Table S1. Main assembly summary assessed with QUAST tool in four *de novo* assemblers used to reconstruct the genome of *Metarhizium* *humberi* ESALQ1638.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Metrics *de novo* assemblers** | **ESALQ1638** | | | |
| **CLC** | **SOAPdenovo2** | **SPAdes** | **IDBA-UD** |
| Genome assembly size (Mb) | 38.07 | 39.30 | 38.38 | 38.33 |
| Number of contigs | 2034 | 7157 | 1990 | 1085 |
| Number of scaffolds\* | 1212 | 291 | 1887 | 1076 |
| Number of Large Scaffolds (>100 kb) | 90 | 19 | 30 | 44 |
| Number of Large Scaffolds (>1 Mb) | 6 | 9 | 11 | 12 |
| Longest scaffold (Mb) | 1.80 | 7.15 | 4.91 | 3.87 |
| N50 scaffold length (Mb) | 0.46 | 3.66 | 2.26 | 1.40 |
| L50 scaffold count | 22 | 4 | 6 | 9 |
| G+C content (%) | 50.71 | 50.08 | 50.19 | 49.84 |
| **Mismatches** |  |  |  |  |
| N's | 449.590 | 1.177.903 | 222.424 | 6.212 |
| N's per 100 kbp | 1180.74 | 2996.85 | 579.41 | 16.14 |

\*≥ 200 nucleotides

Table S2. The Geographical origin and the host/substrate from each *Metarhizium* strain

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| *Metarhizium* species and strains | Host/ substrate | Geographic origin |
| *M. anisopliae* BRIP53293 | Soil | Australia - Queensland |
| *M. anisopliae* ARSEF549 | Recilia dorsalis [Homoptera: Cicadellidae] | Philippines |
| *M. anisopliae* E6 | Deois flavopicta [Homoptera: Cercopidae] | Brazil - Espirito Santos |
| *M. robertsii* ARSEF23 | Conoderus sp. [Coleoptera: Elateridae] | USA - North Carolina |
| *M. brunneum* ARSEF3297 | Boophilus sp. [Acari: Ixodidae] | Mexico |
| *M. guizhouense* ARSEF977 | Melolontha melolontha [Coleoptera: Scarabaeidae] | France |
| *M. majus* ARSEF297 | Xyloryctes jamaicensis [Coleoptera: Scarabaeidae] | Western Samoa: Apia |
| *M. acridum* CQMa102 | Ceracris kiangsu [Orthoptera: Acrididae] | China |
| *M. album* ARSEF1941 | Nephotettix virescens [Hemiptera: Cicadellidae] | Philippines: Roxas, Palawan |
| *M. rileyi* RCEF4871 | Noctuidae | China- Shandong |