

Supplementary Materials

Homology-Based Interactions between Small RNAs and Their Targets Control Dominance Hierarchy of Male Determinant Alleles of Self-Incompatibility in *Arabidopsis lyrata*

Shinsuke Yasuda ^{1,†,‡}, Risa Kobayashi ^{1,‡}, Toshiro Ito ¹, Yuko Wada ^{1,*} and Seiji Takayama ^{2,*}

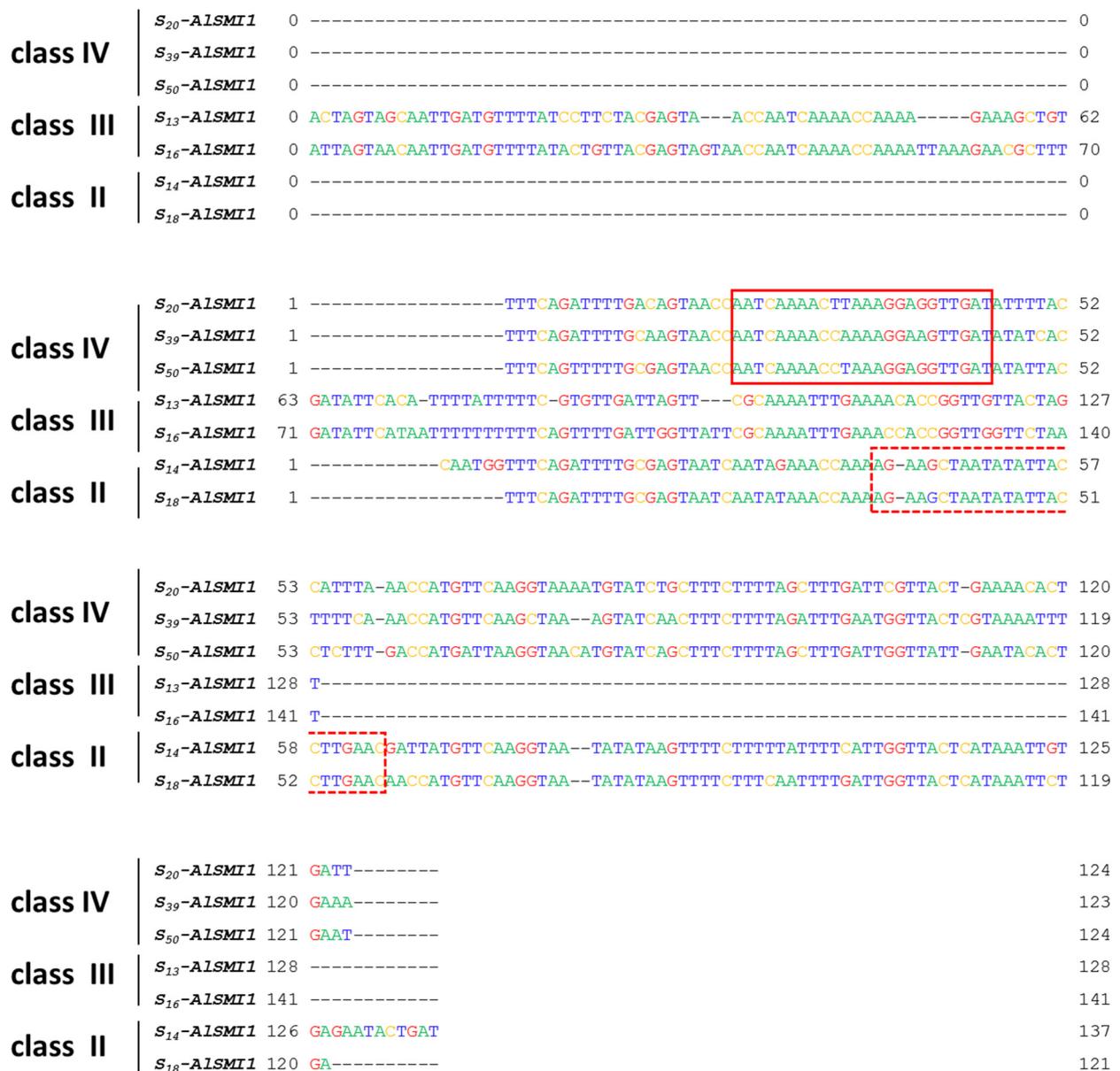
¹ Division of Biological Sciences, Nara Institute of Science and Technology, Nara 630-0192, Japan; shinsuke-yasuda@takii.co.jp (S.Y.); kobayashi.risa.ki7@bs.naist.jp (R.K.); itot@bs.naist.jp (T.I.)

² Department of Applied Biological Chemistry, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo 113-8657, Japan

* Correspondence: yu-wada@gtc.naist.jp (Y.W.); a-taka@g.ecc.u-tokyo.ac.jp (S.T.)

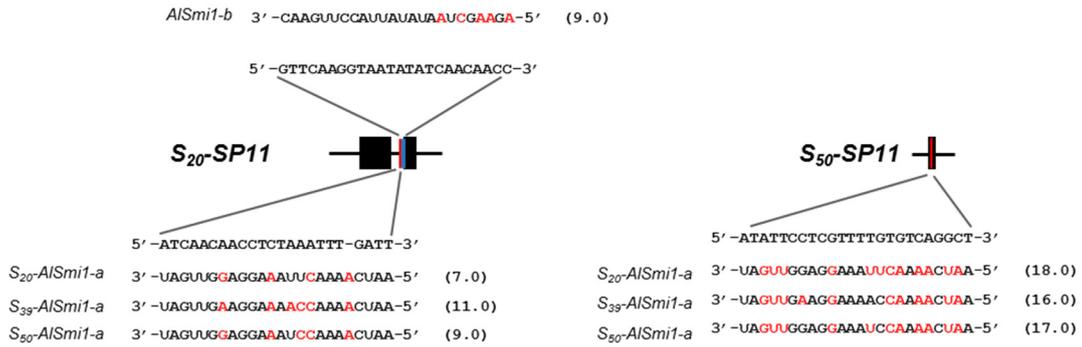
† Present address: Plant Breeding and Experiment Station, Takii and Company, Limited, Konan, Shiga 520-3231, Japan

‡ These authors contributed equally to this work.

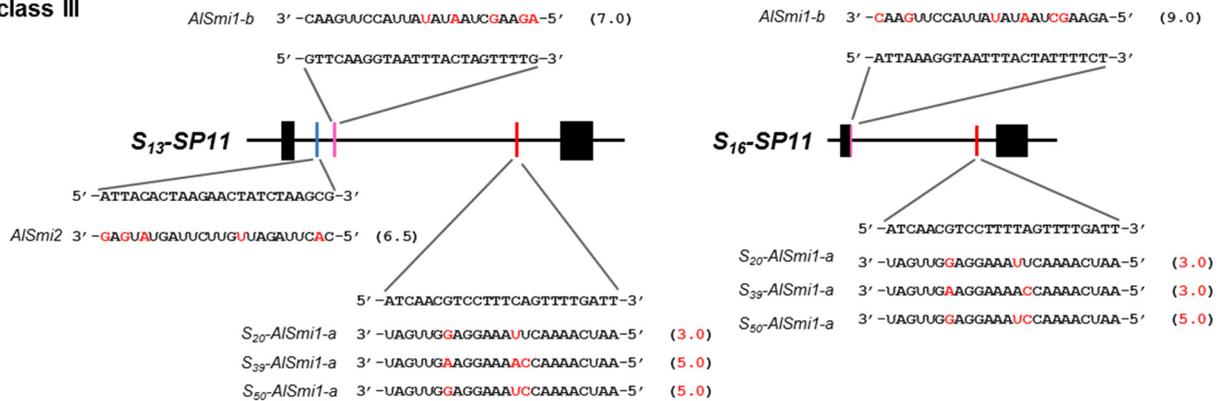


Supplementary Figure S1. Sequence alignment of the inverted repeat sequences of *ALSmi1*. Alignment of *S*₂₀, *S*₅₀, *S*₃₉, *S*₁₃, *S*₁₆, *S*₁₄, and *S*₁₈ haplotypes of *ALSmi1*. Class-IV *ALSmi1-a* sequences and predicted *ALSmi1-b* sequences are highlighted by solid and dashed red boxes, respectively.

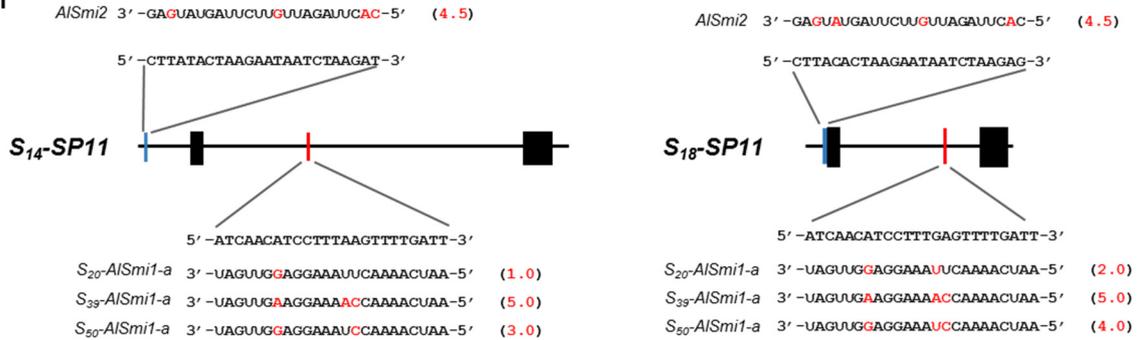
class IV



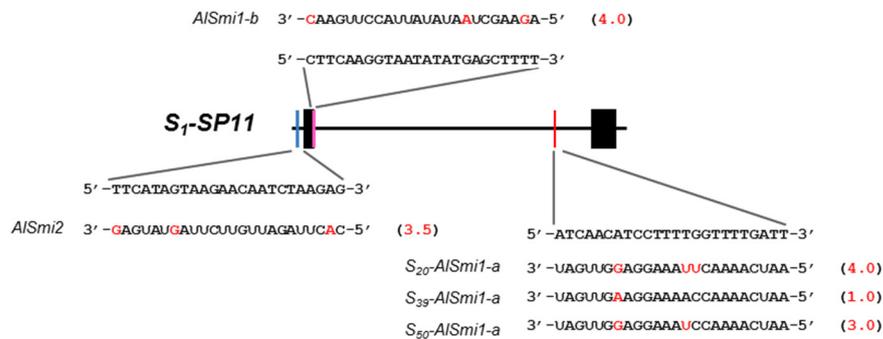
class III



class II



class I



Supplementary Figure S2. Genomic regions of the class-IV, class-III, class-II, and class-I S haplotypes of *SP11*, and sequence similarity between sRNAs and their *SP11* target sites. Schematic diagram of haplotypes *S₂₀*, *S₅₀*, *S₁₃*, *S₁₆*, *S₁₄*, *S₁₈*, and *S₁*. Sequences of *S₂₀-AlSmi1-a*, *S₃₉-AlSmi1-a*, *S₅₀-AlSmi1-a*, *AlSmi1-b*, and *AlSmi2* and their sRNA target sites in *SP11* are shown. Black boxes indicate *SP11* exon regions. Red, magenta, and blue boxes indicate target sites of *AlSmi1-a*, *AlSmi1-b*, and *AlSmi2*, respectively. Bases in red indicate mismatches with each *SP11* target site. Numbers in parentheses indicate the mispair scores between each sRNA and the *SP11* target site. Mispair scores <5.5 are shown in red.

Supplementary Table S1. Number of sequence reads obtained.

sRNA	Obtained Reads Number
<i>S₂₀-AlSmi1-a</i>	100
<i>S₁₃-AlSmi2</i>	2889

Results of massively parallel sequencing of *S₂₀S₁₃* heterozygotes. A total of 44,553,252 bp sequence reads were obtained.