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| **Table S1**. Major features of the genome of *Inocybe terrigena.* |
| Number of scaffolds | 2262 |   |
| Total size of scaffolds | 26127495 |  |
| Longest scaffold | 241864 |  |
| Shortest scaffold | 170 |  |
| Number of scaffolds > 1K nt | 1895 | 83.80% |
| Number of scaffolds > 10K nt | 670 | 29.60% |
| Number of scaffolds > 100K nt | 13 | 0.60% |
| Number of scaffolds > 1M nt | 0 | 0.00% |
| Number of scaffolds > 10M nt | 0 | 0.00% |
| Mean scaffold size | 11551 |  |
| Median scaffold size | 4105 |  |
| N50 scaffold length | 30623 |  |
| L50 scaffold count | 239 |  |
| scaffold %A | 27.14 |  |
| scaffold %C | 22.85 |  |
| scaffold %G | 22.85 |  |
| scaffold %T | 27.16 |  |
| scaffold %N | 0 |  |
| scaffold %non-ACGTN | 0 |  |
| Number of scaffold non-ACGTN nt | 0 |  |
|  |  |  |
| Percentage of assembly in scaffoldedcontigs | 0.00% |  |
| Percentage of assembly in unscaffoldedcontigs | 100.00% |  |
| Average number of contigs per scaffold | 1 |  |
| Average length of break (>25 Ns) between contigs in scaffold | 0 |  |
|  |  |  |
| Number of contigs | 2262 |  |
| Number of contigs in scaffolds | 0 |  |
| Number of contigs not in scaffolds | 2262 |  |
| Total size of contigs | 26127495 |  |
| Longest contig | 241864 |  |
| Shortest contig | 170 |  |
| Number of contigs> 1K nt | 1895 | 83.80% |
| Number of contigs> 10K nt | 670 | 29.60% |
| Number of contigs> 100K nt | 13 | 0.60% |
| Number of contigs> 1M nt | 0 | 0.00% |
| Number of contigs> 10M nt | 0 | 0.00% |
| Mean contig size | 11551 |  |
| Median contig size | 4105 |  |
| N50 contig length | 30623 |  |
| L50 contig count | 239 |  |
| contig %A | 27.14 |  |
| contig %C | 22.85 |  |
| contig %G | 22.85 |  |
| contig %T | 27.16 |  |
| contig %N | 0 |  |
| contig %non-ACGTN | 0 |  |
| Number of contig non-ACGTN nt | 0 |   |