|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Species** | **# CDS** | **CDS Length** | **# Chr** | **Genome Length** | **CDS Density** |
| *Bacillus subtilis* | 4325 | 3731178 | 1 | 4,215,606 | 88.5% |
| *Cryptococcus neoformans* | 6863 | 11110923 | 14 | 19,051,922 | 58.3% |
| *Enterococcus faecalis* | 2680 | 2529763 | 3 | 2,870,381 | 88.1% |
| *Escherichia coli* | 5289 | 4903813 | 3 | 5,594,605 | 87.7% |
| *Lactobacillus fermentum* | 2072 | 1819324 | 2 | 2,103,331 | 86.5% |
| *Listeria monocytogenes* | 2855 | 2627550 | 1 | 2,944,528 | 89.2% |
| *Pseudomonas aeruginosa* | 5571 | 5597565 | 1 | 6,264,404 | 89.4% |
| *Saccharomyces cerevisiae* | 6001 | 8799159 | 17 | 12,157,105 | 72.4% |
| *Salmonella enterica* | 4554 | 4295163 | 2 | 4,951,383 | 86.7% |
| *Staphylococcus aureus* | 2892 | 2399760 | 1 | 2,821,361 | 85.1% |

**Table S1. Genomic characteristics of Zymo Microbial Community Standard species NCBI reference genomes.** *# CDS* describes the total number of coding sequences identified in each assembly, *CDS Length* describes the total base pairs of CDS, *# Chr* identifies the quantity of chromosomes for each species, *Genome Length* defines the total number of base pairs in each assembly, and *CDS density* defines the ratio of CDS Length divided by Genome Length as a percentage.