

Figure S1 The number of transcription factors in the AP2/ERF, bHLH, WRKY, bZIP, MYB, NAC, C2H2, and other families in *Arabidopsis*, maize, *indica* rice, and *japonica* rice. The data were retrieved from the PlantTFDB v5.0 website (http://planttfdb.cbi.pku.edu.cn/).



Figure S2 Structural comparison of putative OsERF106-encoding transcripts between the Rice Annotation Project Database (RAP-DB, http://rapdb.dna.affrc.go.jp/) and the Michigan State University Rice Genome Annotation Project (MSU RGAP, http://rice.plantbiology.msu.edu/). The coding sequences of two Os08t0537900 transcripts (upper panel) and six Os08g42550 transcripts (lower panel) were documented on the RAP-DB and MSU RGAP websites, respectively. One typical AP2/EREBP domain (red bar) is present in the Os08g42550.1-encoded protein. The ScanProsite tool of ExPASy (http://www.expasy.org/) was used to retrieve the AP2/EREBP domain.



Figure S3 Os08t0537900-01 and Os08g42550.2 to Os08g42550.6 encode an O-fucosyltransferase (O-FucT) without the AP2/EREBP domain. The data were analyzed with NCBI SmartBLAST (http://blast.ncbi.nlm.nih.gov/smartblast/).

>Os08t0537900-02 Hypothetical conserved gene. ATCAGTTACTCCTCTTACCAGTGCAGCTCTGCATCGTCAGCGATCAAGGGTACCAGGGTG GATCGCCTACGAGAAGCTAGTGACACAGGGCATCATCGTGGTCGGCACAAGAGGGCCCGC TCCTCTCCTCCACGCCATGACGACGACCGCCGCCGCCGCCGCCGCCGCCGCGGCGGTG ACAGGAGGAGCACACGGCGCGCGCGCGCGCGCGCGCACTCAACGGTGCTCGCGGAGGACGTCGAA ACGGCCGTTCCTCCGGTGACGGTTGCGCCGCCGCAGCGAGCTGCCACGGCTACCATGTTCGGA CAGCAAGCCGCCGCGCGGCTTTCCTCCTCTGCCGTCGTCGAGCGGATCAGCagcqacqqc gccggagcagcagcagccacggcggcgctaccgcggcgtgcggcagcggccgtgggggaa gtgggcggcggagatccgcgacccggtgaaggcggcgcgggtgtgggctcggcaccttcga caccgccgaggacgccgccgcgcctacgacgccgccgccgtccgcttcaagggctccaa qqccaaqqtcaacttcccCGACGAAGTCGCCGGCGCCAGCATCGCCGCCGTCCAGCTGCC ACGCCATCATCAACACCACCCCCCAACGTCACTGCCGCCGCTGCCGGTGCCGGCGCATCT CGTCGCCGCTCCGCCGCGGGGGGGGGGGGGGGGCTTCCCCCGACCTCAGCAGCTACGCGCACATACTGCA GAGCGGCGACCTGGAGTACGACTTCCACGCCGCGGTTTCTGCCGGACTAACGACGACAGC TGGGCGAtcgtcgtcgtcgtcgtcattgtcgatgccgccgccatccgagGATCTTGA

Figure S4 The coding sequence (CDS) of Os08t0537900-02 lacks an ATG-start codon. The image was taken from the Rice Annotation Project Database (RAP-DB, http://rapdb.dna.affrc.go.jp/).



Figure S5 Os08g42550.1 encodes an AP2/EREBP domain-containing O-fucosyltransferase (O-FucT)-like protein, which is homologous to AtO-FucT13 and GmO-FucT13 but not to any AtAP2/ERFs or GmAP2/ERFs. The data were analyzed with NCBI SmartBLAST (http://blast.ncbi.nlm.nih.gov/smartblast/).



Figure S6 Gene structure and amino acid sequence alignment of OsERF106MZ (GenBank accession No. MZ561461). (A) Structure of OsERF106MZ. (B) Amino acid sequence alignment of OsERF105, OsERF106MZ, and OsERF107 together with their homologs, AtERF108 and AtERF113. The predicted AP2/EREBP domain is underlined in green. The conserved alanine 14 and aspartic acid 19 residues of the AP2/EREBP domain are indicated with red and blue asterisks, respectively.



Figure S7 Phylogenetic analysis of OsERF105, OsERF106MZ, and OsERF107 together with AtERF108, AtERF113, AtO-FucT13, and GmO-FucT13 using the neighbor-joining method. Numbers next to the descendants indicate confidence values based on the bootstrap method.



Figure S8 The subcellular localization of OsERF106MZ-GFP and GFP-OsERF106MZ in Oncidium 'Sweet Sugar' suspension cells.



Figure S9 Characterization of a retrotransposon insertion *Oserf106mz* mutant line, H0159. (A) A schematic diagram of the retrotransposon insertion site (indicated with a red triangle) in Os08g42550.1 and the *OsERF106MZ* gene. (B) Identification of homozygous H0159 lines by genomic DNA genotyping. The Arabic numerals represent the individual rice plants within each genotype. (C) Quantification of Os08g42550.s mRNA levels in Hitomebore and *Oserf106mz* plants by qPCR. The values are the mean ± SE of five biological replicates, each with two technical replicates. The positions of the primers used for genotyping (B) and qPCR (C) are indicated by green and blue arrows, respectively, in (A). The primer sequences are listed in Additional file 2: Table S1. The seedlings were grown on basal medium for 11 days and then subjected to genotyping and qPCR assays.



Figure S10 MDA (left panel) and Na⁺ (right panel) contents in the roots of Tainung 67 and OsERF106MZ-overexpressing rice plants.

Biological process GO:0008150 biological_process GO:0071554 (0.0114) D:0065007 (8.35e-0 cell wall GO:0050896 biological regulation organization or biogenesis response to stimulus 79/514 | 2125/24075 11/514 | 148/24075 GO:0009628 (0.0285 D:0050789 (8.53eregulation of GO:0009987 GO:0008152 response to biological process cellular process metabolic process abiotic stimulus 76/514 | 2027/24075 7/514 | 74/24075 D:0050794 (9.56e-0 O:0019222 (9.56e-05) GO:0044237 GO:0006807 GO:0044238 GO:0043170 :0055114 (5.63e-0 regulation of GO:0009058 regulation of cellular metabolic nitrogen compound oxidation reduction primary metabolic macromolecule metaboli cellular process metabolic process biosynthetic process 31/514 | 1351/24075 process metabolic process process process 73/514 | 1955/2407 65/514 | 1664/240 -----2277722222 -----1 GO:0031323 (0.000153 0009889 (9.56e-0 GO:0051171 (9.56e-05) GO:0080090 (8.35e-05) GO:0060255 (8.54e-05) GO:0044036 (8.36e-05) :0005975 (5.5e-0 GO:0044249 GO:0006139 GO:0009059 GO:0044260 GO:0019538 regulation of regulation of regulation of regulation of regulation of GO:0010467 rbohydrate metaboli GO:0009056 cell wall ellular biosynthetic protein metabolic nucleobase, nucleoside nacromolecule biosyntheti ellular macromolecule ellular metabolic process biosynthetic process ogen compound metabolic process mary metabolic process romolecule metabolic proce gene expression process catabolic process cromolecule metabolic process nucleotide and nucleic acid metabolic process metabolic process process process process 62/514 | 1593/24075 62/514 | 1564/2407 61/514 | 1520/24075 65/514 | 1626/24075 65/514 | 1640/24075 47/514 | 833/24075 9/514 | 45/24075 GO:0031326 (9.56e-05) GO:0019219 (9.56e-05) GO:0010556 (9.56e-05) GO:0010468 (0.000118 GO:0009308 (0.0352 GO:0005976 (1.89e-05 O:0016052 (0.00026 GO:0009057 (0.0176) GO:0016998 (6.74e-05) GO:0016070 GO:0034645 GO:0044267 GO:0043412 regulation of regulation of regulation of regulation of amine metabolio lysaccharide metabo arbohydrate catabol macromolecule catabo cell wall RNA metabolic cellular macromolecule cellular protein ucleobase, nucleoside, nucleotide and nucleic acid metabolic process ellular biosynthetic proces molecule biosynthetic proces gene expression process macromolecule modification process process process molecule catabolic process process biosynthetic process metabolic process 62/514 | 1564/24075 61/514 | 1520/24 62/514 | 1564/2407 62/514 | 1577/24 18/514 | 380/2407 16/514 | 143/2407 13/514 | 131/240 17/514 322/2407 9/514 | 42/24075 O:0051252 (0.00959) GO:0032774 (0.0224) O:0006022 (5.5e-0) O:0006350 (0.00027 GO:0006464 RNA biosynthetic regulation of ninoglycan metabol ysaccharide catabo protein modification transcription RNA metabolic proces process 10/514 | 29/24075 process 12/514 | 37/24075 process 62/514 | 1629/24075 process 31/514 | 788/24075 31/514 | 740/24075 GO:0043687 (0.0481) GO:0045449 (9.56e-0 D:0006030 (3.49e-0 D:0006026 (3.49e-0 GO:0006351 (0.0222) regulation of post-translational proteir chitin metabolic minoolvcan cataboli ranscription, DNA-depender transcription modification process process 31/514 | 786/24075 61/514 | 1513/24075 57/514 | 1815/24075 10/514 | 26/2407 10/514 | 26/2407 GO:0006355 (0.00932) regulation of chitin catabolic anscription, DNA-depender process 31/514 | 737/24075 10/514 | 26/2407

Figure S11 GO analysis of the common DEGs according to biological processes and molecular functions.

Molecular function



	1	10	20	30	40	50	60	70	80	90	100	110	120	130
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OsERF106MZ (Hito) Consensus	ATCAG ATCAG ATCAG ATCAG	TTACTCCI TTACTCCI TTACTCCI TTACTCCI	TCTTACCAGTG TCTTACCAGTG TCTTACCAGTG TCTTACCAGTG	CAGCTCTGCA CAGCTCTGCA CAGCTCTGCA CAGCTCTGCA	TCGTCAGCGA TCGTCAGCGA TCGTCAGCGA TCGTCAGCGA	TCAAGGGTAC(TCAAGGGTAC(TCAAGGGTAC(TCAAGGGTAC(CAGGGTGGATC CAGGGTGGATC CAGGGTGGATC CAGGGTGGATC	GCCTACGAG GCCTACGAG GCCTACGAG GCCTACGAG GCCTACGAG	AAGCTAGTGAI AAGCTAGTGAI AAGCTAGTGAI AAGCTAGTGAI	CACAGGGCATI CACAGGGCATI CACAGGGCATI CACAGGGCATI	CATCGTGGTCI CATCGTGGTCI CATCGTGGTCI CATCGTGGTCI CATCGTGGTCI	ggcacaagag ggcacaagag ggcacaagag ggcacaagag ggcacaagag	GGCCCGCTCCT GGCCCGCTCCT GGCCCGCTCCT GGCCCGCTCCT	CTCCTC CTCCTC CTCCTC CTCCTC CTCCTC
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OsERF106MZ (Hito) Consensus	CACGC CACGC CACGC CACGC	CATGACGI CATGACGI CATGACGI CATGACGI CATGACGI	ACGAGCCGCCA ACGAGCCGCCA ACGAGCCGCCA ACGAGCCGCCA ACGAGCCGCCA	CCGCCGCCGC CCGCCGCCGC CCGCCGCCGC CCGCCGC	CGCTGTCTCC CGCTGTCTCC CGCTGTCTCC CGCTGTCTCC CGCTGTCTCC	GGCGGTGACA GGCGGTGACA GGCGGTGACA GGCGGTGACA	ggaggagcaca ggaggagcaca ggaggagcaca ggaggagcaca ggaggagcaca	CGGCGGCGC CGGCGGCGC CGGCGGCGC CGGCGGCGC CGGCGG	CGCGTGGCACT CGCGTGGCACT CGCGTGGCACT CGCGTGGCACT	ICAACGGTGC ICAACGGTGC ICAACGGTGC ICAACGGTGC ICAACGGTGC	tcgcggagga tcgcggagga tcgcggagga tcgcggagga	CGTCGAAAGT CGTCGAAAGT CGTCGAAAGT CGTCGAAAGT CGTCGAAAGT	GCCGTCATCGT GCCGTCATCGT GCCGTCATCGT GCCGTCATCGT GCCGTCATCGT	CGCGGC CGCGGC CGCGGC CGCGGC
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OSERF106MZ (Hito) Consensus	GCTGA GCTGA GCTGA GCTGA	CGCACGTI CGCACGTI CGCACGTI CGCACGTI CGCACGTI	CATCAGCTCCA CATCAGCTCCA CATCAGCTCCA CATCAGCTCCA CATCAGCTCCA	CGGCGGCGGA CGGCGGCGGA CGGCGGCGGA CGGCGGCGGA	GGTGACCACG GGTGACCACG GGTGACCACG GGTGACCACG GGTGACCACG	GCCGTTCCTC(GCCGTTCCTC) GCCGTTCCTC(GCCGTTCCTC)	CGGTGACGGTT CGGTGACGGTT CGGTGACGGTT CGGTGACGGTT	GCGCCGCAG GCGCCGCAG GCGCCGCAG GCGCCGCAG	CGAGCTGCCAI CGAGCTGCCAI CGAGCTGCCAI CGAGCTGCCAI	CGGCTACI ATI CGGCTACI ATI CGGCTACI ATI CGGCTACI ATI	g TCGGACAG G TCGGACAG G TCGGACAG G TCGGACAG G TCGGACAG	CAAG CAAGTGATGCI CAAGTGATGCI CAAGtgatgc	AGCAGCCGCCG AGCAGCCGCCG AGCAGCCGCCG AgcagCCGCCG	CGCGGC CGCGGC CGCGGC CGCGGC
	391 	400	410	420	430	440	450	460	470	480	490	500	510	520 1
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OsERF106MZ (Hito) Consensus		TCCTCTG TCCTCTG TCCTCTG TCCTCTG TCCTCTG	CCGTCGTCGAG CCGTCGTCGAG CCGTCGTCGAG CCGTCGTCGAG	CGGATCAGCA CGGATCAGCA CGGATCAGCA CGGATCAGCA	GCGACGGCGC GCGACGGCGCC GCGACGGCGCC GCGACGGCGCC	CGGAGCAGCA CGGAGCAGCA CGGAGCAGCA CGGAGCAGCA CGGAGCAGCA	GCAGCCACGGC GCAGCCACGGC GCAGCCACGGC GCAGCCACGGC GCAGCCACGGC	GGCGCTACC GGCGCTACC GGCGCTACC GGCGCTACC	GCGGCGTGCGI GCGGCGTGCGI GCGGCGTGCGI GCGGCGTGCGI	SCAGCGGCCG SCAGCGGCCG SCAGCGGCCG SCAGCGGCCG SCAGCGGCCG	TGGGGGAAGTI TGGGGGGAAGTI TGGGGGGAAGTI TGGGGGGAAGTI	GGGCGGCGGA GGGCGGCGGA GGGCGGCGGA GGGCGGCGGA	GATCCGCGACC GATCCGCGACC GATCCGCGACC GATCCGCGACC GATCCGCGACC	CGGTGA CGGTGA CGGTGA CGGTGA
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OsERF106MZ (Hito) Consensus	AGGCG AGGCG AGGCG AGGCG	GCGCGGG GCGCGGG GCGCGGG GCGCGGG	TGTGGCTCGGCI TGTGGCTCGGCI TGTGGCTCGGCI TGTGGCTCGGCI	ACCTTCGACA ACCTTCGACA ACCTTCGACA ACCTTCGACA ACCTTCGACA	CCGCCGAGGA CCGCCGAGGA CCGCCGAGGA CCGCCGAGGA	CGCCGCCCGC(CGCCGCCCGC(CGCCGCCCGC(CGCCGCCCCGC(CGCCGCCCCGC(GCCTACGACGC GCCTACGACGC GCCTACGACGC GCCTACGACGC GCCTACGACGC	CGCCGCCGT CGCCGCCGT CGCCGCCGT CGCCGCCGT	CCGCTTCAAGO CCGCTTCAAGO CCGCTTCAAGO CCGCTTCAAGO CCGCTTCAAGO	GGCTCCAAGG GGCTCCAAGG GGCTCCAAGG GGCTCCAAGG GGCTCCAAGG	CCAAGGTCAA CCAAGGTCAA CCAAGGTCAA CCAAGGTCAA CCAAGGTCAA	CTTCCCCGAC CTTCCCCGAC CTTCCCCGAC CTTCCCCGAC CTTCCCCGAC	GAAGTCGCCGG GAAGTCGCCGG GAAGTCGCCGG GAAGTCGCCGG	icgccag icgccag icgccag icgccag icgccag
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OsERF106MZ (Hito) Consensus	CATCG CATCG CATCG CATCG CATCG	CCGCCGT(CCGCCGT(CCGCCGT(CCGCCGT(CCAGCTGCCAC CCAGCTGCCAC CCAGCTGCCAC CCAGCTGCCAC CCAGCTGCCAC	GCCATCATCA GCCATCATCA GCCATCATCA GCCATCATCA GCCATCATCA	ACACCACCCC ACACCACCCC ACACCACCCC ACACCAC	CCAACGTCACT CCAACGTCACT CCAACGTCACT CCAACGTCACT CCAACGTCACT	TGCCGCCGCTG TGCCGCCGCTG TGCCGCCGCTG TGCCGCCGCTG	CCGGTGCCG CCGGTGCCG CCGGTGCCG CCGGTGCCG	GCGCATCTGAI GCGCATCTGAI GCGCATCTGAI GCGCATCTGAI	GCCACACTT GCCACACTT GCCACACTT GCCACACTT GCCACACTT	CAGCCTCGCC CAGCCTCGCC CAGCCTCGCC CAGCCTCGCC CAGCCTCGCC	GGCGGCCAGA GGCGGCCAGA GGCGGCCAGA GGCGGCCAGA	GCACCACACCG GCACCACACCG GCACCACACCG GCACCACACCG GCACCACACCG	GCGCCC GCGCCC GCGCCC GCGCCC
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OsERF106MZ (Hito) Consensus	GCAGC GCAGC GCAGC GCAGC	CGCCGCCI CGCCGCCI CGCCGCCI CGCCGCCI	GTCGCCGCTCC GTCGCCGCTCC GTCGCCGCTCC GTCGCCGCTCC GTCGCCGCTCC	GCCGCGGGGAG GCCGCGGGGAG GCCGCGGGGAG GCCGCGGGGAG	GAGTTCCCCG GAGTTCCCCG GAGTTCCCCG GAGTTCCCCG	ACCTCAGCAGO ACCTCAGCAGO ACCTCAGCAGO ACCTCAGCAGO ACCTCAGCAGO	CTACGCGCACA CTACGCGCACA CTACGCGCACA CTACGCGCACA CTACGCGCACA	TACTGCAGA TACTGCAGA TACTGCAGA TACTGCAGA	GCGGCGACCT(GCGGCGACCT(GCGGCGACCT(GCGGCGACCT(GCGGCGACCT(GGAGTACGAC GGAGTACGAC GGAGTACGAC GGAGTACGAC	TTCCACGCCG TTCCACGCCG TTCCACGCCG TTCCACGCCG	CGGTTTCTGC CGGTTTCTGC CGGTTTCTGC CGGTTTCTGC CGGTTTCTGC	CGGACTAACGA CGGACTAACGA CGGACTAACGA CGGACTAACGA	icgacag icgacag icgacag icgacag icgacag
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OsERF106MZ (Hito) Consensus	CTGGG CTGGG CTGGG CTGGG	CGATCGTO CGATCGTO CGATCGTO CGATCGTO	CGTCGTCGTCG CGTCGTCGTCG CGTCGTCGTCG CGTCGTCGTCG CGTCGTCGTCG	TCATTGTCGA TCATTGTCGA TCATTGTCGA TCATTGTCGA	TGCCGCCGCC TGCCGCCGCC TGCCGCCGCC TGCCGCCGCC	ATCCGAGGAT(ATCCGAGGAT(ATCCGAGGAT(ATCCGAGGAT(ATCCGAGGAT(CTTGA CTTGACTATAA CTTGACTATAA CTTGActataa	GCCTCCCTT GCCTCCCTT gcctccctt	TGGACCATCTI TGGACCATCTI tggaccatcta	AATTAA CTAI AATTAA CTAI Baa Laa ctai	CTGATTATTC CTGATTATTC ctgattattc	AAATTAGCAT AAATTAGCAT aaattagcat	AGATAGATAAC AGATAGATAAC agatagataac	CCTTTA CCTTTA ccttta
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OsERF106MZ (Hito) Consensus	CAAAA CAAAA caaaa	TCAGGGGG TCAGGGGG Lcaggggg	GAAATTCTGAA GAAATTCTGAA gaaattctgaa	ATTCTGCATT ATTCTGCATT attctgcatt	TTAGGAGTACI TTAGGAGTACI ttaggagtac	AACTTAATTT(AACTTAATTT(aacttaattt{	GTAATAATGGA GTAATAATGGA gtaataatgga	AATGGTTCA AATGGTTCA aatggttca	CGAATTTTAG CGAATTTTAG cgaatttag	TATAATCAGA TATAATCAGA Lataatcaga	AAATAGATAG AAATAGATAG aaatagatag	TATCATCTTG TATCATCTTG Latcatcttg	TAGCAAAGATG TAGCAAAGATG tagcaaagatg	AATAGA AATAGA aataga
	1171	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OsERF106MZ (Hito) Consensus	TAGAA TAGAA Lagaa	CAGTGCA(CAGTGCA(cagtgca;	GTGTGTACATT GTGTGTACATT gtgtgtacatt	TCATTATGTC TCATTATGTC Lcallalgtc	AACTTAACAG AACTTAACAG aacttaacag	TGCTTGGATT(TGCTTGGATT(tgcttggatt{	GAAATGTAGAT GAAATGTAGAT gaaatgtagat	TAAGTAGGA TAAGTAGGA Laagtagga	GAATTAATTG GAATTAATTG gaattaattgl	ITTGTACTTTI ITTGTACTTTI Ltgtacttt	GTAGTAGTAA GTAGTAGTAA gtagtagtaa	GTGGCTCCAT GTGGCTCCAT gtggctccat	CGATCCACTTO CGATCCACTTO cgatccacttg	ATTCTT ATTCTT attctt
	1301	1310	1320	133032										
Os08t0537900-02 (Nip) OsERF106MZ (TNG67) OsERF106MZ (Hito) Consensus	AGAGA AGAGA agaga	CAAAGAT(CAAAGAT(caaagats	GCCTTTGATGG GCCTTTGATGG gcctttgatgg	CTTGATGCC CTTGATGCC cttgatgcc										

Figure S12 Comparison between the coding sequence of Os08t0537900-02 and the cDNA sequence of OsERF106MZ gene from both the TNG67 and Hitomebore (Hito) backgrounds. The 5' UTR, exon 1, exon 2, and 3' UTR within the cDNA sequence of OsERF106MZ gene are underlined in green, red, blue, and purple, respectively. The ATG-start and TAA-stop codons of OsERF106MZ gene are indicated by yellow boxes.

OsERF105	OsERF106MZ	OsERF107	OsbHLH068			
cNLS Mapper Result	cNLS Mapper Result	cNLS Mapper Result	cNLS Mapper Result			
Predicted NLSs in query sequence MADQRRFRGGGDWQASVDDVVDDGGELEAAAAAAARGSVLSGEVQAQEM 59 STMVSALTWVVAAGHDDHGGGQWSGLVDVPATTLAGGGGGDYGHGAQGSY 109 YYYGAAPTSTPEFVAGQQQEQLSSDVPQGGASLGLAMDEHSPTYTVEASS 159 SADQHGGGGGGRRRGVRGVRQRPWGKWAAEIRDPHKAARVWLGTFETAEAAA 200 RAYDEAALRFRGSRAKLNFPEDARLSSPPAGAGAGGATAAAQTVPVAYPA 250 SAVSDVLQVQMLLHGGGGGGGGRPVLYYGGGAAAAMSSLGPYSSIPTSS 300 VTVASVPSSSSAASSSSGYGAPAEHGEAVQWTSWPDGGGWTYPATTSSWS 350 GSSQYPPPPRPPQ 364	Predicted NLSs in query sequence MFGQQVMQQPPRGFPPLPSSSGSAATAPEQQQPRRYRGVRQRPWGKWAA 59 EIRDPVKAARVWLGTFDTAEDAARAYDAAAVRFKGSKAKVNFPDEVAGAS 100 IAAVQLPRHHQHHPTSLPPLPVPAHLRPHFSLAGGGSTTPAPAAAAVAA 150 PPREEFPDLSSYAHILQSGDLEYDFHAAVSAGLTTTAGRSSSSSLSMPP 200 PSEDLDVKPPFGPSN 215 Predicted monopartite NLS Pos. Sequence Score Dos. Sequence Score	Predicted NLSs in query sequence MSSRQPIGSGGGGAPPDWHDVEFQWQPVDDVVTVAAAAAYLAAPAGATLS 59 SESADRRWRPVGPSAAAAAAALQAVEAQGAAAAERHYRGVRRRPWGKWAA 109 EIRDPNKAARVWLGTFDTAEAAAAAYDDAALRFKGAKAKLNPPERVRGRT 159 GQGGFLVSPAVPRPPHGVPAPAPAVAPAPFPLIQVARLLRSGEDAAAA 200 AAVAGIAATAAPAAQILDFAAQRLVGVSPAMAPRPPSTLPTTTTAASSPS 259 AWPHGGGHGS 260 Predicted monopartite NLS Pos. Sequence Score	Predicted NLSs in query sequence MGDHQMMHAAPAAMYNGGGGTTSSHGVWWSNAVGVPAAATCSTTTELAGY 50 TAWSSALAAGYDGMVADNGGKQAKSTTTASSESPGNNSSVTFQEPASIPD 100 PAAVAAVPQPGLAGFTDWTQPFMNNGAGLHEFLQDGHHDMSASSLMMHSS 150 NNLALQQAGHHHELLSSFGSULLSPTSPYGGFQSSLLRSLMEPTAKQQQ 200 QQPALAGLQYHQYQQQMGHAPAAAAKFAQAVGARDSLQFTNDAPFNNPS 250 AGFGMPAAVAVAAAAQDQASVRSAKRSSPAPPRAATLALKTMEGVGD 300 SSSVTTKKETAFKKPRLETPSPLPTFFKVRKEKLGDRITALQQLVSPFGKT 350 DTASVLHETIEYIKFLHDQVGALSAPVLKNGAHQVPHLKNSSPDKSKHGE 400 ISLKGRGLCLVPISSTFAVASEVPVELWTPFGANFIR 437			

Figure S13 Nuclear localization signal (NLS) prediction in OsERF106MZ as well as its homologs OsERF105 and OsERF107. The data were analyzed with NLS Mapper (http://nls-mapper.iab.keio.ac.jp/). OsbHLH068 is a nuclear-localized protein that has been documented in a previous study (Chen et al. 2017) and is used as a positive control.

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
OsERF105	C <mark>G</mark> GTA	CCG <mark>C</mark> GGCG	TGCGGCAGCGG	CCGTGGGG <mark>G</mark> F	AGTGGGCGG	CGGAGATCCGC	GACCCGCAC	AAGGCCGCCC	GCGTCTGGCTC	GGCACCTT	CGAGACCGCCGA	AGGCCGCGGCG	CGCGCCTA	GACGAGG
OsERF106	CGCTA	CCG <mark>C</mark> GGCG	TGCGGC <mark>A</mark> GCGG	CCGTGGGG <mark>G</mark> F	AGTGGGCGG	CGGAGATCCGC	GACCCGGTG	AAGGC <mark>G</mark> GC <mark>G</mark> C	GGGTGTGGCTC	GGCACCTT	CGA <mark>C</mark> ACCGCCGF	AGGACGCCGCC	CGCGCCTAC	GACGCCG
USERF107		CCG166CG CCG 2 66CG	TGCGGC a GCGG	CCGTGGGGGCH CCGTGGGGGGG	18616666666 1861666666	CGGAGATCCG	GACCC a ac	HHGGC <mark>G</mark> GC <mark>G</mark> C AAGGC ₀ GC ₀ C	60010166016 60670766070	GGCACCTT	LGH <mark>L</mark> HLLGLLGH CGA c ACCGCCGA	HGGCLGLLGLLGLL AGGCLGLCGLCG	.GCCGCCTHL .coCGCCTA(GACGacG
consensus	- Series	ccucuucu	Tucuucuucuu	ccuruuugi	maraacaa	counterrecou	uncees.ue	Inducguese		ducineerin	canenceacea		egeucerne	ancaaca
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
OsERF105	CCGCG	CTCCGCTT	CCGCGGCAGCC	GCGCCAAG <mark>C</mark> 1		CGAGGACGCGC	GCCTCAGCA	60000000000000000000000000000000000000	2002202020023	CCGGTGG		CGGCGCAGAC	GGTGCCG <mark>G</mark> 1	GGCCTAC
OsERF106	CCGCC	GTCCGCTT	CAAGGGCTCCA	AGGCCAAGGT	CAACTTCCC	CGA-CGAAGTC	GCCGGC-	GCCAGCATCG	CCGCCGTCCA-	-GCTGCCA	CGCCATCATCA	ACACCACCCC	CAACGTCAC	TGCCGCC
OsERF107	CCGCG	CTCCGCTT	CAAGGGCGCCA	AGGCCAAGC1		CGAGCGCGTCC	GCGGCCGC-	ACCGGCCAGG	GCGGCTTCCTC	GTCTCCCC		GC-CCGCCGCC	GCATGGTG	TCCCGCT
Lonsensus	եենեց	CILLGLII	Laaguul.cla	agullhhuci		LuHgcgcg	նեե.նե.	ցել,նեշ,շն	ICLUGLGLLC.C	g.Ltgcc.	LULCALCC.Lag	gl.clglcgcl	g.a.ggt	tgllgcc
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
OsERF105	CCGGC	CAGCGCGG	TCTCGGACTAC	TT <mark>gcagtac</mark>	CAGATGCTCC	TACA <mark>CGG</mark> AGGA	GGCGGCGGC	G <mark>GCGGCG</mark> GCC	GTTATCCTCTC	TACTACGG	CGCCGCCGCCGC	CCGCTGCCATG	AGTAGCTC7	TTGGGGC
OsERF106	GCTGC	CGGTGCCG	G <mark>CGC</mark> A-TCTGA	G-GCCACAC1	TCAGCCTCG	CCGGCGGCCAG	AGCA-CCAC	ACCGGCGCCC	GCAG-CCGC		CGCCGTCGCCG	CTCC-GCC <mark>G</mark> CG	<mark>GGAGG</mark> AGT	CCCCGAC
OsERF107		GCCCGCCG	TGGCG-CCGGC	GCCGTTCC	CCGACCTGA	TCCAGTACG	CGCGGCTGC	TGCGGAGCGG	iGGAGGACGC		CG <mark>CCGCCGCCGC</mark> CGCCGCCGCCGCCG	CC-GCC <mark>GT</mark> G	GCCGGCATI	GCGGC
consensus	CC . 00	c.geacea		8.8rcgrari	:+Cd+CC1C+	re**rån***å	• arssr•sr	*Scaacacce	a.ag.crgr	•••••	Lacca.cacca	LL.OLLELU	SS*Sac*c1	+C++age
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
OsERF105	CTTAC	TCCTCCAT	CCCCACCTCCT	CGGT <mark>CACCG</mark> T	CGCCTCCGT	GCCGTCGTCGT	CCTCTGCCG	CGTCGTCTTC	TTCGGGTTACG	GCGCGCCG	GCGGAGCACGG	C <mark>GAGGCG</mark> GTGC	.AGTGGA <mark>CC</mark> (
OsERF106	CT	-CAGCAGC	TA <mark>CG</mark> CG <mark>CACAT</mark>	ACT <mark>GCAGAG</mark> (CGGCGACCTG	<mark>Gagtacgactt</mark>	CCAC-GCCG	CGGTTTC	TGCCGGA	-CTAAC-G	ACGACAGO	CTG <mark>GGCG</mark>	AT(GTCGTC-
OsERF107	CA	-CCCCCCCCC	GCCG	eceecec	AGA-TCCTG	GACTTCG	CGGC-GCAG	CGGCTCG	TCG <mark>GGGT</mark>	-CTCTCCG	GCGATGG	C <mark>GCCGCG</mark>	CCC	GCCGTC-
Lonsensus	LC	+LCgL+gc	•cr8••c•c•t	+++gLagcuo	:.uc.tlltg	bacttlb.c.t	ՆՇ ₊ Լ₊նԼՇն	LugcItc	.1.cguut	+LCC+LCU	gluHcgul	ւց․ցնւն․․․․	•••••• <mark>cc</mark> (uccutt.
	521	530	540	550	560	570	580	590	600	611				
OsERF105	GGACG	G <mark>TG</mark> GTGGC	TGGACCTATCC	GGCGACGACG	AGTTCTTGG	TCTGGTTCGAG	CCAGTACCC	G <mark>CCGCCAC</mark> CT	CGGCCTCCTCA	GCAGTAG				
OsERF106	-GTCG	TC <mark>G</mark>	TCATTGTC	GATGCCGCCG	CCATCCGAG	GA <mark>TC</mark> TTGA	CTATAAGCC	TCC-CTTTGG	ACCATCTAA	TTAA				
OsERF107	-GACG	CTG	CCGACGAC	GACGACCGCG	GCGTCG	TCGCCGAG	COCOTOCC	TCA-CGGCGG	CGGCCACGGGA	<mark>gcta</mark> g				
Lonsensus	.uatii	. <mark>tli</mark>	U. <mark>t.g</mark> .U	uactialg.lt	1.C.IUU	tctccgag	L.agtagUU	ttc.t.cgg	cggllacct.H	gcaa				

Figure S14 Nucleotide sequence alignment of *OsERF105* (Os05g36100), *OsERF106* (Os08g42550.1), and *OsERF107* (Os02g32140), three genes belonging to the rice ERF-Xc subgroup, from the region encoding the AP2/EREBP domain (underlined in green) to the translation stop site. The positions of the *OsERF106* gene-specific primers (GSPs) used in 5' and 3' RACE experiments are underlined in red and blue, respectively.