#### **Run Info**

Experiment Name ncov\_ucdh\_env1\_run4
Sample ID ncov\_ucdh\_env1\_run4

Run ID **3ac92cc2-2540-41d6-9128-09ba1ccd31c8** 

Flow Cell Id ABE356

Start Time October 7, 15:55

Run Length 6h 2m

#### **Run Summary**

Reads Generated 1.22 K
Bases Generated 365.27 Kb
Estimated Bases 340.59 Kb

#### **Run Parameters**

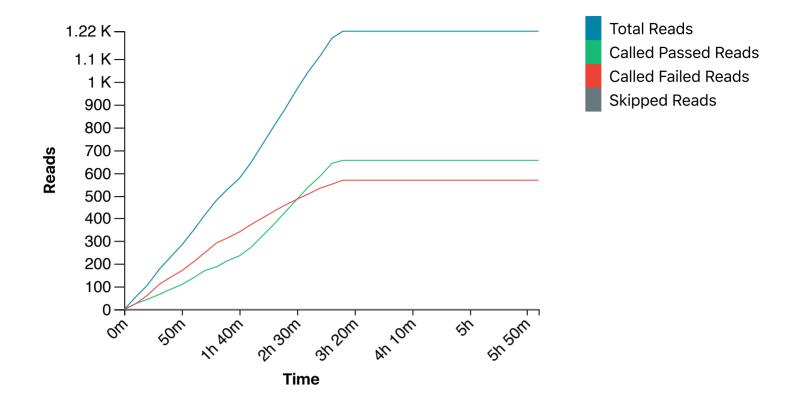
#### **Versions**

 MinKNOW Core
 3.6.5

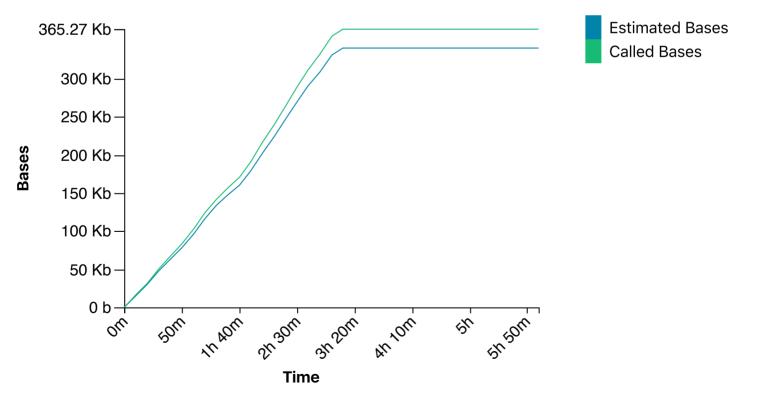
 Bream
 4.3.16

 Guppy
 3.2.10

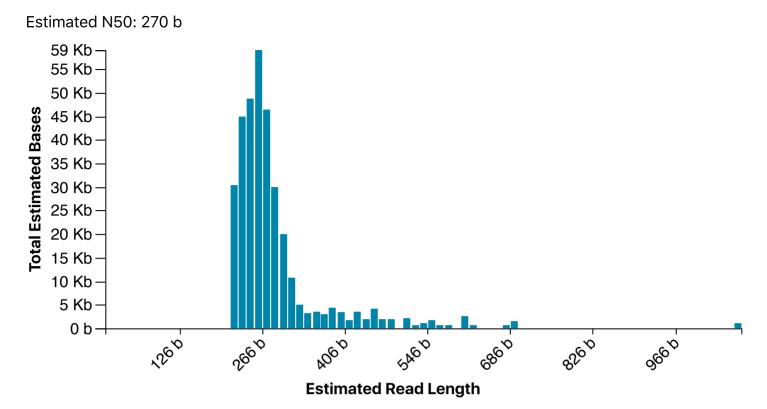
## **Cumulative Output Reads**



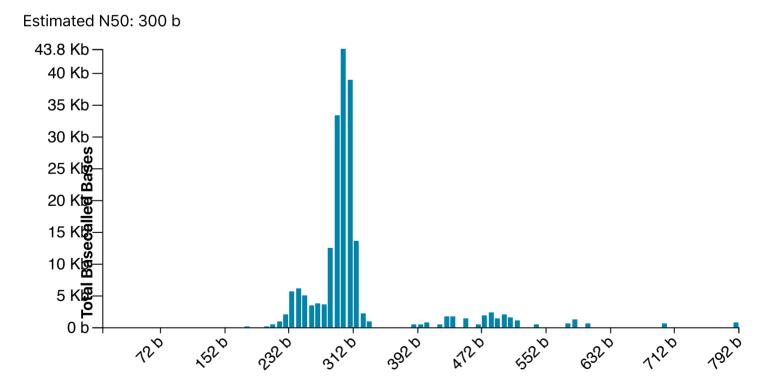
### **Cumulative Output Bases**



## **Read Length Histogram Estimated Bases**

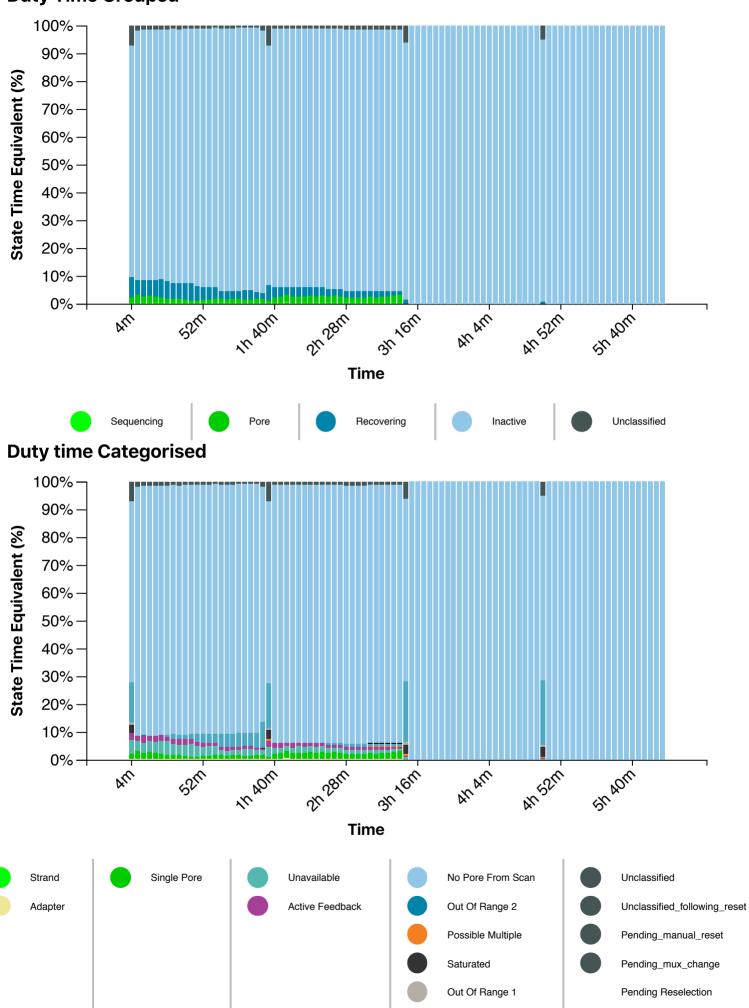


### **Read Length Histogram Basecalled Bases**



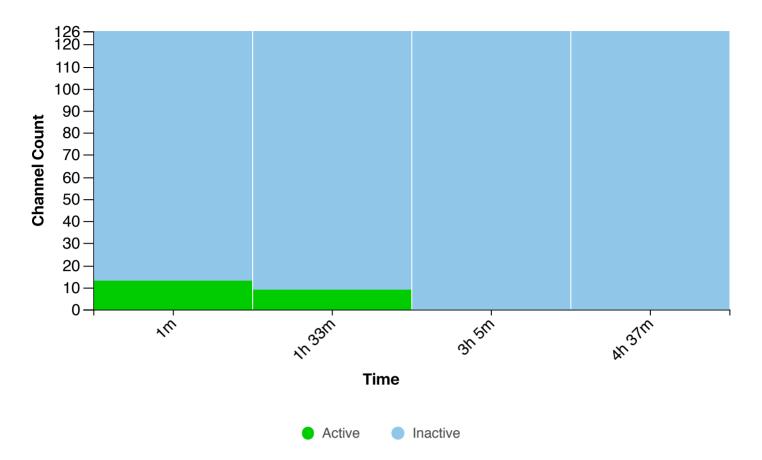
**Read Length** 

### **Duty Time Grouped**

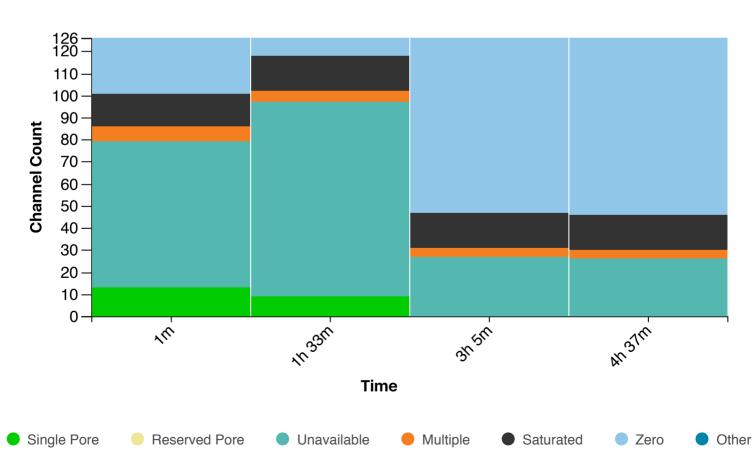


Zero

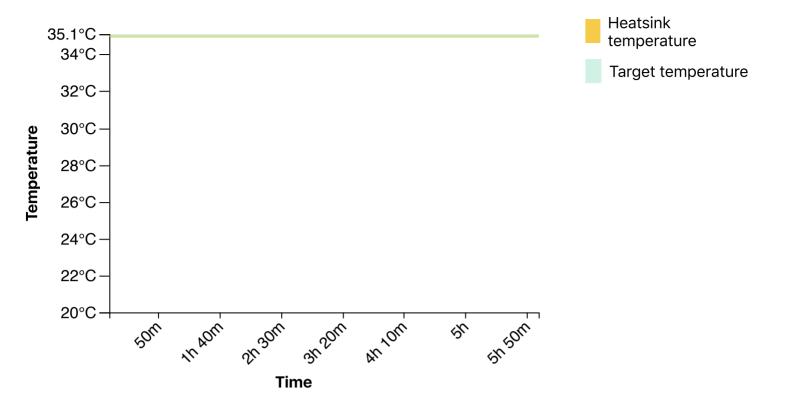
## **Mux Scan Grouped**



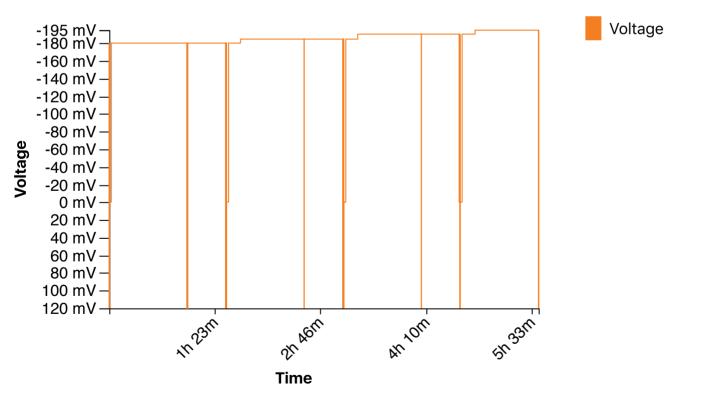
# **Mux Scan Categorised**



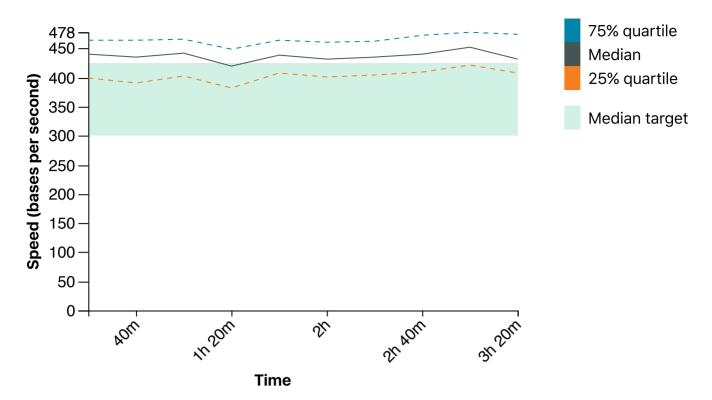
## **Temperature History**



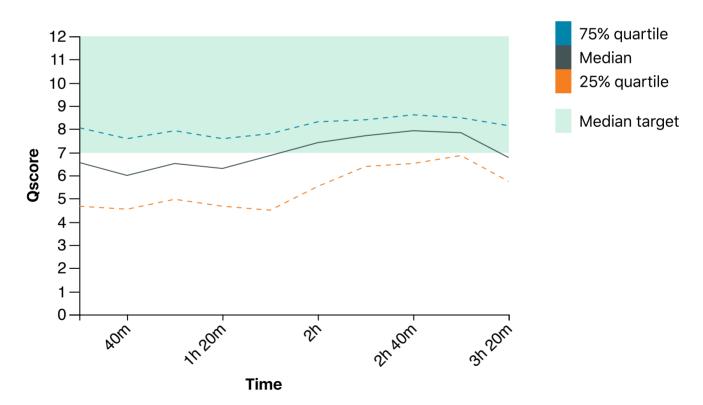
### **Bias Voltage History**



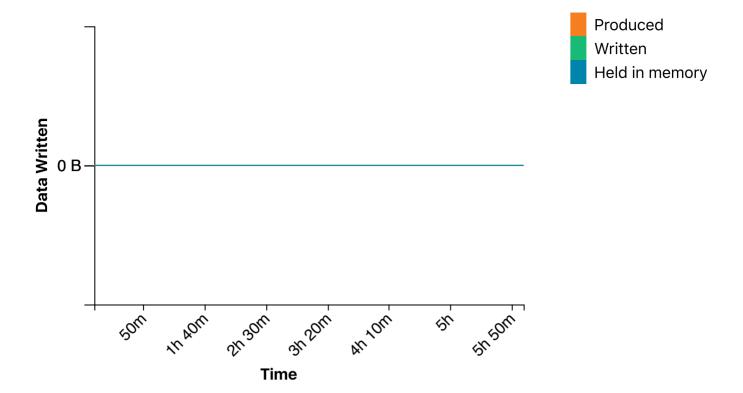
# **Translocation Speed**



## **QScore**



## **Disk Write Performance**



#### **Run Debug Messages**

- The sequencing run has finished, but basecalling may continue October 7, 21:57
- Flow cell ABE356 has 0 pores available for sequencing. Starting sequencing with 0 pores October 7, 20:34
- Performing Channel Scan October 7, 20:33
- Flow cell ABE356 has 0 pores available for sequencing. Starting sequencing with 0 pores October 7, 19:02
- Performing Channel Scan October 7, 19:01
- Flow cell ABE356 has 9 pores available for sequencing. Starting sequencing with 9 pores October 7, 17:30
- Performing Channel Scan October 7, 17:28
- Flow cell ABE356 has 13 pores available for sequencing. Starting sequencing with 13 pores October 7, 15:58
- Performing Channel Scan October 7, 15:57
- Starting sequencing procedure October 7, 15:57
- Waiting up to 300 seconds for temperature to stabilise at 35.0°C October 7, 15:55
- Disk / has 1570 GB space remaining October 7, 15:55