

## Supplementary data

Table S1: 123 DEGs between zws-ms and zws-217 at flowering stage

Gene ID	FDR	log <sub>2</sub> FC	Regulated	GO_annotation	KEGG pathway
BnaA01g10540D	1.06E-07	-3.813455	down	CC: nucleus (GO:0005634);	DNA replication (ko03030)
BnaA03g35870D	5.96E-28	5.4158702	up	MF: guanylate kinase activity (GO:0004385); CC: cytoplasm (GO:0005737); BP: purine nucleotide metabolic process (GO:0006163); BP: response to chitin (GO:0010200); BP: phosphorylation (GO:0016310); BP: endoplasmic reticulum unfolded protein response (GO:0030968); BP: defense response to fungus (GO:0050832);	Purine metabolism (ko00230)
BnaA04g06410D	4.51E-08	Infinity	up	BP: heme biosynthetic process (GO:0006783); BP: response to oxidative stress (GO:0006979); MF: glutamyl-tRNA reductase activity (GO:0008883); CC: chloroplast (GO:0009507); BP: response to wounding (GO:0009611); BP: response to chitin (GO:0010200); BP: defense response by callose deposition (GO:0052542);	Porphyrin and chlorophyll metabolism (ko00860)
BnaA04g20020D	2.50E-04	2.9506573	up	CC: ubiquitin ligase complex (GO:0000151); MF: ubiquitin-protein transferase activity (GO:0004842); BP: plant-type hypersensitive response (GO:0009626); BP: defense response to fungus, incompatible interaction (GO:0009817); BP: protein ubiquitination (GO:0016567);	--
BnaA04g23230D	1.28E-06	4.5110145	up	--	--
BnaA07g04500D	7.06E-33	2.9402076	up	CC: mitochondrion (GO:0005739);	--
BnaA07g33370D	1.72E-05	-Infinity	down	BP: mRNA splicing, via spliceosome (GO:0000398); BP: nuclear-transcribed mRNA catabolic process (GO:0000956); MF: protein binding (GO:0005515); CC: spliceosomal complex (GO:0005681); CC: nucleolus (GO:0005730); BP: N-terminal protein myristoylation (GO:0006499); BP: response to salt stress (GO:0009651); BP: response to abscisic acid (GO:0009737); BP: vegetative to reproductive phase transition of meristem (GO:0010228); BP: response to mannitol (GO:0010555); BP: regulation of circadian rhythm (GO:0042752); BP: positive regulation of transcription, DNA-templated (GO:0045893);	Spliceosome (ko03040)
BnaA08g02930D	1.70E-21	2.2476496	up	MF: nucleotide binding (GO:0000166); BP: endonucleolytic cleavage involved in rRNA processing (GO:0000478); BP: RNA methylation (GO:0001510); MF: nucleic acid binding (GO:0003676); CC: nucleolus (GO:0005730); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: pyrimidine ribonucleotide biosynthetic process (GO:0009220); BP: leaf vascular tissue pattern formation (GO:0010305); BP: cotyledon vascular tissue pattern formation (GO:0010588); BP: root development (GO:0048364); BP: leaf development (GO:0048366); BP: petal vascular tissue pattern formation (GO:0080056); BP: sepal vascular tissue pattern formation (GO:0080057);	--
BnaA08g26960D	3.00E-06	2.6851248	up	CC: nucleus (GO:0005634); CC: plasma membrane (GO:0005886); BP: response to aluminum ion (GO:0010044); MF: malate transmembrane transporter activity (GO:0015140); BP: malate transport (GO:0015743);	--
BnaA09g06740D	4.30E-05	5.9583495	up	CC: nucleus (GO:0005634);	--
BnaA09g26320D	1.76E-07	2.4687526	up	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); BP: regulation of	--

BnaA09g40840D	3.01E-09	-Infinity	down	transcription, DNA-templated (GO:0006355); MF: sequence-specific DNA binding (GO:0043565); CC: mitochondrion (GO:0005739);	--
BnaA09g43250D	4.80E-07	4.8194852	up	CC: mitochondrion (GO:0005739);	--
BnaA09g44370D	3.03E-05	-2.653797	down	MF: DNA binding (GO:0003677); MF: chromatin binding (GO:0003682); MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); BP: protein targeting to membrane (GO:0006612); BP: response to salt stress (GO:0009651); BP: response to ethylene (GO:0009723); BP: response to auxin (GO:0009733); BP: response to abscisic acid (GO:0009737); BP: response to gibberellin (GO:0009739); BP: response to salicylic acid (GO:0009751); BP: response to jasmonic acid (GO:0009753); BP: positive regulation of flavonoid biosynthetic process (GO:0009963); BP: regulation of plant-type hypersensitive response (GO:0010363); BP: response to cadmium ion (GO:0046686);	--
BnaA09g45000D	1.42E-06	-3.148709	down	BP: RNA splicing, via endonucleolytic cleavage and ligation (GO:0000394); MF: DNA binding (GO:0003677); CC: transcription factor TFIID complex (GO:0005669); BP: DNA-templated transcription, initiation (GO:0006352); BP: transcription from RNA polymerase II promoter (GO:0006366); BP: cytokinin-activated signaling pathway (GO:0009736); BP: jasmonic acid mediated signaling pathway (GO:0009867); BP: regulation of ethylene-activated signaling pathway (GO:0010104); MF: protein heterodimerization activity (GO:0046982);	Basal transcription factors (ko03022)
BnaA09g45070D	1.29E-19	-2.480435	down	MF: glutathione transferase activity (GO:0004364); CC: cytoplasm (GO:0005737); BP: toxin catabolic process (GO:0009407); BP: response to cyclopentenone (GO:0010583);	Glutathione metabolism (ko00480)
BnaA09g45300D	3.19E-15	-5.0683	down	MF: serine-type carboxypeptidase activity (GO:0004185); CC: extracellular region (GO:0005576); CC: vacuole (GO:0005773); BP: proteolysis (GO:0006508);	--
BnaA09g45310D	9.62E-08	2.3025883	up	--	--
BnaA09g45320D	2.61E-77	-9.963754	down	MF: copper ion binding (GO:0005507); MF: calmodulin binding (GO:0005516); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: gluconeogenesis (GO:0006094); BP: glycolytic process (GO:0006096); BP: protein folding (GO:0006457); BP: tryptophan catabolic process (GO:0006569); BP: response to heat (GO:0009408); BP: response to cold (GO:0009409); CC: chloroplast thylakoid membrane (GO:0009535); CC: chloroplast stroma (GO:0009570); BP: response to high light intensity (GO:0009644); BP: response to salt stress (GO:0009651); BP: chloroplast organization (GO:0009658); BP: indoleacetic acid biosynthetic process (GO:0009684); CC: chloroplast envelope (GO:0009941); BP: isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway (GO:0019288); BP: cysteine biosynthetic process (GO:0019344); BP: response to endoplasmic reticulum stress (GO:0034976); BP: response to hydrogen peroxide (GO:0042542); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: ovule development (GO:0048481); MF: chaperone binding (GO:0051087); BP: positive regulation of superoxide dismutase activity (GO:1901671);	--
BnaA09g45610D	3.77E-06	2.9104173	up	CC: nucleus (GO:0005634);	--
BnaA09g46080D	1.79E-13	-5.028578	down	CC: nucleus (GO:0005634);	--

BnaA09g46290D	6.71E-06	4.1758547	up	--	--
BnaA09g48320D	1.42E-23	-8.077971	down	MF: structural constituent of ribosome (GO:0003735); CC: nucleolus (GO:0005730); BP: translation (GO:0006412); CC: chloroplast (GO:0009507); CC: cytosolic large ribosomal subunit (GO:0022625); MF: protein serine/threonine phosphatase activity (GO:0004722); CC: plasma membrane (GO:0005886); BP: protein dephosphorylation (GO:0006470); CC: protein serine/threonine phosphatase complex (GO:0008287); BP: negative regulation of abscisic acid-activated signaling pathway (GO:0009788); BP: positive regulation of gibberellic acid mediated signaling pathway (GO:0009939); BP: positive regulation of seed germination (GO:0010030); MF: metal ion binding (GO:0046872); BP: release of seed from dormancy (GO:0048838); BP: negative regulation of seed dormancy process (GO:1902039); BP: response to stimulus (GO:0050896);	Ribosome (ko03010)
BnaA09g49440D	8.98E-05	-2.61411	down		Plant hormone signal transduction (ko04075)
BnaA09g49480D	1.84E-12	-3.203067	down		--
BnaA09g55930D	2.33E-07	-3.511018	down	MF: GTPase activity (GO:0003924); MF: GTP binding (GO:0005525); BP: GTP catabolic process (GO:0006184); BP: small GTPase mediated signal transduction (GO:0007264); BP: protein transport (GO:0015031); CC: membrane (GO:0016020); BP: vesicle-mediated transport (GO:0016192); BP: protein targeting to vacuole (GO:0006623); CC: membrane (GO:0016020); BP: vesicle-mediated transport (GO:0016192); CC: mitochondrion (GO:0005739);	Endocytosis (ko04144); Phagosome (ko04145)
BnaA09g56410D	7.30E-07	-2.479754	down		--
BnaA10g01700D	1.82E-09	-Infinity	down		--
BnaAnng13790D	7.29E-05	4.5871548	up	--	--
BnaAnng23240D	2.38E-04	2.3576336	up	MF: serine-type endopeptidase activity (GO:0004252); BP: proteolysis (GO:0006508); CC: plant-type cell wall (GO:0009505); MF: identical protein binding (GO:0042802); BP: negative regulation of catalytic activity (GO:0043086); CC: apoplast (GO:0048046); BP: mucilage metabolic process involved in seed coat development (GO:0048359); BP: mucilage extrusion from seed coat (GO:0080001);	--
BnaAnng30260D	4.42E-47	3.6884556	up	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: response to xenobiotic stimulus (GO:0009410); BP: response to ethylene (GO:0009723); BP: hormone-mediated signaling pathway (GO:0009755); BP: endoplasmic reticulum unfolded protein response (GO:0030968); BP: positive regulation of transcription, DNA-templated (GO:0045893); MF: protein heterodimerization activity (GO:0046982); BP: positive regulation of seed maturation (GO:2000693);	--
BnaAnng35580D	2.32E-09	-2.847035	down	MF: nucleotide binding (GO:0000166); BP: alternative mRNA splicing, via spliceosome (GO:0000380); MF: double-stranded DNA binding (GO:0003690); MF: single-stranded DNA binding (GO:0003697); MF: mRNA binding (GO:0003729); MF: protein kinase activity (GO:0004672); CC: nucleus (GO:0005634); CC: mitochondrion (GO:0005739); CC: peroxisome (GO:0005777); CC: cytosol (GO:0005829); BP: gluconeogenesis (GO:0006094); BP: glycolytic process (GO:0006096); BP: mRNA export from nucleus (GO:0006406); BP: water transport (GO:0006833); BP: hyperosmotic response (GO:0006972); BP: Golgi organization (GO:0007030); BP: response to cold (GO:0009409); BP: response to water deprivation (GO:0009414); CC: plasmodesma (GO:0009506); CC: chloroplast (GO:0009507); BP: response to salt stress (GO:0009651); BP: etioplast organization (GO:0009662); BP: lignin biosynthetic process (GO:0009809); BP: response to zinc ion	--

				(GO:0010043); BP: regulation of stomatal movement (GO:0010119); BP: response to chitin (GO:0010200); BP: vegetative to reproductive phase transition of meristem (GO:0010228); BP: RNA secondary structure unwinding (GO:0010501); BP: carotenoid biosynthetic process (GO:0016117); BP: brassinosteroid biosynthetic process (GO:0016132); MF: cinnamoyl-CoA reductase activity (GO:0016621); BP: DNA duplex unwinding (GO:0032508); BP: negative regulation of circadian rhythm (GO:0042754); MF: protein homodimerization activity (GO:0042803); BP: innate immune response (GO:0045087); MF: carotenoid isomerase activity (GO:0046608); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: defense response to fungus (GO:0050832);	
BnaC01g02500D	4.60E-33	6.2594148	up	--	--
BnaC01g43270D	7.80E-08	5.0755384	up	MF: magnesium ion binding (GO:0000287); MF: adenosylmethionine-8-amino-7-oxononanoate transaminase activity (GO:0004015); MF: dethiobiotin synthase activity (GO:0004141); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); BP: DNA replication initiation (GO:0006270); BP: regulation of DNA replication (GO:0006275); BP: DNA methylation (GO:0006306); BP: cell proliferation (GO:0008283); BP: biotin biosynthetic process (GO:0009102); MF: pyridoxal phosphate binding (GO:0030170); BP: histone H3-K9 methylation (GO:0051567); BP: regulation of cell cycle (GO:0051726);	Biotin metabolism (ko00780)
BnaC02g06570D	1.20E-17	-7.644264	down	BP: maltose metabolic process (GO:0000023); MF: enzyme inhibitor activity (GO:0004857); CC: cytosol (GO:0005829); BP: pentose-phosphate shunt (GO:0006098); BP: regulation of carbohydrate metabolic process (GO:0006109); BP: glycerol ether metabolic process (GO:0006662); MF: enzyme activator activity (GO:0008047); MF: electron carrier activity (GO:0009055); CC: chloroplast thylakoid (GO:0009534); CC: chloroplast stroma (GO:0009570); MF: protein disulfide oxidoreductase activity (GO:0015035); BP: starch biosynthetic process (GO:0019252); BP: isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway (GO:0019288); BP: glucosinolate metabolic process (GO:0019760); BP: electron transport chain (GO:0022900); BP: positive regulation of catalytic activity (GO:0043085); BP: negative regulation of catalytic activity (GO:0043086); BP: cell redox homeostasis (GO:0045454);	--
BnaC03g09190D	8.34E-08	-5.309902	down	--	--
BnaC03g18930D	8.99E-04	2.3082952	up	CC: chloroplast thylakoid membrane (GO:0009535); CC: photosystem I reaction center (GO:0009538); CC: chloroplast envelope (GO:0009941); CC: plastoglobule (GO:0010287); BP: photosynthesis (GO:0015979); BP: cysteine biosynthetic process (GO:0019344);	Photosynthesis (ko00195)
BnaC03g19830D	2.17E-12	3.2765956	up	--	--
BnaC03g23820D	8.61E-06	2.6246115	up	CC: nucleus (GO:0005634);	Taurine and hypotaurine metabolism (ko00430)
BnaC03g57080D	7.37E-11	4.5819172	up	CC: chloroplast (GO:0009507);	--
BnaC03g65980D	4.61E-14	-6.388435	down	BP: fatty acid biosynthetic process (GO:0006633); CC: membrane (GO:0016020); MF: transferase activity, transferring acyl groups other than amino-acyl groups (GO:0016747);	Fatty acid elongation (ko00062)
BnaC04g10370D	1.76E-51	-9.301434	down	MF: protein kinase activity (GO:0004672); BP: phosphorylation (GO:0016310);	--

BnaC04g29730D	1.61E-12	Infinity	up	CC: cytosol (GO:0005829); BP: response to wounding (GO:0009611); BP: response to salicylic acid (GO:0009751); MF: 12-oxophytodienoate reductase activity (GO:0016629); BP: oxylipin metabolic process (GO:0031407); BP: response to cadmium ion (GO:0046686);	alpha-Linolenic acid metabolism (ko00592)
BnaC04g30180D	1.54E-14	6.1201331	up	--	--
BnaC04g39120D	2.25E-35	-2.801711	down	BP: putrescine biosynthetic process (GO:0009446); MF: N-carbamoylputrescine amidase activity (GO:0050126);	Arginine and proline metabolism (ko00330)
BnaC04g45730D	6.78E-12	2.7698329	up	MF: carboxylic ester hydrolase activity (GO:0004091); CC: extracellular region (GO:0005576); BP: lipid metabolic process (GO:0006629); BP: vegetative to reproductive phase transition of meristem (GO:0010228); BP: protein desumoylation (GO:0016926); BP: hydrogen peroxide biosynthetic process (GO:0050665); CC: nucleus (GO:0005634);	--
BnaC05g05100D	4.90E-05	-3.272942	down	--	--
BnaC05g26860D	1.52E-09	-Infinity	down	--	DNA replication (ko03030); Nucleotide excision repair (ko03420); Mismatch repair (ko03430); Homologous recombination (ko03440)
BnaC06g07110D	2.08E-07	3.1783042	up	--	--
BnaC06g08050D	1.93E-07	4.6921405	up	--	--
BnaC06g16950D	3.12E-07	3.4470044	up	--	--
BnaC06g42000D	3.81E-22	4.5511229	up	--	--
BnaC07g33980D	4.57E-26	5.1079825	up	MF: protein binding (GO:0005515); CC: nucleus (GO:0005634); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: response to auxin (GO:0009733); BP: systemic acquired resistance, salicylic acid mediated signaling pathway (GO:0009862); BP: defense response to bacterium (GO:0042742); MF: ADP binding (GO:0043531);	--
BnaC07g36960D	6.66E-13	5.1718351	up	--	--
BnaC08g01470D	9.32E-10	Infinity	up	CC: plasma membrane (GO:0005886); BP: oligopeptide transport (GO:0006857); MF: kinase activity (GO:0016301);	--
BnaC08g05590D	2.33E-36	4.0764713	up	MF: serine-type carboxypeptidase activity (GO:0004185); CC: extracellular region (GO:0005576); CC: cell wall (GO:0005618); BP: proteolysis (GO:0006508);	--
BnaC08g29060D	9.26E-14	-Infinity	down	BP: RNA splicing, via endonucleolytic cleavage and ligation (GO:0000394); MF: inositol hexakisphosphate binding (GO:0000822); BP: response to molecule of bacterial origin (GO:0002237); MF: ubiquitin-protein transferase activity (GO:0004842); CC: nucleus (GO:0005634); CC: vacuolar membrane (GO:0005774); BP: methionine biosynthetic process (GO:0009086); BP: auxin-activated signaling pathway (GO:0009734); MF: auxin binding (GO:0010011); BP: stomatal complex morphogenesis (GO:0010103); BP: pollen maturation (GO:0010152); BP: protein ubiquitination (GO:0016567); BP: stamen development (GO:0048443); BP: lateral root development (GO:0048527); BP: photoperiodism, flowering (GO:0048573); BP: cellular response to nitrate (GO:0071249); BP: primary root development (GO:0080022);	--
BnaC08g29080D	9.82E-10	-Infinity	down	CC: vacuolar proton-transporting V-type ATPase, V1 domain (GO:0000221); CC: plant-type vacuole	Oxidative phosphorylation

				(GO:0000325); CC: Golgi apparatus (GO:0005794); CC: cytosol (GO:0005829); CC: plasma membrane (GO:0005886); BP: glucose catabolic process (GO:0006007); BP: ubiquitin-dependent protein catabolic process (GO:0006511); BP: calcium ion transport (GO:0006816); BP: Golgi organization (GO:0007030); BP: vacuole organization (GO:0007033); CC: chloroplast (GO:0009507); BP: response to salt stress (GO:0009651); BP: lignin biosynthetic process (GO:0009809); BP: photorespiration (GO:0009853); BP: cell tip growth (GO:0009932); BP: ATP hydrolysis coupled proton transport (GO:0015991); BP: cellulose metabolic process (GO:0030243); BP: regulation of carbohydrate biosynthetic process (GO:0043255); MF: proton-transporting ATPase activity, rotational mechanism (GO:0046961); BP: Golgi vesicle transport (GO:0048193); BP: root hair cell differentiation (GO:0048765); BP: response to misfolded protein (GO:0051788); BP: proteasome core complex assembly (GO:0080129);	(ko00190); Phagosome (ko04145)
BnaC08g35320D	2.13E-05	-2.420617	down	CC: nucleus (GO:0005634); CC: cytosol (GO:0005829); CC: plasma membrane (GO:0005886); CC: plasmodesma (GO:0009506); BP: plant-type cell wall biogenesis (GO:0009832); BP: cellulose biosynthetic process (GO:0030244); BP: anisotropic cell growth (GO:0051211);	--
BnaC08g35500D	5.00E-16	-2.937188	down	MF: GTPase activity (GO:0003924); MF: GTP binding (GO:0005525); BP: GTP catabolic process (GO:0006184); BP: small GTPase mediated signal transduction (GO:0007264); BP: protein transport (GO:0015031); CC: membrane (GO:0016020); BP: vesicle-mediated transport (GO:0016192);	Endocytosis (ko04144); Phagosome (ko04145)
BnaC08g35720D	1.61E-11	8.5817665	up	CC: vacuolar proton-transporting V-type ATPase, V0 domain (GO:0000220); CC: mitochondrion (GO:0005739); CC: Golgi apparatus (GO:0005794); BP: ATP catabolic process (GO:0006200); CC: chloroplast (GO:0009507); MF: hydrogen-translocating pyrophosphatase activity (GO:0009678); CC: plant-type vacuole membrane (GO:0009705); MF: hydrogen ion transmembrane transporter activity (GO:0015078); BP: ATP synthesis coupled proton transport (GO:0015986); BP: ATP hydrolysis coupled proton transport (GO:0015991); MF: ATPase activity (GO:0016887); BP: cellular response to nutrient levels (GO:0031669); BP: sequestering of zinc ion (GO:0032119); BP: vacuolar sequestering (GO:0043181); MF: nutrient reservoir activity (GO:0045735); BP: vacuolar proton-transporting V-type ATPase complex assembly (GO:0070072); BP: cellular response to salt stress (GO:0071472);	Oxidative phosphorylation (ko00190); Phagosome (ko04145)
BnaC08g35850D	9.22E-11	5.0934544	up	MF: microtubule motor activity (GO:0003777); MF: ATP binding (GO:0005524); CC: cytoplasm (GO:0005737); CC: kinesin complex (GO:0005871); CC: microtubule (GO:0005874); CC: plasma membrane (GO:0005886); BP: microtubule-based movement (GO:0007018); MF: microtubule binding (GO:0008017); CC: plasmodesma (GO:0009506);	--
BnaC08g36200D	1.39E-93	-9.329087	down	CC: chloroplast (GO:0009507); BP: photorespiration (GO:0009853);	--
BnaC08g36360D	5.76E-04	2.9369469	up	MF: nucleotide binding (GO:0000166); MF: catalytic activity (GO:0003824); CC: mitochondrial respiratory chain complex I (GO:0005747); BP: ubiquitin-dependent protein catabolic process (GO:0006511); BP: response to salt stress (GO:0009651); BP: photorespiration (GO:0009853); MF: coenzyme binding (GO:0050662); BP: response to misfolded protein (GO:0051788); BP: proteasome core complex assembly (GO:0080129);	Oxidative phosphorylation (ko00190)

BnaC08g36500D	1.42E-08	3.2993725	up	CC: Golgi apparatus (GO:0005794); MF: ceramide glucosyltransferase activity (GO:0008120);	--
BnaC08g37460D	4.44E-16	-Infinity	down	BP: mitotic cell cycle (GO:0000278); MF: RNA binding (GO:0003723); MF: polynucleotide adenyltransferase activity (GO:0004652); MF: protein binding (GO:0005515); CC: nucleus (GO:0005634); BP: transcription, DNA-templated (GO:0006351); BP: RNA polyadenylation (GO:0043631);	mRNA surveillance pathway (ko03015)
BnaC08g37550D	7.16E-06	-Infinity	down	CC: nucleus (GO:0005634); BP: cellular response to phosphate starvation (GO:0016036); BP: dephosphorylation (GO:0016311); BP: galactolipid biosynthetic process (GO:0019375); BP: negative regulation of transcription, DNA-templated (GO:0045892); MF: phosphocholine phosphatase activity (GO:0052731); MF: phosphoethanolamine phosphatase activity (GO:0052732);	Vitamin B6 metabolism (ko00750)
BnaC08g38300D	1.20E-17	-6.204321	down	MF: nucleotide binding (GO:0000166); BP: mRNA splicing, via spliceosome (GO:0000398); MF: RNA binding (GO:0003723); MF: protein binding (GO:0005515); CC: nucleolus (GO:0005730); BP: sugar mediated signaling pathway (GO:0010182); CC: nuclear speck (GO:0016607);	RNA transport (ko03013); mRNA surveillance pathway (ko03015)
BnaC08g39020D	2.22E-16	7.5111994	up	CC: cytosol (GO:0005829); CC: plasmodesma (GO:0009506);	Endocytosis (ko04144)
BnaC08g39120D	4.32E-14	Infinity	up	--	--
BnaC08g39130D	5.42E-57	8.5126957	up	MF: copper ion binding (GO:0005507); MF: calmodulin binding (GO:0005516); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: gluconeogenesis (GO:0006094); BP: glycolytic process (GO:0006096); BP: protein folding (GO:0006457); BP: tryptophan catabolic process (GO:0006569); BP: response to heat (GO:0009408); BP: response to cold (GO:0009409); CC: chloroplast thylakoid membrane (GO:0009535); CC: chloroplast stroma (GO:0009570); BP: response to high light intensity (GO:0009644); BP: response to salt stress (GO:0009651); BP: chloroplast organization (GO:0009658); BP: indoleacetic acid biosynthetic process (GO:0009684); CC: chloroplast envelope (GO:0009941); BP: isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway (GO:0019288); BP: cysteine biosynthetic process (GO:0019344); BP: response to endoplasmic reticulum stress (GO:0034976); BP: response to hydrogen peroxide (GO:0042542); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: ovule development (GO:0048481); MF: chaperone binding (GO:0051087); BP: positive regulation of superoxide dismutase activity (GO:1901671);	--
BnaC08g39360D	7.16E-06	3.2255056	up	MF: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553); CC: cell wall (GO:0005618); BP: cellular glucan metabolic process (GO:0006073); BP: phloem or xylem histogenesis (GO:0010087); BP: fruit development (GO:0010154); MF: xyloglucan:xyloglucosyl transferase activity (GO:0016762); CC: apoplast (GO:0048046); BP: stamen filament development (GO:0080086);	--
BnaC08g39650D	9.40E-10	6.7365643	up	CC: extracellular region (GO:0005576); BP: plant-type cell wall modification (GO:0009827); MF: pectate lyase activity (GO:0030570);	Pentose and glucuronate interconversions (ko00040)
BnaC08g39990D	4.68E-11	2.7036417	up	BP: MAPK cascade (GO:0000165); MF: protein serine/threonine kinase activity (GO:0004674); MF: protein serine/threonine/tyrosine kinase activity (GO:0004712); MF: ATP binding (GO:0005524); CC: nucleus (GO:0005634); CC: cytosol (GO:0005829); BP: protein phosphorylation (GO:0006468); BP: protein targeting to membrane (GO:0006612); BP:	--

				response to cold (GO:0009409); BP: response to water deprivation (GO:0009414); BP: response to ethylene (GO:0009723); BP: auxin-activated signaling pathway (GO:0009734); BP: abscisic acid-activated signaling pathway (GO:0009738); BP: brassinosteroid mediated signaling pathway (GO:0009742); BP: systemic acquired resistance, salicylic acid mediated signaling pathway (GO:0009862); BP: jasmonic acid mediated signaling pathway (GO:0009867); BP: regulation of signal transduction (GO:0009966); BP: leaf vascular tissue pattern formation (GO:0010305); BP: regulation of plant-type hypersensitive response (GO:0010363); BP: endoplasmic reticulum unfolded protein response (GO:0030968); BP: negative regulation of defense response (GO:0031348); BP: hyperosmotic salinity response (GO:0042538); BP: negative regulation of programmed cell death (GO:0043069); BP: defense response to fungus (GO:0050832);	
BnaC08g40040D	3.08E-06	-Infinity	down	MF: acid phosphatase activity (GO:0003993); MF: protein serine/threonine phosphatase activity (GO:0004722); CC: extracellular region (GO:0005576); CC: mitochondrion (GO:0005739); CC: endosome (GO:0005768); CC: Golgi apparatus (GO:0005794); CC: trans-Golgi network (GO:0005802); BP: regulation of carbohydrate metabolic process (GO:0006109); CC: chloroplast (GO:0009507); MF: metal ion binding (GO:0046872);	--
BnaC08g40320D	4.59E-09	5.8280102	up	MF: chromatin binding (GO:0003682); MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); BP: membrane fusion (GO:0006944); MF: identical protein binding (GO:0042802); MF: sequence-specific DNA binding (GO:0043565); BP: Golgi vesicle transport (GO:0048193);	--
BnaC08g40410D	2.27E-11	Infinity	up	MF: Ran GTPase activator activity (GO:0005098); CC: nuclear envelope (GO:0005635); CC: vacuolar membrane (GO:0005774); CC: endoplasmic reticulum (GO:0005783); BP: nucleocytoplasmic transport (GO:0006913); BP: toxin catabolic process (GO:0009407); CC: chloroplast (GO:0009507); BP: photomorphogenesis (GO:0009640); BP: response to salt stress (GO:0009651); BP: cullin deneddylation (GO:0010388); BP: lateral root development (GO:0048527);	RNA transport (ko03013)
BnaC08g40740D	7.86E-08	-Infinity	down	MF: translation initiation factor activity (GO:0003743); CC: cytoplasm (GO:0005737);	--
BnaC08g40810D	4.86E-10	2.7058229	up	MF: protein serine/threonine kinase activity (GO:0004674); BP: protein autophosphorylation (GO:0046777);	--
BnaC08g40940D	4.62E-08	-Infinity	down	MF: ubiquitin-protein transferase activity (GO:0004842); CC: nucleus (GO:0005634); MF: zinc ion binding (GO:0008270); CC: chloroplast (GO:0009507); BP: protein ubiquitination (GO:0016567);	--
BnaC08g41390D	1.83E-05	-8.119765	down	CC: plant-type vacuole (GO:0000325); MF: sucrose alpha-glucosidase activity (GO:0004575); BP: carbohydrate metabolic process (GO:0005975); BP: polyamine catabolic process (GO:0006598); BP: calcium ion transport (GO:0006816); BP: iron ion transport (GO:0006826); BP: Golgi organization (GO:0007030); CC: plant-type cell wall (GO:0009505); BP: response to wounding (GO:0009611); BP: response to bacterium (GO:0009617); BP: response to salt stress (GO:0009651); BP: coumarin biosynthetic process (GO:0009805); BP: cellular response to iron ion starvation (GO:0010106); BP: response to nitrate (GO:0010167); BP: nitrate transport (GO:0015706); BP: brassinosteroid biosynthetic process (GO:0016132); BP: cellular modified amino acid	Galactose metabolism (ko00052); Starch and sucrose metabolism (ko00500)



BnaC08g41540D	6.62E-07	-Infinity	down	<p>biosynthetic process (GO:0042398); BP: cellular response to gibberellin stimulus (GO:0071370); BP: primary root development (GO:0080022); MF: N,N-dimethylaniline monooxygenase activity (GO:0004499); CC: nucleus (GO:0005634); BP: glucosinolate biosynthetic process (GO:0019761); MF: flavin adenine dinucleotide binding (GO:0050660); MF: NADP binding (GO:0050661); BP: oxidation-reduction process (GO:0055114); MF: 8-methylthiopropyl glucosinolate S-oxygenase activity (GO:0080107);</p>	--
BnaC08g41720D	1.12E-23	-8.973216	down	<p>MF: aspartic-type endopeptidase activity (GO:0004190); CC: extracellular region (GO:0005576); CC: vacuole (GO:0005773); CC: cytosol (GO:0005829); BP: glycolytic process (GO:0006096); BP: proteolysis (GO:0006508); BP: protein targeting to vacuole (GO:0006623); BP: lipid metabolic process (GO:0006629); BP: water transport (GO:0006833); BP: hyperosmotic response (GO:0006972); BP: Golgi organization (GO:0007030); BP: response to temperature stimulus (GO:0009266); CC: plasmodesma (GO:0009506); BP: response to salt stress (GO:0009651); BP: response to cadmium ion (GO:0046686); BP: organ development (GO:0048513);</p>	--
BnaC08g41780D	1.45E-10	-Infinity	down	<p>BP: sulfur amino acid metabolic process (GO:0000096); MF: serine-tRNA ligase activity (GO:0004828); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); BP: rRNA processing (GO:0006364); BP: seryl-tRNA aminoacylation (GO:0006434); BP: mitochondrion organization (GO:0007005); BP: cellular amino acid biosynthetic process (GO:0008652); BP: serine family amino acid metabolic process (GO:0009069); CC: chloroplast (GO:0009507); BP: embryo development ending in seed dormancy (GO:0009793); BP: chloroplast relocation (GO:0009902); BP: leaf morphogenesis (GO:0009965); BP: thylakoid membrane organization (GO:0010027); BP: photosystem II assembly (GO:0010207); BP: vegetative to reproductive phase transition of meristem (GO:0010228); BP: iron-sulfur cluster assembly (GO:0016226); BP: cell differentiation (GO:0030154); BP: regulation of protein dephosphorylation (GO:0035304); BP: cell wall modification (GO:0042545); BP: transcription from plastid promoter (GO:0042793); BP: positive regulation of transcription, DNA-templated (GO:0045893); BP: ovule development (GO:0048481);</p>	Aminoacyl-tRNA biosynthesis (ko00970)
BnaC08g42080D	1.06E-05	-3.581727	down	<p>CC: plasma membrane (GO:0005886); MF: transferase activity, transferring phosphorus-containing groups (GO:0016772);</p>	--
BnaC08g42280D	2.57E-12	-Infinity	down	<p>BP: telomere maintenance (GO:0000723); BP: double-strand break repair via homologous recombination (GO:0000724); MF: nucleic acid binding (GO:0003676); MF: ATP binding (GO:0005524); CC: nucleus (GO:0005634); BP: DNA replication (GO:0006260); CC: plasmodesma (GO:0009506); BP: vegetative to reproductive phase transition of meristem (GO:0010228); MF: ATP-dependent 3'-5' DNA helicase activity (GO:0043140); BP: cellular response to cold (GO:0070417); BP: cellular response to abscisic acid stimulus (GO:0071215);</p>	Homologous recombination (ko03440)
BnaC08g42450D	2.43E-05	-5.423095	down	<p>BP: response to molecule of bacterial origin (GO:0002237); MF: protein serine/threonine kinase activity (GO:0004674); MF: ATP binding (GO:0005524); CC: plasma membrane (GO:0005886); BP: N-terminal protein myristoylation (GO:0006499); BP: protein targeting to membrane (GO:0006612); BP: membrane fusion (GO:0006944); BP: response to oxidative stress (GO:0006979); BP: transmembrane receptor protein tyrosine kinase signaling pathway</p>	--

				(GO:0007169); BP: systemic acquired resistance (GO:0009627); BP: seed germination (GO:0009845); BP: stomatal complex morphogenesis (GO:0010103); BP: regulation of plant-type hypersensitive response (GO:0010363); CC: integral component of membrane (GO:0016021); BP: negative regulation of programmed cell death (GO:0043069); BP: protein autophosphorylation (GO:0046777); BP: stamen development (GO:0048443); CC: micropyle (GO:0070825);	
BnaC08g49500D	4.87E-04	Infinity	up	CC: chloroplast (GO:0009507); BP: systemic acquired resistance (GO:0009627); BP: regulation of defense response (GO:0031347);	--
BnaC08g49610D	1.27E-07	-7.011146	down	MF: protein binding (GO:0005515); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); BP: starch catabolic process (GO:0005983); BP: circadian rhythm (GO:0007623); CC: chloroplast stroma (GO:0009570); BP: response to symbiotic fungus (GO:0009610); BP: cold acclimation (GO:0009631); CC: chloroplast envelope (GO:0009941); BP: phosphorylation (GO:0016310); BP: starch biosynthetic process (GO:0019252); MF: alpha-glucan, water dikinase activity (GO:0050521);	--
BnaC08g49940D	5.28E-11	-Infinity	down	CC: nucleus (GO:0005634);	--
BnaC08g49970D	1.75E-08	-Infinity	down	CC: extracellular region (GO:0005576);	--
BnaC09g05690D	7.80E-08	Infinity	up	CC: nuclear pore (GO:0005643); BP: protein import into nucleus (GO:0006606); MF: Ran GTPase binding (GO:0008536); MF: protein transporter activity (GO:0008565); BP: regulation of RNA splicing (GO:0043484);	--
BnaC09g05960D	3.56E-14	7.108321	up	MF: DNA binding (GO:0003677); CC: nucleus (GO:0005634);	--
BnaC09g05970D	2.27E-06	4.4722537	up	BP: pentose-phosphate shunt (GO:0006098); BP: rRNA processing (GO:0006364); BP: protoporphyrinogen IX biosynthetic process (GO:0006782); MF: transaminase activity (GO:0008483); BP: aromatic amino acid family biosynthetic process (GO:0009073); BP: response to light stimulus (GO:0009416); CC: chloroplast stroma (GO:0009570); CC: chloroplast envelope (GO:0009941); BP: leaf morphogenesis (GO:0009965); BP: chlorophyll biosynthetic process (GO:0015995); BP: cysteine biosynthetic process (GO:0019344); BP: cell differentiation (GO:0030154); MF: pyridoxal phosphate binding (GO:0030170); MF: glutamate-1-semialdehyde 2,1-aminomutase activity (GO:0042286); BP: protein targeting to chloroplast (GO:0045036); BP: positive regulation of transcription, DNA-templated (GO:0045893); CC: apoplast (GO:0048046);	Porphyrin and chlorophyll metabolism (ko00860)
BnaC09g06220D	3.04E-14	Infinity	up	CC: plasma membrane (GO:0005886); CC: chloroplast (GO:0009507);	--
BnaC09g06260D	5.58E-09	6.6093421	up	CC: nucleus (GO:0005634);	--
BnaCnng17490D	1.46E-20	3.8154347	up	--	--
BnaCnng23190D	2.71E-13	-3.743504	down	BP: response to cold (GO:0009409); BP: response to light stimulus (GO:0009416); CC: chloroplast thylakoid membrane (GO:0009535); CC: chloroplast stroma (GO:0009570); BP: response to sucrose (GO:0009744); CC: chloroplast envelope (GO:0009941); BP: cellular process (GO:0009987); CC: stromule (GO:0010319); BP: single-organism transport (GO:0044765);	--
BnaCnng24040D	7.33E-18	8.404532	up	MF: protein binding (GO:0005515); CC: cytosol (GO:0005829); BP: glycolytic process (GO:0006096); BP: tricarboxylic acid cycle (GO:0006099); BP: iron ion transport (GO:0006826); BP: water transport (GO:0006833); BP: hyperosmotic response (GO:0006972); BP: Golgi organization (GO:0007030); MF: phosphoenolpyruvate carboxylase activity (GO:0008964); BP: response to temperature stimulus	Pyruvate metabolism (ko00620); Carbon fixation in photosynthetic organisms (ko00710); Carbon metabolism (ko01200)

				(GO:0009266); BP: response to salt stress (GO:0009651); BP: response to sucrose (GO:0009744); BP: response to glucose (GO:0009749); BP: response to fructose (GO:0009750); BP: cellular response to iron ion starvation (GO:0010106); BP: response to nitrate (GO:0010167); BP: nitrate transport (GO:0015706); BP: carbon fixation (GO:0015977); BP: cellular response to phosphate starvation (GO:0016036); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: protein tetramerization (GO:0051262);	
BnaCnng68410D	2.77E-05	5.3691401	up	BP: transcription, DNA-templated (GO:0006351); BP: RNA processing (GO:0006396); BP: translational initiation (GO:0006413); BP: post-embryonic development (GO:0009791); BP: posttranscriptional regulation of gene expression (GO:0010608); CC: macromolecular complex (GO:0032991); BP: macromolecule localization (GO:0033036); CC: cytoplasmic part (GO:0044444); BP: single-organism developmental process (GO:0044767); BP: reproductive structure development (GO:0048608); BP: cellular response to organic substance (GO:0071310); BP: regulation of primary metabolic process (GO:0080090); BP: regulation of cellular macromolecule biosynthetic process (GO:2000112);	RNA transport (ko03013)
BnaCnng75420D	3.74E-11	Infinity	up	CC: vacuolar proton-transporting V-type ATPase, V0 domain (GO:0000220); CC: mitochondrion (GO:0005739); CC: Golgi apparatus (GO:0005794); BP: ATP catabolic process (GO:0006200); CC: chloroplast (GO:0009507); MF: hydrogen-translocating pyrophosphatase activity (GO:0009678); CC: plant-type vacuole membrane (GO:0009705); MF: hydrogen ion transmembrane transporter activity (GO:0015078); BP: ATP synthesis coupled proton transport (GO:0015986); BP: ATP hydrolysis coupled proton transport (GO:0015991); MF: ATPase activity (GO:0016887); BP: cellular response to nutrient levels (GO:0031669); BP: sequestering of zinc ion (GO:0032119); BP: vacuolar sequestering (GO:0043181); MF: nutrient reservoir activity (GO:0045735); BP: vacuolar proton-transporting V-type ATPase complex assembly (GO:0070072); BP: cellular response to salt stress (GO:0071472); MF: binding (GO:0005488);	Oxidative phosphorylation (ko00190); Phagosome (ko04145)
Cole_newGene_1137	4.51E-08	3.7895968	up		--
Cole_newGene_1983	1.76E-10	-Infinity	down	CC: mitochondrion (GO:0005739); CC: chloroplast stroma (GO:0009570); BP: mRNA modification (GO:0016556); MF: carbon-nitrogen ligase activity, with glutamine as amido-N-donor (GO:0016884);	Aminoacyl-tRNA biosynthesis (ko00970)
Cole_newGene_1984	2.67E-18	-Infinity	down	CC: plant-type vacuole (GO:0000325); CC: vacuolar membrane (GO:0005774); CC: chloroplast (GO:0009507); BP: response to salt stress (GO:0009651); BP: proton transport (GO:0015992); BP: CC organization (GO:0016043); MF: pyrophosphatase activity (GO:0016462); MF: transmembrane transporter activity (GO:0022857); BP: ion transmembrane transport (GO:0034220); BP: ATP metabolic process (GO:0046034); BP: maintenance of location (GO:0051235); BP: cellular localization (GO:0051641); BP: cellular response to stimulus (GO:0051716);	Oxidative phosphorylation (ko00190); Phagosome (ko04145)
Cole_newGene_2061	7.80E-08	2.7259809	up	--	--
Cole_newGene_2071	7.42E-22	-9.979161	down	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); MF: protein dimerization activity (GO:0046983);	--
Cole_newGene_2073	1.53E-63	9.6473387	up	CC: intracellular membrane-bounded organelle (GO:0043231); CC: cytoplasmic part (GO:0044444);	Protein processing in endoplasmic reticulum (ko04141);

Cole_newGene_2243	6.93E-11	-7.380299	down	CC: mitochondrion (GO:0005739); CC: Golgi apparatus (GO:0005794); CC: plasma membrane (GO:0005886); BP: response to stress (GO:0006950); CC: integral component of endoplasmic reticulum membrane (GO:0030176); BP: single-organism cellular process (GO:0044763);	Plant-pathogen interaction (ko04626) Protein export (ko03060); Protein processing in endoplasmic reticulum (ko04141)
Cole_newGene_269	1.16E-55	4.0396548	up	--	--
Cole_newGene_3294	4.58E-04	2.1419946	up	--	--
Cole_newGene_3315	4.83E-15	4.344452	up	--	--
Cole_newGene_3682	6.29E-09	-2.684965	down	--	--
Cole_newGene_3766	3.96E-06	-8.02903	down	--	--
Cole_newGene_4151	2.04E-73	-8.612791	down	--	--
Cole_newGene_4384	1.34E-15	7.4681451	up	--	--
Cole_newGene_4761	1.18E-04	2.5715611	up	--	--
Cole_newGene_4855	1.27E-16	2.3247257	up	CC: nucleus (GO:0005634);	--
Cole_newGene_4935	1.40E-05	2.7165926	up	--	--
Cole_newGene_6003	1.83E-05	2.9602378	up	--	--
Cole_newGene_6035	1.53E-04	6.3658568	up	MF: hydrolase activity, acting on ester bonds (GO:0016788);	--
Cole_newGene_6687	1.70E-10	Infinity	up	CC: cell wall (GO:0005618); CC: vacuole (GO:0005773); CC: endoplasmic reticulum (GO:0005783); CC: plasma membrane (GO:0005886); CC: plasmodesma (GO:0009506); MF: transmembrane transporter activity (GO:0022857); BP: transmembrane transport (GO:0055085);	--
Cole_newGene_6749	7.17E-18	2.4653464	up	--	--
Cole_newGene_8277	1.99E-10	-5.957562	down	--	--

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**Table S2:** 268 DEGs between zws-ms and zws-217 at green podding stage

Gene ID	FDR	log <sub>2</sub> FC	Regulated	GO annotation	KEGG pathway
BnaA01g11480D	1.56E-07	8.4670153	up	MF: serine-type endopeptidase activity (GO:0004252); CC: extracellular region (GO:0005576); BP: proteolysis (GO:0006508); CC: plant-type cell wall (GO:0009505); MF: identical protein binding (GO:0042802); BP: negative regulation of catalytic activity (GO:0043086);	--
BnaA01g20280D	8.61E-07	Infinity	up	MF: monooxygenase activity (GO:0004497); MF: iron ion binding (GO:0005506); MF: protein binding (GO:0005515); CC: extracellular region (GO:0005576); MF: electron carrier activity (GO:0009055); MF: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO:0016705); MF: oxygen binding (GO:0019825); MF: heme binding (GO:0020037); BP: oxidation-reduction process (GO:005114);	--
BnaA01g25630D	2.08E-04	Infinity	up	MF: cysteine-type endopeptidase activity (GO:0004197); CC: extracellular space (GO:0005615); BP: proteolysis (GO:0006508); BP: vacuolar protein processing (GO:0006624); CC: chloroplast (GO:0009507); BP: gibberellin biosynthetic process (GO:0009686); BP: response to abscisic acid (GO:0009737); BP: gibberellic acid mediated signaling pathway (GO:0009740); BP: embryo development ending in seed dormancy (GO:0009793); BP: seed germination (GO:0009845); BP: seed dormancy process (GO:0010162); BP: seed coat development (GO:0010214); BP: programmed cell death (GO:0012501);	--
BnaA01g29830D	6.42E-06	3.5126519	up	MF: copper ion binding (GO:0005507); CC: extracellular region (GO:0005576); BP: plant-type cell wall modification (GO:0009827); MF: oxidoreductase activity (GO:0016491); BP: oxidation-reduction process (GO:005114);	--
BnaA01g35470D	3.22E-12	9.1976542	up	CC: cytosol (GO:0005829); MF: O-methyltransferase activity (GO:0008171); CC: chloroplast (GO:0009507); BP: lignin biosynthetic process (GO:0009809);	Phenylpropanoid biosynthesis (ko00940)
BnaA02g06090D	5.85E-04	8.1541922	up	MF: serine-type carboxypeptidase activity (GO:0004185); CC: extracellular region (GO:0005576); BP: proteolysis (GO:0006508);	--
BnaA02g07900D	6.95E-08	-2.316053	down	MF: transporter activity (GO:0005215); CC: extracellular region (GO:0005576); CC: mitochondrion (GO:0005739); CC: vacuolar membrane (GO:0005774); CC: endoplasmic reticulum (GO:0005783); CC: Golgi apparatus (GO:0005794); CC: cytosol (GO:0005829); CC: plasma membrane (GO:0005886); BP: transport (GO:0006810); BP: response to heat (GO:0009408); BP: response to cold (GO:0009409); BP: response to light stimulus (GO:0009416); CC: plasmodesma (GO:0009506); BP: hyperosmotic salinity response (GO:0042538);	--
BnaA02g08870D	1.25E-10	7.0259757	up	CC: cell wall (GO:0005618); CC: anchored component of plasma membrane	--

BnaA02g12810D	3.37E-09	5.8559376	up	(GO:0046658); BP: root development (GO:0048364); BP: shoot system development (GO:0048367); MF: monooxygenase activity (GO:0004497); CC: chloroplast (GO:0009507); BP: photorespiration (GO:0009853); BP: carbon fixation (GO:0015977); BP: photosynthesis (GO:0015979); MF: ribulose-bisphosphate carboxylase activity (GO:0016984); BP: oxidation-reduction process (GO:0055114); MF: enzyme inhibitor activity (GO:0004857); BP: membrane fusion (GO:0006944); CC: plant-type cell wall (GO:0009505); MF: pectinesterase activity (GO:0030599); BP: cell wall modification (GO:0042545); BP: negative regulation of catalytic activity (GO:0043086); MF: aspartyl esterase activity (GO:0045330); BP: pectin catabolic process (GO:0045490); CC: pollen tube (GO:0090406);	Glyoxylate and dicarboxylate metabolism (ko00630); Carbon fixation in photosynthetic organisms (ko00710); Carbon metabolism (ko01200)
BnaA02g30620D	5.21E-06	3.6652093	up	MF: enzyme inhibitor activity (GO:0004857); BP: membrane fusion (GO:0006944); CC: plant-type cell wall (GO:0009505); MF: pectinesterase activity (GO:0030599); BP: cell wall modification (GO:0042545); BP: negative regulation of catalytic activity (GO:0043086); MF: aspartyl esterase activity (GO:0045330); BP: pectin catabolic process (GO:0045490); CC: pollen tube (GO:0090406);	Pentose and glucuronate interconversions (ko00040); Starch and sucrose metabolism (ko00500)
BnaA03g02110D	4.15E-08	5.625901	up	CC: extracellular region (GO:0005576); MF: lipid binding (GO:0008289); BP: plant-type cell wall modification (GO:0009827); BP: pollen hydration (GO:0009859); BP: pollen tube growth (GO:0009860); CC: monolayer-surrounded lipid storage body (GO:0012511); CC: integral component of membrane (GO:0016021); BP: lipid storage (GO:0019915); BP: sexual reproduction (GO:0019953); BP: recognition of pollen (GO:0048544); CC: pollen coat (GO:0070505);	--
BnaA03g05480D	4.05E-08	Infinity	up	MF: enzyme inhibitor activity (GO:0004857); CC: chloroplast (GO:0009507); MF: pectinesterase activity (GO:0030599); BP: negative regulation of catalytic activity (GO:0043086);	--
BnaA03g21590D	9.31E-14	6.6690227	up	CC: extracellular region (GO:0005576); CC: plant-type cell wall (GO:0009505); CC: plasmodesma (GO:0009506); BP: pollen tube growth (GO:0009860); MF: pectinesterase activity (GO:0030599); CC: pollen tube (GO:0090406);	--
BnaA03g23380D	3.75E-08	3.6388567	up	CC: extracellular region (GO:0005576); BP: proteolysis (GO:0006508); MF: cysteine-type peptidase activity (GO:0008234);	--
BnaA03g29100D	8.67E-07	4.4018168	up	MF: enzyme inhibitor activity (GO:0004857); CC: nucleus (GO:0005634); CC: plant-type cell wall (GO:0009505); BP: plant-type cell wall modification (GO:0009827); MF: pectinesterase activity (GO:0030599); BP: negative regulation of catalytic activity (GO:0043086); MF: aspartyl esterase activity (GO:0045330); BP: pectin catabolic process (GO:0045490);	Pentose and glucuronate interconversions (ko00040); Starch and sucrose metabolism (ko00500)
BnaA03g30180D	8.24E-07	3.43196	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975); CC: plant-type cell wall (GO:0009505); BP: plant-type cell wall modification (GO:0009827); BP: pollen tube growth (GO:0009860);	--
BnaA03g32810D	2.41E-08	4.0289988	up	MF: copper ion binding (GO:0005507); CC: extracellular region (GO:0005576); BP: plant-type cell wall modification	--

BnaA03g35870D	1.78E-26	5.3347564	up	(GO:0009827); MF: oxidoreductase activity (GO:0016491); BP: oxidation-reduction process (GO:0055114); MF: guanylate kinase activity (GO:0004385); CC: cytoplasm (GO:0005737); BP: purine nucleotide metabolic process (GO:0006163); BP: response to chitin (GO:0010200); BP: phosphorylation (GO:0016310); BP: endoplasmic reticulum unfolded protein response (GO:0030968); BP: defense response to fungus (GO:0050832);	Purine metabolism (ko00230)
BnaA03g40530D	6.53E-10	Infinity	up	MF: ATP binding (GO:0005524); CC: plasma membrane (GO:0005886); BP: ATP catabolic process (GO:0006200); BP: transport (GO:0006810); CC: plasmodesma (GO:0009506); CC: chloroplast (GO:0009507); BP: plant-type cell wall modification (GO:0009827); BP: pollen tube growth (GO:0009860); MF: ATPase activity, coupled to transmembrane movement of substances (GO:0042626);	--
BnaA03g41530D	1.28E-14	4.4623516	up	MF: secondary active sulfate transmembrane transporter activity (GO:0008271); BP: sulfate transport (GO:0008272); CC: chloroplast (GO:0009507); CC: integral component of membrane (GO:0016021); BP: transmembrane transport (GO:0055085);	--
BnaA03g42690D	4.35E-05	2.283801	up	--	--
BnaA03g47450D	2.33E-04	2.7259849	up	CC: nucleus (GO:0005634); CC: endoplasmic reticulum (GO:0005783); MF: hydrolase activity (GO:0016787);	--
BnaA03g49010D	1.09E-05	3.8585156	up	--	--
BnaA03g51030D	7.20E-05	Infinity	up	BP: very long-chain fatty acid metabolic process (GO:0000038); CC: extracellular region (GO:0005576); CC: endoplasmic reticulum (GO:0005783); BP: response to light stimulus (GO:0009416); CC: membrane (GO:0016020); MF: transferase activity, transferring acyl groups other than amino-acyl groups (GO:0016747); BP: fatty acid elongation (GO:0030497);	Fatty acid elongation (ko00062)
BnaA03g58450D	3.15E-07	4.7052493	up	MF: serine-type endopeptidase activity (GO:0004252); CC: cell wall (GO:0005618); BP: proteolysis (GO:0006508); BP: pattern specification process (GO:0007389); MF: identical protein binding (GO:0042802); BP: negative regulation of catalytic activity (GO:0043086); BP: floral whorl development (GO:0048438); BP: flower morphogenesis (GO:0048439);	--
BnaA03g60670D	3.14E-14	Infinity	up	MF: nucleotide binding (GO:0000166); CC: chloroplast (GO:0009507); BP: negative regulation of flavonoid biosynthetic process (GO:0009964); MF: anthocyanidin reductase activity (GO:0033729); BP: cellular metabolic process (GO:0044237); MF: coenzyme binding (GO:0050662); BP: oxidation-reduction process (GO:0055114);	Flavonoid biosynthesis (ko00941)
BnaA04g06410D	1.94E-08	Infinity	up	BP: heme biosynthetic process (GO:0006783); BP: response to oxidative stress (GO:0006979); MF: glutamyl-tRNA reductase activity (GO:0008883); CC: chloroplast (GO:0009507); BP: response to wounding (GO:0009611); BP: response to chitin (GO:0010200); BP: defense response	Porphyrin and chlorophyll metabolism (ko00860)

				by callose deposition (GO:0052542);	
BnaA04g08590D	1.09E-08	Infinity	up	--	--
BnaA04g11630D	4.93E-05	5.7975683	up	MF: transferase activity (GO:0016740);	--
BnaA04g13390D	2.25E-06	4.1883966	up	MF: DNA binding (GO:0003677); MF: DNA (cytosine-5-)-methyltransferase activity (GO:0003886); MF: protein binding (GO:0005515); CC: nucleus (GO:0005634); BP: DNA-dependent DNA replication (GO:0006261); BP: chromatin assembly or disassembly (GO:0006333); BP: chromatin silencing (GO:0006342); BP: regulation of gene expression by genetic imprinting (GO:0006349); BP: cell proliferation (GO:0008283); BP: DNA mediated transformation (GO:0009294); BP: negative regulation of flower development (GO:0009910); BP: zygote asymmetric cytokinesis in embryo sac (GO:0010069); BP: maintenance of DNA methylation (GO:0010216); BP: DNA methylation on cytosine within a CG sequence (GO:0010424); MF: 2 iron, 2 sulfur cluster binding (GO:0051537); BP: histone H3-K9 methylation (GO:0051567); BP: C-5 methylation of cytosine (GO:0090116);	Cysteine and methionine metabolism (ko00270)
BnaA04g16750D	6.11E-04	6.5732109	up	BP: para-aminobenzoic acid biosynthetic process (GO:0008153); CC: chloroplast (GO:0009507); BP: embryo development ending in seed dormancy (GO:0009793); MF: oxo-acid-lyase activity (GO:0016833); BP: chorismate metabolic process (GO:0046417); BP: folic acid biosynthetic process (GO:0046656); MF: 4-amino-4-deoxychorismate synthase activity (GO:0046820);	Folate biosynthesis (ko00790)
BnaA04g19480D	2.82E-08	4.1935246	up	CC: endoplasmic reticulum (GO:0005783); CC: plasma membrane (GO:0005886); BP: signal peptide processing (GO:0006465); BP: proteolysis (GO:0006508); MF: peptidase activity (GO:0008233); CC: chloroplast (GO:0009507); BP: systemic acquired resistance (GO:0009627); CC: integral component of membrane (GO:0016021); BP: response to endoplasmic reticulum stress (GO:0034976);	Protein export (ko03060)
BnaA04g23760D	4.55E-04	3.3075646	up	BP: regulation of cell growth (GO:0001558); CC: mitochondrion (GO:0005739); CC: endoplasmic reticulum (GO:0005783); BP: post-embryonic organ development (GO:0048569); BP: regulation of cell division (GO:0051302);	--
BnaA04g29280D	4.19E-05	8.4144189	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975);	--
BnaA05g00810D	2.84E-06	3.5252182	up	CC: extracellular region (GO:0005576); CC: plant-type cell wall (GO:0009505); CC: plasmodesma (GO:0009506); BP: pollen tube growth (GO:0009860); MF: pectinesterase activity (GO:0030599); CC: pollen tube (GO:0090406);	--
BnaA05g18870D	1.01E-12	14.852439	up	MF: cysteine-type endopeptidase activity (GO:0004197); CC: extracellular space (GO:0005615); BP: proteolysis (GO:0006508); BP: vacuolar protein processing (GO:0006624); CC: chloroplast	--



				(GO:0009507); BP: gibberellin biosynthetic process (GO:0009686); BP: response to abscisic acid (GO:0009737); BP: gibberellic acid mediated signaling pathway (GO:0009740); BP: embryo development ending in seed dormancy (GO:0009793); BP: seed germination (GO:0009845); BP: seed dormancy process (GO:0010162); BP: seed coat development (GO:0010214); BP: programmed cell death (GO:0012501);	
BnaA05g20190D	6.61E-06	5.9536616	up	MF: nucleotide binding (GO:0000166); MF: sequence-specific DNA binding transcription factor activity (GO:0003700); MF: protein binding (GO:0005515); CC: chromatin silencing complex (GO:0005677); CC: heterotrimeric G-protein complex (GO:0005834); BP: regulation of gene expression by genetic imprinting (GO:0006349); BP: regulation of transcription, DNA-templated (GO:0006355); BP: vernalization response (GO:0010048); BP: histone methylation (GO:0016571); CC: polar nucleus (GO:0043078); CC: Cul4-RING E3 ubiquitin ligase complex (GO:0080008); BP: regulation of endosperm development (GO:2000014);	--
BnaA05g24130D	5.51E-07	3.344237	up	--	--
BnaA05g25890D	1.45E-04	3.370634	up	MF: copper ion binding (GO:0005507); CC: extracellular region (GO:0005576); BP: plant-type cell wall modification (GO:0009827); MF: oxidoreductase activity (GO:0016491); BP: oxidation-reduction process (GO:0055114);	--
BnaA05g31610D	2.25E-05	8.8327283	up	MF: epoxide hydrolase activity (GO:0004301); CC: cytoplasm (GO:0005737); BP: metabolic process (GO:0008152);	--
BnaA05g34730D	5.90E-04	Infinity	up	MF: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553); CC: extracellular region (GO:0005576); CC: cell wall (GO:0005618); BP: carbohydrate metabolic process (GO:0005975); CC: plasmodesma (GO:0009506); BP: response to chitin (GO:0010200); MF: cation binding (GO:0043169);	--
BnaA06g07630D	5.17E-04	4.5200286	up	MF: monooxygenase activity (GO:0004497); MF: iron ion binding (GO:0005506); BP: tryptophan catabolic process (GO:0006569); BP: protein targeting to membrane (GO:0006612); MF: electron carrier activity (GO:0009055); BP: indoleacetic acid biosynthetic process (GO:0009684); BP: positive regulation of flavonoid biosynthetic process (GO:0009963); BP: response to nitrate (GO:0010167); BP: regulation of plant-type hypersensitive response (GO:0010363); BP: nitrate transport (GO:0015706); MF: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO:0016705); MF: oxygen binding (GO:0019825); MF: heme binding (GO:0020037); BP: cellular cation homeostasis (GO:0030003); BP: oxidation-reduction process (GO:0055114); BP: divalent metal ion transport (GO:0070838);	--

BnaA06g08050D	1.14E-05	2.8583035	up	CC: cytoplasm (GO:0005737); BP: photorespiration (GO:0009853); MF: hydroxypyruvate reductase activity (GO:0016618); MF: glyoxylate reductase (NADP) activity (GO:0030267); MF: NAD binding (GO:0051287); BP: oxidation-reduction process (GO:0055114);	--
BnaA06g15390D	6.85E-04	8.5559577	up	CC: extracellular region (GO:0005576); CC: vacuolar membrane (GO:0005774); CC: plant-type cell wall (GO:0009505); BP: methylglyoxal catabolic process to D-lactate (GO:0019243);	--
BnaA06g16030D	3.05E-07	Infinity	up	--	--
BnaA06g20450D	2.28E-12	Infinity	up	MF: iron ion binding (GO:0005506); CC: cytoplasm (GO:0005737); BP: alkaloid biosynthetic process (GO:0009821); MF: 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:0016706); BP: secondary metabolic process (GO:0019748); BP: oxidation-reduction process (GO:0055114);	--
BnaA06g20910D	1.76E-04	9.191123	up	CC: nucleus (GO:0005634); CC: endoplasmic reticulum (GO:0005783); MF: hydrolase activity (GO:0016787);	--
BnaA06g23550D	3.19E-05	2.7072755	up	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); BP: regulation of transcription, DNA-templated (GO:0006355); MF: sequence-specific DNA binding (GO:0043565);	--
BnaA06g28440D	6.52E-06	2.6750732	up	MF: ubiquitin-protein transferase activity (GO:0004842); CC: nucleus (GO:0005634); BP: toxin catabolic process (GO:0009407); BP: protein ubiquitination (GO:0016567);	--
BnaA06g30420D	1.63E-08	4.2548773	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975); BP: plant-type cell wall modification (GO:0009827);	--
BnaA06g33360D	1.65E-09	6.7682958	up	MF: magnesium ion binding (GO:0000287); MF: protein binding (GO:0005515); CC: chloroplast (GO:0009507); MF: sesquiterpene synthase activity (GO:0010334); BP: monoterpenoid biosynthetic process (GO:0016099); MF: (R)-limonene synthase activity (GO:0034002); MF: (E)-beta-ocimene synthase activity (GO:0034768); BP: monoterpene biosynthetic process (GO:0043693); MF: pinene synthase activity (GO:0050550); MF: myrcene synthase activity (GO:0050551); MF: (4S)-limonene synthase activity (GO:0050552); MF: sabinene synthase activity (GO:0080015);	--
BnaA06g34900D	3.38E-04	Infinity	up	MF: serine-type endopeptidase activity (GO:0004252); CC: extracellular region (GO:0005576); CC: cell wall (GO:0005618); BP: proteolysis (GO:0006508); MF: identical protein binding (GO:0042802); BP: negative regulation of catalytic activity (GO:0043086);	--
BnaA06g40340D	3.73E-04	Infinity	up	--	--
BnaA07g04500D	4.29E-17	2.7878588	up	CC: mitochondrion (GO:0005739);	--

BnaA07g09660D	3.01E-05	8.3328631	up	--	Lysine degradation (ko00310)
BnaA07g19690D	3.33E-10	6.1773645	up	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); BP: epidermal cell fate specification (GO:0009957); BP: negative regulation of trichoblast fate specification (GO:0010062); MF: sequence-specific DNA binding (GO:0043565); BP: iron ion transport (GO:0006826); BP: cellular response to iron ion starvation (GO:0010106); BP: response to nitrate (GO:0010167); BP: nitrate transport (GO:0015706); MF: manganese ion binding (GO:0030145); MF: nutrient reservoir activity (GO:0045735); CC: apoplast (GO:0048046);	--
BnaA07g22030D	6.26E-08	4.6514555	up	CC: extracellular region (GO:0005576); BP: alcohol metabolic process (GO:0006066); BP: cell-cell signaling (GO:0007267); MF: choline dehydrogenase activity (GO:0008812); BP: embryo sac development (GO:0009553); BP: fatty acid omega-oxidation (GO:0010430); MF: mandelonitrile lyase activity (GO:0046593); MF: flavin adenine dinucleotide binding (GO:0050660);	Cutin, suberine and wax biosynthesis (ko00073)
BnaA07g22900D	2.81E-04	2.047616	up	MF: nucleotide binding (GO:0000166); BP: endonucleolytic cleavage involved in rRNA processing (GO:0000478); BP: RNA methylation (GO:0001510); MF: nucleic acid binding (GO:0003676); CC: nucleolus (GO:0005730); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: pyrimidine ribonucleotide biosynthetic process (GO:0009220); BP: leaf vascular tissue pattern formation (GO:0010305); BP: cotyledon vascular tissue pattern formation (GO:0010588); BP: root development (GO:0048364); BP: leaf development (GO:0048366); BP: petal vascular tissue pattern formation (GO:0080056); BP: sepal vascular tissue pattern formation (GO:0080057);	--
BnaA08g02930D	2.88E-18	2.9064465	up	MF: catalytic activity (GO:0003824); CC: extracellular region (GO:0005576); BP: metabolic process (GO:0008152);	--
BnaA08g04880D	2.38E-05	6.1174117	up	MF: carboxylic ester hydrolase activity (GO:0004091); CC: extracellular space (GO:0005615); BP: lipid metabolic process (GO:0006629); MF: lipase activity (GO:0016298); MF: cutinase activity (GO:0050525); CC: pollen tube (GO:0090406);	--
BnaA08g13220D	3.90E-09	5.4102242	up	CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975); MF: lyase activity (GO:0016829); MF: carbohydrate binding (GO:0030246);	--
BnaA08g15910D	6.13E-05	Infinity	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975);	--
BnaA08g18330D	1.18E-09	4.1783015	up	BP: metabolic process (GO:0008152); CC: chloroplast (GO:0009507); MF: 4-coumarate-CoA ligase activity (GO:0016207);	alpha-Linolenic acid metabolism (ko00592)
BnaA08g21800D	4.58E-07	4.3108796	up		

BnaA08g23120D	8.29E-04	2.5421555	up	MF: iron ion binding (GO:0005506); CC: chloroplast (GO:0009507); BP: pollen development (GO:0009555); BP: response to wounding (GO:0009611); BP: response to bacterium (GO:0009617); BP: response to fungus (GO:0009620); BP: response to high light intensity (GO:0009644); BP: ethylene biosynthetic process (GO:0009693); BP: jasmonic acid biosynthetic process (GO:0009695); BP: response to jasmonic acid (GO:0009753); BP: ethylene-activated signaling pathway (GO:0009873); BP: anther dehiscence (GO:0009901); BP: response to ozone (GO:0010193); BP: response to chitin (GO:0010200); MF: linoleate 13S-lipoxygenase activity (GO:0016165); BP: oxylipin biosynthetic process (GO:0031408); BP: lipid oxidation (GO:0034440); BP: growth (GO:0040007); BP: defense response by callose deposition (GO:0052542); BP: stamen filament development (GO:0080086);	Linoleic acid metabolism (ko00591); alpha-Linolenic acid metabolism (ko00592)
BnaA08g25320D	4.87E-06	Infinity	up	CC: cell wall (GO:0005618); BP: plant-type cell wall organization (GO:0009664); MF: hydrolase activity, acting on ester bonds (GO:0016788); CC: cytoplasmic part (GO:0044444); BP: pectin metabolic process (GO:0045488);	Pentose and glucuronate interconversions (ko00040); Starch and sucrose metabolism (ko00500)
BnaA08g26310D	8.80E-04	Infinity	up	MF: carboxylic ester hydrolase activity (GO:0004091); CC: extracellular region (GO:0005576);	--
BnaA08g27230D	2.64E-13	4.8401428	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975);	--
BnaA08g29710D	9.41E-05	4.0301762	up	MF: sugar:proton symporter activity (GO:0005351); CC: plasma membrane (GO:0005886); CC: integral component of membrane (GO:0016021); BP: carbohydrate transmembrane transport (GO:0034219);	--
BnaA08g31530D	7.47E-06	3.0428552	up	MF: aminoacyl-tRNA editing activity (GO:0002161); MF: valine-tRNA ligase activity (GO:0004832); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: valyl-tRNA aminoacylation (GO:0006438); BP: regulation of translational fidelity (GO:0006450); CC: chloroplast (GO:0009507); BP: embryo development ending in seed dormancy (GO:0009793);	Aminoacyl-tRNA biosynthesis (ko00970)
BnaA09g02350D	1.65E-07	4.2004776	up	CC: plasma membrane (GO:0005886);	--
BnaA09g02760D	5.76E-04	4.4568915	up	MF: 1-pyrroline-5-carboxylate dehydrogenase activity (GO:0003842); MF: proline dehydrogenase activity (GO:0004657); CC: mitochondrion (GO:0005739); BP: glutamate biosynthetic process (GO:0006537); BP: proline catabolic process (GO:0006562); BP: response to oxidative stress (GO:0006979); BP: response to water deprivation (GO:0009414); BP: defense response to bacterium (GO:0042742); BP: oxidation-reduction process (GO:0051114);	Arginine and proline metabolism (ko00330)
BnaA09g05300D	1.90E-04	Infinity	up	BP: pollination (GO:0009856); CC: cytoplasmic membrane-bounded vesicle (GO:0016023);	--

BnaA09g06740D	7.41E-11	Infinity	up	CC: nucleus (GO:0005634);	--
BnaA09g15210D	4.31E-06	2.4651363	up	MF: carboxylic ester hydrolase activity (GO:0004091); CC: extracellular region (GO:0005576); CC: mitochondrion (GO:0005739); BP: intra-Golgi vesicle-mediated transport (GO:0006891); BP: membrane fusion (GO:0006944); CC: integral component of membrane (GO:0016021); MF: transferase activity, transferring acyl groups (GO:0016746);	--
BnaA09g22810D	1.20E-04	4.6047376	up	MF: DNA binding (GO:0003677); MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); BP: anthocyanin-containing compound biosynthetic process (GO:0009718); BP: response to sucrose (GO:0009744); BP: regulation of flavonoid biosynthetic process (GO:0009962); BP: trichome differentiation (GO:0010026); BP: response to UV-B (GO:0010224); MF: protein dimerization activity (GO:0046983); BP: regulation of proanthocyanidin biosynthetic process (GO:2000029);	--
BnaA09g26320D	3.94E-09	2.8302778	up	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); BP: regulation of transcription, DNA-templated (GO:0006355); MF: sequence-specific DNA binding (GO:0043565);	--
BnaA09g28210D	9.34E-12	Infinity	up	MF: monooxygenase activity (GO:0004497); MF: iron ion binding (GO:0005506); MF: electron carrier activity (GO:0009055); MF: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO:0016705); MF: oxygen binding (GO:0019825); MF: heme binding (GO:0020037); BP: oxidation-reduction process (GO:0055114);	Cutin, suberine and wax biosynthesis (ko00073)
BnaA09g39720D	2.89E-11	5.2425741	up	MF: enzyme inhibitor activity (GO:0004857); CC: extracellular region (GO:0005576); CC: plant-type cell wall (GO:0009505); MF: pectinesterase activity (GO:0030599); BP: cell wall modification (GO:0042545); BP: negative regulation of catalytic activity (GO:0043086); MF: aspartyl esterase activity (GO:0045330); BP: pectin catabolic process (GO:0045490); CC: pollen tube (GO:0090406);	--
BnaA09g41060D	1.01E-07	Infinity	up	BP: mitotic cell cycle (GO:0000278); BP: nuclear division (GO:0000280); BP: double-strand break repair via homologous recombination (GO:0000724); BP: cytokinesis by cell plate formation (GO:0000911); MF: chromatin binding (GO:0003682); MF: ubiquitin-protein transferase activity (GO:0004842); CC: nucleus (GO:0005634); BP: DNA replication initiation (GO:0006270); BP: regulation of DNA replication (GO:0006275); BP: nucleolus organization (GO:0007000); MF: zinc ion binding (GO:0008270); BP: cell proliferation (GO:0008283); MF: methyl-CpG binding (GO:0008327); BP: pollen development (GO:0009555); CC: chromocenter	--

				(GO:0010369); MF: double-stranded methylated DNA binding (GO:0010385); BP: DNA methylation on cytosine within a CG sequence (GO:0010424); MF: methyl-CpNpG binding (GO:0010428); MF: methyl-CpNpN binding (GO:0010429); BP: somatic cell DNA recombination (GO:0016444); BP: protein ubiquitination (GO:0016567); BP: histone phosphorylation (GO:0016572); BP: gene silencing by RNA (GO:0031047); BP: pericentric heterochromatin assembly (GO:0031508); MF: histone binding (GO:0042393); BP: histone H3-K9 methylation (GO:0051567); BP: regulation of cell cycle (GO:0051726); BP: positive regulation of methylation-dependent chromatin silencing (GO:0090309); MF: copper ion binding (GO:0005507); MF: electron carrier activity (GO:0009055); CC: anchored component of membrane (GO:0031225); CC: extracellular region (GO:0005576); MF: growth factor activity (GO:0008083); BP: cell proliferation (GO:0008283); CC: signal peptidase complex (GO:0005787); BP: signal peptide processing (GO:0006465); MF: peptidase activity (GO:0008233); CC: integral component of membrane (GO:0016021); BP: sterol biosynthetic process (GO:0016126); BP: sphingoid biosynthetic process (GO:0046520); MF: GTP binding (GO:0005525); CC: mitochondrion (GO:0005739); CC: Golgi apparatus (GO:0005794); BP: intra-Golgi vesicle-mediated transport (GO:0006891); BP: membrane fusion (GO:0006944); BP: small GTPase mediated signal transduction (GO:0007264); BP: plant-type cell wall modification (GO:0009827); BP: pollen tube growth (GO:0009860); BP: protein transport (GO:0015031); MF: tyrosine decarboxylase activity (GO:0004837); CC: cytoplasm (GO:0005737); BP: L-phenylalanine catabolic process (GO:0006559); BP: response to wounding (GO:0009611); MF: pyridoxal phosphate binding (GO:0030170); MF: phenylacetaldehyde synthase activity (GO:1990055); MF: DNA binding (GO:0003677); MF: chromatin binding (GO:0003682); MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); BP: protein targeting to membrane (GO:0006612); BP: response to salt stress (GO:0009651); BP: response to ethylene (GO:0009723); BP: response to auxin (GO:0009733); BP: response to abscisic acid (GO:0009737); BP: response to gibberellin (GO:0009739); BP: response to salicylic acid (GO:0009751); BP: response to jasmonic acid (GO:0009753); BP: positive regulation of flavonoid biosynthetic process (GO:0009963); BP: regulation of plant-type hypersensitive response (GO:0010363); BP: response to	
BnaA09g41740D	5.64E-04	Infinity	up		--
BnaA09g42260D	5.00E-04	Infinity	up		--
BnaA09g42640D	2.98E-04	-2.707231	down		Protein export (ko03060)
BnaA09g42740D	1.14E-05	4.9324265	up		--
BnaA09g43800D	5.96E-26	6.919077	up		Tyrosine metabolism (ko00350); Isoquinoline alkaloid biosynthesis (ko00950)
BnaA09g44370D	4.81E-16	-3.020588	down		--

				cadmium ion (GO:0046686);	
BnaA09g44770D	1.19E-08	Infinity	up	--	Aminoacyl-tRNA biosynthesis (ko00970)
BnaA09g45300D	1.96E-32	-6.136143	down	MF: serine-type carboxypeptidase activity (GO:0004185); CC: extracellular region (GO:0005576); CC: vacuole (GO:0005773); BP: proteolysis (GO:0006508);	--
BnaA09g45310D	1.32E-04	2.2568262	up	--	--
BnaA09g45320D	3.17E-52	-8.450896	down	MF: copper ion binding (GO:0005507); MF: calmodulin binding (GO:0005516); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: gluconeogenesis (GO:0006094); BP: glycolytic process (GO:0006096); BP: protein folding (GO:0006457); BP: tryptophan catabolic process (GO:0006569); BP: response to heat (GO:0009408); BP: response to cold (GO:0009409); CC: chloroplast thylakoid membrane (GO:0009535); CC: chloroplast stroma (GO:0009570); BP: response to high light intensity (GO:0009644); BP: response to salt stress (GO:0009651); BP: chloroplast organization (GO:0009658); BP: indoleacetic acid biosynthetic process (GO:0009684); CC: chloroplast envelope (GO:0009941); BP: isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway (GO:0019288); BP: cysteine biosynthetic process (GO:0019344); BP: response to endoplasmic reticulum stress (GO:0034976); BP: response to hydrogen peroxide (GO:0042542); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: ovule development (GO:0048481); MF: chaperone binding (GO:0051087); BP: positive regulation of superoxide dismutase activity (GO:1901671);	--
BnaA09g45380D	2.30E-09	-Infinity	down	CC: cytoplasm (GO:0005737); CC: plasma membrane (GO:0005886); BP: response to oxidative stress (GO:0006979);	--
BnaA09g45610D	1.36E-08	3.4292133	up	CC: nucleus (GO:0005634);	--
BnaA09g46070D	4.54E-04	Infinity	up	--	--
BnaA09g46080D	5.89E-04	-3.213456	down	CC: nucleus (GO:0005634);	--
BnaA09g46290D	3.41E-06	6.6743761	up	--	--
BnaA09g48300D	2.22E-05	-2.794932	down	BP: pseudouridine synthesis (GO:0001522); MF: RNA binding (GO:0003723); CC: nucleus (GO:0005634); BP: tRNA processing (GO:0008033); MF: pseudouridine synthase activity (GO:0009982); BP: methylglyoxal catabolic process to D-lactate (GO:0019243);	--
BnaA09g48320D	1.24E-38	-7.856119	down	MF: structural constituent of ribosome (GO:0003735); CC: nucleolus (GO:0005730); BP: translation (GO:0006412); CC: chloroplast (GO:0009507); CC: cytosolic large ribosomal subunit (GO:0022625); BP: response to stimulus (GO:0050896);	Ribosome (ko03010)
BnaA09g49480D	7.37E-18	-6.222013	down	--	--
BnaA09g56660D	1.91E-08	2.3265315	up	CC: nucleus (GO:0005634); CC: SCF ubiquitin ligase complex (GO:0019005); BP: negative regulation of cytokinin-	--

				activated signaling pathway (GO:0080037);	
BnaA10g01390D	1.16E-10	4.337315	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975);	--
BnaA10g13920D	2.14E-07	6.227751	up	BP: cellular process (GO:0009987); MF: oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor (GO:0016620); BP: single-organism metabolic process (GO:0044710);	Cutin, suberine and wax biosynthesis (ko00073); Peroxisome (ko04146)
BnaA10g20480D	2.57E-06	-3.262036	down	MF: nucleotide binding (GO:0000166); MF: RNA binding (GO:0003723); CC: nucleus (GO:0005634);	Spliceosome (ko03040)
BnaA10g22750D	2.75E-05	3.3613442	up	CC: intracellular (GO:0005622);	--
BnaA10g23870D	4.58E-07	4.3140466	up	CC: extracellular region (GO:0005576); CC: plant-type cell wall (GO:0009505); BP: plant-type cell wall modification (GO:0009827); BP: pollen tube growth (GO:0009860); MF: pectinesterase activity (GO:0030599); MF: aspartyl esterase activity (GO:0045330);	--
BnaA10g23970D	6.94E-09	Infinity	up	CC: extracellular region (GO:0005576); MF: lipid binding (GO:0008289); BP: plant-type cell wall modification (GO:0009827); BP: pollen hydration (GO:0009859); BP: pollen tube growth (GO:0009860); CC: monolayer-surrounded lipid storage body (GO:0012511); CC: integral component of membrane (GO:0016021); BP: lipid storage (GO:0019915); BP: sexual reproduction (GO:0019953); BP: recognition of pollen (GO:0048544); CC: pollen coat (GO:0070505);	--
BnaAnng07590D	2.75E-05	5.9971573	up	MF: sucrose alpha-glucosidase activity (GO:0004575); CC: extracellular region (GO:0005576); CC: cell wall (GO:0005618); BP: starch metabolic process (GO:0005982); BP: sucrose catabolic process (GO:0005987); BP: plant-type cell wall modification (GO:0009827); BP: pollen tube growth (GO:0009860); BP: actin filament-based movement (GO:0030048); BP: nectar secretion (GO:0071836);	Galactose metabolism (ko00052); Starch and sucrose metabolism (ko00500)
BnaAnng13710D	4.82E-08	5.6074668	up	CC: extracellular region (GO:0005576); CC: plant-type cell wall (GO:0009505); BP: plant-type cell wall modification (GO:0009827); BP: pollen tube growth (GO:0009860); MF: pectinesterase activity (GO:0030599); MF: aspartyl esterase activity (GO:0045330);	--
BnaAnng13790D	2.28E-11	5.4926253	up	--	--
BnaAnng14640D	7.60E-12	2.294983	up	MF: GTP binding (GO:0005525); CC: nucleus (GO:0005634); CC: cytosol (GO:0005829);	Ribosome biogenesis in eukaryotes (ko03008)
BnaAnng18730D	4.38E-07	-3.440621	down	MF: serine-type endopeptidase activity (GO:0004252); BP: proteolysis (GO:0006508); CC: plant-type cell wall (GO:0009505); MF: identical protein binding (GO:0042802); BP: negative regulation of catalytic activity (GO:0043086); CC: apoplast (GO:0048046); BP: mucilage metabolic process involved in seed coat development (GO:0048359); BP: mucilage extrusion from seed coat (GO:0080001);	--



BnaAnng22470D	8.07E-04	7.2193846	up	MF: carboxylic ester hydrolase activity (GO:0004091); CC: extracellular region (GO:0005576); BP: lipid metabolic process (GO:0006629); MF: lipase activity (GO:0016298);	--
BnaAnng29660D	2.50E-09	#NAME?	down	MF: DNA binding (GO:0003677); MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); CC: cytoplasm (GO:0005737); BP: regulation of transcription, DNA-templated (GO:0006355); BP: response to salt stress (GO:0009651); BP: response to chitin (GO:0010200); BP: regulation of response to water deprivation (GO:2000070);	--
BnaAnng30260D	1.10E-32	3.3123447	up	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: response to xenobiotic stimulus (GO:0009410); BP: response to ethylene (GO:0009723); BP: hormone-mediated signaling pathway (GO:0009755); BP: endoplasmic reticulum unfolded protein response (GO:0030968); BP: positive regulation of transcription, DNA-templated (GO:0045893); MF: protein heterodimerization activity (GO:0046982); BP: positive regulation of seed maturation (GO:2000693);	--
BnaC01g02500D	9.43E-30	6.6261157	up	--	--
BnaC01g12930D	2.60E-19	12.728327	up	MF: serine-type endopeptidase activity (GO:0004252); CC: extracellular region (GO:0005576); BP: proteolysis (GO:0006508); CC: plant-type cell wall (GO:0009505); MF: identical protein binding (GO:0042802); BP: negative regulation of catalytic activity (GO:0043086);	--
BnaC01g14160D	2.87E-05	Infinity	up	CC: plasma membrane (GO:0005886);	--
BnaC01g16500D	2.42E-05	3.6595853	up	CC: vacuole (GO:0005773); CC: chloroplast (GO:0009507); MF: pectinesterase activity (GO:0030599); BP: negative regulation of catalytic activity (GO:0043086); MF: pectinesterase inhibitor activity (GO:0046910); CC: apoplast (GO:0048046);	--
BnaC01g36890D	7.14E-06	5.3564613	up	MF: protein serine/threonine phosphatase activity (GO:0004722); CC: endosome (GO:0005768); CC: Golgi apparatus (GO:0005794); CC: trans-Golgi network (GO:0005802); BP: calcium ion transport (GO:0006816); BP: cellular zinc ion homeostasis (GO:0006882); BP: response to nematode (GO:0009624);	--
BnaC01g37680D	9.18E-11	5.7187688	up	MF: copper ion binding (GO:0005507); CC: extracellular region (GO:0005576); BP: plant-type cell wall modification (GO:0009827); MF: oxidoreductase activity (GO:0016491); BP: oxidation-reduction process (GO:0055114);	--
BnaC01g39620D	3.71E-11	7.1042301	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975); CC: plant-type cell wall (GO:0009505); BP: plant-type cell wall modification (GO:0009827); BP: pollen tube growth (GO:0009860);	--
BnaC01g43270D	1.03E-06	4.6529042	up	MF: magnesium ion binding (GO:0000287); MF: adenosylmethionine-8-amino-7-oxononanoate transaminase	Biotin metabolism (ko00780)

				activity (GO:0004015); MF: dethiobiotin synthase activity (GO:0004141); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); BP: DNA replication initiation (GO:0006270); BP: regulation of DNA replication (GO:0006275); BP: DNA methylation (GO:0006306); BP: cell proliferation (GO:0008283); BP: biotin biosynthetic process (GO:0009102); MF: pyridoxal phosphate binding (GO:0030170); BP: histone H3-K9 methylation (GO:0051567); BP: regulation of cell cycle (GO:0051726); CC: cytoplasm (GO:0005737);	--
BnaC02g06440D	1.26E-12	-2.594987	down		
BnaC02g06570D	4.74E-12	-6.399624	down	BP: maltose metabolic process (GO:0000023); MF: enzyme inhibitor activity (GO:0004857); CC: cytosol (GO:0005829); BP: pentose-phosphate shunt (GO:0006098); BP: regulation of carbohydrate metabolic process (GO:0006109); BP: glycerol ether metabolic process (GO:0006662); MF: enzyme activator activity (GO:0008047); MF: electron carrier activity (GO:0009055); CC: chloroplast thylakoid (GO:0009534); CC: chloroplast stroma (GO:0009570); MF: protein disulfide oxidoreductase activity (GO:0015035); BP: starch biosynthetic process (GO:0019252); BP: isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway (GO:0019288); BP: glucosinolate metabolic process (GO:0019760); BP: electron transport chain (GO:0022900); BP: positive regulation of catalytic activity (GO:0043085); BP: negative regulation of catalytic activity (GO:0043086); BP: cell redox homeostasis (GO:0045454); MF: monooxygenase activity (GO:0004497); MF: copper ion binding (GO:0005507); BP: response to cold (GO:0009409); CC: chloroplast thylakoid membrane (GO:0009535); CC: chloroplast ribulose biphosphate carboxylase complex (GO:0009573); BP: response to blue light (GO:0009637); BP: photorespiration (GO:0009853); CC: chloroplast envelope (GO:0009941); BP: response to red light (GO:0010114); BP: response to far red light (GO:0010218); BP: carbon fixation (GO:0015977); BP: photosynthesis (GO:0015979); MF: ribulose-bisphosphate carboxylase activity (GO:0016984); CC: cytosolic ribosome (GO:0022626); CC: thylakoid lumen (GO:0031977); CC: apoplast (GO:0048046); BP: oxidation-reduction process (GO:0055114); BP: chloroplast ribulose biphosphate carboxylase complex biogenesis (GO:0080158);	--
BnaC02g17140D	1.03E-07	6.1821862	up		Glyoxylate and dicarboxylate metabolism (ko00630); Carbon fixation in photosynthetic organisms (ko00710); Carbon metabolism (ko01200)
BnaC02g19120D	4.68E-04	Infinity	up	--	--
BnaC02g38360D	5.71E-10	Infinity	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975); BP: plant-type cell wall modification (GO:0009827);	--
BnaC02g43450D	7.07E-05	3.1452391	up	MF: calcium ion binding (GO:0005509); MF: calcium-dependent phospholipid binding (GO:0005544); CC: nucleus	--

				(GO:0005634); CC: cytosol (GO:0005829); BP: acetyl-CoA metabolic process (GO:0006084); BP: response to heat (GO:0009408); BP: response to cold (GO:0009409); BP: response to water deprivation (GO:0009414); CC: chloroplast (GO:0009507); CC: thylakoid (GO:0009579); BP: response to salt stress (GO:0009651); CC: cell surface (GO:0009986); BP: polysaccharide transport (GO:0015774); BP: sterol biosynthetic process (GO:0016126); BP: brassinosteroid biosynthetic process (GO:0016132); CC: apoplast (GO:0048046);	
BnaC02g48530D	3.20E-04	Infinity	up	CC: extracellular region (GO:0005576);	--
BnaC03g09190D	2.43E-05	-4.083684	down	--	--
BnaC03g18930D	7.56E-05	2.4286251	up	CC: chloroplast thylakoid membrane (GO:0009535); CC: photosystem I reaction center (GO:0009538); CC: chloroplast envelope (GO:0009941); CC: plastoglobule (GO:0010287); BP: photosynthesis (GO:0015979); BP: cysteine biosynthetic process (GO:0019344);	Photosynthesis (ko00195)
BnaC03g19830D	1.44E-06	3.099261	up	--	--
BnaC03g20530D	7.93E-04	2.7751629	up	MF: peroxidase activity (GO:0004601); CC: extracellular region (GO:0005576); CC: cytosol (GO:0005829); BP: response to oxidative stress (GO:0006979); MF: heme binding (GO:0020037); MF: metal ion binding (GO:0046872); BP: defense response to fungus (GO:0050832); BP: oxidation-reduction process (GO:0055114); CC: integral component of plasma membrane (GO:0005887); BP: carbohydrate transport (GO:0008643); MF: sugar transmembrane transporter activity (GO:0051119);	Phenylalanine metabolism (ko00360); Phenylpropanoid biosynthesis (ko00940)
BnaC03g21870D	4.22E-09	Infinity	up	CC: nucleus (GO:0005634);	--
BnaC03g23820D	5.32E-09	2.956973	up		Taurine and hypotaurine metabolism (ko00430)
BnaC03g23910D	3.23E-05	Infinity	up	--	--
BnaC03g32550D	8.13E-06	4.335782	up	CC: extracellular region (GO:0005576); CC: plasma membrane (GO:0005886); BP: plant-type cell wall modification (GO:0009827); MF: pectate lyase activity (GO:0030570);	Pentose and glucuronate interconversions (ko00040)
BnaC03g35490D	2.17E-05	3.6663128	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975); CC: plant-type cell wall (GO:0009505); BP: plant-type cell wall modification (GO:0009827); BP: pollen tube growth (GO:0009860); BP: rejection of self pollen (GO:0060320);	--
BnaC03g37350D	1.48E-10	Infinity	up		--
BnaC03g37910D	4.98E-07	4.168808	up	MF: copper ion binding (GO:0005507); CC: extracellular region (GO:0005576); BP: plant-type cell wall modification (GO:0009827); MF: oxidoreductase activity (GO:0016491); BP: oxidation-reduction process (GO:0055114);	--
BnaC03g38460D	4.31E-06	7.9453294	up	CC: extracellular region (GO:0005576); CC: nucleus (GO:0005634); CC: endosome (GO:0005768); CC: vacuolar membrane (GO:0005774); CC: Golgi apparatus (GO:0005794); CC: trans-Golgi network (GO:0005802); CC: plasma membrane	Pentose and glucuronate interconversions (ko00040); Starch and sucrose metabolism (ko00500)

				(GO:0005886); CC: plant-type cell wall (GO:0009505); CC: plasmodesma (GO:0009506); BP: response to nitrate (GO:0010167); BP: nitrate transport (GO:0015706); MF: pectinesterase activity (GO:0030599); BP: cell wall modification (GO:0042545); BP: negative regulation of catalytic activity (GO:0043086); MF: aspartyl esterase activity (GO:0045330); BP: pectin catabolic process (GO:0045490); MF: pectinesterase inhibitor activity (GO:0046910); CC: nucleus (GO:0005634); CC: endoplasmic reticulum (GO:0005783); MF: hydrolase activity (GO:0016787); CC: chloroplast (GO:0009507);	--
BnaC03g53130D	5.29E-09	4.8653303	up		--
BnaC03g57080D	6.36E-06	3.1872771	up		--
BnaC03g72420D	6.53E-10	4.4881229	up	CC: extracellular region (GO:0005576); CC: plant-type cell wall (GO:0009505); CC: plasmodesma (GO:0009506); BP: pollen tube growth (GO:0009860); MF: pectinesterase activity (GO:0030599); CC: pollen tube (GO:0090406);	--
BnaC03g76550D	1.29E-09	Infinity	up	CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975); MF: lyase activity (GO:0016829); MF: carbohydrate binding (GO:0030246);	--
BnaC04g00460D	1.72E-08	4.1396092	up	CC: extracellular region (GO:0005576); CC: plant-type cell wall (GO:0009505); CC: plasmodesma (GO:0009506); BP: pollen tube growth (GO:0009860); MF: pectinesterase activity (GO:0030599); CC: pollen tube (GO:0090406);	--
BnaC04g04310D	9.34E-07	4.8353441	up	MF: monooxygenase activity (GO:0004497); MF: iron ion binding (GO:0005506); CC: extracellular region (GO:0005576); MF: electron carrier activity (GO:0009055); MF: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO:0016705); MF: oxygen binding (GO:0019825); MF: heme binding (GO:0020037); BP: oxidation-reduction process (GO:0055114);	--
BnaC04g10370D	8.76E-21	-7.716762	down	MF: protein kinase activity (GO:0004672); BP: phosphorylation (GO:0016310);	--
BnaC04g18950D	6.53E-10	Infinity	up	MF: nucleotide binding (GO:0000166); CC: chloroplast (GO:0009507); BP: negative regulation of flavonoid biosynthetic process (GO:0009964); MF: anthocyanidin reductase activity (GO:0033729); BP: cellular metabolic process (GO:0044237); MF: coenzyme binding (GO:0050662); BP: oxidation-reduction process (GO:0055114);	Flavonoid biosynthesis (ko00941)
BnaC04g21470D	2.88E-18	3.870417	up	MF: enzyme inhibitor activity (GO:0004857); CC: extracellular region (GO:0005576); CC: plant-type cell wall (GO:0009505); MF: pectinesterase activity (GO:0030599); BP: cell wall modification (GO:0042545); BP: negative regulation of catalytic activity (GO:0043086); MF: aspartyl esterase activity (GO:0045330); BP: pectin catabolic process (GO:0045490); CC: pollen tube (GO:0090406);	--
BnaC04g28880D	5.34E-08	4.3466773	up	CC: mitochondrion (GO:0005739); CC: integral component of membrane (GO:0016021);	Peroxisome (ko04146)

BnaC04g29170D	5.60E-05	10.397916	up	MF: cysteine-type endopeptidase activity (GO:0004197); CC: extracellular space (GO:0005615); BP: proteolysis (GO:0006508); BP: vacuolar protein processing (GO:0006624); CC: chloroplast (GO:0009507); BP: gibberellin biosynthetic process (GO:0009686); BP: response to abscisic acid (GO:0009737); BP: gibberellic acid mediated signaling pathway (GO:0009740); BP: embryo development ending in seed dormancy (GO:0009793); BP: seed germination (GO:0009845); BP: seed dormancy process (GO:0010162); BP: seed coat development (GO:0010214); BP: programmed cell death (GO:0012501);	--
BnaC04g29730D	1.48E-10	Infinity	up	CC: cytosol (GO:0005829); BP: response to wounding (GO:0009611); BP: response to salicylic acid (GO:0009751); MF: 12-oxophytodienoate reductase activity (GO:0016629); BP: oxylipin metabolic process (GO:0031407); BP: response to cadmium ion (GO:0046686);	alpha-Linolenic acid metabolism (ko00592)
BnaC04g36880D	6.62E-05	Infinity	up	CC: anchored component of membrane (GO:0031225);	--
BnaC04g39120D	2.31E-11	-2.26584	down	BP: putrescine biosynthetic process (GO:0009446); MF: N-carbamoylputrescine amidase activity (GO:0050126);	Arginine and proline metabolism (ko00330)
BnaC04g40110D	1.98E-04	6.7904842	up	BP: para-aminobenzoic acid biosynthetic process (GO:0008153); CC: chloroplast (GO:0009507); BP: embryo development ending in seed dormancy (GO:0009793); MF: oxo-acid-lyase activity (GO:0016833); BP: chorismate metabolic process (GO:0046417); BP: folic acid biosynthetic process (GO:0046656); MF: 4-amino-4-deoxychorismate synthase activity (GO:0046820);	Folate biosynthesis (ko00790)
BnaC04g55640D	9.39E-07	3.6138378	up	--	--
BnaC05g15230D	2.72E-19	8.2961846	up	CC: nucleus (GO:0005634); CC: cytoplasm (GO:0005737); BP: protein targeting to membrane (GO:0006612); BP: response to water deprivation (GO:0009414); BP: response to wounding (GO:0009611); BP: response to fungus (GO:0009620); BP: jasmonic acid biosynthetic process (GO:0009695); BP: response to ethylene (GO:0009723); BP: response to auxin (GO:0009733); BP: abscisic acid-activated signaling pathway (GO:0009738); BP: salicylic acid mediated signaling pathway (GO:0009863); BP: jasmonic acid mediated signaling pathway (GO:0009867); BP: regulation of plant-type hypersensitive response (GO:0010363); MF: jasmonate O-methyltransferase activity (GO:0030795); BP: oxylipin biosynthetic process (GO:0031408); BP: methylation (GO:0032259); BP: hyperosmotic salinity response (GO:0042538);	alpha-Linolenic acid metabolism (ko00592)
BnaC05g20990D	4.11E-16	Infinity	up	MF: monooxygenase activity (GO:0004497); MF: iron ion binding (GO:0005506); MF: electron carrier activity (GO:0009055); MF: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO:0016705); MF:	Cutin, suberine and wax biosynthesis (ko00073)

BnaC05g26860D	3.09E-09	-Infinity	down	oxygen binding (GO:0019825); MF: heme binding (GO:0020037); BP: oxidation-reduction process (GO:0055114); --	DNA replication (ko03030); Nucleotide excision repair (ko03420); Mismatch repair (ko03430); Homologous recombination (ko03440)
BnaC05g31880D	2.18E-19	10.844813	up	MF: cysteine-type endopeptidase activity (GO:0004197); CC: extracellular space (GO:0005615); BP: proteolysis (GO:0006508); BP: vacuolar protein processing (GO:0006624); CC: chloroplast (GO:0009507); BP: gibberellin biosynthetic process (GO:0009686); BP: response to abscisic acid (GO:0009737); BP: gibberellic acid mediated signaling pathway (GO:0009740); BP: embryo development ending in seed dormancy (GO:0009793); BP: seed germination (GO:0009845); BP: seed dormancy process (GO:0010162); BP: seed coat development (GO:0010214); BP: programmed cell death (GO:0012501);	--
BnaC05g39970D	2.18E-10	5.6619634	up	MF: copper ion binding (GO:0005507); CC: extracellular region (GO:0005576); BP: plant-type cell wall modification (GO:0009827); MF: oxidoreductase activity (GO:0016491); BP: oxidation-reduction process (GO:0055114);	--
BnaC05g46160D	1.23E-06	Infinity	up	MF: epoxide hydrolase activity (GO:0004301); CC: cytoplasm (GO:0005737); BP: metabolic process (GO:0008152);	--
BnaC06g07110D	2.45E-08	3.3782835	up	--	--
BnaC06g14120D	6.80E-07	4.4897048	up	CC: nucleus (GO:0005634); CC: cytosol (GO:0005829); BP: response to mechanical stimulus (GO:0009612); BP: response to parasitic fungus (GO:0009623); BP: defense response, incompatible interaction (GO:0009814); CC: endomembrane system (GO:0012505); MF: kinase activity (GO:0016301); BP: calcium-mediated signaling (GO:0019722); MF: GTPase binding (GO:0051020); BP: cellular response to ethylene stimulus (GO:0071369);	--
BnaC06g16950D	4.53E-09	3.1627956	up	--	--
BnaC06g17050D	6.08E-04	3.8276382	up	CC: plasma membrane (GO:0005886); BP: drug transmembrane transport (GO:0006855); BP: purine nucleobase transport (GO:0006863); CC: plant-type vacuole membrane (GO:0009705); BP: proanthocyanidin biosynthetic process (GO:0010023); BP: maintenance of seed dormancy (GO:0010231); MF: drug transmembrane transporter activity (GO:0015238); MF: solute:proton antiporter activity (GO:0015299);	--
BnaC06g20860D	1.29E-05	Infinity	up	--	--
BnaC06g23520D	1.35E-05	2.3913937	up	BP: maltose metabolic process (GO:0000023); MF: phosphoethanolamine N-methyltransferase activity (GO:0000234); CC: cytoplasm (GO:0005737); BP: phosphatidylcholine	Glycerophospholipid metabolism (ko00564)

BnaC06g34870D	2.58E-04	Infinity	up	<p> biosynthetic process (GO:0006656); BP: starch biosynthetic process (GO:0019252); BP: methylation (GO:0032259); BP: response to hypoxia (GO:0001666); CC: extracellular region (GO:0005576); CC: vacuolar membrane (GO:0005774); CC: Golgi apparatus (GO:0005794); CC: cytosol (GO:0005829); CC: plasma membrane (GO:0005886); BP: amino acid transport (GO:0006865); MF: starch synthase activity (GO:0009011); CC: plant-type cell wall (GO:0009505); CC: plasmodesma (GO:0009506); CC: chloroplast (GO:0009507); BP: response to wounding (GO:0009611); BP: response to jasmonic acid (GO:0009753); BP: amylopectin biosynthetic process (GO:0010021); BP: response to nitrate (GO:0010167); BP: organ senescence (GO:0010260); BP: myo-inositol hexakisphosphate biosynthetic process (GO:0010264); BP: nitrate transport (GO:0015706); MF: strictosidine synthase activity (GO:0016844); BP: galactolipid biosynthetic process (GO:0019375); </p>	--
BnaC06g42000D	1.05E-13	3.2564549	up	--	--
BnaC07g23000D	5.32E-10	4.3150585	up	<p> MF: magnesium ion binding (GO:0000287); MF: protein binding (GO:0005515); CC: chloroplast (GO:0009507); MF: sesquiterpene synthase activity (GO:0010334); BP: monoterpene biosynthetic process (GO:0016099); MF: (R)-limonene synthase activity (GO:0034002); MF: (E)-beta-ocimene synthase activity (GO:0034768); BP: monoterpene biosynthetic process (GO:0043693); MF: pinene synthase activity (GO:0050550); MF: myrcene synthase activity (GO:0050551); MF: (4S)-limonene synthase activity (GO:0050552); MF: sabinene synthase activity (GO:0080015); </p>	--
BnaC07g31470D	7.35E-04	Infinity	up	<p> MF: ATP binding (GO:0005524); CC: endoplasmic reticulum (GO:0005783); CC: plasma membrane (GO:0005886); BP: ATP catabolic process (GO:0006200); BP: positive regulation of triglyceride biosynthetic process (GO:0010867); BP: triglyceride transport (GO:0034197); MF: ATPase activity, coupled to transmembrane movement of substances (GO:0042626); BP: seed morphogenesis (GO:0048317); MF: protein binding (GO:0005515); CC: nucleus (GO:0005634); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: response to auxin (GO:0009733); BP: systemic acquired resistance, salicylic acid mediated signaling pathway (GO:0009862); BP: defense response to bacterium (GO:0042742); MF: ADP binding (GO:0043531); </p>	--
BnaC07g33980D	4.31E-11	3.1306228	up	<p> MF: protein binding (GO:0005515); CC: nucleus (GO:0005634); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: response to auxin (GO:0009733); BP: systemic acquired resistance, salicylic acid mediated signaling pathway (GO:0009862); BP: defense response to bacterium (GO:0042742); MF: ADP binding (GO:0043531); </p>	--
BnaC07g36960D	9.78E-10	3.5926346	up	--	--
BnaC07g37670D	2.88E-05	3.4172659	up	<p> CC: cytoplasm (GO:0005737); BP: vacuole organization (GO:0007033); BP: response to wounding (GO:0009611); BP: anthocyanin-containing compound biosynthetic process (GO:0009718); BP: response to jasmonic acid (GO:0009753); BP: proanthocyanidin biosynthetic process </p>	Flavonoid biosynthesis (ko00941)

BnaC07g47120D	1.59E-04	Infinity	up	(GO:0010023); MF: leucocyanidin oxygenase activity (GO:0050589); BP: oxidation-reduction process (GO:0055114); MF: monooxygenase activity (GO:0004497); MF: iron ion binding (GO:0005506); CC: extracellular region (GO:0005576); MF: electron carrier activity (GO:0009055); BP: gibberellin biosynthetic process (GO:0009686); BP: gibberellic acid mediated signaling pathway (GO:0009740); MF: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO:0016705); MF: oxygen binding (GO:0019825); MF: heme binding (GO:0020037); BP: oxidation-reduction process (GO:0055114); MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975); BP: plant-type cell wall modification (GO:0009827); CC: mitochondrion (GO:0005739); BP: fatty acid biosynthetic process (GO:0006633); CC: integral component of membrane (GO:0016021); MF: 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:0016717); BP: oxidation-reduction process (GO:0055114); MF: catalytic activity (GO:0003824); CC: extracellular region (GO:0005576); BP: metabolic process (GO:0008152);	--
BnaC07g49180D	1.89E-06	4.1564722	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975); BP: plant-type cell wall modification (GO:0009827); CC: mitochondrion (GO:0005739); BP: fatty acid biosynthetic process (GO:0006633); CC: integral component of membrane (GO:0016021); MF: 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:0016717); BP: oxidation-reduction process (GO:0055114); MF: catalytic activity (GO:0003824); CC: extracellular region (GO:0005576); BP: metabolic process (GO:0008152);	--
BnaC08g01790D	6.94E-09	4.3863905	up	MF: 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:0016717); BP: oxidation-reduction process (GO:0055114); MF: catalytic activity (GO:0003824); CC: extracellular region (GO:0005576); BP: metabolic process (GO:0008152);	Biosynthesis of unsaturated fatty acids (ko01040); Fatty acid metabolism (ko01212)
BnaC08g05370D	8.58E-04	4.4536753	up	MF: catalytic activity (GO:0003824); CC: extracellular region (GO:0005576); BP: metabolic process (GO:0008152);	--
BnaC08g11820D	5.57E-05	-3.34022	down	--	--
BnaC08g12180D	2.88E-05	2.5269488	up	MF: S-adenosylmethionine-dependent methyltransferase activity (GO:0008757); MF: gibberellin carboxyl-O-methyltransferase activity (GO:0010341);	--
BnaC08g13870D	8.52E-04	8.4261444	up	CC: plasma membrane (GO:0005886); BP: cellulose microfibril organization (GO:0010215); BP: cell growth (GO:0016049); CC: anchored component of membrane (GO:0031225);	--
BnaC08g17160D	7.10E-04	7.0497994	up	MF: monooxygenase activity (GO:0004497); MF: iron ion binding (GO:0005506); CC: mitochondrion (GO:0005739); MF: electron carrier activity (GO:0009055); BP: response to light stimulus (GO:0009416); BP: unidimensional cell growth (GO:0009826); BP: brassinosteroid biosynthetic process (GO:0016132); MF: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO:0016705); MF: oxygen binding (GO:0019825); MF: heme binding (GO:0020037); BP: oxidation-reduction process (GO:0055114); MF: brassinosteroid binding (GO:0090411);	--
BnaC08g24820D	9.78E-10	Infinity	up	CC: integral component of plasma membrane (GO:0005887); BP: carbohydrate transport (GO:0008643); MF: sugar transmembrane transporter activity (GO:0051119);	--
BnaC08g29060D	2.71E-13	-Infinity	down	BP: RNA splicing, via endonucleolytic cleavage and ligation (GO:0000394); MF: inositol hexakisphosphate binding	--



				(GO:0000822); BP: response to molecule of bacterial origin (GO:0002237); MF: ubiquitin-protein transferase activity (GO:0004842); CC: nucleus (GO:0005634); CC: vacuolar membrane (GO:0005774); BP: methionine biosynthetic process (GO:0009086); BP: auxin-activated signaling pathway (GO:0009734); MF: auxin binding (GO:0010011); BP: stomatal complex morphogenesis (GO:0010103); BP: pollen maturation (GO:0010152); BP: protein ubiquitination (GO:0016567); BP: stamen development (GO:0048443); BP: lateral root development (GO:0048527); BP: photoperiodism, flowering (GO:0048573); BP: cellular response to nitrate (GO:0071249); BP: primary root development (GO:0080022); MF: 6-phosphofructokinase activity (GO:0003872); MF: ATP binding (GO:0005524); CC: 6-phosphofructokinase complex (GO:0005945); BP: fructose 6-phosphate metabolic process (GO:0006002); BP: gluconeogenesis (GO:0006094); BP: glycolytic process (GO:0006096); BP: cytoskeleton organization (GO:0007010); CC: chloroplast (GO:0009507); BP: proteasomal protein catabolic process (GO:0010498); BP: phosphorylation (GO:0016310);	
BnaC08g35040D	1.50E-09	Infinity	up		Glycolysis / Gluconeogenesis (ko00010); Pentose phosphate pathway (ko00030); Fructose and mannose metabolism (ko00051); Galactose metabolism (ko00052); Carbon metabolism (ko01200); Biosynthesis of amino acids (ko01230); RNA degradation (ko03018)
BnaC08g35060D	1.33E-05	-3.201124	down	--	--
BnaC08g35720D	2.96E-18	Infinity	up	CC: vacuolar proton-transporting V-type ATPase, V0 domain (GO:0000220); CC: mitochondrion (GO:0005739); CC: Golgi apparatus (GO:0005794); BP: ATP catabolic process (GO:0006200); CC: chloroplast (GO:0009507); MF: hydrogen-translocating pyrophosphatase activity (GO:0009678); CC: plant-type vacuole membrane (GO:0009705); MF: hydrogen ion transmembrane transporter activity (GO:0015078); BP: ATP synthesis coupled proton transport (GO:0015986); BP: ATP hydrolysis coupled proton transport (GO:0015991); MF: ATPase activity (GO:0016887); BP: cellular response to nutrient levels (GO:0031669); BP: sequestering of zinc ion (GO:0032119); BP: vacuolar sequestering (GO:0043181); MF: nutrient reservoir activity (GO:0045735); BP: vacuolar proton-transporting V-type ATPase complex assembly (GO:0070072); BP: cellular response to salt stress (GO:0071472); MF: microtubule motor activity (GO:0003777); MF: ATP binding (GO:0005524); CC: cytoplasm (GO:0005737); CC: kinesin complex (GO:0005871); CC: microtubule (GO:0005874); CC: plasma membrane (GO:0005886); BP: microtubule-based movement (GO:0007018); MF: microtubule binding (GO:0008017); CC: plasmodesma (GO:0009506);	Oxidative phosphorylation (ko00190); Phagosome (ko04145)
BnaC08g35850D	8.98E-13	4.7076131	up		--
BnaC08g36200D	1.19E-55	-10.0625	down	CC: chloroplast (GO:0009507); BP: photorespiration (GO:0009853); MF: tyrosine decarboxylase activity	--
BnaC08g36370D	1.50E-09	4.7925796	up		Tyrosine metabolism

				(GO:0004837); CC: cytoplasm (GO:0005737); BP: L-phenylalanine catabolic process (GO:0006559); BP: response to wounding (GO:0009611); MF: pyridoxal phosphate binding (GO:0030170); MF: phenylacetaldehyde synthase activity (GO:1990055); BP: mitotic cell cycle (GO:0000278); MF: RNA binding (GO:0003723); MF: polynucleotide adenylyltransferase activity (GO:0004652); MF: protein binding (GO:0005515); CC: nucleus (GO:0005634); BP: transcription, DNA-templated (GO:0006351); BP: RNA polyadenylation (GO:0043631); MF: nucleotide binding (GO:0000166); BP: mRNA splicing, via spliceosome (GO:0000398); MF: RNA binding (GO:0003723); MF: protein binding (GO:0005515); CC: nucleolus (GO:0005730); BP: sugar mediated signaling pathway (GO:0010182); CC: nuclear speck (GO:0016607); CC: cytosol (GO:0005829); CC: plasmodesma (GO:0009506);	(ko00350); Isoquinoline alkaloid biosynthesis (ko00950)
BnaC08g37460D	1.01E-09	-6.793547	down		mRNA surveillance pathway (ko03015)
BnaC08g38300D	6.51E-09	-Infinity	down		RNA transport (ko03013); mRNA surveillance pathway (ko03015)
BnaC08g39020D	1.03E-13	Infinity	up		Endocytosis (ko04144)
BnaC08g39120D	5.75E-12	Infinity	up	--	--
BnaC08g39130D	1.40E-39	Infinity	up	MF: copper ion binding (GO:0005507); MF: calmodulin binding (GO:0005516); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: gluconeogenesis (GO:0006094); BP: glycolytic process (GO:0006096); BP: protein folding (GO:0006457); BP: tryptophan catabolic process (GO:0006569); BP: response to heat (GO:0009408); BP: response to cold (GO:0009409); CC: chloroplast thylakoid membrane (GO:0009535); CC: chloroplast stroma (GO:0009570); BP: response to high light intensity (GO:0009644); BP: response to salt stress (GO:0009651); BP: chloroplast organization (GO:0009658); BP: indoleacetic acid biosynthetic process (GO:0009684); CC: chloroplast envelope (GO:0009941); BP: isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway (GO:0019288); BP: cysteine biosynthetic process (GO:0019344); BP: response to endoplasmic reticulum stress (GO:0034976); BP: response to hydrogen peroxide (GO:0042542); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: ovule development (GO:0048481); MF: chaperone binding (GO:0051087); BP: positive regulation of superoxide dismutase activity (GO:1901671);	--
BnaC08g39360D	1.72E-09	2.9027755	up	MF: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553); CC: cell wall (GO:0005618); BP: cellular glucan metabolic process (GO:0006073); BP: phloem or xylem histogenesis (GO:0010087); BP: fruit development (GO:0010154); MF: xyloglucan:xyloglucosyl transferase activity (GO:0016762); CC: apoplast (GO:0048046); BP: stamen filament development (GO:0080086);	--

BnaC08g39990D	5.45E-07	2.6788586	up	BP: MAPK cascade (GO:0000165); MF: protein serine/threonine kinase activity (GO:0004674); MF: protein serine/threonine/tyrosine kinase activity (GO:0004712); MF: ATP binding (GO:0005524); CC: nucleus (GO:0005634); CC: cytosol (GO:0005829); BP: protein phosphorylation (GO:0006468); BP: protein targeting to membrane (GO:0006612); BP: response to cold (GO:0009409); BP: response to water deprivation (GO:0009414); BP: response to ethylene (GO:0009723); BP: auxin-activated signaling pathway (GO:0009734); BP: abscisic acid-activated signaling pathway (GO:0009738); BP: brassinosteroid mediated signaling pathway (GO:0009742); BP: systemic acquired resistance, salicylic acid mediated signaling pathway (GO:0009862); BP: jasmonic acid mediated signaling pathway (GO:0009867); BP: regulation of signal transduction (GO:0009966); BP: leaf vascular tissue pattern formation (GO:0010305); BP: regulation of plant-type hypersensitive response (GO:0010363); BP: endoplasmic reticulum unfolded protein response (GO:0030968); BP: negative regulation of defense response (GO:0031348); BP: hyperosmotic salinity response (GO:0042538); BP: negative regulation of programmed cell death (GO:0043069); BP: defense response to fungus (GO:0050832);	--
BnaC08g40040D	2.78E-06	-Infinity	down	MF: acid phosphatase activity (GO:0003993); MF: protein serine/threonine phosphatase activity (GO:0004722); CC: extracellular region (GO:0005576); CC: mitochondrion (GO:0005739); CC: endosome (GO:0005768); CC: Golgi apparatus (GO:0005794); CC: trans-Golgi network (GO:0005802); BP: regulation of carbohydrate metabolic process (GO:0006109); CC: chloroplast (GO:0009507); MF: metal ion binding (GO:0046872);	--
BnaC08g40320D	1.04E-12	6.0055506	up	MF: chromatin binding (GO:0003682); MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); BP: membrane fusion (GO:0006944); MF: identical protein binding (GO:0042802); MF: sequence-specific DNA binding (GO:0043565); BP: Golgi vesicle transport (GO:0048193);	--
BnaC08g40330D	9.40E-11	2.3370095	up	MF: glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity (GO:0004365); MF: copper ion binding (GO:0005507); CC: nucleus (GO:0005634); CC: mitochondrial envelope (GO:0005740); CC: vacuolar membrane (GO:0005774); CC: Golgi apparatus (GO:0005794); CC: cytosol (GO:0005829); CC: plasma membrane (GO:0005886); BP: gluconeogenesis (GO:0006094); BP: glycolytic process (GO:0006096); BP: pentose-phosphate shunt (GO:0006098); BP: water transport	Glycolysis / Gluconeogenesis (ko00010); Carbon fixation in photosynthetic organisms (ko00710); Carbon metabolism (ko01200); Biosynthesis of amino acids (ko01230)

				(GO:0006833); BP: hyperosmotic response (GO:0006972); BP: cytoskeleton organization (GO:0007010); BP: Golgi organization (GO:0007030); MF: glyceraldehyde-3-phosphate dehydrogenase (NADP+) (non-phosphorylating) activity (GO:0008886); BP: aerobic respiration (GO:0009060); BP: response to heat (GO:0009408); CC: chloroplast (GO:0009507); BP: response to salt stress (GO:0009651); BP: response to sucrose (GO:0009744); BP: proteasomal protein catabolic process (GO:0010498); BP: response to endoplasmic reticulum stress (GO:0034976); BP: response to hydrogen peroxide (GO:0042542); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: seed development (GO:0048316); MF: NADP binding (GO:0050661); MF: NAD binding (GO:0051287); BP: response to redox state (GO:0051775);	
BnaC08g40410D	2.20E-12	7.2892187	up	MF: Ran GTPase activator activity (GO:0005098); CC: nuclear envelope (GO:0005635); CC: vacuolar membrane (GO:0005774); CC: endoplasmic reticulum (GO:0005783); BP: nucleocytoplasmic transport (GO:0006913); BP: toxin catabolic process (GO:0009407); CC: chloroplast (GO:0009507); BP: photomorphogenesis (GO:0009640); BP: response to salt stress (GO:0009651); BP: cullin deneddylation (GO:0010388); BP: lateral root development (GO:0048527); MF: protein serine/threonine kinase activity (GO:0004674); BP: protein autophosphorylation (GO:0046777); CC: plant-type vacuole (GO:0000325); MF: sucrose alpha-glucosidase activity (GO:0004575); BP: carbohydrate metabolic process (GO:0005975); BP: polyamine catabolic process (GO:0006598); BP: calcium ion transport (GO:0006816); BP: iron ion transport (GO:0006826); BP: Golgi organization (GO:0007030); CC: plant-type cell wall (GO:0009505); BP: response to wounding (GO:0009611); BP: response to bacterium (GO:0009617); BP: response to salt stress (GO:0009651); BP: coumarin biosynthetic process (GO:0009805); BP: cellular response to iron ion starvation (GO:0010106); BP: response to nitrate (GO:0010167); BP: nitrate transport (GO:0015706); BP: brassinosteroid biosynthetic process (GO:0016132); BP: cellular modified amino acid biosynthetic process (GO:0042398); BP: cellular response to gibberellin stimulus (GO:0071370); BP: primary root development (GO:0080022); MF: N,N-dimethylaniline monooxygenase activity (GO:0004499); CC: nucleus (GO:0005634); BP: glucosinolate biosynthetic process (GO:0019761); MF: flavin adenine dinucleotide binding (GO:0050660); MF: NADP binding (GO:0050661); BP: oxidation-reduction process (GO:0055114); MF: 8-methylthiopropyl glucosinolate S-oxygenase activity (GO:0080107);	RNA transport (ko03013)
BnaC08g40810D	7.48E-05	2.2353034	up		--
BnaC08g41390D	1.47E-08	-6.502945	down		Galactose metabolism (ko00052); Starch and sucrose metabolism (ko00500)
BnaC08g41540D	1.17E-12	-8.147759	down		--

BnaC08g41720D	1.46E-11	-7.465454	down	MF: aspartic-type endopeptidase activity (GO:0004190); CC: extracellular region (GO:0005576); CC: vacuole (GO:0005773); CC: cytosol (GO:0005829); BP: glycolytic process (GO:0006096); BP: proteolysis (GO:0006508); BP: protein targeting to vacuole (GO:0006623); BP: lipid metabolic process (GO:0006629); BP: water transport (GO:0006833); BP: hyperosmotic response (GO:0006972); BP: Golgi organization (GO:0007030); BP: response to temperature stimulus (GO:0009266); CC: plasmodesma (GO:0009506); BP: response to salt stress (GO:0009651); BP: response to cadmium ion (GO:0046686); BP: organ development (GO:0048513);	--
BnaC08g41790D	1.05E-07	-Infinity	down	MF: aminomethyltransferase activity (GO:0004047); CC: mitochondrion (GO:0005739); BP: glycine catabolic process (GO:0006546); BP: pattern specification process (GO:0007389); BP: regulation of cell size (GO:0008361); MF: transaminase activity (GO:0008483); CC: chloroplast thylakoid (GO:0009534); CC: chloroplast stroma (GO:0009570); BP: chloroplast organization (GO:0009658); BP: auxin polar transport (GO:0009926); CC: chloroplast envelope (GO:0009941); BP: root morphogenesis (GO:0010015); BP: regulation of meristem growth (GO:0010075); CC: membrane (GO:0016020); BP: carotenoid biosynthetic process (GO:0016117); BP: cysteine biosynthetic process (GO:0019344); CC: cytosolic ribosome (GO:0022626); BP: methylation (GO:0032259); BP: hydrogen peroxide catabolic process (GO:0042744); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: ovule development (GO:0048481);	Glycine, serine and threonine metabolism (ko00260); One carbon pool by folate (ko00670); Carbon metabolism (ko01200)
BnaC08g42280D	8.17E-07	-Infinity	down	BP: telomere maintenance (GO:0000723); BP: double-strand break repair via homologous recombination (GO:0000724); MF: nucleic acid binding (GO:0003676); MF: ATP binding (GO:0005524); CC: nucleus (GO:0005634); BP: DNA replication (GO:0006260); CC: plasmodesma (GO:0009506); BP: vegetative to reproductive phase transition of meristem (GO:0010228); MF: ATP-dependent 3'-5' DNA helicase activity (GO:0043140); BP: cellular response to cold (GO:0070417); BP: cellular response to abscisic acid stimulus (GO:0071215);	Homologous recombination (ko03440)
BnaC08g42450D	1.53E-22	-5.511391	down	BP: response to molecule of bacterial origin (GO:0002237); MF: protein serine/threonine kinase activity (GO:0004674); MF: ATP binding (GO:0005524); CC: plasma membrane (GO:0005886); BP: N-terminal protein myristoylation (GO:0006499); BP: protein targeting to membrane (GO:0006612); BP: membrane fusion (GO:0006944); BP: response to oxidative stress (GO:0006979); BP: transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169); BP: systemic acquired resistance (GO:0009627); BP: seed	--

				germination (GO:0009845); BP: stomatal complex morphogenesis (GO:0010103); BP: regulation of plant-type hypersensitive response (GO:0010363); CC: integral component of membrane (GO:0016021); BP: negative regulation of programmed cell death (GO:0043069); BP: protein autophosphorylation (GO:0046777); BP: stamen development (GO:0048443); CC: micropyle (GO:0070825);	
BnaC08g49500D	7.07E-08	7.657125	up	CC: chloroplast (GO:0009507); BP: systemic acquired resistance (GO:0009627); BP: regulation of defense response (GO:0031347);	--
BnaC08g49610D	6.52E-18	-8.430044	down	MF: protein binding (GO:0005515); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); BP: starch catabolic process (GO:0005983); BP: circadian rhythm (GO:0007623); CC: chloroplast stroma (GO:0009570); BP: response to symbiotic fungus (GO:0009610); BP: cold acclimation (GO:0009631); CC: chloroplast envelope (GO:0009941); BP: phosphorylation (GO:0016310); BP: starch biosynthetic process (GO:0019252); MF: alpha-glucan, water dikinase activity (GO:0050521);	--
BnaC08g49940D	1.46E-11	-Infinity	down	CC: nucleus (GO:0005634);	--
BnaC09g05960D	6.63E-12	Infinity	up	MF: DNA binding (GO:0003677); CC: nucleus (GO:0005634);	--
BnaC09g06220D	1.03E-11	6.3386161	up	CC: plasma membrane (GO:0005886); CC: chloroplast (GO:0009507);	--
BnaC09g06260D	3.75E-04	Infinity	up	CC: nucleus (GO:0005634);	--
BnaC09g17150D	6.19E-04	2.1278744	up	MF: nucleotide binding (GO:0000166); BP: anthocyanin-containing compound biosynthetic process (GO:0009718); BP: response to sucrose (GO:0009744); BP: response to UV-B (GO:0010224); CC: extrinsic component of endoplasmic reticulum membrane (GO:0042406); BP: cellular metabolic process (GO:0044237); MF: dihydrokaempferol 4-reductase activity (GO:0045552); MF: coenzyme binding (GO:0050662);	Flavonoid biosynthesis (ko00941)
BnaC09g22220D	6.39E-04	Infinity	up	MF: cysteine-type endopeptidase inhibitor activity (GO:0004869); CC: cell wall (GO:0005618); BP: negative regulation of peptidase activity (GO:0010466);	--
BnaC09g34450D	9.73E-06	Infinity	up	MF: serine-type endopeptidase activity (GO:0004252); CC: cell wall (GO:0005618); CC: nucleus (GO:0005634); CC: cytoplasm (GO:0005737); BP: proteolysis (GO:0006508); BP: iron ion transport (GO:0006826); BP: cellular response to iron ion starvation (GO:0010106); BP: response to nitrate (GO:0010167); BP: nitrate transport (GO:0015706); BP: brassinosteroid biosynthetic process (GO:0016132); MF: identical protein binding (GO:0042802); BP: negative regulation of catalytic activity (GO:0043086); CC: apoplast (GO:0048046); BP: petal development (GO:0048441); BP: stamen development (GO:0048443);	--
BnaC09g50070D	6.28E-06	-2.185252	down	--	--

BnaC09g54770D	3.86E-08	3.8702678	up	MF: Rab GDP-dissociation inhibitor activity (GO:0005093); CC: cytoplasm (GO:0005737); BP: N-terminal protein myristoylation (GO:0006499); BP: protein transport (GO:0015031); CC: apoplast (GO:0048046);	--
BnaCnng03410D	2.07E-09	5.520551	up	MF: nucleotide binding (GO:0000166); MF: oxidoreductase activity (GO:0016491); BP: oxidation-reduction process (GO:0055114);	--
BnaCnng05770D	7.14E-06	3.705064	up	CC: extracellular region (GO:0005576); CC: plasma membrane (GO:0005886); BP: plant-type cell wall modification (GO:0009827); MF: pectate lyase activity (GO:0030570);	Pentose and glucuronate interconversions (ko00040)
BnaCnng09890D	1.32E-04	9.3407279	up	CC: lytic vacuole within protein storage vacuole (GO:0000327); MF: protein disulfide isomerase activity (GO:0003756); MF: protein binding (GO:0005515); CC: vacuolar membrane (GO:0005774); CC: endoplasmic reticulum (GO:0005783); CC: Golgi apparatus (GO:0005794); CC: plasma membrane (GO:0005886); BP: protein folding (GO:0006457); BP: glycerol ether metabolic process (GO:0006662); MF: electron carrier activity (GO:0009055); BP: response to heat (GO:0009408); CC: plant-type cell wall (GO:0009505); CC: chloroplast (GO:0009507); CC: thylakoid (GO:0009579); BP: systemic acquired resistance (GO:0009627); BP: response to high light intensity (GO:0009644); BP: response to salt stress (GO:0009651); BP: embryo development (GO:0009790); BP: response to zinc ion (GO:0010043); MF: protein disulfide oxidoreductase activity (GO:0015035); BP: response to endoplasmic reticulum stress (GO:0034976); BP: response to hydrogen peroxide (GO:0042542); BP: regulation of programmed cell death (GO:0043067); BP: cell redox homeostasis (GO:0045454); BP: response to cadmium ion (GO:0046686); BP: seed development (GO:0048316);	Protein processing in endoplasmic reticulum (ko04141)
BnaCnng17490D	7.42E-07	2.2433099	up	--	--
BnaCnng23190D	3.65E-07	-2.527136	down	BP: response to cold (GO:0009409); BP: response to light stimulus (GO:0009416); CC: chloroplast thylakoid membrane (GO:0009535); CC: chloroplast stroma (GO:0009570); BP: response to sucrose (GO:0009744); CC: chloroplast envelope (GO:0009941); BP: cellular process (GO:0009987); CC: stromule (GO:0010319); BP: single-organism transport (GO:0044765);	--
BnaCnng24040D	1.46E-13	5.5974175	up	MF: protein binding (GO:0005515); CC: cytosol (GO:0005829); BP: glycolytic process (GO:0006096); BP: tricarboxylic acid cycle (GO:0006099); BP: iron ion transport (GO:0006826); BP: water transport (GO:0006833); BP: hyperosmotic response (GO:0006972); BP: Golgi organization (GO:0007030); MF: phosphoenolpyruvate carboxylase activity (GO:0008964); BP: response to temperature stimulus (GO:0009266); BP: response to salt stress (GO:0009651); BP: response to sucrose (GO:0009744); BP:	Pyruvate metabolism (ko00620); Carbon fixation in photosynthetic organisms (ko00710); Carbon metabolism (ko01200)

				response to glucose (GO:0009749); BP: response to fructose (GO:0009750); BP: cellular response to iron ion starvation (GO:0010106); BP: response to nitrate (GO:0010167); BP: nitrate transport (GO:0015706); BP: carbon fixation (GO:0015977); BP: cellular response to phosphate starvation (GO:0016036); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: protein tetramerization (GO:0051262);	
BnaCnng36050D	1.85E-12	3.9763785	up	--	--
BnaCnng37660D	2.26E-04	Infinity	up	BP: lipid transport (GO:0006869); MF: lipid binding (GO:0008289);	--
BnaCnng40360D	1.24E-04	Infinity	up	--	--
BnaCnng46610D	8.25E-12	5.3399753	up	CC: peroxisome (GO:0005777); MF: oxidoreductase activity (GO:0016491); BP: oxidation-reduction process (GO:0055114); MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975);	--
BnaCnng48740D	1.72E-07	4.1441046	up	CC: nucleosome (GO:0000786); MF: DNA binding (GO:0003677); CC: nucleus (GO:0005634); BP: glucose catabolic process (GO:0006007); BP: nucleosome assembly (GO:0006334); BP: protein targeting (GO:0006605); MF: protein heterodimerization activity (GO:0046982);	--
BnaCnng58100D	5.89E-04	-2.504215	down	BP: metabolic process (GO:0008152); MF: hydrolase activity (GO:0016787);	--
BnaCnng66860D	6.81E-07	-2.284207	down	BP: transcription, DNA-templated (GO:0006351); BP: RNA processing (GO:0006396); BP: translational initiation (GO:0006413); BP: post-embryonic development (GO:0009791); BP: posttranscriptional regulation of gene expression (GO:0010608); CC: macromolecular complex (GO:0032991); BP: macromolecule localization (GO:0033036); CC: cytoplasmic part (GO:0044444); BP: single-organism developmental process (GO:0044767); BP: reproductive structure development (GO:0048608); BP: cellular response to organic substance (GO:0071310); BP: regulation of primary metabolic process (GO:0080090); BP: regulation of cellular macromolecule biosynthetic process (GO:2000112);	RNA transport (ko03013)
BnaCnng68410D	2.06E-11	5.5200274	up	MF: polygalacturonase activity (GO:0004650); CC: extracellular region (GO:0005576); BP: carbohydrate metabolic process (GO:0005975);	--
BnaCnng73190D	1.10E-09	6.8087671	up	CC: vacuolar proton-transporting V-type ATPase, V0 domain (GO:0000220); CC: mitochondrion (GO:0005739); CC: Golgi apparatus (GO:0005794); BP: ATP catabolic process (GO:0006200); CC: chloroplast (GO:0009507); MF: hydrogen-translocating pyrophosphatase activity (GO:0009678); CC: plant-type vacuole membrane (GO:0009705); MF: hydrogen ion transmembrane transporter activity (GO:0015078); BP: ATP synthesis coupled proton transport (GO:0015986); BP: ATP hydrolysis coupled proton transport (GO:0015991); MF: ATPase activity (GO:0016887); BP: cellular response to	--
BnaCnng75420D	4.77E-17	Infinity	up		Oxidative phosphorylation (ko00190); Phagosome (ko04145)



				nutrient levels (GO:0031669); BP: sequestering of zinc ion (GO:0032119); BP: vacuolar sequestering (GO:0043181); MF: nutrient reservoir activity (GO:0045735); BP: vacuolar proton-transporting V-type ATPase complex assembly (GO:0070072); BP: cellular response to salt stress (GO:0071472); CC: extracellular region (GO:0005576); CC: plant-type cell wall (GO:0009505); CC: plasmodesma (GO:0009506); BP: pollen tube growth (GO:0009860); MF: pectinesterase activity (GO:0030599); CC: pollen tube (GO:0090406);	
BnaCnng76410D	1.55E-14	4.5731057	up		--
Cole_newGene_1389	2.26E-05	-2.484461	down	--	--
Cole_newGene_1596	1.12E-06	-Infinity	down	--	--
Cole_newGene_1717	6.96E-06	-5.429251	down	MF: binding (GO:0005488);	--
Cole_newGene_1891	8.16E-13	2.1417662	up	--	--
Cole_newGene_1975	9.78E-10	Infinity	up	--	--
Cole_newGene_1983	8.75E-10	-Infinity	down	CC: mitochondrion (GO:0005739); CC: chloroplast stroma (GO:0009570); BP: mRNA modification (GO:0016556); MF: carbon-nitrogen ligase activity, with glutamine as amido-N-donor (GO:0016884);	Aminoacyl-tRNA biosynthesis (ko00970)
Cole_newGene_1984	2.64E-14	-Infinity	down	CC: plant-type vacuole (GO:0000325); CC: vacuolar membrane (GO:0005774); CC: chloroplast (GO:0009507); BP: response to salt stress (GO:0009651); BP: proton transport (GO:0015992); BP: CC organization (GO:0016043); MF: pyrophosphatase activity (GO:0016462); MF: transmembrane transporter activity (GO:0022857); BP: ion transmembrane transport (GO:0034220); BP: ATP metabolic process (GO:0046034); BP: maintenance of location (GO:0051235); BP: cellular localization (GO:0051641); BP: cellular response to stimulus (GO:0051716);	Oxidative phosphorylation (ko00190); Phagosome (ko04145)
Cole_newGene_2071	4.19E-61	-9.453508	down	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); MF: protein dimerization activity (GO:0046983);	--
Cole_newGene_2073	3.12E-65	Infinity	up	CC: intracellular membrane-bounded organelle (GO:0043231); CC: cytoplasmic part (GO:0044444);	Protein processing in endoplasmic reticulum (ko04141); Plant-pathogen interaction (ko04626)
Cole_newGene_2075	1.26E-17	5.1837421	up	--	--
Cole_newGene_2243	6.53E-10	-Infinity	down	CC: mitochondrion (GO:0005739); CC: Golgi apparatus (GO:0005794); CC: plasma membrane (GO:0005886); BP: response to stress (GO:0006950); CC: integral component of endoplasmic reticulum membrane (GO:0030176); BP: single-organism cellular process (GO:0044763);	Protein export (ko03060); Protein processing in endoplasmic reticulum (ko04141)
Cole_newGene_246	1.47E-08	Infinity	up	BP: microtubule cytoskeleton organization (GO:0000226); BP: cytokinesis by cell plate formation (GO:0000911); MF: binding (GO:0005488); MF: kinase activity (GO:0016301);	--
Cole_newGene_269	2.72E-36	3.9156555	up	--	--

Cole_newGene_2726	3.33E-10	6.9198993	up	--	--
Cole_newGene_3682	1.53E-08	-2.817597	down	--	--
Cole_newGene_3718	5.58E-05	3.7731727	up	--	--
Cole_newGene_4151	8.18E-97	-9.173574	down	--	--
Cole_newGene_4284	2.16E-07	-3.140581	down	--	--
Cole_newGene_4384	6.02E-20	Infinity	up	--	--
Cole_newGene_4855	2.50E-09	2.1296802	up	CC: nucleus (GO:0005634);	--
Cole_newGene_4860	3.18E-08	5.1905863	up	--	--
Cole_newGene_5149	1.27E-08	Infinity	up	--	--
Cole_newGene_5614	4.37E-06	Infinity	up	--	--
Cole_newGene_5961	6.11E-07	Infinity	up	--	--
Cole_newGene_628	8.71E-06	Infinity	up	--	--
Cole_newGene_6351	8.03E-04	2.4526006	up	MF: protein serine/threonine phosphatase activity (GO:0004722); CC: nucleus (GO:0005634); CC: cytoplasm (GO:0005737); BP: response to heat (GO:0009408); BP: blue light signaling pathway (GO:0009785);	--
Cole_newGene_6687	2.01E-05	Infinity	up	CC: cell wall (GO:0005618); CC: vacuole (GO:0005773); CC: endoplasmic reticulum (GO:0005783); CC: plasma membrane (GO:0005886); CC: plasmodesma (GO:0009506); MF: transmembrane transporter activity (GO:0022857); BP: transmembrane transport (GO:0055085);	--
Cole_newGene_7430	1.42E-05	Infinity	up	--	--
Cole_newGene_7507	2.17E-05	3.5129649	up	--	--
Cole_newGene_8277	6.36E-14	-4.716407	down	--	--
Cole_newGene_950	3.36E-05	Infinity	up	--	--

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**Table S3:** GO and KEGG annotation for the 77 stably line-specific DEGs

Gene ID	GO annotation	KEGG pathway
BnaA03g35870D	MF: guanylate kinase activity (GO:0004385); CC: cytoplasm (GO:0005737); BP: purine nucleotide metabolic process (GO:0006163); BP: response to chitin (GO:0010200); BP: phosphorylation (GO:0016310); BP: endoplasmic reticulum unfolded protein response (GO:0030968); BP: defense response to fungus (GO:0050832);	Purine metabolism (ko00230)
BnaA04g06410D	BP: heme biosynthetic process (GO:0006783); BP: response to oxidative stress (GO:0006979); MF: glutamyl-tRNA reductase activity (GO:0008883); CC: chloroplast (GO:0009507); BP: response to wounding (GO:0009611); BP: response to chitin (GO:0010200); BP: defense response by callose deposition (GO:0052542);	Porphyrin and chlorophyll metabolism (ko00860)
BnaA07g04500D	CC: mitochondrion (GO:0005739);	--
BnaA08g02930D	MF: nucleotide binding (GO:0000166); BP: endonucleolytic cleavage involved in rRNA processing (GO:0000478); BP: RNA methylation (GO:0001510); MF: nucleic acid binding (GO:0003676); CC: nucleolus (GO:0005730); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: pyrimidine ribonucleotide biosynthetic process (GO:0009220); BP: leaf vascular tissue pattern formation (GO:0010305); BP: cotyledon vascular tissue pattern formation (GO:0010588); BP: root development (GO:0048364); BP: leaf development (GO:0048366); BP: petal vascular tissue pattern formation (GO:0080056); BP: sepal vascular tissue pattern formation (GO:0080057);	--
BnaA09g06740D	CC: nucleus (GO:0005634);	--
BnaA09g26320D	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); BP: regulation of transcription, DNA-templated (GO:0006355); MF: sequence-specific DNA binding (GO:0043565);	--
BnaA09g44370D	MF: DNA binding (GO:0003677); MF: chromatin binding (GO:0003682); MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); BP: protein targeting to membrane (GO:0006612); BP: response to salt stress (GO:0009651); BP: response to ethylene (GO:0009723); BP: response to auxin (GO:0009733); BP: response to abscisic acid (GO:0009737); BP: response to gibberellin (GO:0009739); BP: response to salicylic acid (GO:0009751); BP: response to jasmonic acid (GO:0009753); BP: positive regulation of flavonoid biosynthetic process (GO:0009963); BP: regulation of plant-type hypersensitive response (GO:0010363); BP: response to cadmium ion (GO:0046686);	--
BnaA09g45300D	MF: serine-type carboxypeptidase activity (GO:0004185); CC: extracellular region (GO:0005576); CC: vacuole (GO:0005773); BP: proteolysis (GO:0006508);	--
BnaA09g45310D	--	--
BnaA09g45320D	MF: copper ion binding (GO:0005507); MF: calmodulin binding (GO:0005516); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: gluconeogenesis (GO:0006094); BP: glycolytic process (GO:0006096); BP: protein folding (GO:0006457); BP: tryptophan catabolic process (GO:0006569); BP: response to heat (GO:0009408); BP: response to cold (GO:0009409); CC: chloroplast thylakoid membrane (GO:0009535); CC: chloroplast stroma (GO:0009570); BP: response to high light intensity (GO:0009644); BP: response to salt stress (GO:0009651); BP: chloroplast organization (GO:0009658); BP: indoleacetic acid biosynthetic process (GO:0009684); CC: chloroplast envelope (GO:0009941); BP: isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway (GO:0019288); BP: cysteine biosynthetic process (GO:0019344); BP: response to endoplasmic reticulum stress (GO:0034976); BP: response to hydrogen peroxide (GO:0042542); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: ovule development (GO:0048481); MF: chaperone binding (GO:0051087); BP: positive regulation of superoxide dismutase activity (GO:1901671);	--
BnaA09g45610D	CC: nucleus (GO:0005634);	--
BnaA09g46080D	CC: nucleus (GO:0005634);	--
BnaA09g46290D	--	--

BnaA09g48320D	MF: structural constituent of ribosome (GO:0003735); CC: nucleolus (GO:0005730); BP: translation (GO:0006412); CC: chloroplast (GO:0009507); CC: cytosolic large ribosomal subunit (GO:0022625); BP: response to stimulus (GO:0050896);	Ribosome (ko03010)
BnaA09g49480D	--	--
BnaAnng13790D	--	--
BnaAnng30260D	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: response to xenobiotic stimulus (GO:0009410); BP: response to ethylene (GO:0009723); BP: hormone-mediated signaling pathway (GO:0009755); BP: endoplasmic reticulum unfolded protein response (GO:0030968); BP: positive regulation of transcription, DNA-templated (GO:0045893); MF: protein heterodimerization activity (GO:0046982); BP: positive regulation of seed maturation (GO:2000693);	--
BnaC01g02500D	--	--
BnaC01g43270D	MF: magnesium ion binding (GO:0000287); MF: adenosylmethionine-8-amino-7-oxononanoate transaminase activity (GO:0004015); MF: dethiobiotin synthase activity (GO:0004141); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); BP: DNA replication initiation (GO:0006270); BP: regulation of DNA replication (GO:0006275); BP: DNA methylation (GO:0006306); BP: cell proliferation (GO:0008283); BP: biotin biosynthetic process (GO:0009102); MF: pyridoxal phosphate binding (GO:0030170); BP: histone H3-K9 methylation (GO:0051567); BP: regulation of cell cycle (GO:0051726);	Biotin metabolism (ko00780)
BnaC02g06570D	BP: maltose metabolic process (GO:0000023); MF: enzyme inhibitor activity (GO:0004857); CC: cytosol (GO:0005829); BP: pentose-phosphate shunt (GO:0006098); BP: regulation of carbohydrate metabolic process (GO:0006109); BP: glycerol ether metabolic process (GO:0006662); MF: enzyme activator activity (GO:0008047); MF: electron carrier activity (GO:0009055); CC: chloroplast thylakoid (GO:0009534); CC: chloroplast stroma (GO:0009570); MF: protein disulfide oxidoreductase activity (GO:0015035); BP: starch biosynthetic process (GO:0019252); BP: isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway (GO:0019288); BP: glucosinolate metabolic process (GO:0019760); BP: electron transport chain (GO:0022900); BP: positive regulation of catalytic activity (GO:0043085); BP: negative regulation of catalytic activity (GO:0043086); BP: cell redox homeostasis (GO:0045454);	--
BnaC03g09190D	--	--
BnaC03g18930D	CC: chloroplast thylakoid membrane (GO:0009535); CC: photosystem I reaction center (GO:0009538); CC: chloroplast envelope (GO:0009941); CC: plastoglobule (GO:0010287); BP: photosynthesis (GO:0015979); BP: cysteine biosynthetic process (GO:0019344);	Photosynthesis (ko00195)
BnaC03g19830D	--	--
BnaC03g23820D	CC: nucleus (GO:0005634);	Taurine and hypotaurine metabolism (ko00430)
BnaC03g57080D	CC: chloroplast (GO:0009507);	--
BnaC04g10370D	MF: protein kinase activity (GO:0004672); BP: phosphorylation (GO:0016310);	--
BnaC04g29730D	CC: cytosol (GO:0005829); BP: response to wounding (GO:0009611); BP: response to salicylic acid (GO:0009751); MF: 12-oxophytodienoate reductase activity (GO:0016629); BP: oxylipin metabolic process (GO:0031407); BP: response to cadmium ion (GO:0046686);	alpha-Linolenic acid metabolism (ko00592)
BnaC04g39120D	BP: putrescine biosynthetic process (GO:0009446); MF: N-carbamoylputrescine amidase activity (GO:0050126);	Arginine and proline metabolism (ko00330)
BnaC05g26860D	--	DNA replication (ko03030); Nucleotide excision repair (ko03420); Mismatch repair (ko03430); Homologous recombination (ko03440)
BnaC06g07110D	--	--
BnaC06g16950D	--	--
BnaC06g42000D	--	--
BnaC07g33980D	MF: protein binding (GO:0005515); CC: nucleus (GO:0005634); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: response to auxin (GO:0009733); BP: systemic acquired resistance, salicylic acid	--

	mediated signaling pathway (GO:0009862); BP: defense response to bacterium (GO:0042742); MF: ADP binding (GO:0043531);	
BnaC07g36960D	--	--
BnaC08g29060D	BP: RNA splicing, via endonucleolytic cleavage and ligation (GO:0000394); MF: inositol hexakisphosphate binding (GO:0000822); BP: response to molecule of bacterial origin (GO:0002237); MF: ubiquitin-protein transferase activity (GO:0004842); CC: nucleus (GO:0005634); CC: vacuolar membrane (GO:0005774); BP: methionine biosynthetic process (GO:0009086); BP: auxin-activated signaling pathway (GO:0009734); MF: auxin binding (GO:0010011); BP: stomatal complex morphogenesis (GO:0010103); BP: pollen maturation (GO:0010152); BP: protein ubiquitination (GO:0016567); BP: stamen development (GO:0048443); BP: lateral root development (GO:0048527); BP: photoperiodism, flowering (GO:0048573); BP: cellular response to nitrate (GO:0071249); BP: primary root development (GO:0080022);	--
BnaC08g35720D	CC: vacuolar proton-transporting V-type ATPase, V0 domain (GO:0000220); CC: mitochondrion (GO:0005739); CC: Golgi apparatus (GO:0005794); BP: ATP catabolic process (GO:0006200); CC: chloroplast (GO:0009507); MF: hydrogen-translocating pyrophosphatase activity (GO:0009678); CC: plant-type vacuole membrane (GO:0009705); MF: hydrogen ion transmembrane transporter activity (GO:0015078); BP: ATP synthesis coupled proton transport (GO:0015986); BP: ATP hydrolysis coupled proton transport (GO:0015991); MF: ATPase activity (GO:0016887); BP: cellular response to nutrient levels (GO:0031669); BP: sequestering of zinc ion (GO:0032119); BP: vacuolar sequestering (GO:0043181); MF: nutrient reservoir activity (GO:0045735); BP: vacuolar proton-transporting V-type ATPase complex assembly (GO:0070072); BP: cellular response to salt stress (GO:0071472);	Oxidative phosphorylation (ko00190); Phagosome (ko04145)
BnaC08g35850D	MF: microtubule motor activity (GO:0003777); MF: ATP binding (GO:0005524); CC: cytoplasm (GO:0005737); CC: kinesin complex (GO:0005871); CC: microtubule (GO:0005874); CC: plasma membrane (GO:0005886); BP: microtubule-based movement (GO:0007018); MF: microtubule binding (GO:0008017); CC: plasmodesma (GO:0009506); CC: chloroplast (GO:0009507); BP: photorespiration (GO:0009853);	--
BnaC08g36200D		--
BnaC08g37460D	BP: mitotic cell cycle (GO:0000278); MF: RNA binding (GO:0003723); MF: polynucleotide adenyltransferase activity (GO:0004652); MF: protein binding (GO:0005515); CC: nucleus (GO:0005634); BP: transcription, DNA-templated (GO:0006351); BP: RNA polyadenylation (GO:0043631);	mRNA surveillance pathway (ko03015)
BnaC08g38300D	MF: nucleotide binding (GO:0000166); BP: mRNA splicing, via spliceosome (GO:0000398); MF: RNA binding (GO:0003723); MF: protein binding (GO:0005515); CC: nucleolus (GO:0005730); BP: sugar mediated signaling pathway (GO:0010182); CC: nuclear speck (GO:0016607); CC: cytosol (GO:0005829); CC: plasmodesma (GO:0009506);	RNA transport (ko03013); mRNA surveillance pathway (ko03015)
BnaC08g39020D		Endocytosis (ko04144)
BnaC08g39120D	--	--
BnaC08g39130D	MF: copper ion binding (GO:0005507); MF: calmodulin binding (GO:0005516); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); CC: cytosol (GO:0005829); BP: gluconeogenesis (GO:0006094); BP: glycolytic process (GO:0006096); BP: protein folding (GO:0006457); BP: tryptophan catabolic process (GO:0006569); BP: response to heat (GO:0009408); BP: response to cold (GO:0009409); CC: chloroplast thylakoid membrane (GO:0009535); CC: chloroplast stroma (GO:0009570); BP: response to high light intensity (GO:0009644); BP: response to salt stress (GO:0009651); BP: chloroplast organization (GO:0009658); BP: indoleacetic acid biosynthetic process (GO:0009684); CC: chloroplast envelope (GO:0009941); BP: isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway (GO:0019288); BP: cysteine biosynthetic process (GO:0019344); BP: response to endoplasmic reticulum stress (GO:0034976); BP: response to hydrogen peroxide (GO:0042542); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: ovule development (GO:0048481); MF: chaperone binding (GO:0051087); BP: positive regulation of superoxide dismutase activity (GO:1901671);	--
BnaC08g39360D	MF: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553); CC: cell wall (GO:0005618); BP: cellular glucan metabolic process (GO:0006073); BP: phloem or xylem histogenesis (GO:0010087); BP: fruit development (GO:0010154); MF: xyloglucan:xyloglucosyl transferase activity (GO:0016762); CC: apoplast (GO:0048046); BP: stamen filament development (GO:0080086);	--

BnaC08g39990D	BP: MAPK cascade (GO:0000165); MF: protein serine/threonine kinase activity (GO:0004674); MF: protein serine/threonine/tyrosine kinase activity (GO:0004712); MF: ATP binding (GO:0005524); CC: nucleus (GO:0005634); CC: cytosol (GO:0005829); BP: protein phosphorylation (GO:0006468); BP: protein targeting to membrane (GO:0006612); BP: response to cold (GO:0009409); BP: response to water deprivation (GO:0009414); BP: response to ethylene (GO:0009723); BP: auxin-activated signaling pathway (GO:0009734); BP: abscisic acid-activated signaling pathway (GO:0009738); BP: brassinosteroid mediated signaling pathway (GO:0009742); BP: systemic acquired resistance, salicylic acid mediated signaling pathway (GO:0009862); BP: jasmonic acid mediated signaling pathway (GO:0009867); BP: regulation of signal transduction (GO:0009966); BP: leaf vascular tissue pattern formation (GO:0010305); BP: regulation of plant-type hypersensitive response (GO:0010363); BP: endoplasmic reticulum unfolded protein response (GO:0030968); BP: negative regulation of defense response (GO:0031348); BP: hyperosmotic salinity response (GO:0042538); BP: negative regulation of programmed cell death (GO:0043069); BP: defense response to fungus (GO:0050832);	--
BnaC08g40040D	MF: acid phosphatase activity (GO:0003993); MF: protein serine/threonine phosphatase activity (GO:0004722); CC: extracellular region (GO:0005576); CC: mitochondrion (GO:0005739); CC: endosome (GO:0005768); CC: Golgi apparatus (GO:0005794); CC: trans-Golgi network (GO:0005802); BP: regulation of carbohydrate metabolic process (GO:0006109); CC: chloroplast (GO:0009507); MF: metal ion binding (GO:0046872);	--
BnaC08g40320D	MF: chromatin binding (GO:0003682); MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); BP: membrane fusion (GO:0006944); MF: identical protein binding (GO:0042802); MF: sequence-specific DNA binding (GO:0043565); BP: Golgi vesicle transport (GO:0048193);	--
BnaC08g40410D	MF: Ran GTPase activator activity (GO:0005098); CC: nuclear envelope (GO:0005635); CC: vacuolar membrane (GO:0005774); CC: endoplasmic reticulum (GO:0005783); BP: nucleocytoplasmic transport (GO:0006913); BP: toxin catabolic process (GO:0009407); CC: chloroplast (GO:0009507); BP: photomorphogenesis (GO:0009640); BP: response to salt stress (GO:0009651); BP: cullin deneddylation (GO:0010388); BP: lateral root development (GO:0048527);	RNA transport (ko03013)
BnaC08g40810D	MF: protein serine/threonine kinase activity (GO:0004674); BP: protein autophosphorylation (GO:0046777);	--
BnaC08g41390D	CC: plant-type vacuole (GO:0000325); MF: sucrose alpha-glucosidase activity (GO:0004575); BP: carbohydrate metabolic process (GO:0005975); BP: polyamine catabolic process (GO:0006598); BP: calcium ion transport (GO:0006816); BP: iron ion transport (GO:0006826); BP: Golgi organization (GO:0007030); CC: plant-type cell wall (GO:0009505); BP: response to wounding (GO:0009611); BP: response to bacterium (GO:0009617); BP: response to salt stress (GO:0009651); BP: coumarin biosynthetic process (GO:0009805); BP: cellular response to iron ion starvation (GO:0010106); BP: response to nitrate (GO:0010167); BP: nitrate transport (GO:0015706); BP: brassinosteroid biosynthetic process (GO:0016132); BP: cellular modified amino acid biosynthetic process (GO:0042398); BP: cellular response to gibberellin stimulus (GO:0071370); BP: primary root development (GO:0080022);	Galactose metabolism (ko00052); Starch and sucrose metabolism (ko00500)
BnaC08g41540D	MF: N,N-dimethylaniline monooxygenase activity (GO:0004499); CC: nucleus (GO:0005634); BP: glucosinolate biosynthetic process (GO:0019761); MF: flavin adenine dinucleotide binding (GO:0050660); MF: NADP binding (GO:0050661); BP: oxidation-reduction process (GO:0055114); MF: 8-methylthiopropyl glucosinolate S-oxygenase activity (GO:0080107);	--
BnaC08g41720D	MF: aspartic-type endopeptidase activity (GO:0004190); CC: extracellular region (GO:0005576); CC: vacuole (GO:0005773); CC: cytosol (GO:0005829); BP: glycolytic process (GO:0006096); BP: proteolysis (GO:0006508); BP: protein targeting to vacuole (GO:0006623); BP: lipid metabolic process (GO:0006629); BP: water transport (GO:0006833); BP: hyperosmotic response (GO:0006972); BP: Golgi organization (GO:0007030); BP: response to temperature stimulus (GO:0009266); CC: plasmodesma (GO:0009506); BP: response to salt stress (GO:0009651); BP: response to cadmium ion (GO:0046686); BP: organ development (GO:0048513);	--
BnaC08g42280D	BP: telomere maintenance (GO:0000723); BP: double-strand break repair via homologous recombination (GO:0000724); MF: nucleic acid binding	Homologous recombination (ko03440)

	(GO:0003676); MF: ATP binding (GO:0005524); CC: nucleus (GO:0005634); BP: DNA replication (GO:0006260); CC: plasmodesma (GO:0009506); BP: vegetative to reproductive phase transition of meristem (GO:0010228); MF: ATP-dependent 3'-5' DNA helicase activity (GO:0043140); BP: cellular response to cold (GO:0070417); BP: cellular response to abscisic acid stimulus (GO:0071215);	
BnaC08g42450D	BP: response to molecule of bacterial origin (GO:0002237); MF: protein serine/threonine kinase activity (GO:0004674); MF: ATP binding (GO:0005524); CC: plasma membrane (GO:0005886); BP: N-terminal protein myristoylation (GO:0006499); BP: protein targeting to membrane (GO:0006612); BP: membrane fusion (GO:0006944); BP: response to oxidative stress (GO:0006979); BP: transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169); BP: systemic acquired resistance (GO:0009627); BP: seed germination (GO:0009845); BP: stomatal complex morphogenesis (GO:0010103); BP: regulation of plant-type hypersensitive response (GO:0010363); CC: integral component of membrane (GO:0016021); BP: negative regulation of programmed cell death (GO:0043069); BP: protein autophosphorylation (GO:0046777); BP: stamen development (GO:0048443); CC: micropyle (GO:0070825);	--
BnaC08g49500D	CC: chloroplast (GO:0009507); BP: systemic acquired resistance (GO:0009627); BP: regulation of defense response (GO:0031347);	--
BnaC08g49610D	MF: protein binding (GO:0005515); MF: ATP binding (GO:0005524); CC: mitochondrion (GO:0005739); BP: starch catabolic process (GO:0005983); BP: circadian rhythm (GO:0007623); CC: chloroplast stroma (GO:0009570); BP: response to symbiotic fungus (GO:0009610); BP: cold acclimation (GO:0009631); CC: chloroplast envelope (GO:0009941); BP: phosphorylation (GO:0016310); BP: starch biosynthetic process (GO:0019252); MF: alpha-glucan, water dikinase activity (GO:0050521); CC: nucleus (GO:0005634);	--
BnaC08g49940D		--
BnaC09g05960D	MF: DNA binding (GO:0003677); CC: nucleus (GO:0005634);	--
BnaC09g06220D	CC: plasma membrane (GO:0005886); CC: chloroplast (GO:0009507);	--
BnaC09g06260D	CC: nucleus (GO:0005634);	--
BnaCnng17490D	--	--
BnaCnng23190D	BP: response to cold (GO:0009409); BP: response to light stimulus (GO:0009416); CC: chloroplast thylakoid membrane (GO:0009535); CC: chloroplast stroma (GO:0009570); BP: response to sucrose (GO:0009744); CC: chloroplast envelope (GO:0009941); BP: cellular process (GO:0009987); CC: stromule (GO:0010319); BP: single-organism transport (GO:0044765);	--
BnaCnng24040D	MF: protein binding (GO:0005515); CC: cytosol (GO:0005829); BP: glycolytic process (GO:0006096); BP: tricarboxylic acid cycle (GO:0006099); BP: iron ion transport (GO:0006826); BP: water transport (GO:0006833); BP: hyperosmotic response (GO:0006972); BP: Golgi organization (GO:0007030); MF: phosphoenolpyruvate carboxylase activity (GO:0008964); BP: response to temperature stimulus (GO:0009266); BP: response to salt stress (GO:0009651); BP: response to sucrose (GO:0009744); BP: response to glucose (GO:0009749); BP: response to fructose (GO:0009750); BP: cellular response to iron ion starvation (GO:0010106); BP: response to nitrate (GO:0010167); BP: nitrate transport (GO:0015706); BP: carbon fixation (GO:0015977); BP: cellular response to phosphate starvation (GO:0016036); BP: response to cadmium ion (GO:0046686); CC: apoplast (GO:0048046); BP: protein tetramerization (GO:0051262);	Pyruvate metabolism (ko00620); Carbon fixation in photosynthetic organisms (ko00710); Carbon metabolism (ko01200)
BnaCnng68410D	BP: transcription, DNA-templated (GO:0006351); BP: RNA processing (GO:0006396); BP: translational initiation (GO:0006413); BP: post-embryonic development (GO:0009791); BP: posttranscriptional regulation of gene expression (GO:0010608); CC: macromolecular complex (GO:0032991); BP: macromolecule localization (GO:0033036); CC: cytoplasmic part (GO:0044444); BP: single-organism developmental process (GO:0044767); BP: reproductive structure development (GO:0048608); BP: cellular response to organic substance (GO:0071310); BP: regulation of primary metabolic process (GO:0080090); BP: regulation of cellular macromolecule biosynthetic process (GO:2000112);	RNA transport (ko03013)
BnaCnng75420D	CC: vacuolar proton-transporting V-type ATPase, V0 domain (GO:0000220); CC: mitochondrion (GO:0005739); CC: Golgi apparatus (GO:0005794); BP: ATP catabolic process (GO:0006200); CC: chloroplast (GO:0009507); MF: hydrogen-translocating pyrophosphatase activity (GO:0009678); CC: plant-	Oxidative phosphorylation (ko00190); Phagosome (ko04145)

	type vacuole membrane (GO:0009705); MF: hydrogen ion transmembrane transporter activity (GO:0015078); BP: ATP synthesis coupled proton transport (GO:0015986); BP: ATP hydrolysis coupled proton transport (GO:0015991); MF: ATPase activity (GO:0016887); BP: cellular response to nutrient levels (GO:0031669); BP: sequestering of zinc ion (GO:0032119); BP: vacuolar sequestering (GO:0043181); MF: nutrient reservoir activity (GO:0045735); BP: vacuolar proton-transporting V-type ATPase complex assembly (GO:0070072); BP: cellular response to salt stress (GO:0071472); CC: mitochondrion (GO:0005739); CC: chloroplast stroma (GO:0009570); BP: mRNA modification (GO:0016556); MF: carbon-nitrogen ligase activity, with glutamine as amido-N-donor (GO:0016884);	
Cole_newGene_1983		Aminoacyl-tRNA biosynthesis (ko00970)
Cole_newGene_1984	CC: plant-type vacuole (GO:0000325); CC: vacuolar membrane (GO:0005774); CC: chloroplast (GO:0009507); BP: response to salt stress (GO:0009651); BP: proton transport (GO:0015992); BP: CC organization (GO:0016043); MF: pyrophosphatase activity (GO:0016462); MF: transmembrane transporter activity (GO:0022857); BP: ion transmembrane transport (GO:0034220); BP: ATP metabolic process (GO:0046034); BP: maintenance of location (GO:0051235); BP: cellular localization (GO:0051641); BP: cellular response to stimulus (GO:0051716);	Oxidative phosphorylation (ko00190); Phagosome (ko04145)
Cole_newGene_2071	MF: sequence-specific DNA binding transcription factor activity (GO:0003700); CC: nucleus (GO:0005634); BP: regulation of transcription, DNA-templated (GO:0006355); MF: protein dimerization activity (GO:0046983);	--
Cole_newGene_2073	CC: intracellular membrane-bounded organelle (GO:0043231); CC: cytoplasmic part (GO:0044444);	Protein processing in endoplasmic reticulum (ko04141); Plant-pathogen interaction (ko04626)
Cole_newGene_2243	CC: mitochondrion (GO:0005739); CC: Golgi apparatus (GO:0005794); CC: plasma membrane (GO:0005886); BP: response to stress (GO:0006950); CC: integral component of endoplasmic reticulum membrane (GO:0030176); BP: single-organism cellular process (GO:0044763);	Protein export (ko03060); Protein processing in endoplasmic reticulum (ko04141)
Cole_newGene_269	--	--
Cole_newGene_3682	--	--
Cole_newGene_4151	--	--
Cole_newGene_4384	--	--
Cole_newGene_4855	CC: nucleus (GO:0005634);	--
Cole_newGene_6687	CC: cell wall (GO:0005618); CC: vacuole (GO:0005773); CC: endoplasmic reticulum (GO:0005783); CC: plasma membrane (GO:0005886); CC: plasmodesma (GO:0009506); MF: transmembrane transporter activity (GO:0022857); BP: transmembrane transport (GO:0055085);	--
Cole_newGene_8277	--	--

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