

Supplement Table S1. 167 catalogues of inbred line materials.

Serial number	Material of name	Pedigree/Origin	Serial number	Material of name	Pedigree/Origin
1	B73	Early core germplasm in the United States	42	Cheng698-3	Unknown
2	Zheng58	Ye478 variant	43	Su75	Unknown
3	Mei68113	unknown	44	7903E	Unknown
4	1145	unknown	45	M1016	American hybrids
5	E600	Mixed species	46	P136	Unknown
6	D15	unknown	47	9711	Unknown
7	D1139	American derivative lineage	48	S53	Unknown
8	Q1261	K12 Modified Series	49	N138	Unknown
9	YE52106	(Ye1075×Ye106)×AiJin525	50	SC24-1	Unknown
10	K12	Huang Zaosi × Weichun	51	DM07	Unknown
11	3335	American derivative lineage	52	B100	Early core germplasm in the United States
12	SC11-1	American derivative lineage	53	L-1	Unknown
13	DF24	unknown	54	W172	French inbred line
14	K22	unknown	55	W668	Unknown
15	1313	unknown	56	18	Unknown
16	Dai6	unknown	57	Ye8112	American Hybrid 3382
17	W499	American hybrids	58	1614	Unknown
18	XOP2	Early core germplasm in the United States	59	B394	Unknown
19	3189	unknown	60	GY3	Unknown
20	D33A	American derivative lineage	61	Chengzi2142	Unknown
21	Lv28	Brigade of the Red Bone	62	Hai9-21	Unknown
22	eQun4	Mixed species	63	N42	Unknown
23	Zheng32	American Hybrid 3382	64	W117	Unknown
24	D864	American derivative lineage	65	HHe01	Unknown
25	D883	American derivative lineage	66	CT109	Unknown
26	N68a	Early core germplasm in the United States	67	Shen135	Unknown
27	Huang C	Unknown	68	Tai184	Unknown

28	8982	Unknown	69	Zong548-1521	Unknown
29	K514	Unknown	70	Han21	Unknown
30	Chang K	Unknown	71	PHJ33	The third batch of inbred lines in the United States
31	624	Unknown	72	Va26	Early core germplasm in the United States
32	M131-5	Early core germplasm in the United States	73	Lo1125	Unknown
33	La2-4	Unknown	74	Ay420	Unknown
34	T24	Unknown	75	DM101B	Unknown
35	08-64	Unknown	76	A632	Unknown
36	Huangy esi3	(Pheasant red × yellow morning four) × yellow morning four	77	E588	Unknown
37	Wenhua ng31413	Unknown	78	Z31B	American derivative lineage
38	Chang7-2	Unknown	79	e220	Unknown
39	Ye488	Unknown	80	P25	Unknown
40	Zhang72	Improved landraces	81	802	Unknown
41	3H2	(WeiDa202× since 330) ×H84	82	Fanrong2	Unknown
83	Yi67	Unknown	127	Yan38	Unknown
84	78371A	Unknown	128	Dan340	Brigade 9 Improved Department
85	PHH93	Unknown	129	DH65232	Unknown
86	HB8229	Unknown	130	BT1	Unknown
87	Bai197	Unknown	131	DF20	Unknown
88	LH123 HT	Unknown	132	68202	American derivative lineage
89	478	Unknown	133	M3	Unknown
90	LH59	Unknown	134	ND246	Unknown
91	Xuan6	Unknown	135	Lx9801	Unknown
92	Q381	Unknown	136	Zong3	Mixed species
93	LH156	Unknown	137	444	A619× Huang Zaosi
94	78002A	Unknown	138	707	Unknown
95	91Huan g15	Unknown	139	L069	Unknown
96	PHW51	Unknown	140	LH74	Unknown
97	BCC03	Unknown	141	WIL900	The third batch of inbred lines in the

					United States
98	PHP85	Unkown	142	ys06	Unknown
99	LH132	Unknown	143	H21	Huang Zaosi × H84
100	CR1HT	The third batch of inbred lines in the United States	144	D857	Unknown
101	B12	Unknown	145	W9706	Unknown
102	IBB15	Unknown	146	SC14	American derivative lineage
103	NS501	The third batch of inbred lines in the United States	147	DH40	Unknown
104	WIL901	Unknown	148	DF27	Unknown
105	Zong31	Unkown	149	17564	American derivative lineage
106	PHN82	The third batch of inbred lines in the United States	150	68122	Unknown
107	764	Unknown	151	Jingnuo2	Unknown
108	PHG86	The third batch of inbred lines in the United States	152	85Bai64	Unknown
109	6M502	Unknown	153	Gan41	Unknown
110	OQ603	Unknown	154	Fu8527	Unknown
111	PHP55	The third batch of inbred lines in the United States	155	H66/6	Unknown
112	PHN37	unknown	156	K14	Unknown
113	Huobai	Unknown	157	H114	Unknown
114	LH128	unknown	158	DH65232 (DH9)	Unknown
115	Lu65	Unknown	159	Fangyin	Unknown
116	LH162	Unknown	160	757	Unknown
117	1538	Unknown	161	Zhong74 1	Unknown
118	MBSJ	Unknown	162	B127	Unknown
119	Qiong51	Unknown	163	ILL12E	Unknown
120	D88	Mixed species	164	268	Unknown
121	B95	Unknown	165	B67	Unknown
122	Yan812	U8112 Improved Series	166	B78	Unknown
					Department 187-2 ×
123	806A	1688×HuangC	167	Mo17	103 of the two-ring system
124	7236	Unknown			
125	y9961	Unknown			
126	9702	Unknown			

Supplement Table S2. Fluorescent quantitative qPCR primers.

Primer name	Sequence (5'-3')
ZmActin-F	GCTACGAGATGCCTGATGGTC
ZmActin-R	CCCCCACTGAGGACAACG
ZmPR3-F	GAACAACTACAGCAGCCAGGTG
ZmPR3-R	GAGACAATAGCTGACATGCGTC
ZmPR4-F	GCGTTCAAGCCCATCGACA
ZmPR4-R	CGTGTGGGATCACATCCATATAAC
ZmPR5-F	TATCGGCCGGAATAGGCTCTG
ZmPR5-R	CGCGTACATACAAATGCGTGTC
ZmBAK1-F	CAACAGCAGTCTTCCTGAGC
ZmBAK1-R	ACCTTCAGTGTTGCAGCTTG
ZmBZR7-F	CTGAGCATCAGAGCATGACG
ZmBZR7-R	TTGAGCACCTCGTTGTTGTC
ZmBZR10-F	GGATGCATTTCGTGCTGAGTT
ZmBZR10-R	AAACAACAGCGTCACCTACG

The qRT-PCR reaction system was 10.0 μ L, including: 5.0 μ L of 2 \times SYBR Green Mix, 0.5 μ L each of forward and reverse primers, 1.0 μ L of cDNA template diluted 6-fold of the original reverse transcription system, and 3.0 μ L of ultrapure water. qRT-PCR reaction procedures were: pre-denaturation at 95°C for 30 s, three-step cycling for 40 cycles: 95°C for 5 s, 57°C for 10 s and 72°C for 20 s, and the lysis curve was plotted. C 10s, 72°C 20s, and the lysis curve was plotted.

Supplementary Table S3

Table S3. Receptor kinases and proteins in signaling transduction screened by transcriptome.

gene function (Gene function)	Gene number (Gene ID)	gene annotation (Gene annotation)	difference in value (log2FC)	P (pValue)
plant receptor kinase	<i>Zm00001eb069530</i>	lectin S-receptor-like protein kinase B120	6.6	6.28E-06
plant receptor kinase	<i>Zm00001eb226690</i>	disease resistance protein RPM1	5.8	2.56E-05
plant receptor kinase	<i>Zm00001eb170180</i>	ZmBAK1	5.2	4.04E-05
plant receptor kinase	<i>Zm00001eb323300</i>	Cysteine-rich receptor-like protein kinase 10	4.9	4.59E-15
plant receptor kinase	<i>Zm00001eb092630</i>	lectin-domain containing receptor kinase S.5	4.6	2.33E-07
plant receptor kinase	<i>Zm00001eb203630</i>	lectin-domain containing receptor kinase SIT2	4.6	6.14E-07
plant receptor kinase	<i>Zm00001eb263010</i>	cysteine-rich receptor-like protein kinase 6	4.2	6.27E-10
plant receptor kinase	<i>Zm00001eb405150</i>	lectin-domain receptor-like protein kinase	3.7	1.92E-06
plant receptor kinase	<i>Zm00001eb034610</i>	wall-associated receptor kinase 5	3.7	2.89E-16
plant receptor kinase	<i>Zm00001eb325300</i>	putative lectin-like receptor protein kinase	3.4	2.34E-19
plant receptor kinase	<i>Zm00001eb413670</i>	probable LRR receptor-like protein kinase	3.3	4.55E-12
plant receptor kinase	<i>Zm00001eb419990</i>	lectin S-receptor-like protein kinase SD2-5	2.9	1.12E-05
plant receptor kinase	<i>Zm00001eb170460</i>	putative receptor-like protein kinase	2.9	1.16E-16
plant receptor kinase	<i>Zm00001eb252380</i>	serine/threonine-pro tein kinase receptor	2.7	3.42E-05
plant receptor	<i>Zm00001eb177830</i>	putative	2.7	5.04E-09

kinase		WAK-related		
		receptor-like protein		
		kinase		
plant receptor	<i>Zm00001eb135120</i>	wall-associated	2.6	6.19E-26
kinase		receptor kinase 2		
plant receptor	<i>Zm00001eb321390</i>	lectin	2.5	2.29E-06
kinase		S-receptor-like protein		
		kinase		
signal	<i>Zm00001eb006850</i>	Ras -related protein	2.0	3.80E-09
transduction		Rab11D		
protein				
signal	<i>Zm00001eb292960</i>	Ras-related protein	2.1	0.00230513
transduction		RIC2		
protein				
signal	<i>Zm00001eb097330</i>	Ras-related protein	1.4	4.61E-05
transduction		RABA4c		
protein				
signal	<i>Zm00001eb006940</i>	Ras-related protein	1.3	1.53E-06
transduction		RABH1e		
protein				
signal	<i>Zm00001eb036050</i>	Ras-related protein	1.1	0.00012725
transduction		RABA5c		
protein				
signal	<i>Zm00001eb285010</i>	Ras-related protein	1.2	2.60E-11
transduction		RGP2		
protein				
signal	<i>Zm00001eb209160</i>	MAPK13	1.7	6.48E-17
transduction				
protein				
signal	<i>Zm00001eb358890</i>	MAPK 10	1.3	2.39E-12
transduction				
protein				
signal	<i>Zm00001eb117980</i>	MAPKKK 5-like	1.1	5.00E-05
transduction				
protein				
signal	<i>Zm00001eb213280</i>	CDPK10	1.7	6.06E-06
transduction				
protein				
signal	<i>Zm00001eb187630</i>	CDPK5	1.3	3.01E-06
transduction				
protein				
signal	<i>Zm00001eb358560</i>	CDPK	1.0	4.10E-09
transduction				
protein				

BR signaling transcription factors	<i>Zm00001eb325550</i>	BZR10	2.4	1.88E-05
BR signaling transcription factors	<i>Zm00001eb107670</i>	BZR7	1.2	1.15E-03

Supplementary Table S4

Table S4. Significant association sites screened by GAPIT software.

mould	SNP	chromosomes	placement	P. value	Phenotypic contribution %
MLMM	4_128393468	4	128393468	2.37E-06	17.30
	4_128393500	4	128393500	4.38E-06	18.07
	7_88700440	7	88700440	4.53E-06	11.59
	7_88695930	7	88695930	8.84E-06	11.50
	7_88700232	7	88700232	1.00E-05	9.88
	7_88699020	7	88699020	1.20E-05	10.48
	7_88699535	7	88699535	1.24E-05	9.21
FarmCPU	4_128393468	4	128393468	2.95E-06	17.30
	4_128393500	4	128393500	3.21E-06	18.07
	7_88700440	7	88700440	8.20E-06	11.59
	7_88695930	7	88695930	1.08E-05	11.50
SUPER	4_128393468	4	128393468	9.30E-07	17.30
	4_128393500	4	128393500	1.30E-06	18.07
	4_128393451	4	128393451	2.24E-06	11.98
	4_128355903	4	128355903	6.88E-06	12.02
BLINK	4_128393468	4	128393468	6.90E-12	17.30
	7_88700440	7	88700440	1.12E-07	11.59
	4_130720344	4	130720344	8.94E-06	7.77
GLM	4_128393468	4	128393468	7.11E-06	17.30
	4_128393500	4	128393500	7.61E-06	18.07
MLM	4_128393468	4	128393468	9.17E-06	17.30

Supplementary Table S5

Table S5. Significant associated sites screened by mrMLM software.

SNP	mould	LOD score	r ² (%)
1_244281660	FAST mrMLM	4.26	1.38
	pKWmEB		1.34
	ISIS EM-BLASSO		0.28
1_59674633	FAST mrMLM	7.02	3.64
	pKWmEB		5.02
1_78993263	FASTmrMLM	5.80	8.23
	pLARmEB		3.48
	pKWmEB		3.88
2_70835476	FASTmrMLM	3.39	3.41
	pKWmEB		6.59
2_87571650	FASTmrMLM	4.80	2.49
	FASTmrEMMA		5.10
	pLARmEB		6.27
	ISIS EM-BLASSO		6.69
4_128393468	FASTmrMLM	7.51	8.78
	pLARmEB		3.60
	pKWmEB		8.20
4_209222445	pLARmEB	4.33	2.43
	ISIS EM-BLASSO		1.35
4_47520061	FASTmrMLM	5.21	3.84
	pKWmEB		7.84
5_220156746	FASTmrMLM	5.58	2.96
	FASTmrEMMA		2.38
	pKWmEB		4.67
5_93407215	FASTmrMLM	3.76	3.66
	pKWmEB		6.56
7_112915305	FASTmrMLM	5.21	4.87
	FASTmrEMMA		4.87
	pLARmEB		2.16
	ISIS EM-BLASSO		5.70
7_48508221	FASTmrMLM	6.03	6.64

	ISIS EM-BLASSO		3.11
7_69407281	pLARmEB	4.52	6.98
	ISIS EM-BLASSO		5.92
7_88700440	FASTmrMLM	6.27	6.06
	FASTmrEMMA		5.34
	pLARmEB		4.91
	pKWmEB		11.71
	ISIS EM-BLASSO		2.26

Supplementary Table S6

Table S6. GAPIT candidate gene mining and functional annotation.

locus of interest (computing)	candidate gene	genetics	NCBI Functional Notes
4_128393468	<i>Zm00001d050880</i>		
	<i>Zm00001d050883</i>		
	<i>Zm00001d050884</i>	<i>LOC100281338</i>	uncharacterized LOC100281338
	<i>Zm00001d050885</i>	<i>galt1</i>	beta-1,3-galactosyl transferase GALT1
	<i>Zm00001d050886</i>	<i>mterf13</i>	Transcription termination factor MTERF2
	<i>Zm00001d050889</i>	<i>LOC103653672</i>	photosynthetic NDH subunit of lumenal location 2, chloroplastic
4_128393500	<i>Zm00001d050880</i>		
	<i>Zm00001d050883</i>		
	<i>Zm00001d050884</i>	<i>LOC100281338</i>	uncharacterized LOC100281338
	<i>Zm00001d050885</i>	<i>galt1</i>	beta-1,3-galactosyl transferase GALT1
	<i>Zm00001d050886</i>	<i>mterf13</i>	Transcription termination factor MTERF2
	<i>Zm00001d050889</i>	<i>LOC103653672</i>	photosynthetic NDH subunit of lumenal location 2, chloroplastic
7_88700440	<i>Zm00001d020043</i>	<i>ereb94</i>	AP2-EREBP-transcription factor 94
	<i>Zm00001d020044</i>		
	<i>Zm00001d020045</i>		
	<i>Zm00001d020046</i>	<i>LOC100273133</i>	SAWADEE HOMEODOMAIN HOMOLOG 1
	<i>Zm00001d020051</i>	<i>LOC103633997</i>	peroxisome biogenesis protein 3-1
	<i>Zm00001d020052</i>	<i>LOC100191349</i>	GDP-mannose transporter GONST4
	<i>Zm00001d020053</i>	<i>LOC100191383</i>	protein phosphatase 2C
	<i>Zm00001d020054</i>		
7_88695930	<i>Zm00001d020043</i>	<i>ereb94</i>	AP2-EREBP-transcription factor 94
	<i>Zm00001d020044</i>		
	<i>Zm00001d020045</i>		
	<i>Zm00001d020046</i>	<i>LOC100273133</i>	SAWADEE HOMEODOMAIN HOMOLOG 1

<i>Zm00001d020051</i>	<i>LOC103633997</i>	peroxisome biogenesis protein 3-1
<i>Zm00001d020052</i>	<i>LOC100191349</i>	GDP-mannose transporter GONST4
<i>Zm00001d020053</i>	<i>LOC100191383</i>	protein phosphatase 2C
<i>Zm00001d020054</i>		

Supplementary Table S7

Table S7. Significant association loci and their candidate genes screened by MrMLM software.

SNP	candidate gene
1_244281660	<i>Zm00001d022947, Zm00001d032937, Zm00001d032938, Zm00001d032939, Zm00001d032942, Zm00001d032943, Zm00001d032944, Zm00001d032945, Zm00001d032946, Zm00001d032947, Zm00001d032948, Zm00001d032949, Zm00001d032950, Zm00001d032951, Zm00001d032952, Zm00001d032953, Zm00001d032954</i>
1_59674633	<i>Zm00001d029129, Zm00001d029130, Zm00001d029132, Zm00001d029133, Zm00001d029134</i>
1_78993263	<i>zm00001d029603, zm00001d029604, zm00001d029605, zm00001d029606, zm00001d029607, zm00001d029608, zm00001d029609</i>
2_70835476	<i>zm00001d003941, zm00001d003943, zm00001d003945</i>
2_87571650	<i>Zm00001d004159</i>
4_128393468	<i>zm00001d050880, zm00001d050883, zm00001d050884, zm00001d050885, zm00001d050886, zm00001d050889</i>
4_209222445	<i>zm00001d053014, zm00001d053015, zm00001d053016, zm00001d053017, Zm00001d053018</i>
4_47520061	<i>zm00001d026804, zm00001d049840, zm00001d049841, zm00001d049842, zm00001d049843, zm00001d049844, zm00001d049846, zm00001d049848</i>
5_220156746	<i>Zm00001d001754, Zm00001d001755, Zm00001d001756, Zm00001d001757, Zm00001d018390, Zm00001d018391, Zm00001d018392, Zm00001d018393, Zm00001d018394, Zm00001d018395, Zm00001d018396, Zm00001d018397, Zm00001d018398, Zm00001d018399, Zm00001d018400, Zm00001d018401, Zm00001d018402, Zm00001d018403, Zm00001d018404, Zm00001d018405, Zm00001d018406, Zm00001d018407, Zm00001d018408, Zm00001d018409, Zm00001d018410, Zm00001d018411, Zm00001d018412, Zm00001d018413, Zm00001d018414, Zm00001d018415, Zm00001d018416, Zm00001d018417, zm00001d018418, zm00001d018419, zm00001d018420, zm00001d018421, zm00001d018422, zma-MIR396f, zma-MIR396g</i>
5_93407215	<i>Zm00001d001605, Zm00001d001606, Zm00001d015490, Zm00001d015491, Zm00001d015493</i>
7_112915305	<i>zm00001d001201, zm00001d020418, zm00001d020419, zm00001d020420, zm00001d020421, zm00001d020423</i>
7_48508221	<i>zm00001d019655, zm00001d019656, zm00001d019659, zm00001d019660, zm00001d019661, zm00001d019662</i>

7_69407281 Zm00001d019850
7_88700440 zm00001d020043, zm00001d020044, zm00001d020045, zm00001d020046, zm00001d020051,
zm00001d020052, zm00001d020053, zm00001d020054

Supplementary Table S8

Table S8. Candidate genes and functional annotations mined by MrMLM software.

SNP	candidate gene	genetic model	Functional Notes
1_244281660	Zm00001d022947		
	Zm00001d032937		
	Zm00001d032938	LOC103643563	uncharacterized LOC103643563
	Zm00001d032939	LOC100275555	uncharacterized LOC100275555
	Zm00001d032942		
	Zm00001d032943	LOC100191647	uncharacterized LOC100191647
	Zm00001d032944	LOC100284867	GTPase family protein
	Zm00001d032945	LOC103643566	myosin-7B
	Zm00001d032946		
	Zm00001d032947	LOC100285638	chitinase 2
	Zm00001d032948	LOC100282655	fatty acid elongase
	Zm00001d032949		
	Zm00001d032950	LOC100192102	GDP-mannose 3,5-epimerase 1
	Zm00001d032951		
	Zm00001d032952		
1_59674633	Zm00001d029129	LOC100277920	uncharacterized LOC100277920
	Zm00001d029130	LOC103634765	uncharacterized LOC103634765
	Zm00001d029132		
	Zm00001d029133	LOC100384700	nuclear cap-binding protein subunit 1
	Zm00001d029134	LOC103644647	uncharacterized LOC103644647
1_78993263	Zm00001d029603	LOC100281290	interferon-related developmental regulator 2
	Zm00001d029604	LOC100272496	uncharacterized LOC100272496
	Zm00001d029605		
	Zm00001d029606		
	Zm00001d029607	LOC103636850	protein SHORT-ROOT 2-like
	Zm00001d029608	LOC103636860	mechanosensitive ion channel protein 2, chloroplastic
	Zm00001d029609		
2_70835476	Zm00001d003941	LOC100192483	putative metal-nicotianamine transporter YSL6
	Zm00001d003943		

	<i>Zm00001d003945</i>	<i>LOC100285383</i>	uncharacterized LOC100285383
2_87571650	<i>Zm00001d004159</i>	<i>LOC100285241</i>	SNARE-interacting protein KEULE
4_128393468	<i>Zm00001d050880</i>		
	<i>Zm00001d050883</i>		
	<i>Zm00001d050884</i>	<i>LOC100281338</i>	uncharacterized LOC100281338
	<i>Zm00001d050885</i>	<i>galt1</i>	beta-1,3-galactosyl transferase GALT1
	<i>Zm00001d050886</i>	<i>mterf13</i>	Transcription termination factor MTERF2
	<i>Zm00001d050889</i>	<i>LOC103653672</i>	photosynthetic NDH subunit of lumenal location 2, chloroplastic
4_209222445	<i>Zm00001d053014</i>	<i>LOC100216607</i>	CBS domain-containing protein CBSCBSPB2
	<i>Zm00001d053015</i>	<i>LOC100272845</i>	uncharacterized LOC100272845
	<i>Zm00001d053016</i>	<i>LOC542703</i>	calcium-dependent protein kinase 24
	<i>Zm00001d053017</i>	<i>LOC100280270</i>	Alkaline/neutral invertase CINV2
	<i>Zm00001d053018</i>	<i>LOC100274308</i>	putative RING zinc finger domain superfamily protein
4_47520061	<i>Zm00001d026804</i>		
	<i>Zm00001d049840</i>	<i>LOC100284838</i>	pollen allergen Phl p 2
	<i>Zm00001d049841</i>	<i>LOC103653221</i>	pollen allergen Phl p 2
	<i>Zm00001d049842</i>	<i>LOC103653222</i>	pollen allergen Phl p 2
	<i>Zm00001d049843</i>	<i>LOC103653227</i>	pollen allergen Phl p 2-like
	<i>Zm00001d049844</i>	<i>LOC101027132</i>	pollen allergen Phl p 2 precursor
	<i>Zm00001d049846</i>	<i>LOC100277477</i>	uncharacterized LOC100277477
	<i>Zm00001d049848</i>		
5_220156746	<i>Zm00001d001754</i>		
	<i>Zm00001d001755</i>		
	<i>Zm00001d001756</i>		
	<i>Zm00001d001757</i>		
	<i>Zm00001d018390</i>	<i>LOC103627863</i>	RING/U-box superfamily protein
	<i>Zm00001d018391</i>	<i>LOC100273142</i>	uncharacterized LOC100273142
	<i>Zm00001d018392</i>	<i>LOC100501247</i>	uncharacterized LOC100501247
	<i>Zm00001d018393</i>	<i>LOC100280948</i>	RING/U-box superfamily pseudogene
	<i>Zm00001d018394</i>	<i>LOC100191216</i>	uncharacterized LOC100191216
	<i>Zm00001d018395</i>		
	<i>Zm00001d018396</i>		
	<i>Zm00001d018397</i>		
	<i>Zm00001d018398</i>		
	<i>Zm00001d018399</i>	<i>LOC100280170</i>	uncharacterized LOC100280170
	<i>Zm00001d018400</i>	<i>LOC103627864</i>	uncharacterized LOC103627864
	<i>Zm00001d018401</i>	<i>LOC103627865</i>	P-loop guanosine triphosphatase YjiA
	<i>Zm00001d018402</i>		
	<i>Zm00001d018403</i>	<i>LOC100217091</i>	putative proteasome maturation factor UMP1 family
	<i>Zm00001d018404</i>	<i>LOC100501670</i>	protein
	<i>Zm00001d018405</i>	<i>LOC100285845</i>	uncharacterized LOC100501670
	<i>Zm00001d018406</i>	<i>LOC100281388</i>	23S RNA methyltransferase 1
	<i>Zm00001d018407</i>		uncharacterized LOC100281388

	<i>Zm00001d018408</i>	<i>LOC100272623</i>	
	<i>Zm00001d018409</i>	<i>LOC100273594</i>	putative vesicle-associated membrane protein family
	<i>Zm00001d018410</i>	<i>LOC100282946</i>	protein
	<i>Zm00001d018411</i>	<i>LOC100194268</i>	uncharacterized LOC100273594
	<i>Zm00001d018412</i>	<i>LOC100285012</i>	40S ribosomal protein S30-like
	<i>Zm00001d018413</i>		methyltransferase WBSCR22
	<i>Zm00001d018414</i>	<i>LOC100281448</i>	50S ribosomal protein L9
	<i>Zm00001d018415</i>	<i>LOC542425</i>	
	<i>Zm00001d018416</i>	<i>LOC100216625</i>	IAA9 - auxin-responsive Aux/IAA family member
	<i>Zm00001d018417</i>	<i>LOC100280395</i>	proliferating cell nuclear antigen 1
	<i>Zm00001d018418</i>	<i>LOC100284272</i>	uncharacterized LOC100216625
	<i>Zm00001d018419</i>	<i>LOC100277099</i>	uncharacterized LOC100280395
	<i>Zm00001d018420</i>	<i>LOC100502250</i>	uncharacterized LOC100284272
	<i>Zm00001d018421</i>	<i>LOC107228387</i>	uncharacterized LOC100277099
	<i>Zm00001d018422</i>	<i>LOC103627873</i>	uncharacterized LOC100502250
	<i>zma-MIR396f</i>	<i>MIR396f</i>	GATA transcription factor 8
	<i>zma-MIR396g</i>	<i>MIR396g</i>	glycosyltransferase family protein 2
			microRNA MIR396f
			microRNA MIR396f
5_93407215	<i>Zm00001d001605</i>		
	<i>Zm00001d001606</i>		
	<i>Zm00001d015490</i>	<i>LOC100276544</i>	uncharacterized LOC100276544
	<i>Zm00001d015491</i>		
	<i>Zm00001d015493</i>	<i>LOC100383018</i>	uncharacterized LOC100383018
7_112915305	<i>Zm00001d001201</i>		
	<i>Zm00001d020418</i>	<i>LOC100501848</i>	putative cytochrome P450 superfamily protein
	<i>Zm00001d020419</i>	<i>LOC100191313</i>	uncharacterized LOC100191313
	<i>Zm00001d020420</i>	<i>LOC103632729</i>	uncharacterized LOC103632729
	<i>Zm00001d020421</i>		
	<i>Zm00001d020423</i>		
7_48508221	<i>Zm00001d019655</i>		
	<i>Zm00001d019656</i>		
	<i>Zm00001d019659</i>		
	<i>Zm00001d019660</i>		
	<i>Zm00001d019661</i>		
	<i>Zm00001d019662</i>		
7_69407281	<i>Zm00001d019850</i>	<i>LOC100501369</i>	Fatty acyl-CoA reductase 1
7_88700440	<i>Zm00001d020043</i>	<i>ereb94</i>	Transcription termination factor MTERF2
	<i>Zm00001d020044</i>		
	<i>Zm00001d020045</i>		
	<i>Zm00001d020046</i>	<i>LOC100273133</i>	SAWADEE HOMEODOMAIN HOMOLOG 1
	<i>Zm00001d020051</i>	<i>LOC103633997</i>	peroxisome biogenesis protein 3-1
	<i>Zm00001d020052</i>	<i>LOC100191349</i>	GDP-mannose transporter GONST4
	<i>Zm00001d020053</i>	<i>LOC100191383</i>	protein phosphatase 2C

Zm00001d020054
