

Table S7. miRNA targets identified by degradome sequencing

SmallRNA	Transcript	Transcript Annotation	GO_Term	KEGG_pathways	Symbol	AllenScore	AllentRange	DegradomeNormReads(TR)	DegradomeNormReads(CT)	pvalue
vvi-MIR159c-p5	VIT_12s0057g00680.t01	PREDICTED: OBERON-like protein	GO:0005634(nucleus);GO:0010071(root meristem specification);GO:0010078(maintenance of root meristem identity);GO:0010468(regulation of gene expression);GO:0010492(maintenance of shoot apical meristem identity);GO:0046872(metal ion binding)	NA	VIT_12s0057g00680	4	1165-1185	0	89.32559178	3.3422E-21
vvi-MIR160b-p3	VIT_08s0058g00690.t01	PREDICTED: probable WRKY transcription factor 26	GO:0003677(DNA binding);GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0009409(response to cold);GO:0009414(response to water deprivation);GO:0009651(response to salt stress);GO:0010120(camalexin biosynthetic process);GO:0010200(response to chitin);GO:0010508(positive regulation of autophagy);GO:0042742(defense response to bacterium);GO:0043565(sequence-specific DNA binding);GO:0044212(transcription regulatory region DNA binding);GO:0050832(defense response to fungus);GO:0070370(cellular heat acclimation)	ko04016(MAPK signaling pathway - plant);ko04626(Plant-pathogen interaction)	VIT_08s0058g00690	4	282-301	276.5231819	0	4.2164E-62
vvi-MIR166h-p5	VIT_11s0016g00600.t01	PREDICTED: 3-oxoacyl-[acyl-carrier-protein] synthase II, chloroplastic	GO:0003824(catalytic activity);GO:0004315(3-oxoacyl-[acyl-carrier-protein] synthase activity);GO:0005739(mitochondrion);GO:0006633(fatty acid biosynthetic process);GO:0009507(chloroplast);GO:0009570(chloroplast stroma);GO:0009631(cold acclimation);GO:0009793(embryo development ending in seed dormancy);GO:0016740(transferase activity);GO:0016747(transferase activity, transferring acyl groups other than amino-acyl groups)	ko00061(Fatty acid biosynthesis);ko00780(Biotin metabolism)	VIT_11s0016g00600	4	750-769	276.5231819	89.32559178	1.2691E-22
vvi-MIR169r-p3	VIT_16s0050g00390.t01	PREDICTED: probable CoA ligase CCL9	GO:0003824(catalytic activity);GO:0009506(plasmodesma);GO:0009570(chloroplast stroma);GO:0009735(response to cytokinin);GO:0010030(positive regulation of seed germination);GO:0010214(seed coat development);GO:0033611(oxalate catabolic process);GO:0046686(response to cadmium ion);GO:0048046(apoplast);GO:0050203(oxalate-CoA ligase activity);GO:0050832(defense response to fungus)	ko00630(Glyoxylate and dicarboxylate metabolism)	VIT_16s0050g00390	4	1225-1246	0	89.32559178	3.3422E-21
vvi-MIR171b-p3	VIT_02s0154g00400.t01	PREDICTED: scarecrow-like protein 22	GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0043565(sequence-specific DNA binding)	NA	VIT_02s0154g00400	2.5	504-524	0	4644.930773	0
vvi-MIR171b-p3	VIT_15s0048g00270.t01	PREDICTED: scarecrow-like protein 27	GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0043565(sequence-specific DNA binding)	NA	VIT_15s0048g00270	2.5	1577-1597	4055.673334	0	0
vvi-MIR3639-p3	VIT_01s0011g005970.t01	PREDICTED: heat stress transcription factor A-8	GO:0000978(RNA polymerase II proximal promoter sequence-specific DNA binding);GO:0003677(DNA binding);GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0034605(cellular response to heat);GO:0043565(sequence-specific DNA binding);GO:0061408(positive regulation of transcription from RNA polymerase II promoter in response to heat stress)	NA	VIT_01s0011g005970	4	297-314	184.3487879	0	5.3983E-42

vvi-MIR3639-p3	VIT_02s0025g01520.t01	NA	GO:0005515(protein binding)	NA	VIT_02s0025g01520	4	644-662	184.3487879	0	5.3983E-42
vvi-MIR3639-p3	VIT_02s0033g00520.t01	PREDICTED: disease resistance protein At4g27190	GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0043531(ADP binding)	NA	VIT_02s0033g00520	3	724-741	0	89.32559178	3.3422E-21
vvi-MIR3639-p3	VIT_04s0008g06480.t01	PREDICTED: hydroxyproline O-galactosyltransferase HPGT2	GO:0000139(Golgi membrane);GO:0005783(endoplasmic reticulum);GO:0005794(Golgi apparatus);GO:0006486(protein glycosylation);GO:0008378(galactosyltransferase activity);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0016740(transferase activity);GO:0016757(transferase activity, transferring glycosyl groups)	NA	VIT_04s0008g06480	3.5	281-299	0	267.9767753	3.0764E-60
vvi-MIR3639-p3	VIT_06s0004g02580.t01	PREDICTED: BEL1-like homeodomain protein 9	GO:0003677(DNA binding);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated)	NA	VIT_06s0004g02580	3.5	1579-1595	0	89.32559178	3.3422E-21
vvi-MIR3639-p3	VIT_08s0007g01790.t01	PREDICTED: protein DEFECTIVE IN EXINE FORMATION 1	GO:0005515(protein binding);GO:0005783(endoplasmic reticulum);GO:0010208(pollen wall assembly);GO:0010584(pollen exine formation);GO:0016020(membrane);GO:0016021(integral component of membrane)	NA	VIT_08s0007g01790	3.5	2341-2358	0	89.32559178	3.3422E-21
vvi-MIR3639-p3	VIT_09s0002g05800.t01	PREDICTED: 26S proteasome regulatory subunit 8 homolog A	GO:0000166(nucleotide binding);GO:0005524(ATP binding);GO:0005737(cytoplasm);GO:0008540(proteasome regulatory particle, base subcomplex);GO:0016787(hydrolase activity);GO:0017025(TBP-class protein binding);GO:0030163(protein catabolic process);GO:0031595(nuclear proteasome complex);GO:0031597(cytosolic proteasome complex);GO:0045899(positive regulation of RNA polymerase II transcriptional preinitiation complex assembly)	ko03050(Proteasome)	VIT_09s0002g05800	4	333-349	92.17439395	89.32559178	0.83252
vvi-MIR3639-p3	VIT_14s0006g02870.t01	NA	GO:0008762(UDP-N-acetylmuramate dehydrogenase activity);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0016491(oxidoreductase activity);GO:0050660(flavin adenine dinucleotide binding);GO:0055114(oxidation-reduction process);GO:0071949(FAD binding)	NA	VIT_14s0006g02870	4	275-292	0	267.9767753	3.0764E-60
vvi-MIR3639-p3	VIT_14s0083g00960.t01	PREDICTED: auxin transport protein BIG	GO:0005515(protein binding);GO:0005829(cytosol);GO:0008270(zinc ion binding);GO:0009506(plasmodesma);GO:0009620(response to fungus);GO:0009640(photomorphogenesis);GO:0009733(response to auxin);GO:0009826(unidimensional cell growth);GO:0009926(auxin polar transport);GO:0010311(lateral root formation);GO:0016020(membrane);GO:0046872(metal ion binding);GO:0048281(inflorescence morphogenesis);GO:0048364(root development)	NA	VIT_14s0083g00960	4	1916-1933	184.3487879	0	5.3983E-42
vvi-MIR3639-p3	VIT_16s0100g01030.t01	PREDICTED: stilbene synthase 2	GO:0003824(catalytic activity);GO:0005737(cytoplasm);GO:0006952(defense response);GO:0009058(biosynthetic process);GO:0016740(transferase activity);GO:0016746(transferase activity, transferring acyl groups);GO:0016747(transferase activity, transferring acyl groups other than amino-acyl groups);GO:0050350(trihydroxystilbene synthase activity)	ko00945(Stilbenoid, diarylheptanoid and gingerol biosynthesis)	VIT_16s0100g01030	4	546-562	276.5231819	0	4.2164E-62

vvi-MIR482-p5	VIT_02s0025g02600.t01	PREDICTED: aldehyde oxidase GLOX	NA	NA	VIT_02s0025g02600	3.5	40-61	0	89.32559178	3.3422E-21
vvi-miR156b	VIT_11s0065g00170.t01	SPL10	GO:0003677(DNA binding);GO:0005634(nucleus);GO:0046872(metal ion binding)	NA	VIT_11s0065g00170	1	1149-1168	829.5695456	267.9767753	1.731E-64
vvi-miR156f	VIT_08s0040g01940.t01	PREDICTED: probable E3 ubiquitin-protein ligase LOG2	GO:0016567(protein ubiquitination);GO:0061630(ubiquitin protein ligase activity)	NA	VIT_08s0040g01940	4	160-180	92.17439395	0	7.9195E-22
vvi-miR156f	VIT_11s0065g00170.t01	SPL10	GO:0003677(DNA binding);GO:0005634(nucleus);GO:0046872(metal ion binding)	NA	VIT_11s0065g00170	2	1149-1169	368.6975758	982.5815096	1.1944E-62
vvi-miR159c	VIT_13s0067g01630.t01	PREDICTED: transcription factor GAMYB	NA	NA	NA	3.5	1370-1390	1382.615909	0	0
vvi-miR159c	VIT_19s0014g01700.t01	PREDICTED: protein SPEAR2	GO:0003700(DNA-binding transcription factor activity);GO:0006355(regulation of transcription, DNA-templated)	NA	VIT_19s0014g01700	3	659-679	460.8719698	1071.907101	5.916E-55
vvi-miR159c	VIT_19s0090g00590.t01	PREDICTED: transcription factor MYB97	GO:0003677(DNA binding);GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0030154(cell differentiation);GO:0043565(sequence-specific DNA binding);GO:0044212(transcription regulatory region DNA binding)	NA	VIT_19s0090g00590	4	845-865	0	357.3023671	1.0546E-79
vvi-miR164a	VIT_14s0108g01070.t01	PREDICTED: NAC domain-containing protein 100	GO:0003677(DNA binding);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated)	NA	VIT_14s0108g01070	3	815-835	0	89.32559178	3.3422E-21
vvi-miR164a	VIT_15s0048g01160.t01	PREDICTED: phospholipase D beta 2	GO:0003824(catalytic activity)	ko00564(Glycerophospholipid metabolism);ko00565(Ether lipid metabolism);ko04144(Endocytosis)	VIT_15s0048g01160	3.5	683-704	92.17439395	0	7.9195E-22
vvi-miR164a	VIT_17s0000g06400.t01	PREDICTED: NAC domain-containing protein 100-like	GO:0003677(DNA binding);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated)	NA	VIT_17s0000g06400	2	928-948	184.3487879	89.32559178	9.2265E-09
vvi-miR166a_L+2	VIT_10s0003g04670.t01	PREDICTED: homeobox-leucine zipper protein HOX32	GO:0003677(DNA binding);GO:0005634(nucleus);GO:0008289(lipid binding)	NA	VIT_10s0003g04670	2.5	584-603	0	535.9535507	0
vvi-miR166a_R+2_1	VIT_09s0002g03740.t01	PREDICTED: homeobox-leucine zipper protein ATHB-15	GO:0003677(DNA binding);GO:0005634(nucleus);GO:0008289(lipid binding);GO:0009855(determination of bilateral symmetry);GO:0009965(leaf morphogenesis);GO:0010014(meristem initiation);GO:0010075(regulation of meristem growth);GO:0010087(phloem or xylem histogenesis);GO:0048263(determination of dorsal identity);GO:0080060(integument development);GO:1905392(plant organ morphogenesis)	NA	VIT_09s0002g03740	3	1099-1119	1843.487879	3483.698079	0
vvi-miR171a	VIT_02s0154g00400.t01	PREDICTED: scarecrow-like protein 22	GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0043565(sequence-specific DNA binding)	NA	VIT_02s0154g00400	1	507-527	4055.673334	5270.209915	1.9544E-36
vvi-miR171a	VIT_04s0023g01380.t01	PREDICTED: scarecrow-like protein 15	GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0030154(cell differentiation);GO:0043565(sequence-specific DNA binding);GO:0048831(regulation of shoot system development)	NA	VIT_04s0023g01380	1	656-676	7281.777122	10183.11746	0

vvi-miR171a	VIT_15s0048g0270.t01	PREDICTED: scarecrow-like protein 27	GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0043565(sequence-specific DNA binding)	NA	VIT_15s0048g00270	1	1580-1600	1198.267121	5180.884323	0
vvi-miR2950-5p_R-1	VIT_04s0008g03190.t01	PREDICTED: F-box only protein 13	GO:0004842(ubiquitin-protein transferase activity);GO:0005515(protein binding);GO:0016567(protein ubiquitination);GO:0031146(SCF-dependent proteasomal ubiquitin-dependent protein catabolic process)	NA	VIT_04s0008g03190	2.5	150-169	184.3487879	0	5.3983E-42
vvi-miR2950-5p_R-1	VIT_07s0031g02090.t01	PREDICTED: peroxisomal membrane protein 11C	GO:0005515(protein binding);GO:0005634(nucleus);GO:0005829(cytosol);GO:0005886(plasma membrane)	NA	VIT_07s0031g02090	4	2050-2070	92.17439395	0	7.9195E-22
vvi-miR2950-5p_R-1	VIT_10s0003g0070.t01	PREDICTED: glyoxysomal processing protease, glyoxysomal	GO:0004175(endopeptidase activity);GO:0004252(serine-type endopeptidase activity);GO:0005777(peroxisome);GO:0006508(proteolysis);GO:0016485(protein processing)	NA	VIT_10s0003g00070	3	1243-1261	0	267.9767753	3.0764E-60
vvi-miR2950-5p_R-1	VIT_11s0052g00830.t01	PREDICTED: VIN3-like protein 2	GO:0005515(protein binding)	NA	VIT_11s0052g00830	4	314-332	0	89.32559178	3.3422E-21
vvi-miR2950-5p_R-1	VIT_17s0000g05800.t01	PREDICTED: probable aldehyde dehydrogenase	GO:0003842(1-pyrroline-5-carboxylate dehydrogenase activity);GO:0005739(mitochondrion);GO:0010133(proline catabolic process to glutamate);GO:0016491(oxidoreductase activity);GO:0016620(oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor);GO:0055114(oxidation-reduction process)	ko00250(Alanine, aspartate and glutamate metabolism);ko00330(Arginine and proline metabolism)	VIT_17s0000g05800	4	1013-1033	645.2207577	535.9535507	0.0014715
vvi-miR2950-5p_R-1	VIT_18s0001g0560.t01	PREDICTED: protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1	GO:0005829(cytosol);GO:0009903(chloroplast avoidance movement);GO:0009904(chloroplast accumulation movement)	NA	VIT_18s0001g10560	4	1238-1257	276.5231819	0	4.2164E-62
vvi-miR319b_R-1	VIT_10s0003g03910.t01	PREDICTED: transcription factor TCP2	GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006351(transcription, DNA-templated);GO:0006355(regulation of transcription, DNA-templated);GO:0043565(sequence-specific DNA binding)	NA	VIT_10s0003g03910	2.5	1786-1804	92.17439395	0	7.9195E-22
vvi-miR319b_R-1	VIT_13s00067g01630.t01	PREDICTED: transcription factor GAMYB	NA	NA	NA	3	1370-1389	0	178.6511836	9.472E-41
vvi-miR3627-3p	VIT_00s0309g00020.t01	PREDICTED: histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH8	NA	NA	NA	4	217-235	92.17439395	0	7.9195E-22
vvi-miR3629a-3p_L+1R-1	VIT_09s0054g01080.t01	PREDICTED: polygalacturonase QRT3	GO:0004650(polygalacturonase activity)	NA	VIT_09s0054g01080	4	776-796	92.17439395	0	7.9195E-22
vvi-miR3631b-3p	VIT_00s0252g00060.t01	NA	NA	NA	NA	4	4341-4360	0	89.32559178	3.3422E-21
vvi-miR3632-3p	VIT_13s00067g00790.t01	PREDICTED: putative disease resistance protein At1g50180	GO:0043531(ADP binding)	NA	VIT_13s00067g00790	2	575-596	276.5231819	714.6047343	4.879E-44
vvi-miR3633a-5p_R-1	VIT_05s0051g00590.t01	PREDICTED: probable pectate lyase 8	GO:0016829(lyase activity);GO:0030570(pectate lyase activity);GO:0045490(pectin catabolic process);GO:0046872(metal ion binding)	ko00040(Pentose and glucuronate interconversions)	VIT_05s0051g00590	3.5	1744-1762	0	178.6511836	9.472E-41
vvi-miR3633a-5p_R-1	VIT_17s0000g08570.t01	PREDICTED: probable BOI-related E3 ubiquitin-protein ligase 2	GO:0004842(ubiquitin-protein transferase activity);GO:0016567(protein ubiquitination)	NA	VIT_17s0000g08570	4	138-154	0	89.32559178	3.3422E-21

vvi-miR3633b-5p_R-1	VIT_03s0180g00280.t01	PREDICTED: UDP-glycosyltransferase 84B1	GO:0008194(UDP-glycosyltransferase activity);GO:0016740(transferase activity);GO:0016757(transferase activity, transferring glycosyl groups);GO:0016758(transferase activity, transferring hexosyl groups);GO:0043231(intracellular membrane-bounded organelle);GO:0080043(quercetin 3-O-glucosyltransferase activity);GO:0080044(quercetin 7-O-glucosyltransferase activity)	NA	VIT_03s0180g00280	3	532-550	0	178.6511836	9.472E-41
vvi-miR3633b-5p_R-1	VIT_17s0000g05110.t01	PREDICTED: cytochrome P450 78A5	GO:0004497(monoxygenase activity);GO:0005506(iron ion binding);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0016491(oxidoreductase activity);GO:0016705(oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen);GO:0016709(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);GO:0020037(heme binding);GO:0046872(metal ion binding);GO:0055114(oxidation-reduction process)	NA	VIT_17s0000g05110	4	521-540	553.0463637	1071.907101	6.0831E-38
vvi-miR3634-3p	VIT_19s0085g00430.t01	NA	GO:0016020(membrane);GO:0016021(integral component of membrane)	NA	VIT_19s0085g00430	2.5	86-107	4055.673334	1429.209469	0
vvi-miR3634-3p	VIT_19s0085g00460.t01	NA	NA	NA	VIT_19s0085g00460	3.5	446-467	92.17439395	0	7.9195E-22
vvi-miR3636-5p_R-3	VIT_17s0000g06970.t01	PREDICTED: diacylglycerol kinase 1	GO:0000166(nucleotide binding);GO:0003951(NAD+ kinase activity);GO:0004143(diacylglycerol kinase activity);GO:0005524(ATP binding);GO:0005622(intracellular);GO:0007165(signal transduction);GO:0007205(protein kinase C-activating G protein-coupled receptor signaling pathway);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0016301(kinase activity);GO:0016310(phosphorylation);GO:0016740(transferase activity);GO:0035556(intracellular signal transduction)	ko00561(Glycerolipid metabolism);ko00564(Glycerophospholipid metabolism);ko04070(Phosphatidylinositol signaling system)	VIT_17s0000g06970	4	1739-1759	92.17439395	0	7.9195E-22
vvi-miR393a_R+1	VIT_07s0104g01320.t01	PREDICTED: protein TRANSPORT INHIBITOR RESPONSE 1	GO:0000822(inositol hexakisphosphate binding);GO:0005515(protein binding);GO:0009734(auxin-activated signaling pathway);GO:0016567(protein ubiquitination);GO:0019005(SCF ubiquitin ligase complex);GO:0031146(SCF-dependent proteasomal ubiquitin-dependent protein catabolic process);GO:0043224(nuclear SCF ubiquitin ligase complex)	ko04075(Plant hormone signal transduction)	VIT_07s0104g01320	2	1505-1527	3502.62697	4376.953997	5.6645E-23
vvi-miR393a_R+1	VIT_14s0068g01330.t01	PREDICTED: protein AUXIN SIGNALING F-BOX 2	GO:0005515(protein binding);GO:0016567(protein ubiquitination);GO:0019005(SCF ubiquitin ligase complex);GO:0031146(SCF-dependent proteasomal ubiquitin-dependent protein catabolic process)	NA	VIT_14s0068g01330	2	1926-1946	0	5538.18669	0
vvi-miR395a_R-2	VIT_02s0025g03270.t01	PREDICTED: puromycin-sensitive aminopeptidase	GO:0004177(aminopeptidase activity);GO:0005737(cytoplasm);GO:0006508(proteolysis);GO:0008237(metallopeptidase activity);GO:0008270(zinc ion binding);GO:0009507(chloroplast);GO:0043171(peptide catabolic process)	NA	VIT_02s0025g03270	3.5	207-224	92.17439395	178.6511836	1.4791E-07
vvi-miR395a_R-2	VIT_05s0020g04210.t01	PREDICTED: ATP sulfurylase 1	GO:0000103(sulfate assimilation);GO:0001887(selenium compound metabolic process);GO:0004020(adenylsulfate kinase activity);GO:0004781(sulfate adenylyltransferase (ATP) activity);GO:0005886(plasma membrane);GO:0009570(chloroplast stroma);GO:0009735(response to cytokinin);GO:0046686(response to cadmium ion)	ko00230(Fumaric acid metabolism);ko00261(Monobactam biosynthesis);ko00450(Selenocompound metabolism);ko00920(Sulfur metabolism)	VIT_05s0020g04210	3.5	367-385	8203.521062	6252.791425	1.2959E-59

vvi-miR395a_R-2	VIT_08s0007g08210.t01	PREDICTED: zinc finger CCH domain-containing protein 30	GO:0005515(protein binding);GO:0005634(nucleus);GO:0005737(cytoplasm);GO:0046872(metal ion binding)	NA	VIT_08s0007g08210	3.5	412-429	184.3487879	267.9767753	0.000084047
vvi-miR396a_R-1	VIT_02s0012g02250.t01	PREDICTED: bZIP transcription factor 16	GO:0003700(DNA-binding transcription factor activity);GO:0006355(regulation of transcription, DNA-templated)	NA	VIT_02s0012g02250	2.5	129-148	0	714.6047343	0
vvi-miR396a_R-1	VIT_06s0009g02520.t01	PREDICTED: replication factor C subunit 1	GO:0000003(reproduction);GO:0000166(nucleotide binding);GO:0000712(resolution of meiotic recombination intermediates);GO:0003677(DNA binding);GO:0003689(DNA clamp loader activity);GO:0005524(ATP binding);GO:0005634(nucleus);GO:0005663(DNA replication factor C complex);GO:0006260(DNA replication);GO:0006281(DNA repair);GO:0006974(cellular response to DNA damage stimulus);GO:0009737(response to abscisic acid);GO:0031935(regulation of chromatin silencing);GO:0051321(meiotic cell cycle);GO:0051570(regulation of histone H3-K9 methylation)	NA	VIT_06s0009g02520	3.5	2058-2076	0	982.5815096	0
vvi-miR396a_R-1	VIT_07s0191g00220.t01	NA	NA	NA	VIT_07s0191g00220	4	494-513	92.17439395	0	7.9195E-22
vvi-miR396b	VIT_02s0012g02250.t01	PREDICTED: bZIP transcription factor 16	GO:0003700(DNA-binding transcription factor activity);GO:0006355(regulation of transcription, DNA-templated)	NA	VIT_02s0012g02250	2.5	129-148	553.0463637	0	0
vvi-miR398a	VIT_14s0030g00830.t01	PREDICTED: superoxide dismutase [Cu-Zn]	GO:0004784(superoxide dismutase activity);GO:0005507(copper ion binding);GO:0005576(extracellular region);GO:0005615(extracellular space);GO:0005737(cytoplasm);GO:0006801(superoxide metabolic process);GO:0008270(zinc ion binding);GO:0016491(oxidoreductase activity);GO:0016532(superoxide dismutase copper chaperone activity);GO:0019430(removal of superoxide radicals);GO:0046872(metal ion binding);GO:0055114(oxidation-reduction process)	ko04146(Peroxisome)	VIT_14s0030g00830	4	17-37	921.7439395	1250.558285	1.6803E-12
vvi-miR398b_R-2	VIT_11s0016g05520.t01	PREDICTED: umecyanin	GO:0009055(electron transfer activity);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0022900(electron transport chain);GO:0046658(anchored component of plasma membrane)	NA	VIT_11s0016g05520	4	17-36	368.6975758	0	3.4751E-82
vvi-miR398b_R-2	VIT_16s0050g00490.t01	PREDICTED: tripeptidyl-peptidase 2	GO:0004252(serine-type endopeptidase activity);GO:0005737(cytoplasm);GO:0005773(vacuole);GO:0005774(vacuolar membrane);GO:0005829(cytosol);GO:0006508(proteolysis);GO:0008240(tripeptidyl-peptidase activity);GO:0009507(chloroplast);GO:0022626(cytosolic ribosome)	NA	VIT_16s0050g00490	4	1672-1689	0	267.9767753	3.0764E-60
vvi-miR403a	VIT_07s0005g01690.t01	NA	NA	NA	VIT_07s0005g01690	3	149-169	92.17439395	446.6279589	1.1706E-52
vvi-miR403a	VIT_10s0042g01180.t01	PREDICTED: protein argonaute 2	GO:0003676(nucleic acid binding);GO:0005515(protein binding);GO:0031047(gene silencing by RNA)	NA	VIT_10s0042g01180	1	2978-2998	15116.60061	0	0
vvi-miR482	VIT_18s0072g01090.t01	PREDICTED: disease resistance protein RPV1	GO:0016020(membrane);GO:0016021(integral component of membrane)	NA	VIT_18s0072g01090	2	224-245	121762.3744	80125.05583	0
vvi-miR535a	VIT_13s0156g00540.t01	PREDICTED: putative disease resistance RPP13-like protein 1 PREDICTED: protein PEP-RELATED DEVELOPMENT ARRESTED 1, chloroplast	NA	NA	VIT_13s0156g00540	4	972-993	276.5231819	0	4.2164E-62
PC-3p-10093_142	VIT_00s0333g00020.t01	PREDICTED: protein PEP-RELATED DEVELOPMENT ARRESTED 1, chloroplast	NA	NA	NA	4	178-195	0	178.6511836	9.472E-41

PC-3p-10093_142	VIT_07s0141g00390.t01	PREDICTED: glutathione reductase, chloroplast	GO:0000166(nucleotide binding);GO:0004362(glutathione-disulfide reductase activity);GO:0004791(thioredoxin-disulfide reductase activity);GO:0005507(copper ion binding);GO:0005524(ATP binding);GO:0005623(cell);GO:0005737(cytoplasm);GO:0005739(mitochondrion);GO:0006749(glutathione metabolic process);GO:0009055(electron transfer activity);GO:0009570(chloroplast stroma);GO:0016491(oxidoreductase activity);GO:0016668(oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor);GO:0022900(electron transport chain);GO:0045454(cell redox homeostasis);GO:0050660(flavin adenine dinucleotide binding);GO:0050661(NADP binding);GO:0055114(oxidation-reduction process);GO:0098869(cellular oxidant detoxification)	ko00480(Glutathione metabolism)	VIT_07s0141g00390	4	745-763	276.5231819	178.6511836	4.4761E-06
PC-3p-109913_6	VIT_02s0012g01040.t01	PREDICTED: NAC domain-containing protein 71	GO:0003677(DNA binding);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated)	NA	VIT_02s0012g01040	4	652-672	0	178.6511836	9.472E-41
PC-3p-111553_6	VIT_02s0087g00770.t01	PREDICTED: ABC transporter E family member 2	GO:0000054(ribosomal subunit export from nucleus);GO:0000166(nucleotide binding);GO:0005506(iron ion binding);GO:0005524(ATP binding);GO:0005622(intracellular);GO:0005623(cell);GO:0006413(translational initiation);GO:0006415(translational termination);GO:0016887(ATPase activity);GO:0043024(ribosomal small subunit binding)	NA	VIT_02s0087g00770	4	1184-1200	0	89.32559178	3.3422E-21
PC-3p-111553_6	VIT_05s0020g01850.t01	PREDICTED: double-stranded RNA-binding protein 2	GO:0003723(RNA binding);GO:0005515(protein binding)	NA	VIT_05s0020g01850	3.5	584-601	92.17439395	0	7.9195E-22
PC-3p-111553_6	VIT_08s0032g01140.t01	NA	GO:0000045(autophagosome assembly);GO:0000407(phagophore assembly site);GO:0005515(protein binding);GO:0006888(endoplasmic reticulum to Golgi vesicle-mediated transport);GO:0030242(autophagy of peroxisome);GO:0031410(cytoplasmic vesicle);GO:0032258(protein localization by the Cvt pathway);GO:0034497(protein localization to phagophore assembly site);GO:1990072(TRAPP3 protein complex)	NA	VIT_08s0032g01140	3.5	2602-2618	0	89.32559178	3.3422E-21
PC-3p-111553_6	VIT_08s0040g01710.t01	PREDICTED: phenylalanine ammonia-lyase-like	GO:0003824(catalytic activity);GO:0005737(cytoplasm);GO:0006559(L-phenylalanine catabolic process);GO:0009698(phenylpropanoid metabolic process);GO:0009800(cinnamic acid biosynthetic process);GO:0016829(lyase activity);GO:0016841(ammonia-lyase activity);GO:0045548(phenylalanine ammonia-lyase activity)	ko00360(Phenylalanine metabolism);ko00940(Phenylpropanoid biosynthesis)	VIT_08s0040g01710	4	1697-1712	553.0463637	0	0
PC-3p-111553_6	VIT_12s0057g01210.t01	PREDICTED: protein NO14	GO:0005886(plasma membrane);GO:0009506(plasmodesma);GO:0010204(defense response signaling pathway, resistance gene-independent)	NA	VIT_12s0057g01210	3.5	152-169	92.17439395	0	7.9195E-22
PC-3p-122670_5	VIT_18s0001g01740.t01	NA	GO:0000785(chromatin);GO:0003676(nucleic acid binding);GO:0004523(RNA-DNA hybrid ribonuclease activity);GO:0005634(nucleus);GO:0005737(cytoplasm);GO:0006355(regulation of transcription, DNA-templated);GO:0007040(lysosome organization);GO:0010452(histone H3-K36 methylation);GO:0016787(hydrolase activity);GO:0046975(histone methyltransferase activity (H3-K36 specific));GO:0090502(RNA phosphodiester bond hydrolysis, endonucleolytic)	NA	VIT_18s0001g01740	3.5	164-181	92.17439395	0	7.9195E-22

PC-3p-127209_5	VIT_13s0073g00560.t01	PREDICTED: dnaJ protein homolog	GO:0005524(ATP binding);GO:0005829(cytosol);GO:0006457(protein folding);GO:0009408(response to heat);GO:0031072(heat shock protein binding);GO:0046872(metal ion binding);GO:0051082(unfolded protein binding)	ko04141(Protein processing in endoplasmic reticulum)	VIT_13s0073g00560	4	613-630	737.3951516	89.32559178	0
PC-3p-130465_5	VIT_04s0008g04060.t01	PREDICTED: BURP domain-containing protein 3	NA	NA	VIT_04s0008g04060	1	491-509	184.3487879	0	5.3983E-42
PC-3p-130465_5	VIT_05s0020g03330.t01	PREDICTED: heat shock 70 kDa protein 8	GO:0000166(nucleotide binding);GO:0005524(ATP binding);GO:0005737(cytoplasm);GO:0006986(response to unfolded protein);GO:0009408(response to heat);GO:0016887(ATPase activity);GO:0031072(heat shock protein binding);GO:0034605(cellular response to heat);GO:0034620(cellular response to unfolded protein);GO:0042026(protein refolding);GO:0042623(ATPase activity, coupled);GO:0044183(protein folding chaperone);GO:0051082(unfolded protein binding);GO:0051085(chaperone cofactor-dependent protein refolding);GO:0051787(misfolded protein binding)	NA	VIT_05s0020g03330	3.5	1169-1185	0	89.32559178	3.3422E-21
PC-3p-130465_5	VIT_07s0031g01640.t01	PREDICTED: ABC transporter F family member 5	GO:0000166(nucleotide binding);GO:0005524(ATP binding);GO:0016887(ATPase activity)	NA	VIT_07s0031g01640	4	559-576	184.3487879	178.6511836	0.76488
PC-3p-130465_5	VIT_13s0064g00570.t01	PREDICTED: protein OBERON 4	GO:0005634(nucleus);GO:0010071(root meristem specification);GO:0010078(maintenance of root meristem identity);GO:0010468(regulation of gene expression);GO:0010492(maintenance of shoot apical meristem identity)	NA	VIT_13s0064g00570	4	445-464	184.3487879	0	5.3983E-42
PC-3p-131526_5	VIT_00s0225g00010.t01	NA	NA	NA	NA	4	475-493	184.3487879	0	5.3983E-42
PC-3p-131526_5	VIT_00s0229g00110.t01	NA	NA	NA	NA	3	5509-5526	368.6975758	0	3.4751E-82
PC-3p-131526_5	VIT_00s0337g00010.t01	PREDICTED: RGG repeats nuclear RNA binding protein B	NA	NA	NA	3.5	310-328	0	89.32559178	3.3422E-21
PC-3p-131526_5	VIT_00s0590g00020.t01	PREDICTED: RGG repeats nuclear RNA binding protein B	NA	NA	NA	3.5	310-328	0	267.9767753	3.0764E-60
PC-3p-131526_5	VIT_00s2512g00010.t01	NA	NA	NA	NA	3.5	1605-1623	368.6975758	0	3.4751E-82
PC-3p-131526_5	VIT_01s0026g01010.t01	PREDICTED: paired amphipathic helix protein Sin3-like 4	GO:0000122(negative regulation of transcription by RNA polymerase II);GO:0000785(chromatin);GO:0003714(transcription corepressor activity);GO:0004407(histone deacetylase activity);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0016575(histone deacetylation)	NA	VIT_01s0026g01010	4	1192-1210	0	178.6511836	9.472E-41
PC-3p-131526_5	VIT_03s0038g04130.t01	PREDICTED: DEAD-box ATP-dependent RNA helicase 42	GO:0000398(mRNA splicing, via spliceosome);GO:0003676(nucleic acid binding);GO:0003723(RNA binding);GO:0005524(ATP binding);GO:0005634(nucleus)	ko03040(Spliceosome)	VIT_03s0038g04130	3	541-559	92.17439395	0	7.9195E-22
PC-3p-131526_5	VIT_06s0004g00860.t01	PREDICTED: F-box/kelch-repeat protein At1g55270-like	GO:0005515(protein binding)	NA	VIT_06s0004g00860	3.5	555-573	0	267.9767753	3.0764E-60
PC-3p-131526_5	VIT_07s0141g00250.t01	PREDICTED: calmodulin-binding transcription activator 3	NA	NA	NA	4	3321-3340	0	178.6511836	9.472E-41

PC-3p-131526_5	VIT_09s0018g00240.t01	probable WRKY transcription factor 40-like	GO:0003677(DNA binding);GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0043565(sequence-specific DNA binding)	NA	VIT_09s0018g00240	4	448-467	368.6975758	0	3.4751E-82
PC-3p-131526_5	VIT_12s0057g01100.t01	PREDICTED: nudix hydrolase 2	GO:0016787(hydrolase activity);GO:0035529(NADH pyrophosphatase activity);GO:0047631(ADP-ribose diphosphatase activity);GO:0051287(NAD binding)	NA	VIT_12s0057g01100	3	876-894	0	267.9767753	3.0764E-60
PC-3p-131526_5	VIT_13s0019g04590.t01	PREDICTED: ATPase GET3B	GO:0000166(nucleotide binding);GO:0005524(ATP binding);GO:0009570(chloroplast stroma);GO:0016887(ATPase activity)	NA	VIT_13s0019g04590	4	906-924	184.3487879	0	5.3983E-42
PC-3p-131526_5	VIT_13s0064g01240.t01	PREDICTED: large ribosomal subunit protein eL31	GO:0002181(cytoplasmic translation);GO:0003735(structural constituent of ribosome);GO:0005622(intracellular);GO:0005840(ribosome);GO:0006412(translation);GO:0022625(cytosolic large ribosomal subunit)	ko03010(Ribosome)	VIT_13s0064g01240	4	315-333	0	89.32559178	3.3422E-21
PC-3p-131526_5	VIT_13s0067g01510.t01	NA	GO:0001401(SAM complex);GO:0016021(integral component of membrane);GO:0019867(outer membrane);GO:0034622(cellular protein-containing complex assembly);GO:0045040(protein insertion into mitochondrial outer membrane)	NA	VIT_13s0067g01510	4	55-73	737.3951516	357.3023671	1.4624E-30
PC-3p-131526_5	VIT_13s0084g00170.t01	PREDICTED: DNA-directed RNA polymerase III subunit 2	GO:0001056(RNA polymerase III activity);GO:0003677(DNA binding);GO:0003899(DNA-directed 5'-3' RNA polymerase activity);GO:0005666(RNA polymerase III complex);GO:0006351(transcription, DNA-templated);GO:0006383(transcription by RNA polymerase III);GO:0032549(ribonucleoside binding)	ko03020(RNA polymerase)	VIT_13s0084g00170	4	174-191	92.17439395	89.32559178	0.83252
PC-3p-131526_5	VIT_14s0060g01630.t01	PREDICTED: eukaryotic translation initiation factor 3 subunit A	GO:0001732(formation of cytoplasmic translation initiation complex);GO:0002183(cytoplasmic translational initiation);GO:0002188(translation reinitiation);GO:0003723(RNA binding);GO:0003729(mRNA binding);GO:0003743(translation initiation factor activity);GO:0005737(cytoplasm);GO:0005829(cytosol);GO:0005852(eukaryotic translation initiation factor 3 complex);GO:0005886(plasma membrane);GO:0006412(translation);GO:0006413(translational initiation);GO:0016282(eukaryotic 43S preinitiation complex);GO:0033290(eukaryotic 48S preinitiation complex);GO:0043614(multi-eIF complex);GO:0071540(eukaryotic translation initiation factor 3 complex, eIF3e);GO:0071541(eukaryotic translation initiation factor 3 complex, eIF3m)	ko03013(RNA transport)	VIT_14s0060g01630	3.5	1766-1785	1382.615909	1250.558285	0.010018
PC-3p-131526_5	VIT_14s0066g00610.t01	NA	NA	NA	VIT_14s0066g00610	3.5	5017-5035	184.3487879	0	5.3983E-42
PC-3p-131526_5	VIT_15s0046g01430.t01	PREDICTED: putative glucose-6-phosphate 1-epimerase	GO:0003824(catalytic activity);GO:0005975(carbohydrate metabolic process);GO:0016853(isomerase activity);GO:0030246(carbohydrate binding);GO:0047938(glucose-6-phosphate 1-epimerase activity)	ko00010(Glycolysis / Gluconeogenesis)	VIT_15s0046g01430	3.5	210-228	184.3487879	714.6047343	5.0558E-70
PC-3p-131526_5	VIT_16s0050g00680.t01	NA	NA	NA	VIT_16s0050g00680	3.5	1153-1171	92.17439395	0	7.9195E-22
PC-3p-131526_5	VIT_17s0000g00390.t01	PREDICTED: coiled-coil domain-containing protein SCD2	GO:0000911(cytokinesis by cell plate formation);GO:0016020(membrane);GO:0016021(integral component of membrane)	NA	VIT_17s0000g00390	4	812-830	184.3487879	0	5.3983E-42

PC-3p-131526_5	VIT_19s0015g00430.t01	PREDICTED: DEK domain-containing chromatin-associated protein 4	GO:0005634(nucleus);GO:0006355(regulation of transcription, DNA-templated);GO:0042393(histone binding);GO:0043565(sequence-specific DNA binding);GO:0046982(protein heterodimerization activity);GO:2000779(regulation of double-strand break repair)	NA	VIT_19s0015g00430	4	554-571	276.5231819	0	4.2164E-62
PC-3p-131526_5	VIT_19s0176g00090.t01	NA	NA	NA	VIT_19s0176g00090	3	1295-1312	368.6975758	178.6511836	4.4988E-16
PC-3p-132433_5	VIT_00s0670g00020.t01	PREDICTED: probable amino-acid acetyltransferase NAGS1	NA	NA	NA	3.5	1037-1055	0	89.32559178	3.3422E-21
PC-3p-132433_5	VIT_00s0823g00020.t01	PREDICTED: probable amino-acid acetyltransferase NAGS1	NA	NA	NA	3.5	1047-1065	0	267.9767753	3.0764E-60
PC-3p-132433_5	VIT_02s0025g04640.t01	NA	GO:0004843(thiol-dependent ubiquitin-specific protease activity);GO:0005634(nucleus);GO:0005829(cytosol);GO:0005886(plasma membrane);GO:0016807(cysteine-type carboxypeptidase activity);GO:0071108(protein K48-linked deubiquitination);GO:1990380(Lys48-specific deubiquitinase activity)	NA	VIT_02s0025g04640	4	1489-1508	92.17439395	0	7.9195E-22
PC-3p-136919_5	VIT_05s0029g00010.t01	NA	GO:0016020(membrane);GO:0016021(integral component of membrane)	NA	VIT_05s0029g00010	4	523-541	1198.267121	1339.883877	0.0049119
PC-3p-136919_5	VIT_05s0049g00760.t01	ripening-induced protein 1-like (MRIP1)	NA	NA	VIT_05s0049g00760	3.5	158-174	30233.20122	29656.09647	0.016651
PC-3p-136919_5	VIT_07s0197g00250.t01	PREDICTED: probable disease resistance protein At5g66900	GO:0043531(ADP binding)	NA	VIT_07s0197g00250	3.5	1520-1537	276.5231819	0	4.2164E-62
PC-3p-136919_5	VIT_09s0018g01420.t01	NA	GO:0016020(membrane);GO:0016021(integral component of membrane)	NA	VIT_09s0018g01420	4	281-298	553.0463637	1429.209469	2.687E-86
PC-3p-136919_5	VIT_14s0068g00250.t01	PREDICTED: exocyst complex component EXO70E2	GO:0000145(exocyst);GO:0006887(exocytosis);GO:0015031(protein transport)	NA	VIT_14s0068g00250	2.5	1385-1403	92.17439395	0	7.9195E-22
PC-3p-136919_5	VIT_16s0039g01690.t01	PREDICTED: protein TORMOZ EMBRYO DEFECTIVE	GO:0000462(maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA));GO:0004611(phosphoenolpyruvate carboxykinase activity);GO:0005515(protein binding);GO:0006094(glucanogenesis);GO:0006364(rRNA processing);GO:0017076(purine nucleotide binding);GO:0030515(snoRNA binding);GO:0032040(small-subunit processome);GO:0034388(Pwp2p-containing subcomplex of 90S preribosome)	ko03008(Ribosome biogenesis in eukaryotes)	VIT_16s0039g01690	4	2702-2720	92.17439395	89.32559178	0.83252
PC-3p-19446_71	VIT_01s0010g00690.t01	PREDICTED: DNA-directed RNA polymerase 1	GO:0003676(nucleic acid binding);GO:0003677(DNA binding);GO:0003899(DNA-directed 5'-3' RNA polymerase activity);GO:0006351(transcription, DNA-templated);GO:0006390(mitochondrial transcription);GO:0009793(embryo development ending in seed dormancy);GO:0009860(pollen tube growth);GO:0015074(DNA integration);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0016740(transferase activity);GO:0016779(nucleotidyltransferase activity);GO:0034245(mitochondrial DNA-directed RNA polymerase complex);GO:0048481(plant ovule development)	NA	VIT_01s0010g00690	4	2793-2808	184.3487879	0	5.3983E-42

PC-3p-19446_71	VIT_15s0048g01870.t01	PREDICTED: serine/arginine-rich splicing factor RS41	GO:0000381(regulation of alternative mRNA splicing, via spliceosome);GO:0003676(nucleic acid binding);GO:0003723(RNA binding);GO:0005634(nucleus);GO:0005681(spliceosomal complex);GO:0016607(nuclear speck);GO:0045292(mRNA cis splicing, via spliceosome)	ko03040(Spliceosome)	VIT_15s0048g01870	4	216-232	92.17439395	178.6511836	1.4791E-07
PC-3p-19446_71	VIT_18s0001g09990.t01	PREDICTED: cysteine proteinase mucunain	GO:0004197(cysteine-type endopeptidase activity);GO:0005615(extracellular space);GO:0005764(lysosome);GO:0006508(proteolysis);GO:0008233(peptidase activity);GO:0008234(cysteine-type peptidase activity);GO:0016787(hydrolase activity);GO:0051603(proteolysis involved in cellular protein catabolic process)	NA	VIT_18s0001g09990	4	960-976	0	267.9767753	3.0764E-60
PC-3p-21754_63	VIT_01s0010g01760.t01	NA	NA	NA	VIT_01s0010g01760	4	144-161	0	535.9535507	0
PC-3p-21754_63	VIT_01s0011g02490.t01	PREDICTED: tRNA(adenine(34)) deaminase	GO:0002100(tRNA wobble adenosine to inosine editing);GO:0003824(catalytic activity);GO:0005886(plasma membrane);GO:0008251(tRNA-specific adenosine deaminase activity);GO:0009507(chloroplast);GO:0052717(tRNA-specific adenosine-34 deaminase activity);GO:0052718(tRNA-specific adenosine-34 deaminase complex)	NA	VIT_01s0011g02490	4	1707-1724	0	178.6511836	9.472E-41
PC-3p-21754_63	VIT_03s0038g02930.t01	NA	GO:0005215(transporter activity);GO:0005887(integral component of plasma membrane);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0022857(transmembrane transporter activity);GO:0055085(transmembrane transport)	NA	VIT_03s0038g02930	3	677-693	184.3487879	0	5.3983E-42
PC-3p-21754_63	VIT_07s0005g01770.t01	PREDICTED: probable pre-mRNA-splicing factor ATP-dependent RNA helicase-like	GO:0000166(nucleotide binding);GO:0003676(nucleic acid binding);GO:0003723(RNA binding);GO:0004386(helicase activity);GO:0005524(ATP binding);GO:0016787(hydrolase activity);GO:0034459(GO_0034459)	ko03040(Spliceosome)	VIT_07s0005g01770	3	1497-1515	553.0463637	0	0
PC-3p-21754_63	VIT_09s0070g00580.t01	PREDICTED: diaminopimelate decarboxylase 2	GO:0003824(catalytic activity);GO:0008836(diaminopimelate decarboxylase activity);GO:0009089(lysine biosynthetic process via diaminopimelate);GO:0009507(chloroplast)	ko00300(Lysine biosynthesis)	VIT_09s0070g00580	3.5	237-253	184.3487879	267.9767753	0.000084047
PC-3p-21754_63	VIT_13s0084g00150.t01	PREDICTED: probable choline kinase 2	NA	ko00564(Glycerophospholipid metabolism)	VIT_13s0084g00150	4	682-698	184.3487879	89.32559178	9.2265E-09
PC-3p-21754_63	VIT_15s0046g01820.t01	PREDICTED: probable E3 ubiquitin-protein ligase RHB1A	GO:0004842(ubiquitin-protein transferase activity);GO:0005829(cytosol);GO:0016567(protein ubiquitination)	NA	VIT_15s0046g01820	2.5	275-292	0	89.32559178	3.3422E-21
PC-3p-21754_63	VIT_17s0000g05580.t01	PREDICTED: LRR receptor-like serine/threonine-protein kinase FEI 2	GO:0000166(nucleotide binding);GO:0004672(protein kinase activity);GO:0004674(protein serine/threonine kinase activity);GO:0005524(ATP binding);GO:0006468(protein phosphorylation);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0016301(kinase activity);GO:0016310(phosphorylation);GO:0016491(oxidoreductase activity);GO:0016740(transferase activity);GO:0030244(cellulose biosynthetic process);GO:0055114(oxidation-reduction process)	NA	VIT_17s0000g05580	4	133-150	92.17439395	714.6047343	0
PC-3p-23087_59	VIT_11s0016g00470.t01	PREDICTED: sucrose synthase	GO:0005985(sucrose metabolic process);GO:0016157(sucrose synthase activity);GO:0016740(transferase activity);GO:0016757(transferase activity, transferring glycosyl groups)	ko00500(Starch and sucrose metabolism)	VIT_11s0016g00470	3.5	1834-1852	184.3487879	0	5.3983E-42

PC-3p-33143_38	VIT_02s0025g01700.t01	PREDICTED: RNA polymerase II transcriptional coactivator KELP	GO:0003677(DNA binding);GO:0003713(transcription coactivator activity);GO:0005634(nucleus);GO:0005667(transcription factor complex);GO:0006355(regulation of transcription, DNA-templated);GO:0060261(positive regulation of transcription initiation from RNA polymerase II promoter)	NA	VIT_02s0025g01700	4	169-189	0	89.32559178	3.3422E-21
PC-3p-48690_22	VIT_11s0016g01780.t01	PREDICTED: protein phosphatase 2C 77	GO:0003824(catalytic activity);GO:0004721(phosphoprotein phosphatase activity);GO:0004722(protein serine/threonine phosphatase activity);GO:0004724(magnesium-dependent protein serine/threonine phosphatase activity);GO:0005634(nucleus);GO:0005829(cytosol);GO:0006470(protein dephosphorylation);GO:0016787(hydrolase activity);GO:0043169(cation binding);GO:0046872(metal ion binding)	ko04016(MAPK signaling pathway - plant);ko04075(Plant hormone signal transduction)	VIT_11s0016g01780	3.5	491-512	0	89.32559178	3.3422E-21
PC-3p-50488_21	VIT_12s0028g01600.t01	PREDICTED: ATP-dependent zinc metalloprotease FTSH 2	GO:0000166(nucleotide binding);GO:0004176(ATP-dependent peptidase activity);GO:0004222(metalloendopeptidase activity);GO:0005524(ATP binding);GO:0006508(proteolysis);GO:0009535(chloroplast thylakoid membrane);GO:0009941(chloroplast envelope);GO:0010027(thylakoid membrane organization);GO:0010205(photoinhibition);GO:0010206(photosystem II repair);GO:0010304(PSII associated light-harvesting complex II catabolic process);GO:0016020(membrane);GO:0016021(integral component of membrane)	NA	VIT_12s0028g01600	3	182-201	645.2207577	714.6047343	0.059809
PC-3p-51246_21	VIT_08s0007g01430.t01	PREDICTED: universal stress protein A-like protein	GO:0003676(nucleic acid binding);GO:0005634(nucleus);GO:0005737(cytoplasm);GO:0005886(plasma membrane);GO:0006979(response to oxidative stress);GO:0009408(response to heat);GO:0009409(response to cold);GO:0009506(plasmodesma);GO:0034337(RNA folding);GO:0061077(chaperone-mediated protein folding)	NA	VIT_08s0007g01430	4	208-228	0	89.32559178	3.3422E-21
PC-3p-52603_20	VIT_01s0011g03350.t01	NA	GO:0004672(protein kinase activity);GO:0005524(ATP binding);GO:0005634(nucleus);GO:0006468(protein phosphorylation)	NA	VIT_01s0011g03350	4	1785-1804	276.5231819	89.32559178	1.2691E-22
PC-3p-73552_12	VIT_02s0025g04530.t01	PREDICTED: DNA-directed RNA polymerase IV subunit 1	GO:0000418(RNA polymerase IV complex);GO:0001056(RNA polymerase III activity);GO:0003677(DNA binding);GO:0003899(DNA-directed 5'-3' RNA polymerase activity);GO:0005654(nucleoplasm);GO:0005666(RNA polymerase III complex);GO:0006351(transcription, DNA-templated);GO:0006383(transcription by RNA polymerase III);GO:0010495(long-distance posttranscriptional gene silencing);GO:0016740(transferase activity);GO:0016779(nucleotidyltransferase activity);GO:0030422(production of siRNA involved in RNA interference)	NA	VIT_02s0025g04530	3.5	590-608	0	178.6511836	9.472E-41
PC-3p-762_2184	VIT_01s0026g02080.t01	PREDICTED: F-box/kelch-repeat protein SKIP11	GO:0005515(protein binding);GO:0005634(nucleus)	NA	VIT_01s0026g02080	4	1706-1725	92.17439395	0	7.9195E-22

PC-3p-91132_8	VIT_13s0019g0020.t01	PREDICTED: metal tolerance protein 11	GO:0005886(plasma membrane);GO:0006812(cation transport);GO:0006876(cellular cadmium ion homeostasis);GO:0006879(cellular iron ion homeostasis);GO:0006882(cellular zinc ion homeostasis);GO:0008324(cation transmembrane transporter activity);GO:0010486(manganese:proton antiporter activity);GO:0015086(cadmium ion transmembrane transporter activity);GO:0015093(ferrous iron transmembrane transporter activity);GO:0015341(zinc efflux active transmembrane transporter activity);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0034220(ion transmembrane transport);GO:0034755(iron ion transmembrane transport);GO:0055085(transmembrane transport);GO:0070574(cadmium ion transmembrane transport);GO:0071421(manganese ion transmembrane transport);GO:0098655(cation transmembrane transport);GO:1902600(proton transmembrane transport)	NA	VIT_13s0019g00020	4	370-392	184.3487879	178.6511836	0.76488
PC-3p-96406_7	VIT_09s0002g07110.t01	PREDICTED: E3 ubiquitin-protein ligase KEG	GO:0004672(protein kinase activity);GO:0005524(ATP binding);GO:0006351(transcription, DNA-templated);GO:0006468(protein phosphorylation);GO:0043565(sequence-specific DNA binding)	NA	VIT_09s0002g07110	4	1206-1225	0	357.3023671	1.0546E-79
PC-3p-96406_7	VIT_12s0034g02010.t01	PREDICTED: kinetochore protein NUF2 homolog	GO:0000776(kinetochore);GO:0000778(condensed nuclear chromosome kinetochore);GO:0007052(mitotic spindle organization);GO:0031262(Ndc80 complex);GO:0044877(protein-containing complex binding);GO:0045132(meiotic chromosome segregation);GO:0051315(attachment of mitotic spindle microtubules to kinetochore);GO:0051383(kinetochore organization)	NA	VIT_12s0034g02010	3	410-427	0	178.6511836	9.472E-41
PC-3p-96406_7	VIT_12s0057g01140.t01	PREDICTED: protein ACTIVITY OF BC1 COMPLEX KINASE 7	GO:0004672(protein kinase activity);GO:0006468(protein phosphorylation);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0046467(membrane lipid biosynthetic process);GO:0055072(iron ion homeostasis);GO:1901031(regulation of response to reactive oxygen species)	ko04626(Plant-pathogen interaction)	VIT_12s0057g01140	3.5	1363-1382	92.17439395	0	7.9195E-22
PC-3p-99556_7	VIT_16s0050g02630.t01	PREDICTED: ATP-dependent zinc metalloprotease FTSH 11	GO:0004176(ATP-dependent peptidase activity);GO:0004222(metalloendopeptidase activity);GO:0005524(ATP binding);GO:0005739(mitochondrion);GO:0006508(proteolysis);GO:0009408(response to heat);GO:0009941(chloroplast envelope);GO:0016020(membrane)	NA	VIT_16s0050g02630	3.5	75-94	276.5231819	178.6511836	4.4761E-06
PC-5p-11177_128	VIT_12s0057g01200.t01	PREDICTED: acetyl-CoA acetyltransferase 2	GO:0003824(catalytic activity);GO:0003857(3-hydroxyacyl-CoA dehydrogenase activity);GO:0003985(acetyl-CoA C-acetyltransferase activity);GO:0003988(acetyl-CoA C-acyltransferase activity);GO:0004300(enoyl-CoA hydratase activity);GO:0005739(mitochondrion);GO:0005829(cytosol);GO:0006635(fatty acid beta-oxidation);GO:0016740(transferase activity);GO:0016746(transferase activity, transferring acyl groups);GO:0016747(transferase activity, transferring acyl groups other than amino-acyl groups)	ko00071(Fatty acid degradation);ko00072(Synthesis and degradation of ketone bodies);ko00280(Valine, leucine and isoleucine degradation);ko00310(Lysine degradation);ko00380(Tryptophan metabolism);ko00620(Pyruvate metabolism);ko00630(Glyoxylate and dicarboxylate metabolism);ko00640(Propanoate metabolism);ko00650(Butanoate metabolism);ko00900(Terpenoid backbone biosynthesis)	VIT_12s0057g01200	2.5	501-520	92.17439395	357.3023671	6.8417E-36

PC-5p-11177_128	VIT_18s0001g01620.t01	NA	NA	NA	NA	3	1040-1056	0	89.32559178	3.3422E-21
PC-5p-111940_6	VIT_07s0031g01160.t01	PREDICTED: heavy metal-associated isoprenylated plant protein 23	GO:0030001(metal ion transport);GO:0046872(metal ion binding)	NA	VIT_07s0031g01160	2.5	218-236	645.2207577	446.6279589	1.8353E-09
PC-5p-111940_6	VIT_07s0141g01030.t01	PREDICTED: putative disease resistance RPP13-like protein 1	NA	NA	NA	4	3701-3721	0	178.6511836	9.472E-41
PC-5p-111940_6	VIT_18s0001g09310.t01	PREDICTED: transcription initiation factor TFIID subunit 4b	GO:0003677(DNA binding);GO:0005669(transcription factor TFIID complex);GO:0006352(DNA-templated transcription, initiation);GO:0008134(transcription factor binding);GO:0045944(positive regulation of transcription by RNA polymerase II);GO:0051123(RNA polymerase II preinitiation complex assembly)	NA	VIT_18s0001g09310	4	2168-2186	0	89.32559178	3.3422E-21
PC-5p-114918_6	VIT_18s0001g1220.t01	NA	GO:0000226(microtubule cytoskeleton organization);GO:0000278(mitotic cell cycle);GO:0000723(telomere maintenance);GO:0000922(spindle pole);GO:0000923(equatorial microtubule organizing center);GO:0000930(gamma-tubulin complex);GO:0005200(structural constituent of cytoskeleton);GO:0005737(cytoplasm);GO:0005813(centrosome);GO:0005815(microtubule organizing center);GO:0005816(spindle pole body);GO:0005856(cytoskeleton);GO:0005874(microtubule);GO:0007020(microtubule nucleation);GO:0008274(gamma-tubulin ring complex);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0031122(cytoplasmic microtubule organization);GO:0043015(gamma-tubulin binding);GO:0051011(microtubule minus-end binding);GO:0051225(spindle assembly);GO:0051321(meiotic cell cycle);GO:0051415(microtubule nucleation by interphase microtubule organizing center);GO:0090307(mitotic spindle assembly)	NA	VIT_18s0001g11220	3.5	2281-2302	0	89.32559178	3.3422E-21
PC-5p-116590_6	VIT_00s0259g00120.t01	PREDICTED: oligopeptide transporter 3	NA	NA	NA	3	1410-1427	0	267.9767753	3.0764E-60
PC-5p-116590_6	VIT_14s0108g00940.t01	PREDICTED: granule-bound starch synthase 2	GO:0004573(glycogen (starch) synthase activity);GO:0009011(starch synthase activity);GO:0009501(amyloplast);GO:0009507(chloroplast);GO:0016757(transferase activity, transferring glycosyl groups);GO:0019252(starch biosynthetic process)	NA	VIT_14s0108g00940	4	1902-1920	0	178.6511836	9.472E-41
PC-5p-116752_6	VIT_02s0025g03520.t01	PREDICTED: 5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase	GO:0006468(protein phosphorylation);GO:0009231(riboflavin biosynthetic process);GO:0016787(hydrolase activity);GO:0043621(protein self-association)	ko00740(Riboflavin metabolism)	VIT_02s0025g03520	4	170-188	0	178.6511836	9.472E-41
PC-5p-116752_6	VIT_08s0056g01670.t01	PREDICTED: BTB/POZ and MATH domain-containing protein 4	GO:0005515(protein binding);GO:0005829(cytosol);GO:0042631(cellular response to water deprivation);GO:0071472(cellular response to salt stress)	NA	VIT_08s0056g01670	4	62-80	184.3487879	0	5.3983E-42

PC-5p-116752_6	VIT_18s0001g04340.t01	PREDICTED: serine hydroxymethyltransferase 7	GO:0003824(catalytic activity);GO:0004372(glycine hydroxymethyltransferase activity);GO:0006544(glycine metabolic process);GO:0006565(L-serine catabolic process);GO:0006730(one-carbon metabolic process);GO:0008270(zinc ion binding);GO:0016597(amino acid binding);GO:0019264(glycine biosynthetic process from serine);GO:0030170(pyridoxal phosphate binding);GO:0035999(tetrahydrofolate interconversion);GO:0046653(tetrahydrofolate metabolic process);GO:0046655(folic acid metabolic process);GO:0050897(cobalt ion binding);GO:0070905(serine binding);GO:1904482(cellular response to tetrahydrofolate)	ko00260(Glycine, serine and threonine metabolism);ko00460(Cyanoamino acid metabolism);ko00630(Glyoxylate and dicarboxylate metabolism);ko00670(One carbon pool by folate)	VIT_18s0001g04340	4	181-199	1659.139091	1429.209469	0.000034634
PC-5p-118019_6	VIT_00s0455g0020.t01	PREDICTED: enhancer of mRNA-decapping protein 4	NA	NA	NA	4	1796-1815	0	89.32559178	3.3422E-21
PC-5p-119769_5	VIT_06s0004g01270.t01	PREDICTED: callose synthase 3	GO:0000148(1,3-beta-D-glucan synthase complex);GO:0003843(1,3-beta-D-glucan synthase activity);GO:0005886(plasma membrane);GO:0006075((1->3)-beta-D-glucan biosynthetic process);GO:0016020(membrane);GO:0016021(integral component of membrane)	NA	VIT_06s0004g01270	4	590-607	184.3487879	0	5.3983E-42
PC-5p-119769_5	VIT_08s0004g03270.t01	PREDICTED: E3 ubiquitin-protein ligase UPL4	GO:0004842(ubiquitin-protein transferase activity);GO:0016567(protein ubiquitination);GO:0016740(transferase activity)	NA	VIT_08s0004g03270	4	3692-3709	0	178.6511836	9.472E-41
PC-5p-119769_5	VIT_11s0103g00420.t01	PREDICTED: factor of DNA methylation 1	GO:0031047(gene silencing by RNA)	NA	VIT_11s0103g00420	4	226-242	0	89.32559178	3.3422E-21
PC-5p-119769_5	VIT_14s00081g0010.t01	indole-3-acetic acid-induced protein 16	GO:0005515(protein binding);GO:0005634(nucleus);GO:0006351(transcription, DNA-templated);GO:0006355(regulation of transcription, DNA-templated);GO:0009734(auxin-activated signaling pathway)	NA	VIT_14s00081g0010	3.5	471-488	0	178.6511836	9.472E-41
PC-5p-125267_5	VIT_04s0008g05220.t01	PREDICTED: cellulose synthase A catalytic subunit 1 [UDP-forming]	GO:0005794(Golgi apparatus);GO:0005802(trans-Golgi network);GO:0005886(plasma membrane);GO:0009833(plant-type primary cell wall biogenesis);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0016740(transferase activity);GO:0016757(transferase activity, transferring glycosyl groups);GO:0016759(cellulose synthase activity);GO:0016760(cellulose synthase (UDP-forming) activity);GO:0030244(cellulose biosynthetic process);GO:0046872(metal ion binding);GO:0071555(cell wall organization)	NA	VIT_04s0008g05220	3.5	1861-1879	368.6975758	0	3.4751E-82
PC-5p-125267_5	VIT_04s0004g01480.t01	PREDICTED: SAL1 phosphatase	GO:0000103(sulfate assimilation);GO:0005737(cytoplasm);GO:0006790(sulfur compound metabolic process);GO:0008441(3'(2'),5'-bisphosphate nucleotidase activity);GO:0016311(dephosphorylation);GO:0042578(phosphoric ester hydrolase activity);GO:0046854(phosphatidylinositol phosphorylation)	ko00562(Inositol phosphate metabolism);ko00920(Sulfur metabolism);ko04070(Phosphatidylinositol signaling system)	VIT_04s0004g01480	4	709-728	0	178.6511836	9.472E-41
PC-5p-125267_5	VIT_06s0004g02090.t01	PREDICTED: nucleolar GTP-binding protein 1	GO:0005525(GTP binding);GO:0005634(nucleus);GO:0005730(nucleolus);GO:0042254(ribosome biogenesis)	ko03008(Ribosome biogenesis in eukaryotes)	VIT_06s0004g02090	4	970-988	276.5231819	0	4.2164E-62
PC-5p-127847_5	VIT_06s0004g07820.t01	PREDICTED: pentatricopeptide repeat-containing protein At1g08070	GO:0005515(protein binding);GO:0008270(zinc ion binding);GO:0009451(RNA modification)	NA	VIT_06s0004g07820	4	214-234	0	89.32559178	3.3422E-21

PC-5p-127847_5	VIT_16s0050g0 0400.t01	NA	NA	NA	VIT_16s0050 g00400	4	53-70	0	89.32559178	3.3422E-21
PC-5p-127847_5	VIT_18s0001g0 1990.t01	NA	NA	NA	NA	3.5	887-905	92.17439395	0	7.9195E-22
PC-5p-130585_5	VIT_05s0020g0 1670.t01	PREDICTED: GTP-binding protein OBGC	GO:0000166(nucleotide binding);GO:0000287(magnesium ion binding);GO:0003924(GTPase activity);GO:0005255(GTP binding);GO:0006364(rRNA processing);GO:0009416(response to light stimulus);GO:0009507(chloroplast);GO:0009570(chloroplast stroma);GO:0009658(chloroplast organization);GO:0009706(chloroplast inner membrane);GO:0009793(embryo development ending in seed dormancy);GO:0010027(thylakoid membrane organization)	NA	VIT_05s0020 g01670	4	762-779	0	89.32559178	3.3422E-21
PC-5p-130585_5	VIT_14s0030g0 2310.t01	PREDICTED: auxin-induced protein 22D	GO:0005515(protein binding);GO:0005634(nucleus);GO:0006351(transcription, DNA-templated);GO:0006355(regulation of transcription, DNA-templated);GO:0009734(auxin-activated signaling pathway)	ko04075(Plant hormone signal transduction)	VIT_14s0030 g02310	4	415-435	0	89.32559178	3.3422E-21
PC-5p-139819_5	VIT_18s0041g0 0560.t01	PREDICTED: protein NRT1/ PTR FAMILY 5.10	GO:0005215(transporter activity);GO:0006857(oligopeptide transport);GO:0015333(peptide:proton symporter activity);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0022857(transmembrane transporter activity);GO:0035672(oligopeptide transmembrane transport);GO:0035673(oligopeptide transmembrane transporter activity);GO:0055085(transmembrane transport);GO:1902600(proton transmembrane transport);GO:1904680(peptide transmembrane transporter activity)	NA	VIT_18s0041 g00560	3	458-481	184.3487879	0	5.3983E-42
PC-5p-141637_5	VIT_04s0008g0 4480.t01	PREDICTED: RING finger and CHY zinc finger domain-containing protein 1-like	GO:0008270(zinc ion binding)	ko04120(Ubiquitin mediated proteolysis)	VIT_04s0008 g04480	4	1141-1161	92.17439395	178.6511836	1.4791E-07
PC-5p-143805_5	VIT_17s0000g0 3200.t01	NA	GO:0016298(lipase activity);GO:0044255(cellular lipid metabolic process)	NA	VIT_17s0000 g03200	2.5	633-652	184.3487879	267.9767753	0.000084047
PC-5p-147830_5	VIT_04s0008g0 0200.t01	PREDICTED: tryptophanyl-tRNA synthetase-like	GO:0000166(nucleotide binding);GO:0003676(nucleic acid binding);GO:0004812(aminoacyl-tRNA ligase activity);GO:0004830(tryptophan-tRNA ligase activity);GO:0005524(ATP binding);GO:0005739(mitochondrion);GO:0005829(cytosol);GO:0006412(translation);GO:0006418(tRNA aminoacylation for protein translation);GO:0006436(tryptophanyl-tRNA aminoacylation);GO:0009507(chloroplast);GO:0016874(ligase activity)	ko00970(Aminoacyl-tRNA biosynthesis)	VIT_04s0008 g00200	2.5	58-76	645.2207577	0	0
PC-5p-147830_5	VIT_06s0061g0 0750.t01	Cu/Zn superoxide dismutase-like (SODCP)	GO:0004784(superoxide dismutase activity);GO:0005507(copper ion binding);GO:0005576(extracellular region);GO:0005615(extracellular space);GO:0005737(cytoplasm);GO:0006801(superoxide metabolic process);GO:0008270(zinc ion binding);GO:0009507(chloroplast);GO:0009536(plastid);GO:0016209(antioxidant activity);GO:0016491(oxidoreductase activity);GO:0016532(superoxide dismutase copper chaperone activity);GO:0019430(removal of superoxide radicals);GO:0046872(metal ion binding);GO:0055114(oxidation-reduction process);GO:0098869(cellular oxidant detoxification)	ko04146(Peroxisome)	VIT_06s0061 g00750	4	81-100	2765.231819	1250.558285	0
PC-5p-147830_5	VIT_12s0028g0 0610.t01	PREDICTED: aspartyl protease family protein 2	GO:0004190(aspartic-type endopeptidase activity);GO:0006508(proteolysis);GO:0008233(peptidase activity);GO:0016787(hydrolase activity);GO:0030163(protein catabolic process)	NA	VIT_12s0028 g00610	4	187-206	460.8719698	0	0

PC-5p-15384_92	VIT_14s0083g01030.t01	PREDICTED: FUL-like protein	GO:000977(RNA polymerase II regulatory region sequence-specific DNA binding);GO:0000982(GO_0000982);GO:0003677(DNA binding);GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006351(transcription, DNA-templated);GO:0006355(regulation of transcription, DNA-templated);GO:0007275(multicellular organism development);GO:0008134(transcription factor binding);GO:0009908(flower development);GO:0010223(secondary shoot formation);GO:0010228(vegetative to reproductive phase transition of meristem);GO:0010311(lateral root formation);GO:0043565(sequence-specific DNA binding);GO:0044212(transcription regulatory region DNA binding);GO:0045944(positive regulation of transcription by RNA polymerase II);GO:0046983(protein dimerization activity);GO:0048366(leaf development)	NA	VIT_14s0083g01030	4	106-123	92.17439395	0	7.9195E-22
PC-5p-23876_57	VIT_06s0004g00810.t01	PREDICTED: phytoene synthase 2	GO:0005515(protein binding);GO:0016020(membrane);GO:0016021(integral component of membrane)	NA	VIT_06s0004g00810	4	1414-1431	276.5231819	0	4.2164E-62
PC-5p-23876_57	VIT_17s0000g06960.t01	PREDICTED: UDP-glucose 6-dehydrogenase-like	GO:0003979(UDP-glucose 6-dehydrogenase activity);GO:0005634(nucleus);GO:0005829(cytosol);GO:0006024(glycoaminoglycan biosynthetic process);GO:0016491(oxidoreductase activity);GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor);GO:0051287(NAD binding);GO:0055114(oxidation-reduction process)	ko00040(Pentose and glucuronate interconversions);ko00053(Ascorbate and aldarate metabolism);ko00520(Amino sugar and nucleotide sugar metabolism)	VIT_17s0000g06960	4	879-895	92.17439395	0	7.9195E-22
PC-5p-27135_49	VIT_05s0020g02000.t01	PREDICTED: chromatin structure-remodeling complex protein SYD	NA	NA	VIT_05s0020g02000	4	1190-1209	92.17439395	178.6511836	1.4791E-07
PC-5p-27135_49	VIT_12s0059g01460.t01	PREDICTED: ethylene-responsive transcription factor 3	GO:0003677(DNA binding);GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006351(transcription, DNA-templated);GO:0006355(regulation of transcription, DNA-templated);GO:0043565(sequence-specific DNA binding)	NA	VIT_12s0059g01460	4	82-101	0	178.6511836	9.472E-41
PC-5p-32453_39	VIT_14s0030g01670.t01	PREDICTED: 26S proteasome non-ATPase regulatory subunit 11-like	GO:0005198(structural molecule activity);GO:0005515(protein binding);GO:0006511(ubiquitin-dependent protein catabolic process);GO:0008541(proteasome regulatory particle, lid subcomplex);GO:0043248(proteasome assembly)	ko03050(Proteasome)	VIT_14s0030g01670	4	552-571	92.17439395	0	7.9195E-22
PC-5p-38584_31	VIT_14s0083g00750.t01	NA	GO:0000902(cell morphogenesis);GO:0005886(plasma membrane);GO:0005938(cell cortex)	NA	VIT_14s0083g00750	3.5	1320-1338	92.17439395	0	7.9195E-22
PC-5p-44362_26	VIT_06s0004g00400.t01	PREDICTED: lysine--tRNA ligase	GO:0000049(tRNA binding);GO:0000166(nucleotide binding);GO:0003676(nucleic acid binding);GO:0004812(aminoacyl-tRNA ligase activity);GO:0004824(lysine-tRNA ligase activity);GO:0005524(ATP binding);GO:0005737(cytoplasm);GO:0005739(mitochondrion);GO:0005829(cytosol);GO:0006418(tRNA aminoacylation for protein translation);GO:0006430(lysyl-tRNA aminoacylation)	ko00970(Aminoacyl-tRNA biosynthesis)	VIT_06s0004g00400	4	101-120	0	89.32559178	3.3422E-21
PC-5p-44362_26	VIT_06s0004g08410.t01	PREDICTED: bifunctional bis(5'-adenosyl)-triphosphatase/adenylylsulfatase FHIT	GO:0003824(catalytic activity);GO:0005829(cytosol);GO:0043530(adenosine 5'-monophosphoramidase activity);GO:0047627(adenylylsulfatase activity)	ko00230(Purine metabolism)	VIT_06s0004g08410	4	308-325	0	178.6511836	9.472E-41
PC-5p-46731_24	VIT_01s0026g02080.t01	PREDICTED: F-box/kelch-repeat protein SKIP11	GO:0005515(protein binding);GO:0005634(nucleus)	NA	VIT_01s0026g02080	3.5	939-957	460.8719698	0	0

PC-5p-46731_24	VIT_14s0128g00390.t01	PREDICTED: peroxisomal adenine nucleotide carrier 1	GO:0005347(ATP transmembrane transporter activity);GO:0005779(integral component of peroxisomal membrane);GO:0006635(fatty acid beta-oxidation);GO:0007031(peroxisome organization);GO:0015217(ADP transmembrane transporter activity);GO:0015866(ADP transport);GO:0015867(ATP transport);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0022857(transmembrane transporter activity);GO:0055085(transmembrane transport)	NA	VIT_14s0128g00390	2.5	552-570	0	446.6279589	0
PC-5p-46731_24	VIT_16s0098g00690.t01	PREDICTED: UNC93-like protein 1	GO:0005887(integral component of plasma membrane);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0055085(transmembrane transport)	NA	VIT_16s0098g00690	3.5	976-994	0	178.6511836	9.472E-41
PC-5p-65472_14	VIT_09s0002g03640.t01	PREDICTED: ABC transporter G family member 29	GO:0000166(nucleotide binding);GO:0005524(ATP binding);GO:0005886(plasma membrane);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0016887(ATPase activity);GO:0042626(ATPase-coupled transmembrane transporter activity);GO:0055085(transmembrane transport)	NA	VIT_09s0002g03640	4	1301-1321	0	89.32559178	3.3422E-21
PC-5p-70654_13	VIT_01s0150g00090.t01	PREDICTED: protein MEI2-like 4	GO:0000381(regulation of alternative mRNA splicing, via spliceosome);GO:0000395(mRNA 5'-splice site recognition);GO:0003676(nucleic acid binding);GO:0003723(RNA binding);GO:0005634(nucleus);GO:0016607(nuclear speck);GO:0045292(mRNA cis splicing, via spliceosome)	NA	VIT_01s0150g00090	3.5	3566-3582	0	357.3023671	1.0546E-79
PC-5p-70654_13	VIT_05s0020g01570.t01	PREDICTED: cysteine-tryptophan domain-containing zinc finger protein 5	GO:0008270(zinc ion binding)	NA	VIT_05s0020g01570	2.5	2654-2671	0	267.9767753	3.0764E-60
PC-5p-70654_13	VIT_06s0004g03580.t01	PREDICTED: general negative regulator of transcription subunit 4	GO:0003676(nucleic acid binding);GO:0003723(RNA binding);GO:0004842(ubiquitin-protein transferase activity);GO:0016567(protein ubiquitination);GO:0030014(CCR4-NOT complex)	ko03018(RNA degradation)	VIT_06s0004g03580	4	2034-2054	0	89.32559178	3.3422E-21
PC-5p-78206_11	VIT_01s0010g03900.t01	MADS-box protein 4	GO:0000977(RNA polymerase II regulatory region sequence-specific DNA binding);GO:0000982(GO_0000982);GO:0003677(DNA binding);GO:0003700(DNA-binding transcription factor activity);GO:0005634(nucleus);GO:0006351(transcription, DNA-templated);GO:0006355(regulation of transcription, DNA-templated);GO:0007275(multicellular organism development);GO:0008134(transcription factor binding);GO:0009908(flower development);GO:0043565(sequence-specific DNA binding);GO:0044212(transcription regulatory region DNA binding);GO:0045944(positive regulation of transcription by RNA polymerase II);GO:0046983(protein dimerization activity);GO:0048481(plant ovule development)	NA	VIT_01s0010g03900	3.5	572-590	184.3487879	0	5.3983E-42
PC-5p-78206_11	VIT_01s0182g00070.t01	PREDICTED: 26S proteasome non-ATPase regulatory subunit 11-like	GO:0005198(structural molecule activity);GO:0005515(protein binding);GO:0006511(ubiquitin-dependent protein catabolic process);GO:0008541(proteasome regulatory particle, lid subcomplex);GO:0043248(proteasome assembly)	ko03050(Proteasome)	VIT_01s0182g00070	4	374-394	0	357.3023671	1.0546E-79

PC-5p-78206_11	VIT_04s0023g01580.t01	PREDICTED: U1 small nuclear ribonucleoprotein 70 kDa	GO:0000243(commitment complex);GO:0000398(mRNA splicing, via spliceosome);GO:0003676(nucleic acid binding);GO:0003723(RNA binding);GO:0003729(mRNA binding);GO:0005634(nucleus);GO:0005685(U1 snRNP);GO:0030619(U1 snRNA binding);GO:0071004(U2-type prespliceosome)	ko03040(Spliceosome)	VIT_04s0023g01580	3	344-362	0	357.3023671	1.0546E-79
PC-5p-78206_11	VIT_05s0020g01850.t01	PREDICTED: double-stranded RNA-binding protein 2	GO:0003723(RNA binding);GO:0005515(protein binding)	NA	VIT_05s0020g01850	2.5	1325-1344	0	267.9767753	3.0764E-60
PC-5p-78206_11	VIT_05s0077g01840.t01	PREDICTED: 60S ribosomal protein L19-like	GO:0003723(RNA binding);GO:0003735(structural constituent of ribosome);GO:0005622(intracellular);GO:0005840(ribosome);GO:0006412(translation);GO:0022625(cytosolic large ribosomal subunit)	ko03010(Ribosome)	VIT_05s0077g01840	3.5	518-536	184.3487879	0	5.3983E-42
PC-5p-78206_11	VIT_07s0031g01190.t01	PREDICTED: MICOS complex subunit MIC60	GO:0005739(mitochondrion);GO:0005743(mitochondrial inner membrane);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0097035(regulation of membrane lipid distribution);GO:0098800(inner mitochondrial membrane protein complex);GO:1901612(cardiolipin binding)	NA	VIT_07s0031g01190	2	672-689	92.17439395	0	7.9195E-22
PC-5p-78206_11	VIT_15s0046g01070.t01	PREDICTED: protein WHAT'S THIS FACTOR 1	GO:0008270(zinc ion binding)	NA	VIT_15s0046g01070	4	411-429	0	89.32559178	3.3422E-21
PC-5p-78206_11	VIT_15s0048g01300.t01	PREDICTED: polygalacturonate 4-alpha-galacturonosyltransferase	GO:0000139(Golgi membrane);GO:0005794(Golgi apparatus);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0016740(transferase activity);GO:0016757(transferase activity, transferring glycosyl groups);GO:0045489(pectin biosynthetic process);GO:0047262(polygalacturonate 4-alpha-galacturonosyltransferase activity);GO:0071555(cell wall organization)	ko00520(Amino sugar and nucleotide sugar metabolism)	VIT_15s0048g01300	3	1052-1070	0	89.32559178	3.3422E-21
PC-5p-78206_11	VIT_16s0039g02270.t01	NA	GO:0005634(nucleus);GO:0005737(cytoplasm);GO:0006470(protein dephosphorylation);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0019888(protein phosphatase regulator activity);GO:0030289(protein phosphatase 4 complex);GO:0043666(regulation of phosphoprotein phosphatase activity)	NA	VIT_16s0039g02270	4	698-716	0	178.6511836	9.472E-41
PC-5p-80402_10	VIT_02s0012g02160.t01	PREDICTED: glycerol-3-phosphate acyltransferase ATS12	GO:0004366(glycerol-3-phosphate O-acyltransferase activity);GO:0006629(lipid metabolic process);GO:0006650(glycerophospholipid metabolic process);GO:0006655(phosphatidylglycerol biosynthetic process);GO:0009507(chloroplast);GO:0009536(plastid);GO:0009570(chloroplast stroma);GO:0016024(CDP-diacylglycerol biosynthetic process);GO:0016740(transferase activity);GO:0016746(transferase activity, transferring acyl groups);GO:0102420(sn-1-glycerol-3-phosphate C16:0-DCA-CoA acyl transferase activity)	ko00561(Glycerolipid metabolism);ko00564(Glycerophospholipid metabolism)	VIT_02s0012g02160	3.5	719-739	184.3487879	178.6511836	0.76488
PC-5p-82241_10	VIT_00s0216g00060.t01	PREDICTED: ninja-family protein 4	NA	NA	NA	3	37-54	0	178.6511836	9.472E-41

PC-5p-95613_7	VIT_17s0000g06710.t01	PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g74360	GO:0000166(nucleotide binding);GO:0002215(defense response to nematode);GO:0004672(protein kinase activity);GO:0004674(protein serine/threonine kinase activity);GO:0005515(protein binding);GO:0005524(ATP binding);GO:0005739(mitochondrion);GO:0005886(plasma membrane);GO:0006468(protein phosphorylation);GO:0009506(plasmodesma);GO:0009825(multidimensional cell growth);GO:0009845(seed germination);GO:0016020(membrane);GO:0016021(integral component of membrane);GO:0016301(kinase activity);GO:0016310(phosphorylation);GO:0016740(transferase activity);GO:0046777(protein autophosphorylation)	NA	VIT_17s0000g06710	4	1819-1839	0	267.9767753	3.0764E-60
PC-5p-97643_7	VIT_05s0020g01610.t01	PREDICTED: protein ALWAYS EARLY 3	GO:0000003(reproduction);GO:0003677(DNA binding);GO:0005634(nucleus);GO:0005654(nucleoplasm);GO:0006351(transcription, DNA-templated);GO:0017053(transcriptional repressor complex);GO:0051726(regulation of cell cycle)	NA	VIT_05s0020g01610	4	242-260	0	446.6279589	0
PC-5p-97643_7	VIT_07s0104g01060.t01	PREDICTED: protein SLOW WALKER 1	GO:0005515(protein binding);GO:0005730(nucleolus);GO:0006364(rRNA processing);GO:0009553(embryo sac development);GO:0009561(megagametogenesis);GO:0045943(positive regulation of transcription by RNA polymerase I)	ko03008(Ribosome biogenesis in eukaryotes)	VIT_07s0104g01060	4	204-222	0	178.6511836	9.472E-41
PC-5p-97643_7	VIT_12s0035g00240.t01	PREDICTED: multiple organellar RNA editing factor 1	GO:0005739(mitochondrion);GO:0016554(cytidine to uridine editing);GO:0080156(mitochondrial mRNA modification)	NA	VIT_12s0035g00240	3,5	189-208	92.17439395	0	7.9195E-22
PC-5p-97643_7	VIT_12s0142g00200.t01	NA	GO:0000470(maturation of LSU-rRNA);GO:0003723(RNA binding);GO:0030686(90S preribosome)	NA	VIT_12s0142g00200	4	249-267	184.3487879	267.9767753	0.000084047
PC-5p-97643_7	VIT_17s0000g05450.t01	PREDICTED: protein EARLY FLOWERING 5	GO:0006396(RNA processing);GO:0045292(mRNA cis splicing, via spliceosome)	NA	VIT_17s0000g05450	4	900-916	0	89.32559178	3.3422E-21
PC-5p-97904_7	VIT_04s0008g03060.t01	PREDICTED: DDB1- and CUL4-associated factor homolog 1	GO:0005515(protein binding);GO:0005634(nucleus);GO:0009793(embryo development ending in seed dormancy);GO:0009908(flower development);GO:0016567(protein ubiquitination);GO:0048366(leaf development);GO:0080008(Cul4-RING E3 ubiquitin ligase complex)	NA	VIT_04s0008g03060	4	4930-4948	460.8719698	625.2791425	6.0404E-07
PC-5p-97904_7	VIT_18s0001g04980.t01	PREDICTED: acetyl-CoA carboxylase 1	GO:0000166(nucleotide binding);GO:0003989(acetyl-CoA carboxylase activity);GO:0005524(ATP binding);GO:0006633(fatty acid biosynthetic process);GO:0016874(ligase activity);GO:0046872(metal ion binding)	ko00061(Fatty acid biosynthesis);ko00620(Pyruvate metabolism);ko00640(Propanoate metabolism)	VIT_18s0001g04980	3,5	4882-4899	184.3487879	0	5.3983E-42