

Accessory Publication

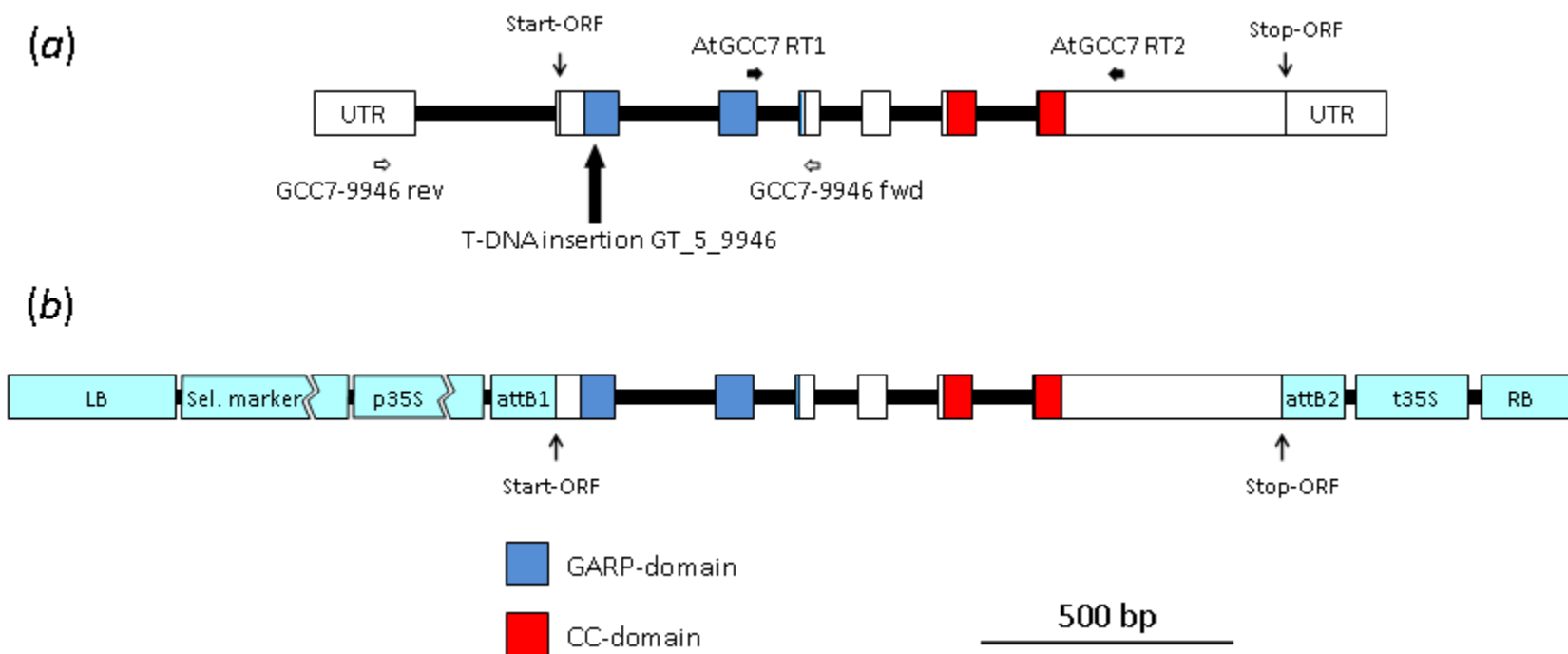


Fig. S1. (a) Intron- and exon structure of the *GCC7* gene (At2g01060). Exons are indicated with wide boxes and introns are indicated with connecting narrow black boxes. UTR indicate upstream and downstream untranslated regions. The GARP-domain is shown in dark blue and the coiled-coil domain in red. The T-DNA insertion site of the *gcc7* mutant *GT_5_9946* is depicted, along with the primers used for screening, *GCC7-9946-fwd* and *-rev* (white arrows), and the primers used for real time RT-PCR, *AtGCC7RT1* and *2* (black arrows). (b) Constructs for expression of *GCC7* in *Wt-Col* background. The selection marker for *pK2GW7-GCC7* is kanamycin resistance. The vector sequences are shown in light blue and the gene structure is as depicted in (a). LB, left border; RB; right border; Sel. marker, kanamycin resistance gene; p35S, 35S promoter; t35S, 35S terminator; attB1 and -2, Gateway recombination sites.

Table S1. Primers used for cloning, mutant screening and real time RT-PCR

AGI, Arabidopsis Gene Identifier

Gene	AGI	Forward primer	Reverse primer	Product (size, bp)
Primers used for cloning				
<i>GCC-attB</i>	At2g01060	5'-GGGGACAAGTTTGTACAAAAAAGCAG GCTTTATCGCCGCCGCCCTGT-3'	5'-GGGGACCAATTTGTACAAGAAAGCTG GGTGCCTAGAGAATTAACGACTTGTG-3'	
Primers used for mutant screening				
<i>GCC7-9946</i>	At2g01060	5'-TTCAGAAGACGAATCTGGAAGATA CTTTG-3'	5'-CAGATAAGATTTAGCTTGGAGAAGA GCA -3'	
Ds3-1	Inserted gene	5' ACCCGACCGGATCGTATCGGT 3'		
Primers used for real time RT-PCR				
<i>Actin</i>	At2g37620	5'-TGGAAGTGGAAATGGTTAAGGCTGG-3'	5'-TCTCCAGAGTCGAGCACAATACCG-3'	435
<i>PHR1/GCC1</i>	At4g28610	5'-AAACCAACCCGCGCATTC-3'	5'-AGCGGTGTCAACTTCCTTCTGG-3'	530
<i>GCC7</i>	At2g01060	5'-TCCTTGTGCTTCTATCCGTAGT-3'	5'-TGAAGGGAAAAAACTGATAAGAA-3'	170
<i>PRI- MIR399d</i>	At2g34202	5'-AATACTCCTATGGCAGATCGCATTGG- 3'	5'-TCCTTTGGCAGAGAAGCATTTTACTTG-3'	62
<i>AT4</i>	At5g03545	5'-AATATGGCCATCCCCTAAAGAAAAC-3'	5'-TAAACCGGAAACAAAGTAAACACG-3'	438
<i>IPS1</i>	At3g09922	5'-GGGGATGGCCTAAATACAAAATG-3'	5'-TCACTATAAAGAGAATCGGAAGC-3'	439
<i>PHO2</i>	At2g33700	5'-AGGTTTGAAGCTCCACCCTCA-3'	5'-CCCAAGATGTGATTGGAGTCC-3'	69
<i>PHT1;1</i>	At5g43350	5'-GGTGACAACTCGGACGAAAAA-3'	5'-CCAAATCCCAACCAAAACCTGAAGA-3'	146
<i>PHT1;4</i>	At2g38940	5'-CAGCTTCAACGATCATTCCACTTCC-3'	5'-GCCACGTCAAGTGCATTCAACA-3'	204
<i>PHT1;8</i>	At1g20860	5'-ACTGCAGAAAACGTCTACGACG-3'	5'-CAGCGATGATGGCTCCTAATTC-3'	62
<i>PHT1;9</i>	At1g76430	5'-GAAACCGCCAGATACACAGCATT-3'	5'-ACGTTTGTGGAGTTGAGGGG-3'	302
<i>PHT2;1</i>	At3g26570	5'-AGCTGGTGCCGTTTTCTGGAG-3'	5'-TAATGCGCGGCTAATGGTC-3'	517
<i>PHT3;1</i>	At5g14040	5'-TGAAGCTGTGAAGGTTCTGTG-3'	5'-AATCTGACGTCCCCAGAGTG-3'	136
<i>PHT3;2</i>	At3g48850	5'-TCGGAGTTAGCTTTGCAGGT-3'	5'-GGTTGGCAATCCAGCTAAAA-3'	248