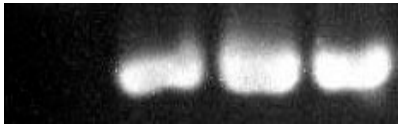

Figure S1. Genotyping of two transgene-silenced G316 plants, S1 and S2.

The *OsNPR1* transgene was detected by PCR using specific primers of transgenic construct listed in Table S2.

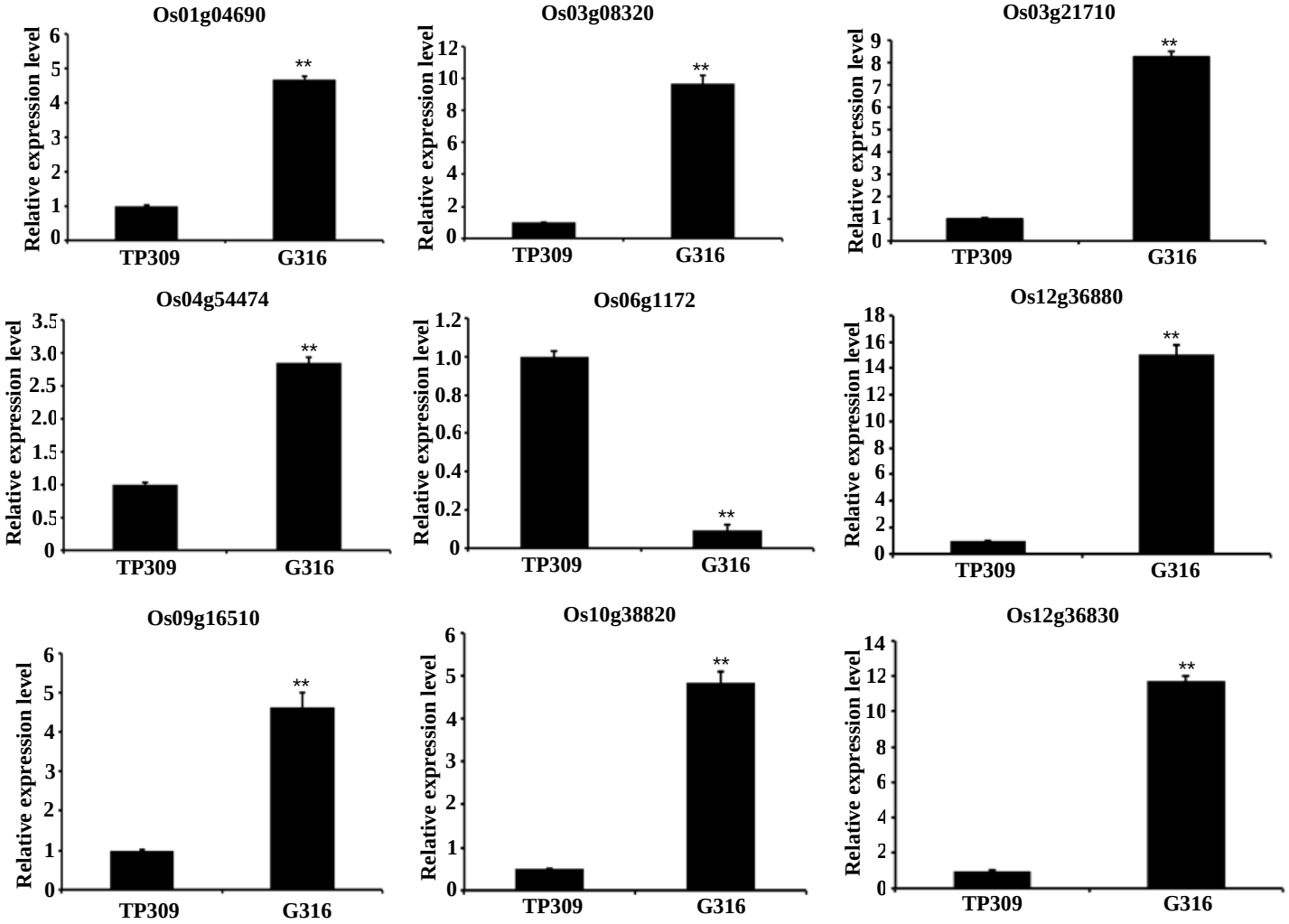

Figure S2. qRT-PCR validation of differentially expressed genes revealed by microarray assay.

RNA was extracted from the young uppermost internodes at heading stage. The rice *OsActin1* gene (Os03g50885) was used as an internal control. Primer sequences are listed in Table S2. Asterisks indicate significant difference in comparison with TP309 (*P*-value < 0.01 by Student's *t*-test).

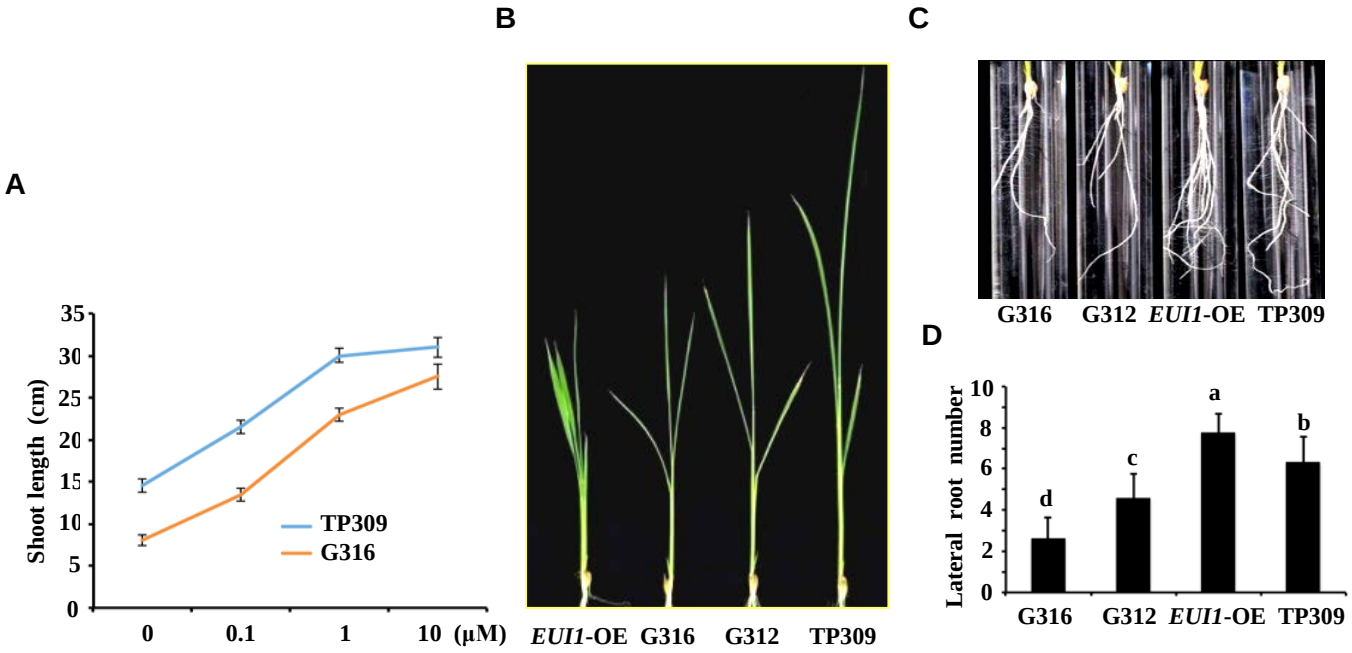

Figure S3. *OsNPR1* overexpression has no effect on GA response.

A, *OsNPR1*-OX plants (G316) were sensitive to exogenous GA similar to the wild-type TP309. Seeds after germinating were grown in 1/2 MS medium with different concentrations of GA_3. The shoot lengths were measured at 17 day after treatment ($n \geq 24$). B and C, Shoot and root morphology of 3-week-old seedlings. *EUI1*-OE is the *OsEUI1* overexpression line in TP309 background (Zhu et al., 2006), used as a GA deficient control. D, Statistics analysis of numbers of lateral roots. Different letters indicate significantly different values at *P*-value < 0.05 (n = 24, ANOVA followed by Duncan's multiple range test).

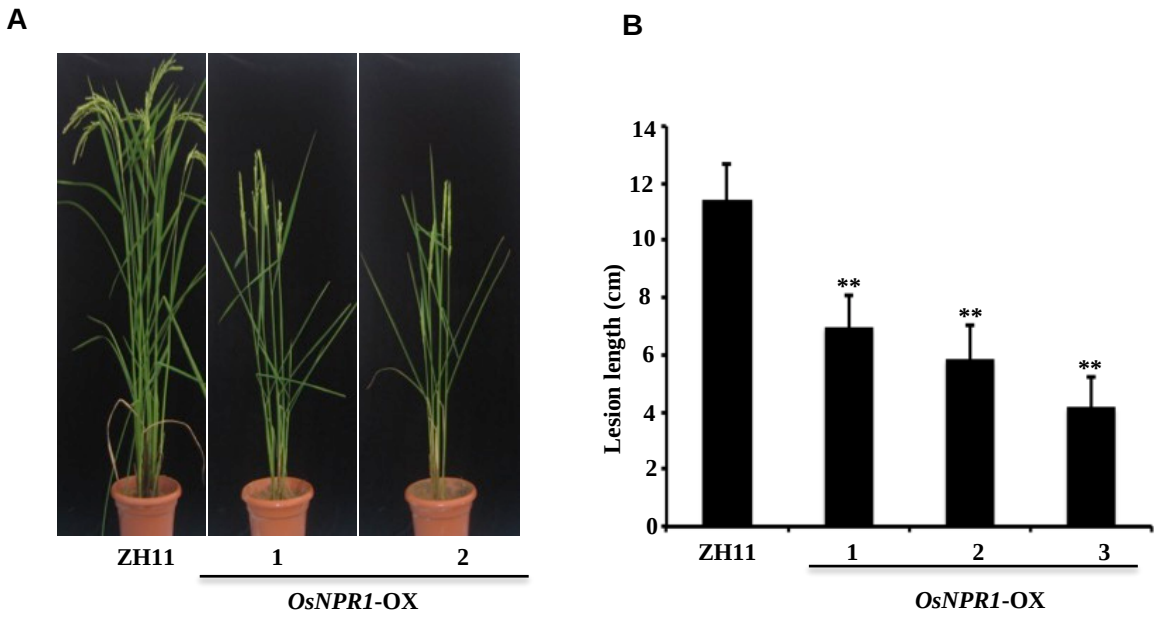

Figure S4. Generation of *OsNPR1* overexpression lines in ZH11.

A, Phenotype of heading plants of the representative transgenic lines in comparison with the wild-type ZH11. B, Statistic analysis of lesion lengths after inoculated with *Xoo* strain PXO99A. Asterisks indicate significant difference in comparison with TP309 ($n \geq 20$, *P*-value < 0.01 by Student's *t*-test).

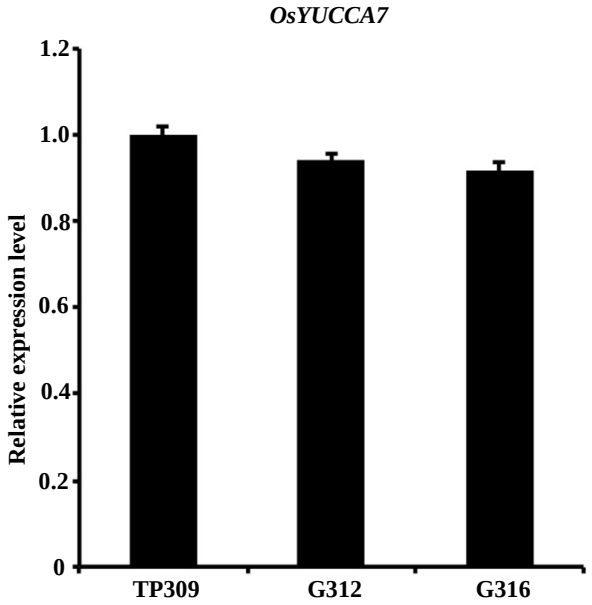

Figure S5. *OsYUCCA7* expression levels at seedling stage.

RNA was extracted from 3-week-old seedlings of TP309, G312 and G316. Statistic analysis indicated that the expression level sof *OsYUCCA7* in G312 and G316 were not significantly changed in comparison with that in TP309.

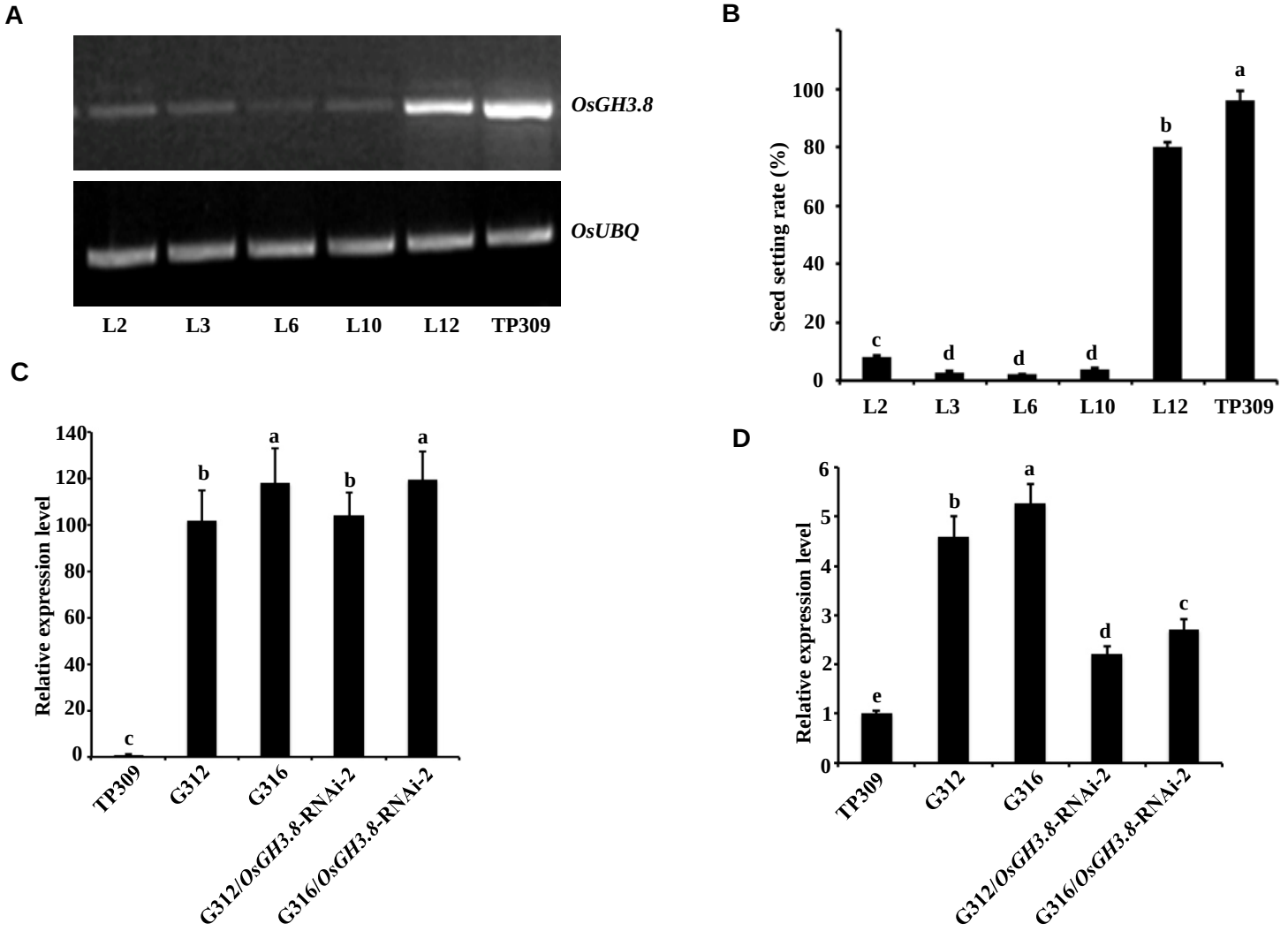

Figure S6. Generation of *OsNPR1*-OX/*OsGH3.8*-RNAi.

A, Expression levels of *OsGH3.8* were examined by semi-quantitative PCR (38cycles) in *OsGH3.8*-RNAi lines L2, L3, L6, L10 and L12, compared with the wild-type TP309. RNA was extracted from the young uppermost internodes at heading stage. The rice ubiquitin gene (Os03g13170) was used as an internal control (25 cycles). B, Statistic analysis of seed setting rates of *OsGH3.8*-RNAi lines. Data collected from transgene plants (T1 generation). C and D, qRT-PCR analysis of *OsNPR1* (C) and *OsGH3.8* (**D**) in the wild-type (TP309), *OsNPR1*-OX (G312, G316) and *OsNPR1*-OX/*OsGH3.8*-RNAi double transgene line. RNA was extracted from the young uppermost internodes at heading stage. The rice *OsActin1* gene *(*Os03g50885) was used as an internal control. Note that the expression level of *OsGH3.8* was only partially decreased in *OsNPR1*-OX/Os*GH3.8*-RNAi compared with *OsNPR1*-OX. Different letters indicate significantly difference (*P*-value < 0.05, ANOVA followed by Duncan‘s multiple range test).