**Table S1. Comparison between draft genome assemblies obtained by the different tools.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **Platanus 1.2.4** | **SOAPdenovo2** | **MaSuRCA 3.3.3** | **wtdbg 2.5** | **Flye 2.6** |
| **Total sequence length** | 1,272,133,741 | 981,942,849 | 1,609,244,920 | 1,390,813,883 | 1,505,080,485 |
| **No. of contigs** | 879,520 | 848,801 | 23,717 | 16,291 | 23,552 |
| **contigs > 10000 bp** | 1,947 | 292 | 18,340 | 12,288 | 18,725 |
| **Largest contig** | 29,328 | 20,266 | 1,951,786 | 1,581,874 | 1,244,054 |
| **Contig N50** | 1,818 | 1,308 | 172,678 | 222,260 | 117,519 |
| **Contig L50** | 194,857 | 215,144 | 2,483 | 1,789 | 3,522 |
| **GC content (%)** | 40.86 | 40.70 | 40.87 | 40.66 | 40.69 |
| **BUSCO complete** |  |  | 91.6% (S:78.0%; D:13.6%) | 91.7% (S:83.9%; D:7.8%) | 91.0% (S:79.4%; D:11.6%) |
| **BUSCO fragmented** |  |  | 2.0% | 2.4% | 2.8% |
| **BUSCO missing** |  |  | 6.4% | 5.9% | 6.2% |