



Term	Observed Frequency	Expected Frequency	p-value	Genes
Cluster #2				
ENERGY	3 out of 6 genes, 50.0%	415 out of 27532 genes, 1.5%	0.00046	At1a35290 At3a62410 At4a426390
chloroplast	4 out of 6 genes, 66.7%	3363 out of 27532 genes, 12.2%	0.01901	At1a35290 At1a18485 At3a62410 At4a418350
plastid	4 out of 6 genes, 66.7%	3386 out of 27532 genes, 12.3%	0.01951	At1a35290 At1a18485 At3a62410 At4a418350
Cluster #8				
metabolism of glycosinolates and derivatives	2 out of 15 genes, 13.3%	14 out of 27532 genes, 0.1%	0.00045	At5a23010 At5a23020
metabolism of leucine	2 out of 15 genes, 13.3%	23 out of 27532 genes, 0.1%	0.00125	At5a23010 At5a23020
metabolism of the oxuvate family (alanine, it)	2 out of 15 genes, 13.3%	41 out of 27532 genes, 0.1%	0.00403	At5a23010 At5a23020
metabolism of secondary products derived from	2 out of 15 genes, 13.3%	43 out of 27532 genes, 0.2%	0.00444	At5a23010 At5a23020
Cluster #18				
unannotated	2 out of 38 genes, 5.3%	out of 27532 genes, 0.0%	0	AtC000660 At3a26782
lead binding	4 out of 38 genes, 10.5%	141 out of 27532 genes, 0.5%	0.00199	At1a35720 At4a27140 At5a65020 At2a27130
metabolism of cysteine	2 out of 38 genes, 5.3%	18 out of 27532 genes, 0.1%	0.01315	At3a1440 At3a01120
metabolism of the cysteine - aromatic group	3 out of 38 genes, 7.9%	133 out of 27532 genes, 0.5%	0.03861	At2a17630 At3a61440 At3a01120
Cluster #20				
ribosomal proteins	5 out of 39 genes, 12.8%	166 out of 27532 genes, 0.6%	0.00017	At2a27720 At5a20290 At3a05590 At1a77940 At3a11510
pyrimidine nucleotide/nucleoside/nucleobase	1 out of 39 genes, 7.7%	71 out of 27532 genes, 0.3%	0.0066	At1a25210 At4a09320 At4a11010
ribosome biogenesis	5 out of 39 genes, 12.8%	388 out of 27532 genes, 1.4%	0.00988	At2a27720 At5a20290 At3a05590 At1a77940 At3a11510
Cluster #17				
C-compound and carbohydrate metabolism	14 out of 66 genes, 21.2%	1631 out of 27532 genes, 5.9%	0.00162	At4a04040 At3a06380 At1a22400 At1a05570 At4a15270 At3a57790 At1a80460 At1a52760 At3a09260 At1a62660 At1a23760 At3a47050 At5a36160 At3a10740
superoxide metabolism	2 out of 66 genes, 3.0%	14 out of 27532 genes, 0.1%	0.01334	At1a12520 At2a26190
METABOLISM	23 out of 66 genes, 34.8%	4848 out of 27532 genes, 17.6%	0.03656	At3a48990 At1a22400 At5a35980 At2a30860 At3a57790 At1a80460 At3a14050 At3a47050 At2a40890 At5a36160 At3a10740 At4a404040 At3a06380 At1a05570 At4a15270 At1a61360 At3a19010 At1a52760 At1a009570 At3a009260 At1a23760 At1a62660 At5a65110
Cluster #15				
ENERGY	7 out of 61 genes, 11.5%	415 out of 27532 genes, 1.5%	0.00309	At4a30190 At4a35260 At3a14940 At4a27180 At4a24620 At3a47520 At5a13420
chemoatraction and response	9 out of 61 genes, 14.8%	770 out of 27532 genes, 2.8%	0.004	At1a74660 At1a19050 At3a14940 At2a38170 At5a50200 At3a60690 At5a62530 At5a61420 At1a69040
metabolism of glutamate	3 out of 61 genes, 4.9%	34 out of 27532 genes, 0.1%	0.00501	At5a53460 At5a53630 At5a62530
tricarboxylic-acid pathway (citrate cycle, Krebs)	3 out of 61 genes, 4.9%	34 out of 27532 genes, 0.1%	0.00501	At4a35260 At3a14940 At3a47520
INTERACTION WITH THE ENVIRONMENT	12 out of 61 genes, 19.7%	1454 out of 27532 genes, 5.3%	0.00598	At5a10030 At1a74660 At1a19050 At3a14940 At2a38170 At5a50200 At3a60690 At5a62530 At5a17880 At5a61420 At4a27180 At1a69040
activity of intercellular mediators	3 out of 61 genes, 4.9%	38 out of 27532 genes, 0.1%	0.00702	At1a74660 At1a19050 At1a69040
cytokines (interleukines, colonv stimulatino fa	3 out of 61 genes, 4.9%	38 out of 27532 genes, 0.1%	0.00702	At1a74660 At1a19050 At1a69040
biosynthesis of glutamate	2 out of 61 genes, 3.3%	7 out of 27532 genes, 0.0%	0.00855	At5a53460 At5a62530
cytokinin response	3 out of 61 genes, 4.9%	41 out of 27532 genes, 0.1%	0.00883	At1a74660 At1a19050 At1a69040
cellular sensina and response to external stim	11 out of 61 genes, 18.0%	1297 out of 27532 genes, 4.7%	0.00988	At5a10030 At1a74660 At1a19050 At3a14940 At2a38170 At5a50200 At3a60690 At5a62530 At5a17880 At5a61420 At1a69040
nitrate transport	2 out of 61 genes, 3.3%	10 out of 27532 genes, 0.0%	0.01825	At5a50200 At5a60770
assimilation of ammonia, metabolism of the	2 out of 61 genes, 4.9%	57 out of 27532 genes, 0.2%	0.02363	At5a53460 At5a53630 At5a62530
Cluster #13				
pentose-phosphate pathway oxidative branch	3 out of 42 genes, 7.1%	15 out of 27532 genes, 0.1%	6.82E-05	At5a41670 At1a64190 At5a13110
pentose-phosphate pathway	3 out of 42 genes, 7.1%	46 out of 27532 genes, 0.2%	0.0022	At5a41670 At1a64190 At5a13110
pentose-phosphate pathway non oxidative br	2 out of 42 genes, 4.8%	8 out of 27532 genes, 0.0%	0.0029	At5a41670 At1a64190
Cluster #12				
peroxidase reaction	4 out of 18 genes, 22.2%	93 out of 27532 genes, 0.3%	1.25E-05	At5a39580 At5a64120 At1a14550 At1a14540
oxygen and radical detoxification	4 out of 18 genes, 22.2%	259 out of 27532 genes, 0.9%	0.00073	At5a39580 At5a64120 At1a14550 At1a14540
detoxification	4 out of 18 genes, 22.2%	264 out of 27532 genes, 1.0%	0.00079	At5a39580 At5a64120 At1a14550 At1a14540
response to biotic stimulus	3 out of 18 genes, 16.7%	221 out of 27532 genes, 0.8%	0.01333	At5a39580 At5a64120 At5a40990
plant defense response	2 out of 18 genes, 11.1%	82 out of 27532 genes, 0.3%	0.04549	At5a40990 At4a39950