

Figure S1. GWAS of root elongation in control conditions. (a). Distribution of root elongation of Ting's core collection grown in control conditions; (b). Box plots for root elongation under high Zn (120 μ M) conditions and without Zn toxicity. The p -value of Student's t -test was shown for comparing root elongation under high and without Zn toxicity; (c). Manhattan plot of GWAS using root elongation without Zn toxicity. Chromosomes are depicted in different colors. The green line depicts the adjusted significant threshold ($p=0.94 \times 10^{-5}$).

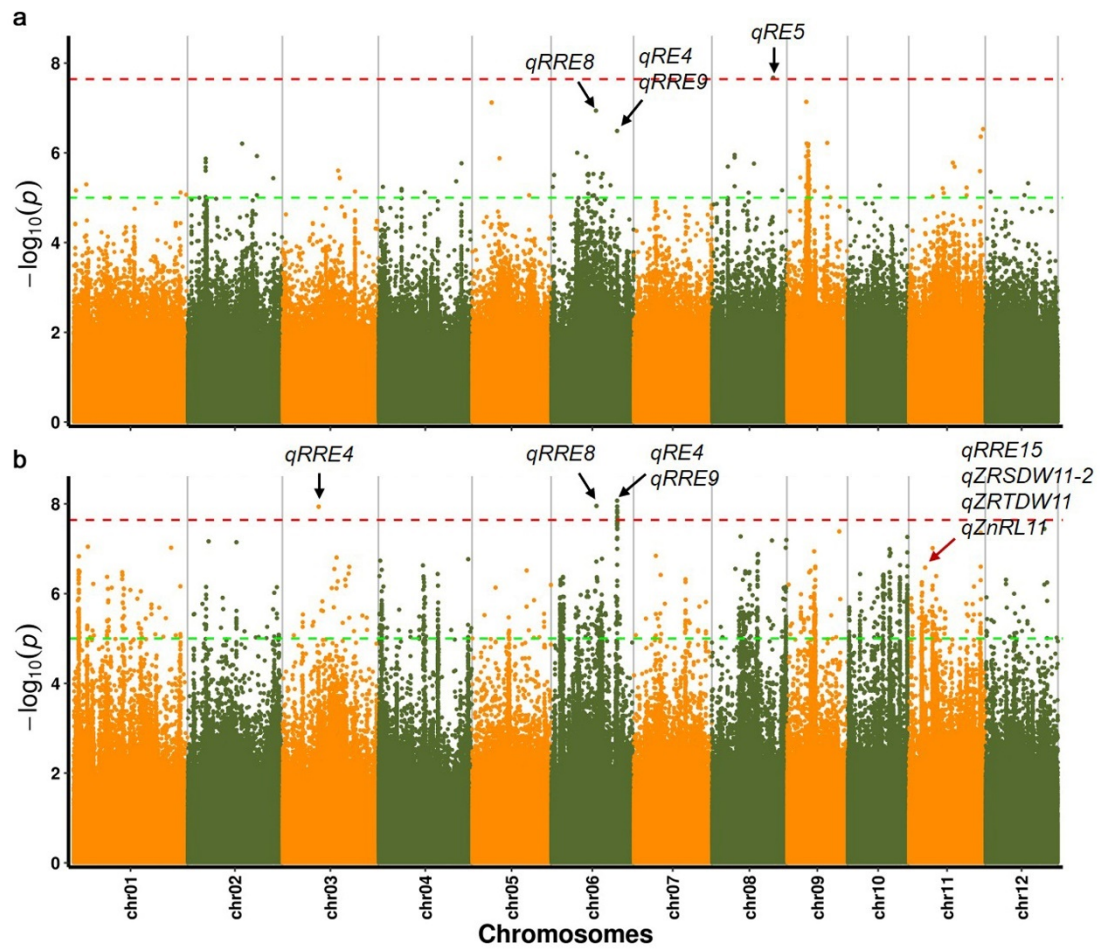


Figure S2. GWAS of Zn tolerance in high Zn conditions using LMM model. **(a).** Manhattan plot of GWAS using root elongation in high Zn conditions; **(b).** Manhattan plot of GWAS using relative root elongation in high Zn conditions. Chromosomes are depicted in different colors. The horizontal red line depicts the significant threshold ($p=2.27 \times 10^{-7}$) and the green line depicts the adjusted significant threshold ($p=0.94 \times 10^{-5}$). The black arrows represent the significant loci detected using EMMAX and LMM models. The red arrow represents the same loci as the previously reported under Zn stress.

Table S1. Root growth of Ting's core collection in control and Zn toxicity conditions.

ID	Variety Name	Root Elongation (mm, control) \pm S.D.	Root Elongation (mm, high Zn) \pm S.D.	Relative Root elongation (%)	Origin
S001	Yin guang	46.30 \pm 2.54	24.67 \pm 2.69	53.28 \pm 5.82	Japan
S005	Guo zhu	40.89 \pm 2.93	17.50 \pm 3.41	42.80 \pm 8.33	Japan
S007	Mang shui dao	45.87 \pm 4.10	21.10 \pm 6.94	46.00 \pm 9.50	Yangtze River region
S008	Bai mang gao li han dao bai	47.13 \pm 3.02	16.06 \pm 2.58	34.06 \pm 5.47	North China
S010	Bi jie ma wei hong gu	42.40 \pm 4.50	18.55 \pm 3.24	43.74 \pm 7.63	Yunnan-Kweichow Plateau
S011	Ai da tou	23.76 \pm 3.15	13.44 \pm 1.46	56.57 \pm 6.16	Yangtze River region
S012	Gui zao bai he	49.50 \pm 4.16	19.80 \pm 5.33	40.00 \pm 9.10	Yangtze River region
S013	Xiang dao	35.62 \pm 4.13	11.19 \pm 2.32	31.41 \pm 6.50	North China
S014	Zi jin gu	42.53 \pm 3.25	21.35 \pm 2.32	50.20 \pm 5.45	Northeast China
S015	Xiang chuan	38.25 \pm 2.12	13.30 \pm 1.70	34.77 \pm 4.45	Japan
S016	Nagabo	16.71 \pm 2.82	13.06 \pm 3.19	78.19 \pm 10.10	Taiwan
S018	San pai zhong	33.43 \pm 5.12	15.38 \pm 2.47	45.99 \pm 7.40	South China
S019	Kai xuan	50.44 \pm 4.24	16.06 \pm 5.07	31.84 \pm 8.58	Japan
S020	Shi ban zhan	45.53 \pm 5.00	21.06 \pm 2.51	46.25 \pm 5.52	North China
S022	Shen shui wan dao	31.50 \pm 6.81	8.75 \pm 0.96	27.78 \pm 3.04	Yangtze River region
S023	Hong ben dao	50.88 \pm 3.26	15.35 \pm 4.03	30.17 \pm 7.92	Yangtze River region
S024	Duan mang zi jin gu	18.82 \pm 5.40	13.19 \pm 1.22	70.08 \pm 6.50	Northeast China
S025	Bei jing jiang mi	46.08 \pm 3.57	22.20 \pm 3.78	48.18 \pm 8.21	Northeast China
S026	Daeri	35.67 \pm 2.91	13.81 \pm 4.78	38.73 \pm 9.34	Celebes
S027	Jian tou nuo	26.5 \pm 5.13	12.38 \pm 5.26	46.70 \pm 9.37	South China

S028	Long you man dao	54.06±3.77	24.06±4.62	44.50±8.54	Yangtze River region
S029	Kun shan zhu zhou dao	54.24±1.99	25.72±3.43	47.43±6.32	Yangtze River region
S031	Sheng fang da bai gu	42.47±3.79	11.19±2.90	26.34±6.84	North China
S032	Xiao du	30.00±7.07	11.00±1.00	36.67±3.33	Japan
S033	Poetih	39.75±4.80	15.65±2.40	39.36±6.03	Celebes
S034	Tebaro	27.44±4.98	9.27±1.62	33.77±5.92	Sumbawa
S035	Ao hua da gui tou hong	47.94±4.23	17.29±1.65	36.08±3.44	Yangtze River region
S036	Hui bei zi	45.87±2.72	15.08±4.11	32.87±8.97	Yunnan-Kweichow Plateau
S037	Ba shi zi	43.43±3.82	21.33±2.63	49.12±6.07	Yangtze River region
S038	Zao sheng da ye	40.46±4.70	14.15±1.77	34.98±4.38	Japan
S039	Bnlastog	37.85±2.27	9.50±3.57	25.10±7.82	Low latitude region
S040	Nuo mi	50.28±3.37	24.47±4.84	48.67±9.62	North China
S041	Xi chuan huang liu	47.77±3.32	21.53±4.91	45.08±9.00	South China
S042	Hei ju dao	25.62±3.78	8.25±1.77	32.21±6.91	Yangtze River region
S043	Guang fu 1 hao	51.89±2.70	25.44±2.71	49.04±5.21	Taiwan
S044	Zhong qi jia qing	47.33±4.33	15.93±2.71	33.66±5.73	Yangtze River region
S045	III-49-4 xi chuan huang	46.81±4.29	22.47±3.66	52.82±8.61	Taiwan
S046	Xin xian li	47.29±3.79	25.07±4.82	53.00±7.62	Yangtze River region
S047	Da liu tiao dao	48.58±5.74	20.46±3.80	42.12±7.82	Yangtze River region
S048	Bai ke	52.56±3.03	26.00±2.93	49.47±5.58	South China
S049	Chuan chi yi hao	52.61±4.92	23.94±4.49	45.51±8.54	Central China
S050	Tai nong 46	32.71±1.38	9.00±3.16	27.51±6.70	Taiwan
S051	Ba chong sui	47.06±4.96	24.00±3.66	51.00±7.78	Japan
S052	Yun nan bai	21.81±4.20	11.25±1.65	51.58±7.58	Central China
S053	Liao yang ben di 4 hao	41.88±3.90	20.88±2.09	49.84±5.00	Northeast China
S054	You zhan hong	40.89±3.36	8.94±3.73	21.86±7.58	South China
S056	Xian zi zhan	45.82±3.30	17.83±3.24	38.92±7.07	Central China
S057	Da tou meng	44.25±2.44	19.28±3.64	43.57±8.23	Central China

S058	Chi bai gan zhan	50.11±4.44	18.89±2.65	37.69±5.30	Central China
S059	Zeng cheng xiang shan zhan	45.47±2.83	24.61±3.05	54.13±6.71	South China
S060	Cang wu shan he zhan	52.00±3.41	23.22±3.73	44.66±7.18	South China
S061	Da gu zao	52.94±4.26	27.12±2.67	51.22±5.04	South China
S062	Jie yang dong liao zhong	47.94±2.41	26.29±3.87	54.85±8.07	South China
S063	Nan xiong ku gua zao	48.18±7.18	25.38±3.43	52.69±7.12	South China
S064	Chang mang	41.59±5.04	24.53±3.72	58.99±8.94	South China
S065	Mandi	42.25±2.72	23.63±4.22	55.92±6.25	Celebes
S066	Bai gu	29.60±7.92	18.25±3.81	61.66±6.72	South China
S068	Can wu shan he zhan	42.36±4.38	22.06±4.34	52.09±6.89	South China
S069	Zao die zhan gu	52.33±4.06	22.94±4.44	43.84±8.48	Central China
S070	Su zhou zhan	20.44±5.34	8.42±2.50	41.17±6.94	Central China
S072	Luo ding zhan 1	45.44±8.19	21.53±2.21	47.38±4.87	South China
S073	Geng yin 29	46.00±3.64	26.28±3.56	57.13±7.74	South China
S074	Wu ke nuo	44.89±7.19	15.53±3.48	34.60±7.76	South China
S075	Hua bai ke	34.44±6.17	23.60±2.01	68.52±5.84	South China
S076	Guang ye hong mi	51.93±3.20	22.50±7.38	43.32±6.74	South China
S077	Da nuo	43.00±4.68	23.00±2.00	53.49±4.65	South China
S078	Bai xu	28.38±4.68	15.00±3.79	52.85±10.14	South China
S079	Mao he	51.06±2.58	22.63±2.50	44.31±4.90	South China
S080	Xu zai	36.50±8.13	19.71±1.38	54.01±3.78	South China
S083	Chi mao zhan	50.94±2.69	25.00±2.12	49.07±4.16	South China
S084	Hu bei zao	43.47±2.85	21.81±2.64	50.18±6.07	Central China
S087	Dong jun zi	44.50±3.54	26.67±4.16	59.93±9.36	Central China
S091	Hei nuo	56.00±4.21	24.88±2.52	44.43±4.50	Unknown
S093	Gai cao zhan	50.82±2.98	25.00±3.02	49.19±5.94	Central China
S094	Gamal	51.59±2.74	25.31±2.44	49.07±4.73	Unknown
S095	Bu gou wei	40.89±7.18	25.29±2.50	61.84±6.11	South China

S096	Bai ke xi nuo	53.80±2.93	27.93±4.11	51.92±7.65	South China
S097	Ben dao	37.36±3.00	16.25±3.77	43.5±4.64	North China
S098	Ba xian shu	56.12±3.22	26.67±5.41	47.52±6.93	Japan
S099	Guang hong mi dao	43.86±2.63	19.94±3.52	45.48±8.03	Yangtze River region
S100	Wu mang yan guo qing	44.14±4.00	17.00±3.98	38.51±7.65	North China
S101	Chang xu nuo	52.33±4.13	25.88±3.64	49.44±6.96	South China
S103	Bai hua er	54.13±4.18	22.33±2.03	41.26±3.75	South China
S104	Liu chang xian	34.00±9.83	14.2±3.70	41.76±9.72	South China
S105	Bai yin 3	24.69±6.05	10.71±2.76	43.40±9.21	South China
S106	Shui zao huang pi	51.83±3.09	29.61±3.53	57.13±6.82	South China
S107	Yin 2 dong 7	31.53±5.88	11.17±3.69	35.43±7.99	South China
S108	Hou ma	50.56±2.76	23.82±2.58	47.12±5.10	South China
S109	Dong zhu 2 hao	53.57±7.08	34.39±2.30	64.19±4.30	South China
S110	Hong gen da mi	52.78±2.02	19.44±4.32	36.83±8.19	South China
S111	Ben cheng guan yin zhan	46.35±5.11	29.07±3.56	62.26±7.75	Central China
S112	Xi miao gu	52.47±5.24	25.69±2.80	48.96±5.33	South China
S113	186-zao guan yin zhan	50.11±4.54	29.08±4.34	58.04±8.66	Central China
S114	Chang mang hei ma zao	52.39±1.75	19.31±2.09	36.86±3.99	Yunnan
S115	Shui tian zhan gu nuo	49.53±2.65	28.10±4.51	56.73±9.10	South China
S116	Chang han da hua ke	45.11±7.26	14.29±2.52	31.69±5.58	South China
S117	Da he	47.41±3.57	22.53±3.07	47.53±6.47	South China
S118	Zeng cheng hei nuo	49.89±3.31	17.71±4.87	35.51±9.77	South China
S119	Mao he	42.00±7.55	29.50±0.71	70.24±1.68	South China
S121	Die zhi	34.00±6.24	16.00±4.98	47.06±8.75	South China
S122	You zhan	52.25±2.54	28.33±3.93	54.23±7.51	South China
S124	Tong ling hu nan xian	38.00±7.79	23.33±2.29	61.40±6.03	Central China
S125	Xiao mao dao	47.13±4.78	29.18±4.03	61.90±8.56	Central China
S127	Zi xing er qu si du xu	46.00±4.03	24.00±2.51	52.17±5.45	Central China

S128	Chen hui fu dao	46.07±2.06	16.69±5.20	36.23±5.74	Central China
S129	Bai gan zi	41.83±7.33	25.35±5.04	60.6±8.35	Central China
S130	Zao lu wei zhan	53.33±2.54	23.22±4.11	43.54±7.71	Central China
S132	Ta gu zhan	52.06±3.17	22.94±2.65	44.08±5.08	Central China
S133	Mian tiao zhan	36.24±3.42	14.27±2.55	39.37±7.03	Central China

Table S2. QTL for root elongation of Ting's core collection in control condition.

QTL	Chromosome	Position	<i>p</i> -value	Allele	Physical interval (bp)
<i>qCRE1</i>	chr02	17,552,474	2.12E-06	G/A	17,446,354–17,645,569
<i>qCRE2</i>	chr02	18,591,797	3.22E-06	A/C	18,495,340–18,662,179
<i>qCRE3</i>	chr02	24,115,867	4.95E-06	C/T	24,021,764–24,201,250
<i>qCRE4</i>	chr02	24,704,915	1.44E-06	T/C	24,645,508–24,786,542
<i>qCRE5</i>	chr02	29,034,587	2.92E-06	T/A	28,935,436–29,120,637

<i>qCRE6</i>	chr03	8,228,307	1.94E-06	G/A	8,130,378–8,328,581
<i>qCRE7</i>	chr03	21,631,477	6.04E-06	A/G	21,539,060–21,731,479
<i>qCRE8</i>	chr03	35,942,382	1.69E-06	C/T	35,840,625–36,043,821
<i>qCRE9</i>	chr04	728,686	1.55E-07	A/T	639,804–798,794
<i>qCRE10</i>	chr05	2,953,058	5.76E-06	C/T	2,852,853–3,056,996
<i>qCRE11</i>	chr06	4,675,238	1.05E-06	A/C	4,577,367–4,764,420
<i>qCRE12</i>	chr06	10,991,829	1.07E-06	T/G	10,891,500–11,094,202
<i>qCRE13</i>	chr06	15,233,394	2.99E-06	A/G	15,189,242–15,254,487
<i>qCRE14</i>	chr06	19,455,509	9.87E-07	A/T	19,357,232–19,553,885
<i>qCRE15</i>	chr06	25,944,857	6.40E-08	C/T	2,5867,747–26,040,374
<i>qCRE16</i>	chr07	12,831,029	1.14E-06	G/A	12,747,743–12,930,673
<i>qCRE17</i>	chr07	17,266,036	5.49E-06	T/C	17,186,673–17,285,379
<i>qCRE18</i>	chr07	26,443,312	2.81E-06	G/A	26,340,582–26,545,180
<i>qCRE19</i>	chr08	6,072,098	2.75E-07	C/G	5,982,519–6,175,794
<i>qCRE20</i>	chr08	10,838,488	5.45E-06	T/C	10,759,593–10,945,133
<i>qCRE21</i>	chr08	19,756,555	3.92E-06	A/G	19,657,493–19,854,635
<i>qCRE22</i>	chr08	20,851,712	6.08E-06	A/T	20,761,382–20,947,979
<i>qCRE23</i>	chr08	22,400,585	7.95E-06	T/C	22,334,606–22,497,785
<i>qCRE24</i>	chr09	346,485	2.93E-07	G/C	244,493–451,698
<i>qCRE25</i>	chr09	6,954,135	1.47E-06	G/A	6,873,236–7,038,397
<i>qCRE26</i>	chr09	7,960,191	6.95E-07	T/G	7,871,403–8,046,886
<i>qCRE27</i>	chr09	10,866,545	4.41E-07	C/T	10,763,252–10,969,484
<i>qCRE28</i>	chr09	13,467,437	1.59E-06	T/C	13,376,227–13,575,139
<i>qCRE29</i>	chr09	19,898,066	2.57E-06	G/A	19,796,232–19,999,811
<i>qCRE30</i>	chr10	11,413,443	3.66E-07	G/A	11,314,672–11,464,119
<i>qCRE31</i>	chr10	16,156,147	1.35E-06	G/A	16,084,478–16,243,154
<i>qCRE32</i>	chr10	18,183,013	2.79E-06	A/T	18,085,539–18,281,584
<i>qCRE33</i>	chr11	16,978,564	1.87E-06	A/G	16,885,485–17,066,284

<i>qCRE34</i>	chr11	21,930,706	1.10E-07	A/T	21,839,186–22,031,935
<i>qCRE35</i>	chr12	20,866,616	5.22E-06	A/T	20,781,339–20,903,625
<i>qCRE36</i>	chr12	26,176,316	3.26E-06	G/A	26,081,664–26,270,792
<i>qCRE37</i>	chr12	27,362,251	4.09E-06	C/T	27,263,777–27,464,059

CRE: root elongation in control conditions.

Table S3. Candidate genes associated with Zn tolerance.

QTL	Gene ID	Annotation
<i>qRE2</i>	<i>Os02g0650300</i>	OsYSL15
	<i>Os02g0650500</i>	protein kinase domain containing protein
	<i>Os02g0650800</i>	CHR740
	<i>Os02g0650900</i>	glutamate dehydrogenase protein
	<i>Os02g0651000</i>	expressed protein
	<i>Os02g0651200</i>	expressed protein
	<i>Os02g0651300</i>	uncharacterized protein
	<i>Os02g0651500</i>	expressed protein
	<i>Os02g0651900</i>	--
	<i>Os02g0652000</i>	cyclin-P4-1-like
	<i>Os02g0652100</i>	OsWRKY34
	<i>Os02g0652300</i>	ELMO/CED-12 family protein
	<i>Os02g0652550</i>	MSP domain containing protein
	<i>Os02g0652575</i>	Hypothetical gene
	<i>Os02g0652600</i>	50S ribosomal protein L19
	<i>Os02g0652800</i>	Transporter
	<i>Os02g0653000</i>	--

	<i>Os02g0653200</i>	plastocyanin-like domain containing protein
	<i>Os02g0653300</i>	Conserved hypothetical protein
	<i>Os02g0653400</i>	transferase family protein
	<i>Os02g0653800</i>	ras-related protein
	<i>Os02g0653850</i>	Hypothetical gene
	<i>Os02g0653900</i>	triacylglycerol lipase like protein
	<i>Os02g0654000</i>	enoyl-CoA hydratase
	<i>Os02g0654100</i>	enoyl-CoA hydratase
	<i>Os08g0470700</i>	bifunctional monodehydroascorbate reductase and carbonic anhydrase nectarin-3 precursor
	<i>Os08g0471000</i>	OsHsfB4a
	<i>Os08g0471150</i>	Hypothetical protein
	<i>Os08g0471300</i>	Similar to Methyl-CpG binding protein-like
	<i>Os08g0471800</i>	remorin C-terminal domain containing protein
<i>qRE5</i>	<i>Os08g0471850</i>	Hypothetical protein
	<i>Os08g0471900</i>	zinc finger family protein
	<i>Os08g0472000</i>	OsZIP66
	<i>Os08g0472400</i>	expressed protein
	<i>Os08g0472600</i>	FucT
	<i>Os08g0472800</i>	OsABA8ox2
	<i>Os08g0473200</i>	Hypothetical protein
	<i>Os01g0199300</i>	lachrymatory factor synthase
	<i>Os01g0199400</i>	Hydrolase
	<i>Os01g0199550</i>	--
<i>qRRE1</i>	<i>Os01g0199700</i>	expressed protein
	<i>Os01g0199900</i>	phosphoribosylaminoimidazole carboxylase
	<i>Os01g0199950</i>	Hypothetical gene

	<i>Os01g0200000</i>	autophagy-related protein 3
	<i>Os01g0200150</i>	Hypothetical gene
	<i>Os01g0200200</i>	expressed protein
	<i>Os01g0200300</i>	OSHB5
	<i>Os01g0200350</i>	Hypothetical protein
	<i>Os01g0200400</i>	expressed protein
	<i>Os01g0200500</i>	MPPN domain containing protein
	<i>Os01g0200600</i>	AP2 domain containing protein
	<i>Os01g0200700</i>	OsMTI-3a
	<i>Os01g0200950</i>	--
	<i>Os01g0201000</i>	protein kinase family protein
	<i>Os01g0201100</i>	xylosyltransferase
	<i>Os01g0201200</i>	protein kinase domain containing protein
	<i>Os01g0201250</i>	HD1
	<i>Os01g0201275</i>	expressed protein
	<i>Os01g0201300</i>	expressed protein
	<i>Os01g0201400</i>	RALFL17
	<i>Os01g0201500</i>	plastocyanin-like domain containing protein
	<i>Os01g0201600</i>	OsGAE1
	<i>Os01g0201700</i>	OSMADS3
	<i>Os01g0201750</i>	--
	<i>Os01g0201800</i>	expressed protein
	<i>Os01g0201850</i>	Hypothetical conserved gene
<i>qRRE4</i>	<i>Os03g0356470</i>	expressed protein
	<i>Os03g0356477</i>	--
	<i>Os03g0356484</i>	tetratricopeptide repeat containing protein
	<i>Os03g0356498</i>	rhythmically expressed gene 2 protein

<i>qRRE8</i>	<i>Os03g0356526</i>	expressed protein
	<i>Os03g0356540</i>	CXXC1
	<i>Os03g0356582</i>	phosphatidylinositol-4-phosphate 5-kinase
	<i>Os03g0356596</i>	phosphatidylinositol-4-phosphate 5-kinase
	<i>Os03g0356638</i>	pleckstrin homology domain-containing protein
	<i>Os03g0356652</i>	TRAF-type zinc finger domain-containing protein 1
	<i>Os03g0356700</i>	VLN2
	<i>Os03g0356801</i>	--
	<i>Os03g0356900</i>	OsIPT2
	<i>Os03g0357200</i>	--
	<i>Os03g0357400</i>	Hypothetical conserved gene
	<i>Os03g0357500</i>	Protease inhibitor
	<i>Os03g0358000</i>	PWWP domain containing protein
	<i>Os06g0493600</i>	OsPHO1,3
	<i>Os06g0493700</i>	Pi homeostasis
	<i>Os06g0493800</i>	Conserved hypothetical protein
	<i>Os06g0493801</i>	pentatricopeptide
	<i>Os06g0493900</i>	Conserved hypothetical protein
	<i>Os06g0494000</i>	expressed protein
	<i>Os06g0494100</i>	Pid2
	<i>Os06g0494250</i>	Hypothetical protein
	<i>Os06g0494400</i>	MATE efflux family protein
	<i>Os06g0494701</i>	retrotransposon protein
	<i>Os06g0495100</i>	MATE domain containing protein
	<i>Os06g0495500</i>	MATE efflux family protein
	<i>Os06g0495632</i>	Similar to F-box domain containing protein
	<i>Os06g0495700</i>	PSP domain containing protein

	<i>Os06g0495800</i>	DUF617 domain containing protein
	<i>Os06g0621600</i>	CC-NBS-LRR protein
	<i>Os06g0621800</i>	retrotransposon protein
	<i>Os06g0621900</i>	expansin precursor
	<i>Os06g0621950</i>	Hypothetical protein
	<i>Os06g0622000</i>	CW-type Zinc Finger
	<i>Os06g0622300</i>	OsARID3
	<i>Os06g0622400</i>	transposon protein
	<i>Os06g0622500</i>	tetratricopeptide repeat domain containing protein
	<i>Os06g0622550</i>	retrotransposon protein
	<i>Os06g0622700</i>	OsZIP50
<i>qRE4/qRRE9</i>	<i>Os06g0622800</i>	guanine nucleotide exchange family protein
	<i>Os06g0622900</i>	RNA recognition motif containing protein
	<i>Os06g0623050</i>	guanine nucleotide exchange family protein
	<i>Os06g0623200</i>	dihydroflavonol-4-reductase
	<i>Os06g0623300</i>	reductase
	<i>Os06g0623600</i>	reductase
	<i>Os06g0623700</i>	TGW6
	<i>Os06g0624000</i>	expressed protein
	<i>Os06g0624100</i>	OsSub51
	<i>Os06g0624200</i>	hypothetical protein
	<i>Os06g0624700</i>	expressed protein
	<i>Os06g0624750</i>	Hypothetical protein
	<i>Os08g0562100</i>	lactate/malate dehydrogenase
<i>qRRE12</i>	<i>Os08g0562200</i>	OsNTL5
	<i>Os08g0562300</i>	C2H2 zinc finger protein
	<i>Os08g0562500</i>	BAHD acyltransferase-like protein gen

	<i>Os08g0562600</i>	C2 domain containing protein
	<i>Os08g0562700</i>	aminopeptidase
	<i>Os08g0562750</i>	--
	<i>Os08g0562800</i>	MATE efflux family protein
	<i>Os08g0562866</i>	Hypothetical protein
	<i>Os08g0563200</i>	DNA binding protein
	<i>Os08g0563300</i>	SNARE domain containing protein
	<i>Os08g0563400</i>	DUF260 domain containing protein
	<i>Os08g0563450</i>	Hypothetical protein
	<i>Os08g0563500</i>	C3HC4 type domain containing protein
	<i>Os08g0564000</i>	OsPT6
	<i>Os08g0564100</i>	ABC transporter
	<i>Os08g0564200</i>	Hypothetical protein
	<i>Os08g0564300</i>	SD8
	<i>Os08g0564400</i>	Hypothetical protein
	<i>Os08g0564500</i>	zinc finger protein 593
	<i>Os08g0564700</i>	protein Kinase-like protein TMKL1 precursor
	<i>Os08g0564750</i>	expressed protein
	<i>Os08g0564800</i>	expressed protein
	<i>Os08g0564900</i>	Conserved hypothetical protein
	<i>Os08g0565200</i>	AP2 domain containing protein
	<i>Os08g0565450</i>	Similar to H0107B07.4 protein
	<i>Os11g0264900</i>	expressed protein
	<i>Os11g0264950</i>	--
	<i>Os11g0265000</i>	uridine/cytidine kinase-like 1
	<i>Os11g0265100</i>	Hypothetical protein
	<i>Os11g0265200</i>	expressed protein

<i>Os11g0265400</i>	oxidoreductase
<i>Os11g0265450</i>	--
<i>Os11g0265500</i>	uncharacterized protein
<i>Os11g0263000</i>	NBS-LRR disease resistance protein
<i>Os11g0263466</i>	--
<i>Os11g0264000</i>	laccase precursor protein
<i>Os11g0264200</i>	F-box domain containing protein
<i>Os11g0264300</i>	NIN
<i>Os11g0264500</i>	expressed protein
<i>Os11g0264600</i>	expressed protein
<i>Os11g0264700</i>	expressed protein

Table S4. Primers used for qRT-PCR

Primer name	Sequence 5'-3'
OsUBQ1-F	GCTCCGTGGCGGTATCAT
OsUBQ1-R	CGGCAGTTGACAGCCCTAG
Os01g0200700-F	TATTTGCTTGCTTTGTGCGT
Os01g0200700-R	TTCGGTTGCTTCGTGACTTC
Os06g0493600-F	AACCCTTGGCTCCGTAATGA
Os06g0493600-R	ACCTCAAGAGCTGCCAAGAT
Os06g0621600-F	TTGGCCATGACAAGTTTCGG
Os06g0621600-R	AGCTGGAGATACGCCATTGA

Os06g0621900-F	CATCTTCAGGTACGGGAGGT
Os06g0621900-R	ATCTCGAAGTGCTCCTTGGG
Os06g0622300-F	CATTGGTTCCTGGCCTTCTG
Os06g0622300-R	ATGGTGCACGGACAAATAGC
Os06g0622700-F	GCGATGATCCCATGAGCAAG
Os06g0622700-R	CCGACAGGCCTATCCTTCAA
Os11g0263000-F	AGAGTGGGATGTTCAGCGAT
Os11g0263000-R	CCAGGTTCTTTAGGGAGCCA
Os11g0264200-F	ATGGTCTGCGATTGGATTGC
Os11g0264200-R	CCTGCAAACCTTGGTCACAA
