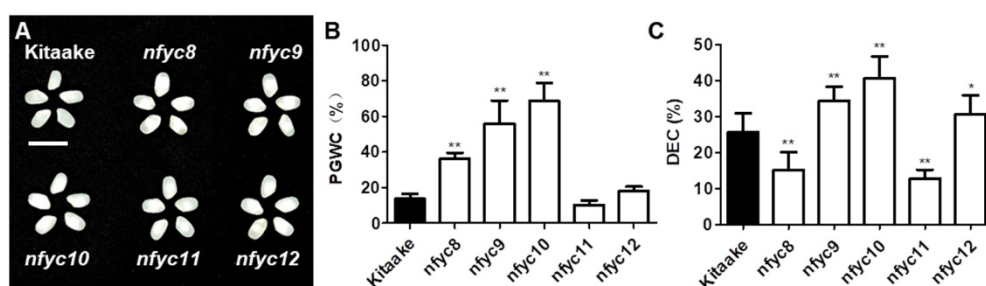
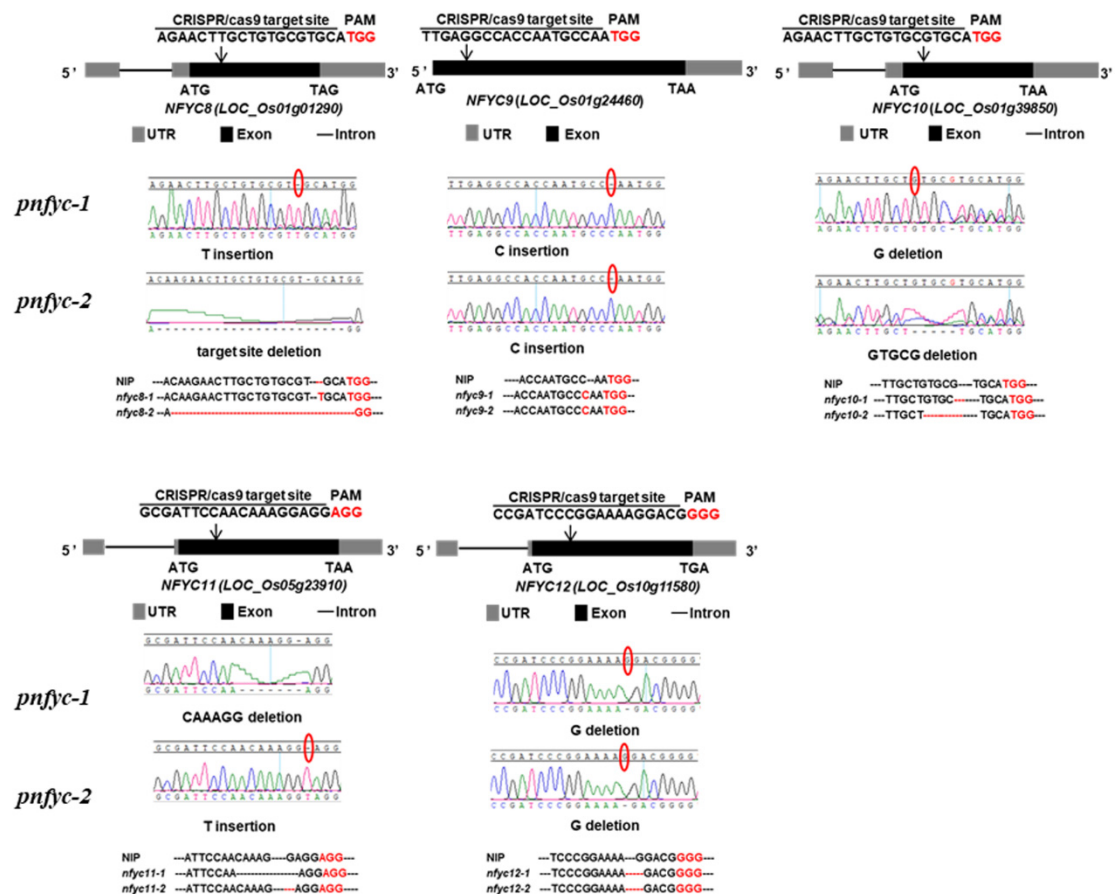


**Figure S1** Genotyping of Kitaake and five *single-nfyc* lines. Sanger sequencing of the target sites in five single gene mutants of *nfyc8* to *nfyc12*. Red bases represent PAM, and red circles indicate insert or delete bases.

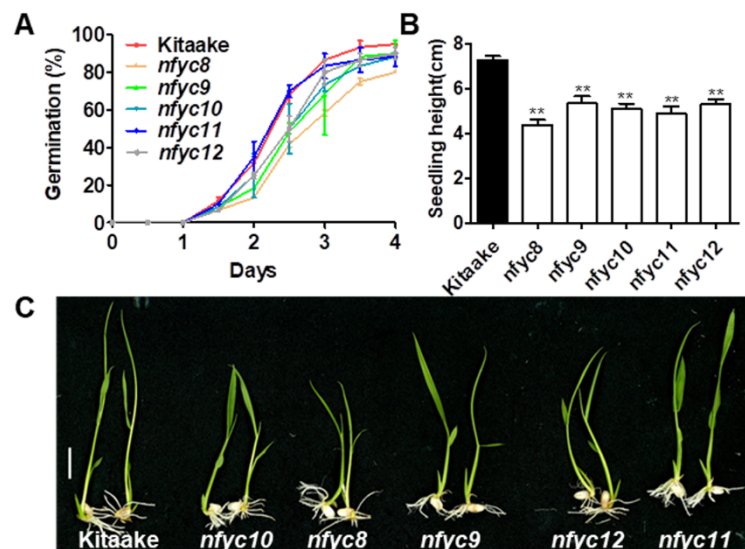


**Figure S2** A Grain chalkiness phenotypical characterization of Kitaake and five single mutants, bar=1cm. **B.** Statistics of chalkiness grain rates of the five single mutants and Kitaake. **C.** Statistics of chalkiness degrees of the five single mutants and Kitaake. Bar=1cm.

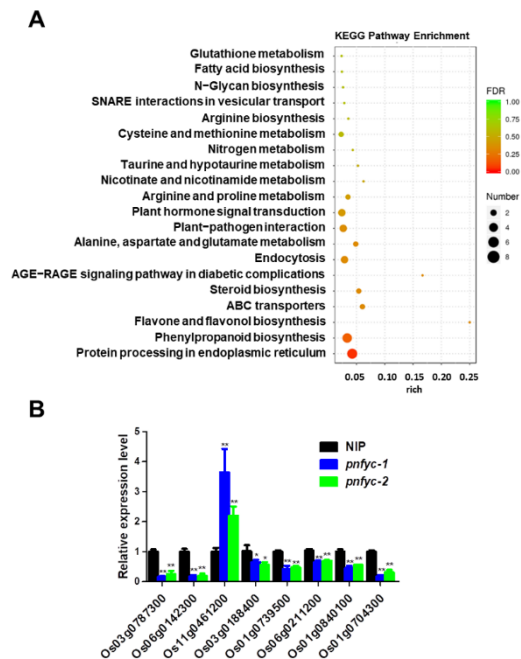
Data are shown as means  $\pm$  SD of at least three biological replicates. (\* $P < 0.05$ , \*\* $P < 0.01$  by two-tailed Student's t-test).



**Figure S3** Genotyping of NIP and *pnfy* lines. Sanger sequencing of the five target sites in *pnfy* (*cr-nfy8/y9/y10/y11/y12*) mutants showed two mutation types. Red bases represent PAM, and red circles indicate insert or delete bases.



**Figure S4** **A** The germination rate of Kitaake and five single mutants in 4 days. **B**. Statistics of the seedling height of Kitaake and five single mutants at 7 days after germination. **C**. The plant morphology of Kitaake and five single mutants at 7 days after germination. Bar=1cm. Data are shown as means  $\pm$  SD of at least three biological replicates. (\* $P < 0.05$ , \*\* $P < 0.01$  by two-tailed Student's t-test).



**Figure S5** **A** One selection of KEGG pathway enrichment assay of the differentially expressed genes (DEGs) as determined by RNA-seq using embryos at 6 hours after germination. **B** qRT-PCR validation of the transcript levels of DEGs obtained from the RNA-seq results.

	Plant height (cm)	Panicle length (cm)	No.primary branch panicle	No.secondary branch panicle	No.effective panicles per plant	Seed setting rate(%)
NIP	99.07±4.31	21.44±1.34	11.56±1.78	16.55±6.78	8.40±2.48	86.41± 8.19
<i>pnfyc-1</i>	99.40±4.09	21.27±1.30	11.11±1.10	15.22±4.94	7.90±1.88	84.93±7.20
<i>Pnfyc-2</i>	97.20±2.66	21.38±1.80	11.21±1.20	15.11±5.11	7.50±1.61	84.05±7.75

**Table S1** Quantification data of the panicle traits and plant height among NIP and *pnfyc* lines. Data are shown as means ± SD of at least three biological replicates. (\*P < 0.05, \*\*P < 0.01 by two-tailed Student's t-test).

	Onset temperature (°C)	Peak temperature (°C)	End set temperature (°C)
NIP	67.84±0.04	72.54±0.08	78.46±0.03
<i>pnfyc-1</i>	65.86±0.33 **	70.57±0.62*	76.61±0.14**
<i>Pnfyc-2</i>	65.77±0.22**	70.48±0.53*	76.12±0.21**

**Table S2 Differential scanning calorimetry assay. Quantification data of gelatinization temperature among NIP and *pnfyc* lines. Data are shown as means ± SD of at least three biological replicates. (\*P < 0.05, \*\*P < 0.01 by two-tailed Student's t-test).**