Supplementary Table 2a. Master table of the identified 14-3-3 client proteins. Spectral counts of proteins identified from each binding experiment are listed below (glycine-sepharose = glycine/BSA-sepharose = BSA/chi-sepharose = chi/epsilon-sepharose = epsilon). Spectral counts were averaged and statistically compared against controls using a student t-test (type 2, array 2). Proteins with a p-value of ≤ 0.33, when compared against controls, were considered statistically significant and labeled 14-3-3 client proteins.

		I				II				III				IV				V			
		control		experimental		control		experimental		control		experimental		control		experimental		control		experimental	
protein name (predicted localization)	accession #	glycine	BSA	chi	epsilon	glycine	BSA	chi	epsilon	glycine	BSA	chi	epsilon	glycine	BSA	chi	epsilon	glycine	BSA	chi	epsilon
01 Metabolism and Catabolism																					
(S)-2-hydroxy-acid oxidase (cytosolic)	At3g14415.1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
6-Phosphogluconate dehydrogenase family protein (chloroplast)	At1g64190.1	0	0	0	0	0	0	0	0	0	0	4	5	0	0	0	0	0	0	0	0
6-Phosphogluconate dehydrogenase family protein (peroxisome)	At3g02360.2	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Aldehyde dehydrogenase (chloroplast)	At1g54100.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aldehyde dehydrogenase (cytoskeleton)	At3g24503.1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
ATP citrate lyase (chloroplast)	At5g49460.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATP citrate lyase (cytosolic)	At1g60810.1	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Beta-fructofuranosidase (cytosolic)	At4g34860.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Biotin carboxylase (chloroplast)	At5g35360.1	0	0	2	0	0	0	5	3	0	0	0	0	0	0	0	0	0	0	0	0
Chalcone-flavanone isomerase (chloroplast)	At1g53520.1	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0
Pyruvate dehydrogenase complex E2 subunit (chloroplast)	At3g25860.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glucosidase (vacuolar membrane)	At5g63840.1	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0
Glyceraldehyde-3-phosphate dehydrogenase (ctyosolic)	At1g13440.1	6	0	14	8	0	0	19	18	23	48	57	40	0	0	6	13	0	8	4	9
Glyceraldehyde-3-phosphate dehydrogenase (ctyosolic)	At3g04120.1	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0
Glyceraldehyde-3-phosphate dehydrogenase (ctyosolic)	At2g24270.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Invertase (cytosolic)	At1g35580.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Isocitrate dehydrogenase (cytosolic)	At1g65930.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Methionine synthase (cytosolic)	At5g17920.1	0	0	0	0	0	0	0	0	0	0	6	8	0	0	0	0	0	0	0	0
Phosphoenolpyruvate carboxylase (cytosolic)	At1g53310.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phosphofructose kinase (chloroplast)	At1g12000.1	0	0	0	0	3	0	2	2	4	3	7	6	0	0	5	4	0	4	0	0
Phosphofructose kinase (ctyosolic)	At1g20950.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phosphoglycerate kinase (chloroplast)	At3g12780.1	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0
Protein disulfide isomerase (chloroplast)	At1g21750.1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Pyridoxal phosphate synthase (cytosolic)	At3g16050.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2
Pyruvate kinase (chloroplast)	At3g25960.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyruvate kinase (cytosolic)	At2g36580.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
S-malonyltransferase acyl-carrier-protein (chloroplast)	At2g30200.1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	3	0	0	0	0
Sucrose synthase (cytosolic)	At5g49190.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Transketolase (chloroplast)	At2g45290.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
UDP-glucose 6-dehydrogenase (extracellular)	At5g15490.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
UDP-glucose dehydrogenase (extracellular)	At1g26570.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
UDP-glucose pyrophosphorylase (cytosolic)	At3g03250.1	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
UDP-glucosyl transferase (chloroplast)	At1g30530.1	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
UDP-glucuronate decarboxylase (chloroplast)	At3g46440.1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Xylose isomerase (endoplasmic reticulum)	At5g57655.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
02 Energy																					
Chlorophyll binding A/B binding protein (chloroplast)	At1g61520.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Chlorophyll binding A/B binding protein (chloroplast)	At1g29910.1	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0
Ketol-acid reductoisomerase (chloroplast)	At3g58610.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ribulose-bisphosphate carboxylase large subunit (mitochondria)	At2g07732.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
03 Cell Growth and Division																					
DNA glycosylase (nucleus)	At3g10010.1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Indole-3-acetic acid-amido synthetase (chloroplast)	At2g47750.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PHD finger transcription factor (cytosolic)	At3g53680.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Proliferating cell nuclear antigen (cell growth and division) (nucleus)	At1g07370.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Replication factor A protein (nucleus)	At5g08020.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
04 Cell Structure																					
Alpha-1,4-glucan protein synthase (cytosolic)	At5g15650.1	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
Tubulin Beta-1 Chain (vacuole)	At1g75780.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
05 Protein Synthesis																					
40S Ribosomal protein S19 (cytoskeleton)	At3g02080.1	0	0	0	0	0	0	2	4	0	0	0	0	4	0	3	3	0	2	0	0
40S Ribosomal protein S19 (cytosolic)	At5g61170.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
40S Ribosomal protein S2 (cytosolic)	At2g41840.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
40S Ribosomal protein S9 (membrane)	At5g39850.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
40S Ribosomal subunit (cytosolic)	At1g72370.1	0	0	0	0	0	0	2	5	0	4	0	0	0	0	2	0	0	0	3	3
60S Ribosomal protein L12 (cytosolic)	At2g37190.1	0	0	0	0	0	0	2	4	0	0	0	2	4	0	5	11	0	0	4	0
60S Ribosomal protein L23 (nucleus)	At2g39460.1	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0
60S Ribosomal protein L26 (cytosolic)	At3g49910.1	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0
60S Ribosomal protein L30 (chloroplast)	At1g36240.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
60S Ribosomal protein L35 (cytosolic)	At1g41880.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
60S Ribosomal protein L4 (chloroplast)	At3g09630.1	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0
Elongation factor 1-alpha (cytosolic)	At1g07920.1	4	3	6	0	0	0	4	4	0	2	13	0	0	0	0	0	0	0	0	0
Elongation factor 1B-gamma (cytosolic)	At1g57720.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Methionine tRNA ligase (cytosolic)	At4g13780.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Ribosomal protein L16 (cytosolic)	At2g42740.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ribosomal protein S21 (chloroplast)	At3g27160.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
Elongation factor 2-like (cytosolic)	At1g56070.1	0	0	2	2	3	0	0	9	2	11	13	8	0	0	2	3	4	0	3	2
06 Protein Destination and Storage																					
20S Proteasome subunit PAA1 (cytosolic)	At5g35590.1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
20S Proteasome subunit PBA1 (cytosolic)	At4g31300.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2S Seed storage protein 4 (chloroplast and extracellular)	At4g27170.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aspartyl protease family protein (chloroplast)	At3g18490.1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Calreticulin 1 (endoplasmic reticulum)	At1g56340.1	0	0	0	0	0	0	0	2	0	0	5	2	0	0	0	0	0	0	0	0
Chaperonin 60 (chloroplast)	At1g55490.1	0	0	0	0	0	0	0	3	0	0	3	0	0	0	0	0	0	0	0	3
Cruciferin 3 (chloroplast)	At4g28520.2	4	5	7	18	0	0	4	5	0	5	0	0	0	0	0	2	0	0	0	0
Cruciferin 3 (chloroplast)	At4g28520.1	2	2	3	10	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
Cupin family protein (cytosolic)	At1g07750.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Heat shock cognate 70 kDa protein 3 (cytosolic)	At3g09440.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	2	4
Heat shock protein 70-1 (chloroplast)	At4g24280.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Heat shock protein 90 (cytosolic)	At5g56030.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Seed storage albumin (chloroplast and extracellular)	At4g27160.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Luminal binding protein (endoplasmic reticulumn)	At5g42020.1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	4
RING-type E3 ubiquitin ligase (nucleus)	At5g22000.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Serine-type endopeptidase (chloroplast)	At5g67360.1	0	0	0	0	0	0	0	0	0	0	6	8	0	0	0	0	0	0	0	0
Subtilase family protein (plasma membrane)	At3g14067.1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
07 Transporters																					
AAA-type ATPases (cytosolic)	At3g09840.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
ATP synthase (chloroplast)	At4g04640.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATP synthase beta-subunit (mitochondrial)	At5g08670.1	0	0	3	0	0	0	6	3	0	0	2	0	0	0	0	0	0	2	0	0
ATPase alpha subunit (cytosolic)	AtCg00120.1	0	0	0	0	0	0	6	0	0	0	4	0	0	0	0	3	0	3	0	0
H+-APTase (chloroplast)	At1g17260.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
08 Disease/Defense																					
2-Cys peroxiredoxin (chloroplast)	At3g11630.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Germin-like protein (chloroplast)	At5g39190.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
MLP-like protein 28 (cytosolic)	At1g70830.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MLP-like protein 423 (cytosolic)	At1g24020.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Translationally controlled tumor protein (cytosolic)	At3g16640.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
09 Signal Transduction																					
14-3-3 Chi (plasma membrane)	At4g09000.1	0	0	148	6	0	0	147	10	0	0	393	37	0	0	118	22	0	0	86	8
14-3-3 Epsilon (mitochondrial)	At1g22300.1	0	0	4	215	0	0	0	145	0	0	0	480	0	0	3	129	0	0	0	57
14-3-3 Nu (plasma membrane)	At3g02520.1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	12	0	0	0	0	0
14-3-3 Omega (plasma membrane)	At1g78300.1	0	0	118	9	0	0	115	9	0	0	168	17	0	0	52	11	0	0	13	2
14-3-3 Phi (chloroplast)	At1g35160.1	0	0	63	4	0	0	25	5	0	0	46	5	0	2	31	12	0	0	33	5
14-3-3 Psi (membrane)	At5g38480.1	0	0	0	0	0	0	16	2	0	0	3	0	0	0	0	0	0	0	0	0
Protein kinase family protein (nuclear)	At1g78940.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
10 Unclear Classification																					
Acid phosphatase (vacuolar membrane)	At5g24780.1	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0
Embryo defective 1211 (nucleus)	At5g22640.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Glycine-rich protein (cytosolic)	At4g02450.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glycine-rich protein (nucleus)	At4g39260.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nucleic acid binding (nucleus)	At3g11770.1	0	0	0	0	0	0	0	0	4	2	0	2	0	0	0	0	0	0	0	0
Transferase family protein- acyl groups (cytosolic)	At4g15390.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Zinc ion binding protein (plasma membrane)	At4g28370.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0

		VI				VII				VIII				IX				Averages												T-test				
		control		experimental		control		experimental		control		experimental		control		experimental		control						experimental										
protein name (predicted localization)	accession #	glycine	BSA	chi	epsilon	glycine	BSA	chi	epsilon	glycine	BSA	chi	epsilon	glycine	BSA	chi	epsilon	glycine	stdev	cv	BSA	stdev	cv	Chi	stdev	cv	Epsilon	stdev	cv	Glycine v. Chi	Glycine v. Epsilon	BSA v. Chi	BSA v. Epsilon	Chi v. Epsilon
01 Metabolism and Catabolism																																		
(S)-2-hydroxy-acid oxidase (cytosolic)	At3g14415.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
6-Phosphogluconate dehydrogenase family protein (chloroplast)	At1g64190.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.44	1.33	3.00	0.56	1.67	3.00	0.33	0.33	0.33	0.33	0.88
6-Phosphogluconate dehydrogenase family protein (peroxisome)	At3g02360.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
Aldehyde dehydrogenase (chloroplast)	At1g54100.1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
Aldehyde dehydrogenase (cytoskeleton)	At3g24503.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
ATP citrate lyase (chloroplast)	At5g49460.1	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.44	1.33	3.00	-	0.33	-	0.33	0.33
ATP citrate lyase (cytosolic)	At1g60810.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Beta-fructofuranosidase (cytosolic)	At4g34860.1	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Biotin carboxylase (chloroplast)	At5g35360.1	7	4	2	3	2	5	3	0	0	3	5	16	0	0	8	8	1.00	2.35	2.35	1.33	2.06	1.55	2.78	2.77	1.00	3.33	5.45	1.64	0.16	0.26	0.23	0.32	0.79
Chalcone-flavanone isomerase (chloroplast)	At1g53520.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.22	0.67	3.00	0.33	0.33	0.33	0.33	1.00
Pyruvate dehydrogenase complex E2 subunit (chloroplast)	At3g25860.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Glucosidase (vacuolar membrane)	At5g63840.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.22	0.67	3.00	0.33	0.33	0.33	0.33	1.00
Glyceraldehyde-3-phosphate dehydrogenase (ctyosolic)	At1g13440.1	5	7	6	13	6	10	10	15	7	9	10	21	5	5	5	13	5.78	7.07	1.22	9.67	14.92	1.54	14.56	16.63	1.14	16.67	9.63	0.58	0.16	0.01	0.52	0.25	0.75
Glyceraldehyde-3-phosphate dehydrogenase (ctyosolic)	At3g04120.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.56	1.67	3.00	-	0.33	-	0.33	0.33
Glyceraldehyde-3-phosphate dehydrogenase (ctyosolic)	At2g24270.2	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
Invertase (cytosolic)	At1g35580.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Isocitrate dehydrogenase (cytosolic)	At1g65930.1	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
Methionine synthase (cytosolic)	At5g17920.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.67	2.00	3.00	0.89	2.67	3.00	0.33	0.33	0.33	0.33	0.84
Phosphoenolpyruvate carboxylase (cytosolic)	At1g53310.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Phosphofructose kinase (chloroplast)	At1g12000.1	0	0	0	0	0	0	0	2	4	2	0	5	0	0	0	3	1.22	1.86	1.52	1.00	1.58	1.58	1.56	2.65	1.70	2.44	2.24	0.92	0.76	0.23	0.60	0.13	0.45
Phosphofructose kinase (ctyosolic)	At1g20950.1	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.44	1.33	3.00	-	0.33	-	0.33	0.33
Phosphoglycerate kinase (chloroplast)	At3g12780.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.56	1.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Protein disulfide isomerase (chloroplast)	At1g21750.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
Pyridoxal phosphate synthase (cytosolic)	At3g16050.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.22	0.67	3.00	0.33	0.33	0.33	0.33	1.00
Pyruvate kinase (chloroplast)	At3g25960.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Pyruvate kinase (cytosolic)	At2g36580.1	0	0	0	0	0	0	0	0	0	0	3	2	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	0.22	0.67	3.00	0.33	0.33	0.33	0.33	0.79
S-malonyltransferase acyl-carrier-protein (chloroplast)	At2g30200.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.33	1.00	3.00	0.33	0.33	0.33	0.33	0.79
Sucrose synthase (cytosolic)	At5g49190.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Transketolase (chloroplast)	At2g45290.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
UDP-glucose 6-dehydrogenase (extracellular)	At5g15490.1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.22	0.67	3.00	0.33	0.33	0.33	0.33	1.00
UDP-glucose dehydrogenase (extracellular)	At1g26570.1	0	0	0	0	0	0	0	2	0	0	0	3	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.56	1.13	2.03	-	0.16	-	0.16	0.16
UDP-glucose pyrophosphorylase (cytosolic)	At3g03250.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.44	1.33	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
UDP-glucosyl transferase (chloroplast)	At1g30530.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
UDP-glucuronate decarboxylase (chloroplast)	At3g46440.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Xylose isomerase (endoplasmic reticulum)	At5g57655.2	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
02 Energy																																		
Chlorophyll binding A/B binding protein (chloroplast)	At1g61520.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Chlorophyll binding A/B binding protein (chloroplast)	At1g29910.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.22	0.67	3.00	0.33	0.33	0.33	0.33	1.00
Ketol-acid reductoisomerase (chloroplast)	At3g58610.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Ribulose-bisphosphate carboxylase large subunit (mitochondria)	At2g07732.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
03 Cell Growth and Division																																		
DNA glycosylase (nucleus)	At3g10010.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Indole-3-acetic acid-amido synthetase (chloroplast)	At2g47750.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
PHD finger transcription factor (cytosolic)	At3g53680.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Proliferating cell nuclear antigen (cell growth and division) (nucleus)	At1g07370.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Replication factor A protein (nucleus)	At5g08020.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
04 Cell Structure																																		
Alpha-1,4-glucan protein synthase (cytosolic)	At5g15650.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.44	1.33	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Tubulin Beta-1 Chain (vacuole)	At1g75780.1	0	0	0	0	0	3	3	6	0	0	0	6	0	0	0	4	0.00	0.00	-	0.33	1.00	3.00	0.33	1.00	3.00	1.78	2.73	1.53	0.33	0.07	1.00	0.16	0.16
05 Protein Synthesis																																		
40S Ribosomal protein S19 (cytoskeleton)	At3g02080.1	0	0	0	0	0	0	2	0	0	2	0	2	0	0	0	2	0.44	1.33	3.00	0.44	0.88	1.98	0.78	1.20	1.55	1.22	1.56	1.28	0.59	0.27	0.51	0.21	0.51
40S Ribosomal protein S19 (cytosolic)	At5g61170.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
40S Ribosomal protein S2 (cytosolic)	At2g41840.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
40S Ribosomal protein S9 (membrane)	At5g39850.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
40S Ribosomal subunit (cytosolic)	At1g72370.1	0	0	0	0	4	0	2	0	2	3	2	3	0	0	2	2	0.67	1.41	2.12	0.78	1.56	2.01	1.44	1.13	0.78	1.44	1.88	1.30	0.22	0.34	0.32	0.43	1.00
60S Ribosomal protein L12 (cytosolic)	At2g37190.1	0	0	2	2	0	0	0	0	2	3	2	2	2	2	2	0	0.89	1.45	1.63	0.56	1.13	2.03	1.89	1.76	0.93	2.33	3.54	1.52	0.21	0.27	0.07	0.17	0.74
60S Ribosomal protein L23 (nucleus)	At2g39460.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.44	1.33	3.00	-	0.33	-	0.33	0.33
60S Ribosomal protein L26 (cytosolic)	At3g49910.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
60S Ribosomal protein L30 (chloroplast)	At1g36240.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
60S Ribosomal protein L35 (cytosolic)	At1g41880.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.22	0.67	3.00	0.33	0.33	0.33	0.33	1.00
60S Ribosomal protein L4 (chloroplast)	At3g09630.1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.56	1.13	2.03	0.33	0.16	0.33	0.16	0.46
Elongation factor 1-alpha (cytosolic)	At1g07920.1	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	3	0.44	1.33	3.00	0.56	1.13	2.03	2.56	4.50	1.76	1.11	1.69	1.52	0.20	0.37	0.21	0.42	0.38
Elongation factor 1B-gamma (cytosolic)	At1g57720.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Methionine tRNA ligase (cytosolic)	At4g13780.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Ribosomal protein L16 (cytosolic)	At2g42740.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Ribosomal protein S21 (chloroplast)	At3g27160.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
Elongation factor 2-like (cytosolic)	At1g56070.1	0	0	0	5	8	9	5	5	7	11	7	13	2	0	6	7	2.89	2.98	1.03	3.44	5.20	1.51	4.22	4.12	0.97	6.00	3.64	0.61	0.44	0.06	0.73	0.24	0.35
06 Protein Destination and Storage																																		
20S Proteasome subunit PAA1 (cytosolic)	At5g35590.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
20S Proteasome subunit PBA1 (cytosolic)	At4g31300.1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
2S Seed storage protein 4 (chloroplast and extracellular)	At4g27170.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.44	1.33	3.00	-	0.33	-	0.33	0.33
Aspartyl protease family protein (chloroplast)	At3g18490.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
Calreticulin 1 (endoplasmic reticulum)	At1g56340.1	0	2	3	3	0	0	0	0	0	0	0	0	0	0	4	0	0.00	0.00	-	0.22	0.67	3.00	1.33	2.06	1.55	0.78	1.20	1.55	0.07	0.07	0.14	0.24	0.49
Chaperonin 60 (chloroplast)	At1g55490.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	0.67	1.32	1.98	0.33	0.15	0.33	0.15	0.55
Cruciferin 3 (chloroplast)	At4g28520.2	0	0	0	0	3	0	0	0	4	3	0	0	0	2	3	11	1.22	1.86	1.52	1.67	2.18	1.31	1.56	2.55	1.64	4.00	6.42	1.61	0.76	0.23	0.92	0.32	0.30
Cruciferin 3 (chloroplast)	At4g28520.1	0	3	0	2	0	0	0	0	0	0	0	2	0	0	2	7	0.22	0.67	3.00	0.56	1.13	2.03	0.56	1.13	2.03	2.56	3.57	1.40	0.46	0.07	1.00	0.13	0.13
Cupin family protein (cytosolic)	At1g07750.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Heat shock cognate 70 kDa protein 3 (cytosolic)	At3g09440.1	0	0	0	0	0	0	6	3	0	0	0	2	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.89	2.03	2.28	1.22	1.56	1.28	0.21	0.03	0.21	0.03	0.70
Heat shock protein 70-1 (chloroplast)	At4g24280.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	2	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.22	0.67	3.00	0.33	0.33	0.33	0.33	1.00
Heat shock protein 90 (cytosolic)	At5g56030.1	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
Seed storage albumin (chloroplast and extracellular)	At4g27160.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	1.11	3.33	3.00	-	0.33	-	0.33	0.33
Luminal binding protein (endoplasmic reticulumn)	At5g42020.1	0	0	0	0	3	0	6	3	0	0	0	5	0	0	0	3	0.33	1.00	3.00	0.00	0.00	-	0.67	2.00	3.00	1.89	1.96	1.04	0.66	0.05	0.33	0.01	0.21
RING-type E3 ubiquitin ligase (nucleus)	At5g22000.2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Serine-type endopeptidase (chloroplast)	At5g67360.1	0	0	0	0	0	0	0	4	0	0	0	3	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.67	2.00	3.00	1.67	2.83	1.70	0.33	0.10	0.33	0.10	0.40
Subtilase family protein (plasma membrane)	At3g14067.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
07 Transporters																																		
AAA-type ATPases (cytosolic)	At3g09840.1	0	0	0	0	0	0	3	0	0	0	0	2	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	0.44	0.88	1.98	0.33	0.15	0.33	0.15	0.81
ATP synthase (chloroplast)	At4g04640.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
ATP synthase beta-subunit (mitochondrial)	At5g08670.1	0	0	0	0	0	3	0	2	0	0	2	7	2	0	5	5	0.22	0.67	3.00	0.56	1.13	2.03	2.00	2.29	1.15	1.89	2.62	1.39	0.04	0.08	0.11	0.18	0.92
ATPase alpha subunit (cytosolic)	AtCg00120.1	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	2	0.00	0.00	-	0.33	1.00	3.00	1.33	2.24	1.68	0.78	1.20	1.55	0.09	0.07	0.24	0.41	0.52
H+-APTase (chloroplast)	At1g17260.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
08 Disease/Defense																																		
2-Cys peroxiredoxin (chloroplast)	At3g11630.1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Germin-like protein (chloroplast)	At5g39190.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	-	0.33	-	0.33	0.33
MLP-like protein 28 (cytosolic)	At1g70830.1	0	0	0	11	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	1.22	3.67	3.00	-	0.33	-	0.33	0.33
MLP-like protein 423 (cytosolic)	At1g24020.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Translationally controlled tumor protein (cytosolic)	At3g16640.1	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.33	1.00	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
09 Signal Transduction																																		
14-3-3 Chi (plasma membrane)	At4g09000.1	0	0	113	3	0	0	125	18	0	0	129	23	0	0	90	10	0.00	0.00	-	0.00	0.00	-	149.89	93.69	0.63	15.22	10.78	0.71	0.00	0.00	0.00	0.00	0.00
14-3-3 Epsilon (mitochondrial)	At1g22300.1	0	0	0	232	0	0	6	177	0	2	7	187	0	0	5	142	0.00	0.00	-	0.22	0.67	3.00	2.78	2.86	1.03	196.00	118.36	0.60	0.01	0.00	0.02	0.00	0.00
14-3-3 Nu (plasma membrane)	At3g02520.1	0	0	0	0	0	0	6	0	0	0	3	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	2.56	4.10	1.60	0.00	0.00	-	0.08	-	0.08	-	0.08
14-3-3 Omega (plasma membrane)	At1g78300.1	0	0	53	2	0	0	40	7	0	0	33	10	0	0	29	0	0.00	0.00	-	0.00	0.00	-	69.00	52.12	0.76	7.44	5.36	0.72	0.00	0.00	0.00	0.00	0.00
14-3-3 Phi (chloroplast)	At1g35160.1	0	0	46	0	0	0	26	6	0	0	32	8	0	0	24	4	0.00	0.00	-	0.22	0.67	3.00	36.22	12.96	0.36	5.44	3.24	0.60	0.00	0.00	0.00	0.00	0.00
14-3-3 Psi (membrane)	At5g38480.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	2.11	5.30	2.51	0.22	0.67	3.00	0.25	0.33	0.25	0.33	0.30
Protein kinase family protein (nuclear)	At1g78940.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
10 Unclear Classification																																		
Acid phosphatase (vacuolar membrane)	At5g24780.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.22	0.67	3.00	0.33	0.33	0.33	0.33	1.00
Embryo defective 1211 (nucleus)	At5g22640.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Glycine-rich protein (cytosolic)	At4g02450.1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33
Glycine-rich protein (nucleus)	At4g39260.1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	-	0.33	-	0.33	0.33
Nucleic acid binding (nucleus)	At3g11770.1	0	0	2	2	0	0	2	2	0	0	2	2	0	0	2	2	0.44	1.33	3.00	0.22	0.67	3.00	0.89	1.05	1.19	1.11	1.05	0.95	0.44	0.26	0.13	0.05	0.66
Transferase family protein- acyl groups (cytosolic)	At4g15390.1	0	0	0	0	0	0	2	0	0	0	0	2	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.22	0.67	3.00	0.33	0.33	0.33	0.33	1.00
Zinc ion binding protein (plasma membrane)	At4g28370.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00	0.00	-	0.00	0.00	-	0.22	0.67	3.00	0.00	0.00	-	0.33	-	0.33	-	0.33

Supplementary Table 2b. The percent protein coverage of all the identified proteins in these binding experiments is listed below (glycine-sepharose = glycine/BSA-sepharose = BSA/chi-sepharose = chilepsilon-sepharose = epsilon).

		I				II				III				IV				V				VI				VII				VIII				IX			
		control		experimental		control		experimental		control		experimental		control		experimental		control		experimental		control		experimental		control		experimental		control		experimental		control		experimental	
protein name (predicted localization)	**accession #**	**glycine**	**BSA**	**chi**	**epsilon**	**glycine**	**BSA**	**chi**	**epsilon**	**glycine**	**BSA**	**chi**	**epsilon**	**glycine**	**BSA**	**chi**	**epsilon**	**glycine**	**BSA**	**chi**	**epsilon**	**glycine**	**BSA**	**chi**	**epsilon**	**glycine**	**BSA**	**chi**	**epsilon**	**glycine**	**BSA**	**chi**	**epsilon**	**glycine**	**BSA**	**chi**	**epsilon**
01 Metabolism and Catabolism																																					
(S)-2-hydroxy-acid oxidase (cytosolic)	At3g14415.1	-	-	-	-	-	-	-	-	0	0	8.70%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6-Phosphogluconate dehydrogenase family protein (chloroplast)	At1g64190.1	-	-	-	-	-	-	-	-	0	0	6.20%	8.80%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6-Phosphogluconate dehydrogenase family protein (peroxisome)	At3g02360.2	-	-	-	-	-	-	-	-	0	0	0	8.20%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Aldehyde dehydrogenase (chloroplast)	At1g54100.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	4.50%	-	-	-	-
Aldehyde dehydrogenase (cytoskeleton)	At3g24503.1	-	-	-	-	-	-	-	-	0	0	7.40%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
ATP citrate lyase (chloroplast)	At5g49460.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	5.80%	-	-	-	-
ATP citrate lyase (cytosolic)	At1g60810.1	-	-	-	-	-	-	-	-	0	0	12%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Beta-fructofuranosidase (cytosolic)	At4g34860.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	3.50%	0	-	-	-	-
Biotin carboxylase (chloroplast)	At5g35360.1	0	0	5.60%	0	0	0	8.20%	7.10%	-	-	-	-	-	-	-	-	-	-	-	-	13%	8.20%	5.20%	5.60%	3.90%	11%	7.40%	0	0	5.80%	6.30%	18%	1.50%	0	2.80%	4.60%
Chalcone-flavanone isomerase (chloroplast)	At1g53520.1	-	-	-	-	-	-	-	-	0	0	9.80%	9.80%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Pyruvate dehydrogenase complex E2 subunit (chloroplast)	At3g25860.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	5.40%	-	-	-	-
Glucosidase (vacuolar membrane)	At5g63840.1	-	-	-	-	0	0	4.00%	5.00%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Glyceraldehyde-3-phosphate dehydrogenase (ctyosolic)	At1g13440.1	14%	0	23%	23%	0	0	31%	31%	35%	52%	56%	53%	0	0	8.60%	19%	0	13%	7.70%	13%	14%	12%	10%	19%	13%	11%	13%	29%	7.70%	11%	11%	32%	7.70%	7.70%	11%	15%
Glyceraldehyde-3-phosphate dehydrogenase (ctysosolic)	At3g04120.1	-	-	-	-	-	-	-	-	0	0	0	14%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Glyceraldehyde-3-phosphate dehydrogenase (ctysosolic)	At2g24270.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	5.80%	-	-	-	-	-	-	-	-	-	-	-	-
Invertase (cytosolic)	At1g35580.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	3.60%	-	-	-	-
Isocitrate dehydrogenase (cytosolic)	At1g65930.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	10%	-	-	-	-	-	-	-	-	-	-	-	-
Methionine synthase (cytosolic)	At5g17920.1	-	-	-	-	-	-	-	-	0	0	9.50%	14%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Phosphoenolpyruvate carboxylase (cytosolic)	At1g53310.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	2.40%	0	-	-	-	-	-	-	-	-
Phosphofructose kinase (chloroplast)	At1g12000.1	-	-	-	-	5.10%	0	6.70%	6.00%	15%	9.20%	22%	9.20%	0	0	7.60%	5.10%	0	5.10%	0	0	-	-	-	-	0	0	0	4.80%	4.80%	4.80%	0	8.00%	0	0	0	4.80%
Phosphofructose kinase (chysosolic)	At1g20950.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	3.10%	-	-	-	-
Phosphoglycerate kinase (chloroplast)	At3g12780.1	-	-	-	-	-	-	-	-	0	0	10%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Protein disulfide isomerase (chloroplast)	At1g21750.1	-	-	-	-	-	-	-	-	0	0	0	14%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Pyridoxal phosphate synthase (cytosolic)	At3g16050.1	-	-	-	-	-	-	-	-	-	-	-	-	0	0	8.90%	0	0	0	0	8.60%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Pyruvate kinase (chloroplast)	At3g25960.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	4.20%	-	-	-	-
Pyruvate kinase (cytosolic)	At2g36580.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	6.10%	4.40%	-	-	-	-
S-malonyltransferase acyl-carrier-protein (chloroplast)	At2g30200.1	-	-	-	-	-	-	-	-	0	0	11%	0	0	0	0	6.40%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Sucrose synthase (cytosolic)	At5g49190.1	-	-	-	-	-	-	-	-	0	0	0	3.70%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Transketolase (chloroplast)	At2g45290.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	3.10%	0	-	-	-	-	-	-	-	-
UDP-glucose 6-dehydrogenase (extracellular)	At5g15490.1	-	-	-	-	0	0	5.80%	0	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	9.00%	-	-	-	-	-	-	-	-	-	-	-	-
UDP-glucose dehydrogenase (extracellular)	At1g26570.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	4.60%	0	0	0	4.60%	-	-	-	-
UDP-glucose pyrophosphorylase (cytosolic)	At3g03250.1	-	-	-	-	-	-	-	-	0	0	9.60%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
UDP-glucosyl transferase (chloroplast)	At1g30530.1	-	-	-	-	-	-	-	-	0	0	7.90%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
UDP-glucuronate decarboxylase (chloroplast)	At3g46440.1	-	-	-	-	-	-	-	-	0	0	17%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Xylose isomerase (endoplasmic reticulum)	At5g57655.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	5.50%	-	-	-	-
02 Energy																																					
Chlorophyll binding A/B binding protein (chloroplast)	At1g61520.1	-	-	-	-	-	-	-	-	0	0	0	16%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Chlorophyll binding A/B binding protein (chloroplast)	At1g29910.1	-	-	-	-	-	-	-	-	0	0	10%	10%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Ketol-acid reductoisomerase (chloroplast)	At3g58610.1	-	-	-	-	-	-	-	-	0	0	0	5.60%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Ribulose-bisphosphate carboxylase large subunit (mitochondria)	At2g07732.1	-	-	-	-	-	-	-	-	0	0	0	16%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
03 Cell Growth and Division																																					
DNA glycosylase (nucleus)	At3g10010.1	0	0	2.80%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Indole-3-acetic acid-amido synthetase (chloroplast)	At2g47750.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	5.10%	-	-	-	-
PHD finger transcription factor (cytosolic)	At3g53680.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	3.00%	0	-	-	-	-	-	-	-	-
Proliferating cell nuclear antigen (cell growth and division) (nucleus)	At1g07370.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	11%	0	-	-	-	-	-	-	-	-
Replication factor A protein (nucleus)	At5g08020.1	-	-	-	-	-	-	-	-	0	0	0	5.80%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
04 Cell Structure																																					
Alpha-1,4-glucan protein synthase (cytosolic)	At5g15650.1	-	-	-	-	-	-	-	-	0	0	8.30%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Tubulin Beta-1 Chain (vacuole)	At1g75780.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	7.80%	4.50%	5.60%	0	0	0	5.60%	0	0	0	5.60%
05 Protein Synthesis																																					
40S Ribosomal protein S19 (cytoskeleton)	At3g02080.1	-	-	-	-	0	0	11%	11%	-	-	-	-	11%	0	11%	20%	0	11%	0	0	-	-	-	-	0	0	11%	0	0	10%	0	10%	0	0	0	10%
40S Ribosomal protein S19 (cytosolic)	At5g61170.1	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	37%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
40S Ribosomal protein S2 (cytosolic)	At2g41840.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	9.80%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
40S Ribosomal protein S9 (membrane)	At5g39850.1	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	5.60%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
40S Ribosomal subunit (cytosolic)	At1g72370.1	-	-	-	-	0	0	8.70%	20%	0	16%	0	0	0	0	10%	0	0	0	10%	8.70%	-	-	-	-	13%	0	10%	0	10%	13%	10%	13%	0	0	8.70%	10%
60S Ribosomal protein L12 (cytosolic)	At2g37190.1	-	-	-	-	0	0	14%	21%	0	0	0	14%	21%	0	34%	41%	0	0	14%	0	0	0	14%	17%	-	-	-	-	14%	14%	14%	14%	14%	17%	14%	0
60S Ribosomal protein L23 (nucleus)	At2g39460.1	-	-	-	-	0	0	0	11%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
60S Ribosomal protein L26 (cytosolic)	At3g49910.1	-	-	-	-	0	0	0	18%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
60S Ribosomal protein L30 (chloroplast)	At1g36240.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	24%	0	-	-	-	-	-	-	-	-
60S Ribosomal protein L35 (cytosolic)	At1g41880.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	9.00%	9.00%
60S Ribosomal protein L4 (chloroplast)	At3g09630.1	-	-	-	-	0	0	6.20%	7.40%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	5.90%	-	-	-	-
Elongation factor 1-alpha (cytosolic)	At1g07920.1	12%	12%	6.90%	0	0	0	15%	9.80%	0	2.70%	17%	0	-	-	-	-	-	-	-	-	0	0	0	13%	-	-	-	-	-	-	-	-	0	0	0	7.80%
Elongation factor 1B-gamma (cytosolic)	At1g57720.1	-	-	-	-	0	0	10%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Methionine tRNA ligase (cytosolic)	At4g13780.1	-	-	-	-	-	-	-	-	0	0	0	5.00%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Ribosomal protein L16 (cytosolic)	At2g42740.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	13%	0	-	-	-	-	-	-	-	-
Ribosomal protein S21 (chloroplast)	At3g27160.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	8.70%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Elongation factor 2-like (cytosolic)	At1g56070.1	0	0	3.20%	3.20%	6.20%	0	0	9.10%	5.10%	13%	15%	10%	0	0	2.70%	5.00%	3.20%	0	3.40%	3.10%	0	0	0	5.10%	3.90%	6.30%	3.40%	3.40%	5.70%	9.40%	4.60%	6.30%	1.50%	0	2.80%	4.60%
06 Protein Destination and Storage																																					
20S Proteasome subunit PAA1 (cytosolic)	At5g35590.1	-	-	-	-	0	0	0	13%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
20S Proteasome subunit PBA1 (cytosolic)	At4g31300.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	13%	-	-	-	-	-	-	-	-	-	-	-	-
2S Seed storage protein 4 (chloroplast and extracellular)	At4g27170.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	25%
Aspartyl protease family protein (chloroplast)	At3g18490.1	-	-	-	-	-	-	-	-	0	0	0	11%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Calreticulin 1 (endoplasmic reticulum)	At1g56340.1	-	-	-	-	0	0	0	6.60%	0	0	19%	9.20%	-	-	-	-	-	-	-	-	0	6.80%	6.60%	11%	-	-	-	-	-	-	-	-	0	0	7.30%	0
Chaperonin 60 (chloroplast)	At1g55490.1	-	-	-	-	0	0	0	10%	0	0	6.70%	0	-	-	-	-	0	0	0	7.80%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Cruciferin 3 (chloroplast)	At4g28520.2	9.40%	9.40%	8.10%	21%	0	0	7.90%	9.90%	0	13%	0	0	0	0	0	9.10%	-	-	-	-	-	-	-	-	5.30%	0	0	0	10%	14%	0	0	0	8.10%	7.40%	8.10%
Cruciferin 3 (chloroplast)	At4g28520.1	5.70%	5.70%	9.50%	13%	0	0	0	2.50%	-	-	-	-	-	-	-	-	-	-	-	-	0	10%	0	7.30%	-	-	-	-	0	0	0	4.20%	0	0	5.30%	5.70%
Cupin family protein (cytosolic)	At1g07750.1	-	-	-	-	-	-	-	-	0	0	0	15%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Heat shock cognate 70 kDa protein 3 (cytosolic)	At3g09440.1	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	2.50%	0	0	2.50%	2.50%	-	-	-	-	0	0	2.50%	2.50%	0	0	0	2.50%	-	-	-	-
Heat shock protein 70-1 (chloroplast)	At4g24280.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	2.80%	0	-	-	-	-	0	0	0	2.80%
Heat shock protein 90 (cytosolic)	At5g56030.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	4.10%	-	-	-	-
Seed storage albumin (chloroplast and extracellular)	At4g27160.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	33%
Luminal binding protein (endoplasmic reticulumn)	At5g42020.1	-	-	-	-	0	0	0	4.50%	-	-	-	-	-	-	-	-	0	0	0	4.00%	-	-	-	-	6.00%	0	6.60%	2.40%	0	0	0	4.50%	0	0	0	3.70%
RING-type E3 ubiquitin ligase (nucleus)	At5g22000.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	6.10%	-	-	-	-	-	-	-	-
Serine-type endopeptidase (chloroplast)	At5g67360.1	-	-	-	-	-	-	-	-	0	0	17%	17%	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	6.90%	0	0	0	3.30%	-	-	-	-
Subtilase family protein (plasma membrane)	At3g14067.1	-	-	-	-	-	-	-	-	0	0	0	3.70%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
07 Transporters																																					
AAA-type ATPases (cytosolic)	At3g09840.1	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	2.30%	-	-	-	-	-	-	-	-	0	0	3.30%	0	0	0	0	2.80%	-	-	-	-
ATP synthase (chloroplast)	At4g04640.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.60%	0
ATP synthase beta-subunit (mitochondrial)	At5g08670.1	0	0	5.90%	0	0	0	15%	8.50%	0	0	4.90%	0	-	-	-	-	0	4.90%	0	0	-	-	-	-	0	4.90%	0	4.70%	0	0	4.90%	13%	4.70%	0	9.00%	7.70%
ATPase alpha subunit (cytosolic)	AtCg00120.1	-	-	-	-	0	0	13%	0	0	0	15%	0	0	0	0	6.90%	0	7.30%	0	0	-	-	-	-	0	0	4.70%	0	0	0	0	4.70%	0	0	0	4.70%
H+-APTase (chloroplast)	At1g17260.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	2.20%
08 Disease/Defense																																					
2-Cys peroxiredoxin (chloroplast)	At3g11630.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	11%	0	-	-	-	-	-	-	-	-	-	-	-	-
Germin-like protein (chloroplast)	At5g39190.1	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	16%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
MLP-like protein 28 (cytosolic)	At1g70830.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	4.80%	-	-	-	-	-	-	-	-	-	-	-	-
MLP-like protein 423 (cytosolic)	At1g24020.1	-	-	-	-	-	-	-	-	0	0	0	18%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Translationally controlled tumor protein (cytosolic)	At3g16640.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	19%	0	-	-	-	-	-	-	-	-
09 Signal Transduction																																					
14-3-3 Chi (plasma membrane)	At4g09000.1	0	0	63%	26%	0	0	61%	39%	0	0	60%	41%	0	0	66%	34%	0	0	42%	23%	0	0	52%	19%	0	0	60%	30%	0	0	45%	41%	0	0	55%	23%
14-3-3 Epsilon (mitochondrial)	At1g22300.1	0	0	7.10%	70%	0	0	0	76%	0	0	0	85%	0	0	12%	76%	0	0	0	50%	0	0	0	64%	0	0	7.10%	67%	0	8.70%	11%	73%	0	0	7.10%	64%
14-3-3 Nu (plasma membrane)	At3g02520.1	-	-	-	-	-	-	-	-	0	0	14%	0	0	0	7.50%	0	-	-	-	-	-	-	-	-	0	0	7.50%	0	0	0	12%	0	-	-	-	-
14-3-3 Omega (plasma membrane)	At1g78300.1	0	0	26%	17%	0	0	37%	17%	0	0	49%	19%	0	0	34%	17%	0	0	18%	11%	0	0	24%	12%	0	0	22%	17%	0	0	22%	17%	0	0	22%	0
14-3-3 Phi (chloroplast)	At1g35160.1	0	0	4.50%	4.50%	0	0	15%	4.50%	0	0	13%	4.50%	0	4.50%	13%	4.50%	0	0	10%	4.50%	0	0	10%	0	0	0	7.50%	4.50%	0	0	7.50%	4.50%	0	0	4.50%	4.50%
14-3-3 Psi (membrane)	At5g38480.1	-	-	-	-	0	0	18%	10%	0	0	19%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Protein kinase family protein (nuclear)	At1g78940.1	-	-	-	-	-	-	-	-	0	0	0	4.40%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
10 Unclear Classification																																					
Acid phosphatase (vacuolar membrane)	At5g24780.1	-	-	-	-	0	0	13%	13%	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Embryo defective 1211 (nucleus)	At5g22640.1	-	-	-	-	0	0	3.80%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Glycine-rich protein (cytosolic)	At4g02450.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	10%	0	-	-	-	-	-	-	-	-
Glycine-rich protein (nucleus)	At4g39260.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	13%	-	-	-	-	-	-	-	-
Nucleic acid binding (nucleus)	At3g11770.1	-	-	-	-	-	-	-	-	25%	17%	0	14%	-	-	-	-	-	-	-	-	0	0	14%	14%	0	0	14%	14%	0	0	11%	11%	0	0	11%	14%
Transferase family protein- acyl groups (cytosolic)	At4g15390.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	4.50%	0	0	0	0	5.20%	-	-	-	-
Zinc ion binding protein (plasma membrane)	At4g28370.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	3.60%	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-