Supplemental Table S2. Summary of differentially expressed genes discovered by RNA-seq

WT(*ZmOXS2b*) VS WT

DEG Number	**GeneID**	**Stress or metal ion transport related genes**	**Log$_2$Ratio WT (*ZmOXS2b*) VS WT**	**Fold Change WT (*ZmOXS2b*) VS WT**	**KEGG Orthology**	**GO Component**	**GO Function**	**GO Process**	**Results of blast against nr database**	**TAIR Annotation (Key Words)**
	AT4G23670	√	0.77	1.71	-	GO:0044444// cytoplasmic part	GO:0046914// transition metal ion binding	GO:0006952// defense response; GO:0006970// response to osmotic stress; GO:0003006// developmental process involved in reproduction; GO:0010038// response to metal ion	SRPBCC ligand-binding domain-containing protein	Involved in defense response, defense response to bacterium, fruit, response to cadmium ion
DEG18	AT5G26220	√	1.45	2.73	K07232|1|2e-51|200|osa: 4335982|cation transport protein ChaC	-	-	GO:0010038// response to metal ion	ChaC-like family protein	response to cadmium ion, response to lead ion

AT2G38390	√	2.44	5.43	K00430|1|0.0|705|ath:AT2G38390|peroxidase [EC:1.11.1.7]	GO:0005618// cell wall; GO:0043231// intracellular membrane-bounded organelle;GO:0031090// organelle membrane; GO:0005576// extracellular region	GO:0016209// antioxidant activity;GO:0003824// catalytic activity; GO:0005506// iron ion binding	GO:0009314// response to radiation;GO:0006952// defense response;GO:0010038// response to metal ion;GO:0000902// cell morphogenesis; GO:0006970// response to osmotic stress;GO:0042743// hydrogen peroxide metabolic process	peroxidase 23	oxidation-reduction process, peroxidase activity, response to oxidative stress

AT5G20250	√	-0.89	0.54	K06617|1|0.0|1504|ath:AT5G20250|raffinose synthase [EC:2.4.1.82]	GO:0009536// plastid; GO:0009536// plastid; GO:0009536// plastid; GO:0009536// plastid	GO:0008378// Galactosyltransferase activity; GO:0008378// galactosyltransferase activity; GO:0008378// galactosyltransferase activity; GO:0008378// galactosyltransferase activity	GO:0006950// response to stress; GO:0009628// response to abiotic stimulus;GO:0006950// response to stress; GO:0009628//response to abiotic stimulus; GO:0006950// response to stress; GO:0009628// response to abiotic stimulus;GO:0006950//response to stress; GO:0009628// response to abiotic stimulus	F5O24_140	response to oxidative stress

AT2G28630		-0.95	0.52	K15397|1|1e-98|358|aly:ARALYDRAFT_887345|3-ketoacyl-CoA synthase [EC:2.3.1.-]	GO:0043231// intracellular membrane-bounded organelle	GO:0016747// transferase activity, transferring acyl groups other than amino-acyl groups	GO:0009314// response toradiation;GO:0006950// response to stress;GO:0006631// fatty acid metabolic process	3-ketoacyl-CoA synthase 12	
AT1G55020	√	0.94	1.91	K15718|1|0.0|1650|ath:AT1G55020|linoleate 9S-lipoxygenase [EC:1.13.11.58]	-	GO:0046914//transition metal ion binding;GO:0016702//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	GO:0006633// fatty acid biosynthetic process;GO:0009694// jasmonic acid metabolic process;GO:0009725// response to hormone stimulus;GO:0042742// defense response to bacterium;GO:0016044// cellular membrane organization; GO:0048527//lateral root development	lipoxygenase 1	defense response, lipid oxidation

DEG5	AT3G49570		1.06	2.09	-	-	-	-	response to low sulfur 3 protein	
DEG1	AT1G75280	√	1.15	2.22	K00224|1|5e-173|605|ath:AT1G75280|[EC:1.3.1.-];K13081|4|1e-64|245|pop:POPTR_835080|leucoanthocyanidin reductase [EC:1.17.1.3]	GO:0016020//membrane	GO:0016491//oxidoreductase activity	GO:0006950//response to stress;GO:0010038//response to metal ion	Isoflavone reductase-P3	Involved in response to oxidative stress.
	AT3G16670	√	-0.83	0.56	-	GO:0044464//cell part	-	GO:0006950//response to stress	Pollen Ole e 1 allergen and extensin family protein	response to oxidative stress
	AT1G70850	√	0.88	1.84	-	-	GO:0005488//binding;GO:0005488//binding;GO:0005488//binding	GO:0006950//response to stress;GO:0006950//response to stress;GO:0006950//response to stress	MLP-like protein 34	response to biotic stimulus, defense response
DEG13	AT3G19710		1.44	2.72	K00826|1|0.0|684|ath:AT3G19710|branched-chain amino acid aminotransferase [EC:2.6.1.42]	GO:0044444//cytoplasmic part	GO:0004084//branched-chain-amino-acid transaminase activity	GO:0019758;GO:0006520//cellular amino acid metabolic process	Probable branched-chain-amino-acid aminotransferase 4	

DEG7	AT5G26260		1.23	2.35	K11838|1|1e-16|85.9|rcu:RCOM_0423090|ubiquitin carboxyl-terminal hydrolase 7 [EC:3.1.2.15]	GO:0031224// intrinsic to membrane;GO:0009536// plastid	-	-	TRAF-like family protein	
	AT2G01520	√	1.46	2.75	-	GO:0044444//cytoplasmic part	GO:0046914// transition metal ion binding	GO:0006950//response to stress;GO:0003006// developmental process involved in reproduction; GO:0010038//response to metal ion	MLP-like protein 328	Involved in defense response
DEG6	AT4G04610	√	1.08	2.12	K05907|1|0.0|861|ath:AT4G04610|adenylyl-sulfate reductase (glutathione) [EC:1.8.4.9]	GO:0031976;GO:0009532// plastid stroma	GO:0016671// oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	GO:0006790// sulfur compound metabolic process;GO:0019725// cellular homeostasis	5'-adenylylsulfate reductase 1	acting on oxidation-reduction process, oxidoreductase activity

AT5G48010	1.25	2.37	K15821|1|0.0|1587|ath:AT5G48010|thalianol synthase [EC:5.4.99.31];K15823|3|0.0|1290|ath:AT4G15340|arabidiol synthase [EC:4.2.1.124];K15813|4|0.0|971|pop:POPTR_764959|beta-amyrin synthase [EC:5.4.99.39]	GO:0031090//organelle membrane;GO:0009526// plastid envelope; GO:0031090//organelle membrane;GO:0009526// plastid envelope	GO:0004721//phosphoprotein phosphatase activity;GO:0015405;GO:0046915//transition metal ion transmembrane transporter activity;GO:0031559//oxidosqualene cyclase activity;GO:0004721//phosphoprotein phosphatase activity;GO:0015405;GO:0046915//transition metal ion transmembrane transporter activity;GO:0031559//oxidosqualene cyclase activity	GO:0015893//drug transport;GO:0050832//defense response to fungus;GO:0006796//phosphate-containing compound metabolic process;GO:0010683;GO:0048513//organ development;GO:0016104//triterpenoid biosynthetic process;GO:0071365//cellular response to auxin stimulus;GO:0009814//defense response, incompatible interaction;GO:0006464//cellular protein modification process;GO:0019762//glucosinolate catabolic process;GO:0010685;GO:0000041//transition metal ion transport	thalianol synthase 1

	AT3G22240		0.81	1.75	-	GO:0016020//membrane	-	GO:0051707//response to other organism	uncharacterized protein	
	AT5G43580	√	-1.24	0.42	-	-	GO:0004866//endopeptidase inhibitor activity	GO:0006950//response to stress	Serine protease inhibitor, potato inhibitor I-type family protein	Involved in defense response
DEG14	AT3G08860		1.36	2.57	K00827|1|0.0|958|ath:AT3G08860|alanine-glyoxylate transaminase / (R)-3-amino-2-methylpropionate-pyruvate transaminase [EC:2.6.1.44 2.6.1.40]	GO:0043231//intracellular membrane-bounded organelle	GO:0008483//transaminase activity;GO:0048037//cofactor binding	GO:0031669//cellular response to nutrient levels	PYRIMIDINE 4	
DEG3	AT2G39310		1.06	2.08	-	GO:0009536//plastid;GO:0009536//plastid;GO:0009536//plastid	GO:0030246//carbohydrate binding;GO:0030246//carbohydrate binding;GO:0030246//carbohydrate binding	GO:0009719;GO:0006970//response to osmotic stress;GO:0009719;GO:0006970//response to osmotic stress;GO:0009719;GO:0006970//response to osmotic stress	jacalin-related lectin 22	
	AT3G05730		-0.79	0.58	-	-	-	-	defensin-like protein 205	

DEG28	AT5G37690	1.72	3.29	K00514|1|2e-23|108|rcu:RCOM_1428040|zeta-carotene desaturase [EC:1.3.5.6];K01206|2|2e-19|95.5|aly:ARALYDRAFT_475890|alpha-L-fucosidase [EC:3.2.1.51]	GO:0031410// cytoplasmic vesicle	GO:0016788// hydrolase activity, acting on ester bonds	GO:0044238// primary metabolic process	lipase
	ATCG00800	-1.41	0.38	K02982|1|3e-113|405|ath:ArthCp061|small subunit ribosomal protein S3	GO:0000314//organellar small ribosomal subunit;GO:0009536// plastid	GO:0003723// RNA binding;GO:0005198//structural molecule activity	GO:0010467// gene expression	ribosomal protein S3
	ATCG00550	-4.03	0.06	-	GO:0009536// plastid	-	-	unnamed protein product (chloroplast)
	AT3G59220	1.13	2.19	K06911|1|6e-123|438|aly:ARALYDRAFT_670248|	GO:0016020// membrane	GO:0005515//protein binding	GO:0009725// response to hormone stimulus;GO:0009637// response to blue light	pirin

AT2G21100	√	2.07	4.19	-	GO:0044464// cell part	-	GO:0006950// response to stress;GO:0009699// phenylpropanoid biosynthetic process	putative disease resistance response protein	Involved in lignan biosynthetic process, defense response;
AT1G11840	√	0.81	1.76	K01759|1|5e-162|569|ath:AT1G11840|lactoylglutathione lyase [EC:4.4.1.5]	GO:0009526// plastid envelope;GO:0016020//membrane;GO:0042579//microbody;GO:0009526//plastid envelope;GO:0016020//membrane;GO:0042579//microbody;GO:0009526//plastid envelope;GO:0016020//membrane;GO:0042579//microbody;GO:0009526//plastid envelope	GO:0043169//cation binding; GO:0016846//carbon-sulfur lyase activity; GO:0043169// cation binding;GO:0016846//carbon-sulfur lyase activity; GO:0043169//cation binding;GO:0016846// carbon-sulfur lyase activity; GO:0043169//cation binding;GO:0016846//carbon-sulfur lyase activity\	GO:0044238//primary metabolic process;GO:0010038//response to metal ion;GO:0044238//primary metabolic process;GO:0010038//response to metal ion;GO:0044238//primary metabolic process;GO:0010038//response to metal ion;GO:0044238//primary metabolic process;GO:0010038//response to metal ion	lactoylglutathione lyase-like protein	response to cadmium ion

	AT4G12490	√	-1.05	0.48	-	GO:0031410//cytoplasmic vesicle	GO:0005488//binding	GO:0010876; GO:0009814//defense response, incompatible interaction	seed storage 2S albumin-like protein	defense response to fungus
	AT1G70890	√	0.81	1.75	-	GO:0009536//plastid	GO:0005488//binding	GO:0006950//response to stress	MLP-like protein 43	Involved in response to biotic stimulus, defense response
	A		-1.94	0.26	-	-	-	-	-	
	AT5G10230		2.58	5.99	-	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0046872//metal ion binding;GO:0005543//phospholipid binding	GO:0006970//response to osmotic stress;GO:0008643//carbohydrate transport;GO:0009416//response to light stimulus	annexin D7	
	AT2G18370		1.21	2.32	-	GO:0044464//cell part	GO:0016787//hydrolase activity;GO:0005488//binding	GO:0051234//establishment of localization;GO:0010876	non-specific lipid-transfer protein 8	
DEG22	AT1G18100		2.00	3.99	K06910|1|5e-06|50.8|smo:SELMODRAFT_143762|	GO:0043231//intracellular membrane-bounded organelle	GO:0016788//hydrolase activity, acting on ester bonds;GO:0003676//nucleic acid binding	GO:0006259//DNA metabolic process;GO:0009725//response to hormone stimulus;GO:0009845//seed germination	protein MOTHER of FT and TF 1	

DEG10	AT1G16410	√	1.53	2.90	K12154|1|0.0|1058|ath:AT1G16410|cytochrome P450, family 79, subfamily F, polypeptide 1 [EC:1.14.13.-];K12155|3|0.0|935|ath:AT1G16400|cytochrome P450, family 79, subfamily F, polypeptide 2 [EC:1.14.13.-];K13027|4|4e-115|414|sbi:SORBI_01g001200|tyrosine N-monooxygenase [EC:1.14.13.41];K11812|5|3e-110|397|aly:ARALYDRAFT_490780|cytochrome P450, family 79, subfamily B, polypeptide 2 (tryptophan N-monooxygenase) [EC:1.14.13.125]	GO:0043231// intracellular membrane-bounded organelle; GO:0043231//intracellular membrane-bounded organelle	GO:0004497// monooxygenase activity;GO:0005506// iron ion binding;GO:0004497//monooxygenase activity; GO:0005506// iron ion binding	GO:0019758; GO:0019758	dihomomethionine N-hydroxylase	oxidoreductase activity
	ATCG01110	√	-0.88	0.54	K05579|1|0.0|778|ath:ArthCp080|NAD(P)H-quinone oxidoreductase subunit H [EC:1.6.5.3]	GO:0009534// chloroplast thylakoid	GO:0016651// oxidoreductase activity, acting on NADH or NADPH;GO:0048037//cofactor binding;GO:0000166//nucleotide binding	GO:0051234// establishment of localization;GO:0006091 //generation of precursor metabolites and energy	NADH dehydrogenase subunit 7	oxidation-reduction process, oxidoreductase activity

DEG21	AT4G13770	√	0.95	1.93	K12156|1|0.0|965|ath:AT4G13770|cytochrome P450, family 83, subfamily A, polypeptide 1 [EC:1.14.-.-];K11818|3|2e-170|597|aly:ARALYDRAFT_913321|cytochrome P450, family 83, subfamily B, polypeptide 1 [EC:1.14.-.-];K00517|5|2e-93|341|ath:AT5G25120|[EC:1.14.-.-]	GO:0016020// membrane;GO:0043231// intracellular membrane-bounded organelle	GO:0004497// monooxygenase activity; GO:0005506// iron ion binding	GO:0048364//root development; GO:0006568//tryptophan metabolic process; GO:0009639//response to red or far red light;GO:0042742// defense response to bacterium;GO:0019761// glucosinolate biosynthetic process;GO:0009683;GO:0052482	cytochrome P450 83A1	oxidoreductase activity
	AT4G13420		2.91	7.52	K03549|1|0.0|1320|aly:ARALYDRAFT_682978|KUP system potassium uptake protein	GO:0044464// cell part	GO:0022820// potassium ion symporter activity	GO:0030001// metal ion transport; GO:0034220//ion transmembrane transport	Potassium transporter 5	
	AT4G04830	√	1.02	2.03	K00391|1|6e-29|125|olu:OSTLU_9083|[EC:1.8.4.-];K07305|2|2e-22|103|vcn:VOLCADRAFT_76054|peptide-methionine (R)-S-oxide reductase [EC:1.8.4.12]	GO:0044444// cytoplasmic part; GO:0044444// cytoplasmic part	GO:0016671//oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	GO:0008152//metabolic process;GO:0008152//metabolic process	peptide methionine sulfoxide reductase B5	oxidation-reduction process, peptide-methionine (S)-S-oxide reductase activity

DEG30	AT5G39110		-1.03	0.49	-	GO:0044421// extracellular region part; GO:0044464// cell part	GO:0046914// transition metal ion binding; GO:0016623; GO:0048037// cofactor binding	GO:0006005// L-fucose biosynthetic process	germin-like protein subfamily 1 member 14	
	AT5G58860	√	1.09	2.13	K15401|1|0.0|1041|ath:AT5G58860|cytochrome P450, family 86, subfamily A, polypeptide 1 (fatty acid omega-hydroxylase) [EC:1.14.-.-]	GO:0043231// intracellular membrane-bounded organelle	GO:0005506// iron ion binding;GO:0016713;GO:0016712// oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	GO:0006631// fatty acid metabolic process	cytochrome P450 86A1	oxidation-reduction process, oxidoreductase activity,

AT4G19690	√	-0.99	0.50	K14709|1|2e-149|527|aly:ARALYDRAFT_330887|solute carrier family 39 (zinc transporter), member 1/2/3	GO:0031224//intrinsic to membrane; GO:0031224//intrinsic to membrane	GO:0005375//copper ion transmembrane transporter activity;GO:0016491//oxidoreductase activity;GO:0005375//copper ion transmembrane transporter activity	GO:0051707//response to other organism;GO:0006829//zinc ion transport;GO:0010039//response to iron ion;GO:0006875//cellular metal ion homeostasis; GO:0006826//iron ion transport;GO:0071241//cellular response to inorganic substance; GO:0009723//response to ethylene stimulus;GO:0051707//response to other organism;GO:0006829//zinc ion transport;GO:0010039//response to iron ion;GO:0006875//cellular metal ion homeostasis;GO:0006826//iron ion transport	Fe(2+) transport protein 1	cadmium ion transmembrane transporter activity, cadmium ion transport

DEG8	AT5G49360		-0.95	0.52	K05349|1|0.0|969|mtr:MTR_7g109390|beta-glucosidase [EC:3.2.1.21]	GO:0005576// extracellular region; GO:0005618// cell wall	GO:0004553// hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0044238// primary metabolic process;GO:0003006//developmental process involved in reproduction	beta-xylosidase 1	
	AT3G45140	√	0.78	1.72	K00454|1|0.0|1810|ath:AT3G45140|lipoxygenase [EC:1.13.11.12]	GO:0009532// plastid stroma; GO:0009534// chloroplast thylakoid	GO:0046914//transition metal ion binding; GO:0016702//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	GO:0051707// response to other organism;GO:0006633// fatty acid biosynthetic process;GO:0009694// jasmonic acid metabolic process;GO:0009719; GO:0006950// response to stress	lipoxygenase 2	oxidoreduction coenzyme metabolic process
	AT4G28940		2.92	7.59	-	GO:0031410// cytoplasmic vesicle	-	GO:0055086// nucleobase-containing small molecule metabolic process	Phosphorylase-like protein protein	

DEG23	AT5G37990	√	2.23	4.69	K08241|1|1e-44|179|rcu:RCOM_1595240|jasmonate O-methyltransferase [EC:2.1.1.141]	GO:0044464// cell part	GO:0008171// O-methyltransferase activity	GO:0006730// one-carbon metabolic process	S-adenosyl-L-methionine-dependent methyltransferase-like protein	transition metal ion transport
	ATCG00820		-1.25	0.42	K02965|1|4e-48|187|ath:ArthCp063|small subunit ribosomal protein S19	GO:0000314// organellar small ribosomal subunit; GO:0009532// plastid stroma	GO:0003723// RNA binding; GO:0005198// structural molecule activity	GO:0010467// gene expression	ribosomal protein S19	
DEG2	AT1G78370	√	1.13	2.18	K00799|1|1e-73|274|gmx:547936|glutathione S-transferase [EC:2.5.1.18]	GO:0009532//plastid stroma;GO:0031090//organelle membrane;GO:0005576//extracellular region	GO:0042277// peptide binding; GO:0016765// transferase activity, transferring alkyl or aryl (other than methyl) groups;	GO:0010038// response to metal ion;GO:0009414//response to water deprivation;GO:0009404//toxin metabolic process;GO:0009639//response to red or far red light	glutathione S-transferase TAU 20	Encodes glutathione transferase belonging to the tau class of GSTs
	AT3G53980		-0.95	0.52	-	GO:0044464// cell part; GO:0044464// cell part	GO:0016787// hydrolase activity; GO:0005488// binding;GO:0016787//hydrolase activity binding	GO:0010876; GO:0010876	seed storage 2S albumin-like protein	

	AT5G23220		1.24	2.35	-	-	GO:0016811// hydrolase activity	GO:0046496// nicotinamide nucleotide metabolic process	nicotinamidase 3	
	AT1G76960		0.91	1.88	-	-	-	-	-	
DEG26	AT5G18600	√	-1.20	0.43	K03676|1|4e-23|106|bdi:100821530|glutaredoxin 3	GO:0044464//cell part	GO:0030611//arsenate reductase activity;GO:0015036//disulfide oxidoreductase activity	GO:0019725//cellular homeostasis	monothiol glutaredoxin-S2	arsenate reductase (glutaredoxin) activity

DEG24	AT5G48000	√	1.93	3.81	K00030|1|3e-79|294|vvi:100242228|isocitrate dehydrogenase (NAD+) [EC:1.1.1.41];K09587|2|8e-66|249|sbi:SORBI_01g041900|cytochrome P450, family 90, subfamily B, polypeptide 1 (steroid 22-alpha-hydroxylase) [EC:1.14.13.-];K09588|3|2e-65|248|gmx:100775886|cytochrome P450, family 90, subfamily A, polypeptide 1 [EC:1.14.-.-]	GO:0043231//intracellular membrane-bounded organelle; GO:0043231//intracellular membrane-bounded organelle; GO:0043231//intracellular membrane-bounded organelle; GO:0043231//intracellular membrane-bounded organelle; GO:0043231//intracellular membrane-bounded organelle	GO:0004497//monooxygenase activity; GO:0005506//iron ion binding; GO:0004497//monooxygenase activity; GO:0005506//iron ion binding; GO:0004497//monooxygenase activity; GO:0005506//iron ion binding; GO:0004497//monooxygenase activity; GO:0005506//iron ion binding; GO:0004497//monooxygenase activity; GO:0005506//iron ion binding	GO:0010683;GO:0048513//organ development;GO:0010683;GO:0048513//organ development;GO:0010683;GO:0048513//organ development;GO:0010683;GO:0048513//organ development;GO:0010683;GO:0048513//organ development	cytochrome P450 708A2	oxidation-reduction process, oxidoreductase activity

AT1G19570		0.77	1.70	K01873|1|2e-57|221|aly:ARALYDRAFT_326110|valyl-tRNA synthetase [EC:6.1.1.9];K00799|2|3e-13|73.9|cre:CHLREDRAFT_146799|glutathione S-transferase [EC:2.5.1.18]	GO:0009532//plastid stroma;GO:0042579//microbody;GO:0005576//extracellular region;GO:0016020//membrane;GO:0009532//plastid stroma;GO:0042579//microbody;GO:0005576//extracellular region;GO:0016020//membrane	GO:0015038//glutathione disulfide oxidoreductase activity;GO:0042277//peptide binding;GO:0046914//transition metal ion binding;GO:0015038//glutathione disulfide oxidoreductase activity;GO:0042277//peptide binding;GO:0046914//transition metal ion binding	GO:0010038//response to metal ion;GO:0009719;GO:0009608//response to symbiont;GO:0043900//regulation of multi-organism process;GO:0006464//cellular protein modification process;GO:0010038//response to metal ion;GO:0009719;GO:0009608//response to symbiont;GO:0043900//regulation of multi-organism process;GO:0006464//cellular protein modification process	glutathione S-transferase DHAR1	
AT4G37410	√	1.07	2.10	K00517|1|0.0|902|ath:AT4G37410||[EC:1.14.-.-]	GO:0043231//intracellular membrane-bounded organelle	GO:0016491//oxidoreductase activity;GO:0005506//iron ion binding	GO:0052482;GO:0019761//glucosinolate biosynthetic process	cytochrome P450, family 81, subfamily F, polypeptide 4	oxidation-reduction process, oxidoreductase activity

AT1G21110		1.11	2.16	K05279|1|2e-80|298|ath:AT5G54160|flavonol 3-O-methyltransferase [EC:2.1.1.76];K13066|5|1e-72|272|pop:POPTR_824484|caffeic acid 3-O-methyltransferase [EC:2.1.1.68]	GO:0044444//cytoplasmic part	GO:0005515//protein binding;GO:0008168//methyltransferase activity	GO:0006730//one-carbon metabolic process	O-methyltransferase family protein	
AT5G13930	√	0.77	1.71	K00660|1|0.0|790|ath:AT5G13930|chalcone synthase [EC:2.3.1.74]	GO:0000325//plant-type vacuole	GO:0016747//transferase activity, transferring acyl groups other than amino-acyl groups	GO:0009411//response to UV;GO:0009718//anthocyanin-containing compound biosynthetic process;GO:0009719;GO:0006950//response to stress	chalcone synthase	response to oxidative stress
AT3G22121		-0.83	0.56	-	-	-	-	-	
AT3G29780		1.48	2.80	-	GO:0005576//extracellular region	-	GO:0007154//cell communication;GO:0023052//signaling	protein ralf-like 27	

DEG29	ATCG00440	√	-1.89	0.27	K05574|1|4e-57|217|ath:ArthCp027|NAD(P)H-quinone oxidoreductase subunit 3 [EC:1.6.5.3]	GO:0031224//intrinsic to membrane;GO:0009534//chloroplast thylakoid	GO:0048037//cofactor binding;GO:0050136//NADH dehydrogenase (quinone) activity	GO:0051234//establishment of localization;GO:0006091//generation of precursor metabolites and energy	NADH dehydrogenase subunit 3	defense response to bacterium, oxidation-reduction process
DEG25	AT5G39120		-1.44	0.37	-	GO:0044421//extracellular region part;GO:0044464//cell part	GO:0046914//transition metal ion binding;GO:0016623;GO:0048037//cofactor binding	GO:0006005//L-fucose biosynthetic process	germin-like protein subfamily 1 member 15	
	AT2G05540		-0.93	0.53	-	-	-	-	Glycine-rich protein family	
	AT3G49960	√	0.96	1.94	K00430|1|0.0|661|ath:AT3G49960|peroxidase [EC:1.11.1.7]	GO:0044424//intracellular part	GO:0005506//iron ion binding;GO:0003824//catalytic activity;GO:0016209//antioxidant activity	GO:0006970//response to osmotic stress;GO:0008152//metabolic process	peroxidase 35	oxidation-reduction process, peroxidase activity, response to oxidative stress,

	AT3G44320	√	0.88	1.84	K01501|1|0.0|707|ath:AT3G44320|nitrilase [EC:3.5.5.1];K13035|4|2e-132|470|aly:ARALYDRAFT_662033|beta-cyano-L-alanine hydratase/nitrilase [EC:3.5.5.1 3.5.5.4]	GO:0009536//plastid;GO:0005576//extracellular region;GO:0016020//membrane	GO:0018822//nitrile hydratase activity;GO:0000257//nitrilase activity	GO:0051707//response to other organism;GO:0009683;GO:0010038//response to metal ion;GO:0009267//cellular response to starvation;GO:0019759	nitrilase 3	response to cadmium ion
DEG27	AT3G15450	√	-1.53	0.35	-	GO:0016020// membrane; GO:0044444// cytoplasmic part;GO:0043231// intracellular membrane-bounded organelle; GO:0016020// membrane; GO:0044444// cytoplasmic part;GO:0043231// intracellular membrane-bounded organelle; GO:0016020//membrane	-	-	aluminum induced protein with YGL and LRDR motif	Aluminum induced protein with YGL and LRDR motif

<table>
<tr><td>AT3G22142</td><td></td><td>-0.85</td><td>0.55</td><td>-</td><td>-</td><td>GO:0005488//binding</td><td>GO:0010876</td><td>seed storage protein-like protein</td><td></td></tr>
<tr><td>AT5G47990</td><td>√</td><td>1.26</td><td>2.39</td><td>K00517|1|0.0|719|ath:AT4G15350|[EC:1.14.-.-];K13261|3|2e-93|341|gmx:100776878|cytochrome P450, family 93, subfamily A, polypeptide 1 (3,9-dihydroxypterocarpan 6a-monooxygenase) [EC:1.14.13.28];K15814|4|8e-92|336|gmx:100037459|beta-amyrin 24-hydroxylase [EC:1.14.99.43];K13257|5|6e-79|293|gmx:100037450|cytochrome P450, family 93, subfamily C (2-hydroxyisoflavanone synthase) [EC:1.14.13.86]</td><td>GO:0043231//intracellular membrane-bounded organelle</td><td>GO:0005506//iron ion binding;GO:0016627//oxidoreductase activity, acting on the CH-CH group of donors</td><td>GO:0010683;GO:0048513//organ development</td><td>cytochrome P450 705A5</td><td>oxidoreductase activity</td></tr>
<tr><td>AT3G22840</td><td></td><td>1.30</td><td>2.46</td><td>-</td><td>-</td><td>-</td><td>GO:0006950//response to stress;GO:0015995//chlorophyll biosynthetic process;GO:0009639//response to red or far red light;GO:0009411//response to UV</td><td>chlorophyll A-B binding, early light-inducible protein</td><td></td></tr>
</table>

DEG12	AT3G49580		1.42	2.68	-	-	-	-	response to low sulfur 1 protein	
	AT1G06640	√	0.96	1.95	K13229|1|1e-84|266|zma:541977|2,4-dihydroxy-1,4-benzoxazin-3-one-glucoside dioxygenase [EC:1.14.20.2];K06892|3|5e-39|137|pop:POPTR_550478|;K05278|5|6e-36|127|rcu:RCOM_1031460|flavonol synthase [EC:1.14.11.23]	-	GO:0016641//oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor;GO:0016706//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	GO:0008152// metabolic process;GO:0008152// metabolic process;GO:0008152// metabolic process	-	oxidation-reduction process, oxidoreductase activity

DEG9	AT5G23010		0.87	1.83	K15741|1|0.0|967|ath:AT5G23010|methylthioalkylmalate synthase 1 [EC:2.3.3.-];K15742|3|0.0|757|ath:AT5G23020|methylthioalkylmalate synthase 3 [EC:2.3.3.-];K01649|5|3e-154|543|aly:ARALYDRAFT_472070|2-isopropylmalate synthase [EC:2.3.3.13]	GO:0009536//plastid	GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	GO:0043436;GO:0019758	methylthioalkylmalate synthase 1	
	AT1G09560		-0.78	0.58	-	GO:0043231//intracellular membrane-bounded organelle;GO:0005576//extracellular region;GO:0030312//external encapsulating structure	GO:0016209//antioxidant activity;GO:0046914//transition metal ion binding;GO:0004871//signal transducer activity;GO:0003824//catalytic activity	GO:0006950//response to stress;GO:0008152//metabolic process	germin-like protein subfamily 2 member 1	
DEG11	AT1G14960	√	1.50	2.83	-	GO:0044444//cytoplasmic part	GO:0046914//transition metal ion binding	GO:0006950//response to stress; GO:0003006//developmental process involved in reproduction;GO:0010038//response to metal ion	major latex-related protein	response to biotic stimulus, defense response

AT3G58550		1.76	3.38	-	GO:0031224//intrinsic to membrane	GO:0016787//hydrolase activity;GO:0005488//binding	GO:0010876	seed storage 2S albumin-like protein	
AT1G18870		1.57	2.96	K02552|1|0.0|959|ath:AT1G18870|menaquinone-specific isochorismate synthase [EC:5.4.4.2]	GO:0043231//intracellular membrane-bounded organelle;GO:0043231//intracellular membrane-bounded organelle	GO:0050486//intramolecular transferase activity, transferring hydroxy groups;GO:0050486//intramolecular transferase activity, transferring hydroxy groups	GO:0009696//salicylic acid metabolic process;GO:0042371//vitamin K biosynthetic process;GO:0009814//defense response, incompatible interaction;GO:0009696//salicylic acid metabolic process	Isochorismate synthase 2	
AT5G44550		1.18	2.26	-	GO:0044464//cell part	-	-	uncharacterized protein	
AT4G14060	√	1.89	3.70	-	GO:0044444//cytoplasmic part	GO:0046914//transition metal ion binding	GO:0006950//response to stress;GO:0003006//developmental process involved in reproduction;GO:0010038//response to metal ion	major latex protein-like protein	response to biotic stimulus, defense response

DEG17	AT5G23020	1.15	2.22	K15742|1|0.0|966|ath:AT5G23020|methylthioalkylmalate synthase 3 [EC:2.3.3.-];K15741|3|0.0|761|ath:AT5G23010|methylthioalkylmalate synthase 1 [EC:2.3.3.-];K01649|5|1e-155|548|rcu:RCOM_1267040|2-isopropylmalate synthase [EC:2.3.3.13]	GO:0009536//plastid	GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	GO:0019758;GO:0006551//leucine metabolic process	methylthioalkylmalate synthase 3
	AT1G45201	0.85	1.81	-	GO:0043231//intracellular membrane-bounded organelle;GO:0043231//intracellular membrane-bounded organelle	GO:0004091//carboxylesterase activity;GO:0004091//carboxylesterase activity	GO:0044238//primary metabolic process;GO:0044238//primary metabolic process	triacylglycerol lipase-like 1 protein
DEG15	AT3G02020	1.34	2.53	K00928|1|0.0|1087|ath:AT3G02020|aspartate kinase [EC:2.7.2.4]	-	GO:0031406//carboxylic acid binding;GO:0016774//phosphotransferase activity, carboxyl group as acceptor	GO:0008652//cellular amino acid biosynthetic process;GO:0006796//phosphate-containing compound metabolic process	aspartokinase 3

DEG20	AT2G43535	√	2.58	5.99	-	GO:0044464//cell part	GO:0016248//channel inhibitor activity;GO:0004866//endopeptidase inhibitor activity	GO:0001906//cell killing;GO:0006952//defense response	defensin-like protein 196	defense response
DEG16	AT4G13860		1.23	2.35	K02965|1|7e-16|80.1|ath:AT5G47320|small subunit ribosomal protein S19;K13195|2|1e-15|79.7|pop:POPTR_712972|cold-inducible RNA-binding protein;K13095|3|8e-15|76.6|zma:100383202|splicing factor 1	GO:0043231//intracellular membrane-bounded organelle	GO:0046914//transition metal ion binding; GO:0043566//structure-specific DNA binding; GO:0032559	GO:0032501//multicellular organismal process;GO:0006950//response to stress	RNA recognition motif-containing protein	
DEG4	AT5G24660	√	1.07	2.10	-	-	-	-	response to low sulfur 2	regulation of defense response
	ATCG00090		-1.31	0.40	-	-	-	-	unnamed protein product (chloroplast)	
	AT2G15960		-1.48	0.36	-	-	-	-	uncharacterized protein	

	AT4G35160	1.16	2.23	K16040|1|8e-49|192|vvi:100233030|trans-resveratrol di-O-methyltransferase [EC:2.1.1.240];K13066|2|1e-36|152|pop:POPTR_824484|caffeic acid 3-O-methyltransferase [EC:2.1.1.68];K05279|3|4e-36|150|pop:POPTR_834247|flavonol 3-O-methyltransferase [EC:2.1.1.76]	GO:0044444//cytoplasmic part	GO:0005515//protein binding;GO:0008168//methyltransferase activity	GO:0006730//one-carbon metabolic process	O-methyltransferase family 2 protein
DEG19	AT5G48850	1.32	2.50	-	-	-	GO:0009267//cellular response to starvation;GO:0006791//sulfur utilization	tetratricopeptide repeat domain-containing protein
	AT5G09480	1.62	3.07	-	GO:0044464//cell part	-	-	PEE-rich protein

WT(*ZmO2L1*) VS WT

DEG Number	**GeneID**	**Stress or metal ion transport related genes**	**Log$_2$Ratio WT(*ZmO2L1*) VS WT**	**Fold Change WT(*ZmO2L1*) VS WT**	**KEGG Orthology**	**GO Component**	**GO Function**	**GO Process**	**Results of blast against nr database**	**TAIR Annotation(Key Words)**
DEG18	AT5G26220	√	1.13	2.18	K07232|1|2e-51|200|osa:4335982|cation transport protein ChaC	-	-	GO:0010038//response to metal ion	ChaC-like family protein	response to cadmium ion, response to lead ion
	AT1G77120	√	1.10	2.15	K00001|1|0.0|741|ath:AT1G77120|alcohol dehydrogenase [EC:1.1.1.1]	GO:0044444//cytoplasmic part;GO:0016020//membrane	GO:0046914//transition metal ion binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0006970//response to osmotic stress;GO:0008152//metabolic process;GO:0010038//response to metal ion	alcohol dehydrogenase class-P	oxidation-reduction process
	AT1G77760	√	-0.88	0.54	K00360|1|0.0|1008|ppp:PHYPADRAFT_184973|nitrate reductase (NADH) [EC:1.7.1.1];K00387|4|1e-108|392|olu:OSTLU_3554|sulfite oxidase [EC:1.8.3.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part;GO:0016020//membrane	GO:0005506//iron ion binding;GO:0050662//coenzyme binding;GO:0008940//nitrate reductase activity	GO:0009314//response to radiation;GO:0009608//response to symbiont;GO:0042126//nitrate metabolic process	nitrate reductase [NADH]	oxidation-reduction process, oxidoreductase activity

	AT4G16260	√	0.76	1.69	-	GO:0031090//organelle membrane;GO:0030312//external encapsulating structure	GO:0016798//hydrolase activity, acting on glycosyl bonds;GO:0043167//ion binding	GO:0006970//response to osmotic stress;GO:0050832//defense response to fungus;GO:0044238//primary metabolic process	catalytic/ cation binding / hydrolase	defense response to fungus, defense response to nematode
	AT5G22460		1.43	2.70	-	GO:0005618//cell wall;GO:0043231//intracellular membrane-bounded organelle;GO:0005618//cell wall;GO:0043231//intracellular membrane-bounded organelle	-	-	esterase/lipase/thioesterase family protein	
DEG5	AT3G49570		1.00	2.00	-	-	-	-	response to low sulfur 3 protein	
DEG1	AT1G75280	√	0.94	1.91	K00224|1|5e-173|605|ath:AT1G75280|[EC:1.3.1.-];K13081|4|1e-64|245|pop:POPTR_835080|leucoanthocyanidin reductase [EC:1.17.1.3]	GO:0016020//membrane	GO:0016491//oxidoreductase activity	GO:0006950//response to stress;GO:0010038//response to metal ion	Isoflavone reductase-P3	Involved in response to oxidative stress
	AT4G01700	√	1.10	2.14	K01183|1|7e-91|332|ath:AT3G12500|chitinase [EC:3.2.1.14]	GO:0030312//external encapsulating structure	GO:0004553//hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0006026	class II chitinase-like protein	defense response to fungus

	AT3G04720	√	0.75	1.68	K01183|1|3e-06|50.8|mtr:MTR_3g118390|chitinase [EC:3.2.1.14]	-	GO:0030247//polysaccharide binding	GO:0050832//defense response to fungus;GO:0009725//response to hormone stimulus;GO:0006970//response to osmotic stress;GO:0009814//defense response, incompatible interaction	hevein-like protein	defense response to bacterium, defense response to fungus
DEG13	AT3G19710		1.49	2.81	K00826|1|0.0|684|ath:AT3G19710|branched-chain amino acid aminotransferase [EC:2.6.1.42]	GO:0044444//cytoplasmic part	GO:0004084//branched-chain-amino-acid transaminase activity	GO:0019758;GO:0006520//cellular amino acid metabolic process	Probable branched-chain-amino-acid aminotransferase 4	
DEG7	AT5G26260		0.98	1.98	K11838|1|1e-16|85.9|rcu:RCOM_0423090|ubiquitin carboxyl-terminal hydrolase 7 [EC:3.1.2.15]	GO:0031224//intrinsic to membrane;GO:0009536//plastid	-	-	TRAF-like family protein	
DEG6	AT4G04610	√	1.03	2.05	K05907|1|0.0|861|ath:AT4G04610|adenylyl-sulfate reductase (glutathione) [EC:1.8.4.9]	GO:0031976;GO:0009532//plastid stroma	GO:0016671//oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	GO:0006790//sulfur compound metabolic process;GO:0019725//cellular homeostasis	5'-adenylylsulfate reductase 1	oxidation-reduction process, oxidoreductase activity
	AT1G08115		1.17	2.24	-	-	-	-	unnamed protein product	

	AT1G51420		1.05	2.07	-	GO:0031090//organelle membrane	GO:0046872//metal ion binding;GO:0016791//phosphatase activity	GO:0005985//sucrose metabolic process;GO:0006796//phosphate-containing compound metabolic process	sucrose-phosphatase 1	
	AT3G09220	√	-1.58	0.33	K00423|1|7e-60|230|ppp:PHYPADRAFT_163787|L-ascorbate oxidase [EC:1.10.3.3]	GO:0005576//extracellular region	GO:0046914//transition metal ion binding;GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	GO:0003006//developmental process involved in reproduction;GO:0009808//lignin metabolic process;GO:0010038//response to metal ion	laccase 7	oxidation-reduction process, oxidoreductase activity
	AT3G58990		0.97	1.96	K01704|1|1e-143|507|ath:AT3G58990|3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit [EC:4.2.1.33 4.2.1.35]	GO:0043234//protein complex;GO:0009532//plastid stroma	GO:0016836//hydro-lyase activity	GO:0006970//response to osmotic stress;GO:0006551//leucine metabolic process	isopropylmalate isomerase 1	
DEG14	AT3G08860		1.57	2.96	K00827|1|0.0|958|ath:AT3G08860|alanine-glyoxylate transaminase / (R)-3-amino-2-methylpropionate-pyruvate transaminase [EC:2.6.1.44 2.6.1.40]	GO:0043231//intracellular membrane-bounded organelle	GO:0008483//transaminase activity;GO:0048037//cofactor binding	GO:0031669//cellular response to nutrient levels	PYRIMIDINE 4	

AT5G02160		-0.83	0.56	-	GO:0009534//chloroplast thylakoid	GO:0005515//protein binding	GO:0044267//cellular protein metabolic process	uncharacterized protein	
AT5G14200	√	0.87	1.83	K00052|1|0.0|701|aly:ARALYDRAFT_473708|3-isopropylmalate dehydrogenase [EC:1.1.1.85]	GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0009532//plastid stroma;GO:0009526//plastid envelope	GO:0046872//metal ion binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding;GO:0046872//metal ion binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding;GO:0046872//metal ion binding	GO:0006551//leucine metabolic process;GO:0008652//cellular amino acid biosynthetic process;GO:0006970//response to osmotic stress;GO:0019758;GO:0006551//leucine metabolic process;GO:0008652//cellular amino acid biosynthetic process;GO:0006970//response to osmotic stress;GO:0019758;GO:0006551//leucine metabolic process;GO:0008652//cellular amino acid biosynthetic process;GO:0006970//response to osmotic stress;GO:0019758	3-isopropylmalate dehydrogenase 3	oxidation-reduction process, oxidoreductase activity

DEG3	AT2G39310		0.92	1.89	-	GO:0009536//plastid;GO:0009536//plastid;GO:0009536//plastid	GO:0030246//carbohydrate binding;GO:0030246//carbohydrate binding;GO:0030246//carbohydrate binding	GO:0009719;GO:0006970//response to osmotic stress;GO:0009719;GO:0006970//response to osmotic stress;GO:0009719;GO:0006970//response to osmotic stress	jacalin-related lectin 22	
	AT1G67148		1.49	2.81	-	-	-	-	-	
	AT2G34430		-1.00	0.50	K08912|1|3e-147|519|ath:AT2G34430|light-harvesting complex II chlorophyll a/b binding protein 1	GO:0031224//intrinsic to membrane;GO:0009521;GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid;GO:0009570//chloroplast stroma;GO:0005576//extracellular region	GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0009746;GO:0006091//generation of precursor metabolites and energy;GO:0009639//response to red or far red light;GO:0006464//cellular protein modification process	light-harvesting complex II chlorophyll a/b binding protein 1	
	AT3G48360	√	-1.07	0.48	K00517|1|0.0|711|ath:AT3G48360|[EC:1.14.-.-];K04498|3|4e-08|57.8|ath:AT3G12980|E1A/CREB-binding protein [EC:2.3.1.48];K10523|5|2e-06|52.4|zma:100191618|speckle-type POZ protein	GO:0043231//intracellular membrane-bounded organelle	GO:0000989//transcription factor binding transcription factor activity;GO:0004468//lysine N-acetyltransferase activity;GO:0046914//transition metal ion binding;GO:0005515//protein binding	GO:0000302//response to reactive oxygen species;GO:0009756//carbohydrate mediated signaling;GO:0048229//gametophyte development;GO:0051347//positive regulation of transferase activity	BTB and TAZ domain protein 2	response to hydrogen peroxide

DEG28	ATCG00800	-0.83	0.56	K02982|1|3e-113|405|ath:ArthCp061|small subunit ribosomal protein S3	GO:0000314//organellar small ribosomal subunit;GO:0009536//plastid	GO:0003723//RNA binding;GO:0005198//structural molecule activity	GO:0010467//gene expression	ribosomal protein S3
	AT1G23730	1.07	2.10	K01673|1|9e-148|521|ath:AT1G23730|carbonic anhydrase [EC:4.2.1.1]	GO:0009526//plastid envelope;GO:0016020//membrane	GO:0046914//transition metal ion binding;GO:0016836//hydro-lyase activity	GO:0010035//response to inorganic substance;GO:0010118//stomatal movement	beta carbonic anhydrase 3
	AT5G04150	-1.18	0.44	-	GO:0043231//intracellular membrane-bounded organelle	GO:0005488//binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-dependent	-
	AT4G13395	2.01	4.03	-	GO:0043231//intracellular membrane-bounded organelle	-	GO:0048513//organ development	protein rotundifolia like 12
	AT2G46390	0.85	1.81	-	-	-	-	uncharacterized protein

DEG22	AT1G18100		1.75	3.37	K06910|1|5e-06|50.8|smo:SELMODRAFT_143762|	GO:0043231//intracellular membrane-bounded organelle	GO:0016788//hydrolase activity, acting on ester bonds;GO:0003676//nucleic acid binding	GO:0006259//DNA metabolic process;GO:0009725//response to hormone stimulus;GO:0009845//seed germination	protein MOTHER of FT and TF 1	
DEG10	AT1G16410	√	1.67	3.17	K12154|1|0.0|1058|ath:AT1G16410|cytochrome P450, family 79, subfamily F, polypeptide 1 [EC:1.14.13.-];K12155|3|0.0|935|ath:AT1G16400|cytochrome P450, family 79, subfamily F, polypeptide 2 [EC:1.14.13.-];K13027|4|4e-115|414|sbi:SORBI_01g001200|tyrosine N-monooxygenase	GO:0043231//intracellular membrane-bounded organelle;GO:0043231//intracellular membrane-bounded organelle	GO:0004497//monooxygenase activity;GO:0005506//iron ion binding;GO:0004497//monooxygenase activity;GO:0005506//iron ion binding	GO:0019758;GO:0019758	dihomomethionine N-hydroxylase	oxidoreductase activity, oxidoreductase activity

DEG21	AT5G66170		0.98	1.98	-	GO:0044424//intracellular part;GO:0044424//intracellular part;GO:0044424//intracellular part	GO:0016783//sulfurtransferase activity;GO:0016783//sulfurtransferase activity;GO:0016783//sulfurtransferase activity	GO:0032502//developmental process;GO:0032502//developmental process;GO:0032502//developmental process	sulfurtransferase 18	
	AT4G13420		1.85	3.61	K03549|1|0.0|1320|aly:ARALYDRAFT_682978|KUP system potassium uptake protein	GO:0044464//cell part	GO:0022820//potassium ion symporter activity	GO:0030001//metal ion transport;GO:0034220//ion transmembrane transport	Potassium transporter 5	
DEG30	AT1G80130	√	1.57	2.97	-	GO:0044464//cell part	-	GO:0006950//response to stress	tetratricopeptide repeat domain-containing protein	response to oxidative stress
	AT5G39110		0.97	1.96	-	GO:0044421//extracellular region part;GO:0044464//cell part	GO:0046914//transition metal ion binding;GO:0016623;GO:0048037//cofactor binding	GO:0006005//L-fucose biosynthetic process	germin-like protein subfamily 1 member 14	
	AT1G61740		-0.92	0.53	-	GO:0031224//intrinsic to membrane	GO:0005488//binding	-	Sulfite exporter TauE/SafE family protein	

DEG8	AT3G45140	√	0.93	1.90	K00454|1|0.0|1810|ath:AT3G45140|lipoxygenase [EC:1.13.11.12]	GO:0009532//plastid stroma;GO:0009534//chloroplast thylakoid	GO:0046914//transition metal ion binding;GO:0016702//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	GO:0051707//response to other organism;GO:0006633//fatty acid biosynthetic process;GO:0009694//jasmonic acid metabolic process;GO:0009719;GO:0006950//response to stress	lipoxygenase 2	Required for wound-induced jasmonic acid accumulation in Arabidopsis
	AT3G54590		0.92	1.89	-	-	-	-	hypothetical protein ARALYDRAFT_917863	
DEG23	AT5G37990	√	1.49	2.82	K08241|1|1e-44|179|rcu:RCOM_1595240|jasmonate O-methyltransferase [EC:2.1.1.141]	GO:0044464//cell part	GO:0008171//O-methyltransferase activity	GO:0006730//one-carbon metabolic process	S-adenosyl-L-methionine-dependent methyltransferase-like protein	transition metal ion transport
DEG2	AT1G78370	√	0.91	1.88	K00799|1|1e-73|274|gmx:547936|glutathione S-transferase [EC:2.5.1.18]	GO:0009532//plastid stroma;GO:0031090//organelle membrane;GO:0005576//extracellular region	GO:0042277//peptide binding;GO:0016765//transferase activity, transferring alkyl or aryl (other than methyl) groups;GO:0005515//protein binding	GO:0010038//response to metal ion;GO:0009414//response to water deprivation;GO:0009404//toxin metabolic process;GO:0009639//response to red or far red light	glutathione S-transferase TAU 20	Encodes glutathione transferase belonging to the tau class of GSTs

DEG26	AT1G43800	√	1.00	2.00	K03921|1|0.0|747|ath:AT1G43800|acyl-[acyl-carrier-protein] desaturase [EC:1.14.19.2]	GO:0009536//plastid	GO:0046872//metal ion binding;GO:0016717//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	GO:0006631//fatty acid metabolic process	stearoyl-acyl-carrier protein desaturase-like protein	oxidation-reduction process, oxidoreductase activity
	AT5G18600	√	-1.40	0.38	K03676|1|4e-23|106|bdi:100821530|glutaredoxin 3	GO:0044464//cell part	GO:0030611//arsenate reductase activity;GO:0015036//disulfide oxidoreductase activity	GO:0019725//cellular homeostasis	monothiol glutaredoxin-S2	Involve in: cell redox homeostasis
	AT2G41090		1.05	2.07	K13448|1|3e-106|382|ath:AT2G41090|calcium-binding protein CML;K02183|2|3e-47|186|ath:AT2G41110|calmodulin	GO:0031090//organelle membrane;GO:0043231//intracellular membrane-bounded organelle	GO:0046872//metal ion binding	GO:0009057//macromolecule catabolic process;GO:0019932//second-messenger-mediated signaling;GO:0009856//pollination	calmodulin-like protein 10	

DEG24	AT5G48000	√	1.35	2.55	K00030|1|3e-79|294|vvi:100242228|isocitrate dehydrogenase (NAD+) [EC:1.1.1.41];K09587|2|8e-66|249|sbi:SORBI_01g041900|cytochrome P450, family 90, subfamily B, polypeptide 1 (steroid 22-alpha-hydroxylase) [EC:1.14.13.-];K09588|3|2e-65|248|gmx:100775886|cytochrome P450, family 90, subfamily A, polypeptide 1 [EC:1.14.-.-]	GO:0043231//intracellular membrane-bounded organelle;GO:0043231//intracellular membrane-bounded organelle;GO:0043231//intracellular membrane-bounded organelle;GO:0043231//intracellular membrane-bounded organelle;GO:0043231//intracellular membrane-bounded organelle	GO:0004497//monooxygenase activity;GO:0005506//iron ion binding;GO:0004497//monooxygenase activity;GO:0005506//iron ion binding;GO:0004497//monooxygenase activity;GO:0005506//iron ion binding;GO:0004497//monooxygenase activity;GO:0005506//iron ion binding;GO:0004497//monooxygenase activity;GO:0005506//iron ion binding	GO:0010683;GO:0048513//organ development;GO:0010683;GO:0048513//organ development;GO:0010683;GO:0048513//organ development;GO:0010683;GO:0048513//organ development;GO:0010683;GO:0048513//organ development	cytochrome P450 708A2	oxidation-reduction process, oxidoreductase activity
	AT2G14610	√	-2.08	0.24	K13449|1|2e-94|343|ath:AT2G14610|pathogenesis-related protein 1	GO:0030312//external encapsulating structure	-	GO:0009725//response to hormone stimulus;GO:0033273//response to vitamin;GO:0009814//defense response, incompatible interaction	-	defense response, defense response to bacterium, defense response to fungus

	AT4G29905		-1.05	0.48	-	-	-	-	uncharacterized protein	
	AT1G29920		-0.76	0.59	K08912|1|1e-154|544|ath:AT1G29920|light-harvesting complex II chlorophyll a/b binding protein 1	GO:0031224//intrinsic to membrane;GO:0009521;GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid;GO:0009570//chloroplast stroma;GO:0005576//extracellular region	GO:0043169//cation binding;GO:0046906//tetrapyrrole binding	GO:0009746;GO:0006091//generation of precursor metabolites and energy;GO:0009639//response to red or far red light;GO:0006464//cellular protein modification process	chlorophyll a-b binding protein 2/3	
	AT4G33070	√	0.96	1.95	K01568|1|0.0|1240|ath:AT4G33070|pyruvate decarboxylase [EC:4.1.1.1]	GO:0044464//cell part	GO:0046872//metal ion binding;GO:0016831//carboxy-lyase activity;GO:0019842//vitamin binding	-	pyruvate decarboxylase	regulation of hydrogen peroxide metabolic process
DEG29	ATCG00440	√	-1.25	0.42	K05574|1|4e-57|217|ath:ArthCp027|NAD(P)H-quinone oxidoreductase subunit 3 [EC:1.6.5.3]	GO:0031224//intrinsic to membrane;GO:0009534//chloroplast thylakoid	GO:0048037//cofactor binding;GO:0050136//NADH dehydrogenase (quinone) activity	GO:0051234//establishment of localization;GO:0006091//generation of precursor metabolites and energy	NADH dehydrogenase subunit 3	Encodes NADH dehydrogenase D3 subunit of the chloroplast NAD(P)H dehydrogenase complex

DEG25	AT3G21850		2.21	4.63	K03094|1|2e-86|315|ath:AT3G21850|S-phase kinase-associated protein 1	GO:0043231//intracellular membrane-bounded organelle;GO:0015630//microtubule cytoskeleton;GO:0031461//cullin-RING ubiquitin ligase complex;GO:0044444//cytoplasmic part;GO:0016020//membrane	GO:0005488//binding	GO:0010038//response to metal ion;GO:0007126//meiosis;GO:0019941//modification-dependent protein catabolic process;GO:0000087//M phase of mitotic cell cycle;GO:0000018//regulation of DNA recombination	-	
	AT3G43190	√	1.25	2.38	K00695|1|0.0|1602|ath:AT3G43190|sucrose synthase [EC:2.4.1.13]	GO:0043231//intracellular membrane-bounded organelle;GO:0016020//membrane	GO:0035251//UDP-glucosyl transferase activity	GO:0005985//sucrose metabolic process;GO:0006950//response to stress;GO:0010038//response to metal ion	sucrose synthase 4	regulation of hydrogen peroxide metabolic process
	AT2G05540		-1.06	0.48	-	-	-	-	Glycine-rich protein family	
	AT3G14210		0.80	1.74	K00514|1|5e-15|80.9|rcu:RCOM_1428040|zeta-carotene desaturase [EC:1.3.5.6];K01206|2|4e-12|71.2|ath:AT1G67830|alpha-L-fucosidase [EC:3.2.1.51]	GO:0005618//cell wall;GO:0005840//ribosome;GO:0009526//plastid envelope;GO:0042579//microbody;GO:0031090//organelle membrane;GO:0005576//extracellular region;GO:0005773//vacuole	GO:0005488//binding;GO:0016788//hydrolase activity, acting on ester bonds	GO:0006952//defense response;GO:0051707//response to other organism;GO:0019759	epithiospecifier modifier 1	

DEG27	AT3G15450	√	-1.16	0.45	-	GO:0016020//membrane;GO:0044444//cytoplasmic part;GO:0043231//intracellular membrane-bounded organelle;GO:0016020//membrane;GO:0044444//cytoplasmic part;GO:0043231//intracellular membrane-bounded organelle;GO:0016020//membrane;GO:0044444//cytoplasmic part;GO:0043231//intracellular membrane-bounded organelle	-	-	aluminum induced protein with YGL and LRDR motif	Aluminum induced protein with YGL and LRDR motif
	ATCG00760		0.83	1.78	K02919|1|1e-07|53.1|gmx:3989331|large subunit ribosomal protein L36	GO:0009536//plastid	GO:0005198//structural molecule activity	GO:0010467//gene expression	ribosomal protein L36	
	AT1G61800		1.27	2.41	K15283|1|0.0|705|ath:AT1G61800|solute carrier family 35, member E1	GO:0031224//intrinsic to membrane;GO:0031090//organelle membrane	GO:0015291//secondary active transmembrane transporter activity;GO:0015119;GO:0005342//organic acid transmembrane transporter activity	GO:0009642//response to light intensity;GO:0051707//response to other organism;GO:0009746;GO:0015712//hexose phosphate transport;GO:0015711//organic anion transport;GO:0015717//triose phosphate	glucose-6-phosphate/phosphate translocator 2	

								transport;GO:0019953//sexual reproduction;GO:0034285;GO:0015979//photosynthesis		
DEG12	AT3G49580		1.38	2.60	-	-	-	-	response to low sulfur 1 protein	
DEG9	AT5G23010		1.02	2.03	K15741|1|0.0|967|ath:AT5G23010|methylthioalkylmalate synthase 1 [EC:2.3.3.-];K15742|3|0.0|757|ath:AT5G23020|methylthioalkylmalate synthase 3 [EC:2.3.3.-];K01649|5|3e-154|543|aly:ARALYDRAFT_472070|2-isopropylmalate synthase [EC:2.3.3.13]	GO:0009536//plastid	GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	GO:0043436;GO:0019758	methylthioalkylmalate synthase 1	
DEG11	AT1G14960	√	1.40	2.64	-	GO:0044444//cytoplasmic part	GO:0046914//transition metal ion binding	GO:0006950//response to stress;GO:0003006//developmental process involved in	major latex-related protein	Response to biotic stimulus, defense

							reproduction;GO:0010038//response to metal ion		response
DEG17	AT5G23020	1.26	2.40	K15742|1|0.0|966|ath:AT5G23020|methylthioalkylmalate synthase 3 [EC:2.3.3.-];K15741|3|0.0|761|ath:AT5G23010|methylthioalkylmalate synthase 1 [EC:2.3.3.-];K01649|5|1e-155|548|rcu:RCOM_1267040|2-isopropylmalate synthase [EC:2.3.3.13]	GO:0009536//plastid	GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	GO:0019758;GO:0006551//leucine metabolic process	methylthioalkylmalate synthase 3	
	AT2G41240	-0.90	0.54	K13422|1|3e-08|57.0|pop:POPTR_676550|transcription factor MYC2	GO:0043231//intracellular membrane-bounded organelle;GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0001071//nucleic acid binding transcription factor activity;GO:0003676//nucleic acid binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-dependent;GO:0006950//response to stress;GO:0006351//transcription, DNA-dependent;GO:0006950//response to stress	transcription factor bHLH100	

DEG15	AT3G02020		1.31	2.47	K00928|1|0.0|1087|ath:AT3G02020|aspartate kinase [EC:2.7.2.4]	-	GO:0031406//carboxylic acid binding;GO:0016774//phosphotransferase activity, carboxyl group as acceptor	GO:0008652//cellular amino acid biosynthetic process;GO:0006796//phosphate-containing compound metabolic process	aspartokinase 3	
	AT3G53040		1.60	3.04	-	-	-	-	late embryogenesis abundant protein-like	
DEG20	AT2G43535	√	1.48	2.79	-	GO:0044464//cell part	GO:0016248//channel inhibitor activity;GO:0004866//endopeptidase inhibitor activity	GO:0001906//cell killing;GO:0006952//defense response	defensin-like protein 196	Encodes a defensin-like (DEFL) family protein
DEG16	AT4G13860		1.33	2.51	K02965|1|7e-16|80.1|ath:AT5G47320|small subunit ribosomal protein S19;K13195|2|1e-15|79.7|pop:POPTR_712972|cold-inducible RNA-binding protein;K13095|3|8e-15|76.6|zma:100383202|splicing factor 1	GO:0043231//intracellular membrane-bounded organelle	GO:0046914//transition metal ion binding;GO:0043566//structure-specific DNA binding;GO:0032559	GO:0032501//multicellular organismal process;GO:0006950//response to stress	RNA recognition motif-containing protein	

	AT5G55050		1.27	2.41	K00514|1|1e-23|109|rcu:RCOM_1428040|zeta-carotene desaturase [EC:1.3.5.6];K01206|2|5e-19|94.4|ath:AT1G67830|alpha-L-fucosidase [EC:3.2.1.51]	GO:0044464//cell part	GO:0016788//hydrolase activity, acting on ester bonds	GO:0044238//primary metabolic process	GDSL esterase/lipase	
DEG4	AT5G24660	√	0.89	1.85	-	-	-	-	response to low sulfur 2	regulation of defense response
DEG19	AT5G48850		1.14	2.21	-	-	-	GO:0009267//cellular response to starvation;GO:0006791//sulfur utilization	tetratricopeptide repeat domain-containing protein	
	AT3G21720		0.82	1.76	K01637|1|0.0|1074|ath:AT3G21720|isocitrate lyase [EC:4.1.3.1]	GO:0005777//peroxisome	GO:0005488//binding;GO:0016833//oxo-acid-lyase activity	GO:0009060//aerobic respiration;GO:0043436;GO:0044262//cellular carbohydrate metabolic process	isocitrate lyase	
	AT4G15700	√	-2.05	0.24	K03676|1|2e-23|106|bdi:100821530|glutaredoxin 3	GO:0044464//cell part	GO:0030611//arsenate reductase activity;GO:0015036//disulfide oxidoreductase activity	GO:0019725//cellular homeostasis	monothiol glutaredoxin-S3	arsenate reductase (glutaredoxin) activity, protein disulfide oxidoreductase activity