

Figure S6 SDpop's inferences of sex-linkage in *Silene latifolia*, using the 12 individuals of the "central cluster" (Figure S4). Contigs were placed on the genetic map of Papadopulos *et al.* (2015). Left panels: posterior probabilities for all placed contigs: autosomal segregation in green, X-hemizygosity in blue, and XY gametology in red; the (uninformative) haploid and paralogous segregation types are indicated in grey. Lines represent running averages, using sliding windows of 10 contigs. The "fuzzy boundary" between the non-recombining region and the pseudoautosomal region on the X chromosome (Krasovec *et al.* 2020) is indicated by the vertical line. Right panel: predicted divergence (black triangles) and nucleotide diversity of X and Y copies (orange circles and cyan squares) based on SDpop's output. The lines are the running averages over 10 genes.

Literature Cited

- Krasovec, M., Y. Zhang, and D. A. Filatov, 2020 The location of the pseudoautosomal boundary in *Silene latifolia*. Genes (Basel). **11**: 610.
- Papadopulos, A. S., M. Chester, K. Ridout, and D. A. Filatov, 2015 Rapid Y degeneration and dosage compensation in plant sex chromosomes. Proc. Natl. Acad. Sci. U.S.A. **112**: 13021–13026.