Fig. S1 (a) Individual internodes W7 (left) and *gw9* mutant (right), panicle-neck internode as the first internode. Bars = 5 cm. (b) Culm cross-sections of individual internodes of W7 and *gw9* mutant. Bars = 5 mm. (c) Average internode length of W7 and *gw9* mutant (n=15). (d) Average internode diameter of W7 and *gw9* mutant (n=15). Error bars represent standard deviation (SD). **, $p < 0.01$; *, $p < 0.05$ (Student's *t*-test).

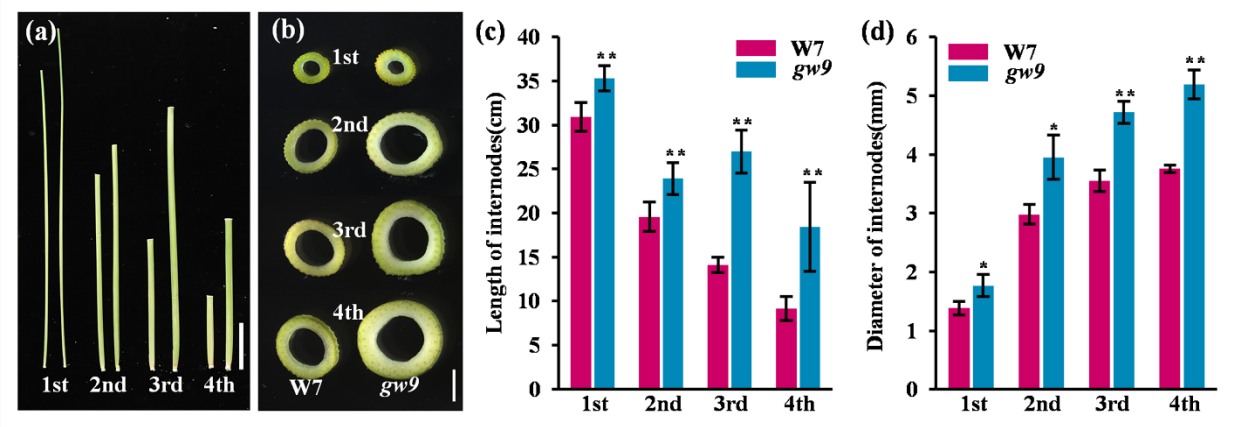

Fig. S2 Grain filling analysis of W7 and *gw9* mutant. (a) Brown grains of W7 and *gw9* mutant after fertilization. (b) Time-course measurement of the fresh weight of brown grain (n=3). (c) Time-course measurement of the dry weight of brown grain (n=3). (d) Grain filling rate of W7 and *gw9* mutant. Error bars represent standard deviation (SD). **, $p < 0.01$ (Student's *t*-test).

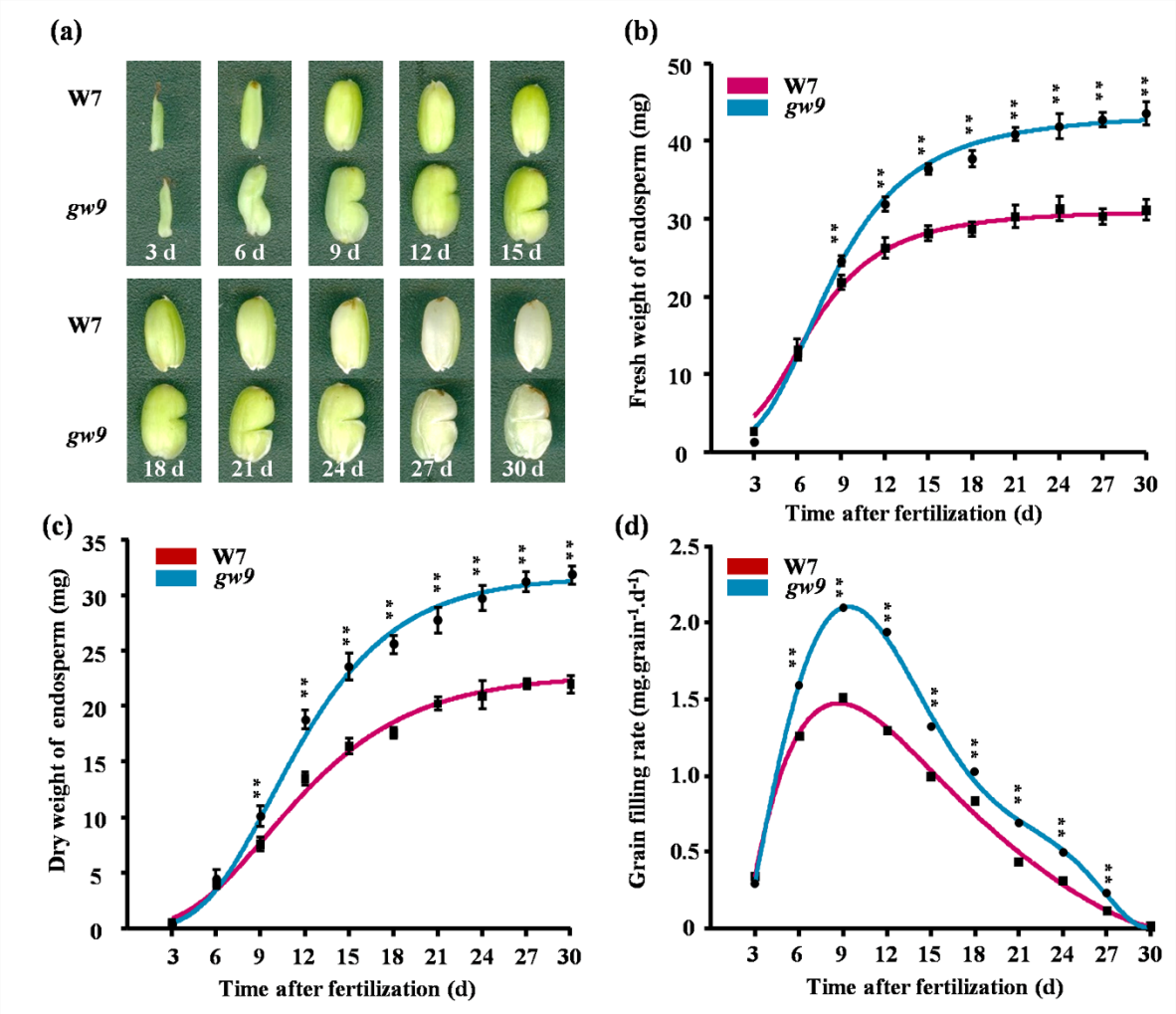

Fig. S3 (a) The relative expression levels of grain size-related genes in W7 and *gw9* mutant. (b) The relative expression levels of cell cycle-related genes in W7 and *gw9* mutant. Error bars represent standard deviation (SD). **, p < 0.01 (Student's *t*-test).

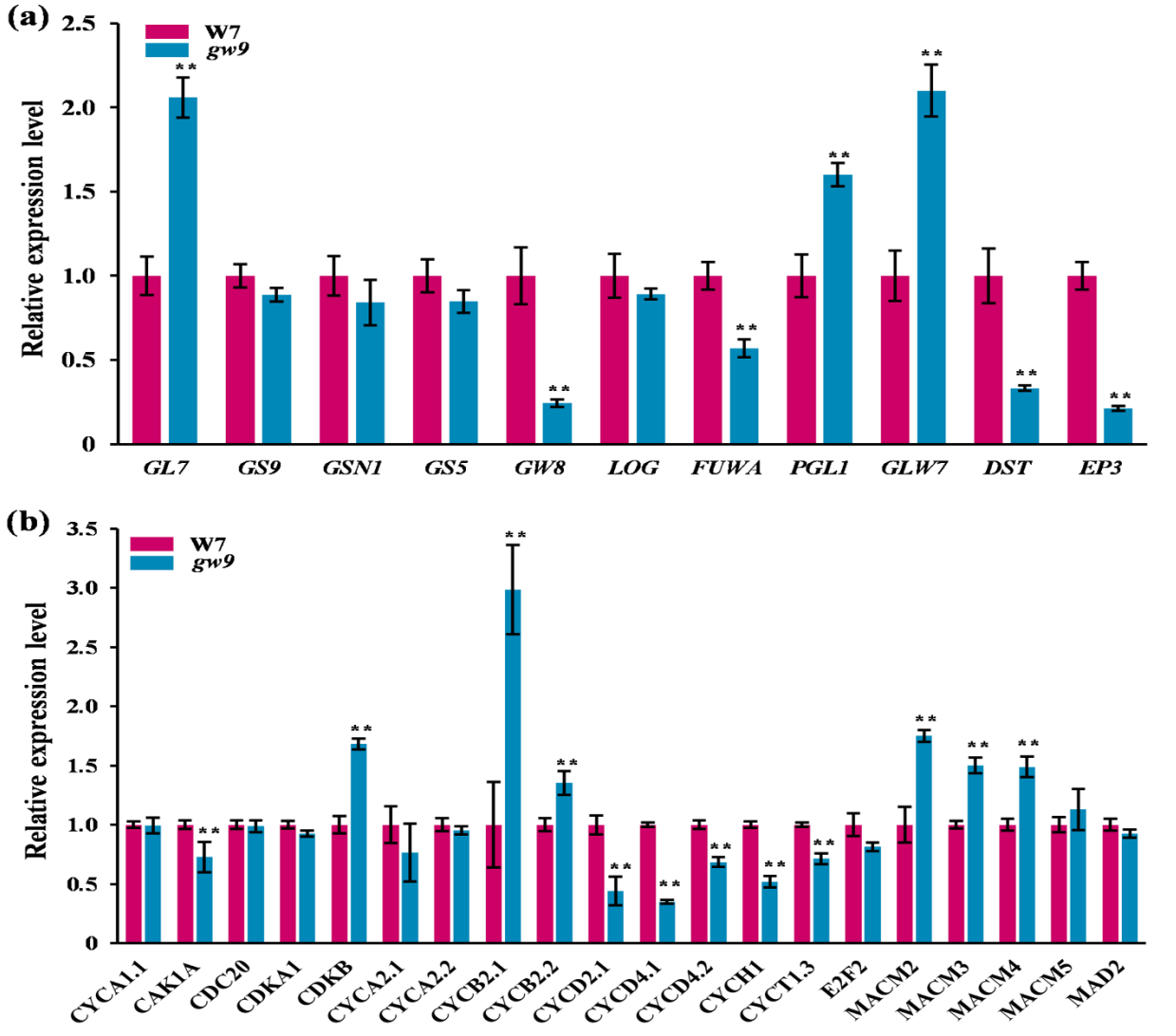

Fig. S4 (a) Sequence analysis of GW9 coding sequence in W7 and *gw9* mutant. The red box indicates the deletion of exon 11 in *gw9* mutant. (b) Protein structure of GW9. The absence of exon 11 results in a deficiency of 18 amino acids in C2H2 zinc finger domain (C2H2-ZnF) in *gw9* mutant.

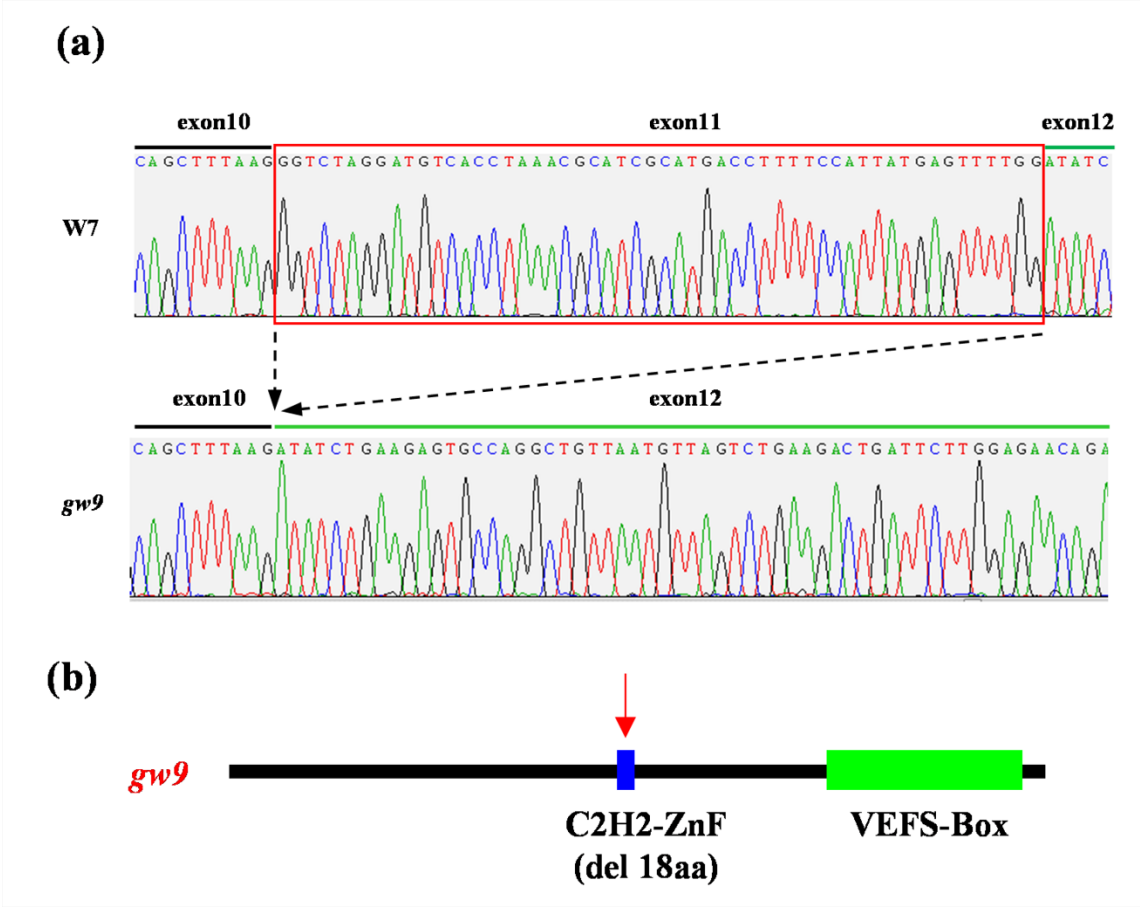

Fig. S5 Transcription level of GW9 in W7, *gw9*, complementation lines (com), and overexpression lines (OE). **, $p < 0.01$ (Student's *t*-test).

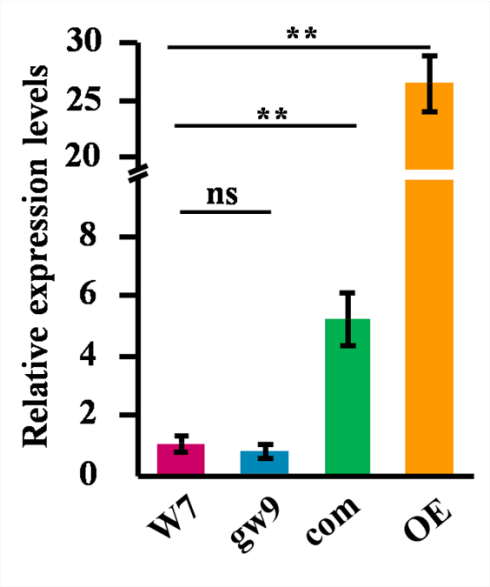

Fig. S6 (a) Comparison of the phenotypes of W7, *gw9*, com, and OE plants at the heading stage. Arrows indicate panicles. (b) Days to flowering of W7, *gw9*, com, and OE. **, $p < 0.01$ (Student's *t*-test).

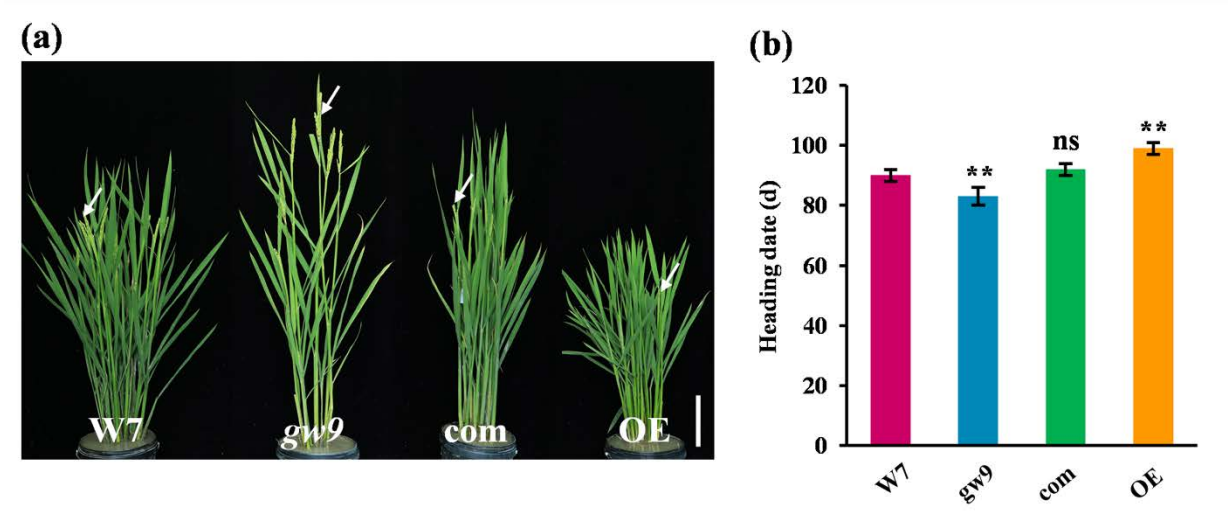

Fig. S7 (a) Schematic diagram of the *GW9* locus, showing the position of the mutations in the *gw9* mutant alleles. Orange box indicate the exons; white box indicates the untranslated regions. Gray arrow indicates T-DNA insertion mutation sites, gray line indicates G7475T mutation in *emf2b-3*, and red line indicates G7213A mutation in *gw9*. (b) Schematic diagram of the protein structure of GW9/EMF2b with the C2H2-ZnF domain deleted. Green box indicate the C2H2-ZnF domain and blue box indicate the VEFS domain. (c) CRISPR/Cas9-mediated mutations at different target sites of *GW9* in representative knockout lines. The PAM motif is indicated in red, and plus and minus signs indicate base insertion and deletion, respectively, relative to W7. (d) Sequence alignment of proteins encoded by different *gw9* alleles.

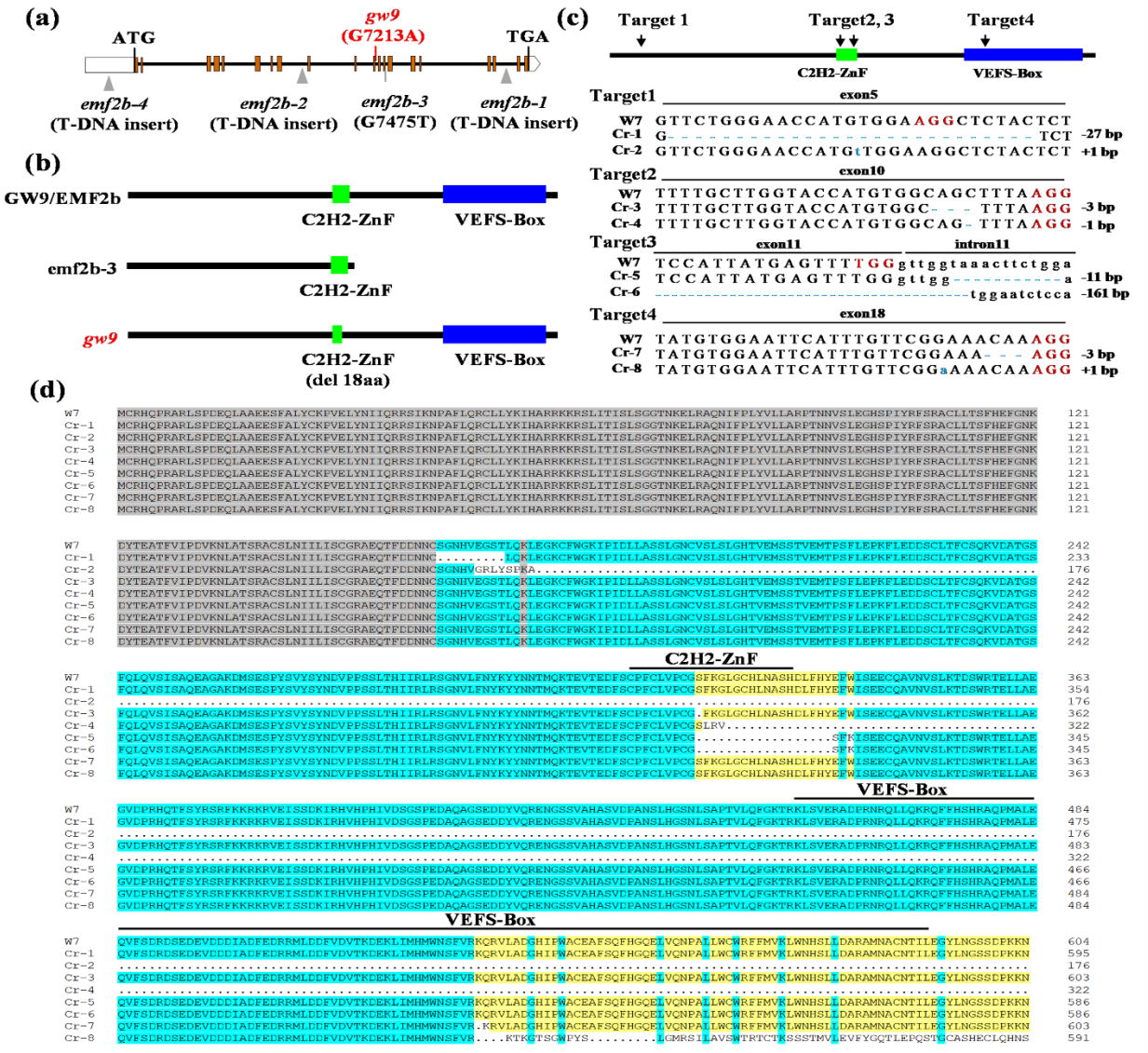

Fig. S8 (a) The representative spikelets morphology of *Cr-2*, *Cr-4*, and *Cr-8* plants. Bars = 2 mm. (b) I_2-KI pollen staining. pollen from W7, *gw9*, and representative mutant plants. Bars = 0.5 mm.

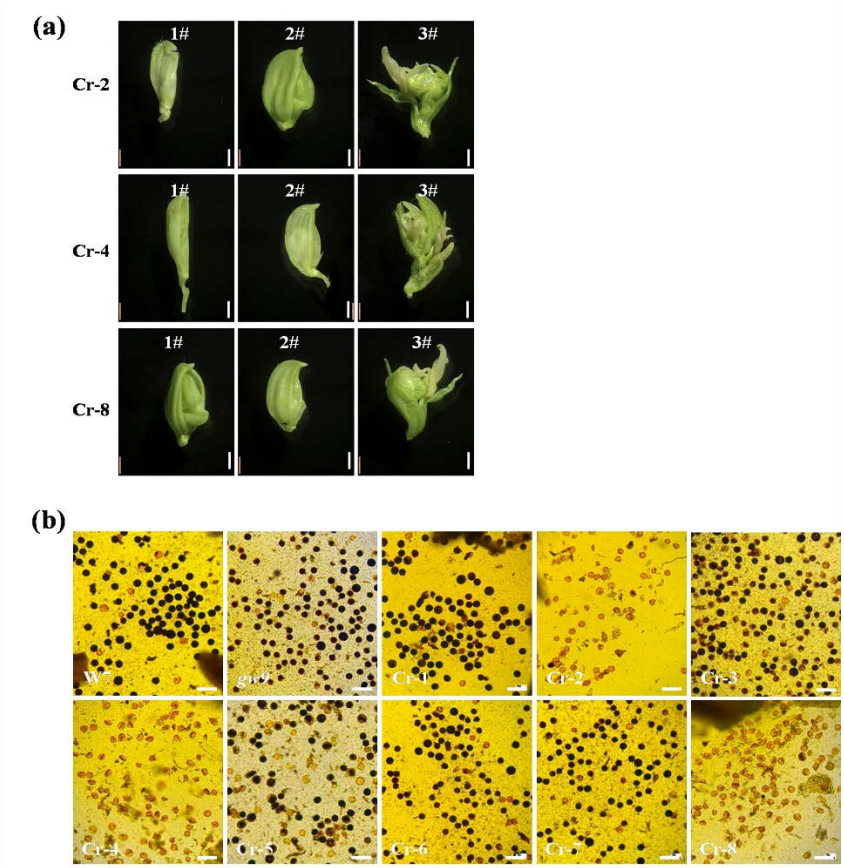

Fig. S9 Heat map of grain size and plant hormone metabolism related gene expression. Three biological replicates were performed.

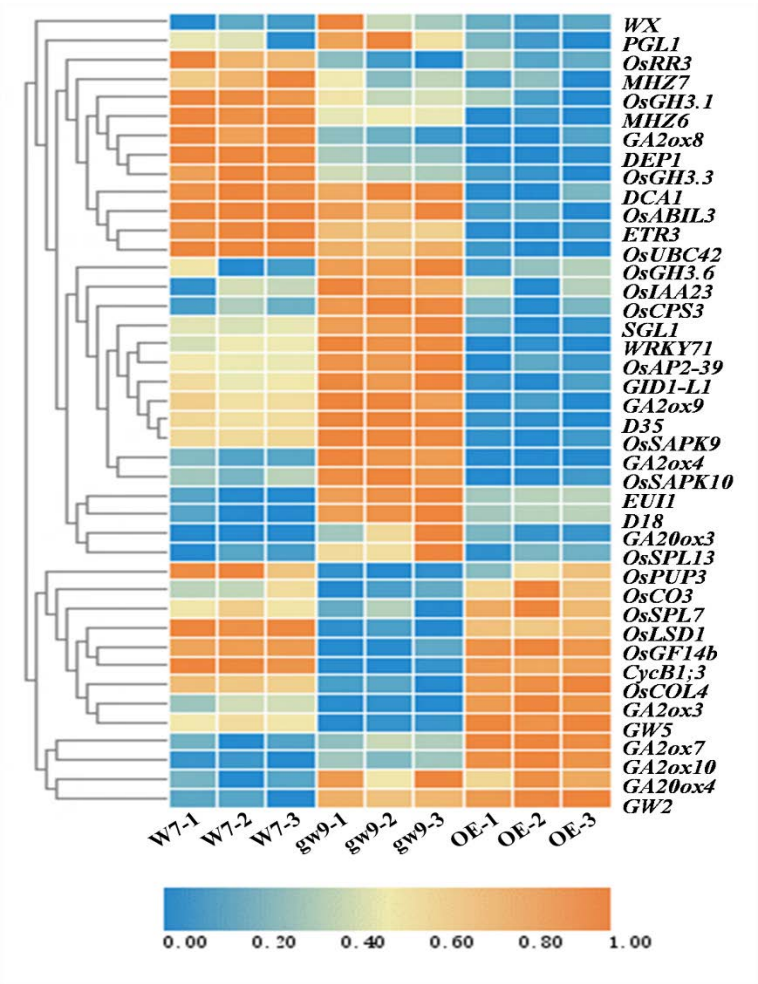

Fig. S10 Y2H assay for the interaction of GW9 with GW2. The transformed yeast cells were cultured on DDO (SD/-Trp-Leu) and QDO (SD/-Trp-Leu-His-Ade/x-α-gal) medium, respectively. α-X-gal staining shows the β-galactosidase activity of the transformants. The PGBKT7-53 and PGADT7-T were used as a positive control, the PGBKT7-empty and PGADT7-empty were used as a negative control.

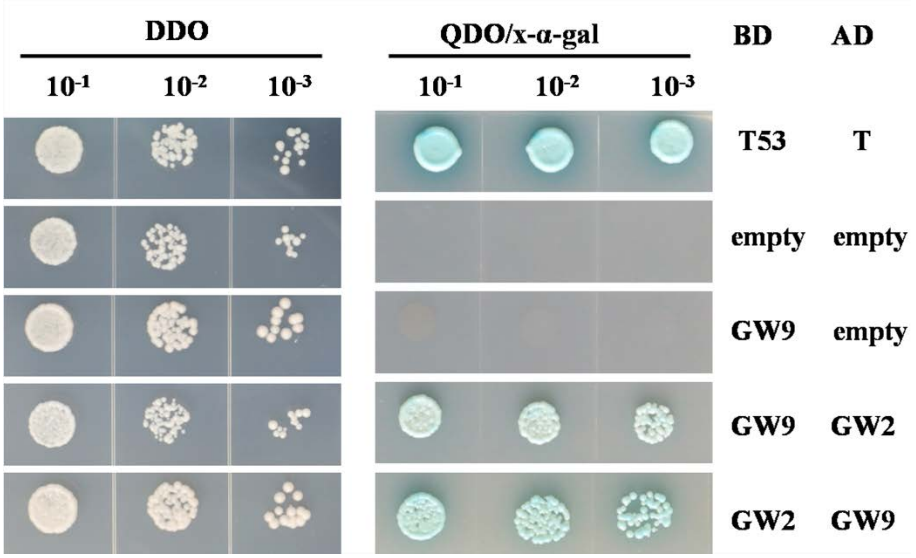

Fig. S11 GW9-GFP and GW2-RFP were co-expressed in rice protoplasts. GW9-GFP was used as the as the nuclear marker. The GFP fluorescence and RFP fluorescence were observed at 488 nm and 561 nm excitation wavelength, respectively. Bars = 10 μm.

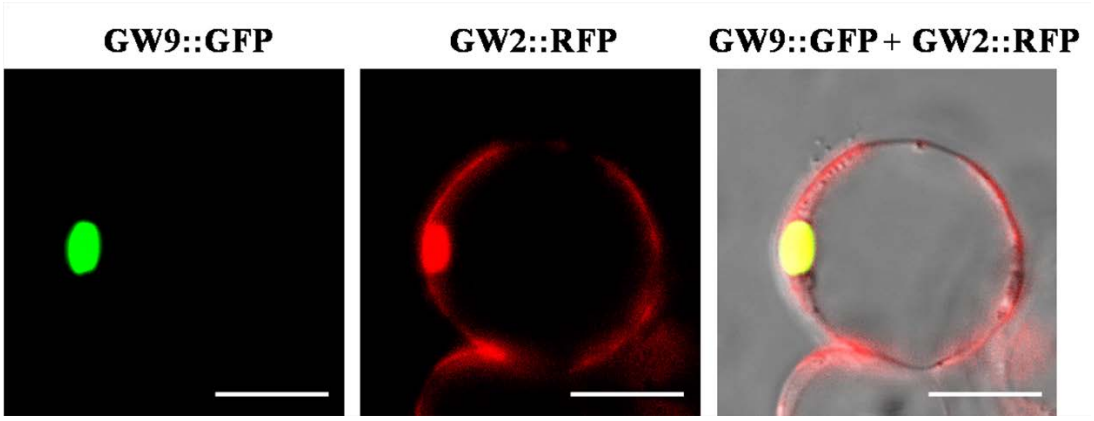

Fig. S12 (a) The representative lines of *GW2* (*gw2-c1* and *gw2-c2*) gene-edited by CRISPR/Cas9. The sequence underlined in black represents sgRNA target for CRISPR/Cas9-mediated gene edition of *GW2*, and PAM motif is indicated in red. (b) Expression levels of *GW2* in *gw2-c1* and *gw2-c2* lines. (c, d) Grain width (c) and grain length (d) of W7, *gw2-c1*, *gw2-c2* lines. Bars=0.5 cm in (b) and (c). (e-g) Quantification of grain width (e), grain length (f), and 1,000-grain weight (g). Error bars represent standard deviation (SD). **Significant difference at $p < 0.01$ compared with the W7 by Student's *t*-test.

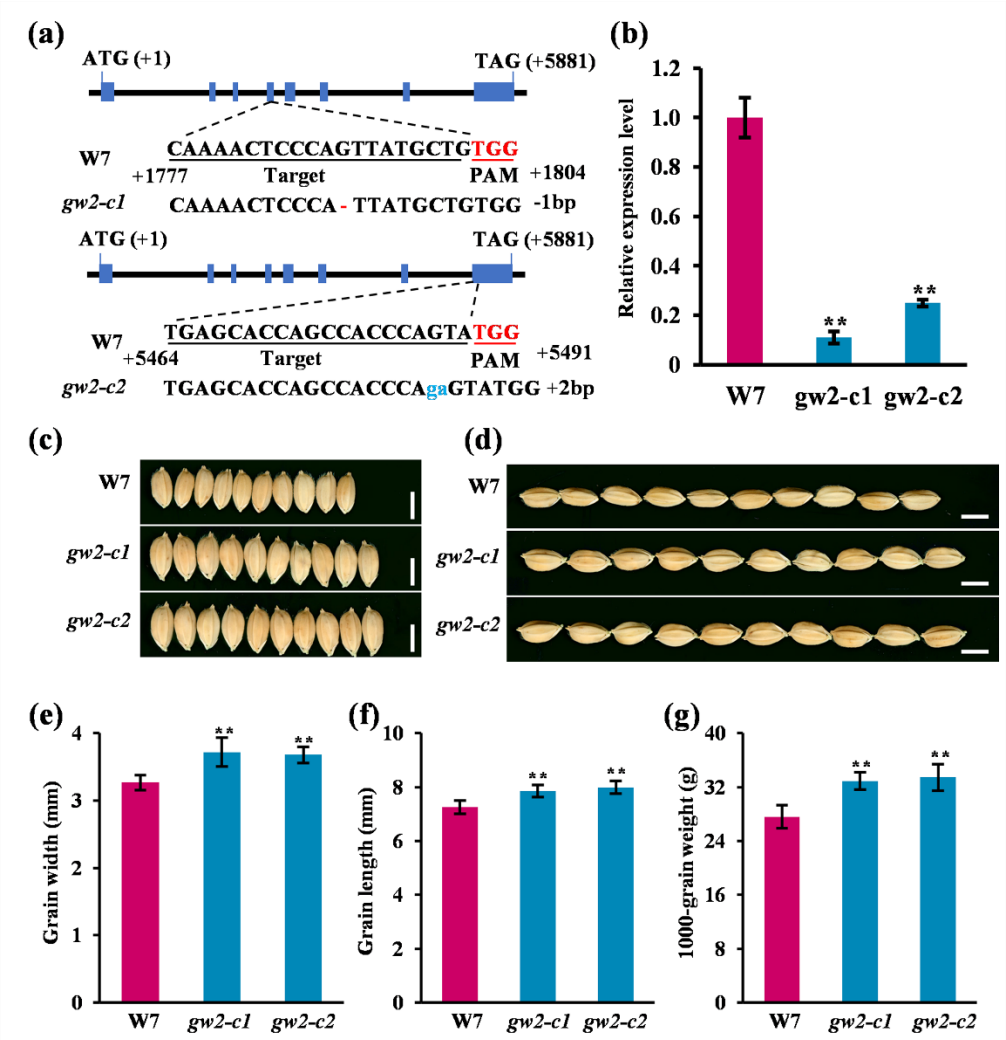

Figure S13. GW9 mediated histone H3K27me3 modification

(a-d)) qRT-PCR analysis of the relative expression level of some reported floral organ identity and grains size development-related genes in W7, *gw9*, and GW9-OE plants. (e) Overall H3K27me3 modification levels in different gene knock out lines. Error bars represent standard deviation (SD). **, $p < 0.01$; ns, no significant difference (Student's *t*-test).