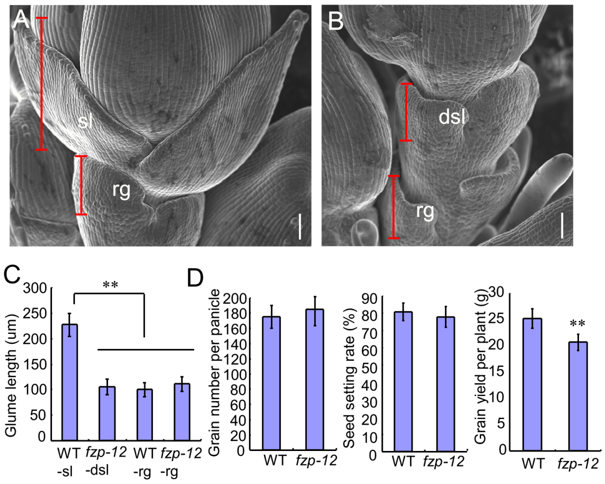
SUPPLEMENTAL FIGURES

Supplemental Figure 1



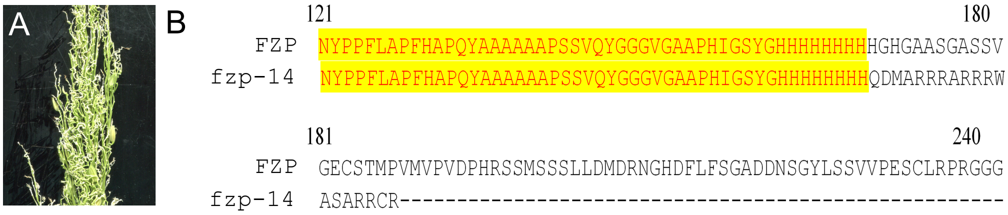
Supplemental Figure 1. A, wild type spikelet at Sp8 stage. B, *fzp-12* spikelet at Sp8 stage. C, length of the sterile lemma, degenerated sterile lemma, rudimentary glume in the wild type and *fzp-12* mutant. D, grain number per panicle, seed setting rate, and grain yield per plant in the wild type and *fzp-12* mutant. rg, rudimentary glume; sl, sterile lemma; dsl, degenerated sterile lemma. Red lines indicate the organ length. Bars = 50 µm. **Significant difference at $P < 0.01$ compared with the wild type by Student's *t*-test.

Supplemental Figure 2

```
       1                                                          60
FZP    MNTRGSGSSSSSSSSQASLMAFSEPPKPASQPSPPSSPMSERPPSGRSRRRAQEPGRFLG
fzp-12 MNTRGSGSSSSSSSSQASLMAFSEPPKPASQPSPPSSPMSERPPSGRSRRRAQEPGRFLG
fzp-13 MNTRGSGSSSSSSSSQASLMAFSEPPKPASQPSPPSSPMSERPPSGRSRRRAQEPGRFLG
       61                                                        120
FZP    VRRRPWGRYAAEIRDPTTKERHWLGTFDTAQEAALAYDRAALSMKGAQARTNFVYTHAAY
fzp-12 VRRRPWGRYAAEIRDPTTKERHWLGTFDTTQEAALAYDRAALSMKGAQARTNFVYTHAAY
fzp-13 VRRRPWGRYAAEIRDSTTKERHWLGTFDTAQEAALAYDRAALSMKGAQARTNFVYTHAAY
       121                                                       180
FZP    NYPPFLAPFHAPQYAAAAAAPSSVQYGGGVGAAPHIGSYGHHHHHHHHHGHGAASGASSV
fzp-12 NYPPFLAPFHAPQYAAAAAAPSSVQYGGGVGAAPHIGSYGHHHHHHHHHGHGAASGASSV
fzp-13 NYPPFLAPFHAPQYAAAAAAPSSVQYGGGVGAAPHIGSYGHHHHHHHHHGHGAASGASSV
       181                                                       240
FZP    GECSTMPVMVPVDPHRSSMSSSLLDMDRNGHDFLFSGADDNSGYLSSVVPESCLRPRGGG
fzp-12 GECSTMPVMVPVDPHRSSMSSSLLDMDRNGHDFLFSGADDNSGYLSSVVPESCLRPRGGG
fzp-13 GECSTMPVMVPVDPHRSSMSSSLLDMDRNGHDFLFSGADDNSGYLSSVVPESCLRPRGGG
       241                                                       300
FZP    AAADHQDMRRYSDADAYGMMGLREDVDDLAQMVAGFWGGGDAADQLGACGFPASGGAADM
fzp-12 AAADHQDMRRYSDADAYGMMGLREDVDDLAQMVAGFWGGGDAADQLGACGFPASGGAADM
fzp-13 AAADHQDMRRYSDADAYGMMGLREDVDDLAQMVAGFWGGGDAADQLGACGFPASGGAADM
       301              318
FZP    VASSQGSDSYSPFSFLSH
fzp-12 VASSQGSDSYSPFSFLSH
fzp-13 VASSQGSDSYSPFSFLSH
```

Supplemental Figure 2. Protein sequence alignment of FZP, fzp-12, and fzp-13. Red arrows indicate the mutated sites in the *fzp-12* and *fzp-13* mutants. *fzp-13* indicates the Cas9 knock-out plant.

Supplemental Figure 3

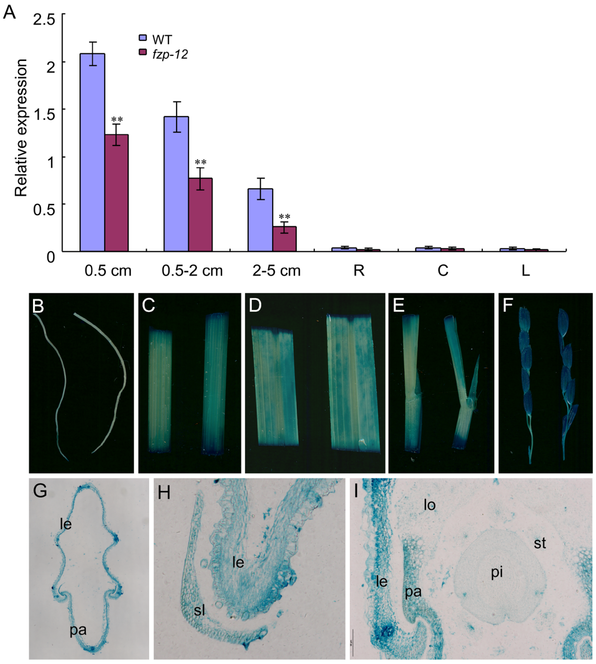


```
         121                                                          180
   FZP  NYPPFLAPFHAPQYAAAAAAAPSSVQYGGGVGAAPHIGSYGHHHHHHHHHGHGAASGASSV
fzp-14  NYPPFLAPFHAPQYAAAAAAAPSSVQYGGGVGAAPHIGSYGHHHHHHHHQDMARRRARRRW

         181                                                        240
   FZP  GECSTMPVMVPVDPHRSSMSSSLLDMDRNGHDFLFSGADDNSGYLSSVVPESCLRPRGGG
fzp-14  ASARRCR-----------------------------------------------------
```

Supplemental Figure 3. *fzp-14* mutant and protein sequence alignment of FZP and fzp-14. A, *fzp-14* mutant. B, protein sequence alignment of FZP and fzp-14. *fzp-14* indicates the Cas9 knock-out plant.

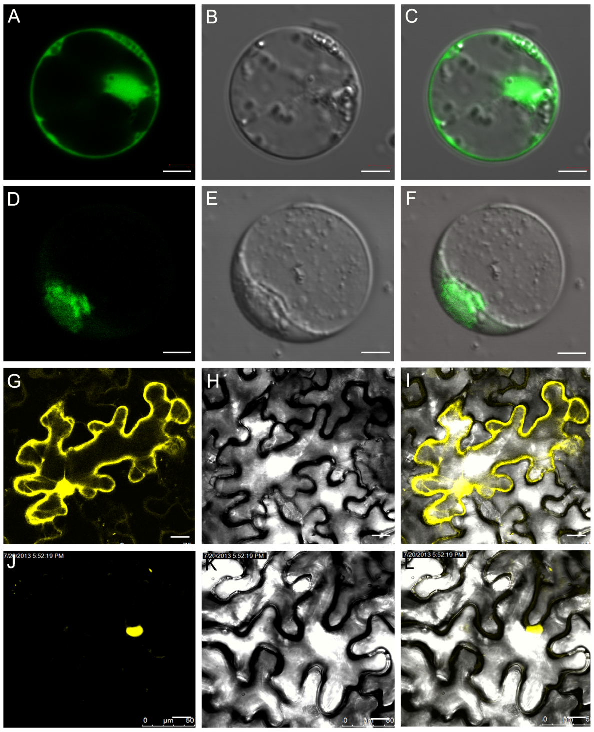
Supplemental Figure 4



Supplemental Figure 4. A, *FZP* expression in different tissues as detected by qPCR. B, GUS staining of root. C, GUS staining of culm. D, GUS staining of leaf. E, GUS staining of leaf sheath. F, GUS staining of spikelet. R, root; C, culm; L, leaf. G-I, Cross-section of the stained spikelets. G, Cross-section of hull. H, Cross-section of sterile lemma. I, Cross-section of inner floral organs. 0.5, young panicles (≤0.5 cm);

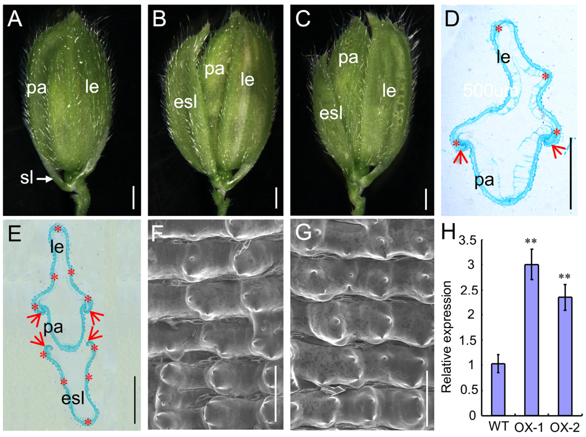
0.5-2, young panicles (0.5-2 cm); 2-5, young panicles (2-5 cm). le, lemma; pa, palea; sl, sterile lemma; st, stamen; pi, pistil. Error bars indicate SD. **Significant difference at $P < 0.01$ compared with the wild type by Student's *t*-test.

Supplemental Figure 5



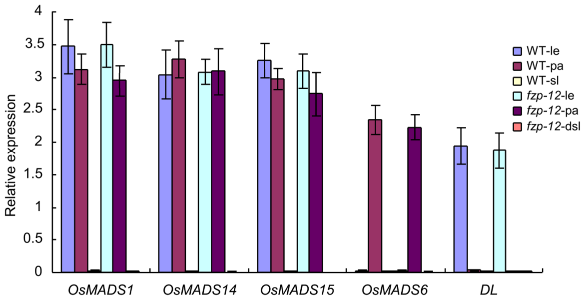
Supplemental Figure 5. Subcellular localization of the FZP protein. A-C, single GFP protein in rice protoplasts. D-F, FZP-GFP in rice protoplasts. G-I, single YFP protein in tobacco (*Nicotiana tabacum*) epidermal cells. J-L, FZP-YFP in tobacco (*Nicotiana tabacum*) epidermal cells. Bars = 5 um in A-F; 10um in G-L.

Supplemental Figure 6



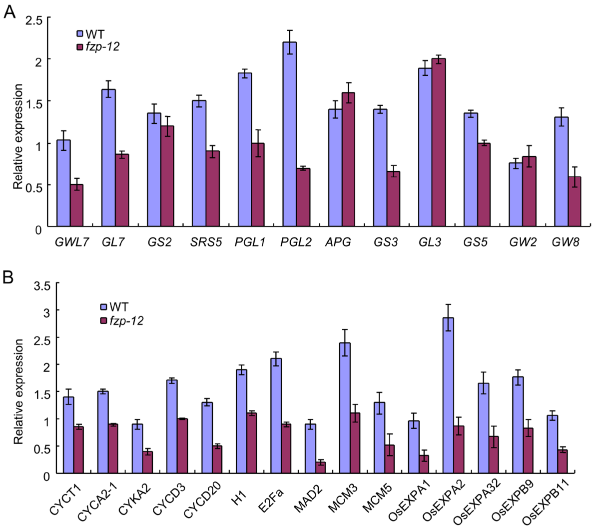
Supplemental Figure 6. A, wild type spikelet. B, spikelet in the *FZP* over-expressing line 1. C, spikelet in the *FZP* over-expressing line 2. D, histological analysis of wild type spikelet. E, histological analysis of spikelet in the *FZP* over-expressing plant. F, epidermal surface of the lemma in the wild type. G, epidermal surface of the sterile lemma in the *FZP* over-expressing plant. H, *FZP* expression analysis in the wild type and *FZP* over-expressing plants. esl, enlarged sterile lemma; sl, sterile lemma; le, lemma; pa, palea. Red stars indicate the vascular bundle. Red arrows indicate the inward hook-like structure. Error bars indicate SD. **Significant difference at $P < 0.01$ compared with the wild type by Student's *t*-test. Bars = 1000 µm in A-C; 500um in D and E; 100um in F and G.

Supplemental Figure 7



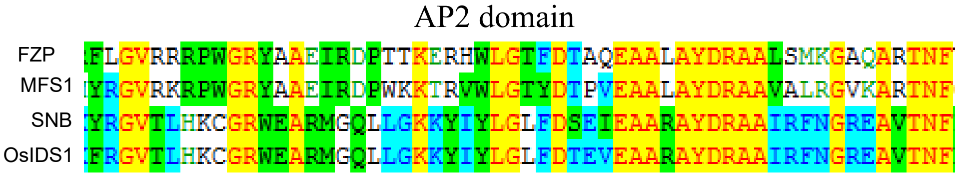
Supplemental Figure 7. Expression of floral organ identity genes in the wild type and *fzp-12* mutant. le, lemma; pa, palea; sl, sterile lemma; dsl, degenerated sterile lemma.

Supplemental Figure 8



Supplemental Figure 8. Expression levels of related genes in wild-type and *fzp-12* mutant. A, Expression analysis of related genes influencing grain size in young panicles. B, Expression analysis of cell proliferation and expansion-related genes in young panicles. Error bars indicate SD. **Significant difference at $P < 0.01$ compared with the wild type by Student's *t*-test.

Supplemental Figure 9. Protein sequence alignment of AP2/ERF genes.


AP2 domain

FZP FLGVRRRPWGRYAAEIRDPTTKERHWLGTFDTAQEAALAYDRAALSMKGAQARTNF
MFS1 YRGVRKRPWGRYAAEIRDPWKKTRVWLGTYDTPVEAALAYDRAAVALRGVKARTNF
SNB YRGVTLHKCGRWEARMGQLLGKKYIYLGLFDSEIEAARAYDRAAIRFNGREAVTNF
OsIDS1 FRGVTLHKCGRWEARMGQLLGKKYIYLGLFDTEVEAARAYDRAAIRFNGREAVTNF

Supplemental Tables

Supplemental Table 1

Cross combination	F1		F2		X^2 (3:1)	P-value
	Wild type	*fzp-12*	Wild type	*fzp-12*		
fzp-12/NJ6	57	0	3612	1189	0.1406	0.7707
NJ6/*fzp-12*	48	0	3025	1043	0.8863	0.3465

Supplemental Table 1. Genetic analysis of the mutant phenotypes of *fzp-12*.

Supplemental Table 2. Primers used in the study.

Purpose	Primer name	Sequence

Mapping	B7-13-1F	ACAGTATCCAAGGCCCTGG
	B7-13-1R	CACGTGAGACAAAGACGGAG
	A7-29-1F	AGTTTTCCTTTCTTTTCTAC
	A7-29-1R	CCTCAGCATGATACCCAC
	A7-33-1F	GCCCAAGATTATGAGA
	A7-33-1R	AAGCTCCGACAATACA
	A7-3-1F	GAGTTCAAGGAAGCACAAAA
	A7-3-1R	CAATGAGACTGTTGCTAACC
	A7-9-1F	TGAGGAGGAGGAGATGGTCG
	A7-9-1R	AGGTGCCCTTTGCAGTTTGA
	A7-13-1F	TGCTACAAGTACGTGCTTTT
	A7-13-1R	GTGGTTGGAGGCGATTTTAT
	A7-25-1F	TGCGTGGTGCAGCATTTGTA
	A7-25-1R	GGCATCACATTGAGCAAGAAA
	A7-26-1F	ACGTGCTTTTCTTGTACCTT
	A7-26-1R	TTTGTGGTTGGAGGCGATTT
	S2-1F	CCTTAAGCTTGCATGGAG
	S2-1R	GGTGGCCGGTGAAAAGT
	S14-1F	GAGCTTTGCCTACAAGG
	S14-1R	CGGGGAACAATGTAACAC
qRT-PCR	*FZP*-1F	GCATGGCTAATCACGCACTTT
	FZP-1R	CCAAGCCACTCTTCTTGTTCG
	OsMADS1-1F	
	OsMADS1-1R	TGATGGTGAGCATGAGGGTG
	OsMADS14-1F	CCATTAACGAGCTTCAACGG
	OsMADS14-1R	TGGTATGGATCTGAAGCCTCC
	OsMADS15-1F	AGTACGCCACTGACTCCAGG
	OsMADS15-1R	TGCTGGCCCCTCACATTC
	OsMADS6-1F	CCAACAATGCACTTTCTGAAAC
	OsMADS6-1R	GGAGGCTTGCTGCATGGC
	DL-1F	CCCATCTGCTTACAACCGCTT
	DL-1R	GTTGGAGGTGGAAACCGTCG
	G1-1F	GGCGTCTACTTGCCATTTCTG
	G1-1R	TCGATCAGCATCAAAGCACAG
	ACTIN-1F	AGCAACTGGGATGATATGGA
	ACTIN-1R	CAGGGCGATGTAGGAAAGC
GUS staining	pro*FZP*-GUS-1F	CAAGAGGAATTAACAGTGCTAATTTC
	pro*FZP*GUS-1R	GTGTTCATGACCAATGCAATATTG
In Situ Hybridization	*G1*H-1F	CGCCTACGACGAGCGTCA
	*G1*SP6-1R	AGATTTAGGTGACACTATAGAAAGCAACCACAGTGAGAAGCACAG
	*DL*H-1F	GGGCCGCAATGGATCTCGTG
	DL SP6-1R	AGATTTAGGTGACACTATAGAATCACAA

		CGAAGGGTGCTCT
Complementation test	*FZP*com-1F	CAAGAGGAATTAACAGTGCTAATTTC
	*FZP*com-1R	CCACCACCTGCGTGTTATATG
	*FZP*OE-1 F	ATGAACACTCGAGGCAGCGG
	*FZP*OE-1 R	TCAATGGGAGAGGAAGCTGAATG
Over-expressing	*FZP*OE-1F	ATGAACACTCGAGGCAGCGG
	*FZP*OE-1R	TCAATGGGAGAGGAAGCTGAATG
EMSA probe (specific)	GCC-1F	CATAAGAGCCGCCACTCATAAGAGCCGCCACTCATAAGAGCCGCCACT
	GCC-1R	GTATTCTCGGCGGTGAGTATTCTCGGCGGTGAGTATTCTCGGCGGTGA
EMSA probe (non-specific)	GCC-2F	CATAAGATACTTGACTCATAAGATACTTGACTCATAAGATACTTGACT
	GCC-2R	GTATTCTATGAACTGAGTATTCTATGAACTGAGTATTCTATGAACTGA
EMSA probe (specific)	DRE-1F	ATACTACCGACATGAGATACTACCGACATGAG ATACTACCGACATGAG
	DRE-1R	TATGATGGCTGTACTCTATGATGGCTGTACTCTATGATGGCTGTACTC
EMSA probe (non-specific)	DRE-2F	ATACGTCTTTGACGAGATACGTCTTTGACGAGATACGTCTTTGACGAG
	DRE-2R	TATGCAGAAACTGCTCTATGCAGAAACTGCTC TATGCAGAAACTGCTC