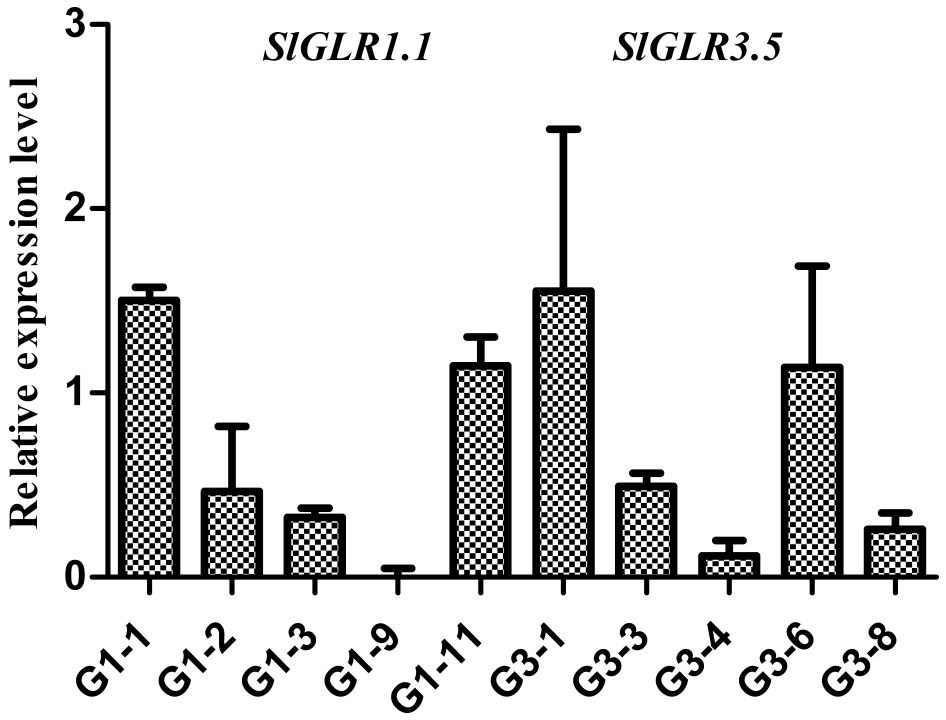
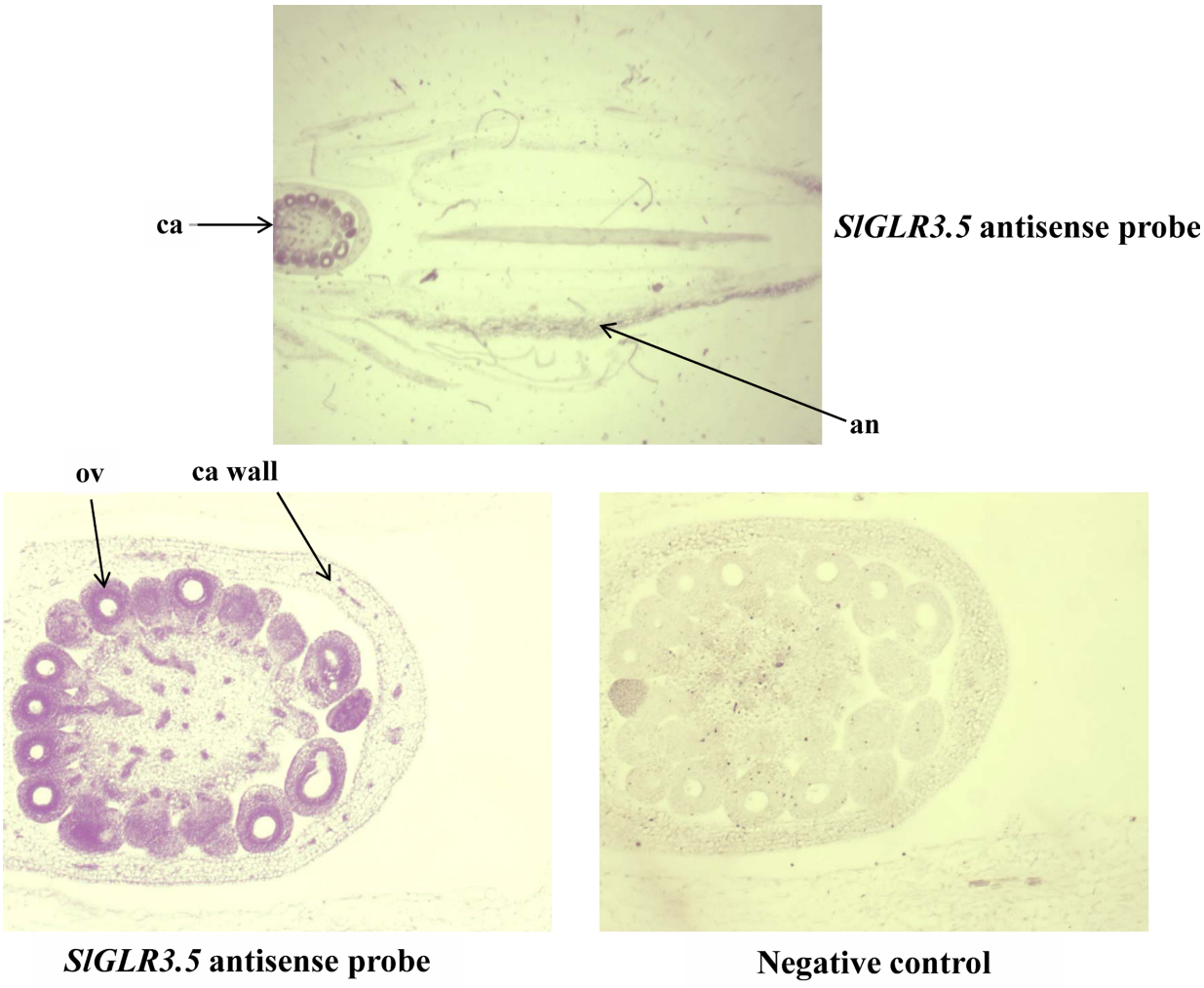


Supplemental Figure S1. Analysis of transgene expression. The expression levels of *SlGLR1.1* and *SlGLR3.5* mRNA in transgenic *Arabidopsis* were analyzed by quantitative real-time PCR. Total RNA was extracted from 3-week-old seedlings of representative lines. Endogenous *SlGLR1.1* and *SlGLR3.5* transcripts were not detected in wild-type Columbia plants.



Supplemental Figure S2. *In situ* hybridization of *SlGLR3.5* in floral organs. Longitudinal sections of flower buds showing the hybridization signal in the carpel (ca), ovule (ov) and anther (an). Because *SlGLR3.5* expression was detected in the flower, the spatial distribution of transcripts in the developing flower was investigated by *in situ* hybridization. *SlGLR3.5* mRNA was more abundant in reproductive organs: carpel and anther. A close examination of the carpel showed high signal intensity on the carpel wall and on the ovule tissue. A control hybridization using the sense probe showed no signal.

Supplemental Table S1. Sets of PCR primers for qRT-PCR analysis

cDNA	Primer sequence 5′→3′	Size (bp)
SlGLR1.1	Sense TTCCTAGGCTGGAACCTTCT	224
	Antisense AAGGAACACTTTGGCATGTG	
SlGLR3.5	Sense CTATGTGGGTTGGCATGTT	251
	Antisense CGGTCAGTTCTTGAACCATT	
AtUBQ10	Sense CCTAACGGGAAAGACGATTA	200
	Antisense GGAGCCTGAGAACAAGATGA	