activity, transferring acyl groups other than amino-acyl groups;ATPase activity, coupled to transmembrane movement of substances;secondary metabolic process;proteolysis involved in cellular protein catabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.4.21;ec:3.4.16 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G233700.1 | 50S ribosomal L21, mitochondrial | mitochondrial large ribosomal subunit;RNA binding;structural constituent of ribosome;translation |  |  |
| Phvul.002G233800.1 | probable ubiquitin-conjugating enzyme E2 24 | cytoplasm;ligase activity;ubiquitin protein ligase binding;ubiquitin protein ligase activity;protein ubiquitination |  |  |
| Phvul.002G235300.1 | pentatricopeptide repeat-containing At4g32450, mitochondrial-like | zinc ion binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G236500.1 | calcium ion-binding | Golgi apparatus;integral component of membrane;nuclear outer membrane- |  |  |

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| | | endoplasmic reticulum membrane network;calcium ion binding | | |
| Phvul.002G236700.1 | chlorophyllide A oxygenase | chloroplast envelope;integral component of membrane;chlorophyllide a oxygenase [overall] activity;metal ion binding;2 iron, 2 sulfur cluster binding;oxidation-reduction process | ec:1.14.13.122-oxygenase;ec:1.13.12 | Porphyrin and chlorophyll metabolism |
| Phvul.002G236800.1 | plant F20M13-60 | endosome;trans-Golgi network;integral component of membrane | | |
| Phvul.002G236800.2 | plant F20M13-60 | endosome;trans-Golgi network;integral component of membrane | | |
| Phvul.002G237900.1 | acyl-activating enzyme 17, peroxisomal , | integral component of membrane;acetate-CoA ligase activity;metabolic process | ec:6.2.1.1-ligase | Carbon fixation pathways in prokaryotes;Pyruvate metabolism;Biosynthesis of antibiotics;Methane metabolism;Glycolysis / Gluconeogenesis;Propanoate metabolism |
| Phvul.002G241200.1 | transmembrane , | | | |
| Phvul.002G242400.1 | adipose-regulatory (seipin), | integral component of membrane;lipid storage | | |
| Phvul.002G243400.1 | probable dolichyl pyrophosphate Man9 c2 alpha-1,3-glucosyltransferase isoform X1 | endoplasmic reticulum membrane;integral component of membrane;dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;protein N-linked glycosylation;oligosaccharide-lipid intermediate biosynthetic process | ec:2.4.1 | |
| Phvul.002G243800.1 | 5 -3 exonuclease family | nucleus;DNA binding;5'-3' exodeoxyribonuclease activity;DNA repair;sister chromatid cohesion;chromatin silencing by small RNA;meiotic chromosome segregation;nucleic acid phosphodiester bond hydrolysis | ec:3.1.15;ec:3.1.11;ec:3.1 | |
| Phvul.002G246100.1 | alpha beta-hydrolase superfamily | | | |
| Phvul.002G249700.1 | Kinetochore Nuf2 | chromosome, centromeric region;vacuolar membrane;plasma membrane;mitotic nuclear division | | |
| Phvul.002G250000.1 | phosphatidylinositol 4-phosphate 5-kinase 7-like | ATP binding;1-phosphatidylinositol-4-phosphate 5-kinase activity;phosphatidylinositol phosphorylation | ec:2.7.1.68-5-kinase;ec:2.7.1 | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.002G250100.2 | Maternal effect embryo arrest 9 | plasma membrane;pollen development;embryo development ending in seed dormancy;hydrogen peroxide catabolic process | | |
| Phvul.002G250300.1 | F-box At1g10780-like | plasmodesma;DNA replication initiation;regulation of DNA replication;cell proliferation;regulation of G2/M transition of mitotic cell cycle;histone phosphorylation | | |
| Phvul.002G250300.2 | F-box At1g10780-like | plasmodesma;DNA replication initiation;regulation of DNA replication;cell proliferation;regulation of G2/M transition of mitotic cell cycle;histone phosphorylation | | |
| Phvul.002G254100.1 | BZIP transcription factor | | | |
| Phvul.002G255300.1 | transmembrane , | endosome;trans-Golgi network;integral component of membrane | | |
| Phvul.002G255500.1 | ABC transporter D family member 1 | integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G257300.1 | chaperone -like | ATP binding;heat shock protein binding;metal ion binding;unfolded protein binding;protein folding;response to heat | | |
| Phvul.002G257300.2 | chaperone -like | ATP binding;heat shock protein binding;metal ion binding;unfolded protein binding;protein folding;response to heat | | |
| Phvul.002G258100.1 | cytochrome b561, DM13 and DOMON domain-containing | endosome;trans-Golgi network;integral component of membrane;monooxygenase | | |

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| | At5g54830-like isoform X1 | activity;heme binding;cytochrome complex assembly;oxidation-reduction process | | |
| Phvul.002G258300.1 | sieve element occlusion | | | |
| Phvul.002G258400.1 | cellulase (glycosyl hydrolase family 5) | integral component of membrane;hydrolase activity, hydrolyzing O-glycosyl compounds;carbohydrate metabolic process | | |
| Phvul.002G258700.1 | myosin heavy chain, | protein glycosylation;calcium ion transport;gravitropism | | |
| Phvul.002G258800.1 | Agglutinin receptor | integral component of membrane | | |
| Phvul.002G260200.1 | clathrin assembly At4g40080 | phospholipid binding;carbohydrate metabolic process | | |
| Phvul.002G261300.1 | tRNA (cytosine(34)-C(5))-methyltransferase | membrane;RNA binding;tRNA (cytosine-5-)-methyltransferase activity;tRNA methylation | ec:2.1.1 | |
| Phvul.002G262400.1 | photosynthetic NDH subunit of lumenal location 4, chloroplastic | endoplasmic reticulum membrane;chloroplast thylakoid membrane;NAD(P)H dehydrogenase complex (plastoquinone);peptidyl-prolyl cis-trans isomerase activity;FK506 binding;NADH dehydrogenase (plastoquinone) activity;protein peptidyl-prolyl isomerization;oxidation-reduction process;chaperone-mediated protein folding | ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:5.2.1.8 | Oxidative phosphorylation |
| Phvul.002G262400.2 | photosynthetic NDH subunit of lumenal location 4, chloroplastic | endoplasmic reticulum membrane;chloroplast thylakoid membrane;NAD(P)H dehydrogenase complex (plastoquinone);peptidyl-prolyl cis-trans isomerase activity;FK506 binding;NADH dehydrogenase (plastoquinone) activity;protein peptidyl-prolyl isomerization;oxidation-reduction process;chaperone-mediated protein folding | ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:5.2.1.8 | Oxidative phosphorylation |
| Phvul.002G262400.3 | photosynthetic NDH subunit of lumenal location 4, chloroplastic | endoplasmic reticulum membrane;chloroplast thylakoid membrane;NAD(P)H dehydrogenase complex (plastoquinone);peptidyl-prolyl cis-trans isomerase activity;FK506 binding;NADH dehydrogenase (plastoquinone) activity;protein peptidyl-prolyl isomerization;oxidation-reduction process;chaperone-mediated protein folding | ec:1.6.99.5;ec:1.6.99.3-dehydrogenase;ec:5.2.1.8 | Oxidative phosphorylation |
| Phvul.002G262600.1 | Binding isoform 1 | cytoplasm;plasma membrane;plasmodesma;plant-type cell wall biogenesis;cellulose biosynthetic process;anisotropic cell growth | | |
| Phvul.002G263800.1 | cytochrome P450 CYP736A12-like | integral component of membrane;iron ion binding;heme binding;flavonoid 3',5'-hydroxylase activity;secondary metabolite biosynthetic process;oxidation-reduction process | ec:1.14.13.88-3',5'-hydroxylase;ec:1.14.13 | Flavone and flavonol biosynthesis;Flavonoid biosynthesis |
| Phvul.002G266600.1 | neutral alkaline invertase 3, chloroplastic | chloroplast;sucrose alpha-glucosidase activity;glycopeptide alpha-N-acetylgalactosaminidase activity;starch metabolic process;sucrose catabolic process;cotyledon development | ec:3.2.1.48-alpha-glucosidase;ec:3.2.1;ec:3.2.1.26-invertase;ec:3.2.1.97 | Starch and sucrose metabolismStarch and sucrose metabolism;Galactose metabolism |
| Phvul.002G267900.1 | ribonucleoside-diphosphate reductase large subunit | ribonucleoside-diphosphate reductase complex;ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor;ATP binding;gluconeogenesis;DNA-dependent DNA replication;cytoskeleton organization;deoxyribonucleoside triphosphate biosynthetic process;deoxyribonucleotide biosynthetic process;proteasomal protein catabolic process;oxidation-reduction process | ec:1.17.4;ec:1.17.4.1-reductase | Purine metabolism;Glutathione metabolism;Pyrimidine metabolism |
| Phvul.002G267900.2 | ribonucleoside-diphosphate reductase large subunit | ribonucleoside-diphosphate reductase complex;ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor;ATP binding;gluconeogenesis;DNA-dependent DNA replication;cytoskeleton organization;deoxyribonucleoside triphosphate biosynthetic process;deoxyribonucleotide biosynthetic process;proteasomal protein catabolic process;oxidation-reduction process | ec:1.17.4;ec:1.17.4.1-reductase | Purine metabolism;Glutathione metabolism;Pyrimidine metabolism |
| Phvul.002G268100.1 | hypothetical protein | | | |

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| | PHAVU_002G268100g | | | |
| Phvul.002G268200.1 | cellulose synthase family | plasma membrane;integral component of membrane;zinc ion binding;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.002G269000.1 | probable plastid-lipid-associated 7, chloroplastic | | | |
| Phvul.002G273000.1 | 50S ribosomal L12, chloroplastic-like | ribosome;structural constituent of ribosome;DNA-templated transcription, elongation;translation | | |
| Phvul.002G273600.1 | trichome birefringence-like 14 | integral component of membrane | | |
| Phvul.002G273900.1 | E3 ubiquitin- ligase RGLG2 | ubiquitin-protein transferase activity;zinc ion binding;ligase activity;response to wounding;cytokinin metabolic process;jasmonic acid mediated signaling pathway;protein ubiquitination;defense response to bacterium | | |
| Phvul.002G274100.1 | hypothetical protein PHAVU_002G274100g | | | |
| Phvul.002G274500.1 | lipase-like PAD4 | membrane;hydrolase activity;lipid metabolic process | | |
| Phvul.002G275100.1 | aspartic ase Asp1-like | integral component of membrane;aspartic-type endopeptidase activity;transferase activity;proteolysis;protein catabolic process | ec:3.4.23 | |
| Phvul.002G275600.1 | alternative NAD(P)H-ubiquinone oxidoreductase C1, chloroplastic mitochondrial | NADH dehydrogenase activity;oxidation-reduction process | ec:1.6.99.3-dehydrogenase | Oxidative phosphorylation |
| Phvul.002G275600.2 | alternative NAD(P)H-ubiquinone oxidoreductase C1, chloroplastic mitochondrial | NADH dehydrogenase activity;oxidation-reduction process | ec:1.6.99.3-dehydrogenase | Oxidative phosphorylation |
| Phvul.002G276200.1 | CBS domain-containing CBSCBSPB3-like | integral component of membrane | | |
| Phvul.002G276300.1 | hypothetical protein PHAVU_002G276300g | | | |
| Phvul.002G276500.1 | chalcone isomerase | chalcone isomerase activity;flavonoid biosynthetic process | ec:5.5.1.6-isomerase | Flavonoid biosynthesis |
| Phvul.002G279100.1 | E3 ubiquitin- ligase CHFR | nucleus;ubiquitin-protein transferase activity;zinc ion binding;ligase activity;ubiquitin-dependent protein catabolic process;sister chromatid cohesion;mitotic cell cycle checkpoint;reciprocal meiotic recombination;response to gamma radiation;protein ubiquitination;regulation of telomere maintenance;meiotic DNA double-strand break formation;telomere maintenance in response to DNA damage;meiotic chromosome segregation | | |
| Phvul.002G279700.1 | respiratory burst oxidase homolog C | integral component of membrane;peroxidase activity;calcium ion binding;oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor;oxidation-reduction process;cellular oxidant detoxification | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.002G280100.1 | staphylococcal nuclease domain-containing 1-like | RISC complex;transcription cofactor activity;posttranscriptional gene silencing by RNA;regulation of nucleic acid-templated transcription | | |
| Phvul.002G282000.1 | signal recognition particle subunit SRP68-like isoform X1 | endoplasmic reticulum;signal recognition particle, endoplasmic reticulum targeting;cytosol;signal recognition particle binding;7S RNA binding;endoplasmic reticulum | | |

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| | | signal peptide binding;SRP-dependent cotranslational protein targeting to membrane | | |
| Phvul.002G282000.2 | signal recognition particle subunit SRP68-like isoform X1 | endoplasmic reticulum;signal recognition particle, endoplasmic reticulum targeting;cytosol;signal recognition particle binding;7S RNA binding;endoplasmic reticulum signal peptide binding;SRP-dependent cotranslational protein targeting to membrane | | |
| Phvul.002G284100.1 | retrotransposon , , unclassified | integral component of membrane | | |
| Phvul.002G285400.1 | integrator complex subunit 9 isoform X1 | integrator complex;snRNA processing | | |
| Phvul.002G287000.1 | methyl- -binding domain-containing 13-like | nucleus;methyl-CpG binding;negative regulation of transcription from RNA polymerase II promoter;methylation-dependent chromatin silencing | | |
| Phvul.002G287900.1 | probable LRR receptor-like serine threonine- kinase At1g63430 | integral component of membrane;protein kinase activity;ATP binding;2-alkenal reductase [NAD(P)] activity;protein phosphorylation;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.002G289600.1 | Mitochondrial substrate carrier family B | integral component of membrane;structural constituent of ribosome;translation;transport | | |
| Phvul.002G289600.2 | Mitochondrial substrate carrier family B | integral component of membrane;structural constituent of ribosome;translation;transport | | |
| Phvul.002G289700.1 | kinesin-4-like isoform X1 | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G289700.2 | kinesin-4-like isoform X1 | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.002G290000.1 | transcription factor EGL1-like | amino acid binding;protein dimerization activity;metabolic process | | |
| Phvul.002G291600.1 | CCT motif | nucleus;ribonuclease P activity;response to light stimulus;regulation of flower development;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1.30;ec:3.1.26;ec:3.1;ec:3.1.26.5 | |
| Phvul.002G293200.1 | probable WRKY transcription factor 29 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.002G296300.1 | myosin heavy chain, cardiac muscle isoform | | | |
| Phvul.002G299100.1 | probable RNA 3 -terminal phosphate cyclase | nucleolus;membrane;RNA binding;RNA-3'-phosphate cyclase activity;endoribonuclease activity;endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | ec:6.5.1.4;ec:3.1 | |
| Phvul.002G299200.1 | patatin-like phospholipase | cytoplasm;membrane;phospholipase activity;acylglycerol lipase activity;lipid catabolic process | ec:3.1.1.23-lipase;ec:3.1.1;ec:3.1.1.1-ali-esterase | Glycerolipid metabolismDrug metabolism - other enzymes |
| Phvul.002G299500.1 | centromere C | kinetochore;centromeric DNA binding;primary metabolic process;cellular macromolecule metabolic process;kinetochore assembly | | |
| Phvul.002G300400.1 | 3-oxoacyl-[acyl-carrier- ] synthase I, chloroplastic-like | 3-oxoacyl-[acyl-carrier-protein] synthase activity;beta-ketoacyl-acyl-carrier-protein synthase II activity;fatty acid biosynthetic process | ec:2.3.1.85-synthase;ec:2.3.1.41-synthase I;ec:2.3.1.179-synthase II | Fatty acid biosynthesisBiotin metabolism;Fatty acid biosynthesisBiotin metabolism;Fatty acid biosynthesis |
| Phvul.002G302200.1 | lupeol synthase | lupeol synthase activity;pentacyclic triterpenoid biosynthetic process | ec:5.4.99 | |
| Phvul.002G303000.1 | superkiller viralicidic activity 2-like 2 | nucleus;cytosol;RNA binding;RNA helicase activity;ATP binding;mitotic cell cycle;mRNA splicing, via spliceosome;RNA catabolic process;cell adhesion;photomorphogenesis;embryo development ending in seed dormancy;seed germination;regulation of flower | ec:3.6.1;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolism;Thiamine metabolism |

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| | | development;meristem structural organization;trichome morphogenesis;specification of floral organ identity;seed dormancy process;sugar mediated signaling pathway;vegetative to reproductive phase transition of meristem;cullin deneddylation;protein ubiquitination;histone methylation;protein deubiquitination;lipid storage;production of siRNA involved in RNA interference;production of miRNAs involved in gene silencing by miRNA;post-translational protein modification;actin nucleation;positive regulation of transcription, DNA-templated;response to freezing | | |
| Phvul.002G304300.1 | K(+) efflux antiporter 4 isoform X1 | integral component of membrane;solute:proton antiporter activity;sodium ion transport;lithium ion transport;hydrogen ion transmembrane transport | | |
| Phvul.002G304300.2 | K(+) efflux antiporter 4 isoform X1 | integral component of membrane;solute:proton antiporter activity;sodium ion transport;lithium ion transport;hydrogen ion transmembrane transport | | |
| Phvul.002G305800.1 | asparagine--tRNA ligase, cytoplasmic 1 | cytoplasm;nucleic acid binding;asparagine-tRNA ligase activity;ATP binding;asparaginyl-tRNA aminoacylation | ec:6.1.1;ec:6.1.1.22-ligase | Aminoacyl-tRNA biosynthesis |
| Phvul.002G307400.1 | derlin-1 | integral component of membrane;protein folding;response to heat;response to high light intensity;response to endoplasmic reticulum stress;response to hydrogen peroxide | | |
| Phvul.002G308100.1 | IQ-DOMAIN 14 | | | |
| Phvul.002G308700.1 | nucleotide-diphospho-sugar transferase domain | integral component of membrane;ceramide glucosyltransferase activity;glucosylceramide biosynthetic process | ec:2.4.1.80-glucosyltransferase;ec:2.4.1 | Sphingolipid metabolism |
| Phvul.002G308800.1 | pentatricopeptide repeat-containing At2g15820 | chloroplast;endonuclease activity;Group II intron splicing;mRNA cis splicing, via spliceosome;photosystem I assembly;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.002G309800.1 | transmembrane , | membrane | | |
| Phvul.002G310300.1 | probable glycosyltransferase At3g07620 | membrane;glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1.224-4-alpha-N-acetylglucosaminyltransferase;ec:2.4.1 | Glycosaminoglycan biosynthesis - heparan sulfate / heparin |
| Phvul.002G310300.2 | probable glycosyltransferase At3g07620 | membrane;glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1.224-4-alpha-N-acetylglucosaminyltransferase;ec:2.4.1 | Glycosaminoglycan biosynthesis - heparan sulfate / heparin |
| Phvul.002G312800.1 | Chloroplast processing peptidase | chloroplast thylakoid membrane;integral component of membrane;mitochondrial inner membrane peptidase complex;serine-type endopeptidase activity;signal peptide processing;protein processing involved in protein targeting to mitochondrion;thylakoid membrane organization;regulation of cellular protein metabolic process;mitochondrial respiratory chain complex assembly;ncRNA metabolic process;posttranscriptional gene silencing by RNA;cellular biosynthetic process;single-organism biosynthetic process;regulation of nitrogen compound metabolic process;production of small RNA involved in gene silencing by RNA;organic substance biosynthetic process;regulation of cellular macromolecule biosynthetic process | ec:3.4.21 | |
| Phvul.002G313300.1 | serine transhydroxymethyl transferase | glycine hydroxymethyltransferase activity;methyltransferase activity;pyridoxal phosphate binding;glycine metabolic process;L-serine metabolic process;methylation;tetrahydrofolate interconversion | ec:2.1.2.1-hydroxymethyltransferase | Biosynthesis of antibiotics;Methane metabolism;One carbon pool by folate;Cyanoamino acid metabolism;Glycine, serine and threonine metabolism;Glyoxylate |

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| Phvul.002G313400.1 | regulator of Vps4 activity in the MVB pathway | | | |
| Phvul.002G314200.1 | leucine-rich repeat extensin 4 | integral component of membrane;transferase activity;metabolic process | | |
| Phvul.002G315600.1 | aluminum-activated malate transporter 9 | plant-type vacuole membrane;integral component of membrane;malate transmembrane transporter activity;malate transmembrane transport | | |
| Phvul.002G317000.1 | Transcription factor MYB21 | DNA binding | | |
| Phvul.002G318800.1 | endoglucanase 8-like | cellulase activity;cellulose catabolic process | ec:3.2.1.4-endo-1,4-beta-D-glucanase | Starch and sucrose metabolism |
| Phvul.002G320100.1 | Histidine--tRNA ligase | mitochondrion;histidine-tRNA ligase activity;ATP binding;histidyl-tRNA aminoacylation;mitochondrial translation | ec:6.1.1;ec:6.1.1.21-ligase | Aminoacyl-tRNA biosynthesis |
| Phvul.002G321200.1 | nuclear pore complex NUP155 | nuclear pore;nucleolus;plasma membrane;plasmodesma;chloroplast;nucleocytoplasmic transporter activity;structural constituent of nuclear pore;RNA methylation;nucleocytoplasmic transport | | |
| Phvul.002G323400.1 | TMV resistance N-like | ADP binding;defense response | | |
| Phvul.002G323800.1 | TMV resistance N-like | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.002G323800.2 | TMV resistance N-like | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.002G323800.3 | TMV resistance N-like | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.002G324500.1 | THO complex subunit 2 | intracellular;phosphorelay sensor kinase activity;phosphorelay signal transduction system;signal transduction by protein phosphorylation | ec:2.7.3;ec:2.7.13.3 | |
| Phvul.002G325900.1 | poly(A) polymerase | nucleus;integral component of membrane;RNA binding;polynucleotide adenylyltransferase activity;mitotic cell cycle;mRNA polyadenylation | ec:2.7.7.19 | |
| Phvul.002G325900.2 | poly(A) polymerase | nucleus;integral component of membrane;RNA binding;polynucleotide adenylyltransferase activity;mitotic cell cycle;mRNA polyadenylation | ec:2.7.7.19 | |
| Phvul.002G325900.3 | poly(A) polymerase | nucleus;integral component of membrane;RNA binding;polynucleotide adenylyltransferase activity;mitotic cell cycle;mRNA polyadenylation | ec:2.7.7.19 | |
| Phvul.002G328600.1 | vacuolar sorting-associated , | integral component of membrane;extrinsic component of membrane | | |
| Phvul.002G328600.2 | vacuolar sorting-associated , | integral component of membrane;extrinsic component of membrane | | |
| Phvul.002G330500.1 | protection of telomeres 1b-like isoform X1 | nuclear telomere cap complex;methyltransferase activity;telomerase inhibitor activity;G-rich strand telomeric DNA binding;telomere capping;regulation of telomere maintenance via telomerase;negative regulation of telomerase activity | | |
| Phvul.002G333400.1 | rhodanese-like domain-containing 8, chloroplastic isoform X1 | integral component of membrane;transferase activity;metabolic process | | |
| Phvul.003G002600.1 | hypothetical protein PHAVU_003G002600g | ADP binding;defense response | | |
| Phvul.003G002600.2 | hypothetical protein PHAVU_003G002600g | ADP binding;defense response | | |
| Phvul.003G005800.1 | zinc finger, C3HC4 type (RING finger) | plasmodesma;zinc ion binding | | |
| Phvul.003G007200.1 | dishevelled Egl-10 leckstrin domain | intracellular;electron carrier activity;protein disulfide oxidoreductase activity;intracellular signal transduction;cell redox homeostasis;oxidation-reduction process | | |

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| Phvul.003G008000.1 | CHROMATIN REMODELING 19 | nucleus;DNA binding;helicase activity;ATP binding;transcription, DNA-templated;regulation of transcription, DNA-templated;cellular response to DNA damage stimulus;gene silencing by RNA;cellular response to UV-C | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.003G009300.1 | cytochrome P450 71D11-like | integral component of membrane;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;secondary metabolite biosynthetic process;oxidation-reduction process | ec:1.14.13 | |
| Phvul.003G010100.1 | deSI At4g17486 | integral component of membrane | | |
| Phvul.003G013100.1 | tobamovirus multiplication 3-like | integral component of membrane | | |
| Phvul.003G013300.1 | GEM 4 | | | |
| Phvul.003G014300.1 | anthranilate synthase beta subunit 2, chloroplastic-like | anthranilate synthase activity;metabolic process | ec:4.1.3.27-synthase | Biosynthesis of antibiotics;Phenylalanine, tyrosine and tryptophan biosynthesis |
| Phvul.003G016400.1 | probable S-adenosylmethionine-dependent methyltransferase At5g38100 | methyltransferase activity;methylation | | |
| Phvul.003G017000.1 | Two-component response regulator ARR2 | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;phosphorelay signal transduction system;transcription, DNA-templated;regulation of transcription, DNA-templated;regulation of multicellular organismal development | | |
| Phvul.003G017500.1 | WD repeat-containing 74 isoform X1 | Cul4-RING E3 ubiquitin ligase complex | | |
| Phvul.003G017500.2 | WD repeat-containing 74 isoform X1 | Cul4-RING E3 ubiquitin ligase complex | | |
| Phvul.003G019100.1 | E3 ubiquitin ligase RIE1 | integral component of membrane;zinc ion binding;hydrolase activity;ligase activity;metabolic process | | |
| Phvul.003G019100.2 | E3 ubiquitin ligase RIE1 | integral component of membrane;zinc ion binding;hydrolase activity;ligase activity;metabolic process | | |
| Phvul.003G019300.1 | tRNA:m(4)X modification enzyme TRM13 homolog | tRNA methyltransferase activity;tRNA methylation | ec:2.1.1 | |
| Phvul.003G019400.1 | VAC14 homolog | integral component of membrane;PAS complex;hydrolase activity;metabolic process;regulation of lipid kinase activity | | |
| Phvul.003G019400.2 | VAC14 homolog | integral component of membrane;PAS complex;hydrolase activity;metabolic process;regulation of lipid kinase activity | | |
| Phvul.003G021200.1 | exosome complex exonuclease RRP41 | | | |
| Phvul.003G022300.1 | DNA gyrase subunit A, chloroplastic mitochondrial | chromosome;nucleoid;mediator complex;DNA binding;DNA topoisomerase type II (ATP-hydrolyzing) activity;ATP binding;DNA topological change;chromosome segregation;pyrimidine ribonucleotide biosynthetic process | ec:5.99.1.3;ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:5.99.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G025500.1 | nuclear matrix constituent , | | | |
| Phvul.003G027400.1 | probable galacturonosyltransferase-like 3 | Golgi apparatus;integral component of membrane;polygalacturonate 4-alpha-galacturonosyltransferase activity;polysaccharide biosynthetic process | ec:2.4.1.43-4-alpha-galacturonosyltransferase | Amino sugar and nucleotide sugar metabolism;Starch and sucrose metabolism |
| Phvul.003G027600.1 | probable receptor kinase At1g49730 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |

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| Phvul.003G028000.1 | probable transcription factor GLK2 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.003G028100.1 | Zn-dependent hydrolase of the beta-lactamase fold | chloroplast;hydrolase activity;photosystem II assembly;myo-inositol hexakisphosphate biosynthetic process | | |
| Phvul.003G030200.1 | endonuclease 2-like | nucleic acid binding;endonuclease activity;DNA catabolic process;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.003G030200.2 | endonuclease 2-like | nucleic acid binding;endonuclease activity;DNA catabolic process;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.003G031400.1 | lipid phosphate phosphatase 2-like isoform X1 | integral component of plasma membrane;acid phosphatase activity;phosphatidate phosphatase activity;phospholipid metabolic process;abscisic acid-activated signaling pathway;phospholipid dephosphorylation | ec:3.1.3.4-phosphatase;ec:3.1.3.2-phosphatase;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase | Sphingolipid metabolism;Ether lipid metabolism;Glycerophospholipid metabolism;Glycerolipid metabolismAminobenzoate degradationAminobenzoate degradation |
| Phvul.003G031400.2 | lipid phosphate phosphatase 2-like isoform X1 | integral component of plasma membrane;acid phosphatase activity;phosphatidate phosphatase activity;phospholipid metabolic process;abscisic acid-activated signaling pathway;phospholipid dephosphorylation | ec:3.1.3.4-phosphatase;ec:3.1.3.2-phosphatase;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase | Sphingolipid metabolism;Ether lipid metabolism;Glycerophospholipid metabolism;Glycerolipid metabolismAminobenzoate degradationAminobenzoate degradation |
| Phvul.003G031400.3 | lipid phosphate phosphatase 2-like isoform X1 | integral component of plasma membrane;acid phosphatase activity;phosphatidate phosphatase activity;phospholipid metabolic process;abscisic acid-activated signaling pathway;phospholipid dephosphorylation | ec:3.1.3.4-phosphatase;ec:3.1.3.2-phosphatase;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase | Sphingolipid metabolism;Ether lipid metabolism;Glycerophospholipid metabolism;Glycerolipid metabolismAminobenzoate degradationAminobenzoate degradation |
| Phvul.003G032200.1 | hypothetical protein PHAVU_003G032200g | integral component of membrane | | |
| Phvul.003G032400.1 | RAE1 | | | |
| Phvul.003G032500.1 | auxin efflux carrier | endoplasmic reticulum;plasma membrane;integral component of membrane;auxin efflux transmembrane transporter activity;auxin-activated signaling pathway;auxin polar transport;auxin homeostasis;auxin efflux;transmembrane transport | | |
| Phvul.003G032900.1 | ATP-dependent DNA helicase | nucleic acid binding;ATP-dependent DNA helicase activity;ATP binding;DNA repair;DNA recombination;DNA duplex unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G034800.1 | hypothetical protein PHAVU_003G034800g | cytoplasm;transition metal ion binding;metal ion transport;cellular transition metal ion homeostasis | | |
| Phvul.003G035400.1 | alpha-xylosidase 1 | alpha-1,4-glucosidase activity;carbohydrate binding;maltose alpha-glucosidase activity;maltose metabolic process | ec:3.2.1;ec:3.2.1.20-maltase | Starch and sucrose metabolism;Galactose metabolism |
| Phvul.003G036700.1 | root meristem growth factor 2 | | | |
| Phvul.003G036900.1 | UDP-glycosyltransferase 89A2-like | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |

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| Phvul.003G037200.1 | GDSL esterase lipase At2g03980-like | hydrolase activity, acting on ester bonds;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.003G039500.1 | BIG GRAIN 1-like E | | | |
| Phvul.003G040200.1 | receptor kinase 2 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;transition metal ion transport;response to molecule of bacterial origin;protein phosphorylation;signal transduction;stomatal complex morphogenesis;regulation of anion channel activity;stamen development | ec:2.7.11 | |
| Phvul.003G041000.1 | serine threonine-kinase dst1 | chromosome, centromeric region;nucleus;mitochondrion;protein serine/threonine kinase activity;ATP binding;[tyrosine 3-monooxygenase] kinase activity;regulation of mitotic cell cycle;signal transduction by protein phosphorylation;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process | ec:2.7.11;ec:2.7.11.6 | |
| Phvul.003G041000.2 | serine threonine-kinase dst1 | chromosome, centromeric region;nucleus;mitochondrion;protein serine/threonine kinase activity;ATP binding;[tyrosine 3-monooxygenase] kinase activity;regulation of mitotic cell cycle;signal transduction by protein phosphorylation;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process | ec:2.7.11;ec:2.7.11.6 | |
| Phvul.003G041900.1 | ATP-dependent RNA helicase DHX33 | ATP-dependent RNA helicase activity;ATP binding;poly(A) RNA binding;RNA processing | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G042400.1 | pentatricopeptide repeat-containing At1g69290 | | | |
| Phvul.003G043400.1 | Quasimodo2 like 2 isoform 2 | S-adenosylmethionine-dependent methyltransferase activity;methylation | | |
| Phvul.003G045600.1 | NAC domain-containing 29 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.003G045700.1 | cell division cycle and apoptosis regulator 1 | calcium ion binding;regulation of transcription, DNA-templated;cell division | | |
| Phvul.003G047700.1 | filament-like plant 7 | cell part;regulation of biological process | | |
| Phvul.003G050000.1 | methyltransferase 13 | methyltransferase activity;hydrolase activity;methylation | | |
| Phvul.003G050400.1 | serine arginine repetitive matrix 2-like | motile cilium;nucleotide binding;RNA binding;metal ion binding;microtubule cytoskeleton organization;cytokinesis by cell plate formation;cell adhesion;organ morphogenesis;trichome morphogenesis;vegetative to reproductive phase transition of meristem;protein desumoylation;regulation of chromosome organization;actin nucleation;hydrogen peroxide biosynthetic process | | |
| Phvul.003G050900.1 | subtilisin-like protease | cell wall;serine-type endopeptidase activity;proteolysis;glucosinolate biosynthetic process | ec:3.4.21 | |
| Phvul.003G050900.2 | subtilisin-like protease | cell wall;serine-type endopeptidase activity;proteolysis;glucosinolate biosynthetic process | ec:3.4.21 | |
| Phvul.003G051300.1 | probable acyl-activating enzyme 16, chloroplastic | long-chain fatty acid-CoA ligase activity;long-chain fatty acid metabolic process | ec:6.2.1.3-ligase;ec:6.2.1 | Fatty acid degradation;Fatty acid biosynthesis |
| Phvul.003G052200.1 | Ulp1 protease family, carboxy-terminal domain | cysteine-type peptidase activity;proteolysis | ec:3.4 | |

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| Phvul.003G052200.2 | Ulp1 protease family, carboxy-terminal domain | cysteine-type peptidase activity;proteolysis | ec:3.4 | |
| Phvul.003G052900.1 | potassium transporter 6-like | plasma membrane;integral component of membrane;potassium ion transmembrane transporter activity;potassium ion transmembrane transport | | |
| Phvul.003G053100.1 | NHL repeat | integral component of membrane;catalytic activity;metabolic process | | |
| Phvul.003G054100.1 | transcription factor DIVARICATA-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.003G054100.2 | transcription factor DIVARICATA-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.003G055300.1 | probable inactive purple acid phosphatase 1 isoform X1 | acid phosphatase activity;metal ion binding;tryptophan catabolic process;systemic acquired resistance;indoleacetic acid biosynthetic process;dephosphorylation;regulation of defense response | ec:3.1.3.2-phosphatase;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase | Aminobenzoate degradationAminobenzoate degradation |
| Phvul.003G055300.2 | probable inactive purple acid phosphatase 1 isoform X1 | acid phosphatase activity;metal ion binding;tryptophan catabolic process;systemic acquired resistance;indoleacetic acid biosynthetic process;dephosphorylation;regulation of defense response | ec:3.1.3.2-phosphatase;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase | Aminobenzoate degradationAminobenzoate degradation |
| Phvul.003G056300.1 | pyruvate dehydrogenase E1 component subunit alpha, mitochondrial-like | nucleus;cytosol;pyruvate dehydrogenase (acetyl-transferring) activity;acetyl-CoA biosynthetic process from pyruvate;oxidation-reduction process | ec:1.2.4.1-dehydrogenase (acetyl-transferring) | Pyruvate metabolism;Biosynthesis of antibiotics;Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis |
| Phvul.003G057400.1 | IQ-DOMAIN 1 | nitrogen compound metabolic process;cellular metabolic process;primary metabolic process;single-organism process;organic substance metabolic process | | |
| Phvul.003G057400.2 | IQ-DOMAIN 1 | nitrogen compound metabolic process;cellular metabolic process;primary metabolic process;single-organism process;organic substance metabolic process | | |
| Phvul.003G057800.1 | hypothetical protein PHAVU_003G057800g | | | |
| Phvul.003G061000.1 | Proteasome subunit beta type-1 | nucleus;cytoplasm;proteasome core complex;threonine-type endopeptidase activity;proteolysis involved in cellular protein catabolic process | ec:3.4.25 | |
| Phvul.003G061200.1 | OBP32pep, | jasmonic acid metabolic process;response to jasmonic acid | | |
| Phvul.003G062400.1 | trichome birefringence-like 2 | Golgi apparatus;integral component of membrane;O-acetyltransferase activity;cell wall organization or biogenesis | ec:2.3.1 | |
| Phvul.003G063000.1 | heme-binding 2-like | | | |
| Phvul.003G063000.2 | heme-binding 2-like | | | |
| Phvul.003G064600.1 | BTB POZ domain-containing At1g67900-like | | | |
| Phvul.003G067800.1 | pre-mRNA-splicing factor CEF1-like | DNA binding;transcription factor activity, sequence-specific DNA binding;regulation of transcription, DNA-templated;cell cycle | | |
| Phvul.003G069200.1 | alpha-amylase 3, chloroplastic | chloroplast stroma;alpha-amylase activity;calcium ion binding;glucan 1,4-alpha-maltotetraohydrolase activity;starch catabolic process;circadian rhythm | ec:3.2.1;ec:3.2.1.1-glycogenase;ec:3.2.1.60 | Starch and sucrose metabolism |
| Phvul.003G072500.1 | TMV resistance N-like isoform X1 | integral component of membrane;ADP binding;defense response;signal transduction | | |

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| Phvul.003G073700.1 | transcription factor VOZ1 | sequence-specific DNA binding;response to symbiotic fungus;positive regulation of transcription, DNA-templated;long-day photoperiodism, flowering;positive regulation of long-day photoperiodism, flowering | | |
| Phvul.003G073700.2 | transcription factor VOZ1 | sequence-specific DNA binding;response to symbiotic fungus;positive regulation of transcription, DNA-templated;long-day photoperiodism, flowering;positive regulation of long-day photoperiodism, flowering | | |
| Phvul.003G073700.3 | transcription factor VOZ1 | sequence-specific DNA binding;response to symbiotic fungus;positive regulation of transcription, DNA-templated;long-day photoperiodism, flowering;positive regulation of long-day photoperiodism, flowering | | |
| Phvul.003G073900.1 | probable glucan endo-1,3-beta-glucosidase A6 | glucan endo-1,3-beta-D-glucosidase activity;carbohydrate metabolic process | ec:3.2.1.39-endo-1,3-beta-D-glucosidase;ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolismStarch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.003G074000.1 | isoflavone synthase 1 | membrane;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;isomerase activity;heme binding;secondary metabolite biosynthetic process;oxidation-reduction process | ec:1.14.13 | |
| Phvul.003G074600.1 | hypothetical protein PHAVU_003G074600g | | | |
| Phvul.003G076200.1 | mitotic spindle assembly checkpoint , | nuclear envelope;mitotic spindle assembly checkpoint;gravitropism | | |
| Phvul.003G076400.1 | DEAD-box ATP-dependent RNA helicase 58, chloroplastic isoform X1 | nucleic acid binding;ATP-dependent RNA helicase activity;ATP binding;RNA secondary structure unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G077300.1 | cardiolipin synthase (CMP-forming), mitochondrial | mitochondrion;membrane;cardiolipin synthase activity;calcium-mediated signaling;cardiolipin biosynthetic process | ec:2.7.8 | |
| Phvul.003G077800.1 | hypothetical protein PHAVU_003G077800g | DNA binding | | |
| Phvul.003G081300.1 | leucine--tRNA ligase, mitochondrial | mitochondrion;chloroplast stroma;integral component of membrane;aminoacyl-tRNA editing activity;leucine-tRNA ligase activity;ATP binding;rRNA processing;leucyl-tRNA aminoacylation;regulation of translational fidelity;chloroplast organization;embryo development ending in seed dormancy;thylakoid membrane organization;stomatal complex morphogenesis;vegetative to reproductive phase transition of meristem;iron-sulfur cluster assembly;mRNA modification;plant ovule development | ec:6.1.1;ec:3.1.1.1-ali-esterase;ec:6.1.1.4-ligase | Drug metabolism - other enzymesAminoacyl-tRNA biosynthesis |
| Phvul.003G081300.2 | leucine--tRNA ligase, mitochondrial | mitochondrion;chloroplast stroma;integral component of membrane;aminoacyl-tRNA editing activity;leucine-tRNA ligase activity;ATP binding;rRNA processing;leucyl-tRNA aminoacylation;regulation of translational fidelity;chloroplast organization;embryo development ending in seed dormancy;thylakoid membrane organization;stomatal complex morphogenesis;vegetative to reproductive phase transition of meristem;iron-sulfur cluster assembly;mRNA modification;plant ovule development | ec:6.1.1;ec:3.1.1.1-ali-esterase;ec:6.1.1.4-ligase | Drug metabolism - other enzymesAminoacyl-tRNA biosynthesis |

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| Phvul.003G081300.3 | leucine--tRNA ligase, mitochondrial | mitochondrion;chloroplast stroma;integral component of membrane;aminoacyl-tRNA editing activity;leucine-tRNA ligase activity;ATP binding;rRNA processing;leucyl-tRNA aminoacylation;regulation of translational fidelity;chloroplast organization;embryo development ending in seed dormancy;thylakoid membrane organization;stomatal complex morphogenesis;vegetative to reproductive phase transition of meristem;iron-sulfur cluster assembly;mRNA modification;plant ovule development | ec:6.1.1;ec:3.1.1.1-ali-esterase;ec:6.1.1.4-ligase | Drug metabolism - other enzymesAminoacyl-tRNA biosynthesis |
| Phvul.003G081500.1 | calcium permeable stress-gated cation channel 1-like | integral component of membrane;4-alpha-glucanotransferase activity;glycogen metabolic process | ec:2.4.1.25-disproportionating enzyme | Starch and sucrose metabolism |
| Phvul.003G082700.1 | tropinone reductase-like 3 | peroxisome;oxidoreductase activity;root hair elongation;oxidation-reduction process;indolebutyric acid metabolic process;response to indolebutyric acid | | |
| Phvul.003G083100.1 | hypothetical protein PHAVU_003G083100g | catalytic activity;metabolic process | | |
| Phvul.003G083700.1 | hypothetical protein PHAVU_003G083700g | integral component of membrane | | |
| Phvul.003G084200.1 | E3 ubiquitin- ligase UPL5 | ubiquitin-protein transferase activity;ligase activity;signal transduction;protein ubiquitination involved in ubiquitin-dependent protein catabolic process | | |
| Phvul.003G084600.1 | cytochrome b561 and DOMON domain-containing At5g47530-like | integral component of membrane;oxidation-reduction process | | |
| Phvul.003G086000.1 | Microtubule-associated 70-5 | microtubule binding;cytoskeleton organization | | |
| Phvul.003G086800.1 | nuclear transcription factor Y subunit B-3-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;protein heterodimerization activity;regulation of transcription, DNA-templated | | |
| Phvul.003G087500.1 | probable ADP-ribosylation factor GTPase-activating AGD13 | vacuole;plasma membrane;phosphatidylserine decarboxylase activity;phospholipase A2 activity;metabolic process | ec:3.1.1;ec:4.1.1.65-decarboxylase;ec:3.1.1.4-A2;ec:3.1.1.1-ali-esterase | Glycerophospholipid metabolismalpha-Linolenic acid metabolism;Linoleic acid metabolism;Arachidonic acid metabolism;Ether lipid metabolism;Glycerophospholipid metabolismDrug metabolism - other enzymes |
| Phvul.003G088200.1 | C2 and GRAM domain-containing At1g03370-like isoform X1 | integral component of membrane;phosphatidylserine decarboxylase activity;ligase activity;metabolic process | ec:4.1.1.65-decarboxylase | Glycerophospholipid metabolism |
| Phvul.003G088400.1 | BTB POZ domain-containing At5g47800-like | | | |
| Phvul.003G092100.1 | Basic 7S globulin | aspartic-type endopeptidase activity;proteolysis;protein catabolic process | ec:3.4.23 | |
| Phvul.003G092200.1 | Basic 7S globulin | aspartic-type endopeptidase activity;proteolysis;protein catabolic process | ec:3.4.23 | |
| Phvul.003G094200.1 | hypothetical protein PHAVU_003G094200g | | | |
| Phvul.003G096500.1 | Glyoxysomal fatty acid beta-oxidation multifunctional MFP-a | cell wall;nucleolus;plasmodesma;3-hydroxyacyl-CoA dehydrogenase activity;enoyl-CoA hydratase activity;long-chain-enoyl-CoA hydratase activity;peroxisome | ec:4.2.1.74-hydratase;ec:4.2.1.17- | Fatty acid degradation;Fatty acid elongationalpha-Linolenic acid |

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| | | organization;fatty acid catabolic process;toxin catabolic process;proteasome-mediated ubiquitin-dependent protein catabolic process;response to misfolded protein;oxidation-reduction process;proteasome core complex assembly | hydratase;ec:1.1.1.35-dehydrogenase | metabolism;Biosynthesis of unsaturated fatty acids;Aminobenzoate degradation;Carbon fixation pathways in prokaryotes;Biosynthesis of antibiotics;Tryptophan metabolism;Geraniol degradation;Valine, leucine and isoleucine degradation;Limonene and pinene degradation;beta-Alanine metabolism;Lysine degradation;Fatty acid degradation;Benzoate degradation;Phenylalanine metabolism;Butanoate metabolism;Fatty acid elongation;Propanoate metabolism;Caprolactam degradationCarbon fixation pathways in prokaryotes;Toluene degradation;Biosynthesis of antibiotics;Tryptophan metabolism;Geraniol degradation;Valine, leucine and isoleucine degradation;Primary bile acid biosynthesis;Lysine degradation;Fatty acid degradation;Benzoate degradation;Butanoate metabolism;Fatty acid elongation;Caprolactam degradation |
| Phvul.003G096600.1 | sericin 1-like | | | |
| Phvul.003G097100.1 | U11 U12 small nuclear ribonucleo 48 kDa | | | |
| Phvul.003G097100.2 | U11 U12 small nuclear ribonucleo 48 kDa | | | |
| Phvul.003G097100.3 | U11 U12 small nuclear ribonucleo 48 kDa | | | |
| Phvul.003G097100.4 | U11 U12 small nuclear ribonucleo 48 kDa | | | |
| Phvul.003G098200.1 | pyruvate, phosphate dikinase, chloroplastic | nucleus;cytosol;chloroplast stroma;ATP binding;kinase activity;metal ion binding;pyruvate, phosphate dikinase activity;pyruvate metabolic process;phosphorylation | ec:2.7.9.1-phosphate dikinase | Carbon fixation pathways in prokaryotes;Pyruvate metabolism;Carbon fixation in photosynthetic organisms |
| Phvul.003G098200.2 | pyruvate, phosphate dikinase, chloroplastic | nucleus;cytosol;chloroplast stroma;ATP binding;kinase activity;metal ion binding;pyruvate, phosphate dikinase activity;pyruvate metabolic process;phosphorylation | ec:2.7.9.1-phosphate dikinase | Carbon fixation pathways in prokaryotes;Pyruvate metabolism;Carbon fixation in photosynthetic organisms |
| Phvul.003G099600.1 | probable 1-deoxy-D-xylulose-5-phosphate synthase, chloroplastic | 1-deoxy-D-xylulose-5-phosphate synthase activity;terpenoid biosynthetic process | ec:2.2.1.7-synthase | Biosynthesis of antibiotics;Terpenoid backbone biosynthesis;Thiamine metabolism |

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| Phvul.003G100000.1 | heat shock amino-terminal domain | | | |
| Phvul.003G100000.2 | heat shock amino-terminal domain | | | |
| Phvul.003G103100.1 | hypothetical protein PHAVU_003G103100g | zinc ion binding | | |
| Phvul.003G105900.1 | Germ cell-less -like 1 | Cul3-RING ubiquitin ligase complex;ubiquitin-protein transferase activity;protein ubiquitination | | |
| Phvul.003G106100.1 | ubiquitin-like-specific protease ESD4 | nucleus;endopeptidase activity;SUMO-specific protease activity;protein desumoylation | ec:3.4 | |
| Phvul.003G108200.1 | catalytic phosphatase type 2C | protein serine/threonine phosphatase activity;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.003G108500.1 | Chaperone dnaJ 49 | cytosol | | |
| Phvul.003G110600.1 | transmembrane , | integral component of membrane | | |
| Phvul.003G114400.1 | serine threonine-kinase STY8 isoform X1 | intracellular;phosphorelay sensor kinase activity;MAP kinase kinase kinase activity;ATP binding;phosphorelay signal transduction system;MAPK cascade;activation of MAPKK activity;regulation of transcription, DNA-templated | ec:2.7.11;ec:2.7.11.25;ec:2.7.3;ec:2.7.13.3 | |
| Phvul.003G116300.1 | probable WRKY transcription factor 48 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated;defense response;single-organism process;localization | | |
| Phvul.003G118000.1 | serine carboxypeptidase-like 33 | vacuole;integral component of membrane;serine-type carboxypeptidase activity;proteolysis involved in cellular protein catabolic process | ec:3.4.21;ec:3.4.16 | |
| Phvul.003G118700.1 | craniofacial development 1 | | | |
| Phvul.003G119200.1 | DNA (cytosine-5)-methyltransferase DRM2 isoform X1 | methyltransferase activity;DNA methylation | | |
| Phvul.003G119200.2 | DNA (cytosine-5)-methyltransferase DRM2 isoform X1 | methyltransferase activity;DNA methylation | | |
| Phvul.003G119300.1 | evolutionarily carboxy-terminal region | membrane | | |
| Phvul.003G119300.2 | evolutionarily carboxy-terminal region | membrane | | |
| Phvul.003G119300.3 | evolutionarily carboxy-terminal region | membrane | | |
| Phvul.003G119300.4 | YTH domain family 2 | membrane | | |
| Phvul.003G119300.5 | YTH domain family 2 | membrane | | |
| Phvul.003G119300.6 | YTH domain family 2 | membrane | | |
| Phvul.003G119400.1 | importin beta-like SAD2 homolog | nuclear envelope;cytosol;Ran GTPase binding;protein transporter activity;protein import into nucleus;signal transduction | | |
| Phvul.003G119700.1 | phragmoplast orienting kinesin-1 | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;nuclear division;cytokinesis by cell plate formation;regulation of DNA replication;nucleolus organization;microtubule-based movement;metabolic process;regulation of G2/M transition of mitotic cell cycle | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G120100.1 | double Clp-N motif P-loop nucleoside triphosphate | | | |

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| | hydrolase superfamily | | | |
| Phvul.003G120400.1 | pleiotropic drug resistance 3-like | plasma membrane;integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G122600.1 | transporter ABC domain | integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G122900.1 | CHUP1, chloroplastic-like isoform X1 | chloroplast outer membrane;chloroplast organization | | |
| Phvul.003G126000.1 | brefeldin A-inhibited guanine nucleotide-exchange 5 | ARF guanyl-nucleotide exchange factor activity;regulation of ARF protein signal transduction;positive regulation of GTPase activity | | |
| Phvul.003G126000.2 | brefeldin A-inhibited guanine nucleotide-exchange 5 | ARF guanyl-nucleotide exchange factor activity;regulation of ARF protein signal transduction;positive regulation of GTPase activity | | |
| Phvul.003G126100.1 | glucan endo-1,3-beta-glucosidase 5 | integral component of membrane;anchored component of membrane;hydrolase activity, hydrolyzing O-glycosyl compounds;protein histidine kinase activity;carbohydrate metabolic process;peptidyl-histidine phosphorylation | ec:2.7.13.3 | |
| Phvul.003G126500.1 | pectinesterase pectinesterase inhibitor PPE8B | extracellular region;cell wall;integral component of membrane;pectinesterase activity;aspartyl esterase activity;pectinesterase inhibitor activity;cell wall modification;negative regulation of catalytic activity;pectin catabolic process | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.003G127000.1 | 1-phosphatidylinositol-3-phosphate 5-kinase FAB1B-like isoform X1 | 1-phosphatidylinositol-3-phosphate 5-kinase activity;ATP binding;metal ion binding;vacuole organization;pollen development;organ morphogenesis;tissue development;vegetative to reproductive phase transition of meristem;endomembrane system organization;positive regulation of organelle organization;protein desumoylation;regulation of chromosome organization;phosphatidylinositol phosphorylation;hydrogen peroxide biosynthetic process | ec:2.7.1.150-5-kinase;ec:2.7.1 | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.003G127000.2 | 1-phosphatidylinositol-3-phosphate 5-kinase FAB1B-like isoform X1 | 1-phosphatidylinositol-3-phosphate 5-kinase activity;ATP binding;metal ion binding;vacuole organization;pollen development;organ morphogenesis;tissue development;vegetative to reproductive phase transition of meristem;endomembrane system organization;positive regulation of organelle organization;protein desumoylation;regulation of chromosome organization;phosphatidylinositol phosphorylation;hydrogen peroxide biosynthetic process | ec:2.7.1.150-5-kinase;ec:2.7.1 | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.003G127200.1 | phosphoinositide phosphatase SAC4 | mannosyl-oligosaccharide 1,2-alpha-mannosidase activity;phosphoric ester hydrolase activity;metabolic process | ec:3.2.1;ec:3.2.1.24-alpha-D-mannosidase;ec:3.1;ec:3.2.1.113-1,2-alpha-mannosidase | Other glycan degradationVarious types of N-glycan biosynthesis;N-Glycan biosynthesis |
| Phvul.003G127400.1 | kinesin NACK2 | kinesin complex;microtubule;plasmodesma;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;male meiosis cytokinesis;metabolic process;pollen development;embryo sac cellularization;radial microtubular system formation | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G127600.1 | Embryogenesis-associated EMB8 | integral component of membrane | | |

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| Phvul.003G128700.1 | Fatty acid biosynthesis 1 isoform 1 | 3-oxoacyl-[acyl-carrier-protein] synthase activity;beta-ketoacyl-acyl-carrier-protein synthase II activity;very long-chain fatty acid metabolic process;sulfur amino acid metabolic process;glycine catabolic process;unsaturated fatty acid biosynthetic process;oxidoreduction coenzyme metabolic process;vitamin metabolic process;cellular amino acid biosynthetic process;aromatic amino acid family metabolic process;lipoate metabolic process;coenzyme biosynthetic process;nucleotide metabolic process;response to light stimulus;cold acclimation;jasmonic acid biosynthetic process;embryo development ending in seed dormancy;plant-type cell wall biogenesis;chlorophyll biosynthetic process;cell growth;carotenoid biosynthetic process;regulation of lipid metabolic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;photosynthesis, light reaction;secondary metabolic process;cellulose metabolic process;oxylipin biosynthetic process;cuticle development;sulfur compound biosynthetic process | ec:2.3.1.85-synthase;ec:2.3.1.41-synthase I;ec:2.3.1.179-synthase II | Fatty acid biosynthesisBiotin metabolism;Fatty acid biosynthesisBiotin metabolism;Fatty acid biosynthesis |
| Phvul.003G128800.1 | auxin response factor 2 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |
| Phvul.003G131200.1 | RNI superfamily | | | |
| Phvul.003G131200.2 | F-box LRR-repeat 3-like | | | |
| Phvul.003G131300.1 | GDP-fucose O-fucosyltransferase | Golgi apparatus;chloroplast;integral component of membrane;transferase activity, transferring glycosyl groups;metabolic process | | |
| Phvul.003G131500.1 | 12-oxophytodienoate reductase 3 | peroxisome;NADPH dehydrogenase activity;FMN binding;12-oxophytodienoate reductase activity;tryptophan catabolic process;response to water deprivation;response to wounding;indoleacetic acid biosynthetic process;jasmonic acid biosynthetic process;response to ethylene;response to auxin;abscisic acid-activated signaling pathway;jasmonic acid mediated signaling pathway;oxylipin biosynthetic process;hyperosmotic salinity response;oxidation-reduction process | ec:1.3.1.42-reductase;ec:1.6.99.1 | alpha-Linolenic acid metabolism |
| Phvul.003G133000.1 | phospholipid:diacylglycerol acyltransferase 1-like | vacuole;endoplasmic reticulum;integral component of membrane;O-acyltransferase activity;phospholipid:diacylglycerol acyltransferase activity;lipid metabolic process | ec:2.3.1.158-acyltransferase;ec:2.3.1 | Glycerolipid metabolism |
| Phvul.003G134000.1 | ribosomal L18ae family | integral component of membrane;cytosolic large ribosomal subunit;structural constituent of ribosome;translation | | |
| Phvul.003G134000.2 | ribosomal L18ae family | integral component of membrane;cytosolic large ribosomal subunit;structural constituent of ribosome;translation | | |
| Phvul.003G134000.3 | ribosomal L18ae family | integral component of membrane;cytosolic large ribosomal subunit;structural constituent of ribosome;translation | | |
| Phvul.003G134500.1 | U-box domain-containing 34 | protein serine/threonine kinase activity;non-membrane spanning protein tyrosine kinase activity;ubiquitin-protein transferase activity;ATP binding;ligase activity;response to stress;protein ubiquitination;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.003G135700.1 | transcription factor bHLH041 | protein dimerization activity | | |
| Phvul.003G135900.1 | valacyclovir hydrolase, | hydrolase activity;metabolic process | | |
| Phvul.003G136100.1 | BAAT acyl- thioester hydrolase carboxy-terminal | hydrolase activity | | |
| Phvul.003G136600.1 | DUF4408 domain | integral component of membrane | | |

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| Phvul.003G136600.2 | DUF4408 domain | integral component of membrane | | |
| Phvul.003G136700.1 | zinc finger CCCH domain-containing 64 | cytosol;catalytic activity;metal ion binding;nuclear-transcribed mRNA catabolic process | | |
| Phvul.003G136700.2 | zinc finger CCCH domain-containing 64 | cytosol;catalytic activity;metal ion binding;nuclear-transcribed mRNA catabolic process | | |
| Phvul.003G140600.1 | Chaperone 1 | protein metabolic process | | |
| Phvul.003G140800.1 | Transcription factor bHLH35 | protein dimerization activity | | |
| Phvul.003G141400.1 | pathogenesis-related homeodomain -like | nucleus;DNA binding;zinc ion binding | | |
| Phvul.003G141400.2 | pathogenesis-related homeodomain -like | nucleus;DNA binding;zinc ion binding | | |
| Phvul.003G142300.1 | DUF4228 domain | | | |
| Phvul.003G143300.1 | glucose-6-phosphate 1-epimerase | integral component of membrane;carbohydrate binding;glucose-6-phosphate 1-epimerase activity;carbohydrate metabolic process | ec:5.1.3.15-1-epimerase | Biosynthesis of antibiotics;Glycolysis / Gluconeogenesis |
| Phvul.003G145300.1 | afadin alpha-actinin-binding | | | |
| Phvul.003G145400.1 | NADPH--cytochrome P450 reductase | endoplasmic reticulum membrane;integral component of membrane;NADPH-hemoprotein reductase activity;iron ion binding;FMN binding;[methionine synthase] reductase activity;oxidation-reduction process | ec:1.16.1.8;ec:1.16.1;ec:1.6.2.4 | |
| Phvul.003G147300.1 | probable xyloglucan endotransglucosylase hydrolase 23 | cell wall;integral component of membrane;apoplast;hydrolase activity, hydrolyzing O-glycosyl compounds;xyloglucan:xyloglucosyl transferase activity;xyloglucan endotransglucosylase activity;xyloglucan metabolic process;cell wall modification;cell wall biogenesis;primary root development | ec:2.4.1;ec:2.4.1.207 | |
| Phvul.003G148900.1 | probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic | 1-deoxy-D-xylulose-5-phosphate synthase activity;terpenoid biosynthetic process | ec:2.2.1.7-synthase | Biosynthesis of antibiotics;Terpenoid backbone biosynthesis;Thiamine metabolism |
| Phvul.003G150000.1 | alpha-rhamnosidase | integral component of membrane | | |
| Phvul.003G150000.2 | alpha-rhamnosidase | | | |
| Phvul.003G150000.3 | alpha-rhamnosidase | integral component of membrane | | |
| Phvul.003G150000.4 | alpha-rhamnosidase | | | |
| Phvul.003G150000.5 | alpha-rhamnosidase | | | |
| Phvul.003G150000.6 | alpha-rhamnosidase | integral component of membrane | | |
| Phvul.003G152500.1 | HAD-superfamily hydrolase, subfamily IG, 5 -nucleotidase isoform 1 | 5'-nucleotidase activity;metal ion binding;dephosphorylation;protein maturation | ec:3.1.3.5-uridine 5'-nucleotidase;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.31 | Purine metabolism;Nicotinate and nicotinamide metabolism;Pyrimidine metabolismAminobenzoate degradation |
| Phvul.003G154500.1 | snRNA-activating complex subunit isoform X1 | integral component of membrane | | |
| Phvul.003G156400.1 | ubiquitin carboxyl-terminal hydrolase 23 | thiol-dependent ubiquitinyl hydrolase activity;ubiquitin-dependent protein catabolic process;protein deubiquitination | ec:3.4;ec:3.4.19.12 | |
| Phvul.003G157600.1 | Fip1 [V] | binding | | |
| Phvul.003G158900.1 | DCN1 5 | ubiquitin ligase complex;ubiquitin conjugating enzyme binding;ubiquitin-like protein binding;cullin family protein binding;protein neddylation;positive regulation of ubiquitin-protein transferase activity | | |

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| Phvul.003G161500.1 | probable receptor kinase At5g20050 | plasma membrane;integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;response to nitrate;nitrate transport;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.003G162700.1 | nudix hydrolase 19, chloroplastic | cytosol;NAD+ diphosphatase activity;metal ion binding;metabolic process | ec:3.6.1;ec:3.6.1.9-diphosphatase;ec:3.6.1.22-diphosphatase | Purine metabolism;Pantothenate and CoA biosynthesis;Nicotinate and nicotinamide metabolism;Starch and sucrose metabolismNicotinate and nicotinamide metabolism |
| Phvul.003G163300.1 | axonemal dynein light chain, | microtubule associated complex;motile cilium;microtubule-based process | | |
| Phvul.003G163600.1 | F-box kelch-repeat At1g55270-like | Cul3-RING ubiquitin ligase complex;ubiquitin-protein transferase activity;protein ubiquitination | | |
| Phvul.003G164500.1 | chaperone -like isoform X1 | chloroplast;heat shock protein binding;unfolded protein binding;pentose-phosphate shunt;rRNA processing;plastid organization;photosynthetic electron transport in photosystem I;photosystem II assembly;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | | |
| Phvul.003G164500.2 | chaperone -like isoform X2 | heat shock protein binding;unfolded protein binding;nucleobase-containing compound metabolic process;cellular component organization;glyceraldehyde-3-phosphate metabolic process;photosynthesis, light reaction;cellular component biogenesis;small molecule metabolic process | | |
| Phvul.003G165500.1 | EIN3-binding F-box 1-like | | | |
| Phvul.003G166400.1 | glycoside hydrolase family 17 | integral component of membrane;anchored component of membrane;hydrolase activity, hydrolyzing O-glycosyl compounds;carbohydrate metabolic process | | |
| Phvul.003G166600.1 | plastocyanin-like domain | integral component of membrane;anchored component of plasma membrane;electron carrier activity | | |
| Phvul.003G167300.1 | clathrin assembly At2g25430 | clathrin-coated vesicle;1-phosphatidylinositol binding;clathrin binding;clathrin coat assembly | | |
| Phvul.003G169100.1 | kDa proline-rich | plasmodesma;chloroplast thylakoid membrane;integral component of membrane;apoplast | | |
| Phvul.003G169300.1 | BSD domain | | | |
| Phvul.003G169300.2 | BSD domain | | | |
| Phvul.003G169700.1 | probable glycosyltransferase At3g42180 | integral component of membrane;glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1.224-4-alpha-N-acetylglucosaminyltransferase;ec:2.4.1 | Glycosaminoglycan biosynthesis - heparan sulfate / heparin |
| Phvul.003G171300.1 | monogalactosyldiacylglycerol synthase 2, chloroplastic | 1,2-diacylglycerol 3-beta-galactosyltransferase activity;glycolipid biosynthetic process | ec:2.4.1.46-synthase;ec:2.4.1 | Glycerolipid metabolism |
| Phvul.003G172900.1 | NUCLEAR FUSION DEFECTIVE 4-like | integral component of membrane | | |
| Phvul.003G173700.1 | scythe ubiquitin-like domain | | | |
| Phvul.003G175300.1 | D111 G-patch domain | nucleic acid binding | | |
| Phvul.003G175700.1 | dicer 4 isoform X1 | nucleus;cytoplasm;RISC complex;DNA binding;RNA binding;helicase activity;ribonuclease III activity;ATP binding;mitotic cell cycle;mRNA splicing, via spliceosome;DNA methylation;chromatin silencing;DNA-templated transcription, termination;cell-cell signaling;virus induced gene silencing;photomorphogenesis;embryo | ec:3.6.1;ec:3.1.30;ec:3.1.26;ec:3.1;ec:3.1.26.3;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |

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| | | development ending in seed dormancy;seed germination;regulation of flower development;meristem structural organization;vegetative phase change;seed dormancy process;sugar mediated signaling pathway;maintenance of DNA methylation;vegetative to reproductive phase transition of meristem;production of ta-siRNAs involved in RNA interference;production of lsiRNA involved in RNA interference;protein ubiquitination;covalent chromatin modification;lipid storage;production of miRNAs involved in gene silencing by miRNA;post-translational protein modification;positive regulation of transcription, DNA-templated;response to freezing;RNA phosphodiester bond hydrolysis, endonucleolytic | | |
| Phvul.003G176600.1 | tRNA (guanine(37)-N1)-methyltransferase 2 isoform X1 | nucleus;mitochondrial matrix;integral component of membrane;hydrolase activity, hydrolyzing O-glycosyl compounds;protein histidine kinase activity;tRNA (guanine(37)-N(1))-methyltransferase activity;carbohydrate metabolic process;peptidyl-histidine phosphorylation;tRNA methylation | ec:2.1.1;ec:2.1.1.228;ec:2.7.13.3 | |
| Phvul.003G177900.1 | translation initiation factor eIF-2B subunit delta-like | eukaryotic translation initiation factor 2B complex;translation initiation factor activity;guanyl-nucleotide exchange factor activity;S-methyl-5-thioribose-1-phosphate isomerase activity;translational initiation;L-methionine biosynthetic process from methylthioadenosine;positive regulation of GTPase activity;negative regulation of translational initiation | ec:5.3.1.23-isomerase | Cysteine and methionine metabolism |
| Phvul.003G178300.1 | Adenine nucleotide alpha hydrolases-like superfamily isoform 2 | response to stress | | |
| Phvul.003G178300.2 | universal stress | response to stress | | |
| Phvul.003G178600.1 | C3HC zinc finger | nucleus;zinc ion binding | | |
| Phvul.003G179000.1 | DEAD-box ATP-dependent RNA helicase 27 | RNA binding;ATP-dependent RNA helicase activity;ATP binding;RNA secondary structure unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G179400.1 | G patch domain-containing TGH | nucleus;primary miRNA binding;pre-miRNA binding;mitotic cell cycle;nuclear-transcribed mRNA catabolic process;phloem or xylem histogenesis;production of siRNA involved in RNA interference;production of miRNAs involved in gene silencing by miRNA | | |
| Phvul.003G179500.1 | phospholipid-transporting ATPase 9 | Golgi membrane;trans-Golgi network;plasma membrane;integral component of membrane;magnesium ion binding;phospholipid-translocating ATPase activity;ATP binding;metabolic process;phospholipid translocation;Golgi vesicle budding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.6.3.1 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G181800.1 | PHD and RING finger domain-containing 1 | zinc ion binding | | |
| Phvul.003G181900.1 | Transcription factor BIM1 | protein dimerization activity | | |
| Phvul.003G183300.1 | presenilins-associated rhomboid , mitochondrial | integral component of membrane;serine-type endopeptidase activity;protein processing | ec:3.4.21 | |
| Phvul.003G184300.1 | glycerophosphodiester phosphodiesterase GDPD6 | vacuole;glycerophosphodiester phosphodiesterase activity;glycerophosphocholine phosphodiesterase activity;lipid metabolic process | ec:3.1;ec:3.1.4.46-phosphodiesterase;ec:3.1.4.2-phosphodiesterase | Glycerophospholipid metabolismGlycerophospholipid metabolism |
| Phvul.003G185800.1 | diacylglycerol kinase 1 | intracellular;integral component of membrane;diacylglycerol kinase activity;calcium ion binding;ATP binding;protein | ec:2.7.1.107-kinase (ATP) | Glycerophospholipid metabolism;Glycerolipid |

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| | | kinase C-activating G-protein coupled receptor signaling pathway;phosphorylation;intracellular signal transduction | | metabolism;Phosphatidylinositol signaling system |
| Phvul.003G186200.1 | centrosomal of 112 kDa-like isoform X1 | | | |
| Phvul.003G186200.2 | centrosomal of 112 kDa-like isoform X1 | | | |
| Phvul.003G186400.1 | LTV1 homolog | | | |
| Phvul.003G186400.2 | LTV1 homolog | | | |
| Phvul.003G186800.1 | carboxy-terminal region remorin | | | |
| Phvul.003G186800.2 | carboxy-terminal region remorin | | | |
| Phvul.003G186900.1 | muscle M-line assembly unc-89 isoform X2 | calmodulin binding | | |
| Phvul.003G186900.2 | muscle M-line assembly unc-89 isoform X2 | calmodulin binding | | |
| Phvul.003G186900.3 | muscle M-line assembly unc-89 isoform X2 | calmodulin binding | | |
| Phvul.003G187800.1 | formin 20 | | | |
| Phvul.003G187800.2 | formin 20 | | | |
| Phvul.003G188200.1 | glycosyltransferase 5 | integral component of membrane;transferase activity, transferring glycosyl groups;metabolic process | | |
| Phvul.003G188300.1 | pentatricopeptide repeat-containing At5g61370, mitochondrial-like | | | |
| Phvul.003G188900.1 | galactoside 2-alpha-L-fucosyltransferase-like isoform X1 | integral component of membrane;Golgi cisterna membrane;galactoside 2-alpha-L-fucosyltransferase activity;protein glycosylation;fucosylation;cell wall biogenesis;cell wall organization | ec:2.4.1.69-2-alpha-L-fucosyltransferase;ec:2.4.1 | Glycosphingolipid biosynthesis - globo series;Glycosphingolipid biosynthesis - lacto and neolacto series |
| Phvul.003G189300.1 | cyclic dof factor 3-like | DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.003G190500.1 | alpha beta hydrolase family | chloroplast thylakoid membrane;chloroplast envelope;integral component of membrane;hydrolase activity;MAPK cascade;regulation of transcription, DNA-templated;protein targeting to membrane;response to bacterium;systemic acquired resistance, salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;regulation of hydrogen peroxide metabolic process;regulation of plant-type hypersensitive response;negative regulation of defense response;regulation of protein dephosphorylation | | |
| Phvul.003G191800.1 | nucleolar and coiled-body phospho 1-like | | | |
| Phvul.003G194000.1 | pentatricopeptide repeat-containing At2g45350, chloroplastic | microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G194600.1 | HIPL1 -like | integral component of membrane;oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor;quinone binding;carbohydrate metabolic process;oxidation-reduction process | | |
| Phvul.003G195300.1 | peroxisomal small heat shock | cellular biosynthetic process | | |
| Phvul.003G197300.1 | probable alpha-mannosidase I MNS5 | endoplasmic reticulum;membrane;mannosyl-oligosaccharide 1,2-alpha-mannosidase activity;calcium ion binding;N-glycan processing;regulation of mitotic cell cycle;ER-associated ubiquitin-dependent protein | ec:3.2.1;ec:3.2.1.24-alpha-D-mannosidase;ec:3.2.1.113-1,2-alpha-mannosidase | Other glycan degradationVarious types of N-glycan biosynthesis;N-Glycan biosynthesis |

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| | | catabolic process;endoplasmic reticulum unfolded protein response;glycoprotein ERAD pathway | | |
| Phvul.003G199600.1 | Phosphoglycerate mutase family isoform 1 | cytosol;phosphatase activity;leaf morphogenesis;dephosphorylation;mRNA modification;cell differentiation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase | Aminobenzoate degradation |
| Phvul.003G200300.1 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic | isomerase activity;manganese ion binding;1-deoxy-D-xylulose-5-phosphate reductoisomerase activity;NADPH binding;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway involved in terpenoid biosynthetic process;oxidation-reduction process | ec:1.1.1.267-reductoisomerase | Biosynthesis of antibiotics;Terpenoid backbone biosynthesis |
| Phvul.003G200600.1 | dof zinc finger | membrane;DNA binding;regulation of transcription, DNA-templated;tissue development | | |
| Phvul.003G200700.1 | pantothenate kinase 2 | cytosol;pantothenate kinase activity;ATP binding;protein N-linked glycosylation;coenzyme A biosynthetic process;phosphorylation | ec:2.7.1.33-kinase | Pantothenate and CoA biosynthesis |
| Phvul.003G201000.1 | iron-sulfur cluster assembly 1-like | mitochondrial matrix;ferrous iron binding;iron-sulfur transferase activity;2 iron, 2 sulfur cluster binding;4 iron, 4 sulfur cluster binding;cellular iron ion homeostasis;[2Fe-2S] cluster assembly;protein maturation by iron-sulfur cluster transfer | | |
| Phvul.003G201700.1 | Mpp10 | small nucleolar ribonucleoprotein complex;cytosol;viral nucleocapsid;small-subunit processome;Mpp10 complex;rRNA processing;protein import into nucleus | | |
| Phvul.003G202200.1 | embryo defective 2759 , | integral component of membrane | | |
| Phvul.003G202900.1 | quinolinate synthase, chloroplastic | integral component of membrane;enzyme activator activity;quinolinate synthetase A activity;transferase activity;protein homodimerization activity;4 iron, 4 sulfur cluster binding;aerobic respiration;NAD biosynthetic process;iron-sulfur cluster assembly;quinolinate biosynthetic process;positive regulation of sulfur metabolic process;positive regulation of transferase activity | | |
| Phvul.003G203100.1 | probable LRR receptor-like serine threonine- kinase At4g26540 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;2-alkenal reductase [NAD(P)] activity;protein phosphorylation;oxidation-reduction process | ec:2.7.11;ec:1.3.1.74 | |
| Phvul.003G203600.1 | LATERAL ORGAN BOUNDARIES-like | carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity;metabolic process;organ boundary specification between lateral organs and the meristem | ec:6.3.5.5-synthase (glutamine-hydrolysing) | Alanine, aspartate and glutamate metabolism;Pyrimidine metabolism |
| Phvul.003G203600.2 | LATERAL ORGAN BOUNDARIES-like | carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity;metabolic process;organ boundary specification between lateral organs and the meristem | ec:6.3.5.5-synthase (glutamine-hydrolysing) | Alanine, aspartate and glutamate metabolism;Pyrimidine metabolism |
| Phvul.003G204700.1 | plant intracellular Ras-group-related LRR 9-like | hydrolase activity;metabolic process | | |
| Phvul.003G206000.1 | Manganese-dependent ADP-ribose CDP-alcohol diphosphatase | ADP-ribose diphosphatase activity;CDP-glycerol diphosphatase activity;metabolic process | ec:3.6.1;ec:3.6.1.16-diphosphatase;ec:3.6.1.13-diphosphatase | Glycerophospholipid metabolismPurine metabolism |
| Phvul.003G208800.1 | hypothetical protein PHAVU_003G208800g | peroxisome;regulation of gene expression | | |
| Phvul.003G209200.1 | Malate synthase, glyoxysomal | glyoxysome;malate synthase activity;glyoxylate cycle;tricarboxylic acid cycle | ec:2.3.3.9-synthase | Pyruvate metabolism;Glyoxylate and dicarboxylate metabolism |
| Phvul.003G210800.1 | probable inactive purple acid phosphatase 27 | integral component of membrane;acid phosphatase activity;metal ion binding;dephosphorylation | ec:3.1.3.2-phosphatase;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase | Aminobenzoate degradationAminobenzoate degradation |

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| Phvul.003G214700.1 | probable calcium-binding CML13 | calcium ion binding | | |
| Phvul.003G216600.1 | chalcone-flavanone isomerase family | chalcone isomerase activity;flavonoid biosynthetic process | ec:5.5.1.6-isomerase | Flavonoid biosynthesis |
| Phvul.003G217400.1 | hypothetical protein PHAVU_003G217400g | integral component of membrane | | |
| Phvul.003G217400.2 | hypothetical protein PHAVU_003G217400g | integral component of membrane | | |
| Phvul.003G218000.1 | probable transaldolase | sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity;carbohydrate metabolic process | ec:2.2.1.2-dihydroxyacetonetransferase | Biosynthesis of antibiotics;Pentose phosphate pathway |
| Phvul.003G218500.1 | NRT1 PTR FAMILY -like | plasma membrane;integral component of membrane;nitrate transmembrane transporter activity;oligopeptide transport;response to water deprivation;response to nitrate;nitrate transport;sterol biosynthetic process;glucosinolate biosynthetic process;plant-type cell wall cellulose metabolic process;cell wall pectin metabolic process | | |
| Phvul.003G218500.2 | NRT1 PTR FAMILY -like | integral component of membrane;transporter activity;oligopeptide transport | | |
| Phvul.003G222300.1 | probable glycosyltransferase At5g03795 | integral component of membrane;glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1.224-4-alpha-N-acetylglucosaminyltransferase;ec:2.4.1 | Glycosaminoglycan biosynthesis - heparan sulfate / heparin |
| Phvul.003G223300.1 | transmembrane , | integral component of membrane | | |
| Phvul.003G223400.1 | dual specificity phosphatase DSP8 | phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity;protein tyrosine phosphatase activity;protein tyrosine/serine/threonine phosphatase activity;peptidyl-tyrosine dephosphorylation;negative regulation of MAP kinase activity | ec:3.1.3;ec:3.1.3.48;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.36-5-phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationInositol phosphate metabolism;Phosphatidylinositol signaling systemT cell receptor signaling pathway |
| Phvul.003G223700.1 | traB domain-containing isoform X1 | | | |
| Phvul.003G224900.1 | ATP-dependent Clp protease proteolytic subunit-related 4, chloroplastic-like | chloroplast stroma;chloroplast envelope;serine-type endopeptidase activity;response to reactive oxygen species;proteolysis;systemic acquired resistance;regulation of gene expression;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;regulation of defense response;regulation of protein localization | ec:3.4.21 | |
| Phvul.003G225000.1 | light harvesting | integral component of membrane | | |
| Phvul.003G227400.1 | lon protease homolog 2, peroxisomal-like | peroxisomal matrix;ATP-dependent peptidase activity;serine-type endopeptidase activity;ATP binding;misfolded or incompletely synthesized protein catabolic process;protein processing;protein import into peroxisome matrix, docking;growth;lateral root development | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.4.21 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G227700.1 | invertase inhibitor | cell periphery;pectinesterase activity;pectinesterase inhibitor activity;negative regulation of catalytic activity | ec:3.1.1.11-pectin demethoxylase;ec:3.1.1.1-ali-esterase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsDrug metabolism - other enzymes |
| Phvul.003G230000.1 | eyes absent homolog 2 isoform X1 | protein tyrosine phosphatase activity, metal-dependent;multicellular organismal development;peptidyl-tyrosine dephosphorylation | ec:3.1.3.48;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.003G230900.1 | hypothetical protein PHAVU_003G230900g | nucleic acid binding;zinc ion binding | | |

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| Phvul.003G231400.1 | leucine-rich repeat receptor-like serine threonine- kinase BAM1 | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.003G232200.1 | CROWDED NUCLEI 4-like | | | |
| Phvul.003G232200.2 | CROWDED NUCLEI 4-like | | | |
| Phvul.003G232500.1 | transmembrane , | integral component of membrane | | |
| Phvul.003G232500.2 | transmembrane , | integral component of membrane | | |
| Phvul.003G232500.3 | transmembrane , | integral component of membrane | | |
| Phvul.003G233200.1 | basic leucine zipper 43-like | transcription factor activity, sequence-specific DNA binding;transferase activity;sequence-specific DNA binding;regulation of transcription, DNA-templated;metabolic process | | |
| Phvul.003G233300.1 | hypothetical protein PHAVU_003G233300g | | | |
| Phvul.003G233900.1 | hypothetical protein PHAVU_003G233900g | | | |
| Phvul.003G234200.1 | unknown | | | |
| Phvul.003G239900.1 | Mortality factor 4 1 | histone acetyltransferase complex;chromatin remodeling;regulation of transcription, DNA-templated;histone acetylation | | |
| Phvul.003G240100.1 | probable cadmium zinc-transporting ATPase HMA1, chloroplastic | integral component of plasma membrane;chloroplast envelope;calcium-transporting ATPase activity;ATP binding;cadmium-exporting ATPase activity;cadmium-transporting ATPase activity;zinc transporting ATPase activity;metal ion binding;cellular copper ion homeostasis;metabolic process;response to toxic substance;response to light intensity;zinc ion homeostasis;cadmium ion transmembrane transport;calcium ion transmembrane transport;zinc II ion transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.6.3.8;ec:3.6.3.3;ec:3.6.3.46 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G240300.1 | oxidoreductase TDA3 | oxidoreductase activity;oxidation-reduction process | | |
| Phvul.003G241900.1 | floral homeotic APETALA 2-like isoform X1 | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;multicellular organismal development | | |
| Phvul.003G242300.1 | PI-PLC X domain-containing | integral component of membrane;phosphoric diester hydrolase activity;lipid metabolic process | ec:3.1 | |
| Phvul.003G243000.1 | Nicotinate phosphoribosyltransferase | nicotinate-nucleotide diphosphorylase (carboxylating) activity;nicotinate phosphoribosyltransferase activity;ligase activity;NAD biosynthetic process;nicotinate nucleotide salvage | ec:2.4.2.19-diphosphorylase (carboxylating);ec:2.4.2.11 | Nicotinate and nicotinamide metabolism |
| Phvul.003G243400.1 | triacylglycerol lipase | integral component of membrane;feruloyl esterase activity;lipid metabolic process | ec:3.1.1.73;ec:3.1.1.1-ali-esterase | Drug metabolism - other enzymes |
| Phvul.003G244900.1 | hypothetical protein PHAVU_003G244900g | intracellular;protein glycosylation;protein targeting to vacuole;vesicle-mediated transport | | |
| Phvul.003G246000.1 | CDPK-related kinase 5-like | cytoplasm;plasma membrane;calmodulin-dependent protein kinase activity;calcium ion binding;calmodulin binding;ATP binding;calcium-dependent protein serine/threonine kinase activity;abscisic acid-activated signaling pathway;peptidyl-serine phosphorylation;intracellular signal transduction;protein autophosphorylation | ec:2.7.11;ec:2.7.11.17 | |

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| Phvul.003G248400.1 | hypothetical protein PHAVU_003G248400g | | | |
| Phvul.003G248600.1 | GDSL esterase lipase At2g23540 | hydrolase activity, acting on ester bonds;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.003G249100.1 | DUF1162 family | integral component of membrane | | |
| Phvul.003G250400.1 | BTB POZ domain-containing At3g50780-like | peptidase activity;proteolysis;cell division | | |
| Phvul.003G251000.1 | probable calcium-binding CML41 | calcium ion binding | | |
| Phvul.003G251300.1 | elongation of fatty acids 3-like | integral component of membrane | | |
| Phvul.003G251700.1 | hypothetical protein PHAVU_003G251700g | | | |
| Phvul.003G252000.1 | G-box-binding factor 1 | cytoplasm;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated;regulation of hydrogen peroxide metabolic process;regulation of cell aging | | |
| Phvul.003G252600.1 | polyol transporter , | integral component of membrane | | |
| Phvul.003G252600.2 | polyol transporter , | integral component of membrane | | |
| Phvul.003G254800.1 | Anaphase-promoting complex subunit 10 | anaphase-promoting complex;nuclear body;mitotic nuclear division;gamete generation;cell proliferation;phloem or xylem histogenesis;regulation of mitotic metaphase/anaphase transition;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;negative regulation of DNA endoreduplication;DNA endoreduplication;proteasome assembly;cell division;regulation of unidimensional cell growth;response to misfolded protein | | |
| Phvul.003G255100.1 | pheophytinase, chloroplastic | chloroplast envelope;1-acylglycerol-3-phosphate O-acyltransferase activity;hydrolase activity;maltose metabolic process;starch biosynthetic process;positive regulation of catalytic activity | ec:2.3.1.51-O-acyltransferase;ec:2.3.1 | Glycerophospholipid metabolism;Glycerolipid metabolism |
| Phvul.003G255200.1 | auxilin 1 | transferase activity;metabolic process | | |
| Phvul.003G255200.2 | auxilin 1 | transferase activity;metabolic process | | |
| Phvul.003G255600.1 | GTPase Era-like isoform X1 | chloroplast;RNA binding;GTP binding;embryo development ending in seed dormancy;iron-sulfur cluster assembly;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;transcription from plastid promoter;protein targeting to chloroplast;positive regulation of transcription, DNA-templated | | |
| Phvul.003G256500.1 | abscisic acid 8 -hydroxylase 3-like | integral component of membrane;iron ion binding;(+)-abscisic acid 8'-hydroxylase activity;heme binding;multicellular organismal development;brassinosteroid homeostasis;sterol metabolic process;brassinosteroid biosynthetic process;oxidation-reduction process | ec:1.14.13.93-acid 8'-hydroxylase;ec:1.14.13 | Carotenoid biosynthesis |
| Phvul.003G257300.1 | AT4G36440 , partial | integral component of membrane | | |
| Phvul.003G258600.1 | amino-terminal domain micro-spherule | | | |

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| Phvul.003G260500.1 | NAC domain-containing 37 | nucleus;integral component of membrane;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.003G263100.1 | armadillo repeat only | | | |
| Phvul.003G266900.1 | probable phosphatase 2C 46 | integral component of membrane;protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.003G267000.1 | Receptor kinase THESEUS 1 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.003G267600.1 | UPF0548 At2g17695 | chloroplast envelope | | |
| Phvul.003G267600.2 | UPF0548 At2g17695 | chloroplast envelope | | |
| Phvul.003G268400.1 | DUF241 domain | | | |
| Phvul.003G268600.1 | Chitinase (Class Ib) Hevein | chitinase activity;chitin binding;polysaccharide catabolic process;chitin catabolic process;defense response;cell wall macromolecule catabolic process | ec:3.2.1.14-chitodextrinase | Amino sugar and nucleotide sugar metabolism |
| Phvul.003G269600.1 | dehydrodolichyl diphosphate synthase 6-like | di-trans,poly-cis-decaprenylcistransferase activity;metabolic process | ec:2.5.1.31-synthase [(2E,6E)-farnesyl-diphosphate specific];ec:2.5.1 | Terpenoid backbone biosynthesis |
| Phvul.003G270100.1 | Syntaxin-binding 5 | cytoplasm;plasma membrane;GTPase activator activity;Rab GTPase binding;syntaxin binding;regulation of exocytosis;positive regulation of GTPase activity | | |
| Phvul.003G270100.2 | Syntaxin-binding 5 | cytoplasm;plasma membrane;GTPase activator activity;Rab GTPase binding;syntaxin binding;regulation of exocytosis;positive regulation of GTPase activity | | |
| Phvul.003G272800.1 | transmembrane 45B-like | integral component of membrane | | |
| Phvul.003G274200.1 | UPF0664 stress-induced | plasma membrane | | |
| Phvul.003G274200.2 | UPF0664 stress-induced | plasma membrane | | |
| Phvul.003G274900.1 | macronuclear actin | structural constituent of cytoskeleton;actin filament-based process | | |
| Phvul.003G275200.1 | glycosyltransferase family 92 | integral component of membrane;transferase activity;metabolic process | | |
| Phvul.003G275500.1 | serine threonine-kinase minibrain-like isoform X1 | cytosol;plasmodesma;protein serine/threonine/tyrosine kinase activity;ATP binding;protein phosphorylation;response to abscisic acid | ec:2.7.12.1 | |
| Phvul.003G276200.1 | inactive RESTRICTED TEV MOVEMENT 2-like | integral component of membrane | | |
| Phvul.003G277700.1 | E3 ubiquitin- ligase MBR1-like isoform X1 | zinc ion binding;ligase activity;metabolic process | | |
| Phvul.003G278500.1 | arabinosyltransferase XEG113-like | integral component of membrane;microtubule-severing ATPase activity;arabinosyltransferase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G279000.1 | probable apyrase 7 | integral component of membrane;hydrolase activity;multicellular organismal development;metabolic process;anatomical structure development | | |
| Phvul.003G279000.2 | probable apyrase 7 | integral component of membrane;hydrolase activity;multicellular organismal development;metabolic process;anatomical structure development | | |
| Phvul.003G280000.1 | probable methyltransferase PMT20 | endosome;trans-Golgi network;integral component of membrane;S-adenosylmethionine-dependent methyltransferase activity;methylation | | |
| Phvul.003G280200.1 | hypothetical protein PHAVU_003G280200g | | | |

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| Phvul.003G280700.1 | translin-associated X | sequence-specific DNA binding | | |
| Phvul.003G281100.1 | ASC1 | endoplasmic reticulum;integral component of membrane;sphingosine N-acyltransferase activity;ceramide biosynthetic process | ec:2.3.1.24-N-acyltransferase;ec:2.3.1 | Sphingolipid metabolism |
| Phvul.003G282200.1 | histone-lysine N-methyltransferase family member SUVH9-like | nucleus;chromosome;zinc ion binding;histone-lysine N-methyltransferase activity;histone binding;histone lysine methylation | ec:2.1.1;ec:2.1.1.43-N-methyltransferase | Lysine degradation |
| Phvul.003G282900.1 | nucleolin 1-like isoform X1 | nucleotide binding;nucleic acid binding | | |
| Phvul.003G282900.2 | nucleolin 1-like isoform X1 | nucleotide binding;nucleic acid binding | | |
| Phvul.003G282900.3 | nucleolin 1-like isoform X1 | nucleotide binding;nucleic acid binding | | |
| Phvul.003G282900.4 | nucleolin 1-like isoform X1 | nucleotide binding;nucleic acid binding | | |
| Phvul.003G283900.1 | ABC transporter B family member 2-like | integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G284800.1 | PLATZ transcription factor family | integral component of membrane | | |
| Phvul.003G285900.1 | phosphoenolpyruvate carboxykinase [ATP]-like | cytosol;phosphoenolpyruvate carboxykinase (ATP) activity;ATP binding;kinase activity;gluconeogenesis;phosphorylation | ec:4.1.1;ec:4.1.1.49-carboxykinase (ATP) | Pyruvate metabolism;Biosynthesis of antibiotics;Carbon fixation in photosynthetic organisms;Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis |
| Phvul.003G290500.1 | guanylate-binding family | GTPase activity;GTP binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.003G290700.1 | PLASMODESMATA CALLOSE-BINDING PROTEIN 3-like | integral component of membrane;protein histidine kinase activity;hydrolase activity;peptidyl-histidine phosphorylation | ec:2.7.13.3 | |
| Phvul.003G292000.1 | glyco 3-alpha-L-fucosyltransferase A | integral component of membrane;Golgi cisterna membrane;glycoprotein 3-alpha-L-fucosyltransferase activity;protein glycosylation;fucosylation | ec:2.4.1;ec:2.4.1.214-3-alpha-L-fucosyltransferase | Various types of N-glycan biosynthesis |
| Phvul.003G293100.1 | pentatricopeptide repeat-containing At2g13600-like | microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.003G295800.1 | Autophagy-related 2 | pre-autophagosomal structure;extrinsic component of membrane;autophagosome assembly;mitophagy;nucleophagy | | |
| Phvul.003G296100.1 | cell division cycle-associated 7 | | | |
| Phvul.003G296300.1 | Sas10 U3 ribonucleo (UTP) family , | nucleolus;small-subunit processome;maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | | |
| Phvul.003G296900.1 | hypothetical protein PHAVU_003G296900g | | | |
| Phvul.004G004800.1 | serine threonine-kinase HT1 | intracellular;MAP kinase kinase kinase activity;protein serine/threonine/tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity;microtubule nucleation | ec:2.7.11;ec:2.7.11.25;ec:2.7.12.1 | |
| Phvul.004G007700.1 | NBS-LRR type disease resistance CNL-J9 | ADP binding;defense response | | |
| Phvul.004G015600.1 | NBS-LRR type disease resistance CNL-B11 | ADP binding;defense response | | |
| Phvul.004G017600.1 | Methyl- -binding domain-containing 9 | nuclear heterochromatin;DNA binding;zinc ion binding;oxidoreductase activity;ubiquitin protein ligase activity;anatomical structure morphogenesis;maintenance of DNA methylation;vegetative to reproductive phase | | |

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| | | transition of meristem;protein ubiquitination;histone acetylation;cell development;oxidation-reduction process;regulation of methylation-dependent chromatin silencing;plant epidermis development | | |
| Phvul.004G017900.1 | pentatricopeptide repeat-containing At3g61360 | | | |
| Phvul.004G018700.1 | Auxin-induced 5NG4 | plasma membrane;integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.004G018900.1 | alpha-dioxygenase 1-like | peroxidase activity;heme binding;dioxygenase activity;response to oxidative stress;oxidation-reduction process;cellular oxidant detoxification | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.004G022600.1 | Hop-interacting THI043 | cellular carbohydrate metabolic process;single-organism carbohydrate metabolic process;single-organism cellular process | | |
| Phvul.004G023100.1 | ABC transporter B family member 15-like | integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.004G023500.1 | glucose-6-phosphate isomerase, cytosolic | cytosol;glucose-6-phosphate isomerase activity;gluconeogenesis;glycolytic process;response to sucrose;flavonoid biosynthetic process;defense response to fungus, incompatible interaction;response to UV-B | ec:5.3.1.9-isomerase | Biosynthesis of antibiotics;Pentose phosphate pathway;Amino sugar and nucleotide sugar metabolism;Glycolysis / Gluconeogenesis;Starch and sucrose metabolism |
| Phvul.004G023500.2 | glucose-6-phosphate isomerase, cytosolic | cytosol;glucose-6-phosphate isomerase activity;gluconeogenesis;glycolytic process;response to sucrose;flavonoid biosynthetic process;defense response to fungus, incompatible interaction;response to UV-B | ec:5.3.1.9-isomerase | Biosynthesis of antibiotics;Pentose phosphate pathway;Amino sugar and nucleotide sugar metabolism;Glycolysis / Gluconeogenesis;Starch and sucrose metabolism |
| Phvul.004G023900.1 | rRNA methyltransferase ylbH | methyltransferase activity;tRNA metabolic process;chloroplast organization;embryo development ending in seed dormancy;production of ta-siRNAs involved in RNA interference;iron-sulfur cluster assembly;rRNA methylation;production of miRNAs involved in gene silencing by miRNA;transcription from plastid promoter;positive regulation of transcription, DNA-templated;defense response to virus | | |
| Phvul.004G025000.1 | probable mitochondrial chaperone BCS1-B | integral component of membrane;ATP binding;hydrolase activity;metabolic process | | |
| Phvul.004G026100.2 | hypersensitive-induced response 2 | vacuolar membrane;plasmodesma;chloroplast;protein histidine kinase binding | | |
| Phvul.004G027800.1 | ABC transporter B family member 19 | integral component of membrane;ATP binding;xenobiotic-transporting ATPase activity;auxin efflux transmembrane transporter activity;polysaccharide biosynthetic process;drug transmembrane transport;regulation of cell size;response to blue light;photomorphogenesis;response to auxin;multidimensional cell growth;cell tip growth;positive gravitropism;vernalization response;formation of organ boundary;response to far red light;auxin efflux;basipetal auxin transport;acropetal auxin transport;xenobiotic transport;anthocyanin accumulation in tissues in response to UV light;carpel development;stamen development;lateral root development;root hair elongation;cell wall organization | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.6.3.44 | Purine metabolismPurine metabolism;Thiamine metabolism |

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| Phvul.004G031600.2 | vesicle transport v-SNARE 13 | Golgi apparatus;integral component of membrane;SNARE binding;SNAP receptor activity;intracellular protein transport;vesicle-mediated transport;membrane fusion | | |
| Phvul.004G032000.1 | SNF1-related kinase catalytic subunit alpha KIN10 | cytoplasm;cAMP-dependent protein kinase activity;ATP binding;protein phosphorylation;intracellular signal transduction | ec:2.7.11;ec:2.7.11.11-protein kinase | mTOR signaling pathway |
| Phvul.004G033900.1 | hypothetical protein PHAVU_004G033900g | | | |
| Phvul.004G037700.1 | transcription factor TCP13 | single-organism process | | |
| Phvul.004G037700.2 | transcription factor TCP13 | single-organism process | | |
| Phvul.004G044300.1 | AF306499_1NBS-LRR resistance B8 | ADP binding;defense response | | |
| Phvul.004G044900.1 | LRR receptor-like kinase family | integral component of membrane | | |
| Phvul.004G045400.1 | ATP sulfurylase 2 | cytosol;adenylylsulfate kinase activity;sulfate adenylyltransferase (ATP) activity;sulfate assimilation;phosphorylation | ec:2.7.1.25-kinase;ec:2.7.7.4-adenylyltransferase;ec:2.7.7 | Sulfur metabolism;Purine metabolismSulfur metabolism;Purine metabolism;Biosynthesis of antibiotics;Monobactam biosynthesis;Selenocompound metabolism |
| Phvul.004G046100.1 | 6-phosphogluconate dehydrogenase, decarboxylating 3 | phosphogluconate dehydrogenase (decarboxylating) activity;pentose-phosphate shunt;oxidation-reduction process | ec:1.1.1.44-dehydrogenase (NADP+-dependent, decarboxylating) | Biosynthesis of antibiotics;Pentose phosphate pathway;Glutathione metabolism |
| Phvul.004G046600.1 | zinc finger CONSTANS-LIKE 2 | nucleus;zinc ion binding;response to light stimulus;regulation of flower development | | |
| Phvul.004G048000.1 | NBS-LRR type disease resistance | ADP binding;defense response | | |
| Phvul.004G048300.1 | tryptophan synthase beta chain 2 | tryptophan synthase activity;pyridoxal phosphate binding;protein homodimerization activity;L-serine hydro-lyase (adding indole, L-tryptophan-forming) activity;tryptophan biosynthetic process | ec:4.2.1;ec:4.2.1.20-synthase | Biosynthesis of antibiotics;Phenylalanine, tyrosine and tryptophan biosynthesis;Glycine, serine and threonine metabolism |
| Phvul.004G048500.1 | zinc finger, C3HC4 type (RING finger) , | zinc ion binding;petal formation;sepal formation | | |
| Phvul.004G048900.1 | trichome birefringence-like 19 | Golgi apparatus;integral component of membrane;O-acetyltransferase activity;cell wall organization or biogenesis | ec:2.3.1 | |
| Phvul.004G049300.1 | endo-1,3(4)-beta-glucanase 2 | cell surface;glucan endo-1,3-beta-D-glucosidase activity;glucan endo-1,3-beta-glucanase activity, C-3 substituted reducing group;glucan endo-1,4-beta-glucanase activity, C-3 substituted reducing group;(1->3)-beta-D-glucan catabolic process | ec:3.2.1.39-endo-1,3-beta-D-glucosidase;ec:3.2.1;ec:3.2.1.21-gentiobiase;ec:3.2.1.6 | Starch and sucrose metabolismStarch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.004G050900.1 | membrane steroid-binding 2-like | endomembrane system;integral component of membrane;dihydrofolate reductase activity;heme binding;oxidation-reduction process | ec:1.5.1.3-reductase | One carbon pool by folate;Folate biosynthesis |
| Phvul.004G052800.1 | bystin-like | | | |
| Phvul.004G052900.1 | UBP1-associated 2A-like | nucleotide binding;nucleic acid binding | | |
| Phvul.004G054400.1 | SWI SNF complex component SNF12 homolog | | | |
| Phvul.004G054400.2 | SWI SNF complex component SNF12 homolog | | | |
| Phvul.004G058100.1 | TPX2 (targeting for Xklp2) family , | | | |

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| Phvul.004G058900.1 | uncharacterized membrane At3g27390-like | integral component of membrane | | |
| Phvul.004G059400.1 | Mitochondrial inner membrane protease ATP23 | metalloendopeptidase activity;proteolysis | ec:3.4.24 | |
| Phvul.004G060400.1 | pentatricopeptide repeat-containing At4g35850, mitochondrial | pyrimidine ribonucleotide biosynthetic process;photomorphogenesis;regulation of flower development;cullin deneddylation;histone lysine methylation | | |
| Phvul.004G064300.1 | ultraviolet-B receptor UVR8 | ligase activity;protein domain specific binding;metabolic process | | |
| Phvul.004G064500.1 | probable dolichyl pyrophosphate Man9 c2 alpha-1,3-glucosyltransferase | endoplasmic reticulum membrane;integral component of membrane;dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;protein N-linked glycosylation;oligosaccharide-lipid intermediate biosynthetic process | ec:2.4.1 | |
| Phvul.004G065200.1 | hypothetical protein PHAVU_004G065200g | | | |
| Phvul.004G065300.1 | phosphoglycerate kinase, cytosolic-like isoform X1 | phosphoglycerate kinase activity;tRNA (guanine-N7-)-methyltransferase activity;glycolytic process;tRNA modification;RNA (guanine-N7)-methylation | ec:2.1.1;ec:2.1.1.33;ec:2.7.2.3-kinase | Biosynthesis of antibiotics;Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis |
| Phvul.004G065300.4 | Phosphoglycerate kinase | phosphoglycerate kinase activity;tRNA (guanine-N7-)-methyltransferase activity;glycolytic process;tRNA modification;RNA (guanine-N7)-methylation | ec:2.1.1;ec:2.1.1.33;ec:2.7.2.3-kinase | Biosynthesis of antibiotics;Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis |
| Phvul.004G065300.6 | phosphoglycerate kinase, cytosolic-like isoform X1 | phosphoglycerate kinase activity;tRNA (guanine-N7-)-methyltransferase activity;glycolytic process;tRNA modification;RNA (guanine-N7)-methylation | ec:2.1.1;ec:2.1.1.33;ec:2.7.2.3-kinase | Biosynthesis of antibiotics;Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis |
| Phvul.004G065600.1 | enhancer of polycomb homolog 2-like | Piccolo NuA4 histone acetyltransferase complex;transcription, DNA-templated;regulation of transcription from RNA polymerase II promoter | | |
| Phvul.004G065600.2 | enhancer of polycomb homolog 2-like | Piccolo NuA4 histone acetyltransferase complex;transcription, DNA-templated;regulation of transcription from RNA polymerase II promoter | | |
| Phvul.004G065900.1 | neoxanthin synthase | integral component of membrane | | |
| Phvul.004G067500.1 | INO80 complex subunit D-like | histone acetyltransferase complex;H4 histone acetyltransferase activity;histone H4 acetylation | ec:2.3.1.48;ec:2.3.1 | |
| Phvul.004G068300.1 | cytochrome P450 81E8-like | integral component of membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.004G068400.1 | cytochrome P450 81E8-like | integral component of membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.004G068600.1 | DUF247 domain | integral component of membrane | | |
| Phvul.004G075000.1 | transmembrane , | mitochondrion;integral component of membrane;RNA methylation | | |
| Phvul.004G075300.1 | IQ-DOMAIN 1-like isoform X1 | integral component of membrane | | |
| Phvul.004G075300.2 | IQ-DOMAIN 1-like isoform X1 | integral component of membrane | | |
| Phvul.004G075300.3 | IQ-DOMAIN 1-like isoform X1 | integral component of membrane | | |

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| Phvul.004G080300.1 | YTH domain family 1 | | | |
| Phvul.004G085100.1 | sucrose transport SUC8-like | integral component of plasma membrane;sucrose transmembrane transporter activity;sucrose transport | | |
| Phvul.004G085700.1 | MATE efflux family 5 | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport;fatty acid catabolic process | | |
| Phvul.004G090900.1 | cell division cycle 5 isoform X2 | chloroplast;DNA binding;transcription factor activity, sequence-specific DNA binding;mitotic cell cycle;regulation of transcription, DNA-templated;RNA processing;defense response signaling pathway, resistance gene-dependent;defense response signaling pathway, resistance gene-independent;defense response to bacterium;defense response to fungus;cell division | | |
| Phvul.004G091600.1 | LHCII type I chlorophyll a b-binding | photosystem I;photosystem II;chloroplast thylakoid membrane;chloroplast envelope;plastoglobule;integral component of membrane;chlorophyll binding;pigment binding;metal ion binding;response to light stimulus;photosynthesis, light harvesting in photosystem I;protein-chromophore linkage | | |
| Phvul.004G098300.1 | hypothetical protein PHAVU_004G0983001g, partial | structural constituent of cell wall;plant-type cell wall organization | | |
| Phvul.004G102700.1 | probable membrane-associated kinase regulator 6 | kinase activity;response to brassinosteroid;phosphorylation | | |
| Phvul.004G102900.1 | P-loop nucleoside triphosphate hydrolase superfamily | ATP binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.004G104900.1 | receptor 12 | integral component of membrane | | |
| Phvul.004G112000.1 | mitogen-activated kinase kinase kinase YODA-like | cytoplasm;protein serine/threonine kinase activity;ATP binding;regulation of mitotic cell cycle;signal transduction by protein phosphorylation;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process | ec:2.7.11 | |
| Phvul.004G113900.1 | hypothetical protein PHAVU_004G113900g | integral component of membrane | | |
| Phvul.004G113900.2 | hypothetical protein PHAVU_004G113900g | integral component of membrane | | |
| Phvul.004G113900.3 | hypothetical protein PHAVU_004G113900g | integral component of membrane | | |
| Phvul.004G113900.4 | hypothetical protein PHAVU_004G113900g | integral component of membrane | | |
| Phvul.004G117900.1 | Methyl- -binding domain-containing 13 | nucleus;methyl-CpG binding;negative regulation of transcription from RNA polymerase II promoter;methylation-dependent chromatin silencing | | |
| Phvul.004G118600.1 | phosphatase inhibitor 2 isoform X2 | protein phosphatase type 1 complex;protein phosphatase inhibitor activity;regulation of signal transduction;negative regulation of catalytic activity;regulation of phosphoprotein phosphatase activity | | |
| Phvul.004G118600.2 | phosphatase inhibitor 2 isoform X2 | protein phosphatase type 1 complex;protein phosphatase inhibitor activity;regulation of signal transduction;negative regulation of catalytic activity;regulation of phosphoprotein phosphatase activity | | |

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| Phvul.004G118600.3 | phosphatase inhibitor 2 isoform X2 | protein phosphatase type 1 complex;protein phosphatase inhibitor activity;regulation of signal transduction;negative regulation of catalytic activity;regulation of phosphoprotein phosphatase activity | | |
| Phvul.004G120400.1 | RHOMBOID 2 | integral component of membrane;serine-type endopeptidase activity;protein processing | ec:3.4.21 | |
| Phvul.004G121900.1 | DETOXIFICATION 49-like | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.004G123200.1 | DUF4378 domain | | | |
| Phvul.004G128900.1 | Fructose-1,6-bisphosphatase, cytosolic | nucleus;cytosol;integral component of membrane;fructose 1,6-bisphosphate 1-phosphatase activity;starch catabolic process;sucrose biosynthetic process;response to abscisic acid;response to fructose;photosynthesis;dephosphorylation;fructose 1,6-bisphosphate metabolic process | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.23;ec:3.1.3.11-hexose diphosphatase | Aminobenzoate degradationBiosynthesis of antibiotics;Pentose phosphate pathway;Methane metabolism;Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis;Fructose and mannose metabolism |
| Phvul.004G129100.1 | DNAJ heat shock N-terminal domain-containing , isoform 1 | | | |
| Phvul.004G131400.1 | clathrin assembly At1g33340 | clathrin-coated vesicle;1-phosphatidylinositol binding;clathrin binding;clathrin coat assembly | | |
| Phvul.004G132600.1 | hypothetical protein PHAVU_004G132600g | | | |
| Phvul.004G133200.1 | DNA (cytosine-5)-methyltransferase 1-like | integral component of membrane;chromatin binding;DNA (cytosine-5-)-methyltransferase activity;transferase activity, transferring acyl groups;C-5 methylation of cytosine | ec:2.1.1;ec:2.1.1.37-(cytosine-5-)-methyltransferase | Cysteine and methionine metabolism |
| Phvul.004G133400.1 | chloride channel CLC-c-like isoform X1 | integral component of membrane;voltage-gated chloride channel activity;chloride transport;ion transmembrane transport;regulation of anion transmembrane transport | | |
| Phvul.004G134300.1 | TMV resistance N-like | ADP binding;defense response;signal transduction | | |
| Phvul.004G134800.1 | UPF0481 At3g02645 | integral component of membrane | | |
| Phvul.004G135100.1 | disease resistance (TIR-NBS-LRR class), | ADP binding;defense response;signal transduction | | |
| Phvul.004G136400.1 | hypothetical protein PHAVU_004G136400g | nucleus | | |
| Phvul.004G136500.1 | receptor kinase HSL1 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.004G136900.1 | hypothetical protein PHAVU_004G136900g | | | |
| Phvul.004G139400.1 | dolichyl-diphosphooligosaccharide--glycosyltransferase subunit STT3B | plasma membrane;oligosaccharyltransferase complex;integral component of membrane;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;protein N-linked glycosylation via asparagine;post-translational protein modification | ec:2.4.1;ec:2.4.1.119 | |
| Phvul.004G139700.1 | TMV resistance N-like | integral component of membrane;ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.004G139800.1 | TMV resistance N-like | integral component of membrane;ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.004G139800.2 | TMV resistance N-like isoform X2 | integral component of membrane;ATP binding;hydrolase activity;ADP binding;defense | | |

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| | | response;signal transduction;RNA phosphodiester bond hydrolysis | | |
| Phvul.004G139800.3 | TMV resistance N | integral component of membrane;ATP binding;hydrolase activity;ADP binding;defense response;signal transduction;RNA phosphodiester bond hydrolysis | | |
| Phvul.004G140300.1 | hypothetical protein PHAVU_004G140300g | | | |
| Phvul.004G142300.1 | nucleotide-diphospho-sugar transferase family | integral component of membrane;transferase activity;metabolic process | | |
| Phvul.004G142900.1 | argonaute 1 | translation initiation factor activity;transferase activity;translational initiation | | |
| Phvul.004G144200.1 | Cyclic nucleotide-binding transporter 1 isoform 1 | integral component of membrane;voltage-gated potassium channel activity;regulation of membrane potential;potassium ion transmembrane transport | | |
| Phvul.004G144800.1 | #NOME? | endoplasmic reticulum membrane;integral component of membrane;protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity;C-terminal protein methylation | ec:2.1.1;ec:2.1.1.100-O-methyltransferase | Biosynthesis of antibiotics;Terpenoid backbone biosynthesis |
| Phvul.004G144800.2 | #NOME? | endoplasmic reticulum membrane;integral component of membrane;protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity;C-terminal protein methylation | ec:2.1.1;ec:2.1.1.100-O-methyltransferase | Biosynthesis of antibiotics;Terpenoid backbone biosynthesis |
| Phvul.004G145300.1 | carbohydrate-binding of the ER | kinase activity;phosphorylation | | |
| Phvul.004G145900.1 | SHOOT GRAVITROPISM 5-like | nucleic acid binding;metal ion binding | | |
| Phvul.004G147000.1 | transcription termination factor family | mitochondrion;double-stranded DNA binding;regulation of transcription, DNA-templated;response to salt stress;chloroplast organization;response to abscisic acid | | |
| Phvul.004G147000.2 | transcription termination factor family | mitochondrion;double-stranded DNA binding;regulation of transcription, DNA-templated;response to salt stress;chloroplast organization;response to abscisic acid | | |
| Phvul.004G147700.1 | PPR containing plant | | | |
| Phvul.004G148200.1 | Ferrochelatase-2, chloroplastic | intracellular;integral component of membrane;ferrochelatase activity;protein targeting to membrane;heme biosynthetic process;response to wounding;regulation of plant-type hypersensitive response;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione;endoplasmic reticulum unfolded protein response;negative regulation of programmed cell death;defense response by callose deposition | ec:4.99.1.1-ferro-protoporphyrin chelatase | Porphyrin and chlorophyll metabolism |
| Phvul.004G149400.1 | Down syndrome critical region 3 homolog | protein transporter activity;protein transport;photoperiodism, flowering | | |
| Phvul.004G149800.1 | Polypeptide deformylase, isoform 1 | chloroplast;iron ion binding;peptide deformylase activity;translation;N-terminal protein amino acid modification;co-translational protein modification | ec:3.5.1.88 | |
| Phvul.004G149800.2 | Polypeptide deformylase, isoform 1 | chloroplast;iron ion binding;peptide deformylase activity;translation;N-terminal protein amino acid modification;co-translational protein modification | ec:3.5.1.88 | |
| Phvul.004G150100.1 | Ketose-bisphosphate aldolase class-II family isoform 1 | phosphogluconate dehydrogenase (decarboxylating) activity;zinc ion binding;aldehyde-lyase activity;NAD binding;carbohydrate metabolic process;oxidation-reduction process | ec:1.1.1.44-dehydrogenase (NADP+-dependent, decarboxylating) | Biosynthesis of antibiotics;Pentose phosphate pathway;Glutathione metabolism |
| Phvul.004G150700.1 | photosystem I assembly ycf3 (chloroplast) | chloroplast thylakoid membrane;photosynthesis | | |
| Phvul.004G151100.1 | zinc finger VAR3, chloroplastic | DNA-directed DNA polymerase activity;zinc ion binding;DNA biosynthetic process | ec:2.7.7.7-DNA polymerase | Purine metabolism;Pyrimidine metabolism |

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| Phvul.004G151700.1 | exonuclease 1 | nucleus;DNA binding;exonuclease activity;DNA repair;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.004G155500.1 | glycerophosphodiester phosphodiesterase kinase domain-containing GDPDL2-like | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.004G155900.1 | SAR DEFICIENT 1-like | calmodulin binding;response to stress | | |
| Phvul.004G156400.1 | plant synaptotagmin | endoplasmic reticulum;integral component of membrane | | |
| Phvul.004G159200.2 | aspartic ase Asp1 | integral component of membrane;aspartic-type endopeptidase activity;transferase activity;N-terminal protein myristoylation;proteolysis;protein catabolic process | ec:3.4.23 | |
| Phvul.004G160000.1 | probable 3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase | intracellular;plasma membrane;integral component of membrane;C-8 sterol isomerase activity;cholestenol delta-isomerase activity;acetyl-CoA metabolic process;sterol metabolic process;brassinosteroid biosynthetic process;second-messenger-mediated signaling;regulation of gene silencing by miRNA | ec:5.3.3.5-Delta-isomerase;ec:5.3.3 | Steroid biosynthesis |
| Phvul.004G162300.1 | Aldehyde dehydrogenase family 2 member C4 | retinal dehydrogenase activity;aldehyde dehydrogenase (NAD) activity;coniferyl-aldehyde dehydrogenase activity;systemic acquired resistance;phenylpropanoid biosynthetic process;response to nitrate;nitrate transport;response to endoplasmic reticulum stress;oxidation-reduction process | ec:1.2.1.68-dehydrogenase;ec:1.2.1.36-dehydrogenase;ec:1.2.1.5-dehydrogenase [NAD(P)+];ec:1.2.1.3-dehydrogenase (NAD+) | Phenylpropanoid biosynthesisRetinol metabolismDrug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;beta-Alanine metabolism;Glycolysis / Gluconeogenesis;Phenylalanine metabolism;Tyrosine metabolism;Histidine metabolismArginine and proline metabolism;Chloroalkane and chloroalkene degradation;Pyruvate metabolism;Biosynthesis of antibiotics;Tryptophan metabolism;Valine, leucine and isoleucine degradation;Limonene and pinene degradation;beta-Alanine metabolism;Lysine degradation;Glycolysis / Gluconeogenesis;Fatty acid degradation;Glycerolipid metabolism;Ascorbate and aldarate metabolism;Histidine metabolism;Pentose and glucuronate interconversions |
| Phvul.004G164500.1 | subtilisin-like protease | cell wall;Golgi apparatus;integral component of membrane;serine-type endopeptidase activity;protein glycosylation;proteolysis;ER to Golgi vesicle-mediated transport;hyperosmotic salinity response | ec:3.4.21 | |
| Phvul.004G164500.2 | subtilisin-like protease | cell wall;Golgi apparatus;integral component of membrane;serine-type endopeptidase activity;protein glycosylation;proteolysis;ER to Golgi vesicle-mediated transport;hyperosmotic salinity response | ec:3.4.21 | |

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| Phvul.004G166900.1 | hypothetical protein PHAVU_004G166900g | | | |
| Phvul.004G168100.1 | Elongation factor Ts | mitochondrial matrix;chloroplast part;translation elongation factor activity;isoprenoid biosynthetic process;plastid organization;mitochondrial translational elongation | | |
| Phvul.004G169700.1 | probable glycosyltransferase At3g07620 | integral component of membrane;glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1.224-4-alpha-N-acetylglucosaminyltransferase;ec:2.4.1 | Glycosaminoglycan biosynthesis - heparan sulfate / heparin |
| Phvul.004G170500.1 | senescence dehydration-associated | | | |
| Phvul.004G171300.1 | tetraspanin family | integral component of membrane | | |
| Phvul.004G172000.1 | hypothetical protein PHAVU_004G172000g | | | |
| Phvul.004G173600.1 | zinc finger CCCH domain-containing 20-like | metal ion binding | | |
| Phvul.004G173700.1 | gamma-glutamyltranspeptidase 3 | integral component of membrane;gamma-glutamyltransferase activity;glutathione gamma-glutamylcysteinyltransferase activity;glutathione catabolic process | ec:2.3.2.2-glutamyl transpeptidase;ec:2.3.2.15 | Taurine and hypotaurine metabolism;Glutathione metabolism;Cyanoamino acid metabolism |
| Phvul.004G173700.2 | gamma-glutamyltranspeptidase 3 | integral component of membrane;gamma-glutamyltransferase activity;glutathione gamma-glutamylcysteinyltransferase activity;glutathione catabolic process | ec:2.3.2.2-glutamyl transpeptidase;ec:2.3.2.15 | Taurine and hypotaurine metabolism;Glutathione metabolism;Cyanoamino acid metabolism |
| Phvul.004G173700.3 | gamma-glutamyltranspeptidase 3 | integral component of membrane;gamma-glutamyltransferase activity;glutathione gamma-glutamylcysteinyltransferase activity;glutathione catabolic process | ec:2.3.2.2-glutamyl transpeptidase;ec:2.3.2.15 | Taurine and hypotaurine metabolism;Glutathione metabolism;Cyanoamino acid metabolism |
| Phvul.004G174000.1 | NAC domain-containing 73 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.004G174000.2 | NAC domain-containing 73 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.004G174000.3 | NAC domain-containing 73 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.004G174700.1 | arginine--tRNA ligase, cytoplasmic-like | cytoplasm;arginine-tRNA ligase activity;ATP binding;arginyl-tRNA aminoacylation | ec:6.1.1;ec:6.1.1.19-ligase | Aminoacyl-tRNA biosynthesis |
| Phvul.004G175000.1 | DNA-directed RNA polymerase III subunit RPC2 | DNA-directed RNA polymerase III complex;integral component of membrane;RNA polymerase III activity;DNA binding;ribonucleoside binding;transcription from RNA polymerase III promoter | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| Phvul.004G175100.1 | phosphoinositide 3-kinase regulatory subunit 4 | nuclear pore;late endosome;phosphatidylinositol 3-kinase complex, class III, type I;phosphatidylinositol 3-kinase complex, class III, type II;nucleus-vacuole junction;Cul4-RING E3 ubiquitin ligase complex;protein serine/threonine kinase activity;ATP binding;response to superoxide;protein phosphorylation;protein targeting to vacuole;fatty acid beta-oxidation;lipid transport;intra-Golgi vesicle-mediated transport;cell death;pollen development;gravitropism;pollen germination;salicylic acid mediated signaling pathway;ethylene-activated signaling | ec:2.7.11 | |

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| | | pathway;lithium ion transport;macroautophagy;protein import into peroxisome matrix;pexophagy;cellular macromolecule catabolic process;late endosome to vacuole transport;photoperiodism, flowering | | |
| Phvul.004G175700.1 | Receptor kinase HSL1 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.004G176100.1 | DNA (cytosine-5)-methyltransferase CMT3 | nucleus;chromatin binding;DNA (cytosine-5-)-methyltransferase activity;DNA replication initiation;regulation of DNA replication;methylation-dependent chromatin silencing;cell proliferation;regulation of flower development;zygote asymmetric cytokinesis in embryo sac;DNA methylation on cytosine within a CNG sequence;histone phosphorylation;chromatin silencing by small RNA;histone H3-K9 methylation;regulation of cell cycle;C-5 methylation of cytosine | ec:2.1.1;ec:2.1.1.37-(cytosine-5-)-methyltransferase | Cysteine and methionine metabolism |
| Phvul.004G176100.2 | DNA (cytosine-5)-methyltransferase CMT3 | nucleus;chromatin binding;DNA (cytosine-5-)-methyltransferase activity;DNA replication initiation;regulation of DNA replication;methylation-dependent chromatin silencing;cell proliferation;regulation of flower development;zygote asymmetric cytokinesis in embryo sac;DNA methylation on cytosine within a CNG sequence;histone phosphorylation;chromatin silencing by small RNA;histone H3-K9 methylation;regulation of cell cycle;C-5 methylation of cytosine | ec:2.1.1;ec:2.1.1.37-(cytosine-5-)-methyltransferase | Cysteine and methionine metabolism |
| Phvul.004G176400.1 | probable RNA-dependent RNA polymerase 5 isoform X1 | RNA-directed RNA polymerase activity;transcription, RNA-templated | ec:2.7.7.48 | |
| Phvul.004G176500.1 | SNW SKI-interacting -like | spliceosomal complex;nucleolus;mRNA splicing, via spliceosome;nuclear-transcribed mRNA catabolic process;N-terminal protein myristoylation;vegetative to reproductive phase transition of meristem;regulation of circadian rhythm;positive regulation of transcription, DNA-templated | | |
| Phvul.004G178400.1 | microtubule-associated TORTIFOLIA1 | DNA replication initiation;regulation of DNA replication;methylation-dependent chromatin silencing;microtubule-based process;cell proliferation;regulation of flower development;chromatin silencing by small RNA;histone H3-K9 methylation;regulation of cell cycle | | |
| Phvul.005G000400.1 | DUF246 domain-containing | integral component of membrane;transferase activity, transferring glycosyl groups;metabolic process | | |
| Phvul.005G000500.1 | Deoxycytidine kinase | nucleus;thymidine kinase activity;hydrolase activity;deoxyribonucleoside monophosphate biosynthetic process;phosphorylation | ec:2.7.1.21-kinase;ec:2.7.1.145 | Drug metabolism - other enzymes;Pyrimidine metabolism |
| Phvul.005G001300.2 | splicing factor U2af large subunit B-like isoform X4 | commitment complex;nuclear speck;U2-type prespliceosome;U2AF;nucleotide binding;poly-pyrimidine tract binding;pre-mRNA 3'-splice site binding;U2-type prespliceosome assembly | | |
| Phvul.005G003000.1 | hypothetical protein PHAVU_005G003000g | mitotic cell cycle;RNA processing | | |
| Phvul.005G003600.1 | phosphatidylinositol phosphatidylcholine transfer SFH13 | vegetative to reproductive phase transition of meristem;protein desumoylation;hydrogen peroxide biosynthetic process | | |
| Phvul.005G003600.2 | phosphatidylinositol phosphatidylcholine transfer SFH13 | vegetative to reproductive phase transition of meristem;protein desumoylation;hydrogen peroxide biosynthetic process | | |
| Phvul.005G003600.3 | phosphatidylinositol phosphatidylcholine transfer SFH13 | vegetative to reproductive phase transition of meristem;protein desumoylation;hydrogen peroxide biosynthetic process | | |
| Phvul.005G006600.1 | vacuolar sorting-associated 9A-like isoform X1 | | | |

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| Phvul.005G008900.1 | U-box domain-containing 35-like isoform X1 | intracellular;MAP kinase kinase kinase activity;ubiquitin-protein transferase activity;ATP binding;ligase activity;MAPK cascade;activation of MAPKK activity;protein ubiquitination | ec:2.7.11;ec:2.7.11.25 | |
| Phvul.005G010900.1 | hypothetical protein PHAVU_005G010900g | single-organism process | | |
| Phvul.005G011000.1 | pentatricopeptide repeat-containing At3g57430, chloroplastic-like | microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.005G012600.1 | histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1-like | nucleus;chromosome;zinc ion binding;histone-lysine N-methyltransferase activity;histone binding;histone lysine methylation | ec:2.1.1;ec:2.1.1.43-N-methyltransferase | Lysine degradation |
| Phvul.005G012800.1 | zinc ion-binding , | zinc ion binding;ligase activity;metabolic process | | |
| Phvul.005G013400.1 | BTB POZ domain-containing At3g05675 | | | |
| Phvul.005G014700.1 | pentatricopeptide repeat-containing At1g11290 | chloroplast;endonuclease activity;zinc ion binding;microtubule-severing ATPase activity;mRNA modification;nucleic acid phosphodiester bond hydrolysis | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.005G015800.1 | Cytochrome P450, isoform 4, partial | integral component of membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;multicellular organismal development;brassinosteroid homeostasis;sterol metabolic process;brassinosteroid biosynthetic process;oxidation-reduction process | | |
| Phvul.005G016000.1 | RING-H2 finger ATL52-like | integral component of membrane;zinc ion binding;hydrolase activity;ligase activity;metabolic process | | |
| Phvul.005G016000.2 | RING-H2 finger ATL52-like | integral component of membrane;zinc ion binding;hydrolase activity;ligase activity;metabolic process | | |
| Phvul.005G016500.1 | TMV resistance N-like | integral component of membrane;ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.005G016500.2 | TMV resistance N-like | integral component of membrane;ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.005G018700.1 | bifunctional purine biosynthesis purH | chloroplast stroma;stromule;IMP cyclohydrolase activity;phosphoribosylaminoimidazolecarboxamide formyltransferase activity;purine nucleotide biosynthetic process;pyrimidine ribonucleotide biosynthetic process | ec:3.5.4.10-cyclohydrolase;ec:2.1.2.3-formyltransferase | Purine metabolism;Biosynthesis of antibioticsPurine metabolism;Biosynthesis of antibiotics;One carbon pool by folate |
| Phvul.005G019200.1 | hypothetical protein PHAVU_005G019200g | integral component of membrane | | |
| Phvul.005G020800.1 | hypothetical protein PHAVU_005G020800g | microtubule cytoskeleton organization;cytokinesis by cell plate formation | | |
| Phvul.005G021200.1 | DNA ligase 1 | nucleus;mitochondrion;DNA binding;DNA ligase (ATP) activity;ATP binding;lagging strand elongation;DNA recombination;DNA ligation involved in DNA repair;DNA biosynthetic process | ec:6.5.1;ec:6.5.1.1 | |
| Phvul.005G021800.1 | Group 2, | integral component of membrane | | |
| Phvul.005G022900.1 | PHYLLO, chloroplastic isoform X1 | thiamine pyrophosphate binding;2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase activity;2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase activity;cellular amino acid catabolic | ec:4.2.99.20-synthase;ec:2.2.1.9-synthase | Ubiquinone and other terpenoid-quinone biosynthesisUbiquinone and other terpenoid-quinone biosynthesis |

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| | | process;menaquinone biosynthetic process;phylloquinone biosynthetic process;photosystem I stabilization | | |
| Phvul.005G023100.1 | RNA polymerase sigma factor sigD, chloroplastic | DNA binding;transcription factor activity, sequence-specific DNA binding;sigma factor activity;DNA-templated transcription, initiation;regulation of transcription, DNA-templated;cellular carbohydrate metabolic process;single-organism carbohydrate metabolic process;single-organism cellular process | | |
| Phvul.005G023100.4 | RNA polymerase sigma factor sigD, chloroplastic | chloroplast;plastid sigma factor activity;DNA binding;transcription factor activity, sequence-specific DNA binding;maltose metabolic process;pentose-phosphate shunt;DNA-templated transcription, initiation;regulation of transcription, DNA-templated;mRNA modification;starch biosynthetic process | | |
| Phvul.005G023100.5 | RNA polymerase sigma factor sigD, chloroplastic | DNA binding;transcription factor activity, sequence-specific DNA binding;sigma factor activity;DNA-templated transcription, initiation;regulation of transcription, DNA-templated;cellular carbohydrate metabolic process;single-organism carbohydrate metabolic process;single-organism cellular process | | |
| Phvul.005G023300.2 | alpha-N-acetylglucosaminidase family | vacuole;alpha-N-acetylglucosaminidase activity;metabolic process | ec:3.2.1.50-alpha-acetylglucosaminidase;ec:3.2.1 | Glycosaminoglycan degradation |
| Phvul.005G026000.1 | calcium-binding CML19 | calcium ion binding | | |
| Phvul.005G026300.1 | LATERAL ROOT PRIMORDIUM 1-like | | | |
| Phvul.005G027200.1 | NBS-LRR type disease resistance | ADP binding;defense response | | |
| Phvul.005G029000.1 | F-box SKIP22-like | | | |
| Phvul.005G029400.1 | E3 ubiquitin- ligase SINAT5-like | nucleus;cytoplasm;zinc ion binding;ligase activity;ubiquitin protein ligase activity;apoptotic process;multicellular organismal development;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;proteasome-mediated ubiquitin-dependent protein catabolic process | | |
| Phvul.005G029500.1 | Translation initiation factor eIF-2B subunit beta | eukaryotic translation initiation factor 2B complex;translation initiation factor activity;guanyl-nucleotide exchange factor activity;transferase activity;S-methyl-5-thioribose-1-phosphate isomerase activity;translational initiation;regulation of translational initiation;L-methionine biosynthetic process from methylthioadenosine;positive regulation of GTPase activity | ec:5.3.1.23-isomerase | Cysteine and methionine metabolism |
| Phvul.005G032400.1 | disease resistance-responsive, dirigent domain | integral component of membrane | | |
| Phvul.005G035600.1 | plasma-membrane choline transporter family | integral component of membrane;cysteine biosynthetic process | | |
| Phvul.005G036800.1 | SURP and G-patch domain-containing 1 isoform X1 | RNA binding;RNA processing | | |
| Phvul.005G037700.1 | ribulose-1,5 bisphosphate carboxylase oxygenase large subunit N-methyltransferase, chloroplastic | chloroplast stroma;protein-lysine N-methyltransferase activity;[ribulose-bisphosphate carboxylase]-lysine N-methyltransferase activity;maltose metabolic process;phosphatidylglycerol biosynthetic process;aromatic amino acid family biosynthetic process;embryo development ending in seed dormancy;chloroplast relocation;thylakoid membrane organization;iron-sulfur cluster assembly;peptidyl-lysine trimethylation;peptidyl-lysine monomethylation;starch biosynthetic | ec:2.1.1;ec:2.1.1.127 | |

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| | | process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;ncRNA metabolic process | | |
| Phvul.005G039000.1 | 30S ribosomal 2, chloroplastic | ribosome;chloroplast thylakoid membrane;chloroplast stroma;chloroplast envelope;viral nucleocapsid;nucleotide binding;nucleic acid binding;photosynthetic electron transport in photosystem I;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;protein targeting to chloroplast | | |
| Phvul.005G040900.1 | callose synthase 2 isoform X1 | 1,3-beta-D-glucan synthase complex;integral component of membrane;1,3-beta-D-glucan synthase activity;(1->3)-beta-D-glucan biosynthetic process | ec:2.4.1.34-synthase;ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.005G040900.2 | callose synthase 2 isoform X1 | 1,3-beta-D-glucan synthase complex;integral component of membrane;1,3-beta-D-glucan synthase activity;(1->3)-beta-D-glucan biosynthetic process | ec:2.4.1.34-synthase;ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.005G042700.1 | serum response factor homolog A-like | xylan metabolic process | | |
| Phvul.005G042800.1 | DUF936 family | | | |
| Phvul.005G043100.1 | DUF946 family | | | |
| Phvul.005G044000.1 | ATPase family AAA domain-containing 3-like | ATP binding;hydrolase activity;metabolic process | | |
| Phvul.005G044700.1 | S-adenosylmethionine-dependent methyltransferase, | methyltransferase activity;methylation | | |
| Phvul.005G044900.1 | myosin-12 isoform X1 | integral component of membrane;unconventional myosin complex;motor activity;actin binding;DNA topoisomerase type I activity;signal transducer activity;ATP binding;signal transduction;response to nematode;xylem development;actin filament-based movement;cell wall macromolecule metabolic process;Golgi localization;mitochondrion localization;peroxisome localization | ec:5.99.1.2;ec:3.6.1;ec:5.99.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.005G047500.1 | plant T8K14-16 | determination of bilateral symmetry;organ morphogenesis;meristem initiation;xylem and phloem pattern formation;meristem maintenance;flower morphogenesis;negative regulation of biological process | | |
| Phvul.005G048400.1 | ALA-interacting subunit 3-like | integral component of membrane | | |
| Phvul.005G049900.1 | cyclin-T1-3-like | cyclin-dependent protein kinase holoenzyme complex;nucleus;cyclin-dependent protein serine/threonine kinase regulator activity;positive regulation of cyclin-dependent protein serine/threonine kinase activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of phosphorylation of RNA polymerase II C-terminal domain | ec:2.7.1 | |
| Phvul.005G049900.2 | cyclin-T1-3-like | cyclin-dependent protein kinase holoenzyme complex;nucleus;cyclin-dependent protein serine/threonine kinase regulator activity;positive regulation of cyclin-dependent protein serine/threonine kinase activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of phosphorylation of RNA polymerase II C-terminal domain | ec:2.7.1 | |
| Phvul.005G050100.1 | rRNA methylase ytqB | chloroplast;methyltransferase activity;methylation | | |
| Phvul.005G053000.1 | pentatricopeptide repeat-containing At1g20230 | zinc ion binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |

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| Phvul.005G054000.1 | glutathione S-transferase | cytoplasm;glutathione transferase activity;glutathione metabolic process;toxin catabolic process | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolism |
| Phvul.005G054100.1 | glutathione S-transferase | cytoplasm;glutathione transferase activity;glutathione metabolic process;toxin catabolic process | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolism |
| Phvul.005G054600.1 | translation initiation factor IF-2, chloroplastic | microtubule;chloroplast stroma;chloroplast envelope;translation initiation factor activity;microtubule motor activity;GTPase activity;ATP binding;GTP binding;microtubule binding;translational initiation;microtubule-based movement;chloroplast relocation;thylakoid membrane organization;regulation of proton transport;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;ncRNA metabolic process;transcription from plastid promoter;protein autophosphorylation | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.005G054900.1 | like subfamily C member 14 | integral component of membrane | | |
| Phvul.005G055300.1 | U5 small nuclear ribonucleo 200 kDa helicase-like | viral nucleocapsid;intracellular ribonucleoprotein complex;nucleic acid binding;helicase activity;ATP binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.005G055300.2 | U5 small nuclear ribonucleo 200 kDa helicase-like | viral nucleocapsid;intracellular ribonucleoprotein complex;nucleic acid binding;helicase activity;ATP binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.005G055500.1 | ribosomal L1 domain-containing 1-like | ribosome;RNA binding | | |
| Phvul.005G055600.1 | RRNAD1-like isoform X1 | methyltransferase activity;methylation | | |
| Phvul.005G055600.2 | RRNAD1-like isoform X1 | methyltransferase activity;methylation | | |
| Phvul.005G056500.1 | PAT1 like 1 | cytoplasmic mRNA processing body;RNA binding;isomerase activity;deadenylation-dependent decapping of nuclear-transcribed mRNA;cytoplasmic mRNA processing body assembly | | |
| Phvul.005G058500.1 | 1-aminocyclopropane-1-carboxylate oxidase | iron ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.005G058700.1 | 2OG-Fe(II) oxygenase family oxidoreductase | oxidoreductase activity;metal ion binding;oxidation-reduction process | | |
| Phvul.005G062300.1 | disease resistance (CC-NBS-LRR class) family | ATP binding;ADP binding;defense response | | |
| Phvul.005G062300.2 | Disease resistance | metabolic process | | |
| Phvul.005G062300.3 | Disease resistance | metabolic process | | |
| Phvul.005G062500.1 | callose synthase 8 | 1,3-beta-D-glucan synthase complex;integral component of membrane;1,3-beta-D-glucan synthase activity;(1->3)-beta-D-glucan biosynthetic process | ec:2.4.1.34-synthase;ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.005G063500.1 | Secologanin synthase | integral component of membrane;acyl-CoA oxidase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;oxidation-reduction process;11-oxo- | ec:1.3.3.6-oxidase;ec:1.14.13 | alpha-Linolenic acid metabolism;Biosynthesis of unsaturated fatty acids;Fatty acid degradation |

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| | | beta-amyrin catabolic process;glycyrrhetinate biosynthetic process | | |
| Phvul.005G063500.2 | 11-oxo-beta-amyrin 30-oxidase-like | integral component of membrane;acyl-CoA oxidase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;oxidation-reduction process;11-oxo-beta-amyrin catabolic process;glycyrrhetinate biosynthetic process | ec:1.3.3.6-oxidase;ec:1.14.13 | alpha-Linolenic acid metabolism;Biosynthesis of unsaturated fatty acids;Fatty acid degradation |
| Phvul.005G064700.1 | receptor-like serine threonine- kinase At1g78530 | intracellular;integral component of membrane;MAP kinase kinase kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.11.25;ec:2.7.10.1 | |
| Phvul.005G064700.2 | receptor-like serine threonine- kinase At1g78530 | intracellular;integral component of membrane;MAP kinase kinase kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.11.25;ec:2.7.10.1 | |
| Phvul.005G067300.1 | increased DNA methylation 1-like | membrane;DNA binding;N-acetyltransferase activity;zinc ion binding;galactosylxylosylprotein 3-beta-galactosyltransferase activity;protein glycosylation;regulation of cellular metabolic process;posttranscriptional gene silencing by RNA;histone H3 acetylation;regulation of nitrogen compound metabolic process;production of small RNA involved in gene silencing by RNA;regulation of primary metabolic process | ec:2.4.1;ec:2.4.1.134-3-beta-galactosyltransferase;ec:2.3.1 | Glycosaminoglycan biosynthesis - heparan sulfate / heparin;Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate |
| Phvul.005G068700.1 | hypothetical protein PHAVU_005G068700g | | | |
| Phvul.005G069700.1 | nuclear pore complex NUP98A | nuclear pore;transport | | |
| Phvul.005G071900.1 | probable serine threonine- kinase At1g54610 | plasma membrane;cyclin-dependent protein serine/threonine kinase activity;ATP binding;protein phosphorylation;regulation of cell cycle | ec:2.7.11;ec:2.7.11.22 | |
| Phvul.005G073600.1 | hypothetical protein VIGAN_07134100 | integral component of membrane | | |
| Phvul.005G075600.1 | nuclear pore complex NUP98A isoform X1 | nuclear pore;transport | | |
| Phvul.005G075600.2 | nuclear pore complex NUP98A isoform X1 | nuclear pore;transport | | |
| Phvul.005G076700.1 | B-box zinc finger 22 | nucleus;transcription factor activity, transcription factor binding;zinc ion binding;regulation of transcription, DNA-templated;photomorphogenesis | | |
| Phvul.005G076700.2 | B-box zinc finger 22 | nucleus;transcription factor activity, transcription factor binding;zinc ion binding;regulation of transcription, DNA-templated;photomorphogenesis | | |
| Phvul.005G080500.1 | WW domain-binding 11-like | integral component of membrane | | |
| Phvul.005G081000.1 | NHL repeat | RNA splicing, via endonucleolytic cleavage and ligation;methionine biosynthetic process;virus induced gene silencing;vegetative phase change | | |
| Phvul.005G082400.1 | choline transporter 2 | plasma membrane;plasmodesma;integral component of membrane | | |
| Phvul.005G082600.1 | Nucleolar GTP-binding 2 | nucleolus;GTPase activity;GTP binding;metabolic process;ribosome biogenesis | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.005G085000.1 | Peroxisomal membrane 22 kDa family isoform 1 | integral component of membrane | | |

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| Phvul.005G085000.2 | Peroxisomal membrane 22 kDa family isoform 1 | integral component of membrane | | |
| Phvul.005G086200.1 | pre-mRNA-processing-splicing factor 8 | U5 snRNP;catalytic step 2 spliceosome;second spliceosomal transesterification activity;U6 snRNA binding;U1 snRNA binding;U2 snRNA binding;U5 snRNA binding;pre-mRNA intronic binding;spliceosomal tri-snRNP complex assembly | | |
| Phvul.005G086600.1 | cyclic nucleotide-gated ion channel 4 | cell;integral component of membrane;voltage-gated potassium channel activity;cellular cation homeostasis;regulation of membrane potential;divalent metal ion transport;potassium ion transmembrane transport | | |
| Phvul.005G088000.1 | S-locus lectin kinase family | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation;defense response;recognition of pollen | ec:2.7.11 | |
| Phvul.005G088400.1 | NADH dehydrogenase subunit 5, partial (mitochondrion) | mitochondrial inner membrane;integral component of membrane;NADH dehydrogenase (ubiquinone) activity;ATP synthesis coupled electron transport | ec:1.6.5.3-reductase (H+-translocating);ec:1.6.99.5;ec:1.6.99.3-dehydrogenase | Oxidative phosphorylationOxidative phosphorylation |
| Phvul.005G090600.1 | kDa class VI heat shock | response to heat;response to high light intensity;response to hydrogen peroxide | | |
| Phvul.005G091300.1 | autophagy-related 18f isoform X1 | cytoplasm;integral component of membrane;cellular response to phosphate starvation;galactolipid biosynthetic process;cellular response to water deprivation | | |
| Phvul.005G091400.1 | UHRF1-binding 1-like | | | |
| Phvul.005G093400.1 | disease resistance (TIR-NBS-LRR class) | purine ribonucleoside binding;adenyl ribonucleotide binding;anion binding;response to stimulus | | |
| Phvul.005G096400.1 | transmembrane , | integral component of membrane | | |
| Phvul.005G096700.1 | transcription factor GTE4 | | | |
| Phvul.005G097500.1 | E3 ubiquitin- ligase ATL41-like | integral component of membrane;zinc ion binding | | |
| Phvul.005G098500.1 | pentatricopeptide repeat-containing At1g06270 | transferase activity, transferring acyl groups other than amino-acyl groups;metabolic process | | |
| Phvul.005G098500.2 | pentatricopeptide repeat-containing At1g06270 | transferase activity, transferring acyl groups other than amino-acyl groups;metabolic process | | |
| Phvul.005G099800.1 | zinc finger MAGPIE | nucleic acid binding;metal ion binding | | |
| Phvul.005G101800.1 | diacylglycerol kinase domain | diacylglycerol kinase activity;ATP binding;protein kinase C-activating G-protein coupled receptor signaling pathway;phosphorylation | ec:2.7.1.107-kinase (ATP) | Glycerophospholipid metabolism;Glycerolipid metabolism;Phosphatidylinositol signaling system |
| Phvul.005G101800.2 | diacylglycerol kinase domain | diacylglycerol kinase activity;ATP binding;protein kinase C-activating G-protein coupled receptor signaling pathway;phosphorylation | ec:2.7.1.107-kinase (ATP) | Glycerophospholipid metabolism;Glycerolipid metabolism;Phosphatidylinositol signaling system |
| Phvul.005G101800.3 | diacylglycerol kinase domain | diacylglycerol kinase activity;ATP binding;protein kinase C-activating G-protein coupled receptor signaling pathway;phosphorylation | ec:2.7.1.107-kinase (ATP) | Glycerophospholipid metabolism;Glycerolipid metabolism;Phosphatidylinositol signaling system |
| Phvul.005G103200.1 | probable L-type lectin-domain containing receptor kinase | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;carbohydrate binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |

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| Phvul.005G104500.1 | Acyl-[acyl-carrier- ]--UDP-N-acetylglucosamine O-acyltransferase | transferase activity | | |
| Phvul.005G104900.1 | pre-mRNA-processing factor 6 | U4/U6 x U5 tri-snRNP complex;catalytic step 2 spliceosome;spliceosomal tri-snRNP complex assembly;RNA-directed DNA methylation;positive regulation of miRNA metabolic process;positive regulation of primary miRNA processing | | |
| Phvul.005G107100.1 | ROOT INITIATION DEFECTIVE 3 | Cul4-RING E3 ubiquitin ligase complex;negative regulation of shoot apical meristem development | | |
| Phvul.005G109300.1 | equilibrative nucleotide transporter 3-like | integral component of membrane;nucleoside transmembrane transporter activity;nucleoside transmembrane transport | | |
| Phvul.005G109300.2 | equilibrative nucleotide transporter 3-like | integral component of membrane;nucleoside transmembrane transporter activity;nucleoside transmembrane transport | | |
| Phvul.005G111500.1 | probable terpene synthase 11 | magnesium ion binding;isoprene synthase activity;metabolic process | ec:4.2.3.27-synthase | Terpenoid backbone biosynthesis |
| Phvul.005G111700.1 | probable terpene synthase 11 | magnesium ion binding;isoprene synthase activity;metabolic process | ec:4.2.3.27-synthase | Terpenoid backbone biosynthesis |
| Phvul.005G114200.2 | syntaxin of plants 122 | plasma membrane;endomembrane system;integral component of membrane;SNARE complex;SNARE binding;SNAP receptor activity;intracellular protein transport;exocytosis;vesicle fusion;vesicle docking | | |
| Phvul.005G114800.1 | glutamate receptor -like | integral component of membrane;G-protein coupled receptor activity;ionotropic glutamate receptor activity;ion transport;G-protein coupled receptor signaling pathway;ionotropic glutamate receptor signaling pathway | | |
| Phvul.005G114900.1 | Glutamate receptor | intracellular;plasma membrane;plasmodesma;integral component of membrane;G-protein coupled receptor activity;ionotropic glutamate receptor activity;calcium channel activity;G-protein coupled receptor signaling pathway;calcium-mediated signaling;ionotropic glutamate receptor signaling pathway;calcium ion transmembrane transport;cellular response to amino acid stimulus | | |
| Phvul.005G116800.1 | linolenate hydroperoxide lyase, chloroplastic | chloroplast envelope;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;hydroperoxide dehydratase activity;tryptophan catabolic process;fatty acid metabolic process;indoleacetic acid biosynthetic process;sterol metabolic process;oxidation-reduction process | ec:4.2.1.92-dehydratase | alpha-Linolenic acid metabolism |
| Phvul.005G119100.1 | E3 ubiquitin- ligase PUB23-like | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.005G120200.1 | histone deacetylase 8 | NAD-dependent histone deacetylase activity (H3-K14 specific);histone H3 deacetylation | ec:3.5.1.98 | |
| Phvul.005G122400.1 | capsanthin capsorubin synthase, chromoplast-like | chromoplast;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;capsanthin synthase activity;capsorubin synthase activity;carotenoid biosynthetic process;oxidation-reduction process | ec:5.3.99.8-synthase | Carotenoid biosynthesis |
| Phvul.005G123900.1 | myb family transcription factor family | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.005G124400.1 | pentatricopeptide repeat-containing At5g48910-like | zinc ion binding | | |
| Phvul.005G125800.1 | flagellar radial spoke 5 isoform X2 | oxidoreductase activity;oxidation-reduction process | | |
| Phvul.005G127300.1 | TIC 100 | kinase activity;phosphorylation | | |

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| Phvul.005G127800.1 | splicing factor U2af small subunit B-like | nucleus;nucleotide binding;RNA binding;metal ion binding | | |
| Phvul.005G128200.1 | AP-2 complex subunit alpha-1-like | clathrin adaptor complex;protein transporter activity;intracellular protein transport;vesicle-mediated transport | | |
| Phvul.005G128200.2 | AP-2 complex subunit alpha-1-like | clathrin adaptor complex;protein transporter activity;intracellular protein transport;vesicle-mediated transport | | |
| Phvul.005G130400.1 | DUF2146 family | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | | |
| Phvul.005G130600.1 | UPSTREAM OF FLC isoform X1 | | | |
| Phvul.005G131000.1 | serine carboxypeptidase-like | vacuole;serine-type carboxypeptidase activity;proteolysis involved in cellular protein catabolic process | ec:3.4.21;ec:3.4.16 | |
| Phvul.005G133500.1 | helicase MOM1-like isoform X1 | | | |
| Phvul.005G133500.2 | helicase MOM1-like isoform X1 | hydrolase activity | | |
| Phvul.005G134300.1 | pleckstrin-like (PH) and lipid-binding START domain | plasma membrane;lipid binding | | |
| Phvul.005G134500.1 | auxin response factor 18 | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;miRNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;pattern specification process;auxin-activated signaling pathway;abscisic acid-activated signaling pathway;response to carbohydrate;fruit development;regulation of anthocyanin biosynthetic process;leaf development;petal development;sepal development;developmental growth;root cap development;cell division | | |
| Phvul.005G134600.1 | Serine threonine-phosphatase 6 regulatory subunit 3 | | | |
| Phvul.005G136900.1 | auxin response factor 4-like isoform X2 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |
| Phvul.005G137600.1 | interactor of constitutive active ROPs 3 isoform X2 | | | |
| Phvul.005G137600.2 | interactor of constitutive active ROPs 3 isoform X2 | | | |
| Phvul.005G137600.3 | interactor of constitutive active ROPs 3 isoform X2 | | | |
| Phvul.005G137600.4 | interactor of constitutive active ROPs 3 isoform X2 | | | |
| Phvul.005G137800.1 | V-type proton ATPase subunit a1 | vacuolar proton-transporting V-type ATPase, V0 domain;plant-type vacuole;endosome;trans-Golgi network;trans-Golgi network transport vesicle membrane;integral component of membrane;proton-transporting ATPase activity, rotational mechanism;ATPase binding;vacuolar acidification;ATP synthesis coupled proton transport;ATP hydrolysis coupled proton transport;vacuolar proton-transporting V-type ATPase complex assembly | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.005G137800.2 | V-type proton ATPase subunit a1 | vacuolar proton-transporting V-type ATPase, V0 domain;plant-type vacuole;endosome;trans-Golgi network;trans-Golgi network transport vesicle membrane;integral component of membrane;proton-transporting ATPase activity, rotational mechanism;ATPase binding;vacuolar acidification;ATP synthesis coupled proton transport;ATP hydrolysis coupled proton transport;vacuolar proton-transporting V-type ATPase complex assembly | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.005G139000.1 | Nfrkb, isoform 1 | Ino80 complex;DNA binding;mitotic cell cycle;RNA processing;sister chromatid cohesion;synapsis;reciprocal meiotic | | |

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| | | recombination;positive regulation of cell proliferation;response to gamma radiation;glucuronoxylan metabolic process;chromatin silencing by small RNA;regulation of telomere maintenance;multicellular organism reproduction;meiotic DNA double-strand break formation;telomere maintenance in response to DNA damage;xylan biosynthetic process;positive regulation of transcription, DNA-templated | | |
| Phvul.005G141100.1 | Aquaporin TIP1-3 | plant-type vacuole membrane;integral component of membrane;central vacuole;water channel activity;glycerol channel activity;water transport;glycerol transport;ion transmembrane transport | | |
| Phvul.005G141200.1 | myb transcription factor | DNA binding | | |
| Phvul.005G141200.2 | myb transcription factor | DNA binding | | |
| Phvul.005G141200.3 | myb transcription factor | DNA binding | | |
| Phvul.005G141600.2 | ras-related RABE1c | intracellular;membrane;GTPase activity;GTP binding;intracellular protein transport;vesicle docking involved in exocytosis;nucleocytoplasmic transport;small GTPase mediated signal transduction;metabolic process;protein secretion | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.005G141800.1 | histone H2A | nucleosome;nuclear chromatin;DNA binding;protein heterodimerization activity;chromatin silencing | | |
| Phvul.005G141900.1 | histone H2A | nucleosome;nuclear chromatin;DNA binding;protein heterodimerization activity;chromatin silencing | | |
| Phvul.005G142400.1 | ACT domain-containing ACR9-like | amino acid binding;nucleotidyltransferase activity;metabolic process;response to sucrose;response to fructose | | |
| Phvul.005G142800.1 | ubiquitin-conjugating enzyme E2 7 | cytoplasm;ATP binding;ligase activity;ubiquitin protein ligase binding;ubiquitin protein ligase activity;protein ubiquitination | | |
| Phvul.005G147200.1 | DUF3527 domain | | | |
| Phvul.005G148600.1 | zinc finger WIP2-like | nucleic acid binding;metal ion binding | | |
| Phvul.005G149800.1 | zinc transporter ZTP29 | integral component of membrane;zinc ion transmembrane transporter activity;zinc II ion transmembrane transport | | |
| Phvul.005G150000.1 | pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 | spliceosomal complex;ATP-dependent RNA helicase activity;ATP binding;poly(A) RNA binding;mRNA splicing, via spliceosome | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.005G152000.1 | probable E3 ubiquitin- ligase ARI7 | ubiquitin ligase complex;cytoplasm;nucleic acid binding;zinc ion binding;ligase activity;ubiquitin conjugating enzyme binding;ubiquitin protein ligase activity;protein polyubiquitination;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;protein ubiquitination involved in ubiquitin-dependent protein catabolic process | | |
| Phvul.005G152500.1 | endonuclease III homolog 1, chloroplastic-like isoform X1 | nucleus;oxidized pyrimidine nucleobase lesion DNA N-glycosylase activity;DNA binding;metal ion binding;4 iron, 4 sulfur cluster binding;base-excision repair, AP site formation;nucleic acid phosphodiester bond hydrolysis | ec:3.2.2;ec:4.2.99.18;ec:3.1 | |
| Phvul.005G152500.2 | endonuclease III homolog 1, chloroplastic-like isoform X1 | nucleus;oxidized pyrimidine nucleobase lesion DNA N-glycosylase activity;DNA binding;metal ion binding;4 iron, 4 sulfur cluster binding;base-excision repair, AP site formation | ec:3.2.2;ec:4.2.99.18;ec:3.1 | |
| Phvul.005G153800.1 | electron transfer flavo -ubiquinone oxidoreductase, mitochondrial | mitochondrion;electron-transferring-flavoprotein dehydrogenase activity;leucine catabolic process;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione;oxidation-reduction process | ec:1.5.5.1 | |

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| Phvul.005G156000.1 | polyadenylate-binding -interacting 3-like isoform X1 | cytoplasmic stress granule;poly(A) RNA binding;regulation of cytoplasmic mRNA processing body assembly;stress granule assembly | | |
| Phvul.005G158000.1 | coatomer subunit zeta-2-like | membrane;viral capsid;protein transport | | |
| Phvul.005G158700.1 | beta-galactosidase 17 | integral component of membrane;nucleic acid binding;beta-galactosidase activity;metal ion binding;vegetative to reproductive phase transition of meristem;glucuronoxylan metabolic process;protein desumoylation;xylan biosynthetic process;hydrogen peroxide biosynthetic process | ec:3.2.1;ec:3.2.1.23-lactase (ambiguous) | Other glycan degradation;Glycosphingolipid biosynthesis - ganglio series;Sphingolipid metabolism;Galactose metabolism;Glycosaminoglycan degradation |
| Phvul.005G160700.1 | inactive kinase SELMODRAFT_444075-like | non-membrane spanning protein tyrosine kinase activity;ATP binding;hydrolase activity;peptidyl-tyrosine phosphorylation | ec:2.7.10;ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.005G161600.1 | eukaryotic translation initiation factor 2 subunit gamma-like | intracellular;integral component of membrane;translation initiation factor activity;GTPase activity;GTP binding;formation of translation preinitiation complex | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.005G163000.1 | leucine-rich repeat receptor kinase At2g19210 isoform X2 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.005G166600.1 | flavonol synthase flavanone 3-hydroxylase-like | integral component of membrane | | |
| Phvul.005G167900.1 | Kinesin-related 6 | nucleus;kinesin complex;microtubule;plasma membrane;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.005G169100.1 | golgin candidate 5 | zinc ion binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.005G169600.1 | auxin-responsive IAA27-like | nucleus;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |
| Phvul.005G170900.1 | ras-related RHN1-like isoform X1 | intracellular;membrane;GTPase activity;GTP binding;intracellular protein transport;nucleocytoplasmic transport;small GTPase mediated signal transduction;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.005G172800.1 | E3 ubiquitin- ligase At1g63170 | integral component of membrane;zinc ion binding;hydrolase activity;ligase activity;metabolic process | | |
| Phvul.005G174500.1 | plant F18G18-200 | plant-type cell wall | | |
| Phvul.005G174900.1 | lys-63-specific deubiquitinase BRCC36-like | integral component of membrane | | |
| Phvul.005G174900.2 | lys-63-specific deubiquitinase BRCC36-like | integral component of membrane | | |
| Phvul.005G175300.1 | Aspartate-glutamate racemase family | amino-acid racemase activity;peptidoglycan biosynthetic process | ec:5.1.1.10-racemase | D-Arginine and D-ornithine metabolism;D-Glutamine and D-glutamate metabolism;Cysteine and methionine metabolism;Glycine, serine and threonine metabolism |
| Phvul.005G175500.1 | nuclear pore complex NUP93A-like | nuclear pore;transferase activity;structural constituent of nuclear pore;protein import into nucleus;poly(A)+ mRNA export from nucleus;nuclear pore complex assembly | | |
| Phvul.005G179700.1 | NUCLEAR FUSION DEFECTIVE 4 | nucleus;integral component of membrane | | |
| Phvul.005G182000.1 | metal transporter Nramp6-like | integral component of membrane;transporter activity;transport | | |

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| Phvul.005G182000.2 | metal transporter Nramp6-like | integral component of membrane;transporter activity;transport | | |
| Phvul.005G183700.1 | AP2-like ethylene-responsive transcription factor At1g16060 | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;multicellular organismal development | | |
| Phvul.005G184300.1 | ribulose bisphosphate carboxylase oxygenase activase, chloroplastic | chloroplast thylakoid membrane;ATP binding;hydrolase activity;thylakoid membrane organization;carotenoid biosynthetic process | | |
| Phvul.005G186000.1 | hypothetical protein PHAVU_005G186000g | integral component of membrane | | |
| Phvul.006G000300.1 | calcium permeable stress-gated cation channel 1-like | integral component of membrane;4-alpha-glucanotransferase activity;glycogen metabolic process | ec:2.4.1.25-disproportionating enzyme | Starch and sucrose metabolism |
| Phvul.006G001200.1 | hypothetical protein PHAVU_006G001200g | | | |
| Phvul.006G001800.1 | UPF0586 C9orf41 | methyltransferase activity;methylation | | |
| Phvul.006G001800.2 | UPF0586 C9orf41 | methyltransferase activity;methylation | | |
| Phvul.006G002500.1 | E3 ubiquitin- ligase MARCH7-like isoform X1 | integral component of membrane;zinc ion binding;ligase activity;metabolic process | | |
| Phvul.006G002500.2 | E3 ubiquitin- ligase MARCH7-like isoform X1 | integral component of membrane;zinc ion binding;ligase activity;metabolic process | | |
| Phvul.006G003000.1 | serine threonine-kinase ATM-like isoform X1 | transferase activity | | |
| Phvul.006G005200.1 | zinc finger CONSTANS-LIKE 9-like | intracellular;integral component of membrane;zinc ion binding | | |
| Phvul.006G005800.1 | breast cancer type 2 susceptibility | nucleus;single-stranded DNA binding;double-strand break repair via homologous recombination;regulation of transcription, DNA-templated | | |
| Phvul.006G008800.1 | anamorsin | mitochondrial intermembrane space;methyltransferase activity;electron carrier activity;metal ion binding;2 iron, 2 sulfur cluster binding;iron-sulfur cluster assembly;methylation;negative regulation of apoptotic process | | |
| Phvul.006G009000.1 | homoserine dehydrogenase | cytosol;homoserine dehydrogenase activity;kinase activity;NADP binding;methionine biosynthetic process;threonine biosynthetic process;isoleucine biosynthetic process;phosphorylation;oxidation-reduction process | ec:1.1.1.3-dehydrogenase | Biosynthesis of antibiotics;Cysteine and methionine metabolism;Lysine biosynthesis;Glycine, serine and threonine metabolism |
| Phvul.006G009100.1 | FAM91A1 isoform X1 | | | |
| Phvul.006G009100.2 | FAM91A1 isoform X1 | | | |
| Phvul.006G009100.3 | FAM91A1 | | | |
| Phvul.006G009200.1 | probable plastidic glucose transporter 1 isoform X1 | integral component of membrane;substrate-specific transmembrane transporter activity;carbohydrate transport;transmembrane transport | | |
| Phvul.006G009200.2 | probable plastidic glucose transporter 1 isoform X1 | integral component of membrane;substrate-specific transmembrane transporter activity;carbohydrate transport;transmembrane transport | | |
| Phvul.006G010300.1 | alcohol dehydrogenase-like 7 | zinc ion binding;S-(hydroxymethyl)glutathione dehydrogenase activity;oxidation-reduction process | ec:1.1.1.284-dehydrogenase | Methane metabolism |

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| Phvul.006G010300.2 | alcohol dehydrogenase-like 7 | zinc ion binding;S-(hydroxymethyl)glutathione dehydrogenase activity;oxidation-reduction process | ec:1.1.1.284-dehydrogenase | Methane metabolism |
| Phvul.006G010900.1 | non-structural maintenance of chromosomes element 1 homolog isoform X1 | nucleus;Smc5-Smc6 complex;ubiquitin-protein transferase activity;double-strand break repair via homologous recombination;postreplication repair;protein ubiquitination | | |
| Phvul.006G012800.1 | Transcription factor PIF1 | integral component of membrane;protein dimerization activity | | |
| Phvul.006G013500.1 | Thymidine kinase | thymidine kinase activity;ATP binding;identical protein binding;deoxyribonucleoside monophosphate biosynthetic process;phosphorylation;DNA biosynthetic process | ec:2.7.1.21-kinase;ec:2.7.1.145 | Drug metabolism - other enzymes;Pyrimidine metabolism |
| Phvul.006G014200.1 | telomerase activating Est1 | meiotic nuclear division | | |
| Phvul.006G016600.1 | Myb SANT-like DNA-binding domain | DNA binding | | |
| Phvul.006G016600.2 | Myb SANT-like DNA-binding domain | DNA binding | | |
| Phvul.006G016900.1 | linoleate 13S-lipoxygenase 2-1, chloroplastic-like | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;metal ion binding;oxylipin biosynthetic process;oxidation-reduction process | ec:1.13.11 | |
| Phvul.006G019400.1 | ubiquitin-associated TS-N domain , | translation elongation factor activity;translational elongation | | |
| Phvul.006G020900.1 | CBL-interacting serine threonine-kinase 3 | protein serine/threonine kinase activity;ATP binding;protein phosphorylation;signal transduction | ec:2.7.11 | |
| Phvul.006G020900.2 | CBL-interacting serine threonine-kinase 3 | protein serine/threonine kinase activity;ATP binding;protein phosphorylation;signal transduction | ec:2.7.11 | |
| Phvul.006G020900.3 | CBL-interacting serine threonine-kinase 3 | protein serine/threonine kinase activity;ATP binding;protein phosphorylation;signal transduction | ec:2.7.11 | |
| Phvul.006G022300.1 | cytochrome b561 domain-containing At2g30890-like | integral component of membrane;oxidation-reduction process | | |
| Phvul.006G022400.1 | VACUOLELESS1 | lysosomal membrane;endosome;plant-type vacuole membrane;HOPS complex;actin binding;protein N-linked glycosylation;protein targeting to vacuole;Golgi organization;vacuole organization;vegetative to reproductive phase transition of meristem;glucuronoxylan metabolic process;endosomal transport;protein desumoylation;regulation of vacuole fusion, non-autophagic;regulation of SNARE complex assembly;xylan biosynthetic process;hydrogen peroxide biosynthetic process | | |
| Phvul.006G027200.1 | ATP-dependent RNA helicase, | ATP-dependent RNA helicase activity;RNA-DNA hybrid ribonuclease activity;ATP binding;poly(A) RNA binding;RNA processing;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.6.1;ec:3.1.30;ec:3.6.1.3-adenylpyrophosphatase;ec:3.1.26;ec:3.1;ec:3.1.26.4;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.006G027400.1 | pentatricopeptide repeat-containing At5g27110-like | | | |
| Phvul.006G028500.1 | transcription factor PIF4-like isoform X1 | protein dimerization activity | | |
| Phvul.006G028500.2 | transcription factor PIF4-like isoform X1 | protein dimerization activity | | |
| Phvul.006G032500.1 | disease resistance RPP13 4 | | | |
| Phvul.006G034000.1 | probable rhamnose biosynthetic enzyme 1 | dTDP-glucose 4,6-dehydratase activity;UDP-glucose 4,6-dehydratase activity;nucleotide-sugar metabolic process | ec:4.2.1.76-4,6-dehydratase;ec:4.2.1.46-4,6-dehydratase | Amino sugar and nucleotide sugar metabolismPolyketide sugar unit biosynthesis;Biosynthesis of |

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| | | | | antibiotics;Streptomycin biosynthesis;Biosynthesis of vancomycin group antibiotics |
| Phvul.006G034500.1 | zinc finger BED domain-containing RICESLEEPER 2-like isoform X1 | DNA binding;protein dimerization activity | | |
| Phvul.006G035800.1 | RNA polymerase II transcription factor SIII (elongin) subunit A | nucleus;integral component of membrane;regulation of transcription, DNA-templated | | |
| Phvul.006G036300.1 | Peptidoglycan-binding domain-containing , isoform 1 | | | |
| Phvul.006G036600.1 | spermidine hydroxycinnamoyl transferase-like | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.006G037700.1 | DDB1- and CUL4-associated factor 13 | nucleolus;small-subunit processome;Cul4-RING E3 ubiquitin ligase complex;mitotic cell cycle;maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);pyrimidine ribonucleotide biosynthetic process | | |
| Phvul.006G037800.1 | glucose-6-phosphate phosphate translocator 1, chloroplastic-like | integral component of membrane;cyclin-dependent protein serine/threonine kinase activity;transporter activity;metabolic process;carbohydrate transmembrane transport;regulation of cell cycle | ec:2.7.11;ec:2.7.11.22 | |
| Phvul.006G039100.1 | DEAD-box ATP-dependent RNA helicase 28 | cytoplasmic ribonucleoprotein granule;nucleic acid binding;ATP-dependent RNA helicase activity;ATP binding;translational initiation;chromosome segregation;regulation of gene expression;RNA secondary structure unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.006G040000.1 | Ankyrin repeat-containing | integral component of membrane | | |
| Phvul.006G040300.1 | plastidial lipoyltransferase 2-like | cytoplasm;octanoyltransferase activity;lipoyl(octanoyl) transferase activity;lipoate biosynthetic process;protein lipoylation | ec:2.3.1.181-transferase;ec:2.3.1 | Lipoic acid metabolism |
| Phvul.006G040300.4 | Plastidial lipoyltransferase 2 | chloroplast;octanoyltransferase activity;ligase activity;lipoyltransferase activity;lipoyl(octanoyl) transferase activity;lipoate biosynthetic process;protein lipoylation | ec:2.3.1.181-transferase;ec:2.3.1 | Lipoic acid metabolism |
| Phvul.006G041000.1 | probable disease resistance At4g19060 | ADP binding | | |
| Phvul.006G041200.1 | Disease resistance RPP13 4 | hydrolase activity;metabolic process | | |
| Phvul.006G041600.1 | ankyrin repeat | integral component of membrane | | |
| Phvul.006G042600.1 | dipeptidyl-peptidase 5-like | cytosol;chloroplast;serine-type peptidase activity;N-terminal protein myristoylation;proteolysis | | |
| Phvul.006G042700.1 | dipeptidyl-peptidase 5-like | cytosol;chloroplast;serine-type peptidase activity;N-terminal protein myristoylation;proteolysis | | |
| Phvul.006G043300.1 | Nucleolar pre-ribosomal-associated 1 | | | |
| Phvul.006G044600.1 | ATP synthase gamma chain, chloroplastic | chloroplast ATP synthase complex;proton-transporting ATP synthase complex, catalytic core F(1);enzyme regulator activity;proton-transporting ATP synthase activity, rotational mechanism;proton-transporting ATPase activity, rotational mechanism;ATP synthesis coupled proton transport;regulation of catalytic activity;regulation of root morphogenesis | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |

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| Phvul.006G045800.1 | GDSL-like lipase acylhydrolase | integral component of membrane;hydrolase activity, acting on ester bonds;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.006G049000.1 | transcription initiation factor TFIID subunit 6-like | nucleus;translation initiation factor activity;protein heterodimerization activity;DNA-templated transcription, initiation;translational initiation;regulation of sequence-specific DNA binding transcription factor activity | | |
| Phvul.006G049900.1 | SWIB MDM2 domain | DNA binding | | |
| Phvul.006G051000.1 | beta-(1,2)-xylosyltransferase | Golgi membrane;Golgi medial cisterna;integral component of membrane;glycoprotein 2-beta-D-xylosyltransferase activity;protein N-linked glycosylation;N-terminal protein myristoylation;posttranslational protein targeting to membrane, translocation | ec:2.4.2.38-2-beta-D-xylosyltransferase | Various types of N-glycan biosynthesis |
| Phvul.006G051200.1 | ankyrin repeat | integral component of membrane | | |
| Phvul.006G051400.1 | probable cytokinin riboside 5 -monophosphate phosphoribohydrolase LOGL3 | lyase activity;metabolic process | | |
| Phvul.006G052700.1 | Kinesin KIF15 | kinesin complex;microtubule;ATP binding;microtubule binding;ATP-dependent microtubule motor activity, plus-end-directed;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.4;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.006G053000.1 | heterogeneous nuclear ribonucleo 1-like | viral nucleocapsid;intracellular ribonucleoprotein complex;nucleotide binding;nucleic acid binding | | |
| Phvul.006G053000.2 | heterogeneous nuclear ribonucleo 1-like | viral nucleocapsid;intracellular ribonucleoprotein complex;nucleotide binding;nucleic acid binding | | |
| Phvul.006G054100.1 | cytochrome P450 family 71 | integral component of membrane;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;secondary metabolite biosynthetic process;oxidation-reduction process | ec:1.14.13 | |
| Phvul.006G059200.1 | probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase | integral component of membrane;RNA binding;S-adenosylmethionine-dependent methyltransferase activity;rRNA processing;methylation;transmembrane transport | | |
| Phvul.006G060800.1 | vacuolar cation proton exchanger 5-like isoform X1 | integral component of membrane;calcium:proton antiporter activity;calcium ion transmembrane transport | | |
| Phvul.006G060800.2 | vacuolar cation proton exchanger 5-like isoform X1 | integral component of membrane;calcium:proton antiporter activity;calcium ion transmembrane transport | | |
| Phvul.006G061200.1 | oxidoreductase transition metal ion-binding | DNA-directed RNA polymerase activity;RNA biosynthetic process | ec:2.7.7.6-RNA polymerase | Purine metabolism;Pyrimidine metabolism |
| Phvul.006G062700.1 | armadillo repeat-containing 8-like | | | |
| Phvul.006G063900.1 | Helicase SKI2W | vacuole;RNA binding;RNA helicase activity;ATP binding;RNA catabolic process;potassium ion transport;sister chromatid cohesion;chromatin silencing by small RNA;response to potassium ion;meiotic chromosome segregation | ec:3.6.1;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolism;Thiamine metabolism |
| Phvul.006G065100.1 | thylakoid soluble phospho TSP9 | chloroplast thylakoid membrane;chloroplast envelope;rRNA processing;response to blue light;chloroplast relocation;thylakoid membrane organization;response to red light;response to far red light;photosynthesis;cellular cation homeostasis;divalent metal ion transport | | |

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| Phvul.006G067600.2 | RING U-box | cytosol;integral component of membrane;zinc ion binding;ligase activity;chlorophyll catabolic process | | |
| Phvul.006G070200.1 | Zinc transporter 6, chloroplastic | plasma membrane;integral component of membrane;zinc ion transmembrane transporter activity;2-alkenal reductase [NAD(P)] activity;oxidation-reduction process;zinc II ion transmembrane transport | ec:1.3.1.74 | |
| Phvul.006G077100.1 | WNK kinase | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.006G082200.1 | hypothetical protein PHAVU_006G082200g | intracellular part | | |
| Phvul.006G084600.1 | cysteine-rich receptor kinase 2 | plasma membrane;integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.006G085300.1 | P-loop nucleoside triphosphate hydrolase superfamily | helicase activity;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.006G087200.1 | plant F12P19-7 | | | |
| Phvul.006G087300.1 | sucrose synthase | sucrose synthase activity;sucrose metabolic process | ec:2.4.1.13-synthase;ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.006G088900.1 | serine threonine-phosphatase PP1 | integral component of membrane;phosphoprotein phosphatase activity;metal ion binding;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.006G088900.2 | serine threonine-phosphatase PP1 | integral component of membrane;phosphoprotein phosphatase activity;metal ion binding;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.006G090000.1 | cell cycle checkpoint control RAD9A | checkpoint clamp complex;3'-5' exonuclease activity;exodeoxyribonuclease III activity;DNA replication checkpoint;DNA repair;intra-S DNA damage checkpoint;cellular response to ionizing radiation;nucleic acid phosphodiester bond hydrolysis | ec:3.1.15;ec:3.1.11;ec:3.1;ec:3.1.11.2 | |
| Phvul.006G090000.2 | cell cycle checkpoint control RAD9A | checkpoint clamp complex;3'-5' exonuclease activity;exodeoxyribonuclease III activity;DNA replication checkpoint;DNA repair;intra-S DNA damage checkpoint;cellular response to ionizing radiation;nucleic acid phosphodiester bond hydrolysis | ec:3.1.15;ec:3.1.11;ec:3.1;ec:3.1.11.2 | |
| Phvul.006G090000.3 | cell cycle checkpoint control RAD9A | checkpoint clamp complex;3'-5' exonuclease activity;exodeoxyribonuclease III activity;DNA replication checkpoint;DNA repair;intra-S DNA damage checkpoint;cellular response to ionizing radiation;nucleic acid phosphodiester bond hydrolysis | ec:3.1.15;ec:3.1.11;ec:3.1;ec:3.1.11.2 | |
| Phvul.006G090700.1 | Acyl- -binding domain-containing 4 | fatty-acyl-CoA binding;N-acylglucosamine 2-epimerase activity;metabolic process | ec:5.1.3.8-2-epimerase | Amino sugar and nucleotide sugar metabolism |
| Phvul.006G090700.2 | Acyl- -binding domain-containing 4 | fatty-acyl-CoA binding;N-acylglucosamine 2-epimerase activity;metabolic process | ec:5.1.3.8-2-epimerase | Amino sugar and nucleotide sugar metabolism |
| Phvul.006G090800.1 | indeterminate-domain 2-like | photosystem II;integral component of membrane;nucleic acid binding;metal ion binding | | |
| Phvul.006G092700.1 | uncharacterized GPI-anchored At5g19250-like | integral component of membrane | | |
| Phvul.006G093300.1 | cation calcium exchanger 5 | plasma membrane;integral component of membrane;nuclear periphery;calcium:sodium antiporter activity;potassium ion transmembrane transporter activity;high-affinity potassium ion import;sodium ion transmembrane transport | | |
| Phvul.006G094000.1 | branched-chain-amino-acid aminotransferase 1 | mitochondrion;catalytic activity;metabolic process | | |

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| Phvul.006G095200.1 | sugar transporter ERD6-like 5 isoform X1 | integral component of plasma membrane;sugar:proton symporter activity;glucose transmembrane transporter activity;2-alkenal reductase [NAD(P)] activity;proton transport;glucose import;oxidation-reduction process;glucose transmembrane transport | ec:1.3.1.74 | |
| Phvul.006G096100.1 | BONZAI 3 | calcium-dependent phospholipid binding;negative regulation of cell death | | |
| Phvul.006G096100.2 | BONZAI 3 | calcium-dependent phospholipid binding;negative regulation of cell death | | |
| Phvul.006G096100.3 | BONZAI 3 | calcium-dependent phospholipid binding;negative regulation of cell death | | |
| Phvul.006G096300.1 | like subfamily B member 14 | | | |
| Phvul.006G096300.2 | like subfamily B member 14 | | | |
| Phvul.006G096700.1 | Transmembrane adipocyte-associated 1 | integral component of membrane | | |
| Phvul.006G096700.2 | Transmembrane adipocyte-associated 1 | integral component of membrane | | |
| Phvul.006G097200.1 | translation initiation factor eIF-2B subunit epsilon-like | translation initiation factor activity;nucleotidyltransferase activity;translational initiation | | |
| Phvul.006G097200.2 | translation initiation factor eIF-2B subunit epsilon-like | translation initiation factor activity;nucleotidyltransferase activity;translational initiation | | |
| Phvul.006G099200.1 | 5 -3 exoribonuclease 4-like isoform X1 | cytosol;nucleic acid binding;exonuclease activity;zinc ion binding;nuclear-transcribed mRNA catabolic process, exonucleolytic;DNA methylation;chromatin silencing;protein N-linked glycosylation;reciprocal meiotic recombination;cell adhesion;cell-cell signaling;positive regulation of cell proliferation;virus induced gene silencing;gravitropism;unidimensional cell growth;ethylene-activated signaling pathway;meristem initiation;trichome morphogenesis;production of ta-siRNAs involved in RNA interference;glucuronoxylan metabolic process;miRNA catabolic process;deadenylation-independent decapping of nuclear-transcribed mRNA;regulation of chromosome organization;production of miRNAs involved in gene silencing by miRNA;post-translational protein modification;actin nucleation;xylan biosynthetic process;regulation of cell differentiation;positive regulation of transcription, DNA-templated | ec:3.1 | |
| Phvul.006G100200.1 | multisubstrate pseudouridine synthase 7 | nucleus;RNA binding;pseudouridylate synthase activity;pseudouridine synthase activity;karyogamy;pseudouridine synthesis;embryo sac egg cell differentiation | ec:5.4.99.12;ec:4.2.1.70-synthase | Pyrimidine metabolism |
| Phvul.006G100800.1 | peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase | cytosol;integral component of membrane;peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase activity;N-terminal protein myristoylation | ec:3.5.1.52 | |
| Phvul.006G101900.1 | mediator of RNA polymerase II transcription subunit 14 | plasmodesma;mediator complex;core mediator complex;RNA polymerase II transcription cofactor activity;catalytic activity;coenzyme binding;regulation of transcription from RNA polymerase II promoter;protein glycosylation;positive regulation of cell proliferation;gravitropism | | |
| Phvul.006G103200.1 | hypothetical protein PHAVU_006G103200g | nucleic acid binding;zinc ion binding | | |
| Phvul.006G104300.1 | pre-mRNA processing PRP39, | integral component of membrane;glycogenin glucosyltransferase activity;metabolic process | ec:2.4.1.186;ec:2.4.1 | |
| Phvul.006G104300.2 | pre-mRNA processing PRP39, | integral component of membrane;glycogenin glucosyltransferase activity;metabolic process | ec:2.4.1.186;ec:2.4.1 | |

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| Phvul.006G107000.1 | translational activator GCN1 | nucleus;transcription factor activity, sequence-specific DNA binding;DNA replication;regulation of transcription, DNA-templated | | |
| Phvul.006G108800.1 | DUF2358 family | | | |
| Phvul.006G109600.1 | BTB POZ domain-containing POB1-like | nucleus;Cul3-RING ubiquitin ligase complex;ubiquitin-protein transferase activity;response to red light;protein ubiquitination | | |
| Phvul.006G110500.1 | tubulin gamma-2 chain | gamma-tubulin complex;microtubule;GTPase activity;GTP binding;microtubule nucleation;metabolic process;cytoplasmic microtubule organization | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.006G110500.2 | tubulin gamma-2 chain | gamma-tubulin complex;microtubule;GTPase activity;GTP binding;microtubule nucleation;metabolic process;cytoplasmic microtubule organization | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.006G111200.1 | extra-large G | membrane | | |
| Phvul.006G111200.2 | extra-large G | | | |
| Phvul.006G113700.1 | ASPARTIC PROTEASE IN GUARD CELL 1 | plant-type cell wall;integral component of membrane;aspartic-type endopeptidase activity;proteolysis;plant-type cell wall organization;protein catabolic process;cell wall modification | ec:3.4.23 | |
| Phvul.006G113900.1 | defective in meristem silencing | DNA metabolic process;chromatin modification;gene silencing by RNA;regulation of gene expression, epigenetic;single-organism metabolic process;regulation of nitrogen compound metabolic process;cellular response to stimulus;regulation of primary metabolic process;regulation of cellular macromolecule biosynthetic process | | |
| Phvul.006G113900.2 | defective in meristem silencing | | | |
| Phvul.006G114200.1 | exportin-2 | nuclear envelope;cytosol;plasmodesma;membrane;nuclear export signal receptor activity;Ran GTPase binding;gluconeogenesis;protein import into nucleus;protein export from nucleus;cytoskeleton organization;response to wounding;response to fungus;jasmonic acid biosynthetic process;response to jasmonic acid;proteasomal protein catabolic process | | |
| Phvul.006G114200.2 | exportin-2 | nuclear envelope;cytosol;plasmodesma;membrane;nuclear export signal receptor activity;Ran GTPase binding;gluconeogenesis;protein import into nucleus;protein export from nucleus;cytoskeleton organization;response to wounding;response to fungus;jasmonic acid biosynthetic process;response to jasmonic acid;proteasomal protein catabolic process | | |
| Phvul.006G115200.1 | bifunctional fucokinase fucose pyrophosphorylase | cytoplasm;ATP binding;fucokinase activity;phosphorylation;cellulose biosynthetic process;GDP-L-fucose salvage;Golgi vesicle transport | ec:2.7.1.52-fucokinase (phosphorylating) | Amino sugar and nucleotide sugar metabolism;Fructose and mannose metabolism |
| Phvul.006G116100.1 | auxin-responsive SAUR32-like | response to auxin | | |
| Phvul.006G116300.1 | Rho GTPase-activating gacA | signal transduction | | |
| Phvul.006G118200.1 | phytochrome B | nucleus;phosphorelay sensor kinase activity;photoreceptor activity;protein homodimerization activity;phosphorelay signal transduction system;transcription, DNA-templated;regulation of transcription, DNA-templated;detection of visible light;red, far-red light phototransduction;protein-tetrapyrrole linkage;protein-chromophore linkage;signal transduction by protein phosphorylation | ec:2.7.3;ec:2.7.13.3 | |
| Phvul.006G118300.1 | Serine threonine-kinase CTR1 | intracellular;MAP kinase kinase kinase activity;ATP binding;MAPK cascade;activation | ec:2.7.11;ec:2.7.11.25 | |

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| | | of MAPKK activity;regulation of transcription, DNA-templated | | |
| Phvul.006G119900.1 | nuclear poly(A) polymerase 3 | nucleus;cytoplasm;integral component of membrane;RNA binding;polynucleotide adenylyltransferase activity;mRNA polyadenylation | ec:2.7.7.19 | |
| Phvul.006G120300.1 | chaperone -domain | integral component of membrane | | |
| Phvul.006G120400.1 | F-box At5g49610 | | | |
| Phvul.006G121000.1 | nuclear export mediator factor NEMF-like isoform X1 | nucleic acid binding;zinc ion binding;nuclear-transcribed mRNA catabolic process | | |
| Phvul.006G121600.1 | YTH domain family 2 | integral component of membrane | | |
| Phvul.006G124500.1 | patellin-4 | nucleus;cytosol;plasma membrane;integral component of membrane;transporter activity;phosphatase activity;transport;sterol biosynthetic process;dephosphorylation;plant-type cell wall cellulose metabolic process;cell wall pectin metabolic process | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase | Aminobenzoate degradation |
| Phvul.006G124600.1 | reticuline oxidase | integral component of membrane;oxidoreductase activity, acting on CH-OH group of donors;flavin adenine dinucleotide binding;oxidation-reduction process | | |
| Phvul.006G125200.1 | midA like, partial | ligase activity;metabolic process | | |
| Phvul.006G125800.1 | Reticuline oxidase | oxidoreductase activity, acting on CH-OH group of donors;reticuline oxidase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.21.3;ec:1.21.3.3-oxidase | Isoquinoline alkaloid biosynthesis |
| Phvul.006G126800.1 | pentatricopeptide repeat-containing At1g51965, mitochondrial | RNA splicing;response to abscisic acid | | |
| Phvul.006G127900.1 | probable receptor kinase At1g30570 | integral component of membrane;protein serine/threonine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;response to brassinosteroid;unidimensional cell growth;peptidyl-tyrosine phosphorylation;regulation of unidimensional cell growth | ec:2.7.11;ec:2.7.10;ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.006G128000.1 | WPP domain-associated | | | |
| Phvul.006G128800.1 | Lysosomal beta glucosidase | plasma membrane;integral component of membrane;anchored component of membrane;beta-glucosidase activity;glucan catabolic process | ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.006G131100.1 | Cysteine desulfurase 2, chloroplastic | pyridoxal phosphate binding;cysteine desulfurase activity;response to reactive oxygen species;selenium compound metabolic process;cysteine metabolic process;aromatic amino acid family biosynthetic process;response to iron ion;response to selenium ion;iron incorporation into metallo-sulfur cluster;iron ion homeostasis | ec:2.8.1.7-desulfurase | Thiamine metabolism |
| Phvul.006G131500.1 | E3 ubiquitin- ligase LIN isoform X1 | ligase activity;metabolic process | | |
| Phvul.006G132500.1 | FAR1-RELATED SEQUENCE 8 | zinc ion binding;regulation of transcription, DNA-templated;vegetative to reproductive phase transition of meristem;protein desumoylation;hydrogen peroxide biosynthetic process | | |
| Phvul.006G132800.1 | vesicle transporter Sec20, | integral component of membrane;single-organism process | | |
| Phvul.006G133500.1 | DNA-3-methyladenine glycosylase 1 | DNA N-glycosylase activity;base-excision repair | ec:3.2.2 | |
| Phvul.006G133800.1 | MLO 13 | plasma membrane;integral component of membrane;hydrolase activity, hydrolyzing O-glycosyl compounds;calmodulin | | |

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| | | binding;polysaccharide catabolic process;defense response;response to biotic stimulus | | |
| Phvul.006G135100.1 | probable galacturonosyltransferase 4 | Golgi membrane;polygalacturonate 4-alpha-galacturonosyltransferase activity;pectin biosynthetic process;cell wall organization | ec:2.4.1.43-4-alpha-galacturonosyltransferase | Amino sugar and nucleotide sugar metabolism;Starch and sucrose metabolism |
| Phvul.006G135600.1 | heavy metal transport detoxification superfamily | cytoplasm;integral component of membrane;transition metal ion binding;metal ion transport;cellular transition metal ion homeostasis | | |
| Phvul.006G136000.1 | BTB POZ domain-containing At5g47800-like | | | |
| Phvul.006G136200.1 | C2 and GRAM domain-containing At1g03370-like | integral component of membrane;phosphatidylserine decarboxylase activity;protein kinase C activity;ligase activity;protein phosphorylation | ec:2.7.11;ec:2.7.11.13-kinase C;ec:4.1.1.65-decarboxylase | Phosphatidylinositol signaling systemGlycerophospholipid metabolism |
| Phvul.006G137300.1 | wall associated kinase | integral component of membrane;protein kinase activity;ATP binding;polysaccharide binding;protein phosphorylation | | |
| Phvul.006G138200.1 | Cytosolic Fe-S cluster assembly factor NARFL | nucleus;cytosol;NADH dehydrogenase activity;ferredoxin hydrogenase activity;iron-sulfur cluster binding;mitotic cell cycle;RNA processing;synapsis;reciprocal meiotic recombination;response to xenobiotic stimulus;iron-sulfur cluster assembly;meiotic DNA double-strand break formation;positive regulation of cellular process;oxidation-reduction process;response to oxygen levels | ec:1.12.7;ec:1.6.99.3-dehydrogenase;ec:1.12.7.2 | Oxidative phosphorylation |
| Phvul.006G138500.1 | TRNA--methyltransferase isoform 1 | methyltransferase activity;tRNA modification;methylation;1-methylguanosine metabolic process | | |
| Phvul.006G141000.1 | mediator of RNA polymerase II transcription subunit 2-like | | | |
| Phvul.006G141900.1 | thymidine kinase-like | thymidine kinase activity;ATP binding;deoxyribonucleoside monophosphate biosynthetic process;phosphorylation;DNA biosynthetic process | ec:2.7.1.21-kinase;ec:2.7.1.145 | Drug metabolism - other enzymes;Pyrimidine metabolism |
| Phvul.006G142400.1 | Inositol monophosphatase 3 | cytosol;plasma membrane;integral component of membrane;magnesium ion binding;inositol monophosphate 1-phosphatase activity;L-galactose-1-phosphate phosphatase activity;inositol monophosphate 3-phosphatase activity;inositol monophosphate 4-phosphatase activity;inositol metabolic process;signal transduction;response to cold;myo-inositol hexakisphosphate biosynthetic process;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione;glucosinolate biosynthetic process;L-ascorbic acid biosynthetic process;phosphatidylinositol phosphorylation;inositol phosphate dephosphorylation | ec:3.1.3;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.25-phosphatase;ec:3.1.3.23 | Aminobenzoate degradationBiosynthesis of antibiotics;Streptomycin biosynthesis;Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.006G142400.2 | Inositol monophosphatase 3 | cytosol;plasma membrane;integral component of membrane;magnesium ion binding;inositol monophosphate 1-phosphatase activity;L-galactose-1-phosphate phosphatase activity;inositol monophosphate 3-phosphatase activity;inositol monophosphate 4-phosphatase activity;inositol metabolic process;signal transduction;response to cold;myo-inositol hexakisphosphate biosynthetic process;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione;glucosinolate biosynthetic process;L-ascorbic acid biosynthetic process;phosphatidylinositol phosphorylation;inositol phosphate dephosphorylation | ec:3.1.3;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.25-phosphatase;ec:3.1.3.23 | Aminobenzoate degradationBiosynthesis of antibiotics;Streptomycin biosynthesis;Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.006G143100.1 | Rho GDP-dissociation inhibitor 1 | cytoplasm;integral component of membrane;Rho GDP-dissociation inhibitor activity;regulation of catalytic activity | | |

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| Phvul.006G143600.1 | Transcription initiation factor IIF subunit alpha | nucleus;photosystem I;integral component of membrane;DNA binding;translation initiation factor activity;catalytic activity;protein C-terminus binding;transcription initiation from RNA polymerase II promoter;translational initiation;photosynthesis;positive regulation of transcription elongation from RNA polymerase II promoter |  |  |
| Phvul.006G143900.1 | hypothetical protein PHAVU_006G143900g |  |  |  |
| Phvul.006G145500.1 | P-loop nucleoside triphosphate hydrolase superfamily | proteasome regulatory particle, base subcomplex;nuclear proteasome complex;cytosolic proteasome complex;ATP binding;TBP-class protein binding;proteasome-activating ATPase activity;ER-associated ubiquitin-dependent protein catabolic process;positive regulation of RNA polymerase II transcriptional preinitiation complex assembly;cell division;positive regulation of proteasomal protein catabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.006G145900.1 | 39S ribosomal L46, mitochondrial | mitochondrial large ribosomal subunit;structural constituent of ribosome;regulation of flower development;histone lysine methylation |  |  |
| Phvul.006G146200.1 | malonyl-decarboxylase, mitochondrial | peroxisome;malonyl-CoA decarboxylase activity;fatty acid biosynthetic process | ec:4.1.1.9-decarboxylase | beta-Alanine metabolism;Propanoate metabolism |
| Phvul.006G147100.1 | proline synthase co-transcribed bacterial homolog -like | pyridoxal phosphate binding;hydrogen peroxide catabolic process |  |  |
| Phvul.006G149800.1 | Myb O | proton-transporting ATP synthase complex, catalytic core F(1);DNA binding;proton-transporting ATP synthase activity, rotational mechanism;proton-transporting ATPase activity, rotational mechanism;anatomical structure morphogenesis;positive regulation of organelle organization;ATP synthesis coupled proton transport;cellular component organization;cellular macromolecule metabolic process;cell development;system development;cell wall organization or biogenesis;plant epidermis development | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.006G151100.1 | adenosine deaminase | adenosine deaminase activity;adenosine catabolic process;hypoxanthine salvage;inosine biosynthetic process | ec:3.5.4.4-deaminase | Purine metabolism |
| Phvul.006G151300.1 | beta-glucosidase 47-like | integral component of membrane;beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.006G152100.1 | trichome birefringence-like 10 | Golgi apparatus;integral component of membrane;O-acetyltransferase activity;cell wall organization or biogenesis | ec:2.3.1 |  |
| Phvul.006G153600.1 | probable E3 ubiquitin- ligase LUL4 | integral component of membrane;zinc ion binding |  |  |
| Phvul.006G153800.1 | RING zinc finger , |  |  |  |
| Phvul.006G154200.1 | adenylate isopentenyltransferase | mitochondrion;AMP dimethylallyltransferase activity;tRNA dimethylallyltransferase activity;tRNA modification | ec:2.5.1.75-dimethylallyltransferase;ec:2.5.1.27-dimethylallyltransferase | Zeatin biosynthesisZeatin biosynthesis |
| Phvul.006G154400.1 | probable serine incorporator | integral component of membrane;L-serine transmembrane transporter activity;L-serine transport |  |  |
| Phvul.006G154500.1 | transmembrane , | mitochondrion;integral component of membrane;cytosolic large ribosomal subunit;RNA binding;structural constituent of ribosome;translation;ribosome biogenesis |  |  |
| Phvul.006G158600.1 | hypothetical protein |  |  |  |

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| | PHAVU_006G158600g | | | |
| Phvul.006G159700.1 | squamosa promoter-binding 7 | nucleus;integral component of membrane;DNA binding | | |
| Phvul.006G160300.1 | BRCT domain DNA repair | | | |
| Phvul.006G160500.1 | serine threonine-kinase ULK4 | plasmodesma;protein kinase activity;ATP binding;microtubule binding;phragmoplast assembly;protein phosphorylation;endosperm cellularization | | |
| Phvul.006G162900.1 | anaphase-promoting complex subunit 7 | mitotic cell cycle;RNA processing;sister chromatid cohesion;reciprocal meiotic recombination;gamete generation;positive regulation of cell proliferation;response to xenobiotic stimulus;photomorphogenesis;response to gamma radiation;cullin deneddylation;glucuronoxylan metabolic process;histone methylation;protein deubiquitination;chromatin silencing by small RNA;regulation of telomere maintenance;regulation of DNA endoreduplication;DNA endoreduplication;meiotic DNA double-strand break formation;proteasome-mediated ubiquitin-dependent protein catabolic process;telomere maintenance in response to DNA damage;proteasome assembly;post-translational protein modification;meiotic chromosome segregation;xylan biosynthetic process;positive regulation of transcription, DNA-templated;regulation of cell division;regulation of unidimensional cell growth;response to misfolded protein | | |
| Phvul.006G165500.1 | F-box kelch-repeat At1g30090 | | | |
| Phvul.006G165600.1 | pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic-like | pyruvate dehydrogenase (acetyl-transferring) activity;oxidation-reduction process | ec:1.2.4.1-dehydrogenase (acetyl-transferring) | Pyruvate metabolism;Biosynthesis of antibiotics;Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis |
| Phvul.006G166300.1 | Mitochondria isoform 1 | mitochondrion | | |
| Phvul.006G166300.2 | Mitochondria isoform 1 | mitochondrion | | |
| Phvul.006G166300.3 | Mitochondria isoform 1 | mitochondrion | | |
| Phvul.006G166900.1 | F-box SKIP19-like | | | |
| Phvul.006G167200.1 | BREAST CANCER SUSCEPTIBILITY 1 homolog isoform X1 | zinc ion binding;ligase activity;DNA repair | | |
| Phvul.006G167200.2 | BREAST CANCER SUSCEPTIBILITY 1 homolog isoform X1 | zinc ion binding;ligase activity;DNA repair | | |
| Phvul.006G167200.3 | BREAST CANCER SUSCEPTIBILITY 1 homolog isoform X2 | zinc ion binding;ligase activity;DNA repair | | |
| Phvul.006G167200.4 | BREAST CANCER SUSCEPTIBILITY 1 homolog isoform X2 | zinc ion binding;ligase activity;DNA repair | | |
| Phvul.006G167500.1 | nucleoporin Ndc1-Nup | integral component of membrane;DNA binding | | |
| Phvul.006G168000.1 | BTB POZ domain-containing At5g03250-like | | | |
| Phvul.006G168000.2 | BTB POZ domain-containing At5g03250-like | | | |
| Phvul.006G168000.3 | BTB POZ domain-containing At5g03250-like | | | |

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| Phvul.006G168000.4 | BTB POZ domain-containing At5g03250-like | | | |
| Phvul.006G168000.5 | BTB POZ domain-containing At5g03250-like | | | |
| Phvul.006G168100.1 | PLASTID TRANSCRIPTIONALLY ACTIVE 12 | nucleoid;plastid;single-organism process | | |
| Phvul.006G168500.1 | Transcription factor GTE12 | | | |
| Phvul.006G168500.2 | Transcription factor GTE12 | | | |
| Phvul.006G172000.1 | ACCELERATED CELL DEATH 6-like | integral component of membrane | | |
| Phvul.006G172000.2 | ACCELERATED CELL DEATH 6-like | integral component of membrane | | |
| Phvul.006G173100.1 | hypothetical protein PHAVU_006G173100g | integral component of membrane | | |
| Phvul.006G174300.1 | RING FYVE PHD zinc finger | integral component of membrane;zinc ion binding | | |
| Phvul.006G174400.1 | probable LRR receptor-like serine threonine- kinase At5g45780 isoform X1 | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;embryo sac egg cell differentiation;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.006G174400.2 | probable LRR receptor-like serine threonine- kinase At5g45780 isoform X1 | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;embryo sac egg cell differentiation;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.006G177100.1 | trichome birefringence-like 38 | Golgi apparatus;O-acetyltransferase activity;cell wall organization or biogenesis | ec:2.3.1 | |
| Phvul.006G177300.1 | phospholipase A1-IIgamma-like | phosphatidylcholine 1-acylhydrolase activity;phosphatidylserine 1-acylhydrolase activity;1-acyl-2-lysophosphatidylserine acylhydrolase activity;lipid metabolic process | ec:3.1.1.32-A1;ec:3.1.1;ec:3.1.1.1-ali-esterase | alpha-Linolenic acid metabolism;Glycerophospholipid metabolismDrug metabolism - other enzymes |
| Phvul.006G178700.1 | IQ-DOMAIN 1 | plasma membrane;RNA splicing, via endonucleolytic cleavage and ligation;methionine biosynthetic process;photoperiodism, flowering | | |
| Phvul.006G179000.1 | probable ATP-dependent RNA helicase DHX35 | spliceosomal complex;ATP-dependent RNA helicase activity;ATP binding;poly(A) RNA binding;RNA processing | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.006G179600.1 | GDSL esterase lipase At5g45960-like | integral component of membrane;hydrolase activity, acting on ester bonds;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.006G179800.1 | pathogenesis-related genes transcriptional activator PTI5-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.006G180000.1 | ras-related RABA1f-like | intracellular;membrane;GTPase activity;GTP binding;intracellular protein transport;nucleocytoplasmic transport;small GTPase mediated signal transduction;metabolic process;vesicle-mediated transport | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.006G180200.1 | probable leucine-rich repeat receptor kinase At5g49770 | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;oxidoreductase activity;peptidyl- | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |

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| | | tyrosine phosphorylation;single-organism metabolic process;regulation of cellular process | | |
| Phvul.006G180400.1 | ribosomal L31 | ribosome | | |
| Phvul.006G181400.2 | guanylate-binding family | GTPase activity;GTP binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.006G181400.3 | guanylate-binding family | GTPase activity;GTP binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.006G181900.1 | transmembrane , | integral component of membrane | | |
| Phvul.006G183400.1 | Zinc finger C-x8-C-x5-C-x3-H type family , isoform 1 | metal ion binding | | |
| Phvul.006G183800.1 | glyoxysomal processing protease, glyoxysomal | peroxisome;serine-type endopeptidase activity;protein processing | ec:3.4.21 | |
| Phvul.006G184400.1 | VQ motif-containing 4 | membrane | | |
| Phvul.006G188200.1 | splicing factor 3B subunit 2 | U2-type spliceosomal complex;U2 snRNP;U12-type spliceosomal complex;chloroplast;precatalytic spliceosome;catalytic step 2 spliceosome;mRNA splicing, via spliceosome | | |
| Phvul.006G188500.1 | Polyphenol oxidase A1, chloroplastic | catechol oxidase activity;metal ion binding;pigment biosynthetic process;oxidation-reduction process | ec:1.10.3.1-oxidase;ec:1.10.3 | Isoquinoline alkaloid biosynthesis;Tyrosine metabolism |
| Phvul.006G189100.1 | serine carboxypeptidase-like 31 | integral component of membrane;serine-type carboxypeptidase activity;proteolysis involved in cellular protein catabolic process | ec:3.4.21;ec:3.4.16 | |
| Phvul.006G189700.1 | BEST plant match is: (TAIR: ) , | | | |
| Phvul.006G189900.1 | katanin p80 WD40 repeat-containing subunit B1 homolog isoform X1 | microtubule;katanin complex;microtubule binding;microtubule severing | | |
| Phvul.006G190800.1 | 60S ribosomal L26-1 | cytosolic large ribosomal subunit;structural constituent of ribosome;cytoplasmic translation;ribosomal large subunit biogenesis | | |
| Phvul.006G191100.1 | pre-mRNA-splicing factor SYF1 | Prp19 complex;prespliceosome;catalytic step 1 spliceosome;catalytic step 2 spliceosome;post-mRNA release spliceosomal complex;generation of catalytic spliceosome for first transesterification step | | |
| Phvul.006G191500.1 | pre-mRNA-splicing factor SYF1 | Prp19 complex;prespliceosome;catalytic step 1 spliceosome;catalytic step 2 spliceosome;post-mRNA release spliceosomal complex;generation of catalytic spliceosome for first transesterification step | | |
| Phvul.006G191800.1 | sphingosine kinase 1 isoform X1 | ceramide kinase activity;sphinganine kinase activity;lipid phosphorylation | ec:2.7.1.91-kinase;ec:2.7.1.138-kinase | Sphingolipid metabolismSphingolipid metabolism |
| Phvul.006G192200.1 | heterogeneous nuclear ribonucleo U 1 isoform X1 | | | |
| Phvul.006G192200.2 | heterogeneous nuclear ribonucleo U 1 isoform X1 | | | |
| Phvul.006G194300.1 | G-type lectin S-receptor-like Serine Threonine-kinase | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;carbohydrate binding;ubiquitin protein ligase binding;protein phosphorylation;innate immune response;recognition of pollen | ec:2.7.11 | |
| Phvul.006G196400.1 | kinesin motor catalytic domain | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.006G196800.1 | salt stress response antifungal domain | integral component of membrane;kinase activity;phosphorylation | | |
| Phvul.006G197000.1 | probably inactive leucine-rich repeat | integral component of membrane;transmembrane receptor protein | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |

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| | receptor kinase At5g48380 | tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | | |
| Phvul.006G198200.1 | receptor kinase HAIKU2 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;peptidase activity;oxidoreductase activity;protein phosphorylation;endosperm development | ec:2.7.11 | |
| Phvul.006G198600.1 | probable sphingolipid transporter spinster homolog 2 | integral component of membrane;transmembrane transport | | |
| Phvul.006G199000.1 | phosphoglycerate mutase 1 isoform X1 | cytosol;sedoheptulose-bisphosphatase activity;cytokinin-activated signaling pathway;dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.37-SBPase | Aminobenzoate degradationCarbon fixation in photosynthetic organisms |
| Phvul.006G200700.1 | U3 small nucleolar RNA-associated 18 homolog | small-subunit processome;Pwp2p-containing subcomplex of 90S preribosome | | |
| Phvul.006G206300.1 | probable phosphatase 2C 9 | protein serine/threonine phosphatase activity;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.006G206300.2 | probable phosphatase 2C 9 | protein serine/threonine phosphatase activity;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.006G206400.1 | calmodulin-binding transcription activator 2 | nucleus;integral component of membrane;transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding;ligase activity;sequence-specific DNA binding;transcription from RNA polymerase II promoter;positive regulation of transcription from RNA polymerase II promoter | | |
| Phvul.006G206600.1 | potassium transporter 7 | plant-type vacuole;vacuolar membrane;integral component of membrane;potassium ion transmembrane transporter activity;potassium ion transmembrane transport | | |
| Phvul.006G206800.1 | pumilio homolog 7, chloroplastic | RNA binding | | |
| Phvul.006G207300.1 | chlorophyll a-b binding CP24 10A, chloroplastic | chloroplast thylakoid membrane;photosystem II antenna complex;chloroplast envelope;plastoglobule;integral component of membrane;chlorophyll binding;pigment binding;calcium ion transport;Golgi organization;response to salt stress;photosynthesis, light harvesting in photosystem I;nonphotochemical quenching;protein-chromophore linkage;cysteine biosynthetic process;regulation of protein dephosphorylation | | |
| Phvul.006G208400.1 | UDP-glucosyltransferase family | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |
| Phvul.006G209700.1 | cytochrome P450 family 71 | integral component of membrane;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;secondary metabolite biosynthetic process;oxidation-reduction process | ec:1.14.13 | |
| Phvul.006G210100.1 | WAT1-related At1g68170-like | plasma membrane;integral component of membrane;transmembrane transporter activity;transmembrane transport | | |
| Phvul.006G212300.1 | transmembrane 87B | Golgi apparatus;integral component of membrane;acetyl-CoA metabolic process;sterol biosynthetic process;brassinosteroid biosynthetic process | | |
| Phvul.006G212600.1 | SUPPRESSOR OF GENE SILENCING 3-like | nucleolar ribonuclease P complex;ribonuclease P activity;gene silencing by RNA;RNA | ec:3.1.30;ec:3.1.26;ec:3.1;ec:3.1.26.5 | |

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| | | phosphodiester bond hydrolysis, endonucleolytic | | |
| Phvul.006G214800.1 | alpha-ketoglutarate-dependent dioxygenase ABH5 | dioxygenase activity;oxidation-reduction process | | |
| Phvul.006G215100.1 | cell division control 48 homolog C | integral component of membrane;ATP binding;mitotic cell cycle;mRNA splicing, via spliceosome;photomorphogenesis;cullin deneddylation;protein ubiquitination;histone methylation;protein deubiquitination;production of siRNA involved in RNA interference;production of miRNAs involved in gene silencing by miRNA;post-translational protein modification;positive regulation of transcription, DNA-templated;cell division | | |
| Phvul.006G215200.1 | importin subunit beta-4 | cytosol;nuclear membrane;nuclear periphery;nuclear localization sequence binding;Ran GTPase binding;protein transporter activity;protein import into nucleus, docking;protein import into nucleus, translocation;gluconeogenesis;NLS-bearing protein import into nucleus;ribosomal protein import into nucleus;cytoskeleton organization;proteasomal protein catabolic process | | |
| Phvul.006G215700.1 | potassium channel AKT2 3 | plasmodesma;integral component of membrane;voltage-gated potassium channel activity;identical protein binding;myo-inositol hexakisphosphate biosynthetic process;regulation of membrane potential;potassium ion transmembrane transport | | |
| Phvul.006G215900.1 | DUF793 family | integral component of membrane | | |
| Phvul.006G216100.1 | T-complex 11 1 | plasmodesma | | |
| Phvul.006G216200.1 | ATP-dependent DNA helicase Q-like 4A | intracellular;nucleic acid binding;ATP binding;ATP-dependent 3'-5' DNA helicase activity;DNA replication;DNA repair;DNA recombination;DNA duplex unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.006G216900.1 | MLO 4 | plasma membrane;integral component of membrane;calmodulin binding;defense response;response to biotic stimulus | | |
| Phvul.006G216900.2 | MLO 4 | plasma membrane;integral component of membrane;calmodulin binding;defense response;response to biotic stimulus | | |
| Phvul.006G218600.1 | Lactoylglutathione lyase glyoxalase I family | integral component of membrane;transferase activity;lyase activity;metabolic process | | |
| Phvul.006G219400.1 | octicosapeptide Phox Bem1p domain-containing | | | |
| Phvul.006G220700.1 | ABC transporter F family member 4 | ATP binding;organic phosphonate transmembrane-transporting ATPase activity;organic phosphonate transport;organophosphate ester transport;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.6.3.28 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.006G220700.2 | ABC transporter F family member 4 | ATP binding;organic phosphonate transmembrane-transporting ATPase activity;organic phosphonate transport;organophosphate ester transport;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.6.3.28 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.006G221100.1 | pentatricopeptide repeat-containing At1g10270-like | | | |
| Phvul.006G221300.1 | zinc finger CCCH domain-containing 5 | nucleus;nucleotide binding;RNA binding;metal ion binding | | |
| Phvul.007G002100.1 | DEAD-box helicase family | helicase activity;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |

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| Phvul.007G002300.1 | sn1-specific diacylglycerol lipase beta | intracellular;integral component of membrane;hydrolase activity;fatty acid beta-oxidation;protein import into peroxisome matrix | | |
| Phvul.007G003000.1 | non-structural maintenance of chromosomes element 4 homolog A-like | nucleus;Smc5-Smc6 complex;DNA repair | | |
| Phvul.007G004700.1 | nucleolar complex 2 homolog | peroxidase activity;cellular oxidant detoxification | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.007G005300.1 | hypothetical protein PHAVU_007G005300g | | | |
| Phvul.007G005700.1 | probable phosphatase 2C 38 | integral component of membrane;protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.007G005900.1 | leukotriene A-4 hydrolase homolog | cytosol;plasma membrane;leukotriene-A4 hydrolase activity;zinc ion binding;peptide binding;metalloaminopeptidase activity;DNA replication;DNA methylation;proteolysis;cell proliferation;leukotriene biosynthetic process;peptide catabolic process;histone H3-K9 methylation | ec:3.3.2.6-hydrolase;ec:3.4.11 | Arachidonic acid metabolism |
| Phvul.007G007900.1 | sucrose-phosphate synthase 2 | | | |
| Phvul.007G007900.2 | sucrose-phosphate synthase 2 | | | |
| Phvul.007G014400.1 | cyclic pyranopterin monophosphate synthase accessory , mitochondrial | chloroplast;cyclic pyranopterin monophosphate synthase activity;Mo-molybdopterin cofactor biosynthetic process | ec:4.1.99.18-pyranopterin phosphate synthase | Folate biosynthesis |
| Phvul.007G016500.1 | ACT-like tyrosine kinase family | cytosol;protein serine/threonine/tyrosine kinase activity;protein tyrosine kinase activity;ATP binding;amino acid binding;actin filament organization;chloroplast organization;peptidyl-tyrosine phosphorylation | ec:2.7.10;ec:2.7.12.1 | |
| Phvul.007G016500.2 | ACT-like tyrosine kinase family | cytosol;protein serine/threonine/tyrosine kinase activity;protein tyrosine kinase activity;ATP binding;amino acid binding;actin filament organization;chloroplast organization;peptidyl-tyrosine phosphorylation | ec:2.7.10;ec:2.7.12.1 | |
| Phvul.007G017100.1 | FAD NAD(P)-binding oxidoreductase family | zeaxanthin epoxidase [overall] activity;zeaxanthin epoxidase activity;antheraxanthin epoxidase activity;FAD binding;secondary metabolite biosynthetic process;oxidation-reduction process | ec:1.14.13.90-epoxidase;ec:1.14.13 | Carotenoid biosynthesis |
| Phvul.007G018200.1 | DUF630 family | | | |
| Phvul.007G018200.2 | DUF630 family | | | |
| Phvul.007G018800.1 | probable ubiquitin-conjugating enzyme E2 23 | cytosol;ligase activity;ubiquitin protein ligase binding;ubiquitin protein ligase activity;postreplication repair;protein ubiquitination | | |
| Phvul.007G019900.1 | Myb family transcription factor At1g14600 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G020200.1 | DUF615 family | | | |
| Phvul.007G020300.1 | transport Sec24-like At4g32640 | COPII vesicle coat;zinc ion binding;intracellular protein transport;ER to Golgi vesicle-mediated transport | | |
| Phvul.007G020500.1 | ACCUMULATION AND REPLICATION OF CHLOROPLASTS 3 | extrinsic component of plastid membrane;GTPase activity;1-phosphatidylinositol-4-phosphate 5-kinase activity;protein self-association;chloroplast fission;phosphatidylinositol phosphorylation | ec:3.6.1;ec:3.6.1.15-phosphatase;ec:2.7.1.68-5-kinase;ec:2.7.1 | Purine metabolism;Thiamine metabolismInositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.007G021700.1 | Germin subfamily 3 member 2 | extracellular region;manganese ion binding;nutrient reservoir activity | | |

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| Phvul.007G022800.1 | ribonuclease H2 subunit A | ribonuclease H2 complex;RNA binding;RNA-DNA hybrid ribonuclease activity;mismatch repair;DNA replication, removal of RNA primer;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1.30;ec:3.1.26;ec:3.1;ec:3.1.26.4 | |
| Phvul.007G024600.1 | RNA-directed DNA methylation 3-like isoform X2 | ribosome;structural constituent of ribosome;translation elongation factor activity;translational elongation;nucleic acid metabolic process | | |
| Phvul.007G024700.1 | NUCLEAR FUSION DEFECTIVE 4-like | integral component of membrane;transmembrane transport | | |
| Phvul.007G026100.1 | Serine Threonine kinase domain | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.007G026100.2 | Serine Threonine kinase domain | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.007G026900.1 | alpha-xylosidase 1-like | alpha-1,4-glucosidase activity;carbohydrate binding;maltose alpha-glucosidase activity;maltose metabolic process | ec:3.2.1;ec:3.2.1.20-maltase | Starch and sucrose metabolism;Galactose metabolism |
| Phvul.007G027600.1 | 50S ribosomal L15, chloroplastic | plastid large ribosomal subunit;chloroplast stroma;chloroplast envelope;structural constituent of ribosome;DNA-templated transcription, elongation;translation;response to stress | | |
| Phvul.007G028000.1 | caffeoylshikimate esterase-like | membrane;acylglycerol lipase activity;lipid metabolic process | ec:3.1.1.23-lipase;ec:3.1.1;ec:3.1.1.1-ali-esterase | Glycerolipid metabolismDrug metabolism - other enzymes |
| Phvul.007G028000.2 | caffeoylshikimate esterase-like | membrane;acylglycerol lipase activity;lipid metabolic process | ec:3.1.1.23-lipase;ec:3.1.1;ec:3.1.1.1-ali-esterase | Glycerolipid metabolismDrug metabolism - other enzymes |
| Phvul.007G031100.1 | serine threonine-kinase | integral component of membrane;protein serine/threonine kinase activity;ATP binding;polysaccharide binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.007G032200.1 | auxin-responsive IAA32 | nucleus;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |
| Phvul.007G034400.1 | Grap2 cyclin-D-interacting | nucleus;regulation of cell cycle | | |
| Phvul.007G035200.1 | pentatricopeptide repeat-containing At5g04780 | zinc ion binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G035700.1 | repressor of RNA polymerase III transcription MAF1 homolog | nucleus;cytoplasm;RNA polymerase III core binding;transcription, DNA-templated;negative regulation of transcription from RNA polymerase III promoter;transcription factor TFIIIB complex assembly | | |
| Phvul.007G035800.1 | hypothetical protein PHAVU_007G035800g | | | |
| Phvul.007G036400.1 | hypothetical protein PHAVU_007G036400g, partial | | | |
| Phvul.007G036900.1 | transmembrane , | integral component of membrane | | |
| Phvul.007G038000.1 | heavy metal-associated domain | cytoplasm;transition metal ion binding;metal ion transport;cellular transition metal ion homeostasis | | |
| Phvul.007G038300.1 | phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity phosphatase PTEN | cytosol;protein tyrosine phosphatase activity;phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase activity;phosphatidic acid binding;peptidyl-tyrosine dephosphorylation;negative regulation of MAP kinase activity;phosphatidylinositol dephosphorylation;Golgi vesicle transport | ec:3.1.3.67-3-phosphatase;ec:3.1.3.48;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Inositol phosphate metabolism;Phosphatidylinositol signaling systemAminobenzoate degradationT cell receptor signaling pathway |
| Phvul.007G039200.1 | Limonoid UDP-glucosyltransferase | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |

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| Phvul.007G040400.1 | receptor kinase At4g34220 | integral component of membrane;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.007G040700.1 | methylthioribose kinase | cytosol;identical protein binding;S-methyl-5-thioribose kinase activity;S-methyl-5-thioribose-1-phosphate isomerase activity;methionine biosynthetic process;phosphorylation | ec:2.7.1.100-kinase;ec:5.3.1.23-isomerase | Cysteine and methionine metabolismCysteine and methionine metabolism |
| Phvul.007G041000.1 | plant basic secretory (BSP) family | | | |
| Phvul.007G041800.1 | homeobox KN domain | nucleus;DNA binding;zinc ion binding;positive regulation of cell proliferation;embryo sac egg cell differentiation;post-translational protein modification;positive regulation of transcription, DNA-templated;chromosome organization | | |
| Phvul.007G046400.1 | nucleobase-ascorbate transporter 4 | integral component of membrane;transporter activity;transmembrane transport | | |
| Phvul.007G047600.1 | pyruvate kinase isozyme A, chloroplastic-like | magnesium ion binding;pyruvate kinase activity;kinase activity;potassium ion binding;glycolytic process | ec:2.7.1.40-kinase | Purine metabolism;Pyruvate metabolism;Biosynthesis of antibiotics;Glycolysis / Gluconeogenesis |
| Phvul.007G048200.1 | dentin sialophospho-like | integral component of membrane | | |
| Phvul.007G048900.1 | receptor kinase At4g00960 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;defense response to bacterium | ec:2.7.11 | |
| Phvul.007G050600.1 | cysteine-rich receptor kinase 10 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;defense response;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.007G051000.1 | cysteine-rich receptor-kinase | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;defense response;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.007G054000.1 | probable ATP-dependent DNA helicase CHR12 isoform X2 | helicase activity;ATP binding;histone binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.007G054600.1 | probable LRR receptor-like serine threonine- kinase At1g67720 | kinase activity;phosphorylation | | |
| Phvul.007G054800.1 | amino-terminal domain cyclin | cyclin-dependent protein kinase holoenzyme complex;nucleus;cyclin-dependent protein serine/threonine kinase regulator activity;positive regulation of cyclin-dependent protein serine/threonine kinase activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of phosphorylation of RNA polymerase II C-terminal domain | ec:2.7.1 | |
| Phvul.007G054800.2 | amino-terminal domain cyclin | cyclin-dependent protein kinase holoenzyme complex;nucleus;cyclin-dependent protein serine/threonine kinase regulator activity;positive regulation of cyclin-dependent protein serine/threonine kinase activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of phosphorylation of RNA polymerase II C-terminal domain | ec:2.7.1 | |
| Phvul.007G056100.1 | thermospermine synthase ACAULIS5-like | cytoplasm;spermidine synthase activity;thermospermine synthase activity;polyamine biosynthetic process | ec:2.5.1.79;ec:2.5.1.16-synthase | Arginine and proline metabolism;Glutathione metabolism;beta-Alanine |

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| | | | | metabolism;Cysteine and methionine metabolism |
| Phvul.007G056400.1 | primary amine oxidase-like | copper ion binding;primary amine oxidase activity;quinone binding;amine metabolic process;oxidation-reduction process | ec:1.4.3.21-oxidase | beta-Alanine metabolism;Tropane, piperidine and pyridine alkaloid biosynthesis;Isoquinoline alkaloid biosynthesis;Phenylalanine metabolism;Glycine, serine and threonine metabolism;Tyrosine metabolism |
| Phvul.007G056400.2 | primary amine oxidase-like | copper ion binding;primary amine oxidase activity;quinone binding;amine metabolic process;oxidation-reduction process | ec:1.4.3.21-oxidase | beta-Alanine metabolism;Tropane, piperidine and pyridine alkaloid biosynthesis;Isoquinoline alkaloid biosynthesis;Phenylalanine metabolism;Glycine, serine and threonine metabolism;Tyrosine metabolism |
| Phvul.007G056800.1 | hypothetical protein PHAVU_007G056800g | | | |
| Phvul.007G060200.1 | type IV inositol polyphosphate 5-phosphatase 7-like | phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity;phosphatidylinositol dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.36-5-phosphatase | Aminobenzoate degradationInositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.007G062700.1 | LRR receptor-like kinase family | intracellular;MAP kinase kinase kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity | ec:2.7.11;ec:2.7.11.25 | |
| Phvul.007G062700.2 | LRR receptor-like kinase family | intracellular;MAP kinase kinase kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity | ec:2.7.11;ec:2.7.11.25 | |
| Phvul.007G066100.1 | Molybdenum cofactor sulfurase | catalytic activity;metabolic process | | |
| Phvul.007G067500.1 | homeobox-leucine zipper ANTHOCYANINLESS 2 isoform X2 | nucleus;lipid binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.007G067500.2 | homeobox-leucine zipper ANTHOCYANINLESS 2 isoform X2 | nucleus;lipid binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.007G068100.1 | 3-hexulose-6-phosphate isomerase, | glutamine-fructose-6-phosphate transaminase (isomerizing) activity;isomerase activity;carbohydrate binding;fructose 6-phosphate metabolic process;UDP-N-acetylglucosamine metabolic process;protein N-linked glycosylation | ec:2.6.1.16-transaminase (isomerizing) | Biosynthesis of antibiotics;Amino sugar and nucleotide sugar metabolism;Alanine, aspartate and glutamate metabolism |
| Phvul.007G068200.1 | phosphatase inhibitor 2 | protein phosphatase type 1 complex;protein phosphatase inhibitor activity;regulation of signal transduction;negative regulation of catalytic activity;regulation of phosphoprotein phosphatase activity | | |
| Phvul.007G068200.2 | phosphatase inhibitor 2 | protein phosphatase type 1 complex;protein phosphatase inhibitor activity;regulation of signal transduction;negative regulation of catalytic activity;regulation of phosphoprotein phosphatase activity | | |
| Phvul.007G069000.1 | F-box LRR-repeat At3g48880-like | | | |
| Phvul.007G069500.1 | remorin-like isoform X1 | | | |

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| Phvul.007G069900.1 | pentatricopeptide repeat-containing At3g60050-like | | | |
| Phvul.007G069900.2 | pentatricopeptide repeat-containing At3g60050-like | | | |
| Phvul.007G069900.3 | pentatricopeptide repeat-containing At3g60050-like | | | |
| Phvul.007G069900.4 | pentatricopeptide repeat-containing At3g60050-like | | | |
| Phvul.007G069900.5 | pentatricopeptide repeat-containing At3g60050-like | | | |
| Phvul.007G070600.1 | cofilin actin-depolymerizing factor | intracellular;nucleic acid binding;zinc ion binding | | |
| Phvul.007G070700.1 | actin depolymerizing factor, | nucleic acid binding;zinc ion binding | | |
| Phvul.007G071000.1 | oxalate-- ligase | plasmodesma;chloroplast stroma;apoplast;oxalate-CoA ligase activity;positive regulation of seed germination;response to nitrate;seed coat development;nitrate transport;oxalate catabolic process;para-aminobenzoic acid metabolic process;defense response to fungus | ec:6.2.1.8-ligase | Glyoxylate and dicarboxylate metabolism |
| Phvul.007G072400.1 | C2H2-like zinc finger , | metal ion binding | | |
| Phvul.007G072800.1 | mitogen-activated kinase kinase kinase YODA-like | cytoplasm;protein serine/threonine kinase activity;ATP binding;regulation of mitotic cell cycle;signal transduction by protein phosphorylation;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process | ec:2.7.11 | |
| Phvul.007G073500.1 | scarecrow 8 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G076700.1 | S-type anion channel SLAH2-like isoform X1 | cell;integral component of membrane;voltage-gated anion channel activity;cellular ion homeostasis;transmembrane transport;regulation of anion transmembrane transport | | |
| Phvul.007G077900.1 | ABC transporter C family member 10-like | integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G078300.1 | chromosome condensation regulator RCC1 repeat | ligase activity;metal ion binding;metabolic process | | |
| Phvul.007G079200.1 | eukaryotic translation initiation factor 5B | intracellular;translation initiation factor activity;GTPase activity;GTP binding;translational initiation | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.007G079200.2 | eukaryotic translation initiation factor 5B | intracellular;translation initiation factor activity;GTPase activity;GTP binding;translational initiation | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.007G080200.1 | UPF0496 4-like | integral component of membrane | | |
| Phvul.007G080800.1 | sterol 3-beta-glucosyltransferase UGT80B1-like isoform X1 | vacuolar membrane;sterol 3-beta-glucosyltransferase activity;flavonoid biosynthetic process;seed germination;seed coat development;sterol metabolic process;lipid glycosylation;flavonoid glucuronidation | ec:2.4.1;ec:2.4.1.173 | |
| Phvul.007G081000.1 | G-box-binding factor 4-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.007G081900.1 | polypyrimidine tract-binding homolog 3-like | nucleus;nucleotide binding;RNA binding;mRNA processing | | |
| Phvul.007G083500.1 | GIGANTEA | nucleoplasm;starch metabolic process;regulation of transcription, DNA- | | |

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| | | templated;circadian rhythm;response to cold;response to blue light;response to far red light;temperature compensation of the circadian clock;response to hydrogen peroxide;long-day photoperiodism, flowering;positive regulation of long-day photoperiodism, flowering | | |
| Phvul.007G083500.2 | GIGANTEA | nucleoplasm;starch metabolic process;regulation of transcription, DNA-templated;circadian rhythm;response to cold;response to blue light;response to far red light;temperature compensation of the circadian clock;response to hydrogen peroxide;long-day photoperiodism, flowering;positive regulation of long-day photoperiodism, flowering | | |
| Phvul.007G083800.1 | gmCK1p isoform X1 | choline kinase activity;CDP-choline pathway;phosphorylation | ec:2.7.1.32-kinase | Glycerophospholipid metabolism |
| Phvul.007G083800.2 | gmCK1p isoform X1 | choline kinase activity;CDP-choline pathway;phosphorylation | ec:2.7.1.32-kinase | Glycerophospholipid metabolism |
| Phvul.007G084400.1 | probable LRR receptor-like serine threonine- kinase At1g34110 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.007G085100.1 | transmembrane , | vacuole;integral component of membrane | | |
| Phvul.007G085300.1 | tRNA pseudouridine(38 39) synthase isoform X2 | RNA binding;pseudouridine synthase activity;pseudouridine synthesis;tRNA processing | ec:5.4.99.12 | |
| Phvul.007G090200.1 | hypothetical protein PHAVU_007G090200g | | | |
| Phvul.007G090400.1 | hypothetical protein PHAVU_007G090400g | chloroplast thylakoid membrane;integral component of membrane;phosphatidylglycerol biosynthetic process;aromatic amino acid family biosynthetic process;thylakoid membrane organization;photosystem II assembly;iron-sulfur cluster assembly;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;cysteine biosynthetic process;photosystem I assembly | | |
| Phvul.007G091100.1 | alpha beta fold hydrolase | integral component of membrane;hydrolase activity;metabolic process | | |
| Phvul.007G092600.1 | beta-taxilin isoform X1 | syntaxin binding | | |
| Phvul.007G093000.1 | pseudouridine synthase Rlu family | RNA binding;pseudouridine synthase activity;deaminase activity;enzyme-directed rRNA pseudouridine synthesis | ec:5.4.99.12 | |
| Phvul.007G093800.1 | Transmembrane 115 | Golgi apparatus;integral component of membrane;serine-type endopeptidase activity;proteolysis;calcium ion transport;retrograde vesicle-mediated transport, Golgi to ER;Golgi organization;response to salt stress | ec:3.4.21 | |
| Phvul.007G094100.1 | Para-aminobenzoate synthase | chloroplast;oxo-acid-lyase activity;4-amino-4-deoxychorismate synthase activity;para-aminobenzoic acid biosynthetic process;chorismate metabolic process;folic acid biosynthetic process | ec:2.6.1.85-synthase | Folate biosynthesis |
| Phvul.007G095400.1 | ENHANCED DISEASE RESISTANCE 2-like | lipid binding | | |
| Phvul.007G096000.1 | synaptotagmin-3 isoform X1 | endoplasmic reticulum;integral component of membrane;lipid binding;sterol biosynthetic process;pentacyclic triterpenoid biosynthetic process | | |
| Phvul.007G096500.1 | probable lysine-specific demethylase ELF6 | nucleic acid binding;methyltransferase activity;oxidoreductase activity;metal ion binding;cellular protein modification process;cellular component organization;methylation;single-organism cellular process;negative regulation of post-embryonic development;negative regulation of | | |

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| | | response to stimulus;response to stimulus;oxidation-reduction process;regulation of photoperiodism, flowering;negative regulation of reproductive process | | |
| Phvul.007G097100.1 | pumilio homolog 4 isoform X1 | mRNA binding | | |
| Phvul.007G097200.1 | vacuolar amino acid transporter 1 | integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.007G098800.1 | exocyst complex component SEC8 | exocyst;cytosol;plasma membrane;plasmodesma;glucose catabolic process;vesicle docking involved in exocytosis;pollen germination;pollen tube growth;protein transport;mucilage biosynthetic process involved in seed coat development | | |
| Phvul.007G100700.1 | ABA induced plasma membrane | integral component of membrane | | |
| Phvul.007G101800.1 | clavata3 esr-related 12 family | integral component of membrane | | |
| Phvul.007G102000.1 | transmembrane fragile-X-F-associated | integral component of membrane;ubiquitin-protein transferase activity;zinc ion binding;ligase activity;regulation of signal transduction;protein ubiquitination | | |
| Phvul.007G102000.2 | transmembrane fragile-X-F-associated | integral component of membrane;ubiquitin-protein transferase activity;zinc ion binding;ligase activity;regulation of signal transduction;protein ubiquitination | | |
| Phvul.007G104200.1 | RAB6-interacting golgin-like | | | |
| Phvul.007G105800.1 | phosphatidylinositol-3-phosphatase myotubularin-1-like isoform X1 | protein tyrosine phosphatase activity;peptidyl-tyrosine dephosphorylation | ec:3.1.3.48;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.007G106300.1 | cytochrome P450 family | integral component of membrane;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;secondary metabolite biosynthetic process;oxidation-reduction process | ec:1.14.13 | |
| Phvul.007G107100.1 | hypothetical protein PHAVU_007G107100g | | | |
| Phvul.007G108200.1 | LIGHT-DEPENDENT SHORT HYPOCOTYLS 4-like | | | |
| Phvul.007G108200.2 | LIGHT-DEPENDENT SHORT HYPOCOTYLS 4-like | | | |
| Phvul.007G108700.1 | hypothetical protein PHAVU_007G108700g, partial | nucleotide binding;nucleic acid binding | | |
| Phvul.007G110400.1 | U-box domain-containing 43-like | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.007G110600.1 | EXORDIUM-like 5 | | | |
| Phvul.007G110800.1 | DUF506 family | | | |
| Phvul.007G111500.1 | 65-kDa microtubule-associated 3-like | microtubule binding;microtubule cytoskeleton organization;cytokinesis | | |
| Phvul.007G113000.1 | chlorophyll a-b binding CP26, chloroplastic | PSII associated light-harvesting complex II;photosystem I;photosystem II antenna complex;chloroplast envelope;plastoglobule;integral component of membrane;chlorophyll binding;pigment binding;metal ion binding;rRNA processing;response to high light intensity;response to sucrose;photosynthesis, light harvesting in photosystem I;regulation of proton transport;nonphotochemical | | |

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| | | quenching;protein-chromophore linkage;cysteine biosynthetic process | | |
| Phvul.007G113600.1 | ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial | ATP binding;peptidase activity;unfolded protein binding;protein folding;proteolysis | | |
| Phvul.007G114400.1 | ribosomal lysine N-methyltransferase 3 isoform X1 | protein-lysine N-methyltransferase activity;peptidyl-lysine monomethylation | ec:2.1.1 | |
| Phvul.007G114500.1 | zinc finger CCCH domain-containing 13-like isoform X1 | | | |
| Phvul.007G114500.2 | zinc finger CCCH domain-containing 13-like isoform X2 | | | |
| Phvul.007G116400.1 | ATP-dependent zinc metalloprotease | mitochondrion;plasmodesma;chloroplast envelope;integral component of membrane;ATP-dependent peptidase activity;metalloendopeptidase activity;ATP binding;microtubule-severing ATPase activity;proteolysis | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase;ec:3.4.24 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G116600.1 | CHROMATIN REMODELING 20 isoform X1 | ATP binding;hydrolase activity;metabolic process | | |
| Phvul.007G116600.2 | CHROMATIN REMODELING 20 isoform X1 | ATP binding;hydrolase activity;metabolic process | | |
| Phvul.007G118300.1 | probable tyrosine-phosphatase At1g05000 | protein tyrosine phosphatase activity;peptidyl-tyrosine dephosphorylation | ec:3.1.3.48;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.007G118700.1 | lysine ketoglutarate reductase trans-splicing | integral component of membrane | | |
| Phvul.007G118700.2 | lysine ketoglutarate reductase trans-splicing | integral component of membrane | | |
| Phvul.007G119900.1 | plastid transcriptionally active | | | |
| Phvul.007G121700.1 | probable serine threonine phosphatase 2A regulatory subunit B delta | calcium ion binding | | |
| Phvul.007G121700.2 | probable serine threonine phosphatase 2A regulatory subunit B delta | calcium ion binding | | |
| Phvul.007G121700.3 | probable serine threonine phosphatase 2A regulatory subunit B delta | calcium ion binding | | |
| Phvul.007G123200.1 | MATH and LRR domain-containing PFE0570w-like isoform X2 | nuclear pore inner ring;structural constituent of nuclear pore;protein import into nucleus, docking;nuclear pore organization;root hair cell differentiation | | |
| Phvul.007G123200.2 | MATH and LRR domain-containing PFE0570w-like isoform X2 | nuclear pore inner ring;structural constituent of nuclear pore;protein import into nucleus, docking;nuclear pore organization;root hair cell differentiation | | |
| Phvul.007G124500.1 | phosphate transporter PHO1 | trans-Golgi network;plasma membrane;integral component of membrane;inositol monophosphate 1-phosphatase activity;inositol monophosphate 3-phosphatase activity;inositol monophosphate 4-phosphatase activity;dephosphorylation | ec:3.1.3;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.25-phosphatase | Aminobenzoate degradationBiosynthesis of antibiotics;Streptomycin biosynthesis;Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.007G124500.2 | phosphate transporter PHO1 | trans-Golgi network;plasma membrane;integral component of membrane;inositol | ec:3.1.3;ec:3.1;ec:3.1.3.41-nitrophenyl | Aminobenzoate degradationBiosynthesi |

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| | | monophosphate 1-phosphatase activity;inositol monophosphate 3-phosphatase activity;inositol monophosphate 4-phosphatase activity;dephosphorylation | phosphatase;ec:3.1.3.25-phosphatase | s of antibiotics;Streptomycin biosynthesis;Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.007G124800.1 | peroxisomal membrane PMP22 | integral component of membrane | | |
| Phvul.007G125800.1 | WVD2-like 1 isoform X1 | integral component of membrane | | |
| Phvul.007G126200.1 | chloroplastic group IIA intron splicing facilitator CRS1, chloroplastic | RNA binding | | |
| Phvul.007G126800.1 | thioredoxin HCF164, chloroplastic | cytoplasm;protein disulfide oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor;sulfate assimilation;protein folding;glycerol ether metabolic process;cellular response to oxidative stress;cell redox homeostasis;oxidation-reduction process | | |
| Phvul.007G128900.1 | probable serine threonine- kinase nek3 | | | |
| Phvul.007G128900.2 | probable serine threonine- kinase nek3 | | | |
| Phvul.007G129000.1 | Actin-related 9 | Ino80 complex;chromatin remodeling;vegetative to reproductive phase transition of meristem | | |
| Phvul.007G129300.1 | replication factor-A carboxy-terminal domain | | | |
| Phvul.007G134400.1 | hypothetical protein PHAVU_007G134400g | | | |
| Phvul.007G134600.1 | hypothetical protein PHAVU_007G134600g | integral component of membrane | | |
| Phvul.007G134600.2 | hypothetical protein PHAVU_007G134600g | integral component of membrane | | |
| Phvul.007G134600.3 | hypothetical protein PHAVU_007G134600g | integral component of membrane | | |
| Phvul.007G134600.4 | hypothetical protein PHAVU_007G134600g | integral component of membrane | | |
| Phvul.007G135800.1 | UDP rhamnose:anthocyanidin-3-glucoside rhamnosyltransferase, partial | integral component of membrane;intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |
| Phvul.007G136200.1 | 2 family | thiol-dependent ubiquitinyl hydrolase activity;ubiquitin-dependent protein catabolic process;protein deubiquitination | ec:3.4;ec:3.4.19.12 | |
| Phvul.007G136200.2 | 2 family | thiol-dependent ubiquitinyl hydrolase activity;ubiquitin-dependent protein catabolic process;protein deubiquitination | ec:3.4;ec:3.4.19.12 | |
| Phvul.007G136700.1 | hypothetical protein PHAVU_007G136700g | | | |
| Phvul.007G136700.2 | hypothetical protein PHAVU_007G136700g | | | |

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| Phvul.007G137100.1 | 7-methylguanosine phosphate-specific 5 -nucleotidase A | cytosol;integral component of membrane;magnesium ion binding;5'-nucleotidase activity;dephosphorylation | ec:3.1.3.5-uridine 5'-nucleotidase;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.31 | Purine metabolism;Nicotinate and nicotinamide metabolism;Pyrimidine metabolismAminobenzoate degradation |
| Phvul.007G137100.2 | 7-methylguanosine phosphate-specific 5 -nucleotidase A | cytosol;integral component of membrane;magnesium ion binding;5'-nucleotidase activity;dephosphorylation | ec:3.1.3.5-uridine 5'-nucleotidase;ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.31 | Purine metabolism;Nicotinate and nicotinamide metabolism;Pyrimidine metabolismAminobenzoate degradation |
| Phvul.007G137800.1 | receptor kinase | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.007G138700.1 | exocyst complex component EXO70A1 | exocyst;exocytosis | | |
| Phvul.007G139200.1 | DUF1635 family | | | |
| Phvul.007G141200.1 | UDP-glycosyltransferase family | endosome;trans-Golgi network;integral component of membrane;transferase activity;metabolic process | | |
| Phvul.007G141200.2 | UDP-glycosyltransferase family | endosome;trans-Golgi network;integral component of membrane;transferase activity;metabolic process | | |
| Phvul.007G141300.1 | DNA-binding PD2 | | | |
| Phvul.007G142900.1 | alanine-tRNA ligase | mitochondrion;cytosol;chloroplast stroma;membrane;tRNA binding;DNA binding;transcription factor activity, sequence-specific DNA binding;alanine-tRNA ligase activity;ATP binding;zinc ion binding;amino acid binding;sigma factor activity;DNA-templated transcription, initiation;regulation of transcription, DNA-templated;tRNA modification;alanyl-tRNA aminoacylation;embryo development ending in seed dormancy | ec:6.1.1;ec:6.1.1.7-ligase | Aminoacyl-tRNA biosynthesis |
| Phvul.007G144000.1 | probable U6 snRNA-associated Sm LSm4 | cytoplasmic mRNA processing body;spliceosomal complex;U6 snRNP;viral nucleocapsid;spliceosomal tri-snRNP complex;U6 snRNA binding;spliceosomal complex assembly;spliceosomal snRNP assembly;nuclear-transcribed mRNA catabolic process;cytoplasmic mRNA processing body assembly | | |
| Phvul.007G146000.1 | phytochrome A-associated F-box | ubiquitin-protein transferase activity;ubiquitin-dependent protein catabolic process;regulation of photomorphogenesis;protein ubiquitination;regulation of protein localization;regulation of circadian rhythm;leaf development;photoperiodism, flowering | | |
| Phvul.007G147000.1 | magnesium proton exchanger | integral component of membrane;iron ion transport;zinc II ion transport;magnesium ion transport;transmembrane transport | | |
| Phvul.007G147100.1 | blue-light photoreceptor PHR2 | lyase activity;maltose metabolic process;phosphatidylglycerol biosynthetic process;carotenoid biosynthetic process;starch biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | | |
| Phvul.007G147200.1 | gamma-tubulin complex component 4 homolog | equatorial microtubule organizing center;gamma-tubulin complex;centrosome;spindle pole body;microtubule;plasmodesma;tubulin complex;structural constituent of cytoskeleton;gamma-tubulin binding;microtubule minus-end binding;meiotic nuclear division;regulation of flower development;histone modification;growth;cortical microtubule organization;floral organ formation;centrosome duplication;interphase microtubule nucleation by interphase microtubule organizing center;positive | | |

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| | | regulation of microtubule nucleation;mitotic spindle assembly | | |
| Phvul.007G148200.1 | transcription termination factor family | mitochondrion;double-stranded DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.007G148600.1 | transmembrane , | membrane | | |
| Phvul.007G149000.1 | auxin response factor 18-like isoform X1 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;auxin-activated signaling pathway | | |
| Phvul.007G151200.1 | probable pectate lyase 12 | integral component of membrane;pectate lyase activity;metal ion binding;pectin catabolic process | ec:4.2.2.2-lyase | Pentose and glucuronate interconversions |
| Phvul.007G152700.1 | hypothetical protein PHAVU_007G152700g | | | |
| Phvul.007G152800.1 | UDP-glycosyltransferase 73C3-like | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |
| Phvul.007G154900.1 | RNA polymerase I termination factor | DNA binding | | |
| Phvul.007G154900.2 | RNA polymerase I termination factor | DNA binding | | |
| Phvul.007G154900.3 | RNA polymerase I termination factor | DNA binding | | |
| Phvul.007G154900.4 | RNA polymerase I termination factor | DNA binding | | |
| Phvul.007G155200.1 | probable indole-3-pyruvate monooxygenase YUCCA5 | integral component of membrane;N,N-dimethylaniline monooxygenase activity;flavin adenine dinucleotide binding;NADP binding;oxidation-reduction process | ec:1.14.13.8-monooxygenase;ec:1.14.13 | Drug metabolism - cytochrome P450 |
| Phvul.007G156300.1 | zinc finger HIT domain-containing 3 | | | |
| Phvul.007G156300.2 | zinc finger HIT domain-containing 3 | | | |
| Phvul.007G157900.1 | PHD zinc finger | DNA binding;helicase activity;N-acetyltransferase activity;zinc ion binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase;ec:2.3.1 | Purine metabolism;Thiamine metabolism |
| Phvul.007G157900.2 | PHD zinc finger | DNA binding;helicase activity;N-acetyltransferase activity;zinc ion binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase;ec:2.3.1 | Purine metabolism;Thiamine metabolism |
| Phvul.007G159500.1 | DUF4378 domain | | | |
| Phvul.007G159700.1 | UDP-glucuronic acid decarboxylase 1 | integral component of membrane | | |
| Phvul.007G161700.1 | probable phosphatase 2C 38 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.007G163300.1 | E3 ubiquitin- ligase UPL4-like | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination involved in ubiquitin-dependent protein catabolic process | | |
| Phvul.007G164300.1 | IQ-DOMAIN 1 | | | |
| Phvul.007G165100.1 | nuclear transcription factor Y subunit B-5 | nucleus;sequence-specific DNA binding;protein heterodimerization activity;regulation of transcription, DNA-templated | | |
| Phvul.007G165500.1 | hypothetical protein PHAVU_007G165500g | | | |
| Phvul.007G166900.1 | CUGBP Elav-like family member 5 | nucleotide binding;RNA binding | | |
| Phvul.007G167200.1 | peroxidase 3-like | extracellular region;plant-type cell wall;peroxidase activity;heme binding;metal ion binding;response to oxidative stress;plant-type cell wall organization;hydrogen peroxide catabolic process;oxidation-reduction process;cellular oxidant detoxification | ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |

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| Phvul.007G168400.1 | methyl- -binding domain | nucleus;thymidine kinase activity;ATP binding;zinc ion binding;methyl-CpG binding;negative regulation of transcription from RNA polymerase II promoter;methylation-dependent chromatin silencing;deoxyribonucleoside monophosphate biosynthetic process | ec:2.7.1.21-kinase;ec:2.7.1.145 | Drug metabolism - other enzymes;Pyrimidine metabolism |
| Phvul.007G169300.1 | BTB POZ and MATH domain-containing 2-like | | | |
| Phvul.007G171800.1 | Rho GTPase | integral component of mitochondrial outer membrane;GTPase activity;calcium ion binding;GTP binding;mitochondrion organization;small GTPase mediated signal transduction;metabolic process;protein transport | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.007G172900.1 | PHD finger , | DNA binding;N-acetyltransferase activity;zinc ion binding;metabolic process | ec:2.3.1 | |
| Phvul.007G173800.1 | hypothetical protein PHAVU_007G173800g | | | |
| Phvul.007G174000.1 | NETWORKED 1D-like | kinase activity;phosphorylation | | |
| Phvul.007G174600.1 | ETO1 1 | RNA splicing, via endonucleolytic cleavage and ligation;cell-cell signaling;serine family amino acid metabolic process;methionine biosynthetic process;virus induced gene silencing;determination of bilateral symmetry;meristem initiation;vegetative phase change;meristem maintenance;production of ta-siRNAs involved in RNA interference;regulation of ethylene biosynthetic process;production of miRNAs involved in gene silencing by miRNA;cell wall modification | | |
| Phvul.007G175700.1 | guanine nucleotide-binding subunit gamma 2 | heterotrimeric G-protein complex;signal transducer activity;GTP binding;G-protein coupled receptor signaling pathway;defense response to fungus, incompatible interaction;seed germination;basipetal auxin transport;acropetal auxin transport;protein prenylation;protein palmitoylation;lateral root development | | |
| Phvul.007G175800.1 | LONGIFOLIA 1 | | | |
| Phvul.007G177300.1 | Photosystem II reaction center W , chloroplastic | chloroplast;photosystem II;integral component of membrane;photosynthesis | | |
| Phvul.007G179200.1 | DEAD-box ATP-dependent RNA helicase 16 | intracellular;nucleic acid binding;ATP-dependent RNA helicase activity;ATP binding;protein import into nucleus;RNA secondary structure unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G179200.2 | DEAD-box ATP-dependent RNA helicase 16 | intracellular;nucleic acid binding;ATP-dependent RNA helicase activity;ATP binding;protein import into nucleus;RNA secondary structure unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G179300.1 | cyclin-H1-1 | cyclin-dependent protein kinase holoenzyme complex;TFIIK complex;protein kinase activity;cyclin-dependent protein serine/threonine kinase regulator activity;mitotic cell cycle;RNA splicing, via endonucleolytic cleavage and ligation;transcription from RNA polymerase II promoter;protein phosphorylation;pyrimidine ribonucleotide biosynthetic process;response to water deprivation;regulation of stomatal movement;stomatal lineage progression;DNA endoreduplication;negative regulation of cyclin-dependent protein serine/threonine kinase activity;positive regulation of cyclin-dependent protein serine/threonine kinase activity;positive regulation of transcription from RNA polymerase II promoter;reactive oxygen species metabolic process;positive regulation of phosphorylation of RNA | ec:2.7.1 | |

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| | | polymerase II C-terminal domain;stomatal opening;regulation of response to water deprivation | | |
| Phvul.007G180200.1 | probable rRNA-processing EBP2 homolog | 2-alkenal reductase [NAD(P)] activity;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.007G180200.2 | probable rRNA-processing EBP2 homolog | 2-alkenal reductase [NAD(P)] activity;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.007G180300.1 | mitochondrial Rho GTPase 1 | integral component of mitochondrial outer membrane;GTPase activity;calcium ion binding;GTP binding;mitochondrion organization;small GTPase mediated signal transduction;metabolic process;protein transport | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.007G181500.1 | heavy-metal-associated domain | cytoplasm;transition metal ion binding;metal ion transport;cellular transition metal ion homeostasis | | |
| Phvul.007G181800.1 | E3 ubiquitin- ligase ATL6-like | integral component of membrane;zinc ion binding | | |
| Phvul.007G183100.1 | breast carcinoma amplified sequence 3 | cytoplasm;nucleotide binding;vacuole organization;cellular response to phosphate starvation;galactolipid biosynthetic process;cellular response to water deprivation | | |
| Phvul.007G184100.1 | Na+ H+ antiporter | vacuolar membrane;plasma membrane;integral component of membrane;sodium:proton antiporter activity;regulation of pH;response to salt stress;sodium ion transmembrane transport;potassium ion homeostasis;hydrogen ion transmembrane transport | | |
| Phvul.007G184300.1 | hypothetical protein PHAVU_007G184300g | | | |
| Phvul.007G185500.1 | mediator-associated 1-like | | | |
| Phvul.007G185700.1 | tRNA(adenine(34)) deaminase, chloroplastic | cytosol;guanosine deaminase activity;RNA modification | ec:3.5.4.15 | |
| Phvul.007G186000.1 | zeta-carotene desaturase, chloroplastic chromoplastic | chromoplast;chloroplast envelope;carotene 7,8-desaturase activity;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;carotenoid biosynthetic process;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.14.99.30;ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.007G186500.1 | pollen-specific SF21-like | | | |
| Phvul.007G186800.1 | serine threonine-kinase Nek2-like | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.007G191900.1 | probable methyltransferase PMT3 | integral component of membrane;S-adenosylmethionine-dependent methyltransferase activity;methylation | | |
| Phvul.007G192000.1 | serine threonine-kinase 19 isoform X1 | kinase activity;phosphorylation | | |
| Phvul.007G192000.2 | serine threonine-kinase 19 isoform X1 | kinase activity;phosphorylation | | |
| Phvul.007G192300.1 | armadillo beta-catenin repeat | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.007G192300.2 | armadillo beta-catenin repeat | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.007G193000.1 | root UVB sensitive 2, chloroplastic | mitochondrion;chloroplast envelope;auxin polar transport;response to UV-B | | |
| Phvul.007G193800.1 | ethylene-responsive transcription factor 1B-like | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G194400.1 | CDT1 a, chloroplastic | | | |
| Phvul.007G197300.1 | DNA-binding , | DNA binding;zinc ion binding | | |

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| Phvul.007G198300.1 | DUF1399 family | plasma membrane | | |
| Phvul.007G198300.2 | DUF1399 family | plasma membrane | | |
| Phvul.007G198300.3 | DUF1399 family | plasma membrane | | |
| Phvul.007G198300.4 | DUF1399 family | plasma membrane | | |
| Phvul.007G198700.1 | probable phosphatase 2C 34 | protein serine/threonine phosphatase activity;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.007G199000.1 | kinesin-4-like | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G199700.1 | syntaxin-43-like isoform X1 | endomembrane system;integral component of membrane;SNARE complex;SNARE binding;SNAP receptor activity;intracellular protein transport;vesicle fusion;vesicle docking | | |
| Phvul.007G203100.1 | alkaline neutral invertase A, mitochondrial-like | nucleus;mitochondrion;sucrose alpha-glucosidase activity;exodeoxyribonuclease III activity;glycopeptide alpha-N-acetylgalactosaminidase activity;sucrose catabolic process;DNA repair;root development | ec:3.2.1.48-alpha-glucosidase;ec:3.2.1;ec:3.2.1.26-invertase;ec:3.1.15;ec:3.1.11;ec:3.1;ec:3.1.11.2;ec:3.2.1.97 | Starch and sucrose metabolismStarch and sucrose metabolism;Galactose metabolism |
| Phvul.007G204600.1 | pentatricopeptide repeat-containing At3g16710, mitochondrial isoform X2 | | | |
| Phvul.007G206100.1 | titin-like isoform X3 | | | |
| Phvul.007G206100.2 | titin-like isoform X3 | | | |
| Phvul.007G206400.1 | NRT1 PTR FAMILY -like | integral component of membrane;transporter activity;transport | | |
| Phvul.007G206500.1 | flap endonuclease 1 isoform X1 | nucleoplasm;nucleolus;mitochondrion;cytosol;DNA binding;endonuclease activity;exonuclease activity;metal ion binding;DNA replication;DNA repair;vegetative to reproductive phase transition of meristem;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.007G206500.2 | flap endonuclease 1 isoform X2 | nucleoplasm;nucleolus;mitochondrion;cytosol;DNA binding;endonuclease activity;exonuclease activity;metal ion binding;DNA replication;DNA repair;vegetative to reproductive phase transition of meristem;nucleic acid phosphodiester bond hydrolysis | ec:3.1 | |
| Phvul.007G208500.1 | Transcription factor PIF3 | protein dimerization activity | | |
| Phvul.007G209300.1 | translocase subunit , chloroplastic | chloroplast thylakoid membrane;chloroplast stroma;ATP binding;protein targeting;protein import | | |
| Phvul.007G209600.1 | ATP binding cassette subfamily B4 isoform 2 | integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G209900.1 | hypothetical protein PHAVU_007G209900g | | | |
| Phvul.007G210600.1 | squamosa promoter-binding 1 | nucleus;integral component of membrane;DNA binding | | |
| Phvul.007G211400.1 | polygalacturonase At1g48100 | extracellular region;polygalacturonase activity;galacturan 1,4-alpha-galacturonidase activity;carbohydrate metabolic process;cell wall organization | ec:3.2.1.15-pectin depolymerase;ec:3.2.1.67-1,4-alpha-galacturonidase | Starch and sucrose metabolism;Pentose and glucuronate interconversionsStarch and sucrose metabolism;Pentose and glucuronate interconversions |

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| Phvul.007G211800.1 | myb transcription factor | DNA binding | | |
| Phvul.007G212600.1 | probable glycerol-3-phosphate acyltransferase 3 | integral component of membrane;glycerol-3-phosphate O-acyltransferase activity;phosphatase activity;glycerol-3-phosphate 2-O-acyltransferase activity;cutin biosynthetic process;dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:2.3.1.15-1-O-acyltransferase;ec:2.3.1 | Aminobenzoate degradationGlycerophospholipid metabolism;Glycerolipid metabolism |
| Phvul.007G215300.1 | DNA replication regulator dpb11, | zinc ion binding | | |
| Phvul.007G216600.1 | kynurenine--oxoglutarate transaminase-like | L-aspartate:2-oxoglutarate aminotransferase activity;kynurenine-oxoglutarate transaminase activity;pyridoxal phosphate binding;cysteine-S-conjugate beta-lyase activity;L-phenylalanine:2-oxoglutarate aminotransferase activity;biosynthetic process;L-kynurenine metabolic process | ec:2.6.1.57-transaminase;ec:4.4.1.13-beta-lyase;ec:2.6.1.9-transaminase;ec:2.6.1.7-transaminase;ec:2.6.1.5-transaminase;ec:2.6.1.1-transaminase | Biosynthesis of antibiotics;Tropane, piperidine and pyridine alkaloid biosynthesis;Cysteine and methionine metabolism;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesis;Isoquinoline alkaloid biosynthesis;Lysine biosynthesis;Phenylalanine metabolism;Tyrosine metabolismSelenocompound metabolismBiosynthesis of antibiotics;Tropane, piperidine and pyridine alkaloid biosynthesis;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesis;Phenylalanine metabolism;Tyrosine metabolism;Histidine metabolismTryptophan metabolismUbiquinone and other terpenoid-quinone biosynthesis;Biosynthesis of antibiotics;Tropane, piperidine and pyridine alkaloid biosynthesis;Cysteine and methionine metabolism;Novobiocin biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesis;Isoquinoline alkaloid biosynthesis;Phenylalanine metabolism;Tyrosine metabolismArginine and proline metabolism;Biosynthesis of antibiotics;Arginine biosynthesis;Carbon fixation in photosynthetic organisms;Tropane, piperidine and pyridine alkaloid biosynthesis;Cysteine and methionine metabolism;Novobiocin |

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| | | | | biosynthesis;Phenylalanine, tyrosine and tryptophan biosynthesis;Isoquinoline alkaloid biosynthesis;Phenylalanine metabolism;Tyrosine metabolism;Alanine, aspartate and glutamate metabolism |
| Phvul.007G217300.1 | RNI superfamily | | | |
| Phvul.007G217400.1 | kinesin-4-like isoform X1 | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G219100.1 | heavy metal-associated domain | cytoplasm;transition metal ion binding;metal ion transport;cellular transition metal ion homeostasis | | |
| Phvul.007G220700.1 | serine threonine-kinase CCR1 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein homodimerization activity;protein phosphorylation;fatty acid catabolic process | ec:2.7.11 | |
| Phvul.007G221000.1 | probable dolichyl pyrophosphate Glc1Man9 c2 alpha-1,3-glucosyltransferase | endoplasmic reticulum membrane;integral component of membrane;dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;microtubule cytoskeleton organization;protein folding;protein N-linked glycosylation;oligosaccharide-lipid intermediate biosynthetic process;response to heat;response to high light intensity;response to endoplasmic reticulum stress;response to hydrogen peroxide | ec:2.4.1 | |
| Phvul.007G221000.2 | probable dolichyl pyrophosphate Glc1Man9 c2 alpha-1,3-glucosyltransferase | endoplasmic reticulum membrane;integral component of membrane;dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity;microtubule cytoskeleton organization;protein folding;protein N-linked glycosylation;oligosaccharide-lipid intermediate biosynthetic process;response to heat;response to high light intensity;response to endoplasmic reticulum stress;response to hydrogen peroxide | ec:2.4.1 | |
| Phvul.007G221200.1 | peptide upstream ORF , | integral component of membrane;S-adenosylmethionine-dependent methyltransferase activity;methylation | | |
| Phvul.007G221300.1 | RING U-box | integral component of membrane;zinc ion binding | | |
| Phvul.007G222100.1 | serine threonine-kinase D6PKL1-like | cytoplasm;plasma membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;intracellular signal transduction | ec:2.7.11 | |
| Phvul.007G223200.1 | polyadenylation and cleavage factor homolog 4-like isoform X1 | cytoplasm;mRNA cleavage factor complex;RNA polymerase II core binding;mRNA binding;metal ion binding;termination of RNA polymerase II transcription;mRNA polyadenylation;mRNA cleavage | | |
| Phvul.007G223200.2 | polyadenylation and cleavage factor homolog 4-like isoform X1 | cytoplasm;mRNA cleavage factor complex;RNA polymerase II core binding;mRNA binding;metal ion binding;termination of RNA polymerase II transcription;mRNA polyadenylation;mRNA cleavage | | |
| Phvul.007G223200.3 | polyadenylation and cleavage factor homolog 4-like isoform X1 | cytoplasm;mRNA cleavage factor complex;RNA polymerase II core binding;mRNA binding;metal ion binding;termination of RNA polymerase II transcription;mRNA polyadenylation;mRNA cleavage | | |
| Phvul.007G223200.4 | polyadenylation and cleavage factor homolog 4-like isoform X1 | cytoplasm;mRNA cleavage factor complex;RNA polymerase II core binding;mRNA binding;metal ion binding;termination of RNA polymerase II transcription;mRNA polyadenylation;mRNA cleavage | | |

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| Phvul.007G223200.5 | polyadenylation and cleavage factor homolog 4-like isoform X1 | cytoplasm;mRNA cleavage factor complex;RNA polymerase II core binding;mRNA binding;metal ion binding;termination of RNA polymerase II transcription;mRNA polyadenylation;mRNA cleavage | | |
| Phvul.007G223200.6 | polyadenylation and cleavage factor homolog 4-like isoform X1 | cytoplasm;mRNA cleavage factor complex;RNA polymerase II core binding;mRNA binding;metal ion binding;termination of RNA polymerase II transcription;mRNA polyadenylation;mRNA cleavage | | |
| Phvul.007G223400.1 | heat stress transcription factor A-3-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.007G224600.1 | Myb SANT-like DNA-binding domain | response to stress;pattern specification process;regulation of cellular metabolic process;meristem development | | |
| Phvul.007G226300.1 | uncharacterized permease | plasma membrane;plastid envelope;integral component of membrane;nucleobase transmembrane transporter activity;response to UV;flavonoid biosynthetic process;nucleobase transport;pyrimidine nucleobase salvage;transmembrane transport | | |
| Phvul.007G228400.1 | glycinol 4-dimethylallyltransferase-like | integral component of membrane;prenyltransferase activity;metabolic process | ec:2.5.1 | |
| Phvul.007G231500.1 | S-adenosyl-L-methionine-dependent methyltransferase superfamily | methyltransferase activity;methylation | | |
| Phvul.007G231500.2 | S-adenosyl-L-methionine-dependent methyltransferase superfamily | methyltransferase activity;methylation | | |
| Phvul.007G231500.3 | S-adenosyl-L-methionine-dependent methyltransferase superfamily | methyltransferase activity;methylation | | |
| Phvul.007G231500.4 | S-adenosyl-L-methionine-dependent methyltransferase superfamily | methyltransferase activity;methylation | | |
| Phvul.007G232400.1 | cation H(+) antiporter 15-like | endomembrane system;integral component of membrane;monovalent cation:proton antiporter activity;regulation of pH;hydrogen ion transmembrane transport | | |
| Phvul.007G234900.1 | pentatricopeptide repeat-containing At5g04810, chloroplastic | nucleotide binding;nucleic acid binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G236300.1 | ankyrin repeat domain-containing 13C-like | | | |
| Phvul.007G238000.1 | hydroxyethylthiazole kinase | hydroxyethylthiazole kinase activity;phosphorylation;thiamine salvage | ec:2.7.1.50-kinase | Thiamine metabolism |
| Phvul.007G239200.1 | thioredoxin-like 3-2, chloroplastic | cytoplasm;protein disulfide oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor;sulfate assimilation;protein folding;glycerol ether metabolic process;cellular response to oxidative stress;cell redox homeostasis;oxidation-reduction process | | |
| Phvul.007G241800.1 | ethylene response factor | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G242000.1 | Mitogen-activated kinase kinase kinase 21, | cytoplasm;protein serine/threonine kinase activity;ATP binding;regulation of mitotic cell cycle;signal transduction by protein | ec:2.7.11 | |

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| | | phosphorylation;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process | | |
| Phvul.007G242100.1 | cucumisin-like | cell wall;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.007G242200.1 | serine carboxypeptidase-like 45 | serine-type carboxypeptidase activity;transferase activity, transferring acyl groups other than amino-acyl groups;secondary metabolic process;proteolysis involved in cellular protein catabolic process | ec:3.4.21;ec:3.4.16 | |
| Phvul.007G242400.1 | vacuolar amino acid transporter 1 | integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.007G242400.2 | vacuolar amino acid transporter 1 | integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.007G243100.1 | CDPK-related kinase 7-like | cytoplasm;plasma membrane;calmodulin-dependent protein kinase activity;calcium ion binding;calmodulin binding;ATP binding;calcium-dependent protein serine/threonine kinase activity;abscisic acid-activated signaling pathway;peptidyl-serine phosphorylation;intracellular signal transduction;protein autophosphorylation | ec:2.7.11;ec:2.7.11.17 | |
| Phvul.007G243200.1 | ABC transporter G family member 24-like | plasma membrane;integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G243300.1 | plant T8M16-80 | integral component of membrane | | |
| Phvul.007G243600.1 | exportin-7 isoform X1 | nuclear pore;cytoplasm;nuclear export signal receptor activity;Ran GTPase binding;protein export from nucleus | | |
| Phvul.007G243600.2 | exportin-7 isoform X1 | nuclear pore;cytoplasm;nuclear export signal receptor activity;Ran GTPase binding;protein export from nucleus | | |
| Phvul.007G243600.3 | exportin-7 isoform X1 | nuclear pore;cytoplasm;nuclear export signal receptor activity;Ran GTPase binding;protein export from nucleus | | |
| Phvul.007G244000.1 | RAP annotation release 2, galactose-binding-like domain | chloroplast | | |
| Phvul.007G244700.1 | transcriptional corepressor LEUNIG_HOMOLOG isoform X3 | transferase activity, transferring glycosyl groups;metabolic process | | |
| Phvul.007G245500.1 | serine threonine-kinase CTR1-like isoform X1 | intracellular;MAP kinase kinase kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity | ec:2.7.11;ec:2.7.11.25 | |
| Phvul.007G245800.1 | serine carboxypeptidase-like | vacuole;cytosol;serine-type carboxypeptidase activity;proteolysis involved in cellular protein catabolic process | ec:3.4.21;ec:3.4.16 | |
| Phvul.007G247800.1 | condensin complex subunit 1 | condensed chromosome, centromeric region;nuclear condensin complex;extracellular region;chromatin binding;hormone activity;histone binding;mitotic chromosome condensation;meiotic chromosome condensation;cell division;chromosome separation | | |
| Phvul.007G247900.1 | L-galactono-1,4-lactone dehydrogenase, mitochondrial | integral component of membrane;D-arabinono-1,4-lactone oxidase activity;galactonolactone dehydrogenase activity;L-gulonolactone oxidase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.1.3.37;ec:1.1.3.8-oxidase;ec:1.3.2.3-dehydrogenase | Ascorbate and aldarate metabolismAscorbate and aldarate metabolism |
| Phvul.007G248100.1 | probable methyltransferase PMT6 | integral component of membrane;S-adenosylmethionine-dependent methyltransferase activity;methylation | | |
| Phvul.007G252500.1 | probable receptor kinase At1g67000 | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |

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| | | tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | | |
| Phvul.007G253800.1 | Guanylate kinase | guanylate kinase activity;phosphorylation;GMP metabolic process;GDP metabolic process | ec:2.7.4.8-kinase | Purine metabolism |
| Phvul.007G254000.1 | G-type lectin S-receptor-like serine threonine- kinase SD3-1 | plasma membrane;integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;carbohydrate binding;flower development;peptidyl-tyrosine phosphorylation;recognition of pollen | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.007G254100.1 | zinc finger CCCH domain-containing 30 | metal ion binding | | |
| Phvul.007G255800.1 | hypothetical protein LR48_Vigan02g029700 | | | |
| Phvul.007G255900.1 | serine threonine-kinase Nek7-like isoform X1 | protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.007G260300.1 | probable L-type lectin-domain containing receptor kinase | integral component of membrane;protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.007G261300.1 | hypothetical protein PHAVU_007G261300g | histamine N-methyltransferase activity;methylation | ec:2.1.1;ec:2.1.1.8-N-methyltransferase | Histidine metabolism |
| Phvul.007G262000.1 | DEAD-box ATP-dependent RNA helicase 37-like | nucleic acid binding;ATP-dependent RNA helicase activity;ATP binding;RNA secondary structure unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G263300.1 | calmodulin-binding family | | | |
| Phvul.007G263400.1 | homogentisate solanesyltransferase, chloroplastic | chloroplast envelope;integral component of membrane;homogentisate farnesyltransferase activity;homogentisate geranylgeranyltransferase activity;homogentisate solanesyltransferase activity;plastoquinone biosynthetic process;carotenoid biosynthetic process | ec:2.5.1 | |
| Phvul.007G263400.2 | homogentisate solanesyltransferase, chloroplastic | chloroplast envelope;integral component of membrane;homogentisate farnesyltransferase activity;homogentisate geranylgeranyltransferase activity;homogentisate solanesyltransferase activity;plastoquinone biosynthetic process;carotenoid biosynthetic process | ec:2.5.1 | |
| Phvul.007G263400.3 | homogentisate solanesyltransferase, chloroplastic | chloroplast envelope;integral component of membrane;homogentisate farnesyltransferase activity;homogentisate geranylgeranyltransferase activity;homogentisate solanesyltransferase activity;plastoquinone biosynthetic process;carotenoid biosynthetic process | ec:2.5.1 | |
| Phvul.007G265400.1 | prolycopene isomerase, chloroplastic | oxidoreductase activity;carotenoid isomerase activity;etioplast organization;carotenoid biosynthetic process;oxidation-reduction process | | |
| Phvul.007G265800.1 | E3 ubiquitin- ligase RHF2A | zinc ion binding;ligase activity;ubiquitin protein ligase activity;protein polyubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;proteasome-mediated ubiquitin-dependent protein catabolic process | | |
| Phvul.007G265800.2 | E3 ubiquitin- ligase RHF2A | zinc ion binding;ligase activity;ubiquitin protein ligase activity;protein polyubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;proteasome-mediated ubiquitin-dependent protein catabolic process | | |
| Phvul.007G266600.1 | EEIG1 EHBP1 amino-terminal domain | | | |

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| Phvul.007G267400.1 | ATP-dependent RNA helicase DHX36 isoform X1 | ATP-dependent RNA helicase activity;ATP binding;poly(A) RNA binding;RNA processing;N-terminal protein myristoylation | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.007G267500.1 | embryo defective 2016 | integral component of membrane | | |
| Phvul.007G268900.1 | YLS9-like | plasmodesma;integral component of membrane;anchored component of plasma membrane;signal transducer activity;defense response;signal transduction | | |
| Phvul.007G269100.1 | Chaperone 1 | protein metabolic process | | |
| Phvul.007G270000.1 | RRP5 homolog isoform X1 | nucleolus;small-subunit processome;RNA binding;mRNA processing | | |
| Phvul.007G270200.1 | serine arginine-rich splicing factor 4-like | nucleotide binding;nucleic acid binding;zinc ion binding | | |
| Phvul.007G270500.1 | pre-mRNA-processing factor 19-like | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.007G271500.1 | MATH domain-containing At5g43560-like isoform X1 | | | |
| Phvul.007G271700.1 | Ethylene receptor 2 | endoplasmic reticulum membrane;integral component of membrane;phosphorelay sensor kinase activity;ethylene receptor activity;ethylene binding;ethylene-activated signaling pathway;negative regulation of ethylene-activated signaling pathway;peptidyl-histidine phosphorylation;signal transduction by protein phosphorylation | ec:2.7.3;ec:2.7.13.3 | |
| Phvul.007G272000.1 | plant T32M21-140 | | | |
| Phvul.007G272200.1 | SWI SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 3-like 3 | chloroplast envelope;nucleic acid binding;helicase activity;ATP binding;zinc ion binding;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.007G272500.1 | CASP 5B3 | plasma membrane;integral component of membrane | | |
| Phvul.007G272600.1 | transcription factor bHLH104-like isoform X1 | protein dimerization activity | | |
| Phvul.007G273000.1 | Ethylene-responsive transcription factor 1B | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.007G273100.1 | Serine threonine-phosphatase PP1 | phosphoprotein phosphatase activity;metal ion binding;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.007G273800.1 | glycoside hydrolase family 1 | beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.007G274800.1 | NRT1 PTR FAMILY -like | integral component of membrane;transporter activity;transport | | |
| Phvul.007G275200.1 | RNA recognition motif | commitment complex;nuclear speck;U2-type prespliceosome;U2AF;nucleotide binding;poly-pyrimidine tract binding;pre-mRNA 3'-splice site binding;U2-type prespliceosome assembly | | |
| Phvul.007G276400.1 | Hemopexin D-tyrosyl-tRNA(Tyr) deacylase | integral component of membrane;metal ion binding | | |
| Phvul.007G276400.2 | Hemopexin D-tyrosyl-tRNA(Tyr) deacylase | integral component of membrane;metal ion binding | | |
| Phvul.007G277200.1 | hypothetical protein PHAVU_007G277200g | | | |

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| Phvul.007G277200.2 | hypothetical protein PHAVU_007G277200g | | | |
| Phvul.007G277200.3 | hypothetical protein PHAVU_007G277200g | | | |
| Phvul.007G277200.4 | hypothetical protein PHAVU_007G277200g | | | |
| Phvul.007G277200.5 | hypothetical protein PHAVU_007G277200g | | | |
| Phvul.007G277200.6 | hypothetical protein PHAVU_007G277200g | | | |
| Phvul.007G277200.7 | hypothetical protein PHAVU_007G277200g | | | |
| Phvul.007G277200.8 | hypothetical protein PHAVU_007G277200g | | | |
| Phvul.007G278800.1 | dentin sialophospho , | | | |
| Phvul.007G279400.1 | armadillo repeat-containing LFR | nucleus;mitotic recombination;embryo sac egg cell differentiation;flower development;leaf development | | |
| Phvul.007G280600.1 | sieve element occlusion | | | |
| Phvul.007G281000.1 | DNA-binding SMUBP-2 | chloroplast stroma;chloroplast envelope;DNA binding;ATP binding;hydrolase activity;chlorophyll catabolic process | | |
| Phvul.008G000200.1 | probable receptor kinase At2g39360 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.008G001800.1 | ras-related RABA5e | intracellular;membrane;GTPase activity;GTP binding;intracellular protein transport;nucleocytoplasmic transport;small GTPase mediated signal transduction;metabolic process | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.008G002200.1 | E3 ubiquitin- ligase LIN-1 | ubiquitin-protein transferase activity;zinc ion binding;amino acid binding;ligase activity;protein ubiquitination | | |
| Phvul.008G002300.1 | callose synthase 3-like | 1,3-beta-D-glucan synthase complex;integral component of membrane;1,3-beta-D-glucan synthase activity;(1->3)-beta-D-glucan biosynthetic process | ec:2.4.1.34-synthase;ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.008G002500.1 | serine threonine-kinase VRK1 | protein serine/threonine kinase activity;ATP binding;protein N-linked glycosylation;Wnt signaling pathway;peptidyl-serine phosphorylation | ec:2.7.11 | |
| Phvul.008G002600.1 | superkiller viralicidic activity 2-like 2 | nucleus;RNA binding;RNA helicase activity;ATP binding;mRNA splicing, via spliceosome;double-strand break repair via homologous recombination;karyogamy;RNA catabolic process;mRNA export from nucleus;protein import into nucleus;embryo sac egg cell differentiation;photomorphogenesis;regulation of flower development;maintenance of meristem identity;response to ionizing radiation;cullin deneddylation;protein ubiquitination;histone methylation;protein deubiquitination;production of siRNA involved in RNA interference;rRNA 3'-end processing;production of miRNAs involved in gene silencing by miRNA;post-translational protein modification;positive regulation of transcription, DNA-templated;cotyledon development;cell division | ec:3.6.1;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolism;Thiamine metabolism |

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| Phvul.008G003600.1 | transaldolase family | mitochondrion;chloroplast stroma;sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity;glycolytic process;pentose-phosphate shunt;aerobic respiration;lignin biosynthetic process;shikimate biosynthetic process | ec:2.2.1.2-dihydroxyacetonetransferase | Biosynthesis of antibiotics;Pentose phosphate pathway |
| Phvul.008G006600.1 | pentatricopeptide repeat-containing At1g20300, mitochondrial-like |  |  |  |
| Phvul.008G006700.1 | ribosomal RNA-processing | integral component of membrane;CURI complex;UTP-C complex;ribosomal small subunit assembly;rRNA processing;protein targeting to mitochondrion;embryo sac egg cell differentiation;vesicle-mediated transport |  |  |
| Phvul.008G007100.1 | DUF4378 domain |  |  |  |
| Phvul.008G008300.1 | lisH domain and HEAT repeat KIAA1468 |  |  |  |
| Phvul.008G008300.2 | lisH domain and HEAT repeat KIAA1468 |  |  |  |
| Phvul.008G008700.1 | hypothetical protein PHAVU_008G008700g |  |  |  |
| Phvul.008G011900.1 | probable mediator of RNA polymerase II transcription subunit 37c | ATP binding |  |  |
| Phvul.008G012400.1 | uncharacterized CRM domain-containing At3g25440, chloroplastic | RNA binding |  |  |
| Phvul.008G012400.2 | uncharacterized CRM domain-containing At3g25440, chloroplastic | RNA binding |  |  |
| Phvul.008G012400.3 | uncharacterized CRM domain-containing At3g25440, chloroplastic | RNA binding |  |  |
| Phvul.008G012400.4 | uncharacterized CRM domain-containing At3g25440, chloroplastic | RNA binding |  |  |
| Phvul.008G012500.1 | dof zinc finger -like | DNA binding;regulation of transcription, DNA-templated |  |  |
| Phvul.008G012500.2 | dof zinc finger -like | DNA binding;regulation of transcription, DNA-templated |  |  |
| Phvul.008G013700.1 | zinc-finger , |  |  |  |
| Phvul.008G014800.1 | F-box plant |  |  |  |
| Phvul.008G017200.1 | sphingosine-1-phosphate lyase | cytoplasm;sphinganine-1-phosphate aldolase activity;carboxy-lyase activity;pyridoxal phosphate binding;fatty acid beta-oxidation;ER to Golgi vesicle-mediated transport;toxin catabolic process;sphingolipid catabolic process;proteasome-mediated ubiquitin-dependent protein catabolic process;response to misfolded protein;proteasome core complex assembly | ec:4.1.2.27-aldolase | Sphingolipid metabolism |
| Phvul.008G017700.1 | bZIP transcription factor bZIP56 precursor | nucleic acid binding;hydrolase activity |  |  |
| Phvul.008G020800.1 | peptide nitrate transporter | integral component of membrane;transporter activity;transport |  |  |

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| Phvul.008G021200.1 | trichome birefringence-like 19 | Golgi apparatus;integral component of membrane;O-acetyltransferase activity;cell wall organization or biogenesis | ec:2.3.1 | |
| Phvul.008G021300.1 | hypothetical protein PHAVU_008G021300g | | | |
| Phvul.008G021500.1 | cell division cycle 27 homolog B-like isoform X1 | spindle;cell plate;mitotic recombination;regulation of mitotic cell cycle;embryo sac egg cell differentiation;response to auxin;leaf morphogenesis;vernalization response;root meristem specification;regulation of DNA endoreduplication;DNA endoreduplication;proteasome-mediated ubiquitin-dependent protein catabolic process;proteasome assembly;root cap development;cell division;regulation of unidimensional cell growth;response to misfolded protein | | |
| Phvul.008G022900.1 | ribosome biogenesis BRX1-like | nucleolus;RNA binding;ribosomal large subunit assembly | | |
| Phvul.008G022900.2 | ribosome biogenesis BRX1-like | nucleolus;RNA binding;ribosomal large subunit assembly | | |
| Phvul.008G023600.1 | hypothetical protein PHAVU_008G023600g, partial | | | |
| Phvul.008G026100.1 | UDP-glucosyltransferase family | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |
| Phvul.008G026100.2 | UDP-glucosyltransferase family | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |
| Phvul.008G026100.3 | UDP-glucosyltransferase family | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |
| Phvul.008G026700.1 | receptor kinase FERONIA | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G027300.1 | serine-threonine kinase isoform X1 | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G027700.1 | ultraviolet-B receptor UVR8 | ligase activity;metabolic process | | |
| Phvul.008G028100.1 | hyoscyamine 6-dioxygenase-like | metal ion binding;dioxygenase activity;oxidation-reduction process | | |
| Phvul.008G028100.2 | hyoscyamine 6-dioxygenase-like | metal ion binding;dioxygenase activity;oxidation-reduction process | | |
| Phvul.008G029500.1 | serine-threonine kinase isoform X1 | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G031100.1 | receptor kinase FERONIA | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G031200.1 | disease resistance At1g50180 | ADP binding;defense response | | |
| Phvul.008G031300.1 | Receptor kinase ANXUR2 | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G031500.1 | ubiquitin-like domain-containing CTD phosphatase 1 isoform X1 | phosphoprotein phosphatase activity;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.008G031500.2 | ubiquitin-like domain-containing CTD phosphatase 1 isoform X1 | phosphoprotein phosphatase activity;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.008G032100.1 | Anthocyanin 5-aromatic acyltransferase | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid |

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| | | | | biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.008G032100.2 | Anthocyanin 5-aromatic acyltransferase | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.008G032200.1 | Anthocyanin 5-aromatic acyltransferase | shikimate O-hydroxycinnamoyltransferase activity;metabolic process | ec:2.3.1;ec:2.3.1.133-O-hydroxycinnamoyltransferase | Stilbenoid, diarylheptanoid and gingerol biosynthesis;Flavonoid biosynthesis;Phenylpropanoid biosynthesis |
| Phvul.008G033900.1 | Magnesium transporter MRS2-3 | integral component of membrane;single-organism transport | | |
| Phvul.008G035600.1 | chaperone 3, chloroplastic | chloroplast stroma;hydrolase activity, hydrolyzing O-glycosyl compounds;ATP binding;carbohydrate metabolic process;response to heat;chloroplast organization;protein processing | | |
| Phvul.008G039500.1 | SNF1-related kinase catalytic subunit alpha KIN10 | nuclear ubiquitin ligase complex;cytoplasm;calmodulin-dependent protein kinase activity;cAMP-dependent protein kinase activity;ATP binding;developmental process involved in reproduction;glucose catabolic process;protein phosphorylation;protein glycosylation;detection of nutrient;abscisic acid-activated signaling pathway;vegetative phase change;sugar mediated signaling pathway;organ senescence;intracellular signal transduction;negative regulation of apoptotic process;primary root development | ec:2.7.11;ec:2.7.11.17;ec:2.7.11.11-protein kinase | mTOR signaling pathway |
| Phvul.008G039500.2 | SNF1-related kinase catalytic subunit alpha KIN10 | nuclear ubiquitin ligase complex;cytoplasm;calmodulin-dependent protein kinase activity;cAMP-dependent protein kinase activity;ATP binding;developmental process involved in reproduction;glucose catabolic process;protein phosphorylation;protein glycosylation;detection of nutrient;abscisic acid-activated signaling pathway;vegetative phase change;sugar mediated signaling pathway;organ senescence;intracellular signal transduction;negative regulation of apoptotic process;primary root development | ec:2.7.11;ec:2.7.11.17;ec:2.7.11.11-protein kinase | mTOR signaling pathway |
| Phvul.008G039600.1 | DUF1336 family | | | |
| Phvul.008G039600.2 | DUF1336 family | | | |
| Phvul.008G039600.3 | DUF1336 family | | | |
| Phvul.008G042700.1 | polyvinylalcohol dehydrogenase-like | | | |
| Phvul.008G044700.1 | LRR receptor-like kinase family | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G045100.1 | Homeobox-leucine zipper HAT3 | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.008G045400.1 | cationic amino acid transporter 9, chloroplastic-like | vacuolar membrane;integral component of membrane;L-amino acid transmembrane transporter activity;antiporter activity;fatty acid beta-oxidation;protein import into peroxisome matrix;L-alpha-amino acid transmembrane transport | | |
| Phvul.008G045400.2 | cationic amino acid transporter 9, chloroplastic-like | vacuolar membrane;integral component of membrane;L-amino acid transmembrane transporter activity;antiporter activity;fatty acid beta-oxidation;protein import into peroxisome matrix;L-alpha-amino acid transmembrane transport | | |

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| Phvul.008G047900.1 | subtilisin-like protease Glyma18g48580 | cell wall;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.008G048900.1 | cysteine protease ATG4B | cytosol;cysteine-type endopeptidase activity;autophagosome assembly;mitophagy;C-terminal protein lipidation;protein targeting to membrane;protein processing;nucleophagy;protein delipidation | ec:3.4;ec:3.4.22 | |
| Phvul.008G048900.2 | cysteine protease ATG4B | cytosol;cysteine-type endopeptidase activity;autophagosome assembly;mitophagy;C-terminal protein lipidation;protein targeting to membrane;protein processing;nucleophagy;protein delipidation | ec:3.4;ec:3.4.22 | |
| Phvul.008G049000.1 | Aldolase-type TIM barrel family isoform 1 | cytoplasm;3-deoxy-8-phosphooctulonate synthase activity;biosynthetic process | ec:2.5.1.55-synthase | Lipopolysaccharide biosynthesis |
| Phvul.008G049100.1 | Heterogeneous nuclear ribonucleo Q | viral nucleocapsid;intracellular ribonucleoprotein complex;nucleotide binding;nucleic acid binding | | |
| Phvul.008G049100.2 | Heterogeneous nuclear ribonucleo Q | viral nucleocapsid;intracellular ribonucleoprotein complex;nucleotide binding;nucleic acid binding | | |
| Phvul.008G050200.1 | acyl-coenzyme A thioesterase 9, mitochondrial | peroxisome;hydrolase activity;isomerase activity;metabolic process | | |
| Phvul.008G051800.1 | chromatin assembly factor 1 subunit FAS1 | nucleus;integral component of membrane;CAF-1 complex;DNA-dependent DNA replication;DNA recombination;nucleosome assembly;multicellular organismal development;single-organism cellular process;anatomical structure development;regulation of cell cycle;regulation of macromolecule metabolic process | | |
| Phvul.008G052000.1 | AP2-like ethylene-responsive transcription factor BBM2 | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;multicellular organismal development | | |
| Phvul.008G052100.1 | phospholipase A(1) LCAT3 | O-acyltransferase activity;lipid metabolic process | ec:2.3.1 | |
| Phvul.008G052900.1 | Membrane-associated VIPP1, chloroplastic | cytosol;plastid chromosome;chloroplast thylakoid membrane;chloroplast stroma;chloroplast envelope;thylakoid membrane organization;vesicle organization | | |
| Phvul.008G053300.1 | thioredoxin F-type, chloroplastic-like | chloroplast;protein disulfide oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor;sulfate assimilation;protein folding;glycerol ether metabolic process;cellular response to oxidative stress;cell redox homeostasis;oxidation-reduction process | | |
| Phvul.008G053400.1 | aspartic ase 2 | integral component of membrane;aspartic-type endopeptidase activity;transferase activity;proteolysis;protein catabolic process | ec:3.4.23 | |
| Phvul.008G054400.1 | photosystem I reaction center subunit XI, chloroplastic | chloroplast thylakoid membrane;photosystem I reaction center;chloroplast envelope;plastoglobule;integral component of membrane;rRNA processing;plastid organization;photosystem II assembly;cellular cation homeostasis;divalent metal ion transport | | |
| Phvul.008G056700.1 | subtilisin-like protease | cell wall;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.008G057500.1 | golgin candidate 3-like isoform X2 | | | |
| Phvul.008G059100.1 | hypothetical protein PHAVU_008G059100g | | | |
| Phvul.008G059100.2 | hypothetical protein | | | |

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| | PHAVU_008G059100g | | | |
| Phvul.008G060200.1 | RIC1 homolog | | | |
| Phvul.008G060300.1 | E3 ubiquitin- ligase RHA1B-like | nucleus;integral component of membrane;zinc ion binding;response to brassinosteroid;response to chitin;single-organism process | | |
| Phvul.008G060800.1 | AT-rich interactive domain-containing 1-like | DNA binding | | |
| Phvul.008G060800.2 | AT-rich interactive domain-containing 1-like | DNA binding | | |
| Phvul.008G060800.3 | AT-rich interactive domain-containing 1-like | DNA binding | | |
| Phvul.008G065600.1 | Beta-amylase 7 | nucleus;transcription factor activity, sequence-specific DNA binding;beta-amylase activity;palmitoyl-CoA hydrolase activity;polysaccharide catabolic process;regulation of transcription, DNA-templated;vernalization response;regulation of shoot system development | ec:3.2.1;ec:3.1.2.2-hydrolase;ec:3.1.2;ec:3.1.2.20;ec:3.2.1.2-saccharogen amylase | Biosynthesis of unsaturated fatty acids;Fatty acid elongationStarch and sucrose metabolism |
| Phvul.008G065800.1 | hypothetical protein PHAVU_008G065800g | membrane | | |
| Phvul.008G067800.1 | K(+) efflux antiporter 2, chloroplastic-like | integral component of membrane;zinc ion binding;solute:proton antiporter activity;potassium ion transport;hydrogen ion transmembrane transport | | |
| Phvul.008G067800.2 | K(+) efflux antiporter 2, chloroplastic-like | integral component of membrane;zinc ion binding;solute:proton antiporter activity;potassium ion transport;hydrogen ion transmembrane transport | | |
| Phvul.008G068800.1 | hypothetical protein PHAVU_008G068800g | mitochondrial respiratory chain complex I;ubiquitin-dependent protein catabolic process;photorespiration;response to misfolded protein;proteasome core complex assembly | | |
| Phvul.008G069600.1 | disease resistance RPP13 4 | | | |
| Phvul.008G069900.1 | SET domain | protein-lysine N-methyltransferase activity;[ribulose-bisphosphate carboxylase]-lysine N-methyltransferase activity;embryo sac egg cell differentiation;peptidyl-lysine monomethylation | ec:2.1.1;ec:2.1.1.127 | |
| Phvul.008G071700.1 | vacuolar 8 | ligase activity;metabolic process | | |
| Phvul.008G071700.2 | ARM repeat superfamily isoform 1 | ligase activity;metabolic process | | |
| Phvul.008G071700.3 | ARM repeat superfamily isoform 1 | ligase activity;metabolic process | | |
| Phvul.008G075100.1 | ankyrin repeat and zinc finger domain-containing 1 | integral component of membrane;Cdc48p-Npl4p-Vms1p AAA ATPase complex;thiol-dependent ubiquitin-specific protease activity;metal ion binding;ER-associated ubiquitin-dependent protein catabolic process;nucleus-associated proteasomal ubiquitin-dependent protein catabolic process;mitochondria-associated ubiquitin-dependent protein catabolic process | ec:3.4;ec:3.4.19.12 | |
| Phvul.008G075200.1 | smad FHA domain | transcription factor activity, sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.008G075400.1 | 4-hydroxy-tetrahydrodipicolinate synthase, chloroplastic | chloroplast;4-hydroxy-tetrahydrodipicolinate synthase;lysine biosynthetic process via diaminopimelate;diaminopimelate biosynthetic process | ec:4.3.3.7-synthase | Biosynthesis of antibiotics;Lysine biosynthesis;Monobactam biosynthesis |
| Phvul.008G075600.1 | brefeldin A-inhibited guanine | trans-Golgi network;cytosol;ARF guanyl-nucleotide exchange factor activity;vesicle-mediated transport;regulation of ARF protein | | |

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| | nucleotide-exchange 2 | signal transduction;positive regulation of GTPase activity | | |
| Phvul.008G077600.1 | cysteine-rich receptor-kinase | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G079500.1 | zinc transporter At3g08650 | Golgi membrane;trans-Golgi network;integral component of membrane;DNA-directed DNA polymerase activity;zinc ion transmembrane transporter activity;zinc II ion transmembrane transport;DNA biosynthetic process | ec:2.7.7.7-DNA polymerase | Purine metabolism;Pyrimidine metabolism |
| Phvul.008G079900.1 | acetyltransferase NSI | chloroplast;protein acetyltransferase complex;peptide alpha-N-acetyltransferase activity;pentose-phosphate shunt;N-terminal protein amino acid acetylation | ec:2.3.1.88;ec:2.3.1 | |
| Phvul.008G080300.1 | 4-hydroxybenzoate polyprenyltransferase, mitochondrial | integral component of membrane;4-hydroxybenzoate decaprenyltransferase activity;4-hydroxybenzoate nonaprenyltransferase activity;ubiquinone biosynthetic process | ec:2.5.1.39-polyprenyltransferase;ec:2.5.1 | Ubiquinone and other terpenoid-quinone biosynthesis |
| Phvul.008G080600.1 | WEB family At1g65010, chloroplastic isoform X1 | | | |
| Phvul.008G081700.1 | phospholipid-transporting ATPase 1-like | plasma membrane;integral component of membrane;magnesium ion binding;phospholipid-translocating ATPase activity;ATP binding;metabolic process;phospholipid translocation | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.6.3.1 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G081700.2 | phospholipid-transporting ATPase 1-like | plasma membrane;integral component of membrane;magnesium ion binding;phospholipid-translocating ATPase activity;ATP binding;metabolic process;phospholipid translocation | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.6.3.1 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G082200.1 | vacuolar-sorting receptor 1-like | integral component of membrane;calcium ion binding | | |
| Phvul.008G082600.1 | transmembrane , | integral component of membrane | | |
| Phvul.008G083000.1 | probable receptor kinase At3g55450 | protein kinase activity;ATP binding;protein phosphorylation;autophagy | | |
| Phvul.008G083900.1 | transmembrane , | plasma membrane;integral component of membrane;helicase activity;response to oxidative stress;metabolic process;pollen development | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.008G084300.1 | adenine guanine permease AZG1-like | integral component of membrane;purine nucleobase transmembrane transporter activity;adenine transport;guanine transport;purine nucleobase transmembrane transport | | |
| Phvul.008G086000.1 | WW domain , | | | |
| Phvul.008G086300.1 | transport SFT2 | integral component of membrane;vesicle-mediated transport | | |
| Phvul.008G089400.1 | tubby C 2 | | | |
| Phvul.008G089400.2 | tubby C 2 | | | |
| Phvul.008G093400.1 | trichome birefringence-like 34 | Golgi apparatus;integral component of membrane;O-acetyltransferase activity;glucuronoxylan metabolic process;xylan biosynthetic process | ec:2.3.1 | |
| Phvul.008G094500.1 | lectin-domain containing receptor kinase -like | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;carbohydrate binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.008G094700.1 | ethylene-overproduction 1-like | protein binding, bridging;protein N-linked glycosylation;hormone-mediated signaling pathway;sugar mediated signaling pathway;regulation of ethylene biosynthetic process;cellular response to phosphate starvation;stem cell division;proteasome-mediated ubiquitin-dependent protein catabolic process;cotyledon | | |

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| | | development;regulation of post-embryonic root development | | |
| Phvul.008G095000.1 | BAG family molecular chaperone regulator 4 | chaperone binding | | |
| Phvul.008G095300.1 | receptor 12 | membrane | | |
| Phvul.008G097300.1 | beta-glucosidase 11-like | beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.008G098000.1 | lethal(2) giant larvae homolog SRO77-like | cytoplasm;plasma membrane;integral component of membrane;GTPase activator activity;Rab GTPase binding;syntaxin binding;vesicle-mediated transport;regulation of exocytosis;positive regulation of GTPase activity | | |
| Phvul.008G099500.1 | U-box domain-containing 13-like isoform X2 | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.008G100700.1 | respiratory burst oxidase homolog H isoform X1 | integral component of membrane;peroxidase activity;calcium ion binding;NAD(P)H oxidase activity;oxidation-reduction process;cellular oxidant detoxification | ec:1.6.3.1;ec:1.11.1.7-lactoperoxidase | Phenylpropanoid biosynthesis |
| Phvul.008G104000.1 | testis-expressed sequence 10 | | | |
| Phvul.008G104000.2 | testis-expressed sequence 10 | | | |
| Phvul.008G104600.1 | probable envelope ADP,ATP carrier , chloroplastic | integral component of membrane;structural constituent of ribosome;translation;transmembrane transport | | |
| Phvul.008G105900.1 | pentatricopeptide repeat-containing At4g28010 | microtubule-severing ATPase activity;metabolic process;petal formation;sepal formation | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G105900.2 | pentatricopeptide repeat-containing At4g28010 | microtubule-severing ATPase activity;metabolic process;petal formation;sepal formation | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G105900.3 | pentatricopeptide repeat-containing At4g28010 | microtubule-severing ATPase activity;metabolic process;petal formation;sepal formation | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.4.3;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G106300.1 | auxin transporter 2 | plasma membrane;integral component of membrane;amino acid transmembrane transporter activity;symporter activity;amino acid transmembrane transport;auxin-activated signaling pathway | | |
| Phvul.008G107600.1 | AT-rich interactive domain-containing 1-like | DNA binding | | |
| Phvul.008G108400.1 | LRR receptor-like serine threonine-kinase GSO1 | integral component of membrane;transferase activity | | |
| Phvul.008G108500.1 | LRR receptor-like serine threonine-kinase GSO1 | | | |
| Phvul.008G109000.1 | LRR receptor-like serine threonine-kinase GSO1 | | | |
| Phvul.008G111500.1 | L-type lectin-domain containing receptor kinase -like | integral component of membrane;kinase activity;carbohydrate binding;phosphorylation | | |
| Phvul.008G113600.1 | glutathione S-transferase | cytoplasm;glutathione transferase activity;glutathione metabolic process;toxin catabolic process | ec:2.5.1.18-transferase | Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Glutathione metabolism |
| Phvul.008G114800.1 | DUF674 family | integral component of membrane | | |

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| Phvul.008G115500.1 | wall-associated receptor kinase-like 20 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;polysaccharide binding;protein phosphorylation;regulation of cellular process | ec:2.7.11 | |
| Phvul.008G115700.1 | bHLH transcription factor | protein dimerization activity | | |
| Phvul.008G119700.1 | scarecrow 9 | transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.008G120800.1 | hypothetical protein PHAVU_008G120800g | integral component of membrane | | |
| Phvul.008G121100.1 | hypothetical protein PHAVU_008G121100g | integral component of membrane | | |
| Phvul.008G122400.1 | kinase TMKL1 | plasma membrane;plasmodesma;integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation;determination of bilateral symmetry;polarity specification of adaxial/abaxial axis;meristem initiation;regulation of meristem growth | | |
| Phvul.008G122500.1 | RINT1 MAG2 | cytosol;extrinsic component of endoplasmic reticulum membrane;protein targeting to vacuole;ER to Golgi vesicle-mediated transport | | |
| Phvul.008G123700.1 | SULFUR DEFICIENCY-INDUCED 1-like | regulation of sulfur utilization | | |
| Phvul.008G125300.1 | root UVB sensitive 4 isoform X2 | integral component of membrane | | |
| Phvul.008G125300.2 | root UVB sensitive 4 isoform X2 | integral component of membrane | | |
| Phvul.008G125300.3 | UPF0420 C16orf58 | integral component of membrane | | |
| Phvul.008G125300.4 | UPF0420 C16orf58 | integral component of membrane | | |
| Phvul.008G125400.1 | Transcriptional corepressor LEUNIG | membrane coat;structural molecule activity;intracellular protein transport;vesicle-mediated transport | | |
| Phvul.008G127100.1 | G-type lectin S-receptor-like Serine Threonine-kinase | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;carbohydrate binding;ubiquitin protein ligase binding;protein phosphorylation;innate immune response;recognition of pollen | ec:2.7.11 | |
| Phvul.008G130900.1 | hypothetical protein PHAVU_008G130900g | | | |
| Phvul.008G132200.1 | galacturonosyltransferase 8 | Golgi membrane;integral component of membrane;polygalacturonate 4-alpha-galacturonosyltransferase activity;pectin biosynthetic process;cell wall organization | ec:2.4.1.43-4-alpha-galacturonosyltransferase | Amino sugar and nucleotide sugar metabolism;Starch and sucrose metabolism |
| Phvul.008G133300.1 | hypothetical protein PHAVU_008G1333001g, partial | oxidoreductase activity;organic cyclic compound binding;heterocyclic compound binding;response to stimulus | | |
| Phvul.008G134400.1 | U-box domain-containing 9 | ubiquitin-protein transferase activity;ligase activity;transmembrane receptor protein serine/threonine kinase binding;protein ubiquitination;protein autophosphorylation;cellular response to abscisic acid stimulus | | |
| Phvul.008G135500.1 | Ubiquinone biosynthesis monooxygenase COQ6 | integral component of membrane;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;FAD binding;ubiquinone biosynthetic process;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione;secondary | ec:1.14.13 | |

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| | | metabolite biosynthetic process;oxidation-reduction process | | |
| Phvul.008G135500.2 | Ubiquinone biosynthesis monooxygenase COQ6 | integral component of membrane;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;FAD binding;ubiquinone biosynthetic process;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione;secondary metabolite biosynthetic process;oxidation-reduction process | ec:1.14.13 | |
| Phvul.008G136000.1 | embryo defective 2752 | integral component of membrane | | |
| Phvul.008G137100.1 | lipid-transfer DIR1 | integral component of membrane | | |
| Phvul.008G137400.1 | SOS response-associated peptidase | | | |
| Phvul.008G137400.2 | SOS response-associated peptidase | | | |
| Phvul.008G139000.1 | Eukaryotic translation initiation factor 4G | translation initiation factor activity;translational initiation | | |
| Phvul.008G139000.2 | Eukaryotic translation initiation factor 4G | translation initiation factor activity;translational initiation | | |
| Phvul.008G142800.1 | hypothetical protein PHAVU_008G142800g | integral component of membrane | | |
| Phvul.008G143400.1 | scarecrow 6 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.008G143400.2 | scarecrow 6 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.008G144900.1 | reticulocyte binding 2 homolog b isoform X4 | | | |
| Phvul.008G145200.1 | guanine nucleotide exchange factor, | intracellular part;cytoskeleton organization;single-multicellular organism process;single-organism developmental process;meristem development;regulation of biological process;organic substance metabolic process;single-organism organelle organization | | |
| Phvul.008G147900.1 | sieve element occlusion | | | |
| Phvul.008G149500.1 | E3 ubiquitin- ligase mib1 | transferase activity;ligase activity;metabolic process | | |
| Phvul.008G150100.1 | transcription factor GTE8 | | | |
| Phvul.008G150100.2 | transcription factor GTE8 | | | |
| Phvul.008G151700.1 | 10 kDa chaperonin | cytoplasm;protein folding | | |
| Phvul.008G152400.1 | RING-H2 finger ATL46-like | integral component of membrane;zinc ion binding | | |
| Phvul.008G152400.2 | RING-H2 finger ATL46-like | integral component of membrane;zinc ion binding | | |
| Phvul.008G153100.1 | GPI ethanolamine phosphate transferase 1 | endoplasmic reticulum membrane;integral component of membrane;sulfuric ester hydrolase activity;mannose-ethanolamine phosphotransferase activity;GPI anchor biosynthetic process | | |
| Phvul.008G155000.1 | cytochrome P450 family 71 | integral component of membrane;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;secondary metabolite biosynthetic process;oxidation-reduction process | ec:1.14.13 | |
| Phvul.008G155100.1 | CASP 4A1 | cytosol;plasma membrane;integral component of membrane;NADH dehydrogenase activity;iron-sulfur cluster binding;iron-sulfur cluster assembly | ec:1.6.99.3-dehydrogenase | Oxidative phosphorylation |

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| Phvul.008G156800.1 | zinc ion-binding | | | |
| Phvul.008G162300.1 | esterase-like isoform X1 | hydrolase activity, acting on ester bonds;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.008G162300.2 | esterase-like isoform X1 | hydrolase activity, acting on ester bonds;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.008G163100.1 | long chain acyl-synthetase 9, chloroplastic-like | membrane;ligase activity;metabolic process | | |
| Phvul.008G165800.1 | seleno K | integral component of membrane;response to stress;response to abiotic stimulus;regulation of biological process;cellular response to stimulus | | |
| Phvul.008G166800.1 | OSBP(oxysterol-binding )-related 1C | | | |
| Phvul.008G167400.1 | ABC transporter C family member 3-like | integral component of membrane;ATP binding;ATPase activity, coupled to transmembrane movement of substances;metabolic process;transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G168300.1 | mediator of RNA polymerase II transcription subunit 1-like | | | |
| Phvul.008G168300.2 | mediator of RNA polymerase II transcription subunit 1-like | | | |
| Phvul.008G169000.1 | transcription factor TGA3-like isoform X1 | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.008G172500.1 | TPR repeat-containing thioredoxin TTL1 | cell;cell redox homeostasis | | |
| Phvul.008G173500.1 | synaptonemal complex 1-like | synaptonemal complex;reciprocal meiotic recombination | | |
| Phvul.008G173500.2 | synaptonemal complex 1-like | synaptonemal complex;reciprocal meiotic recombination | | |
| Phvul.008G173500.3 | synaptonemal complex 1-like | synaptonemal complex;reciprocal meiotic recombination | | |
| Phvul.008G173500.4 | synaptonemal complex 1-like | synaptonemal complex;reciprocal meiotic recombination | | |
| Phvul.008G173500.5 | synaptonemal complex 1-like | synaptonemal complex;reciprocal meiotic recombination | | |
| Phvul.008G174000.1 | probable pectin methyltransferase QUA2 | endosome;trans-Golgi network;integral component of membrane;S-adenosylmethionine-dependent methyltransferase activity;response to cytokinin;homogalacturonan biosynthetic process;methylation;root development;shoot system development | | |
| Phvul.008G175300.1 | 7-deoxyloganetin glucosyltransferase-like | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1 | |
| Phvul.008G175700.1 | EXORDIUM-like | | | |
| Phvul.008G176300.1 | serine threonine-kinase SAPK2-like | ribosome;structural constituent of ribosome;protein serine/threonine kinase activity;ATP binding;translation;protein phosphorylation;intracellular signal transduction | ec:2.7.11 | |

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| Phvul.008G176700.1 | Thylakoid lumenal 29 kDa , chloroplastic | nucleus;chloroplast thylakoid membrane;thylakoid lumen;L-ascorbate peroxidase activity;heme binding;pentose-phosphate shunt;rRNA processing;response to oxidative stress;response to blue light;stomatal complex morphogenesis;response to red light;response to far red light;chlorophyll biosynthetic process;starch biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;photosynthesis, light reaction;glucosinolate metabolic process;oxidation-reduction process;cellular oxidant detoxification | ec:1.11.1.11-peroxidase;ec:1.11.1.7-lactoperoxidase | Glutathione metabolism;Ascorbate and aldarate metabolismPhenylpropanoid biosynthesis |
| Phvul.008G176700.2 | thylakoid lumenal 29 kDa , chloroplastic isoform X1 | nucleus;chloroplast thylakoid membrane;thylakoid lumen;L-ascorbate peroxidase activity;heme binding;pentose-phosphate shunt;rRNA processing;response to oxidative stress;response to blue light;stomatal complex morphogenesis;response to red light;response to far red light;chlorophyll biosynthetic process;starch biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;photosynthesis, light reaction;glucosinolate metabolic process;oxidation-reduction process;cellular oxidant detoxification | ec:1.11.1.11-peroxidase;ec:1.11.1.7-lactoperoxidase | Glutathione metabolism;Ascorbate and aldarate metabolismPhenylpropanoid biosynthesis |
| Phvul.008G176800.1 | DUF246 domain-containing | cytoplasm;integral component of membrane | | |
| Phvul.008G177300.1 | phage capsid scaffolding (GPO) serine peptidase | | | |
| Phvul.008G178500.1 | phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic | chloroplast stroma;phosphoribosylaminoimidazole carboxylase activity;phosphoribosylaminoimidazolesuccinocarboxamide synthase activity;ATP binding;'de novo' IMP biosynthetic process;toxin catabolic process;response to auxin;adenine biosynthetic process | ec:6.3.2.6-synthase;ec:4.1.1.21-carboxylase | Purine metabolism;Biosynthesis of antibioticsPurine metabolism |
| Phvul.008G180300.1 | plant MNA5-17 | | | |
| Phvul.008G181200.1 | clathrin-adaptor medium chain AP-2 | cytosol;clathrin adaptor complex;protein targeting to vacuole;vesicle-mediated transport | | |
| Phvul.008G181800.1 | kinesin FRA1 | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G183800.1 | hypothetical protein PHAVU_008G183800g, partial | | | |
| Phvul.008G184500.2 | glycine-rich domain-containing 2-like | | | |
| Phvul.008G185000.1 | zinc finger (C3HC4-type RING finger) family | zinc ion binding | | |
| Phvul.008G185400.1 | integrase-type DNA-binding superfamily , partial | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;tissue development;floral organ development | | |
| Phvul.008G186500.1 | DUF3133 family | | | |
| Phvul.008G186700.1 | serine threonine-kinase 2 19-like | cytoplasm;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;intracellular signal transduction | ec:2.7.11 | |
| Phvul.008G186700.2 | serine threonine-kinase 2 19-like | cytoplasm;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;intracellular signal transduction | ec:2.7.11 | |

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| Phvul.008G187700.1 | zinc finger with UFM1-specific peptidase domain | integral component of membrane | | |
| Phvul.008G187700.2 | zinc finger with UFM1-specific peptidase domain | membrane | | |
| Phvul.008G187700.3 | zinc finger with UFM1-specific peptidase domain | integral component of membrane | | |
| Phvul.008G188400.1 | DNA mismatch repair MUTS family | endonuclease activity;ATP binding;ATPase activity;mismatched DNA binding;mismatch repair;negative regulation of DNA recombination;nucleic acid phosphodiester bond hydrolysis | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.1;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G190700.1 | probable galacturonosyltransferase 15 | Golgi membrane;integral component of membrane;polygalacturonate 4-alpha-galacturonosyltransferase activity;pectin biosynthetic process;cell wall organization | ec:2.4.1.43-4-alpha-galacturonosyltransferase | Amino sugar and nucleotide sugar metabolism;Starch and sucrose metabolism |
| Phvul.008G190700.2 | probable galacturonosyltransferase 15 | Golgi membrane;integral component of membrane;polygalacturonate 4-alpha-galacturonosyltransferase activity;pectin biosynthetic process;cell wall organization | ec:2.4.1.43-4-alpha-galacturonosyltransferase | Amino sugar and nucleotide sugar metabolism;Starch and sucrose metabolism |
| Phvul.008G191200.1 | neurofilament medium polypeptide-like | | | |
| Phvul.008G191200.2 | neurofilament medium polypeptide-like | | | |
| Phvul.008G192100.1 | pumilio homolog 2-like | RNA binding | | |
| Phvul.008G193300.1 | conserved oligomeric Golgi complex subunit 5-like | cytosol;Golgi transport complex;intra-Golgi vesicle-mediated transport | | |
| Phvul.008G195100.1 | TMV resistance N-like | ADP binding;defense response;signal transduction | | |
| Phvul.008G195300.1 | TMV resistance N | ADP binding;defense response;signal transduction | | |
| Phvul.008G195300.2 | TMV resistance N | ADP binding;defense response;signal transduction | | |
| Phvul.008G195900.1 | nonexpressor of pathogenesis-related 1 | | | |
| Phvul.008G196100.1 | Transmembrane 56-B | integral component of membrane | | |
| Phvul.008G196300.1 | ATP-dependent RNA helicase, | ATP-dependent RNA helicase activity;ATP binding;poly(A) RNA binding;RNA processing | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G197200.1 | pentatricopeptide repeat-containing At5g16860 | zinc ion binding | | |
| Phvul.008G197300.1 | hypothetical protein PHAVU_008G197300g | | | |
| Phvul.008G197400.1 | pentatricopeptide repeat-containing At1g74580 | | | |
| Phvul.008G197500.1 | pentatricopeptide repeat-containing At5g64320, mitochondrial | integral component of membrane;thymidine kinase activity;deoxyribonucleoside monophosphate biosynthetic process | ec:2.7.1.21-kinase;ec:2.7.1.145 | Drug metabolism - other enzymes;Pyrimidine metabolism |
| Phvul.008G197600.1 | auxin response factor 6-like | nucleus;DNA binding;lipid binding;transcription, DNA-templated;regulation of transcription, DNA-templated;lipid transport;auxin-activated signaling pathway | | |
| Phvul.008G199700.1 | DEAD-box ATP-dependent RNA helicase 53-like | nucleic acid binding;ATP-dependent RNA helicase activity;ATP binding;RNA secondary structure unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G199800.1 | CHROMATIN REMODELING 5 | nucleus;DNA binding;ATP binding;ATP-dependent helicase activity;metabolic process | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphata | Purine metabolismPurine |

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|  |  |  | se;ec:3.6.1.15-phosphatase | metabolism;Thiamine metabolism |
| Phvul.008G200100.1 | hypothetical protein PHAVU_008G200100g |  |  |  |
| Phvul.008G200100.2 | hypothetical protein PHAVU_008G200100g |  |  |  |
| Phvul.008G200200.1 | GTP-binding At3g49725, chloroplastic | cytoplasm;GTP binding;ribosome binding |  |  |
| Phvul.008G200300.1 | E3 ubiquitin- ligase HERC1 | ligase activity;metal ion binding;metabolic process |  |  |
| Phvul.008G200400.1 | homeobox leucine zipper | nucleus;DNA binding |  |  |
| Phvul.008G200800.1 | calcium-dependent lipid-binding ( domain) family |  |  |  |
| Phvul.008G200800.2 | calcium-dependent lipid-binding ( domain) family |  |  |  |
| Phvul.008G203700.1 | Nuclear control of ATPase 2 | mitochondrial outer membrane;integral component of membrane;protein complex;cell adhesion;organ morphogenesis;trichome morphogenesis;vegetative to reproductive phase transition of meristem;protein desumoylation;galactolipid biosynthetic process;regulation of chromosome organization;actin nucleation;root hair cell differentiation;hydrogen peroxide biosynthetic process;cell wall organization |  |  |
| Phvul.008G205100.1 | urease accessory F isoform X2 | nickel cation binding;heat shock protein binding;unfolded protein binding;phosphatidylinositol biosynthetic process;nitrogen compound metabolic process;positive regulation of metalloenzyme activity |  |  |
| Phvul.008G205100.2 | urease accessory F isoform X2 | nickel cation binding;heat shock protein binding;unfolded protein binding;phosphatidylinositol biosynthetic process;nitrogen compound metabolic process;positive regulation of metalloenzyme activity |  |  |
| Phvul.008G205700.2 | CBL-interacting serine threonine-kinase 3 | cytoplasm;integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;intracellular signal transduction | ec:2.7.11 |  |
| Phvul.008G206300.1 | la-related 1A |  |  |  |
| Phvul.008G206600.1 | argonaute 4-like | translation initiation factor activity;translational initiation |  |  |
| Phvul.008G206600.2 | argonaute 4-like | translation initiation factor activity;translational initiation |  |  |
| Phvul.008G210200.1 | serine threonine-kinase TOUSLED-like isoform X1 | chromosome;chloroplast;protein kinase activity;ATP binding;identical protein binding;protein phosphorylation;chromosome organization |  |  |
| Phvul.008G210200.2 | serine threonine-kinase TOUSLED-like isoform X2 | chloroplast;protein kinase activity;ATP binding;identical protein binding;protein phosphorylation |  |  |
| Phvul.008G210700.1 | CSC1 At3g21620 | integral component of membrane;4-alpha-glucanotransferase activity;glycogen metabolic process | ec:2.4.1.25-disproportionating enzyme | Starch and sucrose metabolism |
| Phvul.008G211500.1 | lycopene beta epsilon cyclase | chloroplast;oxidoreductase activity;oxidation-reduction process |  |  |
| Phvul.008G211600.1 | plastid transcriptionally active |  |  |  |
| Phvul.008G212400.1 | pentatricopeptide repeat-containing At3g02650, mitochondrial |  |  |  |

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| Phvul.008G212800.1 | nucleobase-ascorbate transporter 1 | plasmodesma;integral component of membrane;transporter activity;transmembrane transport | | |
| Phvul.008G212800.2 | Nucleobase-ascorbate transporter 1 | integral component of membrane;transporter activity;transmembrane transport | | |
| Phvul.008G213300.1 | subtilisin-like protease Glyma18g48580 | cell wall;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.008G213300.2 | subtilisin-like protease Glyma18g48580 | cell wall;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.008G214800.1 | E3 ubiquitin- ligase BRE1-like 2 isoform X1 | zinc ion binding;ligase activity;protein homodimerization activity;regulation of mitotic cell cycle;leaf morphogenesis;seed dormancy process;vegetative to reproductive phase transition of meristem;histone monoubiquitination;histone H2B ubiquitination;post-translational protein modification;positive regulation of transcription, DNA-templated | | |
| Phvul.008G215200.1 | centromere kinetochore zw10 homolog | nucleus;cytoplasm;RZZ complex;ER to Golgi vesicle-mediated transport;chromosome segregation;mitotic nuclear division;mitotic spindle assembly checkpoint | | |
| Phvul.008G215200.2 | centromere kinetochore zw10 homolog | nucleus;cytoplasm;RZZ complex;ER to Golgi vesicle-mediated transport;chromosome segregation;mitotic nuclear division;mitotic spindle assembly checkpoint | | |
| Phvul.008G215200.3 | centromere kinetochore zw10 homolog | nucleus;cytoplasm;RZZ complex;ER to Golgi vesicle-mediated transport;chromosome segregation;mitotic nuclear division;mitotic spindle assembly checkpoint | | |
| Phvul.008G215200.4 | centromere kinetochore zw10 homolog | nucleus;cytoplasm;RZZ complex;ER to Golgi vesicle-mediated transport;chromosome segregation;mitotic nuclear division;mitotic spindle assembly checkpoint | | |
| Phvul.008G217900.1 | SIEVE ELEMENT OCCLUSION C | | | |
| Phvul.008G219800.1 | Neuronal PAS domain-containing 4 | | | |
| Phvul.008G220100.1 | receptor-like kinase | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G221400.1 | peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A | vacuole | | |
| Phvul.008G221900.1 | probable inactive receptor kinase At3g56050 | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G222800.1 | clathrin heavy chain 2 | clathrin coat of trans-Golgi network vesicle;clathrin coat of coated pit;structural molecule activity;intracellular protein transport;vesicle-mediated transport | | |
| Phvul.008G223400.1 | zinc finger CCCH domain-containing 29 | metal ion binding | | |
| Phvul.008G224800.1 | ATP-binding , | ATP binding;vernalization response;anthocyanin accumulation in tissues in response to UV light;carpel development | | |
| Phvul.008G228400.2 | Rop guanine nucleotide exchange factor 1 | Rho guanyl-nucleotide exchange factor activity;positive regulation of GTPase activity | | |
| Phvul.008G228700.1 | cucumisin-like | cell wall;integral component of membrane;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.008G228700.2 | cucumisin-like | cell wall;integral component of membrane;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.008G230700.1 | Regulator of chromosome condensation | kinase activity;ligase activity;phosphorylation | | |

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| | repeat-containing isoform 1 | | | |
| Phvul.008G232400.1 | AP3-complex subunit beta-A | AP-3 adaptor complex;intracellular protein transport;Golgi to vacuole transport;regulation of intracellular pH;lytic vacuole organization | | |
| Phvul.008G233500.1 | AAR2 homolog | spliceosomal tri-snRNP complex assembly;mitotic cell cycle;protein folding;response to heat;response to high light intensity;response to hydrogen peroxide | | |
| Phvul.008G233900.1 | plastid movement impaired | | | |
| Phvul.008G234100.1 | transmembrane , | integral component of membrane | | |
| Phvul.008G234600.1 | serine threonine-kinase CDL1-like | non-membrane spanning protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.10;ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.008G234800.1 | probable fructokinase-4 | chloroplast stroma;ribokinase activity;fructokinase activity;D-ribose metabolic process;cysteine biosynthetic process;carbohydrate phosphorylation | ec:2.7.1.15-deoxyribokinase;ec:2.7.1.4-fructokinase (phosphorylating);ec:2.7.1.1-hexokinase type IV glucokinase | Pentose phosphate pathwayAmino sugar and nucleotide sugar metabolism;Starch and sucrose metabolism;Fructose and mannose metabolismButirosin and neomycin biosynthesis;Biosynthesis of antibiotics;Streptomycin biosynthesis;Amino sugar and nucleotide sugar metabolism;Glycolysis / Gluconeogenesis;Starch and sucrose metabolism;Galactose metabolism;Fructose and mannose metabolism |
| Phvul.008G235900.1 | nucleolar complex 4 homolog | nucleolus;Noc4p-Nop14p complex;small-subunit processome;rRNA processing;single-organism process | | |
| Phvul.008G238100.1 | potassium channel SKOR | integral component of membrane;voltage-gated potassium channel activity;regulation of membrane potential;potassium ion transmembrane transport | | |
| Phvul.008G241300.1 | sucrose synthase | sucrose synthase activity;response to hypoxia;sucrose metabolic process;galactolipid biosynthetic process;callose deposition in phloem sieve plate | ec:2.4.1.13-synthase;ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.008G245200.1 | probable disease resistance At4g27220 | integral component of membrane;ATP binding;ADP binding;defense response | | |
| Phvul.008G245600.1 | probable LRR receptor-like serine threonine- kinase At1g06840 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.008G245600.2 | probable LRR receptor-like serine threonine- kinase At1g06840 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.008G245900.1 | probable inactive receptor kinase At5g58300 | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G245900.2 | probable inactive receptor kinase At5g58300 | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.008G247700.1 | extra-large guanine nucleotide-binding 3-like | zinc ion binding | | |
| Phvul.008G248900.1 | CBL-interacting serine threonine-kinase 10 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;signal transduction | ec:2.7.11 | |

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| Phvul.008G251900.1 | glycolipid transfer (GLTP) family | cytoplasm;integral component of membrane;glycolipid transporter activity;glycolipid binding;glycolipid transport |  |  |
| Phvul.008G252300.1 | exocyst complex component EXO70B1-like | exocyst;integral component of membrane;exocytosis |  |  |
| Phvul.008G252400.1 | exocyst complex component EXO70B1-like | exocyst;integral component of membrane;exocytosis |  |  |
| Phvul.008G252700.1 | hypothetical protein PHAVU_008G252700g | integral component of membrane |  |  |
| Phvul.008G253000.1 | probable phosphatase 2C 60 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.008G255500.1 | exocyst subunit EXO70 family | exocyst;exocytosis |  |  |
| Phvul.008G256100.1 | hypothetical protein PHAVU_008G256100g | integral component of membrane |  |  |
| Phvul.008G256800.1 | UDP-glycosyltransferase 87A1 | intracellular membrane-bounded organelle;indole-3-acetate beta-glucosyltransferase activity;limonoid glucosyltransferase activity;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1;ec:2.4.1.210;ec:2.4.1.121 |  |
| Phvul.008G256800.2 | UDP-glycosyltransferase 87A1 | intracellular membrane-bounded organelle;indole-3-acetate beta-glucosyltransferase activity;limonoid glucosyltransferase activity;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1;ec:2.4.1.210;ec:2.4.1.121 |  |
| Phvul.008G257100.2 | exocyst complex component EXO70B1-like | exocyst;integral component of membrane;exocytosis |  |  |
| Phvul.008G257400.1 | LOB domain-containing 12-like | carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity;metabolic process | ec:6.3.5.5-synthase (glutamine-hydrolysing) | Alanine, aspartate and glutamate metabolism;Pyrimidine metabolism |
| Phvul.008G258300.1 | Nop53 (60S ribosomal biogenesis) | intracellular;mRNA export from nucleus;protein import into nucleus |  |  |
| Phvul.008G258400.1 | Serine Threonine-kinase DDB-G0267514 , | intracellular;MAP kinase kinase kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.11.25;ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.008G258500.1 | ubiquitin-activating enzyme E1 1 | nucleus;cytosol;integral component of membrane;ubiquitin activating enzyme activity;ubiquitin-protein transferase activity;ATP binding;protein ubiquitination;modification-dependent protein catabolic process |  |  |
| Phvul.008G258500.2 | ubiquitin-activating enzyme E1 1 | nucleus;cytosol;integral component of membrane;ubiquitin activating enzyme activity;ubiquitin-protein transferase activity;ATP binding;protein ubiquitination;modification-dependent protein catabolic process |  |  |
| Phvul.008G258500.3 | ubiquitin-activating enzyme E1 1 | nucleus;cytosol;integral component of membrane;ubiquitin activating enzyme activity;ubiquitin-protein transferase activity;ATP binding;protein ubiquitination;modification-dependent protein catabolic process |  |  |
| Phvul.008G261000.1 | double Clp-N motif P-loop nucleoside triphosphate hydrolase superfamily | ATP binding;protein metabolic process |  |  |

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| Phvul.008G261400.1 | inositol 3-kinase-like | ATP binding;inositol 3-kinase activity;myo-inositol hexakisphosphate biosynthetic process;phosphorylation | ec:2.7.1.64-3-kinase | Inositol phosphate metabolism |
| Phvul.008G261900.1 | zinc finger CCCH domain-containing 25 | U2 snRNP;RES complex;precatalytic spliceosome;catalytic step 2 spliceosome;nucleotide binding;first spliceosomal transesterification activity;RNA binding;metal ion binding;mRNA splicing, via spliceosome;mRNA export from nucleus | | |
| Phvul.008G262200.1 | probable NAD(P)H dehydrogenase (quinone) FQR1-like 3 | plasma membrane;FMN binding;oxidoreductase activity;negative regulation of transcription, DNA-templated;oxidation-reduction process | | |
| Phvul.008G264400.1 | LRR receptor-like kinase | plasma membrane;integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;2-alkenal reductase [NAD(P)] activity;peptidyl-tyrosine phosphorylation;oxidation-reduction process | ec:2.7.11;ec:2.7.10;ec:1.3.1.74;ec:2.7.10.1 | |
| Phvul.008G265300.1 | septum-promoting GTP-binding 1 | intracellular;GTP binding;small GTPase mediated signal transduction;protein transport;vesicle-mediated transport | | |
| Phvul.008G265500.1 | hypothetical protein PHAVU_008G265500g | | | |
| Phvul.008G265600.1 | hypothetical protein PHAVU_008G265600g | | | |
| Phvul.008G265600.4 | hypothetical protein PHAVU_008G265600g | | | |
| Phvul.008G266800.3 | reactive Intermediate Deaminase A, chloroplastic-like | | | |
| Phvul.008G266900.1 | ubiquitin thioesterase OTU1 | cytosol;peptidase activity;proteolysis | | |
| Phvul.008G266900.2 | ubiquitin thioesterase OTU1 | cytosol;peptidase activity;proteolysis | | |
| Phvul.008G267500.1 | DEAD-box ATP-dependent RNA helicase 32 | RNA binding;ATP-dependent RNA helicase activity;ATP binding;RNA secondary structure unwinding | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:2.7.7 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.008G268800.1 | GDSL-like lipase acylhydrolase | integral component of membrane;hydrolase activity, acting on ester bonds;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:1.3.5.6-desaturase | Carotenoid biosynthesis |
| Phvul.008G269100.1 | Rab3 GTPase-activating catalytic subunit | cytoplasm;GTPase activator activity;positive regulation of GTPase activity | | |
| Phvul.008G270100.1 | U4 tri-snRNP-associated 2-like | zinc ion binding;thiol-dependent ubiquitinyl hydrolase activity;protein deubiquitination | ec:3.4;ec:3.4.19.12 | |
| Phvul.008G270100.2 | U4 tri-snRNP-associated 2-like | zinc ion binding;thiol-dependent ubiquitinyl hydrolase activity;protein deubiquitination | ec:3.4;ec:3.4.19.12 | |
| Phvul.008G270200.1 | esophageal cancer associated , | intracellular;retromer complex;protein transporter activity;protein transport;retrograde transport, endosome to Golgi | | |
| Phvul.008G270200.2 | esophageal cancer associated , | intracellular;retromer complex;protein transporter activity;protein transport;retrograde transport, endosome to Golgi | | |
| Phvul.008G270600.2 | aspartate carbamoyltransferase 1, chloroplastic | cytosol;chloroplast stroma;aspartate carbamoyltransferase activity;amino acid binding;urea cycle;purine nucleotide biosynthetic process;'de novo' pyrimidine nucleobase biosynthetic process;cellular amino acid metabolic process;'de novo' UMP biosynthetic process | ec:2.1.3.2-carbamoyltransferase | Alanine, aspartate and glutamate metabolism;Pyrimidine metabolism |

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| Phvul.008G273400.1 | ENHANCED DOWNY MILDEW 2-like | methyltransferase activity;zinc ion binding;methylation | | |
| Phvul.008G273400.2 | ENHANCED DOWNY MILDEW 2-like | zinc ion binding;transferase activity | | |
| Phvul.008G273400.3 | ENHANCED DOWNY MILDEW 2-like | methyltransferase activity;zinc ion binding;methylation | | |
| Phvul.008G273400.4 | ENHANCED DOWNY MILDEW 2-like | zinc ion binding;transferase activity | | |
| Phvul.008G276100.1 | receptor 12 | integral component of membrane | | |
| Phvul.008G276800.1 | intracellular transport USO1-like | | | |
| Phvul.008G277500.1 | cytochrome P450 family 71 | integral component of membrane;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;secondary metabolite biosynthetic process;oxidation-reduction process | ec:1.14.13 | |
| Phvul.008G279600.1 | Cellulose synthase E1 | integral component of membrane;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.008G279800.1 | cellulose synthase E6 | integral component of membrane;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.008G280000.1 | sucrase ferredoxin family | integral component of membrane | | |
| Phvul.008G280100.1 | SEC14 cytosolic factor | | | |
| Phvul.008G280600.1 | DUF1296 family | | | |
| Phvul.008G281500.2 | probable LRR receptor-like serine threonine- kinase At4g26540 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.008G282100.1 | late embryogenesis abundant | integral component of membrane | | |
| Phvul.008G282600.1 | probable galactinol--sucrose galactosyltransferase 1 | galactinol-raffinose galactosyltransferase activity;metabolic process | ec:2.4.1.67-galactosyltransferase;ec:2.4.1 | Galactose metabolism |
| Phvul.008G282800.1 | probable amino acid permease 7 | plasma membrane;integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.008G282800.2 | probable amino acid permease 7 | plasma membrane;integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.008G283000.1 | probable amino acid permease 7 | plasma membrane;integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.008G283200.1 | histone deacetylase 9 | nucleus;NAD-dependent histone deacetylase activity (H3-K14 specific);transcription, DNA-templated;regulation of transcription, DNA-templated;histone H3 deacetylation | ec:3.5.1.98 | |
| Phvul.008G283500.1 | armadillo repeat-containing 8-like | | | |
| Phvul.008G284500.1 | disease resistance At4g27190-like isoform X6 | ADP binding;defense response | | |
| Phvul.008G284900.1 | nuclear pore complex NUP133 | chloroplast;nuclear pore outer ring;nucleocytoplasmic transporter activity;structural constituent of nuclear pore;posttranscriptional tethering of RNA polymerase II gene DNA at nuclear periphery;regulation of transcription, DNA-templated;RNA export from nucleus;protein import into nucleus;embryo sac egg cell differentiation | | |
| Phvul.008G286000.1 | scarecrow-like transcription factor PAT1 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |

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| Phvul.008G286300.1 | probable serine threonine- kinase WNK11 | protein kinase activity;ATP binding;protein phosphorylation;organ senescence | | |
| Phvul.008G287900.1 | TBC1 domain family member 2A | hydrolase activity;metabolic process;actin filament-based movement;Golgi localization;mitochondrion localization;peroxisome localization | | |
| Phvul.008G289500.1 | phenylalanine ammonia-lyase | cytoplasm;phenylalanine ammonia-lyase activity;L-phenylalanine catabolic process;cinnamic acid biosynthetic process | ec:4.3.1.25-ammonia-lyase;ec:4.3.1.24-ammonia-lyase | Phenylalanine metabolism;Phenylpropanoid biosynthesisPhenylalanine metabolism;Phenylpropanoid biosynthesis |
| Phvul.008G292300.1 | homoserine kinase | homoserine kinase activity;ATP binding;threonine metabolic process;phosphorylation | ec:2.7.1.39-kinase | Glycine, serine and threonine metabolism |
| Phvul.009G003200.1 | endoglucanase 24-like | cellulase activity;cellulose catabolic process | ec:3.2.1.4-endo-1,4-beta-D-glucanase | Starch and sucrose metabolism |
| Phvul.009G004700.1 | probable phosphoribosylformylglycinamidine synthase, chloroplastic mitochondrial | cytoplasm;phosphoribosylformylglycinamidine synthase activity;ATP binding;transferase activity;'de novo' IMP biosynthetic process;glutamine metabolic process | ec:6.3.5.3-synthase | Purine metabolism;Biosynthesis of antibiotics |
| Phvul.009G006300.1 | canopy-1 | integral component of membrane;systemic acquired resistance;response to endoplasmic reticulum stress | | |
| Phvul.009G008200.1 | xylem cysteine ase 2-like | extracellular space;cell wall;lysosome;cysteine-type endopeptidase activity;regulation of meristem growth;developmental programmed cell death;proteolysis involved in cellular protein catabolic process | ec:3.4;ec:3.4.22 | |
| Phvul.009G009900.1 | Prostaglandin E synthase 2 | mitochondrion;electron carrier activity;protein disulfide oxidoreductase activity;prostaglandin-E synthase activity;protein targeting to mitochondrion;toxin catabolic process;response to cyclopentenone;cell redox homeostasis;oxidation-reduction process | ec:5.3.99.3-synthase | Arachidonic acid metabolism |
| Phvul.009G010900.1 | hypothetical protein PHAVU_009G010900g | | | |
| Phvul.009G011200.1 | NLP4-like isoform X1 | | | |
| Phvul.009G012200.1 | WUSCHEL-related homeobox 8-like | nucleus;DNA binding | | |
| Phvul.009G012300.1 | actin cytoskeleton-regulatory complex pan1 | plasma membrane;calcium ion binding;actin filament-based movement;Golgi localization;mitochondrion localization;peroxisome localization | | |
| Phvul.009G012400.1 | U-box domain-containing 44 | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.009G012500.1 | F-box kelch-repeat At5g42350-like | | | |
| Phvul.009G012500.2 | F-box kelch-repeat At5g42350-like | | | |
| Phvul.009G012500.3 | F-box kelch-repeat At5g42350-like | | | |
| Phvul.009G015200.1 | IQ-DOMAIN 32 | intracellular part | | |
| Phvul.009G015200.2 | IQ-DOMAIN 32 | intracellular part | | |
| Phvul.009G015200.3 | IQ-DOMAIN 32 | intracellular part | | |
| Phvul.009G015700.1 | filament-like plant 4 | | | |
| Phvul.009G015700.2 | filament-like plant 4 | | | |
| Phvul.009G017500.1 | DUF668 family | | | |
| Phvul.009G018600.1 | subtilisin-like serine protease | cell wall;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |

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| Phvul.009G019500.1 | RNA pseudouridine synthase 2, chloroplastic isoform X1 | cytosol;RNA binding;pseudouridine synthase activity;deaminase activity;enzyme-directed rRNA pseudouridine synthesis | ec:5.4.99.12 | |
| Phvul.009G019500.2 | RNA pseudouridine synthase 2, chloroplastic isoform X1 | cytosol;RNA binding;pseudouridine synthase activity;deaminase activity;enzyme-directed rRNA pseudouridine synthesis | ec:5.4.99.12 | |
| Phvul.009G021300.1 | lysine histidine transporter-like 8 | integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.009G021600.1 | DUF630 family | | | |
| Phvul.009G021700.1 | DUF241 domain | | | |
| Phvul.009G021800.1 | transmembrane , | integral component of membrane | | |
| Phvul.009G022100.1 | dihydrofolate reductase-thymidylate synthase | dihydrofolate reductase activity;thymidylate synthase activity;dTMP biosynthetic process;glycine biosynthetic process;one-carbon metabolic process;methylation;tetrahydrofolate biosynthetic process;oxidation-reduction process | ec:1.5.1.3-reductase;ec:2.1.1.45-synthase | One carbon pool by folate;Folate biosynthesisOne carbon pool by folate;Pyrimidine metabolism |
| Phvul.009G023500.1 | transcription factor bHLH63 | membrane;protein dimerization activity | | |
| Phvul.009G025800.1 | hypothetical protein PHAVU_009G025800g | zinc ion binding | | |
| Phvul.009G026300.1 | grpE homolog, mitochondrial | mitochondrial matrix;chloroplast stroma;adenyl-nucleotide exchange factor activity;copper ion binding;protein homodimerization activity;chaperone binding;protein folding;embryo development ending in seed dormancy;thylakoid membrane organization;vegetative to reproductive phase transition of meristem;iron-sulfur cluster assembly;plant ovule development;regulation of catalytic activity | | |
| Phvul.009G026700.1 | phosphopantothenate--cysteine ligase 2-like | phosphopantothenate--cysteine ligase activity;metabolic process | ec:6.3.2.5-ligase | Pantothenate and CoA biosynthesis |
| Phvul.009G027100.1 | alkylated DNA repair alkB homolog 8 | tRNA methyltransferase activity;tRNA wobble uridine modification;tRNA methylation | ec:2.1.1 | |
| Phvul.009G027200.1 | early endosome antigen 1-like isoform X1 | vacuole;regulation of meristem growth | | |
| Phvul.009G027300.1 | F-box kelch-repeat At1g22040-like | | | |
| Phvul.009G028600.1 | probable tRNA modification GTPase | intracellular;GTPase activity;GTP binding;tRNA modification;endocytosis | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.009G030600.1 | sugar transport 5-like | integral component of plasma membrane;sugar:proton symporter activity;glucose transmembrane transporter activity;proton transport;glucose import;glucose transmembrane transport | | |
| Phvul.009G031600.1 | methyl- -binding domain | nucleus;DNA binding;hydrolase activity, acting on ester bonds;metabolic process | | |
| Phvul.009G031800.1 | ROOT PRIMORDIUM DEFECTIVE 1-like | response to oxidative stress;proline transport | | |
| Phvul.009G034100.1 | TRANSPARENT TESTA 12-like | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.009G034200.1 | MATE efflux family | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.009G034200.2 | MATE efflux family | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |

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| Phvul.009G034200.3 | MATE efflux family | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.009G034200.4 | MATE efflux family | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.009G034900.1 | E3 ubiquitin- ligase UPL1-like | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination involved in ubiquitin-dependent protein catabolic process | | |
| Phvul.009G035000.1 | crt homolog 1 | chloroplast;integral component of membrane;defense response to oomycetes;glutathione transport;response to cadmium ion | | |
| Phvul.009G035500.1 | BEACH domain-containing lvsC isoform X1 | | | |
| Phvul.009G035500.2 | BEACH domain-containing lvsC isoform X1 | | | |
| Phvul.009G035500.3 | BEACH domain-containing lvsC isoform X1 | | | |
| Phvul.009G035500.4 | BEACH domain-containing lvsC isoform X1 | | | |
| Phvul.009G035500.5 | BEACH domain-containing lvsC isoform X1 | | | |
| Phvul.009G035500.6 | BEACH domain-containing lvsC isoform X1 | | | |
| Phvul.009G035900.1 | TPR domain | integral component of membrane | | |
| Phvul.009G036300.1 | myb-like DNA-binding domain | nuclear telomere cap complex;double-stranded telomeric DNA binding | | |
| Phvul.009G040100.1 | thaumatin 1 | integral component of membrane | | |
| Phvul.009G041800.1 | hypothetical protein PHAVU_009G041800g | | | |
| Phvul.009G041800.2 | hypothetical protein PHAVU_009G041800g | | | |
| Phvul.009G042600.1 | DUF3133 family | | | |
| Phvul.009G046200.1 | polyadenylate-binding -interacting 12-like | nucleotide binding;nucleic acid binding | | |
| Phvul.009G047400.1 | WD repeat-containing 44 | | | |
| Phvul.009G049600.1 | homeobox-leucine zipper ATHB-12-like | nucleus;transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.009G051000.1 | KH domain-containing At4g18375 | RNA binding | | |
| Phvul.009G053500.1 | probable plastid-lipid-associated 14, chloroplastic | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.009G054100.1 | polynucleotide 5 -hydroxyl-kinase NOL9-like | nucleus;ATP binding;polynucleotide 5'-hydroxyl-kinase activity;cleavage in ITS2 between 5.8S rRNA and LSU-rRNA of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);phosphorylation | ec:2.7.1 | |
| Phvul.009G054200.1 | ATP-dependent zinc metalloprotease FTSH 11, chloroplastic mitochondrial-like | mitochondrion;chloroplast envelope;integral component of membrane;nucleic acid binding;ATP-dependent peptidase activity;metalloendopeptidase activity;ATP binding;proteolysis;response to heat;PSII associated light-harvesting complex II catabolic process;glucosinolate biosynthetic | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.4.24 | Purine metabolismPurine metabolism;Thiamine metabolism |

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| | | process;regulation of protein localization;cell division | | |
| Phvul.009G054700.1 | cyclic nucleotide-gated ion channel 1-like | integral component of membrane;intracellular cyclic nucleotide activated cation channel activity;voltage-gated potassium channel activity;calcium ion transport;regulation of membrane potential;potassium ion transmembrane transport | | |
| Phvul.009G054900.1 | F-box kelch-repeat At3g06240-like | | | |
| Phvul.009G055000.1 | 3-oxoacyl-[acyl-carrier] synthase | | | |
| Phvul.009G056900.1 | DUF4091 domain | transferase activity, transferring glycosyl groups;metabolic process;negative regulation of transcription, DNA-templated | | |
| Phvul.009G057400.1 | GYF domain-containing mpd2 | | | |
| Phvul.009G060400.1 | BEL1-like homeodomain 7 | nucleus;DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.009G060400.2 | BEL1-like homeodomain 7 | nucleus;DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.009G060900.1 | BZIP transcription factor bZIP124 | intracellular;transcription factor activity, sequence-specific DNA binding;MAP kinase activity;sequence-specific DNA binding;MAPK cascade;regulation of transcription, DNA-templated | ec:2.7.11;ec:2.7.11.24-protein kinase | mTOR signaling pathway |
| Phvul.009G061300.1 | Sec14 cytosolic factor | intracellular;integral component of membrane;peptide-aspartate beta-dioxygenase activity;transporter activity;transport;oxidation-reduction process | ec:1.14.11.16;ec:1.14.11 | |
| Phvul.009G061900.1 | Cytochrome b6-f complex subunit 7 | cytochrome b6f complex;integral component of membrane | | |
| Phvul.009G062900.2 | transcription factor | | | |
| Phvul.009G062900.3 | transcription factor | | | |
| Phvul.009G064300.1 | BRI1 kinase inhibitor 1 | kinase activity;phosphorylation | | |
| Phvul.009G067000.1 | SPla RYanodine receptor (SPRY) domain | integral component of membrane | | |
| Phvul.009G067400.1 | basic helix-loop-helix | | | |
| Phvul.009G068400.1 | Chromatin modification-related EAF3 | histone acetyltransferase complex;chromatin remodeling;regulation of transcription, DNA-templated;histone acetylation | | |
| Phvul.009G069700.1 | metal transporter Nramp2-like | integral component of membrane;transporter activity;transport | | |
| Phvul.009G071400.1 | carboxy-terminal domain cyclin | nucleus | | |
| Phvul.009G071400.2 | carboxy-terminal domain cyclin | nucleus | | |
| Phvul.009G072300.1 | calcium-transporting ATPase 3, endoplasmic reticulum-type | trans-Golgi network;integral component of plasma membrane;calcium-transporting ATPase activity;ATP binding;manganese-transporting ATPase activity;metal ion binding;cellular calcium ion homeostasis;intra-Golgi vesicle-mediated transport;metabolic process;root development;manganese ion homeostasis;calcium ion transmembrane transport;manganese ion transmembrane transport | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase;ec:3.6.3.8;ec:3.6.3.35 | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.009G074200.1 | RNA-binding 1-like | nucleotide binding;single-stranded RNA binding;cell proliferation | | |
| Phvul.009G074600.1 | heat shock -binding | integral component of membrane | | |
| Phvul.009G074700.1 | transmembrane , | integral component of membrane | | |
| Phvul.009G075500.1 | zinc finger CCCH domain-containing 23-like | metal ion binding | | |
| Phvul.009G076300.1 | probable phosphatase 2C 72 | protein serine/threonine phosphatase activity;protein dephosphorylation | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |

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| Phvul.009G076600.1 | RNA-binding KH domain | RNA binding | | |
| Phvul.009G077800.1 | alkaline phytoceramidase (APHC) | integral component of membrane;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;ceramide metabolic process | | |
| Phvul.009G078600.1 | graves disease carrier | mitochondrial inner membrane;integral component of membrane;structural constituent of ribosome;coenzyme A transmembrane transporter activity;translation;coenzyme A transmembrane transport | | |
| Phvul.009G081100.1 | BIG GRAIN 1-like A | | | |
| Phvul.009G082900.1 | guanine nucleotide-binding alpha-1 subunit isoform X1 | GTPase activity;signal transducer activity;GTPase inhibitor activity;GTP binding;channel regulator activity;G-protein beta/gamma-subunit complex binding;metal ion binding;G-protein coupled receptor signaling pathway;metabolic process;negative regulation of GTPase activity | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.009G083800.1 | endoribonuclease Dicer homolog 3a isoform X1 | nucleus;cytoplasm;RISC complex;DNA binding;RNA binding;ribonuclease III activity;ATP binding;production of siRNA involved in RNA interference;RNA phosphodiester bond hydrolysis, endonucleolytic | ec:3.1.30;ec:3.1.26;ec:3.1;ec:3.1.26.3 | |
| Phvul.009G084100.1 | eukaryotic translation initiation factor 3 subunit B-like | eukaryotic translation initiation factor 3 complex;eukaryotic 43S preinitiation complex;eukaryotic 48S preinitiation complex;nucleotide binding;translation initiation factor activity;translation initiation factor binding;formation of translation preinitiation complex;regulation of translational initiation | | |
| Phvul.009G086900.1 | BTB POZ domain-containing NPY1 | plasma membrane;signal transducer activity;signal transduction;flower development;positive regulation of flower development;inflorescence development;basipetal auxin transport;apical protein localization;animal organ development;cotyledon development | | |
| Phvul.009G087800.1 | Sister chromatid cohesion PDS5 like B-B | | | |
| Phvul.009G088900.1 | Two-component response regulator ARR12 | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;phosphorelay signal transduction system;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.009G089500.1 | probable receptor kinase At1g80640 isoform X1 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.009G089500.2 | probable receptor kinase At1g80640 isoform X1 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.009G089700.1 | transcriptional regulator family , | nucleus;regulation of transcription, DNA-templated | | |
| Phvul.009G090100.1 | cellulose synthase | plasma membrane;integral component of membrane;cellulose synthase (UDP-forming) activity;metal ion binding;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.009G090400.1 | pentatricopeptide repeat-containing At3g54980, mitochondrial-like isoform X1 | | | |
| Phvul.009G092800.1 | hypothetical protein PHAVU_009G092800g | | | |
| Phvul.009G092900.1 | G-type lectin S-receptor-like serine | plasma membrane;integral component of membrane;peroxidase activity;protein serine/threonine kinase | ec:2.7.11;ec:2.7.10;ec:1.11.1.7- | Phenylpropanoid biosynthesis |

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| | threonine- kinase SD2-5 | activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;heme binding;carbohydrate binding;ubiquitin protein ligase binding;response to oxidative stress;peptidyl-tyrosine phosphorylation;oxidation-reduction process;cellular oxidant detoxification | lactoperoxidase;ec:2.7.10.1 | |
| Phvul.009G093500.1 | Phospholipase D alpha 1 | membrane;phospholipase D activity;calcium ion binding;nucleotidyltransferase activity;N-acylphosphatidylethanolamine-specific phospholipase D activity;lipid catabolic process;phosphatidylcholine metabolic process | ec:3.1.1;ec:3.1;ec:3.1.4.4-D | Ether lipid metabolism;Glycerophospholipid metabolism |
| Phvul.009G097300.1 | TIFY 8 | nucleus;transcription corepressor activity;response to wounding;regulation of defense response;negative regulation of nucleic acid-templated transcription;regulation of jasmonic acid mediated signaling pathway | | |
| Phvul.009G097300.2 | TIFY 8 | nucleus;transcription corepressor activity;response to wounding;regulation of defense response;negative regulation of nucleic acid-templated transcription;regulation of jasmonic acid mediated signaling pathway | | |
| Phvul.009G100600.1 | KAKU4 isoform X1 | | | |
| Phvul.009G100700.1 | COP9 signalosome complex subunit 5b-like | kinase activity;phosphorylation | | |
| Phvul.009G102200.1 | probable xyloglucan glycosyltransferase 5 | integral component of membrane;glucomannan 4-beta-mannosyltransferase activity;mannosylation | ec:2.4.1.32 | |
| Phvul.009G102400.1 | Nucleolysin TIAR | nucleotide binding;nucleic acid binding | | |
| Phvul.009G104700.1 | pentatricopeptide repeat-containing At3g15130 | zinc ion binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.4.3 | |
| Phvul.009G105100.1 | formin 8 | DNA methylation;methylation-dependent chromatin silencing;asymmetric cell division;regulation of flower development;chromatin silencing by small RNA;floral organ formation;histone H3-K9 methylation | | |
| Phvul.009G105200.1 | bromo-adjacent-like (BAH) domain | chromatin;chromatin silencing complex;nucleotide binding;transcription regulatory region sequence-specific DNA binding;chromatin binding;chromatin silencing;heterochromatin assembly | | |
| Phvul.009G106000.1 | hypothetical protein PHAVU_009G106000g | | | |
| Phvul.009G106600.1 | la 1-like | nucleus;intracellular ribonucleoprotein complex;nucleotide binding;RNA binding;RNA processing;nucleocytoplasmic transport;post-embryonic development;macromolecule localization;single-organism cellular process;anatomical structure development;organic substance transport;single-organism intracellular transport | | |
| Phvul.009G107600.1 | EMBRYONIC FLOWER 1 | | | |
| Phvul.009G108600.1 | VAN3-binding -like isoform X1 | | | |
| Phvul.009G108700.1 | probable lactoylglutathione lyase, chloroplast | chloroplast stroma;stromule;thylakoid lumen;lactoylglutathione lyase activity;metal ion binding;dioxygenase activity;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione;oxidation-reduction process | ec:4.4.1.5-lyase | Pyruvate metabolism |
| Phvul.009G108700.2 | probable lactoylglutathione lyase, chloroplast | chloroplast stroma;stromule;thylakoid lumen;lactoylglutathione lyase activity;metal ion binding;dioxygenase activity;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione;oxidation-reduction process | ec:4.4.1.5-lyase | Pyruvate metabolism |

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| Phvul.009G109300.1 | probable glycosyltransferase At5g03795 | integral component of membrane;glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1.224-4-alpha-N-acetylglucosaminyltransferase | Glycosaminoglycan biosynthesis - heparan sulfate / heparin |
| Phvul.009G109900.1 | DUF810 family | plant-type cell wall biogenesis;cell growth;cellulose metabolic process | | |
| Phvul.009G111700.1 | tryptophan--tRNA ligase, mitochondrial isoform X1 | mitochondrion;chloroplast stroma;tryptophan-tRNA ligase activity;ATP binding;tryptophanyl-tRNA aminoacylation;chloroplast organization;embryo development ending in seed dormancy;thylakoid membrane organization;vegetative to reproductive phase transition of meristem;iron-sulfur cluster assembly;plant ovule development | ec:6.1.1.2-ligase | Aminoacyl-tRNA biosynthesis |
| Phvul.009G111900.1 | ribosomal L17 family | ribosome;chloroplast;structural constituent of ribosome;translation | | |
| Phvul.009G115100.1 | Ribonucleoside-diphosphate reductase large subunit | ribonucleoside-diphosphate reductase complex;ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor;ATP binding;DNA replication;deoxyribonucleotide biosynthetic process;oxidation-reduction process | ec:1.17.4.1-reductase | Purine metabolism;Glutathione metabolism;Pyrimidine metabolism |
| Phvul.009G115700.1 | probable galacturonosyltransferase 3 | Golgi membrane;endosome;vacuolar membrane;trans-Golgi network;integral component of membrane;polygalacturonate 4-alpha-galacturonosyltransferase activity;mitotic cell cycle;DNA metabolic process;RNA processing;sister chromatid cohesion;positive regulation of cell proliferation;photomorphogenesis;embryo development ending in seed dormancy;seed germination;regulation of flower development;meristem structural organization;seed dormancy process;sugar mediated signaling pathway;vegetative to reproductive phase transition of meristem;protein ubiquitination;lipid storage;chromatin silencing by small RNA;regulation of chromosome organization;meiotic chromosome segregation;pectin biosynthetic process;positive regulation of transcription, DNA-templated;response to freezing;cell wall organization | ec:2.4.1.43-4-alpha-galacturonosyltransferase | Amino sugar and nucleotide sugar metabolism;Starch and sucrose metabolism |
| Phvul.009G116800.1 | hypothetical protein PHAVU_009G116800g | | | |
| Phvul.009G116800.2 | hypothetical protein PHAVU_009G116800g | | | |
| Phvul.009G116900.1 | probable alanine--tRNA ligase, chloroplastic | mitochondrion;cytosol;chloroplast stroma;membrane;tRNA binding;DNA binding;transcription factor activity, sequence-specific DNA binding;alanine-tRNA ligase activity;ATP binding;zinc ion binding;amino acid binding;sigma factor activity;DNA-templated transcription, initiation;regulation of transcription, DNA-templated;tRNA modification;alanyl-tRNA aminoacylation;embryo development ending in seed dormancy | ec:6.1.1.7-ligase | Aminoacyl-tRNA biosynthesis |
| Phvul.009G117100.1 | PHD and RING finger domain-containing 1 | zinc ion binding;ligase activity;metabolic process | | |
| Phvul.009G117100.2 | PHD and RING finger domain-containing 1 | zinc ion binding;ligase activity;metabolic process | | |
| Phvul.009G117100.3 | PHD and RING finger domain-containing 1 | zinc ion binding;ligase activity;metabolic process | | |
| Phvul.009G117100.4 | PHD and RING finger domain-containing 1 | zinc ion binding;ligase activity;metabolic process | | |

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| Phvul.009G117300.1 | RNA polymerase sigma factor rpoD | cytoplasm;integral component of membrane;plastid sigma factor activity;DNA binding;transcription factor activity, sequence-specific DNA binding;alanine-tRNA ligase activity;ATP binding;pentose-phosphate shunt;DNA-templated transcription, initiation;regulation of transcription, DNA-templated;rRNA processing;alanyl-tRNA aminoacylation;response to blue light;chloroplast relocation;thylakoid membrane organization;response to far red light;carotenoid biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | ec:6.1.1.7-ligase | Aminoacyl-tRNA biosynthesis |
| Phvul.009G120000.1 | subtilisin-like protease | cell wall;membrane;serine-type endopeptidase activity;sulfur amino acid metabolic process;polysaccharide catabolic process;starch metabolic process;proteolysis;microtubule nucleation;cellular amino acid biosynthetic process;serine family amino acid metabolic process;plant-type cell wall modification;plant-type cell wall biogenesis;regulation of meristem growth;glucosinolate biosynthetic process | ec:3.4.21 | |
| Phvul.009G121200.1 | phosphatidylinositol 4-phosphate 5-kinase 1-like | 1-phosphatidylinositol-4-phosphate 5-kinase activity;phosphatidylinositol phosphorylation | ec:2.7.1.68-5-kinase | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.009G121200.2 | phosphatidylinositol 4-phosphate 5-kinase 1-like | 1-phosphatidylinositol-4-phosphate 5-kinase activity;phosphatidylinositol phosphorylation | ec:2.7.1.68-5-kinase | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.009G121600.1 | Serine Threonine kinase family | protein serine/threonine/tyrosine kinase activity;ATP binding;protein phosphorylation;mitotic cell cycle checkpoint;chromosome separation | ec:2.7.12.1 | |
| Phvul.009G121600.2 | Serine Threonine kinase family | protein serine/threonine/tyrosine kinase activity;ATP binding;protein phosphorylation;mitotic cell cycle checkpoint;chromosome separation | ec:2.7.12.1 | |
| Phvul.009G121700.1 | nucleic acid-binding | NAD+ ADP-ribosyltransferase activity;metal ion binding;metabolic process | ec:2.4.2.30 | |
| Phvul.009G122500.1 | pentatricopeptide repeat-containing At3g62890-like | nucleic acid binding;zinc ion binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.4.3 | |
| Phvul.009G122600.1 | G-type lectin S-receptor-like serine threonine- kinase At5g35370 | plasma membrane;integral component of membrane;protein serine/threonine kinase activity;calmodulin binding;ATP binding;carbohydrate binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.009G124200.1 | DNA ligase 1 | membrane;DNA binding | | |
| Phvul.009G124500.1 | P-loop nucleoside triphosphate hydrolase superfamily , | nucleus;DNA repair;cell cycle | | |
| Phvul.009G126000.1 | Replication factor C subunit 5 | DNA clamp loader activity;DNA-directed DNA polymerase activity;ATP binding;mRNA splicing, via spliceosome;DNA-dependent DNA replication;mitotic recombination;methylation-dependent chromatin silencing;embryo sac egg cell differentiation;regulation of flower development;RNA interference;chromatin silencing by small RNA;negative regulation of defense response;floral organ formation;histone H3-K9 methylation;DNA biosynthetic process | ec:2.7.7.7-DNA polymerase | Purine metabolism;Pyrimidine metabolism |
| Phvul.009G128400.1 | chloroplast processing peptidase-like | chloroplast thylakoid membrane;integral component of membrane;mitochondrial inner membrane peptidase complex;serine-type endopeptidase activity;signal peptide processing;protein processing involved in protein targeting to mitochondrion;thylakoid membrane organization;mitochondrial respiratory chain complex assembly | ec:3.4.21 | |

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| Phvul.009G128400.2 | chloroplast processing peptidase-like | chloroplast thylakoid membrane;integral component of membrane;mitochondrial inner membrane peptidase complex;serine-type endopeptidase activity;signal peptide processing;protein processing involved in protein targeting to mitochondrion;thylakoid membrane organization;mitochondrial respiratory chain complex assembly | ec:3.4.21 | |
| Phvul.009G129400.1 | translocase subunit SECA2, chloroplastic isoform X1 | intracellular;membrane;ATP binding;protein targeting;protein import | | |
| Phvul.009G129500.1 | 1-aminocyclopropane-1-carboxylate oxidase 5 | 1-aminocyclopropane-1-carboxylate oxidase activity;metal ion binding;iron ion transport;cellular response to iron ion starvation;response to nitrate;nitrate transport;brassinosteroid biosynthetic process;oxidation-reduction process | ec:1.14.17.4-oxidase | Cysteine and methionine metabolism |
| Phvul.009G130300.1 | probable receptor-like serine threonine- kinase At5g57670 | protein serine/threonine kinase activity;ATP binding;hydrolase activity;protein phosphorylation;response to stress | ec:2.7.11 | |
| Phvul.009G133500.1 | transmembrane , | integral component of membrane | | |
| Phvul.009G133900.1 | thioredoxin M-type, chloroplastic-like | chloroplast;protein disulfide oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor;sulfate assimilation;protein folding;glycerol ether metabolic process;cellular response to oxidative stress;cell redox homeostasis;oxidation-reduction process | | |
| Phvul.009G136800.1 | probable inactive receptor kinase At4g23740 | intracellular;integral component of membrane;MAP kinase kinase kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.11.25;ec:2.7.10.1 | |
| Phvul.009G138900.1 | WRKY family transcription factor | transcription factor activity, sequence-specific DNA binding;sequence-specific DNA binding;regulation of transcription, DNA-templated | | |
| Phvul.009G139100.1 | ABC transporter F family member 5 | ATP binding;ATPase activity;metabolic process | ec:3.6.1.3-adenylpyrophosphatase | Purine metabolism |
| Phvul.009G139500.1 | 4-alpha-glucanotransferase, chloroplastic amyloplastic | 4-alpha-glucanotransferase activity;maltose catabolic process;glycogen metabolic process;starch catabolic process;glucose metabolic process | ec:2.4.1.25-disproportionating enzyme | Starch and sucrose metabolism |
| Phvul.009G139600.1 | VAC14 homolog | vacuolar membrane | | |
| Phvul.009G141300.1 | uncharacterized membrane At1g06890-like | integral component of membrane;carbohydrate transport | | |
| Phvul.009G141400.1 | Poly(A) RNA polymerase cid14 | nucleotidyltransferase activity;metabolic process | | |
| Phvul.009G142600.1 | Exosome complex exonuclease RRP44 | 3'-5'-exoribonuclease activity;endonuclease activity;exoribonuclease II activity;rRNA processing;mRNA catabolic process;rRNA catabolic process;RNA phosphodiester bond hydrolysis, exonucleolytic | ec:3.1.13.1;ec:3.1.13 | |
| Phvul.009G143300.1 | , chloroplastic | copper ion binding;response to metal ion;photoperiodism, flowering | | |
| Phvul.009G144900.1 | probable rhamnogalacturonate lyase B | lyase activity;carbohydrate binding;carbohydrate metabolic process | | |
| Phvul.009G144900.2 | probable rhamnogalacturonate lyase B | lyase activity;carbohydrate binding;carbohydrate metabolic process | | |
| Phvul.009G144900.3 | probable rhamnogalacturonate lyase B | lyase activity;carbohydrate binding;carbohydrate metabolic process | | |
| Phvul.009G149100.1 | zinc finger CCCH domain-containing 38-like | metal ion binding | | |

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| Phvul.009G149800.1 | phosphatidylinositol 4-kinase beta 1-like isoform X1 | intracellular;membrane;1-phosphatidylinositol 4-kinase activity;phosphatidylinositol phosphorylation;phosphatidylinositol-mediated signaling | ec:2.7.1.67-4-kinase | Inositol phosphate metabolism;Phosphatidylinositol signaling system |
| Phvul.009G150000.1 | succinate dehydrogenase subunit 7B, mitochondrial isoform X1 | integral component of membrane | | |
| Phvul.009G150100.1 | plant NAC domain | nucleus;membrane;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.009G153100.1 | beta-galactosidase 10 | plant-type cell wall;beta-galactosidase activity;carbohydrate binding;carbohydrate metabolic process | ec:3.2.1.23-lactase (ambiguous) | Other glycan degradation;Glycosphingolipid biosynthesis - ganglio series;Sphingolipid metabolism;Galactose metabolism;Glycosaminoglycan degradation |
| Phvul.009G153600.1 | amino acid permease 4-like | plasma membrane;integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.009G153700.1 | Amino acid permease 2 | plasma membrane;integral component of membrane;amino acid transmembrane transporter activity;amino acid transmembrane transport | | |
| Phvul.009G153800.1 | auxilin-related 2-like | | | |
| Phvul.009G153900.1 | ultraviolet-B receptor UVR8 isoform X1 | chromatin;chromatin binding;guanyl-nucleotide exchange factor activity;ligase activity;protein homodimerization activity;glucose catabolic process;entrainment of circadian clock;response to UV-B;positive regulation of GTPase activity | | |
| Phvul.009G154000.1 | lipase-like PAD4 | integral component of membrane;hydrolase activity;lipid metabolic process | | |
| Phvul.009G154600.1 | farnesylcysteine lyase | vacuolar membrane;prenylcysteine oxidase activity;lyase activity;abscisic acid-activated signaling pathway;prenylated protein catabolic process;prenylcysteine catabolic process;hydrogen peroxide catabolic process;farnesyl diphosphate metabolic process;oxidation-reduction process | ec:1.8.3.5-oxidase | Biosynthesis of antibiotics;Terpenoid backbone biosynthesis |
| Phvul.009G155700.1 | nuclear snf4 | chloroplast stroma;chloroplast envelope;apoplast;oxidoreductase activity;pentose-phosphate shunt;leaf morphogenesis;thylakoid membrane organization;carotenoid biosynthetic process;cell differentiation;oxidation-reduction process | | |
| Phvul.009G157000.1 | DUF668 family | | | |
| Phvul.009G157600.1 | ferrochelatase-2, chloroplastic-like | ferrochelatase activity;heme biosynthetic process | ec:4.99.1.1-ferro-protoporphyrin chelatase | Porphyrin and chlorophyll metabolism |
| Phvul.009G158900.1 | calcium-binding mitochondrial carrier S -2-B-like | integral component of membrane;structural constituent of ribosome;calcium ion binding;translation;transmembrane transport | | |
| Phvul.009G158900.3 | calcium-binding mitochondrial carrier S -2-like isoform X2 | integral component of membrane;structural constituent of ribosome;calcium ion binding;translation;transmembrane transport | | |
| Phvul.009G159400.1 | FRIGIDA | integral component of membrane | | |
| Phvul.009G160400.1 | DYAD | | | |
| Phvul.009G161300.1 | U5 small nuclear ribonucleo 40 kDa -like | | | |
| Phvul.009G161400.1 | MEI2-like 1 isoform X1 | nucleotide binding;nucleic acid binding | | |
| Phvul.009G161400.2 | MEI2-like 1 isoform X1 | nucleotide binding;nucleic acid binding | | |

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| Phvul.009G161400.3 | MEI2-like 1 isoform X1 | nucleotide binding;nucleic acid binding | | |
| Phvul.009G161600.1 | Lysosomal alpha-mannosidase | alpha-mannosidase activity;zinc ion binding;carbohydrate binding;mannose metabolic process;protein deglycosylation | ec:3.2.1.24-alpha-D-mannosidase | Other glycan degradation |
| Phvul.009G163500.1 | probable serine threonine- kinase At1g54610 | cyclin-dependent protein serine/threonine kinase activity;ATP binding;protein phosphorylation;regulation of cell cycle | ec:2.7.11.22 | |
| Phvul.009G164400.1 | tRNA nucleotidyltransferase poly(A) polymerase | RNA binding;hydrolase activity;CTP:tRNA cytidylyltransferase activity;CTP:3'-cytidine-tRNA cytidylyltransferase activity;ATP:3'-cytidine-cytidine-tRNA adenylyltransferase activity;tRNA 3'-terminal CCA addition | ec:2.7.7.72 | |
| Phvul.009G166500.1 | hypothetical protein PHAVU_009G166500g | integral component of membrane;cytolysis;defense response to Gram-negative bacterium | | |
| Phvul.009G166500.2 | hypothetical protein PHAVU_009G166500g | integral component of membrane;cytolysis;defense response to Gram-negative bacterium | | |
| Phvul.009G166500.3 | hypothetical protein PHAVU_009G166500g | integral component of membrane;cytolysis;defense response to Gram-negative bacterium | | |
| Phvul.009G166500.4 | hypothetical protein PHAVU_009G166500g | | | |
| Phvul.009G166600.1 | snurportin-1 | | | |
| Phvul.009G167100.1 | hypothetical protein PHAVU_009G167100g | ATP binding;microtubule-severing ATPase activity | ec:3.6.4.3 | |
| Phvul.009G168100.1 | transcription factor GTE10-like | | | |
| Phvul.009G168200.1 | nucleic acid-binding, OB-fold | cytosol;plastid chromosome;chloroplast stroma;nucleic acid binding;transcription from plastid promoter;positive regulation of transcription, DNA-templated | | |
| Phvul.009G169100.1 | kelch domain-containing 4 | lipid transport | | |
| Phvul.009G169400.1 | callose synthase 10 | 1,3-beta-D-glucan synthase complex;integral component of membrane;1,3-beta-D-glucan synthase activity;(1->3)-beta-D-glucan biosynthetic process | ec:2.4.1.34-synthase | Starch and sucrose metabolism |
| Phvul.009G170000.1 | probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SPINDLY | transferase activity, transferring glycosyl groups;nuclear-transcribed mRNA catabolic process | | |
| Phvul.009G170000.2 | probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SPINDLY | transferase activity, transferring glycosyl groups;nuclear-transcribed mRNA catabolic process | | |
| Phvul.009G170500.1 | Pectate lyase | pectate lyase activity;metal ion binding;pectin catabolic process | ec:4.2.2.2-lyase | Pentose and glucuronate interconversions |
| Phvul.009G171200.1 | leucine-rich repeat receptor-like serine threonine tyrosine-kinase SOBIR1 | integral component of membrane;calmodulin-dependent protein kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;positive regulation of cell death;peptidyl-tyrosine phosphorylation;positive regulation of defense response;negative regulation of floral organ abscission | ec:2.7.11.17;ec:2.7.10.1 | |
| Phvul.009G172500.1 | transcription factor IWS1 | nucleus;DNA binding;translation elongation factor activity;transcription, DNA-templated;translational elongation | | |
| Phvul.009G172900.1 | manganese-dependent ADP-ribose CDP-alcohol | ADP-ribose diphosphatase activity;CDP-glycerol diphosphatase activity;metabolic process | ec:3.6.1.16-diphosphatase;ec:3.6.1.13-diphosphatase | Glycerophospholipid metabolismPurine metabolism |

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| | diphosphatase-like isoform X1 | | | |
| Phvul.009G172900.2 | manganese-dependent ADP-ribose CDP-alcohol diphosphatase-like isoform X1 | ADP-ribose diphosphatase activity;CDP-glycerol diphosphatase activity;metabolic process | ec:3.6.1.16-diphosphatase;ec:3.6.1.13-diphosphatase | Glycerophospholipid metabolismPurine metabolism |
| Phvul.009G175300.1 | tryptophan aminotransferase-related 2-like | integral component of membrane;transaminase activity;alliin lyase activity;metabolic process | ec:4.4.1.4 | |
| Phvul.009G176400.1 | LRR receptor-like serine threonine-kinase GSO1 | integral component of membrane;kinase activity;2-alkenal reductase [NAD(P)] activity;phosphorylation;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.009G176500.1 | MORC family CW-type zinc finger 3-like | plasmodesma;chloroplast envelope;ATPase activity;sister chromatid cohesion;determination of bilateral symmetry;organ morphogenesis;xylem and phloem pattern formation;chromatin silencing by small RNA;regulation of chromatin silencing;meiotic chromosome segregation;flower morphogenesis;RNA-directed DNA methylation | ec:3.6.1.3-adenylpyrophosphatase | Purine metabolism |
| Phvul.009G176900.1 | transmembrane , | cell;integral component of membrane;maltose metabolic process;pentose-phosphate shunt;chloroplast relocation;stomatal complex morphogenesis;mRNA modification;starch biosynthetic process;positive regulation of catalytic activity | | |
| Phvul.009G177400.1 | transmembrane , | integral component of membrane | | |
| Phvul.009G179300.1 | EXECUTER 2, chloroplastic | thylakoid membrane;singlet oxygen-mediated programmed cell death | | |
| Phvul.009G179300.2 | EXECUTER 2, chloroplastic | thylakoid membrane;singlet oxygen-mediated programmed cell death | | |
| Phvul.009G180300.1 | probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 | alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity;trehalose-phosphatase activity;trehalose biosynthetic process;dephosphorylation | ec:2.4.1.15-synthase (UDP-forming);ec:3.1.3.12-trehalose 6-phosphatase | Starch and sucrose metabolismStarch and sucrose metabolism |
| Phvul.009G184500.1 | probable LRR receptor-like serine threonine- kinase At1g74360 | intracellular;integral component of membrane;MAP kinase kinase kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK activity;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.11.25;ec:2.7.10.1 | |
| Phvul.009G185100.1 | phospholipid-transporting ATPase 9 | Golgi membrane;trans-Golgi network;plasma membrane;integral component of membrane;magnesium ion binding;phospholipid-translocating ATPase activity;ATP binding;metabolic process;phospholipid translocation;Golgi vesicle budding | ec:3.6.3.1 | |
| Phvul.009G187100.1 | E3 ubiquitin- ligase MARCH4-like isoform X7 | integral component of membrane;zinc ion binding | | |
| Phvul.009G187100.2 | E3 ubiquitin- ligase MARCH4-like isoform X7 | integral component of membrane;zinc ion binding | | |
| Phvul.009G187300.1 | probable arabinosyltransferase ARAD1 | integral component of membrane;glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1.224-4-alpha-N-acetylglucosaminyltransferase | Glycosaminoglycan biosynthesis - heparan sulfate / heparin |
| Phvul.009G189600.1 | hypothetical protein PHAVU_009G189600g | | | |
| Phvul.009G191000.1 | 2-aminoethanethiol dioxygenase | cysteamine dioxygenase activity;anaerobic respiration;peptidyl-cysteine oxidation;detection of hypoxia | ec:1.13.11.19-dioxygenase | Taurine and hypotaurine metabolism |
| Phvul.009G191000.2 | 2-aminoethanethiol dioxygenase | cysteamine dioxygenase activity;anaerobic respiration;peptidyl-cysteine oxidation;detection of hypoxia | ec:1.13.11.19-dioxygenase | Taurine and hypotaurine metabolism |

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| Phvul.009G191000.3 | 2-aminoethanethiol dioxygenase | cysteamine dioxygenase activity;anaerobic respiration;peptidyl-cysteine oxidation;detection of hypoxia | ec:1.13.11.19-dioxygenase | Taurine and hypotaurine metabolism |
| Phvul.009G191500.1 | mitochondrial substrate carrier family E | integral component of membrane;structural constituent of ribosome;translation;transmembrane transport | | |
| Phvul.009G193100.1 | dentin sialophospho , | | | |
| Phvul.009G193400.1 | pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 | spliceosomal complex;ATP-dependent RNA helicase activity;ATP binding;poly(A) RNA binding;RNA processing | | |
| Phvul.009G196400.1 | hypothetical protein PHAVU_009G196400g, partial | | | |
| Phvul.009G196600.1 | heat shock family | integral component of membrane | | |
| Phvul.009G196800.1 | structural maintenance of chromosomes 3 isoform X1 | chromatin;nucleus;cohesin core heterodimer;plasmodesma;chromatin binding;ATP binding;DNA repair;mitotic sister chromatid cohesion;production of ta-siRNAs involved in RNA interference;production of miRNAs involved in gene silencing by miRNA;defense response to virus | | |
| Phvul.009G197800.1 | 2-alkenal reductase (NADP(+)-dependent)-like | integral component of membrane;zinc ion binding;2-alkenal reductase [NAD(P)] activity;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.009G200200.1 | acyl ACP-thioesterase | oleoyl-[acyl-carrier-protein] hydrolase activity;myristoyl-[acyl-carrier-protein] hydrolase activity;palmitoyl-[acyl-carrier-protein] hydrolase activity;fatty acid biosynthetic process | ec:3.1.2.14-hydrolase | Fatty acid biosynthesis |
| Phvul.009G202000.1 | ninja-family 2-like isoform X1 | signal transduction | | |
| Phvul.009G202600.1 | pentatricopeptide repeat-containing At2g38420, mitochondrial | | | |
| Phvul.009G203100.1 | COBRA 2 precursor | plant-type cell wall;external side of plasma membrane;longitudinal side of cell surface;integral component of membrane;anchored component of plasma membrane;polysaccharide biosynthetic process;polysaccharide catabolic process;starch metabolic process;glycolytic process;calcium ion transport;water transport;hyperosmotic response;Golgi organization;pattern specification process;regulation of cell size;response to temperature stimulus;response to salt stress;response to fructose;multidimensional cell growth;auxin polar transport;cell tip growth;cellulose microfibril organization;cellulose metabolic process;anthocyanin accumulation in tissues in response to UV light;response to cadmium ion;root hair elongation | | |
| Phvul.009G204500.1 | GDP-fucose O-fucosyltransferase | cytoplasm;integral component of membrane;transferase activity, transferring glycosyl groups;metabolic process | | |
| Phvul.009G204900.1 | Poly(A) polymerase | nucleus;integral component of membrane;RNA binding;polynucleotide adenylyltransferase activity;mRNA polyadenylation | ec:2.7.7.19 | |
| Phvul.009G205100.1 | cellulose synthase A catalytic subunit 7 [UDP-forming] | plasma membrane;integral component of membrane;zinc ion binding;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming) | Starch and sucrose metabolism |
| Phvul.009G205200.1 | Cellulose synthase A catalytic subunit 7 [UDP-forming] | plasma membrane;integral component of membrane;zinc ion binding;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming) | Starch and sucrose metabolism |
| Phvul.009G205400.1 | hypothetical protein PHAVU_009G205400g | | | |

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| Phvul.009G210000.1 | glycerol-3-phosphate transporter 5 | integral component of membrane;transmembrane transporter activity;nitrate transport;transmembrane transport | | |
| Phvul.009G210800.1 | transmembrane , | plasmodesma;integral component of membrane | | |
| Phvul.009G214800.1 | hypothetical protein PHAVU_009G214800g | | | |
| Phvul.009G215600.1 | endoplasmic reticulum oxidoreductin-1-like | endoplasmic reticulum;integral component of membrane;protein disulfide isomerase activity;oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor;protein folding;oxidation-reduction process | ec:5.3.4.1 | |
| Phvul.009G217900.1 | vacuolar sorting-associated 54, chloroplastic | GARP complex;syntaxin binding;Golgi to vacuole transport;retrograde transport, endosome to Golgi | | |
| Phvul.009G218000.1 | vacuolar sorting-associated 2 homolog 2 | ESCRT III complex;microtubule cytoskeleton organization;cytokinesis by cell plate formation;DNA replication;DNA methylation;vacuolar transport;cell proliferation;histone phosphorylation;histone H3-K9 methylation | | |
| Phvul.009G218100.1 | Ferrochelatase-2, chloroplastic | integral component of membrane;ferrochelatase activity;heme biosynthetic process;response to stress;macromolecule localization;regulation of programmed cell death | ec:4.99.1.1-ferro-protoporphyrin chelatase | Porphyrin and chlorophyll metabolism |
| Phvul.009G219000.1 | cytochrome b561 | integral component of membrane | | |
| Phvul.009G219100.1 | pentatricopeptide repeat-containing At3g06430, chloroplastic-like | microtubule-severing ATPase activity;rRNA binding;metabolic process;embryo sac development;pollen development;embryo development;pollen tube development | ec:3.6.4.3 | |
| Phvul.009G219600.1 | hypothetical protein PHAVU_009G219600g | | | |
| Phvul.009G220100.1 | DNA binding , | DNA binding;protein dimerization activity | | |
| Phvul.009G222000.1 | transcription initiation factor TFIID subunit 10 | nucleus;DNA-templated transcription, initiation | | |
| Phvul.009G223200.1 | AT-rich interactive domain-containing 4 | DNA binding;zinc ion binding | | |
| Phvul.009G224700.1 | DEAD-box ATP-dependent RNA helicase 17 | intracellular;RNA binding;ATP-dependent RNA helicase activity;ATP binding;mitotic recombination;mRNA export from nucleus;protein targeting to mitochondrion;embryo sac egg cell differentiation;photomorphogenesis;cullin deneddylation;RNA secondary structure unwinding;transcription factor import into nucleus;protein maturation | | |
| Phvul.009G226100.1 | transmembrane 184 homolog DDB_G0279555 isoform X1 | integral component of membrane;transporter activity;transport;fatty acid catabolic process;plant-type hypersensitive response | | |
| Phvul.009G227400.1 | acyl- N-acyltransferase (NAT) superfamily | protein acetyltransferase complex;peptide alpha-N-acetyltransferase activity;N-terminal protein amino acid acetylation | ec:2.3.1.88 | |
| Phvul.009G227900.1 | DENN domain-containing 5B | integral component of membrane | | |
| Phvul.009G227900.2 | DENN domain-containing 5B | integral component of membrane | | |
| Phvul.009G227900.3 | DENN domain-containing 5B | integral component of membrane | | |
| Phvul.009G228000.1 | growth-regulating factor | nucleus;ATP binding;transcription, DNA-templated;regulation of transcription, DNA-templated;developmental process | | |

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| Phvul.009G228500.1 | replication A 70 kDa DNA-binding subunit A | nuclear chromatin;DNA binding;double-strand break repair via homologous recombination;DNA replication;mitotic recombination;sister chromatid cohesion;male meiosis I;pyrimidine ribonucleotide biosynthetic process;pollen development;embryo sac egg cell differentiation;photomorphogenesis;embryo development ending in seed dormancy;seed germination;regulation of flower development;meristem structural organization;seed dormancy process;sugar mediated signaling pathway;vegetative to reproductive phase transition of meristem;response to gamma radiation;somatic cell DNA recombination;protein ubiquitination;lipid storage;regulation of telomere maintenance;meiotic DNA double-strand break formation;telomere maintenance in response to DNA damage;post-translational protein modification;positive regulation of transcription, DNA-templated;male gamete generation;response to freezing;chiasma assembly | | |
| Phvul.009G229900.1 | probable phosphatase 2C 50 isoform X1 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | | |
| Phvul.009G229900.2 | probable phosphatase 2C 50 isoform X1 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | | |
| Phvul.009G229900.3 | probable phosphatase 2C 50 isoform X1 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | | |
| Phvul.009G229900.4 | probable phosphatase 2C 50 isoform X1 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | | |
| Phvul.009G229900.5 | probable phosphatase 2C 50 isoform X1 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | | |
| Phvul.009G229900.6 | probable phosphatase 2C 50 isoform X1 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | | |
| Phvul.009G229900.7 | probable phosphatase 2C 50 isoform X1 | protein serine/threonine phosphatase activity;metal ion binding;protein dephosphorylation | | |
| Phvul.009G230400.1 | DNA-directed RNA polymerase II subunit RPB2 | DNA-directed RNA polymerase II, core complex;cytosol;plasmodesma;RNA polymerase II activity;DNA binding;ribonucleoside binding;RNA splicing, via endonucleolytic cleavage and ligation;nuclear-transcribed mRNA catabolic process;transcription from RNA polymerase II promoter | | |
| Phvul.009G232100.1 | receptor-like serine threonine- kinase ALE2 isoform X2 | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.009G232100.2 | receptor-like serine threonine- kinase ALE2 isoform X2 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.009G232100.3 | receptor-like serine threonine- kinase ALE2 isoform X2 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.009G232500.1 | beta-galactosidase | cell wall;beta-galactosidase activity;zinc ion binding;carbohydrate binding;carbohydrate metabolic process | ec:3.2.1.23-lactase (ambiguous) | Other glycan degradation;Glycosphingolipid biosynthesis - ganglio series;Sphingolipid metabolism;Galactose metabolism;Glycosaminoglycan degradation |
| Phvul.009G235600.1 | probable inactive purple acid phosphatase 28 | integral component of membrane;acid phosphatase activity;dephosphorylation | ec:3.1.3.2-phosphatase | Aminobenzoate degradation |
| Phvul.009G235800.1 | DNA ligase 4 | cytoplasm;plasmodesma;apoplast;DNA binding;DNA ligase (ATP) activity;NAD+ ADP- | ec:6.5.1.1;ec:2.4.2.30 | |

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| | | ribosyltransferase activity;ATP binding;lagging strand elongation;double-strand break repair;DNA recombination;response to X-ray;DNA ligation involved in DNA repair;DNA biosynthetic process | | |
| Phvul.009G236800.1 | subtilisin-like protease | cell wall;membrane;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.009G237400.1 | core-2 I-branching enzyme | integral component of membrane;acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1 | |
| Phvul.009G237900.1 | pumilio homolog 6, chloroplastic | mRNA binding;nucleotide biosynthetic process | | |
| Phvul.009G237900.2 | pumilio homolog 6, chloroplastic | mRNA binding;nucleotide biosynthetic process | | |
| Phvul.009G239300.1 | adagio 1 | nucleus;cytosol;membrane;SCF ubiquitin ligase complex;scavenger receptor activity;blue light photoreceptor activity;ligase activity;fatty acid beta-oxidation;receptor-mediated endocytosis;circadian rhythm;blue light signaling pathway;flower development;response to red light;protein import into peroxisome matrix;SCF-dependent proteasomal ubiquitin-dependent protein catabolic process;entrainment of circadian clock by photoperiod | | |
| Phvul.009G239900.1 | G-type lectin S-receptor-like serine threonine- kinase | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;carbohydrate binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10.1 | |
| Phvul.009G240000.1 | heavy metal ATPase transporter | integral component of plasma membrane;intracellular membrane-bounded organelle;nucleotide binding;zinc ion transmembrane transporter activity;cadmium-exporting ATPase activity;metal ion binding;metabolic process;cadmium ion transmembrane transport;zinc II ion transmembrane transport | ec:3.6.3.3 | |
| Phvul.009G240000.2 | heavy metal ATPase transporter | integral component of plasma membrane;intracellular membrane-bounded organelle;nucleotide binding;zinc ion transmembrane transporter activity;cadmium-exporting ATPase activity;metal ion binding;metabolic process;cadmium ion transmembrane transport;zinc II ion transmembrane transport | ec:3.6.3.3 | |
| Phvul.009G240500.1 | UPF0481 At3g47200-like | integral component of membrane | | |
| Phvul.009G241100.1 | ATP-dependent zinc metalloprotease FTSH 2, chloroplastic | mitochondrion;chloroplast thylakoid membrane;chloroplast envelope;integral component of membrane;ATP-dependent peptidase activity;metalloendopeptidase activity;ATP binding;zinc ion binding;microtubule-severing ATPase activity;proteolysis;thylakoid membrane organization;photoinhibition;photosystem II repair;PSII associated light-harvesting complex II catabolic process;cell division | ec:3.6.4.3;ec:3.4.24 | |
| Phvul.009G242700.1 | cellulose synthase 4 | plasma membrane;integral component of membrane;zinc ion binding;cellulose synthase (UDP-forming) activity;plant-type secondary cell wall biogenesis;glucuronoxylan metabolic process;cellulose biosynthetic process;defense response to bacterium;xylan biosynthetic process;defense response to fungus;cell wall organization | ec:2.4.1.12-synthase (UDP-forming) | Starch and sucrose metabolism |
| Phvul.009G243500.1 | ribulose-1,5 bisphosphate carboxylase oxygenase large subunit N-methyltransferase, chloroplastic isoform X2 | plastid-encoded plastid RNA polymerase complex;plastid chromosome;chloroplast thylakoid;protein-lysine N-methyltransferase activity;[ribulose-bisphosphate carboxylase]-lysine N-methyltransferase activity;rRNA processing;tRNA metabolic process;phosphatidylglycerol biosynthetic process;chloroplast organization;thylakoid membrane organization;stomatal complex | ec:2.1.1;ec:2.1.1.127 | |

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| | | morphogenesis;peptidyl-lysine monomethylation;transcription from plastid promoter;protein targeting to chloroplast;positive regulation of transcription, DNA-templated | | |
| Phvul.009G243800.1 | vacuolar-sorting receptor 6-like | integral component of membrane;calcium ion binding | | |
| Phvul.009G244300.1 | DDB1- and CUL4-associated factor 4-like isoform X1 | | | |
| Phvul.009G244700.1 | zinc finger, C3HC4 type (RING finger) | ubiquitin-protein transferase activity;zinc ion binding;regulation of signal transduction;protein ubiquitination | | |
| Phvul.009G247100.1 | C2 domain | endoplasmic reticulum membrane;plasma membrane;integral component of membrane;protein storage vacuole membrane;anion transport;regulation of biological process;response to stimulus;organic substance transport;nitrogen compound transport;single-organism intracellular transport | | |
| Phvul.009G247700.1 | probable phosphatase 2C 40 | protein serine/threonine phosphatase activity;protein dephosphorylation | | |
| Phvul.009G247700.2 | probable phosphatase 2C 40 | protein serine/threonine phosphatase activity;protein dephosphorylation | | |
| Phvul.009G248800.1 | condensin-2 complex subunit D3 | condensed chromosome, centromeric region;nuclear condensin complex;chromatin binding;histone binding;mitotic chromosome condensation;meiotic chromosome condensation;chromosome separation | | |
| Phvul.009G249600.1 | sericin 1-like | | | |
| Phvul.009G250700.1 | Acyl-dehydrogenase family member 10 | integral component of membrane;fatty-acyl-CoA binding;acyl-CoA dehydrogenase activity;electron carrier activity;flavin adenine dinucleotide binding;oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor;response to symbiotic fungus;fatty acid beta-oxidation using acyl-CoA dehydrogenase;root hair elongation;lipid homeostasis | ec:1.3.99.3 | |
| Phvul.009G252200.1 | probable polygalacturonase | extracellular region;integral component of membrane;polygalacturonase activity;carbohydrate metabolic process;cell wall organization | ec:3.2.1.15-pectin depolymerase | Starch and sucrose metabolism;Pentose and glucuronate interconversions |
| Phvul.009G254500.1 | calmodulin-binding transcription activator 5-like | nucleus;integral component of membrane;transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding;sequence-specific DNA binding;transcription from RNA polymerase II promoter;positive regulation of transcription from RNA polymerase II promoter | | |
| Phvul.009G254500.2 | calmodulin-binding transcription activator 5-like | nucleus;transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding;sequence-specific DNA binding;transcription from RNA polymerase II promoter;positive regulation of transcription from RNA polymerase II promoter | | |
| Phvul.009G254600.1 | conserved oligomeric Golgi complex subunit 4-like | endoplasmic reticulum;cytosol;Golgi transport complex;retrograde transport, vesicle recycling within Golgi;retrograde vesicle-mediated transport, Golgi to ER;Golgi organization;Golgi vesicle prefusion complex stabilization | | |
| Phvul.009G256200.1 | PH-interacting isoform X1 | nucleus;Cul4-RING E3 ubiquitin ligase complex;DNA binding;regulation of transcription from RNA polymerase II promoter;cytoskeleton organization;regulation of cell shape;response to hormone | | |
| Phvul.009G257900.1 | conserved oligomeric Golgi complex subunit 4 | endoplasmic reticulum;cytosol;Golgi transport complex;retrograde transport, vesicle recycling within Golgi;retrograde vesicle-mediated transport, Golgi to ER;Golgi organization;Golgi vesicle prefusion complex stabilization | | |

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| Phvul.009G258800.1 | caffeic acid 3-O-methyltransferase | O-methyltransferase activity;quercetin 3-O-methyltransferase activity;protein dimerization activity;methylation | ec:2.1.1;ec:2.1.1.76-3-O-methyltransferase | Flavone and flavonol biosynthesis |
| Phvul.009G260300.1 | inactive purple acid phosphatase | hydrolase activity;metabolic process | | |
| Phvul.009G260500.1 | tyrosine-sulfated glycopeptide receptor 1 | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10.1 | |
| Phvul.009G260900.1 | STRUBBELIG-RECEPTOR FAMILY 6 | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.009G260900.2 | STRUBBELIG-RECEPTOR FAMILY 6 | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.009G261000.1 | GDP-fucose O-fucosyltransferase | integral component of membrane;peptide-O-fucosyltransferase activity;signal transduction;protein O-linked fucosylation | ec:2.4.1.221-GDP-L-fucose:polypeptide fucosyltransferase | Other types of O-glycan biosynthesis |
| Phvul.009G261600.1 | pumilio homolog 23 | RNA binding;auxin homeostasis | | |
| Phvul.009G262400.1 | dnaJ homolog subfamily B member 6-like isoform X4 | | | |
| Phvul.009G263000.1 | exportin-T | nuclear pore;cytosol;nuclear matrix;tRNA binding;Ran GTPase binding;nucleobase-containing compound transmembrane transporter activity;mRNA export from nucleus;N-terminal protein myristoylation;protein import into nucleus;photomorphogenesis;embryo development ending in seed dormancy;seed germination;flower development;regulation of flower development;meristem initiation;seed dormancy process;sugar mediated signaling pathway;vegetative to reproductive phase transition of meristem;protein ubiquitination;lipid storage;response to freezing;tRNA re-export from nucleus | | |
| Phvul.010G001900.1 | Pyridoxal biosynthesis PDX2 | cytosol;glutaminase complex;glutaminase activity;transferase activity;protein heterodimerization activity;pyridoxine metabolic process;vitamin B6 biosynthetic process;pyridoxal phosphate biosynthetic process | ec:3.5.1.2-glutaminase I | Arginine biosynthesis;D-Glutamine and D-glutamate metabolism;Alanine, aspartate and glutamate metabolism |
| Phvul.010G002700.1 | DUF247 domain | integral component of membrane | | |
| Phvul.010G003100.1 | lactosylceramide 4-alpha-galactosyltransferase-like | integral component of membrane | | |
| Phvul.010G003200.1 | 30S ribosomal S31, chloroplastic | ribosome;chloroplast stroma;chloroplast envelope;plastid translation | | |
| Phvul.010G003300.1 | DUF247 domain | integral component of membrane | | |
| Phvul.010G004000.1 | NRT1 PTR FAMILY -like | integral component of membrane;transporter activity;transport | | |
| Phvul.010G004700.1 | disease resistance RPP13 1 | ADP binding;defense response | | |
| Phvul.010G004700.2 | disease resistance RPP13 1 | ADP binding;defense response | | |
| Phvul.010G005100.1 | sulfoquinovosyl transferase SQD2 | transferase activity, transferring glycosyl groups;metabolic process | | |
| Phvul.010G005700.1 | DUF3527 domain | | | |
| Phvul.010G005700.2 | DUF3527 domain | | | |
| Phvul.010G005700.3 | DUF3527 domain | | | |
| Phvul.010G006700.1 | fructokinase-like 1, chloroplastic | nucleus;chloroplast nucleoid;kinase activity;phosphotransferase activity, alcohol group as acceptor;rRNA processing;tRNA metabolic process;chloroplast | | |

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| | | organization;embryo development ending in seed dormancy;thylakoid membrane organization;vegetative to reproductive phase transition of meristem;iron-sulfur cluster assembly;phosphorylation;transcription from plastid promoter;positive regulation of transcription, DNA-templated;plant ovule development | | |
| Phvul.010G007200.1 | hypothetical protein PHAVU_010G007200g | | | |
| Phvul.010G007400.1 | GDP-fucose O-fucosyltransferase | cytoplasm;integral component of membrane;transferase activity, transferring glycosyl groups;metabolic process | | |
| Phvul.010G009000.1 | 7-deoxyloganetic acid glucosyltransferase-like | intracellular membrane-bounded organelle;cyanohydrin beta-glucosyltransferase activity;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1.85-beta-glucosyltransferase | Cyanoamino acid metabolism |
| Phvul.010G009400.1 | NRT1 PTR FAMILY -like | integral component of membrane;transporter activity;oligopeptide transport | | |
| Phvul.010G009400.2 | NRT1 PTR FAMILY -like | integral component of membrane;transporter activity;oligopeptide transport | | |
| Phvul.010G011300.1 | NAD(P)-binding rossmann-fold | chloroplast stroma;thylakoid;apoplast;copper ion binding;polysaccharide catabolic process;starch metabolic process;rRNA processing;response to cold;plant-type cell wall organization;salicylic acid biosynthetic process;defense response, incompatible interaction;chlorophyll biosynthetic process;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;photosynthesis, light reaction | | |
| Phvul.010G012400.1 | Mitochondrial import inner membrane translocase subunit Tim9 | mitochondrial intermembrane space protein transporter complex;mitochondrial inner membrane protein insertion complex;mitochondrial protein-transporting ATPase activity;metal ion binding;RNA methylation;photorespiration;protein import into mitochondrial inner membrane;chaperone-mediated protein transport | ec:3.6.3.51 | |
| Phvul.010G013800.1 | UDP-glucose:sterol 3-O-glucosyltransferase | intracellular membrane-bounded organelle;sterol 3-beta-glucosyltransferase activity;flavonoid biosynthetic process;lipid glycosylation;flavonoid glucuronidation | ec:2.4.1.173 | |
| Phvul.010G014200.1 | hypothetical protein PHAVU_010G014200g | chloroplast thylakoid membrane | | |
| Phvul.010G014700.1 | Poly , | integral component of membrane;catalytic activity;binding;cellular metabolic process;primary metabolic process;organic substance metabolic process | | |
| Phvul.010G014900.1 | far-red elongated hypocotyl , | | | |
| Phvul.010G016400.1 | legume-specific | integral component of membrane | | |
| Phvul.010G016900.1 | aldo-keto reductase family 4 member C9-like | alcohol dehydrogenase (NADP+) activity;oxidation-reduction process | ec:1.1.1.2-dehydrogenase (NADP+) | Biosynthesis of antibiotics;Glycolysis / Gluconeogenesis;Glycerolipid metabolism;Caprolactam degradation;Pentose and glucuronate interconversions |
| Phvul.010G018400.1 | disease resistance LAZ5-like isoform X1 | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.010G018600.1 | myosin-binding 7 isoform X1 | integral component of membrane | | |

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| Phvul.010G018900.1 | G-type lectin S-receptor-like Serine Threonine-kinase | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;carbohydrate binding;ubiquitin protein ligase binding;protein phosphorylation;innate immune response;recognition of pollen | ec:2.7.11 | |
| Phvul.010G018900.2 | G-type lectin S-receptor-like Serine Threonine-kinase | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;carbohydrate binding;ubiquitin protein ligase binding;protein phosphorylation;innate immune response;recognition of pollen | ec:2.7.11 | |
| Phvul.010G019500.1 | alkane hydroxylase MAH1-like | integral component of membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.010G020000.1 | XRI1-like isoform X1 | | | |
| Phvul.010G020100.1 | RNA polymerase I-specific transcription initiation factor RRN3 | translation initiation factor activity;translational initiation | | |
| Phvul.010G020200.1 | DNA-directed RNA polymerase III subunit RPC8 | DNA-directed RNA polymerase III complex;RNA polymerase III activity;hydrolase activity;transcription initiation from RNA polymerase III promoter;lipid metabolic process | | |
| Phvul.010G020300.1 | UBX domain-containing 1-like | cytosol;metal ion binding;protein glycosylation;protein targeting to vacuole | | |
| Phvul.010G020700.1 | hypothetical protein PHAVU_010G020700g | intracellular;GTP binding;small GTPase mediated signal transduction;protein transport | | |
| Phvul.010G023900.1 | probable copper-transporting ATPase HMA5 | integral component of plasma membrane;intracellular membrane-bounded organelle;nucleotide binding;copper-exporting ATPase activity;copper ion binding;metabolic process;copper ion export | ec:3.6.3.4 | |
| Phvul.010G026000.1 | TMV resistance N-like | ADP binding;defense response;signal transduction | | |
| Phvul.010G026600.1 | disease resistance LAZ5-like isoform X1 | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.010G026700.1 | disease resistance LAZ5-like isoform X1 | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.010G026900.1 | TMV resistance N-like isoform X2 | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.010G027100.1 | disease resistance LAZ5-like isoform X1 | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.010G027200.1 | TMV resistance N-like | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.010G027600.1 | hypothetical protein PHAVU_010G027600g | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.010G027800.1 | disease resistance LAZ5-like isoform X1 | ATP binding;ADP binding;signal transduction | | |
| Phvul.010G027800.2 | disease resistance LAZ5-like isoform X1 | ATP binding;ADP binding;signal transduction | | |
| Phvul.010G028500.1 | disease resistance TAO1-like | ADP binding;defense response;signal transduction | | |
| Phvul.010G028500.2 | TMV resistance N-like | ADP binding;defense response;signal transduction | | |
| Phvul.010G028500.3 | TMV resistance N-like | ADP binding;defense response;signal transduction | | |
| Phvul.010G028600.1 | TMV resistance N-like | ATP binding;ADP binding;defense response;signal transduction | | |

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| Phvul.010G029200.1 | disease resistance CSA1 | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.010G029400.1 | TMV resistance N-like | ADP binding | | |
| Phvul.010G029600.1 | disease resistance LAZ5-like isoform X1 | ATP binding;ADP binding;defense response;signal transduction | | |
| Phvul.010G031700.1 | Gamma-tubulin complex component 2 | equatorial microtubule organizing center;centrosome;spindle pole body;gamma-tubulin small complex;guanylate cyclase activity;structural constituent of cytoskeleton;gamma-tubulin binding;microtubule minus-end binding;cGMP biosynthetic process;meiotic nuclear division;cytoplasmic microtubule organization;centrosome duplication;interphase microtubule nucleation by interphase microtubule organizing center;positive regulation of microtubule nucleation;mitotic spindle assembly | ec:4.6.1.2-cyclase | Purine metabolism |
| Phvul.010G032700.1 | transport SEC23 | COPII vesicle coat;zinc ion binding;intracellular protein transport;ER to Golgi vesicle-mediated transport | | |
| Phvul.010G036300.1 | ubiquitin-like-conjugating enzyme ATG10 | membrane;ubiquitin activating enzyme activity;autophagy;protein ubiquitination | | |
| Phvul.010G039700.1 | PREDICTED: uncharacterized protein LOC106774021 isoform X1 | | | |
| Phvul.010G043700.1 | Eukaryotic translation initiation factor 4G | translation initiation factor activity;protein kinase activity;ATP binding;translational initiation;protein phosphorylation | | |
| Phvul.010G044700.1 | heterogeneous nuclear ribonucleo | viral nucleocapsid;intracellular ribonucleoprotein complex;nucleotide binding;nucleic acid binding | | |
| Phvul.010G044700.2 | heterogeneous nuclear ribonucleo | viral nucleocapsid;intracellular ribonucleoprotein complex;nucleotide binding;nucleic acid binding | | |
| Phvul.010G044700.3 | heterogeneous nuclear ribonucleo | viral nucleocapsid;intracellular ribonucleoprotein complex;nucleotide binding;nucleic acid binding | | |
| Phvul.010G045600.1 | dol-P-Man:Man(7)c(2)-PP-Dol alpha-1,6-mannosyltransferase | integral component of membrane;alpha-1,6-mannosyltransferase activity;protein N-linked glycosylation;ER-associated ubiquitin-dependent protein catabolic process;mannosylation | ec:2.4.1 | |
| Phvul.010G045600.2 | dol-P-Man:Man(7)c(2)-PP-Dol alpha-1,6-mannosyltransferase | integral component of membrane;alpha-1,6-mannosyltransferase activity;protein N-linked glycosylation;ER-associated ubiquitin-dependent protein catabolic process;mannosylation | ec:2.4.1 | |
| Phvul.010G046200.1 | pentatricopeptide repeat-containing At1g15510, chloroplastic | zinc ion binding;microtubule-severing ATPase activity;RNA modification;chloroplast organization;growth | ec:3.6.4.3 | |
| Phvul.010G048300.1 | pentatricopeptide repeat-containing At4g32430, mitochondrial | | | |
| Phvul.010G048700.1 | cytochrome P450 family | integral component of membrane;monooxygenase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;heme binding;oxidation-reduction process | | |
| Phvul.010G049400.1 | glycyl-tRNA synthetase alpha chain beta chain | mitochondrion;chloroplast stroma;glycine-tRNA ligase activity;ATP binding;protein dimerization activity;glycyl-tRNA aminoacylation;chloroplast organization;embryo development ending in seed dormancy;regulation of embryonic development;plant ovule development | ec:6.1.1.14-ligase | Aminoacyl-tRNA biosynthesis |

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| Phvul.010G049800.1 | phospholipase A(1) DAD1, chloroplastic-like | phosphatidylcholine 1-acylhydrolase activity;phosphatidylserine 1-acylhydrolase activity;1-acyl-2-lysophosphatidylserine acylhydrolase activity;lipid metabolic process | ec:3.1.1.32-A1 | alpha-Linolenic acid metabolism;Glycerophospholipid metabolism |
| Phvul.010G050000.1 | serine threonine-kinase D6PK-like | nucleus;cytoplasm;plasma membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;determination of bilateral symmetry;organ morphogenesis;meristem initiation;xylem and phloem pattern formation;meristem maintenance;xylem development;intracellular signal transduction;cell wall macromolecule metabolic process;flower morphogenesis;negative regulation of biological process | ec:2.7.11 | |
| Phvul.010G054200.2 | TMV resistance N-like | ADP binding;defense response;signal transduction | | |
| Phvul.010G056500.1 | pentatricopeptide repeat-containing At2g17670 | intracellular;protein targeting to mitochondrion | | |
| Phvul.010G057800.1 | transmembrane 87B-like | integral component of membrane | | |
| Phvul.010G058700.1 | cell wall integrity and stress response component 4-like | | | |
| Phvul.010G063700.1 | disease resistance At3g14460 | ADP binding;defense response | | |
| Phvul.010G065600.1 | ferritin-2, chloroplastic | chloroplast;ferroxidase activity;ferric iron binding;iron ion transport;cellular iron ion homeostasis;oxidation-reduction process | ec:1.16.3.1-ceruloplasmin | Porphyrin and chlorophyll metabolism |
| Phvul.010G068200.1 | DETOXIFICATION 53-like | integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.010G070600.1 | Transcription factor UNE10 | protein dimerization activity | | |
| Phvul.010G070600.2 | transcription factor UNE10-like | protein dimerization activity | | |
| Phvul.010G070600.3 | transcription factor UNE10-like | protein dimerization activity | | |
| Phvul.010G071600.1 | Holliday junction resolvase | nucleic acid binding;hydrolase activity;rRNA processing | | |
| Phvul.010G071900.1 | Anthocyanidin 3-O-glucosyltransferase 5 | intracellular membrane-bounded organelle;coniferyl-alcohol glucosyltransferase activity;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | ec:2.4.1.111-glucosyltransferase | Phenylpropanoid biosynthesis |
| Phvul.010G072500.1 | EF-hand pair | calcium ion binding | | |
| Phvul.010G072500.2 | EF-hand pair | calcium ion binding | | |
| Phvul.010G072500.3 | EF-hand pair | calcium ion binding | | |
| Phvul.010G072700.1 | Scarecrow 6 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.010G072900.1 | scarecrow 6 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.010G073200.1 | transcription factor bHLH140 | DNA binding;DNA 5'-adenosine monophosphate hydrolase activity;DNA repair;DNA recombination;meiosis I;regulation of nucleobase-containing compound metabolic process;regulation of chromosome organization;xylan metabolic process;chromosome organization;regulation of macromolecule metabolic process;regulation of biological quality;nucleic acid phosphodiester bond hydrolysis;nuclear chromosome segregation | | |
| Phvul.010G073300.1 | receptor 12 | integral component of membrane;transferase activity;metabolic process | | |
| Phvul.010G073800.1 | laccase-4-like | apoplast;copper ion binding;L-ascorbate oxidase activity;oxidoreductase activity, oxidizing metal ions;hydroquinone:oxygen oxidoreductase activity;lignin biosynthetic process;glucuronoxylan metabolic | ec:1.10.3.3-oxidase;ec:1.10.3.2 | Ascorbate and aldarate metabolism |

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| | | process;xylan biosynthetic process;lignin catabolic process;oxidation-reduction process | | |
| Phvul.010G081900.1 | pentatricopeptide repeat-containing At2g22410, mitochondrial | nucleic acid binding;zinc ion binding;protein methyltransferase activity;protein methylation | ec:2.1.1 | |
| Phvul.010G081900.2 | pentatricopeptide repeat-containing At2g22410, mitochondrial | nucleic acid binding;zinc ion binding;protein methyltransferase activity;protein methylation | ec:2.1.1 | |
| Phvul.010G084900.1 | LOB domain-containing 19 | | | |
| Phvul.010G086700.1 | Poly(A) RNA polymerase cid11 | RNA uridylyltransferase activity;nuclear-transcribed mRNA catabolic process;protein N-linked glycosylation;photoperiodism, flowering | ec:2.7.7.52 | |
| Phvul.010G089100.1 | transcription factor TCP9 | integral component of membrane;biological regulation | | |
| Phvul.010G091000.1 | F-box PP2-A13 | carbohydrate binding;response to sucrose;response to fructose | | |
| Phvul.010G092500.1 | E3 ubiquitin- ligase ATL59 | integral component of membrane;zinc ion binding;ligase activity;metabolic process | | |
| Phvul.010G093900.1 | methionine adenosyltransferase 2 subunit beta | methionine adenosyltransferase activity;metabolic process | ec:2.5.1.6-adenosyltransferase | Cysteine and methionine metabolism |
| Phvul.010G094300.1 | hypothetical protein PHAVU_010G094300g | | | |
| Phvul.010G094300.2 | hypothetical protein PHAVU_010G094300g | | | |
| Phvul.010G094400.1 | zinc finger C-x8-C-x5-C-x3-H type | metal ion binding | | |
| Phvul.010G096400.1 | myb transcription factor MIXTA | DNA binding;regulation of biological process | | |
| Phvul.010G097800.1 | MATH domain and coiled-coil domain-containing At3g58250-like | | | |
| Phvul.010G098500.1 | transcription factor EGL1 isoform X1 | protein dimerization activity | | |
| Phvul.010G098500.2 | transcription factor EGL1 isoform X2 | protein dimerization activity | | |
| Phvul.010G099200.1 | phosphatidylinositol N-acetyglucosaminlytransferase subunit P | | | |
| Phvul.010G099500.1 | signal peptide peptidase-like 4 | integral component of membrane;aspartic-type endopeptidase activity;proteolysis | ec:3.4.23 | |
| Phvul.010G100100.1 | ATP-dependent helicase BRM-like | nucleus;helicase activity;ATP binding;DNA-dependent ATPase activity;transferase activity;regulation of transcription, DNA-templated;metabolic process;regulation of gene expression, epigenetic;ATP-dependent chromatin remodeling | | |
| Phvul.010G101500.1 | ferric reduction oxidase 2-like | integral component of membrane;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.010G102500.1 | N6-adenosine-methyltransferase MT-A70-like | chloroplast;nuclear speck;mRNA (2'-O-methyladenosine-N6-)-methyltransferase activity;mRNA methylation | ec:2.1.1.62 | |
| Phvul.010G103800.1 | FK506-binding 4 | cytoplasm;transition metal ion binding;metal ion transport;cellular transition metal ion homeostasis | | |
| Phvul.010G104900.1 | 3-methyl-2-oxobutanoate hydroxymethyltransferase 1, mitochondrial-like | 3-methyl-2-oxobutanoate hydroxymethyltransferase activity;methyltransferase activity;pantothenate biosynthetic process;methylation | ec:2.1.2.11-hydroxymethyltransferase | Pantothenate and CoA biosynthesis |
| Phvul.010G105900.1 | group 1 family glycosyltransferase | endosome;trans-Golgi network;integral component of membrane;transferase activity;response to hypoxia;galactolipid biosynthetic process | | |

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| Phvul.010G107600.1 | dihydroorotase, mitochondrial-like | chloroplast;dihydroorotase activity;pyrimidine nucleobase biosynthetic process | ec:3.5.2.3-carbamoylaspartic dehydrase | Pyrimidine metabolism |
| Phvul.010G107600.2 | dihydroorotase, mitochondrial-like | chloroplast;dihydroorotase activity;pyrimidine nucleobase biosynthetic process | ec:3.5.2.3-carbamoylaspartic dehydrase | Pyrimidine metabolism |
| Phvul.010G107700.1 | F-box kelch-repeat At3g61590 | ubiquitin-protein transferase activity;lipid transport;protein ubiquitination;animal organ development | | |
| Phvul.010G107700.2 | F-box kelch-repeat At3g61590 | ubiquitin-protein transferase activity;lipid transport;protein ubiquitination;animal organ development | | |
| Phvul.010G109100.1 | hypothetical protein PHAVU_010G109100g | DNA binding;protein dimerization activity | | |
| Phvul.010G110700.1 | Proline-, glutamic acid- and leucine-rich 1 | | | |
| Phvul.010G110800.1 | mediator of RNA polymerase II transcription subunit 19a-like | | | |
| Phvul.010G112300.1 | dentin sialophospho | | | |
| Phvul.010G112700.1 | Poly(A) RNA polymerase cid14 | DNA-directed DNA polymerase activity;DNA biosynthetic process | ec:2.7.7.7-DNA polymerase | Purine metabolism;Pyrimidine metabolism |
| Phvul.010G114600.1 | Embryo defective 1703, isoform 1 | integral component of membrane | | |
| Phvul.010G115100.1 | kinesin light chain | | | |
| Phvul.010G115800.1 | probable serine threonine- kinase WNK10 isoform X1 | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.010G116400.1 | U-box domain-containing 44-like | ubiquitin-protein transferase activity;ligase activity;protein ubiquitination | | |
| Phvul.010G117400.1 | auxin-responsive family | response to auxin | | |
| Phvul.010G118300.1 | CBL-interacting serine threonine-kinase 9 | cytoplasm;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;intracellular signal transduction | ec:2.7.11 | |
| Phvul.010G118400.1 | probable L-gulonolactone oxidase 6 | membrane;D-arabinono-1,4-lactone oxidase activity;L-gulonolactone oxidase activity;flavin adenine dinucleotide binding;oxidation-reduction process | ec:1.1.3.37;ec:1.1.3.8-oxidase | Ascorbate and aldarate metabolism |
| Phvul.010G119300.1 | Granule-bound starch synthase 1, chloroplastic amyloplastic | amyloplast;chloroplast;glycogen (starch) synthase activity;response to hypoxia;myo-inositol hexakisphosphate biosynthetic process;starch biosynthetic process;galactolipid biosynthetic process | ec:2.4.1.11-synthase | Starch and sucrose metabolism |
| Phvul.010G120800.1 | Soluble inorganic pyrophosphatase | nucleus;cytosol;membrane;magnesium ion binding;inorganic diphosphatase activity;RNA splicing, via endonucleolytic cleavage and ligation;phosphate-containing compound metabolic process;methionine biosynthetic process;lipid storage | ec:3.6.1.1-diphosphatase | Oxidative phosphorylation |
| Phvul.010G121700.1 | transcription factor 25 | cytosol | | |
| Phvul.010G122100.1 | STRUBBELIG-RECEPTOR FAMILY 6 | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.010G122300.1 | K+-H+ exchange | mitochondrion;vacuolar membrane;plastid;integral component of membrane | | |
| Phvul.010G123900.1 | AT-rich interactive domain-containing 4-like | DNA binding;zinc ion binding | | |
| Phvul.010G124800.1 | GDSL esterase lipase 5-like | lipase activity;9,9'-dicis-carotene:quinone oxidoreductase activity;7,9,9'-tricis-neurosporene:quinone oxidoreductase activity;proline transport;9,9'-di-cis-zeta-carotene desaturation to 7,9,7',9'-tetra-cis-lycopene;oxidation-reduction process | ec:3.1.1;ec:1.3.5.6-desaturase | Carotenoid biosynthesis |

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| Phvul.010G126600.1 | auxin-repressed kDa isoform X1 | membrane | | |
| Phvul.010G126700.1 | chaperone domain | | | |
| Phvul.010G127600.1 | exocyst complex component EXO70A1-like | exocyst;exocytosis | | |
| Phvul.010G131900.1 | disease resistance RML1A-like | integral component of membrane;ADP binding;defense response;signal transduction | | |
| Phvul.010G132100.1 | hypothetical protein PHAVU_010G132100g | | | |
| Phvul.010G132200.1 | disease resistance RML1A-like | integral component of membrane;ADP binding;defense response;signal transduction | | |
| Phvul.010G132900.1 | phospholipid:diacylglycerol acyltransferase 1-like | vacuole;endoplasmic reticulum;integral component of membrane;O-acyltransferase activity;phospholipid:diacylglycerol acyltransferase activity;lipid metabolic process | ec:2.3.1.158-acyltransferase;ec:2.3.1 | Glycerolipid metabolism |
| Phvul.010G133700.1 | hypothetical protein PHAVU_010G133700g | integral component of membrane | | |
| Phvul.010G136000.1 | telomere repeat-binding factor 4-like | nucleosome;nucleus;DNA binding;nucleosome assembly | | |
| Phvul.010G136600.1 | probable phospholipid-transporting ATPase 4 isoform X1 | Golgi membrane;trans-Golgi network;plasma membrane;integral component of membrane;magnesium ion binding;phospholipid-translocating ATPase activity;ATP binding;metabolic process;phospholipid translocation;Golgi vesicle budding | ec:3.6.3.1 | |
| Phvul.010G136600.2 | probable phospholipid-transporting ATPase 4 isoform X1 | Golgi membrane;trans-Golgi network;plasma membrane;integral component of membrane;magnesium ion binding;phospholipid-translocating ATPase activity;ATP binding;metabolic process;phospholipid translocation;Golgi vesicle budding | ec:3.6.3.1 | |
| Phvul.010G138000.1 | F-box RNI superfamily | | | |
| Phvul.010G138200.1 | indeterminate-domain 11-like | nucleic acid binding;metal ion binding | | |
| Phvul.010G139100.1 | ROOT HAIR DEFECTIVE 3-like | endoplasmic reticulum membrane;integral component of membrane;GTPase activity;GTP binding;metabolic process | | |
| Phvul.010G139600.1 | cytochrome P450 family 90 | integral component of membrane;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;brassinosteroid homeostasis;sterol metabolic process;brassinosteroid biosynthetic process;leaf development;petal development;stamen development;oxidation-reduction process | ec:1.14.13 | |
| Phvul.010G139800.1 | phospholipase D alpha | membrane;phospholipase D activity;calcium ion binding;N-acylphosphatidylethanolamine-specific phospholipase D activity;lipid catabolic process;phosphatidylcholine metabolic process | ec:3.1.4.4-D | Ether lipid metabolism;Glycerophospholipid metabolism |
| Phvul.010G139800.2 | phospholipase D alpha | membrane;phospholipase D activity;calcium ion binding;N-acylphosphatidylethanolamine-specific phospholipase D activity;lipid catabolic process;phosphatidylcholine metabolic process | ec:3.1.4.4-D | Ether lipid metabolism;Glycerophospholipid metabolism |
| Phvul.010G140200.1 | inactive kinase SELMODRAFT_444075 | non-membrane spanning protein tyrosine kinase activity;ATP binding;hydrolase activity;peptidyl-tyrosine phosphorylation | ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.010G141800.1 | dentin sialophospho | | | |
| Phvul.010G142900.1 | EARLY FLOWERING 3-like isoform X1 | regulation of transcription, DNA-templated | | |
| Phvul.010G142900.2 | EARLY FLOWERING 3-like isoform X1 | | | |
| Phvul.010G142900.3 | EARLY FLOWERING 3-like isoform X1 | regulation of transcription, DNA-templated | | |

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| Phvul.010G142900.4 | EARLY FLOWERING 3-like isoform X1 | | | |
| Phvul.010G142900.5 | EARLY FLOWERING 3-like isoform X1 | regulation of transcription, DNA-templated | | |
| Phvul.010G142900.6 | EARLY FLOWERING 3-like isoform X1 | regulation of transcription, DNA-templated | | |
| Phvul.010G143200.1 | glucose-6-phosphate 1-dehydrogenase, chloroplastic-like | chloroplast stroma;glucose-6-phosphate dehydrogenase activity;NADP binding;glucose metabolic process;pentose-phosphate shunt, oxidative branch;response to blue light;regulation of proton transport;photosynthesis;isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway;protein autophosphorylation;oxidation-reduction process | ec:1.1.1.49-dehydrogenase (NADP+) | Biosynthesis of antibiotics;Pentose phosphate pathway;Glutathione metabolism |
| Phvul.010G143400.1 | pentatricopeptide repeat-containing At4g26680, mitochondrial | | | |
| Phvul.010G144400.1 | stress response NST1-like | | | |
| Phvul.010G144400.2 | stress response NST1-like | | | |
| Phvul.010G144800.1 | nuclear poly(A) polymerase 4-like isoform X2 | nucleus;RNA binding;polynucleotide adenylyltransferase activity;mRNA polyadenylation | ec:2.7.7.19 | |
| Phvul.010G145100.1 | lysM domain receptor-like kinase 3 isoform X1 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;microtubule nucleation | ec:2.7.11 | |
| Phvul.010G145900.1 | Casein kinase I-2 | protein serine/threonine kinase activity;ATP binding;Wnt signaling pathway;peptidyl-serine phosphorylation | ec:2.7.11 | |
| Phvul.010G147600.1 | transcription factor bHLH68-like isoform X1 | nucleus;core promoter sequence-specific DNA binding;transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding;protein dimerization activity;transcription from RNA polymerase II promoter;positive regulation of transcription from RNA polymerase II promoter | | |
| Phvul.010G147900.1 | NRT1 PTR FAMILY -like | integral component of membrane;transporter activity;oligopeptide transport | | |
| Phvul.010G148100.1 | Thioesterase superfamily , | | | |
| Phvul.010G149300.1 | proline-rich receptor kinase PERK1 | integral component of membrane;protein serine/threonine kinase activity;structural constituent of cell wall;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.010G149400.1 | sorting nexin carboxy-terminal | integral component of membrane;transferase activity;phosphatidylinositol binding;metabolic process | | |
| Phvul.010G149400.2 | sorting nexin carboxy-terminal | integral component of membrane;transferase activity;phosphatidylinositol binding;metabolic process | | |
| Phvul.010G151300.1 | stress response NST1-like | cytoplasm;transition metal ion binding;metal ion transport;cellular transition metal ion homeostasis | | |
| Phvul.010G151600.1 | N-alpha-acetyltransferase 15, auxiliary subunit-like | cytoplasm;peptide alpha-N-acetyltransferase activity;N-terminal peptidyl-methionine acetylation | ec:2.3.1.88 | |
| Phvul.010G152600.1 | DUF2921 family | endosome;trans-Golgi network;integral component of membrane | | |
| Phvul.010G152600.2 | DUF2921 family | endosome;trans-Golgi network;integral component of membrane | | |
| Phvul.010G154600.1 | DUF246 domain-containing | cytoplasm;transferase activity, transferring glycosyl groups;metabolic process | | |
| Phvul.010G155600.1 | TPR repeat | | | |
| Phvul.010G157200.1 | clustered mitochondria homolog | cytosol;translation initiation factor activity;translational initiation | | |

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| Phvul.010G157200.2 | clustered mitochondria homolog | cytosol;translation initiation factor activity;translational initiation | | |
| Phvul.010G157900.1 | mediator of RNA polymerase II transcription subunit 15a-like isoform X1 | transcription cofactor activity;regulation of transcription, DNA-templated | | |
| Phvul.010G160600.1 | DNA mismatch repair Msh6-1 | | | |
| Phvul.010G160600.2 | DNA mismatch repair Msh6-1 | | | |
| Phvul.011G000600.1 | TVP38 TMEM64 family membrane slr0305 | chloroplast;integral component of membrane;myo-inositol hexakisphosphate biosynthetic process | | |
| Phvul.011G000800.1 | FKBP-type peptidyl-prolyl cis-trans isomerase | endoplasmic reticulum membrane;peptidyl-prolyl cis-trans isomerase activity;FK506 binding;protein peptidyl-prolyl isomerization;single-organism process;chaperone-mediated protein folding | ec:5.2.1.8 | |
| Phvul.011G000800.2 | FKBP-type peptidyl-prolyl cis-trans isomerase | endoplasmic reticulum membrane;peptidyl-prolyl cis-trans isomerase activity;FK506 binding;protein peptidyl-prolyl isomerization;single-organism process;chaperone-mediated protein folding | ec:5.2.1.8 | |
| Phvul.011G001200.1 | phosphoinositide phosphatase SAC1 | mannosyl-oligosaccharide 1,2-alpha-mannosidase activity;phosphatidylinositol-3,5-bisphosphate 5-phosphatase activity;protein N-linked glycosylation;cell adhesion;unidimensional cell growth;plant-type cell wall biogenesis;trichome morphogenesis;glucuronoxylan metabolic process;inositol trisphosphate metabolic process;phosphatidylinositol-3-phosphate biosynthetic process;actin nucleation;xylan biosynthetic process;inositol phosphate dephosphorylation;root hair cell differentiation;cell wall organization | ec:3.1.3;ec:3.2.1.113-1,2-alpha-mannosidase | Various types of N-glycan biosynthesis;N-Glycan biosynthesis |
| Phvul.011G002700.1 | shoot gravitropism 2 (SGR2) | plasmodesma;plant-type vacuole membrane;phosphatidylcholine 1-acylhydrolase activity;metal ion binding;metabolic process;detection of gravity;amyloplast organization;negative gravitropism | ec:3.1.1.32-A1 | alpha-Linolenic acid metabolism;Glycerophospholipid metabolism |
| Phvul.011G002700.2 | shoot gravitropism 2 (SGR2) | plasmodesma;plant-type vacuole membrane;phosphatidylcholine 1-acylhydrolase activity;metal ion binding;metabolic process;detection of gravity;amyloplast organization;negative gravitropism | ec:3.1.1.32-A1 | alpha-Linolenic acid metabolism;Glycerophospholipid metabolism |
| Phvul.011G003700.1 | hypothetical protein PHAVU_011G003700g | | | |
| Phvul.011G005800.1 | MADS-box transcription factor | nucleus;DNA binding;transcription factor activity, sequence-specific DNA binding;protein dimerization activity;transcription, DNA-templated;regulation of transcription, DNA-templated;iron ion transport;cellular response to iron ion starvation;response to nitrate;vegetative to reproductive phase transition of meristem;nitrate transport;plant ovule development;lateral root development;developmental growth;root hair cell differentiation | | |
| Phvul.011G006200.1 | COP9 signalosome complex subunit 4 | proteasome complex;cytosol;COP9 signalosome;NEDD8-specific protease activity;photomorphogenesis;cullin deneddylation;positive regulation of G2/M transition of mitotic cell cycle | | |
| Phvul.011G009600.1 | dentin sialophospho-like | | | |
| Phvul.011G009800.1 | tRNA-dihydrouridine(47) synthase | nucleus;cytosol;phragmoplast;tRNA dihydrouridine synthase activity;flavin adenine dinucleotide binding;tRNA dihydrouridine synthesis;methylglyoxal catabolic process to D- | | |

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| | [NAD(P)(+)]-like isoform X1 | lactate via S-lactoyl-glutathione;oxidation-reduction process | | |
| Phvul.011G011000.1 | RETICULATA-RELATED 4, chloroplastic-like | mitochondrion;chloroplast inner membrane;integral component of membrane | | |
| Phvul.011G011400.1 | hypothetical protein PHAVU_011G0114000g, partial | DNA binding | | |
| Phvul.011G012000.1 | aspartokinase-homoserine dehydrogenase | chloroplast;aspartate kinase activity;homoserine dehydrogenase activity;amino acid binding;NADP binding;aspartate family amino acid biosynthetic process;phosphorylation;oxidation-reduction process | ec:1.1.1.3-dehydrogenase;ec:2.7.2.4-kinase | Biosynthesis of antibiotics;Cysteine and methionine metabolism;Lysine biosynthesis;Glycine, serine and threonine metabolismBiosynthesis of antibiotics;Cysteine and methionine metabolism;Lysine biosynthesis;Monobactam biosynthesis;Glycine, serine and threonine metabolism |
| Phvul.011G012000.2 | aspartokinase-homoserine dehydrogenase | chloroplast;aspartate kinase activity;homoserine dehydrogenase activity;amino acid binding;NADP binding;aspartate family amino acid biosynthetic process;phosphorylation;oxidation-reduction process | ec:1.1.1.3-dehydrogenase;ec:2.7.2.4-kinase | Biosynthesis of antibiotics;Cysteine and methionine metabolism;Lysine biosynthesis;Glycine, serine and threonine metabolismBiosynthesis of antibiotics;Cysteine and methionine metabolism;Lysine biosynthesis;Monobactam biosynthesis;Glycine, serine and threonine metabolism |
| Phvul.011G012700.1 | OBERON 4 | cell fate specification;embryonic pattern specification;embryonic meristem initiation | | |
| Phvul.011G016300.1 | glycerol-3-phosphate transporter 1 | integral component of membrane;transmembrane transporter activity;anion transport;transmembrane transport | | |
| Phvul.011G016600.1 | DNA topoisomerase 1-like | nucleolus;replication fork protection complex;DNA binding;DNA topoisomerase type I activity;DNA topoisomerase type II (ATP-hydrolyzing) activity;2-alkenal reductase [NAD(P)] activity;DNA replication;DNA topological change;chromatin remodeling;chromosome segregation;oxidation-reduction process | ec:5.99.1.3;ec:5.99.1.2;ec:1.3.1.74 | |
| Phvul.011G016600.2 | DNA topoisomerase 1-like | nucleolus;replication fork protection complex;DNA binding;DNA topoisomerase type I activity;DNA topoisomerase type II (ATP-hydrolyzing) activity;2-alkenal reductase [NAD(P)] activity;DNA replication;DNA topological change;chromatin remodeling;chromosome segregation;oxidation-reduction process | ec:5.99.1.3;ec:5.99.1.2;ec:1.3.1.74 | |
| Phvul.011G016900.1 | bromodomain-containing DDB_G0280777 | | | |
| Phvul.011G017900.1 | Bromodomain adjacent to zinc finger domain 1A | zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.011G017900.2 | RING FYVE PHD zinc finger , | zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.011G017900.3 | RING FYVE PHD zinc finger , | zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.011G017900.4 | Bromodomain adjacent to zinc finger domain 1A | zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |

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| Phvul.011G017900.5 | Bromodomain adjacent to zinc finger domain 1A | zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.011G017900.6 | Bromodomain adjacent to zinc finger domain 1A | zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.011G017900.7 | Bromodomain adjacent to zinc finger domain 1A | zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.011G017900.8 | RING FYVE PHD zinc finger , | zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.011G017900.9 | Bromodomain adjacent to zinc finger domain 1A | zinc ion binding;oxidoreductase activity;oxidation-reduction process | | |
| Phvul.011G018800.1 | impaired sucrose induction , | regulation of carbohydrate metabolic process | | |
| Phvul.011G019900.1 | probable arabinosyltransferase ARAD1 | Golgi apparatus;integral component of membrane;glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity;metabolic process | ec:2.4.1.224-4-alpha-N-acetylglucosaminyltransferase | Glycosaminoglycan biosynthesis - heparan sulfate / heparin |
| Phvul.011G020800.1 | probable methionine--tRNA ligase | cytoplasm;tRNA binding;methionine-tRNA ligase activity;ATP binding;methionyl-tRNA aminoacylation | ec:6.1.1.10-ligase | Aminoacyl-tRNA biosynthesis;Selenocompound metabolism |
| Phvul.011G021900.1 | myosin-related family | | | |
| Phvul.011G023300.1 | biotin synthase | biotin synthase activity;zinc ion binding;2 iron, 2 sulfur cluster binding;4 iron, 4 sulfur cluster binding;acetyl-CoA metabolic process;microtubule nucleation;biotin biosynthetic process;regulation of meristem growth;sterol biosynthetic process;brassinosteroid biosynthetic process;anther development | ec:2.8.1.6-synthase | Biotin metabolism |
| Phvul.011G023300.2 | biotin synthase | integral component of membrane;biotin synthase activity;zinc ion binding;2 iron, 2 sulfur cluster binding;4 iron, 4 sulfur cluster binding;acetyl-CoA metabolic process;microtubule nucleation;biotin biosynthetic process;regulation of meristem growth;sterol biosynthetic process;brassinosteroid biosynthetic process;anther development | ec:2.8.1.6-synthase | Biotin metabolism |
| Phvul.011G023500.1 | hypothetical protein PHAVU_011G023500g | | | |
| Phvul.011G023900.1 | Nucleosome-remodeling factor subunit BPTF | zinc ion binding | | |
| Phvul.011G023900.2 | Nucleosome-remodeling factor subunit BPTF | zinc ion binding | | |
| Phvul.011G024200.1 | probable S-acyltransferase 19 | integral component of membrane;zinc ion binding;protein-cysteine S-palmitoyltransferase activity;metabolic process | ec:2.3.1.225 | |
| Phvul.011G024200.2 | probable S-acyltransferase 19 | integral component of membrane;zinc ion binding;protein-cysteine S-palmitoyltransferase activity;metabolic process | ec:2.3.1.225 | |
| Phvul.011G025300.1 | signal recognition particle 43 kDa , chloroplastic | chloroplast thylakoid membrane;chloroplast envelope;signal recognition particle, chloroplast targeting;identical protein binding;response to blue light;response to sucrose;response to red light;regulation of proton transport;response to far red light;cysteine biosynthetic process;protein import into chloroplast thylakoid membrane;protein autophosphorylation | | |
| Phvul.011G026500.1 | Transcription factor bHLH121 | intracellular;transcription factor activity, sequence-specific DNA binding;protein dimerization activity;regulation of transcription, DNA-templated;fatty acid beta-oxidation;protein import into peroxisome matrix | | |

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| Phvul.011G026800.1 | Nucleoporin NUP188 like | nuclear pore inner ring;structural constituent of nuclear pore;RNA export from nucleus;protein import into nucleus | | |
| Phvul.011G029000.1 | Cytochrome P450, family 86, subfamily B, polypeptide 1 isoform 1 | integral component of membrane;iron ion binding;heme binding;aromatase activity;oxidation-reduction process | ec:1.14.14.1-monooxygenase | Linoleic acid metabolism;Arachidonic acid metabolism;Drug metabolism - cytochrome P450;Metabolism of xenobiotics by cytochrome P450;Caffeine metabolism;Aminobenzoate degradation;Tryptophan metabolism;Fatty acid degradation;Retinol metabolism;Steroid hormone biosynthesis |
| Phvul.011G029100.1 | RNI superfamily | nucleotide binding;DNA binding;DNA-directed DNA polymerase activity;3'-5' exonuclease activity;DNA replication;DNA biosynthetic process;nucleic acid phosphodiester bond hydrolysis | ec:2.7.7.7-DNA polymerase | Purine metabolism;Pyrimidine metabolism |
| Phvul.011G029200.1 | hypothetical protein PHAVU_011G029200g | integral component of membrane | | |
| Phvul.011G029800.1 | photosystem II stability assembly factor HCF136, chloroplastic | chloroplast stromal thylakoid;chloroplast envelope;thylakoid lumen;pentose-phosphate shunt;rRNA processing;response to blue light;chloroplast relocation;thylakoid membrane organization;response to red light;photosystem II assembly;response to far red light;PSII associated light-harvesting complex II catabolic process;chlorophyll biosynthetic process;carotenoid biosynthetic process;regulation of protein dephosphorylation;hydrogen peroxide catabolic process;transcription from plastid promoter;positive regulation of transcription, DNA-templated | | |
| Phvul.011G029800.2 | photosystem II stability assembly factor HCF136, chloroplastic | chloroplast stromal thylakoid;chloroplast envelope;thylakoid lumen;pentose-phosphate shunt;rRNA processing;response to blue light;chloroplast relocation;thylakoid membrane organization;response to red light;photosystem II assembly;response to far red light;PSII associated light-harvesting complex II catabolic process;chlorophyll biosynthetic process;carotenoid biosynthetic process;regulation of protein dephosphorylation;hydrogen peroxide catabolic process;transcription from plastid promoter;positive regulation of transcription, DNA-templated | | |
| Phvul.011G030700.1 | hypothetical protein PHAVU_011G030700g | ATP binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.4.3 | |
| Phvul.011G030700.2 | hypothetical protein PHAVU_011G030700g | ATP binding;microtubule-severing ATPase activity;metabolic process | ec:3.6.4.3 | |
| Phvul.011G031400.1 | DPH4 homolog | | | |
| Phvul.011G031400.2 | DPH4 homolog | | | |
| Phvul.011G032300.1 | DUF3067 family | chloroplast | | |
| Phvul.011G032700.1 | hypothetical protein PHAVU_011G032700g | | | |

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| Phvul.011G034700.1 | subtilisin-like protease | cell wall;membrane;serine-type endopeptidase activity;sulfur amino acid metabolic process;polysaccharide catabolic process;starch metabolic process;proteolysis;microtubule nucleation;cellular amino acid biosynthetic process;serine family amino acid metabolic process;plant-type cell wall modification;plant-type cell wall biogenesis;regulation of meristem growth;glucosinolate biosynthetic process | ec:3.4.21 | |
| Phvul.011G035600.1 | Kinase with adenine nucleotide alpha hydrolases-like domain, isoform 1 | non-membrane spanning protein tyrosine kinase activity;ATP binding;hydrolase activity;peptidyl-tyrosine phosphorylation | ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.011G035600.2 | Kinase with adenine nucleotide alpha hydrolases-like domain, isoform 1 | non-membrane spanning protein tyrosine kinase activity;ATP binding;hydrolase activity;peptidyl-tyrosine phosphorylation | ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.011G037800.1 | transcription initiation factor TFIID subunit 14b-like | regulation of transcription, DNA-templated;vegetative to reproductive phase transition of meristem;regulation of timing of transition from vegetative to reproductive phase;regulation of histone H4 acetylation | | |
| Phvul.011G039100.1 | fructose-bisphosphate aldolase 1, chloroplastic | fructose-bisphosphate aldolase activity;glycolytic process | ec:4.1.2.13-aldolase | Biosynthesis of antibiotics;Pentose phosphate pathway;Methane metabolism;Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis;Fructose and mannose metabolism |
| Phvul.011G039100.2 | fructose-bisphosphate aldolase 1, chloroplastic | fructose-bisphosphate aldolase activity;glycolytic process | ec:4.1.2.13-aldolase | Biosynthesis of antibiotics;Pentose phosphate pathway;Methane metabolism;Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis;Fructose and mannose metabolism |
| Phvul.011G040300.1 | MATE efflux family 4, chloroplastic | chloroplast envelope;integral component of membrane;drug transmembrane transporter activity;antiporter activity;drug transmembrane transport | | |
| Phvul.011G040700.1 | kinesin motor catalytic domain | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;zinc ion binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1.3-adenylpyrophosphatase | Purine metabolism |
| Phvul.011G040700.2 | kinesin motor catalytic domain | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;zinc ion binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1.3-adenylpyrophosphatase | Purine metabolism |
| Phvul.011G040700.3 | kinesin-related 11-like isoform X2 | kinesin complex;microtubule;microtubule motor activity;ATP binding;microtubule binding;zinc ion binding;ATPase activity;microtubule-based movement;metabolic process | ec:3.6.1.3-adenylpyrophosphatase | Purine metabolism |
| Phvul.011G040800.1 | salt tolerance | nucleus;transcription factor activity, transcription factor binding;zinc ion binding;regulation of transcription, DNA-templated;photomorphogenesis | | |
| Phvul.011G040800.2 | salt tolerance | nucleus;transcription factor activity, transcription factor binding;zinc ion binding;regulation of transcription, DNA-templated;photomorphogenesis | | |
| Phvul.011G040800.3 | salt tolerance | nucleus;transcription factor activity, transcription factor binding;zinc ion binding;regulation of transcription, DNA-templated;photomorphogenesis | | |

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| Phvul.011G046200.1 | SWI SNF complex subunit SWI3D | nucleus;DNA binding;zinc ion binding | | |
| Phvul.011G046300.1 | BURP domain-containing 3-like | protein storage vacuole;seed development | | |
| Phvul.011G049000.1 | pentatricopeptide repeat-containing At2g15980 | | | |
| Phvul.011G050100.1 | extra-large guanine nucleotide-binding 1-like | GTPase activity;signal transducer activity;GTP binding;G-protein beta/gamma-subunit complex binding;G-protein coupled receptor signaling pathway;metabolic process;response to abiotic stimulus;response to abscisic acid;response to hexose;regulation of defense response;macromolecule localization;regulation of programmed cell death;innate immune response;negative regulation of biological process;cellular response to acid chemical;cellular response to organic substance;defense response to other organism;cellular response to oxygen-containing compound;single-organism intracellular transport | | |
| Phvul.011G050100.2 | extra-large GTP-binding | intracellular;GTPase activity;signal transducer activity;GTP binding;G-protein beta/gamma-subunit complex binding;protein targeting to membrane;G-protein coupled receptor signaling pathway;response to water deprivation;response to wounding;systemic acquired resistance;salicylic acid biosynthetic process;response to ethylene;response to auxin;abscisic acid-activated signaling pathway;response to sucrose;response to glucose;response to fructose;response to jasmonic acid;salicylic acid mediated signaling pathway;regulation of plant-type hypersensitive response;response to mannitol;endoplasmic reticulum unfolded protein response;negative regulation of defense response;hyperosmotic salinity response;defense response to bacterium;negative regulation of programmed cell death;Golgi vesicle transport;lateral root development;defense response by callose deposition;regulation of root morphogenesis | | |
| Phvul.011G050100.3 | extra-large guanine nucleotide-binding 1-like | GTPase activity;signal transducer activity;GTP binding;G-protein beta/gamma-subunit complex binding;response to acid chemical;defense response;G-protein coupled receptor signaling pathway;metabolic process;response to hormone;response to carbohydrate | | |
| Phvul.011G050100.4 | extra-large guanine nucleotide-binding 1-like | GTPase activity;signal transducer activity;GTP binding;G-protein beta/gamma-subunit complex binding;response to acid chemical;defense response;G-protein coupled receptor signaling pathway;metabolic process;response to hormone;response to carbohydrate;localization;cellular response to organic substance | | |
| Phvul.011G050300.1 | serine threonine-kinase SMG1-like | protein serine/threonine kinase activity;ATP binding;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;DNA repair;protein phosphorylation | ec:2.7.11 | |
| Phvul.011G050300.2 | serine threonine-kinase SMG1-like | protein serine/threonine kinase activity;ATP binding;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;DNA repair;protein phosphorylation | ec:2.7.11 | |
| Phvul.011G050600.1 | B3 domain-containing transcription factor VRN1 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.011G050600.2 | B3 domain-containing transcription factor VRN1-like isoform X2 | nucleus;DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated | | |

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| Phvul.011G051400.1 | orn lys arg decarboxylase major region | lysine decarboxylase activity;metabolic process | ec:4.1.1.18-decarboxylase | Lysine degradation;Tropane, piperidine and pyridine alkaloid biosynthesis |
| Phvul.011G051900.1 | ribosome biogenesis BMS1 homolog | nucleus;hydrolase activity;mRNA export from nucleus;protein import into nucleus;ribosome biogenesis | | |
| Phvul.011G054400.1 | probable serine threonine- kinase GCN2 | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.011G054900.1 | ATPase family AAA domain | nucleus;chromatin binding;ATP binding;ATPase activity;histone binding;negative regulation of chromatin silencing;positive regulation of transcription from RNA polymerase II promoter;cell division | ec:3.6.1.3-adenylpyrophosphatase | Purine metabolism |
| Phvul.011G055500.1 | probable E3 ubiquitin- ligase ARI7 | ubiquitin ligase complex;cytoplasm;nucleic acid binding;zinc ion binding;ligase activity;ubiquitin conjugating enzyme binding;ubiquitin protein ligase activity;protein polyubiquitination;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;protein ubiquitination involved in ubiquitin-dependent protein catabolic process | | |
| Phvul.011G056200.1 | cyanogenic beta-glucosidase, | integral component of membrane;lactase activity;beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1.21-gentiobiase;ec:3.2.1.108-lactase-phlorizin hydrolase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesisGalactose metabolism |
| Phvul.011G056600.1 | multiple C2 and transmembrane domain-containing 1-like | plasmodesma;integral component of membrane;phosphatidylserine decarboxylase activity;calcium ion binding;calcium-dependent phospholipid binding;transferase activity, transferring glycosyl groups;metabolic process | ec:4.1.1.65-decarboxylase | Glycerophospholipid metabolism |
| Phvul.011G057300.1 | hypothetical protein PHAVU_011G057300g | plasma membrane | | |
| Phvul.011G057500.1 | LOB domain-containing 4 | carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity;metabolic process;determination of bilateral symmetry;polarity specification of adaxial/abaxial axis;meristem initiation;regulation of meristem growth | ec:6.3.5.5-synthase (glutamine-hydrolysing) | Alanine, aspartate and glutamate metabolism;Pyrimidine metabolism |
| Phvul.011G058200.1 | hypothetical protein PHAVU_011G058200g | integral component of membrane | | |
| Phvul.011G060300.1 | UDP-glucose iridoid glucosyltransferase-like | intracellular membrane-bounded organelle;quercetin 3-O-glucosyltransferase activity;quercetin 7-O-glucosyltransferase activity;flavonoid biosynthetic process;flavonoid glucuronidation | | |
| Phvul.011G061000.1 | pentatricopeptide repeat-containing At4g01570 | | | |
| Phvul.011G063100.1 | scarecrow 14 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.011G064300.1 | ENTH VHS family | | | |
| Phvul.011G066000.1 | THO complex subunit 4A | nucleotide binding;nucleic acid binding | | |
| Phvul.011G068900.1 | 3-ketoacyl-synthase 12-like | integral component of membrane;transferase activity, transferring acyl groups other than amino-acyl groups;fatty acid biosynthetic process | | |
| Phvul.011G069600.1 | receptor kinase HERK 1 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.011G070100.1 | DNA-directed RNA polymerase III subunit rpc1 | DNA-directed RNA polymerase III complex;RNA polymerase III activity;DNA binding;transcription from RNA polymerase III promoter | | |

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| Phvul.011G070400.1 | transmembrane , | integral component of membrane | | |
| Phvul.011G071200.1 | CCR4-NOT transcription complex subunit 4 | CCR4-NOT complex;nucleotide binding;nucleic acid binding;ubiquitin-protein transferase activity;zinc ion binding;ligase activity;protein ubiquitination | | |
| Phvul.011G071400.2 | mitogen-activated kinase 3 | intracellular;MAP kinase activity;ATP binding;MAPK cascade;activation of MAPK activity involved in osmosensory signaling pathway;response to hypoxia;regulation of transcription, DNA-templated;protein targeting to membrane;response to osmotic stress;response to cold;detection of biotic stimulus;salicylic acid biosynthetic process;abscisic acid-activated signaling pathway;systemic acquired resistance, salicylic acid mediated signaling pathway;jasmonic acid mediated signaling pathway;camalexin biosynthetic process;response to UV-B;inflorescence development;regulation of hydrogen peroxide metabolic process;regulation of plant-type hypersensitive response;stomatal complex development;photosynthesis, light reaction;negative regulation of defense response;regulation of protein dephosphorylation;defense response to bacterium;negative regulation of programmed cell death;regulation of multi-organism process;plant ovule development;defense response to fungus;priming of cellular response to stress;regulation of stomatal complex patterning;regulation of stomatal complex development | ec:2.7.11.24-protein kinase | mTOR signaling pathway |
| Phvul.011G071800.1 | arogenate dehydratase prephenate dehydratase 2, chloroplastic-like | chloroplast stroma;prephenate dehydratase activity;amino acid binding;arogenate dehydratase activity;L-phenylalanine biosynthetic process;vernalization response;anthocyanin accumulation in tissues in response to UV light;carpel development | ec:4.2.1.91-dehydratase;ec:4.2.1.51-dehydratase | Biosynthesis of antibiotics;Phenylalanine, tyrosine and tryptophan biosynthesisBiosynthesis of antibiotics;Phenylalanine, tyrosine and tryptophan biosynthesis |
| Phvul.011G072000.1 | interactor of constitutive active ROPs 3 isoform X2 | | | |
| Phvul.011G072500.1 | RNA ligase, | RNA ligase (ATP) activity;2',3'-cyclic-nucleotide 3'-phosphodiesterase activity;ATP binding;polynucleotide 5'-hydroxyl-kinase activity;tRNA splicing, via endonucleolytic cleavage and ligation;phosphorylation | ec:6.5.1.3;ec:3.1.4.37;ec:2.7.1 | |
| Phvul.011G072500.2 | RNA ligase, | RNA ligase (ATP) activity;2',3'-cyclic-nucleotide 3'-phosphodiesterase activity;ATP binding;polynucleotide 5'-hydroxyl-kinase activity;tRNA splicing, via endonucleolytic cleavage and ligation;phosphorylation | ec:6.5.1.3;ec:3.1.4.37;ec:2.7.1 | |
| Phvul.011G074500.1 | fasciclin-like arabinogalactan 11 | integral component of membrane | | |
| Phvul.011G077800.1 | root cap late embryogenesis | | | |
| Phvul.011G078000.1 | heat shock with TPR , | cellular component organization;single-organism cellular process;single-organism developmental process;anatomical structure development | | |
| Phvul.011G079600.1 | SAND isoform X1 | cell;calcium ion transport;cellular zinc ion homeostasis;response to nematode;vesicle-mediated transport | | |
| Phvul.011G080000.1 | serine threonine-phosphatase 6 regulatory subunit 3 | | | |
| Phvul.011G080500.1 | glycosyltransferase family 2 | integral component of membrane;transferase activity;metabolic process | | |
| Phvul.011G080600.1 | cytokinin riboside 5 -monophosphate | nucleus;cytosol;hydrolase activity, hydrolyzing N-glycosyl compounds;cytokinin biosynthetic process | | |

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| | phosphoribohydrolase LOG1 | | | |
| Phvul.011G080800.1 | cyclic nucleotide-gated ion channel 15 | integral component of membrane;voltage-gated potassium channel activity;regulation of membrane potential;potassium ion transmembrane transport | | |
| Phvul.011G082700.1 | P-loop NTPase domain-containing LPA1 homolog 1-like | kinase activity;hydrolase activity;phosphorylation | | |
| Phvul.011G082700.2 | P-loop NTPase domain-containing LPA1 homolog 1-like | kinase activity;hydrolase activity;phosphorylation | | |
| Phvul.011G082800.1 | hypothetical protein PHAVU_011G082800g | | | |
| Phvul.011G083800.1 | cell division cycle 48 homolog | plasma membrane;ATP binding;microtubule-severing ATPase activity;cell cycle;metabolic process;cell division | ec:3.6.4.3 | |
| Phvul.011G084000.1 | ABC transporter F family member 1 | transporter activity;ATP binding;ATPase activity;glucose catabolic process;transport;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.011G084000.2 | ABC transporter F family member 1 | transporter activity;ATP binding;ATPase activity;glucose catabolic process;transport;methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione | ec:3.6.1.3-adenylpyrophosphatase | Purine metabolism |
| Phvul.011G085500.1 | hypothetical protein PHAVU_011G085500g | | | |
| Phvul.011G086700.1 | pheophorbide a oxygenase, chloroplastic | chloroplast thylakoid;chloroplast envelope;chlorophyllide a oxygenase [overall] activity;pheophorbide a oxygenase activity;metal ion binding;2 iron, 2 sulfur cluster binding;cell death;embryo development ending in seed dormancy;defense response to bacterium, incompatible interaction;leaf morphogenesis;thylakoid membrane organization;vegetative to reproductive phase transition of meristem;iron-sulfur cluster assembly;cell differentiation;positive regulation of transcription, DNA-templated;plant ovule development;oxidation-reduction process | ec:1.8;ec:1.14.13.122-oxygenase | Porphyrin and chlorophyll metabolism |
| Phvul.011G088100.1 | vacuolar sorting-associated 41 homolog | late endosome;HOPS complex;CORVET complex;zinc ion binding;GTPase binding;protein targeting to vacuole;gravitropism;vesicle-mediated transport;regulation of SNARE complex assembly;vacuole fusion, non-autophagic | | |
| Phvul.011G088300.1 | aspartic ase 2 | integral component of membrane;aspartic-type endopeptidase activity;transferase activity;proteolysis;protein catabolic process | ec:3.4.23 | |
| Phvul.011G089000.1 | ribulose-1,5-bisphosphate carboxylase oxygenase large subunit, partial (chloroplast) | chloroplast;magnesium ion binding | | |
| Phvul.011G090800.1 | WD repeat and FYVE domain-containing 3 | RNA polymerase I transcription factor complex;transcription from RNA polymerase I promoter | | |
| Phvul.011G090800.2 | WD repeat and FYVE domain-containing 3 | RNA polymerase I transcription factor complex;transcription from RNA polymerase I promoter | | |
| Phvul.011G090800.3 | WD repeat and FYVE domain-containing 3 | RNA polymerase I transcription factor complex;transcription from RNA polymerase I promoter | | |
| Phvul.011G091900.1 | DNA polymerase epsilon catalytic subunit A | nucleus;nucleotide binding;DNA binding;DNA-directed DNA polymerase activity;zinc ion binding;3'-5' exonuclease activity;DNA replication;DNA biosynthetic process;nucleic acid phosphodiester bond hydrolysis | ec:3.1;ec:2.7.7.7-DNA polymerase | Purine metabolism;Pyrimidine metabolism |

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| Phvul.011G092500.1 | Fatty acyl-reductase 3 | intracellular membrane-bounded organelle;fatty-acyl-CoA reductase (alcohol-forming) activity;wax biosynthetic process;suberin biosynthetic process;long-chain fatty-acyl-CoA metabolic process;oxidation-reduction process | | |
| Phvul.011G092600.1 | subtilisin-like protease | cell wall;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.011G092600.2 | subtilisin-like protease | cell wall;serine-type endopeptidase activity;proteolysis | ec:3.4.21 | |
| Phvul.011G093800.1 | F-box LRR-repeat At1g67190-like | | | |
| Phvul.011G095900.1 | mitochondrial fission ELM1-like | mitochondrial fission | | |
| Phvul.011G099500.1 | FAF-like, chloroplastic | | | |
| Phvul.011G099600.1 | BRI1 suppressor 1 (BSU1)-like 2 isoform 1 | phosphoprotein phosphatase activity;protein dephosphorylation;brassinosteroid mediated signaling pathway | ec:3.1;ec:3.1.3.41-nitrophenyl phosphatase;ec:3.1.3.16-phosphatase | Aminobenzoate degradationT cell receptor signaling pathway |
| Phvul.011G100500.1 | replication factor C1 | nucleus;DNA replication factor C complex;DNA clamp loader activity;ATP binding;resolution of meiotic recombination intermediates;DNA replication;DNA repair;response to abscisic acid;regulation of chromatin silencing;regulation of histone H3-K9 methylation | ec:3.6.1;ec:3.6.1.3-adenylpyrophosphatase;ec:3.6.1.15-phosphatase | Purine metabolismPurine metabolism;Thiamine metabolism |
| Phvul.011G101500.1 | cellulose synthase H1 | integral component of membrane;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming) | Starch and sucrose metabolism |
| Phvul.011G101700.1 | cellulose synthase H1 | integral component of membrane;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming) | Starch and sucrose metabolism |
| Phvul.011G101700.2 | cellulose synthase H1 | integral component of membrane;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming) | Starch and sucrose metabolism |
| Phvul.011G102500.1 | L-ascorbate oxidase homolog | plant-type cell wall;plasmodesma;copper ion binding;L-ascorbate oxidase activity;oxidoreductase activity, oxidizing metal ions;oxidation-reduction process | ec:1.10.3.3-oxidase;ec:1.10.3 | Ascorbate and aldarate metabolism |
| Phvul.011G102900.1 | hypothetical protein PHAVU_011G102900g | integral component of membrane | | |
| Phvul.011G103400.1 | probable beta-1,3-galactosyltransferase 2 | Golgi apparatus;integral component of membrane;galactosylxylosylprotein 3-beta-galactosyltransferase activity;protein glycosylation | ec:2.4.1.134-3-beta-galactosyltransferase | Glycosaminoglycan biosynthesis - heparan sulfate / heparin;Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate |
| Phvul.011G103700.1 | aconitate hydratase, cytoplasmic | cell wall;vacuolar membrane;cytosol;chloroplast stroma;aconitate hydratase activity;copper ion binding;ATP binding;4 iron, 4 sulfur cluster binding;response to superoxide;gluconeogenesis;glycolytic process;citrate metabolic process;isocitrate metabolic process;protein N-linked glycosylation;ubiquitin-dependent protein catabolic process;water transport;hyperosmotic response;Golgi organization;response to temperature stimulus;response to auxin;response to carbohydrate;photorespiration;ethylene-activated signaling pathway;response to iron ion;photosynthesis;response to misfolded protein;iron ion homeostasis;proteasome core complex assembly | ec:4.2.1.3-hydratase | Carbon fixation pathways in prokaryotes;Biosynthesis of antibiotics;Citrate cycle (TCA cycle);Glyoxylate and dicarboxylate metabolism |
| Phvul.011G104000.1 | DUF4228 domain | | | |
| Phvul.011G107700.1 | beta-amylase | beta-amylase activity;polysaccharide catabolic process | ec:3.2.1.2-saccharogen amylase | Starch and sucrose metabolism |
| Phvul.011G109900.1 | myb-related Myb4-like | DNA binding | | |

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| Phvul.011G110000.1 | cyclin-D6-1 | nucleus;integral component of membrane;cell cycle;regulation of cell cycle | | |
| Phvul.011G110000.2 | cyclin-D6-1 | nucleus;integral component of membrane;cell cycle;regulation of cell cycle | | |
| Phvul.011G111800.1 | embryo defective 1923 , | integral component of membrane;rRNA processing;tRNA metabolic process;chloroplast organization | | |
| Phvul.011G112400.1 | H ACA ribonucleo complex non-core subunit NAF1 | viral nucleocapsid;intracellular ribonucleoprotein complex;pseudouridine synthesis;ribosome biogenesis | | |
| Phvul.011G114500.1 | hypothetical protein PHAVU_011G114500g, partial | integral component of membrane | | |
| Phvul.011G115100.1 | transmembrane E3 ubiquitin- ligase 1-like | integral component of membrane;zinc ion binding;ligase activity;ubiquitin protein ligase activity;protein polyubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;proteasome-mediated ubiquitin-dependent protein catabolic process | | |
| Phvul.011G115600.1 | transcription factor VOZ1-like | positive regulation of biological process;response to stimulus | | |
| Phvul.011G116300.1 | translation factor GUF1 homolog, organellar chromatophore | intracellular;translation elongation factor activity;GTPase activity;GTP binding;translational elongation | ec:3.6.1;ec:3.6.1.15-phosphatase | Purine metabolism;Thiamine metabolism |
| Phvul.011G117500.1 | expansin-B3-like precursor | extracellular region;plasmodesma;hydrolase activity;syncytium formation;metabolic process;sexual reproduction | | |
| Phvul.011G117600.1 | alpha-expansin 20 precursor family | extracellular region;cell wall;integral component of membrane;plant-type cell wall organization | | |
| Phvul.011G119200.1 | probable L-type lectin-domain containing receptor kinase | integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;carbohydrate binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10;ec:2.7.10.1 | |
| Phvul.011G124600.1 | M48 family peptidase | integral component of membrane;metalloendopeptidase activity;proteolysis | ec:3.4.24 | |
| Phvul.011G124700.1 | peroxisomal membrane 22 kDa (Mpv17 PMP22) family | mitochondrion;peroxisomal membrane;chloroplast envelope;integral component of membrane | | |
| Phvul.011G128000.1 | shaggy-related kinase eta isoform X1 | protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.011G128800.1 | multi -bridging factor 1a | cytoplasm;transcription coactivator activity;sequence-specific DNA binding;response to high light intensity;response to hydrogen peroxide;positive regulation of transcription, DNA-templated | | |
| Phvul.011G136200.1 | TMV resistance N-like | ADP binding;defense response;signal transduction | | |
| Phvul.011G136200.2 | disease resistance (TIR-NBS-LRR class), | ADP binding;defense response;signal transduction | | |
| Phvul.011G140300.1 | disease resistance (TIR-NBS-LRR class), | ADP binding;defense response;signal transduction | | |
| Phvul.011G141900.1 | Formin 5 isoform 1 | cell wall;phragmoplast;integral component of membrane;actin binding;structural constituent of cell wall;endosperm development;actin filament polymerization;seed morphogenesis | | |
| Phvul.011G142300.1 | scarecrow 21 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.011G142300.2 | scarecrow 21 | transcription, DNA-templated;regulation of transcription, DNA-templated | | |
| Phvul.011G144300.1 | ACCELERATED CELL DEATH 6-like | integral component of membrane;regulation of defense response;cellular response to salicylic acid stimulus;regulation of salicylic acid mediated signaling pathway | | |

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| Phvul.011G144400.1 | chromosome transmission fidelity 18 homolog | ATP binding | | |
| Phvul.011G146000.1 | mRNA cap guanine-N7 methyltransferase 1 | nucleus;mRNA cap binding complex;RNA binding;mRNA (guanine-N7-)-methyltransferase activity;7-methylguanosine mRNA capping;proline transport;RNA (guanine-N7)-methylation | ec:2.1.1;ec:2.1.1.56 | |
| Phvul.011G148800.1 | homogentisate 1,2-dioxygenase | cytosol;homogentisate 1,2-dioxygenase activity;L-phenylalanine catabolic process;tyrosine metabolic process;fatty acid beta-oxidation;response to sucrose;response to fructose;chlorophyll catabolic process;protein import into peroxisome matrix;homogentisate catabolic process | ec:1.13.11.5-1,2-dioxygenase | Tyrosine metabolism;Styrene degradation |
| Phvul.011G149500.1 | S-locus lectin kinase family | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;ubiquitin protein ligase binding;protein phosphorylation;innate immune response;recognition of pollen | ec:2.7.11 | |
| Phvul.011G151000.1 | G-type lectin S-receptor-like serine threonine- kinase At4g27290 isoform X2 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation;defense response;recognition of pollen | ec:2.7.11 | |
| Phvul.011G151700.1 | ankyrin repeat domain-containing 13C | | | |
| Phvul.011G152300.1 | G-type lectin S-receptor-like serine threonine- kinase At4g27290 isoform X1 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;defense response;recognition of pollen | ec:2.7.11 | |
| Phvul.011G152300.2 | G-type lectin S-receptor-like serine threonine- kinase At4g27290 isoform X1 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;defense response;recognition of pollen | ec:2.7.11 | |
| Phvul.011G152300.3 | G-type lectin S-receptor-like serine threonine- kinase At4g27290 isoform X2 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;defense response;recognition of pollen | ec:2.7.11 | |
| Phvul.011G152700.1 | G-type lectin S-receptor-like serine threonine- kinase At4g27290 isoform X1 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation;defense response;recognition of pollen | ec:2.7.11 | |
| Phvul.011G158100.1 | SAWADEE HOMEODOMAIN HOMOLOG 2 | integral component of membrane;DNA binding;chromatin binding | | |
| Phvul.011G158200.1 | SAWADEE HOMEODOMAIN HOMOLOG 2 | nucleus;integral component of membrane;DNA binding;chromatin binding | | |
| Phvul.011G159200.1 | Fiber Fb32 isoform 3 | | | |
| Phvul.011G159500.1 | Serine threonine-phosphatase 4 regulatory subunit 2-A, | DNA binding | | |
| Phvul.011G159700.1 | serine threonine-kinase isoform X2 | plasma membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;signal transduction;peptidyl-tyrosine phosphorylation;innate immune response;cellular response to organic substance | ec:2.7.11;ec:2.7.10.1 | |
| Phvul.011G161000.1 | phytosulfokine receptor 2-like | chloroplast;integral component of membrane;peptide receptor activity;MAP kinase kinase kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;MAPK cascade;activation of MAPKK | ec:2.7.11;ec:2.7.11.25;ec:2.7.10.1 | |

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| | | activity;response to wounding;peptidyl-tyrosine phosphorylation | | |
| Phvul.011G161100.1 | 11-oxo-beta-amyrin 30-oxidase-like | integral component of membrane;acyl-CoA oxidase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;oxidation-reduction process;11-oxo-beta-amyrin catabolic process;glycyrrhetinate biosynthetic process | ec:1.3.3.6-oxidase;ec:1.14.13 | alpha-Linolenic acid metabolism;Biosynthesis of unsaturated fatty acids;Fatty acid degradation |
| Phvul.011G161100.2 | cytochrome P450 monooxygenase | integral component of membrane;acyl-CoA oxidase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;oxidation-reduction process;11-oxo-beta-amyrin catabolic process;glycyrrhetinate biosynthetic process | ec:1.3.3.6-oxidase;ec:1.14.13 | alpha-Linolenic acid metabolism;Biosynthesis of unsaturated fatty acids;Fatty acid degradation |
| Phvul.011G161200.2 | cytochrome P450 monooxygenase | integral component of membrane;acyl-CoA oxidase activity;iron ion binding;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen;heme binding;oxidation-reduction process;11-oxo-beta-amyrin catabolic process;glycyrrhetinate biosynthetic process | ec:1.3.3.6-oxidase;ec:1.14.13 | alpha-Linolenic acid metabolism;Biosynthesis of unsaturated fatty acids;Fatty acid degradation |
| Phvul.011G162500.1 | hypothetical protein PHAVU_011G162500g | | | |
| Phvul.011G163800.1 | ankyrin repeat | integral component of membrane | | |
| Phvul.011G164700.1 | germinal center kinase 1-like isoform X1 | cytoplasm;cyclin-dependent protein serine/threonine kinase activity;ATP binding;Rac GTPase binding;Rho protein signal transduction;regulation of mitotic cell cycle;cell migration;signal transduction by protein phosphorylation;actin cytoskeleton organization;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process;regulation of MAPK cascade | ec:2.7.11.22 | |
| Phvul.011G164700.2 | germinal center kinase 1-like isoform X1 | cytoplasm;cyclin-dependent protein serine/threonine kinase activity;ATP binding;Rac GTPase binding;Rho protein signal transduction;regulation of mitotic cell cycle;cell migration;signal transduction by protein phosphorylation;actin cytoskeleton organization;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process;regulation of MAPK cascade | ec:2.7.11;ec:2.7.11.22 | |
| Phvul.011G164700.3 | germinal center kinase 1-like isoform X1 | cytoplasm;cyclin-dependent protein serine/threonine kinase activity;ATP binding;Rac GTPase binding;Rho protein signal transduction;regulation of mitotic cell cycle;cell migration;signal transduction by protein phosphorylation;actin cytoskeleton organization;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process;regulation of MAPK cascade | ec:2.7.11.22 | |
| Phvul.011G164700.4 | germinal center kinase 1-like isoform X1 | cytoplasm;cyclin-dependent protein serine/threonine kinase activity;ATP binding;Rac GTPase binding;Rho protein signal transduction;regulation of mitotic cell cycle;cell migration;signal transduction by protein phosphorylation;actin cytoskeleton organization;stress-activated protein kinase signaling cascade;activation of protein kinase activity;regulation of apoptotic process;regulation of MAPK cascade | ec:2.7.11;ec:2.7.11.22 | |

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| Phvul.011G165500.1 | anaphase-promoting complex subunit 6 | double-strand break repair via homologous recombination;cytokinesis by cell plate formation;DNA replication initiation;DNA methylation;methylation-dependent chromatin silencing;synapsis;reciprocal meiotic recombination;cell adhesion;gamete generation;cell proliferation;nucleotide biosynthetic process;pollen development;regulation of flower development;leaf morphogenesis;phloem or xylem histogenesis;trichome morphogenesis;regulation of G2/M transition of mitotic cell cycle;somatic cell DNA recombination;chromatin silencing by small RNA;regulation of DNA endoreduplication;DNA endoreduplication;post-translational protein modification;actin nucleation;positive regulation of transcription, DNA-templated;root hair cell differentiation;spindle assembly;regulation of cell division;regulation of unidimensional cell growth;histone H3-K9 methylation;cell wall organization | | |
| Phvul.011G166400.1 | receptor kinase | integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.011G166600.1 | hypothetical protein PHAVU_011G166600g | | | |
| Phvul.011G168400.1 | S-locus lectin kinase family | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;carbohydrate binding;protein phosphorylation;defense response;recognition of pollen | ec:2.7.11 | |
| Phvul.011G169300.1 | probable LRR receptor-like serine threonine- kinase At1g56130 | plasma membrane;integral component of membrane;protein serine/threonine kinase activity;transmembrane receptor protein tyrosine kinase activity;ATP binding;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10.1 | |
| Phvul.011G170000.1 | PHD finger family | zinc ion binding | | |
| Phvul.011G170000.2 | Jade-1-like isoform X2 | zinc ion binding | | |
| Phvul.011G170200.1 | amidophosphoribosyltransferase, chloroplastic-like | amidophosphoribosyltransferase activity;metal ion binding;iron-sulfur cluster binding;'de novo' IMP biosynthetic process;purine nucleobase biosynthetic process;nucleoside metabolic process | ec:2.4.2.14-phosphoribosyldiphosphate 5-amidotransferase | Purine metabolism;Biosynthesis of antibiotics;Alanine, aspartate and glutamate metabolism |
| Phvul.011G172100.1 | hypothetical protein PHAVU_011G172100g | ADP binding;defense response | | |
| Phvul.011G172100.2 | hypothetical protein PHAVU_011G172100g | ADP binding;defense response | | |
| Phvul.011G172200.1 | tRNA (adenine(58)-N(1))-methyltransferase catalytic subunit TRMT61A | nucleus;tRNA (m1A) methyltransferase complex;tRNA (adenine-N1-)-methyltransferase activity;tRNA methylation | ec:2.1.1 | |
| Phvul.011G172900.1 | vacuolar sorting-associated 8 homolog | | | |
| Phvul.011G173800.1 | disease resistance RPP13 1 | ADP binding;defense response | | |
| Phvul.011G174000.1 | cationic amino acid transporter 8, vacuolar | integral component of membrane;intracellular membrane-bounded organelle;L-glutamate transmembrane transporter activity;L-lysine transmembrane transporter activity;antiporter activity;response to brassinosteroid;L-arginine import;L-glutamate import;L-lysine transmembrane transport | | |

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| Phvul.011G174800.1 | obg-like ATPase 1 | chloroplast stroma;ATP binding;GTP binding;ATPase activity;ribosome binding;ribosomal large subunit binding;heme biosynthetic process | ec:3.6.1.3-adenylpyrophosphatase | Purine metabolism |
| Phvul.011G175400.1 | cysteine-rich RLK (receptor-like kinase) | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.011G175400.2 | cysteine-rich RLK (receptor-like kinase) | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.011G175600.1 | cysteine-rich RLK (receptor-like kinase) | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.011G177600.1 | guanine nucleotide exchange factor, | nucleus;cytosol;plasma membrane;extrinsic component of membrane;endoplasmic reticulum exit site;guanyl-nucleotide exchange factor activity;cytokinesis by cell plate formation;acetyl-CoA metabolic process;microtubule nucleation;small GTPase mediated signal transduction;determination of bilateral symmetry;meristem initiation;regulation of meristem growth;trichome morphogenesis;sterol biosynthetic process;brassinosteroid biosynthetic process;vesicle-mediated transport;positive regulation of GTPase activity;actin nucleation | | |
| Phvul.011G179000.1 | cyclin-B3-1 isoform X2 | nucleus | | |
| Phvul.011G179600.1 | MYND finger | zinc ion binding | | |
| Phvul.011G179600.3 | MYND finger | zinc ion binding | | |
| Phvul.011G180100.1 | strawberry notch-like | zinc ion binding;regulation of transcription, DNA-templated | | |
| Phvul.011G181200.1 | exosome complex component RRP43-like | nuclear exosome (RNase complex);cytoplasmic exosome (RNase complex);cytosol;exonuclease activity;AU-rich element binding;exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5';U1 snRNA 3'-end processing;U4 snRNA 3'-end processing;U5 snRNA 3'-end processing;transcription factor import into nucleus;exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay;nuclear mRNA surveillance;nuclear polyadenylation-dependent rRNA catabolic process;nuclear polyadenylation-dependent tRNA catabolic process;nuclear polyadenylation-dependent mRNA catabolic process | | |
| Phvul.011G181600.1 | resistance KR4 | ADP binding;defense response | | |
| Phvul.011G182300.1 | probable leucine-rich repeat receptor kinase At1g35710 | integral component of membrane;protein kinase activity;ATP binding;protein phosphorylation | | |
| Phvul.011G186500.1 | SWIM zinc finger family | zinc ion binding | | |
| Phvul.011G186900.1 | calcium and calcium calmodulin-dependent serine threonine- kinase | cytoplasm;integral component of membrane;calmodulin-dependent protein kinase activity;calcium ion binding;calmodulin binding;ATP binding;calcium-dependent protein serine/threonine kinase activity;response to symbiont;nodulation;peptidyl-serine phosphorylation;intracellular signal transduction;protein autophosphorylation | ec:2.7.11;ec:2.7.11.17 | |
| Phvul.011G190200.1 | histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1-like | nucleus;chromosome;zinc ion binding;histone-lysine N-methyltransferase activity;histone binding;histone lysine methylation | ec:2.1.1.43-N-methyltransferase | Lysine degradation |
| Phvul.011G192800.1 | cilia- and flagella-associated 20 | | | |

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| Phvul.011G193000.1 | hypothetical protein PHAVU_011G193000g | ADP binding;defense response | | |
| Phvul.011G194000.1 | hypothetical protein PHAVU_011G194000g | ADP binding;defense response | | |
| Phvul.011G194300.1 | cysteine-rich receptor kinase 10 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;defense response | ec:2.7.11 | |
| Phvul.011G194300.2 | cysteine-rich receptor kinase 10 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;ATP binding;protein phosphorylation;defense response | ec:2.7.11 | |
| Phvul.011G194600.1 | cysteine-rich receptor kinase 25 | plasma membrane;plasmodesma;integral component of membrane;protein serine/threonine kinase activity;non-membrane spanning protein tyrosine kinase activity;ATP binding;defense response;peptidyl-tyrosine phosphorylation | ec:2.7.11;ec:2.7.10.2-protein-tyrosine kinase | T cell receptor signaling pathway |
| Phvul.011G195200.1 | hypothetical protein PHAVU_011G195200g | ADP binding;defense response | | |
| Phvul.011G197900.1 | disease resistance RPP13 1 | ADP binding;defense response | | |
| Phvul.011G200400.1 | probable receptor kinase At1g67000 isoform X1 | integral component of membrane;protein serine/threonine kinase activity;ATP binding;polysaccharide binding;protein phosphorylation | ec:2.7.11 | |
| Phvul.011G200900.1 | disease resistance RPP13 1 | ADP binding;defense response | | |
| Phvul.011G201100.1 | disease resistance RPP13 1 | ADP binding;defense response | | |
| Phvul.011G201200.1 | retinoblastoma-related 1 | nucleus;cytosol;DNA binding;transcription factor binding;G1/S transition of mitotic cell cycle;regulation of cell growth;cell fate specification;regulation of gene expression by genetic imprinting;transcription, DNA-templated;regulation of transcription from RNA polymerase II promoter;asymmetric cell division;embryo sac development;trichome morphogenesis;generative cell differentiation;regulation of DNA endoreduplication;DNA endoreduplication;leaf development;regulation of nuclear division;regulation of stem cell population maintenance | | |
| Phvul.011G201200.2 | retinoblastoma-related 1 | nucleus;cytosol;DNA binding;transcription factor binding;G1/S transition of mitotic cell cycle;regulation of cell growth;cell fate specification;regulation of gene expression by genetic imprinting;transcription, DNA-templated;regulation of transcription from RNA polymerase II promoter;asymmetric cell division;embryo sac development;trichome morphogenesis;generative cell differentiation;regulation of DNA endoreduplication;DNA endoreduplication;leaf development;regulation of nuclear division;regulation of stem cell population maintenance | | |
| Phvul.011G201700.2 | glycoside hydrolase family 1 | integral component of membrane;beta-glucosidase activity;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.21-gentiobiase | Starch and sucrose metabolism;Cyanoamino acid metabolism;Phenylpropanoid biosynthesis |
| Phvul.011G201800.1 | hypothetical protein PHAVU_011G201800g | | | |

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| Phvul.011G202100.1 | disease resistance At3g14460 | ADP binding;defense response | | |
| Phvul.011G204500.1 | leginsulin 1 | nutrient reservoir activity;pathogenesis | | |
| Phvul.011G206500.1 | amidohydrolase , | endoplasmic reticulum;perinuclear region of cytoplasm;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;regulation of mitotic cell cycle;metabolic process | | |
| Phvul.011G206600.1 | hypothetical protein PHAVU_011G206600g | mitochondrion;structural constituent of ribosome | | |
| Phvul.011G206600.2 | hypothetical protein PHAVU_011G206600g | mitochondrion;structural constituent of ribosome | | |
| Phvul.011G206800.1 | beta-galactosidase | beta-galactosidase complex;beta-galactosidase activity;carbohydrate binding;carbohydrate metabolic process | ec:3.2.1;ec:3.2.1.23-lactase (ambiguous) | Other glycan degradation;Glycosphingolipid biosynthesis - ganglio series;Sphingolipid metabolism;Galactose metabolism;Glycosaminoglycan degradation |
| Phvul.011G210000.2 | chaperone dnaJ 10-like isoform X1 | | | |
| Phvul.011G212400.1 | FACT complex subunit SSRP1 | nuclear euchromatin;FACT complex;DNA binding;transcription factor activity, sequence-specific DNA binding;2-alkenal reductase [NAD(P)] activity;RNA splicing, via endonucleolytic cleavage and ligation;DNA methylation;methylation-dependent chromatin silencing;transcription from RNA polymerase II promoter;cell-cell signaling;virus induced gene silencing;determination of bilateral symmetry;organ morphogenesis;meristem initiation;vegetative phase change;xylem and phloem pattern formation;meristem maintenance;vegetative to reproductive phase transition of meristem;production of ta-siRNAs involved in RNA interference;production of miRNAs involved in gene silencing by miRNA;flower morphogenesis;oxidation-reduction process | ec:1.3.1.74 | |
| Phvul.011G215500.1 | organic cation carnitine transporter | plant-type vacuole membrane;integral component of membrane;substrate-specific transmembrane transporter activity;transmembrane transport | | |
| Phvul.011G215800.1 | Eukaryotic translation initiation factor 2D | translation initiation factor activity;translational initiation | | |
| Phvul.L000500.1 | transmembrane , | integral component of membrane;nucleotide binding;nucleic acid binding | | |
| Phvul.L000800.1 | probable receptor kinase At1g67000 | integral component of membrane;protein kinase activity;ATP binding;polysaccharide binding;protein phosphorylation | | |
| Phvul.L004300.1 | pentatricopeptide repeat-containing At5g40400 | | | |
| Phvul.L004400.1 | truncated NBS-LRR resistance isoforms JA68, JA76, and JA80 | ADP binding;defense response | | |
| Phvul.L008300.1 | Cellulose synthase E1 | integral component of membrane;cellulose synthase (UDP-forming) activity;cellulose biosynthetic process;cell wall organization | ec:2.4.1.12-synthase (UDP-forming);ec:2.4.1 | Starch and sucrose metabolism |
| Phvul.L008400.1 | Magnesium transporter MRS2-3 | integral component of membrane;magnesium ion transmembrane transporter activity;magnesium ion transport;magnesium ion transmembrane transport | | |
| Phvul.L009100.1 | transcription factor bHLH91-like | DNA binding;protein dimerization activity | | |
| Phvul.L009100.2 | transcription factor bHLH91-like | DNA binding;protein dimerization activity | | |

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| Phvul.L009100.3 | transcription factor bHLH91-like | DNA binding;protein dimerization activity | | |
| Phvul.L009500.1 | hypothetical protein PHAVU_L009500g | | | |