

Illumina Short Read Assembly and Annotation (Prokaryotic)

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 Bakta³. 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
bakta	1.8.1	default parameters; db version 5.0

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 Schwengers O., Jelonek L., Dieckmann M. A., Beyvers S., Blom J., Goesmann A. (2021). Bakta: rapid and standardized annotation of bacterial genomes via alignment-free sequence identification. *Microbial Genomics*, 7(11).