Run Info

Host Name	**GXB02243 (localhost)**
Experiment Name	**GZFN211103**
Sample ID	**UL_DNA**
Run ID	**0caf19ef-7d95-443e-bff9-324a83ceec97**
Flow Cell Id	**FAO61000**
Start Time	**September 29, 10:30**
Run Length	**3d 0h 3m**

Run Summary

Reads Generated	**581.6 K**
Passed Bases	**10.56 Gb**
Failed Bases	**1.14 Gb**
Estimated Bases	**12.05 Gb**

Run Parameters

Flow Cell Type	**FLO-MIN106**
Kit	**SQK-RAD004**
Initial Bias Voltage	**-180 mV**
FAST5 Output	**Enabled**
FASTQ Output	**Enabled**
BAM Output	**Disabled**
Active Channel Selection	**Enabled**
Basecalling	**on**
Specified Run Length	**72 hours**
FAST5 Reads per File	**4000**
FAST5 Output Options	**zlib_compress,fastq,raw**
FASTQ Reads per File	**4000**
Mux Scan Period	**6 hours**
Reserved Pores	**0 %**
Basecall Model	**High-accuracy basecalling**
Read Filtering	**min_qscore=7**

Versions

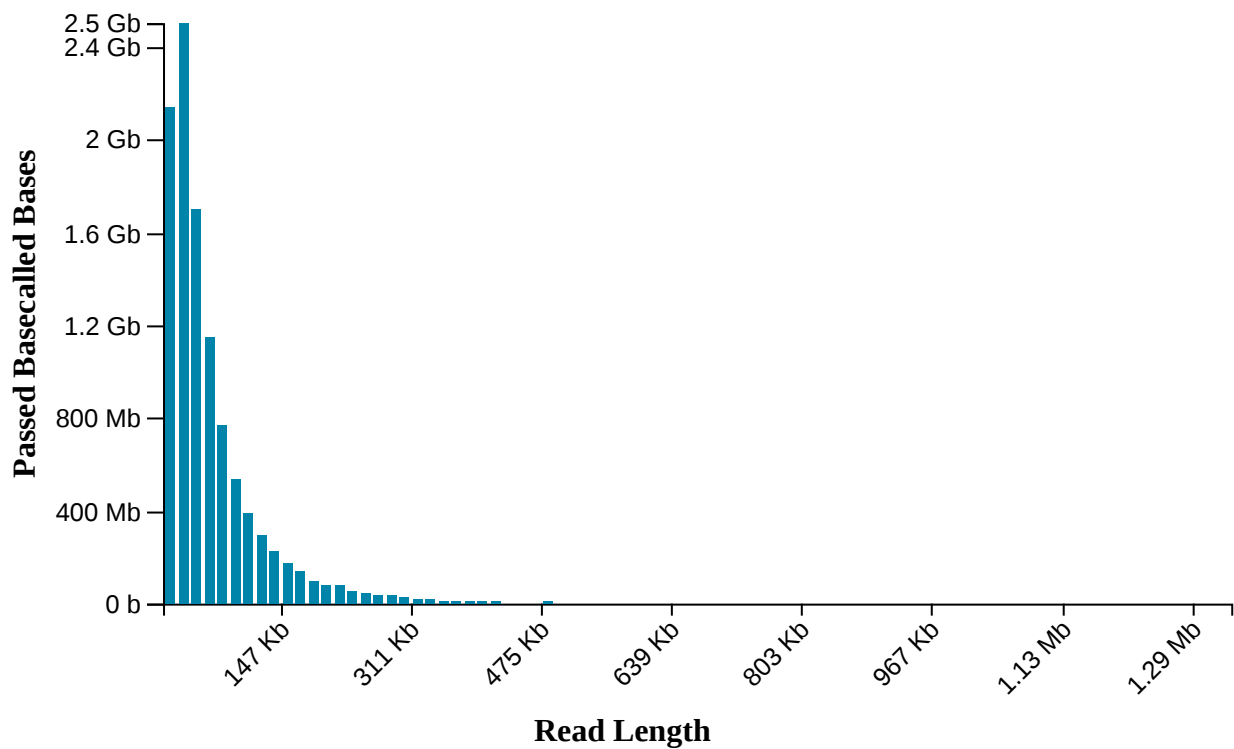|	
MinKNOW	**20.06.9**
MinKNOW Core	**4.0.3**
Bream	**6.0.7**
Guppy	**4.0.11**

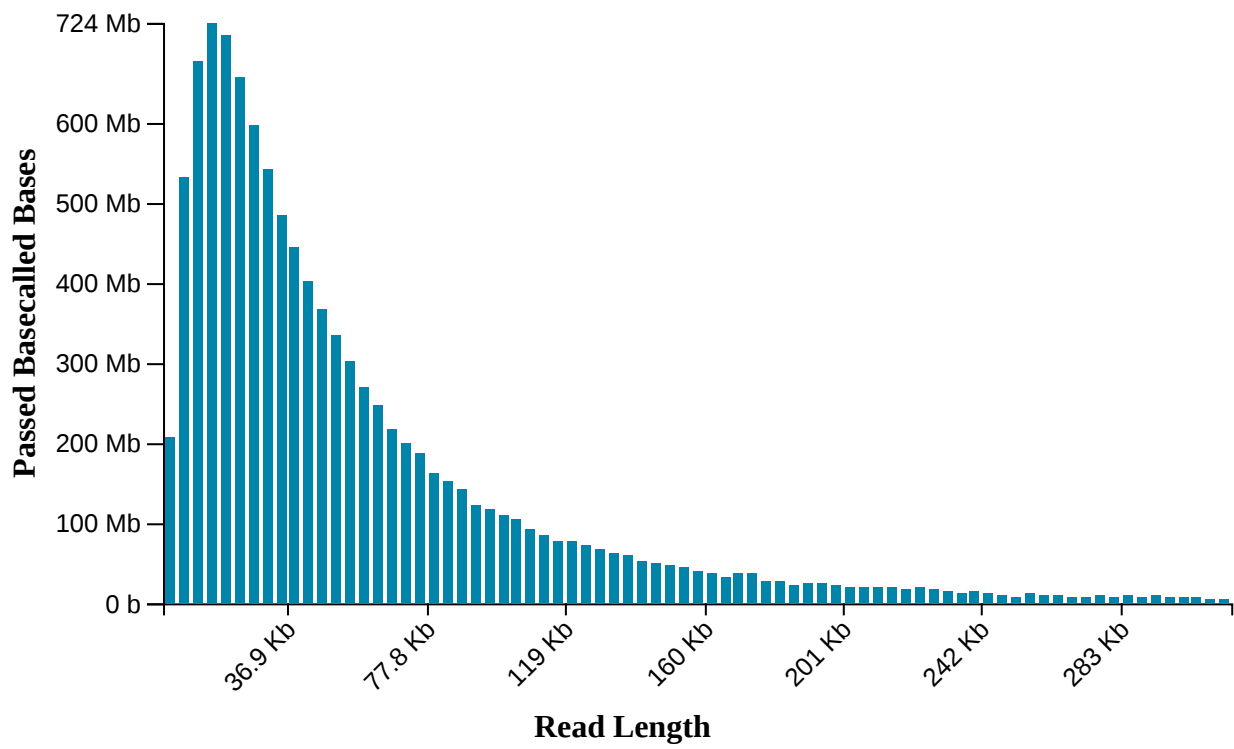## Cumulative Output Reads
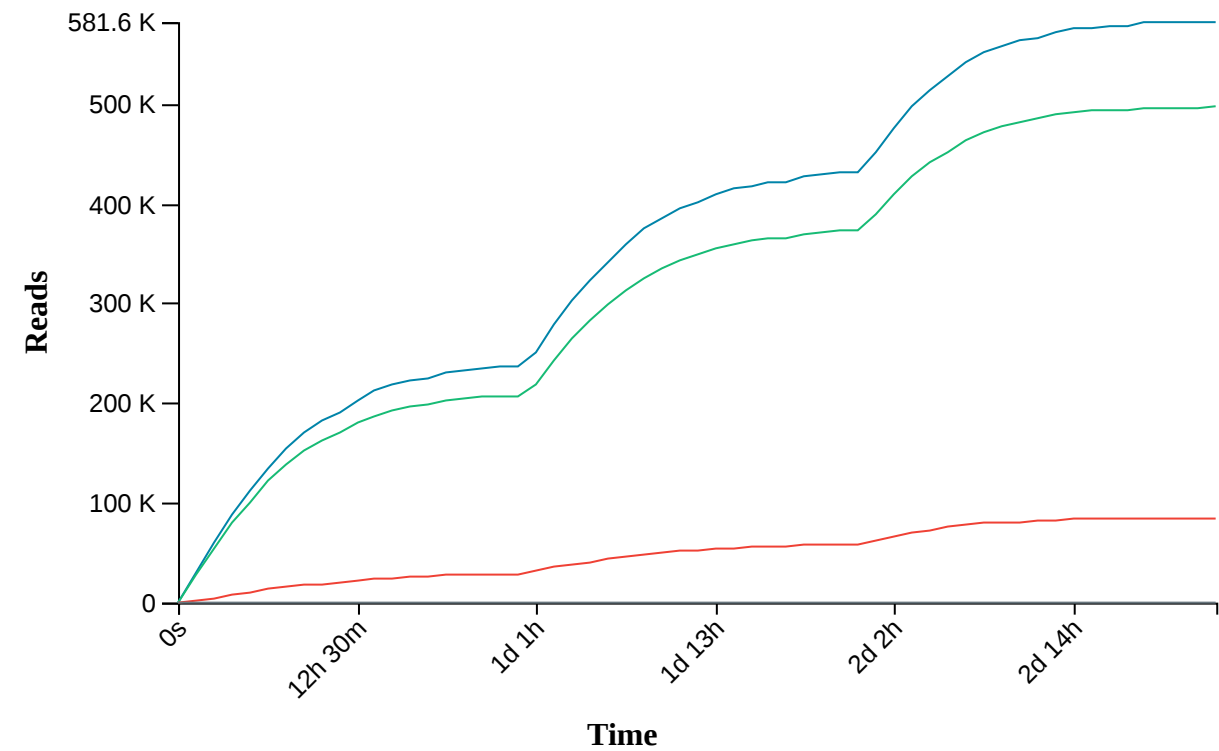
Cumulative Output Bases
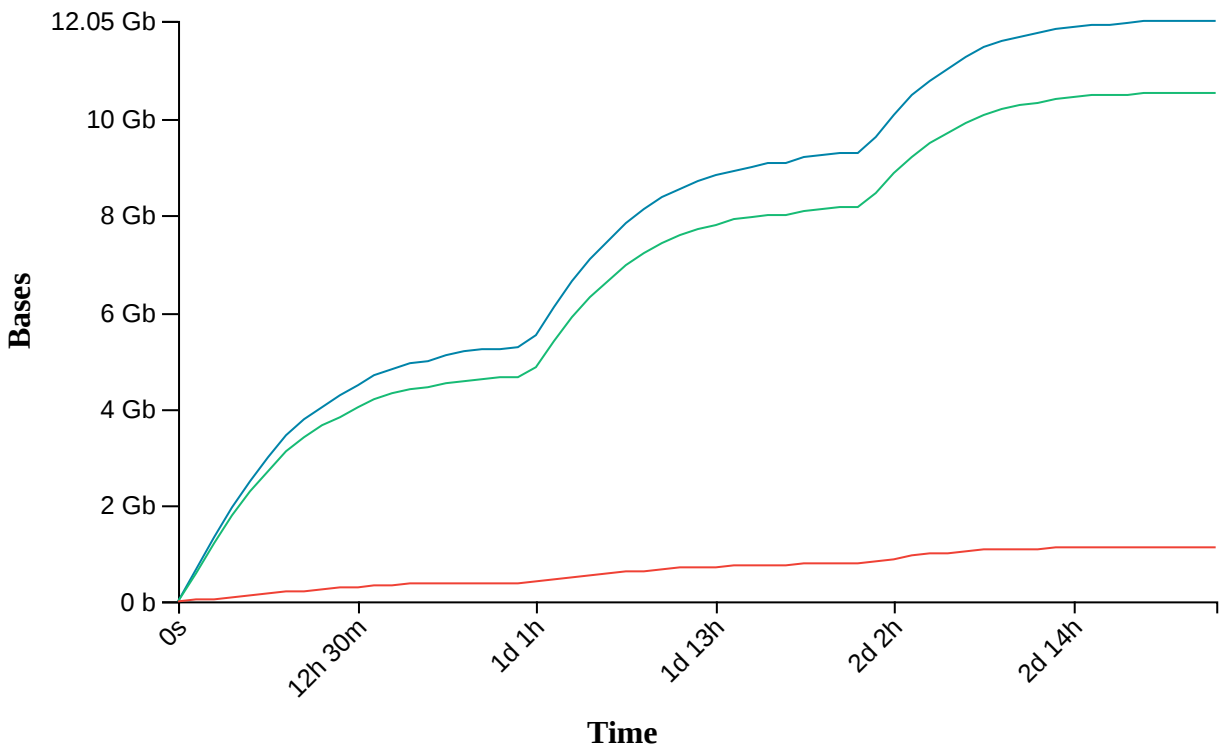
Read Length Histogram Estimated Bases - Outliers Discarded
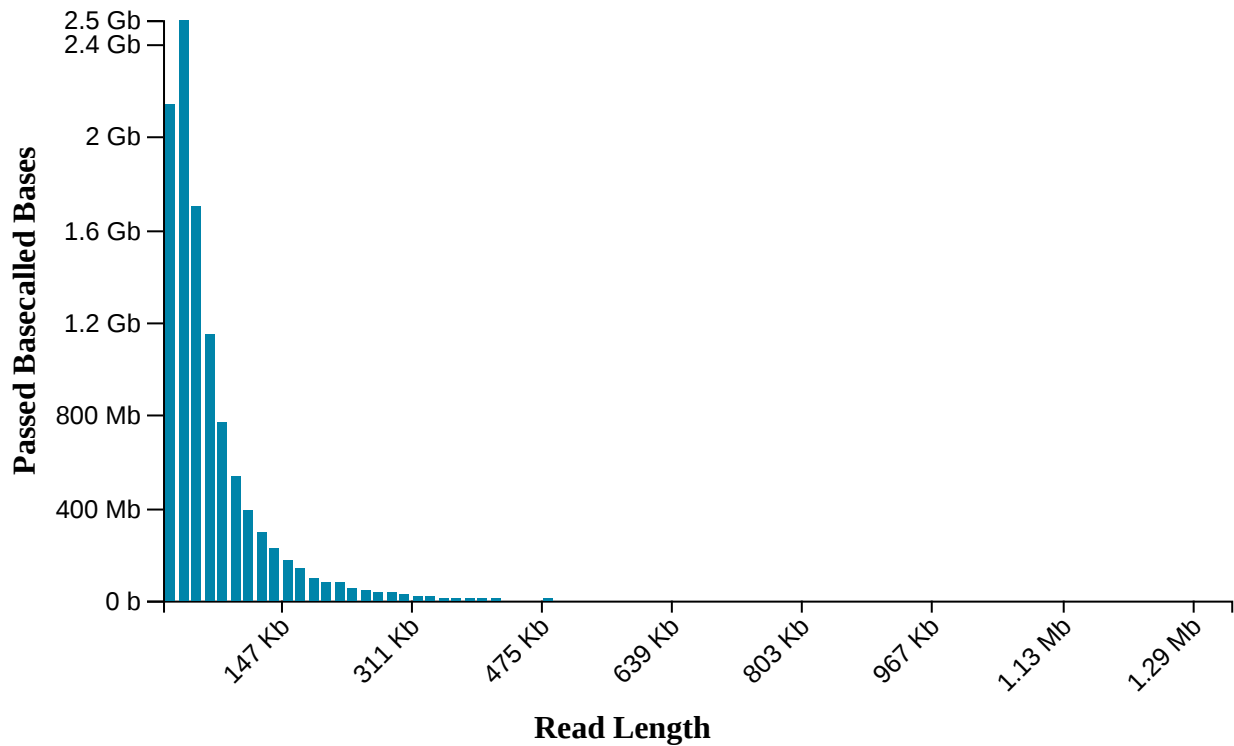
Estimated N50: 38.23 Kb

Read Length Histogram Basecalled Bases - Outliers Discarded
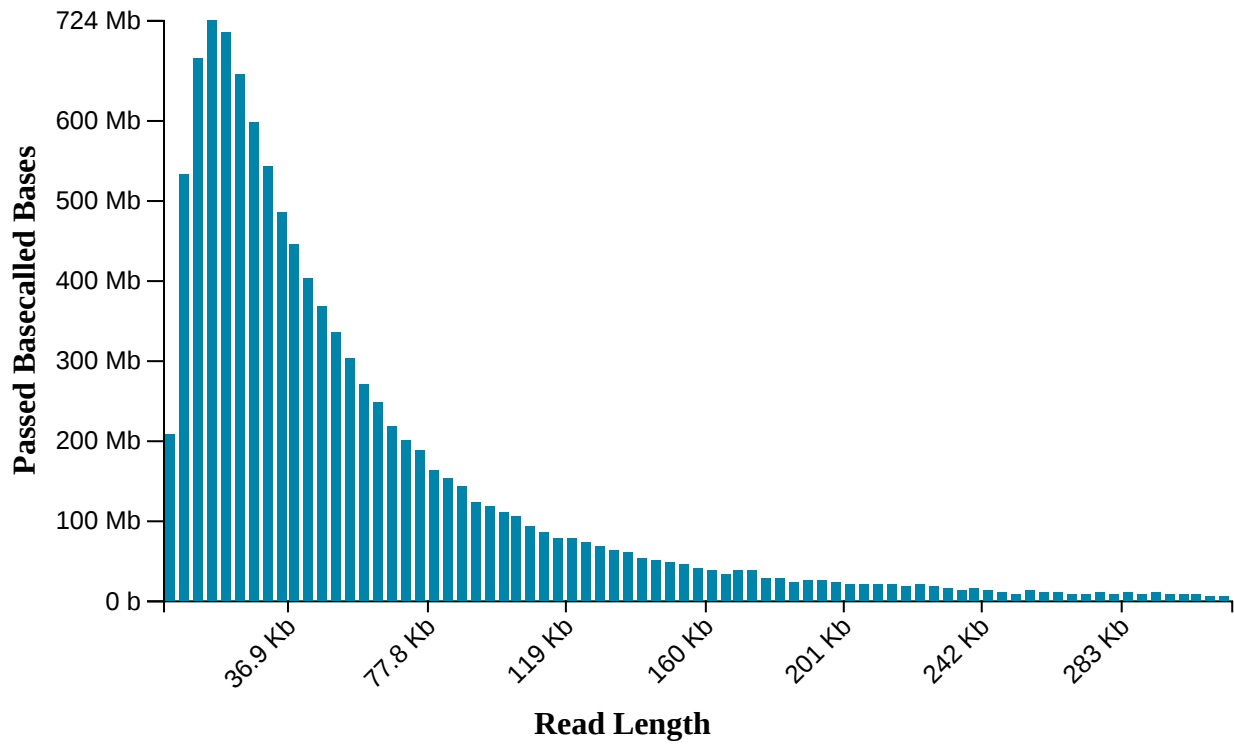
Estimated N50: 37.76 Kb

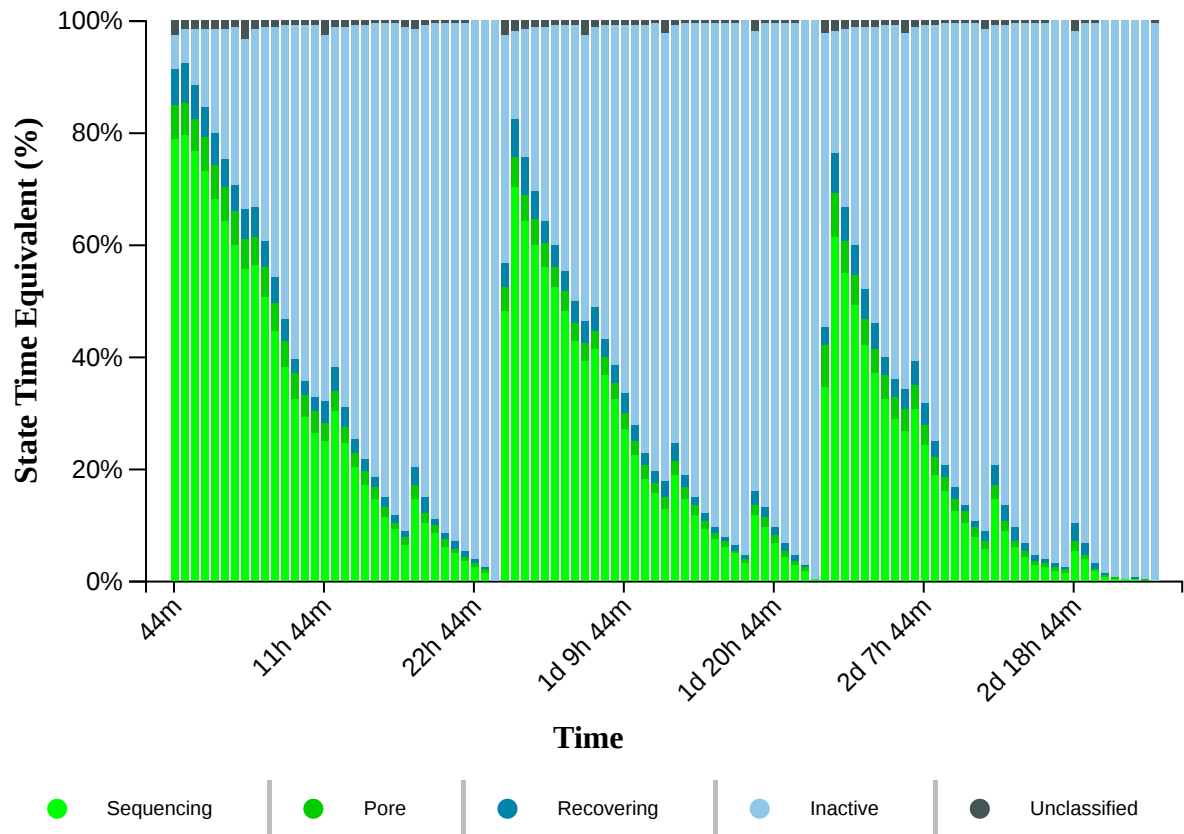## Read Length Histogram Estimated Bases

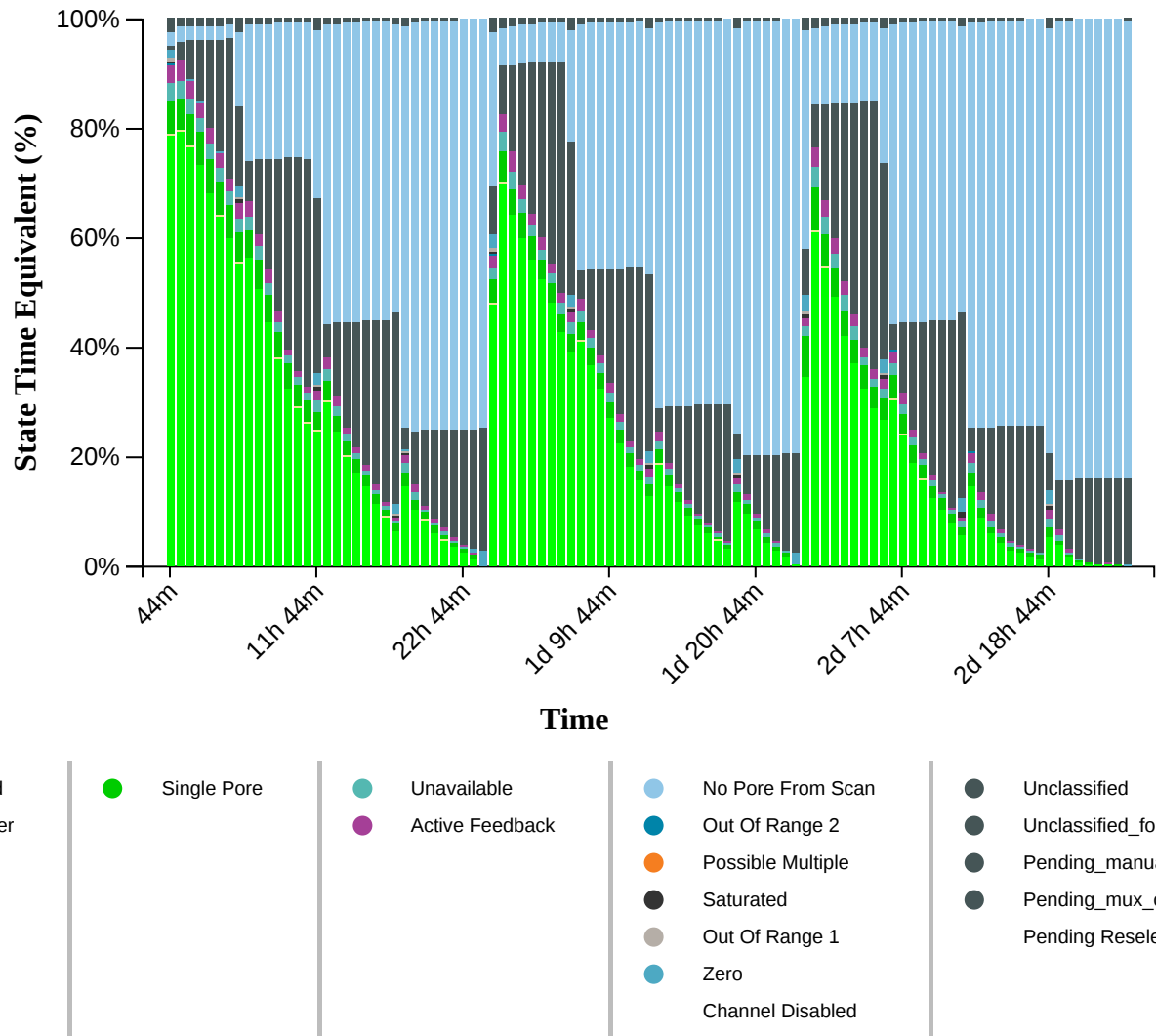Estimated N50: 38.23 Kb

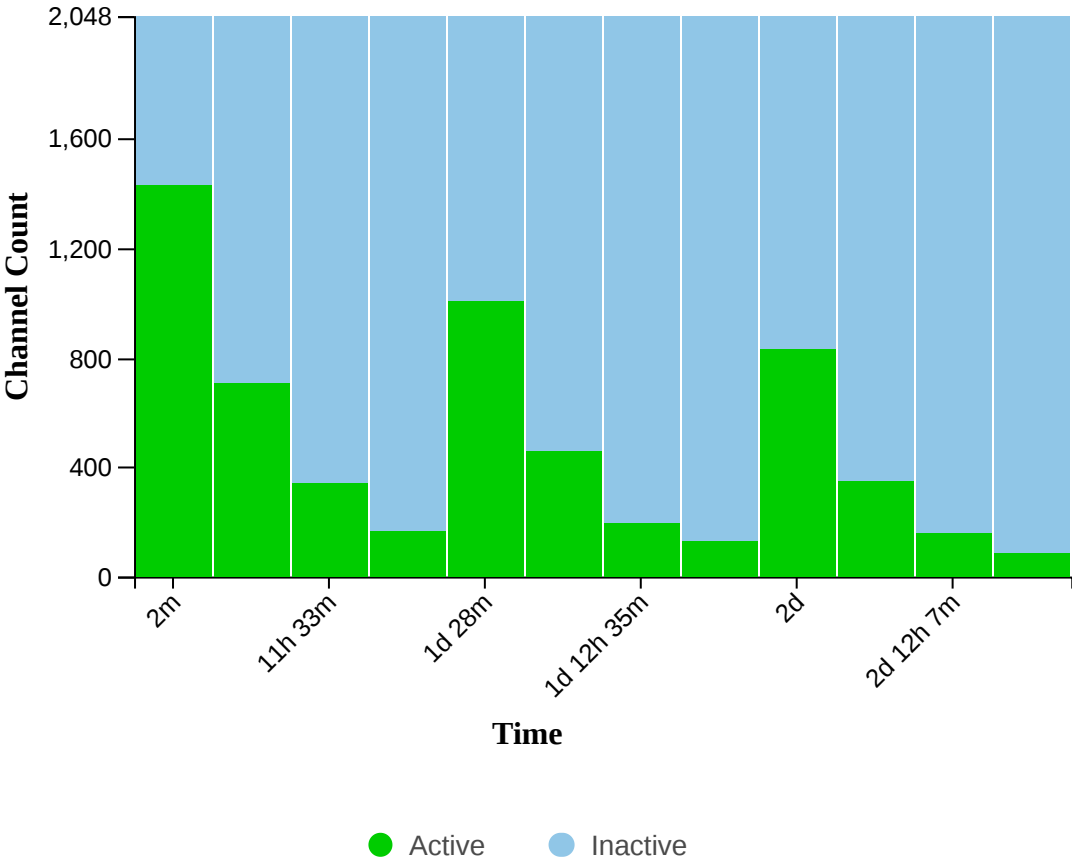## Read Length Histogram Basecalled Bases

Estimated N50: 37.76 Kb

Duty Time Grouped

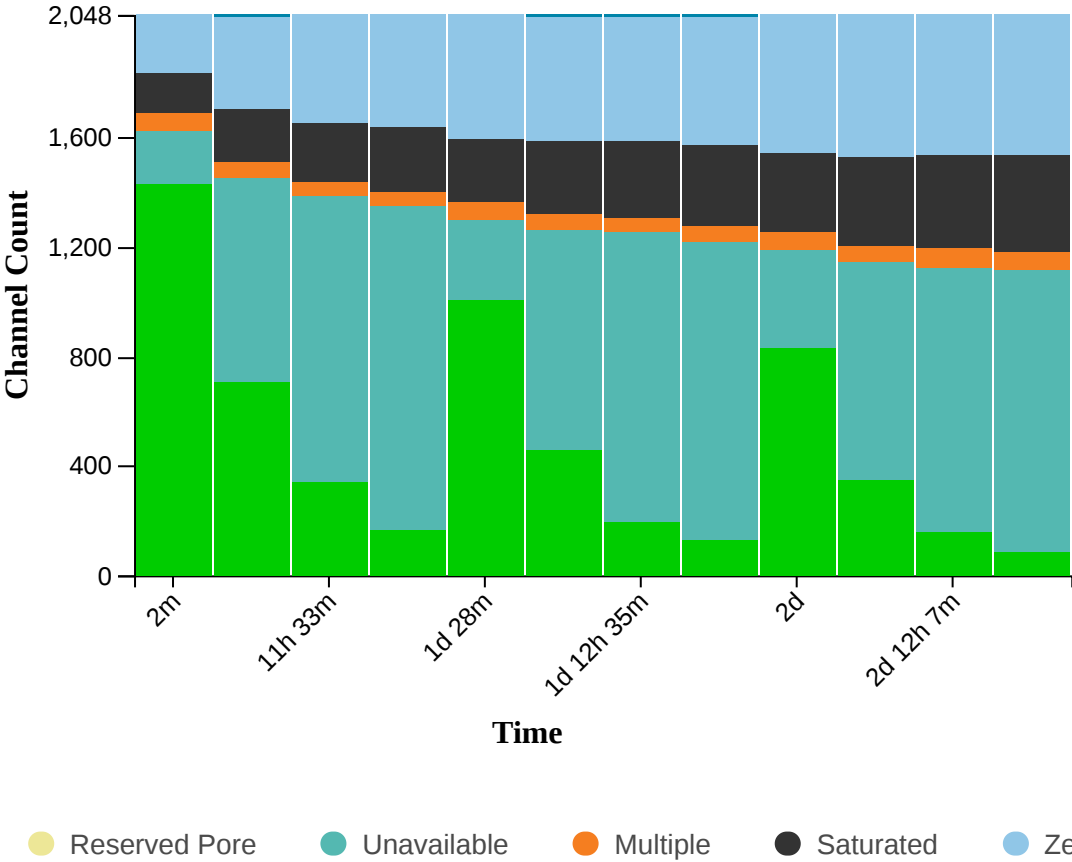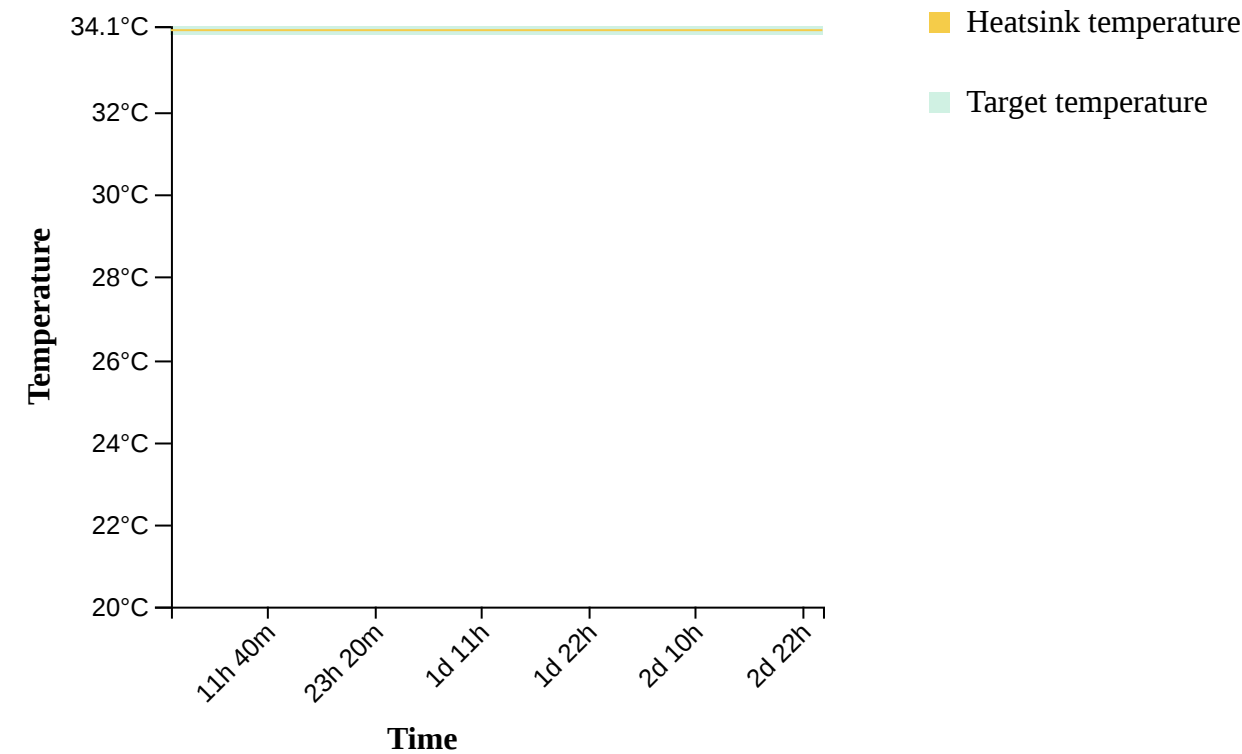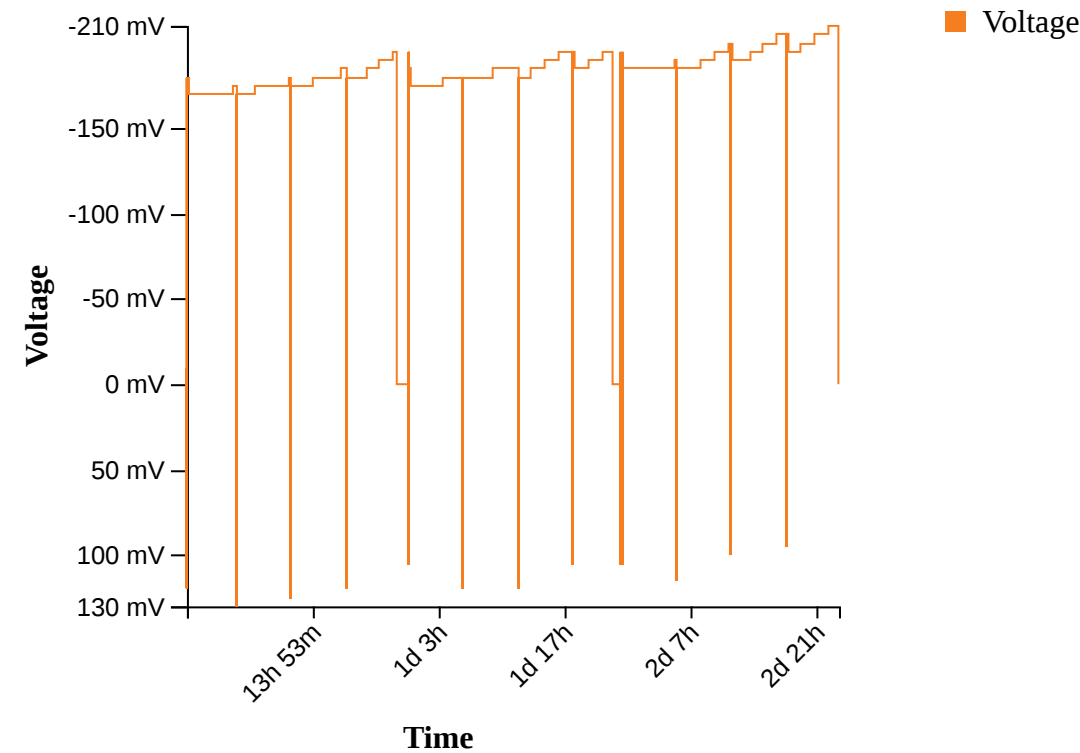## Duty time Categorised
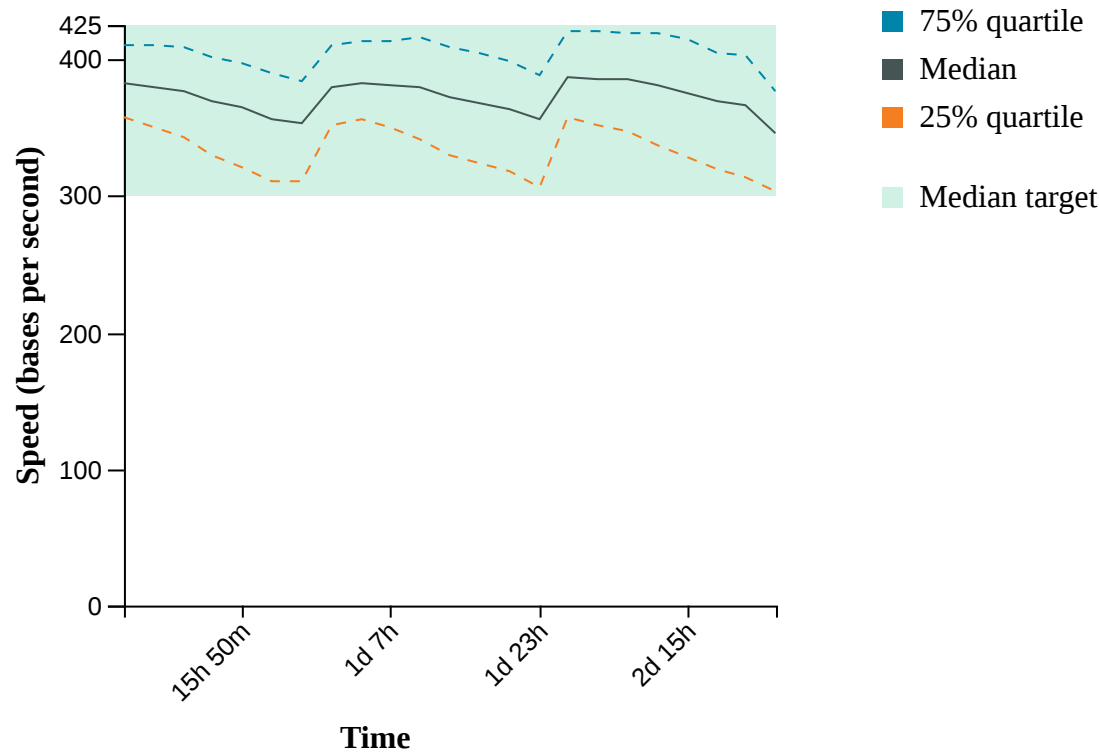
Mux Scan Grouped

Mux Scan Categorised
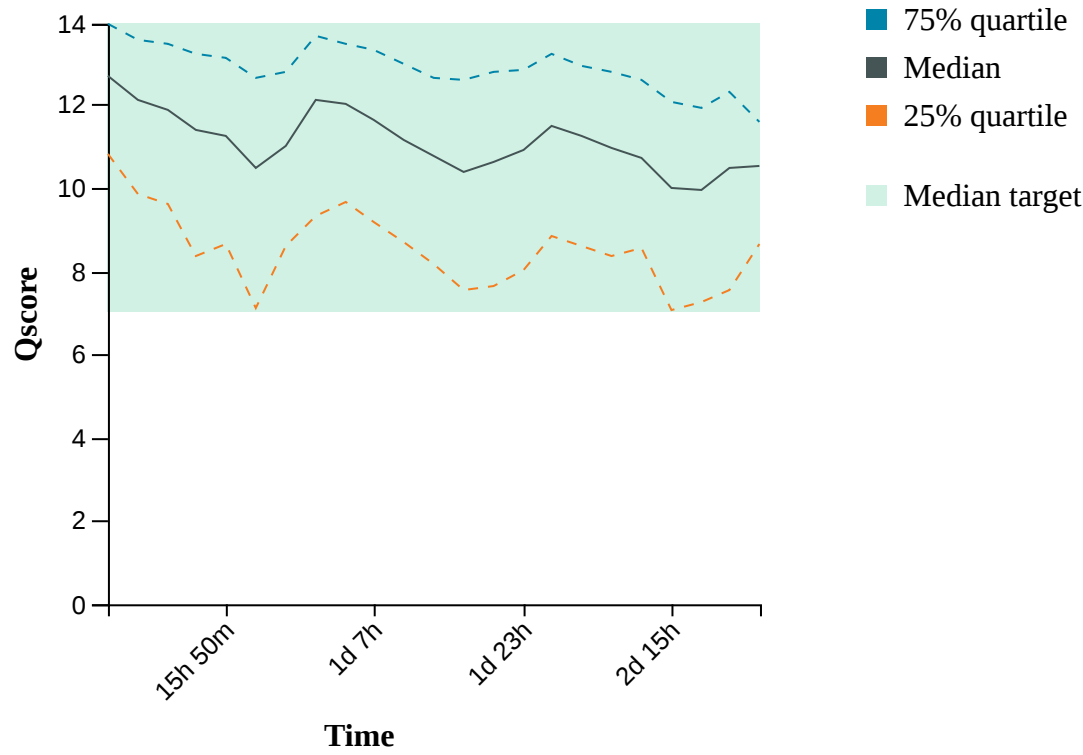
Temperature History
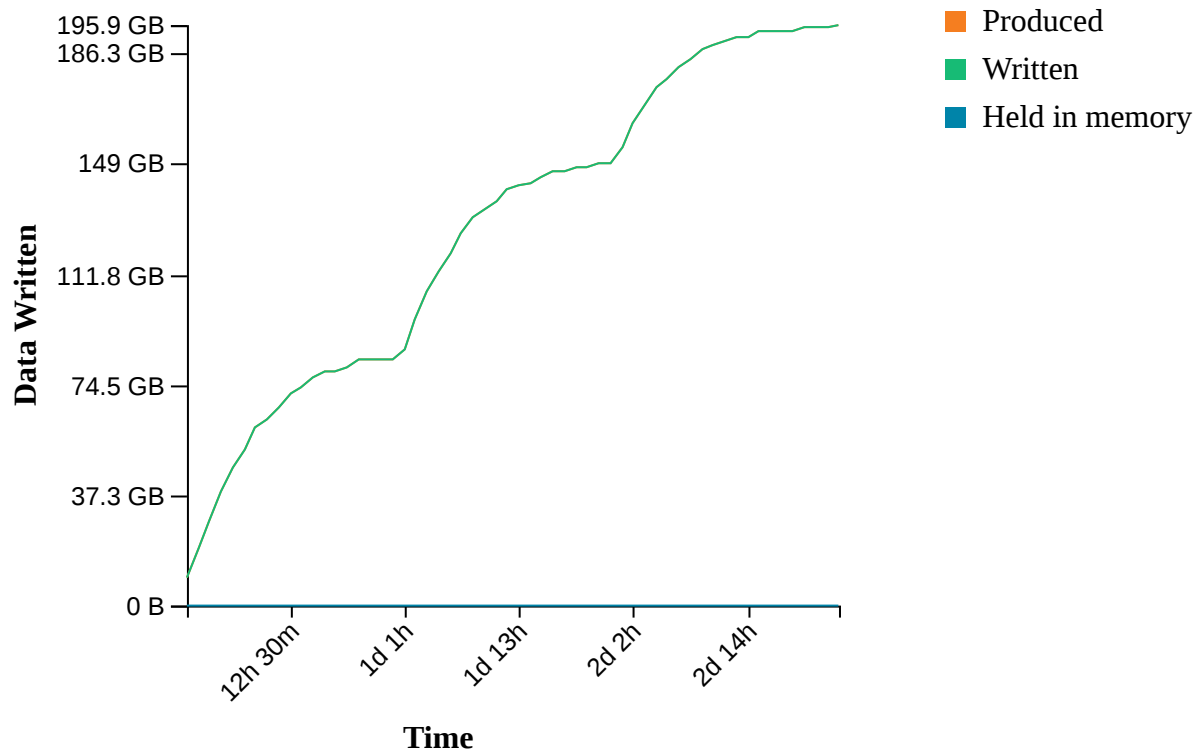

Bias Voltage History

Translocation Speed

QScore

Disk Write Performance

<u>Run Debug Messages</u>

- The sequencing run has finished, but basecalling may continue   October 2, 10:33
- Mux scan for flow cell FAO61000 has found a total of 89 pores. 82 pores available for immediate sequencing   October 2, 04:43
- Performing Mux Scan   October 2, 04:41
- Mux scan for flow cell FAO61000 has found a total of 162 pores. 133 pores available for immediate sequencing   October 1, 22:41
- Performing Mux Scan   October 1, 22:38
- Mux scan for flow cell FAO61000 has found a total of 352 pores. 232 pores available for immediate sequencing   October 1, 16:37
- Performing Mux Scan   October 1, 16:35
- Mux scan for flow cell FAO61000 has found a total of 836 pores. 439 pores available for immediate sequencing   October 1, 10:34
- Performing Mux Scan   October 1, 10:31
- Mux scan for flow cell FAO61000 has found a total of 130 pores. 106 pores available for immediate sequencing   October 1, 05:12
- Performing Mux Scan   October 1, 05:09
- Mux scan for flow cell FAO61000 has found a total of 197 pores. 152 pores available for immediate sequencing   September 30, 23:09
- Performing Mux Scan   September 30, 23:06
- Mux scan for flow cell FAO61000 has found a total of 460 pores. 282 pores available for immediate sequencing   September 30, 17:05
- Performing Mux Scan   September 30, 17:03
- Mux scan for flow cell FAO61000 has found a total of 1010 pores. 476 pores available for immediate sequencing   September 30, 11:02
- Performing Mux Scan   September 30, 10:59
- Mux scan for flow cell FAO61000 has found a total of 165 pores. 129 pores available for immediate sequencing   September 30, 04:10
- Performing Mux Scan   September 30, 04:08
- Mux scan for flow cell FAO61000 has found a total of 346 pores. 233 pores available for immediate sequencing   September 29, 22:07
- Performing Mux Scan   September 29, 22:04
- Mux scan for flow cell FAO61000 has found a total of 713 pores. 385 pores available for immediate sequencing   September 29, 16:03
- Performing Mux Scan   September 29, 16:01
- Mux scan for flow cell FAO61000 has found a total of 1436 pores. 499 pores available for immediate sequencing   September 29, 10:36
- Performing Mux Scan   September 29, 10:33
- Starting sequencing procedure   September 29, 10:33
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   September 29, 10:30
- Disk /data has 2479 GB space remaining   September 29, 10:30