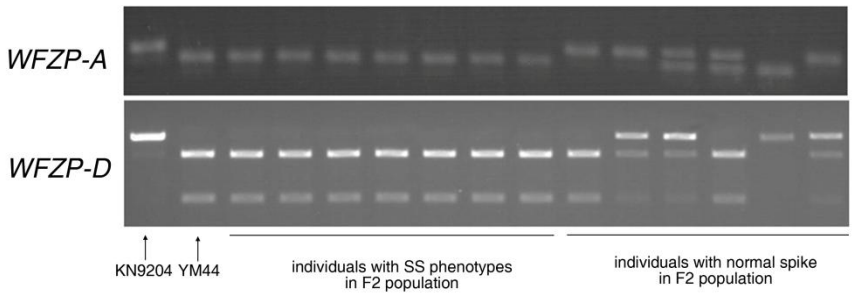

Fig. S1 Linkage analysis of *WFZP-A*, *WFZP-D* and YM44 SSs phenotype. This linkage analysis was conducted using another batch of individuals in the F_2 population differing from those used in Fig. 2A.

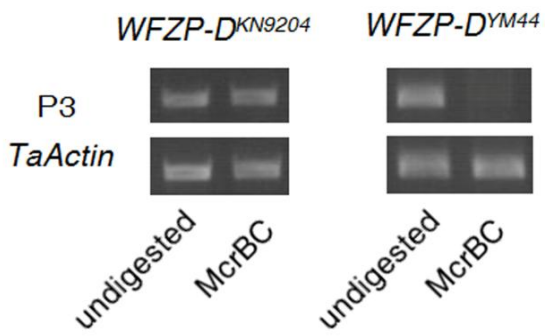

Fig. S2 McrBC analysis of the promoter of *WFZP-D* in the P3 region in the individuals of F_2 crossed by KN9204 and YM44. *WFZP*^{KN9204} indicating individuals with the *WFZP-D* homozygous genotype deriving from KN9204, and *WFZP*^{YM44} indicating individuals with the *WFZP-D* homozygous genotype deriving from YM44.

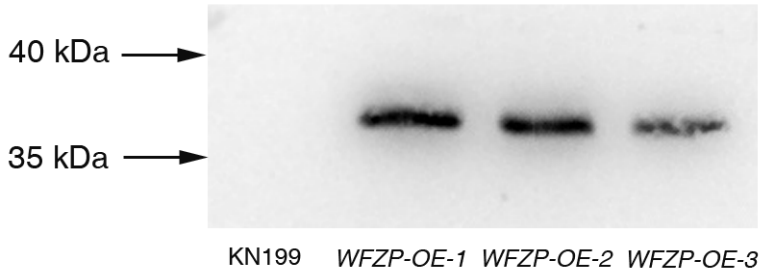

Fig. S3 Western blotting of *WFZP* OE lines expressing the protein of WFZP fused with 3 FLAGs.

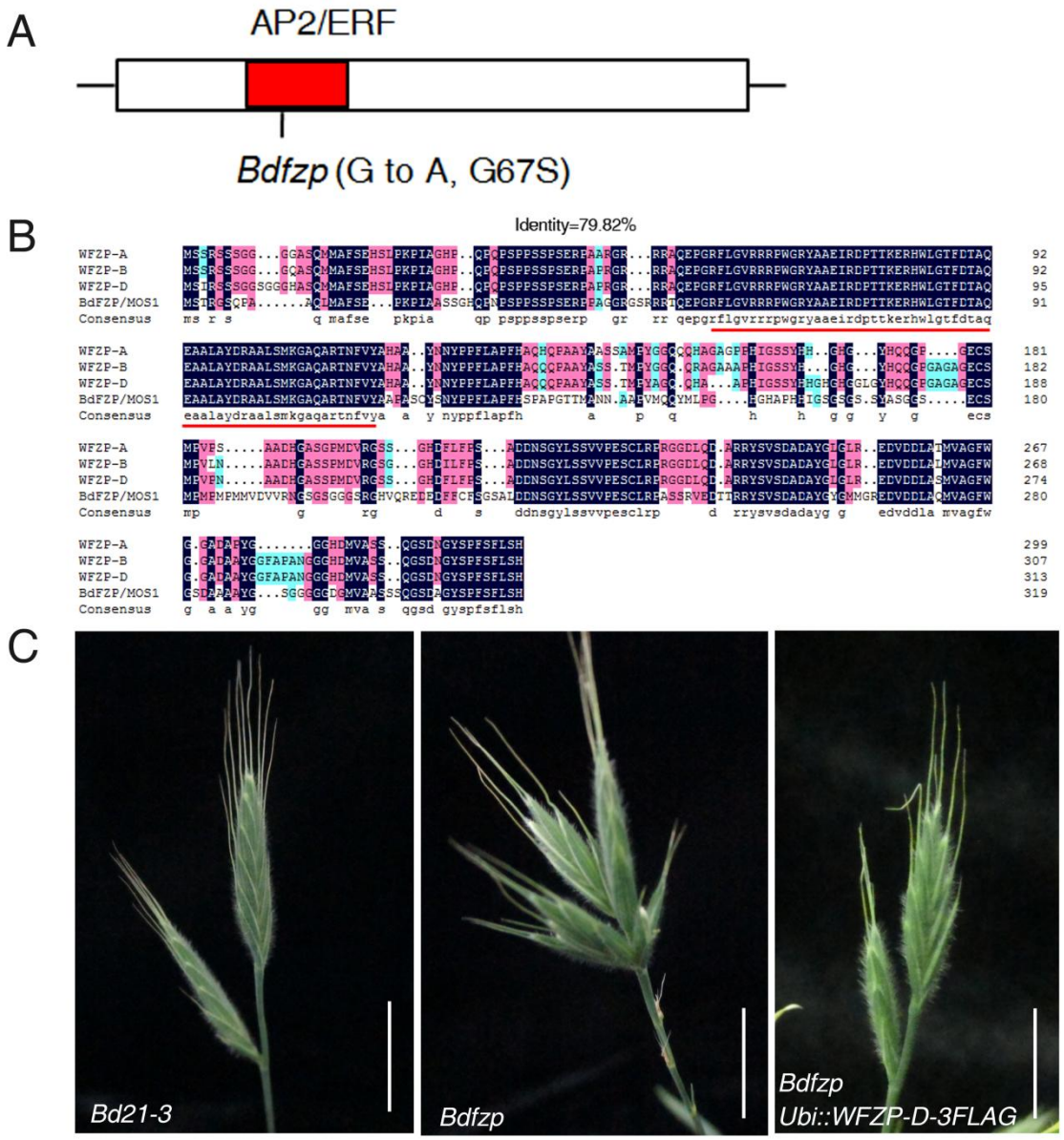

Fig. S4 Functional verification of *WFZP*. (A) The schematic diagram of the sequence of *BdFZP* in *Bdfzp* mutant. A G-to-A mutation occurred in AP2/ERF domain (red color). (B) The protein alignment of WFZP-A, B, D and BdFZP. (C) The spike of *Bd21-3*, *Bdfzp* and *Ubi::WFZP-D* in *Bdfzp*. Bars = 1cm in C.

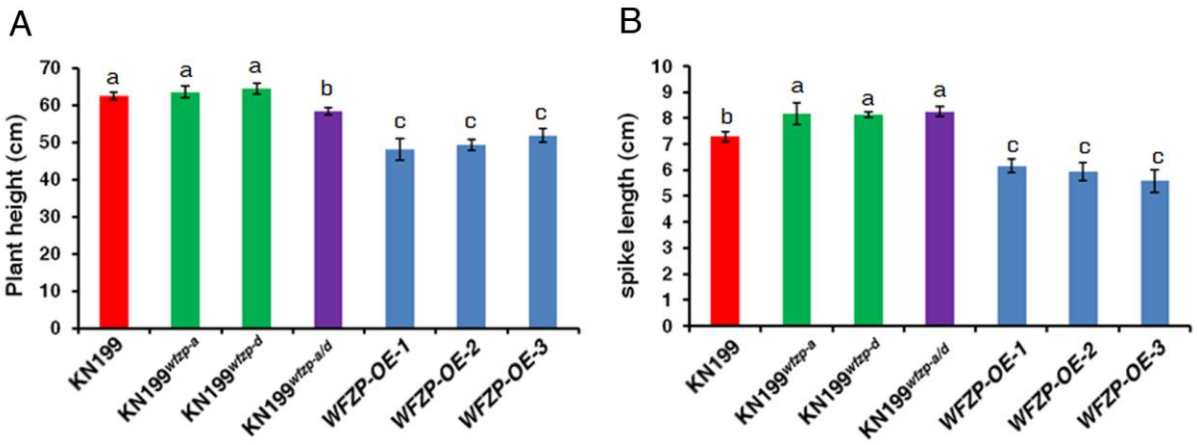

Fig. S5 Statistics comparison of plant height (A) and spike length (B) between KN199, KN199$^{wfzp\text{-}a}$, KN199$^{wfzp\text{-}d}$, KN199$^{wfzp\text{-}a/d}$ and *WFZP* OE lines. The error bars denote ± SE. Different letters mean significant difference at $P<0.01$.

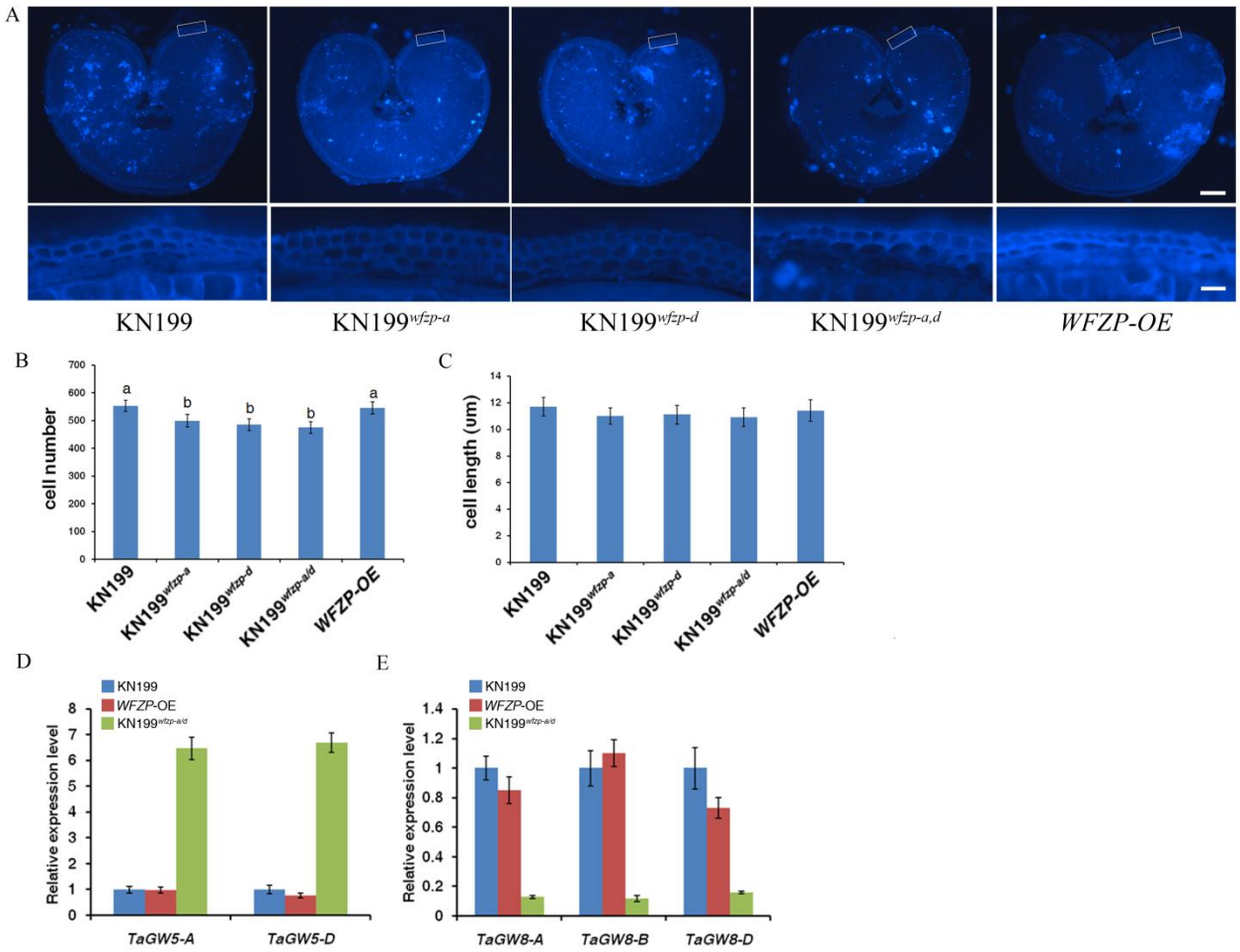

Fig. S6 Effects of *WFZP* on seed coat cell proliferation. (A) Cross sections at the middle of seeds of KN199, KN199$^{wfzp\text{-}a}$, KN199$^{wfzp\text{-}d}$, KN199$^{wfzp\text{-}a/d}$ and *WFZP* OE lines stained with Fluorescent Brightener 28. Figures in the bottom part were magnified figures in the pane in the upper part. (B) and (C) Statistics comparison of cell number (B) and cell length (C) in the cross section of the outer seed integuments of KN199, KN199$^{wfzp\text{-}a}$, KN199$^{wfzp\text{-}d}$, KN199$^{wfzp\text{-}a/d}$ and *WFZP* OE lines. The error bars denote ± SE. Different letters mean significant difference at P<0.01. (D) and (E) The expression level of *TaGW5* (D) and *TaGW8* (E) in KN199, *WFZP OE*, and KN199$^{wfzp\text{-}a/d}$ detected by qPCR. The error bars denote ± SE.

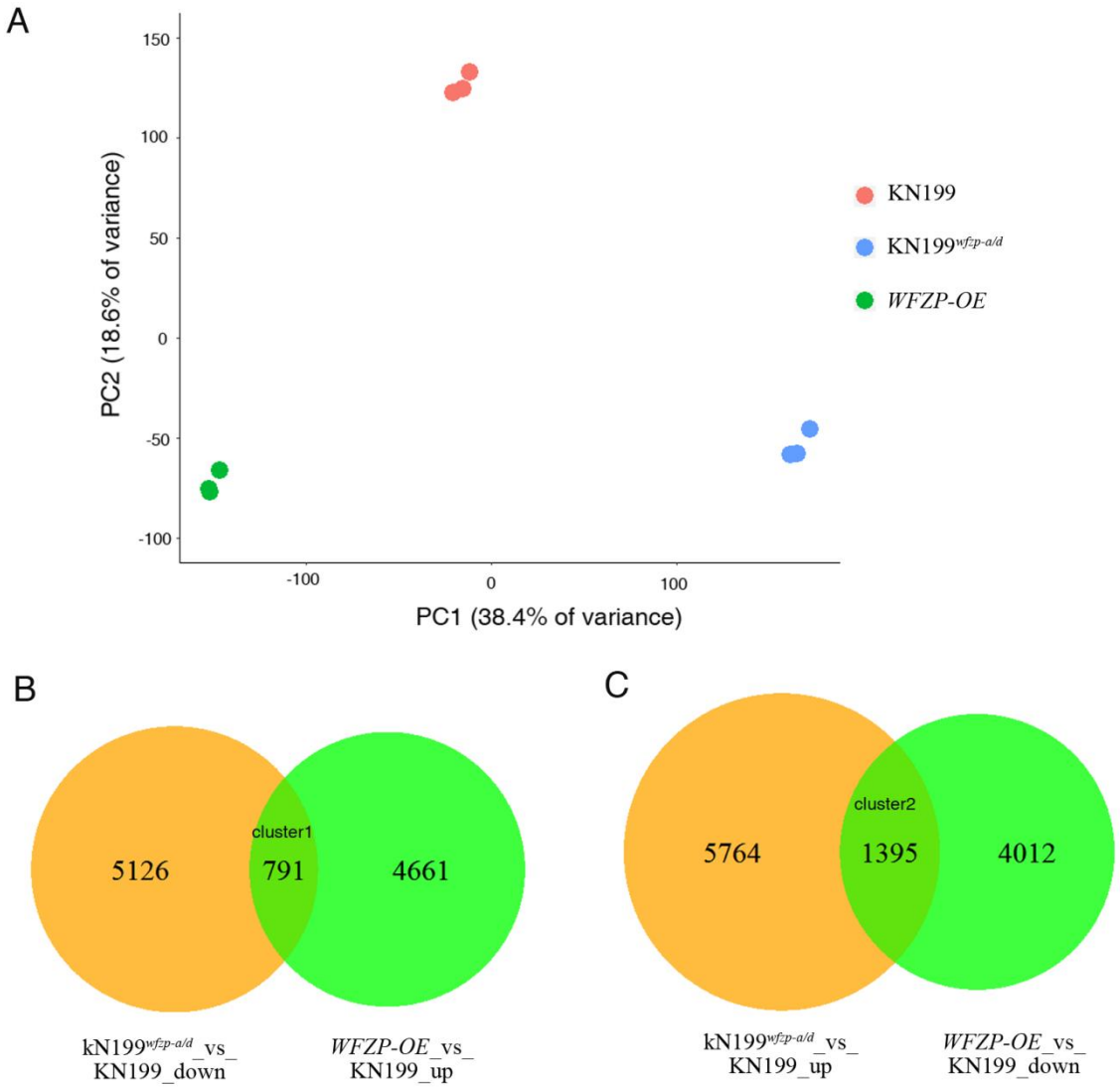

Fig. S7 The overall view of RNA-seq data. (A) The PCA result of RNA-seq data of different samples. (B) The overlapped DEGs between KN199$^{wfzp\text{-}a/d}$_vs_KN199 down-regulated genes and *WFZP-OE*_vs_KN199 up-regulated genes. (C) The overlapped DEGs between KN199$^{wfzp\text{-}a/d}$_vs_KN199 up-regulated genes and *WFZP-OE*_vs_KN199 down-regulated genes.

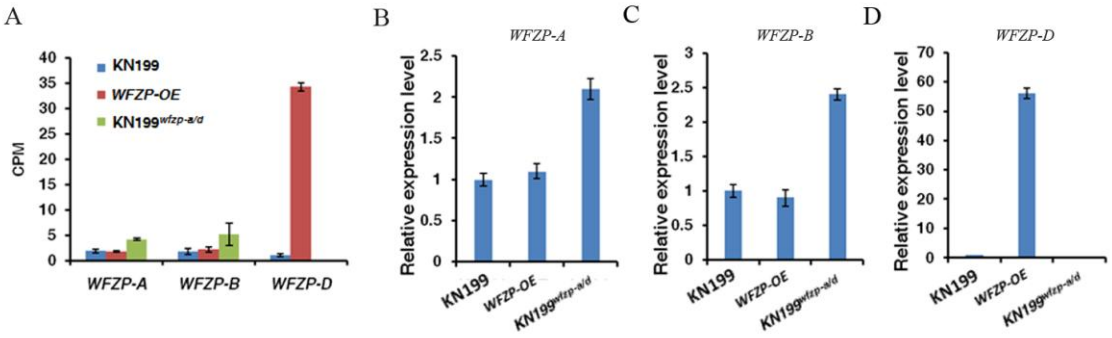

Fig. S8 The expression level of *WFZP-A*, *B* and *D* in KN199, KN199$^{wfzp\text{-}a/d}$ and *WFZP* OE lines detected by RNA-seq (A) and qPCR (B to D). The error bars denote ± SE.

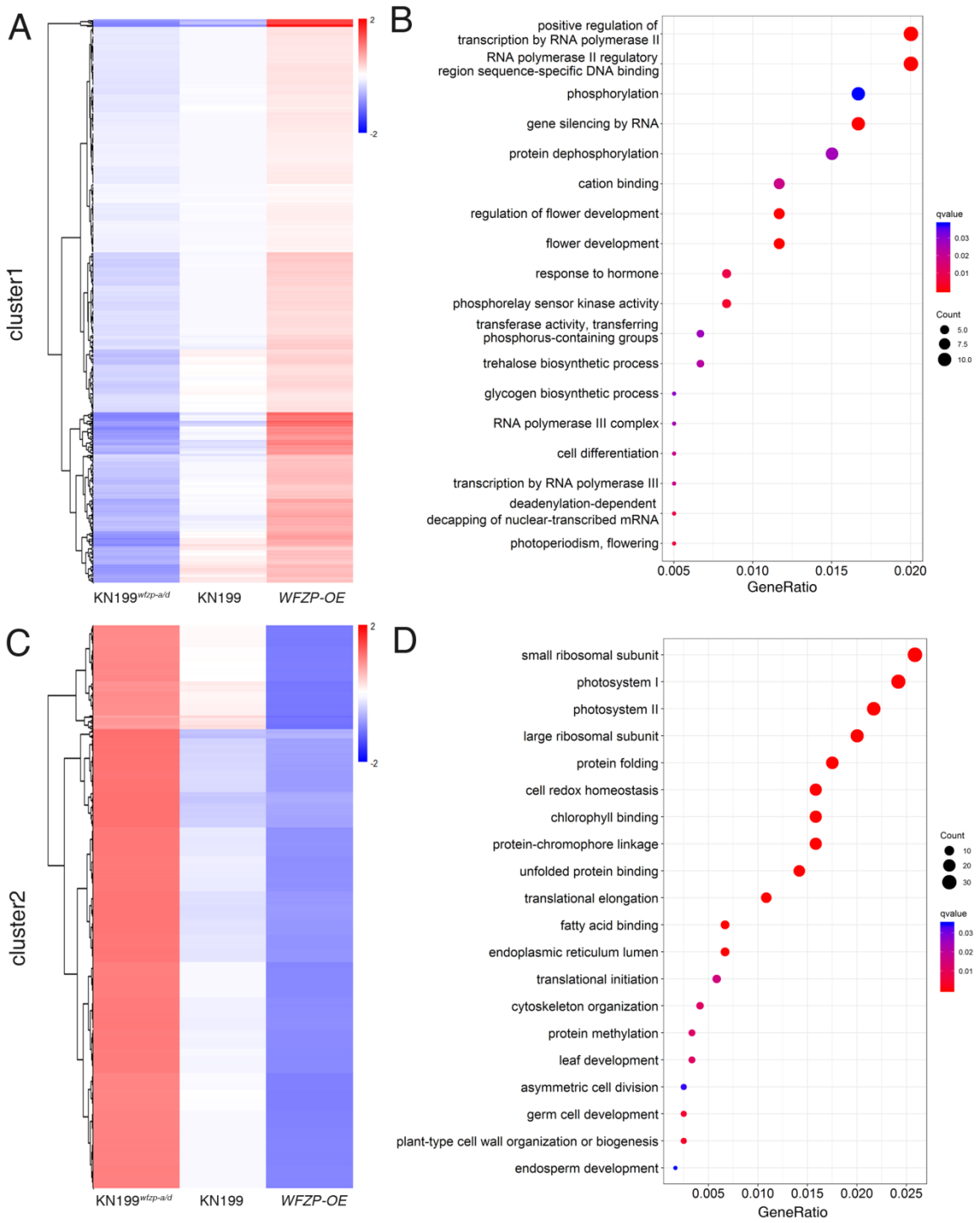

Fig. S9 GO enrichment analysis of genes in the overlapped DEGs of KN199$^{wfzp\text{-}a/d}$ up-regulated/down-regulated genes and *WFZP-OE* down-regulated/up-regulated genes. (A) Heatmap of genes down-regulated in KN199$^{wfzp\text{-}a/d}$ and up-regulated in *WFZP-OE* line. (B) GO enrichment analysis of genes down-regulated in KN199$^{wfzp\text{-}a/d}$ and up-regulated in *WFZP-OE* line. (C) Heatmap of genes up-regulated in KN199$^{wfzp\text{-}a/d}$ and down-regulated in

WFZP-OE line. (D) GO enrichment analysis of genes up-regulated in KN199$^{wfzp\text{-}a/d}$ and down-regulated in *WFZP-OE* line.

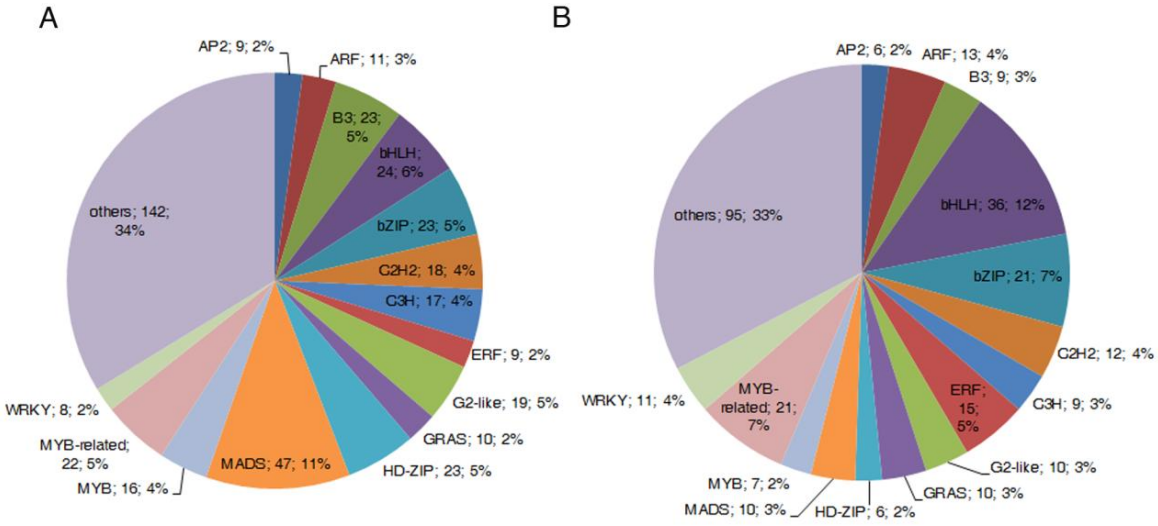

Fig. S10 Transcription factors in the KN199$^{wfzp\text{-}a/d}$_vs_KN199 down-regulated genes (A) and KN199$^{wfzp\text{-}a/d}$ _vs_KN199 up-regulated genes (B).

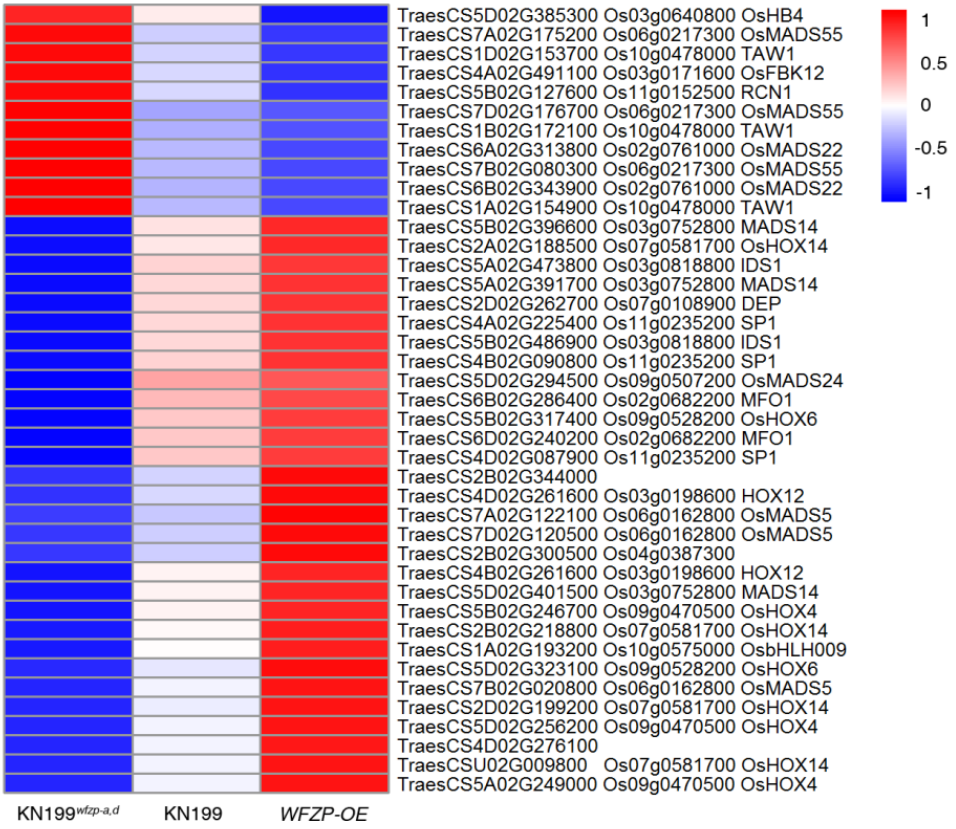

Fig. S11 Heatmap of MADS family TFs, HD-ZIP family TFs and other development related genes in the overlapped DEGs of KN199$^{wfzp\text{-}a/d}$ up-regulated/down-regulated genes and *WFZP-OE* down-regulated/up-regulated genes.

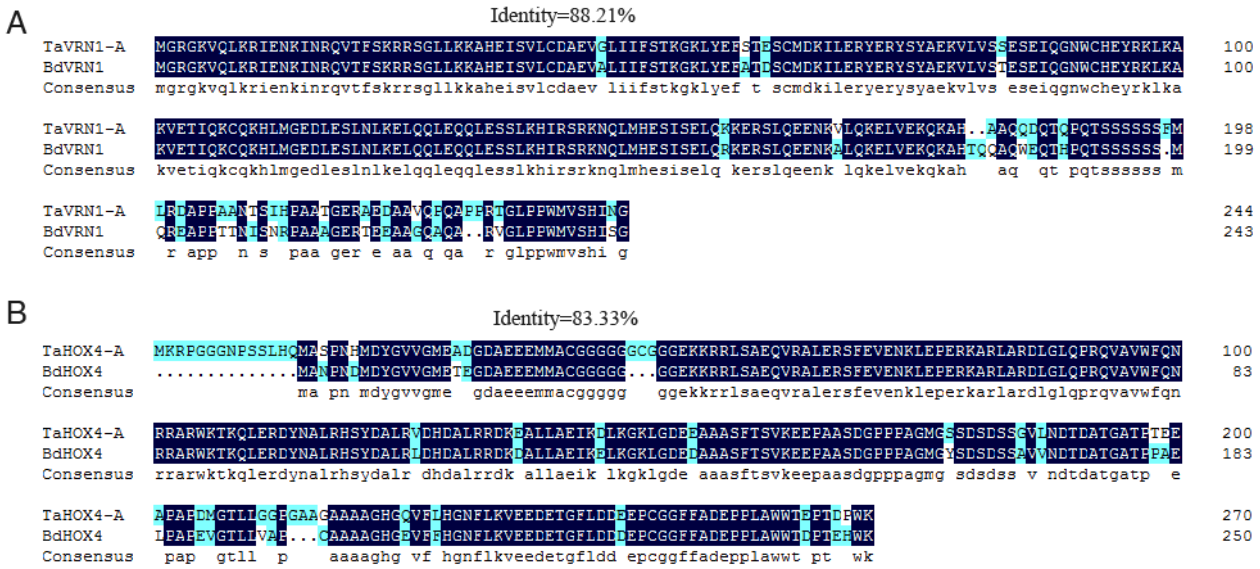

Fig. S12 The protein alignment of TaVRN1-A and BdVRN1 (A) and TaHOX4-A and BdHOX4 (B).

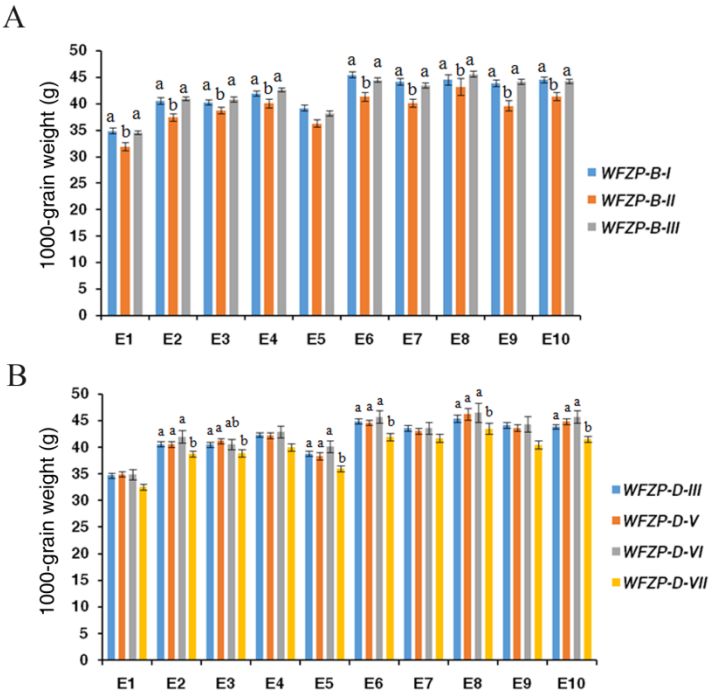

Fig. S13 1000-grain weight of cultivars with different haplotypes of *WFZP-B* (A) and *WFZP-D* (B) in ten growing environments. The error bars denote ± SE. Different letters mean significant difference at $P<0.05$. Note that the number of cultivars with *WFZP-D-I*, *II* and *IV* were too few (2, 3 and 2 for each, Supplemental dataset S7), so only the other four haplotypes were analyzed.

Table S1. The polymorphism of *WFZP-B*

No.	Site	Variation type	*WFZP-B-I*	*WFZP-B-II*	*WFZP-B-III*
1	-1987 - -1933	Indel	Del	Del	In
2	-1839	SNP	T	T	C
3	-1809- -1808	SNP	CT	CT	TC
4	-1747	SNP	T	T	C
5	-1726	SNP	C	C	T
6	-1419	SNP	T	T	C
7	-1208	SNP	T	T	C
8	-1187	SNP	A	A	G
9	-867	SNP	C	C	G
10	-785	SNP	A	A	G
11	-752- -750	Indel	Del	Del	In
12	-559	SNP	G	G	A
13	-545	SNP	T	T	C
14	-484	SNP	G	A	G
15	-482	SNP	A	A	G
16	-469	SNP	C	C	A
17	-424- -412	Indel	Del	Del	In
18	-392	SNP	T	T	C
19	-374	SNP	C	C	T
20	-362	SNP	A	A	G
21	-330- -315	Indel	Del	Del	In
22	-311	SNP	T	T	C
23	-308	SNP	A	A	G
24	-269	SNP	G	G	A
25	-137	SNP	T	T	A
26	144	SNP	T	T	C
27	491	SNP	G	G	A
28	619	SNP	T	T	A

Variations labeled with the same color were linked.

Variations highlighted were selected to develop molecular markers.

Table S2. The polymorphism of *WFZP-D*

No.	Site	Variation type	*WFZP-D-I*	*WFZP-D-II*	*WFZP-D-III*	*WFZP-D-IV*	*WFZP-D-V*	*WFZP-D-VI*	*WFZP-D-VII*
1	-1974	SNP	G	G	G	C	C	C	G
2	-1425	SNP	G	G	G	A	A	A	G
3	-1410	Indel	In	Del	In	Del	In	Del	Del
4	-1344	SNP	T	T	T	C	C	C	T
5	-1261	SNP	T	T	T	G	G	G	T
6	-1183	SNP	T	T	T	C	C	C	T
7	-1166	SNP	C	C	C	T	T	T	C
8	-1164	SNP	C	T	C	T	C	T	T
9	-1063	SNP	T	C	C	T	T	C	T
10	-908	SNP	T	T	T	A	A	A	T
11	-843	SNP	C	A	C	A	C	A	A
12	-742	SNP	T	T	T	A	A	A	T
13	-528	SNP	A	G	A	G	A	G	G
14	-378	SNP	T	T	T	A	A	A	T
15	552	SNP	C	C	C	G	G	G	C

Variations labeled with the same color were linked.

Variations highlighted were selected to develop molecular markers.

Table S3. Association analysis of *WFZP* with SNS and TGW

environment	Years	location	Water and temperature	P-value					
				WFZP-A		*WFZP-B*		*WFZP-D*	
				SNS	TGW	SNS	TGW	SNS	TGW
E1	2015	Shunyi	DS+HS	**0.00496***	**0.0075***	0.77482	**0.03662***	0.96727	0.05439
E2	2015	Shunyi	DS	**0.01641***	**0.0001376***	0.74611	**5.026E-06***	0.33573	**0.02965***
E3	2015	Shunyi	WW+HS	**0.02615***	0.22213	0.39132	**0.03341***	0.92688	**0.03128***
E4	2015	Shunyi	WW	0.08337	**0.0006261***	0.93637	**0.006***	0.74899	0.06958
E5	2016	Shunyi	DS+HS	**0.02464***	0.53468	0.07453	0.07095	0.95462	**0.02916***
E6	2016	Shunyi	DS	**0.00316***	**0.00358***	0.14227	**5.388E-05***	0.733	**0.01924***
E7	2016	Shunyi	WW+HS	0.18959	0.08703	0.18488	**5.749E-05***	0.95009	0.66021
E8	2016	Shunyi	WW	**0.02339***	**6.935E-05***	0.14266	**0.00689***	0.61586	**0.0176***
E9	2016	Changping	WW	**0.00663***	0.07545	0.05396	**0.0001063***	0.93546	0.0554
E10	2016	Changping	DS	**5.201E-05***	**0.00313***	0.31636	**0.0002177***	0.19367	**0.0003555***

SNS, spikelet number per spike; TGW, thousand grain weight; DS, drought stress; HS, heat stress; WW, well-watered.

Table S4. Primers used in this study

Primer name	**Sequence**	**Aim and introduction**	**Reference**
Primers for construction			
WFZP-2DOE-F	CGACTCTAGAGGATCCTCAGTTCTGCCATGAGCATC	Clone *WFZP-D* into pTCK303-3FLAG vector	
WFZP-2DOE-R	GCTTGGCGCGACTAGTGTTGTTTCTGTGGGAGAGGAAG		
VRN1-OE-F	CGACTCTAGAGGATCCATGGGGCGGGGGAAGGT	Clone *VRN1-A* into pTCK303-3FLAG vector	
VRN1-OE-R	GCTTGGCGCGACTAGTCCCGTTGATGTGGCTCACC		
TaHOX4-OE-F	CGACTCTAGAGGATCCATGAAGCGGCCCGGCGG	Clone *TaHOX4-A* into pTCK303-3FLAG vector	
TaHOX4-OE-R	GCTTGGCGCGACTAGTCTTCCAGGGATCCGTCGG		
WFZP-pMN6-F	TTGACTGTATCGCCCGGGATGAGCATCCGCAGCAGCA	Clone *WFZP-D* into pMN6 vector	
WFZP-pMN6-R	GGAAATTCGAGCTCGGTACCTCAGTGGGAGAGGAAGCTGAA		
WFZP-A-P-F3	GACCCCATAAAGCCATAGATTAGG	Clone *WFZP-A* promoter into ENTR1A-T vector	
WFZP-A-P-R	GGCAGAAGTGAAGTGAGGTTGG		
LUC-F1-KpnI	CGGGGTACCCCGATGGAAGACGCCAAAAACATA	Clone *LUC* into the downstream of *WFZP-A* promoter	
LUC-R1-NotI	ATTTGCGGCCGCTTTATTACAATTTGGACTTTCCGCC		
RLUC-F-SalI	ACGCGTCGACGTCGATGACTTCGAAAGTTTATGATCC	Clone *R-LUC* into ENTR1A-T vector	
RLUC-R-EcoRI	CGGAATTCCGTTATTGTTCATTTTTGAGAACTCG		

Primers for genotyping			
Xwmc522-F	AAAAATCTCACGAGTCGGGC	SSR marker for linkage analysis	https://wheat.pw.usda.gov/GG3
Xwmc522-R	CCCGAGCAGGAGCTACAAAT		
Cfd56-F	TTGCATAATTACTTGCCCTCC		
Cfd56-R	CTGGTCCAACTTCCATCCAT		
WFZP-D-P-F3	GACCCCATAAAGCCATGGATTAGG	Linkage analysis of *WFZP-D* and SSs. PCR product was digested using *EcoNI*.	
WFZP-D-P-R2	CGTCTGAGATAACGCTTTTAGCTG		
WFZP_F3	GCTCACAGTCTCAGCAACCA	Linkage analysis of *WFZP-D* and SSs. WFZP_F3 + WFZP_2A_R3 used for first round PCR.	(Dobrovolskaya et al., 2015)
WFZP_2A_R3	CACTGGGCACCGGCATGGAA		
WFZP-A-indel-F2	AGCCGCAGCCGTCCCCG		
WFZP-A-indel-R2	AAGCGCCCGGGCTCCTG		
Me-4F	GCAGGCATCTTTACACCATCTTA	dCAPs primer of *WFZP-A* at -387 loci, Me-4F+2A-R2 used for first round PCR, 387F+ 387R used for second round PCR, using *HinfI* to digest the PCR product	
WFZP-2A-R2	TGGCAGAAGTGAAGTGAGGT		(Dobrovolskaya et al., 2015)
WFZP-A-387F	GCAAGGATTGTGGCATGCA		
WFZP-A-387R	CAAAGAGATGAGGAGAATGTTGAG		
WFZP-B-P-F1	GCGGATTAACTTTGACCTCTG	Indel marker for *WFZP-B* at -1987 - -1933 loci, F1+Indel-R used for first round PCR, F5+Indel-R used for second round PCR	
WFZP-B-P-F5	GAGCATCTTCAACAGGCGTCA		
WFZP-B-Indel-R	GGGAGCGACGAAGAGGTTT		

WFZP-B-484F	CATTCCCTCCTTTTACTCCT	dCAPs primer of *WFZP-B* at -484 loci, 484F+P-R used for first round PCR, 484F+484R used for second round PCR, using *ScaI* to digest the PCR product	
WFZP-B-484R	TATGGTCTTATAGGGACTTATAAGTAC		
WFZP-AB-P-R	GGCAGCGAATGCTCCGAGAAG		
WFZP-D-P-F3	GACCCCATAAAGCCATGGATTAGG	dCAPs primer of *WFZP-D* at -1974 loci, P-F3+Me1R used for first round PCR, 1974F+ 1974R used for second round PCR, using *SalI* to digest the PCR product	
Me1R	GTATCATCAGCGGTCAAAGTTAACG		
WFZP-D-1974F	TGATCCTTGTCCAAGCATTTGTCGA		
WFZP-D-1974R	CTCTCACATGAGGGGAGGGC		
Me-3F	GCCTGCAAATTCTGGGTG	dCAPs primer of *WFZP-D* at -1063 loci, Me3F+Me3R used for first round PCR, 1063F+ 1063R used for second round PCR, using *ApaLI* to digest the PCR product	
Me-3R	CTTCAATTATATGGCCCTACATGT		
WFZP-D-1063F	TCTCCTATGTTCATTCTAGTGTGCA		
WFZP-D-1063R	GATACATGCCAAAATGCTACAC		
Me-3F	GCCTGCAAATTCTGGGTG	dCAPs primer of *WFZP-D* at -843 loci, Me3F+Me3R used for first round PCR, 843F+ 843R used for second round PCR, using *HinfI* to digest the PCR product	
Me-3R	CTTCAATTATATGGCCCTACATGT		
WFZP-D-843F	GGCAAGCTCTCTTCTTTCGATT		
WFZP-D-843R	GCCTTGCATGCTTTGATGAT		
Primers for qPCR or ChIP-PCR			
WFZP_F3	GCTCACAGTCTCAGCAACCA	qPCR of *WFZP-A*	(Dobrovolskaya et al., 2015)
WFZP_2A_R2	TGGCAGAAGTGAAGTGAGGT		

WFZP_F5	ACGACATGGTCGCCTCGT	qPCR of *WFZP-B*	(Dobrovolskaya et al., 2015)
WFZP_2B_R3	CGGTGCATTTGCTTCAGTGT		
WFZP_F5	ACGACATGGTCGCCTCGT	qPCR of *WFZP-D*	(Dobrovolskaya et al., 2015)
WFZP_2D_R5	CTGGCTGGTGCATTTGTTG		
WFZP-D-OE-q-F	CACATTGGCAGCTCGTACCA	qPCR of *WFZP-D* in *WFZP* overexpression lines	
WFZP-D-OE-q-R	TGGGGAAGAGGAAGTCGTG		
VRN1-q-F	GATCAAACTCAGCCTCAAACCA	qPCR of selected genes	
VRN1-q-F	CCGCATCCTCTGCCCTCT		
TaHOX4-q-F	TGGCCAGCCCCAATCATAT		
TaHOX4-q-R	GGCTCCAGCTTGTTCTCCA		
BdVRN1-q-F	GCTCTGCAGAAGGAACTTGTGG		(Ream et al., 2014)
BdVRN1-q-R	CTAGTTTGCGGGTGTGTTTGCTC		
BdHOX4-q-F	GAGATCAAGGAGCTGAAGGG		
BdHOX4-q-R	CTGGAGTCGCTGTCGGAATA		
TaGW5-A-F	CACGGTTCATGGCAGTGAG		
TaGW5-A-R	CACATGATTGATCACAACGATG		
TaGW5-D-F	GTGCAACCGGGTGGAGGA		
TaGW5-D-R	TCACCACCTCCTCTGCAAGG		

TaGW8-7A-RTF	GCAGGCAGCATTTTGGTGTA		(Ma et al., 2019)
TaGW8-7A-RTR	TGGGGATGTGTTCAGTCTGC		
TaGW8-7B-RTF	CTGACTCCAGTGCTGGACTCA		(Ma et al., 2019)
TaGW8-7B-RTR	GTTGCTCATTTTCCCCCACA		
TaGW8-7D-RTF	ACAGGCAGCATTTTGGTCTC		(Ma et al., 2019)
TaGW8-7D-RTR	TCTGGCCAACATCGATACCG		
VRN1-ChIP-F1	GGAAACCAAGTAATCACTAACTTG	ChIP-PCR of certain regions of selected genes	
VRN1-ChIP-R1	TGCGGTGTATCTCCAAGAATG		
VRN1-ChIP-F2	GACCTAGCCAGCCAGCATT		
VRN1-ChIP-R2	GAAGGGAAAGAGCGGAGTT		
VRN1-ChIP-F3	CCTCACCCAACCACCTGA		
VRN1-ChIP-R3	CAACCCTACGCCCCTACC		
TaHOX4-ChIP-F1	CTATGGGAGATGTCCTAAACC		
TaHOX4-ChIP-R1	ACATTACACTCCAGCAAAGAA		
TaHOX4-ChIP-F2	CTCTTCTCGCAGTAATCGG		
TaHOX4-ChIP-R2	GGAGGGAGGAGGGGTTT		
Primers for amplifying templates of in situ probes			
WFZP- FSP6	GATTTAGGTGACACTATAGAATACATGAGCATCCGCAGCAGCAG	To amplify templates of in situ	

WFZP- RT7	TGTAATACGACTCACTATAGGGCGATCAGTGGGAGAGGAAGCTG A	probes of selected genes	
VRN1-FSP6	GATTTAGGTGACACTATAGAATACATGGGGCGGGGGAAGGT		
VRN1-RT7	TGTAATACGACTCACTATAGGGCGACCCGTTGATGTGGCTCACC		
TaHOX4-FSP6	GATTTAGGTGACACTATAGAATACATGAAGCGGCCCGGCGG		
TaHOX4-RT7	TGTAATACGACTCACTATAGGGCGACTTCCAGGGATCCGTCGG		
Primers for McrBC analysis			
Me-1F	GACCCCATAAAGCCATGGATTAGG	McrBC analysis of certain region in the promoter of *WFZP-D*	
Me-1R	GTATCATCAGCGGTCAAAGTTAACG		
Me-2F	AGTCTGAGTGGTCAAGACGCG		
Me-2R	AAACACGGCACCCAATCC		
Me-3F	GCCTGCAAATTCTGGGTG		
Me-3R	CTTCAATTATATGGCCCTACATGT		
Me-4F	GCAGGCATCTTTACACCATCTTA		
Me-4R	GGATGAGATGGCGTGATAGG		
Me-5F	GACTGGCACAACATTCTCCTCC		
Me-5R	TGCTGCTGCGGATGCTCA		
Primers for SAAB			

SAAB-oligonucleotide	GAGAGGATCCAGTCAGCATGNNNNNNNNNNNNNNNNNNNCTCAGCCTCGAGAATTCCAA		(Smith et al., 2002)
SAAB-F	GGGCTGGCAAGCCACGTTTGGTG		
SAAB-R	CCGGGAGCTGCATGTGTCAGAGG		

Reference

Dobrovolskaya, O., Pont, C., Sibout, R., Martinek, P., Badaeva, E., Murat, F., Chosson, A., Watanabe, N., Prat, E., Gautier, N., Gautier, V., Poncet, C., Orlov, Y.L., Krasnikov, A.A., Berges, H., Salina, E., Laikova, L. and Salse, J. (2015) *FRIZZY PANICLE* Drives Supernumerary Spikelets in Bread Wheat. *Plant Physiology* **167**, 189-199.

Ma, L., Hao, C., Liu, H., Hou, J., Li, T. and Zhang, X. (2019) Diversity and sub-functionalization of TaGW8 homoeologs hold potential for genetic yield improvement in wheat. *Crop Journal* **7**, 830-844.

Ream, T.S., Woods, D.P., Schwartz, C.J., Sanabria, C.P., Mahoy, J.A., Walters, E.M., Kaeppler, H.F. and Amasino, R.M. (2014) Interaction of Photoperiod and Vernalization Determines Flowering Time of Brachypodium distachyon. *Plant Physiology* **164**, 694-709.

Smith, H.M.S., Boschke, I. and Hake, S. (2002) Selective interaction of plant homeodomain proteins mediates high DNA-binding affinity. *P Natl Acad Sci USA* **99**, 9579-9584.