



Novel mechanisms and transcription factors involved in the control of stomatal behavior in *Arabidopsis thaliana*

Nuevos mecanismos y factores de transcripción involucrados en el control del comportamiento estomático en *Arabidopsis thaliana*

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Table 1: Miss-expressed genes in TOC1-ox.

AGI ID UP- REGULATED	Affy ID	pvalue	BH	mean M	mean A	C1.CEL	C3.2.CEL	C3.CEL	T1.CEL	T3.2.CEL	T3.CEL	Annotation
At4g15210	245275_at	4,6691E-05	0,018420543	9,710778992	7,99549146	2,354259123	2,342744793	4,723301978	13,19289997	13,03404979	12,32569311	AT-BETA-AMY_ATBETA-AMY_BMY1_RAM1__BAM5 (BETA-AMYLASE 5); beta-amylase
At3g60140	251428_at	7,5165E-05	0,020170651	7,433218659	7,109155992	3,206441485	3,225904932	3,74529357	11,69989145	11,29579699	9,481607521	BGLU30_SRG2__DIN2 (DARK INDUCIBLE 2);catalytic/ cation binding /hydrolase, hydrolyzing O-glycosyl compounds
At5g61380	247525_at	7,9946E-07	0,005994532	5,56309923	11,3401487	8,398893886	8,79657494	8,480328423	14,25877703	14,31917182	13,78714608	APRR1_PRR1__TOC1 (TIMING OF CAB EXPRESSION 1); transcription regulator/ two-component response regulator
At4g33720	253301_at	0,00040926	0,038559756	5,387458725	4,913080972	2,540803657	2,117976791	1,999274379	8,338148608	8,291025382	6,191257012	pathogenesis-related protein, putative
At1g43800	260869_at	0,00065031	0,044950062	5,021864672	6,958426414	3,121166127	4,866997705	5,354318403	8,946436762	10,0361826	9,425456886	acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative
At5g20230	246099_at	0,00015902	0,027068898	4,93793178	5,083465409	2,604396957	2,57711517	2,66198643	8,490181308	7,565647113	6,601465477	BCB__ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier
At5g07990	250558_at	0,00014046	0,025227635	4,608984364	7,309852657	4,259168806	5,470254352	5,286658267	10,02826611	9,836739355	8,978029053	CYP75B1_D501__TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding
At1g03495 A	265091_s_at	0,00084121	0,04906509	4,602894764	7,796734303	4,865705146	6,691912055	4,928243561	10,52572451	10,48579282	9,28302772	transferase/ transferase, transferring acyl groups other than amino-acyl groups
At4g24890	254111_at	0,00037921	0,037216203	4,463376364	4,412772592	2,184928839	2,186594539	2,171729851	7,351495939	7,113452977	5,468433405	ATPAP24__PAP24 (PURPLE ACID PHOSPHATASE 24); acid phosphatase/ protein serine/threonine phosphatase
At1g02940	262103_at	6,4801E-05	0,019224063	4,440022206	4,372801494	2,364274816	2,086899657	2,007196699	7,28106696	6,575288318	5,922082513	ATGSTF5__GSTF5 (GLUTATHIONE S-TRANSFERASE (CLASS PHI) 5); glutathione transferase
At4g14090	245624_at	0,00060795	0,043066232	4,429003541	7,573332336	4,648300531	6,336225375	5,09196579	10,26043046	10,12869208	8,974379781	UDP-glucuronosyl/UDP-glucosyl transferase family protein
At5g14650	250142_at	5,7972E-05	0,018874816	4,414940945	4,304318248	2,099977602	2,189380155	2,001185569	5,916049526	6,368905687	7,250410948	polygalacturonase, putative / pectinase, putative
At5g54060	248185_at	0,00029512	0,033103505	4,335385814	8,277336322	5,841463045	6,83251696	5,654950241	10,88689173	10,81140557	9,636790385	UF3GT (udp-glucose:flavonoid 3-O-glucosyltransferase); transferase, transferring glycosyl groups
At3g59930 A	251438_s_at	0,00032782	0,034144073	4,126698009	5,729705297	3,286460082	3,272897232	4,439711562	8,109526957	8,201150045	7,068485904	Encodes a defensin-like (DEFL) family protein.
At2g40100	265722_at	3,1281E-06	0,00644066	4,088557943	8,683348959	6,708387868	6,635674164	6,573147932	10,74533215	10,3791832	11,05836844	LHCB4.3 (light harvesting complex PSII); chlorophyll binding
At4g33560	253298_at	0,00024998	0,031274333	4,073789273	6,674072532	4,615995534	4,297603126	4,997935029	8,999541006	9,307241262	7,826119239	unknown protein
At4g01630	255591_at	4,5344E-05	0,018420543	4,060451526	4,729626448	2,749848453	2,740761344	2,607592259	6,4869762	6,352422861	7,440157572	ATEXP17__ATHEXP ALPHA 1.13__ATEXPA17 (ARABIDOPSIS THALIANA EXPANSIN A17)
At3g29590	256924_at	0,00012717	0,024460803	3,994206302	5,534290011	3,27372863	4,141839432	3,195992518	7,949413603	7,675276925	6,969488957	AT5MAT; O-malonyltransferase/ transferase
At5g09470	245882_at	0,00027231	0,03218351	3,978008746	5,131622873	2,739491277	2,868913264	3,819450959	7,421815663	7,526295579	6,413770495	mitochondrial substrate carrier family protein
At1g65500	264635_at	7,4103E-05	0,020170651	3,932431522	6,09721136	4,47139985	4,210268389	3,711325277	8,56098219	7,538207381	8,091098511	unknown protein
At1g17710	259399_at	0,00013425	0,024662247	3,834679304	8,624777056	6,755387354	6,383858988	6,983065869	11,03327774	10,77418573	9,818886663	phosphatase
At5g09570	250515_at	5,2448E-05	0,018874816	3,766086752	6,941569555	5,046480963	4,742804118	5,386293454	9,070935626	9,122548516	8,280354649	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast;
At5g08030	250561_at	0,00050216	0,041449563	3,742204894	4,513541333	2,487615088	2,732314867	2,707386702	5,929950171	5,800491285	7,423489884	glycerophosphoryl diester phosphodiesterase family protein
At2g19970	265588_at	0,00016123	0,027182166	3,712449674	7,268794206	5,43113917	4,69356332	6,113005615	9,175208024	9,080298553	9,119550551	pathogenesis-related protein, putative

At1g43910	259507_at	1,6649E-05	0,011169642	3,707198756	5,940696815	4,001192655	3,795156411	4,464943246	7,984228226	7,471670274	7,926990078 AAA-type ATPase family protein
At3g19550	256569_at	0,00051698	0,041926418	3,69879747	4,618211899	2,374550545	2,468057	3,463831948	6,889097852	6,826866504	5,686867546 unknown protein
At1g73010	262369_at	0,00064991	0,044950062	3,664053269	10,69420197	8,700760993	8,605422722	9,280342277	13,07653143	12,97904969	11,52310468 phosphatase
At1g27730	261648_at	0,00083019	0,048828545	3,658907082	4,652574571	2,159729562	2,752632373	3,557001153	7,254022564	6,315817363	5,876244407 ZAT10__STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding
At5g64000	247314_at	0,00024402	0,031266832	3,656166702	4,887105538	3,566037916	2,875021396	2,736007248	7,21829692	6,907244011	6,020025735 AT2SAL2__SAL2; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase
At3g15310	257057_at	6,9428E-05	0,020046198	3,637275929	4,094756776	2,277770666	2,311750866	2,238834904	5,896898416	6,504962557	5,338323249
At5g42800	249215_at	0,00072062	0,047199623	3,549166323	10,58599016	9,344680835	9,157023345	7,932516811	12,77644193	12,54693672	11,75834131 M318__TT3__DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase
At2g36750	265197_at	1,4402E-05	0,010440956	3,548019728	4,702486528	3,014955304	3,149819812	2,620654876	6,680667903	6,124786312	6,624034959 UGT73C1 (UDP-GLUCOSYL TRANSFERASE 73C1); UDP-glucosyltransferase/ UDP-glycosyltransferase/
At2g47520	245173_at	5,267E-05	0,018874816	3,540799917	4,540990805	2,313570086	3,01601221	2,982190242	5,926798135	6,647542307	6,359831848 AP2 domain-containing transcription factor, putative
At3g10150	258932_at	7,4509E-05	0,020170651	3,499266005	4,187913414	2,120783963	2,182112321	3,01194495	6,171807319	5,629269492	6,011562437 ATPAP16__PAP16 (PURPLE ACID PHOSPHATASE 16); acid phosphatase/ protein serine/threonine phosphatase
At5g58770	247780_at	0,00010826	0,02287736	3,444913129	6,913929758	4,960918231	5,307540635	5,305960715	8,417428161	8,20491285	9,286817958 dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative
At1g76650	259879_at	0,00030809	0,033800422	3,432556868	5,331632744	3,855698748	3,488023909	3,502340272	7,2979229	7,613927758	6,231882876 CML38__calcium-binding EF hand family protein
At2g39330	266989_at	4,3099E-05	0,018408786	3,419434298	4,88252776	2,941131359	3,098395741	3,478904733	6,770238557	6,886798502	6,119697669 JAL23 (JACALIN-RELATED LECTIN 23)
At1g65060	261907_at	0,00016783	0,027942325	3,353181769	8,41757297	6,744459487	7,086659627	6,391827143	10,54899733	10,24532667	9,488167566 4CL3; 4-coumarate-CoA ligase
At2g19990	265586_at	8,2354E-05	0,021435549	3,351901531	5,426103239	3,472014698	3,408521114	4,369921609	7,096147468	7,252828614	6,957185932 PR-1-LIKE (PATHOGENESIS-RELATED PROTEIN-1-LIKE)
At1g62580 A	265105_s_at	3,5562E-05	0,017929746	3,13050149	3,815071055	2,385845522	2,207529133	2,156086273	4,955362682	5,391079444	5,794523273 flavin-containing monooxygenase family protein / FMO family protein
At5g41080	249337_at	5,4433E-05	0,018874816	3,128554622	5,042160369	3,393801842	3,339973975	3,699873355	6,450421077	7,098553365	6,270338598 glycerophosphoryl diester phosphodiesterase family protein
At4g22870 A	254283_s_at	0,00057974	0,042332139	3,108681088	9,697647978	8,064931878	8,639887922	7,725102502	11,77329181	11,4288342	10,55383955 leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase, putative
At5g48880	248625_at	5,021E-06	0,007244828	3,094924914	8,868752032	7,173217865	7,581797382	7,208853478	10,57090506	10,45186612	10,22587229 KAT5__PKT1__PKT2 (PEROXISOMAL 3-KETO-ACYL-COA THIOLASE 2); acetyl-CoA C-acyltransferase/ catalytic
At1g06000	260955_at	9,7942E-05	0,022072294	3,062756088	9,558715966	7,56847844	8,211249958	8,30228537	11,31853436	11,25741523	10,69433244 UDP-glucuronosyl/UDP-glucosyl transferase family protein
At5g24150	249774_at	0,00069387	0,046425208	3,059323766	7,32519589	5,352966647	5,664458471	6,369176904	8,805574295	8,275868282	9,483130742 SQP1; squalene monooxygenase
At5g46050	248932_at	5,8482E-06	0,007410981	3,033150032	4,100191576	2,434437699	2,409301751	2,90711023	5,651562364	5,664326686	5,534410727 ATPTR3__PTR3 (PEPTIDE TRANSPORTER 3); dipeptide transporter/ transporter/ tripeptide transporter
At1g23140	264893_at	9,4312E-05	0,022072294	2,986643374	8,453435597	6,931413782	6,846452965	7,102474983	10,28189075	10,17808438	9,380296725 C2 domain-containing protein
At3g02550	258487_at	0,00032194	0,03399751	2,886669506	8,26299366	6,727768416	6,420495087	7,310713217	9,34491986	10,21168035	9,562385026 LBD41 (LOB DOMAIN-CONTAINING PROTEIN 41)
At5g51720	248377_at	0,0003901	0,037619787	2,858655263	8,015864648	6,84127239	6,960758334	5,957580326	9,362135981	9,128210092	9,845230764 unknown protein
At1g29720	246633_at	3,1767E-05	0,017673137	2,791861931	4,038413904	2,671906611	2,667403468	2,588138737	5,01661085	5,746595723	5,539828036 protein kinase family protein
At1g69880	260408_at	1,2505E-05	0,00983553	2,729950058	4,757617656	3,247016084	3,20056088	3,730350919	6,105958224	6,051013168	6,210806664 ATH8 (thioredoxin H-type 8)
At5g20410	246075_at	0,00013515	0,024662247	2,719508327	8,333937447	6,808423782	7,001681022	7,112445045	9,935150728	10,00061108	9,14531302 ATMGD2__MGD2; 1,2-diacylglycerol 3-beta-galactosyltransferase/ UDP-galactosyltransferase/ transferase, transferring glycosyl
At3g15650	258270_at	0,00042611	0,038723411	2,65226808	8,470377081	6,58516579	7,283636324	7,563927009	10,14509256	9,827457378	9,416983421 phospholipase/carboxylesterase family protein
At1g77120	264953_at	0,00069615	0,046425208	2,650245778	10,61052595	9,210988747	9,348642396	9,29657805	12,03800072	12,5664689	11,2024769 ATADH__ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase

At3g51240	252123_at	0,00058739	0,042332139	2,62849183	10,43574813	8,857999805	9,577339458	8,929167374	12,1648535	11,93043165	11,15469698	F3'H_TT6__F3H (FLAVANONE 3-HYDROXYLASE); naringenin 3-dioxygenase
At3g16330	257517_at	3,6158E-05	0,017929746	2,6212777	5,996054291	5,027206885	4,597717358	4,431322081	7,533504672	7,206939861	7,17963489	unknown protein
At1g09240	264261_at	0,00015762	0,027068898	2,523878024	4,555530336	3,192387703	3,156441284	3,531944985	6,282365209	5,428875629	5,741167207	ATNAS3__NAS3 (NICOTIANAMINE SYNTHASE 3); nicotianamine synthase
At1g19200	256014_at	0,00030822	0,033800422	2,518257856	6,489076475	4,863225544	5,117903303	5,708713793	8,058763168	7,800665178	7,385187863	senescence-associated protein-related
At1g05680	263231_at	0,00026073	0,031479337	2,517774161	8,552275029	7,020425914	7,178032618	7,681705314	9,580057995	9,575634671	10,27779366	UDP-glucuronosyl/UDP-glucosyl transferase family protein
At1g30040	260023_at	0,00065452	0,045104372	2,460341005	5,082104313	3,774430516	3,70439699	4,076973925	6,793654005	6,504395363	5,638775079	ATGA2OX2 (GIBBERELLIN 2-OXIDASE); gibberellin 2-beta-dioxygenase
At4g02330	255524_at	0,00073045	0,047199623	2,458631462	6,976986089	5,697526826	5,190363121	6,355121128	8,52849131	8,026116847	8,064297302	ATPMEPCRB; pectinesterase
At3g10040	258930_at	0,00025464	0,031274333	2,450297176	5,536912834	4,567173085	3,995831437	4,372288215	6,666528806	7,226434276	6,393221183	transcription factor
At2g04032	263480_at	5,8677E-05	0,018874816	2,434308932	6,043826777	4,936673525	4,489542043	5,053801365	7,410026276	7,373563638	6,999353816	ZIP7 (ZINC TRANSPORTER 7 PRECURSOR); cation transmembrane transporter/ metal ion transmembrane transporter/ zinc ion
At3g59140	251503_at	0,00076155	0,047924887	2,425571816	7,827036737	6,281491499	6,325490489	7,235770498	9,34147879	9,127687828	8,650301318	ATMRP14; ATPase, coupled to transmembrane movement of substances
At2g16060	263096_at	0,00048228	0,041201286	2,399190375	9,437110596	8,298814957	7,970007325	8,443723944	10,03572529	10,87699683	10,99739523	ARATH GLB1_ATGLB1_GLB1_NSHB1__AHB1 (ARABIDOPSIS HEMOGLOBIN 1); oxygen binding / oxygen transporter
At3g29810	245228_at	4,0226E-05	0,018408786	2,371247275	5,640273974	4,64661637	4,201421297	4,515913341	6,850503263	7,05952305	6,567666519	COBL2 (COBRA-LIKE PROTEIN 2 PRECURSOR)
At2g45220	245148_at	5,83E-05	0,018874816	2,354353927	5,096788839	3,577693162	4,014215254	4,166927209	6,374484048	6,395592343	6,051821017	pectinesterase family protein
At2g17280	264907_at	5,5031E-05	0,018874816	2,350197493	7,886387077	6,381319118	6,751716686	7,000829187	8,963703416	8,959810066	9,260943989	phosphoglycerate/bisphosphoglycerate mutase family protein
At5g15120	250152_at	5,9219E-05	0,018874816	2,335403589	7,499393301	6,472566645	6,046751825	6,47575605	8,659418901	8,932434148	8,409432237	unknown protein
At3g21560	258167_at	0,00052489	0,041926418	2,33063435	9,075596526	7,648245656	8,16514309	7,917449306	10,40412751	10,64846812	9,670145472	UGT84A2; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase
At2g29670	266617_at	0,0002151	0,030656428	2,321098409	9,888489352	8,674349732	8,697370657	8,812100055	11,22367577	11,400303	10,5231369	binding
At2g03020 A	266772_s_at	9,6425E-05	0,022072294	2,313943403	7,080237844	5,635157268	5,950667269	6,183973891	7,932316955	8,287654085	8,491657598	heat shock protein-related
At5g05270	250794_at	0,00028499	0,032976083	2,245843701	7,566763316	5,89743146	6,750254751	6,683838185	8,625520419	8,654399315	8,789135766	chalcone-flavanone isomerase family protein
At5g59490	247727_at	0,00052451	0,041926418	2,216411312	5,272419494	4,010303324	4,213189404	4,269148785	6,621077899	6,742570613	5,778226936	haloacid dehalogenase-like hydrolase family protein
At2g29350	266292_at	9,8701E-05	0,022072294	2,213969879	4,715433577	3,855404966	3,206027511	3,763913436	5,978204086	5,790309403	5,698742062	SAG13; alcohol dehydrogenase/ oxidoreductase
At1g02920 A	262119_s_at	1,699E-06	0,005994532	2,167180981	11,78747163	10,5925735	10,75156244	10,76750749	13,0009043	12,77454837	12,8377337	ATGSTF7_ATGSTF8_GST11__GSTF7; copper ion binding / glutathione binding / glutathione transferase
At1g65490	264636_at	0,00068666	0,046339137	2,160018913	7,1585385	5,954971241	5,713084363	6,567531527	8,302262373	7,864605134	8,548776362	unknown protein
At3g04000	258815_at	0,00011133	0,02287736	2,149877172	7,043262347	5,875370183	6,031572082	5,998029017	8,190131806	7,719102622	8,44536837	short-chain dehydrogenase/reductase (SDR) family protein
At3g10450	258923_at	0,00085716	0,049124973	2,122451528	6,524766809	5,074061966	5,195157291	6,12140388	7,500771053	7,615058857	7,64214781	SCPL7 (SERINE CARBOXYPEPTIDASE-LIKE 7); serine-type carboxypeptidase
At1g71330 A	259937_s_at	6,7295E-05	0,019679447	2,120611976	7,28743359	5,924662044	6,175171508	6,581549254	8,297575984	8,374944652	8,370698099	ATNAP5; ATPase, coupled to transmembrane movement of substances / transporter
At4g08770	255110_at	0,00023345	0,030973716	2,100840635	7,821074133	6,964851529	6,305814927	7,04129499	8,896912756	9,008451824	8,709118771	peroxidase, putative
At1g01060	261569_at	0,00038179	0,037216203	2,093289869	3,41544724	2,299751567	2,497749306	2,308906042	3,928721268	4,677036938	4,780518316	LHY1__LHY (LATE ELONGATED HYPOCOTYL); DNA binding / transcription factor
At1g76190	261776_at	0,00031142	0,033917894	2,081382308	3,78541491	2,849442647	2,848708857	2,536019764	5,270129172	4,766586323	4,441602696	auxin-responsive family protein
At5g52320	248353_at	0,00042182	0,038723411	2,073887121	6,735552542	5,163938564	5,992563775	5,939324604	7,847518885	7,856439734	7,613529688	CYP96A4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding

At5g10130	250469_at	0,00039088	0,037619787	2,065532135	6,571994762	5,535168148	5,132271483	5,950246451	7,497838226	7,879140005	7,437304257	pollen Ole e 1 allergen and extensin family protein
At5g24160	249775_at	0,00011976	0,023753925	2,059901133	8,651986508	7,737167147	7,296990043	7,831950635	9,803118218	9,826525391	9,416167613	SQE6 (SQUALENE MONOOXYGENASE 6); FAD binding / oxidoreductase/ squalene monooxygenase
At1g50110	261636_at	0,00020431	0,030330161	2,053722648	6,76594309	5,392438722	5,804269301	6,020537275	8,077233054	7,725269291	7,575910898	branched-chain amino acid aminotransferase 6 / branched-chain amino acid transaminase 6 (BCAT6)
At5g49330	248596_at	5,0185E-05	0,018874816	2,036662373	7,070811496	5,916683025	6,200507379	6,040250524	8,237602472	8,246993392	7,782832184	AtMYB111 (myb domain protein 111); DNA binding / transcription factor
At2g23910	266578_at	0,00023965	0,031179193	2,032069871	8,631306019	7,722991776	7,859315816	7,263505657	9,849954082	9,764768578	9,327300203	cinnamoyl-CoA reductase-related
At5g01840	251062_at	0,00066781	0,045606769	2,025374694	5,25056662	3,838075788	4,092228156	4,783333876	6,141163042	6,176705154	6,471893706	ATOFP1__OFP1 (OVATE FAMILY PROTEIN 1); protein binding / transcription repressor
At3g59010	251509_at	0,00072891	0,047199623	2,024114769	7,419103663	6,702727833	6,249942684	6,268468317	8,747769	8,649234125	7,896480015	pectinesterase family protein
At3g27220	257153_at	0,00021644	0,030656428	2,021468391	6,66658794	5,970627859	5,412336333	5,58459704	7,509468382	8,014030041	7,508467982	kelch repeat-containing protein
At5g15070	246551_at	0,00010383	0,02287736	1,987551813	5,171646814	4,127748148	4,002278142	4,403586431	6,289427616	6,356249154	5,850591391	acid phosphatase/ oxidoreductase/ transition metal ion binding
At2g32190 A	265670_s_at	0,00017274	0,027992881	1,982297249	6,39948801	5,201366677	5,626929719	5,396721762	7,746117468	7,140226507	7,285565929	unknown protein
At5g13930	250207_at	0,00031826	0,03399751	1,96999062	12,54635745	11,77456654	11,68394785	11,22557201	13,80786585	13,59972993	13,18646249	ATCHS_CHS__TT4 (TRANSPARENT TESTA 4); naringenin-chalcone synthase
At1g09500	264514_at	0,00083272	0,048828545	1,965733777	6,739563989	6,270411657	5,625931158	5,373748487	8,023161222	7,594751551	7,549379859	cinnamyl-alcohol dehydrogenase family / CAD family
At2g25000	263536_at	0,00019769	0,030330161	1,942332013	5,865009489	5,059996851	4,900747658	4,720785938	7,047831281	7,022516834	6,43817837	ATWRKY60__WRKY60; transcription factor
At5g20400	246098_at	0,00039766	0,038112151	1,921972329	8,182495101	7,436788841	7,105566506	7,122171463	9,421068387	9,325249863	8,684125548	oxidoreductase, 2OG-Fe(II) oxygenase family protein
At5g51500	248407_at	0,00041711	0,038676323	1,92084896	4,216127386	3,118977568	2,924314451	3,723816699	5,350044875	5,036670282	5,142940443	pectinesterase family protein
At5g49520	248611_at	2,072E-06	0,005994532	1,918074083	3,078272773	2,204729335	1,994275058	2,158702803	4,031173599	4,121458682	3,959297164	AtWRKY48__WRKY48; transcription factor
At5g63580	247358_at	0,00085406	0,049124973	1,906499552	3,543243867	2,958719715	2,443241049	2,36802151	4,721963973	4,739586749	4,027930208	FLS2 (FLAVONOL SYNTHASE 2); flavonol synthase
At4g17970	254697_at	0,00045005	0,039635644	1,90189433	7,101668044	6,429436768	6,130739389	5,891986478	8,128668724	8,36800788	7,661169023	unknown protein
At2g45210	245136_at	0,00056023	0,042332139	1,90082534	7,793289689	6,759586202	6,900411073	6,868633781	8,996308545	9,027668494	8,207130036	auxin-responsive protein-related
At1g75388 A	261114_at	0,00042052	0,038723411	1,880540862	8,338725491	7,433722534	7,01258773	7,749054917	9,26163961	9,521519223	9,053828935	CPuORF5 (Conserved peptide upstream open reading frame 5)
At5g38710	249527_at	0,00037738	0,037216203	1,877745438	4,706210539	3,743692351	3,783455615	3,774865496	6,044965586	5,196645743	5,693638445	proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative
At3g60160 A	251457_s_at	1,2202E-05	0,00983553	1,875311857	5,515069079	4,607726552	4,645390342	4,479122559	6,660044912	6,31552962	6,382600492	ATMRP9; ATPase, coupled to transmembrane movement of substances
At1g17420	261037_at	0,00043349	0,039082426	1,865435868	3,110233384	2,04048153	2,041336155	2,450728666	4,452662191	3,932534201	3,743657563	LOX3; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incor
At5g55930	248037_at	2,2109E-06	0,005994532	1,843706923	4,842809583	4,026182428	3,792241677	3,94444426	5,765192928	5,823959471	5,704836734	ATOPT1__OPT1 (OLIGOPEPTIDE TRANSPORTER 1); oligopeptide transporter
At4g21680	254396_at	9,1236E-06	0,008429685	1,837759547	4,647190491	3,694180278	3,685809269	3,804942606	5,420986938	5,757473653	5,519750204	proton-dependent oligopeptide transport (POT) family protein
At4g21990	254343_at	0,00057959	0,042332139	1,812039198	11,73864514	10,97621492	10,6033461	10,91831562	12,96284822	12,78191514	12,18923087	ATAPR3__PRH-26__PRH26__APR3 (APS REDUCTASE 3); adenylyl-sulfate reductase
At3g17998 A	258218_at	3,2598E-05	0,017703586	1,805037291	9,540038413	8,44135009	8,571705447	8,899503767	10,47296718	10,38506261	10,46964138	CPuORF30 (Conserved peptide upstream open reading frame 30)
At5g50200	248551_at	0,00019912	0,030330161	1,798273616	7,793144674	7,017273755	7,006992338	6,657757504	8,663884811	8,416770743	8,996188893	ATNRT3.1__NRT3.1__WR3 (WOUND-RESPONSIVE 3); nitrate transmembrane transporter
At5g51850	248372_at	6,811E-07	0,005994532	1,78990205	4,383432731	3,545560282	3,5213691	3,398515735	5,303107964	5,309499718	5,222543585	unknown protein
At3g27170	256751_at	1,2437E-06	0,005994532	1,766296834	5,695570844	4,800189371	4,795948884	4,841129027	6,549714697	6,695263853	6,491179233	ATCLC-B__CLC-B (CHLORIDE CHANNEL B); anion channel/ voltage-gated chloride channel

At1g61380	264767_at	9,5747E-06	0,008429685	1,765709789	5,670936742	4,891566965	4,69277617	4,779902407	6,725561142	6,470266712	6,465547054	SD1-29 (S-DOMAIN-1 29); carbohydrate binding / kinase/ protein kinase
At1g28600	262745_at	0,000254	0,031274333	1,764147994	9,283163421	8,044917934	8,684584187	8,47376615	10,30024821	10,22044226	9,975021782	lipase, putative
At5g17050	246468_at	0,00061578	0,043485873	1,75989526	8,82460891	7,47929533	8,302711996	8,051976512	9,800652562	9,767340402	9,545676655	UGT78D2 (UDP-GLUCOSYL TRANSFERASE 78D2); UDP-glycosyltransferase/ anthocyanidin 3-O-glucosyltransferase/ quercetin 3
At4g14680	245254_at	4,2469E-05	0,018408786	1,733254445	7,951539757	6,928474915	6,967216503	7,359046186	8,876610348	8,764410679	8,813479913	APS3; sulfate adenyltransferase (ATP)
At1g72920	262382_at	0,00034717	0,035039549	1,728570513	4,258489964	3,507796938	3,534227855	3,140589328	5,429761594	5,1398629	4,798701166	disease resistance protein (TIR-NBS class), putative
At2g23560	267123_at	0,00049933	0,041449563	1,721473049	4,449874439	3,262918488	3,765835603	3,738659652	5,262615582	5,033948388	5,63526892	ATMES7__MES7 (METHYL ESTERASE 7); hydrolase/ hydrolase, acting on ester bonds / methyl indole-3-acetate esterase/ methyl
At4g10120	255016_at	0,00048975	0,041449563	1,720686278	9,694054636	8,892414144	8,917107012	8,691613335	10,777909	10,78579017	10,09949415	ATSP54F; transferase, transferring glycosyl groups
At5g02190	251025_at	0,00058973	0,042332139	1,707357891	2,976580459	2,154803602	2,140783444	2,073117494	4,129904364	4,016234185	3,344639663	ATASP38__PCS1 (PROMOTION OF CELL SURVIVAL 1); aspartic-type endopeptidase/ peptidase
At5g20830	245998_at	0,00016207	0,027182166	1,705111766	8,928481827	8,011925388	8,000060585	8,215791858	9,735005323	10,09946697	9,508640832	ASUS1__atus1__SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase
At3g14850	256600_at	0,00076924	0,047924887	1,700697128	5,203740131	4,515829168	4,478771819	4,065573714	6,470200986	5,948793859	5,743271241	unknown protein
At1g65840	262933_at	9,6016E-05	0,022072294	1,696136905	9,08355906	7,936990568	8,48463387	8,284847384	9,853141127	9,985273515	9,956467897	PAO4__ATPAO4 (ARABIDOPSIS THALIANA POLYAMINE OXIDASE 4); amine oxidase/ polyamine oxidase
At4g15490	245352_at	0,00028683	0,032976083	1,695051882	8,547862196	7,460833997	7,992038248	7,648136519	9,121224461	9,577710042	9,487229906	UGT84A3; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase/ transferase, transferring glycosyl groups
At1g74710	262177_at	0,00046567	0,040387681	1,687334912	5,535330016	4,860457811	4,278547643	4,935982225	6,566219609	6,352640962	6,218131845	EDS16__ICS1__SID2__isochorismate synthase 1 (ICS1) / isochorismate mutase
At5g67400	246991_at	0,00041079	0,038559756	1,68026091	8,815138434	7,870905969	7,931705856	8,122412112	9,833043834	9,897262751	9,23550008	peroxidase 73 (PER73) (P73) (PRXR11)
At5g44110	249063_at	5,0641E-05	0,018874816	1,662515712	9,474729001	8,472892795	8,539883002	8,91763764	10,26112002	10,31563985	10,3412007	ATNAP2__ATPOP1__POP1; transporter
At4g23600	254232_at	4,0389E-05	0,018408786	1,661742745	13,08631027	12,03003229	12,45340318	12,28288124	13,97166836	13,81309333	13,96678325	JR2__CORI3 (CORONATINE INDUCED 1); cystathionine beta-lyase/ transaminase
At5g08640	250533_at	2,7306E-05	0,015571283	1,650942227	9,794040831	9,151038287	8,9723169	8,782353964	10,72876164	10,6021792	10,52759499	FLS (FLAVONOL SYNTHASE); flavonol synthase
At4g11890	254869_at	0,00050278	0,041449563	1,632890049	3,541768852	2,563378118	2,643588812	2,969004552	4,641586765	4,436806031	3,996248834	protein kinase family protein
At1g21460	260876_at	0,00044325	0,039635644	1,616416517	7,975724689	7,023187248	7,028075789	7,451286254	8,964148766	8,936311779	8,451338298	nodulin MtN3 family protein
At1g69870	260410_at	1,5105E-05	0,010440956	1,603015013	10,71367323	9,731864857	10,00095852	10,00367378	11,48999947	11,61071509	11,44482764	proton-dependent oligopeptide transport (POT) family protein
At5g35970	249677_at	0,00072879	0,047199623	1,5796517	6,545426656	5,732130431	5,684743923	5,849928063	7,079437022	7,125502395	7,800818101	DNA-binding protein, putative
258288_at	258288_at	0,0001924	0,030058964	1,572431021	5,075921118	4,376638651	4,146483597	4,345994577	5,853133482	5,886406443	6,146869962	
At5g44190	249035_at	8,0304E-06	0,008429685	1,5655492	8,753368945	8,049709394	7,998453625	7,863620017	9,404283699	9,607111078	9,597035859	ATGLK2__GPRI2__GLK2 (GOLDEN2-LIKE 2); DNA binding / transcription factor/ transcription regulator
At2g28690	263436_at	0,00059361	0,042416886	1,540535402	3,256850516	2,548581907	2,473481137	2,437685401	3,671261381	3,982312536	4,427780733	unknown protein
At3g52190	256677_at	8,9711E-05	0,021769263	1,538646992	8,555845791	7,61661769	7,715592488	8,027356709	9,40910379	9,398156014	9,168248058	PHF1 (PHOSPHATE TRANSPORTER TRAFFIC FACILITATOR1); nucleotide binding
At4g27280	253915_at	0,00081938	0,048828545	1,525231588	8,05186365	7,540946648	7,245729361	7,081067559	9,076020164	8,93137315	8,436045016	calcium-binding EF hand family protein
At2g41010	267069_at	0,00046203	0,040378934	1,517892373	5,926198068	4,833304652	5,491248528	5,177202464	6,536822948	6,819259287	6,699350528	ATCAMP25 (ARABIDOPSIS THALIANA CALMODULIN (CAM)-BINDING PROTEIN OF 25 KDA); calmodulin binding
At3g13650	256781_at	0,00062333	0,043883299	1,493641015	8,48116922	7,447758882	7,62467092	8,130616334	9,266783043	9,330918425	9,086267713	disease resistance response
At3g12700	257697_at	7,7355E-06	0,008429685	1,466756375	8,588688321	7,964568255	7,737025731	7,864336416	9,349350699	9,236809539	9,380039289	aspartyl protease family protein
At3g23290	256942_at	0,00056826	0,042332139	1,461540293	6,954794031	6,307696636	6,434732368	5,92964265	7,604121073	7,48953861	7,963032851	LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4)

At4g17840	254691_at	0,00022493	0,030656428	1,460634031	9,299579845	8,253876089	8,734332186	8,719580213	10,14926656	10,00300458	9,937419432	unknown protein
At2g31160	266479_at	0,0008774	0,049661382	1,441360749	6,299838527	5,820359265	5,204276004	5,712839187	7,163904413	6,777099876	7,120552414	LSH3 (LIGHT SENSITIVE HYPOCOTYLS 3)
At3g44990	252607_at	0,00062782	0,044063392	1,426013444	10,15633426	9,209110031	9,781333384	9,339539193	10,91272843	11,0421179	10,65317661	ATXTR8_XTR8 (XYLOGLUCAN ENDO-TRANSGLYCOSYLASE-RELATED 8); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucan
At1g72900	262381_at	0,00018335	0,028843601	1,420802073	7,184246851	6,448301374	6,258913898	6,714322173	7,955055402	7,725020768	8,003867492	disease resistance protein (TIR-NBS class), putative
At5g33290	246682_at	0,00082991	0,048828545	1,412653518	8,197085342	7,692802709	7,321345778	7,458127261	9,181784665	8,987781963	8,540669674	XGD1 (XYLOGALACTURONAN DEFICIENT 1); UDP-xylosyltransferase/ catalytic
At5g52810	248330_at	0,0002179	0,030656428	1,402848075	7,934786987	7,303145206	7,390156965	7,006786676	8,762756245	8,412107849	8,733768979	ornithine cyclodeaminase/mu-crystallin family protein
At1g73260	260101_at	0,00025502	0,031274333	1,382679769	9,428568912	8,655063103	8,744765498	8,811858483	10,43321587	10,00278642	9,923724102	trypsin and protease inhibitor family protein / Kunitz family protein
At1g64900	262882_at	8,3003E-05	0,021435549	1,359729438	7,427928042	6,669251961	6,829294707	6,745643301	7,963985562	8,019194488	8,340198234	CYP89A2 (CYTOCHROME P450 89A2); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding
At3g55120	251827_at	0,00046521	0,040387681	1,359695867	9,323904198	8,329907203	8,929347382	8,67291421	10,09397565	10,03549228	9,881788468	A11_CFI__TT5 (TRANSPARENT TESTA 5); chalcone isomerase
At1g06550	262619_at	0,00019886	0,030330161	1,355681787	9,457502424	8,856783174	8,650137441	8,832063977	10,36131992	10,15977472	9,884935311	enoyl-CoA hydratase/isomerase family protein
At2g31750	263473_at	0,00012761	0,024460803	1,353449443	10,54092036	9,865047379	9,687710162	10,03982939	11,37830233	11,22013144	11,05450148	UGT74D1 (UDP-glucosyl transferase 74D1); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ transferase, transferring
At4g08850	255116_at	0,00042792	0,038733791	1,340136779	8,868950295	8,054796256	8,077923241	8,463926219	9,556577776	9,737000828	9,32347745	kinase
At1g48320	262237_at	0,00012564	0,024460803	1,30844952	8,525747822	7,843670361	7,69056649	8,080332334	9,302979226	9,172392381	9,064546137	thioesterase family protein
At1g64405	259735_at	0,00080551	0,048606425	1,305689993	5,157335236	4,541468623	4,53697686	4,435025233	5,66956223	6,199531692	5,561446774	unknown protein
At3g49360	252282_at	7,1518E-05	0,020139907	1,300680088	8,083624427	7,572154457	7,458276091	7,269422601	8,778974736	8,836070255	8,586848423	glucosamine/galactosamine-6-phosphate isomerase family protein
At3g22540	256926_at	0,00081188	0,048606425	1,29061701	5,991111659	5,220585123	5,095082031	5,721742308	6,536857455	6,665551759	6,706851277	unknown protein
At5g45650	248961_at	0,00076795	0,047924887	1,289383086	7,257923963	6,706312298	6,247740193	6,885644768	7,836653954	7,991992727	7,879199837	subtilase family protein
At4g38950	252916_at	0,00066759	0,045606769	1,269717503	6,167753327	5,690563519	5,294088466	5,61403174	6,586512404	6,752349675	7,068974155	kinesin motor family protein
At1g22150	255958_at	0,00015876	0,027068898	1,259704245	2,741964867	2,136357468	2,120693886	2,079286878	3,635873038	3,210327661	3,269250269	SULTR1;3; sulfate transmembrane transporter
At1g12320	259520_at	0,00082782	0,048828545	1,24380986	4,71078228	4,424718787	3,942009502	3,899903762	5,153408198	5,452498562	5,39215487	unknown protein
At1g19450	260676_at	0,00011537	0,023288885	1,243619981	8,473598403	7,694974356	7,900289802	7,960101079	8,972260357	9,035378297	9,278586525	integral membrane protein, putative / sugar transporter family protein
At1g02520 A	260932_s_at	7,8467E-05	0,020811905	1,213607764	4,630445747	3,926082562	4,013440668	4,131402363	5,053175327	5,318626136	5,339947423	PGP11 (P-GLYCOPROTEIN 11); ATPase, coupled to transmembrane movement of substances
At3g50480	252170_at	0,00033941	0,03474939	1,208398083	5,931540618	5,389817157	5,250598369	5,341609203	6,6517505	6,710934543	6,244533936	HR4 (HOMOLOG OF RPW8 4)
At3g13760	256774_at	7,3455E-05	0,020170651	1,196435896	3,413398328	2,671265112	2,756538045	3,017737983	4,05416252	3,992132981	3,988553326	DC1 domain-containing protein
At4g33030	253386_at	6,3741E-05	0,019224063	1,196195261	11,73876748	11,13832398	11,07635565	11,20732991	12,44004471	12,42488736	12,14566325	SQD1; UDPsulfoquinovose synthase/ sulfotransferase
At3g08940	258993_at	0,0005592	0,042332139	1,178002659	12,58410906	12,11831234	11,72958196	12,1374289	12,97952808	13,23412182	13,30568128	LHCB4.2 (light harvesting complex PSII); chlorophyll binding
At5g06320	250676_at	0,00086421	0,049281754	1,170204508	9,664663605	9,108067117	8,90288781	9,227729126	10,49485666	10,29082769	9,963613232	NHL3
At5g54960	248138_at	0,00056548	0,042332139	1,157670932	9,493487531	8,663748952	9,011482773	9,06872447	9,946024167	10,27614898	9,994795844	PDC2 (pyruvate decarboxylase-2); carboxy-lyase/ catalytic/ magnesium ion binding / pyruvate decarboxylase/ thiamin pyrophosphat
At5g43980	249068_at	0,00053089	0,042047458	1,137547461	4,016875318	3,517861858	3,4868989	3,339544006	4,562294179	4,852748113	4,341904854	PDLP1 (PLASMODESMATA-LOCATED PROTEIN 1)
At1g74000	260335_at	0,00050902	0,041474262	1,130763164	3,534684246	3,014969965	2,96725694	2,925681085	4,041411323	3,868966964	4,389819196	SS3 (STRICTOSIDINE SYNTHASE 3); strictosidine synthase

At3g49110 A	252291_s_at	0,00084321	0,04906509	1,125563119	12,15644549	11,45820077	11,48816286	11,83462817	12,89362745	12,78529809	12,47875562	ATPCA_ATPRX33_PRX33__PRXCA (PEROXIDASE CA); peroxidase
At3g26690	257830_at	1,2029E-05	0,00983553	1,119215368	8,482064146	7,964465476	7,965881931	7,837021979	9,132250629	8,989530269	9,003234591	ATNUDT13__ATNUDX13 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 13); bis(5'-adenosyl)-pentaphosphate/ hydrolyzing
At1g33811	261981_at	0,00010951	0,02287736	1,113895513	9,992413603	9,466836746	9,376346561	9,463214234	10,4639223	10,42873015	10,75543163	GDSL-motif lipase/hydrolase family protein
At5g43060	249187_at	0,00013115	0,024662247	1,096883618	10,39230156	9,870796444	9,681767902	9,97901492	11,00230286	11,0151259	10,80480136	cysteine proteinase, putative / thiol protease, putative
At3g61220	251309_at	5,5622E-05	0,018874816	1,094741456	9,34126707	8,822880187	8,644000663	8,914808176	9,920344259	9,805448369	9,940120767	short-chain dehydrogenase/reductase (SDR) family protein
At1g22400	261934_at	0,00050607	0,041474262	1,068530113	6,742128612	6,078919563	6,167008619	6,377662485	7,308712646	7,061078802	7,459389558	ATUGT85A1__UGT85A1; UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ glucuronosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase
At4g34580	253244_at	0,00018205	0,028836448	1,062192236	6,271941413	5,858875553	5,575949343	5,78771099	6,657055025	6,920068596	6,831988973	SRH1__COW1 (CAN OF WORMS1); phosphatidylinositol transporter/ transporter
At4g27970	253828_at	0,0001049	0,02287736	1,054114782	3,922905647	3,460114144	3,455857899	3,271572726	4,337653764	4,411107272	4,601128079	SLAH2 (SLAC1 HOMOLOGUE 2); transporter
At2g19880	266703_at	0,00013994	0,025227635	1,035931674	7,481809004	6,982962843	6,955452205	6,953114454	7,875701579	8,207708682	7,915914264	ceramide glucosyltransferase, putative
At2g19570	265943_at	0,00026501	0,031649064	1,024880242	8,628235609	8,319715058	8,069885222	7,957786184	9,165948252	9,221257667	9,034821271	AT-CDA1_DESZ__CDA1 (CYTIDINE DEAMINASE 1); cytidine deaminase
At2g30490	267470_at	0,00049986	0,041449563	1,017221439	10,6676022	9,933712542	10,14371755	10,39954436	11,19700719	11,21607334	11,11555825	ATC4H_CYP73A5__C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase
At5g67300	246987_at	0,00029231	0,033047875	1,012670781	9,348652341	9,010615315	8,850943048	8,665392487	9,954208115	9,889594201	9,721160877	ATMYB44__ATMYBR1__MYBR1 (MYB DOMAIN PROTEIN R1); DNA binding / transcription factor
At3g56040	251741_at	0,00059506	0,042416886	1,005239452	8,726074777	8,005209474	8,405256144	8,259899533	9,298951301	9,06798361	9,319148597	UGP3 (UDP-GLUCOSE PYROPHOSPHORYLASE 3)
At1g17170	262518_at	0,00068969	0,04640631	1,004208292	10,34792684	9,88018657	9,973159775	9,684121741	11,08517971	10,76889149	10,69602176	GST__ATGSTU24 (GLUTATHIONE S-TRANSFERASE TAU 24); glutathione binding / glutathione transferase
At5g64870	247208_at	0,00029606	0,033103505	1,001513671	3,044500821	2,663323011	2,662925418	2,304983528	3,527353809	3,577004332	3,53141483	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole
At3g44720	252652_at	0,000854	0,049124973	0,988371474	7,579801166	6,791388155	7,171871093	7,293587039	8,057586454	8,086835778	8,077538476	ADT4 (arogenate dehydratase 4); arogenate dehydratase/ prephenate dehydratase
At3g51330	252098_at	0,00087133	0,0495637	0,984694958	5,098887599	4,437717538	4,481377984	4,900524838	5,619412334	5,632395206	5,521897694	aspartyl protease family protein
At2g23960	266561_at	9,8049E-05	0,022072294	0,980721479	2,612307838	2,291991246	2,06043547	2,013414579	3,151498842	3,102674503	3,053832387	defense-related protein, putative
At3g19000	256892_at	0,00011506	0,023288885	0,979129382	9,183874921	8,69059367	8,630665175	8,761671845	9,714829236	9,797372848	9,508116753	oxidoreductase, 2OG-Fe(II) oxygenase family protein
At4g14030 A	245285_s_at	0,00082666	0,048828545	0,961223568	10,84417167	10,19051024	10,28671504	10,61345437	11,23248436	11,27938829	11,46247771	SBP1 (selenium-binding protein 1); selenium binding
At4g23190	254241_at	4,4234E-05	0,018408786	0,957977406	6,404871497	5,966873648	5,841652032	5,9691227	7,000816983	6,823877907	6,826885709	AT-RLK3__CRK11 (CYSTEINE-RICH RLK11); kinase/ protein kinase
At5g38530	249515_at	0,0003328	0,034349098	0,950687563	9,616146191	9,126583757	8,969889499	9,325933971	10,13827081	9,981676232	10,15452288	tryptophan synthase-related
At2g31730	263467_at	0,00036374	0,036390055	0,947153726	7,566052179	7,107314448	7,166894213	7,003217289	7,978109869	7,889736292	8,251040965	ethylene-responsive protein, putative
At4g14010	245386_at	0,00031958	0,03399751	0,937688368	9,835667139	9,232561897	9,280216216	9,587690751	10,2553533	10,33214349	10,32603718	RALFL32 (ralf-like 32); signal transducer
At1g22410	261933_at	0,00078419	0,047924887	0,934552489	11,57553984	11,05928113	11,07453897	11,19097069	12,20731933	12,14289414	11,77823479	2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, putative / hydrolyzing
At3g04640	258792_at	0,00050911	0,041474262	0,910430627	6,800689535	6,510647386	6,23845574	6,287319537	7,378316914	7,30914577	7,08025186	glycine-rich protein
At5g64100	247297_at	0,00074629	0,0476833	0,906445073	8,804036696	8,59867822	8,272093719	8,18167054	9,321394173	9,275484665	9,17489886	peroxidase, putative
At1g58370	256025_at	0,0008068	0,048606425	0,903089025	6,483428196	6,11440356	5,829796535	6,151450954	7,111835023	6,875609216	6,817473886	ATXN1__RXF12; endo-1,4-beta-xylanase/ hydrolase, hydrolyzing O-glycosyl compounds
At5g60300	247626_at	0,00021808	0,030656428	0,887593072	6,85384803	6,372792143	6,406694822	6,450667517	7,386336961	7,399218217	7,107378519	lectin protein kinase family protein
At1g24020	263034_at	0,00060228	0,042797616	0,881882538	12,72933421	12,22677189	12,1284946	12,50991235	13,22581888	13,20779413	13,07721344	MPL423 (MPL-LIKE PROTEIN 423)

At3g51090	252097_at	0,00057466	0,042332139	0,869355403	5,570978084	5,072098634	5,074263619	5,262538895	6,046609708	6,158957495	5,811400156	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component un
At4g36010	253104_at	5,0819E-06	0,007244828	0,860202639	7,206378454	6,766196755	6,76761486	6,795019787	7,607427709	7,613320282	7,688691329	pathogenesis-related thaumatin family protein
At3g63300	251162_at	0,00070421	0,046425208	0,851921164	5,944313199	5,452242184	5,389559779	5,713255889	6,444954788	6,442629061	6,223237495	phosphoinositide binding
At1g51070	245746_at	0,00031963	0,03399751	0,839915903	9,74179042	9,397043789	9,210494399	9,357959215	10,22705062	10,26149971	9,996694781	basic helix-loop-helix (bHLH) family protein
At1g06420	259394_at	0,00063287	0,044281541	0,8351927	6,415189283	5,933768052	5,977752724	6,081258023	6,850371189	7,012727676	6,635258035	unknown protein
At3g06500	258507_at	9,1661E-06	0,008429685	0,826323958	6,89731761	6,468059961	6,530696988	6,453709943	7,336392601	7,261744319	7,333301847	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative
At2g43018	265244_at	0,00065007	0,044950062	0,820437408	6,878404053	6,467256833	6,287402892	6,649896323	7,356241581	7,189939763	7,319686927	CPuORF17 (Conserved peptide upstream open reading frame 17)
At3g16520	257205_at	0,00032956	0,034169696	0,813669549	11,31899313	10,97285346	10,73274024	11,03088138	11,68751848	11,69394185	11,79602339	UGT88A1__UDP-glucuronosyl/UDP-glucosyl transferase family protein
At2g34070	256725_at	0,00025019	0,031274333	0,810317541	9,407096749	9,115760481	8,830078619	9,059974836	9,861992407	9,780326133	9,794448019	unknown protein
At1g25450	255732_at	0,00025738	0,031394962	0,80894839	9,731828344	9,397118592	9,302358489	9,282585366	9,998793909	10,28964097	10,12047274	CER60__KCS5 (3-KETOACYL-COA SYNTHASE 5); fatty acid elongase
At2g19110	267488_at	0,0002257	0,030656428	0,799572267	7,955824037	7,679160338	7,57589185	7,413061524	8,28416125	8,42356587	8,359103393	HMA4; cadmium ion transmembrane transporter/ cadmium-transporting ATPase/ zinc ion transmembrane transporter
At2g41640	245119_at	0,0002061	0,030330161	0,775501326	5,106344519	4,656679086	4,632352438	4,866750043	5,562612364	5,472647542	5,44702564	transferase, transferring glycosyl groups
At4g24130	254201_at	0,00038983	0,037619787	0,757206284	7,459093216	7,022413111	7,089953566	7,129103544	8,005229839	7,802919133	7,704940101	unknown protein
At1g80360	260328_at	0,00017093	0,027992881	0,750817258	8,34505365	8,03268211	8,044336919	7,831329934	8,679589172	8,703698792	8,778098875	aminotransferase class I and II family protein
At5g49890	248580_at	0,0003042	0,033800422	0,73219987	7,048753902	6,540356727	6,77103023	6,736574945	7,493603378	7,338364578	7,412593555	ATCLC-C__CLC-C (CHLORIDE CHANNEL C); anion channel/ voltage-gated chloride channel
At1g36940	261292_at	0,00071517	0,047011595	0,719239355	5,956901488	5,738514597	5,641768778	5,411562056	6,279772876	6,286702734	6,383087886	unknown protein
At5g07830	250604_at	0,00077232	0,047924887	0,71355944	8,46512859	8,213915434	7,944829293	8,166301884	8,944145512	8,779264615	8,742314804	AtGUS2 (Arabidopsis thaliana glucuronidase 2); beta-glucuronidase
At3g03300	258863_at	0,00013127	0,024662247	0,709953341	6,414993028	6,052133914	6,053393861	6,074521299	6,88095529	6,772515421	6,656438384	ATDCL2__DCL2 (DICER-LIKE 2); ATP binding / ATP-dependent helicase/ RNA binding / double-stranded RNA binding / helicase/
At2g25820	266661_at	0,00027909	0,032792886	0,706276233	2,505628583	2,172753273	2,174490957	2,11022717	2,761183252	3,009402636	2,805714211	transcription factor
At3g55520	251799_at	0,00070386	0,046425208	0,68732723	9,27316655	9,050992465	8,78776278	8,949753558	9,557068612	9,735559369	9,557862514	immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative
At4g34050	253276_at	0,00027192	0,03218351	0,681375873	12,46026671	12,11207227	12,03832151	12,20834252	12,85675363	12,85911171	12,68699858	caffeoyl-CoA 3-O-methyltransferase, putative
At2g26530	245041_at	0,00024117	0,031179193	0,671498601	5,639122097	5,383170707	5,242170712	5,28477697	6,076016943	5,974028946	5,874568302	AR781
At2g04650	263619_at	4,4068E-05	0,018408786	0,664665416	6,439984777	6,088521296	6,173223651	6,06121126	6,735433246	6,818733508	6,7627857	ADP-glucose pyrophosphorylase family protein
At2g05260	263049_at	0,00020564	0,030330161	0,66048931	7,298954098	6,980382187	6,979219678	6,946526466	7,644779441	7,735207675	7,507609143	lipase class 3 family protein
At2g04450	263852_at	4,6839E-05	0,018420543	0,652771792	2,597209239	2,280246742	2,268279749	2,263943537	2,939856971	2,985016303	2,845912129	ATNUDT6 (Arabidopsis thaliana Nudix hydrolase homolog 6); ADP-ribose diphosphatase/ NAD or NADH binding / hydrolase
At5g51190	248448_at	0,00088194	0,049794485	0,641906776	2,487344034	2,172185698	2,173386053	2,153600187	2,863019284	2,624180534	2,937692447	AP2 domain-containing transcription factor, putative
At4g37310	253052_at	0,00077863	0,047924887	0,639309406	8,143895425	7,787472203	7,825889913	7,85936005	8,469622296	8,614588437	8,306439652	CYP81H1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding
At3g55980	251745_at	0,00023492	0,030973716	0,62405815	7,971370886	7,773507357	7,605221349	7,599296726	8,26314594	8,342558549	8,244495394	ATSZF1__SZF1 (SALT-INDUCIBLE ZINC FINGER 1); transcription factor
At1g09780	264668_at	0,0001474	0,026064047	0,610221104	11,34292142	10,93479477	11,09669544	11,08194238	11,6208808	11,64310506	11,68011005	2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative
At5g18630	250008_at	0,00047204	0,040784898	0,604959217	8,3844567	8,054563995	8,190212707	8,001154572	8,590715221	8,756421406	8,713672299	lipase class 3 family protein

At2g26080	266892_at	0,00017745	0,028504409	0,579286966	11,38415427	11,07457235	11,11770577	11,09125423	11,61133276	11,6332288	11,77683169	AtGLDP2 (Arabidopsis thaliana glycine decarboxylase P-protein 2); ATP binding / glycine dehydrogenase (decarboxylating)
At1g79720	261346_at	0,00054758	0,042332139	0,563885555	7,98342367	7,79203413	7,681283204	7,631125343	8,371513674	8,22151472	8,203070948	aspartyl protease family protein
At4g37870	253041_at	0,00035005	0,035174286	0,549650788	11,19823705	10,82187371	10,92265988	11,02570138	11,44979552	11,50216257	11,46722925	PEPCK_PCK1 (PHOSPHOENOLPYRUVATE CARBOXYKINASE 1); ATP binding / phosphoenolpyruvate carboxykinase (ATP)/ phosphoenolpyruvate carboxykinase (ATP)
At5g58870	247766_at	7,0609E-05	0,020132459	0,548146799	8,134468983	7,831788403	7,901819553	7,847578793	8,418053329	8,449793995	8,357779823	ftsH9 (FtsH protease 9); ATP-dependent peptidase/ ATPase/ metallopeptidase
At1g51890	246368_at	0,00057433	0,042332139	0,544097649	2,794026212	2,544192623	2,541680531	2,480059009	3,130398723	2,934360588	3,133465799	leucine-rich repeat protein kinase, putative
At5g52560	248305_at	0,00078818	0,047942471	0,515809109	8,768416066	8,557529639	8,403571576	8,570433319	8,937846443	9,050678392	9,090437028	ATUSP (ARABIDOPSIS THALIANA UDP-SUGAR PYROPHOSPHORYLASE); UTP-monosaccharide-1-phosphate uridylyltransferase/ UDP-glucose 4-epimerase
At4g17230	245247_at	0,00069643	0,046425208	0,512001048	7,302718641	7,059388061	7,014213177	7,066553113	7,654293053	7,58813703	7,433727411	SCL13 (Scarecrow-like 13); transcription factor
At1g12140	260993_at	0,00032089	0,03399751	0,456644686	8,367894272	8,162863301	8,132696955	8,123155533	8,574558234	8,535378134	8,678713478	FMO GS-OX5 (FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 5); 8-methylthiopropyl glucosinolate S-oxygenase/ flavin monooxygenase
At3g27380	257713_at	0,00083243	0,048828545	0,41939558	10,10596849	9,94635545	9,917077593	9,825379061	10,38116708	10,32109323	10,24473853	SDH2-1; electron carrier/ succinate dehydrogenase
At2g29630	266673_at	0,00043901	0,039424329	0,394307725	11,83771056	11,61926106	11,64667423	11,6557348	12,07990791	12,06236522	11,96232013	THIC (ThiaminC); ADP-ribose pyrophosphohydrolase/ catalytic/ iron-sulfur cluster binding
At2g39110	266196_at	0,00015743	0,027068898	0,381328232	5,65156525	5,4524621	5,44252554	5,487715763	5,856367165	5,819754166	5,850566769	protein kinase, putative

AGI ID	Affy ID	pvalue	BH	mean M	mean A	C1.CEL	C3.2.CEL	C3.CEL	T1.CEL	T3.2.CEL	T3.CEL	Annotation
DOWN-REGULATED												
At1g27690	261646_at	0,00088687	0,049949166	-0,296443669	7,570971065	7,742993774	7,688090415	7,72649451	7,409662706	7,466599211	7,391985776	unknown protein
At3g48750	252337_at	0,00067776	0,046148526	-0,341542652	10,03598317	10,22582477	10,19742729	10,19701142	9,799978533	9,889501771	9,906155221	CDC2A_CDC2AAT_CDK2_CDKA1_CDKA;1__CDC2 (CELL DIVISION CONTROL 2); cyclin-dependent protein kinase/ kinase/ protein binding
At1g74170	259902_at	0,00085492	0,049124973	-0,399430082	5,114861831	5,30700554	5,26069854	5,376026536	4,840985345	4,942708349	4,961746675	AtRLP13 (Receptor Like Protein 13); protein binding
At3g63120	251150_at	0,0004086	0,038559756	-0,431292062	7,932836707	8,211499977	8,166205946	8,06774229	7,699932267	7,712906833	7,738732929	CYCP1;1 (cyclin p1;1); cyclin-dependent protein kinase
At3g62370	251270_at	0,00081026	0,048606425	-0,446690105	8,553994033	8,835691387	8,726305543	8,770020327	8,250573289	8,419671673	8,321701978	unknown protein
At4g11960	254848_at	0,00041296	0,038604726	-0,451213794	8,756319625	8,928725115	9,033899416	8,983155034	8,457702919	8,560912947	8,573522318	PGRL1B (PGR5-Like B)
At5g27670	246735_at	0,00054656	0,042332139	-0,461455801	10,22337188	10,4856464	10,37391539	10,50273754	9,923253387	10,04440515	10,0102734	HTA7 (HISTONE H2A 7); DNA binding
At5g65490	247187_at	0,00077153	0,047924887	-0,46532091	6,993691972	7,28194548	7,272979195	7,124132608	6,712781907	6,745774827	6,824537818	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: chloroplast
At3g29035	258059_at	0,00075767	0,047924887	-0,484186359	7,383425275	7,625819029	7,525032153	7,725704182	7,186067693	7,146164891	7,091763703	ANAC059__ATNAC3 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 3); protein heterodimerization/ transcription factor
At3g01690	259181_at	0,00021033	0,030656428	-0,487587657	10,14703313	10,43877702	10,31934374	10,41436012	9,858979761	9,927650142	9,923088007	EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Alpha/beta hydrolase
At2g02760	267484_at	0,0008524	0,049124973	-0,489975864	12,20804415	12,5413504	12,47122949	12,34651634	11,89970307	12,02392824	11,96553733	UBC2__ATUBC2 (UBIQUITING-CONJUGATING ENZYME 2); ubiquitin-protein ligase
At3g20410	257621_at	0,00070291	0,046425208	-0,490359185	8,614730414	8,883099591	8,768878969	8,927751459	8,377625114	8,43920579	8,29182156	CPK9 (calmodulin-domain protein kinase 9); calmodulin-dependent protein kinase/ kinase
At5g58960	247741_at	0,00022847	0,030837281	-0,530971275	8,347495298	8,674223194	8,528753974	8,635965639	8,061181135	8,051401538	8,133446309	GIL1 (GRAVITROPIC IN THE LIGHT)
At4g14270	245602_at	0,00033972	0,03474939	-0,531991168	10,30873398	10,54132301	10,49941052	10,68345516	10,04155295	10,06845391	10,01820833	Protein containing PAM2 motif which mediates interaction with the PABC domain of polyadenyl binding proteins.
At1g49320	262388_at	0,00057843	0,042332139	-0,544598194	4,185429842	4,423215135	4,56463111	4,385340572	3,879972939	3,861368737	3,998050559	BURP domain-containing protein

At3g60390	251374_at	0,00049422	0,041449563	-0,554324246	7,07406409	7,45733118	7,289793939	7,306553518	6,715290975	6,8195581	6,855856825 HAT3 (HOMEODOMAIN-LEUCINE ZIPPER PROTEIN 3); transcription factor
At2g44900	266815_at	0,00083617	0,048905042	-0,570483573	6,843493613	7,089178355	7,037472921	7,259554923	6,648365367	6,527363796	6,499026316 armadillo/beta-catenin repeat family protein / F-box family protein
At1g30690	263226_at	0,00010886	0,02287736	-0,589871829	7,915864332	8,277605698	8,233517687	8,121277356	7,611982342	7,629448458	7,621354454 SEC1A cytosolic factor family protein / phosphoglyceride transfer family protein
At1g30210	245774_at	0,00077456	0,047924887	-0,595584375	8,085586843	8,407032057	8,346500562	8,396604474	7,781609236	7,64933447	7,932440261 ATTCP24__TCP24 (TEOSINTE BRANCHED1, CYCLOIDEA, AND PCF FAMILY 24); transcription factor
At2g38000	266090_at	0,00057847	0,042332139	-0,597651338	7,187914413	7,597237557	7,510790186	7,352192503	6,828911816	6,908841784	6,929512631 chaperone protein dnaJ-related
At2g45280	245147_at	0,00034444	0,034918303	-0,60354422	5,376725772	5,573380331	5,724864704	5,737248611	5,153163475	5,000596581	5,071100929 RAD51C__ATRAD51C; ATP binding / damaged DNA binding / protein binding / recombinase/ single-stranded DNA binding
At2g41890	267530_at	4,1679E-05	0,018408786	-0,616233196	6,624368463	6,892976559	6,967689342	6,936789284	6,370549883	6,281347108	6,296858604 curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein
At3g01310	259118_at	0,00017009	0,027992881	-0,616333647	9,575577001	9,826032665	9,914424392	9,910774417	9,215419002	9,367421091	9,219390441 acid phosphatase/ oxidoreductase/ transition metal ion binding
At4g31450	253539_at	0,00010916	0,02287736	-0,624272141	5,599204576	5,941036842	5,843264177	5,949720922	5,210845823	5,332284163	5,318075531 zinc finger (C3HC4-type RING finger) family protein
At5g19030	249966_at	8,8696E-05	0,021769263	-0,627028538	7,164458134	7,513637038	7,397448987	7,522831183	6,800839983	6,860913233	6,891078379 RNA recognition motif (RRM)-containing protein
At3g21650	258176_at	0,00075853	0,047924887	-0,643042272	8,837815162	9,27570881	9,024140224	9,178159858	8,615970124	8,50560632	8,427305633 serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative
At5g39590	249442_at	0,00028766	0,032976083	-0,646008382	10,72333776	11,18760192	10,98080108	10,97062284	10,39941595	10,41850757	10,38307718 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component
At1g17455	261039_at	0,00042513	0,038723411	-0,677678854	7,168902464	7,600965774	7,360044277	7,562215621	6,753418243	6,86367105	6,873099818 ELF4-L4 (ELF4-Like 4)
At3g04910	259080_at	0,00077999	0,047924887	-0,682470283	10,37175766	10,82508715	10,76588318	10,54800809	10,09556111	10,06679248	9,929213978 ATWNK1_ZIK4__WNK1 (WITH NO LYSINE (K) 1); kinase/ protein kinase/ protein serine/threonine kinase
At1g06390	259396_at	4,4388E-05	0,018408786	-0,693705671	9,365748091	9,754502397	9,633363453	9,749936928	9,011299952	9,059359893	9,896025922 ATGSK1__GSK1 (GSK3/SHAGGY-LIKE PROTEIN KINASE 1); glycogen synthase kinase 3/ kinase
At1g49740	261609_at	0,00026083	0,031479337	-0,703373315	7,735826719	8,020352746	8,206003513	8,036183871	7,455241184	7,40888084	7,288298161 phospholipase C/ phosphoric diester hydrolase
At1g51950	246376_at	0,00020595	0,030330161	-0,709797993	9,676078287	10,09888807	9,95191684	10,04212694	9,217169422	9,321435558	9,424932893 IAA18 (INDOLE-3-ACETIC ACID INDUCIBLE 18); transcription factor
At5g40610	249366_at	0,00053055	0,042047458	-0,727215798	7,468210884	7,868864877	7,857208686	7,769382785	7,030289516	6,997399612	7,286119826 glycerol-3-phosphate dehydrogenase (NAD+) / GPDH
At3g53950	251931_at	0,00057277	0,042332139	-0,731650814	7,657554246	8,122036317	7,830628814	8,117473828	7,33707033	7,27209927	7,266016919 glyoxal oxidase-related
At1g07250	256033_at	0,00058807	0,042332139	-0,733923773	8,71557499	9,20114002	9,134689734	8,911780876	8,25250875	8,385823449	8,40750711 UGT71C4 (UDP-GLUCOSYL TRANSFERASE 71C4); quercetin 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase
At1g05140	264584_at	0,00020553	0,030330161	-0,734253525	9,399747374	9,858819092	9,777885261	9,663918057	9,121294972	8,941063645	9,035503218 membrane-associated zinc metalloprotease, putative
At5g05100	250819_at	0,00030731	0,033800422	-0,739365836	9,864572997	10,32686893	10,1869651	10,18893372	9,413938647	9,431511298	9,639220293 nucleic acid binding
At1g12580	259484_at	0,00052569	0,041926418	-0,771618452	7,0803293	7,34718588	7,522788226	7,528441473	6,627150502	6,594637866	6,861771856 PEPKR1 (Phosphoenolpyruvate carboxylase-related kinase 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase
At5g52450	248335_at	0,0008107	0,048606425	-0,787370025	8,315978026	8,603583571	8,711149589	8,814255956	7,835260775	7,809976649	8,121641618 MATE efflux protein-related
At3g27820	257227_at	0,00086068	0,049203154	-0,791244585	10,2902356	10,77565996	10,80929994	10,47261378	9,884972672	9,990288725	9,80857852 ATMDAR4__MDAR4 (MONODEHYDROASCORBATE REDUCTASE 4); monodehydroascorbate reductase (NADH)
At5g22310	249887_at	0,00068657	0,046339137	-0,794076865	5,16107652	5,566145646	5,592695387	5,515503824	4,54299282	4,853005086	4,896116357 unknown protein
At5g23920	249810_at	0,00051851	0,041926418	-0,797015306	8,887840633	9,351472621	9,124552539	9,383019699	8,559307741	8,351830406	8,556860795 unknown protein
At1g50575	261867_at	0,00045249	0,039697336	-0,801712508	8,366549096	8,830783068	8,871450361	8,599982621	7,944137847	7,873779482	8,079161197 lysine decarboxylase family protein
At1g04400	263669_at	0,00015184	0,026642155	-0,836061173	10,11295638	10,69137221	10,43425829	10,4673304	9,696964719	9,657742754	9,730069912 AT-PHH1__FHA_PHH1__CRY2 (CRYPTOCHROME 2); blue light photoreceptor/ protein homodimerization
At1g55510	265070_at	9,3104E-05	0,022072294	-0,843142781	6,731373859	7,234745662	7,067454396	7,15663569	6,24246102	6,264759047	6,422187339 BCDH BETA1 (BRANCHED-CHAIN ALPHA-KETO ACID DECARBOXYLASE E1 BETA SUBUNIT); 3-methyl-2-oxobutanoate dehydrogenase

At2g36490	263909_at	0,00029087	0,033047875	-0,848216304	5,804752043	6,366644872	6,280427327	6,039508385	5,413129128	5,351014163	5,37778838	ROS1__DML1 (DEMETER-LIKE 1); DNA N-glycosylase/ DNA-(apurinic or apyrimidinic site) lyase/ protein binding
At2g42590	263494_at	0,000533	0,042068349	-0,854458009	11,48960921	12,05270006	11,92862984	11,76918474	11,17592555	11,10787496	10,9033401	GF14 MU__GRF9 (GENERAL REGULATORY FACTOR 9); calcium ion binding / protein binding / protein phosphorylated amino acid binding
At4g26530	253971_at	0,00023297	0,030973716	-0,861169316	10,16131069	10,46916	10,69898118	10,60754485	9,858901753	9,710652088	9,622624245	fructose-bisphosphate aldolase, putative
At1g68540	260260_at	0,00050336	0,041449563	-0,878652344	6,874695909	7,09904123	7,373672629	7,469352385	6,491642684	6,357929506	6,456537022	oxidoreductase family protein
At2g18280	265321_at	0,00032549	0,034056667	-0,89495346	9,528679531	10,05180507	10,00165739	9,875006317	9,057129707	9,256588515	8,92989018	AtTLP2 (TUBBY LIKE PROTEIN 2); phosphoric diester hydrolase/ transcription factor
At5g07950	250555_at	0,00055812	0,042332139	-0,911132481	7,119664637	7,611323023	7,511536818	7,602832791	6,877241997	6,659164853	6,455888338	unknown protein
At2g44660	266869_at	8,8907E-05	0,021769263	-0,92935492	7,099647729	7,488239173	7,503732352	7,70100404	6,640545361	6,551305132	6,713060313	transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
At1g48240	262245_at	0,00082056	0,048828545	-0,932587794	7,101255124	7,757605816	7,294392425	7,650648824	6,649368741	6,600772092	6,654742848	NPSN12__ATNPSN12; protein transporter
At5g63810	247348_at	9,3364E-05	0,022072294	-0,941452376	8,04260181	8,465532253	8,553065213	8,521386528	7,661402548	7,409477566	7,644746754	BGAL10 (beta-galactosidase 10); beta-galactosidase/ catalytic/ cation binding
At3g16450	259384_at	0,00044501	0,039635644	-0,952523038	11,89886685	12,25490541	12,44878095	12,42169873	11,5441655	11,51984516	11,20380532	jacalin lectin family protein
At5g58140	247853_at	8,9313E-05	0,021769263	-0,956970434	9,610065328	10,10442142	10,069224	10,09200621	9,295309062	9,091788001	9,00764327	NPL1__PHOT2 (PHOTOTROPIN 2); FMN binding / blue light photoreceptor/ kinase/ protein serine/threonine kinase
At3g25690	256754_at	0,0005597	0,042332139	-0,97658787	10,80463007	11,50020898	11,32064946	11,05791359	10,39372215	10,24188969	10,31339657	CHUP1 (CHLOROPLAST UNUSUAL POSITIONING 1)
At5g12440	245183_at	0,00022227	0,030656428	-0,99376023	6,736006408	7,385874422	7,205025688	7,107759459	6,252636145	6,100524383	6,364218353	nucleic acid binding / nucleotide binding / zinc ion binding
At4g16330	245360_at	0,00022562	0,030656428	-0,995473516	8,732971839	9,250071667	9,127880559	9,314173566	8,127920659	8,146580974	8,431203609	oxidoreductase/ oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as
At1g61900	264307_at	2,3455E-05	0,014459665	-1,010667043	8,161911612	8,780806709	8,625727724	8,595200969	7,64856398	7,713756611	7,607413681	unknown protein
267495_at	267495_at	0,00085542	0,049124973	-1,030190414	4,412238884	5,025612857	5,138434748	4,617954666	3,883729954	3,89218171	3,915519367	
At3g14690	258094_at	0,00067979	0,046148962	-1,037275875	9,047721805	9,656151581	9,741123642	9,301804005	8,57724655	8,392335245	8,617669809	CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding
At1g10760	262784_at	0,00029266	0,033047875	-1,048946292	11,23935574	11,81150084	11,92550203	11,55448378	10,84020351	10,65510591	10,64933835	GWD_GWD1_SOP_SOP1__SEX1 (STARCH EXCESS 1); alpha-glucan, water dikinase
At2g33390	255833_at	2,5337E-05	0,01520891	-1,062309822	7,497204543	8,103165241	8,063691573	7,918221547	6,921698451	6,923256794	7,053193651	unknown protein
At5g43700	249109_at	0,00056046	0,042332139	-1,066457536	9,020944377	9,839995293	9,44844316	9,37408098	8,430506028	8,557142	8,475498799	IAA4__ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor
At1g13640	256071_at	0,00055273	0,042332139	-1,083484018	7,815374925	8,633523236	8,206876588	8,230950977	7,167661477	7,274052868	7,379184403	phosphatidylinositol 3- and 4-kinase family protein
At2g03710	264041_at	0,00055633	0,042332139	-1,083627456	6,496707421	7,332159007	6,888890268	6,894514171	5,927965688	5,908078496	6,028636893	AGL3__SEP4 (SEPALLATA 4); DNA binding / transcription factor
At2g32480	267061_at	0,0003722	0,036912307	-1,096964969	9,756611507	10,23405581	10,38996709	10,29125908	9,195974354	8,984937785	9,44347493	membrane-associated zinc metalloprotease, putative
At5g16000	246483_at	0,00064732	0,044950062	-1,110760657	7,863707681	8,34549436	8,489066193	8,422703476	7,432091649	7,493557341	6,999333069	NIK1 (NSP-INTERACTING KINASE 1); kinase
At2g39400	266983_at	1,5031E-05	0,010440956	-1,128857431	7,035057208	7,520730618	7,57360881	7,704118342	6,470834884	6,402817745	6,538232847	hydrolase, alpha/beta fold family protein
At3g57190	251670_at	0,00079084	0,047976068	-1,135849107	7,053226366	7,910535058	7,605055077	7,347862623	6,566530819	6,514624279	6,374750339	peptide chain release factor, putative
At3g26030	258060_at	4,0814E-06	0,006657245	-1,146532423	8,231746111	8,854022527	8,785004822	8,776009619	7,676061578	7,582896911	7,71648121	ATB' DELTA; protein phosphatase type 2A regulator
At1g68550 A	260209_at	0,00024536	0,031266832	-1,174288261	8,376445886	8,909897515	8,963736938	9,017135597	7,566017638	7,773615316	8,028272312	AP2 domain-containing transcription factor, putative
At3g57040	251665_at	0,0003244	0,034056667	-1,211220135	7,852989666	8,519382326	8,27913031	8,57286564	7,323236501	7,011691989	7,407210306	ATRR4__ARR9 (RESPONSE REGULATOR 9); transcription regulator/ two-component response regulator
At1g52340	259669_at	0,00047515	0,040898532	-1,216107685	7,382483078	8,192737324	7,767686603	8,011186833	6,693739921	6,637311358	6,992236427	ATABA2_GIN1_ISI4_SDR1_SIS4_SRE1__ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase

At1g03520	264844_at	0,00022096	0,030656428	-1,246140708	5,981697848	6,647346673	6,33939697	6,827560965	5,359992368	5,374724499	5,341165617	glycosyltransferase family 14 protein / core-2/-l-branching enzyme family protein
At3g48610	252343_at	5,8307E-06	0,007410981	-1,26309753	7,341992502	8,032687522	8,017332366	7,870603912	6,740159645	6,742676879	6,648494686	phosphoesterase family protein
At2g39010	266172_at	0,00038122	0,037216203	-1,268680968	11,60351937	11,97194346	12,47330402	12,26833207	10,9772712	11,09754021	10,83272525	PIP2,6_PIP2E (PLASMA MEMBRANE INTRINSIC PROTEIN 2E); water channel
At1g68020	260010_at	2,628E-06	0,005994532	-1,272453618	7,281070205	7,85947325	7,986197201	7,906220592	6,642726677	6,593435149	6,698368363	TPS6__ATTPS6; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-p
At4g25020	254100_at	0,00040129	0,038298579	-1,278139868	3,135692868	3,914146079	3,459944939	3,950197389	2,6094663	2,430582264	2,449820238	KOW domain-containing protein / D111/G-patch domain-containing protein
At5g57040	247931_at	0,00023632	0,030980279	-1,31339752	9,560254989	10,29696209	10,40945641	9,944442746	8,809119749	8,79937379	9,021611559	lactoylglutathione lyase family protein / glyoxalase I family protein
At5g01075	251141_at	0,00026445	0,031649064	-1,314568014	5,945998012	6,369843117	6,853466518	6,586536423	5,239622099	5,195659128	5,430860789	beta-galactosidase
At5g16820	246450_at	0,00058929	0,042332139	-1,317799628	5,165267566	5,97068651	5,743745718	5,758069911	4,683669649	4,676350207	4,159083399	ATHSFA1B_HSFA1B__HSF3 (HEAT SHOCK FACTOR 3); DNA binding / transcription factor
At3g14650	258113_at	0,00014477	0,025799078	-1,32547718	8,500474078	9,186695025	9,35095727	8,95198571	7,762463302	7,991156177	7,759586987	CYP72A11; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding
At3g62550	251221_at	0,00013413	0,024662247	-1,326975733	12,03301186	12,77453258	12,75095371	12,5640129	11,43187994	11,1387426	11,53794945	universal stress protein (USP) family protein
At1g21130	261453_at	0,0006629	0,045544203	-1,348831203	9,276558494	10,04782946	9,622926337	10,18216649	8,703119959	8,709925787	8,393382929	O-methyltransferase, putative
At3g18930	256917_at	0,00040746	0,038559756	-1,354757155	3,410488403	3,988669446	4,357815875	3,917115621	2,696289548	2,554173153	2,948866776	zinc finger (C3HC4-type RING finger) family protein
At5g06270	250734_at	0,00024721	0,031274333	-1,390018599	7,774544072	8,342737399	8,649860487	8,416062231	6,947438923	6,939790832	7,351374563	unknown protein
At1g12990	262768_at	0,00028769	0,032976083	-1,453126724	6,201528542	7,127632014	7,004272417	6,652371281	5,48301796	5,285532962	5,656344618	glycosyl transferase family 17 protein
At1g35612	262010_at	0,00034226	0,034852692	-1,470332599	6,678419343	7,500351878	7,433521033	7,306884015	5,91193469	5,650757875	6,267066563	
At3g47620	252425_at	0,00021301	0,030656428	-1,50757684	9,297492995	9,946098237	10,36690416	9,840841846	8,483270906	8,474167458	8,673675361	AtTCP14 (TEOSINTE BRANCHED1, CYCLOIDEA and PCF (TCP) 14); transcription factor
At5g19500	245943_at	0,00076772	0,047924887	-1,52272761	4,016371394	4,812005162	4,73832072	4,782879715	3,012406096	3,035540321	3,71707635	tryptophan/tyrosine permease family protein
At1g62030	264310_at	0,00010876	0,02287736	-1,525705266	6,977495934	7,658303122	7,582424215	7,980318363	6,094856658	6,390711443	6,158361801	DC1 domain-containing protein
At3g17930	258161_at	0,00056948	0,042332139	-1,543334039	9,186084156	10,01058436	10,28246861	9,580200549	8,486121573	8,250446746	8,506683091	unknown protein
At3g47250	252462_at	0,00022008	0,030656428	-1,544708254	9,753392307	10,8526008	10,37959066	10,34504784	8,994513335	8,849031921	9,099569284	unknown protein
At3g20810	257985_at	0,00017888	0,028533488	-1,546959995	9,905175711	10,44739015	10,74386832	10,84470866	9,1872328	9,311827791	8,896026551	transcription factor jumonji (jmi) domain-containing protein
At2g46680	266327_at	0,00072935	0,047199623	-1,583669811	8,527177167	9,355920315	8,923686112	9,67742979	7,843370706	7,82086314	7,541792939	ATHB7__ATHB-7 (ARABIDOPSIS THALIANA HOMEBOX 7); transcription activator/ transcription factor
At4g25910	254038_at	0,00025434	0,031274333	-1,587260254	8,734465663	9,429271713	9,589676521	9,565339134	7,761163327	7,753515696	8,307827585	AtCNFU3__NFU3; structural molecule
At4g34250	253285_at	5,3684E-05	0,018874816	-1,617765541	7,714005539	8,714604275	8,536972467	8,317088186	7,01993615	6,759914591	6,935517564	KCS16 (3-KETOACYL-COA SYNTHASE 16); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl gr
At1g06040	260956_at	6,4895E-05	0,019224063	-1,639511027	4,999795751	5,904608348	5,985937466	5,56810798	4,259491247	4,039192428	4,241437037	STO (SALT TOLERANCE); DNA binding / protein binding / transcription factor/ zinc ion binding
At1g28330	245668_at	0,00076728	0,047924887	-1,6543868	10,51410914	11,12299069	11,46607831	11,43483863	9,348584296	10,12009802	9,592064908	DRM1__DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)
At4g38690	252950_at	2,7122E-05	0,015571283	-1,67246913	8,87504944	9,940531294	9,642412728	9,550907992	8,107878768	8,024029482	7,984536374	1-phosphatidylinositol phosphodiesterase-related
At2g23240	245070_at	0,00023454	0,030973716	-1,674957862	4,252485029	4,858949479	4,945050924	5,465891478	3,470653748	3,470611415	3,303753131	plant EC metallothionein-like family 15 protein
At5g25460	246919_at	5,9579E-05	0,018874816	-1,678105045	11,83384861	12,78895081	12,66342856	12,56632403	10,77794144	10,97274758	11,23397224	unknown protein
At3g16240	258054_at	0,00031953	0,03399751	-1,72862627	12,4056445	13,38595915	13,31768253	13,10623123	11,19855449	11,52949573	11,89594387	AQP1__ATTIP2;1__DELTA-TIP1_TIP2;1__DELTA-TIP; ammonia transporter/ methylammonium transmembrane transporter/ water c

At3g56080	251713_at	0,00074308	0,0476833	-1,759085151	4,892427736	5,822625575	5,29289224	6,200393118	3,956606737	3,97855113	4,103497613	dehydration-responsive protein-related
At1g02700	260917_at	0,0007276	0,047199623	-1,786494514	4,159487289	4,6449031	4,95746491	5,555835627	3,219378041	3,234739401	3,344602655	unknown protein
At2g33790	267457_at	0,00055179	0,042332139	-1,819209691	6,370811092	7,486893864	6,770915706	7,583438243	5,518013083	5,475949475	5,389656182	AGP30 (ARABINOGALACTAN PROTEIN30)
At2g37870	266098_at	0,00059016	0,042332139	-1,861136437	9,458379259	10,34369961	10,20782295	10,61531987	9,009550557	8,294811262	8,279071302	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
At3g28007	257271_at	0,00052298	0,041926418	-1,893277905	7,024125664	7,498268239	8,164920041	8,249105569	5,869601861	6,07308854	6,289769733	nodulin MtN3 family protein
At2g21830	263883_at	0,00078579	0,047924887	-1,90319378	6,131202432	6,633909703	7,176553554	7,43793471	5,522180002	4,971420112	5,045216513	DC1 domain-containing protein
At3g53800	251919_at	0,00074599	0,0476833	-1,934644364	6,469298487	7,757968904	7,204928947	7,346964155	5,385958955	5,150432148	5,969537812	armadillo/beta-catenin repeat family protein
At1g25520	255735_at	0,00075435	0,047924887	-2,018291591	6,710800262	7,301164262	8,134311099	7,72436281	5,323120463	5,954777018	5,827065918	unknown protein
At5g43840	249117_at	0,00087485	0,049639988	-2,024196923	3,807563772	4,41993515	4,85085302	5,18819853	3,108983415	2,928558061	2,348854454	HSFA6A__AT-HSFA6A; DNA binding / transcription factor
At4g28040	253829_at	6,2238E-05	0,019184479	-2,038097674	6,218121425	7,357351209	7,169859462	7,184300114	5,472558546	5,242781241	4,881877975	nodulin MtN21 family protein
At1g74670	260221_at	0,00028034	0,032792886	-2,042214373	12,57360136	13,96210813	13,70271478	13,11930274	11,57730357	11,48111482	11,59906414	gibberellin-responsive protein, putative
At4g34650	253254_at	0,00024194	0,031179193	-2,094054653	4,370657361	5,260651002	5,256893477	5,735509583	3,066440675	3,201919927	3,702529501	SQS2 (SQUALENE SYNTHASE 2); farnesyl-diphosphate farnesyltransferase
At5g57345	247899_at	0,00044769	0,039635644	-2,134093822	7,95862511	9,269602042	8,708789411	9,09862461	6,918621434	6,464032095	7,292081069	unknown protein
At5g01300	251137_at	3,4993E-05	0,017929746	-2,13906099	4,756466323	5,892695622	5,676795873	5,908498957	3,984592931	3,591804759	3,484409794	phosphatidylethanolamine-binding family protein
At1g75770	262952_at	0,00058623	0,042332139	-2,16042698	3,539306088	4,360835367	5,174482719	4,323240649	2,309100076	2,746414069	2,321763651	unknown protein
At2g25200	264379_at	5,632E-05	0,018874816	-2,21419836	6,389234494	7,570260794	7,565333304	7,353406925	5,10581268	5,096956148	5,643637113	unknown protein
At5g44310	249039_at	0,0007853	0,047924887	-2,269732466	4,283901745	4,888871875	5,288814934	6,078617127	3,168393654	3,175240337	3,103472546	late embryogenesis abundant domain-containing protein / LEA domain-containing protein
At2g29300	266278_at	0,00036636	0,036491989	-2,31947469	4,919903317	6,168484941	5,938018424	6,132418621	3,289149646	3,687638659	4,303709612	tropinone reductase, putative / tropine dehydrogenase, putative
At1g66130	256514_at	0,00050221	0,041449563	-2,333377639	6,68071892	8,380871997	7,708697065	7,452654157	5,29542911	5,388742107	5,857919086	oxidoreductase N-terminal domain-containing protein
At4g32980	253411_at	0,00011106	0,02287736	-2,416187853	4,698265547	5,924342331	5,796490655	5,998245433	3,017441789	3,67228482	3,780788252	ATH1 (ARABIDOPSIS THALIANA HOMEODOMAIN GENE 1); DNA binding / sequence-specific DNA binding / transcription factor
At1g07430	261077_at	0,00057777	0,042332139	-2,44877556	6,054117747	7,109434945	7,209942246	7,516139388	5,075165447	5,241462537	4,172561916	protein phosphatase 2C, putative / PP2C, putative
At4g39770	252858_at	0,00055564	0,042332139	-2,459761252	3,462257817	5,317477386	4,618747022	4,140190921	2,35931164	2,269640962	2,06817897	trehalose-6-phosphate phosphatase, putative
At5g59130	247760_at	2,529E-06	0,005994532	-2,52637283	3,620160907	4,682255341	4,915025204	5,052761421	2,431229402	2,311943474	2,327750601	subtilase family protein
At2g36050	263953_at	3,5223E-07	0,005994532	-2,534951999	4,245259121	5,419426523	5,510827283	5,607951556	2,92973435	2,931483246	3,072131768	ATOFFP15__OFFP15 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 15)
At3g05640	258901_at	0,00012701	0,024460803	-2,56271043	5,959603656	7,102117143	7,351924278	7,268835192	4,257354778	4,629899554	5,14749099	protein phosphatase 2C, putative / PP2C, putative
At1g62290	264741_at	0,00011784	0,023578705	-2,59788099	8,503243975	9,518240729	9,851904405	10,03640828	6,805883117	7,238674148	7,568353176	aspartyl protease family protein
At4g21020	254440_at	0,00077816	0,047924887	-2,607504041	5,363903981	6,259211885	7,23021119	6,513544927	4,415080886	4,253209216	3,512165779	late embryogenesis abundant domain-containing protein / LEA domain-containing protein
At1g02340	259417_at	0,00041601	0,038676323	-2,709073915	4,390754952	5,450152491	5,391615131	6,394108106	2,895466626	3,368722033	2,844465323	FBI1_REP1_RSF1_HFR1 (LONG HYPOCOTYL IN FAR-RED); DNA binding / protein binding / transcription factor
At5g60100	247668_at	0,00044955	0,039635644	-2,736561506	3,921556667	5,44901871	5,69422409	4,726269461	2,779173767	2,801825123	2,078828853	PRR3__APRR3 (ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 3); transcription regulator/ two-component response regulator
At1g29430 A	259790_s_at	0,00049921	0,041449563	-2,740099577	5,394853143	7,256518693	6,655760938	6,382429164	3,545529439	3,998837863	4,530042761	auxin-responsive family protein

At1g05510	263175_at	0,00074172	0,0476833	-2,789955887	3,369445954	5,330003411	5,032615591	3,930652691	2,015410748	1,951899949	1,956093336	Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds.
At5g42900	249174_at	8,3637E-05	0,021435549	-2,917069356	8,3763078	9,882357895	9,988681624	9,633487915	7,185480289	7,169920776	6,397918301	unknown protein
At1g54040	263174_at	0,00017304	0,027992881	-3,018298807	7,777884121	9,303461113	9,555071381	9,002568079	5,838989358	6,125599916	6,841614877	ESR_TASTY__ESP (EPITHIOSPECIFIER PROTEIN); enzyme regulator
At2g45660	267509_at	9,6086E-06	0,008429685	-3,057763264	5,48542562	6,742734649	6,994644575	7,305542531	4,084155455	4,008424265	3,777052243	SOC1__AGL20 (AGAMOUS-LIKE 20); transcription factor
At5g44260	249065_at	4,279E-05	0,018408786	-3,092190878	5,489535835	7,273591645	6,932448724	6,900853453	3,604598799	4,381227036	3,844495353	zinc finger (CCCH-type) family protein
At3g01510	259188_at	0,00013484	0,024662247	-3,186711607	6,730559149	8,61066296	8,120397938	8,240683959	5,412718937	4,527476981	5,471414117	5'-AMP-activated protein kinase beta-1 subunit-related
At2g33830	267461_at	0,00049056	0,041449563	-3,41370308	12,4030795	14,59928458	14,19122197	13,53928657	11,05201147	11,06942648	9,967245928	dormancy/auxin associated family protein
At3g50750	252178_at	0,00020567	0,030330161	-3,423741109	5,939775673	8,245198152	7,814983657	6,894756873	4,208761811	4,234212627	4,240740916	brassinosteroid signalling positive regulator-related
At3g53250	251977_at	3,3883E-06	0,00644066	-3,500797316	6,054891656	7,971790475	7,694788382	7,749292086	4,004441992	4,425639557	4,483397446	auxin-responsive family protein
At2g29650	266672_at	1,7258E-05	0,011247298	-3,637991214	3,818667523	5,451830718	6,128764049	5,332394623	2,055600343	2,043679265	1,899736139	ANTR1__PHT4;1; carbohydrate transmembrane transporter/ inorganic diphosphate transmembrane transporter/ inorganic phospho
At1g54870	256354_at	0,0004253	0,038723411	-3,641043581	4,254329961	5,955566601	5,303052697	6,965935957	2,603745466	2,446799888	2,250879159	binding / catalytic/ oxidoreductase
At3g16800	257650_at	2,2758E-06	0,005994532	-3,704896914	4,3940159	6,270516719	6,401497616	6,067378736	2,789510032	2,311998216	2,52319408	protein phosphatase 2C, putative / PP2C, putative
At1g14280	261480_at	6,1471E-05	0,019184479	-3,735924137	7,400470452	9,691667478	9,37953022	8,734099863	5,339222256	5,905801448	5,352501445	PKS2 (PHYTOCHROME KINASE SUBSTRATE 2)
At5g47610	248759_at	6,9191E-06	0,008306551	-3,757572241	4,533637548	6,019835186	6,479692355	6,737743464	2,598084063	2,607489739	2,758980479	zinc finger (C3HC4-type RING finger) family protein
At1g62510	265111_at	3,4987E-05	0,017929746	-3,806922215	9,045484209	11,26964672	11,12326126	10,45392796	7,026566387	7,487893645	6,911609272	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
At5g45310	248969_at	9,199E-06	0,008429685	-3,810863955	3,979192246	5,535190897	5,792737925	6,325943848	2,069901425	2,074757985	2,076621396	unknown protein
At2g02120	266141_at	8,6098E-05	0,021769263	-3,877463085	8,387517762	10,21277631	10,27107713	10,49489447	6,712489028	5,724423665	6,909445965	LCR70__PDF2.1; peptidase inhibitor
At2g25890	266654_at	2,0134E-05	0,012756986	-3,93115622	4,257402635	5,954416539	6,023426114	6,691099584	2,436037864	2,461681052	1,97775466	glycine-rich protein / oleosin
At3g20210	257130_at	0,00055052	0,042332139	-4,035190555	4,662482145	6,927276021	7,303922182	5,809034066	3,377100888	2,278655434	2,278904281	DELTA_VPE; cysteine-type endopeptidase
At2g28490	264079_at	0,00031226	0,033917894	-4,582853328	4,742645103	7,201861404	7,806593426	6,093760473	3,04755959	2,152711989	2,153383738	cupin family protein
At2g22980	267265_at	1,3003E-05	0,00988671	-4,693847369	6,127804263	8,794978928	8,652853886	7,976351028	3,706360364	4,120788389	3,515492981	SCPL13__serine-type carboxypeptidase
At3g17520	258347_at	0,00047994	0,041155612	-4,783181771	5,154334334	6,484376668	7,820929092	8,332469899	3,481667703	2,596460368	2,210102273	late embryogenesis abundant domain-containing protein / LEA domain-containing protein
At5g52300	248352_at	0,00069992	0,046425208	-4,890825116	5,691614701	7,163633115	8,16562336	9,081825301	4,20871678	2,927016601	2,602873048	RD29B__LTI65 (LOW-TEMPERATURE-INDUCED 65)
At3g28290 A	256601_s_at	0,00022579	0,030656428	-4,99455562	8,632019364	10,12979936	11,81965719	11,43843497	5,577946178	6,210860746	6,615417738	AT14A
At5g36910	249645_at	4,086E-06	0,006657245	-5,290282007	4,947555025	7,62383759	7,69507181	7,459178685	2,589406051	2,547927594	1,769908419	THI2.2 (THIONIN 2.2); toxin receptor binding

Table 2: Miss-expressed genes in *toc1-2*.

AGI ID	mean M	SD M	z-score	p-value	Annotation
UP-REGULATED					
At1g22410	4,94	0,09	4,67	0,00834562	2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, putative / DAHP synthetase, putative
At3g16870	2,82	0,11	2,92	0,01759777	zinc finger (GATA type) family protein
At2g05070	2,61	0,18	6,87	0,03167028	LHCB2.2; chlorophyll binding
At2g20670	2,31	0,08	3,31	0,01537953	unknown protein
At3g27690	2,28	0,17	7,29	0,03373512	LHCB2.4__LHCB2.3; chlorophyll binding
At5g06980	2,14	0,14	6,97	0,02911086	unknown protein
At4g27310	2,04	0,08	7,55	0,01700636	zinc finger (B-box type) family protein; FUNCTIONS IN: transcription factor activity,
At1g32900	2,04	0,19	7,08	0,04239512	starch synthase, putative
At4g12480	2,01	0,14	7,45	0,03084948	pEARL1 1; lipid binding
At5g54270	1,91	0,02	5,01	0,00579224	LHCB3*1__LHCB3 (LIGHT-HARVESTING CHLOROPHYLL B-BINDING PROTEIN 3); structural molecule
At5g38910	1,85	0,19	6,8	0,04715827	germin-like protein, putative
At2g46830	1,75	0,1	6,22	0,02652615	CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); DNA binding / transcription activator/ transcription factor/ transcription repressor
At3g01060	1,62	0,18	6,03	0,04920739	unknown protein
At2g21650	1,49	0,16	4,4	0,04775082	ATRL2__MEE3 (MATERNAL EFFECT EMBRYO ARREST 3); DNA binding / transcription factor
At1g73870	1,5	0,14	5,27	0,04307449	zinc finger (B-box type) family protein
At5g44420	1,47	0,11	5,12	0,03440976	LCR77_PDF1.2A__PDF1.2
At3g09450	1,45	0,14	4,3	0,04328338	unknown protein; (TAIR:AT2G28780.1);
At4g12490	1,45	0,04	4,91	0,01091224	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
At4g12470	1,42	0,01	5,19	0,00426885	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
At3g54890	1,41	0,03	3,67	0,00824455	LHCA1; chlorophyll binding
At2g46790	1,38	0,05	4,02	0,01574358	PRR9_TL1__APRR9 (ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 9); protein binding / transcription regulator/ two-component response regulator
At4g31940	1,32	0,14	4,71	0,04759347	CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding
At2g30810	1,32	0,03	3,92	0,01095082	gibberellin-regulated family protein
At2g29650	1,32	0,1	4,62	0,03330509	ANTR1__PHT4;1; carbohydrate transmembrane transporter/ inorganic diphosphate transmembrane transporter/ inorganic phosphate transmembrane transporter/

At5g17220	1,31	0,08	4,76	0,02611401 GST26_TT19__ATGSTF12 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE PHI 12); glutathione transferase
At1g73600	1,26	0,11	4,43	0,04029142 methyltransferase/ phosphoethanolamine N-methyltransferase
At3g30210	1,25	0,09	4,44	0,03333462 ATMYB121__MYB121 (MYB DOMAIN PROTEIN 121); DNA binding / transcription factor
At5g67030	1,23	0,05	3,98	0,01926764 ATABA1_ATZEP_IBS3_LOS6_NPQ2_ZEP__ABA1 (ABA DEFICIENT 1); zeaxanthin epoxidase
At2g43010	1,19	0,02	4,24	0,00570904 SRL2__PIF4 (phytochrome interacting factor 4); DNA binding / protein binding / transcription factor
At3g30150	1,17	0,07	4,15	0,02836648 ransposable element gene; similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G31990.1);
At3g29970	1,17	0,02	4,18	0,00768389 germination protein-related
At1g06040	1,17	0,1	4,03	0,03670569 STO (SALT TOLERANCE); DNA binding / protein binding / transcription factor/ zinc ion binding
At5g13630	1,14	0,05	3,33	0,02028202 CCH_CCH1_CHLH__GUN5 (GENOMES UNCOUPLED 5); magnesium chelatase
At5g43570	1,14	0,11	2,94	0,04476899 cellular component unknown, defense response, response to wounding, serine-type endopeptidase inhibitor activity
At5g14760	1,13	0,03	4,03	0,01344975 AO (L-ASPARTATE OXIDASE); L-aspartate oxidase/ electron carrier/ oxidoreductase
At4g08300	1,11	0,07	3,99	0,02990736 nodulin MtN21 family protein
At1g75830	1,11	0,05	4,13	0,01923131 PDF1.1__LCR67
At1g09932	1,1	0,06	3,88	0,0240769 phosphoglycerate/bisphosphoglycerate mutase-related;
At2g24915	1,09	0,1	3,2	0,03974277 transposable element gene; similar to zinc ion binding [Arabidopsis thaliana]
At5g54060	1,08	0,1	3,44	0,03992945 UF3GT (udp-glucose:flavonoid 3-O-glucosyltransferase); transferase, transferring glycosyl groups
At2g39030	1,07	0	3,7	0,00059526 GCN5-related N-acetyltransferase (GNAT) family protein
At3g30220	1,04	0,04	3,61	0,01689137 unknown protein
At2g30770	1,04	0,06	3,79	0,02601924 CYP71A13 (cytochrome P450, family 71, subfamily A, polypeptide 13); indoleacetaldoxime dehydratase/ oxygen binding
At2g02320	1,04	0,01	3,61	0,00311847 Phloem protein 2-B7 (AtPP2-B7); FUNCTIONS IN: carbohydrate binding; INVOLVED IN: biological_process unknown;
At5g44570	1,02	0,03	3,4	0,01173 unknown protein
At3g29765	0,99	0,05	3,42	0,02498835 hAT dimerisation domain-containing protein
At2g34610	0,97	0,07	3,58	0,03089971 unknown protein
At1g75040	0,97	0,07	3,01	0,0302647 PR-5__PR5 (PATHOGENESIS-RELATED GENE 5)
At5g18990	0,97	0,1	2,76	0,04557261 pectinesterase family protein
At2g30750	0,96	0,05	3,55	0,02409207 CYP71A12 (cytochrome P450, family 71, subfamily A, polypeptide 12); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding
At2g19050	0,96	0,01	2,86	0,00245912 GDSL-motif lipase/hydrolase family protein
At3g30200	0,94	0,01	3,44	0,00337147 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown;
At3g13950	0,94	0,03	2,92	0,01521568 unknown protein
At2g28780	0,94	0,08	3,33	0,0370455 unknown protein

At1g14880	0,93	0,09	2,42	0,04181504 unknown protein
At4g01430	0,92	0,04	3,15	0,01936939 nodulin MtN21 family protein
At2g36820	0,92	0,09	3,33	0,04478828 similar to Hypothetical protein [Oryza sativa] (GB:AAK98733.1); contains domain MAESTRO-RELATED HEAT DOMAIN-CONTAINING (PTHR23120); contains domain gb def: Hypothetical protein At2g36820 (PTHR23120:SF6)
At5g64840	0,91	0,02	2,92	0,00953603 ATGCN5 (A. THALIANA GENERAL CONTROL NON-REPRESSIBLE 5); transporter
At4g34150	0,91	0,01	3,34	0,00263183 C2 domain-containing protein
At3g30420	0,91	0,04	3,32	0,01836761 transposable element gene; similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G54430.1);
At1g61480	0,91	0,04	3,3	0,01870858 S-locus protein kinase, putative
At2g46450	0,89	0,02	3,34	0,00838359 CNGC12__ATCNGC12; cation channel/ cyclic nucleotide binding / ion channel
At2g32680	0,9	0,04	3,38	0,01898081 ATRLP23 (Receptor Like Protein 23); kinase/ protein binding
At2g42540	0,89	0,06	3,07	0,03196695 COR15A (COLD-REGULATED 15A)
At5g25250	0,87	0,07	3,19	0,03650515 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole;
At5g01540	0,85	0,02	3,08	0,01074247 LECRKA4.1 (LECTIN RECEPTOR KINASE A4.1); kinase
At5g48540	0,83	0,01	2,87	0,00515859 33 kDa secretory protein-related
At1g26380	0,82	0,09	2,97	0,04688352 FAD-binding domain-containing protein
At5g45105	0,82	0,01	2,33	0,00619403 ZINC TRANSPORTER 8 PRECURSOR (ZIP8); FUNCTIONS IN: cation transmembrane transporter activity;
At5g22545	0,8	0,01	2,78	0,00453322 unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown;
At2g23270	0,8	0,04	2,48	0,019768 unknown protein
At1g75100	0,8	0,05	3,03	0,02542763 JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMULATION RESPONSE 1); heat shock protein binding
At2g39510	0,8	0,09	2,85	0,04873724 nodulin MtN21 family protein
At5g20190	0,79	0,01	2,74	0,00622811 FUNCTIONS IN: binding; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Tetratricopeptide-like helical (InterPro:IPRO11990),
At5g15725	0,79	0,06	2,3	0,03512302 unknown protein
At4g14365	0,76	0,07	2,44	0,04279796 zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein
At5g64120	0,74	0,06	2,61	0,03391388 peroxidase, putative
At2g46440	0,73	0,02	2,68	0,01360816 CNGC11__ATCNGC11 (CYCLIC NUCLEOTIDE-GATED CHANNELS); calmodulin binding / cation channel/ cyclic nucleotide binding / ion channel
At1g56060	0,72	0,06	2,35	0,03757542 unknown protein
At4g24110	0,71	0,04	2,06	0,02256161 unknown protein
At4g09400	0,71	0,01	2,66	0,00632313 transposable element gene; similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G33230.1);
At3g30480	0,72	0,07	2,26	0,04649892 transposable element gene; similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G24915.1);
At3g26830	0,71	0,08	2,66	0,0484835 CYP71B15__PAD3 (PHYTOALEXIN DEFICIENT 3); dihydrocamalexin acid decarboxylase/ monooxygenase/ oxygen binding
At4g13010	0,7	0,07	2,49	0,04209768 oxidoreductase, zinc-binding dehydrogenase family protein

At2g21045	0,7	0,06	2,55	0,03991947 INVOLVED IN: aging; EXPRESSED IN: hypocotyl, root; CONTAINS InterPro DOMAIN/s: Rhodanese-like (InterPro:IPR001763); .
At1g13340	0,69	0,03	2,44	0,01965831 unknown protein
At3g28580	0,69	0,04	2,49	0,02327698 AAA-type ATPase family protein
At2g29360	0,69	0,04	2,6	0,0261892 tropinone reductase, putative / tropine dehydrogenase, putative
At2g19440	0,69	0,02	2,49	0,01408829 glycosyl hydrolase family 17 protein
At1g80130	0,67	0,07	2,36	0,0436481 binding
At1g70610	0,67	0,03	2,52	0,02275764 ATTAP1; ATPase, coupled to transmembrane movement of substances / transporter
At5g43910	0,66	0,04	2,17	0,025519 pfkB-type carbohydrate kinase family protein
At3g51895	0,65	0,02	2,05	0,01473757 AST12__SULTR3;1 (SULFATE TRANSPORTER 3;1); secondary active sulfate transmembrane transporter/ sulfate transmembrane transporter/ transporter
At5g28770	0,63	0,04	2,26	0,02966612 AtbZIP63__BZO2H3; DNA binding / protein heterodimerization/ transcription factor
At2g34430	0,63	0,02	2,05	0,01080349 LHCB1.4__LHB1B1; chlorophyll binding
At3g51660	0,61	0,06	2,21	0,04086759 macrophage migration inhibitory factor family protein / MIF family protein
At1g20510	0,62	0,04	2,13	0,02554491 OPCL1 (OPC-8:0 COA LIGASE1); 4-coumarate-CoA ligase
At1g74590	0,6	0,01	2,21	0,00375599 ATGSTU10__GSTU10 (GLUTATHIONE S-TRANSFERASE TAU 10); glutathione transferase
At3g18250	0,6	0,02	2,14	0,01433683 unknown protein
At1g07700	0,59	0,01	2,18	0,00601164 thioredoxin family protein

AGI ID DOWN- REGULATED	mean M	SD M	z-score	p-value	Annotation
At5g57655	-0,56	0,05	-2,06	0,03854887	xylose isomerase family protein
At4g29270	-0,56	0,02	-2,04	0,0151007	acid phosphatase class B family protein
At5g01520	-0,58	0,03	-2,1	0,02461368	zinc finger (C3HC4-type RING finger) family protein
At2g34650	-0,58	0,06	-2,02	0,04795156	ABR__PID (PINOID); kinase/ protein kinase/ protein serine/threonine kinase
At1g02205	-0,57	0,03	-2,02	0,02355299	CER1 (ECERIFERUM 1); octadecanal decarbonylase
At3g61160	-0,59	0,02	-2,14	0,01483991	shaggy-related protein kinase beta / ASK-beta (ASK2)
At5g11070	-0,59	0,03	-2,16	0,02408757	unknown protein
At1g30260	-0,59	0,02	-2,16	0,01638343	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cytokinin stimulus;
At3g24240	-0,6	0,03	-2,11	0,02489997	leucine-rich repeat transmembrane protein kinase, putative
At3g09770	-0,6	0,01	-2,19	0,00918813	zinc finger (C3HC4-type RING finger) family protein

At2g19810	-0,6	0,01	-2,21	0,00505354 zinc finger (CCCH-type) family protein
At4g17730	-0,62	0,02	-2,14	0,01476344 ATSP23__SYP23 (SYNTAXIN OF PLANTS 23); SNAP receptor
At1g66140	-0,62	0,01	-2,2	0,01062545 ZFP4 (ZINC FINGER PROTEIN 4); nucleic acid binding / transcription factor/ zinc ion binding
At2g22420	-0,64	0,06	-2,13	0,0403906 peroxidase 17 (PER17) (P17)
At2g29630	-0,65	0,06	-2,26	0,04437722 THIC (ThiaminC); ADP-ribose pyrophosphohydrolase/ catalytic/ iron-sulfur cluster binding
At2g15440	-0,65	0,02	-2,2	0,01660213 unknown protein
At5g56040	-0,67	0,04	-2,4	0,02780267 leucine-rich repeat protein kinase, putative
At4g12290	-0,67	0,03	-2,38	0,02276264 amine oxidase/ copper ion binding / quinone binding
At4g25250	-0,68	0,02	-2,49	0,01411808 invertase/pectin methylesterase inhibitor family protein
At2g42900	-0,67	0,06	-2,35	0,04158303 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown;
At1g25230	-0,68	0	-2,47	0,00297608 purple acid phosphatase family protein
At4g11211	-0,69	0,03	-2,23	0,01843259 expressed protein
At3g50440	-0,7	0,01	-2,41	0,00828774 ATMES10__MES10 (METHYL ESTERASE 10); hydrolase/ hydrolase, acting on ester bonds / methyl jasmonate esterase
At1g18100	-0,7	0,03	-2,55	0,02211597 E12A11; phosphatidylethanolamine binding
At3g43920	-0,71	0,03	-2,44	0,02218235 DCL3__ribonuclease III family protein
At1g61097	-0,71	0,01	-2,05	0,00763785 Expressed protein
At3g48510	-0,72	0,05	-2,24	0,03244026 unknown protein
At2g39570	-0,73	0,07	-2,61	0,04591165 ACT domain-containing protein
At2g01530	-0,73	0,07	-2,54	0,04438064 MLP329 (MLP-LIKE PROTEIN 329); copper ion binding
At3g53040	-0,74	0,07	-2,5	0,04312414 late embryogenesis abundant protein, putative / LEA protein, putative
At5g11550	-0,75	0,02	-2,58	0,00911706 binding
At4g25580	-0,75	0,05	-2,2	0,03146301 stress-responsive protein-related
At1g64590	-0,75	0,08	-2,68	0,04924875 short-chain dehydrogenase/reductase (SDR) family protein
At5g57685	-0,79	0	-2,74	0,00072217 expressed protein
At5g37260	-0,79	0,05	-2,54	0,02565712 CIR1__RVE2 (REVEILLE 2); DNA binding / transcription factor
At5g48250	-0,83	0,04	-2,93	0,02429748 zinc finger (B-box type) family protein
At4g34950	-0,83	0,09	-3,02	0,047508 nodulin family protein
At2g16005	-0,82	0,06	-2,85	0,03254025 MD-2-related lipid recognition domain-containing protein / ML domain-containing protein
At4g14270	-0,84	0,07	-2,75	0,03585933 Protein containing PAM2 motif which mediates interaction with the PABC domain of polyadenyl binding proteins.
At5g22460	-0,84	0,02	-2,91	0,00927797 esterase/lipase/thioesterase family protein

At2g21910	-0,84	0,06	-2,98	0,03218642 CYP96A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding
At1g47960	-0,86	0,01	-3,19	0,00452361 ATC/VIF1__C/VIF1 (CELL WALL / VACUOLAR INHIBITOR OF FRUCTOSIDASE 1); enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor
At4g15440	-0,87	0,03	-2,79	0,01488535 CYP74B2__HPL1 (HYDROPEROXIDE LYASE 1); electron carrier/ heme binding / iron ion binding / monooxygenase
At4g11210	-0,87	0,04	-3,11	0,02306559 disease resistance-responsive family protein / dirigent family protein
At2g01200	-0,9	0	-2,76	0,00134682 auxin-responsive AUX/IAA family protein contains Pfam profile: PF02309 AUX/IAA family
At3g12120	-0,91	0,04	-2,55	0,02056321 FAD2 (FATTY ACID DESATURASE 2); delta12-fatty acid dehydrogenase/ omega-6 fatty acid desaturase
At5g40420	-0,93	0,06	-3,26	0,02827901 OLE2__OLEO2 (OLEOSIN 2)
At3g45680	-0,93	0,06	-3,29	0,0268898 proton-dependent oligopeptide transport (POT) family protein
At5g45690	-0,96	0,09	-3,25	0,04012337 unknown protein
At3g60530	-0,96	0	-3,34	0,00140746 zinc finger (GATA type) family protein
At3g07650	-0,97	0,08	-3,52	0,03817486 COL9 (CONSTANS-LIKE 9); transcription factor/ zinc ion binding
At4g12545	-1	0,01	-3,57	0,00570129 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains protease inhibitor/seed storage/LTP family domain
At4g32340	-1,03	0,07	-3,68	0,02927602 EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: binding (TAIR:AT1G80130.1);
At2g23240	-1,03	0,03	-3,21	0,01406474 plant EC metallothionein-like family 15 protein
At4g14096	-1,06	0,09	-3,51	0,03913139 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; G14103.1;
At1g21670	-1,07	0,04	-3,73	0,01483471 INVOLVED IN: proteolysis; LOCATED IN: cell wall, plant-type cell wall; EXPRESSED IN: 23 plant structures;
At5g47640	-1,09	0,06	-3,89	0,0265802 NF-YB2 (NUCLEAR FACTOR Y, SUBUNIT B2); transcription factor
At5g45310	-1,13	0,05	-3,89	0,01881858 unknown protein
At1g73190	-1,15	0,1	-4,01	0,03942847 ALPHA-TIP__TIP3;1; water channel
At2g18050	-1,17	0,01	-4,02	0,00554767 HIS1-3 (HISTONE H1-3); DNA binding / nucleosomal DNA binding
At3g26880	-1,19	0,07	-4,25	0,02696947 self-incompatibility protein-related
At4g09600	-1,22	0,07	-4,37	0,02466843 GASA3 (GAST1 PROTEIN HOMOLOG 3)
At1g07050	-1,26	0,03	-4,45	0,01029785 CONSTANS-like protein-related
At2g21820	-1,27	0,06	-4,49	0,02218859 unknown protein
At4g16146	-1,32	0,08	-4,57	0,02859129 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown;
At5g59570	-1,34	0,15	-4,89	0,04947473 myb family transcription factor
At1g72100	-1,44	0,07	-4,2	0,02245275 late embryogenesis abundant domain-containing protein / LEA domain-containing protein
At2g15890	-1,55	0,13	-5,36	0,03860733 MEE14 (maternal effect embryo arrest 14)
At4g28520	-1,83	0,02	-6,64	0,00445694 CRC__CRU3 (CRUCIFERIN 3); nutrient reservoir
At2g40170	-1,85	0,14	-4,36	0,03316107 ATEM6__GEA6 (LATE EMBRYOGENESIS ABUNDANT 6)

At3g22640	-2,09	0,19	-6,33	0,04129628 PAP85; nutrient reservoir
At3g15670	-2,18	0,19	-7,86	0,03953088 late embryogenesis abundant protein, putative / LEA protein, putative
At4g08530	-2,41	0,16	-2,23	0,03076199 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
At2g19190	-2,67	0,15	-2,67	0,0248235 FRK1 (FLG22-INDUCED RECEPTOR-LIKE KINASE 1); kinase
At1g75870	-2,95	0,01	-3,1	0,00145122 unknown protein

Table 4: ABA-related genes miss-expressed in *toc1-2*.

AGI ID	Affy ID	Annotation (Lookup from 2008-05-29) - for multiple identifier mappings only the annotation for the first identifier is shown, except in the case of the multi-line output option
AT3G16870	257571_at	zinc finger (GATA type) family protein
AT2G05070	263345_s_a	LHCB2.2_LHCB2__LHCB2.2 (Photosystem II light harvesting complex gene 2.2); chlorophyll binding
AT2G20670	265387_at	similar to unknown protein(TAIR:AT4G32480.1); similar to unnamed protein product (GB:CAO69754.1); contains InterPro domain Protein of unknown function DUF506
AT3G27690	258239_at	LHCB2:4_LHCB2__LHCB2:4 (Photosystem II light harvesting complex gene 2.3); chlorophyll binding
AT5G06980	250665_at	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G12320.1)
AT4G27310		zinc finger (B-box type) family protein; similar to zinc finger (B-box type) family protein [Arabidopsis thaliana] (TAIR:AT5G54470.1)
AT1G32900	261191_at	starch synthase, putative
AT4G12480	254805_at	pEARLI 1__pEARLI 1; lipid binding
AT5G54270	248151_at	LHCB3__LHCB3 (LIGHT-HARVESTING CHLOROPHYLL BINDING PROTEIN 3)
AT2G46830	266719_at	CCA1__CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); transcription factor
AT3G01060	259275_at	similar to unnamed protein product [Vitis vinifera] (GB:CAO15045.1); similar to unknown [Brassica rapa] (GB:ABC41272.1)
AT1G73870	260380_at	zinc finger (B-box type) family protein
AT4G12490	254832_at	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
AT4G12470	254818_at	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
AT2G46790	266720_s_a	APRR9_PRR9_TL1__APRR9 (PSEUDO-RESPONSE REGULATOR 9); transcription regulator
AT4G31940	253502_at	CYP82C4__CYP82C4 (cytochrome P450, family 82, subfamily C, polypeptide 4); oxygen binding
AT2G29650	266672_at	inorganic phosphate transporter, putative
AT1G73600	259842_at	phosphoethanolamine N-methyltransferase
AT3G30210	257307_at	ATMYB121_MYB121__MYB121 (myb domain protein 121); DNA binding / transcription factor
AT5G67030	247025_at	ABA1_ATZEP_IBS3_LOS6_NPQ2_ZEP__ABA1 (ABA DEFICIENT 1); zeaxanthin epoxidase
AT1G06040	260956_at	STO__STO (SALT TOLERANCE); transcription factor/ zinc ion binding
AT5G13630	250243_at	GUN5_CCH_CHLH__GUN5 (GENOMES UNCOUPLED 5)
AT5G43570		Predicted to encode a PR (pathogenesis-related) peptide that belongs to the PR-6 proteinase inhibitor family.
AT4G08300	255127_at	nodulin MtN21 family protein
AT2G39030	266142_at	GCN5-related N-acetyltransferase (GNAT) family protein

AT2G34610 266900_at similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G30190.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG12037.1)

AT3G13950 258203_at similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G13266.1); similar to Ankyrin [Medicago truncatula] (GB:ABN08906.1)

AT2G28780 266222_at similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G09450.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21693.1)

AT5G64840 247222_at ATGCN5__ATGCN5 (Arabidopsis thaliana general control non-repressible 5)

AT4G34150 253284_at C2 domain-containing protein

AT2G46450 263777_at ATCNGC12_CNGC12__ATCNGC12 (cyclic nucleotide gated channel 12); cyclic nucleotide binding / ion channel

AT2G42540 263497_at COR15A_COR15__COR15A (COLD-REGULATED 15A)

AT5G25250 246927_s_a similar to unknown protein(TAIR:AT5G64870.1); (TAIR:AT5G25260.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO44306.1);

AT5G48540 248686_at 33 kDa secretory protein-related

AT1G26380 261021_at FAD-binding domain-containing protein

AT1G75100 259927_at JAC1__JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMULATION RESPONSE 1); heat shock protein binding

AT2G39510 266965_at nodulin MtN21 family protein

AT4G14365 245329_at zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein

AT5G64120 247327_at peroxidase, putative

AT1G56060 262085_at similar to unknown protein (TAIR:AT2G32190.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68639.1); contains domain PD188784 (PD188784)

AT4G24110 254200_at similar to unnamed protein product [Vitis vinifera] (GB:CAO62924.1)

AT4G13010 254804_at oxidoreductase, zinc-binding dehydrogenase family protein

AT1G13340 259410_at similar to unknown protein (TAIR:AT1G34220.2); similar to unknown (GB:ABS01355.1); contains InterPro domain Protein of unknown function DUF292, (InterPro:IPR005061)

AT1G80130 262050_at binding

AT3G51895 246310_at SULTR3;1_AST12_ATST1__SULTR3;1 (SULFATE TRANSPORTER 1); sulfate transmembrane transporter

AT1G20510 259518_at OPCL1__OPCL1 (OPC-8:0 COA LIGASE1); 4-coumarate-CoA ligase

AT1G74590 260225_at ATGSTU10__ATGSTU10 (Arabidopsis thaliana Glutathione S-transferase (class tau) 10); glutathione transferase

AT3G18250 257061_at contains domain PROKAR_LIPOPROTEIN (P551257)

AT1G07700 261417_at thioredoxin family protein

AT4G24380 254158_at similar to unknown protein (TAIR:AT5G65400.1); similar to unknown (GB:ABK94545.1); contains InterPro domain Protein of unknown function DUF341 (InterPro:IPR005645)

AT4G04770 255305_at ATABC1_ATNAP1_LAF6__ATABC1 (ARABIDOPSIS THALIANA NUCLEOSOME ASSEMBLY PROTEIN 1)

AT5G57655 247924_at xylose isomerase family protein

AT5G01520 251084_at zinc finger (C3HC4-type RING finger) family protein

AT3G61160 251358_at shaggy-related protein kinase beta / ASK-beta (ASK2)

AT5G11070 245906_at similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G35090.1)

AT1G30260 245776_at AGL79__AGL79 (AGAMOUS-LIKE 79)

AT3G09770 258714_at zinc finger (C3HC4-type RING finger) family protein

AT2G19810 266695_at zinc finger (CCCH-type) family protein

AT4G17730 245278_at SYP23__SYP23 (syntaxin 23)

AT1G66140 256528_at ZFP4__ZFP4 (ZINC FINGER PROTEIN 4); nucleic acid binding / transcription factor/ zinc ion binding

AT2G22420 264001_at peroxidase 17 (PER17) (P17)

AT4G12290 254833_s_a copper amine oxidase, putative

AT1G25230 245637_at purple acid phosphatase family protein

AT3G50440 252168_at hydrolase

AT1G18100 256073_at E12A11__E12A11; phosphatidylethanolamine binding

AT3G48510 252321_at similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63350.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68256.1)

AT2G39570 266984_at ACT domain-containing protein

AT3G53040 252019_at late embryogenesis abundant protein, putative / LEA protein, putative

AT4G25580 245233_at stress-responsive protein-related

AT5G37260 249606_at CIR1_RVE2__CIR1/RVE2 (CIRCADIAN 1); DNA binding / transcription factor

AT5G48250 248744_at zinc finger (B-box type) family protein

AT2G16005 263098_at MD-2-related lipid recognition domain-containing protein / ML domain-containing protein

AT5G22460 249917_at esterase/lipase/thioesterase family protein

AT1G47960 259616_at C/VIF1__C/VIF1 (CELL WALL / VACUOLAR INHIBITOR OF FRUCTOSIDASE 1); pectinesterase inhibitor

AT5G45690 248915_at similar to unknown protein(TAIR:AT4G18920.1); similar to unnamed protein product (GB:CAO47983.1); InterPro domain of unknown function DUF1264 (InterPro:IPRO10686)

AT3G60530 251373_at zinc finger (GATA type) family protein

AT3G07650 259244_at COL9__COL9 (CONSTANS-LIKE 9)

AT1G21670 262503_at similar to unknown protein (TAIR:AT1G21680.1); similar to hypothetical protein(GB:CAN73514.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61906.1);

AT5G47640 248764_at CCAAT-box binding transcription factor subunit B (NF-YB) (HAP3) (AHAP3) family (Hap3b)

AT5G45310 248969_at similar to unnamed protein product [Vitis vinifera] (GB:CAO63757.1)

AT2G18050 265817_at HIS1-3__HIS1-3 (HISTONE H1-3); DNA binding

AT4G09600 255048_at GASA3__GASA3 (GAST1 PROTEIN HOMOLOG 3)

AT2G21820 263881_at similar to hypothetical protein MtrDRAFT_AC155884g16v2 [Medicago truncatula] (GB:ABN08202.1)

AT5G59570 252475_s_a myb family transcription factor

AT2G40170 263385_at ATEM6_GEA6__ATEM6/GEA6 (ARABIDOPSIS EARLY METHIONINE-LABELLED 6)

AT3G22640 258327_at cupin family protein

AT3G15670 258224_at late embryogenesis abundant protein, putative / LEA protein, putative

Table 5: ABA-related genes miss-expressed in TOC1-ox.

AGI ID	Affy ID	Annotation (Lookup from 2008-05-29) - for multiple identifier mappings only the annotation for the first identifier is shown, except in the case of the multi-line output option
AT4G15210	245275_at	BMY1_ATBETA-AMY_AT-BETA-AMY_RAM1__ATBETA-AMY (BETA-AMYLASE); beta-amylase
AT3G60140	251428_at	DIN2_SRG2__DIN2 (DARK INDUCIBLE 2); hydrolase, hydrolyzing O-glycosyl compounds
AT5G61380	247525_at	TOC1_APRR1_PRR1__TOC1 (TIMING OF CAB EXPRESSION 1); transcription regulator
AT1G43800	260869_at	acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative
AT5G20230	246099_at	ATBCB_BCB__ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding
AT5G07990	250558_at	TT7_CYP75B1_D501__TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding
AT5G14650	250142_at	polygalacturonase, putative / pectinase, putative
AT5G09470	245882_at	mitochondrial substrate carrier family protein
AT2G19970	265588_at	pathogenesis-related protein, putative
AT1G43910	259507_at	AAA-type ATPase family protein
AT1G73010	262369_at	phosphoric monoester hydrolase
AT1G27730	261648_at	STZ_ZAT10__STZ (SALT TOLERANCE ZINC FINGER); nucleic acid binding / transcription factor/ zinc ion binding
AT3G15310	257057_at	transposable element gene; similar to unknown protein [Arabidopsis thaliana]
AT2G36750	265197_at	UGT72C1__UGT72C1 (UDP-GLUCOSYL TRANSFERASE 72C1); UDP-glycosyltransferase/ transferase, transferring glycosyl groups
AT2G47520	245173_at	AP2 domain-containing transcription factor, putative
AT3G10150	258932_at	ATPAP16_PAP16__ATPAP16/PAP16 (purple acid phosphatase 16); acid phosphatase/ protein serine/threonine phosphatase
AT5G58770	247780_at	dehydrodolicyl diphosphate synthase, putative / DEDOL-PP synthase, putative
AT1G76650	259879_at	CML38__CML38
AT2G39330	266989_at	jacalin lectin family protein
AT1G65060	261907_at	4CL3__4CL3 (4-coumarate:CoA ligase 3); 4-coumarate-CoA ligase
AT2G19990	265586_at	PR-1-LIKE__PR-1-LIKE (PATHOGENESIS-RELATED PROTEIN-1-LIKE)
AT5G41080	249337_at	glycerophosphoryl diester phosphodiesterase family protein
AT5G48880	248625_at	KAT5_PKT1_KAT5_PKT2__KAT5/PKT1/PKT2 (PEROXISOMAL 3-KETO-ACYL-COA THIOLASE 1, PEROXISOMAL 3-KETO-ACYL-COA THIOLASE 2); acetyl-CoA C-acyltransferase
AT1G06000	260955_at	UDP-glucuronosyl/UDP-glucosyl transferase family protein
AT5G24150	249774_at	SQP1__SQP1 (Squalene monooxygenase 1)

AT5G46050	248932_at	ATPTR3_PTR3__ATPTR3/PTR3 (PEPTIDE TRANSPORTER PROTEIN 3); transporter
AT3G02550	258487_at	LBD41__LBD41 (LOB DOMAIN-CONTAINING PROTEIN 41)
AT5G51720	248377_at	similar to Os07g0467200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001059590.1); similar to hypothetical protein Osl_025030 [Oryza sativa (indica cultivar-group)] (GB:EAZ03798.1);
AT1G69880	260408_at	ATH8__ATH8 (thioredoxin H-type 8); thiol-disulfide exchange intermediate
AT1G77120	264953_at	ADH1_ADH__ADH1 (ALCOHOL DEHYDROGENASE 1)
AT3G51240	252123_at	F3H_F3'H__TT6__F3H (TRANSPARENT TESTA 6); naringenin 3-dioxygenase
AT3G16330	257517_at	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G52140.1); similar to hypothetical protein [Vitis vinifera] (GB:CA N64915.1)
AT1G09240	264261_at	nicotianamine synthase, putative
AT1G19200	256014_at	senescence-associated protein-related
AT1G05680	263231_at	UDP-glucuronosyl/UDP-glucosyl transferase family protein
AT1G30040	260023_at	ATGA2OX2__ATGA2OX2; gibberellin 2-beta-dioxygenase
AT4G02330	255524_at	ATPMEPCRB__ATPMEPCRB; pectinesterase
AT2G04032	263480_at	ZIP7__ZIP7 (ZINC TRANSPORTER 7 PRECURSOR); cation transmembrane transporter
AT3G59140	251503_at	ATMRP14__ATMRP14 (Arabidopsis thaliana multidrug resistance-associated protein 14)
AT3G29810	245228_at	COBL2__COBL2 (COBRA-LIKE PROTEIN 2 PRECURSOR)
AT2G45220	245148_at	pectinesterase family protein
AT2G17280	264907_at	phosphoglycerate/bisphosphoglycerate mutase family protein
AT5G15120	250152_at	similar to unknown protein(TAIR:AT5G39890.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14912.1); contains InterPro domain of unknown function DUF1637 (InterPro:IPRO12864)
AT2G29670	266617_at	binding LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures
AT5G05270	250794_at	chalcone-flavanone isomerase family protein
AT5G59490	247727_at	haloacid dehalogenase-like hydrolase family protein
AT2G29350	266292_at	SAG13__SAG13 (Senescence-associated gene 13); oxidoreductase
AT1G65490	264636_at	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G65486.1)
AT3G04000	258815_at	short-chain dehydrogenase/reductase (SDR) family protein
AT3G10450	258923_at	SCPL7__SCPL7; serine carboxypeptidase
AT4G08770	255110_at	peroxidase, putative
AT1G01060	261569_at	LHY__LHY (LATE ELONGATED HYPOCOTYL)
AT1G76190	261776_at	auxin-responsive family protein
AT5G24160	249775_at	squalene monooxygenase 1,2 / squalene epoxidase 1,2 (SQP1,2)
AT5G49330	248596_at	AtMYB111__AtMYB111 (myb domain protein 111); DNA binding / transcription factor

AT2G23910	266578_at	cinnamoyl-CoA reductase-related
AT3G59010	251509_at	pectinesterase family protein
AT3G27220	257153_at	kelch repeat-containing protein
AT5G13930	250207_at	CHS_TT4__ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
AT1G09500	264514_at	cinnamyl-alcohol dehydrogenase family / CAD family
AT2G25000	263536_at	WRKY60__WRKY60 (WRKY DNA-BINDING PROTEIN 60); transcription factor
AT5G49520	248611_at	WRKY48__WRKY48 (WRKY DNA-binding protein 48); transcription factor
AT5G63580	247358_at	flavonol synthase, putative
AT2G45210	245136_at	auxin-responsive protein-related
AT5G38710	249527_at	proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative
AT1G17420	261037_at	LOX3__(Lipoxygenase 3); iron ion binding lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
AT4G21680	254396_at	proton-dependent oligopeptide transport (POT) family protein
AT4G21990	254343_at	APR3_PRH26_PRH-26__APR3 (APS REDUCTASE 3)
AT5G50200	248551_at	ATNRT3.1_NRT3.1_WR3__WR3 (WOUND-RESPONSIVE 3); nitrate transmembrane transporter
AT3G27170	256751_at	CLC-B__CLC-B (chloride channel protein B); anion channel/ voltage-gated chloride channel
AT1G28600	262745_at	lipase, putative
AT5G17050	246468_at	UDP-glucuronosyl/UDP-glucosyl transferase family protein
AT4G14680	245254_at	APS3__APS3 (ATP sulfurylase 2); sulfate adenylyltransferase (ATP)
AT4G10120	255016_at	ATSPS4F__ATSPS4F
AT5G02190	251025_at	ATASP38_PCS1__ATASP38/PCS1 (PROMOTION OF CELL SURVIVAL1); aspartic-type endopeptidase/ peptidase
AT5G20830	245998_at	SUS1__SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase
AT3G14850	256600_at	similar to unknown protein (TAIR:AT1G29050.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39470.1); contains InterPro domain of unknown function DUF231, plant (InterPro:IPR004253)
AT1G65840	262933_at	ATPAO4__ATPAO4 (POLYAMINE OXIDASE 4); amine oxidase
AT4G15490	245352_at	UGT84A3__UGT84A3; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase/ transferase, transferring glycosyl groups
AT1G74710	262177_at	ICS1_EDS16_SID2__ICS1 (ISOCHORISMATE SYNTHASEI); isochorismate synthase
AT5G67400	246991_at	peroxidase 73 (PER73) (P73) (PRXR11)
AT5G44110	249063_at	POP1_ATNAP2_ATPOP1__POP1
AT4G23600	254232_at	COR13_JR2__COR13 (CORONATINE INDUCED 1, JASMONIC ACID RESPONSIVE 2); transaminase
AT5G08640	250533_at	FLS__FLS (FLAVONOL SYNTHASE)
AT4G11890	254869_at	protein kinase family protein

AT1G21460	260876_at	nodulin MtN3 family protein
AT1G69870	260410_at	proton-dependent oligopeptide transport (POT) family protein
AT5G35970	249677_at	DNA-binding protein, putative
AT5G44190	249035_at	GLK2_GPRI2__GLK2 (GOLDEN2-LIKE 2); DNA binding / transcription factor
AT4G27280	253915_at	calcium-binding EF hand family protein
AT3G12700	257697_at	aspartyl protease family protein
AT3G44990	252607_at	XTR8__XTR8 (xyloglucan:xyloglucosyl transferase 8); hydrolase, acting on glycosyl bonds
AT1G72900	262381_at	disease resistance protein (TIR-NBS class), putative
AT5G33290	246682_at	XGD1__XGD1 (XYLOGALACTURONAN DEFICIENT 1); catalytic
AT1G73260	260101_at	trypsin and protease inhibitor family protein / Kunitz family protein
AT1G64900	262882_at	CYP89A2_CYP89__CYP89A2 (CYTOCHROME P450 89A2); oxygen binding
AT4G08850	255116_at	leucine-rich repeat family protein / protein kinase family protein
AT1G48320	262237_at	thioesterase family protein
AT3G22540	256926_at	similar to unknown protein(TAIR:AT4G14819.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71190.1); contains InterPro domain of unknown function DUF1677 plant (InterPro:IPR012876)
AT5G45650	248961_at	subtilase family protein
AT4G38950	252916_at	kinesin motor family protein
AT1G19450	260676_at	integral membrane protein, putative / sugar transporter family protein
AT3G50480	252170_at	HR4__HR4 (HOMOLOG OF RPW8 4)
AT3G13760	256774_at	DC1 domain-containing protein
AT4G33030	253386_at	SQD1__SQD1 (sulfoquinovosyldiacylglycerol 1); UDPsulfoquinovose synthase
AT3G08940	258993_at	LHCB4.2__LHCB4.2 (LIGHT HARVESTING COMPLEX PSII)
AT5G06320	250676_at	NHL3__NHL3 (NDR1/HIN1-like 3)

Table 6: Over-represented promoter motifs significantly enriched in TOC1-ox and *toc1-2* miss-expressed genes.

TOC1-ox				
	P-value	Name	Number of promoters with TF sites	Number of predicted TF sites
	< 10 ⁻⁸	ACGTABREMOTIFA2OSEM	97	129
	< 10 ⁻⁷	ABRE-like binding site motif	121	184
	< 10 ⁻⁵	ABRE binding site motif	38	43
	< 10 ⁻⁵	EveningElement promoter motif	51	57
	< 10 ⁻⁴	AtMYC2 BS in RD22	163	220
	< 10 ⁻⁴	CACGTGMOTIF	86	212
	< 10 ⁻⁴	MYCATERD1	163	220
<i>toc1-2</i>				
	P-value	Name	Number of promoters with TF sites	Number of predicted TF sites
	< 10 ⁻⁹	ABRE-like binding site motif	69	121
	< 10 ⁻⁵	ACGTABREMOTIFA2OSEM	46	79
	< 10 ⁻⁶	CACGTGMOTIF	49	124
	< 10 ⁻⁷	GADOWNAT	36	48
	< 10 ⁻⁴	MYB1AT	153	353