

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
H	Up-regulated in KO analysis:															
**	AT1G51890.2	AT1G51890	--	139	224	337	402	23.21 ± 4.79	11.21 ± 1.55	-1.38 ± 0.48	-0.62 ± 0.38	3.25E-04	5.40E-10	7.56E-02	5.51E-01	Leucine-rich repeat protein kinase family protein
	AT5G44925.1	AT5G44925	--	192	44	15	16	9.58 ± 1.52	7.40 ± 1.73	1.92 ± 1.25	-2.50 ± 1.20	1.86E-07	2.75E-03	6.73E-01	2.87E-01	transposable element gene
	AT5G60300.2	AT5G60300	LecRK-1.9	168	394	66	234	9.38 ± 1.63	10.57 ± 1.49	-0.47 ± 1.09	-0.34 ± 0.45	3.98E-06	1.28E-09	1.00E+00	9.97E-01	Concanavalin A-like lectin protein kinase family protein
	AT3G53780.1	AT3G53780	--	50	25	43	80	9.09 ± 1.76	8.03 ± 2.03	0.09 ± 2.02	2.45 ± 4.57	7.89E-05	8.85E-03	1.00E+00	1.00E+00	RHOMBOID-like protein 4
	AT1G62981.1	AT1G62981	--	39	40	25	43	8.72 ± 1.84	8.70 ± 1.83	0.31 ± 1.22	-0.74 ± 0.74	5.11E-04	3.88E-04	1.00E+00	9.07E-01	Protein of unknown function (DUF1191)
	AT2G43190.4	AT2G43190	POP4	35	25	7	81	8.58 ± 2.02	8.03 ± 2.33	-6.38 ± 4.25	0.88 ± 3.00	4.01E-03	4.65E-02	6.96E-01	1.00E+00	ribonuclease P family protein
	AT5G26280.2	AT5G26280	--	272	962	2470	4457	8.51 ± 1.12	10.28 ± 2.07	-1.44 ± 0.64	-0.72 ± 0.15	3.74E-11	1.59E-04	2.66E-01	8.51E-05	TRAF-like family protein
**	AT2G20110.2	AT2G20110	--	32	28	10	14	8.44 ± 2.16	8.23 ± 2.28	-6.86 ± 2.21	1.38 ± 2.02	1.37E-02	2.99E-02	4.31E-02	1.00E+00	Tesmin/TSO1-like CXC domain-containing protein
	AT1G59218.1	AT1G59218	--	142	94	91	60	6.81 ± 1.03	6.16 ± 1.56	0.15 ± 0.63	0.91 ± 0.64	3.08E-08	9.30E-03	1.00E+00	6.83E-01	Disease resistance protein (CC-NBS-LRR class) family
**	AT4G25800.2	AT4G25800	--	40	89	154	41	6.32 ± 1.89	7.42 ± 1.76	-0.47 ± 0.70	-4.80 ± 0.92	7.94E-02	3.45E-03	1.00E+00	8.41E-06	Calmodulin-binding protein
	AT5G26120.1	AT5G26120	ASD2	82	190	13	12	5.52 ± 1.04	6.70 ± 1.32	-0.76 ± 1.10	-1.04 ± 1.14	4.07E-05	9.44E-05	1.00E+00	9.46E-01	alpha-L-arabinofuranosidase 2
	AT5G39150.1	AT5G39150	--	1541	1589	22	13	4.26 ± 0.20	4.24 ± 0.45	0.49 ± 1.00	1.03 ± 1.16	3.74E-96	9.45E-18	1.00E+00	9.56E-01	RmlC-like cupins superfamily protein
	AT3G20395.1	AT3G20395	--	66	53	2	1	4.18 ± 1.28	3.76 ± 1.15	-3.16 ± 3.10	3.93 ± 4.62	9.49E-02	7.72E-02	NA	NA	RING/U-box superfamily protein
	AT5G39100.1	AT5G39100	GLP6	131	119	3	0	4.16 ± 0.54	3.95 ± 0.87	-0.50 ± 2.15	-1.52 ± 4.99	2.58E-11	9.49E-04	1.00E+00	NA	germin-like protein 6
	AT5G39120.1	AT5G39120	--	1250	1287	52	24	4.07 ± 0.21	4.04 ± 0.44	0.72 ± 0.63	-0.91 ± 0.91	8.48E-82	1.24E-16	8.72E-01	9.07E-01	RmlC-like cupins superfamily protein
	AT5G39110.1	AT5G39110	--	1595	1996	13	7	3.78 ± 0.22	4.04 ± 0.28	0.53 ± 1.09	-0.31 ± 1.80	1.77E-64	2.65E-44	1.00E+00	1.00E+00	RmlC-like cupins superfamily protein
	AT4G25490.1	AT4G25490	CBF1	58	54	7	3	3.66 ± 1.10	3.50 ± 0.94	0.62 ± 1.44	3.30 ± 2.80	7.95E-02	2.04E-02	1.00E+00	NA	C-repeat/DRE binding factor 1
	AT5G35935.1	AT5G35935	--	1549	1476	340	353	3.46 ± 0.23	3.34 ± 0.28	0.01 ± 0.25	-0.27 ± 0.45	1.11E-45	9.70E-30	1.00E+00	1.00E+00	transposable element gene
	AT2G31280.4	AT2G31280	CPUORF7	1131	1216	905	937	3.16 ± 0.20	3.23 ± 0.27	0.80 ± 0.31	0.41 ± 1.98	6.66E-50	1.19E-28	1.38E-01	1.00E+00	conserved peptide upstream open reading frame 7
	AT1G66170.1	AT1G66170	MMD1	83	79	8	12	2.83 ± 0.65	2.68 ± 0.70	1.02 ± 1.68	-0.45 ± 1.21	2.67E-03	1.46E-02	1.00E+00	1.00E+00	RING/FYVE/PHD zinc finger superfamily protein
	AT4G24380.2	AT4G24380	--	148	200	17	28	2.38 ± 0.65	2.81 ± 0.61	-0.03 ± 0.94	-0.65 ± 0.90	3.29E-02	6.75E-04	1.00E+00	1.00E+00	
	AT3G12502.1	AT3G12502	--	520	598	194	220	2.36 ± 0.38	2.52 ± 0.40	0.12 ± 0.43	0.33 ± 0.34	4.73E-07	1.21E-07	1.00E+00	9.24E-01	other RNA
	AT4G24350.1	AT4G24350	--	122	163	49	35	2.32 ± 0.64	2.75 ± 0.64	-0.89 ± 0.67	-0.54 ± 0.79	3.65E-02	3.02E-03	7.87E-01	1.00E+00	Phosphorylase superfamily protein
	AT1G07920.1	AT1G07920	--	40315	45841	45591	57463	2.24 ± 0.29	2.40 ± 0.31	0.16 ± 0.04	0.06 ± 0.07	2.54E-11	8.49E-12	9.90E-04	9.59E-01	GTP binding Elongation factor Tu family protein
	AT3G04720.1	AT3G04720	PR4	15495	22904	2564	4129	2.23 ± 0.24	2.82 ± 0.32	-0.14 ± 0.10	0.15 ± 0.20	2.52E-17	2.50E-15	7.57E-01	9.98E-01	pathogenesis-related 4
	AT3G12500.1	AT3G12500	HCHIB	4878	6791	1631	1922	2.18 ± 0.30	2.68 ± 0.37	0.36 ± 0.19	0.25 ± 0.16	5.63E-10	6.51E-10	4.39E-01	5.64E-01	basic chitinase
	AT4G17785.1	AT4G17785	MYB39	535	612	95	64	2.15 ± 0.33	2.33 ± 0.34	-0.18 ± 0.42	-0.54 ± 0.53	3.39E-08	5.34E-09	1.00E+00	9.03E-01	myb domain protein 39
	AT4G11190.1	AT4G11190	--	3413	4387	4122	1617	2.09 ± 0.34	2.44 ± 0.20	-0.10 ± 0.12	-0.56 ± 0.28	4.50E-07	1.38E-31	9.78E-01	3.18E-01	Disease resistance-responsive (dirigent-like protein) family protein
	AT3G29000.1	AT3G29000	--	257	265	24	18	1.96 ± 0.55	1.93 ± 0.35	0.11 ± 0.79	1.63 ± 1.31	4.49E-02	1.64E-05	1.00E+00	7.84E-01	Calcium-binding EF-hand family protein
**	AT4G11290.1	AT4G11290	--	12770	15274	1888	2169	1.77 ± 0.17	2.04 ± 0.25	-0.68 ± 0.17	-1.03 ± 0.21	1.75E-21	2.09E-13	3.07E-03	4.83E-05	Peroxidase superfamily protein
	AT1G76650.1	AT1G76650	CML38	788	911	94	46	1.75 ± 0.30	1.94 ± 0.35	-0.81 ± 0.48	0.15 ± 0.82	1.59E-06	9.76E-06	5.80E-01	1.00E+00	calmodulin-like 38
	AT5G39670.1	AT5G39670	--	529	503	160	103	1.70 ± 0.33	1.53 ± 0.30	0.60 ± 0.77	-0.05 ± 0.48	7.59E-05	9.36E-05	9.88E-01	1.00E+00	Calcium-binding EF-hand family protein
	AT4G13395.1	AT4G13395	RTFL12	163	221	28	12	1.70 ± 0.48	2.14 ± 0.39	0.06 ± 0.74	0.80 ± 1.26	4.10E-02	1.40E-05	1.00E+00	1.00E+00	ROTUNDIFOLIA like 12
	AT2G28210.1	AT2G28210	ACA2	211	228	73	52	1.66 ± 0.47	1.72 ± 0.42	-0.17 ± 0.49	-0.61 ± 0.60	4.35E-02	6.58E-03	1.00E+00	8.97E-01	alpha carbonic anhydrase 2
	AT3G23250.1	AT3G23250	MYB15	349	318	273	145	1.62 ± 0.40	1.37 ± 0.38	-0.06 ± 0.28	0.67 ± 0.44	7.76E-03	2.65E-02	1.00E+00	6.06E-01	myb domain protein 15
	AT1G17400.1	AT1G17400	DRO3	464	462	48	64	1.60 ± 0.30	1.53 ± 0.31	-0.70 ± 0.66	0.04 ± 0.57	2.61E-05	2.10E-04	9.00E-01	1.00E+00	
	AT5G51190.1	AT5G51190	ERF105	1565	1734	323	169	1.60 ± 0.32	1.71 ± 0.26	-0.40 ± 0.32	0.99 ± 0.58	1.67E-04	1.49E-08	8.40E-01	5.08E-01	Integrase-type DNA-binding superfamily protein
	AT2G38380.1	AT2G38380	--	62907	76890	28764	20670	1.56 ± 0.16	1.88 ± 0.19	-0.31 ± 0.07	-0.56 ± 0.11	3.00E-19	7.18E-19	1.47E-04	9.68E-06	Peroxidase superfamily protein
**	AT5G52710.1	AT5G52710	--	498	547	27	61	1.56 ± 0.29	1.68 ± 0.26	-1.52 ± 0.77	2.43 ± 0.58	3.43E-05	7.32E-08	4.14E-01	7.41E-04	Copper transport protein family
	AT3G61190.1	AT3G61190	BAP1	452	524	160	130	1.51 ± 0.43	1.71 ± 0.34	-0.51 ± 0.48	0.21 ± 0.39	5.42E-02	1.05E-04	9.03E-01	1.00E+00	BON association protein 1
	AT5G45340.2	AT5G45340	CYP707A3	513	565	44	91	1.50 ± 0.39	1.62 ± 0.38	-0.38 ± 0.94	-0.86 ± 0.56	1.77E-02	2.73E-03	1.00E+00	5.98E-01	cytochrome P450, family 707, subfamily A, polypeptide 3
	AT1G28370.1	AT1G28370	ERF11	557	712	43	52	1.48 ± 0.45	1.87 ± 0.35	0.18 ± 0.60	0.42 ± 0.67	9.19E-02	2.77E-05	1.00E+00	1.00E+00	ERF domain protein 11
	AT5G17350.1	AT5G17350	--	776	771	114	70	1.41 ± 0.38	1.32 ± 0.26	-0.62 ± 0.39	0.69 ± 0.52	2.29E-02	1.54E-04	6.47E-01	7.28E-01	
**	AT1G53940.1	AT1G53940	GLIP2	3233	3502	206	297	1.38 ± 0.19	1.47 ± 0.21	-1.40 ± 0.47	-1.57 ± 0.35	1.01E-09	4.87E-09	5.59E-02	1.81E-04	GDSL-motif lipase 2
	AT1G35210.1	AT1G35210	--	422	492	44	28	1.37 ± 0.42	1.58 ± 0.28	-0.57 ± 0.67	0.17 ± 1.02	9.60E-02	4.56E-06	9.69E-01	1.00E+00	
	AT3G32980.1	AT3G32980	--	153011	175105	41422	45300	1.29 ± 0.15	1.49 ± 0.19	-0.28 ± 0.06	-0.28 ± 0.09	1.84E-14	2.43E-12	4.75E-05	4.97E-02	Peroxidase superfamily protein
	AT2G29330.1	AT2G29330	TRI	2003	2165	751	588	1.24 ± 0.24	1.32 ± 0.26	-0.23 ± 0.17	0.11 ± 0.21	7.22E-05	9.36E-05	7.46E-01	1.00E+00	tropinone reductase
**	AT1G27730.1	AT1G27730	STZ	3744	3684	1012	783	1.22 ± 0.22	1.10 ± 0.21	-0.02 ± 0.25	2.08 ± 0.38	1.57E-05	2.82E-05	1.00E+00	1.59E-06	salt tolerance zinc finger
	AT1G06160.1	AT1G06160	ORA59	555	683	106	99	1.19 ± 0.32	1.53 ± 0.38	-1.07 ± 0.44	-0.83 ± 0.50	2.56E-02	6.70E-03	1.91E-01		

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				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
**	AT3G44540.1	AT3G44540	FAR4	2576	2384	2613	4889	-1.03 ± 0.18	-1.58 ± 0.36	0.33 ± 0.13	1.24 ± 0.13	2.44E-06	1.81E-03	1.73E-01	1.06E-18	fatty acid reductase 4
**	AT2G48140.1	AT2G48140	EDA4	3903	3612	4976	11726	-1.04 ± 0.17	-1.64 ± 0.30	0.83 ± 0.14	2.59 ± 0.18	5.31E-07	1.22E-05	8.66E-07	1.59E-42	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
**	AT4G36610.1	AT4G36610	--	2739	2777	3820	8575	-1.05 ± 0.15	-1.15 ± 0.18	1.47 ± 0.18	2.98 ± 0.18	1.46E-09	4.91E-08	3.19E-13	7.79E-56	alpha/beta-Hydrolases superfamily protein
**	AT4G29800.2	AT4G29800	PLP8	903	907	1152	2026	-1.05 ± 0.20	-1.17 ± 0.21	0.75 ± 0.21	1.91 ± 0.19	4.51E-05	8.97E-06	9.03E-03	5.11E-21	PATATIN-like protein 8
**	AT2G23540.1	AT2G23540	--	4632	4296	9162	20039	-1.06 ± 0.26	-1.62 ± 0.27	-0.02 ± 0.14	1.74 ± 0.13	9.89E-03	6.93E-07	1.00E+00	1.78E-39	GDSL-like Lipase/Acylhydrolase superfamily protein
**	AT5G12420.1	AT5G12420	--	5070	4878	6270	12483	-1.06 ± 0.24	-1.41 ± 0.22	0.69 ± 0.15	2.24 ± 0.16	2.30E-03	1.21E-07	1.65E-04	3.07E-41	O-acyltransferase (WSD1-like) family protein
**	AT5G13580.1	AT5G13580	ABCG6	2981	2669	6684	18175	-1.06 ± 0.30	-1.81 ± 0.29	1.12 ± 0.19	3.14 ± 0.16	4.60E-02	3.17E-07	6.39E-07	2.09E-78	ABC-2 type transporter family protein
**	AT2G40370.1	AT2G40370	LAC5	904	867	2210	6275	-1.09 ± 0.25	-1.45 ± 0.43	0.80 ± 0.18	2.61 ± 0.16	2.99E-03	5.12E-02	7.08E-04	4.41E-59	laccase 5
**	AT2G41170.1	AT2G41170	--	987	1007	1807	4950	-1.11 ± 0.32	-1.17 ± 0.25	1.92 ± 0.23	3.10 ± 0.20	5.54E-02	5.73E-04	3.51E-14	1.04E-50	F-box family protein
**	AT1G28470.1	AT1G28470	NAC010	586	597	586	787	-1.11 ± 0.22	-1.18 ± 0.24	0.06 ± 0.18	0.38 ± 0.17	1.38E-04	2.77E-04	1.00E+00	2.21E-01	NAC domain containing protein 10
**	AT1G49430.1	AT1G49430	LAC52	2270	2126	3702	6839	-1.11 ± 0.29	-1.61 ± 0.27	0.04 ± 0.13	1.51 ± 0.12	1.58E-02	8.90E-07	1.00E+00	1.91E-35	long-chain acyl-CoA synthetase 2
**	AT1G45201.1	AT1G45201	TLL1	5372	4945	8676	8523	-1.22 ± 0.17	-1.87 ± 0.51	-0.11 ± 0.10	0.04 ± 0.10	1.70E-10	2.30E-02	8.84E-01	1.00E+00	triacylglycerol lipase-like 1
**	AT5G18840.1	AT5G18840	--	1266	1260	1280	1148	-1.23 ± 0.19	-1.41 ± 0.33	-0.11 ± 0.18	0.05 ± 0.21	1.11E-07	3.56E-03	1.00E+00	1.00E+00	Major facilitator superfamily protein
**	AT5G63560.1	AT5G63560	FACT	4020	3751	7586	6324	-1.27 ± 0.12	-1.85 ± 0.46	0.07 ± 0.07	0.19 ± 0.08	6.86E-24	7.04E-03	9.66E-01	1.74E-01	HXXXD-type acyl-transferase family protein
**	AT2G22510.1	AT2G22510	--	3465	3291	6896	22549	-1.30 ± 0.29	-1.86 ± 0.39	0.35 ± 0.13	2.77 ± 0.15	2.08E-03	3.02E-04	1.17E-01	1.11E-72	hydroxyproline-rich glycoprotein family protein
**	AT2G01580.1	AT2G01580	--	237	223	277	491	-1.31 ± 0.36	-1.91 ± 0.42	0.27 ± 0.33	1.24 ± 0.29	3.13E-02	9.05E-04	9.78E-01	4.88E-04	
**	AT3G58550.1	AT3G58550	--	3326	3124	4335	6047	-1.31 ± 0.25	-1.96 ± 0.40	0.03 ± 0.09	0.11 ± 0.12	6.83E-05	2.46E-04	1.00E+00	9.51E-01	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
**	AT3G06390.1	AT3G06390	CASPL1D2	1714	1585	2639	5385	-1.33 ± 0.29	-2.06 ± 0.39	0.08 ± 0.14	1.80 ± 0.19	8.06E-04	3.73E-05	1.00E+00	3.01E-18	Uncharacterised protein family (UPF0497)
**	AT4G38080.1	AT4G38080	--	8110	7744	13206	36992	-1.33 ± 0.22	-1.90 ± 0.37	0.16 ± 0.13	2.19 ± 0.14	8.45E-07	1.08E-04	8.69E-01	2.57E-50	hydroxyproline-rich glycoprotein family protein
**	AT5G19410.1	AT5G19410	ABCG23	650	617	2069	6340	-1.37 ± 0.27	-1.85 ± 0.42	1.00 ± 0.23	3.17 ± 0.15	1.73E-04	1.62E-03	8.78E-04	5.59E-99	ABC-2 type transporter family protein
**	AT1G73410.1	AT1G73410	MYB54	352	342	338	1133	-1.38 ± 0.32	-1.74 ± 0.34	0.22 ± 0.25	1.92 ± 0.22	2.68E-03	6.47E-05	9.57E-01	1.30E-15	myb domain protein 54
**	AT5G58860.1	AT5G58860	CYP86A1	4342	4142	9297	17669	-1.39 ± 0.30	-1.85 ± 0.29	-0.28 ± 0.13	1.05 ± 0.10	1.09E-03	8.67E-08	2.77E-01	1.20E-23	cytochrome P450, family 86, subfamily A, polypeptide 1
**	AT2G33205.1	AT2G33205	--	470	441	638	854	-1.39 ± 0.28	-2.00 ± 0.40	-0.14 ± 0.16	0.01 ± 0.15	1.56E-04	1.35E-04	9.62E-01	1.00E+00	Serine-domain containing serine and sphingolipid biosynthesis protein
**	AT1G29000.1	AT1G29000	--	147	130	218	531	-1.40 ± 0.41	-2.55 ± 0.50	-0.21 ± 0.27	1.09 ± 0.20	7.24E-02	7.49E-05	9.84E-01	1.69E-06	Heavy metal transport/detoxification superfamily protein
**	AT1G17950.1	AT1G17950	MYB52	316	319	375	1384	-1.40 ± 0.42	-1.55 ± 0.38	0.83 ± 0.25	2.53 ± 0.23	8.52E-02	6.58E-03	2.73E-02	1.50E-26	myb domain protein 52
**	AT1G55990.1	AT1G55990	--	943	909	1529	3007	-1.42 ± 0.24	-2.06 ± 0.35	0.77 ± 0.20	3.44 ± 0.19	1.59E-06	1.40E-06	4.36E-03	3.17E-69	glycine-rich protein
**	AT5G09520.1	AT5G09520	PELPK2	1106	1114	2120	2602	-1.44 ± 0.30	-1.74 ± 0.31	0.77 ± 0.18	2.45 ± 0.22	3.68E-04	1.00E-05	1.32E-03	2.72E-26	hydroxyproline-rich glycoprotein family protein
**	AT2G18370.1	AT2G18370	--	3621	3516	3387	4450	-1.45 ± 0.18	-1.92 ± 0.36	0.16 ± 0.08	0.54 ± 0.15	1.19E-12	2.97E-05	3.24E-01	9.16E-03	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
**	AT3G03530.1	AT3G03530	NPC4	434	407	562	1912	-1.47 ± 0.28	-2.07 ± 0.44	0.19 ± 0.25	0.98 ± 0.19	4.80E-05	4.27E-04	9.96E-01	5.59E-06	non-specific phospholipase C4
**	AT1G78950.1	AT1G78950	BAS	498	468	982	565	-1.52 ± 0.30	-2.13 ± 0.36	-0.08 ± 0.17	0.00 ± 0.21	1.20E-04	1.40E-06	1.00E+00	1.00E+00	Terpenoid cyclases family protein
**	AT3G47790.1	AT3G47790	ABCA8	1236	1121	1188	1444	-1.54 ± 0.26	-2.44 ± 0.59	-0.08 ± 0.13	0.30 ± 0.14	3.05E-06	4.67E-03	1.00E+00	2.22E-01	ABC2 homolog 7
**	AT4G33450.1	AT4G33450	MYB69	198	179	167	221	-1.57 ± 0.39	-2.62 ± 0.64	-0.30 ± 0.35	0.20 ± 0.30	8.56E-03	5.13E-03	9.67E-01	1.00E+00	myb domain protein 69
**	AT5G20860.1	AT5G20860	--	208	204	559	1182	-1.62 ± 0.38	-1.95 ± 0.48	0.94 ± 0.19	3.69 ± 0.21	4.60E-03	6.71E-03	7.14E-05	7.72E-69	Plant invertase/pectin methylesterase inhibitor superfamily
**	AT2G47200.1	AT2G47200	--	626	623	763	1807	-1.67 ± 0.31	-2.07 ± 0.34	-0.06 ± 0.14	0.73 ± 0.20	2.64E-05	8.33E-07	1.00E+00	6.66E-03	
**	AT3G07970.1	AT3G07970	QRT2	291	290	610	1215	-1.68 ± 0.33	-1.91 ± 0.50	0.18 ± 0.16	2.36 ± 0.21	1.39E-04	1.57E-02	8.93E-01	1.28E-26	Pectin lyase-like superfamily protein
**	AT4G33610.1	AT4G33610	--	3637	3540	5930	12934	-1.68 ± 0.18	-2.19 ± 0.30	0.82 ± 0.17	3.85 ± 0.16	1.02E-17	5.40E-10	1.52E-04	#####	glycine-rich protein
**	AT5G07130.1	AT5G07130	LAC13	1216	1170	2763	6151	-1.70 ± 0.17	-2.19 ± 0.32	1.00 ± 0.19	3.19 ± 0.17	5.22E-19	9.81E-09	1.56E-05	1.08E-73	laccase 13
**	AT1G73290.1	AT1G73290	SCPL5	205	215	350	640	-1.77 ± 0.36	-1.69 ± 0.39	1.45 ± 0.24	3.44 ± 0.39	2.18E-04	2.83E-03	4.38E-07	1.25E-16	serine carboxypeptidase-like 5
**	AT3G50400.1	AT3G50400	--	976	941	1923	4777	-1.78 ± 0.29	-2.31 ± 0.31	1.36 ± 0.20	3.19 ± 0.19	7.16E-07	2.60E-10	5.48E-09	1.03E-62	GDSL-like Lipase/Acylhydrolase superfamily protein
**	AT4G15396.1	AT4G15396	CYP702A6	301	281	752	696	-1.81 ± 0.38	-2.62 ± 0.56	-0.40 ± 0.20	-0.09 ± 0.22	3.94E-04	6.46E-04	3.98E-01	1.00E+00	cytochrome P450, family 702, subfamily A, polypeptide 6
**	AT2G43390.1	AT2G43390	--	205	227	365	1170	-1.84 ± 0.46	-1.63 ± 0.46	1.39 ± 0.32	3.74 ± 0.31	9.85E-03	3.68E-02	8.88E-04	1.74E-31	
**	AT4G24140.1	AT4G24140	--	1548	1526	2830	6291	-1.90 ± 0.38	-2.25 ± 0.38	-0.15 ± 0.14	0.81 ± 0.10	1.73E-04	1.27E-06	9.07E-01	3.47E-13	alpha/beta-Hydrolases superfamily protein
**	AT3G12720.1	AT3G12720	MYB67	334	320	231	325	-1.96 ± 0.38	-2.60 ± 0.59	-0.06 ± 0.28	-0.01 ± 0.23	7.77E-05	1.55E-03	1.00E+00	1.00E+00	myb domain protein 67
**	AT1G44180.1	AT1G44180	--	151	143	181	372	-1.97 ± 0.45	-2.73 ± 0.59	-0.41 ± 0.31	0.14 ± 0.25	2.28E-03	5.99E-04	8.01E-01	1.00E+00	Peptidase M20/M25/M40 family protein
**	AT4G20390.1	AT4G20390	CASPL1B2	2324	2273	3517	9915	-1.97 ± 0.36	-2.50 ± 0.37	-0.03 ± 0.14	1.55 ± 0.17	2.50E-05	6.94E-09	1.00E+00	3.56E-17	Uncharacterised protein family (UPF0497)
**	AT1G64000.1	AT1G64000	WRKY56	242	229	476	976	-2.07 ± 0.52	-2.99 ± 0.61	0.53 ± 0.20	1.73 ± 0.24	9.79E-03	2.33E-04	1.46E-01	6.17E-11	WRKY DNA-binding protein 56
**	AT2G19200.1	AT2G19200	--	311	309	632	1769	-2.07 ± 0.34	-2.42 ± 0.37</							

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes							
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description			
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line					
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H				
	AT1G55490.1	AT1G55490	CPN60B	153	158	0	2	-10.70 ± 1.95	-8.36 ± 1.57	NA ± NA	-1.57 ± 3.29	1.72E-05	3.42E-05	NA	NA	chaperonin 60 beta			
	AT2G17500.3	AT2G17500	PILS5	108	111	179	499	-23.60 ± 4.79	-23.68 ± 4.79	-2.85 ± 2.93	2.27 ± 3.22	2.28E-04	1.74E-04	9.37E-01	1.00E+00	Auxin efflux carrier family protein			
H Up-regulated in TPL-OE (6H) analysis:																			
	AT2G17500.1	AT2G17500	PILS5	74	24	254	69	2.02 ± 2.06	-0.74 ± 3.30	11.31 ± 1.47	0.59 ± 1.87	1.00E+00	1.00E+00	6.42E-12	1.00E+00	Auxin efflux carrier family protein			
	AT3G15880.3	AT3G15880	WSIP2	170	130	72	48	-1.22 ± 3.35	-3.99 ± 4.57	9.49 ± 1.57	-1.44 ± 4.57	1.00E+00	1.00E+00	2.21E-07	1.00E+00	WUS-interacting protein 2			
	AT1G06680.2	AT1G06680	PSBP-1	149	140	61	139	-1.13 ± 1.03	-1.62 ± 3.21	9.24 ± 1.62	0.76 ± 0.54	1.00E+00	1.00E+00	1.31E-06	6.91E-01	photosystem II subunit P-1			
	AT1G77460.1	AT1G77460	CS13	122	87	51	36	-1.21 ± 4.56	-23.35 ± 4.79	9.01 ± 1.75	8.60 ± 4.79	1.00E+00	2.33E-04	2.32E-05	4.45E-01	Armadillo/beta-catenin-like repeat ; C2 calcium/lipid-binding domain (CaLB) protein			
	AT4G32660.3	AT4G32660	AME3	973	1318	50	203	-0.30 ± 0.77	0.46 ± 0.72	8.96 ± 1.73	0.74 ± 1.13	1.00E+00	1.00E+00	1.92E-05	1.00E+00	Protein kinase superfamily protein			
	AT1G12650.3	AT1G12650	--	235	187	49	75	0.88 ± 0.77	0.23 ± 0.68	8.94 ± 1.61	-0.04 ± 0.62	1.00E+00	1.00E+00	2.97E-06	1.00E+00				
	AT2G26150.2	AT2G26150	HSFA2	297	272	47	114	0.39 ± 0.40	0.06 ± 0.43	8.87 ± 1.66	-1.07 ± 0.91	1.00E+00	1.00E+00	9.28E-06	8.21E-01	heat shock transcription factor A2			
	AT1G61660.4	AT1G61660	AtbHLH112	208	139	46	75	1.14 ± 1.28	0.09 ± 3.22	8.85 ± 1.73	-0.27 ± 3.92	1.00E+00	1.00E+00	2.57E-05	1.00E+00	basic helix-loop-helix (bHLH) DNA-binding superfamily protein			
	AT1G67500.2	AT1G67500	REV3	159	141	45	34	-1.17 ± 4.56	-2.01 ± 4.56	8.80 ± 1.69	-8.57 ± 4.79	1.00E+00	1.00E+00	1.79E-05	4.48E-01	recovery protein 3			
	AT3G15095.2	AT3G15095	HCF243	54	93	44	117	-9.20 ± 3.60	-0.60 ± 4.56	8.79 ± 2.18	-1.40 ± 3.70	5.10E-01	1.00E+00	2.46E-03	1.00E+00				
	AT1G25275.2	AT1G25275	--	51	54	41	0	-2.63 ± 2.07	-2.81 ± 1.98	8.65 ± 1.67	-1.50 ± 4.99	1.00E+00	1.00E+00	2.09E-05	NA				
	AT4G22120.5	AT4G22120	--	489	570	210	118	-0.35 ± 0.56	0.02 ± 0.73	8.58 ± 1.09	0.48 ± 3.14	1.00E+00	1.00E+00	1.49E-12	1.00E+00	ERD (early-responsive to dehydration stress) family protein			
	AT5G60100.3	AT5G60100	PRR3	467	349	38	26	1.21 ± 0.74	0.49 ± 0.84	8.56 ± 1.76	-2.24 ± 2.89	1.00E+00	1.00E+00	8.73E-05	9.89E-01	pseudo-response regulator 3			
	AT3G12620.2	AT3G12620	--	364	311	35	66	0.30 ± 0.41	-0.25 ± 0.53	8.46 ± 1.68	-1.65 ± 1.82	1.00E+00	1.00E+00	3.69E-05	9.49E-01	Protein phosphatase 2C family protein			
	AT1G29120.2	AT1G29120	UP9	0	0	32	12	NA ± NA	NA ± NA	8.32 ± 1.78	7.05 ± 3.80	NA	NA	1.86E-04	4.09E-01	Hydrolase-like protein family			
	AT3G10420.1	AT3G10420	--	128	158	28	50	-0.17 ± 0.59	0.34 ± 0.83	8.15 ± 1.82	-0.88 ± 0.66	1.00E+00	1.00E+00	4.50E-04	7.37E-01	P-loop containing nucleoside triphosphate hydrolases superfamily protein			
	AT5G44120.3	AT5G44120	CRA1	0	0	28	0	NA ± NA	NA ± NA	8.15 ± 1.75	NA ± NA	NA	NA	1.95E-04	NA	RmlC-like cupins superfamily protein			
	AT5G58330.3	AT5G58330	NADP-MDH	160	232	74	285	-2.90 ± 0.93	-0.75 ± 0.81	8.09 ± 1.67	-0.46 ± 0.34	1.39E-01	1.00E+00	9.48E-05	7.14E-01	lactate/malate dehydrogenase family protein			
	AT1G33980.2	AT1G33980	UPF3	0	17	27	88	NA ± NA	7.52 ± 4.00	8.06 ± 1.74	-0.01 ± 3.10	NA	1.00E+00	2.30E-04	1.00E+00	Smg-4/UPF3 family protein			
	AT2G14120.3	AT2G14120	DRP3B	104	200	26	101	-1.90 ± 1.09	0.45 ± 0.98	8.05 ± 2.74	0.29 ± 1.69	1.00E+00	1.00E+00	6.66E-02	1.00E+00	dynamain related protein			
	AT4G01610.2	AT4G01610	AtCATHB3	182	191	25	26	-1.87 ± 1.06	-1.77 ± 1.28	7.96 ± 1.86	0.82 ± 0.90	1.00E+00	1.00E+00	9.67E-04	9.46E-01	Cysteine proteinases superfamily protein			
	AT4G13940.2	AT4G13940	HOG1	18168	30277	135	746	-1.08 ± 0.93	0.46 ± 0.44	7.94 ± 1.17	-2.32 ± 1.06	1.00E+00	1.00E+00	2.89E-09	2.40E-01	S-adenosyl-L-homocysteine hydrolase			
	AT1G21350.2	AT1G21350	--	11	14	24	12	-0.64 ± 1.35	-0.09 ± 2.46	7.90 ± 1.77	6.99 ± 3.83	1.00E+00	1.00E+00	4.67E-04	4.28E-01	Thioredoxin superfamily protein			
	AT5G47620.1	AT5G47620	--	85	154	23	14	-1.01 ± 2.12	0.71 ± 0.76	7.81 ± 1.79	2.77 ± 2.30	1.00E+00	1.00E+00	7.06E-04	8.07E-01	RNA-binding (RRM/RBD/RNP motifs) family protein			
	AT4G33770.2	AT4G33770	ITPK2	206	212	22	131	-0.34 ± 0.67	-0.37 ± 0.49	7.78 ± 1.94	-0.62 ± 0.45	1.00E+00	1.00E+00	2.70E-03	7.05E-01	Inositol 1,3,4-trisphosphate 5/6-kinase family protein			
	AT5G28910.1	AT5G28910	--	52	68	21	27	-4.17 ± 1.72	-1.59 ± 1.96	7.70 ± 1.83	1.34 ± 1.88	6.47E-01	1.00E+00	1.21E-03	1.00E+00				
	AT2G41100.4	AT2G41100	TCH3	28	52	21	48	1.13 ± 2.21	2.25 ± 3.02	7.70 ± 1.90	-1.71 ± 4.57	1.00E+00	1.00E+00	2.36E-03	1.00E+00	Calcium-binding EF hand family protein			
	AT1G77300.2	AT1G77300	EFS	2	2	20	3	-4.26 ± 4.82	-4.35 ± 4.82	7.64 ± 1.96	-5.03 ± 4.80	1.00E+00	NA	3.82E-03	NA	histone methyltransferases(H3-K4 specific);histone methyltransferases(H3-K36 specific)			
	AT1G69840.2	AT1G69840	AtHIR1	90	70	20	18	2.05 ± 1.99	1.51 ± 1.97	7.63 ± 1.90	0.68 ± 3.07	1.00E+00	1.00E+00	2.54E-03	1.00E+00	SPFH/Band 7/PHB domain-containing membrane-associated protein family			
	AT2G21590.2	AT2G21590	APL4	102	69	19	17	0.01 ± 0.96	-1.68 ± 2.02	7.56 ± 1.86	1.35 ± 3.10	1.00E+00	1.00E+00	2.14E-03	1.00E+00	Glucose-1-phosphate adenylyltransferase family protein			
	AT2G37500.2	AT2G37500	--	15	96	18	21	0.55 ± 3.66	3.80 ± 1.64	7.48 ± 1.94	0.89 ± 3.01	1.00E+00	6.69E-01	4.80E-03	1.00E+00	arginine biosynthesis protein ArgJ family			
	AT1G72370.2	AT1G72370	P40	80	118	18	18	-0.83 ± 0.94	0.29 ± 1.08	7.47 ± 2.04	-0.03 ± 3.07	1.00E+00	1.00E+00	8.86E-03	1.00E+00	40s ribosomal protein SA			
	AT3G12530.2	AT3G12530	PSF2	101	51	17	20	0.12 ± 4.56	-9.15 ± 3.33	7.41 ± 2.43	0.27 ± 3.04	1.00E+00	2.88E-01	4.98E-02	1.00E+00	PSF2			
	AT4G36540.2	AT4G36540	BEE2	15	22	17	21	-1.50 ± 3.68	-0.09 ± 2.29	7.38 ± 2.15	-0.18 ± 3.02	1.00E+00	1.00E+00	1.78E-02	1.00E+00	BR enhanced expression 2			
	AT3G05380.3	AT3G05380	ALY2	69	38	15	32	0.66 ± 3.26	-1.40 ± 3.14	7.25 ± 1.95	-0.32 ± 4.57	1.00E+00	1.00E+00	7.30E-03	1.00E+00	DIRP ;Myb-like DNA-binding domain			
	AT3G54000.3	AT3G54000	--	48	46	15	5	0.65 ± 1.24	0.45 ± 1.31	7.19 ± 1.97	-5.93 ± 2.77	1.00E+00	1.00E+00	8.98E-03	2.63E-01				
	AT4G14160.1	AT4G14160	AtSEC23F	85	61	14	43	-0.65 ± 2.18	-2.88 ± 1.86	7.11 ± 2.00	0.51 ± 2.04	1.00E+00	1.00E+00	1.21E-02	1.00E+00	Sec23/Sec24 protein transport family protein			
	AT2G24960.1	AT2G24960	--	14	13	14	20	0.98 ± 3.72	0.75 ± 2.38	7.10 ± 2.04	1.73 ± 3.01	1.00E+00	1.00E+00	1.50E-02	1.00E+00				
	AT5G44120.1	AT5G44120	CRA1	1	2	13	0	-3.45 ± 4.84	-0.47 ± 4.69	7.07 ± 2.47	NA ± NA	NA	NA	7.77E-02	NA	RmlC-like cupins superfamily protein			
	AT3G50210.2	AT3G50210	--	22	10	13	0	7.91 ± 4.17	6.68 ± 4.58	7.06 ± 2.08	NA ± NA	1.00E+00	1.00E+00	2.03E-02	NA	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein			
	AT1G49050.2	AT1G49050	APCB1	0	0	13	14	NA ± NA	NA ± NA	7.03 ± 2.03	-7.30 ± 3.65	NA	NA	1.56E-02	3.28E-01	Eukaryotic aspartyl protease family protein			
	AT4G22990.1	AT4G22990	PHT5;3	35	14	13	42	0.64 ± 3.42	-7.29 ± 4.19	7.00 ± 2.16	2.09 ± 1.87	1.00E+00	1.00E+00	2.97E-02	8.55E-01	Major Facilitator Superfamily with SPX (SYG1/Pho81/XPR1) domain-containing protein			
	AT1G06640.3	AT1G06640	--	0	0	12	7	NA ± NA	NA ± NA	6.96 ± 2.10	6.13 ± 2.58	NA	NA	2.48E-02	1.72E-01	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein			
	AT2G43490.5	AT2G43490	--	6	11	12	3	6.11 ± 3.32	6.89 ± 4.40	6.93 ± 2.16	-4.88 ± 4.81	1.00E+00	1.00E+00	3.24E-02	NA	Ypt/Rab-GAP domain of gyp1p superfamily protein			
	AT4G27800.3	AT4G27800	TAP38	22	24	12	14	2.04 ± 2.15	2.17 ± 2.11	6.90 ± 2.09	0.78 ± 1.07	1.00E+00	1.00E+00	2.60E-02	9.99E-01	thylakoid-associated phosphatase 38			
	AT1G29460.1	AT1G29460	SAUR65	4	3	64	0	-1.68 ± 3.19	-3.68 ± 3.40	6.84 ± 2.11	-2.40 ± 4.90	1.00E+00	1.00E+00	2.97E-02	NA	SAUR-like auxin-responsive protein family			
	AT4G10120.2	AT4G10120	AtSPS4F	310	246	61	90	-0.18 ± 0.51	-1.14 ± 0.63	6.84 ± 2.18	1.52 ± 1.41	1.00E+00	1.00E+00	3.91E-02	8.71E-01	Sucrose-phosphate synthase family protein			
	AT5G54130.4	AT5G54130	--	85	54	11	21	0.87 ± 1.31	-0.41 ± 2.12	6.81 ± 2.11	1.62 ± 1.89	1.00E+00	1.00E+00	3.12E-02	9.66E-01	Calc			

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT3G18850.1	AT3G18850	LPAT5	134	197	63	77	-0.27 ± 0.78	0.69 ± 0.66	5.87 ± 1.29	1.21 ± 0.57	1.00E+00	1.00E+00	3.23E-04	2.82E-01	lysophosphatidyl acyltransferase 5
	AT1G21080.2	AT1G21080	--	517	628	30	138	0.63 ± 3.75	0.99 ± 3.43	5.72 ± 1.42	-4.89 ± 2.42	1.00E+00	1.00E+00	2.38E-03	3.19E-01	DNAI heat shock N-terminal domain-containing protein
	AT5G59310.1	AT5G59310	LTP4	0	2	38	16	NA ± NA	4.10 ± 4.82	5.55 ± 1.93	1.20 ± 1.44	NA	NA	7.53E-02	9.73E-01	lipid transfer protein 4
	AT4G18380.2	AT4G18380	--	10	0	115	57	5.32 ± 3.76	-1.54 ± 5.00	5.47 ± 1.10	9.25 ± 4.79	1.00E+00	NA	4.70E-05	3.67E-01	F-box family protein
	AT2G13115.1	AT2G13115	--	12	19	70	11	-0.78 ± 2.05	0.53 ± 1.76	5.37 ± 1.72	-0.05 ± 1.29	1.00E+00	1.00E+00	4.03E-02	1.00E+00	
	AT1G27600.2	AT1G27600	IRX9-L	5	5	46	33	-5.76 ± 4.80	-5.85 ± 4.80	5.09 ± 1.51	8.46 ± 4.79	1.00E+00	1.00E+00	2.07E-02	4.62E-01	Nucleotide-diphospho-sugar transferases superfamily protein
	AT3G47836.2	AT3G47836	--	7	0	20	0	6.38 ± 4.79	NA ± NA	4.45 ± 1.58	NA ± NA	1.00E+00	NA	8.83E-02	NA	
	AT1G71000.1	AT1G71000	--	2	1	12	6	1.06 ± 3.71	0.54 ± 4.74	4.33 ± 1.52	3.35 ± 2.20	NA	NA	8.02E-02	6.13E-01	Chaperone DnaJ-domain superfamily protein
	AT1G76990.4	AT1G76990	ACR3	194	107	47	49	1.84 ± 0.75	0.54 ± 0.65	4.15 ± 1.25	-1.26 ± 1.82	6.19E-01	1.00E+00	2.40E-02	1.00E+00	ACT domain repeat 3
	AT3G04640.3	AT3G04640	--	91	75	36	25	0.43 ± 0.63	-0.23 ± 0.78	3.96 ± 0.85	-1.59 ± 1.35	1.00E+00	1.00E+00	2.00E-04	8.25E-01	glycine-rich protein
	AT5G17020.2	AT5G17020	XPO1A	496	506	447	885	0.02 ± 1.20	0.00 ± 0.73	3.74 ± 0.67	0.04 ± 0.33	1.00E+00	1.00E+00	2.91E-06	1.00E+00	exportin 1A
	AT3G52970.1	AT3G52970	CYP76G1	5	8	29	94	-0.68 ± 2.77	0.58 ± 1.69	3.64 ± 0.96	2.12 ± 1.13	1.00E+00	1.00E+00	5.52E-03	4.00E-01	cytochrome P450, family 76, subfamily G, polypeptide 1
	AT2G37870.1	AT2G37870	--	20	17	46	42	2.04 ± 1.29	1.65 ± 1.23	3.20 ± 0.70	1.06 ± 0.90	1.00E+00	1.00E+00	2.54E-04	8.22E-01	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT4G27160.1	AT4G27160	SESA3	0	0	35	9	NA ± NA	NA ± NA	3.09 ± 1.12	0.81 ± 1.60	NA	NA	9.94E-02	1.00E+00	seed storage albumin 3
	AT3G49010.1	AT3G49010	BBC1	655	1723	98	10	-2.92 ± 1.82	0.90 ± 2.24	3.01 ± 0.59	0.89 ± 1.67	1.00E+00	1.00E+00	2.90E-05	1.00E+00	breast basic conserved 1
	AT5G18420.2	AT5G18420	--	1160	1007	363	480	0.72 ± 0.29	0.29 ± 0.24	2.95 ± 0.62	-0.10 ± 0.71	6.13E-01	1.00E+00	1.19E-04	1.00E+00	
	AT3G21110.2	AT3G21110	PUR7	848	992	114	306	-0.93 ± 0.50	-0.47 ± 0.60	2.88 ± 1.00	-2.08 ± 3.09	1.00E+00	1.00E+00	7.46E-02	1.00E+00	purin 7
	AT3G15670.1	AT3G15670	LEA76	13	20	75	115	-0.87 ± 1.40	0.38 ± 1.24	2.74 ± 0.91	1.95 ± 0.97	1.00E+00	1.00E+00	5.59E-02	3.19E-01	Late embryogenesis abundant protein (LEA) family protein
	AT1G19350.6	AT1G19350	BES1	403	662	157	279	-0.79 ± 3.61	0.59 ± 1.00	2.70 ± 0.96	-0.51 ± 3.42	1.00E+00	1.00E+00	9.16E-02	1.00E+00	Brassinosteroid signalling positive regulator (BZR1) family protein
	AT5G63880.2	AT5G63880	VPS20.1	122	121	54	39	-0.06 ± 0.72	-0.20 ± 1.37	2.69 ± 0.74	-0.91 ± 2.19	1.00E+00	1.00E+00	8.94E-03	1.00E+00	SNF7 family protein
	AT3G20130.2	AT3G20130	CYP705A22	257	349	148	347	-0.33 ± 0.42	0.44 ± 0.57	2.48 ± 0.56	-0.23 ± 0.57	1.00E+00	1.00E+00	4.92E-04	1.00E+00	cytochrome P450, family 705, subfamily A, polypeptide 22
	AT4G19710.1	AT4G19710	AK-HSDH II	132	95	57	45	0.11 ± 0.91	-1.12 ± 1.00	2.45 ± 0.72	0.87 ± 0.73	1.00E+00	1.00E+00	2.08E-02	8.11E-01	aspartate kinase-homoserine dehydrogenase ii
	AT1G43170.9	AT1G43170	RP1	76	144	69	100	1.47 ± 2.09	2.56 ± 1.76	2.38 ± 0.63	2.43 ± 2.80	1.00E+00	1.00E+00	5.72E-03	9.61E-01	ribosomal protein 1
	AT2G15780.1	AT2G15780	--	4	4	56	20	3.85 ± 2.89	3.82 ± 2.95	2.33 ± 0.68	1.14 ± 1.31	1.00E+00	1.00E+00	1.73E-02	9.61E-01	Cupredoxin superfamily protein
	AT3G08580.1	AT3G08580	AAC1	16558	25670	1439	13025	-0.53 ± 2.69	0.62 ± 2.36	2.22 ± 0.43	-0.88 ± 0.73	1.00E+00	1.00E+00	2.57E-05	8.05E-01	ADP/ATP carrier 1
	AT5G15950.2	AT5G15950	SAMDC2	240	302	44	2303	-0.15 ± 0.58	0.40 ± 0.59	2.19 ± 0.64	0.29 ± 0.27	1.00E+00	1.00E+00	1.74E-02	8.82E-01	Adenosylmethionine decarboxylase family protein
	AT5G59210.2	AT5G59210	--	114	104	73	80	-0.31 ± 2.15	-0.74 ± 2.05	2.00 ± 0.53	-1.17 ± 0.56	1.00E+00	1.00E+00	5.90E-03	2.91E-01	myosin heavy chain-related
	AT2G29190.2	AT2G29190	PUM2	864	790	462	207	-0.10 ± 0.87	-0.48 ± 0.90	1.98 ± 0.21	0.98 ± 0.58	1.00E+00	1.00E+00	6.41E-18	5.08E-01	pumilio 2
	AT4G31180.2	AT4G31180	IBI1	1555	1797	655	1099	1.62 ± 0.81	1.84 ± 0.72	1.90 ± 0.23	0.23 ± 0.28	1.00E+00	4.44E-01	6.85E-14	9.79E-01	Class II aminoacyl-tRNA and biotin synthetases superfamily protein
	AT2G46370.1	AT2G46370	JAR1	1123	1299	257	213	-0.57 ± 0.44	-0.19 ± 0.51	1.89 ± 0.27	-1.07 ± 0.63	1.00E+00	1.00E+00	1.24E-09	5.15E-01	Auxin-responsive GH3 family protein
	AT4G29930.3	AT4G29930	--	66	62	52	61	-0.61 ± 0.71	-1.03 ± 0.76	1.86 ± 0.65	1.18 ± 0.67	1.00E+00	1.00E+00	7.57E-02	4.58E-01	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
	AT1G73220.1	AT1G73220	OCT1	40	48	307	1468	-0.33 ± 0.91	0.16 ± 1.02	1.81 ± 0.58	2.04 ± 0.14	1.00E+00	1.00E+00	3.92E-02	4.67E-44	organic cation/carnitine transporter1
	AT2G47770.1	AT2G47770	TSPO	5	4	62	49	-0.86 ± 2.06	-1.66 ± 2.23	1.81 ± 0.54	1.02 ± 0.62	1.00E+00	1.00E+00	2.42E-02	5.42E-01	TSPO(outer membrane tryptophan-rich sensory protein)-related
	AT3G61490.2	AT3G61490	--	48	47	115	59	0.93 ± 2.31	0.83 ± 0.83	1.78 ± 0.48	2.32 ± 1.70	1.00E+00	1.00E+00	7.16E-03	7.17E-01	Pectin lyase-like superfamily protein
	AT3G03950.1	AT3G03950	ECT1	683	929	346	554	-1.74 ± 1.84	-0.49 ± 0.44	1.77 ± 0.40	0.32 ± 0.36	1.00E+00	1.00E+00	6.79E-04	9.55E-01	evolutionarily conserved C-terminal region 1
	AT3G02480.1	AT3G02480	ABR	33	33	234	219	1.01 ± 0.96	0.88 ± 0.88	1.72 ± 0.53	1.70 ± 0.75	1.00E+00	1.00E+00	2.94E-02	2.16E-01	Late embryogenesis abundant protein (LEA) family protein
	AT1G53165.2	AT1G53165	AtMAP4Kα1	443	525	514	596	0.26 ± 1.00	0.61 ± 0.90	1.71 ± 0.47	0.31 ± 0.20	1.00E+00	1.00E+00	8.08E-03	6.03E-01	Protein kinase superfamily protein
	AT1G04580.1	AT1G04580	A04	11	9	62	30	-0.54 ± 1.42	-1.15 ± 1.55	1.69 ± 0.52	1.25 ± 0.83	1.00E+00	1.00E+00	2.90E-02	6.28E-01	aldehyde oxidase 4
	AT5G65685.2	AT5G65685	--	749	789	127	208	-0.34 ± 0.23	-0.28 ± 0.24	1.69 ± 0.59	-0.44 ± 0.30	1.00E+00	1.00E+00	8.33E-02	6.43E-01	UDP-Glycosyltransferase superfamily protein
	AT1G55900.2	AT1G55900	TIM50	267	233	154	115	-0.04 ± 0.64	-0.58 ± 0.54	1.68 ± 0.45	0.91 ± 0.42	1.00E+00	1.00E+00	6.71E-03	2.39E-01	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
	AT1G23950.1	AT1G23950	--	253	257	61	75	0.60 ± 0.59	0.56 ± 0.54	1.68 ± 0.57	-0.70 ± 0.52	1.00E+00	1.00E+00	6.18E-02	7.25E-01	Protein of unknown function (DUF626)
	AT5G12440.3	AT5G12440	--	695	702	236	135	-0.39 ± 0.47	-0.46 ± 0.78	1.62 ± 0.59	0.53 ± 0.65	1.00E+00	1.00E+00	9.97E-02	9.76E-01	CCCH-type zinc fingerfamily protein with RNA-binding domain
	AT1G03830.1	AT1G03830	--	413	552	231	386	-0.44 ± 1.31	0.33 ± 0.28	1.61 ± 0.43	-0.10 ± 0.28	1.00E+00	1.00E+00	7.58E-03	1.00E+00	guanylate-binding family protein
	AT2G46390.1	AT2G46390	SDH8	710	1082	384	254	-0.84 ± 0.79	0.43 ± 0.59	1.54 ± 0.33	-1.07 ± 0.44	1.00E+00	1.00E+00	1.58E-04	1.51E-01	
	AT3G49060.2	AT3G49060	--	187	160	147	174	0.18 ± 0.86	-0.38 ± 0.80	1.53 ± 0.45	0.57 ± 0.34	1.00E+00	1.00E+00	2.08E-02	5.15E-01	U-box domain-containing protein kinase family protein
	AT5G59290.2	AT5G59290	UXS3	1853	2753	378	1192	-0.52 ± 0.50	0.52 ± 0.48	1.53 ± 0.52	-0.02 ± 0.15	1.00E+00	1.00E+00	6.80E-02	1.00E+00	UDP-glucuronic acid decarboxylase 3
	AT5G43990.4	AT5G43990	SUVR2	281	196	203	180	-0.09 ± 1.14	-1.66 ± 1.11	1.50 ± 0.39	0.88 ± 3.18	1.00E+00	1.00E+00	4.94E-03	1.00E+00	SET-domain containing protein lysine methyltransferase family protein
	AT3G25830.1	AT3G25830	TPS-CIN	12510	5825	8162	2739	0.45 ± 1.84	-3.87 ± 1.96	1.50 ± 0.15	2.36 ± 0.93	1.00E+00	1.00E+00	1.88E-20	1.21E-01	terpene synthase-like sequence-1,8-cineole
	AT3G61060.2	AT3G61060	PP2-A13													

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes					
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description	
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line			
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H		
	AT4G15530.6	AT4G15530	PPDK	68	42	209	62	5.24 ± 1.47	4.48 ± 1.65	1.29 ± 0.35	1.69 ± 4.57	4.11E-02	3.18E-01	8.54E-03	1.00E+00	pyruvate orthophosphate dikinase	
	AT1G66260.2	AT1G66260	ALY3	1340	1400	682	414	0.52 ± 0.52	0.54 ± 0.39	1.28 ± 0.36	0.69 ± 0.47	1.00E+00	1.00E+00	1.09E-02	6.47E-01	RNA-binding (RRM/RBD/RNP motifs) family protein	
	AT4G28040.3	AT4G28040	UMAMIT33	163	258	154	280	-1.85 ± 1.97	-0.07 ± 0.58	1.25 ± 0.39	0.36 ± 0.45	1.00E+00	1.00E+00	3.47E-02	9.82E-01	nodulin MtN21 /EamA-like transporter family protein	
	AT5G44200.1	AT5G44200	CBP20	574	831	206	211	-0.17 ± 0.32	0.72 ± 0.32	1.24 ± 0.37	-0.19 ± 0.58	1.00E+00	7.45E-01	2.36E-02	1.00E+00	CAP-binding protein 20	
	AT5G52230.1	AT5G52230	MBD13	471	505	228	413	-0.16 ± 0.24	-0.04 ± 0.34	1.21 ± 0.39	0.23 ± 0.24	1.00E+00	1.00E+00	4.84E-02	9.24E-01	methyl-CPG-binding domain protein 13	
	AT2G01170.2	AT2G01170	BAT1	499	452	239	176	0.55 ± 0.80	0.22 ± 0.78	1.18 ± 0.32	0.46 ± 0.50	1.00E+00	1.00E+00	7.55E-03	9.43E-01	bidirectional amino acid transporter 1	
	AT5G65060.2	AT5G65060	MAF3	188	245	145	198	0.72 ± 0.45	1.21 ± 0.42	1.18 ± 0.35	0.37 ± 0.37	1.00E+00	2.32E-01	2.04E-02	9.03E-01	K-box region and MADS-box transcription factor family protein	
	AT1G25275.1	AT1G25275	--	1197	1638	820	399	-0.46 ± 0.60	0.27 ± 0.41	1.17 ± 0.42	-2.81 ± 1.43	1.00E+00	1.00E+00	9.31E-02	3.51E-01		
	AT4G32950.1	AT4G32950	--	422	429	104	129	-0.04 ± 0.54	-0.10 ± 0.34	1.15 ± 0.39	-0.01 ± 0.67	1.00E+00	1.00E+00	6.65E-02	1.00E+00	Protein phosphatase 2C family protein	
	AT1G23950.5	AT1G23950	--	598	690	296	403	-0.12 ± 0.41	0.19 ± 0.30	1.12 ± 0.37	-0.44 ± 0.34	1.00E+00	1.00E+00	5.18E-02	7.48E-01	Protein of unknown function (DUF626)	
	AT1G79880.2	AT1G79880	--	350	418	151	153	-1.61 ± 0.53	-0.90 ± 0.35	1.08 ± 0.35	-0.22 ± 0.52	1.78E-01	4.49E-01	4.81E-02	1.00E+00	RNA recognition motif (RRM)-containing protein	
	AT3G21720.1	AT3G21720	ICL	802	660	844	557	1.33 ± 0.65	0.85 ± 0.31	1.06 ± 0.30	0.96 ± 0.57	1.00E+00	3.13E-01	1.10E-02	5.14E-01	isocitrate lyase	
	AT3G45780.1	AT3G45780	PHOT1	2182	2359	1192	1049	-0.56 ± 0.27	-0.39 ± 0.29	1.04 ± 0.17	-0.41 ± 0.34	1.00E+00	1.00E+00	1.18E-07	8.11E-01	phototropin 1	
	AT2G19900.1	AT2G19900	NADP-ME1	57	42	491	602	0.24 ± 0.93	-0.88 ± 0.84	1.03 ± 0.22	0.78 ± 0.26	1.00E+00	1.00E+00	2.26E-04	4.81E-02	NADP-malic enzyme 1	
	AT1G80160.1	AT1G80160	GLY17	156	171	401	272	-0.82 ± 0.55	-0.65 ± 0.51	1.01 ± 0.31	0.90 ± 0.46	1.00E+00	1.00E+00	2.91E-02	3.53E-01	Lactoylglutathione lyase / glyoxalase I family protein	
H	Down-regulated in TPL-OE (6H) analysis:																
*	AT4G18020.1	AT4G18020	APRR2	853	1080	301	636	0.08 ± 0.30	0.61 ± 0.26	-1.00 ± 0.25	0.26 ± 0.35	1.00E+00	6.42E-01	2.06E-03	9.97E-01	CheY-like two-component responsive regulator family protein	
	AT5G62360.1	AT5G62360	PMEI13	124	153	519	109	-0.46 ± 0.46	0.07 ± 0.51	-1.00 ± 0.23	-1.20 ± 0.49	1.00E+00	1.00E+00	7.74E-04	1.49E-01	Plant invertase/pectin methyltransferase inhibitor superfamily protein	
	AT4G12770.2	AT4G12770	AUXILIN-LIKE2	249	193	223	124	0.29 ± 1.00	-0.57 ± 0.99	-1.02 ± 0.27	0.63 ± 0.50	1.00E+00	1.00E+00	7.13E-03	7.71E-01	Chaperone DnaJ-domain superfamily protein	
	AT1G73602.1	AT1G73602	--	738	391	703	625	0.82 ± 1.91	-1.27 ± 0.32	-1.02 ± 0.21	0.44 ± 1.56	1.00E+00	9.70E-03	6.29E-05	1.00E+00	conserved peptide upstream open reading frame 32	
	AT1G65860.1	AT1G65860	FMO GS-OX1	114	112	208	375	0.49 ± 0.51	0.37 ± 0.52	-1.02 ± 0.31	-0.10 ± 0.29	1.00E+00	1.00E+00	2.77E-02	1.00E+00	flavin-monoxygenase glucosinolate S-oxygenase 1	
	AT1G72360.2	AT1G72360	ERF73	3515	4082	1106	1528	0.92 ± 0.36	1.15 ± 0.41	-1.03 ± 0.13	-0.33 ± 0.14	5.29E-01	2.50E-01	1.49E-12	1.57E-01	Integrase-type DNA-binding superfamily protein	
	AT3G01260.1	AT3G01260	--	1770	1954	943	1319	0.05 ± 0.24	0.23 ± 0.29	-1.03 ± 0.15	-0.95 ± 0.21	1.00E+00	1.00E+00	3.84E-10	1.66E-04	Galactose mutarotase-like superfamily protein	
	AT1G07890.6	AT1G07890	APX1	4746	3450	3863	7140	1.37 ± 1.10	0.60 ± 1.45	-1.03 ± 0.25	0.53 ± 0.12	1.00E+00	1.00E+00	1.39E-03	6.41E-04	ascorbate peroxidase 1	
	AT2G20080.1	AT2G20080	TIE2	358	358	212	407	0.23 ± 0.35	0.12 ± 0.45	-1.03 ± 0.36	-1.19 ± 0.57	1.00E+00	1.00E+00	7.23E-02	2.93E-01		
	AT2G39200.1	AT2G39200	MLO12	4818	4423	1959	2024	0.06 ± 0.11	-0.30 ± 0.17	-1.04 ± 0.12	-0.88 ± 0.21	1.00E+00	1.00E+00	6.12E-15	8.72E-04	Seven transmembrane MLO family protein	
	AT5G06110.2	AT5G06110	AtGLSA2	3219	3499	921	1850	-0.20 ± 1.00	-0.04 ± 0.49	-1.04 ± 0.17	0.27 ± 0.24	1.00E+00	1.00E+00	2.93E-07	8.47E-01	DnaJ domain ;Myb-like DNA-binding domain	
	AT2G02170.2	AT2G02170	--	334	387	257	157	1.56 ± 0.70	1.78 ± 0.67	-1.04 ± 0.35	1.20 ± 0.58	8.66E-01	3.50E-01	6.13E-02	3.00E-01	Remorin family protein	
	AT1G55450.1	AT1G55450	--	1187	1204	493	482	0.18 ± 0.39	0.13 ± 0.40	-1.05 ± 0.28	-0.83 ± 0.23	1.00E+00	1.00E+00	7.44E-03	5.53E-03	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	
	AT5G16510.1	AT5G16510	RGP5	638	1049	700	1234	-0.64 ± 0.44	0.69 ± 0.77	-1.05 ± 0.17	0.12 ± 0.14	1.00E+00	1.00E+00	8.00E-08	9.60E-01	Alpha-1,4-glucan-protein synthase family protein	
	AT3G09920.2	AT3G09920	PIP5K9	1125	847	864	563	0.41 ± 0.56	-0.51 ± 0.53	-1.05 ± 0.37	0.52 ± 0.47	1.00E+00	1.00E+00	8.65E-02	8.56E-01	phosphatidyl inositol monophosphate 5 kinase	
	AT5G25100.2	AT5G25100	TMN9	5596	5590	625	1079	-0.02 ± 0.14	-0.11 ± 0.15	-1.06 ± 0.18	0.70 ± 0.34	1.00E+00	1.00E+00	2.36E-07	2.96E-01	Endomembrane protein 70 protein family	
	AT4G15330.1	AT4G15330	CYP705A1	747	626	643	441	0.37 ± 0.28	-0.22 ± 0.42	-1.06 ± 0.17	-0.80 ± 0.26	1.00E+00	1.00E+00	1.38E-07	3.41E-02	cytochrome P450, family 705, subfamily A, polypeptide 1	
	AT5G15320.2	AT5G15320	--	201	145	160	97	1.52 ± 1.48	0.69 ± 1.42	-1.06 ± 0.37	0.28 ± 3.08	1.00E+00	1.00E+00	7.61E-02	1.00E+00		
	AT1G11185.1	AT1G11185	sORF2	1023	1130	323	222	0.23 ± 0.31	0.33 ± 0.27	-1.06 ± 0.31	0.08 ± 0.38	1.00E+00	1.00E+00	1.85E-02	1.00E+00	other RNA	
	AT5G14200.1	AT5G14200	IMD1	20355	22536	11314	29019	0.15 ± 0.18	0.33 ± 0.23	-1.07 ± 0.11	-0.36 ± 0.10	1.00E+00	1.00E+00	7.04E-20	4.40E-03	isopropylmalate dehydrogenase 1	
	AT3G59710.1	AT3G59710	--	143	141	140	134	0.07 ± 0.67	-0.07 ± 0.45	-1.08 ± 0.36	-0.79 ± 0.42	1.00E+00	1.00E+00	5.59E-02	4.00E-01	NAD(P)-binding Rossmann-fold superfamily protein	
	AT3G03190.1	AT3G03190	GSTF11	1085	1256	505	773	0.24 ± 0.31	0.50 ± 0.30	-1.08 ± 0.27	-0.37 ± 0.23	1.00E+00	1.00E+00	2.78E-03	5.94E-01	glutathione S-transferase F11	
	AT1G21120.1	AT1G21120	IGMT2	671	491	790	295	0.84 ± 0.24	-0.04 ± 0.31	-1.08 ± 0.27	-0.06 ± 0.32	4.11E-02	1.00E+00	2.06E-03	1.00E+00	O-methyltransferase family protein	
	AT3G61220.2	AT3G61220	SDR1	902	713	345	285	0.65 ± 0.60	-0.06 ± 0.43	-1.09 ± 0.27	0.48 ± 0.37	1.00E+00	1.00E+00	2.18E-03	7.59E-01	NAD(P)-binding Rossmann-fold superfamily protein	
	AT1G10390.1	AT1G10390	DRA2	1362	1464	652	568	-0.85 ± 0.56	-0.68 ± 0.69	-1.09 ± 0.36	0.77 ± 0.35	1.00E+00	1.00E+00	5.27E-02	2.37E-01	Nucleoporin autopeptidase	
	AT1G27020.1	AT1G27020	--	1751	1675	856	454	0.45 ± 0.27	0.25 ± 0.29	-1.10 ± 0.14	-0.51 ± 0.28	1.00E+00	1.00E+00	8.86E-13	4.06E-01		
	AT4G27430.2	AT4G27430	CIP7	590	355	273	439	1.08 ± 0.93	-0.29 ± 0.99	-1.12 ± 0.36	0.20 ± 0.21	1.00E+00	1.00E+00	4.32E-02	9.36E-01	COP1-interacting protein 7	
	AT1G09090.2	AT1G09090	RBOHB	3701	3812	776	722	1.06 ± 0.14	1.06 ± 0.15	-1.12 ± 0.22	-0.80 ± 0.21	2.65E-10	5.40E-10	2.10E-05	3.65E-03	respiratory burst oxidase homolog B	
	AT5G41300.1	AT5G41300	--	564	511	141	134	0.19 ± 0.34	-0.21 ± 0.39	-1.13 ± 0.36	-0.30 ± 0.37	1.00E+00	1.00E+00	4.05E-02	9.81E-01	Receptor-like protein kinase-related family protein	
	AT1G61210.1	AT1G61210	DWA3	515	303	370	423	1.97 ± 0.28	0.86 ± 1.41	-1.13 ± 0.27	0.56 ± 0.58	1.02E-09	1.00E+00	1.14E-03	9.27E-01	Transducin/WD40 repeat-like superfamily protein	
	AT5G64120.1	AT5G64120	PRX71	944	666	6435	3780	0.81 ± 0.32	-0.19 ± 0.38	-1.15 ± 0.18	-1.12 ± 0.68	5.49E-01	1.00E+00	3.16E-08	5.37E-01	Peroxidase superfamily protein	
	AT5G60410.2	AT5G60410	SIZ1	222	113	162	218	0.52 ± 0.76	-2.31 ± 1.89	-1.15 ± 0.38	-0.20 ± 3.32	1.00E+00	1.00E+00	5.23E-02	1.00E+00	DNA-binding protein with MIZ/SP-RING zinc finger, PHD-finger and SAP domain	
	AT2G26560.1	AT2G26560	PLA2A	146	115	379	201	-0.66 ± 0.50	-2.08 ± 0.62	-1.15 ± 0.26	-0.84 ± 0.47	1.00E+00	6.24E-02	7.42E-04	4.49E-01	phospholipase A 2A	
	AT1G55450.2	AT1G55450	--	804	754	346	217	0.13 ± 0.21	-0.15 ± 0.38	-1.15 ± 0.30	-0.25 ± 0.46	1.00E+00	1.00E+00	4.94E-03	1.00E+00	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	
	AT4G25110.1	AT4G25110	MC2	514	480	338	293	0.11 ± 0.31	-0.19 ± 0.29	-1.17 ±							

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes					
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN		LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description			
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis			TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2		6 H	15 H	
*	AT4G14710.2	AT4G14710	AtARD2	2966	2415	1506	2164	0.54 ± 0.20	-0.11 ± 0.51	-1.21 ± 0.24	0.00 ± 0.24	3.72E-01	1.00E+00	3.02E-05	1.00E+00	RmlC-like cupins superfamily protein	
	AT3G27610.2	AT3G27610	--	592	613	237	249	-0.21 ± 0.37	-0.20 ± 0.37	-1.22 ± 0.30	-0.58 ± 0.47	1.00E+00	1.00E+00	1.76E-03	7.96E-01	Nucleotidyl transferase superfamily protein	
	AT5G20300.2	AT5G20300	TOC90	812	711	330	477	-0.81 ± 0.39	-1.58 ± 0.33	-1.22 ± 0.38	0.17 ± 0.29	1.00E+00	3.04E-04	3.14E-02	1.00E+00	Avirulence induced gene (AIG1) family protein	
	AT1G77480.2	AT1G77480	--	483	435	108	115	0.30 ± 0.29	-0.09 ± 0.29	-1.22 ± 0.41	-0.07 ± 0.46	1.00E+00	1.00E+00	5.58E-02	1.00E+00	Eukaryotic aspartyl protease family protein	
	AT3G02470.4	AT3G02470	SAMDC	1584	644	3487	4278	1.96 ± 1.71	-0.10 ± 0.75	-1.23 ± 0.21	0.50 ± 0.58	1.00E+00	1.00E+00	6.92E-07	9.66E-01	S-adenosylmethionine decarboxylase	
	AT5G19240.1	AT5G19240	--	1146	1214	447	843	0.25 ± 0.22	0.29 ± 0.27	-1.24 ± 0.21	-0.90 ± 0.31	1.00E+00	1.00E+00	6.51E-07	5.57E-02	Glycoprotein membrane precursor GPI-anchored	
	AT3G47040.2	AT3G47040	--	474	506	110	124	-0.47 ± 0.32	-0.36 ± 0.40	-1.25 ± 0.39	-0.48 ± 0.48	1.00E+00	1.00E+00	3.50E-02	9.11E-01	Glycosyl hydrolase family protein	
	AT1G79860.1	AT1G79860	ROPGEF12	327	347	95	73	-0.20 ± 0.34	-0.12 ± 0.41	-1.26 ± 0.45	-1.14 ± 0.53	1.00E+00	1.00E+00	8.71E-02	2.58E-01	RHO guanyl-nucleotide exchange factor 12	
	AT2G47850.1	AT2G47850	--	1521	968	406	185	0.28 ± 0.68	-1.45 ± 3.57	-1.28 ± 0.26	0.21 ± 2.24	1.00E+00	1.00E+00	7.80E-05	1.00E+00	Zinc finger C-x8-C-x5-C-x3-H type family protein	
	AT1G19250.1	AT1G19250	FMO1	73	57	99	25	0.05 ± 0.67	-0.89 ± 0.72	-1.28 ± 0.42	-0.95 ± 0.86	1.00E+00	1.00E+00	4.53E-02	8.62E-01	flavin-dependent monooxygenase 1	
	AT2G22122.1	AT2G22122	--	1489	1547	484	675	-0.25 ± 0.16	-0.32 ± 0.19	-1.29 ± 0.19	-0.96 ± 0.22	1.00E+00	1.00E+00	4.67E-09	3.08E-04		
	AT1G17410.1	AT1G17410	--	170	180	104	98	0.23 ± 0.42	0.27 ± 0.47	-1.29 ± 0.46	-0.41 ± 0.65	1.00E+00	1.00E+00	8.85E-02	1.00E+00	Nucleoside diphosphate kinase family protein	
	AT4G25080.3	AT4G25080	CHLM	626	685	315	319	0.03 ± 0.35	0.19 ± 0.31	-1.30 ± 0.25	-0.28 ± 0.34	1.00E+00	1.00E+00	1.77E-05	9.73E-01	magnesium-protoporphyrin IX methyltransferase	
	AT3G63460.3	AT3G63460	SEC31B	1338	1429	641	920	-0.15 ± 0.40	-0.04 ± 0.65	-1.30 ± 0.46	0.72 ± 0.40	1.00E+00	1.00E+00	8.83E-02	4.23E-01	transducin family protein / WD-40 repeat family protein	
	AT5G14200.3	AT5G14200	IMD1	908	829	306	357	-0.06 ± 0.37	-0.46 ± 0.35	-1.32 ± 0.26	-0.61 ± 0.42	1.00E+00	1.00E+00	2.26E-05	6.58E-01	isopropylmalate dehydrogenase 1	
	AT1G35340.3	AT1G35340	--	0	3	130	147	NA	NA	4.86 ± 4.80	-1.32 ± 0.42	-0.40 ± 0.57	NA	NA	4.31E-02	1.00E+00	ATP-dependent protease La (LON) domain protein
	AT5G26320.1	AT5G26320	--	349	358	71	59	0.00 ± 0.42	-0.04 ± 0.52	-1.32 ± 0.47	-1.48 ± 0.57	1.00E+00	1.00E+00	8.85E-02	1.10E-01	TRAF-like family protein	
	AT1G70770.2	AT1G70770	--	176	175	189	192	0.79 ± 0.95	0.70 ± 0.94	-1.32 ± 0.37	-0.33 ± 0.34	1.00E+00	1.00E+00	1.28E-02	9.27E-01	Protein of unknown function DUF2359, transmembrane	
	AT3G12490.1	AT3G12490	CYSB	1080	843	365	713	0.14 ± 0.85	-0.82 ± 0.84	-1.33 ± 0.40	-0.03 ± 0.40	1.00E+00	1.00E+00	2.69E-02	1.00E+00	cystatin B	
	AT3G16450.1	AT3G16450	JAL33	1737	1696	2710	3047	-0.76 ± 0.45	-0.99 ± 0.40	-1.33 ± 0.18	-0.37 ± 0.36	1.00E+00	4.99E-01	1.65E-10	8.97E-01	Mannose-binding lectin superfamily protein	
	AT1G48500.2	AT1G48500	JAZ4	1936	1940	306	358	0.10 ± 0.18	0.02 ± 0.27	-1.33 ± 0.45	-0.91 ± 0.45	1.00E+00	1.00E+00	5.90E-02	3.22E-01	jasmonate-zim-domain protein 4	
	AT1G53165.1	AT1G53165	AtMAP4Ka1	2003	1814	861	671	0.12 ± 0.39	-0.26 ± 0.44	-1.33 ± 0.20	-0.16 ± 0.24	1.00E+00	1.00E+00	1.36E-08	1.00E+00	Protein kinase superfamily protein	
	AT1G14710.2	AT1G14710	--	1246	1141	153	104	-0.14 ± 0.48	-0.52 ± 0.45	-1.33 ± 0.37	1.29 ± 0.61	1.00E+00	1.00E+00	9.90E-03	2.73E-01	hydroxyproline-rich glycoprotein family protein	
	AT5G22340.2	AT5G22340	--	211	218	96	91	-0.08 ± 0.75	-0.09 ± 0.75	-1.34 ± 0.47	0.28 ± 0.88	1.00E+00	1.00E+00	8.06E-02	1.00E+00		
	AT4G38360.1	AT4G38360	LAZ1	261	222	176	143	0.25 ± 0.57	-0.31 ± 0.58	-1.34 ± 0.43	0.40 ± 0.44	1.00E+00	1.00E+00	4.04E-02	9.54E-01	Protein of unknown function (DUF300)	
	AT4G13770.1	AT4G13770	CYP83A1	9566	9981	3445	13406	0.18 ± 0.16	0.21 ± 0.16	-1.34 ± 0.19	-0.37 ± 0.08	1.00E+00	1.00E+00	5.60E-10	1.10E-04	cytochrome P450, family 83, subfamily A, polypeptide 1	
	AT5G61410.2	AT5G61410	RPE	303	427	291	299	-0.05 ± 0.62	0.74 ± 0.55	-1.35 ± 0.43	-0.37 ± 0.27	1.00E+00	1.00E+00	3.65E-02	7.26E-01	D-ribulose-5-phosphate-3-epimerase	
	AT3G20380.1	AT3G20380	--	4046	4468	415	602	0.35 ± 0.24	0.51 ± 0.28	-1.35 ± 0.28	-0.94 ± 0.23	1.00E+00	1.00E+00	1.10E-04	1.65E-03	TRAF-like family protein	
	AT3G19710.1	AT3G19710	BCAT4	13070	14262	8672	25135	0.30 ± 0.23	0.44 ± 0.23	-1.37 ± 0.18	-0.38 ± 0.13	1.00E+00	1.00E+00	2.18E-11	5.25E-02	branched-chain aminotransferase4	
	AT4G30190.2	AT4G30190	HA2	241	98	140	140	1.64 ± 1.08	-0.69 ± 0.81	-1.37 ± 0.44	0.68 ± 0.42	1.00E+00	1.00E+00	4.29E-02	5.55E-01	H(+)-ATPase 2	
	AT1G51890.2	AT1G51890	--	139	224	337	402	23.21 ± 4.79	11.21 ± 1.55	-1.38 ± 0.48	-0.62 ± 0.38	3.25E-04	5.40E-10	7.56E-02	5.51E-01	Leucine-rich repeat protein kinase family protein	
	AT5G20250.3	AT5G20250	DIN10	1658	861	1246	389	0.75 ± 0.72	-1.50 ± 0.53	-1.39 ± 0.28	0.12 ± 0.64	1.00E+00	2.39E-01	6.92E-05	1.00E+00	Raffinose synthase family protein	
	AT5G42930.1	AT5G42930	--	83	79	134	107	0.00 ± 0.54	-0.25 ± 0.59	-1.40 ± 0.42	-0.41 ± 0.52	1.00E+00	1.00E+00	2.64E-02	9.84E-01	alpha/beta-Hydrolases superfamily protein	
	AT1G63670.3	AT1G63670	TRM12	350	350	162	55	0.11 ± 0.61	0.02 ± 0.59	-1.40 ± 0.50	-0.42 ± 1.86	1.00E+00	1.00E+00	9.64E-02	1.00E+00	Protein of unknown function (DUF3741)	
	AT1G21100.1	AT1G21100	IGMT1	1408	1146	1590	860	0.49 ± 0.26	-0.17 ± 0.43	-1.41 ± 0.18	-0.81 ± 0.47	1.00E+00	1.00E+00	3.96E-13	4.88E-01	O-methyltransferase family protein	
	AT4G38510.5	AT4G38510	VAB2	653	322	700	487	1.83 ± 0.98	0.23 ± 0.60	-1.44 ± 0.18	1.31 ± 0.54	1.00E+00	1.00E+00	6.56E-13	1.57E-01	ATPase, V1 complex, subunit B protein	
	AT1G01830.1	AT1G01830	--	361	650	311	358	0.35 ± 1.19	1.57 ± 1.08	-1.44 ± 0.45	-0.46 ± 1.53	1.00E+00	1.00E+00	3.30E-02	1.00E+00	ARM repeat superfamily protein	
	AT5G23020.1	AT5G23020	IMS2	9775	10366	9718	23245	0.28 ± 0.13	0.35 ± 0.16	-1.47 ± 0.11	-0.40 ± 0.13	9.60E-01	7.39E-01	1.06E-34	4.20E-02	2-isopropylmalate synthase 2	
	AT5G23010.1	AT5G23010	MAM1	2858	2916	2961	6492	0.37 ± 0.17	0.34 ± 0.20	-1.49 ± 0.17	-0.33 ± 0.19	9.54E-01	1.00E+00	5.59E-15	4.88E-01	methylthioalkylmalate synthase 1	
	AT3G26850.2	AT3G26850	--	116	109	125	103	-0.64 ± 2.32	-1.05 ± 2.15	-1.49 ± 0.46	-0.22 ± 0.57	1.00E+00	1.00E+00	2.95E-02	1.00E+00	histone-lysine N-methyltransferases	
	AT1G49570.1	AT1G49570	--	3305	3866	1091	2709	0.17 ± 0.16	0.49 ± 0.28	-1.49 ± 0.36	-0.10 ± 0.27	1.00E+00	1.00E+00	1.54E-03	1.00E+00	Peroxidase superfamily protein	
	AT4G25090.1	AT4G25090	--	715	712	404	495	-0.24 ± 0.24	-0.35 ± 0.26	-1.51 ± 0.36	-0.90 ± 0.24	1.00E+00	1.00E+00	1.24E-03	3.95E-03	Riboflavin synthase-like superfamily protein	
	AT5G59090.3	AT5G59090	SBT4.12	372	449	515	386	-0.12 ± 0.63	0.32 ± 0.61	-1.51 ± 0.41	-0.07 ± 0.61	1.00E+00	1.00E+00	8.77E-03	1.00E+00	subtilase 4.12	
	AT2G07698.1	AT2G07698	--	418	401	267	287	0.60 ± 0.30	0.43 ± 0.38	-1.52 ± 0.29	-0.02 ± 0.48	1.00E+00	1.00E+00	1.85E-05	1.00E+00	ATPase, F1 complex, alpha subunit protein	
	AT1G13930.2	AT1G13930	--	10143	6348	6068	5262	1.57 ± 0.93	0.46 ± 0.59	-1.54 ± 0.18	0.56 ± 0.25	1.00E+00	1.00E+00	1.55E-14	2.29E-01		
	AT3G03670.1	AT3G03670	--	319	329	296	184	0.17 ± 0.31	0.16 ± 0.37	-1.56 ± 0.50	-0.85 ± 0.59	1.00E+00	1.00E+00	4.34E-02	6.67E-01	Peroxidase superfamily protein	
	AT4G36220.1	AT4G36220	FAH1	1139	1193	347	360	-0.06 ± 0.32	-0.01 ± 0.33	-1.57 ± 0.23	-1.12 ± 0.47	1.00E+00	1.00E+00	2.33E-09	1.69E-01	ferulic acid 5-hydroxylase 1	
	AT3G27430.3	AT3G27430	PBB1	355	246	307	344	1.69 ± 0.79	0.87 ± 1.17	-1.57 ± 0.32	0.00 ± 0.30	9.86E-01	1.00E+00	5.25E-05	1.00E+00	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	
	AT2G16380.1	AT2G16380	--	313	327	146	122	0.00 ± 0.42	0.04 ± 0.56	-1.59 ± 0.38	-1.07 ± 0.54	1.00E+00	1.00E+00	1.54E-03	3.34E-01	Sec14p-like phosphatidylinositol transfer family protein	
	AT5G22555.1	AT5G22555	--	28	34	129	76	-0.35 ± 0.92	0.03 ± 0.98	-1.60 ± 0.49	0.00 ± 0.62	1.00E+00	1.00E+00	3.08E-02	1.00E+00		
	AT4G06477.1	AT4G06477	--	781	570	476	878	1.40 ± 0.46	0.66 ± 0.43								

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT2G01010.1	AT2G01010	--	299	213	200	228	0.89 ± 0.48	-0.04 ± 0.43	-1.85 ± 0.38	-0.02 ± 0.76	1.00E+00	1.00E+00	8.07E-05	1.00E+00	rRNA
	AT5G59090.2	AT5G59090	SBT4.12	107	127	197	149	1.12 ± 2.07	1.40 ± 1.89	-1.89 ± 0.36	0.50 ± 0.38	1.00E+00	1.00E+00	1.74E-05	7.36E-01	subtilase 4.12
	AT5G61240.2	AT5G61240	--	523	420	171	195	1.12 ± 3.52	0.55 ± 3.40	-1.90 ± 0.55	0.58 ± 0.48	1.00E+00	1.00E+00	1.67E-02	8.13E-01	Leucine-rich repeat (LRR) family protein
	ATMG01190.1	ATMG01190	ATP1	232	152	165	182	1.04 ± 0.58	-0.10 ± 0.58	-1.92 ± 0.40	-0.55 ± 0.59	1.00E+00	1.00E+00	1.43E-04	9.43E-01	ATP synthase subunit 1
	AT4G39838.1	AT4G39838	--	155	102	89	52	1.43 ± 0.74	0.43 ± 0.74	-1.93 ± 0.51	0.66 ± 0.76	1.00E+00	1.00E+00	6.11E-03	9.60E-01	
	ATMG00090.1	ATMG00090	RPS3	126	94	68	72	1.19 ± 0.62	0.46 ± 0.64	-1.93 ± 0.64	-0.31 ± 0.79	1.00E+00	1.00E+00	5.41E-02	1.00E+00	structural constituent of ribosome;protein binding
	AT2G42850.1	AT2G42850	CYP718	971	1000	115	164	0.22 ± 0.17	0.21 ± 0.30	-1.94 ± 0.53	-1.32 ± 0.58	1.00E+00	1.00E+00	8.04E-03	1.98E-01	cytochrome P450, family 718
	AT2G33620.3	AT2G33620	AHL10	577	630	225	357	-0.27 ± 0.31	-0.10 ± 0.29	-1.94 ± 0.41	0.31 ± 0.48	1.00E+00	1.00E+00	1.36E-04	1.00E+00	AT hook motif DNA-binding family protein
	ATCG00350.1	ATCG00350	PSAA	54	71	68	51	0.64 ± 0.66	1.15 ± 0.88	-1.97 ± 0.61	0.01 ± 0.81	1.00E+00	1.00E+00	3.23E-02	1.00E+00	Photosystem I, PsA/PsaB protein
	AT2G01750.2	AT2G01750	MAP70-3	90	120	59	46	0.02 ± 0.84	0.67 ± 1.03	-1.98 ± 0.70	-0.08 ± 1.05	1.00E+00	1.00E+00	8.82E-02	1.00E+00	microtubule-associated proteins 70-3
	AT3G41768.1	AT3G41768	--	561452	462726	459825	480562	1.20 ± 0.19	0.71 ± 0.25	-1.98 ± 0.31	-0.39 ± 0.54	3.58E-07	2.29E-01	3.34E-08	1.00E+00	rRNA
	AT3G43720.2	AT3G43720	LTPG2	56	61	73	85	0.20 ± 0.80	0.30 ± 0.76	-1.99 ± 0.72	0.36 ± 0.50	1.00E+00	1.00E+00	9.53E-02	1.00E+00	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT5G60100.1	AT5G60100	PRR3	760	742	98	64	-0.35 ± 0.27	-0.54 ± 0.61	-2.00 ± 0.63	0.17 ± 1.91	1.00E+00	1.00E+00	3.61E-02	1.00E+00	pseudo-response regulator 3
	AT5G28630.1	AT5G28630	--	424	457	110	84	0.24 ± 0.26	0.30 ± 0.28	-2.02 ± 0.46	-0.78 ± 0.51	1.00E+00	1.00E+00	7.15E-04	6.02E-01	glycine-rich protein
	AT5G18240.4	AT5G18240	MYR1	277	205	154	72	0.58 ± 3.31	-0.35 ± 3.32	-2.02 ± 0.62	-0.29 ± 1.32	1.00E+00	1.00E+00	2.85E-02	1.00E+00	myb-related protein 1
	ATMG01390.1	ATMG01390	RRN18	15599	13840	19159	19796	1.20 ± 0.23	0.87 ± 0.31	-2.04 ± 0.30	-0.56 ± 0.53	1.10E-04	2.25E-01	2.69E-09	8.85E-01	
	AT5G18380.2	AT5G18380	--	2120	2293	1689	834	-0.79 ± 0.50	-0.71 ± 0.63	-2.05 ± 0.74	0.43 ± 1.17	1.00E+00	1.00E+00	9.50E-02	1.00E+00	Ribosomal protein S5 domain 2-like superfamily protein
	AT2G47940.2	AT2G47940	DEG2	657	434	519	565	0.76 ± 0.79	-0.46 ± 0.71	-2.06 ± 0.29	1.15 ± 0.47	1.00E+00	1.00E+00	7.29E-10	1.48E-01	DEGP protease 2
	AT5G18240.3	AT5G18240	MYR1	90	69	87	44	4.25 ± 1.62	3.79 ± 1.63	-2.11 ± 0.56	0.45 ± 1.48	4.57E-01	6.56E-01	6.26E-03	1.00E+00	myb-related protein 1
	AT5G02470.3	AT5G02470	DPA	185	217	86	56	0.34 ± 0.85	0.65 ± 0.84	-2.11 ± 0.49	0.88 ± 1.87	1.00E+00	1.00E+00	8.90E-04	1.00E+00	Transcription factor DP
	AT3G09560.3	AT3G09560	PAH1	30	50	209	360	-0.09 ± 2.67	1.08 ± 1.55	-2.14 ± 0.76	0.36 ± 1.42	1.00E+00	1.00E+00	8.99E-02	1.00E+00	Lipin family protein
	AT5G50520.1	AT5G50520	--	1135	1626	409	681	-0.44 ± 0.68	0.50 ± 0.52	-2.15 ± 0.66	0.97 ± 0.53	1.00E+00	1.00E+00	2.83E-02	4.28E-01	Major facilitator superfamily protein
	AT1G35580.1	AT1G35580	CINV1	920	680	519	1886	-0.43 ± 0.37	-2.01 ± 0.88	-2.15 ± 0.33	0.11 ± 0.78	1.00E+00	7.04E-01	8.43E-09	1.00E+00	cytosolic invertase 1
	AT5G26850.3	AT5G26850	--	783	1121	226	619	-2.25 ± 2.13	-0.55 ± 1.99	-2.19 ± 0.77	-0.46 ± 1.95	1.00E+00	1.00E+00	7.98E-02	1.00E+00	Uncharacterized protein
	AT2G31960.2	AT2G31960	GSL03	2434	1092	792	1316	1.49 ± 1.37	-0.59 ± 0.82	-2.26 ± 0.38	2.52 ± 1.05	1.00E+00	1.00E+00	4.63E-07	1.60E-01	glucan synthase-like 3
	AT2G43020.1	AT2G43020	PAO2	684	2118	671	563	0.44 ± 0.49	2.60 ± 0.29	-2.39 ± 0.40	-0.17 ± 0.61	1.00E+00	1.89E-16	2.99E-07	1.00E+00	polyamine oxidase 2
	AT1G34510.1	AT1G34510	--	275	276	40	19	0.09 ± 0.41	0.00 ± 0.42	-2.43 ± 0.84	-2.05 ± 1.10	1.00E+00	1.00E+00	6.99E-02	4.02E-01	Peroxidase superfamily protein
	ATCG01210.1	ATCG01210	RRN16S.2	3710	4246	5879	4702	0.45 ± 0.42	0.69 ± 0.60	-2.50 ± 0.49	-0.53 ± 0.85	1.00E+00	1.00E+00	2.93E-05	1.00E+00	
	ATCG00920.1	ATCG00920	RRN16S.1	3710	4246	5879	4702	0.45 ± 0.42	0.69 ± 0.60	-2.50 ± 0.49	-0.53 ± 0.85	1.00E+00	1.00E+00	2.93E-05	1.00E+00	
	ATCG00020.1	ATCG00020	PSBA	202	169	194	165	1.28 ± 0.44	0.81 ± 0.51	-2.54 ± 0.58	-0.65 ± 0.66	2.55E-01	1.00E+00	5.67E-04	9.17E-01	photosystem II reaction center protein A
	AT3G14415.3	AT3G14415	GOX2	93	32	148	113	2.52 ± 2.13	0.36 ± 2.17	-2.54 ± 0.75	1.25 ± 0.95	1.00E+00	1.00E+00	1.88E-02	7.43E-01	Aldolase-type TIM barrel family protein
	AT3G05165.1	AT3G05165	--	1429	1019	692	1100	1.76 ± 0.67	1.02 ± 0.85	-2.61 ± 0.34	-0.33 ± 0.31	4.60E-01	1.00E+00	3.10E-12	8.69E-01	Major facilitator superfamily protein
	AT4G00560.3	AT4G00560	--	41	47	20	18	-1.17 ± 2.25	-0.76 ± 1.28	-2.63 ± 0.95	1.02 ± 1.16	1.00E+00	1.00E+00	9.84E-02	9.57E-01	NAD(P)-binding Rossmann-fold superfamily protein
	ATCG00950.1	ATCG00950	RRN23S.1	5190	4884	7263	6063	0.87 ± 0.33	0.66 ± 0.45	-2.65 ± 0.57	-0.36 ± 0.84	4.76E-01	1.00E+00	2.26E-04	1.00E+00	
	ATCG01180.1	ATCG01180	RRN23S.2	5190	4884	7263	6063	0.87 ± 0.33	0.66 ± 0.45	-2.65 ± 0.57	-0.36 ± 0.84	4.76E-01	1.00E+00	2.26E-04	1.00E+00	
	AT4G32930.2	AT4G32930	--	119	82	88	232	1.71 ± 2.23	0.84 ± 2.30	-2.89 ± 0.83	0.76 ± 0.29	1.00E+00	1.00E+00	1.62E-02	1.03E-01	
	AT4G25770.2	AT4G25770	--	135	79	130	76	0.57 ± 0.85	-1.27 ± 0.74	-2.89 ± 0.47	0.63 ± 0.95	1.00E+00	1.00E+00	1.02E-07	1.00E+00	alpha/beta-Hydrolases superfamily protein
	AT2G30390.2	AT2G30390	FC2	74	63	47	51	0.06 ± 0.75	-0.51 ± 1.02	-2.99 ± 0.91	-2.85 ± 1.62	1.00E+00	1.00E+00	2.74E-02	4.67E-01	ferrochelatase 2
	ATCG00490.1	ATCG00490	RBCL	69	74	105	106	1.54 ± 0.80	1.59 ± 0.74	-3.10 ± 0.67	-0.45 ± 0.76	1.00E+00	8.74E-01	2.26E-04	1.00E+00	ribulose-bisphosphate carboxylases
	AT5G55300.2	AT5G55300	TOP1α	184	75	65	42	1.22 ± 3.50	-1.63 ± 2.13	-3.12 ± 0.57	0.62 ± 0.77	1.00E+00	1.00E+00	5.17E-06	9.79E-01	DNA topoisomerase I alpha
	AT1G48410.3	AT1G48410	AGO1	443	183	351	309	2.80 ± 3.67	1.13 ± 1.40	-3.20 ± 0.57	0.29 ± 0.34	1.00E+00	1.00E+00	1.93E-06	9.69E-01	Stabilizer of iron transporter SufD / Polynucleotidyl transferase
	AT2G30520.2	AT2G30520	RPT2	293	87	121	235	1.78 ± 3.63	-1.80 ± 2.21	-3.32 ± 0.87	0.94 ± 0.80	1.00E+00	1.00E+00	5.66E-03	8.17E-01	Phototropic-responsive NPH3 family protein
	ATMG00510.1	ATMG00510	NAD7	28	21	18	19	0.76 ± 0.98	-0.17 ± 1.50	-3.40 ± 1.23	-0.93 ± 1.41	1.00E+00	1.00E+00	9.91E-02	1.00E+00	NADH dehydrogenase subunit 7
	AT1G22920.2	AT1G22920	CSN5A	99	41	115	148	2.50 ± 1.58	0.72 ± 2.24	-3.59 ± 0.64	1.46 ± 0.67	1.00E+00	1.00E+00	2.31E-06	2.41E-01	COP9 signalosome 5A
	AT2G01830.3	AT2G01830	WOL	245	847	56	1074	-1.16 ± 3.70	1.95 ± 2.45	-3.63 ± 0.86	-0.38 ± 0.95	1.00E+00	1.00E+00	1.29E-03	1.00E+00	CHASE domain containing histidine kinase protein
	AT1G80640.2	AT1G80640	--	33	51	47	41	0.01 ± 1.18	0.99 ± 1.08	-4.26 ± 1.38	-0.26 ± 1.99	1.00E+00	1.00E+00	4.65E-02	1.00E+00	Protein kinase superfamily protein
	AT5G13220.3	AT5G13220	JAZ10	5	4	33	13	-0.30 ± 4.30	-0.81 ± 4.28	-4.44 ± 1.41	-0.45 ± 2.31	1.00E+00	1.00E+00	3.82E-02	1.00E+00	jasmonate-zim-domain protein 10
	AT2G41430.5	AT2G41430	ERD15	2364	406	1817	1683	3.11 ± 3.94	-0.74 ± 0.93	-5.20 ± 0.36	1.43 ± 1.22	1.00E+00	1.00E+00	5.51E-42	8.25E-01	dehydration-induced protein (ERD15)
	AT3G55630.1	AT3G55630	DFD	0	25	25	8	NA ± NA	8.06 ± 2.04	-5.23 ± 1.54	6.33 ± 2.47	NA	9.06E-03	2.03E-02	1.15E-01	DHFS-FPGS homolog D
	AT2G47640.4	AT2G47640	--	373	649	39	153	-1.13 ± 2.32	0.49 ± 0.70	-5.89 ± 1.78	-1.83 ± 1.26	1.00E+00	1.00E+00	2.53E-02	6.56E-01	Small nuclear ribonucleoprotein family protein
	AT1G10340.2	AT1G10340	--	8	38	36	20	6.46 ± 4.79	8.64 ± 3.47	-6.33 ± 1.54	0.52 ± 1.52					

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes					
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description	
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line			
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H		
	AT5G43910.1	AT5G43910	--	16	22	12	9	0.29 ± 2.44	0.90 ± 2.28	-7.15 ± 2.08	-0.17 ± 3.34	1.00E+00	1.00E+00	1.00E+00	1.71E-02	1.00E+00	ptkB-like carbohydrate kinase family protein
	AT4G18740.2	AT4G18740	--	7	3	12	6	1.77 ± 4.06	-0.05 ± 4.64	-7.17 ± 2.19	-0.05 ± 1.51	1.00E+00	1.00E+00	2.81E-02	1.00E+00		Rho termination factor
	AT2G33120.3	AT2G33120	SAR1	73	79	13	22	1.56 ± 1.29	1.64 ± 1.20	-7.21 ± 2.43	3.46 ± 1.80	1.00E+00	1.00E+00	6.03E-02	3.76E-01		synaptobrevin-related protein 1
	AT4G08980.3	AT4G08980	FBW2	5	36	14	12	-5.84 ± 4.80	2.51 ± 1.92	-7.37 ± 2.00	-7.06 ± 3.77	1.00E+00	1.00E+00	8.14E-03	3.98E-01		F-BOX WITH WD-40 2
	AT2G36480.3	AT2G36480	--	72	86	14	2	0.06 ± 0.83	0.47 ± 0.99	-7.40 ± 1.99	-4.75 ± 4.81	1.00E+00	1.00E+00	7.32E-03	NA		ENTH/VHS family protein
	AT1G10670.3	AT1G10670	ACLA-1	34	21	15	24	1.08 ± 2.39	-0.14 ± 1.17	-7.50 ± 1.95	-0.74 ± 2.09	1.00E+00	1.00E+00	4.85E-03	1.00E+00		ATP-citrate lyase A-1
	AT1G77890.2	AT1G77890	--	103	89	17	33	-0.70 ± 1.16	-1.48 ± 0.85	-7.68 ± 2.22	2.91 ± 1.74	1.00E+00	1.00E+00	1.66E-02	5.25E-01		DNA-directed RNA polymerase II protein
	AT3G21600.2	AT3G21600	--	72	65	19	36	0.25 ± 0.94	-0.14 ± 0.89	-7.82 ± 1.89	0.07 ± 1.26	1.00E+00	1.00E+00	1.70E-03	1.00E+00		Senescence/dehydration-associated protein-related
	AT1G18870.2	AT1G18870	ICS2	46	62	20	111	1.89 ± 2.33	2.36 ± 1.90	-7.87 ± 1.86	-0.28 ± 0.87	1.00E+00	1.00E+00	1.15E-03	1.00E+00		isochorismate synthase 2
	AT1G70280.1	AT1G70280	--	105	115	21	20	-0.03 ± 1.04	0.14 ± 1.11	-7.96 ± 2.10	0.58 ± 0.93	1.00E+00	1.00E+00	5.80E-03	1.00E+00		NHL domain-containing protein
	AT5G55730.2	AT5G55730	FLA1	7	0	21	0	6.33 ± 4.79	NA ± NA	-7.97 ± 1.99	NA ± NA	1.00E+00	NA	2.63E-03	NA		FASCICLIN-like arabinogalactan 1
	AT1G62610.1	AT1G62610	--	17	73	23	31	7.54 ± 4.35	9.58 ± 1.66	-8.10 ± 2.06	1.20 ± 2.92	1.00E+00	3.57E-06	3.45E-03	1.00E+00		NAD(P)-binding Rossmann-fold superfamily protein
	AT1G59265.1	AT1G59265	--	0	2	24	13	NA ± NA	4.31 ± 4.81	-8.14 ± 1.81	-0.23 ± 3.15	NA	NA	3.91E-04	1.00E+00		transposable element gene
	AT3G13030.3	AT3G13030	--	328	225	24	56	0.56 ± 0.69	-0.62 ± 0.73	-8.16 ± 1.88	0.84 ± 1.97	1.00E+00	1.00E+00	7.60E-04	1.00E+00		hAT transposon superfamily protein
	AT3G18200.2	AT3G18200	UMAMIT4	63	39	25	35	-0.55 ± 3.28	-8.76 ± 3.46	-8.22 ± 1.80	-1.67 ± 1.79	1.00E+00	4.55E-01	2.86E-04	9.39E-01		nodulin MtN21 /EamA-like transporter family protein
	AT5G09890.2	AT5G09890	--	50	45	26	9	-1.10 ± 0.82	-1.81 ± 0.86	-8.26 ± 1.87	-1.33 ± 2.12	1.00E+00	9.06E-01	5.67E-04	1.00E+00		Protein kinase family protein
	AT5G43960.2	AT5G43960	--	10	192	358	1141	-6.81 ± 4.79	4.10 ± 2.76	-8.27 ± 0.97	0.36 ± 1.11	1.00E+00	1.00E+00	1.08E-14	1.00E+00		Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain
	AT1G10920.1	AT1G10920	LOV1	90	71	28	50	1.17 ± 2.05	0.56 ± 2.05	-8.36 ± 1.73	-0.06 ± 0.62	1.00E+00	1.00E+00	9.48E-05	1.00E+00		NB-ARC domain-containing disease resistance protein
	AT1G68010.2	AT1G68010	HPR	15	10	28	22	0.02 ± 2.51	-1.54 ± 3.66	-8.40 ± 1.79	-0.85 ± 1.33	1.00E+00	1.00E+00	1.69E-04	1.00E+00		hydroxypyruvate reductase
	AT5G18590.2	AT5G18590	--	0	107	30	49	NA ± NA	22.86 ± 4.79	-8.45 ± 2.67	-7.39 ± 4.75	NA	3.59E-04	3.68E-02	5.97E-01		Galactose oxidase/kelch repeat superfamily protein
	AT5G54130.3	AT5G54130	--	0	10	30	0	NA ± NA	6.75 ± 4.52	-8.47 ± 1.81	NA ± NA	NA	1.00E+00	1.92E-04	NA		Calcium-binding endonuclease/exonuclease/phosphatase family
	AT3G14010.2	AT3G14010	CID4	378	253	85	31	-0.44 ± 0.50	-3.00 ± 2.96	-8.52 ± 1.50	-5.19 ± 2.24	1.00E+00	1.00E+00	1.68E-06	1.91E-01		CTC-interacting domain 4
	AT5G57930.1	AT5G57930	APO2	15	41	31	39	5.89 ± 3.56	7.31 ± 1.74	-8.53 ± 2.68	-8.75 ± 4.79	1.00E+00	3.80E-03	3.48E-02	4.26E-01		Arabidopsis thaliana protein of unknown function (DUF794)
	AT3G01410.2	AT3G01410	--	18	43	31	21	0.60 ± 3.64	2.29 ± 2.06	-8.54 ± 1.91	-7.82 ± 3.42	1.00E+00	1.00E+00	4.43E-04	2.03E-01		Polynucleotidyl transferase, ribonuclease H-like superfamily protein
	AT5G47620.3	AT5G47620	--	48	45	34	79	-0.22 ± 2.27	-0.50 ± 3.11	-8.64 ± 1.86	-0.29 ± 3.25	1.00E+00	1.00E+00	2.09E-04	1.00E+00		RNA-binding (RRM/RBD/RNP motifs) family protein
	AT3G26890.3	AT3G26890	--	244	157	34	58	0.78 ± 4.56	-0.52 ± 3.29	-8.66 ± 1.68	1.28 ± 0.63	1.00E+00	1.00E+00	2.09E-05	3.18E-01		
	AT4G09250.1	AT4G09250	--	0	8	37	0	NA ± NA	6.35 ± 4.79	-8.79 ± 2.13	NA ± NA	NA	1.00E+00	1.73E-03	NA		SPLa/Ryanodine receptor (SPRY) domain-containing protein
	AT1G09840.5	AT1G09840	SK41	201	124	39	15	0.19 ± 0.84	-1.80 ± 1.94	-8.86 ± 1.66	7.37 ± 3.65	1.00E+00	1.00E+00	8.59E-06	3.20E-01		shaggy-like protein kinase 41
	AT2G34150.1	AT2G34150	WAVE1	166	157	40	9	-0.90 ± 0.53	-1.32 ± 0.53	-8.89 ± 1.75	-6.69 ± 3.99	1.00E+00	5.02E-01	3.03E-05	5.19E-01		SCAR family protein
	AT5G49110.1	AT5G49110	--	46	96	41	61	-0.07 ± 3.33	1.58 ± 3.91	-8.91 ± 1.72	-0.45 ± 4.57	1.00E+00	1.00E+00	1.87E-05	1.00E+00		
	AT1G12900.4	AT1G12900	GAPA-2	0	2	41	40	NA ± NA	4.20 ± 4.81	-8.93 ± 2.09	1.13 ± 2.03	NA	NA	9.97E-04	1.00E+00		glyceraldehyde 3-phosphate dehydrogenase A subunit 2
	AT3G20920.2	AT3G20920	--	112	172	49	126	-3.13 ± 2.04	-0.60 ± 1.11	-9.19 ± 1.74	-0.11 ± 0.61	1.00E+00	1.00E+00	1.28E-05	1.00E+00		translocation protein-related
	AT1G03780.3	AT1G03780	TPX2	102	177	52	44	-1.23 ± 1.13	0.49 ± 0.92	-9.26 ± 1.60	-0.61 ± 2.04	1.00E+00	1.00E+00	9.15E-07	1.00E+00		targeting protein for XKLP2
	AT2G47060.3	AT2G47060	PTI1-4	33	72	52	44	-3.00 ± 1.96	0.48 ± 1.01	-9.28 ± 1.60	-3.47 ± 1.50	1.00E+00	1.00E+00	8.09E-07	1.91E-01		Protein kinase superfamily protein
	AT5G40840.3	AT5G40840	SYN2	0	0	56	46	NA ± NA	NA ± NA	-9.38 ± 2.11	-8.98 ± 4.79	NA	NA	5.07E-04	3.98E-01		Rad21/Rec8-like family protein
	AT4G21150.2	AT4G21150	HAP6	98	74	69	70	-0.96 ± 2.22	-3.32 ± 1.90	-9.68 ± 2.08	1.80 ± 1.75	1.00E+00	1.00E+00	2.00E-04	8.96E-01		ribophorin II (RPN2) family protein
	AT4G09770.2	AT4G09770	--	209	150	79	117	0.45 ± 0.71	-0.65 ± 0.75	-9.88 ± 1.54	-1.91 ± 2.85	1.00E+00	1.00E+00	2.85E-08	1.00E+00		TRAF-like family protein
	AT3G53740.1	AT3G53740	--	866	23	419	168	5.92 ± 3.60	-0.92 ± 3.31	-12.31 ± 2.94	1.40 ± 0.77	1.00E+00	1.00E+00	1.35E-03	4.30E-01		Ribosomal protein L36e family protein
H Up-regulated in TPL-OE (6H and 15H) analysis:																	
	AT2G26430.2	AT2G26430	RCY1	64	58	39	93	-0.77 ± 2.15	-1.39 ± 1.99	8.62 ± 1.64	9.96 ± 1.74	1.00E+00	1.00E+00	1.43E-05	6.63E-07		arginine-rich cyclin 1
	AT3G56580.2	AT3G56580	RZF1	1	4	163	188	-3.44 ± 4.84	1.44 ± 4.41	10.67 ± 1.56	9.52 ± 1.74	NA	1.00E+00	1.88E-09	2.32E-06		RING/U-box superfamily protein
	AT4G09770.1	AT4G09770	--	158	211	56	52	-0.83 ± 0.80	0.02 ± 0.75	6.11 ± 1.09	9.11 ± 1.75	1.00E+00	1.00E+00	2.25E-06	9.17E-06		TRAF-like family protein
	AT1G05830.2	AT1G05830	ATX2	17	4	68	18	7.49 ± 2.38	5.56 ± 4.80	9.41 ± 1.57	7.58 ± 2.00	1.33E-01	1.00E+00	3.23E-07	3.67E-03		trithorax-like protein 2
	AT5G41810.2	AT5G41810	--	9	10	35	13	0.56 ± 3.94	0.73 ± 3.73	8.44 ± 1.69	7.11 ± 2.14	1.00E+00	1.00E+00	4.28E-05	1.61E-02		
	AT5G65230.1	AT5G65230	MYB53	194	351	4651	16043	-4.90 ± 0.52	-0.32 ± 0.34	4.31 ± 0.26	5.80 ± 0.22	1.63E-17	1.00E+00	2.40E-59	#####		myb domain protein 53
	AT1G62760.1	AT1G62760	AtPMEI10	8	5	65	349	1.17 ± 1.56	-0.28 ± 2.24	1.47 ± 0.50	5.70 ± 0.47	1.00E+00	1.00E+00	6.11E-02	1.88E-31		Plant invertase/pectin methyltransferase inhibitor superfamily protein
	AT1G05450.2	AT1G05450	--	152	156	278	796	-0.99 ± 0.56	-1.04 ± 0.49	3.46 ± 0.38	4.97 ± 0.27	1.00E+00	9.19E-01	4.83E-17	6.10E-73		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT5G06090.1	AT5G06090	GPAT7	464	428	1480	3329	-0.75 ± 0.37	-1.25 ± 0.30	2.43 ± 0.26	4.18 ± 0.19	1.00E+00	4.99E-03	3.62E-17	#####		glycerol-3-phosphate acyltransferase 7
	AT3G55090.1	AT3G55090	ABCG16	190	151	692	1385	0.58 ± 0.66	-0.12 ± 0.67	3.04 ± 0.38	4.15 ± 0.28	1.00E+00	1.00E+00	9.66E-13	4.52E-46		ABC-2 type transporter family protein
	AT1G21540.1	AT1G21540	--	3	4	28	70	-3.36 ± 3.24	-1.09 ± 2.30	4.29 ± 1.08	4.10 ± 0.77	1.00E+00	1.00E+00	3.04E-03	5.19E-06		AMP-dependent synthetase and ligase family protein

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
*	AT5G59050.2	AT5G59050	--	207	206	92	206	-0.51 ± 0.48	-0.64 ± 0.47	1.59 ± 0.50	3.03 ± 0.41	1.00E+00	1.00E+00	3.62E-02	9.87E-12	mitogen-activated protein kinase kinase kinase 18 alpha/beta-Hydrolases superfamily protein ABC-2 type transporter family protein HXXXD-type acyl-transferase family protein Cytochrome P450 superfamily protein GDSL-like Lipase/Acylhydrolase superfamily protein Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein cytochrome P450, family 86, subfamily B, polypeptide 1 laccase 12 ATP binding microtubule motor family protein RING/U-box superfamily protein other RNA Auxin-responsive family protein Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein RING/U-box superfamily protein HXXXD-type acyl-transferase family protein myb domain protein 41 senescence associated gene 18 heptahelical transmembrane protein1 myb domain protein 9 Matrixin family protein Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein methyl esterase 6 SCAR family protein 4 cytochrome P450, family 86, subfamily A, polypeptide 8 Auxin-responsive family protein Papain family cysteine protease protein affected trafႡcking 2 Uncharacterised protein family (UPF0497) O-Glycosyl hydrolases family 17 protein serine carboxypeptidase-like 28 highly ABA-induced PP2C gene 1 lysophosphatidyl acyltransferase 3 Protein kinase superfamily protein NIMA-related kinase 5 Tetratricopeptide repeat (TPR)-like superfamily protein branched-chain amino acid transaminase 2 RING/U-box superfamily protein 6-phosphogluconate dehydrogenase family protein
	AT1G05100.1	AT1G05100	MAPKKK18	173	163	288	434	0.07 ± 0.50	-0.20 ± 0.61	2.16 ± 0.30	3.02 ± 0.34	1.00E+00	1.00E+00	1.62E-10	4.42E-17	
	AT4G36610.1	AT4G36610	--	2739	2777	3820	8575	-1.05 ± 0.15	-1.15 ± 0.18	1.47 ± 0.18	2.98 ± 0.18	1.46E-09	4.91E-08	3.19E-13	7.79E-56	
	AT1G53270.1	AT1G53270	ABCG10	482	453	987	2230	-0.66 ± 0.38	-1.04 ± 0.35	1.27 ± 0.18	2.96 ± 0.20	1.00E+00	1.79E-01	4.66E-10	3.50E-47	
	AT5G41040.2	AT5G41040	RWP1	2622	2344	3103	6035	0.02 ± 0.21	-0.42 ± 0.24	1.47 ± 0.18	2.96 ± 0.15	1.00E+00	1.00E+00	2.46E-13	3.16E-84	
	AT5G08250.1	AT5G08250	--	530	462	1016	1702	-1.59 ± 0.57	-2.99 ± 0.32	1.32 ± 0.21	2.90 ± 0.17	3.37E-01	2.45E-17	8.09E-08	1.38E-60	
	AT4G26790.2	AT4G26790	--	314	345	488	1315	-1.92 ± 0.68	-1.55 ± 0.65	1.24 ± 0.23	2.83 ± 0.28	3.07E-01	5.76E-01	7.59E-06	4.68E-22	
	AT5G13900.1	AT5G13900	--	1040	1096	914	2238	-0.73 ± 0.23	-0.75 ± 0.29	1.38 ± 0.24	2.81 ± 0.20	1.15E-01	3.68E-01	1.07E-06	6.67E-44	
	AT5G23190.1	AT5G23190	CYP86B1	2119	1963	4405	10266	-0.93 ± 0.25	-1.44 ± 0.25	1.12 ± 0.17	2.76 ± 0.16	3.02E-02	4.01E-06	2.73E-08	3.09E-66	
	AT5G05390.1	AT5G05390	LAC12	96	89	246	776	0.74 ± 0.51	0.49 ± 0.57	2.11 ± 0.53	2.66 ± 0.28	1.00E+00	1.00E+00	2.68E-03	1.92E-19	
	AT4G38950.2	AT4G38950	--	1623	1641	1805	4240	-0.32 ± 0.18	-0.38 ± 0.19	1.10 ± 0.20	2.64 ± 0.19	1.00E+00	1.00E+00	4.15E-06	5.47E-43	
	AT5G55970.1	AT5G55970	--	795	785	1397	2832	-0.77 ± 0.47	-0.97 ± 0.41	1.11 ± 0.19	2.61 ± 0.22	1.00E+00	6.01E-01	6.92E-07	2.11E-30	
	AT5G01732.1	AT5G01732	--	209	218	210	416	0.00 ± 0.35	0.04 ± 0.41	1.26 ± 0.39	2.59 ± 0.30	1.00E+00	1.00E+00	2.98E-02	8.88E-16	
	AT4G17280.1	AT4G17280	--	3659	3725	5480	9007	-0.94 ± 0.13	-1.00 ± 0.18	1.30 ± 0.16	2.56 ± 0.20	2.78E-09	1.55E-05	1.23E-12	5.14E-35	
	AT3G22620.1	AT3G22620	--	8567	8593	8990	18561	-0.80 ± 0.17	-0.95 ± 0.17	1.52 ± 0.16	2.55 ± 0.17	4.76E-04	6.13E-06	1.51E-18	7.84E-50	
	AT3G25030.2	AT3G25030	--	141	197	192	462	0.32 ± 0.91	1.00 ± 0.84	1.04 ± 0.33	2.54 ± 0.46	1.00E+00	1.00E+00	3.81E-02	1.45E-06	
	AT2G37530.1	AT2G37530	--	275	296	241	648	-0.23 ± 0.33	-0.16 ± 0.44	1.12 ± 0.28	2.48 ± 0.30	1.00E+00	1.00E+00	2.48E-03	6.57E-15	
	AT5G41040.1	AT5G41040	RWP1	8668	8776	7953	16916	-0.17 ± 0.15	-0.23 ± 0.17	1.56 ± 0.17	2.48 ± 0.17	1.00E+00	1.00E+00	5.91E-17	3.14E-43	
	AT4G28110.1	AT4G28110	MYB41	351	299	464	636	0.51 ± 0.46	-0.03 ± 0.47	1.86 ± 0.34	2.48 ± 0.26	1.00E+00	1.00E+00	7.04E-06	1.01E-18	
	AT1G71190.2	AT1G71190	SAG18	21	52	13	99	-5.48 ± 3.32	0.53 ± 3.08	5.56 ± 1.88	2.40 ± 0.48	1.00E+00	1.00E+00	6.17E-02	2.41E-05	
	AT5G20270.1	AT5G20270	HHP1	1125	1097	1789	3858	-0.73 ± 0.20	-0.97 ± 0.21	1.06 ± 0.17	2.38 ± 0.16	3.23E-02	5.68E-04	1.76E-07	2.04E-48	
	AT5G16770.1	AT5G16770	MYB9	1090	1060	687	966	-0.19 ± 0.26	-0.39 ± 0.27	1.29 ± 0.22	2.35 ± 0.23	1.00E+00	1.00E+00	9.89E-07	1.51E-21	
	AT2G45040.1	AT2G45040	--	121	131	156	245	-0.74 ± 0.52	-0.58 ± 0.54	1.63 ± 0.41	2.35 ± 0.31	1.00E+00	1.00E+00	2.96E-03	2.79E-12	
	AT3G22600.1	AT3G22600	LTPG5	12671	13047	7251	14333	-0.12 ± 0.16	-0.16 ± 0.17	1.61 ± 0.16	2.30 ± 0.17	1.00E+00	1.00E+00	2.90E-20	2.66E-38	
	AT2G23550.1	AT2G23550	MES6	181	172	92	188	-0.90 ± 0.53	-1.31 ± 0.58	1.60 ± 0.54	2.26 ± 0.41	1.00E+00	7.09E-01	6.03E-02	1.85E-06	
	AT5G01730.1	AT5G01730	SCAR4	1429	1389	1148	2100	-0.54 ± 0.30	-0.76 ± 0.37	1.21 ± 0.20	2.23 ± 0.12	1.00E+00	9.78E-01	5.10E-07	5.60E-69	
	AT2G45970.1	AT2G45970	CYP86A8	2352	2197	2437	4290	-0.46 ± 0.19	-0.82 ± 0.19	1.03 ± 0.16	2.21 ± 0.18	7.21E-01	3.45E-03	5.80E-08	1.99E-30	
	AT5G47530.1	AT5G47530	--	476	492	499	827	-0.29 ± 0.34	-0.29 ± 0.35	1.32 ± 0.25	2.21 ± 0.28	1.00E+00	1.00E+00	1.73E-05	4.01E-13	
	AT2G21430.1	AT2G21430	--	200	215	208	343	-0.66 ± 0.37	-0.52 ± 0.42	1.55 ± 0.32	2.17 ± 0.30	1.00E+00	1.00E+00	9.95E-05	3.45E-11	
	AT3G56275.1	AT3G56275	--	141	137	248	634	-0.53 ± 0.50	-0.85 ± 0.51	1.15 ± 0.36	2.14 ± 0.27	1.00E+00	1.00E+00	3.65E-02	1.00E-13	
	AT3G55480.1	AT3G55480	PAT2	501	400	144	139	0.24 ± 0.50	-0.54 ± 0.80	2.29 ± 0.42	2.06 ± 0.59	1.00E+00	1.00E+00	5.72E-06	9.71E-03	
	AT4G03540.1	AT4G03540	CASPL1C1	212	222	220	396	-0.40 ± 0.63	-0.48 ± 0.56	1.07 ± 0.32	2.03 ± 0.26	1.00E+00	1.00E+00	2.45E-02	2.40E-13	
	AT5G55180.2	AT5G55180	--	357	325	604	819	-0.15 ± 0.55	-0.56 ± 0.47	1.58 ± 0.37	2.02 ± 0.45	1.00E+00	1.00E+00	9.65E-04	2.44E-04	
	AT2G35770.1	AT2G35770	SCPL28	1514	1500	1301	2061	0.02 ± 0.17	-0.10 ± 0.21	1.43 ± 0.22	1.95 ± 0.17	1.00E+00	1.00E+00	1.20E-08	1.26E-26	
	AT5G59220.1	AT5G59220	HAI1	76	76	215	530	0.00 ± 0.65	-0.09 ± 0.84	1.80 ± 0.43	1.91 ± 0.45	1.00E+00	1.00E+00	1.29E-03	7.30E-04	
	AT1G51260.1	AT1G51260	LPAT3	122	101	64	112	-0.01 ± 0.61	-0.75 ± 0.64	2.00 ± 0.58	1.81 ± 0.48	1.00E+00	1.00E+00	1.80E-02	3.51E-03	
	AT2G39110.1	AT2G39110	--	2151	2188	1947	3903	-0.09 ± 0.16	-0.14 ± 0.20	1.05 ± 0.16	1.70 ± 0.14	1.00E+00	1.00E+00	4.67E-09	4.67E-31	
	AT3G20860.1	AT3G20860	NEK5	1711	1794	1929	2074	-0.26 ± 0.17	-0.22 ± 0.21	1.09 ± 0.14	1.63 ± 0.12	1.00E+00	1.00E+00	1.91E-12	2.02E-40	
	AT5G48850.1	AT5G48850	ATSD11	190	199	153	473	-0.27 ± 0.49	-0.24 ± 0.49	1.15 ± 0.34	1.60 ± 0.22	1.00E+00	1.00E+00	1.75E-02	1.39E-11	
	AT1G10070.2	AT1G10070	BCAT-2	249	258	881	548	-0.49 ± 1.12	-0.48 ± 1.08	1.21 ± 0.37	1.39 ± 0.42	1.00E+00	1.00E+00	3.06E-02	1.63E-02	
	AT4G26580.2	AT4G26580	--	214	190	117	170	-0.67 ± 0.47	-1.35 ± 0.88	1.20 ± 0.37	1.38 ± 0.50	1.00E+00	1.00E+00	3.31E-02	7.31E-02	
	AT2G41540.3	AT2G41540	GPDHC1	470	417	385	420	0.19 ± 2.16	-0.25 ± 2.16	1.89 ± 0.60	1.25 ± 0.43	1.00E+00	1.00E+00	4.04E-02	4.78E-02	
	AT5G66780.1	AT5G66780	--	8	8	367	464	1.63 ± 1.79	1.60 ± 1.73	1.12 ± 0.30	1.22 ± 0.21	1.00E+00	1.00E+00	6.85E-03	4.91E-07	
H Down-regulated in TPL-OE (6H and 15H) analysis:																
	AT1G21110.1	AT1G21110	IGMT3	1762	1580	1516	653	0.47 ± 0.17	0.09 ± 0.24	-1.31 ± 0.12	-1.01 ± 0.20	3.06E-01	1.00E+00	1.53E-24	2.76E-05	O-methyltransferase family protein
	AT5G43520.1	AT5G43520	--	1765	1851	926	656	0.06 ± 0.14	0.07 ± 0.25	-1.21 ± 0.20	-1.04 ± 0.28	1.00E+00	1.00E+00	2.40E-07	4.92E-03	Cysteine/Histidine-rich C1 domain family protein
	AT1G26250.1	AT1G26250	EXT18	15463	13921	9164	8468	-0.23 ± 0.15	-0.70 ± 0.20	-1.80 ± 0.45	-1.09 ± 0.26	1.00E+00	4.51E-02	2.50E-03	1.02E-03	Proline-rich extensin-like family protein
	AT4G37070.2	AT4G37070	PLP1	2248	2040	2136	2050	-0.26 ± 0.21	-0.72 ± 0.21	-1.03 ± 0.22	-1.09 ± 0.24	1.00E+00	4.51E-02	1.66E-04	2.18E-04	Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein
	AT3G02850.1	AT3G02850	SKOR	1281	1176	424	714	-0.04 ± 0.30	-0.40 ± 0.32	-1.23 ± 0.27	-1.14 ± 0.17	1.00E+00	1.00E+00	2.54E-04	9.30E-10	STELAR K+ outward rectifier
	AT1G21210.1	AT1G21210	WAK4	1167	1120	191	232	-0.07 ± 0.21	-0.29 ± 0.23	-1.22 ± 0.37	-1.14 ± 0.30	1.00E+00	1.00E+00	2.86E-02	3.13E-03	wall associated kinase 4
	AT3G10710.1	AT3G10710	RHS12	1324	1335	417	363	0.01 ± 0.17	-0.06 ± 0.30	-1.03 ± 0.31	-1.17 ± 0.33	1.00E+00	1.00E+00	2.29E-02	6.78E-03	root hair specific 12
	AT1G05250.1	AT1G05250	PRX2	12884	15227	2395	2259	0.02 ± 0.23	0.38 ± 0.38	-1.05 ± 0.11	-1.17 ± 0.36	1.00E+00	1.00E+00	6.11E-20	1.96E-02	Peroxidase superfamily protein
	AT3G51350.1	AT3G51350	--	3490	3670	801	1036	-0.09 ± 0.13	-0.04 ± 0.20	-1.17 ± 0.25	-1.20 ± 0.14	1.00E+00	1.00E+00	2.57E-04	5.59E-15	Eukaryotic aspartyl protease family protein
	AT5G64100.1	AT5G64100	--	35509	36150	14490	12448	0.01 ± 0.12	-0.04 ± 0.19	-1.09 ± 0.17	-1.21 ± 0.17	1.00E+00	1.00E+00	1.28E-08	1.35E-10	Peroxidase superfamily protein

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
*	AT4G09420.1	AT4G09420	--	842	787	178	241	0.51 ± 0.28	0.25 ± 0.25	-1.04 ± 0.36	-1.36 ± 0.29	1.00E+00	1.00E+00	7.19E-02	1.22E-04	Disease resistance protein (TIR-NBS class)
	AT5G44130.1	AT5G44130	FLA13	1255	1374	343	330	-0.26 ± 0.18	-0.10 ± 0.34	-1.31 ± 0.43	-1.37 ± 0.31	1.00E+00	1.00E+00	4.95E-02	2.56E-04	FASCICLIN-like arabinogalactan protein 13 precursor
	AT4G27290.1	AT4G27290	--	396	402	176	165	0.09 ± 0.35	0.05 ± 0.31	-1.14 ± 0.30	-1.39 ± 0.37	1.00E+00	1.00E+00	5.46E-03	4.07E-03	S-locus lectin protein kinase family protein
	AT3G29250.1	AT3G29250	SDR4	1816	1878	1950	1781	0.03 ± 0.21	0.02 ± 0.23	-1.06 ± 0.22	-1.40 ± 0.24	1.00E+00	1.00E+00	1.30E-04	4.14E-07	NAD(P)-binding Rossmann-fold superfamily protein
	AT1G01580.1	AT1G01580	FRO2	21226	16650	433	2194	0.34 ± 0.26	-0.46 ± 0.26	-1.58 ± 0.29	-1.41 ± 0.28	1.00E+00	1.00E+00	7.05E-06	1.59E-05	ferric reduction oxidase 2
	AT4G08410.1	AT4G08410	--	2349	2062	760	607	-0.46 ± 0.30	-1.09 ± 0.35	-1.02 ± 0.33	-1.42 ± 0.28	1.00E+00	1.11E-01	4.10E-02	1.26E-05	Proline-rich extensin-like family protein
	AT4G22666.1	AT4G22666	--	3048	3386	579	1095	-0.15 ± 0.15	0.03 ± 0.35	-1.10 ± 0.27	-1.44 ± 0.26	1.00E+00	1.00E+00	2.11E-03	2.04E-06	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT4G15390.1	AT4G15390	--	18128	19013	3305	6443	0.14 ± 0.09	0.17 ± 0.16	-1.00 ± 0.14	-1.45 ± 0.16	1.00E+00	1.00E+00	8.63E-11	3.09E-18	HXXXD-type acyl-transferase family protein
	AT3G29250.2	AT3G29250	SDR4	1856	1785	2216	2053	0.00 ± 0.26	-0.24 ± 0.27	-1.07 ± 0.23	-1.45 ± 0.25	1.00E+00	1.00E+00	2.26E-04	2.73E-07	NAD(P)-binding Rossmann-fold superfamily protein
	AT4G22080.1	AT4G22080	RHS14	657	777	208	176	-0.28 ± 0.27	0.12 ± 0.39	-1.11 ± 0.33	-1.47 ± 0.34	1.00E+00	1.00E+00	2.06E-02	4.23E-04	root hair specific 14
	AT5G59680.1	AT5G59680	--	1837	1840	537	555	-0.23 ± 0.18	-0.32 ± 0.20	-1.43 ± 0.30	-1.48 ± 0.23	1.00E+00	1.00E+00	1.69E-04	6.24E-09	Leucine-rich repeat protein kinase family protein
	AT2G24980.1	AT2G24980	--	4263	3898	942	759	-0.46 ± 0.27	-0.92 ± 0.25	-1.50 ± 0.31	-1.49 ± 0.29	1.00E+00	2.56E-02	6.95E-05	9.85E-06	Proline-rich extensin-like family protein
	AT2G45360.1	AT2G45360	--	2401	2415	533	527	0.00 ± 0.20	-0.11 ± 0.27	-1.25 ± 0.22	-1.50 ± 0.29	1.00E+00	1.00E+00	2.02E-06	1.70E-05	Protein of unknown function (DUF1442)
	AT3G18200.1	AT3G18200	UMAMIT4	2073	2260	531	931	-0.04 ± 0.16	0.11 ± 0.28	-1.00 ± 0.27	-1.50 ± 0.28	1.00E+00	1.00E+00	7.19E-03	4.37E-06	nodulin MtN21 /EamA-like transporter family protein
	AT5G57625.1	AT5G57625	AtCAPE5	3847	4104	961	872	-0.06 ± 0.13	0.01 ± 0.34	-1.01 ± 0.20	-1.51 ± 0.21	1.00E+00	1.00E+00	2.27E-05	1.99E-11	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein
	AT5G06640.1	AT5G06640	EXT10	3495	3098	856	852	-0.47 ± 0.30	-1.06 ± 0.30	-1.53 ± 0.35	-1.52 ± 0.28	1.00E+00	3.68E-02	7.67E-04	2.03E-06	Proline-rich extensin-like family protein
	AT5G06630.1	AT5G06630	--	3748	3390	612	510	-0.31 ± 0.21	-0.79 ± 0.22	-1.35 ± 0.33	-1.54 ± 0.29	1.00E+00	2.95E-02	1.98E-03	5.02E-06	proline-rich extensin-like family protein
	AT4G12470.1	AT4G12470	AZI1	452	712	1159	678	-1.33 ± 0.41	0.15 ± 0.55	-1.35 ± 0.37	-1.54 ± 0.27	9.81E-02	1.00E+00	1.08E-02	4.05E-07	azelaic acid induced 1
	AT5G20470.1	AT5G20470	HDK	638	642	128	200	-0.24 ± 0.23	-0.32 ± 0.25	-1.34 ± 0.40	-1.55 ± 0.32	1.00E+00	1.00E+00	2.36E-02	5.30E-05	myosin, putative
	AT1G73120.1	AT1G73120	--	556	560	40	308	-0.04 ± 0.26	-0.20 ± 0.74	-2.51 ± 0.78	-1.55 ± 0.51	1.00E+00	1.00E+00	3.34E-02	3.39E-02	
	AT5G06060.1	AT5G06060	PIP2;4	2965	3120	874	1435	-0.13 ± 0.25	-0.08 ± 0.34	-1.08 ± 0.21	-1.57 ± 0.19	1.00E+00	1.00E+00	3.68E-05	1.93E-14	plasma membrane intrinsic protein 2;4
	AT3G62680.1	AT3G62680	PRP3	4067	3922	1160	1002	-0.20 ± 0.23	-0.43 ± 0.16	-1.25 ± 0.28	-1.57 ± 0.21	1.00E+00	3.24E-01	3.26E-04	2.94E-12	proline-rich protein 3
	AT2G26370.1	AT2G26370	--	42	39	149	109	-0.37 ± 0.81	-0.75 ± 0.91	-1.34 ± 0.40	-1.57 ± 0.55	1.00E+00	1.00E+00	2.08E-02	5.71E-02	MD-2-related lipid recognition domain-containing protein
	AT1G53940.1	AT1G53940	GLIP2	3233	3502	206	297	1.38 ± 0.19	1.47 ± 0.21	-1.40 ± 0.47	-1.57 ± 0.35	1.01E-09	4.87E-09	5.59E-02	1.81E-04	GDSL-motif lipase 2
	AT5G57530.1	AT5G57530	XTH12	1753	2017	147	140	-0.06 ± 0.14	0.23 ± 0.42	-1.60 ± 0.50	-1.62 ± 0.51	1.00E+00	1.00E+00	3.42E-02	2.66E-02	xyloglucan endotransglucosylase/hydrolase 12
	AT4G37060.2	AT4G37060	PLP5	18	33	109	103	-1.90 ± 1.31	0.31 ± 1.00	-1.25 ± 0.39	-1.71 ± 0.56	1.00E+00	1.00E+00	3.30E-02	3.57E-02	PATATIN-like protein 5
	AT2G03720.1	AT2G03720	MRH6	729	798	158	176	-0.18 ± 0.25	-0.03 ± 0.43	-1.19 ± 0.37	-1.71 ± 0.40	1.00E+00	1.00E+00	2.91E-02	6.96E-04	Adenine nucleotide alpha hydrolases-like superfamily protein
	AT5G04960.1	AT5G04960	PME46	3639	3614	765	625	0.06 ± 0.14	-0.05 ± 0.27	-1.16 ± 0.28	-1.74 ± 0.30	1.00E+00	1.00E+00	1.47E-03	4.01E-07	Plant invertase/pectin methyltransferase inhibitor superfamily
	AT2G36690.1	AT2G36690	--	1558	1640	718	1030	0.54 ± 0.22	0.58 ± 0.18	-1.33 ± 0.34	-1.74 ± 0.25	6.48E-01	8.74E-02	3.70E-03	1.59E-10	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
	AT1G19900.1	AT1G19900	--	1293	1341	261	443	0.18 ± 0.30	0.20 ± 0.38	-1.32 ± 0.45	-1.78 ± 0.28	1.00E+00	1.00E+00	6.29E-02	1.35E-08	glyoxal oxidase-related protein
	AT4G25790.1	AT4G25790	AtCAPE4	612	655	132	99	-0.04 ± 0.33	0.03 ± 0.36	-1.53 ± 0.43	-1.79 ± 0.47	1.00E+00	1.00E+00	1.24E-02	3.78E-03	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein
	AT5G24880.1	AT5G24880	--	890	904	161	141	0.16 ± 0.21	0.10 ± 0.24	-1.20 ± 0.33	-1.79 ± 0.45	1.00E+00	1.00E+00	1.09E-02	1.57E-03	
	AT4G12510.1	AT4G12510	AZI5	2565	2841	493	1028	-0.22 ± 0.26	-0.09 ± 0.30	-1.14 ± 0.19	-1.80 ± 0.16	1.00E+00	1.00E+00	3.36E-07	3.01E-26	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT1G66800.1	AT1G66800	--	661	611	845	584	0.24 ± 0.43	-0.08 ± 0.46	-1.27 ± 0.21	-1.81 ± 0.38	1.00E+00	1.00E+00	4.63E-07	6.75E-05	NAD(P)-binding Rossmann-fold superfamily protein
	AT4G15290.1	AT4G15290	ATCSLB05	1584	1659	239	566	-0.06 ± 0.30	-0.01 ± 0.33	-1.56 ± 0.35	-1.81 ± 0.21	1.00E+00	1.00E+00	4.86E-04	3.17E-15	Cellulose synthase family protein
	AT5G22410.1	AT5G22410	RHS18	1014	1100	309	295	0.09 ± 0.18	0.22 ± 0.47	-1.57 ± 0.32	-1.84 ± 0.28	1.00E+00	1.00E+00	5.40E-05	3.89E-09	root hair specific 18
	AT4G12545.1	AT4G12545	--	3233	3013	4490	4963	0.55 ± 0.26	0.24 ± 0.21	-1.59 ± 0.22	-1.87 ± 0.23	1.00E+00	1.00E+00	5.09E-11	2.61E-14	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT2G23620.1	AT2G23620	MES1	418	413	221	206	-0.17 ± 0.28	-0.33 ± 0.30	-1.38 ± 0.33	-1.88 ± 0.51	1.00E+00	1.00E+00	1.66E-03	4.85E-03	methyl esterase 1
	AT2G24720.1	AT2G24720	GLR2.2	451	542	307	215	-1.03 ± 0.40	-0.44 ± 0.30	-1.34 ± 0.34	-1.89 ± 0.30	4.67E-01	1.00E+00	2.89E-03	3.13E-08	glutamate receptor 2.2
	AT4G08620.1	AT4G08620	SULTR1;1	834	903	53	63	-0.38 ± 0.27	-0.22 ± 0.35	-1.73 ± 0.60	-1.89 ± 0.67	1.00E+00	1.00E+00	7.53E-02	6.29E-02	sulphate transporter 1;1
	AT5G36870.1	AT5G36870	GSL09	633	545	82	141	-0.35 ± 0.49	-1.01 ± 0.54	-1.54 ± 0.47	-1.90 ± 0.38	1.00E+00	1.00E+00	2.76E-02	3.22E-05	glucan synthase-like 9
	AT5G49080.1	AT5G49080	--	2936	2648	460	253	-0.36 ± 0.30	-0.85 ± 0.31	-1.77 ± 0.37	-1.91 ± 0.33	1.00E+00	2.71E-01	1.12E-04	4.71E-07	transposable element gene
	AT5G46900.1	AT5G46900	--	3169	3288	568	1512	-0.44 ± 0.29	-0.48 ± 0.26	-1.31 ± 0.24	-1.91 ± 0.26	1.00E+00	1.00E+00	8.25E-06	2.73E-11	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT5G46890.1	AT5G46890	--	2264	2388	488	1423	-0.31 ± 0.31	-0.31 ± 0.31	-1.33 ± 0.20	-1.92 ± 0.20	1.00E+00	1.00E+00	4.46E-09	8.35E-19	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT4G29740.2	AT4G29740	CKX4	1492	1247	845	414	0.53 ± 0.23	-0.03 ± 0.26	-1.03 ± 0.15	-1.95 ± 0.29	8.29E-01	1.00E+00	1.61E-09	3.26E-09	cytokinin oxidase 4
	AT2G25410.1	AT2G25410	--	274	300	105	120	-0.22 ± 0.31	-0.06 ± 0.33	-1.99 ± 0.57	-2.00 ± 0.51	1.00E+00	1.00E+00	1.41E-02	2.01E-03	RING/U-box superfamily protein
	AT5G47990.1	AT5G47990	CYP705A5	983	803	2858	2202	0.28 ± 0.36	-0.41 ± 0.44	-1.05 ± 0.24	-2.01 ± 0.34	1.00E+00	1.00E+00	4.34E-04	2.30E-07	cytochrome P450, family 705, subfamily A, polypeptide 5
	AT3G14850.2	AT3G14850	TBL41	350	377	51	64	0.06 ± 0.39	0.17 ± 0.44	-1.77 ± 0.59	-2.04 ± 0.74	1.00E+00	1.00E+00	5.53E-02	7.13E-02	TRICHOME BIREFRINGENCE-LIKE 41
	AT2G19060.1	AT2G19060	--	925	952	464	483	-0.07 ± 0.29	-0.08 ± 0.28	-1.36 ± 0.23	-2.10 ± 0.34	1.00E+00	1.00E+00	7.79E-07	2.71E-08	SGNH hydrolase-type esterase superfamily protein
	AT5G35190.1	AT5G35190	EXT13	3512	3182	924	763	-0.33 ± 0.22	-0.82 ± 0.27	-1.60 ± 0.33	-2.11 ± 0.19	1.00E+00	1.			

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes							
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description			
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line					
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H				
	AT1G63770.1	AT1G63770	--	3	4	34	12	5.19 ± 4.80	5.22 ± 4.80	-8.67 ± 1.69	-7.01 ± 2.24	1.00E+00	1.00E+00	2.57E-05	2.83E-02	Peptidase M1 family protein			
	AT1G25210.2	AT1G25210	LpxC5	91	125	24	16	-8.48 ± 1.82	-1.60 ± 1.72	-6.64 ± 2.36	-7.45 ± 2.69	7.63E-04	1.00E+00	8.79E-02	7.10E-02	UDP-3-O-acyl N-acetylglucosamine deacetylase family protein			
	AT3G57760.2	AT3G57760	--	17	6	17	25	7.56 ± 4.37	5.95 ± 4.79	-7.69 ± 1.89	-8.13 ± 1.84	1.00E+00	1.00E+00	2.14E-03	3.17E-04	Protein kinase superfamily protein			
	AT5G12330.2	AT5G12330	LRP1	398	229	74	155	0.42 ± 0.60	-1.74 ± 1.59	-7.33 ± 1.20	-10.74 ± 1.51	1.00E+00	1.00E+00	1.77E-07	1.27E-10	Lateral root primordium (LRP) protein-related			
H	Inconsistent Common DE Targets in TPL-OE (6H and 15H) analysis:																		
	AT1G54510.2	AT1G54510	NEK1	237	162	50	103	-0.37 ± 0.63	-2.51 ± 0.67	-9.21 ± 1.61	10.10 ± 1.57	1.00E+00	1.91E-02	1.37E-06	9.79E-09	NIMA-related serine/threonine kinase 1			
	AT4G13630.1	AT4G13630	--	38	64	103	93	0.21 ± 3.40	1.32 ± 4.57	-6.21 ± 0.73	9.96 ± 1.93	1.00E+00	1.00E+00	1.13E-14	1.18E-05	Protein of unknown function, DUF593			
	AT3G59210.4	AT3G59210	--	57	23	170	129	0.62 ± 3.27	-8.03 ± 3.77	-10.98 ± 1.58	7.99 ± 1.11	1.00E+00	8.82E-01	9.39E-10	7.57E-11	F-box/RNI-like superfamily protein			
	AT3G61050.1	AT3G61050	NTMC2T4	14	0	201	15	7.20 ± 3.34	NA ± NA	-3.54 ± 1.13	7.34 ± 2.52	9.71E-01	NA	4.03E-02	5.03E-02	Calcium-dependent lipid-binding (CaLB domain) family protein			
	AT5G25360.2	AT5G25360	--	810	1007	344	238	-1.24 ± 0.34	-0.51 ± 0.59	-1.88 ± 0.51	2.61 ± 0.96	3.13E-02	1.00E+00	8.67E-03	8.25E-02				
	AT1G50500.2	AT1G50500	HIT1	218	110	166	153	4.27 ± 4.57	3.15 ± 1.83	-10.94 ± 1.49	2.24 ± 0.66	1.00E+00	1.00E+00	7.48E-11	1.22E-02	Membrane trafficking VPS53 family protein			
	AT1G67950.4	AT1G67950	--	85	48	25	39	1.11 ± 1.28	-0.47 ± 2.14	-8.21 ± 1.84	1.93 ± 0.71	1.00E+00	1.00E+00	4.50E-04	8.35E-02	RNA-binding (RRM/RBD/RNP motifs) family protein			
	AT1G16340.3	AT1G16340	ATKDSA2	65	47	15	83	-0.22 ± 0.99	-1.74 ± 1.08	-7.49 ± 2.17	1.57 ± 0.50	1.00E+00	1.00E+00	1.70E-02	2.66E-02	Aldolase superfamily protein			
	AT4G12880.2	AT4G12880	ENODL19	122	60	338	319	0.64 ± 2.15	-2.45 ± 2.99	-1.44 ± 0.48	1.47 ± 0.53	1.00E+00	1.00E+00	6.03E-02	6.87E-02	early nodulin-like protein 19			
	AT3G54380.2	AT3G54380	SAC3C	100	99	57	166	1.15 ± 2.05	1.05 ± 2.03	-2.38 ± 0.57	1.43 ± 0.34	1.00E+00	1.00E+00	1.26E-03	6.62E-04	SAC3/GANP/Nin1/mts3/eIF-3 p25 family			
	AT1G79230.3	AT1G79230	MST1	473	312	284	452	0.72 ± 0.57	-0.54 ± 0.35	-2.17 ± 0.35	1.31 ± 0.26	1.00E+00	1.00E+00	1.05E-07	1.40E-05	mercaptopryuvate sulfurtransferase 1			
	AT3G04400.2	AT3G04400	EMB2171	7071	7956	3074	6026	0.28 ± 1.45	0.47 ± 0.42	-1.14 ± 0.28	1.15 ± 0.23	1.00E+00	1.00E+00	1.63E-03	2.82E-05	Ribosomal protein L14p/L23e family protein			
	AT1G25275.3	AT1G25275	--	894	591	1034	1219	1.40 ± 0.71	0.33 ± 0.99	-1.37 ± 0.34	1.13 ± 0.24	1.00E+00	1.00E+00	2.83E-03	1.06E-04				
	AT2G43490.1	AT2G43490	--	319	405	283	304	-3.92 ± 3.74	-1.67 ± 4.56	-2.24 ± 0.60	1.06 ± 0.28	1.00E+00	1.00E+00	7.14E-03	3.78E-03	Ypt/Rab-GAP domain of gyp1p superfamily protein			
	AT2G36880.2	AT2G36880	MAT3	6420	9548	1962	1330	-0.86 ± 0.98	0.30 ± 1.06	1.20 ± 0.22	-1.03 ± 0.38	1.00E+00	1.00E+00	4.58E-06	7.88E-02	methionine adenosyltransferase 3			
	AT1G07780.2	AT1G07780	PAI1	337	270	236	211	0.17 ± 0.50	-0.63 ± 0.58	1.22 ± 0.43	-1.16 ± 0.31	1.00E+00	1.00E+00	7.59E-02	4.47E-03	phosphoribosylanthranilate isomerase 1			
	AT1G27650.2	AT1G27650	ATU2AF35A	1057	1503	64	299	-1.14 ± 0.81	-0.01 ± 0.60	4.67 ± 0.90	-1.18 ± 0.36	1.00E+00	1.00E+00	2.02E-05	1.70E-02	U2 snRNP auxiliary factor small subunit, putative			
	AT1G64230.3	AT1G64230	UBC28	1934	2460	593	587	0.06 ± 0.60	0.58 ± 0.19	1.12 ± 0.30	-2.16 ± 0.43	1.00E+00	1.26E-01	6.03E-03	2.41E-05	ubiquitin-conjugating enzyme 28			
	AT1G24510.2	AT1G24510	--	730	903	372	111	-0.98 ± 0.78	-0.31 ± 0.37	3.35 ± 0.71	-2.92 ± 0.81	1.00E+00	1.00E+00	1.47E-04	6.59E-03	TCP-1/cpn60 chaperonin family protein			
	AT3G06130.2	AT3G06130	--	154	192	73	52	0.11 ± 0.73	0.61 ± 0.66	2.53 ± 0.85	-4.19 ± 1.30	1.00E+00	1.00E+00	5.74E-02	2.18E-02	Heavy metal transport/detoxification superfamily protein			
	AT2G38290.2	AT2G38290	AMT2	23	11	17	15	1.39 ± 1.31	-0.39 ± 2.48	7.39 ± 2.00	-7.34 ± 2.02	1.00E+00	1.00E+00	7.65E-03	6.02E-03	ammonium transporter 2			
H	Up-regulated in TPL-OE (15H) analysis:																		
	AT5G25980.2	AT5G25980	TGG2	0	0	0	134	NA ± NA	NA ± NA	NA ± NA	23.19 ± 4.79	NA	NA	NA	4.95E-05	glucoside glucohydrolase 2			
	AT2G44130.1	AT2G44130	KMD3	0	0	53	284	NA ± NA	NA ± NA	9.05 ± 4.79	11.57 ± 1.51	NA	NA	4.65E-01	2.42E-12	Galactose oxidase/kelch repeat superfamily protein			
	AT4G36070.2	AT4G36070	CPK18	5	5	25	107	-0.63 ± 2.87	-1.08 ± 2.05	1.03 ± 0.91	10.17 ± 1.55	1.00E+00	1.00E+00	8.75E-01	4.36E-09	calcium-dependent protein kinase 18			
	AT3G62090.1	AT3G62090	PIL2	189	77	108	98	1.27 ± 4.56	-1.58 ± 4.57	1.00 ± 3.31	10.03 ± 1.53	1.00E+00	1.00E+00	1.00E+00	5.34E-09	phytochrome interacting factor 3-like 2			
	AT3G52950.2	AT3G52950	--	79	87	47	95	0.23 ± 4.56	0.39 ± 2.06	-0.30 ± 1.98	10.00 ± 1.53	1.00E+00	1.00E+00	1.00E+00	5.90E-09	CBS / octicosapeptide/Phox/Bemp1 (PB1) domains-containing protein			
	AT5G60360.3	AT5G60360	ALP	1290	259	415	261	2.06 ± 4.26	-8.01 ± 4.62	-6.27 ± 2.43	9.97 ± 3.13	1.00E+00	1.00E+00	1.47E-01	2.41E-02	aleurain-like protease			
	AT1G61140.3	AT1G61140	EDA16	566	535	161	91	-1.43 ± 0.53	-1.96 ± 0.73	0.16 ± 3.28	9.93 ± 1.56	3.98E-01	3.24E-01	1.00E+00	1.54E-08	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related			
	AT4G24230.3	AT4G24230	ACBP3	25	41	157	79	-8.06 ± 4.07	-0.69 ± 3.14	-0.21 ± 0.81	9.73 ± 1.56	1.00E+00	1.00E+00	1.00E+00	2.96E-08	acyl-CoA-binding domain 3			
	AT1G73960.2	AT1G73960	TAF2	46	19	9	215	8.97 ± 1.90	7.65 ± 3.93	1.30 ± 3.30	9.72 ± 1.46	5.41E-04	1.00E+00	1.00E+00	2.81E-09	TBP-associated factor 2			
	AT2G45740.3	AT2G45740	PEX11D	166	161	74	74	0.00 ± 0.90	-0.20 ± 1.10	0.08 ± 0.84	9.62 ± 1.65	1.00E+00	1.00E+00	1.00E+00	3.58E-07	peroxin 11D			
	AT3G45090.2	AT3G45090	--	0	0	14	72	NA ± NA	NA ± NA	7.13 ± 3.74	9.59 ± 1.62	NA	NA	4.55E-01	2.21E-07	P-loop containing nucleoside triphosphate hydrolases superfamily protein			
	AT4G34530.1	AT4G34530	CIB1	39	49	253	64	0.75 ± 3.39	1.18 ± 2.09	0.27 ± 0.37	9.43 ± 1.62	1.00E+00	1.00E+00	9.97E-01	4.00E-07	cryptochrome-interacting basic-helix-loop-helix 1			
	AT1G79280.1	AT1G79280	NUA	2292	1501	1172	145	0.18 ± 3.95	-1.48 ± 4.56	-0.23 ± 0.76	9.14 ± 1.61	1.00E+00	1.00E+00	1.00E+00	8.24E-07	nuclear pore anchor			
	AT2G20900.4	AT2G20900	DGK5	161	132	61	51	-0.85 ± 3.18	-2.09 ± 1.84	-0.42 ± 0.63	9.08 ± 1.63	1.00E+00	1.00E+00	1.00E+00	1.47E-06	diacylglycerol kinase 5			
	AT5G18830.2	AT5G18830	SPL7	56	129	47	50	-2.17 ± 2.05	0.78 ± 0.73	2.78 ± 1.62	9.07 ± 1.71	1.00E+00	1.00E+00	5.72E-01	5.61E-06	squamosa promoter binding protein-like 7			
	AT1G06230.3	AT1G06230	GTE4	46	33	314	49	0.75 ± 2.21	-0.22 ± 3.20	0.19 ± 0.64	9.04 ± 1.66	1.00E+00	1.00E+00	1.00E+00	2.57E-06	global transcription factor group E4			
	AT4G25450.3	AT4G25450	ABCB28	200	179	85	49	-2.74 ± 2.90	-10.98 ± 1.55	0.04 ± 0.77	9.03 ± 1.67	1.00E+00	1.65E-09	1.00E+00	3.05E-06	non-intrinsic ABC protein 8			
	AT3G47250.1	AT3G47250	--	2	0	23	46	4.59 ± 4.81	NA ± NA	1.51 ± 2.00	8.93 ± 2.02	1.00E+00	NA	9.93E-01	3.37E-04	Plant protein of unknown function (DUF247)			
	AT1G78510.2	AT1G78510	SPS1	19	32	30	44	-0.30 ± 3.58	0.95 ± 3.21	0.89 ± 4.57	8.87 ± 1.85	1.00E+00	1.00E+00	1.00E+00	6.00E-05	solanesyl diphosphate synthase 1			
	AT1G80245.2	AT1G80245	--	82	116	43	42	-2.17 ± 4.57	-0.61 ± 2.07	-2.14 ± 1.76	8.81 ± 1.69	1.00E+00	1.00E+00	8.44E-01	8.41E-06	Spe97 / Spe98 family of spindle pole body (SBP) component			
	AT3G01090.3	AT3G01090	KIN10	69	52	71	42	9.56 ± 1.87	9.11 ± 3.33	1.07 ± 1.82	8.81 ± 1.65	1.10E-04	2.99E-01	1.00E+00	4.56E-06	SNF1 kinase homolog 10			
	AT3G20280.2	AT3G20280	--	97	107	86	39	1.71 ± 1.83	1.85 ± 3.93	0.47 ± 0.62	8.71 ± 1.69	1.00E+00	1.00E+00	9.93E-01	1.13E-05	RING/FYVE/PHD zinc finger superfamily protein			
	AT1G28630.4	AT1G28630	--	0	0	1	39	-1.45 ± 5.00	-1.54 ± 5.00	0.16 ± 4.75	8.69 ± 1.70	NA	NA	NA	1.49E-05				
	AT5G27830.2	AT5G27830	--	0	1	0	37	-1.42 ± 5.00	1.55 ± 4.85	NA ± NA	8.63 ± 2.56	NA	NA	NA	1.38E-02				
	AT1G75080.2	AT1G75080	BZR1	78	23	56	32	2.09 ± 2.40	-0.98 ± 2.33	-1.77 ± 1.94	8.41 ± 1.82	1.00E+00	1.00E+00	9.53E-01	1.39E-04	Brassinosteroid signalling positive regulator (BZR1) family protein			
	AT1G75880.1	AT1G75880	--</																

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes						
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN		LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]								FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line				
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H			
	AT1G43170.3	AT1G43170	RP1	3	3	0	26	-1.88 ± 4.67	-1.78 ± 4.57	NA ± NA	8.09 ± 2.62	1.00E+00	1.00E+00	NA	3.14E-02	ribosomal protein 1		
	AT1G28260.1	AT1G28260	--	150	163	39	25	-0.33 ± 0.93	-0.15 ± 1.02	-2.08 ± 0.76	8.07 ± 1.95	1.00E+00	1.00E+00	1.04E-01	9.70E-04	Telomerase activating protein Est1		
	AT5G36790.3	AT5G36790	--	0	0	1	25	NA ± NA	NA ± NA	-3.35 ± 4.85	8.04 ± 2.46	NA	NA	NA	1.86E-02	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein		
	AT5G51230.3	AT5G51230	EMF2	87	37	26	25	2.20 ± 2.06	0.40 ± 3.16	0.84 ± 3.02	8.04 ± 1.98	1.00E+00	1.00E+00	1.00E+00	1.34E-03	VEFS-Box of polycomb protein		
	AT4G21060.1	AT4G21060	GALT2	0	0	52	24	NA ± NA	NA ± NA	-1.10 ± 0.86	8.01 ± 2.22	NA	NA	8.09E-01	6.77E-03	Galactosyltransferase family protein		
	AT3G01345.1	AT3G01345	--	234	242	1	63	-11.32 ± 4.78	-9.00 ± 3.53	-2.69 ± 4.89	7.96 ± 2.44	7.11E-01	4.43E-01	NA	1.91E-02	Expressed protein		
	AT2G47300.3	AT2G47300	POP1	41	8	11	23	2.04 ± 2.05	-6.53 ± 4.76	0.22 ± 3.29	7.95 ± 1.81	1.00E+00	1.00E+00	1.00E+00	3.85E-04	ribonuclease Ps		
	AT1G04945.2	AT1G04945	--	236	389	69	21	-1.38 ± 0.50	0.27 ± 0.50	0.61 ± 0.76	7.84 ± 1.84	3.18E-01	1.00E+00	9.78E-01	6.34E-04	HIT-type Zinc finger family protein		
	AT1G04870.1	AT1G04870	PRMT10	24	16	31	21	-0.90 ± 3.49	-7.53 ± 4.03	-1.07 ± 2.07	7.79 ± 1.95	1.00E+00	1.00E+00	1.00E+00	1.73E-03	protein arginine methyltransferase 10		
	AT4G30710.2	AT4G30710	QWRf8	0	0	5	20	NA ± NA	NA ± NA	-5.78 ± 4.72	7.75 ± 1.88	NA	NA	8.39E-01	1.02E-03	Family of unknown function (DUF566)		
	AT2G47230.2	AT2G47230	DUF6	96	106	25	20	0.25 ± 1.05	0.45 ± 0.59	1.37 ± 2.01	7.74 ± 1.89	1.00E+00	1.00E+00	1.00E+00	1.18E-03	DOMAIN OF UNKNOWN FUNCTION 724 6		
	AT4G13610.1	AT4G13610	MEE57	0	0	7	20	NA ± NA	NA ± NA	3.00 ± 1.57	7.71 ± 1.88	NA	NA	4.53E-01	1.21E-03	DNA (cytosine-5-)-methyltransferase family protein		
	AT4G16830.3	AT4G16830	AuRGGA	39	31	8	19	-0.17 ± 0.79	-1.10 ± 0.93	-6.62 ± 4.09	7.68 ± 2.00	1.00E+00	1.00E+00	6.28E-01	3.13E-03	Hyaluronan / mRNA binding family		
	AT2G35140.3	AT2G35140	--	185	274	40	19	0.24 ± 1.13	1.10 ± 1.10	-1.04 ± 1.94	7.63 ± 1.90	1.00E+00	1.00E+00	1.00E+00	1.58E-03	DCD (Development and Cell Death) domain protein		
	AT2G33070.1	AT2G33070	NSP2	0	0	0	18	NA ± NA	NA ± NA	NA ± NA	7.57 ± 2.52	NA	NA	NA	3.91E-02	nitrile specifier protein 2		
	AT2G25840.2	AT2G25840	OVA4	56	32	37	17	1.88 ± 2.03	0.68 ± 3.20	-0.74 ± 2.05	7.48 ± 2.02	1.00E+00	1.00E+00	1.00E+00	4.94E-03	Nucleotidyl transferase superfamily protein		
	AT4G20980.3	AT4G20980	--	20	21	17	17	-7.79 ± 4.22	-7.88 ± 3.84	7.40 ± 3.59	7.48 ± 1.95	1.00E+00	9.79E-01	3.65E-01	3.06E-03	Eukaryotic translation initiation factor 3 subunit 7 (eIF-3)		
	AT1G29355.1	AT1G29355	--	0	0	32	17	NA ± NA	NA ± NA	1.88 ± 4.57	7.47 ± 2.13	NA	NA	1.00E+00	8.98E-03			
	AT3G06870.1	AT3G06870	--	5	5	8	17	-5.83 ± 4.79	-5.94 ± 4.79	0.17 ± 2.62	7.47 ± 2.13	1.00E+00	1.00E+00	1.00E+00	8.98E-03	proline-rich family protein		
	AT1G26330.2	AT1G26330	--	21	97	82	44	7.83 ± 3.12	10.00 ± 4.45	-1.15 ± 3.88	7.44 ± 2.41	5.49E-01	7.42E-01	1.00E+00	3.14E-02	DNA binding		
	AT1G63690.2	AT1G63690	SPPL2	5	10	8	16	-5.84 ± 4.80	-0.36 ± 3.73	0.31 ± 3.39	7.42 ± 1.98	1.00E+00	1.00E+00	1.00E+00	4.06E-03	SIGNAL PEPTIDE PEPTIDASE-LIKE 2		
	AT5G59280.1	AT5G59280	PUM16	0	0	0	16	2.31 ± 4.90	NA ± NA	2.07 ± 4.90	7.41 ± 2.13	NA	NA	NA	9.82E-03	pumilio 16		
	AT3G46220.2	AT3G46220	--	104	62	40	15	-0.43 ± 0.67	-9.44 ± 1.77	0.92 ± 1.91	7.30 ± 2.01	1.00E+00	3.07E-05	1.00E+00	6.10E-03			
	AT3G660510.3	AT3G660510	--	9	23	2	15	-6.66 ± 4.79	0.49 ± 3.32	4.31 ± 4.81	7.30 ± 2.34	1.00E+00	1.00E+00	NA	2.93E-02	ATP-dependent caseinolytic (Clp) protease/crotonase family protein		
	AT4G13470.1	AT4G13470	--	2	2	12	155	-4.58 ± 4.52	-4.71 ± 4.52	3.05 ± 1.74	7.27 ± 0.89	1.00E+00	NA	5.49E-01	4.14E-14	transposable element gene		
	AT5G38520.2	AT5G38520	CLD1	8	6	2	14	-0.92 ± 3.95	-6.00 ± 4.79	4.31 ± 4.81	7.25 ± 2.03	1.00E+00	1.00E+00	NA	7.39E-03	alpha/beta-Hydrolases superfamily protein		
	AT2G32390.1	AT2G32390	GLR3.5	128	88	38	14	3.02 ± 2.00	2.35 ± 1.81	-0.52 ± 1.97	7.22 ± 2.04	1.00E+00	1.00E+00	1.00E+00	8.45E-03	glutamate receptor 3.5		
	AT1G29200.1	AT1G29200	--	60	72	20	14	1.03 ± 0.95	1.35 ± 1.42	-7.91 ± 3.48	7.18 ± 2.09	1.00E+00	1.00E+00	2.60E-01	1.14E-02	O-fucosyltransferase family protein		
	AT3G57620.1	AT3G57620	--	0	0	2	36	NA ± NA	NA ± NA	4.31 ± 3.88	7.15 ± 1.63	NA	NA	NA	3.93E-04	glyoxal oxidase-related protein		
	AT1G10840.2	AT1G10840	TIF3H1	15	19	23	13	7.31 ± 2.44	7.68 ± 3.90	-1.11 ± 0.80	7.13 ± 2.21	1.94E-01	1.00E+00	7.57E-01	2.11E-02	translation initiation factor 3 subunit H1		
	AT5G57050.2	AT5G57050	ABI2	31	33	63	103	0.08 ± 2.55	0.13 ± 3.20	-0.34 ± 1.91	7.06 ± 1.01	1.00E+00	1.00E+00	1.00E+00	2.88E-10	Protein phosphatase 2C family protein		
	AT5G06250.1	AT5G06250	DPA4	29	28	8	12	0.87 ± 1.79	0.66 ± 1.78	6.32 ± 2.34	7.03 ± 2.17	1.00E+00	1.00E+00	1.12E-01	2.06E-02	AP2/B3-like transcriptional factor family protein		
	AT4G09500.1	AT4G09500	--	43	9	24	12	2.04 ± 3.28	-6.62 ± 4.69	-0.13 ± 2.04	6.95 ± 2.20	1.00E+00	1.00E+00	1.00E+00	2.58E-02	UDP-Glycosyltransferase superfamily protein		
	AT5G61850.1	AT5G61850	LFY	5	7	4	11	-5.83 ± 3.36	-1.92 ± 1.81	0.42 ± 1.87	6.94 ± 2.28	1.00E+00	1.00E+00	1.00E+00	3.54E-02	floral meristem identity control protein LEAFY (LFY)		
	AT5G22608.3	AT5G22608	--	0	0	7	11	NA ± NA	NA ± NA	-6.47 ± 4.21	6.92 ± 2.25	NA	NA	6.73E-01	3.24E-02			
	AT1G60730.2	AT1G60730	--	0	0	21	11	NA ± NA	NA ± NA	1.83 ± 1.97	6.89 ± 2.18	NA	NA	9.48E-01	2.63E-02	NAD(P)-linked oxidoreductase superfamily protein		
	AT5G24630.2	AT5G24630	BIN4	34	36	19	10	-0.03 ± 1.16	0.00 ± 1.07	-0.24 ± 1.34	6.79 ± 2.33	1.00E+00	1.00E+00	1.00E+00	5.03E-02	double-stranded DNA binding		
	AT2G17470.1	AT2G17470	ALMT6	0	0	1	10	NA ± NA	NA ± NA	1.77 ± 3.50	6.78 ± 2.32	NA	NA	NA	4.90E-02	Aluminium activated malate transporter family protein		
	AT1G76440.2	AT1G76440	--	8	0	5	10	6.43 ± 4.79	NA ± NA	1.69 ± 3.51	6.75 ± 2.28	1.00E+00	NA	1.00E+00	4.40E-02	HSP20-like chaperones superfamily protein		
	AT4G38900.1	AT4G38900	bZIP29	24	18	17	10	-1.53 ± 2.19	-7.66 ± 2.26	-1.29 ± 1.98	6.75 ± 2.24	1.00E+00	5.64E-02	1.00E+00	3.88E-02	Basic-leucine zipper (bZIP) transcription factor family protein		
	AT4G28520.1	AT4G28520	CRU3	0	0	33	9	NA ± NA	NA ± NA	0.70 ± 4.57	6.66 ± 2.28	NA	NA	1.00E+00	4.95E-02	cruciferin 3		
	AT2G40570.2	AT2G40570	--	49	73	0	9	-0.97 ± 1.29	0.22 ± 1.17	NA ± NA	6.60 ± 2.43	1.00E+00	1.00E+00	NA	8.24E-02	initiator tRNA phosphoribosyl transferase family protein		
	AT3G12250.4	AT3G12250	TGA6	0	0	5	9	NA ± NA	NA ± NA	-5.86 ± 4.67	6.59 ± 2.32	NA	NA	8.23E-01	5.99E-02	TGACG motif-binding factor 6		
	AT3G25800.2	AT3G25800	PP2AA2	9	12	31	9	-6.54 ± 4.79	-1.44 ± 3.58	1.13 ± 4.57	6.58 ± 2.36	1.00E+00	1.00E+00	1.00E+00	6.91E-02	protein phosphatase 2A subunit A2		
	AT3G62800.3	AT3G62800	DRB4	44	25	25	9	2.41 ± 1.99	1.26 ± 2.37	-0.41 ± 3.01	6.56 ± 2.33	1.00E+00	1.00E+00	1.00E+00	6.57E-02	double-stranded-RNA-binding protein 4		
	AT5G36790.2	AT5G36790	--	0	6	0	9	NA ± NA	6.00 ± 4.79	NA ± NA	6.55 ± 2.34	NA	1.00E+00	NA	6.64E-02	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein		
	AT1G55560.1	AT1G55560	SKS14	0	0	1	22	NA ± NA	NA ± NA	-2.35 ± 4.76	6.40 ± 1.79	NA	NA	NA	7.24E-03	SKU5 similar 14		
	AT2G10940.1	AT2G10940	--	3	2	2	265	1.87 ± 3.23	0.65 ± 3.64	2.77 ± 2.89	6.31 ± 2.36	1.00E+00	NA	NA	9.05E-02	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein		
	AT1G67623.1	AT1G67623	--	8	9	10	61	-3.05 ± 2.47	-1.71 ± 1.70	4.00 ± 1.82	6.29 ± 1.11	1.00E+00	1.00E+00	2.97E-01	7.67E-07	F-box family protein		
	AT4G33150.1	AT4G33150	--	32	0	1	95	6.96 ± 3.27	-1.54 ± 5.00	2.68 ± 4.86	6.25 ± 1.42	9.99E-01	NA	NA	3.42E-04	lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme		
	AT5G61530.3	AT5G61530	--	128	135	14	19	0.70 ± 2.08	0.75 ± 1.94	0.61 ± 3.18	6.22 ± 1.82	1.00E+00	1.00E+00	1.00E+00	1.21E-02	small G protein family protein / RhoGAP family protein		
	AT3G19530.1	AT3G19530	--	18	19	22	75	-1.50 ± 1.08	-1.44 ± 1.32	1.96 ± 0.98	6.20 ± 0.95							

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				TAIR10 Gene Description
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT2G45580.1	AT2G45580	CYP76C3	4	2	0	38	-0.33 ± 3.06	-4.70 ± 4.81	1.28 ± 4.98	5.18 ± 1.02	1.00E+00	NA	NA	1.57E-05	cytochrome P450, family 76, subfamily C, polypeptide 3
	AT4G10507.1	AT4G10507	--	3	3	3	17	-1.88 ± 3.14	-1.70 ± 2.41	-0.06 ± 2.02	5.07 ± 1.49	1.00E+00	1.00E+00	1.00E+00	1.29E-02	other RNA
	AT5G47000.1	AT5G47000	--	7	7	9	61	-1.34 ± 2.85	-1.38 ± 3.01	0.65 ± 1.32	5.04 ± 0.91	1.00E+00	1.00E+00	1.00E+00	1.71E-06	Peroxidase superfamily protein
	AT5G35390.1	AT5G35390	PRK1	1	1	6	17	-1.89 ± 4.82	-2.11 ± 4.84	2.58 ± 1.68	5.02 ± 1.60	NA	NA	6.75E-01	2.85E-02	Leucine-rich repeat protein kinase family protein
	AT4G22030.1	AT4G22030	--	1	0	5	24	2.45 ± 4.89	NA ± NA	2.04 ± 1.81	4.94 ± 1.29	NA	NA	8.80E-01	3.15E-03	F-box family protein with a domain of unknown function (DUF295)
	AT2G05935.1	AT2G05935	--	15	10	3	16	1.89 ± 1.31	1.03 ± 1.55	1.40 ± 2.63	4.92 ± 1.47	1.00E+00	1.00E+00	1.00E+00	1.44E-02	transposable element gene
	AT5G05000.2	AT5G05000	TOC34	128	219	19	28	-1.72 ± 4.56	0.20 ± 4.56	-2.06 ± 1.92	4.79 ± 1.33	1.00E+00	1.00E+00	8.97E-01	6.87E-03	translocon at the outer envelope membrane of chloroplasts 34
	AT5G35380.1	AT5G35380	--	1	2	5	71	0.11 ± 4.98	2.27 ± 4.83	5.72 ± 2.68	4.73 ± 0.74	NA	NA	3.25E-01	1.61E-08	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain
	AT2G33070.2	AT2G33070	NSP2	6	6	27	249	-2.51 ± 1.85	-4.56 ± 2.64	0.33 ± 0.84	4.73 ± 0.47	1.00E+00	1.00E+00	1.00E+00	4.13E-21	nitrile specifier protein 2
	AT4G36070.1	AT4G36070	CPK18	0	0	8	49	NA ± NA	NA ± NA	0.88 ± 2.20	4.72 ± 0.87	NA	NA	1.00E+00	3.42E-06	calcium-dependent protein kinase 18
	AT4G21065.2	AT4G21065	--	49	19	6	21	2.37 ± 2.08	0.38 ± 3.40	-6.08 ± 4.48	4.69 ± 1.49	1.00E+00	1.00E+00	7.71E-01	2.61E-02	Tetratricopeptide repeat (TPR)-like superfamily protein
	AT2G02640.1	AT2G02640	--	18	17	23	20	-1.20 ± 2.32	-1.93 ± 1.53	0.29 ± 1.09	4.61 ± 1.59	1.00E+00	1.00E+00	1.00E+00	5.26E-02	Cysteine/Histidine-rich C1 domain family protein
	AT2G37760.5	AT2G37760	AKR4C8	20	20	32	73	1.03 ± 2.48	0.84 ± 2.40	-1.49 ± 1.11	4.58 ± 1.28	1.00E+00	1.00E+00	7.79E-01	7.43E-03	NAD(P)-linked oxidoreductase superfamily protein
	AT1G27461.1	AT1G27461	--	0	0	5	18	NA ± NA	NA ± NA	5.51 ± 3.01	4.58 ± 1.68	NA	NA	5.01E-01	8.04E-02	
	AT3G56920.1	AT3G56920	--	5	4	5	37	0.17 ± 2.24	-0.46 ± 3.21	1.47 ± 2.31	4.51 ± 1.15	1.00E+00	1.00E+00	1.00E+00	2.28E-03	DHHC-type zinc finger family protein
	AT1G01980.1	AT1G01980	AtBBE1	0	0	3	43	NA ± NA	NA ± NA	0.04 ± 2.02	4.51 ± 0.91	NA	NA	NA	3.31E-05	FAD-binding Berberine family protein
	AT3G50390.1	AT3G50390	--	5	9	12	30	0.44 ± 2.23	1.77 ± 1.58	1.65 ± 1.12	4.48 ± 1.03	1.00E+00	1.00E+00	7.11E-01	4.42E-04	Transducin/WD40 repeat-like superfamily protein
	AT3G14420.6	AT3G14420	GOX1	5	0	64	63	5.77 ± 4.80	2.39 ± 4.89	-3.43 ± 1.78	4.48 ± 1.47	1.00E+00	NA	4.44E-01	3.48E-02	Aldolase-type TIM barrel family protein
	AT1G80740.1	AT1G80740	CMT1	7	10	7	29	-1.64 ± 1.73	-0.23 ± 1.52	1.92 ± 1.52	4.47 ± 1.02	1.00E+00	1.00E+00	8.16E-01	3.89E-04	chromomethylase 1
	AT4G19880.3	AT4G19880	--	68	35	2	28	9.53 ± 1.72	8.54 ± 3.52	-2.80 ± 4.43	4.42 ± 1.55	1.40E-05	5.59E-01	NA	5.91E-02	Glutathione S-transferase family protein
	AT4G26390.1	AT4G26390	--	2	3	6	57	-4.45 ± 4.81	-1.50 ± 3.53	2.11 ± 1.60	4.42 ± 0.75	1.00E+00	1.00E+00	7.90E-01	2.37E-07	Pyruvate kinase family protein
	AT2G17280.2	AT2G17280	--	270	197	123	76	0.62 ± 0.51	-0.36 ± 0.72	-0.08 ± 0.42	4.28 ± 1.38	1.00E+00	1.00E+00	1.00E+00	3.00E-02	Phosphoglycerate mutase family protein
	AT5G09730.1	AT5G09730	BXL3	6	8	20	99	-0.86 ± 2.77	-0.22 ± 2.09	1.34 ± 0.87	4.28 ± 0.59	1.00E+00	1.00E+00	6.69E-01	3.85E-11	beta-xylosidase 3
	AT3G47640.3	AT3G47640	PYE	265	333	221	213	0.17 ± 1.18	0.66 ± 1.00	-0.16 ± 0.33	4.10 ± 0.90	1.00E+00	1.00E+00	1.00E+00	1.99E-04	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
	AT2G02800.2	AT2G02800	APK2B	258	141	550	109	-0.17 ± 3.54	-24.00 ± 4.79	0.08 ± 0.39	4.09 ± 1.38	1.00E+00	1.33E-04	1.00E+00	4.43E-02	protein kinase 2B
	AT5G02560.2	AT5G02560	HTA12	34	19	13	35	0.68 ± 1.30	-1.22 ± 2.27	-2.67 ± 1.26	4.06 ± 1.03	1.00E+00	1.00E+00	3.35E-01	2.26E-03	histone H2A 12
	AT4G14450.1	AT4G14450	PHI	6	3	7	13	2.28 ± 2.58	0.83 ± 3.31	0.01 ± 1.46	3.98 ± 1.46	1.00E+00	1.00E+00	1.00E+00	8.10E-02	
	AT1G18520.1	AT1G18520	TET11	0	0	0	24	1.58 ± 4.98	1.39 ± 4.99	-1.68 ± 4.99	3.91 ± 1.16	NA	NA	NA	1.38E-02	tetraspanin11
*	AT4G33610.1	AT4G33610	--	3637	3540	5930	12934	-1.68 ± 0.18	-2.19 ± 0.30	0.82 ± 0.17	3.85 ± 0.16	1.02E-17	5.40E-10	1.52E-04	#####	glycine-rich protein
	AT1G76610.1	AT1G76610	--	14	11	9	54	-0.13 ± 1.60	-1.38 ± 1.84	0.28 ± 1.22	3.84 ± 0.72	1.00E+00	1.00E+00	1.00E+00	5.04E-06	Protein of unknown function, DUF617
	AT1G18270.2	AT1G18270	--	134	407	189	386	-0.53 ± 1.91	1.99 ± 1.96	-1.77 ± 2.17	3.81 ± 0.70	1.00E+00	1.00E+00	9.76E-01	2.72E-06	ketose-bisphosphate aldolase class-II family protein
	AT4G14165.1	AT4G14165	--	6	4	3	15	0.18 ± 3.13	-0.92 ± 3.22	-0.56 ± 1.94	3.80 ± 1.38	1.00E+00	1.00E+00	1.00E+00	7.67E-02	F-box family protein-related
	AT2G47015.1	AT2G47015	MIR408	12	12	12	71	-0.12 ± 1.79	-0.35 ± 2.53	2.31 ± 1.36	3.73 ± 0.79	1.00E+00	1.00E+00	5.80E-01	9.53E-05	MIR408; miRNA
	AT5G10150.1	AT5G10150	--	44	50	62	262	-0.22 ± 0.75	0.04 ± 0.77	0.77 ± 0.50	3.72 ± 0.33	1.00E+00	1.00E+00	6.73E-01	1.21E-26	Domain of unknown function (DUF966)
	AT1G69560.1	AT1G69560	MYB105	17	17	33	82	-4.93 ± 2.08	-7.58 ± 2.46	0.58 ± 0.70	3.72 ± 0.56	7.02E-01	1.30E-01	9.72E-01	2.55E-09	myb domain protein 105
*	AT5G20860.1	AT5G20860	--	208	204	559	1182	-1.62 ± 0.38	-1.95 ± 0.48	0.94 ± 0.19	3.69 ± 0.21	4.60E-03	6.71E-03	7.14E-05	7.72E-69	Plant invertase/pectin methyltransferase inhibitor superfamily
	AT1G22290.2	AT1G22290	--	4	4	3	17	-5.33 ± 3.77	-5.44 ± 3.74	2.36 ± 2.47	3.64 ± 1.18	1.00E+00	1.00E+00	9.41E-01	3.21E-02	14-3-3 family protein
	AT4G25580.1	AT4G25580	--	2	2	20	27	-0.86 ± 4.72	-0.09 ± 3.69	0.92 ± 0.98	3.62 ± 1.18	NA	NA	9.47E-01	3.44E-02	CAP160 protein
	AT1G20030.2	AT1G20030	--	154	166	159	224	-0.92 ± 0.80	-0.74 ± 0.88	0.19 ± 0.49	3.58 ± 0.40	1.00E+00	1.00E+00	1.00E+00	5.42E-17	Pathogenesis-related thaumatin superfamily protein
	AT3G17760.1	AT3G17760	GAD5	9	7	8	16	6.59 ± 2.80	6.28 ± 3.10	0.10 ± 1.47	3.52 ± 1.29	7.24E-01	1.00E+00	1.00E+00	8.04E-02	glutamate decarboxylase 5
	AT3G60780.1	AT3G60780	--	6	8	4	15	-1.37 ± 2.03	-0.51 ± 1.92	1.79 ± 2.43	3.51 ± 1.25	1.00E+00	1.00E+00	9.96E-01	6.57E-02	Protein of unknown function (DUF1442)
	AT2G36560.1	AT2G36560	--	7	6	6	43	-1.13 ± 1.70	-1.47 ± 1.86	-0.51 ± 1.59	3.45 ± 0.77	1.00E+00	1.00E+00	1.00E+00	2.69E-04	AT hook motif DNA-binding family protein
	AT4G24790.1	AT4G24790	--	7	0	0	52	4.84 ± 3.92	-0.11 ± 5.00	1.29 ± 4.98	3.44 ± 1.23	1.00E+00	NA	NA	6.84E-02	AAA-type ATPase family protein
*	AT1G55990.1	AT1G55990	--	943	909	1529	3007	-1.42 ± 0.24	-2.06 ± 0.35	0.77 ± 0.20	3.44 ± 0.19	1.59E-06	1.40E-06	4.36E-03	3.17E-69	glycine-rich protein
	AT4G26830.1	AT4G26830	--	44	44	48	185	0.02 ± 0.74	-0.09 ± 1.02	1.22 ± 0.70	3.36 ± 0.48	1.00E+00	1.00E+00	5.55E-01	3.42E-10	O-Glycosyl hydrolases family 17 protein
	AT4G19645.2	AT4G19645	--	140	128	43	121	0.34 ± 0.74	0.00 ± 0.73	0.75 ± 0.83	3.31 ± 0.52	1.00E+00	1.00E+00	9.58E-01	1.42E-08	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein
	AT5G53210.1	AT5G53210	SPCH	7	6	13	32	-1.91 ± 2.58	-4.47 ± 2.66	1.03 ± 1.09	3.26 ± 0.83	1.00E+00	1.00E+00	9.45E-01	2.36E-03	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
	AT5G66670.2	AT5G66670	--	46	43	9	58	0.04 ± 0.97	-0.29 ± 0.93	1.10 ± 2.16	3.23 ± 0.62	1.00E+00	1.00E+00	1.00E+00	9.05E-06	Protein of unknown function (DUF677)
	AT2G40170.1	AT2G40170	GEA6	24	28	32	57	-1.04 ± 1.05	-0.63 ± 1.01	1.32 ± 0.78	3.23 ± 0.70	1.00E+00	1.00E+00	5.88E-01	1.29E-04	Stress induced protein
	AT3G54310.1	AT3G54310	--	45	39	53	370	-0.61 ± 0.87	-1.35 ± 1.01	0.66 ± 0.67	3.22 ± 0.30	1.00E+00	1.00E+00	9.28E-01	3.51	

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
*	AT4G13840.1	AT4G13840	CER26	96	95	158	522	-0.19 ± 0.51	-0.34 ± 0.79	-0.30 ± 0.34	2.83 ± 0.21	1.00E+00	1.00E+00	9.65E-01	6.44E-37	HXXXD-type acyl-transferase family protein
	AT4G17100.2	AT4G17100	--	161	66	98	81	1.29 ± 3.25	-1.46 ± 4.57	-1.10 ± 3.22	2.82 ± 0.67	1.00E+00	1.00E+00	1.00E+00	7.38E-04	
	AT3G23110.1	AT3G23110	RLP37	82	72	40	111	0.30 ± 0.56	-0.14 ± 0.62	0.90 ± 0.69	2.81 ± 0.49	1.00E+00	1.00E+00	8.06E-01	7.53E-07	
	AT2G22510.1	AT2G22510	--	3465	3291	6896	22549	-1.30 ± 0.29	-1.86 ± 0.39	0.35 ± 0.13	2.77 ± 0.15	2.08E-03	3.02E-04	1.17E-01	1.11E-72	
	AT3G17240.3	AT3G17240	mtLPD2	80	79	53	59	-0.84 ± 0.78	-0.98 ± 0.85	-1.08 ± 1.93	2.76 ± 0.78	1.00E+00	1.00E+00	1.00E+00	8.47E-03	
	AT4G14440.1	AT4G14440	HCD1	1548	1551	2902	7425	-0.72 ± 0.25	-0.86 ± 0.24	0.94 ± 0.16	2.76 ± 0.18	2.39E-01	3.56E-02	4.38E-07	1.29E-48	
	AT5G60040.2	AT5G60040	NRPC1	63	31	23	21	0.98 ± 1.31	-1.22 ± 1.55	-0.13 ± 0.85	2.71 ± 0.99	1.00E+00	1.00E+00	1.00E+00	7.89E-02	
	AT1G17960.1	AT1G17960	--	225	222	367	999	-0.67 ± 0.49	-0.84 ± 0.49	0.70 ± 0.30	2.68 ± 0.24	1.00E+00	1.00E+00	2.36E-01	8.26E-27	
	AT2G32810.2	AT2G32810	BGAL9	96	73	38	26	1.17 ± 0.60	0.47 ± 0.78	-0.61 ± 0.66	2.67 ± 0.92	1.00E+00	1.00E+00	9.53E-01	5.09E-02	
	AT1G08630.2	AT1G08630	THA1	43	47	450	404	-0.13 ± 2.25	0.03 ± 2.16	1.73 ± 0.79	2.64 ± 0.54	1.00E+00	1.00E+00	2.95E-01	3.64E-05	
*	AT5G55970.2	AT5G55970	--	940	812	764	1348	-0.47 ± 0.33	-1.18 ± 0.25	1.00 ± 0.29	2.63 ± 0.33	1.00E+00	6.59E-04	1.56E-02	9.84E-14	RING/U-box superfamily protein
	AT5G57780.1	AT5G57780	--	136	143	121	300	-0.52 ± 0.42	-0.50 ± 0.54	0.97 ± 0.45	2.62 ± 0.33	1.00E+00	1.00E+00	3.18E-01	5.83E-13	
	AT2G40370.1	AT2G40370	LAC5	904	867	2210	6275	-1.09 ± 0.25	-1.45 ± 0.43	0.80 ± 0.18	2.61 ± 0.16	2.99E-03	5.12E-02	7.08E-04	4.41E-59	
	AT2G48140.1	AT2G48140	EDA4	3903	3612	4976	11726	-1.04 ± 0.17	-1.64 ± 0.30	0.83 ± 0.14	2.59 ± 0.18	5.31E-07	1.22E-05	8.66E-07	1.59E-42	
	AT4G38950.1	AT4G38950	--	208	164	114	277	-0.77 ± 0.79	-2.25 ± 0.70	0.68 ± 0.56	2.58 ± 0.36	1.00E+00	9.34E-02	8.40E-01	1.12E-10	
	AT1G20030.1	AT1G20030	--	84	75	312	408	-0.08 ± 1.02	-0.58 ± 1.30	0.65 ± 0.29	2.57 ± 0.32	1.00E+00	1.00E+00	2.60E-01	1.39E-13	
	AT3G11430.1	AT3G11430	GPAT5	1418	1328	2874	7773	-0.99 ± 0.26	-1.46 ± 0.32	0.95 ± 0.19	2.54 ± 0.15	2.00E-02	9.54E-04	4.84E-05	4.24E-60	
	AT4G29800.1	AT4G29800	PLP8	171	154	165	359	-1.11 ± 0.52	-1.87 ± 0.71	0.42 ± 0.44	2.54 ± 0.27	9.99E-01	3.86E-01	9.45E-01	5.12E-19	
	AT1G17950.1	AT1G17950	MYB52	316	319	375	1384	-1.40 ± 0.42	-1.55 ± 0.38	0.83 ± 0.25	2.53 ± 0.23	8.52E-02	6.58E-03	2.73E-02	1.50E-26	
	AT2G05540.1	AT2G05540	--	90	108	359	655	-0.51 ± 0.57	-0.07 ± 0.59	0.35 ± 0.38	2.53 ± 0.47	1.00E+00	1.00E+00	9.57E-01	2.95E-06	
*	AT1G08630.1	AT1G08630	THA1	45	43	153	111	1.35 ± 0.84	1.16 ± 0.95	0.79 ± 0.70	2.52 ± 0.79	1.00E+00	1.00E+00	8.79E-01	2.27E-02	P-loop containing nucleoside triphosphate hydrolases superfamily protein
	AT4G24860.1	AT4G24860	--	39	39	31	75	-0.36 ± 0.95	-0.51 ± 0.92	0.47 ± 0.77	2.50 ± 0.60	1.00E+00	1.00E+00	1.00E+00	7.88E-04	
	AT3G25855.1	AT3G25855	--	95	101	92	281	-0.08 ± 0.57	-0.08 ± 0.66	0.28 ± 0.41	2.49 ± 0.36	1.00E+00	1.00E+00	1.00E+00	8.03E-10	
	AT5G22270.1	AT5G22270	SIED1	110	116	76	160	0.10 ± 0.58	0.12 ± 0.62	0.59 ± 0.46	2.49 ± 0.43	1.00E+00	1.00E+00	8.02E-01	4.06E-07	
	AT3G27690.1	AT3G27690	LHCB2.3	3	5	21	268	-2.44 ± 2.30	-0.59 ± 2.20	0.18 ± 1.02	2.48 ± 0.89	1.00E+00	1.00E+00	1.00E+00	6.96E-02	
	AT1G68850.1	AT1G68850	--	2255	2130	3742	8938	-0.74 ± 0.26	-1.12 ± 0.34	0.76 ± 0.13	2.48 ± 0.17	3.09E-01	7.25E-02	1.04E-06	3.39E-43	
	AT1G30450.2	AT1G30450	CCC1	383	183	95	252	2.54 ± 3.63	1.11 ± 3.22	-0.43 ± 3.09	2.48 ± 0.60	1.00E+00	1.00E+00	1.00E+00	9.71E-04	
	AT3G03660.2	AT3G03660	WOX11	117	89	34	42	0.21 ± 0.55	-0.79 ± 0.64	1.44 ± 0.93	2.48 ± 0.73	1.00E+00	1.00E+00	6.73E-01	1.27E-02	
	AT5G10480.3	AT5G10480	PAS2	37	36	11	47	-0.63 ± 1.44	-0.85 ± 1.40	-1.11 ± 2.20	2.47 ± 0.87	1.00E+00	1.00E+00	1.00E+00	6.26E-02	
	AT2G19200.1	AT2G19200	--	311	309	632	1769	-2.07 ± 0.34	-2.42 ± 0.37	0.71 ± 0.20	2.47 ± 0.21	5.02E-07	5.54E-08	1.42E-02	3.62E-28	
*	AT1G01070.2	AT1G01070	UMAMIT28	16	8	9	35	0.48 ± 1.45	-1.94 ± 2.46	-1.24 ± 3.33	2.47 ± 0.83	1.00E+00	1.00E+00	1.00E+00	4.31E-02	cytochrome P450, family 86, subfamily A, polypeptide 4
	AT1G31490.1	AT1G31490	--	449	460	258	738	-0.55 ± 0.43	-0.57 ± 0.39	0.42 ± 0.35	2.46 ± 0.27	1.00E+00	1.00E+00	8.44E-01	5.47E-17	
	AT5G26667.3	AT5G26667	PYR6	234	64	82	92	3.19 ± 0.73	0.75 ± 0.75	-0.95 ± 0.80	2.46 ± 0.49	2.40E-03	1.00E+00	8.55E-01	2.73E-05	
	AT5G16770.2	AT5G16770	MYB9	367	335	327	400	-0.24 ± 0.37	-0.67 ± 0.35	0.92 ± 0.35	2.46 ± 0.28	1.00E+00	1.00E+00	1.27E-01	7.96E-17	
	AT5G09520.1	AT5G09520	PELPK2	1106	1114	2120	2602	-1.44 ± 0.30	-1.74 ± 0.31	0.77 ± 0.18	2.45 ± 0.22	3.68E-04	1.00E-05	1.32E-03	2.72E-26	
	AT4G02830.2	AT4G02830	--	283	300	155	390	-0.98 ± 0.38	-0.89 ± 0.45	0.76 ± 0.32	2.44 ± 0.24	4.61E-01	1.00E+00	2.34E-01	3.18E-22	
	AT1G18290.1	AT1G18290	--	293	324	162	361	-0.26 ± 0.36	-0.08 ± 0.36	0.51 ± 0.32	2.44 ± 0.32	1.00E+00	1.00E+00	6.32E-01	1.47E-12	
	AT1G01600.1	AT1G01600	CYP86A4	755	848	1367	4231	-0.52 ± 0.23	-0.24 ± 0.32	0.88 ± 0.20	2.43 ± 0.13	8.48E-01	1.00E+00	8.21E-04	4.17E-72	
	AT5G52710.1	AT5G52710	--	498	547	27	61	1.56 ± 0.29	1.68 ± 0.26	-1.52 ± 0.77	2.43 ± 0.58	3.43E-05	7.32E-08	4.14E-01	7.41E-04	
	AT5G36790.1	AT5G36790	--	16	12	34	80	-1.08 ± 1.39	-3.59 ± 2.11	-0.53 ± 1.01	2.40 ± 0.60	1.00E+00	1.00E+00	1.00E+00	1.64E-03	
*	AT5G36700.1	AT5G36700	PGLP1	16	12	34	80	-1.08 ± 1.39	-3.59 ± 2.11	-0.53 ± 1.01	2.40 ± 0.60	1.00E+00	1.00E+00	1.00E+00	1.64E-03	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
	AT2G42860.1	AT2G42860	--	42	57	11	47	-0.21 ± 0.85	0.55 ± 0.76	-0.65 ± 1.14	2.40 ± 0.82	1.00E+00	1.00E+00	1.00E+00	5.04E-02	
	AT5G63440.1	AT5G63440	--	108	119	44	134	-0.98 ± 0.54	-0.71 ± 0.58	1.29 ± 0.86	2.39 ± 0.51	1.00E+00	1.00E+00	6.93E-01	1.10E-04	
	AT4G37220.1	AT4G37220	--	30	31	10	47	-1.21 ± 1.05	-1.25 ± 0.99	0.52 ± 1.65	2.38 ± 0.87	1.00E+00	1.00E+00	1.00E+00	7.69E-02	
	AT4G15120.1	AT4G15120	--	370	400	463	1051	-0.26 ± 0.39	-0.15 ± 0.38	0.80 ± 0.27	2.37 ± 0.26	1.00E+00	1.00E+00	5.78E-02	2.73E-17	
	AT1G35330.1	AT1G35330	--	247	249	197	578	-0.36 ± 0.33	-0.45 ± 0.35	0.30 ± 0.45	2.37 ± 0.25	1.00E+00	1.00E+00	1.00E+00	6.15E-19	
	AT2G16760.1	AT2G16760	--	958	1008	1140	1891	-0.55 ± 0.19	-0.49 ± 0.29	0.83 ± 0.19	2.37 ± 0.19	2.76E-01	1.00E+00	6.06E-04	2.03E-31	
	AT3G07970.1	AT3G07970	QRT2	291	290	610	1215	-1.68 ± 0.33	-1.91 ± 0.50	0.18 ± 0.16	2.36 ± 0.21	1.39E-04	1.57E-02	8.93E-01	1.28E-26	
	AT2G32190.2	AT2G32190	AthCYSTM4	47	42	29	63	0.60 ± 1.15	0.20 ± 1.20	-0.26 ± 0.71	2.33 ± 0.59	1.00E+00	1.00E+00	1.00E+00	1.82E-03	
	AT1G15830.1	AT1G15830	--	18	19	17	52	-0.83 ± 1.19	-0.70 ± 1.60	0.42 ± 0.97	2.32 ± 0.61	1.00E+00	1.00E+00	1.00E+00	3.38E-03	
*	AT1G21326.1	AT1G21326	--	87	91	15	36	0.60 ± 0.70	0.60 ± 0.63	0.05 ± 0.95	2.30 ± 0.78	1.00E+00	1.00E+00	1.00E+00	4.60E-02	VQ motif-containing protein
	AT1G22160.1	AT1G22160	--	256	225	78	186	-0.16 ± 0.40	-0.75 ± 0.39	1.02 ± 0.45	2.29 ± 0.42	1.00E+00	1.00E+00	2.63E-01	2.89E-06	
	AT3G02940.1	AT3G02940	MYB107	191	182	158	337	-0.57 ± 0.46	-0.89 ± 0.63	0.84 ± 0.37	2.29 ± 0.26	1.00E+00	1.00E+00	2.60E-01	8.59E-16	
	AT4G38390.1	AT4G38390	RHS17	349	328	140	364	-0.01 ± 0.28	-0.29 ± 0.38	-0.13 ± 0.40	2.26 ± 0.29	1.00E+00	1.00E+00	1.00E+00	1.64E-12	
	AT5G04220.1	AT5G04220	SYTC	274	282	554	1755	-0.85 ± 0.45	-0.86 ± 0.46	0.55 ± 0.28	2.24 ± 0.16	1.00E+00	1.00E+00	3.98E-01	3.23E-42	
	AT5G06120.2	AT5G06120	--	509	298	419	306	-0.36 ± 1.08	-6.40 ± 2.78	-0.15 ± 0.57	2.24 ± 0.68	1.00E+00	6.69E-01	1.00E+00	1.83E-02	
	AT2G37760.4	AT2G37760	AKR4C8	95	27	187	225	2.								

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT1G05410.2	AT1G05410	--	198	252	93	190	0.17 ± 1.19	0.69 ± 1.21	-0.44 ± 4.56	2.16 ± 0.52	1.00E+00	1.00E+00	1.00E+00	9.83E-04	Protein of unknown function (DUF1423)
	AT2G484140.2	AT2G484140	EDA4	183	186	353	814	-0.65 ± 0.52	-0.75 ± 0.68	0.43 ± 0.36	2.15 ± 0.29	1.00E+00	1.00E+00	8.51E-01	2.24E-11	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT1G72920.1	AT1G72920	--	70	98	103	233	0.10 ± 0.76	0.85 ± 0.63	0.40 ± 0.42	2.15 ± 0.45	1.00E+00	1.00E+00	9.44E-01	7.97E-05	Toll-Interleukin-Resistance (TIR) domain family protein
	AT2G43920.1	AT2G43920	HOL2	1604	1493	1256	1118	-0.35 ± 0.40	-0.74 ± 0.30	-0.37 ± 0.15	2.15 ± 0.43	1.00E+00	4.75E-01	1.92E-01	2.94E-05	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
	AT3G49330.1	AT3G49330	--	572	573	394	698	-0.68 ± 0.26	-0.91 ± 0.30	0.82 ± 0.26	2.13 ± 0.26	4.30E-01	1.56E-01	4.34E-02	5.96E-14	Plant invertase/pectin methyltransferase inhibitor superfamily protein
	AT1G71860.2	AT1G71860	PTP1	175	194	45	69	-0.07 ± 0.80	0.14 ± 0.62	0.00 ± 0.74	2.13 ± 0.78	1.00E+00	1.00E+00	1.00E+00	7.56E-02	protein tyrosine phosphatase 1
	AT4G34510.1	AT4G34510	KCS17	72	66	72	183	-0.12 ± 0.90	-0.50 ± 0.79	0.55 ± 0.50	2.13 ± 0.34	1.00E+00	1.00E+00	8.86E-01	4.27E-08	3-ketoacyl-CoA synthase 17
	AT2G38185.1	AT2G38185	APD1	417	416	121	346	0.05 ± 0.30	-0.05 ± 0.31	-1.58 ± 1.10	2.13 ± 0.72	1.00E+00	1.00E+00	7.31E-01	4.33E-02	RING/U-box superfamily protein
	AT5G66070.2	AT5G66070	--	123	137	36	98	0.08 ± 0.78	0.26 ± 0.73	-0.37 ± 0.66	2.13 ± 0.52	1.00E+00	1.00E+00	1.00E+00	1.07E-03	RING/U-box superfamily protein
	AT2G34200.1	AT2G34200	--	304	368	272	513	0.00 ± 0.29	0.40 ± 0.37	0.61 ± 0.25	2.12 ± 0.30	1.00E+00	1.00E+00	2.00E-01	1.38E-10	RING/FYVE/PHD zinc finger superfamily protein
	AT1G50590.1	AT1G50590	--	697	696	222	553	-0.20 ± 0.32	-0.34 ± 0.32	0.98 ± 0.34	2.12 ± 0.31	1.00E+00	1.00E+00	7.19E-02	1.12E-09	RmlC-like cupins superfamily protein
	AT1G24735.2	AT1G24735	--	293	334	162	478	0.11 ± 0.37	0.36 ± 0.43	0.08 ± 0.32	2.12 ± 0.34	1.00E+00	1.00E+00	1.00E+00	4.76E-08	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
	AT5G59050.1	AT5G59050	--	1690	1628	1004	2705	-0.09 ± 0.18	-0.31 ± 0.19	0.65 ± 0.15	2.11 ± 0.16	1.00E+00	1.00E+00	9.78E-04	3.76E-37	WRKY DNA-binding protein 43
	AT2G46130.1	AT2G46130	WRKY43	97	104	153	453	-1.44 ± 0.83	-1.33 ± 0.59	0.68 ± 0.40	2.11 ± 0.33	1.00E+00	7.28E-01	5.68E-01	8.98E-09	WRKY DNA-binding protein 43
	AT2G46130.2	AT2G46130	WRKY43	16	9	20	59	-0.15 ± 1.18	-6.67 ± 2.77	0.88 ± 0.91	2.11 ± 0.59	1.00E+00	5.78E-01	9.37E-01	7.32E-03	GDSL-like Lipase/Acylhydrolase superfamily protein
	AT4G26790.1	AT4G26790	--	403	382	297	659	-0.96 ± 0.52	-1.37 ± 0.57	0.15 ± 0.37	2.11 ± 0.27	1.00E+00	5.68E-01	1.00E+00	1.12E-12	Transketolase
	AT3G60750.2	AT3G60750	TKL1	392	119	154	263	1.71 ± 3.71	-1.91 ± 2.08	-0.85 ± 0.47	2.10 ± 0.40	1.00E+00	1.00E+00	5.14E-01	9.20E-06	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT4G33550.1	AT4G33550	--	47	63	47	196	0.30 ± 0.73	0.86 ± 0.90	1.57 ± 0.68	2.10 ± 0.48	1.00E+00	1.00E+00	2.49E-01	4.23E-04	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT2G48130.1	AT2G48130	--	5027	5080	5077	9502	-0.62 ± 0.23	-0.75 ± 0.23	0.78 ± 0.17	2.10 ± 0.17	4.51E-01	7.72E-02	4.14E-04	7.65E-31	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT5G55180.1	AT5G55180	--	4176	4404	7054	14609	-0.40 ± 0.12	-0.33 ± 0.18	0.51 ± 0.12	2.09 ± 0.16	1.09E-01	1.00E+00	1.55E-03	2.34E-38	O-Glycosyl hydrolases family 17 protein
	AT5G23240.1	AT5G23240	DJC76	303	340	239	164	0.25 ± 0.44	0.46 ± 0.50	0.44 ± 0.33	2.09 ± 0.35	1.00E+00	1.00E+00	7.86E-01	1.02E-07	DNAJ heat shock N-terminal domain-containing protein
	AT1G27730.1	AT1G27730	STZ	3744	3684	1012	783	1.22 ± 0.22	1.10 ± 0.21	-0.02 ± 0.25	2.08 ± 0.38	1.57E-05	2.82E-05	1.00E+00	1.59E-06	salt tolerance zinc finger
	AT1G79700.2	AT1G79700	WR14	873	895	1145	1871	-0.34 ± 0.33	-0.38 ± 0.35	0.43 ± 0.17	2.08 ± 0.19	1.00E+00	1.00E+00	1.44E-01	1.15E-24	Integrase-type DNA-binding superfamily protein
	AT2G47240.2	AT2G47240	LACS1	270	311	269	309	-0.73 ± 0.59	-0.34 ± 0.55	0.26 ± 0.28	2.08 ± 0.31	1.00E+00	1.00E+00	9.55E-01	1.17E-09	AMP-dependent synthetase and ligase family protein
	AT4G40085.1	AT4G40085	--	134	128	111	92	-0.83 ± 0.64	-1.17 ± 0.54	-0.31 ± 0.40	2.07 ± 0.78	1.00E+00	8.38E-01	9.90E-01	9.43E-02	other RNA
	AT5G30340.2	AT5G30340	IQD2	294	19	151	383	3.90 ± 2.84	-6.28 ± 3.27	-1.57 ± 3.86	2.07 ± 0.38	1.00E+00	1.00E+00	1.00E+00	2.78E-06	IQ-domain 2
	AT5G23170.1	AT5G23170	--	492	494	346	724	0.15 ± 0.25	0.06 ± 0.27	0.77 ± 0.22	2.07 ± 0.23	1.00E+00	1.00E+00	1.33E-02	9.57E-17	Protein kinase superfamily protein
	AT2G17410.2	AT2G17410	--	201	122	163	100	0.77 ± 0.94	-0.76 ± 0.72	0.23 ± 0.49	2.07 ± 0.51	1.00E+00	1.00E+00	1.00E+00	1.59E-03	ARID/BRIGHT DNA-binding domain-containing protein
	AT3G49055.1	AT3G49055	--	62	56	62	189	0.01 ± 0.61	-0.39 ± 0.75	0.30 ± 0.57	2.06 ± 0.37	1.00E+00	1.00E+00	1.00E+00	1.73E-06	Calcosin-related family protein
	AT2G33380.1	AT2G33380	RD20	0	0	8	80	NA ± NA	NA ± NA	0.43 ± 1.27	2.06 ± 0.65	NA	NA	1.00E+00	2.57E-02	TATA BOX ASSOCIATED FACTOR II 59
	AT1G04950.1	AT1G04950	TAFII59	254	356	131	118	-1.38 ± 0.73	-0.18 ± 0.72	-1.35 ± 1.29	2.06 ± 0.42	1.00E+00	1.00E+00	9.05E-01	3.93E-05	Protein kinase superfamily protein
	AT5G58540.1	AT5G58540	--	191	114	105	179	0.57 ± 0.45	-1.22 ± 0.53	-1.69 ± 2.96	2.06 ± 0.73	1.00E+00	6.75E-01	1.00E+00	6.17E-02	CAP160 protein
	AT5G52300.1	AT5G52300	LTI65	3	6	149	115	-1.70 ± 2.29	0.35 ± 2.90	0.84 ± 1.26	2.05 ± 0.57	1.00E+00	1.00E+00	1.00E+00	6.38E-03	acyl-activating enzyme 18
	AT1G55320.2	AT1G55320	AAE18	655	646	159	151	-0.21 ± 0.25	-0.35 ± 0.28	-0.80 ± 0.86	2.05 ± 0.53	1.00E+00	1.00E+00	9.45E-01	2.54E-03	transcription factor-related
	AT4G17020.3	AT4G17020	--	389	388	193	132	-0.27 ± 0.72	-0.38 ± 0.55	0.15 ± 0.32	2.05 ± 0.76	1.00E+00	1.00E+00	1.00E+00	8.35E-02	nodulin MtN21 /EamA-like transporter family protein
	AT3G56620.1	AT3G56620	UMAMIT10	199	195	165	106	0.81 ± 0.37	0.69 ± 0.42	1.11 ± 0.45	2.04 ± 0.43	9.20E-01	1.00E+00	1.80E-01	7.47E-05	organic cation/carnitine transporter1
	AT1G73220.1	AT1G73220	OCT1	40	48	307	1468	-0.33 ± 0.91	0.16 ± 1.02	1.81 ± 0.58	2.04 ± 0.14	1.00E+00	1.00E+00	3.92E-02	4.67E-44	serine protease inhibitor, Kazal-type family protein
	AT4G01575.1	AT4G01575	KPI-2	197	233	108	244	-0.09 ± 0.44	0.25 ± 0.38	0.80 ± 0.42	2.03 ± 0.37	1.00E+00	1.00E+00	4.51E-01	2.07E-06	Galactose oxidase/kelch repeat superfamily protein
	AT2G03460.1	AT2G03460	--	14	14	11	31	0.42 ± 1.42	0.26 ± 1.50	0.82 ± 1.16	2.02 ± 0.76	1.00E+00	1.00E+00	1.00E+00	9.58E-02	Protein of unknown function, DUF547
	AT5G66600.3	AT5G66600	--	196	137	88	155	1.20 ± 0.94	0.31 ± 0.88	2.27 ± 2.73	2.00 ± 0.65	1.00E+00	1.00E+00	9.72E-01	3.07E-02	xyloglucan endotransglucosylase/hydrolase 24
	AT1G56660.1	AT1G56660	--	4531	5490	2324	5988	-0.31 ± 0.25	0.16 ± 0.23	0.29 ± 0.18	2.00 ± 0.12	1.00E+00	1.00E+00	6.33E-01	6.56E-62	Phosphoglycerate mutase family protein
	AT4G30270.1	AT4G30270	XTH24	2593	2750	2085	3375	-0.27 ± 0.30	-0.20 ± 0.58	0.38 ± 0.23	2.00 ± 0.32	1.00E+00	1.00E+00	5.83E-01	1.66E-08	WRKY DNA-binding protein 24
	AT5G64460.1	AT5G64460	--	94	104	130	76	0.15 ± 0.69	0.32 ± 0.63	-0.12 ± 0.54	2.00 ± 0.70	1.00E+00	1.00E+00	1.00E+00	6.11E-02	long chain acyl-CoA synthetase 9
	AT5G41570.1	AT5G41570	WRKY24	215	200	581	1678	-0.96 ± 0.43	-1.52 ± 0.67	0.46 ± 0.23	2.00 ± 0.22	8.77E-01	7.24E-01	3.79E-01	7.83E-18	Developmental regulator, ULTRAPETALA
	AT4G02830.1	AT4G02830	--	248	256	306	546	-0.86 ± 0.45	-0.91 ± 0.53	0.52 ± 0.28	1.99 ± 0.30	1.00E+00	1.00E+00	4.88E-01	2.17E-09	ATP-citrate lyase A-1
	AT1G77590.1	AT1G77590	LACS9	4964	5111	5649	11942	-0.52 ± 0.13	-0.52 ± 0.15	0.65 ± 0.12	1.99 ± 0.12	1.12E-02	4.65E-02	4.71E-06	2.85E-63	dihydroflavonol 4-reductase-like1
	AT2G20825.1	AT2G20825	ULT2	45	51	50	123	0.03 ± 0.90	0.27 ± 0.99	1.08 ± 0.62	1.99 ± 0.56	1.00E+00	1.00E+00	5.59E-01	8.11E-03	Cysteine/Histidine-rich C1 domain family protein
	AT1G10670.2	AT1G10670	ACLA-1	848	1041	430	875	-0.27 ± 0.31	0.23 ± 0.25	0.93 ± 0.36	1.98 ± 0.23	1.00E+00	1.00E+00	1.38E-01	3.57E-15	C2H2-like zinc finger protein
	AT4G35420.1	AT4G35420	DRL1	781	805	982	1369	-0.97 ± 0.26	-0.99 ± 0.28	0.54 ± 0.17	1.94 ± 0.23	2.76E-02	3.98E-02	2.91E-02	2.10E-15	C2H2-like zinc finger protein
	AT1G62030.1	AT1G62030	--	197	215	27	36	0.12 ± 0.68	0.28 ± 0.48	-0.23 ± 0.74	1.9					

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT2G37070.1	AT2G37070	GPT1	107	93	87	176	-0.20 ± 0.62	-0.77 ± 0.59	0.58 ± 0.44	1.87 ± 0.38	1.00E+00	1.00E+00	7.82E-01	4.00E-05	
	AT1G73480.1	AT1G73480	MAGL4	747	707	732	2088	-0.56 ± 0.25	-0.89 ± 0.36	0.62 ± 0.18	1.86 ± 0.20	8.87E-01	5.38E-01	1.66E-02	1.22E-17	alpha/beta-Hydrolases superfamily protein
	AT1G48700.1	AT1G48700	--	29	34	21	65	-0.48 ± 0.91	-0.02 ± 0.88	0.93 ± 0.93	1.85 ± 0.61	1.00E+00	1.00E+00	9.27E-01	3.88E-02	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
	AT2G16750.1	AT2G16750	--	9967	9875	2545	4530	0.56 ± 0.09	0.47 ± 0.16	0.28 ± 0.11	1.85 ± 0.18	3.74E-07	2.33E-01	1.78E-01	1.56E-21	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain
	AT3G52790.1	AT3G52790	--	469	504	564	1238	-1.11 ± 0.42	-1.11 ± 0.42	0.30 ± 0.22	1.84 ± 0.26	4.51E-01	3.73E-01	7.74E-01	7.03E-11	peptidoglycan-binding LysM domain-containing protein
	AT2G29380.1	AT2G29380	HAI3	7	12	27	90	-0.66 ± 1.61	0.65 ± 1.37	1.03 ± 0.98	1.83 ± 0.48	1.00E+00	1.00E+00	9.04E-01	3.05E-03	highly ABA-induced PP2C gene 3
	AT1G01610.1	AT1G01610	GPAT4	3634	3602	5852	10940	-0.60 ± 0.19	-0.75 ± 0.23	0.75 ± 0.13	1.83 ± 0.15	1.47E-01	9.88E-02	1.43E-06	3.56E-31	glycerol-3-phosphate acyltransferase 4
	AT4G10480.2	AT4G10480	--	239	264	78	100	1.10 ± 3.26	1.23 ± 3.44	0.09 ± 0.46	1.82 ± 0.47	1.00E+00	1.00E+00	1.00E+00	2.51E-03	Nascent polypeptide-associated complex (NAC), alpha subunit family protein
	AT3G25640.1	AT3G25640	--	833	911	969	1980	-0.69 ± 0.22	-0.50 ± 0.24	0.68 ± 0.13	1.82 ± 0.21	1.49E-01	9.96E-01	2.77E-05	1.10E-15	Protein of unknown function, DUF617
	AT1G03790.1	AT1G03790	SOM	15	9	48	76	0.15 ± 1.31	-2.14 ± 1.63	0.69 ± 0.57	1.81 ± 0.50	1.00E+00	1.00E+00	8.53E-01	6.88E-03	Zinc finger C-x8-C-x5-C-x3-H type family protein
*	AT3G56580.3	AT3G56580	RZF1	557	460	879	1906	-0.82 ± 0.41	-1.98 ± 3.29	0.50 ± 0.24	1.81 ± 0.27	1.00E+00	1.00E+00	3.32E-01	2.03E-09	RING/U-box superfamily protein
	AT1G78990.1	AT1G78990	--	672	667	2064	5120	-3.85 ± 0.30	-5.29 ± 0.44	-0.27 ± 0.22	1.81 ± 0.15	3.19E-33	3.99E-29	8.27E-01	8.38E-30	HXXXD-type acyl-transferase family protein
	AT1G21520.1	AT1G21520	--	67	73	54	113	0.11 ± 0.74	0.17 ± 0.73	1.01 ± 0.53	1.80 ± 0.52	1.00E+00	1.00E+00	4.56E-01	1.03E-02	
*	AT3G06390.1	AT3G06390	CASPL1D2	1714	1585	2639	5385	-1.33 ± 0.29	-2.06 ± 0.39	0.08 ± 0.14	1.80 ± 0.19	8.06E-04	3.73E-05	1.00E+00	3.01E-18	Uncharacterised protein family (UPF0497)
	AT1G70170.1	AT1G70170	MMP	920	928	1064	2108	-0.18 ± 0.24	-0.26 ± 0.24	0.69 ± 0.28	1.79 ± 0.18	1.00E+00	1.00E+00	1.73E-01	2.16E-20	matrix metalloproteinase
	AT5G04220.2	AT5G04220	SYTC	248	245	446	1030	-1.40 ± 0.43	-1.65 ± 0.88	-0.60 ± 0.23	1.79 ± 0.22	9.24E-02	1.00E+00	1.40E-01	1.94E-14	Calcium-dependent lipid-binding (CaLB domain) family protein
	AT2G32510.1	AT2G32510	MAPKKK17	535	505	1125	1709	-0.88 ± 0.28	-1.31 ± 0.35	0.76 ± 0.15	1.79 ± 0.21	1.39E-01	1.59E-02	3.95E-05	9.49E-16	mitogen-activated protein kinase kinase kinase 17
	AT2G43670.1	AT2G43670	--	377	354	260	606	-0.90 ± 0.42	-1.49 ± 0.42	-0.14 ± 0.27	1.78 ± 0.32	9.96E-01	3.16E-02	1.00E+00	1.19E-06	Carbohydrate-binding X8 domain superfamily protein
	AT3G60500.2	AT3G60500	CER7	319	168	163	169	2.42 ± 0.78	1.16 ± 0.78	-0.69 ± 0.44	1.78 ± 0.41	1.51E-01	1.00E+00	6.54E-01	4.11E-04	3'-5'-exoribonuclease family protein
	AT3G19020.1	AT3G19020	LRX8	381	373	302	619	-0.57 ± 0.39	-0.76 ± 0.54	0.20 ± 0.24	1.77 ± 0.20	1.00E+00	1.00E+00	9.69E-01	1.10E-16	Leucine-rich repeat (LRR) family protein
	AT3G54840.2	AT3G54840	ARA6	334	276	211	338	0.58 ± 0.85	-0.02 ± 0.59	-1.72 ± 0.64	1.77 ± 0.63	1.00E+00	1.00E+00	1.16E-01	6.86E-02	Ras-related small GTP-binding family protein
	AT1G01120.1	AT1G01120	KCS1	3893	3899	5896	10664	-0.79 ± 0.13	-0.91 ± 0.26	0.79 ± 0.14	1.76 ± 0.14	7.46E-07	4.89E-02	5.05E-06	7.55E-33	3-ketoacyl-CoA synthase 1
	AT2G03200.1	AT2G03200	--	1113	1081	1897	4423	-0.73 ± 0.27	-0.99 ± 0.23	0.19 ± 0.20	1.76 ± 0.17	3.50E-01	3.19E-03	9.44E-01	4.22E-24	Eukaryotic aspartyl protease family protein
	AT4G09760.3	AT4G09760	CEK3	209	245	77	291	-0.82 ± 0.41	-0.37 ± 0.57	-0.14 ± 0.62	1.76 ± 0.29	1.00E+00	1.00E+00	1.00E+00	1.34E-07	Protein kinase superfamily protein
	AT2G38100.1	AT2G38100	NPF5.5	64	72	23	75	-0.64 ± 0.68	-0.35 ± 0.83	-0.33 ± 0.82	1.75 ± 0.49	1.00E+00	1.00E+00	1.00E+00	7.24E-03	proton-dependent oligopeptide transport (POT) family protein
	AT5G09670.2	AT5G09670	--	748	766	989	709	-0.10 ± 0.88	-0.12 ± 1.99	-0.46 ± 0.29	1.75 ± 0.19	1.00E+00	1.00E+00	6.45E-01	4.82E-17	loricrin-related
	AT1G29230.1	AT1G29230	CIPK18	110	106	63	86	0.00 ± 0.58	-0.22 ± 0.64	1.60 ± 0.66	1.75 ± 0.53	1.00E+00	1.00E+00	1.97E-01	1.85E-02	CBL-interacting protein kinase 18
*	AT5G53220.3	AT5G53220	--	282	332	152	295	-0.21 ± 0.68	0.16 ± 0.62	-0.14 ± 0.41	1.75 ± 0.26	1.00E+00	1.00E+00	1.00E+00	2.02E-09	
	AT2G23540.1	AT2G23540	--	4632	4296	9162	20039	-1.06 ± 0.26	-1.62 ± 0.27	-0.02 ± 0.14	1.74 ± 0.13	9.89E-03	6.93E-07	1.00E+00	1.78E-39	GDSL-like Lipase/Acylhydrolase superfamily protein
*	AT2G47630.1	AT2G47630	MAGL9	2688	2782	1856	3539	0.02 ± 0.19	0.02 ± 0.22	0.37 ± 0.13	1.74 ± 0.16	1.00E+00	1.00E+00	1.01E-01	1.17E-26	alpha/beta-Hydrolases superfamily protein
	AT1G64000.1	AT1G64000	WRKY56	242	229	476	976	-2.07 ± 0.52	-2.99 ± 0.61	0.53 ± 0.20	1.73 ± 0.24	9.79E-03	2.33E-04	1.46E-01	6.17E-11	WRKY DNA-binding protein 56
	AT4G28930.1	AT4G28930	--	20	21	52	65	-2.45 ± 1.11	-2.45 ± 1.15	0.06 ± 0.54	1.72 ± 0.55	8.87E-01	8.81E-01	1.00E+00	2.88E-02	
	AT5G63130.1	AT5G63130	--	291	278	104	176	0.36 ± 0.34	0.13 ± 0.36	0.86 ± 0.45	1.72 ± 0.37	1.00E+00	1.00E+00	4.42E-01	1.29E-04	Octicosa peptide/Phox/Bem1p family protein
	AT1G21400.1	AT1G21400	--	290	329	1259	806	-0.51 ± 0.75	-0.20 ± 0.58	0.79 ± 0.39	1.71 ± 0.48	1.00E+00	1.00E+00	3.98E-01	7.38E-03	Thiamin diphosphate-binding fold (THDP-binding) superfamily protein
	AT1G54540.1	AT1G54540	NHL11	1360	1360	1150	2076	0.02 ± 0.17	-0.10 ± 0.19	0.87 ± 0.18	1.71 ± 0.24	1.00E+00	1.00E+00	5.70E-05	3.58E-11	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
	AT3G21530.1	AT3G21530	--	875	931	642	1287	0.21 ± 0.24	0.29 ± 0.34	0.29 ± 0.19	1.71 ± 0.21	1.00E+00	1.00E+00	6.86E-01	1.39E-14	DNase I-like superfamily protein
	AT3G44730.1	AT3G44730	KP1	2042	2022	1578	3657	-0.50 ± 0.14	-0.63 ± 0.32	0.28 ± 0.15	1.71 ± 0.14	4.49E-02	1.00E+00	5.25E-01	3.28E-32	kinesin-like protein 1
	AT3G56130.2	AT3G56130	BLP3	1197	1142	493	879	0.03 ± 0.26	-0.21 ± 0.30	0.73 ± 0.24	1.71 ± 0.23	1.00E+00	1.00E+00	5.57E-02	2.92E-11	biotin/lipoyl attachment domain-containing protein
	AT5G26030.2	AT5G26030	FC1	19	70	777	313	1.06 ± 3.61	3.36 ± 1.93	-0.65 ± 0.36	1.70 ± 0.44	1.00E+00	1.00E+00	5.24E-01	2.92E-03	ferrochelatase 1
	AT1G28815.1	AT1G28815	--	140	175	79	158	-0.70 ± 0.48	-0.19 ± 0.48	0.95 ± 0.52	1.69 ± 0.42	1.00E+00	1.00E+00	5.01E-01	1.34E-03	
	AT3G62590.1	AT3G62590	--	358	381	472	1100	-0.99 ± 0.31	-0.85 ± 0.32	0.71 ± 0.25	1.69 ± 0.19	1.12E-01	3.67E-01	8.63E-02	5.92E-16	alpha/beta-Hydrolases superfamily protein
	AT1G18070.3	AT1G18070	--	394	275	220	165	1.46 ± 1.38	0.63 ± 0.97	-1.01 ± 0.77	1.69 ± 0.36	1.00E+00	1.00E+00	7.94E-01	8.31E-05	Translation elongation factor EF1A/initiation factor IF2gamma family protein
	AT1G80520.1	AT1G80520	--	344	364	157	242	-0.15 ± 0.31	-0.16 ± 0.31	0.45 ± 0.37	1.68 ± 0.40	1.00E+00	1.00E+00	8.44E-01	8.45E-04	Sterile alpha motif (SAM) domain-containing protein
	AT2G01275.2	AT2G01275	--	147	146	116	172	-0.42 ± 0.50	-0.58 ± 0.45	0.71 ± 0.72	1.68 ± 0.52	1.00E+00	1.00E+00	9.35E-01	2.08E-02	RING/FYVE/PHD zinc finger superfamily protein
	AT4G20440.2	AT4G20440	smB	522	391	519	435	0.60 ± 0.37	-0.29 ± 0.45	-0.24 ± 0.45	1.66 ± 0.57	1.00E+00	1.00E+00	1.00E+00	5.24E-02	small nuclear ribonucleoprotein associated protein B
	AT3G19002.1	AT3G19002	--	80	67	67	143	0.27 ± 0.65	-0.34 ± 0.66	-0.11 ± 0.54	1.65 ± 0.38	1.00E+00	1.00E+00	1.00E+00	4.06E-04	other RNA
	AT2G01275.1	AT2G01275	--	140	156	129	216	-0.61 ± 0.55	-0.37 ± 0.53	0.22 ± 0.53	1.65 ± 0.39	1.00E+00	1.00E+00	1.00E+00	7.80E-04	RING/FYVE/PHD zinc finger superfamily protein
	AT2G40160.1	AT2G40160	TBL30	1463	1482	783	1483	-0.27 ± 0.20	-0.33 ± 0.22	0.23 ± 0.19	1.65 ± 0.19	1.00E+00	1.00E+00	8.58E-01	6.85E-16	Plant protein of unknown function (DUF828)
	AT1G10790.1	AT1G10790	--	127	130	115	252	-0.83 ± 0.44	-0.88 ± 0.56	0.39 ± 0.40	1.65 ± 0.35	1.00E+00	1.00E+00	9.31E-01	8.55E-05	
	AT1G52155.1	AT1G52155	--	863	893	286	430	-0.39 ± 0.20	-0.39 ± 0.23	0.45 ± 0.28	1.64 ± 0.33	1.00E+00	1.00E+00	6.32E-01	2.30E-05	
	AT5G02840.2	AT5G02840	LCL1	86	95	54	66	-0.22 ± 0.58	-0.04 ± 0.59	-1.28 ± 0.56	1.64 ± 0.60	1.00E+00	1.00E+00	2.58E-01	7.69E-02	LHY/CCA1-like 1
	AT1G02205.2	AT1G02205	CER1	65	66	114	190	-0.82 ± 0.75	-0.91 ± 0.78	1.23 ± 0.45	1.64 ± 0.52	1.00E+00	1.00E+00	1.07E-01	2.88E-02	Fatty acid hydroxylase superfamily super

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
*	AT5G58330.2	AT5G58330	NADP-MDH	301	218	291	153	-0.76 ± 0.42	-3.14 ± 0.50	-1.20 ± 0.69	1.57 ± 0.57	1.00E+00	1.82E-07	5.58E-01	7.12E-02	lactate/malate dehydrogenase family protein
	AT4G20390.1	AT4G20390	CASPL1B2	2324	2273	3517	9915	-1.97 ± 0.36	-2.50 ± 0.37	-0.03 ± 0.14	1.55 ± 0.17	2.50E-05	6.94E-09	1.00E+00	3.56E-17	Uncharacterised protein family (UPF0497)
	AT4G30850.2	AT4G30850	HHP2	2155	2006	1207	3354	0.03 ± 0.23	-0.29 ± 0.22	0.48 ± 0.14	1.55 ± 0.19	1.00E+00	1.00E+00	2.46E-02	6.01E-14	heptahelical transmembrane protein2
	AT3G49780.1	AT3G49780	PSK4	877	781	779	509	0.02 ± 0.21	-0.57 ± 0.33	0.35 ± 0.25	1.55 ± 0.30	1.00E+00	1.00E+00	7.66E-01	1.21E-05	phytosulfokine 4 precursor
	AT1G24600.1	AT1G24600	--	59	76	45	81	-0.22 ± 0.91	0.31 ± 0.62	1.13 ± 0.65	1.54 ± 0.52	1.00E+00	1.00E+00	5.55E-01	4.17E-02	
	AT4G02380.2	AT4G02380	SAG21	1229	986	184	261	1.03 ± 0.59	0.37 ± 0.60	-0.61 ± 0.69	1.54 ± 0.48	1.00E+00	1.00E+00	9.63E-01	2.14E-02	senescence-associated gene 21
	AT2G34470.2	AT2G34470	UREG	715	739	192	391	-0.39 ± 0.56	-0.41 ± 0.65	-1.05 ± 0.48	1.54 ± 0.33	1.00E+00	1.00E+00	3.09E-01	1.17E-04	urease accessory protein G
	AT1G24735.1	AT1G24735	--	218	231	56	221	0.06 ± 0.47	0.09 ± 0.49	-0.14 ± 0.52	1.54 ± 0.39	1.00E+00	1.00E+00	1.00E+00	2.46E-03	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
	AT1G27720.1	AT1G27720	TAF4B	204	212	93	106	-0.17 ± 0.35	-0.15 ± 0.41	0.32 ± 0.45	1.53 ± 0.43	1.00E+00	1.00E+00	1.00E+00	8.51E-03	TBP-associated factor 4B
	AT2G44630.1	AT2G44630	--	154	148	98	148	-0.16 ± 0.63	-0.40 ± 0.66	0.03 ± 0.41	1.53 ± 0.42	1.00E+00	1.00E+00	1.00E+00	5.28E-03	Galactose oxidase/kelch repeat superfamily protein
*	AT2G41540.2	AT2G41540	GPDHC1	1368	1269	1355	1688	0.02 ± 0.55	-0.30 ± 0.43	0.27 ± 0.25	1.53 ± 0.20	1.00E+00	1.00E+00	8.90E-01	7.27E-12	6-phosphogluconate dehydrogenase family protein
	AT2G38060.1	AT2G38060	PH4T4.2	543	535	522	1028	-0.20 ± 0.26	-0.35 ± 0.30	0.48 ± 0.23	1.53 ± 0.25	1.00E+00	1.00E+00	3.80E-01	3.40E-08	phosphate transporter 4;2
	AT5G04340.1	AT5G04340	ZAT6	2256	2481	1605	2099	0.22 ± 0.30	0.37 ± 0.30	0.16 ± 0.15	1.52 ± 0.22	1.00E+00	1.00E+00	9.01E-01	1.31E-09	zinc finger of Arabidopsis thaliana 6
	AT1G19530.1	AT1G19530	--	8997	8811	1940	1069	0.54 ± 0.78	0.37 ± 0.47	0.47 ± 0.19	1.52 ± 0.39	1.00E+00	1.00E+00	1.72E-01	2.50E-03	
	AT1G01060.2	AT1G01060	LHY	44	43	10	120	-4.45 ± 3.15	-8.93 ± 3.40	-6.92 ± 3.93	1.52 ± 0.50	1.00E+00	3.79E-01	5.42E-01	3.48E-02	Homeodomain-like superfamily protein
	AT2G44230.1	AT2G44230	--	407	435	1339	2386	-1.31 ± 0.32	-1.13 ± 0.44	0.69 ± 0.17	1.52 ± 0.16	6.15E-03	4.32E-01	2.56E-03	1.81E-19	Plant protein of unknown function (DUF946)
	AT4G37550.3	AT4G37550	--	335	296	92	139	-0.51 ± 0.43	-1.13 ± 0.51	0.88 ± 0.60	1.51 ± 0.41	1.00E+00	7.51E-01	7.19E-01	4.82E-03	Acetamidase/Formamidase family protein
	AT1G49430.1	AT1G49430	LACS2	2270	2126	3702	6839	-1.11 ± 0.29	-1.61 ± 0.27	0.04 ± 0.13	1.51 ± 0.12	1.58E-02	8.90E-07	1.00E+00	1.91E-35	long-chain acyl-CoA synthetase 2
	AT3G23780.2	AT3G23780	NRPD2A	750	1043	565	519	0.08 ± 0.32	0.83 ± 0.41	-0.89 ± 0.26	1.51 ± 0.44	1.00E+00	1.00E+00	1.91E-02	1.04E-02	nuclear RNA polymerase D2A
	AT2G38110.1	AT2G38110	GPAT16	816	761	1955	4800	-0.60 ± 0.23	-0.99 ± 0.36	0.16 ± 0.11	1.50 ± 0.13	5.11E-01	2.57E-01	7.57E-01	5.26E-30	glycerol-3-phosphate acyltransferase 6
*	AT5G43810.2	AT5G43810	AGO10	468	335	253	178	0.41 ± 1.11	-0.68 ± 1.04	-0.02 ± 0.34	1.50 ± 0.46	1.00E+00	1.00E+00	1.00E+00	1.81E-02	Stabilizer of iron transporter SufD / Polynucleotidyl transferase
	AT5G20710.1	AT5G20710	BGAL7	13	13	31	100	-2.49 ± 2.27	-2.36 ± 1.44	0.28 ± 0.76	1.50 ± 0.56	1.00E+00	1.00E+00	1.00E+00	9.44E-02	beta-galactosidase 7
	AT2G32560.1	AT2G32560	--	2845	3119	1310	2191	0.09 ± 0.20	0.25 ± 0.21	0.55 ± 0.16	1.50 ± 0.20	1.00E+00	1.00E+00	2.37E-02	2.59E-11	F-box family protein
	AT4G39330.2	AT4G39330	CAD9	92	61	167	97	0.21 ± 0.51	-1.36 ± 0.78	0.19 ± 0.34	1.50 ± 0.50	1.00E+00	1.00E+00	1.00E+00	4.35E-02	cinnamyl alcohol dehydrogenase 9
	AT2G13360.2	AT2G13360	AGT	799	854	579	581	-0.65 ± 0.62	-0.53 ± 0.56	-0.80 ± 0.38	1.50 ± 0.25	1.00E+00	1.00E+00	3.45E-01	1.08E-07	alanine:glyoxylate aminotransferase
	AT1G33050.2	AT1G33050	--	723	526	229	200	0.94 ± 0.37	0.09 ± 0.37	-0.37 ± 0.51	1.49 ± 0.47	5.42E-01	1.00E+00	9.98E-01	2.72E-02	
	AT4G32420.1	AT4G32420	--	2525	1825	1383	549	0.44 ± 1.36	-0.60 ± 1.35	0.21 ± 0.20	1.49 ± 0.40	1.00E+00	1.00E+00	9.06E-01	4.67E-03	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein
	AT4G16690.1	AT4G16690	MES16	28	29	191	309	-0.61 ± 1.13	-0.54 ± 1.14	0.00 ± 0.50	1.48 ± 0.41	1.00E+00	1.00E+00	1.00E+00	6.94E-03	methyl esterase 16
	AT4G18910.1	AT4G18910	NIP1;2	984	1080	642	1379	-0.36 ± 0.31	-0.18 ± 0.30	0.27 ± 0.18	1.48 ± 0.21	1.00E+00	1.00E+00	6.73E-01	7.82E-11	NOD26-like intrinsic protein 1;2
	AT1G74000.1	AT1G74000	SS3	305	320	335	568	-0.17 ± 0.34	-0.13 ± 0.33	0.26 ± 0.24	1.48 ± 0.23	1.00E+00	1.00E+00	8.80E-01	1.81E-08	strictosidine synthase 3
*	AT2G25290.3	AT2G25290	PHOX1	176	144	152	119	-0.21 ± 1.57	-1.06 ± 0.96	0.66 ± 0.67	1.47 ± 0.41	1.00E+00	1.00E+00	9.36E-01	6.32E-03	Octicosaepptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein
	AT1G62320.1	AT1G62320	--	622	635	375	490	-0.34 ± 0.32	-0.37 ± 0.31	0.22 ± 0.23	1.45 ± 0.27	1.00E+00	1.00E+00	9.28E-01	5.24E-06	ERD (early-responsive to dehydration stress) family protein
	AT4G30850.1	AT4G30850	HHP2	2528	2518	2433	4087	-0.34 ± 0.17	-0.46 ± 0.25	0.37 ± 0.16	1.45 ± 0.09	1.00E+00	1.00E+00	2.19E-01	6.56E-62	heptahelical transmembrane protein2
	AT2G28470.1	AT2G28470	BGAL8	6061	6013	3127	4870	-0.06 ± 0.18	-0.17 ± 0.14	0.61 ± 0.17	1.45 ± 0.13	1.00E+00	1.00E+00	1.26E-02	5.58E-25	beta-galactosidase 8
	AT2G18050.1	AT2G18050	HIS1-3	1381	1315	308	367	-0.15 ± 0.38	-0.45 ± 0.46	0.07 ± 0.25	1.45 ± 0.27	1.00E+00	1.00E+00	1.00E+00	4.70E-06	histone H1-3
	AT3G13920.4	AT3G13920	EIF4A1	3796	1922	3408	3664	1.25 ± 1.21	-0.61 ± 0.57	-0.72 ± 0.24	1.45 ± 0.24	1.00E+00	1.00E+00	6.24E-02	2.10E-07	eukaryotic translation initiation factor 4A1
	AT1G61190.1	AT1G61190	--	179	167	109	185	0.08 ± 0.38	-0.23 ± 0.50	-0.31 ± 0.40	1.45 ± 0.34	1.00E+00	1.00E+00	9.88E-01	6.66E-04	LRR and NB-ARC domains-containing disease resistance protein
	AT3G13275.1	AT3G13275	--	207	220	156	292	-0.03 ± 0.35	-0.01 ± 0.45	0.29 ± 0.32	1.45 ± 0.32	1.00E+00	1.00E+00	9.50E-01	2.84E-04	
	AT5G24380.1	AT5G24380	YSL2	1109	1062	1549	2840	-0.01 ± 0.17	-0.23 ± 0.28	0.50 ± 0.12	1.43 ± 0.17	1.00E+00	1.00E+00	1.37E-03	1.71E-14	YELLOW STRIPE like 2
	AT5G43760.1	AT5G43760	KCS20	4777	4853	6566	9338	-0.35 ± 0.11	-0.41 ± 0.18	0.75 ± 0.12	1.43 ± 0.11	1.11E-01	7.76E-01	3.37E-07	3.64E-36	3-ketoacyl-CoA synthase 20
*	AT2G44500.1	AT2G44500	--	4373	4453	3053	4920	-0.19 ± 0.12	-0.23 ± 0.18	0.54 ± 0.14	1.43 ± 0.15	1.00E+00	1.00E+00	5.87E-03	1.49E-18	O-fucosyltransferase family protein
	AT1G16060.1	AT1G16060	ADAP	2553	2690	1411	3346	0.21 ± 0.24	0.26 ± 0.22	0.37 ± 0.15	1.42 ± 0.19	1.00E+00	1.00E+00	2.01E-01	2.62E-12	ARIA-interacting double AP2 domain protein
	AT5G37690.1	AT5G37690	--	2670	2700	6478	17505	-2.77 ± 0.20	-3.05 ± 0.22	-0.21 ± 0.11	1.41 ± 0.12	1.32E-38	9.86E-41	5.11E-01	3.28E-31	SGNH hydrolase-type esterase superfamily protein
	AT3G03700.1	AT3G03700	--	350	365	355	781	-0.93 ± 0.32	-0.89 ± 0.32	0.65 ± 0.26	1.41 ± 0.40	2.55E-01	2.56E-01	1.79E-01	8.93E-03	Plasma-membrane choline transporter family protein
	AT2G37360.1	AT2G37360	ABCG2	2516	2349	3403	5473	-0.92 ± 0.18	-1.38 ± 0.28	0.59 ± 0.12	1.40 ± 0.14	1.34E-04	1.46E-04	6.95E-05	3.73E-21	ABC-2 type transporter family protein
	AT1G79160.1	AT1G79160	--	467	453	680	1293	-0.29 ± 0.28	-0.52 ± 0.30	0.24 ± 0.21	1.40 ± 0.19	1.00E+00	1.00E+00	8.75E-01	6.87E-12	
	AT1G20020.1	AT1G20020	FNR2	199	224	237	181	-0.56 ± 0.41	-0.28 ± 0.41	-1.01 ± 0.88	1.40 ± 0.51	1.00E+00	1.00E+00	8.71E-01	7.33E-02	ferredoxin-NADP(+)-oxidoreductase 2
	AT4G28040.2	AT4G28040	UFAMIT33	43	25	107	124	1.37 ± 3.31	-0.03 ± 2.26	0.68 ± 0.74	1.40 ± 0.48	1.00E+00	1.00E+00	9.54E-01	5.05E-02	nodulin MtN21 /EamA-like transporter family protein
	AT3G44550.1	AT3G44550	FAR5	3182	2877	4862	8571	-0.33 ± 0.17	-0.81 ± 0.39	0.27 ± 0.09	1.40 ± 0.12	1.00E+00	9.34E-01	7.04E-02	5.84E-28	fatty acid reductase 5
	AT4G17215.1	AT4G17215	--	1082	1126	1814	3384	-0.93 ± 0.30	-0.98 ± 0.32	0.19 ± 0.19	1.40 ± 0.18	1.47E-01	1.43E-01	9.25E-01	1.96E-12	Pollen Ole e 1 allergen and extensin family

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT1G17380.1	AT1G17380	JAZ5	231	241	215	227	0.34 ± 0.46	0.36 ± 0.45	-0.24 ± 0.27	1.35 ± 0.42	1.00E+00	1.00E+00	9.68E-01	2.04E-02	jasmonate-zim-domain protein 5
	AT5G41160.1	AT5G41160	PUP12	155	163	58	134	-0.69 ± 0.41	-0.65 ± 0.45	0.41 ± 0.59	1.35 ± 0.43	1.00E+00	1.00E+00	1.00E+00	2.66E-02	purine permease 12
	AT2G43400.1	AT2G43400	ETFQO	2344	2311	2221	2831	-0.24 ± 0.17	-0.38 ± 0.23	0.63 ± 0.14	1.34 ± 0.15	1.00E+00	1.00E+00	4.67E-04	2.21E-16	electron-transfer flavoprotein:ubiquinone oxidoreductase
	AT1G09155.1	AT1G09155	PP2-B15	370	416	246	226	-0.54 ± 0.31	-0.27 ± 0.37	0.59 ± 0.30	1.34 ± 0.34	1.00E+00	1.00E+00	4.01E-01	2.56E-03	phloem protein 2-B15
	AT1G19190.1	AT1G19190	--	498	507	566	772	-0.33 ± 0.33	-0.39 ± 0.28	0.25 ± 0.18	1.34 ± 0.28	1.00E+00	1.00E+00	7.44E-01	7.00E-05	alpha/beta-Hydrolases superfamily protein
	AT3G51630.1	AT3G51630	WNK5	2185	2205	1018	1901	-0.24 ± 0.20	-0.30 ± 0.19	0.12 ± 0.14	1.33 ± 0.16	1.00E+00	1.00E+00	9.70E-01	8.60E-15	with no lysine (K) kinase 5
	AT3G51632.1	AT3G51632	--	2185	2205	1018	1901	-0.24 ± 0.20	-0.30 ± 0.19	0.12 ± 0.14	1.33 ± 0.16	1.00E+00	1.00E+00	9.70E-01	8.60E-15	conserved peptide upstream open reading frame 44
	AT2G36430.1	AT2G36430	--	226	214	201	287	-0.54 ± 0.54	-0.86 ± 0.49	0.58 ± 0.34	1.33 ± 0.31	1.00E+00	1.00E+00	5.87E-01	5.78E-04	Plant protein of unknown function (DUF247)
	AT1G10070.1	AT1G10070	BCAT-2	240	274	896	502	-0.74 ± 1.22	-0.39 ± 0.51	0.69 ± 0.33	1.32 ± 0.38	1.00E+00	1.00E+00	3.50E-01	9.91E-03	branched-chain amino acid transaminase 2
	AT3G09770.2	AT3G09770	LOG2	77	72	71	108	0.16 ± 0.83	-0.13 ± 0.84	0.70 ± 0.67	1.31 ± 0.41	1.00E+00	1.00E+00	9.05E-01	2.06E-02	RING/U-box superfamily protein
	AT4G39320.1	AT4G39320	--	417	548	225	370	0.12 ± 0.34	0.69 ± 0.37	0.94 ± 0.32	1.31 ± 0.39	1.00E+00	1.00E+00	5.86E-02	1.36E-02	microtubule-associated protein-related
	AT1G67148.1	AT1G67148	--	220	256	120	235	-0.03 ± 0.38	0.21 ± 0.36	0.44 ± 0.37	1.31 ± 0.39	1.00E+00	1.00E+00	8.52E-01	1.50E-02	
	AT4G28640.3	AT4G28640	IAA11	72	72	68	105	1.34 ± 1.04	1.29 ± 1.00	-0.72 ± 0.48	1.31 ± 0.44	1.00E+00	1.00E+00	6.94E-01	3.97E-02	indole-3-acetic acid inducible 11
	AT3G16470.2	AT3G16470	JR1	1552	1519	2249	2013	-0.50 ± 0.73	-0.70 ± 0.41	-0.50 ± 0.64	1.31 ± 0.40	1.00E+00	1.00E+00	9.88E-01	1.70E-02	Mannose-binding lectin superfamily protein
	AT1G53100.1	AT1G53100	--	73	62	87	281	-1.02 ± 0.98	-2.18 ± 1.10	0.02 ± 0.42	1.31 ± 0.25	1.00E+00	1.00E+00	1.00E+00	1.26E-05	Core-2/1-branching beta-1,6-N-acetylglucosaminyltransferase family protein
	AT5G54020.1	AT5G54020	--	862	886	299	646	-0.12 ± 0.18	-0.13 ± 0.24	0.78 ± 0.28	1.31 ± 0.30	1.00E+00	1.00E+00	1.04E-01	4.84E-04	Cysteine/Histidine-rich C1 domain family protein
	AT2G35710.1	AT2G35710	PGSIP7	537	472	307	461	0.12 ± 0.49	-0.36 ± 0.35	-0.31 ± 0.29	1.30 ± 0.25	1.00E+00	1.00E+00	9.03E-01	1.39E-05	Nucleotide-diphospho-sugar transferases superfamily protein
	AT3G11210.1	AT3G11210	--	872	964	856	1369	-0.32 ± 0.35	-0.12 ± 0.41	0.34 ± 0.17	1.30 ± 0.18	1.00E+00	1.00E+00	4.15E-01	1.21E-11	SGNH hydrolase-type esterase superfamily protein
	AT1G50050.1	AT1G50050	--	1254	1403	105	154	0.44 ± 0.34	0.59 ± 0.53	0.12 ± 0.44	1.30 ± 0.37	1.00E+00	1.00E+00	1.00E+00	8.98E-03	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein
	AT1G28400.1	AT1G28400	--	33460	33971	21233	30002	0.01 ± 0.10	-0.05 ± 0.22	0.22 ± 0.04	1.30 ± 0.16	1.00E+00	1.00E+00	4.42E-05	6.75E-14	
	AT3G19000.2	AT3G19000	--	491	513	256	600	-0.27 ± 0.44	-0.23 ± 0.43	0.23 ± 0.35	1.29 ± 0.26	1.00E+00	1.00E+00	1.00E+00	3.47E-05	2-oxoglutarate (ZOG) and Fe(II)-dependent oxygenase superfamily protein
	AT2G28140.1	AT2G28140	--	688	796	306	486	-0.14 ± 0.27	0.17 ± 0.29	0.19 ± 0.25	1.28 ± 0.34	1.00E+00	1.00E+00	9.94E-01	4.44E-03	Protein of unknown function (DUF1635)
	AT5G28510.1	AT5G28510	BGLU24	135	130	369	209	0.45 ± 0.45	0.27 ± 0.48	0.79 ± 0.36	1.28 ± 0.41	1.00E+00	1.00E+00	3.01E-01	2.73E-02	beta glucosidase 24
	AT1G02030.1	AT1G02030	--	110	104	72	98	-0.67 ± 0.49	-1.03 ± 0.58	1.10 ± 0.52	1.28 ± 0.44	1.00E+00	1.00E+00	3.23E-01	5.09E-02	C2H2-like zinc finger protein
	AT5G62580.1	AT5G62580	--	4661	4622	3822	5553	-0.25 ± 0.18	-0.37 ± 0.22	0.39 ± 0.09	1.27 ± 0.11	1.00E+00	1.00E+00	1.38E-03	1.55E-27	ARM repeat superfamily protein
	AT5G18290.1	AT5G18290	SIP1.2	175	174	151	201	-0.51 ± 0.39	-0.66 ± 0.49	-0.54 ± 0.39	1.27 ± 0.32	1.00E+00	1.00E+00	7.44E-01	1.84E-03	Aquaporin-like superfamily protein
	AT2G16720.1	AT2G16720	MYB7	2368	2582	908	1709	0.41 ± 0.18	0.53 ± 0.18	0.49 ± 0.14	1.26 ± 0.19	7.97E-01	2.10E-01	1.39E-02	6.06E-09	myb domain protein 7
	AT4G00440.2	AT4G00440	TRM15	296	257	325	449	0.20 ± 0.70	-0.30 ± 0.69	0.51 ± 0.40	1.25 ± 0.47	1.00E+00	1.00E+00	8.12E-01	9.18E-02	Protein of unknown function (DUF3741)
	AT2G21100.1	AT2G21100	--	1181	1238	1548	1967	-0.81 ± 0.38	-0.80 ± 0.38	0.25 ± 0.12	1.25 ± 0.20	1.00E+00	8.77E-01	3.88E-01	4.01E-08	Disease resistance-responsive (dirigent-like protein) family protein
	AT1G08430.1	AT1G08430	ALMT1	13	18	374	424	-1.34 ± 1.39	-0.22 ± 1.26	0.60 ± 0.30	1.24 ± 0.29	1.00E+00	1.00E+00	4.02E-01	7.11E-04	aluminum-activated malate transporter 1
*	AT2G01580.1	AT2G01580	--	237	223	277	491	-1.31 ± 0.36	-1.91 ± 0.42	0.27 ± 0.33	1.24 ± 0.29	3.13E-02	9.05E-04	9.78E-01	4.88E-04	
	AT5G47880.2	AT5G47880	ERF1-1	560	253	419	674	1.95 ± 0.84	0.17 ± 1.02	-0.93 ± 0.45	1.24 ± 0.35	7.82E-01	1.00E+00	3.55E-01	7.29E-03	eukaryotic release factor 1-1
	AT1G74010.1	AT1G74010	--	441	435	678	842	-0.18 ± 0.38	-0.33 ± 0.32	0.53 ± 0.22	1.24 ± 0.20	1.00E+00	1.00E+00	1.98E-01	4.23E-08	Calcium-dependent phosphotriesterase superfamily protein
*	AT3G44540.1	AT3G44540	FAR4	2576	2384	2613	4889	-1.03 ± 0.18	-1.58 ± 0.36	0.33 ± 0.13	1.24 ± 0.13	2.44E-06	1.81E-03	1.73E-01	1.06E-18	fatty acid reductase 4
	AT5G23660.1	AT5G23660	SWEET12	210	206	130	108	-0.15 ± 0.38	-0.33 ± 0.61	0.61 ± 0.39	1.23 ± 0.46	1.00E+00	1.00E+00	6.54E-01	9.62E-02	homolog of Medicago truncatula MTN3
	AT2G48100.3	AT2G48100	--	1126	1389	702	561	-0.28 ± 0.77	0.23 ± 0.67	0.04 ± 0.34	1.23 ± 0.43	1.00E+00	1.00E+00	1.00E+00	5.97E-02	Exonuclease family protein
	AT1G67730.1	AT1G67730	KCR1	12650	12839	7391	10313	-0.07 ± 0.09	-0.13 ± 0.13	0.77 ± 0.11	1.22 ± 0.14	1.00E+00	1.00E+00	3.49E-10	8.24E-16	beta-ketoacyl reductase 1
	AT3G51860.1	AT3G51860	CAX3	1017	1082	736	1735	-0.86 ± 0.23	-0.74 ± 0.24	0.01 ± 0.16	1.22 ± 0.15	3.13E-02	1.53E-01	1.00E+00	1.39E-14	cation exchanger 3
	AT2G44500.2	AT2G44500	--	1393	1164	579	1134	-0.38 ± 0.37	-1.21 ± 0.35	0.60 ± 0.20	1.22 ± 0.21	1.00E+00	4.89E-02	5.76E-02	3.25E-07	O-fucosyltransferase family protein
	AT5G43170.1	AT5G43170	ZF3	744	815	463	662	0.29 ± 0.20	0.40 ± 0.23	0.43 ± 0.19	1.21 ± 0.30	1.00E+00	1.00E+00	2.63E-01	1.44E-03	zinc-finger protein 3
	AT4G31240.2	AT4G31240	NRX2	426	414	302	414	0.07 ± 0.37	-0.11 ± 0.30	0.20 ± 0.38	1.21 ± 0.32	1.00E+00	1.00E+00	1.00E+00	3.13E-03	protein kinase C-like zinc finger protein
	AT5G19130.2	AT5G19130	--	491	646	328	214	-0.18 ± 0.81	0.49 ± 0.79	0.35 ± 0.33	1.21 ± 0.43	1.00E+00	1.00E+00	9.03E-01	6.99E-02	GPI transamidase component family protein / Gaa1-like family protein
	AT3G45590.1	AT3G45590	SEN1	210	219	127	143	0.50 ± 0.38	0.51 ± 0.37	-0.52 ± 0.35	1.21 ± 0.36	1.00E+00	1.00E+00	7.20E-01	1.37E-02	splicing endonuclease 1
	AT5G39610.1	AT5G39610	NAC6	1138	1148	696	609	0.16 ± 0.34	0.08 ± 0.40	0.61 ± 0.16	1.20 ± 0.33	1.00E+00	1.00E+00	7.84E-03	5.52E-03	NAC domain containing protein 6
	AT2G45685.1	AT2G45685	--	137	140	80	101	0.26 ± 0.73	0.24 ± 0.47	0.25 ± 0.48	1.20 ± 0.42	1.00E+00	1.00E+00	1.00E+00	5.74E-02	other RNA
	AT3G08860.1	AT3G08860	PYD4	2433	2347	2074	2457	-0.03 ± 0.39	-0.23 ± 0.50	0.77 ± 0.10	1.19 ± 0.30	1.00E+00	1.00E+00	3.69E-13	2.25E-03	PYRIMIDINE 4
	AT2G34355.1	AT2G34355	--	296	311	348	479	-0.48 ± 0.40	-0.43 ± 0.41	0.77 ± 0.23	1.19 ± 0.27	1.00E+00	1.00E+00	2.72E-02	2.79E-04	Major facilitator superfamily protein
	AT1G64660.1	AT1G64660	MGL	2824	2570	4098	2814	-0.05 ± 0.32	-0.45 ± 0.36	0.37 ± 0.13	1.18 ± 0.27	1.00E+00	1.00E+00	9.32E-02	3.17E-04	methionine gamma-lyase
	AT4G33240.1	AT4G33240	FAB1A	1182	1078	1188	916	0.14 ± 0.58	-0.21 ± 0.65	-0.41 ± 0.38	1.18 ± 0.24	1.00E+00	1.00E+00	8.99E-01	4.61E-05	1-phosphatidylinositol-4-phosphate 5-kinases;zinc ion binding;1-phosphatidylinositol-3-phosphate 5-kinases
	AT3G19830.1	AT3G19830	NTMC2T5.2	993	998	622	973	-0.16 ± 0.19	-0.23 ± 0.26	0.06 ± 0.18	1.17 ± 0.18	1.00E+00	1.00E+00	1.00E+00	8.32E-09	Calcium-dependent lipid-binding (CaLB domain) family protein
	AT5G56150.2	AT5G56150	UBC30	307	286	202	239	0.59 ± 0.33	0.29 ± 0.37	-0.62 ± 0.50	1.17 ± 0.40	1.00E+00	1.00E+00	8.37E-01	5.06E-02	ubiquitin-conjugating enzyme 30
	AT2G17710.1	AT2G17710	--	4202	4214											

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT4G30900.2	AT4G30900	--	859	757	355	270	0.75 ± 0.25	0.37 ± 0.27	-0.17 ± 0.32	1.14 ± 0.32	1.56E-01	1.00E+00	1.00E+00	8.99E-03	DNase I-like superfamily protein
	AT1G80940.1	AT1G80940	--	1767	1834	1150	1946	-0.01 ± 0.22	-0.01 ± 0.24	0.22 ± 0.18	1.13 ± 0.21	1.00E+00	1.00E+00	8.40E-01	2.44E-06	
	AT4G15248.1	AT4G15248	--	115	122	39	253	-0.22 ± 0.70	-0.24 ± 0.71	0.66 ± 0.63	1.13 ± 0.42	1.00E+00	1.00E+00	9.08E-01	8.79E-02	B-box type zinc finger family protein
	AT5G44550.1	AT5G44550	CASPL1B1	3905	3684	6615	15806	-0.80 ± 0.30	-1.23 ± 0.30	-0.19 ± 0.09	1.13 ± 0.14	4.52E-01	6.30E-03	3.68E-01	2.72E-13	Uncharacterised protein family (UPF0497)
	AT3G28030.1	AT3G28030	UVH3	1788	1699	1072	1482	0.09 ± 0.27	-0.14 ± 0.27	0.08 ± 0.13	1.13 ± 0.14	1.00E+00	1.00E+00	1.00E+00	2.75E-14	5'-3' exonuclease family protein
	AT3G20475.1	AT3G20475	MSH5	165	165	111	159	-0.11 ± 0.45	-0.22 ± 0.43	0.28 ± 0.38	1.13 ± 0.35	1.00E+00	1.00E+00	9.97E-01	2.21E-02	MUTS-homologue 5
	AT2G37150.3	AT2G37150	--	312	329	299	403	-0.36 ± 0.62	-0.29 ± 0.62	-0.20 ± 0.30	1.13 ± 0.28	1.00E+00	1.00E+00	1.00E+00	1.35E-03	RING/U-box superfamily protein
	AT2G44080.1	AT2G44080	ARL	3513	4083	305	326	0.63 ± 0.38	0.89 ± 0.35	-0.20 ± 0.29	1.12 ± 0.26	1.00E+00	4.80E-01	1.00E+00	5.26E-04	ARGOS-like
	AT4G33330.1	AT4G33330	PGSIP3	680	768	354	578	-0.34 ± 0.27	-0.06 ± 0.25	0.54 ± 0.21	1.11 ± 0.27	1.00E+00	1.00E+00	1.50E-01	1.27E-03	plant glycogenin-like starch initiation protein 3
	AT1G34420.1	AT1G34420	--	752	669	485	769	0.05 ± 0.24	-0.40 ± 0.36	-0.13 ± 0.20	1.11 ± 0.17	1.00E+00	1.00E+00	1.00E+00	6.72E-09	leucine-rich repeat transmembrane protein kinase family protein
	AT3G16950.1	AT3G16950	LPD1	8151	8459	4422	7457	-0.09 ± 0.16	-0.07 ± 0.18	0.38 ± 0.07	1.11 ± 0.10	1.00E+00	1.00E+00	3.02E-06	3.62E-28	lipamide dehydrogenase 1
	AT4G24800.2	AT4G24800	ECIP1	808	859	828	544	-0.69 ± 0.30	-0.57 ± 0.36	0.17 ± 0.19	1.11 ± 0.21	7.71E-01	1.00E+00	9.68E-01	9.59E-06	MA3 domain-containing protein
	AT1G04100.1	AT1G04100	IAA10	627	661	320	477	0.02 ± 0.24	0.07 ± 0.27	0.45 ± 0.26	1.10 ± 0.25	1.00E+00	1.00E+00	5.78E-01	4.13E-04	indoleacetic acid-induced protein 10
	AT5G62430.1	AT5G62430	CDF1	275	275	154	611	-0.37 ± 0.42	-0.49 ± 0.34	0.35 ± 0.42	1.10 ± 0.25	1.00E+00	1.00E+00	9.72E-01	2.39E-04	cycling DOF factor 1
	AT3G17110.1	AT3G17110	--	153	151	116	218	-0.08 ± 0.41	-0.24 ± 0.46	0.82 ± 0.44	1.10 ± 0.39	1.00E+00	1.00E+00	4.77E-01	6.84E-02	
	AT4G31990.1	AT4G31990	ASP5	2082	2183	782	1378	-0.22 ± 0.69	-0.17 ± 0.60	-0.82 ± 0.31	1.10 ± 0.39	1.00E+00	1.00E+00	1.17E-01	6.30E-02	aspartate aminotransferase 5
	AT3G02030.1	AT3G02030	--	711	773	576	1038	-0.51 ± 0.25	-0.33 ± 0.23	0.15 ± 0.18	1.09 ± 0.15	1.00E+00	1.00E+00	9.69E-01	5.26E-11	transferases, transferring acyl groups other than amino-acyl groups;acyltransferases
	AT5G10480.1	AT5G10480	PAS2	6536	7012	4008	5917	-0.20 ± 0.15	-0.10 ± 0.18	0.40 ± 0.09	1.09 ± 0.14	1.00E+00	1.00E+00	1.17E-03	4.06E-13	Protein-tyrosine phosphatase-like, PTPLA
*	AT1G08820.2	AT1G08820	VAP27-2	3558	3767	2937	3627	-0.05 ± 0.16	0.02 ± 0.18	0.28 ± 0.13	1.09 ± 0.14	1.00E+00	1.00E+00	2.94E-01	2.03E-13	vamp/synaptobrevin-associated protein 27-2
	AT1G29000.1	AT1G29000	--	147	130	218	531	-1.40 ± 0.41	-2.55 ± 0.50	-0.21 ± 0.27	1.09 ± 0.20	7.24E-02	7.49E-05	9.84E-01	1.69E-06	Heavy metal transport/detoxification superfamily protein
	AT5G44510.1	AT5G44510	TAO1	1433	1300	578	1264	0.03 ± 0.32	-0.35 ± 0.39	0.09 ± 0.18	1.09 ± 0.18	1.00E+00	1.00E+00	1.00E+00	4.51E-08	target of AVR8 operation1
	AT3G47950.1	AT3G47950	HA4	2143	1931	1088	1744	0.07 ± 0.13	-0.34 ± 0.49	0.02 ± 0.18	1.08 ± 0.12	1.00E+00	1.00E+00	1.00E+00	1.19E-18	H(+)-ATPase 4
	AT1G79900.1	AT1G79900	BAC2	57	65	155	178	-0.38 ± 0.80	-0.07 ± 0.68	0.39 ± 0.33	1.08 ± 0.38	1.00E+00	1.00E+00	8.59E-01	6.32E-02	Mitochondrial substrate carrier family protein
	AT1G75760.1	AT1G75760	--	2877	2939	1581	2142	0.08 ± 0.16	0.05 ± 0.17	0.57 ± 0.12	1.08 ± 0.19	1.00E+00	1.00E+00	8.88E-05	6.27E-07	ER lumen protein retaining receptor family protein
	AT1G72230.1	AT1G72230	--	2305	2538	1737	2784	-0.54 ± 0.21	-0.35 ± 0.19	0.75 ± 0.14	1.08 ± 0.19	4.57E-01	1.00E+00	4.05E-06	6.22E-07	Cupredoxin superfamily protein
	AT5G23920.1	AT5G23920	--	2425	2650	1673	2610	0.17 ± 0.19	0.29 ± 0.18	0.13 ± 0.15	1.08 ± 0.21	1.00E+00	1.00E+00	9.72E-01	1.33E-05	
	AT1G23330.1	AT1G23330	--	2457	2442	2941	4763	-0.46 ± 0.14	-0.60 ± 0.23	0.49 ± 0.11	1.07 ± 0.12	7.11E-02	4.13E-01	5.01E-04	5.91E-17	alpha/beta-Hydrolases superfamily protein
	AT3G07650.4	AT3G07650	COL9	956	1180	1079	208	-0.98 ± 0.87	-0.32 ± 0.25	-0.11 ± 0.19	1.07 ± 0.35	1.00E+00	1.00E+00	1.00E+00	3.48E-02	CONSTANS-like 9
	AT1G79470.1	AT1G79470	--	4067	4469	3345	4138	-0.27 ± 0.13	-0.08 ± 0.17	0.44 ± 0.07	1.07 ± 0.14	1.00E+00	1.00E+00	3.76E-07	1.15E-11	Aldolase-type TIM barrel family protein
	AT3G04030.1	AT3G04030	MYR2	251	215	132	149	-0.34 ± 0.62	-1.05 ± 0.87	0.31 ± 0.42	1.07 ± 0.34	1.00E+00	1.00E+00	9.94E-01	3.00E-02	Homeodomain-like superfamily protein
	AT5G17600.1	AT5G17600	--	370	386	289	437	-0.39 ± 0.28	-0.37 ± 0.29	0.44 ± 0.24	1.07 ± 0.26	1.00E+00	1.00E+00	4.95E-01	9.93E-04	RING/U-box superfamily protein
	AT2G41100.3	AT2G41100	TCH3	872	890	968	675	0.58 ± 0.27	0.55 ± 0.27	0.71 ± 0.88	1.07 ± 0.19	9.99E-01	9.85E-01	9.78E-01	1.14E-06	Calcium-binding EF hand family protein
	AT5G06100.2	AT5G06100	MYB33	1555	1647	974	1633	-0.20 ± 0.21	-0.12 ± 0.29	0.24 ± 0.17	1.06 ± 0.14	1.00E+00	1.00E+00	7.31E-01	2.39E-12	myb domain protein 33
	AT3G44540.2	AT3G44540	FAR4	111	93	201	267	-0.82 ± 0.84	-1.89 ± 1.14	1.47 ± 0.71	1.06 ± 0.36	1.00E+00	1.00E+00	3.68E-01	4.99E-02	fatty acid reductase 4
	AT5G06750.3	AT5G06750	APD8	314	283	274	336	0.92 ± 0.69	0.60 ± 0.42	-0.53 ± 0.51	1.05 ± 0.35	1.00E+00	1.00E+00	9.07E-01	3.50E-02	Protein phosphatase 2C family protein
	AT3G19000.1	AT3G19000	--	1344	1399	1230	2091	-0.07 ± 0.17	-0.05 ± 0.19	-0.01 ± 0.12	1.05 ± 0.15	1.00E+00	1.00E+00	1.00E+00	7.39E-10	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
	AT1G16510.1	AT1G16510	SAUR41	651	721	129	381	0.40 ± 0.46	0.55 ± 0.30	0.10 ± 0.37	1.05 ± 0.33	1.00E+00	1.00E+00	1.00E+00	2.55E-02	SAUR-like auxin-responsive protein family
	AT2G18890.1	AT2G18890	--	572	619	713	733	-0.29 ± 0.23	-0.15 ± 0.27	0.20 ± 0.17	1.05 ± 0.22	1.00E+00	1.00E+00	8.65E-01	4.91E-05	Protein kinase superfamily protein
	AT1G31814.1	AT1G31814	FRL2	747	743	468	785	-0.18 ± 0.30	-0.30 ± 0.32	0.02 ± 0.21	1.05 ± 0.18	1.00E+00	1.00E+00	1.00E+00	2.06E-07	FRIGIDA like 2
	AT1G11860.2	AT1G11860	--	147	423	317	462	-0.88 ± 3.28	1.72 ± 3.26	-1.10 ± 0.54	1.05 ± 0.26	1.00E+00	1.00E+00	3.90E-01	1.36E-03	Glycine cleavage T-protein family
	AT2G02610.1	AT2G02610	--	692	702	258	389	-0.22 ± 0.34	-0.27 ± 0.34	0.12 ± 0.31	1.05 ± 0.26	1.00E+00	1.00E+00	1.00E+00	1.27E-03	Cysteine/Histidine-rich C1 domain family protein
*	AT5G58860.1	AT5G58860	CYP86A1	4342	4142	9297	17669	-1.39 ± 0.30	-1.85 ± 0.29	-0.28 ± 0.13	1.05 ± 0.10	1.09E-03	8.67E-08	2.77E-01	1.20E-23	cytochrome P450, family 86, subfamily A, polypeptide 1
	AT4G34060.1	AT4G34060	DML3	355	301	111	210	0.34 ± 0.36	-0.20 ± 0.54	-0.40 ± 0.38	1.05 ± 0.32	1.00E+00	1.00E+00	9.07E-01	1.74E-02	demeter-like protein 3
	AT2G24150.1	AT2G24150	HHP3	1199	1201	970	1409	-0.20 ± 0.17	-0.31 ± 0.26	-0.23 ± 0.17	1.05 ± 0.14	1.00E+00	1.00E+00	7.56E-01	5.01E-11	heptahelical protein 3
	AT4G15530.2	AT4G15530	PPDK	206	265	1657	1430	-0.09 ± 1.00	0.52 ± 0.46	0.47 ± 0.40	1.04 ± 0.34	1.00E+00	1.00E+00	8.55E-01	3.48E-02	pyruvate orthophosphate dikinase
	AT1G22980.1	AT1G22980	--	430	432	114	183	0.22 ± 0.30	0.15 ± 0.30	0.49 ± 0.39	1.04 ± 0.34	1.00E+00	1.00E+00	8.21E-01	3.39E-02	
	AT1G31470.1	AT1G31470	NFD4	1226	1168	941	1383	-0.42 ± 0.19	-0.71 ± 0.36	0.14 ± 0.16	1.04 ± 0.16	8.43E-01	1.00E+00	9.62E-01	2.11E-09	Major facilitator superfamily protein
	AT3G04000.1	AT3G04000	--	57	55	208	265	-0.56 ± 0.88	-0.83 ± 0.95	0.45 ± 0.32	1.04 ± 0.36	1.00E+00	1.00E+00	7.49E-01	5.36E-02	NAD(P)-binding Rossmann-fold superfamily protein
	AT5G44520.1	AT5G44520	--	443	407	207	331	0.16 ± 0.24	-0.19 ± 0.30	-0.01 ± 0.28	1.04 ± 0.25	1.00E+00	1.00E+00	1.00E+00	8.44E-04	NagB/RpiA/CoA transferase-like superfamily protein
	AT2G23430.1	AT2G23430	ICK1	486	511	202	271	0.16 ± 0.23	0.19 ± 0.27	0.51						

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT3G55840.1	AT3G55840	--	526	547	256	402	-0.03 ± 0.24	-0.01 ± 0.27	0.43 ± 0.34	1.02 ± 0.24	1.00E+00	1.00E+00	8.11E-01	7.98E-04	Hs1pro-1 protein
	AT1G04360.1	AT1G04360	ATL1	728	724	869	1758	-0.71 ± 0.20	-0.86 ± 0.24	0.12 ± 0.16	1.02 ± 0.15	6.14E-02	2.76E-02	1.00E+00	2.40E-10	RING/U-box superfamily protein
	AT5G25280.2	AT5G25280	--	634	824	265	265	-0.44 ± 0.24	0.25 ± 0.31	0.08 ± 0.27	1.02 ± 0.27	1.00E+00	1.00E+00	1.00E+00	4.83E-03	serine-rich protein-related
	AT4G28025.2	AT4G28025	--	173	168	133	156	0.26 ± 0.51	0.05 ± 0.52	-0.48 ± 0.44	1.01 ± 0.34	1.00E+00	1.00E+00	8.99E-01	3.97E-02	
	AT3G50980.1	AT3G50980	XERO1	195	215	140	206	-0.24 ± 0.59	-0.10 ± 0.58	0.34 ± 0.33	1.01 ± 0.31	1.00E+00	1.00E+00	9.14E-01	1.62E-02	dehydrin xero 1
	AT4G00360.1	AT4G00360	CYP86A2	1724	1680	2910	6817	-0.87 ± 0.28	-1.12 ± 0.21	0.07 ± 0.16	1.01 ± 0.11	1.37E-01	1.92E-05	1.00E+00	1.83E-19	cytochrome P450, family 86, subfamily A, polypeptide 2
	AT1G48490.3	AT1G48490	--	1365	1045	768	484	0.62 ± 2.07	-0.17 ± 2.03	-0.34 ± 0.18	1.01 ± 0.25	1.00E+00	1.00E+00	4.96E-01	1.43E-03	Protein kinase superfamily protein
	AT3G06850.1	AT3G06850	BCE2	1364	1180	2055	1454	0.03 ± 0.17	-0.53 ± 0.27	0.55 ± 0.22	1.01 ± 0.37	1.00E+00	1.00E+00	1.72E-01	7.53E-02	2-oxoacid dehydrogenases acyltransferase family protein
	AT2G05510.3	AT2G05510	--	9128	9058	6405	6256	1.04 ± 0.32	0.90 ± 0.49	-0.35 ± 0.12	1.01 ± 0.19	9.20E-02	1.00E+00	6.80E-02	8.96E-06	Glycine-rich protein family
	AT2G19150.1	AT2G19150	--	349	343	158	206	0.36 ± 0.31	0.21 ± 0.33	-0.09 ± 0.32	1.01 ± 0.33	1.00E+00	1.00E+00	1.00E+00	3.18E-02	Pectin lyase-like superfamily protein
	AT3G53460.3	AT3G53460	CP29	1159	1182	472	340	-0.43 ± 0.35	-0.47 ± 0.34	-0.77 ± 0.36	1.01 ± 0.28	1.00E+00	1.00E+00	3.09E-01	7.71E-03	chloroplast RNA-binding protein 29
	AT4G09760.1	AT4G09760	CEK3	271	271	268	725	-0.09 ± 0.42	-0.20 ± 0.45	-0.12 ± 0.25	1.01 ± 0.19	1.00E+00	1.00E+00	1.00E+00	5.97E-06	Protein kinase superfamily protein
	AT1G64860.1	AT1G64860	SIGA	1158	1213	1046	1501	-0.36 ± 0.23	-0.31 ± 0.20	0.28 ± 0.16	1.00 ± 0.15	1.00E+00	1.00E+00	5.64E-01	5.37E-10	sigma factor A
	AT1G70140.1	AT1G70140	FH8	569	528	461	648	-0.02 ± 0.27	-0.34 ± 0.30	0.29 ± 0.22	1.00 ± 0.21	1.00E+00	1.00E+00	7.97E-01	7.12E-05	formin 8
	AT4G24610.1	AT4G24610	--	2156	2165	1620	2092	-0.43 ± 0.16	-0.52 ± 0.26	0.04 ± 0.20	1.00 ± 0.17	3.77E-01	1.00E+00	1.00E+00	2.91E-07	
H	Down-regulated in TPL-OE (15H) analysis:															
	AT2G25680.1	AT2G25680	MOT1	491	503	192	200	0.09 ± 0.28	0.06 ± 0.37	-0.48 ± 0.31	-1.00 ± 0.31	1.00E+00	1.00E+00	6.68E-01	1.87E-02	molybdate transporter 1
	AT3G21351.1	AT3G21351	--	220	217	230	186	0.41 ± 0.57	0.19 ± 0.52	-0.79 ± 0.33	-1.00 ± 0.37	1.00E+00	1.00E+00	2.13E-01	8.84E-02	
	AT2G21020.1	AT2G21020	--	2686	2688	616	551	0.04 ± 0.18	-0.06 ± 0.24	-0.67 ± 0.19	-1.01 ± 0.19	1.00E+00	1.00E+00	1.62E-02	6.91E-06	
	AT1G52200.1	AT1G52200	--	5373	5266	2823	1802	0.06 ± 0.15	-0.12 ± 0.18	-0.96 ± 0.09	-1.01 ± 0.24	1.00E+00	1.00E+00	1.45E-22	7.65E-04	PLAC8 family protein
	AT3G07750.2	AT3G07750	RRP42	628	537	253	196	-0.07 ± 0.42	-0.72 ± 0.48	0.45 ± 0.63	-1.01 ± 0.32	1.00E+00	1.00E+00	1.00E+00	2.44E-02	3'-5'-exoribonuclease family protein
	AT5G23220.1	AT5G23220	NIC3	308	331	371	305	0.04 ± 0.42	0.12 ± 0.39	-0.15 ± 0.27	-1.01 ± 0.35	1.00E+00	1.00E+00	1.00E+00	5.27E-02	nicotinamidase 3
	AT4G18070.2	AT4G18070	--	1633	1792	294	614	-0.23 ± 0.27	-0.06 ± 0.38	-0.11 ± 0.43	-1.01 ± 0.28	1.00E+00	1.00E+00	1.00E+00	5.28E-03	
	AT2G43590.1	AT2G43590	--	449	495	844	1168	-0.46 ± 0.54	-0.26 ± 0.53	-0.90 ± 0.23	-1.01 ± 0.19	1.00E+00	1.00E+00	4.40E-03	3.31E-06	Chitinase family protein
	AT3G50740.1	AT3G50740	UGT72E1	7398	6746	2199	3664	0.23 ± 0.11	-0.13 ± 0.15	-0.68 ± 0.12	-1.01 ± 0.17	1.00E+00	1.00E+00	4.70E-06	1.21E-07	UDP-glucosyl transferase 72E1
	AT1G67110.1	AT1G67110	CYP735A2	1341	1503	1001	361	0.62 ± 0.18	0.81 ± 0.25	0.17 ± 0.30	-1.02 ± 0.34	5.52E-02	9.62E-02	1.00E+00	3.88E-02	cytochrome P450, family 735, subfamily A, polypeptide 2
	AT3G14540.1	AT3G14540	TPS19	769	832	445	609	-0.32 ± 0.27	-0.17 ± 0.24	-0.38 ± 0.23	-1.02 ± 0.18	1.00E+00	1.00E+00	5.85E-01	4.37E-07	Terpenoid cyclases/Protein prenyltransferases superfamily protein
	AT3G11550.1	AT3G11550	CASP2	1404	1493	612	745	-0.17 ± 0.23	-0.12 ± 0.25	-0.29 ± 0.18	-1.02 ± 0.18	1.00E+00	1.00E+00	6.15E-01	8.53E-07	Uncharacterised protein family (UPF0497)
	AT4G23550.1	AT4G23550	WRKY29	1546	1541	870	626	0.04 ± 0.22	-0.08 ± 0.25	-0.79 ± 0.16	-1.02 ± 0.25	1.00E+00	1.00E+00	5.73E-05	1.54E-03	WRKY family transcription factor
	AT3G25597.1	AT3G25597	--	571	552	158	201	0.28 ± 0.32	0.07 ± 0.34	-0.31 ± 0.34	-1.02 ± 0.30	1.00E+00	1.00E+00	9.55E-01	1.12E-02	
	AT3G26290.1	AT3G26290	CYP71B26	1108	1094	234	501	-0.13 ± 0.18	-0.27 ± 0.20	-0.45 ± 0.27	-1.02 ± 0.32	1.00E+00	1.00E+00	5.78E-01	2.16E-02	cytochrome P450, family 71, subfamily B, polypeptide 26
	AT5G01050.1	AT5G01050	--	1268	1205	471	398	0.01 ± 0.18	-0.24 ± 0.20	-0.87 ± 0.22	-1.02 ± 0.27	1.00E+00	1.00E+00	2.84E-03	4.64E-03	Laccase/Diphenol oxidase family protein
	AT4G40010.1	AT4G40010	SNRK2.7	655	721	512	647	0.20 ± 0.28	0.35 ± 0.43	-0.37 ± 0.19	-1.02 ± 0.22	1.00E+00	1.00E+00	4.07E-01	9.82E-05	SNF1-related protein kinase 2.7
	AT5G22310.1	AT5G22310	--	700	770	267	362	-0.06 ± 0.27	0.13 ± 0.37	-0.54 ± 0.31	-1.02 ± 0.28	1.00E+00	1.00E+00	5.38E-01	4.82E-03	
	AT5G37450.1	AT5G37450	--	1809	1791	316	291	0.08 ± 0.15	-0.03 ± 0.20	-1.07 ± 0.43	-1.02 ± 0.27	1.00E+00	1.00E+00	1.73E-01	3.58E-03	Leucine-rich repeat protein kinase family protein
	AT3G61430.1	AT3G61430	PIP1A	20724	23616	8441	10843	-0.09 ± 0.37	0.18 ± 0.12	-0.31 ± 0.34	-1.02 ± 0.22	1.00E+00	1.00E+00	9.56E-01	1.51E-04	plasma membrane intrinsic protein 1A
	AT3G01190.1	AT3G01190	--	33220	35654	8567	10105	0.05 ± 0.16	0.15 ± 0.29	-0.82 ± 0.13	-1.03 ± 0.07	1.00E+00	1.00E+00	2.85E-08	3.30E-52	Peroxidase superfamily protein
	AT4G11290.1	AT4G11290	--	12770	15274	1888	2169	1.77 ± 0.17	2.04 ± 0.25	-0.68 ± 0.17	-1.03 ± 0.21	1.75E-21	2.09E-13	3.07E-03	4.83E-05	Peroxidase superfamily protein
	AT3G51330.1	AT3G51330	--	5283	5152	2844	3001	-0.13 ± 0.11	-0.31 ± 0.15	-0.64 ± 0.14	-1.03 ± 0.16	1.00E+00	8.82E-01	2.87E-04	5.54E-09	Eukaryotic aspartyl protease family protein
	AT1G27140.1	AT1G27140	GSTU14	839	967	495	623	-0.48 ± 0.29	-0.17 ± 0.33	-0.34 ± 0.22	-1.03 ± 0.24	1.00E+00	1.00E+00	6.73E-01	6.53E-04	glutathione S-transferase tau 14
	AT3G12977.1	AT3G12977	--	1181	1055	440	384	0.26 ± 0.21	-0.17 ± 0.27	-0.25 ± 0.21	-1.03 ± 0.36	1.00E+00	1.00E+00	8.47E-01	5.54E-02	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
	AT2G14510.1	AT2G14510	--	1710	1594	291	378	-0.01 ± 0.25	-0.31 ± 0.22	-0.73 ± 0.26	-1.03 ± 0.39	1.00E+00	1.00E+00	9.34E-02	9.48E-02	Leucine-rich repeat protein kinase family protein
	AT2G28990.1	AT2G28990	--	1198	1107	240	282	-0.10 ± 0.23	-0.44 ± 0.22	-0.92 ± 0.37	-1.03 ± 0.28	1.00E+00	9.97E-01	1.78E-01	4.33E-03	Leucine-rich repeat protein kinase family protein
	AT1G48500.1	AT1G48500	JAZ4	1610	1506	715	730	0.16 ± 0.18	-0.13 ± 0.25	-0.42 ± 0.15	-1.03 ± 0.20	1.00E+00	1.00E+00	9.09E-02	1.23E-05	jasmonate-zim-domain protein 4
	AT4G19690.2	AT4G19690	IRT1	25531	21597	779	3790	0.39 ± 0.23	-0.17 ± 0.17	-0.71 ± 0.21	-1.03 ± 0.19	1.00E+00	1.00E+00	1.74E-02	2.60E-06	iron-regulated transporter 1
	AT5G04950.1	AT5G04950	NAS1	4812	4539	641	2710	-0.28 ± 0.25	-0.60 ± 0.26	-0.42 ± 0.22	-1.03 ± 0.29	1.00E+00	6.44E-01	4.35E-01	7.11E-03	nicotianamine synthase 1
	AT5G46060.1	AT5G46060	--	952	917	151	201	0.01 ± 0.29	-0.21 ± 0.29	-0.50 ± 0.34	-1.04 ± 0.33	1.00E+00	1.00E+00	7.12E-01	3.03E-02	Protein of unknown function, DUF599
	AT5G01330.1	AT5G01330	PDC3	1141	1199	279	447	-0.11 ± 0.35	-0.05 ± 0.34	-0.43 ± 0.24	-1.04 ± 0.21	1.00E+00	1.00E+00	5.07E-01	4.08E-05	pyruvate decarboxylase-3
	AT2G44010.1	AT2G44010	--	622	673	452	436	-0.17 ± 0.32	-0.07 ± 0.37	-0.67 ± 0.20	-1.04 ± 0.32	1.00E+00	1.00E+00			

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT1G51850.1	AT1G51850	SIF2	2701	2642	979	1023	-0.01 ± 0.20	-0.17 ± 0.19	-0.82 ± 0.14	-1.06 ± 0.19	1.00E+00	1.00E+00	6.63E-07	9.82E-07	Leucine-rich repeat protein kinase family protein
	AT1G66200.1	AT1G66200	GSR2	68702	74908	38449	45171	-0.15 ± 0.13	0.00 ± 0.23	-0.32 ± 0.12	-1.06 ± 0.07	1.00E+00	1.00E+00	1.08E-01	1.30E-50	glutamine synthase clone F11
	AT2G29750.1	AT2G29750	UGT71C1	5852	5990	2299	2582	-0.08 ± 0.14	-0.11 ± 0.18	-0.46 ± 0.11	-1.06 ± 0.10	1.00E+00	1.00E+00	1.59E-03	7.97E-22	UDP-glucosyl transferase 71C1
	AT3G21180.1	AT3G21180	ACA9	1307	1227	291	406	0.03 ± 0.26	-0.25 ± 0.30	-0.47 ± 0.33	-1.06 ± 0.21	1.00E+00	1.00E+00	7.31E-01	3.20E-05	autoinhibited Ca(2+)-ATPase 9
	AT3G07900.1	AT3G07900	--	736	734	165	241	-0.10 ± 0.29	-0.20 ± 0.29	-0.73 ± 0.35	-1.06 ± 0.30	1.00E+00	1.00E+00	3.51E-01	9.58E-03	O-fucosyltransferase family protein
	AT1G14540.1	AT1G14540	PER4	235	210	476	264	0.50 ± 0.43	0.11 ± 0.43	-0.58 ± 0.32	-1.06 ± 0.34	1.00E+00	1.00E+00	5.01E-01	2.92E-02	Peroxidase superfamily protein
	AT4G30170.1	AT4G30170	--	17333	19107	9309	9521	0.00 ± 0.14	0.17 ± 0.31	-0.64 ± 0.10	-1.06 ± 0.11	1.00E+00	1.00E+00	4.46E-09	6.35E-20	Peroxidase family protein
	AT3G45700.1	AT3G45700	NPF2.4	1099	1111	1085	881	-0.20 ± 0.26	-0.26 ± 0.30	-0.95 ± 0.17	-1.06 ± 0.29	1.00E+00	1.00E+00	6.39E-06	4.96E-03	Major facilitator superfamily protein
	AT3G25930.1	AT3G25930	--	8558	8640	675	948	0.28 ± 0.12	0.18 ± 0.25	-0.62 ± 0.26	-1.06 ± 0.30	6.90E-01	1.00E+00	2.34E-01	9.67E-03	Adenine nucleotide alpha hydrolases-like superfamily protein
	AT1G01340.1	AT1G01340	CNGC10	1072	1060	285	309	-0.22 ± 0.47	-0.35 ± 0.41	-0.58 ± 0.52	-1.06 ± 0.38	1.00E+00	1.00E+00	8.79E-01	7.09E-02	cyclic nucleotide gated channel 10
	AT4G04745.1	AT4G04745	--	986	1189	144	328	0.04 ± 0.42	0.39 ± 0.28	-0.16 ± 0.39	-1.06 ± 0.29	1.00E+00	1.00E+00	1.00E+00	6.30E-03	
	AT4G15380.1	AT4G15380	CYP705A4	1127	1186	279	440	0.00 ± 0.19	0.06 ± 0.19	-0.71 ± 0.31	-1.07 ± 0.33	1.00E+00	1.00E+00	2.50E-01	2.01E-02	cytochrome P450, family 705, subfamily A, polypeptide 4
	AT4G23420.1	AT4G23420	--	975	1023	1519	855	0.15 ± 0.21	0.19 ± 0.24	-0.82 ± 0.13	-1.07 ± 0.30	1.00E+00	1.00E+00	2.80E-08	7.71E-03	NAD(P)-binding Rossmann-fold superfamily protein
	AT3G07195.1	AT3G07195	--	1099	1143	387	454	-0.07 ± 0.25	-0.08 ± 0.32	-0.88 ± 0.21	-1.07 ± 0.21	1.00E+00	1.00E+00	1.00E-03	1.98E-05	RPM1-interacting protein 4 (RIN4) family protein
	AT4G37530.1	AT4G37530	--	2362	2511	1331	1295	-0.29 ± 0.16	-0.21 ± 0.29	-0.51 ± 0.17	-1.07 ± 0.17	1.00E+00	1.00E+00	6.48E-02	2.21E-08	Peroxidase superfamily protein
	AT2G26480.1	AT2G26480	UGT76D1	773	803	471	595	-0.23 ± 0.20	-0.22 ± 0.22	-0.34 ± 0.20	-1.08 ± 0.35	1.00E+00	1.00E+00	5.50E-01	3.62E-02	UDP-glucosyl transferase 76D1
	AT1G12040.1	AT1G12040	LXR1	2416	2195	990	1050	-0.37 ± 0.19	-0.83 ± 0.23	-0.94 ± 0.28	-1.08 ± 0.17	1.00E+00	3.35E-02	2.30E-02	6.74E-09	leucine-rich repeat/extensin 1
	AT4G26010.1	AT4G26010	--	11285	12084	2279	2256	0.10 ± 0.13	0.19 ± 0.31	-0.67 ± 0.21	-1.08 ± 0.22	1.00E+00	1.00E+00	2.95E-02	4.04E-05	Peroxidase superfamily protein
	AT2G21880.1	AT2G21880	RAB7A	664	679	148	250	-0.03 ± 0.28	-0.08 ± 0.39	-0.46 ± 0.35	-1.08 ± 0.28	1.00E+00	1.00E+00	8.00E-01	2.23E-03	RAB GTPase homolog 7A
	AT1G48930.1	AT1G48930	GH9C1	2767	2890	846	910	-0.08 ± 0.15	-0.05 ± 0.26	-0.72 ± 0.23	-1.08 ± 0.16	1.00E+00	1.00E+00	4.65E-02	2.96E-09	glycosyl hydrolase 9C1
	AT5G67450.1	AT5G67450	ZF1	1113	1144	334	396	-0.02 ± 0.22	-0.05 ± 0.32	-0.83 ± 0.24	-1.08 ± 0.30	1.00E+00	1.00E+00	1.47E-02	5.95E-03	zinc-finger protein 1
	AT5G48320.1	AT5G48320	--	402	402	138	125	-0.13 ± 0.35	-0.22 ± 0.36	-0.79 ± 0.38	-1.08 ± 0.40	1.00E+00	1.00E+00	3.35E-01	8.89E-02	Cysteine/Histidine-rich C1 domain family protein
	AT2G42210.4	AT2G42210	OEP16-3	204	184	63	135	0.63 ± 0.47	0.26 ± 0.42	0.17 ± 0.75	-1.09 ± 0.41	1.00E+00	1.00E+00	1.00E+00	9.05E-02	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein
	AT3G45650.1	AT3G45650	NPF2.7	3092	3021	1125	1118	0.14 ± 0.18	-0.01 ± 0.23	-0.63 ± 0.15	-1.09 ± 0.17	1.00E+00	1.00E+00	1.49E-03	4.44E-09	nitrate excretion transporter1
	AT1G34760.1	AT1G34760	GRF11	760	665	74	160	0.07 ± 0.38	-0.46 ± 0.41	-0.94 ± 0.49	-1.09 ± 0.33	1.00E+00	1.00E+00	4.53E-01	1.77E-02	general regulatory factor 11
	AT5G50560.1	AT5G50560	--	639	678	150	217	0.08 ± 0.32	0.05 ± 0.31	-0.56 ± 0.34	-1.09 ± 0.33	1.00E+00	1.00E+00	6.16E-01	1.63E-02	Protein of unknown function (DUF 3339)
	AT2G37130.1	AT2G37130	--	8714	8496	9339	9556	0.06 ± 0.15	-0.11 ± 0.29	-0.59 ± 0.17	-1.09 ± 0.14	1.00E+00	1.00E+00	1.34E-02	7.71E-13	Peroxidase superfamily protein
	AT2G02960.4	AT2G02960	--	2202	2007	730	632	0.16 ± 0.37	-0.21 ± 0.39	0.20 ± 0.26	-1.09 ± 0.22	1.00E+00	1.00E+00	9.94E-01	3.07E-05	RING/FYVE/PHD zinc finger superfamily protein
	AT4G36480.2	AT4G36480	LCB1	1007	1337	446	888	-0.21 ± 1.44	0.48 ± 0.70	0.37 ± 0.49	-1.10 ± 0.27	1.00E+00	1.00E+00	9.93E-01	9.29E-04	long-chain base1
	AT2G28970.1	AT2G28970	--	1612	1540	472	610	-0.03 ± 0.20	-0.26 ± 0.24	-0.61 ± 0.24	-1.10 ± 0.19	1.00E+00	1.00E+00	1.58E-01	2.75E-07	Leucine-rich repeat protein kinase family protein
	AT3G24300.1	AT3G24300	AMT1;3	9500	9515	4038	5131	-0.07 ± 0.12	-0.16 ± 0.13	-0.30 ± 0.13	-1.10 ± 0.14	1.00E+00	1.00E+00	1.97E-01	1.47E-12	ammonium transporter 1;3
	AT5G06200.1	AT5G06200	CASP4	579	628	155	266	0.10 ± 0.25	0.18 ± 0.36	-0.52 ± 0.40	-1.11 ± 0.28	1.00E+00	1.00E+00	8.04E-01	1.82E-03	Uncharacterised protein family (UPF0497)
	AT1G70410.1	AT1G70410	BCA4	6007	7317	1502	2341	-0.55 ± 0.36	-0.03 ± 0.34	-0.40 ± 0.17	-1.11 ± 0.36	1.00E+00	1.00E+00	2.04E-01	3.54E-02	beta carbonic anhydrase 4
	AT4G19030.1	AT4G19030	NLM1	7340	7677	2372	2914	-0.01 ± 0.15	0.02 ± 0.20	-0.83 ± 0.10	-1.12 ± 0.12	1.00E+00	1.00E+00	3.46E-15	3.74E-18	NOD26-like major intrinsic protein 1
	AT1G13300.1	AT1G13300	HRS1	5269	5460	3127	1692	0.16 ± 0.13	0.16 ± 0.16	-0.61 ± 0.08	-1.12 ± 0.21	1.00E+00	1.00E+00	5.15E-11	5.69E-06	myb-like transcription factor family protein
	AT2G26820.1	AT2G26820	PP2-A3	1651	1828	767	634	0.08 ± 0.14	0.27 ± 0.34	-0.75 ± 0.27	-1.12 ± 0.22	1.00E+00	1.00E+00	9.49E-02	2.23E-05	phloem protein 2-A3
	AT5G20165.1	AT5G20165	--	664	918	297	279	-0.12 ± 0.49	0.57 ± 0.32	0.48 ± 0.33	-1.12 ± 0.34	1.00E+00	1.00E+00	7.22E-01	1.52E-02	
	AT3G14550.1	AT3G14550	GGPS3	430	481	265	368	-0.38 ± 0.29	-0.13 ± 0.27	-0.26 ± 0.25	-1.12 ± 0.26	1.00E+00	1.00E+00	9.00E-01	5.26E-04	geranylgeranyl pyrophosphate synthase 3
	AT3G13610.1	AT3G13610	F6H1	9388	8514	2870	2265	0.36 ± 0.26	0.00 ± 0.23	-0.64 ± 0.20	-1.12 ± 0.19	1.00E+00	1.00E+00	3.26E-02	3.76E-07	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
	AT2G34810.1	AT2G34810	AtBBE16	1186	1250	358	280	-0.06 ± 0.21	0.00 ± 0.35	-0.23 ± 0.25	-1.12 ± 0.27	1.00E+00	1.00E+00	9.48E-01	8.40E-04	FAD-binding Berberine family protein
	AT5G45340.1	AT5G45340	CYP707A3	2712	2597	871	719	0.31 ± 0.17	0.10 ± 0.18	-0.81 ± 0.21	-1.13 ± 0.25	1.00E+00	1.00E+00	5.79E-03	2.00E-04	cytochrome P450, family 707, subfamily A, polypeptide 3
	AT3G54580.1	AT3G54580	--	21103	19235	11234	12095	-0.47 ± 0.28	-0.93 ± 0.30	-0.83 ± 0.37	-1.13 ± 0.08	1.00E+00	1.39E-01	2.56E-01	5.38E-44	Proline-rich extensin-like family protein
	AT1G53830.1	AT1G53830	PME2	1672	1718	553	1015	-0.21 ± 0.34	-0.22 ± 0.40	-0.85 ± 0.25	-1.13 ± 0.24	1.00E+00	1.00E+00	1.67E-02	1.01E-04	pectin methylesterase 2
	AT4G31710.1	AT4G31710	GLR2.4	212	209	107	103	-0.33 ± 0.37	-0.48 ± 0.40	-0.85 ± 0.38	-1.13 ± 0.41	1.00E+00	1.00E+00	2.69E-01	7.82E-02	glutamate receptor 2.4
	AT5G25810.1	AT5G25810	TNY	5373	5671	1886	1740	0.14 ± 0.16	0.18 ± 0.21	-0.40 ± 0.11	-1.13 ± 0.21	1.00E+00	1.00E+00	1.06E-02	3.61E-06	Integrase-type DNA-binding superfamily protein
	AT5G66490.1	AT5G66490	--	1199	1226	210	244	0.23 ± 0.19	0.12 ± 0.23	-0.98 ± 0.29	-1.13 ± 0.30	1.00E+00	1.00E+00	1.91E-02	4.32E-03	
	AT1G27740.1	AT1G27740	RSL4	758	709	352	439	0.05 ± 0.31	-0.26 ± 0.37	-0.89 ± 0.27	-1.13 ± 0.21					

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT3G45920.1	AT3G45920	--	789	948	122	215	-0.06 ± 0.51	0.31 ± 0.45	-0.82 ± 0.41	-1.16 ± 0.39	1.00E+00	1.00E+00	4.07E-01	4.10E-02	Protein kinase superfamily protein
	AT3G45710.1	AT3G45710	NPF2.5	8300	7754	2593	2793	0.16 ± 0.12	-0.13 ± 0.17	-0.68 ± 0.12	-1.17 ± 0.18	1.00E+00	1.00E+00	1.36E-06	1.86E-08	Major facilitator superfamily protein
	AT5G05340.1	AT5G05340	PRX52	37	34	285	399	-0.04 ± 0.98	-0.45 ± 0.96	1.25 ± 0.58	-1.17 ± 0.21	1.00E+00	1.00E+00	3.22E-01	2.50E-06	Peroxidase superfamily protein
	AT5G14340.1	AT5G14340	MYB40	441	469	77	135	0.01 ± 0.29	0.07 ± 0.43	-0.13 ± 0.46	-1.18 ± 0.41	1.00E+00	1.00E+00	1.00E+00	5.52E-02	myb domain protein 40
	AT3G09925.1	AT3G09925	--	1054	1193	342	362	-0.12 ± 0.21	0.05 ± 0.38	-0.77 ± 0.30	-1.18 ± 0.23	1.00E+00	1.00E+00	1.66E-01	1.30E-05	Pollen Ole e 1 allergen and extensin family protein
	AT1G62980.1	AT1G62980	EXPA18	1847	2041	558	524	0.02 ± 0.14	0.19 ± 0.38	-0.92 ± 0.26	-1.18 ± 0.27	1.00E+00	1.00E+00	1.60E-02	4.00E-04	expansin A18
	AT1G06120.1	AT1G06120	--	579	627	98	215	-0.32 ± 0.26	-0.19 ± 0.37	-0.71 ± 0.48	-1.18 ± 0.38	1.00E+00	1.00E+00	7.19E-01	2.77E-02	Fatty acid desaturase family protein
	AT5G47450.1	AT5G47450	TIP2;3	2124	1861	415	1040	-0.04 ± 0.36	-0.59 ± 0.23	-0.02 ± 0.39	-1.18 ± 0.16	1.00E+00	3.84E-01	1.00E+00	2.92E-11	tonoplast intrinsic protein 2;3
	AT4G15417.1	AT4G15417	RTL1	379	379	129	148	0.16 ± 0.28	0.05 ± 0.30	-0.69 ± 0.38	-1.18 ± 0.36	1.00E+00	1.00E+00	5.06E-01	1.74E-02	RNAse II-like 1
	AT5G05500.1	AT5G05500	MOP10	2647	2938	705	649	-0.07 ± 0.20	0.10 ± 0.32	-0.79 ± 0.22	-1.19 ± 0.20	1.00E+00	1.00E+00	1.36E-02	1.47E-07	Pollen Ole e 1 allergen and extensin family protein
	AT4G01680.1	AT4G01680	MYB55	1192	1108	173	271	0.18 ± 0.31	-0.13 ± 0.22	-0.87 ± 0.39	-1.19 ± 0.27	1.00E+00	1.00E+00	2.67E-01	2.98E-04	myb domain protein 55
	AT3G51360.1	AT3G51360	--	1240	1256	278	352	-0.06 ± 0.16	-0.12 ± 0.19	-0.70 ± 0.29	-1.19 ± 0.29	1.00E+00	1.00E+00	2.15E-01	1.13E-03	Eukaryotic aspartyl protease family protein
	AT1G08670.1	AT1G08670	--	490	579	142	143	0.48 ± 0.25	0.77 ± 0.30	-0.42 ± 0.34	-1.19 ± 0.36	1.00E+00	4.08E-01	8.39E-01	1.54E-02	ENTH/VHS family protein
	AT4G11210.1	AT4G11210	--	508	549	250	440	-0.40 ± 0.47	-0.34 ± 0.39	-0.81 ± 0.26	-1.19 ± 0.31	1.00E+00	1.00E+00	4.07E-02	2.60E-03	Disease resistance-responsive (dirigent-like protein) family protein
	AT5G17820.1	AT5G17820	PER57	17853	17967	5577	7110	0.08 ± 0.09	0.00 ± 0.28	-0.85 ± 0.17	-1.20 ± 0.09	1.00E+00	1.00E+00	2.83E-05	2.88E-39	Peroxidase superfamily protein
	AT5G09978.1	AT5G09978	PEP7	911	1071	238	372	-0.25 ± 0.23	0.05 ± 0.37	-0.67 ± 0.27	-1.20 ± 0.26	1.00E+00	1.00E+00	1.87E-01	2.00E-04	elicitor peptide 7 precursor
	AT2G04090.1	AT2G04090	--	339	333	218	260	-0.08 ± 0.32	-0.25 ± 0.42	-0.40 ± 0.31	-1.20 ± 0.31	1.00E+00	1.00E+00	8.08E-01	2.33E-03	MATE efflux family protein
	AT1G05660.1	AT1G05660	--	1273	1229	284	408	0.03 ± 0.35	-0.18 ± 0.32	-0.33 ± 0.33	-1.21 ± 0.33	1.00E+00	1.00E+00	9.21E-01	4.82E-03	Pectin lyase-like superfamily protein
	AT3G44326.1	AT3G44326	CFB	182	159	428	448	0.16 ± 0.46	-0.36 ± 0.49	-0.65 ± 0.29	-1.21 ± 0.44	1.00E+00	1.00E+00	2.82E-01	7.17E-02	F-box family protein
	AT2G25160.1	AT2G25160	CYP82F1	1294	1386	1451	1376	0.72 ± 0.21	0.81 ± 0.25	-0.52 ± 0.16	-1.21 ± 0.23	7.10E-02	8.84E-02	3.14E-02	4.49E-06	cytochrome P450, family 82, subfamily F, polypeptide 1
	AT1G69240.1	AT1G69240	MES15	677	679	178	185	-0.12 ± 0.31	-0.21 ± 0.40	-0.75 ± 0.36	-1.22 ± 0.36	1.00E+00	1.00E+00	3.51E-01	1.31E-02	methyl esterase 15
	AT4G23400.1	AT4G23400	PIP1;5	9860	9213	2377	3270	0.09 ± 0.09	-0.21 ± 0.13	-0.88 ± 0.14	-1.23 ± 0.22	1.00E+00	1.00E+00	9.52E-08	1.27E-06	plasma membrane intrinsic protein 1;5
	AT3G45410.1	AT3G45410	LecRK-1.3	1241	1164	542	426	0.02 ± 0.21	-0.27 ± 0.31	-0.55 ± 0.27	-1.23 ± 0.32	1.00E+00	1.00E+00	3.80E-01	2.60E-03	Concanavalin A-like lectin protein kinase family protein
	AT4G37520.2	AT4G37520	--	947	853	643	1131	0.14 ± 0.89	-0.28 ± 0.81	-1.64 ± 0.62	-1.23 ± 0.27	1.00E+00	1.00E+00	1.21E-01	2.21E-04	Peroxidase superfamily protein
	AT5G61350.1	AT5G61350	CAP1	435	441	177	160	0.00 ± 0.36	-0.05 ± 0.36	-0.97 ± 0.39	-1.23 ± 0.34	1.00E+00	1.00E+00	1.68E-01	6.30E-03	Protein kinase superfamily protein
	AT3G18170.1	AT3G18170	--	2813	3077	696	1095	-0.05 ± 0.15	0.10 ± 0.27	-0.66 ± 0.18	-1.23 ± 0.20	1.00E+00	1.00E+00	8.68E-03	2.34E-08	Glycosyltransferase family 61 protein
	AT1G18420.1	AT1G18420	--	602	621	219	246	-0.03 ± 0.36	-0.03 ± 0.40	-0.76 ± 0.35	-1.23 ± 0.31	1.00E+00	1.00E+00	2.97E-01	1.75E-03	Aluminium activated malate transporter family protein
	AT1G73300.1	AT1G73300	SCPL2	784	694	228	223	-0.23 ± 0.23	-0.78 ± 0.43	-0.65 ± 0.38	-1.24 ± 0.43	1.00E+00	1.00E+00	5.63E-01	5.81E-02	serine carboxypeptidase-like 2
	AT3G60330.2	AT3G60330	HA7	4152	3838	724	961	0.08 ± 0.23	-0.24 ± 0.33	-0.82 ± 0.21	-1.24 ± 0.31	1.00E+00	1.00E+00	4.78E-03	1.53E-03	H(+)-ATPase 7
	AT5G61250.2	AT5G61250	GUS1	944	755	360	296	0.27 ± 0.38	-0.49 ± 0.32	-0.40 ± 0.40	-1.24 ± 0.44	1.00E+00	1.00E+00	9.26E-01	6.84E-02	glucuronidase 1
	AT5G24270.1	AT5G24270	SOS3	746	841	112	231	-0.36 ± 0.50	-0.10 ± 0.39	-2.24 ± 2.88	-1.24 ± 0.29	1.00E+00	1.00E+00	9.88E-01	7.32E-04	Calcium-binding EF-hand family protein
	AT1G12150.1	AT1G12150	--	395	394	130	160	-0.28 ± 0.32	-0.39 ± 0.40	-0.33 ± 0.38	-1.24 ± 0.37	1.00E+00	1.00E+00	9.68E-01	1.40E-02	Plant protein of unknown function (DUF827)
	AT3G54590.1	AT3G54590	HRGP1	7808	6525	3525	3195	-0.33 ± 0.28	-1.13 ± 0.35	-0.99 ± 0.27	-1.25 ± 0.09	1.00E+00	8.61E-02	7.16E-03	3.51E-40	hydroxyproline-rich glycoprotein
	AT4G04450.1	AT4G04450	WRKY42	359	355	321	218	-0.09 ± 0.29	-0.22 ± 0.40	-0.41 ± 0.24	-1.26 ± 0.40	1.00E+00	1.00E+00	5.70E-01	2.74E-02	WRKY family transcription factor
	AT3G02885.1	AT3G02885	GASA5	6933	7749	825	849	0.57 ± 0.28	0.72 ± 0.31	-0.29 ± 0.15	-1.26 ± 0.30	1.00E+00	6.55E-01	4.51E-01	7.18E-04	GAST1 protein homolog 5
	AT1G01540.1	AT1G01540	--	299	303	130	137	0.00 ± 0.46	-0.06 ± 0.55	0.40 ± 0.37	-1.26 ± 0.43	1.00E+00	1.00E+00	8.91E-01	4.34E-02	Protein kinase superfamily protein
	AT2G28160.1	AT2G28160	FRU	7128	6869	1721	2974	0.06 ± 0.18	-0.15 ± 0.20	-0.41 ± 0.14	-1.26 ± 0.21	1.00E+00	1.00E+00	7.06E-02	5.07E-08	FER-like regulator of iron uptake
	AT2G32270.1	AT2G32270	ZIP3	2187	2472	1946	1770	-0.10 ± 0.13	0.16 ± 0.20	-0.76 ± 0.19	-1.26 ± 0.20	1.00E+00	1.00E+00	2.00E-03	3.23E-08	zinc transporter 3 precursor
	AT1G52820.1	AT1G52820	--	201	261	299	785	-1.24 ± 0.51	-0.36 ± 0.48	0.08 ± 0.25	-1.27 ± 0.44	6.29E-01	1.00E+00	1.00E+00	5.14E-02	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
	AT1G05240.1	AT1G05240	PR9	7586	7381	2066	1592	-0.20 ± 0.24	-0.39 ± 0.29	-0.76 ± 0.22	-1.28 ± 0.26	1.00E+00	1.00E+00	1.66E-02	5.14E-05	Peroxidase superfamily protein
	AT2G01530.1	AT2G01530	MLP329	17835	17886	7981	7969	0.10 ± 0.20	-0.03 ± 0.21	-0.61 ± 0.16	-1.28 ± 0.21	1.00E+00	1.00E+00	5.72E-03	6.41E-08	MLP-like protein 329
	AT1G70880.1	AT1G70880	--	175	181	130	100	0.04 ± 0.44	0.00 ± 0.57	-0.53 ± 0.47	-1.28 ± 0.44	1.00E+00	1.00E+00	8.75E-01	5.01E-02	Polyketide cyclase/dehydrase and lipid transport superfamily protein
	AT3G01310.2	AT3G01310	AtVIP1	2920	2852	1793	881	-0.04 ± 0.21	-0.20 ± 0.27	0.26 ± 0.21	-1.28 ± 0.44	1.00E+00	1.00E+00	8.40E-01	4.69E-02	Phosphoglycerate mutase-like family protein
	AT3G22570.1	AT3G22570	--	699	730	400	396	-0.08 ± 0.20	-0.10 ± 0.28	-0.96 ± 0.20	-1.29 ± 0.37	1.00E+00	1.00E+00	1.69E-04	9.43E-03	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT5G27930.1	AT5G27930	EGR2	816	892	340	464	-0.15 ± 0.60	0.01 ± 0.45	-0.90 ± 0.27	-1.29 ± 0.21	1.00E+00	1.00E+00	2.29E-02	2.43E-08	Protein phosphatase 2C family protein
	AT1G49310.1	AT1G49310	--	1057	1191	450	537	0.28 ± 0.20	0.42 ± 0.23	-0.47 ± 0.25	-1.30 ± 0.26	1.00E+00	1.00E+00	4.59E-01	3.40E-05	
	AT5G27930.2	AT5G27930	EGR2	1062	1066	192	264	0.20 ± 0.35	0.12 ± 0.33	-0.65 ± 0.29	-1.30 ± 0.29	1.00E+00	1.00E+00	2.61E-01	2.69E-04	Protein phosphatase 2C family protein
	AT1G23020.1	AT1G23020														

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
	AT1G05650.1	AT1G05650	--	1092	1163	137	347	-0.17 ± 0.28	-0.09 ± 0.35	-0.82 ± 0.33	-1.34 ± 0.39	1.00E+00	1.00E+00	1.91E-01	1.12E-02	Pectin lyase-like superfamily protein
	AT2G48080.1	AT2G48080	ALKBH10A	1813	2111	734	1216	-0.62 ± 0.40	-0.22 ± 0.25	-0.13 ± 0.23	-1.34 ± 0.29	1.00E+00	1.00E+00	1.00E+00	1.30E-04	oxidoreductase, 2OG-Fe(II) oxygenase family protein
	AT5G48290.2	AT5G48290	--	843	996	251	226	0.00 ± 0.23	0.34 ± 0.31	-0.68 ± 0.29	-1.34 ± 0.33	1.00E+00	1.00E+00	2.46E-01	1.57E-03	Heavy metal transport/detoxification superfamily protein
	AT1G71740.1	AT1G71740	--	152	179	63	92	0.07 ± 0.42	0.37 ± 0.48	-0.22 ± 0.53	-1.35 ± 0.51	1.00E+00	1.00E+00	1.00E+00	1.00E-01	
	AT4G30140.1	AT4G30140	CDEF1	928	1152	996	950	-0.10 ± 0.33	0.40 ± 0.45	-0.94 ± 0.15	-1.35 ± 0.15	1.00E+00	1.00E+00	4.70E-08	2.38E-17	GDSL-like Lipase/Acylhydrolase superfamily protein
	AT2G27040.2	AT2G27040	AGO4	341	234	308	203	0.53 ± 4.56	-0.68 ± 3.40	-0.08 ± 3.36	-1.35 ± 0.48	1.00E+00	1.00E+00	1.00E+00	6.09E-02	Argonaute family protein
	AT4G25820.1	AT4G25820	XTH14	6482	6872	1249	1184	0.04 ± 0.12	0.10 ± 0.32	-0.93 ± 0.29	-1.35 ± 0.23	1.00E+00	1.00E+00	3.26E-02	1.68E-07	xyloglucan endotransglucosylase/hydrolase 14
	AT2G48100.2	AT2G48100	--	1169	1162	372	633	-0.44 ± 0.28	-0.58 ± 0.40	0.08 ± 0.41	-1.36 ± 0.28	1.00E+00	1.00E+00	1.00E+00	3.81E-05	Exonuclease family protein
	AT4G37700.1	AT4G37700	--	404	368	138	115	0.15 ± 0.37	-0.29 ± 0.40	-0.84 ± 0.38	-1.36 ± 0.46	1.00E+00	1.00E+00	2.78E-01	4.47E-02	
	AT4G40070.1	AT4G40070	--	767	762	378	289	0.25 ± 0.30	0.14 ± 0.33	-0.77 ± 0.28	-1.36 ± 0.36	1.00E+00	1.00E+00	1.13E-01	3.49E-03	RING/U-box superfamily protein
	AT4G30290.1	AT4G30290	XTH19	4425	4579	1043	1510	0.01 ± 0.27	0.00 ± 0.20	-0.37 ± 0.19	-1.37 ± 0.13	1.00E+00	1.00E+00	4.65E-01	5.87E-24	xyloglucan endotransglucosylase/hydrolase 19
	AT2G32620.1	AT2G32620	CSLB02	581	560	155	167	-0.13 ± 0.27	-0.34 ± 0.49	-0.65 ± 0.35	-1.37 ± 0.52	1.00E+00	1.00E+00	4.94E-01	9.21E-02	cellulose synthase-like B
	AT1G70860.2	AT1G70860	--	281	294	73	119	0.04 ± 0.45	-0.03 ± 0.46	-0.88 ± 0.48	-1.37 ± 0.52	1.00E+00	1.00E+00	4.99E-01	9.62E-02	Polyketide cyclase/dehydrase and lipid transport superfamily protein
	AT1G03850.2	AT1G03850	GRXS13	996	990	868	696	-0.23 ± 0.22	-0.42 ± 0.25	-0.54 ± 0.22	-1.39 ± 0.46	1.00E+00	1.00E+00	1.70E-01	3.54E-02	Glutaredoxin family protein
	AT1G78000.2	AT1G78000	SULTR1;2	1581	2354	1769	2201	-1.46 ± 0.72	-0.05 ± 0.71	-0.43 ± 0.27	-1.39 ± 0.15	1.00E+00	1.00E+00	6.55E-01	1.92E-19	sulfate transporter 1;2
	AT2G29620.1	AT2G29620	--	601	592	165	163	-0.17 ± 0.23	-0.31 ± 0.35	-0.83 ± 0.40	-1.40 ± 0.34	1.00E+00	1.00E+00	3.73E-01	1.20E-03	
	AT3G07230.1	AT3G07230	--	1692	2195	469	476	-0.26 ± 0.42	0.39 ± 0.24	0.76 ± 0.37	-1.41 ± 0.22	1.00E+00	1.00E+00	3.78E-01	5.29E-09	wound-responsive protein-related
	AT2G32060.1	AT2G32060	--	1601	1836	776	812	0.73 ± 0.55	0.93 ± 0.35	0.71 ± 0.49	-1.41 ± 0.28	1.00E+00	3.67E-01	7.23E-01	2.76E-05	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein
	AT5G02090.1	AT5G02090	--	1280	1165	436	393	0.03 ± 0.20	-0.42 ± 0.21	-0.60 ± 0.20	-1.42 ± 0.52	1.00E+00	1.00E+00	6.08E-02	7.67E-02	
	AT1G07550.1	AT1G07550	--	603	572	86	110	0.01 ± 0.27	-0.23 ± 0.26	-0.85 ± 0.57	-1.42 ± 0.44	1.00E+00	1.00E+00	6.96E-01	2.00E-02	Leucine-rich repeat protein kinase family protein
	AT3G02560.2	AT3G02560	--	237	218	70	154	1.63 ± 0.86	1.38 ± 0.45	-0.49 ± 0.62	-1.42 ± 0.53	1.00E+00	1.37E-01	9.87E-01	9.18E-02	Ribosomal protein S7e family protein
	AT3G07070.1	AT3G07070	--	677	680	146	170	-0.03 ± 0.24	-0.11 ± 0.38	-1.18 ± 0.43	-1.43 ± 0.33	1.00E+00	1.00E+00	1.07E-01	4.77E-04	Protein kinase superfamily protein
	AT4G37070.1	AT4G37070	PLP1	660	578	664	693	-0.57 ± 0.27	-1.26 ± 0.35	-0.60 ± 0.24	-1.44 ± 0.21	1.00E+00	3.29E-02	1.76E-01	1.86E-09	Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein
	AT2G37760.1	AT2G37760	AKR4C8	311	443	847	451	-0.72 ± 0.50	0.27 ± 0.61	0.51 ± 0.44	-1.44 ± 0.28	1.00E+00	1.00E+00	8.73E-01	1.96E-05	NAD(P)-linked oxidoreductase superfamily protein
	AT2G15370.1	AT2G15370	FUT5	759	792	188	279	-0.09 ± 0.30	-0.06 ± 0.35	-0.80 ± 0.30	-1.44 ± 0.27	1.00E+00	1.00E+00	1.20E-01	4.13E-06	fucosyltransferase 5
	AT5G14330.1	AT5G14330	--	6222	6870	1305	1880	-0.07 ± 0.24	0.04 ± 0.34	-0.92 ± 0.17	-1.44 ± 0.22	1.00E+00	1.00E+00	9.02E-06	2.23E-09	
	AT4G16563.1	AT4G16563	--	695	690	792	352	-0.11 ± 0.26	-0.23 ± 0.28	-0.38 ± 0.15	-1.44 ± 0.27	1.00E+00	1.00E+00	1.82E-01	3.11E-06	Eukaryotic aspartyl protease family protein
	AT5G67400.1	AT5G67400	RHS19	7293	7768	1492	1223	-0.08 ± 0.16	0.00 ± 0.32	-0.98 ± 0.22	-1.44 ± 0.28	1.00E+00	1.00E+00	3.70E-04	1.80E-05	root hair specific 19
	AT3G09220.1	AT3G09220	LAC7	1789	1788	4057	3326	-0.96 ± 0.24	-1.10 ± 0.18	-0.90 ± 0.14	-1.45 ± 0.29	7.92E-03	1.32E-06	1.03E-08	2.75E-05	laccase 7
	AT1G53640.1	AT1G53640	--	437	406	192	152	0.59 ± 0.28	0.31 ± 0.41	-0.99 ± 0.35	-1.45 ± 0.46	1.00E+00	1.00E+00	7.93E-02	2.46E-02	
	AT4G08400.1	AT4G08400	--	1427	1222	503	445	-0.34 ± 0.32	-1.05 ± 0.32	-0.98 ± 0.32	-1.46 ± 0.33	1.00E+00	7.49E-02	4.86E-02	2.99E-04	Proline-rich extensin-like family protein
	AT3G16420.2	AT3G16420	PBP1	10881	12809	8398	9694	0.23 ± 0.40	0.56 ± 0.29	-0.24 ± 0.40	-1.46 ± 0.07	1.00E+00	1.00E+00	1.00E+00	#####	PYK10-binding protein 1
	AT5G40730.1	AT5G40730	ABP24	3473	4086	803	1211	-0.22 ± 0.21	0.05 ± 0.37	-0.65 ± 0.26	-1.48 ± 0.16	1.00E+00	1.00E+00	1.55E-01	1.62E-18	arabinogalactan protein 24
	AT3G47740.1	AT3G47740	ABCA3	393	380	89	92	0.01 ± 0.28	-0.17 ± 0.30	-0.79 ± 0.47	-1.50 ± 0.45	1.00E+00	1.00E+00	5.91E-01	1.61E-02	ABC2 homolog 2
	AT4G18975.3	AT4G18975	--	331	267	161	94	0.38 ± 0.47	-0.34 ± 0.70	-0.34 ± 0.43	-1.51 ± 0.55	1.00E+00	1.00E+00	9.88E-01	8.07E-02	Pentatricopeptide repeat (PPR) superfamily protein
	AT4G17340.1	AT4G17340	TIP2;2	15691	15627	2399	4729	-0.01 ± 0.19	-0.14 ± 0.26	-0.60 ± 0.23	-1.51 ± 0.18	1.00E+00	1.00E+00	1.48E-01	2.21E-15	tonoplast intrinsic protein 2;2
	AT2G18740.2	AT2G18740	--	869	1244	243	212	-0.52 ± 0.43	0.37 ± 0.38	0.50 ± 0.47	-1.51 ± 0.34	1.00E+00	1.00E+00	8.98E-01	2.55E-04	Small nuclear ribonucleoprotein family protein
	AT5G53550.2	AT5G53550	YSL3	1342	1069	509	355	0.43 ± 0.52	-0.29 ± 0.50	0.27 ± 0.24	-1.52 ± 0.40	1.00E+00	1.00E+00	8.80E-01	4.08E-03	YELLOW STRIPE like 3
	AT5G48000.3	AT5G48000	CYP708A2	961	924	1616	1389	0.61 ± 0.44	0.44 ± 0.36	-0.16 ± 0.23	-1.53 ± 0.28	1.00E+00	1.00E+00	1.00E+00	2.55E-06	cytochrome P450, family 708, subfamily A, polypeptide 2
	AT3G49960.1	AT3G49960	--	3391	3528	642	433	-0.09 ± 0.13	-0.07 ± 0.28	-0.86 ± 0.33	-1.55 ± 0.26	1.00E+00	1.00E+00	1.43E-01	1.86E-07	Peroxidase superfamily protein
	AT1G10550.1	AT1G10550	XTH33	434	485	173	152	0.04 ± 0.27	0.25 ± 0.40	-0.64 ± 0.31	-1.55 ± 0.44	1.00E+00	1.00E+00	3.56E-01	8.50E-03	xyloglucan:xyloglucosyl transferase 33
	AT4G12520.1	AT4G12520	--	10734	11299	3064	5020	-0.13 ± 0.19	-0.12 ± 0.29	-0.97 ± 0.11	-1.55 ± 0.11	1.00E+00	1.00E+00	7.74E-16	2.73E-39	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	AT5G23840.1	AT5G23840	--	423	427	437	325	-0.08 ± 0.55	-0.18 ± 0.56	-1.03 ± 0.39	-1.55 ± 0.43	1.00E+00	1.00E+00	1.20E-01	6.51E-03	MD-2-related lipid recognition domain-containing protein
	AT5G48290.1	AT5G48290	--	1084	1041	284	245	0.03 ± 0.31	-0.22 ± 0.29	-0.50 ± 0.24	-1.55 ± 0.34	1.00E+00	1.00E+00	3.35E-01	1.86E-04	Heavy metal transport/detoxification superfamily protein
	AT1G47230.2	AT1G47230	CYCA3;4	332	417	73	170	-0.27 ± 0.75	0.28 ± 0.41	-0.52 ± 0.55	-1.57 ± 0.59	1.00E+00	1.00E+00	9.43E-01	9.21E-02	CYCLIN A3;4
	AT2G01880.1	AT2G01880	PAP7	2698	2474	752	505	0.17 ± 0.19	-0.18 ± 0.16	-0.98 ± 0.18	-1.57 ± 0.22	1.00E+00	1.00E+00	5.05E-06	1.99E-10	purple acid phosphatase 7
	AT2G44380.1	AT2G44380	--	2503	2582	1336	992	-0.02 ± 0.18	-0.05 ± 0.21	-0.92 ± 0.13	-1.57 ± 0.29	1.00E+00	1.00E+00	2.47E-09	4.64E-06	Cysteine/Histidine-rich C1 domain family protein
	AT1G23060.1	AT1G23060	MDP40	469	508	156	130	-0.39 ± 0.27	-0.24 ± 0.38	0.02 ± 0.36	-1.58 ± 0.47	1.00E+00	1.00E+00	1.00E+00	1.38E-02	
	AT5G65720.2	AT5G65720	NFS1	1317	1837	312	1107	-0.15 ± 2.59	0.65 ± 1.74	-0.48 ± 3.50	-1.58 ± 0.40	1.00E+00	1.00E+00	1.00E+00	2.03E-03	nitrogen fixation S (NIFS)-like 1
	AT5G54700.1	AT5G54700	--	1377	1410	253	350	-0.32 ± 0.23	-0.							

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes				
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN				LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]				FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	
*	AT5G42590.1	AT5G42590	CYP71A16	544	563	412	435	-0.50 ± 0.44	-0.49 ± 0.33	-0.88 ± 0.22	-1.70 ± 0.39	1.00E+00	1.00E+00	2.50E-03	4.77E-04	cytochrome P450, family 71, subfamily A, polypeptide 16
	AT4G32420.4	AT4G32420	--	309	369	199	618	-2.06 ± 2.51	-1.21 ± 2.13	0.51 ± 0.67	-1.70 ± 0.19	1.00E+00	1.00E+00	9.92E-01	1.76E-16	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein
	AT5G36180.1	AT5G36180	sep1l	2337	2447	794	1024	-0.15 ± 0.19	-0.11 ± 0.21	-0.73 ± 0.20	-1.70 ± 0.27	1.00E+00	1.00E+00	9.57E-03	4.48E-08	serine carboxypeptidase-like 1
	AT4G22470.1	AT4G22470	--	42	56	225	113	-0.20 ± 0.78	0.50 ± 0.72	-1.03 ± 0.74	-1.70 ± 0.45	1.00E+00	1.00E+00	7.49E-01	3.37E-03	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
	AT5G11440.1	AT5G11440	CID5	362	399	75	102	-0.04 ± 0.32	0.12 ± 0.42	-0.63 ± 0.54	-1.70 ± 0.43	1.00E+00	1.00E+00	8.67E-01	1.90E-03	CTC-interacting domain 5
	AT2G19990.1	AT2G19990	PR-1-LIKE	926	967	63	64	1.25 ± 0.40	1.24 ± 0.45	-0.67 ± 0.64	-1.71 ± 0.65	1.39E-01	3.00E-01	9.06E-01	9.78E-02	pathogenesis-related protein-1-like
	AT1G26390.1	AT1G26390	AtBBE4	141	121	343	86	-1.30 ± 0.46	-2.64 ± 0.77	-0.53 ± 0.48	-1.73 ± 0.52	3.13E-01	5.09E-02	8.89E-01	1.47E-02	FAD-binding Berberine family protein
	AT5G62420.1	AT5G62420	--	839	756	127	214	0.29 ± 0.53	-0.11 ± 0.37	-0.55 ± 0.47	-1.78 ± 0.39	1.00E+00	1.00E+00	8.56E-01	1.84E-04	NAD(P)-linked oxidoreductase superfamily protein
	AT2G44100.2	AT2G44100	GDI1	109	93	36	67	1.19 ± 1.34	0.78 ± 1.28	-0.02 ± 0.66	-1.78 ± 0.61	1.00E+00	1.00E+00	1.00E+00	4.65E-02	guanosine nucleotide diphosphate dissociation inhibitor 1
	AT1G51880.1	AT1G51880	RHS6	208	211	63	80	0.03 ± 0.44	-0.03 ± 0.48	-0.72 ± 0.55	-1.82 ± 0.48	1.00E+00	1.00E+00	7.93E-01	4.05E-03	root hair specific 6
	AT3G60280.1	AT3G60280	UCC3	326	346	72	86	-0.16 ± 0.41	-0.11 ± 0.35	-1.23 ± 0.51	-1.82 ± 0.54	1.00E+00	1.00E+00	1.91E-01	1.40E-02	uclacyanin 3
	AT4G30280.1	AT4G30280	XTH18	4207	4720	729	1135	-0.01 ± 0.16	0.21 ± 0.28	-0.99 ± 0.20	-1.83 ± 0.17	1.00E+00	1.00E+00	3.74E-05	9.77E-26	xyloglucan endotransglucosylase/hydrolase 18
	AT4G31970.1	AT4G31970	CYP82C2	111	75	140	81	-0.25 ± 0.69	-2.22 ± 0.97	0.50 ± 1.06	-1.84 ± 0.63	1.00E+00	6.86E-01	1.00E+00	4.86E-02	cytochrome P450, family 82, subfamily C, polypeptide 2
	AT5G10330.2	AT5G10330	HPA1	423	862	72	216	-3.43 ± 2.23	0.21 ± 0.46	9.48 ± 4.79	-1.85 ± 0.66	1.00E+00	1.00E+00	4.11E-01	6.81E-02	histidinol phosphate aminotransferase 1
	AT5G09672.1	AT5G09672	--	1545	1490	448	740	0.17 ± 0.37	-0.02 ± 0.33	0.56 ± 0.48	-1.85 ± 0.19	1.00E+00	1.00E+00	8.68E-01	1.89E-20	conserved peptide upstream open reading frame 21
	AT1G27170.2	AT1G27170	--	621	674	240	262	-1.05 ± 0.79	-0.83 ± 0.59	0.29 ± 0.32	-1.85 ± 0.45	1.00E+00	1.00E+00	9.57E-01	9.83E-04	transmembrane receptors;ATP binding
	AT3G44510.2	AT3G44510	--	308	367	61	160	-0.84 ± 0.49	-0.34 ± 0.34	-0.82 ± 0.65	-1.86 ± 0.53	1.00E+00	1.00E+00	8.14E-01	1.02E-02	alpha/beta-Hydrolases superfamily protein
	AT1G09350.1	AT1G09350	GolS3	48	74	88	299	-0.69 ± 0.82	0.53 ± 0.74	-0.84 ± 0.44	-1.87 ± 0.27	1.00E+00	1.00E+00	4.61E-01	4.26E-10	galactinol synthase 3
	AT2G20080.2	AT2G20080	TIE2	120	145	67	149	-0.48 ± 0.48	-0.03 ± 0.52	0.17 ± 0.52	-1.89 ± 0.52	1.00E+00	1.00E+00	1.00E+00	5.97E-03	
	AT3G44310.2	AT3G44310	NT11	566	830	204	1125	-1.11 ± 4.56	0.10 ± 3.72	1.40 ± 3.13	-1.91 ± 0.25	1.00E+00	1.00E+00	1.00E+00	1.68E-12	nitrilase 1
	AT5G43540.1	AT5G43540	--	455	578	58	59	1.03 ± 0.28	1.40 ± 0.28	-1.24 ± 0.60	-1.91 ± 0.63	2.54E-02	1.37E-04	3.58E-01	3.86E-02	C2H2 and C2HC zinc fingers superfamily protein
	AT3G07300.1	AT3G07300	--	750	765	259	215	-0.37 ± 0.77	-0.41 ± 0.80	-1.37 ± 0.72	-1.91 ± 0.62	1.00E+00	1.00E+00	4.53E-01	3.02E-02	NagB/RpiA/CoA transferase-like superfamily protein
	AT3G45130.1	AT3G45130	LAS1	163	160	109	99	-0.59 ± 0.49	-0.76 ± 0.50	-1.30 ± 0.59	-1.93 ± 0.52	1.00E+00	1.00E+00	2.97E-01	5.22E-03	lanosterol synthase 1
	AT1G79580.1	AT1G79580	SMB	349	331	108	72	0.61 ± 0.60	0.40 ± 0.60	0.61 ± 0.54	-1.93 ± 0.67	1.00E+00	1.00E+00	8.77E-01	5.76E-02	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
	AT1G77990.1	AT1G77990	SULTR2;2	534	600	131	166	-0.29 ± 0.23	-0.02 ± 0.27	-0.88 ± 0.35	-1.93 ± 0.39	1.00E+00	1.00E+00	1.70E-01	2.41E-05	STAS domain / Sulfate transporter family
	AT1G67840.2	AT1G67840	CSK	312	307	145	232	-0.40 ± 0.41	-0.56 ± 0.44	1.05 ± 0.42	-1.95 ± 0.50	1.00E+00	1.00E+00	1.73E-01	2.16E-03	chloroplast sensor kinase
	AT5G48010.1	AT5G48010	THAS1	66	79	193	134	-1.22 ± 1.11	-0.56 ± 2.02	-0.68 ± 0.38	-1.95 ± 0.68	1.00E+00	1.00E+00	5.24E-01	5.66E-02	thalianol synthase 1
	AT3G15370.1	AT3G15370	EXPA12	693	698	41	126	0.26 ± 0.24	0.17 ± 0.33	-1.19 ± 0.81	-1.96 ± 0.65	1.00E+00	1.00E+00	7.20E-01	3.94E-02	expansin 12
	AT3G61440.2	AT3G61440	CYSC1	2426	3275	112	362	-1.13 ± 1.98	-0.16 ± 1.65	-0.12 ± 0.82	-2.00 ± 0.72	1.00E+00	1.00E+00	1.00E+00	6.90E-02	cysteine synthase C1
	AT5G51470.1	AT5G51470	--	255	270	49	54	-0.15 ± 0.43	-0.07 ± 0.38	-0.66 ± 0.68	-2.01 ± 0.61	1.00E+00	1.00E+00	9.38E-01	1.88E-02	Auxin-responsive GH3 family protein
	AT2G22300.1	AT2G22300	SR1	3066	2760	723	596	-0.10 ± 0.33	-0.54 ± 0.21	-0.38 ± 0.27	-2.03 ± 0.30	1.00E+00	4.36E-01	7.54E-01	2.10E-09	signal responsive 1
	AT5G03570.2	AT5G03570	IREG2	562	514	91	76	-0.18 ± 0.44	-0.58 ± 0.45	-0.64 ± 0.56	-2.04 ± 0.52	1.00E+00	1.00E+00	8.75E-01	2.15E-03	iron regulated 2
	AT3G46270.1	AT3G46270	--	173	223	47	84	-0.79 ± 0.46	-0.04 ± 0.57	-1.53 ± 0.67	-2.07 ± 0.54	1.00E+00	1.00E+00	2.54E-01	3.05E-03	receptor protein kinase-related
	AT2G02310.1	AT2G02310	PP2-B6	186	176	57	46	-0.04 ± 0.38	-0.33 ± 0.55	-0.99 ± 0.56	-2.10 ± 0.74	1.00E+00	1.00E+00	5.39E-01	6.14E-02	phloem protein 2-B6
	AT3G20060.2	AT3G20060	UBC19	140	209	9	130	-0.18 ± 1.47	0.71 ± 1.12	1.28 ± 3.33	-2.18 ± 0.56	1.00E+00	1.00E+00	1.00E+00	2.51E-03	ubiquitin-conjugating enzyme19
	AT1G06923.1	AT1G06923	--	299	327	45	41	-0.09 ± 0.37	0.07 ± 0.55	-1.15 ± 0.65	-2.19 ± 0.72	1.00E+00	1.00E+00	5.35E-01	3.83E-02	
	AT4G37950.1	AT4G37950	--	86	87	13	52	-0.96 ± 0.72	-1.07 ± 0.73	-2.53 ± 1.18	-2.19 ± 0.65	1.00E+00	1.00E+00	3.22E-01	1.36E-02	Rhamnogalacturonate lyase family protein
	AT1G66200.2	AT1G66200	GSR2	167	172	53	85	0.03 ± 0.42	0.02 ± 0.51	-0.07 ± 0.54	-2.22 ± 0.56	1.00E+00	1.00E+00	1.00E+00	2.14E-03	glutamine synthase clone F11
	AT2G33120.2	AT2G33120	SAR1	222	380	108	106	-2.56 ± 2.95	-0.10 ± 0.32	1.05 ± 2.97	-2.23 ± 0.80	1.00E+00	1.00E+00	1.00E+00	6.62E-02	synaptobrevin-related protein 1
	AT5G65800.1	AT5G65800	ACS5	151	118	52	116	0.25 ± 0.64	-0.60 ± 0.72	-1.60 ± 0.64	-2.25 ± 0.43	1.00E+00	1.00E+00	1.66E-01	8.48E-06	ACC synthase 5
	AT1G07960.1	AT1G07960	PDIL5-1	339	431	100	132	-0.93 ± 0.44	-0.22 ± 0.45	-0.03 ± 0.79	-2.29 ± 0.83	1.00E+00	1.00E+00	1.00E+00	7.57E-02	PDI-like 5-1
	AT1G48598.1	AT1G48598	--	1989	3601	1588	2497	-1.88 ± 1.27	0.30 ± 1.48	-1.25 ± 1.57	-2.30 ± 0.15	1.00E+00	1.00E+00	9.83E-01	3.70E-49	conserved peptide upstream open reading frame 31
	AT4G01890.1	AT4G01890	--	87	93	30	58	-0.40 ± 0.75	-0.32 ± 0.71	-1.26 ± 0.73	-2.37 ± 0.60	1.00E+00	1.00E+00	5.57E-01	2.06E-03	Pectin lyase-like superfamily protein
	AT1G11100.1	AT1G11100	FRG5	199	197	143	86	1.05 ± 0.92	0.97 ± 1.06	-0.90 ± 0.42	-2.44 ± 0.49	1.00E+00	1.00E+00	3.22E-01	3.46E-05	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related
	AT4G33730.1	AT4G33730	ATCAPE1	119	114	29	33	0.13 ± 0.53	-0.18 ± 0.61	-1.36 ± 0.76	-2.45 ± 0.76	1.00E+00	1.00E+00	5.25E-01	2.13E-02	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein
	AT4G19680.1	AT4G19680	IRT2	365	328	39	70	0.11 ± 0.35	-0.31 ± 0.41	0.18 ± 0.93	-2.47 ± 0.72	1.00E+00	1.00E+00	1.00E+00	1.11E-02	iron regulated transporter 2
	AT3G06400.3	AT3G06400	CHR11	336	263	177	126	0.34 ± 0.83	-0.48 ± 0.83	1.51 ± 0.67	-2.47 ± 0.62	1.00E+00	1.00E+00	2.66E-01	1.61E-03	chromatin-remodeling protein 11
	AT3G49720.2	AT3G49720	CGR2	1183	1590	1033	712	-0.35 ± 1.36	0.39 ± 1.40	1.02 ± 0.98	-2.53 ± 0.29	1.00E+00	1.00E+00	9.08E-01	3.24E-16	
	AT5G52350.1	AT5G52350	EXO70A3	425	557	25	29	-0.21 ± 0.47	0.45 ± 0.55	-1.67 ± 0.99	-2.55 ± 0.95	1.00E+00	1.00E+00	8.58E-01	9.02E-02	exocyst subunit exo70 family protein A3
	AT2G45330.2	AT2G45330	emb1067	492	694	366	302	-1.07 ± 0.73	0.01 ± 0.75	0.59 ± 0.62	-2.55 ± 0.38	1.00E+00	1.00E+00	9.42E-01	2.22E-09	RNA 2'-phosphotransferase, Tpt1 / KptA family
	AT4G22230.1	AT4G22230	--	101	149	54	28	0.19 ± 0.91	1.18 ± 0.64	-0.01 ± 0.80	-2.5					

Triple knockout (TKO) DE Genes				TPL-OE (6H) DE Genes				TPL-OE (6H and 15H) DE Genes				TPL-OE (15H) DE Genes						
(*)	MODEL ID	LOCUS ID	GENE ID	BASE MEAN		LOG BASE 2 FOLD CHANGE (±SE) [Mutant line compared to control]								FDR p-VALUE				TAIR10 Gene Description
				KO Analysis		TPL-OE line		KO Analysis		TPL-OE line		KO Analysis		TPL-OE line				
				TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H	TKO-1	TKO-2	6 H	15 H			
*	AT2G25510.2	AT2G25510	--	6	5	12	14	0.03 ± 2.85	-0.82 ± 2.06	-0.17 ± 2.41	-4.10 ± 1.53	1.00E+00	1.00E+00	1.00E+00	9.05E-02	Basic-leucine zipper (bZIP) transcription factor family protein SGNH hydrolase-type esterase superfamily protein Calmodulin-binding protein Protein of unknown function (DUF1666) NAC domain containing protein 69 detoxifying efflux carrier 35 Protein of unknown function DUF92, transmembrane 1-deoxy-D-xylulose 5-phosphate reductoisomerase rotamase FKBP 1 NAC domain containing protein 52 sterol 4-alpha-methyl-oxidase 2-2 PNAS-3 related Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region Phosphoglycerate mutase family protein D-3-phosphoglycerate dehydrogenase transposable element gene dicarboxylate transporter 1 Glucose-6-phosphate/phosphate translocator-related cysteine-rich RLK (RECEPTOR-like protein kinase) 18 actin-related protein C1A calmodulin-binding family protein 5'-3' exonuclease family protein eukaryotic translation initiation factor 4A1 CVP2 like 1 RHOMBOID-like protein 14 squamosa promoter-like 11 Family of unknown function (DUF566) Protein of unknown function (DUF567) Seven transmembrane MLO family protein tubulin beta 8 Ribosomal L29 family protein tonoplast monosaccharide transporter2 SIN3-like 5 rotamase cyclophilin 2 cation exchanger 5 peptide deformylase 1B NAC domain containing protein 48 eukaryotic translation initiation factor-related DNA repair protein Rad4 family Protein of unknown function (DUF581) MATE efflux family protein F-box family protein MIF4G domain-containing protein / MA3 domain-containing protein cyclic nucleotide gated channel 3 MAP kinase 17		
	AT1G58110.1	AT1G58110	--	293	489	11	96	-6.24 ± 4.58	-0.66 ± 3.55	6.77 ± 3.91	-4.35 ± 1.59	1.00E+00	1.00E+00	5.63E-01	7.69E-02			
	AT3G26890.4	AT3G26890	--	161	79	140	69	1.23 ± 3.09	-0.77 ± 4.57	-1.55 ± 3.90	-4.51 ± 1.29	1.00E+00	1.00E+00	1.00E+00	9.15E-03			
	AT1G75880.2	AT1G75880	--	19	17	41	25	-0.35 ± 2.21	-0.80 ± 2.18	-0.16 ± 0.65	-4.60 ± 1.12	1.00E+00	1.00E+00	1.00E+00	1.08E-03			
	AT4G25800.2	AT4G25800	--	40	89	154	41	6.32 ± 1.89	7.42 ± 1.76	-0.47 ± 0.70	-4.80 ± 0.92	7.94E-02	3.45E-03	1.00E+00	8.41E-06			
	AT5G39785.2	AT5G39785	--	33	32	9	9	0.74 ± 2.35	0.54 ± 0.91	-0.20 ± 3.39	-6.60 ± 2.39	1.00E+00	1.00E+00	1.00E+00	7.43E-02			
	AT4G01550.2	AT4G01550	NAC069	0	0	2	9	NA ± NA	NA ± NA	4.48 ± 4.81	-6.64 ± 2.38	NA	NA	NA	6.84E-02			
	AT4G09060.2	AT4G09060	--	13	20	2	9	-7.10 ± 2.76	-0.86 ± 2.39	-4.43 ± 4.82	-6.68 ± 2.30	4.97E-01	1.00E+00	NA	5.14E-02			
	AT4G25640.2	AT4G25640	DTX35	10	23	32	9	-1.25 ± 2.56	1.01 ± 1.23	1.64 ± 2.01	-6.68 ± 2.31	1.00E+00	1.00E+00	9.77E-01	5.32E-02			
	AT1G78620.2	AT1G78620	VTE6	40	15	10	10	2.66 ± 2.03	0.66 ± 3.51	-1.32 ± 3.31	-6.79 ± 2.31	1.00E+00	1.00E+00	1.00E+00	4.76E-02			
	AT5G62790.2	AT5G62790	DXR	34	39	15	10	-0.45 ± 2.33	-0.15 ± 2.20	-0.08 ± 2.11	-6.79 ± 2.28	1.00E+00	1.00E+00	1.00E+00	4.26E-02			
	AT3G25230.2	AT3G25230	ROF1	16	0	0	11	7.40 ± 4.47	NA ± NA	NA ± NA	-6.88 ± 2.20	1.00E+00	NA	NA	2.83E-02			
	AT3G10490.1	AT3G10490	NAC052	40	57	49	11	0.36 ± 0.81	1.12 ± 0.76	-0.93 ± 2.10	-6.96 ± 2.20	1.00E+00	1.00E+00	1.00E+00	2.51E-02			
	AT1G23110.1	AT1G23110	--	22	14	2	12	-0.36 ± 1.22	-2.95 ± 2.19	1.29 ± 4.40	-7.03 ± 2.34	1.00E+00	1.00E+00	NA	3.97E-02			
	AT2G29390.5	AT2G29390	SMO2-2	0	10	0	13	NA ± NA	6.76 ± 4.51	NA ± NA	-7.10 ± 2.14	NA	1.00E+00	NA	1.63E-02			
	AT2G25355.2	AT2G25355	--	34	30	5	13	-2.33 ± 2.25	-8.37 ± 2.28	-5.78 ± 4.74	-7.15 ± 2.15	1.00E+00	2.46E-02	8.41E-01	1.60E-02			
	AT4G14740.3	AT4G14740	--	63	82	9	13	1.27 ± 1.02	1.72 ± 1.10	-0.36 ± 2.24	-7.17 ± 2.23	1.00E+00	1.00E+00	1.00E+00	2.25E-02			
	AT5G64460.7	AT5G64460	--	120	139	27	14	1.21 ± 0.97	1.43 ± 0.96	0.39 ± 2.00	-7.25 ± 2.06	1.00E+00	1.00E+00	1.00E+00	8.71E-03			
	AT1G17745.2	AT1G17745	PGDH	54	58	10	14	-0.19 ± 3.32	-0.08 ± 3.06	0.69 ± 2.15	-7.26 ± 2.05	1.00E+00	1.00E+00	1.00E+00	8.09E-03			
	AT3G61330.1	AT3G61330	--	15	16	3	14	-0.58 ± 2.39	-0.37 ± 1.23	4.79 ± 4.80	-7.32 ± 2.24	1.00E+00	1.00E+00	NA	1.86E-02			
	AT5G12860.2	AT5G12860	DiT1	4	0	0	15	5.61 ± 4.80	NA ± NA	NA ± NA	-7.33 ± 2.21	1.00E+00	NA	NA	1.63E-02			
	AT5G46110.2	AT5G46110	APE2	136	105	34	15	-1.56 ± 2.13	-10.20 ± 1.88	0.62 ± 1.94	-7.37 ± 2.01	1.00E+00	2.13E-05	1.00E+00	5.36E-03			
	AT4G23260.1	AT4G23260	CRK18	4	2	55	15	0.73 ± 4.52	-4.12 ± 4.82	-2.71 ± 1.27	-7.37 ± 2.35	1.00E+00	NA	3.26E-01	2.73E-02			
	AT2G30910.2	AT2G30910	ARPC1A	48	82	9	16	-1.28 ± 1.01	0.44 ± 0.64	-1.07 ± 2.15	-7.44 ± 2.03	1.00E+00	1.00E+00	1.00E+00	5.37E-03			
	AT4G33050.4	AT4G33050	EDA39	24	11	23	16	0.95 ± 2.27	-1.93 ± 3.62	-0.51 ± 1.13	-7.49 ± 2.24	1.00E+00	1.00E+00	1.00E+00	1.53E-02			
	AT3G52050.4	AT3G52050	OEX1	133	116	4	17	-0.73 ± 0.82	-1.50 ± 0.92	5.40 ± 4.80	-7.53 ± 2.04	1.00E+00	1.00E+00	8.79E-01	5.04E-03			
	AT3G13920.2	AT3G13920	EIF4A1	23	35	9	18	-2.68 ± 2.03	-0.61 ± 2.17	-0.45 ± 3.34	-7.65 ± 1.91	1.00E+00	1.00E+00	1.00E+00	1.70E-03			
	AT1G19010.2	AT1G19010	--	52	124	34	19	-1.75 ± 1.09	1.01 ± 0.87	0.18 ± 0.79	-7.71 ± 2.04	1.00E+00	1.00E+00	1.00E+00	3.82E-03			
	AT2G32010.2	AT2G32010	CVL1	17	14	6	20	7.51 ± 2.26	7.21 ± 2.57	5.79 ± 4.54	-7.75 ± 2.02	8.48E-02	2.50E-01	8.13E-01	3.09E-03			
	AT3G17611.2	AT3G17611	RBL14	100	80	3	21	0.91 ± 1.05	0.29 ± 1.03	4.91 ± 3.26	-7.86 ± 1.85	1.00E+00	1.00E+00	6.93E-01	6.36E-04			
	AT1G27360.1	AT1G27360	SPL11	39	30	22	23	-1.44 ± 2.15	-8.38 ± 1.95	2.46 ± 1.89	-7.98 ± 1.97	1.00E+00	2.59E-03	8.01E-01	1.39E-03			
	AT3G19570.1	AT3G19570	SCO3	20	20	8	25	-0.24 ± 3.60	-0.39 ± 3.39	6.33 ± 4.15	-8.09 ± 1.90	1.00E+00	1.00E+00	6.79E-01	6.24E-04			
	AT2G14560.1	AT2G14560	LURP1	6	1	0	27	1.92 ± 4.13	-3.85 ± 4.83	-1.67 ± 4.99	-8.22 ± 2.57	1.00E+00	NA	NA	2.31E-02			
	AT1G67700.3	AT1G67700	HHL1	42	33	25	28	-0.62 ± 0.75	-1.98 ± 1.14	-2.09 ± 2.98	-8.28 ± 1.75	1.00E+00	1.00E+00	1.00E+00	8.44E-05			
	AT1G61560.3	AT1G61560	MLO6	74	81	88	79	-0.74 ± 0.87	-0.56 ± 0.84	-0.37 ± 3.02	-8.38 ± 2.16	1.00E+00	1.00E+00	1.00E+00	2.54E-03			
	AT5G23860.2	AT5G23860	TUB8	73	76	311	32	-0.91 ± 2.16	-0.87 ± 0.93	0.22 ± 0.59	-8.46 ± 1.78	1.00E+00	1.00E+00	1.00E+00	7.60E-05			
	AT3G55170.2	AT3G55170	--	164	149	196	34	-2.53 ± 0.95	-10.71 ± 1.82	0.15 ± 0.82	-8.54 ± 1.71	4.31E-01	1.76E-06	1.00E+00	2.66E-05			
	AT4G35300.4	AT4G35300	TMT2	84	126	206	35	0.71 ± 2.72	1.51 ± 1.95	0.74 ± 3.20	-8.59 ± 2.66	1.00E+00	1.00E+00	1.00E+00	2.07E-02			
	AT1G59890.3	AT1G59890	SNL5	11	108	24	101	1.73 ± 3.78	5.35 ± 2.05	-8.14 ± 3.39	-8.64 ± 1.89	1.00E+00	3.92E-01	2.08E-01	1.68E-04			
	AT5G07940.2	AT5G07940	--	17	10	98	40	7.49 ± 4.37	6.67 ± 3.40	1.02 ± 3.23	-8.79 ± 2.08	1.00E+00	1.00E+00	1.00E+00	6.93E-04			
	AT3G56070.2	AT3G56070	ROC2	264	354	20	109	-0.39 ± 4.56	0.33 ± 3.39	-4.27 ± 2.90	-8.82 ± 1.74	1.00E+00	1.00E+00	7.12E-01	1.69E-05			
	AT1G55730.1	AT1G55730	CAX5	168	206	54	43	-0.77 ± 3.20	-0.17 ± 0.82	0.67 ± 1.94	-8.90 ± 1.82	1.00E+00	1.00E+00	1.00E+00	3.87E-05			
	AT5G14660.2	AT5G14660	PDF1B	0	0	49	44	NA ± NA	NA ± NA	-0.31 ± 2.17	-8.91 ± 1.65	NA	NA	1.00E+00	3.36E-06			
	AT3G04420.2	AT3G04420	NAC048	131	92	21	44	2.71 ± 1.56	2.04 ± 1.60	-0.33 ± 3.06	-8.92 ± 1.65	1.00E+00	1.00E+00	1.00E+00	3.03E-06			
	AT1G11480.2	AT1G11480	--	15	16	35	44	-7.38 ± 4.47	-7.47 ± 4.07	1.38 ± 1.85	-8.93 ± 1.81	1.00E+00	1.00E+00	9.94E-01	3.39E-05			
	AT5G16630.1	AT5G16630	RAD4	205	178	94	50	1.89 ± 3.08	1.57 ± 3.11	1.02 ± 2.96	-9.11 ± 1.65	1.00E+00	1.00E+00	1.00E+00	1.71E-06			
	AT1G53885.1	AT1G53885	--	113	210	105	55	-0.39 ± 2.19	1.08 ± 3.23	-1.97 ± 2.88	-9.24 ± 1.61	1.00E+00	1.00E+00	1.00E+00	5.91E-07			
	AT1G51340.1	AT1G51340	--	137	88	2	57	1.41 ± 3.87	0.35 ± 2.09	4.48 ± 4.81	-9.29 ± 1.66	1.00E+00	1.00E+00	NA	1.17E-06			
	AT1G25055.1	AT1G25055	--	2684	3619	637	776	-1.05 ± 3.71	-0.10 ± 0.41	3.14 ± 3.16	-9.34 ± 0.68	1.00E+00	1.00E+00	9.28E-01	1.70E-40			
	AT5G57870.2	AT5G57870	elFiso4G1	213	269	143	83	-1.42 ± 3.20	-0.55 ± 3.32	-0.81 ± 0.65	-9.84 ± 1.77	1.00E+00	1.00E+00	8.29E-01	1.45E-06			
	AT2G46430.1	AT2G46430	CNGC3	487	605	108	167	-1.21 ± 0.52	-0.46 ± 0.43	0.90 ± 0.85	-10.85 ± 1.64	7.65E-01	1.00E+00	9.04E-01	3.15E-09			
	AT2G01450.4	AT2G01450	MPK17	0	1	0	124	NA ± NA	3.39 ± 4.84	NA ± NA	-23.82 ± 4.79	NA	NA	NA	2.73E-05			