Nanopore Read Assembly and Annotation (Eukaryotic)

Porechop[1] was used to trim residual adapter sequence from the Oxford Nanopore Technology (ONT) reads that may have been missed during basecalling and demultiplexing. *De novo* genome assemblies were generated from the Oxford Nanopore Technologies (ONT) read data with Flye[2] under the nano-hq (ONT high-quality reads) model. Additional Flye options initiate the assembly by first using reads longer than an estimated N50 based on a genome size of 12Mbp.

Assembled genome sequences were annotated with funannotate[3]. Queried funannotate databases include: dbCAN, go, interpro, merops, mibig, pfam, repeats, and uniprot. Final assembly statistics were recorded with QUAST[4] and are reported in the "*Assembly Metrics.tsv*" file. The assembly and annotation files are "*SampleName.fasta*", "*SampleName.gff*", and "*SampleName.gbk*" respectively. A summary of the assembled contigs can be found in each sample's respective '*Contig Summary.tsv*' file.

Tool	Version	Parameters
porechop	0.2.4	default parameters
flye	2.9.2	--asm-coverage 50 --genome-size 12000000 --nano-hq
funannotate	1.8.15	interproscan and eggnog mapper enabled
quast	5.2.0	default parameters

---

[1] An open source software for the QC and adapter trimming of ONT technologies. https://github.com/rrwick/Porechop

[2] Mikhail Kolmogorov, Jeffrey Yuan, Yu Lin and Pavel Pevzner. Assembly of Long Error-Prone Reads Using Repeat Graphs. *Nature Biotechnology* (2019)

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

[4] Alexey Gurevich, Vladislav Saveliev, Nikolay Vyahhi and Glenn Tesler, QUAST: quality assessment tool for genome assemblies, *Bioinformatics* (2013) 29 (8): 1072-1075.