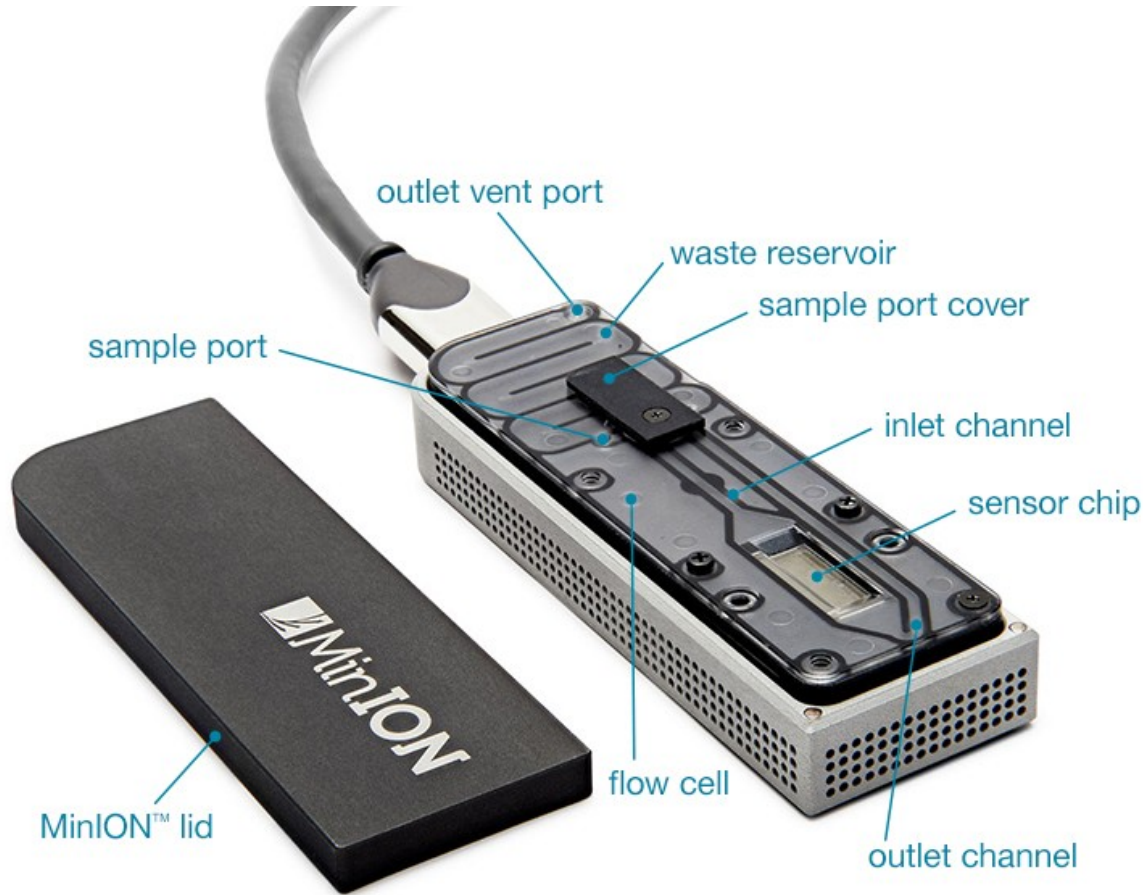
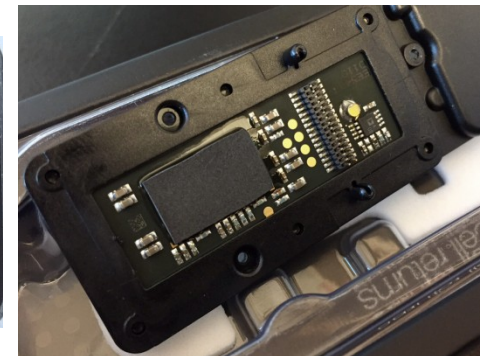


MinION Anatomy



Pre-Run Check List

- ① **Make sure required Software is installed:-**
 - MinKNOW** Control of MinION device & run parameters
 - Metrichor** Cloud basecalling of event data
 - MinoTour** Live monitoring / control of run while sequencing
 - Chronolapse** Screen image grabber for record keeping
 - Poretools, poRe** Sequence extraction and data summaries
 - TeamViewer** Remote control of MinION computer
- ② **Confirm automatic software updates and sleep modes are disabled**
- ③ **Check computer SSD for available storage space >150Gb**
- ④ **Flowcell inspection** Remove bubbles in fluid lines and on surface of flowcell where possible if present, & confirm conductive heat pad is installed on bottom surface of ASIC chip.



Preparing & Loading MinION Device

- 1 Attach Flowcell to MinION device and plug into USB3 port



- 2 Start MinKNOW software and start device



- 3 Name Run and start platform-QC protocol



If flow-cell good proceed
(Single Good pores >650)

- 4 Prime flow-cell with 2x 500 μ l 1xRBF1 for 10 mins each
(500 μ l 2xRBF1 + 500 μ l H₂O)



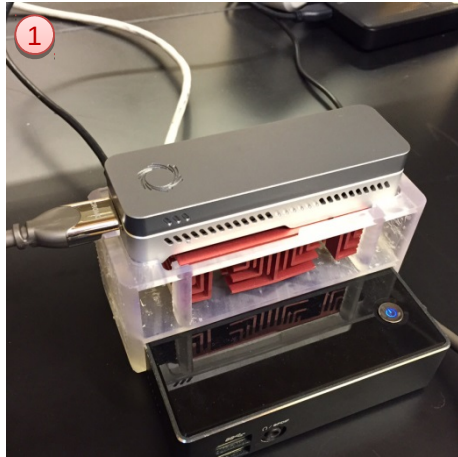
- 5 Load 150 μ l of Library in 1xRBF1
(75 μ l 2xRBF1 + x μ l H₂O + 4 μ l Fuel + 6-11 μ l Pre-sequencing Mix)



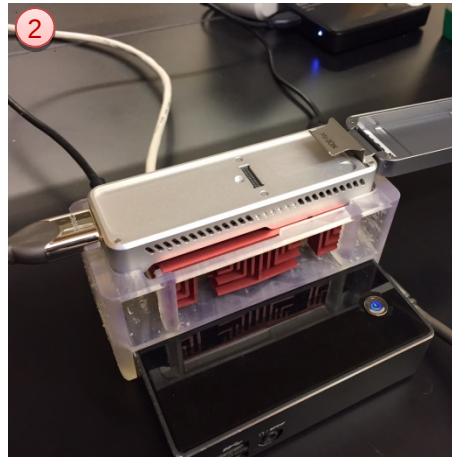
- 6 Name run and start Sequencing Protocol – Standard / Modified :o)
(Start Metrichor & required workflow plus screen capture software)



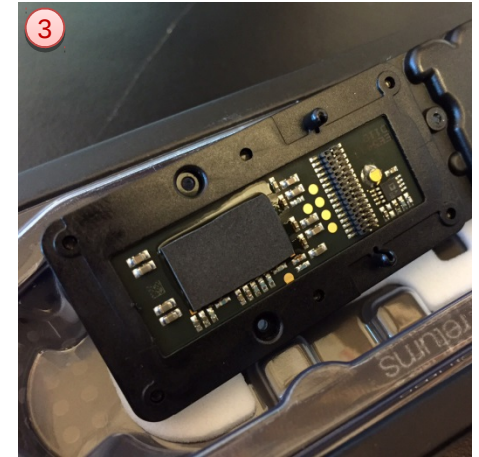
Inserting Flow-cell into MinION Device



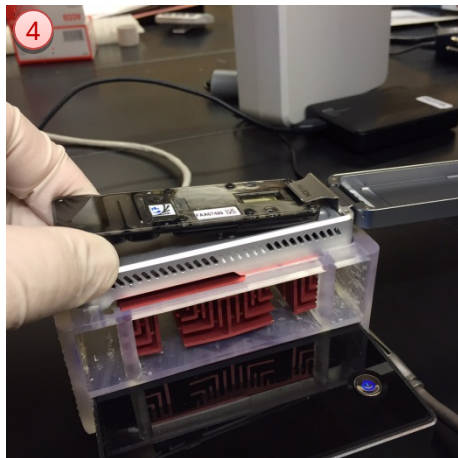
Ready MinION



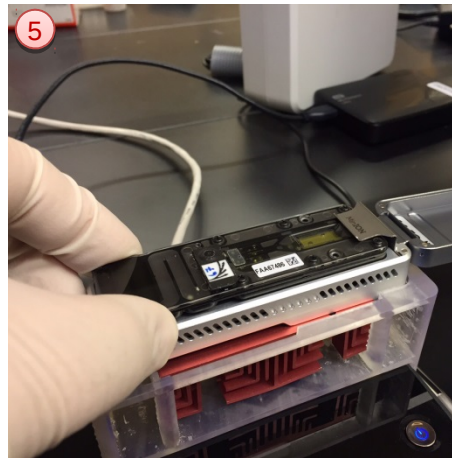
Open lid



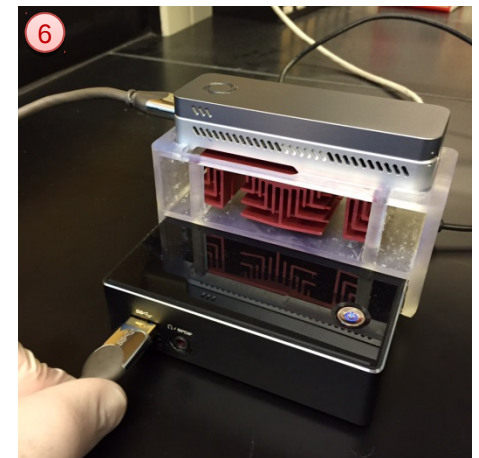
Unpack flow-cell, check heat pad intact & ASIC bubble free



Slide flow-cell into place



Make sure flow-cell is seated properly



Plug MinION into USB3 port

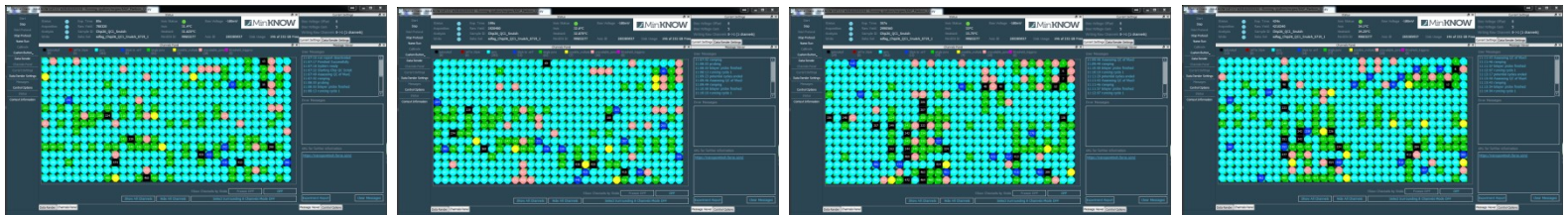
Flow-cell Quality Assessment

Platform-QC scans the 2048 channels as 4 Mux groups @ -180mV with R9 & reports back single good channel assignment to each of g1 to g4 groups with up to 512 wells each. Expect Good correlation using R9 flowcells between Platform QC pore numbers and those obtained at the start of a run.

Good

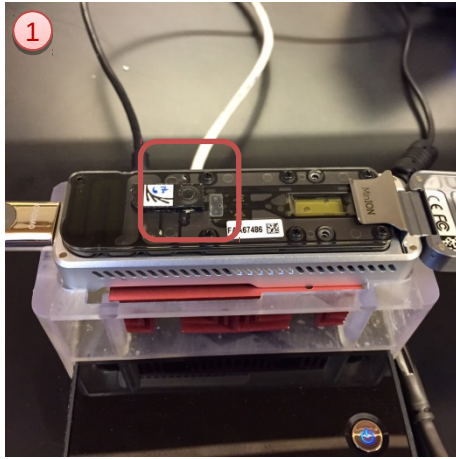


Bad

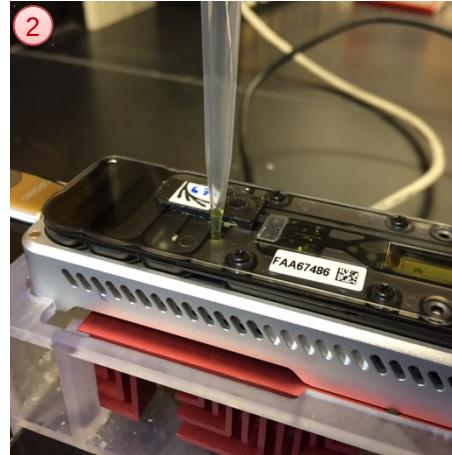


>650 Pore Guarantee

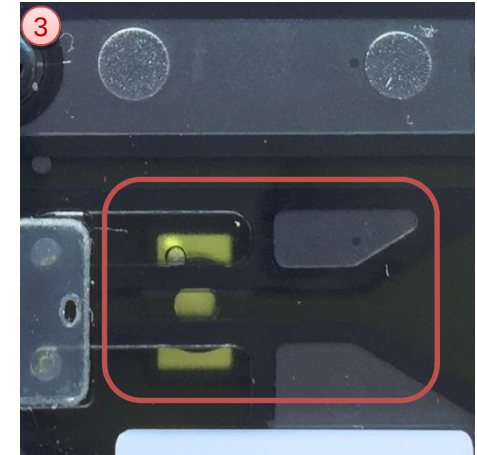
Priming and Loading Flow-cell



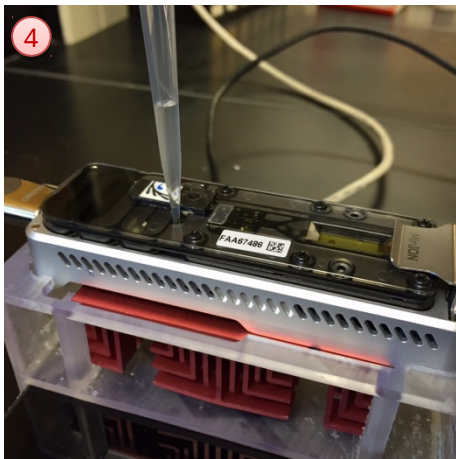
Open sample port



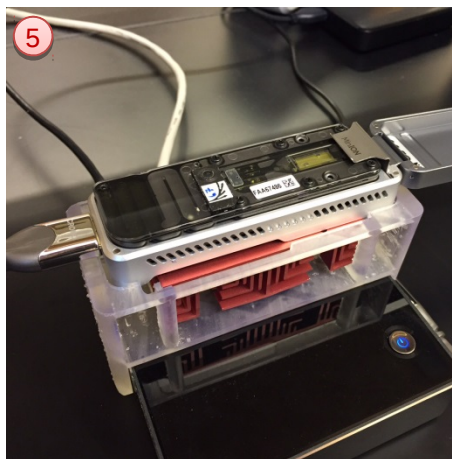
Slowly remove any air from sample port with pipette



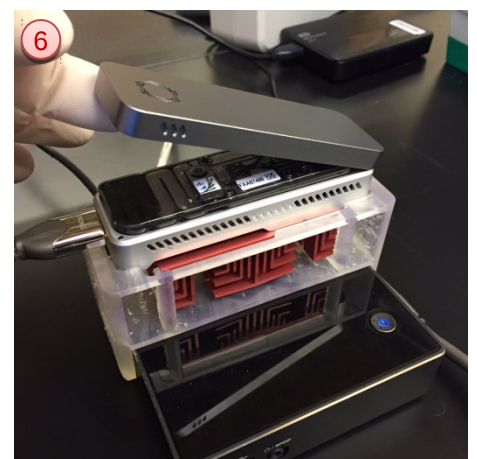
Confirm fluidic channel is free of bubbles



2 x 10 min 500µl 1xRBF1 followed by 150µl Library



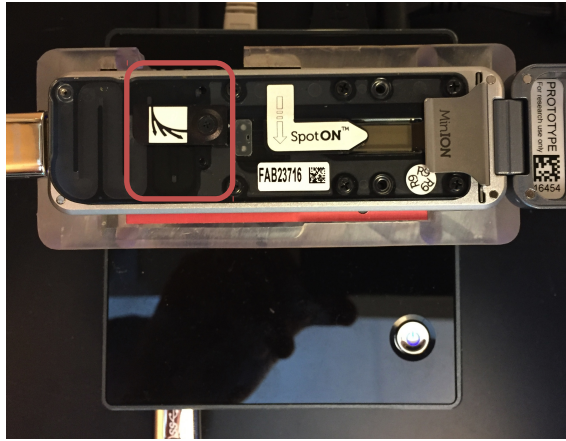
Close sample port



Close lid and GO!

Priming and a Loading SpotON Flow-cell

1



Open sample port

2

Flowcell Priming

Slowly remove any air from sample port with pipette

1x 10 min 500 μ l RBF1 through sample port

1x 10 min 300 μ l RBF1 through sample port

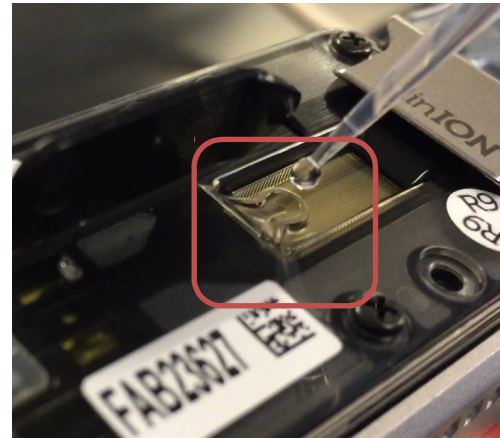


3



Open SpotON port and then add 200 μ l RBF1 through sample port, NOT SpotON port.

4



Add 75 μ l of Sequencing Mix to SpotON well dropwise



Close ports, lid and GO!

Start Run

1 Start Sequencing Recipe Script

Name run and select required Recipe Script

2 Start Chronolapse screen capture

Image grab every 30 seconds and as required at start

3 Start Metrichor workflow

Select desired workflow:- 2D basecall or WIMP

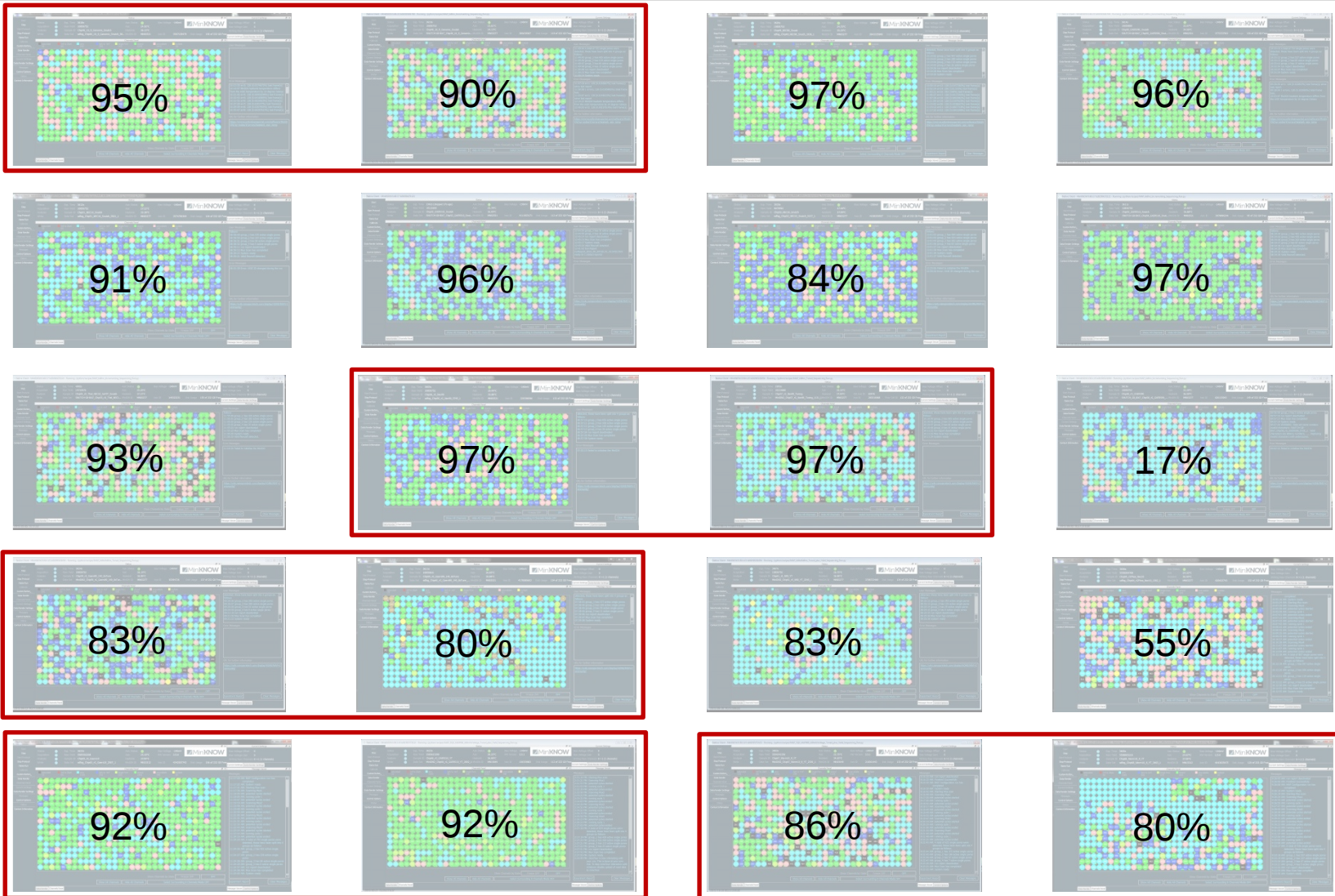
4 Start MinUp & Open MinoTour Browser Window

Issue command line parameters for read mapping and device control as below or use MinUP-GUI:

```
minUP.exe -dbh minotour.nottingham.ac.uk -dbu USER -pw PWD -w d:\data -f c:\reference\REF.txt -u USER  
-c -bwa -d -ip xxx.xxx.xxx.xxx -pin XXX -s minion
```



Good or Bad Library/Flowcell ?



% of Single Good pores in Strand

Single Good Pore % in Strand as Library QC

Use the relative quantity of in Strand reads as a measure of library quality independent of pore number



$$292 / 302 = 97\%$$

The screenshot shows the MinKNOW software interface. The main window displays a grid of pore counts, with a red box highlighting a specific row of pores. The interface includes various control panels and status indicators.

Channels Panel Legend:

- saturated (7)
- -Inf to 20pA (0)
- zero (36)
- SpA to -Inf (119)
- Single Pore (10)
- strand (292)
- unavailable (46)
- multiple (2)

Status: Exp. Time 3611s, Raw Yield 10850752, Sample ID Chip54_GAERS10_Snutch, Data Set SNUTCH-GB-BX17_Chip54_GAERS10_Snut...

Current Settings: Bias Voltage -140mV, Bias Voltage Offset 0, Bias Voltage Gain 5, Writing Raw Channels 0->1 (1 channels)

User Messages:

- 08:34:04 group_1 has 481 active single pores
- 08:34:05 group_2 has 405 active single pores
- 08:34:06 group_3 has 263 active single pores
- 08:34:07 group_4 has 87 active single pores
- 08:34:28 run report deactivated
- 08:34:29 Mux Scan has completed
- 08:34:32 System ready
- 08:34:39 Valid flowcell detected.

URL for further information: <https://wiki.nanoporetech.com/display/HOME/MAP+Community/>

Buttons: Show All Channels, Hide All Channels, Select Surrounding 8 Channels Mode OFF, Experiment Report, Clear Messages

Footer: 2015-04-30 08:34:36.10

Script Tinkering

① Bias-Voltage Setting & Remux

Bias voltage directly controls induced current flow across the membrane, and current flow is used to assign pores to different categories. With time greater bias-voltage is required to produce current that is in the “single good” pore range. Bias-voltage is the master control. Selection or “re-mux” of pores at a particular targeted voltage must be carried out for maximum efficiency.

② Yield Monitoring

As pore numbers fall and/or reagent is depleted you will see a drop in the event yield over time. Gaining access to still functional, but unselected, pores once event accumulation rate drops below a set value makes much better use of a flow-cell. This lessens unproductive electrochemical gradient deterioration observed with standard recipe scripts.

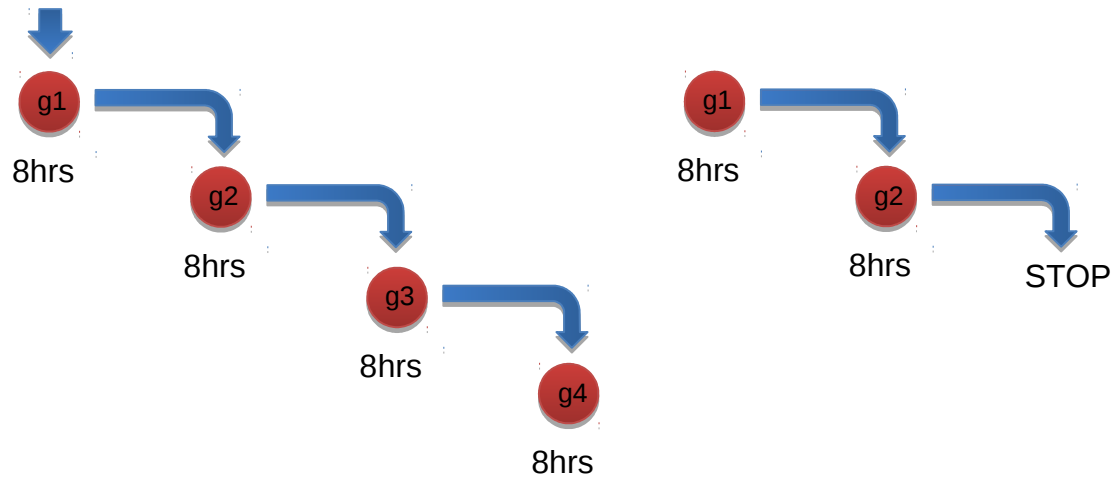
③ Pore Shepherding

Wells actively sequencing experience an electrochemical gradient deterioration that is twice that of inactive pores, but even inactive pores show a deterioration that requires bias-voltage increases for optimal functioning. Because of the 4-1 (wells - electrical channel) nature of current flow-cells this results in a spreading of the optimal bias-voltage required for a particular well depending on its on/off history. To mitigate this, sub-peak bias-voltage selection can “shepherd” well population more tightly by attempting to deplete least used wells.

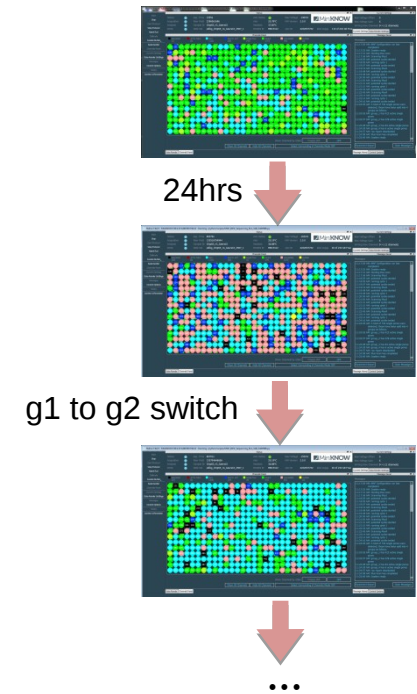
Standard 48hr Sequencing Recipe Script

R9 48hr Genomic DNA Sequencing Script

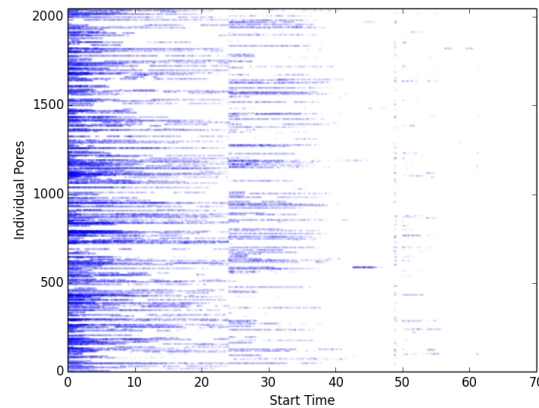
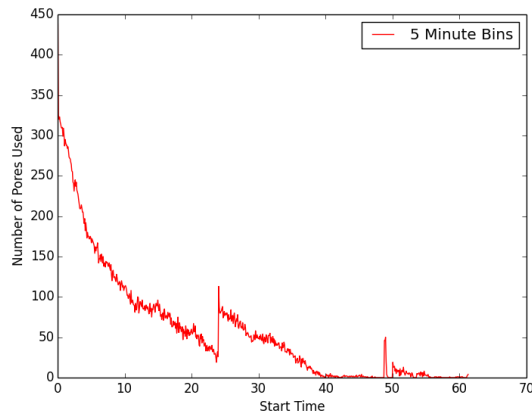
Mux @-180mV to assign g1, g2, g3 & g4 pores



(example from previous R7.3 Version)



Example Pore Usage from retired R7.3



Modified Scripts to Maximise Flowcell Yields

Yield-Monitoring_Voltage-Tuning Scripts

(If new flowcell use -180mV to start)

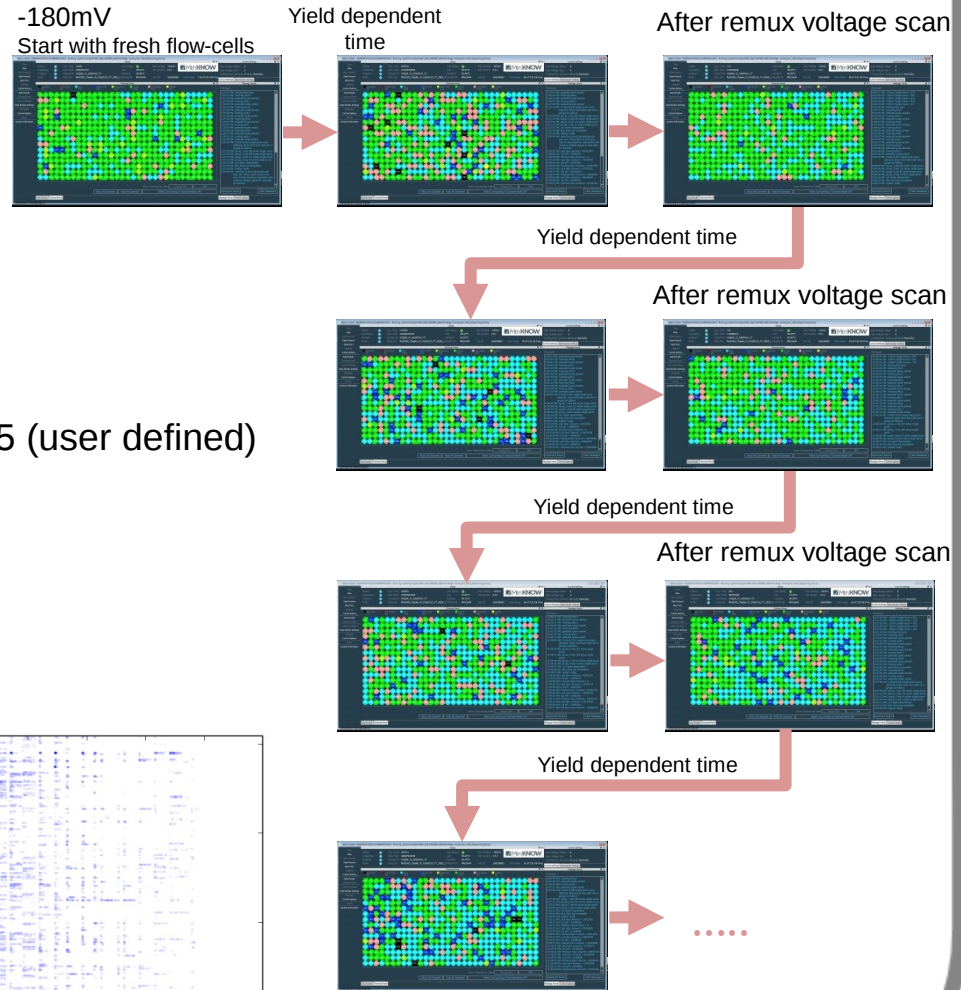
Multi-Voltage Re-mux scan selecting one within a defined range of the greatest "single good pore" count voltage

15 min
Mux / Re-Mux Scan
(Voltage tuned across 30mV range)

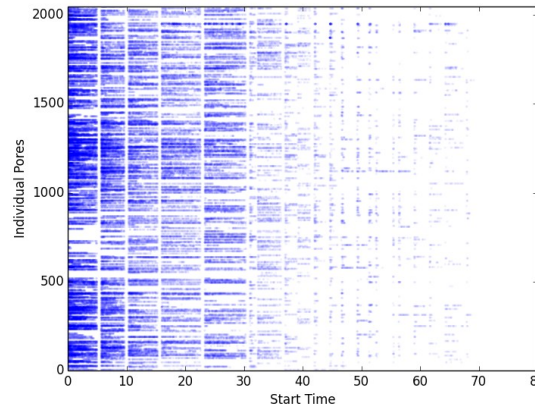
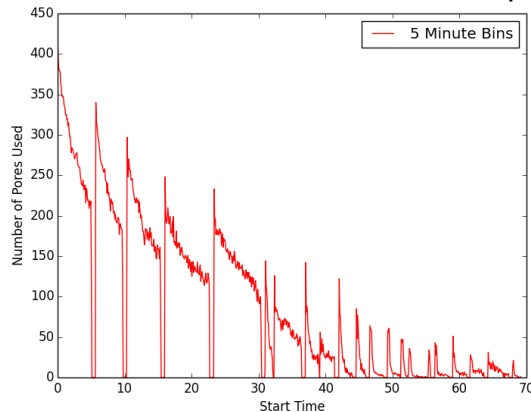
Switch when hourly event yield drops below 67% of first hour of this segment

Yield Dependent Time
(~1-5 hrs)

x5 (user defined)

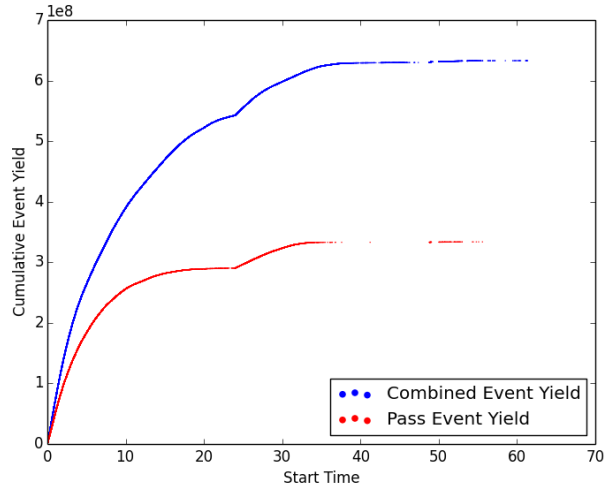


Example Pore Usage

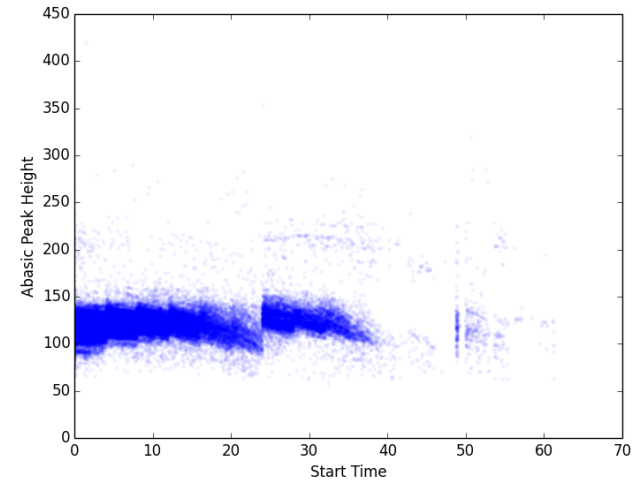


Run Dynamics:- SQK006 Standard Recipe Script

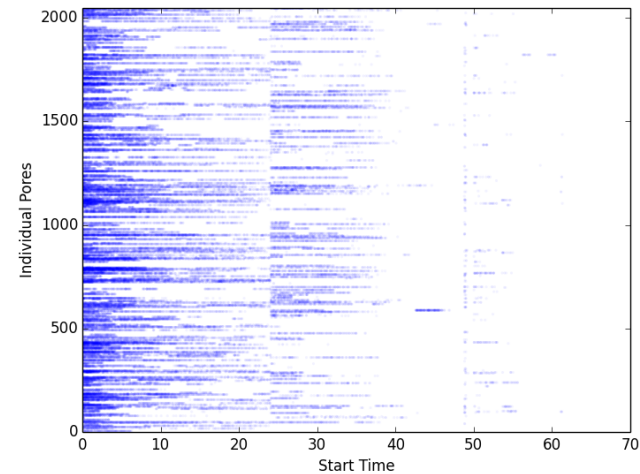
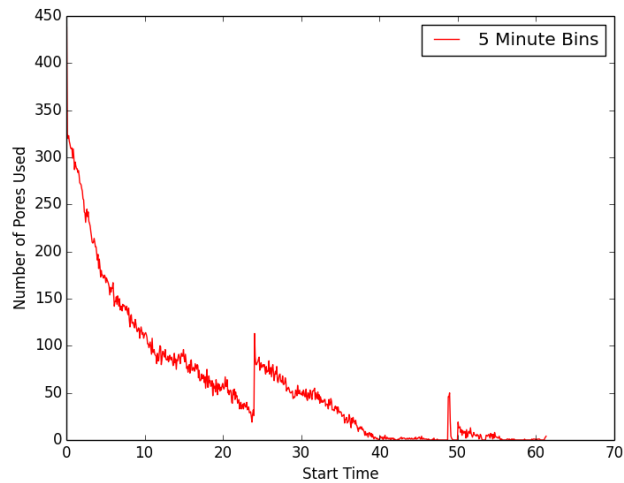
Event Accumulation



Abasic Current

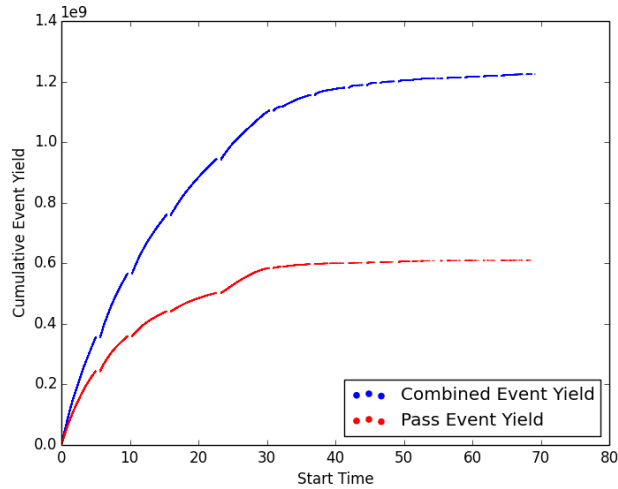


Pore Usage

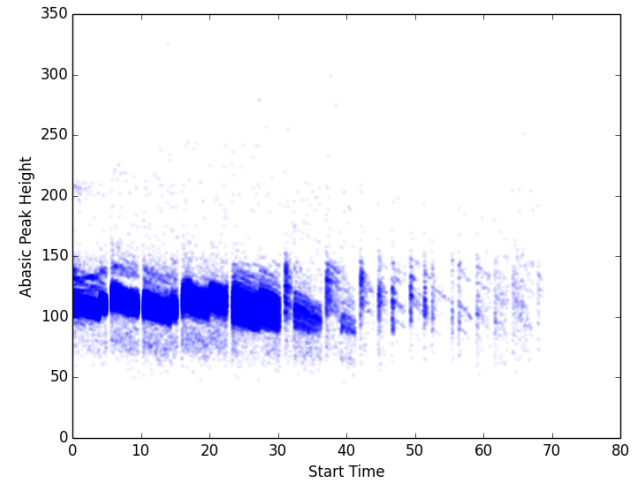


Run Dynamics:- SQK006 Tuning Recipe Script

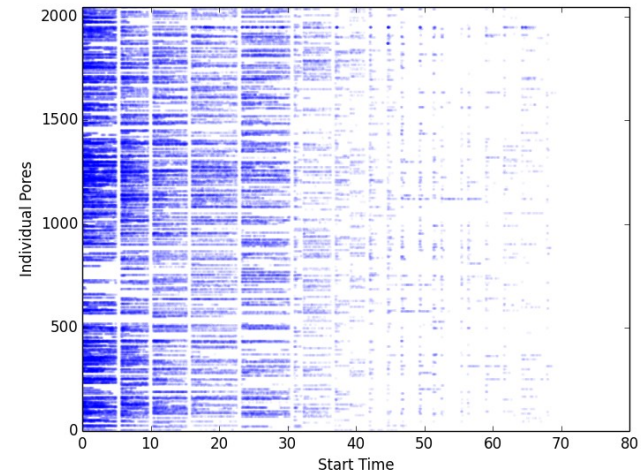
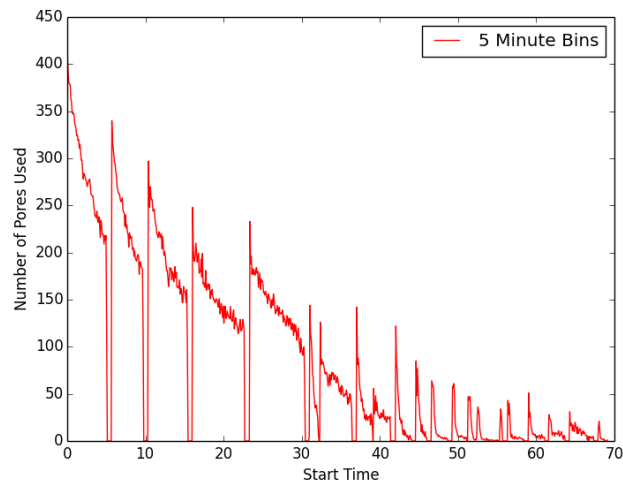
Event Accumulation



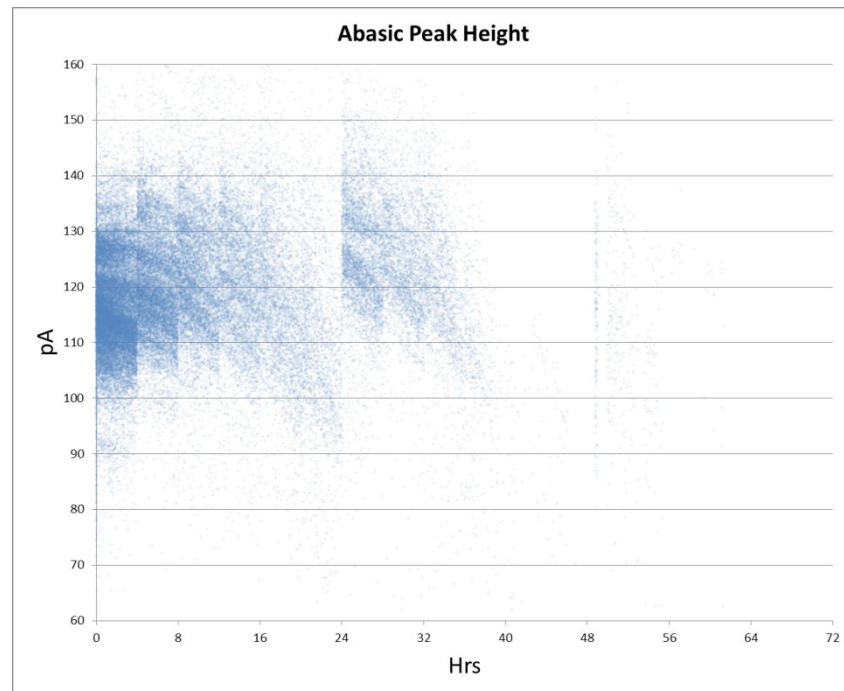
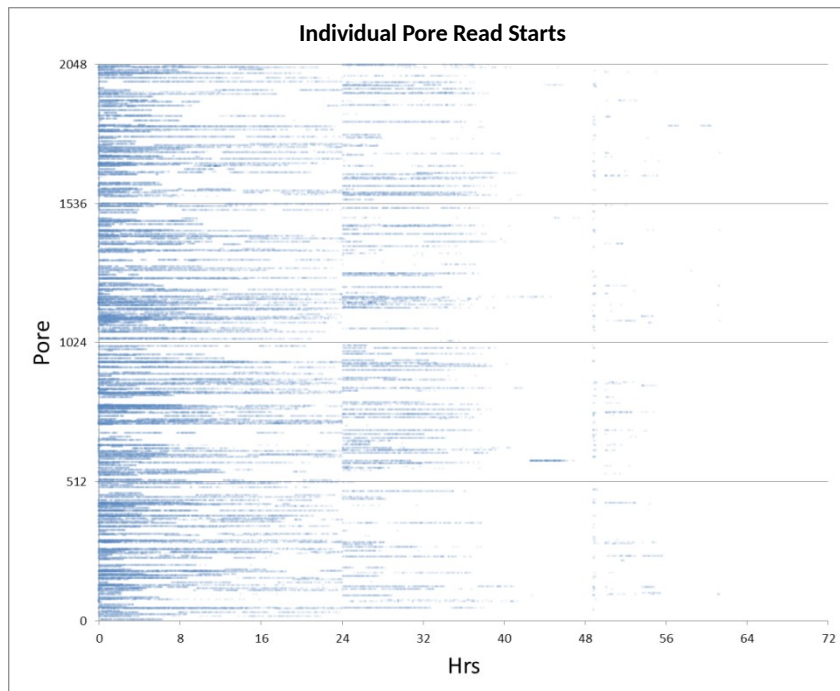
Abasic Current



Pore Usage



Standard Script
(Chip65)



Tuning Script
(Chip66)

