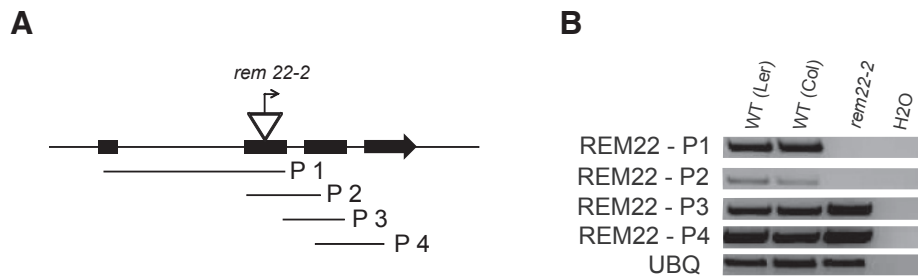


SUPPLEMENTARY MATERIAL

corresponding to:

***Reproductive Meristem22* is a unique marker
for the early stages of stamen development**

ELISSON ROMANEL, PRADEEP DAS, RICHARD M. AMASINO, JAN TRAAS,
ELLIOT MEYEROWITZ and MARCIO ALVES-FERREIRA



Supplementary Fig. 1. Position of the T-DNA insertion in the *REM22* gene and gene expression analysis. (A) The triangle indicates the location of T-DNA insertion in the second exon of *REM22* gene. The lines below the gene diagram show the PCR fragments produced by distinct primer combination used in the RT-PCR analysis (Supplementary Table 1). Exons are represented as black solid boxes. (B) *REM22* expression in inflorescence of distinct ecotypes (*Ler* - Landsberg erecta; *Col* - Columbia) and in the insertion line (*SALK_091149*). Gene-specific primer combinations for *REM22* used in the RT-PCR are indicated in the left side. *UBIQUITIN10 (UBQ)* was used as a control for loading. Complete *REM22* transcripts were only detected in WT plants.



Supplementary Fig. 2. Genomic structure of *REM22* gene. *REM22* gene, the promoter region and the 5th exon of the gene *At1g17000* are shown. The cloned promoter region (1022 bp upstream the *REM22* ATG) is indicated by the black line below the gene diagram. The exons (dark gray), the UTRs (light gray) and the scale bar in base pairs (bp) are shown below the diagram.

SUPPLEMENTARY TABLE 1

PRIMER LIST

Gene – RT-PCR fragment	Forward	Reverse
REM22 – P1	GGGCAGATCTATCCTCTGACTG	CGAGGTTTACGCATCTCTAAGC
REM22 – P2	GGAAGACATGGGATGTAGAAGTC	TCTATGAGGCTGTTCTCTCCTTCT
REM22 – P3	GGTCCTTCTAGTGGGATCAAG	GGTATTGCCAGGAACCTTGAGGT
REM22 – P4	GGACGAGCTGAGTTCTAGTTAGA	AGATTGTCCGAATCTCCCTCAC
UBQ10 (AT4G05320)	GATCTTTGCCGAAAACAATTGGAGG	CGACTTGTCCATTAGAAAGAAAGAGAT