

GO-ID	GO-TERM	STATS		QUERY GENES		ALL ANNOTATED GENES			FDR	
		<i>p</i> -VALUE	FDR <i>p</i> -VALUE	HITS	PERCENT	HITS	TOTAL	PERCENT	RATE	<EXP>

**Up-regulated in KO analysis: (58 genes analyzed)**

Unknown identifiers (2)										
GO:0050896	response to stimulus	1.22E-07	2.17E-05	31	53.45%	6897	31767	21.71%	0	0
GO:0006950	response to stress	1.27E-07	2.27E-05	23	39.66%	3910	31767	12.31%	0.00%	0
GO:0009611	response to wounding	1.65E-07	2.93E-05	7	12.07%	222	31767	0.70%	0.00%	0
GO:0009723	response to ethylene	2.07E-06	3.69E-04	7	12.07%	324	31767	1.02%	0.00%	0
GO:0042221	response to chemical	3.34E-05	5.95E-03	17	29.31%	3171	31767	9.98%	1.20%	0.06
GO:0042744	hydrogen peroxide catabolic process	3.44E-05	6.13E-03	4	6.90%	100	31767	0.31%	1.00%	0.06
GO:0017001	antibiotic catabolic process	4.17E-05	7.42E-03	4	6.90%	105	31767	0.33%	0.86%	0.06
GO:0016999	antibiotic metabolic process	6.79E-05	1.21E-02	5	8.62%	233	31767	0.73%	1.25%	0.1
GO:0042743	hydrogen peroxide metabolic process	7.48E-05	1.33E-02	4	6.90%	122	31767	0.38%	1.11%	0.1
GO:0042737	drug catabolic process	1.06E-04	1.88E-02	5	8.62%	256	31767	0.81%	1.20%	0.12
GO:0051187	cofactor catabolic process	1.08E-04	1.92E-02	4	6.90%	134	31767	0.42%	1.09%	0.12
GO:0042493	response to drug	1.56E-04	2.78E-02	7	12.07%	637	31767	2.01%	1.00%	0.12
GO:0006952	defense response	2.11E-04	3.75E-02	11	18.97%	1690	31767	5.32%	1.54%	0.2
GO:0009861	jasmonic acid and ethylene-dependent systemic resistance	3.39E-04	6.03E-02	2	3.45%	15	31767	0.05%	3.14%	0.44
GO:0072593	reactive oxygen species metabolic process	3.93E-04	6.99E-02	4	6.90%	188	31767	0.59%	3.07%	0.46
GO:0010035	response to inorganic substance	4.28E-04	7.62E-02	8	13.79%	994	31767	3.13%	2.88%	0.46
GO:0009873	ethylene-activated signaling pathway	4.60E-04	8.18E-02	4	6.90%	196	31767	0.62%	2.94%	0.5

**Down-regulated in KO analysis: (66 genes analyzed)**

Unknown identifiers (2)										
GO:2000652	regulation of secondary cell wall biogenesis	1.46E-07	3.04E-05	4	6.06%	23	31767	0.07%	0	0
GO:1903338	regulation of cell wall organization or biogenesis	1.32E-06	2.75E-04	4	6.06%	39	31767	0.12%	0	0
GO:0009698	phenylpropanoid metabolic process	2.02E-06	4.20E-04	6	9.09%	179	31767	0.56%	0	0
GO:0019748	secondary metabolic process	4.70E-06	9.78E-04	8	12.12%	456	31767	1.44%	0	0
GO:0010345	suberin biosynthetic process	9.52E-06	1.98E-03	3	4.55%	20	31767	0.06%	0	0
GO:0010345	suberin biosynthetic process	9.52E-06	1.98E-03	3	4.55%	20	31767	0.06%	0.00%	0
GO:0006629	lipid metabolic process	1.74E-05	3.61E-03	11	16.67%	1115	31767	3.51%	1.33%	0.08
GO:0009834	plant-type secondary cell wall biogenesis	2.51E-05	5.21E-03	4	6.06%	81	31767	0.25%	1.14%	0.08
GO:0071554	cell wall organization or biogenesis	1.25E-04	2.61E-02	8	12.12%	724	31767	2.28%	2.25%	0.18
GO:0009699	phenylpropanoid biosynthetic process	1.78E-04	3.71E-02	4	6.06%	134	31767	0.42%	2.44%	0.22
GO:0016042	lipid catabolic process	1.99E-04	4.14E-02	5	7.58%	257	31767	0.81%	2.20%	0.22
GO:0044087	regulation of cellular component biogenesis	2.67E-04	5.56E-02	4	6.06%	149	31767	0.47%	2.36%	0.26
GO:0071669	plant-type cell wall organization or biogenesis	4.31E-04	8.96E-02	5	7.58%	304	31767	0.96%	3.00%	0.36

GO-ID	GO-TERM	STATS		QUERY GENES		ALL ANNOTATED GENES			FDR	
		<i>p-VALUE</i>	<i>FDR p-VALUE</i>	<i>HITS</i>	<i>PERCENT</i>	<i>HITS</i>	<i>TOTAL</i>	<i>PERCENT</i>	<i>RATE</i>	<i>&lt;EXP&gt;</i>

***Up-regulated in TPL-OE (6H) analysis: (135 genes analyzed)***

Unknown identifiers (1)										
GO:0006592	ornithine biosynthetic process	1.79E-05	8.55E-03	2	1.48%	2	31767	0.01%	0.00%	0
GO:0044281	small molecule metabolic process	3.37E-05	1.61E-02	22	16.30%	1988	31767	6.26%	0.00%	0
GO:0019752	carboxylic acid metabolic process	1.01E-04	4.83E-02	15	11.11%	1135	31767	3.57%	2.00%	0.06
GO:0043436	oxoacid metabolic process	1.37E-04	6.55E-02	16	11.85%	1303	31767	4.10%	4.00%	0.16
GO:0006082	organic acid metabolic process	1.41E-04	6.73E-02	16	11.85%	1306	31767	4.11%	3.20%	0.16

***Down-regulated in TPL-OE (6H) analysis: (210 genes analyzed)***

Unknown identifiers (7)										
GO:1901659	glycosyl compound biosynthetic process	3.24E-08	1.95E-05	9	4.29%	104	31767	0.33%	0.00%	0
GO:1901657	glycosyl compound metabolic process	1.45E-07	8.71E-05	12	5.71%	254	31767	0.80%	0.00%	0
GO:0055114	oxidation-reduction process	1.97E-07	1.18E-04	29	13.81%	1489	31767	4.69%	0.00%	0
GO:0016144	S-glycoside biosynthetic process	3.10E-07	1.86E-04	7	3.33%	67	31767	0.21%	0.00%	0
GO:0019758	glycosinolate biosynthetic process	3.10E-07	1.86E-04	7	3.33%	67	31767	0.21%	0.00%	0
GO:0019761	glucosinolate biosynthetic process	3.10E-07	1.86E-04	7	3.33%	67	31767	0.21%	0.00%	0
GO:0009628	response to abiotic stimulus	7.93E-07	4.76E-04	36	17.14%	2262	31767	7.12%	0.00%	0
GO:1901135	carbohydrate derivative metabolic process	7.96E-07	4.77E-04	21	10.00%	911	31767	2.87%	0.00%	0
GO:0016143	S-glycoside metabolic process	1.43E-06	8.60E-04	9	4.29%	162	31767	0.51%	0.00%	0
GO:0019757	glycosinolate metabolic process	1.43E-06	8.60E-04	9	4.29%	162	31767	0.51%	0.00%	0
GO:0019760	glucosinolate metabolic process	1.43E-06	8.60E-04	9	4.29%	162	31767	0.51%	0.00%	0
GO:0044281	small molecule metabolic process	2.81E-06	1.69E-03	32	15.24%	1988	31767	6.26%	0.00%	0
GO:0006950	response to stress	2.89E-06	1.73E-03	50	23.81%	3910	31767	12.31%	0.00%	0
GO:0044272	sulfur compound biosynthetic process	3.12E-06	1.87E-03	9	4.29%	178	31767	0.56%	0.00%	0
GO:0009098	leucine biosynthetic process	4.13E-06	2.48E-03	4	1.90%	17	31767	0.05%	0.00%	0
GO:1901137	carbohydrate derivative biosynthetic process	5.37E-06	3.22E-03	15	7.14%	559	31767	1.76%	0.25%	0.04
GO:0051186	cofactor metabolic process	7.97E-06	4.78E-03	16	7.62%	652	31767	2.05%	0.24%	0.04
GO:1901564	organonitrogen compound metabolic process	1.59E-05	9.53E-03	67	31.90%	6234	31767	19.62%	0.22%	0.04
GO:0043436	oxoacid metabolic process	1.95E-05	1.17E-02	23	10.95%	1303	31767	4.10%	0.21%	0.04
GO:0009081	branched-chain amino acid metabolic process	2.00E-05	1.20E-02	5	2.38%	50	31767	0.16%	0.20%	0.04
GO:0006082	organic acid metabolic process	2.02E-05	1.21E-02	23	10.95%	1306	31767	4.11%	0.19%	0.04
GO:0009082	branched-chain amino acid biosynthetic process	2.11E-05	1.26E-02	4	1.90%	25	31767	0.08%	0.27%	0.06
GO:0006979	response to oxidative stress	2.23E-05	1.34E-02	13	6.19%	483	31767	1.52%	0.26%	0.06
GO:0006790	sulfur compound metabolic process	3.33E-05	2.00E-02	12	5.71%	431	31767	1.36%	0.42%	0.1

GO-ID	GO-TERM	STATS		QUERY GENES		ALL ANNOTATED GENES			FDR	
		p-VALUE	FDR p-VALUE	HITS	PERCENT	HITS	TOTAL	PERCENT	RATE	<EXP>
GO:0006551	leucine metabolic process	3.36E-05	2.01E-02	4	1.90%	28	31767	0.09%	0.40%	0.1
GO:0071456	cellular response to hypoxia	5.08E-05	3.05E-02	4	1.90%	31	31767	0.10%	0.54%	0.14
GO:0019748	secondary metabolic process	5.73E-05	3.44E-02	12	5.71%	456	31767	1.44%	0.59%	0.16
GO:0036294	cellular response to decreased oxygen levels	6.53E-05	3.92E-02	4	1.90%	33	31767	0.10%	0.71%	0.2
GO:0071453	cellular response to oxygen levels	6.53E-05	3.92E-02	4	1.90%	33	31767	0.10%	0.69%	0.2
GO:0019752	carboxylic acid metabolic process	7.13E-05	4.28E-02	20	9.52%	1135	31767	3.57%	0.73%	0.22
GO:1901566	organonitrogen compound biosynthetic process	7.52E-05	4.51E-02	34	16.19%	2563	31767	8.07%	0.71%	0.22
GO:0050896	response to stimulus	1.19E-04	7.14E-02	69	32.86%	6897	31767	21.71%	0.75%	0.24
GO:0016053	organic acid biosynthetic process	1.23E-04	7.38E-02	14	6.67%	652	31767	2.05%	0.73%	0.24
GO:0046394	carboxylic acid biosynthetic process	1.23E-04	7.38E-02	14	6.67%	652	31767	2.05%	0.71%	0.24
GO:0044550	secondary metabolite biosynthetic process	1.27E-04	7.60E-02	8	3.81%	223	31767	0.70%	0.69%	0.24
GO:0042743	hydrogen peroxide metabolic process	1.66E-04	9.97E-02	6	2.86%	122	31767	0.38%	0.94%	0.34

*Up-regulated in TPL-OE (6H and 15H) analysis: (65 genes analyzed)*

Unknown identifiers (1)

GO:0010345	suberin biosynthetic process	9.09E-06	2.77E-03	3	0.046154	20	31767	0.00063	0.00%	0
GO:0009698	phenylpropanoid metabolic process	3.37E-05	1.03E-02	5	0.076923	179	31767	0.005635	0.00%	0
GO:0019748	secondary metabolic process	4.07E-05	1.24E-02	7	0.107692	456	31767	0.014355	0.00%	0
GO:0033239	negative regulation of cellular amine metabolic process	4.11E-05	1.25E-02	2	0.030769	5	31767	0.000157	0.00%	0
GO:0045763	negative regulation of cellular amino acid metabolic process	4.11E-05	1.25E-02	2	0.030769	5	31767	0.000157	0.00%	0

*Down-regulated in TPL-OE (6H and 15H) analysis: (86 genes analyzed)*

Unknown identifiers (4)

GO:0071669	plant-type cell wall organization or biogenesis	6.66E-10	1.78E-07	11	0.127907	304	31767	0.00957	0.00%	0
GO:0071554	cell wall organization or biogenesis	9.81E-10	2.62E-07	15	0.174419	724	31767	0.022791	0.00%	0
GO:0048364	root development	2.57E-08	6.86E-06	12	0.139535	541	31767	0.01703	0.00%	0
GO:0022622	root system development	2.68E-08	7.14E-06	12	0.139535	543	31767	0.017093	0.00%	0
GO:0071555	cell wall organization	1.92E-07	5.12E-05	11	0.127907	528	31767	0.016621	0.00%	0
GO:0009664	plant-type cell wall organization	2.89E-07	7.73E-05	7	0.081395	161	31767	0.005068	0.00%	0
GO:0045229	external encapsulating structure organization	3.82E-07	1.02E-04	11	0.127907	566	31767	0.017817	0.00%	0
GO:0010015	root morphogenesis	9.91E-07	2.65E-04	8	0.093023	281	31767	0.008846	0.00%	0
GO:0010054	trichoblast differentiation	1.57E-05	4.19E-03	5	0.05814	115	31767	0.00362	1.33%	0.12
GO:0006869	lipid transport	2.48E-05	6.62E-03	6	0.069767	212	31767	0.006674	1.60%	0.16
GO:0048528	post-embryonic root development	3.91E-05	1.04E-02	5	0.05814	139	31767	0.004376	1.45%	0.16
GO:1905392	plant organ morphogenesis	3.94E-05	1.05E-02	8	0.093023	466	31767	0.014669	1.33%	0.16

GO-ID	GO-TERM	STATS		QUERY GENES		ALL ANNOTATED GENES			FDR	
		<i>p</i> -VALUE	FDR <i>p</i> -VALUE	HITS	PERCENT	HITS	TOTAL	PERCENT	RATE	<EXP>
GO:0099402	plant organ development	4.11E-05	1.10E-02	12	0.139535	1102	31767	0.03469	1.23%	0.16
GO:0010053	root epidermal cell differentiation	4.48E-05	1.20E-02	5	0.05814	143	31767	0.004502	1.43%	0.2
GO:0010876	lipid localization	5.56E-05	1.48E-02	6	0.069767	245	31767	0.007712	1.33%	0.2
GO:0042546	cell wall biogenesis	5.56E-05	1.48E-02	6	0.069767	245	31767	0.007712	1.25%	0.2
GO:0090627	plant epidermal cell differentiation	9.08E-05	2.42E-02	5	0.05814	166	31767	0.005226	1.88%	0.32
GO:0009653	anatomical structure morphogenesis	1.43E-04	3.81E-02	11	0.127907	1067	31767	0.033588	2.11%	0.38
GO:0090558	plant epidermis development	1.45E-04	3.88E-02	6	0.069767	292	31767	0.009192	2.00%	0.38
GO:0090696	post-embryonic plant organ development	1.51E-04	4.03E-02	5	0.05814	185	31767	0.005824	2.00%	0.4
GO:0048764	trichoblast maturation	2.09E-04	5.58E-02	4	0.046512	107	31767	0.003368	2.00%	0.42
GO:0048765	root hair cell differentiation	2.09E-04	5.58E-02	4	0.046512	107	31767	0.003368	1.91%	0.42
GO:0048469	cell maturation	2.17E-04	5.78E-02	4	0.046512	108	31767	0.0034	1.83%	0.42
GO:0005976	polysaccharide metabolic process	3.44E-04	9.17E-02	7	0.081395	483	31767	0.015204	2.58%	0.62
GO:0048527	lateral root development	3.45E-04	9.21E-02	4	0.046512	122	31767	0.00384	2.48%	0.62

### *Up-regulated in TPL-OE (15H) analysis: (534 genes analyzed)*

Unknown identifiers (10)

GO:0006631	fatty acid metabolic process	2.40E-14	2.26E-11	28	0.052434	271	31767	0.008531	0.00%	0
GO:0006633	fatty acid biosynthetic process	1.33E-13	1.25E-10	22	0.041199	169	31767	0.00532	0.00%	0
GO:0032787	monocarboxylic acid metabolic process	7.67E-11	7.20E-08	34	0.06367	545	31767	0.017156	0.00%	0
GO:0019752	carboxylic acid metabolic process	8.14E-11	7.64E-08	52	0.097378	1135	31767	0.035729	0.00%	0
GO:0043436	oxoacid metabolic process	4.60E-10	4.32E-07	55	0.102996	1303	31767	0.041017	0.00%	0
GO:0006082	organic acid metabolic process	5.00E-10	4.70E-07	55	0.102996	1306	31767	0.041112	0.00%	0
GO:0072330	monocarboxylic acid biosynthetic process	5.40E-09	5.07E-06	24	0.044944	343	31767	0.010797	0.00%	0
GO:1901568	fatty acid derivative metabolic process	7.65E-09	7.18E-06	11	0.020599	63	31767	0.001983	0.00%	0
GO:0010345	suberin biosynthetic process	2.34E-08	2.20E-05	7	0.013109	20	31767	0.00063	0.00%	0
GO:0010025	wax biosynthetic process	5.19E-08	4.87E-05	9	0.016854	45	31767	0.001417	0.00%	0
GO:0010166	wax metabolic process	7.74E-08	7.27E-05	9	0.016854	47	31767	0.00148	0.00%	0
GO:0010143	cutin biosynthetic process	9.85E-08	9.25E-05	7	0.013109	24	31767	0.000756	0.00%	0
GO:0044281	small molecule metabolic process	1.08E-07	1.01E-04	66	0.123596	1988	31767	0.062581	0.00%	0
GO:1901570	fatty acid derivative biosynthetic process	1.13E-07	1.06E-04	9	0.016854	49	31767	0.001542	0.00%	0
GO:0044255	cellular lipid metabolic process	1.51E-07	1.42E-04	36	0.067416	809	31767	0.025467	0.00%	0
GO:0006629	lipid metabolic process	1.86E-07	1.75E-04	44	0.082397	1115	31767	0.035099	0.00%	0
GO:0016053	organic acid biosynthetic process	2.74E-07	2.57E-04	31	0.058052	652	31767	0.020524	0.00%	0
GO:0046394	carboxylic acid biosynthetic process	2.74E-07	2.57E-04	31	0.058052	652	31767	0.020524	0.00%	0
GO:0008610	lipid biosynthetic process	1.27E-06	1.19E-03	29	0.054307	630	31767	0.019832	0.00%	0
GO:0000038	very long-chain fatty acid metabolic process	2.00E-06	1.87E-03	7	0.013109	36	31767	0.001133	0.00%	0

GO-ID	GO-TERM	STATS		QUERY GENES		ALL ANNOTATED GENES			FDR	
		<i>p</i> -VALUE	FDR <i>p</i> -VALUE	HITS	PERCENT	HITS	TOTAL	PERCENT	RATE	<EXP>
GO:0042221	response to chemical	3.39E-06	3.18E-03	87	0.162921	3171	31767	0.099821	0.00%	0
GO:1901700	response to oxygen-containing compound	5.27E-06	4.95E-03	56	0.104869	1778	31767	0.05597	0.00%	0
GO:0009646	response to absence of light	5.91E-06	5.55E-03	7	0.013109	42	31767	0.001322	0.00%	0
GO:0006970	response to osmotic stress	6.46E-06	6.07E-03	29	0.054307	685	31767	0.021563	0.00%	0
GO:0044283	small molecule biosynthetic process	6.71E-06	6.30E-03	33	0.061798	837	31767	0.026348	0.00%	0
GO:0042761	very long-chain fatty acid biosynthetic process	9.42E-06	8.84E-03	5	0.009363	18	31767	0.000567	0.00%	0
GO:0009698	phenylpropanoid metabolic process	1.17E-05	1.10E-02	13	0.024345	179	31767	0.005635	0.00%	0
GO:0010035	response to inorganic substance	1.63E-05	1.53E-02	36	0.067416	994	31767	0.03129	0.00%	0
GO:0009737	response to abscisic acid	2.97E-05	2.79E-02	26	0.048689	630	31767	0.019832	0.14%	0.04
GO:0097305	response to alcohol	3.31E-05	3.10E-02	26	0.048689	634	31767	0.019958	0.13%	0.04
GO:0010033	response to organic substance	3.44E-05	3.23E-02	64	0.11985	2268	31767	0.071395	0.13%	0.04
GO:0009725	response to hormone	3.71E-05	3.48E-02	56	0.104869	1905	31767	0.059968	0.19%	0.06
GO:0009719	response to endogenous stimulus	4.78E-05	4.49E-02	56	0.104869	1923	31767	0.060535	0.24%	0.08
GO:0001101	response to acid chemical	5.05E-05	4.74E-02	43	0.080524	1347	31767	0.042402	0.24%	0.08
GO:0009628	response to abiotic stimulus	5.83E-05	5.47E-02	63	0.117978	2262	31767	0.071206	0.23%	0.08

**Down-regulated in TPL-OE (15H) analysis: (353 genes analyzed)**

Unknown identifiers (8)										
GO:0042744	hydrogen peroxide catabolic process	9.42E-11	6.10E-08	13	3.68%	100	31767	0.31%	0	0
GO:0017001	antibiotic catabolic process	1.76E-10	1.14E-07	13	3.68%	105	31767	0.33%	0	0
GO:0017001	antibiotic catabolic process	1.76E-10	1.14E-07	13	3.68%	105	31767	0.33%	0.00%	0
GO:0042743	hydrogen peroxide metabolic process	1.17E-09	7.56E-07	13	3.68%	122	31767	0.38%	0.00%	0
GO:0051187	cofactor catabolic process	3.73E-09	2.42E-06	13	3.68%	134	31767	0.42%	0.00%	0
GO:0072593	reactive oxygen species metabolic process	2.86E-08	1.85E-05	14	3.97%	188	31767	0.59%	0.00%	0
GO:0006979	response to oxidative stress	3.13E-08	2.02E-05	22	6.23%	483	31767	1.52%	0.00%	0
GO:0016999	antibiotic metabolic process	6.36E-08	4.11E-05	15	4.25%	233	31767	0.73%	0.00%	0
GO:0042737	drug catabolic process	2.16E-07	1.40E-04	15	4.25%	256	31767	0.81%	0.00%	0
GO:0055114	oxidation-reduction process	2.69E-07	1.74E-04	40	11.33%	1489	31767	4.69%	0.00%	0
GO:0071555	cell wall organization	6.04E-07	3.91E-04	21	5.95%	528	31767	1.66%	0.00%	0
GO:0071554	cell wall organization or biogenesis	7.04E-07	4.55E-04	25	7.08%	724	31767	2.28%	0.00%	0
GO:0045229	external encapsulating structure organization	1.82E-06	1.18E-03	21	5.95%	566	31767	1.78%	0.00%	0
GO:0006811	ion transport	1.89E-06	1.22E-03	25	7.08%	765	31767	2.41%	0.00%	0
GO:0006722	triterpenoid metabolic process	3.71E-06	2.40E-03	5	1.42%	22	31767	0.07%	0.29%	0.04
GO:0050896	response to stimulus	1.24E-05	8.04E-03	111	31.44%	6897	31767	21.71%	0.40%	0.06
GO:0006950	response to stress	1.92E-05	1.25E-02	71	20.11%	3910	31767	12.31%	0.38%	0.06
GO:0010411	xyloglucan metabolic process	4.06E-05	2.63E-02	6	1.70%	57	31767	0.18%	0.35%	0.06
GO:0010054	trichoblast differentiation	4.52E-05	2.93E-02	8	2.27%	115	31767	0.36%	0.33%	0.06

GO-ID	GO-TERM	STATS		QUERY GENES		ALL ANNOTATED GENES			FDR	
		<i>p-VALUE</i>	<i>FDR p-VALUE</i>	<i>HITS</i>	<i>PERCENT</i>	<i>HITS</i>	<i>TOTAL</i>	<i>PERCENT</i>	<i>RATE</i>	<i>&lt;EXP&gt;</i>
GO:0015698	inorganic anion transport	6.50E-05	4.20E-02	8	2.27%	121	31767	0.38%	0.53%	0.1
GO:0009825	multidimensional cell growth	8.58E-05	5.55E-02	6	1.70%	65	31767	0.20%	0.70%	0.14
GO:0006820	anion transport	9.68E-05	6.26E-02	13	3.68%	331	31767	1.04%	0.67%	0.14
GO:0006826	iron ion transport	1.12E-04	7.27E-02	4	1.13%	23	31767	0.07%	0.64%	0.14