

## Supplement table 1

A list of genes that were differentially expressed in NtAAA1-RNAi transgenic tobacco plants upon pathogen infection.

Clone ID	Putative function	Ratio	P-value
stress and defense/21			
1 L-095_g04	Sar8.2b protein	3.22	0.020215
2 R-112_F03	putative Regulatory protein NPR1	1.58	0.01859
3 SOD		2.79	0.09843
4 L-095_g05	superoxide dismutase [Nicotiana plumbaginifolia]	2.01	0.04643
5 R-011_b10	putative translationally controlled tumor protein [Nicotiana tabacum]	1.5	0.12357
6 I-013_b04	putative translationally controlled tumor protein	1.52	0.341044
7 I-105_b01	salicylic acid binding catalase	1.81	0.001289
8 I-002_a11	putative translationally controlled tumor protein [Nicotiana tabacum]	2.91	0.00567
9 R-064_e07	isocitrate dehydrogenase (NAD+) [Nicotiana tabacum]	1.71	0.194574
10 R-016_c04	pleiotropic drug resistance like protein [Nicotiana tabacum]	2.01	0.5
11 L-096_e08	stress responsive protein homolog [Arabidopsis thaliana]	1.63	0.00046
12 L-010_c02	elicitor resposable protein [Nicotiana tabacum]	1.32	0.99998
13 L-098_c05	elicitor resposable protein [Nicotiana tabacum]	1.58	0.00167
14 R-057_c09	ACC oxidase [Nicotiana tabacum]	1.59	0.4562
15 R-044_A01	DnaJ-like protein [Arabidopsis thaliana]	1.5	0.078666
16 ACC oxidase		1.51	0.001023
17 I-011_d08	elicitor resposable protein [Nicotiana tabacum]	2.62	0.99479
18 I-013_e12	salicylic acid binding catalase	1.7	0.031812
19 I-093_b11	salicylic acid binding catalase	1.68	0.031583
20 I-031_e03	phospholipase D delta isoform 1a [Gossypium hirsutum]	1.81	0.093642
21 R-101_h08	ADP-ribosylation factor [Glycine max]	1.64	0.043165
transporte/6			
1 R-039_A01	vesicle transport v-SNARE	1.57	0.093642
2 I-001_e03	putative VAMP protein SEC22 [Arabidopsis thaliana]	1.56	0.021416
3 R-056_D01	putative equilibrative nucleoside transporter ENT3 [Arabidopsis thaliana]	1.7	0.999977
4 R-024_E01	mRNA export protein, putative [Arabidopsis thaliana]	1.88	0.071697
5 I-012_f02	vacuolar processing enzyme-1a [Nicotiana tabacum]	1.52	0.040698
6 R-021_A05	putative ABC transporter [Oryza sativa (japonica cultivar-group)]	1.62	0.058594
cell structure /7			
1 R-073_D11	reversibly glycosylated polypeptide [Oryza sativa (japonica cultivar-group)]	1.57	0.030907
2 R-040_f11	putative phytochelatin synthetase [Oryza sativa (japonica cultivar-group)]	1.79	0.112317
3 R-120_A01	extensin-like protein Dif54 [Lycopersicon esculentum]	2.35	0.000425

4 I-089_d03	alpha-tubulin [Gossypium hirsutum]	2.32	0.022612
5 R-101_f12	endomembrane protein 70, putative [Arabidopsis thaliana]	1.93	0.021674
6 L-076_E07	pectin methylesterase PME1 [Vitis vinifera]	2.02	0.772815
7 I-063_c05	P-Protein precursor [Flaveria trinervia]	1.65	0.312384
protein distribution and stoge/7			
1 R-068_c12	aspartic protease [Pyrus pyrifolia]	2.66	0.042508
2 L-041_F11	20S proteasome alpha 6 subunit [Nicotiana benthamiana]	2.56	0.034587
3 R-115_C0t	putative AAA-metalloprotease [Oryza sativa (japonica cultivar-group)]	1.814	0.015645
4 L-046_E10	putative quinone reductase [Vitis vinifera]	2.09	0.646948
5 I-056_h06	similar to cdc2 protein kinase [Arabidopsis thaliana]	1.74	0.004357
6 I-088_f05	putative senescence-associated protein [Pisum sativum]	1.54	0.01943
7 I-019_g07	cysteine protease [Nicotiana tabacum]	1.66	0.010892
transcription/7			
1 I-108_c01	RNA helicase like protein DB10 [Nicotiana sylvestris]	2.66	0.950577
2 L-095_h03	putative eukaryotic translation initiation factor 6 [Oryza sativa (japonica cu	1.68	0.334242
3 L-095_g08	putative eukaryotic translation initiation factor 6 [Oryza sativa (japonica cu	1.98	0.175753
4 I-062_h06	transport protein particle component Bet3-like protein [Oryza sativa (japon	3.13	0.02998
5 I-108_c01	RNA helicase like protein DB10 [Nicotiana sylvestris]	1.5	0.637169
6 L-066_E07	elongation factor 1 alpha subunit [Malus x domestica]	2.89	0.500107
7 I-012_a12	elongation factor-1 alpha [Nicotiana tabacum]	1.55	0.287566
sinal transduction/1			
1 L-046_F02	signal recognition particle receptor protein [Cucumis sativus]	1.86	0.039849
secondary metabolism/2			
1 R-103_d0e	3-hydroxy-3-methylglutaryl-CoA reductase [Nicotiana attenuata]	2.62	0.027357
2 I-086_h09	acetyl Co-A acetyltransferase [Hevea brasiliensis]	2.48	0.605333
cell cycles/1			
1 R-034_F0e	carboxypeptidase C cbp31 [Oryza sativa (japonica cultivar-group)]	1.72	0.01809
metabolism/11			
1 R-011_f10	metallothionein-like protein	2.05	0.033537
2 R-018_E0f	fatty acid alpha-oxidase [Oryza sativa]	1.68	0.010448
3 R-011_a02	ubiquitin carrier protein	1.84	0.207371
4 R-017_g0e	metallothionein-like protein	3.77	0.598548
5 R-015_c03	metallothionein-like protein	2.1	0.506746
6 R-103_h09	hydroxymethylglutaryl coenzyme A synthase [Hevea brasiliensis]	1.96	0.047806
7 I-028_e06	Contains PF00561 alpha/beta hydrolase fold. [Arabidopsis thaliana]	1.87	0.030907
8 I-017_g12	ubiquitin conjugating protein [Avicennia marina]	1.51	0.635666

	9 R-105_H0: cyprosin [Cynara cardunculus]	1.55	0.039221
	10 I-002_b06 ferredoxin-I [Lycopersicon esculentum]	1.68	0.000425
	11 I-029_c10 39 kDa EF-Hand containing protein [Solanum tuberosum]	3.31	0.032796
energy	/3		
	1 L-037_E03 cytochrome c1 precursor [Solanum tuberosum]	2.53	0.013758
	2 I-012_h09 PSI-D2 [Nicotiana glauca]	1.96	0.006959
	3 L-098_h06 ribulose-1,5-bisphosphate carboxylase small subunit	2.44	0.004357
others	/16		
	1 R-011_d05 endomembrane protein 70, putative [Arabidopsis thaliana]	3.29	0.006773
	2 R-068_h07 Putative FH protein interacting protein FIP1 [Oryza sativa (japonica cultivar group)]	2.13	0.015118
	3 R-016_f04 far-red impaired response protein (FAR1) [Arabidopsis thaliana]	2.04	0.033628
	4 L-039_B08 putative ribosomal protein L10 [Arabidopsis thaliana]	1.81	0.021416
	5 R-059_B0: putative 40S ribosomal protein S2 [Oryza sativa (japonica cultivar group)]	1.66	0.050271
	6 R-010_g10 putative multiprotein bridging factor 1 [Nicotiana glauca]	2.16	0.020219
	7 I-105_b12 40S ribosomal protein S2 [Arabidopsis thaliana]	2.56	0.47585
	8 I-094_c08 putative 60s ribosomal protein L37 [Arabidopsis thaliana]	1.99	0.009954
	9 R-027_D0: putative nucleosome assembly protein [Arabidopsis thaliana]	1.69	0.045576
	10 R-110_c05 putative multiprotein bridging factor 1 [Nicotiana glauca]	2.01	0.031207
	11 L-010_a06 putative 40S ribosomal protein s12	1.52	0.011059
	12 I-001_e09 ribosomal protein L19 [Triticum aestivum]	1.6	0.209446
	13 I-056_a05 putative ribosomal protein CtrL6e, 5'-partial [Oryza sativa (japonica cultivar group)]	1.71	0.002549
	14 R-055_B0: ribosomal protein L9 [Pisum sativum]	1.5	0.017694
	15 I-001_f06 putative 40S ribosomal protein s12	1.52	0.039733
	16 R-031_c04 tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	2.28	0.04178
unknown	/9		
	1 L-095_g04		
	2 R-027_C12		
	3 L-040_C12		
	4 R-032_E09		
	5 L-066_B08		
	6 R-122_A05		
	7 L-041_C04		
	8 I-016_e12		
	9 L-098_f08		

## List of down-regulated gene

	Clone ID	Putative funcion	Ratio	P-value
stress and defense /22				
1	I-105_d10	heat shock protein 70 [Nicotiana tabacum]	0.02	0.5
2	I-013_a01	putative stress protein [Arabidopsis thaliana]	0.015	0.028404
3	I-027_h06	glutathione S-transferase [Capsicum annuum]	0.15	0.032977
4	L-099_b10	secretory peroxidase [Nicotiana tabacum]	0.09	0.000969
5	L-006_F11	WRKY 12 [Theobroma cacao]	0.18	0.010448
6	R-026_G07	putative thioredoxin M [Arabidopsis thaliana]	0.3	0.035258
7	R-016_h01	dehydration stress-induced protein [Brassica napus]	0.31	0.597247
8		acidic chitinase III	0.1	0.002717
9	R-112_C07	70 kDa heat shock protein [Chlamydomonas reinhardtii]	0.072	0.620387
10	R-038_A11	lipoygenase [Nicotiana attenuata]	0.28	0.001932
11	R-040_b11	lipoygenase [Nicotiana attenuata]	0.17	0.035721
12	R-120_C11	isoflavone reductase-like protein [Nicotiana sylvestris]	0.17	0.028404
13	NM-18-3	AAA protein	0.27	0.002526
14	I-012_a01	Oxygen-evolving enhancer protein 1	0.11	0.033547
15	L-077_H12	ethylene-inducible protein	0.51	0.048167
16	I-012_c01	33kDa precursor protein of oxygen-evolving complex [Solanum tuberosum]	0.12	0.028404
17	L-038_F04	Np-ypt3 [Nicotiana plumbaginifolia]	0.3	0.035684
18	R-124_C12	germin-like protein [Lycopersicon esculentum]	0.06	0.002526
19	GRP		0.06	0.033547
20	I-032_c12	WD40-repeat protein [Arabidopsis thaliana]	0.14	0.049621
21	I-088_e03	thionin like protein [Nicotiana tabacum]	0.19	0.0399
22	I-003_e04	thionin like protein [Nicotiana tabacum]	0.01	0.002439
transporte/6				
1	I-084_e02	putative sugar transporter protein [Oryza sativa (japonica cultivar-group)]	0.01	0.001037
2	R-083_F09	amino acid transporter [Lycopersicon esculentum]	0.06	0.02949
3	L-065_B09	sucrose transporter [Nicotiana tabacum]	0.12	0.033502
4	I-024_g10	utative golgi transport complex protein; 67058-70172 [Arabidopsis thaliana]	0.3	0.031041
5	R-031_b07	Similar to nitrate and oligopeptide transporters [Arabidopsis thaliana]	0.11	0.032078
6	I-023_a06	vacuolar processing enzyme-3 [Nicotiana tabacum]	0.26	0.001
cell structure/11				
1	R-125_E05	alpha-tubulin [Streblomastix strix]		
2	R-046_H12	proline-rich protein family [Arabidopsis thaliana]	0.14	0.003
3	R-078_F12	putative hydroxyproline-rich glycoprotein [Oryza sativa (japonica cultivar-g	0.04	0.034984

4	I-106_f07	major intrinsic protein 1 [Solanum tuberosum]	0.3	0.048289
5	I-127_d07	Putative integral membrane protein [Arabidopsis thaliana]	0.19	0.054233
6	R-020_F07	actin-depolymerizing factor 2 [Petunia x hybrida]	0.22	0.047695
7	R-040_b03	fiber protein Fb11 [Gossypium barbadense]	0.24	0.038652
8	R-057_a07	endosperm-specific protein-like protein [Arabidopsis thaliana]	0.17	0.032977
9	R-020_B03	putative coatomer protein gamma 2-subunit [Oryza sativa (japonica cultivar-group)]	0.15	0.00061
10	I-108_d04	endoxyloglucan transferase [Daucus carota]	0.25	0.038962
11	I-107_a10	putative microtubule-associated protein [Arabidopsis thaliana]	0.07	0.031041
protein distribution and stoge/10				
1	R-117_D03	putative protein kinase [Arabidopsis thaliana]	0.21	0.004817
2	I-093_c01	proteasome alpha subunit [Petunia x hybrida]	0.19	0.046765
3	R-101_f01	putative alpha3 proteasome subunit [Nicotiana tabacum]	0.27	0.033478
4	I-089_h06	aspartic proteinase 2 [Glycine max]	0.08	0.00039
5	I-057_g07	putative serine/threonine kinase [Oryza sativa (japonica cultivar-group)]	0.01	0.028404
6	I-058_c07	carbohydrate kinase-like protein [Arabidopsis thaliana]	0.15	0.054233
7	R-074_D07	putative chaperonin gamma chain [Arabidopsis thaliana]	0.1	0.003347
8	R-104_D07	putative ubiquitin-specific protease [Oryza sativa (japonica cultivar-group)]	0.18	0.054233
9	L-078_D06	mitochondrial Lon protease homolog 1 precursor [Arabidopsis thaliana]	0.15	0.065248
10	R-031_f05	putative FtsH protease [Oryza sativa (japonica cultivar-group)]	0.14	0.003861
transcription/21				
1	R-063_D08	elongation factor 1B gamma [Oryza sativa]	0.01	0.038207
2	R-121_A01	bHLH transcriptional regulator [Lycopersicon esculentum]	0.09	0.012284
3	R-086_G07	putative exonuclease RRP41 [Arabidopsis thaliana]	0.25	0.046943
4	I-029_g04	telomere binding protein TBP1 [Nicotiana glutinosa]	0.11	0.05043
5	I-001_c09	putative C2H2-type zinc finger protein [Arabidopsis thaliana]	0.28	0.032753
6	L-064_E08	isoleucine-tRNA ligase - like protein [Arabidopsis thaliana]	0.19	0.042835
7	L-100_a12	transcription factor LIM [Nicotiana tabacum]	0.08	0.037505
8	R-002_E01	Putative CAF protein [Oryza sativa (japonica cultivar-group)]	0.12	0.046326
9	L-066_D06	nucleic acid binding protein-like [Arabidopsis thaliana]	0.18	0.032078
10	I-106_e02	poly(A) polymerase [Pisum sativum]	0.3	0.041078
11	I-094_f11	putative small nuclear ribonucleoprotein Prp4p [Arabidopsis thaliana]	0.19	0.05726
12	I-012_b04	putative ribosomal protein L18 [Arabidopsis thaliana]	0.09	0.0399
13	R-103_b03	Putative splicing factor Prp8 [Arabidopsis thaliana]	0.23	0.047236
14	R-098_H07	putative DEAD/DEAH box RNA helicase protein [Arabidopsis thaliana]	0.17	0.032365
15	R-062_C10	putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]	0.21	0.002409
16	I-017_a01	DEAD-Box RNA helicase-like protein [Arabidopsis thaliana]	0.3	0.091046

17	R-065_g12	multifunctional aminoacyl-tRNA ligase-like protein [Arabidopsis thaliana]	0.21	0.049621
18	R-056_H11	putative lipase [Arabidopsis thaliana]	0.17	0.058699
19	I-022_e12	mRNA-binding protein precursor [Nicotiana tabacum]	0.16	0.032078
20	R-001_g07	putative RNA helicase [Arabidopsis thaliana]	0.28	0.029161
21	I-105_c11	elongation factor EF-2 [Arabidopsis thaliana]	0.19	0.015118
sinal transduction/2				
1	R-077_C12	Probable microsomal signal peptidase 12 kDa subunit (EC -related [Arabido	0.21	0.046326
2	L-097_F08	putative EBNA1-binding protein homolog; Ebp2p [Oryza sativa (japonica cul	0.37	0.47585
secondary metabolism/5				
1	I-106_d03	Ubiquitin conjugating enzyme [Cicer arietinum]	0.26	0.034667
2	L-014_h03	polyubiquitin [Pinus sylvestris]	0.26	0.060158
3	I-092_c1	putative C-4 sterol methyl oxidase [Arabidopsis thaliana]	0.15	0.096741
4	R-012_a07	flavonoid O-methyltransferase [Catharanthus roseus]	0.19	0.014762
5	I-012_e07	squalene synthase [Nicotiana tabacum]	0.21	0.047162
cell cycles /0				
metabolism/29				
1	R-001_f11	putative phosphatidylglycerolphosphate synthase [Oryza sativa (japonica cu	0.31	0.038054
2	L-046_G06	chorismate mutase [Arabidopsis thaliana]	0.25	0.002232
3	R-015_b08	kinesin-like protein A, putative [Arabidopsis thaliana]	0.03	0.009871
4	L-005_F12	probable [acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) T27E13	0.01	0.051006
5	R-041_E04	homocysteine S-methyltransferase AtHMT-2 [Arabidopsis thaliana]	0.34	0.097779
6	I-086_e06	GTP-binding membrane protein LepA homolog [Arabidopsis thaliana]	0.24	0.045963
7	L-020_B01	putative GTP-binding protein [Cucumis sativus]	0.15	0.040146
8	R-036_G07	putative calcium channel [Arabidopsis thaliana]	0.3	0.03799
9	R-069_d08	cytosolic cysteine synthase [Solanum tuberosum]	0.27	0.034143
10	I-012_a04	putative serine carboxypeptidase II-like protein [Oryza sativa (japonica cult	0.25	0.032753
11	R-125_D11	glycolate oxidase [Lycopersicon esculentum]	0.13	0.030127
12	I-103_h11	NADPH:protochlorophyllide oxidoreductase [Nicotiana tabacum]	0.06	0.074208
13	R-094_F09	protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]	0.35	0.010135
14	I-034_g11	Mg protoporphyrin IX chelatase [Nicotiana tabacum]	0.3	0.036181
15	R-004_d08	progesterone 5-beta-reductase [Digitalis purpurea]	0.2	0.028609
16	R-092_F08	LAX1 / AUX1-like permease [Arabidopsis thaliana]	0.03	0.028404
17	R-044_B09	GAST-like gene product [Fragaria x ananassa]	0.04	0.046326
18	L-017_G07	cytosolic NADP-malic enzyme [Lycopersicon esculentum]	0.16	0.031799
19	R-003_a06	ubiquinol--cytochrome c reductase [Solanum tuberosum]	0.36	0.095518
20	.R-034_F05	geraniol 10-hydroxylase [Catharanthus roseus]	0.24	0.045048

21	wFAD		0.13	0.001932
22	L-041_H01	purple acid phosphatase [Nicotiana tabacum]	0.1	0.021006
23	I-086_f12	extracellular calcium sensing receptor [Arabidopsis thaliana]	0.31	0.051707
24	R-010_e11	putative serine carboxypeptidase [Oryza sativa (japonica cultivar-group)]	0.03	0.037393
25	R-020_D12	catechol O-methyltransferase [Nicotiana tabacum]	0.12	0.009871
26	L-008_G01	UDP-glucose:protein transglucosylase [Solanum tuberosum]	0.34	0.274367
27	R-008_a09	putative PHD-type zinc finger protein [Arabidopsis thaliana]	0.04	0.001932
28	I-026_d09	hydroxymethylglutaryl coenzyme A synthase [Hevea brasiliensis]	0.38	0.082511
29	I-015_a08	putative RING zinc finger ankyrin protein [Arabidopsis thaliana]	0.18	0.051006
energy/14				
1	I-012_e12	chlorophyll a/b binding protein [Nicotiana tabacum]	0.12	0.063852
2	L-097_C12	chlorophyll a/b binding protein [Petunia x hybrida]	0.1	0.977005
3	R-123_G09	cytochrome P450 CYP74C3 [Lycopersicon esculentum]	0.31	0.039962
4	I-057_f03	light-harvesting chlorophyll a /b binding protein [Nicotiana tabacum]	0.22	0.035399
5	L-097_D08	chlorophyll a/b-binding protein (cab-12) - tomato	0.18	0.049643
6	I-092_f05	putative chlorophyll A-B binding protein of LHCII type III, [Oryza sativa (japc	0.01	0.037017
7	L-086_E07	photosystem I reaction center subunit X psaK [Nicotiana tabacum]	0.12	0.032365
8	I-017_g01	light-harvesting chlorophyll a /b binding protein [Nicotiana tabacum]	0.34	0.098793
9	R-106_E06	mitochondrial ATPase beta subunit [Nicotiana glauca]	0.14	0.057312
10	L-007_C03	putative chlorophyll A-B binding protein type I [Pinus pinaster]	0.17	0.047378
11	I-057_c04	light-harvesting chlorophyll a /b binding protein [Nicotiana tabacum]	0.27	0.036509
12	-088_c05	light harvesting chlorophyll a/b-binding protein [Nicotiana glauca]	0.2	0.051612
13	R-101_a09	Cryptochrome 1b [Lycopersicon esculentum]	0.14	0.005077
14	I-104_g07	photosystem I light-harvesting chlorophyll a/b-binding protein [Nicotiana glauca]	0.13	0.009282
others/43				
1	I-024_d03	unnamed protein product [Nicotiana glauca]	0.21	0.063815
2	I-089_a09	ribosomal protein L11-like protein [Arabidopsis thaliana]	0.28	0.00429
3	L-079_C08	expressed protein [Arabidopsis thaliana]	0.26	0.044846
4	R-115_H12	5.8 kb basic protein [Phaseolus vulgaris]	0.2	0.039441
5	L-054_B07	water channel-like protein [Arabidopsis thaliana]	0.01	0.036181
6	I-104_d11	SPP30 [Solanum chacoense]	0.18	0.049464
7	R-010_b07	pheromone receptor, putative (AR401) [Arabidopsis thaliana]	0.29	0.067234
8	R-123_H06	putative carrier protein [Arabidopsis thaliana]	0.31	0.062997
9	I-109_d09	Putative amp-binding protein [Arabidopsis thaliana]	0.11	0.046077
10	R-001_f07	P69C protein [Lycopersicon esculentum]	0.16	0.001521
11	L-103_e07	ribosomal protein L23a [Fritillaria agrestis]	0.1	0.03348

12	L-103_C07	NtpII10 [Nicotiana tabacum]	0.08	0.032365
13	R-018_G11	putative urease accessory protein F [Lycopersicon esculentum]	0.17	0.005506
14	R-078_G10	putative AtHVA22a protein [Arabidopsis thaliana]	0.17	0.037264
15	R-115_F05	putative ribosomal protein S29 [Oryza sativa (japonica cultivar-group)]	0.11	0.021268
16	I-093_d04	putative inward rectifying potassium channel [Solanum tuberosum]	0.24	0.032365
17	R-095_C06	histone H3	0.25	0.008844
18	I-002_h08	succinate dehydrogenase iron-sulfur protein subunit [Cucumis sativus]	0.04	0.020292
19	I-087_h01	histone H2A:ISOTYPE=9	0.05	0.035721
20	R-101_a12	homeobox gene [Nicotiana tabacum]	0.31	0.034667
21	I-090_c11	starch (bacterial glycogen) synthase [Solanum tuberosum]	0.33	0.044846
22	I-068_f12	ribonuclease NGR2 [Nicotiana glutinosa]	0.36	0.08948
23	R-057_c11	RNA-binding glycine-rich protein-1 (RGP-1a) [Nicotiana sylvestris]	0.06	0.022615
24	L-014_a10	SLL2-S9-protein [Brassica rapa]	0.23	0.018151
25	R-103_e09	F12A21.11 [Arabidopsis thaliana]	0.32	0.043065
26	R-092_B09	pollen-related protein -related [Arabidopsis thaliana]	0.19	0.053641
27	R-115_H11	class II knotted-like homeodomain protein [Lycopersicon esculentum]	0.31	0.02161
28	L-010_h11	putative peptide chain release factor subunit 1 (ERF1) [Oryza sativa (japonica cultivar-group)]	0.38	0.016064
29	I-017_b04	putative leaf development protein Argonaute [Arabidopsis thaliana]	0.07	0.093499
30	I-062_a10	plastid ribosomal protein S9 precursor [Spinacia oleracea]	0.15	0.052251
31	O19-C-1		0.31	0.019222
32	I-074_c11	potassium channel [Nicotiana paniculata]	0.01	0.041596
33	I-001_e01	putative ripening-related protein [Vitis vinifera]	0.11	0.008104
34	I-027_h08	ripening-related protein-like [Arabidopsis thaliana]	0.34	0.213417
35	L-080_G05	alcohol dehydrogenase [Petunia x hybrida]	0.15	0.040437
36	L-102_b07	6b-interacting protein 1 [Nicotiana tabacum]	0.32	0.079608
37	R-064_e10	GCN4-complementing protein (GCP1) [Arabidopsis thaliana]	0.01	0.009552
38	I-108_e05	PP2A regulatory subunit-like protein [Oryza sativa (japonica cultivar-group)]	0.18	0.033123
39	R-035_F09	putative trehalose-6-phosphate phosphatase (AtTPPA) [Arabidopsis thaliana]	0.17	0.009794
40	I-094_c07	transformer-SR ribonucleoprotein [Nicotiana tabacum]	0.21	0.047713
41	I-105_h08	synaptobrevin-like protein [Arabidopsis thaliana]	0.34	0.038054
42	R-121_B07	putative ring box-1 protein [Oryza sativa (japonica cultivar-group)]	0.34	0.03799
43	I-103_g07	ribosomal protein L23a [Fritillaria agrestis]	0.12	0.683756

unkown/76

- 1 I-093\_a01
- 2 R-040\_h08
- 3 R-032\_C01



4 R-019\_A02  
5 L-046\_E09  
6 R-006\_b06  
7 L-006\_G02  
8 R-057\_e01  
9 L-048\_D09  
10 L-010\_b11  
11 I-084\_c07  
12 L-035\_B06  
13 L-098\_b08  
14 I-092\_f01  
15 R-030\_g12  
16 R-101\_c12  
17 L-079\_C02  
18 R-003\_f11  
19 I-012\_d10  
20 I-093\_e01  
21 I-093\_g05  
22 I-024\_a08  
23 I-057\_c07  
24 L-010\_g05  
25 I-057\_g11  
26 I-072\_e03  
27 L-097\_B09  
28 I-088\_a07  
29 I-029\_c05  
30 R-063\_A05  
31 I-033\_g12  
32 R-018\_C05  
33 I-106\_f08  
34 I-105\_a11  
35 I-022\_a11  
36 R-066\_c06  
37 L-014\_c09  
38 R-106\_B09  
39 L-098\_f01

40 R-019\_H03  
41 R-119\_D04  
42 I-070\_d03  
43 R-056\_F07  
44 I-062\_f05  
45 I-086\_a03  
46 I-057\_e01  
47 I-012\_e05  
48 R-076\_G02  
49 L-049\_C05  
50 L-102\_d05  
51 I-105\_c09  
52 R-021\_D03  
53 I-093\_e07  
54 R-004\_g09  
55 R-028\_B05  
56 R-026\_E02  
57 I-056\_d02  
58 I-001\_a09  
59 L-046\_B10  
60 R-014\_H10  
61 I-033\_d05  
62 R-123\_G12  
63 R-079\_G11  
64 R-101\_a07  
65 R-059\_B05  
66 I-022\_b12  
67 R-011\_b07  
68 R-097\_C03  
69 L-044\_A01  
70 I-002\_g02  
71 I-057\_g01  
72 L-096\_e07  
73 R-100\_h11  
74 I-087\_b03  
75 L-038\_G08

76 I-094\_b12