Run Info

Experiment Name	**SARS2**
Sample ID	**A549_SCoV2_totRNA**
Run ID	**43d615e8-5fa6-490c-bebc-f856a9b0215f**
Flow Cell Id	**FAO33670**
Start Time	**July 31, 14:23**
Run Length	**2d 19h 48m**

Run Summary

Reads Generated	**2.15 M**
Bases Generated	**634.54 Mb**
Estimated Bases	**2.75 Gb**
Percentage Basecalled	**26%**

Run Parameters

Flow Cell Type	**FLO-MIN106**
Kit	**SQK-RNA002**
Basecalling	**on**
Specified Run Length	**72 hours**
Initial Bias Voltage	**-180 mV**
FAST5 Output	**Enabled**
FAST5 Output Options	**zlib_compress,fastq,raw**
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	**High-accuracy basecalling**

Versions

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

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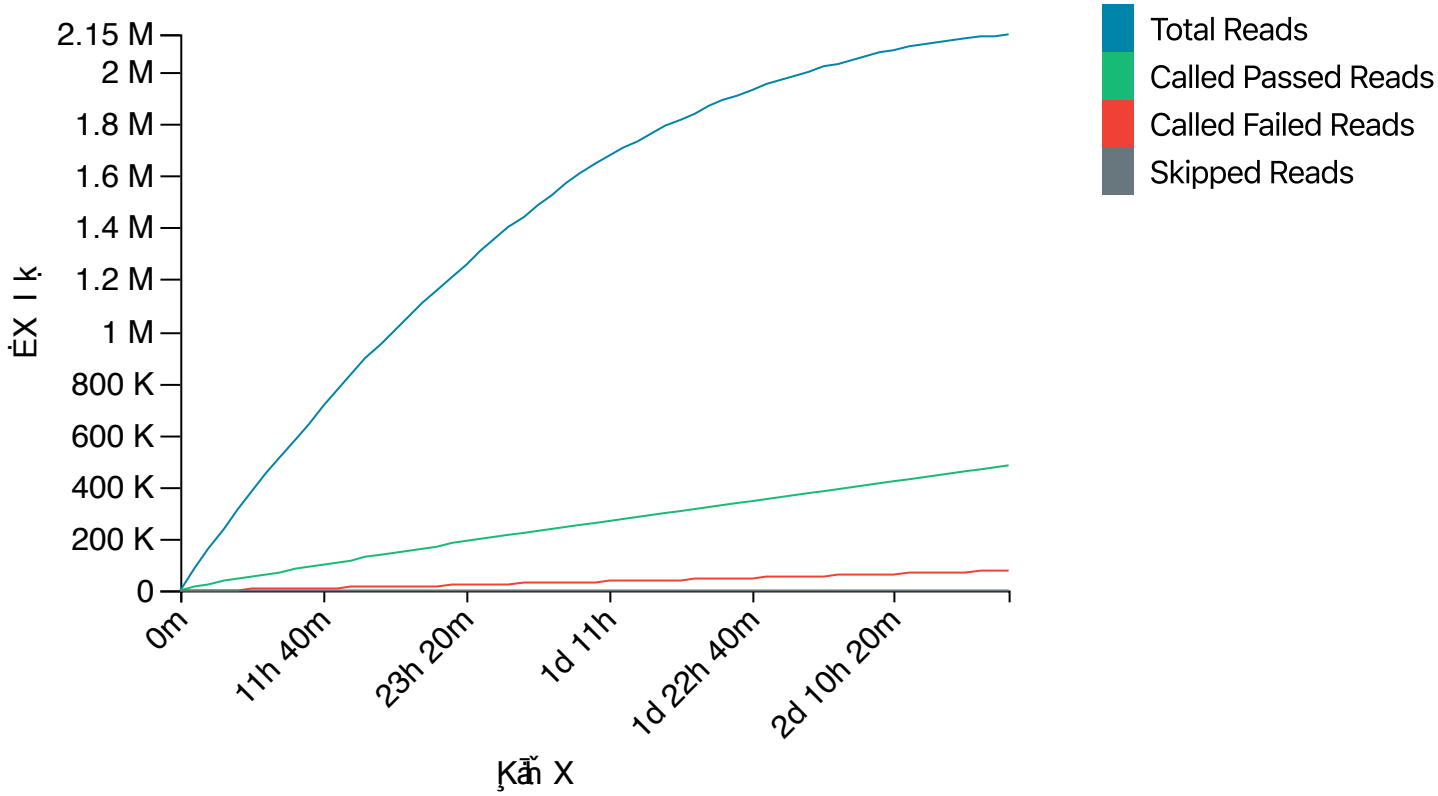

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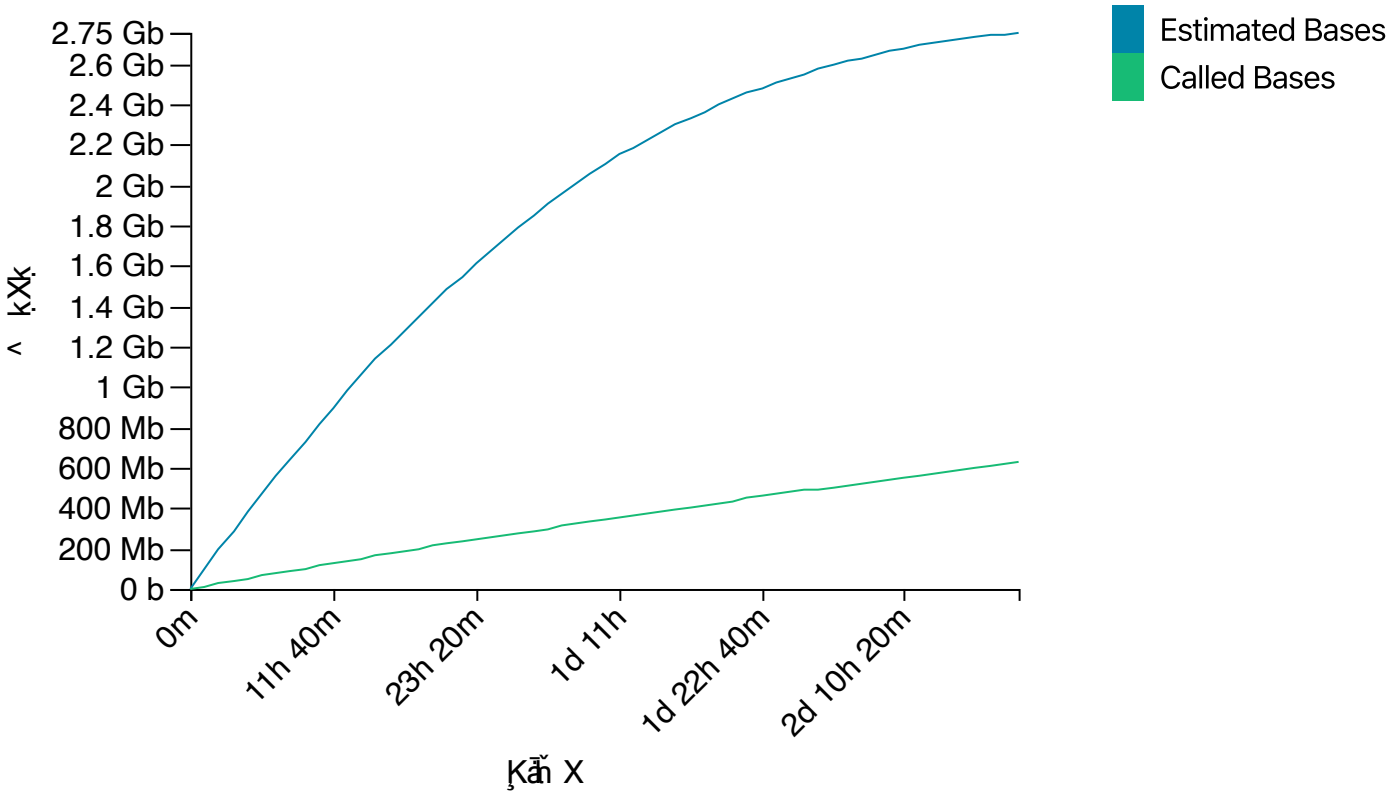

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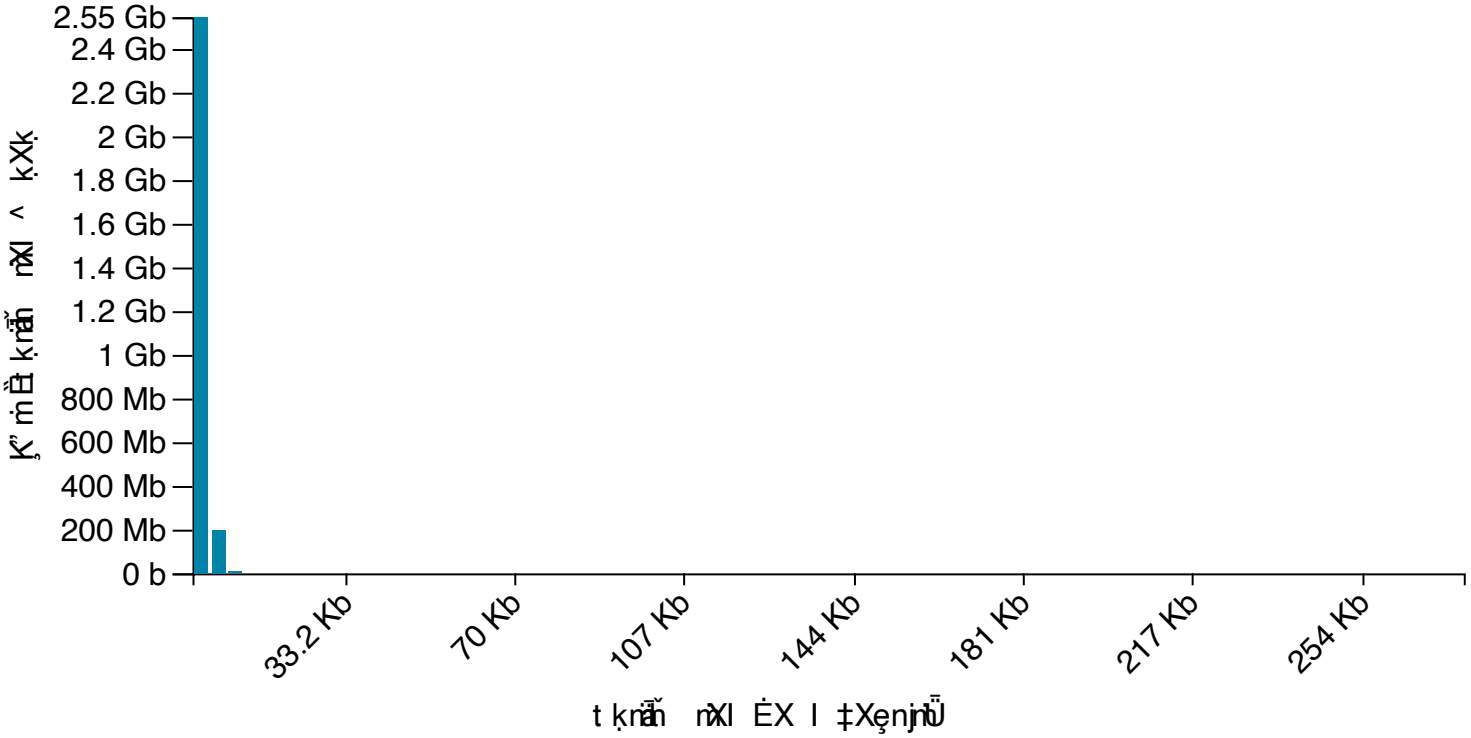
Estimated N50: 1.56 Kb



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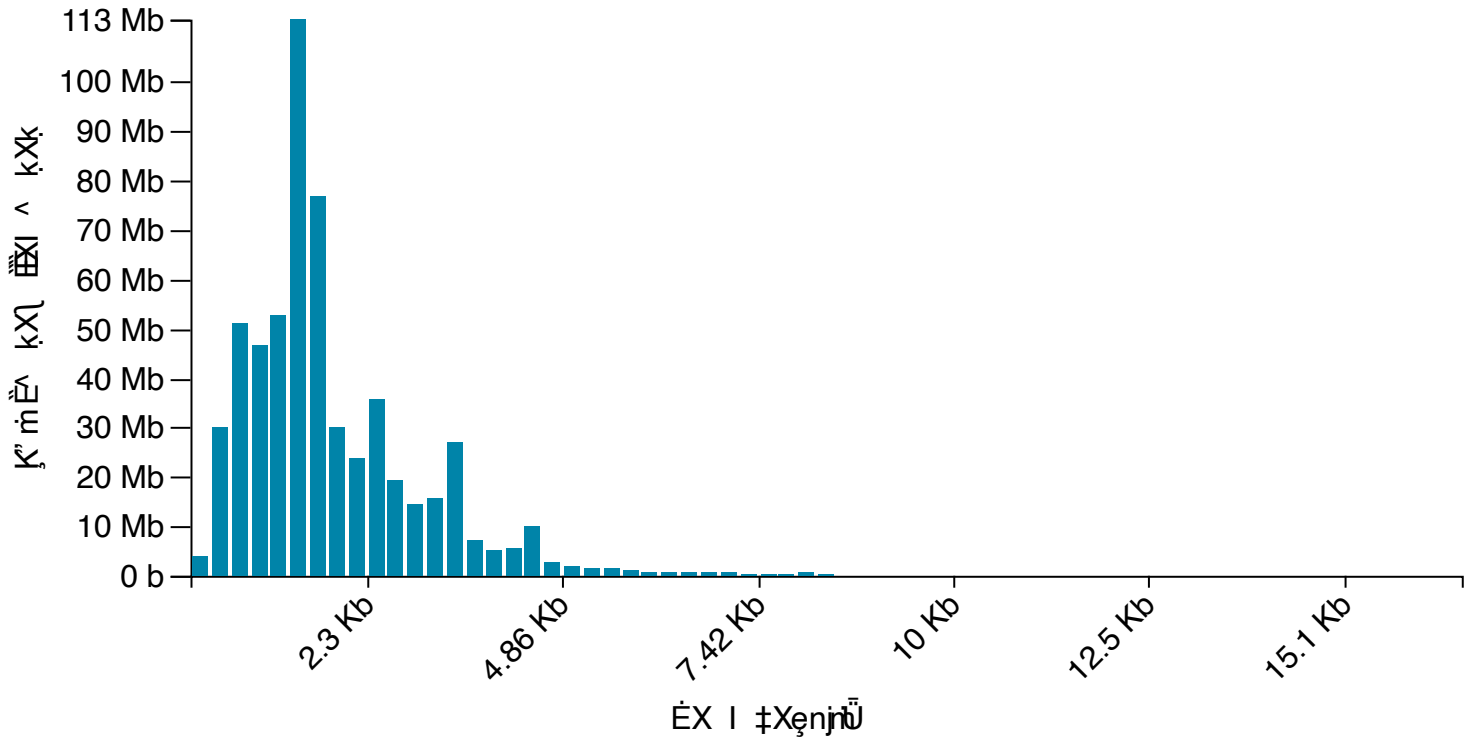
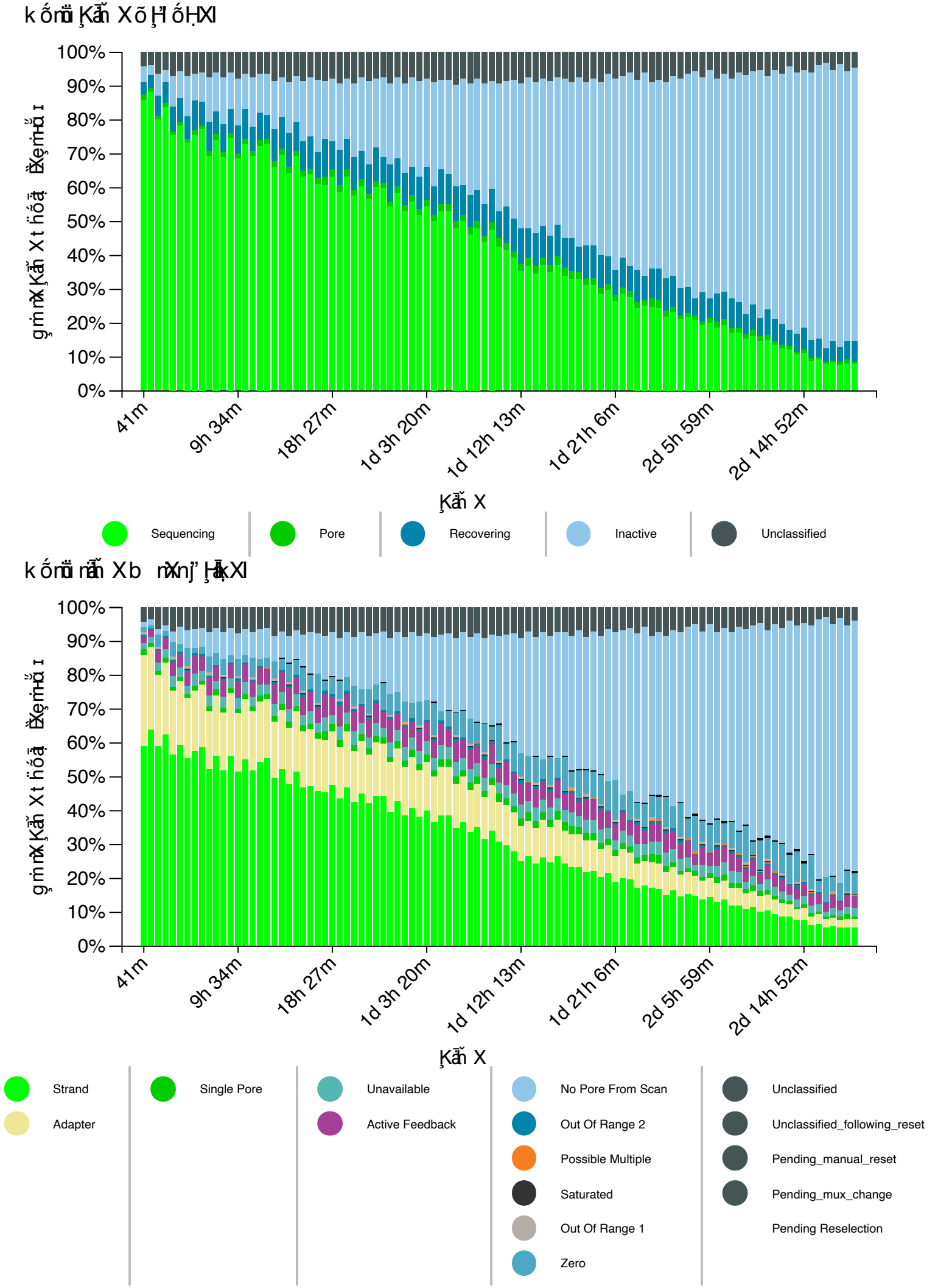
Estimated N50: 1.51 Kb




100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
41m
9h 34m
18h 27m
1d 3h 20m
1d 12h 13m
1d 21h 6m
2d 5h 59m
2d 14h 52m
Sequencing
Pore
Recovering
Inactive
Unclassified
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

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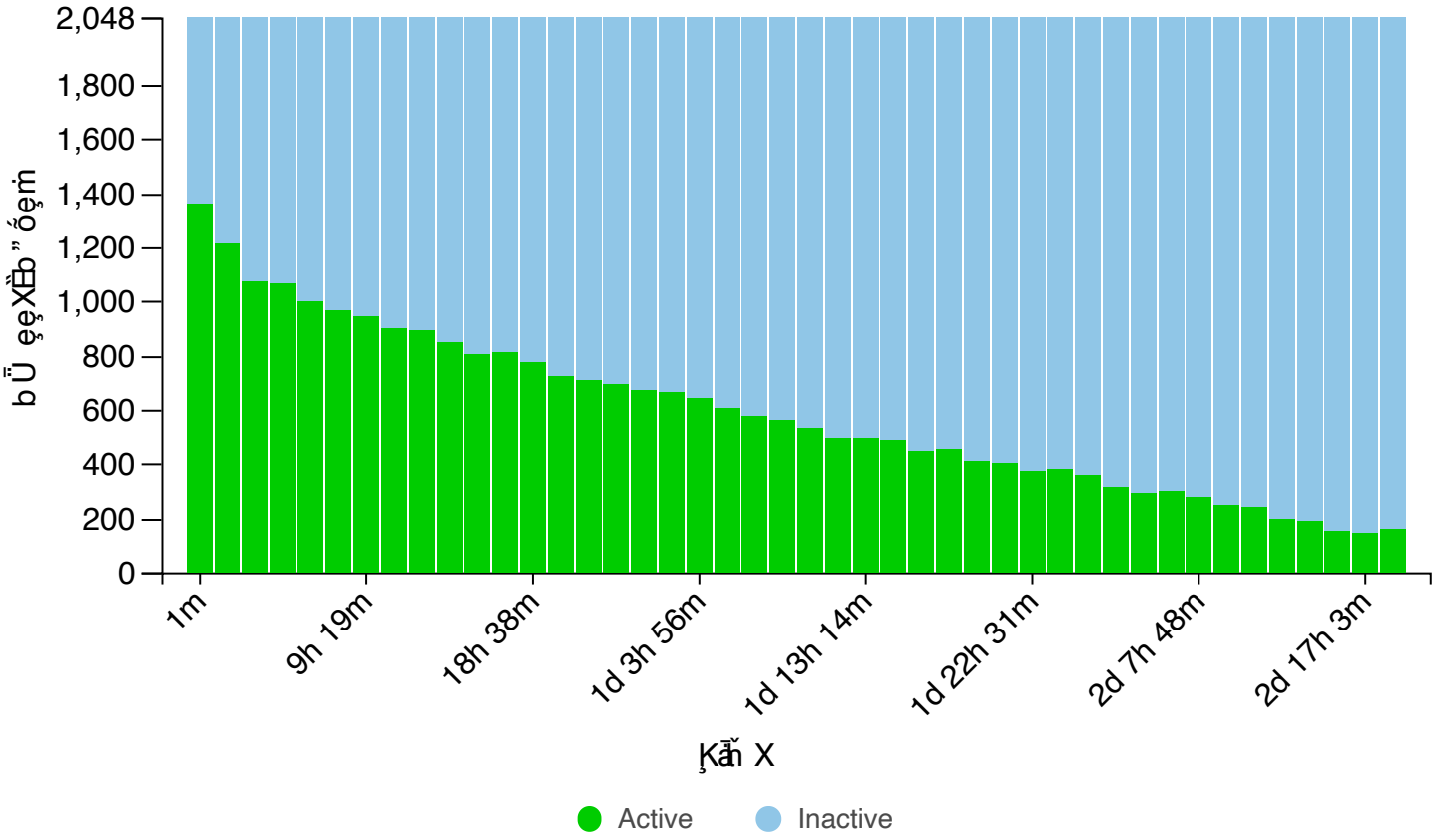

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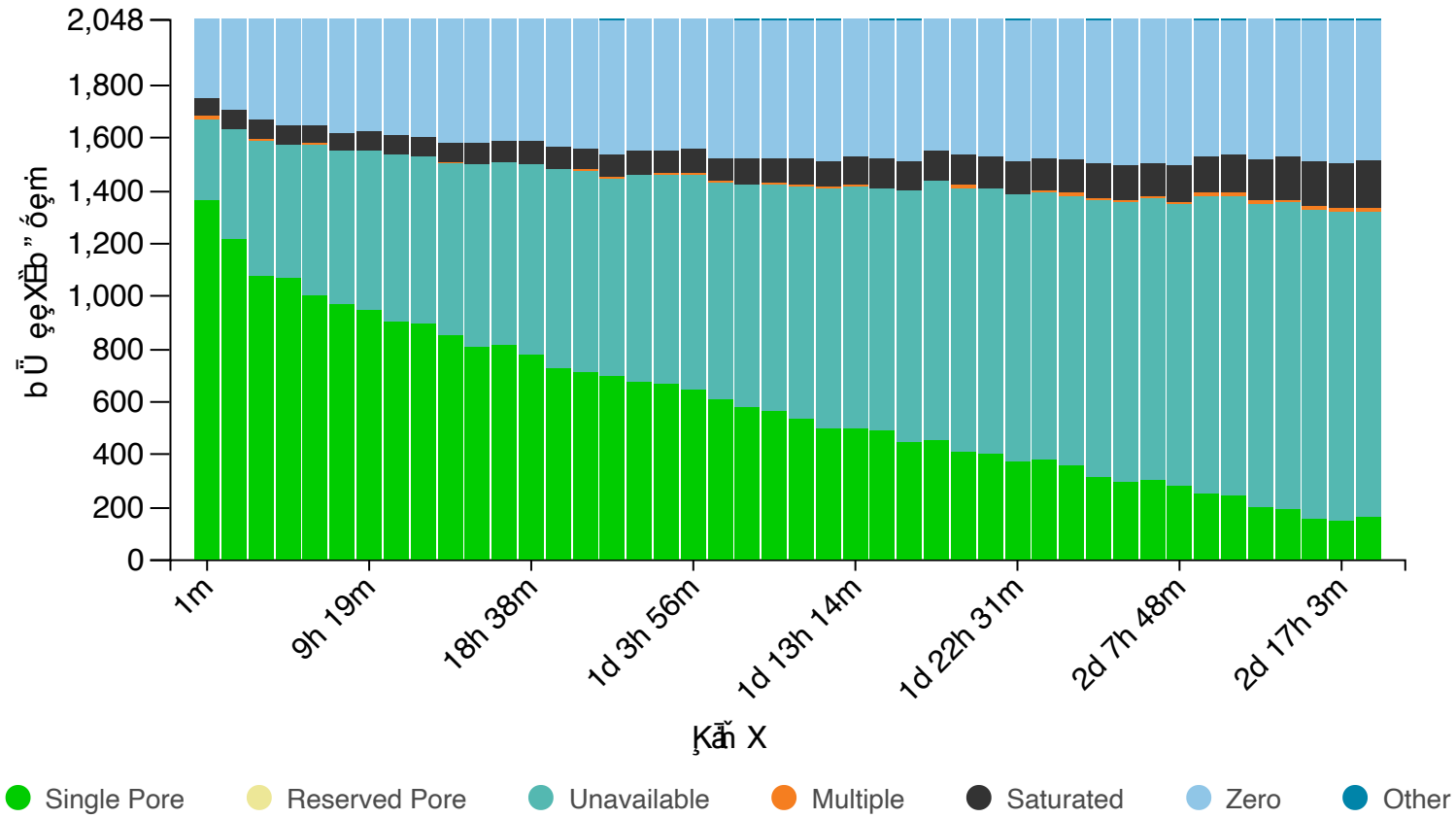

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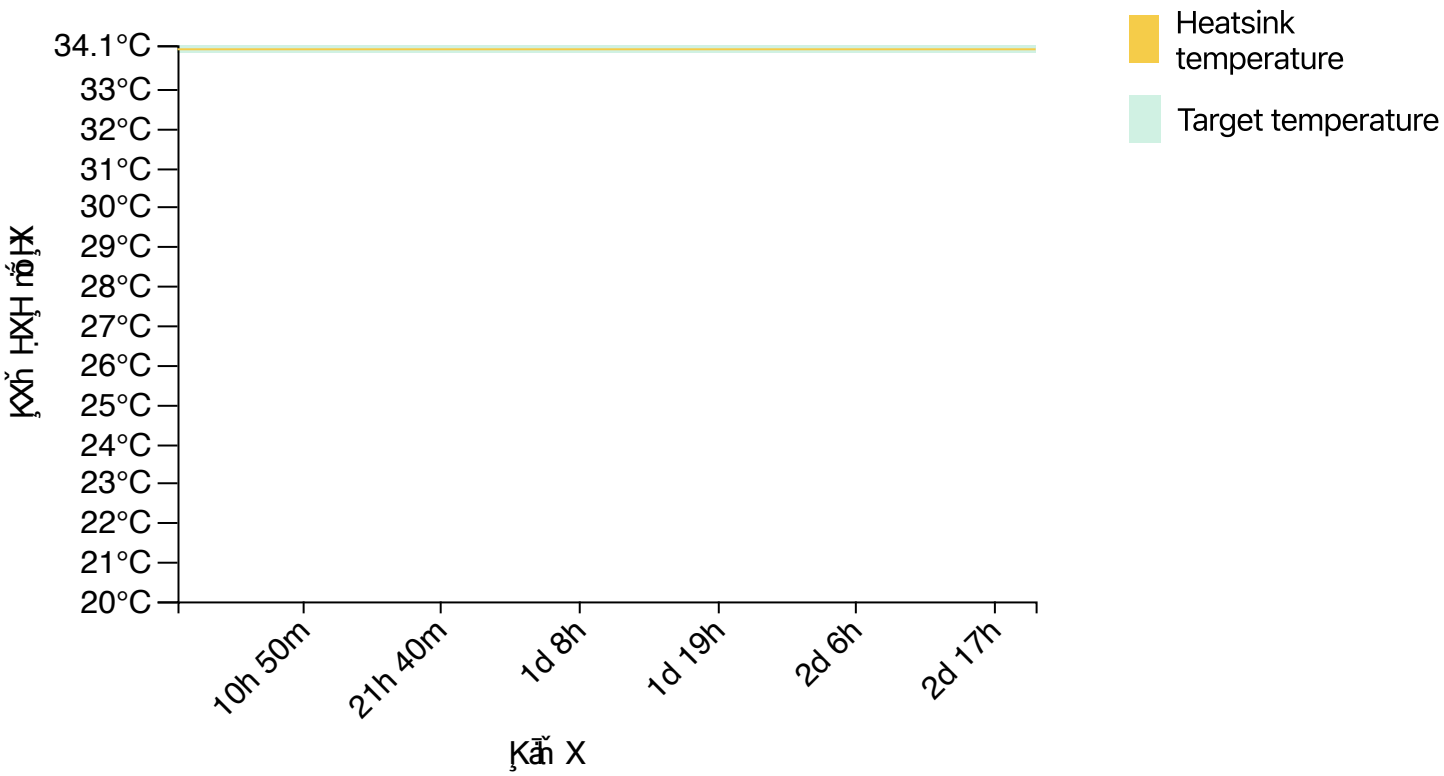

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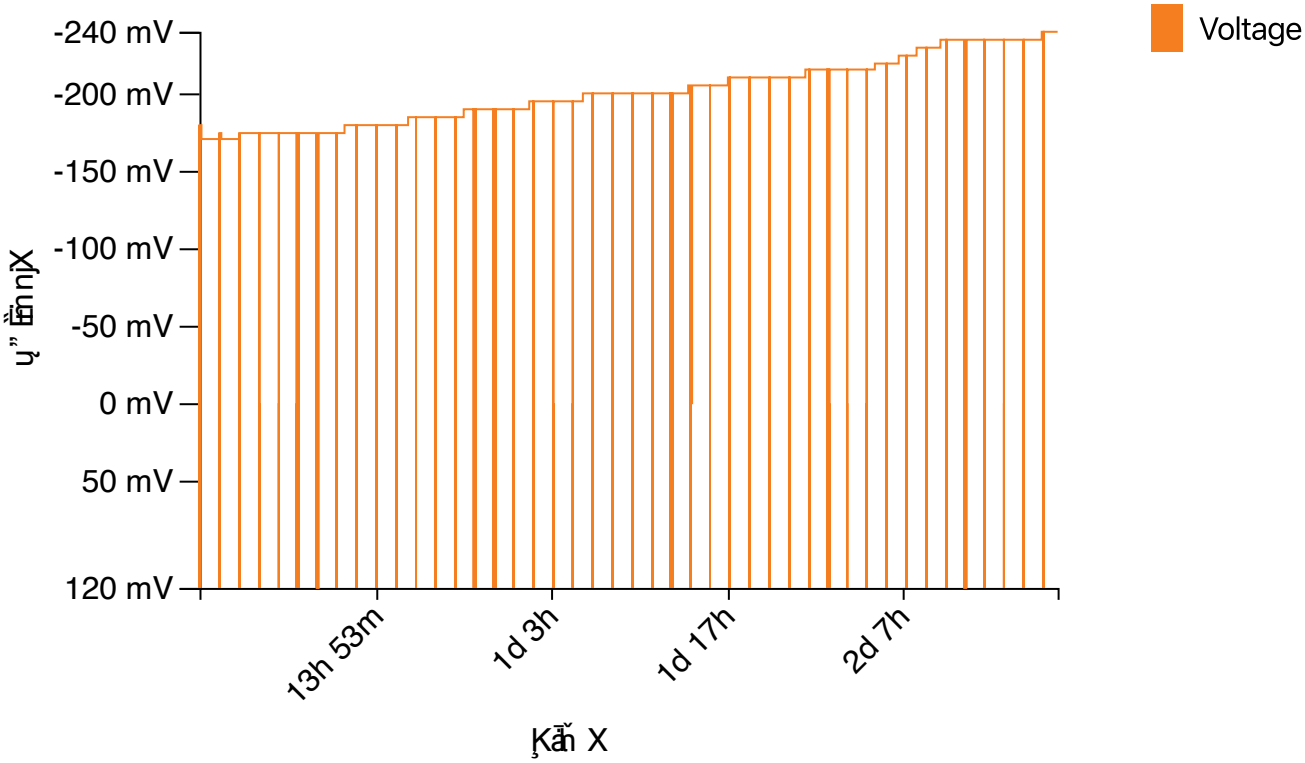

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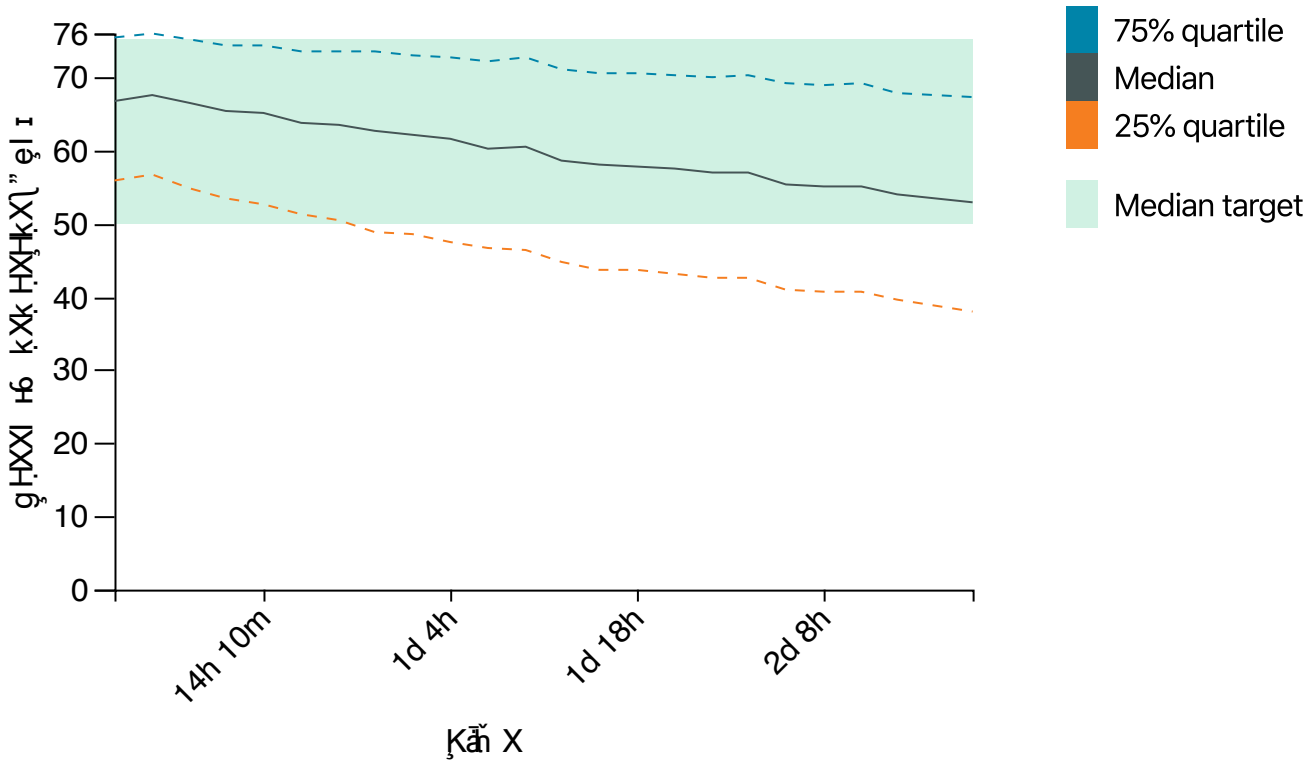

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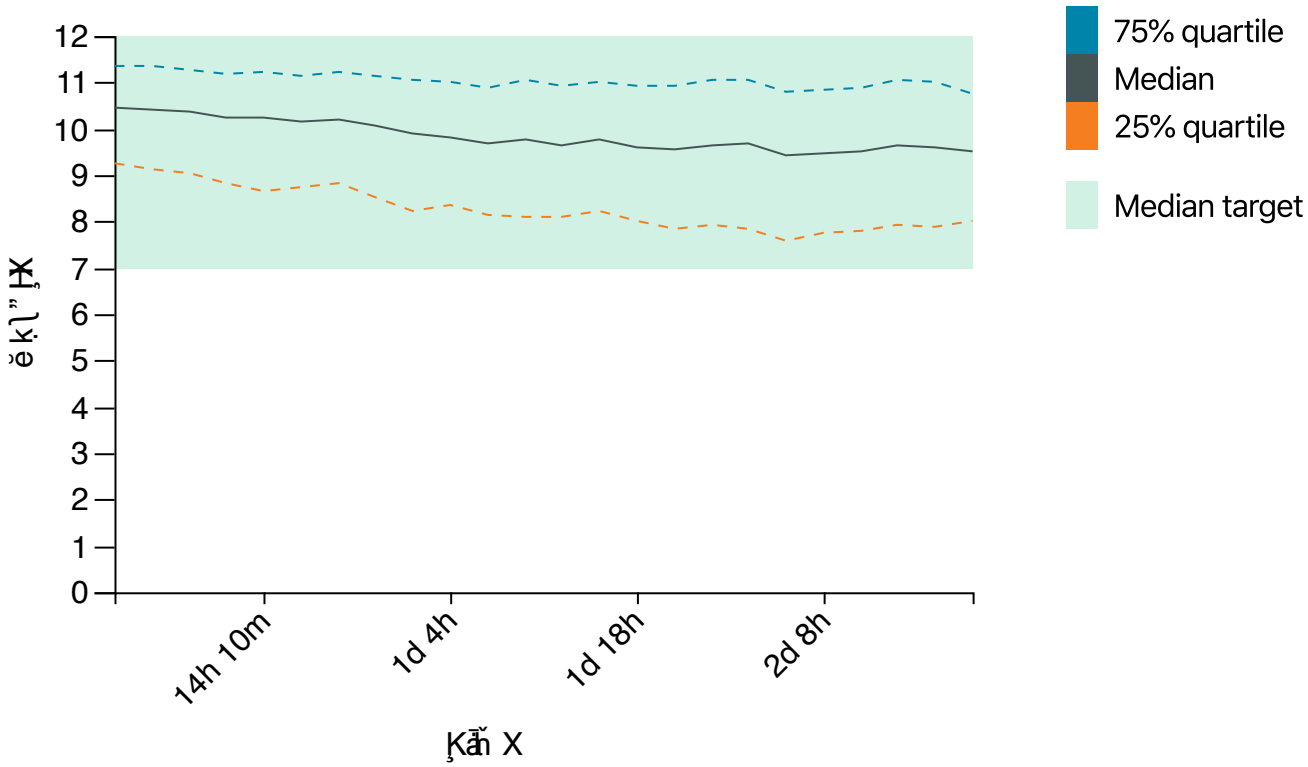

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- Flow cell FAO33670 has 158 pores available for sequencing. Starting sequencing with 133 pores 2őnƤķm̈ ĥ⁰ ⁿ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁰ ⁿ ′Ή
- Flow cell FAO33670 has 146 pores available for sequencing. Starting sequencing with 112 pores 2őnƤķm̈ ĥ⁰ ⁽ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁰ ⁽ ′Ή
- Flow cell FAO33670 has 150 pores available for sequencing. Starting sequencing with 119 pores 2őnƤķm̈ ĥ⁰ ⁺ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁰ ⁺ ′Ή
- Flow cell FAO33670 has 192 pores available for sequencing. Starting sequencing with 152 pores 2őnƤķm̈ ĥ⁰ ⁸ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁰ ⁸ ′Ή
- Flow cell FAO33670 has 200 pores available for sequencing. Starting sequencing with 160 pores 2őnƤķm̈ ĥ⁰ ⁶ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁰ ⁶ ′Ή
- Flow cell FAO33670 has 239 pores available for sequencing. Starting sequencing with 185 pores 2őnƤķm̈ ĥ⁰ ⁵ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁰ ⁵ ′Ή
- Flow cell FAO33670 has 251 pores available for sequencing. Starting sequencing with 187 pores 2őnƤķm̈ ĥ⁶ ⁷ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁶ ⁷ ′Ή
- Flow cell FAO33670 has 279 pores available for sequencing. Starting sequencing with 203 pores 2őnƤķm̈ ĥ⁶ ⁶ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁶ ⁶ ′Ή
- Flow cell FAO33670 has 298 pores available for sequencing. Starting sequencing with 218 pores 2őnƤķm̈ ĥ⁶ ⁰ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁶ ⁰ ′Ή
- Flow cell FAO33670 has 291 pores available for sequencing. Starting sequencing with 211 pores 2őnƤķm̈ ĥ⁵ⁿ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁵ⁿ ′Ή
- Flow cell FAO33670 has 315 pores available for sequencing. Starting sequencing with 224 pores 2őnƤķm̈ ĥ⁵⁽ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁵⁽ ′Ή
- Flow cell FAO33670 has 359 pores available for sequencing. Starting sequencing with 246 pores 2őnƤķm̈ ĥ⁵⁻ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁵⁻ ′Ή
- Flow cell FAO33670 has 380 pores available for sequencing. Starting sequencing with 267 pores 2őnƤķm̈ ĥ⁵⁸ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁵⁸ ′Ή
- Flow cell FAO33670 has 374 pores available for sequencing. Starting sequencing with 245 pores 2őnƤķm̈ ĥ⁵⁷ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁵⁶ ′Ή
- Flow cell FAO33670 has 399 pores available for sequencing. Starting sequencing with 265 pores 2őnƤķm̈ ĥ⁵⁵ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁵⁵ ′Ή
- Flow cell FAO33670 has 413 pores available for sequencing. Starting sequencing with 282 pores 2őnƤķm̈ ĥ⁰ ⁿ ′Ή
- Performing Mux Scan 2őnƤķm̈ ĥ⁰ ⁿ ′Ή

- Flow cell FAO33670 has 450 pores available for sequencing. Starting sequencing with 302 pores
- Performing Mux Scan
- Flow cell FAO33670 has 446 pores available for sequencing. Starting sequencing with 303 pores
- Performing Mux Scan
- Flow cell FAO33670 has 488 pores available for sequencing. Starting sequencing with 322 pores
- Performing Mux Scan
- Flow cell FAO33670 has 498 pores available for sequencing. Starting sequencing with 321 pores
- Performing Mux Scan
- Flow cell FAO33670 has 500 pores available for sequencing. Starting sequencing with 325 pores
- Performing Mux Scan
- Flow cell FAO33670 has 533 pores available for sequencing. Starting sequencing with 349 pores
- Performing Mux Scan
- Flow cell FAO33670 has 566 pores available for sequencing. Starting sequencing with 375 pores
- Performing Mux Scan
- Flow cell FAO33670 has 578 pores available for sequencing. Starting sequencing with 378 pores
- Performing Mux Scan
- Flow cell FAO33670 has 606 pores available for sequencing. Starting sequencing with 395 pores
- Performing Mux Scan
- Flow cell FAO33670 has 641 pores available for sequencing. Starting sequencing with 397 pores
- Performing Mux Scan
- Flow cell FAO33670 has 667 pores available for sequencing. Starting sequencing with 411 pores
- Performing Mux Scan
- Flow cell FAO33670 has 673 pores available for sequencing. Starting sequencing with 406 pores
- Performing Mux Scan
- Flow cell FAO33670 has 697 pores available for sequencing. Starting sequencing with 423 pores
- Performing Mux Scan
- Flow cell FAO33670 has 708 pores available for sequencing. Starting sequencing with 435 pores
- Performing Mux Scan
- Flow cell FAO33670 has 722 pores available for sequencing. Starting sequencing with 425 pores
- Performing Mux Scan
- Flow cell FAO33670 has 775 pores available for sequencing. Starting sequencing with 446 pores
- Performing Mux Scan
- Flow cell FAO33670 has 809 pores available for sequencing. Starting sequencing with 446 pores
- Performing Mux Scan
- Flow cell FAO33670 has 803 pores available for sequencing. Starting sequencing with 449 pores

- Performing Mux Scan 2ốnp̃ķm̃ñ⁰⁺ʺH
- Flow cell FAO33670 has 850 pores available for sequencing. Starting sequencing with 468 pores 2ốnp̃ķm̃ñ⁰⁸ʺH
- Performing Mux Scan 2ốnp̃ķm̃ñ⁰⁸ʺH
- Flow cell FAO33670 has 890 pores available for sequencing. Starting sequencing with 472 pores 2ốnp̃ķm̃ñ⁰⁶ʺH
- Performing Mux Scan 2ốnp̃ķm̃ñ⁰⁶ʺH
- Flow cell FAO33670 has 898 pores available for sequencing. Starting sequencing with 467 pores 2ốnp̃ķm̃ñ⁰⁵ʺH
- Performing Mux Scan 2ốnp̃ķm̃ñ⁰⁵ʺH
- Flow cell FAO33670 has 946 pores available for sequencing. Starting sequencing with 472 pores ÷ốb̃⁷⁵ñ⁶⁷ʺH
- Performing Mux Scan ÷ốb̃⁷⁵ñ⁶⁷ʺH
- Flow cell FAO33670 has 969 pores available for sequencing. Starting sequencing with 469 pores ÷ốb̃⁷⁵ñ⁶⁶ʺH
- Performing Mux Scan ÷ốb̃⁷⁵ñ⁶⁶ʺH
- Flow cell FAO33670 has 1005 pores available for sequencing. Starting sequencing with 473 pores ÷ốb̃⁷⁵ñ⁶⁰ʺH
- Performing Mux Scan ÷ốb̃⁷⁵ñ⁶⁰ʺH
- Flow cell FAO33670 has 1069 pores available for sequencing. Starting sequencing with 483 pores ÷ốb̃⁷⁵ñ⁵ⁿʺH
- Performing Mux Scan ÷ốb̃⁷⁵ñ⁵ⁿʺH
- Flow cell FAO33670 has 1075 pores available for sequencing. Starting sequencing with 485 pores ÷ốb̃⁷⁵ñ⁵(ʺH
- Performing Mux Scan ÷ốb̃⁷⁵ñ⁵(ʺH
- Flow cell FAO33670 has 1215 pores available for sequencing. Starting sequencing with 502 pores ÷ốb̃⁷⁵ñ⁵⁻ʺH
- Performing Mux Scan ÷ốb̃⁷⁵ñ⁵⁻ʺH
- Flow cell FAO33670 has 1361 pores available for sequencing. Starting sequencing with 504 pores ÷ốb̃⁷⁵ñ⁵⁸ʺH
- Performing Mux Scan ÷ốb̃⁷⁵ñ⁵⁸ʺH
- Starting sequencing procedure ÷ốb̃⁷⁵ñ⁵⁸ʺH
- Failed to reach 34.0°C within 300 seconds(with 0.1 tolerance). The experiment will continue anyway. ÷ốb̃⁷⁵ñ⁵⁸ʺH
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C ÷ốb̃⁷⁵ñ⁵⁸ʺH
- Disk / has 631 GB space remaining ÷ốb̃⁷⁵ñ⁵⁸ʺH