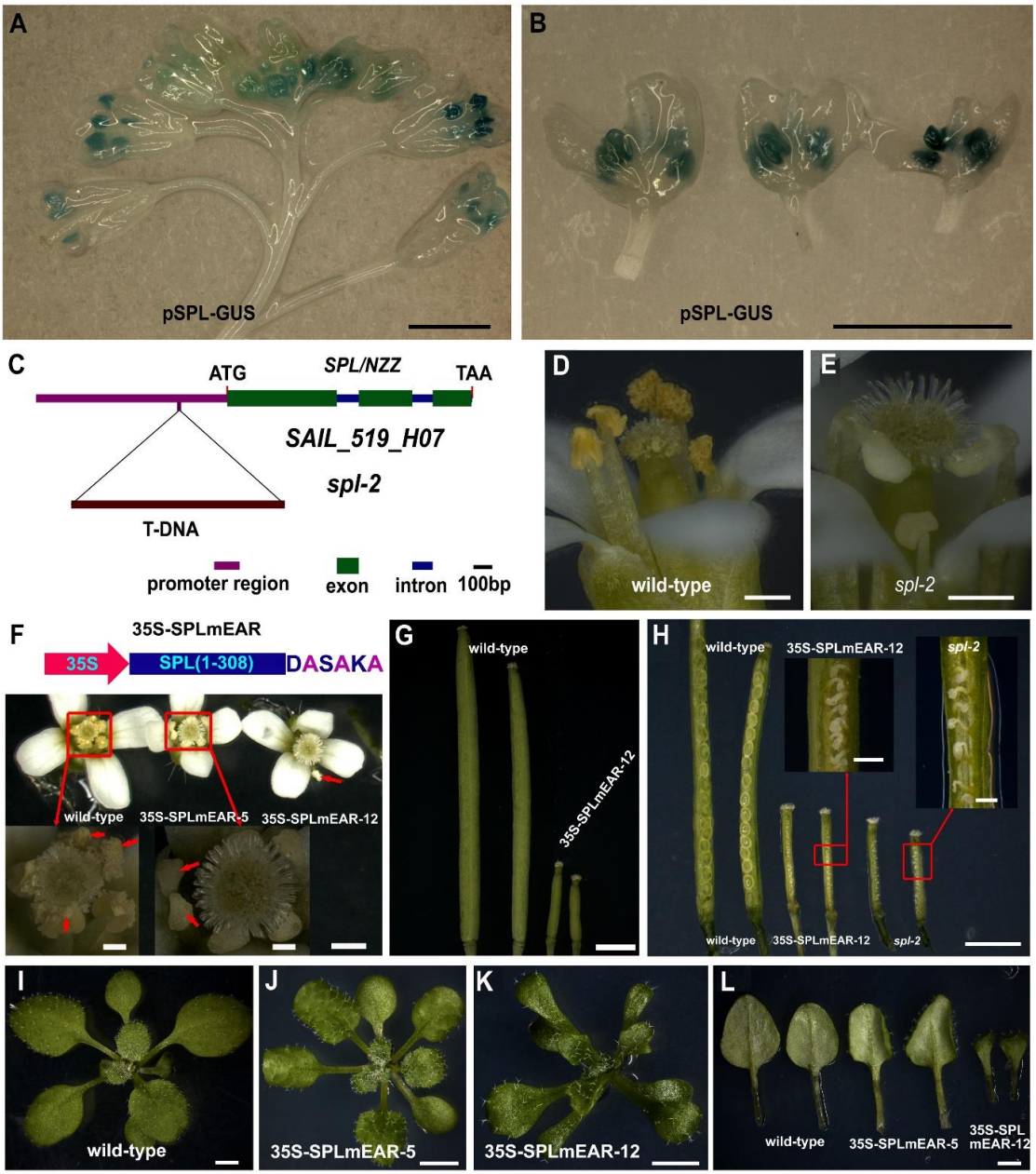

Supplementary information, Figure S2 Identification of 4.4-kb-long promoter of *SPL* and *spl-2*.

(A) and **(B)** The GUS activity of pSPL-GUS transgenic line in which GUS was driven by 4.4-kb-long promoter of *SPL*. Bars, 1 mm. **(C)** Schematic representation of T-DNA insertion site in *spl-2* (*SAIL_519_H07*). The T-DNA was located in the promoter region of *SPL*. **(D)** and **(E)** The mutant *spl-2* displayed male sterility **(E)** as compared to wild-type **(D)**. **(F)** to **(H)** Overexpression of SPLmEAR in which the three conserved leucine

residues of C-terminal EAR motif were mutated to alanines caused the male and female sterility as observed in *spl-2* mutants. **(F)** Top, schematic representation of 35S-SPLmEAR construct. Bottom, from left to right, the opening flowers from wild-type with mature pollens in the stamens (red arrows), two independent lines of 35S-SPLmEAR with no pollens in the stamens (red arrows). **(G)** The siliques from wild-type and 35S-SPLmEAR line. **(H)** The dissected siliques from wild-type, 35S-SPLmEAR and *spl-2*. The 35S-SPLmEAR lines and *spl-2* all displayed the similar sterility. Bars, 1 mm and 250 μm in the insets. **(I)** to **(L)** SPLmEAR overexpression lines displayed down-curled leaves opposite to those observed in *spl-D* mutants. **(I)** 21-day-old wild-type plant. **(J)** and **(K)** Two independent lines of 35S-SPLmEAR. **(L)** The close-up views of the 4^{th} and 5^{th} leaves from 21-day-old wild-type and two independent lines of 35S-SPLmEAR plants. Bars, 1 mm.