Supplemental Data Set S3. List of differentially expressed genes between wild-type-1 and almt9-1 in shoots under salinity conditions.

Gene ID	**Short description**	**Curator summary**	**log2 Rat**	**pValue**	**fdr**	**WT-S1 [**	**WT-S2 [**	**WT-S3 [**	**WTplusS**	**WTplusS**	**WTplusS**	**KO-S1 [r**	**KO-S2 [r**	**KO-S3 [r**	**KOplusS**	**KOplusS**	**KOplusS**	**WT-S1 [**	**WT-S2 [**	**WT-S3 [**	**WTplusS**	**WTplusS**	**WTplusS**	**KO-S1 [F**	**KO-S2 [F**	**KO-S3 [F**	**KOplusS**	**KOplusS**	**KOplusS3 [FPKM]**
AT2G11410	transposable element gene		-7,79	4,33E-93	8,26E-89	415,3	331,9	471,6	293,3	360,9	308,3	0	0	0	0	0	4,186	6,457	5,249	7,099	4,029	5,434	4,568	0	0	0	0	0	0,0659
AT4G08093		pseudogene_of_unknown_protein	-7,016	2,12E-40	2,02E-36	231,3	142,9	183	101,1	143	151,6	0	0	2,254	1,343	1,175	0	9,824	6,173	7,524	3,792	5,883	6,134	0	0	0,0937	0,0534	0,0475	0
AT3G18440	aluminum-activated malate transporter 9	Belongs_to_the_aluminum-activated_malate_transporter_family._Encodes_a_vacuolar_malate_channel._Expressed_in_all_parts_of_plants._Almost_exclusively_expressed_in_mesophyll_cells_of_leaves.	-1,195	1,28E-17	8,13E-14	457,2	539,3	543,7	465,7	441,2	484	215,3	169,6	182,5	221,5	184,5	196,8	14,13	16,95	16,26	12,72	13,21	14,25	6,612	5,028	5,522	6,409	5,43	6,157
AT4G23140	cysteine-rich RLK (RECEPTOR-like protein kinase) 6	Arabidopsis_thaliana_receptor-like_protein_kinase._Naming_convention_from_Chen_et_al_2003_(PMID_14756307)	1,229	8,88E-17	4,23E-13	834,7	936,8	371,3	223,6	218,8	246,1	1004	300,7	530,9	618,8	513,9	462,8	23,34	26,64	10,05	5,523	5,924	6,556	27,9	8,066	14,53	16,2	13,68	13,11
AT1G75230	DNA glycosylase superfamily protein		-1,134	1,19E-12	4,55E-09	272	300,4	284,8	582	751,5	523,7	287,1	125,8	167,9	316,9	259,7	266,5	11,25	12,64	11,4	21,27	30,1	20,64	11,8	4,991	6,798	12,27	10,23	11,16
AT2G11405			-7,388	2,41E-12	7,67E-09	25,5	29,2	29,24	25,1	19,8	25,84	0	0	0	0	0	0	4,54	5,288	5,04	3,949	3,415	4,383	0	0	0	0	0	0
AT4G34410	redox responsive transcription factor 1	encodes_a_member_of_the_ERF_(ethylene_response_factor)_subfamily_B-3_of_ERF/AP2_transcription_factor_family._The_protein_contains_one_AP2_domain._There_are_18_members_in_this_subfamily_including_ATERF-1,_ATERF-2,_AND_ATERF-5.	-1,458	2,87E-12	7,83E-09	100,2	168,3	231,8	931,4	1110	628,7	173,4	71,54	172,4	345,1	236,2	386,5	4,482	7,657	10,04	36,81	48,1	26,8	7,706	3,07	7,55	14,45	10,06	17,51
AT2G34600	jasmonate-zim-domain protein 7		-1,23	2,17E-11	4,65E-08	316,4	732,2	536,6	1554	2051	1492	503,6	126,9	169	892,9	524,2	745,1	28,95	68,16	47,54	125,7	181,8	130,1	45,79	11,14	15,14	76,5	45,69	69,06
AT2G32680	receptor like protein 23		1,073	2,19E-11	4,65E-08	1645	2072	1014	195,5	263	206,7	2770	1052	1816	404,2	504,2	478,6	35,81	45,89	21,37	3,761	5,545	4,288	59,91	21,98	38,71	8,237	10,45	10,55
AT2G32150	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein		-1,332	4,23E-11	8,07E-08	1619	1955	2192	2671	3384	2058	1936	1224	1170	1423	940,2	845,6	90,03	110,6	118	131,2	182,3	109,1	107	65,32	63,68	74,11	49,8	47,63
AT3G26210	cytochrome P450, family 71, subfamily B, polypeptide 23	putative_cytochrome_P450	1,137	1,37E-10	2,38E-07	244,7	301,9	126,2	108,3	102,3	91,3	318,1	234,2	246,8	230,9	213,9	221,9	8,693	10,91	4,339	3,4	3,521	3,091	11,23	7,983	8,582	7,681	7,237	7,982
AT5G53750	CBS domain-containing protein		-1,158	2,19E-10	3,48E-07	219,2	537	562,1	626,9	644,7	406,5	699,1	143,1	148,7	298,1	230,4	223,3	9,721	24,23	24,13	24,56	27,7	17,18	30,8	6,088	6,458	12,38	9,73	10,03
AT1G18710	myb domain protein 47	Member_of_the_R2R3_factor_gene_family.	-1,05	3,21E-10	4,70E-07	461,5	456,4	633	540,3	718,5	611,5	427,4	221,5	175,8	370,6	288	238,6	25,55	25,7	33,93	26,43	38,53	32,26	23,51	11,77	9,528	19,21	15,18	13,38
AT2G16367		Encodes_a_defensin-like_(DEFL)_family_protein.	-1,188	7,23E-10	9,20E-07	133	43,02	114,8	525,8	318	348	29,82	28,85	28,17	193,4	175,1	153,5	31,21	10,27	26,08	109	72,28	77,81	6,953	6,495	6,472	42,48	39,14	36,48
AT1G19960			-1,063	8,51E-10	1,02E-06	624,2	209	474,3	1317	1090	768,3	296	240	210,7	561,3	430,2	523,3	90,99	30,99	66,94	169,7	154	106,7	42,87	33,57	30,07	76,6	59,72	77,25
AT5G24850	cryptochrome 3	Binds_flavin_adenine_dinucleotide_and_DNA._It_does_not_have_photolyase_activity,_and_it_is_likely_to_act_as_photoreceptor._Closely_related_to_Synechocystis_cryptochrome.	2,51	2,90E-09	3,26E-06	9,715	6,146	2,707	10,57	8,802	3,445	28,71	28,85	38,31	53,71	44,66	44,65	0,3364	0,2165	0,0908	0,3234	0,2953	0,1137	0,988	0,9584	1,299	1,741	1,473	1,566
AT1G70700	TIFY domain/Divergent CCT motif family protein	JAZ9_is_a_protein_presumed_to_be_involved_in_jasmonate_signaling._JAZ9_transcript_levels_rise_in_response_to_a_jasmonate_stimulus._JAZ9_can_interact_with_the_COI1_F-box_subunit_of_an_SCF_E3_ubiquitin_ligase_in_a_yeast-two-hybrid_assay_only_in_the_presence_of_jasmonate-isoleucine_(JA-ILE)_or_coronatine._The_Jas_domain_appears_to_be_important_for_JAZ9-COI1_interactions_in_the_presence_of_coronatine._Two_positive_residues_(R205_and_R206)_in_the_Jas_domain_shown_to_be_important_for_coronatine_-dependent_COI1_binding_are_not_required_for_binding_AtMYC2.	-1,071	4,58E-09	4,60E-06	7843	11900	11990	5183	6609	4608	10480	6238	4851	3265	2252	2251	401,3	619,2	594,1	234,3	327,5	224,6	532,9	306,2	243	156,4	109,7	116,6
AT1G19670	chlorophyllase 1	Chlorophyllase_is_the_first_enzyme_involved_in_chlorophyll_degradation._It_catalyzes_the_hydrolysis_of_the_ester_bond_to_yield_chlorophyllide_and_phytol._AtCLH1_lacks_a_typical_signal_sequence_for_the_chloroplast.__Its_expression_is_induced_rapidly_by_methyljasmonate,_a_known_promoter_of_senescence_and_chlorophyll_degradation.	-1,198	7,21E-09	6,88E-06	3632	5612	6227	504,7	553,4	332,5	3819	2219	1294	259,1	158,7	188,4	175,7	276,1	291,6	21,57	25,93	15,32	183,5	103	61,25	11,73	7,308	9,227
AT2G27690	cytochrome P450, family 94, subfamily C, polypeptide 1	Encodes_a_CYP94C1._Has_highest_omega-hydroxylase_activity_with_9,10-epoxystearic_acid,_while_also_metabolized_lauric_acid_(C12:0)_and_C18_unsaturated_fatty_acids._Gene_expression_is_induced_in_response_to_wounding_and_jasmonic_acid_treatment	-1,088	1,14E-08	9,85E-06	788,8	3474	2964	3062	4013	2279	3509	1184	929,7	1747	1242	1388	25,59	114,6	93,08	87,75	126,1	70,44	113,1	36,84	29,52	53,05	38,38	45,61
AT1G12610	Integrase-type DNA-binding superfamily protein	Encodes_a_member_of_the_DREB_subfamily_A-1_of_ERF/AP2_transcription_factor_family_(DDF1)._The_protein_contains_one_AP2_domain._There_are_six_members_in_this_subfamily,_including_CBF1,_CBF2,_and_CBF3._Overexpression_of_this_gene_results_in_delayed_flowering_and_dwarfism,_reduction_of_gibberellic_acid_biosynthesis,_and_increased_tolerance_to_high_levels_of_salt._This_gene_is_expressed_in_all_tissues_examined,_but_most_abundantly_expressed_in_upper_stems._Overexpression_of_this_gene_is_also_correlated_with_increased_expression_of_GA_biosynthetic_genes_and_RD29A_(a_cold_and_drought_responsive_gene)._Under_salt_stress_it_induces_the_expression_of_GAOX7,_which_encodes_ad_C20-GA_inhibitor.	-1,717	1,28E-08	1,06E-05	30,36	76,06	117,5	171,7	113,3	120,6	77,3	36,92	91,27	60,42	25,86	37,68	1,751	4,464	6,562	8,754	6,332	6,628	4,431	2,044	5,155	3,263	1,421	2,201
AT4G36950	mitogen-activated protein kinase kinase kinase 21	member_of_MEKK_subfamily	-1,592	1,69E-08	1,29E-05	96,55	168,3	186,3	228,6	259,7	124	146,9	27,69	30,42	88,62	64,64	50,23	4,497	7,973	8,4	9,407	11,72	5,505	6,798	1,238	1,387	3,865	2,868	2,37
AT3G44860	farnesoic acid carboxyl-O-methyltransferase	Encodes_a_farnesoic_acid_carboxyl-O-methyltransferase.	-1,101	1,90E-08	1,39E-05	5768	7124	7543	2149	1693	1395	6826	2537	1718	1098	634,7	696,3	289,6	363,9	366,6	95,33	82,34	66,75	340,5	122,2	84,46	51,63	30,35	35,41
AT4G27654			-1,117	2,97E-08	2,10E-05	19,43	33,04	37,9	369,3	440,1	270,4	13,25	24,23	46,2	206,8	136,3	154,9	2,498	4,32	4,717	41,94	54,79	33,13	1,692	2,988	5,814	24,88	16,69	20,16
AT3G51450	Calcium-dependent phosphotriesterase superfamily protein		-1,193	6,97E-08	4,15E-05	3812	6376	6179	2093	2007	1111	5152	3699	2383	946,6	564,1	756,3	182	309,6	285,5	88,29	92,78	50,54	244,3	169,4	111,4	42,3	25,64	36,56
AT1G02920	glutathione S-transferase 7	Encodes_glutathione_transferase_belonging_to_the_phi_class_of_GSTs._Naming_convention_according_to_Wagner_et_al._(2002).	1,576	7,33E-08	4,24E-05	222,3	582,1	403,2	118,2	89,85	93,69	631,4	581,6	984	487,8	203,7	210,2	14,89	39,66	26,14	6,997	5,829	5,98	42,02	37,37	64,52	30,59	13	14,26
AT2G29350	senescence-associated gene 13	senescence-associated_gene_SAG13_encoding_a_short-chain_alcohol_dehydrogenase	1,564	1,40E-07	6,85E-05	41,29	67,61	139,2	107	51,71	101,6	16,57	19,62	15,78	371,9	224,5	170,3	2,032	3,386	6,631	4,654	2,465	4,767	0,8102	0,9263	0,7602	17,14	10,52	8,487
AT1G25430	transposable element gene		-1,005	1,74E-07	8,31E-05	369,2	148,3	256,1	438	267,4	404,8	249,6	161,5	146,5	204,1	193,9	150,7	4,294	1,754	2,884	4,501	3,012	4,486	2,884	1,803	1,668	2,222	2,148	1,775
AT5G18470	Curculin-like (mannose-binding) lectin family protein		1,104	2,17E-07	9,87E-05	109,3	156	134,3	161,2	162,8	155	161,2	121,2	336,9	448,5	358,5	219,1	4,548	6,602	5,409	5,926	6,563	6,147	6,666	4,836	13,72	17,47	14,2	9,232
AT2G43535	Scorpion toxin-like knottin superfamily protein	Encodes_a_defensin-like_(DEFL)_family_protein.	-1,16	2,50E-07	0,00011	121,4	120,6	171,1	140,7	169,4	130,9	72,89	99,23	43,95	64,45	62,29	69,77	13,27	13,41	18,1	13,58	17,93	13,63	7,913	10,4	4,701	6,593	6,482	7,721
AT1G21240	wall associated kinase 3	encodes_a_wall-associated_kinase	2,093	2,62E-07	0,00011	61,7	61,98	54,97	11,62	25	22,17	103,4	50,02	81,67	124,3	59,89	61,61	1,624	1,659	1,401	0,2702	0,6373	0,556	2,705	1,263	2,104	3,063	1,501	1,642

AT1G05680	Uridine diphosphate glycosyltransferase 74E2	Encodes_a_UDP-glucosyltransferase,_UGT74E2,__that_acts_on_IBA_(indole-3-butyric_acid)_and_affects_auxin_homeostasis._The_transcript_and_protein_levels_of_this_enzyme_are_strongly_induced_by_H2O2_and_may_allow_integration_of_ROS_(reactive_oxygen_species)_and_auxin_signaling._This_enzyme_can_also_transfer_glycosyl_groups_to_several_compounds_related_to_the_explosive_TNT_when_this_synthetic_compound_is_taken_up_from_the_environment.	3,338	2,90E-07	0,00012	248,3	1,537	11,37	11,89	5,501	37,9	0	1,154	7,888	374,6	102,3	58,61	10,14	0,0638	0,4493	0,4288	0,2175	1,474	0	0,0452	0,3152	14,31	3,975	2,422
AT3G60170	transposable element gene		2,57	3,23E-07	0,00013	4,858	11,52	11,37	7,266	2,2	6,89	43,07	24,23	21,41	28,2	35,26	36,28	0,0749	0,1807	0,1697	0,099	0,0329	0,1012	0,6595	0,3583	0,323	0,4068	0,5175	0,5663
AT1G62440	leucine-rich repeat/extensin 2	encodes_a_paralog_of_LRX1_(LEUCINE-RICH_REPEAT/EXTENSIN_1)_which_acts_synergistically_with_LRX1_in_root_hair_cell_morphogenesis.	2,792	7,26E-07	0,00028	15,18	63,77	50,36	2,642	9,902	3,445	24,3	57,69	64,23	51,02	35,26	23,72	0,3791	1,62	1,217	0,0583	0,2395	0,082	0,6028	1,382	1,57	1,193	0,8386	0,5999
AT3G48520	cytochrome P450, family 94, subfamily B, polypeptide 3	member_of_CYP94B	-1,371	7,55E-07	0,00028	184	609,3	1046	375,2	174,9	263,6	342,3	159,2	182,5	108,8	70,52	134	6,729	22,67	37,04	12,12	6,197	9,185	12,44	5,587	6,536	3,724	2,456	4,962
AT3G25010	receptor like protein 41		1,593	1,29E-06	0,00044	325,7	570,5	170,5	20,42	54,68	37,9	610,3	140,8	215,1	115,2	122	94,8	7,627	13,59	3,866	0,4224	1,24	0,8456	14,2	3,162	4,932	2,526	2,721	2,248
AT1G74930	Integrase-type DNA-binding superfamily protein	encodes_a_member_of_the_DREB_subfamily_A-5_of_ERF/AP2_transcription_factor_family._The_protein_contains_one_AP2_domain._There_are_15_members_in_this_subfamily_including_RAP2.1,_RAP2.9_and_RAP2.10.	-1	1,35E-06	0,00044	34	39,18	63,9	591,2	509,4	389,3	34,23	79,62	133	334,3	181	228,8	2,295	2,69	4,175	35,26	33,3	25,04	2,296	5,155	8,785	21,12	11,63	15,64
AT2G04495			1,243	2,80E-06	0,0008	33,4	33,04	41,15	36,33	60,51	46,51	39,76	31,15	89,02	124,9	102,3	106,1	2,199	2,213	2,623	2,114	3,859	2,918	2,601	1,968	5,738	7,697	6,412	7,071
AT5G10930	CBL-interacting protein kinase 5	Encodes_CBL-interacting_protein_kinase_5_(CIPK5)	-1,098	3,07E-06	0,00083	499,7	72,99	106,7	183	203,5	117,1	136,9	101,5	74,37	72,51	81,1	82,33	17,7	2,63	3,658	5,727	6,984	3,954	4,82	3,451	2,579	2,405	2,736	2,954
AT3G15630			1,089	3,36E-06	0,00089	250,2	485,6	403,4	61,43	77,02	79,24	512,4	851,6	920,5	138,3	131,6	184,2	20,58	40,64	32,13	4,466	6,138	6,213	41,89	67,22	74,15	10,65	10,31	15,35
ATCG01050	NADH-Ubiquinone/plastoquinone (complex I) protein	Represents_a_plastid-encoded_subunit_of_a_NAD(P)H_dehydrogenase_complex.__Its_mRNA_is_edited_at_four_positions.__Translation_data_is_not_available_for_this_gene.	-1,405	4,89E-06	0,00121	88,65	50,71	92,05	110,3	78,12	91,3	68,47	35,77	47,33	30,88	24,68	50,23	3,611	2,101	3,63	3,97	3,082	3,544	2,771	1,398	1,887	1,178	0,9575	2,072
AT5G52020	Integrase-type DNA-binding superfamily protein	encodes_a_member_of_the_DREB_subfamily_A-4_of_ERF/AP2_transcription_factor_family._The_protein_contains_one_AP2_domain._There_are_17_members_in_this_subfamily_including_TINY.	-1,396	8,35E-06	0,00194	3,643	5,378	21,66	72	70,42	89,57	4,417	3,462	19,16	30,88	19,98	36,28	0,2278	0,342	1,311	3,977	4,264	5,336	0,2744	0,2076	1,172	1,808	1,19	2,297
AT1G52200	PLAC8 family protein		1,005	1,11E-05	0,00246	221,6	331,1	234,5	94,46	63,81	122,3	589,7	483,5	791	166,5	184,5	199,5	15,29	23,24	15,66	5,758	4,264	8,041	40,43	32	53,43	10,75	12,12	13,94
AT1G01250	Integrase-type DNA-binding superfamily protein	encodes_a_member_of_the_DREB_subfamily_A-4_of_ERF/AP2_transcription_factor_family._The_protein_contains_one_AP2_domain._There_are_17_members_in_this_subfamily_including_TINY.	-1,078	1,13E-05	0,00249	37,65	9,22	25,99	120,9	112,2	105,1	11,04	13,85	6,761	56,39	63,47	39,07	2,777	0,6918	1,856	7,878	8,017	7,385	0,8093	0,9798	0,4882	3,894	4,458	2,919
AT3G26830	Cytochrome P450 superfamily protein	Mutations_in_pad3_are_defective_in_biosynthesis_of_the_indole_derived_phytoalexin_camalexin._Encodes_a_cytochrome_P450_enzyme_that_catalyzes_the_conversion_of_dihydrocamalexic_acid_to_camalexin.	4,411	1,32E-05	0,00284	30,36	23,82	7,039	2,642	5,501	5,168	13,25	3,462	11,27	261,8	5,877	16,74	1,133	0,9043	0,2543	0,0871	0,1989	0,1838	0,4914	0,1239	0,4117	9,149	0,2089	0,6329
AT2G18190	P-loop containing nucleoside triphosphate hydrolases superfamily protein		4,674	1,58E-05	0,00317	24,97	1,537	0	0,6606	0	0	0	0,0346	1,127	18,89	12,93	2,791	1,042	0,0652	0	0,0244	0	0	0	0,0014	0,046	0,7379	0,5137	0,1179
AT1G78440	Arabidopsis thaliana gibberellin 2-oxidase 1	Encodes_a_gibberellin_2-oxidase_that_acts_on_C19_gibberellins.	-2,445	2,12E-05	0,00413	15,79	6,915	2,166	36,33	26,41	22,39	1,104	5,769	1,127	9,399	5,877	0	0,7991	0,3561	0,1061	1,625	1,295	1,08	0,0555	0,2802	0,0558	0,4454	0,2833	0
AT2G38240	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein		-2,247	2,76E-05	0,00527	936,9	6140	5256	65,4	68,21	24,12	3524	2294	844	17,46	14,1	1,395	43,42	289,5	235,8	2,678	3,062	1,065	162,2	102	38,29	0,7573	0,6224	0,0655
AT4G27970	SLAC1 homologue 2	Encodes_a_protein_with_ten_predicted_transmembrane_helices._The_SLAH2_protein_has_similarity_to_the_SLAC1_protein_involved_in_ion_homeostasis_in_guard_cells._But,_it_is_not_expressed_in_guard_cells_and_cannot_complement_a_slac1-2_mutant_suggesting_that_it_performs_a_different_function._SLAH2:GFP_localizes_to_the_plasma_membrane.	1,205	2,82E-05	0,00528	72,86	236,6	181,9	63,41	89,12	62,01	271,7	200,8	286,2	126,2	126,9	238,6	2,875	9,5	6,951	2,211	3,406	2,332	10,65	7,601	11,06	4,663	4,77	9,536
AT1G30135	jasmonate-zim-domain protein 8		-1,275	3,18E-05	0,00572	117,2	381,1	302,1	229,2	333,4	186	361,1	75	121,7	166,5	64,64	78,14	12,87	42,58	32,13	22,25	35,47	19,47	39,41	7,904	13,09	17,12	6,763	8,693
AT1G53903	Protein of unknown function (DUF581)		-1,021	3,21E-05	0,00572	1233	1267	1587	901,2	1380	652,2	1261	621,3	541,1	666,2	394,3	382,5	121,1	126,6	150,9	78,19	131,3	61,02	123	58,52	52,01	61,24	36,87	38,03
AT1G49530	geranylgeranyl pyrophosphate synthase 6	encodes_a_mitochondria-targeted_geranylgeranyl_pyrophosphate_synthase	-1,11	3,24E-05	0,00573	251,4	330,4	420,7	91,82	117,7	84,41	234,1	113,1	133	48,34	38,79	48,84	12,35	16,51	20,01	3,986	5,602	3,952	11,43	5,33	6,396	2,223	1,815	2,43
AT2G04050	MATE efflux family protein		2,535	3,38E-05	0,00588	452,3	5,37	3,79	18,5	28,61	56,86	7,73	8,077	21,41	440,4	103,4	48,84	19,58	0,2365	0,1589	0,7076	1,2	2,346	0,3325	0,3355	0,9075	17,85	4,265	2,141
AT4G25000	alpha-amylase-like	Predicted_to_be_secreted_protein_based_on_signalP_prediction._Involved_in_starch_mobilization.__Mutants_are_defective_in_alpha-amylase_activity._(Note:_AMY1_has_been_found_in_the_literature_to_be_referred_to_as_AMY3,_which_is_not_to_be_confused_with_AMY3/At1g69830).	1,482	3,40E-05	0,00588	24,29	101,4	95,3	33,03	35,21	53,4	47,49	69,23	33,81	165,2	109,3	57,21	1,051	4,464	3,992	1,263	1,475	2,202	2,041	2,874	1,432	6,689	4,504	2,507
AT3G44300	nitrilase 2	Encodes_an_enzyme_that_catalyzes_the_hydrolysis_of_indole-3-acetonitrile_(IAN)_to_indole-3-acetic_acid_(IAA)_(nitrile_aminohydrolase,_EC_3.5.5.1)_and_IAN_to_indole-3-acetamide_(IAM)_at_lower_levels._Mutants_have_reduced_sensitivity_to_IAN_and_are_sensitive_to_IAA._This_enzyme_likely_participates_in_other_non-auxin-related_metabolic_pathways.	3,217	3,46E-05	0,00588	3,036	348	57,05	72,77	15,41	27,58	1,104	40,39	3,381	829,5	30,9	223,1	0,1322	15,41	2,405	2,799	0,65	1,144	0,0478	1,687	0,1441	33,81	1,281	9,837
AT2G04040	MATE efflux family protein	AtDTX1_(At2g04040)_has_been_identified_as_a_detoxifying_efflux_carrier_for_plant-derived_antibiotics_and_other_toxic_compounds,_including_CD2+.	3,998	4,70E-05	0,00753	48,52	5,378	1,083	0,6606	0	6,89	1,104	4,615	4,507	80,56	10,55	11,16	1,95	0,2198	0,0421	0,0235	0	0,2638	0,0441	0,1779	0,1773	3,03	0,4039	0,4542
AT3G57240	beta-1,3-glucanase 3	encodes_a_member_of_glycosyl_hydrolase_family_17	1,514	5,12E-05	0,00814	459,7	421	385	35,67	18,7	34,45	650,5	410,8	456,4	45,65	98,73	107,4	23,15	21,57	18,77	1,588	0,9125	1,654	32,55	19,85	22,5	2,153	4,736	5,481
AT1G29715			3,98	5,93E-05	0,00898	9,715	13,83	7,039	0	1,1	0	13,25	12,69	13,52	8,056	7,052	6,977	0,2602	0,3768	0,1825	0	0,0286	0	0,3527	0,3262	0,3546	0,202	0,1799	0,1893
AT2G38760	annexin 3	Annexins_are_calcium_binding_proteins_that_are_localized_in_the_cytoplasm._When_cytosolic_Ca2+_increases,_they_relocate_to_the_plasma_membrane.	-1,48	6,50E-05	0,00947	114,2	255,1	170	50,2	92,42	51,68	122,6	101,5	57,47	25,51	19,98	23,72	5,717	13	8,244	2,222	4,484	2,466	6,1	4,879	2,818	1,196	0,953	1,203
AT1G26380	FAD-binding Berberine family protein		3,478	7,06E-05	0,00997	9,715	34,57	7,581	5,945	4,401	5,168	4,417	15	14,65	157,1	11,75	9,768	0,3359	1,216	0,2537	0,1816	0,1474	0,1703	0,1517	0,4976	0,4958	5,085	0,387	0,342
AT1G14780	MAC/Perforin domain-containing protein		1,125	8,42E-05	0,01131	60,72	152,9	233,9	31,71	36,31	56,84	87,24	106,2	122,8	80,56	92,85	86,52	1,715	4,394	6,398	0,7915	0,9935	1,53	2,449	2,877	3,397	2,131	2,498	2,475
AT5G02490	Heat shock protein 70 (Hsp 70) family protein		1,285	9,44E-05	0,01251	90,47	173,6	102,9	81,25	86,92	136,1	90,56	48,46	76,63	402,8	190,4	138,1	2,432	4,748	2,677	1,93	2,263	3,485	2,418	1,25	2,016	10,14	4,874	3,76

AT4G21380	receptor kinase 3	encodes_a_putative_receptor-like_serine/threonine_protein_kinases_that_is_similar_to_Brassica_self-incompatibility_(S)_locus._Expressed_in_root._Shoot_expression_limited_to_limited_to_the_root-hypocotyl_transition_zone_and_at_the_base_of_lateral_roots_as_well_as_in_axillary_buds,_and_pedicels.	0,4797	9,53E-05	0,01253	1699	1208	1398	686,3	634,8	623,6	1206	949,6	839,5	828,5	861,5	1006	35,29	25,52	28,1	12,6	12,77	12,34	24,89	18,92	17,07	16,11	17,04	21,16
AT3G19030			-0,471	9,62E-05	0,01257	919,9	885,9	1443	2616	2291	2491	1029	1168	1707	1862	1795	1642	127,8	125,2	194,1	321,1	308,2	329,7	142,1	155,6	232,2	242,2	237,4	231,1
AT1G56650	production of anthocyanin pigment 1	Encodes_a_putative_MYB_domain_containing_transcription_factor_involved_in_anthocyanin_metabolism_and_radical_scavenging._Essential_for_the_sucrose-mediated_expression_of_the_dihydroflavonol_reductase_gene	-1,148	9,99E-05	0,01296	76,51	43,79	46,57	152,6	152,9	80,96	22,09	18,46	6,761	72,51	63,47	39,07	5,186	3,02	3,056	9,139	10,04	5,229	1,488	1,201	0,4487	4,601	4,097	2,682
AT2G18193	P-loop containing nucleoside triphosphate hydrolases superfamily protein		2,007	0,0001	0,01336	485,1	27,66	22,2	23,12	37,41	65,46	39,76	46,12	64,23	339,6	85,8	71,17	17,71	1,027	0,7847	0,7458	1,323	2,277	1,442	1,615	2,296	11,61	2,983	2,631
AT3G28890	receptor like protein 43		1,085	0,00015	0,01779	131,2	108,3	95,06	53,51	31,91	44,79	122,1	89,89	63,1	115,5	77,58	85,12	3,523	2,96	2,471	1,27	0,83	1,146	3,258	2,316	1,659	2,903	1,984	2,315
AT4G08570	Heavy metal transport/detoxification superfamily protein		-1,14	0,0002	0,02248	24,29	2,305	3,249	87,2	94,62	63,73	2,209	5,769	1,127	38,94	48,19	23,72	1,379	0,1332	0,1786	4,375	5,205	3,449	0,1246	0,3143	0,0627	2,07	2,606	1,364
AT2G18690			1,119	0,0002	0,02248	154,8	269,7	187,4	146,6	205,7	189,5	323,6	211,2	496,9	656,6	289,1	226,1	7,08	12,54	8,293	5,925	9,112	8,256	14,7	9,263	22,24	28,11	12,59	10,47
AT1G16370	organic cation/carnitine transporter 6		-1,236	0,00021	0,02316	72,26	273,5	167,9	62,09	75,92	49,95	89,45	102,7	61,98	32,23	19,98	27,91	2,552	9,828	5,74	1,938	2,597	1,681	3,139	3,48	2,143	1,066	0,6721	0,9983
AT1G17170	glutathione S-transferase TAU 24	Encodes_glutathione_transferase_belonging_to_the_tau_class_of_GSTs._Naming_convention_according_to_Wagner_et_al._(2002).	1,956	0,00022	0,02362	6,072	3,842	20,58	16,51	15,4	10,34	5,522	9,231	2,254	48,34	19,98	99,07	0,44	0,2832	1,443	1,057	1,081	0,7137	0,3976	0,6417	0,1599	3,279	1,379	7,271
AT3G28580	P-loop containing nucleoside triphosphate hydrolases superfamily protein		3,371	0,00023	0,02454	21,86	3,842	2,166	1,982	6,601	5,168	2,209	3,462	7,888	123,5	9,402	8,372	0,7934	0,1418	0,0761	0,0636	0,2321	0,1787	0,0797	0,1205	0,2803	4,197	0,325	0,3078
AT1G77855			-1,048	0,00023	0,02454	32,18	20,74	15,16	72	96,82	78,36	12,15	23,08	12,4	32,23	43,49	41,86	1,716	1,125	0,7826	3,392	5	3,981	0,6435	1,18	0,647	1,609	2,208	2,26
AT1G17960	Threonyl-tRNA synthetase		2,573	0,00031	0,03072	66,19	1,537	3,79	2,642	3,301	0	3,313	4,615	4,507	20,14	8,227	13,95	2,62	0,0619	0,1453	0,0924	0,1266	0	0,1303	0,1753	0,1747	0,7465	0,3102	0,5595
AT3G22275			-1,287	0,00031	0,03108	116	303,5	188,4	64,08	95,72	105,1	226,4	40,39	33,81	57,74	28,21	20,93	10,94	29,11	17,2	5,339	8,743	9,442	21,21	3,654	3,121	5,097	2,533	1,999
AT3G23550	MATE efflux family protein		1,47	0,00042	0,03735	247,1	997,3	1047	46,9	44,01	5,168	1443	1518	1836	75,19	104,6	97,68	9,451	38,8	38,77	1,585	1,63	0,1883	54,85	55,72	68,73	2,692	3,81	3,783
AT3G09640	ascorbate peroxidase 2	Encodes_a_cytosolic_ascorbate_peroxidase_APX2.__Ascorbate_peroxidases_are_enzymes_that_scavenge_hydrogen_peroxide_in_plant_cells.__Eight_types_of_APX_have_been_described_for_Arabidopsis:_three_cytosolic_(APX1,_APX2,_APX6),_two_chloroplastic_types_(stromal_sAPX,_thylakoid_tAPX),_and_three_microsomal_(APX3,_APX4,_APX5)_isoforms.	-1,669	0,00045	0,0399	0,6072	1,537	1,083	25,1	36,31	39,62	1,104	2,308	0	9,386	15,28	5,582	0,0368	0,0946	0,0635	1,343	2,129	2,285	0,0664	0,134	0	0,5319	0,8808	0,3422
AT1G63030	Integrase-type DNA-binding superfamily protein	encodes_a_member_of_the_DREB_subfamily_A-1_of_ERF/AP2_transcription_factor_family_(DDF2)._The_protein_contains_one_AP2_domain._There_are_six_members_in_this_subfamily,_including_CBF1,_CBF2,_and_CBF3._Overexpression_of_this_gene_results_in_the_reduction_of_gibberellic_acid_biosynthesis._This_gene_is_expressed_in_all_tissues_examined,_but_most_abundantly_expressed_in_rosette_leaves_and_stems._Overexpression_of_DDF1,_a_putative_paralog_of_this_gene,_also_reduces_gibberellic_acid_biosynthesis_and_makes_the_plants_more_tolerant_to_high-salinity_levels.	-2,258	0,00052	0,04448	1,214	0,7683	2,707	21,14	12,1	25,84	1,104	3,462	12,4	8,056	1,175	2,791	0,0895	0,0576	0,1932	1,377	0,8641	1,815	0,0809	0,2448	0,8945	0,556	0,0825	0,2083
AT5G60250	zinc finger (C3HC4-type RING finger) family protein		1,473	0,00053	0,04497	8,501	13,06	8,122	17,84	14,3	13,78	14,36	6,923	10,14	40,28	28,21	61,4	0,2421	0,3785	0,224	0,4489	0,3946	0,3741	0,4063	0,1892	0,2828	1,074	0,7652	1,771
AT5G66740	Protein of unknown function (DUF620)		-1,711	0,00059	0,04865	15,18	19,21	25,99	23,78	26,41	29,28	13,25	12,69	6,761	5,371	5,877	12,56	0,845	1,088	1,401	1,17	1,424	1,553	0,7329	0,6778	0,3684	0,2799	0,3115	0,708
AT1G30730	FAD-binding Berberine family protein		1,303	0,00064	0,05201	5,465	20,74	14,08	25,1	14,3	13,78	5,522	24,23	61,98	49,68	49,36	37,68	0,2014	0,7778	0,5023	0,8174	0,5106	0,484	0,2022	0,8568	2,236	1,714	1,733	1,406
AT2G22770	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	regulates_the_development_of_ER_bodies._also_involves_in_response_to_the_endophytic_fungus_Piriformospora_indica.	-1,018	0,00067	0,05347	302,4	623,9	342,8	171,1	331,2	144,7	293,8	171,9	102,5	84,59	94,02	139,5	13,67	28,7	15,01	6,836	14,51	6,235	13,2	7,459	4,54	3,581	4,05	6,391
AT5G10970	C2H2 and C2HC zinc fingers superfamily protein		-2,031	0,00069	0,05452	6,679	9,988	8,122	19,82	18,7	20,67	3,313	18,46	10,14	5,371	8,227	0	0,5053	0,7686	0,5948	1,325	1,37	1,49	0,249	1,34	0,7511	0,3804	0,5927	0
AT5G13790	Glycosyl hydrolases family 32 protein	Encodes_a_protein_with_invertase_activity.	1,137	0,00072	0,05568	150	347,3	250,7	23,12	29,71	18,95	265	278,1	333,5	48,34	58,77	51,63	4,744	11,18	7,678	0,6462	0,9102	0,5712	8,331	8,44	10,33	1,432	1,77	1,654
AT1G76930	extensin 4	Encodes_an_Arabidopsis_extensin_gene_that_belongs_to_cell-wall_hydroxyproline-rich_glycoproteins.__The_cross-link_of_extensins_enforces_cell_wall_strength._Transgenic_plants_overexpressing_this_gene_show_an_increase_in_stem_thickness.	1,38	0,00074	0,05672	10,93	167,4	24,37	12,55	19,8	17,23	15,46	25,38	38,31	29,54	44,66	51,63	0,6253	9,742	1,349	0,6344	1,097	0,939	0,8788	1,393	2,146	1,582	2,433	2,991
AT1G13520	Protein of unknown function (DUF1262)		3,313	0,00074	0,05672	4,25	8,451	0,5415	1,321	2,2	3,445	4,417	0	0	53,71	12,93	1,395	0,2077	0,4201	0,0256	0,057	0,1041	0,1604	0,2145	0	0	2,457	0,6016	0,0691
AT1G35230	arabinogalactan protein 5	Encodes_arabinogalactan-protein_(AGP5).	1,001	0,00075	0,05676	77,72	55,32	39,53	46,9	29,71	29,28	53,01	28,85	54,09	75,19	76,4	65,58	7,83	5,669	3,855	4,175	2,899	2,811	5,306	2,788	5,334	7,092	7,329	6,691
AT2G03760	sulphotransferase 12	Encodes_a_brassinosteroid_sulfotransferase._In_vitro_experiements_show_that_this_enzyme_has_a_preference_for_24-epibrassinosteroids,_particularly_24-epicathasterone,_but_does_not_act_on_castasterone_and_brassinolide.__It_is_differentially_expressed_during_development,_being_more_abundant_in_young_seedlings_and_actively_growing_cell_cultures._Expression_is_induced_in_response_to_salicylic_acid_and_methyl_jasmonate_and_bacterial_pathogens.	1,031	0,00085	0,06186	505,2	175,9	164,6	186,3	161,7	206,7	172,3	211,2	197,2	655,2	236,2	237,2	23,59	8,356	7,44	7,685	7,314	9,196	7,992	9,458	9,013	28,64	10,5	11,22
AT1G58225			1,015	0,00089	0,06393	115,4	148,3	36,82	33,69	37,41	60,29	129,2	35,77	72,12	107,4	82,27	65,58	11,08	14,49	3,424	2,859	3,48	5,518	12,33	3,296	6,782	9,661	7,526	6,38
AT5G25260	SPFH/Band 7/PHB domain-containing membrane-associated protein family		1,957	0,00105	0,07193	15,18	11,52	4,873	13,21	12,15	12,06	21,05	8,077	6,772	104,9	21,03	20,93	0,5659	0,437	0,1759	0,4352	0,4386	0,4283	0,7796	0,2889	0,2471	3,661	0,7465	0,7902
AT3G04220	Disease resistance protein (TIR-NBS-LRR class) family		1,2	0,00106	0,07193	21,25	26,89	10,83	36,33	42,91	41,34	22,09	12,69	36,06	149	78,75	47,44	0,5056	0,6508	0,2494	0,7638	0,9889	0,9373	0,5221	0,2897	0,8399	3,32	1,784	1,143
AT5G02550			-1,334	0,00106	0,07193	21,25	26,89	3,79	47,56	41,81	32,73	14,36	8,077	7,888	20,14	9,402	19,54	2,607	3,356	0,4502	5,156	4,968	3,826	1,75	0,9507	0,9474	2,313	1,099	2,427
AT4G04490	cysteine-rich RLK (RECEPTOR-like protein kinase) 36	Encodes_a_cysteine-rich_receptor-like_protein_kinase	1,583	0,0011	0,0741	100,2	59,93	41,15	27,74	25,31	41,34	76,2	25,38	55,22	186,6	42,31	50,23	3,14	1,91	1,248	0,7682	0,7681	1,235	2,373	0,7632	1,694	5,476	1,263	1,594
AT4G27140	seed storage albumin 1		-3,441	0,00111	0,07434	15,79	264,3	144	6,606	7,702	3,445	85,04	62,31	29,3	0	0	1,395	1,391	23,69	12,29	0,5144	0,6574	0,2893	7,446	5,268	2,528	0	0	0,1245
AT5G12340			-1,304	0,00117	0,07683	61,33	145,2	107,2	101,1	148,5	56,84	104,9	24,23	30,42	71,16	27,03	26,51	5,731	13,8	9,699	8,345	13,44	5,062	9,741	2,172	2,783	6,226	2,406	2,509
AT5G47850	CRINKLY4 related 4		1,359	0,0013	0,08238	4,858	10,76	29,24	23,12	14,3	18,95	16,57	23,08	70,99	76,53	36,43	33,49	0,1263	0,2846	0,7363	0,5313	0,3603	0,4696	0,4281	0,5759	1,808	1,864	0,9025	0,8822
AT5G01550	lectin receptor kinase a4.1	Encodes_LecRKA4.2,_a_member_of_the_lectin_receptor_kinase_subfamily_A4_(LecRKA4.1_At5g01540;_LecRKA4.2_At5g01550;_LecRKA4.3_At5g01560)._Together_with_other_members_of_the_subfamily,_functions_redundantly_in_the_negative_regulation_of_ABA_response_in_seed_germination.	2,724	0,00144	0,08955	11,54	7,683	3,249	5,945	6,601	3,445	4,417	1,154	3,381	95,33	7,052	8,372	0,3458	0,2343	0,0943	0,1575	0,1917	0,0984	0,1316	0,0332	0,0992	2,675	0,2013	0,2542

AT1G16420	metacaspase 8	Encodes_a_metacaspase_(cysteine-type_endopeptidase)_that_is_involved_in_promoting_programmed_cell_death_in_response_to_hydrogen_peroxide_(H2O2),_UV_light,_and_methyl_viologen_(MV)._Transcript_levels_rise_in_response_to_UV-C,_H2O2,_and_MV._In_vitro_assays_demonstrate_that_this_enzyme_has_a_preference_for_cleaving_after_an_arginine_residue,_and_it_has_a_pH_optimum_of_8.0.	2,497	0,00179	0,1026	9,715	5,378	13	3,963	5,501	1,723	3,313	3,462	23,66	51,02	7,052	9,768	0,4499	0,2533	0,5826	0,1622	0,2467	0,076	0,1524	0,1538	1,073	2,212	0,311	0,4581
AT3G59710	NAD(P)-binding Rossmann-fold superfamily protein		-1,082	0,00181	0,1026	81,37	29,96	72,02	62,09	103,4	56,84	45,28	36,92	20,28	25,51	31,73	47,44	4,229	1,584	3,624	2,852	5,207	2,815	2,338	1,841	1,032	1,241	1,571	2,497
AT3G27270	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein		-1,649	0,00184	0,1038	29,15	4,61	7,581	23,78	16,5	25,84	7,73	5,769	6,761	5,371	10,58	4,186	2,05	0,3298	0,5161	1,478	1,124	1,732	0,5401	0,3892	0,4655	0,3536	0,7084	0,2981
AT2G47000	ATP binding cassette subfamily B4	Multidrug_resistance__P-glycoprotein_(MDR/PGP)_subfamily_of_ABC_transporters._Functions_in_the_basipetal__redirection_of_auxin_from_the_root_tip._Exhibits_apolar_plasma_membrane_localization_in_the_root_cap_and_polar_localization_in_tissues_above.	1,636	0,00192	0,1072	238	113,7	93,68	61,43	59,41	120,6	97,18	102,7	94,66	541,1	130,5	73,96	3,544	1,722	1,35	0,8082	0,8569	1,711	1,438	1,467	1,38	7,543	1,85	1,115
AT2G04070	MATE efflux family protein		3,05	0,00195	0,108	326,7	6,922	4,332	4,624	12,1	60,27	5,522	5,769	6,761	570,7	39,96	18,14	12,47	0,2688	0,1601	0,156	0,4475	2,192	0,2094	0,2113	0,2527	20,39	1,453	0,7013
AT5G03270	lysine decarboxylase family protein		-1,653	0,00201	0,1087	13,97	43,79	24,91	17,84	34,11	18,95	16,57	16,15	11,27	6,714	7,052	8,372	1,254	4	2,165	1,415	2,966	1,621	1,478	1,392	0,9905	0,5644	0,603	0,7613
AT4G23210	cysteine-rich RLK (RECEPTOR-like protein kinase) 13	Encodes_a_Cysteine-rich_receptor-like_kinase_(CRK13).__Overexpression_of_CRK13_leads_to_hypersensitive_response_cell_death,_and_induces_defense_against_pathogens_by_causing_increased_accumulation_of_salicylic_acid.	1,566	0,00202	0,1087	20,31	25,96	29,38	11,3	4,742	7,82	40,24	35,89	46,88	31,85	20,85	21,17	0,5635	0,7327	0,7892	0,2771	0,1274	0,2068	1,109	0,9552	1,273	0,8273	0,5509	0,5948
AT4G24040	trehalase 1	Encodes_a_trehalase,_member_of_Glycoside_Hydrolase_Family_37.	1,141	0,00216	0,1109	58,9	80,67	92,59	36,99	26,41	27,56	162,3	169,6	170,2	106,1	47,01	50,23	1,725	2,404	2,626	0,9575	0,7492	0,7693	4,725	4,767	4,88	2,909	1,312	1,49
AT5G18270	Arabidopsis NAC domain containing protein 87		1,184	0,00222	0,1127	20,64	23,82	12,45	20,48	18,7	17,23	9,939	8,077	5,634	57,74	42,31	29,3	0,8387	0,9843	0,4898	0,7351	0,736	0,6669	0,4012	0,3148	0,2241	2,196	1,637	1,206
AT4G12410	SAUR-like auxin-responsive protein family		-1,49	0,00235	0,1163	7,894	3,073	11,37	23,78	18,7	29,28	8,835	4,615	4,507	8,056	7,052	9,768	0,7702	0,305	1,074	2,05	1,768	2,723	0,8565	0,432	0,4305	0,7359	0,6553	0,9652
AT3G57765	U2.3; snRNA	encodes_a_small_nuclear_RNA,_which_is_a_part_of_small_nuclear_ribonuclear_particle_(snRNP)_and_is_involved_in_RNA_processing_such_as_splicing_and_polyadenylation.	-1,149	0,00242	0,1186	19,95	27,27	27,1	61,1	42,39	40,89	54,95	28,15	41,31	19,87	14,79	31,09	1,419	1,973	1,866	3,84	2,921	2,772	3,884	1,921	2,877	1,323	1,002	2,24
AT3G13950			1,803	0,00243	0,1186	27,32	15,37	15,16	15,85	15,4	10,34	26,5	18,46	29,3	106,1	18,8	23,72	1,982	1,134	1,065	1,016	1,082	0,7145	1,91	1,285	2,081	7,204	1,299	1,743
AT3G29250	NAD(P)-binding Rossmann-fold superfamily protein		1,764	0,00249	0,1206	39,47	43,02	49,28	5,285	13,2	8,613	41,97	18,46	16,9	53,71	18,8	18,14	2,5	2,773	3,022	0,2958	0,8101	0,5199	2,641	1,122	1,048	3,185	1,135	1,164
AT4G24000	cellulose synthase like G2	encodes_a_protein_similar_to_cellulose_synthase	1,324	0,0026	0,1248	6,072	14,6	15,16	50,2	23,11	36,17	1,104	6,923	1,127	155,8	85,8	34,89	0,1545	0,3778	0,3735	1,129	0,5694	0,8771	0,0279	0,169	0,0281	3,71	2,079	0,8989
AT4G04540	cysteine-rich RLK (RECEPTOR-like protein kinase) 39	Encodes_a_cysteine-rich_receptor-like_protein_kinase	2,675	0,00262	0,125	5,228	12,92	1,18	2,735	8,373	1,946	4,716	2,481	18,87	68,28	16,1	2,958	0,1636	0,4114	0,0358	0,0756	0,2538	0,058	0,1466	0,0745	0,5782	2	0,4798	0,0938
AT5G19100	Eukaryotic aspartyl protease family protein		-2,774	0,00262	0,125	17,61	84,51	39,53	6,606	18,7	3,445	33,13	13,85	15,78	1,343	1,175	1,395	0,9277	4,529	2,016	0,3075	0,9544	0,173	1,734	0,6999	0,8136	0,0662	0,059	0,0745
AT1G53540	HSP20-like chaperones superfamily protein		-1,386	0,00271	0,1272	1,214	0	0	37,65	20,9	29,28	2,209	0	2,254	10,74	14,1	8,372	0,1161	0	0	3,181	1,936	2,668	0,2098	0	0,2109	0,9615	1,284	0,8107
AT1G49310			2,079	0,00275	0,1283	3,643	17,67	17,33	1,321	2,2	5,168	8,835	16,15	5,634	10,74	12,93	8,372	0,5311	2,621	2,445	0,1702	0,3107	0,7179	1,28	2,259	0,8041	1,466	1,795	1,236
AT1G67810	sulfur E2	Encodes_a_protein_capable_of_stimulating_the_cysteine_desulfurase_activity_of_CpNifS_(AT1G08490)_in_vitro._SufE2:GFP_localizes_to_the_chloroplasts_where_it_is_likely_to_play_a_role_in_iron-sulfur_cluster_assembly._Transcript_levels_for_this_gene_are_high_in_the_pollen_relative_to_other_organs_based_on_RT-PCR_analysis.	1,088	0,00296	0,1345	27,93	32,27	21,66	24,44	18,7	18,95	49,7	28,85	52,96	57,74	38,79	37,68	2,008	2,359	1,507	1,552	1,302	1,298	3,549	1,989	3,727	3,885	2,655	2,742
AT1G28480	Thioredoxin superfamily protein	Encodes_GRX480,_a_member_of_the_glutaredoxin_family_that_regulates_protein_redox_state.__GRX480_interacts_with_TGA_factors_and_suppresses_JA-responsive_PDF1.2_transcription.__GRX480_transcription_is_SA-inducible_and_requires_NPR1.__Maybe_involved_in_SA/JA_cross-talk.	-1,165	0,003	0,135	71,04	36,88	62,27	124,2	151,8	49,95	48,59	6,923	21,41	63,11	24,68	58,61	7,336	3,874	6,225	11,33	15,19	4,915	4,985	0,6859	2,164	6,101	2,427	6,129
AT1G66390	myb domain protein 90	production_of_anthocyanin_pigment_2_protein_(PAP2)	3,74	0,00305	0,1367	0	0,7683	0,5415	0	1,1	0	0	0	0	10,74	8,227	0	0	0,0491	0,0329	0	0,067	0	0	0	0	0,6319	0,4923	0
AT3G48240	Octicosapeptide/Phox/Bem1p family protein		-2,131	0,00358	0,1506	80,76	3,073	7,581	8,587	9,902	12,06	3,313	2,308	4,507	2,685	3,526	0	5,064	0,196	0,4602	0,4758	0,6014	0,7205	0,2064	0,1388	0,2767	0,1577	0,2106	0
AT2G12930	transposable element gene		-2,199	0,0037	0,153	1,84	9,135	6,157	11,56	11,18	8,819	10,09	1,05	11,21	1,893	0	5,721	0,0186	0,0939	0,0602	0,1032	0,1094	0,0849	0,1014	0,0102	0,1109	0,0179	0	0,0586
AT1G61810	beta-glucosidase 45		1,58	0,00398	0,161	4,858	49,94	30,86	8,581	12,1	6,89	5,522	12,7	6,761	38,93	11,75	33,49	0,2343	2,451	1,441	0,3657	0,5655	0,3167	0,2647	0,588	0,3193	1,758	0,54	1,636
AT4G00700	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein		1,378	0,00422	0,1678	63,76	73,76	30,86	12,55	37,41	25,84	65,16	15	30,42	108,8	52,89	32,09	1,17	1,377	0,5485	0,2036	0,6651	0,452	1,188	0,2642	0,5468	1,869	0,9246	0,5967
AT3G63380	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein		1,865	0,00431	0,1698	32,79	63,77	62,81	17,84	9,902	3,445	77,3	45	69,86	81,91	28,21	11,16	0,5417	1,072	1,005	0,2604	0,1585	0,0542	1,269	0,7133	1,13	1,267	0,4438	0,1868
AT1G46480	WUSCHEL related homeobox 4	Encodes_a_WUSCHEL-related_homeobox_gene_family_member_with_65_amino_acids_in_its_homeodomain._Proteins_in_this_family_contain_a_sequence_of_eight_residues_(TLPLFPMH)_downstream_of_the_homeodomain_called_the_WUS_box._This_protein_also_contains_an_acidic_domain_approximately_10_residues_upstream_of_the_WUS_box._Part_of_the_TDIF-TDR-WOX4_signaling_pathway_that_plays_a_crucial_role_in_the_maintenance_of_the_vascular_meristem_organization_during_secondary_growth.	-1,061	0,00465	0,1769	20,64	39,95	33,03	44,26	49,51	44,79	22,09	31,15	27,04	18,8	15,28	32,09	1,183	2,329	1,833	2,241	2,749	2,446	1,258	1,713	1,517	1,009	0,834	1,863
AT2G31910	cation/H+ exchanger 21	member_of_Putative_Na+/H+_antiporter_family	-1,848	0,00499	0,1837	12,14	3,842	4,873	13,21	14,3	20,67	9,939	6,923	12,4	4,028	8,227	0	0,3011	0,0969	0,117	0,2894	0,3435	0,4883	0,2448	0,1647	0,3008	0,0935	0,1943	0
AT1G43910	P-loop containing nucleoside triphosphate hydrolases superfamily protein		1,597	0,00518	0,1876	73,47	70,68	31,95	9,909	35,21	18,95	35,34	11,54	20,28	126,2	25,86	40,47	2,803	2,743	1,18	0,334	1,301	0,6888	1,34	0,4223	0,7575	4,508	0,9394	1,563
ATMG00980	Ribosomal protein S12/S23 family protein	ribosomal_protein_L2	-1,11	0,00525	0,1883	47,75	20,55	52,78	50,96	49,33	40,45	31,52	18,43	29,68	24,13	10,81	31,03	7,826	3,427	8,375	7,38	7,832	6,317	5,133	2,898	4,763	3,702	1,688	5,151
AT3G62920			-1,016	0,00545	0,192	41,29	37,65	32,49	42,94	45,11	43,06	39,76	38,08	31,55	18,8	29,38	15,35	6,091	5,649	4,64	5,596	6,445	6,053	5,827	5,389	4,556	2,596	4,128	2,293
AT4G37370	cytochrome P450, family 81, subfamily D, polypeptide 8	member_of_CYP81D	1,198	0,00632	0,2078	313,3	106	78,52	201,5	90,22	163,6	94,97	72,69	64,23	699,6	193,9	149,3	11,67	4,018	2,832	6,632	3,256	5,81	3,516	2,598	2,343	24,4	6,881	5,633
AT2G26750	alpha/beta-Hydrolases superfamily protein		-2,606	0,00639	0,2093	4,979	1,79	5,637	3,805	6,271	7,769	1,391	0,1385	2,682	0,1746	1,457	1,73	0,2952	0,108	0,3235	0,1993	0,3601	0,4389	0,082	0,0079	0,1557	0,0097	0,0823	0,1039
AT1G57630	Toll-Interleukin-Resistance (TIR) domain family protein		1,464	0,00685	0,2191	32,18	42,26	40,07	22,46	23,11	15,5	49,7	24,23	60,85	115,5	37,61	18,14	3,842	5,132	4,631	2,369	2,672	1,764	5,894	2,775	7,111	12,91	4,276	2,193
AT3G10320	Glycosyltransferase family 61 protein		1,397	0,00696	0,222	3,643	3,842	24,91	6,606	6,601	18,95	1,104	4,615	0	30,88	27,03	19,54	0,1222	0,1311	0,8089	0,1958	0,2145	0,6057	0,0368	0,1485	0	0,9698	0,8636	0,6637
AT4G20000	VQ motif-containing protein		2,045	0,007	0,2229	4,25	0	0,5415	1,321	2,2	1,723	1,104	0	0	8,056	8,227	5,582	0,3161	0	0,039	0,0868	0,1585	0,1221	0,0816	0	0	0,561	0,5828	0,4204
AT2G29110	glutamate receptor 2.8	member_of_Putative_ligand-gated_ion_channel_subunit_family	1,065	0,00716	0,2255	17,61	16,9	7,581	36,99	16,5	49,95	25,4	8,077	9,015	103,4	61,12	47,44	0,3836	0,3746	0,1599	0,712	0,3482	1,037	0,5498	0,1688	0,1923	2,109	1,268	1,047
AT2G29460	glutathione S-transferase tau 4	Encodes_glutathione_transferase_belonging_to_the_tau_class_of_GSTs._Naming_convention_according_to_Wagner_et_al._(2002).	1,415	0,00719	0,2258	16,39	34,57	59,56	36,99	9,902	17,23	14,36	12,69	12,4	107,4	35,26	33,49	1,121	2,405	3,943	2,235	0,6559	1,122	0,9754	0,8327	0,8298	6,877	2,296	2,319
AT4G04409		Pseudogene_of_AT3G54560;_HTA11;_DNA_binding_protein	-1,21	0,0074	0,2283	26,11	19,21	22,2	25,1	29,71	27,56	15,46	19,62	14,65	6,714	14,1	13,95	5,428	4,062	4,468	4,611	5,982	5,46	3,194	3,913	2,982	1,307	2,793	2,938

AT4G23200	cysteine-rich RLK (RECEPTOR-like protein kinase) 12	Encodes_a_cysteine-rich_receptor-like_protein_kinase	1,082	0,00742	0,2287	27,32	54,55	76,35	21,8	25,31	24,12	90,56	81,92	171,3	63,11	62,29	23,72	0,8695	1,766	2,352	0,6129	0,78	0,7313	2,863	2,501	5,336	1,88	1,888	0,7645
AT5G51440	HSP20-like chaperones superfamily protein		1,664	0,00747	0,2292	59,51	7,683	8,664	8,587	9,902	20,67	5,522	6,923	13,52	81,91	14,1	23,72	4,051	0,5321	0,571	0,5166	0,653	1,341	0,3735	0,4522	0,9013	5,221	0,9145	1,636
AT5G38120	AMP-dependent synthetase and ligase family protein		-1,052	0,00781	0,2366	191,3	607	337,9	32,37	42,91	31,01	123,7	227,3	70,99	14,77	15,28	20,93	6,854	22,13	11,72	1,025	1,489	1,059	4,404	7,815	2,49	0,4955	0,5214	0,7596
AT2G30750	cytochrome P450, family 71, subfamily A, polypeptide 12	putative_cytochrome_P450	2,619	0,00834	0,2451	3,036	27,66	4,873	5,285	6,601	3,445	4,417	16,15	2,254	89,96	1,175	6,977	0,1116	1,034	0,1734	0,1716	0,235	0,1206	0,1613	0,5695	0,0811	3,095	0,0411	0,2597
AT1G30370	alpha/beta-Hydrolases superfamily protein		1,672	0,00867	0,2513	1,214	4,61	5,956	6,606	2,2	3,445	1,104	8,077	28,17	20,14	14,1	8,372	0,0473	0,1827	0,2247	0,2274	0,0831	0,1279	0,0428	0,3019	1,075	0,7347	0,5234	0,3304
AT1G11340	S-locus lectin protein kinase family protein		1,535	0,0091	0,258	26,11	54,55	54,15	7,266	4,401	3,445	61,84	60	87,89	20,14	9,402	18,14	0,5978	1,271	1,2	0,147	0,0976	0,0752	1,407	1,318	1,97	0,4317	0,205	0,4206
AT1G15405	other RNA	Unknown_gene	-1,12	0,0097	0,2698	24,9	10,76	14,62	30,39	31,91	29,28	43,07	17,31	33,81	8,056	14,1	19,54	5,282	2,322	3,003	5,697	6,557	5,921	9,08	3,523	7,022	1,6	2,85	4,198
AT3G28740	Cytochrome P450 superfamily protein	Encodes_a_member_of_the_cytochrome_p450_family._Expression_is_upregulated_in_response_to_cis-jasmonate_treatment._Overexpression_induces_synthesis_of_volatile_compounds_that_affect_chemical_ecology_and_insect_interactions.	2,19	0,00974	0,2701	0,6072	14,6	14,08	4,624	1,1	0	3,313	1,154	0	18,8	3,526	11,16	0,0236	0,5761	0,5287	0,1585	0,0413	0	0,1277	0,043	0	0,6827	0,1303	0,4386
AT5G06800	myb-like HTH transcriptional regulator family protein		1,343	0,00999	0,2743	27,93	17,67	41,15	4,624	11	12,06	59,64	35,77	40,57	22,83	25,86	16,74	1,278	0,8225	1,823	0,1869	0,4876	0,5258	2,711	1,57	1,817	0,9778	1,127	0,776