No.	Chromosome	Position	Reference	Alteration	Gene	Note
SNP1	Chr1	5236843	С	т	LOC_Os01g10040	nonsynonymous
SNP2	Chr1	5655212	С	т	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). (a)

N1: membrane anchor domain

N2: proline-rich domain

()			·
OsCYP90D2 OsCYP90D3 AtCYP90C1 AtCYP90D1 AtCYP90A1 OsCYP90A/OsCPD1 OsCYP90A/OsCPD2	1 1 1 1 1 1	MVSAAAGWAAPAFAVAAVVIWVVIC MQPLAAGGGVSWPLYAATVAAALIVTAI MQPPASAGLFRSPENLPWPYNYMDYLVAGFLVLTAG-IIL MDTSSSLLFFSFFFFIIVIF MAFTAFUII LSSIA MAAAALUUTAAAAAIVVVAMV MAAAALUUTAAAAA	SELURRRRRGACSGKGDAAAAARIPPGSFGWPVVGETLE. VURUARSTAAACKARPPAGSIGWPLVGETLQ. RPWLWFRLRNSKTKDGDEEEDNEEKKKGMIPNGSIGWPVIGETLN. NKINGURSSPASKKKLNDHHVTSQSHGPKFPHGSIGWPVIGETIE. AGFTLU-LRRTRYRRMGLPPGSIGLPLIGETFO. 'LRWLLD-LGCPAAGRLGKRALMPPGSTGLPLIGETLR LRWLLD-LG
OSCYP90D2 OSCYP90D3 AtCYP90C1 AtCYP90D1 AtCYP90A1 OSCYP90A/OSCPD1 OSCYP90A/OSCPD2	65 61 85 67 47 58 58	FVSCAYSPREBAFVDKRRKLHGSAVFRSHLFGSATVVTADAEVS FISAAYSSREBSFVEKRCRRYG-KVFRSHLWGSPAVVSADABAS FIACGYSSREVTFMDKRKSLYG-KVFKTNIIGTPIIISTDAEVNK FVSSAYSDREBSFMDKRRLMYG-RVFKSHIFGTATIVSTDAEVNK LIGAYKTENEBFFIDERVARHG-SVFMHLFGEFTIFSADEFTNK LISAYKTENEBFFIDERVARHG-GVFTHVFGERTVFSADEAFNK LISAYKTENEBFFIDERVARHG-GVFTHVFGERTVFSADEAFNK	FVLCSDARAFVPWYPRSLTELMGRSSILLINGAICRRVHGUVGAF AVLCSDASAFVPWYPRSLMELMGESSILVLCGALORRVHGUAGAF VVLONHGNTFVPAYPRSITELLGENSILSINGPHOKRLHTLIGAF AVLOSDSTAFVPFYPKTVRELMGRSSILLINGSLHRRFHGUVGSF FVLONEGRIFECSYPASICNLLGKHSLLLMRGSLHRRMHSLIMSF ILLIAAEGRAVHSSYPSSIATLLGARSILLTRGAAHRRIHSLTTR ILLIAAEGRAVHSSYPSSIATLLGARSILLTRGAAHRRIHSLTTR
OsCYP90D2 OsCYP90D3 AtCYP90C1 AtCYP90D1 AtCYP90A1 OsCYP90A/OsCPD1 OsCYP90A/OsCPD2	155 150 174 156 136 147 147	FKSSHLKSOLTAD MRRRISPALSSEPDSSLLHVOHLARS FKSELKARVTADMRSRLAAAMDAWRATAATGAGAAVRVODEAR IRSEHLKDRITRDIEASVVLTIASWAQLPLVHVODEIK IKSELLKACIVRDMHKELSESMDLWSEDQVVLLODVSR ANSSIIKDHLMLDIDRLVRFNLDSWSSRVLLMEEAR IGRE-ASPELIAHIDRLVLATMROWEPAATVRLMDEAK IGRE-ASPELIAHIDRLVLATMROWEPAATVRLMDEAK	VVEELIVRGLIGHBAGEE-MOOLKQQEQEFIVGLMSHPIKLPG IVFELIVRALIGHECGQE-MNYLRQQSHIPIAGLISHPIKLPG MTFELIVRVIMSTSPGED-MNILKLEFEEFIKGHICHPIKFPG VAFKVIAKALISVEKGED-LBELKREFENFISGLMSHPINFPG LIFELIVRQLMSEDPGEW-SESLRKEYHLVIEGFFSHPIPIFS KITFNLTVRQLVSIEPGPW-TESLRREYVKHIDGFFSHPFPIANLL KITFNLTVRQLVSIEPGPW-TESLRREYVKHIDGFFSHPFPIANLL
OsCYP90D2 OsCYP90D3 AtCYP90C1 AtCYP90D1 AtCYP90A1	236 237 255 237 215	TRLYRSICAKKKMARIICRITREKRARRAA TQLYRSIKAKKRMTSIIONIICEKRRIFEGKDL TRLYKSIKAKERLIKMVKKVVEERQVAMTT	
OsCYP90A/OsCPD1 OsCYP90A/OsCPD2	229 229	PFTTYGOALKARKKVAGALREVIKKRMEEKAENGGSIGDD PFTTYGOALKARKKVAGALREVIKKRMEEKAENGGSIGDD	EGKKEKRDMVBE <mark>LT</mark> EAEGGSFSEB <mark>E</mark> MVDFCLS EGKKEKKDMVB <mark>ELL</mark> QAEGGSFSEB <mark>E</mark> MVDFCLS
OsCYP90A/OsCPD1 OsCYP90A/OsCPD2	229 229	PFNTYGOALKARKKVAGALREVTKKRMEEKAENGGSIGDD: PFNTYGOALKARKKVAGALREVTKKRMEEKAENGGSIGDD: N3: dioxygen binding domain	EGKKEKKDMVEBILTEAEGGSFSBBBMVDFCILS EGKKEKKDMVEBILTOAEGGSFSBBBMVDFCILS N4: steroid binding domain
OSCYP90A/OSCPD1 OSCYP90A/OSCPD2 OSCYP90D2 OSCYP90D3 AtCYP90C1 AtCYP90D1 AtCYP90A1 OSCYP90A/OSCPD1 OSCYP90A/OSCPD2	229 229 303 319 301 275 301 301	PFTTYGQALKARKKVAGALREV TKRRMEEKAENGGSIGDD PFTTYGQALKARKKVAGALREV TKRRMEEKAENGGSIGDD N3: dioxygen binding domain IMI BAEDSVPVLITLAVKFLSECELALHQIEEENIOLKRRKTDM FMI BAEDSVPVLITLAVKFLSECELALHQIEEENIOLKRRKTDM FMI BAEDSVPVLITLAVKFLSECELALQOIEEENMELKROKSDV MMI PGETMPTAMTLAVKFLSDNPVALAKIVEENMEMKRRKLELO MMI PGHDSVPVLITLAVKFLSDSPALNILTEENMELKSLKELT LLVAGYETTSTITTLAVKFLSDSPALNILTEENMELKSLKELT LLVAGYETTSTITTLAVKFLSDSPALNILTEENMELKSLKELT LLVAGYETTSMINTLAVKFLSDFPALADIKEEHANIIDMKG1 LLVAGYETTSVLMTLAVKFLSDFPALADIKEEHANIIDMKG1	EGKKEKKDMVEBLIEAEGGSFSBEBWVDFCLS EGKKEKKDMVEBLIEAEGGSFSBEBWVDFCLS N4: steroid binding domain EB-TLOWTDYMSLSFTCHVITETLRIGNIIGGTMRKAVRDVEVKGH EB-TLEWTDYMSLSFTCHVITETLRIGNIIGGTMRKAVRDVEVKGQ E-EYKWTDYMSLSFTCHVITETLRIGNIIGGTMRKAVRDVEVKGQ E-EYKWTDYMSLSFTCNVINETLRMANIINGVWRKALKDVEIKGY EB-FLYWNDYLSIFTCKVITETLRMGNVIIGGVFRRAMTDVEIKGY SYSLEWSDYKSMPFTCCVINETLRVGNIIGGVFRRAMTDIHYRDY KNOPLEWSDYKSMPFTCCVINETLRVGNIISGVFRRAMTDIHYRDY
OSCYP90A/OSCPD1 OSCYP90A/OSCPD2 OSCYP90D2 OSCYP90D3 AtCYP90D1 AtCYP90D1 AtCYP90A1 OSCYP90A/OSCPD1 OSCYP90A/OSCPD2	229 229 303 319 301 275 301 301	PFTTYGQALKARKKVAGALREV TKKRMEEKAENGGSIGDD PFTTYGQALKARKKVAGALREV TKKRMEEKAENGGSIGDD N3: dioxygen binding domain IMT PAEDSVPVLITLAVKFLSECPLATHCLEEENICLKRRKTDM FMIPAEDSVPVLITLAIKKLSECPLATQCLEEENMELKROKSDV MMI PGEETMPTAMTLAVKFLSECPLATQCLEEENMELKROKSDV MMI PGEETMPTAMTLAVKFLSECPLATQCLEEENMELKROKSDV ILVAGYETTSTIMTLAVKFLSESPAAMILITEENMELKSIKELTG LLVAGYETTSTIMTLAVKFLTETPLATAELKEEHANIRDMKG1 LLVAGYETTSVIMTLAVKFLTETPAALAELKEEHANIRDMKG1	EGKKERKDMVPELLEAEGGSFSBEEMVDFCLS EGKKER
OsCYP90A/OsCPD1 OsCYP90A/OsCPD2 OsCYP90D2 OsCYP90D3 AtCYP90C1 AtCYP90C1 AtCYP90A1 OsCYP90A/OsCPD1 OsCYP90A/OsCPD2 OsCYP90D3 AtCYP90D1 AtCYP90C1 AtCYP90D1 AtCYP90D1 OsCYP90A1 OsCYP90A1 OsCYP90A/OsCPD1 OsCYP90A/OsCPD2	229 229 303 319 301 275 301 301 301 385 392 408 390 363 389 389	PFTTYGQALKARKKVAGALREV TKKRMEEKAENGGSIGDD PFTTYGQALKARKKVAGALREV TKKRMEEKAENGGSIGDD N3: dioxygen binding domain IMT PAEDSVEVLITLAVKFLSECPLATHCTEEENICIKRRKTDM FMIPAEDSVEVLITLAVKFLSECPLATHCTEEENICIKRRKTDM MIPGETMPTAMTLAVKFLSECPLATQOTEEENMELKROKSDV MIPGETMPTAMTLAVKFLSECPLATQOTEEENMELKROKSDV MIPGETMPTAMTLAVKFLSECPLATQOTEEENMELKROKSDV MIPGETMPTAMTLAVKFLSECPLATQOTEEENMELKROKSDV MIPGETMPTAMTLAVKFLSECPLATQOTEEENMELKROKSDV MIPGETMPTAMTLAVKFLSECPLATQOTEEENMELKROKSDV MIPGETMPTAMTLAVKFLSECPLATQOTEEENMELKROKSDV MIPGETMPTAMTLAVKFLSECPLATQOTEEENMELKROKSLKELU UVAGVETTSTIMTLAVKFLSECPLATQOTEEENMELKSLKELU ILVAGVETTSTIMTLAVKFLSETPLATACKEEHEKTRAMKS GDVVIPKGWCVIVYFRSVHLDANIYDEYAFNPWRWKEKDMAAAT LIPKGWCVIVYFRSVHLDANIYDEYAFNPWRWKEKDMAAAT 	EGKKEKKDMVPELLEAEGGSFSBEEMVDFCLS EGKKEK

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 μ M 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.