**Table S1. Genome statistics of *M. haptotylum*.**

|  |  |
| --- | --- |
| General features | Valuesa |
| Total number of reads assembled | Shotgun XLR70: 2.1×106Paired end: 1.0×106 |
| Size (Mb) | 40.4 |
| GC content | 45.24 |
| Coverage | 28x |
| Number of scaffolds | 1279 |
| Mean scaffold size (bp) | 67,560 |
| N50 scaffold size (kb) | 194  |
| Largest scaffold size (kb) | 937  |
| Number of scaffolds >3 kb | 25 |
| Number of scaffolds >2 kb  | 28 |
| Number of scaffolds >1 kb | 83 |
| Contigs | 1,543  |
| Largest contig (kb) | 818  |
| N50 contig size (kb) | 177 |
| Number of contigs >2 kb  | 49 |
| Number of contigs >1 kb  | 85 |
| Number of predicted gene models | 10,965 |
| Total number of exons  | 36,272 |
| Average length of the exons (bp) | 469 |
| Number of single exon genes | 2,336 |
| Average length of introns (bp) | 108.60 |
| Total number of gaps  | 34,178 |
| Total number of tRNA genes | 149 |

aValues were calculated using the Eval software [1]

1 Keibler E, Brent MR (2003) Eval: a software package for analysis of genome annotations. BMC Bioinformatics 4: 50.