



Figure S2. Plots generated by genome size estimators for 21-mer with Illumina raw reads. A-B. 21-mer histogram frequencies plots generated by GenomeScope and FindGSE. **C.** 21-mer comparison plot. Colors show the coverage of the 21-mer in the assembly. In black, many rare 21-mers (resulting from sequencing errors) are not in the assembly. In red, 21-mer are present in the assembly once and in purple few 21-mers are duplicated in the assembly. The three plots show that *S. nonagrioides* genome is mainly homozygous, since they have only one peak.