

CORRECTION

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Yu L.-X. and Setter T.L. Comparative Transcriptional Profiling of Placenta and Endosperm in Developing Maize Kernels in Response to Water Deficit.

The correct Table I for the above article appears below.

Accession #	Annotation	WS/C ratio	R/WS ratio	SAM relative difference statistic, <i>df</i>	Control Signal (fluor. units)
Cell division, growth and organization					
AI714488	xyloglucan endotransglycosylase (XET) [<i>Hordeum vulgare</i>]	2.45	0.84	1.87	11280
AI714505	histone H2A [<i>Allium cepa</i>]	1.94	1.14	2.20	3080
AI691345	expansin [<i>Gossypium hirsutum</i>]	1.68	1.11	2.48	797
AI691489	alpha tubulin 1 [<i>Eleusine indica</i>]	0.69	1.26	-3.41	19352
AI738162	ribonucleotide reductase [<i>Nicotiana tabacum</i>]	0.69	1.30	-2.02	5774
Metabolism					
AI714854	anthranilate synthase alpha 1 subunit [<i>Oryza sativa</i>]	9.65	1.64	1.71	2276
AI714511	phosphofructokinase [<i>Arabidopsis thaliana</i>]	2.91	1.27	1.40	11282
AI666136	trans-cinnamate 4-monooxygenase	2.28	0.69	2.48	2535
AI691886	1-acyl-glycerol-3-phosphate acyltransferase [<i>Zea mays</i>]	2.23	0.73	2.91	5597
AI665879	cytochrome-c oxidase [<i>Triticum aestivum</i>]	1.81	0.98	3.74	1309
AI881719	S-adenosyl-L-homocysteine hydrolase [<i>Arabidopsis thaliana</i>]	0.67	1.23	-5.04	8851
AI770628	alcohol dehydrogenase 1 [<i>Zea mays</i>]	0.66	1.08	-4.57	12967
AI881961	glyceraldehyde phosphate dehydrogenase [<i>Zea mays</i>]	0.66	1.04	-2.75	13995
AI770613	UDP-glucose dehydrogenase [<i>Glycine max</i>]	0.64	0.92	-4.99	6609
AI691424	ADP-ribosylation factor [<i>Capsicum annum</i>]	0.55	0.64	-4.46	17139
Protein synthesis and destination					
AI734306	mitochondrial 26S rRNA [<i>Zea mays</i>]	4.63	1.40	2.14	6531
AI770708	25S ribosomal RNA [<i>Oryza sativa</i>]	3.45	1.20	3.12	2350
AI738370	eukaryotic initiation factor 4A [<i>Oryza sativa</i>]	3.34	0.98	2.06	7011
AI738189	mitochondrial gene for 18S rRNA [<i>Zea mays</i>]	1.94	0.97	4.93	1603
AI734820	60S ribosomal protein L13 [<i>Arabidopsis thaliana</i>]	1.63	1.50	1.67	3705
Cellular communication and signal transduction					
AI691885	protein kinase PK4 [<i>Zea mays</i>].	2.36	0.93	1.04	1897
AI734622	gibberellin-induced protein 1 [<i>Petunia x hybrida</i>]	1.97	0.92	2.07	2177
AI714724	phosphatidylinositol-transfer protein domain, Sec14, CRAL/TRIO	1.84	0.93	3.67	702
AI881783	protein kinase, putative [<i>Arabidopsis thaliana</i>]	1.75	1.23	2.01	1803
AI834156	calcium dependent protein kinase (CDPK) [<i>Arabidopsis thaliana</i>]	1.73	0.60	2.17	5869
AI734411	ABA insensitive 1/2 protein phosphatase 2C [<i>Arabidopsis thaliana</i>]	1.71	0.40	1.92	6334
Stress response					
AI714517	senescence-associated protein, putative [<i>Pisum sativum</i>]	4.07	1.16	1.36	2498
AI834437	heat shock protein HSP83	3.06	0.21	1.41	9262
AI691707	heat shock protein, HSP18 [<i>Zea mays</i>]	2.89	0.62	1.44	5614
AI691409	heat shock protein HSP80-2 [<i>Triticum aestivum</i>]	2.45	0.43	1.94	6731
AI855025	heat shock protein HSP82 [<i>Oryza sativa</i>]	2.38	0.32	5.37	1688
AI881616	heat shock protein HSP70 [<i>Triticum aestivum</i>]	2.37	0.40	3.31	6182
AI691249	DnaJ, seed maturation protein PM3 [<i>Glycine max</i>]	2.07	0.84	4.60	3225
AI666018	heat shock protein HSP70 kDa [<i>Zea mays</i>]	2.07	0.58	4.14	4550
AI770766	MIP, plasma membrane intrinsic protein [<i>Zea mays</i>]	2.06	0.82	2.23	5722
AI714415	chaperonin, rubisco subunit binding-protein [<i>Triticum aestivum</i>]	1.87	0.40	1.66	10905
AI734741	MIP1, membrane intrinsic protein [<i>Sorghum bicolor</i>]	1.85	0.86	2.82	9034
AI737385	trehalose-6-phosphate synthase, putative [<i>Arabidopsis thaliana</i>]	1.83	1.06	2.28	2543
AI881838	DnaJ protein [<i>Hevea brasiliensis</i>]	1.80	0.82	2.64	4681
AI666231	heat shock protein HSP90, GRP94 homologue [<i>Hordeum vulgare</i>]	1.75	0.58	2.32	2537

AI881722	glutathione S-transferase (GST6) [Arabidopsis thaliana].	1.74	0.64	4.83	2646
AI738145	glutathione S-transferase, putative [Oryza sativa]	1.68	0.31	1.56	5618
AI714853	cyclophilin [Zea mays].	1.67	1.28	2.39	20146
AI881357	heat shock cognate protein HSP80.	1.65	0.35	2.49	7923
AI734803	MIP, plasma membrane intrinsic protein 1 [Triticum aestivum]	1.63	1.19	1.67	5104
AI881790	lipid transfer protein [Hordeum vulgare]	1.60	0.99	1.17	2502
Transcription and RNA processing					
AI714525	homeo domain-leucine zipper transcription factors [Zea mays]	3.00	0.94	2.41	1747
AI881804	zinc-finger protein [Oryza sativa].	2.10	0.80	5.92	9569
AI738123	high mobility group, HMGd1 [Zea mays]. DNA-binding protein[N.t.]	1.91	1.26	1.26	6609
AI738168	QM protein	0.68	1.33	-3.99	8465
Transport					
AI691896	integral membrane protein, putative [Oryza sativa]	1.73	0.64	8.71	3505
Unclassified or unknown					
AI770703	unknown	4.94	1.49	2.60	2919
AI714513	gag polyprotein (similarity) [Zea mays]	4.59	1.23	1.89	6022
AI692115	Unknown	2.92	1.06	1.94	4935
AI881769	Unknown	2.61	0.51	1.81	1248
AI714831	Unknown	2.59	0.30	1.66	6171
AI739749	Unknown	2.48	0.51	2.01	2218
AI770716	Unknown	2.45	0.68	1.97	3938
AI715020	Unknown	2.29	1.07	1.86	6568
AI714813	Unknown	2.17	0.85	1.51	673
AI737418	Unknown	2.16	1.24	1.92	2041
AI714781	Unknown	2.15	1.34	2.91	2238
AI854983	hypothetical protein [Oryza sativa]	2.02	0.56	2.54	997
AI666137	Unknown	2.01	1.28	3.01	2381
AI714830	Unknown	1.94	0.97	2.08	4174
AI834513	Unknown	1.88	0.35	2.07	6278
AI737204	Unknown	1.83	0.48	2.53	2771
AI715035	Unknown	1.82	1.33	2.23	6401
AI881770	Unknown	1.81	0.49	1.98	1574
AI737276	Unknown	1.72	0.56	1.83	4797
AI714514	hypothetical protein [Arabidopsis thaliana].	1.79	0.84	2.02	7248
AI881975	Unknown	1.76	0.63	2.04	954
AI734552	Unknown	1.76	1.04	2.14	2411
AI770419	Hypothetical protein [Arabidopsis thaliana]	1.70	0.33	2.48	9132
AI737857	Unknown	1.63	0.56	1.34	795
AI665898	Unknown	1.62	0.36	4.08	3922
AI691449	Unknown	1.62	0.44	2.06	2145
AI737285	Unknown	1.62	0.74	3.18	7254
AI714877	Unknown	0.55	0.55	-2.59	10821