Run Info

Experiment Name	**Dcoel010720**
Sample ID	**Dcoel**
Run ID	**87acb637-f3b9-4f14-b587-768f6b7270f1**
Flow Cell Id	**FAO01594**
Start Time	**July 1, 09:51**
Run Length	**7h 10m**

Run Summary

Reads Generated	**593.68 K**
Bases Generated	**571.21 Mb**
Estimated Bases	**516.87 Mb**

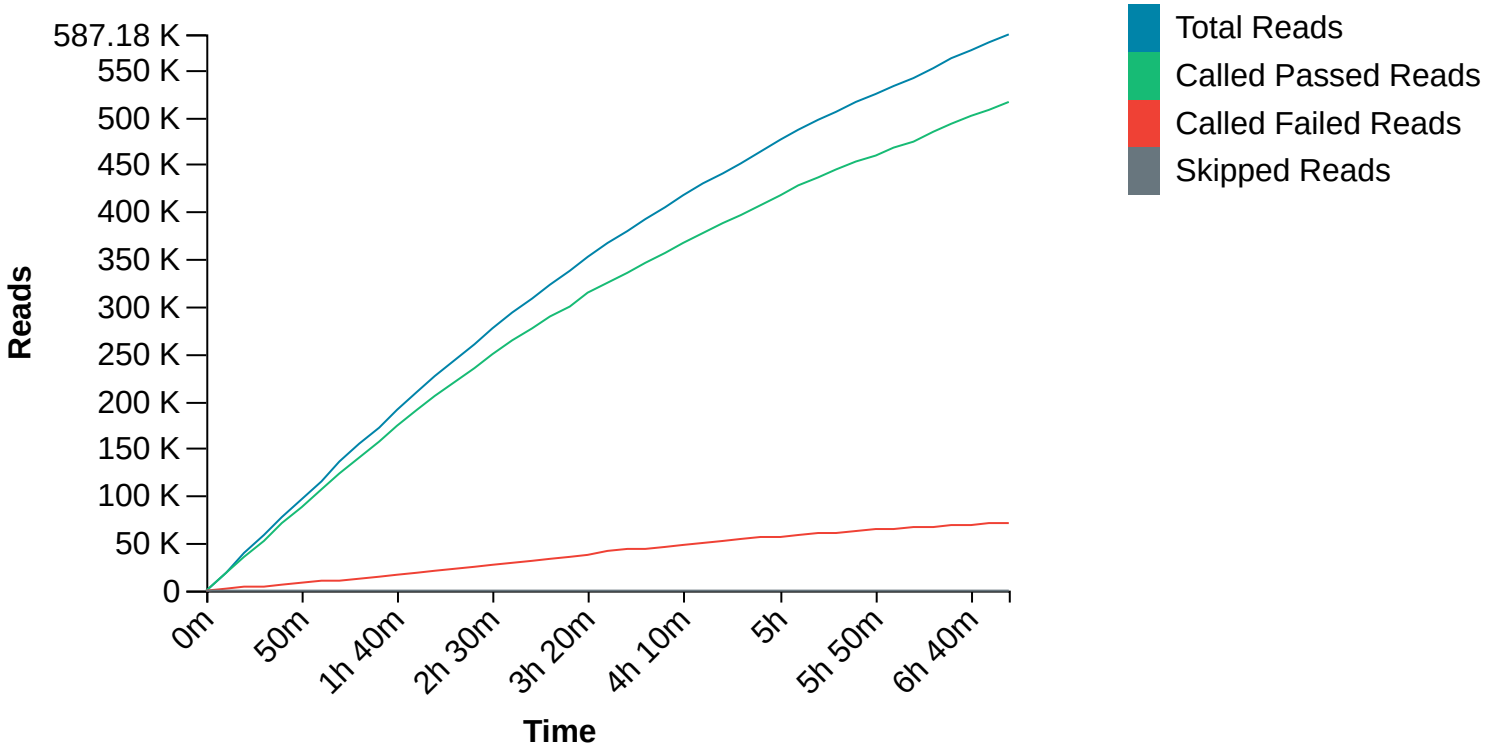
Run Parameters

Flow Cell Type	**FLO-MIN106**
Kit	**SQK-LSK109**
Basecalling	**on**
Specified Run Length	**72 hours**
Initial Bias Voltage	**-180 mV**
FAST5 Output	**Enabled**
FAST5 Output Options	**zlib_compress,fastq,raw**
FASTQ Output Options	**compress**
FAST5 Reads per File	**4000**
FASTQ Output	**Enabled**
FASTQ Reads per File	**4000**
Active Channel Selection	**Enabled**
Mux Scan Period	**1 hour 30 minutes**
Reserved Pores	**0 %**
Basecall Model	**Fast basecalling**

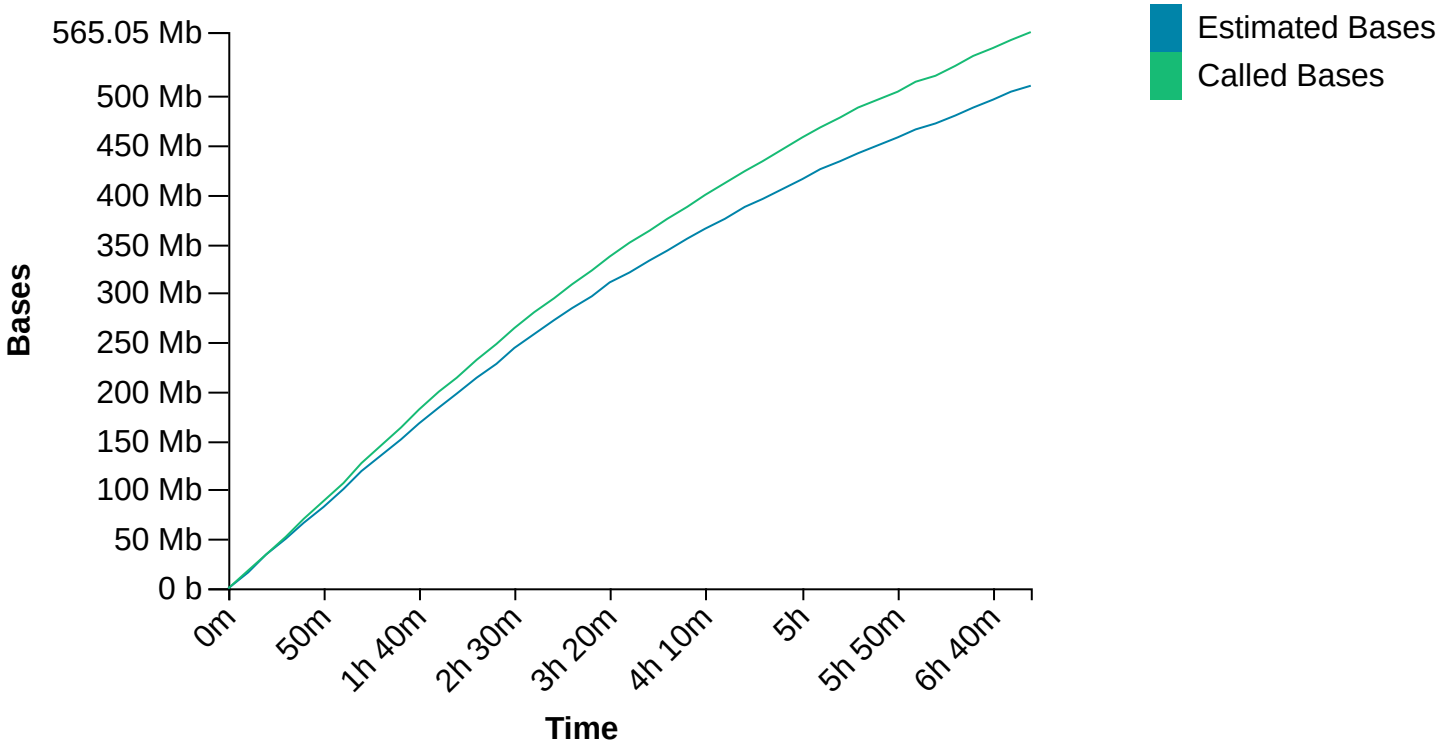
Versions

MinKNOW Core	**3.6.5**
Bream	**4.3.16**
Guppy	**3.2.10**

Cumulative Output Reads

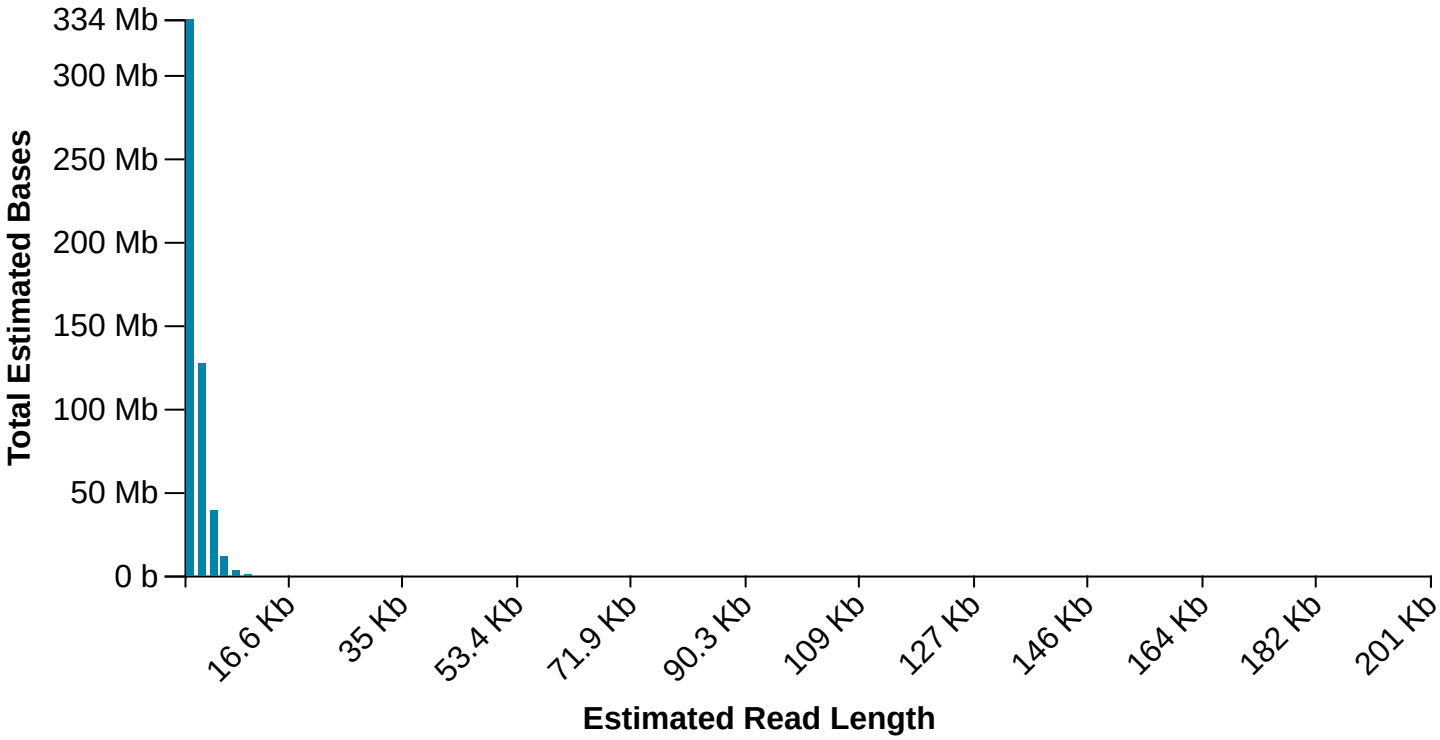


Cumulative Output Bases



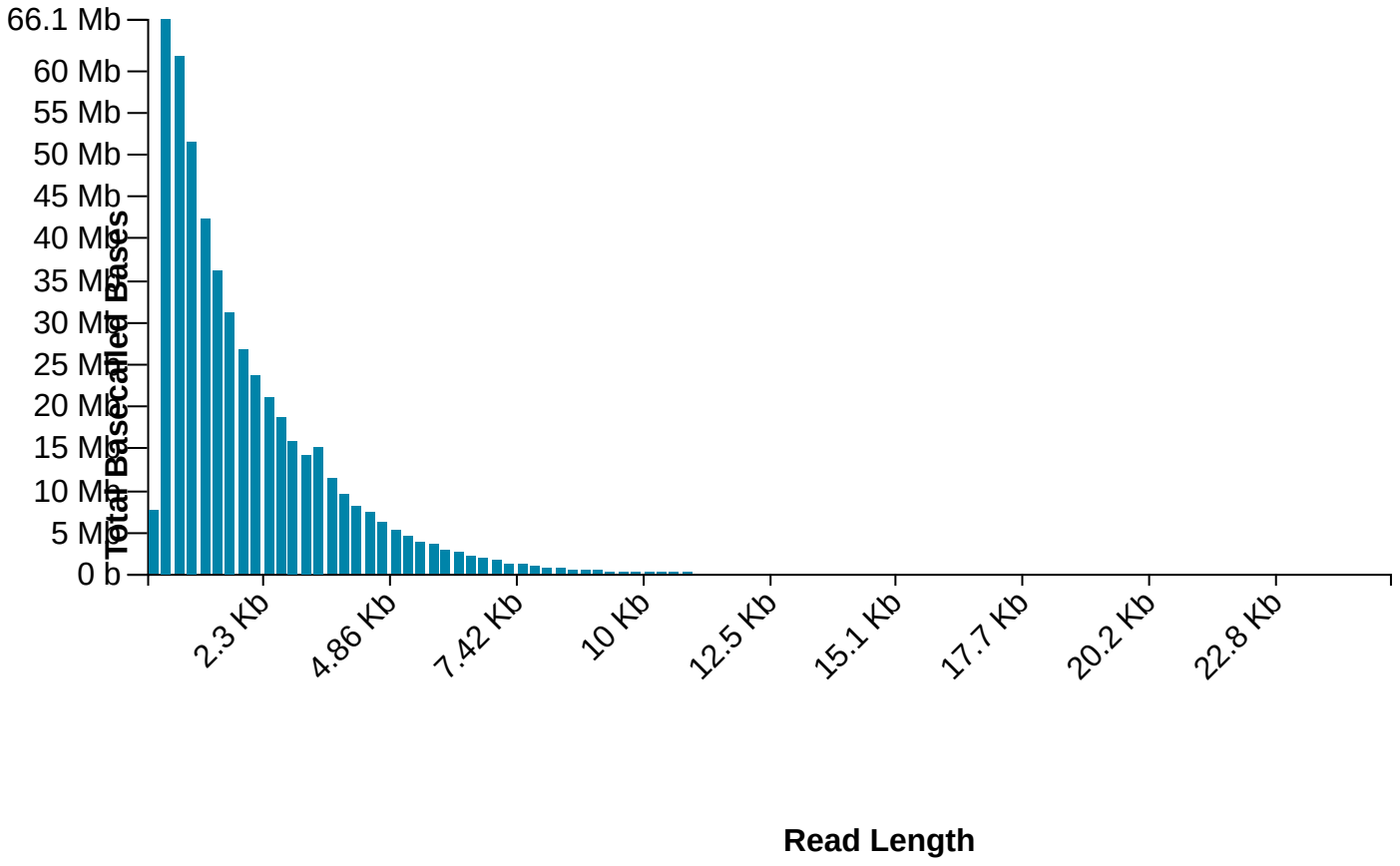
Read Length Histogram Estimated Bases

Estimated N50: 1.28 Kb

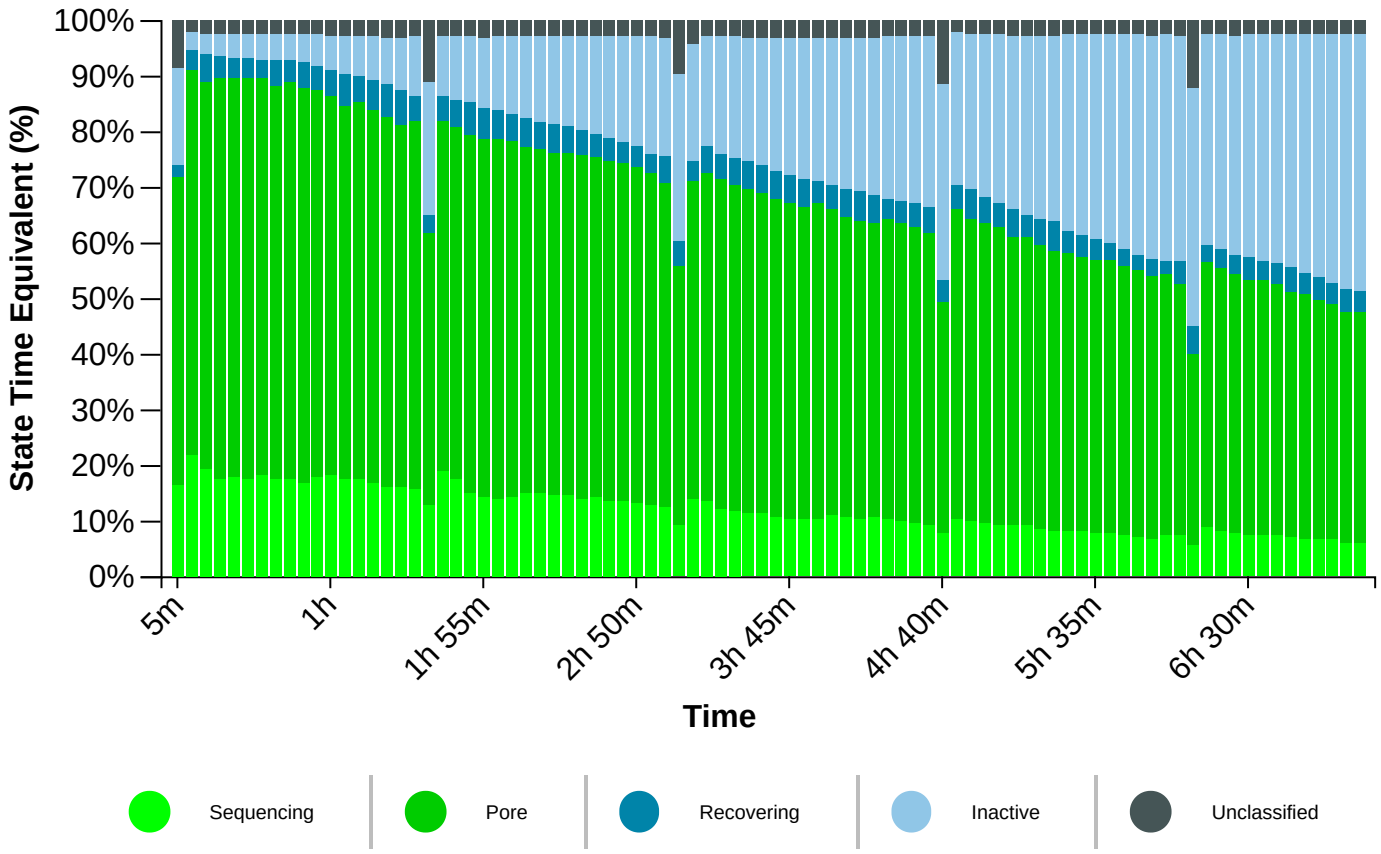


Read Length Histogram Basecalled Bases

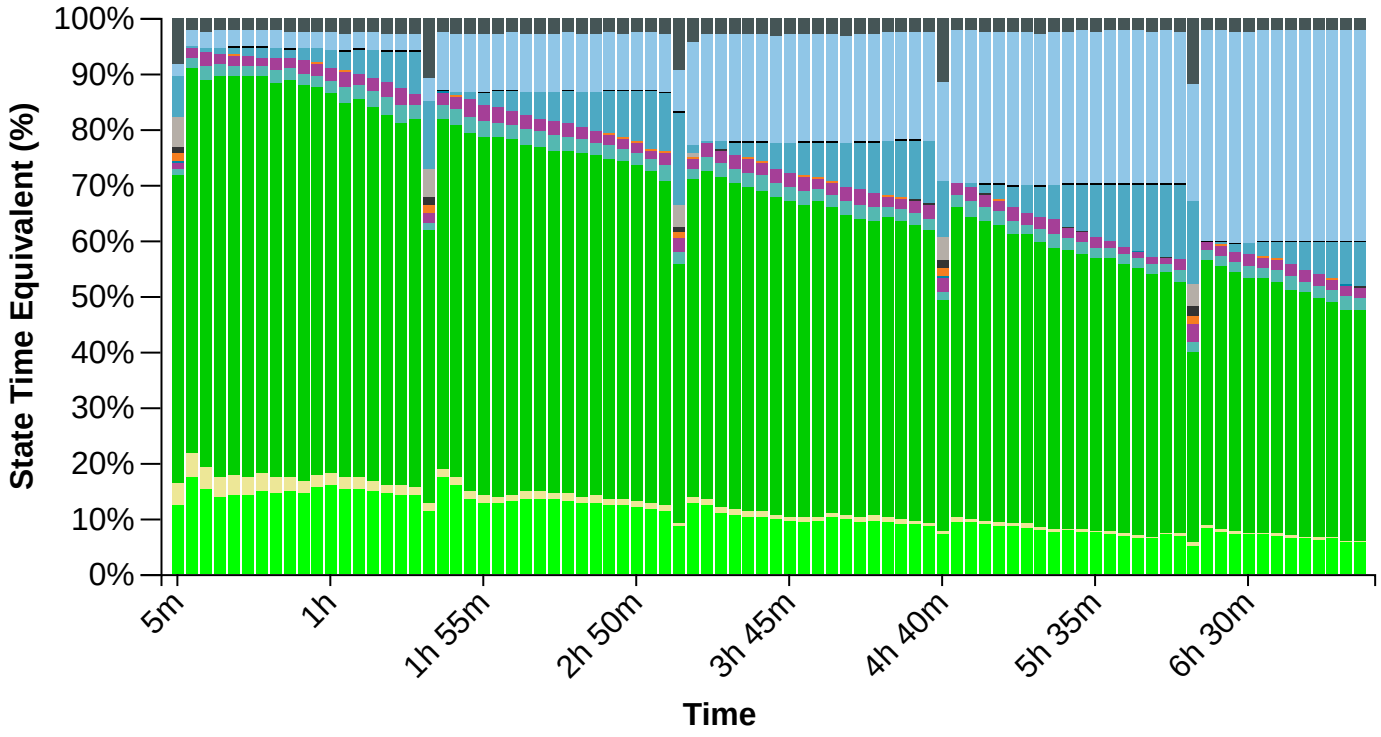
Estimated N50: 1.46 Kb



Duty Time Grouped

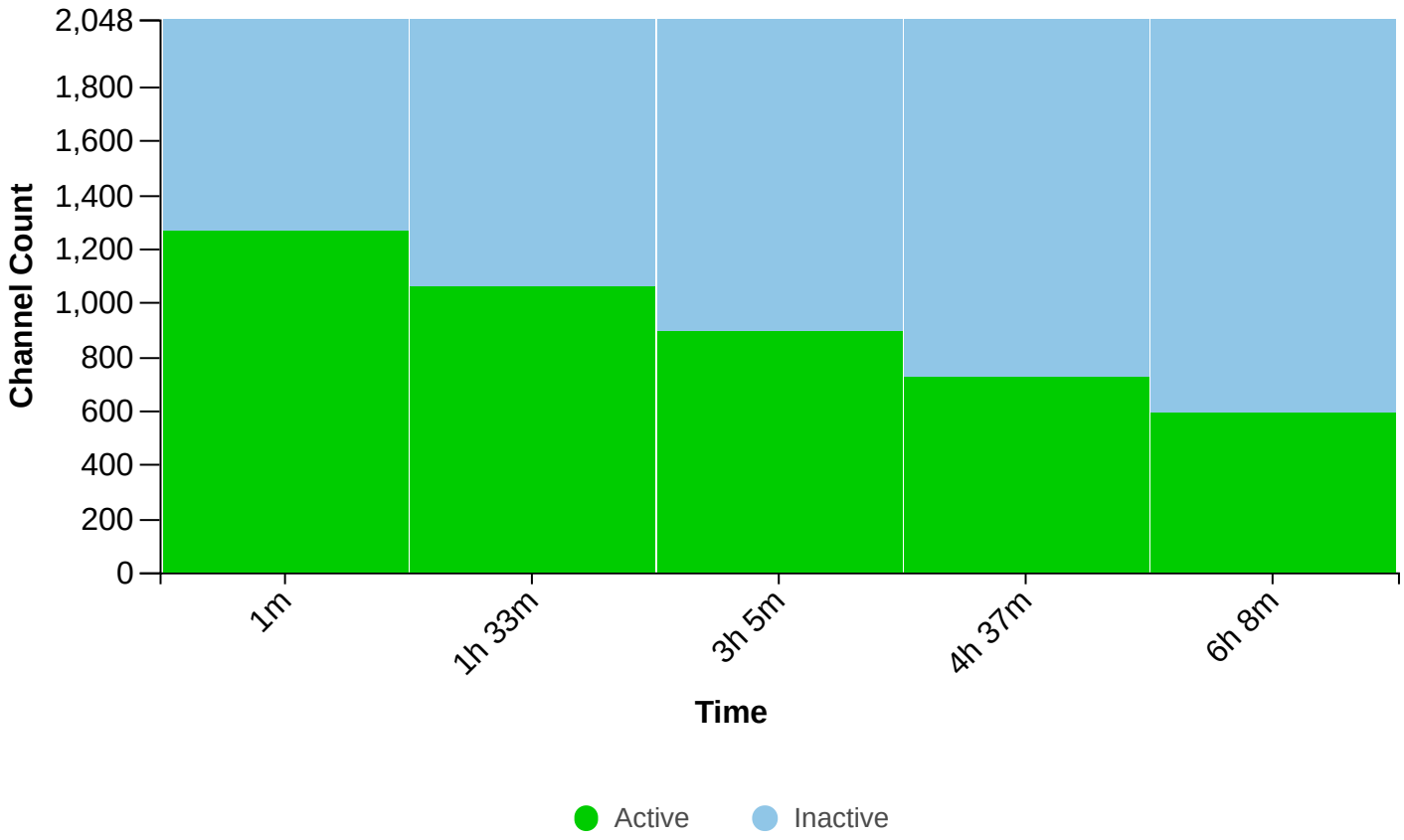


Duty time Categorised

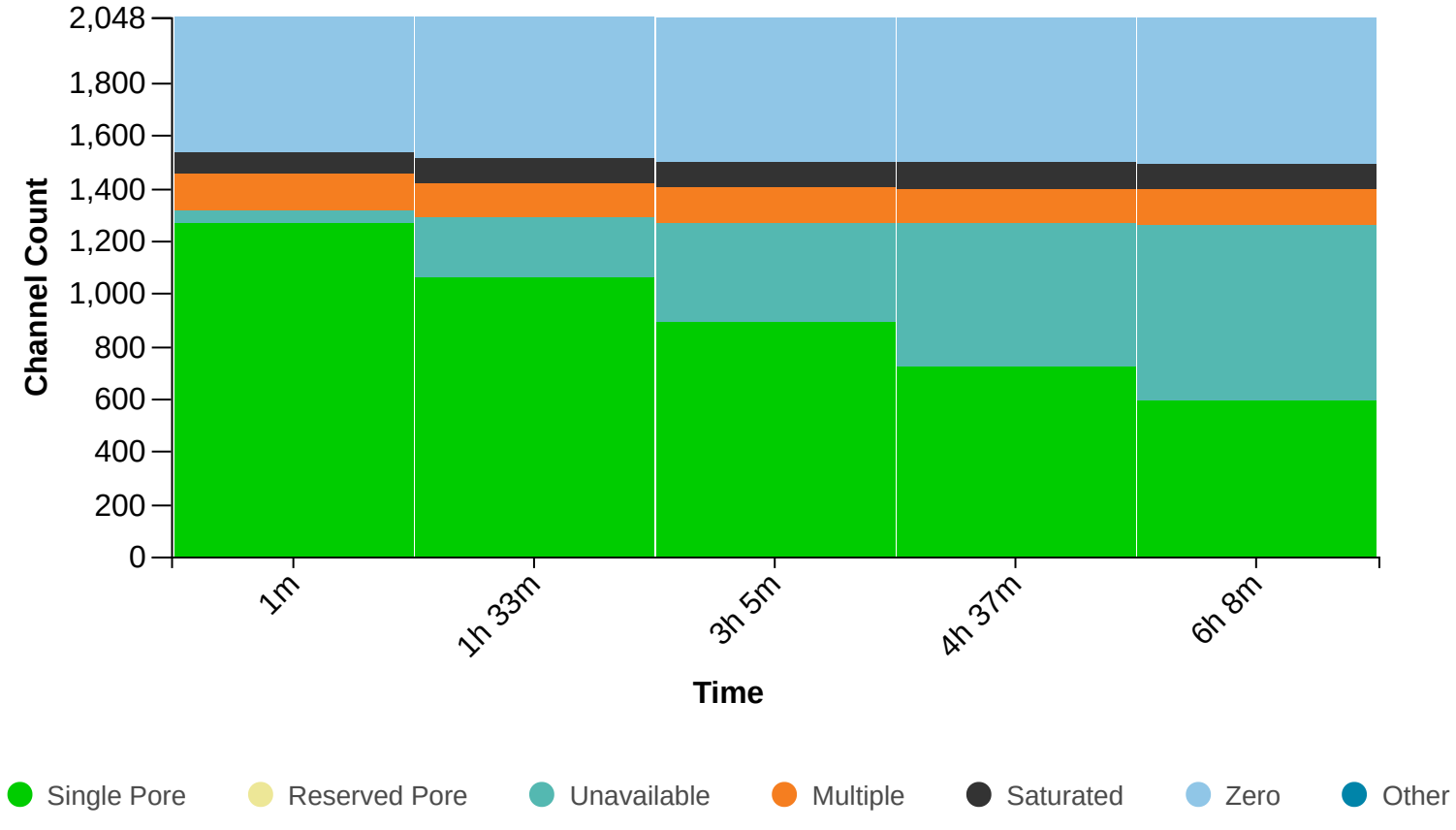


Strand
Adapter
Single Pore
Unavailable
Active Feedback
No Pore From Scan
Out Of Range 2
Possible Multiple
Saturated
Out Of Range 1
Zero
Unclassified
Unclassified_following_reset
Pending_manual_reset
Pending_mux_change
Pending Reselection

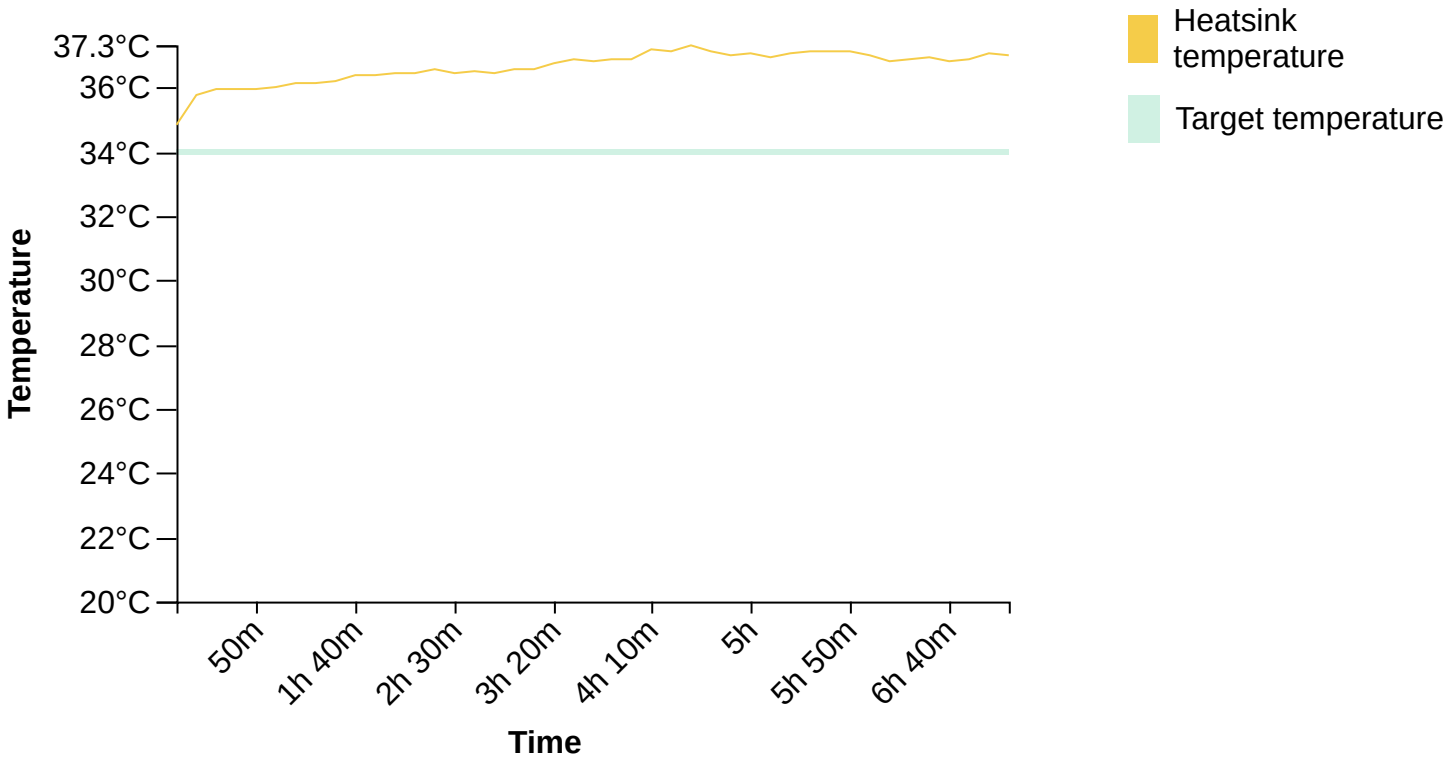
Mux Scan Grouped



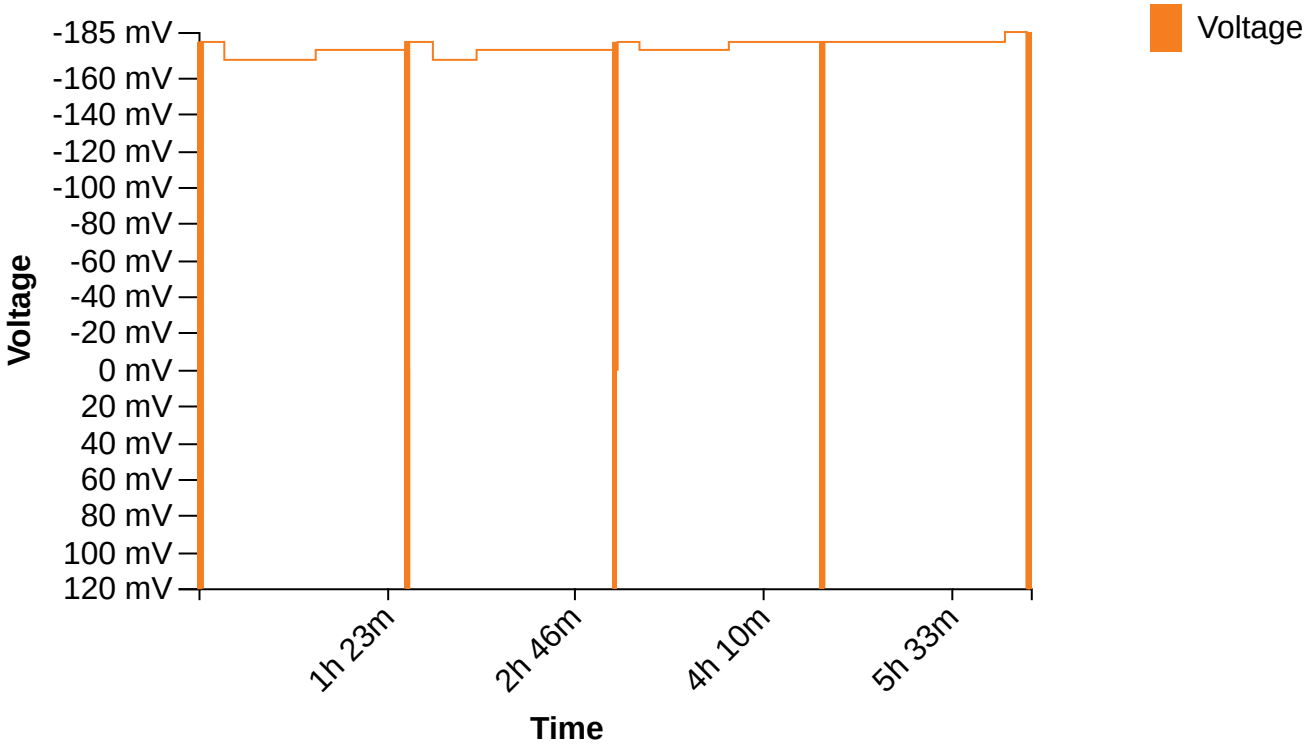
Mux Scan Categorised



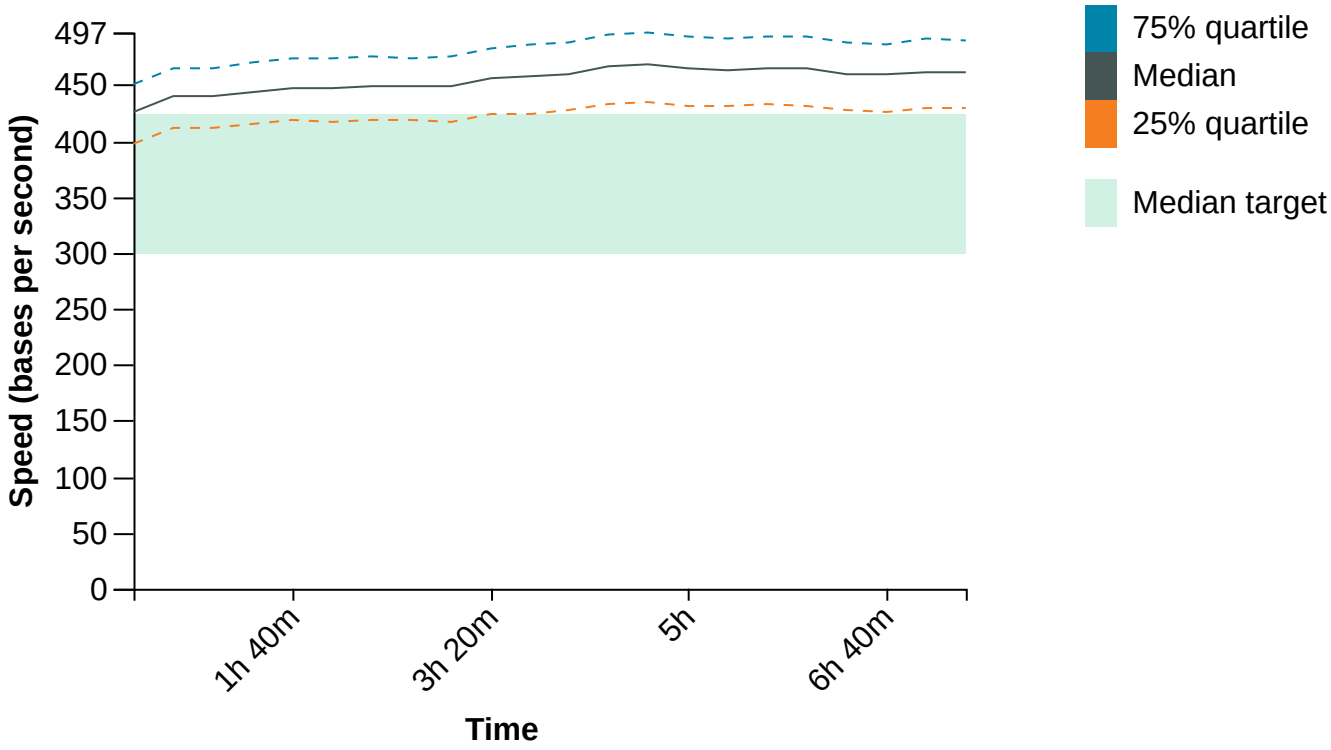
Temperature History



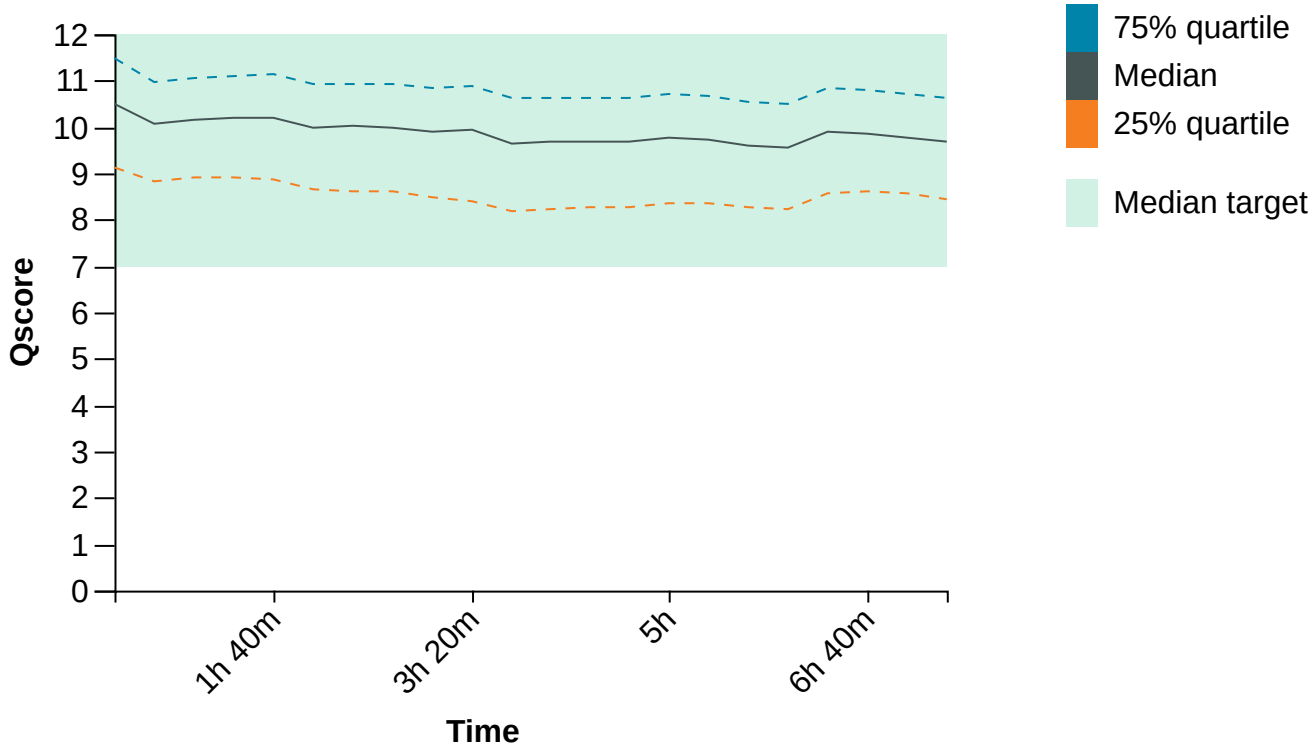
Bias Voltage History



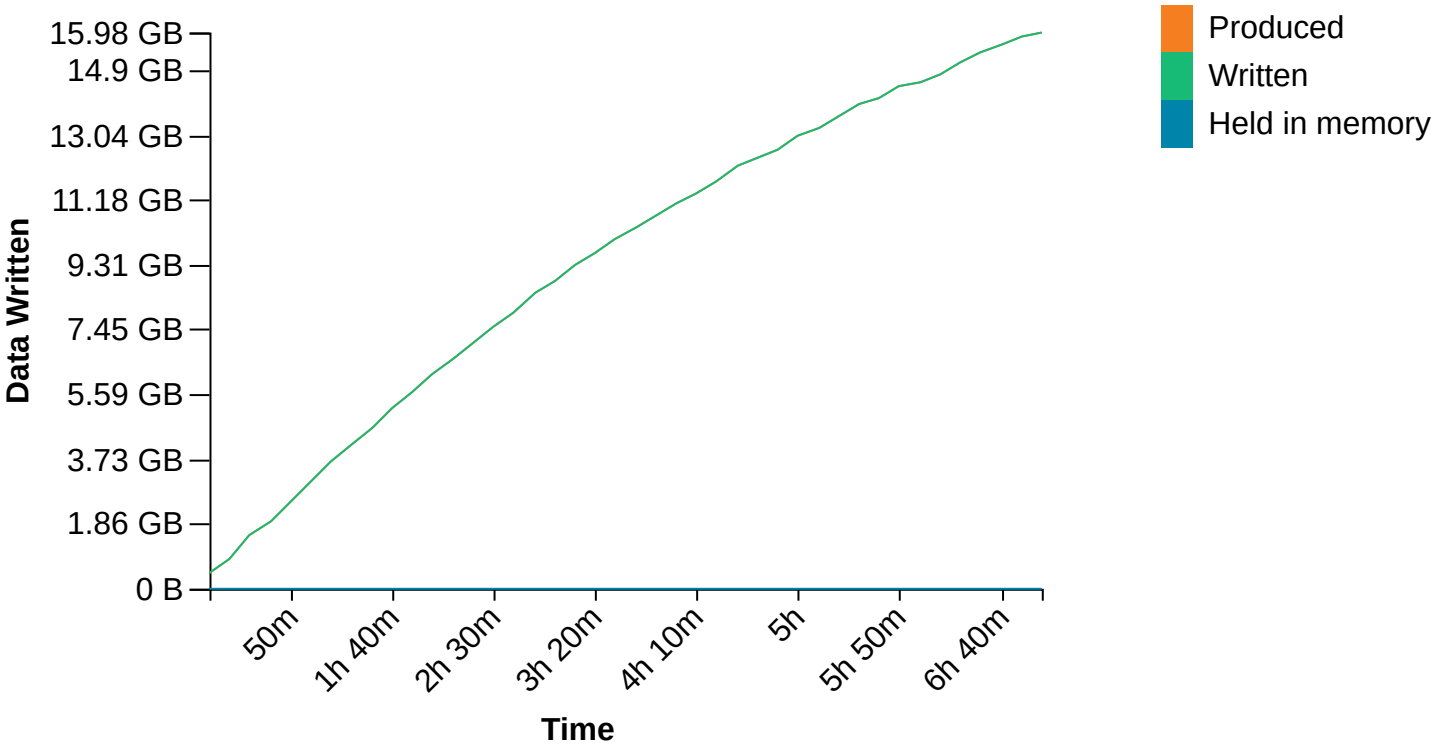
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Flow cell FAO01594 has 591 pores available for sequencing. Starting sequencing with 318 pores July 1, 16:02
- Performing Mux Scan July 1, 16:00
- Flow cell FAO01594 has 727 pores available for sequencing. Starting sequencing with 372 pores July 1, 14:30
- Performing Mux Scan July 1, 14:28
- Flow cell FAO01594 has 892 pores available for sequencing. Starting sequencing with 413 pores July 1, 12:58
- Performing Mux Scan July 1, 12:57
- Flow cell FAO01594 has 1063 pores available for sequencing. Starting sequencing with 459 pores July 1, 11:27
- Performing Mux Scan July 1, 11:25
- Flow cell FAO01594 has 1263 pores available for sequencing. Starting sequencing with 497 pores July 1, 09:55
- Performing Mux Scan July 1, 09:53
- Starting sequencing procedure July 1, 09:53
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C July 1, 09:51
- Disk / has 410 GB space remaining July 1, 09:51