

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 KO analysis: (58 genes analyzed)

Unknown identifiers (2)										
GO:0005576	extracellular region	0.000000889	4.27E-05	19	32.76%	3019	31767	9.50%	0	0
GO:0005618	cell wall	0.00000172	8.24E-05	10	17.24%	801	31767	2.52%	0	0
GO:0005618	cell wall	1.72E-06	8.24E-05	10	17.24%	801	31767	2.52%	0.00%	0
GO:0030312	external encapsulating structure	1.72E-06	8.24E-05	10	17.24%	801	31767	2.52%	0.00%	0
GO:0071944	cell periphery	4.30E-04	2.07E-02	19	32.76%	4675	31767	14.72%	1.00%	0.04
GO:0009505	plant-type cell wall	7.73E-04	3.71E-02	5	8.62%	395	31767	1.24%	0.80%	0.04

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

Unknown identifiers (2)

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

Unknown identifiers (1)										
GO:0005829	cytosol	1.38E-04	1.40E-02	23	17.04%	2345	31767	7.38%	2.00%	0.02

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

Unknown identifiers (7)										
GO:0000313	organellar ribosome	1.47E-06	2.17E-04	7	3.33%	84	31767	0.26%	0.00%	0
GO:0009532	plastid stroma	1.68E-06	2.48E-04	19	9.05%	797	31767	2.51%	0.00%	0
GO:0071944	cell periphery	9.92E-06	1.47E-03	55	26.19%	4675	31767	14.72%	0.00%	0
GO:0005886	plasma membrane	1.24E-05	1.84E-03	49	23.33%	4003	31767	12.60%	0.00%	0
GO:0044435	plastid part	2.61E-05	3.86E-03	25	11.90%	1517	31767	4.78%	0.00%	0
GO:0016020	membrane	5.58E-05	8.25E-03	83	39.52%	8594	31767	27.05%	0.33%	0.02
GO:0044391	ribosomal subunit	6.33E-05	9.36E-03	11	5.24%	390	31767	1.23%	0.29%	0.02
GO:0000314	organellar small ribosomal subunit	7.37E-05	1.09E-02	4	1.90%	34	31767	0.11%	0.25%	0.02
GO:0005829	cytosol	7.45E-05	1.10E-02	32	15.24%	2345	31767	7.38%	0.22%	0.02
GO:0005840	ribosome	7.92E-05	1.17E-02	13	6.19%	547	31767	1.72%	0.20%	0.02
GO:0015935	small ribosomal subunit	1.11E-04	1.65E-02	7	3.33%	163	31767	0.51%	0.18%	0.02
GO:0005737	cytoplasm	1.13E-04	1.68E-02	121	57.62%	14209	31767	44.73%	0.17%	0.02
GO:0044444	cytoplasmic part	1.64E-04	2.43E-02	102	48.57%	11518	31767	36.26%	0.31%	0.04
GO:0009547	plastid ribosome	1.71E-04	2.52E-02	4	1.90%	42	31767	0.13%	0.29%	0.04

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:0009570	chloroplast stroma	1.80E-04	2.66E-02	15	7.14%	761	31767	2.40%	0.27%	0.04
GO:0009941	chloroplast envelope	2.86E-04	4.23E-02	14	6.67%	708	31767	2.23%	0.62%	0.1
GO:0009536	plastid	3.23E-04	4.78E-02	47	22.38%	4308	31767	13.56%	0.59%	0.1
GO:0009526	plastid envelope	3.72E-04	5.51E-02	14	6.67%	727	31767	2.29%	0.56%	0.1
GO:0044446	intracellular organelle part	3.78E-04	5.60E-02	57	27.14%	5594	31767	17.61%	0.53%	0.1
GO:0044422	organelle part	3.93E-04	5.81E-02	57	27.14%	5602	31767	17.63%	0.50%	0.1
GO:0033178	proton-transporting two-sector ATPase complex, catalytic domain	5.20E-04	7.70E-02	3	1.43%	24	31767	0.08%	0.57%	0.12
GO:0009506	plasmodesma	6.03E-04	8.93E-02	17	8.10%	1042	31767	3.28%	0.64%	0.14
GO:0055044	symplast	6.03E-04	8.93E-02	17	8.10%	1042	31767	3.28%	0.61%	0.14
GO:0005911	cell-cell junction	6.16E-04	9.12E-02	17	8.10%	1044	31767	3.29%	0.58%	0.14
GO:0030054	cell junction	6.16E-04	9.12E-02	17	8.10%	1044	31767	3.29%	0.56%	0.14

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

Unknown identifiers (1)

GO:0031225	anchored component of membrane	0.000543225	0.027704465	5	0.076923	325	31767	0.010231	4.00%	0.04
GO:0005886	plasma membrane	0.000857477	0.043731341	18	0.276923	4003	31767	0.126011	5.00%	0.1
GO:0031012	extracellular matrix	0.000927449	0.047299889	2	0.030769	22	31767	0.000693	4.00%	0.12
GO:0016020	membrane	0.001735331	0.088501866	29	0.446154	8594	31767	0.270532	5.00%	0.2

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

Unknown identifiers (4)

GO:0005576	extracellular region	2.92E-09	1.43E-07	28	32.56%	3019	31767	9.50%	0	0
GO:0005576	extracellular region	2.92E-09	1.43E-07	28	32.56%	3019	31767	9.50%	0.00%	0
GO:0005618	cell wall	1.69E-06	8.26E-05	12	13.95%	801	31767	2.52%	0.00%	0
GO:0030312	external encapsulating structure	1.69E-06	8.26E-05	12	13.95%	801	31767	2.52%	0.00%	0
GO:0009505	plant-type cell wall	1.21E-05	5.94E-04	8	9.30%	395	31767	1.24%	0.00%	0
GO:XXXXXXXX	unannotated	1.32E-04	6.44E-03	13	15.12%	1443	31767	4.54%	2.00%	0.1
GO:0071944	cell periphery	1.85E-04	9.05E-03	26	30.23%	4675	31767	14.72%	2.00%	0.12
GO:0009506	plasmodesma	2.04E-03	9.99E-02	9	10.47%	1042	31767	3.28%	6.00%	0.42
GO:0055044	symplast	2.04E-03	9.99E-02	9	10.47%	1042	31767	3.28%	5.25%	0.42

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

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>
Unknown identifiers (10)										
GO:0044464	cell part	3.31E-06	5.52E-04	445	83.33%	23895	31767	75.22%	0.00%	0
GO:0005623	cell	3.44E-06	5.74E-04	445	83.33%	23900	31767	75.24%	0.00%	0
GO:0005623	cell	0.00000344	5.74E-04	445	83.33%	23900	31767	75.24%	0.00%	0
GO:0009923	fatty acid elongase complex	0.000282052	4.71E-02	2	0.37%	2	31767	0.01%	0.67%	0.02

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

Unknown identifiers (8)										
GO:0005576	extracellular region	8.59E-12	1.14E-09	76	21.53%	3019	31767	9.50%	0	0
GO:0005576	extracellular region	8.59E-12	1.14E-09	76	21.53%	3019	31767	9.50%	0.00%	0
GO:0071944	cell periphery	3.93E-06	5.23E-04	84	23.80%	4675	31767	14.72%	0.00%	0
GO:0005618	cell wall	1.29E-05	1.72E-03	24	6.80%	801	31767	2.52%	0.00%	0
GO:0030312	external encapsulating structure	1.29E-05	1.72E-03	24	6.80%	801	31767	2.52%	0.00%	0
GO:0016021	integral component of membrane	6.54E-05	8.70E-03	72	20.40%	4135	31767	13.02%	0.00%	0
GO:0031224	intrinsic component of membrane	9.97E-05	1.33E-02	75	21.25%	4416	31767	13.90%	0.00%	0
GO:0016020	membrane	1.38E-04	1.83E-02	127	35.98%	8594	31767	27.05%	0.57%	0.04
GO:0009505	plant-type cell wall	5.33E-04	7.09E-02	13	3.68%	395	31767	1.24%	2.75%	0.22
GO:0048046	apoplast	7.26E-04	9.65E-02	14	3.97%	461	31767	1.45%	2.44%	0.22