

## 1 May 17th 2018

### 1.1 Canu test with all reads of best qual that mapped to the MBELA01182 Illumina contig

The file from Canu\_tests/data 2018-05-17-MBELA01182\_nanopore\_reads\_subset.fastq was used to test canu.

Command used: `canu -p 2018-05-17-testMBELA01182 -d 2018-05-17-testMBELA01182 genomeSize`  
Script in `src/scripts/2018-05-17-MBELA01182_canu.script`  
Results in `results/2018-05-17-testMBELA01182`

### 1.2 Canu test with all reads of best qual

The file used from Canu\_tests/data 2018-05-17-Nanopore\_all\_reads\_best\_qual.fastq

Command used: `canu -p 2018-05-17-first_test_assembly -d 2018-05-17-first_test_assembly`  
Script in `src/scripts/2018-05-17-first_test_assembly.script`  
Results in `results/2018-05-17-first_test_assembly`

ABORTED because most of the reads were too short ,1000kb we will retry by changing this parameter

### 1.3 Canu test with all reads of best qual test 2 changing parameters

The file used from Canu\_tests/data 2018-05-17-Nanopore\_all\_reads\_best\_qual.fastq

Command used: `canu -p 2018-05-17-assembly_test_2 -d 2018-05-17-assembly_test_2 genomeSi`  
Script in `src/scripts/2018-05-17-assembly_test_2.script`  
Results in `results/2018-05-17-assembly_test_2` Job aborted

## 2 May 18th 2018

### 2.1 Removing *E.coli* reads from nanopore reads

*E. coli* contamination was removed from the nanopore reads 2018-05-17-Nanopore\_all\_reads\_best\_qual.f