**Supplementary Table 1. Runtimes for alignment of whole-genome assemblies**

Pairwise alignments:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Microbial genome:** | **Size** | **Microbial genome:** | **Size** | **Runtime** |
| Bartonella bacilliformis KC583 | 1.4Mb | Bartonella Quintana st r. Toulouse | 1.6Mb | 7 min |
| Bartonella bacilliformis KC583 | 1.4Mb | Bartonella henselae str. Houston-1 | 1.9Mb | 8 min |
| Bartonella henselae str. Houston-1 | 1.9Mb | Bartonella - tribocorum CIP 105476 plasmidBtr | 2.6Mb | 31 min |
|  |  |  |  |  |
| **Yeast genome**: Candida tenuis | 10.7Mb | **Yeast genome:** Spathaspora assalidarum | 13.3Mb | 1 h. 52 min |
| **Fungal genome:** Batrachochytrium dendrobatidis JAM81 | 30Mb | **Fungal genome:** Piromyces sp. E2 | 71Mb | 7 h. 13 min |
| **Fungal genome:** Batrachochytrium dendrobatidis JAM81 | 30Mb | **Fungal genome:** Batrachochytrium dendrobatidis JEL423 | 23.7Mb | 7 h. 30 min |

 Multiple alignment of microbial genomes:

Acetobacter pasteurianus IFO 3283-07 (2.9Mb)

Acetohalobium arabaticum DSM 5501 (2.5Mb)

Coprococcus sp. ART55/1 (3.1Mb)

Runtime: 4 h.10 min.