

The assembly was made up of 230 sequences, with 130,056 more bases than the reference sequence. Of these 99.98% align with the reference sequence. 154 alignments were made, with an average length of 12,000 bases. There are 21 SNPs and 3 GSNPs. Additionally, there are 45 Indels and 21 GIndels. There are 20637 contigs, with an average size of 893. The graph below shows individual alignments made (not in sequence order). While the alignment did well, many of the sections are in reverse order. From all these results, it appears the assembly was not successful.

