

Supplementary Material

Supplementary Figures and Tables

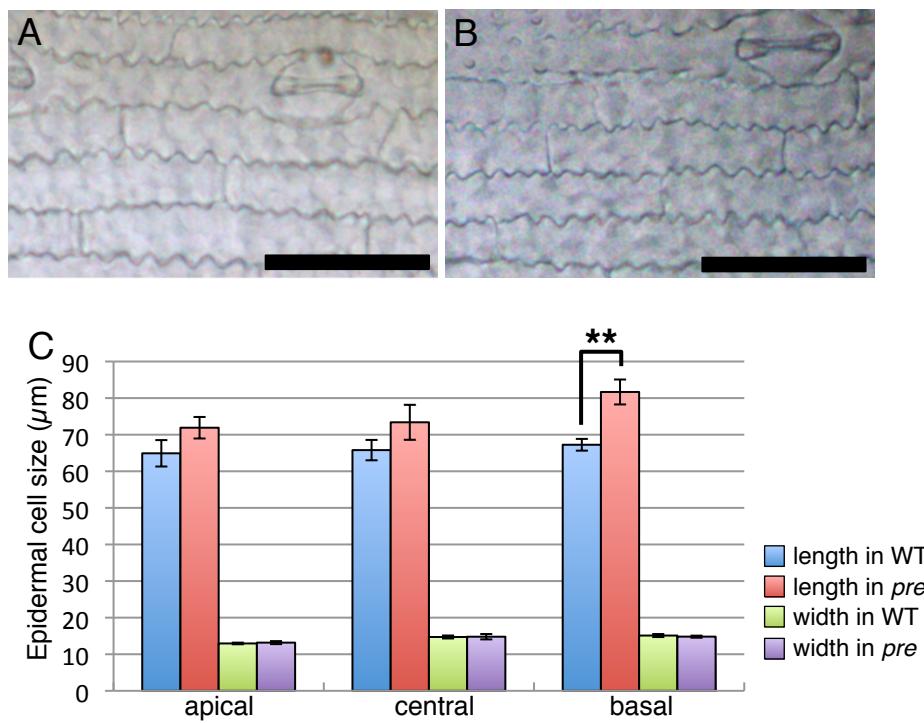


Fig. S1. Comparison of epidermal cell size between wild type and *pre*.

(A, B) Epidermal cells in the basal region of the second leaf blade in wild type (A) and *pre* (B). Scale bars = 5 μm. (C) Comparison of epidermal cell sizes in apical, central and basal regions of the second leaf blade in wild type and *pre* ($n \geq 10$). Data are shown as means ± s.e.m. ** = $P < 0.01$ (Student's *t*-test).

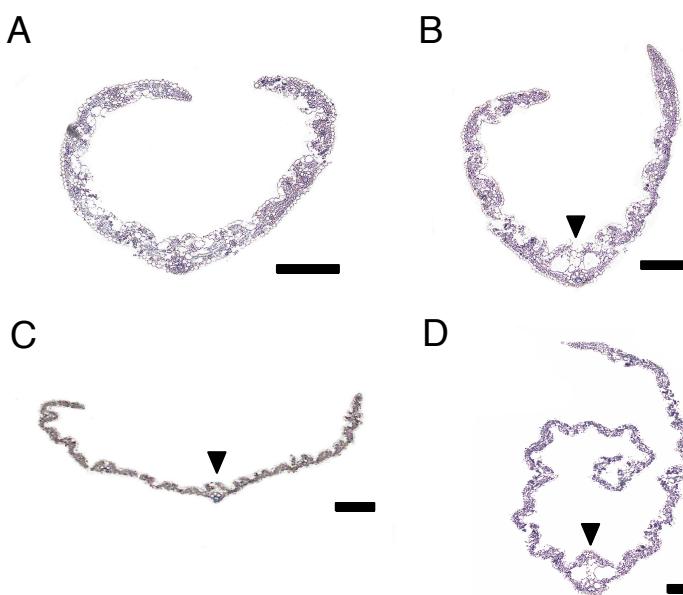
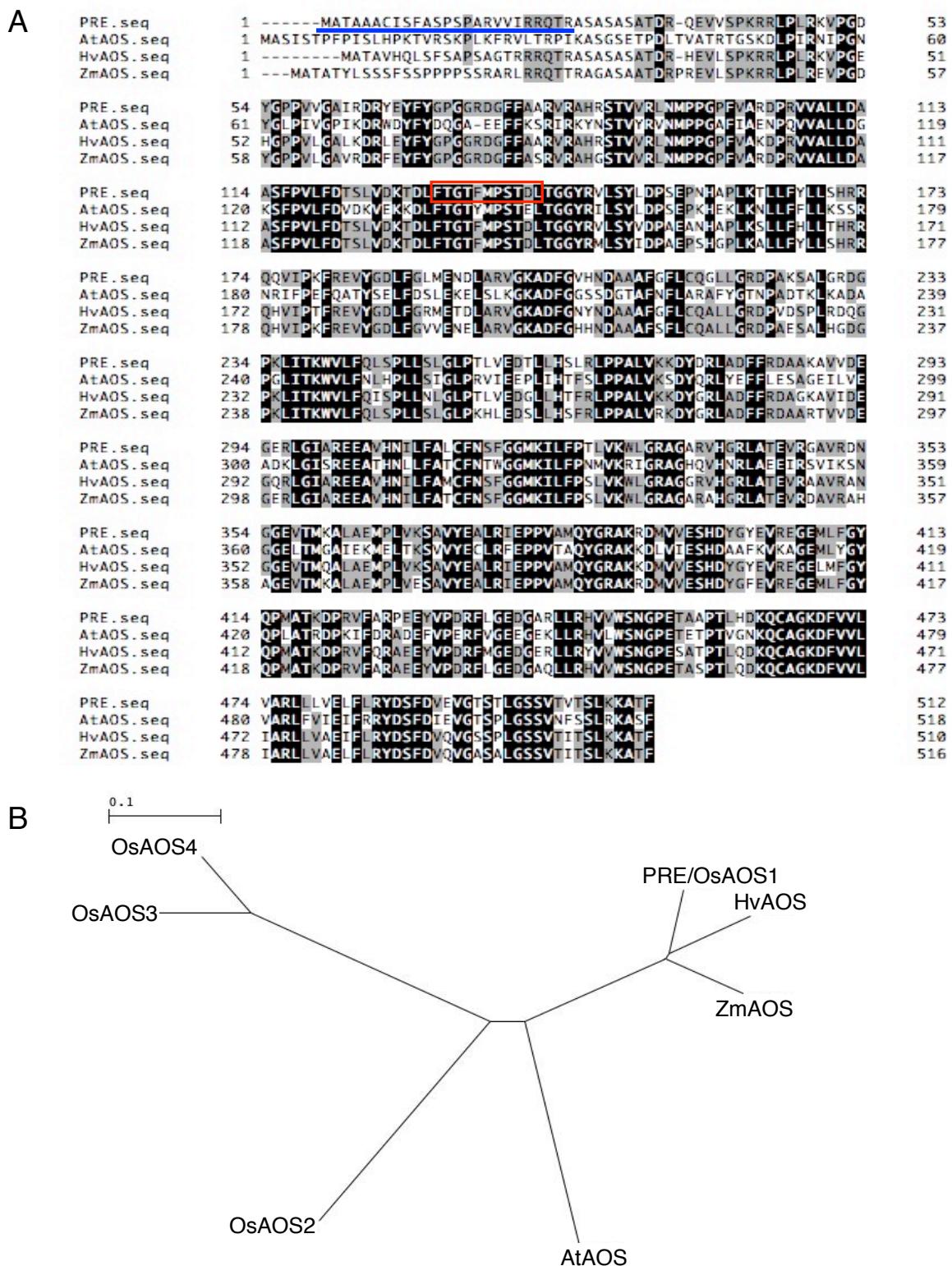


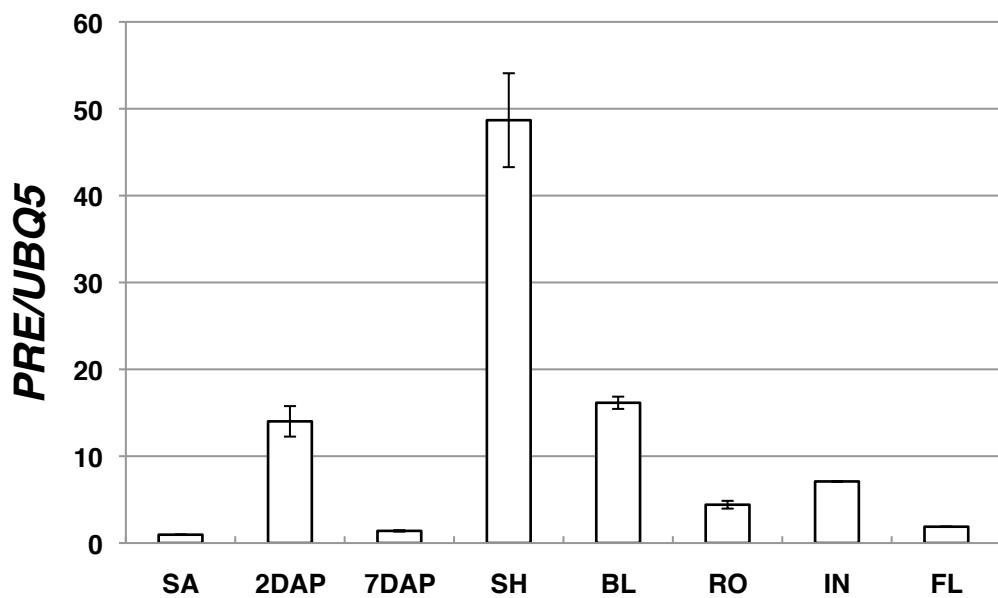
Fig. S2. Cross-sections of leaf blade in wild type and *pre*.

(A) Cross section of wild-type second leaf blade cut at 8 % from the base to the tip. (B) Cross section of *pre* second leaf blade cut at 22 % from the base. (C) Cross section of wild-type third leaf blade cut at 50 % from the base. (D) Cross section of *pre* third leaf blade cut at 60 % from the base. Arrowheads indicate midribs. Scale bars = 100 μm in (A, B) and 200 μm in (C, D).

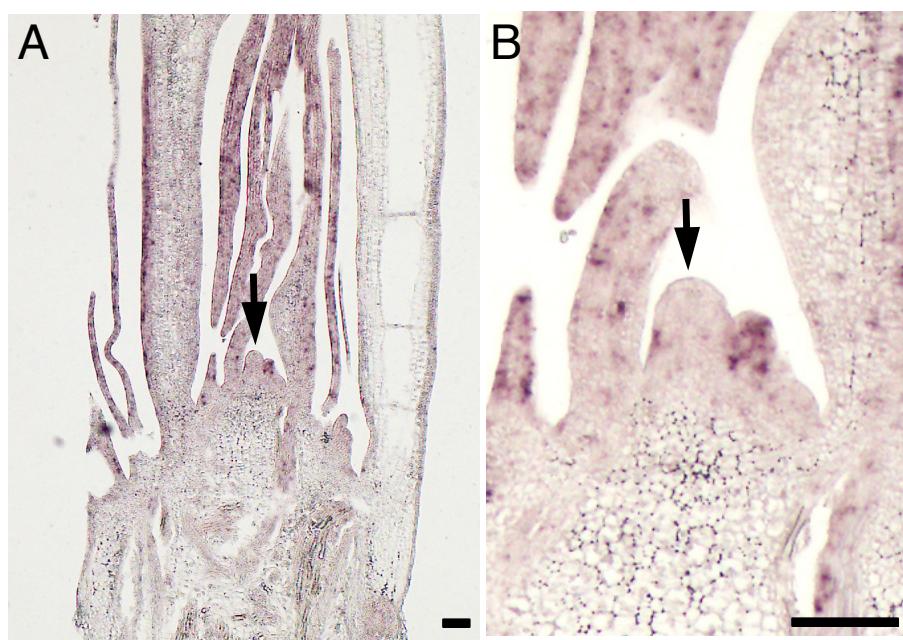
**Figure S3. Alignments of amino acid sequences and the phylogenetic tree of PRE/AOS proteins.**

(A) Alignment of deduced amino acid sequences of PRE protein and three AOS proteins from arabidopsis (At), barley (Hv) and maize (Zm). Blue underline indicates a chloroplast transit peptide. Deletion site in *pre* is indicated as a red box. Residues conserved in all four proteins are shaded in black, and those conserved in three proteins are shaded in grey.

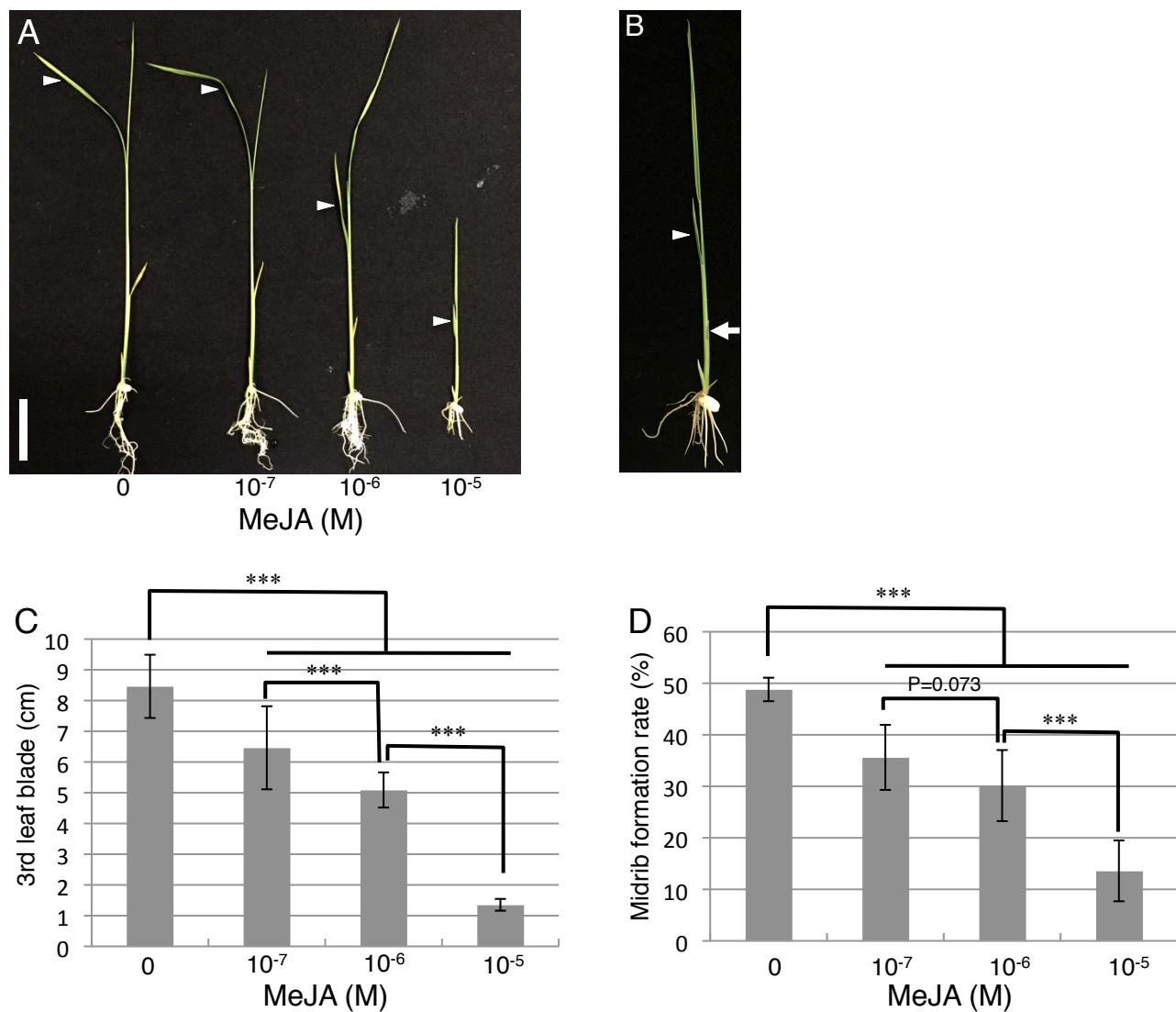
(B) The phylogenetic tree of PRE/AOS proteins from rice (Os), arabidopsis (At), barley (Hv) and maize (Zm) constructed by the neighbor-joining method. The bootstrap values based on 1000 replicates are shown as the numbers.

**Fig. S4. Expression profile of *PRE* gene.**

qPCR analysis of *PRE* gene expression in wild-type tissues including shoot apex at 14 days after sowing (SA), ovary at 2 or 7 days after pollination (2 DAP and 7 DAP), the third leaf sheath (SH), the third leaf blade (BL), root (RO), young panicle at the primary rachis branch differentiation stage (IN) and flower (FL). *OsUBQ5* was used as an internal control. Values are shown as means of three technical replicates \pm s.d.

**Fig. S5. *in situ* hybridization using *PRE* sense probe.**

(A) Expression pattern in 14 day-old wild type shoot apex when *PRE* sense probe was used. (B) Magnified view of shoot apex in (A). Accumulation of complementary mRNA to *PRE* mRNA implies the expression of *Os03t0766900-02* transcripts (Figure 3). Arrows indicate shoot apical meristems. Scale bars = 100 μ m.

**Fig. S6. Effect of JA on leaf length and midrib formation**

(A) Wild-type seedlings in 13 days after germination on the medium containing different concentrations of MeJA. Arrowheads indicate the third leaves. Scale bar = 3cm. (B) Higher magnification of the seedling grown on the medium containing 10^{-5} M MeJA in (A). Arrow indicates the second leaf. (C) Comparison of the third leaf blade on the medium containing different concentrations of MeJA. ($n \geq 10$). (D) The percentage of midrib length against total leaf blade length in 3rd leaf blades ($n \geq 10$). Data are shown as means \pm SD. ***= $P < 0.001$ (Student's *t*-test).

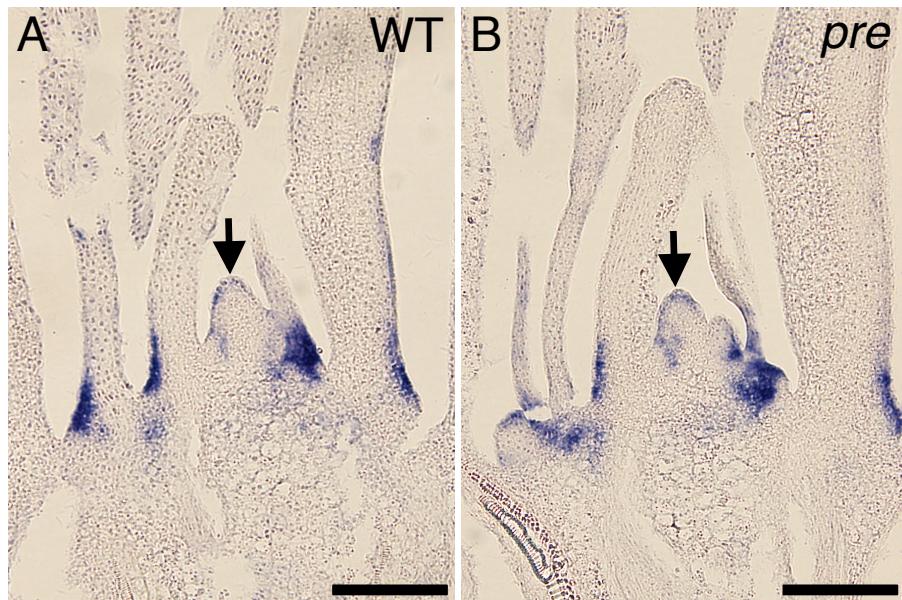


Fig. S7. *in situ* hybridization analysis of *PLA1* in wild type and *pre*.

(A, B) Longitudinal sections of 10-day-old shoot apices in wild type (A) and *pre* (B). Arrows indicate shoot apical meristems. Scale bars = 200 μ m.

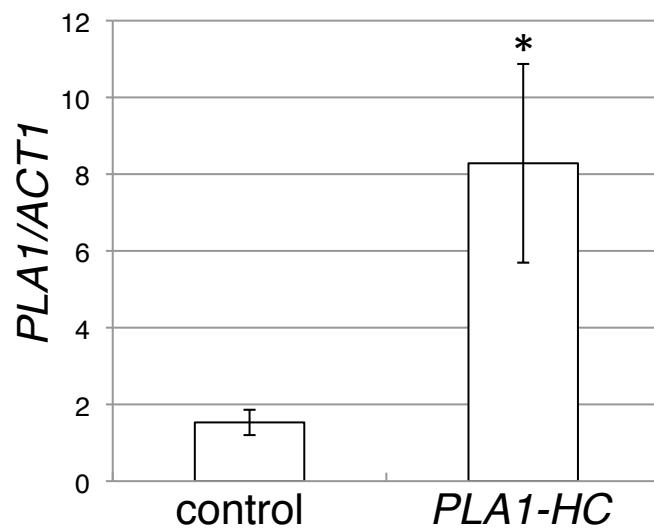


Fig. S8. Expression of *PLA1* in *PLA1-HC*.

Expression level of *PLA1* in the control and *PLA1-HC* shoot apices. Expression level was normalized by that of *OsACTIN1* (*ACT1*). The data shown are as means of three biological replicates \pm SD. * $P < 0.05$ (Student's *t*-test).

Table S1. Primer sequence used for the experiment

Primers for Mapping			
name	Marker type	Forward Primer	Reverse Primer
K0437	Direct sequence	ctgttcatgtggcggttt	tttgccatcacgactatga
0079B15	SSLP	ggacttcacccatgggttgt	gctcgatgtccagtcagg
K0320	CAPS(PstI)	tgtgtccccgtctatggaat	agtttatcgccatggcctg
K0011	CAPS(MboI)	actttgcgttcggagcagtg	tttgcgttctgtttgaaggaa

Primers for RT-PCR		
Transcripts	Forward Primer (name)	Reverse Primer (name)
<i>Os03t0766900-01,-02</i>	cagaagatgtactggtgatc (F1)	cactagataggcttcaagtc (R1)
<i>Os03t0766900-02</i>	gtgaaattccaagctccaag (F2)	gcacatccacaaaactgcac (R2)
<i>Os03t0767000-01</i>	tcctccgatacgtactcc (F3)	tgatcacaccatacagagtga (R3)
<i>OsACTIN1</i>	tccatcttgcgttc (F4)	gtaccctcatcaggcatctg (R4)