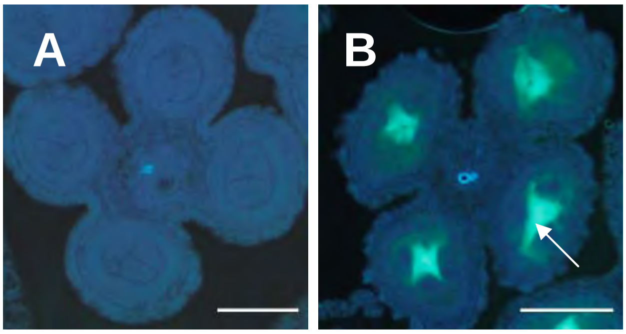
Supplemental File Contents:

Supplemental Figure 1

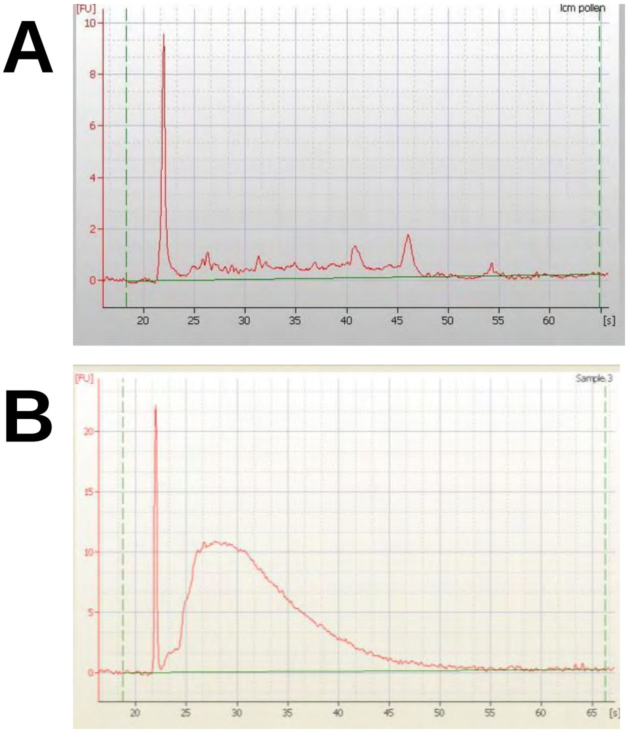


Supplemental Figure 1 Aniline blue staining of cross section of anthers about 2mm long.

Anthers about 2mm long were stained with aniline blue to detect callose. Most anthers were in the pre-meiosis stage, and callose was not detectable in PMCs (A). Some anthers were in the early meiosis stage, and callose was deposited around the PMCs (B). Callose deposition is shown as bright-yellow fluorescence (indicated by arrows). The pre-meiosis and early meiosis stage were distinguished according to the results of Chen(2007).
Bar=50 μ m.

Chen RZ, Zhao X, Shao Z *et al* (2007). Rice UDP-Glucose Pyrophosphorylase1 Is Essential for Pollen Callose Deposition and Its Cosuppression Results in a New Type of Thermosensitive Genic Male Sterility. Plant Cell, 19: 847–861.

Supplemental Figure 2



Supplemental Figure 2. Assessment of the quality of total RNA (A) extracted from laser microdissected sample of pollen mother cells and amplified RNA for microarray hybridization (B) by Agilent bioanalyzer 2100.

Supplemental Figure 3

A. 59% (17,196 of 29,008) of rice genes are expressed in PMCs.

B.

C.

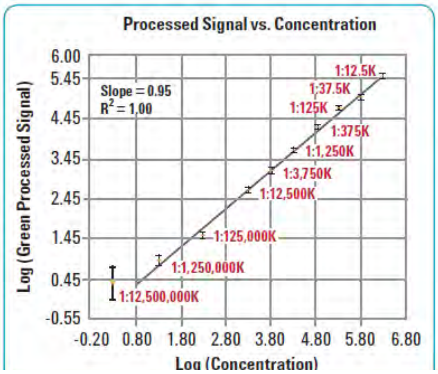


Chart from LeProust 2008

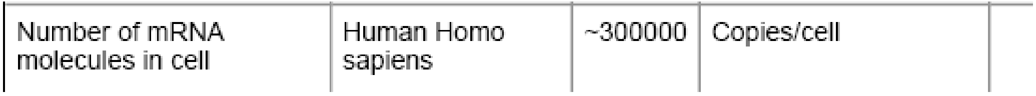
D.

	mRNA copy number per pollen mother cell	intensity in microarray
Os03g0650400	~1000	114,355
Os09g0480300	~600	79,423
all mRNA	3,650,000	455,220,997

A1=455220997x1000/114355=3980770
A2=455220997x600/79423=3324371
AVERAGE=3652571

E. Total intensity of all genes expressed in TCP in our microarray is 312,524,120, therefore total mRNA copy in TCP is estimated as 2,500,000.

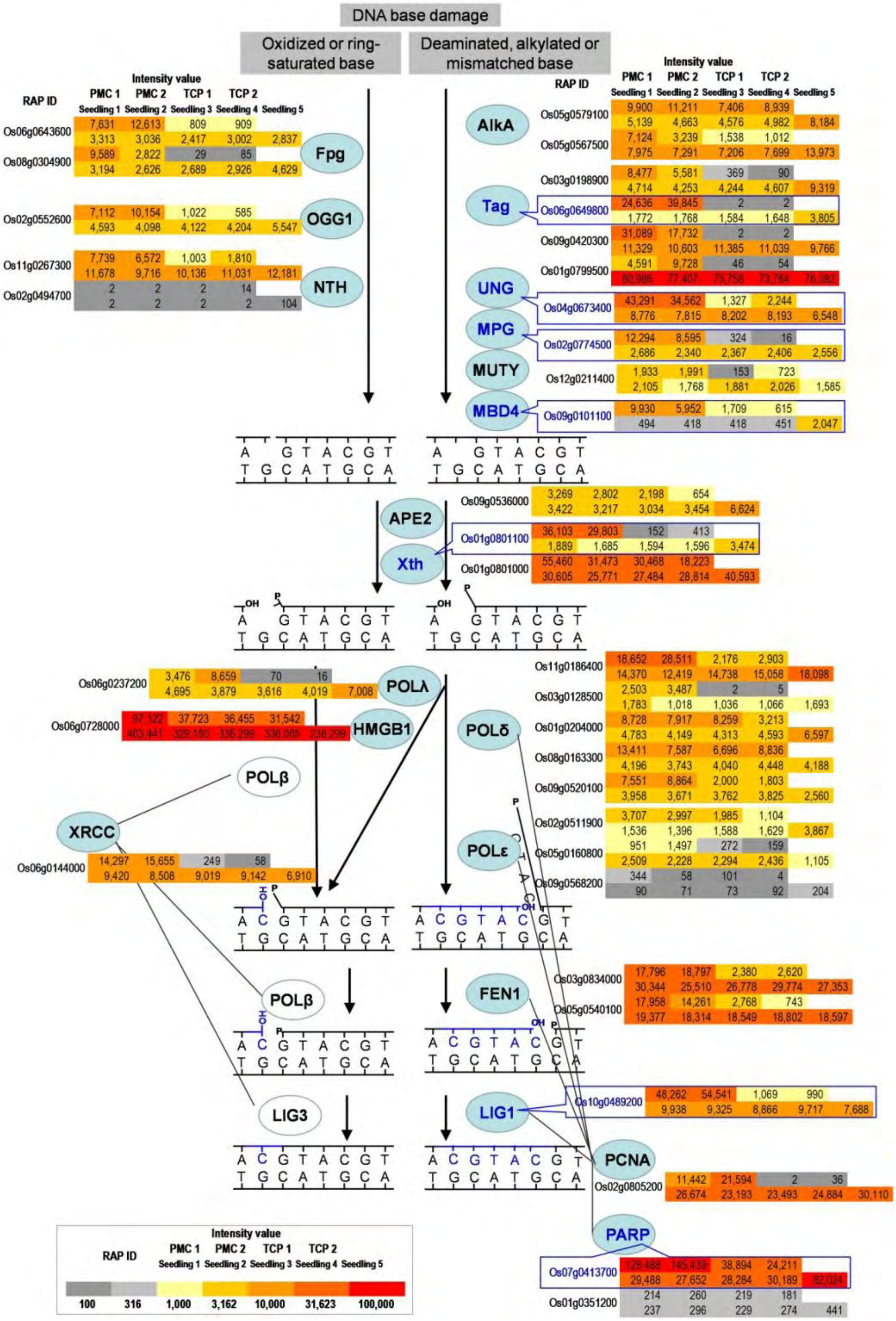
F.



Number of mRNA molecules in cell	Human Homo sapiens	~300000	Copies/cell

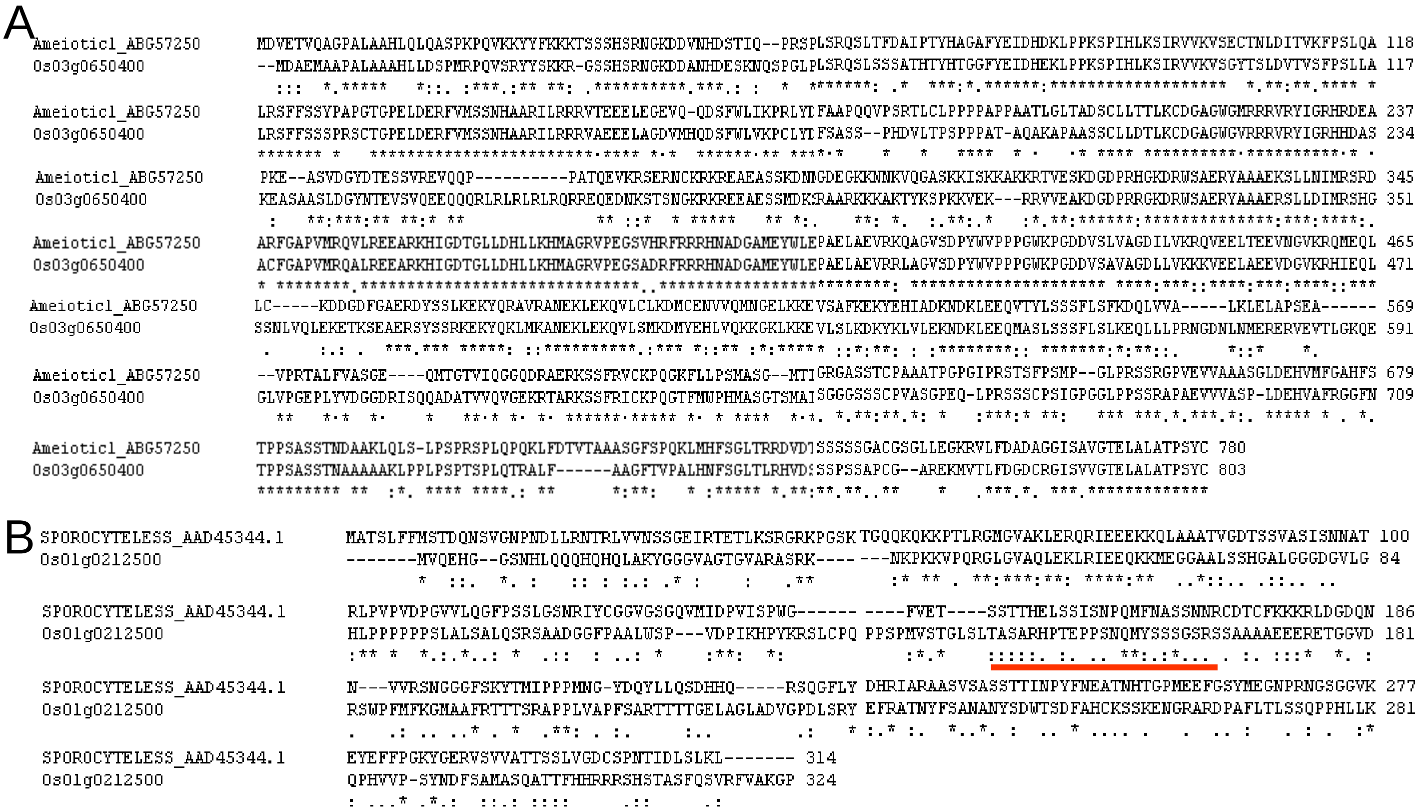
Supplemental Figure 3. Calculation of total mRNA copy number per PMC. A. The number of genes that expressed in PMCs, which is different concept from total copy number. B. Laser microdissection can count how many cells captured. C. Linear relationship of mRNA concentration to signal intensity measured by Agilent microarray. Chart from LeProust (2008) Agilent's Microarray Platform: How High-Fidelity DNA Synthesis Maximizes the Dynamic Range of Gene Expression Measurements. D. Calculation table for PMC. E. Similar calculation for TCP . F. Noteworthy that our calculation is about 10 fold of that number calculated in human (data from bionumbers).

Supplemental Figure 4



Supplemental Figure 4. Rice genes in both the short-patch (left branch) and long-patch (right branch) base excision repair pathways with expression data from our microarray. The absolute intensity values (with background subtraction) of individual genes from the two biological replicates of pollen mother cells (PMC1, PMC2), two biological replicates of tricellular pollen (TCP1, TCP2) and five replicates of seedling samples (Seedling 1-5) are listed beside the gene RAP ID, and color-coded as indicated. Gene names as KEGG. Fpg, formamidopyrimidine-DNA glycolase; OGG1, 8-oxoguanine-DNA glycosylase; NTH, endonuclease III; AlkA, DNA-3-methyladenine glycosylase II; Tag, DNA-3-methyladenine glycosylase I; UNG, uracil-DNA glycosylase; MUTY, A/G-specific adenine glycosylase; MPG, N-methylpurine-DNA glycosylase; MBD4, methyl-CpG binding domain protein 4; APE2, AP endonuclease 2; Xth, exodeoxyribonuclease III; HMGB1, high mobility group protein B1; XRCC1, BRCT domain containing; POL, DNA polymerase; FEN1, flap structure-specific endonuclease 1; LIG, DNAligase; PCNA, proliferating cell nuclear antigen; PARP, Poly(ADP)-ribose polymerase. POL□ and LIG3 are unknown in rice. The genes expressing significantly higher in pollen mother cells than in tri-cellular pollen and in seedling are in blue.

Supplemental Figure 5



A

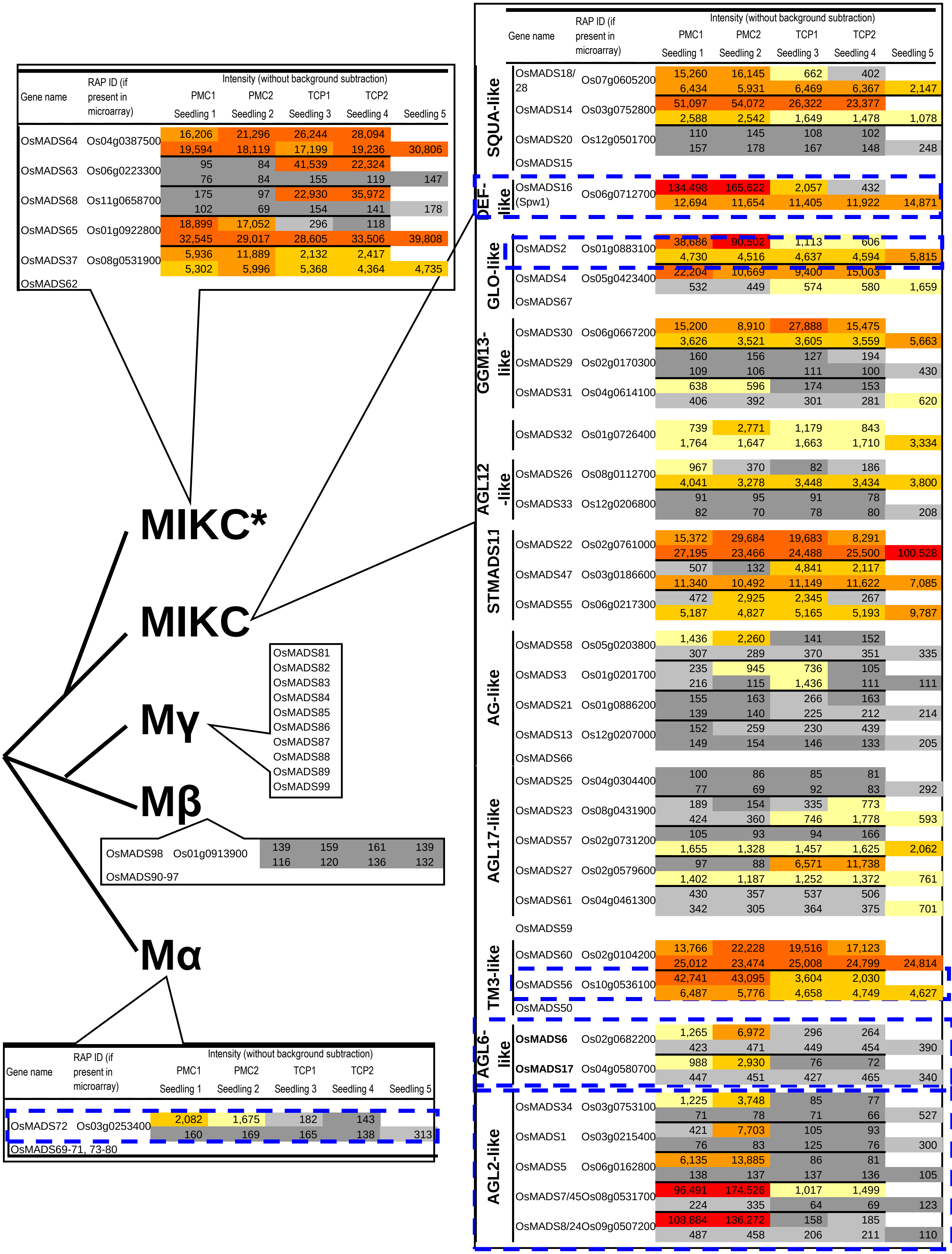
```
Ameiotic1_ABG57250    MDVETVQAGPALAAHLQLQASPKPQVKKYYFKKKTSSSHSRNGKDDVNHDSTIQ--PRSPLSRQSLTFDAIPTYHAGAFYEIDHDKLPPKSPIHLKSIRVVKVSECTNLDITVKFPSLQA 118
Os03g0650400          --MDAEMAAPALAAAHLLDSPMRPQVSRYYSKKR-GSSHSRNGKDDANHDESKNQSPGLPLSRQSLSSSATHTYHTGGFYEIDHEKLPPKSPIHLKSIRVVKVSGYTSLDVTVSFPSLLA 117
                        :::  *.*****   *::. :***.:** **: .**********.***.: :  *  *******: .*  ***:*.******:********************  *.**:**.**** *

Ameiotic1_ABG57250    LRSFFSSYPAPGTGPELDERFVMSSNHAARILRRRVTEEELEGEVQ-QDSFWLIKPRLYI FAAPQQVPSRTLCLPPPPAPPAATLGLTADSCLLTTLKCDGAGWGMRRRVRYIGRHRDEA 237
Os03g0650400          LRSFFSSSPRSCTGPELDERFVMSSNHAARILRRRVAEEELAGDVMHQDSFWLVKPCLYI FSASS--PHDVLTPSPPPAT-AQAKAPAASSCLLDTLKCDGAGWGVRRRVRYIGRHHDAS 234
                      ******* *   *************************.**** *.*  ******.** ***:*.*    *    *    ****  * .    .* **** ***********.***********.* .

Ameiotic1_ABG57250    PKE--ASVDGYDTESSVREVQQP----------PATQEVKRSERNCKRKREAEASSKDNNGDEGKKNNKVQGASKKISKKAKKRTVESKDGDPRHGKDRWSAERYAAAEKSLLNIMRSRD 345
Os03g0650400          KEASAASLDGYNTEVSVQEEQQQRLRLRLRLRQRREQEDNKSTSNGKRKREEAESSMDKSRAARKKKAKTYKSPKKVEK---RRVVEAKDGDPRRGKDRWSAERYAAAERSLLDIMRSHG 351
                       :   **:***:** **:* **                ** ::*  * *****   ** *:.    **: *.   :.**:.*   :*.**:******:***************:***:****:.

Ameiotic1_ABG57250    ARFGAPVMRQVLREEARKHIGDTGLLDHLLKHMAGRVPEGSVHRFRRRHNADGAMEYWLEPAELAEVRKQAGVSDPYWVPPPGWKPGDDVSLVAGDILVKRQVEELTEEVNGVKRQMEQL 465
Os03g0650400          ACFGAPVMRQALREEARKHIGDTGLLDHLLKHMAGRVPEGSADRFRRRHNADGAMEYWLEPAELAEVRRLAGVSDPYWVPPPGWKPGDDVSAVAGDLLVKKKVEELAEEVDGVKRHIEQL 471
                      * ********.*********************************..*************************: ********************* ****:***::****:***:****::***

Ameiotic1_ABG57250    LC-----KDDGDFGAERDYSSLKEKYQRAVRANEKLEKQVLCLKDMCENVVQMNGELKKE VSAFKEKYEHIADKNDKLEEQVTYLSSSFLSFKDQLVVA-----LKLELAPSEA------ 569
Os03g0650400          SSNLVQLEKETKSEAERSYSSRKEKYQKLMKANEKLEKQVLSMKDMYEHLVQKKGKLKKE VLSLKDKYKLVLEKNDKLEEQMASLSSSFLSLKEQLLLPRNGDNLNMERERVEVTLGKQE 591
                       .     :.: .  ***.*** *****: ::**********.:*** *::** :*:***** ::*:**: : :********:: *******:*:**::.     *::*    *.

Ameiotic1_ABG57250    --VPRTALFVASGE----QMTGTVIQGGQDRAERKSSFRVCKPQGKFLLPSMASG--MTI GRGASSTCPAAATPGPGIPRSTSFPSMP--GLPRSSRGPVEVVAAASGLDEHVMFGAHFS 679
Os03g0650400          GLVPGEPLYVDGGDRISQQADATVVQVGEKRTARKSSFRICKPQGTFMWPHMASGTSMAI SGGGSSSCPVASGPEQ-LPRSSSCPSIGPGGLPPSSRAPAEVVVASP-LDEHVAFRGGFN 709
                        **    *.*  *.     *    **.* *. *. ******.***** *. * ****  *.*. *.**:**.*: *   :***:* **:    *** ***.*.***.*:. ***** * . *.

Ameiotic1_ABG57250    TPPSASSTNDAAKLQLS-LPSPRSPLQPQKLFDTVTAAASGFSPQKLMHFSGLTRRDVD SSSSSGACGSGLLEGKRVLFDADAGGISAVGTELALATPSYC 780
Os03g0650400          TPPSASSTNAAAAAKLPPLPSPTSPLQTRALF------AAGFTVPALHNFSGLTLRHVD SSPSSAPCG--AREKMVTLFDGDCRGISVVGTELALATPSYC 803
                      ********* **  :*. **** ****.: **      *:**:   * :***** *.**:**.**..**    *   .***.*. ***.*************
```

B

```
SPOROCYTELESS_AAD45344.1    MATSLFFMSTDQNSVGNPNDLLRNTRLVVNSSGEIRTETLKSRGRKPGSK TGQQKQKKPTLRGMGVAKLERQRIEEEKKQLAAATVGDTSSVASISNNAT 100
Os01g0212500                -------MVQEHG--GSNHLQQQHQHQLAKYGGGVAGTGVARASRK---- ---NKPKKVPQRGLGVAQLEKLRIEEQKKMEGGAALSSHGALGGGDGVLG 84
                                   *  ::.  *. :   :: : :.: .* :    :   .**       :* ** . **:***:**: ****:**  ..*::.. .::.. ..

SPOROCYTELESS_AAD45344.1    RLPVPVDPGVVLQGFPSSLGSNRIYCGGVGSGQVMIDPVISPWG------ ----FVET----SSTTHELSSISNPQMFNASSNNRCDTCFKKKRLDGDQN 186
Os01g0212500                HLPPPPPPSLALSALQSRSAADGGFPAALWSP---VDPIKHPYKRSLCPQ PPSPMVSTGLSLTASARHPTEPPSNQMYSSSGSRSSAAAAEEERETGGVD 181
                            :** *  *.:.*..: *  .::  : ..: *    :**:  *:            :*.*    :::::. :. ..  **:.:*... . :. :::*  *. :

SPOROCYTELESS_AAD45344.1    N---VVRSNGGGFSKYTMIPPPMNG-YDQYLLQSDHHQ-----RSQGFLY DHRIARAASVSASSTTINPYFNEATNHTGPMEEFGSYMEGNPRNGSGGVK 277
Os01g0212500                RSWPFMFKGMAAFRTTTSRAPPLVAPFSARTTTTGELAGLADVGPDLSRY EFRATNYFSANANYSDWTSDFAHCKSSKENGRARDPAFLTLSSQPPHLLK 281
                            .   .: .. ..* . *  .**: . :.     :..        .:   * :.* :.  *..*. :  .. * .... .    .  .. :   . : .  :*

SPOROCYTELESS_AAD45344.1    EYEFFPGKYGERVSVVATTSSLVGDCSPNTIDLSLKL------- 314
Os01g0212500                QPHVVP-SYNDFSAMASQATTFHHRRRSHSTASFQSVRFVAKGP 324
                            : ...* .*.:  ::.: ::::     .::      .:
```

Supplemental Figure 5. Protein sequence alignments. A. The alignment of maize Ameiotic 1 and its rice homolog Os03g0650400 shows significant similarity, suggesting Os03g0650400 is the ortholog of Ameiotic 1. B. The alignment of Arabidopsis SPOROCYTELESS (SPL) and its rice homolog Os01g0212500 (B) shows weak similarity between these two proteins. Red underline indicated the helix 1 of the MADS domain from SPL protein with significant similarity.

Supplemental Figure 6



Gene name	RAP ID (if present in microarray)	PMC1 Seedling 1	PMC2 Seedling 2	TCP1 Seedling 3	TCP2 Seedling 4	Seedling 5
OsMADS64	Os04g0387500	16,206	21,296	26,244	28,094	
		19,594	18,119	17,199	19,236	30,806
OsMADS63	Os06g0223300	95	84	41,539	22,324	
		76	84	155	119	147
OsMADS68	Os11g0658700	175	97	22,930	35,972	
		102	69	154	141	178
OsMADS65	Os01g0922800	18,899	17,052	296	118	
		32,545	29,017	28,605	33,506	39,808
OsMADS37	Os08g0531900	5,936	11,889	2,132	2,417	
		5,302	5,996	5,368	4,364	4,735
OsMADS62						

	Gene name	RAP ID (if present in microarray)	PMC1 Seedling 1	PMC2 Seedling 2	TCP1 Seedling 3	TCP2 Seedling 4	Seedling 5
SQUA-like	OsMADS18/28	Os07g0605200	15,260	16,145	662	402	
			6,434	5,931	6,469	6,367	2,147
	OsMADS14	Os03g0752800	51,097	54,072	26,322	23,377	
			2,588	2,542	1,649	1,478	1,078
	OsMADS20	Os12g0501700	110	145	108	102	
			157	178	167	148	248
	OsMADS15						
DEF-like	OsMADS16 (Spw1)	Os06g0712700	134,498	165,622	2,057	432	
			12,694	11,654	11,405	11,922	14,871
GLO-like	OsMADS2	Os01g0883100	38,686	90,502	1,113	606	
			4,730	4,516	4,637	4,594	5,815
	OsMADS4	Os05g0423400	22,204	10,669	9,400	15,003	
			532	449	574	580	1,659
	OsMADS67						
GGM13-like	OsMADS30	Os06g0667200	15,200	8,910	27,888	15,475	
			3,626	3,521	3,605	3,559	5,663
	OsMADS29	Os02g0170300	160	156	127	194	
			109	106	111	100	430
	OsMADS31	Os04g0614100	638	596	174	153	
			406	392	301	281	620
	OsMADS32	Os01g0726400	739	2,771	1,179	843	
			1,764	1,647	1,663	1,710	3,334
AGL12-like	OsMADS26	Os08g0112700	967	370	82	186	
			4,041	3,278	3,448	3,434	3,800
	OsMADS33	Os12g0206800	91	95	91	78	
			82	70	78	80	208
STMADS11	OsMADS22	Os02g0761000	15,372	29,684	19,683	8,291	
			27,195	23,466	24,488	25,500	100,528
	OsMADS47	Os03g0186600	507	132	4,841	2,117	
			11,340	10,492	11,149	11,622	7,085
	OsMADS55	Os06g0217300	472	2,925	2,345	267	
			5,187	4,827	5,165	5,193	9,787
AG-like	OsMADS58	Os05g0203800	1,436	2,260	141	152	
			307	289	370	351	335
	OsMADS3	Os01g0201700	235	945	736	105	
			216	115	1,436	111	111
	OsMADS21	Os01g0886200	155	163	266	163	
			139	140	225	212	214
	OsMADS13	Os12g0207000	152	259	230	439	
			149	154	146	133	205
	OsMADS66						
AGL17-like	OsMADS25	Os04g0304400	100	86	85	81	
			77	69	92	83	292
	OsMADS23	Os08g0431900	189	154	335	773	
			424	360	746	1,778	593
	OsMADS57	Os02g0731200	105	93	94	166	
			1,655	1,328	1,457	1,625	2,062
	OsMADS27	Os02g0579600	97	88	6,571	11,738	
			1,402	1,187	1,252	1,372	761
	OsMADS61	Os04g0461300	430	357	537	506	
			342	305	364	375	701
	OsMADS59						
TM3-like	OsMADS60	Os02g0104200	13,766	22,228	19,516	17,123	
			25,012	23,474	25,008	24,799	24,814
	OsMADS56	Os10g0536100	42,741	43,095	3,604	2,030	
			6,487	5,776	4,658	4,749	4,627
	OsMADS50						
AGL6-like	**OsMADS6**	Os02g0682200	1,265	6,972	296	264	
			423	471	449	454	390
	OsMADS17	Os04g0580700	988	2,930	76	72	
			447	451	427	465	340
AGL2-like	OsMADS34	Os03g0753100	1,225	3,748	85	77	
			71	78	71	66	527
	OsMADS1	Os03g0215400	421	7,703	105	93	
			76	83	125	76	300
	OsMADS5	Os06g0162800	6,135	13,885	86	81	
			138	137	137	136	105
	OsMADS7/45	Os08g0531700	96,491	174,526	1,017	1,499	
			224	335	64	69	123
	OsMADS8/24	Os09g0507200	108,884	136,272	158	185	
			487	458	206	211	110

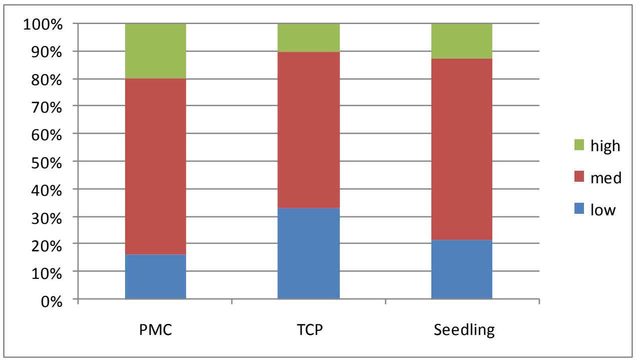
OsMADS81
OsMADS82
OsMADS83
OsMADS84
OsMADS85
OsMADS86
OsMADS87
OsMADS88
OsMADS89
OsMADS99

OsMADS98	Os01g0913900	139	159	161	139
		116	120	136	132
OsMADS90-97					

Gene name	RAP ID (if present in microarray)	PMC1 Seedling 1	PMC2 Seedling 2	TCP1 Seedling 3	TCP2 Seedling 4	Seedling 5
OsMADS72	Os03g0253400	2,082	1,675	182	143	
		160	169	165	138	313
OsMADS69-71, 73-80						

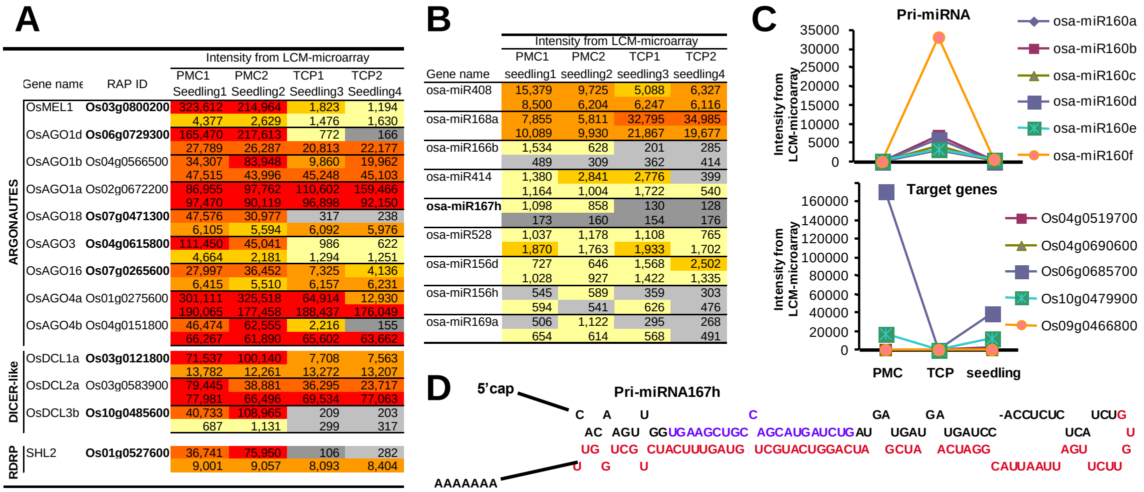
Supplemental Figure 6. Expression data of rice MADS transcription factors with a phylogenic view. The blue boxes indicate the PMC-preferential expressed ones.

Supplemental Figure 7



Supplemental Figure 7. Highly expressed transcription factors occupy more percentage in pollen mother cells than in tri-cellular pollen or seedling.

Supplemental Figure 8



A

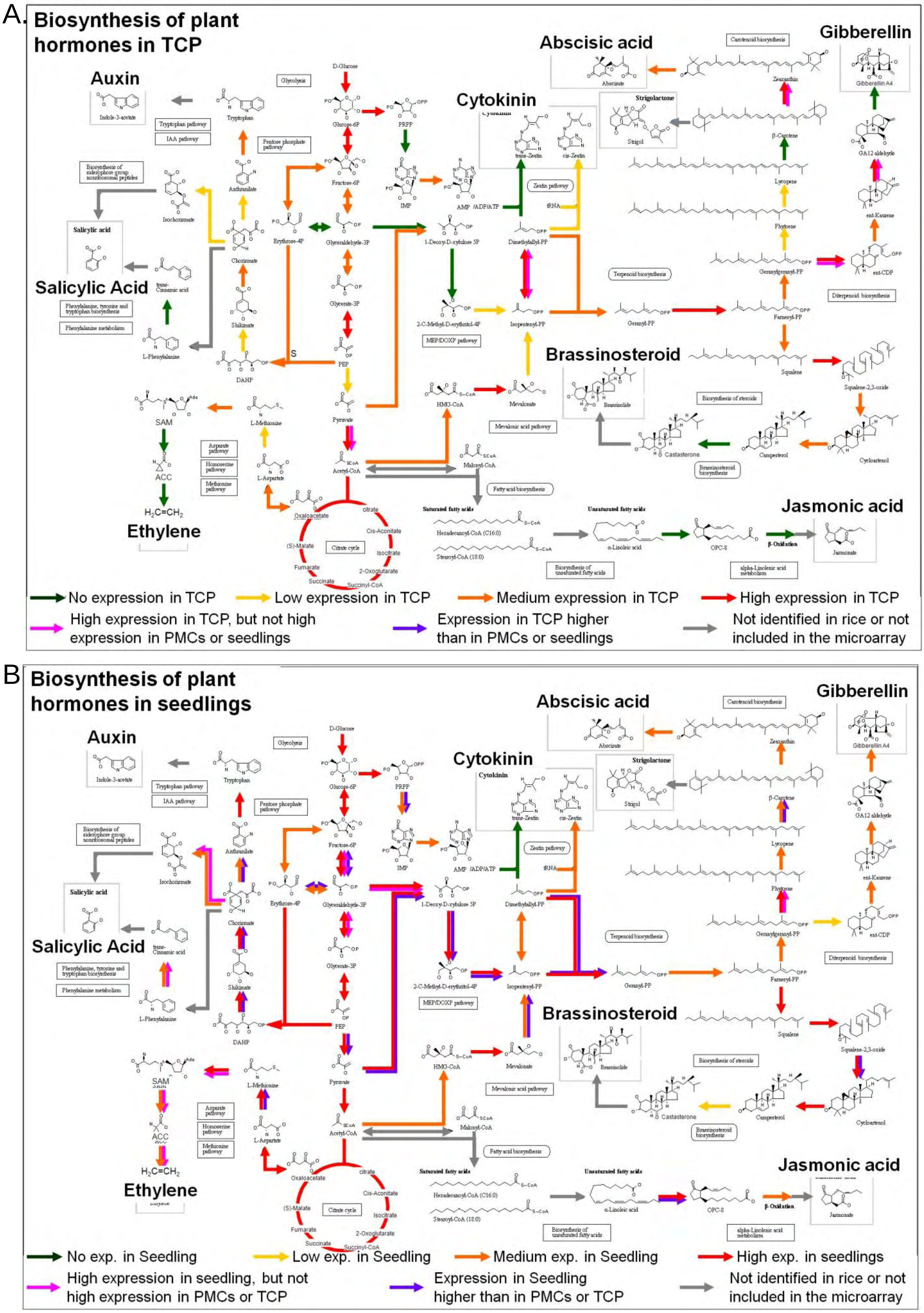
	Gene name	RAP ID	Intensity from LCM-microarray PMC1 Seedling1	PMC2 Seedling2	TCP1 Seedling3	TCP2 Seedling4
ARGONAUTES	OsMEL1	**Os03g0800200**	323,612	214,964	1,823	1,194
			4,377	2,629	1,476	1,630
	OsAGO1d	**Os06g0729300**	165,470	217,613	772	166
			27,789	26,287	20,813	22,177
	OsAGO1b	Os04g0566500	34,307	83,948	9,860	19,962
			47,515	43,996	45,248	45,103
	OsAGO1a	Os02g0672200	86,955	97,762	110,602	159,466
			97,470	90,119	96,898	92,150
	OsAGO18	**Os07g0471300**	47,576	30,977	317	238
			6,105	5,594	6,092	5,976
	OsAGO3	**Os04g0615800**	111,450	45,041	986	622
			4,664	2,181	1,294	1,251
	OsAGO16	**Os07g0265600**	27,997	36,452	7,325	4,136
			6,415	5,510	6,157	6,231
	OsAGO4a	Os01g0275600	301,111	325,518	64,914	12,930
			190,065	177,458	188,437	176,049
	OsAGO4b	Os04g0151800	46,474	62,555	2,216	155
			66,267	61,890	65,602	63,662
DICER-like	OsDCL1a	**Os03g0121800**	71,537	100,140	7,708	7,563
			13,782	12,261	13,272	13,207
	OsDCL2a	Os03g0583900	79,445	38,881	36,295	23,717
			77,981	66,496	69,534	77,063
	OsDCL3b	**Os10g0485600**	40,733	108,965	209	203
			687	1,131	299	317
RDRP	SHL2	**Os01g0527600**	36,741	75,950	106	282
			9,001	9,057	8,093	8,404

B

Gene name	Intensity from LCM-microarray PMC1 seedling1	PMC2 seedling2	TCP1 seedling3	TCP2 seedling4
osa-miR408	15,379	9,725	5,088	6,327
	8,500	6,204	6,247	6,116
osa-miR168a	7,855	5,811	32,795	34,985
	10,089	9,930	21,867	19,677
osa-miR166b	1,534	628	201	285
	489	309	362	414
osa-miR414	1,380	2,841	2,776	399
	1,164	1,004	1,722	540
osa-miR167h	1,098	858	130	128
	173	160	154	176
osa-miR528	1,037	1,178	1,108	765
	1,870	1,763	1,933	1,702
osa-miR156d	727	646	1,568	2,502
	1,028	927	1,422	1,335
osa-miR156h	545	589	359	303
	594	541	626	476
osa-miR169a	506	1,122	295	268
	654	614	568	491

Supplemental Figure 8. MicroRNA pathways in pollen mother cells. A. The expression data of microRNA biosynthesis pathway genes. B. The expression data of rice microRNA encoding genes that expressed in pollen mother cells. C. The expression of osa miR160 encoding genes and their putative target genes are anti-correlated in pollen mother cells (PMC), tri-cellular pollen (TCP) and seedling, as a successful case of using miRNA coding gene probes to represent the expression of miRNA. This result shows that multiple miR160-encoding genes are expressed in TCP, while their putative target genes are not expressed in TCP, suggesting that miR160 genes are functional in TCP. This is consistent with recent reports (Grant-Downton et al., 2009; Chambers and Shuai 2009) demonstrating miR160 expression in Arabidopsis mature pollen, a stage very similar to TCP (Honys and Twell 2004). This result also suggests that none of the miR160-encoding genes are expressed in PMCs, consistent with the high expression of its putative target gene in PMCs, OsARF18 (Os06g0685700). D. The structure of pri-miR167h, the letters in red indicate the binding site of the 60mer probe in Agilent microarray, the letters in purple indicate the sequence of mature miR167.

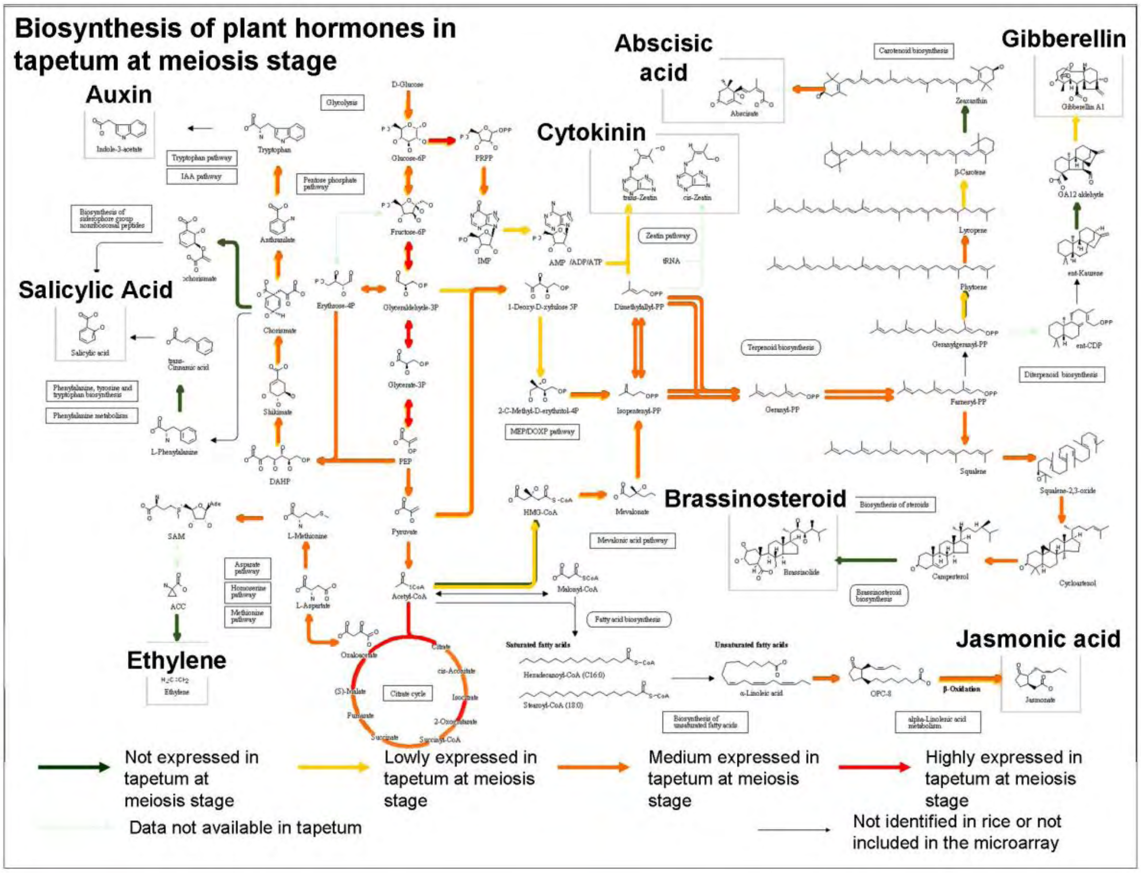
Supplemental Figure 9



Supplemental Figure 9. Overview of plant hormone biosynthesis pathways in rice TCP (A), seedling (B) and tapetum (C) with colored arrows indicating the gene expression patterns. Tapetum expression data according to Hirano *et al., 2008.*

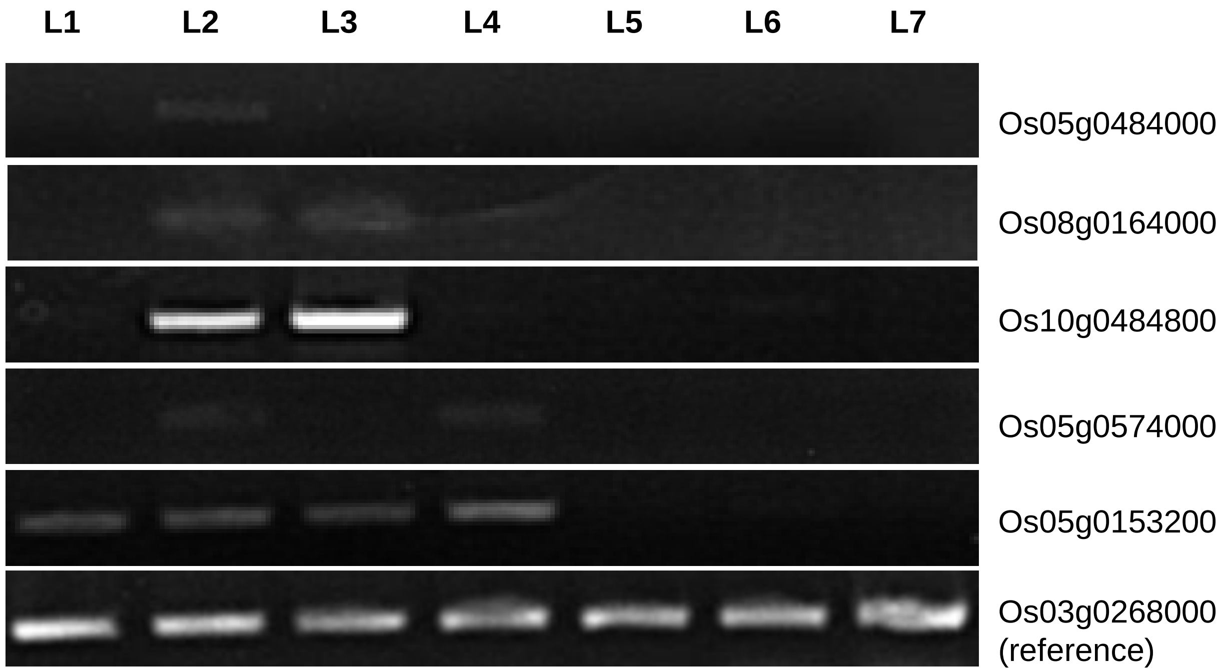
Supplemental Figure 9 continue

C.



Supplemental Figure 9. Overview of plant hormone biosynthesis pathways in rice TCP (A), seedling (B) and tapetum (C) with colored arrows indicating the gene expression patterns. Tapetum expression data according to Hirano *et al., 2008.*

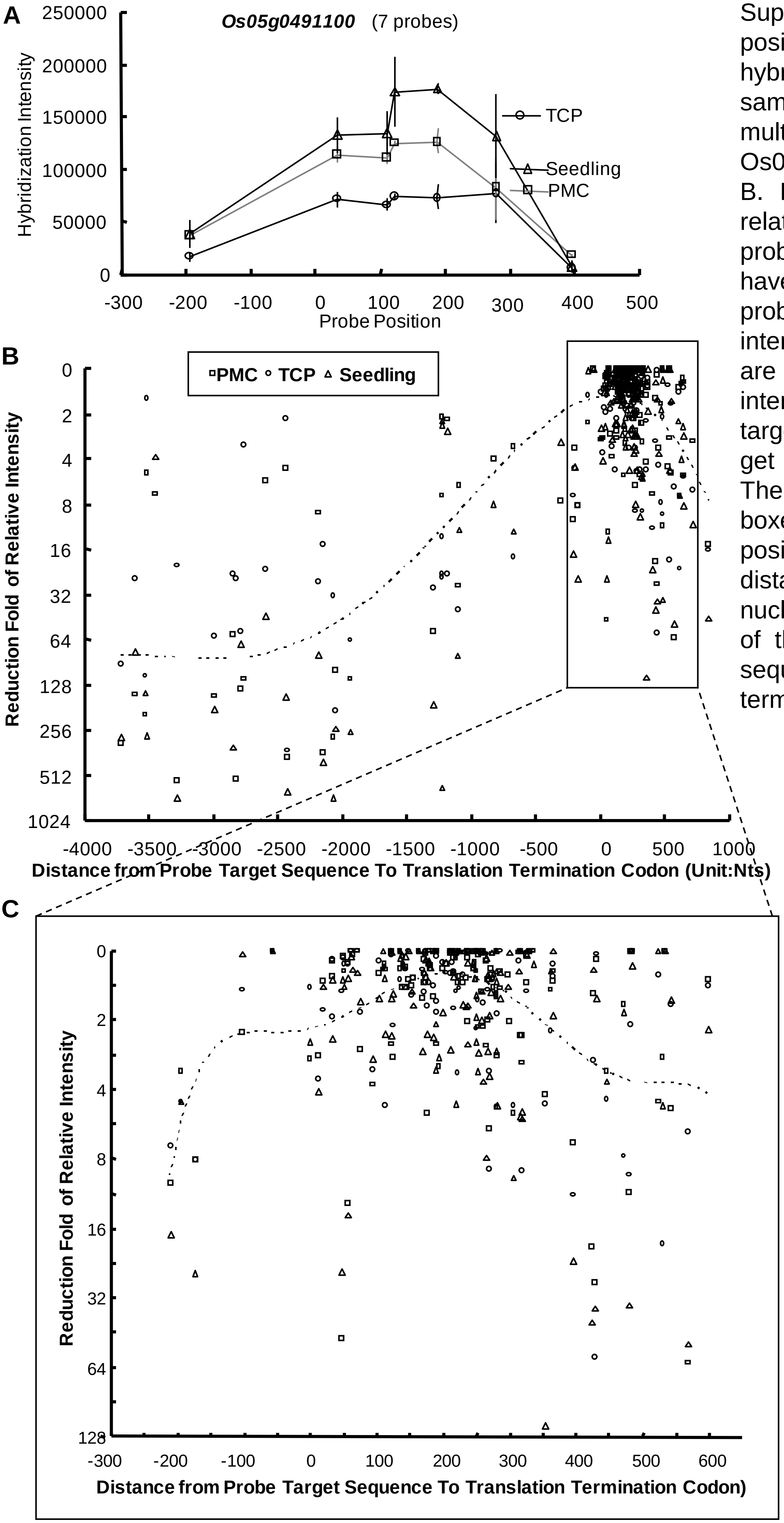
Supplemental Figure 10



Supplemental Figure 10. RT-PCR results for 5 genes in rice panicles at different developmental stages and other organs (young rice leaf, stem and root), using Os03g0268000 as a reference gene. The RT-PCR were repeated at least twice for each gene.

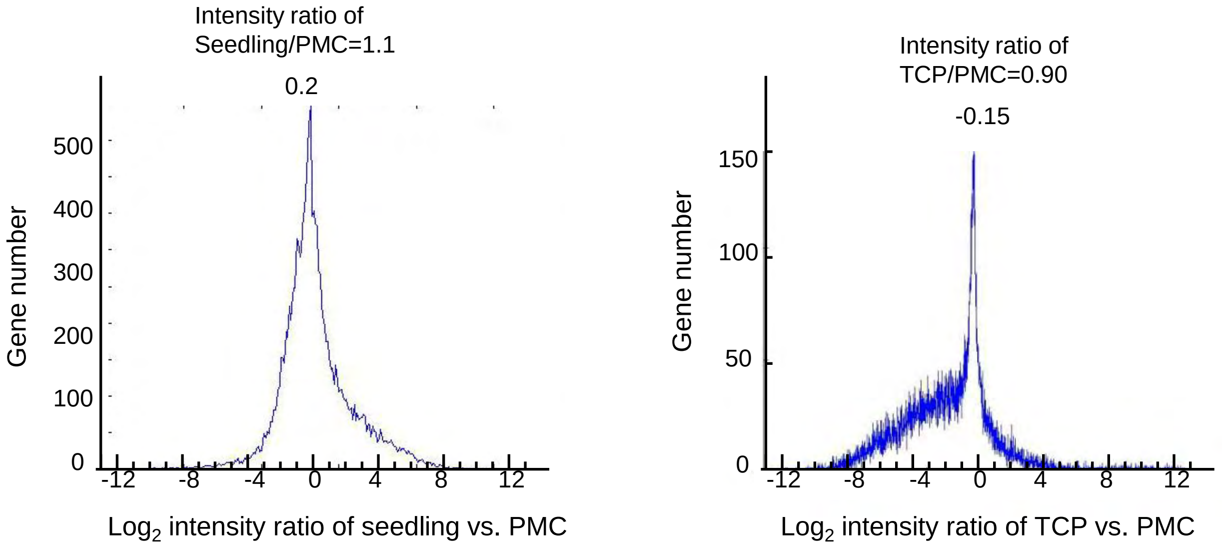
L1: Immature panicle at anther stage 3.
L2: Immature panicle at anther stage 5 (PMC stage).
L3: Immature panicle at anther stage 7.
L4: Mature panicle (TCP stage).
L5: leaf
L6: stem
L7: root

Supplemental Figure 11 probe position effects

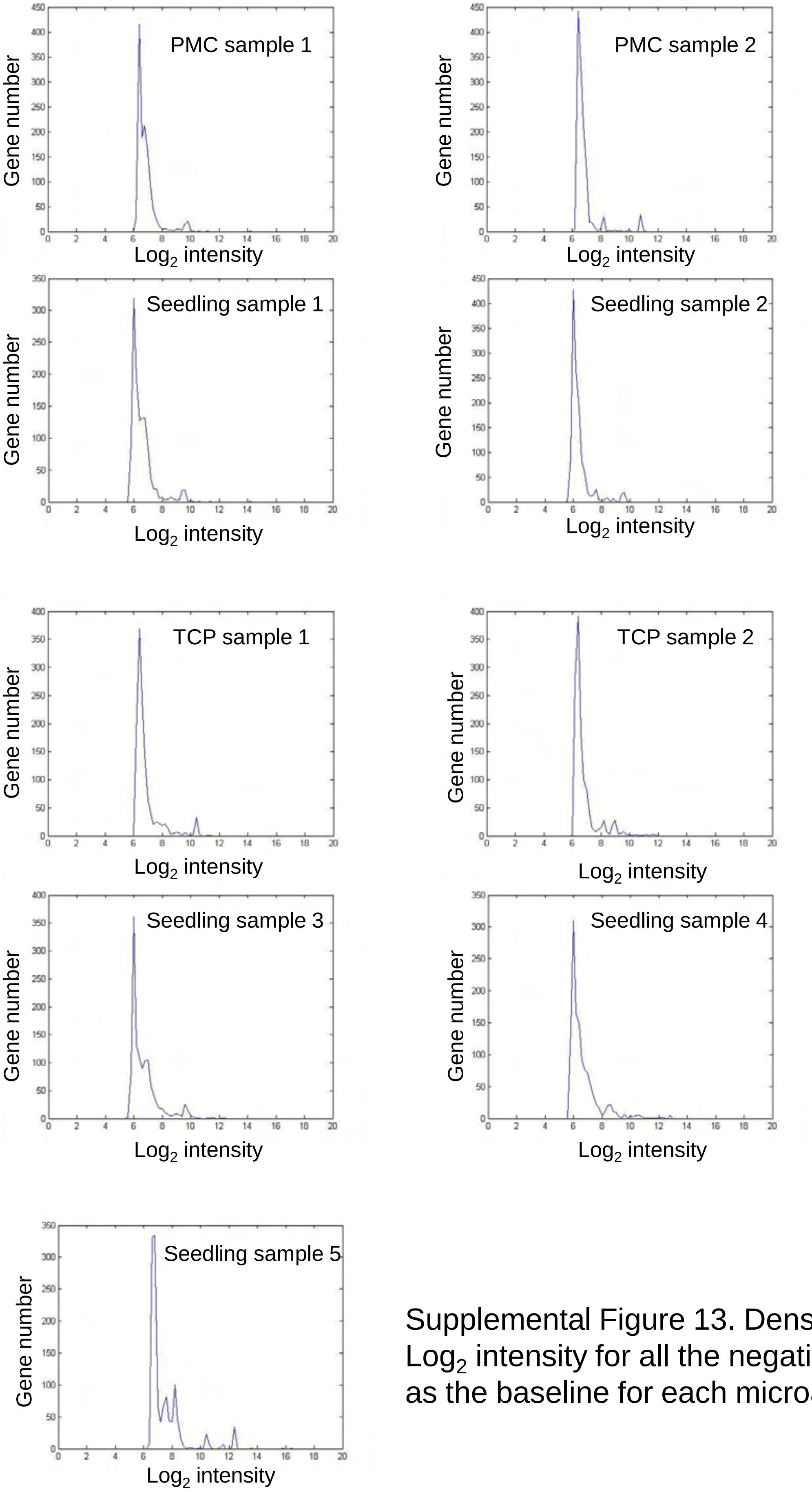


Supplemental Figure 11. Probe position effects on hybridization Intensities for the same gene. A. Intensities for multiple probes of Os05g0491100, as an example; B. Plots of reduction fold of relative intensities of all the probes for 27 genes, which have 6 to 9 representing probes each. The hybridization intensities for individual probes are divided by the maximum intensities for all the probes targeted to the same genes to get the relative intensities. C. The enlarged plot for the boxed area in B. The probe position is represented by the distance (number of nucleotides) from the 5’ end of the 60-mer probe targeted sequence to the translation termination codon.

Supplemental Figure 12



Supplemental figure 12. The density plots shows that among the intensity ratios of Seedling/PMC (left) and TCP/PMC (right) of all the genes in the microarray, the most abundant genes' ratios are very close to 1:1. (Density plots made by MATLAB)



Supplemental Figure 13. Density plot of Log$_2$ intensity for all the negative probes as the baseline for each microarray.

Supplemental table 1. Microarray data for the 26 genes that have been suggested roles in rice early stamen development

			Intensity value (without background subtraction)					Intensity value (with background subtraction)				
Accession number*	Description	RAP ID	PMC1	PMC2	TCP1	TCP2		PMC1	PMC2	TCP1	TCP2	
			Seedling 1	Seedling 2	Seedling 3	Seedling 4	Seedling 5	Seedling 1	Seedling 2	Seedling 3	Seedling 4	Seedling 5
AB004461	**DNA polymerase alpha catalytic subunit (EC 2.7.7.7).**	**Os01g0868300**	10,072	12,292	5,582	4,301		9,951	12,186	5,468	4,201	
			5,797	5,197	5,275	5,783	7,835	5,687	5,111	5,131	5,662	7,779
AK064973	OsATK1-1 (kinesin)	Os04g0629700	16,760	37,536	180	153		16,625	37,424	59	43	
			98,918	95,505	99,523	100,732	105,753	98,787	95,420	99,379	100,599	105,677
AK065897	**Tesmin/TSO1-like, CXC domain containing protein.**	**Os07g0176200**	17,147	45,307	1,104	2,105		17,020	45,203	995	2,002	
			8,882	7,802	9,297	8,917	9,320	8,763	7,727	9,168	8,793	9,262
AK069222	Hypothetical protein.	Os03g0302900	25,145	28,751	482	96		25,026	28,649	380	2	
			31,966	29,664	31,828	31,031	41,550	31,851	29,587	31,712	30,924	41,486
AK073124	EH-domain containing protein 4 (FKSG7 protein) .	Os02g0158100	43,261	26,684	884	106		43,161	26,591	796	20	
			18,212	15,369	15,424	17,125	20,467	18,122	15,302	15,345	17,045	20,399
AK073684	FYVE/PHD zinc finger domain containing protein.	Os03g0421000	1,608	7,339	1,768	1,546		1,503	7,249	1,677	1,455	
			166	143	136	142	285	79	70	37	56	232
AK071997	**Transcriptional factor B3 family**	**Os11g0523800**	13,848	52,029	90	81		13,742	51,931	2	2	
			6,056	5,953	5,785	5,911	5,515	5,954	5,880	5,680	5,818	5,447
AK103514	SMC2-1.	Os01g0904400	20,892	30,149	2,274	543		20,763	30,045	2,164	440	
			13,624	13,206	14,039	13,618	13,592	13,503	13,131	13,907	13,493	13,530
U78891	**OsMADS7/45**	**Os09g0507200**	108,884	136,272	158	185		108,780	136,178	65	95	
			487	458	206	211	110	398	389	121	131	51
X82036	OsCycB2;2	Os06g0726800	7,114	30,365	597	466		7,007	30,263	492	374	
			39,676	36,677	39,193	39,741	56,193	39,572	36,600	39,089	39,649	56,100
AK063381	Kinesin-related protein	Os03g0114000	44,932	39,709	2,286	553		44,828	39,609	2,186	463	
			13,259	12,073	12,425	12,120	17,795	13,157	11,996	12,328	12,031	17,734
AK065367	Protein kinase-like domain containing protein.	Os11g0308800	3,521	10,931	89	91		3,418	10,827	2	2	
			11,722	10,948	10,694	11,689	12,495	11,637	10,871	10,596	11,599	12,444
AK066916	Plant protein of unknown function DUF869 family	Os03g0246500	85,538	151,554	468	524		85,414	151,448	353	429	
			102,777	90,192	98,065	102,006	173,025	102,665	90,106	97,945	101,900	172,962
AK071939	Homeobox domain containing	Os10g0575600	1,260	6,457	157	167		1,145	6,355	47	72	
			12,479	9,630	11,421	12,415	36,291	12,372	9,545	11,288	12,301	36,217
AK073282	IQ calmodulin-binding region domain containing protein.	Os01g0194200	9,250	1,891	266	190		9,147	1,795	175	101	
			26,859	24,692	25,239	25,878	43,456	26,764	24,620	25,143	25,793	43,390
AK101994	TPR-like domain containing	Os11g0598800	99,853	52,807	1,987	5,000		99,741	52,706	1,878	4,904	
			1,029	520	94	133	147	928	436	2	11	89
AK102192	Relative to SR12 protein	Os03g0165400	117,125	160,745	131	105		116,992	160,635	11	2	
			106,254	98,568	103,574	106,756	107,887	106,126	98,484	103,436	106,627	107,814
AK102525	IQ calmodulin-binding region domain containing protein.	Os12g0619000	3,172	5,985	770	297		3,067	5,891	678	207	
			3,440	3,178	3,385	3,524	4,150	3,351	3,109	3,298	3,445	4,077
AK102637	Non-protein coding transcript, uncharacterized transcript.	Os02g0792600	16,406	34,925	360	333		16,265	34,808	235	221	
			25,496	24,370	24,838	26,847	55,733	25,373	24,281	24,676	26,712	55,662

Supplemental table 1 continue. 26 genes from Lu et al., 2006

AK109536	B-type cell cycle switch protein	Os01g0972900	796	6,966	234	78		684	6,855	134	2	
			3,145	2,954	2,885	3,103	7,946	3,044	2,871	2,773	3,004	7,886
AK109777	Acyl CoA synthetase (EC 6.2.1.3).	Os11g0558300	716	1,698	129	102		595	1,593	16	3	
			5,937	5,309	5,169	6,087	7,752	5,827	5,224	5,031	5,970	7,696
AK061599	Conserved hypothetical protein.	Os03g0672400	9,457	7,515	423	264		9,310	7,394	295	146	
			18,480	17,290	20,446	20,300	16,284	18,346	17,199	20,282	20,157	16,220
AK106279	Hypothetical protein.	Os02g0742800	82,950	63,629	103,546	101,566		82,839	63,533	103,443	101,471	
			21,653	18,846	21,753	22,571	25,660	21,559	18,769	21,636	22,459	25,575
AF210816	putative kinesin	Os04g0350300	42,766	35,852	409	752		42,639	35,745	290	643	
			14,492	13,614	13,364	14,026	15,506	14,374	13,531	13,214	13,891	15,436
AK070863	**Conserved hypothetical protein.**	**Os04g0506900**	118,416	89,564	6,339	2,894		118,284	89,456	6,223	2,788	
			10,265	9,375	10,485	10,193	10,417	10,139	9,295	10,341	10,062	10,342
BP432938	Dehydrin COR410 (Cold-induced COR410 protein).	Os02g0669100	43,737	307,173	433	366		43,602	307,061	308	252	
			130,842	118,373	135,981	133,077	297,741	130,715	118,287	135,826	132,937	297,675

* in the same order as Lu et al., Plant Mol Biol (2006) 61:845–861 table 3

Lu XC, Gong HQ, Huang ML, Bai SL, He YB, Mao X, Geng Z, Li SG, Wei L, Yuwen JS, Xu ZH, Bai SN (2006) Molecular analysis of early rice stamen development using organ-specific gene expression profiling. Plant Mol Biol 61: 845-851

Supplemental Table 2. KEGG enrichment analysis

		PMC expressed				TCP expressed				Seedling expressed				Expressed higher in PMC than in TCP and Seedling				Expressed higher in TCP than in PMC and Seedling				Expressed higher in Seedling than in PMC & Seedling			
KEGG pathways that have 10 or more genes on this microarray	# of genes presenting in microarray overlapping with each pathway	# of genes overlapping with each pathway	more or less than expected # if random	chi-square	probability of enrichment *	# of genes overlapping with each pathway	more or less than expected # if random	chi-square	probability of enrichment	# of sgenes overlapping with each pathway	more or less tnan expected # if there was no relationship between the variables	chi-square	probability of enrichment	# of genes overlapping with each pathway	more or less than expected # if random	chi-square	probability of enrichment	# of genes overlapping with each pathway	more or less than expected # if random	chi-square	probability of enrichment	# of genes overlapping with each pathway	more or less than expected # if random	chi-square	probability of enrichment
1. Metabolism																									
1.1 Carbohydrate Metabolism																									
Glycolysis Gluconeogenesis	88	71	less	2.21		59	more	0.31	0.58	79	less	1.12		4	more	0.76	0.38	3	more	0.13	0.72	15	more	0.11	0.74
Starch and sucrose metabolism	68	47	less	16.55		37	less	2.84		55	less	14.1		2	less	0.00		11	more	45.13	<0.0001	13	more	0.58	0.45
Pentose and glucuronate interconversions	14	11	less	0.68		9	more	0.00	1.00	13	more	0.00	0.98	0	less	0.43		2	more	6.85	0.009	2	less	0.02	
Galactose metabolism	30	22	less	4.14		18	less	0.23		28	more	0.02	0.90	3	more	5.16	0.023	3	more	5.78	0.016	2	less	1.87	
Citrate cycle (TCA cycle)	34	31	more	0.72	0.40	30	more	8.54	0.0035	32	more	0.10	0.75	1	less	0.00		0	less	0.97		3	less	1.23	
Pyruvate metabolism	55	51	more	1.99	0.16	40	more	1.73	0.19	51	more	0.00	1.00	0	less	1.68		3	more	1.45	0.23	8	less	0.06	
Fructose and mannose metabolism	40	30	less	4.17		22	less	1.48		36	less	0.43		2	more	0.57	0.45	1	less	0.01		8	more	0.54	0.46
Glyoxylate and dicarboxylate metabolism	31	24	less	1.98		21	more	0.17	0.68	27	less	1.44		0	less	0.95		0	less	0.89		12	more	12.30	0.0005
Pentose phosphate pathway	42	35	less	0.28		25	less	0.40		41	more	1.50	0.22	1	less	0.05		2	more	0.61	0.43	10	more	2.05	0.15
Inositol phosphate metabolism	16	16	more	2.57	0.11	10	less	0.02		15	more	0.03	0.87	1	more	0.60	0.44	1	more	0.71	0.40	4	more	1.03	0.31
Ascorbate and aldarate metabolism	19	16	less	0.06		12	less	0.01		18	more	0.12	0.73	0	less	0.58		1	more	0.43	0.51	6	more	3.58	0.059
Butanoate metabolism	32	28	more	0.05	0.83	21	more	0.03	0.86	29	less	0.21		0	less	0.98		1	more	0.01	0.92	4	less	0.26	
Propanoate metabolism	17	16	more	0.90	0.34	9	less	0.94		16	more	0.05	0.82	0	less	0.52		0	less	0.49		1	less	1.25	
Aminosugars metabolism	23	14	less	12.33		11	less	2.69		19	less	3.47		0	less	0.70		0	less	0.66		6	more	1.85	0.17
Nucleotide sugars metabolism	11	10	more	0.21	0.65	8	more	0.35	0.56	10	less	0.05		1	more	1.43	0.23	1	more	1.62	0.20	1	less	0.37	
1.2 Energy Metabolism																									
Carbon fixation	64	52	less	1.29		46	more	1.63	0.20	60	more	0.10	0.75	2	more	0.01	0.92	2	more	0.03	0.86	25	more	26.18	<.0001
Methane metabolism	28	13	less	37.05		10	less	9.90		23	less	4.62		2	more	1.70	0.19	1	more	0.06	0.80	14	more	24.73	<.0001
Photosynthesis	32	26	less	0.65		10	less	15.13		31	more	0.82	0.36	0	less	0.98		0	less	0.92		28	more	124.0	<.0001
Reductive carboxylate cycle (CO2 fixation)	26	24	more	0.82	0.36	20	more	1.83	0.18	25	more	0.46	0.50	1	more	0.07	0.79	1	more	0.11	0.74	3	less	0.35	
Oxidative phosphorylation	90	83	more	2.78	0.10	76	more	16.03	<.0001	83	less	0.03		2	less	0.17		4	more	0.92	0.34	7	less	4.32	
Nitrogen metabolism	28	21	less	2.92		14	less	2.46		24	less	2.03		1	more	0.04	0.84	2	more	1.97	0.16	9	more	5.66	0.017
Sulfur metabolism	19	16	less	0.06		12	less	0.01		17	less	0.29		0	less	0.58		0	less	0.54		5	more	1.59	0.21

Supplemental table 2 continue. KEGG enrichment analysis

1.3 Lipid Metabolism																			
alpha-Linolenic acid metabolism	26	11 less	41.91		10 less	7.50		24 less	0.01		0 less	0.79		0 less	0.74		11 more	13.80	0.0002
Linoleic acid metabolism	14	2 less	60.63		5 less	4.95		11 less	4.14		0 less	0.43		0 less	0.40		6 more	7.74	0.0054
Ether lipid metabolism	13	8 less	6.60		8 less	0.04		11 less	1.26		0 less	0.40		2 more	7.64	0.0057	5 more	5.05	0.025
Glycerophospholipid metabolism	30	24 less	0.95		20 more	0.08	0.78	27 less	0.33		0 less	0.92		3 more	5.78	0.016	6 more	0.41	
Fatty acid biosynthesis	14	12 less	0.00		9 more	0.00	1.00	14 more	1.10	0.29	0 less	0.43		0 less	0.40		0 less	2.62	
Biosynthesis of unsaturated fatty acids	18	15 less	0.12		10 less	0.59		18 more	1.42	0.23	0 less	0.55		0 less	0.51		3 more	0.01	0.92
Biosynthesis of steroids	39	33 less	0.08		23 less	0.47		36 less	0.01	0.92	1 less	0.02		1 less	0.01		7 more	0.14	0.71
Bile acid biosynthesis	13	10 less	0.93		6 less	1.85		11 less	1.26		0 less	0.40		0 less	0.37		2 less	0.00	
1.4 Nucleotide Metabolism																			
Purine metabolism	83	79 more	5.67	0.017	53 less	0.00		80 more	1.66	0.20	1 less	0.89		1 less	0.76		5 less	5.93	
Pyrimidine metabolism	72	68 more	4.15	0.042	46 less	0.00		69 more	1.04	0.31	0 less	2.20		1 less	0.52		4 less	5.65	
1.5 Amino Acid Metabolism																			
Alanine and aspartate metabolism	46	43 more	2.07	0.15	33 more	1.13	0.29	44 more	0.59	0.44	0 less	1.41		3 more	2.38	0.12	6 less	0.26	
Arginine and proline metabolism	18	17 more	1.04	0.31	13 more	0.50	0.48	17 more	0.08	0.78	1 more	0.42	0.52	1 more	0.51	0.48	1 less	1.41	
Cysteine metabolism	21	17 less	0.48		13 less	0.05		18 less	1.52		0 less	0.64		0 less	0.60		4 more	0.17	0.68
Glutamate metabolism	39	33 less	0.08		22 less	1.03		37 more	0.27	0.60	1 less	0.02		2 more	0.79	0.37	9 more	1.57	0.21
Glycine, serine and threonine metabolism	38	37 more	4.01	0.045	22 less	0.66		37 more	1.22	0.27	0 less	1.16		1 less	0.00		6 more	0.00	1.00
Histidine metabolism	20	20 more	3.21	0.073	9 less	3.21		20 more	1.57	0.21	0 less	0.61		0 less	0.57		1 less	1.74	
Lysine biosynthesis	13	11 less	0.03		6 less	1.85		12 less	0.00		0 less	0.40		0 less	0.37		1 less	0.64	
Lysine degradation	17	16 more	0.90	0.34	10 less	0.22		16 more	0.05	0.82	0 less	0.52		0 less	0.49		1 less	1.25	
Methionine metabolism	31	19 less	16.07		11 less	11.14		25 less	6.67		1 more	0.01	0.92	2 more	1.54	0.21	9 more	4.11	0.043
Phenylalanine, tyrosine and tryptophan biosynth	43	35 less	0.82		28 more	0.02	0.90	38 less	1.20		0 less	1.31		1 less	0.03		3 less	2.50	
Phenylalanine metabolism	28	13 less	37.05		8 less	15.48		24 less	2.03		2 more	1.70	0.19	1 more	0.06	0.81	11 more	11.67	0.0006
Tryptophan metabolism	25	22 more	0.07	0.79	10 less	6.38		24 more	0.40	0.53	0 less	0.76		0 less	0.72		4 more	0.00	1.00
Tyrosine metabolism	26	22 less	0.05		15 less	0.48		25 more	0.46	0.50	0 less	0.79		0 less	0.74		3 less	0.35	
Urea cycle and metabolism of amino groups	27	23 less	0.02		16 less	0.29		25 less	0.00		0 less	0.83		1 more	0.08	0.78	4 less	0.02	
Valine, leucine and isoleucine degradation	32	28 more	0.05	0.83	18 less	0.88		31 more	0.82	0.36	1 more	0.00	1.00	0 less	0.92		4 less	0.26	
Valine, leucine and isoleucine biosynthesis	26	23 more	0.12	0.73	19 more	0.89	0.35	24 less	0.01		0 less	0.79		0 less	0.74		2 less	1.27	
1.6 Metabolism of Other Amino Acids																			
beta-Alanine metabolism	21	17 less	0.48		13 less	0.05		20 more	0.20	0.66	0 less	0.64		2 more	3.53	0.060	5 more	1.02	0.31
Cyanoamino acid metabolism	15	12 less	0.48		7 less	2.01		15 more	1.18	0.28	0 less	0.46		0 less	0.43		9 more	22.11	<.0001
Glutathione metabolism	40	28 less	8.75		22 less	1.48		35 less	1.60		1 less	0.03		0 less	1.14		10 more	2.57	0.11
Selenoamino acid metabolism	23	21 more	0.51	0.47	12 less	1.45		23 more	1.81	0.18	0 less	0.70		0 less	0.66		7 more	3.73	0.053
1.7 Glycan Biosynthesis and Metabolism																			

Supplemental table 2 continue. KEGG enrichment analysis

Glycan structures	23	22 more	1.74	0.19	18 more	1.97	0.16	22 more	0.30	0.59	0 less	0.70		0 less	0.66		0 less	4.30	
Glycan structures	11	10 more	0.21	0.65	7 less	0.00		9 less	1.93		0 less	0.34		1 more	1.62	0.20	0 less	2.06	
Glycosylphosphatidylinositol(GPI)	10	10 more	1.61	0.20	7 more	0.15	0.70	9 less	0.11		0 less	0.31		1 more	1.93	0.16	0 less	1.87	
N-Glycan biosynthesis	25	24 more	2.03	0.15	20 more	2.71	0.10	24 more	0.40	0.53	0 less	0.76		1 more	0.14	0.71	0 less	4.68	
1.9 Metabolism of Cofactors and Vitamins																			
Folate biosynthesis	10	10 more	1.61	0.20	7 more	0.15	0.70	10 more	0.79	0.38	0 less	0.31		0 less	0.29		0 less	1.87	
One carbon pool by folate	17	17 more	2.73	0.10	11 more	0.00	0.97	16 more	0.05	0.54	0 less	0.52		0 less	0.49		5 more	2.39	0.12
Pantothenate and CoA biosynthesis	18	16 more	0.11	0.74	14 more	1.44	0.23	18 more	1.42	0.23	0 less	0.55		1 more	0.51	0.48	2 less	0.29	
Porphyrin and chlorophyll metabolism	26	25 more	2.18	0.14	14 less	1.22		25 more	0.46	0.50	0 less	0.79		0 less	0.74		12 more	18.09	<.0001
Ubiquinone biosynthesis	10	9 more	0.12	0.72	4 less	2.55		9 less	0.11		0 less	0.31		0 less	0.29		4 more	4.43	0.035
1.10 Biosynthesis of Secondary Metabolites																			
Carotenoid biosynthesis	17	15 more	0.06	0.80	8 less	2.18		16 more	0.05	0.82	2 more	4.57	0.03	1 more	0.60	0.44	1 less	1.25	
Flavonoid biosynthesis	10	4 less	17.86		3 less	5.09		8 less	2.39		0 less	0.31		1 more	1.93	0.16	3 more	1.53	0.22
Limonene and pinene degradation	20	14 less	4.38		7 less	7.43		18 less	0.22		0 less	0.61		0 less	0.57		5 more	1.29	0.26
Terpenoid biosynthesis	13	10 less	0.93		9 more	0.14	0.71	12 less	0.00		1 more	1.01	0.31	1 more	1.16	0.28	3 more	0.52	0.47
Phenylpropanoid biosynthesis	40	15 less	79.39		5 less	46.55		32 less	9.55		2 more	0.57	0.45	1 less	0.01		20 more	35.32	<.0001
Streptomycin biosynthesis	13	11 less	0.03		9 more	0.14	0.71	12 less	0.00		0 less	0.40		0 less	0.37		0 less	2.43	
1.11 Xenobiotics Biodegradation																			
3-Chloroacrylic acid degradation	10	8 less	0.32		5 less	0.88		9 less	0.11		0 less	0.31		0 less	0.29		2 more	0.14	0.71
Benzoate degradation via CoA ligation	16	14 more	0.02	0.88	8 less	1.41		14 less	0.64		0 less	0.49		0 less	0.46		1 less	1.09	
Drug metabolism - other enzymes - Oryza	10	10 more	1.61	0.20	6 less	0.08		10 more	0.79	0.38	0 less	0.31		0 less	0.29		0 less	1.87	
Drug metabolism - cytochrome P450 - Ory	13	7 less	11.38		5 less	3.75		11 less	1.26		0 less	0.40		0 less	0.37		5 more	5.05	0.025
gamma-Hexachlorocyclohexane degradation	13	6 less	17.44		3 less	9.57		11 less	1.26		0 less	0.40		0 less	0.37		5 more	5.05	0.025
Metabolism of xenobiotics by cytochrome P450	11	6 less	9.22		5 less	1.68		9 less	1.93		0 less	0.34		0 less	0.31		4 more	3.52	0.061
Naphthalene and anthracene degradation	16	9 less	12.00		2 less	18.62		13 less	3.11		0 less	0.49		0 less	0.46		4 more	1.03	0.31
2. Genetic Information Processing																			
2.1 Transcription																			
Basal transcription factors	21	21 more	3.37	0.066	20 more	8.80	0.0030	21 more	1.65	0.20	2 more	3.14	0.08	0 less	0.60		0 less	3.93	
RNA polymerase	29	24 less	0.28		19 more	0.02	0.88	27 more	0.01	0.93	0 less	0.89		1 more	0.05	0.82	2 less	1.72	
2.2 Translation																			
Aminoacyl-tRNA biosynthesis	41	39 more	2.76	0.096	18 less	7.36		38 less	0.00		0 less	1.25		0 less	1.17		0 less	7.67	
Ribosome	189	184 more	19.87	<.0001	153 more	23.04	<.0001	183 more	4.74	0.029	2 less	2.39		0 less	5.41		20 less	3.82	
2.3 Folding, Sorting and Degradation																			
Regulation of autophagy	10	10 more	1.61	0.20	10 more	5.57	0.018	10 more	0.79	0.38	0 less	0.31		0 less	0.29		0 less	1.87	
SNARE interactions in vesicular transport	26	25 more	2.18	0.14	22 more	4.71	0.030	24 less	0.01		1 more	0.07	0.79	1 more	0.11	0.74	0 less	4.86	

Supplemental table 2 continue. KEGG enrichment analysis

Proteasome	46	45	more	5.25	0.022	41	more	12.43	0.0004	45	more	1.78	0.18	1	less	0.10		0	less	1.32		0	less	8.61	
Ubiquitin mediated proteolysis	46	44	more	3.48	0.062	40	more	10.35	0.0013	45	more	1.78	0.18	2	more	0.30	0.58	0	less	1.32		1	less	6.40	
2.4 Replication and Repair																									
DNA replication	37	36	more	3.85	0.050	25	more	0.18	0.67	36	more	1.15	0.28	4	more	7.91	0.0049	0	less	1.06		0	less	6.92	
Homologous recombination	23	23	more	3.70	0.055	14	less	0.11		22	more	0.30	0.59	3	more	8.11	0.0044	0	less	0.66		0	less	4.30	
Base excision repair	34	31	more	0.72	0.40	18	less	1.88		31	less	0.12		6	more	25.45	<0.0001	0	less	0.97		2	less	2.50	
Mismatch repair	26	25	more	2.18	0.14	18	more	0.28	0.59	26	more	2.05	0.15	4	more	13.93	0.0002	0	less	0.74		0	less	4.86	
Nucleotide excision repair	38	36	more	2.35	0.13	31	more	4.99	0.026	37	more	1.22	0.27	4	more	7.54	0.0060	0	less	1.09		0	less	7.11	
3. Environmental Information Processing																									
3.1 Membrane Transport																									
Protein export	23	22	more	1.74	0.19	13	less	0.59		23	more	1.81	0.18	1	more	0.15	0.70	0	less	0.66		2	less	0.86	
3.2 Signal Transduction																									
Phosphatidylinositol signaling system	39	35	more	0.42	0.19	24	less	0.12		36	less	0.01		2	more	0.63	0.43	3	more	3.48	0.062	5	less	0.25	
All KEGG pathways	1618	1394				1039				1500				48				45				255			

*. P values were only provided for those candidate enriched pathways, not provided for those candidate depleted pathways. P<0.01 were highlighted.

Supplemental Table 3. The twelve known meiotic genes and brief functional description.

Meiotic chromosome behavior	Gene name	RAP ID	Fold change		Description
			PMC/TCP	PMC/seedling	
Double-strand break formation	*OsSPO11-1*	Os03g0752200	12.3	17.3	OsSPO11-1 catalyzes DNA double-strand breaks and initiates homologous chromosome recombination (Yu *et al*., 2010).
	PAIR1	Os03g0106300	45.9	34.8	PAIR1 is a coiled-coil protein, has been reported to perform unknown function during DSB formation (Nonomura *et al.*, 2004).
Strand invasion	*OsDMC1*	Os11g0146800	178.0	52.6	OsDMC1 is a recombinase mediating homologous pairing between a single strand DNA and double stranded DNA (Ding *et al.*, 2001; Kant *et al.*, 2005).
	OsRPA1a	Os02g0776800	2.4	2.9	OsRPA1a is a subunit of the heterotrimeric complex replication protein A required for meiotic DNA repair (Chang *et al.*, 2009a).
	OsRAD51	Os11g0615800	0.5	1.2	OsRAD51 is a recombinase that function in both meiosis and mitosis (Rajanikant *et al.*, 2008).
Interfering crossovers	*PAIR2*	Os09g0506800	114.9	19.6	PAIR2, a homolog of yeast axial elements-associated protein HOP1, is essential for rice homologous chromosome synapsis (Nonomura *et al.*, 2006).
	ZEP1	Os04g0452500	67.7	29.9	ZEP1 is a central element protein of the synaptonemal complex, regulates the number of crossovers during meiosis (Wang *et al.*, 2010).
	OsMER3 /OsRCK	Os02g0617500	N.A.	N.A.	*OsMER3/OsRCK* functions in the formation of meiotic crossovers. *OsMER3/OsRCK* has been reported to be preferentially expressed in young flowers by RT-PCR (Chang *et al*., 2009), while our microarray data didn't detect any expression in tested samples with Os02g0617500 probe. The sequence of 60mer probe representing Os02g0617500 in our microarray is 5'-AGGGA AGGCT TTGGT TCCAT GTTGT TGGTG CAAAT GGGAA AAGGA AGAAG CGTAT TCAAA-3'. It was designed based on previous incorrect annotation (Chang *et al.*, 2009 updated its annotation) and is targeted to the 1.7kb upstream of the stop codon of the corrected ORF. Only the probes targeted to the region within 0-300 nts downstream of translation termination codon are good probes to represent the gene expression (see methods section and supplemental fig. 11 for probe position effects). Therefore the Os02g0617500 probe in our microarray is not capable to reflect expression of *OsMER3*/*OsRCK*.
Sister chromatid cohesion	*OsRAD21-4*	Os05g0580500	23.2	28.8	OsRAD21-4, an orthologue of Yeast Rec8 Protein, is Required for homologous pairing and cohesion at sister chromatid arms at meiotic prophase I (Zhang *et al.*, 2006).
Pairing and synapsis	*PAIR3*	Os10g0405500	56.0	12.2	PAIR3, a putative coiled-coil protein, is required for homologous chromosome pairing and synapsis at diakinesis (Yuan *et al.*, 2009).
Meiotic cell cycle control	*OsSDS*	Os03g0225200	42.2	34.6	OsSDS, a N-type cyclin, regulates meiotic cell cycle (Chang *et al.*, 2009).
	OsMEL1	Os03g0800200	178.5	76.9	*OsMEL1*, is an *ARGONAUTE* (*AGO*) gene regulating the cell division of premeiotic germ cell**s,** the proper modification of meiotic chromosomes, and the faithful progression of meiosis (Nonomura *et al.*, 2007)**.**

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Supplemental Table 4. The detailed microarray data for rice genes similar to meiotic genes identified in other species

Groups	Gene name	RAP ID	Intensity (with background subtraction)				
			PMC1	PMC2	TCP1	TCP2	
			seedling1	seedling2	seedling3	seedling4	seedling5
1. Meiotic commitment	probable SPL/NZZ homologue	Os01g0212500	6,865	3,598	673	203	
			14	9	2	2	107
2. Meiosis Initiation	homlogue of maize Ameiotic (am) 1	Os03g0650400	140,046	88,469	13,261	5,783	
			13,163	11,948	12,431	12,604	11,800
3. Meiosis progression regulation	homologue of maize pollenless3	Os05g0506000	7,196	14,410	2,296	1,268	
			2,566	2,296	2,387	2,490	5,026
	homologue of Arabidopsis POLLENLESS3-LIKE1	Os08g0130300	331	416	198	166	
			2	2	2	2	60
	homologue of Arabidopsis POLLENLESS3-LIKE2	Os09g0538500	6,034	19,133	166	8	
			21,370	18,075	19,522	21,310	19,003
	OsCycA1;1	Os12g0298700	1,738	2,990	1,268	901	
			2,371	2,145	2,410	2,408	2,498
	OsCycA1;2	Os01g0233500	12,705	11,725	5,353	2,462	
			19,726	18,469	19,837	19,635	24,865
	OsCycA2;1	Os12g0502300	4,910	14,482	2,181	2,178	
			13,972	12,642	13,848	14,175	18,246
	OsCycA3;1	Os03g0607600	5,288	6,349	237	217	
			5,577	5,084	5,340	5,595	4,009
	OsCycB1;1	Os01g0805600	2,584	10,849	883	79	
			13,603	13,216	13,040	13,552	14,507
	OsCycB1;2	Os05g0493500	9,690	12,533	352	100	
			21,716	19,406	20,467	21,820	41,425
	OsCycB1;4	Os01g0281200	632	973	2,514	760	
			501	560	622	596	1,372
	OsCycB2;1	Os04g0563700	2,834	11,292	4,655	2,208	
			6,663	5,804	6,493	6,730	9,554
	OsCycB2;2 (Lu *et al* .,2006, -10)	Os06g0726800	7,007	30,263	492	374	
			39,572	36,600	39,089	39,649	56,100
	OsCycD1;1	Os09g0382300	1,682	137	106	452	
			2,148	471	541	811	719
	OsCycD1;2	Os06g0217900	4,330	10,867	2	2	
			9,851	8,872	8,918	9,951	20,720
	OsCycD2;1	Os07g0620800	4,394	3,445	447	471	
			9,432	8,776	7,021	6,063	11,150
	OsCycD2;3	Os03g0203800	14,115	10,362	78	232	
			4,464	4,006	3,978	4,417	3,352
	OsCycD4;1	Os09g0466100	5,887	7,725	323	154	
			20,664	17,144	18,114	17,515	21,990
	OsCycD4;2	Os08g0479300	2,099	858	1,106	2,550	
			6,531	6,246	7,260	7,717	13,186
	OsCycD3;1	Os09g0111100	1,481	244	1,107	532	
			7,904	7,342	7,910	8,137	17,037
	OsCycD5;1	Os12g0588800	695	362	45	119	
			30,397	27,531	29,788	30,924	24,093
	OsCycD5;2	Os03g0617500	40,393	3,697	67	61	
			12,808	11,179	11,361	11,446	22,570
	OsCycD7;1	Os11g0706600	5,381	721	2	51	
			809	282	256	285	419
	OsCycH1;1	Os03g0737600	18,521	11,683	4,377	2,943	
			8,992	8,214	8,326	8,634	9,310
	OsCycL1;1	Os01g0377500	44,246	59,528	50,391	33,051	
			24,670	23,894	23,743	25,834	36,919
	OsCycT1;2	Os02g0438200	11,189	7,977	3,611	1,061	
			4,604	4,260	4,652	4,396	10,971
	OsCycT1;3	Os02g0133000	2,274	5,191	5,852	6,545	
			2,781	2,587	2,876	2,986	5,617
	OsCycT1;4	Os11g0157100	30,225	38,673	13,171	8,341	
			15,883	14,439	16,085	16,005	18,894
	OsCycT1;6	Os12g0485400	48,560	70,999	9,412	9,354	
			26,691	24,722	25,048	25,360	51,087
	OsSDS (homologue of Arabidopsis SOLO DANCERS, N-type of cyclin)	Os03g0225200	11,394	4,207	6	187	
			163	137	82	101	188
	OsCycU1;1	Os04g0628900	86	318	44	36	
			561	580	500	503	1,131
	OsCycU2;1	Os04g0552300	216	501	7	43	
			17,048	15,840	16,763	16,805	14,540
	OsCycU3;1	Os05g0398000	520	440	2	2	
			655	689	610	664	816
	OsCycU4;4	Os02g0652000	1,132	167	29	24	

Supplemental Table 4 cont. putative meiotic genes

			6,037	5,592	6,123	5,957	6,740
	OsCycU4;1	Os10g0563900	2,933	842	728	37	
			16,497	15,990	16,129	16,365	26,631
	OsCycU4;2	Os04g0544200	143	185	99	145	
			5,609	5,224	4,942	5,261	8,099
	CYCD1;3 Rice Os08g32540	Os08g0413100	1,161	1,578	1,936	2,566	
			977	944	876	972	1,018
	homolog of Arabidopsis MMD1 (MALE MEIOCYTE DEATH 1) AT1G66170	Os03g0716200	34,708	32,212	1,340	2	
			702	614	187	207	2,216
4. Sister chromatid cohesion(SCC)	OsRAD21-1	Os01g0897800	30,094	89,264	1,443	1,678	
			46,232	45,789	49,541	49,560	175,882
	OsRAD21-2	Os04g0488100	4,360	3,410	1,206	1,014	
			2,677	2,389	2,598	2,765	2,982
	OsRAD21-3*	Os08g0266700	19	424	4,883	5,247	
			1,407	1,145	1,242	1,375	883
	OsRAD21-4	Os05g0580500	16,124	10,602	213	736	
			360	371	335	324	187
5. Recombination	homolog of AtRAD51C (AT2G45280)	Os01g0578000	7,854	10,410	1,870	1,384	
			4,908	4,570	4,874	4,978	3,826
	homolog of AtRAD51 (AT5G20850)	Os11g0615800	1,403	17,449	17,982	18,319	
			8,234	7,853	7,878	8,382	8,796
	homolog of AtRAD51 (AT5G20850)	Os12g0497300	6,127	8,661	1,533	1,319	
			4,405	3,777	3,847	4,243	4,182
	homolog of AtSPO11-1 (AT3G13170)	Os03g0284800	7,333	6,299	2	2	
			2,000	1,801	2,042	2,120	1,735
	homolog of AtSPO11-1 (AT3G13170)	Os12g0622500	16,394	14,374	1,136	775	
			18,287	16,322	16,534	17,448	23,400
	homolog of AtXRCC3 (AT5G57450)	Os02g0562100	4,635	959	71	47	
			762	428	455	395	1,127
	homolog of AtRAD50 (AT2G31970)	Os02g0497500	9,672	18,524	4	2	
			8,902	8,040	8,542	9,188	7,774
6. Chiasmata resolution and sister chromatid cohesion	skp1-like-All expressed	Os07g0625400	598,132	320,978	87,041	38,829	
			12,720	5,977	2,512	1,413	3,432
	skp1-like-All expressed	Os09g0539500	327,377	124,768	8,641	4,787	
			17,892	16,777	17,939	17,812	29,811
	skp1-like-All expressed	Os11g0456300	203,410	138,409	69,147	67,159	
			114,590	98,637	125,166	132,864	108,195
	skp1-like-N.A.	Os07g0625500	150,575	50,144	27	92	
			12,650	2,800	44	112	151
	skp1-like-N.A.	Os07g0625600	520,530	192,882	121	131	
			21,881	6,269	469	472	716
	skp1-like-no expression	Os06g0113800	117	92	30	180	
			47	29	2	27	323
	skp1-like-no expression	Os07g0144900	197	10	2	2	
			198	7	2	2	82
	skp1-like-no expression	Os08g0375200	2	8	10	22	
			2	2	2	6	101
	skp1-like-no expression	Os08g0375700	2	2	637	20	
			2	2	1,231	26	64
	skp1-like-no expression	Os09g0273800	31	42	29	46	
			35	37	11	38	117
	skp1-like-no expression	Os09g0274700	2	19	2	2	
			2	7	2	12	641
	skp1-like-no expression	Os09g0274800	44	36	10	3	
			31	37	31	37	93
	skp1-like-no expression	Os10g0438100	250	242	16	2	
			85	201	13	7	187
	skp1-like-PMC only	Os07g0409500	206,639	108,526	95	426	
			1,582	930	515	501	185
	skp1-like-PMC only	Os07g0624900**	1,017	1,383	5	2	
			81	179	2	2	327
	skp1-like-Seedling only	Os09g0272900	13	20	24	32	
			5,409	4,870	5,097	5,151	5,182
	skp1-like-TCP only	Os09g0275200	172	2	1,072	645	
			2	2	9	2	50
7. separation of sister and homologous chromatids	putative kinesin	Os02g0644400	13,276	18,657	1,098	1,100	
			25,371	23,864	24,010	22,943	33,485
	putative kinesin	Os02g0645100	51,063	63,917	3,001	136	
			54,216	45,799	48,232	51,358	86,984
	putative kinesin	Os03g0152900	1,827	2,683	235	489	
			710	626	684	2,084	1,522
	putative kinesin	Os03g0773600	10,774	17,807	1,468	90	
			43,113	38,552	42,565	42,750	51,720

Supplemental Table 4 cont. putative meiotic genes

	homolog of AtATK3	Os03g0862200	4,805	3,292	1,934	1,820	
			20,447	18,064	18,720	19,441	18,897
	putative kinesin; Bai-24	Os04g0350300	42,639	35,745	290	643	
			14,374	13,531	13,214	13,891	15,436
	homolog of AtATK5	Os04g0629700	16,625	37,424	59	43	
			98,787	95,420	99,379	100,599	105,677
	putative kinesin	Os06g0206700	11,383	9,275	264,876	387,688	
			3,846	3,654	5,306	6,515	7,050
	homolog of AtATK3	Os07g0105700	3,765	6,082	4,690	1,461	
			19,007	17,825	18,515	18,733	22,132
	putative kinesin	Os08g0117000	56,928	44,454	4,400	4,005	
			10,538	9,356	9,654	9,771	20,929
	putative kinesin	Os10g0512800	1,712	1,736	993	1,438	
			1,472	1,365	1,442	1,410	2,005
	putative kinesin	Os01g0243100	82,969	51,502	573	265	
			12,847	12,443	12,635	12,774	19,802
	putative kinesin	Os02g0229600	79	5	1,566	2,395	
			2	6	18	2	79
8. microspore development	OsMS2 (Male sterility protein 2)	Os03g0167600	395	975	218	206	
			2	2	2	8	146
	OsUGP (UDP-glucose pyrophosphorylase)	Os09g0553200	182,465	192,742	2,324	787	
			187,444	178,268	186,246	186,685	156,277
	OsUGP-like	Os02g0117700	109,531	167,936	341,680	320,683	
			1,469	1,711	3,275	2,954	2,965
9. other anther specific gene	rice anther specific YY1	Os09g0525500	381,005	661,884	91	3,044	
			5,487	8,240	537	517	725

OsRAD21-3*: This gene expression patterns in our microarray are not consistance with RT-PCR results of Tao *et al.,* (2007). Using RT-PCR, Tao et al. showed that OsRAD21-3 expressed higher in PMC stage than in TCP stage. However, our microarray data showed the opposite pattern. We also checked the probe position of OsRAD21-3, it was targeted in the 3' UTR of the gene ORF correctly. Because our microarray detected the expression of 29008 genes simultaneously, with only two biological replicates, errors in some genes expression are statistically possible. It is also possible that OsRAD21-3 expressed higher in cells surrounding PMCs, but not as high in PMCs, because Tao et al. used florets as sample for RT-PCR, can not distinguish expression in PMCs or other cells surrounding it. In this case we couldn't tell which possibility is true. Reference: Tao J, Zhang L, Chong K, Wang T. (2007) OsRAD21-3, an orthologue of yeast RAD21, is required for pollen development in Oryza sativa. Plant J 51: 919-30

Os07g0624900**: The probe position of Os07g0624900 in the 144-203 bp downstream of the ORF start condon, which is 461-520 bp upstream of ORF stop codon. This is not within the optimum probe region. So the probe signal value probably is smaller than the real expression of this gene.

Supplemental Table 5 Microarray data of 127 genes that significantly expressed in pollen mother cells, but not in tri-cellular pollen or seedling.

Major category	Minor category	Sub-category	RAP ID	Intensity (without background subtraction)					Intensity (with background subtraction)					Tapetum[a]	40 cell- tYespesb	RT-PCR[c]
				PMC1 seedling1	PMC2 seedling2	TCP1 seedling3	TCP2 seedling4	seedling5	PMC1 seedling1	PMC2 seedling2	TCP1 seedling3	TCP2 seedling4	seedling5			
1. Metabolic Enzymes		lipase family	Os05g0574000	14,839	6,219	169	166		14,722	6,117	68	69		No		No
				186	111	172	137	341	72	35	56	31	265			
			Os01g0651300	4,382	2,203	115	111		4,245	2,091	2	2		No	Yes	
				157	113	123	119	132	28	27	2	2	70			
			Os06g0129600	1,229	2,202	81	76		1,118	2,109	2	2			Yes	
				92	88	84	71	258	2	15	2	2	202			
			Os11g0129500	1,180	827	99	87		1,051	708	2	2		No	Yes	
				201	151	134	124	274	84	60	2	5	206			
			Os01g0309900	662	704	110	140		549	601	2	45		Yes	Yes	
				150	115	102	106	235	40	36	2	6	172			
		peptidase family	**Os05g0153200**	6,792	9,940	86	78		6,666	9,829	2	2		Yes	No	No
				162	145	121	111	323	38	61	2	2	259			
			Os01g0554100	1,454	2,331	112	109		1,348	2,234	7	18			Yes	
				124	115	116	111	251	26	31	2	2	167			
			Os07g0570200	715	640	101	82		615	544	4	2		Y/N		
				189	171	158	158	230	96	99	66	75	162			
		Chalcone and stilbene synthases, N-terminal family.	Os10g0484800	47,118	36,296	84	88		47,020	36,193	2	2			No	No
				182	133	78	56	89	105	58	2	2	29			
			Os07g0411300	6,577	8,692	105	98		6,475	8,599	10	9		Yes	Yes	
				173	195	86	86	178	82	126	2	2	100			
		putative secretory peroxidase	**Os08g0302000**	58,987	84,775	81	79		58,883	84,681	2	2		Y/N	Yes	No
				152	168	77	73	146	64	99	2	2	77			
		other types of enzymes	Os04g0573100	27,615	33,559	94	76		27,507	33,466	2	2			Yes	
				155	126	132	89	105	69	48	21	2	28			
			Os01g0264100	10,242	4,620	70	77		10,139	4,524	2	2			Yes	
				108	88	84	91	120	19	15	2	9	53			
			Os01g0361700	9,973	33,876	93	79		9,861	33,776	2	2		No	Yes	
				126	145	109	101	305	17	70	2	2	249			
			Os07g0688000	1,814	1,199	97	83		1,706	1,105	2	2			Yes	
				93	83	90	77	239	2	11	2	2	170			
			Os12g0456700	733	2,343	87	90		626	2,233	2	2				
				72	112	79	73	155	2	30	2	2	92			
			Os01g0370900	603	644	88	84		477	526	2	2		Yes		
				166	148	148	133	298	60	59	24	23	235			
			Os03g0326100	578	1,399	105	99		463	1,300	3	2		Yes		
				165	135	141	106	121	63	62	28	2	58			
2. Genetic Information Processing	Ubiquitin mediated proteolysis components	cylcin-like F-box family protein	Os05g0468100	115,976	36,451	99	92		115,872	36,358	9	3		No		
				330	161	88	88	144	242	94	10	12	83			
			Os01g0243900	46,579	23,978	89	81		46,476	23,884	2	2		Y/N	Yes	
				344	170	72	71	142	252	99	2	2	70			
			Os05g0468200	29,120	8,205	80	75		29,020	8,109	2	2		Y/N	Yes	
				159	89	70	61	127	67	18	2	2	74			
			Os05g0570300	25,355	6,668	82	80		25,254	6,574	2	2		No	Yes	
				139	81	63	64	97	50	14	2	2	30			
			Os04g0208400	22,769	16,936	86	81		22,666	16,842	2	2		Yes	Yes	
				220	157	102	100	114	130	87	14	18	56			
			Os01g0595800	14,107	9,093	69	65		14,000	9,001	2	2		Y/N	Yes	
				265	172	66	60	116	183	101	2	2	54			
			Os06g0685200	10,476	7,801	112	100		10,376	7,707	22	13				
				149	122	100	89	116	60	54	16	11	54			
			Os05g0484000	10,117	7,831	91	78		10,016	7,734	2	2		Yes	Yes	Yes
				92	87	72	60	126	2	14	2	2	60			
			Os12g0595300	8,212	3,620	154	139		8,091	3,516	39	33		No		
				199	134	141	127	166	87	52	2	2	104			
			Os04g0208600	7,743	4,780	120	100		7,605	4,667	2	2		No	Yes	
				139	93	122	109	132	7	8	2	2	67			
			Os06g0492900	5,655	4,796	83	74		5,551	4,702	2	2		Y/N	No	
				127	101	62	55	133	37	31	2	2	67			
			Os10g0125300	5,139	1,653	84	77		5,038	1,555	2	2		Y/N	Yes	
				112	105	94	94	287	15	31	2	12	222			
			Os12g0607800	2,725	1,751	92	89		2,622	1,654	2	2		No		
				74	83	77	66	124	2	11	2	2	52			
			Os04g0193300	1,153	1,575	87	122		1,016	1,454	2	19		No	Yes	
				125	110	93	150	201	5	18	2	28	132			
			Os01g0774300	1,097	1,235	83	76		972	1,117	2	2			Yes	
				82	92	72	66	153	2	3	2	2	91			
			Os10g0126800	1,070	1,203	137	173		951	1,101	31	72		No	No	
				105	81	117	137	151	2	6	2	18	93			
			Os04g0341200	907	1,275	94	98		784	1,170	2	2		No	No	
				92	95	80	80	353	2	12	2	2	291			
			Os11g0201800	502	1,687	106	104		371	1,579	2	2			Yes	

				125	110	115	141	192	2	29	2	10	133			
		putative RPN10, 26S proteasome	Os10g0141400	2,837	1,930	96	177		2,736	1,839	9	88			Yes	
				102	75	67	68	204	9	6	2	2	146			
		putative SKP1 component family	Os07g0624900	1,117	1,478	97	88		1,017	1,383	5	2			Yes	
				170	250	83	78	385	81	179	2	2	327			
		RING domain	Os05g0352700	1,023	601	146	94		902	501	42	2			Yes	
				137	97	102	90	176	22	24	2	2	110			
	Related to transcription, translation and RNA processing	Pentatricopeptide repeat family protein	Os11g0607100	2,091	1,918	86	120		1,990	1,819	2	33			Yes	
				181	173	162	166	401	83	98	68	83	332			
			Os04g0676200	667	1,264	76	75		566	1,170	2	2		No	No	
				68	68	67	65	110	2	2	2	2	46			
			Os11g0109800	1,008	847	87	77		905	753	2	2		No	Yes	
				115	91	86	79	201	21	19	2	2	142			
			Os03g0216400	4,189	1,060	84	79		4,089	966	2	2			No	
				163	93	81	73	391	76	24	2	2	330			
			Os07g0513200	2,588	870	89	81		2,479	758	2	2		No	Yes	
				91	82	76	89	220	3	2	2	2	147			
		RNA-binding region RNP-1 containing	Os03g0374500	503	1,084	99	90		373	973	2	2		Yes		
				181	127	160	153	270	68	40	39	43	216			
		putative protein synthesis initiation	Os07g0692800	2,567	4,085	90	83		2,459	3,992	2	2				
				87	80	68	73	271	2	10	2	2	217			
	others related to genetic information processing		Os03g0687400	3,430	4,782	77	91		3,315	4,683	2	2			Yes	
				155	152	80	209	153	52	80	2	94	94			
3. Environmental Information Processing	Membrane Transport	ABC transporter domain containing	Os09g0360900	1,351	698	71	69		1,247	607	2	2				
				254	102	109	104	205	166	29	8	17	148			
		Zinc/iron permease family.	Os06g0566300	585	567	127	146		481	474	39	46		No	Yes	
				146	125	134	161	203	68	56	46	56	137			
	Signal transduction	Plant lipid transfer/trypsin-alpha amylase inhibitor domain containing protein	Os06g0341500	39,897	13,843	81	81		39,798	13,748	2	2			Yes	
				194	105	91	82	158	112	35	4	9	74			
			Os07g0489000	25,899	9,662	82	88		25,784	9,563	2	2		Yes		
				111	90	72	92	99	11	18	2	2	26			
			Os10g0148000	1,748	1,023	172	181		1,622	915	56	79		Yes	No	
				76	116	215	148	186	2	29	71	26	124			
		Protein kinase domain containing	Os01g0608000	1,263	3,392	81	81		1,161	3,296	2	2		Yes		
				118	192	67	68	180	24	120	2	2	111			
		No apical meristem (NAM) protein	Os07g0566500	11,816	5,158	77	78		11,699	5,058	2	2			Yes	
				120	72	68	64	117	15	2	2	2	54			
			Os07g0456900	3,303	1,102	151	109		3,154	980	28	2			Yes	
				131	116	216	141	265	7	25	65	9	201			
			Os12g0156100	1,481	3,418	81	77		1,357	3,300	2	2		No	No	
				85	114	92	74	242	2	25	2	2	174			
		Tetratricopeptide-like helical family	Os11g0598900	3,518	5,289	114	102		3,414	5,197	23	11			No	
				122	121	111	103	156	32	48	14	17	87			
			Os07g0514400	927	1,965	178	159		823	1,873	88	68		No	Yes	
				155	148	152	142	242	65	76	56	56	186			
			Os09g0327200	699	547	85	84		577	436	2	2		Yes	No	
				102	83	90	91	295	2	2	2	2	232			
		WD40 repeat	Os03g0746600	1,510	797	165	154		1,359	673	37	37		No	Yes	
				151	80	217	169	395	17	2	51	27	339			
		Ankyrin repeat	Os01g0691200	1,363	966	144	161		1,262	870	54	74		No		
				163	158	150	156	237	69	86	59	74	170			
		Leucine-rich repeats containing	Os02g0798800	907	1,084	120	116		800	987	16	25				
				93	90	100	144	200	2	7	2	29	136			
	Transcription factors	GRAS transcription	Os11g0139600	6,288	7,236	99	81		6,169	7,133	2	2				No
				138	144	121	102	142	30	63	2	2	72			
			Os05g0574900	740	1,058	78	77		637	965	2	2		No	Yes	
			SLRL2	72	66	65	63	137	2	2	2	2	71			
		MADS-box family.	Os06g0162800	6,135	13,885	86	81		6,034	13,791	2	2		No	No	
			OsMADS5	138	137	137	136	105	48	68	52	55	39			
		B3 family.	Os07g0183300	5,735	5,292	87	114		5,631	5,201	2	23				
				255	139	78	78	132	167	66	2	2	69			
			Os07g0183200	3,594	8,074	98	177		3,484	7,978	2	83		Yes	Yes	
				172	293	98	77	148	79	216	2	2	91			
		FAR1 family	Os05g0471800	992	1,318	87	82		890	1,225	2	2		Y/N		
				144	179	74	83	282	57	113	2	6	210			
			Os04g0615900	1,898	729	145	118		1,794	629	46	28		No	No	
				145	140	131	153	478	50	64	31	65	400			
		Auxin responsive SAUR protein family.	Os09g0546100	4,943	2,731	89	89		4,842	2,639	2	3		Yes		
				74	74	70	70	168	2	9	2	2	95			
			Os02g0143400	651	502	111	118		539	404	12	19			Yes	
				271	102	94	113	242	174	30	2	2	183			
		other putative transcription factors	Os03g0358000	2,271	811	87	140		2,172	714	2	53			No	
				199	127	106	104	264	106	55	15	25	203			
			Os05g0473300	992	546	78	78		887	452	2	2		Y/N	Yes	
				61	63	60	65	174	2	2	2	2	117			

			Os02g0149600	1,352	506	81	138		1,252	412	2	51			No	
				74	67	75	68	181	2	2	2	2	123			
4. Cellular Processes	Related to chromosomal behaviours	Histone deacetylase	Os02g0214900	3,542	4,657	77	69		3,442	4,563	2	2		Y/N	Yes	
				97	103	71	69	123	9	35	2	2	62			
		containing XH (rice gene X Homology)	Os01g0126600	17,749	24,842	91	180		17,631	24,729	2	84		No	No	No
				126	138	76	78	167	18	52	2	2	90			
5. Unknown protein		Protein of unknown function DUF569 family	**Os08g0164000**	9,211	6,044	119	99		9,068	5,925	2	2			Yes	No
				109	89	129	103	177	2	2	2	2	119			
			Os08g0163900	16,644	13,705	114	114		16,513	13,594	2	12			Yes	
				242	162	161	148	128	127	74	24	31	69			
			Os08g0164300	13,551	7,234	86	81		13,449	7,140	2	2			No	
				104	86	69	66	191	14	17	2	2	96			
			Os03g0721700	7,353	18,078	120	109		7,223	17,973	9	5		Yes	Yes	
				262	153	126	129	141	138	75	2	4	85			
		Protein of unknown function DUF295 family	Os07g0184200	20,895	12,501	74	74		20,794	12,404	2	2		Yes		
				173	110	66	73	149	77	37	2	2	88			
			Os05g0570200	17,349	5,675	115	132		17,220	5,569	2	26		No	Yes	
				255	144	140	140	265	133	64	2	11	192			
		Protein of other unknown function domains	Os01g0276300	2,190	1,714	94	81		2,090	1,621	5	2		Y/N	Yes	
				99	83	93	74	281	10	17	14	2	213			
			Os08g0135500	554	1,774	101	100		448	1,680	12	11		Yes		
				128	129	112	126	233	39	62	36	51	169			
			Os11g0557400	557	1,074	87	85		455	979	2	2				
				83	71	76	79	138	2	2	2	2	77			
		Zinc-finger containing protein	Os07g0138400	4,131	5,241	116	81		4,028	5,146	23	2		Y/N	Yes	
				113	128	107	72	191	24	57	16	2	131			
			Os11g0103400	542	2,131	79	81		438	2,040	2	2		Yes	Yes	
				74	75	66	65	134	2	2	2	2	74			
		similar to function unknown proteins	Os09g0480900	9,222	2,847	114	102		9,111	2,751	16	8		Yes	No	
				246	138	135	137	147	149	67	14	34	86			
			Os01g0122200	3,253	3,491	77	75		3,149	3,396	2	2			Yes	
				68	65	70	63	129	2	2	2	2	65			
			Os02g0461100	651	1,528	73	71		541	1,429	2	2			Yes	
				192	159	163	160	181	93	76	26	40	115			
			Os04g0617900	1,503	1,899	97	91		1,392	1,800	2	2		Y/N	Yes	
				126	148	118	105	261	19	75	5	4	203			
			Os07g0177100	630	574	91	74		508	470	2	2		No	No	
				173	177	186	175	184	62	94	40	45	113			
		hypothetical proteins	Os05g0366900	103,301	53,786	169	170		103,179	53,680	55	69		Yes	Yes	
				179	137	146	114	203	68	51	4	2	136			
			Os09g0566300	628	931	74	86		515	828	2	2		Y/N		
				104	80	58	76	95	2	2	2	2	37			
			Os06g0243900	996	602	80	81		891	508	2	2				
				71	68	61	69	96	2	2	2	2	33			
			Os12g0576200	23,607	54,940	68	78		23,497	54,841	2	2		No		
				146	218	62	68	101	46	134	2	2	37			
			Os03g0373100	564	680	79	72		461	582	2	2		Y/N	No	
				66	65	67	59	94	2	2	2	2	22			
			Os08g0449400	1,406	699	82	86		1,302	603	2	2		Yes		
				119	87	67	70	197	29	15	2	2	135			
			Os07g0151700	12,319	18,907	85	84		12,217	18,809	2	2		No	Yes	
				106	110	70	75	214	7	36	2	2	150			
			Os03g0569000	5,198	1,848	78	93		5,098	1,754	2	7		Y/N	No	
				88	80	71	69	309	2	11	2	2	251			
			Os02g0318400	2,037	928	84	163		1,937	832	2	75		No	Yes	
				88	78	74	62	127	5	7	2	2	71			
			Os11g0666100	6,082	5,589	75	73		5,982	5,496	2	2		No		
				114	97	77	79	171	24	29	2	2	104			
			Os08g0476000	1,713	1,620	94	90		1,607	1,528	2	2			Yes	
				131	92	79	72	244	42	19	2	2	186			
			Os09g0512100	6,422	6,370	89	84		6,293	6,251	2	2				
				92	92	80	75	166	2	2	2	2	106			
			Os01g0733000	1,288	3,104	102	99		1,184	3,012	12	9		No		
				147	227	83	89	155	57	156	2	5	101			
			Os03g0345300	3,658	6,489	95	99		3,556	6,391	2	9		Yes	No	
				172	187	86	74	149	75	113	2	2	80			
			Os12g0604000	594	1,527	98	88		493	1,431	2	2				
				95	120	88	77	269	2	49	2	2	214			
			Os11g0604400	553	1,795	125	109		451	1,701	29	20		No		
				101	155	92	85	323	10	85	3	2	262			
			Os08g0520600	1,300	581	85	140		1,169	469	2	32		No	Yes	
				108	93	96	198	142	2	6	2	68	83			
			Os04g0664300	973	652	99	90		871	556	2	2		Y/N	Yes	
				108	103	96	84	276	12	31	3	2	220			
			Os07g0479400	2,982	783	88	79		2,883	683	2	2		Yes	Yes	

			109	85	104	95	396	29	11	12	11	328		
		Os03g0419200	1,060	1,031	164	138		956	940	74	47		Yes	Yes
			111	110	107	106	209	22	38	12	21	158		
		Os12g0540100	3,889	4,576	94	90		3,792	4,480	4	2		Yes	
			139	128	110	99	165	62	58	22	26	104		
		Os03g0158000	1,113	851	94	159		1,007	755	2	68		Yes	
			125	110	119	84	399	27	38	12	2	318		
		Os05g0506400	8,398	2,725	112	133		8,280	2,624	7	32			No
			331	143	122	151	198	222	69	5	33	135		
		Os06g0630200	653	904	118	107		545	809	22	13			
			104	100	124	130	158	11	29	7	26	109		
		Os12g0148700	700	1,253	77	112		582	1,136	2	15		Yes	Yes
			157	169	128	141	304	61	82	13	38	205		
		Os05g0249900	4,287	2,630	102	107		4,155	2,518	2	6		No	
			208	107	129	146	206	93	20	2	29	153		
		Os07g0679400	2,904	893	103	68		2,777	785	2	2		No	No
			99	67	132	64	140	2	2	2	2	80		
		Os02g0160300	2,563	1,109	81	77		2,439	1,003	2	2		Y/N	
			151	122	133	128	449	31	42	12	10	382		
		Os02g0213000	2,094	1,180	88	81		1,999	1,083	2	2		Y/N	
			162	161	142	146	197	87	91	57	76	137		
		Os01g0929600	985	1,322	103	176		866	1,220	2	75		Yes	Yes
			135	130	160	132	242	27	56	42	14	179		
		Os01g0799100	802	1,396	100	120		649	1,272	2	10		Yes	Yes
			180	150	174	230	161	54	57	23	96	89		
		Os04g0428500	1,359	1,793	133	130		1,224	1,682	12	20		Yes	Yes
			126	118	184	140	173	2	34	42	8	108		
		Os08g0293200	594	1,743	153	116		444	1,621	28	3		No	Yes
			162	122	217	143	223	36	31	56	7	165		
6. Non-protein	Non-protein coding transcript	Os05g0463100	2,512	1,233	79	101		2,408	1,137	2	11			
			116	82	78	73	146	25	10	2	2	84		
	miRNA	osa-miR167h	1,098	858	130	128		976	750	15	26			
			173	160	154	176	321	53	78	32	62	266		

[a] Whether the gene is significantly expressed in tapetum according to microarray data reported by Hobo et al., (2008)

[b] Whether the gene is significantly expressed in any of the 40 cell types according to LM microarray data reported by Jiao et al., (200

[c] Whether the gene expression in root, stem or leaf is detected by RT-PCR (Supplemental Figure)

Supplemental Table 6. Microarray data for 34 rice SET domain containing proteins

			Intensity (without background subtraction)					Intensity (without background subtraction)				
Sub-family	Gene Name	RAP ID	PMC1	PMC2	TCP1	TCP2		PMC1	PMC2	TCP1	TCP2	
		(TIGR locus ID)	Seedling 1	Seedling 2	Seedling 3	Seedling 4	Seedling 5	Seedling 1	Seedling 2	Seedling 3	Seedling 4	Seedling 5
A	**OsSET25**	Os07g0435900	40,665	58,924	14,645	9,097		40,561	58,825	14,544	9,007	
		(LOC_Os07g25450)	12,703	12,484	12,501	11,914	14,381	12,607	12,408	12,401	11,826	14,322
A	OsSET32	Os08g0565700	54,191	48,653	170	126		54,072	48,553	64	26	
		(LOC_Os08g45130)	13,805	13,119	14,088	13,627	16,446	13,698	13,045	13,965	13,511	16,384
A	**OsSET05**	Os01g0927000	6,777	5,344	83	217		6,662	5,245	2	120	
		(LOC_Os01g70220)	996	890	965	978	2,493	896	813	840	862	2,431
A	OsSET19	Os04g0544100	13,443	22,631	6,704	5,346		13,337	22,540	6,612	5,257	
		(LOC_Os04g45990)	8,028	7,228	7,399	7,570	11,049	7,940	7,155	7,289	7,479	10,960
A	**OsSET30**	Os08g0400200	10,127	9,954	174	117		9,996	9,849	63	12	
		(LOC_Os08g30910)	965	857	944	814	846	841	780	808	684	780
A	OsSET35	Os09g0362900	34,560	85,781	34,379	35,626		34,446	85,683	34,279	35,526	
		(LOC_Os09g19830)	13,423	12,562	11,799	12,693	15,605	13,323	12,490	11,691	12,580	15,539
A	OsSET21	Os05g0490700	79,494	103,746	18,489	18,217		79,389	103,641	18,394	18,125	
		(LOC_Os05g41172)	128,611	123,429	127,529	123,924	197,298	128,521	123,350	127,428	123,831	197,223
A	**OsSET03**	Os01g0811300	3,515	2,321	407	448		3,404	2,221	299	355	
		(LOC_Os01g59620)	491	406	443	437	1,584	388	321	314	325	1,521
A	**OsSET16**	Os03g0320400	842	3,858	247	531		736	3,768	156	441	
		(LOC_Os03g20430)	108	130	92	100	403	21	56	2	10	345
A	OsSET41	Os11g0602200	53,402	60,667	797	975		53,285	60,566	694	874	
		(LOC_Os11g38900)	60,055	56,891	62,813	63,122	55,717	59,951	56,818	62,700	63,007	55,648
A	OsSET11	Os02g0708600	68,206	98,566	46,080	37,823		68,054	98,442	45,958	37,713	
		(LOC_Os02g47900)	35,685	31,543	32,384	36,082	43,510	35,561	31,451	32,238	35,950	43,454
A	OsSET10	Os02g0621100	29,122	21,164	21,225	17,302		28,993	21,054	21,103	17,192	
		(LOC_Os02g40770)	161	117	230	181	442	41	30	73	48	366
B	OsSET08	Os02g0554000	36,143	54,748	36,754	35,667		36,019	54,641	36,639	35,570	
		(LOC_Os02g34850)	21,681	18,700	21,398	22,536	39,700	21,568	18,614	21,273	22,427	39,629
B	OsSET09	Os02g0611300	7,800	6,225	1,543	507		7,700	6,130	1,448	419	
		(LOC_Os02g39800)	6,204	5,761	6,010	6,234	8,806	6,112	5,690	5,920	6,153	8,735
B	OsSET34	Os09g0307800	31,947	20,697	458	542		31,823	20,595	350	440	
		(LOC_Os09g13740)	9,701	8,798	10,230	10,384	29,772	9,588	8,723	10,104	10,264	29,715
B	OsSET43	Os12g0613200	21,031	61,838	6,407	5,912		20,888	61,719	6,281	5,799	
		(LOC_Os12g41900)	15,189	13,928	15,532	15,943	28,775	15,065	13,838	15,368	15,807	28,705
B	OsSET18	Os04g0429100	3,377	9,403	940	1,719		3,251	9,300	832	1,616	
		(LOC_Os04g34976)	3,347	3,044	3,244	3,348	3,451	3,230	2,970	3,117	3,225	3,388
C	OsSET37	Os09g0556700	13,055	13,684	82	79		12,955	13,591	2	2	
		(LOC_Os09g38440)	6,828	5,799	5,973	6,550	8,062	6,738	5,732	5,893	6,470	7,999
C	OsSET33	Os09g0134500	18,048	36,143	13,012	10,312		17,946	36,050	12,924	10,224	
		(LOC_Os09g04890)	9,458	8,366	8,385	9,070	11,903	9,367	8,297	8,301	8,989	11,847
C	OsSET02	Os01g0655300	37,625	50,178	37,171	20,212		37,510	50,080	37,069	20,115	
		(LOC_Os01g46700)	15,203	13,795	15,548	15,307	23,755	15,101	13,723	15,422	15,200	23,655
C	OsSET01	Os01g0218800	29,125	34,173	26,034	19,732		28,980	34,051	25,907	19,617	
		(LOC_Os01g11952)	29,964	27,891	30,190	28,996	32,143	29,827	27,800	30,032	28,853	32,081
C	OsSET06	Os01g0965500	7,869	1,774	6,262	5,326		7,768	1,676	6,168	5,237	
		(LOC_Os01g73460)	2,175	1,967	2,005	2,045	7,726	2,089	1,893	1,911	1,960	7,654
D	OsSET15	Os03g0307800	11,733	7,160	3,643	2,095		11,623	7,059	3,544	2,001	
		(LOC_Os03g19480)	3,176	2,978	3,109	3,022	4,896	3,066	2,900	3,004	2,927	4,828
D	OsSET24	Os06g0275500	74,469	126,101	46,013	28,218		74,368	126,008	45,921	28,130	
		(LOC_Os06g16390)	56,988	53,161	47,818	48,992	93,360	56,901	53,093	47,735	48,915	93,292
E	OsSET27	Os08g0180100	26,893	30,232	18,326	10,384		26,748	30,113	18,203	10,275	
		(LOC_Os08g08210)	11,268	10,806	11,509	11,734	21,361	11,146	10,716	11,357	11,604	21,297
E	**OsSET20**	Os04g0629100	3,176	2,463	133	89		3,073	2,368	39	2	
		(LOC_Os04g53700)	690	615	600	640	971	600	545	510	558	899
E	OsSET29	Os08g0244400	1,605	5,448	204	101		1,498	5,339	112	8	
		(LOC_Os08g14660)	2,815	2,573	2,589	2,720	6,206	2,727	2,491	2,486	2,625	6,130
E	OsSET12	Os02g0725200	3,053	5,918	1,594	1,672		2,943	5,814	1,488	1,579	
		(LOC_Os02g49326)	20,317	19,318	19,774	20,079	24,096	20,210	19,238	19,664	19,981	24,037
E	OsSET42	Os12g0236900	17,243	18,025	14,058	9,268		17,092	17,900	13,935	9,156	
		(LOC_Os12g13460)	54,361	50,722	54,773	56,524	47,563	54,229	50,627	54,615	56,387	47,498
E	OsSET13	Os02g0733800	17,242	12,483	1,401	655		17,131	12,383	1,293	560	
		(LOC_Os02g50100)	13,343	11,202	12,594	13,071	22,710	13,242	11,118	12,457	12,953	22,650
E	OsSET22	Os05g0587200	954	4,609	194	126		835	4,507	84	24	
		(LOC_Os05g50980)	14,818	13,715	15,916	16,213	14,124	14,709	13,636	15,781	16,092	14,058
E	OsSET23	Os06g0127200	1,611	1,150	782	372		1,494	1,036	683	276	
		(LOC_Os06g03676)	1,400	1,316	1,234	1,397	1,654	1,298	1,229	1,118	1,292	1,594
E	OsSET26	Os07g0471100	7,020	6,094	1,920	2,829		6,916	6,003	1,830	2,738	
		(LOC_Os07g28840)	810	702	732	754	2,104	721	630	635	669	2,037
E	OsSET04	Os01g0879500	666	1,952	332	291		563	1,858	242	202	
		(LOC_Os01g65730)	1,913	1,684	1,826	1,862	2,455	1,821	1,612	1,734	1,779	2,392

Supplemental Table 7. Transcription factors and transcriptional regulators expression summary

	number of genes								number of genes						
		expressed			highly expressed					expressed			highly expressed		
Family name	in the microarry	in pollen mother cell	in tricellular pollen	in seedling	in pollen mother cell	in tricellular pollen	in seedling	Family name	in the microarry	in pollen mother cell	in tricellular pollen	in seedling	in pollen mother cell	in tricellular pollen	in seedling
MYB	103	40	19	69 *	6		3	ARID	4	4	3	4		1	
MYB-related	45	32 *	29 *	41 *	8	3	9	**HMG**	9	9 *	7	9	6 *	1	6 *
E2F-DP	8	8 *	5	8	1			JUMONJI	14	12 *	8	12	1	2	1
NAC	88	32	14	58	8		9	CPP	8	6	5	6			
HSF	23	15	7	19 *				MADS	38	21	15	19	6		2
FHA	16	13	10	15 *	4	2	2	S1Fa-like	2	2	2	2	1		1
HB	71	39	20	55 *	5	1	11	EIL	5	4	3	4			2
Alfin	9	9 *	7	9	7 *		5	Trihelix	19	14	6	16	5		3
PHD	55	50 *	43 *	50 *	18 *	6	8	TUB	14	13 *	7	13 *	2	2	3
C3H	49	43 *	26 *	42 *	15 *	5	10	ABI3-VP1	34	17	8	21	1	1	2
C2C2-GATA	17	15 *	5	16 *				ARF	25	21 *	4	22 *	6		7
C2C2-CO-like	31	19	13	30 *	3	3	7	AUX-IAA	27	13	2	25 *	2	1	8
C2C2-Dof	24	7	3	18	1		3	CAMTA	6	6	5	6	2	1	1
BBR-BPC	3	3	2	3	1		2	CCAAT-Dr1	1	1	1	1	1		
C2C2-YABBY	8	3	1	7	1			CCAAT-HAP2	10	7	3	8			
C2H2	77	31	18	51	1	2	3	CCAAT-HAP3	11	4	2	6	1		
TAZ	6	5	5	5			1	CCAAT-HAP5	14	9	5	9	1	1	2
HRT-like	1	1	1	1				GARP-ARR-B	7	3	2	4			
LIM	10	5	4	7	1	3	1	GARP-G2-like	41	23	10	33 *	4	1	6
PLATZ	11	3	1	6			1	LFY	1		1	1			
SBP	17	13	7	16 *	2			ULT	1	1	1	1			
SRS	3	2	2 *	3				VOZ	2	2	1	2			
WRKY	74	27	11	54 *	2	1	3	PBF-2-like	1	1	0	1	1		
ZF-HD	13	5	2	10				NZZ	1	1	0	*			
ZIM	16	13	9	13	3	2	3	BES1	5	5	0	5			
bHLH	110	55	23	84 *	8	2	11	GRAS	37	26 *	10	30 *	3		4
TCP	16	8	2	14	3		3	GRF	11	9	1	11 *			
bZIP	73	54 *	24	64 *	9	2	9	GIF	3	3	0	3	1		
GeBP	13	12 *	9	12	3			MBF1	2	2	2	2	2	1	1
AS2	27	10	6	18		1	0	LUG	6	4	2	4	1		1
Nin-like	8	6	2	5			1	**PcG**	29	29 *	18 *	27 *	9 *	4	5
AP2-EREBP	128	58	29	92 *	14	1	17	total	1541	908	493	1202	180	50	177

* significantly enriched at P level 0.001

Transcription regulators without DNA-binding domains are with space

Supplemental Table 8. Microarray data for 288 genes in plant hormone biosynthesis and signaling pathways

note: 1) The included hormones are brassinosteroid (BR), cytokinin (CK), ethylene (ET), gibberellin (GA), jasmonic acid (JA), salic acids (SA), abscisic acid (ABA) and auxin. 2) The genes are ordered in the sequence of biosynthetic procedure and signaling steps within the group of individual hormone.

				Intensity (without background subtraction)					Intensity (with background subtraction)				
	Pathway type	Gene name	RAP ID	PMC1	PMC2	TCP1	TCP2		PMC1	PMC2	TCP1	TCP2	
				seedling1	seedling2	seedling3	seedling4	seedling5	seedling1	seedling2	seedling3	seedling4	seedling5
BR	biosynthesis	OsSMT1	Os07g0206700	48,862	71,033	31,898	18,273		48,757	70,940	31,808	18,183	
				135,826	123,365	130,458	132,880	262,584	135,738	123,299	130,382	132,804	262,512
BR	biosynthesis	OsFACKEL1	Os01g0354200	6,946	7,603	92	406		6,833	7,492	2	312	
				16,060	14,665	15,331	15,896	30,838	15,959	14,581	15,218	15,795	30,772
BR	biosynthesis	OsFACKEL2	Os09g0565600	28,840	22,613	278	441		28,740	22,519	185	354	
				17,430	15,082	16,069	17,314	30,119	17,342	15,013	15,982	17,236	30,047
BR	biosynthesis	OsHYD1	Os01g0103600	3,948	5,311	303	294		3,846	5,218	212	200	
				503	389	120	184	438	418	320	13	83	383
BR	biosynthesis	OsDWF7	Os01g0134500	35,406	62,474	145	290		35,306	62,381	57	205	
				36,973	31,778	32,731	35,739	27,653	36,883	31,712	32,652	35,661	27,587
BR	biosynthesis	OsDWF5	Os02g0465400	41,269	55,479	14,452	9,317		41,159	55,377	14,350	9,221	
				60,994	58,635	59,617	60,482	74,789	60,884	58,557	59,513	60,385	74,717
BR	biosynthesis	OsDIM	Os10g0397400	31,749	33,032	534	112		31,624	32,928	424	9	
				108,628	96,001	110,200	106,177	168,606	108,510	95,925	110,070	106,053	168,541
BR	biosynthesis	OsDET2;1	Os11g0184100	2,931	4,676	1,006	279		2,815	4,576	903	179	
				1,856	1,702	1,888	1,901	3,551	1,752	1,628	1,775	1,785	3,491
BR	biosynthesis	OsDET2;2	Os01g0851600	14,113	6,038	10,813	8,791		13,995	5,936	10,702	8,698	
				7,972	7,365	8,224	8,571	6,990	7,862	7,279	8,103	8,467	6,930
BR	biosynthesis	OsDWARF4/CYP90B2	Os03g0227700	136	116	109	126		13	14	2	25	
				2,029	1,888	2,020	2,043	2,656	1,916	1,814	1,896	1,923	2,598
BR	biosynthesis	D11/CYP724B1	Os04g0469800	2,670	2,548	688	602		2,564	2,455	595	511	
				23,554	21,298	22,819	22,157	17,643	23,462	21,226	22,711	22,065	17,586
BR	biosynthesis	D2/CYP90D2	Os07g0136800	78	92	75	79		2	2	2	2	
				75	82	79	90	122	2	2	2	2	55
BR	biosynthesis	OsCPD1/CYP90A3	Os11g0143200	6,800	9,327	319	306		6,673	9,221	202	199	
				22,509	21,376	23,217	23,258	28,307	22,390	21,293	23,070	23,126	28,232
BR	biosynthesis	OsCPD2/CYP90A4	Os12g0139300	3,403	3,731	91	99		3,289	3,634	2	2	
				7,632	6,876	7,372	7,312	11,877	7,534	6,802	7,261	7,202	11,812
BR	biosynthesis	OsDWARF/CYP85A1	Os03g0602300	1,521	2,603	100	93		1,406	2,505	2	2	
				11,650	10,701	12,013	11,444	13,848	11,544	10,629	11,891	11,339	13,784
BR	deactivation	OsBAS1L1/CYP734A4	Os06g0600400	676	1,157	205	243		567	1,049	107	150	
				2,937	2,885	2,826	2,755	3,778	2,841	2,803	2,720	2,659	3,703
BR	deactivation	OsBAS1L2/CYP734A6	Os01g0388000	1,095	2,002	119	116		992	1,912	29	24	
				4,472	3,400	3,860	4,370	6,134	4,384	3,327	3,765	4,286	6,080
BR	deactivation	OsBAS1L3/CYP734A2	Os02g0204700	93	1,513	98	161		2	1,420	6	72	
				77	76	82	74	617	2	9	2	2	560
BR	signaling	OsBRI1	Os01g0718300	13,771	26,047	483	613		13,651	25,930	390	516	
				49,881	43,742	36,960	41,132	75,423	49,787	43,654	36,844	41,030	75,362
BR	signaling	OsBRL1	Os09g0293500	271	395	114	115		167	293	18	24	
				1,573	1,496	1,557	1,554	930	1,482	1,418	1,457	1,463	864
BR	signaling	OsBRL2	Os10g0114400	167	154	130	144		63	59	35	54	
				2,353	2,058	2,147	2,337	1,755	2,262	1,986	2,054	2,254	1,691
BR	signaling	OsBRL3	Os08g0342300	301	859	134	88		179	756	27	2	
				1,730	1,620	1,879	1,816	4,057	1,617	1,545	1,755	1,696	3,986
BR	signaling	OsBAK1;1	Os08g0174700	78,531	88,750	3,400	1,819		78,420	88,645	3,293	1,726	
				36,206	35,110	33,654	35,198	36,578	36,097	35,029	33,542	35,099	36,515
BR	signaling	OsBAK1;2	Os04g0457800	36,869	48,849	14,802	3,768		36,765	48,756	14,712	3,679	
				71,017	62,670	63,636	65,273	100,039	70,930	62,603	63,559	65,197	99,961
BR	signaling	OsBKI1	Os09g0459500	94	103	112	92		2	2	2	2	
				13,343	11,646	12,657	13,245	31,803	13,239	11,561	12,517	13,124	31,741
BR	signaling	OsBIN2;4/OsSKetha	Os05g0207500	1,360	1,181	104	106		1,260	1,084	10	19	
				2,505	2,353	2,461	2,422	3,716	2,411	2,280	2,369	2,342	3,655
BR	signaling	OsBSL1	Os05g0144400	47,560	55,763	191	221		47,465	55,663	101	133	
				43,129	39,093	39,270	42,081	49,699	43,057	39,021	39,183	42,003	49,629
BR	signaling	OsBSL2	Os12g0617900	16,084	17,005	1,327	702		15,979	16,911	1,234	607	
				19,090	17,032	18,188	18,029	34,857	19,002	16,963	18,080	17,926	34,791
BR	signaling	OsBZR1/BES1	Os07g0580500	2,589	1,628	92	83		2,485	1,531	2	2	
				21,121	19,922	21,230	21,761	23,090	21,021	19,849	21,129	21,672	23,033
CK	biosynthesis	OsIPT2	Os03g0356900	88	275	77	86		2	176	2	2	
				77	61	81	82	125	2	2	2	2	50
CK	biosynthesis	OSIPT3	Os05g0312000	31,709	41,057	142	93		31,581	40,948	25	2	
				7,409	6,928	7,458	7,885	11,981	7,295	6,841	7,312	7,763	11,919
CK	biosynthesis	OsIPT7	Os05g0551700	3,331	5,809	86	73		3,230	5,712	2	2	
				276	377	138	125	109	180	304	45	40	41
CK	biosynthesis	LOG	Os01g0588900	12,725	7,844	2,803	4,735		12,623	7,750	2,713	4,647	

Supplemental Table 8 cont. hormone pathways

				19,836	13,295	14,662	18,269	26,579	19,743	13,224	14,571	18,186	26,518
CK	deactivation	OsCKX1	Os01g0187600	238	367	281	230		105	258	161	121	
				1,412	1,428	1,568	1,505	2,968	1,284	1,345	1,431	1,375	2,904
CK	deactivation	Gn1/OsCKX2	Os01g0197600	326	111	110	109		226	15	19	23	
				158	149	146	135	218	65	77	56	54	158
CK	deactivation	OsCKX3	Os10g0483500	16,584	3,473	328	303		16,436	3,352	205	193	
				5,874	5,211	5,704	6,154	9,568	5,750	5,120	5,550	6,022	9,497
CK	deactivation	OsCKX5	Os01g0775400	488	1,151	719	91		355	1,043	604	2	
				1,215	1,072	1,172	1,154	2,621	1,088	992	1,029	1,022	2,564
CK	deactivation	OsCKX9	Os05g0374200	1,679	193	158	116		1,538	76	32	2	
				3,086	1,455	1,680	1,630	3,405	2,961	1,365	1,515	1,493	3,347
CK	deactivation	OsCKX11	Os08g0460600	372	236	1,646	739		267	143	1,557	650	
				6,344	5,485	5,587	6,108	10,972	6,256	5,419	5,513	6,033	10,898
CK	signaling	OsHK1	Os02g0738500	14,438	19,614	263	175		14,319	19,511	152	72	
				12,383	11,160	13,439	13,594	21,053	12,275	11,080	13,298	13,470	20,989
CK	signaling	OsHK2	Os10g0362300	173	2,138	121	93		55	2,035	8	2	
				15,952	13,645	14,906	15,300	42,245	15,845	13,559	14,764	15,179	42,168
CK	signaling	OsHK3	Os01g0923700	10,942	19,392	588	1,416		10,842	19,294	492	1,328	
				26,349	25,016	25,992	26,746	50,139	26,252	24,941	25,898	26,662	50,077
CK	signaling	OsHK4	Os03g0717700	10,676	19,763	8,617	8,323		10,575	19,669	8,522	8,234	
				21,988	20,271	21,319	22,374	15,868	21,897	20,202	21,230	22,290	15,807
CK	signaling	OsHKL1/OsCRL4	Os12g0454800	973	122	112	114		868	29	22	25	
				13,589	11,650	11,783	12,745	7,058	13,500	11,584	11,707	12,670	6,993
CK	signaling	OsHP2	Os08g0557700	207,964	190,749	440	315		207,853	190,653	343	220	
				59,568	53,964	54,178	54,531	105,800	59,468	53,893	54,059	54,431	105,725
CK	signaling	OsHP3	Os01g0743800	6,291	15,288	8,449	4,587		6,156	15,177	8,326	4,474	
				3,953	3,714	4,192	3,983	5,263	3,826	3,629	4,040	3,843	5,187
CK	signaling	OsHP4	Os05g0521300	12,375	20,264	8,366	7,191		12,265	20,161	8,259	7,098	
				21,736	20,496	21,245	22,125	31,168	21,628	20,417	21,137	22,027	31,109
CK	signaling	OsHP5	Os05g0186100	281	614	5,793	6,634		139	491	5,685	6,529	
				5,007	5,218	5,608	5,620	4,237	4,892	5,125	5,469	5,500	4,172
CK	signaling	OsRR1	Os04g0442300	541	523	126	129		407	403	15	26	
				3,879	3,606	3,414	3,779	3,907	3,758	3,514	3,276	3,657	3,851
CK	signaling	OsRR2	Os02g0557800	3,042	1,543	108	127		2,936	1,441	8	37	
				14,427	13,667	14,344	15,233	18,060	14,330	13,589	14,242	15,142	17,985
CK	signaling	OsRR3	Os02g0830200	542	475	152	153		421	373	45	52	
				1,222	1,111	1,308	1,290	2,234	1,111	1,037	1,186	1,170	2,169
CK	signaling	OsRR4	Os01g0952500	1,550	2,467	80	85		1,424	2,359	2	2	
				3,514	3,355	3,492	3,423	3,520	3,392	3,273	3,366	3,305	3,460
CK	signaling	OsRR5	Os04g0524300	135	124	101	88		35	31	14	2	
				922	794	791	898	664	832	728	713	819	601
CK	signaling	OsRR6	Os04g0673300	34,881	40,355	88	86		34,785	40,259	2	2	
				8,365	7,419	6,941	7,601	16,408	8,287	7,349	6,854	7,530	16,334
CK	signaling	OsRR9	Os11g0143300	10,436	16,514	138	137		10,333	16,419	50	48	
				1,082	902	1,004	1,100	698	997	833	918	1,027	631
CK	signaling	OsRR10	Os12g0139400	22,340	51,047	372	355		22,237	50,948	279	266	
				7,399	9,398	5,603	5,593	1,837	7,298	9,323	5,505	5,506	1,775
CK	signaling	OsRR11	Os02g0631700	99	270	131	126		2	151	8	17	
				474	441	518	535	748	352	351	366	405	680
CK	signaling	OsRR13	Os04g0212200	259	279	765	478		135	172	650	375	
				196	204	299	263	206	76	122	177	147	130
CK	signaling	OsRR14	Os03g0742300	99	84	88	108		2	2	2	14	
				72	59	82	109	123	2	2	2	6	70
CK	signaling	OsRR15	Os08g0376700	194	95	86	83		91	2	2	2	
				73	73	77	71	119	2	3	2	2	56
CK	signaling	OsRR16	Os01g0904700	1,120	724	249	76		1,013	629	155	2	
				5,773	5,084	5,533	5,634	6,033	5,684	5,013	5,430	5,528	5,972
CK	signaling	OsRR17	Os02g0182100	14,333	19,816	3,508	1,063		14,220	19,716	3,411	968	
				10,155	9,659	9,923	9,802	15,669	10,046	9,586	9,810	9,700	15,607
CK	signaling	OsRR18	Os02g0796500	3,190	13,807	126	104		3,089	13,712	36	17	
				16,392	15,221	16,106	15,359	20,949	16,300	15,150	16,018	15,278	20,889
CK	signaling	OsRR19	Os03g0224200	23,138	26,339	2,737	3,871		23,022	26,239	2,638	3,774	
				23,376	20,667	23,601	23,560	31,828	23,265	20,593	23,483	23,454	31,761
CK	signaling	OsRR20	Os06g0183100	277	221	91	86		171	127	3	2	
				2,286	1,998	2,028	2,177	1,842	2,199	1,929	1,946	2,102	1,780
CK	signaling	OsRR21	Os06g0647200	215	139	120	109		112	44	29	20	
				143	97	111	100	315	49	25	16	15	255
CK	signaling	OsRR22/Ehd	Os10g0463400	76	82	184	75		2	2	78	2	
				60	68	272	66	180	2	2	149	2	116
ET	biosynthesis	OsACS1	Os03g0727600	411	114	117	103		309	22	27	16	
				2,293	1,839	1,916	2,009	6,080	2,206	1,773	1,837	1,933	6,014
ET	biosynthesis	OsACS2	Os04g0578000	93	85	175	382		2	2	79	293	

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				293	277	310	294	420	203	202	212	206	357
ET	biosynthesis	OsACS5	Os01g0192900	80	93	82	88		2	2	2	2	
				404	379	356	393	1,500	317	312	277	315	1,422
ET	biosynthesis	OsACS6	Os06g0130400	2,251	3,573	34,485	40,153		2,128	3,459	34,375	40,054	
				39,384	36,459	39,712	40,130	34,717	39,267	36,372	39,583	40,015	34,652
ET	biosynthesis	OsACO1	Os09g0451400	480	3,167	167	150		378	3,074	77	62	
				16,079	14,411	16,298	16,823	50,721	15,993	14,345	16,221	16,748	50,654
ET	biosynthesis	OsACO2	Os02g0771600	956	1,822	623	170		815	1,701	499	58	
				55,586	54,595	56,835	56,161	113,341	55,451	54,503	56,683	56,023	113,268
ET	biosynthesis	OsACO3	Os09g0451000	471	745	411	525		367	646	310	436	
				63,469	59,752	61,186	60,611	76,300	63,371	59,677	61,087	60,524	76,233
ET	biosynthesis	OsACO4	Os11g0186900	133	163	149	292		2	42	30	183	
				422	444	514	958	337	292	351	365	825	273
ET	biosynthesis	OsACO5	Os05g0149400	93	100	98	89		2	6	3	2	
				28,819	26,157	28,483	27,216	18,439	28,725	26,085	28,367	27,120	18,380
ET	biosynthesis	OsACO6	Os05g0149300	93	79	82	69		2	2	2	2	
				189	175	167	167	109	100	106	81	89	38
ET	biosynthesis	OsACO7	Os01g0580500	284	582	110	99		180	489	21	10	
				28,089	25,026	25,718	27,894	44,739	28,001	24,959	25,641	27,818	44,666
ET	signaling	OsETR1;1	Os03g0701700	63,794	64,644	208	517		63,660	64,535	91	410	
				74,809	71,900	75,916	74,656	113,420	74,680	71,819	75,770	74,523	113,345
ET	signaling	OsETR1;2	Os05g0155200	1,805	868	100	113		1,690	769	2	14	
				2,500	2,241	2,467	2,480	2,581	2,396	2,168	2,345	2,368	2,516
ET	signaling	OsEIN4	Os04g0169100	20,567	12,845	206	417		20,457	12,748	108	318	
				21,842	19,145	21,647	22,151	35,502	21,747	19,073	21,537	22,042	35,438
ET	signaling	OsETR2;1	Os02g0820900	6,719	12,124	223	258		6,617	12,025	128	168	
				16,782	15,998	16,727	16,552	16,882	16,695	15,923	16,631	16,465	16,815
ET	signaling	OsETR2;2	Os07g0259100	194	124	139	123		78	22	27	24	
				179	103	159	105	204	74	19	16	2	150
ET	signaling	OsCTR1;1	Os02g0527600	5,033	3,664	485	662		4,933	3,566	392	575	
				17,133	15,879	17,253	17,676	15,222	17,036	15,805	17,159	17,594	15,150
ET	signaling	OsCTR1;2	Os09g0566500	105	219	100	113		2	109	2	7	
				96	96	97	142	211	2	12	2	19	162
ET	signaling	OsEIN2;1	Os07g0157000	9,930	13,059	235	169		9,811	12,948	126	72	
				5,028	4,797	4,992	4,769	8,826	4,913	4,712	4,869	4,658	8,767
ET	signaling	OsEIN2;2	Os03g0700800	15,897	10,352	145	123		15,781	10,252	46	26	
				26,985	25,221	26,750	26,428	21,719	26,873	25,147	26,633	26,323	21,645
ET	signaling	OsEIN3;1	Os03g0324200	2,341	5,318	3,690	2,596		2,239	5,226	3,600	2,508	
				37,181	32,266	31,686	34,696	50,319	37,094	32,201	31,610	34,621	50,255
ET	signaling	OsEIN3;2	Os03g0324300	21,702	41,040	4,126	6,419		21,578	40,922	4,026	6,320	
				129,405	125,362	126,775	130,629	151,376	129,300	125,273	126,652	130,520	151,308
ET	signaling	OsEIN3;3	Os07g0685700	4,473	8,387	134	125		4,368	8,285	35	36	
				49,357	45,452	51,077	50,448	82,641	49,262	45,375	50,976	50,357	82,577
ET	signaling	OsEIN3;4	Os09g0490200	3,067	2,250	857	2,142		2,969	2,147	766	2,053	
				4,242	3,781	4,071	4,491	3,521	4,168	3,706	3,981	4,408	3,443
ET	signaling	OsEIN3;5	Os08g0508700	2,355	1,247	12,952	3,826		2,253	1,151	12,853	3,736	
				1,354	1,252	1,340	1,299	1,958	1,258	1,181	1,247	1,213	1,901
ET	signaling	OsEIN3;6	Os02g0574800	109	109	90	333		2	3	2	228	
				97	89	108	449	129	2	9	2	327	61
ET	signaling	OsEIN3;7	Os04g0456700	8,654	8,585	1,498	780		8,554	8,493	1,411	695	
				80,406	70,733	72,255	78,349	111,259	80,317	70,669	72,180	78,273	111,184
GA	biosynthesis	CPS	Os02g0278700	160	146	47,711	27,487		7	21	47,585	27,373	
				881	715	880	897	1,336	752	622	718	760	1,260
GA	biosynthesis	KS	Os04g0611800	2,002	5,931	8,991	6,197		1,899	5,838	8,901	6,108	
				10,859	10,251	10,562	10,750	12,179	10,768	10,179	10,470	10,665	12,120
GA	biosynthesis	KO1a	Os06g0570600	132	89	98	83		2	2	2	2	
				122	78	119	86	230	2	2	2	2	172
GA	biosynthesis	KO2	Os06g0569900	4,723	105	1,793	1,169		4,606	5	1,688	1,070	
				109	69	85	110	211	5	2	2	2	163
GA	biosynthesis	KAO	Os06g0110000	129	655	218,724	154,745		28	563	218,633	154,657	
				1,502	1,343	2,062	1,859	2,453	1,415	1,276	1,981	1,782	2,372
GA	biosynthesis	GA20ox1	Os03g0856700	1,553	2,257	513	483		1,452	2,164	425	398	
				3,609	3,529	3,488	3,636	7,324	3,521	3,464	3,412	3,560	7,256
GA	biosynthesis	GA20ox2	Os01g0883800	233	253	221	205		133	155	129	118	
				1,827	1,728	1,637	1,717	2,382	1,732	1,654	1,545	1,636	2,321
GA	biosynthesis	GA20ox3	Os07g0169700	14,938	8,004	223,688	140,147		14,833	7,910	223,598	140,058	
				78	79	433	248	293	2	11	352	169	224
GA	biosynthesis	GA20ox4	Os05g0421900	293	133	160	165		138	8	36	53	
				267	107	226	231	341	137	13	65	95	279
GA	biosynthesis	GA3ox1	Os05g0178100	7,916	4,105	64,479	34,053		7,764	3,981	64,351	33,936	
				202	105	258	221	350	70	13	91	80	288
GA	biosynthesis	GA3ox2	Os01g0177400	125	108	164	133		22	14	71	44	

Supplemental Table 8 cont. hormone pathways

				436	396	397	381	467	347	327	312	300	407
GA	deactivation	GA2ox1	Os05g0158600	228	95	83	425		112	2	2	326	
				760	725	793	798	977	646	647	683	692	892
GA	deactivation	GA2ox3	Os01g0757200	243	618	279	133		139	519	177	42	
				6,935	6,369	7,375	7,173	7,764	6,834	6,294	7,278	7,083	7,698
GA	deactivation	GA2ox4	Os05g0514600	98	93	465	198		2	2	374	102	
				490	445	494	584	718	405	376	392	481	643
GA	deactivation	GA2ox5	Os07g0103500	116	99	108	96		2	2	2	2	
				453	381	481	482	558	341	295	362	377	497
GA	deactivation	GA2ox6	Os04g0522500	96	103	118	104		2	7	24	12	
				624	613	618	592	845	528	542	510	499	781
GA	deactivation	GA2ox7	Os05g0560900	217	203	200	224		63	78	79	114	
				1,109	1,001	1,031	1,081	3,011	984	907	877	949	2,935
GA	deactivation	EUI	Os05g0482400	103	324	138	111		2	223	32	10	
				774	775	858	818	653	659	702	728	703	589
GA	deactivation	EUIL1	Os07g0681300	114	165	105	94		2	42	2	2	
				204	204	241	236	300	81	110	96	108	238
GA	deactivation	EUIL2	Os12g0118900	138	102	87	84		37	8	2	2	
				574	522	557	571	422	485	454	471	492	361
GA	deactivation	EUIL3	Os12g0119000	257	933	177	165		158	841	92	78	
				5,231	4,478	4,735	5,174	4,821	5,138	4,411	4,660	5,093	4,744
GA	deactivation	EUIL4	Os03g0332000	135	102	186	113		4	2	74	8	
				532	513	646	549	682	407	435	508	419	610
GA	signaling	GID1	Os05g0407500	764	2,566	355	418		660	2,471	265	328	
				1,979	1,818	1,800	1,906	3,814	1,891	1,748	1,714	1,829	3,744
GA	signaling	SLR1	Os03g0707600	31,797	25,620	94	92		31,696	25,527	3	5	
				16,406	14,157	14,479	15,849	27,700	16,319	14,090	14,397	15,772	27,633
GA	signaling	SLRL1	Os01g0646300	259	276	143	119		129	157	38	18	
				581	545	630	591	540	469	454	499	476	469
GA	signaling	SLRL2	Os05g0574900	740	1,058	78	77		637	965	2	2	
				72	66	65	63	137	2	2	2	2	71
GA	signaling	GID2	Os02g0580300	72,251	69,135	2,983	1,749		72,152	69,036	2,891	1,660	
				305,381	271,931	266,329	276,912	433,748	305,300	271,858	266,238	276,830	433,680
GA	signaling	EL1	Os03g0793500	11,994	16,950	12,040	11,958		11,894	16,855	11,945	11,870	
				6,972	6,427	6,679	6,878	7,341	6,880	6,355	6,588	6,797	7,263
GA	signaling	OsSPY	Os08g0559300	22,208	34,364	6,485	3,863		22,102	34,268	6,383	3,774	
				13,120	11,078	12,092	12,371	20,389	13,026	10,995	11,964	12,258	20,324
GA	signaling	OsSEC	Os01g0915400	1,007	522	408	463		863	403	286	356	
				506	468	526	579	424	385	378	381	452	362
GA	signaling	OsGAMYB	Os01g0812000	58,756	93,245	108	464		58,626	93,140	2	360	
				8,475	7,469	7,743	8,483	9,732	8,351	7,392	7,610	8,359	9,663
GA	signaling	OsGAMYBL1	Os06g0605600	92,248	49,637	2,376	340		92,149	49,545	2,290	255	
				8,005	6,615	6,866	7,362	23,497	7,914	6,550	6,791	7,282	23,430
GA	signaling	OsGAMYBL2	Os03g0578900	58,003	34,752	112	93		57,903	34,659	25	8	
				573	404	362	365	521	484	340	288	291	460
GA	putative GAMYB regulated		Os03g0168600	92,289	68,116	100	83		92,178	68,016	3	2	
				1,029	782	375	354	776	921	707	266	255	721
GA	putative GAMYB regulated		Os07g0103100	11,121	8,229	104	93		11,015	8,122	10	2	
				2,045	1,893	1,993	2,066	4,975	1,957	1,813	1,892	1,972	4,919
GA	putative GAMYB regulated		Os04g0404400	9,814	12,833	174	102		9,712	12,741	85	14	
				446	407	483	348	491	359	341	408	273	420
GA	putative GAMYB regulated		Os06g0228500	13,785	8,528	135	101		13,651	8,409	18	2	
				1,680	1,592	1,724	1,655	1,086	1,552	1,502	1,581	1,527	1,027
GA	putative GAMYB regulated		Os06g0539400	11,903	14,587	135	361		11,803	14,494	48	274	
				1,153	961	1,010	1,060	2,578	1,061	893	931	978	2,512
GA	putative GAMYB regulated		Os07g0566500	11,816	5,158	77	78		11,699	5,058	2	2	
				120	72	68	64	117	15	2	2	2	54
JA	biosynthesis	OsDAD1;2	Os08g0143600	180	80	157	110		80	2	69	24	
				160	150	155	162	349	70	81	72	82	289
JA	biosynthesis	OsDAD1;3	Os02g0653900	342	1,356	166	102		201	1,240	39	2	
				15,957	14,986	15,987	15,505	15,357	15,825	14,898	15,832	15,362	15,287
JA	biosynthesis	OsDAD1;4	Os10g0562200	107	104	162	175		2	10	65	78	
				188	160	197	193	191	95	87	93	86	133
JA	biosynthesis	OsPLA1	Os07g0520900	12,151	10,336	10,876	8,781		12,039	10,242	10,779	8,684	
				4,907	4,211	4,925	4,779	4,767	4,814	4,138	4,822	4,672	4,707
JA	biosynthesis	OsLOX2;1	Os08g0508800	93	98	96	89		2	2	2	2	
				597	566	582	588	594	485	487	471	485	530
JA	biosynthesis	OsLOX2;2	Os12g0559200	513	425	5,208	6,903		406	331	5,115	6,803	
				9,178	8,469	9,140	9,111	16,259	9,092	8,399	9,044	9,003	16,206
JA	biosynthesis	OsLOX2;3	Os08g0509100	110	94	103	103		6	2	13	15	
				422	355	337	358	246	335	289	263	284	186
JA	biosynthesis	OsLOX2;4	Os02g0194700	93	105	85	261		2	7	2	174	

Supplemental Table 8 cont. hormone pathways

				19,598	18,512	18,868	19,191	12,197	19,502	18,438	18,775	19,109	12,135
JA	biosynthesis	OsLOX2;5	Os03g0179900	306	404	194	209		154	279	69	93	
				1,163	1,168	1,206	1,242	1,535	1,029	1,074	1,044	1,101	1,469
JA	biosynthesis	OsAOS1	Os03g0225900	145	126	141	199		7	12	16	85	
				1,252	1,169	1,288	1,345	1,755	1,121	1,083	1,135	1,206	1,697
JA	biosynthesis	OsAOS2	Os03g0767000	4,504	10,565	119	120		4,402	10,467	25	30	
				18,769	17,844	17,808	18,098	42,039	18,681	17,769	17,713	18,012	41,966
JA	biosynthesis	OsAOC	Os03g0438100	85,914	77,467	142	187		85,780	77,351	21	79	
				147,331	143,746	147,761	139,720	158,585	147,200	143,659	147,619	139,589	158,514
JA	biosynthesis	OsOPR7	Os08g0459600	39,761	52,213	19,559	11,176		39,611	52,090	19,431	11,059	
				52,975	49,334	55,653	55,175	57,005	52,843	49,241	55,486	55,034	56,940
JA	biosynthesis	OsOPCL1	Os03g0132000	13,142	11,193	86	240		13,046	11,096	2	153	
				17,453	15,506	16,302	17,204	17,518	17,376	15,434	16,214	17,130	17,454
JA	biosynthesis	OsACX	Os06g0103500	43,716	70,951	8,494	4,270		43,599	70,843	8,384	4,174	
				64,783	60,246	64,335	62,148	113,176	64,670	60,164	64,217	62,042	113,114
JA	biosynthesis	OaAIM1	Os02g0274100	28,134	35,927	2,166	294		28,034	35,833	2,078	207	
				86,610	79,751	85,638	89,294	97,372	86,521	79,682	85,554	89,214	97,300
JA	biosynthesis	OsKAT	Os02g0817700	12,109	12,821	373	597		11,973	12,712	254	488	
				44,915	42,665	45,951	45,221	47,659	44,784	42,583	45,806	45,087	47,587
JA	biosynthesis	OsJMT1	Os01g0701700	5,078	3,204	123	103		4,954	3,098	6	2	
				522	455	578	532	860	410	369	426	402	802
JA	biosynthesis	OsJMT2	Os06g0329900	79	75	69	69		2	2	2	2	
				1,802	1,503	1,592	1,691	3,582	1,713	1,438	1,517	1,617	3,528
JA	biosynthesis	OsJMT3	Os06g0314600	105	116	145	120		2	2	21	8	
				3,057	2,909	3,238	3,073	4,781	2,925	2,822	3,088	2,934	4,720
JA	biosynthesis	OsJMT4	Os06g0323100	98	86	78	70		2	2	2	2	
				171	155	145	146	119	71	82	43	56	59
JA	biosynthesis	OsJMT5	Os05g0102000	88	92	87	234		2	2	2	145	
				301	279	273	294	347	225	204	182	210	288
JA	biosynthesis	OsJAR1;2	Os05g0586200	5,855	6,027	12,591	4,298		5,729	5,923	12,481	4,195	
				13,007	11,733	12,847	12,756	13,499	12,888	11,658	12,717	12,631	13,429
JA	biosynthesis	OsJAR1;3	Os01g0221100	93	93	91	84		2	2	2	2	
				87	92	99	97	324	2	19	2	2	256
JA	signaling	OsCOI1	Os01g0853400	14,434	23,974	55,962	29,375		14,316	23,870	55,852	29,275	
				33,252	31,156	33,919	33,087	52,762	33,138	31,076	33,806	32,980	52,688
JA	signaling	OsJAZ1	Os03g0180900	11,790	17,230	4,949	8,225		11,685	17,136	4,857	8,135	
				9,088	8,154	8,895	9,083	10,736	8,999	8,085	8,809	9,004	10,660
JA	signaling	OsJAZ2	Os10g0392400	5,940	10,396	5,709	3,841		5,810	10,291	5,598	3,737	
				7,881	7,340	7,865	7,638	11,896	7,757	7,263	7,729	7,510	11,827
JA	signaling	OsJAZ3	Os07g0615200	7,761	7,635	113	115		7,639	7,527	2	15	
				222,006	206,007	214,336	213,139	163,084	221,887	205,925	214,215	213,026	163,012
JA	signaling	OsJAZ4	Os03g0402800	5,071	7,834	5,744	8,690		4,945	7,725	5,628	8,586	
				8,924	8,543	8,775	8,719	8,251	8,802	8,460	8,649	8,600	8,186
JA	signaling	OsJAZ5	Os03g0181100	12,131	6,537	6,154	3,801		12,003	6,429	6,033	3,691	
				8,161	8,363	9,412	9,692	25,077	8,043	8,277	9,259	9,557	25,007
JA	signaling	OsJAZ6	Os03g0180800	83,186	83,375	289,543	173,353		83,060	83,270	289,429	173,248	
				21,362	19,330	24,605	23,309	49,070	21,243	19,250	24,464	23,183	49,014
JA	signaling	OsJAZ7	Os09g0439200	2,763	6,266	347	672		2,654	6,175	256	573	
				28,173	24,459	27,292	28,578	36,758	28,090	24,388	27,201	28,472	36,692
JA	signaling	OsJAZ9	Os04g0395800	108	278	93	159		2	183	2	64	
				231	223	237	245	456	140	153	124	142	402
JA	signaling	OsMYC	Os10g0575000	1,797	1,278	943	1,308		1,663	1,170	826	1,201	
				4,492	4,266	4,869	4,353	2,789	4,364	4,186	4,725	4,220	2,733
SA	biosynthesis	OsICS1	Os09g0361500	2,426	3,123	118	502		2,273	2,998	2	392	
				14,606	12,712	13,528	14,394	16,977	14,481	12,618	13,373	14,263	16,894
SA	biosynthesis	OsPAL2	Os04g0518400	285	220	115	190		182	124	22	100	
				2,947	2,730	2,629	2,932	1,433	2,858	2,658	2,538	2,851	1,382
ABA	biosynthesis	OsZEP1	Os04g0448900	637	10,869	26,099	35,984		533	10,773	26,003	35,894	
				27,555	26,879	27,464	29,309	45,396	27,464	26,806	27,370	29,226	45,329
ABA	biosynthesis	OsABA4	Os01g0128300	149	280	117	100		38	183	20	6	
				126	132	134	131	239	25	60	17	31	177
ABA	biosynthesis	OsNCED1	Os03g0645900	11,369	14,483	931	724		11,220	14,360	809	616	
				8,170	6,822	5,712	5,310	7,473	8,048	6,732	5,570	5,180	7,415
ABA	biosynthesis	OsNCED2	Os12g0617400	252	405	125	1,490		146	311	35	1,401	
				411	353	386	451	347	322	285	309	375	285
ABA	biosynthesis	OsABA2	Os03g0810800	9,517	13,852	90	92		9,417	13,757	2	6	
				24,829	22,807	23,153	24,475	23,733	24,739	22,736	23,065	24,397	23,670
ABA	biosynthesis	OsAAO3;1	Os07g0281700	82	84	80	76		2	2	2	2	
				483	400	421	437	132	402	321	323	346	65
ABA	biosynthesis	OsAAO3;2	Os07g0282300	111	106	87	77		11	14	2	2	
				898	813	837	900	934	806	745	759	818	870
ABA	biosynthesis	OsAAO3;3	Os07g0164900	5,099	1,004	121	85		4,966	892	2	2	

Supplemental Table 8 cont. hormone pathways

				2,567	2,309	2,409	2,510	4,751	2,450	2,222	2,256	2,382	4,680
ABA	biosynthesis	OsAAO3;4	Os10g0168100	11,169	29,635	34,169	47,909		11,050	29,530	34,057	47,808	
				5,067	5,197	5,369	5,633	8,753	4,952	5,117	5,255	5,524	8,694
ABA	deactivation	OsABA8OX1	Os02g0703600	8,369	24,611	188	194		8,266	24,518	97	104	
				16,460	15,082	14,980	15,767	26,200	16,372	15,015	14,901	15,689	26,125
ABA	deactivation	OsABA8OX2	Os08g0472800	388	242	103	138		247	124	2	33	
				1,227	1,086	1,144	1,191	3,334	1,109	997	1,007	1,068	3,272
ABA	deactivation	OsABA8OX3	Os09g0457100	623	1,056	105	100		488	940	2	2	
				305	244	304	297	731	173	155	160	165	659
ABA	signaling	OsPLDα1	Os01g0172400	23,912	36,409	1,700	829		23,792	36,293	1,600	732	
				95,915	90,180	93,120	93,810	97,607	95,810	90,093	93,000	93,703	97,536
ABA	signaling	OsPLDα2	Os03g0119100	617	1,155	56,033	33,054		511	1,060	55,931	32,966	
				1,216	1,131	3,207	2,357	2,656	1,125	1,050	3,086	2,247	2,593
ABA	signaling	OsPLDα3	Os03g0391400	135	123	195	381		2	2	73	273	
				3,651	3,172	3,356	3,545	3,735	3,528	3,081	3,207	3,415	3,673
ABA	signaling	OsPLDα4	Os03g0840800	413	428	166,196	212,076		259	304	166,074	211,965	
				155	201	33,170	46,391	30,637	28	109	33,016	46,257	30,567
ABA	signaling	OsPLDα5	Os05g0171000	122	86	52,749	46,128		6	2	52,639	46,028	
				61	60	180	178	147	2	2	43	57	84
ABA	signaling	OsPLDα6	Os06g0604200	176	1,900	559	140		74	1,806	462	51	
				7,779	7,349	7,458	7,669	10,435	7,687	7,279	7,369	7,585	10,367
ABA	signaling	OsPLDα7	Os06g0604300	96	787	99	105		2	685	2	3	
				4,281	3,946	4,355	4,183	2,326	4,168	3,872	4,227	4,064	2,269
ABA	signaling	OsPLDα8	Os06g0604400	537	90	110	146		421	2	8	48	
				330	229	276	283	405	227	154	157	170	346
ABA	signaling	OsPLDα9	Os07g0260400	1,496	901	127,564	111,745		1,387	805	127,466	111,651	
				2,006	1,953	2,603	2,407	2,324	1,911	1,882	2,485	2,303	2,248
ABA	signaling	OsPLDα10	Os08g0401800	1,391	1,225	1,320	840		1,267	1,115	1,205	737	
				1,920	1,613	1,281	1,062	1,903	1,798	1,529	1,154	944	1,843
ABA	signaling	OsPLDα11	Os09g0421300	1,452	816	207	190		1,320	707	86	80	
				308	264	337	386	479	183	180	186	250	408
ABA	signaling	OsPLDα12	Os09g0543100	30,962	60,490	97,617	153,263		30,858	60,397	97,527	153,174	
				16,090	13,642	13,087	15,071	17,753	16,002	13,576	13,013	14,997	17,686
ABA	signaling	OsPLDα13	Os10g0524400	26,497	64,109	20,433	20,945		26,392	64,009	20,331	20,853	
				8,609	7,806	8,094	8,126	11,933	8,505	7,729	7,996	8,034	11,868
ABA	signaling	OsPP2C1	Os01g0583100	14,177	22,998	27,337	23,284		14,077	22,903	27,244	23,197	
				15,928	14,692	15,215	15,895	27,572	15,838	14,622	15,127	15,817	27,511
ABA	signaling	OsPP2C2	Os01g0656200	35,000	54,357	281	99		34,879	54,254	169	2	
				4,200	4,059	4,043	4,135	8,832	4,088	3,979	3,901	4,010	8,763
ABA	signaling	OsPP2C3	Os01g0846300	58,203	17,459	4,410	5,941		58,070	17,352	4,296	5,835	
				17,587	16,792	18,905	18,364	17,767	17,461	16,713	18,765	18,233	17,704
ABA	signaling	OsPP2C4	Os03g0268600	5,090	4,836	714	795		4,963	4,717	618	695	
				308	721	193	200	500	207	632	71	93	439
ABA	signaling	OsPP2C5	Os05g0457200	5,013	2,228	366,052	379,125		4,910	2,129	365,951	379,034	
				1,336	1,238	5,187	5,067	4,833	1,236	1,163	5,091	4,979	4,766
ABA	signaling	OsPP2C6	Os05g0537400	5,593	7,710	578	1,341		5,489	7,617	487	1,252	
				3,940	3,440	3,625	3,803	5,869	3,852	3,372	3,543	3,723	5,807
ABA	signaling	OsPP2C7	Os05g0572700	920	115	2,561	136		802	16	2,457	37	
				905	797	3,567	864	640	799	723	3,447	750	579
ABA	signaling	OsPP2C8	Os05g0592800	18,998	17,441	2,605	1,082		18,869	17,329	2,486	976	
				9,399	8,833	9,070	8,860	17,024	9,272	8,748	8,935	8,735	16,963
ABA	signaling	OsPP2C9	Os09g0325700	5,871	2,667	805	371		5,769	2,574	714	283	
				1,425	1,235	1,254	1,387	2,533	1,338	1,169	1,175	1,311	2,467
ABA	signaling	SAPK8	Os03g0764800	32,165	57,617	9,032	6,367		32,026	57,503	8,907	6,251	
				63,596	56,575	70,350	68,761	72,346	63,467	56,487	70,193	68,620	72,266
ABA	signaling	SAPK9	Os12g0586100	6,466	2,691	92	130		6,333	2,578	2	21	
				5,200	4,407	4,529	4,615	4,328	5,070	4,321	4,388	4,485	4,270
ABA	signaling	SAPK10	Os03g0610900	5,463	1,683	611	771		5,360	1,589	519	682	
				4,655	4,205	4,574	4,655	10,350	4,566	4,136	4,489	4,575	10,291
ABA	signaling	OsVP1	Os01g0911700	211	146	649	412		85	41	534	306	
				251	195	266	248	469	132	115	123	121	407
ABA	signaling	TRAB1	Os08g0472000	27,284	34,687	3,081	1,377		27,141	34,568	2,955	1,262	
				7,910	5,513	6,226	6,125	12,056	7,783	5,423	6,062	5,988	11,990
ABA	signaling	OsbZIP9	Os01g0813100	84	339	81	73		2	241	2	2	
				75	79	108	94	132	2	7	2	2	65
ABA	signaling	OsbZIP10	Os01g0859300	3,109	1,173	348	245		2,996	1,072	238	150	
				1,481	1,192	1,294	1,361	1,490	1,377	1,107	1,161	1,247	1,418
ABA	signaling	OsbZIP12	Os01g0867300	19,498	17,754	30,394	17,756		19,394	17,659	30,303	17,667	
				16,020	13,603	14,664	15,235	44,430	15,932	13,533	14,576	15,158	44,366
ABA	signaling	OsbZIP23	Os02g0766700	4,880	13,289	607	155		4,778	13,192	514	65	
				12,398	11,459	11,293	12,458	13,639	12,311	11,386	11,201	12,377	13,552
ABA	signaling	OsbZIP24	Os02g0833600	272	962	187	212		154	862	82	112	

Supplemental Table 8 cont. hormone pathways

				20,837	19,500	21,488	20,387	23,232	20,731	19,426	21,366	20,272	23,165
ABA	signaling	OsbZIP40	Os05g0437700	48,528	42,242	32,515	20,303		48,428	42,147	32,425	20,217	
				36,605	33,384	34,910	35,317	45,200	36,515	33,313	34,823	35,238	45,128
ABA	signaling	OsbZIP42	Os05g0489700	32,219	26,150	4,536	3,735		32,081	26,035	4,411	3,622	
				10,095	8,767	9,315	9,140	18,904	9,970	8,678	9,154	9,005	18,849
ABA	signaling	OsbZIP46	Os06g0211200	71,912	81,533	8,579	7,790		71,779	81,415	8,463	7,685	
				49,143	48,027	51,544	50,203	75,819	49,016	47,936	51,403	50,076	75,749
ABA	signaling	OsbZIP62	Os07g0686100	6,819	3,501	163	142		6,687	3,395	51	37	
				2,641	2,228	2,585	2,549	2,721	2,515	2,149	2,447	2,419	2,662
ABA	signaling	OsbZIP69	Os08g0549600	1,141	218	88	99		1,037	123	2	9	
				6,313	6,041	6,016	6,393	5,592	6,224	5,970	5,926	6,313	5,522
ABA	signaling	OsbZIP72	Os09g0456200	1,859	1,335	469	90		1,759	1,242	381	4	
				9,314	7,855	7,889	8,805	10,329	9,224	7,789	7,809	8,727	10,257
Auxin	biosynthesis	OsASA1	Os03g0826500	25,588	21,168	1,469	596		25,444	21,045	1,360	491	
				9,541	8,053	8,083	8,558	9,293	9,427	7,960	7,941	8,439	9,231
Auxin	biosynthesis	OsASA2	Os03g0264400	28,873	21,151	132	147		28,719	21,026	7	33	
				38,739	34,801	35,270	37,907	23,990	38,608	34,707	35,109	37,770	23,927
Auxin	biosynthesis	OsASB1	Os04g0463500	67,202	84,126	2,707	891		67,048	84,002	2,585	780	
				33,383	29,430	31,045	33,185	34,472	33,257	29,337	30,892	33,051	34,400
Auxin	biosynthesis	OsASB2	Os03g0718000	4,612	1,493	3,544	2,872		4,515	1,394	3,453	2,783	
				6,321	5,705	6,132	6,525	12,048	6,244	5,632	6,043	6,446	11,991
Auxin	biosynthesis	OsTAA1;1	Os01g0169800	134	2,145	103	107		28	2,050	15	17	
				10,018	8,441	8,849	9,537	16,045	9,930	8,372	8,766	9,462	15,984
Auxin	biosynthesis	OsTAA1;2	Os01g0717400	92	93	2,850	721		2	2	2,757	634	
				6,817	6,017	6,371	6,872	7,418	6,729	5,947	6,285	6,794	7,348
Auxin	biosynthesis	OsTAA1;3	Os01g0717700	142	706	134	123		12	596	13	13	
				14,909	13,422	14,215	14,963	16,925	14,790	13,335	14,058	14,830	16,854
Auxin	biosynthesis	OsTAA1;4	Os05g0169300	785	245	35,155	16,644		643	123	35,039	16,537	
				227	173	318	246	682	100	80	172	116	606
Auxin	biosynthesis	OsYUCCA1	Os01g0645400	184	676	109	106		65	572	2	3	
				742	675	768	821	1,329	634	591	621	693	1,262
Auxin	biosynthesis	OsYUCCA4	Os01g0224700	136	106	74,682	35,993		5	2	74,571	35,889	
				116	77	559	376	587	2	2	422	247	522
Auxin	biosynthesis	OsYUCCA5	Os12g0512000	412	312	308	442		298	209	199	345	
				2,625	2,401	2,572	2,591	3,481	2,514	2,322	2,464	2,489	3,426
Auxin	biosynthesis	OsYUCCA6	Os07g0437000	96	89	76	133		2	2	2	41	
				1,430	1,318	1,284	1,413	949	1,327	1,243	1,184	1,321	894
Auxin	biosynthesis	OsYUCCA7	Os04g0128900	125	140	98	96		24	48	10	8	
				2,676	2,343	2,225	2,418	4,127	2,584	2,273	2,143	2,337	4,062
Auxin	biosynthesis	COW1	Os03g0162000	5,435	1,152	4,782	3,506		5,332	1,057	4,686	3,416	
				312	167	283	252	877	221	96	191	169	818
Auxin	signaling	OsTIR1;1	Os05g0150500	1,381	2,305	88	82		1,278	2,212	2	2	
				1,065	971	890	996	1,034	978	906	815	921	976
Auxin	signaling	OsTIR1;2	Os02g0759700	27,650	59,671	20,784	19,748		27,549	59,576	20,688	19,659	
				44,447	42,908	42,147	43,337	73,144	44,354	42,837	42,057	43,253	73,080
Auxin	signaling	OsTIR1;3	Os04g0395600	138,639	193,260	43,587	21,316		138,508	193,146	43,468	21,210	
				143,576	134,827	142,402	140,646	245,119	143,448	134,741	142,264	140,519	245,058
Auxin	signaling	OsTIR1;4	Os11g0462900	115	112	535	83		2	9	423	2	
				93	82	118	82	157	2	2	2	2	104
Auxin	signaling	OsTIR1;5	Os11g0515500	9,561	25,810	3,570	4,263		9,450	25,718	3,477	4,164	
				12,564	11,121	11,977	12,852	19,925	12,477	11,049	11,882	12,746	19,869
Auxin	signaling	OsIAA1	Os01g0178500	20,757	23,300	728	391		20,608	23,177	600	274	
				27,367	26,391	27,374	27,749	58,462	27,236	26,299	27,207	27,608	58,406
Auxin	signaling	OsIAA2	Os01g0190300	1,048	13,122	124	124		943	13,030	32	34	
				15,024	13,347	14,768	14,367	47,781	14,936	13,276	14,655	14,272	47,707
Auxin	signaling	OsIAA3	Os01g0231000	10,032	11,228	328	299		9,932	11,132	233	212	
				116,776	108,704	115,741	114,606	76,589	116,684	108,633	115,650	114,525	76,512
Auxin	signaling	OsIAA4	Os01g0286900	94	86	88	77		2	2	2	2	
				209	180	207	194	624	104	104	79	76	570
Auxin	signaling	OsIAA5	Os01g0675700	30,977	20,618	5,714	3,597		30,872	20,525	5,622	3,507	
				28,559	25,018	28,750	27,710	31,419	28,470	24,946	28,636	27,615	31,348
Auxin	signaling	OsIAA6	Os01g0741900	2,265	5,885	95	88		2,158	5,786	2	2	
				11,826	11,085	11,574	11,533	17,142	11,724	11,010	11,476	11,442	17,087
Auxin	signaling	OsIAA7	Os02g0228900	7,033	17,950	122	127		6,902	17,844	10	21	
				10,310	9,900	10,382	10,370	12,281	10,186	9,821	10,250	10,244	12,209
Auxin	signaling	OsIAA8	Os02g0723400	120	106	106	104		2	2	2	2	
				100	77	118	137	155	2	2	2	18	94
Auxin	signaling	OsIAA9	Os02g0805100	105	103	81	81		2	2	2	2	
				1,335	1,221	1,236	1,286	3,314	1,229	1,145	1,134	1,191	3,242
Auxin	signaling	OsIAA10	Os02g0817600	22,198	18,856	392	442		22,095	18,764	303	352	
				120,779	109,264	118,586	117,339	147,277	120,688	109,192	118,495	117,255	147,204
Auxin	signaling	OsIAA11	Os03g0633500	176	114	139	192		37	2	14	79	

Supplemental Table 8 cont. hormone pathways

				901	790	903	968	680	769	704	750	829	622
Auxin	signaling	OsIAA12	Os03g0633800	82	123	83	81		2	29	2	2	
				3,547	3,198	3,329	3,541	2,452	3,455	3,126	3,228	3,453	2,389
Auxin	signaling	OsIAA13	Os03g0742900	494	5,920	592	135		394	5,827	500	48	
				98,882	88,412	96,428	102,767	153,985	98,793	88,343	96,342	102,690	153,913
Auxin	signaling	OsIAA14	Os03g0797800	7,903	9,219	118	273		7,749	9,094	2	161	
				9,096	9,452	9,915	10,147	12,298	8,967	9,359	9,755	10,011	12,246
Auxin	signaling	OsIAA15	Os05g0178600	13,255	10,200	4,755	3,936		13,153	10,104	4,655	3,846	
				60,323	56,583	60,020	57,325	53,231	60,228	56,511	59,927	57,240	53,163
Auxin	signaling	OsIAA16	Os05g0186900	3,834	545	102	124		3,703	439	2	19	
				4,500	4,218	4,612	4,570	7,658	4,376	4,140	4,474	4,439	7,586
Auxin	signaling	OsIAA17	Os05g0230700	33,414	58,314	125	144		33,309	58,220	33	53	
				122,389	118,823	126,926	127,917	149,985	122,296	118,751	126,824	127,828	149,926
Auxin	signaling	OsIAA18	Os05g0523300	155	420	81	351		57	328	2	266	
				2,161	1,842	1,979	2,511	3,841	2,067	1,777	1,906	2,429	3,771
Auxin	signaling	OsIAA19	Os05g0559400	17,749	79,012	62,649	97,239		17,643	78,909	62,549	97,148	
				64,003	60,217	62,929	64,804	84,153	63,905	60,139	62,827	64,713	84,086
Auxin	signaling	OsIAA20	Os06g0166500	148	115	101	132		20	10	2	28	
				2,869	2,574	2,876	2,927	3,171	2,747	2,497	2,739	2,800	3,106
Auxin	signaling	OsIAA21	Os06g0335500	11,470	9,746	109	96		11,375	9,650	21	9	
				52,431	45,548	50,066	51,910	53,001	52,355	45,478	49,981	51,840	52,937
Auxin	signaling	OsIAA22	Os06g0355300	307	442	109	96		210	342	18	7	
				1,072	946	1,078	1,145	940	994	872	988	1,064	867
Auxin	signaling	OsIAA23	Os06g0597000	33,586	56,708	1,701	414		33,481	56,611	1,608	324	
				25,523	24,117	25,518	25,328	37,305	25,424	24,045	25,415	25,238	37,237
Auxin	signaling	OsIAA24	Os07g0182400	544	1,886	129	95		395	1,762	13	2	
				15,867	14,424	15,569	15,995	12,727	15,744	14,330	15,418	15,865	12,669
Auxin	signaling	OsIAA25	Os08g0109400	356	456	109	79		252	361	14	2	
				809	717	759	785	675	718	646	667	702	611
Auxin	signaling	OsIAA26	Os09g0527700	148	130	119	118		36	34	17	22	
				684	585	701	662	1,582	590	509	584	551	1,499
Auxin	signaling	OsIAA27	Os11g0221000	83	84	78	76		2	2	2	2	
				4,164	3,820	3,953	4,066	4,739	4,070	3,748	3,855	3,980	4,672
Auxin	signaling	OsIAA29	Os11g0221300	108	103	92	84		8	10	2	2	
				70	70	69	68	149	2	2	2	2	85
Auxin	signaling	OsIAA30	Os12g0601300	318	308	267	307		164	184	143	195	
				26,750	25,152	26,371	26,648	56,896	26,623	25,059	26,213	26,512	56,830
Auxin	signaling	OsARF1	Os01g0236300	33,163	24,135	90	78		33,061	24,037	2	2	
				2,634	2,520	2,553	2,598	4,852	2,545	2,446	2,457	2,512	4,787
Auxin	signaling	OsARF2	Os01g0670800	6,014	3,244	899	107		5,910	3,153	809	16	
				16,244	13,859	14,091	15,039	21,056	16,155	13,786	13,995	14,953	20,992
Auxin	signaling	OsARF3	Os01g0753500	9,139	9,506	601	331		9,038	9,413	510	243	
				13,043	11,002	11,433	12,084	25,555	12,956	10,935	11,351	12,007	25,491
Auxin	signaling	OsARF4	Os01g0927600	62,585	83,976	4,218	3,808		62,485	83,880	4,123	3,720	
				34,174	31,140	31,961	33,999	50,184	34,082	31,069	31,870	33,918	50,120
Auxin	signaling	OsARF6	Os02g0164900	23,040	27,408	188	252		22,911	27,295	70	146	
				33,292	30,923	31,943	31,933	53,241	33,166	30,838	31,809	31,809	53,152
Auxin	signaling	OsARF7	Os02g0557200	46,687	25,914	436	298		46,582	25,820	345	208	
				16,936	14,767	15,563	15,976	31,020	16,847	14,698	15,479	15,897	30,964
Auxin	signaling	OsARF9	Os04g0442000	48,361	91,043	372	212		48,251	90,946	274	114	
				54,358	48,470	54,490	42,437	55,564	54,264	48,399	54,379	42,329	55,488
Auxin	signaling	OsARF10 miF	Os04g0519700	113	117	142	163		2	16	43	67	
				2,471	2,269	2,386	2,269	5,061	2,358	2,192	2,275	2,168	4,996
Auxin	signaling	OsARF11	Os04g0664400	9,275	14,210	108	118		9,137	14,094	2	6	
				6,184	6,049	6,328	6,418	4,280	6,051	5,962	6,178	6,279	4,201
Auxin	signaling	OsARF12	Os04g0671900	39,510	20,230	339	93		39,404	20,132	245	2	
				78,688	73,570	79,124	78,641	72,291	78,587	73,498	79,018	78,548	72,235
Auxin	signaling	OsARF13 miF	Os04g0690600	209	100	84	271		101	4	2	179	
				92	70	74	111	110	2	2	2	2	54
Auxin	signaling	OsARF14	Os05g0515400	7,362	6,064	39,376	22,535		7,218	5,945	39,250	22,420	
				15,804	13,180	18,271	16,363	17,867	15,677	13,090	18,106	16,225	17,810
Auxin	signaling	OsARF15	Os05g0563400	34,329	59,586	140	173		34,227	59,491	42	84	
				123,184	113,326	119,328	122,747	191,146	123,091	113,256	119,238	122,662	191,077
Auxin	signaling	OsARF16	Os06g0196700	1,834	6,588	112	334		1,694	6,472	2	220	
				5,524	5,080	5,417	5,350	8,279	5,391	4,993	5,263	5,207	8,212
Auxin	signaling	OsARF17	Os06g0677800	3,407	5,130	82	80		3,288	5,023	2	2	
				22,762	21,038	22,060	22,635	27,305	22,646	20,957	21,942	22,526	27,229
Auxin	signaling	OsARF18, mi	Os06g0685700	141,442	201,845	106	115		141,294	201,724	2	7	
				42,253	37,710	38,193	39,989	51,006	42,131	37,620	38,049	39,860	50,930
Auxin	signaling	OsARF19	Os06g0702600	1,939	3,870	201	241		1,788	3,747	73	124	
				9,400	8,831	9,524	9,499	10,150	9,267	8,739	9,357	9,357	10,089
Auxin	signaling	OsARF21	Os08g0520500	3,096	15,139	230	165		2,958	15,024	106	53	

Supplemental Table 8 cont. hormone pathways

				12,665	12,481	13,371	13,220	18,994	12,532	12,394	13,221	13,081	18,932
Auxin	signaling	OsARF23	Os11g0523800	13,848	52,029	90	81		13,742	51,931	2	2	
				6,056	5,953	5,785	5,911	5,515	5,954	5,880	5,680	5,818	5,447
Auxin	signaling	OsARF24	Os12g0479400	217,787	351,520	1,039	904		217,685	351,428	950	816	
				58,153	47,762	46,558	51,554	102,016	58,067	47,696	46,482	51,479	101,945
Auxin	signaling	OsARF25	Os12g0613700	21,516	15,299	11,673	6,290		21,416	15,201	11,578	6,202	
				31,827	30,221	31,630	32,791	28,181	31,730	30,146	31,536	32,708	28,117

Supplemental Table 9. 29 genes that significantly expressed in PMCs and contain putative MYB binding motif in the promoter region

RAP ID	Intensity (without background subtraction)					Putative binding site in promoter region	binding motif*	Description
	PMC1	PMC2	TCP1	TCP2				
	seedling1	seedling2	seedling3	seedling4	seedling5			
Os08g0131100	121,726	27,448	1,895	1,058		CAACTAAC; TAACCAA	148; 97	Cytochrome P450.
	1,414	380	208	227	389			
Os08g0241300	62,380	50,319	2,034	4,369		CAACCAAA; TAACGAC	169; 359	Conserved hypothetical protein.
	2,005	1,515	781	770	10,447			
Os03g0168600	92,289	68,116	100	83		CAACGAAC	277	Cytochrome P450 family protein.
	1,029	782	375	354	776			
Os04g0645600	65,984	79,370	176,426	322,596		CAACGGCC	267	Conserved hypothetical protein.
	16,575	15,226	15,854	16,561	25,872			
Os07g0103100	11,121	8,229	104	93		CAACAAAC	219	Metabotropic gamma-aminobutyric acid receptor, type B family protein.
	2,045	1,893	1,993	2,066	4,975			
Os08g0280200	14,071	11,247	28,591	20,544		CAACGAAC; CAACCAA	408; 457	Actin-binding FH2 domain containing protein.
	3,593	3,391	3,694	3,650	2,159			
Os04g0404400	9,814	12,833	174	102		CAACTGTC	82	Bipartite response regulator, C-terminal effector domain containing protein.
	446	407	483	348	491			
Os06g0228500	13,785	8,528	135	101		CAACCACA	88	Amino acid/polyamine transporter II family protein.
	1,680	1,592	1,724	1,655	1,086			
Os04g0465600	7,749	25,372	1,488	1,547		CAACCAAC; CAACGGC	261; 379	Bet v I allergen family protein.
	289,504	272,267	274,694	295,450	428,563			
Os06g0539400	11,903	14,587	135	361		TAACCACC	447	Amino acid/polyamine transporter I family protein.
	1,153	961	1,010	1,060	2,578			
Os02g0138900	24,705	33,634	183,220	183,411		CAACCAAA	246	Low affinity calcium antiporter CAX2.
	2,299	2,098	3,537	3,434	1,267			
Os01g0647000	16,963	21,327	640	469		CAACCAAA; CAACCAC	61; 144	Cyclin-like F-box domain containing protein.
	10,596	9,761	11,242	11,385	10,485			
Os04g0650700	5,230	20,475	52,363	87,386		CAACGCCG;CAACGCCG;TAACCGCG	234; 174; 43	L-asparaginase (L-asparagine amidohydrolase).
	78,602	73,191	66,429	72,122	88,944			
Os01g0761400	42,992	2,204	114	98		TAACTACC	109	TGF-beta receptor, type I/II extracellular region family protein.
	1,024	203	175	163	258			
Os03g0680200	8,018	31,968	147	165		CAACGACA	62	TPR-like domain containing protein.
	278	468	191	255	322			
Os03g0245100	9,370	12,029	2,243	1,543		CAACGAAC	61	Dihydrodipicolinate reductase family protein.
	8,891	8,489	9,135	9,194	15,226			

Os06g0108500	4,957	12,060	316	101		CAACAAAC	477	(No Hit)
	810	794	799	783	1,806			
Os01g0551000	4,312	5,137	309	313		CAACGCGA	337	Conserved hypothetical protein.
	2,965	2,452	2,432	2,757	5,169			
Os07g0503500	4,203	9,270	66,195	68,791		CAACCGCA;CAACCAAC;CAACCACC	134; 141; 17	UDP-glucuronosyl/UDP-glucosyltransferase family protein.
	61,136	56,585	60,800	63,366	156,200			
Os02g0564600	5,355	2,436	2,720	2,589		CAACGCGA;CAACCGAA:CAACGAAC;CAAC	42; 76; 46; 1	(No Hit)
	1,631	1,393	1,520	1,581	1,405			
Os03g0785900	4,424	4,140	395	970		CAACCAAA;TAACCAA	176; 327	Glutathione S-transferase GST 19 (EC 2.5.1.18).
	51,354	46,697	51,750	49,236	42,484			
Os07g0680000	5,336	3,668	44,956	35,468		CAACGGCA	285	Vacuolar sorting receptor homolog.
	1,562	1,336	1,587	1,784	2,484			
Os01g0149800	12,177	3,546	336,729	221,771		CAACAAAC;CAACCGA	425; 311	Metallothionein-like protein type 2.
	68,806	61,968	75,775	75,498	55,137			
Os02g0790600	7,889	1,954	105	100		CAACCAAA	165	Zn-finger, RING domain containing protein.
	5,112	4,567	4,472	4,729	5,999			
Os12g0554100	5,067	1,995	79	69		CAACCACC;TAACCAC	27; 260	Protein of unknown function DUF231 domain containing protein.
	937	770	782	810	1,233			
Os10g0576900	1,761	5,657	92	80		CAACAAAC	220	Conserved hypothetical protein.
	16,732	15,778	16,404	16,253	22,214			
Os01g0225400	4,590	1,086	509	458		TAACCAAC	110	Ketopantoate hydroxymethyltransferase family protein.
	3,361	3,172	3,393	3,483	5,652			
Os07g0566500	11,816	5,158	77	78		CAACAAAC;TAACCGA	86; 98	No apical meristem (NAM) protein domain containing protein.
	120	72	68	64	117			
Os07g0565800	2,458	5,499	328	321		CAACCACA	287	Conserved hypothetical protein.
	116,117	106,074	108,172	114,321	205,464			

*(bp to start coden)   Reference: Aya *et al.* , 2009

Supplemental Table 10. 20 housekeeping genes that used for normalization

RAP ID	TCP1-Intensity	TCP2-Intensity	PMC1-Intensity	PMC2-Intensity	Seedling1-Intensity	Seedling2-Intensity	Seedling3-Intensity	Seedling4-Intensity
Os03g0313000	66,587	60,845	73,453	51,400	61,819	62,337	60,170	58,621
Os01g0328700	97,834	65,877	99,863	111,836	108,543	106,818	104,640	96,159
Os07g0222800	69,761	38,804	80,565	33,257	50,476	48,704	50,721	48,380
Os07g0134800	165,144	75,132	96,505	119,434	99,981	100,736	102,907	94,367
Os01g0962300	25,526	21,304	27,205	23,790	28,838	28,121	27,610	26,213
Os02g0601300	167,842	93,235	164,893	194,000	199,574	202,992	212,807	196,141
Os05g0482700	149,020	89,661	156,254	145,244	186,307	181,220	171,239	163,601
Os02g0816800	35,933	24,760	32,777	25,761	24,650	24,467	25,307	22,740
Os04g0390000	100,127	52,016	56,149	61,848	72,138	72,773	71,438	66,687
Os01g0612200	102,935	83,276	123,474	129,402	99,844	99,084	108,801	96,664
Os03g0416500	2,704	1,694	1,193	6,497	2,269	2,388	2,227	2,024
Os07g0585800	108,282	60,111	91,041	60,388	58,252	61,057	61,594	55,546
Os07g0495200	75,275	35,550	54,169	48,426	36,654	39,349	42,499	37,702
Os04g0137500	29,658	28,253	30,086	26,685	20,700	21,020	21,657	19,994
Os07g0645400	83,853	60,602	68,487	78,207	92,187	93,424	97,282	88,093
Os02g0751800	16,023	9,874	24,388	10,039	11,625	11,333	11,441	10,699
Os07g0640100	67,525	48,828	59,056	33,457	59,767	59,589	58,136	50,984
Os02g0520800	120,277	83,255	106,027	95,474	73,644	74,135	72,100	67,696
Os08g0161700	56,427	36,367	46,182	30,127	54,412	55,023	53,568	51,232
Os12g0168900	154,374	127,010	135,247	98,966	174,987	173,163	170,155	163,560

Supplemental Table 11. Saturated intensity values and number of probes at saturated level.

	PMC-1	PMC-2	TCP-1	TCP-2	Seedling-1	Seedling-2	Seedling-3	edling-4
Saturated intensity value	661347	661995	658203	657354	632392	632075	601030	6E+05
Log2 Saturated intensity value	19.34	19.34	19.33	19.33	19.27	19.27	19.2	19.21
Number of probes with saturated intensity	2	3	5	5	1	1	2	1

Supplemental Table 12. Primer sequences (5'→3')

Real-time PCR primers

Gene	Forward	Reverse
Os03g0289300	AATCCGTTTCTTGGTTGGGTG	CACATAACCGCAGCCACCG
Os06g0492900	GCCTCCAGAAGCACATCAAGAAG	TCAGCACAACGACAACCTTCTCC
Os09g0480300	AAGAAAGTAGGGAGACCAAAGAA	TTATTCCTATTGTGTCCAGCCC
Os04g0208600	TAGTGGTCCTTGAGAGTGATGCT	CAGAGATGTCAAGCCGAGAAGAT
Os12g0512000	GCCTCTCAGTGTTCCTTCTCAA	AAGTCCTCCCTACAGCCATTCAC
Os01g0717400	GAAATGCGAGTGGGTGGAAGAC	GCTCTGCCGTGCTTCTCG
Os02g0635200	GGCAGGTCCCAACTACGAAGG	GAGGTGCGGCTGGTCATTCA
Os03g0268000	CGTGCAGGCGTTAGGCTTGAAGC	GGCAACTTCATCCTTCCATAATC
Os02g0161900	TGGTCAGTAATCAGCCAGTTTGG	GCACCACAAATACTTGACGAACAG
Os07g0574800	CTAAGCGTGCGTTTGTG	CGTCGTTCTCGTCGTCT
Os03g0264400	GCCAAGCCACAACACGATG	CTATCAGCGACAATGCCAGC
Os07g0108900	GGTGGAGAGGCAGAAGAATGTGAG	GGTGGAAGAAGTGCCTGCTGAT
Os03g0681800	GAGAGGAACATAACGAGCCACT	TGTCATCTCCCGAAGCCT
Os03g0718100	CTTCATAGGAATGGAAGCTGCGGGTA	CGACCACCTTGATCTTCATGCTGCTA

Real time PCR primers for measuring the absolute mRNA copy number

Gene	Forward	Reverse
Os09g0480300	AAGAAAGTAGGGAGACCAAAGAA	TTATTCCTATTGTGTCCAGCCC
Os03g0650400	ATGCGGTGCTAGGGAGAAGATG	ATCAGCAGTAGGACGGAGTGGC
	GGTTTGAGTCCCCATGTCTGTA	CAATGGCAATGATGAATAATGAAT

Primers used in the in situ hybridization as below:

Gene	Forward	Reverse
Os03g0650400	GGTACCTGCTGCTGCCAAGAAATG	GAGCTCGGAGAAGTTGTGTAATGCCG
Os07g0409500	GGTACCCAAATCTCCTCCGGTATCTTC	GAGCTCCGAACCTACCAGAGATAACTACG
Os01g0212500	CCGCGGCTGTGCCCACAGCCTCCAT	GGTACCGAACCGGACCGACTGGAAG

References for in situ hybridization:

Langdale JA (1993) In situ hybridization. The Maize Handbook, Springer-Verlag, New York pp.165-180

Cox KH, Goldberg RB (1988) Analysis of gene expression. In CH Shaw, ed, Plant Molecular Biology: A Practical Approach. Oxford IRL Press, Oxford, UK, pp 1-35

Schichnes D, Nemson J, Sohlberg L, Ruzin SE (1999) Microwave Protocols for Paraffin Microtechnique and In Situ Localization in Plants. Microsc Microanal 4(5): 491-496

Conventional RT-PCR

Total RNA of the seven organs were extracted directly by Trizol reagent (Chomczynski and Sacchi, 1987).Their cDNA synthesis utilizes Reverse Transcriptase M-MLV kit (TakaRa Code: D2649A, China). RT-PCR was performed using the following protocol: Cycle 1(1X); step 1, 95.0℃ for 2:00; Cycle 2(30X); step 1,95.0 ℃ for 00:30; step2, 60.0 ℃ for 00:30; step 3, 72.0 ℃ for 00:30; Cycle 3(1X); 72.0 ℃ for 05:00. Each reaction was set to 20 μl of final volume containing 1 μl of 10 uM of each primer, 2 ul of cDNA, 2ul of 2mM dNTPs, 0.3 ul of 2.5U/ul Taq DNA Polymerase (TIANGEN Code: PT080530, China). RT-PCR primers as below:

Gene	Forward	Reverse
Os10g0484800	GATGTATTCTGGGCTGTGC	CAAATGTGATGCCTGGG
Os05g0153200	GATGCGGTGACAAATGCTCTG	GCCTTCTCTTGGTCGCCTTG
Os08g0164000	GATGAAGACAATGCCACGA	AACACCCATTGAACACACTG
Os05g0574000	GCTGGCGAACAAGTCCTAC	CACTATCCTCATCTTCCTCGC
Os05g0484000	TATGATTCGCTGTTGATTTGAT	TTTCTCCAGCATCATAGCAAC

Supplemental Table 13. 1158 PMC-preferential genes as meiosis-related core.

RAP ID	PMC1-intensity	PMC2-intensity	TCP1-intensity	TCP2-intensity	Seedling 1-intensity	Seedling 2-intensity	Seedling 3-intensity	Seedling 4-intensity	Seedling 5-intensity	foldchange PMC /seedling	foldchange PMC /TCP	Probe Sequence
Os01g0103100	14,162	3,756	73	83	1,068	589	499	527	715	10.8	93.8	TCTAGTACTAGTAGTATCTGCTAAGTGACATTATATTGATCAATCAAACAAATTAAGGGC
Os01g0103600	3,948	5,311	303	294	503	389	120	184	438	13.7	15.3	AAAGAATCGATTCTAAGGGTATGGAAGGATCTAGTTTTGGTATAAGTTTCATGAAGGATG
Os01g0109500	32,420	21,254	89	81	1,687	1,463	1,451	1,652	3,336	11.5	310	TGGAGTAGTAGACAAAGAAAAAGTTGTAGGTAGACGGGCAGATCAATTACATTCTACGCC
Os01g0112300	31,877	36,405	3,113	2,260	11,124	10,216	9,672	9,497	6,927	4.1	12.8	TTGTGACCAGAACGTCGTCTATTAGGGAAGGATCTCCTGAATCTTCAAATGGAGCCTCAT
Os01g0114800	12,043	15,494	1,014	1,296	2,401	2,297	1,589	1,483	3,356	5.4	11.9	CTGCTTGTATCCTGTCTCAGTCCCCTGCTGCTTTGTGTTTGTCTGTAAATAACTTTTATT
Os01g0122200	3,253	3,491	77	75	68	65	70	63	129	36.4	44.4	CAACCTCGTTTTTAATCTTCAATGGATAGAAGTAGATGCCAAAAAGATCCTAATTGAAGC
Os01g0126600	17,749	24,842	91	180	126	138	76	78	167	162	164	CTGCCAGTGAGATACGTAACTTGTTTGGACTACTGTTGTTAATCTTTCCTCCATGTGCAT
Os01g0127900	10,715	19,224	94	243	1,330	812	919	904	1,067	14.1	94.9	TTCAGCCATTCTATTCTATTACATTGTAGTTCAGAACTAAAATGTGAACTGGTCTCAAGC
Os01g0129200	7,968	2,573	254	189	201	111	205	145	197	25.5	20.7	AGCGCTGGGTGGCCACATGAATCGCCACCGCCAAGGCAATATCACACAACAACCTACCTA
Os01g0150400	1,436	2,474	124	132	195	201	226	211	278	7.8	14.8	TTGTACGTTCCAGGATGCTACCATTTCTGGAACAAAGAAGCAAAGCTGTTGATTGCTGAG
Os01g0156300	36,909	13,363	235	321	1,922	1,684	1,600	1,554	1,759	12.9	80.9	ATTGGTTGATTTTGTGCAGTTGTGCTACCTCTATATCGATCCTCACCTGGATTCTGTGGA
Os01g0157200	16,001	13,203	75	252	320	237	64	63	123	114	106	GGTGGACTCGAAATTCTTGATCAGTTTGAAAACAACCACTTGGATGTTTCTGTTTCTTCT
Os01g0157500	17,497	12,909	133	800	890	648	139	211	169	60.9	46.1	TGACAGCCTGAGGCCCTTGTGCTTCTGAAACTTCTGATCAATTTGATGATTCGAACCTGA
Os01g0157600	5,643	7,084	81	252	196	167	100	106	121	49.3	44.4	AATTTTAGGGAGGAATTCGTCCTAGCTTCTCTGTAAACATGATCATTTGATTCACTGATC
Os01g0164800	21,844	32,270	1,490	1,092	4,373	4,004	4,381	4,529	5,959	5.2	20.8	CTCAAATTGGAGAACAGCCCTGACGCAATTATATGGTTGTATTTCTCACTCCAATATCCA
Os01g0165200	123,675	113,627	433	163	5,166	4,723	3,739	3,638	5,210	25.1	446	CTGTCTACAGGACACTAGTTACTTAGAGAAGTTCGAATGAACAAACTTTAGCTGGTGATA
Os01g0166200	12,940	13,837	139	101	1,054	1,084	186	131	195	47.5	113	CTGAGCTGTCTCCAATTCAGGTCTGTTTATGACAAAGTCATTGGATGTTTGTTCCCTTCG
Os01g0171200	29,246	24,029	79	91	1,051	706	109	135	339	80.0	314	CTCCGTTTGGATGTTGCAGTAGTATGCTTGTACGGTTCTACCACATACTACTCCGTATTG
Os01g0175200	14,102	10,838	132	118	2,151	1,965	1,751	1,827	2,758	5.4	99.2	CTGAACATTGTATCAGTTGATTCAGTTCCACGCAATTATCAGAACATTGCTGAATGCTTA
Os01g0175600	38,604	20,683	136	202	1,404	1,232	1,305	1,294	1,208	22.5	170	CGGCGGCCGTATGATATGATATGCTTGTCAGTTGTCACATTGTGCATGGAGTAAACAGAA
Os01g0180700	40,555	39,202	4,831	7,056	8,569	7,921	8,320	8,819	10,193	4.3	6.8	TCGCTGCTTGCTGTGAAATATTTTGTGCCTGTACTTTGGGCGTTGGAGGGAGTTGAATTT
Os01g0182100	4,809	6,467	746	676	446	422	468	496	569	10.9	7.9	ATCATCGTGGATTTATGTCATACTACTAATAGTGTTGGGCTCTTCAAATCCAACATTGTA
Os01g0184100	311,139	202,004	3,612	260	8,879	7,710	7,403	7,303	10,908	27.2	259	ACATGGTGGTCTGTATGCCGTATGCGATGTGATGATGATGGATGGTTTGATGTTTGGTAA
Os01g0189200	93,993	105,004	873	553	3,211	2,707	810	923	1,246	70.4	143	AAACTGTCCTAGAGCATCTCAACAAACTGCTGTCCTAACTGTCCTAGAGCATCCAACTGA
Os01g0206200	287,682	340,583	197	141	17,659	16,281	16,642	16,519	32,227	13.5	1877	GCTGCATGTTTCCATTTTGATTCGTAACCTGATTAAACCCTCAATGCCCAAACTTGGTGT
Os01g0209200	85,972	63,220	153	1,073	13,773	11,154	11,035	12,100	12,060	6.1	182	TGATTCTTCGACTTCTTGAGCAACATCGTGTACTAAGCACTCGCTGATCGCTCTTTTGCA
Os01g0209500	74,651	98,559	7,889	4,108	335	324	178	198	898	181	15.1	ATGGAACAATCCGTTGTAGTGCGTTGCCATTGCTGTACAGATGGCCTCCATTTCTTACAT
Os01g0212500	6,976	3,691	769	299	104	82	93	83	184	39.4	10.6	GTTGTGTGAAAAAAAGTAGAAACTTGTTTAGTCAGTAAGACCAGATGTATAATCAGTTGC
Os01g0219200	35,021	15,435	508	319	702	304	187	192	310	76.8	57.8	GCCTTGTTTGCGATGATATAAGTTCTGTCAGGGATAAATCATGAGAGGGAGTACAGTTAT
Os01g0222800	3,453	3,554	402	371	1,046	1,006	1,026	1,026	800	3.9	9.1	TTGAGGTCCCTCCTATTCCGAGGTCACTTCAGTACTTTGTGGGCATGGAGGATAATAATA
Os01g0232500	25,212	21,596	4,592	3,261	6,183	5,712	6,263	6,038	5,295	4.1	6.0	CTGTTGACCAAGATGATGAATTAAATAGATATATGCCTATCCATCTCAAGGCTCTTAAGA
Os01g0236300	33,163	24,135	90	78	2,634	2,520	2,553	2,598	4,852	8.0	337	TAGTCAAAACCTTAATGGTGCTTAAGGAATAACGTGAAGCTATAAAACTGGTGTGTAAGT
Os01g0236400	38,751	25,591	86	82	5,268	4,641	4,812	5,071	6,889	5.4	374	ATCTGATATTTGAGATTTTAGCTTTTTTGTCCAAATGGAGGCATTTTCGCCTTATCTTTC
Os01g0243900	46,579	23,978	89	81	344	170	72	71	142	245	391	ACACTGGGAAATGACAAGTACTCTCATGCTGGCATGTTTTTGGCTATCGCGGTGTACGGT
Os01g0244000	9,220	2,973	132	157	910	361	186	239	269	17.1	36.3	CTACGAGCTGGTCGCGCCGCCGAGCGAGGTCCTCGCTACTCGCTTCGTCCGCGCTTGGGA
Os01g0244400	3,472	1,515	275	149	87	76	86	67	92	27.0	11.4	TTTCGTGGACCTATGTTGGGATATTTCATAGCACCATTTGTTTTTCCTAAATGTAGATTG
Os01g0245700	15,716	4,927	221	133	253	132	267	158	284	37.5	51.4	TGCTATCTTACACAACCAGTGTTTGTTAATTGGTGGATGGCTGATGACATTGTTCGTGAT
Os01g0245800	9,877	6,329	99	134	693	390	120	180	276	28.6	68.8	ATGAGACAGATGAATCTGACGGATGAGCTTGACTTGAACTTTTCGAGTGACAAAGCTGAC

Os01g0249900	11,498	5,781	169	385	1,881	1,487	1,324	1,393	1,415	5.6	32.0 TTTGTTCTCTTGTTTCATAGTCCCGTCGATACTTTCTCTCATTAGCAGGGAGTACTTTCA
Os01g0260000	1,019	1,107	83	326	134	121	77	77	181	7.9	6.5 AGGATAAAAGTTGGCCAAGCCTTTCTTCTTCAGTTAAAGGTACGGGCAACATCTAAACAG
Os01g0263600	2,301	1,799	551	454	221	202	210	209	351	7.5	4.1 TACCATGACCATGTAGACAATATTCTTGAACTACCAGCACCAGACCAGGAGCATGAAGCA
Os01g0264100	10,242	4,620	70	77	108	88	84	91	120	65.3	93.4 AAGTGATAGGTTCATACGCTGTTGAACTTAATTACGACATTGAGCACTATGCAGAACCGC
Os01g0271500	26,857	21,666	2,899	1,791	5,606	4,975	4,622	4,575	4,874	4.9	10.6 CACACCACATTCAAAACTGTTTATTTGTTTAAATGAAATTGGCTAAAAAAAGAGAAAATG
Os01g0274800	18,213	9,510	324	399	1,628	1,377	1,399	1,410	1,565	8.7	36.6 TCTCGCAGATGGATCAGCAACATCAAGCATTGCCGCATTGTCTCTCTCTTTGTGTTCATT
Os01g0275200	7,436	14,517	885	291	3,280	3,293	3,129	3,383	1,582	4.6	20.5 AAGGAATCTGTCATCCCAGGAACTGTGATTTCTACATGTGTGCTCATGCTGGGATGATTG
Os01g0276300	2,190	1,714	94	81	99	83	93	74	281	12.4	22.2 TCTGTAATGTAAATATGTAATGCGGCAGTTAAAAGTAATAAAATATCCCCTAATCACTTG
Os01g0283700	2,136	2,331	129	156	237	222	209	234	192	10.7	15.8 AACTGAATCTGCGTGTATGCATTGTGAAAAGGAATGGAGTTGAATCCTAGTGAGTCAATG
Os01g0293100	220,345	212,886	114	117	741	590	88	85	162	1,101	1879 AGCTTTTGGGAGATCTTTGGTATGTCATGGTTTGCATGTATTATTTTGGTCTACTTGGAT
Os01g0293200	11,018	11,078	1,108	4,323	3,786	3,188	3,275	3,452	1,512	4.9	5.0 ATATCACTCAAAACCTTTCCTTTCATTGAACTATCTAAACATGTTTGCATCATGTCATGC
Os01g0318400	56,459	76,209	704	515	7,831	7,621	6,511	7,309	10,271	7.6	109 ATGAACAAGGGTAGCAGCAGTAGATTTGCCTTAGCTAGGGAGGAGTGAGATTTGTGAGAT
Os01g0321800	13,136	12,499	1,218	381	2,525	2,342	2,559	2,831	2,665	4.9	18.8 CAGCGGTGATGATAATTTGATAACGAAAACAATACTAATGCACGAATACACTTATAACCC
Os01g0332200	3,127	4,997	505	414	492	456	484	508	696	6.8	8.7 ACAGTGATCAGTGTCCTTGTGCATTAGTGCATATTGTATAGGCTACAGCATAATTATATG
Os01g0332500	7,416	6,243	89	83	790	684	697	737	640	10.0	79.2 ATCCAGCCTGAAGCTCTTGGTAACTTTTGTTGGTAAAGCATCTCAAGTCTCAAGCAATTA
Os01g0342700	4,371	2,667	82	257	95	73	79	87	460	17.5	23.5 GCAGAGCAGAGGCAATAACTTCATCTCAAGAAATGCTGCTGTATTTGACAATTAAATAAA
Os01g0343200	48,037	44,041	3,899	2,196	2,959	2,526	2,506	2,647	6,340	11.2	15.7 CTTGGAAGCTGTAAAGCCATAGTTTACATTGTTGTTAATCATGAGAACCCAGTGGGTTTT
Os01g0351300	17,354	25,536	132	859	1,082	1,005	1,018	1,000	3,492	11.1	62.5 TCTGAAGCTTATCATGTGAATTGGGTAATTAACATTGCATGGTCATCAAGTCTCTCCTTA
Os01g0354700	52,142	66,541	3,069	5,875	1,194	1,181	705	869	1,303	52.6	13.9 TGGTATCTGATACTGCAAGTGATATAGCGGACAGGCTAAGGGAGCTCAATTGTCATGGAT
Os01g0360000	9,775	6,161	114	108	140	97	117	159	502	30.9	70.1 TGTATTCGAGGAAAGAAGTGGTAACATGTTGGACCTGTATTAATTATGCTGTATTTCTAC
Os01g0360100	1,973	2,669	219	226	129	111	139	120	280	12.3	10.3 ATTACTACACGATTGCTACGAGATCATGGGCTATATCGAGAGGAAGGTGGCAATTGTTTT
Os01g0361700	9,973	33,876	93	79	126	145	109	101	305	96.5	215 TCTTTGTTGTTCTTGTAAATCTGATATAAACCAAGGAGATGTGACAGAATACATGGTACC
Os01g0369200	260,182	226,918	1,241	691	18,721	10,992	370	324	705	194	262 TCGGCTGTGACTGTGAACCACATTTACATGTTTAGCTTTGACGCCCTTTGCTCTACCTTT
Os01g0383900	45,457	38,815	271	75	1,333	1,124	1,089	1,193	1,437	32.2	294 GTACGGATAGCTGGATACTTCTGGACGAAATAACTTTAGCTATAAAAACTGCCTTTGTTG
Os01g0496900	6,462	14,528	314	227	539	479	496	526	403	21.4	36.3 TTAATCTAGACAAACCATCCTTACCCACATATGTATTGAAGAACATGTATGAATCACAGC
Os01g0514700	4,452	6,965	86	85	1,038	958	958	1,042	748	6.4	65.0 GTCTGAATGAACAAGAACTGATAGGATTATATGGAGCACTTTGTTTGGAGAACAGAGCCA
Os01g0518400	6,044	5,167	385	122	238	199	80	66	158	39.7	25.8 GCGTAGAGCTTATGGAATTAAACGTGTTGATACTAACTGAGAGCTCCTGAGCTCCTGGTT
Os01g0527600	36,741	75,950	106	282	9,001	9,057	8,093	8,404	7,698	6.5	306 TCAGTTGAGGGCTGTCTATATTATGAAATGCACAAATATACGCTGCCTGCAGCTTTTGGC
Os01g0530500	20,092	21,422	398	93	2,779	2,371	2,420	2,513	4,004	6.5	108 TGGTGGTCACATTATGGAACCATTCAACTCCTGTTTTAGGGTGGTGGTCTCTGATTTTCT
Os01g0532100	19,733	35,339	133	107	235	199	174	207	323	103	221 GGAACTGGGAAGTGATACAAGGGCAATCATAACCCTCCATTTAGGATGGTGTCTATGGTA
Os01g0554100	1,454	2,331	112	109	124	115	116	111	251	10.8	16.7 AATGTTTCCGATTAAAAATAAATCATTTATGAACAGTGCATTTTTACAATTTCTCGGATT
Os01g0566000	103,883	39,461	491	306	1,244	539	252	187	276	188	165 ATTGCGGACTTGAGAAAATTGAGATGTGTGGTTTGGTTTCTGACTGTTTGGGACTATTTG
Os01g0571300	4,952	8,051	259	1,279	1,147	1,067	1,094	1,128	745	6.9	11.0 CAATACTGTCTCTGCAATGTAGCCGAGGAAAAATACGAATGCCAGTCTTATCAATGTGAA
Os01g0584100	36,818	18,182	359	112	4,964	4,098	3,762	3,854	2,107	8.8	129 CGGCTTCTAACTACTAAGGTAGCGACGTGAGGTGTGGCACTGACCCTGAAAAAAAAAGAG
Os01g0589400	1,972	3,120	264	320	257	252	249	280	416	7.6	8.5 AAACACCACCACCAACTTGTCATATTAAAGCCATGTCCATAAATTAGCACAGCTCATACG
Os01g0595800	14,107	9,093	69	65	265	172	66	60	116	97.8	169 GTAGTTCTCGTGCAATGGCTTATCAGCTTAAGCTATTTAACTATTTTAAGCACTACATTT
Os01g0596000	53,088	43,977	2,528	4,513	662	461	121	184	283	170	14.3 CGCGTTCAGCTACATGAGAGCATCTGATCTTTCTCTGAGTGACCCATTCTTTGTTTCGAA
Os01g0596100	26,262	14,860	905	576	207	162	133	181	97	155	27.4 ATTATATGATTCATGCAGTCACTCTGATAATCTCTGTATGTTTTCTTCTACTGCGTGTGC
Os01g0596300	15,204	13,884	200	422	417	175	283	139	129	84.2	50.1 CAATATTACTAAGTGGCTGTAAGCGTTTAAATTTGTAGTACTATGGTTTACTGCAAGGAC
Os01g0598400	17,843	8,985	89	79	471	385	376	392	308	35.9	150 GGTTGCGGAAGTACTAAAACTTTGGTGCGTATTGTTTTGGGCCAAAATCCACAATCCTGT
Os01g0600300	113,260	146,644	2,847	846	20,984	18,901	19,792	19,583	31,132	5.2	83.0 CCTTTTATGTTATCCCACGGAACATCTTTTAAGTTAGTGAAATCTTAGCATTTGTGTAGC
Os01g0605700	91,504	56,209	95	90	654	554	569	605	506	131	773 TAGTTGAAGTTTGATGAGACAATACAATGATACAATATCACCCGCCAGTGGCGGATTTAG

Os01g0606000	40,843	34,076	1,390	1,771	10,787	8,298	1,339	1,284	1,181	18.3	23.8	TCTATGCTTGCTACTACCGGACCACACCTAAGAAGACCAAGGCCGCCAAGGACGTCGAGA
Os01g0608000	1,263	3,392	81	81	118	192	67	68	180	15.4	25.5	TGCGCGGGGATTTTTCGACATGAGATCGGCATTACGCGCGAGCGGAAATCACCAAGTCCA
Os01g0609200	13,414	22,324	448	317	3,080	3,200	2,224	2,299	2,327	7.0	45.9	TCTGGTACCTCTTCTTCATGTTCTTCACGTTTCTATACTTCACATTCTATGGCATGATGG
Os01g0609300	30,365	39,917	862	324	2,358	2,318	1,837	1,844	2,258	16.1	65.8	ACTACTGTTACACCTAGTAATTTTGTTATTAGTACCCTTCTTTTTATAGAAAGATGGTAC
Os01g0616600	74,399	24,555	6,939	3,674	7,812	7,248	7,606	7,660	7,130	5.8	8.5	TCTGAGGATGCGAGAATCACTCAAATTTTGTCAAACTAGCTTCTTGAATCACACCATAAA
Os01g0617600	4,208	4,644	359	597	365	294	353	336	1,251	6.8	9.6	CTCTCCACTTAAAAGGTATTTATATCTTGAGGATTGGCATTGCCATCTCAAAATTCTGTG
Os01g0622800	3,271	3,507	126	216	282	253	292	322	863	6.8	20.5	TATCCCACCCATCTTATAGAGTGGCATATTGTTCGTTTTCTCAACTAAGTTGTGGCGTTT
Os01g0623500	44,068	89,476	1,485	731	7,635	7,471	7,410	7,703	6,769	8.8	60.2	CCCTAGTTGATTTATTGAATAATAATGCTGAACCTTCTTGATTCGGGAATACAATTGGTC
Os01g0632700	3,996	2,416	609	365	3,378	219	350	318	634	5.3	6.6	ATTTCAGACAGCTGTACATGTCATTGGTTGTTCATTCCAATAAAGTGTGCATTGTCGAGC
Os01g0633100	298,738	323,012	12,192	11,050	10,157	9,153	4,132	4,523	5,586	51.7	26.8	GGTTTATGTACTTGGTTTGTTTTGGAATGGGAACTCTATTATTGGTATTCTGAAGTTTGC
Os01g0642900	46,610	41,380	1,590	1,597	12,553	11,385	11,301	11,607	10,870	3.9	27.6	ACAGTTGGACATCATTGTCGAAACCCTCTAATAATTGAACAACTGATTGTACTGTATAAC
Os01g0648700	18,887	12,642	135	86	493	375	355	357	936	25.5	144	TTGGTGAACTAGAAGGGGAAAATATGCAAAAATATGCAGTGCAAACTCTTATGTAGTGTA
Os01g0651300	4,382	2,203	115	111	157	113	123	119	132	24.0	27.5	ACTACCTCCGTCTCAAAAGACTTTATTACTTGCTAAAATAAAATCTTTTTGAGTGGAGGC
Os01g0656200	35,000	54,357	281	99	4,200	4,059	4,043	4,135	8,832	7.2	261	CTTAAGCTGACATTTCGGCCGAGGCAGCATGAAGCATGTGCTGATTTCGTCTGTTCTGAT
Os01g0659800	8,524	6,826	107	243	693	588	675	601	951	9.8	47.2	TCGTTTGAAGCAATATAAGCCTGAATGCCTGAGTATTTCCACTCATCTTAATGGCATATG
Os01g0660800	125,465	75,485	92	90	6,709	6,280	6,711	6,814	7,595	13.7	1068	AAACGTTGTGCCGATCTTCTGATCTAGACTATGGTTAATGAAAATTTCCAGTGCCGATCC
Os01g0663400	75,775	31,641	4,233	1,753	4,303	3,756	3,903	4,178	5,920	10.0	18.0	TCTCAAAACCTGTCTGTTTTAATTTGGCTAAGCTAAATATAAGTAGGCAGAATTCAGACG
Os01g0666700	7,969	7,925	202	175	1,154	1,127	1,227	1,219	830	8.0	42.3	AACCACCGTTTGTACTGTTTGTGAAAAAGTACAGATATGCAACATTTATATTTCTCAGGC
Os01g0685400	20,280	22,288	173	353	4,429	4,261	4,620	4,584	5,122	4.4	86.2	TCCCCCTTCTTCCCGACGAGATTATTACATGTACATTATCCTATCTGTACTACGGCTGTT
Os01g0688000	2,540	3,263	500	318	833	786	199	219	242	9.1	7.2	ACAATAATTGCATACTACACTATTAATATCTGGTCTCACCTGTCATACACATACTGCATC
Os01g0691200	1,363	966	144	161	163	158	150	156	237	6.0	7.5	CGTGGTTAATGTATGGCAAATAGTAGTAAATTTTGCCCCCATTGGTCTGGCTGAGATAGA
Os01g0691300	369,982	272,331	129	193	23,521	12,445	189	292	236	462	2009	ACCATTGTTCAGTGAGGCAGAAAACCTGTCACCGCTCCCAGTACTTCTTTCGAGAAAATT
Os01g0697700	6,918	3,535	628	377	1,166	581	259	202	197	16.9	10.2	GGTGCCCACGTTCGAGACCTTCGGGATGATCTTCACCCGGTTGATGTGCTTCTTCCTCTA
Os01g0698000	493,097	248,878	744	981	22,711	20,244	23,613	24,101	39,854	11.7	410	TGAAACAATTTGTGATGCGTAACTGAGGAACGCCGAATGGTTGCTGTGCGGTTATGCTTT
Os01g0701700	5,078	3,204	123	103	522	455	578	532	860	6.0	35.8	GTTGTTGTATTGAGTAACTGATGATATTAACAAATTCCATGTGTACTTAACTGGTAGGAT
Os01g0706200	9,381	7,468	818	216	200	150	99	99	424	35.5	19.9	TGCATGCTGTGATACTGATACTGACACGCATTGTAATTATTCTCGTGGCGAGATGTGCTT
Os01g0710100	4,410	4,264	125	237	1,074	996	1,052	1,068	717	5.0	25.2	TTAGTTTTCAATTTTGGGTGTTTTTGAAGTTCATTTATCTCGTGTATGTTCGACTCAGGT
Os01g0710800	9,640	10,345	2,100	918	2,097	1,926	2,052	1,949	2,705	4.3	7.2	AGAAAATGCAAGGTGACAATATCTTGTGGCCATCAAAAATTGAGATTTTCAGTGACTGTC
Os01g0715500	90,239	96,458	1,527	457	1,313	1,085	482	509	625	135	112	ACTTCACCAAGTACGATGCTGGACTGACCATCAACAATTCAGATCTTGCTGCTGATCTGA
Os01g0716300	4,894	6,629	181	110	877	759	777	826	937	6.5	40.4	AGCGACATTGCAGTGAACTGGAATGCTCCATTACTGATGTTGTGGTGGATGATGAGCATT
Os01g0723000	262,407	89,432	88	85	6,149	1,193	76	66	173	557	1773	TGTGCCAGTCAGTTTAGGATGAAATGGTGAGTTAAGTAGTTGCAAGTTATGTTTACCTTT
Os01g0733000	1,288	3,104	102	99	147	227	83	89	155	14.3	19.9	GGCTGGCCAAATGTAGCCAGTCTCTCCACTGGCTAAAGGTGGGTCCCACTACCACTCTTA
Os01g0737300	80,003	61,952	5,709	530	5,478	5,163	5,148	5,027	6,290	12.3	40.5	ACAGTACTTATTAGTGAGAATCTTTCTAACAGTCAAAATCTCTTATATTTGGGGACACGG
Os01g0771900	29,681	37,995	100	99	1,788	1,648	1,116	1,127	1,977	20.3	339	CATGTGACACTCCACAGAAAGTAAAGGAATATTAAAATGTGGGTAAGAAATTGATGGGTT
Os01g0772000	90,262	119,134	4,730	4,801	7,505	6,397	6,935	7,207	10,564	12.1	21.8	CCAACTATCTTAGCAGCAACGTGAATTGAACTTCTATTATAGTTCCCAACCTTAATTAAC
Os01g0774300	1,097	1,235	83	76	82	92	72	66	153	10.7	14.6	TGATTCAATCATTAGTATATTCCTGTTGCAACTGATTTTCAGTGCGGACATGTGCGTATG
Os01g0799100	802	1,396	100	120	180	150	174	230	161	6.2	9.6	CATTCCATCCATGATGCCATCGTTATACTTGTACCACACAATCATCCTCTACAGGTTGTG
Os01g0801100	36,231	29,907	261	515	2,011	1,762	1,725	1,717	3,532	13.1	89.8	GTCCTGAGACCTTCTGTATATAACGCGATGCATTTGTTTGCTGTCTCTGGGCCAAACTTT
Os01g0812000	58,756	93,245	108	464	8,475	7,469	7,743	8,483	9,732	8.4	330	TTAGAGAACCCTTTTTGTCATCTCTATTGCCCGAATTCTGTTGGAAATTCGTCATGTTTG
Os01g0812100	14,106	8,642	103	2,862	883	737	772	828	529	16.9	20.3	TTGATCATCCTAATGCCAAAATCGTGTTGTAGTTGTGATGTTCATGAGTTGCACCTATGT
Os01g0840100	590,922	384,642	2,901	700	82,301	69,153	67,898	70,801	91,868	5.8	335	AAGCTTTTGTAAGTGTGTATCGCCGTATGGTTTTACCTGAACTTGCTCTGAAATAGTTTA
Os01g0841400	4,591	3,924	123	180	288	175	185	173	853	10.3	28.6	GAATGCCAAGGCAAGATTGAGAGGTTCTACTGATGGCTCTTTTGTGTAAGTAGGAATTCA

Os01g0841600	101,678	182,202	3,021	1,198	31,208	26,653	29,637	30,931	25,981	4.9	71.5	CTGTATTATCAGAAGTTTGTTGATGGCTTGATGCTATAATAGTTGAACCTGATACTTCCT
Os01g0842600	92,584	96,605	22,082	21,275	2,827	2,576	2,765	2,852	2,244	38.1	4.4	TTCCTGTAAGGCTGTAACCTAGCACTAGGGCATGAGAAGTTGTATAAAGGTGTTCGTGGT
Os01g0843300	5,095	3,393	676	470	741	514	510	552	374	9.0	7.4	CGAAACACCAATTCCTATTAGTGTAAGGTTGAGGGATTTGAACAATATTTTCTGCCGGAT
Os01g0857000	36,256	61,203	2,366	2,123	2,873	2,529	2,515	2,584	3,325	16.0	21.0	ATGTTGAAATGTGAGGCCAGCTGTTGATAACATGCCATTTTCAAAATTGTGGCATTCTGG
Os01g0857100	5,712	14,380	558	240	1,213	1,165	1,270	1,289	766	9.3	24.7	TAAAAGGGGGGACATTCCTATGCACACATGCTTCAGGTGCACTTTGTGCACAACAACTAA
Os01g0857200	57,549	31,845	106	103	4,579	2,705	1,034	1,051	1,528	25.0	409	ATTTCGGGGAGGCTGATTACCTCGAAGCGCTTTGCTCCTTCCAGAGCAGAGACAGGCGAT
Os01g0869300	54,272	69,439	846	111	5,924	5,463	5,847	5,734	13,543	7.0	200	CACTGGAAAAAGTGGCACAGCCGTTCAGCATAGTCAGTAAAAGTCAGAGCACGTGTTTTA
Os01g0875400	118,135	135,259	155	87	15,147	13,505	12,483	14,056	14,760	8.9	1085	CGTTCGATCTGCACAAAAACATTTCCAAACTGCAACAGTTATTTTTTAACCTTCCTGTGT
Os01g0876800	13,417	18,885	427	133	4,551	4,124	4,166	4,415	3,521	4.1	66.7	TTGCACAGGCGAAGCCTGATGCATTGGTAGCAGAAGAGAACTTGCAAAAGTCGGTAAAAA
Os01g0877400	38,085	16,073	249	103	148	100	67	62	126	234	154	CCCTTTATATAGTTCGTTTACCTTTCAAAAAGTGCAGCCGTGAGATGTAATTTCTACTCT
Os01g0878400	53,708	14,258	1,768	1,448	2,959	2,500	2,858	2,761	2,265	11.1	17.3	ATAGCAGAAAGAGGTTGGAATATGTAGTAGTATTGGAATAACCTGTACAACGGCCTTTGC
Os01g0881000	9,852	4,931	242	216	229	138	75	70	139	55.5	30.5	ATGAAACTGACAGCGCTCTGCAGCTGCAAATAGTTACAGTACCGGACATTGATGCAGATT
Os01g0883100	38,686	90,502	1,113	606	4,730	4,516	4,637	4,594	5,815	11.4	72.1	CCAATATATAGTCTGTCTCTAGTACAAGCTCTGTGCTTGCCATTCTGCCTCGCTGTAGAT
Os01g0891000	451,251	462,149	122,712	56,724	1,731	1,411	570	323	2,349	329	5.5	AGTTAACCTATTATCCCTATTTTTCCCCTCTTCCAATTTTCAACAGAATAATTTTGAGGA
Os01g0891300	30,452	23,026	1,415	440	2,405	2,137	2,189	2,198	2,366	11.5	33.6	ATTCTGATGAGTATCAGAAACCTCTCTGAATTGAGGTGATAAGTAATAGATGTTTGTCTT
Os01g0895000	5,264	2,885	99	79	188	150	204	164	199	20.9	44.2	TCTGAACATTTGTGTACATAAAGATGAACACAACGTGAGAAATTAAGCTACTGATGATCG
Os01g0898900	14,438	9,395	1,323	173	2,117	1,849	2,108	2,096	2,557	5.1	24.3	CTGGGTGTAAAGGGCAAGCGTTCGAGCGCGGACCAGAAAAGTTTATACGTACAAATTTTT
Os01g0911300	83,565	117,118	8,383	3,738	14,529	12,437	13,033	13,806	13,809	7.3	17.7	ATCAGAGTCAAGACCATCGGAAATCATAACTTATATACTCTGCAGGGAAAGTTTACTCCA
Os01g0914800	19,726	26,582	5,589	4,657	2,917	2,674	2,864	2,973	4,643	6.3	4.5	TTGTGGAACTACATATGATCTCATATCTCGAGCACCTGTCAATCTATGAGGCAGATGCTG
Os01g0917500	54,829	40,829	180	158	3,571	3,105	3,109	3,207	2,001	18.6	281	TGTGAGTGCTTAATGTGCTGTCGTTTGAATAAAAGTACTGCTTGCCTGTTTCTAAGTGTT
Os01g0927500	30,019	15,732	108	97	1,674	1,461	1,269	1,272	2,069	12.7	212	CTTTGCCCTTACATGATTTGGAGGAGGTAGGCAAGGAAGATGTGAATATTGTGGTGTCTT
Os01g0929600	985	1,322	103	176	135	130	160	132	242	6.2	8.5	TCTCTCTGTGCCATGCCTGTACTGCATTGAAATGAATCTGCATGCAGCCATGAACTGATA
Os01g0931300	43,478	49,686	9,333	7,404	9,811	8,988	9,157	10,054	12,255	4.3	5.6	GGGGCAACTTGAATGGCATATGCATTTCGCTTCTCAAGAATCATATAATACGCATGGTTT
Os01g0933400	9,182	9,421	1,161	749	2,086	1,835	2,103	2,001	2,560	4.1	10.0	TGTTTGGTAATATATAAATACTATAGATTGGATCTGAAACGTGTTGTGGTGAGCTATGGC
Os01g0934900	18,894	20,987	5,086	1,859	2,543	2,232	2,293	2,546	4,374	6.1	6.5	ATGTAATCAGTGGTTCGGTTGTGTTTTGTGAAGCTAATGATAATATCTCACCAGATCAAT
Os01g0935300	68,351	59,494	7,339	2,802	9,964	9,193	9,416	9,230	9,298	6.8	14.1	CCTGTCCACATCAAAAGTTTGTGGCATGACATCTGATGAATGGGTACGCGTAATCTGTTG
Os01g0939200	2,541	1,134	102	112	1,179	259	276	312	243	5.4	15.9	CTTGAACATCGTGAAGATGGAGAATTTGTAATCTCTTTGGTGAAGATGGAGAATGTGTAA
Os01g0939300	6,372	10,591	116	253	1,769	1,715	1,607	1,567	1,418	5.4	47.9	ATTTCTGTGGGTAGACACCAAGCTCTTGTGTGAAGAAGAATGATGATGTCATTAACATGG
Os01g0940100	21,934	12,285	158	81	2,923	2,528	2,337	2,447	3,330	5.6	145	TAAAAAAGGGACATTGTTTGATATCTATATTCATATATATAAAAATCTGGGTCTTGTGCA
Os01g0946300	2,289	5,050	202	343	170	283	82	111	131	24.8	12.9	TCATCTCCGATGAATTAGCGCTCAAGCGTGTGGTCAGCGAAATTCTTGGAGCAAATTCAA
Os01g0960200	1,867	5,361	148	201	400	374	457	503	531	6.6	18.3	GAGAAGACCAAGCATGATGAGATTGTAAAACATGCCCATCTTGCAGCTTCAGCTACTCTA
Os01g0961300	3,407	1,855	112	97	436	422	354	417	400	6.2	24.1	TGATAACACAGTTTGCTCCCTTAAAATTGTTCTTGAGAGCTGAAGCAAAGCACATTCGAT
Os01g0966700	29,870	23,387	80	139	4,197	3,918	4,070	4,121	4,874	5.9	250	CACAGACTTGTTGATGACATCTACTTGCTTTGTAGCAATATGTTTTTACTTGTAGAAAGG
Os01g0967700	12,213	4,340	110	121	259	171	107	149	530	24.8	63.2	GCTGACCTGTCCCTGACATTGTACAAACTATTGTGGATCGTGGTATCACTGATCCTAGTA
Os01g0974700	41,629	53,626	2,671	1,435	9,916	9,062	10,193	9,890	9,773	4.8	24.1	AGCCTTGATGGCAGTACGCCCGACCGATAAATATTCTTTTCCCAGCTCATATATGTGATA
Os01g0977400	9,604	2,958	101	103	2,573	2,416	2,586	2,583	605	4.3	52.5	TTTGTGGGGACTGTCATACTGTAATCAAGCACATAAGCTTAGTGAAGCGCAGGGCTATCA
Os02g0101900	97,227	40,677	107	80	993	288	157	107	251	244	680	TGTCTCGACTCAATACTTAATTGGTGGATGGATTTTAATACTACACTACTACTACTGGAG
Os02g0108000	7,965	3,455	143	137	771	639	726	703	537	8.5	37.4	CTAACATGGGTGGGACCCACAAACATGTATTGTGCACTGTGAAGTGTGGTTCTTTACGGC
Os02g0108100	6,215	5,120	173	206	264	222	302	223	180	26.6	29.9	TTCCTGATTGTAAGCCACGTTGGAGGCTATTTCCAACTGAGATCAATATATTCGTGCGGC
Os02g0110400	13,040	9,939	181	195	1,560	1,386	1,363	1,462	2,015	6.7	60.7	ACATGTTTAATAATCAATGAAGATGTACTTGCTATGAATTTCATTGAGAAATTGAGCTGC
Os02g0113400	7,503	18,105	1,109	121	154	196	115	117	1,097	29.6	31.8	TTTAATCCCCTTTCTTATTGTTGGCTATTTCTTGTCATGCTACCCTCATGGAAATATCGA
Os02g0114400	28,844	37,212	127	160	7,538	7,690	7,215	7,398	5,612	5.1	229	ATCCATCTTTCTAAAGATGGCAGGCCACCTACCACCTGATTAGGCCACTTGGCGCCCCTA

Os02g0117500	24,526	34,585	92	98	3,655	3,284	3,346	3,399	3,696	8.2	308	GGCAACTGAAAAACTGTATAGAAAGTTATTCTTGTCCTTGATGGTATTTTGAATGGAGGA
Os02g0119700	5,131	4,115	267	72	637	593	594	551	632	7.5	33.2	TTGTTGTATTACAATGAAATATGCAAATTCAGATGAATCTGTGATATGATTGTTTGATCT
Os02g0120300	4,574	4,586	331	1,650	901	782	862	882	1,017	4.9	6.2	AGATTCACCAAACCAATAGTTATGACAGAATATTACACATCTCTACACGGGATGTTCCAA
Os02g0120500	120,877	48,282	104	126	678	365	227	273	240	263	666	TGATAAGTAGTTGTCTAGTATTTGTGATTAATGGCATATATGCATAATGACTTGATGACT
Os02g0121500	15,299	19,337	1,606	901	4,915	4,498	4,676	4,712	4,090	3.9	14.3	CTGTAATTAATTTGAGATGTTTTATGTTGCTCGATCGAAAGGTACTCGAGTGTAGTGAAG
Os02g0125800	33,346	34,918	1,292	1,884	7,828	6,873	7,107	8,054	9,796	4.0	21.9	AACAGGTCAAGCTAGTAGATGGCAAATCATTTTTCTTGTCATGGTGACACAGGTTGCGCT
Os02g0126800	107,253	84,176	10,004	3,885	21,484	19,401	20,067	20,825	23,499	4.3	15.2	TAACCTGTCCTACATGTACAGTACAGAGCAATTTTGCTTTCCAAAGTAACTTGTCTGGCT
Os02g0135200	58,331	95,099	299	106	3,014	2,888	2,553	2,633	2,896	26.3	418	AGTGTGTGATGACTCTATCTGCCATATGAACAATCTGGCACTTTTTTACCTTAGTACCAT
Os02g0136000	6,062	3,149	308	118	206	191	204	196	397	15.5	22.9	GGAACATGCCTTAGAGAGTGTCAATATACCATGAACATTGTTTCATCTTGAATAATAACC
Os02g0142400	7,870	3,218	1,862	327	495	408	435	409	128	21.3	6.5	GAATCCCTATGCAGGTTAATTTCCTGGGTTCATGTAACAATGCAAACCCATGATTTTGCT
Os02g0142800	11,896	16,906	2,152	299	550	499	557	546	1,039	19.0	17.7	GTCCGATCTTTTGAGTTGTGTCGTTGTTGTTATTTGTAATCATTTTGTGATCAGATATGG
Os02g0148600	15,301	10,153	1,043	884	2,476	2,100	1,795	1,768	1,636	6.9	13.0	GGGTTGATCTAGGACTGCACATTCTTCAGTTAAAATGAATGCAACCAATTCAGTCACTTA
Os02g0163300	38,328	24,624	10,199	5,138	341	290	303	314	857	59.5	4.2	CTTTATTAGAAAGGCTGTAAACCCATGAGATGATCTATGATCATTCCTTGATTTTGTGGT
Os02g0176300	9,276	6,671	254	207	831	671	396	395	1,110	10.1	34.3	CTTGTACCCTTTGTAAGCATAGTAGGCAATTCTTGTGTAGTAGAACCCAGGGATGAACAT
Os02g0178000	13,284	31,562	2,921	1,807	2,194	2,138	2,214	2,162	2,283	9.2	8.9	GTTGCATGCAAAGGGAACATGCAAGCCATTTCCATGTATTGGATTTTTTCCCCCCTGAAC
Os02g0181900	19,337	27,670	3,391	2,695	2,844	2,853	2,339	2,361	2,956	8.4	7.7	CATATGGCTTTCTATAGAAAGTCTGTCCAGTTGAAAAGAATGTAACTTGCAAAGGATGTT
Os02g0187000	29,242	53,287	754	1,083	3,310	5,151	928	769	647	35.9	43.7	CGGCTTCCCCTCCTCGTGGTTGCACGGCCTCATGCCGCTCTCCCCACTAAGTACTGTAAT
Os02g0192400	30,814	45,825	8,095	1,127	9,083	8,724	8,754	8,142	8,664	4.3	12.4	TTCTGTTGTGGTTTTAGGTTCCAGAAGGAAGAATTGGTACTCCATGTGCGAGCATTCGAT
Os02g0194400	11,395	6,856	3,146	641	256	159	192	191	616	25.4	6.2	TCTCATCTTATATGCGGACACAGAGATGCAGCAGAAACTCAATTTTTTAACAAGTTCATA
Os02g0194600	35,114	26,921	1,102	168	422	323	92	93	177	170	71.4	TGCTCGGAATGCTCTTTCTAGTGAACTCTAACAGGCAGGTCCAGCCTTATCTTCCCCTGA
Os02g0204500	19,903	33,378	3,743	5,954	4,274	4,130	4,219	4,379	2,883	7.4	5.5	TAGATTTACCATAACTTCTCAAATGCTACCTTTGCCCCAATTAACTCAAGGCTTTCTTCT
Os02g0207100	62,837	86,634	749	499	568	739	124	137	429	209	121	AAGGTGGACGATGACAGGTTTTCGGGTTTATGGGGTAATTTGGAGGACCGCGATAGTTCG
Os02g0213000	2,094	1,180	88	81	162	161	142	146	197	9.1	18.6	AAAGTCCTCTTGATCCTGAGGCTTTTATATTGGCATGAACTAGGTGCTGATTTTTGCGAA
Os02g0214600	1,329	1,281	103	300	100	106	104	100	226	8.6	7.4	AAGTCAGCTCTCCAGGGGGTATAATCTCTAGTTCAGTAGTATGTCCAGGTTGTGCAATCT
Os02g0214900	3,542	4,657	77	69	97	103	71	69	123	40.0	55.8	GTAACGTGAAGCAAGTTAAAATGTACAGTCTGTTAGACTGTTAGATGGAGATATGGAATT
Os02g0216500	1,439	1,510	121	116	235	219	231	243	421	4.7	12.4	GCTTTCTTGCCCTATACATCTCTTGCATACCACCCTTGAGAGTTTCTGAGAATATTTGCA
Os02g0217900	26,578	19,239	752	579	5,442	4,323	3,178	2,656	1,697	9.0	34.3	GTGCTCACCGTCACCGTCGACAAGAAGCCGCCACCGGAGCCCAAGAAGCCGCGCGTCGTC
Os02g0221300	14,517	36,328	3,044	3,479	1,554	2,783	877	885	262	38.6	7.1	ATAACTAGCACCGATGAGCGTGTGTTCTCTACCATCCAGAAGTTCTGCAACACCCAAATA
Os02g0226000	84,749	85,283	8,402	11,463	11,686	10,287	10,873	18,350	10,910	7.3	8.7	GTTATGACTTATGATGAACCCAAAGTATGATTTGATATCTATGGATGAGCTTGGCCTGCC
Os02g0246300	84,380	65,507	6,411	3,401	15,373	14,455	15,544	14,490	18,373	4.5	15.9	AAAGTTTGGCACTCCATACAGATTATTAGTGAATTATTAGCTTGTGTGGCTTCTGTCCCA
Os02g0251700	38,547	32,566	4,547	1,769	7,836	7,228	7,751	7,459	7,791	4.6	12.5	GTAAGTCTTTGCAGTCCGCACCATTCAGATTCAGTGTTTCCTTAGTTGCATCATCTTGAT
Os02g0252300	10,202	2,598	120	109	1,515	718	536	577	412	9.2	44.9	GCCTGTGGGACTCTGTCTGGGACTGGACGGTGGGAGACTGGGAGTGGACTGGATCTGAAT
Os02g0272400	24,978	24,609	1,240	920	3,628	3,176	3,228	3,506	6,396	5.3	23.2	TTTCCCCTAGAGGAAACAAATGTTGAGGGTTAGTTAGCCACTGAAGTTCATACAAGAGGT
Os02g0273900	6,257	3,534	254	168	549	530	545	525	1,034	6.3	22.7	GGTAAAAGTTTGGTTGTTTTCTGCTATACTAGCTATTTTTCTGTGATAAGAATGCTTATT
Os02g0288000	1,580	2,150	284	238	535	478	485	515	404	4.1	7.1	GTCGAAGATTAATGTACTATGCATCAAGAATATATATTACCTGATGCTATCTTTGTCTGC
Os02g0289300	5,550	4,720	1,608	981	834	589	588	640	612	8.1	4.1	TGGGTGAACAGGATGGAAGGCATTTTTTATAGGCCCTTGTCAGATGATGGCTTTTGGCTT
Os02g0293300	28,957	22,103	142	173	425	314	474	379	584	52.8	162	CTTTCTGATATTCACTACATTCTGATAGAATTGTGCTGTCAGAGCATAAATCTTTTTGGG
Os02g0313700	23,231	27,429	6,375	5,924	7,960	7,412	8,043	8,041	4,267	4.4	4.1	AGGAACAATACCTCTGTACATGTCGTATGCAGACTGTCTAAGCTGTTTGCTTCTTGGACA
Os02g0317200	24,470	6,418	1,679	781	625	446	418	430	435	27.6	10.9	GCGCAATACGTTTGAGTACCATGAATCCTTGTTGCTATTTTTTCCATTGCTATGATGCCT
Os02g0317500	56,279	67,460	1,637	1,197	14,964	13,682	14,512	14,650	12,926	4.5	44.0	TGTATCCAACTGCAAGTCTGCAACCGGTCTAGTGACCTCATGTGTAGTGGTAAAACCTTT
Os02g0318200	10,045	9,018	154	138	260	236	259	240	239	39.1	65.4	ATGACTGATGATGCAGTAAGGTTGTGATCTGTCTTGCTGTTTCTTCCATTGATATGATGC
Os02g0318400	2,037	928	84	163	88	78	74	62	127	14.1	11.7	TTTTGTGGACACGTTCAGTAATCTGTTAATTCAGGGATGGTAACGCTTTTAGATTTCCCA

Os02g0320300	2,056	2,180	785	336	431	425	413	368	529	4.6	4.1	GTTTGGTTATATATATGAATATCTAATTAAACTCAAATACATTTCTAACATGAACATTGG
Os02g0323000	151,180	72,273	20,013	3,013	1,486	1,019	956	938	951	103	13.5	GCCGTAGTTTAATCCAAAAACAAAATGACCACGTTGTTCTTTTAGTTATAAAGAGGGTCT
Os02g0325600	6,524	6,960	216	253	1,481	1,256	1,285	1,328	1,015	5.8	28.8	TTAAGGGTTAATTACTGATTGCTTCGTGATCGCACACACCACATTTGCTGTTTTGTTTGT
Os02g0433200	5,693	5,555	193	166	870	789	799	800	683	7.5	31.4	AGTCATGTTCGGTGTCACAGTTTTTTGATGAGGATGATGACTAGACTATGAGGATTTCGT
Os02g0453100	11,383	7,024	612	307	1,229	1,115	1,119	1,079	536	11.5	20.6	TGCTTGTGGTGTACATTGAAATTTTCTTCACGATTATCGTCCTTGCTATGAAATGCTTAT
Os02g0459600	9,917	3,396	79	85	697	383	267	282	925	9.8	70.9	CTGCTGGGTGGTATGAAAATCCTGATAGTTTTCTTTACCAAGAATCGTAACTAGATTCGG
Os02g0461100	651	1,528	73	71	192	159	163	160	181	5.7	13.8	TCCCTGTTGTCCAATTAGTCATAGATGTTTACAGAAGTTTGGACTGGACATACTATATTT
Os02g0491300	631,850	324,263	183	348	4,745	1,796	232	275	187	1,130	1794	ATCGTGCTACTGCCTGTACGGTTCTCGGTTCATGCCATGGATCAGCAACTGCTTGAAATG
Os02g0492000	21,890	18,691	910	262	927	718	860	834	1,370	19.0	41.4	AACCTTTTGCAACTGGCACGGCTTTGTAAATTTTACTTGAAACTGATCGCAACTATTATC
Os02g0492900	6,746	9,755	223	79	146	173	74	67	149	64.7	61.2	GCGGAGAATAGTATTATCGCTGATTATGAACAAACTATTATCACTGATTATGATACAAAT
Os02g0493100	25,128	33,195	184	284	8,221	7,741	7,821	7,588	6,555	4.0	126	AGTCCACAGATGTTCTCACATTTTGCCTGGAGACTTCGATACCCAGAACCAGAATGGTTT
Os02g0493300	16,830	15,734	2,639	1,908	740	589	356	274	343	41.2	7.3	GCTCTACCGCGAGATCGAACGGACGATGTTGGTGGGGGAACCAATATGTAATTAATAAAA
Os02g0494000	6,855	9,176	93	124	1,022	959	969	969	1,172	7.4	73.8	AGGATTATCTATCTGCAACAGGATTCTACAGTAAGGCACTGTACCTTTACCCTGATGATG
Os02g0504100	26,652	27,682	262	99	2,982	2,849	2,803	2,763	3,356	8.8	169	CCTACATGAGACGCTAAATTCAAGTGAAGTTGAAATGACTATGCAATTATGCATTCTTCT
Os02g0512300	4,707	6,525	138	238	1,311	1,129	1,011	1,232	1,408	4.3	30.5	TGACCTTGGGAACAATGATACAAACGAAGATACAGAAGCCGATGAGGAGTTCAGCATCGA
Os02g0513000	9,366	19,522	75	277	1,085	1,130	906	982	1,320	11.6	93.7	TGTTGTACTTGTAAATTCTCAGAAATTTTTGTGAGAATGAAAGGACACTTTTGAGTTCCC
Os02g0538900	127,565	102,893	86	100	5,495	4,718	5,603	5,760	7,189	18.4	1237	GAATTCTGCAATGACTTCCATCGAACACATATGAGATGAAGCAATCTTTGCATTGCTTAA
Os02g0543300	8,475	2,642	97	527	204	125	87	96	783	15.4	20.9	GCAACGAAGCTCATGAATTCTGTGAGGCGAAGAAAGGGACTGCACGTTGAAGAGAAAATT
Os02g0549200	84,599	164,134	325	95	20,757	20,109	20,334	20,042	17,245	6.3	671	CATGCCGAAGGAACATATTAGCCCTAGTAATATTTTTTCTCGGTTTATTTATCCGATTAG
Os02g0549700	4,467	3,226	85	122	868	730	786	857	862	4.5	37.4	ATGGAAGTGTTTATGTTAGTAATTATTCAAGCTCCTTGGGTAGAATCTAATGAAATTGAA
Os02g0580500	76,537	37,112	3,568	1,362	3,726	3,234	3,377	3,667	2,660	17.5	24.2	TGCCCAAAATATGTGGCAATTTGTTGAATTTTGTGATCCTTCAACTACTGCAATGCAGGA
Os02g0580700	11,617	20,492	1,578	1,039	2,710	2,532	2,577	2,629	1,847	7.0	12.0	TTCAGAGGTGAAACATCTGCTCATGTAAAGCAACTTACTTTTCTCTAGTTTTGGGGAAAA
Os02g0584700	1,459	1,975	97	117	531	475	262	379	384	4.3	15.9	TTTGAAGAAAAAAGTTGAAAGTTTATGTATGTAGAAAAGTTTCTGATGTGATAGAAAATT
Os02g0586800	44,024	64,666	6,794	702	6,671	6,092	14,082	6,385	12,513	5.4	24.4	ACTGCGTACACACACGGTGCACGCATCTACTGATCTTCCTAAAATAACTCTGCCAAAGTT
Os02g0594800	21,238	18,581	3,188	4,643	1,725	1,616	1,722	1,721	4,207	7.4	5.2	AAACTTGCATATTTCGTGGTTCCTCCTAAAAGATGATCATGAGAACCCATGCATTTCTAT
Os02g0598500	146,758	125,351	5,006	2,665	8,024	5,896	1,581	1,407	2,037	53.1	37.1	CTGTACGTTAACTACTTGCACCTGTACGTTAACTACTTTGCTTTTGGTGAAGTTTTCCTC
Os02g0598800	127,479	96,810	2,955	1,608	1,133	909	665	659	1,944	88.0	51.0	TTTCCTCATTCTTCTAGCTCTATGTGATACGTTTTGGTTTTAAATCGATTCATGCATTGG
Os02g0599200	71,638	23,769	5,479	2,767	730	361	282	244	547	92.1	10.6	GAGTAGTTGGTTTCTGCTACCTTGTTTTTGGTTTATGACTCCTGGTTGGCTGGGTACGTT
Os02g0599700	104,150	89,973	4,893	3,696	5,325	4,798	4,581	4,625	3,986	22.1	22.8	GTTTACGAATCATCTCTAGCCTTTTTAGTTCTGAAGGTGATTGATCTAGTGATGCTTTTG
Os02g0606600	49,510	28,678	88	99	1,307	1,232	1,266	1,236	2,025	23.6	403	TAGTGCAGAACCGAAATCCGCATGAAAGTACTCTGTATCTGTTATCTGATAAACTGAGAA
Os02g0606900	341,708	301,091	6,869	7,913	15,140	11,780	7,673	7,788	21,070	21.9	43.5	CGTTTAACGCACCTTTATCATTGTACTCTGGATTACTGAAGATTTTGGTCGATGTAGTAA
Os02g0609500	4,183	5,021	1,101	799	385	364	368	359	742	8.8	4.9	TCCTGACAGAGTGCTAAAAATTAAAACGAATGTAAATTTCAATGCTATTAAAGTGAACCC
Os02g0612100	13,057	9,186	193	164	2,909	2,436	1,934	1,947	1,222	6.6	61.5	GCACGACGGGGACGACGGTTACTCTGACTAGTGTTAACATGGAGACCGTTGCAGCAGGTT
Os02g0618000	18,142	14,957	152	118	1,711	1,419	1,576	1,651	1,094	12.5	123	TTCGGTTCGATTTACTTTTGCGTCGTCGATTTTTGCCAGTTTGTGTCTCGGCTTCTCTCA
Os02g0620400	36,094	76,578	102	163	4,588	4,789	4,038	3,911	7,554	9.2	409	GGGCTGTTCAAAGTATTCTTGTTTATTCCTCCGAGTGCAATCCACTTTGAATGCTCTCTT
Os02g0622500	21,191	54,063	6,129	2,790	2,109	2,027	2,027	2,092	3,973	11.8	8.2	CGTTGTGAACGGTACGAAGTTCTCTTATGATGAACTCCTGTAGCGTGGAGCAATTCGATT
Os02g0637800	6,686	8,694	687	546	798	689	618	733	1,912	6.6	12.5	ATGAGTGTACACTGTACAAATATATGATCGAAAACAAATTAATGCTGTATTTTCTTTCGT
Os02g0639500	78,912	144,461	95	89	12,930	12,408	12,157	12,389	22,447	6.4	1157	CTGATGTTTGCAGTTATTTGTTCTGAAACTACGCATACAATCAATAATTGGTTTGCCTTC
Os02g0639700	49,868	45,325	10,685	6,430	2,682	2,361	1,988	1,949	4,788	14.6	5.7	GCAGATGAATGGTCTCACTTGTTTAACACTGATGTGCGCAAAATGGCATGCTGCATCTCT
Os02g0642600	3,674	4,519	242	317	619	522	609	600	517	7.4	14.7	TCATTTGTTACATATGGGAAGGAAAAACAGAGCAAGCTGGTCTGGCGAAACCAGAACAGC
Os02g0654500	249,458	168,281	3,854	1,600	29,179	27,036	28,644	28,360	34,209	6.6	82.5	AGATCATAGACCAATGTGTTTGGATGATGTATTCACGTTTTGTCAATCGAGAGGTTATCA
Os02g0659500	10,516	5,164	663	252	96	88	108	66	317	44.1	18.0	AGCTATGGAATCGATGTAGATTTGAGCAACTGACAGTGCAACAAGAACTAGCCCCTGTTC

Os02g0668100	74,935	94,069	2,749	4,182	11,446	10,496	11,288	11,269	12,372	7.2	24.8 TGACTAAATGAAGAATTCTTAGGATAAACTACCACAATTGCTATGCCTTGGTGTTACATG
Os02g0669700	40,705	32,478	2,644	2,277	5,786	4,969	4,272	4,784	5,740	6.8	14.8 CTGTCGGATGCTGTCTATTATGCATGTCTGAAATTAACTTGCTGTTGATTAATCGGAGGT
Os02g0679200	2,936	4,957	121	81	658	622	639	650	700	5.7	38.6 CATTTGATGTTCTCGAAACATTTGAGATTATGTTCATCCTGAGGCTTAGTTACAGAAGTG
Os02g0686600	43,901	61,896	311	270	2,952	2,999	1,949	2,113	2,431	21.3	180 TCGAACGACGAGTTTATGATTACATTTTATAAAGATTAGAAAAGATGATGGGACATATCC
Os02g0693500	133,367	83,923	85	81	28,566	26,238	28,093	28,521	21,463	4.3	1274 ATCGAAGGAACAGCTGATCTTATCATCATTGTATATGCACTGCTAACCAGATTCAGTTTT
Os02g0694600	1,915	4,130	118	87	427	377	444	404	386	7.0	27.8 TCGTTGCAACCAGGCAATTAAAGGATACGAGCATTTCTGGGGTGGAAATTGTGTGCTGTT
Os02g0697600	16,307	13,322	145	364	1,628	1,636	1,524	1,591	3,416	6.3	64.2 TAACGCAGTGTCACTTGCGACAAGATGGGAAATTTACTGGACAATATCATTGATCAGCTC
Os02g0702100	7,891	6,972	115	117	710	643	704	667	658	11.1	63.9 TGTATGTGAATCTTATGTTGTTCCCTGTTGAATTCTTTCTGCTAAATATTCTTTTACCCG
Os02g0711100	9,140	10,714	80	272	2,249	2,071	2,032	2,055	2,160	4.6	66.9 GCTAGGTGTACAATGTAGTGACATATTTGGTAAGGTAGTTTGGTAAATTAAACTTGACTC
Os02g0712000	47,246	60,070	2,418	950	6,107	5,582	5,082	5,304	6,123	9.2	35.1 CTTTTTGTATAATCTATTCTATTGCTACAATTTTTGCAGTAATAATAAATCTTTAGCTCT
Os02g0712800	2,668	1,705	105	95	342	232	112	111	222	10.8	21.4 AAACAGTACATATTATGGACGTTTGCGTTGCAGCCTTGCAGTTGCGGGTTAGTTGGATCA
Os02g0730100	9,560	8,773	190	89	86	94	138	92	895	30.5	70.5 TTGTGCAAGTAGATGTGTTACATTCGTTCCTGGCACTATCATCGCCTAAATAATCACATA
Os02g0733500	15,659	8,701	450	221	220	212	249	229	365	40.5	37.0 ATTTGACGAATACTGATATGGATGAGTCCAAATGTATTGGAAAATCTCAATGAAACGAGC
Os02g0739100	4,822	13,137	83	91	706	697	616	716	1,234	8.7	91.8 TAAGAACGTGGATAGATTTTTGTTTAGAAACTTGTACAAAATTTGATACAAGGATATCAA
Os02g0740300	7,076	3,763	82	228	829	746	842	891	763	6.5	37.7 AAGAAATGTACATTGCCTTGGAACTTGTGTACCTATATGCAAGCATGCAGTATTGCCAAA
Os02g0741800	196,733	392,846	156	167	19,715	17,721	20,572	20,224	36,949	10.4	1720 GGAATTATGGCACGGATGTATATTTTAACCTATCTGGGGGCAATAGTAGGAAATTTTGGC
Os02g0743800	82,438	48,868	6,180	2,546	2,381	1,502	1,171	1,201	596	67.2	16.0 TCGAGATTTTGTGCTCTAAGCTCTGGTGGTTGTGCAAATGGATATCGGCATCTACAAAGC
Os02g0754500	169,781	140,353	727	84	4,427	4,182	3,560	3,831	11,725	22.6	625 GTGTTTGTATAGGAATTAAGCCACATATTTTGGCCAGGCGATGACGGAAGAAACATTTGG
Os02g0761100	91,496	61,595	173	85	11,461	8,324	8,887	9,780	17,899	5.7	621 TATCGTAGGAAATGTCTGGCGGATTGAATTGTCAAACTCTTGGAAAGGCCTTTTGAATGA
Os02g0761700	8,324	8,285	2,383	1,109	1,316	1,293	1,152	1,150	1,564	6.0	5.1 ATGTAAACTCATATTACTAAGATAACCTACAAAAATTTTGAGTAAAATTGGTTTTAGAAG
Os02g0767800	3,427	6,224	153	159	239	203	206	208	748	11.6	29.6 AGCTTTCCATGGAGCAAAACTCCCCTCAATTCCATGTCATACCATGTGTAAAAGTGGTGT
Os02g0773600	6,275	4,639	401	693	1,201	989	873	899	492	7.8	10.2 TGATCCGGCGATCAGGAGTACTACAGGAGAGCGTCTCGTCAACGGCGTCGTCCGGGCAAT
Os02g0774100	4,842	1,919	83	228	141	110	109	408	193	17.2	22.1 TTCTATCTTCAGAAAATGCCCACTATCCAGTTATGGAAGGATGGAGAATGGGCAGCGGAA
Os02g0774500	12,402	8,688	418	108	2,778	2,412	2,481	2,500	2,613	4.0	48.9 CGCCATGTTTGATGTTCAGAAACTCTTAGTTTCATCGACACGGCAGTGTCGGATAGAGAT
Os02g0780600	11,285	17,160	439	436	4,866	2,114	2,335	2,395	3,269	4.6	31.8 TAGGCTCTACCTGTAAAAAGAAAACCTTTCAGTTATTCTTGAGAAGATAGAATTAGCACC
Os02g0782800	29,643	34,143	2,468	215	5,529	5,042	4,969	5,272	3,372	7.6	43.6 GTAAATAGCGGCCGATTTTCGGGTGTAAATAAAATTATGGTACTCCTATTTGCTTATTAC
Os02g0793200	6,895	6,464	586	450	499	350	378	450	579	13.6	13.0 TTGCTCCAGACCAGACGATACAGAGCAAGCAATTAAAAAGAAGTACAAAAAGCTGCAGAT
Os02g0796700	43,140	35,854	6,933	3,727	8,200	6,928	6,838	7,432	7,659	5.2	7.7 AATCCTCACCGATGTACATAAGATGATGATGATTTCTACCAATACAAAGCAAGAATTGCC
Os02g0798000	1,437	2,496	312	362	318	267	456	315	328	5.7	5.6 CTGAATCGATTCATGTATATGGTTTTACCAGACTGAAGCTCTTGATTTAGAGAAACTTTG
Os02g0798800	907	1,084	120	116	93	90	100	144	200	6.8	8.4 TCAGATTATCTTTACATTGCTTGTCGAGACCCCCAAAAAGTCATAAAATGTATTTGCACG
Os02g0806300	5,310	6,619	83	77	888	858	828	836	510	9.0	74.3 TGGAAACATTTGGGGACAGTGAGAAAAAATGTGCAAATTCTGAGAGGCAATACGCCGGCA
Os02g0806600	6,816	18,831	483	3,796	741	933	581	686	1,130	12.5	8.4 CAATGCTACAACTACTGTGTTGTGTTGGATGCAAAGCCTTAATACTATAATCATCAATGT
Os02g0807000	70,782	77,378	2,764	2,066	3,238	2,944	2,484	2,648	3,195	24.7	31.0 GGCTTGTTCAGATGAAAATTGAATCCAAAAACATGAGAAAATTTCTGTGAATTGCTGCAG
Os02g0807100	8,170	17,884	287	88	1,351	1,393	951	1,071	766	12.7	75.9 AATGTTGCTTGATAACCGGCCGATTGAATACCTGTAACGACTTTCAGAGCTAACGTGAAC
Os02g0809100	30,127	18,881	609	95	2,206	2,252	1,981	2,088	3,274	9.0	99.4 CTGGACATAATGGATATTATATTAGCCTATTGGATGAGTTCATAACGATGTCTTAAGGTG
Os02g0822800	46,897	45,462	10,856	5,547	12,495	11,599	13,051	13,274	10,194	4.1	6.0 CGGCGAGGGGATGAATACATTGTTTATATACCTCAAACTTGCAAATATACTATTCAGATA
Os02g0824300	96,949	108,185	3,641	1,817	9,421	8,029	7,080	7,249	16,031	9.1	39.8 ATGAGAATGAAGGATCCGGATCGTACCCTATTATATTATATAGAGGAAGAAAAAAGAACC
Os03g0100800	73,012	149,416	2,867	1,601	3,292	2,592	1,690	1,808	4,374	33.2	48.8 TTCCTTTCCCATCCCATTTGGTTTATTGCATGTGGATCGAACATTTACTCTCCTCGTAAT
Os03g0101700	58,568	66,412	3,443	2,138	6,928	6,517	5,631	5,973	11,858	7.2	23.0 TGCCTCGCGTCAGTTAGCTACGAAAAATGTTTGTCTGAACAAGTGAACCGAAAACGAAAA
Os03g0103900	9,915	5,510	399	308	528	428	471	506	673	13.0	21.1 AACTCTGGGTTCAGCCCATATTCGATAAGATTAAACCTGGTCTATCTCCTGTTCTTGAAT
Os03g0106300	11,196	4,682	150	196	278	179	198	187	448	23.8	42.2 AAGCCAAACAAAGGAAAGAGATAAAGATTACGACAAGACGAAATTAAAAGGTAAATCAAC
Os03g0108700	26,833	12,373	699	668	2,471	2,031	1,846	1,911	2,471	8.1	26.7 TCAAAACCGGTTTCACAAACCCTATCTACATCAATATTAGATGGTGCTATGTATGCTAGC

Os03g0117000	8,835	5,409	150	160	2,920	2,663	2,733	2,598	1,001	4.2	44.7	TAATCTGCTTAGGGATACTAAACTCTGCCACGTGTAAACATCGTATTAGAAAGGAAAACT
Os03g0118900	26,606	18,845	87	77	2,074	1,881	2,083	2,047	4,462	7.5	273	GTTGCATCAAAACAGTGATGTGATGAGATGTTTCTAGATCCACTCTTATCATAGGCGTCC
Os03g0120500	7,710	5,675	544	491	6,904	5,579	1,435	1,403	718	4.5	12.8	AGCTCGGAGGGCGGCGTCCTCCTTGGCGATGGCGGCGGTTATGCATTTAGAATCATGTAT
Os03g0127500	3,667	8,776	85	117	2,497	2,336	2,445	2,538	816	4.0	56.8	TTGGTGAACCTCCTTTTACCTTTCTATGTTCATTGATTCTTTGGATGATACAGTTGTCAT
Os03g0132300	58,021	31,908	1,619	1,649	4,914	4,699	4,840	4,820	9,464	6.4	26.3	AAGTATGCGTGACTGACTTGCCGAAAATCATCACAAAAATCAAATGGGTAATTAGTATAG
Os03g0133000	147,490	239,140	79	79	6,092	6,684	3,169	3,493	2,895	51.4	2388	TGGATTCGATTGTACATATAGTAGTAGCACCGAGATATCAATCAATCTTTTGGTCTTCTC
Os03g0143400	4,659	5,809	95	90	873	824	867	843	1,334	4.9	56.2	TTAATCTTAACTTTCAGCCACTTCTAACTCAAAGCAAAGAATGAAGCTACTGTGGCAATT
Os03g0144000	52,738	36,426	3,679	3,123	11,339	10,793	10,504	11,029	10,040	4.2	12.9	TTGAAGTGAAATACCGTTGTGATTGAGGCTGCTAATATGCTATGAATGACTGGAGCCCAA
Os03g0146300	197,102	135,000	3,986	4,645	36,654	32,943	35,413	34,703	26,084	5.4	37.9	CGTCTGTGTTATCTTGGATACTTTTCATTGCTAAGCTATTATATGTGATGCTGGTACTGT
Os03g0147700	33,831	39,646	6,105	3,487	5,729	5,196	5,104	5,335	9,779	5.1	7.9	ACAGCTCTATTTCAAAGAAAATCATTCAGTATTTGCCTTGTTGGTACATCGGTCACATAT
Os03g0148300	61,500	17,336	4,783	4,541	3,293	2,308	2,359	2,509	1,117	19.2	7.0	AGATGCTACAGAAACAGAAGAGTACTATGCTCAGCCAAGATCCTGGCTCGCAACAGTATA
Os03g0148400	6,681	8,454	203	571	1,237	1,202	1,262	1,338	1,744	5.1	22.1	TGCTGCTCTATTCTTTTAAGATGTTGTTTATAGATGAAATCTGGACAGAGCTGTGCAGAT
Os03g0153400	2,781	4,256	151	175	246	249	261	279	767	7.7	21.1	ATATGTTGCTCCTGTTTGAGGGTGGTTTTTTAACGAAACCACTTTTGAAAGTGGCATTCC
Os03g0160400	48,812	147,803	2,567	571	4,204	4,569	4,089	4,004	9,372	13.5	70.2	AAACTCCGAAACTGATTATCTTGCTAGCTATGGCAATATATATAGCATCCTCACTTGCTG
Os03g0161000	87,628	108,057	13,902	4,975	17,329	16,155	16,463	17,024	19,838	5.3	11.7	TTTGTGATGCTGCTATTATACTTGCGAGATACTACTATTTTGTGATGCTATGATACTTGC
Os03g0165000	9,380	7,543	528	145	888	738	822	844	1,841	6.8	30.4	GTTGAATCTTTCTGGTGTGACCAATCTCAGTTTGAACTCCTTGAATAATCAACTAAGCCT
Os03g0165200	8,365	20,226	78	71	868	1,817	105	107	142	57.1	175	AGCCAGTATGTGCGCTCTTTGATTTTCTTGGAAAAGCAGATGCTACAGTCTTCTTTGGCT
Os03g0168600	92,289	68,116	100	83	1,029	782	375	354	776	119	873	GGATTTGTTGGTCCTAGACCGTGCTTGAAACGGTGCGAATTTCATCTAAATGGTTGAGAA
Os03g0177300	97,725	78,453	11,379	21,133	21,321	19,893	22,149	21,429	22,724	4.0	5.6	TTTTGTTGGCTCTCCCTTCTCATGTCTGTGCATTCTGTAAAGATGGTTTTGCCGCTAGCA
Os03g0184000	184,343	271,643	4,093	1,206	44,765	41,131	43,937	39,801	51,299	4.8	101	TTAGTGGGTGCCCAACTCTCCACCAATTTACACATGATGGAACTTGAAAGATGCCTATTT
Os03g0194400	46,324	29,594	529	424	3,234	3,042	3,173	3,118	2,931	12.2	78.2	GTGCATTCGATTCGAGATCTGTAACTTGTACTGGTAGTAACTTGTAAGCCAGAAATGCCT
Os03g0194500	98,100	105,364	5,292	3,225	16,005	14,851	14,958	14,970	18,095	6.1	24.6	ATCTGGGATGCTGAACGTTATCAGTTATCACTGAAAGCAATGGTATTCTTCATATTTATC
Os03g0204500	34,424	16,571	637	133	448	296	265	254	352	72.6	81.9	AGGCTACCAATGGATGAATGTTGCGAAGTATTTGCGATGAACCTTCGTGATGCATTTCCT
Os03g0204900	44,910	23,935	1,664	419	585	426	374	367	360	83.4	39.3	GATATCTGGTTGTGATGATGTTGCCAAGTGATATACCTGATTGTGATGCTGATGTTGCCA
Os03g0208600	6,060	2,952	87	111	621	548	615	586	157	13.9	43.1	TCTGCAAGCTGAATGCCTGGATGTAAAATCACAACTACTGTGTAGAGACACTTCAACATT
Os03g0212400	30,145	40,240	3,059	1,528	5,851	5,200	5,101	5,410	7,292	5.6	16.1	ATCTGTACTCCTAAATATGCCAGAACGAGATGAGAAGAGAATTGAATCAAGCGATAGAAT
Os03g0213100	156,104	141,790	15,675	6,989	39,114	37,064	32,763	32,031	41,990	3.9	14.2	GTTGCGATCAATTTTTATTATCTTTTAAACTGGATAGTATATTTGATTCCTGATCTCTTT
Os03g0213600	77,708	83,024	8,459	4,103	3,356	2,952	2,656	2,783	2,398	30.3	13.6	CTTGCGAGGTGTAGCTAACGAGTAACCTGGTACCACCAAATATCAACGAAACCATTTGCT
Os03g0217900	61,941	41,270	2,437	1,170	2,889	2,601	2,548	2,979	5,036	13.6	29.9	GGTATATCGGAAAGGATCCCGTAATGTTCAATTGTAATTGCCTTAACAATCATGTAAGGA
Os03g0225200	11,494	4,304	99	276	246	210	174	183	249	31.4	42.7	ACCAAAGGTTGAGACTTTGTTGTTCTAATCAAACATCCTGTTTACAAATTGCAACTGGTG
Os03g0237500	9,026	6,288	177	80	892	706	740	812	1,436	7.1	63.5	GTACTTGCGTCAAAAGATGAAATCGTGTTGCCAAACTGTACAGTAATACAATTGAACTTT
Os03g0238300	12,895	15,771	87	89	3,040	2,603	2,717	2,965	2,574	5.3	162	CTGACTTCCTGTAACTATACATATGTACTCTTCATGATCAGAAATTCACAATACCAGATC
Os03g0240600	4,444	3,410	84	78	332	320	330	339	464	9.9	48.1	GATTGTAAATCTAATTGCAAAAACAAGTTTCCTACTTTCCTCACTGTAAATATTTTGCAT
Os03g0245300	620,661	404,908	134	120	17,342	11,654	5,500	5,553	8,568	57.5	3959	GTTTCAGACTTTCAGTTCGTTGCTTTGTTTGTGAAATAAAGATTGTGGTCTATTCAGAGG
Os03g0245800	2,293	1,827	265	83	272	86	74	100	214	13.1	13.8	GTGTACTAGAGGTTGTAATTACTCAGCGAACGAGCGAATGAATGGAATAATGCTAGTATG
Os03g0253400	2,082	1,675	182	143	160	169	165	138	313	8.4	11.6	CCAAAAGGTCTGGTCAGCGCCCTCATCATCACGGCATTACACATCGAGGGGAGTAGCCAT
Os03g0262000	8,647	16,365	82	84	974	911	933	941	1,545	9.9	144	ATTACTATTTACAAACTGGTGCATCCTGTCAAAATCTAAAAAAGAACGAGGATGTCCATC
Os03g0266300	650,913	515,765	31,250	12,636	37,237	34,423	25,803	25,173	92,517	11.0	29.2	GCGCCGTTCATCAGCCGATCAGCGTCTGTACCGGTCTTTTGCAACTAGTTAAGTGATGAA
Os03g0266900	34,019	23,646	139	125	4,615	1,689	1,656	1,737	1,748	14.5	215	TCGAACTACTCCGCTATGTAAAACGGTAAAACCTGTTGTCTCATTATGAAAGTGAACTAT
Os03g0267000	46,773	19,045	383	176	7,174	5,441	4,697	4,879	2,023	9.0	115	GAAACTTCGGGTGTGACATGCACGGTGGAGAGCTTCGATTCGAGCCTTCGGTTTGTGATC
Os03g0268600	5,090	4,836	714	795	308	721	193	200	500	12.7	6.6	AAAGCTCATGTGTTTCCGATGTTTGAAGAGAAACTTCCTCAAGCGTCAGAGAAATTGTAG
Os03g0281800	13,134	11,676	217	268	2,853	2,259	2,361	2,464	3,425	4.3	51.4	CTATAATCGAACTCTCTGATGAATTGGATGTCTATTTTGTCTGTACTAAACGAAGGTGAT

Os03g0283900	4,150	6,831	88	81	322	294	294	307	376	15.8	63.0	CTTTGTTTTAAGGTTACACCGAAGTGTCAGTTCAACCTCTGTCCATTTGTTGTATGGATG
Os03g0292900	13,533	14,147	160	98	664	636	798	700	1,224	15.0	110	GTCCCAATACTCCTAGATCAGATATTGACATGTTATAGGAAACCATTTGAAAAGAGAACA
Os03g0293400	10,919	10,137	3,052	2,002	3,248	3,086	3,194	3,128	2,156	4.0	4.3	CTGCAGTGCATCTGATCGTTAAAAAGAAAAACAGAGATCTGAAGTGTTGCAAGCCCTTTC
Os03g0296000	633,588	403,596	118	99	54,976	22,408	91	90	123	1,082	4688	TTAACTCATCGATCCGTTCTGGTGTCTACGAGACTACGATATATCCGATCCCCATTCGAT
Os03g0300700	95,199	89,373	6,652	4,766	4,373	3,856	3,231	3,321	4,944	21.7	16.4	TGGGATTCAGTTATGCGTTGCTTCTGAAGATCTTGGTTAGTTGGTTAGATGCGAATTTTC
Os03g0302500	129,724	105,969	270	449	32,098	28,737	31,884	31,527	27,710	4.0	337	GTTAGGAGCTTTCTGATGAGATTGCTTCTCTTGCCGATGCTGTTGTTACTGTCTGCTAAT
Os03g0307900	1,579	2,596	110	130	198	158	218	248	416	7.0	16.9	GTTTTGGCATGATATTTGCTATATTATGGACATTGAACAAAGTAGAAATCCATTTCCCCC
Os03g0308600	111,976	68,907	638	135	710	561	446	465	1,793	89.6	300	ATCCGTGTTAAAGGATCAAACCTAACATGCTTACTCAATTAAAGCTGTTTGCTGTTTCGT
Os03g0308700	175,106	168,581	92	89	6,429	4,882	886	916	1,697	88.0	1907	TGTACTGTTGATCCTAATTGTTGTTTGTAATCACCTGTTGCAGCTATGGGATCATTATGG
Os03g0310000	126,030	96,238	137	112	15,078	14,053	15,186	15,579	16,211	7.1	887	TTCTGTCCGTTTGGACGCATATTTTGGGGAGACGCACTGATGGATATGTGCATGTGATGC
Os03g0313100	23,980	6,260	443	2,123	204	111	80	84	143	97.2	12.6	TGGGTCTAAGCTCAAAATGAGCTTGTGGTATGCCCCAGATATGCTTAGTTGTTAATTAAT
Os03g0326100	578	1,399	105	99	165	135	141	106	121	7.0	8.8	GTTCAGTAACTGAACAACTGCAGGAAGTGCTTCATTTTGGTTGACTTTTGTAGGTGGATG
Os03g0340500	67,090	70,121	9,376	4,101	13,382	12,397	13,588	13,892	12,258	5.4	11.1	GAACTTGGGAGTTGGGACTCTGTAAAACTAGATTTGTCAAACATCTTGTCTATGTACATT
Os03g0343800	404,289	406,463	122	137	32,346	29,080	23,701	25,170	56,423	10.3	3126	ATTATTTTACCAGGAGTACCCCGTTTCGTCGGGTTGCTCTGCACAAGGCTGAAGCTTCTG
Os03g0345100	29,533	32,322	111	83	5,728	5,314	5,759	5,926	6,639	5.0	322	TTAACAATGTGACTTGTTTGTATCCGATGTGGCTATGGCATTTCTCATAGTGCAGAGATT
Os03g0345300	3,658	6,489	95	99	172	187	86	74	149	36.5	50.2	CACGGTGTCTAATTAGCTATGCCTACAATTGGTAAATGGGTCCTATCCTCCTATTACCTC
Os03g0346700	4,575	6,167	93	94	1,285	998	1,071	1,114	962	5.1	56.8	TTGAACTTGTTACAGTGAGCAATCTGTATTCTGGAGATTGGCACTGTTTTATCATGGTGA
Os03g0346900	149,008	369,947	16,288	13,245	10,915	10,423	10,790	10,419	18,601	16.7	16.0	AGTAGGAGCAGCAAGTGGCTGTATCCATTTTACCGTCCTTTAACTTACCATGCAATGCAA
Os03g0353000	225,936	115,589	104	99	21,720	19,748	20,864	20,801	19,923	7.9	1597	CTTGAGTTGTTTGGTGCTAAGGCCGATTCGAATTGCTCTTATCAATTCAGAATTCACAAG
Os03g0353300	19,039	35,621	637	600	393	673	89	82	212	123	42.2	AGCTGGTCAAATGATGTATGCTAAGTGAGCGAATTGTGAATGATGCTCTCTTTGAGTCTG
Os03g0353900	77,451	67,874	383	570	2,613	2,296	2,061	1,990	2,960	28.2	155	TATCTAACCTTTGTTCTCTGTATGATATTTGCCTCATCAGCTGCTCTGCTCAAAATGCTT
Os03g0357500	96,025	79,023	630	79	439	273	104	65	152	545	390	TGATGAGGTCCTTGACTATCAGCTAGATTTTAAAAATCTGAACTTCGGGATTTATGTTTC
Os03g0369700	12,975	5,736	104	106	483	434	518	541	449	18.3	82.0	CCGTTTCAGATGCCATAGATGCAGAATTTAGCTAGAACTTTGGTATATTGAAATTTTGAC
Os03g0373100	564	680	79	72	66	65	67	59	94	8.0	8.2	GTCCTCTGATTCTTCAAGAGTTCTAGTTGTAGCAATACATTAAGACTTAGTACCAATTTG
Os03g0381300	61,305	38,194	91	77	5,895	5,219	5,373	5,950	7,453	7.5	578	TGTTCGTGACTGTAAAAATAAACTGAAGTATCCAGCTTGCTCAATCCATATTGTTACTGC
Os03g0383900	113,733	105,496	91	75	1,188	1,084	652	632	243	241	1323	TGTTGCACATGTTTCACCACTCATTAAAAGATGTTTCAATAAACTTGTTTCAGATGTCCG
Os03g0412400	4,556	7,687	84	77	1,613	1,526	1,524	1,602	848	5.1	73.4	TTTTTGGATTTTGTTCACTGATGAAATTAAAACCAAACCGCCTAGTTTGGGAATGGCCGA
Os03g0415500	22,247	17,723	1,404	1,141	144	101	154	76	390	94.0	15.7	TGCTCTACTGAAAGTGAAGTTAGTCCAGATATCTCCATTCTATTACGTAGGTGAAGAGGC
Os03g0419200	1,060	1,031	164	138	111	110	107	106	209	6.9	7.0	AGCCACAACAGATTCTTCCAAGTACCAATCACGATGAATCAAATATCAAATATATATATT
Os03g0421300	9,224	9,998	1,478	1,663	157	143	132	144	295	46.6	6.1	AGTATAGTTCTGTTAGTAGGGGTTGACCCCTCCTAGGATTAATCTCAATGGAGGCATCCA
Os03g0422200	2,310	2,965	95	123	314	301	191	224	467	7.6	24.2	ACTGGTGTGTCATGCACATTTAATAGGGGTAAGACTGAATAAAAAATGATTATTTGCATG
Os03g0563200	1,986	3,924	876	362	991	988	939	911	191	6.5	5.0	TTGCCATCTTCCTTTCACTCAATTTGTTGTTTTGTCTACCATGATTGTTTCGCACGAAAC
Os03g0569000	5,198	1,848	78	93	88	80	71	69	309	20.1	36.2	TGTACTAATTCTGTAAATGTGACGCACCAGCTTTTGGTGGGTGAATGATGGCGCACTTTC
Os03g0576500	15,358	27,193	340	206	1,418	1,858	695	636	975	20.3	77.2	GAAGATTTCATCTTTTTTGCAGGAATTTCTTGGCTTCTTGCCAAGTTGCCATTGCCAGAT
Os03g0578900	58,003	34,752	112	93	573	404	362	365	521	96.2	440	TTAGGTTGTATCGATCGTGACTGAGCAAAGTGCAAATCTTCGATGCCCCCAGTGAGGCTT
Os03g0580200	38,435	17,695	77	81	408	302	280	279	401	73.6	332	CCATGTAAAGTATACTAGTGTATTTACTTACGATTGGTACATATAGCGGTAGAATCATAT
Os03g0588600	13,113	16,765	2,927	3,449	389	381	219	209	181	65.0	4.7	GTCAGAGTAGTAGTACTTGATACCATTACTGTTTGACTGAACTGAAGATAAAGATAGTAG
Os03g0589300	4,142	7,198	96	95	621	616	519	551	351	12.2	57.3	TATATACGCTACAGCAGCTGGAGATTTATATAGTCAGCACTCGTTTGCCCTCTGGGCCCC
Os03g0601000	19,865	10,582	1,332	1,332	364	262	214	224	336	49.1	10.9	CATGTAGGTGTGTGTAGGAGTTGGATGTAGGTCTTTCTTCTTTGGGTGCTTTTGCTTTGA
Os03g0604600	14,733	23,842	1,514	1,660	3,573	3,382	3,501	3,581	4,157	4.9	11.8	CGTTAATTCTGGGATCTTCATATCAGAAAACAAGAAGATCAGCAACTTTCTGCCAAACAA
Os03g0617800	3,565	1,533	81	125	718	608	672	687	376	4.7	23.2	TGATGAAATGTGGATGTACGCACCGATTGCTTACAACGGGATGAACATCGGGATCGATTT
Os03g0621400	6,718	3,606	126	113	214	160	198	209	503	15.8	41.2	GTCTTTTTGGACGGAGGGAGTACTAGACAAGCACAATATGACTGCGAGATGGTAATGGAT

Os03g0639100	2,153	1,007	114	223	82	71	94	77	97	16.7	9.2	TTGTCCTATTGTTGGCTTATCGTTCTGAAATAAACATGTTTATCGGTTGAAATAGAGTGG
Os03g0643300	49,587	43,931	450	464	11,433	10,442	10,210	10,603	8,065	5.0	102	ACAAATGGGGTAGCATTATTCTAGTCTATCATATCATGCAGAAGAATCTTGAATTGGATG
Os03g0645200	9,731	8,160	1,959	560	880	771	830	1,067	1,465	7.8	8.5	TAGTAATATTTTGCAACTTGGGGATAGTTAGATACATACCGATTTTCAAGCTGCATGGAA
Os03g0647400	36,758	27,448	273	1,025	2,282	2,083	2,088	2,075	4,162	10.7	60.1	CAAATTCATTTTTGGGTGGAAACTATACACGAGTTCTGAATTATACGGAGATCTCATGCT
Os03g0650400	140,147	88,564	13,358	5,872	13,255	12,018	12,520	12,688	11,860	9.1	12.6	TAGGTCCGCTATTTTGTCCTGGATACATATTCATTATTCATCATTGCCATTGGTAGTATA
Os03g0650700	25,529	27,143	4,986	5,039	5,036	4,555	4,940	4,701	3,780	6.2	5.3	CCTGATAGACCCAAATACTATAATCAAATACAGAATTCGATGTGACCACATGGTTTTGTT
Os03g0653900	100,818	146,865	99	101	216	219	78	89	155	842	1218	ATTAGCAGTTAGGTAATGCCAGGTTGAGATGAATTGCTGTTGTGGTATGAGTAAAGGACG
Os03g0655300	16,359	22,215	357	226	2,539	2,413	2,412	2,492	1,630	9.5	67.1	CAGCAGCTAGGATGTTATTATGCTTTTATGGATTCTGAGCACCTTCTCTCAGATTTGAGA
Os03g0663100	11,090	8,974	139	1,080	582	538	551	594	1,006	13.2	25.7	TGTCGATAGTAATCTACTATGTACTAACACGCACGCTGTGAACTATGTACCTCTTGTGCG
Os03g0663900	659,396	556,993	103	146	7,806	4,627	166	147	465	903	4932	TCTATCTCCAGTAGCTGAACAAGTATGTCAACTGAATGCTGCAATGAAGTGAATGGATGC
Os03g0664700	8,823	11,279	183	81	186	177	205	167	923	24.3	82.1	CTCTGCATATAACTGATCCTCACAAAGAACATGCATGATGTTTGTGACTGTCAAGGCTAT
Os03g0666600	39,286	44,408	298	122	653	660	71	66	128	254	219	TACTTCCTCTGTTACAGAATAAGTTAATTTAGTACAGGGTGTAACACATCCTACTAAACT
Os03g0679300	2,192	3,392	154	265	738	674	726	747	152	8.3	13.5	CTGTCTGGGTTGGTTAAACACTTCGGTGAAATTTTATTTTGGTGTCGGATTCAAGATCCG
Os03g0679800	191,614	120,377	748	661	5,873	2,784	84	94	163	486	216	TCACATAACATTTCTTGAAACTGTACTTAACGTTACCTGTTTGCATGAGCGTGTTCTTTG
Os03g0680100	25,091	22,936	93	148	436	364	246	217	206	96.1	204	AGCGATGAAATGCAGAATGCATTTTGGGAGGCAGCTAAAGCAATGAAGAATGAATATATG
Os03g0680200	8,018	31,968	147	165	278	468	191	255	322	53.1	103	TGCCCTGATGTCGCTCAAGGAATACAAAGAAGCATGTGATGCATTCATGGATGGAGTGAA
Os03g0680500	3,311	1,035	455	112	94	84	83	85	111	18.9	8.2	CTCGGTGTTTCATTACTCGAGTATCTTGATATCCTCTCGGACTCCTTATCATTTCATCGC
Os03g0683500	421,707	183,209	114	170	3,910	1,206	105	109	179	948	1996	TCCAGCAGGAGATCGGCCTAGCTGGTGTCTTAATTAATTATATGTGATGTGCTGTTCCGT
Os03g0684100	96,469	81,306	1,403	154	8,028	7,519	9,414	8,394	11,213	9.2	191	TCTGCCAATTTACATTGATGTGGTTACATTATTGGTGCTAGCGATGTAATGAACGCGCAT
Os03g0684300	44,147	37,832	5,943	5,537	7,135	6,446	6,232	7,014	7,205	5.9	7.1	GAGACGTAAACTTTTATCCCAAAGAAACTTGTCCAGAGTAATACTAACCTTTCATGTTGG
Os03g0687400	3,430	4,782	77	91	155	152	80	209	153	27.6	48.5	AAGATTAGATTACGACACGCAAAAATAAAAAAGTATTAGCATATTATTAATTGAGTTTAA
Os03g0687800	182,527	63,960	90	91	1,103	331	74	73	124	668	1194	GACAAGTTCTCGTTCATTTGTGTATGTGTGTGAGTCCACAATTTCCAGCAGCAGATTAGC
Os03g0687900	3,973	2,264	178	123	252	183	271	163	602	8.4	20.2	ATCATCATATTGCTGTCGACCTGTCGTTCATCCGAGCTGCTTTGATTCGATCTGAGTTGA
Os03g0688000	500,797	252,298	103	104	11,228	3,142	382	384	187	670	3443	TGTGTTTTGTGTTTTCAGATCAAAGTGTTTAGAACTTAATTTGGTGAGCCGCCTCTGACG
Os03g0688200	129,418	115,531	8,621	9,547	13,515	12,340	13,153	13,646	31,507	6.0	13.5	CCCCTCAGAGTTCTTTTGTCACTCCAATGACTTTCATATGGATGGTTGGTTGATAATGCG
Os03g0689300	8,321	8,826	793	428	2,163	2,131	1,904	2,322	1,695	4.5	14.7	AATGTAATCAACCAACAGTTCATACAATCTATAAATCAAATCATCAAAGGGGATTGTTGA
Os03g0694700	56,029	32,940	11,057	4,764	7,835	7,245	7,867	7,991	8,500	5.3	5.9	AAAGTGGTAAACTGAGGATTTTATCATGGCATAATATTTAGTATCTCTGATTGGACTATT
Os03g0699100	4,040	4,130	80	78	1,037	1,040	810	907	1,174	3.9	51.6	CTCAATATAGCTACAGGTGCCTGAAAAAATAACTTTAAAGTTTTGAACATCGATTTCACT
Os03g0701100	4,474	14,507	400	1,883	240	291	198	267	240	33.1	9.3	ACTATATCCTGTCGCCCTTGGAGGCTTGGACTGTGTTAATTGGAATGATGATTAGTGGTG
Os03g0709300	21,376	20,125	100	98	6,741	5,828	6,527	6,529	3,337	4.5	209	GATTTATGTGATGTGTATTTTGAGAAGAATTTAATAAAAGCCAAACAGCTGCGTTCTGGC
Os03g0711300	57,731	63,893	14,741	9,740	15,187	13,650	11,561	12,110	12,825	4.7	5.1	TTTGGCTGCTGCAACATGTAAGCTTTTTTCATTTGGTTGTTGAATCCAGTATAGCAACCA
Os03g0712800	167,893	146,255	88	74	4,032	2,951	757	758	431	188	1946	GCATCTCATGAAATAGATCTATTGCAATGACAATACCAATGGCAACGCAAAATTTTATGG
Os03g0715600	22,521	9,920	157	161	214	206	157	160	237	71.9	94.2	TGATGCTAACTGCATATCCTGTAACTCTCCGGTCGCTCTTCACCCACGAATGATGAATTA
Os03g0716200	34,811	32,313	1,436	79	792	690	285	297	2,285	32.6	99.7	TAGCTATTCGACTGGAAATTTTGTACCTGATACACTACAGAAGATGATATAGCTAGATGT
Os03g0716400	661,346	522,024	102	88	9,200	6,302	3,843	3,878	4,128	124	6185	GTGGTTACTACTGCTGTGATCTCCGGATGTTTCTACCTGAAAAAATATGTGAACCTTGAA
Os03g0721700	7,353	18,078	120	109	262	153	126	129	141	76.8	101	TTGGCACTTCGCTGGAAGTATGACTATGAGTATGCTTCTTGCTCATAGGAATGTGCTGAA
Os03g0721900	113,498	55,038	2,195	1,222	5,386	4,604	4,736	4,950	6,136	14.4	48.3	CTCTGGGTTCATTAAAGGTGGATGAATAGATGATATAAACAAGAAAGAAATGATGGCTTC
Os03g0722700	13,045	11,741	1,717	1,031	661	665	575	642	515	21.6	9.3	TTCCATGAAAGAAAGAGATAATCATTTATGCTAACATGACTGACAATCAGAAACAAATCC
Os03g0724600	90,886	49,399	80	91	1,010	767	644	688	800	85.7	785	GGGGATGATATACCCACTGGATTCATCTTGGTTTTCTGAATGCAAGGGTCAATTAGCACT
Os03g0725300	19,822	11,820	358	891	2,503	2,129	2,282	2,392	2,989	5.8	27.1	GAATTGAATGGGATGTGTAGACGAATGATCTTTCATTGTGTGTATTAACTTGATTTGCAG
Os03g0725400	63,072	38,090	2,311	776	6,890	6,149	6,146	6,373	6,507	7.6	36.6	TTCCTGAACACCAACAGTGCTGCTTTCTTTTCTGTGCCATTTCATTGGGCACCTAGGAAT
Os03g0740900	907	2,091	444	272	168	367	982	178	174	5.8	4.0	AGCCGATGGTCAACTGCAAATTCTGTCGACTGAAAAGCTGGTCAGATAATTGCCGACATA

Os03g0752200	24,413	58,176	3,991	2,726	2,483	2,298	2,337	2,439	5,124	10.8	11.4	AACTGTAGTCACATGTATGGCACTCTGGTAGTTTAACCCCCAGCAAGTATTTTGTAGCAA
Os03g0759700	66,213	82,387	5,049	2,229	7,461	6,800	6,872	6,584	3,542	14.9	22.0	TGTAAATGGAGGGTGGGGTTTTAGCTGATTAAAGTACAAGTACTAATGCTCCTGCTTAAG
Os03g0760800	138,934	122,977	207	139	16,308	15,086	16,457	16,202	19,856	7.3	773	AATGTATACATGCATGCCTGGTGATAATAATGGTGTGTGTGCTGTAATAAAGTGTTGGCT
Os03g0775300	30,620	69,613	407	290	4,172	3,580	3,599	3,787	8,619	8.1	134	ACATGGAGCTCTGTTTTATTTCTCTGACCAGATGGTTTAAAAATGTTGTGATGTTTTTCG
Os03g0778000	36,629	65,623	298	108	5,669	5,167	5,365	5,421	5,950	8.6	273	TAATTTGTTCCGCTCACGTTAAATTTGCTGCCTGCACATTTGGCATAGTTTGTTTGTACT
Os03g0788500	96,666	207,493	1,543	828	27,196	31,217	21,823	21,754	23,255	5.9	125	TGGGTCACTCTTGGGTCATTGGTTCGATTGTTTTCTTCTGACGTTAAAAATACAAGAGAG
Os03g0798300	9,757	10,991	73	90	534	474	440	471	608	19.2	128	TTTTGTGAGCAATTGGACTCCTAAAATTAATTCTGGGATGGTTACATGGATTACCTTTTG
Os03g0800200	323,612	214,964	1,823	1,194	4,377	2,629	1,476	1,630	5,202	76.4	179	TCTTTAAGGCCTTAACTCTGCTTGAGACAATGCAAGTCTTTTAAATTTCCCTGTGGCTTT
Os03g0800400	12,307	6,037	545	201	825	649	657	729	859	11.0	26.0	CCATGCATATCTTTCTCATCTATGCTGGCTTGCTTGCTATTAGTGTTGATGCGTTGTACC
Os03g0800700	95,587	70,077	195	196	16,181	15,320	16,421	16,896	16,835	5.0	418	ACGCGTTTAAGACAATAAACTTGTGATACTTGGGAATGGAAATGTAATTGCCTGTTGCTC
Os03g0800900	54,518	53,067	604	184	1,933	1,635	1,688	1,594	4,884	18.6	161	ACGATCTGCATGTAAGGAAGGATTTTTACGAGTGGCTATACTCATCAATTTTCCCAGCTC
Os03g0809900	316,848	206,341	372	90	6,827	5,154	4,687	4,646	12,651	31.3	1399	TGACGTTGAGATGGAAGTGTCTGCCGACTTAAAAGCCTACTACTACATTTTAAGGAAAAC
Os03g0813700	5,141	6,166	358	301	958	852	870	878	906	6.3	17.1	ATTATTCCCCTTATGTGTAACACCTTATTTGTGTACTAAGCTTTGCCCTGGAAAACCGCA
Os03g0820100	92,159	79,494	7,803	2,859	11,853	10,558	9,669	10,869	16,806	6.4	18.1	TGTCAGATTTGGAATTATCATCGTATTTACATGGGAAAAGGTCAAAATACCCCTTGAAAC
Os03g0823800	42,951	158,762	91	86	8,214	9,666	7,487	7,431	7,643	10.5	933	CTGAGGAAGGAGAAATGACTCGGTATTTTTGGGTGTATATTAGTTCGGATTAACAGTTAA
Os03g0825900	22,483	11,765	147	179	772	710	766	795	1,117	17.7	100	AGTGATCCTGGATGTAGGTTTCACCACCACCCGAGGAAAAAATACAAGCCGAGATGAATT
Os03g0826700	20,308	17,887	1,493	465	2,840	2,528	2,518	2,606	3,642	6.2	22.9	CTTTCCTGTACACATTCTTATATGTGGAGAAATGGTGAAACACTGAAATGCTATACATCG
Os03g0832200	61,656	69,620	4,829	1,802	10,576	9,706	9,919	9,783	7,303	7.7	22.2	TACTACATTGTCAAACTTCACTGGTACTAGTACTACTGTAAAATCACATCATGCATGTCT
Os03g0837000	35,301	25,088	2,880	1,081	1,385	1,150	1,202	1,265	1,135	25.0	16.9	GTTTTTGTAACGGCCTGTTTTTGGGCAGCTAGTACCATTATTTTTGGATATTACTCCCCC
Os03g0837800	18,080	17,981	1,139	160	640	534	2,450	443	801	22.8	42.3	AACCTCTTTGGCCTGATTTTCCTTCTTATATAGGAGTAAGTCATAACCAGTAGCTCGCTA
Os03g0841700	119,747	95,731	89	1,053	14,142	13,025	13,096	13,368	18,200	6.9	349	ATTCCTGTGCTAACTAGGCAGCAGTGAGCATCGAATGGCTAGAACTTGACTGCCATTTTT
Os03g0845300	23,469	12,666	1,434	1,860	384	227	100	127	169	98.4	10.6	GGAAAGTTTTTGTACCGGATTTTGCATGCTTTTCGGCGTTAATTCTCTCATTTTTTGTAA
Os03g0847800	4,845	1,715	229	423	875	469	265	389	498	6.1	9.3	CCTCGCACCTGCTCGAAAAGGAGAAACACAAGGAGAAGAAGCATAAGAAGGACAAGAAGG
Os03g0851400	8,127	21,346	78	178	905	899	773	845	676	17.3	112	TCATTTCAATAGTGGCCTCATTAAGAAAGCTCCGTTTACTTATTCCTATATTAGTGAGTC
Os04g0125100	1,488	1,139	81	87	280	277	257	255	226	5.3	15.5	TATGGCTCTATTGCCCTAGTTATAATTTCTTAGACAAAGGTTATTTTCTCCTGTGTTCTG
Os04g0129600	3,053	1,891	107	218	815	762	622	683	467	4.2	15.8	CTGGTTGGCATGTGGAAATACATCATACTAAATACTGATATTATGTAGCAGTTTGGGTAG
Os04g0192800	40,676	21,264	1,247	932	2,435	2,125	2,245	2,324	2,806	11.6	27.3	GCCGGCTCGTTGTTTAACCGGCGTGATTATATCCACTAATATATGTTGATGACCGGCATT
Os04g0193300	1,153	1,575	87	122	125	110	93	150	201	8.8	13.1	TGCAGTAGAGAGGGCTGTTCAGTTAAATGATCAGTTCCTATTATATTCTAACAGAGTCAT
Os04g0208400	22,769	16,936	86	81	220	157	102	100	114	157	236	GTACGATTAGCTTTAATTTAGTAGCAAGTTTATTCTAGCCAACAAGTGCCATTCCACAGA
Os04g0208600	7,743	4,780	120	100	139	93	122	109	132	49.5	55.6	TTCCAGCAGAAGACAAATGTTATCTCAGATGAATGTTGTATTGACCTGGCATTGATCATG
Os04g0209200	13,312	11,801	298	79	1,214	1,124	1,073	1,193	1,913	8.5	81.8	AACTAAAATGTGGATGGTTTTATTTCTGGCATTAACAAAGATCCCTTCTTGATTTGTATT
Os04g0209300	22,978	36,599	587	208	2,182	1,861	2,018	2,090	2,752	12.3	83.0	TGGGTACATAAACTCTTTGCACATGAGCTATTGAAGCTTCGAAGGAAAAACACTCGTTCT
Os04g0223500	75,578	71,621	108	118	2,565	2,246	2,445	2,554	4,743	21.6	652	TGGTTTCTTGGATTTCTGCTGTTTTGCATAGTGCAAATTCAGTAAACCGTGTGAAGTGTA
Os04g0223900	130,272	133,690	113	78	1,849	1,575	1,474	1,613	3,207	57.9	1407	AGTGCAAATTCAGTAAACCGTGTTTAGGGGAGGATGAAAATTAAACTCGTTACTTGTTAG
Os04g0224100	182,754	60,935	88	81	28,675	7,405	78	74	281	194	1251	ATCTTGAGGTGAGAATTTCGCTACGGCTTTGCGTGGAGGAAGTTTCCAAATTTGCTGGAA
Os04g0229100	513,728	371,617	117	178	20,914	18,368	17,471	17,872	6,564	39.5	3033	GTTGGCCACGTGAAGTAACTGTACGCACTTTGTACTTATTCGAGAAATGATCAGTGATAA
Os04g0244400	51,646	40,346	2,704	1,619	3,785	3,526	3,836	3,979	6,826	9.0	21.8	GAATGTGTGACAATGTAATAATGTGACATCATATATTTAGTACACAGAGAATTGAACATG
Os04g0252400	8,696	6,173	656	614	250	180	151	153	182	40.5	11.5	GACTTGCATAAGCAAAAGGTGCATTGTTGAAGCTTCTTCTACCTACTTATTTTCCAAAAG
Os04g0274400	28,911	13,799	2,642	1,510	4,816	4,290	4,843	4,517	3,600	4.9	10.0	TTCTCGTGCACCATAGCCGAAATTACTTTCTGGATTGCCCTGATCTTTATCAAGGAATGC
Os04g0278900	5,458	3,938	223	199	917	836	849	910	1,130	4.7	22.0	AACACTATTGATTGTAAGTTGAAACAAACATCATGAAATGTGTATATATTCTTTGGGAGG
Os04g0284600	21,593	24,991	5,210	4,779	993	857	850	966	1,688	18.7	4.7	ATTTGAGGCTCATAGTAGGAAGCTAATCAGAAAAGGCAACAATTGTTTTTGATAACCTTG
Os04g0329500	19,098	23,245	538	104	3,902	3,603	4,061	3,817	4,154	5.3	89.0	GCTTACTTGTCATTAGACTCTTTGGTCATGACTATAACATGTATAATCTGCTATGCTCTT

Os04g0330800	14,444	11,672	1,758	3,222	2,498	2,173	1,628	1,929	1,135	8.5	5.5	GAAGCATTAGATTCCTAGGTTTTGGCGAGGCCTTCTCCTTCTTGGCTCCTTTCTTGTATT
Os04g0361900	6,246	3,333	92	80	911	803	850	865	484	7.1	53.1	GAGCTGTACCGGCATGTATATATGTAAACTGGATGAGATCAATACACCTGCGCGTTGTAT
Os04g0376400	22,124	21,018	963	551	1,303	1,167	1,156	1,204	2,422	12.6	29.6	TCCAATAGGAATTCACATTAACAATGGAGTAAAAACAGTGTGTTTTTGTGACTGACCGTC
Os04g0382100	32,978	34,379	1,856	990	9,972	9,100	8,490	8,805	7,472	4.1	24.8	TTTTGGTGTAGAAACAAGCTATCTGTTATGTACTAGTAAAAATTCAGATATGTTAGCGAC
Os04g0386700	7,328	1,973	105	265	217	176	207	231	247	16.8	22.8	TTGGTGTTCGAGTGTCACGTCGTTGAATTGGTAGTTAAAATTTGCTAATAACTTGCTGAT
Os04g0390600	24,322	28,058	2,578	2,872	2,279	2,012	2,224	2,284	4,854	8.0	9.6	CTGTGTACAATTGTGTAGAAAATGGGACATTGGAATTTAGAGCCGTTGTCCACGATGAAC
Os04g0398900	165,515	75,589	82	79	1,497	509	71	74	163	554	1389	ACTAGTTAGTTCGATTAATTTCGATGCTGGATGTGTTTAGTATATTTACCTACTGTTTGA
Os04g0403700	2,571	6,327	106	89	507	853	199	178	331	11.8	41.4	TGGCCCGATTCCCATCGCTCTGAACTTGATGGATGCATCTGTGAACGCCAAGAAGATTAG
Os04g0404400	9,814	12,833	174	102	446	407	483	348	491	24.8	84.5	TCAGTGTGTGTTTTGTTATAGAACTTGCATGGATAAATTGGGGAGTGTATACATGCATAC
Os04g0428500	1,359	1,793	133	130	126	118	184	140	173	10.0	11.9	TTTCAAAGTTTGTGGACGTTTTTGCCCATGGGCCCACCTGTCAGATCAAAGAGAGAAATA
Os04g0437700	7,875	16,701	1,483	1,522	1,715	2,156	511	492	1,408	9.8	7.6	TTAGAGTCCGTGCTACAGCTGGTATAAATCTGTAGCCCGCTGCTTTTCTCTCTCCTTATT
Os04g0444900	63,083	61,403	3,208	5,835	11,954	10,556	10,669	11,864	17,646	4.4	14.4	TTCTGCCTCCTTGGTTGGATGGATTGGTTAAGTGTCTAAACTCTCTGATTAATGATGTGA
Os04g0445000	28,906	13,507	556	607	869	607	495	498	575	33.6	34.0	ACTAATTGCAATGAAATATTCTTTCTGAGGCAGTGAGAAAGCTTGTCACAGGATTTCCTG
Os04g0446500	58,763	56,681	1,195	867	4,574	4,287	4,418	6,235	6,186	10.6	56.7	TCAACTGACTGGATTACGAGAAACCGCTGTAACTATTTCGTTTACTGCATTGATCGTCCT
Os04g0448100	17,850	7,987	1,721	1,570	1,408	1,163	1,158	1,244	1,918	7.7	7.3	CATGTGTTCTTCTTGTCCAGTGGATCTGCAACTTTCAGTGATAACAATGTGCTAGCAGTT
Os04g0449800	556,287	190,657	129	111	18,912	6,981	3,690	3,822	2,952	74.0	2720	CGCCGTGGCGCTTGACAAGAAAAACCGATGGAACCGGATCGTGTGGTTGGGCGTTGAATT
Os04g0452500	7,447	8,770	134	106	285	257	164	156	650	22.0	67.9	CACCCTGCAAACATTGGTGAATTGTTTTCTGAGGGCTCGTTGAATCCATATGCCGAAGAT
Os04g0462200	348,213	376,776	2,200	2,287	2,641	1,650	211	229	228	922	161	GAAGTTATTTAGTTGTCCCCTGTTGTTTTTTTCATAGCAAATGGATTTAGCAGTTGAGGC
Os04g0463700	33,035	26,237	5,142	699	2,273	2,044	2,083	2,082	5,377	8.7	15.5	TATAAGATGACCTTTGCAGCTACTTATCTACCCATTTATGAGCAATGAAGTACATTGATC
Os04g0477200	15,489	14,297	94	101	5,433	5,006	5,385	5,319	2,182	4.4	153	CTCAAGATTCGGCTTGGCTATATCAGAACTCACTCTGTTTATTTGGTTTTCTCATTGTCA
Os04g0477300	9,783	13,249	3,138	1,143	1,554	1,467	1,567	1,513	1,478	7.6	6.0	ATTTGCGTATTAACACCAGCTCTATGTAGCCGAGCAGTAAGTATAGTAGTCTCTCTTCCC
Os04g0479900	80,686	43,618	116	115	8,148	7,549	7,892	7,831	6,484	8.3	513	TAGCAGATGCAGATCGCTTCGAGCACTGTAAATTGAATCCAAGCAATTATACCATGAAAT
Os04g0480500	5,130	9,870	520	336	319	316	268	120	313	26.0	17.0	CGCGGAAAGTGAAAAATGAAGCTTGGTGGTCAATAATAAATAGAGGGAAACAACAATATG
Os04g0490300	218,649	63,672	175	177	11,216	6,618	5,802	6,035	12,152	12.7	671	TGCTTGGCTAAAGTTGTTTTAGCTGACTGCTTGTAGTTGCTTTCCCTCTGAAAACAAAAC
Os04g0496400	23,947	34,914	1,712	1,587	5,841	5,403	6,222	6,390	7,101	4.4	17.5	TTGACATATTAACTTCTACTTCTAGGCTTGTAGCAACTTGCTATCCTCCTTGGTATGCAT
Os04g0497300	9,221	4,185	313	253	111	79	109	72	322	36.3	22.0	TACCTGACATGTTTGTAGAGCATCAGCTGAGTGGTGACTTCAAGCAGCAGGACATCATAT
Os04g0499100	11,197	14,457	100	77	1,228	1,127	1,141	1,134	1,462	9.8	145	TTGTGTTTTGTTCAAGCGTCCTTTTGGGACGTACGATTTTTAGAGGAATTTCATGTGACT
Os04g0506900	118,416	89,564	6,339	2,894	10,265	9,375	10,485	10,193	10,417	10.1	24.0	GCAGCAGAACACTGCTCCATATGACCATATGCTGCAAAGAGTATTATATAATGCATTCCG
Os04g0507000	36,116	46,439	472	351	6,972	6,689	6,244	6,280	3,913	8.1	101	TACTACTAACTCTTTATAATATGCAATCTAATCGAACTCTAGGAGAGTAAATTCTGATCC
Os04g0509200	6,342	8,507	1,186	506	1,650	1,584	1,652	1,744	1,656	4.4	9.5	CAAACAGCAGCAATTGTAGAAAACTTTATTTAGATGTTGATATGAATCGAGATGCCTCTG
Os04g0513000	29,243	28,807	10,562	4,027	6,516	6,023	6,125	6,326	7,893	4.1	4.5	GTTAGTGAATATCCGGCATTTCAATTAAAAGAATGGATGGTTTAATTTTCACATAATGAG
Os04g0514800	51,774	81,398	12,690	7,723	18,832	17,911	17,069	18,202	15,389	3.9	6.6	TATGAGCTGCCGCTCCACTATTGGTACGTTGAAATGCAATCATAATGAACAGATGTGTCG
Os04g0526600	9,664	35,914	108	100	1,271	1,660	993	1,026	1,225	15.3	179	GCGCATGTGCTGGTTGAATAATGTGTGAAGAGGCTAGCAGGTATTGCTCCGTGGTTCTGT
Os04g0527900	5,410	3,787	670	701	366	265	293	192	410	13.6	6.6	GAGGATTACTGATGTATCGAGCTGAATCATAGCACCTGCATATTTGCTCTAGTGTACCAT
Os04g0528200	113,151	55,821	99	113	9,938	3,415	98	132	132	242	751	TGCTAAGTCGGATATAATTTTTCGCCCTCGTACTATGTTTCTTCCACGTGAATGATCGAT
Os04g0528400	4,835	4,910	104	140	579	491	530	550	1,206	6.1	40.3	ATCCTGTCCAGAGGATCGTCCGACCTCTCGATCTTCAATGAGAATGCCCAAAAATTAGAT
Os04g0531300	4,909	7,285	150	98	1,228	1,139	1,289	1,070	955	5.6	49.3	AGTAGACAAATTATGGCGTGGTTGTCATCTTGTACACTTCCAGAAATTCAGTTTCTTGCA
Os04g0543700	5,125	5,157	817	181	444	427	317	320	516	11.7	13.4	GGATGGAGTTGTACGATGAATGAATAACATGTATACATACACTATACTCGTGTTCGAGCA
Os04g0546100	7,375	4,806	138	186	411	363	370	386	1,387	8.2	37.3	TCAGTCTGTGGTTGATGGTGCAAAACATATACTTATAGCCCTCTCTAAATAGCATGAGAA
Os04g0552700	2,532	7,242	757	1,009	152	213	137	129	223	23.0	4.9	TGTCTTTTTGTTTGTTTCAAGCTACCCGAACAGTGTACATTGGGGCAACTAGCAGAGCTT
Os04g0566600	207,457	136,458	164	159	3,183	2,662	2,697	2,598	6,682	39.1	1039	TGTTAGGAAGTTAGCCAATTGCAAGATGTCAGTGTAGGGCCTTGAGTATGCAGTGCAATG
Os04g0566700	7,152	2,520	686	726	187	172	164	175	194	23.1	6.0	GTCGGCTTATGGATATCTAGATGTGTATTGAGAATGATTAAAAGTTTATGCCTCCATTTG

Os04g0572600	81,637	180,954	3,236	2,761	11,832	12,267	10,547	10,436	8,118	12.7	40.7	GTCGTCGTTATCCTTGCATCAATTGTATGCGGAAATGATCCATATTCTAAATGAGAATCA
Os04g0573100	27,615	33,559	94	76	155	126	132	89	105	268	360	TCTTATGTACTACTCAAATTCAAATGAAATTATGTTCACTCAATAAGAAACCTTTGTTCA
Os04g0576700	23,463	20,500	3,816	2,999	6,127	5,600	6,267	6,398	5,001	4.0	6.5	ATAGAAGGTGGCAATCCACTCCTGGGAGTGGGGATGGATATATGTTGTCACAAGTATGAT
Os04g0577600	14,976	6,237	92	656	871	448	79	1,347	832	15.8	39.3	TGTAACTGTAGCATATGTACCGTGTACCCATCCGTTCGTGACGTGACATGCAACACCGTT
Os04g0578700	179,349	194,015	1,949	1,792	24,081	22,756	24,526	23,886	24,617	7.7	99.8	TAACAGAGAGAAGCACTGCCAATGAGCCACGGTAAACATTTTGGTCCGCATGCTGATAAT
Os04g0580300	160,990	52,442	1,048	1,632	10,267	9,428	10,657	10,602	9,815	9.2	70.3	AGTTGTAGCAACTCATAATTCTTGGTAGCTAATGCTTATATATGGAAAAAGAGTAAATTA
Os04g0582600	1,956	6,347	145	75	1,069	966	1,003	1,056	362	5.8	33.8	GACAAATCATACTCCGTAACTTTTTGTACTGTATTAGTATAATCCAATGCCATTCTCTGG
Os04g0585000	37,441	33,280	139	247	3,804	3,467	3,873	3,731	6,929	7.0	190	TCAGAGATCCTGGTTTGCAACTTGCAAGTGGATGGCTGCAGCTTTTTCGCTTTGTACATT
Os04g0585300	7,774	14,564	455	126	2,080	2,011	1,890	2,029	1,736	5.7	44.4	TACTACCAGTGAAAGATGTAGCCTTGAAAGTTATCAACTCTAGAGTAAATGCCATTTAGC
Os04g0588900	114,348	133,030	1,261	739	4,112	3,632	1,228	1,212	1,415	70.4	128	AAACTGTCCTAGAGCATCTCAACAACTGCTGTCCTAACTGTCCTAGAGCATCCAAACTGA
Os04g0595000	12,297	13,144	97	68	199	209	130	61	133	95.2	157	ACAGAAGTTAGCAGCCACTATCAGTGAGAAATCATTATTTTTATACATTATATTCCCTTT
Os04g0599300	332,345	456,180	212	122	2,119	3,195	441	286	522	550	2419	TAGCTACCTAGCAAAACTTCTTAACAATTTGGCCATGTAACGGCTTGCTGCTGTCCGGTT
Os04g0599600	23,718	13,305	285	262	2,494	1,968	1,184	1,055	2,665	8.7	65.0	CATACTGAAATCGTTTTTGACAGCGACACGGTCTCCCAAAACACAACTTTAACTTCCTGT
Os04g0600200	20,896	12,832	767	934	2,633	2,447	2,556	2,450	2,526	6.5	19.3	ACACCTGAATTTCTTTCGTTGAACTATTGGCAGCTGAGTTATATATACTACATACCATTC
Os04g0603900	26,158	13,498	137	91	1,238	1,029	963	1,038	1,847	13.4	168	TAGCTAAAGGTGAGCAGAGCTGGGAAAACAAGCAAGAAGTTGACCTGATTAAGTGTTCGT
Os04g0615800	111,450	45,041	986	622	4,664	2,181	1,294	1,251	1,817	37.0	90.4	AACTGCCTGGAGTCTCTCATGTCTTTGGGTGGTTTATCCATAGTAAATTTTTGTCCGTGT
Os04g0617900	1,503	1,899	97	91	126	148	118	105	261	9.4	18.0	GTTACACCTCTTTATGAAATAATAACAAAGTTGGATATTTATGTGCTGCCTATGCACAGG
Os04g0618400	2,610	2,173	88	84	355	353	339	334	496	5.8	27.6	CAAAGCAGAGAGTCCTTGAGAGGATCGTTGTGGTGTGTTCTTTACGTGAAAACCATCGGT
Os04g0625100	8,424	14,207	846	278	754	639	707	824	1,192	11.7	22.6	GAGTAGAATGACATGGTTTATGTCGGAGAATATAATCACATAACAAAGCTTCAACTGTTC
Os04g0637500	10,530	4,959	558	484	1,158	1,236	1,142	1,189	1,279	5.9	13.9	TACATTATTATTGAAGAAGTGTAAAACATTCGATTCTGAAATATCTACCCATTTCGTGTT
Os04g0644300	70,860	90,204	12,068	5,679	12,478	11,212	12,179	12,397	11,154	6.9	9.7	ATAGTTTTTATCAAACCTCAGAAAGAAATATAGTCAGCCTCAATCCGAGAGAGTTTGCTT
Os04g0652500	9,411	5,755	645	989	663	568	479	452	1,062	9.8	9.2	TCCTGTACATACTAACGTCACATCCGACAATATCAGAAGCTCGCCCTGGTGCTACATTTT
Os04g0659400	15,748	17,079	2,750	2,491	4,871	4,610	5,071	5,048	3,290	4.1	6.3	TGAAGGAACTCTAATCATCTAGAAATGATTATTAACATTCCAAAACTGTTAAACCCTTTG
Os04g0663800	32,080	25,378	4,598	3,934	6,456	5,990	6,380	6,573	4,738	5.2	6.7	GCTCAAGACAACCTATGAATATTGATTGTTACAACATGTTTGGAATTAGCTGAACTGAGC
Os04g0673400	43,408	34,661	1,429	2,342	8,882	7,887	8,329	8,301	6,614	5.2	21.2	GGGACTATCTGCCATTGATTGGCAACTCTAGACCATTTGAAGACATCATGTGGTCTGTCT
Os04g0676200	667	1,264	76	75	68	68	67	65	110	10.7	12.1	TCCTTCGTAAACGAAATTGGTTTTCAGTAGGGCAAATATTATCATTTGAACTTGCTTAGC
Os04g0677200	32,226	57,453	103	97	3,343	3,008	2,742	2,878	5,962	10.2	431	GTATTGGGCACTGTAGCTGCGTACTAATTTCGTTTCTGTCATACGTATCTAATTGAGTTT
Os04g0677600	149,482	318,812	1,288	524	1,704	3,284	162	151	144	738	266	CTCATATATGTCGTCGAATTAATTTGTTTAGGCCCAATGTTTGTTGTTGTTCTAGTCTTC
Os04g0682400	12,080	19,922	105	116	619	506	540	593	368	34.1	141	AACTGATGACCACTCTGATGAGTGAGAGATGCTTGGTTGGAGCTTCATGCTATCTGAACT
Os04g0682600	26,585	33,089	104	107	1,589	1,522	1,319	1,339	3,463	13.3	282	CCCTTCAGTTGATCAGTAATATACCTGTGCTTCTATCTGCTATGTTTTTGGAAAACTAGG
Os04g0691200	3,779	3,911	1,056	475	781	731	823	830	1,076	4.2	5.4	TTTTTTGTGTTTCGTCTAAGAAAGGCCACTGAATCAAAGTTTTGCAAGTTTACTCCCTAA
Os04g0692500	109,764	88,626	21,777	12,145	10,614	9,697	10,080	10,755	21,619	6.6	6.1	TCCTCAAGGTTAAAATCTGAAACAGCGAGGACTAGTCAAACAAGAGGTCGTGTAACTGAA
Os05g0102600	122,408	178,913	2,070	1,922	19,216	18,188	19,529	19,099	32,781	5.9	74.2	TTACCTGTATGGATGTATGATGGATGTTCCTCATACAACTTTCCAATTCCAATTACTGGC
Os05g0106700	1,577	701	102	150	916	113	146	205	125	6.1	8.5	GCCTTTCGATCTTTACTGTACCATAATATTATTATGATACTCCATATCAATAGCCAAATT
Os05g0107900	137,939	71,810	112	73	3,424	2,780	2,866	2,808	1,716	44.2	1100	ACATGTATACCTACAATGTTTGGATATCTATATAATCATCAATCGTAATCCTATCAATTT
Os05g0113300	20,108	5,791	117	177	490	284	265	308	561	25.2	75.1	TAATTAGCTAGCTTGTAATCGAATGGCAGAAAAAAATTTAAAATAAGCCAGATTTGCTAG
Os05g0114800	10,434	13,637	118	149	1,341	1,123	996	1,140	851	12.1	89.9	ACCAAAAGTGAACTTATTGCAAGCCTGAATGATATATTACTTGGGCCGGATTAAGTTGCT
Os05g0116000	544,678	507,824	111,319	39,447	57,377	53,579	57,375	57,535	59,044	9.1	7.9	TGCGGTTGAACTGTGGTGATTCGCCACTTAAAATTCTATTCTATTCGAGAGTGCCTTCTG
Os05g0121700	2,893	3,156	139	142	763	719	796	783	777	3.9	21.5	TAATTTTTGCTACTGAATTGCATTCCGACTGTAATAGACAGTTACCAATCCATCTTTACG
Os05g0122500	20,971	15,031	257	127	937	816	368	145	194	60.2	98.3	TCCGGCTCAACTACTCGATGTCGGCTTCGCCGATCGATTCTCCAGAGTGCTCACTGAACA
Os05g0145000	28,707	20,477	404	564	3,278	2,909	3,326	3,369	5,268	5.9	50.8	TGTGTGCAGAGTGTATAAATATTATGTAAAGGAGATCATTATTGCAAGCTTTTGTTTCCC
Os05g0146100	27,319	36,773	8,229	6,653	223	164	112	93	149	220	4.3	ATAACTATCTGTGAACATGGAGATGATGTCCATGAGCATGTTCTAGCTTTTCATTATGTC

Os05g0147800	7,108	5,283	100	88	278	323	169	138	275	25.3	65.5	GAATCCTGATTTGTCATTTCAAACATTCGAATGAAATTTGTGGCGGTTTTTGCTTTCAAC
Os05g0153200	6,792	9,940	86	78	162	145	121	111	323	39.6	100	TGACTGATAGTCTGTGTATTCTACTTGCCAAACTTAATTTATGGCCAGTCTGGGCTGACC
Os05g0155000	17,413	14,533	1,110	857	2,689	2,454	2,597	2,668	2,476	6.3	16.3	GACGTGATGACATACTACATGCAGCTCGGATTCTTATACGGCTGCTTAAAAGGCCTCATT
Os05g0158400	20,738	19,447	1,083	1,044	2,023	1,815	1,858	1,900	4,723	6.7	18.9	TGGCTGAACTGCTAATATTCATATGAACGACTGTCATATATATTCAGCCCGATTGGTCCT
Os05g0162600	49,161	23,400	492	218	1,688	1,349	1,282	1,251	3,833	14.7	104	TGTATGCTTGTGCTAAATCTTGGTTGGCTGTAATCATTAATGACGTGTTACATCAAAATG
Os05g0164900	359,429	427,379	2,173	309	13,644	12,631	12,602	12,445	17,140	26.4	479	TCACCTACTGTTGAGAAACACCCTGTTTTATCAGGTACCATGTAAATCTCTTGGAATGCA
Os05g0176400	7,467	3,593	91	240	400	390	382	359	174	20.1	35.1	TTGAACAAATTCTTATGAGTTAACCTGCCAGTGAATGTGCGGATGAAGAAGGGATCCATA
Os05g0180700	31,754	14,564	4,955	1,483	3,256	2,740	2,496	2,568	2,642	8.0	7.9	ATCGATGCAGATATTGTGAACAATCGCAAATGAGTTAGTAAGTATACTACTTCAGAGTTC
Os05g0181000	116,803	83,095	18,467	20,834	19,853	18,588	18,195	18,859	20,253	5.0	5.0	TTTGTCCAATGGTCCATAACATCTAAGGAAAAACAAATTTTGGTCCATGGGAAGAAACGC
Os05g0188100	381,886	406,094	3,833	1,301	42,722	35,066	38,866	40,660	93,208	6.5	176	TGTTGGAGTCTTCGGTTCGGTTCTTTGGCCTAAACCGATTTATCTTTTATCTCAGCCGTA
Os05g0193700	8,231	16,390	1,060	90	1,433	1,289	1,383	1,473	1,986	7.0	37.5	GGATGCAACAGTTTACCTATGTATGATATCTATTCACAGAAATTTAAGTGTGTTGTGTTG
Os05g0193900	3,994	1,839	515	179	792	684	752	812	347	5.3	8.9	GTGCAGTAAACCAAAGTTAGATTAAAAACTCTATCTGAAGATTGCAACAGTGATTTGGTC
Os05g0203800	1,436	2,260	141	152	307	289	370	351	335	5.4	12.3	CCATAATTCAGGCTTGGCACTATCAAGGTGATGTACCTAAGTATTGGTTCAACCTGTGAA
Os05g0211800	13,588	27,318	144	225	210	241	146	134	280	86.5	107	TGATTCTTCGTGTTTGCCATTGGTATGTGTTTGAATATTGTATTTGCCCTTGTCCTCGTC
Os05g0212100	2,990	2,262	127	108	696	622	721	650	391	5.1	22.2	GTTGCTTTGTATAGTTCATAATTTTTTAGTTGCTTTCTGTTTTGTACAATCACATGTTGG
Os05g0214400	1,392	4,103	148	108	195	176	259	267	335	8.8	18.9	AATCAACAAGCTGCAGAAATGGAAGCTGTTAAAGCTATTGCAAAATTTGTGCAGAACTCC
Os05g0223200	555,814	466,999	451	1,406	2,410	2,035	800	892	1,800	325	640	TACTAGGGTTTAAGAGATGGATGGGATGGTTAATTGTCAGGCTCTGTTGGTAACCTCCTG
Os05g0223300	127,459	116,904	112	125	1,189	953	389	391	1,216	138	1031	CCTGAGTGTGTGTAAGTTTGATGGCTAGCGTTTATGTTAAGAATGACTCTATCTGCTGCC
Os05g0249900	4,287	2,630	102	107	208	107	129	146	206	19.5	32.1	TGCAACAAAGGTGATGCCAAAGGCAAGACTTTATCAGACATGTTGGTTCGTGTACACAGC
Os05g0313600	4,747	3,279	357	1,164	904	808	805	830	737	5.0	6.1	CCAAATCTTGATGTGGTGTAGCCCATAAACAGAAGCAATTACTTTTAGCTGCTGAAATGT
Os05g0316800	259,190	144,579	131	123	13,953	10,958	6,295	6,430	20,774	14.3	1521	AGCTGCCTTGAATGGCACGTCTCCCGCGTGGAAACGGAACAGTGTAATTGCGTGGCAGAT
Os05g0323200	2,434	1,405	338	323	253	227	198	165	296	7.5	5.6	AATAGCTTGCTATTGTACCTGCTCTTATGGCACCCTCGATGTATAATACTCTCTCCGTCC
Os05g0324600	5,348	7,364	92	92	501	478	477	467	741	10.5	68.0	CTGTAAATGGATATATTGTGCCGTTAATTTTTGGTGTTAATGAATCAAGCTGGCATATGT
Os05g0326400	60,647	39,248	12,539	5,251	2,846	2,200	2,100	1,962	2,106	22.4	6.0	GGATGTTTAGCAACTGTTAGCTCTGTCAAATTATCAATCCCTGTCTTGAATTTCCATCTT
Os05g0348400	3,542	2,247	113	103	332	306	260	254	493	7.5	26.1	AAAGAAAAACTTTGTACTTTGTTTCCTTCCACTCTTAATGAAATTTGTCGGCCTCTTTCG
Os05g0352700	1,023	601	146	94	137	97	102	90	176	5.8	6.7	AACCACGAGAGAGACCATCGGTGCTCGACTACGCCAGATGGGTGTTCAGAAACTCAGGCA
Os05g0361000	3,449	2,818	78	105	740	341	159	195	248	11.5	34.5	TTTTCTTAAAACCGCAGCAGAACTGCGTTTCATTTCATTAAGGTAAAGAAAAGAAAAATA
Os05g0366900	103,301	53,786	169	170	179	137	146	114	203	439	440	TGATGTGGGTTTTTATTCAGGCATGATTAGAAGACAGTACTAGCATTTCACAGGATTTTA
Os05g0367800	5,885	2,935	338	234	1,228	846	496	454	512	7.0	14.8	GCAAGGAGGAGTACGAGGAGAAGCTCCGGGAGCTGGAGGACGTGTGCAACCCGGTCATGT
Os05g0368600	4,934	9,707	122	75	753	1,072	392	318	369	15.2	72.2	GCAGCGTCATGTGAAACCAAGCTCGAAAAAATTAATTCAGATTACATGTTTAGACTTGCT
Os05g0373300	34,697	10,588	552	454	946	728	643	657	700	26.7	38.3	AGTAATTAGCTCGCAGCCTCGCACTACATTTGGTTTGGTGGTGGTGTAATTTGTGCGGTG
Os05g0376400	42,053	60,845	105	109	4,351	4,349	3,337	3,209	5,436	11.2	473	TCAAGACACTGCTGAATTTTCCGTCCTTGTCGCAGATGATTCTAGCTGTCATGCTCTGAA
Os05g0409800	5,306	4,041	713	301	385	351	335	367	347	13.1	10.0	GTTGACAAGCTTCCTGGATATAGTTCAGTTGAATTTGATGTTAATGTCTCTGAACCAAGA
Os05g0410800	943	1,236	92	75	230	186	232	199	280	4.4	13.0	TAATTAGGGAGTGACTTATTGACATCAGTGAAGTAATTTGGTCAGAGCTATCTTTCTTTT
Os05g0415400	756	2,250	114	84	214	200	231	180	122	8.2	13.3	GCTCTGATCTGTGCTGGAGAGTGAATTTAGTATCTATTGTACCAGATAGAATAAAACCAG
Os05g0417100	2,835	8,830	1,100	534	1,115	1,031	1,178	1,062	576	6.3	6.5	GCTCGATGAAAATCCACAATAAGTTTCTTATGTACTTTCTTGGTAAATTATCACCCTTGC
Os05g0427200	498,108	472,905	701	801	2,801	2,425	1,249	1,194	2,478	231	648	TGAGCCTCACTGATACTCCATCCGTGGGTAAGTGATCTTGTCCTTTGTAGTTTGTCTTCA
Os05g0427900	76,661	40,451	14,076	6,274	7,713	6,920	6,770	7,282	7,283	7.7	5.9	GATCGAGTATGAGATCTGAGCGACCGTTTTGACGCATATACGTATATAAATACGGGATGG
Os05g0439300	4,592	2,760	95	333	292	200	188	197	792	8.6	20.1	CAAATCTGGCAAACGATTGATGACAAATTGGCAATCACATATATGAAATGAGAGGGGGAA
Os05g0455600	38,012	28,669	8,575	7,097	6,821	6,198	6,206	6,398	7,510	4.8	4.2	CCAAGCATTGGAAAAAGAACAGCATGTAAAGGATGTAAACAAGTATTCTAATCAACACAG
Os05g0455900	25,559	28,601	5,926	5,378	3,920	3,626	3,495	4,059	2,939	8.1	4.8	GAGTGTCATCTAAATTTGCATAGTGAACCTTGGACCATTTTGAAGTACAATAACCATTTG
Os05g0460000	174,430	44,310	161	142	3,332	2,611	3,111	3,397	294	92.1	582	TTTTTTATCTGTGCAATGCTCGACTCTGGGCCAAACGGGTCTCTCCTTCGACAGCTTTGA

Os05g0460700	9,071	8,213	1,314	1,373	1,010	1,021	913	1,039	1,064	8.4	6.4	TTAGAACATGAATAACATTATGCAAGATACTTGTTCTATATGATAATTCTGTTAGCGATC
Os05g0463100	2,512	1,233	79	101	116	82	78	73	146	15.8	19.7	AATATCTGATGCATTTGTGCCCGTAAAGATCGTGAGGTCGACGTGCAAAGATAGCTTGAT
Os05g0467400	49,125	22,966	126	84	7,141	6,280	6,782	7,261	6,833	4.9	326	TAGAAGCTGGGCATGGTACTCCTATGAACCCAATGTTTGTTTTCAGGACACTTATCTCTC
Os05g0467600	6,643	13,794	2,619	1,385	497	461	494	449	1,077	13.4	5.0	GCTGTGATATGGATGCTTGTATGTTTTCCAAAGTTTGAGTCACCCGTTGAAGTAGGGACT
Os05g0467700	67,763	29,638	134	94	2,396	2,126	2,308	2,227	2,382	19.3	400	AGTGAAATGACTTGATTCCATCGCCAGTTGAGCTTTGAACCGCAGTCTAGAACAACACAT
Os05g0467800	42,178	14,144	81	303	176	89	70	66	691	96.7	156	ACTAGTGAATTTGTGAGAGATCTTATTATTATGGCTATGGAAAGCGTGATGTTTATGTGC
Os05g0468100	115,976	36,451	99	92	330	161	88	88	144	455	679	AACGTTTTGCAACTTCTCCTTGCTGTATGTGCTATGAACCATGTTTACTTTATTCAGTGA
Os05g0468200	29,120	8,205	80	75	159	89	70	61	127	146	200	TCGGTTCAATCAGCATGTAATGGCTACTATAAAGTACAAACAGCTTGCATGGCATCAGTT
Os05g0468400	5,354	3,160	91	89	1,079	957	1,005	993	125	11.6	45.7	GGCCTCCTTATTCTTCCTGTTCAGTAAGATTTAGGAGTCTGTGATTGTACTGTTTGACTG
Os05g0471800	992	1,318	87	82	144	179	74	83	282	6.4	13.5	GGTGAGTAGTAGCAAGCACCATCATATGGCGAAGGCAGAAGATGGAACCATTACAGTTAT
Os05g0481900	8,058	3,538	108	165	716	595	636	645	1,014	6.6	40.0	GTGTCAGCACCTCTTGTACATTTGATCGTAAAATACAGGATATCTCCAACTAATAGAGAG
Os05g0484000	10,117	7,831	91	78	92	87	72	60	126	90.6	106	TCAGAACTACATGAATCGTGAACGCAGTATGAAACTATGAATTTGTGTGATCTGATGCTG
Os05g0484700	27,544	8,004	107	327	181	103	108	106	118	124	79.5	TGGACTCTGGTCTGATGATTTGTATGAATGCAGCAACGTTTTGGCTTTCAGTACTTGGAT
Os05g0490300	5,166	6,091	671	577	1,325	1,217	1,362	1,284	1,412	4.1	9.0	TCTCCCAATGCCATGTCATGATTTTATGCAACTAACATCATGCAAGCTGATTGTTTGCTC
Os05g0500900	60,047	123,916	165	357	2,055	1,853	2,054	1,978	4,197	29.9	356	GTAGTAGTACGTACGTATGATCATCTAGCTATTGGGCTTTTGTTTTCTTTTCTTTTCTCC
Os05g0502800	17,403	14,156	535	193	4,140	3,994	4,180	4,326	2,151	5.2	48.9	AGACATGATCAGTTGCATGTAATATTCAATTTGTTTCGTTTACGGTGAACTTCACTTTGG
Os05g0506400	8,398	2,725	112	133	331	143	122	151	198	25.9	39.2	AAGCATGGGAGCAGCCTAGCCGAGCTGGTGATGGCGAAAGACTTGGAGCTAGTTGTACGT
Os05g0506900	2,218	4,449	81	78	353	308	301	335	390	8.8	39.5	CTCTAGTTTTTGCCTTTGTAATGAATTCCACAACAATATTGAGCATGCTGGACTTAACAT
Os05g0512000	2,988	4,441	448	545	865	814	800	843	373	6.6	7.4	GAGACTTAAATTATTTGAAAATAAGTTTACTATGCGTTGCAAAAGAAACTAGACTGCATT
Os05g0513200	980	2,580	122	116	495	443	480	479	240	4.7	13.3	CAGCTCAGTTTGTTGTAATGCATGAAAGTAATATATCAAAAGTAAGGTCCCGAAGCAATT
Os05g0515900	149,588	106,336	105	724	4,175	2,896	1,153	1,198	417	137	457	TAGGAACTTGGTGGTAGCAACTTTGGTGAACAATTGTCTACTATTTGTCCTCATGCCGCG
Os05g0517400	661,347	661,995	115	592	8,514	6,084	114	691	385	894	2532	TCGGTCTTCGGTCAGTTAAAGGTGCCTTTTCAGTTTCAGTTTGTTCAATTGCAGTTCCTC
Os05g0517800	30,493	21,484	1,232	237	3,275	2,972	3,165	3,238	3,579	7.6	47.3	TGTACTTGTTTATTAAGGCTTTGGACATGAAATATATCACATATGGAGGGGCTACTGACC
Os05g0519700	104,320	58,321	236	1,053	6,989	3,228	774	790	1,665	43.5	157	TGTGAATGAATGTGGGGTGTCTCCGTTGAATAAGCTGTGAAATATGGTGTTTTTCCGATG
Os05g0524400	100,011	160,969	405	104	28,708	26,514	27,549	28,397	18,100	5.7	619	GTATGAATCCACGGATACTCTCCTGGATTGCTGGTAACTACAAGCGTAATAAGAAAAGCG
Os05g0526400	108,020	102,100	1,161	875	11,099	9,647	10,832	10,702	27,831	6.1	104	GCGATGTGCTGAACTTCAATGAATTCGAATTATGCCAGCATGCTCTATCTATATCCTGTT
Os05g0526600	7,638	10,353	850	397	555	464	441	457	1,255	11.5	15.3	GCACTGAAGCAGACATGCAGTGTATATACATTGTTTTTCCATTCGGATATAGTAGCTTT
Os05g0526900	53,685	145,210	82	81	800	1,015	553	588	468	152	1085	CTTGTTTAGGTTTCGTTCAATAAGGTTAAACCACGCAGCATCTGGTGCTAGCGGTCTGTT
Os05g0535100	28,451	22,971	114	92	745	617	550	560	1,013	32.4	249	TTGGCGGTACAGAGTCATATGTGAATGAACGCTCTGCAATTTTAGCTGCTCTTGAATTGC
Os05g0537700	3,370	7,666	227	100	105	93	306	127	167	33.3	33.7	TGCATTTCTTTGTGGTGCAAAGCTGAAGGCAGAACCCGTTTAGTGCTGAATTGCTACAGA
Os05g0548200	14,025	6,420	82	78	91	84	75	71	497	47.6	119	AAACGTGAAGCCTGTTCTTGCGAGACAATCTGACAATTATTCAGATTTTTAGCAATGAGA
Os05g0551700	3,331	5,809	86	73	276	377	138	125	109	29.4	55.5	GCACTGTATGTATGTAGTGAGTAGTACTAATCATCTAATTATCCACCGTGTTCAGAATTT
Os05g0552300	106,958	128,697	4,728	3,631	18,527	18,038	21,765	21,181	24,178	5.4	28.3	ACTTTCGGAGCCTCATTGCCTAGATGTAAATAATGCTTCATCAATTGCTATTTTCTGATG
Os05g0556800	1,074	1,068	85	273	88	83	78	76	143	9.9	7.0	GTTGCATGGATCAGTAGACCGACTGTCTGTGCTTGTAACTGATGGGTTAGCTTGATTTGT
Os05g0557200	166,917	404,659	1,112	3,336	27,130	27,471	23,163	24,576	41,547	8.0	135	GAGATGATGGATGTACCACCTGTGTTCCTGGTGCGCTAAACATGTCTTTGACGACCGAAG
Os05g0570200	17,349	5,675	115	132	255	144	140	140	265	47.7	80.5	GGGGATAGGATTGTTGCTGATTAGTCTGGTACAGTTACAATGACACGGTGGATATTAGCT
Os05g0570300	25,355	6,668	82	80	139	81	63	64	97	146	161	GTCCTTGTCACATTTCTGATAATTCCTGATAATTCAGTAGCTCTCTAAATGTCAGTGGAT
Os05g0571600	231,322	77,498	16,990	9,118	4,793	3,784	3,688	3,859	6,690	25.9	10.8	TTTGGTTCAAATCGTGGTGTTCCTCTCCAAAGCTGTACGTACCTGATGGAGGTTTTGAAC
Os05g0572000	9,793	6,936	90	291	561	555	553	565	1,391	9.4	51.1	AGGTTATAACCTAGAAATATTAGAAGGATATCAGCAATAAATCGTCCCGAGAAAATTGGG
Os05g0573200	16,666	35,043	4,445	2,059	5,105	4,343	4,423	4,877	3,222	6.2	8.0	ATCACTTGGTAGGTGGAGATTACAAATAAAGTTTCAGAGCTATTCATGAGAAAGCTCCAG
Os05g0574000	14,839	6,219	169	166	186	111	172	137	341	42.7	57.3	GCATTTGACTGGACAGAGTTCTATTTACAAATGAATTATGTGATATGAGGGGGAAATCCC
Os05g0574900	740	1,058	78	77	72	66	65	63	137	9.3	11.5	TTGCATTTAGTCTGAGAGAGCAACATGTTGGTTTTCGAATTAATAATAAAATGTCGTTTC

Os05g0576300	28,100	27,570	114	121	553	522	494	559	588	49.8	237	TTATTTGGATATCTGAATTATGTATGGAACACTTGTACGCTATGAAAGTGCCTGAAGGCT
Os05g0578500	19,195	19,601	506	267	919	833	780	839	1,943	15.2	52.7	TAAACCTAGCTAGATAGAACTTGTACAGTACAAAACATGAATATGGATAGAAATTAGAAG
Os05g0580500	16,247	10,715	325	836	479	457	463	440	246	39.3	25.3	TTTGTGTAGGAAAGAAATTTTGTAAGTATGCTGAATGGCTTGATAGCTGGTGCAAGGTTA
Os05g0583200	9,534	10,230	89	127	937	836	866	858	754	12.2	92.8	ATCTTAAGCCATGTGACTGAGAGTTCGAAGTTATAAAGGATATTAGGAGCCATCTTCAAT
Os05g0583400	7,760	13,983	81	73	902	890	784	834	1,654	8.8	135	GCTGGAAATTCCAAAGATGAATACCTGTTTTCTTTACTGTATCTTGAATTCCAGTTCTTG
Os05g0584600	124,010	230,998	137	178	10,414	9,631	10,529	10,831	8,119	18.5	1084	AAGCTTCAGTTAGTTTAGCCATAGAAAGCTGTGATGTAAATTCTTACATATGTTCGATGC
Os05g0591600	9,131	13,557	1,857	1,864	707	611	592	617	226	29.5	6.0	TTTGACCCTGGAAGAAATTCATATAGCAGTATATAATTTATCCAACCAAAGCTATGTCCC
Os05g0594900	12,293	9,555	461	268	2,352	2,009	125	99	299	28.3	30.8	TTGGTTTCCATTGTATTGTATTGTTTGTGCAGCTGTATCAATGTACATGAATGAGGAAGG
Os05g0595100	98,057	96,904	25,028	17,143	10,245	9,384	10,318	10,083	10,220	9.6	4.7	ATCCCATCTGATGGACCGCATTGTATAGGGGGCTTGTAGGGGTCCAGCAGCTTCATCATC
Os06g0103400	107,344	77,714	123	99	11,287	10,506	11,313	11,138	16,818	6.7	827	AGTTGGATCTTGTGTCGCTGATGGTTCTACATATACGATGAAGAATATTTCTGGGATGTC
Os06g0103700	42,870	46,274	3,351	2,230	6,638	5,949	6,876	6,768	7,409	6.4	16.3	TTCGGAGACTTGTGTTGTATCTCGACAAAATTGAGTGTATTTACTGATCTGATGGTAGCT
Os06g0129600	1,229	2,202	81	76	92	88	84	71	258	11.2	21.0	TGGACAAGTTTGTATGGGGAGTAGATGTCATATAGCGAACTCTCAGTAACAAAGGGATTT
Os06g0132600	10,628	6,054	558	294	842	653	839	633	1,337	8.1	19.8	AGTTCTTTGTAAAGCCAGAGGAATATGAGATAAATGATGCGTAGGGATTGTGGTATGACT
Os06g0138900	199,325	105,307	2,096	1,254	19,705	18,596	18,596	19,170	23,490	6.9	89.4	CCCTGCGTCCTAAGATGTCTTTGAGTCGTACAGGGATGACAGTCTGATGTCTTTCAGTCG
Os06g0147400	16,543	13,129	4,261	3,025	1,688	1,577	1,640	1,608	2,029	8.1	4.1	CACCTGGACATTTCAAGGTCTATCTCACATTTTCTCCTCGATTGCATTACAGGGGGAAAA
Os06g0148600	18,423	22,292	4,946	3,917	4,297	3,798	3,918	4,338	3,728	5.2	4.6	TGCTACTTGTCATGTCTACTCTTATGCTAGAATGATTTGCTCTGGATTCAGAAAGCATTG
Os06g0151600	48,542	51,642	2,979	1,279	6,025	5,214	5,502	5,675	8,469	7.3	25.6	GAACCCTTTACCTCTACCTTAAGTATGTAAGATGTCTTCTATACACTAGTCTGAAAATGA
Os06g0158200	14,251	13,741	2,428	2,314	1,439	1,357	1,339	1,306	2,266	8.0	5.9	CCTCAGATGAGCAATGAAACAATTGACTGTTTTGCTAGAAAAAGAGAGAAATACAAGATG
Os06g0159400	6,087	3,833	178	109	880	764	877	826	874	5.7	34.7	TTTTGTAAAGAACCATCATTAAGATTTAGTACTAAGTTATGTGACATCGTATTTCAGATA
Os06g0159900	11,638	18,490	102	106	3,831	3,450	3,937	3,779	2,525	4.8	141	GCCTTGTACACACAGGTCGATATAATTCATGCCAGAATGCAACATAAACACAGCATTCAG
Os06g0161400	17,103	13,008	134	97	131	102	145	131	1,719	32.0	131	GTTGGCCATTATGCCGTGAAGTTTACAAACTGCTGAAATTTCCAACTACGTAGAATGTGC
Os06g0161800	2,549	7,362	239	419	84	93	79	77	422	23.2	13.7	TCCATACATTTGCAGATGTGAAATGTTGTGCTCAAGTCTGAATACACAGAGCTCATCTGT
Os06g0161900	2,644	7,367	556	232	83	97	84	72	482	22.0	12.3	TAGTTTCTCCATCGTTATCTGTGATTCTGTATGACACGAGTGATGATCATCCATACATTT
Os06g0162800	6,135	13,885	86	81	138	137	137	136	105	77.0	111	GAATGATCCCGGTTTGATTGATGAATGCTGCAAGAACATAATCTATATGTTAGTCTGAAT
Os06g0174300	18,612	9,398	92	83	4,162	1,709	98	80	102	59.5	152	TGTCGTTTGGAATCTTTGGATGTTAGTTTCCATATGTTTAAGCGTTTCTGCAAATTAAGG
Os06g0196500	2,539	2,472	95	108	230	175	225	251	632	6.7	24.8	CCACTTGCTGAGAGCACCTTATGAACCATGGTAGTAATATGTATCATGTTTTGTGTGTGT
Os06g0197200	1,469	3,723	80	79	270	256	246	264	134	12.6	29.4	TCGGAACAATTGTTGGGCTATATGCAAAGATTTGTGCATGTACTGAGCCAAGCGAGAAAA
Os06g0201000	3,679	6,747	118	229	424	409	376	409	778	8.9	30.4	GTGATGTTTTAATTGTTGATTCGTTCTGTATTCAGGTGAGATAATTAACAGTGAAGTTTC
Os06g0202100	26,361	18,170	8,775	3,310	3,868	3,104	3,390	3,732	2,277	7.7	4.1	TCGGTCAGTGGGCTGAACTGGATATCATCTCGTTGAAGGAATGGGCAAGAAATGGAATAT
Os06g0208200	19,338	14,012	1,622	1,178	3,708	3,456	3,639	3,652	3,155	4.9	11.9	GCTTGTGTAAAGATCATGAGATACAACTAAATTACGCCATGACAAATTCAGATTCATCTG
Os06g0212900	21,741	18,527	85	86	1,382	1,217	1,108	1,095	893	19.4	235	CTAACCACTAAATAATTGTTCATTTCCCTGTGAAATTCTGAATGAGACACCTCCTTTTGT
Os06g0214100	44,983	21,232	270	272	11,231	9,737	7,476	8,790	4,842	4.6	114	CAAGTTGAAATCATTGTGTTTGCCTGCCCGGTACTTATGTTACAGCTGTGTTGATGCGCT
Os06g0219400	12,454	7,702	379	120	1,431	1,314	1,479	1,213	1,415	7.1	45.9	CTGTAAATCTGGAAGCATGGTGCTAACATACATAACCAGGGGACATTAGTACTGTAAATC
Os06g0219500	566,040	261,061	200	185	33,405	15,221	10,665	11,071	13,084	26.9	1995	CCTGTGGGGGTTTCTGATGTTTTGTTCATCTGTGGAGTTTCTGATGGTGGTGAAAACAGT
Os06g0224100	88,063	71,863	7,591	8,289	8,527	7,861	8,175	8,293	9,256	9.1	10.0	TCGCATGTAAATTCTGTAAAGTTACATTGATCTGGTTCAGAGGTGGATGAAAACGTCCAA
Os06g0228500	13,785	8,528	135	101	1,680	1,592	1,724	1,655	1,086	8.1	92.8	ACAGGTGGTGTCAACCATGATGTTATGCATAAATCACTTGAGAAAGAAATCCATATGCCG
Os06g0237100	6,960	6,968	735	418	1,876	1,653	1,415	1,574	1,828	4.0	12.6	AGAACAAGGAGCTTCTTGAGCGCTTCATCGACAGGGAGGAGATGCTTGGAGGTGGTCCCA
Os06g0238700	54,674	46,167	159	141	4,544	3,541	967	979	1,621	28.1	335	GCTGCTCTCGTTTGCAGTGGCTCGTTGGACTGTGACGTCAAGCTTTGGAGAGTGACGGTT
Os06g0243900	996	602	80	81	71	68	61	69	96	9.7	9.6	CCACTGCGCATCTTCATCTAGTACTCTTTGTTCTATATATAGAGTATAAAAGAGTGGTTT
Os06g0252800	8,554	25,417	111	769	200	214	170	170	193	77.5	50.6	ATTTTCTCGCCGTTCACCCGATTGTATTAATTAATTTAGGATAAAAATCTGAATACTTGG
Os06g0257200	145,860	75,872	9,647	7,234	16,191	14,106	14,580	15,264	20,386	6.0	12.6	AAAGAACTGAGTACCTTATTACACTGTGGCCTGATCAGAAAAACAATCAAATCTTCAACC
Os06g0272500	3,546	4,835	85	81	953	880	754	811	1,061	4.4	49.9	ATACTTGTGAGAGTTGTATTCAAGCTTGTTGTTACTAATTGGGAGAAGAGGGTTCCTAAA

Os06g0281300	2,205	4,297	712	126	211	431	201	114	512	9.3	10.3	ACGATGGTGGTGCATCAAAGATGGATGGCTCGGCTTCATCTTTGGTCGTGCGTCACCGCA
Os06g0288400	4,035	5,455	1,031	645	375	359	341	336	725	9.3	5.8	AACACGACCTGAAAACAAGTGACCATGATTTTCCTTTTTTGTTGAAGTTAGTGAACAATC
Os06g0298500	3,521	3,168	1,263	573	813	755	831	804	840	4.1	3.9	GAGAGATGCACTATACATGATGTATCCTGAAGCTGGTCATTCCGTTTGTTTGGGAAAGTA
Os06g0341500	39,897	13,843	81	81	194	105	91	82	158	177	291	GACCACTAATTTTTGTAACAGCCAATGACATCATAATATATGAAGGCATCTCTCCAGACG
Os06g0342700	2,132	2,674	313	726	303	263	341	355	570	5.7	5.0	TTGCCCCATCTCGAGTGCCATCCTCTTCTCAATAAGAGTAACCATTGAAGTTCTAACAGA
Os06g0343900	1,584	1,423	244	342	252	240	267	216	297	5.6	5.2	TTTTTATGTTTTATCCTCCTTTTTTGGGACTGTTTTACCCCTGGCCCCACTTGTCAGGTA
Os06g0360500	2,992	6,117	453	394	879	794	781	763	613	6.1	10.1	ATTCGTGTGGCTCCTGTTCTTTGCTGGTTAGAGATGTTTCTACTATTTTCTACTCCTAAT
Os06g0473000	42,331	26,724	79	166	423	312	201	195	1,192	59.5	294	GAACAGGTCCTCTGTTTTATATACATGTTATCTGAATTGTTGAGAGCATGCTACCCCATA
Os06g0487900	130,794	181,968	11,968	5,321	34,876	35,500	27,966	28,206	38,030	4.5	19.3	CGCTCTTAAAACCATGCTTTTGGGGACACTTGTACATTTGGTGCTAGTAAAAGTCAGGCG
Os06g0492900	5,655	4,796	83	74	127	101	62	55	133	50.1	66.2	TGGCTTCTACAAGATTGGCCAATGAAGACTGTAAGCTGATTGTCTATGAGAGTCCATTTC
Os06g0505700	30,324	33,160	3,552	3,259	6,734	5,815	5,333	5,599	7,464	4.8	9.3	AATCCTTGTACCAGTAGAGCTAGCTATGTGAGGATAAACAGAATTTAGGTGAGGTTGAGG
Os06g0507400	25,419	53,707	9,677	5,217	11,484	9,319	18,431	11,595	7,137	3.9	5.2	GCATTGTTATCGAACTGTGAAAAGTGATTCTTCTAATCAAAGTTATGCTGAATGGTCCAC
Os06g0520600	9,136	24,129	216	82	96	107	78	77	1,176	46.0	111	TCCTATGTAATTGGTAGTATGTACAGTGTGGCCTATCGAGTTGTTTCGCTAGAGAATGCA
Os06g0524400	20,411	13,703	102	89	2,838	2,421	2,636	2,618	3,216	5.8	176	CAACTTGAGATAGTTGATTTAAAGAGTCAAATATAAGTCTCATCAGCTACTCGTCTTCTG
Os06g0539400	11,903	14,587	135	361	1,153	961	1,010	1,060	2,578	8.0	59.7	CCACCCATGCATTTAGTTGGAACTCTATGAGCAGAGGTTTTTCTTTTTCCAATTACATTT
Os06g0573600	129,860	137,869	249	289	35,364	35,056	34,822	35,617	33,977	3.9	499	GGTCGCCGTCGATTATTTATTATTTTACTAGTTATTTATTCTGAGCCGTGGATGATGGCT
Os06g0574900	359,489	346,384	312	381	10,007	7,017	154	579	116	824	1024	CCAAATTAATTTATATGTAATTTCTGTTGCTTGCTTGAAGAATTAATTACTTCATCAGTG
Os06g0583500	3,765	5,218	668	80	864	809	814	820	746	5.6	19.2	GATGATTATTCGAGATACACTTGGATTTACTTCATGAAACACCGTTCACAACTTTTATCC
Os06g0592500	333,066	144,398	1,795	780	7,014	5,406	5,636	5,866	3,472	48.2	185	AAACTATGATATGCTAACTGGCTCAGACGCATGTGAAGTGATGATGGCTAGAAATTGAAT
Os06g0602400	274,272	178,724	72	78	3,320	1,767	63	83	142	908	2951	GTGGCAGCTGATCGACACTGCTATATTTACCAGTGTTTAAGGAAGAACTTTATATTCCTT
Os06g0610100	40,324	26,003	95	334	2,348	1,445	90	106	237	102	182	AGCTCCTCTGCGAGAAGTCGTCCACGATGGTGACACTGGAAGGCAAAGTAACACGAACTC
Os06g0611000	56,971	61,011	12,792	3,568	9,397	8,821	9,042	8,824	11,423	5.8	8.7	GATTTGTTGCTGTCCATTTGCTGGTAGTGGATCGAATGGATCGAGTGGGTGCAGCCGTGC
Os06g0611400	104,907	78,250	256	143	850	580	456	188	203	299	474	GACCGATGACGAGATTGATCCTTAATTATGGGGACATCTTGTTCTCCCCTGTAATGGAAC
Os06g0612200	100,329	80,450	135	109	20,684	19,084	18,691	20,076	21,056	4.4	741	AGCAGGAAACGAACATGTGAACACTGATACTCCCTTTGGTAGTAGTATGGACATTAGTCT
Os06g0613400	4,312	6,990	97	122	318	292	277	305	376	16.4	50.5	AGAATGTACTTACTGTCACATCGATTCTATGTAAATGACATCTGACATTGAAAAGCAGTC
Os06g0627500	65,145	46,097	477	164	342	197	598	135	173	253	196	TTGAGTTAAAAAAATGTAAAGTAGTTATGGTATTGGTTGTGCTACTAACAAGAAACAAGT
Os06g0630200	653	904	118	107	104	100	124	130	158	5.7	6.8	GATGGAACCATTACAGTTAATGGTGACAAGCAGCATAATCCTGCCGCAGATAGGAATGGT
Os06g0633500	59,907	47,348	6,606	7,000	4,722	4,193	4,579	4,582	7,021	9.5	7.8	GTGCGTAGCTGTCATGATTGGTAATTGAACGGTAAGAACAATTGCTAGAATTTAGAACTG
Os06g0634600	100,759	96,881	12,534	7,938	18,899	17,675	18,775	18,836	16,621	5.6	9.9	CCAATAGCTGCTCCAGGTATGAAGAGTGTAAAACAGTGAGATCTGGGTATCTCGTCCTTA
Os06g0635200	119,320	86,822	2,064	1,744	7,142	6,358	5,952	6,536	16,033	10.0	53.6	CTGTGCAGTTGGATCCTCGTGAGTGGAGTCATTTTTGGGTGCTCACGATAGTAGCGTGCG
Os06g0635300	86,747	56,285	103	123	797	474	73	124	101	448	622	CATCCATCAGTACATCTTTGTCATGTCAAAGTATATATGTCAGTTCCACCATGCTAGATA
Os06g0646900	32,655	27,063	575	204	1,050	770	588	562	922	36.5	86.7	TCTACGCTGAGTATTTCCTTATACCATTTGTGCAGTGAGCACTATATACACAAGGGCAAG
Os06g0649800	24,741	39,941	94	78	1,871	1,841	1,686	1,737	3,858	12.0	368	GAGAAGGATGATGACCATTTTACTGATGCAGAAACTGGACCATCTCCATCAAACCAGGCA
Os06g0650600	26,795	39,534	97	75	4,468	3,862	4,303	4,353	7,286	5.9	382	CTCTCTTATCCCCGGATGCTTCAGGGGATCTACAGTTTAGTCAAGTTGTACTAGTAGCTT
Os06g0652100	40,545	14,740	330	194	1,190	416	94	80	338	84.7	96.5	GCCGTCATGGAGAGGGCCATTTCCGGCCGGGAGTACGAGAAGCTCGTCATGTTCGACTGA
Os06g0666600	222,668	242,176	29,440	13,540	9,013	7,689	3,625	3,382	1,768	75.2	11.6	TGCCGACATGAAGATACATGCTGTGTTGTGATAATCCGAGCTTATTTTTGGCCTGTTTGA
Os06g0668200	120,894	139,681	37,092	19,852	26,642	25,102	22,753	22,165	22,009	5.6	4.8	AGAAATGCCCGGCACAAACAAACTATAATGGTGTACTATATTTTGCCATATTCTAGTTGC
Os06g0672700	52,400	51,417	86	84	11,677	10,794	11,357	11,297	13,515	4.2	610	TATGTACAGTACCTTACTGCCTTGTATACATAGAAGATAGAACCTTGTGTGAAATATGTG
Os06g0678700	925	2,684	188	190	163	146	173	180	104	12.0	8.3	AGTTGGATTCTTGACTGCTATTCAGATTTGGAAATGTCAACAATCTGCAATTTTTGTGCG
Os06g0680900	14,322	6,152	1,285	829	928	629	502	503	1,445	9.9	9.1	GTGTGCAGTAGAACACTGTACACTGCATTTCTGCATTTATAGACAATAGGTTGTGTTCGA
Os06g0682900	28,399	27,017	7,414	3,871	4,993	4,376	4,730	5,133	5,770	5.3	5.2	TCTCTACTCCTGCCCGGAAACTTATTACTCCTTGTCACAGTTTATAGGGTGTTCTTTTAC
Os06g0685200	10,476	7,801	112	100	149	122	100	89	116	79.1	85.6	AGTACAGTCTCGTCATACCTTGATTTCTTTTTTCCTTCTGTTTTACTTGAGAGAAGGTGA

Os06g0693300	102,068	41,179	4,124	3,005	1,653	1,151	1,333	1,417	2,429	35.5	18.4	TTTGCACTCGGAAACTGTGATTGCTGAATGGATCTGTTTATTACTGCATACAAAGGTCAC
Os06g0704800	4,655	6,001	183	560	364	330	310	356	571	12.0	16.5	GAGTCTAGGAGGATGGCTTCTGTAAATGAGAGGGTAAGGCAAAGAGTTGCAGAAGTAACT
Os06g0705000	7,045	5,532	78	77	1,474	1,242	1,214	1,323	1,472	4.5	80.6	ATTGTACAAACTGATTCTTTGGAGGAGATATTGTACACCTGAAACTAAAGCTTTGGATTG
Os06g0710900	11,511	14,856	84	73	2,188	1,865	1,926	2,121	2,539	5.8	167	ATGGGATATGTAATGTGGTCAGGAGATGTAGAAATGAAGTACAGACTTCTTGCCAAAATT
Os06g0712700	134,498	165,622	2,057	432	12,694	11,654	11,405	11,922	14,871	11.2	158	ATCCAGCGGTTAAACCGTGTGTTGTCTCTTGACATTTTGTACCAGTTACTGATGATGTTG
Os06g0713500	115,530	98,298	3,589	2,967	22,702	19,783	9,146	10,346	14,619	7.4	32.7	AACTTGGAGGCGATGGCGGCGGAGGCTCCGATCCTGTTGGATCGAGAGAGTTACTAAAGT
Os06g0724500	30,840	43,908	8,953	6,783	5,029	5,109	4,789	4,747	8,367	5.7	4.7	GCCTGAGATAGCTAAGCAAAAGCATACTTACATGTGGACAAATTTGAGTGGATGGAGAAT
Os06g0724600	1,881	3,195	84	542	89	81	68	75	144	23.2	11.5	TGTTGGATTGGATGATGGAACCGAATGGATCATGTGAGTTAATCTACTAGTACAGTATTA
Os06g0729300	165,470	217,613	772	166	27,789	26,287	20,813	22,177	33,204	6.7	531	GGCTCTATTTGTACTCTAATTCGTATGGACCTGTTTCATCATTTCAAAATGGTCAATTGT
Os07g0108900	10,327	14,969	742	969	2,132	1,756	1,787	1,677	1,583	7.3	14.7	GCCTGCTGCCCCCTACCCTACAGGCTACATATGATTTGCAAGAAATTAATTATGAGCAAG
Os07g0112800	35,148	33,458	5,269	3,348	7,413	6,716	6,899	7,144	9,905	4.1	8.2	GAGTGGCAGCTGTAATTCGTATAGTAAAAGTGGGAAATCCATTCTGCTATGAGATGTGCC
Os07g0113500	12,330	8,222	383	209	2,072	1,894	2,469	2,127	1,216	6.3	35.6	GGTTACATTTTACAGTCTGCTTCCGGCTTTCCTGATCATGTTTGCAGCCATGTTGGGAAA
Os07g0114500	16,629	21,507	2,222	1,812	3,429	3,034	2,962	3,137	4,166	5.2	9.4	ATGATTTGCCCCCCTTTCATATGAACAATTAGTTAATGATTTAACGTGTCTGACAACTTC
Os07g0120200	7,565	16,646	1,088	519	246	259	338	278	306	38.5	14.9	TAGGACCGTTACCCTCAATCTTATAGGTTTACATTTCTTCTTATTTGAGGCAATGCTCAA
Os07g0120400	40,101	35,625	153	426	1,106	988	906	961	1,160	35.3	148	AACTGAGAAAGGATGGCTCACACAGTGAACATTTGTTTCTTCTCATTTAACTGCTTATGA
Os07g0120600	32,962	32,218	1,677	732	2,173	1,854	412	391	450	51.3	29.4	CTACTATGCCGTCATTCCCTACATGAGCTTCTACACTTCAGATCTTGCTAGGAAGAGGTT
Os07g0124400	22,998	49,561	112	534	1,030	943	958	965	4,031	17.0	138	CTGCACAAACTCGCCCATTAGTAAAAACATTTGTATTGACGGCTTGCAATGTTAAATCTC
Os07g0124600	35,998	34,808	278	979	7,099	5,984	5,113	5,853	8,570	4.9	67.9	CTGCTTCTTGTACCGATGTTTAAATTCTTTGTTGATTTAATGTACCAGGATCAGAACATC
Os07g0129100	35,387	26,710	2,213	1,271	5,397	5,114	5,231	5,028	7,445	4.9	18.3	AAAGGGTGATTTTTACAGACGATTTACCGCATGGAAAGATGGTTCTCAGCCGTATGGAAA
Os07g0136300	93,443	77,997	13,474	8,847	627	462	281	294	455	202	7.8	CATCGATGTGTAACGTACCATCGTACTATAGTTGCACTCTATAATAGTTTGTGATGGTTG
Os07g0136400	1,564	1,811	84	346	97	83	73	167	116	15.7	9.9	CCCACACCAATGCTTCCTAGGAGTATGTAATGATCATCCTGCTAGCTCTATGGCAATCTA
Os07g0138400	4,131	5,241	116	81	113	128	107	72	191	33.2	48.0	CAGGGTCTAGGGGAAAAAGATTACTAGAACCCATGAATTTGATTTTGAGTCCTAATAAAC
Os07g0143900	3,462	1,871	233	78	110	103	387	91	185	15.8	18.9	AATCTCGGGCTGAAGCAATTTGCAGCTCATTCTAGCTCCAATATAACACCTGCCAATTTT
Os07g0151700	12,319	18,907	85	84	106	110	70	75	214	111	180	TTGGCTATGTGATGGTTAAGGGTGGTAGTGAACACCATATTATTGTTGCATCGATCTTTA
Os07g0151800	246,844	230,442	23,604	14,057	13,674	12,464	13,400	12,998	15,211	16.9	13.1	AAATGAAGTCGTTTTCACAAACAGCTTGTGGCTATGACATATTTATGCTGGGTTAAGTTG
Os07g0151900	1,326	2,297	97	204	154	145	156	145	260	8.8	12.4	CATATTTGCTTACACGAGTATATAGGGCATGGAAATTTTCCTCGTTGTATTGTACTACCT
Os07g0154400	8,404	7,332	124	111	1,220	964	919	874	657	9.8	66.8	AACAATGATCACAAGCAAGATACCTGTTGCGAAGAGATCCCTGGAGCGTTTCGTATTCCA
Os07g0154800	64,738	55,481	5,643	1,794	4,144	3,753	4,091	4,338	9,763	9.5	18.8	TTTATATTAGCTAGGGCCTAGAAAATGCCTTCAGTAATGGATAGCGCTAGACCCGTGAGG
Os07g0158400	8,691	4,720	259	218	1,195	1,008	1,127	1,081	867	6.6	26.9	AAGCCGATTACGGAATAATTGTTGGACATGATAAGCAATTTACTGAGGAAATTTTGATGC
Os07g0163500	178,409	124,579	6,309	547	16,909	15,274	16,455	17,094	29,503	6.8	80.2	CTGTGCGTTGTAACGGGACAATAGTTGTACATACATAAACAATACATAAACAATGAATGG
Os07g0165700	24,696	16,414	306	88	1,724	1,487	2,031	1,535	3,058	8.9	123	TTTTTTGCCCTTGCTTTTGGATGGGACCATTCCTATCAAAACAGTAAATACTGTTGTTCT
Os07g0168700	13,272	28,703	103	91	1,801	1,920	1,439	1,516	373	24.8	202	TAGGACCTAGGGGGCATTGGAGGACTGAACTTTGGGTTCAATACCAAGATGCAAATTCTT
Os07g0170900	7,144	6,909	88	88	628	557	548	564	366	15.3	80.2	TTTGTTTCTCTAGACTATATATGAACTCTTATGCTTTCAAGAAAAAGCAGGGCGTAATGC
Os07g0183200	3,594	8,074	98	177	172	293	98	77	148	37.5	40.9	GGCCAAGTACACCTGCTTGTGACTAACTCAAGTAAAAATTAGTTCTGTCACTTGCGAGTT
Os07g0183300	5,735	5,292	87	114	255	139	78	78	132	43.6	55.2	TTGTGACTTTGCGAGACTGGGTCCGTCATGAATCATCTATGCCAGCTTTGGTCTGAATTT
Os07g0184200	20,895	12,501	74	74	173	110	66	73	149	134	218	TGCTAGGTGATTTCTTCATGTGAATTCTATCTGTGAGTAAATTTCATGCGAATTACTTCA
Os07g0189400	26,985	44,505	3,562	4,838	116	131	68	71	117	333	8.3	TGGGCAAAGTTTTCACAGAATTTTATATTCGTCTTACTACATACAGATTGCATTGTTCCC
Os07g0191700	103,320	93,368	6,926	2,964	19,024	16,955	16,071	15,814	17,156	5.8	21.7	TCGGGGATTACAGGACAGGTCGAGGTATTGTTTTTTATGTTTGAATTTGGTGAAAAATGA
Os07g0218000	1,219	1,428	126	134	275	254	354	305	304	4.4	10.2	CATTCATGAATAAAGAGGTACTCTGTTATGAATGTTTAAACTTGCCATTGCTCTATCGAG
Os07g0228900	7,625	10,354	116	109	505	464	354	354	915	14.4	79.0	TCTGTTGTAAGGATGTTTGTCTCTCGTGATATAGGGATTAATTATGTATTTGAGCATGGT
Os07g0229100	6,785	4,016	117	161	709	551	587	557	1,089	6.5	38.1	TGCTGGTGAAAATTGTCTGATCGAAAGTTTGTTCCATTTAAATGTGAATGCTGCCTGACC
Os07g0229200	5,460	6,871	93	90	477	423	418	455	427	14.1	66.9	TATACTTGGGTATTGTTGACTGCACGCACTAACAACTTGGGCCCCAACGTGTGTTTACAT

Os07g0258100	39,308	37,160	84	78	6,508	6,149	6,219	6,400	8,714	5.2	471	CCATCAGTATATTTTGTACTCTCTATCCCAATTTAACTATCACCTAAGCAAAGTTCTTCC
Os07g0274700	75,382	60,107	7,369	3,962	20,770	19,808	19,427	19,948	11,659	4.4	12.5	TGAGCGTATACAAATATTGGTCTCTGATCTGAATAATATTCATCAGACAAATGCGTATGC
Os07g0297300	8,307	4,695	648	230	713	504	694	395	635	10.5	16.2	TCATTTTAACATGTTCATAACAGTCAATTTTTTAATTAAACAAAGGCAGAATTAGATGGC
Os07g0408100	11,060	5,554	2,007	1,546	1,968	1,250	1,425	1,374	1,063	6.2	4.5	CATGTTACAGAAAAACATCTGAAATACAAAGTAACTTGAAAAGGAGCGAGACGCAAGTGG
Os07g0409500	206,770	108,632	207	532	1,707	1,009	649	628	249	314	452	ATCGAAATGTTCAACTGCTTAATTGTTTGCATCAACTGAAATGTTTTGCCCCTGCCGCTT
Os07g0411300	6,577	8,692	105	98	173	195	86	86	178	50.6	74.2	AGACTAATAAAAGGCGAAAGTGTTTTCTTCCCTATAAAAGATATCCTCTCGTTGCGTGCA
Os07g0419300	5,361	1,640	360	145	650	550	577	584	320	6.8	13.0	ATGTATGTTTCGGAGCATCTCTCAAGTTTCGATCATTATTTGGAACCTTCCATGGGAATA
Os07g0421000	31,140	25,194	89	81	1,986	1,656	1,593	1,783	2,224	14.2	330	CTGTTGGGCAATGTAGGTATGAGCAATTCGAGTCATCATGTTCGAATATGGTCATCGTAT
Os07g0439100	26,944	19,562	731	714	844	680	437	357	331	54.0	31.8	TTAATCCTTTTGTGCTCTTGCTGCTGGGGGAGGCCTTAATTGAGATGGATATCTGCCTAT
Os07g0456900	3,303	1,102	151	109	131	116	216	141	265	9.7	14.9	TTCTGGTGTAATCTGTAGACTAGAGGCAGAGTAGATAGATGTTCCTTAGTTTATTGACTA
Os07g0464600	24,736	29,272	5,312	4,220	4,603	4,159	3,776	4,397	5,915	5.4	5.7	ACATGTATCAAAGTTTACACTCAAAACACCGAAGGTCTCAATAGGCTGTGCTCACAAAAT
Os07g0468900	1,932	2,075	630	190	495	477	454	484	532	4.0	5.8	GCAACAATCAAGCACAAAATAAAACATAGTTGGGGAGTTCATGATGTTTCAGAAACTTGG
Os07g0471300	47,576	30,977	317	238	6,105	5,594	6,092	5,976	2,144	10.8	140	CGGTGTTACTATCTCAGCACTTTGGATGTTTTATTTTGTTATGTCTGAAGATATAGACAC
Os07g0476500	68,222	69,234	14,594	15,995	13,951	12,147	13,040	14,105	17,942	4.5	4.5	GATGCTTGGTTGTTTCATTGTAAATTTGAAGCCCATTTGGATCATGAATCATAGAACTTG
Os07g0486000	13,161	9,971	2,314	2,177	420	316	274	241	414	32.2	5.1	GTAAAAAGGAGTTTTTGTTTCTCTCTCCTACAGCTGGCAGCATGTATGGATTATGGTCGT
Os07g0489000	25,899	9,662	82	88	111	90	72	92	99	168	186	ACAGCTGTAATGTGTACTCTATTGTAATCTTGTTGTGGAATAAACTACATGATGTTCAGC
Os07g0492300	1,706	1,115	439	103	161	135	133	119	174	9.0	6.5	GTGGATTCGTTGTGTATCTATCCTATGTGGCATACGAGGTAACGCAAATGAGGTGCTGTG
Os07g0503700	55,815	53,692	4,480	3,113	12,359	11,183	10,443	10,841	6,558	6.4	14.7	GTTTATTGAAAGCTTGAAGAATCTTGACATGCGGACTTTCATGCTAGCAAAGAGCACTAT
Os07g0505200	100,082	142,464	149	166	16,252	15,643	14,691	14,686	27,518	5.8	759	TGTGCCTATGTATGCTGTTGTGCCGGGATGGCAGTGGTAATATATGCTGTTTGAGTCAAA
Os07g0507500	13,231	14,905	1,111	938	694	631	558	295	203	43.4	13.8	CGTTGAATTCAGGTTATGTAGCATTTGATTTGACTACTATGGATTTGATGACTACGCTAG
Os07g0510800	9,581	12,872	240	355	871	814	733	764	1,449	10.4	38.1	GAGGGCTAAGAGAGAAGAGGGTGTCGAAAGTGTAAACACAAAACACAAAACTATTCCCCA
Os07g0511500	28,869	25,087	6,544	5,404	7,445	6,702	6,239	6,317	6,213	4.2	4.5	GCGTCGCGTTCTTGTTGAATCTTTGCAAGAACAAAATACGGAGTAGCTGATAGTTTGCCT
Os07g0513200	2,588	870	89	81	91	82	76	89	220	11.0	17.7	CTCTGTATTTCCATAGTGAAATGATAGAAAAGGGATTCAGGCTTACTGCAAGCTCATACA
Os07g0514400	927	1,965	178	159	155	148	152	142	242	7.1	8.0	TGTCGTCTGTTTCTTCTTCTGGTTGCTACCTGCAAATTTGCAAATACCGTGATTGTCATA
Os07g0516700	208,666	147,284	92	86	11,777	10,500	10,749	10,975	5,863	21.8	1975	GTATGCGTTTAGGTGGACTGTAGCACGCAAAAAATGTAATGTAAAGATGTTCCTGTTGTG
Os07g0517400	68,003	28,169	3,779	1,178	1,319	960	820	844	1,911	32.2	20.7	TTGGCTTTTGGGAGGTGATTTAGGGCACACTCTAGAGGTGTTTGCCATGAGCTTTTTGTA
Os07g0518200	2,431	2,255	419	428	236	201	268	287	568	6.3	5.5	TTTTTTGCCGGGTTGGCCGAAAGAAAGGGCGACCAAATTTCATTAAGATTGGGTGTGTGT
Os07g0546400	49,523	81,360	91	83	9,201	9,187	9,202	9,298	11,880	6.1	732	TGTGAAAATTGGGAGTGTCTGAACTCTGAAGAACATGGCAATGCATATAGATTGTGAATA
Os07g0548000	7,341	3,332	81	85	926	563	335	352	191	16.0	59.6	CGCTGTTTATCCTTATGGATTGCAGAACGTTTTCTTCAATCGGAGCTGTCAGATGCTTCT
Os07g0549600	26,181	23,243	189	180	258	222	207	200	488	75.2	134	GATGACATAGAAGGGGGAAAAAAGGACTAAATTTTGTGTTGAAATTGAGCACAGTGGCAC
Os07g0551300	13,544	19,124	106	97	2,355	2,004	1,955	2,223	2,450	7.0	159	TGTCATATATAAAATGGCATGTAAGTTTTGTGAAATGAAGCATGTGTAGATGATTGTGGT
Os07g0552800	1,548	2,238	108	811	190	202	238	198	132	11.3	6.3	TGCTCTATACGAGTGAGACTTGGATTGTTCTTCTTTAAAAATGACAAGATTTGAATTTCT
Os07g0554900	40,722	43,569	6,119	1,151	519	411	367	294	101	212	15.9	TACACTTTCGTTGTGTTTCGATCTAAGCTGCTTGCTAGGTACTAGCTAGCTTATTATGTT
Os07g0556000	227,518	126,509	370	515	10,132	8,998	10,365	10,910	23,974	10.9	388	TTCAGAAGTACTGGATGTTAAGGGCGATGAATATATTGTGGTGAGAGGGAGAGGGGGATA
Os07g0561300	16,271	17,507	537	709	1,666	1,529	1,773	1,676	1,164	12.1	27.4	ACGACGCCTTGTGTAATAAGTTTCATATAAGCATCGAATGCATGAATTATCAGGAGATCT
Os07g0564200	80,771	82,518	93	95	12,832	10,785	9,974	11,475	21,626	5.2	869	AGTATGTTGTACATATGCTGGAGATGAAGAGAGGAAGTTGATTAAATTTTTGTTACCGGT
Os07g0566500	11,816	5,158	77	78	120	72	68	64	117	81.6	101	CGTTTGTACCATATATAGCGGATGCAGAAAGTAGCTAGTTGCACTGTTCATCATTATCCC
Os07g0572500	9,638	5,690	141	370	2,019	1,799	1,778	1,857	988	5.5	32.4	TGATCACGACATCTCTATTCCCTTGAGACCCTCGATCCTTCAAATCCTGGCATTTGAAAC
Os07g0572900	14,737	7,597	94	107	2,104	1,846	2,000	1,982	2,027	5.3	106	TCGCAATGATATGAAGTTCAATTTACACCTTGACTTTGGGTAGTTCTTTCTAAAGATGTG
Os07g0588500	11,018	9,301	118	105	545	402	129	110	175	49.8	90.7	ACGCAATCTTTATCCGTGATGTCAACGAAGTACAAGTAAAGCCCAGGCCCAAGATCACAT
Os07g0591700	72,810	76,576	146	141	3,674	3,319	3,478	3,288	5,264	17.6	520	TTGGCCACTAGAACATGTAAGGAACTTCATAATATGCCGTATGATGCATCTCTATCTGAA
Os07g0595800	39,599	51,176	94	445	5,925	5,393	5,895	5,741	8,838	6.3	220	TGTTGTGCAAAAGATGGTTTCATACACTCATCCCTGTAATAACATTCATCTAATCAGATT

Os07g0603100	63,948	64,748	4,285	3,141	14,817	13,768	13,536	14,511	13,259	4.7	17.5	TATATGCATTAGTATTTATGGCACGCAGATGGATGAAGGATCTGTTGTGTGCTTTTCCTT
Os07g0603700	112,554	49,615	162	406	728	328	159	151	838	156	291	AAATTTGCTTTGCCAGTCTTTTGGTTTAAATCGAGGCATTAGTTGTGAAACATCATGAGA
Os07g0605200	15,260	16,145	662	402	6,434	5,931	6,469	6,367	2,147	4.3	30.4	CCATCTTCCAGCGATATTGATATATCGGCATTCGGCATAGCCAATATATATTAATGTAAT
Os07g0608500	193,431	186,091	15,326	6,831	29,407	27,653	31,292	31,126	46,718	5.1	18.5	AGTAAAGAGTTCTAGTTTTTAAGTTGCAAACATCAGCAACTAATACAAGATTCGTCACTA
Os07g0614000	174,014	222,884	1,057	408	12,416	13,091	15,065	16,154	12,387	14.9	300	ATAACTTCCATGCTGTAAAAGATTTGAAAGACTGGTGATCGTCCTATATCGAGCACTTTG
Os07g0615400	80,631	113,944	172	94	6,520	6,438	6,018	6,405	7,796	13.6	753	ATATGTGTGTGAAGGATGTAAGCTGACAATTTTATATAATCTTAGTCTAATGTTATTGCT
Os07g0618700	33,121	45,928	3,871	2,940	4,689	4,233	4,787	4,714	4,177	8.9	11.6	TTTTTTAGAGTGTAGCTTTTCCAGCTCTTGATAATGGTTAGTAGGGAACCAAAGTGTTCT
Os07g0622900	13,483	19,150	130	322	3,352	3,178	3,171	3,180	2,693	5.5	78.5	TTATCTGATACAGTAGTCTCATGTTTTATCAGACACTCTTGTTATTCACCAGTATATCGC
Os07g0625400	598,232	321,072	87,135	38,917	12,809	6,047	2,599	1,492	3,486	115	7.5	AGTCGATTGGCTGTGTTGTTGAATGCTTTGAACTGCTGGATCGCTTGCATGATCGTGAAT
Os07g0625500	150,704	50,251	145	201	12,772	2,883	192	245	219	174	510	TGCCCCCGTAAGCCGTAGTGTCCTCGTCGTAACGATTGTTCTCTCGTAGTTGCGCGTTGT
Os07g0625600	520,634	192,974	213	222	21,968	6,340	582	569	781	222	1458	TGTGTGTTGTGTCTCTGGTGGATTCAGATCTGATCAGCTTACCTTTGAGTTCGTGCATCC
Os07g0626200	40,509	21,836	1,155	181	2,713	2,111	2,020	2,175	1,975	14.1	65.0	TTCAATGTTGATGAACTGGGGGAATGCATATGTGCTAAGTCGCAGCATTTCCCCCCTAAA
Os07g0633400	1,061	1,748	110	104	537	498	524	534	168	4.6	12.7	CATGTAGATCTTGTAGTAGAGTCTCAAAAAAGAGATCTTGTAGCAAGAGTGATATACACA
Os07g0642400	48,677	44,994	6,829	4,214	6,528	5,819	5,168	5,199	10,186	6.2	8.7	GCATTGCATCCGGCATCCTGTCCTTTTCCTTTTGCTTATTTTTGTATACCATATTAGCGG
Os07g0662700	5,508	3,430	102	156	1,006	886	931	912	854	4.9	34.3	TGCAATGATTTTTGGTAGTAGAGAAATCTGGAATAGTGGCATAAAGTATGCTTTCTTGTC
Os07g0674300	3,136	2,756	89	91	445	393	403	425	464	6.7	32.6	ATTATTTATGACTTCTTAGAGCAAATGTAGCTACTGAAATATATATCAGATTTTGCTGTC
Os07g0679400	2,904	893	103	68	99	67	132	64	140	14.6	19.3	AAGTGTTAACTCCTGGTAGGAGCCTTAATTGTAAAAGAACTAGCTCATCTTTTTAGCTTT
Os07g0688000	1,814	1,199	97	83	93	83	90	77	239	10.3	16.4	AATATCACAAATTAGAACATGCTTGTTTCTTGAATATTGGACAAATATCAGAAAATAGAG
Os07g0689300	12,364	16,103	594	527	1,897	1,546	1,667	1,814	1,449	8.9	25.2	TGGGGAAGTATCACAAAGAAAAAACTATTGTAAACTAATTCTTATAATGAACGAGGTCTG
Os07g0690500	8,810	4,924	169	547	1,379	1,220	1,432	2,222	555	7.2	21.7	GGCATGTATATATGTAAACTGGATGAGATCAATACACCTGCGCGTTGTATCCAAACTCTT
Os07g0692800	2,567	4,085	90	83	87	80	68	73	271	22.5	37.4	CTAGAGCTGTGAGCGAGAGAGAGGATAGGCTGTTCATGGATGACATAGAAAAGCTGAAAA
Os07g0693500	40,243	35,059	5,337	1,847	9,007	8,094	9,050	8,501	6,706	4.9	12.0	CACATGTGCTGTAAGCTATTACTAGTACACGCGTACATTTATACATGTGATGCCGTTCGA
Os07g0695700	5,113	7,922	413	264	705	616	722	622	573	10.3	19.3	AAACCATGATGTTCCCAGCACAGCTGAAACCAGAGCTAAGAACAAAGCCTGTCAGTGTTT
Os07g0695900	72,111	79,633	11,051	8,000	11,801	10,545	10,611	10,875	15,797	5.8	8.1	GGGGAACTTCCTGCTCTGAACGCTTATTTTCTATCTTCTATCTTCATGGCTATCCTTGTT
Os08g0104900	152,970	166,210	24,624	10,378	15,566	13,867	9,676	10,434	10,793	13.9	10.0	TTTGCTCGTAACTATGCTACTATTGCTACACATTTGATCACACAGCATTGTTCAGTTGAC
Os08g0107500	209,057	169,731	20,851	14,697	35,127	31,624	28,866	28,739	40,189	5.3	10.8	TTGTGTAACCGCAATGTACGCTACTTGCAATCTACTGAAATGGAGTGGTCTATCCACATT
Os08g0110600	26,868	31,160	792	174	396	245	1,513	289	167	105	77.8	TAGCCAAAACTATAAACTTGTATGTAAATCGAAAAAGAATAGATGATTGGCATGCAATAG
Os08g0114200	46,800	69,795	222	844	9,559	10,559	5,060	5,568	3,121	12.0	132	GTATCGTTCGTTGACTTTGTCGTGTATTCGACGCAACAAACAGTATTTGCACGGAGTACG
Os08g0121800	36,819	19,968	5,225	5,712	3,878	3,628	3,807	3,733	5,496	6.0	5.0	ATGTGGCAAAATACCTAGTCTGAACCGATTCCTCTGTTGTGTGTTAATTGCCAATTTGCT
Os08g0122700	3,009	7,373	103	111	600	565	633	689	519	8.3	43.9	TTTTTCCTATACAAACACTGTTTGTGAGGGGCCTATACGTAATTAAAGAAAACCGGAGGG
Os08g0126500	1,473	4,192	185	334	113	125	108	91	177	17.9	10.0	TAGGCTGAATTCTGTGATAAGAGACAGAAGTTTTGGCTGTCTTCGTTGCTGTCATTCCGA
Os08g0128200	42,789	44,650	6,478	5,337	6,110	5,546	6,045	6,175	10,862	5.4	7.4	GGTATAGACCACATGATCGATACTACAACTGAATCTAAAGTTTTCGTTTATGGTTGAGTG
Os08g0141400	36,722	51,057	7,733	3,843	7,916	7,807	8,113	8,310	5,630	6.4	7.9	AAAGATAAGCAAAAGAAAACCACTTTGGACCTGACCTCTTTTTGTTACTGTCAAATCTTG
Os08g0154200	2,043	2,857	271	82	1,284	1,159	1,151	1,251	312	3.9	16.2	TAAAGTGAGATCGTTGTTCGTTGAGTTATACAGAACAATGAAAAGCTGTTTGAGCAAAGG
Os08g0158500	405,319	266,147	6,327	1,620	40,606	36,067	37,351	36,636	35,903	8.9	103	AAATGCATGGATTATCAGTCGTTCATGAAACAAGTTCACCATGACGGCAATGGCTCATGG
Os08g0160300	15,707	19,533	107	106	700	647	582	526	393	35.8	164	AGCACCAGCGAGCTGAACCTCGAGTTCACGCTAGGGCGACCACAAAACCGACCAAACTAA
Os08g0163900	16,644	13,705	114	114	242	162	161	148	128	101	133	GCCGATGCTGGAATGCAGTTTTACGTTCTCTCAGCTGTAGAATGGCTGAAAAACCTCAAA
Os08g0164000	9,211	6,044	119	99	109	89	129	103	177	54.4	68.7	GATTGACGCCAAAAATGTGCTTATTCCTGAAGTATATTAGTGTTCATGCTAAACTTGGTA
Os08g0164300	13,551	7,234	86	81	104	86	69	66	191	80.1	118	ACAATGGGTGTTTTTACGCAGTTTACATACTTCGAAAACCCGGTAAAAGTGAAACAGGGT
Os08g0165200	8,567	8,113	1,380	465	725	661	480	484	802	12.2	10.4	AATGGAGGAGGGCTCCGCATGCTGAAGCACAGGTCTGAGATGTACAAGCTCACCAGCGAA
Os08g0165800	17,718	14,775	414	998	2,343	2,181	2,472	2,508	3,612	5.5	25.2	TGAGAGTGTCGTTCATGTTCTACAAATGTTAATAAGGAAGTGAATCTCCACTATATCTAC
Os08g0166100	12,613	15,177	157	217	520	516	80	76	199	69.2	75.0	AGAGGCCACAGATGAAGACAATGCCACGATTGAGTGAATCCTTTTGTGCTGAAGTTCTGA

Os08g0180400	36,899	22,713	2,736	1,389	2,287	2,020	2,033	2,058	3,158	11.3	14.8	CGAAGGTGATACAGTTTATTCTAGCCCTGTGAAGCAAAGAAAACAGTTTGCAAAACAGTT
Os08g0184800	12,040	9,041	4,664	1,400	2,681	2,473	2,409	2,410	2,351	4.3	4.1	AGGGTGATTTCATAGTGATCTACTCCGATATCAAGTCCAACAAATATGTAATGTTCCCAC
Os08g0191800	2,429	3,399	241	131	247	192	186	180	202	14.3	16.2	CCGTGAGCACTTTGAAAACAACAAGGAAGCCAAATTCTTGCGTGATACAGTTAAGGGCTA
Os08g0193500	1,102	2,166	178	83	384	391	365	346	160	6.3	12.7	TCTCATCCCCTGAGTCTTGCGTCGACTCAAAGGATGTATATTGTGATGACCCCAATGTTT
Os08g0197100	8,281	9,189	86	74	149	131	127	101	566	32.7	110	CTATATGCACAGTGTTAGTACAGTTACCTGGATATATGAAAAATTTTGCATTCGTTGGTG
Os08g0197200	22,890	16,176	292	133	500	377	150	237	489	51.4	97.5	CTGGATGTGTATATGCATCAGTTTTAGTACAGGTACCTGGGTATGTGCAAGACTTTGCAT
Os08g0197300	18,464	19,917	106	316	1,211	1,052	1,078	1,115	967	18.5	105	GGCATATTGTTCTAAACTCGTTACTTTTTGCTTTGGGATTAAATGGATTATGAGAGCAAG
Os08g0205300	12,565	13,305	1,186	934	2,473	2,369	2,256	2,372	3,771	4.3	12.3	TTATCTAGAATGGTGATTTAGACTTGAGAAATTTATGCAGTCAGAAGCTGATCTCCTGTG
Os08g0207800	235,170	174,122	93	154	598	477	336	346	1,575	247	1690	TCACGGCTGTCTTAGTTTACTATTGATGACTGCTGAAATGGACCTGCTACTTCGTTGAGT
Os08g0208200	13,076	6,097	77	74	460	382	401	443	470	20.1	118	TTTTTTATTAATATCACATAGCTTGCCAATTCATGCTGGGCAAGACATGCAGGTTGTTAC
Os08g0241300	62,380	50,319	2,034	4,369	2,005	1,515	781	770	10,447	16.1	18.8	CCTCATGACACAGTGGATGAAATCAGCTTCTGTTTCAAGAGAATAATCATATCCATATTT
Os08g0246700	12,019	12,294	2,259	699	878	788	654	744	1,808	10.4	9.7	TCCTGGATTTTTATTTTTACGTGCGGATGCGCTACCTTTACATATAAATCAGATTTTTGC
Os08g0248700	1,256	1,483	181	102	285	138	287	184	235	6.1	10.0	AAGGTATGGTAAAAAATATATATACCAGGTCCAAGAGATGATGTAATCTTGGCACCATTC
Os08g0260400	15,471	13,416	135	129	1,938	1,719	1,527	1,640	2,381	7.2	109	CTCAAGACGCAGGTCGAGCTCATGCACAGCCTCTGCAAAGGATCCCAGCAGAAGCTGCAT
Os08g0267800	3,105	10,490	77	369	118	148	90	104	110	51.3	34.0	CAGGCTTGTTTGTGAAACACTACGATTACTCGAGATGTATACACTGATATAGCATGTGGC
Os08g0270900	10,733	8,399	163	147	357	346	406	385	410	24.3	61.3	CGAACAAAGAACAAAGTTTTTTGATCACTTACTTCGCTCGCCCTTTTTGATCGGGGAAGA
Os08g0277200	70,946	49,846	445	396	964	556	125	112	198	246	142	GTCCTTTTCGGAGCACCTATAAATCGGGCACCGATTAGTTTGTCAAAAATAGCGTGCTGT
Os08g0299400	8,185	6,498	505	597	436	382	311	312	542	16.6	13.3	GAAGGTTGGTCCGCTTGCTGAAGAACTTGTACATACTGAATTGGATTTGTTCGTTTGTCC
Os08g0302000	58,987	84,775	81	79	152	168	77	73	146	560	887	GACTATCCTGCATGTAATCGAATAACTATACTAATAAAATCGGGCAAGTCATTTTCAGTC
Os08g0321600	13,914	8,734	82	76	3,456	3,252	3,215	3,301	1,247	5.4	140	TGAAGATGGATGAACTTTTGTTGTTGCATCAAACTGGTTCGGTGACTGAATACCGTTTCA
Os08g0324300	5,653	11,464	205	677	974	878	1,005	951	1,590	6.5	21.6	TTTTTTGGGTGATACACTAGGGGGGTTCCCTTGCTAATTAATGACCCATGTAATTACTGA
Os08g0326000	4,317	5,133	727	625	705	700	628	686	1,250	5.1	7.0	TGCTAATTGCAACCGCAGGATTAATCCGGCGCTAATTGCAATCGCGGTGTTAATTACACT
Os08g0339200	129,670	114,723	7,365	7,593	13,049	11,457	12,447	12,807	33,057	6.0	16.3	TATGTGTATGCTAAAGACCTCGCCTCCACGGCCCTGAGATAATAAAATTAATATTTTGAG
Os08g0367400	20,203	16,824	1,537	1,104	2,920	2,605	1,952	2,566	4,402	5.6	14.2	ATTGAGTGAGAGAGAGAATTGCACACAAGAATATAGAGAATGAATGAGCGGAATCTTTAT
Os08g0376300	159,600	81,280	79	75	2,968	2,495	2,522	2,524	3,395	38.2	1484	AGTATTTTCATGGGTTAATGTACTACTACCAGTTTGTCTAAAGTATCAATGCCAACAAGG
Os08g0384100	429,925	275,607	21,868	13,608	16,971	13,988	15,726	17,061	27,339	16.5	20.0	AGTCGGGATGATCAGCAAATGATTTTGTTCTTCTATGCACTGAGAATCCAGATGCATTTA
Os08g0389800	8,830	7,488	99	291	643	561	541	532	913	11.3	47.9	GGCGGATTTACAAGTCTTTTATTTGGAGTTCAGCAAGATTCAGCCATGGCTGCTAGAAAG
Os08g0399500	6,603	7,539	221	110	306	153	147	168	277	31.2	45.2	TTTACTTATGACGGGTTGTATCATGTGGTGGATTACTGGAGAGAAGGTCTAAAAGGTTCT
Os08g0400000	21,601	32,911	122	113	438	509	158	137	221	111	228	GTACAAAAATGTTCTTGGAAAGGTTGTGCGGTTGGGCCAGGTGTGGCCACTACTAAAAAA
Os08g0400200	10,127	9,954	174	117	965	857	944	814	846	11.6	70.3	CAGAGTAAAAGTTAAAGATTGCCATTGTGGTTCTCCACAGTGCTGCGGCAGGCTCTATTA
Os08g0418600	134,988	84,274	137	84	1,261	709	67	67	128	595	995	GACCGCAAGCTGTCCGAGTAACTATGTGATCCGACTTTTATGCTACTACATGTTGCAGTT
Os08g0419000	10,969	6,956	541	227	244	189	132	134	158	53.4	24.9	GGTTTGAATTGGTGAAGAATGATGAGTTAGCAAATTAAGCGATTAGATTTTCGATTCGAC
Os08g0419100	114,629	67,449	78	210	843	636	528	536	927	116	688	AGATTGGTTTTGCAAATCCAGCGGACAATTATGTTGCAAAGTACGTACATCATGTTCTGG
Os08g0419200	1,013	1,944	143	190	605	119	85	79	246	7.3	8.5	AGGTTTATCAAGGAGGAGGAGGTACTTTCCCTTTTTGAACTGGGGATCCTGAACTTGACT
Os08g0421100	20,846	12,802	104	120	1,362	952	393	400	634	25.0	146	TGCTCTGATTCACAGAATATTTACATGGATTGGTGAATGAGGCCTTGTTTAGTTACAAAC
Os08g0421700	27,069	9,947	110	100	315	231	247	254	1,126	30.3	156	TGTTGCAAACTTGTGTTCTGGGAATCGGGGAAGATGCTGGGTGCATGGAAGATATACTTT
Os08g0439900	28,683	14,118	417	103	1,827	1,546	1,457	1,581	2,054	11.1	97.1	TTCAGGACGAATTGGTTCACTAGTTTATCAAATGGTTTATACTCTACTGTGCTTCTCATC
Os08g0444400	9,208	3,128	965	599	1,114	1,194	1,148	1,116	461	7.4	7.1	AACTCATTTAACTATCAGTACCTTGTCTTGTGTGCTCTCTAATGCAGCCACACTTTTCAC
Os08g0445700	201,176	115,298	106	108	9,021	5,140	3,808	3,801	6,734	26.0	1418	CGATCGGTAGGTTACAGATGTTCATGTTTTACCCGGTAGGCAGTTCTTTTGTACAAACGT
Os08g0449400	1,406	699	82	86	119	87	67	70	197	7.7	11.8	AACTAAGGTGGTCTACGTAAAGAGAAGTTCTGATGATAAGGTATTGTTCTTTTCTGATTC
Os08g0451500	7,613	3,340	450	341	919	817	847	806	845	6.0	12.9	CACAAACCAAGATGAAGATGAAGCTATTGCAAATGGTCTATATCACCATCCGCCAAGATG
Os08g0453700	115,383	101,976	179	115	8,229	7,588	5,983	6,404	7,285	15.2	757	GTCTAGTACTGGCAGTGGCATTGCGCAGTGATACTATATATGGATATTCAGTTGGGCCTT

Os08g0458200	21,748	57,633	7,022	5,225	2,314	2,039	2,189	2,142	4,322	11.6	5.8	TTAGCATACTACATACTGATATCGATGGCCTAAGCCCTAAGGTGTATGTCTGTATCATGC
Os08g0474000	9,939	12,534	1,558	1,752	1,401	1,293	1,333	1,308	1,595	7.7	6.8	AATTGAACAAAGCAGAGTTTGTAAATTATCCATAGAGTTGACTACTAAACTGTATTGAAC
Os08g0476000	1,713	1,620	94	90	131	92	79	72	244	11.2	18.1	TGAAAACTTATCTGATCGATTTCATGGTACAAAAGATTGACGCCCCGTCGTTCGGGCGTA
Os08g0480200	278,134	173,880	216	133	4,688	2,895	1,071	1,071	2,372	101	1297	TTGCAGGCGCTGATTCGTTGTAAAGCTCGAACTGTGATATGTGGAATGTTCATCATCATC
Os08g0483100	16,254	8,845	1,783	1,841	2,081	1,699	1,679	1,860	1,416	7.5	6.6	TGGTTGTGAAGTTTGTGTAGATAGGATTATCATCACGCAAAATTGGCATCATTTCTATTC
Os08g0486200	92,743	99,616	5,081	12,433	16,540	15,708	15,127	14,353	17,881	5.8	12.1	CTTGGTATTGACACACTGATGTTGTTCACTGCTGACAGAGTTCCTTGAATTGTTTTTGTT
Os08g0494300	32,641	41,290	7,481	3,998	944	879	769	698	3,251	22.5	6.7	ACTCATGGTATTCAAACTAGTACTGGTCATTTTGGATAGCATTTGTGAAATGAATGTTCC
Os08g0499400	1,220	1,444	518	113	220	140	1,068	179	268	4.9	5.5	CTTATCCATCTCTTGCTTTGTCAGTCAAATACCTGAGGAAATCAAGCTCTTCGATGGCAC
Os08g0502000	105,525	105,711	5,388	2,517	1,745	1,404	427	476	395	183	28.7	TCCAAAACTCTCCTTGCCAATCCACGCCTGTTGATGTACTAGGACGTATTTTGCCTCTTT
Os08g0515900	31,056	45,319	133	126	575	572	168	166	206	149	290	AGAATCATCAGTTGCACACAGGAAAAATGTGTCTCTGTGTCAGAGAAGGTTGTGCGCTAC
Os08g0516600	91,888	122,284	6,797	5,264	9,534	6,082	12,069	12,999	22,349	7.2	17.7	AAAGGAGAAAGGAGTTGTAAGAGAAATTCCCGGAGATCTTGTTAATTATTTATTAAGTAT
Os08g0518200	2,641	3,172	99	153	823	769	862	835	673	3.9	23.5	CCAGATGATTAGCCTGATATGTTATATTTTTCTTTCTCATCAACTTACTTTTTTGCTGGC
Os08g0519600	39,924	43,165	167	398	5,016	4,554	4,506	4,708	4,315	9.2	161	AATGCCTTTAGGTTTAAATGCTCATACTAAAACGATACCTAAGAAGAGTTGCTGCTAGAT
Os08g0520600	1,300	581	85	140	108	93	96	198	142	6.7	8.0	CTGTACTGTAGAAATCAGTTTTCAACTGAAATAGAGATGAATTTGGATCGATTCAAAAAG
Os08g0520900	41,987	32,953	1,148	1,078	4,632	3,934	3,801	3,825	3,305	10.2	33.4	AAACATATGTTTATAGCCCTTTTTGCGTATATGTTGAAGTTGTGCGGTCCTTCAATTTTG
Os08g0524200	96,769	139,354	3,443	3,762	24,673	22,678	26,850	27,531	27,410	4.4	32.3	TGTATGATATTTGTATACTGCACACTATACTGGAGATGAGAGATGCCAGTACAGCTTGTT
Os08g0525500	12,846	7,615	861	741	1,643	1,500	1,447	1,469	1,559	6.4	12.4	AGCATAATCCTTGTGAACTGTGATTATCATTGGTTGCACTAAATAGCAGATTTAGGCATG
Os08g0525600	155,363	124,671	805	94	19,362	17,109	19,450	20,907	26,430	6.2	505	TTTCTGGATGAATGTTACAACCATACGCCATGTCGGGTCCAGTTTGCCACGAAAGATCAA
Os08g0527900	4,039	6,936	422	406	394	370	361	363	260	17.0	12.8	GTTGCCACCTGTATTGACCATTCATCTGATGAGATATTTGGAGGATTTAACGAAGGTGAT
Os08g0528100	1,436	545	214	81	95	78	221	66	89	9.3	6.7	GGACCTCCAAATATCCAATTTTTGATTTGTTCGTACTCACGTTGGATCAAAATCAAGAAG
Os08g0529100	35,100	27,957	6,410	2,858	3,320	3,169	2,931	3,508	2,464	11.1	7.3	ACGGAAGTGGTTACGTAAGACATTTTGTAGTCTTTCTATCTGAACTATGCGTATCTGAAT
Os08g0530100	45,057	20,504	1,581	1,712	1,292	1,125	1,130	1,177	1,354	24.1	18.5	CCCTCTTGTTGGGATCTAAGTGGGACTGATTGATATCAGGAGCATTGTAAAAGTGTTCTT
Os08g0531700	96,491	174,526	1,017	1,499	224	335	64	69	123	1,006	105	ATACTACCTTAAAAACTATCGGTGTCTGTTGAACATATTCTGCGATCAACTTTAAGCGTA
Os08g0532500	2,525	2,043	345	435	151	145	163	901	424	7.1	5.9	TAAATGACTGGGATGTTCTGGTTACTGTACATTGATGTACTGCTTATGAGTGACTTGTAG
Os08g0544600	2,543	1,673	218	229	297	262	269	325	355	6.5	9.2	ATGGAGATAGTAGTGTAAATTGTTGGAAATTTTATGTTTTGTATTGTGTATTAATTTGAT
Os08g0545800	69,325	114,193	79	69	183	222	71	61	115	774	1209	ATAGTAGAGAAGCTATGAGTTTGATGTCATATTGCAGTGCATTACATCGTTTTGTTATTA
Os08g0548000	38,835	66,864	2,095	2,965	1,920	1,914	1,699	1,769	2,932	22.0	20.4	GACACGTTTGCATGTATACATGCTTCTGTTCAGAAATATGAGAGGTCATCTCCATTCTCC
Os08g0548300	53,264	69,296	149	471	7,688	6,298	6,836	7,261	11,136	6.9	230	AAGCAATTAATTTATAGTCTCCTGGTGGCCTGAGGCCTGTTGTAGCCTATAAGTTCCGAA
Os08g0555800	3,353	1,814	130	95	542	513	610	576	311	5.9	22.2	AGTTCCTAATATCTGACAGCTTCAACAATTGGCTATGCCGTGATCATTTTGACAGAAATT
Os08g0559000	466,854	287,604	373	593	27,470	19,560	13,245	13,645	37,694	14.2	779	TTTTTGGAGGGTGATCTTTTTGATCTGTACGGAGTAGAAGATTGTGCCCTTTTTGTCATA
Os09g0103800	16,064	27,406	901	560	1,905	1,688	1,499	1,583	2,525	10.2	29.5	GCTGCTGCTGTATATATGACTATAATGGGGAGCCTTGCAATATATATATGGGACTATATA
Os09g0114700	28,970	41,797	168	95	574	712	242	251	419	85.3	275	TGAATCCGATAACGAGGAACAGCCTGCCAGATTGATTTGTAAGAGGAAGCGTCCGAGTAG
Os09g0115600	23,295	22,614	871	333	3,950	3,604	3,397	3,432	5,713	5.1	42.6	GTACCCATCACGAAGTAATACAAAGAAATTGAATGGATTAATGGTCCTATGGGTTGGCAC
Os09g0124800	27,607	46,473	1,136	1,269	1,389	1,598	832	834	807	37.8	29.8	ACATGCCCACATCATCTGATGGATTTGTGGCCGTCCTTGCTGTAAATTGGACATGCAAAT
Os09g0242300	1,876	2,015	553	230	114	122	154	142	152	13.7	5.5	TTCATATTTTCAGGATCTCATAGCATTAGTTGTAACCATGGTCACCGGTACGAAAGGTGG
Os09g0260000	21,058	8,483	425	267	1,465	773	650	583	548	20.1	39.7	GGCTACTGAAGATGGAAAGGAGTATGGCCACCCCATCTACGCCTACTACGTGGCCTGGCC
Os09g0260200	2,238	712	272	205	293	268	266	290	171	5.8	5.3	CGGATTTCTAGTTGTAGGATATGTATGGTCATATAATTTCCAAGTAATAACATTCTAGTT
Os09g0261100	27,527	14,471	2,124	251	1,519	1,263	1,294	1,381	2,523	10.8	27.4	AGAAAGTGGGATGACATTGCACATTGTGCTGGGTAAGTTTGGCAAATTGTGGTTTGAAAT
Os09g0261500	21,510	24,624	3,085	2,807	2,591	2,457	2,271	2,344	2,345	9.7	7.8	TAACGGAGGTAGTATATTTTTCCGAGTAGCCATCATAGGATGAAAAAGAACAGTTATTTG
Os09g0279200	31,831	22,863	101	105	888	735	728	757	1,038	30.1	262	CCCTGAAGAGTCCTTGTTTTTGTTCACTTTCTTGGTTTTTAAGTTCAGGATTAAGGGTTC
Os09g0280600	25,742	22,520	902	358	4,044	3,846	4,181	4,013	5,619	5.1	42.4	CCCAATATGCTCCATATTTTCTGCTTTGTAAGTAAGGTACCTATGGAATGCTGTCAGAAA
Os09g0284400	53,774	78,698	2,168	4,542	16,656	14,477	13,586	14,858	14,356	4.5	20.7	AAGAGGAGCGTTATTTTTTGTTCTAACCAGCACAAGCTATTGCACTGTAAGCAATGACAA

Os09g0309700	16,427	38,233	539	415	3,834	4,088	3,068	3,374	3,257	7.4	53.0	GGTTGTGTATTTGTTGGACGCCATTATTATATTTGTTAATTTTGATATTGTTCTTGTGAT
Os09g0314400	4,786	6,751	285	349	637	617	537	599	1,361	6.3	18.0	TGGTATGACTAATCCAGTAAATTAGGTTGCTATATTTTGAGATTTTTGAGATGGAGGGAG
Os09g0318600	3,255	4,448	227	370	377	377	356	381	418	9.6	13.1	ATCCCATGCCAAAAACAAAATGTTCCTATTCGGACAAGAGAAAACTAATTATGTTGCATC
Os09g0321900	52,669	49,443	1,818	144	2,565	2,411	2,498	2,457	5,192	14.2	99.6	GTACTGGAATCATGTAAGCGCAACGATGTTTAAACTGAAATGTCAAATGATGTTTGGAAC
Os09g0326100	5,014	15,268	264	278	205	290	149	162	881	21.1	32.3	ATAATGTTGGAAATATTTAGTCGGGTTCAGCTCTGCATGAATGAAATGTGCATGTTGCTA
Os09g0326800	65,968	63,972	8,308	4,123	13,440	12,368	12,675	12,635	14,230	4.8	11.1	AGACAATGCATACTTGATACGGTGAGGACTGAGTTGTAACAAAGAGTTCAGGTATAATGG
Os09g0337500	24,861	35,796	123	322	5,897	5,303	5,544	5,471	5,969	5.2	150	GAAGTTCCAAGTTGACAAAGACTGGCGTCGTGGAGTTGCTACAAAGTTCTGTCCATCTAG
Os09g0348800	67,347	54,850	2,680	1,208	5,869	5,523	5,479	5,452	9,782	8.2	33.8	TTGCCATGTTGGCATGCGCTGGAACTTGTGAACTGGAAGTTCGGTTCTTTTGGTCATATA
Os09g0360900	1,351	698	71	69	254	102	109	104	205	5.9	13.9	TTTTGTTTATTTTAAATGTACAAATGACTCAATATATCATTGCAGATATGCGGGAATTAC
Os09g0361200	826	1,518	420	184	257	267	237	228	238	4.6	4.0	AGAATGTCCCTGGAACCACTGCAAAGGATATCATGGACATGGTTCTTGTTACCCAGTACT
Os09g0364800	14,739	29,402	455	72	217	291	753	116	252	79.4	115	TCCATCCCAAAATATAAAAGAATCTAGAATCTGGATAGTTGTCTAGATTCATAGTATTAG
Os09g0370200	35,223	47,729	7,505	4,504	6,355	6,502	5,238	4,617	6,464	6.8	7.1	AGCTCCTGTTCCCCGCTCCTTTGTGTGTAAGAATTGAGCAAAACTGTACAGCGCCTCCTC
Os09g0371700	26,335	21,249	4,777	2,899	2,104	1,717	1,795	2,057	6,169	6.9	6.4	CAAACAGCAACTGATTGGATACATGCAACAACAATGGTACATTTCCCACCCTATACATCT
Os09g0380600	27,042	26,936	121	690	563	542	497	466	489	53.8	93.3	TACCAAGTACTCCGTACTACTTTACTTTACCTCATTTATAAATAGTTAATGAATTCAGTT
Os09g0407300	6,274	9,967	96	148	1,719	1,552	1,676	1,678	1,209	5.6	66.1	CAGCAGGATCTCAGAAGTAGACTCTTATATCTTGGGCACAAACCTCTGAATTATGATATG
Os09g0413100	42,243	43,559	2,828	2,645	10,722	9,393	9,771	10,531	10,053	4.3	15.7	CCATATATACCCATCTCCTTTTTTGTAAGGATACCTTGGAACCTATTGAAAATGTGAGAA
Os09g0415300	21,395	22,022	3,988	4,990	215	207	196	163	220	105	4.9	TTTGGGGGAGCGCACAAGACTTCGTGGTTATTTCTGTTTTTGGAGAAGATGTTTTGGTTG
Os09g0419500	14,103	16,904	79	411	694	724	327	322	696	26.7	85.6	TTAATTAGCTCGTATATTACCACTCTGATGTCATTTGTCAATCAATATCAGTAGTATTAC
Os09g0432300	19,411	11,792	172	100	904	652	344	394	382	33.6	115	TGCAGTGCAAGAAAGGAGCTTTCTTGAACCAAAAGAAAAAAGAAAACTTTTCTTTGTCTC
Os09g0449800	24,189	11,014	92	471	2,725	2,227	2,137	2,455	2,910	6.2	78.4	AGCTTGCTGTCAGTTTCTGGTTATCCACTTCATGTACTCGCAGTCTCACGGGTAGGCCAG
Os09g0459600	2,335	7,522	943	542	648	557	598	612	360	9.0	5.9	TTCTTGGCAAAATAGATTGAAGATTTGTTAATTGGTTGGATTAACATAGCACTATCTAAC
Os09g0465800	31,635	38,098	113	157	4,844	4,559	4,762	4,640	8,646	5.4	261	TGAAAAAGTTGTTATGAACATTTAATATGTTATCTTAGTGCTTTAGTGCTGGTTCTGAAT
Os09g0471100	175,162	59,603	724	270	8,550	6,106	5,989	6,229	5,967	16.2	231	CCTACCTGTAAGCTTGTGATTTCAGGGTTACCCGCTTATTGCCGATTATTGAATGGTGAT
Os09g0473300	11,465	16,954	1,231	710	2,044	1,986	1,988	2,065	2,663	6.0	14.9	CACTACAAACGTTTAACATGTTAAACAATGGTTATCGTACCATTGGTTTTCATATCCGAG
Os09g0475700	12,525	6,784	91	78	1,673	1,492	1,492	1,569	1,931	5.3	109	CGTCATCAGATTGCATGTAACACTCATATGTACATTTTGTGATGTAGTCCATATCTGCGA
Os09g0479300	24,769	19,581	154	90	2,811	2,756	2,790	2,839	2,632	8.1	187	TTTGTGTCTCAAAACTCTGACTGACCACAACAGCCAAGTTCCTTTTTGTAATGCAGGTGC
Os09g0479900	25,804	8,149	560	285	554	469	404	491	722	24.7	36.3	CCTGACCAAAGAAGGTTTGGCTAGTTTGGTGAACAGACTTAGAAATGATAAACTGAAACT
Os09g0480300	85,187	73,659	149	84	1,594	1,226	797	730	1,593	61.8	709	ACTTCAGTGTTGACTACTTTATTAGAACAGGCAACATCAACTCAATCCTCCATTAACCAG
Os09g0480900	9,222	2,847	114	102	246	138	135	137	147	33.6	47.4	CCGCTTGCGCAGACGGCATCCTTGTATCACCCACTTGCAAAAAGTTTTTGGGGGCAAAAA
Os09g0483400	650,797	383,165	139,175	39,865	10,725	8,829	8,490	8,607	7,190	61.7	6.7	CGAAGCTGCGACTGGGATGTTGAACCCTCTATCATCACTCTGAATGAAGAAGTTATCGTT
Os09g0489500	49,931	32,959	124	99	5,995	5,675	5,973	5,831	3,637	8.8	366	TAGCGGATCTTACCTCAGCAGCTGGTTCATCAAGTGTTGATGCAGCTCAATCAAACTTTT
Os09g0494500	58,346	55,273	107	146	1,368	1,316	686	768	1,185	52.5	454	ACTGGTGATTACGCGGAGTTTTGTTCTGCTTGTACATGGTCAGTGTGGTACTGGTACGGT
Os09g0497500	13,534	24,923	856	88	97	156	102	80	176	135	67.0	CGGAAAACCATTGTGTCACTGTATAAAGTTATAAAGAAAGCACGAACATCTCTGATATAC
Os09g0499400	129,250	34,945	262	508	768	265	154	125	190	309	184	TTGCTGGATGCTTAATTTGGTTGATCTAATGAATGAAATCTAGTGAGATATCACGCCTTG
Os09g0499500	105,177	29,815	130	132	865	300	177	172	472	149	428	ACTCTAGCTATCTGCTATCTCCTCTGTTAAAATCTAGCTATAATCGAATTGAGTTTGATC
Os09g0500100	1,468	2,029	305	466	105	93	97	96	391	8.8	4.6	CCACTTCTTGAGTTAGGCGACATTTAATTATTGTTTACACGTGTACAATCAGATGTTTAG
Os09g0506800	511,402	348,626	5,370	2,113	26,109	17,730	11,321	11,264	16,190	26.6	125	CCGCTGTCCCAAATGGCAAATGGAGATAGACGCTACTATGTGCTAACACACACTCAAATT
Os09g0507200	108,884	136,272	158	185	487	458	206	211	110	655	713	AGTGCAGTGCCTGTACATTTCATAATTTGCGGTAAAGTTTATTGACTATATATCCAGTGT
Os09g0512100	6,422	6,370	89	84	92	92	80	75	166	54.0	73.9	TATCAGTACCTGTTATTAGGACCTGACTCTGTTGGGGATTTTTTCAGGACCTTTTATTAG
Os09g0513800	19,229	16,301	1,972	1,043	1,776	1,588	1,497	1,603	964	14.2	12.3	TTTTTCAACTTCGTGAATTCAGCTATGGTTCAAATTAAAATTGGCCTGTATGGATGAGTG
Os09g0514500	141,518	362,300	6,280	10,307	1,329	1,791	993	981	1,032	201	28.1	CTGCAGGTGCAGTGTGAATTTTGTAGTCATTTTAAACAATAGATCTTGGTGAACATGTCT
Os09g0525500	381,140	661,995	215	3,158	5,614	8,325	690	657	781	388	610	TGTCCTGCTTGCTCTGCTGATCGTTCAATGAACGACAAATTAATCTAACTCTGGAGTGAC

Os09g0526000	9,122	6,542	894	562	646	568	505	499	1,057	10.1	10.9	TGAGTGAGGACTGAGGAGCAGAATCATACTGTGGTACTAACATCAACTAAGGAAGCTTGC
Os09g0527500	11,350	9,646	552	866	1,485	1,306	1,306	1,452	2,383	5.8	15.1	GTTGGTATGGATGTGTTGATAACTATTGGTTGGATGGAAACAAAGTAGATGGGGCTGAAA
Os09g0533600	4,379	2,350	77	75	504	438	400	426	470	7.0	42.1	TATTTTTTAGGCTTATTTAGGATGAGGATAGTAGTATGAGAATACATTTGATTTGATTGG
Os09g0536800	3,402	1,387	271	99	167	147	162	175	309	9.7	13.3	ATGATTGATTGAAAAGGGAAGATTTTCTCCCATTTAAATAGCTGTTGTACTCATGTACGG
Os09g0539500	327,490	124,876	8,747	4,882	18,002	16,859	18,054	17,915	29,890	8.8	30.9	AGCAGACTATTTAGCTGACTCCGTTCTGTTTTGTGCACTCTGGAGCGAGAAGGAAATGAT
Os09g0546100	4,943	2,731	89	89	74	74	70	70	168	33.5	41.3	GAAAGAGGAAAATTGCCATGTAAGCCTGTCAATATTGCAAGCAATCAAAGAAAACGTCCA
Os09g0546200	8,858	7,155	88	83	245	183	224	175	151	45.3	93.0	GAATTGTTGACCATACAGAGTACTTTCAATACTCAACAAGTTTCTGTACAATCTATCTGC
Os09g0547900	16,654	12,670	94	338	2,576	927	919	955	857	14.3	81.3	TCACACACCGTTTTCTTCATCGATCTTTTCCCTGACACAAGAGTGGCAAATATGTTTAAA
Os09g0550000	13,353	12,678	517	492	2,278	2,058	2,077	2,285	2,492	5.6	25.8	GGTAGAATTAGATAGCATAGCAGATCATATATAGGCTTGCAAGATATGAAAGTTCATCAC
Os09g0566100	40,547	72,868	1,835	3,708	8,697	8,423	8,912	10,325	10,023	5.7	20.8	ATCTTCCGAGGACTAGAGATTTTGTACCTAAAAAGAACTGATAATAGAACATCATGGAGG
Os09g0566300	628	931	74	86	104	80	58	76	95	8.9	9.6	AAACTGGAAGAAGATTGATATTTGTATGTTAAATTACAGTTAAATTTCACCTAAAATATG
Os09g0569600	13,025	10,349	1,050	953	3,057	2,172	1,466	1,512	1,558	6.6	11.6	TTGGTGTTCTTCTCTGTATTGTTCGTTTCTTTTTTGTGTGGATGGAATCATGGAAATGGA
Os09g0569700	12,349	9,656	161	123	1,277	1,014	648	678	1,051	11.4	77.4	GATCGAATCTCTCACAAAGGGGACTTTTGGCTTCGCTTGTATGTCGTCTGGCAACTTTTA
Os09g0569900	8,215	12,596	97	97	544	552	371	399	1,225	13.6	105	GTTTGGATGTCTCATCCTTCCCAGAATCTCTACCTGTAATGTATTGGCAAAATCACATAT
Os09g0571400	17,773	11,711	236	108	2,061	1,811	1,915	1,947	1,331	9.0	90.4	CTTCTTGTATCAATAACAATCCAATGTTAGAAAACATTTATTTATAACTATGCTCTTAGC
Os09g0572500	1,553	928	85	226	125	91	67	62	105	12.9	8.7	ACATGCATCCATGTATAATTCCATCCATTATATTCCTGCATACAAACCTCAATTATATCC
Os10g0120300	3,927	2,905	275	111	249	290	508	398	328	10.0	19.3	TGGACCAGATGGATGAACACTACAAATTAATTAAGCACAGTAAGGAAATGTGTTACTAGC
Os10g0124700	4,699	1,356	346	99	252	204	285	272	162	12.5	13.7	AAACAGTGATAACAGAATGTGTGGCTACTTCTGTTGATGCTCAAAGAACAAAGTGAACTG
Os10g0125300	5,139	1,653	84	77	112	105	94	94	287	17.1	36.3	TTGTCTTGAGTTTTTGACGAGATGAGTAGAGGAATCAAAGGATTATGCATAACGTCGTAA
Os10g0126500	37,771	40,990	1,613	1,223	4,658	4,350	4,301	3,942	5,415	8.1	28.0	GCTCTCTTCCGTCTTCCTCCTTTGATTCCAGTTGACTTCGAAAGCACAGAGACATGTTTA
Os10g0126700	1,500	1,193	80	114	292	258	270	283	230	5.3	14.0	CACTGCCTACTGTCAGGATGTGACCATTCTGACAATGGAAGAGATACATCATTTGTTTCT
Os10g0126800	1,070	1,203	137	173	105	81	117	137	151	8.9	7.4	AGTCCTATACTTGTATATATGTTGCTTCTGTTTAAATACTCCATTTGGCCTATGTTCTGC
Os10g0128100	12,304	12,526	2,362	398	2,752	2,408	1,505	1,507	1,545	7.1	12.8	TGCACGCGGTAGACGGGATCGAACGGTTGGCGGACAGTGAATAGTGGCAGCTGAGAAAAG
Os10g0128600	4,390	3,597	327	258	407	334	483	663	642	7.3	13.7	TGTGATGTTCTGTTGTACAGAAGATACTGCATGTCTGCATGTACATGCTTGGGTACTCTA
Os10g0128800	2,637	1,820	136	277	161	120	141	122	272	11.4	11.3	AGGAAAAAACACAAAGAATCATTGGCAAGATTGAAGATAGATCATTTACATGTGAGCACC
Os10g0141400	2,837	1,930	96	177	102	75	67	68	204	18.7	18.0	TTTCAGTTTGAAGTGGAAGATATCATCAATTTGATATGCTGGCAAGGGTGGCAGCAATGC
Os10g0145100	7,955	9,780	313	216	1,055	972	1,120	1,041	1,817	6.4	33.9	CTGCGGTAGTAGATTAGATATATTGGTCTCTGCATTTTATTTGTCTTAGCTAGGAAGATT
Os10g0148000	1,748	1,023	172	181	76	116	215	148	186	8.6	7.6	ACAAACATGACGCTTGAATAGCAGAAGAGAAGTTCTATCCAGCAATATCAAAAGTACAGC
Os10g0154500	3,889	2,627	161	600	492	456	471	488	603	6.0	10.3	TTTGTAAGCATAATTATGTAAATCCTATTCAATTTGTACAAAGCAATTCAAGGCCCTCTT
Os10g0177200	17,897	23,675	99	112	2,329	2,008	1,565	1,885	816	16.4	196	ATTAAGCCAGCAGTTGAACAACGGGGAATAATTTATTTCAAGCTTTTGTTTTGGGTGCAG
Os10g0183000	1,628	1,761	162	100	845	749	794	764	203	4.2	13.3	AGTTTCAGCTACAAGAAAGCTTATATTCTTTCCCCATTTTGGATAAATTGCAATTTTGTT
Os10g0198100	2,998	2,041	78	89	654	553	592	597	335	5.5	29.7	TGTGAGGATACCAAGTGGATGTGATTAAATAAGTTTAAGAAATACCCCTGTTTTATGTTG
Os10g0205500	13,096	7,598	593	218	429	337	320	356	166	41.0	27.7	CACCAGTTAATGTGAGGACAATGTTTGCTGATGCAGCTAAAAGAAATATAGCTAATTTTG
Os10g0359500	8,021	4,899	141	160	2,487	2,334	2,447	2,329	1,050	4.0	41.8	AGTACTAATACTGATTGCTCAATACTTAGTTATCCTGCTTGCATTTGAAGGAGTATAAGC
Os10g0368400	8,194	6,135	2,072	1,595	1,369	1,312	1,299	1,353	1,431	5.1	3.9	CAGATGACGTCTCTGTTCTTTAATGTTATCTTGCTGTGAGTTGTGTTATTTACTCTAGGA
Os10g0373400	11,532	6,234	84	75	293	278	296	297	554	21.1	107	CATATTCTAAACTGTGAAAGCTTTACTTATTGCTCTCGATTAGACATGGATATTGCAACG
Os10g0374600	766	918	233	146	243	207	217	230	198	4.0	4.5	GCTTCCATGCGACCAGGCCGTTCCCAACGCTACCCACCATCGTTGTCGCTACGGGAATCT
Os10g0375000	5,908	22,705	88	92	339	324	323	352	675	24.4	128	ATTTTTTGCTGATGTAATCCATTTATTGGTGATCCCAAACCATTAGCAATCAATGGTGCT
Os10g0382100	161,528	98,678	143	75	4,812	2,389	242	142	128	396	1219	TGCGTCCAAATGACGAGGCGATCTGAACTGTTATATGTAATTCTACTTATATCATGTTTG
Os10g0386300	63,111	22,360	91	83	780	639	650	708	1,221	40.9	432	TTAGTTGTGATCCTGAGTTATTGTTATCAAGAGTGCAAGATCTTCTGATATTTATCGACC
Os10g0389200	3,354	3,678	301	126	592	562	568	588	866	5.0	18.1	ACAATCAGATATATTGTGTGATTATAAATTTATAATTGCAAATACCATCAGATGTCATAA
Os10g0391600	41,697	31,584	2,333	1,638	11,771	10,393	13,053	12,070	5,604	4.5	18.6	GCTTTGGGGAAATTATGAGGGGATCTCTCAGGGTTTTGCATATCATCAGTACCTTGTTTG

Os10g0398600	31,571	12,510	970	1,203	786	580	545	481	358	43.3	18.4	GGGCCCATGAGCCCCTATAATATTATGTACCCCTGTAAATGTCCCTTTCGTAAGGGTAAT
Os10g0400200	8,408	14,632	507	760	731	661	783	738	1,819	9.6	17.9	TAAAAGTTTCTTATAATATCAGTTCTGAATGCTAAGGACATCCCTCAAGATGGTCTTTCT
Os10g0405500	20,266	23,277	457	321	1,816	1,743	1,160	1,168	3,050	10.4	56.7	AAGAGGATGAAGGGCCTCAAATTTGTGCTCAAGGAGCTCATTGCAGAAACTGCAGAGTAA
Os10g0413700	207,908	62,204	340	111	949	422	818	432	127	408	586	TGAGATTGCAATTCTGATCTGCAACTGCTTGTAATCTGGATGATCAATAGCTGCTTCCCT
Os10g0413900	14,131	6,161	984	134	160	121	1,737	162	156	45.3	25.7	ACTAGTATTAATCTTGGTGATCTGTTGTTCTGAAATGCTTATAAATTTTGCCCTTGTGCC
Os10g0414500	30,169	13,313	72	265	1,606	1,342	1,434	1,517	2,360	10.8	145	CATTTTGTCTTAGATTCACATTTATCGAAATCATTATTATGGAGCTAATGGGCCGAATCC
Os10g0414700	6,047	14,320	94	92	663	590	601	651	1,503	9.6	100	GGGTAAGTGATGTACAAGATATGTGCCCTCAGATGTTTGAGAGACAGTTTGTATTACATG
Os10g0415300	17,043	29,765	4,148	3,168	1,106	999	890	991	1,720	17.2	6.2	AAAGAAAGAAATGCTTCAGGATGTTGATAGTATTGCCGCATGAAATTTTTTGATTAAACA
Os10g0430600	10,525	12,527	117	117	1,972	1,823	1,776	1,758	2,710	5.2	98.0	CTGCAGTTTGTTAGCACGATGTAAGCAACATCTATATCTCAAACATGGAGAAATTGTTGG
Os10g0432300	10,772	7,599	1,571	3,180	1,353	1,310	1,192	1,307	679	9.7	4.0	GTTTGATTGTGAGAGAAGTGGTACTCCATACGAAGTATGGAAAATATCACATTCTTCTCT
Os10g0437200	24,199	17,475	856	210	6,351	5,796	5,590	5,966	4,779	3.9	48.4	CATGATTCAGAACATTGAGGATACTTATACCAGATATTGAATCATTTCAGTAAAGCACGC
Os10g0457000	31,402	29,687	511	220	5,388	4,774	4,816	5,125	6,937	5.2	91.1	TTTCCATGTAACTTGCAAACACTAGGAGAGGATCAGAATTCAGTGAGTTTAGCTGACACT
Os10g0484800	47,118	36,296	84	88	182	133	78	56	89	437	481	TCTTGACAGCATCTGTGCACTACATAGTTATTGTTTTACTGTAATCTATGTTTTATGTAT
Os10g0485600	40,733	108,965	209	203	687	1,131	299	317	521	128	323	GCCAATGCCAGAATTCGAATTTGTGGAACAAAGGTTCAGGGAACATAAGAACCAACCATA
Os10g0487500	46,122	71,278	2,578	2,174	3,893	3,639	3,762	3,630	6,197	11.9	24.2	TATTTTGCGACCTCACTACTGTATATATTCTGCTTAGTAAGTTTATTGACGAGGGTAATT
Os10g0489200	48,376	54,644	1,175	1,087	10,050	9,404	8,974	9,820	7,758	6.0	45.5	TGCACAAAAGATATACCATGCGAACAACAATAACGATGATGAGGATGATGACTAGACTAT
Os10g0494300	57,922	104,157	146	181	1,406	1,345	1,376	1,402	2,681	40.3	478	TATTGTATTGATAATTACTAATATCAAGGTGTATATCAGCAGCTGAATGCAAGTTTAGCT
Os10g0498100	10,363	11,161	4,051	1,626	2,341	2,158	2,201	2,292	700	8.6	4.2	ATTGTACTCGCACACAATTTATAATCCACGTGTAATAGTGGGAGTGAATGTGACCGTGGG
Os10g0501200	35,989	33,492	5,979	4,932	3,050	2,637	2,620	2,783	5,607	8.8	6.4	GATTATAAACCTCTGTACAACTGCTTATATAGGAACTTGCCATTCTTCTATGCATGTGAT
Os10g0518200	20,752	19,676	635	433	3,419	3,024	3,180	3,316	3,360	6.1	38.5	AGCTATATTAGGTGAAATGATTTGGATCAAAAGAACTAAATAATGATATTTGTTGAGGGG
Os10g0519600	151,709	164,550	12,105	5,159	42,621	38,432	35,545	34,990	26,376	5.0	20.0	GAGTGTGATGATCGATGCTTAACCATTTTGGATGCAAAACATATTGAGTAGTGTAACAAA
Os10g0534500	2,613	3,547	684	95	176	120	153	113	194	18.6	12.0	GTGGAACCATTGTGGCATTCTAGCTTTTTAGCATTAAGTTCCAGCCTACTATTTATTTGT
Os10g0536100	42,741	43,095	3,604	2,030	6,487	5,776	4,658	4,749	4,627	8.6	15.9	GCATGCAGTTCTCGGTGGGTAAATTATTATCTCGCATTATTAGCTATATGCGTGTCCTTG
Os10g0537600	9,160	7,238	1,545	796	1,363	957	1,090	1,075	2,159	5.3	7.3	ACCTGGGAAGCAATATGTAAAAGACTAGAAGGTAGCTCAATAAAAAGGAAAAGAAAGCGT
Os10g0545500	206,498	149,621	91	97	23,547	21,877	22,480	22,989	35,329	6.2	1872	TATGCAATGCGTCAGTTGTATCATAATGTGGTTGCAGTGACTTAAGTAGCACCATAAGAT
Os10g0546600	4,217	5,703	337	316	726	696	516	590	1,146	5.8	15.0	AAAGCAAAAGATGTACATCGACACACATGAGATGTAATCTACAAGTTTAAATTTATTGCT
Os10g0555100	48,779	64,469	82	128	5,703	4,989	4,831	5,362	8,837	8.3	548	TCATTTGGACAGAATCACATTCTCTAATTCTTGATTCATTCTGACGATTTTGGCTCAGGC
Os10g0557700	3,737	4,217	240	86	190	174	154	146	213	21.2	27.6	TGAACCACATGTACTAGTCTTTGTAATGAGTAAATCTTTTCAAATTATTAGTACTGGGAA
Os10g0557800	8,646	8,559	600	341	1,281	1,147	1,202	1,280	1,267	6.9	19.0	ATTCTGTATTAATTTGACTGCTAAAAGGCCTATATATATTGTAAGAAGAGAAACTGAGAA
Os10g0561300	76,465	110,829	104	104	10,494	9,828	9,710	9,317	9,144	9.7	884	CCGTGACTGGCTCTTTCAGATGGTAATTACAAAGAAATGTAACATTAATGTTGTAACAAG
Os10g0580900	76,124	101,356	7,419	6,506	10,585	7,835	9,961	10,382	12,764	7.9	12.6	TTGTATTCATTGTGTTGTGCCTTAGTCTTTATACTAAATATTACGTTGGATGCTTCTCCC
Os11g0103400	542	2,131	79	81	74	75	66	65	134	11.1	13.4	TTACTATGTTGGAGAAGGCCTTCAGTACAATGTGGATTACCATCGTCAGTATGATGGAGG
Os11g0109800	1,008	847	87	77	115	91	86	79	201	6.8	11.3	TACTTCTTTCGTTGTAACAATGTTTGGAAGAAAGCAAGTAAATCCTGGAAACATGTGTGG
Os11g0115600	5,020	10,549	88	84	469	498	352	367	1,142	10.5	84.7	AACCACAGTGGGTTTTGGATAATGTTTCCGATTAAAAATAAATCATTTATGAACAGTGCA
Os11g0135400	109,968	66,872	4,760	1,838	10,070	8,831	8,973	8,866	8,832	9.5	29.0	ATCTTTAGCGTATTAAGCTTGTGCTAGTCAAGAACCATGTTGGACTTAGCGTGTATATTC
Os11g0137500	4,470	2,272	86	77	123	107	107	109	365	15.8	39.1	TTTTTTCGAGACAAAGCCATTTCTGCGTTTTCGCCTTATGTGTCTATAAAAGAACTTACA
Os11g0139600	6,288	7,236	99	81	138	144	121	102	142	50.6	75.6	ACGAGCGTTCATTGTCCACTAATGTCATACCGGGATGTATCATGTATGAAGGCTAGCTCA
Os11g0143300	10,436	16,514	138	137	1,082	902	1,004	1,100	698	15.6	95.5	CGTAAAAGGGATACTAACATCTAGTTTACAAAATAGAATGGAATCCGTTAACGGATACTG
Os11g0146200	4,106	4,061	538	587	751	708	779	823	434	7.1	7.3	ATCTGCATGCAAACAGCTGACAGATTAATTCTTCAGAAATGAATGAGGCGGCTGAAGTTG
Os11g0146800	66,214	50,248	368	286	1,239	974	897	919	2,867	34.1	178	AAGAATACAACTACTGCTGCTGCTATGTTTTTGCCACTGCTGAGGAAAGAGGCAACCTCA
Os11g0148200	23,219	14,721	2,582	1,011	3,349	2,759	2,787	2,907	2,509	6.8	11.4	GAGCTCCAGCAATGAATGATGTAAATATATAATTCTACTACAATCCGCGAGAAACGTGAC
Os11g0150800	25,618	25,414	9,171	2,142	3,974	3,714	3,915	3,881	4,332	6.2	5.8	CAGTTGGGACAATCAGAACCGATAGATTCAAAGACATGGTTGGAAAGAAAAATTGAGATG

Os11g0160100	81,430	67,536	6,240	10,278	11,835	10,719	12,098	11,762	14,581	5.7	9.3	CAACCTCACCTAGAACTGTCATGCATGAAGTGCCATCACTACTCTGCAAGTCTATTTGAA
Os11g0184500	2,156	5,375	136	113	231	409	158	151	111	21.9	27.4	AGCTGCCACCAGGCATGCGTTGCGTTATTGCTCACTCCAAAATGCATCTTTCCTTTTTAA
Os11g0184600	19,718	31,119	795	1,867	1,522	1,462	1,460	1,491	1,324	17.7	20.3	TTACAATGCAGGATCAGATGGTGATATATGATAACGAGAGAGAACAGCTTGGATGGATCC
Os11g0184800	16,055	21,721	495	442	225	218	103	98	125	137	39.9	AATGAATGATAAAGCATGTATGCTTCTGCCCATAAATAATGAAATGAAGTAATATTTTAG
Os11g0190700	8,682	8,369	85	91	662	1,190	374	456	1,114	10.4	96.6	GCATGTATTGATGTTTATTTGTTGAGAATGAAGTAAGAAATTGATGTAGTGTTCTCTTGA
Os11g0215300	293,345	254,808	368	789	48,087	40,031	361	1,297	309	210	508	CGATTCGGCGCTCCGCACCATCCCTGCCAATGCCATCGCCATGTCCGCAATATTGCTGCT
Os11g0230700	12,539	3,764	1,114	990	416	148	101	115	224	35.9	6.5	TAGAGAGCAAATTGAGCCTTTTATTCGTTTTAAATTGGATATCTACCCTATAGTATGAAT
Os11g0237900	1,465	1,510	142	215	105	101	103	101	269	8.9	8.5	AAGGAGATTATCAAGTCTGTTATCGGTGACAAAATCAAGATGCTTCCCCATAATCCCAAG
Os11g0256200	97,935	49,715	3,227	1,608	10,148	9,131	10,041	9,820	14,107	5.9	30.6	GGAACCACACTTTGTTGCAGAGCTGATTTATCGAAAGATGGTGCAATAATAGAAGATGAT
Os11g0261900	33,880	14,845	651	1,196	922	799	918	896	651	29.6	25.4	ACCATTATCATCATTATTTATCGAGATGTGCTAATCAATTGCTGATATGTGCAAATTGTG
Os11g0433800	13,330	18,075	315	1,026	2,818	2,711	2,648	2,680	2,899	5.5	27.3	AACTTGCTGGTACAAGAGCTAGCTCTGTGCTGCTATGTTCTGTTCCAACTGTGGATGTAT
Os11g0506800	53,507	37,875	3,582	733	314	209	135	193	213	216	27.8	TTGGTTTCTTTCGTTTTTTGATTTGGTTTGTAGTCCTTTCGAATGCGAATCAAACGATAC
Os11g0507400	6,858	3,829	248	76	283	237	261	273	668	12.2	37.4	AGTGCAACCAGAATGTAGTGAAGATAGTAAAATCAAGAGACGTGAAACTGATGTACTGAT
Os11g0514100	2,917	3,582	393	144	730	734	645	681	740	4.5	13.6	GAGTTCTTGCTGAAGTCCAAGAATCTGCAGCTATTCCCTGAGGACGAAGAGTTTTTGGAT
Os11g0516800	12,925	12,376	1,475	2,088	2,730	2,232	2,386	2,531	2,444	5.2	7.2	TGATCCGATTGCACCATTAAATTCGTTGTAATTAAATATTCGAAACAAGATCACACGTGG
Os11g0517400	12,412	16,172	1,600	1,937	423	438	376	359	1,068	21.7	8.0	GCTTGTAGGGTTCCCCGTAAGGAAAAAAGAGTACAACAACTATTTTACATTTTAGCATCA
Os11g0518600	5,690	4,836	488	356	169	162	180	168	197	28.7	12.6	GATAATTCATACTGTAGCTATTGAGATACACTGCGAATAAAACTTTGCATGAAGTGTCTC
Os11g0527000	16,599	11,773	82	76	554	382	144	157	99	86.9	177	TGGAGTTGCAGTTTTTCGTTTGACTTGACTATTGTAAACAGCTGGTTTATGTCAACAAAT
Os11g0532000	11,604	6,854	883	762	285	220	189	203	589	24.7	10.9	AGTTTGTTTTTTGTTCTTGCTATCCCTTTTTGAAAATGATTGAATATGTGCCTTGCCTGG
Os11g0533600	2,789	3,708	240	1,132	228	228	255	216	415	10.4	6.2	TACGATGGATGCCCTTCCAAAATTTATGTGGCAATAGAAGATGCTTTTTAGTGGTTAGAC
Os11g0547000	22,104	10,519	91	95	691	661	640	691	2,317	12.2	164	AACAAAAAGAGGATTACTGGTAGTTTTCATCCTTAGAAGTTAGGAAAAAGATCTGAAAAA
Os11g0552100	40,328	31,484	5,378	3,841	9,939	9,292	9,941	10,100	7,842	4.1	7.8	GATCTACCTATCTCTGTACTTATTTCTTCCTAAAATTTGCCAGCTATCTGCTGTTATTAG
Os11g0557400	557	1,074	87	85	83	71	76	79	138	7.5	9.0	TCTCTAGAAGCATAGTGTAATCTTGTCAAAATATCGAGTCTGGGATTTTTAGGCAGTTGT
Os11g0577700	6,980	2,335	254	347	609	598	463	558	125	15.3	13.6	CTACTTTACAGCTTGCTCTCATTTCTTGTCTTTAGTGTCAAATATGATGGTGAATATGTC
Os11g0579700	16,765	18,716	2,022	1,122	5,452	4,917	4,993	4,918	4,072	3.9	11.8	TGTGTGTGTTGGAAATCAGTGATTCAGTTCTTGTAATTTATGTAGACAGCAACTGGATGG
Os11g0579900	15,966	6,137	900	765	312	210	303	317	334	32.3	11.9	TTGTAATCACTAGTCTGATCAGATGAGCTGTATCATCTGCAAGGGTTTATATTCCGGTTG
Os11g0581900	66,615	52,713	16,853	8,034	420	300	273	191	199	249	5.1	TGCAGTGATCTGCACTACATCGGTTTAGATCTAATCAGTGGAGCGAAAAACTTCAATGGA
Os11g0594000	3,909	7,730	166	168	431	437	252	264	241	19.4	32.9	TCATACAATAGTTGCTTGCTATATTATTATATAATGTATGGTCCCACCTGTCATAAAAAA
Os11g0595100	7,230	6,963	83	272	742	637	661	656	730	10.1	47.2	TGAGTACATGTCACAGATCTACTTTGATTGCAATATACTTATCATGCCCTGTTTGACACT
Os11g0598800	99,853	52,807	1,987	5,000	1,029	520	94	133	147	354	23.0	TTCCAGTTATGCACTACTTTTAGGATGATATACCAGGTATCTTAATTACTTCGAAACAGC
Os11g0598900	3,518	5,289	114	102	122	121	111	103	156	32.4	40.0	TGCTCTGTAATTCTGCTGCTTACATACTCATGTGATCTTGTGTGGGTAACATGGGTGATG
Os11g0599000	9,482	10,006	255	793	203	159	126	101	105	79.9	21.7	TTTGGCTTGTTGTTACATGTCACCATCTTGATGCAAACTGTTCTGATACACGACCTCCTT
Os11g0600900	33,560	56,398	3,059	893	1,740	1,638	1,803	1,648	2,024	23.4	26.3	GAGCTTCTAGTTTCGATTATTCATTCATCATGTACATGCGAAAATTGAAGTTTGCTTTGG
Os11g0601700	2,543	2,476	564	243	166	141	199	205	167	14.7	6.8	AAGTCATGAAAATCTGATCTTGTATGTTCATGGGCAGCTTGTTTCAGCATTACAAGTTGA
Os11g0607100	2,091	1,918	86	120	181	173	162	166	401	7.7	19.6	ATGAAGAACAAGTCTTTCTTGAATACTTGGGAGATAGTAGTCACTAACAAAATCCATCTG
Os11g0616300	12,681	22,656	91	75	576	588	537	501	1,055	22.3	205	GTGTCATGTGTATCAAAAAACTCTGATTTTTCAAGGTGATATATACCAGATTGCTGAATG
Os11g0619700	54,932	23,061	139	776	2,680	2,214	2,206	2,171	4,780	10.7	108	TCTATGTAAGTGAGTGTTTGGCACCCAGTCCATGTGTTTTCTCTATTCGTATAATATTTA
Os11g0648400	2,039	2,204	93	1,287	66	64	74	59	146	21.7	6.1	AATGTTTCTCGATCGGTTTGATCTGTATCAAAATTTACACGGTTACTTCCTATATGTTCG
Os11g0648800	11,210	7,341	123	85	356	329	339	317	109	47.5	88.5	GAATGCTAACTTGTTAACTTTCAAACTCATGCATGCATGGTTGATGCGTGTGTAGCCACC
Os11g0649300	16,185	22,877	1,066	867	126	98	85	92	500	86.5	20.0	TTGGTAGTATGTTGCTCGTTAAGATGTTGGCACATTGTATTGAAGTAGTCATGAGAACAA
Os11g0666100	6,082	5,589	75	73	114	97	77	79	171	46.9	78.6	AGGTTGCCACAAAGTTTGTTCGGACAGAAATCCATGGAGTAAAAGAATTCACTTTTAAGC
Os11g0672800	88,601	42,240	253	111	1,136	631	245	122	1,611	77.9	365	TGAGTTTCGGGGGGTGAGGTGGTAATGTAATTGTCCCGGTGATCAGATCTGAACCCTCTT

Os11g0679700	14,300	24,345	94	77	814	724	851	843	2,774	12.5	219	GTGTTTTAATCAAATTAATGATTGTATAGAAACAACAAGAAGCTGGCACCATCAAGGAGC
Os11g0702900	3,072	3,414	143	100	396	274	404	279	358	9.4	27.1	CTGCCTGACACATCATGTACAACTGCCTTATACAATTGAATCAAGAACCACTTGGCCGTT
Os11g0703000	641,105	466,737	85	86	13,174	7,515	1,482	1,501	403	439	6391	TTAGAAATGCATGCTGTACGTGTGATTCATTCAATAAATGGTTTAACTCCGAATCTGCCA
Os12g0103300	25,893	34,782	1,518	877	3,688	3,414	3,481	3,727	7,351	5.9	26.0	GCAAAATGTGCCTCTTGGGAATTTTGATTGTTACAGTGTAGTTACTGTTACTGAAGATGC
Os12g0109600	5,530	3,474	467	232	661	607	615	654	839	6.0	13.3	AGGATGTGTAAAAAATGCACAGATATGGTAAGGGATTATAACACTACGCTAATTTTAATC
Os12g0111000	28,659	22,698	9,963	2,424	1,458	1,191	3,874	1,403	1,793	14.4	5.2	ATCGTGGATTGGTACAGTTGCTACAAATGCTGGATAGTAGTATTAATTTCTCCCTTTTCT
Os12g0136300	15,652	14,002	1,427	2,150	729	534	188	181	160	63.5	8.5	ATTGTGCATCTGTGTACTATGTTTACCATGTCAACTTGAGGCAATTCTATATAAATCCTG
Os12g0139400	22,340	51,047	372	355	7,399	9,398	5,603	5,593	1,837	9.5	93.0	CACAAGAGAAAGGCAGTCGATGAAGAAATTTTGCCCCACACAATAAGACCAAGGCATAGT
Os12g0141000	8,319	30,518	81	92	262	479	169	203	510	44.1	184	ACATAGTTCTATGTTGAATTTGATTTCCATATGTGTAGGAATTTCTAGTTTACTTGGTTT
Os12g0141800	2,019	2,374	84	419	102	90	87	834	120	15.8	11.7	TGAGTGACTAGGAGATCTATGTTTATCCTGACTCAGTAATACCTTTTTTGTGTTGGATGC
Os12g0143800	40,410	27,640	4,506	2,121	863	739	687	684	1,118	36.8	10.8	CCACTGTCGAGGAAATATGCAACCTCATTTATCCAGACGATTATACCTTAAAATGGGTAT
Os12g0152900	13,973	8,219	89	83	3,110	2,642	2,644	2,979	1,970	4.5	125	CCAGTGACAACAAAAAGGGGTTAGCTAGATTTTGTTGCTGAAATACTACTTATTTATGTG
Os12g0154000	292,068	333,426	93,023	67,737	36,207	30,537	32,811	35,543	50,488	7.6	3.9	CTTGCCTGGCGTCTTCGTTTAGTGCTGAAGCCGTAGATTTGCCATCTAGAAACTCAGCAT
Os12g0156100	1,481	3,418	81	77	85	114	92	74	242	15.3	28.5	CTCTCAATTCTGCTTGTCTTTAATTTTTCTTGAATAAATTCTGAACTATGGCCTGTTCTT
Os12g0158300	43,340	64,580	81	79	3,227	2,979	3,019	3,099	3,884	15.3	661	AGGTTTGTACCGAACTTGATTTTGCATGATGATGATATGTTAACCACGGCCACTGTTTGG
Os12g0178000	4,058	4,488	306	94	643	618	604	649	872	5.8	25.2	GAAGAGAACATTTCAGTGCAGTTGTGGGTATAAAATAAATATGTATAGTAGGATTGGCAG
Os12g0178200	7,828	9,317	78	79	192	188	184	191	581	25.8	109	CTCGAAAAAGAGCAACCAAATTTGTTCAGGTCAACAATTAGATGCATCACAACCTCAGTT
Os12g0183100	32,519	49,009	182	117	2,666	2,835	1,791	1,982	2,624	16.3	274	AGTAACTATTGATAATTTAGGTTCATAGCATTGATAAATAATAACAACAATAATTCAGGC
Os12g0197500	202,508	244,763	8,832	4,754	57,825	52,209	60,045	58,033	31,419	5.3	34.4	ACTGATGACTGTGCGCTGCGCTTTTACAGCAAGCGTGGAAATCGAATATATATCTAGTTT
Os12g0198400	4,561	2,774	140	113	797	734	888	752	605	5.1	28.3	GCCCTATGCCGATGTTTTGGGCATTTTGGATAAGTCGATTGACAAAGCATTTCAGAAACG
Os12g0224000	64,217	53,827	10,323	7,028	13,621	11,726	11,819	12,811	13,298	4.6	6.9	TAGGGTGTATCGGTGGCCTATACAAAAGGTATGAATGTAAGTTTAATCCCTCGTTTTTTG
Os12g0228400	1,295	3,038	423	527	401	457	404	428	357	5.1	4.2	CTTAATCTGTTATTCTCCCCCTAAGTCTTGTGTGGCGCCTTCTGGGGAATTTGAACCATT
Os12g0233300	31,646	23,700	116	223	6,570	6,040	5,600	5,747	6,939	4.3	170	ATTGGGCTTGTTAAACTTGGTAGGCTTTAGCTCTGTGGTTTCATGGAAGCGAAGAACTGG
Os12g0233900	168,618	72,935	98	90	18,785	6,443	91	95	176	263	1182	CTGCAGCAGAAAGCCCTCAAAGTTCAGACACTTCCACGTCACAAATTGCATCTTCTTATA
Os12g0242700	40,452	11,912	5,071	2,169	583	196	131	93	121	144	6.6	CTTGTAAACCAAGTGAATGTAATAGACTCTAAAGATATCACGATGCTTTTCTTGAAAATC
Os12g0244000	84,488	119,475	940	1,480	1,417	1,562	271	325	722	145	85.2	TCATGTACTTCGGGTATAAATATGGCCCGACCCCATGTAATCAAGGGACGACAGTTCAAT
Os12g0256400	11,626	16,144	655	490	569	624	311	294	640	26.3	24.2	GCTTTGGGTTGGTCGTCCTAGGCCCATTGGATAGGATTAGGGTTTGTTAGGATTAGATTA
Os12g0279600	1,017	2,114	186	118	222	214	212	203	200	7.1	9.9	CATTTGTTCCATTGTTTTTAATCCGAAGAAAAACAATATATGCAAGCTAATTCTGGTCCG
Os12g0410200	120,703	89,976	1,833	1,439	15,321	11,419	20,097	19,493	25,203	5.2	64.2	CGGTTTGCACAAATCGCTCAGGACATGGAAATATATGACTAACAAAAATTTATTTGGAAG
Os12g0422200	79,351	29,428	80	80	484	424	388	385	298	137	604	GTGTAAGCTGAAGCAGGATTGCTCAATTCAGTGGAGAAATTGATCTGCAGGTGACTTACC
Os12g0424600	23,483	14,683	121	111	602	408	130	119	192	85.0	160	GATCGTTGCTAAGCTTTCTGTTAGTGTGTTTGTACGTTGATGAGTTGGATGGTTTTCTCG
Os12g0425600	76,011	63,838	10,491	2,731	17,869	16,521	17,422	17,119	17,428	4.0	13.0	ATGGGTACTTCAAGGTTGTCGTAATGTCAACCAGAGTTTAAACGATATGCGATAAAATAT
Os12g0433700	61,204	65,762	98	148	8,938	8,051	8,632	9,001	4,966	9.7	527	CACTCCGTGTATTCTCCAATCCATATTTGAATGTCTTATACATACTTTCGCAAGAAATTG
Os12g0451400	18,369	20,212	198	403	2,271	2,184	1,748	1,788	2,800	8.2	68.2	GATCCAATCTAATCCGGTTACTCTGATTAGTTTGAATGGAGATGGAGATTGATCCATTTG
Os12g0456700	733	2,343	87	90	72	112	79	73	155	11.6	14.8	ATGGACGGTGTGACGCTACAATAATGTATAACTTGGCTTTATAATATTAATGGTGCTTAA
Os12g0472500	80,187	36,956	11,189	6,521	1,147	705	526	527	2,475	41.7	6.4	TTTTTTTGACCCCATGTCAGTATCACTCACAGAACAACAGCTCACCATTTGCTACGCCTC
Os12g0516800	7,486	2,488	87	86	783	633	618	647	744	6.1	49.9	ACCTGATGTTATCATCATCTGAGAAAAAGCAGCTATTTTTCATGTAAATCTGGGATAACC
Os12g0516900	21,438	8,453	1,265	2,836	877	801	888	816	2,483	9.3	7.1	ATAAGGCATCTGATGTGTGAAAACCATGGTAATGGTCAACACAATGGTACCCTGCAACCA
Os12g0517100	18,693	20,744	238	823	292	292	177	179	977	41.7	44.5	AACTGGTCCGAAAGGCATTGGATCATTGGGTGTAGTCAACAATGTACACTGCATTACCTG
Os12g0540100	3,889	4,576	94	90	139	128	110	99	165	30.3	46.1	TACGTTCTTTTCTGGATTGATATAATGTAATAATTGGCTGTAGCTTGTAAAGGCTGGGAT
Os12g0552400	17,604	26,312	5,347	2,011	188	200	173	145	294	94.8	6.6	AAATCCTAGGTGAAGATGTGACTCCTCCTTATACAACGAATAAGAGTGGTCACTTCCTCT
Os12g0552800	16,397	9,672	3,526	1,580	2,093	1,854	2,062	2,115	2,876	5.2	5.3	GACAGGGCAACCAGCAACAAAACTATGTTGAAATTGTGATGAACAACATGCAGTTTATAC

Os12g0566500	98,307	118,750	5,398	4,526	25,645	23,312	26,291	25,390	28,878	4.0	21.9	CAGATTTCTTGATCTGTTTCAGGTTTATGTTTGTTTACCCTGTTGCAGTGTATGGCATGC
Os12g0572500	100,245	181,063	14,413	8,965	14,612	13,806	13,280	12,876	12,278	10.4	11.9	GCTTGTGCACCCAGCTCATTACATGCTATAGTATGTATTTACATGAGACCTATAGTTAAT
Os12g0572800	29,290	46,892	2,262	1,622	954	1,350	416	382	142	120	19.3	TTCAGTAACATTACTCAAGGGCTGCACCACTTGTGGCTGCATGATTGAGCACTTCAAGTT
Os12g0573700	2,844	3,635	691	362	519	462	556	508	403	7.1	6.4	ATGTTTACCATTGACTAGCCCTGCTCGAGGTATTTGCATTACAAGCCGTGCACTGTTTGA
Os12g0573900	28,708	50,842	4,802	1,302	3,254	3,126	3,001	3,043	4,080	10.7	15.3	ATGTCTTGGGCAATCTTGCTAGAGCAATGATAAACTTTTGTAAACATTTGCGTGATGCTA
Os12g0576200	23,607	54,940	68	78	146	218	62	68	101	346	495	GTGGCCACATTCAGATGTAATGCATAATGTTTCAGTATAACTGTTACCTCACTGAAGTCA
Os12g0578200	469,670	208,406	86	78	3,819	1,230	490	507	595	398	3816	TTGGTACTGAATTGCAACTTGAATGGAGGTTGTCTGAATTGAAAAGCCAAGATTTGAGCT
Os12g0578300	22,400	22,294	142	133	2,058	1,886	1,473	1,456	809	19.1	162	CTGAGCTGAATGATGTGTGTTTTCGTTTTGGAGCTTGTGAACTTCCTGTAAATTTTGGAG
Os12g0578700	1,951	2,654	174	137	309	315	507	557	409	5.6	14.8	GTATTCTTTGCACTCTTGCTTCGATAGTGAAGCAGTGTTATTCAGTTACATGCAATGGAT
Os12g0580300	29,323	38,694	3,359	2,350	6,263	6,177	5,448	5,393	7,160	5.2	12.0	TGTTGCTAAACTTTTACTAACTTGTTAACAGACAGACAGAATGATAACATGGACTGTGGA
Os12g0586500	1,982	1,191	92	172	185	147	147	1,037	136	8.3	12.2	CTACTGCACCAGTCTTTGAGACCACTTGTGTTATTATGAAAAATACTATTCTGTCCTCAT
Os12g0594600	200,405	97,893	14,101	2,242	5,865	4,228	3,424	3,331	2,167	47.0	24.9	CTGCTTAATTCAGTCATATTTGGTACTCCTGTGTACGGTACTAATTGAGAAAAACTGGTT
Os12g0595300	8,212	3,620	154	139	199	134	141	127	166	34.8	37.3	GCAGTGAATGATGATGCCCTCTCTCAGTCTGAACAATATGTTAGTATTGAGCAAAGTCAA
Os12g0595500	104,668	58,542	119	97	3,479	2,971	3,179	2,921	3,331	24.2	728	GCAGATCATCACCCCTCTATACCTAGCTAGTGAAGTATATACTGCCTATGTTTCAGGATA
Os12g0595600	23,316	10,662	1,407	368	509	449	475	423	346	39.4	21.9	CCATCGAAGAACATGAGTTAATTGGTCATAAAATCATTGTGCATTTCGAATACTAGCAAG
Os12g0599900	48,840	35,676	129	114	2,176	1,905	1,924	2,046	6,426	11.6	345	TTGTCTTCCCTTTGTGTGCGACTCTAATGCAAGCGCAGACTGGCAGCATGATATTTGTAT
Os12g0600100	7,395	7,890	1,104	1,154	643	609	581	619	602	12.6	6.8	CAACTCATGCAAGTGCAAACTGGCAGTAATAGTATATGATATGTAAAGTTCGTCAGTTTC
Os12g0603900	4,475	15,402	141	157	226	216	265	313	705	19.7	55.9	TTTTGCAGTTCTAGCTAGCAATTTCACTGTAAAACATGTGTATTACCGATCAATACTGGC
Os12g0605900	11,901	4,231	132	286	126	100	163	120	245	40.5	36.4	TGGATCCATGAATGGTGTTGGGATATTGGCATTAAAGCAAGGATTGGTGAGTTGGATCCA
Os12g0607000	345,325	488,947	249	663	39,319	39,813	50,402	51,876	80,184	6.8	1013	GTGTACTACTACTACTGCTGTACTACTACTACCCTGTGAACTCTTGTTTTGCTATACAAG
Os12g0607800	2,725	1,751	92	89	74	83	77	66	124	22.7	24.1	GTGACTTTTCTTTTTTCCTTCTAAATTAAATTTTGTGCTGATAAGACTAGACTTCTTTTT
Os12g0618000	104,332	61,053	90	83	4,287	1,843	94	81	102	355	924	CTCAGACTTCTGGGCTTTGCCCCTACATTAGCACTACACTCACTTGTGAAGTTGTGAATT
Os12g0628300	20,111	16,036	590	202	4,172	3,891	4,132	4,065	4,693	4.1	52.0	ACTGCAAATCGCATTCCTTCTTTACTCTGAATTAAGAAGTGAAATGTTGGTGTTGTTATG
Os12g0631600	164,626	67,774	14,251	4,151	6,181	3,666	2,614	2,276	5,824	23.7	13.7	TCCAAACTAGTTGATCGAGTGGGTAAACTTTGAAACTACCACCGTCTCTGGTGTTCCTGA
Os12g0633700	6,894	11,123	96	96	794	717	658	738	665	12.6	91.4	CGAGCTGCTACCGAGGGAAGAATAGTAGAGCAACAAGTTCTCGAAGTAATGAATCGAGTT
Os12g0634400	27,686	15,771	123	120	3,495	2,824	2,475	2,452	2,201	8.4	172	GCTTGTTGCCTGAATCTTTGACACCTCCTGAATGTAAATAAATTCCAATTGGGCACAACA
Os12g0634900	50,406	44,303	86	167	2,008	1,637	1,155	1,224	1,511	31.7	393	CGCAGGAATGATGGCTTTTATTTGCTCCAGATGGAGAAGAAATGTTGTTGGAATGATGAA
Os12g0636100	122,244	121,164	2,108	2,052	5,072	4,654	4,593	4,417	6,031	22.9	58.5	CTGTTGCTAGTATGGGCAGAGGATGATCAACTGTCTAAGCAAGCTGGAATGATATGAATT

Supplemental Table 14. Microarray data for rice kinase genes (Genes that expressed >4-fold higher in PMC than in TCP and Seedling are indicated by *)

		Intensity (without background subtraction)					Intensity (with background subtraction)				
RAP ID*	Kinase Group	PMC1	PMC2	TCP1	TCP2		PMC1	PMC2	TCP1	TCP2	
TIGR Locus ID		seedling1	seedling2	seedling3	seedling4	seedling5	seedling1	seedling2	seedling3	seedling4	seedling5
Os01g0577600	CMGC_other	3,745	3,757	279	285		3,622	3,652	162	179	
LOC_Os01g39600		7,966	7,632	8,528	8,726	18,559	7,852	7,549	8,380	8,595	18,496
Os10g0154300	CMGC_other	3,632	8,366	2,011	2,841		3,530	8,272	1,918	2,751	
LOC_Os10g06560		1,676	1,773	1,475	1,633	3,048	1,587	1,705	1,390	1,551	2,978
Os10g0154500*	CMGC_other	3,889	2,627	161	600		3,786	2,530	61	510	
LOC_Os10g06580		492	456	471	488	603	397	383	375	403	538
Os10g0153900	CMGC_other	2,392	4,939	1,389	1,875		2,270	4,837	1,281	1,773	
LOC_Os10g06510		570	535	563	558	1,077	456	459	433	438	1,003
Os10g0157400	CMGC_other	522	540	86	153		414	431	2	60	
LOC_Os10g06950		613	628	576	609	308	522	546	470	512	243
Os06g0693900	CMGC_other	122	121	105	137		2	12	2	28	
LOC_Os06g47880		100	89	117	138	115	2	7	2	4	57
Os12g0424700	CMGC_other	3,113	1,275	769	761		2,997	1,159	677	666	
LOC_Os12g23700		810	868	751	720	1,359	718	782	639	619	1,297
Os01g0201000	CMGC_other	49,523	63,519	108	134		49,395	63,416	2	33	
LOC_Os01g10430		36,560	33,740	36,584	34,832	43,212	36,440	33,665	36,453	34,712	43,145
Os08g0112500	CMGC_other	27,838	41,488	16,894	6,041		27,689	41,364	16,772	5,929	
LOC_Os08g02050		40,490	38,336	40,974	40,694	50,273	40,358	38,242	40,818	40,557	50,210
Os03g0349200	CMGC_other	15,835	13,653	160	178		15,699	13,540	35	64	
LOC_Os03g22700		17,756	16,700	18,474	18,631	35,320	17,630	16,612	18,314	18,493	35,254
Os11g0242500	CMGC_other	12,728	10,626	137,041	217,345		12,621	10,528	136,936	217,253	
LOC_Os11g13860		8,705	7,511	7,105	7,621	11,201	8,608	7,428	6,972	7,504	11,140
Os12g0203000	CMGC_other	257	241	3,864	3,242		149	145	3,767	3,145	
LOC_Os12g10190		146	121	167	155	245	53	51	54	49	180
Os01g0925700	CMGC_other	1,332	1,035	1,702	865		1,229	933	1,607	775	
LOC_Os01g70130		5,683	5,116	5,076	5,451	5,350	5,594	5,039	4,976	5,360	5,291
Os12g0577700	CMGC_other	117	123	247,944	360,554		15	28	247,846	360,465	
LOC_Os12g38860		602	567	4,162	6,982	2,677	509	496	4,071	6,897	2,602
Os02g0322400	MEKK_ste11_MAP3K	127	134	106	100		25	36	6	10	
LOC_Os02g21700		107	101	97	101	209	9	27	2	14	147
Os01g0629900	MAPK(CMGC_2)	3,920	9,683	89,866	151,998		3,771	9,559	89,739	151,882	
LOC_Os01g43910		5,931	5,367	5,273	5,424	5,562	5,794	5,274	5,111	5,282	5,500
Os01g0665200	MAPK(CMGC_2)	31,421	39,325	126,721	101,671		31,322	39,233	126,634	101,585	
LOC_Os01g47530		68,407	58,204	59,684	65,477	94,723	68,316	58,137	59,606	65,396	94,647
Os05g0566400	MAPK(CMGC_2)	15,241	37,816	91	84		15,139	37,722	2	2	
LOC_Os05g49140		32,563	30,241	31,961	32,954	36,051	32,471	30,169	31,870	32,871	35,988
Os06g0367900	MAPK(CMGC_2)	17,453	24,126	303	285		17,338	24,020	193	189	
LOC_Os06g26340		36,333	35,172	33,783	34,138	54,787	36,220	35,091	33,668	34,033	54,722
Os01g0643800	MAPK(CMGC_2)	5,445	9,860	172,178	107,241		5,300	9,737	172,065	107,134	
LOC_Os01g45620		554	557	2,811	2,098	1,630	433	464	2,666	1,972	1,566
Os05g0576800	MAPK(CMGC_2)	5,034	6,954	276,756	249,595		4,929	6,860	276,666	249,505	
LOC_Os05g50120		2,640	2,216	4,734	4,563	7,932	2,552	2,146	4,647	4,486	7,868
Os02g0135200*	MAPK(CMGC_2)	58,331	95,099	299	106		58,225	95,005	210	17	
LOC_Os02g04230		3,014	2,888	2,553	2,633	2,896	2,925	2,819	2,472	2,556	2,841
Os05g0143500	MAPK(CGMC_2)	13,366	15,918	95	93		13,249	15,815	2	2	
LOC_Os05g05160		59,125	56,019	59,612	59,291	57,977	59,011	55,940	59,502	59,184	57,909
Os06g0699400	MAPK(CMGC_2)_SLT2	9,098	13,308	26,879	22,907		8,988	13,211	26,774	22,812	
LOC_Os06g48590		33,216	29,522	33,377	34,495	47,552	33,120	29,442	33,249	34,380	47,484
Os02g0148100	MAPK(CMGC_2)_SLT2	2,440	7,080	38,522	27,675		2,318	6,977	38,413	27,573	
LOC_Os02g05480		49,259	44,849	51,347	53,431	84,578	49,145	44,773	51,215	53,311	84,512
Os03g0285800	MAPK(CGMC_2)_ERK	3,105	9,809	265	213		3,003	9,711	171	124	
LOC_Os03g17700		10,970	9,995	10,379	10,397	8,160	10,882	9,921	10,285	10,313	8,089
Os06g0154500	MAPK(CMGC_2)_ERK	16,428	34,362	19,525	10,584		16,328	34,268	19,433	10,497	
LOC_Os06g06090		26,930	23,581	24,921	26,653	76,242	26,842	23,512	24,836	26,576	76,173
Os08g0157000	MAPK(CMGC_2)_ERK	140	216	289	278		6	107	171	170	
LOC_Os08g06060		333	355	350	399	266	206	274	214	270	205
Os10g0533600	MAPK(CMGC_2)_ERK	20,491	36,179	1,507	1,914		20,384	36,084	1,411	1,821	
LOC_Os10g38950		30,686	27,024	30,839	30,567	32,944	30,593	26,953	30,722	30,465	32,880
Os02g0700600	CMGC_other_ICKh	88,020	89,407	525,269	657,221		87,913	89,313	525,181	657,132	
LOC_Os02g47220		146,314	127,728	135,155	123,371	180,711	146,226	127,659	135,074	123,296	180,637
Os06g0116100	CMGC_other_ICKh	81,489	87,866	102,248	67,997		81,388	87,773	102,156	67,908	
LOC_Os06g02550		98,180	86,663	92,534	96,044	217,854	98,093	86,595	92,453	95,966	217,779
Os03g0847600	CMGC_other_ICKh	16,695	35,826	36,204	29,338		16,577	35,726	36,100	29,237	
LOC_Os03g63020		17,271	15,751	17,641	18,229	25,111	17,166	15,678	17,527	18,113	25,051
Os01g0897000	CDK(CMGC_1)_CDC2	24,964	35,969	378	879		24,855	35,863	276	787	
LOC_Os01g67160		9,500	8,632	9,508	9,797	16,453	9,398	8,551	9,401	9,703	16,393
Os08g0512600	CDK(CMGC_1)_CDC2	42,664	43,000	2,043	1,398		42,556	42,891	1,946	1,305	
LOC_Os08g40170		27,543	27,402	24,441	27,344	36,557	27,449	27,320	24,335	27,248	36,499
Os02g0123100	CDK(CMGC_1)_CDC2	51,760	18,699	1,003	167		51,657	18,603	905	77	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os02g03060		21,722	20,357	19,970	20,622	35,361	21,629	20,285	19,875	20,538	35,295
Os03g0108800	CDK(CMGC_1)_CDC2	44,801	105,275	343	255		44,672	105,168	226	146	
LOC_Os03g01850		31,438	30,446	30,733	30,509	32,583	31,316	30,363	30,585	30,376	32,514
Os03g0118400	CDK(CMGC_1)_CDC2	89,217	224,705	404	326		89,098	224,606	301	227	
LOC_Os03g02680		84,511	78,426	88,510	85,277	112,741	84,403	78,353	88,382	85,166	112,653
Os01g0958000	CMGC_other_CDK9h_(	56,016	88,550	15,764	4,301		55,894	88,444	15,651	4,199	
LOC_Os01g72790		41,979	38,155	39,146	39,395	55,153	41,861	38,074	39,026	39,283	55,088
Os05g0389700	CMGC_other_CDK9h_CHEDh_CTK1y	73,197	70,553	24,859	16,117		73,071	70,448	24,750	16,014	
LOC_Os05g32360		11,915	11,310	11,710	11,588	12,220	11,794	11,232	11,582	11,468	12,142
Os08g0453800	CMGC_other_CDK9h_(	4,477	3,895	487	806		4,323	3,770	365	696	
LOC_Os08g35220		847	759	647	676	3,454	721	665	494	543	3,389
Os02g0602100	CMGC_other_PITSLRE	5,242	16,655	1,152	1,891		5,142	16,563	1,064	1,805	
LOC_Os02g39010		2,963	2,696	2,789	2,840	7,682	2,875	2,632	2,714	2,764	7,615
Os05g0392300	CDK(CMGC_1)_CDK7	19,651	18,521	13,688	7,375		19,522	18,406	13,570	7,270	
LOC_Os05g32600		22,021	20,339	22,091	21,610	21,359	21,894	20,252	21,955	21,486	21,277
Os10g0580300	CDK8_SSN3y	30,256	39,928	14,733	11,640		30,156	39,828	14,641	11,551	
LOC_Os10g42950		32,465	28,581	30,231	31,337	32,738	32,383	28,506	30,138	31,254	32,665
Os01g0205700	GSK(CMGC_3)	53,325	72,902	3,028	1,415		53,202	72,793	2,914	1,314	
LOC_Os01g10840		45,875	42,969	45,846	44,696	77,922	45,754	42,886	45,722	44,582	77,856
Os05g0207500	GSK(CMGC_3)	1,360	1,181	104	106		1,260	1,084	10	19	
LOC_Os05g11730		2,505	2,353	2,461	2,422	3,716	2,411	2,280	2,369	2,342	3,655
Os02g0236200	GSK(CMGC_3)	1,041	2,858	125	553		906	2,743	5	451	
LOC_Os02g14130		1,350	1,118	1,075	1,312	3,110	1,235	1,031	948	1,196	3,052
Os06g0547900	GSK(CMGC_3)	18,049	27,913	2,124	909		17,901	27,789	2,009	801	
LOC_Os06g35530		83,709	78,557	81,396	84,410	108,238	83,585	78,463	81,247	84,281	108,168
Os01g0252100	GSK(CGMC_3)	68,526	105,159	8,223	4,316		68,377	105,036	8,095	4,199	
LOC_Os01g14860		57,630	52,630	51,885	54,443	54,318	57,495	52,538	51,720	54,298	54,235
Os01g0296100	GSK(CMGC_3)	19,455	38,100	81,997	91,878		19,347	38,005	81,905	91,778	
LOC_Os01g19150		26,342	23,282	26,570	26,865	37,582	26,256	23,212	26,475	26,757	37,515
Os03g0841800	GSK(CMGC_3)	85,869	94,844	7,212	821		85,747	94,743	7,105	720	
LOC_Os03g62500		71,722	67,250	75,177	72,234	104,409	71,611	67,176	75,048	72,117	104,346
Os10g0521700	GSK(CMGC_3)	29,860	44,180	283,540	340,879		29,760	44,083	283,444	340,791	
LOC_Os10g37740		69,658	67,412	68,984	69,624	55,267	69,563	67,338	68,891	69,541	55,205
Os03g0207300	CK2(CMGC_4)	43,442	29,093	83,243	49,649		43,337	28,999	83,153	49,560	
LOC_Os03g10940		34,562	31,065	32,726	34,724	25,512	34,473	30,997	32,648	34,647	25,437
Os07g0114400	CK2(CMGC_4)	69,659	71,772	9,959	8,196		69,556	71,676	9,859	8,106	
LOC_Os07g02350		68,466	65,678	69,023	68,368	77,475	68,371	65,606	68,930	68,283	77,404
Os03g0763000	CK2(CMGC_4)	8,922	11,328	7,079	6,286		8,816	11,228	6,984	6,195	
LOC_Os03g55490		8,827	8,089	8,608	8,549	10,102	8,722	8,013	8,508	8,459	10,045
Os01g0198200	CaseinKinase_1a	26,053	31,656	7,887	4,972		25,947	31,555	7,784	4,882	
LOC_Os01g10150		16,616	16,050	16,391	16,552	21,825	16,514	15,973	16,289	16,461	21,762
Os05g0200500	CaseinKinase_1a	7,073	17,427	13,284	5,634		6,970	17,329	13,183	5,543	
LOC_Os05g11140		7,307	6,596	7,016	6,690	7,601	7,207	6,521	6,920	6,602	7,534
Os01g0744300	CaseinKinase_1a	44,608	84,400	7,437	6,086		44,503	84,307	7,346	5,997	
LOC_Os01g54100		49,776	43,258	46,576	49,401	85,131	49,687	43,189	46,492	49,322	85,059
Os03g0793500	CaseinKinase_1a	11,994	16,950	12,040	11,958		11,894	16,855	11,945	11,870	
LOC_Os03g57940		6,972	6,427	6,679	6,878	7,341	6,880	6,355	6,588	6,797	7,263
Os07g0171300	CaseinKinase_1a	60,064	105,828	94,900	74,502		59,965	105,731	94,806	74,415	
LOC_Os07g07560		35,321	34,765	33,567	35,839	44,562	35,226	34,691	33,474	35,758	44,491
Os01g0772600	CaseinKinase_1a	81,309	96,631	56,142	32,956		81,205	96,535	56,048	32,866	
LOC_Os01g56580		76,296	70,601	71,885	73,657	97,053	76,206	70,529	71,793	73,575	96,980
Os01g0231500	CaseinKinase_1	1,697	2,423	1,849	1,589		1,593	2,324	1,755	1,499	
LOC_Os01g13060		2,745	2,517	2,753	2,728	3,188	2,642	2,442	2,654	2,640	3,125
Os02g0280400	CaseinKinase_1	11,472	10,403	660	922		11,371	10,308	570	834	
LOC_Os02g17910		8,449	7,652	7,824	8,350	11,428	8,357	7,580	7,735	8,268	11,359
Os02g0622100	CaseinKinase_1	5,113	9,486	4,096	4,024		5,012	9,385	4,004	3,934	
LOC_Os02g40860		6,590	5,789	6,242	6,535	8,685	6,507	5,714	6,148	6,448	8,626
Os04g0514800	CaseinKinase_1	51,774	81,398	12,690	7,723		51,670	81,299	12,589	7,633	
LOC_Os04g43490		18,832	17,911	17,069	18,202	15,389	18,734	17,836	16,970	18,115	15,319
Os02g0810400	CaseinKinase_1	57,585	78,913	48,091	36,259		57,464	78,811	47,982	36,158	
LOC_Os02g56560		73,837	67,231	78,328	80,532	90,112	73,724	67,154	78,198	80,413	90,040
Os10g0476300	CaseinKinase_1	783	748	384,394	364,047		646	637	384,273	363,936	
LOC_Os10g33650		1,771	1,699	19,710	19,667	14,374	1,639	1,616	19,561	19,531	14,281
Os01g0570500	CaseinKinase_1	37,910	49,818	36,314	26,805		37,800	49,713	36,208	26,713	
LOC_Os01g38950		36,730	34,743	35,371	36,087	52,006	36,623	34,663	35,262	35,989	51,945
Os01g0708400	CaseinKinase_1	28,787	34,451	249	769		28,678	34,354	151	672	
LOC_Os01g51200		42,483	36,843	40,811	39,549	47,554	42,388	36,772	40,697	39,441	47,484
Os05g0593800	CaseinKinase_1	9,253	10,691	2,242	1,573		9,146	10,590	2,141	1,480	
LOC_Os05g51560		5,738	5,502	5,415	5,618	10,635	5,633	5,425	5,315	5,526	10,558
Os03g0748400	CLK(CMGC_5)_SRPKh	22,268	22,027	5,045	4,362		22,166	21,933	4,951	4,273	
LOC_Os03g53720		10,324	9,415	9,437	9,947	8,730	10,235	9,346	9,351	9,865	8,675
Os07g0472400	CLK(CMGC_5)_SRPKh	813	493	28,486	44,087		663	370	28,363	43,978	
LOC_Os07g28930		5,867	5,070	6,081	6,242	2,300	5,744	4,979	5,934	6,110	2,240

Supplemental Table 14 continue. Microarray data for rice kinase genes

Os12g0460800	CLK(CMGC_5)_CLK2_	122,181	248,939	63,056	47,336		122,077	248,845	62,964	47,242	
LOC_Os12g27520		94,681	88,744	93,121	96,409	110,567	94,594	88,675	93,012	96,307	110,494
Os01g0837900	CLK(CMGC_5)_CLK2_	47,780	67,164	11,834	18,423		47,652	67,061	11,727	18,322	
LOC_Os01g62080		35,650	33,468	36,320	36,050	33,930	35,529	33,393	36,189	35,931	33,859
Os01g0590900	CLK(CMGC_5)_CLK2_	16,405	28,088	3,813	7,130		16,298	27,995	3,721	7,039	
LOC_Os01g40840		11,641	10,385	11,006	11,081	12,229	11,551	10,312	10,896	10,990	12,166
Os02g0702500	CLK(CMGC_5)_YAKy_	28,454	23,537	48,196	32,869		28,351	23,445	48,106	32,780	
LOC_Os02g47410		49,506	43,285	45,607	47,552	108,391	49,419	43,218	45,529	47,476	108,327
Os04g0602800	CLK(CMGC_5)_YAKy	137,364	114,114	32,478	17,851		137,251	114,017	32,377	17,755	
LOC_Os04g51370		91,300	83,680	87,638	86,333	147,953	91,199	83,608	87,514	86,228	147,887
Os01g0832900	CLK(CMGC_5)_PRP4h	12,017	24,823	102	105		11,913	24,728	9	15	
LOC_Os01g61620		13,959	12,254	13,325	14,041	20,850	13,869	12,183	13,236	13,961	20,786
Os05g0466900	CLK(CMGC_5)_PRP4h	18,222	22,363	2,791	1,827		18,085	22,250	2,667	1,715	
LOC_Os05g39080		42,321	39,638	43,912	42,261	54,036	42,189	39,553	43,764	42,123	53,940
Os03g0719500	CLK(CMGC_5)_PRP4h	30,391	69,009	15,894	15,235		30,282	68,913	15,797	15,140	
LOC_Os03g51020		56,284	51,866	58,724	56,981	79,865	56,191	51,795	58,607	56,877	79,789
Os12g0640800	CLK(CMGC_5)_PRP4h	27,084	46,862	30,093	10,992		26,976	46,762	29,987	10,899	
LOC_Os12g44330		22,487	20,450	22,742	21,611	45,342	22,382	20,374	22,641	21,518	45,281
Os03g0704400	TTKh_MPS1y	7,576	5,191	279	98		7,473	5,099	190	10	
LOC_Os03g49750		3,879	3,337	3,349	3,506	12,388	3,792	3,272	3,274	3,431	12,325
Os02g0591900	NimA_AAKh_BIKEh_N	55,847	39,232	98,474	98,092		55,741	39,135	98,370	98,001	
LOC_Os02g37880		34,889	30,409	33,875	35,538	39,614	34,791	30,325	33,745	35,426	39,540
Os09g0279100	NimA_AAKh_BIKEh_N	2,929	5,106	93	82		2,819	5,010	2	2	
LOC_Os09g10720		1,405	1,394	1,447	1,392	1,756	1,308	1,322	1,329	1,294	1,692
Os09g0237600	MPSKh_like	179	363	112	110		36	243	2	2	
LOC_Os09g06230		252	198	225	243	267	117	107	70	101	208
Os09g0372800	MPSKh_like	3,275	4,611	765	719		3,175	4,512	672	629	
LOC_Os09g20640		4,094	3,604	3,729	3,989	3,395	4,011	3,530	3,636	3,905	3,343
Os01g0622600	CAMK_like(CAMK_1)	29,820	46,199	314	286		29,718	46,106	226	198	
LOC_Os01g43410		83,389	74,755	80,659	82,934	112,072	83,298	74,685	80,574	82,852	111,997
Os05g0585500	CAMK_like(CAMK_1)	36,254	75,933	1,971	2,892		36,130	75,829	1,859	2,788	
LOC_Os05g50810		25,786	23,223	27,507	27,611	29,758	25,669	23,145	27,368	27,488	29,700
Os01g0808400	CAMK_like(CAMK_1)	86	85	237,961	328,043		2	2	237,872	327,956	
LOC_Os01g59360		65	60	22,114	30,588	12,197	2	2	22,038	30,513	12,135
Os05g0491900	CAMK_like(CAMK_1)	82	90	158,065	188,952		2	2	157,976	188,864	
LOC_Os05g41270		62	65	3,203	5,106	1,215	2	2	3,116	5,023	1,155
Os11g0136600	CAMK_like(CAMK_1)	162	444	208,433	232,840		30	338	208,321	232,735	
LOC_Os11g04170		168	116	1,605	1,752	1,356	42	38	1,468	1,622	1,287
Os12g0133500	CAMK_like(CAMK_1)	102	1,035	235,387	298,746		2	937	235,281	298,652	
LOC_Os12g03970		259	246	1,972	2,905	1,993	162	166	1,843	2,790	1,910
Os04g0560600	CAMK_like(CAMK_1)	236	157	281	152		84	32	155	35	
LOC_Os04g47300		2,236	2,046	2,344	2,366	1,594	2,101	1,953	2,179	2,224	1,540
Os02g0685900	CAMK_like(CAMK_1)	23,785	99,056	299	358		23,681	98,958	199	269	
LOC_Os02g46090		56,109	54,123	53,104	55,445	85,859	56,015	54,048	53,007	55,360	85,780
Os04g0584600	CAMK_like(CAMK_1)	45,339	128,750	219	188		45,226	128,652	118	90	
LOC_Os04g49510		127,792	119,946	130,876	127,865	209,308	127,692	119,874	130,757	127,755	209,240
Os02g0832000	CAMK_like(CAMK_1)	442	132	119,920	103,998		337	42	119,829	103,909	
LOC_Os02g58520		225	218	555	502	820	139	144	447	414	755
Os03g0128700	CAMK_like(CAMK_1)	8,513	40,827	4,197	2,747		8,414	40,731	4,106	2,661	
LOC_Os03g03660		50,443	47,578	48,400	50,477	44,452	50,353	47,507	48,311	50,400	44,377
Os10g0539600	CAMK_like(CAMK_1)	3,662	6,704	1,002	2,649		3,562	6,606	908	2,562	
LOC_Os10g39420		15,842	14,935	15,658	16,167	12,900	15,746	14,861	15,565	16,085	12,834
Os03g0788500*	CAMK_like(CAMK_1)	96,666	207,493	1,543	828		96,561	207,393	1,442	738	
LOC_Os03g57450		27,196	31,217	21,823	21,754	23,255	27,098	31,141	21,723	21,666	23,185
Os12g0486600	CAMK_like(CAMK_1)	94	87	32,837	32,076		2	2	32,750	31,978	
LOC_Os12g30150		71	65	142	130	173	2	2	48	29	114
Os03g0789000	CAMK_like(CAMK_1)	99	98	9,306	14,927		2	2	9,203	14,837	
LOC_Os03g57510		102	84	248	279	351	2	6	144	188	291
Os07g0161600	CAMK_like(CAMK_1)	12,792	23,333	3,963	3,697		12,685	23,238	3,868	3,605	
LOC_Os07g06740		14,824	12,842	14,205	13,755	15,690	14,732	12,771	14,088	13,655	15,639
Os11g0171500	CAMK_like(CAMK_1)	27,857	47,571	150	312		27,747	47,473	54	218	
LOC_Os11g07040		41,572	37,976	39,712	39,982	41,367	41,466	37,903	39,600	39,882	41,302
Os12g0169800	CAMK_like(CAMK_1)	8,469	21,265	30,877	20,382		8,363	21,169	30,774	20,293	
LOC_Os12g07230		25,361	22,207	23,969	25,561	33,822	25,269	22,126	23,847	25,449	33,754
Os01g0832300	CAMK_like(CAMK_1)	103,034	132,300	1,622	1,551		102,932	132,207	1,531	1,462	
LOC_Os01g61590		104,047	93,666	83,324	87,053	107,329	103,960	93,599	83,243	86,975	107,263
Os05g0467000	CAMK_like(CAMK_1)	8,376	7,270	118	113		8,231	7,146	5	6	
LOC_Os05g39090		7,170	6,485	7,308	7,261	13,063	7,049	6,391	7,162	7,135	12,988
Os03g0808600	CAMK_like(CAMK_1)	26,031	39,081	243	132		25,898	38,975	129	26	
LOC_Os03g59390		15,872	14,759	15,887	15,253	13,044	15,745	14,681	15,747	15,121	12,982
Os07g0568600	CAMK_like(CAMK_1)	12,873	48,751	465	221		12,768	48,658	375	132	
LOC_Os07g38120		7,426	7,530	6,042	7,181	15,401	7,337	7,463	5,964	7,104	15,335
Os12g0230200	CAMK_like(CAMK_1)	118	94	299,460	396,536		2	2	299,352	396,434	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os12g12860		121	85	1,435	1,874	729	4	11	1,303	1,754	658
Os08g0540400	CAMK_like(CAMK_1)	1,221	680	317,481	393,588		1,121	584	317,386	393,501	
LOC_Os08g42750		316	309	10,336	18,170	2,126	223	237	10,245	18,089	2,067
Os09g0514200	CAMK_like(CAMK_1)	140	1,040	280,351	404,009		36	945	280,260	403,920	
LOC_Os09g33910		908	805	3,087	4,453	2,238	814	733	2,991	4,368	2,173
Os03g0688300	CAMK_like(CAMK_1)	696	373	86	89		594	278	2	2	
LOC_Os03g48270		5,300	4,341	4,663	4,896	9,261	5,216	4,272	4,577	4,824	9,192
Os07g0409900	CAMK_like(CAMK_1)	9,742	25,950	5,301	7,387		9,641	25,854	5,210	7,300	
LOC_Os07g22710		23,794	22,523	23,800	25,041	21,736	23,700	22,450	23,708	24,960	21,671
Os03g0366200	CAMK_like(CAMK_1)	16,449	23,513	1,154	584		16,350	23,421	1,069	498	
LOC_Os03g25070		20,439	17,367	17,361	19,865	12,167	20,347	17,302	17,287	19,785	12,106
Os07g0641200	CAMK_like(CAMK_1)	14,728	27,016	202	181		14,624	26,918	110	92	
LOC_Os07g44710		25,579	24,196	24,588	25,582	32,924	25,479	24,123	24,488	25,495	32,857
Os07g0619800	CAMK_like(CAMK_1)	28,872	42,944	157	158		28,751	42,842	54	58	
LOC_Os07g42770		40,964	38,311	38,888	36,221	57,502	40,848	38,236	38,765	36,109	57,416
Os06g0714200	CAMK_like(CAMK_1)	5,244	6,044	9,082	9,537		5,147	5,944	8,991	9,449	
LOC_Os06g50030		11,631	10,474	11,418	12,140	15,989	11,555	10,400	11,329	12,060	15,927
Os10g0510700	CAMK_like(CAMK_1)	64,728	58,174	13,031	4,151		64,599	58,067	12,915	4,045	
LOC_Os10g36710		17,034	15,834	16,079	15,828	30,614	16,913	15,754	15,934	15,699	30,554
Os09g0466900	CAMK_like(CAMK_1)	1,903	3,443	992	1,087		1,787	3,343	888	987	
LOC_Os09g29170		2,969	2,741	3,106	2,753	2,595	2,863	2,667	2,990	2,638	2,528
Os02g0625300	CAMK_like(CAMK_1)	437	216	708	93		314	110	594	2	
LOC_Os02g41580		361	307	1,483	293	567	249	221	1,352	181	502
Os04g0517500	CAMK_like(CAMK_1)	5,104	859	15,669	9,313		4,976	755	15,559	9,209	
LOC_Os04g43710		9,765	8,940	8,952	9,556	9,905	9,645	8,865	8,822	9,430	9,834
Os02g0807000*	L-LEC	70,782	77,378	2,764	2,066		70,641	77,260	2,639	1,953	
LOC_Os02g56310		3,238	2,944	2,484	2,648	3,195	3,114	2,855	2,320	2,513	3,135
Os02g0135300	Swe1y_Wee1	13,194	10,596	93	114		13,087	10,500	2	22	
LOC_Os02g04240		5,065	4,733	4,921	4,825	2,887	4,967	4,662	4,813	4,732	2,824
Os05g0511400	AGC_other_NDRh_TR	33,462	56,800	2,180	1,659		33,353	56,702	2,074	1,567	
LOC_Os05g43570		52,092	43,492	50,702	52,499	33,400	51,989	43,407	50,577	52,391	33,346
Os12g0290100	AGC_other_NDRh_TR	37,433	34,374	786	643		37,305	34,269	676	540	
LOC_Os12g19290		19,273	16,334	17,712	18,794	20,925	19,150	16,256	17,580	18,671	20,858
Os10g0476100	AGC_other_NDRh_TR	362	122	37,424	33,050		230	10	37,305	32,950	
LOC_Os10g33640		382	291	1,090	1,643	1,580	268	204	964	1,530	1,517
Os01g0186700	AGC_other_NDRh_TR	115,013	90,451	3,826	3,542		114,878	90,338	3,701	3,428	
LOC_Os01g09200		95,560	86,551	87,443	86,112	118,498	95,435	86,463	87,284	85,975	118,432
Os02g0281000	PKA/PKG_like(AGC_1)	13,924	28,871	207	89		13,816	28,767	105	2	
LOC_Os02g17970		12,012	11,281	12,086	11,963	17,669	11,910	11,201	11,980	11,870	17,612
Os03g0334000	AGC_other++RS6K_like(AGC_6)	1,901	4,688	2,233	2,461		1,798	4,590	2,132	2,370	
LOC_Os03g21620		582	577	559	573	660	482	503	463	485	586
Os07g0680900	AGC_other++RS6K_like	23,556	32,913	43,729	38,265		23,441	32,812	43,619	38,169	
LOC_Os07g48290		7,973	7,835	9,063	9,522	14,725	7,868	7,750	8,925	9,404	14,650
Os03g0711800	AGC_other_GWLd	37,970	61,139	525	217		37,866	61,043	430	128	
LOC_Os03g50390		27,975	25,714	25,998	27,284	37,617	27,885	25,642	25,906	27,201	37,543
Os12g0621500	AGC_other_GWLd	1,140	175	21,835	13,776		1,041	82	21,748	13,690	
LOC_Os12g42660		159	135	331	248	194	68	69	254	168	112
Os01g0872800	AGC_other_PDK1_Pk6	8,730	9,407	19,789	6,802		8,614	9,308	19,689	6,705	
LOC_Os01g65230		14,232	13,046	14,616	13,856	11,235	14,124	12,974	14,492	13,750	11,174
Os03g0642200	PVPK_like(AGC_8)_kin82y	164	86	610	201		65	2	518	115	
LOC_Os03g44020		2,301	2,081	2,112	2,020	4,614	2,209	2,008	2,021	1,940	4,543
Os12g0614600	PVPK_like(AGC_8)_kin82y	4,770	7,974	87	82		4,664	7,879	2	2	
LOC_Os12g42020		3,646	3,437	3,575	3,517	3,475	3,550	3,366	3,468	3,426	3,409
Os01g0174700	PVPK_like(AGC_8)_kin	5,128	1,587	1,593	738		5,026	1,491	1,494	648	
LOC_Os01g07940		1,237	1,182	1,203	1,165	2,031	1,141	1,110	1,111	1,079	1,972
Os01g0233800	PVPK_like(AGC_8)_kin	117	84	54,354	64,244		9	2	54,262	64,144	
LOC_Os01g13270		87	81	258	241	162	2	10	164	133	97
Os05g0237400	PVPK_like(AGC_8)_kin	127	235	122,746	119,029		8	134	122,640	118,928	
LOC_Os05g14750		102	66	1,480	1,342	560	2	2	1,360	1,224	497
Os02g0654300	PVPK_like(AGC_8)_kin	7,277	7,772	84	78		7,175	7,679	2	2	
LOC_Os02g43740		12,334	10,563	11,569	12,493	11,872	12,247	10,498	11,496	12,420	11,811
Os04g0546300	PVPK_like(AGC_8)_kin	39,892	52,915	1,339	1,395		39,792	52,818	1,243	1,308	
LOC_Os04g46180		16,792	15,782	16,343	15,864	23,650	16,698	15,709	16,250	15,782	23,597
Os10g0562500	PVPK_like(AGC_8)_kin	1,664	531	821	1,471		1,564	439	732	1,385	
LOC_Os10g41290		2,705	2,355	2,444	2,569	2,642	2,616	2,290	2,367	2,492	2,582
Os02g0725000	PVPK_like(AGC_8)_kin	4,022	23,385	155	147		3,922	23,289	65	58	
LOC_Os02g49310		17,164	15,206	15,961	16,683	16,408	17,079	15,135	15,872	16,606	16,347
Os06g0291600	PVPK_like(AGC_8)_kin	2,911	4,607	2,188	1,619		2,793	4,508	2,084	1,520	
LOC_Os06g18830		10,727	10,144	10,905	10,619	12,971	10,620	10,072	10,777	10,508	12,896
Os09g0258500	PVPK_like(AGC_8)_kin	2,387	3,412	1,044	844		2,257	3,293	946	744	
LOC_Os09g08420		4,985	4,345	4,782	5,047	6,214	4,882	4,255	4,657	4,938	6,141
Os08g0491200	PVPK_like(AGC_8)_kin	952	158	209	111		810	41	82	2	
LOC_Os08g38320		1,516	1,363	1,535	1,459	1,113	1,383	1,274	1,378	1,315	1,045

Supplemental Table 14 continue. Microarray data for rice kinase genes

Os09g0478500	PVPK_like(AGC_8)_kin	18,936	14,959	2,282	1,053		18,806	14,851	2,161	942	
LOC_Os09g30150		19,295	17,877	20,984	20,940	18,001	19,174	17,793	20,832	20,803	17,947
Os12g0480200	PVPK_like(AGC_8)_kin	6,906	13,324	102	84		6,787	13,220	2	2	
LOC_Os12g29580		9,491	8,079	8,697	9,406	10,038	9,383	7,994	8,557	9,287	9,980
Os11g0150700	PVPK_like(AGC_8)_kin	676	90	98	129		559	2	2	28	
LOC_Os11g05320		2,395	2,136	2,449	2,466	6,820	2,289	2,063	2,335	2,349	6,746
Os04g0304200	PVPK_like(AGC_8)_kin	1,359	1,302	399	372		1,228	1,196	286	267	
LOC_Os04g23890		25,235	24,142	26,290	26,381	34,155	25,110	24,064	26,152	26,251	34,071
Os11g0102200	PVPK_like(AGC_8)_kin	133	151	135	135		2	26	10	21	
LOC_Os11g01140		14,190	13,121	14,065	14,513	24,892	14,060	13,028	13,902	14,375	24,835
Os12g0101800	PVPK_like(AGC_8)_kin	93	112	84	99		2	18	2	12	
LOC_Os12g01140		13,794	12,343	13,059	13,808	23,178	13,706	12,274	12,972	13,731	23,108
Os03g0253200	PVPK_like(AGC_8)_kin	117	156	117	102		16	64	30	3	
LOC_Os03g14840		2,288	1,907	2,330	2,418	2,692	2,209	1,839	2,238	2,316	2,638
Os08g0504800	PVPK_like(AGC_8)_CD	450	139	655,539	657,352		336	40	655,431	657,253	
LOC_Os08g39460		5,676	5,249	56,159	90,467	44,092	5,574	5,170	56,026	90,348	44,030
Os09g0486700	PVPK_like(AGC_8)_CD	102	114	86	78		2	20	2	2	
LOC_Os09g31210		5,456	5,006	5,399	5,275	4,154	5,363	4,934	5,284	5,179	4,090
Os01g0191800	CAMK_like(CAMK_1)_ Aur_like	61,491	57,826	18,768	24,730		61,386	57,732	18,680	24,641	
LOC_Os01g09580		53,404	47,030	49,061	53,243	85,177	53,317	46,961	48,978	53,169	85,109
Os01g0759400	KIN1/SNF1/Nim1_like(CAMK_2)	5,233	936	195	205		5,123	826	97	112	
LOC_Os01g55450		2,240	2,175	2,047	2,188	2,209	2,144	2,092	1,940	2,091	2,146
Os05g0514200	KIN1/SNF1/Nim1_like(CAMK_2)	1,329	6,620	1,652	868		1,202	6,512	1,532	758	
LOC_Os05g43840		4,316	3,816	4,501	4,332	7,249	4,198	3,731	4,348	4,197	7,182
Os01g0206300	KIN1/SNF1/Nim1_like(C	90	97	98	113		2	4	7	24	
LOC_Os01g10870		97	94	97	99	173	9	26	15	19	110
Os03g0339900	KIN1/SNF1/Nim1_like(C	143	113	192	180		18	11	87	80	
LOC_Os03g22050		571	523	598	587	303	453	448	469	472	244
Os07g0678600	KIN1/SNF1/Nim1_like(C	19,903	51,369	2,958	1,624		19,764	51,255	2,833	1,509	
LOC_Os07g48100		200,841	193,587	203,986	210,128	168,752	200,711	193,501	203,831	209,987	168,662
Os05g0332300	KIN1/SNF1/Nim1_like(C	5,408	15,994	7,464	4,609		5,283	15,890	7,354	4,506	
LOC_Os05g26820		22,202	21,347	20,839	21,203	26,780	22,083	21,269	20,716	21,085	26,720
Os01g0206700	KIN1/SNF1/Nim1_like(C	15,766	26,172	248,590	372,031		15,652	26,076	248,490	371,934	
LOC_Os01g10890		5,742	5,498	19,016	25,854	9,748	5,644	5,424	18,904	25,744	9,687
Os05g0208100	KIN1/SNF1/Nim1_like(C	4,440	3,621	34,627	28,887		4,339	3,523	34,533	28,797	
LOC_Os05g11790		110	110	194	191	241	23	35	99	107	176
Os01g0759200	KIN1/SNF1/Nim1_like(C	162	116	543,492	654,013		33	6	543,375	653,914	
LOC_Os01g55440		243	182	41,906	61,077	36,586	129	96	41,778	60,965	36,499
Os09g0418000	KIN1/SNF1/Nim1_like(C	2,220	1,108	192	134		2,088	998	70	22	
LOC_Os09g25090		7,446	6,827	7,472	7,547	8,634	7,323	6,742	7,318	7,409	8,565
Os08g0441100	KIN1/SNF1/Nim1_like(C	72,246	29,882	12,418	6,121		72,142	29,788	12,326	6,030	
LOC_Os08g34240		30,700	20,892	20,693	23,299	39,866	30,606	20,821	20,593	23,211	39,802
Os09g0418500	KIN1/SNF1/Nim1_like(C	123	130	124	82		4	27	20	2	
LOC_Os09g25100		147	119	168	133	455	30	41	52	23	397
Os01g0824600	KIN1/SNF1/Nim1_like(C	4,950	2,439	89	556		4,829	2,324	2	459	
LOC_Os01g60910		6,674	6,456	6,228	6,764	5,133	6,566	6,368	6,105	6,655	5,074
Os02g0161000	KIN1/SNF1/Nim1_like(C	2,042	1,829	100	125		1,925	1,717	2	29	
LOC_Os02g06570		777	699	782	818	3,146	666	613	661	711	3,076
Os11g0113700	KIN1/SNF1/Nim1_like(C	7,780	33,980	124	543		7,638	33,861	2	429	
LOC_Os11g02240		8,553	8,008	8,603	8,343	11,466	8,418	7,919	8,449	8,201	11,405
Os12g0113500	KIN1/SNF1/Nim1_like(C	18,321	61,589	125	655		18,207	61,490	26	559	
LOC_Os12g02200		21,836	19,777	21,677	20,714	27,442	21,729	19,705	21,556	20,609	27,384
Os06g0606000	KIN1/SNF1/Nim1_like(C	1,845	3,116	5,900	6,942		1,702	2,998	5,773	6,826	
LOC_Os06g40370		4,335	4,132	4,379	4,485	3,089	4,206	4,042	4,215	4,346	3,033
Os07g0687000	KIN1/SNF1/Nim1_like(C	85	96	88	98		2	2	2	2	
LOC_Os07g48760		1,273	1,162	1,298	1,322	1,590	1,177	1,091	1,189	1,212	1,521
Os12g0132200	KIN1/SNF1/Nim1_like(C	8,356	5,462	105	103		8,239	5,363	3	6	
LOC_Os12g03810		13,308	11,784	12,090	12,556	13,433	13,201	11,712	11,964	12,448	13,371
Os11g0134300	KIN1/SNF1/Nim1_like(C	9,278	5,052	83	82		9,174	4,958	2	2	
LOC_Os11g03970		23,275	20,244	20,885	22,611	19,564	23,185	20,175	20,800	22,530	19,512
Os07g0150700	KIN1/SNF1/Nim1_like(C	469	1,048	148	294		349	943	36	193	
LOC_Os07g05620		3,703	3,440	3,565	3,546	3,998	3,587	3,360	3,449	3,436	3,944
Os03g0126800	KIN1/SNF1/Nim1_like(C	101	95	95	568		2	2	6	480	
LOC_Os03g03510		230	209	230	247	790	139	138	143	164	726
Os01g0292200	KIN1/SNF1/Nim1_like(C	3,893	9,656	937	532		3,788	9,560	845	442	
LOC_Os01g18800		78,991	75,006	79,469	80,263	88,664	78,894	74,934	79,368	80,175	88,597
Os05g0136200	KIN1/SNF1/Nim1_like(C	1,388	4,995	1,097	198		1,287	4,902	1,005	110	
LOC_Os05g04550		9,986	8,821	9,013	9,593	16,120	9,898	8,753	8,930	9,515	16,060
Os07g0637000	KIN1/SNF1/Nim1_like(C	440	1,440	537	822		328	1,344	439	723	
LOC_Os07g44290		1,702	1,566	1,784	1,766	3,048	1,606	1,493	1,679	1,656	2,982
Os02g0178000*	KIN1/SNF1/Nim1_like(C	13,284	31,562	2,921	1,807		13,162	31,462	2,816	1,707	
LOC_Os02g08140		2,194	2,138	2,214	2,162	2,283	2,082	2,065	2,083	2,048	2,224
Os06g0543400	KIN1/SNF1/Nim1_like(C	16,531	6,735	4,348	4,277		16,381	6,613	4,224	4,165	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os06g35160		11,011	10,350	11,528	11,350	17,489	10,885	10,259	11,369	11,215	17,422
Os03g0634400	KIN1/SNF1/Nim1_like(C	119	91	98	85		2	2	2	2	
LOC_Os03g43440		11,001	10,620	10,771	10,329	10,012	10,880	10,545	10,639	10,208	9,948
Os12g0603700	KIN1/SNF1/Nim1_like(C	6,290	1,082	87	85		6,186	986	2	2	
LOC_Os12g41090		1,771	1,537	1,475	1,516	1,156	1,679	1,464	1,380	1,432	1,097
Os05g0334800	KIN1/SNF1/Nim1_like(CAMK_2)	8,932	2,649	1,920	3,791		8,803	2,544	1,809	3,687	
LOC_Os05g26940		6,370	5,825	6,520	6,532	5,166	6,249	5,749	6,387	6,405	5,092
Os05g0333000	KIN1/SNF1/Nim1_like(CAMK_2)	1,703	1,334	1,735	2,356		1,596	1,232	1,632	2,265	
LOC_Os05g26870		412	344	340	328	251	310	266	236	237	181
Os07g0678300	KIN1/SNF1/Nim1_like(CAMK_2)	72,786	54,616	32,893	36,748		72,687	54,524	32,808	36,661	
LOC_Os07g48090		75,400	63,275	58,525	67,000	105,837	75,307	63,208	58,450	66,918	105,767
Os02g0551100	CAMK_like(CAMK_1)	5,132	4,403	1,230	917		4,993	4,287	1,105	805	
LOC_Os02g34600		3,375	3,286	3,535	3,551	5,984	3,242	3,198	3,383	3,410	5,894
Os04g0432000	CAMK_like(CAMK_1)	7,244	17,708	275	282		7,125	17,602	163	183	
LOC_Os04g35240		19,718	18,613	19,395	19,147	9,826	19,602	18,531	19,278	19,039	9,744
Os04g0691100	CAMK_like(CAMK_1)	100	161	103	134		2	64	12	46	
LOC_Os04g59450		13,289	11,171	11,877	13,038	21,880	13,208	11,099	11,787	12,960	21,818
Os01g0869900	CAMK_like(CAMK_1)	52,113	48,966	144,484	153,909		52,010	48,867	144,390	153,819	
LOC_Os01g64970		49,232	45,092	49,236	50,321	54,609	49,130	45,017	49,138	50,234	54,527
Os03g0390200	CAMK_like(CAMK_1)	19,984	15,014	20,490	12,278		19,867	14,905	20,380	12,181	
LOC_Os03g27280		44,312	42,038	42,575	44,137	41,339	44,198	41,955	42,455	44,029	41,268
Os07g0622000	CAMK_like(CAMK_1)	24,243	47,754	1,319	310		24,109	47,636	1,202	205	
LOC_Os07g42940		49,139	43,535	51,018	50,454	54,027	49,011	43,445	50,877	50,327	53,971
Os03g0610900	CAMK_like(CAMK_1)	5,463	1,683	611	771		5,360	1,589	519	682	
LOC_Os03g41460		4,655	4,205	4,574	4,655	10,350	4,566	4,136	4,489	4,575	10,291
Os12g0586100	CAMK_like(CAMK_1)	6,466	2,691	92	130		6,333	2,578	2	21	
LOC_Os12g39630		5,200	4,407	4,529	4,615	4,328	5,070	4,321	4,388	4,485	4,270
Os03g0764800	CAMK_like(CAMK_1)	32,165	57,617	9,032	6,367		32,026	57,503	8,907	6,251	
LOC_Os03g55600		63,596	56,575	70,350	68,761	72,346	63,467	56,487	70,193	68,620	72,266
Os10g0564500	CAMK_like(CAMK_1)	1,261	1,007	243	272		1,153	905	142	178	
LOC_Os10g41490		30,552	27,762	30,333	29,449	31,843	30,444	27,684	30,231	29,356	31,772
Os08g0484600	KIN1/SNF1/Nim1_like(C	38,683	40,317	407	415		38,577	40,223	318	326	
LOC_Os08g37800		22,692	18,999	19,305	19,441	35,113	22,603	18,932	19,229	19,366	35,056
Os07g0194100	KIN1/SNF1/Nim1_like(C	169	166	96	82		69	69	2	2	
LOC_Os07g09610		204	175	193	762	196	111	102	101	682	143
Os03g0711300*	KIN1/SNF1/Nim1_like(C	57,731	63,893	14,741	9,740		57,631	63,801	14,653	9,654	
LOC_Os03g50330		15,187	13,650	11,561	12,110	12,825	15,098	13,584	11,482	12,033	12,757
Os01g0259400	NimA_ULK4h	34,260	46,408	2,468	1,413		34,145	46,308	2,369	1,317	
LOC_Os01g15480		24,236	22,332	23,425	23,584	23,854	24,126	22,260	23,307	23,479	23,773
Os12g0433500	NimA_Fused	7,071	10,334	3,161	1,102		6,952	10,234	3,056	1,002	
LOC_Os12g24550		3,102	3,051	3,221	3,022	3,996	2,995	2,978	3,096	2,907	3,933
Os03g0122000	CAMK_like(CAMK_1)_ ULKh_APGy	5,441	9,466	445	379		5,337	9,372	353	289	
LOC_Os03g02980		2,754	2,515	2,702	2,804	4,781	2,665	2,446	2,614	2,724	4,724
Os03g0268200	CAMK_like(CAMK_1)_ ULKh_APGy	74,585	86,837	38,852	19,521		74,481	86,739	38,752	19,431	
LOC_Os03g16130		82,039	80,924	83,160	79,690	102,628	81,944	80,850	83,063	79,604	102,548
Os04g0686600	CAMK_like(CAMK_1)_ ULKh_APGy	9,880	17,499	7,190	6,456		9,766	17,404	7,089	6,360	
LOC_Os04g58990		3,769	3,244	3,488	3,650	9,839	3,673	3,170	3,375	3,541	9,777
Os05g0489900	CAMK_like(CAMK_1)_ CG18020d	354	737	272	173		253	642	176	84	
LOC_Os05g41090		2,866	2,737	2,685	2,867	1,557	2,774	2,667	2,595	2,783	1,489
Os03g0749800	NimA++CAMK_like(CA	39,127	43,269	8,766	4,941		39,023	43,170	8,664	4,851	
LOC_Os03g53880		14,004	13,154	13,679	13,624	14,903	13,906	13,079	13,579	13,537	14,838
Os07g0471000	Eph/Elk/Eck(PTK_11)_	9,468	20,584	2,484	1,742		9,365	20,487	2,383	1,652	
LOC_Os07g28820		9,333	8,877	9,211	9,085	8,348	9,238	8,804	9,117	9,000	8,278
Os01g0864700	NimA_NEK_like	2,734	4,267	4,515	1,227		2,608	4,160	4,399	1,131	
LOC_Os01g64490		37,794	32,310	37,721	39,047	45,341	37,682	32,224	37,599	38,940	45,274
Os05g0440800	NimA_NEK_like	11,510	10,471	5,475	3,803		11,379	10,352	5,365	3,701	
LOC_Os05g36960		13,179	12,230	13,076	13,724	15,838	13,059	12,139	12,940	13,604	15,768
Os03g0636800	NimA_NEK_like	5,991	14,936	3,751	2,046		5,893	14,839	3,660	1,957	
LOC_Os03g43590		491	609	413	378	733	412	537	324	301	662
Os12g0604700	NimA_NEK_like	31,826	20,372	98	97		31,727	20,278	6	10	
LOC_Os12g41180		7,492	6,406	6,170	6,500	8,454	7,404	6,337	6,084	6,423	8,382
Os07g0176600	NimA_NEK_like	107	338	108,987	163,404		2	242	108,891	163,305	
LOC_Os07g08000		3,687	3,106	3,833	4,055	4,208	3,595	3,036	3,727	3,947	4,119
Os02g0590800	NimA_NEK_like	11,788	5,544	651	212		11,649	5,428	526	100	
LOC_Os02g37830		62,561	56,823	60,383	62,647	54,694	62,438	56,734	60,221	62,512	54,622
Os05g0108300	PAK_Ste20++Translati	7,073	9,319	12,775	5,487		6,953	9,215	12,666	5,387	
LOC_Os05g01780		7,741	7,381	7,802	7,590	16,853	7,625	7,302	7,688	7,479	16,793
Os07g0572800	PAK_Ste20_Slob_Wnk	9,385	16,019	89	93		9,267	15,918	2	2	
LOC_Os07g38530		20,362	19,103	20,428	20,380	21,388	20,255	19,026	20,297	20,261	21,306
Os02g0672800	Raf++PAK_Ste20_Slob	12,888	18,176	170,089	226,495		12,757	18,071	169,978	226,390	
LOC_Os02g45130		14,856	13,549	14,104	13,877	20,839	14,731	13,471	13,967	13,749	20,776
Os11g0160300	Raf++PAK_Ste20_Slob	606	106	31,903	22,279		497	10	31,806	22,179	
LOC_Os11g06140		123	98	274	201	469	31	27	172	92	414

Supplemental Table 14 continue. Microarray data for rice kinase genes

Os12g0162100	PAK_Ste20_Slob_Wnk	86,511	106,545	18,849	8,700		86,383	106,442	18,741	8,598	
LOC_Os12g06490		31,512	28,887	31,362	31,818	49,169	31,390	28,809	31,231	31,697	49,113
Os11g0114600	PAK_Ste20_Slob_Wnk	529	147	524	439		422	52	428	348	
LOC_Os11g02300		7,681	6,698	7,514	7,676	7,096	7,588	6,626	7,397	7,579	7,034
Os12g0114100	PAK_Ste20_Slob_Wnk	115	130	160	115		2	8	56	12	
LOC_Os12g02250		12,236	11,169	11,334	11,838	10,116	12,126	11,078	11,200	11,723	10,045
Os07g0185000	PAK_Ste20_Slob_Wnk	199	113	130	465		57	2	3	348	
LOC_Os07g08750		14,531	13,440	14,311	14,770	14,236	14,400	13,350	14,151	14,628	14,172
Os07g0584100	PAK_Ste20_Slob_Wnk	9,342	4,003	10,553	14,979		9,243	3,907	10,461	14,892	
LOC_Os07g39520		3,374	3,087	3,289	3,374	3,641	3,283	3,015	3,198	3,295	3,582
Os03g0225100	MEK_ste7_MAP2K	806	893	76	78		705	801	2	2	
LOC_Os03g12390		3,601	3,145	3,180	3,392	6,510	3,514	3,081	3,104	3,317	6,445
Os01g0510100	MEK_ste7_MAP2K	29,489	51,919	847	574		29,379	51,825	746	481	
LOC_Os01g32660		56,400	48,051	57,958	60,618	89,982	56,310	47,974	57,844	60,507	89,916
Os06g0473200	MEK_ste7_MAP2K	4,028	12,985	3,029	365		3,930	12,889	2,940	277	
LOC_Os06g27890		3,889	3,354	3,509	3,697	16,100	3,808	3,283	3,421	3,624	16,035
Os02g0787300	MEK_ste7_MAP2K	8,118	5,881	1,699	882		7,995	5,779	1,591	781	
LOC_Os02g54600		4,114	3,692	3,513	3,358	5,096	4,002	3,618	3,389	3,238	5,037
Os01g0699100	MEKK_ste11_MAP3K	14,526	13,000	68,932	64,410		14,401	12,897	68,824	64,307	
LOC_Os01g50370		10,029	9,403	10,490	10,562	27,899	9,912	9,328	10,363	10,439	27,838
Os05g0545400	MEKK_ste11_MAP3K	2,072	2,512	6,656	7,257		1,968	2,420	6,568	7,157	
LOC_Os05g46760		863	780	912	1,002	972	784	711	823	897	915
Os01g0699500	MEKK_ste11_MAP3K	965	268	11,037	12,472		829	153	10,915	12,363	
LOC_Os01g50410		2,583	2,473	2,731	2,713	4,912	2,452	2,386	2,587	2,579	4,858
Os01g0699600	MEKK_ste11_MAP3K	7,681	4,563	18,351	19,148		7,581	4,467	18,258	19,061	
LOC_Os01g50420		12,128	11,130	11,277	12,211	20,960	12,038	11,058	11,187	12,132	20,893
Os01g0699400	MEKK_ste11_MAP3K	2,056	3,050	3,422	2,022		1,923	2,938	3,300	1,912	
LOC_Os01g50400		603	580	686	633	785	483	493	527	501	717
Os05g0545300	MEKK_ste11_MAP3K	170	2,015	20,688	23,974		47	1,910	20,579	23,872	
LOC_Os05g46750		279	276	581	630	648	160	198	460	514	592
Os10g0129000	MEKK_ste11_MAP3K	4,325	1,760	94	99		4,216	1,667	2	2	
LOC_Os10g04000		272	241	253	282	910	187	170	160	174	850
Os03g0292600	MEKK_ste11_MAP3K	543	531	2,522	2,818		409	422	2,401	2,707	
LOC_Os03g18170		500	301	542	381	2,149	373	217	392	244	2,088
Os02g0791700	PAK_Ste20_STLK	1,123	1,269	41,578	29,748		980	1,151	41,450	29,631	
LOC_Os02g54900		638	528	782	744	933	506	439	621	602	875
Os06g0486400	PAK_Ste20_STLK	3,708	7,365	608	360		3,602	7,270	513	266	
LOC_Os06g29120		5,380	4,842	5,296	5,066	5,704	5,289	4,772	5,181	4,964	5,648
Os03g0114300	PAK_Ste20_STLK	34,874	34,565	2,018	1,218		34,757	34,463	1,906	1,116	
LOC_Os03g02320		21,085	19,103	20,846	21,787	42,297	20,979	19,021	20,704	21,662	42,236
Os10g0518800	PAK_Ste20_STLK	8,283	13,165	88	107		8,141	13,048	2	2	
LOC_Os10g37480		9,814	9,169	9,279	10,152	11,920	9,693	9,080	9,129	10,024	11,866
Os03g0678100	PAK_Ste20_STLK	129	109	146	403		21	13	48	308	
LOC_Os03g47470		549	531	626	674	1,554	455	460	509	570	1,491
Os03g0755000	PAK_Ste20_KHSh_GC	44,727	50,944	39,925	23,791		44,625	50,849	39,828	23,701	
LOC_Os03g54780		18,973	17,684	18,341	19,491	36,957	18,881	17,614	18,250	19,407	36,888
Os07g0507300	PAK_Ste20_MST_like	32,532	47,946	26,891	18,804		32,379	47,822	26,769	18,693	
LOC_Os07g32400		13,888	12,233	13,924	14,659	19,381	13,762	12,140	13,771	14,525	19,332
Os04g0437600	MEKK_ste11_MAP3K	12,090	27,558	205	132		11,973	27,458	102	31	
LOC_Os04g35700		43,209	39,363	44,681	44,285	55,791	43,105	39,289	44,569	44,170	55,734
Os02g0555900	MEKK_ste11_MAP3K	1,828	2,269	121	91		1,690	2,153	2	2	
LOC_Os02g35010		2,308	1,190	1,258	1,212	852	2,187	1,101	1,101	1,081	793
Os11g0207200	MEKK_ste11_MAP3K	15,697	26,065	1,736	599		15,576	25,963	1,630	498	
LOC_Os11g10100		42,416	39,684	45,648	45,267	92,037	42,304	39,609	45,523	45,148	91,973
Os02g0666300	MEKK_ste11_MAP3K	16,293	18,780	6,610	7,973		16,168	18,674	6,498	7,870	
LOC_Os02g44642		33,151	31,186	33,243	32,116	30,009	33,031	31,107	33,121	31,998	29,943
Os03g0764300	MEKK_ste11_MAP3K	24,274	24,230	6,189	3,509		24,179	24,134	6,099	3,422	
LOC_Os03g55560		12,130	11,544	12,390	13,045	23,660	12,054	11,473	12,303	12,972	23,595
Os07g0119000	MEKK_ste11_MAP3K	95	87	6,661	7,528		2	2	6,569	7,437	
LOC_Os07g02780		390	364	380	403	406	301	291	274	313	351
Os09g0383300	MEKK_ste11_MAP3K	5,405	10,398	120	119		5,304	10,300	22	30	
LOC_Os09g21510		2,348	2,070	2,278	2,300	5,563	2,250	1,995	2,184	2,214	5,501
Os08g0421800	MEKK_ste11_MAP3K	28,611	30,530	18,685	11,139		28,511	30,436	18,597	11,052	
LOC_Os08g32600		16,924	14,978	15,623	16,429	29,391	16,834	14,910	15,541	16,349	29,321
Os03g0262200	MEKK_ste11_MAP3K	9,107	15,019	959	116		9,005	14,926	869	29	
LOC_Os03g15570		4,421	3,941	3,724	3,890	12,886	4,334	3,875	3,647	3,814	12,826
Os03g0703400	MEKK_ste11_MAP3K	14,399	42,329	204	136		14,301	42,237	118	51	
LOC_Os03g49640		7,574	6,781	6,510	6,906	17,283	7,483	6,717	6,437	6,827	17,217
Os02g0769800	MEKK_ste11_MAP3K	9,660	14,987	96	314		9,538	14,884	2	212	
LOC_Os02g53040		10,071	6,758	7,124	7,270	6,381	9,958	6,683	7,001	7,149	6,322
Os04g0660500	MEKK_ste11_MAP3K	115,105	179,033	54,332	36,855		114,979	178,931	54,226	36,753	
LOC_Os04g56530		51,263	48,718	53,199	52,174	104,771	51,144	48,644	53,069	52,057	104,706
Os01g0107300	Raf	158	121	96	83		50	24	2	2	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os01g01740		246	193	214	207	287	145	121	104	112	220
Os06g0636600	Raf	103	110	79	96		2	17	2	2	
LOC_Os06g43030		4,285	3,905	3,993	4,131	2,509	4,207	3,836	3,904	4,027	2,449
Os01g0201200	Raf	12,416	5,195	345	245		12,293	5,084	231	144	
LOC_Os01g10450		13,751	12,414	13,638	13,066	17,085	13,630	12,329	13,511	12,949	17,020
Os05g0519200	Raf	16,561	29,548	42,523	36,593		16,437	29,443	42,408	36,488	
LOC_Os05g44290		49,859	44,677	52,741	52,687	49,996	49,744	44,596	52,596	52,558	49,938
Os01g0747400	Raf	777	4,633	84	213		678	4,542	2	126	
LOC_Os01g54350		1,619	1,397	1,442	1,524	2,088	1,525	1,330	1,367	1,442	2,030
Os02g0120100	Raf	281	421	635	598		151	317	525	495	
LOC_Os02g02780		230	201	255	371	418	107	124	120	245	357
Os09g0544300	Raf	14,351	21,561	219	281		14,249	21,466	129	192	
LOC_Os09g37230		6,305	5,435	5,631	5,932	19,986	6,218	5,365	5,543	5,856	19,923
Os07g0475900	Raf	26,015	11,489	177	143		25,871	11,370	51	29	
LOC_Os07g29330		28,539	3,122	3,353	3,293	5,110	28,413	3,031	3,189	3,156	5,051
Os06g0724900	Raf	521	1,040	1,344	725		397	937	1,235	623	
LOC_Os06g50920		3,209	2,798	3,242	3,346	2,324	3,094	2,724	3,117	3,224	2,256
Os12g0163800	Raf	535	446	98	122		431	352	8	23	
LOC_Os12g06670		85	76	76	123	192	2	7	2	18	133
Os02g0174200	Raf	37,906	60,403	5,444	3,027		37,787	60,290	5,338	2,930	
LOC_Os02g07790		45,009	43,546	44,732	47,332	41,728	44,897	43,460	44,609	47,223	41,669
Os06g0663400	Raf	20,328	16,280	1,897	3,366		20,194	16,167	1,778	3,266	
LOC_Os06g45300		22,428	18,796	20,217	22,102	24,549	22,314	18,708	20,090	21,987	24,489
Os04g0608900	Raf	4,230	14,076	165	129		4,095	13,962	45	27	
LOC_Os04g51950		3,290	3,067	2,983	2,978	3,501	3,173	2,979	2,847	2,859	3,437
Os08g0224100	Raf	49,651	63,968	17,504	8,331		49,539	63,858	17,403	8,237	
LOC_Os08g12750		55,068	51,102	54,070	53,462	78,188	54,966	51,019	53,958	53,363	78,129
Os03g0816100	Raf	3,055	5,107	129	93		2,946	5,011	34	2	
LOC_Os03g60150		10,434	9,713	10,160	10,140	4,642	10,337	9,642	10,044	10,043	4,585
Os01g0641000	Raf	29,052	14,259	86	80		28,951	14,162	2	2	
LOC_Os01g45380		11,164	10,319	10,483	10,536	4,935	11,069	10,245	10,390	10,453	4,879
Os05g0577700	Raf	7,850	28,613	162	969		7,750	28,514	67	881	
LOC_Os05g50190		30,983	29,634	31,065	29,872	50,036	30,884	29,559	30,970	29,789	49,973
Os03g0638800	Raf	21,282	42,699	286	235		21,177	42,600	182	144	
LOC_Os03g43760		33,559	31,425	34,210	34,487	48,318	33,459	31,350	34,111	34,399	48,253
Os12g0605900*	Raf	11,901	4,231	132	286		11,777	4,125	20	183	
LOC_Os12g41260		126	100	163	120	245	6	20	42	2	187
Os03g0745700	Raf	144	116	160,486	168,714		26	16	160,382	168,614	
LOC_Os03g53410		136	97	1,010	1,207	512	29	23	893	1,090	444
Os03g0160100	Raf	48,651	64,195	6,175	2,418		48,521	64,091	6,066	2,314	
LOC_Os03g06410		44,827	40,463	43,834	43,416	51,931	44,704	40,387	43,700	43,291	51,866
Os10g0430900	Raf	12,529	15,432	11,131	7,473		12,396	15,320	11,012	7,372	
LOC_Os10g29540		13,193	10,373	12,140	13,667	21,616	13,078	10,285	12,006	13,550	21,555
Os02g0220700	Raf	119	149	126	111		2	46	17	8	
LOC_Os02g12810		100	77	140	133	140	2	3	10	11	81
Os06g0232100	Raf	6,193	9,567	92	86		6,089	9,476	2	2	
LOC_Os06g12590		11,192	10,104	10,355	10,954	15,380	11,105	10,031	10,254	10,867	15,320
Os02g0527600	Raf	5,033	3,664	485	662		4,933	3,566	392	575	
LOC_Os02g32610		17,133	15,879	17,253	17,676	15,222	17,036	15,805	17,159	17,594	15,150
Os09g0566500	Raf	105	219	100	113		2	109	2	7	
LOC_Os09g39320		96	96	97	142	211	2	12	2	19	162
Os04g0610900	Raf	96	126	100	99		2	20	2	2	
LOC_Os04g52140		11,184	10,891	11,139	11,316	10,147	11,059	10,811	11,006	11,189	10,084
Os11g0678000	Raf	220	104	86	147		120	11	2	61	
LOC_Os11g45280		11,209	9,881	11,070	11,213	18,746	11,120	9,815	10,992	11,135	18,680
Os12g0562500	Raf	3,339	478	174	139		3,221	375	62	36	
LOC_Os12g37570		4,961	988	1,079	1,030	2,279	4,853	906	936	904	2,223
Os12g0562600	Raf	7,261	8,377	193	105		3,221	375	62	36	
LOC_Os12g37570		33,179	29,861	33,710	33,169	30,103	33,062	29,786	33,583	33,046	30,042
Os01g0674100	Raf_CG8767 fly	20,472	28,570	104	117		20,364	28,457	14	23	
LOC_Os01g48330		44,554	39,506	38,145	40,913	85,334	44,470	39,423	38,041	40,818	85,272
Os06g0181200	Raf	8,530	12,272	4,529	2,322		8,426	12,173	4,433	2,232	
LOC_Os06g08280		2,184	2,132	2,055	2,176	3,694	2,093	2,057	1,957	2,089	3,631
Os06g0646400	Raf	25,260	40,670	2,481	681		25,149	40,574	2,383	587	
LOC_Os06g43840		21,731	19,741	22,692	22,026	30,104	21,632	19,669	22,572	21,926	30,044
Os07g0438500	Raf	177	570	135	108		48	461	18	10	
LOC_Os07g25680		302	257	286	284	303	188	170	161	174	249
Os12g0594300	Raf	5,754	7,795	74,710	71,559		5,648	7,703	74,622	71,459	
LOC_Os12g40279		8,378	7,492	8,821	9,130	10,525	8,300	7,423	8,734	9,024	10,464
Os02g0786200	Raf	9,210	9,939	17,979	17,666		9,110	9,845	17,889	17,580	
LOC_Os02g54510		5,316	4,779	4,880	5,145	9,901	5,227	4,711	4,796	5,067	9,843
Os03g0401100	Raf	1,037	142	113	105		906	31	2	2	
LOC_Os03g28300		16,195	14,781	15,079	14,760	10,334	16,068	14,697	14,944	14,633	10,274

Supplemental Table 14 continue. Microarray data for rice kinase genes

Os02g0608500	Raf++Eph/Elk/Eck(PTK_11)	5,363	3,459	144	157		5,214	3,336	17	40	
LOC_Os02g39560		25,147	22,303	26,089	25,662	33,560	25,011	22,211	25,927	25,518	33,493
Os01g0748600	Eph/Elk/Eck(PTK_11)++Src(PTK_1)	14,340	13,438	179	719		14,237	13,345	89	631	
LOC_Os01g54480		21,393	19,126	19,490	20,535	20,378	21,307	19,060	19,413	20,460	20,322
Os07g0632800	Raf++MixedLineageKinase	74,916	74,927	59,296	41,185		74,814	74,831	59,202	41,095	
LOC_Os07g43900		24,974	22,535	23,808	24,332	40,868	24,886	22,462	23,716	24,250	40,804
Os01g0541900	ILK_BMPR_ALK_ACTR	11,760	18,682	5,123	2,120		11,627	18,571	5,000	2,007	
LOC_Os01g36080		15,463	14,145	15,696	15,607	21,602	15,339	14,060	15,543	15,468	21,550
Os01g0621600	Src(PTK_1)++HGF(PTK_21)	107,389	35,488	20,522	13,992		107,240	35,365	20,395	13,875	
LOC_Os01g43350		5,888	3,386	3,561	3,233	3,395	5,754	3,294	3,395	3,090	3,342
Os05g0585800	Src(PTK_1)++HGF(PTK_21)	156	80	55,208	54,506		55	2	55,116	54,418	
LOC_Os05g50830		149	63	683	610	223	52	2	589	527	165
Os04g0492500	TranslationKinase_GCN2	29,924	31,605	1,184	1,734		29,776	31,482	1,057	1,617	
LOC_Os04g41510		18,355	16,644	18,921	18,548	29,948	18,219	16,552	18,759	18,404	29,876
Os03g0295600	Eph/Elk/Eck(PTK_11)_HH498h	22,725	19,379	593	403		22,592	19,261	478	298	
LOC_Os03g18430		17,434	16,421	16,246	16,196	18,328	17,308	16,330	16,105	16,070	18,261
Os06g0334400	RLCK-XIII-sis_unique	14,368	14,148	8,868	10,110		14,267	14,055	8,779	10,024	
LOC_Os06g22820		17,343	14,784	15,390	16,085	22,138	17,256	14,718	15,310	16,009	22,076
Os08g0275200	RLCK-XIII-sis_unique	83	80	77	72		2	2	2	2	
LOC_Os08g17320		62	60	62	62	96	2	2	2	2	29
Os03g0251700	RLCK-XIII-sis-b	10,239	19,923	219	246		10,141	19,827	129	158	
LOC_Os03g14710		5,475	5,059	4,622	4,725	11,971	5,395	4,988	4,535	4,651	11,875
Os10g0187500	RLCK-XIII-sis-b	10,144	25,125	4,281	873		10,022	25,016	4,167	771	
LOC_Os10g10870		6,442	6,238	5,797	5,846	19,714	6,322	6,155	5,673	5,731	19,648
Os02g0648100	RLCK-XIII	3,085	4,731	160	219		2,978	4,632	55	127	
LOC_Os02g43290		19,352	17,969	19,082	19,192	18,354	19,249	17,894	18,984	19,101	18,286
Os04g0540900	RLCK-XIII	667	1,298	118	132		550	1,198	15	31	
LOC_Os04g45730		1,458	1,252	819	952	3,745	1,353	1,179	705	836	3,676
Os03g0113000	RLCK-XIII	243	180	959	3,626		117	75	847	3,522	
LOC_Os03g02190		7,452	6,870	7,370	7,331	5,592	7,332	6,793	7,233	7,205	5,532
Os10g0516200	RLCK-XIII	175	579	190	184		50	473	73	76	
LOC_Os10g37190		15,851	14,952	16,111	16,439	14,616	15,735	14,868	15,961	16,305	14,554
Os02g0106900	RLCK-XIII	163	107	127	137		29	2	11	30	
LOC_Os02g01730		1,496	1,358	1,531	1,431	1,295	1,368	1,278	1,387	1,299	1,239
Os02g0192900	LysM-II	136	156	108	95		12	40	3	2	
LOC_Os02g09960		108	113	117	94	267	2	25	2	2	208
Os06g0625200	LysM-II	81	88	77	74		2	2	2	2	
LOC_Os06g41960		56	66	63	57	182	2	2	2	2	120
Os06g0625300	LysM-II	889	342	229	263		747	221	109	153	
LOC_Os06g41980		827	339	409	391	563	695	246	259	256	508
Os11g0557500	LysM-II	121	88	98	109		5	2	2	8	
LOC_Os11g35330		359	329	369	363	328	254	248	229	240	255
Os02g0681700	LysM-II	1,484	1,652	79	72		1,385	1,560	2	2	
LOC_Os02g45750		1,531	1,321	1,312	1,449	2,558	1,441	1,257	1,237	1,373	2,498
Os02g0819900	LysM-II-b	289	427	196	181		189	331	106	94	
LOC_Os02g57440		650	638	629	555	800	558	566	540	475	733
Os04g0689400	URK-I	12,349	24,627	1,015	87		12,236	24,531	914	2	
LOC_Os04g59320		17,336	15,871	17,771	18,188	42,005	17,239	15,796	17,656	18,077	41,946
Os07g0159700	URK-I-sis	102	94	164	91		2	2	54	2	
LOC_Os07g06570		2,205	1,844	2,040	2,276	1,025	2,098	1,758	1,911	2,166	966
Os10g0351500	URK-I-sis-b	93	84	76	80		2	2	2	2	
LOC_Os10g21090		561	472	503	506	819	472	404	425	430	751
Os01g0206800	LRR-VI	17,210	19,638	221,042	266,313		17,094	19,535	220,933	266,215	
LOC_Os01g10900		4,130	4,124	35,842	38,649	16,698	4,019	4,045	35,733	38,546	16,623
Os05g0560300	LRR-VI	220	228	152	160		103	118	43	64	
LOC_Os05g48660		26,970	26,989	29,680	29,486	18,438	26,856	26,905	29,560	29,378	18,365
Os01g0674800	LRR-VI	5,171	8,555	16,234	21,573		5,071	8,459	16,141	21,486	
LOC_Os01g48390		8,992	8,113	8,090	8,337	24,656	8,901	8,041	8,000	8,259	24,579
Os03g0294800	LRR-VI	8,575	7,709	100	87		8,457	7,608	2	2	
LOC_Os03g18370		46,974	41,884	47,769	47,941	54,705	46,867	41,810	47,654	47,824	54,633
Os07g0693000	LRR-VI	2,326	5,992	105	101		2,199	5,889	2	2	
LOC_Os07g49240		3,833	3,688	4,043	3,919	7,880	3,717	3,613	3,914	3,798	7,823
Os05g0353500	LRR-VI	1,031	1,671	83	82		929	1,573	2	2	
LOC_Os05g28520		8,967	8,425	8,768	8,614	10,372	8,867	8,350	8,672	8,526	10,314
Os05g0471000	LRR-VI	2,133	4,476	105	99		1,981	4,352	2	2	
LOC_Os05g39410		2,908	2,506	2,547	2,973	4,358	2,786	2,412	2,396	2,843	4,302
Os12g0105800	LRR-VI	683	156	79	77		584	59	2	2	
LOC_Os12g01510		2,035	1,712	1,777	1,962	1,067	1,952	1,640	1,687	1,884	1,000
Os04g0683600	LRR-VI	36,036	48,608	1,444	572		35,896	48,487	1,330	466	
LOC_Os04g58700		53,174	48,950	49,258	50,193	49,389	53,049	48,856	49,114	50,065	49,326
Os04g0534200	LRR-VI	1,250	1,592	685	342		1,104	1,469	564	231	
LOC_Os04g45170		4,125	3,820	3,927	4,038	1,523	3,993	3,726	3,773	3,901	1,448
Os03g0773300	LRR-XIV	3,577	3,587	4,387	1,560		3,466	3,486	4,280	1,466	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os03g56250		7,782	7,042	7,007	7,068	9,663	7,675	6,965	6,903	6,972	9,593
Os07g0134600	LRR-XIV	8,571	13,786	174	162		8,448	13,685	67	60	
LOC_Os07g04220		2,277	2,127	2,279	2,337	6,174	2,164	2,053	2,151	2,218	6,107
Os03g0724300	LRR-XIV	8,709	14,095	238	186		8,594	13,994	128	89	
LOC_Os03g51440		14,777	12,379	13,375	14,397	18,594	14,672	12,294	13,238	14,280	18,532
Os03g0791700	LRR-VI	1,177	1,670	176	220		1,032	1,550	48	102	
LOC_Os03g57780		27,873	26,236	28,777	28,646	38,395	27,741	26,146	28,613	28,504	38,326
Os07g0166700	LRR-VI	104	129	92	75		2	34	2	2	
LOC_Os07g07230		166	141	169	147	316	71	69	58	53	250
Os06g0589600	LRR-VI	6,290	5,535	480	593		6,179	5,441	379	499	
LOC_Os06g38970		26,594	23,660	26,732	27,545	52,517	26,504	23,583	26,620	27,436	52,445
Os01g0104000	C-LEC	7,787	11,409	2,853	1,642		7,657	11,304	2,743	1,538	
LOC_Os01g01410		6,126	5,895	6,393	6,212	8,169	6,003	5,819	6,259	6,084	8,109
Os06g0134700	LRR-IV	11,080	4,582	127	154		10,938	4,464	2	39	
LOC_Os06g04370		4,292	3,875	4,105	4,119	3,937	4,158	3,786	3,949	3,976	3,876
Os08g0117700	LRR-IV	564	459	105	97		465	366	18	10	
LOC_Os08g02440		5,139	4,420	4,623	4,961	7,260	5,049	4,353	4,543	4,882	7,201
Os01g0822200	RLCK-II	2,472	4,214	468	2,165		2,358	4,115	367	2,064	
LOC_Os01g60700		5,185	4,680	5,269	5,118	5,600	5,085	4,607	5,160	5,005	5,539
Os03g0132800	RLCK-XII	2,901	8,062	3,579	2,765		2,791	7,968	3,485	2,666	
LOC_Os03g04050		9,326	7,830	9,089	9,319	12,643	9,237	7,759	8,993	9,210	12,570
Os10g0542800	RLCK-XII	13,465	32,055	5,963	1,034		13,322	31,937	5,835	917	
LOC_Os10g39670		17,227	15,492	17,622	17,372	25,579	17,097	15,403	17,460	17,231	25,527
Os10g0571300	RLCK-XII	43,820	50,997	2,694	2,111		43,705	50,882	2,599	2,016	
LOC_Os10g42110		9,890	9,185	9,499	9,464	24,657	9,793	9,099	9,386	9,361	24,595
Os03g0825300	RLCK-XII	102,206	82,172	120	179		102,103	82,077	24	89	
LOC_Os03g61010		28,405	26,259	27,543	29,064	30,240	28,314	26,188	27,452	28,980	30,181
Os11g0692300	LRR-XII	114	108	95	94		2	2	2	2	
LOC_Os11g47000		230	196	153	203	293	135	112	43	102	235
Os11g0691800	LRR-XII	103	113	145	97		2	15	38	4	
LOC_Os11g46960		598	494	590	567	753	495	409	462	457	700
Os11g0692100	LRR-XII	186	148	138	137		35	24	11	20	
LOC_Os11g46980		774	714	811	831	801	640	621	645	689	742
Os06g0272000	LRR-XII	184	142	152	169		29	16	27	55	
LOC_Os06g16070		159	96	161	246	140	29	3	2	108	87
Os01g0228200	LRR-XII	254	114	401	87		144	19	298	2	
LOC_Os01g12790		613	476	997	522	822	522	399	880	410	758
Os11g0208900	LRR-XII	112	94	115	91		2	2	2	2	
LOC_Os11g10310		1,442	1,299	1,459	1,518	1,726	1,327	1,213	1,306	1,386	1,660
Os07g0132000	LRR-XII	95	88	269	168		2	2	177	78	
LOC_Os07g03990		367	304	388	386	514	283	230	294	301	438
Os11g0692500	LRR-XII	103	92	98	178		2	2	2	83	
LOC_Os11g47030		375	355	397	402	266	276	283	275	299	208
Os11g0695000	LRR-XII	158	89	199	223		35	2	93	122	
LOC_Os11g47240		972	896	940	847	314	859	823	810	731	256
Os11g0695700	LRR-XII	106	235	129	127		2	134	28	33	
LOC_Os11g47300		84	154	92	199	1,058	2	77	2	106	993
Os11g0695800	LRR-XII	96	101	87	97		2	2	2	2	
LOC_Os11g47310		837	765	812	852	386	723	687	700	748	325
Os01g0694000	LRR-XII	118	102	130	119		10	6	32	24	
LOC_Os01g49910		932	832	956	1,005	796	837	761	840	900	727
Os01g0694100	LRR-XII	392	165	98	88		265	58	2	2	
LOC_Os01g49920		149	105	126	116	376	31	22	2	2	305
Os11g0559200	LRR-XII	188	208	124	112		88	115	35	26	
LOC_Os11g35500		4,183	3,451	3,673	4,107	4,293	4,094	3,384	3,593	4,028	4,221
Os11g0569600	LRR-XII	192	89	89	85		68	2	2	2	
LOC_Os11g36160		896	778	859	835	1,329	782	705	729	719	1,270
Os11g0569500	LRR-XII	146	1,042	2,923	2,181		44	948	2,831	2,092	
LOC_Os11g36150		970	881	907	950	1,276	882	813	825	871	1,203
Os11g0569800	LRR-XII	436	516	2,903	2,634		336	422	2,811	2,547	
LOC_Os11g36190		1,053	940	961	1,037	2,328	965	871	875	960	2,270
Os11g0570000	LRR-XII	90	242	87	82		2	135	2	2	
LOC_Os11g36200		985	948	910	1,021	1,942	893	867	806	926	1,882
Os02g0635600	LRR-XII	545	1,487	96	98		435	1,391	2	2	
LOC_Os02g42370		1,214	1,052	1,149	1,199	1,644	1,119	981	1,035	1,092	1,571
Os02g0215500	LRR-XII	1,146	1,353	90	164		1,042	1,254	2	74	
LOC_Os02g12400		4,485	4,225	4,370	4,551	871	4,391	4,150	4,272	4,465	817
Os02g0215700	LRR-XII	90	146	131	149		2	48	37	59	
LOC_Os02g12420		254	240	249	252	374	152	166	150	165	308
Os02g0215900	LRR-XII	113	208	94	89		13	115	5	3	
LOC_Os02g12440		75	75	78	77	315	2	9	2	2	257
Os08g0248100	LRR-XII	84	546	92	83		2	451	2	2	
LOC_Os08g14990		124	118	118	116	345	34	47	30	38	280

Supplemental Table 14 continue. Microarray data for rice kinase genes

Os08g0247600	LRR-XII	98	109	86	76		2	13	2	2	
LOC_Os08g14940		73	77	73	73	166	2	5	2	2	107
Os10g0337400	LRR-XII	97	100	88	87		2	6	2	2	
LOC_Os10g19160		81	80	79	78	161	2	11	2	2	85
Os02g0211200	LRR-XII	314	1,646	81	75		209	1,556	2	2	
LOC_Os02g11980		532	314	304	303	251	445	240	203	216	193
Os02g0210700	LRR-XII	84	79	81	78		2	2	2	2	
LOC_Os02g11930		66	57	64	61	93	2	2	2	2	20
Os06g0587000	LRR-XII	130	97	135	125		2	2	27	23	
LOC_Os06g38730		447	404	511	526	205	329	329	379	405	135
Os06g0587500	LRR-XII	114	92	111	1,868		2	2	2	1,767	
LOC_Os06g38780		104	99	146	3,389	186	2	15	2	3,264	129
Os04g0227000	LRR-XII	160	132	97	95		19	15	2	2	
LOC_Os04g15650		721	637	704	718	147	589	550	549	575	84
Os02g0231700	LRR-XII	99	155	102	78		2	54	4	2	
LOC_Os02g13780		92	90	107	85	200	2	16	2	2	135
Os06g0581500	LRR-XII	160	129	135	133		37	26	27	31	
LOC_Os06g38340		437	401	467	426	261	322	326	341	303	195
Os08g0331900	LRR-XII	108	93	91	87		2	2	2	2	
LOC_Os08g24310		250	233	252	254	200	128	152	127	132	141
Os11g0625200	LRR-XII	705	301	89	77		592	203	2	2	
LOC_Os11g40890		72	65	74	90	134	2	2	2	2	70
Os11g0625900	LRR-XII	562	84	88	79		462	2	2	2	
LOC_Os11g40970		564	86	90	93	242	472	17	10	11	183
Os01g0149700	LRR-XII	98	114	101	101		2	5	7	8	
LOC_Os01g05640		905	820	861	942	230	814	739	756	846	168
Os01g0153000	LRR-XII	88	95	87	80		2	2	2	2	
LOC_Os01g05980		64	70	63	65	132	2	2	2	2	63
Os01g0152800	LRR-XII	97	81	81	84		2	2	2	2	
LOC_Os01g05960		173	141	157	197	348	80	62	35	83	278
Os01g0152600	LRR-XII	101	113	96	86		2	21	6	2	
LOC_Os01g05940		69	73	77	70	193	2	7	2	2	137
Os01g0152000	LRR-XII	91	193	79	78		2	99	2	2	
LOC_Os01g05870		174	151	159	164	447	85	82	72	83	387
Os06g0667000	LRR-XII	86	86	87	81		2	2	2	2	
LOC_Os06g45630		59	60	63	63	112	2	2	2	2	52
Os10g0375000*	LRR-XII	5,908	22,705	88	92		5,778	22,591	2	2	
LOC_Os10g22890		339	324	323	352	675	212	237	186	227	610
Os11g0490200	LRR-XII	122	95	96	87		13	2	2	2	
LOC_Os11g29790		89	61	71	79	374	2	2	2	2	319
Os02g0615300	LRR-XII	95	87	93	91		2	2	2	2	
LOC_Os02g40180		73	69	71	72	156	2	2	2	2	89
Os02g0615500	LRR-XII	152	150	113	117		37	47	9	19	
LOC_Os02g40200		812	738	811	803	249	699	659	702	701	185
Os02g0615800	LRR-XII	89	91	77	75		2	2	2	2	
LOC_Os02g40240		6,107	5,024	5,071	5,537	6,914	6,019	4,959	4,996	5,462	6,848
Os07g0121200	LRR-XII	220	149	242	127		70	25	114	9	
LOC_Os07g03000		203	143	436	224	384	67	50	272	80	318
Os11g0173100	LRR-XII	126	94	102	122		10	2	2	23	
LOC_Os11g07200		105	62	88	140	218	2	2	2	25	163
Os11g0173500	LRR-XII	678	1,654	861	1,001		580	1,556	770	913	
LOC_Os11g07230		2,370	2,041	2,151	2,347	2,385	2,291	1,968	2,061	2,268	2,321
Os11g0173700	LRR-XII	137	95	108	91		22	2	5	2	
LOC_Os11g07250		116	69	137	76	194	14	2	22	2	128
Os11g0173800	LRR-XII	9,690	8,155	3,624	2,149		9,554	8,044	3,503	2,038	
LOC_Os11g07260		996	950	1,075	1,081	3,405	864	866	926	944	3,330
Os07g0251900	LRR-XII	193	147	162	164		68	43	51	61	
LOC_Os07g14820		1,053	949	1,076	1,106	295	934	872	941	982	221
Os11g0171800	LRR-XII	706	721	223	209		593	624	121	112	
LOC_Os11g07060		858	796	832	821	595	761	721	715	709	534
Os11g0172800	LRR-XII	95	113	85	81		2	19	2	2	
LOC_Os11g07180		84	87	85	87	169	2	19	6	9	104
Os11g0172700	LRR-XII	143	94	113	109		2	2	2	2	
LOC_Os11g07170		117	82	135	125	320	2	2	2	2	266
Os06g0186300	LRR-XII	101	93	86	90		2	2	2	3	
LOC_Os06g08710		76	77	73	67	153	2	10	2	2	79
Os06g0186000	LRR-XII	110	82	157	601		2	2	56	508	
LOC_Os06g08680		92	60	68	86	122	4	2	2	2	72
Os06g0339500	LRR-XII	175	315	2,476	126		63	215	2,367	29	
LOC_Os06g23190		87	84	4,568	168	597	2	2	4,429	46	525
Os04g0618700	LRR-XII	444	687	123	100		337	593	30	8	
LOC_Os04g52780		4,490	3,883	4,234	4,341	12,479	4,397	3,811	4,126	4,249	12,422
Os04g0465900	RLCK-OS3	96	95	156	76		2	2	62	2	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os04g39180		647	563	638	661	946	557	494	552	579	887
Os01g0155500	CrRLK1L-1	866	1,890	105	618		759	1,795	9	526	
LOC_Os01g06280		3,656	3,215	3,638	3,557	3,081	3,563	3,144	3,521	3,457	3,019
Os01g0769700	CrRLK1L-1	32,847	55,949	105	103		32,743	55,856	12	13	
LOC_Os01g56330		32,219	29,388	31,449	31,950	56,815	32,130	29,318	31,363	31,869	56,731
Os03g0333200	CrRLK1L-1	34,913	40,247	180	181		34,791	40,138	67	80	
LOC_Os03g21540		32,813	31,055	32,713	32,473	44,974	32,693	30,972	32,589	32,358	44,909
Os05g0318700	CrRLK1L-1	211	318	169	158		80	213	57	53	
LOC_Os05g25450		1,960	1,856	1,995	1,926	1,099	1,834	1,778	1,858	1,797	1,030
Os05g0280700	CrRLK1L-1	89	79	415,135	471,809		2	2	415,046	471,720	
LOC_Os05g20150		73	63	9,138	13,917	5,670	2	2	9,061	13,842	5,606
Os05g0317700	CrRLK1L-1	687	1,453	76	76		588	1,360	2	2	
LOC_Os05g25350		1,786	1,519	1,580	1,760	1,413	1,695	1,454	1,504	1,681	1,351
Os05g0317900	CrRLK1L-1	91	83	86	75		2	2	2	2	
LOC_Os05g25370		65	58	71	67	995	2	2	2	2	936
Os03g0124200	CrRLK1L-1	102	174	101	97		2	76	2	7	
LOC_Os03g03280		3,589	3,385	3,495	3,566	2,272	3,491	3,311	3,400	3,478	2,214
Os10g0534500*	CrRLK1L-1	2,613	3,547	684	95		2,480	3,428	572	2	
LOC_Os10g39010		176	120	153	113	194	53	28	14	2	129
Os05g0162500	CrRLK1L-1	2,605	4,383	868	331		2,505	4,287	777	242	
LOC_Os05g06990		2,888	2,552	2,473	2,737	5,347	2,803	2,480	2,384	2,660	5,276
Os06g0334300	CrRLK1L-1	5,609	7,207	158	140		5,499	7,116	64	42	
LOC_Os06g22810		16,393	13,845	16,095	16,542	12,459	16,307	13,773	15,998	16,437	12,384
Os03g0281500	CrRLK1L-1	245	113	319	93		115	10	210	2	
LOC_Os03g17300		1,086	924	1,249	947	834	962	848	1,115	823	770
Os04g0619600	CrRLK1L-1	932	3,528	2,380	1,352		828	3,436	2,290	1,261	
LOC_Os04g52860		3,880	3,392	3,559	3,760	5,826	3,790	3,320	3,462	3,674	5,771
Os07g0147600	CrRLK1L-1	615	120	85	122		483	7	2	14	
LOC_Os07g05370		3,846	3,633	3,790	3,779	2,700	3,717	3,548	3,652	3,651	2,636
Os07g0568100	LRR-Ic	2,133	667	120	133		2,032	565	27	42	
LOC_Os07g38070		157	148	108	119	1,264	73	72	12	31	1,169
Os01g0816600	LRR-VIII-1	147	99	87	81		34	2	2	2	
LOC_Os01g60060		430	312	333	355	211	328	230	193	233	144
Os03g0329700	LRR-VIII-1	141	129	477	80		27	30	370	2	
LOC_Os03g21230		1,166	1,101	1,956	1,200	844	1,064	1,022	1,826	1,083	788
Os05g0305900	LRR-VIII-1	1,810	2,913	115	115		1,676	2,805	2	9	
LOC_Os05g24010		3,339	3,115	3,443	3,328	3,522	3,211	3,035	3,301	3,196	3,457
Os11g0245200	LRR-VIII-1	292	268	198	244		140	144	73	131	
LOC_Os11g14050		1,022	898	937	1,094	306	894	805	776	957	219
Os12g0210400	LRR-VIII-1	213	102	106	109		78	2	2	5	
LOC_Os12g10740		18,062	16,694	17,506	18,328	23,340	17,945	16,606	17,364	18,206	23,267
Os01g0818600	LRR-VIII-1	6,266	2,801	102	101		6,166	2,708	14	15	
LOC_Os01g60280		12,071	10,175	10,493	11,577	33,592	11,981	10,108	10,413	11,498	33,529
Os01g0960400	LRR-VIII-1	6,340	8,758	125	273		6,236	8,660	23	183	
LOC_Os01g72990		3,704	3,500	3,029	3,488	3,319	3,606	3,426	2,933	3,401	3,257
Os09g0375600	RLCK-VIIb	96	97	87	81		2	2	2	2	
LOC_Os09g20880		2,939	2,716	2,824	2,926	2,230	2,847	2,644	2,733	2,846	2,178
Os01g0852100	RLCK-IV	422	77	104	147		294	2	2	37	
LOC_Os01g63280		672	618	728	701	928	554	533	574	568	849
Os03g0148700	RLCK-IV	6,772	15,051	3,067	1,631		6,672	14,951	2,974	1,542	
LOC_Os03g05470		3,272	2,907	2,868	3,230	3,466	3,189	2,832	2,774	3,145	3,405
Os02g0821400	RLCK-IV	104	285	90	91		2	185	2	2	
LOC_Os02g57560		5,386	4,858	5,057	5,114	6,128	5,281	4,782	4,956	5,020	6,070
Os04g0503600	RLCK-IV	3,896	8,269	139	128		3,794	8,176	47	39	
LOC_Os04g42480		18,320	16,415	16,755	17,575	20,091	18,232	16,347	16,673	17,494	20,022
Os01g0689900	WAK/LRK10L-1	6,307	9,474	308	265		6,201	9,376	203	174	
LOC_Os01g49529		31,893	26,595	27,546	29,193	34,798	31,796	26,511	27,415	29,077	34,734
Os05g0550800	WAK/LRK10L-1	631	460	106	75		520	364	9	2	
LOC_Os05g47770		2,811	2,629	2,777	2,849	1,319	2,713	2,557	2,657	2,749	1,258
Os01g0136800	WAK/LRK10L-1	598	1,099	1,134	2,378		501	1,004	1,046	2,291	
LOC_Os01g04450		1,574	1,373	1,390	1,561	1,371	1,494	1,304	1,305	1,491	1,307
Os03g0802100	WAK/LRK10L-1	433	436	130	123		317	336	26	22	
LOC_Os03g58750		225	207	231	216	733	121	134	117	101	671
Os03g0225700	WAK/LRK10L-1	422	364	85	81		317	274	2	2	
LOC_Os03g12470		2,171	1,919	1,887	2,036	2,245	2,084	1,846	1,780	1,948	2,173
Os12g0595800	WAK/LRK10L-1	2,872	4,216	78	77		2,771	4,124	2	2	
LOC_Os12g40419		6,381	5,442	5,538	5,993	6,748	6,294	5,376	5,458	5,917	6,673
Os05g0318100	WAK/LRK10L-1	106	100	85	98		2	2	2	2	
LOC_Os05g25390		118	88	100	131	162	2	2	2	2	105
Os01g0310400	WAKL-OS	160	98	109	124		54	6	16	34	
LOC_Os01g20880		81	68	90	109	161	2	2	2	17	67
Os01g0310800	WAKL-OS	590	2,242	94	89		488	2,150	6	2	
LOC_Os01g20900		520	496	540	544	422	429	427	456	462	359

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Os11g0555600	WAKL-OS	1,428	1,847	1,513	1,780		1,323	1,747	1,412	1,688	
LOC_Os11g35220		4,418	4,064	4,215	4,264	2,281	4,315	3,987	4,117	4,174	2,215
Os11g0556400	WAKL-OS	112	99	100	88		2	2	2	2	
LOC_Os11g35274		337	275	323	315	216	215	198	185	188	153
Os10g0112700	WAKL-OS	98	102	99	230		2	9	7	139	
LOC_Os10g02360		5,223	5,315	5,785	5,551	3,888	5,132	5,243	5,680	5,461	3,824
Os11g0553500	WAKL-OS	88	97	77	72		2	2	2	2	
LOC_Os11g35120		137	132	124	126	176	39	59	30	39	114
Os10g0142600	WAKL-OS	123	98	99	97		2	2	2	2	
LOC_Os10g05250		110	83	124	125	212	2	2	2	5	159
Os07g0493200	WAKL-OS	2,289	7,166	16,051	16,944		2,182	7,065	15,955	16,852	
LOC_Os07g31130		5,806	5,442	5,702	5,800	3,853	5,699	5,365	5,600	5,708	3,794
Os07g0493800	WAKL-OS	908	3,229	147	96		777	3,124	35	2	
LOC_Os07g31190		1,228	1,146	1,340	1,187	977	1,104	1,069	1,204	1,058	896
Os07g0494800	WAKL-OS	538	134	98	86		438	39	9	2	
LOC_Os07g31250		1,491	1,247	1,409	1,499	1,281	1,407	1,177	1,321	1,423	1,214
Os10g0151100	WAKL-OS	82	81	83	75		2	2	2	2	
LOC_Os10g06030		67	64	70	64	184	2	2	2	2	126
Os10g0151500	WAKL-OS	150	156	142	124		4	35	14	7	
LOC_Os10g06090		133	120	182	93	187	2	29	22	2	125
Os10g0174800	WAKL-OS	125	132	110	100		2	11	2	2	
LOC_Os10g09620		114	97	127	120	185	2	7	2	2	128
Os10g0116600	WAKL-OS	122	93	85	77		14	2	2	2	
LOC_Os10g02720		89	65	68	64	156	2	2	2	2	88
Os11g0691600	WAKL-OS	107	104	107	88		11	6	17	2	
LOC_Os11g46950		3,560	3,100	3,181	3,624	2,751	3,483	3,028	3,092	3,546	2,690
Os01g0363900	WAKa	16,345	24,479	1,039	1,463		16,229	24,380	937	1,364	
LOC_Os01g26160		14,427	13,031	14,835	14,877	16,917	14,324	12,957	14,723	14,763	16,864
Os01g0364800	WAKa	102	101	77	158		2	2	2	59	
LOC_Os01g26280		1,134	1,067	1,113	1,078	849	1,030	991	989	963	801
Os02g0623600	WAKa	373	125	629	87		248	8	523	2	
LOC_Os02g41480		1,240	1,017	1,072	1,060	294	1,127	928	943	946	233
Os09g0373800	WAKa	110	86	93	81		5	2	3	2	
LOC_Os09g20740		80	66	72	68	193	2	2	2	2	133
Os09g0471600	WAKa	110	107	95	85		8	15	7	2	
LOC_Os09g29584		79	81	84	79	645	2	10	2	2	588
Os09g0471800	WAKa	126	99	87	91		2	2	2	2	
LOC_Os09g29600		311	266	250	277	729	201	176	122	164	666
Os09g0471200	WAKa	100	91	74	103		2	2	2	2	
LOC_Os09g29510		327	290	353	403	789	213	213	220	283	728
Os09g0471500	WAKa	83	84	82	77		2	2	2	2	
LOC_Os09g29540		309	295	276	301	247	219	225	189	218	152
Os09g0471400	WAKa	76	128	72	78		2	34	2	2	
LOC_Os09g29520		881	770	841	864	687	798	700	749	756	617
Os02g0807900	WAKa	93	87	79	78		2	2	2	2	
LOC_Os02g56380		1,280	1,150	1,222	1,243	534	1,175	1,077	1,107	1,128	469
Os02g0808300	WAKa	121	134	136	106		2	22	12	2	
LOC_Os02g56420		106	96	182	145	123	2	11	33	7	60
Os02g0811200	WAKa	91	86	79	71		2	2	2	2	
LOC_Os02g56630		72	58	72	63	140	2	2	2	2	83
Os02g0807200	WAKa	126	185	128	91		2	64	23	2	
LOC_Os02g56330		120	136	350	141	429	7	44	216	24	357
Os02g0111600	WAKa	91	84	72	97		2	2	2	2	
LOC_Os02g02120		289	239	241	314	227	206	169	148	207	167
Os06g0142500	WAKa	155	159	147	139		40	56	39	42	
LOC_Os06g05050		130	136	145	134	278	19	57	36	31	208
Os03g0643200	WAKa	154	102	121	220		23	2	4	113	
LOC_Os03g44140		124	64	121	144	180	2	2	2	12	115
Os12g0614800	WAKa	109	218	95	86		2	119	2	2	
LOC_Os12g42040		73	76	80	69	135	2	2	2	2	68
Os12g0615300	WAKa	5,832	3,943	1,286	1,511		5,697	3,832	1,164	1,399	
LOC_Os12g42070		2,240	2,009	2,259	2,194	3,789	2,112	1,925	2,109	2,056	3,714
Os12g0615100	WAKa	1,303	700	928	774		1,182	596	813	669	
LOC_Os12g42060		550	539	582	674	736	440	455	435	544	670
Os03g0841100	WAKb	3,029	926	9,395	15,633		2,922	832	9,307	15,544	
LOC_Os03g62430		1,268	1,085	1,153	1,239	3,028	1,178	1,017	1,075	1,164	2,953
Os04g0127500	WAKb	143	130	134	175		15	26	24	71	
LOC_Os04g03830		130	109	175	195	177	10	34	44	70	119
Os02g0632100	WAKb	78	85	99	76		2	2	2	2	
LOC_Os02g42110		63	64	123	71	202	2	2	2	2	140
Os05g0135100	WAKb	81	89	88	79		2	2	2	2	
LOC_Os05g04460		114	104	116	121	118	35	34	28	47	54
Os02g0632800	WAKb	95	111	90	87		2	15	2	2	

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LOC_Os02g42150		106	107	104	118	364	13	24	2	5	303
Os04g0308100	WAKb	121	130	277	175		2	15	153	63	
LOC_Os04g24300		241	257	588	266	297	108	170	438	127	230
Os04g0307500	WAKb	81	79	78	78		2	2	2	2	
LOC_Os04g24220		1,773	1,462	1,635	1,692	2,738	1,681	1,390	1,550	1,610	2,682
Os04g0286300	WAKb	83	76	72	75		2	2	2	2	
LOC_Os04g21820		73	66	71	75	126	2	2	2	2	52
Os04g0366000	WAKb	114	99	76	102		5	2	2	8	
LOC_Os04g29680		150	124	132	206	199	51	40	2	87	142
Os10g0178800	WAKb	147	104	97	102		7	2	2	2	
LOC_Os10g10030		111	73	107	121	276	2	2	2	2	195
Os10g0180800	WAKb	107	94	99	108		2	2	2	7	
LOC_Os10g10130		539	512	564	631	288	434	428	421	506	216
Os09g0561600	WAKb	222	119	115	95		89	11	2	2	
LOC_Os09g38850		346	210	348	273	213	220	129	214	144	148
Os02g0807800	WAKb	455	1,551	82	84		351	1,457	2	2	
LOC_Os02g56370		5,564	4,928	5,531	5,517	3,712	5,476	4,858	5,418	5,416	3,645
Os09g0561000	WAKb	140	161	127	154		28	48	34	60	
LOC_Os09g38800		6,054	5,391	5,785	6,052	2,919	5,964	5,306	5,677	5,952	2,858
Os09g0561500	WAKb	187	198	189	155		76	97	83	61	
LOC_Os09g38840		336	320	344	322	641	229	243	241	227	574
Os12g0265900	WAKb	89	95	89	88		2	2	2	2	
LOC_Os12g16520		502	466	495	500	147	412	395	406	422	87
Os09g0562600	WAKb	174	1,056	483	240		21	931	358	125	
LOC_Os09g38910		569	545	604	667	492	436	451	443	528	410
Os11g0565300	WAKb	106	84	96	83		5	2	9	2	
LOC_Os11g35860		75	63	63	65	198	2	2	2	2	136
Os08g0501700	WAKb	230	110	348	134		90	2	222	19	
LOC_Os08g39240		231	121	702	197	189	99	34	547	54	126
Os08g0501500	WAKb	724	282	1,789	1,665		572	157	1,669	1,556	
LOC_Os08g39210		505	485	469	537	584	380	390	313	406	520
Os04g0651500	WAKb	87	84	77	79		2	2	2	2	
LOC_Os04g55760		62	59	66	60	104	2	2	2	2	45
Os04g0598800	WAKb	92	86	76	76		2	2	2	2	
LOC_Os04g51030		145	141	121	133	182	57	74	40	55	119
Os04g0598900	WAKb	206	171	117	148		93	62	12	54	
LOC_Os04g51040		206	201	158	181	209	98	118	43	79	147
Os04g0599000	WAKb	360	1,856	447	102		257	1,761	357	14	
LOC_Os04g51050		2,261	2,043	2,219	2,259	1,702	2,167	1,972	2,127	2,176	1,642
Os04g0371700	WAKc	176	125	141	129		23	2	19	18	
LOC_Os04g30330		146	90	154	154	270	20	2	2	20	203
Os04g0275100	WAKc	92	129	83	87		2	17	2	2	
LOC_Os04g20680		148	140	126	160	441	40	54	7	54	377
Os04g0370100	WAKc	105	85	69	68		2	2	2	2	
LOC_Os04g30160		117	92	85	91	122	20	9	2	2	61
Os04g0368000	WAKc	122	127	119	116		18	34	29	27	
LOC_Os04g29960		455	423	396	427	456	367	355	317	349	391
Os04g0370900	WAKc	94	94	87	75		2	2	2	2	
LOC_Os04g30240		912	859	903	893	589	811	786	801	804	510
Os04g0372100	WAKc	87	88	82	78		2	2	2	2	
LOC_Os04g30370		65	62	75	62	196	2	2	2	2	145
Os04g0368800	WAKc	161	114	146	245		32	10	37	141	
LOC_Os04g30010		2,405	2,173	2,338	2,270	1,339	2,281	2,096	2,204	2,145	1,282
Os01g0581400	RLCK-IXb	345	212	59,179	93,178		244	117	59,089	93,090	
LOC_Os01g39970		78	72	266	413	833	2	2	177	331	765
Os02g0787200	RLCK-IXb	445	365	94,393	141,202		325	249	94,294	141,105	
LOC_Os02g54590		214	220	1,582	3,092	751	111	132	1,462	2,986	680
Os06g0191900	RLCK-IXb	6,308	1,111	344,264	338,142		6,204	1,012	344,162	338,051	
LOC_Os06g09230		2,097	1,932	10,579	12,387	7,284	1,997	1,858	10,483	12,298	7,215
Os02g0218400	RLCK-IXb	104	97	84,355	130,578		2	3	84,266	130,489	
LOC_Os02g12660		82	79	1,108	1,399	575	2	10	1,026	1,324	513
Os02g0152300	RLCK-IXb	724	1,165	36,329	45,624		622	1,068	36,235	45,534	
LOC_Os02g05820		78	80	171	162	590	2	7	77	79	527
Os10g0561500	RLCK-IXb	11,221	11,200	5,816	1,861		11,096	11,098	5,709	1,760	
LOC_Os10g41220		373	347	414	465	1,296	255	272	284	349	1,232
Os03g0101200	RLCK-IXb	2,164	1,391	477	170		2,037	1,283	361	65	
LOC_Os03g01160		655	495	735	755	3,235	533	413	608	634	3,173
Os06g0140800	RLCK-IXb	1,530	2,214	755	1,839		1,378	2,089	633	1,727	
LOC_Os06g04880		26,210	24,273	25,636	28,037	24,972	26,081	24,178	25,478	27,902	24,892
Os02g0218600	RLCK-IXb	1,305	1,427	10,049	5,815		1,202	1,334	9,959	5,717	
LOC_Os02g12670		240	226	459	388	640	157	157	360	285	581
Os06g0574200	RLCK-IXb	4,117	7,627	94	203		4,013	7,525	2	113	
LOC_Os06g37620		1,766	1,650	1,577	1,633	6,782	1,676	1,573	1,478	1,542	6,708

Supplemental Table 14 continue. Microarray data for rice kinase genes

Os02g0665700	RLCK-IXb	108	85	83	71		2	2	2	2	
LOC_Os02g44610		78	59	107	64	123	2	2	2	2	62
Os10g0548700	RLCK-IXb	8,360	9,954	257	555		8,250	9,862	163	457	
LOC_Os10g40100		5,397	2,756	2,952	3,052	2,215	5,309	2,684	2,854	2,946	2,157
Os06g0163000	RLCK-IXb	20,715	29,276	267	142		20,569	29,156	144	34	
LOC_Os06g06760		15,178	13,671	13,911	14,921	14,132	15,057	13,580	13,767	14,794	14,072
Os10g0548300	RLCK-IXb	3,982	3,730	5,168	2,076		3,874	3,632	5,073	1,984	
LOC_Os10g40060		1,402	1,221	1,329	1,263	2,982	1,298	1,149	1,222	1,168	2,921
Os03g0424200	RLCK-IXb	7,173	2,626	121	386		7,031	2,509	2	269	
LOC_Os03g31070		2,718	2,484	2,647	2,711	4,108	2,587	2,395	2,486	2,569	4,045
Os09g0569800	RLCK-IXb	289	544	170	495		143	424	45	382	
LOC_Os09g39620		540	421	556	533	1,381	414	330	392	396	1,322
Os09g0570000	RLCK-IXb	279	679	122	97		160	579	17	2	
LOC_Os09g39640		1,212	1,127	1,217	1,274	1,739	1,103	1,051	1,092	1,157	1,673
Os10g0100500	RLCK-IXb	1,603	1,220	159	373		1,487	1,121	59	276	
LOC_Os10g01060		2,946	2,753	2,753	2,738	8,451	2,839	2,681	2,630	2,632	8,387
Os02g0822900	RLCK-IXb	90	94	117	139		2	2	2	29	
LOC_Os02g57700		258	243	316	384	304	127	161	171	249	243
Os11g0618300	RLCK-IXb	1,438	144	87	301		1,327	45	2	206	
LOC_Os11g40370		113	104	113	106	2,209	15	22	2	2	2,144
Os09g0570100	RLCK-IXb	240	307	85	88		124	208	2	2	
LOC_Os09g39650		672	618	647	630	486	563	546	524	523	422
Os07g0597200	LRR-Xb	793	732	598	708		677	633	495	610	
LOC_Os07g40630		4,254	4,076	4,427	4,462	4,138	4,150	4,004	4,301	4,353	4,065
Os01g0935800	RLCK-IXa	1,762	543	1,738	1,172		1,624	429	1,612	1,057	
LOC_Os01g70970		11,995	10,965	11,697	11,832	4,329	11,868	10,877	11,538	11,693	4,269
Os05g0371600	RLCK-IXa	156	274	105	117		48	162	15	23	
LOC_Os05g30820		1,161	999	1,081	1,218	1,433	1,077	917	978	1,123	1,330
Os01g0929200	RLCK-IXa	2,545	2,376	120	316		2,441	2,279	18	226	
LOC_Os01g70410		33,681	31,697	33,481	34,040	27,084	33,582	31,623	33,386	33,953	27,015
Os01g0170300	LRR-XI	1,632	1,540	852	753		1,491	1,423	726	639	
LOC_Os01g07560		16,301	15,244	16,155	16,121	23,579	16,167	15,155	16,002	15,979	23,516
Os05g0169600	LRR-XI	4,427	2,671	3,289	1,500		4,314	2,572	3,188	1,400	
LOC_Os05g07740		9,278	8,321	8,877	8,879	15,241	9,179	8,249	8,764	8,768	15,178
Os08g0493800	LRR-XI	364	346	791	1,045		241	244	683	943	
LOC_Os08g38560		703	691	921	667	635	590	617	797	547	574
Os09g0479200	LRR-XI	250	215	273	298		135	114	175	201	
LOC_Os09g30190		238	230	203	199	305	126	156	89	95	241
Os04g0132500	LRR-XI	117	135	116	316		14	31	22	224	
LOC_Os04g04330		6,402	5,728	5,979	6,213	3,195	6,314	5,650	5,880	6,122	3,136
Os06g0589800	LRR-XI	1,041	426	160	130		891	303	33	15	
LOC_Os06g38990		5,841	5,324	5,661	5,740	3,433	5,712	5,232	5,495	5,600	3,363
Os02g0111800	LRR-XI	149	80	397	168		47	2	307	80	
LOC_Os02g02140		312	318	320	332	309	220	247	230	250	246
Os03g0145000	LRR-XI	150	134	101	101		40	35	2	7	
LOC_Os03g05140		123	114	109	110	325	23	30	2	2	266
Os08g0148300	LRR-XI	194	177	145	144		71	63	35	45	
LOC_Os08g05290		2,916	2,862	2,528	2,387	6,933	2,799	2,774	2,400	2,272	6,871
Os04g0506100	LRR-XI	296	915	112	254		188	813	7	162	
LOC_Os04g42700		2,596	2,427	2,419	2,564	2,430	2,491	2,349	2,313	2,470	2,366
Os07g0152200	LRR-XI	826	3,002	90	92		726	2,910	2	6	
LOC_Os07g05740		4,218	3,683	3,621	3,832	4,432	4,130	3,617	3,541	3,755	4,365
Os03g0773700	LRR-XI	63,292	53,478	556	315		63,171	53,377	453	216	
LOC_Os03g56270		33,923	31,582	32,689	31,893	54,296	33,806	31,507	32,565	31,781	54,231
Os07g0134200	LRR-XI	8,784	6,271	83	74		8,683	6,175	2	2	
LOC_Os07g04190		5,228	4,888	4,818	5,062	5,396	5,135	4,816	4,728	4,981	5,336
Os03g0228800	LRR-XI	485	372	130	134		380	272	29	44	
LOC_Os03g12730		2,399	2,315	2,054	1,977	3,035	2,302	2,239	1,954	1,890	2,964
Os11g0233800	LRR-XI	370	430	104	100		247	327	2	2	
LOC_Os11g12620		3,793	3,539	3,745	3,631	7,897	3,673	3,462	3,621	3,516	7,837
Os06g0717200	LRR-XI	18,213	7,032	123	107		18,110	6,938	32	17	
LOC_Os06g50340		16,975	14,856	15,298	15,927	17,425	16,887	14,788	15,216	15,847	17,352
Os07g0498400*	LRR-XI	42,335	36,985	404	227		42,215	36,883	298	126	
LOC_Os07g31500		5,948	4,589	5,193	5,739	11,949	5,837	4,515	5,073	5,620	11,887
Os01g0239700	LRR-XI	5,248	12,636	119	131		5,129	12,521	18	34	
LOC_Os01g13800		69,483	66,094	69,992	70,503	102,092	69,378	66,007	69,872	70,397	102,019
Os08g0376300*	LRR-XI	159,600	81,280	79	75		159,488	81,186	2	2	
LOC_Os08g28870		2,968	2,495	2,522	2,524	3,395	2,876	2,423	2,422	2,417	3,335
Os09g0326100*	LRR-XI	5,014	15,268	264	278		4,895	15,151	168	181	
LOC_Os09g15700		205	290	149	162	881	105	202	32	58	806
Os01g0878300	LRR-XI	283	240	266	123		150	128	145	14	
LOC_Os01g65650		5,790	5,298	6,309	6,224	8,151	5,661	5,214	6,169	6,094	8,089
Os11g0232100	LRR-XI	895	100	87	108		793	5	2	19	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os11g12530		11,285	10,424	10,413	11,349	10,057	11,198	10,352	10,322	11,269	9,995
Os12g0632900	LRR-XI	98	116	125	115		2	2	26	17	
LOC_Os12g43660		5,035	4,660	4,864	5,061	5,556	4,932	4,572	4,744	4,954	5,500
Os12g0632800	URK-I	102	116	117	95		2	2	2	2	
LOC_Os12g43640		2,946	2,808	2,936	2,986	4,669	2,822	2,714	2,788	2,857	4,606
Os01g0742400	LRR-XV	902	1,520	1,333	668		789	1,406	1,241	573	
LOC_Os01g53920		1,833	1,378	1,175	1,513	6,132	1,743	1,293	1,065	1,413	6,066
Os05g0522600	LRR-XV	5,258	2,086	214	217		5,108	1,963	87	101	
LOC_Os05g44770		27,405	24,292	27,250	28,052	16,011	27,273	24,200	27,083	27,911	15,949
Os02g0228300	LRR-XV	194	616	238	110		48	494	114	2	
LOC_Os02g13510		26,833	26,442	27,288	28,805	25,196	26,698	26,349	27,131	28,665	25,139
Os02g0227700	LRR-XV	199	96	87	78		95	2	2	2	
LOC_Os02g13430		98	74	74	77	139	11	6	2	4	69
Os06g0557700	LRR-XV	83	90	115	81		2	2	4	2	
LOC_Os06g36320		308	281	342	332	244	204	196	201	211	184
Os02g0552600	LRR-XIIb	7,216	10,245	1,111	675		7,112	10,154	1,022	585	
LOC_Os02g34750		4,684	4,170	4,210	4,287	5,605	4,593	4,098	4,122	4,204	5,547
Os02g0553000	LRR-XIIb	97	92	86	148		2	2	2	51	
LOC_Os02g34790		74	72	84	101	115	2	2	2	2	53
Os01g0296000	LRR-XIIb	2,159	7,507	148	132		2,030	7,404	39	29	
LOC_Os01g19160		3,181	2,802	3,748	3,674	1,720	3,062	2,727	3,616	3,552	1,651
Os10g0119200	LRR-XIIb	95	86	103	95		2	2	2	2	
LOC_Os10g02970		77	65	129	118	95	2	2	2	2	33
Os02g0277700	LRR-XIIb	472	129	121	177		344	12	13	76	
LOC_Os02g17710		1,256	1,034	991	914	954	1,139	944	858	797	884
Os10g0467900	LRR-XIIb	157	198	390	339		27	94	281	236	
LOC_Os10g32990		201	173	251	206	229	79	97	117	80	168
Os10g0468500	LRR-XIIb	161	2,602	99	100		59	2,507	12	11	
LOC_Os10g33040		1,081	927	982	1,080	1,304	996	859	897	1,008	1,224
Os08g0342300	LRR-Xb	301	859	134	88		179	756	27	2	
LOC_Os08g25380		1,730	1,620	1,879	1,816	4,057	1,617	1,545	1,755	1,696	3,986
Os09g0293500	LRR-Xb	271	395	114	115		167	293	18	24	
LOC_Os09g12240		1,573	1,496	1,557	1,554	930	1,482	1,418	1,457	1,463	864
Os01g0718300	LRR-Xb	13,771	26,047	483	613		13,651	25,930	390	516	
LOC_Os01g52050		49,881	43,742	36,960	41,132	75,423	49,787	43,654	36,844	41,030	75,362
Os10g0114400	LRR-Xb	167	154	130	144		63	59	35	54	
LOC_Os10g02500		2,353	2,058	2,147	2,337	1,755	2,262	1,986	2,054	2,254	1,691
Os01g0917500*	LRR-Xb	54,829	40,829	180	158		54,699	40,723	68	54	
LOC_Os01g68870		3,571	3,105	3,109	3,207	2,001	3,447	3,028	2,973	3,077	1,911
Os02g0194400*	LRR-Xb	11,395	6,856	3,146	641		11,262	6,747	3,026	531	
LOC_Os02g10100		256	159	192	191	616	129	76	42	55	547
Os02g0629400	LRR-Xb	131	100	90	89		4	2	2	2	
LOC_Os02g41890		929	840	916	951	1,844	804	754	784	830	1,776
Os04g0672100	LRR-Xb	2,255	1,136	489	124		2,118	1,014	387	22	
LOC_Os04g57630		6,084	5,417	5,703	5,986	8,599	5,976	5,325	5,571	5,873	8,535
Os07g0107800	LRR-Xb	529	2,617	89	83		429	2,524	2	2	
LOC_Os07g01710		4,515	3,847	4,058	4,509	5,489	4,426	3,781	3,979	4,431	5,427
Os02g0116700	LRR-Xb	19,726	16,295	73,305	87,839		19,602	16,189	73,187	87,733	
LOC_Os02g02490		41,720	40,504	77,626	71,222	33,382	41,607	40,418	77,474	71,094	33,312
Os02g0153100	LRR-Xb	125	129	159	150		23	31	65	60	
LOC_Os02g05910		1,883	1,673	1,724	1,797	1,175	1,795	1,599	1,630	1,713	1,109
Os02g0153200	LRR-XV	93	86	80	83		2	2	2	2	
LOC_Os02g05920		478	432	464	481	483	388	362	377	400	425
Os02g0153700	LRR-Xb	82	79	85	81		2	2	2	2	
LOC_Os02g05950		621	597	563	611	377	533	529	482	532	315
Os02g0153900	LRR-Xb	127	129	93	100		22	29	2	11	
LOC_Os02g05960		1,630	1,511	1,666	1,692	1,488	1,532	1,435	1,566	1,604	1,434
Os02g0153400	LRR-Xb	116	91	100	85		2	2	2	2	
LOC_Os02g05930		110	84	106	106	169	2	6	2	2	100
Os02g0154000	LRR-Xb	495	2,336	130	105		372	2,230	14	2	
LOC_Os02g05970		470	428	496	481	191	358	342	346	355	126
Os02g0153500	LRR-Xb	572	2,619	108	100		440	2,504	2	2	
LOC_Os02g05940		555	357	340	364	289	425	270	200	235	226
Os02g0154200	LRR-XV	296	759	147	95		151	637	23	2	
LOC_Os02g05980		1,922	1,780	1,925	1,914	3,295	1,787	1,688	1,769	1,775	3,238
Os06g0691800	LRR-Xb	4,533	8,899	81	95		4,427	8,805	2	2	
LOC_Os06g47650		4,251	3,876	4,054	4,336	5,452	4,167	3,806	3,961	4,229	5,392
Os06g0692500	LRR-Xb	83	101	267	82		2	5	169	2	
LOC_Os06g47740		88	90	98	94	186	2	17	2	2	112
Os06g0692600	LRR-Xb	106	93	312	91		2	2	203	2	
LOC_Os06g47750		104	89	142	135	206	2	8	4	13	136
Os06g0692100	LRR-Xb	124	179	91	85		23	85	2	2	
LOC_Os06g47700		1,809	1,740	1,724	1,872	1,154	1,716	1,670	1,634	1,788	1,089

Supplemental Table 14 continue. Microarray data for rice kinase genes

Os11g0168700	SD-2b	127	151	88	84		25	46	2	2	
LOC_Os11g06780		105	109	106	93	176	22	31	9	3	111
Os02g0777400	LRR-XIIIb	72,705	67,878	584	157		72,607	67,782	497	69	
LOC_Os02g53720		32,076	28,147	29,343	31,823	89,725	31,996	28,079	29,257	31,754	89,651
Os06g0203800	LRR-XIIIb	4,139	6,252	85	141		4,040	6,159	2	56	
LOC_Os06g10230		9,284	7,224	7,977	8,993	12,983	9,193	7,159	7,901	8,913	12,917
Os06g0130100	LRR-XIIIb-sis	146,746	162,915	479	516		146,633	162,816	379	416	
LOC_Os06g03970		69,619	62,518	61,992	63,124	98,219	69,521	62,446	61,884	63,011	98,152
Os08g0446200	LRR-XI	4,319	13,755	38,491	28,209		4,204	13,653	38,389	28,112	
LOC_Os08g34640		7,891	7,384	7,809	8,015	13,216	7,778	7,306	7,699	7,913	13,158
Os08g0446400	LRR-XI	1,923	89	180	75		1,826	2	93	2	
LOC_Os08g34650		472	333	369	326	518	391	265	284	257	462
Os01g0247500	LRR-XIIIa	460	100	79	77		358	3	2	2	
LOC_Os01g14510		1,428	1,316	1,353	1,413	4,045	1,331	1,244	1,260	1,326	3,993
Os03g0266800	LRR-XIIIa	7,703	15,245	724	424		7,599	15,151	632	334	
LOC_Os03g16010		35,097	31,773	31,912	34,616	44,922	35,008	31,703	31,825	34,536	44,866
Os12g0638100	LRR-XIIIa	849	2,024	124	77		724	1,917	9	2	
LOC_Os12g44090		15,461	14,114	14,713	15,647	28,695	15,348	14,028	14,573	15,530	28,630
Os10g0155800	LRR-XI_sgk192h	115	275	125	425		2	164	3	315	
LOC_Os10g06760		347	302	346	380	430	227	215	187	247	368
Os03g0756200	LRR-XV	331	359	116	162		230	262	17	73	
LOC_Os03g54900		341	296	266	364	269	247	224	173	279	204
Os07g0602700	LRR-XV	15,689	29,346	82	75		15,583	29,253	2	2	
LOC_Os07g41140		5,127	4,709	4,848	4,881	11,275	5,037	4,636	4,741	4,790	11,200
Os01g0821900	LRR-VIIa	6,502	9,270	1,106	311		6,393	9,168	999	218	
LOC_Os01g60670		21,682	20,193	21,947	22,100	32,321	21,575	20,115	21,841	22,004	32,257
Os05g0478300	LRR-VIIa	1,577	107	127	103		1,444	2	13	2	
LOC_Os05g40050		371	278	391	355	320	245	198	256	226	257
Os03g0335500	LRR-VIIa	3,998	15,259	142	128		3,897	15,166	53	41	
LOC_Os03g21730		19,887	17,907	18,038	19,181	28,378	19,796	17,837	17,953	19,099	28,319
Os01g0957100	LRR-VIIa	131,775	37,343	181	178		131,626	37,220	53	61	
LOC_Os01g72700		49,139	44,277	47,503	47,504	60,764	49,003	44,185	47,338	47,360	60,698
Os03g0127700	LRR-VIIa	18,283	16,418	105	80		18,174	16,321	9	2	
LOC_Os03g03570		6,588	5,802	6,397	6,251	11,885	6,496	5,731	6,293	6,142	11,818
Os10g0531700	LRR-VIIa	103	107	127	86		2	12	33	2	
LOC_Os10g38800		7,289	6,678	6,855	7,143	6,898	7,199	6,608	6,747	7,039	6,845
Os05g0414700	LRR-Xa	1,821	1,857	87	184		1,716	1,759	2	94	
LOC_Os05g34270		6,759	6,246	6,545	6,855	10,254	6,658	6,173	6,441	6,764	10,190
Os11g0249900	LRR-Xa	2,238	4,639	91	82		2,136	4,546	2	2	
LOC_Os11g14420		5,919	5,429	5,499	5,818	16,860	5,832	5,362	5,419	5,739	16,786
Os04g0487200	LRR-Xa	95	328	85	75		2	232	2	2	
LOC_Os04g41030		355	324	334	318	124	260	252	242	233	68
Os02g0655800	LRR-III	6,246	10,677	117	374		6,119	10,575	9	272	
LOC_Os02g43870		21,539	21,024	23,206	22,231	31,954	21,422	20,949	23,075	22,111	31,889
Os04g0548400	LRR-III	2,180	1,630	429	315		2,080	1,536	340	229	
LOC_Os04g46320		2,464	2,099	2,255	2,396	1,548	2,375	2,031	2,172	2,318	1,494
Os03g0297800	LRR-III	808	220	88	88		707	126	2	2	
LOC_Os03g18630		8,205	7,612	8,465	8,776	3,991	8,115	7,543	8,382	8,696	3,934
Os08g0564700	LRR-III	1,529	926	343	307		1,412	826	239	207	
LOC_Os08g45060		4,380	3,952	4,479	4,162	13,259	4,273	3,878	4,361	4,047	13,197
Os07g0145400	LRR-III	3,487	4,361	82	104		3,382	4,267	2	5	
LOC_Os07g05190		2,932	2,768	2,975	2,947	15,882	2,847	2,699	2,877	2,842	15,825
Os07g0626500	LRR-III	57,327	128,042	285	354		57,227	127,945	190	267	
LOC_Os07g43350		55,871	54,258	60,252	60,071	76,642	55,776	54,185	60,159	59,989	76,585
Os03g0320800	LRR-III	15,690	20,651	168	160		15,586	20,555	70	70	
LOC_Os03g20450		40,232	38,985	38,824	38,374	34,008	40,140	38,912	38,729	38,289	33,943
Os06g0288100	LRR-III-like	148	540	173	212		25	439	66	110	
LOC_Os06g18000		17,206	16,066	18,914	18,222	22,626	17,094	15,992	18,785	18,104	22,558
Os01g0819100	LRR-III	42,676	40,768	3,735	2,072		42,531	40,649	3,609	1,958	
LOC_Os01g60330		41,650	21,559	23,309	24,047	52,974	41,524	21,468	23,144	23,910	52,909
Os05g0480400	LRR-III	1,729	6,252	726	196		1,627	6,159	637	108	
LOC_Os05g40200		6,722	6,057	6,113	6,037	6,012	6,631	5,987	6,026	5,955	5,951
Os03g0332900	LRR-III	196,346	87,461	192	184		196,196	87,338	65	68	
LOC_Os03g21510		32,230	30,506	32,401	33,580	51,459	32,101	30,414	32,234	33,440	51,391
Os07g0681100	LRR-III	47,401	31,530	233	224		47,249	31,405	107	107	
LOC_Os07g48310		18,795	17,523	17,445	18,104	25,788	18,662	17,430	17,280	17,963	25,703
Os01g0223600	LRR-III	14,318	8,810	111	100		14,209	8,712	5	6	
LOC_Os01g12390		18,246	16,569	18,150	18,460	22,428	18,148	16,487	18,017	18,344	22,364
Os05g0588300	LRR-III	102	339	382	102		2	244	285	4	
LOC_Os05g51070		5,706	4,948	5,587	5,711	11,289	5,612	4,876	5,483	5,604	11,234
Os03g0223000	LRR-III	55,716	23,093	2,602	1,386		55,615	22,997	2,504	1,297	
LOC_Os03g12250		54,962	57,755	63,594	60,604	102,453	54,867	57,683	63,501	60,519	102,382
Os03g0712400	LRR-III	515	120	123	119		412	17	29	28	

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LOC_Os03g50450		437	395	412	412	155	350	317	313	322	103
Os04g0463000	LRR-III	805	684	222	267		694	586	126	172	
LOC_Os04g38910		4,302	4,102	3,866	3,948	8,598	4,200	4,031	3,750	3,849	8,535
Os09g0400500	LRR-III	88	90	89	80		2	2	2	2	
LOC_Os09g23570		1,253	1,167	1,233	1,168	1,917	1,147	1,094	1,124	1,070	1,859
Os01g0133900	LRR-III	39,353	24,245	246	183		39,223	24,135	127	78	
LOC_Os01g04230		58,900	51,898	58,494	58,048	177,549	58,783	51,811	58,342	57,921	177,473
Os09g0376600	LRR-III	170	130	145	148		21	8	21	36	
LOC_Os09g20970		392	341	386	405	455	266	250	229	270	400
Os01g0711200	LRR-III	132	89	93	79		6	2	2	2	
LOC_Os01g51400		770	665	796	724	937	651	590	668	599	875
Os10g0492400	LRR-III	1,119	676	94	78		1,019	584	7	2	
LOC_Os10g35040		1,349	1,138	1,123	1,171	3,214	1,257	1,070	1,046	1,089	3,151
Os08g0521200	LRR-III	96	98	80,434	117,130		2	2	80,339	117,040	
LOC_Os08g40990		423	384	496	585	754	332	313	404	502	674
Os06g0198900	LRR-III	111	89	282,416	303,828		2	2	282,316	303,732	
LOC_Os06g09860		102	65	5,790	4,845	2,866	8	2	5,679	4,737	2,803
Os11g0620500	LRR-III	506	456	298,146	444,450		370	342	298,025	444,344	
LOC_Os11g40550		176	89	1,860	3,544	592	58	2	1,709	3,417	524
Os02g0830700	LRR-III	8,727	5,269	164	127		8,602	5,163	52	24	
LOC_Os02g58390		7,531	7,177	7,610	7,423	12,652	7,411	7,097	7,488	7,304	12,583
Os04g0649700	LRR-III	15,109	10,283	124	104		15,008	10,186	28	16	
LOC_Os04g55620		19,794	18,243	18,971	19,236	28,298	19,699	18,169	18,878	19,153	28,234
Os07g0574100	LRR-III	84	82	78	74		2	2	2	2	
LOC_Os07g38640		68	70	74	67	120	2	2	2	2	57
Os06g0638500	LRR-III	114,728	89,794	133	108		114,605	89,693	26	7	
LOC_Os06g43170		24,600	22,870	25,358	24,281	27,727	24,489	22,796	25,230	24,163	27,665
Os09g0110100	LRR-III	19,642	5,101	107	142		19,518	4,998	2	40	
LOC_Os09g02250		9,032	8,262	9,350	8,980	12,977	8,918	8,188	9,224	8,859	12,913
Os01g0514700*	LRR-III	4,452	6,965	86	85		4,352	6,871	2	2	
LOC_Os01g33090		1,038	958	958	1,042	748	948	889	870	964	684
Os08g0506400	LRR-III	5,110	2,614	345	233		5,007	2,514	247	143	
LOC_Os08g39590		35,761	32,419	34,044	34,785	58,003	35,659	32,343	33,947	34,698	57,924
Os07g0207100	LRR-Xc	3,970	4,613	131	99		3,844	4,511	24	2	
LOC_Os07g10630		1,777	1,549	1,703	1,608	4,553	1,656	1,473	1,573	1,490	4,483
Os12g0182300	LRR-Xc	1,697	6,918	284	255		1,579	6,814	174	155	
LOC_Os12g08180		1,259	1,223	1,201	1,191	873	1,144	1,143	1,089	1,081	799
Os04g0576900	LRR-VIIa	26,675	44,396	9,192	5,418		26,564	44,286	9,094	5,324	
LOC_Os04g48760		19,880	20,434	19,963	19,249	57,798	19,781	20,352	19,854	19,151	57,674
Os04g0472500	not_assigned	183	190	88	96		62	89	2	2	
LOC_Os04g39650		1,526	1,359	1,542	1,543	1,194	1,415	1,284	1,419	1,425	1,138
Os02g0176100	LRR-V	26,554	23,934	440	227		26,446	23,837	335	134	
LOC_Os02g07960		31,420	27,833	27,021	28,183	49,972	31,323	27,751	26,889	28,068	49,899
Os06g0660800	LRR-V	11,757	14,085	118	291		11,616	13,969	2	184	
LOC_Os06g45020		7,612	6,724	7,422	7,862	7,620	7,492	6,634	7,272	7,735	7,562
Os07g0565400	LRR-V	100	112	84	81		2	17	2	2	
LOC_Os07g37810		81	80	92	104	155	2	10	2	2	87
Os02g0136900	LRR-V	591	522	98	183		491	424	3	96	
LOC_Os02g04430		218	197	146	150	417	122	123	52	67	347
Os02g0190500	LRR-V	962	1,372	96	210		832	1,262	2	110	
LOC_Os02g09740		2,953	2,617	2,781	3,039	3,824	2,838	2,530	2,645	2,923	3,754
Os06g0634500	LRR-V	348	918	120	90		235	821	20	2	
LOC_Os06g42800		9,242	8,530	9,463	9,536	13,962	9,141	8,458	9,340	9,431	13,901
Os03g0183800	LRR-V	3,452	7,795	100	100		3,352	7,700	6	13	
LOC_Os03g08550		28,519	25,993	27,564	28,950	24,627	28,428	25,923	27,475	28,871	24,568
Os10g0389800	LRR-V	40,118	30,590	214	228		39,988	30,483	100	123	
LOC_Os10g25090		43,940	40,467	43,229	43,310	22,998	43,816	40,389	43,088	43,180	22,946
Os03g0397700	LRR-V	679	1,086	272	157		559	981	157	54	
LOC_Os03g27990		49,333	44,435	46,656	46,048	52,571	49,223	44,350	46,507	45,921	52,508
Os07g0618500	LRR-V	760	2,848	308	492		643	2,735	209	396	
LOC_Os07g42632		1,438	1,449	1,509	1,530	2,766	1,336	1,363	1,392	1,426	2,703
Os09g0559900	LRR-V	150	123	102,722	108,030		18	14	102,602	107,920	
LOC_Os09g38700		126	104	702	766	821	2	21	554	631	753
Os02g0194600*	LRR-V	35,114	26,921	1,102	168		35,013	26,826	1,005	79	
LOC_Os02g10110		422	323	92	93	177	329	253	2	9	110
Os02g0241100	LRR-VIIb	89	94	99	84		2	2	2	2	
LOC_Os02g14480		3,531	3,126	3,418	3,348	7,731	3,438	3,056	3,308	3,241	7,669
Os06g0544100	LRR-VIIb	1,109	575	102	95		997	478	2	2	
LOC_Os06g35200		7,484	6,614	8,034	7,898	7,909	7,385	6,542	7,915	7,790	7,843
Os08g0276400	LRR-VIIb	2,035	1,790	98	95		1,935	1,691	6	6	
LOC_Os08g17410		6,480	5,678	5,744	6,183	8,346	6,398	5,604	5,652	6,100	8,293
Os12g0257900	SD-1d	132	116	111	114		30	20	12	24	
LOC_Os12g15550		522	492	507	515	182	427	421	416	430	123

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Os01g0113800	LRK10L-2	113	152	532	109		2	35	412	2	
LOC_Os01g02360		918	882	1,546	894	297	788	793	1,403	764	235
Os01g0114100	LRK10L-2	2,662	1,333	4,188	1,974		2,556	1,225	4,094	1,882	
LOC_Os01g02390		2,488	2,398	2,031	2,205	3,286	2,398	2,317	1,929	2,111	3,223
Os01g0114500	LRK10L-2	148	165	123	157		46	64	30	66	
LOC_Os01g02420		200	199	186	202	328	114	123	89	113	263
Os01g0116300	LRK10L-2	148	141	143	114		2	19	18	3	
LOC_Os01g02690		120	96	162	130	121	2	4	4	2	59
Os01g0114900	LRK10L-2	95	92	86	81		2	2	2	2	
LOC_Os01g02460		268	236	235	271	429	181	164	144	191	364
Os01g0115900	LRK10L-2	152	201	105	114		48	103	4	24	
LOC_Os01g02600		713	667	588	648	357	616	591	489	561	300
Os01g0116000	LRK10L-2	145	222	128	106		2	100	2	2	
LOC_Os01g02610		207	159	181	128	213	71	67	22	2	152
Os01g0114300	LRK10L-2	126	1,048	126	106		2	934	2	2	
LOC_Os01g02400		3,070	2,826	3,035	3,092	1,342	2,937	2,740	2,885	2,953	1,269
Os01g0115600	LRK10L-2	100	78	75	73		2	2	2	2	
LOC_Os01g02560		84	47	52	51	103	2	2	2	2	41
Os01g0117500	LRK10L-2	95	96	119	115		2	2	32	27	
LOC_Os01g02810		68	70	76	67	540	2	2	2	2	482
Os01g0117700	LRK10L-2	90	118	103	123		2	26	18	37	
LOC_Os01g02840		595	572	640	649	596	501	506	567	567	533
Os01g0117100	LRK10L-2	129	97	96	104		18	2	2	9	
LOC_Os01g02770		155	133	143	177	488	59	55	20	63	420
Os01g0116900	LRK10L-2	117	105	90	151		2	2	2	46	
LOC_Os01g02750		1,666	1,498	1,593	1,728	1,438	1,545	1,419	1,468	1,607	1,377
Os01g0117300	LRK10L-2	102	87	79	81		2	2	2	2	
LOC_Os01g02790		80	66	62	69	109	2	2	2	2	53
Os01g0114700	LRK10L-2	99	108	105	85		2	16	16	2	
LOC_Os01g02440		73	80	79	70	148	2	9	2	2	82
Os01g0113200	LRK10L-2	97	90	91	80		2	2	2	2	
LOC_Os01g02290		127	124	130	119	994	45	49	36	32	915
Os01g0113400	LRK10L-2	5,531	4,057	6,975	7,189		5,432	3,965	6,890	7,104	
LOC_Os01g02320		2,028	1,767	1,845	2,302	3,614	1,937	1,702	1,770	2,222	3,556
Os01g0113700	LRK10L-2	2,344	802	76	73		2,241	706	2	2	
LOC_Os01g02350		2,475	2,115	2,234	2,295	1,275	2,381	2,043	2,138	2,210	1,209
Os01g0114400	LRK10L-2	122	99	1,839	92		4	2	1,728	2	
LOC_Os01g02410		111	65	158	96	176	4	2	17	2	111
Os01g0116200	LRK10L-2	81	94	1,373	78		2	2	1,255	2	
LOC_Os01g02680		58	75	108	67	82	2	2	2	2	15
Os01g0115800	LRK10L-2	193	839	1,418	1,329		80	744	1,317	1,233	
LOC_Os01g02590		268	234	278	288	592	174	159	166	179	529
Os01g0117200	LRK10L-2	79	79	80	77		2	2	2	2	
LOC_Os01g02780		60	57	55	56	104	2	2	2	2	45
Os01g0115700	LRK10L-2	116	108	146	352		2	2	21	238	
LOC_Os01g02570		133	115	221	204	127	6	28	62	66	67
Os01g0114600	LRK10L-2	105	377	7,176	3,881		2	255	7,069	3,777	
LOC_Os01g02430		1,741	1,632	2,018	1,881	1,023	1,629	1,540	1,878	1,763	963
Os01g0116400	LRK10L-2	103	1,636	17,570	10,957		5	1,539	17,480	10,869	
LOC_Os01g02700		2,568	2,147	2,451	2,462	1,558	2,489	2,075	2,363	2,386	1,485
Os01g0117400	LRK10L-2	867	9,441	6,079	6,083		747	9,325	5,980	5,986	
LOC_Os01g02800		1,108	1,323	1,260	1,425	3,101	1,004	1,235	1,140	1,318	3,036
Os01g0117600	LRK10L-2	166	2,645	1,979	1,664		37	2,535	1,862	1,563	
LOC_Os01g02830		220	166	305	191	601	105	79	166	73	517
Os01g0113300	LRK10L-2	3,613	5,337	31,562	47,936		3,502	5,240	31,463	47,838	
LOC_Os01g02300		2,565	2,306	2,730	3,148	2,923	2,468	2,235	2,616	3,040	2,857
Os01g0137200	LRK10L-2	178	6,604	116	94		38	6,484	2	2	
LOC_Os01g04480		159	158	154	113	177	25	67	4	2	114
Os01g0137500	LRK10L-2	102	96	104	102		2	2	8	8	
LOC_Os01g04520		189	160	188	181	155	89	89	72	83	99
Os01g0138400	LRK10L-2	99	92	83	81		2	2	2	2	
LOC_Os01g04580		997	968	995	979	1,032	896	893	896	891	966
Os01g0138300	LRK10L-2	167	156	249	231		47	52	137	136	
LOC_Os01g04570		980	857	974	1,042	1,815	869	771	850	936	1,754
Os01g0137400	LRK10L-2	157	100	133	142		23	2	11	30	
LOC_Os01g04490		90	67	143	97	170	2	2	2	2	99
Os01g0691000	LRK10L-2	92	81	174	68		2	2	72	2	
LOC_Os01g49630		73	62	103	58	175	2	2	2	2	122
Os04g0655300	RLCK-OS4	138	105	114	109		2	2	2	2	
LOC_Os04g56110		427	375	430	453	793	300	280	275	319	720
Os04g0655400	RLCK-Os4	583	248	127	116		442	133	2	2	
LOC_Os04g56120		449	399	367	383	895	319	311	210	241	832
Os11g0441900	RLCK-OS4	89	81	92	76		2	2	2	2	

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LOC_Os11g25510		76	57	78	58	83	2	2	2	2	26
Os06g0241100	RLCK-Os4	309	361	534	464		196	261	425	367	
LOC_Os06g13320		161	144	176	184	295	60	60	36	62	237
Os07g0141200	RLCK-OS4	100	94	86	78		2	2	2	2	
LOC_Os07g04820		292	280	318	316	186	192	207	216	227	122
Os07g0141100	RLCK-Os4	100	95	104	97		2	2	2	2	
LOC_Os07g04810		289	246	321	306	552	180	174	192	193	490
Os04g0303100	SD-2b	193	143	154	188		79	40	45	91	
LOC_Os04g23700		558	538	571	550	233	447	460	462	448	174
Os04g0303300	SD-2b	304	98	101	113		205	2	12	24	
LOC_Os04g23720		1,611	1,219	1,281	1,379	1,329	1,529	1,150	1,194	1,307	1,262
Os04g0303500	SD-2b	126	99	131	167		15	2	24	72	
LOC_Os04g23760		273	240	249	277	289	172	156	114	161	227
Os06g0551800	SD-2b	93	132	84	82		2	37	2	2	
LOC_Os06g35850		313	283	295	315	353	224	213	207	237	281
Os02g0234500	SD-2b	237	489	264	86		137	397	178	2	
LOC_Os02g13970		4,847	3,916	4,138	4,474	7,056	4,755	3,850	4,062	4,393	6,994
Os06g0494100	SD-2b	889	2,433	93	96		785	2,339	2	6	
LOC_Os06g29810		7,264	6,612	6,846	7,163	4,394	7,172	6,540	6,749	7,077	4,331
Os03g0838100	SD-2b	3,110	1,374	423	195		2,978	1,261	302	87	
LOC_Os03g62180		18,564	15,950	19,271	20,004	29,833	18,434	15,865	19,131	19,874	29,770
Os04g0103500	SD-2b	116	89	132	79		2	2	25	2	
LOC_Os04g01310		642	627	791	670	2,590	541	548	659	551	2,533
Os07g0186200	SD-2b	129	274	119	106		27	180	23	17	
LOC_Os07g08860		1,859	1,718	1,674	1,827	1,788	1,768	1,648	1,585	1,743	1,715
Os04g0103700	SD-2b	377	1,132	384	453		235	1,015	257	336	
LOC_Os04g01320		3,058	2,734	3,330	3,328	4,924	2,928	2,645	3,168	3,188	4,862
Os05g0165900	SD-2b	168	145	316	285		38	37	200	178	
LOC_Os05g07300		862	820	930	920	1,573	738	739	801	795	1,507
Os04g0356600	SD-2b	101	100	91	83		2	2	2	2	
LOC_Os04g28780		1,037	939	1,007	992	262	943	862	907	903	201
Os11g0208700	SD-2b	175	138	129	1,532		76	46	44	1,446	
LOC_Os11g10280		12,020	10,553	10,976	13,651	17,859	11,927	10,487	10,903	13,570	17,796
Os04g0420400	SD-2b	104	106	84	83		2	10	2	2	
LOC_Os04g34320		85	80	66	74	162	2	8	2	2	105
Os04g0419900	SD-2b	92	1,094	86	89		2	999	2	2	
LOC_Os04g34270		1,380	1,300	1,445	1,476	971	1,289	1,228	1,351	1,393	913
Os04g0420600	SD-2b	117	143	85	82		18	52	2	2	
LOC_Os04g34330		116	106	103	114	161	22	39	29	32	100
Os04g0420900	SD-2b	87	82	81	82		2	2	2	2	
LOC_Os04g34370		1,413	1,203	1,261	1,371	2,262	1,326	1,137	1,185	1,295	2,187
Os10g0342300	SD-2b	189	123	125	118		45	4	2	2	
LOC_Os10g20160		793	683	828	817	1,056	661	593	667	674	986
Os04g0161800	SD-2b	102	100	81	76		2	8	2	2	
LOC_Os04g08000		79	77	80	67	156	2	4	2	2	90
Os01g0587400	SD-2b	85	146	1,049	443		2	52	955	353	
LOC_Os01g40499		86	77	81	88	844	2	8	2	6	784
Os01g0889900	SD-2b	114	89	75	75		2	2	2	2	
LOC_Os01g66610		1,900	1,776	1,812	1,935	4,459	1,795	1,693	1,670	1,811	4,407
Os01g0870500	SD-2b	1,263	325	114	91		1,145	222	8	2	
LOC_Os01g65030		171	154	218	164	639	55	76	105	56	555
Os01g0890600	SD-2b	504	121	457	648		355	2	329	531	
LOC_Os01g66680		354	300	609	379	507	220	209	443	236	451
Os03g0221700	SD-2b	2,626	125	188	181		2,472	2	62	66	
LOC_Os03g12150		7,396	4,556	5,510	5,486	7,018	7,265	4,463	5,346	5,348	6,959
Os01g0222800	SD-2b	3,453	3,554	402	371		3,323	3,444	284	269	
LOC_Os01g12290		1,046	1,006	1,026	1,026	800	930	919	882	905	736
Os01g0223700	SD-2b	1,431	3,517	761	826		1,329	3,418	662	736	
LOC_Os01g12400		2,511	2,245	2,384	2,376	6,170	2,411	2,169	2,288	2,289	6,109
Os01g0223900	SD-2b	1,354	1,012	97	94		1,236	912	2	2	
LOC_Os01g12420		3,121	3,005	3,321	3,113	3,794	3,015	2,932	3,198	2,999	3,707
Os01g0224000	SD-2b	422	104	86	74		322	11	2	2	
LOC_Os01g12430		68	66	69	67	185	2	2	2	2	118
Os07g0553500	SD-2b	96	101	86	86		2	2	2	2	
LOC_Os07g36760		77	76	77	80	178	2	2	2	2	123
Os02g0767400	SD-2b	120	126	4,522	3,583		16	30	4,430	3,493	
LOC_Os02g52850		2,430	2,316	2,414	2,447	967	2,332	2,244	2,314	2,360	907
Os12g0640700	SD-2b	1,316	90	78	74		1,213	2	2	2	
LOC_Os12g44320		1,803	1,532	1,491	1,682	1,991	1,715	1,467	1,418	1,608	1,925
Os09g0454900	SD-2b	116	90	107	95		3	2	10	2	
LOC_Os09g28180		842	804	883	848	953	734	732	767	744	891
Os01g0668600	SD-2a	105	90	93	97		2	2	2	2	
LOC_Os01g47820		447	407	468	498	160	344	335	342	389	105

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Os01g0670600	SD-2a	104	87	98	182		2	2	2	84	
LOC_Os01g48040		77	65	91	96	390	2	2	2	2	334
Os01g0669100	SD-2a	83	80	72	81		2	2	2	2	
LOC_Os01g47900		1,023	880	907	997	425	932	810	817	915	357
Os01g0670100	SD-2a	109	106	104	110		9	15	18	22	
LOC_Os01g48000		862	793	824	839	1,218	768	725	747	756	1,161
Os01g0885700	SD-2a	98	83	103	69		2	2	2	2	
LOC_Os01g66250		79	65	114	61	109	2	2	2	2	55
Os12g0177800	SD-2a	2,721	905	8,379	12,176		2,609	811	8,278	12,082	
LOC_Os12g07800		3,145	2,660	2,764	2,670	981	3,053	2,584	2,652	2,560	910
Os12g0130200	SD-2a	85	81	83	79		2	2	2	2	
LOC_Os12g03640		351	342	357	381	448	261	270	267	304	381
Os03g0422800	SD-2a	5,998	3,391	9,172	6,781		5,893	3,297	9,078	6,688	
LOC_Os03g30890		1,345	1,152	1,264	1,260	3,116	1,256	1,082	1,150	1,158	3,056
Os06g0575400	SD-2a	81	82	77	72		2	2	2	2	
LOC_Os06g37750		1,490	1,429	1,476	1,480	800	1,399	1,358	1,388	1,399	747
Os06g0578200	SD-2a	128	136	172	156		2	24	47	42	
LOC_Os06g38100		104	115	232	155	175	2	28	74	17	114
Os06g0574700	SD-2a	906	322	393	133		783	219	284	30	
LOC_Os06g37670		259	210	211	232	336	143	133	77	112	275
Os06g0602500	SD-2a	235	80	88	79		135	2	2	2	
LOC_Os06g40030		1,666	1,529	1,596	1,678	7,410	1,577	1,459	1,508	1,601	7,342
Os12g0130300	SD-2a	1,968	7,921	2,175	2,333		1,844	7,806	2,066	2,234	
LOC_Os12g03650		271	259	259	271	658	154	171	130	156	593
Os12g0130500	SD-2a	137	371	125	101		2	249	2	2	
LOC_Os12g03670		1,030	1,089	1,054	1,068	1,053	902	998	888	929	997
Os11g0133500	SD-2a	101	92	89	80		2	2	2	2	
LOC_Os11g03880		103	99	92	99	137	3	25	2	10	76
Os06g0164900	SD-2a	108	114	105	237		2	20	3	146	
LOC_Os06g06930		243	214	217	467	474	155	135	102	355	415
Os06g0165200	SD-2a	103	98	110	85		2	2	6	2	
LOC_Os06g06940		112	82	163	104	335	2	7	40	2	252
Os06g0165500	SD-2a	118	86	97	79		2	2	2	2	
LOC_Os06g06960		100	65	95	68	153	2	2	2	2	90
Os12g0527700	SD-2a	4,337	5,412	97	85		4,197	5,290	2	2	
LOC_Os12g34320		5,117	4,777	4,748	4,763	7,076	4,991	4,683	4,603	4,634	7,005
Os04g0655000	SD-2a	140	113	109	105		12	3	2	8	
LOC_Os04g56090		289	235	270	278	269	176	148	150	170	206
Os08g0230800	SD-2b	92	111	89	89		2	19	2	2	
LOC_Os08g13420		608	557	604	617	178	527	487	515	510	121
Os03g0828800	SD-2b	2,318	1,741	3,137	596		2,217	1,648	3,047	510	
LOC_Os03g61310		203	161	179	189	369	116	94	97	112	302
Os04g0202300	SD-2b	101	104	102	105		2	12	12	14	
LOC_Os04g12560		143	140	161	161	250	54	68	67	76	187
Os04g0202500	SD-2b	155	106	142	125		21	2	24	17	
LOC_Os04g12580		153	104	181	158	263	23	22	34	24	188
Os04g0202800	SD-2b	112	108	182	111		3	17	91	12	
LOC_Os04g12600		118	101	262	149	273	36	30	171	43	219
Os04g0201900	SD-2b	651	183	183	159		537	84	82	59	
LOC_Os04g12540		181	143	181	165	229	80	71	72	51	164
Os06g0620200	SD-2b	95	116	79	79		2	15	2	2	
LOC_Os06g41560		762	670	705	761	746	659	586	563	639	677
Os10g0101000	SD-2b	1,108	247	157	115		992	145	45	15	
LOC_Os10g01100		887	244	334	265	733	782	160	190	140	673
Os01g0127700	DUF26-Ig	348	437	79	78		248	341	2	2	
LOC_Os01g03690		2,335	2,132	2,033	2,280	2,006	2,252	2,061	1,944	2,203	1,949
Os01g0366300	DUF26-1h_AtRLK4_like	162	114	105	86		24	2	2	2	
LOC_Os01g26390		298	266	286	265	529	184	174	150	147	457
Os01g0535400	DUF26-Ih_AtRLK4_like	4,148	5,562	95	98		4,024	5,458	2	2	
LOC_Os01g35160		2,695	2,353	2,629	2,711	4,972	2,578	2,276	2,494	2,589	4,912
Os01g0545500	DUF26-Ih	115	102	88	86		11	8	2	2	
LOC_Os01g36500		85	78	81	81	196	2	6	2	2	125
Os11g0601500	DUF26-Ia	447	457	211	184		348	362	118	97	
LOC_Os11g38850		142	131	140	137	205	52	59	50	58	140
Os10g0136500	DUF26-Ia	122	86	89	138		2	2	2	34	
LOC_Os10g04730		219	163	187	295	196	98	86	51	167	131
Os10g0136400	DUF26-Ia	127	103	100	178		16	5	2	82	
LOC_Os10g04720		327	294	338	331	245	229	215	209	214	187
Os07g0534700	DUF26-Ia	108	91	79	79		8	2	2	2	
LOC_Os07g35004		727	648	660	698	870	648	580	566	597	802
Os07g0534500	DUF26-Ih	83	83	84	81		2	2	2	2	
LOC_Os07g34980		65	67	73	63	156	2	2	2	2	91
Os07g0550900	SD-1a	259	836	91	77		150	738	2	2	

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LOC_Os07g36570		380	354	354	337	462	276	281	246	241	401
Os07g0551300*	SD-1a	13,544	19,124	106	97		13,413	19,012	2	2	
LOC_Os07g36590		2,355	2,004	1,955	2,223	2,450	2,241	1,917	1,828	2,110	2,384
Os01g0784700	SD-1a	123	128	315	95		2	27	208	2	
LOC_Os01g57560		1,121	1,051	1,433	1,096	1,349	1,005	977	1,303	980	1,284
Os04g0634500	SD-1a	7,709	3,789	25,178	20,168		7,597	3,692	25,080	20,073	
LOC_Os04g54190		5,428	4,969	5,567	5,631	6,284	5,330	4,897	5,446	5,530	6,217
Os01g0784200	SD-1a	117	132	553	2,114		2	12	455	2,014	
LOC_Os01g57510		92	104	150	189	394	2	14	25	80	316
Os01g0784500	SD-1a	5,108	4,606	544	365		4,994	4,505	446	269	
LOC_Os01g57540		5,112	4,729	4,946	4,880	2,905	5,000	4,654	4,834	4,778	2,837
Os03g0556600	SD-1a	83	83	128	80		2	2	37	2	
LOC_Os03g35600		834	728	815	820	1,245	748	654	709	732	1,184
Os07g0550500	SD-1a	94	86	80	79		2	2	2	2	
LOC_Os07g36544		83	68	69	66	107	2	2	2	2	52
Os05g0493100	DUF26-Ia	316	134	105	79		167	10	2	2	
LOC_Os05g41370		527	358	404	365	506	401	263	253	234	436
Os02g0710500	SD-1a	151	148	119	126		47	53	28	36	
LOC_Os02g48080		2,492	2,258	2,211	2,374	1,735	2,399	2,186	2,114	2,288	1,666
Os06g0496800	SD-1a	290	1,542	134	124		189	1,450	43	37	
LOC_Os06g30130		7,625	6,616	6,606	7,208	11,671	7,538	6,550	6,526	7,132	11,604
Os04g0226600	SD-1c	82	81	80	80		2	2	2	2	
LOC_Os04g15580		1,854	1,666	1,658	1,772	2,125	1,753	1,590	1,562	1,687	2,057
Os04g0632700	SD-1c	127	120	131	101		2	7	12	2	
LOC_Os04g54020		869	845	787	763	428	740	759	649	636	367
Os04g0633200	SD-1c	96	95	88	91		2	2	2	2	
LOC_Os04g54070		66	69	66	65	217	2	2	2	2	155
Os04g0633300	SD-1c	117	114	170	112		2	3	49	2	
LOC_Os04g54080		85	79	269	125	203	2	2	127	2	140
Os04g0632600	SD-1c	244	400	198	194		128	299	95	93	
LOC_Os04g54010		490	430	492	500	501	386	357	379	384	432
Os04g0633800	SD-1c	109	102	89	86		2	2	2	2	
LOC_Os04g54120		118	94	121	118	129	2	4	2	2	73
Os08g0179000	SD-1c	889	178	4,175	2,296		789	86	4,087	2,210	
LOC_Os08g08140		4,842	4,215	4,439	4,738	9,618	4,753	4,150	4,361	4,661	9,548
Os09g0550500	SD-1c	96	173	914	2,240		2	62	807	2,144	
LOC_Os09g37790		66	86	81	85	297	2	2	2	2	230
Os09g0551500	SD-1c	124	542	143	86		2	418	23	2	
LOC_Os09g37890		104	409	98	86	881	2	316	2	2	825
Os10g0329700	DUF26-Ic	94	97	88	90		2	2	2	2	
LOC_Os10g18260		130	117	128	137	304	49	48	43	68	245
Os04g0197200	DUF26-Ic	8,580	136	4,196	1,026		8,478	44	4,109	938	
LOC_Os04g12080		3,507	3,039	3,217	3,347	3,780	3,414	2,970	3,136	3,265	3,714
Os07g0537300	DUF26-Ic	238	365	106	350		121	262	2	250	
LOC_Os07g35290		1,388	1,276	1,311	1,314	799	1,274	1,197	1,199	1,207	736
Os07g0537400	DUF26-Ic	619	1,192	84	227		519	1,099	2	140	
LOC_Os07g35300		1,177	1,044	1,161	1,197	1,656	1,087	976	1,080	1,118	1,589
Os07g0540100	DUF26-Ic	1,348	4,777	2,216	970		1,236	4,678	2,119	875	
LOC_Os07g35580		6,210	5,774	5,995	5,883	6,112	6,102	5,701	5,883	5,782	6,049
Os07g0537000	DUF26-Ic	635	669	84	86		516	566	2	2	
LOC_Os07g35260		923	859	899	929	599	807	781	783	821	538
Os07g0541000	DUF26-Ic	223	248	5,307	7,436		110	153	5,206	7,340	
LOC_Os07g35660		169	138	208	250	243	74	63	94	140	185
Os07g0541200	DUF26-Ic	86	94	81	75		2	2	2	2	
LOC_Os07g35680		1,356	1,295	1,304	1,337	424	1,259	1,222	1,206	1,251	365
Os07g0538200	DUF26-Ic	203	196	153	195		100	90	61	103	
LOC_Os07g35370		16,076	13,968	13,624	15,788	18,817	15,993	13,890	13,527	15,697	18,750
Os07g0538400	DUF26-Ic	128	87	85	74		2	2	2	2	
LOC_Os07g35390		802	677	723	751	821	688	590	594	640	754
Os07g0537500	DUF26-Ic	2,426	401	35,084	29,096		2,284	278	34,971	28,990	
LOC_Os07g35310		8,704	7,710	8,380	9,153	13,357	8,582	7,616	8,237	9,027	13,285
Os07g0628700	DUF26-Ic	178	122	620	113		44	8	498	4	
LOC_Os07g43560		3,928	3,642	4,762	3,862	2,761	3,797	3,556	4,619	3,729	2,702
Os07g0540800	DUF26-Ic	321	185	97	127		189	77	2	18	
LOC_Os07g35650		294	254	308	347	216	168	172	160	213	144
Os07g0541400	DUF26-Ic	783	188	93	174		668	85	2	76	
LOC_Os07g35690		1,295	1,153	1,279	1,386	892	1,182	1,075	1,170	1,280	833
Os07g0541500	DUF26-Ic	96	93	84	75		2	2	2	2	
LOC_Os07g35700		1,318	1,205	1,212	1,368	1,953	1,231	1,134	1,123	1,291	1,896
Os07g0541700	DUF26-Ic	89	89	82	74		2	2	2	2	
LOC_Os07g35730		4,547	4,138	4,476	4,650	8,183	4,472	4,067	4,390	4,576	8,120
Os07g0541900	DUF26-Id	432	83	211	66		322	2	108	2	
LOC_Os07g35750		524	189	462	208	564	433	112	344	95	493

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Os07g0542400	DUF26-Id	93	92	102	116		2	2	8	16	
LOC_Os07g35790		2,661	2,505	2,762	2,742	4,583	2,573	2,434	2,663	2,635	4,528
Os07g0541800	DUF26-Id	82	79	131	71		2	2	31	2	
LOC_Os07g35740		195	177	295	187	510	105	96	176	78	455
Os07g0542600	DUF26-Id	1,317	1,013	487	399		1,171	892	360	283	
LOC_Os07g35810		15,424	14,223	15,055	15,099	16,786	15,294	14,132	14,889	14,959	16,727
Os07g0628900	DUF26-Ic	88	86	227	78		2	2	138	2	
LOC_Os07g43570		1,837	1,617	1,911	1,876	1,580	1,750	1,553	1,836	1,801	1,518
Os11g0549300	DUF26-Ic	92	85	86	88		2	2	2	2	
LOC_Os11g34624		67	66	72	65	258	2	2	2	2	203
Os07g0537900	DUF26-Ic	176	123	105	103		24	2	2	2	
LOC_Os07g35340		212	153	177	189	369	80	60	11	48	307
Os07g0539700	DUF26-Ic	366	375	578	428		262	282	487	338	
LOC_Os07g35540		320	258	277	270	612	232	190	198	192	558
Os07g0538300	DUF26-Ic	119	235	117	131		8	138	17	33	
LOC_Os07g35380		926	834	967	995	1,579	828	762	850	886	1,518
Os07g0537600	DUF26-Ic	144	147	104	129		29	45	2	29	
LOC_Os07g35330		4,223	3,564	4,065	4,255	7,984	4,119	3,480	3,921	4,130	7,918
Os07g0537200	DUF26-Ic	131	102	84	78		2	2	2	2	
LOC_Os07g35280		522	484	464	501	1,224	389	392	314	365	1,150
Os06g0541600	DUF26	143	607	118	116		9	498	2	8	
LOC_Os06g34960		160	124	159	163	289	32	42	12	30	233
Os06g0690200	DUF26-Ih	470	132	108	97		341	29	2	2	
LOC_Os06g47530		7,780	7,452	7,895	7,232	5,972	7,659	7,377	7,763	7,110	5,907
Os06g0689600	DUF26-Ih	90	96	91	88		2	4	2	2	
LOC_Os06g47470		79	85	80	77	178	2	20	3	2	114
Os08g0343000	not_assigned	494	523	317	192		379	418	207	95	
LOC_Os08g25430		1,011	926	966	931	419	899	846	853	827	360
Os12g0249900	not_assigned	180	203	581	141		37	82	458	29	
LOC_Os12g14699		13,453	12,628	13,567	13,753	5,716	13,318	12,535	13,413	13,616	5,654
Os11g0670100	not_assigned	111	109	97	85		5	9	2	2	
LOC_Os11g44750		146	159	173	157	136	41	84	71	66	74
Os11g0672200	not_assigned	94	93	89	103		2	2	2	13	
LOC_Os11g44860		569	543	547	547	992	478	473	457	464	918
Os04g0634000	SD-1d	256	250	403	335		152	153	310	245	
LOC_Os04g54140		499	469	465	439	228	401	396	366	352	156
Os04g0634400	SD-1d	162	135	1,743	1,904		34	28	1,624	1,795	
LOC_Os04g54180		827	742	860	894	230	708	659	711	760	157
Os04g0633900	DUF26-Id	115	223	77	117		9	125	2	26	
LOC_Os04g54130		650	615	672	762	148	553	532	540	645	86
Os01g0548600	DUF26-If	106	100	106	96		2	2	4	2	
LOC_Os01g36790		839	801	862	849	769	735	729	736	741	680
Os05g0130100	DUF26-If	90	83	83	80		2	2	2	2	
LOC_Os05g03920		63	60	65	68	160	2	2	2	2	98
Os10g0483400	DUF26-If	140	516	1,185	318		14	413	1,077	216	
LOC_Os10g34220		325	296	371	325	133	210	222	243	204	78
Os11g0470200	DUF26-If	100	150	470	580		2	57	379	491	
LOC_Os11g28104		700	598	583	603	135	612	532	506	527	69
Os04g0658700	RLCK-OS1	93	96	94	100		2	2	4	9	
LOC_Os04g56360		83	84	104	96	186	3	6	7	5	127
Os06g0676600	LRR-VIII-2	547	758	85	80		439	652	2	2	
LOC_Os06g46330		1,839	1,715	1,757	1,772	1,752	1,742	1,635	1,653	1,678	1,684
Os02g0165100	LRR-VIII-2	1,014	17,105	194	179		906	17,011	101	80	
LOC_Os02g06930		2,758	2,517	2,758	2,674	7,570	2,673	2,447	2,664	2,566	7,507
Os04g0619400	LRR-VIII-2	2,450	9,392	78	92		2,334	9,278	2	2	
LOC_Os04g52840		5,164	4,723	4,197	4,750	6,490	5,062	4,638	4,081	4,647	6,418
Os08g0200500	LRR-VIII-2	961	1,564	142	115		817	1,442	24	6	
LOC_Os08g10070		2,794	2,653	2,113	2,223	1,903	2,665	2,559	1,963	2,091	1,852
Os12g0611100	LRR-VIII-2	116	108	99	89		16	7	6	2	
LOC_Os12g41710		3,195	2,821	2,814	3,114	4,129	3,111	2,745	2,719	3,028	4,069
Os03g0264300	RLCK-XII	228	233	105	102		96	121	2	2	
LOC_Os03g15770		326	299	342	331	407	197	214	204	202	316
Os04g0679200	LRR-VIII-2	4,585	3,974	98	98		4,485	3,876	4	11	
LOC_Os04g58250		16,662	15,198	15,223	16,170	12,697	16,567	15,124	15,130	16,089	12,638
Os05g0256500	LRR-VIII-2	2,775	105	104	101		2,644	2	2	2	
LOC_Os05g16740		11,500	10,908	12,106	11,712	2,511	11,376	10,830	11,968	11,582	2,438
Os05g0256100	LRR-VIII-2	506	1,362	429	209		380	1,256	317	105	
LOC_Os05g16670		3,187	3,020	3,166	3,128	4,274	3,067	2,941	3,043	3,008	4,206
Os05g0258400	LRR-VIII-2	92	122	113	82		2	9	2	2	
LOC_Os05g16930		1,733	1,565	1,766	1,725	1,060	1,615	1,477	1,613	1,597	1,003
Os05g0261700	LRR-VIII-2	278	280	177	206		178	182	83	118	
LOC_Os05g17604		521	527	504	502	938	424	452	410	419	879
Os08g0203100	LRR-VIII-2	276	100	315	182		174	8	225	94	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os08g10290		944	806	851	924	626	858	740	774	848	558
Os08g0203300	LRR-VIII-2	130	112	82	80		8	8	2	2	
LOC_Os08g10300		100	75	74	74	209	2	2	2	2	142
Os08g0203600	LRR-VI	944	1,533	78	74		842	1,439	2	2	
LOC_Os08g10320		4,258	3,932	3,898	4,179	8,927	4,166	3,860	3,807	4,096	8,865
Os04g0616300	LRR-VIII-2	2,040	2,653	84	195		1,886	2,529	2	84	
LOC_Os04g52600		3,294	3,048	3,199	3,400	4,858	3,167	2,955	3,044	3,266	4,794
Os04g0616700	LRR-VIII-2	7,966	3,002	99	170		7,848	2,898	2	71	
LOC_Os04g52640		15,595	14,607	15,347	15,654	16,702	15,481	14,528	15,235	15,545	16,633
Os04g0616400	LRR-VIII-2	13,195	8,207	4,493	1,131		13,070	8,105	4,385	1,029	
LOC_Os04g52606		11,017	10,542	11,567	11,351	17,465	10,902	10,467	11,440	11,231	17,397
Os04g0616200	LRR-VIII-2	26,115	8,292	9,179	6,255		25,980	8,179	9,055	6,143	
LOC_Os04g52590		7,841	7,090	7,977	8,145	8,196	7,717	7,002	7,816	8,010	8,135
Os08g0201700	LRR-VIII-2	93	94	148	159		2	2	58	71	
LOC_Os08g10150		1,168	1,039	1,057	1,219	765	1,082	974	982	1,144	696
Os09g0345300	LRR-VIII-2	553	1,511	108	91		452	1,417	11	2	
LOC_Os09g17630		2,377	2,208	2,214	2,314	3,012	2,285	2,138	2,125	2,230	2,938
Os04g0369000	RLCK-OS2	88	674	85	78		2	572	2	2	
LOC_Os04g30030		1,523	1,421	1,502	1,491	1,623	1,433	1,344	1,403	1,400	1,561
Os04g0369100	RLCK-OS2	94	94	93	92		2	2	2	3	
LOC_Os04g30040		72	64	69	77	436	2	2	2	2	369
Os11g0607900	RLCK-OS2	169	165	544	104		38	59	433	2	
LOC_Os11g39420		163	164	1,073	117	153	38	86	938	2	81
Os11g0213000	RLCK-OS2	109	84	83	85		2	2	2	2	
LOC_Os11g10710		1,085	1,004	1,002	1,019	1,330	978	927	899	923	1,262
Os11g0212300	RLCK-OS2	322	293	495	988		219	190	401	897	
LOC_Os11g10640		220	231	251	264	894	134	154	153	174	805
Os11g0274700	RLCK-OS2	113	102	206	96		2	2	98	2	
LOC_Os11g17440		98	79	170	115	152	2	5	39	2	85
Os11g0225000	RLCK-OS2	101	99	99	92		2	2	2	2	
LOC_Os11g11780		702	605	679	682	277	583	516	540	559	217
Os10g0200000	RLCK-OS2	1,522	418	1,280	511		1,409	313	1,172	417	
LOC_Os10g12620		1,901	1,746	1,884	1,838	429	1,791	1,665	1,772	1,737	362
Os12g0486900	RLCK-OS2	191	101	134	109		54	2	14	2	
LOC_Os12g30180		383	286	352	363	242	252	202	204	227	137
Os02g0728500*	LRR-II	7,444	2,171	84	84		7,326	2,071	2	2	
LOC_Os02g49600		784	730	733	706	1,221	674	658	609	598	1,143
Os06g0274500	LRR-II	3,398	3,978	163	103		3,251	3,856	36	2	
LOC_Os06g16330		710	603	757	688	2,451	574	511	596	544	2,382
Os08g0442700	LRR-II	11,728	8,152	163	156		11,601	8,044	46	53	
LOC_Os08g34380		6,430	5,591	6,068	6,005	8,363	6,317	5,505	5,921	5,882	8,295
Os01g0171000	LRR-II	3,764	5,964	959	791		3,642	5,858	846	688	
LOC_Os01g07630		19,374	18,635	18,413	18,241	26,309	19,257	18,554	18,296	18,127	26,246
Os02g0236100	LRR-II	31,497	31,153	315	444		31,388	31,056	217	345	
LOC_Os02g14120		21,071	17,836	18,513	18,292	31,335	20,977	17,765	18,403	18,184	31,267
Os05g0170700	LRR-II	141	133	123	127		2	12	2	10	
LOC_Os05g07850		125	112	159	181	468	2	21	2	36	402
Os02g0283800	LRR-II	7,493	14,139	101	106		7,352	14,023	2	2	
LOC_Os02g18320		7,742	6,898	7,349	7,317	6,560	7,609	6,810	7,195	7,175	6,499
Os03g0703200	LRR-II	20,956	34,058	111	413		20,842	33,958	2	321	
LOC_Os03g49620		51,378	43,770	46,336	50,320	53,643	51,270	43,684	46,212	50,214	53,552
Os11g0607200	LRR-II	1,392	1,326	107	96		1,287	1,223	9	6	
LOC_Os11g39370		29,344	26,615	29,081	28,256	20,412	29,251	26,537	28,980	28,164	20,353
Os04g0457800	LRR-II	36,869	48,849	14,802	3,768		36,765	48,756	14,712	3,679	
LOC_Os04g38480		71,017	62,670	63,636	65,273	100,039	70,930	62,603	63,559	65,197	99,961
Os08g0174700	LRR-II	78,531	88,750	3,400	1,819		78,420	88,645	3,293	1,726	
LOC_Os08g07760		36,206	35,110	33,654	35,198	36,578	36,097	35,029	33,542	35,099	36,515
Os08g0176200	LRR-II	9,350	8,780	8,453	5,366		9,196	8,655	8,328	5,252	
LOC_Os08g07890		7,470	7,109	7,612	7,538	22,288	7,340	7,016	7,450	7,400	22,212
Os08g0174800	LRR-II	16,163	21,176	741	956		16,059	21,086	651	865	
LOC_Os08g07774		28,897	24,347	26,513	28,017	45,093	28,808	24,274	26,418	27,933	45,038
Os06g0225300	LRR-II	1,476	5,846	572	755		1,375	5,739	482	664	
LOC_Os06g12120		2,012	1,804	1,742	2,093	3,333	1,935	1,727	1,648	2,005	3,276
Os02g0186500	RLCK-XV	12,607	13,186	110	122		12,510	13,084	20	34	
LOC_Os02g09359		58,949	53,240	54,706	58,981	49,756	58,875	53,166	54,616	58,899	49,695
Os06g0654500	RLCK-XV	261	266	662	456		156	176	572	367	
LOC_Os06g44430		171	191	187	182	500	85	117	79	94	442
Os09g0531800	RLCK-XV	2,201	3,192	1,047	598		2,100	3,099	960	511	
LOC_Os09g36180		953	891	958	971	1,053	862	821	876	890	992
Os06g0166900	RLCK-XV	304	3,798	85	86		200	3,703	2	2	
LOC_Os06g07070		1,097	1,028	1,067	1,134	2,108	1,007	957	976	1,054	2,043
Os01g0883000	RKF3	381	544	110	98		259	443	4	2	
LOC_Os01g66020		186	144	198	190	556	75	71	68	75	501

Supplemental Table 14 continue. Microarray data for rice kinase genes

Os05g0423500	RKF3	1,672	398	84	81		1,530	276	2	2	
LOC_Os05g34950		2,301	2,101	2,355	2,211	4,134	2,175	2,007	2,210	2,082	4,055
Os01g0384300	RKF3	4,462	6,445	187	146		4,363	6,353	101	60	
LOC_Os01g28730		4,549	3,801	3,949	4,341	4,785	4,457	3,735	3,874	4,261	4,730
Os11g0108800	RLCK-V	3,218	3,140	193	707		3,113	3,044	90	618	
LOC_Os11g01740		10,829	9,211	9,738	11,487	8,762	10,734	9,128	9,609	11,373	8,686
Os12g0108100	RLCK-V	10,201	10,071	255	193		10,101	9,975	164	106	
LOC_Os12g01740		58,833	54,478	36,211	30,800	36,925	58,739	54,405	36,121	30,719	36,861
Os01g0323000	RLCK-V	23,791	38,169	100	85		23,672	38,068	2	2	
LOC_Os01g21960		7,437	6,785	7,664	7,270	13,600	7,330	6,711	7,546	7,154	13,541
Os01g0631700	RLCK-V	3,243	13,020	99	94		3,140	12,928	11	5	
LOC_Os01g44110		6,156	5,575	5,921	6,176	18,672	6,065	5,505	5,836	6,094	18,615
Os10g0497600	RLCK-V	95,924	90,606	770	166		95,794	90,499	655	60	
LOC_Os10g35450		54,115	49,359	55,604	55,131	92,301	53,991	49,280	55,463	55,002	92,237
Os01g0664200	RLCK-V	8,883	16,328	142	198		8,759	16,217	28	96	
LOC_Os01g47470		17,041	16,341	17,025	17,121	16,798	16,919	16,257	16,898	17,004	16,716
Os01g0601200	RLCK-V	9,546	8,408	1,664	1,437		9,418	8,301	1,550	1,332	
LOC_Os01g41730		15,743	15,497	12,524	12,225	16,135	15,621	15,417	12,398	12,103	16,065
Os02g0549200*	RLCK-V	84,599	164,134	325	95		84,481	164,030	214	2	
LOC_Os02g34430		20,757	20,109	20,334	20,042	17,245	20,642	20,029	20,220	19,934	17,176
Os04g0430000	RLCK-V	800	1,192	108	115		655	1,069	2	10	
LOC_Os04g35080		1,163	1,028	1,109	1,162	3,577	1,047	934	965	1,040	3,524
Os05g0436100	RLCK-V	2,045	3,319	254	251		1,936	3,223	158	157	
LOC_Os05g36050		98,437	92,059	90,461	91,774	173,526	98,338	91,987	90,348	91,677	173,442
Os03g0125600	RLCK-V	2,696	785	154	133		2,598	687	63	45	
LOC_Os03g03410		15,562	13,595	14,549	15,411	37,255	15,485	13,523	14,460	15,333	37,194
Os03g0227900	RLCK-V	911	10,525	138	141		800	10,432	39	46	
LOC_Os03g12680		3,058	3,159	3,075	3,053	3,435	2,968	3,085	2,967	2,946	3,381
Os01g0110500	PERK	1,289	931	133	107		1,159	824	18	2	
LOC_Os01g02040		2,578	2,358	2,610	2,588	4,452	2,454	2,279	2,466	2,459	4,396
Os05g0100700	PERK	11,864	20,624	122	98		11,744	20,524	17	2	
LOC_Os05g01040		13,354	12,327	13,556	12,969	11,120	13,245	12,254	13,428	12,855	11,050
Os01g0738300	PERK	3,902	3,147	142	115		3,802	3,055	55	28	
LOC_Os01g53640		3,677	3,232	3,416	3,498	3,313	3,585	3,164	3,338	3,416	3,252
Os03g0568800	PERK	194	239	338,999	465,780		88	145	338,910	465,691	
LOC_Os03g37120		146	145	12,879	21,647	6,072	56	77	12,801	21,572	6,006
Os06g0486000	PERK	118	87	12,024	15,401		3	2	11,923	15,303	
LOC_Os06g29080		95	64	128	154	137	2	2	15	43	81
Os01g0227200	PERK	954	1,247	114	110		850	1,153	21	20	
LOC_Os01g12720		8,369	7,426	7,734	8,083	9,215	8,280	7,356	7,648	8,003	9,149
Os05g0218400	PERK	39,689	68,610	114	114		39,585	68,512	10	23	
LOC_Os05g12680		43,462	40,668	42,674	43,268	24,544	43,362	40,594	42,578	43,180	24,483
Os03g0776100	PERK	1,528	369	234	371		1,393	260	118	263	
LOC_Os03g56470		5,888	5,232	5,725	5,715	6,304	5,759	5,152	5,582	5,582	6,238
Os03g0226800	PERK	236	181	641,429	656,795		99	71	641,310	656,685	
LOC_Os03g12570		198	113	31,942	47,226	14,607	67	31	31,796	47,092	14,540
Os10g0104800	PERK	91	79	29,915	20,364		2	2	29,827	20,278	
LOC_Os10g01560		70	54	2,621	3,168	393	2	2	2,542	3,091	330
Os07g0137800	PERK	103	110	17,686	17,438		3	17	17,593	17,350	
LOC_Os07g04520		84	81	105	102	158	2	12	19	23	92
Os01g0750600	PERK	32,546	9,825	3,585	3,348		32,441	9,721	3,490	3,257	
LOC_Os01g54700		11,342	10,919	11,456	11,475	14,379	11,252	10,840	11,355	11,382	14,323
Os05g0516400	PERK	87	90	2,433	1,004		2	2	2,342	915	
LOC_Os05g44030		128	125	221	161	298	40	57	140	82	234
Os03g0269300	PERK	123	113	130	101		2	7	16	2	
LOC_Os03g16260		283	248	331	279	197	160	170	189	152	145
Os01g0602800	PERK	40,284	77,403	1,425	2,310		40,147	77,291	1,301	2,196	
LOC_Os01g41870		20,830	20,309	21,044	20,974	36,447	20,700	20,224	20,891	20,834	36,384
Os05g0589700	PERK	2,229	2,155	117	108		2,123	2,061	29	19	
LOC_Os05g51190		5,391	4,427	4,690	4,799	13,877	5,303	4,359	4,610	4,723	13,812
Os01g0195200	Extensin	4,534	3,137	104	85		4,430	3,040	12	2	
LOC_Os01g09860		9,507	8,845	9,268	9,675	28,856	9,407	8,772	9,169	9,588	28,777
Os01g0709500	Extensin	20,820	37,462	2,101	2,296		20,716	37,371	2,010	2,208	
LOC_Os01g51290		128,519	122,105	124,404	128,381	164,280	128,432	122,033	124,293	128,290	164,214
Os02g0815900	Extensin	37,592	26,202	389	423		37,466	26,100	281	321	
LOC_Os02g57080		26,296	24,495	26,251	24,498	37,827	26,180	24,421	26,123	24,376	37,769
Os04g0509000	Extensin	108	319	111	124		2	210	2	15	
LOC_Os04g43020		105	83	136	164	273	2	2	2	29	191
Os05g0207700	Extensin	18,949	11,425	113	100		18,847	11,333	26	12	
LOC_Os05g11750		17,617	16,099	16,249	17,296	28,277	17,525	16,029	16,166	17,214	28,208
Os05g0398800	Extensin	133	105	82	85		15	4	2	2	
LOC_Os05g33080		20,995	19,253	22,070	21,632	21,111	20,888	19,176	21,942	21,514	21,050
Os01g0936100	RLCK-VIIa	16,184	24,267	102	93		16,055	24,162	2	2	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os01g71000		16,435	15,561	16,299	16,528	19,360	16,312	15,483	16,168	16,404	19,293
Os05g0372100	RLCK-VIIa	48,092	70,596	56,358	50,157		47,988	70,505	56,269	50,067	
LOC_Os05g30870		45,776	39,516	41,807	44,350	83,405	45,685	39,444	41,718	44,266	83,351
Os07g0668900	RLCK-VIIa	163	2,389	70	68		56	2,295	2	2	
LOC_Os07g47270		4,620	3,948	4,523	4,583	3,683	4,531	3,867	4,406	4,472	3,623
Os07g0695300	RLCK-VIIa	11,003	14,572	131	117		10,902	14,479	38	29	
LOC_Os07g49470		9,612	8,675	8,947	9,633	16,795	9,524	8,606	8,862	9,555	16,732
Os02g0513000*	RLCK-VIIa	9,366	19,522	75	277		9,267	19,427	2	190	
LOC_Os02g30900		1,085	1,130	906	982	1,320	996	1,060	818	905	1,253
Os04g0393900	RLCK-VIIa	30,178	7,215	161	153		30,047	7,100	42	47	
LOC_Os04g32310		9,613	8,405	8,696	8,319	14,550	9,484	8,318	8,558	8,191	14,491
Os01g0789200	RLCK-VIIa	216	115	264,810	338,448		83	9	264,697	338,342	
LOC_Os01g57940		191	102	4,330	4,934	1,145	65	23	4,191	4,803	1,068
Os05g0498900	RLCK-VIIa	1,274	2,395	65,596	67,716		1,162	2,301	65,497	67,620	
LOC_Os05g41950		1,165	1,021	1,670	1,705	1,151	1,072	947	1,563	1,599	1,088
Os09g0572600	RLCK-VIIa	104	96	196,878	228,190		2	2	196,766	228,085	
LOC_Os09g39930		83	72	1,633	1,714	1,087	2	2	1,495	1,583	1,021
Os05g0125300	RLCK-VIIa	114	117	95	101		2	13	2	2	
LOC_Os05g03460		77	72	101	114	241	2	2	2	2	175
Os05g0463000	RLCK-VIIa	410	256	189,675	251,784		276	145	189,551	251,670	
LOC_Os05g38770		85	84	1,102	1,671	733	2	2	946	1,531	675
Os02g0833000	RLCK-VIIa	81	85	8,857	11,269		2	2	8,764	11,178	
LOC_Os02g58610		62	59	249	334	404	2	2	151	244	349
Os03g0130900	RLCK-VIIa	82,070	49,705	3,818	3,168		81,958	49,604	3,720	3,073	
LOC_Os03g03880		72,706	64,681	64,460	66,205	74,424	72,596	64,604	64,354	66,108	74,348
Os03g0283900*	RLCK-VIIa	4,150	6,831	88	81		4,049	6,735	2	2	
LOC_Os03g17550		322	294	294	307	376	229	222	204	226	313
Os01g0588500	RLCK-VIIa	5,920	10,730	865	216		5,799	10,630	762	117	
LOC_Os01g40590		6,900	6,728	7,022	6,730	6,990	6,787	6,655	6,895	6,618	6,927
Os09g0361100	RLCK-VIIa	8,863	14,887	101	90		8,763	14,795	15	3	
LOC_Os09g19700		20,482	17,063	18,002	18,773	20,999	20,389	16,994	17,925	18,691	20,944
Os06g0168800	RLCK-VIIa	3,119	10,868	541	187		2,999	10,758	430	89	
LOC_Os06g07230		61,738	58,885	62,029	61,132	111,939	61,622	58,801	61,906	61,021	111,856
Os01g0973500*	RLCK-VIIa	81,334	8,470	118	209		81,230	8,377	28	120	
LOC_Os01g74200		3,644	2,477	2,473	2,757	4,512	3,556	2,410	2,397	2,681	4,444
Os05g0110900	RLCK-VIIa	37,468	11,639	121	115		37,330	11,523	2	2	
LOC_Os05g02020		11,400	10,664	11,451	11,378	12,281	11,267	10,576	11,300	11,238	12,202
Os03g0274800	RLCK-VIIa	8,970	4,018	173	166		8,840	3,901	61	64	
LOC_Os03g16740		43,017	39,808	42,949	41,971	50,044	42,895	39,717	42,813	41,849	49,980
Os03g0821900*	RLCK-VIIa	27,437	17,035	1,002	708		27,331	16,942	908	617	
LOC_Os03g60710		3,806	3,046	3,239	3,303	7,458	3,716	2,975	3,124	3,205	7,397
Os11g0121400	RLCK-VIIa	10,655	25,405	18,718	8,759		10,528	25,296	18,602	8,660	
LOC_Os11g02830		25,701	21,951	23,389	25,540	81,181	25,588	21,864	23,259	25,428	81,099
Os12g0121100	RLCK-VIIa	12,007	41,855	27,802	12,889		11,900	41,748	27,704	12,797	
LOC_Os12g02810		31,770	31,083	31,388	31,541	94,719	31,675	31,003	31,284	31,446	94,652
Os06g0663200	RLCK-VIIa	1,109	1,299	108	240		991	1,198	4	139	
LOC_Os06g45280		561	507	545	854	626	454	433	429	736	557
Os06g0703000	RLCK-VIIa	213	128	394,588	396,179		73	6	394,476	396,074	
LOC_Os06g48980		117	101	144,167	168,214	35,918	2	8	144,025	168,089	35,844
Os03g0159100	RLCK-VIIa	6,234	13,698	887	408		6,113	13,598	782	308	
LOC_Os03g06330		7,683	7,166	7,846	7,380	10,340	7,571	7,093	7,716	7,266	10,278
Os10g0431900	RLCK-VIIa	161	161	152	199		44	60	51	102	
LOC_Os10g29620		25,211	23,688	24,250	24,266	30,004	25,097	23,611	24,136	24,161	29,946
Os02g0777800	RLCK-VIIa	563	150	172	173		414	27	44	55	
LOC_Os02g53750		8,426	7,806	8,356	8,415	10,946	8,292	7,713	8,190	8,271	10,889
Os06g0202900	RLCK-VIIa	602	585	88	178		497	494	2	87	
LOC_Os06g10160		3,729	3,312	3,585	3,581	6,907	3,641	3,239	3,480	3,493	6,850
Os08g0457400	RLCK-VIIa	173	85	103	213		62	2	5	119	
LOC_Os08g35600		848	851	873	1,089	446	751	779	753	989	390
Os09g0442100	RLCK-VIIa	139	173	182	251		5	62	59	139	
LOC_Os09g27010		3,463	3,245	3,470	3,429	4,257	3,336	3,161	3,319	3,290	4,200
Os03g0179400	RLCK-VIIa	1,012	2,695	117	82		864	2,573	2	2	
LOC_Os03g08170		8,216	7,078	7,753	7,949	15,185	8,094	6,987	7,606	7,820	15,122
Os10g0395000	RLCK-VIIa	304	158	109	83		155	33	2	2	
LOC_Os10g25550		437	316	337	330	247	311	221	184	198	197
Os03g0407900	RLCK-VIIa	265	223	243	506		127	103	125	399	
LOC_Os03g29410		3,647	3,387	3,883	3,943	1,964	3,518	3,295	3,737	3,812	1,902
Os07g0613500	RLCK-VIIa	2,830	3,643	9,050	4,204		2,698	3,533	8,927	4,092	
LOC_Os07g42200		15,993	14,857	15,391	15,716	12,461	15,870	14,771	15,237	15,578	12,398
Os03g0364400	RLCK-VIIa	1,696	3,807	74	77		1,585	3,701	2	2	
LOC_Os03g24930		866	851	848	872	1,546	758	769	736	773	1,488
Os02g0118200	RLCK-VIIa	2,972	5,393	101	97		2,855	5,294	2	2	
LOC_Os02g02600		6,208	5,892	6,394	6,289	4,127	6,102	5,817	6,274	6,175	4,066

Supplemental Table 14 continue. Microarray data for rice kinase genes

Os06g0727400	RLCK-VIIa	802	131	130	88		667	9	29	2	
LOC_Os06g51170		6,532	5,712	6,241	6,776	10,384	6,425	5,621	6,110	6,664	10,313
Os02g0670100	RLCK-VIIa	214	122	104	105		103	29	10	7	
LOC_Os02g44920		283	150	147	139	189	194	78	49	33	129
Os04g0563900	RLCK-VIIa	635	914	306	262		534	821	214	173	
LOC_Os04g47620		1,019	761	848	945	2,000	932	694	765	867	1,930
Os03g0131000	RLCK-VIIa	167	560	245	230		19	438	117	113	
LOC_Os03g03890		4,485	4,564	4,734	4,677	3,429	4,353	4,473	4,568	4,536	3,364
Os03g0170400	RLCK-VIIa	2,804	5,589	495	161		2,704	5,498	409	73	
LOC_Os03g07430		19,652	16,100	17,457	18,636	17,418	19,559	16,031	17,378	18,554	17,360
Os10g0405100	RLCK-VIIa	30,104	38,579	239	124		29,999	38,485	150	35	
LOC_Os10g26520		16,165	13,727	14,678	15,102	26,933	16,076	13,660	14,600	15,026	26,860
Os02g0650500	RLCK-VIIa	473	364	79	83		358	264	2	2	
LOC_Os02g43430		2,023	1,647	1,749	1,868	1,439	1,915	1,561	1,628	1,764	1,379
Os04g0543000	RLCK-VIIa	324	393	251	165		211	297	148	70	
LOC_Os04g45920		512	441	511	550	1,429	417	365	393	437	1,372
Os06g0714900	RLCK-VIIa	2,583	3,075	7,958	6,833		2,476	2,980	7,862	6,741	
LOC_Os06g50100		2,049	1,877	2,005	2,097	2,069	1,957	1,806	1,888	1,998	2,009
Os09g0533600	RLCK-VIIa	4,379	2,350	77	75		4,275	2,251	2	2	
LOC_Os09g36320		504	438	400	426	470	402	363	302	338	393
Os02g0819600	RLCK-VIIa	18,420	25,418	118	158		18,315	25,318	15	68	
LOC_Os02g57420		13,299	12,530	13,505	13,667	32,877	13,197	12,454	13,403	13,578	32,822
Os10g0442800	RLCK-VIIa	158	594	99	85		45	497	2	2	
LOC_Os10g30600		14,461	13,348	15,147	14,794	7,152	14,360	13,276	15,024	14,690	7,090
Os05g0525000	LRR-Ia	95	105	82	78		2	12	2	2	
LOC_Os05g44960		72	61	67	63	147	2	2	2	2	88
Os05g0524600	LRR-Ia	95	100	81	77		2	7	2	2	
LOC_Os05g44940		83	86	71	64	113	2	17	2	2	43
Os05g0524500	LRR-Ia	89	110	79	75		2	2	2	2	
LOC_Os05g44930		372	342	324	351	109	262	251	194	237	58
Os05g0525600	LRR-Ia	108	102	114	95		2	2	8	2	
LOC_Os05g44990		1,925	1,768	2,069	2,039	283	1,814	1,693	1,942	1,920	220
Os08g0518400	LRR-Ia	94	104	108	144		2	2	2	39	
LOC_Os08g40650		73	76	122	162	227	2	2	2	36	159
Os12g0567500	LRR-Ia	228	159	2,851	1,738		79	35	2,730	1,626	
LOC_Os12g37980		237	221	273	309	993	106	126	117	172	924
Os02g0151100	LRR-Ia	5,551	5,125	429	582		5,443	5,031	335	489	
LOC_Os02g05730		1,254	1,146	1,160	1,171	2,407	1,159	1,074	1,048	1,077	2,352
Os05g0246600	LRR-Ia	437	97	465	558		324	2	362	462	
LOC_Os05g15720		116	69	139	122	272	21	2	22	11	220
Os09g0349100	LRR-Ia	120	111	83	89		18	9	2	2	
LOC_Os09g17970		89	80	72	92	212	6	4	2	4	102
Os09g0349600	LRR-Ia	85	95	126	82		2	2	35	2	
LOC_Os09g18010		534	469	486	534	179	457	395	395	451	104
Os09g0349700	LRR-Ia	146	135	96	92		22	18	2	2	
LOC_Os09g18020		145	121	106	94	513	31	33	2	2	450
Os09g0349800	LRR-Ia	145	212	168	104		36	116	72	4	
LOC_Os09g18030		115	125	148	88	1,130	24	54	48	2	1,065
Os09g0350900	LRR-Ia	89	86	80	125		2	2	2	36	
LOC_Os09g18159		193	174	187	188	150	102	103	99	105	84
Os09g0352000	LRR-Ia	130	101	99	93		11	2	2	2	
LOC_Os09g18260		361	314	361	354	519	252	240	243	235	462
Os09g0351700	LRR-Ia	161	154	117	99		32	45	2	2	
LOC_Os09g18230		4,567	4,288	4,445	4,292	6,904	4,443	4,206	4,315	4,168	6,843
Os09g0353200	LRR-Ia	107	98	102	83		3	5	9	2	
LOC_Os09g18360		83	70	101	74	146	2	2	2	2	83
Os09g0355400	LRR-Ia	536	159	94	80		406	51	2	2	
LOC_Os09g18594		528	456	536	498	267	404	375	406	373	204
Os09g0356200	LRR-Ia	98	92	101	79		2	2	5	2	
LOC_Os09g19160		1,504	1,465	1,523	1,502	2,005	1,405	1,394	1,405	1,403	1,937
Os01g0810600	LRR-Ia	114	119	84	104		3	23	2	4	
LOC_Os01g59560		107	88	98	131	294	13	16	2	20	235
Os01g0810900	LRR-Ia	187	96	114	124		65	2	2	21	
LOC_Os01g59580		195	113	156	188	270	78	33	38	73	206
Os11g0102900	LRR-Ic	194	233	124	144		72	130	20	44	
LOC_Os11g01200		186	171	197	218	295	69	94	78	107	236
Os12g0102500	LRR-Ic	9,519	9,695	144	159		9,420	9,602	57	74	
LOC_Os12g01200		39,190	34,069	33,744	36,224	26,607	39,100	34,004	33,667	36,146	26,545
Os01g0976900	LRR-Ic	190	194	220	166		70	93	116	67	
LOC_Os01g74550		2,311	2,158	2,551	2,431	2,554	2,198	2,085	2,424	2,319	2,478
Os06g0283200	LRR-Ib	4,118	13,100	1,537	1,197		4,001	12,998	1,436	1,100	
LOC_Os06g17280		4,667	4,310	4,421	4,320	3,712	4,553	4,233	4,308	4,216	3,654
Os08g0138700	LRR-Ib	328	276	972	468		219	178	866	373	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os08g04420		677	596	685	714	1,499	580	514	551	597	1,448
Os01g0546000	LysM-I	364	148	4,467	2,345		238	45	4,360	2,244	
LOC_Os01g36550		303	99	174	177	237	182	23	45	60	165
Os01g0741200	LysM-I	16,484	15,336	102	101		16,383	15,243	11	14	
LOC_Os01g53840		14,232	12,380	12,937	14,018	16,357	14,144	12,312	12,852	13,941	16,295
Os09g0509400	LysM-I	18,665	25,685	56,044	64,656		18,532	25,574	55,924	64,547	
LOC_Os09g33520		10,555	9,831	10,487	10,913	9,942	10,427	9,747	10,348	10,784	9,888
Os09g0511000	LysM-I	18,211	16,361	4,537	2,270		18,082	16,253	4,418	2,162	
LOC_Os09g33630		16,059	14,783	15,939	15,200	17,528	15,937	14,701	15,791	15,066	17,464
Os08g0538300	LysM-I	10,966	22,487	397	156		10,866	22,395	309	71	
LOC_Os08g42580		13,501	11,368	11,552	12,752	19,177	13,413	11,304	11,476	12,676	19,116
Os03g0717000	LRR-IX	48,554	29,183	212	172		48,455	29,091	124	86	
LOC_Os03g50810		34,443	27,376	25,034	24,724	50,416	34,353	27,310	24,956	24,646	50,362
Os04g0685900	LRR-IX	8,100	7,828	137	135		7,967	7,720	20	28	
LOC_Os04g58910		19,162	18,085	19,900	19,140	23,745	19,035	18,004	19,755	19,008	23,669
Os11g0448000	LRR-IX	19,003	25,300	25,648	14,062		18,883	25,198	25,542	13,960	
LOC_Os11g26130		31,788	29,468	32,117	33,142	33,440	31,677	29,394	31,996	33,022	33,378
Os02g0182600	RLCK-X	973	1,019	105	107		866	927	12	16	
LOC_Os02g08530		1,292	1,166	1,286	1,302	2,913	1,201	1,093	1,173	1,209	2,850
Os05g0319700	RLCK-X	541	170	158	115		412	60	37	4	
LOC_Os05g25540		4,298	4,129	4,690	4,623	3,748	4,178	4,043	4,535	4,487	3,689
Os08g0285600	RLCK-X	5,705	5,959	325	401		5,552	5,834	198	284	
LOC_Os08g18920		16,154	15,011	15,220	15,328	14,488	16,022	14,918	15,054	15,187	14,428
Os12g0608500	L-LEC	834	319	80	80		732	226	2	2	
LOC_Os12g41490		156	144	143	139	282	65	73	58	57	216
Os12g0608700	L-LEC	200	126	145	134		65	17	28	26	
LOC_Os12g41510		348	323	372	379	303	219	242	227	245	231
Os12g0608900	L-LEC	106	99	84	77		2	5	2	2	
LOC_Os12g41530		81	72	74	68	377	2	2	2	2	291
Os07g0569600	L-LEC	10,196	11,763	100	87		10,085	11,667	4	2	
LOC_Os07g38230		20,532	18,502	20,646	20,360	29,490	20,435	18,430	20,529	20,262	29,426
Os01g0779300	L-LEC	3,836	1,979	138	627		3,732	1,882	41	537	
LOC_Os01g57100		1,990	1,936	2,162	2,267	3,350	1,898	1,863	2,067	2,183	3,298
Os07g0569800	L-LEC	414	237	255	223		292	131	142	121	
LOC_Os07g38250		467	284	279	327	629	350	203	161	213	568
Os12g0606000	L-LEC	288	117	231	309		165	16	126	209	
LOC_Os12g41270		164	91	176	156	334	47	17	49	43	265
Os12g0609000	L-LEC	108	100	107	98		6	6	14	8	
LOC_Os12g41540		104	93	92	94	173	15	24	7	13	106
Os08g0124500	L-LEC	101	106	96	78		2	2	2	2	
LOC_Os08g03020		6,888	6,251	6,594	6,781	12,093	6,773	6,163	6,465	6,666	12,021
Os08g0125200	L-LEC	137	154	123,806	81,802		2	33	123,684	81,694	
LOC_Os08g03170		106	81	3,248	2,080	1,201	2	2	3,104	1,951	1,136
Os08g0125800	L-LEC	104	99	83	87		2	2	2	2	
LOC_Os08g03240		637	581	569	642	473	548	500	466	546	414
Os08g0124000	L-LEC	112	125	104	128		6	28	2	38	
LOC_Os08g02996		5,411	4,689	5,006	5,427	7,271	5,315	4,606	4,876	5,312	7,198
Os08g0124900	L-LEC	144	140	130	127		42	47	37	38	
LOC_Os08g03090		988	906	932	983	852	899	838	849	903	784
Os09g0339000	L-LEC	896	1,031	156	173		762	921	36	62	
LOC_Os09g16950		200	133	186	250	445	72	50	36	114	385
Os09g0341100	L-LEC	538	724	994	960		431	629	902	859	
LOC_Os09g17110		612	553	563	579	552	526	483	468	472	499
Os09g0334800	L-LEC	1,298	288	11,076	10,665		1,196	195	10,988	10,577	
LOC_Os09g16540		226	208	322	310	356	135	138	238	228	287
Os12g0454800	L-LEC	973	122	112	114		868	29	22	25	
LOC_Os12g26940		13,589	11,650	11,783	12,745	7,058	13,500	11,584	11,707	12,670	6,993
Os04g0125700	L-LEC	113	100	85	89		10	5	2	2	
LOC_Os04g03579		72,173	65,460	70,119	73,313	36,105	72,087	65,391	70,033	73,240	36,031
Os04g0140400	L-LEC	114	113	103	89		14	21	17	2	
LOC_Os04g05470		738	604	655	675	313	645	536	578	593	257
Os04g0141200	L-LEC	153	105	129	107		23	2	20	4	
LOC_Os04g05560		807	693	795	739	581	685	617	662	614	517
Os04g0141400	L-LEC	108	104	90	88		4	9	2	2	
LOC_Os04g05580		2,082	1,850	1,994	2,069	2,117	1,988	1,779	1,898	1,983	2,056
Os04g0109100	L-LEC	5,868	3,999	1,829	1,127		5,754	3,900	1,728	1,027	
LOC_Os04g01874		15,931	15,842	15,142	14,826	14,060	15,831	15,769	15,033	14,712	13,989
Os08g0514000	L-LEC	601	464	648	478		476	363	542	377	
LOC_Os08g40270		464	431	444	358	724	347	357	314	242	652
Os02g0712600	L-LEC	109	108	209	211		2	11	110	112	
LOC_Os02g48200		4,309	3,837	3,962	4,033	1,976	4,212	3,764	3,857	3,922	1,918
Os02g0712700	L-LEC	299	809	97	153		171	700	2	47	
LOC_Os02g48210		913	888	935	903	2,056	789	806	806	780	1,984

Supplemental Table 14 continue. Microarray data for rice kinase genes

Os06g0328400	L-LEC	322	128	112	123		210	21	5	29	
LOC_Os06g22290		4,157	3,973	4,011	4,169	1,917	4,048	3,892	3,898	4,068	1,851
Os08g0514100	L-LEC	111	90	77	68		2	2	2	2	
LOC_Os08g40280		433	388	423	420	181	325	305	279	293	134
Os12g0500400	L-LEC	118	94	88	75		11	2	2	2	
LOC_Os12g31610		107	75	86	81	178	10	3	2	2	115
Os06g0285400	L-LEC	4,166	3,263	232	160		4,044	3,161	125	58	
LOC_Os06g17490		6,193	5,495	6,059	6,109	5,842	6,080	5,420	5,937	5,988	5,787
Os05g0125200	L-LEC	6,292	4,148	104	87		6,186	4,044	7	2	
LOC_Os05g03450		9,518	8,746	9,202	9,184	19,101	9,425	8,667	9,101	9,091	19,038
Os02g0459600	L-LEC	9,917	3,396	79	85		9,805	3,288	2	2	
LOC_Os02g26160		697	383	267	282	925	592	300	155	183	867
Os11g0445300	L-LEC	164	118	77	74		60	22	2	2	
LOC_Os11g25860		1,308	1,238	1,227	1,225	1,107	1,216	1,166	1,133	1,141	1,037
Os02g0298200	L-LEC	812	119	128	138		676	7	4	26	
LOC_Os02g19550		779	79	131	150	133	650	2	2	11	70
Os02g0640500	L-LEC	113	87	640	459		2	2	535	358	
LOC_Os02g42780		115	81	123	122	367	5	7	5	3	308
Os04g0531400	L-LEC	689	1,544	111	126		558	1,433	2	19	
LOC_Os04g44900		3,194	2,939	3,160	3,110	3,234	3,066	2,854	3,024	2,984	3,172
Os03g0258000	L-LEC	88	85	77	75		2	2	2	2	
LOC_Os03g15250		65	66	62	64	114	2	2	2	2	55
Os07g0575700	L-LEC	103	101	407	104		2	2	299	8	
LOC_Os07g38810		1,292	1,079	1,845	1,336	778	1,192	996	1,706	1,215	727
Os04g0531500	L-LEC	742	1,350	130	100		643	1,258	44	15	
LOC_Os04g44910		19,372	16,408	16,728	19,498	16,158	19,281	16,344	16,654	19,420	16,080
Os10g0442000	L-LEC	3,167	147	131	116		3,045	34	21	18	
LOC_Os10g30540		2,119	1,858	1,970	2,043	3,111	2,002	1,772	1,844	1,930	3,050
Os07g0575600	L-LEC	118	92	106	101		2	2	2	2	
LOC_Os07g38800		1,216	1,097	1,290	1,225	1,519	1,108	1,023	1,169	1,109	1,457
Os07g0132100	L-LEC	100	101	91	93		2	2	2	3	
LOC_Os07g04000		80	88	80	79	137	2	12	2	2	75
Os07g0129800	L-LEC	104	96	93	78		2	2	2	2	
LOC_Os07g03780		117	92	122	101	194	12	20	2	2	128
Os07g0130900	L-LEC	95	103	83	81		2	7	2	2	
LOC_Os07g03880		76	71	72	65	198	2	2	2	2	135
Os07g0130100	L-LEC	160	145	187	136		16	25	60	21	
LOC_Os07g03810		232	229	297	227	603	97	139	140	83	534
Os07g0130300	L-LEC	116	110	92	100		15	14	2	13	
LOC_Os07g03830		98	91	83	87	155	4	19	2	5	93
Os07g0130800	L-LEC	85	197	101	77		2	83	2	2	
LOC_Os07g03870		314	387	338	307	184	193	298	179	175	119
Os07g0262600	L-LEC	107	97	86	84		2	4	2	2	
LOC_Os07g15930		87	67	84	76	153	4	2	2	2	89
Os07g0133000	L-LEC	88	79	80	73		2	2	2	2	
LOC_Os07g04110		340	296	322	320	2,624	253	222	216	232	2,551
Os07g0130400	L-LEC	133	92	91	77		17	2	2	2	
LOC_Os07g03840		110	65	100	63	124	7	2	2	2	60
Os07g0130200	L-LEC	101	83	84	82		2	2	2	2	
LOC_Os07g03820		131	117	124	122	138	32	42	26	34	78
Os07g0130700	L-LEC	103	106	89	81		4	13	2	2	
LOC_Os07g03860		67	70	73	67	215	2	4	2	2	158
Os07g0131000	L-LEC	121	96	86	86		12	2	2	2	
LOC_Os07g03890		107	71	84	79	183	8	2	2	2	100
Os07g0131100	L-LEC	124	136	110	113		12	42	14	15	
LOC_Os07g03900		94	99	122	117	132	2	27	21	10	70
Os07g0262800	L-LEC	104	172	98	87		2	72	3	2	
LOC_Os07g15940		105	107	108	111	178	17	31	12	23	120
Os07g0132500	L-LEC	893	85	76	77		794	2	2	2	
LOC_Os07g04040		236	186	185	183	1,205	143	118	110	101	1,137
Os09g0315600	L-LEC	186	98	88	80		85	5	2	2	
LOC_Os09g14660		140	61	70	70	164	48	2	2	2	102
Os07g0133100	L-LEC	84	92	98	91		2	2	6	2	
LOC_Os07g04130		92	86	121	122	188	5	17	13	20	111
Os05g0224700	L-LEC	126	124	127	119		2	16	6	9	
LOC_Os05g13770		809	748	912	952	129	690	664	760	816	66
Os10g0441900	L-LEC	146	229	193	97		2	106	70	2	
LOC_Os10g30530		459	437	587	457	578	325	343	430	318	521
Os03g0823000	L-LEC	198	191	122	92		56	74	2	2	
LOC_Os03g60810		2,552	2,342	2,536	2,503	3,843	2,420	2,254	2,380	2,359	3,777
Os06g0210400	L-LEC	142	80	93	75		25	2	2	2	
LOC_Os06g10790		501	412	471	448	282	395	339	356	332	215
Os10g0533800	L-LEC	286	166	174	190		158	58	56	83	

Supplemental Table 14 continue. Microarray data for rice kinase genes

LOC_Os10g38960		459	330	297	308	376	336	248	168	184	310
Os01g0267800	CR4L	290	113	164	96		191	16	73	8	
LOC_Os01g16230		405	392	388	429	819	325	320	299	353	760
Os05g0387600	CR4L	298	98	590	171		176	2	483	70	
LOC_Os05g32170		292	81	1,014	145	228	181	7	888	27	168
Os04g0439600	CR4L	1,262	926	1,806	2,642		1,136	822	1,695	2,538	
LOC_Os04g35890		2,270	1,786	2,430	2,731	1,673	2,151	1,709	2,295	2,606	1,604
Os11g0222000	CR4L	534	299	94	95		433	206	2	6	
LOC_Os11g11490		2,231	2,126	2,211	2,359	2,225	2,142	2,057	2,126	2,278	2,153
Os08g0109800	CR4L	138	111	103	119		15	9	2	17	
LOC_Os08g01830		546	448	526	551	1,042	434	373	401	432	967
Os05g0127300	CR4L	27,395	26,949	94	115		27,288	26,855	2	23	
LOC_Os05g03620		9,370	8,583	9,515	9,510	14,289	9,277	8,511	9,407	9,418	14,235
Os08g0374600	RLCK-OS1	1,717	1,406	125	499		1,605	1,309	28	404	
LOC_Os08g28710		335	305	239	277	555	234	234	119	177	500
Os11g0667700	RLCK-OS1	148	145	187	227		44	52	98	138	
LOC_Os11g44560		101	101	97	92	166	13	35	23	17	106
Os11g0666200	RLCK-OS1	112	144	117	100		2	23	15	2	
LOC_Os11g44430		1,322	1,186	1,153	1,306	1,059	1,214	1,096	1,023	1,192	999
Os11g0664000	RLCK-OS1	1,653	10,920	120	104		1,553	10,827	32	18	
LOC_Os11g44250		308	548	201	189	204	218	482	122	110	128
Os11g0666100*	N/A	6,082	5,589	75	73		5,982	5,496	2	2	
LOC_Os11g44420		114	97	77	79	171	24	29	2	2	104
Os06g0151700	RLCK-OS1	129	151	97	84		5	47	2	2	
LOC_Os06g05830		1,344	1,174	1,401	1,481	152	1,228	1,095	1,260	1,355	71
Os03g0637800	CR4L	1,401	3,136	83	81		1,299	3,043	2	2	
LOC_Os03g43670		10,733	9,218	9,723	10,231	17,634	10,646	9,151	9,645	10,154	17,571
Os01g0323100	RLCK-VIII	13,348	3,067	165,991	231,524		13,240	2,973	165,898	231,424	
LOC_Os01g21970		1,619	1,343	2,634	3,649	2,003	1,533	1,273	2,540	3,541	1,943
Os05g0135800	RLCK-VIII	106,900	204,499	109	117		106,801	204,404	17	31	
LOC_Os05g04520		70,809	63,488	67,564	69,736	98,753	70,720	63,418	67,476	69,659	98,681
Os01g0899000	RLCK-VIII	16,718	34,831	3,954	2,529		16,616	34,734	3,855	2,439	
LOC_Os01g67340		18,392	16,927	18,293	17,235	14,631	18,296	16,855	18,200	17,150	14,572
Os09g0513600	RLCK-VIII	14,227	3,815	410	860		14,107	3,715	307	761	
LOC_Os09g33860		11,323	10,584	11,212	11,006	9,825	11,210	10,511	11,086	10,894	9,749
Os03g0844100	RLCK-VIII	78,992	47,918	298	314		78,877	47,818	200	218	
LOC_Os03g62700		80,009	74,450	78,361	75,790	95,518	79,898	74,376	78,247	75,688	95,451
Os02g0565500	RLCK-VIII	4,168	105	2,675	3,465		4,059	12	2,574	3,374	
LOC_Os02g35760		4,040	68	111	78	235	3,952	2	2	2	167
Os03g0226300	RLCK-VIII	82	88	14,646	17,975		2	2	14,559	17,890	
LOC_Os03g12520		61	62	192	208	155	2	2	117	131	85
Os04g0490500	RLCK-VIII	1,603	3,564	124	92		1,481	3,459	10	2	
LOC_Os04g41310		2,418	2,035	2,079	2,402	3,039	2,307	1,949	1,944	2,287	2,975
Os11g0194900	RLCK-VI	239	1,144	472	254		140	1,048	380	168	
LOC_Os11g08950		1,645	1,504	1,590	1,609	1,858	1,555	1,432	1,501	1,532	1,789
Os03g0839900	RLCK-VI	5,692	17,931	38,292	21,902		5,562	17,827	38,183	21,799	
LOC_Os03g62340		33,708	31,626	33,646	33,088	29,255	33,584	31,550	33,512	32,964	29,198
Os03g0241600	RLCK-VI	81,009	12,372	367	145		80,908	12,279	277	59	
LOC_Os03g13820		49,538	42,096	44,111	48,169	55,126	49,450	42,029	44,029	48,091	55,052
Os04g0654600	RLCK-VI	276	127	172	110		150	25	66	8	
LOC_Os04g56060		11,376	10,726	11,353	10,927	14,297	11,257	10,651	11,222	10,809	14,242
Os08g0249100	RLCK-VI	104	101	86	78		2	7	2	2	
LOC_Os08g15060		3,698	3,328	3,394	3,694	2,087	3,610	3,260	3,312	3,614	2,030
Os06g0663900	RLCK-VI	390	1,777	333	430		270	1,662	230	332	
LOC_Os06g45350		53,282	52,625	55,304	56,663	98,077	53,174	52,538	55,182	56,554	97,995

Supplemental Table 15. Microarray data for genes in oxidative phosphorylation pathway

A. Microarray data without background subtraction

RAP ID	PMC1-Cy3_MS	PMC2-Cy3_MS	TCP1-Cy3_MS	TCP2-Cy3_MS	Seedling 1-	Seedling 2-	Seedling 3-	Seedling 4-	Seedling 5-	TCP (mean)	PMC (mean)	seedling (mean)	KEGG ID	Description
Os07g0134800	96,505	119,434	165,144	75,132	102,907	94,367	99,981	100,736	79,351	120,138	107,969	88,855	K00234	succinate dehydrogenase (ubiquinone) flavoprotein subunit
Os08g0120000	102,156	53,698	136,392	107,605	65,885	56,204	62,961	64,852	90,521	121,999	77,927	75,202	K00235	succinate dehydrogenase (ubiquinone) iron-sulfur protein
Os09g0370300	158	91	79	92	61	59	65	110	87	86	125	80	K00235	succinate dehydrogenase (ubiquinone) iron-sulfur protein
Os10g0579300	27,056	16,141	49,368	40,575	26,990	25,583	28,173	26,463	21,318	44,972	21,599	23,903	K00329	NADH dehydrogenase
Os02g0520800	106,027	95,474	120,277	83,255	72,100	67,696	73,644	74,135	93,439	101,766	100,751	81,962	K00411	ubiquinol-cytochrome c reductase iron-sulfur subunit
Os04g0398500	111,325	60,073	185,655	197,029	149,228	129,967	139,953	149,060	157,675	191,342	85,699	149,660	K00411	ubiquinol-cytochrome c reductase iron-sulfur subunit
Os05g0301700	101,928	130,049	162,250	148,158	101,693	93,212	109,193	111,190	103,875	155,204	115,989	103,849	K00413	ubiquinol-cytochrome c reductase cytochrome c1 subunit
Os01g0935700	45,778	50,397	63,028	42,617	15,860	14,823	15,415	15,609	19,277	52,822	48,087	17,245	K00413	ubiquinol-cytochrome c reductase cytochrome c1 subunit
Os11g0162200	55,783	36,083	26,028	25,443	61,457	58,012	64,569	63,064	87,795	25,736	45,933	73,645	K00416	ubiquinol-cytochrome c reductase subunit 6
Os03g0806900	64,270	46,453	76,387	67,592	48,956	47,511	44,182	50,092	42,346	71,990	55,362	44,936	K00417	ubiquinol-cytochrome c reductase subunit 7
Os07g0205000	9,183	16,422	6,054	3,098	8,581	7,938	8,762	8,589	10,188	4,576	12,802	9,288	K00417	ubiquinol-cytochrome c reductase subunit 7
Os05g0400400	243,457	126,239	210,564	179,361	80,361	70,639	70,985	78,662	107,573	194,963	184,848	89,919	K00419	ubiquinol-cytochrome c reductase subunit 9
Os01g0866500	2,041	1,039	167	756	3,040	2,630	2,645	2,891	6,299	462	1,540	4,201	K01507	inorganic pyrophosphatase
Os02g0537900	104,224	152,898	22,086	15,245	63,947	58,736	65,261	68,510	103,430	18,666	128,561	81,433	K01507	inorganic pyrophosphatase
Os02g0802500	4,754	5,979	440	259	9,617	8,966	8,454	8,948	9,315	349	5,366	9,154	K01507	inorganic pyrophosphatase
Os02g0704900	293,988	213,601	7,458	4,619	138,037	126,942	123,048	121,966	103,896	6,039	253,795	115,094	K01507	inorganic pyrophosphatase
Os06g0178900	78,395	62,573	9,489	2,514	211,318	205,324	199,733	203,841	236,110	6,001	70,484	220,035	K01507	inorganic pyrophosphatase
Os06g0644200	91,172	61,795	321	269	241,633	216,204	237,185	223,320	236,612	295	76,484	233,072	K01507	inorganic pyrophosphatase
Os01g0974700	41,629	53,626	2,671	1,435	9,916	9,062	10,193	9,890	9,773	2,053	47,627	9,769	K01507	inorganic pyrophosphatase
Os05g0114000	6,828	7,778	93	113	27,289	23,760	24,217	26,763	25,918	103	7,303	25,712	K01507	inorganic pyrophosphatase
Os02g0768600	13,388	15,192	9,063	5,276	142,244	131,517	144,994	147,884	110,327	7,169	14,290	125,016	K01507	inorganic pyrophosphatase
Os04g0687100	18,749	19,586	528	474	97,375	92,633	99,735	98,927	78,875	501	19,168	87,545	K01507	inorganic pyrophosphatase
Os05g0438500	2,505	3,008	77,866	81,391	766	702	1,240	1,730	723	79,628	2,756	896	K01507	inorganic pyrophosphatase
Os01g0337500	88	88	7,316	5,319	573	483	687	635	221	6,318	88	362	K01507	inorganic pyrophosphatase
Os05g0156900	666	271	2,422	1,087	93	105	102	110	207	1,754	468	146	K01507	inorganic pyrophosphatase
Os01g0966000	10,564	19,907	11,657	2,417	30,323	28,443	29,921	29,486	27,163	7,037	15,236	28,328	K01535	H+-transporting ATPase
Os12g0638700	26,636	32,775	1,668	468	24,928	23,597	25,140	26,277	22,936	1,068	29,705	23,939	K01535	H+-transporting ATPase
Os03g0689300	8,321	8,826	793	428	2,163	2,131	1,904	2,322	1,695	611	8,573	1,900	K01535	H+-transporting ATPase
Os07g0191200	22,797	50,169	794	906	15,576	14,866	10,139	10,842	11,594	850	36,483	12,209	K01535	H+-transporting ATPase
Os03g0100800	73,012	149,416	2,867	1,601	3,292	2,592	1,690	1,808	4,374	2,234	111,214	3,203	K01535	H+-transporting ATPase
Os04g0656100	7,407	2,718	114	123	95,714	87,158	94,082	96,275	110,945	119	5,062	101,745	K01535	H+-transporting ATPase
Os03g0183900	81	94	80	83	104	98	101	111	185	81	87	138	K01535	H+-transporting ATPase
Os05g0319800	140	121	103,761	44,264	110	90	541	318	829	74,013	130	469	K01535	H+-transporting ATPase
Os10g0527100	1,024	331	82	84	5,428	4,403	4,637	4,853	1,105	83	677	2,310	K02108	F-type H+-transporting ATPase subunit a

Supplemental Table 15 continue. Microarray data for genes in oxidative phosphorylation pathway

Os04g0235600	756	906	981	662	10,084	9,097	4,877	6,920	534	822	831	2,034	K02109	F-type H+-transporting ATPase subunit b
Os03g0278900	2,225	6,014	324	536	101,138	97,390	94,956	109,582	98,903	430	4,120	99,830	K02109	F-type H+-transporting ATPase subunit b
Os10g0355800	135	1,622	80	82	209	172	122	113	151	81	878	152	K02112	F-type H+-transporting ATPase subunit beta
Os02g0750100	3,549	3,306	872	881	95,585	89,467	96,815	93,959	75,571	877	3,428	84,264	K02113	F-type H+-transporting ATPase subunit delta
Os07g0513000	3,052	4,358	1,382	1,498	56,119	49,821	53,189	54,830	93,047	1,440	3,705	70,548	K02115	F-type H+-transporting ATPase subunit gamma
Os01g0791500	97	98	123	87	334	303	344	320	288	105	97	306	K02126	F-type H+-transporting ATPase subunit a
Os05g0553000	106,986	92,119	173,265	119,790	159,787	143,890	140,623	159,596	191,532	146,528	99,553	170,048	K02133	F-type H+-transporting ATPase subunit beta
Os01g0685800	88,794	112,112	143,762	99,808	277,069	271,715	298,278	292,552	287,465	121,785	100,453	286,181	K02133	F-type H+-transporting ATPase subunit beta
Os07g0495200	54,169	48,426	75,275	35,550	42,499	37,702	36,654	39,349	38,415	55,412	51,298	38,732	K02134	F-type H+-transporting ATPase subunit delta
Os08g0250200	312	218	241	330	218	200	256	217	571	286	265	357	K02135	F-type H+-transporting ATPase subunit epsilon
Os10g0320400	81,567	89,140	90,041	50,145	209,035	187,941	203,551	215,854	172,687	70,093	85,353	187,735	K02136	F-type H+-transporting ATPase subunit gamma
Os06g0646500	71,046	63,879	77,748	80,837	131,542	114,019	131,008	132,182	103,488	79,293	67,462	114,728	K02137	F-type H+-transporting ATPase oligomycin sensitivity conferral
Os08g0478200	63,185	52,740	130,421	74,755	80,074	76,607	80,264	70,660	114,577	102,588	57,962	93,867	K02138	F-type H+-transporting ATPase subunit d
Os07g0549700	34,306	52,153	53,942	30,588	91,043	87,205	93,306	91,717	75,202	42,265	43,230	82,642	K02144	V-type H+-transporting ATPase 54 kD subunit
Os02g0175400	13,535	10,734	36,089	26,287	16,854	15,257	16,332	16,497	13,776	31,188	12,134	14,955	K02145	V-type H+-transporting ATPase subunit A
Os06g0662000	45,889	39,255	54,612	44,579	120,186	115,185	111,506	121,466	99,264	49,596	42,572	107,807	K02145	V-type H+-transporting ATPase subunit A
Os01g0587000	45,224	58,546	20,269	13,691	61,277	57,543	58,200	60,412	80,601	16,980	51,885	69,169	K02146	V-type H+-transporting ATPase subunit AC39
Os06g0568200	104,822	82,309	157,810	76,683	243,809	227,023	271,568	241,838	291,584	117,246	93,565	267,856	K02147	V-type H+-transporting ATPase subunit B
Os01g0711000	9,838	7,150	33,163	26,551	18,970	17,551	18,147	19,296	21,927	29,857	8,494	20,136	K02147	V-type H+-transporting ATPase subunit B
Os05g0593100	35,872	42,026	16,881	12,105	18,496	16,699	18,402	17,693	17,948	14,493	38,949	17,885	K02148	V-type H+-transporting ATPase subunit C
Os04g0643100	69,948	44,866	114,170	77,199	97,070	91,809	97,624	99,209	166,840	95,684	57,407	126,839	K02149	V-type H+-transporting ATPase subunit D
Os01g0222500	12,187	13,896	66,949	39,836	9,765	9,556	9,746	10,656	10,130	53,392	13,041	10,030	K02150	V-type H+-transporting ATPase subunit E
Os01g0659200	40,425	38,438	494	506	172,908	154,549	173,138	162,956	97,870	500	39,431	127,418	K02150	V-type H+-transporting ATPase subunit E
Os05g0480700	515	416	159,164	107,773	96	91	548	311	623	133,469	466	404	K02150	V-type H+-transporting ATPase subunit E
Os04g0137500	30,086	26,685	29,658	28,253	21,657	19,994	20,700	21,020	16,207	28,955	28,385	18,379	K02151	V-type H+-transporting ATPase subunit F
Os02g0824700	18,284	15,391	8,344	5,003	20,473	18,795	19,523	20,792	19,176	6,674	16,837	19,533	K02151	V-type H+-transporting ATPase subunit F
Os04g0601700	10,721	11,796	20,741	21,168	27,662	25,373	27,871	29,158	20,909	20,954	11,259	23,986	K02152	V-type H+-transporting ATPase subunit G
Os04g0660600	39,229	28,909	60,519	36,250	38,400	33,220	36,806	37,634	36,457	48,385	34,069	36,486	K02153	V-type H+-transporting ATPase subunit H
Os01g0834200	184,751	303,114	77,823	42,852	83,399	78,995	80,788	83,467	112,826	60,338	243,933	95,988	K02154	V-type H+-transporting ATPase subunit I
Os03g0251500	38,455	35,783	354,678	295,089	87,473	80,884	87,690	89,191	115,891	324,884	37,119	100,012	K02154	V-type H+-transporting ATPase subunit I
Os01g0962300	27,205	23,790	25,526	21,304	27,610	26,213	28,838	28,121	45,402	23,415	25,497	35,460	K02155	V-type H+-transporting ATPase 16kDa proteolipid subunit
Os12g0168900	135,247	98,966	154,374	127,010	170,155	163,560	174,987	173,163	162,702	140,692	117,106	166,539	K02155	V-type H+-transporting ATPase 16kDa proteolipid subunit
Os11g0169900	118,262	95,225	204,722	120,754	131,096	121,179	124,862	132,580	158,647	162,738	106,743	142,184	K02155	V-type H+-transporting ATPase 16kDa proteolipid subunit
Os02g0550100	52,085	49,888	107,666	59,938	38,110	34,298	35,703	37,365	43,178	83,802	50,986	39,627	K02155	V-type H+-transporting ATPase 16kDa proteolipid subunit
Os05g0106100	7,845	9,661	33,718	23,416	12,219	10,479	10,781	11,903	13,559	28,567	8,753	12,403	K02155	V-type H+-transporting ATPase 16kDa proteolipid subunit
Os03g0718600	20,762	13,728	9,479	8,038	11,537	9,948	10,557	11,374	14,922	8,758	17,245	12,727	K02258	cytochrome c oxidase subunit XI assembly protein
Os08g0496000	39,908	56,558	3,715	2,083	25,103	23,705	25,599	24,571	29,416	2,899	48,233	26,979	K02259	cytochrome c oxidase subunit XV assembly protein
Os02g0794600	7,550	7,976	5,787	2,509	1,608	1,511	1,549	1,629	3,058	4,148	7,763	2,194	K02260	cytochrome c oxidase subunit XVII assembly protein

Supplemental Table 15 continue. Microarray data for genes in oxidative phosphorylation pathway

Os01g0612200	123,474	129,402	102,935	83,276	108,801	96,664	99,844	99,084	173,536	93,105	126,438	132,454	K02265	cytochrome c oxidase subunit Vb
Os06g0142700	11,181	11,342	46,082	41,412	18,005	15,254	14,784	17,095	28,642	43,747	11,261	21,597	K02265	cytochrome c oxidase subunit Vb
Os03g0772800	52,608	28,861	105,925	55,110	72,534	64,178	65,810	69,938	91,873	80,518	40,734	79,107	K02266	cytochrome c oxidase subunit VIa
Os03g0390400	101,603	96,453	23,126	12,768	74,677	72,396	95,046	96,904	94,030	17,947	99,028	89,273	K02267	cytochrome c oxidase subunit VIb
Os04g0498200	19,764	31,813	97,079	71,797	23,852	22,084	23,681	22,751	26,422	84,438	25,788	24,701	K02267	cytochrome c oxidase subunit VIb
Os02g0791400	103	102	101	107	604	480	588	607	102	104	102	241	K02267	cytochrome c oxidase subunit VIb
Os01g0610100	92,847	135,750	96,365	45,540	40,791	37,499	40,107	41,753	89,817	70,953	114,299	59,967	K03661	V-type H+-transporting ATPase 21kDa proteolipid subunit
Os06g0684000	3,774	8,234	29,424	9,459	13,258	12,316	13,595	13,221	14,429	19,441	6,004	13,747	K03885	NADH dehydrogenase
Os05g0331200	62,164	68,280	132,613	83,851	5,967	5,692	7,658	7,174	7,109	108,232	65,222	6,862	K03885	NADH dehydrogenase
Os06g0214900	740	541	119	105	1,499	1,324	1,462	1,544	874	112	640	1,129	K03885	NADH dehydrogenase
Os03g0713400	39,292	45,778	88,424	68,074	113,419	111,107	113,970	116,841	104,044	78,249	42,535	108,829	K03934	NADH dehydrogenase (ubiquinone) Fe-S protein 1
Os07g0585800	91,041	60,388	108,282	60,111	61,594	55,546	58,252	61,057	80,379	84,196	75,715	68,930	K03937	NADH dehydrogenase (ubiquinone) Fe-S protein 4
Os08g0556600	61,472	31,294	98,822	60,960	66,369	62,538	70,317	68,917	79,664	79,891	46,383	73,077	K03938	NADH dehydrogenase (ubiquinone) Fe-S protein 5
Os08g0161700	46,182	30,127	56,427	36,367	53,568	51,232	54,412	55,023	54,114	46,397	38,155	53,836	K03939	NADH dehydrogenase (ubiquinone) Fe-S protein 6
Os01g0720300	51,211	64,748	82,307	92,513	79,503	71,649	77,473	81,559	107,125	87,410	57,979	91,143	K03940	NADH dehydrogenase (ubiquinone) Fe-S protein 7
Os05g0533700	10,376	18,261	3,941	2,610	56,733	53,154	55,069	56,856	54,239	3,276	14,319	54,843	K03940	NADH dehydrogenase (ubiquinone) Fe-S protein 7
Os03g0774200	11,056	6,900	15,979	11,556	17,198	15,090	15,793	17,041	20,620	13,768	8,978	18,322	K03941	NADH dehydrogenase (ubiquinone) Fe-S protein 8
Os07g0645400	68,487	78,207	83,853	60,602	97,282	88,093	92,187	93,424	78,950	72,227	73,347	85,571	K03942	NADH dehydrogenase (ubiquinone) flavoprotein 1
Os05g0509200	63,309	94,020	58,644	44,869	105,231	93,177	41,729	62,081	55,952	51,757	78,664	65,019	K03943	NADH dehydrogenase (ubiquinone) flavoprotein 2
Os05g0481600	58,683	48,375	79,734	49,529	91,513	86,243	88,618	90,742	106,658	64,632	53,529	97,582	K03945	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 1
Os04g0310500	81,380	67,780	203,407	119,996	97,050	79,747	98,140	115,428	161,625	161,702	74,580	125,591	K03946	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 2
Os03g0313000	73,453	51,400	66,587	60,845	60,170	58,621	61,819	62,337	47,136	63,716	62,426	53,506	K03949	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5
Os07g0640100	59,056	33,457	67,525	48,828	58,136	50,984	59,767	59,589	85,270	58,176	46,256	69,789	K03950	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 6
Os03g0295500	56,276	36,486	91,130	51,956	100,570	83,534	86,055	95,763	92,488	71,543	46,381	91,983	K03952	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 8
Os02g0816800	32,777	25,761	35,933	24,760	25,307	22,740	24,650	24,467	20,284	30,346	29,269	22,197	K03953	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 9
Os07g0222800	80,565	33,257	69,761	38,804	50,721	48,380	50,476	48,704	52,676	54,282	56,911	51,100	K03955	NADH dehydrogenase (ubiquinone) 1 alpha/beta subcomplex 1
Os03g0352800	86,868	76,232	29,022	25,652	97,138	90,737	99,398	102,314	97,054	27,337	81,550	97,225	K03955	NADH dehydrogenase (ubiquinone) 1 alpha/beta subcomplex 1
Os03g0129900	36,500	27,517	71,461	31,648	30,964	29,152	29,622	31,648	22,340	51,555	32,009	26,037	K03963	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 7
Os06g0714100	36,149	21,922	38,895	38,975	38,942	35,269	35,505	38,397	42,332	38,935	29,036	39,591	K03965	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 9
Sum of mean intensities										5.1E+06	4.8E+06	6.3E+06		

Supplemental Table 15 continue. Microarray data for genes in oxidative phosphorylation pathway

B. Microarray data with background subtraction (note: signal value is set to 2 if the signal<2 after background subtraction, to ease later log transformation)

RAP ID	PMC1-Signal	PMC2-Signal	TCP1-Signal	TCP2-Signal	Seedling 1-Signal	Seedling 2-Signal	Seedling 3-Signal	Seedling 4-Signal	Seedling 5-Signal	PMC Signal (average)	TCP Signal (average)	seedling Signal (average)
Os07g0134800	96,405	119,339	165,054	75,045	102,816	94,296	99,894	100,656	79,278	107,872	120,050	89,347
Os08g0120000	102,042	53,596	136,282	107,509	65,779	56,119	62,826	64,737	90,450	77,819	121,896	76,408
Os09g0370300	54	2	2	2	2	2	2	6	23	25	2	3
Os10g0579300	26,930	16,040	49,261	40,474	26,873	25,509	28,042	26,346	21,254	21,485	44,868	23,973
Os02g0520800	105,893	95,363	120,153	83,141	71,974	67,610	73,490	73,996	93,372	100,628	101,647	82,570
Os04g0398500	111,220	59,982	185,564	196,940	149,141	129,894	139,844	148,970	157,596	85,601	191,252	149,779
Os05g0301700	101,805	129,945	162,140	148,055	101,577	93,135	109,057	111,068	103,816	115,875	155,097	103,763
Os01g0935700	45,672	50,296	62,927	42,527	15,763	14,746	15,313	15,520	19,202	47,984	52,727	17,269
Os11g0162200	55,667	35,984	25,924	25,345	61,356	57,936	64,448	62,951	87,725	45,826	25,635	74,699
Os03g0806900	64,129	46,334	76,263	67,480	48,822	47,420	44,030	49,954	42,275	55,232	71,871	44,916
Os07g0205000	9,065	16,321	5,950	2,997	8,475	7,865	8,647	8,472	10,112	12,693	4,474	9,238
Os05g0400400	243,363	126,141	210,474	179,274	80,288	70,568	70,898	78,587	107,504	184,752	194,874	91,295
Os01g0866500	1,941	947	80	669	2,949	2,562	2,566	2,811	6,236	1,444	375	4,479
Os02g0537900	104,124	152,803	21,993	15,158	63,856	58,665	65,172	68,431	103,352	128,463	18,576	83,691
Os02g0802500	4,650	5,885	349	169	9,525	8,895	8,357	8,862	9,254	5,268	259	9,082
Os02g0704900	293,880	213,500	7,353	4,527	137,932	126,865	122,944	121,873	103,828	253,690	5,940	115,616
Os06g0178900	78,290	62,478	9,396	2,416	211,231	205,254	199,631	203,737	236,035	70,384	5,906	220,499
Os06g0644200	91,059	61,698	220	172	241,532	216,132	237,062	223,212	236,552	76,378	196	233,018
Os01g0974700	41,493	53,515	2,550	1,324	9,784	8,979	10,046	9,755	9,714	47,504	1,937	9,677
Os05g0114000	6,727	7,685	4	27	27,201	23,693	24,136	26,685	25,861	7,206	16	25,645
Os02g0768600	13,259	15,073	8,956	5,176	142,129	131,427	144,862	147,768	110,273	14,166	7,066	125,910
Os04g0687100	18,617	19,479	414	369	97,249	92,555	99,594	98,795	78,794	19,048	391	87,921
Os05g0438500	2,400	2,915	77,776	81,291	685	633	1,148	1,625	668	2,658	79,534	845
Os01g0337500	2	2	7,225	5,230	485	416	607	556	159	2	6,227	337
Os05g0156900	555	163	2,318	994	2	23	2	12	148	359	1,656	75
Os01g0966000	10,442	19,800	11,543	2,315	30,203	28,361	29,800	29,372	27,101	15,121	6,929	28,268
Os12g0638700	26,506	32,671	1,558	365	24,806	23,521	25,007	26,152	22,869	29,588	962	23,870
Os03g0689300	8,207	8,716	690	334	2,056	2,047	1,788	2,219	1,618	8,462	512	1,823
Os07g0191200	22,695	50,073	695	816	15,482	14,795	10,047	10,756	11,533	36,384	756	12,152
Os03g0100800	72,913	149,323	2,780	1,514	3,201	2,524	1,612	1,727	4,315	111,118	2,147	3,290
Os04g0656100	7,304	2,625	25	24	95,632	87,089	93,986	96,172	110,876	4,965	25	102,048
Os03g0183900	2	2	2	2	14	27	11	32	121	2	2	71
Os05g0319800	36	26	103,668	44,174	20	20	450	237	758	31	73,921	470
Os10g0527100	919	240	2	2	5,340	4,330	4,536	4,766	1,045	580	2	2,894

Supplemental Table 15 continue. Microarray data for genes in oxidative phosphorylation pathway

Os04g0235600	632	788	882	563	9,979	9,008	4,754	6,811	470	710	723	4,054
Os03g0278900	2,106	5,900	219	439	101,027	97,303	94,833	109,473	98,840	4,003	329	99,749
Os10g0355800	30	1,528	2	2	120	103	38	35	86	779	2	80
Os02g0750100	3,447	3,212	783	794	95,494	89,397	96,728	93,878	75,505	3,330	789	84,689
Os07g0513000	2,948	4,263	1,292	1,408	56,031	49,751	53,101	54,752	92,987	3,606	1,350	73,198
Os01g0791500	2	2	22	2	233	222	237	225	224	2	9	227
Os05g0553000	106,881	92,009	173,175	119,698	159,707	143,810	140,524	159,505	191,476	99,445	146,436	171,181
Os01g0685800	88,692	112,016	143,671	99,719	276,974	271,643	298,183	292,468	287,394	100,354	121,695	286,105
Os07g0495200	54,068	48,334	75,185	35,463	42,412	37,637	36,576	39,274	38,345	51,201	55,324	38,660
Os08g0250200	186	115	131	227	101	125	127	92	499	151	179	305
Os10g0320400	81,467	89,046	89,953	50,058	208,945	187,873	203,469	215,774	172,612	85,257	70,006	188,314
Os06g0646500	70,933	63,780	77,648	80,737	131,443	113,947	130,901	132,069	103,414	67,356	79,193	115,252
Os08g0478200	63,084	52,644	130,323	74,666	79,979	76,535	80,171	70,575	114,513	57,864	102,495	95,664
Os07g0549700	34,170	52,041	53,820	30,476	90,912	87,121	93,155	91,580	75,112	43,106	42,148	82,902
Os02g0175400	13,389	10,612	35,961	26,170	16,719	15,165	16,171	16,352	13,715	12,000	31,066	14,908
Os06g0662000	45,764	39,137	54,512	44,480	120,080	115,096	111,382	121,356	99,192	42,451	49,496	108,085
Os01g0587000	45,112	58,432	20,176	13,596	61,186	57,458	58,091	60,312	80,525	51,772	16,886	69,893
Os06g0568200	104,716	82,208	157,707	76,592	243,707	226,946	271,466	241,748	291,515	93,462	117,149	268,741
Os01g0711000	9,729	7,039	33,070	26,457	18,881	17,468	18,041	19,198	21,847	8,384	29,764	20,122
Os05g0593100	35,744	41,923	16,773	12,003	18,373	16,622	18,269	17,571	17,879	38,833	14,388	17,794
Os04g0643100	69,839	44,765	114,074	77,105	96,961	91,733	97,519	99,114	166,782	57,302	95,590	131,557
Os01g0222500	12,078	13,785	66,855	39,743	9,675	9,473	9,640	10,558	10,073	12,932	53,299	9,955
Os01g0659200	40,325	38,343	402	419	172,818	154,478	173,049	162,878	97,803	39,334	410	131,804
Os05g0480700	396	315	159,058	107,672	2	17	429	194	565	355	133,365	361
Os04g0137500	29,980	26,593	29,566	28,162	21,568	19,921	20,593	20,930	16,146	28,286	28,864	18,449
Os02g0824700	18,182	15,298	8,256	4,916	20,381	18,725	19,441	20,710	19,111	16,740	6,586	19,463
Os04g0601700	10,590	11,685	20,622	21,066	27,547	25,285	27,729	29,038	20,836	11,137	20,844	24,118
Os04g0660600	39,125	28,816	60,428	36,159	38,314	33,150	36,693	37,535	36,397	33,971	48,294	36,410
Os01g0834200	184,647	303,018	77,727	42,762	83,308	78,922	80,693	83,383	112,769	243,832	60,244	97,173
Os03g0251500	38,347	35,688	354,584	294,997	87,377	80,812	87,579	89,097	115,828	37,018	324,790	101,022
Os01g0962300	27,101	23,693	25,434	21,215	27,511	26,140	28,739	28,034	45,332	25,397	23,325	36,469
Os12g0168900	135,144	98,872	154,284	126,921	170,064	163,489	174,896	173,079	162,613	117,008	140,603	166,497
Os11g0169900	118,159	95,130	204,631	120,665	131,002	121,107	124,767	132,495	158,582	106,644	162,648	142,962
Os02g0550100	51,983	49,788	107,570	59,848	38,008	34,222	35,606	37,279	43,103	50,885	83,709	39,691
Os05g0106100	7,748	9,565	33,630	23,328	12,140	10,410	10,695	11,832	13,489	8,656	28,479	12,379
Os03g0718600	20,645	13,625	9,367	7,940	11,430	9,863	10,418	11,256	14,862	17,135	8,653	12,802
Os08g0496000	39,777	56,446	3,595	1,975	24,974	23,620	25,461	24,443	29,328	48,111	2,785	26,976
Os02g0794600	7,439	7,875	5,680	2,415	1,501	1,434	1,444	1,533	2,994	7,657	4,047	2,236

Supplemental Table 15 continue. Microarray data for genes in oxidative phosphorylation pathway

Os01g0612200	123,368	129,308	102,846	83,187	108,713	96,596	99,763	99,007	173,438	126,338	93,016	137,229
Os06g0142700	11,081	11,250	45,997	41,325	17,912	15,186	14,709	17,012	28,576	11,166	43,661	22,390
Os03g0772800	52,504	28,767	105,834	55,021	72,446	64,110	65,728	69,858	91,816	40,636	80,427	79,926
Os03g0390400	101,486	96,354	23,025	12,670	74,569	72,324	94,921	96,796	93,957	98,920	17,848	89,305
Os04g0498200	19,628	31,704	96,961	71,689	23,723	22,003	23,539	22,619	26,354	25,666	84,325	24,663
Os02g0791400	2	9	9	7	519	409	495	499	43	2	8	262
Os01g0610100	92,706	135,633	96,240	45,428	40,667	37,410	39,944	41,617	89,759	114,170	70,834	64,834
Os06g0684000	3,639	8,119	29,303	9,350	13,127	12,229	13,452	13,090	14,368	5,879	19,326	13,671
Os05g0331200	62,052	68,172	132,507	83,757	5,858	5,610	7,544	7,073	7,045	65,112	108,132	6,783
Os06g0214900	617	435	4	4	1,388	1,238	1,318	1,422	808	526	4	1,074
Os03g0713400	39,184	45,675	88,320	67,982	113,315	111,029	113,865	116,748	103,977	42,429	78,151	108,858
Os07g0585800	90,939	60,294	108,187	60,021	61,504	55,477	58,165	60,974	80,304	75,617	84,104	69,667
Os08g0556600	61,318	31,169	98,701	60,850	66,243	62,444	70,162	68,784	79,580	46,244	79,776	73,244
Os08g0161700	46,075	30,024	56,326	36,276	53,468	51,153	54,308	54,932	54,039	38,050	46,301	53,752
Os01g0720300	51,111	64,654	82,218	92,427	79,413	71,581	77,391	81,480	107,055	57,882	87,322	92,260
Os05g0533700	10,277	18,166	3,850	2,524	56,643	53,082	54,980	56,778	54,181	14,221	3,187	54,776
Os03g0774200	10,957	6,800	15,888	11,467	17,118	15,016	15,702	16,958	20,544	8,879	13,677	18,371
Os07g0645400	68,349	78,085	83,744	60,498	97,165	88,000	92,049	93,303	78,854	73,217	72,121	85,742
Os05g0509200	63,207	93,929	58,557	44,781	105,138	93,107	41,648	61,999	55,887	78,568	51,669	65,680
Os05g0481600	58,573	48,265	79,638	49,436	91,419	86,160	88,511	90,644	106,592	53,419	64,537	97,887
Os04g0310500	81,256	67,676	203,293	119,891	96,935	79,667	97,997	115,302	161,552	74,466	161,592	129,513
Os03g0313000	73,352	51,303	66,489	60,756	60,074	58,547	61,725	62,253	47,076	62,327	63,622	53,863
Os07g0640100	58,936	33,355	67,415	48,726	58,026	50,906	59,632	59,468	85,194	46,145	58,071	71,101
Os03g0295500	56,176	36,393	91,041	51,870	100,481	83,468	85,976	95,685	92,429	46,285	71,456	91,916
Os02g0816800	32,671	25,668	35,839	24,668	25,214	22,668	24,541	24,374	20,218	29,169	30,254	22,208
Os07g0222800	80,460	33,153	69,663	38,713	50,628	48,301	50,374	48,612	52,612	56,806	54,188	51,045
Os03g0352800	86,756	76,123	28,920	25,559	97,034	90,654	99,286	102,215	96,984	81,440	27,239	97,141
Os03g0129900	36,353	27,394	71,339	31,536	30,830	29,059	29,465	31,509	22,280	31,873	51,437	26,248
Os06g0714100	36,050	21,830	38,808	38,890	38,852	35,204	35,428	38,319	42,274	28,940	38,849	39,612
Sum of average signals										4.7E+06	5.1E+06	6.3E+06

Supplemental Table 16 Plant hormones function in anther or pollen development.

Hormone	**Functions**
Auxin	Auxin flow has been reported to be important for late pollen development (Feng *et al*., 2006), and high temperatures in barley and Arabidopsis can cause male sterility probably through repressing YUCCA auxin biosynthesis genes to reduce endogenous auxin levels (Sakata *et al*., 2010).
Abscisic acid	Abscisic acid is a potential signal for cold-induced pollen sterility in rice (Oliver *et al*., 2007).
Brassinosteroids	Brassinosteroids have been reported to regulate Arabidopsis male fertility probably through the downstream BES1 transcription factor regulating the expression of key genes involved in anther and pollen development such as SPL/NZZ (Ye *et al*., 2010).
Ethylene	Ethylene promotes female cucumber flower development by specifically inducing DNA damage in primordial anthers (Wang *et al*., 2010).
Jasmonate	Jasmonate controls the expression of MYBs to promote stamen filament growth in Arabidopsis (Cheng *et al*., 2009; Mandaokar and Browse 2009).
Gibberellin	Gibberellin has been reported to modulate anther development in rice via the transcriptional regulation of GAMYB (Aya *et al*., 2009).
cytokinin	Trans-zeatin is an active form of cytokinin. ZOG1 is a zeatin O-glucosyltransferase that temporarily inactivates trans-zeatin. Using Ubi::ZOG1 transgenic maize, Rodo´ *et al.*, (2008) found that Ubi:ZOG1 causes reduction of tassel size and feminization of florets, indicating cytokinin involved in early anther development.

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