Supplemental Table 3. Comparison of transcripts in Col and Ler ecotype using fullgenome oligoarrays.

Supplemental Table 3A. Genes expressed at higher level in Col (p-values<0.05)

Locus Ratio At1g22400-1	rmalized (Col/Ler) 2.26 3.83	Annotation	Function
Locus Ratio At1g22400-1	2.26		Function
At1g22400-1 At2g16730 At2g47030-m	2.26		
At2g16730 At2g47030-m	3.83	UDP-glucosyl transferase family protein	carbon metabolism
At2g47030-m		glycosyl hydrolase family protein	carbon metabolism
1	2.58	pectinesterase family protein	carbon metabolism
At3g17060	3.58	pectinesterase family protein	carbon metabolism
	2.51	glucosamine/galactosamine family protein	carbon metabolism
At3g52600	3.75	beta-fructosidase	carbon metabolism
	2.34	pectate lyase family protein	carbon metabolism
	2.84	F-box family protein (FKF1)	cell communication
At3g19310	2.14	protein kinase	cell communication
At5g01950	2.12	leucine-rich repeat	cell communication
At1g61070	2.19	plant defensin-fusion protein	cell defense
At4g19500	5.77	disease resistance protein	cell defense
At4g25780	2.32	pathogenesis-related protein	cell defense
At5g14380	2.16	hydroxyproline-rich glycoprotein	development
At1g67290	2.80	glyoxal oxidase-related	lipid metabolism
At4g11840-m	2.30	phospholipase D gamma 3 /(PLDGAMMA3)	lipid metabolism
At4g30140	2.43	GDSL-motif lipase/hydrolase	lipid metabolism
At5g15720	2.12	GDSL-motif lipase/hydrolase	lipid metabolism
At1g61580	2.54	60S ribosomal protein L3 (RPL3B)	protein folding and processing
At1g65150-m	7.25	meprin and TRAF homology domain containing protein	protein folding and processing
At2g22970	2.73	serine carboxypeptidase S10 family protein	protein folding and processing
At3g58210	2.73	meprin and TRAF homology domain containing protein	protein folding and processing
At5g03330	2.15	OTU-like cysteine protease family protein	protein folding and processing
At5g50680-m	2.20	SUMO activating enzyme (SAE1b)	protein folding and processing
At5g59120	2.47	subtilase family protein	protein folding and processing
At1g74010	2.36	strictosidine synthase family protein	secondary metabolism
At2g29460	2.34	glutathione S-transferase	secondary metabolism
At4g00040	3.64	chalcone and stilbene synthase	secondary metabolism
At5g24670	2.15	cytidine/deoxycytidylate deaminase family protein	secondary metabolism
At1g15720-m	2.18	myb family transcription factor	transcription
At1g57820	2.09	C3HC4-type RING finger family protein	transcription
At3g07610	3.05	transcription factor jumonji (jmjC)	transcription
At4g02540	2.60	DC1 domain-containing protein	transcription
At5g01070	2.12	C3HC4-type RING finger family protein	transcription
··· J · · · ·	2.19	squamosa promoter-binding protein	transcription
At5g65080	2.06	MADS-box family protein	transcription
	2.01	RNA-binding protein	translation
	2.10	exocyst subunit EXO70 family protein	transport
	2.37	oligopeptide transporter OPT family protein	transport
	4.23	non-LTR retrotransposon family protein	transposable element
	2.20	expressed protein	unknown
	6.38	expressed protein	unknown
	3.15	expressed protein	unknown
	8.85	hypothetical protein	unknown
At2g02790	5.04	calmodulin-binding family protein	unknown

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At2g14520	2.49	CBS domain-containing protein	unknown
At2g29950	2.02	expressed protein	unknown
At2g30010	2.13	expressed protein	unknown
At2g36550	2.40	expressed protein	unknown
At2g40680-m	2.59	hypothetical protein	unknown
At3g58800	3.20	expressed protein	unknown
At4g22860	2.46	expressed protein	unknown
At5g50440	2.19	Golgi SNARE protein membrin 12	unknown
At5g64770	3.11	expressed protein	unknown
Leaf			
At3g16950	2.06	dihydrolipoamide dehydrogenase	amino acid metabolism
At1g22360	2.12	UDP-glucoronosyl/UDP-glucosyl transferase	carbon metabolism
At1g22400-1	2.79	UDP-glucoronosyl/UDP-glucosyl transferase	carbon metabolism
At1g22650	5.96	beta-fructofuranosidase	carbon metabolism
At2g06850	2.43	xyloglucan:xyloglucosyl transferase	carbon metabolism
At3g07010	2.78	pectate lyase family protein	carbon metabolism
At3g18270	2.58	mandelate racemase/muconate lactonizing enzyme	carbon metabolism
At3g49360	2.55	galactosamine-6-phosphate isomerase family protein	carbon metabolism
At3g54690	2.11	sugar isomerase (SIS) domain containing protein	carbon metabolism
At4g04040-m	2.30	pyrophosphate-fructose-6-phosphate 1-phosphotransferase	carbon metabolism
At4g23820	2.07	glycoside hydrolase family protein	carbon metabolism
At1g11350	2.95	S-locus lectin protein kinase	cell communication
At1g66940	2.19	protein kinase-related	cell communication
At2g17220	2.08	protein kinase	cell communication
At2g21370	2.00	xylulose kinase	cell communication
At3g23340	3.15	casein kinase	cell communication
At4g16970	5.49	protein kinase family protein	cell communication
At4g23160	6.76	protein kinase family protein	cell communication
At5g02760	3.10	protein phosphatase 2C family protein	cell communication
At1g02360	2.64	chitinase	cell defense
At1g59124-m	2.13	disease resistance protein	cell defense
At1g63870	6.09	disease resistance protein	cell defense
At1g66100	50.02	thionin	cell defense
At3g25020-m	2.45	disease resistance family protein	cell defense
At3g44630	2.71	disease resistance protein	cell defense
At3g50440	2.13	hydrolase alpha/beta fold	cell defense
At4g37530	2.05	peroxidase	cell defense
At5g36930	14.98	disease resistance protein	cell defense
At5g39190-m	7.95	germin-like protein (GER2)	cell defense
At5g45490	14.45	disease resistance protein	cell defense
At5g63020	2.89	disease resistance protein	cell defense
At2g37640	3.00	expansin (EXP3)	cell structure
At4g17030	4.77	expansin-related	cell structure
At4g29270	3.52	acid phosphatase class B family protein	energy metabolism
At1g29420	4.62	auxin-responsive family protein	hormone regulation
At1g29450-m	4.31	auxin-responsive protein	hormone regulation
At1g29460-m	5.73	auxin-responsive protein	hormone regulation
At1g29490	3.39	auxin-responsive family protein	hormone regulation
At1g29500	3.59	auxin-responsive protein	hormone regulation
At3g03820-m	3.53	auxin-responsive protein	hormone regulation
At3g23050	3.06	auxin-responsive protein	hormone regulation
At4g32280	5.18	auxin-responsive AUX/IAA family protein	hormone regulation
At4g34770	3.67	auxin-responsive family protein	hormone regulation
At5g18010-m	3.67	auxin-responsive protein	hormone regulation
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At5g18030-m	3.84	auxin-responsive protein	hormone regulation
At5g18050	3.28	auxin-responsive protein	hormone regulation
At5g18060	3.42	auxin-responsive protein	hormone regulation
At5g18080-m	3.74	auxin-responsive protein	hormone regulation
At2g03980	3.55	GDSL-motif lipase/hydrolase	lipid metabolism
At2g19570	2.01	cytidine deaminase (CDD)	nucleotide metabolism
At1g31090	2.67	F-box family protein	protein folding and processing
At1g52480	6.40	F-box family protein	protein folding and processing
At1g68050-m	2.63	F-box family protein (FKF1)	protein folding and processing
At2g40920	13.07	F-box family protein	protein folding and processing
At3g55170	2.00	60S ribosomal protein L35	protein folding and processing
At1g76160	2.11	multi-copper oxidase type I	secondary metabolism
At3g26210	2.89	cytochrome P450 (CYP71B23)	secondary metabolism
At4g12730	2.16	fasciclin-like arabinogalactan-protein	secondary metabolism
At5g25980	48.74	thioglucoside glucohydrolase protein (TGG2)	secondary metabolism
At3g16770	3.06	AP2 domain-containing protein	transcription
At3g24954	2.51	leucine-rich repeat family protein	transcription
At5q45510	2.09	leucine-rich repeat family protein	transcription
At5g65310	2.84	homeobox-leucine zipper protein	transcription
At1g66230	3.15	myb family transcription factor (MYB20)	transcription factor
At3q07200	2.00	zinc finger (C3HC4-type RING finger) family protein	transcription factor
At5g13080	2.00	WRKY family transcription	transcription factor
At5g65410	2.07		· · · · ·
At1g13950	2.11	zinc finger homeobox family protein eukaryotic translation initiation factor	transcription factor
At1g58380-m	2.37	40S ribosomal protein S2 (RPS2A)	translation
			translation
At1g52190	2.92	proton-dependent oligopeptide transport (POT)	transport
At2g11240-1	2.05	non-LTR retrotransposon family protein	transposable element
At2g13970	2.25	Mutator-like transposase family protein	transposable element
At1g07090 At1g31580	2.42 2.96	expressed protein	unknown
At1g35612	35.46	expressed protein	unknown
	2.74	expressed protein	unknown
At1g56320 At1g62480	2.14	expressed protein	unknown
	22.14	vacuolar calcium-binding protein	unknown unknown
At1g67020 At1g78460	8.63	hypothetical protein SOUL heme-binding family protein	
	2.88	protease inhibitor/seed storage/LTP	unknown
At2g10940			unknown
At2g23640	3.70	reticulon family protein	unknown
At2g25510	51.08	expressed protein	unknown
At2g30010	4.44	expressed protein	unknown
At2g33330	2.21	33 kDa secretory protein-related	unknown
At3g08670	5.21	expressed protein	unknown
At3g19520	2.41	expressed protein	unknown
At3g22240	4.28	expressed protein	unknown
At3g25717	2.63	expressed protein	unknown
At3g28857	2.31	expressed protein	unknown
At3g47965	23.36	expressed protein	unknown
At3g56030	2.22	pentatricopeptide (PPR) repeat-containing protein	unknown
At3g59880	2.13	expressed protein	unknown
At3g60440-2	5.73	expressed protein	unknown
At4g01590	3.21	expressed protein	unknown
At4g07410	2.18	transducin family protein	unknown
At4g07800	2.81	hypothetical protein	unknown
At4g08110	16.41	CACTA-like transposase family protein	unknown
At5g03090	6.40	hypothetical protein	unknown
At5g12240	3.04	expressed protein	unknown

At5g26800	2.05	expressed protein	unknown
At5g35800	4.28	pseudogene	unknown
At5g57760-m	2.84	expressed protein	unknown
At5g64870	3.01	expressed protein	unknown

Table3B. Genes expressed at higher level in Ler (p-values<0.05)</th>

Flower			
	Normalized		
Locus	Ratio (Col/Ler)	Annotation	Function
At2g43100	0.39	aconitase C-terminal domain-containing protein	amino acid metabolism
At1g51490	0.27	glycosyl hydrolase family	carbon metabolism
At2g20520	0.34	fasciclin-like arabinogalactan-protein (FLA6)	carbon metabolism
At5g44400	0.39	FAD-linked oxidoreductase family	carbon metabolism
At5g49180	0.45	pectinesterase family protein	carbon metabolism
At5g53610	0.38	glycosyl hydrolase family	carbon metabolism
At4g01420	0.45	calcineurin B-like protein 5	cell communication
At1g23935	0.49	apoptosis inhibitory protein 5 (API5)	cell defense
At1g58520	0.43	ERD protein-related	cell defense
At1g78370	0.42	glutathione S-transferase	cell defense
At4g16930-m	0.30	disease resistance protein	cell defense
At4g35090	0.39	catalase 2	cell defense
At3g27690	0.32	chlorophyll A-B binding protein	energy metabolism
At1g12010	0.19	1-aminocyclopropane-1-carboxylate oxidase	hormone regulation
At4g15440	0.25	hydroperoxide lyase (HPL1)/cytochrome P450 (CYP74B2)	lipid metabolism
At1g27540-m	0.15	F-box family protein	protein folding and processing
At1g27560	0.15	F-box family protein	protein folding and processing
At1g73260	0.47	trypsin and protease inhibitor	protein folding and processing
At5g37640	0.31	polyubiquitin (UBQ9)	protein folding and processing
At1g12350	0.34	DNA/panthothenate metabolism flavoprotein	secondary metabolism
At4g03050	0.34	2-oxoglutarate-dependent dioxygenase (AOP3)	secondary metabolism (glucosinolate synthesis)
At4g27070	0.42	tryptophan synthase, beta subunit 2 (TSB2)	secondary metabolism
At4g13770	0.21	cytochrome P450 (CYP83A1)	secondary metabolism (glucosinolate synthesis)
At1g73230-m	0.40	nascent polypeptide-associated complex (NAC)	transcription
At3g61950-1	0.44	basic helix-loop-helix family protein	transcription
At3g61950-2	0.44	basic helix-loop-helix family protein	transcription
At1g32150	0.40	bZIP transcription factor	transcription factor
At2g25640	0.41	transcription elongation factor	transcription factor
At5g37280	0.31	zinc finger (C3HC4-type) family protein	transcription factor
At3g26618	0.05	eRF1 family protein	translation
At5g24510	0.38	60S acidic ribosomal protein	translation
At2g37180	0.34	plasma membrane intrinsic protein 2C (PIP2C)	transport
At3g29100	0.39	vesicle transport v-SNARE 13 (VTI13)	transport
At4g08680-m	0.25	Mutator-like transposase	transposable element
At1q11990	0.21	expressed protein	unknown
At1g23940	0.49	adaptin family protein	unknown
At1g24370	0.13	hypothetical protein	unknown
At1g27480	0.42	lecithin:cholesterol acyltransferase family protein	unknown
At1g30020-m	0.34	expressed protein	unknown
At1g48310-m	0.46	SNF2 domain-containing protein	unknown
At1g48750-m	0.27	protease inhibitor/seed storage/LTP	unknown
At1g50290	0.08	expressed protein	unknown
At1g52590	0.46	expressed protein	unknown
At1g58025	0.11	DNA-binding bromodomain-containing protein	unknown
71900020	0.11		dina of the

At2g21140	0.40	hydroxyproline-rich glycoprotein family protein	unknown
At2g30230	0.22	hypothetical protein	unknown
At2g35810	0.49	expressed protein	unknown
At2g35820	0.29	expressed protein	unknown
At2g40960	0.29	expressed protein	unknown
At2g47270	0.50	expressed protein	unknown
At3g18280	0.31	protease inhibitor/seed storage/LTP	unknown
At3g26510-1	0.42	octicosapeptide/Phox/Bem1p	unknown
At3g44070	0.33	expressed protein	unknown
At3g49270	0.32	expressed protein	unknown
At4g16215	0.25	expressed protein	unknown
At4g24420	0.17	RNA recognition motif (RRM)	unknown
At4g29760	0.27	hypothetical protein	unknown
At4g32050	0.23	neurochondrin family protein	unknown
At5g15360	0.37	hypothetical protein	unknown
At5g17090	0.19	expressed protein	unknown
Leaf			
At5g23020	0.38	2-isopropylmalate synthase 2 (IMS2)	amino acid metabolism
At2g43100	0.31	aconitase C-terminal domain-containing protein	amino acid metabolism
At3g19710-m	0.36	branched-chain amino acid aminotransferase	amino acid metabolism
At4g23600	0.22	coronatine-responsive tyrosine aminotransferase	amino acid metabolism
At3g22740	0.39	homocysteine S-methyltransferase 3 (HMT-3)	amino acid metabolism
At1g44350	0.39	IAA-amino acid hydrolase 6	amino acid metabolism
At4g27070	0.14	tryptophan synthase beta	amino acid metabolism
At2g20340	0.34	tyrosine decarboxylase	amino acid metabolism
At5g14200	0.40	3-isopropylmalate dehydrogenase, chloroplast	carbohydrate metabolism
At5g57655	0.41	xylose isomerase family protein	carbohydrate metabolism
At3g06500	0.30	beta-fructofuranosidase	carbon metabolism
At2g28470	0.46	beta-galactosidase	carbon metabolism
At5g56870	0.15	beta-galactosidase	carbon metabolism
At2g39800	0.42	delta 1-pyrroline-5-carboxylate synthetase A	carbon metabolism
At5g42800	0.37	dihydroflavonol 4-reductase	carbon metabolism
At5g50950	0.38	fumarate hydratase	carbon metabolism
At1g09420	0.17	glucose-6-phosphate 1-dehydrogenase	carbon metabolism
At1g12570	0.19	glucose-methanol-choline	carbon metabolism
At2g40840	0.41	glycoside hydrolase family protein	carbon metabolism
At4g23500	0.47	glycoside hydrolase family protein	carbon metabolism
At1g60140	0.48	glycosyl hydrolase family protein	carbon metabolism
At1g70090	0.49	glycosyl hydrolase family protein	carbon metabolism
At2g18700	0.43	glycosyl hydrolase family protein	carbon metabolism
At3g62740-2-m	0.35	glycosyl hydrolase family protein	carbon metabolism
At4g27820	0.22	glycosyl hydrolase family protein	carbon metabolism
At5g55180	0.21	glycosyl hydrolase family protein	carbon metabolism
At5g63800	0.45	glycosyl hydrolase family protein	carbon metabolism
At1g32480	0.29	isocitrate/isopropylmalate	carbon metabolism
At1g75290	0.46	isoflavone reductase	carbon metabolism
At1g75300	0.38	isoflavone reductase	carbon metabolism
At4g30270	0.46	MERI-5 protein (MERI-5)	carbon metabolism
At4g15760	0.49	monooxygenase putative (MO1)	carbon metabolism
At5g20250	0.31	raffinose synthase family/seed imbibition protein	carbon metabolism
At5g65140	0.21	trehalose-6-phosphate phosphatase	carbon metabolism
At2g36770	0.36	UDP-glucoronosyl/UDP-glucosyl transferase	carbon metabolism
At2g36780	0.31	UDP-glucoronosyl/UDP-glucosyl transferase	carbon metabolism
At2g36800	0.26	UDP-glucoronosyl/UDP-glucosyl transferase	carbon metabolism
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Ard 92120 0.45 blunctional aspartate kinase/homesem dehydrogenase oell communication Ard 920200 0.43 calcium-binding profein oell communication Ard 920500 0.43 calcium-binding profein oell communication Ard 920500 0.45 calcium-binding profein oell communication Ard 920500 0.45 calcium-binding profein oell communication Ard 920500 0.44 calcium-dependent profein oell communication Ard 920500 0.45 calcium-dependent profein oell communication Ard 920500 0.46 calmodulin-binding profein oell communication Ard 920500 0.41 Cell vietracing profein frame oell communication Ard 920500 0.41 Cell vietracing profein frame oell communication Ard 920500 0.41 Cell vietracing profein frame oell communication Ard 920500 0.41 insole olyphysicphate 5 phosphates il (PSPI) oell communication Ard 920500 0.42 iscalin methy profein cell communication Ard 920500 0.43 iscal				
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At2g34930 0.36 disease resistance protein cell defense	At1g72950		i i i i i i i i i i i i i i i i i i i	
	At2g34930	0.36	disease resistance protein	cell defense

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At3g44480-m	0.19	disease resistance protein	cell defense
At3g44670-1	0.40	disease resistance protein	cell defense
At3g44670-2-m	0.40	disease resistance protein	cell defense
At4g16890	0.43	disease resistance protein	cell defense
At4g16920-1	0.39	disease resistance protein	cell defense
At4g16930-m	0.18	disease resistance protein	cell defense
At4g16950	0.19	disease resistance protein	cell defense
At5g43740	0.36	disease resistance protein	cell defense
At5g45060	0.46	disease resistance protein	cell defense
At5g46470-2	0.46	disease resistance protein	cell defense
At1g11960	0.45	early-responsive to dehydration protein-related	cell defense
At5g53730	0.37	harpin-induced family protein	cell defense
At4g11660	0.46	heat shock factor protein 7 (HSF7)	cell defense
At5g47600	0.16	heat shock protein-related	cell defense
At1g02660-1	0.37	lipase class 3 family protein	cell defense
At1g02660-2	0.37	lipase class 3 family protein	cell defense
At1g52030-1-m	0.34	myrosinase-binding protein	cell defense
At1g52030-2-m	0.34	myrosinase-binding protein	cell defense
At4g36010	0.29	pathogenesis-related thaumatin family protein	cell defense
At2g20145-m	0.40	Toll-Interleukin-Resistance(TIR)	cell defense
At5g24780	0.16	vegetative storage protein (VSP1)	cell defense
At5g24770	0.14	vegetative storage protein (VSP2)	cell defense
At1g52080	0.07	actin binding protein family	cell structure
At5g11740	0.43	arabinogalactan-protein (AGP15)	cell structure
At2g20870	0.37	cell wall protein precursor	cell structure
At1g12350	0.27	DNA/panthothenate metabolism flavoprotein family protein	cell structure
At2g03090	0.39	expansin (EXP15)	cell structure
At3g45970-m	0.37	expansin family protein (EXPL1)	cell structure
At4g18280	0.39	glycine-rich cell wall protein	cell structure
At4g30460	0.41	glycine-rich protein	cell structure
At5g07530	0.22	glycine-rich protein (GRP1)	cell structure
At5g07550	0.20	glycine-rich protein (GRP1)	cell structure
At5g07560	0.27	glycine-rich protein (GRP2)	cell structure
At3g15400	0.25	anther development protein	development
At3g61190	0.15	BON1-associated protein 1 (BAP1)	development
At1g65480	0.30	flowering locus T protein (FT)	development
At1g76110	0.38	high mobility group (HMG1)	development
At1g01470	0.33	late embryogenesis	development
At2g03850	0.31	late embryogenesis	development
At1g75520	0.23	lateral root primordium	development
At1g52890	0.32	no apical meristem (NAM)	development
At3g29035	0.30	no apical meristem (NAM)	development
At4g01520	0.49	no apical meristem (NAM)	development
At4g01540	0.37	no apical meristem (NAM)	development
At4g27410	0.44	no apical meristem (NAM)	development
At4g08290	0.30	nodulin MtN21 family protein	development
At5g50800	0.27	nodulin MtN3 family protein	development
At2g17840	0.36	senescence/dehydration-associated protein-related (ERD7)	development
At1g66330	0.46	senescence-associated family protein	development
At3g22550	0.43	senescence-associated protein	development
At4g35770	0.35	senescence-associated protein (SEN1)	development
At1g75460-1	0.42	ATP-dependent protease La (LON)	energy metabolism
At2g06050	0.34	12-oxophytodienoate reductase (OPR3/DDE1)	hormone (JA synthesis)
At2g44840	0.46	ethylene-responsive element	hormone regulation
At3g25780	0.45	allene oxide cyclase	hormone regulation
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At5g08350	0.20	GRAM domain-containing protein	hormone regulation
At5g13200	0.25	GRAM domain-containing protein	hormone regulation
At5g23360-m	0.25	GRAM domain-containing protein	hormone regulation
At5g23370	0.31	GRAM domain-containing protein	hormone regulation
At4g24960	0.36	ABA-responsive protein (HVA22d)	hormone regulation (hyperosmotic salinity response)
At1g02205	0.47	CER1 protein	lipid metabolism
At1g75910	0.31	family II extracellular lipase 4	lipid metabolism
At4g15440	0.45	hydroperoxide lyase (HPL1)/cytochrome P450 (CYP74B2)	lipid metabolism
At1g72520	0.38	lipoxygenase	lipid metabolism
At3g45140	0.30	lipoxygenase (LOX2)	lipid metabolism
At1g17420	0.40	lipoxygenase (LOX3)	lipid metabolism
At1g54000	0.47	myrosinase-associated protein	lipid metabolism
At1g80950	0.50	phospholipid/glycerol acyltransferase	lipid metabolism
At4g22240	0.50	plastid-lipid associated	lipid metabolism
At3g55290	0.15	short-chain dehydrogenase/reductase (SDR) family protein	lipid metabolism
At4g18440-m	0.48	adenylosuccinate lyase	nucleotide metabolism
At5g67520	0.20	adenylylsulfate kinase	nucleotide metabolism
At3g23890	0.38	ATP-hydrolyzing / DNA topoisomerase II	nucleotide metabolism
At4g20320	0.30	CTP synthase	nucleotide metabolism
At2g18190	0.30	AAA-type ATPase family protein	protein catabolism
At1g66180	0.37	aspartyl protease family protein	protein folding and processing
At4g11320	0.36	cysteine proteinase	protein folding and processing
At2g31980	0.20	cysteine proteinase inhibitor	protein folding and processing
At1g54290	0.49	eukaryotic translation initiation factor SUI1	protein folding and processing
At5g57870	0.47	eukaryotic translation initiation factor SUI2	protein folding and processing
At1g10110	0.29	F-box family protein	protein folding and processing
At1g27540-m	0.14	F-box family protein	protein folding and processing
At1g27560	0.11	F-box family protein	protein folding and processing
At1g61340	0.42	F-box family protein	protein folding and processing
At4g27050	0.41	F-box family protein	protein folding and processing
At1g24140	0.40	matrixin family protein	protein folding and processing
At3g19170	0.45	peptidase M16 family protein	protein folding and processing
At3g27110	0.32	peptidase M48 family protein	protein folding and processing
At5g07460	0.44	peptide methionine sulfoxide	protein folding and processing
At4g12910	0.44	serine carboxypeptidase S10 family protein	protein folding and processing
At4g21326	0.31	subtilase family protein c	protein folding and processing
At5g45650	0.37	subtilase family protein c	protein folding and processing
At5g58820	0.46	subtilase family protein c	protein folding and processing
At5g59130	0.40	subtilase family protein c	protein folding and processing
At2g43530	0.42	trypsin inhibitor	protein folding and processing
At2g16740	0.39	ubiquitin-conjugating enzyme	protein folding and processing
At5g56150	0.48	ubiquitin-conjugating enzyme	protein folding and processing
At5g43450	0.21	2-oxoglutarate-dependent dioxygenase	secondary metabolism
At5g51260	0.41	acid phosphatase putative	secondary metabolism
At2g37770	0.38	aldo/keto reductase family protein	secondary metabolism
At4g08870	0.32	arginase	secondary metabolism
At1g58180	0.43	carbonic anhydrase family protein	secondary metabolism
At1g62810	0.35	copper amine oxidase	secondary metabolism
At1g16410	0.42	cytochrome P450 (CYP79F1)	secondary metabolism (glucosinolate synthesis)
At4g13770	0.44	cytochrome P450 (CYP83A1)	secondary metabolism (glucosinolate synthesis)
At1g64940-m	0.43	cytochrome P450 (CYP89A6)	secondary metabolism
At1g69500	0.28	cytochrome P450 (CYP704B1)	secondary metabolism
At3g48520	0.24	cytochrome P450 (CYP94B3)	secondary metabolism
At5g26030	0.48	ferrochelatase I	secondary metabolism
At1g69720	0.38	heme oxygenase 3 (HO3)	secondary metabolism
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At5g13800	0.47	hydrolase alpha/beta fold	secondary metabolism
At5g09530	0.21	hydroxyproline-rich glycoprotein	secondary metabolism
At4g34030-1	0.41	methylcrotonyl-CoA carboxylase	secondary metabolism
At4g34030-2	0.41	methylcrotonyl-CoA carboxylase	secondary metabolism
At1g01290	0.44	molybdopterin biosynthesis	secondary metabolism
At1g21440	0.38	mutase family protein	secondary metabolism
At5g05600	0.33	oxidoreductase 2OG-Fe(II)	secondary metabolism
At1g65980	0.49	peroxiredoxin type 2	secondary metabolism
At3g61070	0.38	peroxisomal biogenesis	secondary metabolism
At3g54020	0.40	phosphatidic acid phosphatase	secondary metabolism
At5g24240	0.38	phosphatidylinositol 3- and 4-kinase	secondary metabolism
At2g22860	0.37	phytosulfokines 2 (PSK2)	secondary metabolism
At5g65870	0.49	phytosulfokines 5 (PSK5)	secondary metabolism
At5g24160	0.10	squalene monooxygenase (SQP1,2)	secondary metabolism
At2g03760	0.18	steroid sulfotransferase	secondary metabolism
At4g32770	0.43	tocopherol cyclase (VTE1/SXD1)	secondary metabolism
At4g03050	0.08	2-oxoglutarate-dependent dioxygenase (AOP3)	secondary metabolism (glucosinolate synthesis)
At1g62940	0.31	4-coumarateCoA ligase family protein	secondary metabolism (phenylpropanoid metabolism)
At5g60910	0.31	agamous-like MADS box protein	transcription factor
At1g74930-1	0.13	AP2 domain-containing transcription factor	transcription factor
At1g78080	0.45	AP2 domain-containing transcription factor	transcription factor
At5g51190	0.34	AP2 domain-containing transcription factor	transcription factor
At1g75390	0.36	bZIP transcription factor	transcription factor
At1g76650	0.26	calcium-binding EF hand family protein	transcription factor
At4g27280	0.34	calcium-binding EF hand family protein	transcription factor
At5g54490	0.41	calcium-binding EF hand family protein	transcription factor
At3g44260	0.28	CCR4-NOT transcription transcription complex protein	transcription factor
At5g22250	0.26	CCR4-NOT transcription transcription complex protein	transcription factor
At3g02310-1	0.39	developmental protein SEPALLATA2 (AGL4)	transcription factor
At3g02310-2	0.39	developmental protein SEPALLATA2 (AGL4)	transcription factor
At1g12610	0.15	DRE-binding protein	transcription factor
At4g25470	0.33	DRE-binding protein (DREB1C)	transcription factor
At4g25490	0.36	DRE-binding protein (DREB1C)	transcription factor
At1g28370	0.11	ERF domain protein 11 (ERF11)	transcription factor
At1g62360	0.32	homeobox protein SHOOT MERISTEMLESS	transcription factor
At2g46680	0.35	homeobox-leucine zipper protein	transcription factor
At2g45660	0.43	MADS-box protein (AGL20)	transcription factor
At1g74430-m	0.18	myb family transcription factor	transcription factor
At3g23250	0.21	myb family transcription factor	transcription factor
At3g50060	0.31	myb family transcription factor	transcription factor
At4g01060	0.09	myb family transcription factor	transcription factor
At5g67300-m	0.49	myb family transcription factor	transcription factor
At5g59450	0.31	scarecrow-like transcription factor 11 (SCL11)	transcription factor
At3g45950	0.44	splicing factor-related	transcription factor
At4g37610	0.45	TAZ zinc finger family protein	transcription factor
At5g05140	0.44	transcription elongation factor	transcription factor
At4g10920	0.18	transcriptional coactivator p15 (PC4) family protein (KELP)	transcription factor
At1g80840	0.23	WRKY family transcription factor	transcription factor
At4g31800	0.38	WRKY family transcription factor	transcription factor
At1g27730	0.21	zinc finger (C2H2 type) family protein	transcription factor
At2g28200	0.29	zinc finger (C2H2 type) family protein	transcription factor
At3g46080	0.34	zinc finger (C2H2 type) family protein	transcription factor
At5g04340	0.26	zinc finger (C2H2 type) family protein	transcription factor
At3g19580	0.30	zinc finger (C2H2 type) protein	transcription factor
At1g66500	0.25	zinc finger (C2H2-type) family protein	transcription factor

4+4 = 00070	0.00	ring finger (C211C4 type DINC finger) family protein	
At1g62370	0.28	zinc finger (C3HC4-type RING finger) family protein	transcription factor
At1g69330	0.43	zinc finger (C3HC4-type RING finger) family protein	transcription factor
At3g46620	0.48	zinc finger (C3HC4-type RING finger) family protein	transcription factor
At4g15975	0.30	zinc finger (C3HC4-type RING finger) family protein	transcription factor
At5g63780	0.45	zinc finger (C3HC4-type RING finger) family protein	transcription factor
At5g36240	0.06	zinc knuckle (CCHC-type) family protein	transcription factor
At5g46710	0.45	zinc-binding family protein	transcription factor
At3g59140	0.40	ABC transporter family protein	transport
At5g09220	0.45	amino acid permease 2 (AAP2)	transport
At5g04770	0.39	amino acid permease family protein	transport
At3g30390	0.41	amino acid transporter family protein	transport
At4g29900-1	0.46	calcium-transporting ATPase	transport
At4g29900-2	0.46	calcium-transporting ATPase	transport
At1g02300-m	0.47	cathepsin B-like cysteine protease	transport
At5g49730	0.31	ferric reductase-like transmembrane component family	transport
At5g49740	0.36	ferric reductase-like transmembrane component family	transport
At2g32390	0.37	glutamate receptor family	transport
At5g16570	0.38	glutamine synthetase	transport
At1g28480	0.22	glutaredoxin family protein	transport
At2g29420	0.41	glutathione S-transferase	transport
At2g29490	0.33	glutathione S-transferase	transport
At4g00630	0.48	K+ efflux antiporter	transport
At3g51590	0.27	lipid transfer protein	transport
At5g59320	0.10	lipid transfer protein 3	transport
At5g59310	0.14	lipid transfer protein 4	transport
At2g04080	0.37	MATE efflux family protein	transport
At5g52050	0.26	MATE efflux protein	transport
At4g24570	0.31	mitochondrial substrate	transport
At1g69850	0.33	nitrate transporter (NTL1)	transport
At1g80830	0.46	NRAMP metal ion transport	transport
At1g70300	0.36	potassium transporter	transport
At1g69870	0.45	proton-dependent oligopeptide	transport
At3g47960-m	0.48	proton-dependent oligopeptide	transport
At5g62680-m	0.47	proton-dependent oligopeptide	transport
At4g18210	0.45	purine permease family protein	transport
At5g56160	0.41	SEC14 cytosolic factor family protein	transport
At5g07880	0.30	SNAP25 homologous protein	transport
At1g54370	0.30	sodium proton exchanger	transport
At3g05160	0.45	sugar transporter	transport
At1g36035-m	0.14	copia-like retrotransposon	transposable element
At4g07840	0.21	copia-like retrotransposon	transposable element
At1g35970-m	0.25	gypsy-like retrotransposon	transposable element
At4g08680-m	0.03	Mutator-like transposase family	transposable element
At2g38760	0.45	annexin 3 (ANN3)	unknown
At2g38750	0.39	annexin 4 (ANN4)	unknown
At2g30600-1	0.32	BTB/POZ domain-containing protein	unknown
At2g30600-2	0.37	BTB/POZ domain-containing protein	unknown
At1g52410	0.34	caldesmon-related	unknown
At3g25990	0.39	DNA-binding protein GT-1-related	unknown
At5g02310-2	0.46	eceriferum3 protein	unknown
At1g05340	0.35	expressed protein	unknown
At1g10380	0.40	expressed protein	unknown
At1g13650	0.30	expressed protein	unknown
At1g17380	0.14	expressed protein	unknown
At1g18740	0.31	expressed protein	unknown
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At1g19180	0.34	expressed protein	unknown
At1g20310	0.16	expressed protein	unknown
At1g28375	0.32	expressed protein	unknown
At1g32920	0.35	expressed protein	unknown
At1g35210	0.49	expressed protein	unknown
At1g35780	0.34	expressed protein	unknown
At1g36640	0.38	expressed protein	unknown
At1g50290	0.12	expressed protein	unknown
At1g52590	0.24	expressed protein	unknown
At1g58280	0.48	expressed protein	unknown
At1g59590	0.37	expressed protein	unknown
At1g64360	0.25	expressed protein	unknown
At1g64370	0.42	expressed protein	unknown
At1g70700	0.41	expressed protein	unknown
At1g72240	0.41	expressed protein	unknown
At1g72450	0.34	expressed protein	unknown
At1g74450	0.32	expressed protein	unknown
At1g76600	0.40	expressed protein	unknown
At2g18210	0.09	expressed protein	unknown
At2g23120	0.36	expressed protein	unknown
At2g25250	0.45	expressed protein	unknown
At2g26530	0.48	expressed protein	unknown
At2g32160	0.36	expressed protein	unknown
At2g34600	0.13	expressed protein	unknown
At2g40960	0.46	expressed protein	unknown
At2g42760	0.37	expressed protein	unknown
At2g46100	0.49	expressed protein	unknown
At2g47270	0.23	expressed protein	unknown
At3g02140	0.28	expressed protein	unknown
At3g19550	0.33	expressed protein	unknown
At3g23170	0.31	expressed protein	unknown
At3g27210	0.26	expressed protein	unknown
At3g52360	0.47	expressed protein	unknown
At3g55840-m	0.31	expressed protein	unknown
At4g04200	0.48	expressed protein	unknown
At4g13970	0.06	expressed protein	unknown
At4g16215	0.07	expressed protein	unknown
At4g19240	0.33	expressed protein	unknown
At4g23880	0.38	expressed protein	unknown
At4g29780	0.17	expressed protein	unknown
At5g03210	0.28	expressed protein	unknown
At5g12960	0.40	expressed protein	unknown
At5g13220	0.33	expressed protein	unknown
At5g17090	-0.09	expressed protein	unknown
At5g22430	0.22	expressed protein	unknown
At5g24660	0.47	expressed protein	unknown
At5g24740	0.42	expressed protein	unknown
At5g43210-2	0.46	expressed protein	unknown
At5g43680	0.27	expressed protein	unknown
At5g46500-2	0.49	expressed protein	unknown
At5g47860	0.46	expressed protein	unknown
At5g48480	0.44	expressed protein	unknown
At5g54145	0.39	expressed protein	unknown
At5g54730	0.45	expressed protein	unknown
At5g55570	0.08	expressed protein	unknown
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415-50000	0.47	Laurana da stata	1
At5g59080	0.47	expressed protein	unknown
At5g61340	0.46	expressed protein	unknown
At5g62090	0.39	expressed protein	unknown
At5g64170	0.48	expressed protein	unknown
At5g65480	0.48	expressed protein	unknown
At1g02990	0.40	expressed protein	unknown
At1g03660	0.30	expressed protein	unknown
At1g11210	0.25	expressed protein	unknown
At1g26920	0.42	expressed protein	unknown
At1g28400	0.47	expressed protein	unknown
At1g67040	0.20	expressed protein	unknown
At1g71240	0.33	expressed protein	unknown
At1g73750	0.41	expressed protein	unknown
At1g79245	0.38	expressed protein	unknown
At2g28305	0.49	expressed protein	unknown
At2g32130	0.44	expressed protein	unknown
At2g41640	0.29	expressed protein	unknown
At2g44500	0.47	expressed protein	unknown
At3g06210	0.38	expressed protein	unknown
At4g21570	0.39	expressed protein	unknown
At4g24380	0.27	expressed protein	unknown
At4g32020	0.49	expressed protein	unknown
At4g32350	0.47	expressed protein	unknown
At5g03545	0.26	expressed protein	unknown
At5g43660	0.23	expressed protein	unknown
At5g45630	0.32	expressed protein	unknown
At5g56980	0.44	expressed protein	unknown
At5g61820	0.34	expressed protein	unknown
At5g65610	0.42	expressed protein	unknown
At5g66650	0.23	expressed protein	unknown
At3g07540	0.43	formin homology 2	unknown
At1g51090	0.20	heavy-metal-associated	unknown
At2g23840	0.46	HNH endonuclease	unknown
At1g77960	0.33	hypothetical protein	unknown
At2g11570	0.06	hypothetical protein	unknown
At5g08150	0.46	hypothetical protein	unknown
At5g15360	0.29	hypothetical protein	unknown
At5g44570	0.26	hypothetical protein	unknown
At1g24370	0.31	hypothetical protein	unknown
At3g48390	0.33	MA3 domain-containing protein	unknown
At1g34770	0.23	MAGE-8 antigen-related	unknown
At4g00780	0.45	meprin and TRAF homology	unknown
At1g16860	0.50	merozoite surface protein	unknown
At1g07610	0.41	metallothionein-like protein	unknown
At2g11000	0.37	natC N(alpha)-terminal acetyltransferase	unknown
At1g09240	0.14	nicotianamine synthase	unknown
At5g56080	0.44	nicotianamine synthase	unknown
At3g26510-1	0.35	octicosapeptide/Phox/Bem1p	unknown
At5g09620	0.50	octicosapeptide/Phox/Bem1p	unknown
At5g63130	0.42	octicosapeptide/Phox/Bem1p	unknown
At3g22470-m	0.24	pentatricopeptide (PPR) repeat	unknown
At4g36850	0.39	PQ-loop repeat family protein	unknown
At1g80480	0.49	PRLI-interacting factor L	unknown
At1g73330	-0.02	protease inhibitor	unknown
At1g66850	0.15	protease inhibitor/seed storage/LTP	unknown
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At4g12480	0.31	protease inhibitor/seed storage/LTP	unknown
At5g62080	0.19	protease inhibitor/seed storage/LTP	unknown
At4g08596-m	0.20	pseudogene FAR1 -related	unknown
At2g29160	0.27	pseudogene similar	unknown
At3g16810	0.36	pumilio/Puf RNA-binding do	unknown
At4g14020	0.22	rapid alkalinization factor (RALF) family protein	unknown
At4g24420	0.06	RNA recognition motif (RRM)-containing protein	unknown
At5g45160	0.42	root hair defective 3 GTP-binding (RHD3) family protein	unknown
At3g58620	0.47	tetratricopeptide repeat (TPR)-containing protein	unknown
At5g37130	0.20	tetratricopeptide repeat (TPR)-containing protein	unknown
At3g06170	0.46	TMS membrane family protein/tumor differentially expressed (TDE) family protein	unknown
At4g01870	0.34	tolB protein-related	unknown
At1g66160	0.35	U-box domain-containing protein	unknown
At2g22880-m	0.35	VQ motif-containing protein	unknown
At5g46780	0.44	VQ motif-containing protein	unknown
At1g78070-1	0.42	WD-40 repeat family protein	unknown
At1g78070-2	0.42	WD-40 repeat family protein	unknown
At1g78070-2 At3g14440	0.42 0.39	WD-40 repeat family protein 9-cis-epoxycarotenoid dioxygenase	unknown unknown