

Supplementary information

The genome of medicinal leech (*Whitmania pigra*) and comparative genomic study for exploration of bioactive ingredients

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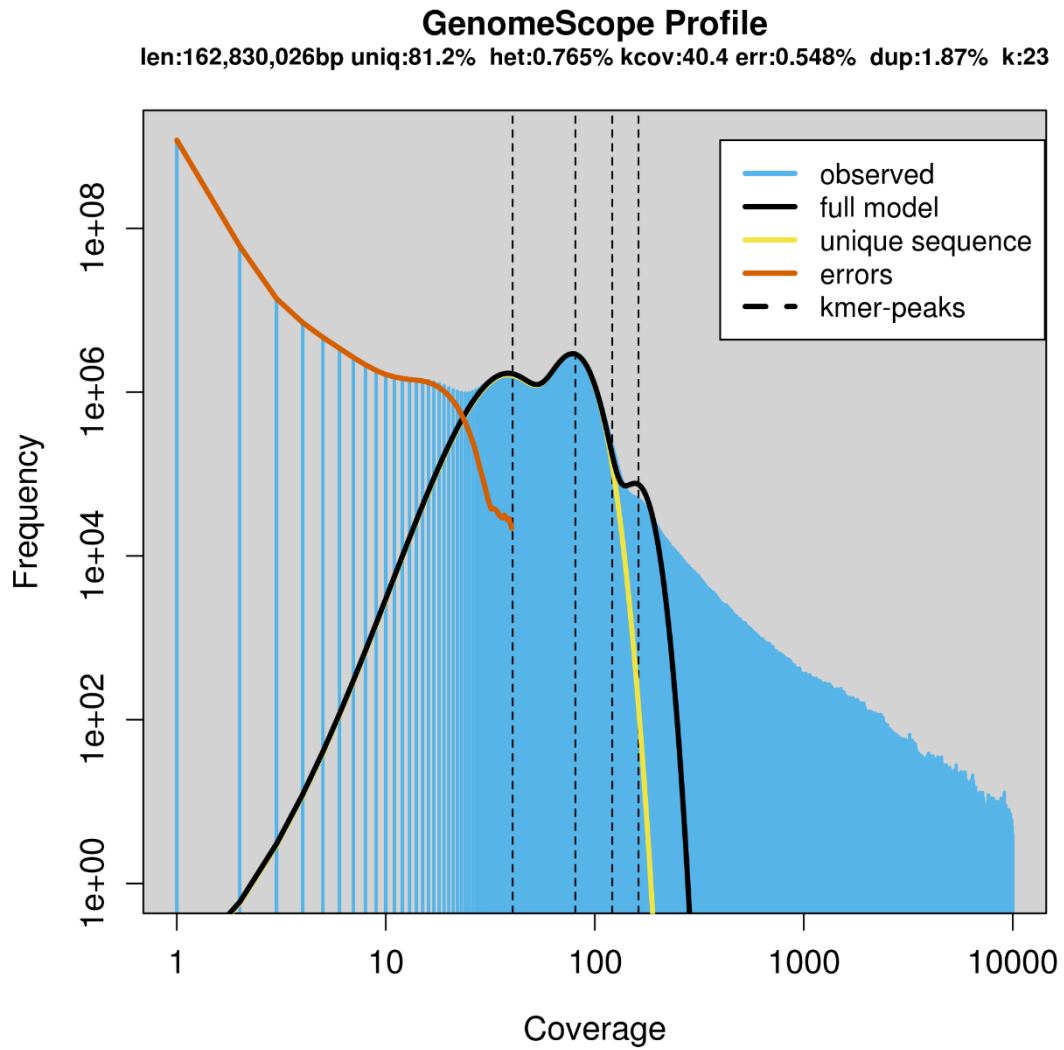


Figure S1. GenomeScope Analysis of the 23-mers for *W. Pigra* genome sequencing data. Estimate of the heterozygous portion is 0.765%. The estimated genome size of *W. Pigra* was ~ 162 Mbp

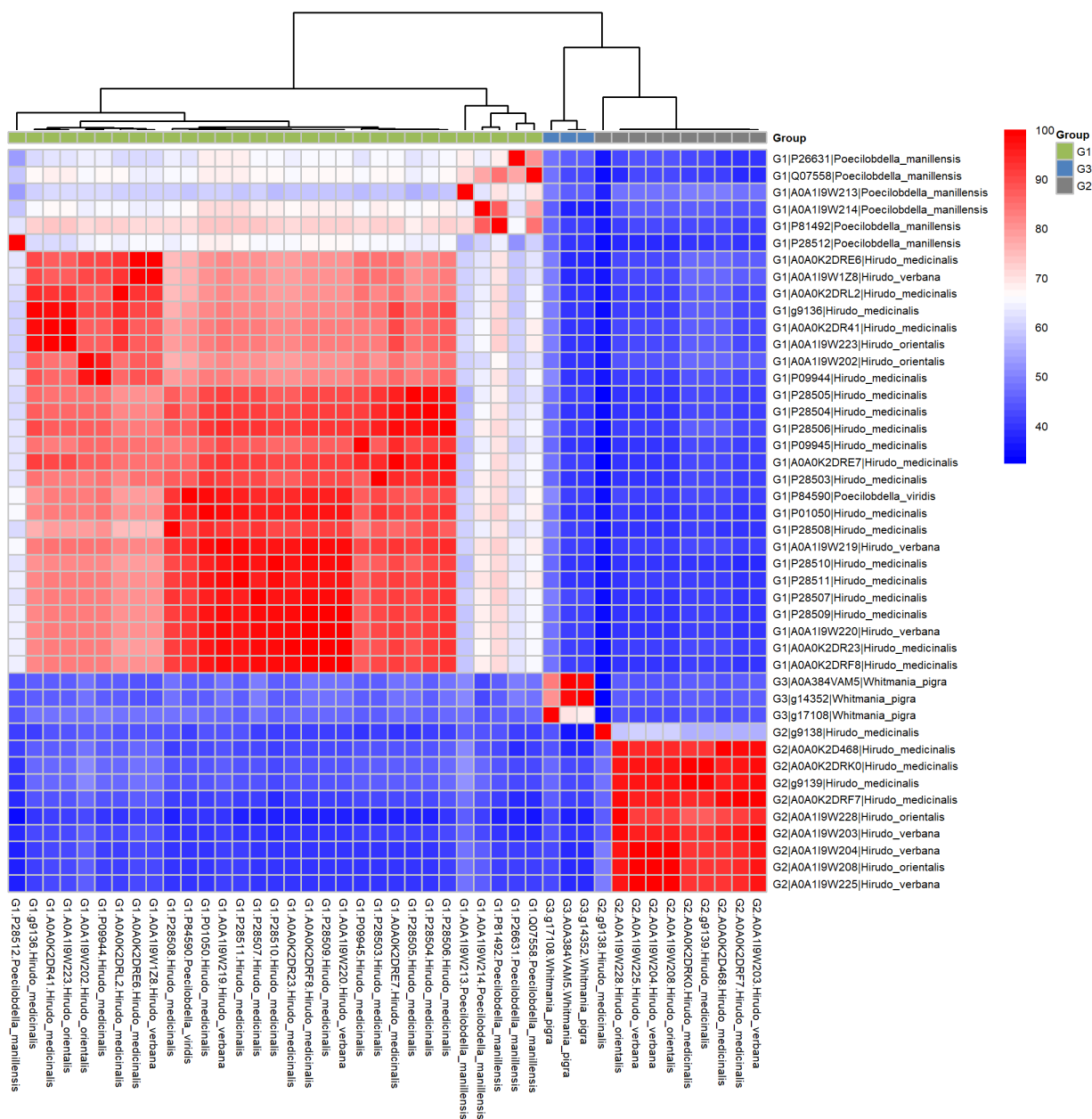


Figure S2. The heatmap displays the pairwise similarities values among the Hirudin sequences in **Figure 4**. The Hirudin sequences belong to G1, G2, G3, respectively. Within the group, the pairwise similarities of Hirudins are more than 60%. In contrast, in different groups, the pairwise similarities of Hirudins are between 30% and 60%. Whether between G2 and G1 or between G3 and G1, the pairwise similarities are always below 60%.