Supplemental Data

OsmiR396d-regulated OsGRFs Function in Floral Organogenesis in Rice through Binding to their Targets *OsJMJ706* and *OsCR4*

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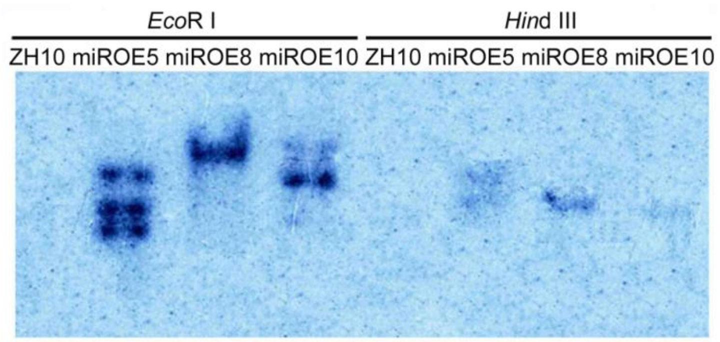
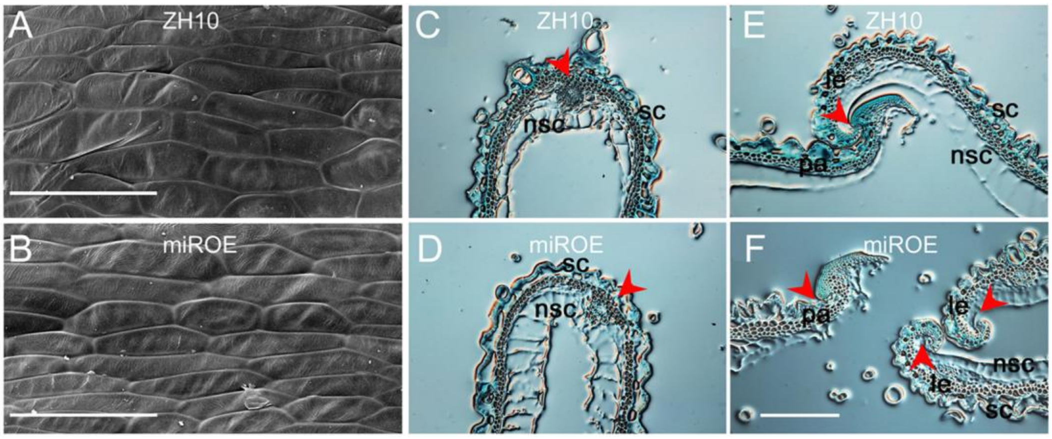
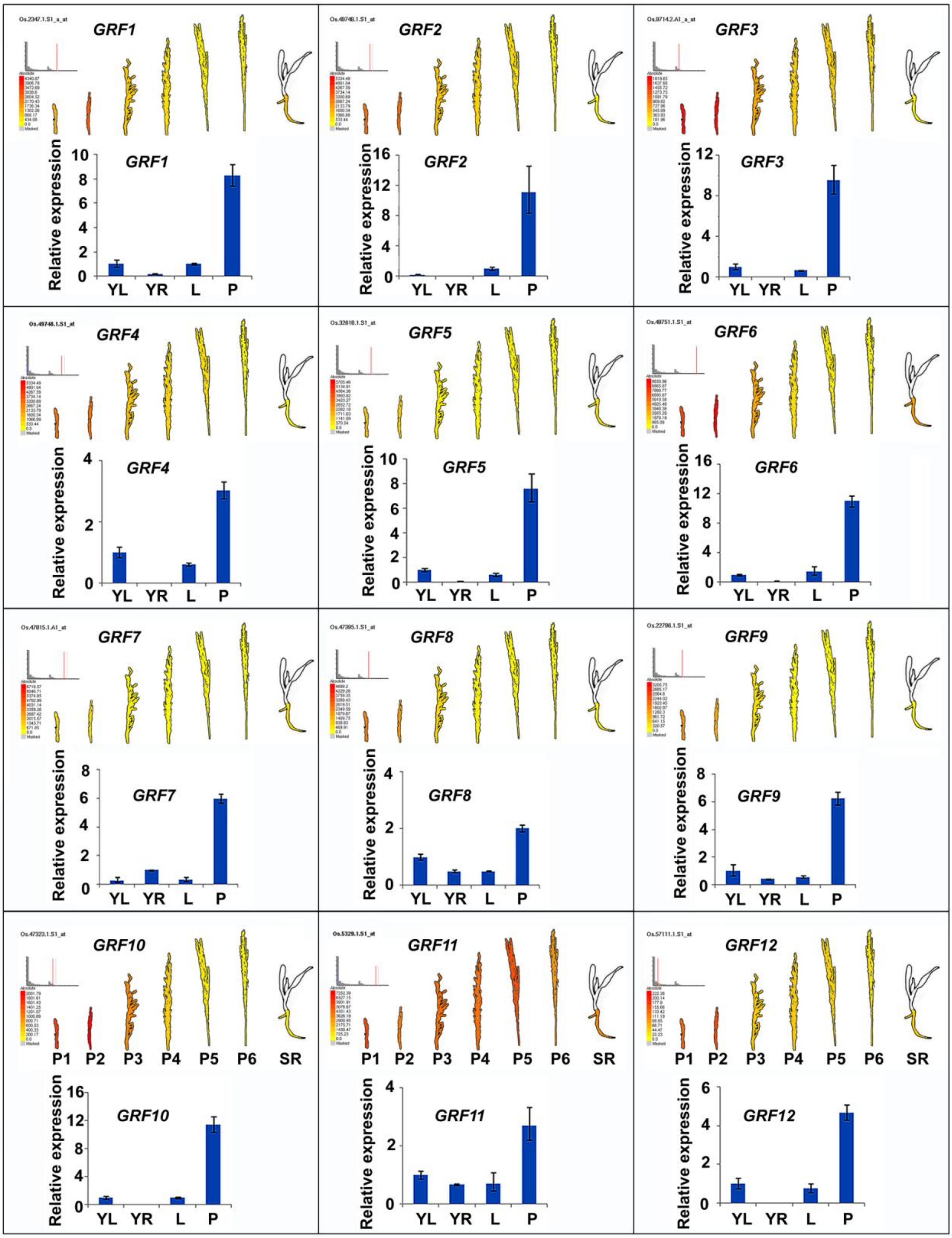


Supplemental Figure S1. Southern blot assay of miROE transformed rice plants. Southern blot assay of genomic DNA isolated from wild type and miROE transformed plants were digested with *Eco*R I or *Hin*d III. The blot was hybridized with the open reading frame of the *GUS* gene labeled with α-^{32}P-dCTP. ZH10, miROE5, miROE8 and miROE10 representing zhonghua10, overexpression (OE) lines of OsmiR396d transgenic rice, respectively.

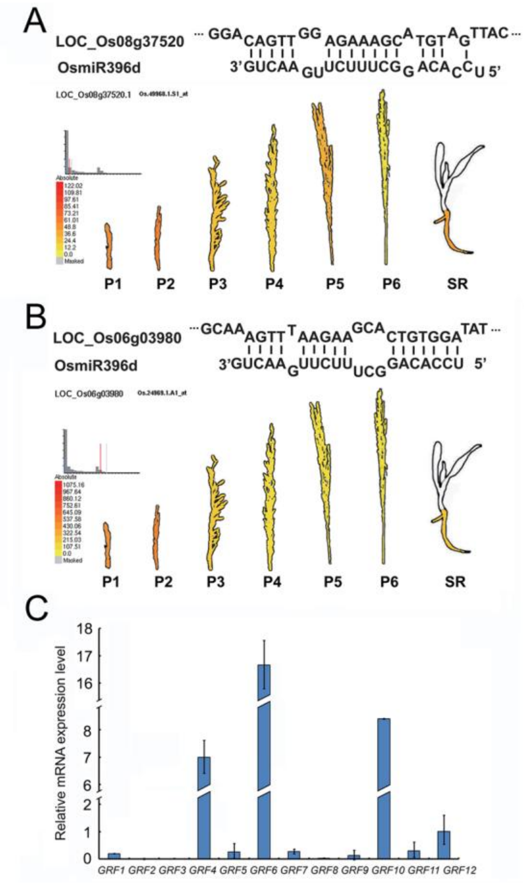


Supplemental Figure S2. Phenotypic analysis of floret inner organs in miROE8 and ZH10. A to B, SEM analysis of the surfaces of lodicules in ZH10 and miROE plants. Scale bars = 50 µm. C to D, Transverse section of lemma of florets in ZH10 and miROE plants. (Red arrowheads indicate the vascular bundles). E to F, Transverse sections of the interlocking regions of florets in ZH10 and miROE plants. (Red arrowheads indicate the interlocking region in E or the self-fusion region in F of the palea and lemma). Scale bars = 200 µm in C to F.

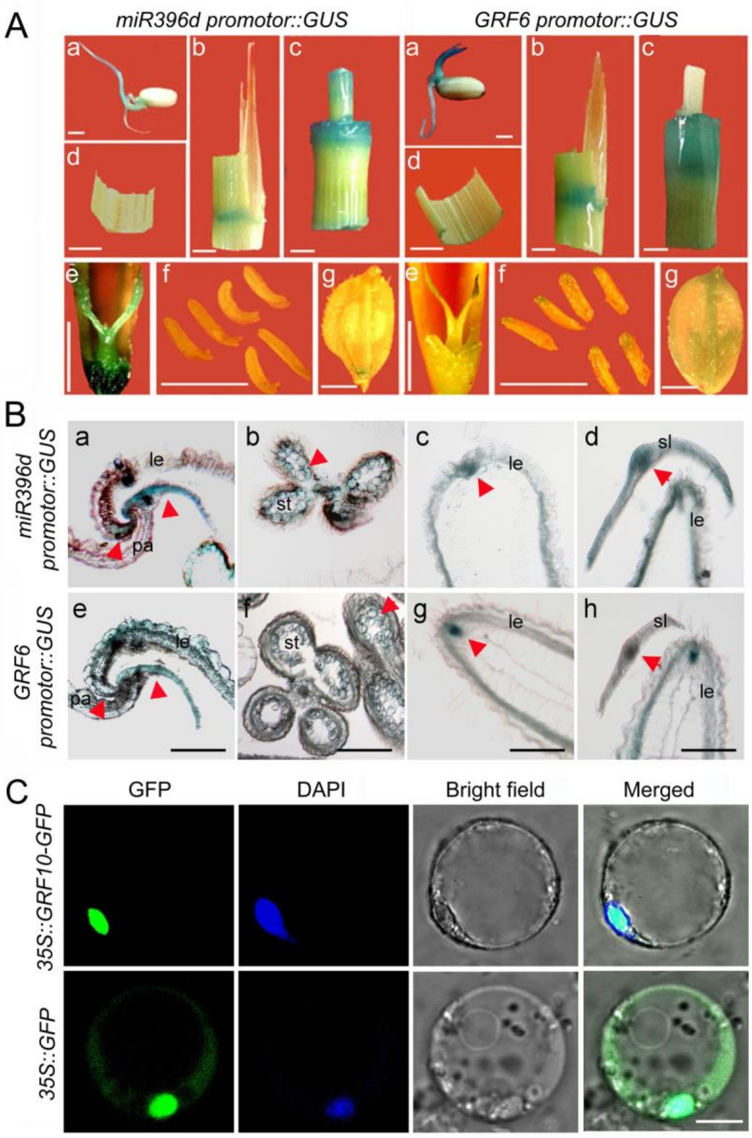


Supplemental Figure S3. Expression patterns of *OsGRF* genes in different tissues. Relative expression levels of *OsGRF* genes based on microarray data displayed in the eFP browser (http://bar.utoronto.ca/efprice/cgi-bin/efpWeb.cgi) in Young Inflorescence (P1), Inflorescence (P2), Inflorescence (P3), Inflorescence (P4), Inflorescence (P5), Inflorescence (P6) and

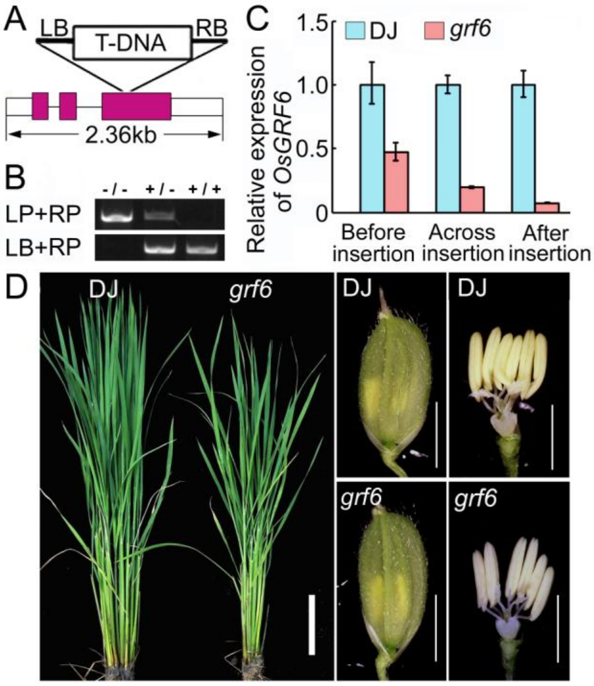
Seedling Root (ST). Color scale shows the microarray signal level. The expression levels of *OsGRF* genes were also detected by RT-Q-PCR in various organs, including Young Leaf (YL), Young Root (YR), leaves (L) and Young panicles (P). Values are means ± SD of three independent experiments.



Supplemental Figure S4. Expression patterns of predicted targets of OsmiR396d and *OsGRF* genes. Expression pattern analysis of two predicated target genes of OsmiR396d are processed by rice eFP browser (http://bar.utoronto.ca/efprice/cgi-bin/efpWeb.cgi) and *OsGRF* genes in young inflorescence of ZH10 by RT-Q-PCR. A to B, Expression pattern analysis of two predicated target genes of OsmiR396d by rice eFP browser. C, Relative expression levels of *OsGRF* genes with Q-RT-PCR in young inflorescence of wild type ZH10, expression level of *OsGRF12* was set as 1. Values are means ± SD of three independent experiments.

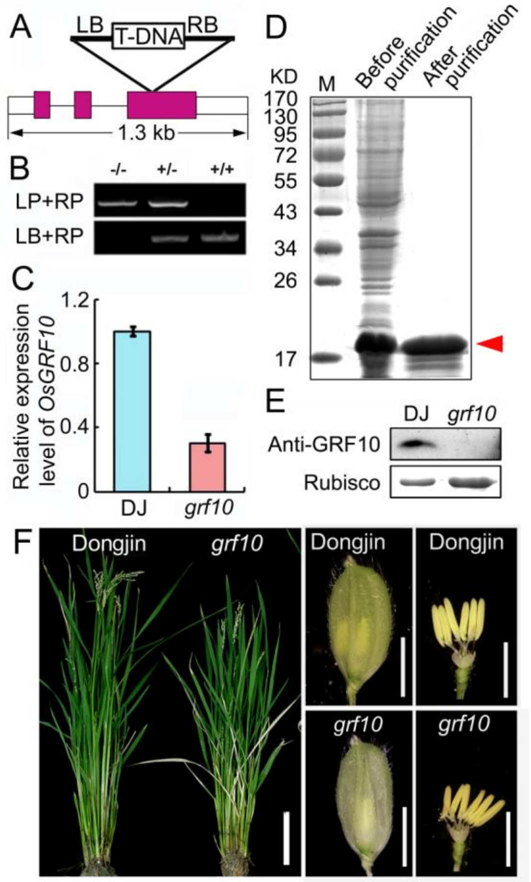


Supplemental Figure S5. Expression pattern of OsmiR396d and its target genes. A, p*OsmiR396d promotor::GUS* and p*OsGRF6 promotor::GUS* expression patterns are shown as GUS staining. (a), Seeds after germinating for 3 days; (b), Pulvinus; (c), Node; (d), Mature leaf; (e), pistil and lodicules; (f), stamens; (g), Old floret. Bars = 2 mm. B, Sections of GUS staining florets in p*OsmiR396d promotor::GUS* and p*OsGRF6 promotor::GUS* plants. Red arrow heads in a-d or e-h indicates the interlocking region of palea and lemma; pollens; the vascular bundles of the lemma and sterile lemma respectively. Pa: palea, le: lemma, st: stamen, sl: sterile lemma. Scale bars = 100 μm. C, Subcellular localization of OsGRF10-GFP in rice leaf protoplast, *35S::GFP* was used as a control. Bar = 10 μm.

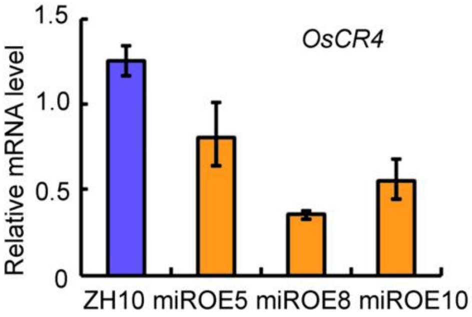


Supplemental Figure S6. Molecular identification of *osgrf6* mutant.

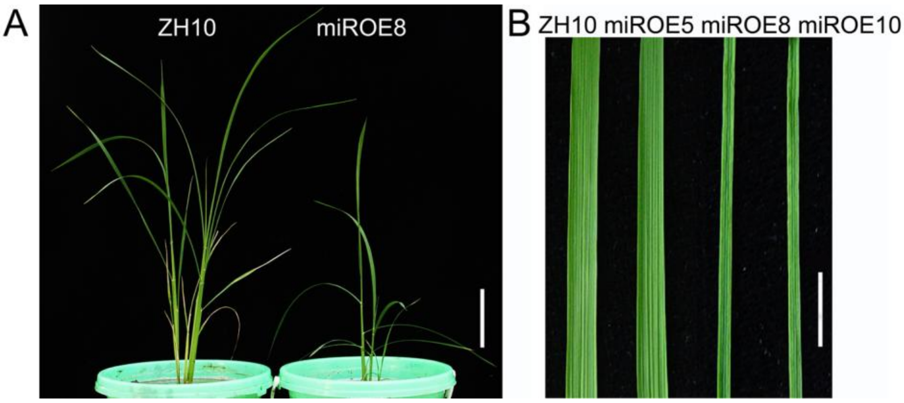
A, Scheme representing the *osgrf6* mutant. B, Genomic identification of the *osgrf6* mutant. DJ (DongJin -/-) is the wild type and +/+ indicates the homozygous mutant. C, Relative expression levels of *OsGRF6* gene before the insertion site, across the insertion site and after the insertion site in DJ (DongJin) and *osgrf6*. Values are means ± SD of three independent experiments. D, Plants of *osgrf6* mutant and the DJ wild type plants (Scale bar = 20 cm) as well as their florets before flowering (Scale bars = 3 mm).



Supplemental Figure S7. Molecular identification of *osgrf10* mutant. A, Scheme representing the *osgrf10* mutant. B, Genomic identification of the *osgrf10* mutant. C, Expression level of *OsGRF10* was detected in *osgrf10* and Dongjin wild type. Values are means ± SD of three independent experiments. D, OsGRF10-His protein was expressed in *E. coli* and purified. The red head indicates the purified OsGRF10-His protein. E, Expression levels of OsGRF10 protein were detected in *osgrf10* and Dongjin wild type plants. The rubisco was used as the loading control. F, Plants of *osgrf10* mutant and the DJ wild type plants (Scale bar = 20 cm) as well as the florets before flowering (Scale bars = 3 mm).



Supplemental Figure S8. Expression levels of *OsCR4* were detected in young spikelets. Values are means ±SD of three independent experiments.



Supplemental Figure S9. Small leaves were occasionally found in miROE plants. Bars = 10 cm in A and 1 cm in B.

Supplemental Table S1. Microarray analysis of OsmiR396d OE plants. (Down-regulated genes with ｜$\log_2$ ratio｜⩾2. P value is showed as $\log_2$ of fold change value.)

Locus[a]	**Description**[b]	**Fold Change ($\log_2$)**[C]
LOC_Os01g45914	expressed protein	-5.9
LOC_Os02g43370	transposon protein, putative, unclassified, expressed	-4.7
LOC_Os03g03724	expressed protein	-4.5
LOC_Os07g34520	isocitrate lyase, putative, expressed	-3.8
LOC_Os03g59330	polygalacturonase, putative, expressed	-3.4
LOC_Os06g38980	polyadenylate-binding protein, putative, expressed	-3.4
LOC_Os08g38810	BURP domain containing protein, expressed	-3.4
LOC_Os08g43290	LTPL44, Protease inhibitor/seed storage/LTP family protein precursor, expressed	-3.3
LOC_Os01g57599	retrotransposon protein, putative, unclassified, expressed	-3.2
LOC_Os05g15300	expressed protein	-3.2
LOC_Os10g38050	HOTHEAD precursor, putative, expressed	-3.2
LOC_Os05g07060	fasciclin domain containing protein, expressed	-3.1
LOC_Os02g30910	nodulin MtN3 family protein, putative, expressed	-3
LOC_Os01g65690	4,5-DOPA dioxygenase extradiol, putative, expressed	-2.9
LOC_Os01g66700	beta-hexosaminidase precursor, putative, expressed	-2.9
LOC_Os05g06670	gibberellin 2-oxidase, putative, expressed	-2.9
LOC_Os09g21370	cysteine proteinase EP-B 1 precursor, putative, expressed	-2.9
LOC_Os04g33080	protein phosphatase 2C, putative, expressed	-2.8
LOC_Os08g05820	monocopper oxidase, putative, expressed	-2.8
LOC_Os09g08190	sulfotransferase domain containing protein, expressed	-2.8
LOC_Os01g65100	peptide transporter, putative, expressed	-2.7
LOC_Os03g32490	DUF1230 domain containing protein, expressed	-2.7
LOC_Os05g31670	AWPM-19-like membrane family protein, putative, expressed	-2.7
LOC_Os06g13390	SAM dependent carboxyl methyltransferase, putative, expressed	-2.7
LOC_Os07g14600	hydrolase, putative, expressed	-2.7
LOC_Os08g03682	cytochrome P450, putative, expressed	-2.7

LOC_Os08g38170	putative, expressed	-2.7
LOC_Os03g53900	universal stress protein domain containing protein, putative, expressed	-2.6
LOC_Os04g33920	LTPL102 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	-2.6
LOC_Os05g48300	purine permease, putative, expressed	-2.6
LOC_Os09g30320	BURP domain containing protein, expressed	-2.6
LOC_Os02g52040	phosphate-induced protein 1 conserved region domain containing protein, expressed	-2.5
LOC_Os09g35800	UDP-glucose 4-epimerase, putative, expressed	-2.5
LOC_Os11g47580	glycosyl hydrolase, putative, expressed	-2.5
LOC_Os04g25440	cytokinin-O-glucosyltransferase 2, putative, expressed	-2.3
LOC_Os07g48550	no apical meristem protein, putative, expressed	-2.3
LOC_Os01g46120	GDSL-like lipase/acylhydrolase, putative, expressed	-2.2
LOC_Os03g61270	OsMan04 - Endo-Beta-Mannanase, expressed	-2.2
LOC_Os04g15920	dehydrogenase, putative, expressed	-2.2
LOC_Os04g44600	CRP1 - Cysteine-rich family protein precursor, expressed	-2.2
LOC_Os05g09740	HAD superfamily phosphatase, putative, expressed	-2.2
LOC_Os07g30640	ubiquitin fusion protein, putative, expressed	-2.2
LOC_Os08g38170	methyladenine glycosylase, putative, expressed	-2.2
LOC_Os10g39770	zinc finger, C3HC4 type, domain containing protein, expressed	-2.2
LOC_Os11g02054	ACT domain containing protein, expressed	-2.2
LOC_Os01g21120	AP2 domain containing protein, expressed	-2.1
LOC_Os01g46720	expressed protein	-2.1
LOC_Os01g48710	heavy metal-associated domain containing protein, expressed	-2.1
LOC_Os01g52130	sulfate transporter, putative, expressed	-2.1
LOC_Os02g17620	isochorismatase family protein, putative, expressed	-2.1
LOC_Os02g35770	homeobox associated leucine zipper, putative, expressed	-2.1
LOC_Os02g47660	basic helix-loop-helix, putative, expressed	-2.1
LOC_Os03g54000	oligopeptide transporter, putative, expressed	-2.1
LOC_Os04g14680	OsAPx3 - Peroxisomal Ascorbate Peroxidase encoding gene 5,8, expressed	-2.1

LOC_Os05g27350	hypothetical protein	-2.1
LOC_Os05g50080	zinc finger C-x8-C-x5-C-x3-H type family protein, expressed	-2.1
LOC_Os01g22352	peroxidase precursor, putative, expressed	-2
LOC_Os01g50750	zinc finger, C3HC4 type domain containing protein, expressed	-2
LOC_Os02g33060	expressed protein	-2
LOC_Os02g48710	expressed protein	-2
LOC_Os03g58350	OsIAA14 - Auxin-responsive Aux/IAA gene family member, expressed	-2
LOC_Os04g28620	male sterility protein, putative, expressed	-2
LOC_Os05g48850	no apical meristem protein, putative, expressed	-2
LOC_Os06g38960	expressed protein	-2
LOC_Os10g42690	**jmjC domain containing protein, expressed**	**-0.3**

a TIGR locus number.

b Gene annotation in the TIGR database.

c Fold change of the OsmiR396d OE plants compared with the wild type. Value is showed as $\log_2$ of fold change value.

Supplemental Table S2. Microarray analysis of OsmiR396d OE plants. (Up-regulated genes with ｜$\log_2$ ratio｜$\geqslant$2. P value is showed as $\log_2$ of fold change value.)

Locus^a	**Description**^{b}	**Fold Change (log$_2$)**^{C}
LOC_Os10g11580	histone-like transcription factor and archaeal histone, putative, expressed	6.4
LOC_Os10g40430	LTPL139 - Protease inhibitor/seed storage/LTP family protein precursor, expressed	5.6
LOC_Os01g60640	OsWRKY21 - Superfamily of TFs having WRKY and zinc finger domains, expressed	5.4
LOC_Os07g18680	retrotransposon, putative, centromere-specific	4.8
LOC_Os06g06490	U-box domain containing heat shock protein, putative, expressed	4.7
LOC_Os06g11830	hAT dimerisation domain-containing protein, putative,	4.7

	expressed	
LOC_Os06g39240	endothelial differentiation-related factor 1, putative, expressed	4.6
LOC_Os05g44340	heat shock protein 101, putative, expressed	4.5
LOC_Os11g31060	IQ calmodulin-binding and BAG domain containing protein, putative, expressed	4.2
LOC_Os01g03680	BBTI8, Bowman-Birk type bran trypsin inhibitor precursor, expressed	4.1
LOC_Os10g26910	transposon protein, putative, CACTA, En/Spm sub-class	3.9
LOC_Os06g31930	thionin precursor protein, putative, expressed	3.5
LOC_Os03g52860	lipoxygenase, putative, expressed	3.4
LOC_Os03g49430	pre-mRNA-splicing factor, putative, expressed	3.3
LOC_Os05g48810	dnaJ domain containing protein, expressed	3.3
LOC_Os03g03980	coiled-coil domain-containing protein 124, putative, expressed	3.1
LOC_Os11g37960	WIP4 - Wound-induced protein precursor, expressed	3
LOC_Os02g07630	copper-transporting ATPase, putative, expressed	2.9
LOC_Os10g34930	secretory protein, putative, expressed	2.9
LOC_Os04g44460	sulfotransferase domain containing protein, expressed	2.9
LOC_Os11g38260	PAP fibrillin family domain containing protein, expressed	2.8
LOC_Os08g34249	inhibitor I family protein, putative	2.8
LOC_Os08g27870	EARLY flowering protein, putative	2.7
LOC_Os04g34490	nodulin, putative, expressed	2.6
LOC_Os01g55270	SGS domain containing protein, expressed	2.6
LOC_Os04g01874	protein kinase, putative, expressed	2.5
LOC_Os05g06920	relA-SpoT like protein RSH4, putative, expressed	2.5
LOC_Os08g36340	potassium transporter, putative, expressed	2.5
LOC_Os02g56900	thioredoxin family protein, putative, expressed	2.4
LOC_Os10g28340	heat stress transcription factor, putative, expressed	2.4
LOC_Os03g57340	chaperone protein dnaJ, putative, expressed	2.4
LOC_Os07g03840	lectin-like receptor kinase, putative, expressed	2.3
LOC_Os10g03050	leucine-rich repeat receptor protein kinase EXS precursor, putative	2.3
LOC_Os04g48030	heat stress transcription factor B-1, putative, expressed	2.2

LOC_Os06g32600	THION15 - Plant thionin family protein precursor, expressed	2.2
LOC_Os04g13220	ABC transporter family protein, putative, expressed	2.2
LOC_Os11g36160	receptor-like protein kinase 2 precursor, putative, expressed	2.1
LOC_Os01g20160	OsHKT1;5 - Na+ transporter, expressed	2.1
LOC_Os09g36700	ribonuclease T2 family domain containing protein, expressed	2.1
LOC_Os05g01444	polygalacturonase inhibitor precursor, putative, expressed	2
LOC_Os01g14410	early light-induced protein, chloroplast precursor, putative, expressed	2
LOC_Os01g03310	BBTI1 - Bowman-Birk type bran trypsin inhibitor precursor, expressed	2
LOC_Os01g35330	circumsporozoite protein precursor, putative, expressed	2

a TIGR locus number.

b Gene annotation in the TIGR database.

c Fold change of the OsmiR396d OE compared with the wild type. Value is showed as $\log_2$ of fold change value.

Supplemental Table S3. Primers used in this work.

Experiment	**Primer name**	**Sequence**
Q-PCR analysis	*Ubi* RT F:	5'-AACCAGCTGAGGCCCAAGA-3'
	Ubi RT R:	5'-AACCAGTCCATGAACCCGG-3'
	OsGIF1 RT F:	5'-CCACCGAGCAGATCCAAAAG-3'
	OsGIF1 RT R:	5'-GAGCACATTCAGCCAACTTCC-3'
	OsGRF1 RT P1:	5'-GCGTACCCGGACTCCAAGTA-3'
	OsGRF1 RT P2:	5'-CAAGGACATTTCCACAGGCTTT-3'
	OsGRF2 RT P1:	5'-GCGTACGGCGAGTCCAAGTA-3'
	OsGRF2 RT P2:	5'-GGGCGGCATTTCCACAG-3'
	OsGRF3 RTP1:	5'-ACTCGCCTCGCGCTTCTAC-3'
	OsGRF3 RTP2:	5'-TCCGGGCTCCGGGT-3'
	OsGRF4 RT P1:	5'-ATTCCAAGTACTGCGAGCGC-3'
	OsGRF4 RT P2:	5'-GGCGACCAGCTGCGTTT-3'
	OsGRF5 RT P1:	5'-ACTCCAAGTACTGCGAGCGC-3'
	OsGRF5 RT P2:	5'-GGGCAGCGGTCTTGGATT-3'

	OsGRF6 RT P1:	5'-CGGACGGACGGCAAG-3'
	OsGRF6 RT P2:	5'-GGTTCATGTGTCGCTCACAG-3'
	OsGRF7 RT P1:	5'-AAGTACTGCGAGCGGCACATA-3'
	OsGRF7 RT P2:	5'-AGATTGGCCTTCCACATGCT-3'
	OsGRF8 RT P1:	5'-TTGTGAGCGACACATAAACCG-3'
	OsGRF8 RT P2:	5'-GCAATGGTGAGTGTCGCCTT-3'
	OsGRF9 RT P1:	5'-CACATCAACAGAAACCGCCA-3'
	OsGRF9 RT P2:	5'-CAGCACACGGTGTCTCTTTCAC-3'
	OsGRF10 RT P1:	5'-ACAAGGCGACGGCGC-3'
	OsGRF10 RT P2:	5'-GCGAAGTAGCGGTAGATGAGC-3'
	OsGRF11 RT P1:	5'-GGAAGAGTGTTACTGGTGCATCT-3'
	OsGRF11 RT P2:	5'-AGTCCAAGCAGAGTGTTGCC-3'
	OsGRF12 RT P1:	5'-GGCCGTTCAAGAAAGCCTATG-3'
	OsGRF12 RT P2:	5'-GGACCGGGAGATATGTGGG-3'
	GRF6-as RT p1:	5'-GCCTGGTGTGAGCTTCTTGAT-3'
	GRF6-as RT p2:	5'-TGAATCGTTTCCTCATGCCTG-3'
	JMJ706 RT P1:	5'-GTCCGACCAAAGCGACTGAA-3'
	JMJ706 RT P2:	5'-GCTCAACCACTCTGTTCGTGC-3'
	MADS47 RT P1:	5'-TGCACAGGCTGAATGTGGAA-3'
	MADS47 RT P2:	5'-CCTAGACCGGACTCGAGGCT-3'
	DH1 RT P1:	5'-GCGATGATGAGATCAACCTCC-3'
	DH1 RT P2:	5'-CAAAGCGTTGCATTGTTTGATTT-3'
	CR4 RT P1:	5'-GGAAATCCTCGGCATCTGAA-3'
	CR4 RT P2:	5'-TCCCAACGTTCCTTCCATCT-3'
	396d stem-loop:	5'-GTCTCCTCTGGTGCAGGGTCCGAGGTATTCGCACCAGAGGAGACMAGTTC-3'
	396 stem loop P1:	5'-GGCGGTCCACAGGCTTTCTT-3'
	396 stem loop p2:	5'-TGGTGCAGGGTCCGAGGTATT-3´
	U6 P1:	5´-GGGACATCCGATAAAATTGGAA-3´
	U6 P2:	5´-CGATTTGTGCGTGTCATCCTT -3´
ChIP	*JMJ706* a p1:	5´-CCAATTCATACAAACCGTTGGTG-3´
	JMJ706 a p2:	5´-TGTGCAAAATCTGGGAAGGC-3´
	JMJ706 b p1:	5´-TGACTTGGTTGGGACTTGCC-3´
	JMJ706 b p2:	5´-AGAGTGAACAAGCACCAACGG-3´
	JMJ706 c p1:	5´-TCTGACCACGTCCAGTCCAC-3´
	JMJ706 c p2:	5´-AATGTAGGGCCTTGGAAGAGAAA-3´
	JMJ706 d p1:	5´-CTAATTTGGCCCCGGGTC-3´

	JMJ706 d p2:	5´-TTGTGGCCCGGTCTAAGGTA-3´
	CR4 a p1:	5´-GCTGTTGCAAAGGTGGAGGA-3´
	CR4 a p2:	5´-GTGGAAGCATACAATCCCCAAT-3´
	CR4 b p1:	5´-GCAAAAGGCGAAGGTGAGAG-3´
	CR4 b p2:	5´-GCGATGGTAAATGGGAGAATTG-3´
	CR4 c p1:	5´-TTGTTGCGTAACCGTATTTCTGT-3´
	CR4 c p2:	5´-GGGATTCAGATGATGCAGGA-3´
EMSA	*JMJ706* P1P1:	5´-CACTCTGCTGTCTCTGTTGGTCAATGCCAC-3´
	JMJ706 P1P2:	5´-GTGGCATTGACCAACAGAGACAGCAGAGTG-3´
	JMJ706 M1P1:	5´-CACTCTGCTGTCTGGGAAGGTCAATGCCAC-3´
	JMJ706 M1P2:	5´-GTGGCATTGACCTTCCCAGACAGCAGAGTG-3´
	JMJ706 M2P1:	5´-CACTCTGCTGTCTCCCCCGGTCAATGCCAC-3´
	JMJ706 M2P2:	5´-GTGGCATTGACCGGGGGAGACAGCAGAGTG-3´
	CR4 P1P1:	5´-TAACCGTATTTCTGTTAAAATCCCGTG-3´
	CR4 P1P2:	5´-CACGGGATTTTAACAGAAATACGGTTA-3´
Subcellular localization	*OsGRF6* P1:	5´-GC TCTAGA ATGCAGGGTGCAATG-3´
	OsGRF6 P2:	5´-GG GGTACC CACCAGGCGGATGC-3´
	OsGRF10 P1:	5´-TGCTCTAGA ATGGATGAGGAGAAG-3´
	OsGRF10 P2:	5´-GGGGTACC GGTGGCGCGCGCGG-3´
Mutant identify	2715 LB:	5´-TTGGGGTTTCTACAGGACGTAAC-3´
	OsGRF6 MT LP:	5´-TCGCTATCAACCATCAGCAC-3´
	OsGRF6 MT RP:	5´-AAAACCTCTCCCAATGGTCC-3´
	2707-LB:	5´-GGTGAATGGCATCGTTTGAA-3´
	GRF10 LP :	5´-TCATTCCTCTTCCCACCAAG-3´
	GRF10 RP :	5´-ACGGTGAGAATTGTTTTGGC-3´
Luciferase and GUS assay	*OsGIF1* P1:	5'-TCCCCCGGGGATGCAGCAGCAGATG-3'
	*OsGIF1*P2:	5'-GCGTCGACGGATTGATCGCCG-3'
	OsGIF2 p1:	5´-TCCCCCGGGGATGCAGCAGCAGCCG-3´
	OsGIF2 p2:	5´-GCGTCGACGGATTGATCGCC-3´
	OsGRF6 P1:	5´-TCCCCCGGGGATGCAGGGTGCAATGGC-3´
	OsGRF6 P2:	5´-GCGTCGACCACCAGGCGGATGC-3´

	OsGRF10 p1:	5´-TCCCCCGGGGATGGATGAGGAGAAG-3´
	OsGRF10 P2:	5´-GCGTCGACGGTGGCGCGCGGTGCC-3´
	JMJ706 promoter P1:	5´-CCCAAGCTTACGACACGACACCACACG-3´
	JMJ706 promoter P2:	5´-AAAACTGCAGTAGGTGTTTCTGCCCTCCAC-3´
	CR4 promoter P1:	5´-AAAACTGCAG ATCCCAATGCAAGTATTCG-3´
	CR4 promoter P2:	5´-GAAGATCTTTCTTGAAACTTGGAGGGGTC-3´
RNA *in situ* hybridization	*T7-OsGRF6*-F1	5´-TAATACGACTCACTATAGGGGAGAAGCTGATGTTGTCAC-3´
	OsGRF6-R1	5´-GACTCCGATAGGCAATTC-3´
	OsGRF6-F2	5´- GAGAAGCTGATGTTGTCAC-3´
	T7-OsGRF6-R2	5´-TAATACGACTCACTATAGGGGACTCCGATAGGCAATTC-3´
	T7-OsGRF10-F1	5´-TAATACGACTCACTATAGGGATGGATGAGGAGAAGGAAG-3´
	OsGRF10-R1	5´-CATGAACGTCAGCGCCGTC-3´
	OsGRF10-F2	5´-ATGGATGAGGAGAAGGAAG-3´
	T7-OsGRF10-R2	5´-TAATACGACTCACTATAGGGCATGAACGTCAGCGCCGTC-3´
	T7-JMJ706-F1	5´-TAATACGACTCACTATAGGGATGCAACAGGTGGAGGGC-3´
	JMJ706-R1	5´-TAGAGCTGTGCCATTGTTAG-3´
	JMJ706-F2	5´-ATGCAACAGGTGGAGGGC-3´
	T7-JMJ706-R2	5´-TAATACGACTCACTATAGGGTAGAGCTGTGCCATTGTTAG-3´
	T7-CR4-F1	5´-TAATACGACTCACTATAGGGATGGACATTGTGCCTGTTG-3´
	CR4-R1	5´-CGAACGGGATCCTGCTG-3´
	CR4-F2	5´-ATGGACATTGTGCCTGTTG-3´
	T7-CR4-R2	5´-TAATACGACTCACTATAGGGCGAACGGGATCCTGCTG-3´
	T7-Actin-F1	5´-TAATACGACTCACTATAGGGGTCAGCCACACCGTGCCAATC-3´
	Actin-R1	5´-TGTCCCTTACAATTTCCCG-3´
	Actin-F2	5´-GTCAGCCACACCGTGCCAATC-3´

	T7-Actin-R2	5´-TAATACGACTCACTATAGGGTGTCCCTTACAATTTCCCG-3´
Yeast two hybrid	*OsGIF1* N p1:	5'-CGGAATTCATGCAGCAGCAGATG-3'
	OsGIF1 N p2:	5'-CGGGATCCCGACATGTATTGCCC-3'
	OsGIF1 C p1:	5'-CGGAATTCCAGGTGCCAATGTTC-3'
	OsGIF1 C p2:	5'-CGGGATCCGGATTGATCGCCG-3'
	OsGIF2 Np1:	5'-CGGAATTCATGCAGCAGCAGCCG-3'
	OsGIF2 N p2:	5'-CGGGATCCCCCAGCACCTGGGGTAG-3'
	OsGIF2 C p1:	5'-CGGAATTCCATTACATGTCCCAAG-3'
	OsGIF2 C p2:	5´-CGGGATCCTTAGGATTGATCGCC-3´
	OsGIF3 N p1:	5´-CGGAATTCATGCAGCAGCAACAC-3´
	OsGIF3 N p2:	5'-CGGGATCCCGCCCCGGACTGC-3'
	OsGIF3 C p1:	5'-CGGAATTCAGGTACATGCCGCAGC-3'
	OsGIF3 C p2:	5´-CGGGATCCCTAGCTGCCTTCCTC-3´
	OsGRF6 N P1:	5´-CGGAATTCATGCAGGGTGCAATGGC-3´
	OsGRF6 N P2:	5´-GCGTCGACGCCTTCCACATGCTTTC-3´
	OsGRF6 C P1:	5´-CGGAATTCCAGCCTGGCCATGCCG-3´
	OsGRF6 C P2:	5´-CGGGATCCCACCAGGCGGATGC-3´
	OsGRF10 p1:	5´-CGGAATTCATGGATGAGGAGAAG-3´
	OsGRF10 p2 :	5´-CGGGATCCGGTGGCGCGCGCGGTGCC-3´
Protein expression	*OsGIF1* P1:	5´-CGGAATTCATGCAGCAGCAGATG-3´
	OsGIF1 P2:	5´-GCGTCGACGGACTTCTCCGCTATG-3´
	OsGRF6 N P1:	5´-CGGAATTCATGCAGGGTGCAATGGC-3´
	OsGRF6 N P2:	5´-GCGTCGACGCCTTCCACATGCTTTC-3´
	OsGRF10 P1:	5´-CGGAATTCATGGATGAGGAGAAGG-3´
	OsGRF10 P2:	5´-GCGTCGACGGTGGCGCGCGCGGTGCCG-3´
	OsGRF6-pro-P1:	5´-GCGTCGACCAACCCGCACAGCGAGAG-3´
	OsGRF6-pro-P2:	5´-GGGGTACCGCTGCTGCTCAAGCTCACTG-3´
	miR396d-pro-P1:	5´-GCGTCGACTTTGGGGCCCTCACAAAC-3´
	miR396d-pro-P2:	5´-GGGGTACCCGGAATTCCATGCTCTGC-3´
	rOsGRF6 P1:	5´-GGACGCCACCGTTCTAGGAAACACGTCGAAGGCCAGCCTGG-3´
	rOsGRF6 P2:	5´-CCAGGCTGGCCTTCGACGTGTTTCCTAGAACGGTGGCGTCC-3´
	*OsGRF6*1301 P1:	5´-CCCCCGGG ATGCAGGGTG CAATG-3´
	*OsGRF6*1301 P2:	5´-GGGGTACC TCACACCAGGCGGATG-3´
	miROE-1301P1:	5´-CGGGATCCTGGAATTCCGGGAGTCCC-3´

	miROE-1301P2:	5´-GGGGTACCAAGCCACAGAAGTCAACAAACA-3´
	GRF6 as P1:	5´-GGGGTACCATGCAGGGTGCAATGGC-3´
	GRF6 as P2:	5´-GAAGATCTCACCAGGCGGATGCTCGGATG-3´

Supplemental Table S4. Statistical analysis of different kinds of florets as well as expression level of *JMJ706* in miROE and miROE/*JMJ706*OE crossed plants.

No of six independent miROE/*JMJ706*OE crossed lines	Ratio of florets with open husks or long sterile lemmas in independent plants of miROE8	Ratio of florets with open husks or long sterile lemmas in miROE/*JMJ706* OE crossed lines	*JMJ706* expression levels in independent plants of *JMJ706OE* line1 (/Ubiqutin)	*JMJ706* expression levels in crossed lines (/Ubiqutin)
Line1	17%	8%	2.50	1.26
Line2	16%	6%	2.60	1.51
Line3	20%	10%	2.28	1.19
Line4	15%	7%	2.62	1.30
Line5	17%	9%	2.39	1.20
Line6	19%	10%	2.41	1.10
Averaged value	17.3%	8.3%	2.47	1.26