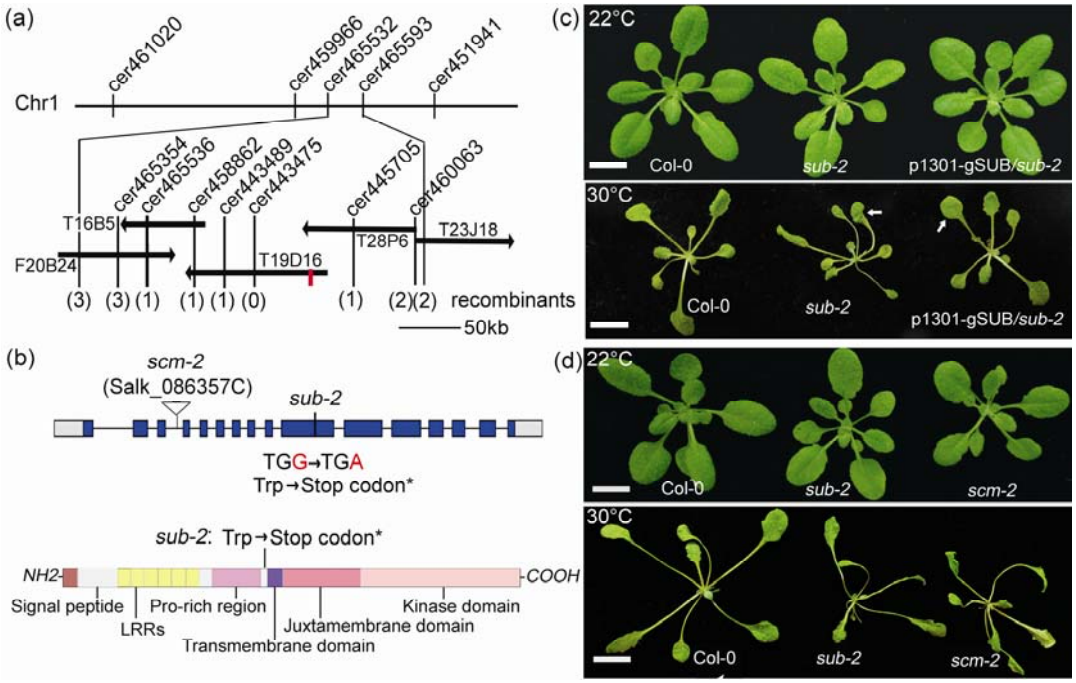

Figure S1. Map-based cloning of the *SCM/SUB* gene.

(a) The mutant locus was mapped to a 112-kb region between two markers cer443489 and cer445705 on chromosome 1 using a F2 population from the cross of *sub-2* with L*er*. Numbers in brackets represent recombination events.

(b) Upper, diagram of the genomic locus of *SCM/SUB* including exons (blue boxes), introns (lines) and untranslational regions (grey boxes). Lower, diagram of structural domains of the SCM/SUB protein. The G-to-A mutation in *sub-2* that creates a premature stop codon TGA (*) at amino acid 337 before transmembrane domain and the T-DNA insertion position in *scm-2* were indicated.

(c) Genetic complementation of *sub-2* at 22°C and 30°C. Note that the incomplete leaf in *sub-2* was rescued in a transgenic line (arrows).

(d) *scm-2* with leaf phenotypes similar to *sub-2* at both 22°C and 30°C. Scale bars = 1cm.

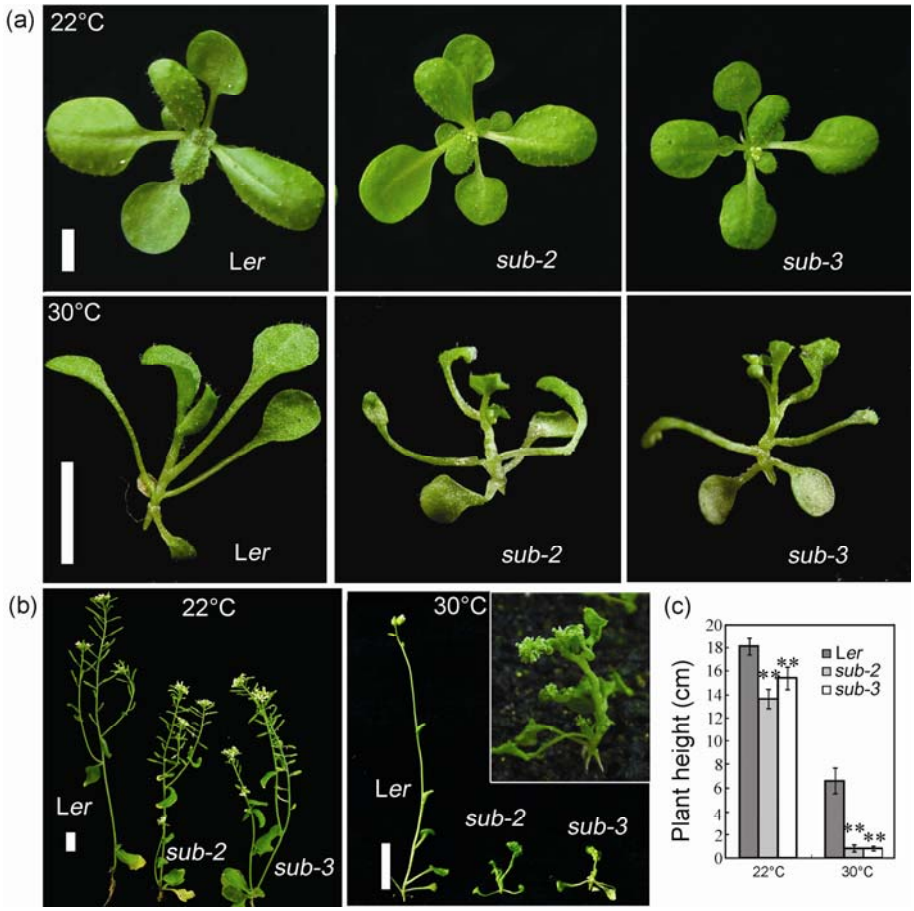

Figure S2. Temperature-sensitive phenotypes of the *sub* mutants in L*er* background.
(a) Morphological phenotypes of L*er*, *sub-2* and *sub-3* plants at the rosette stage. The leaves of the *sub* mutants were only slightly smaller than those of L*er* grown at 22°C; whereas at 30°C, the *sub* mutants produced narrow and twisted leaves similar to *sub-2* in Col-0 background.
(b) Comparison of L*er* and *sub* plants during the flowering stage at 22°C and 30°C. Note that the *sub* mutant plants are shorter than L*er* at both temperatures and extremely dwarf at 30°C. Inset shows a magnified *sub* plant for details.
(c) Statistical analysis of plant heights of L*er* and *sub* mutants grown at 22°C and 30°C. Values are means ± SD, Student's *t*-test, ** P≤0.001 (n=12). Scale bars = 1cm.

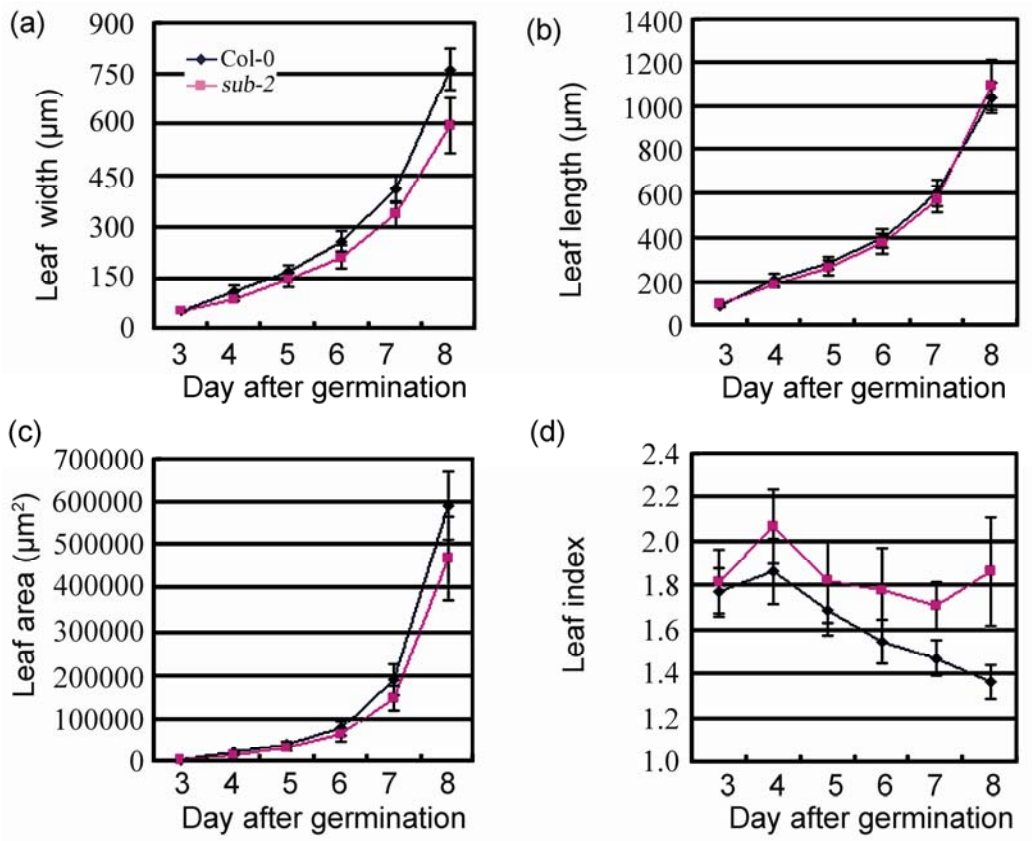

Figure S3. Time course of early leaf growth.

The leaf width (a), leaf length (b), leaf area (c) and leaf index (d) were measured on the first-pair leaves of Col-0 and *sub-2* seedlings grown at 30°C from 3 to 8 DAG. Values are means ± SD (n≥12).

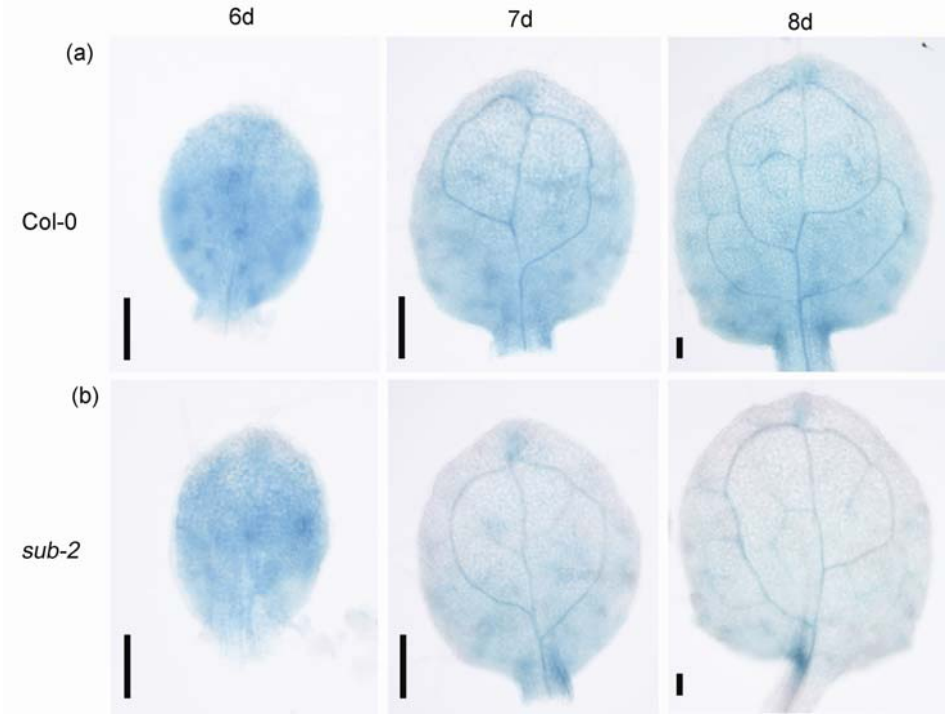

Figure S4. CYCB1;1-GUS activity in the Col-0 and *sub-2* leaves at 22°C.

The accumulation of CYCB1;1-GUS is decreased and diminished earlier in the first leaf from 6- to 8-day-old *sub-2* seedlings (b) grown at 22°C than that in Col-0 (a**)**. Scale bars = 200μm.

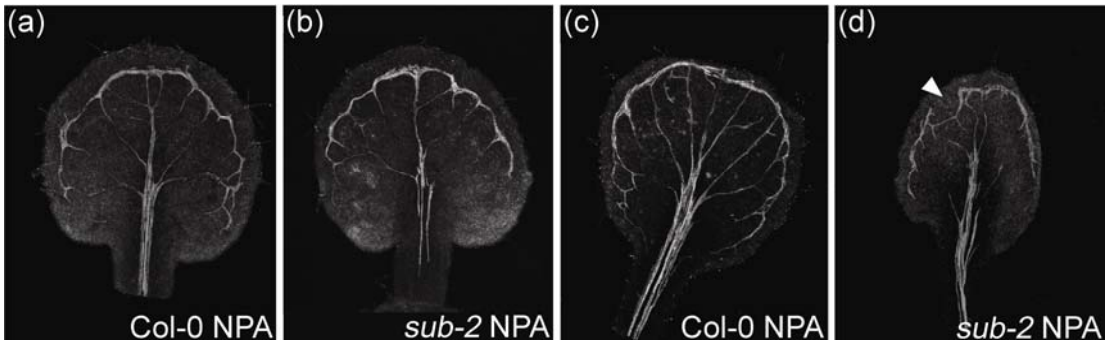

Figure S5. Venation pattern in NPA-treated leaves of *sub-2*.

(a, b) Cleared first leaves of the 5μM NPA-treated 12-day-old Col-0 and *sub-2* seedlings grown at 22°C.

(c, d) Cleared first leaves of the 5μM NPA-treated 12-day-old Col-0 and *sub-2* seedlings grown at 30°C. Arrowhead indicates a gap of vascular strands along leaf margin of *sub-2*.

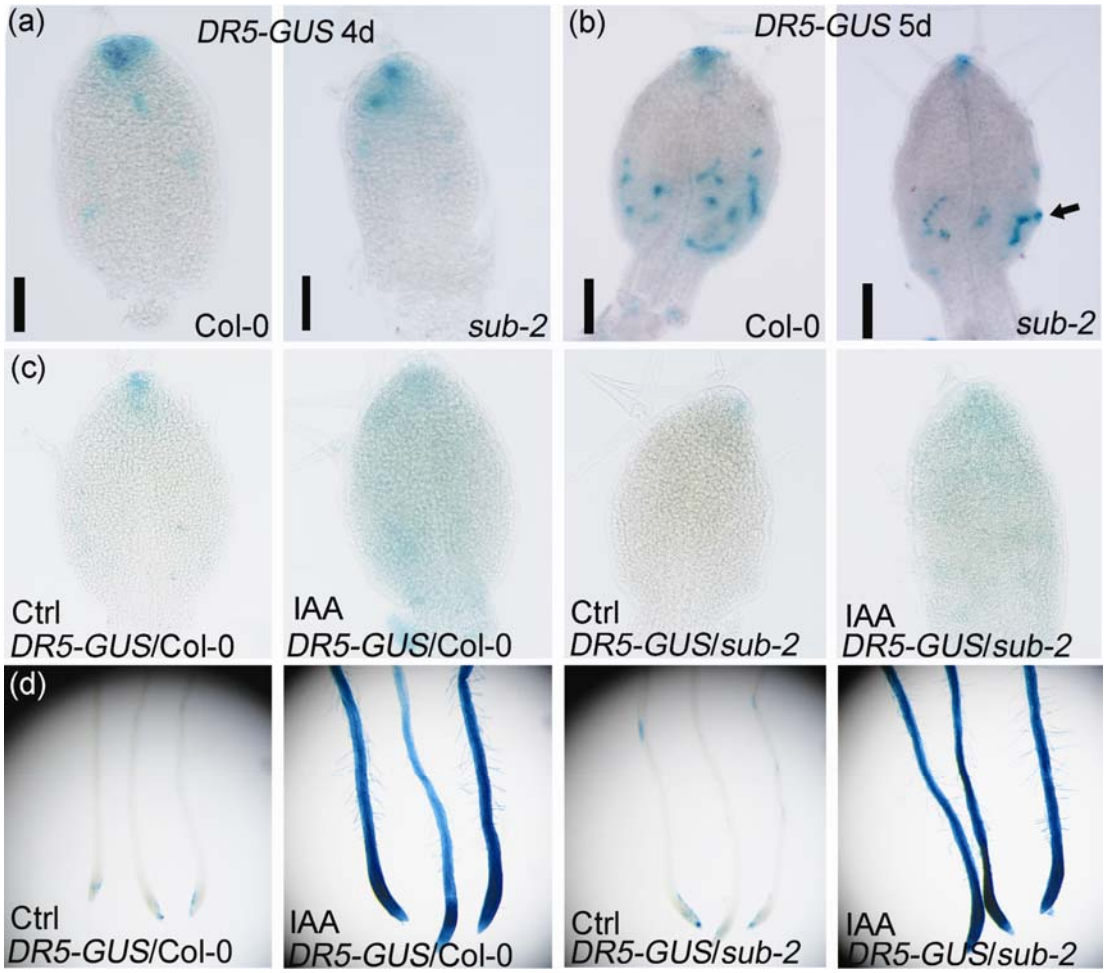

Figure S6. *DR5-GUS* expression in Col-0 and *sub-2* seedling with or without exogenous IAA treatment.

(a, b) *DR5-GUS* expression in 4- and 5-day-old first leaves at 30°C. Note that *DR5-GUS* expression was slightly reduced in *sub-2* compared with Col-0. Arrow indicates *DR5-GUS* expression in ectopic hydathodes in *sub-2*.

(c) Induction of the *DR5-GUS* expression by 5μM IAA for 6 hours in the leaf primordia of 4-day-old Col-0 and *sub-2* seedlings grown at 30°C, with non-IAA treatment as control (Ctrl).

(d) Induction of the *DR5-GUS* expression by 5μM IAA for 6 hours in the roots of 4-day-old Col-0 and *sub-2* seedlings grown at 30°C, with non-IAA treatment as control.

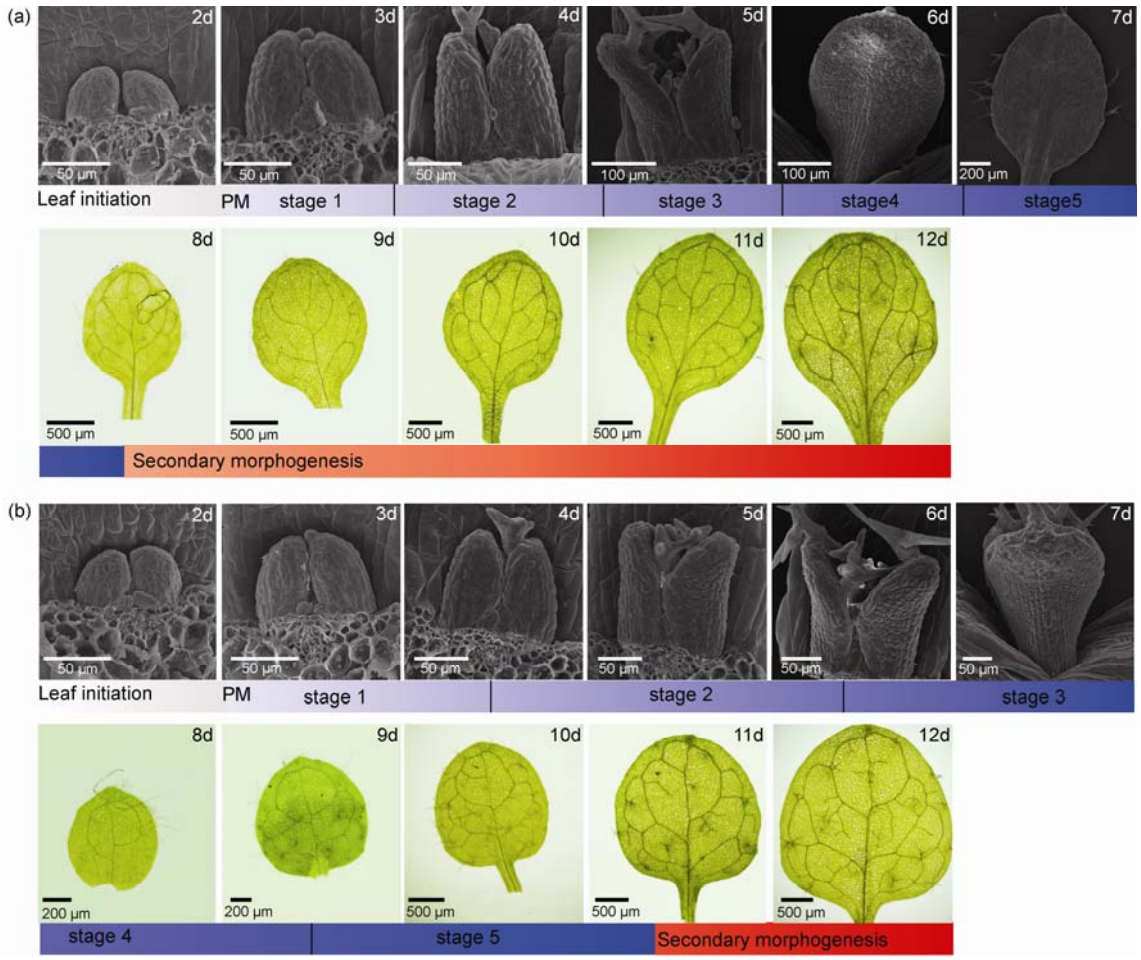

Figure S7. Analysis of leaf developmental stage at the time of temperature shift.

SEM and light-microscope images show the leaves that were harvested from 2- to 12-day-old Col-0 seedlings continuously grown at 30°C (a) and 22°C (b) in temperature-shift experiments. Leaf initiation has happened at 2 DAG. The leaf developmental stages during primary morphogenesis (PM) were estimated based on leaf length and morphological characteristics such as trichome initiation, the appearance of midrib and petiole, and the elongation of petiole as described by Carland and McHale (1996). The transition from PM to secondary morphogenesis was determined by the disappearance of CYCB1;1-GUS accumulation in leaves.

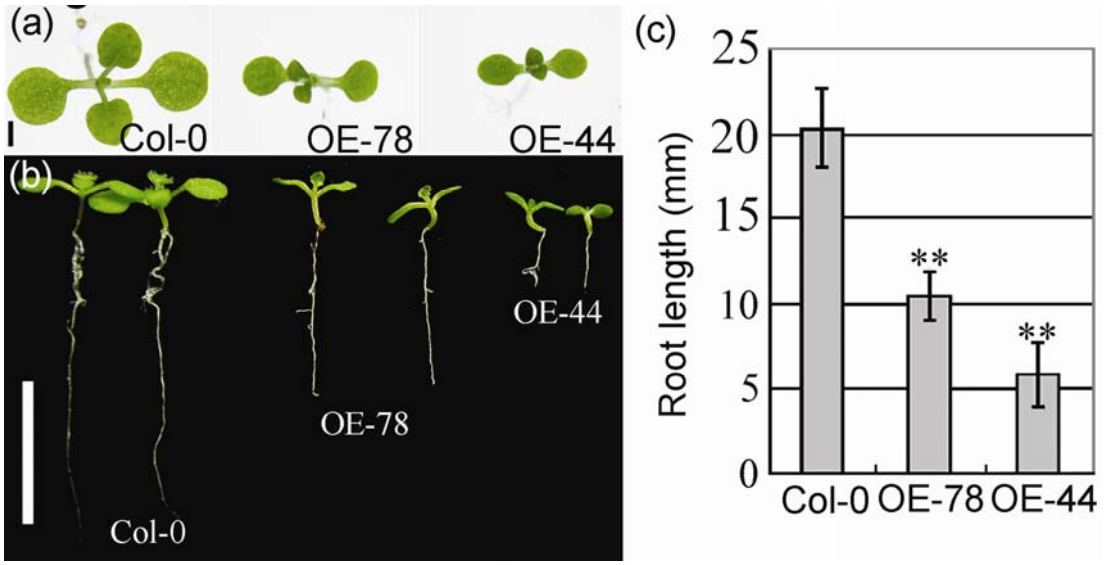

Figure S8. Comparison of wild-type and *SUB*-OE seedlings.

(a) The *SUB*-OE seedlings (OE-78 and OE-44) are smaller than wild-type Col-0.

(b) The roots of the *SUB*-OE seedlings are shorter that those of the wild type.

(c) Statistical analysis of root length of Col-0 and *SUB*-OE seedlings in (b). Values are means ± SD, Student's *t*-test, ** P≤0.001 (n = 12). Scale bars = 1mm in (a), 1cm in (b).

Table S1. Primers used in this study

Primers for map-based cloning		
CER461020-F	5'-GTCTGGAATATTCACAAATGGC-3'	
CER461020-R	5'-GTACGCAACCAGTAAAAGGTATC-3'	
CER459966-F	5'-TCGTGGAATCTTTGTGGTCA-3'	
CER459966-R	5'-AAGGGATTGATTTTCGCTGA-3'	
CER465532-F	5'-ATCGTTTTGTTCTCATTA-3'	
CER465532-R	5'-ATTTGACATACCGTATCA-3'	
CER465354-F	5'-TAACCTTTTGACTTACCAA-3'	(*Mse*I 65°C enzymetic reaction)
CER465354-R	5'-CCACCCGACTGAACCAAAT-3'	
CER465536-F	5'-AAATAAAGGAAAATGCGTCG-3'	
CER465536-R	5'-CTCGGAGTTTTGAGGGAGA-3'	
CER458862-F	5'-CGAGATTCCTGGACTATGC-3'	
CER458862-R	5'-CCTTACAAGACTTCGCCAT-3'	
CER443489-F	5'-ACCTACTTTATCGAGGAATA-3'	(*Hind*III 37°C enzymetic reaction)
CER443489-R	5'-ATGTAGCCTTAACACTTTAC-3'	
CER443475-F	5'-GCTCACCATAGGCATAGTCAC-3'	(*Pst*I 37°C enzymetic reaction)
CER443475-R	5'-TTCTAATAGGCTCCCTTGTC-3'	
CER445705-F	5'-ATGCTATTGCTGGTGTTGCT-3'	(*Bcl*I 55°C enzymetic reaction)
CER445705-R	5'-AAAGTTGGGATCTTGCTTGG-3'	
CER460063-F	5'-CACAGACGCAGATAACAAA-3'	
CER460063-R	5'-GAGGCTGAATCTTCTGACC-3'	
CER465593-F	5'-ATGGTTCGTCGGAAGTGAC-3'	
CER465593-R	5'-AAATCAACAATGGGAAATG-3'	
CER451941-F	5'-AAGCCAAGTACCTCCAAGCA-3'	
CER451941-R	5'-GATCATCCCAAGGTCATGCT-3'	
Primers for plasmid constructions		
pSUB(*Sal*I)-F	5'-ACATGTCGACAATCCACGATTTGAATATG-3' (*Sal*I site underlined)	
pSUB(*Sma*I)-R	5'-ATCCCGGGAACTTCAGCCACTGAAGATG-3' (*Sma*I site underlines)	
gSUBa(*Kpn*I)-F	5'-ACGGTACCAAGTTCAAGGGTTTTCTCAT-3' *(Kpn*I site underlines)	
gSUBa(*Bam*HI)-R	5'-CGGATCCATTATTTGTGTATTGCTGAAG-3' (*Sma*I site underlined)	
gSUBb-F	5'-ACCACCGAGGCAGTTCCA-3'	
gSUBb-R(*Bam*HI)	5'-ACGGATCCACTATTGCTTCTGCGTCTTA-3' (*BamH*I site underlined)	
UTR(*Sac*I)-F	5'-GAGCTCGATACACAACCTTGGACTAA-3'(*Sac*I site underlined)	
UTR(*Eco*RI)-R	5'-TGAATTCAAGAGCCTCATTCGTGACATCC-3'(*Eco*RI site underlined)	
gSUBma(*Kpn*I)-F	5'-GGTACCATGAGCTTTACAAGATGGGA-3'*(Kpn*I site underlines)	
gSUBa(*Bam*HI)-R	5'-CGGATCCATTATTTGTGTATTGCTGAAG-3'(*BamH*I site underlined)	
gSUBb-F	5'-ACCACCGAGGCAGTTCCA-3'	

gSUBmb(*Bam*HI)-R	5'-GGATCCGATCATATGTTGAAGATCTTGG-3'(*BamH*I site underlined)
Primers for real-time RT-PCR	
qActin2-F	5'-GCACCCTGT TCTTCTTACCG-3'
qActin2-R	5'-AACCCTCGTAGATTGGCACA-3'
qSUB-F	5'-TTTGCTCCTTTTGCTCCACT-3'
qSUB-R	5'-GTTCCAGGGATC TCCTCCTC-3'