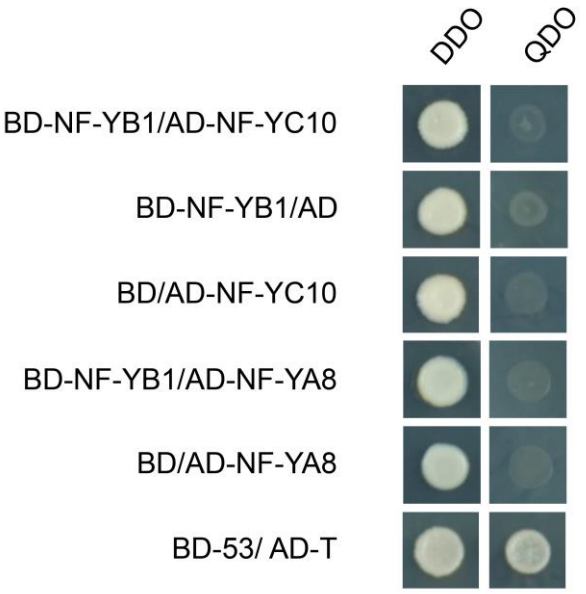
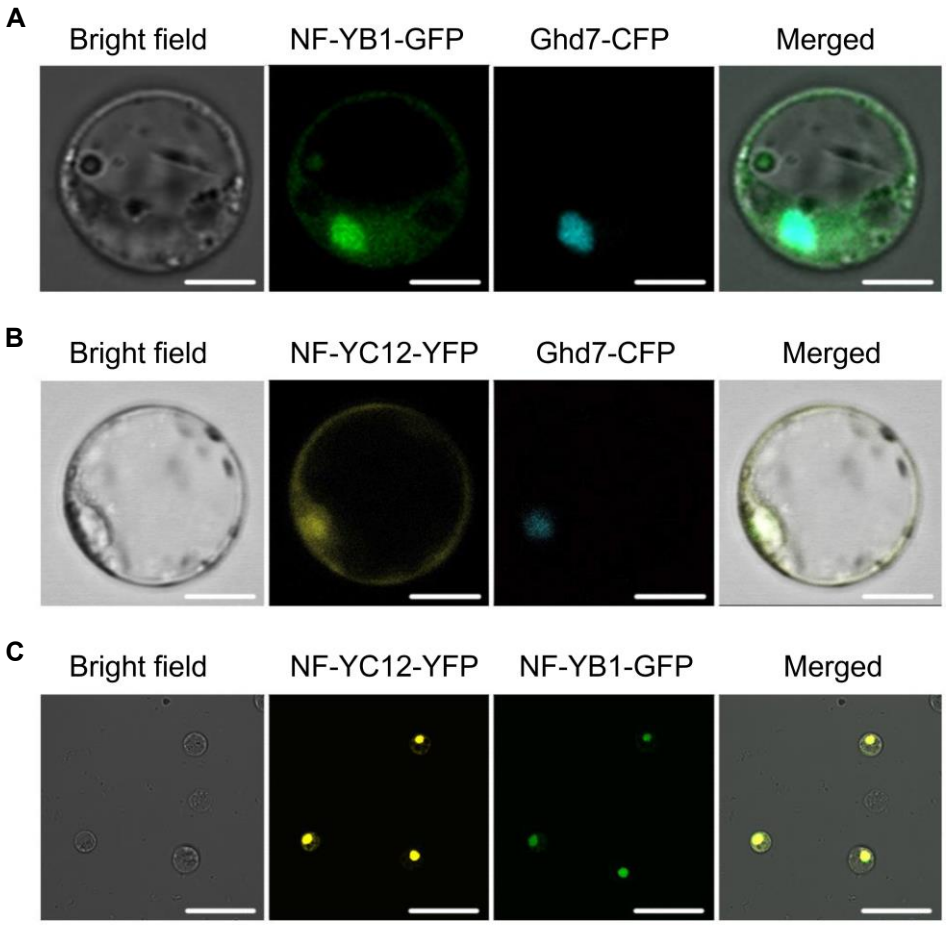
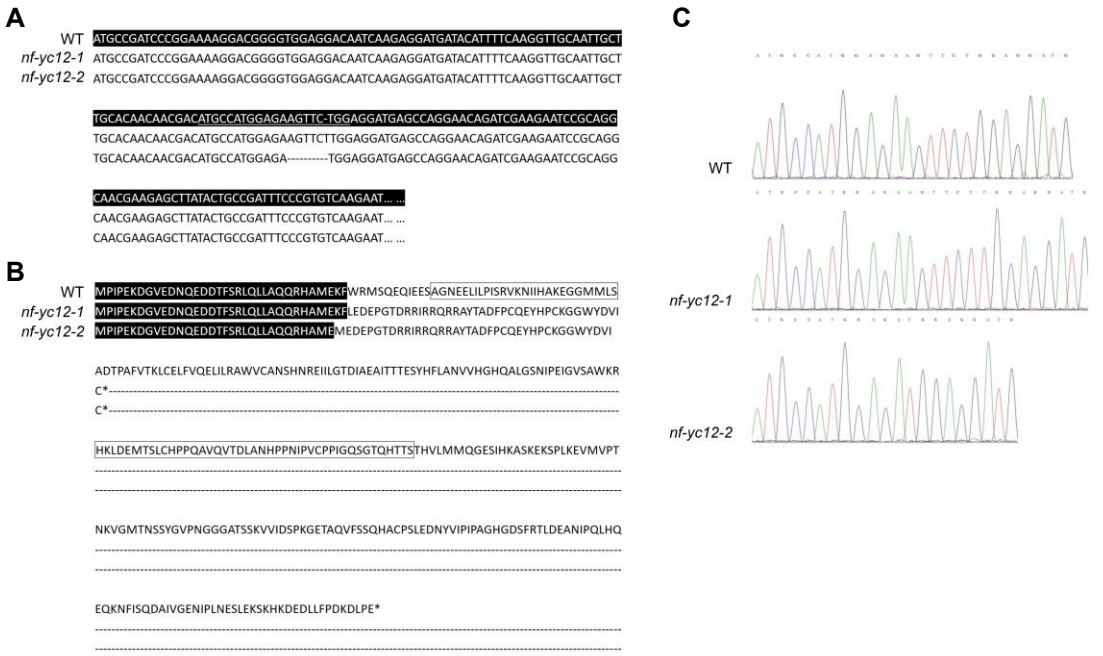
Supplementary Fig. S1 Interactions between the selected rice endosperm-specific NF-Ys. Yeast two hybrid assay shows NF-YB1 can not interact with NF-YA8 or NF-YC10. The transfomants were grown on DDO (SD/-Leu/-Trp) and QDO (SD/-Leu/-Trp/-His/-Ade) plates. Vector pGBKT7-53 (BD-53) paired with pGADT7-T (AD-T) were as the positive control. The growth pictures were taken 5 d after the selections.



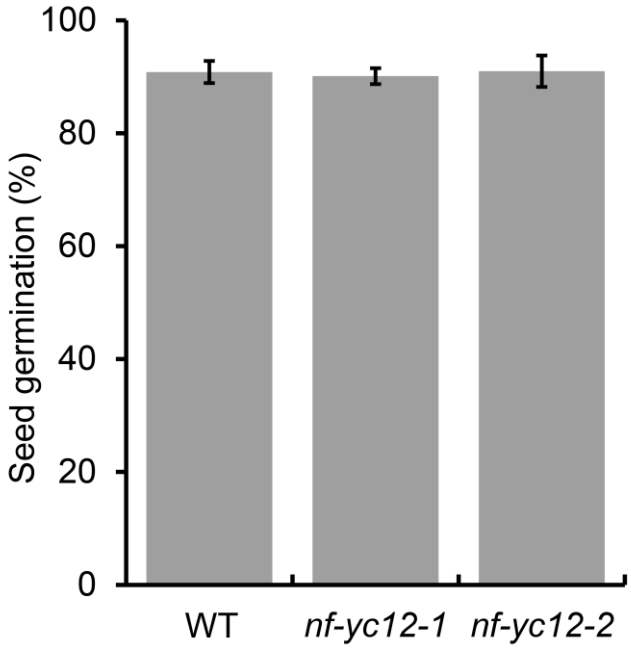
Supplementary Fig. S2. **Subcellular localization of the NF-YB1 and NF-YC12 protein in rice protoplasts.** Rice Ghd7 protein fused with CFP was used as a nuclear localization marker. Scale bars, 5 μm (A, B) and 30 μm (C).



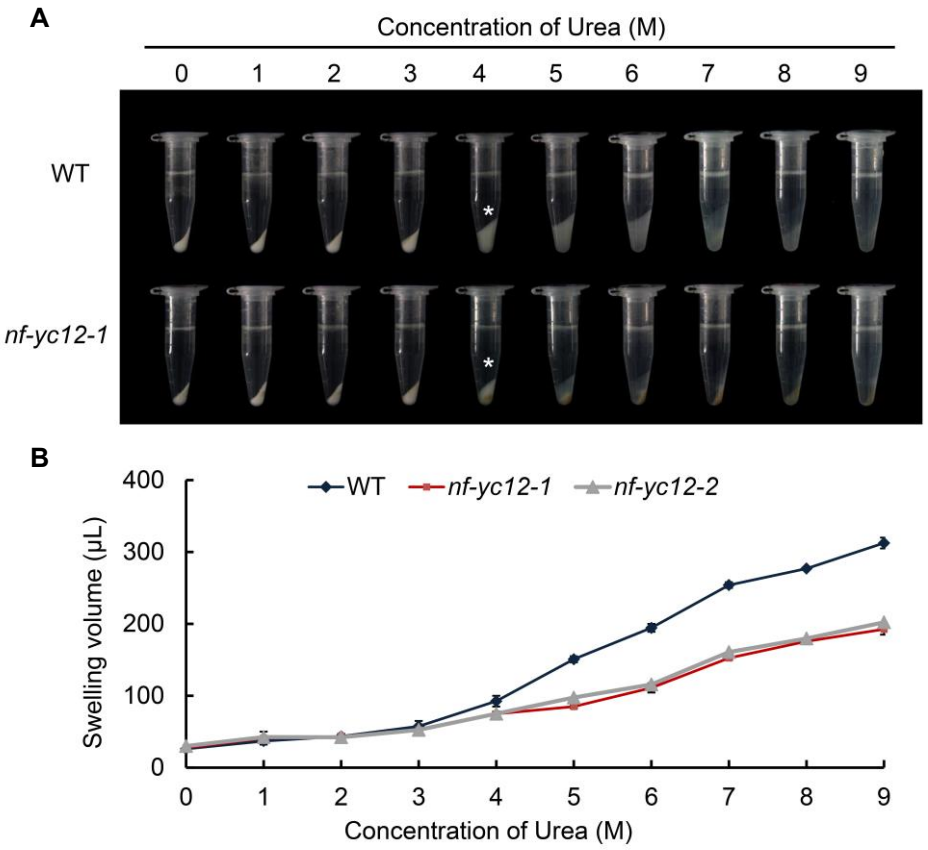
Supplementary Fig. S3 Identification of CRISPR/Cas9-induced target mutations. A and B. Genomic (A) and polypeptide sequences (B) of *NF-YC12* from the WT and *nf-yc12-1* and *nf-yc12-2* mutants generated using CRISPR-Cas9 system, showing the presence of an T insertion and 5 bp deletion in *NF-YC12* from *nf-yc12-1* and *nf-yc12-2* mutants, respectively, leading to truncations of the NF-YC12 protein. *, stop codon. Black wire frame is highly conserved domain. C. Direct PCR/sequencing and alignment for the mutations.



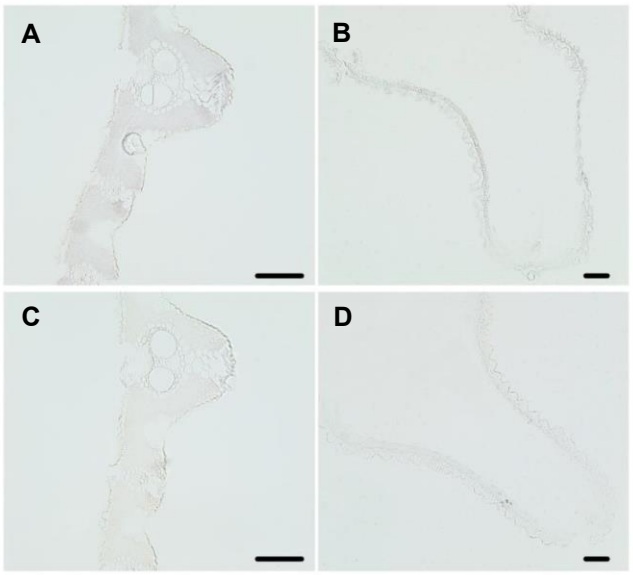
Supplementary Fig. S4 Seed germination rate of WT and *nf-yc12* mature seeds. Data are means ± SD for three replicates with each replicate containing at least 35 seeds. **P* < 0.05, ***P* < 0.01. *P* values were produced by two-tailed Student's *t*-test.



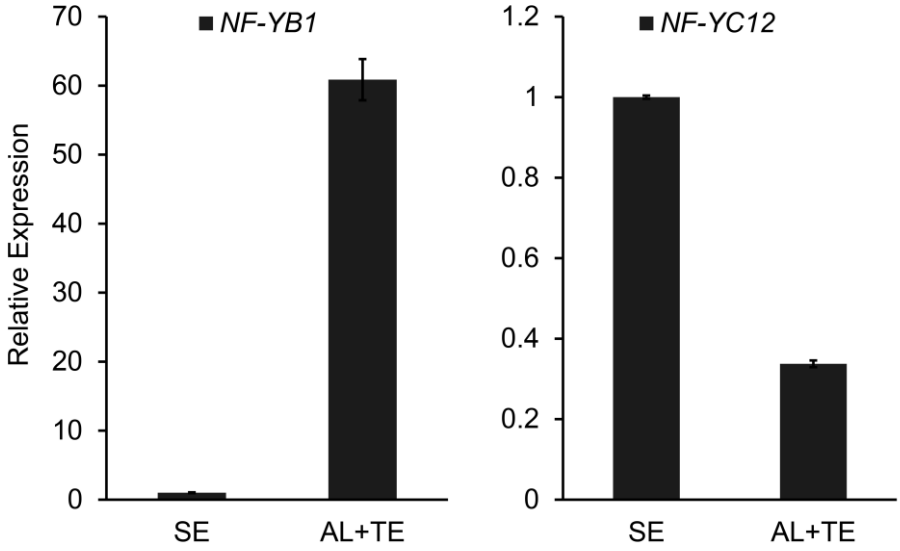
Supplementary Fig. S5 Gelatinization characteristics of starch from *nf-yc12* mutant seeds. A. Starch powder was mixed with different concentrations (0-9 M) of urea solution. B. The swollen volume of WT and *nf-yc12* starch in different concentration urea solutions (0-9 M).



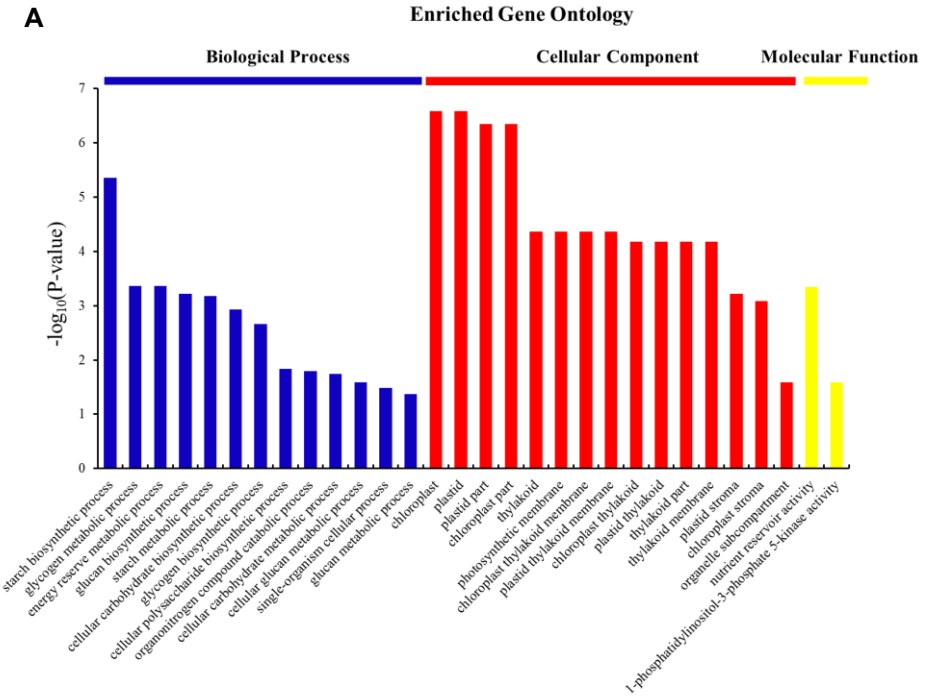
Supplementary Fig. S6 *In situ* hybridization of *NF-YC12* in vegetative organs. leaves and panicles collected at flowering stage using antisense (A and B) and sense probes (C and D). Bar = 100 um.

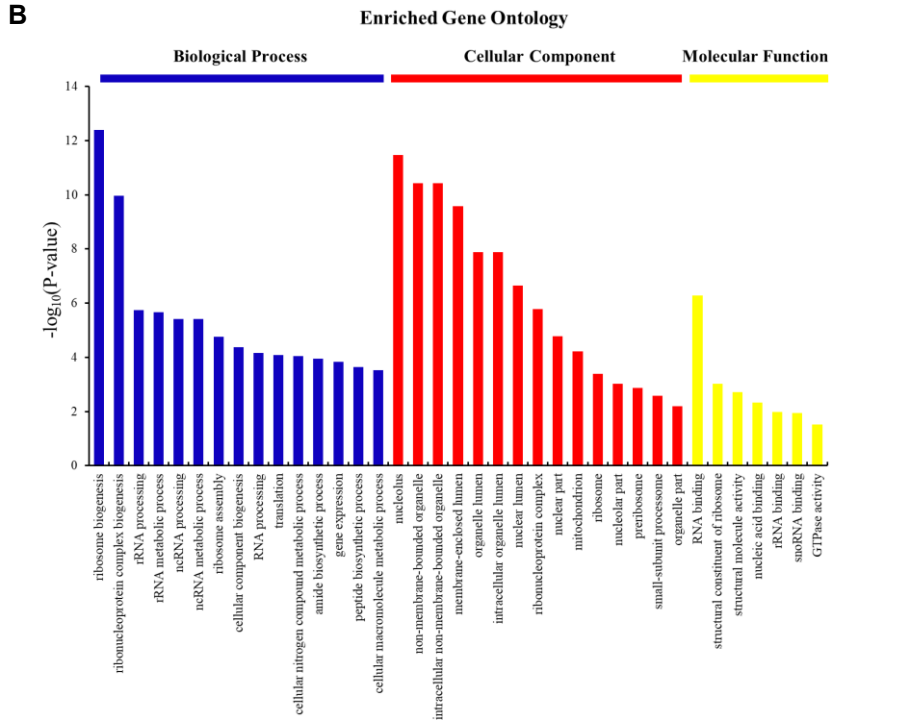


Supplementary Fig. S7 Expression levels of *NF-YB1* and *NF-YC12* in different endosperm tissues. SE and AL+TE, starchy endosperm and mixed aleurone and testa samples collected at 10 DAP, respectively. Data are presented as means ± SD (n = 3).

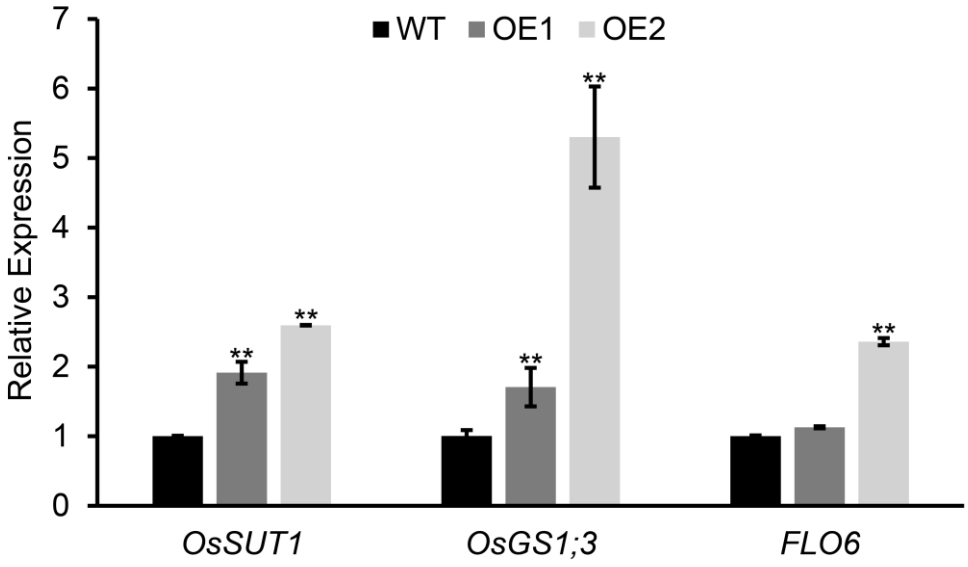


Supplementary Fig. S8 GO analysis of DEGs that were down-regulated (A) and up-regulated (B) in *nf-yc12*.

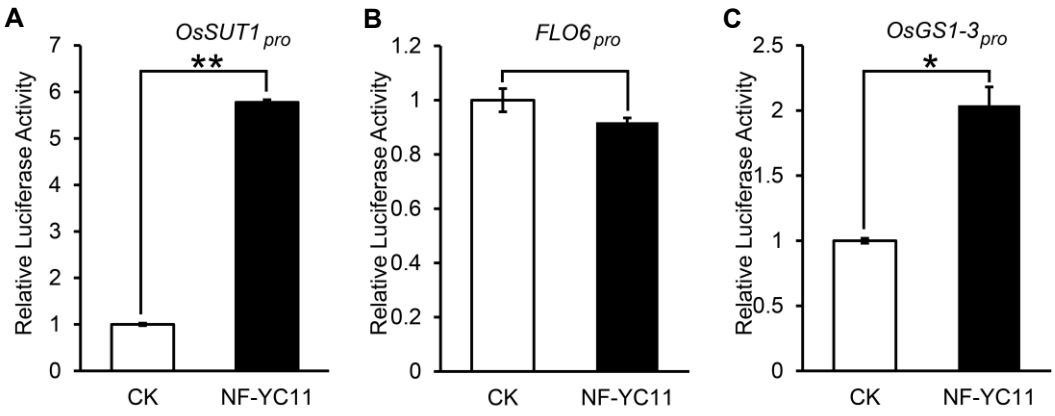




Supplementary Fig. S9 Expression level of NF-YC12 potential targets in the developing seeds at 7 DAP of the WT and overexpression lines. Data are means ± SD for three replicates. *P < 0.05, **P < 0.01. P values were produced by two-tailed Student's t-test.



Supplementary Fig. S10 LUC transient transcriptional activity assay in rice protoplast. Relative luciferase activity (fLUC/rLUC) are shown. The target promoters are indicated above each panel. Error bars indicates ± SD (n=3). *P < 0.05, **P < 0.01. P values were produced by two-tailed Student's t-test. CK, without NF-YC12 present.



Supplementary Fig. S11 Real-time PCR analysis of the expression pattern of *OsGS1;3* in endosperm. *OsGS1;3* is highly expressed in endosperm. P, panicles; S1, caryopses collected at 1 DAP; S3, caryopses collected at 3 DAP; En5 to 21, endosperm collected at 5 to 21 DAP.