
No.	Chromosome	Position	Reference	Alteration	Gene	Note
SNP1	Chr1	5236843	C	T	LOC_Os01g10040	nonsynonymous
SNP2	Chr1	5655212	C	T	LOC_Os01g10590	synonymous

Figure S1. Identification of the *smg11* mutation.

The whole genome sequencing reveals the SNP1 and SNP2 in the gene regions that are associated with the *smg11* phenotype.

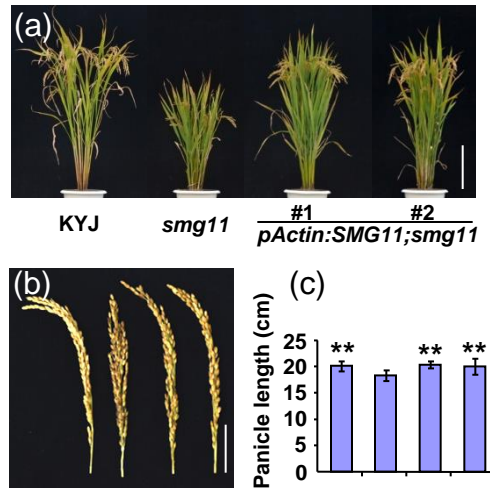


Figure S2. Overexpression of *SMG11* complements the phenotypes of *smg11*.

(a) Plants of KYJ, *smg11*, *pActin:SMG11;smg11#1* and *pActin:SMG11;smg11#2*.

pActin:SMG11;smg11 is *smg11* transformed with *pActin:SMG11*.

(b) Panicles of KYJ, *smg11*, *pActin:SMG11;smg11#1* and *pActin:SMG11;smg11#2*.

(c) Panicle length of KYJ, *smg11*, *pActin:SMG11;smg11#1* and *pActin:SMG11;smg11#2*.

Values (c) are given as mean \pm SD. **P < 0.01 compared with *smg11* by Student's t-test.

Bars: 20cm in (a), 5 cm in (b).

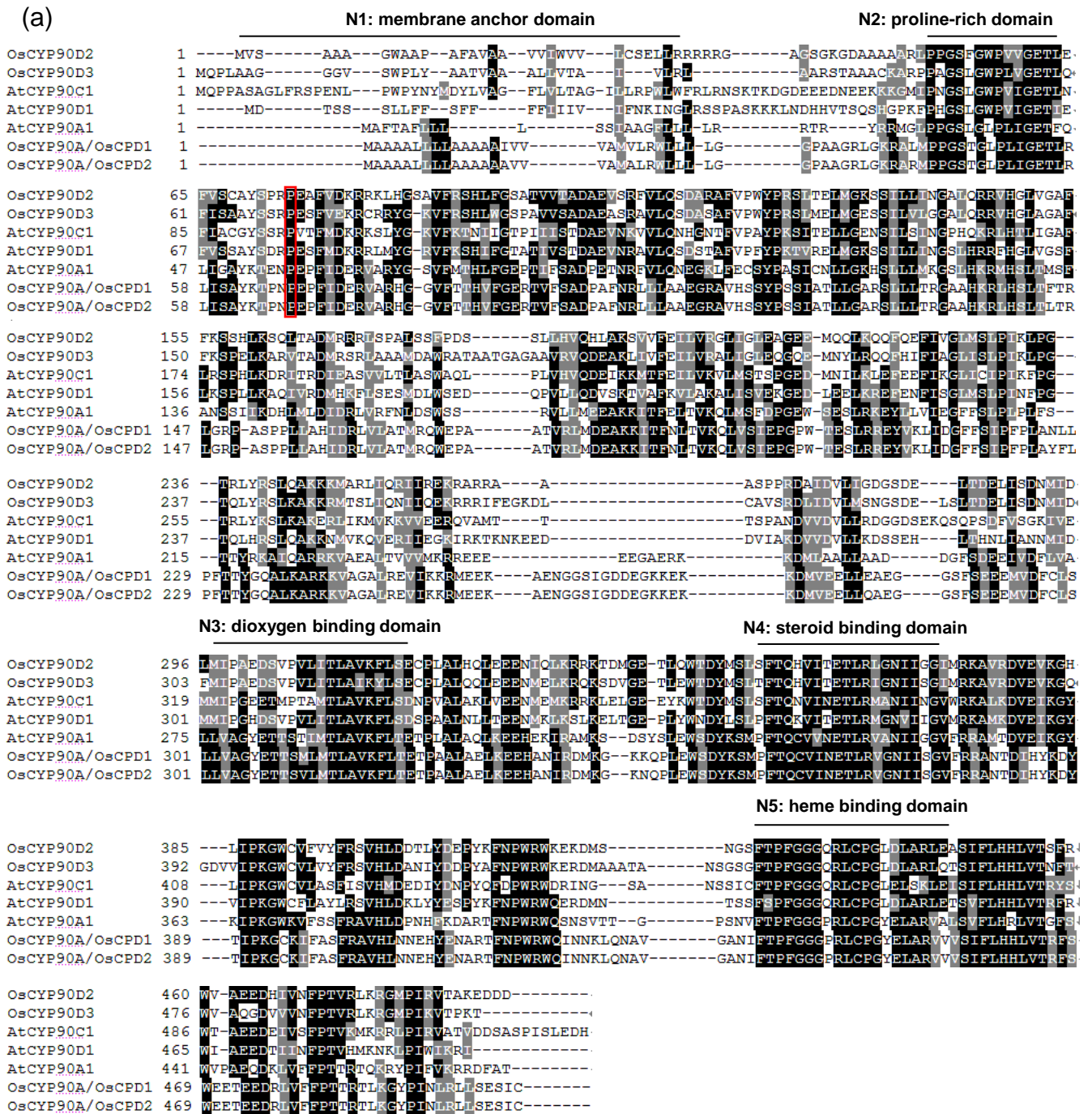


Figure S3. Alignment of D2/SMG11 homologs in rice and Arabidopsis.

The red box shows the conserved amino acid (Pro) at the position 74. The predicted domains are shown.

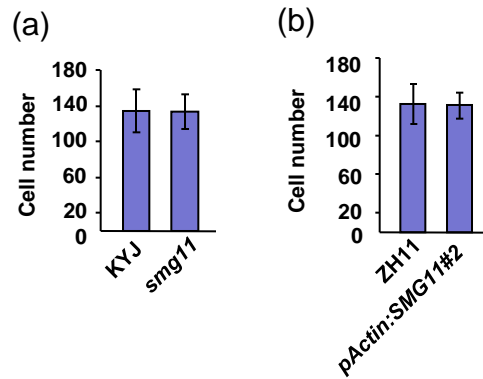


Figure S4. Effects of *SMG11* on cell number in spikelet hulls.

(a) The calculated number of outer epidermal cells in the grain-length direction in KYJ and *smg11* lemmas.

(b) The calculated number of outer epidermal cells in the grain-length direction in ZH11 and *pActin:SMG11#2* lemmas.

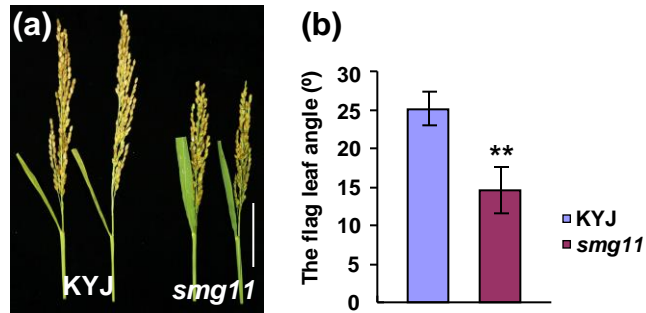


Figure S5. *smg11* influences leaf angle.

(a) Comparison of KYJ and *smg11* lamina joints at the mature stage.

(b) The flag leaf angle of KYJ and *smg11* plants at the mature stage.

Values (b) are given as mean \pm SD. **P < 0.01 compared with KYJ by Student's t-test.

Bars: 5cm in (a).

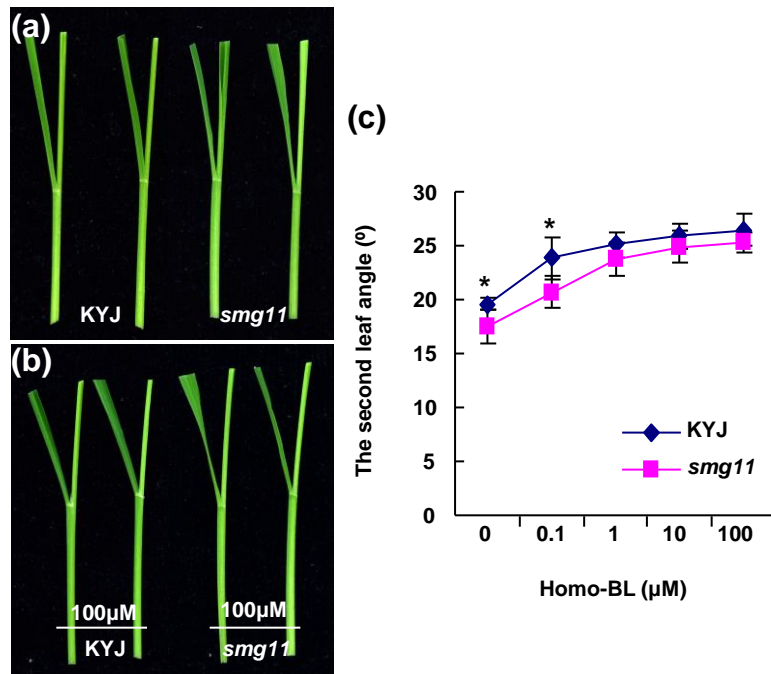


Figure S6. Exogenous application of BL rescues the leaf angle phenotype of *smg11*.

(a) The second leaf joint of KYJ and *smg11* seedlings without homo-BL (in the trefoil stage).

(b) The second leaf joint of KYJ and *smg11* seedlings with 100 μM homo-BL (in the trefoil stage).

(c) The second leaf angle of KYJ and *smg11* treated by different concentrations of homo-BL.

Values (c) are given as mean \pm SD. *P < 0.05 compared with KYJ by Student's t-test.