**Table S1** Statistical results for Oxford Nanopore Technology’s sequencing data

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Data type** | **SeqNum** | **SumBase** | **N50Len** | **N90Len** | **MeanLen** | **MaxLen** | **MeanQual** |
| Raw\_data | 1,204,217 | 8,861,673,022 | 13,927 | 3,288 | 7,358 | 144,872 | 8.89 |
| Clean\_data | 842,473 | 8,244,475,872 | 14,418 | 4,356 | 9,786 | 134,093 | 9.02 |

**Table S2** Summary of the mapping results.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Library | Mapped(%) | Properly mapped(%) | Coverage(%) | Depth(X) |
| 350bp | 81.72 | 78.74 | 98.74 | 91.85 |

**Table 3** Summary of BUSCO evaluation results.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Complete BUSCOs(C) | Complete and single-copy BUSCOs(S) | Complete and duplicated BUSCOs(D) | Fragmented BUSCOs(F) | Missing BUSCOs(M) | Total Lineage BUSCOs |
| 267 (92.07%) | 258 (88.97%) | 9 (3.10%) | 8 (2.76%) | 15 (5.17%) | 290 |

**Table S4** Summary of Hi-C auxiliary assembly results

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Read Pairs Number | Base Number | GC content (%) | Q20 ratio (%) | Q30 ratio (%) |
| 39,539,679 | 11,808,003,574 | 53.12 | 97.24 | 92.39 |

**Table S5** Statistics of mapping results between Hi-C library and genome

|  |  |  |
| --- | --- | --- |
| Mapping Type | Number | Ratio（%） |
| Total Read Pairs | 39,539,679 | 100 |
| Mapped Reads | 71,824,112 | 90.83 |
| Unique Mapped Read Pairs | 24,609,611 | 62.24 |

**Table S6** Statistics of each type of Hi-C sequencing data

|  |  |  |
| --- | --- | --- |
| Type | Number | Ratio（%） |
| Unique Paired Alignments | 24,609,611 | 100 |
| Valid Interaction Pairs | 21,328,573 | 86.67 |
| Dangling End Pairs | 2,494,100 | 10.13 |
| Re-ligation Pairs | 487,628 | 1.98 |
| Self-cycle Pairs | 53,489 | 0.22 |
| Dumped Pairs | 245,821 | 1 |

**Table S7** Statistical results of genomic repeat sequencing

|  |  |  |  |
| --- | --- | --- | --- |
| **Type** | **Number** | **Length (bp)** | **Percentage (%)** |
| ClassI | 4,350 | 4,599,659 | 11.11 |
| ClassI/DIRS | 53 | 72,803 | 0.18 |
| ClassI/LINE | 34 | 20,635 | 0.05 |
| ClassI/LTR | 7 | 2,986 | 0.01 |
| ClassI/LTR/Copia | 863 | 1,033,608 | 2.50 |
| ClassI/LTR/Gypsy | 1,866 | 2,184,684 | 5.28 |
| ClassI/PLE|LARD | 1,494 | 1,239,886 | 2.99 |
| ClassI/TRIM | 29 | 78,132 | 0.19 |
| ClassI/Unknown | 4 | 13,793 | 0.03 |
| ClassII | 1,420 | 727,422 | 1.76 |
| ClassII/Helitron | 110 | 57,207 | 0.14 |
| ClassII/MITE | 979 | 365,998 | 0.88 |
| ClassII/Maverick | 13 | 26,232 | 0.06 |
| ClassII/TIR | 309 | 276,291 | 0.67 |
| ClassII/Unknown | 9 | 1,821 | 0.00 |
| PotentialHostGene | 82 | 361,311 | 0.87 |
| SSR | 14 | 1,561 | 0.00 |
| Unknown | 3,110 | 1,880,488 | 4.54 |
| Total | 5,866 | 7,234,336 | 17.47 |

**Table S8** The number of protein coding genes supported by de novo, transcriptome data and homology prediction

| **Method** | **Software** | **Species** | **Gene number** |
| --- | --- | --- | --- |
| Ab initio based | Augustus |  | 9,433 |
| Genscan |  | 7,184 |
| GeneID |  | 13,463 |
| GlimmerHMM |  | 12,444 |
| SNAP |  | 11,193 |
| RNA-seq based | PASA |  | 16,570 |
| TransDecoder |  | 34,952 |
| Homology based | GeMoMa | Laetiporus sulphureus | 9,403 |
| Sparassis crispa | 13,876 |
| Dichomitus squalens | 8,556 |
| Integration | EVM |  | 13,103 |

**Table S9** Basic information for genes.

|  |  |
| --- | --- |
| GeneNum | 13103 |
| Genelen | 24672670 |
| AveGenlen | 1882.98 |
| ExonLen | 19381226 |
| AveExonLen | 238.51 |
| ExonNum | 81260 |
| AveExonNum | 6.2 |
| CDSLen | 17464707 |
| AveCDSlen | 220.98 |
| CDSNum | 79033 |
| AveCDSNum | 6.03 |
| IntronLen | 5291444 |
| AveIntronLen | 77.64 |
| IntronNum | 68157 |
| AveIntronnum | 5.2 |

**Table S10** Summary of gene function annotations

|  |  |  |  |
| --- | --- | --- | --- |
| **Database** | **Number** | **100<=length<300** | **length>=300** |
| GO\_Annotation | 3,341 | 824 | 2,443 |
| KEGG\_Annotation | 3,497 | 940 | 2,459 |
| KOG\_Annotation | 5,608 | 1,359 | 4,167 |
| Pfam\_Annotation | 7,344 | 1,808 | 5,403 |
| Swissprot\_Annotation | 5,967 | 1,407 | 4,442 |
| TrEMBL\_Annotation | 11,187 | 3,297 | 7,558 |
| nr\_Annotation | 11,252 | 3,340 | 7,576 |
| All\_Annotated | 11,281 | 3,355 | 7,586 |

**Table S11** Statistics of non-coding RNAs

|  |  |  |
| --- | --- | --- |
| **RNA classify** | **Number** | **Family Number** |
| rRNA | 75 | 4 |
| tRNA | 126 | 48 |
| other ncRNA | 36 | 14 |

**Table 1****2** Statistics of Pesudogene

|  |  |  |
| --- | --- | --- |
| **Pesudogene number** | **Pesudogene size (bp)** | **Average Pesudogene Length (bp)** |
| 452 | 971,967 | 2,150.36 |