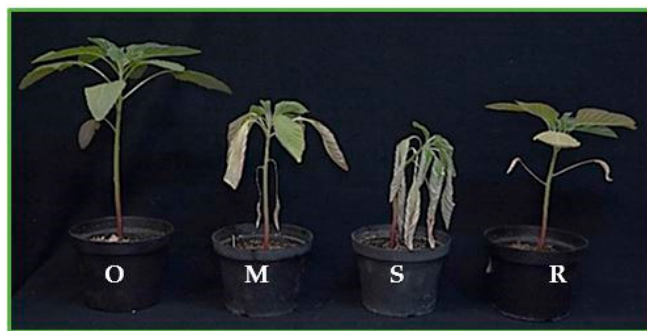




(A)



(B)



(C)



(D)



(E)

Figure S1. Response to water-deficit stress (WDS) in different amaranth species. Images of representative (A) *Amaranthus hypochondriacus* cv. Gabriela and (B) *A. cruentus* cv. Amaranteca plants used in the first selection experiment under optimal conditions [O], and 5 [M] and 10 [S] days after watering was withheld, and in [R], one day after watering was restored, after S. Panels (C) and (D) show *A. caudatus* and *A. hybridus* plants during one of the two formal WDS experiments performed under moderate WDS. Wilting is evident in both groups of plants even before the final 30% field capacity was reached. In panel (E), an image of the extreme desiccation suffered by *A. hybridus* plants during the preliminary 5- and 10-day WDS experiments. Also shown, is this species' ability to partially recover several days after watering was restored.

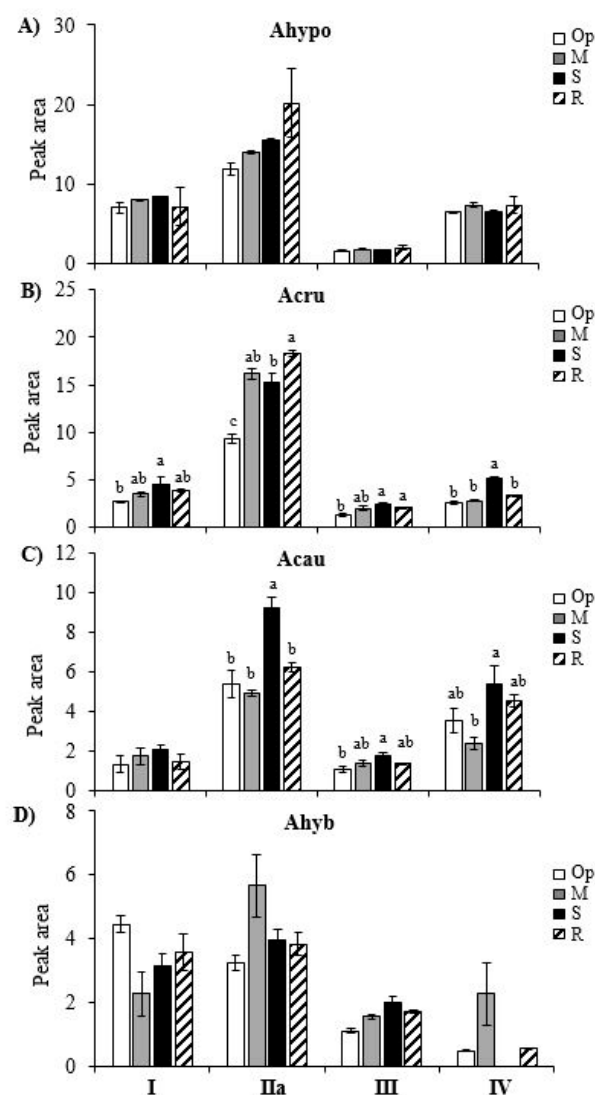


Figure S2. Unidentified RFO-like compounds quantified by HPAEC-PAD in leaf extracts of four species of amaranth plants. (A) *Amaranthus hypochondriacus* [Ahypo], (B) *A. cruentus* [Acru], (C) *A. caudatus* [Acau], and (D) *A. hybridus* [Ahyb] growing in optimal conditions (Op; empty bars), subjected to moderate (M) or severe (S) water deficit stress (gray and black bars respectively) or allowed to recover from S, 1 day after normal watering was restored (R; striped bars). The unidentified compounds analyzed, possibly RFO with increased degree of polymerization, are labelled in Roman numerals in ascending order in correspondence with their longer elution times, as follows: peak I (16 min); peak IIa (21.2 min); peak III (31.4 min) and Peak IV (33.8 min). The bars represent peak areas. Different letters over the bars represent statistically significant differences at $P \leq 0.05$ (Tukey Kramer test). Bars and error bars indicate mean values and ES, respectively ($n = 3$ pools of four plants each). The results shown are those obtained from a representative experiment that was repeated in the spring-summer and summer-autumn seasons of 2014, respectively, with similar results.

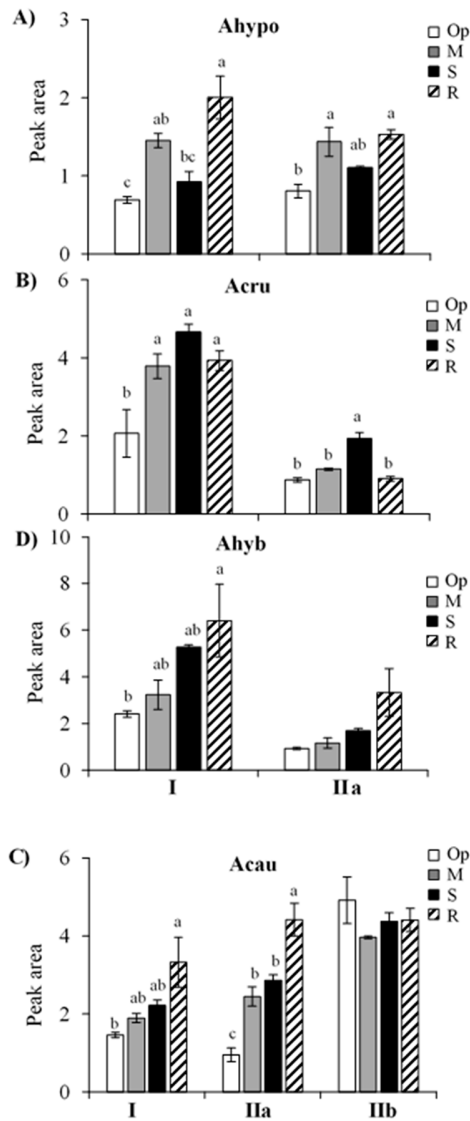


Figure S3. Unidentified RFO-like compounds quantified by HPAEC-PAD in root extracts of four species of amaranth plants. (A) *Amaranthus hypochondriacus* [Ahypo], (B) *A. cruentus* [Acru], (C) *A. caudatus* [Acau], and (D) *A. hybridus* [Ahyb] growing in optimal conditions (Op; empty bars), subjected to moderate (M) or severe (S) water deficit stress (gray and black bars respectively) or allowed to recover from S, 1 day after normal watering was restored (R; striped bars). The unidentified compounds analyzed, possibly RFO with increased degree of polymerization, are labelled in Roman numerals in ascending order, in correspondence with their longer elution times, as follows: peak I (16 min); peak IIa (21.2 min), and Peak IIb (22.8 min). The bars represent peak areas. Different letters over the bars represent statistically significant differences at $P \leq 0.05$ (Tukey Kramer test). Bars and error bars indicate mean values and ES, respectively ($n = 3$ pools of four plants each). The results shown are those obtained from a representative experiment that was repeated in the spring-summer and summer-autumn seasons.

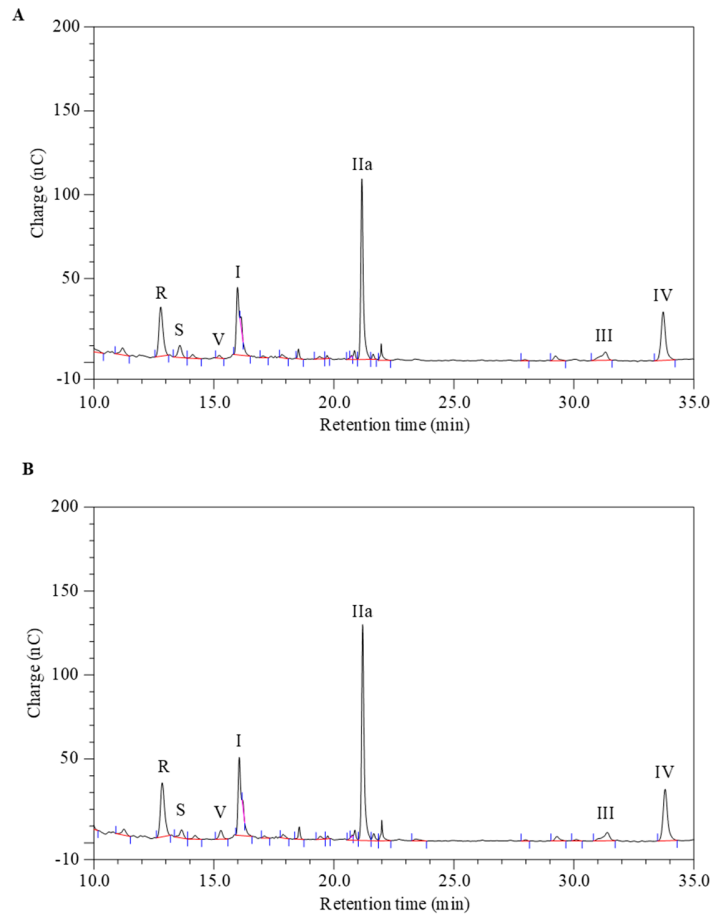


Figure S4. Representative HPAEC-PAD separation of soluble raffinose family oligosaccharides (RFOs) and unknown RFO-like compounds extracted from leaf extracts of *Amaranthus hypochondriacus*. The traces were obtained from plants growing in (A) optimal conditions or (B) subjected to severe water deficit stress. The peaks shown correspond to known raffinose (R), stachyose (S) and verbascose (V) oligosaccharides. Unknown RFO-like compounds were labeled with Roman numerals assigned according to their increasing retention time: I (16 min), IIa (21.2 min), III (31.4 min), and IV (33.8 min).

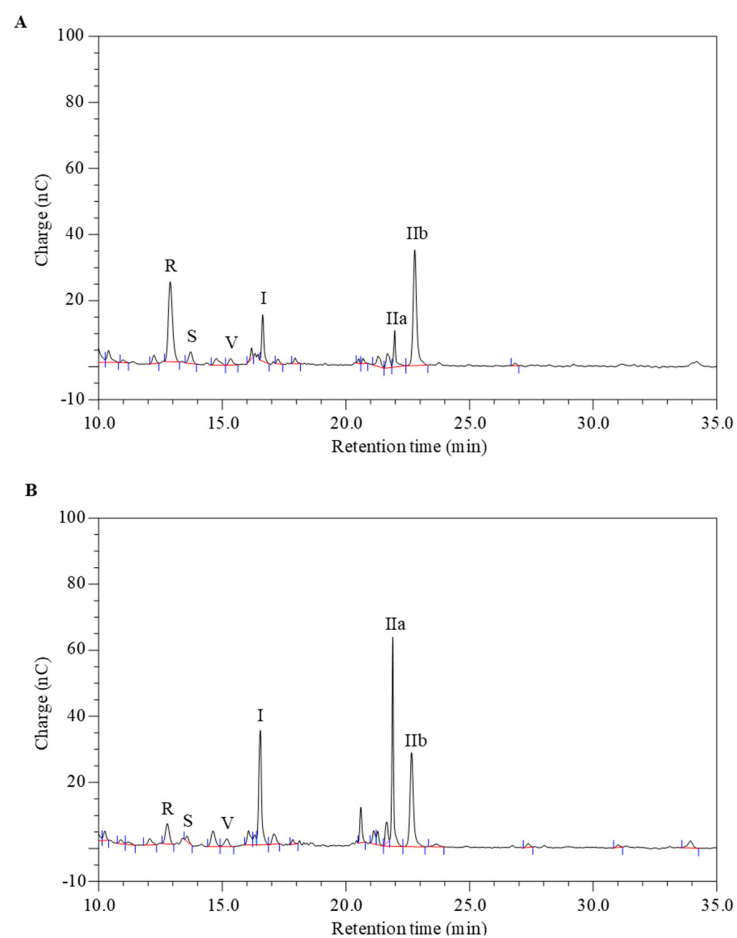


Figure S5. Representative HPAEC-PAD separation of soluble raffinose family oligosaccharides (RFOs) and unknown RFO-like compounds extracted from root extracts of *Amaranthus hypochondriacus*. The traces were obtained from plants growing in **(A)** optimal conditions or **(B)** subjected to severe water deficit stress. The peaks shown correspond to known raffinose (R), stachiose (S) and verbascose (V) oligosaccharides. Unknown RFO-like compounds were labeled with Roman numerals assigned according to their retention time: I (16 min), IIa (21.2 min), IIb (22.8 min).

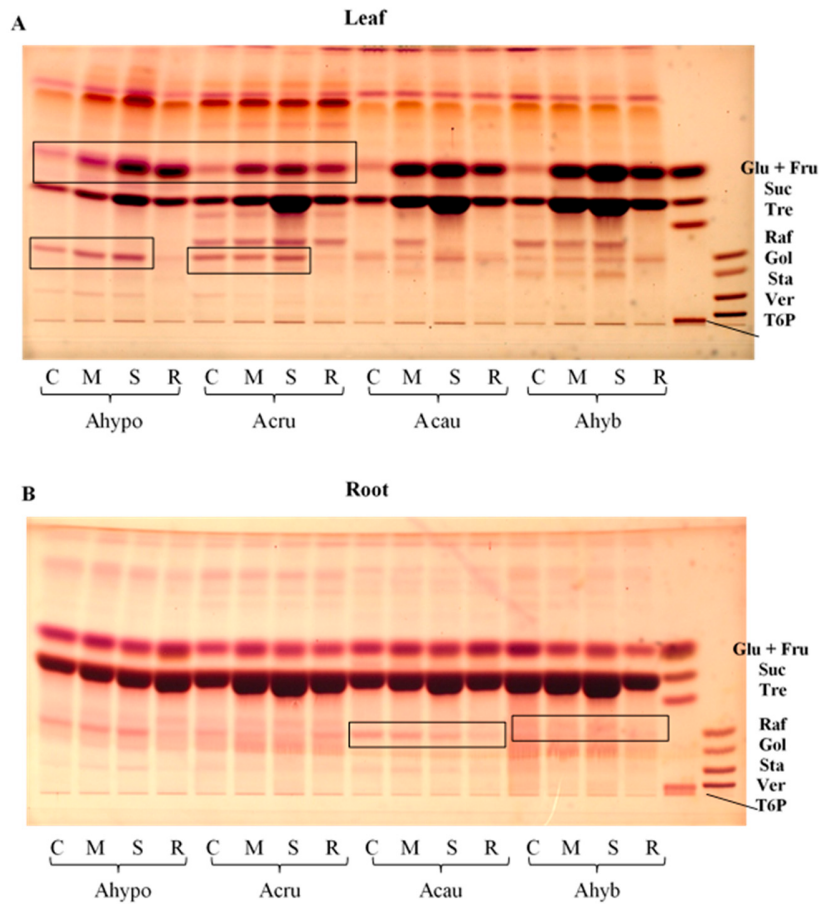


Figure S6. Thin layer chromatography separation of soluble non-structural carbohydrates and raffinose family oligosaccharides (RFOs). These were extracted from **(A)** leaves and **(B)** roots of four species of amaranth plants: *Amaranthus hypochondriacus* [Ahypo], *A. cruentus* [Acru], *A. caudatus* [Acau], and *A. hybridus* [Ahyb]) growing in optimal conditions (Op), subjected to moderate (M) or severe (S) water deficit stress or allowed to recover from S, 1 day after normal watering was restored (R). The position of the RFO and their respective precursor standards are shown in last two lanes on the right edge of the plate: These were the following: galactinol (Gol), raffinose (Raf), stachiose (Sta) and verbascose (Ver). Also included were glucose + fructose (Glu + Fru), sucrose (Suc), trehalose (Tre) and trehalose-6-phosphate (TGP) standards. Unidentified compounds, perhaps representing unknown RFOs that were constitutively accumulated in these tissues and/or were further increased in treated plants are enclosed in boxes.

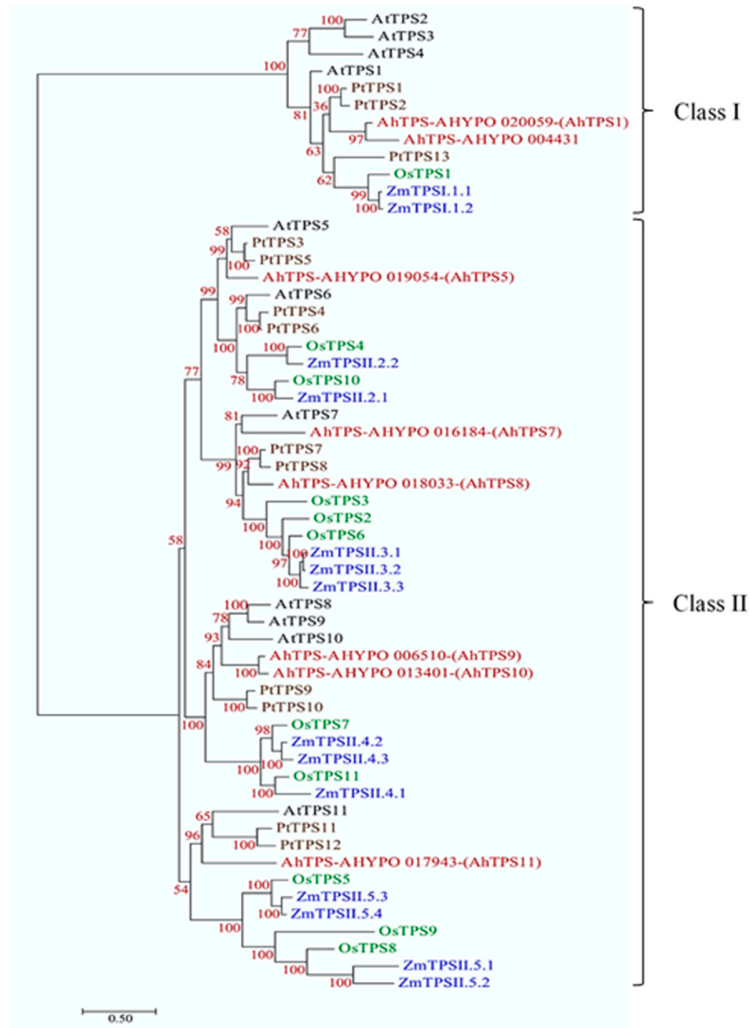


Figure S7. Phylogenetic analysis of the class I and II trehalose phosphate synthase proteins. The AhTPS proteins, shown in red text, were obtained from their respective genes, themselves contained in the *Amaranthus hypochondriacus* genome (Clouse et al., 2016). The phylogeny of AhTPS proteins with members reported in other plant species is shown. Abbreviations used are the following: Ah, *Amaranthus hypochondriacus*; At, *Arabidopsis thaliana* (black text); Os, *Oryza sativa* (green text); Pt, *Populus trichocarpa* (brown text), and Zm, *Zea mays* (blue text). The tree was obtained using the maximum likelihood method.

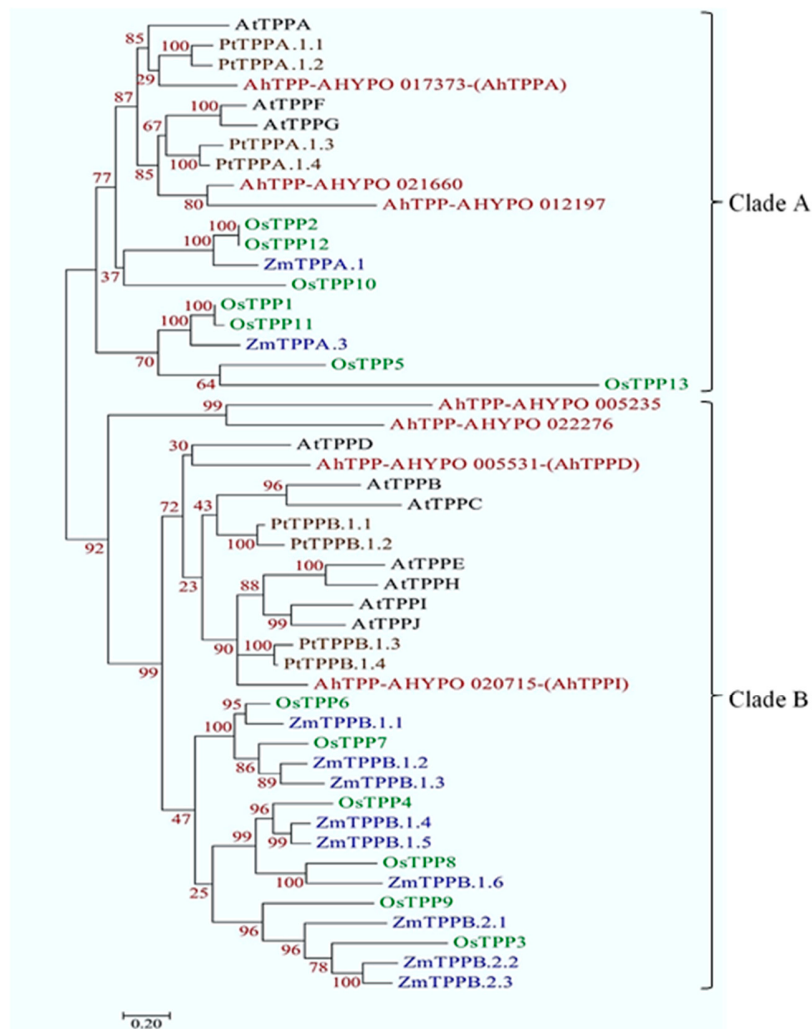


Figure S8. Phylogenetic analysis of the amaranth trehalose phosphate phosphatase proteins. The AhTPP proteins, shown in red text, were obtained from their respective genes, themselves contained in the *Amaranthus hypochondriacus* genome as reported by Clouse et al. [31]. The phylogeny of AhTPP proteins with members reported in other plant species is shown. Abbreviations used are the following: Ah, *Amaranthus hypochondriacus*, At, *Arabidopsis thaliana* (black text); Os, *Oryza sativa* (green text); Pt, *Populus trichocarpa* (brown text), and Zm, *Zea mays* (blue text). The tree was obtained using the maximum likelihood method.

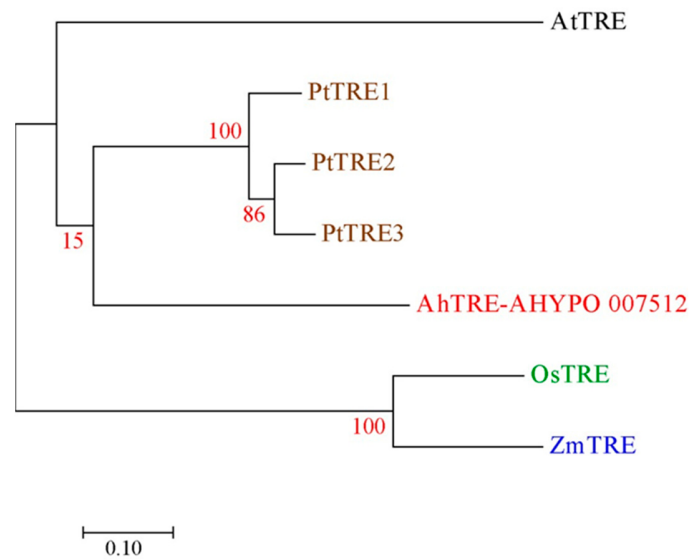


Figure S9: Phylogenetic analysis of the amaranth trehalase protein. The predicted AhTRE protein, shown in red text, was obtained from its respective gene, itself contained in the *Amaranthus hypochondriacus* genome as reported by Clouse et al. [31]. The phylogeny of the AhTRE protein with members reported in other plant species is shown. Abbreviations used are the following: Ah, *Amaranthus hypochondriacus*, At, *Arabidopsis thaliana* (black text); Os, *Oryza sativa* (green text); Pt, *Populus trichocarpa* (brown text), and Zm, *Zea mays* (blue text). The tree was obtained using the maximum likelihood method.

Table S1. Relative expression levels¹ of selected *SnRK*, *SnGRIK* and *SnRK2* genes in amaranth leaves. Gene expression was determined in leaves of four *Amaranthus* species subjected to two levels of water-deficit stress (moderate [M] and severe [S]) and to subsequent recovery ([R]). Induced (normalized expression values ≥ 2.0 ; in normal text) and repressed (normalized expression values ≤ 0.5 ; in italicized text) expression values are emphasized in bold.

Gene	<i>A. hypochondriacus</i>			<i>A. cruentus</i>			<i>A. caudatus</i>			<i>A. hybridus</i>		
	M	S	R	M	S	R	M	S	R	M	S	R
<i>AhGRIK2-like</i>	1.281	1.163	1.483	0.777	0.846	0.532	1.048	1.803	1.628	0.966	2.744	1.443
<i>AhSnRK1</i>	0.783	0.495	0.648	0.613	0.707	0.741	1.286	1.323	1.276	1.437	1.299	0.885
<i>AhSnRK2.1</i>	0.447	0.322	0.586	0.467	0.364	0.547	0.805	0.702	1.216	0.54	0.504	0.853
<i>AhSnRK2.2</i>	1.301	0.922	1.053	0.806	0.485	0.595	1.224	1.334	1.198	2.239	1.789	0.964

Calculated according to the comparative cycle threshold method (Livak and Schmittgen, 2001) using the *AhACT7*, *AhEF1a* and *Ah β Tub5* amaranth genes for data normalization.

Table S2. Relative expression values¹ of selected *SnRK*, *SnGRIK* and *SnRK2* genes in amaranth roots. Gene expression was determined in roots of four *Amaranthus* species subjected to two levels of water-deficit stress (moderate [M] and severe [S]) and to subsequent recovery ([R]). Induced (normalized expression values ≥ 2.0 ; in normal text) and repressed (normalized expression values ≤ 0.5 ; in italicized text) expression values are emphasized in bold.

Gene	<i>A. hypochondriacus</i>			<i>A. cruentus</i>			<i>A. caudatus</i>			<i>A. hybridus</i>		
	M	S	R	M	S	R	M	S	R	M	S	R
<i>AhGRIK2-like</i>	4.857	3.352	3.100	0.956	1.516	0.842	0.617	1.031	0.881	0.827	1.156	0.652
<i>AhSnRK1</i>	1.183	1.933	1.464	0.544	1.408	0.791	0.297	0.712	0.162	1.818	1.371	0.801
<i>AhSnRK2.1</i>	0.672	0.688	0.638	0.964	0.918	0.638	0.952	0.957	0.929	0.604	0.679	0.392
<i>AhSnRK2.2</i>	0.925	0.654	0.981	0.962	1.338	1.220	0.952	0.957	0.929	1.103	1.074	1.172

Calculated according to the comparative cycle threshold method (Livak and Schmittgen, 2001) using the *AhACT7*, *AhEF1a* and *Ah β Tub5* amaranth genes for data normalization.

Table S3. List of qPCR primers used in this study.

Gene		Sequence
<i>AhTPS1</i>	Forward	CTCCTTACAGTTGAGAAATCGC
	Reverse	TAACACTCTTGACCCAGATCG
<i>AhTPS5</i>	Forward	AACATCCTTAGTATCTCGCCTG
	Reverse	AGAACAACCTCCTTCACTCTCG
<i>AhTPS7</i>	Forward	AGGAAGCGATATTGAGGAGA
	Reverse	GCAATGGTGAAGTAAGCGAT
<i>AhTPS8</i>	Forward	CACCATTAGTAGGTCCAACAG
	Reverse	CAAGTGATGATGAGCCAGG
<i>AhTPS9</i>	Forward	TTCTTGCTCTGCCACTCAC
	Reverse	ATTGTCTCGGCGTATAGGA
<i>AhTPS10</i>	Forward	TCCTTGAAAGACGGTCAGAAT
	Reverse	CTGCTTGTTGTGCTTGAAGTTA
<i>AhTPS11</i>	Forward	AACAACGACAGGCTCATTAG
	Reverse	GGCATTATCAAGACTCCGA
<i>AhTPPA</i>	Forward	TGTTTCGTATTACTGCTTGGC
	Reverse	TGAGAGGGCTGACGGATA
<i>AhTPPD</i>	Forward	GCAGATGGATGATTGACC
	Reverse	TTCCAACCTCCTCCTTC
<i>AhTPPI</i>	Forward	TTGGATTACGATGGCACTCT
	Reverse	GGCACCTTCCACTCACTATT
<i>AhTRE</i>	Forward	AACAACGGTAACGGTAGGAG
	Reverse	GCAAGCACAGATCAATGC
<i>AhGOLS1</i>	Forward	AGCCCAACTACACCCTTTATG
	Reverse	TAATGGCACCAACAACTTCG
<i>AhGOLS2</i>	Forward	TCCTCCTACTCAAATATCCAA
	Reverse	AAAGGATCTAAGCAGCAGAAG
<i>AhReFS</i>	Forward	AAGCAGTTGAGTCACTATTCCA
	Reverse	AGATGGTTTCGTCTTGGCATAA
<i>AhSTaS</i>	Forward	CAATCCAAGGCAAAATCAAACAC
	Reverse	TCAAATGAGGCACCAAAGAAG
<i>AhGRIK2-like</i>	Forward	CTCCTGTAGTGCTCTCCGATA
	Reverse	CCCGAATGTTGCTTAGGT
<i>AhSnRK1</i>	Forward	GGACCTCAGATGCTCTTCCTT
	Reverse	TGAAACACGACCATAACATCAT
<i>AhSnRK2.1</i>	Forward	ATCCCAAAGTCTGAACAAGTA
	Reverse	CGGCTCATTACAATCGTTT
<i>AhSnRK2.2</i>	Forward	TCACAACAGAGGGACAATAAA
	Reverse	GCTCTCTTCTTGGGTGGA
<i>AhRAB18</i>	Forward	GCCCAGTGAAACAAGCAATAC
	Reverse	GCCAGAGACTCCGTAACTTC
<i>AhDREB2C</i>	Forward	TAACTCCGCAACAACAACACC
	Reverse	TCGATTGACCAACTGACTGA
<i>AhABI5</i>	Forward	TTTCTGAACTTCTTGCTCCAAT
	Reverse	AGAGGAGACAAAGGCGTATGA
<i>AhLEA14</i>	Forward	CCCGACAATATCTCCCTGGTA
	Reverse	ACGTACTCTGCTAAAGTTGGTG
<i>AhActin (ACT)</i>	Forward	CGTGACCTGACTGATTACCTTA
	Reverse	GCTCGTAGTTCTTCTCAATGGC
<i>Ahβ-Tubulin (TUB)</i>	Forward	TCTCAGCAGTATGTCTCCCTCA
	Reverse	TCTACTTCTTTGGTGCTCATCTT
<i>AhElongation factor 1α (EF1α)</i>	Forward	GCCAAATATCTAAGAAACAAATGC
	Reverse	TAGCACAACCACATGATATTTCTT

Table S4. Genes found to be differentially expressed in *A. hypochondriacus* plants subjected to water-deficit stress. Induced (relative expression value ≥ 1.5) or repressed (relative expression value ≤ 0.5) genes in each category are shown.

CELL WALL/ CYTOSKELETON RELATED				
XYLOGLUCANS				
0.1	gb AAB39950.1 xylucan endotransglycosylase			
0.2	gb AAK51119.1 xylucan endo-transglycosylase [<i>Carica papaya</i>]			
0.2	gb ABB72441.1 xylucan endotransglucosylase [<i>Betula pendula</i>]			
0.4	Bifunctional endo-1,4-beta-xylanase XylA precursor			
0.1	gb ABV27475.1 fasciclin-like arabinogalactan protein 4			
0.3	gb AAM62616.1 arabinogalactan protein-like [<i>Arabidopsis thaliana</i>]			
0.1	gb ABV27490.1 fasciclin-like arabinogalactan protein 19 [<i>Gossypium</i> spp.]			
PECTIN MATRIX				
0.1	gb AAK66161.1 pectate lyase [<i>Fragaria x ananassa</i>] 430 e-118	3.5	gb ABG47806.1 pectin methylesterase inhibitor protein 1 [<i>Capsicum</i> spp.]	
0.2	dbj BAE98780.1 pectinesterase like protein [<i>Arabidopsis thaliana</i>]	2.3	gb ABS18954.1 PGIP2 [<i>Populus deltoides</i>]	
0.1	ref NP_200149.1 ATPMEPCRF; pectinesterase [<i>Arabidopsis thaliana</i>]			
0.5	gb AAA53547.1 polygalacturonase inhibitor protein 231			
0.2	ref NP_566170.1 GAUT9 (Galacturonosyltransferase 9); polygalacturonase			
0.2	ref NP_196051.2 pectate lyase family protein [<i>Arabidopsis thaliana</i>]			
0.3	ref NP_001118545.1 GAUT13 (Galacturonosyltransferase 13) [<i>Arabidopsis thaliana</i>]			
0.4	ref NP_186753.2 GAUT13 (Galacturonosyltransferase 13); polygalacturonase			
0.3	ref NP_194113.1 glycoside hydrolase family 28 protein / polygalacturonase			
0.5	gb ACF05806.1 Pectin acetyl esterase [<i>Litchi chinensis</i>]			
0.2	gb AAT40110.1 putative UDP-glucuronate decarboxylase 4 [<i>Nicotiana</i> spp.]			
0.1	dbj BAD91079.1 beta-D-galactosidase [<i>Pyrus pyrifolia</i>]			
0.3	ref NP_197193.1 ATCSLD2 (Cellulose synthase-like D2); cellulose.	6.5	gb AAZ79231.1 cellulose synthase-like protein CslG [<i>Nicotiana tabacum</i>]	
0.3	sp A2YU42.1 CSLD2_ORYSI RecName: Full=Cellulose synthase-like protein	1.9	gb AAK49454.1 AF304374_1 cellulose synthase catalytic subunit	
0.5	gb AAZ60847.1 cellulose synthase 5 [<i>Eucalyptus grandis</i>]			
0.1	ref NP_193893.1 glycine-rich protein [<i>Arabidopsis thaliana</i>]	2.2	gb ABG76000.1 GRP-like protein 2 [<i>Gossypium hirsutum</i>]; glycine-rich protein	

0.2	ref NP_190109.1 hydroxyproline-rich glycoprotein family protein		
0.3	gb AAM65462.1 glycine rich protein-like [Arabidopsis thaliana]		
0.2	dbj BAC67189.1 expansin [Pyrus communis]	2.8	ggb AAR09170.1 alpha-expansin 3 [Populus tremula x Populus tremula]
0.3	gb AAN87551.1 AF376053_1 gamma-tubulin [Lupinus albus]	2.1	ref NP_567094.1 ADL4/ADLP2/DRP1E/EDR3 (DYNAMIN-LIKE PROTEIN 4)
0.3	ref NP_176252.1 dynamin family protein [Arabidopsis thaliana]	1.9	gb AAF35902.1 AF230333_1 expansin 3 [Zinnia elegans]
0.1	gb ABO28522.1 kinesin-related protein [Gossypium hirsutum]	5.2	sp Q9ZPN9.1 TBB2_ELEIN Tubulin beta-2 chain (Beta-2-tubulin)
0.2	dbj BAB40710.1 BY-2 kinesin-like protein 10 [Nicotiana tabacum]		
0.4	gb ACG39191.1 actin-1 [Zea mays]		
0.5	dbj BAA82639.1 Beta-tubulin [Zinnia elegans]		
0.1	sp P51074.2 ANX4_FRAAN RecName: Full=Annexin-like protein		
0.1	sp P83304.1 LEC_PARPC RecName: Full=Mannose/glucose-specific lectin	4.1	dbj BAB18761.1 lectin [Helianthus tuberosus]
0.1	emb CAA61158.1 SIEP1L protein [Beta vulgaris subsp. vulgaris], LECTIN	3.2	gb ABA94728.1 Jacalin-like lectin domain containing protein
0.3	gb AAT37529.1 purple acid phosphatase 1 [Solanum tuberosum]		
0.4	gb ABD28734.1 UDP-N-acetylglucosamine transferase subunit ALG14		
0.2	gb AAL77689.1 AT5g55180/MCO15_13 [Arabidopsis thaliana]; O-glycosyl transferase family 17		
0.4	gb ACG27548.1 heparanase-like protein 2 precursor [Zea mays]		
0.3	gb AAP97493.1 UDP-Glc-4-epimerase [Solanum tuberosum]		
		11.9	ref NP_176737.2 ATHEX1/HEXO3 (BETA-HEXOSAMINIDASE 3);
		4.5	ref NP_683538.1 glycosyl hydrolase family 17 protein [Arabidopsis thaliana]
		2.1	gb ACC91241.1 aldose 1-epimerase family protein [Arabidopsis thaliana]
PRIMARY/ SECONDARY METABOLISM			
0.5	gb AAB99757.1 malate dehydrogenase precursor [Medicago sativa]; partitioning of carbon and energy in leaves	4.5	sp P46488.1 MDHG_CUCSA RecName: Full= Malate dehydrogenase , glyoxysomal
		5.9	sp Q05145.1 MDHP_MESCR RecName: Full= Malate dehydrogenase [NADP]
		8.6	emb CAD33240.1 putative mitochondrial NAD-dependent malate dehydrogenase
0.1	ref NP_190421.1 CYP94B3 (cytochrome P450, family 94, subfamily	1.6	ref NP_563789.1 SMO2-2 (sterol 4-alpha-methyl-oxidase 2); C-4 m.
0.1	ref ZP_01308190.1 methyl-accepting chemotaxis domain/unknown domain	7.1	sp P46255.1 DCAM_SPIOL RecName: Full=S-adenosylmethionine decarboxylase

0.5	sp P49297.1 ACEA_SOLLC RecName: Full=Isocitrate lyase (Glioxyate cycle associate with senescence)	1.5	pdb 2AKJ A Chain A, Structure of spinach Nitrite Reductase; coordination of nitrogen and carbon metabolism
0.1	gb AAP74755.1 chalcone synthase [<i>Gypsophila paniculata</i>]	2.8	ATPDX2/EMB2407/PDX2 (PYRIDOXINE BIOSYNTHESIS 2)
0.3	ref NP_197195.2 AAA-type ATPase family protein [<i>Arabidopsis thaliana</i>]	3.1	gb ACF17659.1 putative 3-isopropylmalate dehydrogenase small subunit
0.1	ref NP_173857.2 methyltransferase [<i>Arabidopsis thaliana</i>]	3.9	dbj BAD80839.1 2-Hydroxyisoflavanone dehydratase [<i>Glycyrrhiza</i> spp.]
0.1	dbj BAE92730.1 3-hydroxy-3-methylglutaryl coenzyme A reductase	1.5	emb CAC33003.1 urease accessory protein G [<i>Solanum tuberosum</i>]; nitrogen recycling
0.1	gb AAP96920.1 pyruvate decarboxylase [<i>Dianthus caryophyllus</i>]	1.6	gb ABC02881.1 ACS2 [<i>Ricinus communis</i>]; Acyl-CoA synthetase
0.3	gb ABK76265.1 beta-amyrin synthase [<i>Vaccaria hispanica</i>], saponins, drought stress	2.1	gb AAT12274.1 putative 14alpha-demethylase [<i>Solanum chacoense</i>]
0.2	gb AAC06319.1 putative cinnamyl alcohol dehydrogenase [<i>Malus</i> spp.]	5.3	ref NP_172724.2 membrane bound O-acyl transferase (MBOAT) family
0.3	ref NP_188226.1 A37 (PYRIDOXINE BIOSYNTHESIS 1.2)	2.6	ref NP_567228.1 epoxide hydrolase, putative [<i>Arabidopsis thaliana</i>]
0.2	sp Q07510.1 FABH_SPIOL RecName: Full=3-oxoacyl-[acyl-carrier-protein	3.1	sp Q84KI6.1 SQD1_SPIOL RecName: Full=UDP-sulfoquinovose synthase.
0.3	gb ABC74567.1 acetoacetyl-CoA thiolase [<i>Picrorhiza kurrooa</i>]	5.5	emb CAC91565.1 hydroperoxide lyase [<i>Nicotiana attenuata</i>]
0.3	sp O65162.1 CAMT_MESCR RecName: Full=Caffeoyl-CoA O-methyltransferase	1.9	gb AAR29980.1 sterol delta-7 reductase [<i>Tropaeolum majus</i>]
0.3	emb CAD23248.1 squalene monooxygenase 2 [<i>Medicago truncatula</i>]	1.9	ref NP_566011.1 MTHFR2 (METHYLENETETRAHYDROFOLATE REDUCTASE 2)
0.3	gb ACC63870.1 coumaroyl 3-hydroxylase [<i>Populus trichocarpa</i>]	4.5	gb ACB56924.1 glycosyltransferase UGT88A8 [<i>Hieracium pilosella</i>]
0.4	dbj BAF98285.1 diphosphomevelonate decarboxylase [<i>Hevea brasiliensis</i>]		
0.5	gb AAC49114.1 acetyl-CoA carboxylase biotin-containing subunit		
0.2	gb AAP96921.1 alcohol dehydrogenase [<i>Dianthus caryophyllus</i>]		
0.5	dbj BAF98279.1 hydroxymethylglutaryl-CoA synthase [<i>Hevea brasiliensis</i>]		
0.1	tpe CAI56335.1 TPA: isoflavone reductase-like protein 6 [<i>Vitis</i> spp.]		
0.2	gb AAF76143.1 AF258339_4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplastic/chromoplastic		
0.1	gb ABB89006.1 CXE carboxylesterase [<i>Malus pumila</i>]		
RNA-DNA BINDING PROTEINS			
0.1	ref NP_565175.1 RNA recognition motif (RRM)-containing protein	1.5	chloroplast RNA binding protein [<i>Arabidopsis thaliana</i>].
0.1	ref NP_177158.1 DNA-binding family protein [<i>Arabidopsis thaliana</i>]	3.1	dbj BAG09558.1 chloroplast RNA binding protein [<i>Mesembryanthemum</i> sp.]
0.5	dbj BAA22083.1 RNA binding protein [<i>Nicotiana sylvestris</i>]		
PHYTOHORMONE-RELATED (development/ stress)			
0.3	ref NP_200336.1 IAMT1 (IAA CARBOXYLMETHYLTRANSFERASE 1); converts IAA to methyl-IAA ester (MeIAA) <i>in vitro</i> ,	5.0	gb ACL81167.1 auxin-responsive protein IAA1 [<i>Mirabilis jalapa</i>]

	suggesting that methylation of IAA plays an important role in regulating plant development and auxin homeostasis.		
0.2	gb ABL67651.1 putative auxin-repressed/dormancy-associated protein		
0.4	gb ACL81159.1 putative auxin/aluminum-responsive protein		
0-4	gb ABN81351.1 auxin influx transport protein [<i>Casuarina glauca</i>]		
0.2	gb ABB52080.1 putative 9-cis epoxycarotenoid dioxygenase (ABA biosynthesis)	2.6	sp Q40412.1 ABA2_NICPL RecName: Full=Zeaxanthin epoxidase; ABA biosynthesis
		2.1	gb AAP41850.1 1-aminocyclopropane-1-carboxylate oxidase [<i>Hevea</i> sp.] (ethylene biosynthesis)
0.1	gb AAP83138.1 lipoxygenase [<i>Nicotiana attenuata</i>]	6.5	gb AAP83137.1 lipoxygenase [<i>Nicotiana attenuata</i>] (jasmonic acid)
0.3	ref NP_568914.1 gibberellin-regulated family protein [<i>Arabidopsis thaliana</i>]		
0.3	emb CAB45241.1 GEG protein [Gerbera hybrid cultivar]; Gerbera hybrid homolog of the gibberellin [GA]-stimulated transcript 1 [GAST1] from tomato		
0.1	ref NP_191705.1 BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein		
0.1	ref NP_197535.2 TIP1 (TIP GROWTH DEFECTIVE 1) [<i>Arabidopsis thaliana</i>]	5.6	gb ACC95130.1 COL2 [<i>Beta vulgaris</i> subsp. vulgaris]; Constans-like protein
		6.7	ref NP_569012.2 GRF8 (GENERAL REGULATORY FACTOR 8); 14:3:3. This protein is reported to interact with the BZR1 transcription factor involved in brassinosteroid signaling and may affect the nucleocytoplasmic shuttling of BZR1.
		7.6	ref NP_851274.1 GRF8 (GENERAL REGULATORY FACTOR 8).
STRESS-RELATED			
0.1	sp P09887.1 HS22C_SOYBN RecName: Full= Small heat shock protein	2.4	gb AAB62947.1 LTCOR11 [<i>Lavatera thuringiaca</i>], cold-responsive
0.1	ref NP_565824.1 DNAJ heat shock N-terminal domain-containing protein	2.2	dbj BAB70509.1 DNAJ homoue [<i>Oryza sativa</i>]
0.3	ref NP_195570.1 ATEP6 (FARNESYLATED PROTEIN 6); metal ion binding; ACBP2-overexpressing plants were more tolerant to hydrogen peroxide than wild-type plants, further supporting a role for ACBP2 in post-stress membrane repair.		ref NP_568342.1 ENH1 (ENHANCER OF SOS3-1); metal ion binding, enhanced salinity tolerance by excluding Na⁺ from the cytosol
0.4	gb ACK99529.1 LEA protein [<i>Knorringia sibirica</i>]	3.7	gb AAT01418.1 putative stress-responsive protein [<i>Tamarix</i> sp.]
0.1	gb ABB02409.1 chloroplast lipocalin [<i>Ipomoea nil</i>]		gb AAO72532.1 aldehyde dehydrogenase 1 precursor [<i>Lotus</i> sp.]; Different plant ALDH genes have been reported to respond to environmental stress conditions such as dehydration, salinity, or excessive light

0.3	gb AAC69177.1 peroxisomal targeting signal 1 receptor	1.7	gb ACF06568.1 disulfide-isomerase precursor-like protein; chaperone
0.3	ref NP_174368.1 CTP synthase, putative / UTP--ammonia ligase, glutamine synthetase, salt stress	1.6	ref NP_175812.1 ALDH7B4 (ALDEHYDE DEHYDROGENASE 7B4)
0.4	ref NP_030521.1 dehydration-responsive family protein [<i>Arabidopsis thaliana</i>]	1.6	gb AAX09646.1 aldehyde dehydrogenase family 7 member A1
0.3	ref NP_001119417.1 glucose-methanol-choline (GMC) oxidoreductase	2.1	ref NP_192626.1 arginase, putative [<i>Arabidopsis thaliana</i>]
0.1	emb CAR67806.1 Chaperone protein htpG (Heat shock protein htpG)	2.2	emb CAC85228.1 salt tolerance protein 2 [<i>Beta vulgaris</i>]
0.1	ref NP_179374.1 ERD7 (EARLY-RESPONSIVE TO DEHYDRATION 7) [<i>Arabidopsis thaliana</i>]	3.9	ref NP_564093.1 wound-responsive family protein [<i>Arabidopsis thaliana</i>]
0.1	gb ACH87168.1 senescence-related protein [<i>Camellia sinensis</i>]	3.5	gb AAR17080.1 heat shock protein 70-3 [<i>Nicotiana tabacum</i>]
0.4	gb ABX60218.1 heat shock protein [<i>Ammopiptanthus mongolicus</i>]	3.8	sp P17202.1 BADH_SPIOL RecName: Full= Betaine aldehyde dehydrogenase
0.2	dbj BAA11766.1 high mobility group protein [<i>Canavalia gladiata</i>]	4.9	gb ABB02383.1 temperature-induced lipocalin' [<i>Solanum lycopersicum</i>]
0.1	ref NP_568974.1 AFTP3 (<i>Arabidopsis thaliana</i> farnesylated protein)	4.1	gb AAA87042.1 putative 32.7 kDa jasmonate-induced protein [<i>Hordeum vulgare</i>]
0.5	gb AAA61609.1 pyrophosphatase [<i>Beta vulgaris</i>]	10.8	gb ABC26011.1 carotenoid cleavage dioxygenase 4a [<i>Citrus clementine</i>]
TRANSCRIPTION FACTORS			
0.1	gb ABO48369.1 TINY-like protein 2 [<i>Populus trichocarpa</i>], AP2/ERF		
0.1	ref NP_188299.1 ATEBP/ERF72/RAP2.3 (RELATED TO AP2 3); DNA binding		
0.1	gb AAV66332.1 ethylene response factor 1 [<i>Cucumis sativus</i>]		
0.2	gb AAK92213.1 bZIP transcription factor BZI-2 [<i>Nicotiana tabacum</i>]		
0.5	ABSCISIC ACID-INSENSITIVE 5-like protein 5//AREB-like protein//bZIP transcription factor//abscisic acid responsive elements-binding factor 2		
0.1	ref NP_849712.1 transcription regulator [<i>Arabidopsis thaliana</i>]	2.1	gb ABV53916.1 GAGA-motif binding transcriptional activator
0.1	gb AAY40250.1 Cys2/His2 zinc-finger transcription factor [<i>Silene latifolia</i>]	3.5	gb ABN05686.1 Zinc finger, CCHC-type [<i>Medicago truncatula</i>]
0.2	dbj BAD06717.1 WRKY transcription factor 1 [<i>Spinacia oleracea</i>]		
0.2	gb AAY90122.1 basic helix-loop-helix transcription factor protein		
0.5	gb AAZ30376.1 PHB1 [<i>Nicotiana benthamiana</i>], prohibitin		
TRANSPORT			
0.3	dbj BAD91179.1 putative mitochondrial dicarboxylate transporter	2.6	ref NP_187290.1 integral membrane family protein [<i>Arabidopsis thaliana</i>]
0.1	gb AAT35231.1 nodulin 26-like protein [<i>Medicago truncatula</i>]	1.9	sp P93690.1 SECY_SPIOL RecName: Full=Preprotein translocase subunit
0.1	ref NP_200682.1 nuclear movement family protein [<i>Arabidopsis thaliana</i>]	2.5	sp P42767 PIP1_ATRCA Aquaporin PIP-type
0.4	dbj BAB11940.1 Na/H antiporter Nhx1 [<i>Atriplex gmelini</i>]	1.5	ref NP_566180.1 integral membrane family protein [<i>Arabidopsis thaliana</i>]

0.4	gb AAD31848.1 AF133532.1 water channel protein MipK [<i>Mesembryanthemum crystallinum</i>]	2.1	ref NP_201094.1 permease, putative [<i>Arabidopsis thaliana</i>]
0.2	sp Q43748.1 NLTP_BETVU RecName: Full=Non-specific lipid-transfer	5.1	gb AAB67869.1 plasma membrane major intrinsic protein 2 [<i>Beta vulgaris</i>]
0.3	gb AAB95302.1 putative nitrate transporter [<i>Arabidopsis thaliana</i>]	2.1	dbj BAD29977.1 putative ammonium transporter [<i>Camellia sinensis</i>]
0.1	ref NP_179257.1 nodulin family protein [<i>Arabidopsis thaliana</i>]	1.5	ref NP_566806.1 YSL6 (YELLOW STRIPE LIKE 6); oligopeptide transporter
0.3	ref NP_568091.2 CAX4 (cation exchanger 4); cation:cation antiporter	4.6	emb CAC84547.1 dicarboxylate/ tricarboxylate carrier [<i>Nicotiana</i> spp.]
		4.5	emb CAD92450.1 amino acid permease 6 [<i>Brassica napus</i>]
		2.1	gb ACF06527.1 secretory carrier membrane protein [<i>Elaeis</i> spp.]
		5.5	emb CAN99590.1 Na⁺/H⁺ antiporter [<i>Mesembryanthemum crystallinum</i>]
		6.7	dbj BAD91181.1 putative mitochondrial adenylate transporter.
		7.1	BAD91180.1 putative plastidic ANT1 - ADP,ATP carrier protein - [<i>Mesembryanthemum crystallinum</i>]
		15.4	ref NP_182239.1 ARF1A1c (ADP-RIBOSYLATION FACTOR 1); GTP binding
CARBOHYDRATE METABOLISM			
0.2	gb ABR87939.1 sucrose synthase 1 [<i>Beta vulgaris</i>]	1.8	ref NP_195020.1 GAMMA-VPE (Vacuolar processing enzyme gamma)
0.1	ref YP_534971.1 neopullulanase / cyclomaltodextrinase / maltoge.	1.5	dbj BAD93291.1 beta-amylase [<i>Glycine max</i>]
0.2	emb CAA59464.1 alpha-glucan phosphorylase [<i>Spinacia oleracea</i>]	2.7	gb AA989374.1 beta-amylase 1 [<i>Nicotiana langsdorffii</i> x <i>Nicotiana</i>]
		4.9	dbj BAA09462.1 beta-amylase [<i>Glycine max</i>]
		6.9	gb ACH72975.1 granule-bound starch synthase [<i>Nelumbo nucifera</i>]
		7.7	dbj BAD91175.1 plastidic glucose 6-phosphate/phosphate translocator
		2.1	gb ACF04278.1 UTP-glucose 1 phosphate uridylyltransferase; gluconeogenesis .
GLYCOLYSIS			
0.2	gb AAA80675.1 fructokinase [<i>Beta vulgaris</i>]	1.8	emb CAA53507.1 phosphoglucomutase [<i>Spinacia oleracea</i>]
		2.4	sp P22418.2 F16P1_SPIOL RecName: Full=Fructose-1,6-bisphosphatase
		4.4	ref XP_001351443.1 phosphoglycerate mutase
		5.4	glyceraldehyde-3-phosphate dehydrogenase; glycolysis
		2.3	gb AAC18055.1 fructose-6-phosphate 2-kinase /fructose-2,6-bisphosphatase
		8.5	sp P14766.2 F16P2_SPIOL RecName: Full=Fructose-1,6-bisphosphatase
		4.3	emb CAA03982.1 glucose-6-phosphate isomerase [<i>Spinacia oleracea</i>]
		2.5	gb AAB61592.1 fructose-biphosphate aldolase [<i>Mesembryanthemum</i> spp.]
		3.1	gb AAR24912.1 fructokinase 3 [<i>Solanum lycopersicum</i>]

	4.9	sp P29356.1 ALF_SPIOL RecName: Full=Fructose-bisphosphate aldolase	
	9.9	sp P29409.2 PGKH_SPIOL RecName: Full=Phosphoglycerate kinase	
SUGAR TRANSPORT			
	1.5	gb AAB68029.1 putative sugar transporter; member of major facilitator family	
	1.6	N3 - Bidirectional sugar transporter SWEET – [<i>Glycine max</i>]	
	22.6	emb CAA58730.1 sucrose/proton-symporter [<i>Beta vulgaris</i>]	
	3.4	emb CAB52689.1 hexose transporter [<i>Solanum lycopersicum</i>]	
	17.1	gb AAF86907.1 AF223359_1 phosphoenolpyruvate/phosphate translocator	
DEFENSE			
0.4	gb AAY15221.1 antifungal protein [<i>Sinapis alba</i>]	1.6	gb ABK58702.1 anti-microbial protein 2 [<i>Amaranthus caudatus</i>]
0.1	ref NP_192169.1 ATMLO1/MLO1 (MILDEW RESISTANCE LOCUS O 1)	7.8	gb AAW48295.1 pore-forming toxin-like protein Hfr-2 [<i>Triticum aestivum</i>]
0.4	sp P82010.1 AX2_BETVU RecName: Full=Antifungal protein	1.8	emb CAB56619.1 phragmoplastin [<i>Nicotiana tabacum</i>]; callose deposition
0.5	gb AAP03878.1 Avr9/Cf-9 rapidly elicited protein 189 [<i>Nicotiana spp.</i>]	2.5	gb AAR26482.1 harpin binding protein 1 [<i>Malus x domestica</i>]
0.3	dbj BAB86893.1 syringolide-induced protein 1-3-1B [<i>Glycine max</i>]	3.2	gb ACK38253.1 pathogenesis-related protein [<i>Tamarix hispida</i>]
0.1	gb AAB48305.1 Hs1pro-1 [<i>Beta procumbens</i>]	1.5	gb AAC61805.1 Pto kinase interactor 1 [<i>Solanum lycopersicum</i>]
0.3	gb AAD13216.1 latex-abundant protein [<i>Hevea brasiliensis</i>]	2.6	ref NP_973870.1 pathogenesis-related thaumatin family protein
0.3	gb ABS01349.1 hypersensitive-induced response protein [<i>Carica papaya</i>]	21.3	dbj BAA22966.1 chitinase [<i>Chenopodium amaranticolor</i>]
0.5	emb CAJ44458.1 ALY protein [<i>Nicotiana benthamiana</i>] 197 3e-48	5.5	sp P42820.1 CHIP_BETVU RecName: Full=Acidic endochitinase SP2
AMINES/ AMINOACID METABOLISM/ SYNTHESIS			
0.1	gb ABN08767.1 Amine oxidase [<i>Medicago truncatula</i>] 594 e-168	3.1	emb CAA45022.1 aspartate aminotransferase [<i>Panicum miliaceum</i>]
0.5	gb ABI35986.1 methionine synthase [<i>Phelipanche ramosa</i>]	1.8	gb AAA18948.1 ferredoxin-dependent glutamate synthase (GLUTAMATE)
		1.9	gb AAC19395.1 cystathionine gamma-synthase [<i>Mesembryanthemum spp.</i>] (METHIONINE)
		1.8	gb ABW76425.1 branched-chain aminotransferase [<i>Nicotiana benthamiana</i>]
		4.3	gb ABS72164.1 acetolactate synthase [<i>Amaranthus hypochondriacus</i>]; branched amino acids
		5.3	gb AAD31898.1 AF145480_1 glutamine synthetase leaf
		2.2	gb AAK14401.1 AF343667_1 cytosolic glutamine synthetase [<i>Beta vulgaris</i>]
		6.1	sp Q00834.1 CYSK_SPIOL RecName: Full=Cysteine synthase.
		5.7	emb CAA47329.1 cysteine synthase [<i>Spinacia oleracea</i>]
		18.8	sp P93263.1 METE_MESCR RecName: 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase; methionine synthesis

ANTIOXIDANTS			
0.1	gb ABO77632.1 peroxidase [<i>Medicago truncatula</i>]	3.6	gb ABA00455.1 MnSOD [<i>Gossypium hirsutum</i>]
0.2	gb AAF63025.1 AF244922_1 peroxidase prx13 precursor [<i>Spinacia oleracea</i>]	7.3	gb ABL60875.1 germin-like protein 6 [<i>Vitis vinifera</i>]
0.3	emb CAA71494.1 peroxidase [<i>Spinacia oleracea</i>]	2.3	dbj BAF36564.1 alternative oxidase [<i>Nicotiana tabacum</i>]
0.5	emb CAA71495.1 peroxidase [<i>Spinacia oleracea</i>]	3.1	ref NP_181046.1 ATO1 (Arabidopsis THIOREDOXIN O1)
		3.1	dbj BAA08535.1 ascorbate peroxidase [<i>Spinacia oleracea</i>]
		4.5	dbj BAG84436.1 NADP-dependent isocitrate dehydrogenase
		1.9	emb CAC82727.1 monodehydroascorbate reductase [<i>Mesembryanthemum</i> spp.]
		4.2	ref NP_567725.1 ACD1-LIKE; electron carrier [<i>Arabidopsis thaliana</i>]
		2.8	ref NP_568630.1 ATARD4; acireductone dioxygenase
		4.6	ref NP_849444.1 ACD1-LIKE; electron carrier [<i>Arabidopsis thaliana</i>]
		1.9	sp Q04522.3 GSTF_SILCU RecName: Full= Glutathione S-transferase
		3.1	emb CAA57973.1 class III ADH, glutathione-dependent formaldehyde dehydrogenase
		4.6	emb CAK22416.1 cationic peroxidase [<i>Beta vulgaris</i>]
		2.4	emb CAA71491.1 peroxidase [<i>Spinacia oleracea</i>]
		12.7	gb AAK67359.2 AF390210_1 catalase [<i>Suaeda maritima</i> subsp. <i>salsa</i>]
		8.9	gb AAO61856.1 glutathione S-transferase Z1 [<i>Malva pusilla</i>]
		6.3	ref NP_180873.1 KAT2/PED1 (PEROXISOME DEFECTIVE 1)
		5.8	sp O23814.1 GPX4_SPIOL RecName: Full= Probable phospholipid hydroperoxide glutathione peroxidase
		10.8	emb CAC17803.1 peroxiredoxin [<i>Phaseolus vulgaris</i>]
		6.3	gb AAA99518.1 ascorbate peroxidase
		6.4	emb CAA71490.1 peroxidase [<i>Spinacia oleracea</i>]
		7.4	sp P22233.1 SODC_SPIOL RecName: Full= Superoxide dismutase [Cu-Zn]
		13	gb AAS92464.1 Fe-superoxide dismutase 1 precursor [<i>Lotus japonicus</i>]
		18.4	emb CAE22480.1 superoxide dismutase [Fe] [<i>Solanum</i> [<i>Solanum lycopersicum</i>]]
		53.8	gb AAC19398.1 root catalase [<i>Mesembryanthemum crystallinum</i>]
PROTEIN DEGRADATION/ MODIFICATION			
0.3	tpe CAG29028.1 TPA: putative cystatin [<i>Zea mays</i>]	11	gb ABQ10199.1 cysteine protease Cp1 [<i>Actinidia deliciosa</i>]
		9.7	gb ABQ10204.1 cysteine protease Cp6 [<i>Actinidia deliciosa</i>]
		33.7	dbj BAD29954.1 cysteine protease [<i>Daucus carota</i>]
		7.9	emb CAD59764.1 cysteine proteinase inhibitor [<i>Celosia cristata</i>]
		9.0	gb AAF61440.1 AF138264_1 papain-like cysteine proteinase isoform.
		2.2	gb ABD28731.1 C2; Peptidase, cysteine peptidase active site

0.1	dbj BAC66627.1 F-box [<i>Prunus mume</i>]	1.6	sp O24361.1 PSB5_SPIOL RecName: Full= Proteasome subunit beta
0.2	gb ACL14907.1 L-isoaspartyl methyltransferase 2 TIS II alpha-om.	2.1	ref NP_568892.1 FTSH9 (FtsH protease 9) ; ATP-dependent peptidase
0.1	pir IJC5562 trypsin inhibitor ETIb precursor - <i>Erythrina variegata</i>	20.1	dbj BAB20972.1 aspartic proteinase 4 [<i>Nepenthes alata</i>]
0.5	sp O49939.1 TLP40_SPIOL RecName: Full=Peptidyl-prolyl cis-trans isomerase, chloroplastic PPIases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides. Has a regulatory effect on thylakoid protein phosphorylation.		
0.5	gb ABI84264.1 ubiquitin-conjugating enzyme [<i>Arachis hypogaea</i>]		
0.1	emb CAC86004.1 aspartic proteinase [<i>Theobroma cacao</i>]		
RNA/ DNA DEGRADATION/ MODIFICATION/ EPIGENETIC CONTROL			
0.2	ref NP_195467.1 ribonuclease III family protein [<i>Arabidopsis thaliana</i>]	4.2	gb AAM62421.1 AF515795_1 Drm3 [<i>Pisum sativum</i> ; Encodes DRM3 (Domains Rearranged Methyltransferase3), a catalytically mutated paralog of the cytosine methyltransferase DRM2. Despite being catalytically mutated, DRM3 is required for normal maintenance of non-CG DNA methylation: Chromatin-Based Epigenetic Regulation of Plant Abiotic Stress Response.
0.5	ref NP_565843.1 inosine-uridine preferring nucleoside hydrolase	1.6	emb CAC43291.1 putative linker histone H1 variant protein [<i>Beta vulgaris</i>]
0.3	ref XP_002171493.1 DNA ligase [<i>Schizosaccharomyces japonicas</i>]	2.1	gb ACK75561.1 allantoate amidohydrolase [<i>Glycine max</i>]; recycling purine-ring nitrogen in all plants
0.4	gb ACG39790.1 pre-mRNA-splicing factor 19 [<i>Zea mays</i>]	1.7	gb ABD32395.1 Histone-fold/TFIID-TAF/NF-Y [<i>Medicago truncatula</i>]
0.1	gb AAP31307.1 histone H1 [<i>Lens nigricans</i>]	2.9	sp P0C2M6.1 DED1_EMENI RecName: Full=ATP-dependent RNA helicase.
		7.1	ref NP_001078516.1 histone H3.2 [<i>Arabidopsis thaliana</i>]
LIPID MODIFICATION/ DEGRADATION			
FATTY ACID DESATURASES			
		6.9	gb AAM63459.1 putative delta 9 desaturase [<i>Arabidopsis thaliana</i>]
		3.6	gb ABG88131.1 chloroplast omega-3 fatty acid desaturase
		3.6	gb ABL61262.1 chloroplast omega-3 desaturase [<i>Portulaca oleracea</i>]
		4.2	emb CAK54360.1 putative desaturase-like protein [<i>Trifolium repens</i>]
		8.7	gb ABS86965.1 delta-9 fatty acid desaturase [<i>Descurainia sophia</i>]
WAX SYNTHESIS			
		2.7	gb AAZ08051.1 wax synthase [<i>Petunia x hybrida</i>]
		1.5	gb AAY23355.1 3-ketoacyl-CoA reductase 2 [<i>Gossypium hirsutum</i>]; Very-long-chain fatty acids (VLCFAs) are essential precursors of cuticular waxes and aliphatic suberins in roots.

0.1	gb ABD32376.1 Lipolytic enzyme, G-D-S-L [<i>Medicago truncatula</i>]	3.7	sp P52877.1 SERC_SPIOL RecName: Full=Phosphoserine aminotransferase
0.1	gb AAP55714.1 GDSL-lipase [<i>Chenopodium rubrum</i>]	2.1	gb AAB53764.1 aminoalcohol phosphotransferase [<i>Brassica rapa</i>], phospholipids
0.5	ref ZP_01692219.1 glycerophosphoryl diester phosphodiesterase		
SIGNALING			
KINASES/ PHOSPHATASES/ OTHERS			
0.1	emb CAB82852.1 protein kinase MK6 [<i>Mesembryanthemum crystallinum</i>]	4.6	ref NP_199595.1 AMK2 (ADENOSINE MONOPHOSPHATE KINASE); AMPK plays critical roles in regulating growth and reprogramming metabolism.
0.1	emb CAB89490.1 CRK1 protein [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>]; The CDPK-related kinases (CRKs) are a type of serine-threonine kinases belonging to the CDPK-SnRK superfamily.		
0.1	gb AAK62444.1 AF386999_1 similar to wpk4 protein kinase [<i>Arabidopsis thaliana</i>]; The first identified serine/threonine protein kinase, which according to Halford and Hardie (1998) belongs to the SnRK3 subfamily, was WPK4 from wheat.		
0.1	emb CAC82999.1 calcium-dependent protein kinase 3 [<i>Nicotiana tabacum</i>]		
0.2	emb CAC24490.1 choline kinase [<i>Pisum sativum</i>]		
0.4	gb AAD31900.1 AF145482_1 putative serine/threonine protein kinase		
0.3	gb ABW80999.1 PI-phospholipase C PLC5 [<i>Solanum lycopersicum</i>]	1.7	emb CAC10358.1 protein phosphatase 2C [<i>Nicotiana tabacum</i>]
		3.4	gb AAC36700.1 protein phosphatase-2C ; PP2C [<i>Mesembryanthemum spp.</i>]
		2.3	gb AAD11430.1 protein phosphatase 2C homo [<i>Mesembryanthemum spp.</i>]
0.3	ref NP_201227.3 calmodulin-binding protein [<i>Arabidopsis thaliana</i>]	2.1	sp O81919.1 CALR_BETVU RecName: Full=Calreticulin;
0.2	gb ABM55247.1 calmodulin-binding protein [<i>Beta vulgaris</i>]		
RECEPTOR-LIKE KINASES			
0.2	gb AAL40864.1 receptor protein kinase-like protein [<i>Capsicum annuum</i>]		
0.2	gb ABY40731.1 FERONIA receptor-like kinase [<i>Poncirus trifoliata</i>]		
0.2	dbj BAE46451.1 putative receptor protein kinase PERK1 [Glycine]; The proline-rich, extensin-like receptor kinase-1; wound-inducible.		
0.1	ref NP_196408.2 leucine-rich repeat family protein	5.7	ref NP_175397.1 leucine-rich repeat family protein [<i>Arabidopsis thaliana</i>]
INOSITOL METABOLISM			
0.4	sp O49071.1 IMPP_MESCR RecName: Full= Inositol monophosphatase		
0.5	gb AAL28131.1 AF433879_1 myo-inositol-1- phosphate synthase [<i>Suaeda salsa</i>]		
PHOTOSYNTHESIS/ ENERGY/ PHOTORESPIRATION			
0.3	sp Q9XGX4.1 RBS3_AMAHP RecName: Full= Ribulose biphosphate carboxylase	1.7	sp P16016.2 CAHC_SPIOL RecName: Full=Carbonic anhydrase, chloroplast

0.3	emb CAK18840.1 subunit IV of photosystem I (PSI-E) precursor	6.6	sp P37224.1 MAOM_AMAHP RecName: Full=NAD-dependent malic enzyme
0.4	emb CAA04157.1 Rieske iron-sulfur protein Tic55 [<i>Pisum sativum</i>]	5.4	sp P52765.1 NU3C_LUPLU RecName: Full=NAD(P)H-quinone oxidoreductase
0.3	ref NP_194457.2 quinone reductase family protein [<i>Arabidopsis t.</i>]	2.5	sp P00289.2 PLAS_SPIOL RecName: Full=Plastocyanin, chloroplastic
0.3	sp Q41014.2 FENR2_PEA RecName: Full= Ferredoxin--NADP reductase	1.6	gb AAL77589.1 L43068_1 chloroplast ribose-5-phosphate isomerase
		3.0	emb CAA29590.1 Rieske FeS-precursor [<i>Spinacia oleracea</i>]
		3.2	sp P10690.1 PSBR_SPIOL RecName: Full= Photosystem II 10 kDa polypeptide
		1.7	gb AAT02656.1 mitochondrial pyruvate dehydrogenase kinase isoform
		2.0	sp P41348.2 FTRC1_SPIOL RecName: Full= Ferredoxin-thioredoxin reductase
		15.1	gb AAM78591.1 Rubisco activase [<i>Chenopodium quinoa</i>]
		1.9	sp Q9SM43.2 VDE_SPIOL RecName: Full= Violaxanthin de-epoxidase
		2.4	sp P12357.1 PSAG_SPIOL RecName: Full= Photosystem I reaction center
		1.7	ref NP_189086.1 HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE 101)
		2.1	gb ABD52327.1 plastid protoporphyrinogen oxidase [<i>Amaranthus ssp.</i>]
		3.2	gb AAB40396.1 glycolate oxidase [<i>Mesembryanthemum crystallinum</i>]
		3.1	gb ACK56136.1 transaldolase [<i>Dimocarpus longan</i>]; Calvin cycle
		7.5	gb AAB95218.1 putative serine-glyoxylate aminotransferase
		2.4	gb ABA54865.1 putative 3-deoxy-D-arabino-heptulosonate 7-phosphate phosphatase
		3.6	gb ACF06473.1 light-inducible protein ATLS1 [<i>Elaeis guineensis</i>]
		5.0	emb CAA04526.1 magnesium chelatase subunit [<i>Glycine max</i>]
		2.7	emb CAC43293.1 putative phosphoenolpyruvate carboxylase kinase
		2.1	ref NP_191434.1 CSY2 (CITRATE SYNTHASE 2)
		2.4	gb ACG31979.1 mo-molybdopterin cofactor sulfurase [<i>Zea mays</i>]
		3.1	ref NP_181092.1 plastid-lipid associated protein PAP
		9.9	sp P05435.2 ATPG_SPIOL RecName: Full=ATP synthase gamma chain
		5.9	ref NP_564093.1 wound-responsive family protein [<i>Arabidopsis thaliana</i>] sp O20250.1 TKTC_SPIOL RecName: Full=Transketolase, chloroplastic; Calvin cycle
		3.1	sp P21239.2 RUB1_BRANA RecName: Full= RuBisCO large subunit
		2.6	emb CAJ77390.1 major chlorophyll a/b binding protein LHCb1.2
		8.0	sp P12355.1 PSAF_SPIOL RecName: Full= Photosystem I reaction center subunit III, chloroplastic.
		4.6	emb CAA96568.1 CP12 [<i>Spinacia oleracea</i>]

	6.5	ref NP_054960.1 photosystem II 47 kDa protein [<i>Spinacia olerace</i>]	
	8.1	sp P31853.2 ATPX_SPIOL RecName: Full= ATP synthase B' chain , chloroplastic	
	12.5	gb AAC24709.1 ribulose-phosphate 3-epimerase transit.	
	3.9	dbj BAE07183.1 putative serine decarboxylase [<i>Beta vulgaris</i>]	
	12.8	sp P50433.1 GLYM_SOLTU RecName: Full= Serine hydroxymethyltransferase	
	17	sp P12301.1 PSBQ_SPIOL RecName: Full= Oxygen-evolving enhancer protein	
	13.7	sp Q41385.1 PSAL_SPIOL RecName: Full= Photosystem I reaction center subunit XI, chloroplastic	
	27.9	sp Q42910.1 PPKD_MESCR RecName: Full= Pyruvate, phosphate dikinase	
	6.5	gb ABO61376.1 serine hydroxymethyltransferase [<i>Populus tremuloides</i>]	
	14.1	ref YP_319761.1 photosystem II 44 kDa protein [<i>Acorus calamus</i>]	
	21	ref NP_064080.2 NADH dehydrogenase subunit 4 [<i>Beta vulgaris</i>]	
TRANSCRIPTION/ TRANSLATION			
	2.2	gb AAT01416.1 translation initiation factor 5A [<i>Tamarix sp.</i>]	
	3.3	sp Q43467.1 EFTU1_SOYBN RecName: Full=Elongation factor Tu, chloroplast	
	3.4	ref NP_173165.1 FUG1 (FU-GAERII); translation initiation factor	
	3.8	sp O23755.1 EF2_BETVU RecName: Full=Elongation factor 2.	
	7.5	gb ACF06581.1 translational initiation factor eIF1 [<i>Elaeis guinea</i>]	
0.1	gb ABO31952.1 ribosomal protein S3 [<i>Peridiscus lucidus</i>]	2.3	sp O80360.1 RK3_TOBAC RecName: Full=50S ribosomal protein L3,
0.3	gb AAT39969.1 60S ribosomal protein L34, putative [<i>Solanum demisum</i>]	2.9	gb AAA34039.1 ribosomal protein 30S subunit
0.4	gb ACF06518.1 40S ribosomal protein S23 [<i>Elaeis guineensis</i>]	2.1	gb AAL91663.1 60s acidic ribosomal protein [<i>Prunus dulcis</i>]
0.4	sp Q9ST69.1 RR5_SPIOL RecName: Full=30S ribosomal protein S5	3.5	emb CAA63651.1 ribosomal protein L4 [<i>Spinacia oleracea</i>]
0.5	gb AAY41426.1 putative L24 ribosomal protein [<i>Ipomoea batatas</i>]	2.7	sp P29344.1 RR1_SPIOL RecName: Full=30S ribosomal protein S1, chloroplast
		3.4	emb CAG47084.1 40S ribosomal protein S9 [<i>Catharanthus roseus</i>]
		4.9	ref NP_563847.1 60S ribosomal protein L21 (RPL21A) [<i>Arabidopsis thaliana</i>]
		4.9	ref NP_187574.1 60S ribosomal protein L4/L1 (RPL4A) [<i>Arabidopsis thaliana</i>]
0.1	ref NP_001099678.1 poly(A) binding protein, cytoplasmic 3		
OTHERS			

0.1	gb ABD65058.1 GRF zinc finger containing protein [<i>Brassica oleraceae</i>]	3.3	gb AAC18788.1 AAC18788 Contains similarity to beta scruiin gb
0.3	gb ABC88375.1 Smad4 [<i>Nematostella vectensis</i>] 35 3.0	4.9	ref NP_192259.1 ankyrin repeat family protein [<i>Arabidopsis thaliana</i>]
0.1	ref NP_568721.1 short-chain dehydrogenase/reductase (SDR) family	2.7	gb AAL57201.1 AF355597_1 putative nodule membrane protein [<i>Medicago spp.</i>]
0.4	gb AAO43000.1 early tobacco anther 1 [<i>Nicotiana tabacum</i>]	2.6	gb AAZ85265.1 CT099 [<i>Lycopersicon pimpinellifolium</i>]
0.1	gb ABD98040.1 epicotyl-specific tissue protein [<i>Striga asiatica</i>]		
0.1	emb CAA66109.3 specific tissue protein 2 [<i>Cicer arietinum</i>]		
0.1	gb ACG30449.1 PGPS/D12 [<i>Zea mays</i>]		
0.1	ref NP_973902.1 NHL repeat-containing protein [<i>Arabidopsis thaliana</i>]		
0.2	gb ABL86674.1 PDF [<i>Gossypium barbadense</i>]		
0.5	gb AAY51975.1 GIR1 [<i>Vigna radiata</i>]		
0.5	ref NP_190741.1 saposin B domain-containing protein [<i>Arabidopsis thaliana</i>]		
0.5	gb ACG42167.1 DAG protein [<i>Zea mays</i>]		
0.1	gb AAK71662.1 AF395901_1 mature anther-specific protein LAT61		
0.2	gb ACJ02356.1 GAST-like protein [<i>Populus euphratica</i>]		
0.3	ref NP_680660.2 BTB/POZ domain-containing protein [<i>Arabidopsis thaliana</i>]		
	gb ABD83324.1 Fgenes protein 108 [<i>Beta vulgaris</i>] 49 0.001		
0.5	gb AAD22104.1 B12D protein [<i>Ipomoea batatas</i>]		
0.4	ref NP_564385.1 NFD3 (NUCLEAR FUSION DEFECTIVE 3)		