Supplementary Table 4: Information on sequenced Symphyta genomes

Organism	**Sequencing Technology used**	**Total length**	**Number of contigs**	**N50**	**Assembly completeness (BUSCO score, %)**	**Reference**
Sirex noctilio	Illumina	185 Mb	6215	825 kb	95.4%	Current study
Cephus cinctus	Illumina	162 Mb	1976	622 kb	98%	(Robertson et al., 2018)
Athalia rosae	Illumina	164 Mb	522	1.37 Mb	96%	(Oeyen et al., 2020)
Orussus abietinus	Illumina	201 Mb	936	2.37 Mb	93%	(Oeyen et al., 2020)
Euura lapo	10X, Oxford Nanopore and Illumina	259 Mb	2503	209 kbp	93.5%	(Michell et al., 2021)
Eupontania aestiva	10X, Oxford Nanopore and Illumina	222 Mb	16952	49.7 kbp	90.2%	(Michell et al., 2021)