

Figure 1

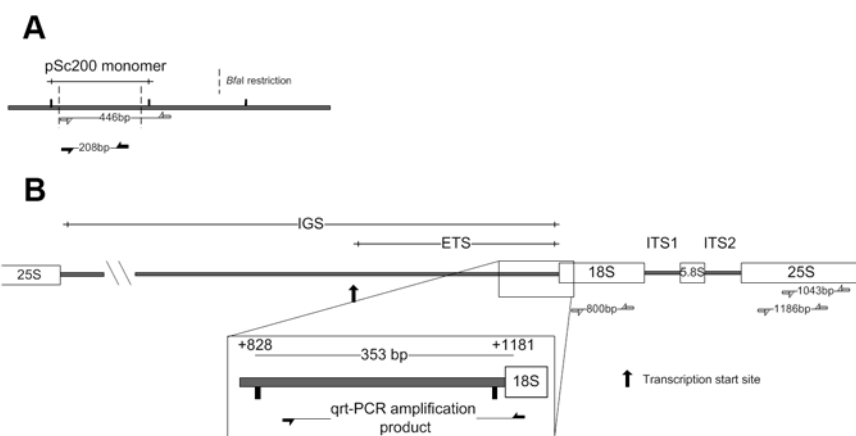


Figure 2

A

Accession	ID	Query start	Query end	Subject start	Subject end	Strand	Score	Evalue
MI0013263	osa-MIR2921	43	90	129	176	-	87	3.3
MI0010876	sbi-MIR169k	25	52	11	38	+	86	3.9
MI0010897	sbi-MIR396d	254	288	48	82	+	85	4.8
MI0019046	osa-MIR5526	194	228	20	54	+	85	4.8

B

Query: 43-90	<u>osa-MIR2921</u> : 129-176	score: 87	evalue: 3.3
pSc200	90 aaauuugagcuguaaaauugcgauaacuucauuuuuccaaucugcau 43		
osa-MIR2921	129 aaguucuaucuaaaaauugugauaucuagcuuguuuuauaugaucauuau 176		
Query: 25-52	<u>sbi-MIR169k</u> : 11-38	score: 86	evalue: 3.9
pSc200	25 ugauaugccggcucucaaaaaauugagc 52		
sbi-MIR169k	11 ugacuugccggcuccucaaaaaugaagc 38		
Query: 254-288	<u>sbi-MIR396d</u> : 48-82	score: 85	evalue: 4.8
pSc200	254 ugcuuuguucacacuugcuuuugagagucucgaucaa 288		
sbi-MIR396d	48 ugcuuugcucucgcgucgcuuuugugaugguucaa 82		
Query: 194-228	<u>osa-MIR5526</u> : 20-54	score: 85	evalue: 4.8
pSc200	194 aaguccuaucaccucaauuuccccaauagcuuucca 228		
osa-MIR5526	20 aagaccucucaccucagcucucaaacacauuacca 54		

Supplementary Material (Legends)

Figure 1. Schematic representation of pSc200 and 45S rDNA sequences. **A** Schematic representation of the tandem organization of pSc200 repetitive sequence showing *Bfa*I restriction sites and primers used to produce pSc200 FISH probe (gray arrows) and for quantitative real time PCR analysis (black arrows). **B** Schematic representation of 45S rDNA subunit showing primers used to produce the rDNA FISH probe (gray arrows) and for quantitative real time PCR analysis (black arrows).

Figure 2. pSc200 microRNA prediction. MicroRNA prediction for pSc200 sequence (EU333404.1) obtained from miRBase (<http://www.mirbase.org/>) using BLASTN searching for stem-loop sequences in the Monocotyledons database. **A** Matches for pSc200 nucleotide sequence. **B** Alignment of pSc200 to hairpin miRNAs.