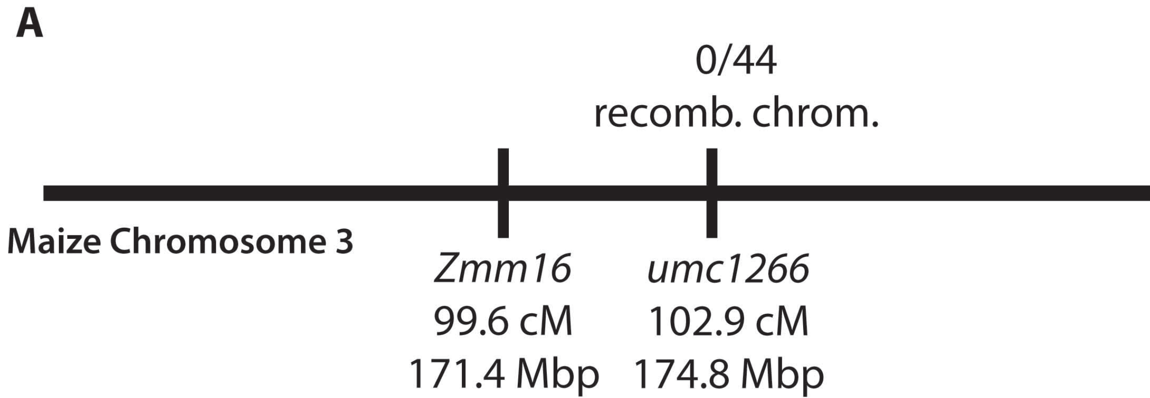
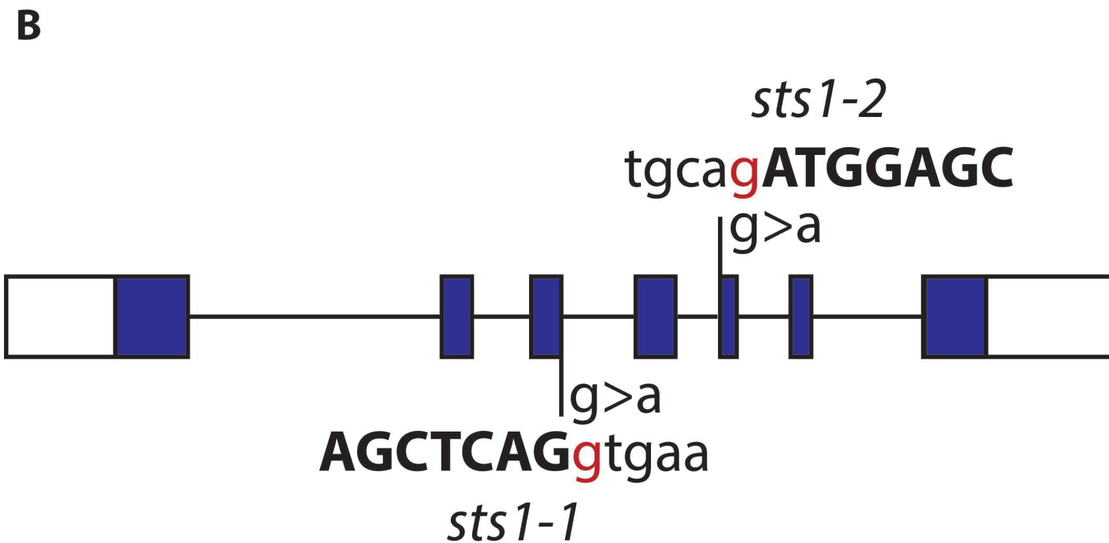
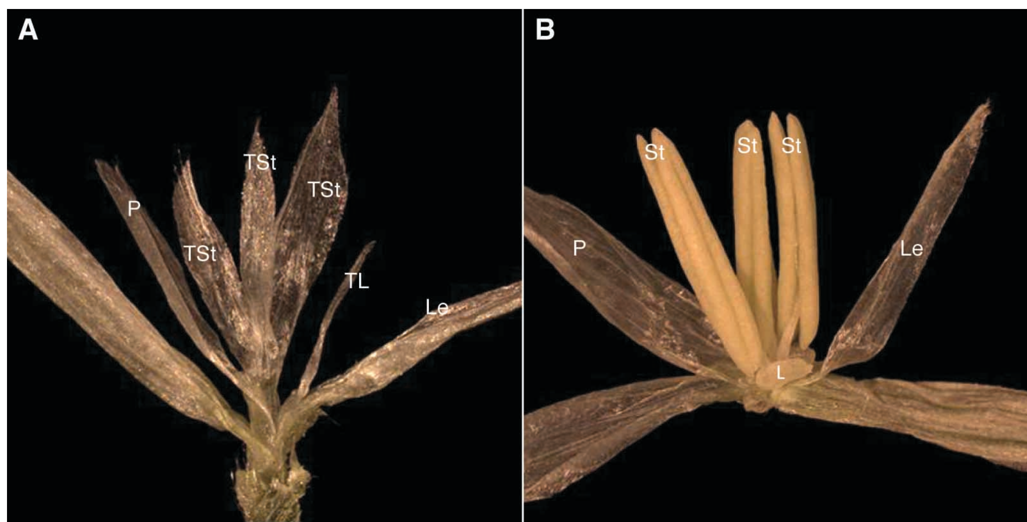
Supplemental Figure 1 Positional cloning of *sts1*
(A) Bulked-segregant mapping of *sts1* identified linkage to the SSR marker *umc1266*, which is tightly linked to *Zmm16* on chromosome 3.
(B) Gene structure of *sts1* (*Zmm16*), showing the splice site mutations in two independent mutant *sts1* alleles.





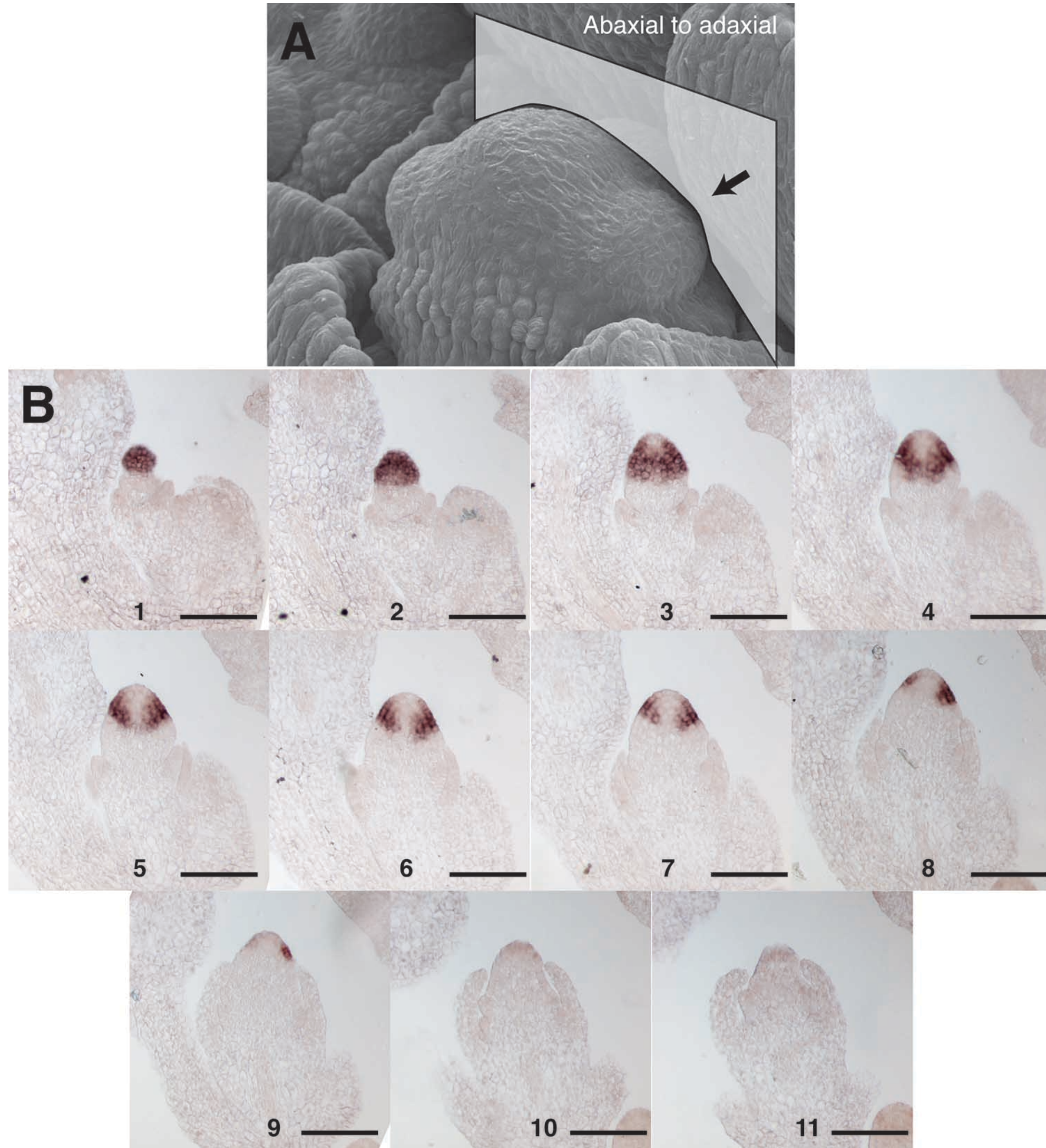
Supplemental Figure 2 Complementation of *sts1-1* by *Zmm16-YFP*
(A) *sts1-1* homozygote lacking *Zmm16-YFP* transgene
(B) *sts1-1* homozygote with *Zmm16-YFP* transgene shows complete rescue of the floral phenotype.
P = Palea, Le = lemma, TSt = transformed stamen, TL = transformed lodicule, St = stamen

Table shows the number of wild-type and *sts1* mutant flowers. All plants were F2 progeny of a cross between *sts1* mutant x *Zmm16-YFP* transgenic plants. Progeny were genotyped for the *sts1-1* locus as described in the materials and methods, and presence of *Zmm16-YFP* determined by scoring for BASTA resistance.

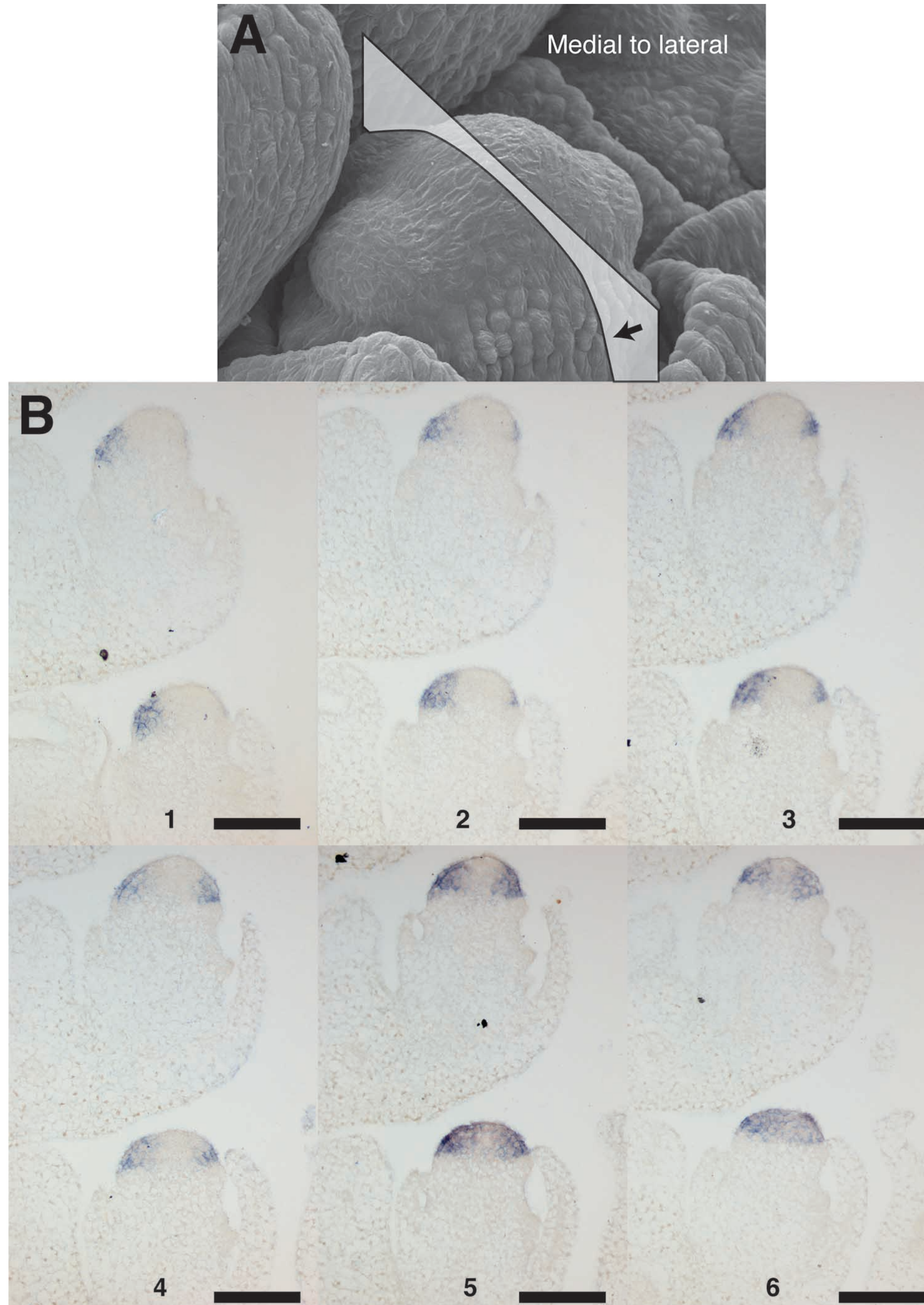


***sts1* Genotype**	***Zmm16-YFP***	**Phenotype Wild-type**	***sts1***
sts1-1/sts1-1	Present	6	0
sts1-1/sts1-1	Absent	0	5
+/sts1-1	Present	8	0
+/sts1-1	Absent	8	0
+/+	Present	9	0
+/+	Absent	3	0

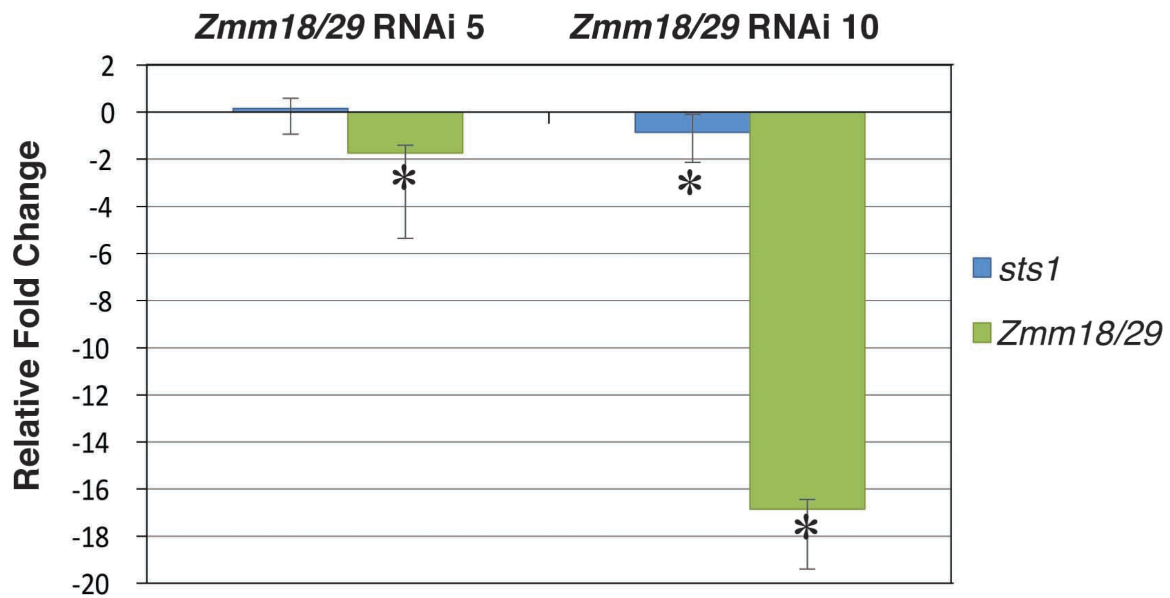
Supplemental Figure 3 *sts1* expression in male florets
(A) Orientation and direction of sections
(B) Adjacent serial sections through an entire floret ordered from abaxial to adaxial (1-11) probed with anti-*sts1* probe. Note the lack of expression in the adaxial region (floret shown in (A) is at an older stage than the sections). Scale bar = 100μm.



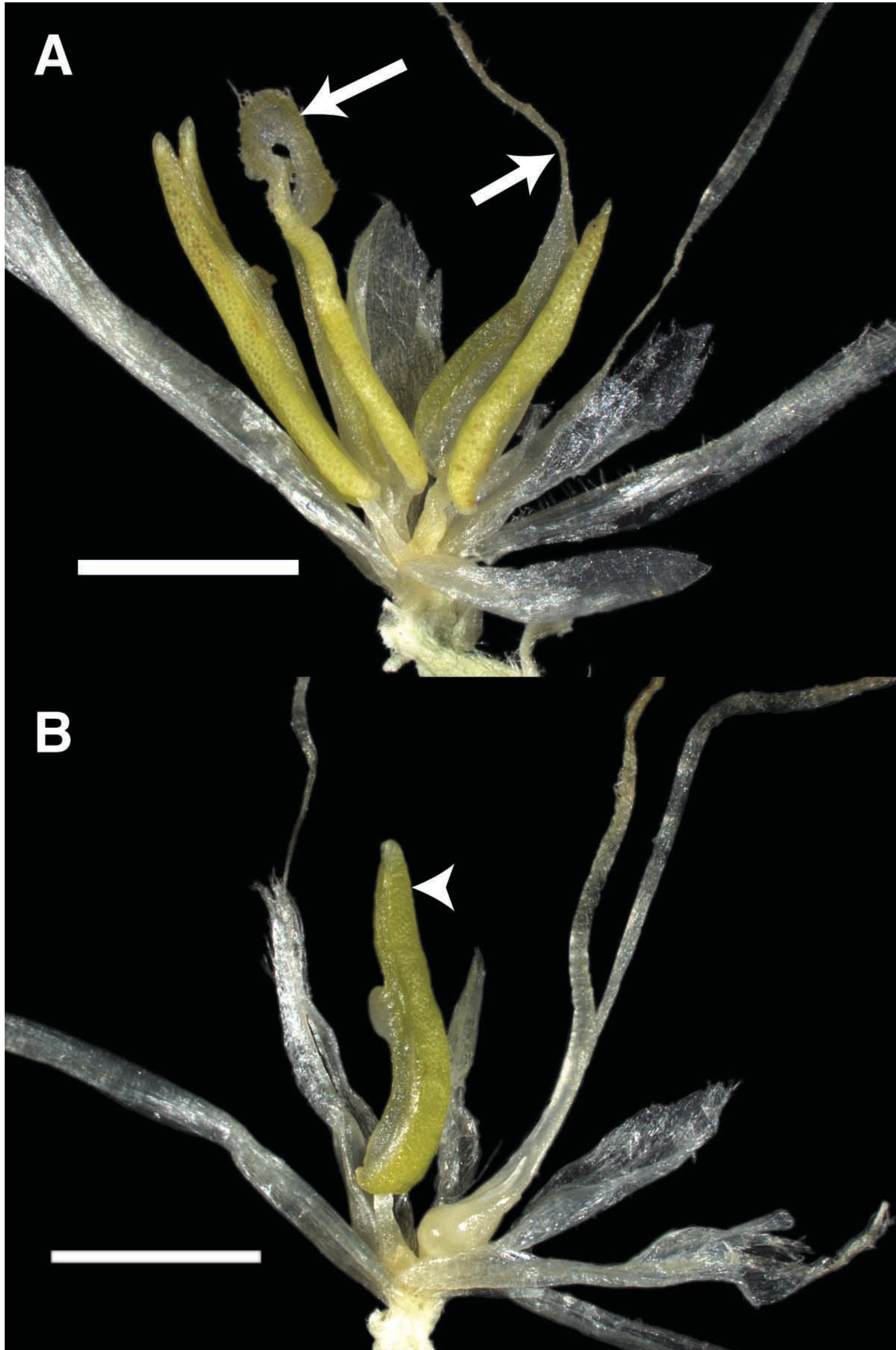
Supplemental Figure 4 *si1* expression in male florets
(A) Orientation and direction of sections
(B) Adjacent serial sections through half of a floret ordered from medial to lateral (1-6) probed with anti-*si1* probe. Two florets from successive nodes are shown in each panel. Sections are ordered from abaxial to adaxial. Note the lack of expression in the adaxial region (floret shown in (A) is at an older stage than the sections). Scale bar = 100µm.



Supplemental Figure 5 Expression analysis of *Zmm18/29* RNAi knockdown lines
Expression levels of *Zmm18/29* (assayed together with primers that recognize both paralogs) and *sts1* were determined by RT-qPCR using cDNA from florets of tassels just prior to emergence from vegetative leaves. *sts1* levels were assayed as a control for specificity of RNAi to *Zmm18/29*. The slight but significant down-regulation of *sts1* in line #10 could be due to either non-specific silencing of this paralogous gene, or positive regulation of *sts1* by *Zmm18/29*. Error bars represent standard deviation from the mean, and * indicate a significant difference ($P \leq 0.05$) from wild-type (lacking transgene) expression levels at the same stage.



Supplemental Figure 6 Partial stamen identity in *gt1 sts1* double mutants
(A) and (B) *sts1-1 gt1* double mutants have organs with partial stamen identity. Some organs are mosaic with both stamen and carpel identity as evidenced by anthers tipped by silk tissue (arrows), while others are deformed stamens (arrowhead). Scale bar is 2.0 mm.



Supplemental Table 1.

Primer Name	Primer Sequence
Genotyping primers for *sts1-1*, *gt1-1*, and *si1-mum2*	
Sts1-CAPS-For	TCGGATAGGGGAACAGACAG
Sts1-CAPS-Rev	ATCAGGTCTTTGGGTTGCAG
Sts1-CAPS-Rev1	GCATCCAGCAGTCTAATTGT
Gt1-CAPS-For	AGGTGGCCGTCTGGTTCCAGAA
Gt1-CAPS-Rev	TGGTGCGTCACCGTCGAGAAC
Si1-For	GTGCTGCTGTGCTCATCAAT
Si1-Rev	TAGGTATCAGTCTGCGTGCTG
Mu-TIR6	AGAGAAGCCAACGCCAWCGCCTCYATTTCGTC
Zmm19/29 RNAi Vector Construction Primers	
Zmm18/ZMM29-5'SpeI-For	GCGACTAGTTAAAGATCCACACCACTTGAGC
Zmm18/ZMM29-5'-Rev	CTACTCGTCTACTGCGTTCTCCACTCCCAA
Zmm18/ZMM29-3'-For	AGAACGCAGTAGACGAGTAGCTACAGCCTG
Zmm18/ZMM29-3'XmaI-Rev	GCGCCCGGGAGCCCAGCAAAGTCAAAAGAGA
Zmm18/ZMM29-5'AscI-For	GCGGGCGCGCCTAAAGATCCACACCACTTGAGC
Zmm18/ZMM29-3'AvrII-Rev	GCGCCTAGGAGCCCAGCAAAGTCAAAAGAGA
Primers and probes for qRT-PCR	
Sts1-RTPCR-For	ATAATGGACTGACGAACCTGAATG
Sts1-RTPCR- Rev	GCGATATCTTGCTGGTGGAGT
Si1-RTPCR- For	CACAGAGATTAGGCAAAGGATGG
Si1-RTPCR-Rev	AGTCTGCGTGCTGATCACATG
Zmm18/29-RTPCR-For	ATGCAGATTCAGCTCAGGCAT
Zmm18/29-RTPCR-Rev	CAGTAGTCCATCTGCTTCTCGC
αTubulin-RTPCR-For	GAGCATGGCATTCAGGCTG
αTubulin-RTPCR-Rev	CAAGGTCAACAAAAACAGCACG
Sts1-Probe	6FAM-AAGGCCAGCAATTTGTTCTCGTCTTCCAT-TAMRA
Si1-Probe	6FAM-ATCTGGACAGTCTGGACTTCGACGAGCT-TAMRA
Zmm18/29-Probe	6FAM-ATGTTGGTCTGCCCATTCTGGAGGC-TAMRA
αTubulin-Probe	6FAM-CAGATGCCCGGTGACAAGACCATTG-TAMRA
Primers for creation of *sts1-YFP*	
sts1_attB4	GGGGACAACTTTGTATAGAAAAGTTGTGCCAACGCAGCTATCTCTA
sts1_attB1(R)	GGGGACTGCTTTTTTGTACAAACTTG**C**ATTGTTCTCCTGCAAGTTGG
sts1_attB2	GGGGACAGCTTTCTTGTACAAAGTGG**GA**TAGACTGCTGGATGCCCTCG
sts1_attB3(R)	GGGGACAACTTTGTATAATAAAGTTGAGACGACGGAACACCAAATC
YFP_attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAGGCCGGCCTGGAGGTGGAGGTGGAGCTGTGAGC
YFP_attB2(R)	GGGGACCACTTTGTACAAGAAAGCTGGGTGGGCCCCAGCGGCCGCAGCAGCACCAGCAGGATC

The *att* sites required for Gateway cloning are underlined. Nucleotides inserted to maintain the reading frame are bolded