

New Phytologist Supporting Information

Article title: **OsmiR530 acts downstream of OsPIL15 to regulate grain yield in rice**

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The following Supporting Information is available for this article:

Fig. S1 Agronomic traits of OsmiR530-overexpressing (miR530-OE) and target mimic (MIM530) lines. **(a)** Results of the qRT-PCR analysis of the expression of OsmiR530 in rice miR530-OE lines. 5.8S rRNA was used as an internal control for qRT-PCR. Three biological replicates were analyzed. **(b)** Results of the qRT-PCR analysis of the expression of the OsmiR530 target mimic in MIM530 lines. *OsEF-1 α* was used as a reference gene for the qRT-PCR. Because the OsmiR530 target mimic was not expressed in rice wild-type (WT) plants, the expression level of the OsmiR530 target mimic in MIM530-#2 was set as the baseline. Three biological replicates were analyzed. **(c)** Rice transgenic and WT plants heights ($n = 20$ plants). **(d)** Phenotypes of the main panicle of rice transgenic and WT plants. Scale bars, 5 cm. **(e)** Primary panicle lengths of rice transgenic and WT plants ($n = 20$ panicles). **(f)** Seed-setting rates of rice transgenic and WT plants ($n = 20$ panicles). **(g)** Spikelet hull lengths and widths in rice transgenic and WT plants ($n = 20$ spikelets). For all histogram, the gray bar represents WT, blue bars represent miR530-OE transgenic lines #a1, #b5, and #c2 (from left to right), and red bars represent MIM530 transgenic lines #2, #3, and #6 (from left to right). The data in **(a)**, **(b)**, **(c)**, **(e)**, **(f)**, and **(g)** are presented as the mean \pm standard deviation. Significant differences were determined with Student's *t*-test (* $P < 0.05$, ** $P < 0.01$).

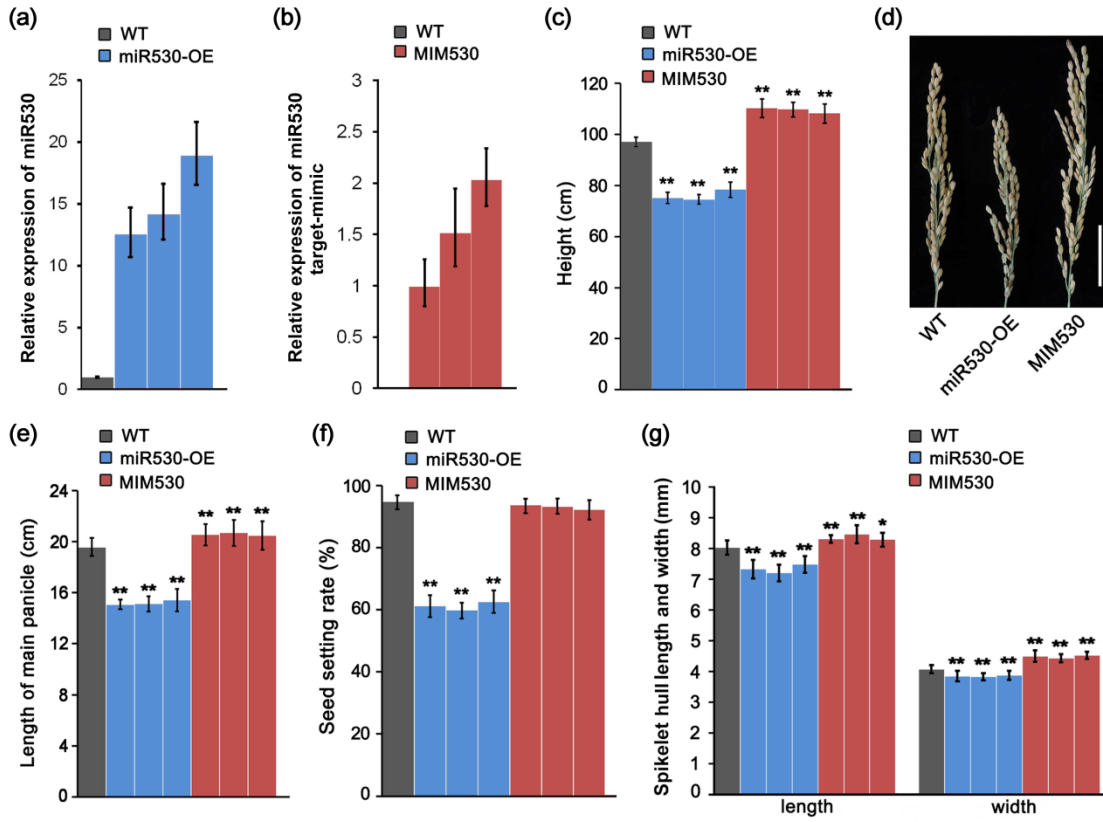


Fig. S2 Comparison of the peduncle in miR530-overexpressing (miR530-OE), target mimic (MIM530) and wild-type (WT) plants. **(a)** Comparison of the peduncle diameters of rice transgenic and WT plants ($n = 10$ plants). **(b)** Cross-sections of the peduncles of rice transgenic and WT plants. LV, large vascular bundles; SV, small vascular bundles. Scale bars, 200 μm . Comparison of the number of LV **(c)** and SV **(d)** in the peduncles of rice transgenic and WT plants ($n = 10$ plants). Data are presented as the mean \pm standard deviation. Significant differences were determined with Student's t -test (* $P < 0.05$, ** $P < 0.01$).

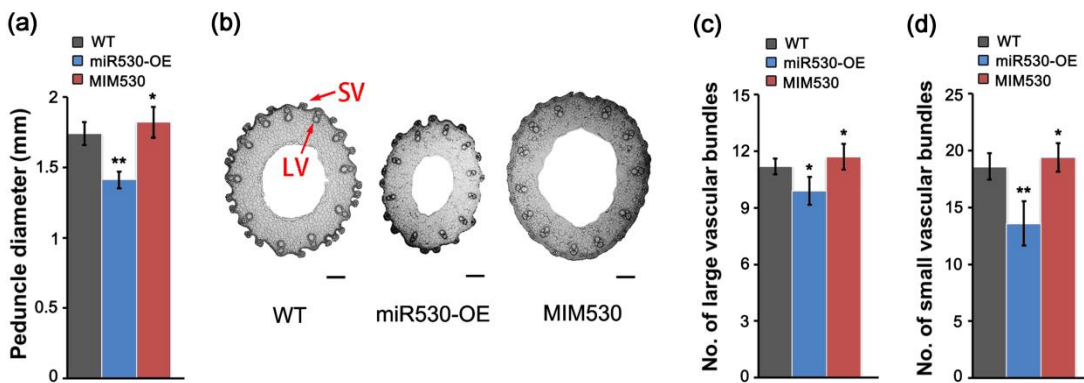


Fig. S3 Expression of *OsmiR530* and *OsPL3* in various rice tissues. **(a)** Expression of *OsmiR530* in various rice tissues. R, root; IN, internode; FL, flag leaf; SP1, spikelet (0.5-1 cm long); SP2, spikelet (3-5 cm long); E, embryo; S, immature seed. 5.8S rRNA was used as an internal control for the qRT-PCR. Data are presented as the mean \pm standard deviation of three biological replicates. **(b)** Expression of *OsPL3* in various rice tissues. R, root; IN, internode; FL, flag leaf; SP1, spikelet (0.5-1 cm long); SP2, spikelet (3-5 cm long); E, embryo; S, immature seed. *OsEF1 α* was used as a reference gene for the qRT-PCR. Data are presented as the mean \pm standard deviation of three biological replicates.

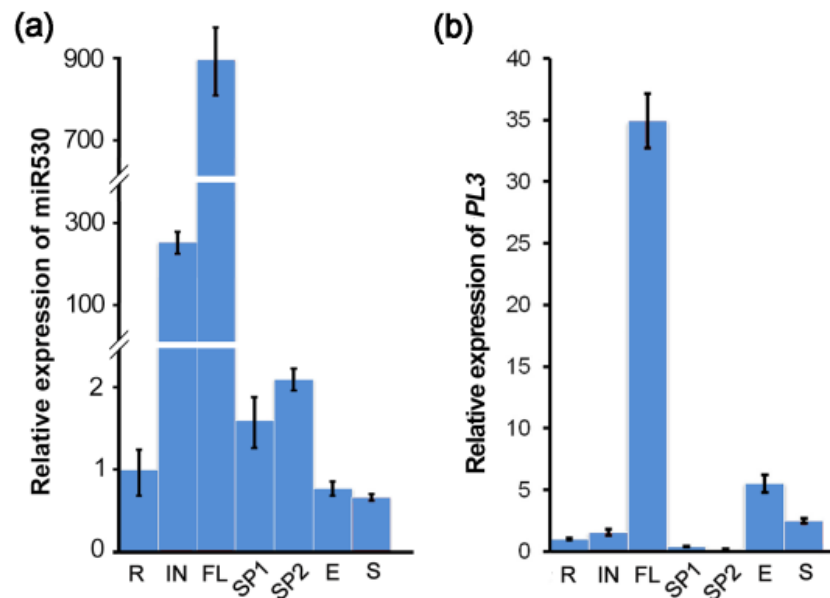


Fig. S4 Diagram of two single-guide RNAs (sgRNAs) targeting *OsPL3* in the rice genome.

Target sites are marked in red, whereas the protospacer-adjacent motif (PAM) is marked in green.

Sequences in boxes are the target sequences in the wild-type (WT) rice. Black dashes represent deleted bases and inserted nucleotides are indicated with red lowercase letters.

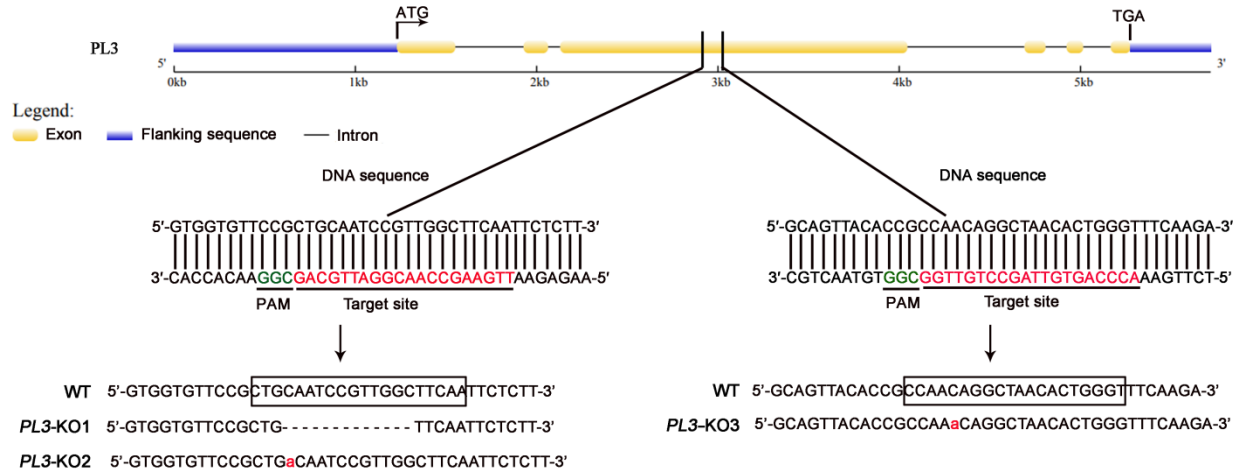
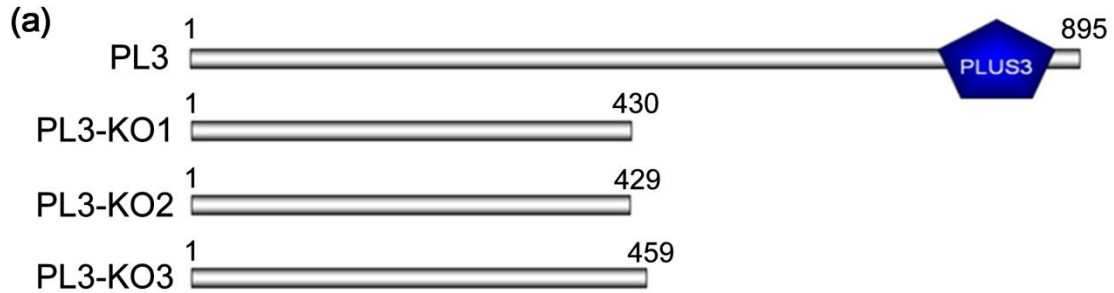


Fig. S5 Analysis of the OsPL3 protein sequence of in the wild-type (WT) and *OsPL3*-knockout (*PL3*-KO) lines. **(a)** Protein structure of OsPL3 in rice WT and *PL3*-KO lines. **(b)** Changes in the OsPL3 amino acid sequences in *PL3*-KO lines.



(b)

PL3-KO1.seq	MRSVSELVWSPDEGLSIRKIAAASLSTRKTSLHWNADTLIVISSPQQSGAGESGHIIDATVEDAEKMFQCLRTSPSSARVFMSSPSRIRNTDAQQSTIRSHGQDSWYCGGMVWNEGK	120
PL3-KO2.seq	MRSVSELVWSPDEGLSIRKIAAASLSTRKTSLHWNADTLIVISSPQQSGAGESGHIIDATVEDAEKMFQCLRTSPSSARVFMSSPSRIRNTDAQQSTIRSHGQDSWYCGGMVWNEGK	120
PL3-KO3.seq	MRSVSELVWSPDEGLSIRKIAAASLSTRKTSLHWNADTLIVISSPQQSGAGESGHIIDATVEDAEKMFQCLRTSPSSARVFMSSPSRIRNTDAQQSTIRSHGQDSWYCGGMVWNEGK	120
WT.seq	MRSVSELVWSPDEGLSIRKIAAASLSTRKTSLHWNADTLIVISSPQQSGAGESGHIIDATVEDAEKMFQCLRTSPSSARVFMSSPSRIRNTDAQQSTIRSHGQDSWYCGGMVWNEGK	120
Consensus	mrsvselvwspeqlsirkiaaaslstrktslhwadtlivisspqqsgagesghiidatvedaeakmpqlrtspssarvfmsspsrirntdaqgstirshgqdsyccgmvwneqk	
PL3-KO1.seq	ETSDNFCVDRLEKEDEVGSCPTRYCNDTSHSLGASRREVMPIIAEKQAFCAITVHDERSWAANAWRARLVRAISQKDSVLFKNADNIHSTSAFGSIGNTENMPGKLTSLGNRNDSSQD	240
PL3-KO2.seq	ETSDNFCVDRLEKEDEVGSCPTRYCNDTSHSLGASRREVMPIIAEKQAFCAITVHDERSWAANAWRARLVRAISQKDSVLFKNADNIHSTSAFGSIGNTENMPGKLTSLGNRNDSSQD	240
PL3-KO3.seq	ETSDNFCVDRLEKEDEVGSCPTRYCNDTSHSLGASRREVMPIIAEKQAFCAITVHDERSWAANAWRARLVRAISQKDSVLFKNADNIHSTSAFGSIGNTENMPGKLTSLGNRNDSSQD	240
WT.seq	ETSDNFCVDRLEKEDEVGSCPTRYCNDTSHSLGASRREVMPIIAEKQAFCAITVHDERSWAANAWRARLVRAISQKDSVLFKNADNIHSTSAFGSIGNTENMPGKLTSLGNRNDSSQD	240
Consensus	etsdnfcvdrlekedevgscptrycndtshslgsasrrevmpiiiaekeqafcaitvhderswaanawrarlvraisqkdsvlfnknadnihstsafigsigntenmpgkltslgnrndssqd	
PL3-KO1.seq	QAMQEKHKDGLIVARCESYSAVNPVAVARCELASGVNPLARHSTSGCNPRKLEKGEKELIYDMNCVSNITNEGDDSNESIESCPSTKAPKRKHGQFSAAEMTSGNKRCRREDNESSCGLF	360
PL3-KO2.seq	QAMQEKHKDGLIVARCESYSAVNPVAVARCELASGVNPLARHSTSGCNPRKLEKGEKELIYDMNCVSNITNEGDDSNESIESCPSTKAPKRKHGQFSAAEMTSGNKRCRREDNESSCGLF	360
PL3-KO3.seq	QAMQEKHKDGLIVARCESYSAVNPVAVARCELASGVNPLARHSTSGCNPRKLEKGEKELIYDMNCVSNITNEGDDSNESIESCPSTKAPKRKHGQFSAAEMTSGNKRCRREDNESSCGLF	360
WT.seq	QAMQEKHKDGLIVARCESYSAVNPVAVARCELASGVNPLARHSTSGCNPRKLEKGEKELIYDMNCVSNITNEGDDSNESIESCPSTKAPKRKHGQFSAAEMTSGNKRCRREDNESSCGLF	360
Consensus	qamqekhkdgliivarcesyavnpvarcelasgvnplarhestsgcnprklekgekeliydmncvsnitnegddsnesiescpstkapkrkhgqfsaaemtsgnkrcreddnesccglf	
PL3-KO1.seq	HKNDSSFFNMSTLTNGVKVFDETTAVPLNQRKFSAAATGEEFPTNFVPLQNNCGVPLASILEFNIIVRML.....	430
PL3-KO2.seq	HKNDSSFFNMSTLTNGVKVFDETTAVPLNQRKFSAAATGEEFPTNFVPLQNNCGVPLIRWQCFSSISL.....	429
PL3-KO3.seq	HKNDSSFFNMSTLTNGVKVFDETTAVPLNQRKFSAAATGEEFPTNFVPLQNNCGVPLQSVGNSHLSQSLYSQNVMTSRNTCHQSESSYTAKQANTGFQE.....	459
WT.seq	HKNDSSFFNMSTLTNGVKVFDETTAVPLNQRKFSAAATGEEFPTNFVPLQNNCGVPLQSVGNSHLSQSLYSQNVMTSRNTCHQSESSYTAARLTLGFRSKRFVSMGRELTINVAETLTAAG	480
Consensus	hkndssffnmstltngvkvfdeettavplnqrkfsaatgeefptnfvplqnncgvplf	
PL3-KO1.seq	430
PL3-KO2.seq	429
PL3-KO3.seq	RIQMDSYGDGRGAFQWGIIFLRAERNQNGFHGSSNAASGHKDDFSESIVSRLLKPTFMKVMWDTTRCDEETDFCSANFKGLGDSSSPQDFWVRELNNSQYFTSKGSDNETTSSCAA	459
WT.seq	600
Consensus	
PL3-KO1.seq	430
PL3-KO2.seq	429
PL3-KO3.seq	FQDENKFEETMASIFAKRLDALRHANTSAVHVAITCDHGTFRGRNHKTSFVSVYNSHDEQESGQKTHRSSGGEGRIVLWTKGKGEQLSEGNDRDELGEKVLKSHENQCEGSSDGKVVV	720
WT.seq	
Consensus	
PL3-KO1.seq	430
PL3-KO2.seq	429
PL3-KO3.seq	FKCNLETNYIIIEIDRRKRLQNHGAFNSMENQFDNKQWVYGIIVFDVYDEASVFGALQRLRLSRSDIIRWHRFSVMHTLIDGFFLLRFRGWEEALGGTYHVARINGLDKRNLSVT	840
WT.seq	
Consensus	
PL3-KO1.seq	430
PL3-KO2.seq	429
PL3-KO3.seq	459
WT.seq	IRNSTCQVDSRFVSNHDFHQDELKAWWSAAMKSGWKLFSQEELNTRLERELLA	894
Consensus	

Fig. S6 Agronomic traits of *OsPL3*-knockout (*PL3*-KO) lines. **(a)** The rice *PL3*-KO and wild-type (WT) plant heights ($n = 20$ plants). **(b)** Phenotypes of the main panicle of rice *PL3*-KO and WT plants. **(c)** Primary panicle lengths of rice *PL3*-KO and WT plants ($n = 20$ panicles). **(d)** Number of primary branches per main panicle in rice *PL3*-KO and WT plants. **(e)** Seed-setting rates of rice *PL3*-KO and WT plants ($n = 20$ panicles). For all histograms, the gray bar represents WT and green bars represent *PL3*-KO transgenic lines #12, #13, and #16 (from left to right). The data in **(a)** and **(c–e)** are presented as the mean \pm standard deviation. Significant differences were determined with Student's *t*-test (* $P < 0.05$, ** $P < 0.01$).

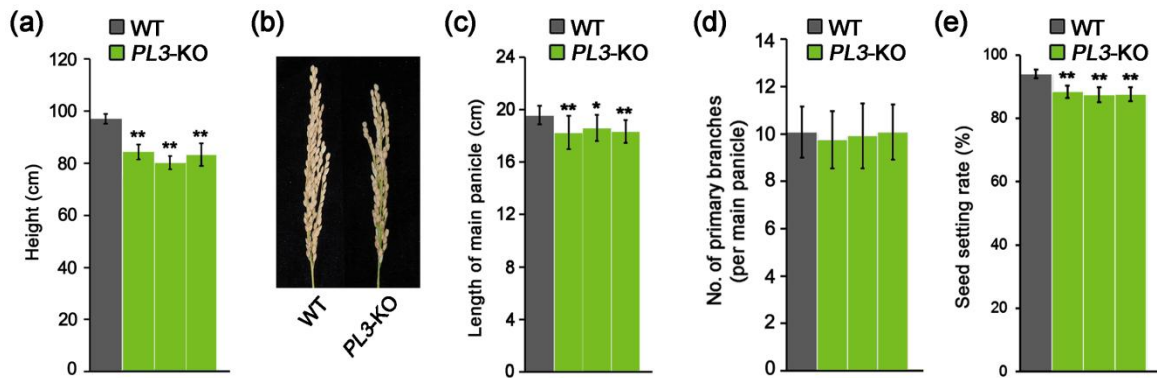


Fig. S7 Diagram of two single-guide RNAs (sgRNAs) targeting *OsPIL15* in the rice genome. Target sites are marked in red, whereas the protospacer-adjacent motif (PAM) is marked in green. Sequences in boxes are the target sequences in the wild-type (WT) rice. Black dashes represent deleted bases and inserted nucleotides are indicated with red lowercase letters.

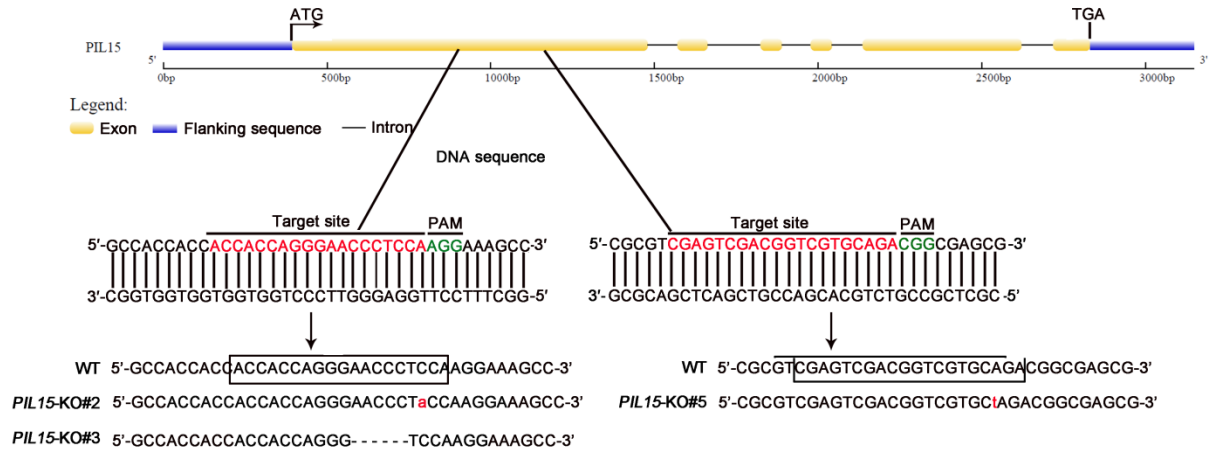


Fig. S8 Analysis of the OsPIL15 protein sequence in the rice wild-type (WT) and *OsPIL15*-knockout (*PIL15*-KO) lines.

WT.seq	MSDGNDFAE LLWENGQAVVHGRKKHPQAFPPFFGFGGTGGGGGSSSRAQERQ PGGIDAF AKVGGGFGALGMAPAVHDF	80
PL15-KO#2.seq	MSDGNDFAE LLWENGQAVVHGRKKHPQAFPPFFGFGGTGGGGGSSSRAQERQ PGGIDAF AKVGGGFGALGMAPAVHDF	80
PIL15-KO#3.seq	MSDGNDFAE LLWENGQAVVHGRKKHPQAFPPFFGFGGTGGGGGSSSRAQERQ PGGIDAF AKVGGGFGALGMAPAVHDF	80
PIL15-KO#5.seq	MSDGNDFAE LLWENGQAVVHGRKKHPQAFPPFFGFGGTGGGGGSSSRAQERQ PGGIDAF AKVGGGFGALGMAPAVHDF	80
Consensus	msdgndfaellwengqavvhgrkkhpqafppffgfggtgggggssssraqerqppgidafakvgggfgalgmavpavhdf	
WT.seq	ASGFGATTQDNGDDDTVPWIHYPIIDDEDA AAAPAALAAADYGSDF FSEIQAAAAAAAAA APPTDLASLPASNHN GATNNR	160
PL15-KO#2.seq	ASGFGATTQDNGDDDTVPWIHYPIIDDEDA AAAPAALAAADYGSDF FSEIQAAAAAAAAA APPTDLASLPASNHN GATNNR	160
PIL15-KO#3.seq	ASGFGATTQDNGDDDTVPWIHYPIIDDEDA AAAPAALAAADYGSDF FSEIQAAAAAAAAA APPTDLASLPASNHN GATNNR	160
PIL15-KO#5.seq	ASGFGATTQDNGDDDTVPWIHYPIIDDEDA AAAPAALAAADYGSDF FSEIQAAAAAAAAA APPTDLASLPASNHN GATNNR	160
Consensus	asfggattqdnngdddtvpwihypiiddedaaapaalaaadygsdffselqaaaaaaaaapptdlaslpasnhngatnnr	
WT.seq	NAPVATTTTR... EPSKESHGGLSVETTR EFQ QPQLAAAKLFR SSGSGGEGVMN FLFSRFAV LARATLES AGRTQ G	237
PL15-KO#2.seq	NAPVATTTTREPYQ GKPRR FV GS HH SRRA AAAA TARRSQAA SVER QRRRRGR DELLALL PPGRF ...GEGDAGE BRAED	235
PIL15-KO#3.seq	NAPVATTTTR...VQ GKPRR FV GS HH SRRA AAAA TARRSQAA SVER QRRRRGR DELLALL PPGRF ...GEGDAGE BRAED	233
PIL15-KO#5.seq	NAPVATTTTR... EPSKESHGGLSVETTR EFQ QPQLAAAKLFR SSGSGGEGVMN FLFSRFAV LARATLES AGRTQ G	237
Consensus	napvat tttr ... g p a a a r g r p r	
WT.seq	TDNKASNV TASN RVESTV V QTASGPR SAPAFADQRAAAWPPQKEMP FASTAAAPMA FAVNLHHEMGRDRAGRT MPVHKT	317
PL15-KO#2.seq	AGHRQZ.....	241
PIL15-KO#3.seq	AGHRQZ.....	239
PIL15-KO#5.seq	TDNKASNV TASN RVESTV V LDGERAKERTG VRRSEGGGVA AAAE GD AVRVH GS RS HGFGRZ	298
Consensus		
WT.seq	EARKAPEATVATSSVCSGNGAGS DELWRQ Q KRKCAQA EC SASQ DDDL DDEPGVLRKSGTR STKRSRTAEVH NLSERRRR	397
PL15-KO#2.seq	241
PIL15-KO#3.seq	239
PIL15-KO#5.seq	298
Consensus		
WT.seq	DRINEKMRALQELIPNCNKIDKASMLDEAIEYLKTLQLQVQMMSMG TGLCIP PMLLPTAMQHLQIP PM AHFPHLGMGLGY	477
PL15-KO#2.seq	241
PIL15-KO#3.seq	239
PIL15-KO#5.seq	298
Consensus		
WT.seq	GMGVFDM SNTGALQMP MPGAHFPC PMIPGAS PQGLGIPGTST MPMFGV PGQTI PSSASSV PPFASLAGLPVR PSG V PQV	557
PL15-KO#2.seq	241
PIL15-KO#3.seq	239
PIL15-KO#5.seq	298
Consensus		
WT.seq	SGAMANMVQDQQGGIANQQ QCLNKEA IQGAN PGDS QM QIIM QGD NENFRIP SSAQTKSS QFSDGTG KGTNARERDGAET	637
PL15-KO#2.seq	241
PIL15-KO#3.seq	239
PIL15-KO#5.seq	298
Consensus		

Fig. S9 Expression of OsmiR530 in rice *OsPIL15* transgenic lines. The expression of mature OsmiR530 in *OsPIL15*-overexpressing (*PIL15*-OE) and knockout (*PIL15*-KO) lines. 5.8S rRNA was used as an internal control for the qRT-PCR. Data are presented as the mean \pm standard deviation of three biological replicates.

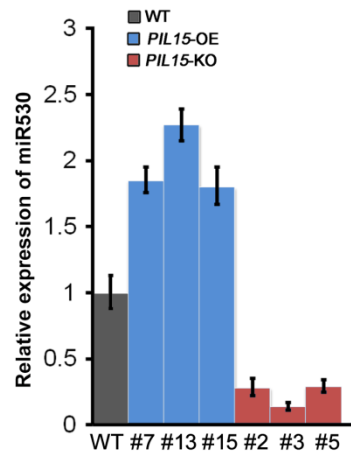


Fig. S10 Alignment of mature miR530 sequences identified in miRBase. tae, *Triticum aestivum*; mdm, *Malus domestica*; stu, *Solanum tuberosum*; ppe, *Prunus persica*; eun, *Eugenia uniflora*; mtr, *Medicago truncatula*; gma, *Glycine max*; cme, *Cucumis melo*; tcc, *Theobroma cacao*; fve, *Fragaria vesca*; aqc, *Aquilegia caerulea*; bdi, *Brachypodium distachyon*; ptc, *Populus trichocarpa*; csi, *Citrus sinensis*; lus, *Linum usitatissimum*; htu, *Helianthus tuberosus*; mes, *Manihot esculenta*; gra, *Gossypium raimondii*; sly, *Solanum lycopersicum*.

tae-miR530	---UGCAGUGGCAUAUGCAACUCU	21
mdm-miR530a	---UGCAUUUGCACCUGCACUUGU	21
mdm-miR530b	---UGCAUUUGCACCUGCACUUGU	21
mdm-miR530c	---UGCAUUUGCACCUGCACUUGU	21
stu-miR530	-UCUGCAUUUGCACCUGCACCU--	21
ppe-miR530	-UCUGCAUUUGCACCUGCACCU--	21
eun-miR530-5p	-UCUGCAUUUGCACCUGCACCU--	21
mtr-miR530	---UGCAUUUGCACCUGCACUUUC	21
gma-miR530a	---UGCAUUUGCACCUGCACUUU-	20
gma-miR530b	---UGCAUUUGCACCUGCACUUUA	21
gma-miR530c	---UGCAUUUGCACCUGCACUUUA	21
gma-miR530d	---UGCAUUUGCACCUGCACUUUA	21
gma-miR530e	---UGCAUUUGCACCUGCACUUUA	21
cme-miR530b	---UGCAUUUGCACCUACACCUU-	20
tcc-miR530a	---UGCAUUUGCACCUGCACCU--	20
fve-miR530	---UGCAUUUGCACCUGCACCUU	21
aqc-miR530	---UGCAUUUGCACCUGCAUCUC-	20
OsmiR530	---UGCAUUUGCACCUGCACCUAC	21
bdi-miR530a	---UGCAUUUGCACCUGCACCUAC	21
bdi-miR530b	---UGCAUUUGCACCUGCACCUAC	21
ptc-miR530b	---UGCAUUUGCACCUGCAUCUU-	20
csi-miR530b-5p	---UGCAUUUGCACCUGCAUCUUG	21
mes-miR530b	---UGCAUUUGCACCUGCACCUUA	21
ptc-miR530a	---UGCAUUUGCACCUGCACCUU-	20
csi-miR530a-5p	---UGCAUUUGCACCUGCACCUUG	21
tcc-miR530b	---UGCAUUUGCACCUGCACCUU-	20
lus-miR530a	---UGCAUUUGCACCUGCACCUU-	20
lus-miR530b	---UGCAUUUGCACCUGCACCUU-	20
htu-miR530	---UGCAUUUGCACCUGCACCUU-	20
cme-miR530a	---UGCAUUUGCACCUGCACCUU-	20
mes-miR530a	---UGCAUUUGCACCUGCACCUU-	20
gra-miR530a	AGGUGCAGAUGCAGUUGCAGG---	21
gra-miR530b	AGGUGCAGGUGCAGGCGCAGC---	21
sly-miR530	AGGUGUAGGUGUUC AUGCAGA---	21

** * * **

Fig. S11 PHYB physically interacts with OsPIL15. **(a)** Yeast two-hybrid analysis of the interaction between PHYB and OsPIL15. The full-length *OsPIL15* open reading frame and the C-terminal *PHYB* cDNA sequences were inserted into GAL4-AD and GAL4-BD vectors to generate AD-*OsPIL15* and BD-*PHYB-C* constructs, respectively. Yeast AH109 cells were co-transformed with the two constructs. The AD/BD-*PHYB-C* combination was used as a negative control. Transformed yeast cells were selected on synthetic dextrose medium lacking Leu and Trp (SD/-L/-W) and then transferred to medium lacking Leu, Trp and His (SD/-L/-W/-H). **(b)** A firefly luciferase complementation imaging (LCI) assay revealed the interaction between PHYB and OsPIL15 in *Nicotiana benthamiana* leaves. The constructs are listed on the right. The signals were analyzed at 48 h after the infiltrations. At least 10 independent *N. benthamiana* leaves were infiltrated for each experiment. **(c)** Semi-*in vivo* pull-down assays confirming that PHYB specifically interacts with OsPIL15 under red light conditions.

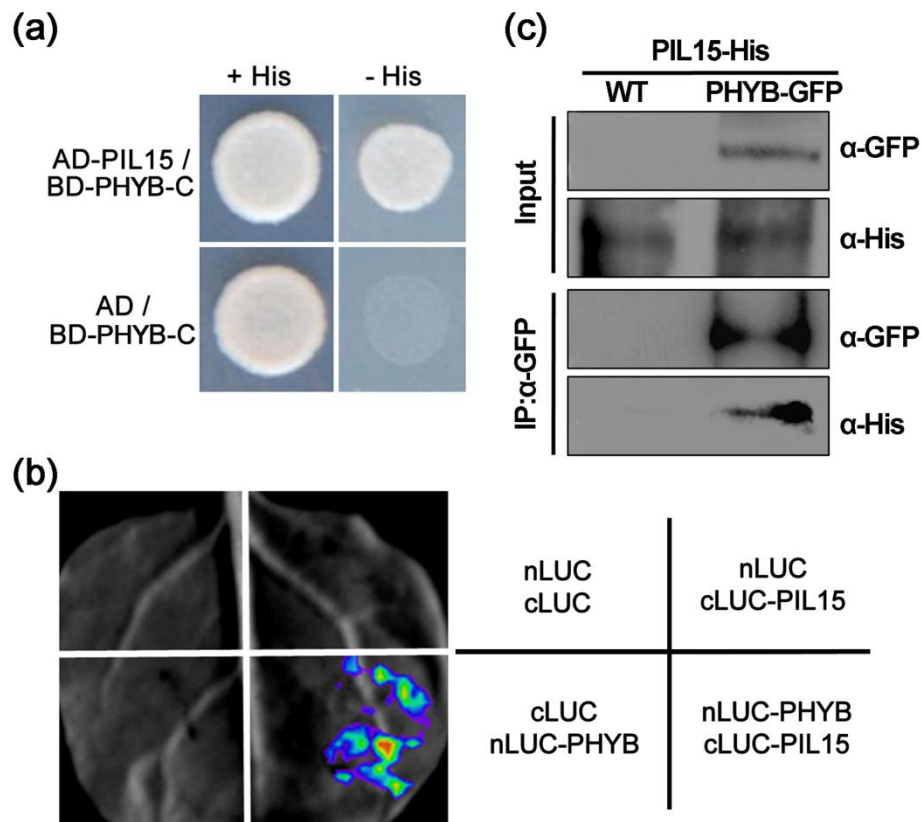


Fig. S12 Knockout of *PHYB* in rice results in smaller seed. **(a)** Grains with hulls of wild-type (WT) and *phyB* mutant. Bar, 1 cm. **(b)** Grain length and width of WT and *phyB* mutant. **(c)** The 1,000-grain weight of WT and *phyB* mutant. The data in **(b)** and **(c)** are presented as the mean \pm standard deviation (**b**, $n > 300$ seeds; **c**, $n = 3$ replicates). Significant differences were determined with Student's *t*-test (* $P < 0.05$, ** $P < 0.01$).

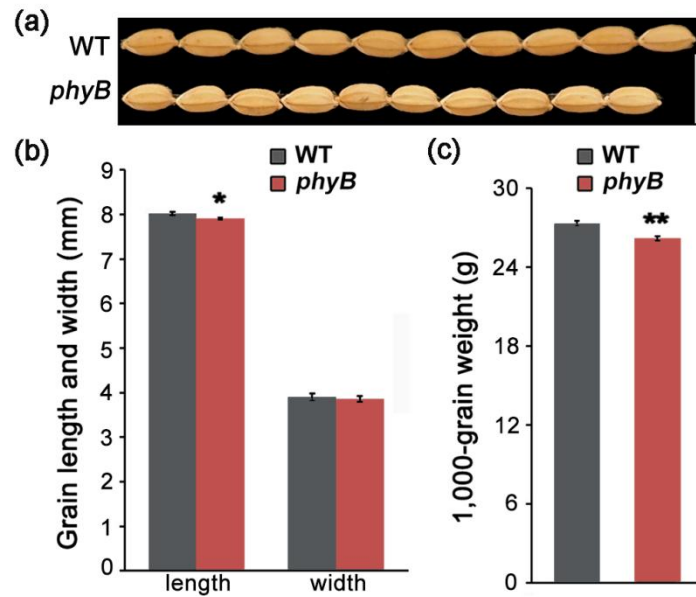


Table S1 Details regarding the primers and DNA fragments used in this study.

miR530-OE-F	5'-gg actagtATGCTCATTGATTGAAACTTC-3'	For OsmiR530 overexpression construct
miR530-OE-R	5'-cg g gatccCTGATCCACGTGTAAACCG-3'	
osa-5.8S	5'-GAACGACTCTCGGCGGCTA-3'	For detecting the expression of the 5.8S rRNA by qRT-PCR
osa-miR530	5'-cgccTGCATTTGCACCTGCACCTAC-3'	For detecting the expression of the mature OsmiR530 by qRT-PCR
MIM530-RF1	5'-TCTCTCTTCTCTATGCTTTG-3'	For detecting OsmiR530 target mimic by qRT-PCR
MIM530-RR1	5'-CACTGGTCTGACTATTCTC-3'	
miR530Pre-F	5'-AGGAAGATGAAGCAGCAA-3'	For detecting the precursor of OsmiR530 by qRT-PCR
miR530Pre-R	5'-AAGAGACCAGGAACAACAT-3'	
IPS1-F	5'-caccAAACACCACAAAAACAAAAGA-3'	For OsmiR530 target mimic construct (MIM530)
IPS1-R	5'-ACTATAAAGAGAATCGGAAGCA-3'	
MIM530-F	5'-AATAGGTGCAGGTGTTGCAAATGCAAGCTTCGGTCCCCCTC-3'	
MIM530-R	5'-CT TGCATTTGCAACACCTGCACCTA TTTCTAGAGGGAGATAA-3'	
PHYB-F	5'- aatctaga ATGGCCTCGGGTAGCCG-3'	For PHYB-GFP construct
PHYB-R	5'- atggtacc GCTTGTCCTTACTT G-3'	
eGFP-F	5'- aaggtcaccATGGTGAGCAAGGGCGAG-3'	For eGFP amplification
eGFP-R	5'- atggtcaccT TACTTGTACAGCTCGTCCATG-3'	
pMIR530-A	<u>gagctcCGGTCTTGGACGAGAAAGCAGCTTTGATACGCAAATCTTT</u> <u>AGCTGCCGTTGAACGGCCGGCCAAATCCGACAGAACGAAGCTT</u> <u>TTGGCTACATCTACATGTGACATGTACTGCAGCAGCTAGCAAT</u> <u>ATATCCAACATTGTTGCTAGCTAACTGATCCACGTGTAAACCGG</u> <u>CACGTGTCGCCGTGCCATTGGCCTGCCGTGCAAGTCCCATGTGA</u> <u>ACCGTGGCGATGTGCctcgag</u>	For yeast one-hybrid (Fragment A, G-box were underlined)
pMIR530-Am	<u>gagctcCGGTCTTGGACGAGAAAGCAGCTTTGATACGCAAATCTTT</u> <u>AGCTGCCGTTGAACGGCCGGCCAAATCCGACAGAACGAAGCTT</u> <u>TTGGCTACATCTACATGTGACATGTACTGCAGCAGCTAGCAAT</u> <u>ATATCCAACATTGTTGCTAGCTAACTGATCTGACTTTAAACCGG</u> <u>TGACTTTTCGCCGTGCCATTGGCCTGCCGTGCAAGTCCCATGTGA</u> <u>ACCGTGGCGATGTGCctcgag</u>	For yeast one-hybrid (mutant fragment A, mutant G-box were underlined)
pMIR530-B	<u>gagctcCGACAGGTAATATGGGACAGAGGTTAGTAGATATTTCCC</u> <u>ACGTGCACTACAGATGGTTTCTCTTAGAAGCTGCTAGCTAGCTct</u> <u>cgag</u>	For yeast one-hybrid (Fragment B, G-box were underlined)
pMIR530-Bm	<u>gagctcCGACAGGTAATATGGGACAGAGGTTAGTAGATATTTCCCT</u> <u>GACTTCACTACAGATGGTTTCTCTTAGAAGCTGCTAGCTAGCTct</u> <u>cgag</u>	For yeast one-hybrid (mutant fragment B, mutant G-box were underlined)
Probe A-F	5'-TGATCCACGTGTAAACCGGCACGTGTCGCC-3'	For EMSA assay (Probe A, G-box were underlined)
Probe A-R	5'-GGCGACACGTGCCGTTTACACGTGGATCA-3'	
Probe Am-F	5'-TGATCTGACTTTAAACCGGTGACTTTCGCC-3'	For EMSA assay (mutant probe A, mutant G-box were underlined)
Probe Am-R	5'-GGCGAAAGTCACCGGTTTAAAGTCAGATCA-3'	
Probe B-F	5'- ATTTTCCCACGTGCACTACAGATGGTT -3'	For EMSA assay (Probe B, G-box were underlined)
Probe B-R	5'- AACCATCTGTAGTGCACGTGGGAAAAT -3'	

Probe Bm-F	5'- ATTTTCCTGACTTCACTATGACTTGTT -3'	For EMSA assay (mutant probe B, mutant G-box were underlined)
Probe Bm-R	5'- AACAAAGTCATAGTGAAGTCAGGAAAAT-3'	
PHYB-1300-nLUC-Infusion-F	5'-TCGGTACCCGGGATCCAATGGCCTCGGGTAGCCGC-3'	For LCI assay
PHYB-1300-nLUC-Infusion-R	5'-ACGAGATCTGGTCGACTCAGCTTGCCCCCTACTTGCTG-3'	
PIL15-1300-cLUC-Infusion-F	5'-GCGGTACCCGGGATCCAATGTCCGACGGCAACGACTTC-3'	For LCI assay
PIL15-1300-cLUC-Infusion-R	5'-AGCTCTGCAGGTCGACTTATGTTTTAGCCCCATCTCTCTCT-3'	
OsPIL15NdeF1	5'-CAC ATA TGT CCG ACG GCA ACG ACT-3'	For yeast one-hybrid and two-hybrid assays
OsPIL15LxhoR1	5'-ATC TCG AGT GTT TCA GCC CCA TCT CTC-3'	
phyB-C-F	5'-AACCATGGCAGAGGGCACAAGTAAC-3'	For yeast two-hybrid assay
phyB-C-R	5'-ATCTGCAGCTTGCCCCCTACTTG-3'	
PIL15-Infusion-F	5'-CGAAATCGATGGATCCTATGTCCGACGGCAACGACTTC-3'	For Luciferase activity assay
PIL15-Infusion-R	5'-ATTCGAGCTCACTAGTTTTATGTTTCAGCCCCATCTCTCTCT-3'	
p530-LUC-F	5'-caccAGGAAGCGGATTACATAGAAC-3'	Luciferase activity assay
p530-LUC-R	5'-GCTCTATCACACATCACTTGC-3'	
p530Chip-AF	5'-GCTTTTGGCTACATCTACAT-3'	For ChIP-qPCR (Fragment A)
p530Chip-AR	5'-CGGTTACATGGGACTTG-3'	
p530Chip-BF	5'-GGTAATATGGGACAGAGGTA-3'	For ChIP-qPCR (Fragment B)
p530Chip-BR	5'-GAACTATTGTCGATGGGTT-3'	
p530Chip-CF	5'-TTGACAACCGGCACCTAA-3'	For ChIP-qPCR (Fragment C)
p530Chip-CR	5'-AAACATTTATGGGCTTATCGCTAT-3'	
PL3-GSP1	5'-AACAGGATTCACAGCAGACACG-3'	For RLM5' -RACE
PL3-GSP2	5'-AGCCCATCCTTATGCTTTTCCTG-3'	For RLM5' -RACE
PL3-TS	5'-cgggatccATGAGATCTGTCTCTGAGCTGGTG-3'	For subcellular localization of OsPL3
PL3-TAS	5'-gctctagaAAAACGAAGCAGCTCTCTT-3'	
PL3-RS	5'-AAGCTGTGAAATGAGATG-3'	For detection of <i>OsPL3</i> expression by qRT-PCR
PL3-RAS	5'-ATGCCGAATATTATGACTG-3'	