

contig2	numOutSnps	prop	NumTempOut	NumPrecipOut	Annotation
comp60064_c0	46	0.613333333	46	1	NA protein_coding acclimation of photosynthesis to environment mutant has Altered acclimation responses; Proteasome maturation factor UMP1 (TAIR:AT5G38650.1).
comp1563_c0	19	0.76	16	2	NA
comp73926_c0	13	0.928571429	13	0	NA
comp1180_c0	3	0.1875	3	0	NA
comp21748_c0	2	0.0625	2	1	heavy metal atpase 5 The Arabidopsis P-type ATPase HMA5 is involved in Cu detoxification. hma5 mutant plants exhibit Cu hypersensitivity, which is especially dramatic in roots where HMA5 is mostly expressed. heavy metal atpase 5 (HMA5); FUNCTIONS IN: ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism; INVOLVED IN: detoxification of copper ion, response to copper ion; LOCATED IN: integral to membrane, membrane;
comp8237_c0	5	0.11627907	2	0	protein_coding Transducin/WD40 repeat-like superfamily protein Encodes a protein with similarity to yeast Pfs2p, an mRNA processing factor. Involved in regulation of flowering time; affects FCA mRNA processing. Homozygous mutants are late flowering, null alleles are embryo lethal.
comp6762_c0	7	0.152173913	1	7	NA
comp19776_c1	2	0.037037037	1	2	NA
comp29496_c0	4	0.2	1	2	protein_coding Duplicated homeodomain-like superfamily protein \Putative protein_coding nuclear factor Y, subunit A7 \nuclear
comp4611_c0	1	0.022727273	1	1	protein_coding similar to RCD one 2 Encodes a protein with similarity to RCD1 but without the WWE domain. The protein does have a PARP signature upstream of the C-terminal protein interaction domain. The PARP signature may bind NAD+ and attach the ADP-ribose-moiety from NAD+ to the target molecule. Its presence suggests a role for the protein in ADP ribosylation.
comp1011_c0	2	0.048780488	1	0	similar to RCD one 2 (SRO2); protein_coding plastid division1 An integral outer envelope membrane protein (as its homolog PDV2), component of the plastid division machinery. Similar to ARC5, PDV1 localized to a discontinuous ring at the division site in wild-type plants. PDV1 and PDV2 are required for localization of ARC5 at the chloroplast division site. Topological analysis showed that the large N-terminal region of PDV1 upstream of the transmembrane helix bearing a putative coiled-coil domain is exposed to the cytosol. Mutation of the conserved PDV1 C-terminal Gly residue did not block PDV1 insertion into the outer envelope membrane but did abolish its localization to the division site.
comp13145_c1	1	0.011764706	1	0	protein_coding peroxin 14 mutant has a defect in the intracellular transport of thiolase from the cytosol to glyoxysomes (formerly known as ped2) peroxin 14 (PEX14); FUNCTIONS IN: protein transporter activity, protein binding;
comp1439_c0	2	0.034482759	1	0	INVOLVED IN: peroxisome organization, protein targeting to peroxisome;
comp15605_c0	2	0.043478261	1	0	NA
comp28687_c0	1	0.083333333	1	0	NA
comp31135_c0	1	0.037037037	1	0	protein_coding Pentatricopeptide repeat (PPR-like) superfamily protein Pentatricopeptide repeat (PPR-like) superfamily protein; FUNCTIONS IN: molecular_function unknown; Pentatricopeptide repeat (PPR-like) superfamily protein
comp1565_c0	34	0.267716535	0	24	protein_coding Insulinase (Peptidase family M16) protein Insulinase (Peptidase family M16) protein; FUNCTIONS IN: metalloendopeptidase activity, ATP binding; INVOLVED IN: proteolysis, response to salt stress;
comp2237_c0	11	0.25	0	9	protein_coding DNA-binding bromodomain-containing protein DNA-binding bromodomain-containing protein; CONTAINS InterPro DOMAIN/s: Bromodomain (InterPro:IPR001487);
comp9553_c0	9	0.132352941	0	8	protein_coding histone acetyltransferase of the GNAT family 2 Encodes an enzyme with histone acetyltransferase activity. Histone H4 is the primary substrate for the enzyme. Prior acetylation of lysine 12 of histone H4 reduces radioactive acetylation by HAG2. HAG2 acetylates histone H4 lysine 12. histone acetyltransferase of the GNAT family 2 (HAG2); FUNCTIONS IN: histone acetyltransferase activity, H4 histone acetyltransferase activity; INVOLVED IN: histone acetylation, chromatin modification, chromatin silencing at telomere;
comp1964_c0	12	0.3	0	7	protein_coding SWIB/MDM2 domain superfamily protein SWIB/MDM2 domain superfamily protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast;
comp4147_c0	8	0.114285714	0	7	protein_coding Protein of unknown function (duplicated DUF1399) Protein of unknown function (duplicated DUF1399);
comp6329_c0	8	0.444444444	0	7	NA
comp24588_c0	5	0.227272727	0	5	protein_coding YUCCA 3 YUCCA 3 (YUC3); FUNCTIONS IN: NADP or NADPH binding, oxidoreductase activity, FAD binding, flavin-containing monooxygenase activity; INVOLVED IN: auxin biosynthetic process;

comp4835_c0	8	0.163265306	0	5	NA
comp64053_c0	5	0.138888889	0	5	NA
comp1027_c0	4	0.111111111	0	4	protein_coding myo-inositol oxygenase 4 Encodes a myo-inositol oxygenase. myo-inositol oxygenase 4 (MIOX4); FUNCTIONS IN: inositol oxygenase activity; INVOLVED IN: L-ascorbic acid biosynthetic process, syncytium formation;
comp25728_c1	5	0.238095238	0	4	NA
comp12654_c0	3	0.088235294	0	3	protein_coding ATP binding microtubule motor family protein ATP binding microtubule motor family protein; FUNCTIONS IN: microtubule motor activity, ATP binding;
comp26296_c0	3	0.230769231	0	3	NA
comp3285_c0	3	0.096774194	0	3	protein_coding Zinc finger C-x8-C-x5-C-x3-H type family protein Encodes SOMNUS (SOM), a nucleus-localized CCCH-type zinc finger protein. SOM negatively regulates light-dependent seed germination downstream of PIL5 (AT2G20180). SOMNUS (SOM);
comp6268_c0	3	0.3	0	3	protein_coding RNA-binding (RRM/RBD/RNP motifs) family protein RNA-binding (RRM/RBD/RNP motifs) family protein; FUNCTIONS IN: RNA binding, nucleotide binding, nucleic acid binding; INVOLVED IN: biological_process unknown;
comp7067_c0	2	0.066666667	0	2	protein_coding K+ efflux antiporter 4 member of Putative potassium proton antiporter family K+ efflux antiporter 4 (KEA4); FUNCTIONS IN: potassium:hydrogen antiporter activity, potassium ion transmembrane transporter activity; INVOLVED IN: potassium ion transport, cation transport, transmembrane transport; LOCATED IN: endomembrane system, integral to membrane;
comp8064_c0	2	0.074074074	0	2	protein_coding TIFY domain protein 8 TIFY domain protein 8 (TIFY8);
comp9706_c0	3	0.125	0	2	protein_coding Pentatricopeptide repeat (PPR) superfamily protein Pentatricopeptide repeat (PPR) superfamily protein;
comp11553_c0	1	0.01	0	1	protein_coding ubiquitin-specific protease 23 Encodes a ubiquitin-specific protease. ubiquitin-specific protease 23 (UBP23); FUNCTIONS IN: ubiquitin-specific protease activity, ubiquitin thiolesterase activity; INVOLVED IN: ubiquitin-dependent protein catabolic process; LOCATED IN: chloroplast;
comp1506_c0	2	0.036363636	0	1	protein_coding Tubulin/FtsZ family protein Encodes one of two FtsZ proteins, tubulin-like proteins, in Arabidopsis. It is involved in chloroplast division. FTSZ2. 1; FUNCTIONS IN: protein binding, structural molecule activity; INVOLVED IN: chloroplast fission; LOCATED IN: chloroplast stroma, chloroplast;
comp33268_c0	1	0.043478261	0	1	NA
comp33846_c0	15	0.625	0	1	protein_coding sodium proton exchanger, putative (NHX7) (SOS1) Encodes a plasma membrane-localized Na+/H+ antiporter SOS1. Functions in the extrusion of toxic Na+ from cells and is essential for plant salt tolerance. Has 12 predicted transmembrane domains in the N-terminal region and a long cytoplasmic tail of approx. 700 aa at the C-terminal side. SOS1 interacts through its predicted cytoplasmic tail with RCD1, a regulator of oxidative-stress responses, suggesting that SOS1 might function in oxidative-stress tolerance.
comp3516_c0	1	0.027027027	0	1	protein_coding signal peptide peptidase Encodes a putative protease SppA (SppA). signal peptide peptidase (SPPA); FUNCTIONS IN: serine-type endopeptidase activity; INVOLVED IN: proteolysis, response to light intensity;
comp51036_c0	1	0.027777778	0	1	NA
comp730_c0	1	0.033333333	0	1	protein_coding ARF-GAP domain 2 A member of ARF GAP domain (AGD), A thaliana has 15 members, grouped into four classes. AGD2 belongs to the class 1, together with AGD1, AGD3, and AGD4. ARF-GAP domain 2 (AGD2);
comp90150_c0	2	0.074074074	0	1	FUNCTIONS IN: ARF GTPase activator activity, zinc ion binding; INVOLVED IN: regulation of ARF GTPase activity;
comp93351_c0	2	0.046511628	0	1	NA