Supplemental Information

SI Materials and Methods

Field growth condition of rice plants. The rice plants examined under natural field conditions were grown in normal rice growing seasons in the Experimental Station of Huazhong Agricultural University, Wuhan, China. Following Zhang and Yuan (1), for natural long-day conditions, seeds of Nongken 58 and Nongken 58S as well as the transgenic plants were sown in a seed bed in mid-April, and seedlings were transplanted to the field in mid-May, ensuring the day-length at young panicle developing stage to be longer than 14 h. For natural short-day conditions, seeds were sown in mid-June, and seedlings transplanted to the field in mid-July, which placed young panicle developing stage at day-length of ~13.5 h.

Assay of transgenic plants and fertility examination. For co-segregation analysis, the *GUS* (β-glucuronidase) gene was amplified by using a primer pair GUS1.6F and GUS1.6R (Table S4). An internal marker in the *Transcript-1* sequence was obtained by amplifying the genomic DNA with a primer pair 210115F and 210225R resulting in a fragment of 1392 bp in length. Digestion of the 58N fragment with *Acc*I resulted in two fragments of 930 bp and 462 bp, while the corresponding fragment from 58S could not be digested. During flowering time, anthers of 6-9 mature flowers from each plant were sampled, and pollen fertility was examined using the method of I_2-KI solution staining. A total of 300-800 pollen grains were observed per plant. Five

panicles were harvested for examining spikelet fertility scored as the ratio of number of filled grains to the total number of spikelet.

Primer walking and strand-specific RT-PCR to detect transcripts around the SNP genomic region. Primers spanning the 3-kb genomic regions around SNP site were designed at intervals of about 60 bases (Fig. S3*A* and Table S4). Each primer was paired to other primers one by one. The reverse transcription was performed with oligo (dt) as reverse transcribed primer. And the RT-PCR products were confirmed by gel electrophoresis and sequencing analysis (Fig. S3*B*). The strand-specific RT-PCR method was used to determine the strand from which the expressed sequence was transcribed (2). In brief, 1 μg total RNA from young panicles of Nongken 58 at pollen-mother cell formation stage was reverse-transcribed using SuperScript III reverse transcriptase (Invitrogen) with the mixture of gene-specific-primers (for sense: SNP-R5, pms3-R8, 195210R2, and UBQR1; for antisense: 210225F, pms3-F9, and UBQR1). The temperature of the reaction was set to 55℃ to inhibit non-specific reverse-transcription. And the strand-specific RT-PCR products were confirmed by gel electrophoresis and sequencing analysis (Fig. S3*C*).

Determination of full-length transcripts. Total RNA was isolated from developing young panicles of Nongken 58 using a RNA extraction kit (TRIzol reagent, Invitrogen). To synthesize the first-strand cDNA, 1 μg total RNA was reverse-transcribed using the protocol provided by the SMARTTM RACE cDNA Amplification Kit (Clontech) with a final volume to 100 μL. The primers used for 5'RACE and 3'RACE of different transcripts were listed in Table S4. We defined the number of transcripts and their structures according two rules: first, sequences from

RACE results fully or partially overlapped with each other were classified as a RACE cluster; and second, regions between the nearest 5'-RACE cluster and 3'-RACE cluster were regarded as a transcript (Fig. S3*D*).

RNA *in situ* hybridization. Tissue preparation, *in situ* hybridization, and detection were as described previously (3). In our study, sections containing different tissues (sheath, leaf and panicles at different developing stages) were placed in the same glass slide. The detection of *Transcript-1* to *3* was performed in parallel with three corresponding probes, to make the signals of three transcripts directly comparable. To prepare the probes, we used two pairs of primers, 3UTRSacIF/3UTRSalIR and pms3-F3/pms3-R8 (Table S4), to amplify 610-bp and 467-bp sequences respectively from cDNA clones of *Transcript-1* and *Transcript-2*. Each fragment was then inserted into the pGEM-T vector (Promega) for RNA transcription. The sense and antisense RNA probes were produced by T7 and SP6 transcriptase labelled with digoxigenin (Roche).

Histochemical analysis and TUNEL Assays. Anthers at different developmental stages were fixed in a solution containing 50% ethanol, 5% glacial acetic acids, and 3.7% formaldehyde for 24 h at 4℃. Fixed tissue was dehydrated with a 50–100% ethanol series and embedded in paraffin. The paraffin embedded samples were sliced into 6.0–8.0 μm using microtome YD-1508A and stained with 0.25% toluidine blue O (Merck). Images were captured with a Leica DFC480 Digital Camera system. The 8.0 μm paraffin sections of treated anthers were used for *in situ* nick-end labelling of nuclear DNA fragmentation with a TUNEL apoptosis detection kit (DeadEnd Fluorometric TUNEL system, Promega) according to the supplier's instructions.

Samples were analyzed under a laser scanning confocal microscope (TCS SP2; Leica).

One-tube stem-loop qRT-PCR. Total RNA was isolated from panicles of Nongken 58. Primers (Table S4) used for stem-loop qRT-PCR were designed according to a published protocol (4). One-tube stem-loop qRT-PCR was performed as described previously (5).

1. Zhang Z, Yuan S (1987) The influence of photoperiod on pollenfertility change of Hubei photoperiod-sensitive genic male sterile rice. *Chin J Rice Sci* 1:137-143.
2. Swiezewski S, Liu F, Magusin A, Dean C (2009) Cold-induced silencing by long antisense transcripts of an Arabidopsis Polycomb target. *Nature* 462:799-802.
3. Xue W, *et al.* (2008) Natural variation in *Ghd7* is an important regulator of heading date and yield potential in rice. *Nat Genet* 40:761-767.
4. Chen C, *et al*. (2005) Real-time quantification of microRNAs by stem-loop RT-PCR. *Nucleic Acids Res* 33:e179.
5. Shen J, Xie K, Xiong L (2010) Global expression profiling of rice microRNAs by one-tube stem-loop reverse transcription quantitative PCR revealed important roles of microRNAs in abiotic stress responses. *Mol Genet Genomics* 284:477-488.

Table S1. Accessions of rice germplasm used for *pms3* genotype analysis

Code (Number)	Variety name	Accession ID*	Species	Origin	Genotype
1	Nongken 58S		*O. sativa*	China	C
2	Nongken 58		*O. sativa*	China	G
3	Nanjing 11		*O. sativa*	China	G
4	Zhenshan 97		*O. sativa*	China	G
5	Minghui 63		*O. sativa*	China	G
6	9311		*O. sativa*	China	G
7	Balilla		*O. sativa*	Italy	G
8	Nipponbare		*O. sativa*	Japan	G
9	Zhonghua 11		*O. sativa*	China	G
10	Mudanjiang 8		*O. sativa*	China	G
11	Dular		*O. sativa*	India	G
12	02428		*O. sativa*	China	G
13		IRGC 1012	*O. sativa*	China	G
14		IRGC 1034	*O. sativa*	China	G
15		IRGC 14619	*O. sativa*	Indonesia	G
16		IRGC 17376	*O. sativa*	Indonesia	G
17		IRGC 26977	*O. sativa*	Indonesia	G
18		IRGC 27635	*O. sativa*	Nepal	G
19		IRGC 30346	*O. sativa*	China	G
20		IRGC 53453	*O. sativa*	China	G
21		IRGC 53454	*O. sativa*	China	G
22		IRGC 66515	*O. sativa*	Sri lanka	G
23		IRGC 66528	*O. sativa*	Sri lanka	G
24		IRGC 66560	*O. sativa*	Indonesia	G
25		IRGC 66627	*O. sativa*	Indonesia	G
26		IRGC 66809	*O. sativa*	Bangladesh	G
27		IRGC 66813	*O. sativa*	Bangladesh	G
28		IRGC 66831	*O. sativa*	Bangladesh	G
29		IRGC 77144	*O. sativa*	Malaysia	G
30		IRGC 73118	*O. sativa*	Pakistan	G
31		IRGC 74730	*O. sativa*	India	G
32		IRGC 76290	*O. sativa*	India	G
33		IRGC 76404	*O. sativa*	Pakistan	G
34		IRGC 77143	*O. sativa*	China	G
35		IRGC 77144	*O. sativa*	China	G
36		IRGC 77529	*O. sativa*	India	G
37		IRGC 77636	*O. sativa*	Indonesia	G
38		IRGC 77645	*O. sativa*	Korea	G
39		IRGC 77665	*O. sativa*	Korea	G
40		IRGC 78269	*O. sativa*	Thailand	G

41	IRGC 80180	*O. sativa*	Laos	G
42	IRGC 81586	*O. sativa*	Indonesia	G
43	IRGC 82097	*O. sativa*	Myanmar	G
44	IRGC 84154	*O. sativa*	Myanmar	G
45	IRGC 104921	*O. glaberrima*	Egypt	G
46	IRGC 113509	*O. sativa*	Myanmar	G
47	IRGC 80622	*O. nivara*	India	G
48	IRGC 81831	*O. nivara*	India	G
49	IRGC 81845	*O. nivara*	India	G
50	IRGC 81883	*O. rufipogon*	India	G
51	IRGC 81915	*O. nivara*	India	G
52	IRGC 81928	*O. nivara*	India	G
53	IRGC 82037	*O. nivara*	Thailand	G
54	IRGC 83795	*O. rufipogon*	India	G

*Rice accession ID from the International Rice Research Institute (IRRI, Los Banos, the Philippines).

Table S2. Tissues used for analyzing expression profile of transcripts in Fig. 2*A*

Number	Tissue
1	root of seedling with two tillers
2	leaf of seedling with two tillers
3	leaf before secondary branch primordium differentiation stage
4	sheath at secondary branch primordium differentiation stage
5	stem at pistil/stamen primordium differentiation stage
6	leaf at secondary branch primordium differentiation stage
7	leaf at pistil/stamen primordium differentiation stage
8	leaf at pollen-mother cell formation stage
9	flag leaf at pollen mitosis stage
10	panicle at secondary branch primordium differentiation stage
11	panicle at pistil/stamen primordium differentiation stage
12	panicle at pollen-mother cell formation stage
13	panicle at pollen meiosis stage
14	panicle at pollen mitosis stage
15	panicle at heading stage

Table S3. Morphological traits of homozygous transgenic plants harboring Actin:NT1 and Actin:ST1 in comparison to Nongken 58S under natural long-day conditions

Traits	Nongken 58S	Actin:NT1	Actin:ST1
Plant height (cm)	106.3 ±0.67	108.6 ±1.15	108.1 ±0.85
P		0.0944	0.1024
No. days to heading	117.1 ±0.50	115.8 ±0.61	118.6 ±0.69
P		0.1108	0.0812
No. panicles	14.6 ±0.97	13.8 ±0.58	13.6 ±0.87
P		0.5049	0.4471
No. spikelets per panicle	117.1 ±4.28	110.9 ±5.39	105.8 ±4.39
P		0.3766	0.0737
Seed-setting rate (%)	17.1 ±1.72	80.7 ±0.99	84.0 ±1.34
P		0.0000	0.0000

All data are given as mean ± SEM. (n=21). Each *P* value for each trait was obtained from a *t* test between Nongken 58S and the transgenic line.

Table S4. Primers used in this study

Primer name	Sequence(5'→3')	Purpose
RF1	CAAGCCACCGGATGTTGGGT	"Primer walking"
RF2	AGGTGGATGGAAGAGATGAGA	
RF3	AGGCTAGTGCTGGGCCTCTA	
RF4	ATCCTGGGAAAGCTTGTGGT	
RF5	CCTCTCTACGACACCCTCCT	
RF6	TCCACCTCGTCGGCACCGGAT	
RF8	CTCTCCCTCCCTCTCATTGGT	
RF9	CATATGTCCATTGAGTAGCA	
RF10	CACCGGATGTTGGGTTTGGTGGAG	
RF11	TAACTGAGGGCACTCCCAGGGGCACA	
RR1	CTACCTTGCGTGGTGTGAAGT	
RR2	GAAGAGAGGGGTAGTACAGA	
RR3	GGTGATACAATGACATGTCCT	
RR4	ATCCCACAAATCCTTTAGCAT	
RR5	CTGGCTCAGTATAACGGTGT	
RR6	AGAGAGAGAGAGGGAGAGAGT	
RR7	GGGGAAGACAGGGAGAGATT	
RR8	CCGCCATGCGGAGGCAAAGA	
RR9	ACAGCCAACATTGCCCAAGT	
RR10	TCCCCTCACGTGCGTACCTGT	
RR11	CAAGGGCGGAGACAAGAGTAGAGC	
RR12	CAACCAAGATGGGCCGCATGGAAA	
SNP-F1	ACTCAGATCATCCCATTCAC	
SNP-F2	CACTATACATTGTTTGCTCCAT	
SNP-F3	CTAGGAGCAAGCTACCACTG	
SNP-F4	CTGGTGAAGATTCAGTGGTACCT	
SNP-F5	TAGAGTATCTGAACTGCGTGTTG	
SNP-R1	ACAAGACTATTTCATAGCACCT	
SNP-R3	GAGGCATGGTGAAGCAAAGA	
SNP-R5	TATCTTGTCCAGTGCTCATGCCA	
pms3-F1	TGGGTTGTTAGATGGCACGA	
pms3-F2	CTTTAGGCTTGGAAGACATCA	
pms3-F3	AAGGCAAGCAAGAAGTAGGTGT	
pms3-F4	ACATTGGATCTAGCGATTGG	
pms3-F5	TTGGTCGATTGTGAGGTCAGC	
pms3-F6	TAGATGGCACGAACATTGAG	
pms3-F7	ATCTCTTCCATCCACCTCATC	
pms3-F8	TGGGTTCAGACTGTGTTAGTG	
pms3-F9	TCCCAGGATGCACATACTGAA	
pms3-R1	TGTTTGCTCCATTGGTTAGG	

pms3-R2	GTTATAGATAGACCCGAGAAG	
pms3-R5	AACATGGCATGAGCACTGGA	
pms3-R6	CCAAGCTCTAGCTGCTCTAC	
pms3-R8	GGAAGAACCATGGACGAACAC	
pms3-R9	GCTGAAGTTCTCATGTTGCTCA	
12R	TCGTGCCATCTAACAACCCA	
195210R2	GCATCTACGCACATGTAGGA	
RACEF1	TGGGTGTCCCAACCCAAAAAGCCCAC	RACE
RACEF2	CATGTAGGATTTCCATGCGGCCCATC	
RACEF3	GTCTCCGCCCTTGGATACAAGTGTCCC	
RACEF4	GGGGGGGATTTGGGGCAGTTTTCTGTC	
RACEF5	GTGTAACCGCTGGCCGGCTTCCTCTT	
RACEF6	CTCTCCCTCCACACGGCGCCTCTCTCT	
RACER1	TCGGAACAGCTACAGAGTGCGCCCA	
RACER2	AAAACTGCCCCAAATCCCCCCCAAG	
RACER3	GCCATGCGGAGGCAAAGAAAGGGCGT	
RACER4	AGAGATGTGTGCCCCTGGGAGTGCCC	
RACER5	GGAGAGAGAGGCGCCGTGTGGAGGGA	
RACER6	GTGAGGGAGGAGACCGTCGCTGGGAA	
MEF1	ATGTTGTAGTTTTTGATATAAATAGAATAA	Bisulfite squencing
MEF2	TTATGAAGTTTTATTAAAAATTTTAAGATA	
MEF5	TATAATTGGGTTGGGTTTTTTTGTA	
MEF6	TGATGTTTTTGGATTGTTTTTTAAAG	
MEF9	GGTATGATTATTTTTTATTTTTGTGG	
MEF11	TTATTTATATTTGGTTTGAAATTGG	
MEF12	GTAATGTTGGTTGTAGTTAAGATGT	
MEF14	ATAGAGTAAAGGAAGAAATAAAGGA	
MEF15	TTATGAAATTTGGAGTAGTAGTTTTTAA	
MEF16	TTAAAGGATTTGTGGGATGTAT	
MEF17	GGTATGAGTATTGGATAAGATATA	
MEF18	TGTATTTAGAGTATTTGAATTG	
MEF19	TTTGTAAAGTAGTAGTAATTGA	
MER1	AAAAACATTAATCAATAATCTCCTC	
MER2	AAAAAAACAAACAAAAAATAAATATAC	
MER4	AATAAATCTATTTAACCATTCCCAACTT	
MER5	AAAAATACATTATTTATCTACCATCCATCA	
MER6	CAAAAAAATACATTATTTATCTACCATCC	
MER10	CCCATTATAAATTTATATATCTTCACC	
MER11	ACTCTACCTTTATCAATAAAATAATTC	
MER12	ACTTTACTATATTATACTCCCTCATCATAA	
MER19	AAATACACATACTAAATCTCTCTATATT	
GUS1.6F	CCAGGCAGTTTTAACGATCAGTTCGC	Positive test
GUS1.6R	GAGTGAAGATCCCTTTCTTGTTACCG	

210225L	CAGTAGGGACACTTGTATCCA	
210225R	TGCACCGTGCAAATGTACCA	
3UTRSacIF	ATGAAAGAGCTCCAGAGACATAGATGAGCA ACAT	*in situ* hybridization
3UTRSalIR	ACCGTGGTCGACTACCAGGTTCTTTCTGAGT A	
UBQF1	GAAGAAGTGTGGTCACAGCA	qRT-PCR
UBQR1	GAGATAACAACGGAAGCATAA	
P-R1	ATTTGTGGGTGACGAGGAGA	
ASNPF	TTCTTTCATCAAATTGCCTGCTTCACCAGCA CGTCCATATTGAAT	Vector construction
ASNPR	ATTCAATATGGACGTGCTGGTGAAGCAGGC AATTTGATGAAAGAA	
DSNPEcoRIF	GAATTCAGATACTCTAGATGCAGT	
DSNPEcoRIR	GAATTCTTTGCTTCACCATGCCT	
OSNPF	GTTGGATCCGTATCAGAAGCTACAACATGT	
OSNPR	AGGCTGCAGCTGAGTAGGAAAATCATCTGA	
HSNPR	CTCCTGCAGAGCGTAATCTGGAACATCGTAT GGGTATATGTCCATTGAGTAGCATTTATGT	
GSNPF	CCAGGATCCCCCCAAGTCCTTTGTTTCTT	
ST-RT-small RNA-1	GTCGTATCCAGTGCAGGGTCCGAGGTATTCG CACTGGATACGACATGGAT	Stem-loop qRT-PCR
Forward-small RNA-1	GCGGCGGCATTGTTTGTCTACC	
ST-RT-small RNA-2	GTCGTATCCAGTGCAGGGTCCGAGGTATTC GCACTGGATACGACCTAACC	
Forward-small RNA-2	GCGGCGGGCATTGTTTGCTCCATT	
ST-RT-small RNA-3	GTCGTATCCAGTGCAGGGTCCGAGGTATTCG CACTGGATACGACCATTGT	
Forward-small RNA-3	GCGGCGGGATGGATGGTAGACAA	
Universal reverse primer	CCAGTGCAGGGTCCGAGGT	
U6F	TACAGATAAGATTAGCATGGCCCC	
U6R	GGACCATTTCTCGATTTGTACGTG	

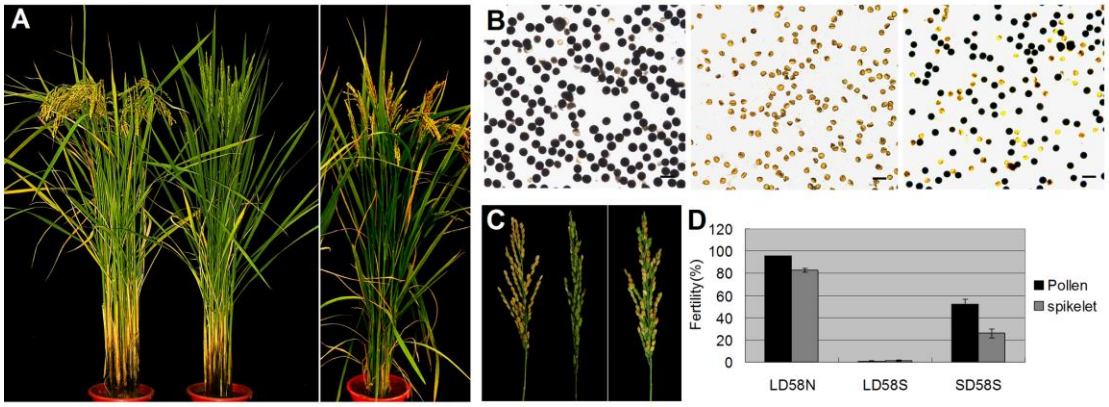


Fig. S1. Fertility of 58N and 58S under natural long-day and short-day conditions. (*A*) 58N (left) and 58S (middle) under natural long-day conditions and 58S (right) under natural short-day conditions in the Experimental Station of Huazhong Agricultural University, Wuhan, China. Following Zhang et al (25), for natural long-day conditions, seeds were sown in a seed bed in mid-April, and the day-length at young panicle developing stage was longer than 14 h; for natural short-day conditions, seeds were sown in mid-June, which placed young panicle developing stage at day-length of ~ 13.5 h. (*B*) Pollen fertility of 58N (left) and 58S (middle) under natural long-day conditions, and 58S (right) under natural short-day conditions. Scale bars: 50 μm. (*C*) Panicles of 58N (left, spikelets highly fertile) and 58S (middle, spikelets highly sterile) under natural long-day conditions, and 58S (right, spikelets partly fertile) under natural short-day conditions. (*D*) Fertility scores of 58N (left) and 58S (middle) under natural long-day conditions, and 58S (right) under natural short-day conditions. Data are means ± SEM. (n=3).

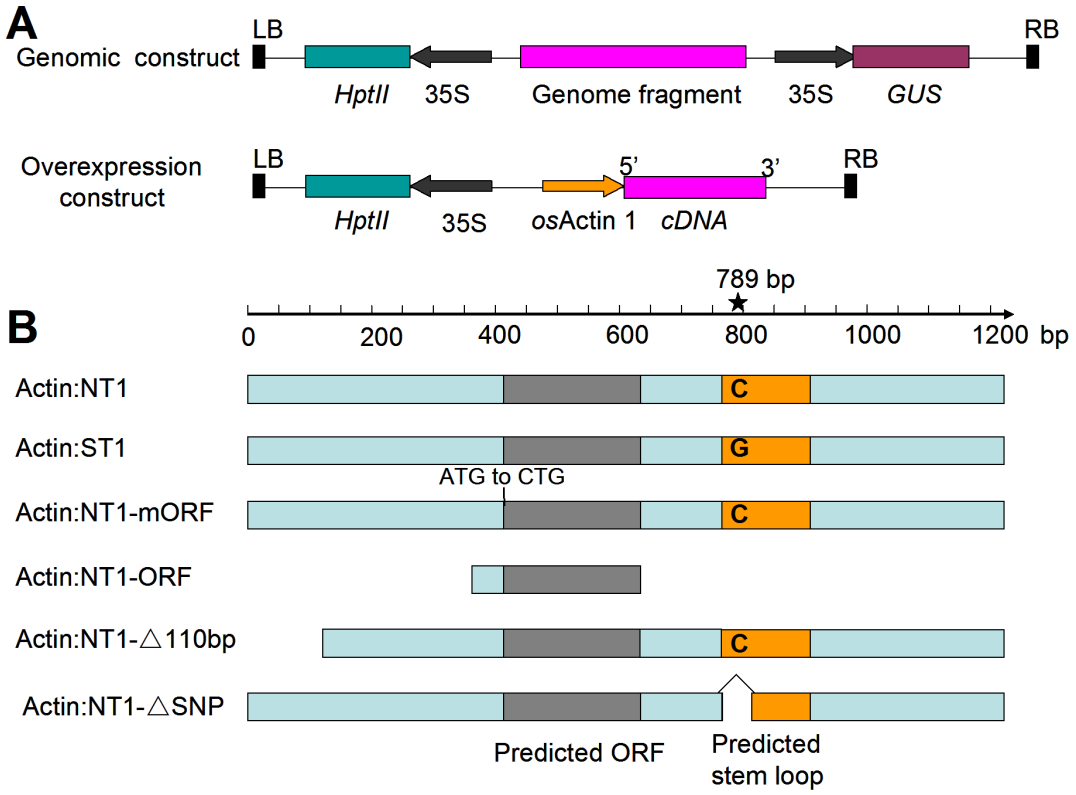


Fig. S2. Schematic representation of constructs used for transformation. (*A*) Genomic constructs: genomic DNA fragments (HB614, SH5800, B9K and N6K) were cut from 58N BAC library and cloned into pCAMIA1301. Overexpression constructs: the transcript was under the control of *β-actin1* promoter from rice. (*B*) Schematic representation of the *Transcript-1* (LDMAR) sequences in the constructs. Actin, rice *β-actin1* promoter; NT1, full length *Transcript-1* from Nongken 58; ST1, full length *Transcript-1* (LDMAR) from 58S; NT1-mORF, the predicted start codon ATG was changed to CTG; NT1-ORF, only containing the predicted ORF; NT1-△110bp, an 110-bp fragment at the 5'-end of *Transcript-1* deleted; NT1-△SNP, 52-bp surrounding the SNP deleted; ★, the SNP site.

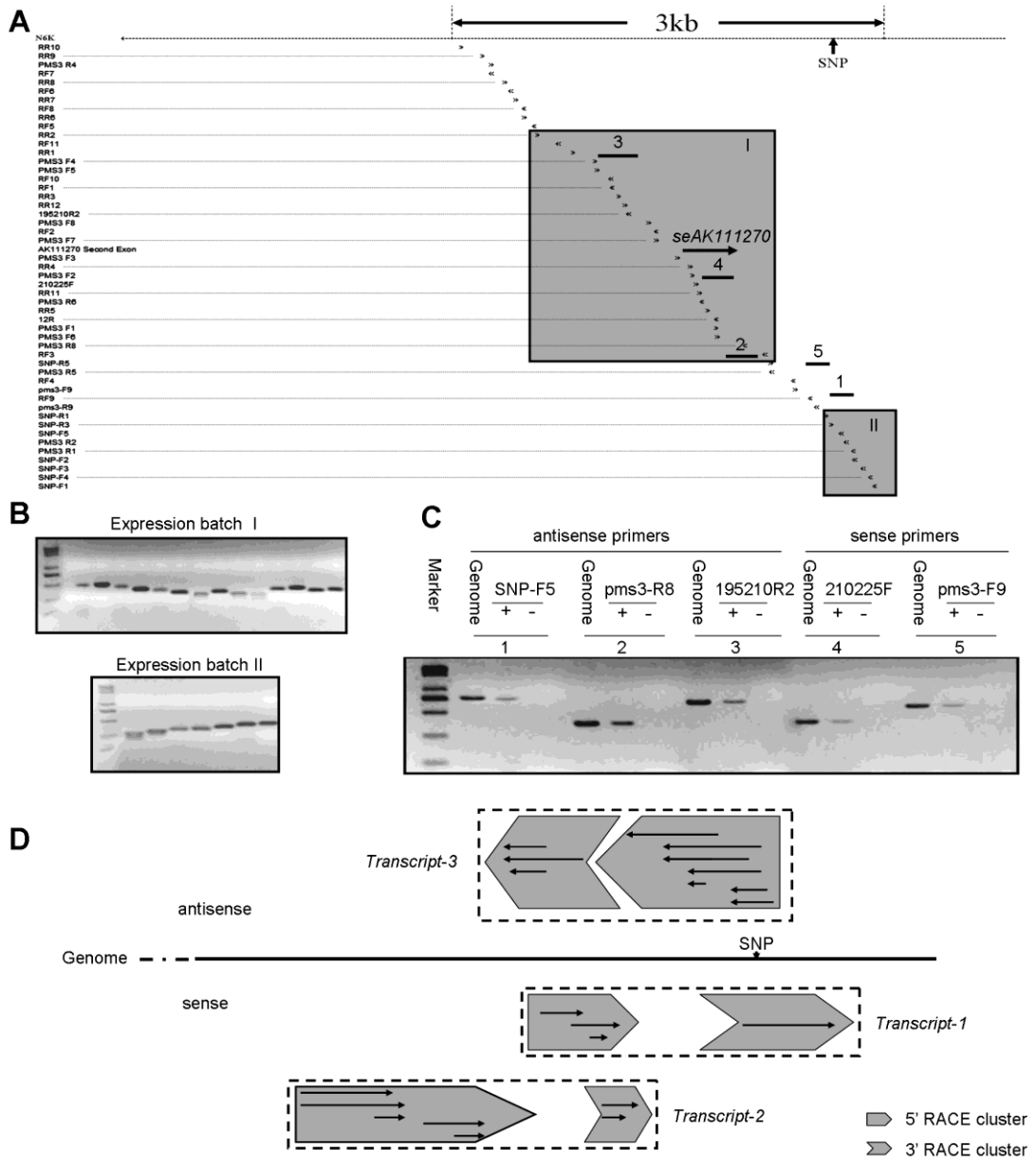


Fig. S3. Characterization of the transcription units. (*A*) Names and positions of the primers used for primer walking. The two shaded boxes indicate regions (I and II) where transcripts were detected; lines labeled with numbers (1 to 5) represent transcripts detected using strand-specific PCR. The site of SNP and the second exon of *AK111270* (*seAK111270*) are also indicated. (*B*) Primer walking to determine expression units and showed the two expression batches, which were also indicated in (*A*). (*C*) Strand-specific RT-PCR for determining the direction of transcripts: SNP-R5, pms3-R8 and 195210R2 were used for sense reverse transcription; 210225F and pms3-F9 were used for antisense reverse transcription. Marker indicates a 2-kb ladder.

The genome lane was obtained by reverse-transcription without Dnase I pre-treatment. The inclusion or exclusion of reverse-transcriptase is indicated by + and -, respectively. (*D*) Schematic representation of the 5'RACE and 3'RACE results. Lines with arrow heads in the shaded area indicate the RACE fragments and their directions. Dashed boxes represent deduced transcripts. All above digital photograph of the ethidiumbromide-stained gels are shown in inverted contrast for clarity.

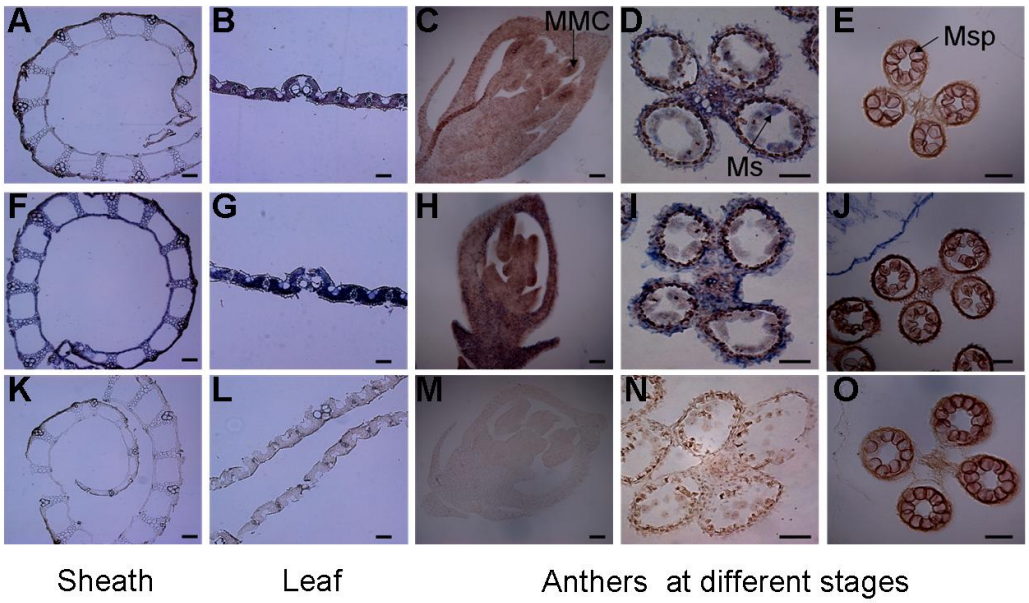
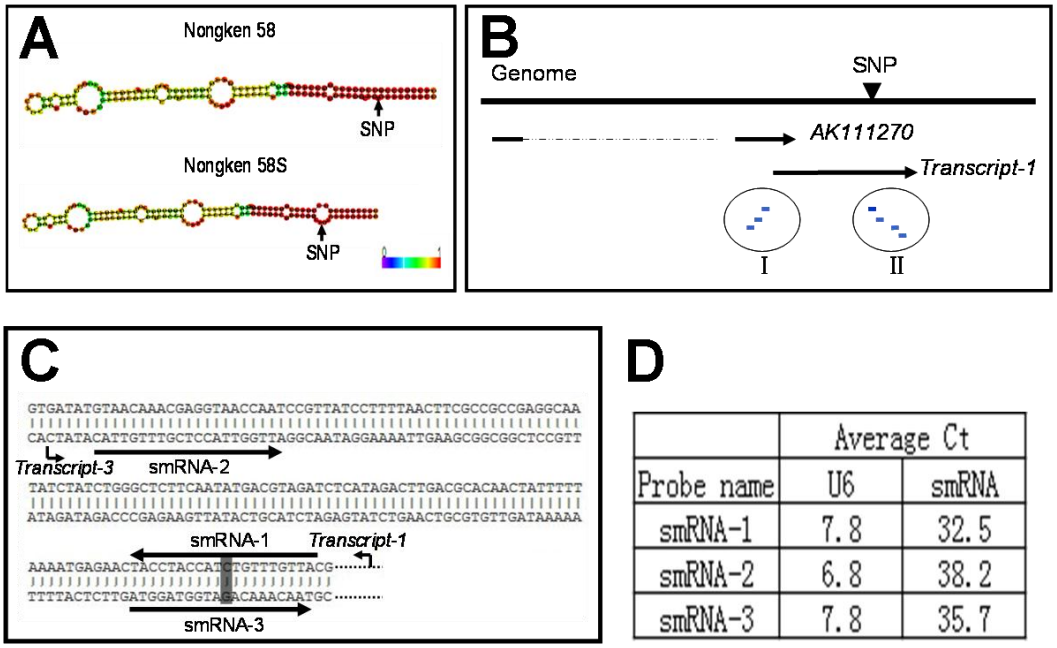


Fig. S4. Expression of *Transcript-1 to 3* in various tissues of 58N detected by *in situ* hybridization. (*A*) to (*E*) *Transcript-1* (LDMAR); (*F*) to (*J*) *Transcript-2*; (*K*) to (*O*) *Transcript-3*. Sections containing different tissues were placed in the same glass slide and the detection of the transcripts was performed in parallel with sense and antisense probes, to make the signals of three transcripts directly comparable. MMC, microspore mother cell; Ms, microsporocyte; Msp, microspore. Scale bars = 50 μm.



	Average Ct	
Probe name	U6	smRNA
smRNA-1	7.8	32.5
smRNA-2	6.8	38.2
smRNA-3	7.8	35.7

Fig. S5. Bioinformatic analysis of the LDMAR region. (*A*) Predicted stem-loop structure involving 145 bases of LDMAR according to the RNA secondary structure prediction website (http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi). (*B*) Two regions (Ⅰ, Ⅱ) that are predicted to produce small RNAs (http://sundarlab.ucdavis.edu/smrnas/). (*C*) Small RNAs in the 145-bp region verified using a stem-loop qRT-PCR method. (*D*) The average Ct values of three predicted small RNAs.

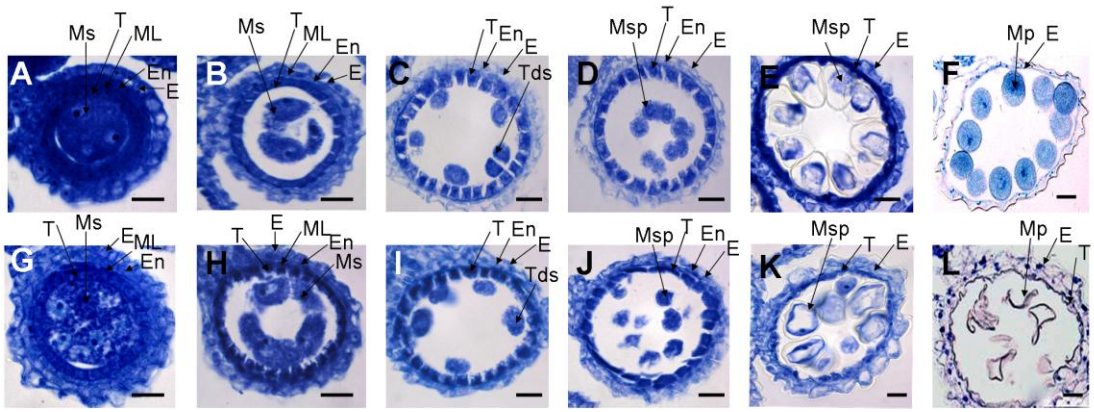


Fig. S6. Cytological comparison of male gametogenesis between 58N and 58S. (*A*) to (*F*) 58N; (*G*) to (*L*) 58S. The cross sections are stained with 0.25% toluidine blue. E, epidermis; En, endothecium; ML, middle layer; Ms, microsporocyte; Msp, microspore; MP, mature pollen; T, tapetum. Bars = 15 μm.

(*A*) and (*G*) Cross section of single locule at the microspore mother cell stage.

(*B*) and (*H*) Cross section of single locule at the meiosis stage (dyads).

(*C*) and (*I*) Cross section of single locule at the meiosis stage (tetrads).

(*D*) and (*J*) Cross section of single locule at the young microspore stage.

(*E*) and (*K*) Cross section of single locule at the vacuolated pollen grain stage.

(*F*) and (*L*) Cross section of single locule at the mature pollen stage.

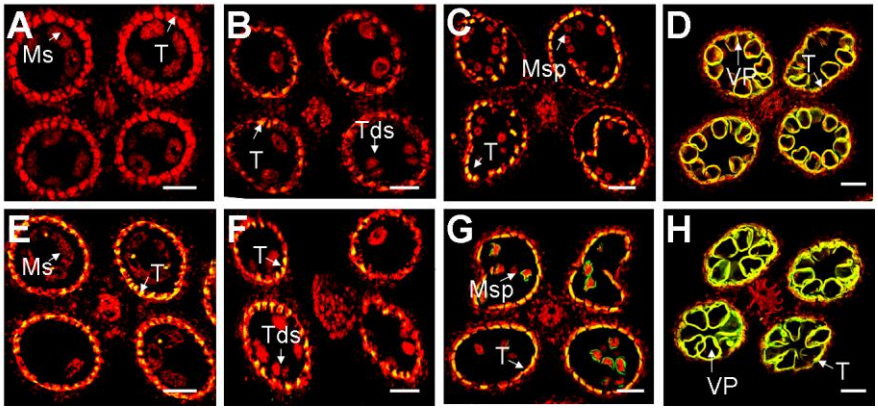


Fig. S7. Comparison of DNA fragmentation in the anthers between 58N and 58S. DNA fragmentation in anthers of 58N (*A-D*) and 58S (*E-H*) assayed using the TUNEL method. T, tapetum; Tds, tetrads; Ms, microsporocyte; Msp, microspore; VP, vacuolated pollen. Bars = 50 μm.

(*A*) and (*E*) Cross section at the meiosis stage (dyads).

(*B*) and (*F*) Cross section at the meiosis stage (tetrads).

(*C*) and (*G*) Cross section at the young microspore stage.

(*D*) and (*H*) Cross section at the vacuolated pollen stage.

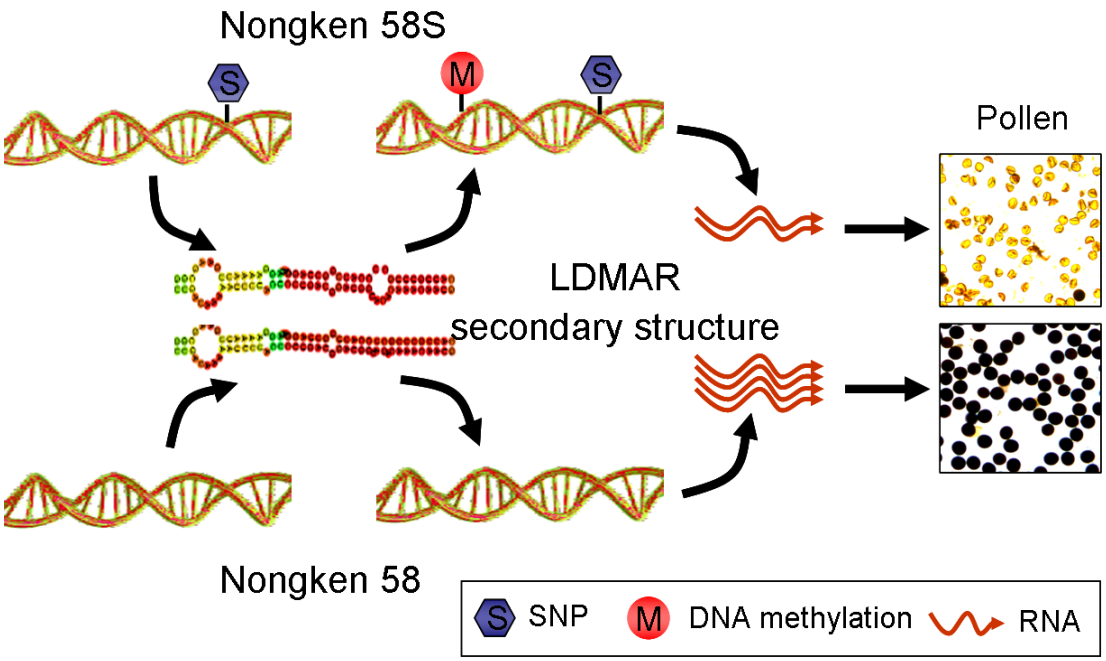


Fig. S8. Schematic representation of the role of LDMAR on PSMS under long-day conditions regulated by SNP, RNA secondary structure and DNA methylation.