

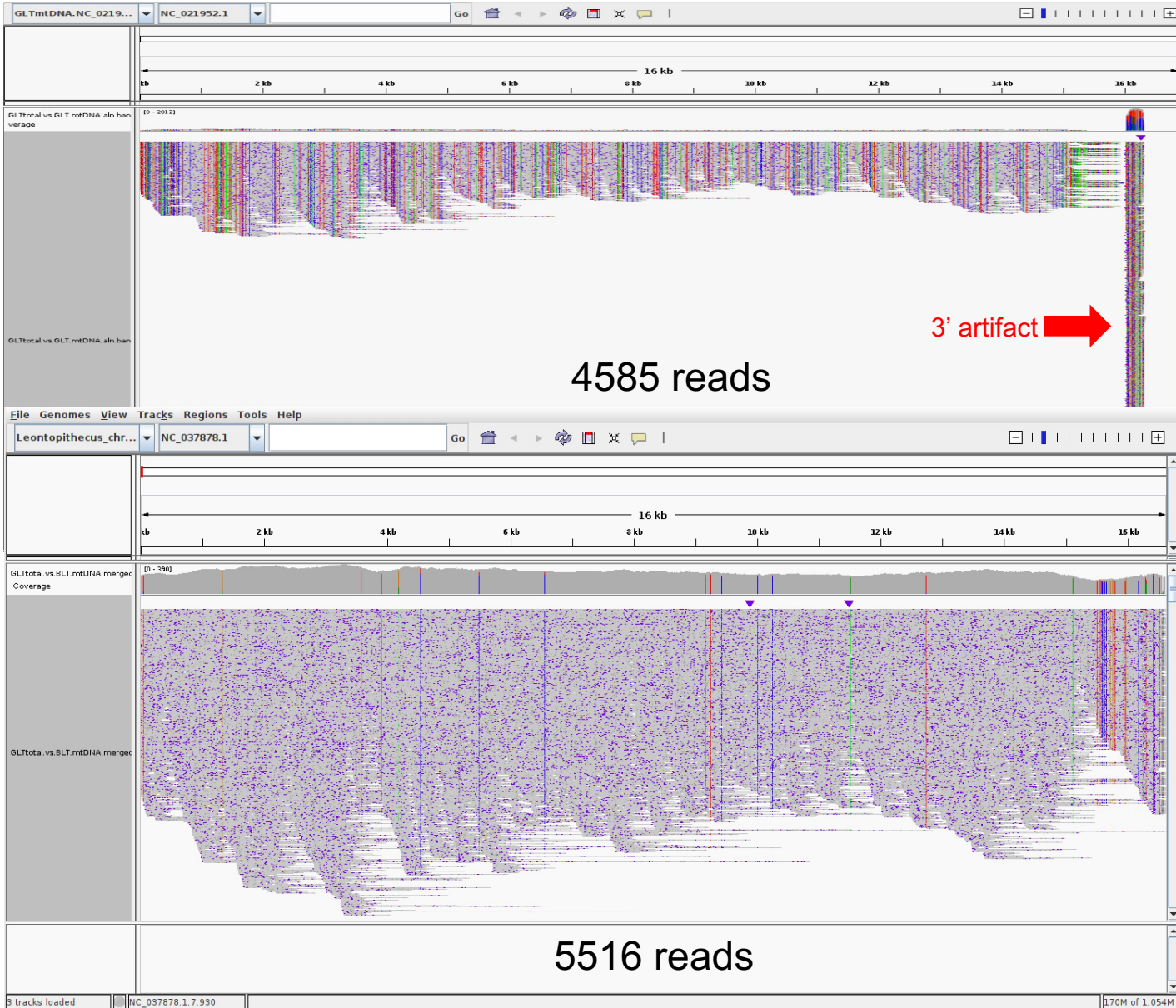


Fig S1. Alignment of reads to *L. rosalia* from the first 24 hr run to the reference mitogenome (KC757399) has 96.83% contig identity over 92% of its length, with 5' gaps (top). Alignment to *L. chrysopygus* reference (NC_037878) improves to 99% with complete coverage over the full length (bottom). The 5516 reads are combined from 2810 (1st run) and 2706 (2nd run).