

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

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

Unknown identifiers (2)										
GO:0046872	metal ion binding	1.57E-08	8.79E-07	21	36.21%	2893	31767	9.11%	0	0
GO:0043169	cation binding	1.79E-08	1.00E-06	21	36.21%	2915	31767	9.18%	0	0
GO:0043169	cation binding	1.79E-08	1.00E-06	21	36.21%	2915	31767	9.18%	0.00%	0
GO:0045735	nutrient reservoir activity	1.51E-07	8.44E-06	5	8.62%	67	31767	0.21%	0.00%	0
GO:0030145	manganese ion binding	1.83E-06	1.03E-04	4	6.90%	48	31767	0.15%	0.00%	0
GO:0043167	ion binding	2.85E-06	1.60E-04	24	41.38%	5022	31767	15.81%	0.00%	0
GO:0004601	peroxidase activity	6.74E-06	3.78E-04	5	8.62%	144	31767	0.45%	0.00%	0
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	8.22E-06	4.60E-04	5	8.62%	150	31767	0.47%	0.00%	0
GO:0016209	antioxidant activity	1.78E-05	9.98E-04	5	8.62%	176	31767	0.55%	0.25%	0.02
GO:0005509	calcium ion binding	5.76E-05	3.22E-03	5	8.62%	225	31767	0.71%	0.44%	0.04
GO:0005488	binding	1.39E-04	7.79E-03	36	62.07%	11961	31767	37.65%	0.80%	0.08
GO:0003700	DNA-binding transcription factor activity	3.50E-04	1.96E-02	11	18.97%	1793	31767	5.64%	3.64%	0.4
GO:0020037	heme binding	3.93E-04	2.20E-02	4	6.90%	188	31767	0.59%	3.50%	0.42
GO:0140110	transcription regulator activity	6.29E-04	3.52E-02	11	18.97%	1922	31767	6.05%	3.85%	0.5
GO:0046906	tetrapyrrole binding	7.83E-04	4.39E-02	4	6.90%	226	31767	0.71%	4.86%	0.68
GO:0008061	chitin binding	8.09E-04	4.53E-02	2	3.45%	23	31767	0.07%	4.80%	0.72

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

Unknown identifiers (2)										
GO:0052716	hydroquinone:oxygen oxidoreductase activity	0.000566644	4.48E-02	2	3.03%	17	31767	0.05%	0.2	0.2
GO:0016787	hydrolase activity	0.000711975	5.62E-02	17	25.76%	3539	31767	11.14%	0.13	0.26

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

Unknown identifiers (1)										
GO:0043424	protein histidine kinase binding	1.61E-04	2.22E-02	3	2.22%	25	31767	0.08%	8.00%	0.08
GO:0016652	oxidoreductase activity, acting on NAD(P)H, NAD(P) as acceptor	4.94E-04	6.81E-02	2	1.48%	8	31767	0.03%	8.00%	0.16
GO:0005488	binding	5.32E-04	7.35E-02	70	51.85%	11961	31767	37.65%	5.33%	0.16
GO:0003729	mRNA binding	6.00E-04	8.28E-02	8	5.93%	439	31767	1.38%	5.00%	0.2
GO:0000978	RNA polymerase II proximal promoter sequence-specific DNA binding	6.13E-04	8.46E-02	3	2.22%	39	31767	0.12%	4.00%	0.2

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

Unknown identifiers (7)										
GO:0016491	oxidoreductase activity	8.10E-06	1.35E-03	28	13.33%	1698	31767	5.35%	0.00%	0
GO:0003824	catalytic activity	1.76E-05	2.92E-03	96	45.71%	10118	31767	31.85%	0.00%	0
GO:0004601	peroxidase activity	5.10E-05	8.47E-03	7	3.33%	144	31767	0.45%	0.67%	0.02
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	6.61E-05	1.10E-02	7	3.33%	150	31767	0.47%	0.50%	0.02
GO:0010177	2-(2'-methylthio)ethylmalate synthase activity	1.30E-04	2.16E-02	2	0.95%	3	31767	0.01%	1.20%	0.06
GO:0046906	tetrapyrrole binding	1.39E-04	2.31E-02	8	3.81%	226	31767	0.71%	1.00%	0.06

GO-ID	GO-TERM	STATS		QUERY GENES		ALL ANNOTATED GENES			FDR	
		p-VALUE	FDR p-VALUE	HITS	PERCENT	HITS	TOTAL	PERCENT	RATE	<EXP>
GO:0016209	antioxidant activity	1.79E-04	2.97E-02	7	3.33%	176	31767	0.55%	0.86%	0.06
GO:0046912	transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	2.16E-04	3.59E-02	3	1.43%	18	31767	0.06%	3.50%	0.28
GO:0003852	2-isopropylmalate synthase activity	2.59E-04	4.29E-02	2	0.95%	4	31767	0.01%	4.22%	0.38

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

Unknown identifiers (1)										
GO:0016787	hydrolase activity	0.000016	0.001454564	20	0.307692	3539	31767	0.111405	0.00%	0
GO:0046914	transition metal ion binding	0.0000878	0.007992556	11	0.169231	1355	31767	0.042654	1.00%	0.02
GO:0003824	catalytic activity	0.000195078	0.017752127	35	0.538462	10118	31767	0.318507	2.00%	0.06
GO:0043167	ion binding	0.000263336	0.023963576	22	0.338462	5022	31767	0.158089	1.50%	0.06
GO:0052716	hydroquinone:oxygen oxidoreductase activity	0.000549646	0.050017773	2	0.030769	17	31767	0.000535	2.00%	0.1
GO:0046872	metal ion binding	0.000608737	0.055395067	15	0.230769	2893	31767	0.091069	1.67%	0.1
GO:0043169	cation binding	0.000658956	0.059964995	15	0.230769	2915	31767	0.091762	1.43%	0.1

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

Unknown identifiers (4)										
GO:0005199	structural constituent of cell wall	9.96E-09	0.000000886	5	0.05814	27	31767	0.00085	0.00%	0
GO:0052689	carboxylic ester hydrolase activity	0.000367044	0.032666897	6	0.069767	347	31767	0.010923	8.00%	0.16
GO:0022838	substrate-specific channel activity	0.000911261	0.081102262	4	0.046512	158	31767	0.004974	17.33%	0.52
GO:0016298	lipase activity	0.001046331	0.093123422	4	0.046512	164	31767	0.005163	14.50%	0.58

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

Unknown identifiers (10)										
GO:0102391	decanoate-CoA ligase activity	9.30E-06	2.83E-03	4	0.75%	9	31767	0.03%	0.00%	0
GO:0004467	long-chain fatty acid-CoA ligase activity	1.53E-05	4.65E-03	4	0.75%	10	31767	0.03%	1.00%	0.02
GO:0009922	fatty acid elongase activity	1.53E-05	4.65E-03	4	0.75%	10	31767	0.03%	0.67%	0.02
GO:0031956	medium-chain fatty acid-CoA ligase activity	1.53E-05	4.65E-03	4	0.75%	10	31767	0.03%	0.50%	0.02
GO:0003824	catalytic activity	2.20E-05	6.69E-03	215	40.26%	10118	31767	31.85%	0.40%	0.02
GO:0015645	fatty acid ligase activity	2.37E-05	7.21E-03	4	0.75%	11	31767	0.03%	0.33%	0.02
GO:0004312	fatty acid synthase activity	2.74E-05	8.32E-03	5	0.94%	22	31767	0.07%	0.29%	0.02
GO:0016746	transferase activity, transferring acyl groups	2.96E-05	9.01E-03	20	3.75%	415	31767	1.31%	0.25%	0.02
GO:0048037	cofactor binding	4.78E-05	1.45E-02	29	5.43%	764	31767	2.41%	0.22%	0.02
GO:0018685	alkane 1-monooxygenase activity	1.57E-04	4.78E-02	3	0.56%	7	31767	0.02%	0.80%	0.08
GO:0046914	transition metal ion binding	2.34E-04	7.11E-02	41	7.68%	1355	31767	4.27%	0.73%	0.08
GO:0043167	ion binding	2.67E-04	8.11E-02	115	21.54%	5022	31767	15.81%	0.67%	0.08
GO:0009674	potassium:sodium symporter activity	2.82E-04	8.57E-02	2	0.37%	2	31767	0.01%	1.69%	0.22
GO:0031957	very long-chain fatty acid-CoA ligase activity	2.82E-04	8.57E-02	2	0.37%	2	31767	0.01%	1.57%	0.22
GO:0102419	sn-2-glycerol-3-phosphate omega-OH-C22:0-CoA acyl transferase activity	2.82E-04	8.57E-02	2	0.37%	2	31767	0.01%	1.47%	0.22

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

Unknown identifiers (8)

GO-ID	GO-TERM	STATS		QUERY GENES		ALL ANNOTATED GENES			FDR	
		p-VALUE	FDR p-VALUE	HITS	PERCENT	HITS	TOTAL	PERCENT	RATE	<EXP>
GO:0004601	peroxidase activity	9.07E-10	2.19E-07	14	3.97%	144	31767	0.45%	0.00%	0
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	1.55E-09	3.76E-07	14	3.97%	150	31767	0.47%	0.00%	0
GO:0016209	antioxidant activity	1.24E-08	2.99E-06	14	3.97%	176	31767	0.55%	0.00%	0
GO:0003824	catalytic activity	2.14E-08	5.17E-06	162	45.89%	10118	31767	31.85%	0.00%	0
GO:0020037	heme binding	2.86E-08	6.91E-06	14	3.97%	188	31767	0.59%	0.00%	0
GO:0048037	cofactor binding	4.36E-08	1.06E-05	28	7.93%	764	31767	2.41%	0.00%	0
GO:0016491	oxidoreductase activity	1.76E-07	4.25E-05	44	12.46%	1698	31767	5.35%	0.00%	0
GO:0046906	tetrapyrrole binding	2.80E-07	6.78E-05	14	3.97%	226	31767	0.71%	0.00%	0
GO:0015318	inorganic molecular entity transmembrane transporter activity	4.51E-07	1.09E-04	27	7.65%	806	31767	2.54%	0.00%	0
GO:0016709	oxidoreductase activity...NAD(P)H as one donor, and incorporation of one atom of oxygen	2.13E-06	5.17E-04	12	3.40%	195	31767	0.61%	0.00%	0
GO:0022857	transmembrane transporter activity	2.18E-06	5.28E-04	34	9.63%	1264	31767	3.98%	0.00%	0
GO:0043167	ion binding	1.07E-05	2.58E-03	87	24.65%	5022	31767	15.81%	0.17%	0.02
GO:0015075	ion transmembrane transporter activity	1.14E-05	2.76E-03	25	7.08%	849	31767	2.67%	0.15%	0.02
GO:0004497	monooxygenase activity	1.41E-05	3.40E-03	14	3.97%	316	31767	0.99%	0.14%	0.02
GO:0036094	small molecule binding	2.22E-05	5.37E-03	55	15.58%	2789	31767	8.78%	0.13%	0.02
GO:0016705	oxidoreductase activity... molecular oxygen	2.62E-05	6.33E-03	15	4.25%	379	31767	1.19%	0.12%	0.02
GO:0016762	xyloglucan:xyloglucosyl transferase activity	3.03E-05	7.32E-03	5	1.42%	33	31767	0.10%	0.12%	0.02
GO:0008144	drug binding	3.35E-05	8.11E-03	43	12.18%	2017	31767	6.35%	0.11%	0.02
GO:0005215	transporter activity	5.17E-05	1.25E-02	34	9.63%	1473	31767	4.64%	0.11%	0.02
GO:0019825	oxygen binding	6.87E-05	1.66E-02	11	3.12%	234	31767	0.74%	0.10%	0.02
GO:0005372	water transmembrane transporter activity	7.87E-05	1.91E-02	5	1.42%	40	31767	0.13%	0.10%	0.02
GO:0015250	water channel activity	7.87E-05	1.91E-02	5	1.42%	40	31767	0.13%	0.09%	0.02
GO:0015103	inorganic anion transmembrane transporter activity	8.65E-05	2.09E-02	8	2.27%	126	31767	0.40%	0.09%	0.02
GO:0005516	calmodulin binding	9.95E-05	2.41E-02	10	2.83%	203	31767	0.64%	0.08%	0.02
GO:0015267	channel activity	1.46E-04	3.54E-02	9	2.55%	173	31767	0.54%	0.24%	0.06
GO:0022803	passive transmembrane transporter activity	1.46E-04	3.54E-02	9	2.55%	173	31767	0.54%	0.23%	0.06
GO:0008509	anion transmembrane transporter activity	2.23E-04	5.39E-02	12	3.40%	313	31767	0.99%	0.52%	0.14
GO:0046527	glucosyltransferase activity	3.59E-04	8.70E-02	10	2.83%	238	31767	0.75%	1.07%	0.3
GO:0022838	substrate-specific channel activity	4.08E-04	9.87E-02	8	2.27%	158	31767	0.50%	1.24%	0.36