Supplementary Data

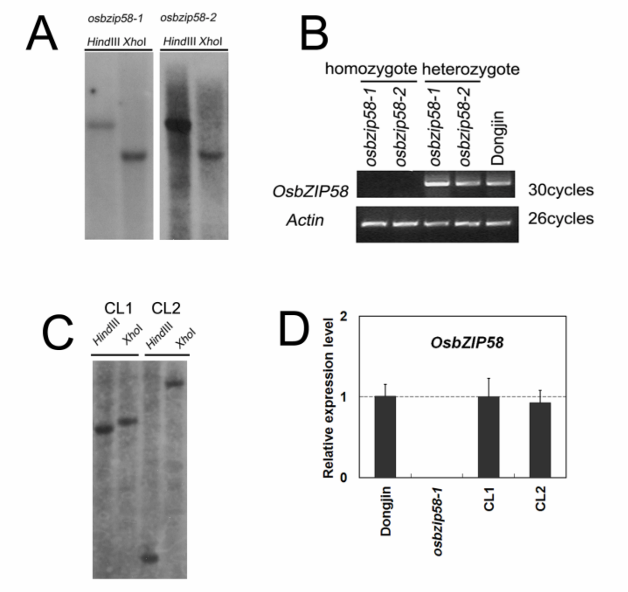

Figure S1 Identification and characterization of the *osbzip58* mutants and CLs.

(A) Southern blot analysis of *osbzip58-1* and *osbzip58-2*. Genomic DNA isolated from homozygous mutants of the T_4 generation were digested with *Hind*III or *Xho*I and hybridized with labeled *HPTII* coding sequences.

(B) Expression levels of *OsbZIP58* in developing seed of homozygous, heterozygous mutants and wild-type plants analyzed by semi-quantitative RT–PCR. The rice *OsAct1* was used as control.

(C) Southern blot analysis of CL1 and CL2. Genomic DNA isolated from homozygous transgenic plants of the T_2 generation were digested with

*Hind*III or *Xho*I and hybridized with labeled NPTII coding sequences.

(D) Expression level of *OsbZIP58* in its CL transgenic plants. Total RNA was extracted from seeds at 10 DAF. The expression of wild-type seeds was used as control. All the data are shown as mean ± s.d. from four replicates.

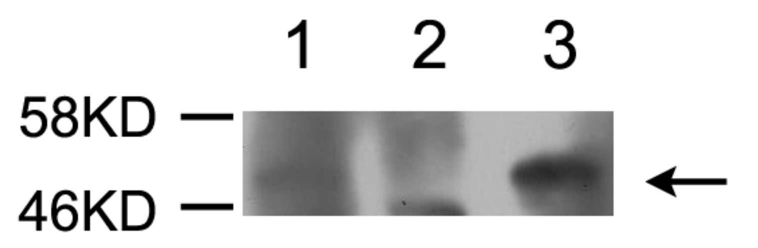

Figure S2 Western blot detecting the specificity of the anti-OsbZIP58 antibody

Lane 1: 40ug total protein of immature seed of *Dongjin*. Lane 2: 40ug total protein of immature seed of *osbzip58-1*. Lane 3: 40ug total protein of immature seed of CL3 (Complemented line 3, a transformant with a wild type *OsbZIP58* gene in the *osbzip58-1* mutant and the expression of *OsbZIP58* in it was 8 times higher than the wild type in this line). The black arrow indicates the OsbZIP58 protein, about 46 kD.

Table S1 Information of primers used in this study

Assay	Primer ID	Primer Specific Name	Primer Sequence （from 5' to 3’）	Restricted Enzyme Site	Reference
Yeast one-hybrid screening	GE0121	OsbZIP58 F	G GAATTCTGGAGCACGTGTTCGCCG	EcoRI	LOC_Os07g08420
	GE0122	OsbZIP58 R	GCAGATCTCTACTGAAGCTCCATGTTGACAAG	BglII	
	GE0140	OsbZIP15 F	GGAATTCTGGACATCGAGGCGTTCATC	EcoRI	LOC_Os02g07840, RISBZ4
	GE0141	OsbZIP15 R	GCGAGCTCAGCCCCAGGCGTCAACCAC	SacI	
	GE0241	OsbZIP20 F	GGAATTCTGAAGAAGTGCCCGTCGGAG	EcoRI	LOC_Os02g16680
	GE0242	OsbZIP20 R	GCGAGCTCCGTAGCTGAGCTGACAAAGCAG	SacI	
	GE0142	OsbZIP33 F	GGAATTCCGATGGAGCGGGTGTTCT	EcoRI	LOC_Os03g58250, REB
	GE0143	OsbZIP33 R	GCGAGCTCTCTGGGTTTCGGTCTCAGG	SacI	
	GE0123	OsbZIP34 F	GGAATTCTGGCATCCTCGGCCGCCT	EcoRI	LOC_Os03g59460,
	GE0124	OsbZIP34 R	GCGAGCTCCTACCCTTTGCTGTCATCATTTGTG	SacI	
	GE0144	OsbZIP35 F	GGAATTCTGGAGGGTGAACCCTCACG	EcoRI	LOC_Os04g10260
	GE0145	OsbZIP35 R	TCCCCGCGGTTATTGTGGCTGATTATGCTGGA	SacII	
	GE0243	OsbZIP40 F	GGAATTCTGGCGTCGTCGAGGGTGA	EcoRI	LOC_Os05g36160 TIGR
	GE0244	OsbZIP40 R	GCGAGCTCCCATTCCATTGAGTTGGTTCTTC	SacI	

	GE0146	OsbZIP50 F	GGAATTCTGGATGTAGAGTTCTTCGCC	EcoRI	LOC_Os06g41770
	GE0147	OsbZIP50 R	GCACTAGTAGCTGCTGCTAAACGGAACG	SpeI	
	GE0148	OsbZIP52 F	GGAATTCTGATGAAGAAGTGCCCGTCG	EcoRI	LOC_Os06g45140，RISBZ5
	GE0149	OsbZIP52 R	GCGAGCTCCCACACATCAGCCGAGCAG	SacI	
	GE0152	OsbZIP76 F	GGAATTCCTAGT CCT TGCACC CCTAACA	EcoRI	LOC_Os09g34880，
	GE0153	OsbZIP76 R	GCGAGCTCTCATCAGAAATCACCCTAAAGC	SacI	
Antibody and *in situ*	GE0336	OsbZIP58-ET F	GCGGATCCATGGAGCACGTGTTCGCCG	BamHI	Os07g08420 ORF
	GE0311	OsbZIP58-ET R	GCAAGCTTAAGGATCATATTTCCCATTGCC	HinDIII	
Mutant Identification	GE0295	pGA2715 R	CCACAGTTTTCGCGATCCAGACTG		pGA2715
	GE0301	Os07g08420 R	CCCCATCTACAATCGACTGG		Os07g08420 DNA 1219
	GE0279	Os07g08420 F	GCGGATCC GGGTTGCTGGAGCGGTGC		
RT-PCR	GE0013	OsRAC F	CCTGCTATGTACGTCGCCATC		Actin
	GE0014	OsRAC R	CCGCAGCTTCCATTCCTATGA		
	GE0332	OsbZIP58-RT F	AGACATTGAAGCCCTAAGAGC		Os07g08420
	GE0333	OsbZIP58-RT R	ACGATCCCCATGCTGTATATTC		
qRT-PCR	GE0348	OsAGPS2b F	AACAATCGAAGCGCGAGAAA		AGPS2b，AK103906
	GE0349	OsAGPS2b R	GCCTGTAGTTGGCACCCAGA		
	GE0352	OsAGPL2 F	AGTTCGATTCAAGACGGATAGC		OsAGPL2，U66041
	GE0353	OsAGPL2 R	CGACTTCCACAGGCAGCTTATT		
	GE0548	OsAGPL3 F	AAGCCAGCCATGACCATTTG		AK069296
	GE0549	OsAGPL3 R	CACACGGTAGATTCACGAGACAA		
	GE0354	OsSSI F	GGGCCTTCATGGATCAACC		

	GE0355	OsSSI R	CCGCTTCAAGCATCCTCATC		
	GE0356	OsSSIIa F	GCTTCCGGTTTGTGTGTTCA		OsSSIIa，OsSSII-3，AF419099
	GE0357	OsSSIIa R	CTTAATACTCCCTCAACTCCACCAT		
	GE0556	OsSSIIIa F	GCCTGCCCTGGACTACATTG		AY100469
	GE0557	OsSSIIIa R	GCAAACATATGTACACGGTTCTGG		
	GE0360	OsSSIVb F	ATGCAGGAAGCCGAGATGTT		OsSSIVb，OsSSIVb，AY373258
	GE0361	OsSSIVb R	ACGACAATGGGTGCCAAGAT		
	GE0362	OsGBSSI F	AACGTGGCTGCTCCTTGAA		OsGBSSI，X62134
	GE0363	OsGBSSI R	TTGGCAATAAGCCACACACA		
	GE0364	OsBEIIb F	ATGCTAGAGTTTGACCGC		OsBEIIb，SBE3， D16201
	GE0365	OsBEIIb R	AGTGTGATGGATCCTGCC		
	GE0366	OsISA1 F	TGCTCAGCTACTCCTCCATCATC		OsISA1，AB093426
	GE0367	OsISA1 R	AGGACCGCACAACTTCAACATA		
	GE0368	OsPUL F	ACCTTTCTTCCATGCTGG		OsPUL，AB012915
	GE0369	OsPUL R	CAAAGGTCTGAAAGATGGG		
	GE0386	OsBEI F	TGGCCATGGAAGAGTTGGC		OsBEI,D11082
	GE0387	OsBEI R	CAGAAGCAACTGCTCCACC		
	GE0422	UBQ10 F	TGGTCAGTAATCAGCCAGTTTGG		AK101547；06-BBRC-housekeeping gene in rice
	GE0423	UBQ10 R	GCACCACAAATACTTGACGAACAG		
	GE0841	OsPHOL F	TTGGCAGGAAGGTTTCGCT		AK063766
	GE0842	OsPHOL R	CGAAGCCTGAAGTGAACTTGCT		
	GE0566	OsISA2 F	TAGAGGTCCTCTTGGAGG		AC132483
	GE0567	OsISA2 R	AATCAGCTTCTGAGTCACCG		
	GE0390	OsbZIP58 F	CTCCAACGCTAACAATGC		LOC_Os07g08420M,RISBZ1
	GE0391	OsbZIP58 R	GCTCTATTCTGAAGATGCTG		

Table S2 Locations of promoter regions and sequences of primers used in the ChIP-PCR assays

Fragment Name	NCBI ID	Primer Name	Primer Sequence (from 5’ to 3’)	“ACGT” Site	“ACGT” number
OsAGPL2	Os01g0633100	GE0600	TGCGTTACGGCATCTCCACCT	+2194~+2489	3
		GE0601	TGCAGAGGAAGGAAGCAGGGT		
OsAGPL3	Os03g0735000	GE0614	CTTGGCTGCCTGCCACTCCC	-241~-76	4
		GE0615	CTAGGGACACAACCGCGGCG		
Wx/GBSSI-a	Os06g0133000	GE0677	CCGCTGGCACCGGAGGACTA	-1670~-1506	7
		GE0678	TCCGTCCTTCAACCGCAAAACCA		
Wx/GBSSI-b		GE0679	CGCAGGTAATTGACACCCCACG	-1051~-770	6
		GE0680	CATGCAGGGCGAGGCTAGCG		
Wx/GBSSI-c		GE0681	GGCAGGCACTCAGCTCGCTG	-684~-551	3
		GE0682	GTACGTCGCTCGCGTGTGCT		
OsSSIIa-a	Os06g0229800	GE0624	ACCCTGGTGGCCGAAATGAA	-1551~-1394	3
		GE0625	ATCCAAGCGAACTCCCACAGTG		
OsSSIIa-b		GE0628	ACCTGCATCCGCAACTGGCA	-420~-217	4
		GE0629	ACGTTAACGGCTCGGGGTGC		
OsSSIIIa	OSJNBa0056O06.4, LOC_Os08g09230	GE0651	CCAGTTTGGTATGGTTTCCATTGA	-1559~-1281	3
		GE0652	ACCGGGAATGTAATTATCCGGGT		
OsSSIVb	Os05g0533600	GE0675	TGGGTTTGGACTTGTAGATGGGCA	-655~-351	3
		GE0676	ACTCCCTCCGTCCCAAAATAAGT		
SBE1-a	Os06g0726400	GE0697	ACATATGCCTTTGTGCCGGGA	-831~-663	3
		GE0698	AGGCTCATTAGATTCGTCTCGCA		
SBE1-b		GE0463	GGTTTGTATTTATTTGCGTCTGG	-178~+146	3
		GE0467	GGAGGAGGAAGAGGAGGTGAG		

OsSBEIIb-a	Os02g0528200	GE0707	CGCTCGATGGCATGAGGGTC	-1660~-1378	3
		GE0708	AGTGGGTTGTAGGTTGCATTTAGAC		
OsSBEIIb-b		GE0709	CGGTTAGACCGAATGCCCACCC	-968~-757	3
		GE0710	ACACCGGTGCTCTGTTGTTTCA		
OsISA1	Os08g0520900	GE0711	CGGCCCAAGCCGTCTGTTGA	-1898~-1585	5
		GE0712	TGTGGTGTGGCCGTCTTTTTCT		
OsISA2	OSJNBa0014C03.3, LOC_Os05g32710	GE0719	GACAACGGTCAGCCCAGCCC	-744~-641	3
		GE0720	GTGGCGTCGTCCTGCTGTCC		
Actin	OsActin1	GE0424	CAGCCACACTGTCCCCATCTA		
		GE0425	AGCAAGGTCGAGACGAAGGA		