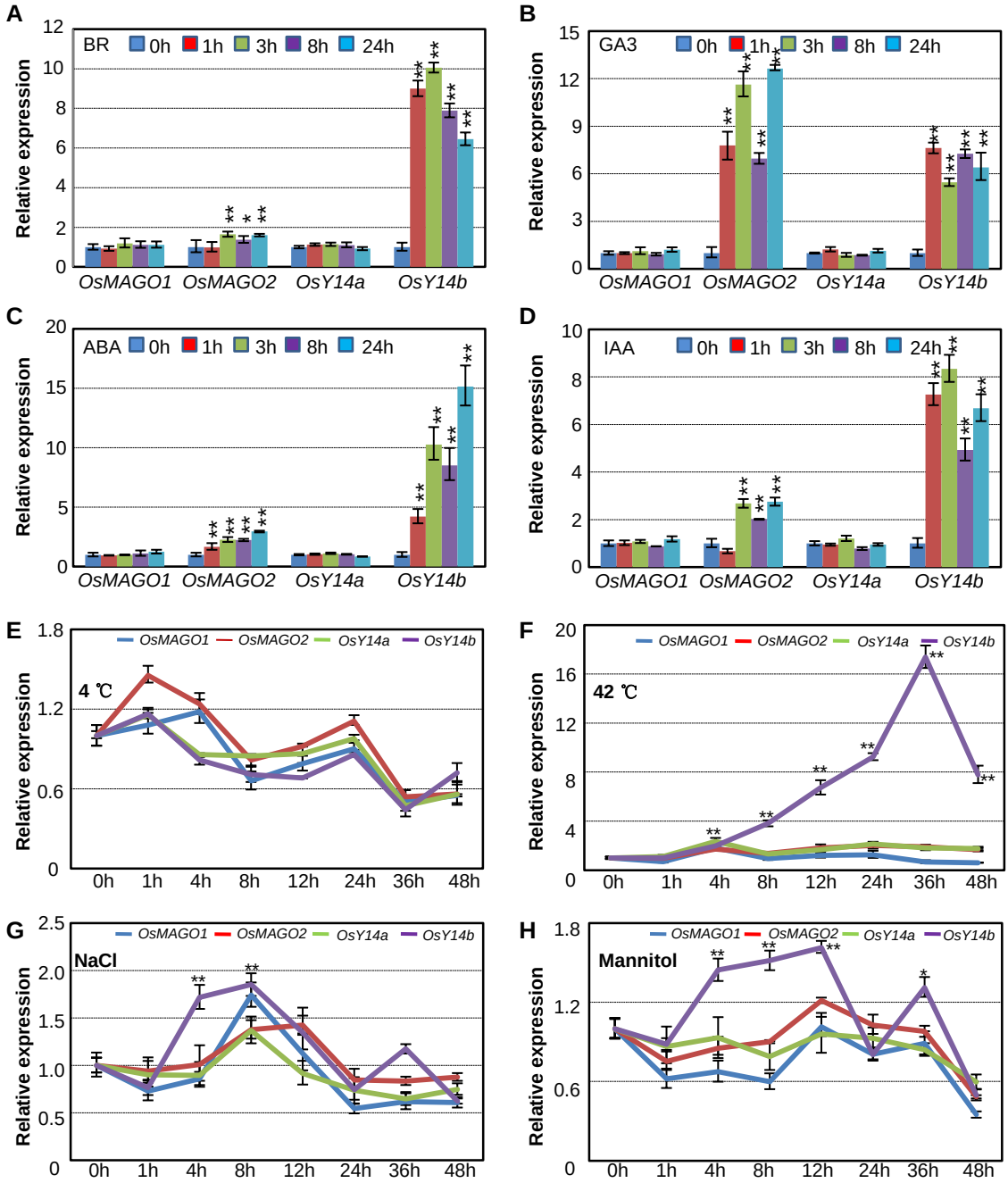

Figure S1. Gene Expressions of Rice *MAGO* and *Y14* under Different Types of Stresses.
(A-D) Gene expression in response to hormonal treatments. BR, brassinolide; GA3, gibberellic acid; ABA, abscisic acid; and IAA, indole acetic acid. (E-H) Gene expression in response to abiotic stresses indicated. *OsACTIN1* was used as an internal control. Expression data were expressed as results of three independent biological samples were. The expression for each gene without treatment was set to 1. The average expression and the standard deviation are presented. A two-tailed *t*-test was used to determine the significance of means. * indicates $P < 0.05$ and ** indicate $P < 0.01$.

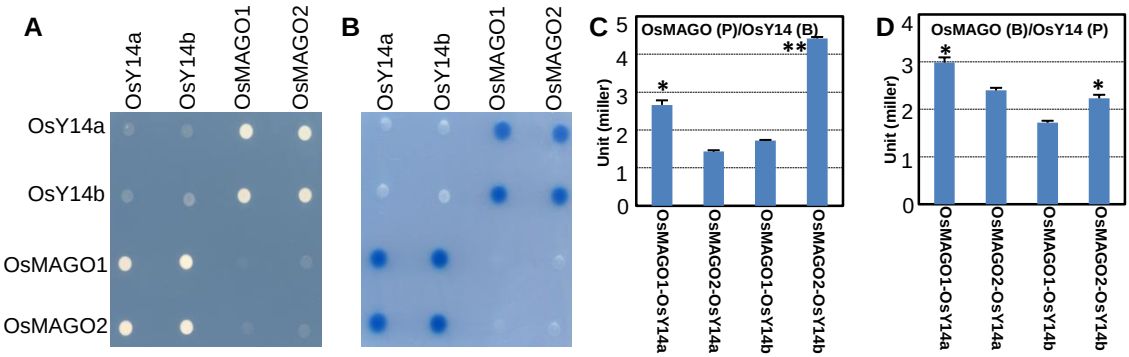

Figure S2. Interaction of Rice MAGO and Y14 Proteins in Yeast.
(A) Yeast cell growth on a high-stringency selective plate (SD/-Trp-His-Leu-Ade). (B) Non-lethal β-galactosidase assay. The expressed prey proteins (AD) are indicated above and the bait proteins (BD) to the left of the panels. (C and D) The interaction strength of OsMAGO1/2 and OsY14a/b using ONPG as substrate. P: prey; B: bait. The experiments were repeated three times. The average enzyme activity and the standard deviation are presented. The significance was evaluated by two-tailed *t*-test. * indicates $P < 0.05$, and ** indicate $P < 0.01$.

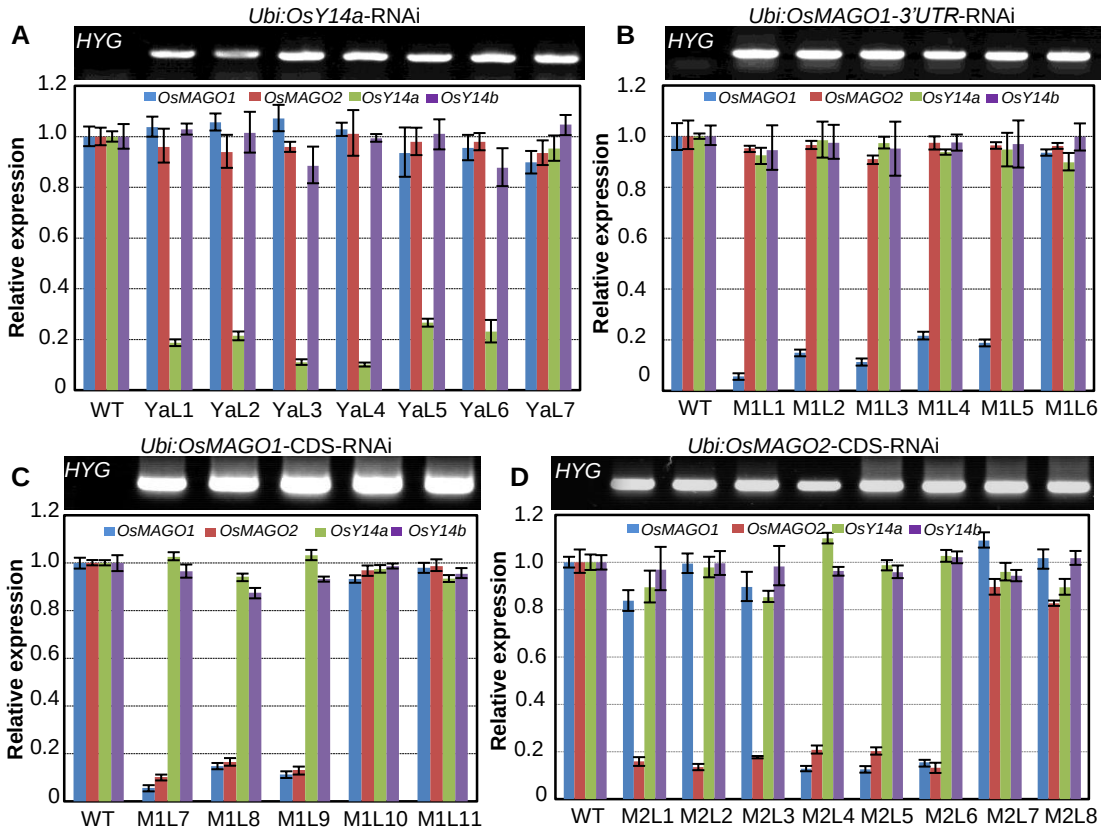

Figure S3. Genotyping Analyses of the RNAi Transgenic Rice Plants.
(A) *Ubi:OsY14a*-RNAi. (B) *Ubi:OsMAGO1*-3'UTR-RNAi. (C) *Ubi:OsMAGO1*-CDS-RNAi. (D) *Ubi:OsMAGO2*-CDS-RNAi. *OsACTIN1* was used as an internal control. The expressions were detected with three independent biological samples. . The expression for each gene in wild-type was set to 1. The average expression and the standard deviation are presented. Hygromycin resistant gene (*HYG*) expression was determined by RT-PCR.

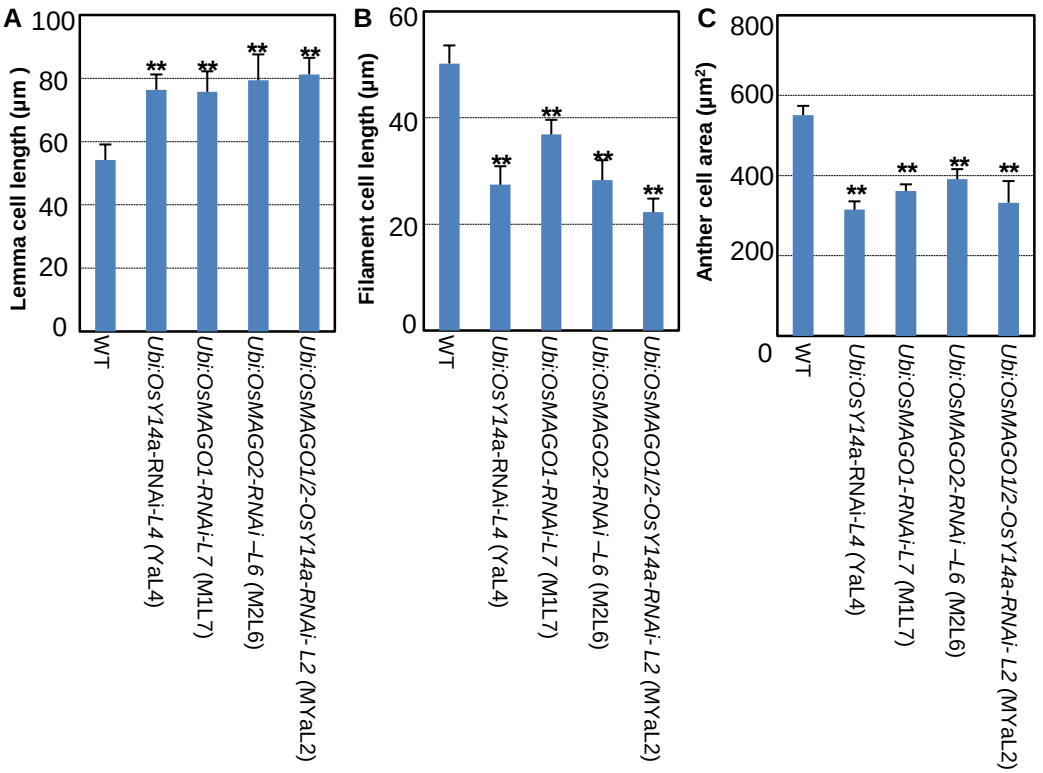

Figure S4. Variation in Cell Size in the Wild Type and Transgenic Rice Plants.
(A) Cell length of lemma. (B) Cell length of filament. (C) Cell area of anther. A two-tailed *t*-test was used determine the significance of means. ** indicate $P < 0.01$.

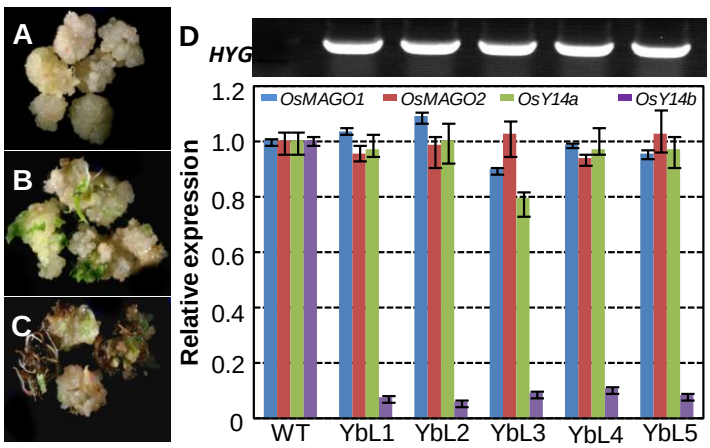

Figure S5. *Ubi:OsY14b*-RNAi Transgenic Rice Plants.
(A-C) Callus on MS medium with hygromycin for 2, 6 weeks and 2 months. (D) Gene expression of *OsMAGO1*, *OsMAGO2*, *OSY14a* and *OsY14b* in different *Ubi:OsY14b*-RNAi callus (green points, randomly picked as YbL1-YbL5). Expression of the gene resistance to hygromycin (*HYG*) was checked by RT-PCR. *OsACTIN1* was used as an internal control. Three-time PCR based on one biological sample were performed. The expression for each gene in wild-type was set to 1. The average expression and the standard deviation are presented. The results indicate a lethal effect of downregulating *OsY14b*.

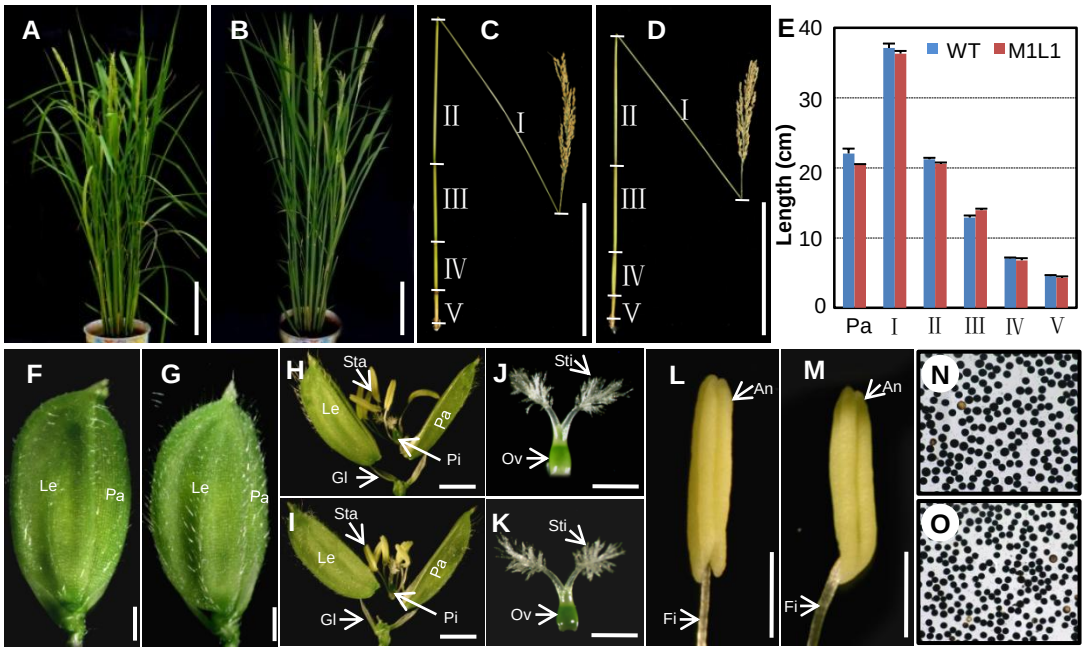

Figure S6. Phenotype of *OsMAGO1-3'UTR*-RNAi Transgenic Rice Plants.
(A and B) Rice plant at heading stage of wild-type (WT) and *OsMAGO1*-3'UTR RNAi line 1 (M1L1). Bars = 20 cm. (C and D) Internodes and panicle of wild-type (WT) and M1L1 after seed maturation. Bars = 20 cm. (E) Size quantification of the internode (I to V, where I is the uppermost) and panicle (Pa) between WT and M1L1. (F and G) Floret of WT and M1L1. Bars = 1 mm. (H and I) Artificial opened floret of WT and M1L1. Bars = 1 mm. (J and K) Pistil of WT and M1L1. Bars = 1 mm. (L and M) Stamen of WT and M1L1. Bars = 1 mm. Glumes (Gl), lemma (Le), palea (Pa), stamen (Sta), anther (An), filament (Fi), pistil (Pi), stigma (Sti) and ovary (Ov) are indicated in F-M. (N and O) The I_2-KI staining pollen grains of the WT and M1L1.

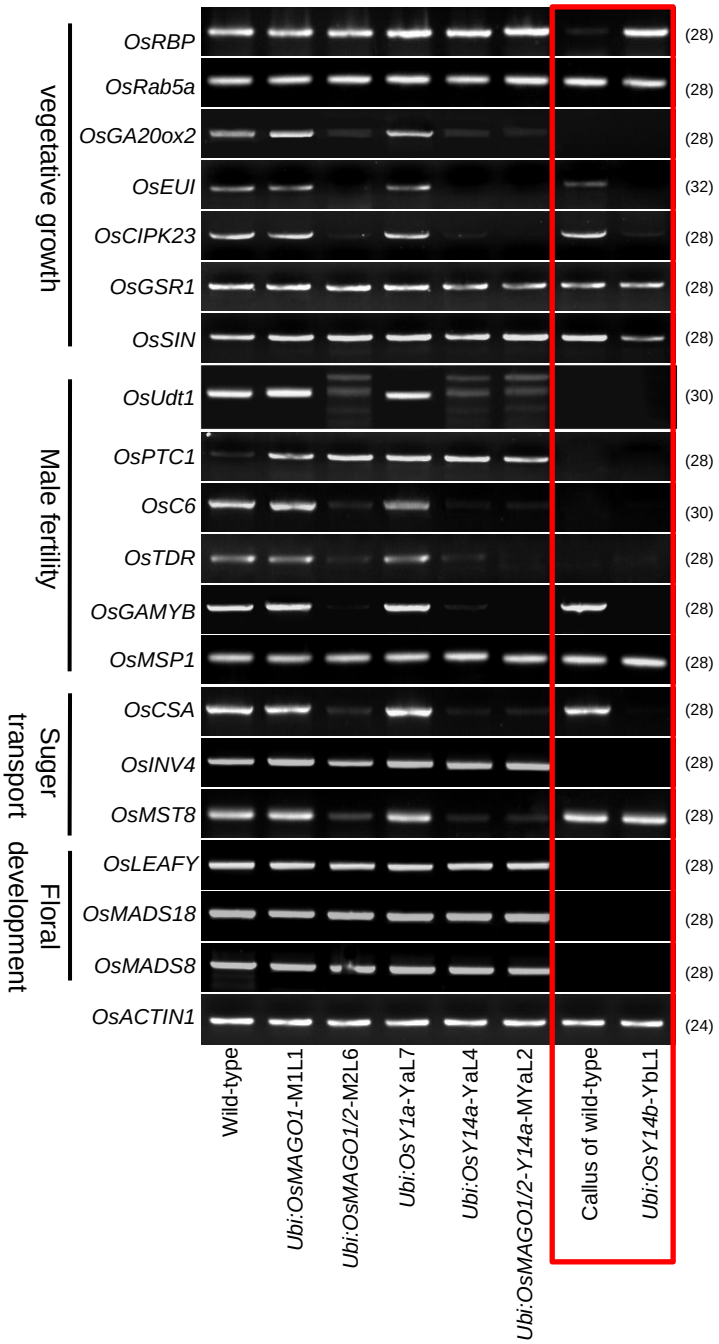

Figure S7. Gene Expression Profiles in the Transgenic Rice Plants.
Expression of 20 genes as indicated was revealed using RT-PCR in different genotypes indicated. The primers for each gene basically flank the whole coding region. The amplification cycle for each gene was given in the parenthesis. In *Ubi:OsY14b* line, callus was used to isolate the total RNA and wild-type callus was used as a control for all gene expression. In other backgrounds, the panicles were sampled for expression analyses with an exception of *OsGA20ox2* and *OsGSR1* sampled from flag leaves of these lines. The gene expression in callus of wild-type and *Ubi:OsY14b* are boxed in red. The information of these genes is presented in Table S4.

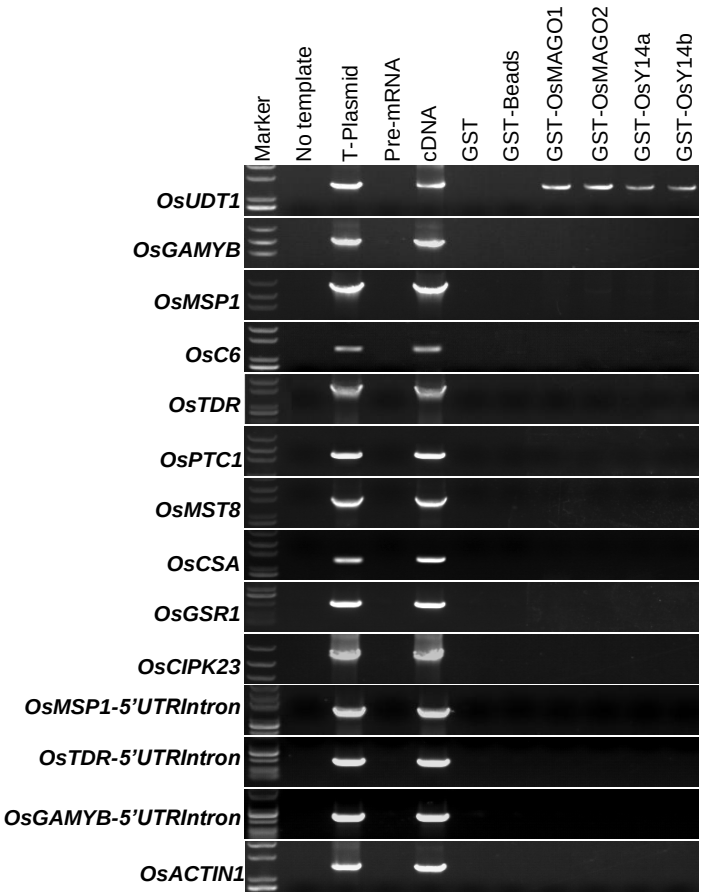

Figure S8. Rice MAGO and Y14 Specifically Bind to the *OsUDT1* Pre-mRNA. Saturated RT-PCR of different cDNAs indicated from the GST-MAGO and GST-Y14 beads. The "No template" and "pre-mRNA" were as negative controls, and plasmids and the corresponding cDNAs were used as positive controls. 1 μg GST, Glutathione beads (GST-Beads), GST-MAGO and GST-Y14, were separately incubated with 250 ng different pre-mRNAs indicated.

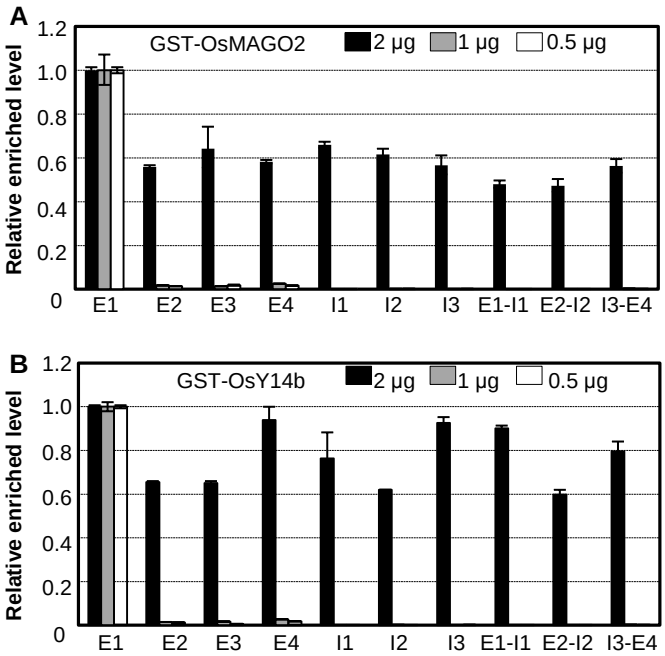

Figure S9. OsMAGO2 and OsY14b Proteins Bind to the *OsUDT1* Pre-mRNA. (A and B) Pre-mRNA competitive binding assays. The mixture of each exon (E) and intron (I) pre-mRNA fragment (125ng each) was incubated with the indicated concentrations of GST-OsMAGO2 (A) or GST-Y14b (B). Relative enriched level of the bond pre-mRNA was shown by qRT-PCR assays. The bound E1 pre-mRNA level was set to 1. Each experiment was performed with three independent samples, and error bars represent standard deviations.

Table S1. Transformation of Rice RNAi Lines.

RNAi construct	Callus number	Resistant callus (HYG^+)	Transformation efficiency (%)	Resistant seedlings
Ubi:OsY14a	95	8	8.42	48
Ubi:OsY14b	405	33	8.15	0
Ubi:OsMAGO1-3'UTR	167	15	8.98	45
Ubi:OsMAGO1-CDS	310	19	6.13	57
Ubi:OsMAGO2-CDS	285	18	6.32	72
Ubi:OsMAGO1-CDS-OsY14a	102	9	8.82	36

Table S2. Phenotypic Variations in RNAi Transgenic Rice Plants.

Gene for silencing	Lines	Plant height (cm)	Floret length (mm)	Anther length (μm)	Filament length (μm)	Pollen maturation (%)	Seed setting rate (%)
	WT	104.97±2.31	6.99±0.17	2780.39±111.81	2330.99±133.32	95.89	93.27±0.5
OsY14a	**YaL1**	**62.13±2.25****	**7.50±0.25****	**2268.13±143.41****	**1947.10±120.90****	**21.64****	**15.43±0.43****
	YaL2	**62.13±3.12****	**7.45 ±0.19****	**2213.83±145.24****	**1954.83±135.42****	**22.37****	**17.63±0.42****
	YaL3	**63.25±3.12****	**7.47 ±0.16****	**2238.25±120.28****	**1978.34±123.35****	**24.85****	**15.34±0.61****
	YaL4	**62.55±2.22****	**7.52±0.23****	**2179.16±113.51****	**1953.19±125.92****	**25.62****	**10.35±0.42****
	YaL5	**62.39±2.21****	**7.39 ±0.19****	**2272.59±156.28****	**1898.85±135.12****	**24.75****	**10.21±0.36****
	YaL6	**64.67±3.21****	**7.43 ±0.13****	**2225.37±125.13****	**1918.12±123.38****	**21.59****	**14.12±0.33****
	YaL7	103.54±2.30	6.98±0.12	2785.12±121.51	2332.21±103.23	95.49	92.15±0.19
OsY14b	**Transgenic plants were not generated indicating that the importance of OsY14b in embryonic organogenesis.**						
OsMAGO1 3'UTR	M1L1	102.5±2.46	6.98±0.14	2735.62±125.36	2369.38±162.62	96.12	94.33±0.25
	M1L2	103.13±2.59	6.88±0.15	2719.54±131.32	2354.32±156.32	95.23	95.14±0.21
	M1L3	102.25±2.36	6.95±0.13	2752.32±151.25	2338.26±167.23	96.25	92.65±0.34
	M1L4	103.55±2.28	7.03±0.15	2746.98±136.24	2312.36±151.21	96.54	93.78±0.46
	M1L5	101.40±2.54	7.11±0.16	2769.12±127.63	2321.65±165.84	95.21	91.12±0.18
	M1L6	104.67±2.42	6.98±0.16	2783.25±121.21	2331.09±113.22	95.43	94.63±0.37
OsMAGO1 CDS	**M1L7**	**67.97±2.21****	**7.42±0.17****	**2474.84±121.83****	**1970.80±127.45****	**20.83****	**12.54±0.32****
	M1L8	**68.33±3.15****	**7.35±0.43***	**2413.83±118.84****	**2003.93±117.45****	**32.61****	**17.96±0.25****
	M1L9	**68.17±3.18****	**7.39±0.15****	**2435.27±108.32****	**1985.64±105.37****	**22.45****	**13.36±0.46****
	M1L10	104.88±3.21	7.00±0.13	2753.31±100.11	2325.94±126.12	93.24	93.45±0.62
	M1L11	105.02±3.25	7.01±0.15	2782.63±103.23	2333.14±106.31	96.02	92.55±0.49
OsMAGO2 CDS	M2L1	na	na	na	na	93.12	92.35±0.36
	M2L2	na	na	na	na	92.35	93.66±0.43
	M2L3	na	na	na	na	94.53	91.86±0.56
	M2L4	**63.61±2.55****	**7.59±0.26****	**2206.15±120.96****	**1932.96±188.27****	**12.88****	**11.55±0.21****
	M2L5	**64.52±2.36****	**7.69±0.29****	**2212.34±120.98****	**1858.01±281.05****	**13.56****	**11.95±0.25****
	M2L6	**62.45±2.70****	**7.73±0.25****	**2195.63±110.22****	**1862.25±256.62****	**12.43****	**9.37±0.34****
	M2L7	101.32±2.37	7.02±0.18	2769.95±100.93	2315.96±113.25	94.62	94.33±0.43
	M2L8	102.65±2.33	6.95±0.23	2778.69±102.65	2328.12±124.63	94.73	93.74±0.32
OsMAGO1 OsMAGO2 OsY14a *(OsMAGO1-CDS-OsY14a)*	**MYaL1**	**52.93±2.88****	**7.56±0.21****	**1725.22±49.54****	**1852.22±77.38****	**10.32****	**9.22±0.32****
	MYaL2	**55.13±2.63****	**7.62 ±0.15****	**1722.36±54.32****	**1836.33±69.86****	**5.49****	**8.35±0.21****
	MYaL3	**57.25±2.32****	**7.48 ±0.13****	**1698.65±54.36****	**1795.22±83.59****	**7.86****	**10.23±0.64****
	MYaL4	**53.55±2.25****	**7. 61±0.12****	**1702.33±49.59****	**1802.34±75.63****	**6.43****	**10.59±0.33****
	MYaL5	**54.39±2.35****	**7.39 ±0.11****	**1695.21±51.20****	**898.85±66.652****	**15.92****	**11.33±0.25****
	MYaL6	**64.65±2.42****	**7.45 ±0.16****	**1688.87±59.63****	**1798.12±59.87****	**12.59****	**12.72±0.54****
	MYaL7	101.54±2.52	7.12±0.09	2654.28±69.61	2302.15±59.64	90.03	91.99±0.38

Transgenic plants with obvious phenotype are showed by overstriking letters and numbers, while the WT and WT-like transgenic plants are in normal. CDS, coding regions. 3'UTR, 3' untranslated regions. WT, wild-type. na, not analyzed. *T*-tests, * P <0.05, ** P < 0.01.

Table S3. Ovary Fertility Comparison between the Wild-Type and Transgenic Rice Plants.

	WT	*Ubi:OsY14a*-YaL4	*Ubi:OsMAGO1*-CDS-M1L7	*Ubi:OsMAGO2*-CDS-M2L6	*Ubi:OsMAGO1-CDS-OsY14a*-MYaL2	*Ubi:OsMAGO1-3'UTR*-M1L1
Ovary fertility (%)	68.63	65.37	67.21	64.39	61.38	69.33
Number	N=118	N=109	N=112	N=125	N=115	N=117

Table S4. Gene Information Used in Expression Studies.

Gene name	Accession No. Of CDS (Phytozome)	Sequence length (bp)	Exon number	Intron number	Largest intron length (bp)	Near centrosome area
OsRBP	LOC_Os12g01916.1	3986	4	3	2163 (2)	no
OsRBA5A	LOC_Os12g43550.1	2922	6	5	859 (3)	no
OsGA20OX2	LOC_Os01g66100.1	2827	3	2	1471 (2)	no
OsEUI	LOC_Os05g40384.1	9784	2	1	7874 (1)	no
OsCIPK23	LOC_Os07g05620.1	4075	14	13	595 (2)	no
OsGSR1	LOC_Os06g15620.1	475	2	1	104 (1)	no
OsSIN	LOC_Os03g22510.1	330	1	0	0	no
OsUDT1	LOC_Os07g36460.1	1830	4	3	521 (2)	no
OsPTC1	LOC_Os09g27620.1	2215	3	2	101 (2)	no
OsC6	LOC_Os11g37280.1	1067	2	1	591 (1)	no
OsTDR	LOC_Os02g02820.1	2987	8	7	337 (1)	no
OsGAMYB	LOC_Os01g59660.1	3946	4	3	1257 (2)	no
OsMSP1	LOC_Os01g68870.2	6977	4	3	2091 (2)	no
OsCSA	LOC_Os01g16810.1	1217	2	1	81 (1)	no
OsINV4	LOC_Os04g33720.1	2461	6	5	223 (1)	no
OsMST8	LOC_Os01g38670.1	2084	4	3	291 (2)	no
OsLEAFY	LOC_Os04g51000.1	3014	3	2	1555 (2)	no
OsMADS8	LOC_Os09g32948.1	6032	8	7	2606 (1)	no
OsMADS18	LOC_Os07g41370.1	4955	8	7	2726 (1)	no
OsACTIN	LOC_Os03g50885.1	1558	4	3	249 (2)	no

Sequence length ranges from the putative transcription initiation site to the stop codon. The “no” indicates the gene is not near the centrosome. The location of the largest intron in each gene is given in parenthesis.

Table S5. List of Primers Used in the Present Study.

Usage	Gene name	Forward sequences (5'-3')	Reverse sequences (5'-3')
RNA-binding	*OsUDT1*	GAGTTTGAGACTTGAGGCTGC	AGTGTCTCAGATGCTTGGAAC
	OsGAMYB	ATGTATCGGGTGAAGAGCGAGAG	TTTGAATTCTGACATTTCACAGGC
	OsGAMYB-5UTRIntron	TGTTCTTGCGGAATTCTGGC	CTACACCGGAAAATTTGGAAG
	OsMSP1	TCCAATAGTTTCTGGCTTTTCATCCTG	CATGTCCCTGGAGACGGTCACCACCAG
	OsMSP1-5UTRIntron	GGTGAAGCGAGGTTCTGGAC	TTGAACATGTAATGGCCGAAC
	OsC6	AGCTAGCTCAAGCTCTAATCCAC	CATATATACTCAGGCAGATGGAGC
	OsTDR	TGATCACCACATGGGAAGAGGAG	CAATCAAACGCGAGGTAATGCAGG
	OsTDR-5UTRIntron	GAAGGTATCTTTCTTTCTCTGC	CTAGCAGTGACACATGAAAGC
	OsPTC1	ATGGCGCCTAAGATGGTGATCAG	TGCAGCAGCCTCAGCTCCATG
	OsMST8	ATGGCCGGCGGCGCCATGACCGAC	GCAATGGATCGATGTAGCCAGCAG
	OsCSA	ATGGCTCACGAGATGATGGGTG	CGTCGCCGGTAATCATGTCGC
	OsGSR1	TAAGTCCCTAACCCACCCAAAC	AAGGCATGCATCTTAGGGGC
	OsCIPK23	GATCTGAGAGGGACAGGGGAAG	GTTTTCCTGGCTGGTTATCTAC
	OsUDT1-Exon1	AGTTTGAGACTTGAGGCTGC	CTTGGTGATCTTGGGCACGAC
	OsUDT1-Exon2	ATGAGCAAGGAGGCCACCTTG	CTGATAATGGGCGTTCTCAG
	OsUDT1-Exon3	GGTCAGGTGGAATTGATCTC	CTCGATGGTGAAGAAACTCTC
	OsUDT1-Exon4	GTGAAGGGTGAGCAGGATGTTG	AGTGTCTCAGATGCTTGGAAC
	OsUDT1-Exon1-Intron1	AAGAACCTGGAGGCCGAGCGG	TTCCAGAGAATCGAGAGAGGG
	OsUDT1-Exon2-Intron2	CTTGGGAGAAGCAAGGCAGCG	TGTTCAGAATTAGTCCCAGGG
	OsUDT1Intron3-Exon4	ATTGCATGTAGATTTCGCTG	AGTGTCTCAGATGCTTGGAAC
RT-PCR for gene expression	*OsRBP*	GAGGTGGGAATGGACATGCCGC	CTACTCCTTTACGACCCTAGCG
	OsRAB5A	ATCCCTCATCCGATCTGAATC	GTTGTCACATACTCCACACTTG
	OsGA20OX2	ATGGACTCCACCGCCGGCTCTG	CCAGGTGAAGTCCGGGTAGTGCTG
	OsEUI	GAAAGAGAGAGTAGGCTGCC	TGTAGAACTCCGGCGCGATGAC
	OsCIPK23	GATCTGAGAGGGACAGGGGAAG	GTTTTCCTGGCTGGTTATCTAC
	OsGSR1	TAAGTCCCTAACCCACCCAAAC	AAGGCATGCATCTTAGGGGC
	OsSIN	GTGAGTTGGATGGCGGGGAC	GCTAGCTAGTTATCAAGGACC
	OsUDT1	GAGTTTGAGACTTGAGGCTGC	AGTGTCTCAGATGCTTGGAAC
	OsPTC1	ATGGCGCCTAAGATGGTGATCAG	CTCCTGGCTGAAGCACGACAG
	OsC6	AGCTAGCTCAAGCTCTAATCCAC	CATATATACTCAGGCAGATGGAGC
	OsTDR	ATGGGAAGAGGAGACCACCTG	ACTTCGTCGTGGTAGTGCTCTCC
	OsGAMYB	ATGTATCGGGTGAAGAGCGAGAG	TTTGAATTCTGACATTTCACAGGC
	OsMSP1	TCCAATAGTTTCTGGCTTTTCATCCTG	CATGTCCCTGGAGACGGTCACCACCAG
	OsINV4	ATGGCGACGGCGAGGGCGAGGGCC	CTACTCCTCCGCGTTCATCTTCGG
	OsCSA	ATGGCTCACGAGATGATGGGTG	CGTCGCCGGTAATCATGTCGC
	OsMST8	ATGGCCGGCGGCGCCATGACCGAC	TCATACTGTGGAGGTAATCTCGAC
	OsLEAFY	ATGGATCCCAACGATGCCTTCTCG	TCTCCGGCGAGCTTAGAACAAGGG
	OsMADS8	ACTCCTCGCACACTTCGGAATTCC	ATGTAGCCAGCAGATTCAATTACG
	OsMADS18	ATGGGGAGAGGGCCGGTGCAG	TCATGTGTGACTTGTCCGGAG
	OsACTIN1	ATGGCTGACGCCGAGGATATCC	GAAGCATTTCCTGTGCACAATGG
RT-PCR	*Hygromycin*	GTCGTCCATCACAGTTTGCC	TGACATTGGGGAGTTTAGCG
qRT-PCR for identification of transgenics	*OsMAGO1*	GAGGATGACAGCAACTGGCCG	CGTTCCCCATCACGATCTCC
	OsMAGO2	CCGGAGGATCATCCAGGAGTC	CACGAAACATTTCAGATCCTG
	OsY14a	GAAGGATGGATTGTGCTAGTC	GCATTCTAAAGCACCATCATCAC
	OsY14b	GGCGATCTCGGACTCCACCTC	CTCAGTCAGTACAACAGCCTC
	OsACTIN1	AGGCTCCTCTCAACCCCAAGGC	GACACCATCACCAGAGTCCAACAC
RNAi	*OsMAGO1-3UTR*	TAGGTACCACTAGTGCTCCTTTCAGTTTCTTAATTG	AGGGATCCGAGCTCCTGCCAAAAGGATGTAAAGAAGC
	OsMAGO1-CDS	TAGGTACCACTAGTGAGTTCTACCTGCGGTACTAC	ATGGATCCGAGCTCTTGAAGTGGAGATTGATGAG
	OsMAGO2-CDS	TAGGTACCACTAGTATGGCGACGGGCGGCGCC	ATGGATCCGAGCTCGTTGCCCATAACAATCTCG
	OsY14a	TAGGTACCACTAGTTGAAGGATGGATTGTGCTAG	ATGGATCCGAGCTCAGTATCTTCTCCTCGGTG
	OsY14b	TAGGTACCACTAGTGGATATGCATTAGTTGAATATG	AGGGATCCGAGCTCGGAAGATATATCACACCATAC
Subcellular Localization	*OsMAGO1*	ATCCATGGCGACGGTGGCCGGC	ATACTAGTAGATTGAATAGGCTTGATCTTG
	OsMAGO2	ATTCTAGATGGCGACGGGCGGCGCCGC	ATGGTACCAGATTGAATAGGCTTGATCTTG
	OsY14a	ATCCATGGCTGCGGTGACCAACG	GCACTAGTGTATCTTCTCCTCGGTGGGGATC
	OsY14b	AACCATGGCGGCGGCGGCGGAGGACG	ATACTAGTACATGTCAAGGCAGCAAGCCTG
BiFC	*OsMAGO1*	ATTCTAGAATGGCGACGGTGGCCGGCGAC	ATACTAGTAGATTGAATAGGCTTGATCTTG
	OsMAGO2	ATTCTAGAATGGCGACGGGCGGCGCC	ATACTAGTAGATTGAATAGGCTTGATCTTG
	OsY14a	ATTCTAGAATGGCTGCGGTGACCAACG	GCACTAGTGTATCTTCTCCTCGGTGGGGATC
	OsY14b	ATTCTAGAATGGCGGCGGCGGCGGAGGACG	ATACTAGTACATGTCAAGGCAGCAAGCCTG