

Illumina Short Read Assembly and Annotation (Eukaryotic)

Short read assembly was performed with Unicycler¹. Assembly statistics were recorded with QUAST². Assembly statistics are now available for all samples in the “*Assembly Metrics.tsv*” file. Samples were annotated with Funannotate³. Assembled and annotated genomes can be found in the “*SampleName.fasta*”, “*SampleName.gbk*”, and “*SampleName.gff*” files, respectively.

Tool	Version	Parameters
unicycler	0.5.0	default parameters
quast	5.2.0	default parameters
funannotate	1.8.15	interproscan and eggno mapper enabled

¹ Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads Wick RR, Judd LM, Gorrie CL, Holt KE (2017) Unicycler: Resolving bacterial genome assemblies from short and long sequencing reads. PLOS Computational Biology 13(6): e1005595.
<https://doi.org/10.1371/journal.pcbi.1005595>

² Alexey Gurevich, Vladislav Saveliev, Nikolay Vyahhi and Glenn Tesler. QUAST: quality assessment tool for genome assemblies, Bioinformatics (2013) 29 (8): 1072-1075. doi: 10.1093/bioinformatics/btt086

³ Palmer J (2017) Funannotate: Fungal genome annotation scripts.
<https://github.com/nextgenusfs/funannotate>