

***Zm401p10*, encoded by an anther-specific gene with short open reading frames, is essential for tapetum degeneration and anther development in maize**

Dongxue Wang^{A,B}, Chengxia Li^{A,C}, Qian Zhao^A, Linna Zhao^A, Meizhen Wang^A, Dengyun Zhu^A, Guangming Ao^A and Jingjuan Yu^{A,D}

^AState Key Laboratory for Agro-biotechnology, College of Biological Sciences, China Agricultural University, No. 2 Yuanmingyuan West Road, Beijing 100094, China.

^BPresent address: Department of Biology, Stanford University, Stanford, CA 94305-5020, USA.

^CPresent address: Department of Plant Sciences, University of California, Davis, CA 95616, USA.

^DCorresponding author. Email: yujj@cau.edu.cn

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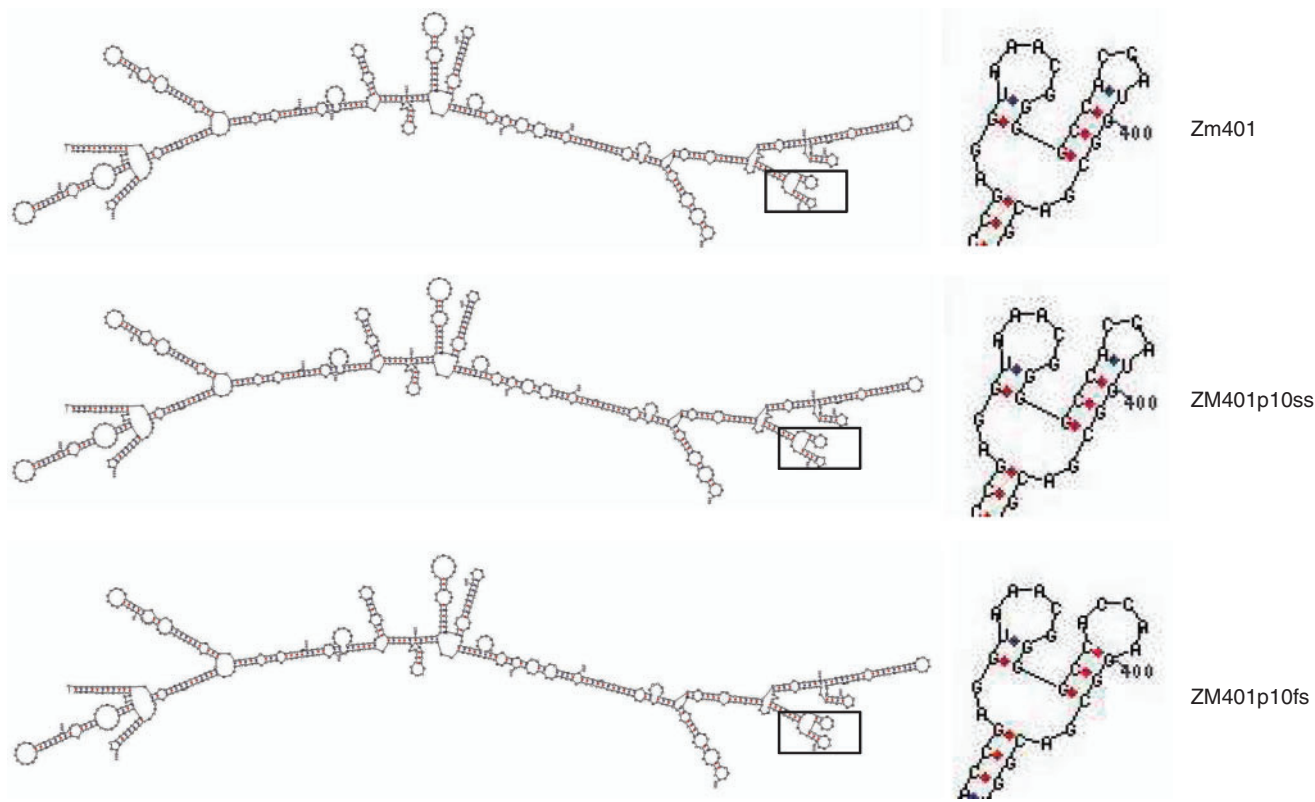


Fig. S1. Mfold predicted structures of the RNA variants and control structures. Zm401: *Zm401* RNA; ZM401p10ss: the Zm401 RNA with the site specific mutant of the *Zm401p10* ORF (An A was substituted for a U at position 792, the transcription start site is designated position 1); ZM401p10fs: the Zm401 RNA with frame shift mutation constructed by inserting a C at position 794.

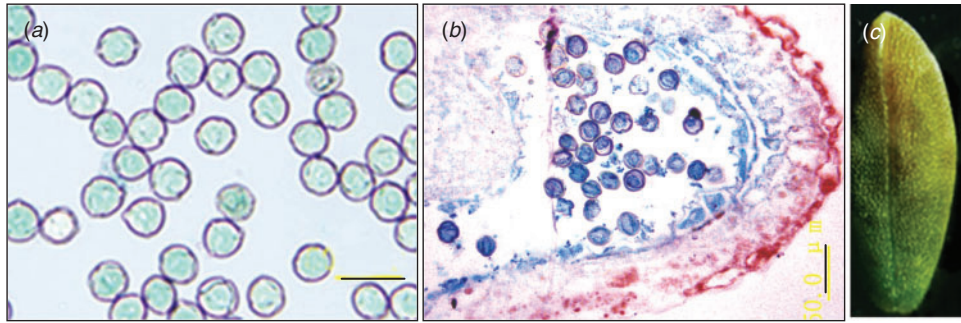


Fig. S2. Histological analysis of GUS activity under the control of the Zm401 promoter (Zm401::GUS) in tobacco. (a) Pollen grains from 20 mm-stage transgenic anther. (b) A cross section of 25 mm-stage transgenic anther. (c) An anther at the 25-stage of a transgenic plant. Bars = 50 μ m in (a) and (b).

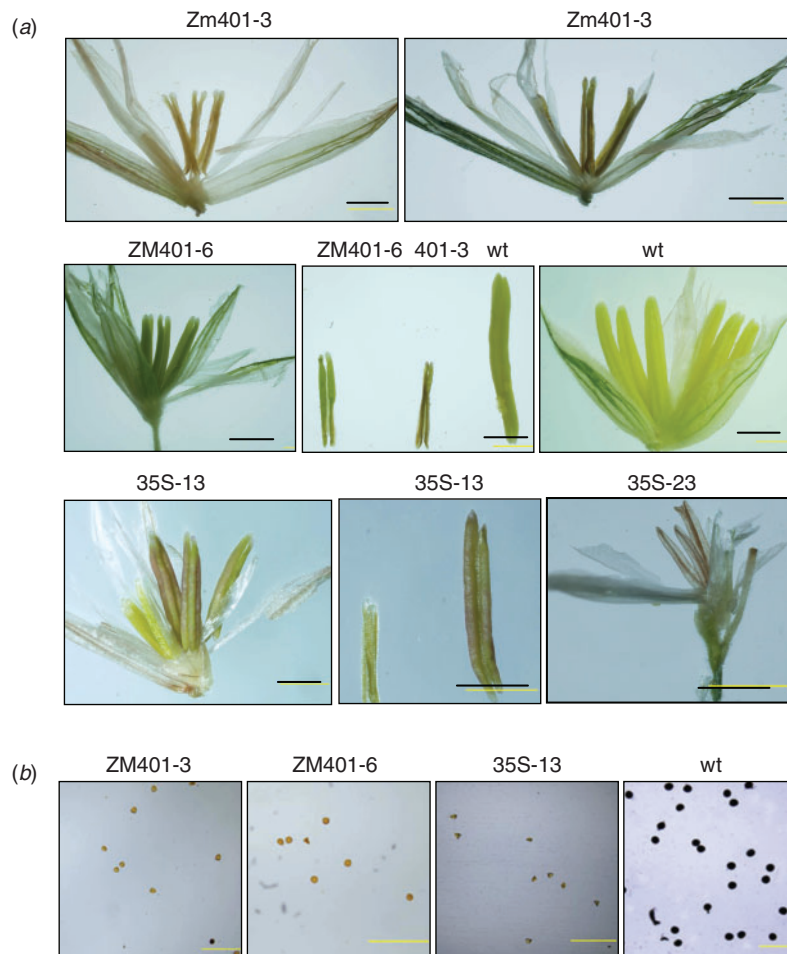


Fig. S3. Phenotypic and microscopic analysis of transgenic maize anthers. (a) Phenotype of mature anthers from transgenic maize lines, the wild type anther (Z31 \times Q31) was used as a control, bar = 2 mm. (b) Phenotype of pollen grains. Pollen grains from wild type and transgenic maize plants were stained with I₂-KI solution. Bar = 500 μ m.

Table S1. Primers used in plasmid construction and molecular analysis

Construct/gene name	Primer	Primer sequences
pETZm401p10::GFP	270gfp-1	5'-CCGGGGATCCATGGCGACGGTCGCAC-3'
	270gfp-2	5'-CCGGGAGCTCTTATTGTATAGTTCATCC-3'
	270gfpf	5'-TGTTCTTCGGTTTTTCATGATGAGTAAAGGAGAAGAA-3'
	270gfpr	5'-TTCTTCTCCTTTACTCATCATGAAAACCGAAGAACA-3'
35S::GFP::Zm401p10	gfp270-1	5'-CCGGGGATCCATGAGTAAAGGAGAAG-3'
	gfp270-2	5'-CCGGGAGCTCTCACATGAAAACCGAA-3'
	gfp270f	5'-ATGGATGAACTATACAAAATGGCGACGGTCGCACGG-3'
	gfp270r	5'-CCGTGCGACCGTCGCCATTTGTATAGTTCATCCAT-3'
NPT::35S::Zm401p10	orf	5'-CGGGATCCCGCCACCATGGCGACGG-3'
	orf	5'-CGGAGCTCCGTCACATGAAAACCGAAGAAC-3'
NPT::35S::Zm401p10ss	401f	5'-CGGGATCCCGTTGCTGTCGGATGTGGAAT-3'
	401r	5'-CGGAGCTCGTTGCTGTCGGTTCGTCACAT-3'
	ssf	5'-GGCCACCAAGCGACGGT-3'
	ssr	5'-GACCGTCGCCTTGGTGGC-3'
NPT::35S::Zm401p10fs	fsf	5'-GGCCACCATGCGCGACGGT-3'
	fsr	5'-GACCGTCGCGCATGGTGGC-3'
	Zm401 promoter	5'-TTAGTGCGGATTGGTGC-3'
Zm401 promoter	Zm401promoterf	5'-TTCACCTTGATTTCCACTAATTTT-3'
	Zm401promoterr	5'-CTTACGCAGCAGGTTCATCA-3'
CaMV 35S promoter	35sf	5'-CCACCTTCCTTTTCCACTATCTT-3'
	35sr	5'-ATGAGTAAAGGAGAAG-3'
gfp	gfpf	5'-TCACATGAAAACCGAA-3'
	gfpr	5'-GGCGAAGAAATCTCGTGCTTTCA-3'
htp	hptf	5'-CAGGACATTGTTGGAGCCGAAA-3'
	hptr	5'-CTGAAAGAGCAGTATGCGTGTT-3'
actin	actinf	5'-ATCAGCACCCGCAAGGCCCGGC-3'
	actinr	5'-GTATGTTGCTATCGAGGCTGTTCT-3'
actin	qActinF	5'-GGAGAATAGCATGAGGAAGTGTGT-3'
	qActinR	5'-ATCTTTTCACTCCTGCGGTAATATC-3'
Zm401p10	qZm401p10F	5'-TGGTAAATGAGCTATTCAAAATGAAC-3'
	qZm401p10R	5'-TTACGCATACAATACGACCAC-3'
Knl	Kn1f	5'-GCCGCACGCATGAGCT-3'
	Kn1r	5'-TGAGCGGCATCACGAGCAT-3'
Yabby	Yabbyf	5'-AAACGGTTGTATGCGGAAGGAA-3'
	Yabbyr	5'-CAAAGTTATCACGGTGTATGGC-3'
Ctyo	Ctyof	5'-TGCCCATCATCTTCATTCAC-3'
	Ctyor	5'-CGGTGCGAGCGAGAAAAG-3'
Dfr	Dfir	5'-GTCCAGCTTTCCTCGTCGA-3'
	Dfir	5'-ATGATTGGCGGTAACAAGGGAAA-3'
Hsp	Hspf	5'-CGGACAACGCCGAAGTGA-3'
	Hspr	5'-GCAGATTGGTGGTCCGTTG-3'
Spk	Spkf	5'-GATTCTGTGGGACACTGGAC-3'
	Spkr	

Table S2. A list of genes significantly affected in transgenic maize anthers during overexpression of the Zm401p10

Affymetrix number	Fold change* (OE vs WT)	P value (10 ⁻³)	Swissprot_id
Zm.1002.1.A1_at	-2.08631	8.348	PHD finger protein, putative
Zm.1002.2.S1_s_at	-1.14966	9.332	PHD finger protein, putative
Zm.10090.1.A1_x_at	1.38898	7.127	Rhodanese-like domain containing protein
Zm.10091.1.A1_at	2.30475	9.623	expressed protein
Zm.10156.1.A1_a_at	-3.54937	9.520	Pathogenesis-related protein Bet v I family protein
Zm.10182.2.S1_a_at	-1.73334	7.127	MoeZ/MoeB domain containing protein
Zm.10204.1.A1_at	-5.73330	7.499	farnesylated protein 2
Zm.10213.2.S1_at	-2.18725	8.998	reticulon family protein, putative
Zm.10213.2.S1_x_at	-1.43493	6.641	protein reticulon family protein
Zm.10234.1.S1_at	1.48907	7.830	ABA/WDS induced protein
Zm.10247.1.S1_at	-5.50984	2.128	none
Zm.10338.1.S1_at	1.46350	7.127	protein hypothetical protein
Zm.10372.1.S1_at	-4.23365	4.196	EF hand family protein
Zm.10383.4.S1_at	-1.29121	6.083	CCAAT-binding transcription factor subunit HAP3A, putative
Zm.1039.1.A1_x_at	2.22356	4.299	expressed protein
Zm.10435.1.S1_at	-6.83228	5.688	none
Zm.10450.1.S1_at	5.62339	7.127	expressed protein
Zm.10498.1.S1_at	1.53373	9.212	expressed protein
Zm.10500.1.S1_at	-4.52053	3.080	none
Zm.10510.1.S1_at	3.33827	3.080	none
Zm.10528.1.A1_at	1.61915	8.700	oxidoreductase, putative
Zm.10579.1.S1_at	-3.11175	6.755	hypothetical protein
Zm.10642.1.A1_at	-1.66814	6.824	expressed protein
Zm.10716.1.S1_at	-2.85306	6.818	zinc finger family protein
Zm.1076.1.S1_x_at	-1.72230	7.494	expressed protein
Zm.10773.1.A1_at	2.36356	4.985	Phosphatase
Zm.1079.1.A1_a_at	-5.62451	4.394	Carbonic anhydrase, chloroplast precursor
Zm.10811.2.S1_at	-0.96892	8.114	expressed protein
Zm.10827.1.S1_at	-3.03313	7.236	none
Zm.10837.1.S1_at	-7.43398	8.114	none
Zm.1085.1.A1_a_at	-2.23542	5.947	Acidic endochitinase precursor
Zm.1113.1.A1_at	3.02796	6.818	Harpin-induced protein 1 containing protein
Zm.11259.1.A1_at	0.82175	9.086	SHORT VEGETATIVE PHASE protein
Zm.11385.1.A1_at	-3.98952	3.708	L-ascorbate peroxidase 6, chloroplast precursor
Zm.11469.2.A1_a_at	-1.74608	9.623	DNA polymerase III, delta subunit family
Zm.11476.1.A1_at	1.10557	6.641	expressed protein
Zm.11636.1.A1_at	-4.74824	3.133	expressed protein
Zm.11657.1.A1_at	-2.00098	4.127	none
Zm.11679.1.A1_at	-3.22004	2.887	none
Zm.11734.1.A1_at	-3.20413	6.133	Polygalacturonase inhibitor 1 precursor
Zm.11745.1.A1_at	-2.55799	4.177	Protein kinase domain containing
Zm.11748.1.A1_at	-5.26995	2.278	expressed protein
Zm.11804.1.A1_s_at	-3.83887	3.080	Glucose transporter, putative
Zm.11825.1.S1_at	-2.39114	9.332	expressed protein
Zm.11865.1.A1_at	-1.30034	5.947	none
Zm.11874.1.A1_at	-1.99822	8.308	Protein kinase domain containing protein
Zm.11943.1.S1_at	-3.40209	5.340	Dihydroflavonol-4-reductase
Zm.12177.1.A1_at	4.39473	2.128	none
Zm.12184.1.A1_at	-2.22698	9.378	expressed protein
Zm.12240.1.S1_a_at	1.15694	7.127	F-box domain containing protein
Zm.12288.1.A1_at	1.33861	8.957	SNF7 family protein
Zm.12295.2.S1_a_at	-4.46768	6.641	stress responsive protein, putative
Zm.12352.1.S1_at	6.32809	3.708	none
Zm.12367.1.S1_at	-5.90021	9.000	none
Zm.12385.1.S1_at	-3.80089	7.448	expressed protein
Zm.12385.1.S1_s_at	-1.90892	3.708	expressed protein
Zm.12387.1.S1_at	-3.01684	6.115	none
Zm.12422.1.S1_at	4.70921	4.067	Isoflavone reductase homolog, putative
Zm.12605.1.S1_at	1.72458	6.210	none

Table S2. (continued)

Affymetrix number	Fold change* (OE vs WT)	P value (10 ⁻³)	Swissprot_id
Zm.12622.1.A1_at	1.54430	9.954	expressed protein
Zm.1263.1.A1_at	-1.77946	7.272	chlorophyll synthase, ChlG family protein
Zm.12700.1.A1_at	2.23237	3.880	Serine carboxypeptidase family protein
Zm.12716.2.A1_at	-4.18672	6.133	expressed protein
Zm.12757.1.A1_at	-3.50607	3.080	Secretory carrier-associated membrane protein, putative
Zm.12796.1.A1_at	1.33678	6.791	Uncharacterized conserved protein, putative
Zm.12825.1.S1_at	-1.47429	7.127	Aquaporin TIP3.1, putative
Zm.12843.1.A1_at	1.51724	8.110	protein phosphatase 2C family protein, putative
Zm.12873.1.A1_at	1.00002	7.127	expressed protein
Zm.12954.1.A1_at	1.68396	8.998	ADP-ribosylation factor At2g18390, putative
Zm.12997.2.S1_a_at	0.97444	8.308	chloroplastic outer envelope membrane protein, putative
Zm.12998.1.S1_at	1.94142	6.641	Uncharacterised protein family containing protein
Zm.13013.1.A1_at	2.64576	6.989	none
Zm.13057.1.A1_at	2.13862	5.688	DNA-binding protein, putative
Zm.1319.1.S1_at	-3.26516	7.830	none
Zm.1323.1.S1_at	-1.56497	6.133	none
Zm.1323.1.S1_x_at	-1.91538	3.708	none
Zm.13239.2.A1_at	-2.66272	4.177	Chlorophyll a-b binding protein 2, chloroplast precursor, putative
Zm.13261.2.S1_x_at	1.03393	6.818	none
Zm.13266.1.S1_at	1.86172	6.611	expressed protein
Zm.13273.2.A1_x_at	-2.17000	9.954	none
Zm.13296.1.S1_at	-1.02083	9.573	expressed protein
Zm.13307.1.S1_at	-3.96952	3.080	none
Zm.13324.1.S1_at	4.53988	5.688	expressed protein
Zm.13343.1.S1_at	-3.18159	7.716	none
Zm.13365.3.A1_at	-1.15023	8.378	Tubulin alpha-2 chain, putative
Zm.13376.1.S1_s_at	-1.09134	8.114	Plasma membrane ATPase, putative
Zm.1341.1.A1_at	-1.74694	9.662	PAP_fibrillin family protein
Zm.13452.2.A1_at	-1.24010	6.791	ZIP zinc/iron transport family protein
Zm.13480.1.S1_at	-1.60500	8.899	oxidoreductase, 2OG-Fe oxygenase family protein
Zm.1350.1.S1_at	-1.23866	6.309	HEAT repeat family protein
Zm.13559.2.A1_a_at	-0.96275	8.087	PB1 domain containing protein
Zm.1360.1.S1_at	-4.39475	7.515	none
Zm.13631.1.A1_at	-2.00917	6.791	XYPPX repeat family protein
Zm.13642.1.S1_at	2.94045	9.623	csAtPR5, putative
Zm.13645.1.S1_at	0.93393	8.193	Indole-3-glycerol phosphate lyase, chloroplast precursor, putative
Zm.1375.1.S1_at	3.50905	9.456	60S ribosomal protein L30, putative
Zm.13818.1.S1_at	-2.82486	7.162	D-tyrosyl-tRNA deacylase family protein
Zm.13840.1.S1_at	-4.04056	3.483	Cytochrome P450 family protein
Zm.13844.1.A1_at	2.18191	9.954	hypothetical protein
Zm.13986.1.A1_at	-2.50965	5.955	translocon Tic40, putative
Zm.14088.2.A1_at	-2.19394	4.705	Aconitate hydratase, cytoplasmic, putative
Zm.14099.1.A1_at	-1.24231	8.700	Nodule membrane protein, putative
Zm.1418.1.A1_at	-2.73164	3.080	Male sterility protein
Zm.1419.1.S1_at	-2.79442	5.955	xylanase inhibitor TAXI-IV, putative
Zm.14352.3.S1_at	-1.45864	7.127	expressed protein
Zm.14380.1.A1_at	-4.10217	2.278	magnesium-chelatase subunit H family protein
Zm.14392.1.S1_at	-5.86775	6.726	Dehydrin family protein
Zm.14463.1.A1_at	-2.40563	9.573	expressed protein
Zm.14516.1.S1_at	1.58782	8.110	Transcription initiation factor TFIID subunit 10, putative
Zm.14563.1.A1_s_at	-4.11115	2.128	Peroxidase 11 precursor, putative
Zm.14566.1.S1_at	-3.83005	2.887	possible Photosystem II reaction center Psb27 protein, putative
Zm.14596.3.S1_at	-2.69452	8.315	Magnesium-protoporphyrin IX monomethyl ester cyclase, chloroplast precursor, putative
Zm.14692.1.A1_s_at	0.97940	9.954	none
Zm.14706.1.S1_at	-1.43858	6.818	Histone H2A, putative
Zm.14760.1.S1_at	-1.35893	7.127	ubiquitin-conjugating enzyme E2, putative
Zm.1480.1.A1_at	-2.45522	9.925	hypothetical protein
Zm.1482.3.A1_at	-4.25353	4.196	N3 like protein, putative
Zm.14838.1.A1_at	-1.69576	9.623	Plasma membrane ATPase, putative

Table S2. (continued)

Affymetrix number	Fold change* (OE vs WT)	P value (10 ⁻³)	Swissprot_id
Zm.14873.1.A1_at	-2.06973	8.553	none
Zm.14975.1.S1_at	1.79389	7.947	none
Zm.15.1.A1_at	-5.27730	8.957	NADP-dependent malic enzyme, chloroplast precursor, putative
Zm.150.2.A1_at	-3.01760	9.954	Triose phosphate/phosphate translocator, chloroplast precursor, putative
Zm.15004.1.S1_at	5.82673	4.177	EF hand family protein
Zm.15027.1.A1_at	1.20303	6.641	haloacid dehalogenase-like hydrolase family protein, putative
Zm.15083.2.A1_at	-3.30231	4.177	heavy metal-associated domain containing protein
Zm.15183.1.A1_at	-3.89966	3.708	Nonphototropic hypocotyl protein 1, putative
Zm.1519.1.S1_at	-2.66611	9.332	lysine and histidine specific transporter, putative
Zm.15307.1.A1_at	-1.94391	8.235	expressed protein
Zm.15320.1.S1_at	-2.50619	8.110	Heat shock factor protein HSF30, putative
Zm.15325.1.A1_at	-3.44558	4.302	O-methyltransferase family protein
Zm.1544.1.A1_a_at	-5.38717	6.641	Chlorophyll a-b binding protein 1, chloroplast precursor, putative
Zm.15442.1.A1_at	-2.30730	6.083	Xyloglucan galactosyltransferase KATAMARI 1, putative
Zm.15456.1.A1_at	0.96574	9.954	Protein kinase domain containing protein
Zm.15530.1.A1_at	1.89898	8.892	C2 domain-containing protein, putative
Zm.1556.1.A1_at	-2.78880	2.887	f13j11 PRLI-interacting factor G, putative
Zm.1561.1.A1_at	-1.60338	7.302	expressed protein
Zm.15702.1.S1_at	-2.63922	6.791	Chlorophyll A-B binding protein
Zm.1578.1.A1_at	-1.75634	6.133	yabby14 protein, putative
Zm.15822.1.S1_at	-6.32911	6.641	Chlorophyll A-B binding protein
Zm.15835.1.A1_at	-2.72483	5.744	Phenylalanine ammonia-lyase, putative
Zm.15903.2.A1_at	1.66960	4.365	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha subunit, putative
Zm.1592.1.A1_at	-0.87058	9.954	Endochitinase A precursor, putative
Zm.1595.1.S1_at	-4.06010	7.515	Peptidyl-prolyl cis-trans isomerase 1, putative
Zm.15995.2.A1_at	-6.35520	3.080	Peptidyl-prolyl cis-trans isomerase 1, putative
Zm.15995.2.A1_x_at	-5.14011	9.447	none
Zm.16025.2.A1_at	-5.94960	3.080	none
Zm.16049.1.S1_x_at	1.11065	9.954	none
Zm.16056.1.S1_at	1.75228	9.323	Profilin A, putative
Zm.16171.1.A1_at	-4.23571	6.133	Inositol oxygenase, putative
Zm.16227.1.A1_at	-2.85747	8.351	Potassium channel SKOR, putative
Zm.1629.1.A1_at	-4.17585	7.830	none
Zm.1631.1.S1_at	-6.46594	2.128	expressed protein
Zm.16360.1.A1_at	-3.06178	3.725	Pyrophosphate-fructose 6-phosphate 1-phosphotransferase, putative
Zm.16443.1.S1_at	-3.71644	9.954	none
Zm.16449.1.S1_at	7.11788	7.991	IAA-amino acid hydrolase homolog 2 precursor, putative
Zm.16472.2.S1_at	0.86806	8.744	RNA recognition motif family protein
Zm.16475.2.S1_at	-3.03756	8.308	none
Zm.16481.1.A1_at	2.02416	9.460	Acetyl-CoA acetyltransferase, cytosolic 1, putative
Zm.16489.1.S1_at	1.31811	6.818	3-methyl-2-oxobutanoate hydroxymethyltransferase family protein
Zm.16490.1.S1_at	1.47420	9.719	expressed protein
Zm.16502.4.A1_at	-1.94754	5.079	17.5 kDa class II heat shock protein, putative
Zm.16504.2.A1_at	5.38465	9.954	none
Zm.16524.5.A1_at	-2.61427	8.901	60S ribosomal protein L18a, putative
Zm.16532.4.S1_at	4.15246	4.177	none
Zm.1659.1.A1_at	-3.29099	8.268	Signal peptidase subunit family protein
Zm.16593.2.S1_at	1.90802	9.623	tropomyosin, putative
Zm.1665.1.A1_at	-1.44335	8.468	Chlorophyll a-b binding protein, chloroplast precursor, putative
Zm.16683.1.S1_at	-3.87058	2.128	ZIP Zinc transporter family protein
Zm.16699.1.A1_at	1.31873	5.611	expressed protein
Zm.16931.1.A1_s_at	-1.01851	7.909	Dolichol-phosphate mannosyltransferase, putative
Zm.17122.1.A1_at	1.35418	6.115	expressed protein
Zm.17168.2.A1_at	5.16531	2.128	tRNA methyltransferase family protein
Zm.17200.1.S1_at	2.95569	2.554	expressed protein
Zm.17249.1.A1_at	1.22535	5.947	Ribose-phosphate pyrophosphokinase 3, putative
Zm.1727.1.A1_at	2.86360	4.365	expressed protein
Zm.17329.1.A1_at	-1.79950	6.764	Photosystem I reaction center subunit III, chloroplast precursor, putative
Zm.1735.1.S1_at	-3.58643	5.688	Zinc finger, C3HC4 type family protein

Table S2. (continued)

Affymetrix number	Fold change* (OE vs WT)	P value (10 ⁻³)	Swissprot_id
Zm.17350.1.A1_at	-1.19725	6.791	D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain containing protein
Zm.17494.1.A1_at	-1.93707	7.947	Thiamine pyrophosphate enzyme, central domain containing protein
Zm.17533.1.S1_at	7.26927	2.128	expressed protein
Zm.17544.1.A1_at	-2.91789	3.708	expressed protein
Zm.17551.1.S1_at	-4.98844	4.177	Haemolysin-III related family protein
Zm.17557.1.A1_at	-3.18667	6.791	none
Zm.1758.1.S1_at	-2.74450	7.272	expressed protein
Zm.17617.1.A1_at	4.35851	7.580	Adapter-related protein complex 4 sigma 1 subunit, putative
Zm.17661.1.A1_at	5.30242	4.177	none
Zm.17674.1.S1_at	-2.76408	6.641	none
Zm.17705.1.A1_at	-1.12067	6.641	expressed protein
Zm.17740.1.A1_at	3.54202	3.483	none
Zm.17740.2.A1_a_at	4.52082	8.892	Rfl1 protein, mitochondrial precursor, putative
Zm.17743.1.S1_at	4.16737	2.278	ABC transporter family protein
Zm.17745.1.A1_at	1.30832	9.954	none
Zm.17748.1.S1_at	-6.45396	4.177	none
Zm.17809.1.A1_at	-2.98584	7.127	60S ribosomal protein L38, putative
Zm.17856.2.A1_at	1.71997	4.543	ABA/WDS induced protein
Zm.1794.1.S1_at	-6.25249	2.128	Sybindin-like family protein
Zm.17957.1.A1_at	0.94801	8.998	Peroxin-3 family protein
Zm.17972.1.A1_at	4.14505	2.128	none
Zm.1798.1.A1_a_at	5.88894	4.995	AAA-type ATPase family protein, putative
Zm.18031.1.A1_at	-3.54055	6.641	expressed protein
Zm.18075.1.S1_at	1.25795	8.123	pyrrolidone-carboxylate peptidase family protein
Zm.18076.1.S1_at	1.10535	7.127	LysM domain containing protein
Zm.18088.1.A1_at	-3.64076	6.665	MazG nucleotide pyrophosphohydrolase domain protein, putative
Zm.18112.1.A1_at	-4.93603	9.954	expressed protein
Zm.18243.1.A1_at	-2.40036	8.899	protein phosphatase 2C family protein, putative
Zm.18251.1.A1_at	-1.68254	4.196	Magnesium-chelatase subunit chlI, chloroplast precursor, putative
Zm.18314.1.S1_at	-2.23163	4.669	fertility restorer homologue, putative
Zm.18423.1.A1_at	1.09218	6.641	expressed protein
Zm.18429.1.A1_at	1.64201	4.711	MAP kinase-activating protein C22orf5 homolog, putative
Zm.18441.1.S1_at	1.61692	4.669	DHHC zinc finger domain containing protein
Zm.18450.1.A1_at	-2.05801	4.177	ICE-like protease p20 domain containing protein
Zm.18453.1.A1_at	-5.29357	7.127	Glutaredoxin, putative
Zm.1850.1.A1_at	0.84126	9.925	UDP-glucuronosyl and UDP-glucosyl transferase family protein
Zm.18507.1.A1_at	2.11970	3.160	Glycosyl hydrolase family 1 protein
Zm.18516.1.A1_a_at	-5.72088	5.611	Homeobox domain containing protein
Zm.18537.1.S1_at	-5.97090	2.128	Cytochrome P450 family protein
Zm.18666.1.A1_at	-3.59011	4.672	embryo-abundant protein, putative
Zm.1871.1.A1_at	-1.29576	7.947	fructose-1,6-bisphosphatase family protein
Zm.18781.1.A1_at	-1.17130	7.272	none
Zm.18828.1.A1_at	-1.18753	9.169	hypothetical protein
Zm.18946.1.A1_at	-1.90234	7.448	hydrolase, alpha/beta fold family protein
Zm.18987.1.A1_at	-4.27646	4.123	Transferase family protein
Zm.19027.1.A1_at	3.89834	2.278	Sugar transporter family protein
Zm.19048.1.A1_at	1.32127	9.954	glycosyl transferase, group 2 family protein
Zm.19075.1.A1_at	1.66513	7.370	RER1B protein, putative
Zm.19085.1.S1_at	1.77955	9.086	Peroxidase 43 precursor, putative
Zm.19094.1.S1_at	-2.04044	7.127	hypothetical protein
Zm.19097.1.A1_at	3.38567	9.378	none
Zm.19106.1.A1_at	1.42080	7.937	Pirin, putative
Zm.19144.1.A1_at	1.92154	7.512	Calcium-dependent protein kinase, putative
Zm.19155.2.A1_at	-3.57361	6.641	expressed protein
Zm.19192.1.A1_at	2.49736	5.611	Will die slowly protein, putative
Zm.19200.1.S1_at	2.01239	6.133	oxidoreductase, short chain dehydrogenase/reductase family protein
Zm.19227.1.S1_at	-2.59835	7.839	GRAM domain-containing protein, putative
Zm.19228.1.A1_at	-1.68760	5.688	expressed protein
Zm.19290.1.A1_at	-0.96422	8.085	Lecithin:cholesterol acyltransferase family protein

Table S2. (continued)

Affymetrix number	Fold change* (OE vs WT)	P value (10 ⁻³)	Swissprot_id
Zm.19319.1.A1_at	-3.42952	2.650	2-isopropylmalate synthase B, putative
Zm.19348.1.A1_at	1.19156	9.447	C2 domain containing protein
Zm.1977.1.A1_at	-1.22869	8.744	Ferredoxin-1, chloroplast precursor, putative
Zm.2.1.A1_at	-3.30858	6.726	expressed protein
Zm.2025.1.A1_at	-1.43493	8.998	Metallothionein family protein
Zm.2031.4.A1_at	-4.33648	7.346	Metallothionein family protein
Zm.2031.4.A1_x_at	-4.10093	4.196	expressed protein
Zm.2047.1.S1_at	-4.14293	8.308	none
Zm.2181.1.S1_at	4.67847	4.196	Serine/threonine-protein kinase RLCKVII, putative
Zm.2220.3.S1_at	-5.30295	6.641	expressed protein
Zm.2221.1.S1_at	-1.78788	6.641	Papain family cysteine protease containing protein
Zm.2276.1.S1_at	-2.65128	4.196	hypothetical protein
Zm.2306.1.A1_at	5.76338	4.302	Alanine aminotransferase 2, putative
Zm.2321.1.A1_at	-1.06366	9.954	DNA polymerase delta small subunit, putative
Zm.2330.1.S1_at	1.96633	5.611	none
Zm.2343.1.S1_at	5.36758	2.128	subtilase family protein, putative
Zm.2374.1.A1_at	-0.95798	8.892	Dirigent-like protein
Zm.2400.1.A1_at	1.48835	7.499	Adenosine kinase 2, putative
Zm.247.2.A1_at	-4.09839	6.791	stress-induced protein sti1, putative
Zm.2497.1.S1_at	0.98331	7.580	Spermidine synthase 2, putative
Zm.2540.1.A1_at	-3.06910	7.689	oxidoreductase, aldo/keto reductase family protein
Zm.2558.1.S1_at	1.10761	8.901	G-box binding factor 1, putative
Zm.263.1.A1_at	-2.39739	4.177	Ribose-phosphate pyrophosphokinase 2, putative
Zm.2695.1.S1_at	-1.45478	9.378	PrMC3, putative
Zm.2710.1.S1_at	1.30334	9.378	Auxin response factor 3, putative
Zm.2806.1.A1_at	1.13286	9.925	YT521-B-like family protein
Zm.2836.1.S1_at	1.45251	9.908	Asparagine synthetase, putative
Zm.2869.1.A1_at	1.23780	9.954	expressed protein
Zm.2910.1.S1_a_at	-2.22686	8.586	none
Zm.2922.1.A1_at	-4.80000	4.177	expressed protein
Zm.2968.1.A1_at	3.58993	9.323	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplast precursor, putative
Zm.298.1.S1_a_at	-3.12987	4.177	Sterol esterification protein, putative
Zm.2991.1.A1_at	3.70860	9.925	Subtilisin-chymotrypsin inhibitor CI-1B, putative
Zm.301.1.A1_a_at	-2.88662	9.954	FLOWERING LOCUS T protein, putative
Zm.3034.1.A1_at	-4.59243	2.128	Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform, putative
Zm.3058.1.A1_at	-1.71347	6.133	17.5 kDa class II heat shock protein, putative
Zm.311.1.A1_at	2.77565	6.641	29 kDa ribonucleoprotein A, chloroplast precursor, putative
Zm.3118.1.S1_at	-1.22400	6.083	Regulator of chromosome condensation family protein
Zm.3132.2.S1_at	0.99688	7.302	Clathrin coat assembly protein AP17, putative
Zm.3174.1.A1_at	1.08483	7.699	expressed protein
Zm.3188.1.A1_at	-1.94362	6.726	auxin response factor 3, putative
Zm.3190.1.A1_at	-1.30884	9.944	ZIM motif family protein
Zm.3225.1.S1_at	3.91304	8.468	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative
Zm.3309.1.S1_at	3.15529	2.424	ribosomal protein S21 containing protein
Zm.3316.1.A1_at	-2.64580	9.086	Dormancy/auxin associated protein
Zm.3339.1.A1_at	-0.96173	9.925	Cyclin, N-terminal domain containing protein
Zm.3420.1.A1_at	4.08795	5.688	PGR5, putative
Zm.3459.1.A1_at	-2.26354	3.080	expressed protein
Zm.3500.1.S1_at	-2.54467	7.786	protein kinase, putative
Zm.3551.1.S1_at	5.22515	2.128	DSBA-like thioredoxin domain containing protein
Zm.3587.1.S1_at	-4.24440	9.447	Non-cyanogenic beta-glucosidase precursor, putative
Zm.3633.1.A1_at	-2.70722	4.129	Acetyl-coenzyme A synthetase, putative
Zm.3669.1.A1_at	1.68177	6.641	Stem-specific protein TSJT1, putative
Zm.3670.4.S1_at	-1.50376	8.582	4F5 protein family protein
Zm.3731.2.A1_at	2.07062	7.909	Hsp20/alpha crystallin family protein
Zm.3740.1.A1_at	3.43700	6.133	nuclear protein, putative
Zm.3785.1.S1_at	2.32293	7.675	none
Zm.3855.1.S1_at	-5.78784	9.272	Oxygen-evolving enhancer protein 1, chloroplast precursor, putative
Zm.3895.1.A1_at	-0.94655	7.909	3' exoribonuclease family, domain 1 containing protein

Table S2. (continued)

Affymetrix number	Fold change* (OE vs WT)	P value (10 ⁻³)	Swissprot_id
Zm.3913.1.A1_at	1.97210	6.989	Peroxidase 11 precursor, putative
Zm.3932.1.S1_at	-3.27533	5.955	Kelch motif family protein
Zm.4049.1.A1_at	5.77331	6.484	Ubiquitin-conjugating enzyme family protein
Zm.4067.1.S1_at	-2.48656	4.177	zinc finger family protein, putative
Zm.4087.1.A1_at	-1.94664	7.302	Sugar carrier protein C, putative
Zm.4089.1.S1_at	-3.53967	4.177	Non-cyanogenic beta-glucosidase precursor, putative
Zm.418.1.A1_at	-3.45712	3.133	NAD binding domain of 6-phosphogluconate dehydrogenase family protein
Zm.4188.1.A1_at	-1.58998	6.641	expressed protein
Zm.4189.1.S1_at	-4.01835	5.341	expressed protein
Zm.4223.1.S1_at	0.78696	9.400	expressed protein
Zm.4284.1.A1_at	1.63856	8.582	Sigma-70 region 2 family protein
Zm.431.1.S1_at	-2.68545	9.954	expressed protein
Zm.4376.1.A1_at	-2.61933	6.641	expressed protein
Zm.4384.1.A1_at	2.33651	7.127	Sigma-70 region 2 family protein
Zm.439.1.A1_at	-2.38774	9.254	methionyl-tRNA formyltransferase family protein
Zm.4438.1.A1_at	2.39997	7.302	IQ calmodulin-binding motif family protein
Zm.4448.1.A1_at	1.10470	7.127	Pyruvate, phosphate dikinase, chloroplast precursor, putative
Zm.4471.1.A1_a_at	-2.59336	3.133	Pyruvate, phosphate dikinase, chloroplast precursor, putative
Zm.4471.1.A1_x_at	-2.57268	6.641	Pyruvate, phosphate dikinase, chloroplast precursor, putative
Zm.4471.2.S1_a_at	-2.98292	5.611	Pyruvate, phosphate dikinase, chloroplast precursor, putative
Zm.4471.3.A1_x_at	-2.47415	3.708	RNA recognition motif family protein
Zm.4478.1.A1_at	1.41974	7.699	cation exchanger, putative
Zm.4505.1.A1_a_at	1.78691	6.641	Enoyl, chloroplast precursor, putative
Zm.4508.1.A1_at	1.33854	9.086	expressed protein
Zm.4527.1.A1_at	-3.94833	6.641	seed specific protein Bn15D1B, putative
Zm.4561.2.A1_a_at	-2.69077	3.133	LysM domain containing protein
Zm.4611.1.A1_at	-4.78603	5.938	none
Zm.4707.1.A1_at	5.55861	8.583	GRAS family transcription factor containing protein
Zm.4742.1.A1_at	-2.74772	4.216	lysine ketoglutarate reductase/saccharopine dehydrogenase, putative
Zm.476.1.S1_at	-0.88237	9.829	Dehydrin family protein
Zm.4870.1.A1_a_at	1.23399	9.113	yabby15 protein, putative
Zm.4882.1.S1_at	-4.10752	9.323	Tetraspanin family protein
Zm.4899.1.A1_at	3.79510	6.641	inositol 1, 3, 4-trisphosphate 5/6-kinase, putative
Zm.4953.1.A1_at	-1.03803	7.689	4-methyl-5-thiazole monophosphate biosynthesis protein, putative
Zm.4980.1.A1_at	-2.07042	7.127	Neutral/alkaline invertase, putative
Zm.5062.1.A1_at	-1.87051	3.880	xyloglucan endotransglucosylase/hydrolase protein 15 precursor, putative
Zm.5108.1.A1_at	3.19226	4.177	40S ribosomal protein SA, putative
Zm.5139.1.S1_at	0.81249	9.113	ATP-dependent Clp protease proteolytic subunit 1, putative
Zm.5146.2.S1_at	-0.88769	9.323	Fructokinase, putative
Zm.5169.1.A1_at	2.02950	8.121	Auxin-induced protein PCNT115, putative
Zm.5214.1.S1_at	-1.01440	8.085	Copine family protein
Zm.5267.1.A1_at	3.23204	6.755	Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor, putative
Zm.5274.1.S1_at	-2.07219	3.880	expressed protein
Zm.5340.1.A1_at	-3.30717	4.177	KH domain-containing protein, putative
Zm.5398.1.A1_at	-1.15284	7.198	expressed protein
Zm.5420.1.A1_at	-2.90310	9.113	expressed protein
Zm.5466.1.A1_a_at	-3.31383	9.776	expressed protein
Zm.5466.1.A1_at	-5.76304	7.515	none
Zm.5466.2.S1_a_at	-2.46980	7.909	Glutathione S-transferase, N-terminal domain containing protein
Zm.556.2.A1_a_at	3.03536	6.641	Cycloartenol synthase, putative
Zm.5671.1.S1_at	-1.63785	7.042	NADP-dependent oxidoreductase P2, putative
Zm.5748.1.A1_at	6.17130	2.618	protein disulfide isomerase, putative
Zm.5770.1.S1_at	0.88945	8.357	MADS2, putative
Zm.578.1.S1_at	-3.94491	2.278	Photosystem II reaction centre X protein containing protein
Zm.5797.2.A1_a_at	-1.89102	8.998	expressed protein
Zm.5801.1.A1_at	-6.66068	9.332	Peroxidase 3 precursor, putative
Zm.5808.1.A1_at	2.57633	6.082	expressed protein
Zm.5835.1.S1_at	-3.60957	2.128	reticulin family protein, putative

Table S2. (continued)

Affymetrix number	Fold change* (OE vs WT)	P value (10 ⁻³)	Swissprot_id
Zm.5948.1.A1_at	-0.98009	9.623	expressed protein
Zm.5953.1.A1_at	0.87164	9.447	Vacuolar sorting receptor 1 precursor, putative
Zm.5966.1.A1_at	1.30483	5.968	Elongation factor Tu, chloroplast precursor, putative
Zm.6033.1.A1_at	-1.79913	4.410	Elongation factor Tu, chloroplast precursor, putative
Zm.6033.1.A1_s_at	-1.43130	6.791	Cell elongation protein DIMINUTO, putative
Zm.6146.1.A1_at	-1.23583	7.302	60S ribosomal protein L35, putative
Zm.6206.1.A1_at	4.40126	3.483	uncharacterized plant-specific domain TIGR01589 family protein
Zm.6217.1.A1_at	1.07135	9.662	Homeobox protein OSH1, putative
Zm.6265.1.A1_at	-3.21170	4.196	none
Zm.6298.1.A1_at	4.25149	6.818	none
Zm.6364.1.A1_at	2.18477	7.515	TPR Domain containing protein
Zm.6370.1.A1_at	-3.33240	4.177	MADS-box protein CMB1, putative
Zm.6382.1.A1_at	4.07163	2.128	amino acid transporter family protein, putative
Zm.6460.1.A1_at	-1.36507	5.039	peroxisomal membrane protein, putative
Zm.6522.2.A1_a_at	-2.63337	4.995	F-box domain containing protein
Zm.6524.1.S1_at	-0.78718	9.954	Photosystem I reaction centre subunit IV/PsaE family protein
Zm.6532.8.A1_at	-2.35296	7.566	none
Zm.6549.1.A1_at	1.07444	6.898	jasmonate-induced protein, putative
Zm.6569.3.S1_at	-6.05875	2.618	expressed protein
Zm.6586.1.A1_at	-1.82549	4.067	Alpha-expansin 11 precursor, putative
Zm.667.1.A1_at	-3.21825	6.133	expressed protein
Zm.6680.1.A1_at	-3.66139	7.127	Glucan endo-1,3-beta-glucosidase GII precursor, putative
Zm.6689.1.A1_s_at	-4.06665	7.909	Alpha-expansin 1 precursor, putative
Zm.669.1.S1_at	-2.28074	3.483	Translation initiation factor IF-2, chloroplast precursor, putative
Zm.6732.5.S1_at	-2.15065	5.341	Saposin-like type B, region 1 family protein
Zm.7023.1.S1_at	1.10359	6.641	GTPase activating protein, putative
Zm.7035.1.A1_at	-1.14915	9.124	harpin binding protein 1, putative
Zm.705.1.S1_at	-1.58131	4.196	expressed protein
Zm.7055.1.A1_at	-2.53748	3.483	Chlorophyll a-b binding protein CP24 10B, chloroplast precursor, putative
Zm.7091.1.A1_at	-2.92495	3.483	11974.m08831 protein Chlorophyll a-b binding protein CP24 10B, chloroplast precursor, putative
Zm.7091.2.S1_a_at	-3.07622	4.299	11971.m10749 protein hypothetical protein
Zm.7132.1.A1_a_at	-3.64410	9.789	Thioredoxin M-type, chloroplast precursor, putative
Zm.719.1.A1_at	-2.16005	8.123	Thioredoxin M-type, chloroplast precursor, putative
Zm.719.2.S1_x_at	-2.30392	3.708	expressed protein
Zm.7275.1.A1_at	-2.45855	4.299	tetratricopeptide repeat, putative
Zm.7276.1.S1_at	-2.47147	5.419	Cysteine proteinase 2 precursor, putative
Zm.737.2.A1_at	5.25953	7.909	TBC domain containing protein
Zm.7416.1.A1_s_at	-2.55272	4.177	Clathrin assembly protein, putative
Zm.7429.1.A1_at	-1.51066	5.039	expressed protein
Zm.743.1.S1_at	-3.75632	7.515	prefoldin subunit 4, putative
Zm.7460.1.A1_at	-1.37139	7.127	ADP,ATP carrier protein, mitochondrial precursor, putative
Zm.75.2.S1_at	-1.98779	8.892	negatively light-regulated protein, putative
Zm.7501.1.S1_at	-2.30744	4.685	none
Zm.7538.1.A1_at	2.69315	5.688	Ribulose-phosphate 3-epimerase, chloroplast precursor, putative
Zm.7577.1.S1_at	-1.16505	8.582	Harpin-induced protein 1 containing protein
Zm.7596.1.A1_at	-4.05278	9.456	AUX/IAA family protein
Zm.7611.1.A1_a_at	1.55427	7.302	Complex 1 protein containing protein
Zm.7644.1.A1_at	1.05831	9.272	ribosomal protein L15 containing protein
Zm.7667.1.A1_at	1.32149	7.127	expressed protein
Zm.767.1.A1_at	-2.66050	8.123	heavy metal-associated domain containing protein
Zm.7677.1.A1_at	-4.12857	4.482	Mpv17/PMP22 family protein
Zm.7709.1.A1_at	-1.43332	6.641	expressed protein
Zm.7768.1.A1_at	-4.98577	2.887	YABBY protein, putative
Zm.7769.1.S1_at	-2.89413	6.641	MATH domain containing protein
Zm.787.1.A1_at	1.46282	7.515	Uncharacterized BCR, COG1963 family protein
Zm.7953.1.A1_at	-2.31501	4.822	ChaC-like protein
Zm.7963.1.A1_at	0.84723	9.942	Glycine cleavage system H protein, mitochondrial precursor, putative
Zm.7973.1.S1_at	1.09978	7.127	expressed protein

Table S2. (continued)

Affymetrix number	Fold change* (OE vs WT)	P value (10 ⁻³)	Swissprot_id
Zm.8061.1.S1_at	1.71208	6.083	hypothetical protein
Zm.8097.1.A1_at	-2.70658	3.483	Rho termination factor, N-terminal domain containing protein
Zm.8101.1.A1_at	-4.49944	5.611	Glutathione S-transferase, putative
Zm.813.1.S1_at	2.50064	4.610	SnRK1-interacting protein 1, putative
Zm.8134.1.S1_at	3.34589	9.086	expressed protein
Zm.8161.1.S1_at	-1.40493	5.914	SNARE-interacting protein KEULE, putative
Zm.8278.1.A1_at	6.35066	2.128	MtN3/saliva family protein
Zm.8559.1.A1_at	-5.86079	5.947	expressed protein
Zm.8680.1.A1_at	-2.37794	9.954	none
Zm.8708.1.S1_at	-5.28592	5.968	Aldose 1-epimerase family protein
Zm.8850.1.A1_at	1.67704	4.871	Peptidyl-prolyl cis-trans isomerase, putative
Zm.889.2.S1_at	-5.61752	5.341	Serine/threonine-protein kinase SNT7, chloroplast precursor, putative
Zm.8898.1.A1_at	-2.28050	6.818	expressed protein
Zm.8914.1.S1_at	-4.28312	4.275	Chlorophyll a-b binding protein 8, chloroplast precursor, putative
Zm.892.1.A1_at	-1.63451	7.127	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic, putative
Zm.8992.1.S1_at	-3.64138	2.787	none
Zm.9058.1.A1_at	1.82179	4.299	Eukaryotic aspartyl protease family protein
Zm.9124.1.A1_at	-0.83076	8.892	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative
Zm.9223.1.A1_at	-3.96119	3.435	Protein of unknown function, DUF614 containing protein
Zm.9241.1.A1_at	0.92124	9.400	Cytochrome P450 72A1, putative
Zm.9289.1.A1_at	-2.57411	6.082	none
Zm.9319.1.A1_at	-1.13144	6.641	none
Zm.934.1.S1_at	-5.7177	3.080	heavy metal-associated domain containing protein
Zm.949.1.A1_at	-4.38784	6.083	glycerophosphoryl diester phosphodiesterase 1 precursor, putative
Zm.953.1.A1_at	2.58400	3.133	none
Zm.9601.1.A1_at	-3.88202	5.611	Nicotianamine synthase 3, putative
Zm.9637.1.A1_at	-4.72947	4.196	expressed protein
Zm.9651.1.A1_at	-1.77212	6.989	none
Zm.966.1.A1_at	-2.82604	5.955	none
Zm.9696.1.S1_at	4.81887	7.566	Nitrate-induced NOI protein
Zm.9751.1.A1_at	-1.38763	7.076	Bromodomain associated family protein
Zm.9770.1.A1_at	0.98986	7.947	expressed protein
Zm.9803.1.A1_at	-4.78015	2.790	aminotransferase, classes I and II family protein
Zm.9829.1.A1_at	1.48272	7.830	chorismate mutase family protein
Zm.9867.1.A1_at	-4.34165	3.708	Lichenase II precursor, putative
Zm.9873.1.A1_at	-4.54790	6.755	none
Zm.9944.1.A1_at	3.59992	9.378	none
Zm.9973.1.A1_at	1.37438	9.619	GUN4-like family protein
ZmAffx.1079.1.A1_at	-3.36910	4.672	none
ZmAffx.1082.1.A1_at	-2.19531	4.735	none
ZmAffx.1087.1.S1_s_at	-5.64635	4.365	none
ZmAffx.389.1.A1_at	0.88830	9.378	Zinc finger, C3HC4 type family protein
ZmAffx.543.1.A1_at	1.40629	8.799	60S ribosomal protein L27, putative
ZmAffx.64.1.A1_at	4.83484	3.708	Mechanosensitive ion channel family protein
ZmAffx.704.1.A1_at	2.42265	3.133	expressed protein
ZmAffx.705.1.A1_at	4.30561	4.985	none
ZmAffx.726.1.A1_at	2.07426	3.880	Rare lipoprotein A like double-psi beta-barrel containing protein
ZmAffx.728.1.A1_at	2.26691	6.641	nucleoporin family protein, putative
ZmAffx.734.1.A1_at	-1.64469	7.512	none
ZmAffx.743.1.A1_at	-0.91704	9.749	none
ZmAffx.936.1.A1_at	7.85959	3.483	oxidoreductase, 2OG-Fe oxygenase family protein
ZmAffx.998.1.A1_at	-1.87004	8.468	PHD finger protein, putative

*Log ratios with base 2 for the *Zm401p10*/wild type anthers at young microspore stages are average values from two replicate experiments. OE: transgenics with overexpression of *Zm401p10*, WT: wild type.