

Table S1. Comparison of match parameters of all BUSCO genes present in the genome assembly to those present in the genome assembly, but absent from the genome annotation. Reported are the percentage of genes that were fragmented and the bitscore and length of the alignment to the BUSCO profile.

	%fragmented		mean bitscore		mean length	
	overall	missing	overall	missing	overall	missing
<i>G. legneri</i>	0.4	0.4	476.9	366.4	308.7	253.3
<i>A. bilineata</i>	3.5	9	418.3	280.6	284.7	214.7
<i>P. maculata</i>	5.1	11.7	434.1	311.7	292.4	223.9

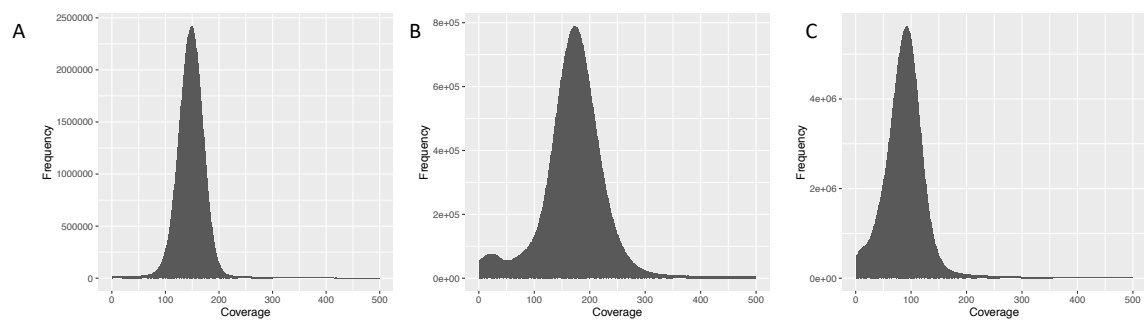


Figure S1. Coverage histograms for (A) *G. legneri*, (B) *A. bilineata* and (C) *P. maculata*.

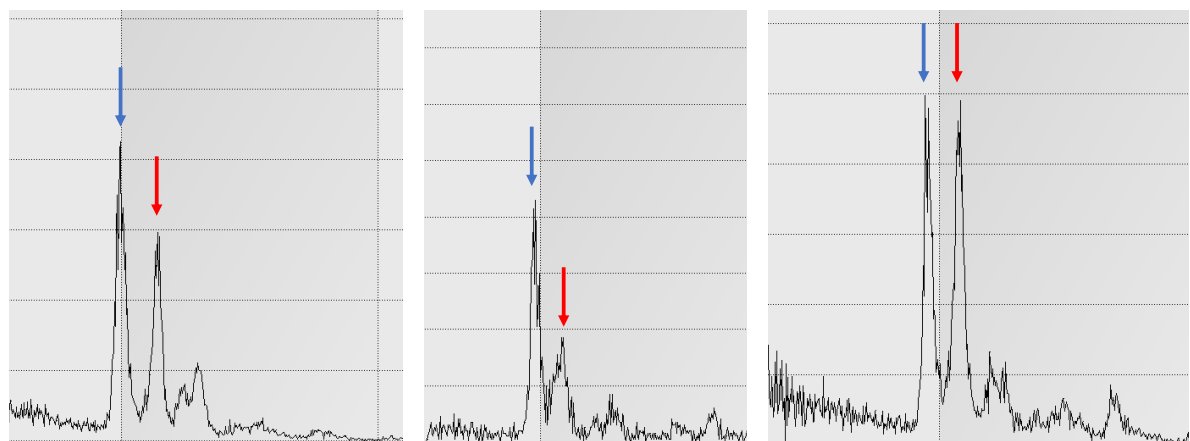


Figure S2. Traces of three flow cytometry replicates comparing *A. bilineata* (red arrows) to *D. melanogaster* (blue arrows).

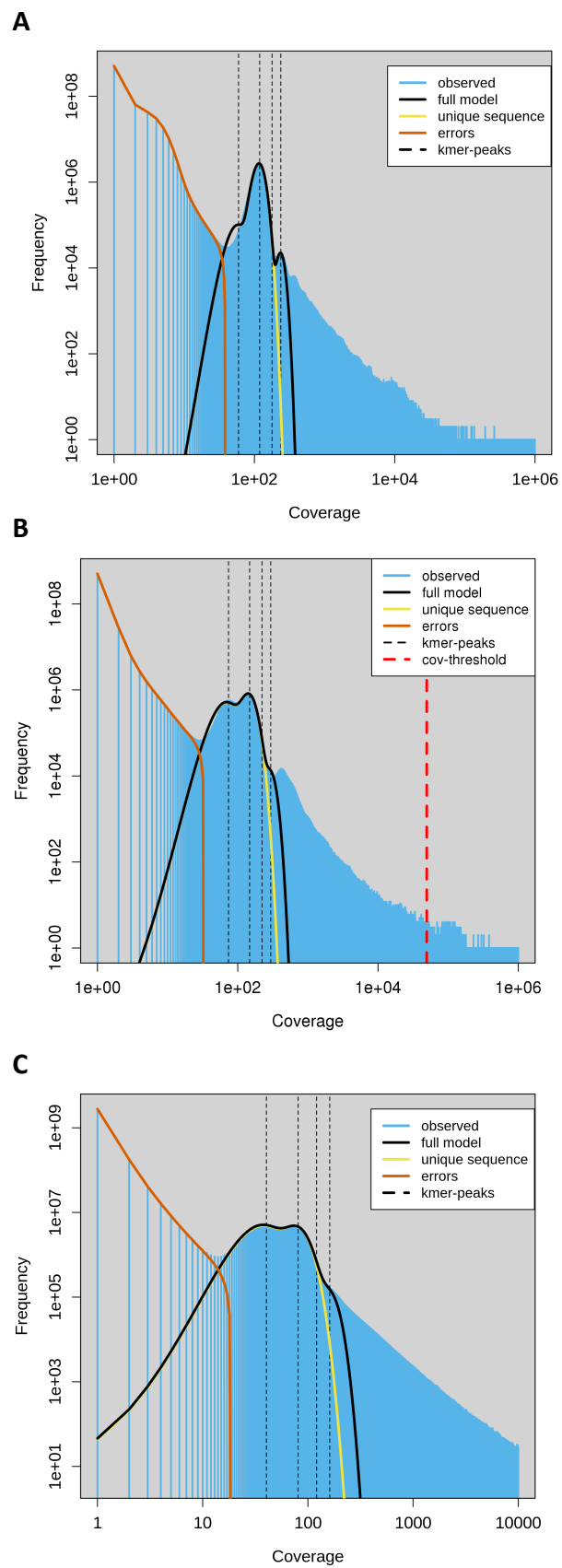


Figure S2. K-mer profiles generated from sequence data using GenomeScope for (A) *G. legneri*, (B) *A. bilineata* and (C) *P. maculata*.

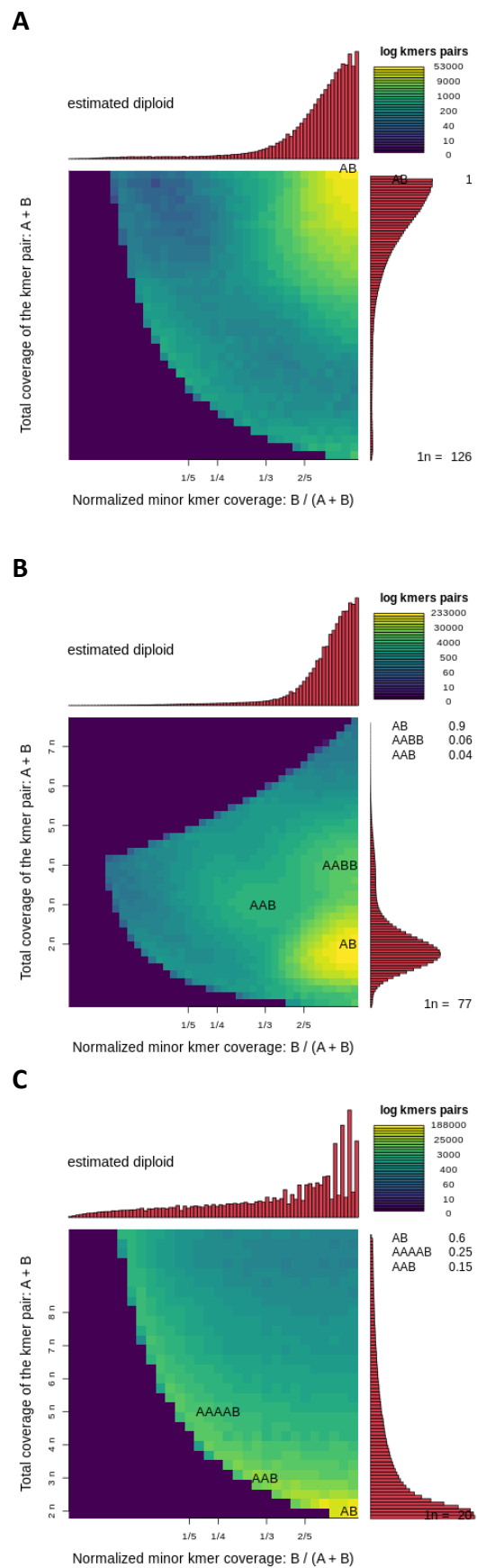


Figure S3. Results of Smudgeplot analysis for *A. bilineata* sequence data for (A) *G. legneri*, (B) *A. bilineata* and (C) *P. maculata*.