Supplementary information

Title: *De novo* Assembly of the *Brugia malayi* Genome Using Long Reads from a Single MinION Flowcell

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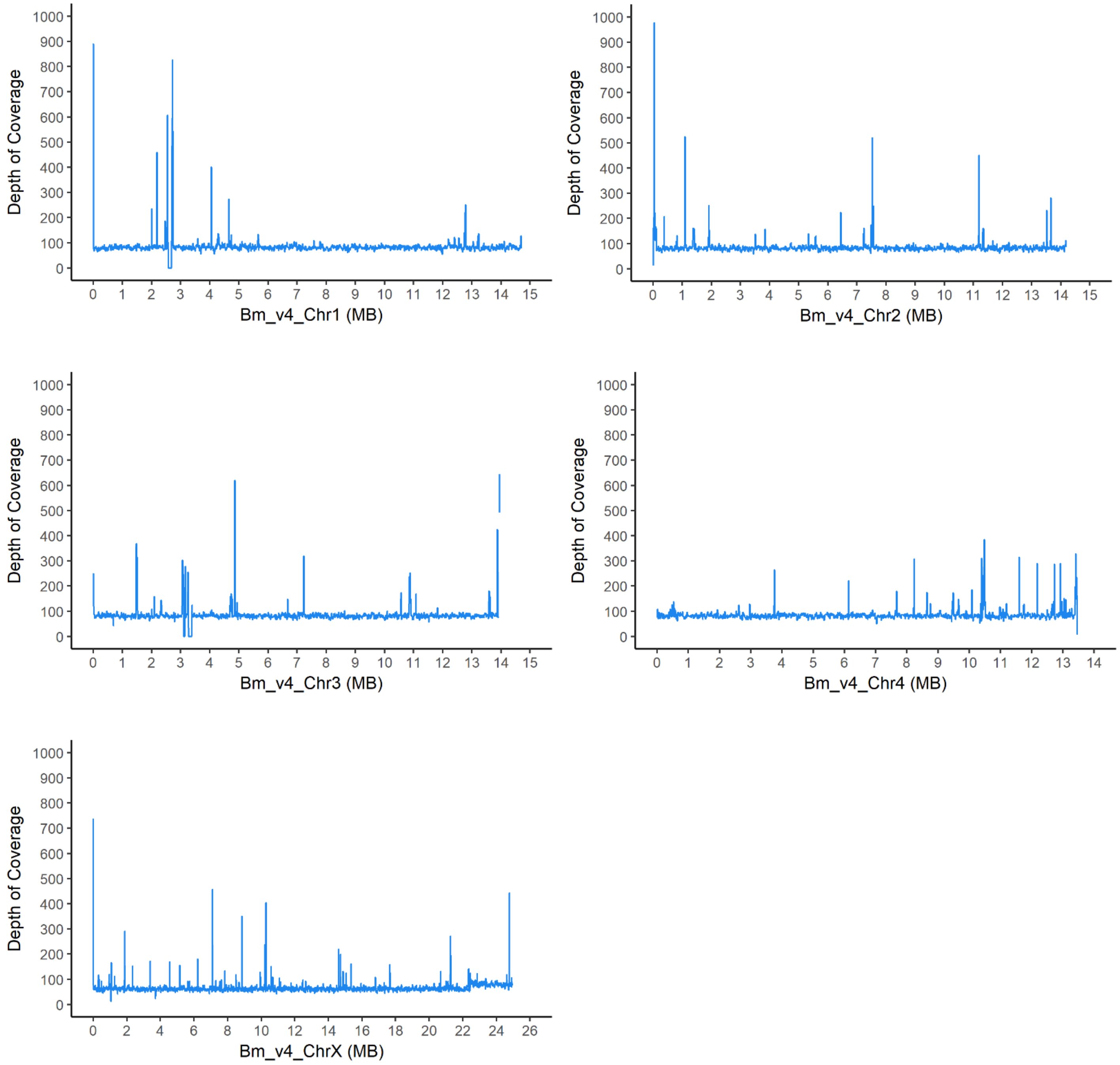
Supplementary Figure 1- Depth of coverage across each major contig in the reference genome, mitochondrial genome, and wBM genome.

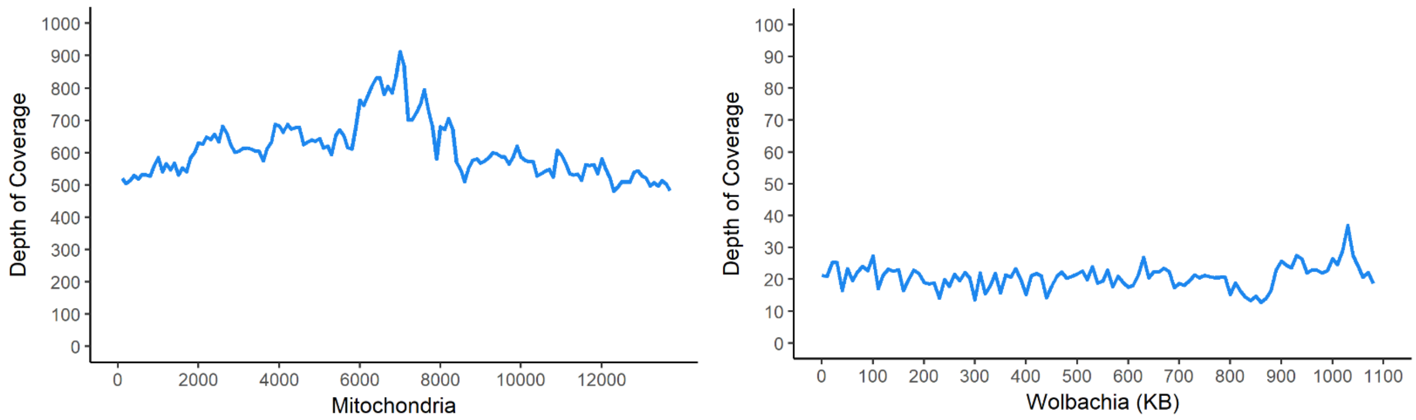
Supplementary Figure 2- Percent nucleotide identity of reads covering greater than 90% of the mitochondrial genome

Supplementary File 1- Gene features identified in areas of no coverage in the reference genome.

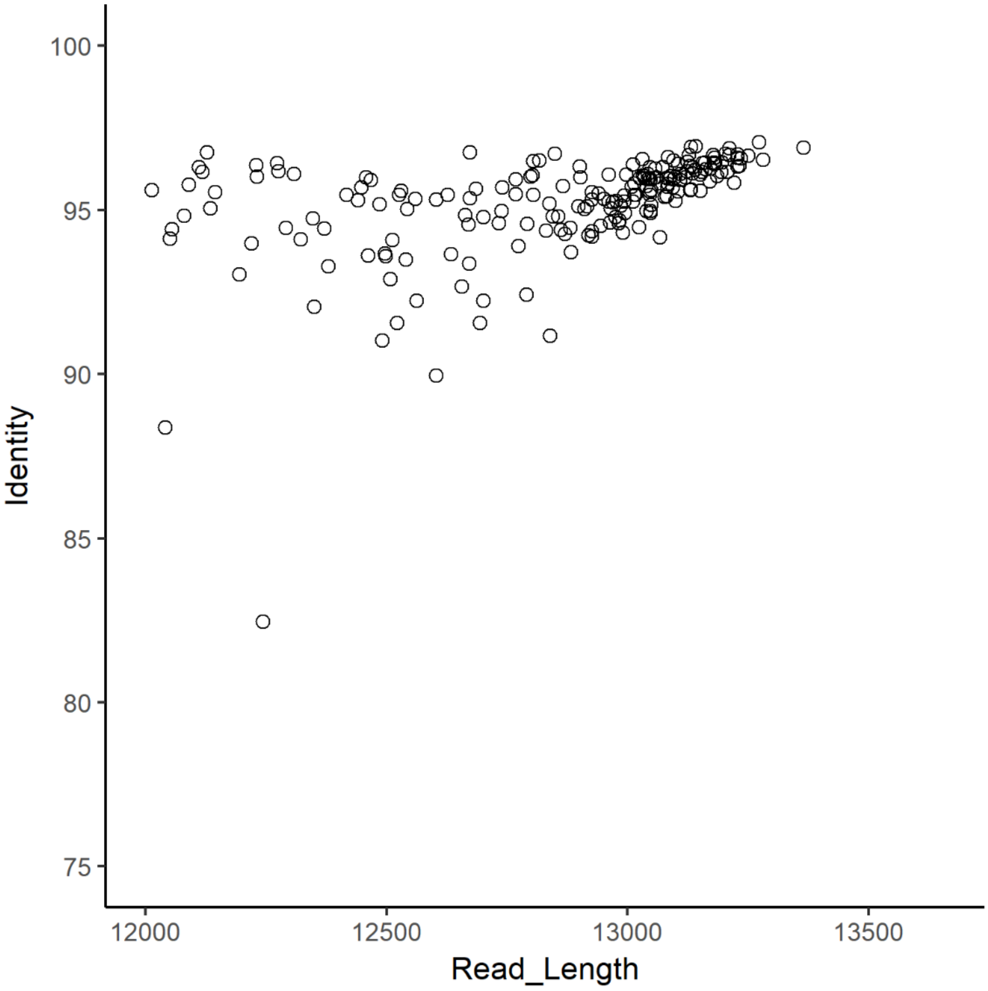
Supplementary Figure 1



Supplementary Figure 1 continued



Supplementary Figure 2



Supplementary Table 1: Assembly mismatches compared to the reference genome

		ONT Assembly Pre-Polishing			ONT Assembly Post-Polishing		
Genome Segment	**Length (b.p.)**	**Total Mismatches**	**Mismatches per b.p.**	**Mismatches per 1kb**	**Total Mismatches**	**Mismatches per b.p.**	**Mismatches per 1kb**
Bm_v4_Chr1	14701151	198499	0.01	13.50	112895	0.008	7.68
Bm_v4_Chrm2	14214749	195689	0.01	13.77	111435	0.008	7.84
Bm_v4_Chr3	13951302	188196	0.01	13.49	103327	0.007	7.41
Bm_v4_Chr4	13467244	194188	0.01	14.42	110512	0.008	8.21
Bm_v4_ChrX	24943668	279625	0.01	11.21	146124	0.006	5.86
Remaining contigs	5877599	65291	0.01	11.11	46229	0.008	7.87
5 Major Contigs	81278114	1056197	0.01	12.99	584293	0.007	7.19
Nuclear Genome	87155713	1121588	0.01	12.87	630522	0.007	7.23

Supplementary Table 2: BUSCO/CDS Statistics for Reference and MinION Assemblies

BUSCOs (N=303)	Reference Assembly	Canu_Filtlong Assembly	Canu_Filtlong_Polished
Complete and single-copy BUSCOs	289	262	277
Complete and duplicated BUSCOs	4	0	2
Fragmented BUSCOs	1	24	11
Missing BUSCOs	9	17	13
Total BUSCOs identified	294	286	290
Proportion of BUSCOs identified	97.00%	94.40%	95.71%
Avg CDS Length (b.p.) per shared BUSCO*	133.7	106.8	120
Avg Number of CDS per shared BUSCO	9.6	10.5	10.5

*- The assemblies shared a total of 160 complete single-copy BUSCOs