Run Info

Host Name	**GXb03422 (localhost)**
Position	**X1**
Experiment Name	**ReadUntil_Hydrogenophaga_Refenr_051021**
Sample ID	**ReadUntil_Hydrogenophaga_Refenr_051021**
Run ID	**ea62a72a-32a6-48e4-8a85-7819d37146f5**
Acquisition ID(s)	**dbd22c0b2569bf7fc80624b73a5d45d958231261, ad84e2ea249cb571d329436590d3a1e5562679fc**
Flow Cell Id	**FAQ86094**
Start Time	**October 5, 16:19**
Run Length	**1h 3m**

Run Summary

Reads Generated	**275.19 k**
Passed Bases	**375.31 Mb**
Failed Bases	**36.19 Mb**
Estimated Bases	**422.35 Mb**

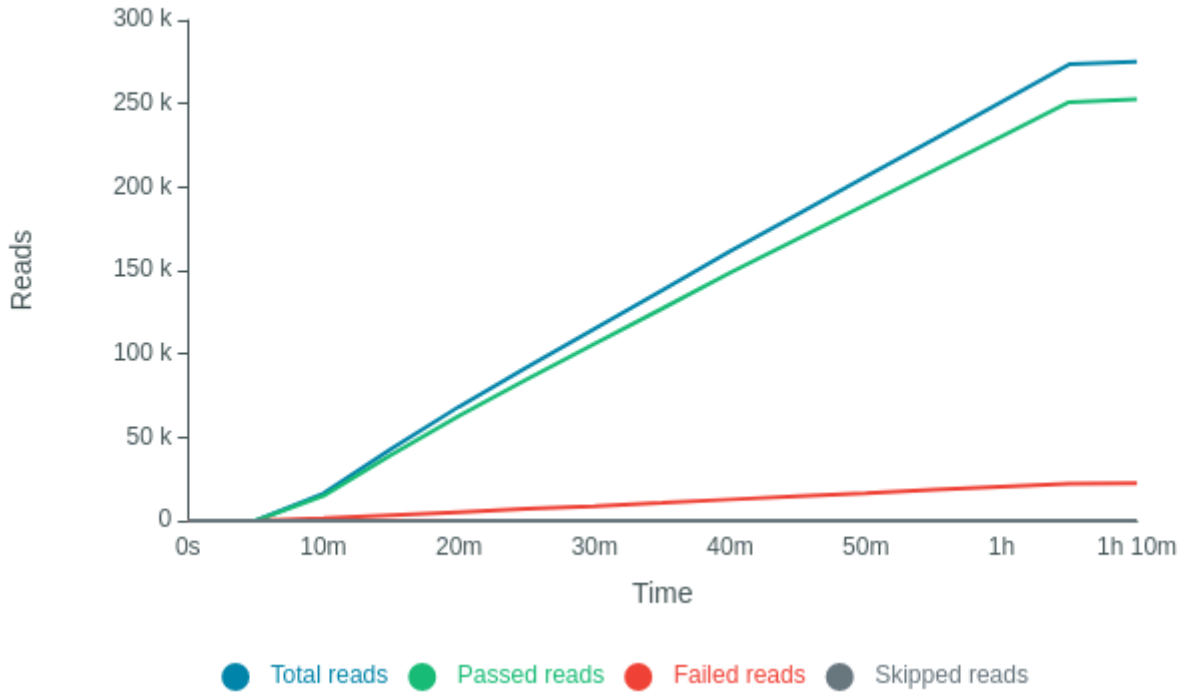
Run Parameters

Flow Cell Type	**FLO-MIN106**
Kit	**SQK-LSK109**
Initial bias voltage	**-180 mV**
FAST5 output	**Enabled**
FASTQ output	**Enabled**
BAM output	**Enabled**
Bulk file output	**Disabled**
Active channel selection	**Enabled**
Basecalling	**Enabled**
Specified run length	**72 hours**
Adaptive sampling	**reference_files= ["/data/references/compost_3/Hydrogenophaga_PBC_ref.fasta"],filter_type=enrich,first_channel=1,last_channel=256**
FAST5 reads per file	**4000**
FAST5 output options	**vbz_compress,fastq,raw**
FASTQ reads per file	**4000**
FASTQ output options	**compress**
Mux scan period	**1 hour 30 minutes**
Reserved pores	**0 %**
Basecall model	**High-accuracy basecalling**
Alignment	**reference_files= ["/data/references/compost_3/Hydrogenophaga_all.fasta"]**
Read filtering	**min_qscore=9**

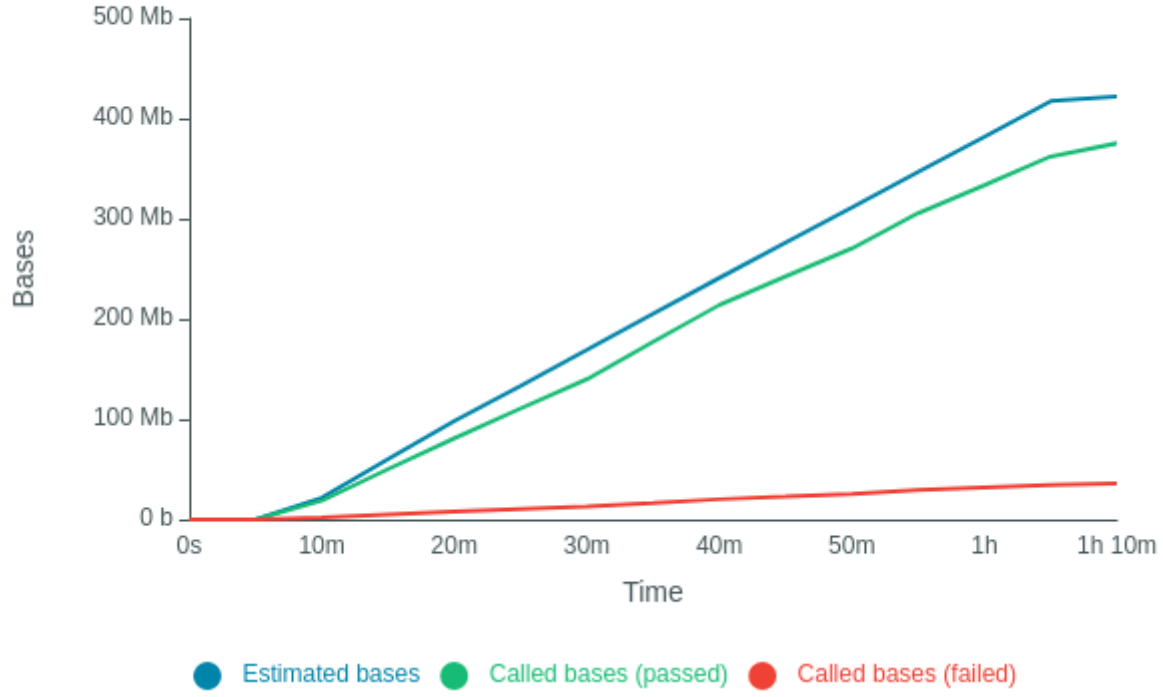
Versions

MinKNOW	**21.05.21**
MinKNOW Core	**4.3.12**
Bream	**6.2.6**
Guppy	**5.0.13**

Cumulative Output Reads

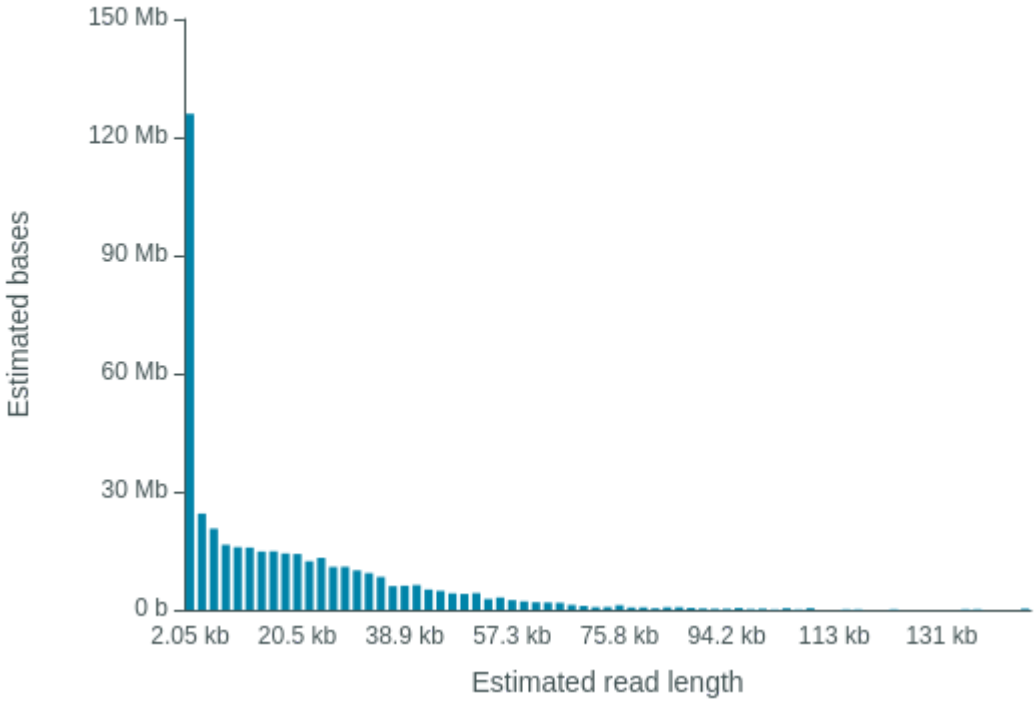


Cumulative Output Bases



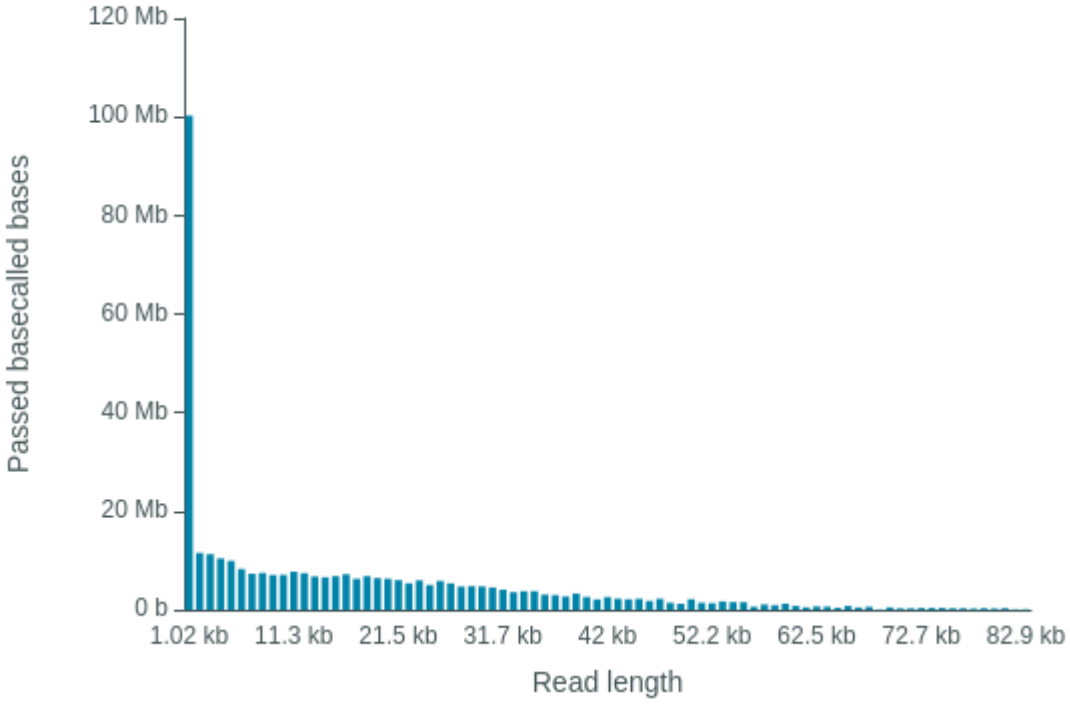
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 11.22 kb



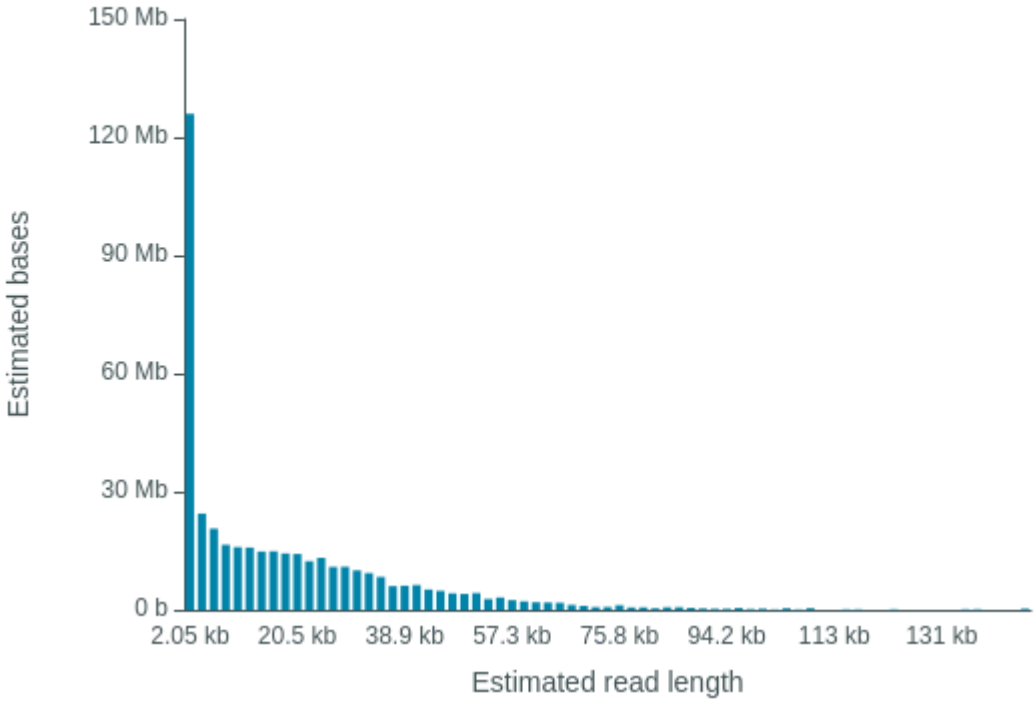
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 10.94 kb



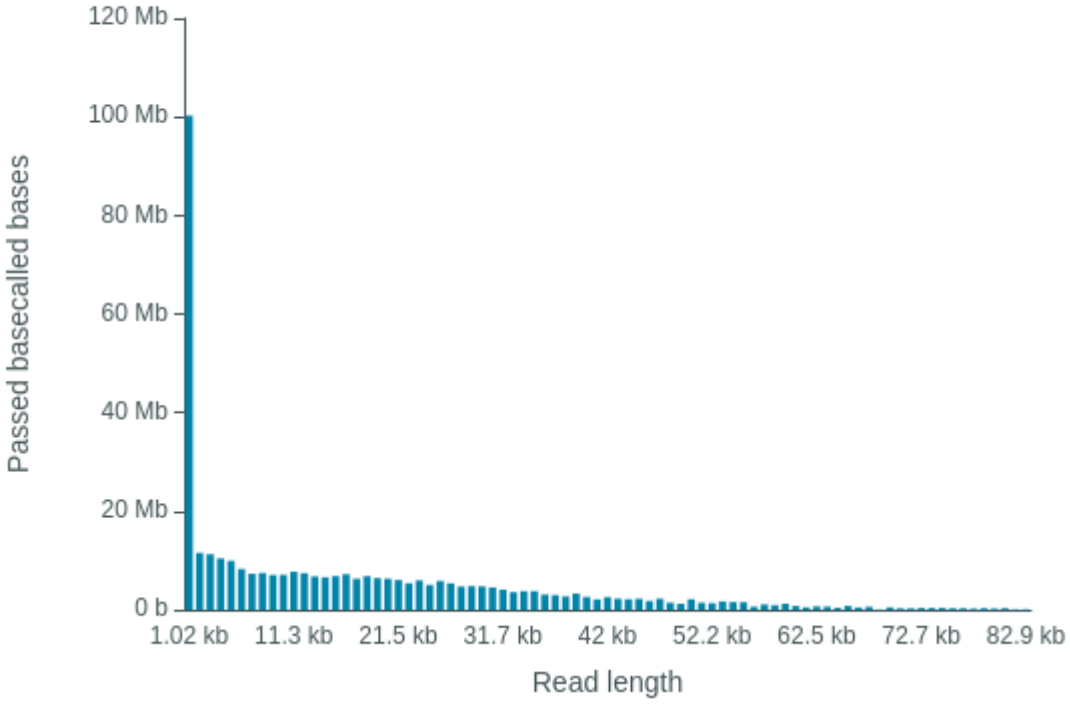
Read Length Histogram Estimated Bases

Estimated N50: 11.22 kb

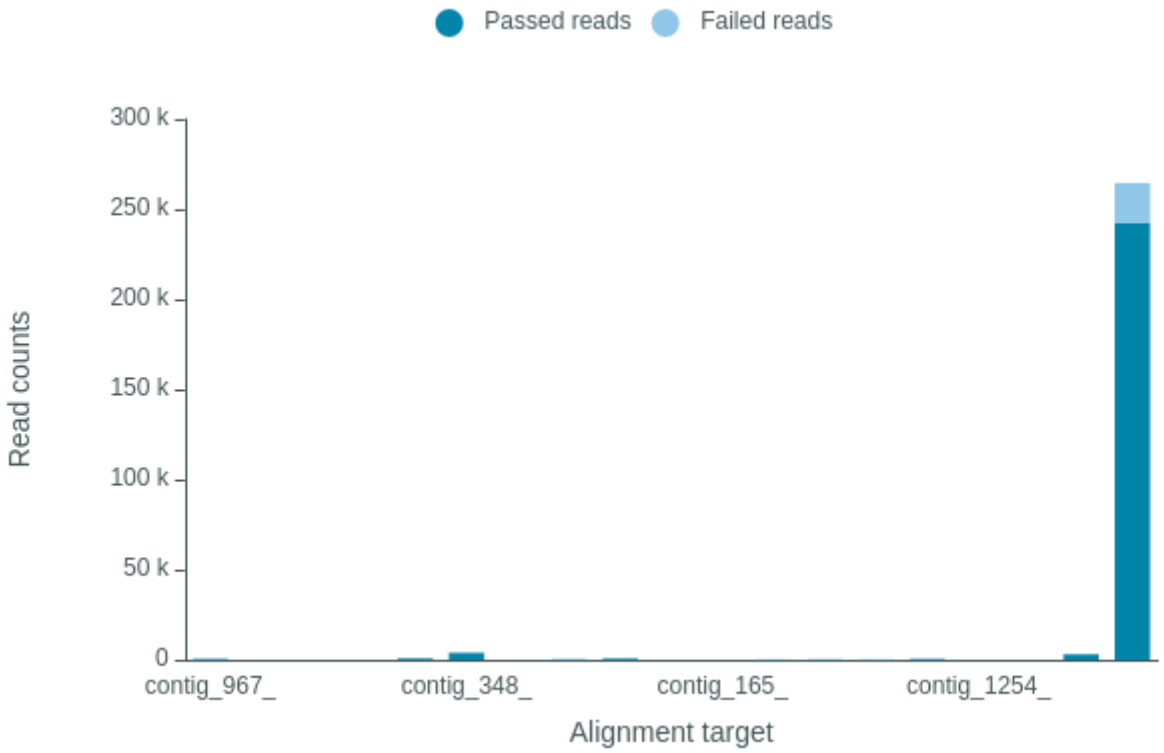


Read Length Histogram Basecalled Bases

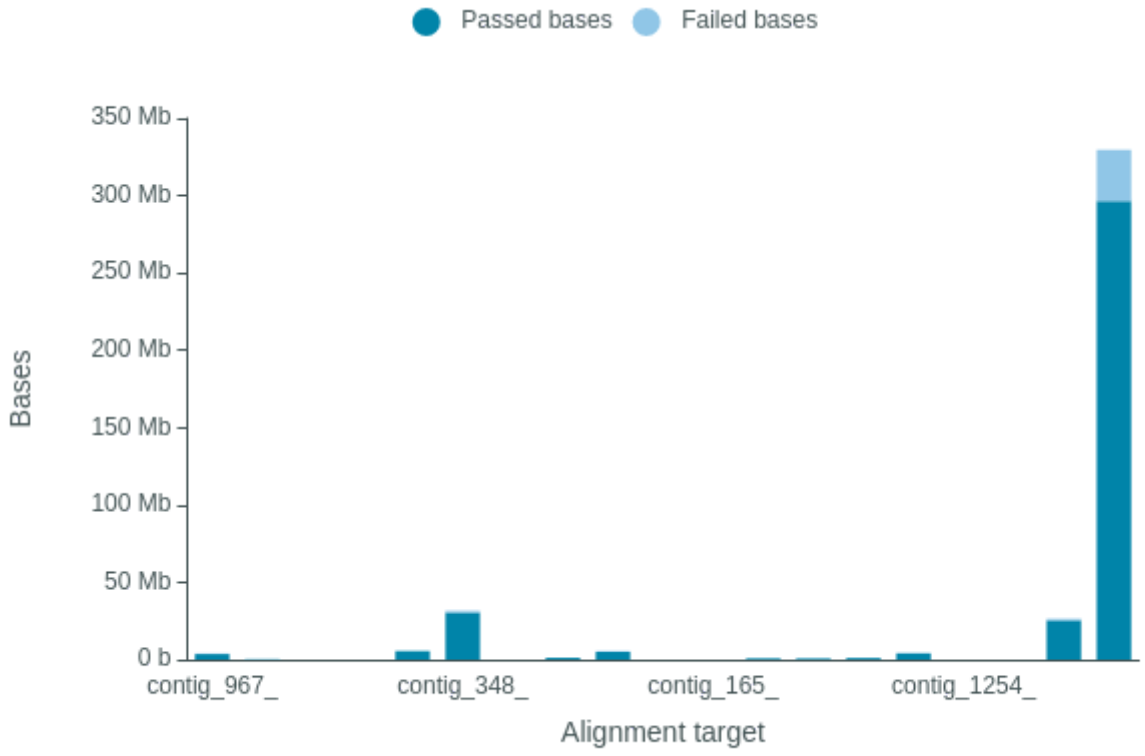
Estimated N50: 10.94 kb



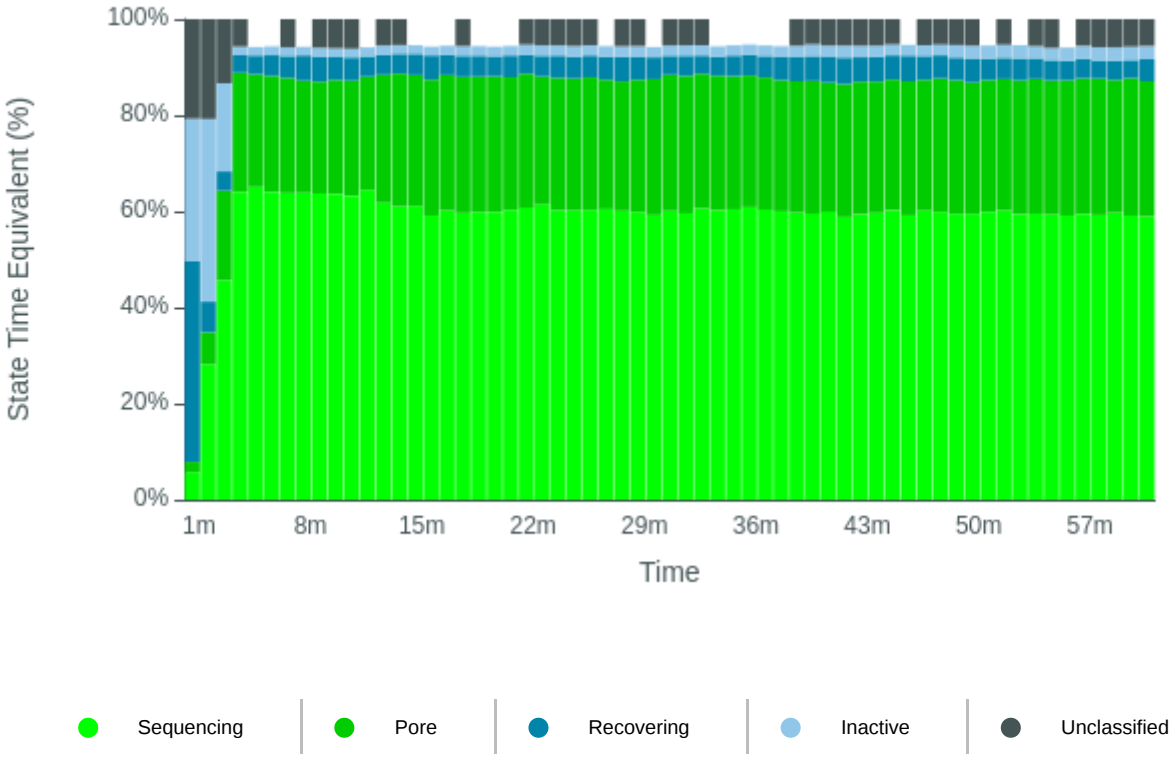
Alignment Target Hits (reads)



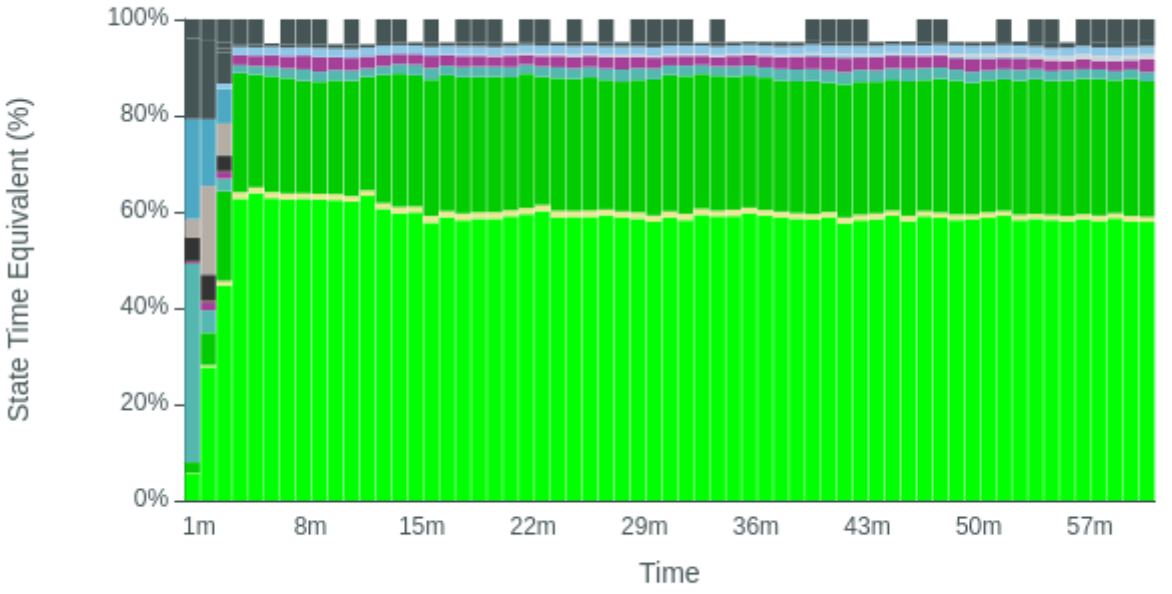
Alignment Target Hits (bases)



Duty Time Grouped

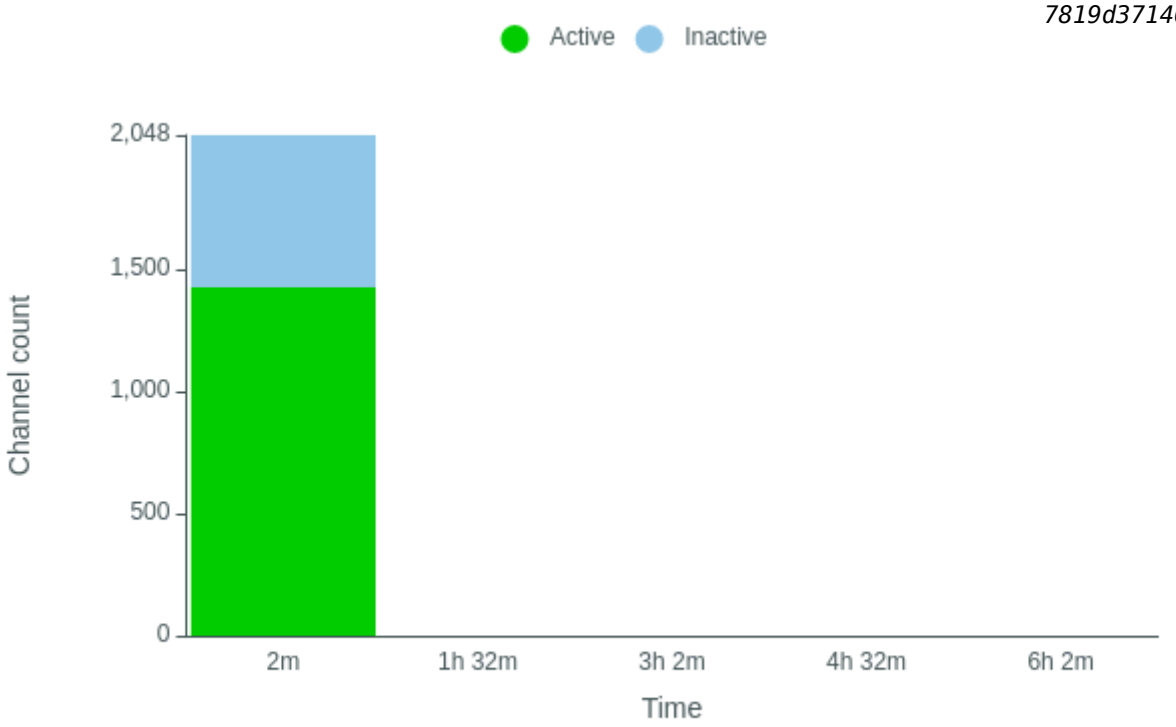


Duty time Categorised

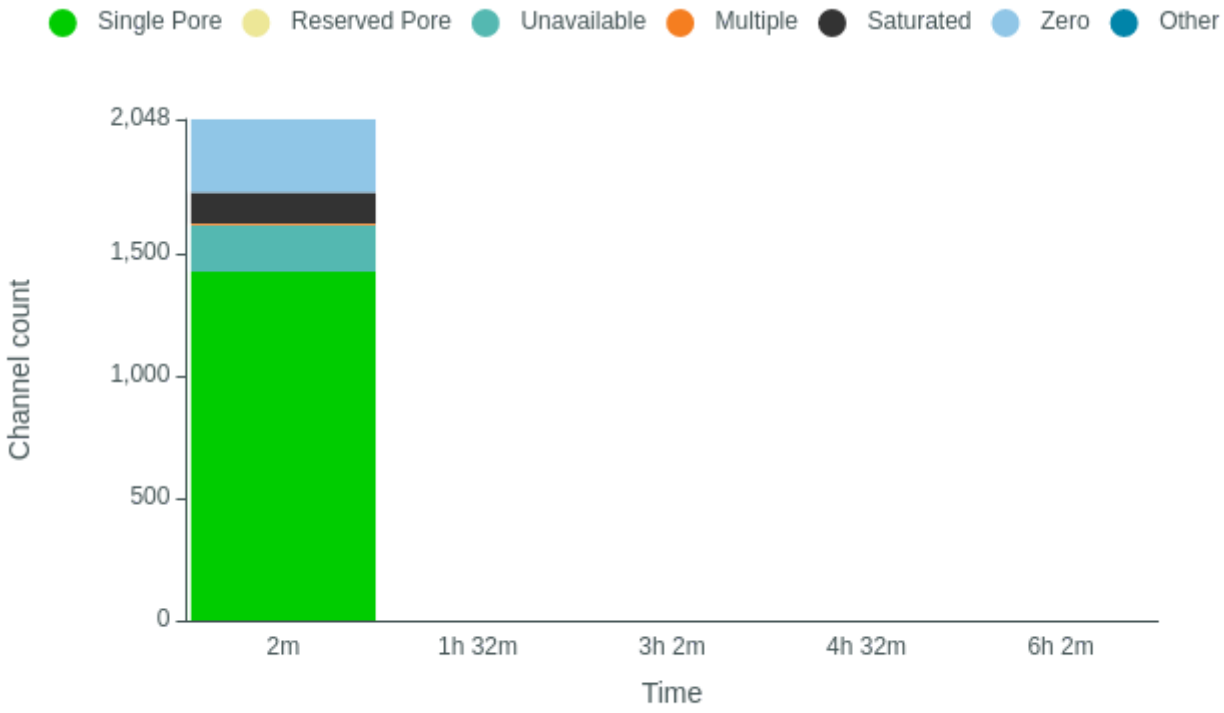


Strand
Adapter
Single Pore
Unavailable
Active Feedback
No Pore From Scan
Out Of Range 2
Possible Multiple
Saturated
Out Of Range 1
Zero
Channel Disabled
Unclassified
Unclassified_following_reset
Pending_manual_reset
Pending_mux_change
Pending Reselection

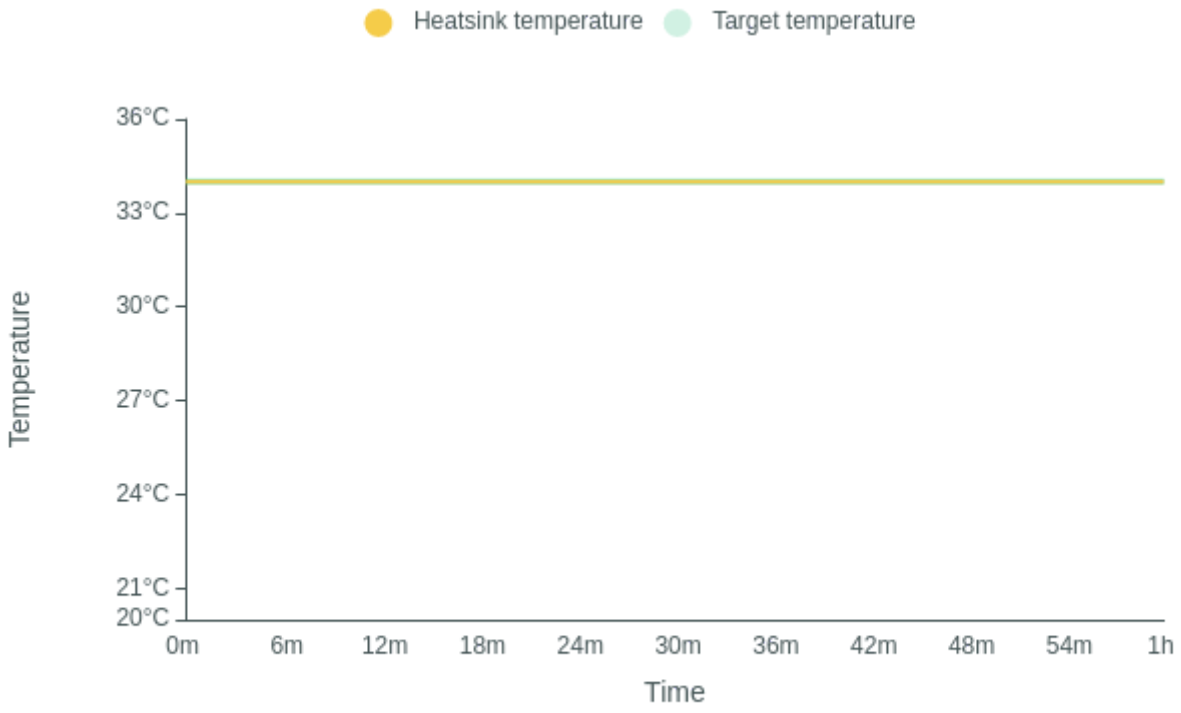
Mux Scan Grouped



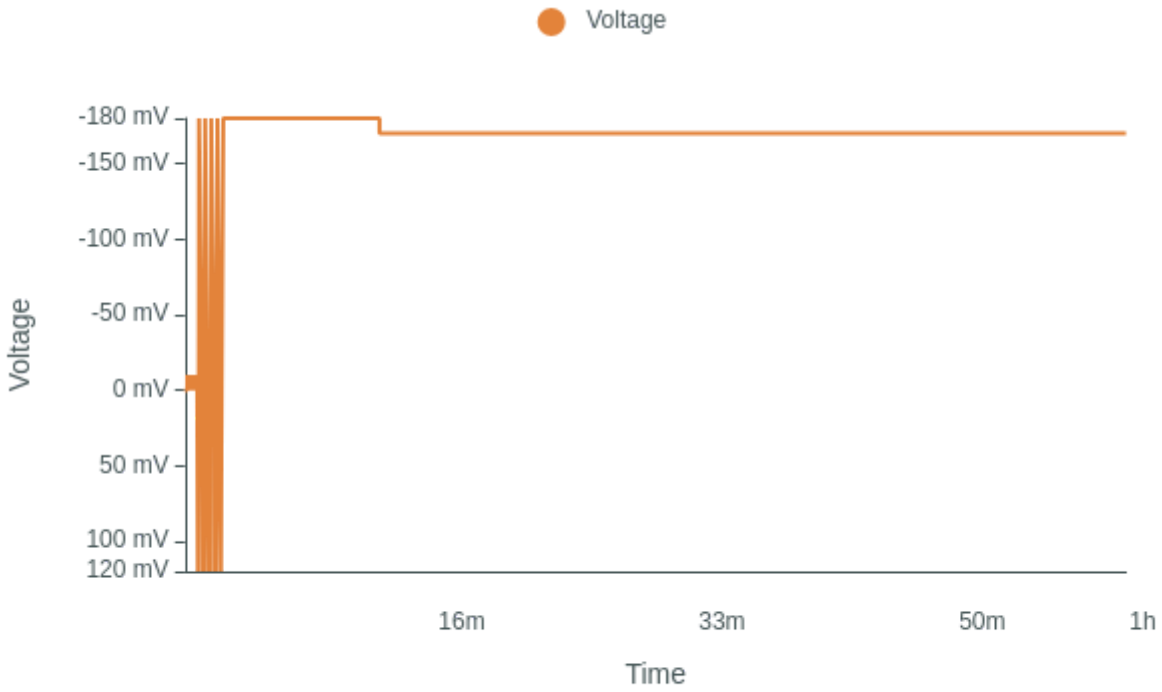
Mux Scan Categorised



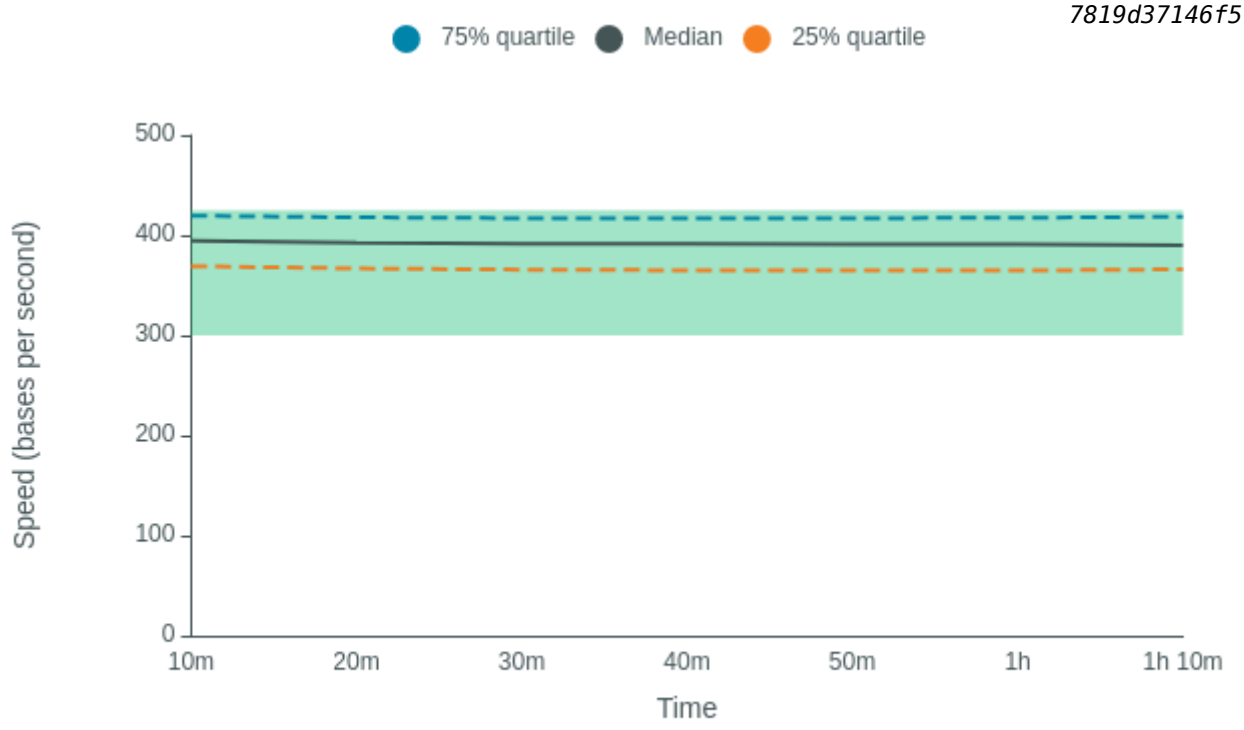
Temperature History



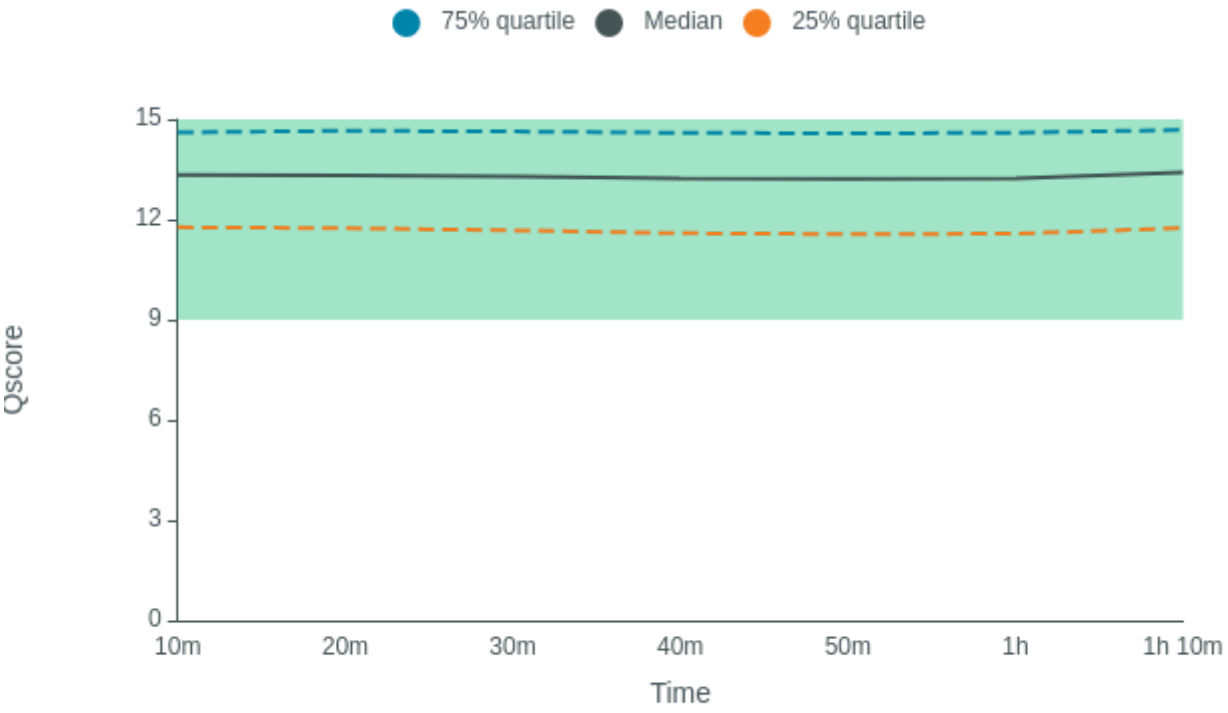
Bias Voltage History



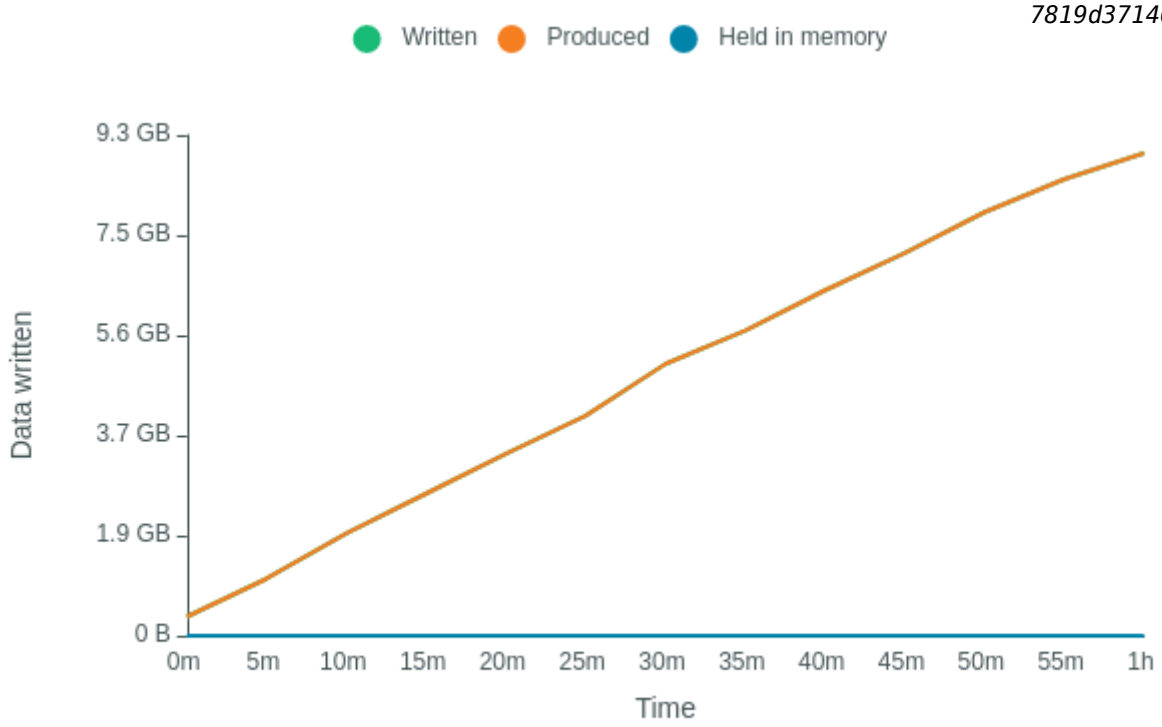
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAQ86094 has found a total of 1425 pores. 503 pores available for immediate sequencing October 5, 16:24
- Performing Mux Scan October 5, 16:22
- Starting sequencing procedure October 5, 16:22
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C October 5, 16:19