|  |  |  |  |
| --- | --- | --- | --- |
| **Assembly statistics\*** | **Short read**† | **Long read** ‡ | **Hybrid**§ |
| Number of contigs | 554 | 4 | 33 |
| Total length (bp) | 4314964 | 4703397 | 4865484 |
| Reference length (bp) | 4788855 | 4788855 | 4788855 |
| Number of misassembled contigs | 4 | 0 | 1 |
| Misassembled contigs length (bp) | 47430 | 0 | 4742328 |
| Genome fraction of reference (%) | 89.969 | 98.247 | 99.815 |
| Largest alignment (bp) | 60767 | 2669051 | 3233973 |
| Total aligned length (bp) | 4308655 | 4703397 | 4826756 |
|  |  |  |  |

∗ Assembly was done using Unicycler and SH-ancestor was used as the reference genome (4,788,855 bp)

† Illumina short technology was used for sequencing.

‡ PacBio long read sequencing technology was used.

§ Illumina short reads and PacBio long reads were combined.