|  |  |  |  |
| --- | --- | --- | --- |
| **Type** | **Initial Genome** | **Polished Genome** | **Ultimate Genome** |
| Genome size (bp) | 1,217,613,942 | 1,223,597,352 | 945,583,264 |
| Number of contigs | 2,474 | 2,474 | 967 |
| N50 contig length (bp) | 1,338,548 | 1,343,606 | 1,645,408 |
| TGS Coverage Raito (%) | / | 100.00 | 100.00 |
| NGS Coverage Raito (%) | / | 100.00 | 100.00 |
| Number of Homo SNP | / | 20,573 | 21,743 |
| Number of Homo Indel | / | 32,871 | 32,171 |
| Error rate by homo variants (%) | / | 0.00533 | 0.005702 |
| Accuracy of genome (%) | / | 99.99467 | 99.994298 |
| BUSCO | / | 97.20 | 95.36 |

Table 1. Statistics of genome assembly and assessment

Table 2. Result of all predicted genes compared with five databases

|  |  |  |
| --- | --- | --- |
| Database | Gene Number | Annotation Ratio / % |
| KOG | 17,388 | 61.36 |
| KEGG | 16,205 | 57.18 |
| NR | 26,411 | 93.2 |
| SwissProt | 24,886 | 87.82 |
| GO | 18,122 | 63.95 |
| Total Gene Number | 28339 | - |
| Overall Annotated Gene | 27,817 | 98.16 |