**Supplementary File 1.** Sequencing depth statistics for MIC genome assemblies

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|  | ***Oxytricha trifallax*\*** | ***Tetmemena sp.*** | ***Euplotes woodruffi*** |
| Illumina coverage (X) | 118 | 69 | 190 |
| PacBio coverage (X) | 34 | 28 | 29 |
| Nanopore coverage (X) | - | - | 62 |

\*Sequencing data from Chen et al. (1).

\*\*Raw reads were mapped to the MIC genome assembly by Minimap2 and Bowtie2 (97). Average coverage was calculated with BBmap ([sourceforge.net/projects/bbmap/](http://sourceforge.net/projects/bbmap/)) pileup.sh for MDS-containing contigs in the MIC genome assembly.