

## Appendix A

Functional categories	EST accession number	Putative identification	Organism	E-value
Genes responded to stress	GT917037	oxidoreductase, 2OG-Fe(II) oxygenase family protein	<i>Arabidopsis thaliana</i>	7e-07
	GT917043	novel protein similar to vertebrate calcium channel, voltage-dependent, alpha 1 family subunit (CANNA1)	<i>Danio rerio</i>	8.0
	GT917084	multidrug resistance protein ABC transporter family	<i>Populus trichocarpa</i>	2e-56
	GT917121	sphingosine kinase related protein	<i>Dictyostelium discoideum AX4</i>	7.9
	GT917132	plasma membrane integral protein ZmPIP2-7	<i>Zea mays</i>	1e-20
	GT917139	sensor histidine kinase/response regulator	<i>Aspergillus fumigatus Af293</i>	6.0
	GT917142	copia LTR rider	<i>Solanum lycopersicum</i>	0.050
	GT917143	glycerol-3-phosphate acyltransferase	<i>Culex quinquefasciatus</i>	7.9
	GU385812	NOI protein	<i>Arabidopsis thaliana</i>	3e-22
	GT917183	zinc finger (AN1-like) family protein	<i>Arabidopsis thaliana</i>	8e-18
	GT917190	Phospholipase A22	<i>Ricinus communis</i>	3e-09
	GT917192	envelope-like protein	<i>Glycine max</i>	1e-09
	GT917197	calmodulin binding protein, putative	<i>Ricinus communis</i>	5e-45
	GT917204	putative senescence-associated protein	<i>Lilium longiflorum</i>	9e-17
	GT917206	dolichyl-diphosphooligosaccharide--protein glycosyltransferase, putative	<i>Ricinus communis</i>	1e-14
	GT917218	NADPH-dependent reductase-like protein codeinone	<i>Papaver rhoeas</i>	2e-06
	GT917219	putative serine carboxypeptidase precursor	<i>Gossypium hirsutum</i>	8e-24
	GT917239	kinesin family protein (KipA), putative	<i>Aspergillus clavatus NRRL 1</i>	6.1
	GT917242	Flavonol synthase/flavanone 3-hydroxylase, putative	<i>Ricinus communis</i>	2e-09
	GT917257	envelope-like protein	<i>Glycine max</i>	4e-25
GT917263	envelope-like protein	<i>Glycine max</i>	7e-07	
GT917267	envelope-like protein	<i>Glycine max</i>	1e-25	
GT917274	NADPH-dependent reductase-like protein codeinone	<i>Papaver rhoeas</i>	2e-06	
GT917275	Flavonol synthase/flavanone 3-hydroxylase,	<i>Ricinus communis</i>	2e-09	

Hypothetical genes	GT917088	putative hypothetical protein MC7420_5697	<i>Microcoleus chthonoplastes</i> <i>PCC 7420</i>	0.72
	GT917094	hypothetical protein - soybean transposable element Tgm5 (fragment)	<i>Glycine max</i>	7e-09
	GT917042	conserved hypothetical protein	<i>Medicago truncatula</i>	0.92
	GT917044	hypothetical protein	<i>Sulfolobus islandicus</i>	2.7
	GT917125	hypothetical protein	<i>Flavobacterium johnsoniae</i> UW101	0.72
	GT917128	Putative gag-pol polyprotein, identical	<i>Solanum demissum</i>	2e-11
	GT917162	hypothetical protein	<i>Vitis vinifera</i>	0.93
	GT917194	hypothetical protein	<i>Theileria parva</i> strain Muguga	2.0
	GT917207	hypothetical protein	<i>Coprinopsis cinerea</i> okayama7#130	5.9
	GT917232	hypothetical chloroplast RF1	<i>Glycine max</i>	1e-61
	GT917252	retrotransposon protein, putative, unclassified	<i>Oryza sativa</i> (japonicacultivar-group)	6e-18
	GT917258	hypothetical protein	<i>Vitis vinifera</i>	0.022
	Others	GT917016	reverse transcriptas	<i>Arabidopsis thaliana</i>
GT917022		Putative gag-pol polyprotein, identical	<i>Solanum demissum</i>	9e-10
GT917027		Transposable element protein, putative, Retrotrans_gag	<i>Oryza sativa</i> (japonica cultivar-group)	2.0
GT917028		putative athila transposon protein	<i>Arabidopsis thaliana</i>	3e-06
GT917059		Polynucleotidyl transferase, Ribonuclease H	<i>Medicago truncatula</i>	4e-14
GT917072		Integrase, catalytic region; Ribonuclease H	<i>Medicago truncatula</i>	2e-22
GT917075		RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H	<i>Medicago truncatula</i>	3e-05
GT917100		integrase	<i>Populus trichocarpa</i>	2e-05
GT917107		gag-protease polyprotein-like protein	<i>Cicer arietinum</i>	2e-08
GT917114		gag/pol polyprotein	<i>Pisum sativum</i>	0.14
GT917115	retroelement pol polyprotein-like	<i>Arabidopsis thaliana</i>	1e-04	
GT917122	gag-protease polyprotein	<i>Glycine max</i>	2e-04	
GT917123	integrase	<i>Populus trichocarpa</i>	2e-20	

GT917126	gag/pol polyprotein	<i>Pisum sativum</i>	1e-07
GT917134	gag/pol polyprotein	<i>Pisum sativum</i>	9e-33
GT917140	ribosome binding protein 1 homolog 180kDa	<i>Gallus gallus</i>	0.24
GT917156	gag/pol polyprotein	<i>Pisum sativum</i>	2e-31
GT917166	40S ribosomal S4 protein	<i>Glycine max</i>	3e-35
GT917167	RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H	<i>Medicago truncatula</i>	5e-08
GT917169	reverse transcriptase	<i>Glycine max</i>	1e-07
GT917170	Beta-galactosidase alpha peptide	<i>Cloning vector pUC1918</i>	6e-10
GT917177	gag-protease polyprotein-like protein	<i>Cicer arietinum</i>	0.003
GT917200	pol polyprotein	<i>Zea mays</i>	5e-05
GT917231	Ribonuclease H	<i>Phaseolus vulgaris</i>	0.19
GT917240	retroelement polyprotein-like	<i>Malus x domestica</i>	0.029
GT917253	soybean transposable element Tgm5 (fragment)	<i>Glycine max</i>	1e-14
GT917271	integrase	<i>Beta vulgaris</i>	3e-09

## Appendix B

Sample No.	EST accession number	Putative identification	Organism	E-value
Genes responded to stress	GT917284	phosphoesterase (RecJ-like)	<i>methanogenic archaeon RC-I</i>	0.009
	GT917289	metal ion binding protein	<i>Zea mays</i>	4e-13
	GT917290	MLO1	<i>Lotus corniculatus var. japonicus</i>	4e-06
	GT917302	Serine carboxypeptidase precursor	<i>Matricaria chamomilla</i>	3e-18
	GT917303	chaperone protein DnaJ	<i>Plesiocystis pacifica SIR-1 uncultured</i>	0.001
	GT917293	response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	<i>Synechococcus elongatus PCC 7942</i>	1.6
	GT917295	Homoserine dehydrogenase	<i>Leptotrichia buccalis DSM 1135</i>	6.0
	GT917309	copper-binding family protein	<i>Arabidopsis thaliana</i>	1e-26
	GT917310	MLO1	<i>Lotus corniculatus var. japonicus</i>	4e-06
	GT917317	increased sodium tolerance protein 2	<i>Saccharomyces cerevisiae RM11-1a</i>	0.28

	GT917345	multi-sensor hybrid histidine kinase	<i>Burkholderia ubonensis Bu</i>	3.5
	GT917358	copper ion binding protein, putative	<i>Ricinus communis</i>	3e-33
	GT917365	phytoene dehydrogenase	<i>Azoarcus sp. BH72</i>	0.049
	GT917384	ferrichrome-binding protein	<i>Bacillus cereus</i>	0.048
	GT917393	oxidative stress induced growth inhibitor family member 2	<i>Bos taurus</i>	3.5
Hypothetical genes	GT917299	retrotransposon protein, putative, unclassified, expressed	<i>Oryza sativa (japonica cultivar-group)</i>	4e-21
	GT917306	FMRFamide neuropeptide precursor, putative	<i>Bacillus cereus G9241</i>	0.049
	GT917338	hypothetical protein	<i>Tetrahymena thermophila</i>	4.7
	GT917352	unnamed protein product	<i>Vitis vinifera</i>	3e-07
	GT917374	putative phage regulatory protein	<i>Clostridium difficile CD196</i>	7.9
	GT917353	copper ion binding protein, putative	<i>Ricinus communis</i>	3e-34
	GT917382	hypothetical protein	<i>Sorghum bicolor</i>	0.41
Others	GT917291	Integrase, atalytic region; Ribonuclease H	<i>Medicago truncatula</i>	2e-33
	GT917308	SAM-dependent methyltransferase	<i>Plasmodium yoelii yoelii</i>	0.42
	GT917311	gag/pol polyprotein	<i>Pisum sativum</i>	4e-35
	GT917315	putative gag-pol polyprotein	<i>Petunia x hybrida</i>	2e-09
	GT917316	cellulose synthase catalytic subunit(UDP-forming)	<i>Methylobacterium radiotolerans JCM 2831</i>	0.46
	GT917319	CTP synthetase	<i>Fingoldia magna ATCC 29328</i>	0.91
	GT917324	beta-galactosidase alpha peptide	<i>Cloning vector</i>	4e-10
	GT917328	Peptidase aspartic,catalytic; Polynucleotidyl	<i>Arabidopsis thaliana</i>	2e-33
	GT917336	Integrase, catalytic region; Ribonuclease H	<i>Medicago truncatula</i>	2e-32
	GT917340	gag-pol polyprotein	<i>Glycine max</i>	2e-57
	GT917343	Ribonuclease H	<i>Medicago truncatula</i>	3e-25
	GT917344	Ribonuclease H	<i>Medicago truncatula</i>	7e-20
	GT917354	gag/pol polyprotein	<i>Pisum sativum</i>	6e-34
	GT917357	Peptidase aspartic, catalytic; Polynucleotidyl	<i>Arabidopsis thaliana</i>	4e-34
	GT917359	RNA-directed DNA polymerase	<i>Medicago truncatula</i>	2e-32
	GT917366	gastrula zinc finger protein XICGF17.1	<i>Verticillium albo-atrum VaMs.102</i>	1.2

GT917372	Beta-lactamase regulatory protein 1	<i>Bacillus cereus</i>	6.4
GT917373	erythrocyte binding protein 3	<i>Plasmodium yoelii</i>	0.049
		<i>yoelii</i>	
GT917375	ribosomal protein L6	<i>Thraustochytrium aureum</i>	2.7
GT917376	26S proteasome regulatory subunit 4, putative	<i>Plasmodium falciparum 3D7</i>	0.65
GT917383	enhanced green fluorescent protein.	<i>Bacillus cereus</i>	0.004
GT917385	enhanced green fluorescent protein	<i>Bacillus cereus</i>	5e-07
GT917386	SJCHGC09076 protein	<i>Schistosoma japonicum</i>	8e-08
GT917388	similar to CG11148-PA, isoform A	<i>Apis mellifera</i>	4.5
GT917390	gag-pol polyprotein	<i>Glycine max</i>	2e-57
GT917392	Retrovirus-related Pol polyprotein from transposon TNT 1-94 , putative	<i>Solanum demissum</i>	1e-14