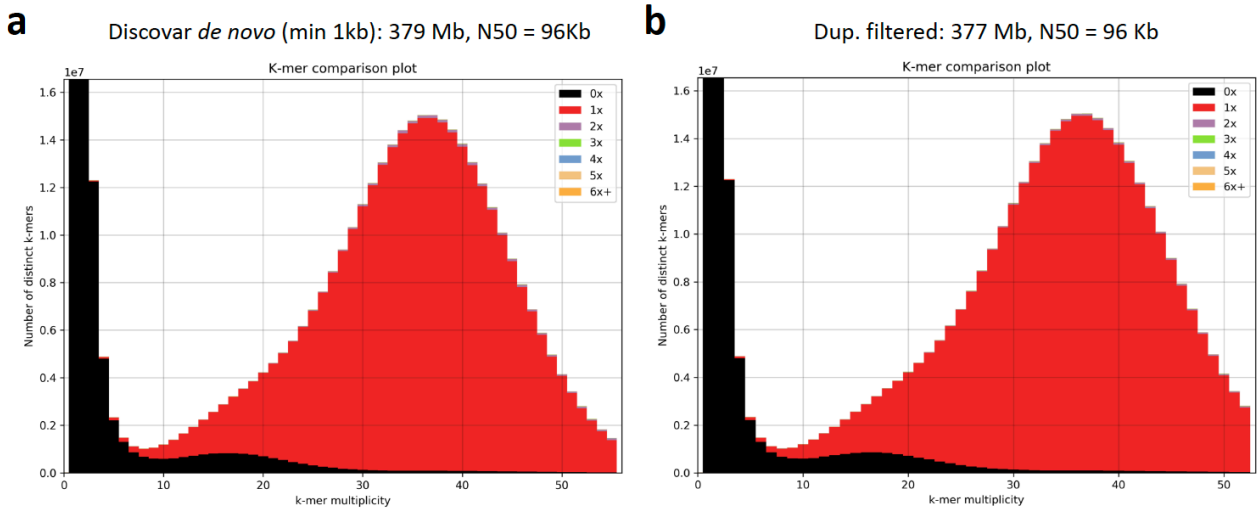
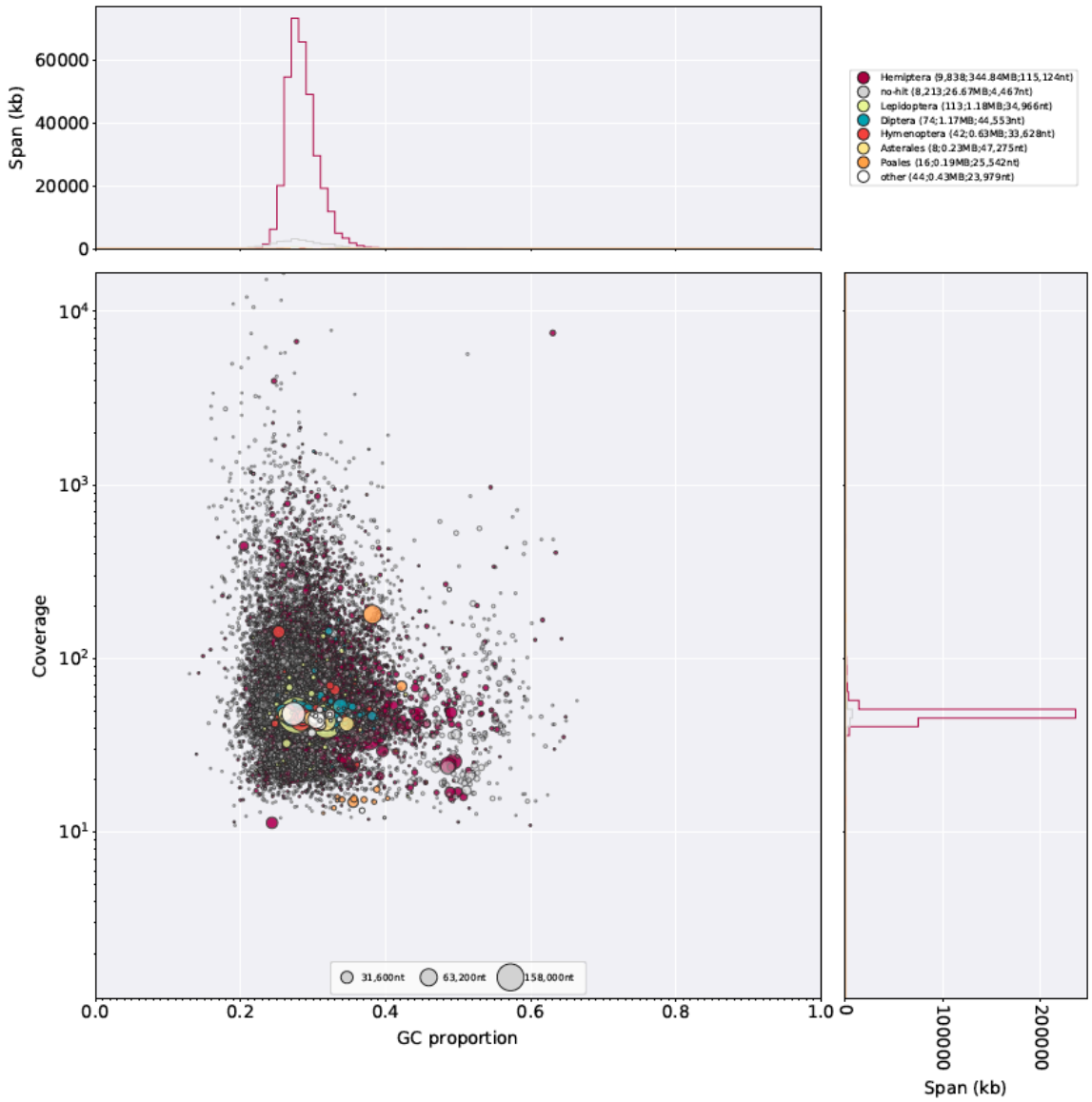
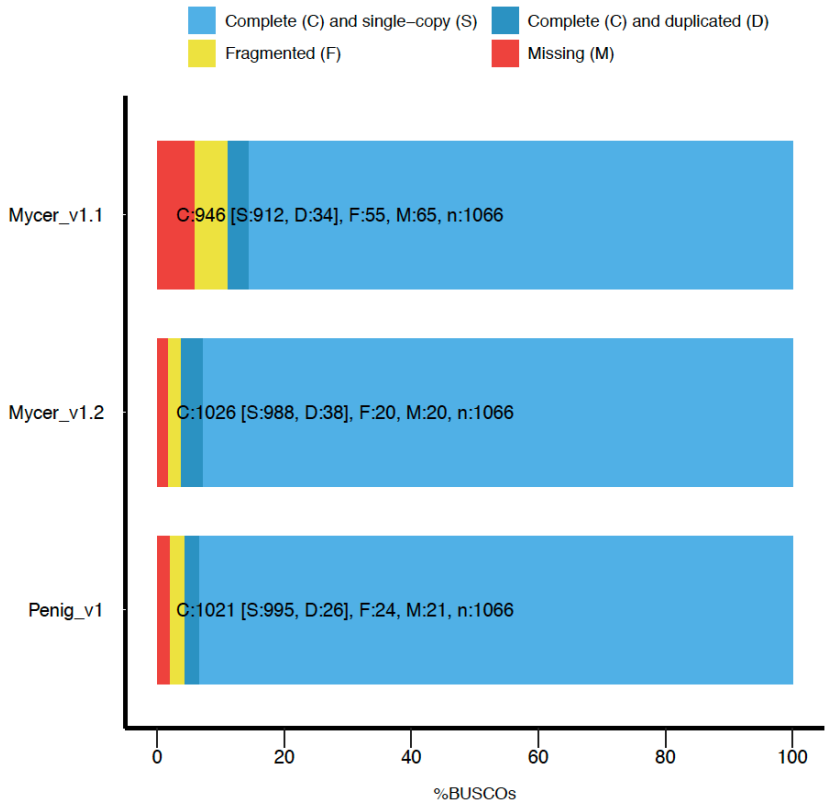


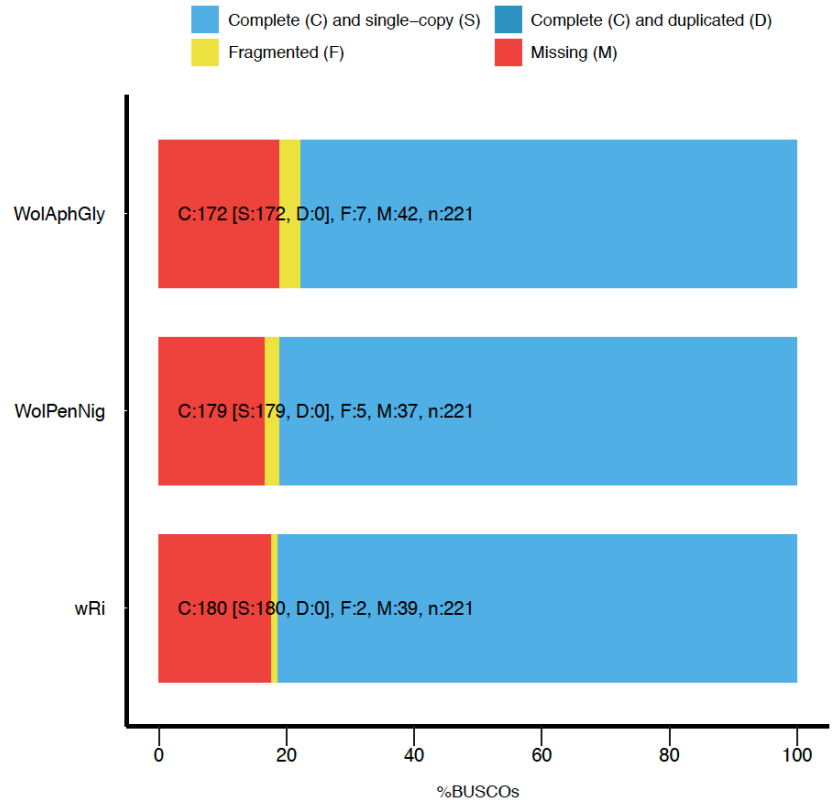
Supplementary Figure 1: KAT k-mer spectra plot comparing k-mer content of PCR-free *P. nigronervosa* Illumina reads to k-mer content of the initial discovar de novo genome assembly (**a**) and the same assembly after processing with our de-duplication pipeline (**b**) (see Methods). Colours indicate how many times fixed length words (k-mers) from the reads appear in the assembly. Red indicates k-mers found only once in the assembly, black indicates content present in the reads but missing from the assembly and other colours indicate k-mers that are duplicated in the assembly. The x-axis shows the number of times each k-mer is found in the reads (k-mer multiplicity) and the y-axis shows the count of distinct k-mers in 1x k-mer multiplicity bins.



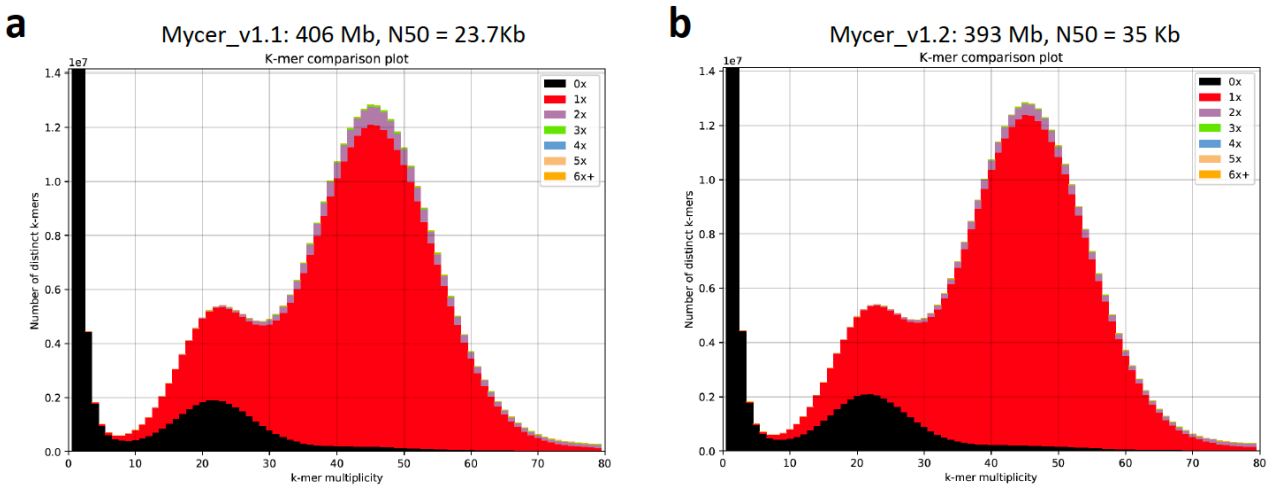
Supplementary Figure 2: Taxon-annotated GC content-coverage plot of the frozen *P. nigronervosa* genome assembly (Penig_v1). Each circle represents a scaffold in the assembly, scaled by length, and coloured by order-level NCBI taxonomy assigned by BlobTools. The X axis corresponds to the average GC content of each scaffold and the Y axis corresponds to the average coverage based on alignment of *P. nigronervosa* PCR-free Illumina short reads. Marginal histograms show cumulative genome content (in Kb) for bins of coverage (Y axis) and GC content (X axis).



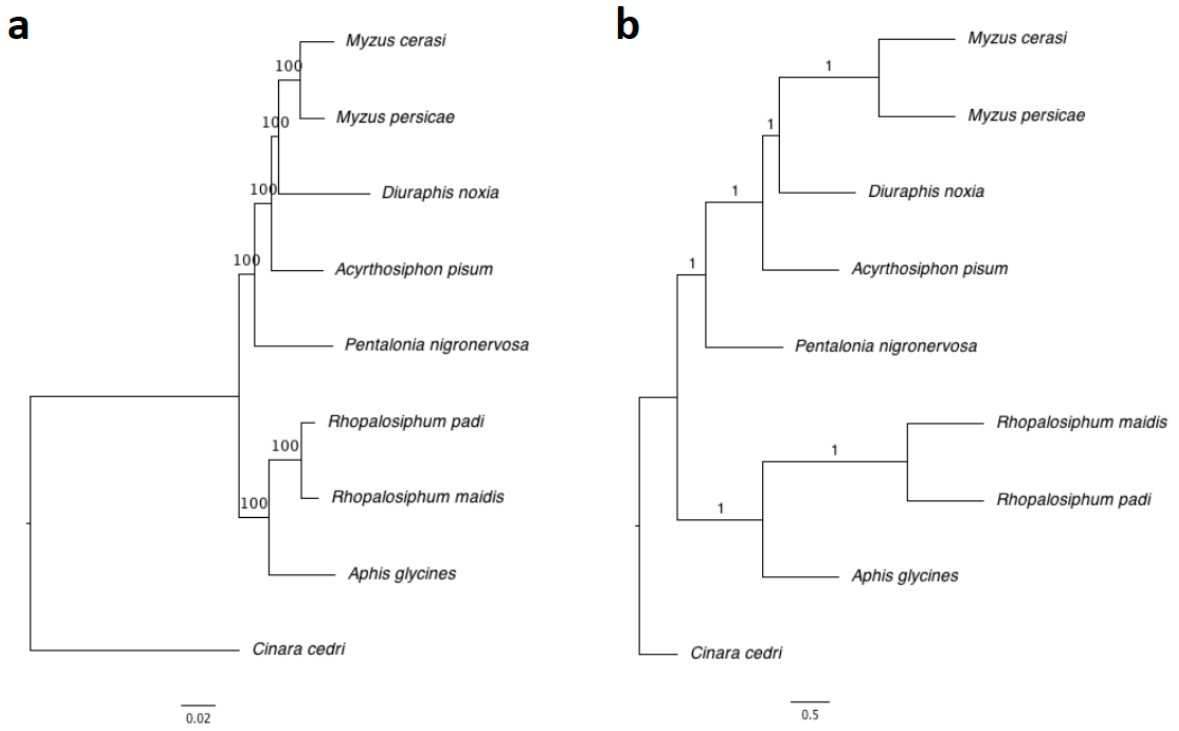
Supplementary Figure 3: BUSCO analysis of the *P. nigronervosa* v1 (Penig_v1), *M. cerasi* v1.1 (Mycer_v1.1) and *M. cerasi* v1.2 (Mycer_v1.2) gene sets (protein sequences). Where multiple transcripts of a gene where annotated we used the longest transcript to represent the gene. The protein sets were assessed using the Arthropoda gene set (n=1,066).



Supplementary Figure 4: The *P. nigronervosa* Wolbachia genome (WolPenNig) extracted from the discovar de novo genome assembly has similar completeness to the reference Wolbachia wRi genome (NCBI Reference Sequence: NC_012416.1) and a long-read assembly of a Wolbachia strain infecting the soybean aphid (WolAphGly). BUSCO gene-level completeness was assessed for each genome assembly using the proteobacteria gene set (n = 221).



Supplementary Figure 5: KAT k-mer spectra plot comparing k-mer content of genomic PCR-free *Myzus cerasi* Illumina reads (NCBI accession: ERR2236145) to k-mer content of the published assembly of *M. cerasi* (**a**; Mycer_v1.1 [Thorpe et. al. 2018]) and the same assembly after processing with our de-duplication pipeline (**b**) (see Methods). The *stacked-histograms* are as described in **Supplementary Figure 1**.



Supplementary Figure 6: (**a**) IQ-Tree maximum likelihood phylogeny of selected aphid species that have sequenced genomes based on a concatenated protein alignment of 4,721 conserved one-to-one orthologs. Sequence evolution was modelled using the JTT+F+R8 model (selected by ModelFinder based on Bayesian Information Criterion score). Branch lengths are in amino acid substitutions per site. Values on branches show IQ-Tree ultrafast bootstrap support values based on 1000 replicates. (**b**) Coalescent species tree estimated from 3,919 gene trees with ASTRAL-III. Values on branches show local posterior probabilities. Branch lengths are in coalescent units.