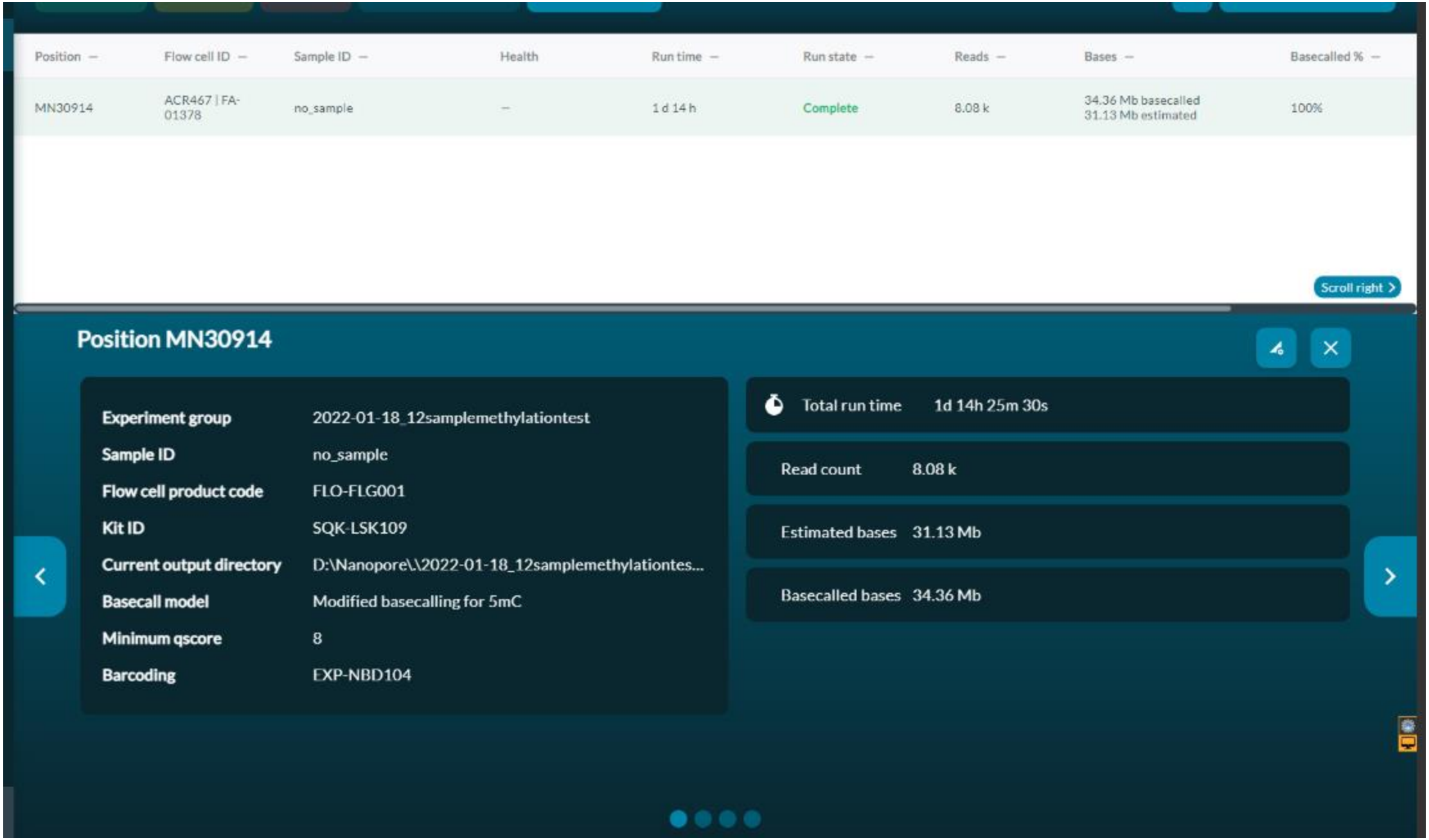
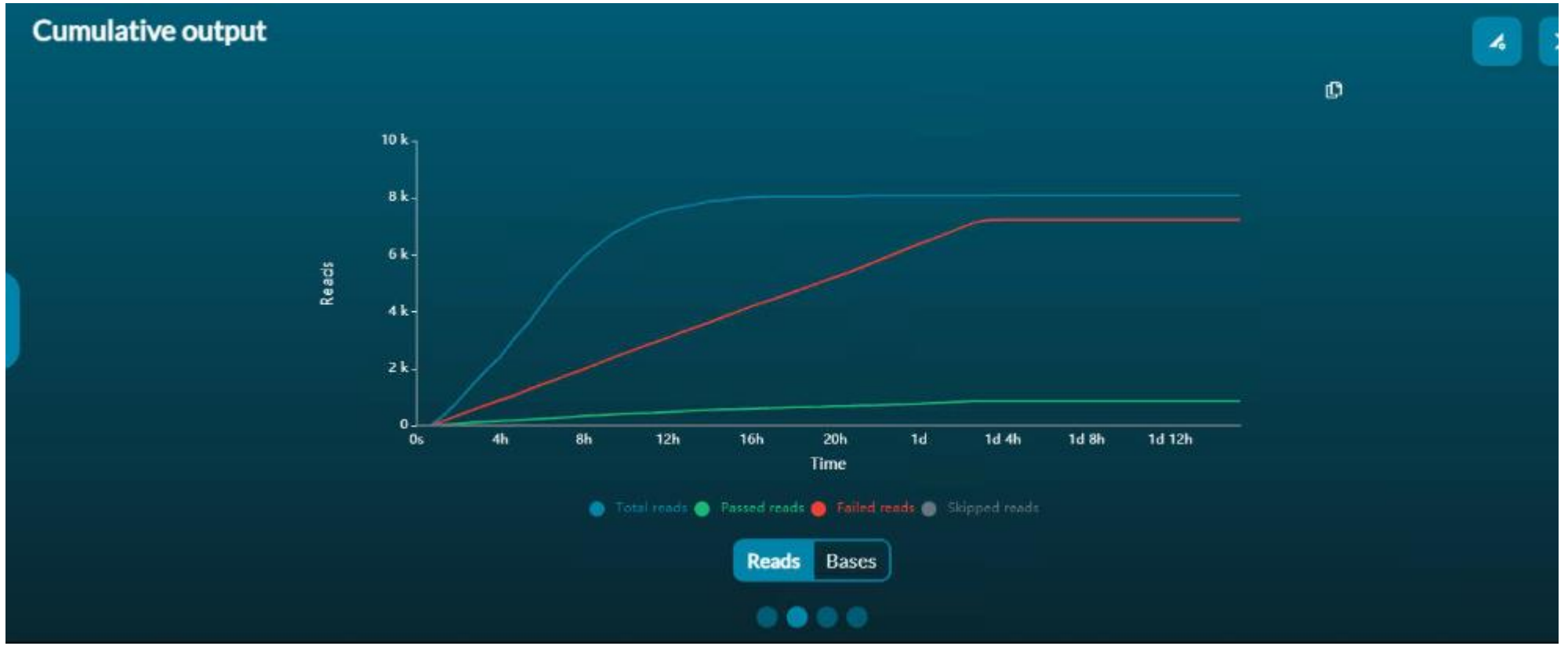
Nanopore experiment samples

Sample nr.	Description	Type	Methylation enzymes
1	DNA 16*601 (50) to test Hia5	Bare DNA	Hia5
2	DNA 16*601 (50) to test Hia5	Bare DNA	x
3	DNA 16*601 (50) to test Hia5 (with other enzymes)	Bare DNA	M.Cvipi +M.SssI
4	DNA to test Hia5 (with other enzymes)	Bare DNA	Hia5 + M.Cvipi +M.SssI
5	Reconstituted DNA for Hia5 testing (16*601, 50bp)	Reconstitution	Hia5
6	Reconstituted DNA for Hia5 testing (16*601, 20bp)	Reconstitution	Hia5
7	Reconstituted DNA for Hia5 testing (16*601, 50bp)	Reconstitution	Hia5 + M.Cvipi +M.SssI
8	Reconstituted DNA for Hia5 testing (16*601, 20bp)	Reconstitution	Hia5 + M.Cvipi +M.SssI
9	Reconstituted DNA for Hia5 testing (16*601, 50bp) (suboptimal, not enough nucleosomes)	Reconstitution	Hia5 + M.Cvipi +M.SssI
10	Wt yeast grown in GAL	Native chromatin	M.Cvipi +M.SssI
11	Wt yeast grown in RAF	Native chromatin	M.Cvipi +M.SssI
12	Wt yeast grown in RAF	Native chromatin	Hia5


Position
Flow cell ID
Sample ID
Health
Run time
Run state
Reads
Bases
Basecalled %
MN30914
ACR467 | FA-01378
no_sample
–
1 d 14 h
Complete
8.08 k
34.36 Mb basecalled
31.13 Mb estimated
100%
Scroll right
Position MN30914
Experiment group
2022-01-18_12samplemethylationtest
Sample ID
no_sample
Flow cell product code
FLO-FLG001
Kit ID
SQK-LSK109
Current output directory
D:\Nanopore\\2022-01-18_12samplemethylationtes...
Basecall model
Modified basecalling for 5mC
Minimum qscore
8
Barcoding
EXP-NBD104
Total run time
1d 14h 25m 30s
Read count
8.08 k
Estimated bases
31.13 Mb
Basecalled bases
34.36 Mb


Cumulative output
10 k
8 k
6 k
4 k
2 k
0
Reads
0s
4h
8h
12h
16h
20h
1d
1d 4h
1d 8h
1d 12h
Time
Total reads
Passed reads
Failed reads
Skipped reads
Reads
Bases

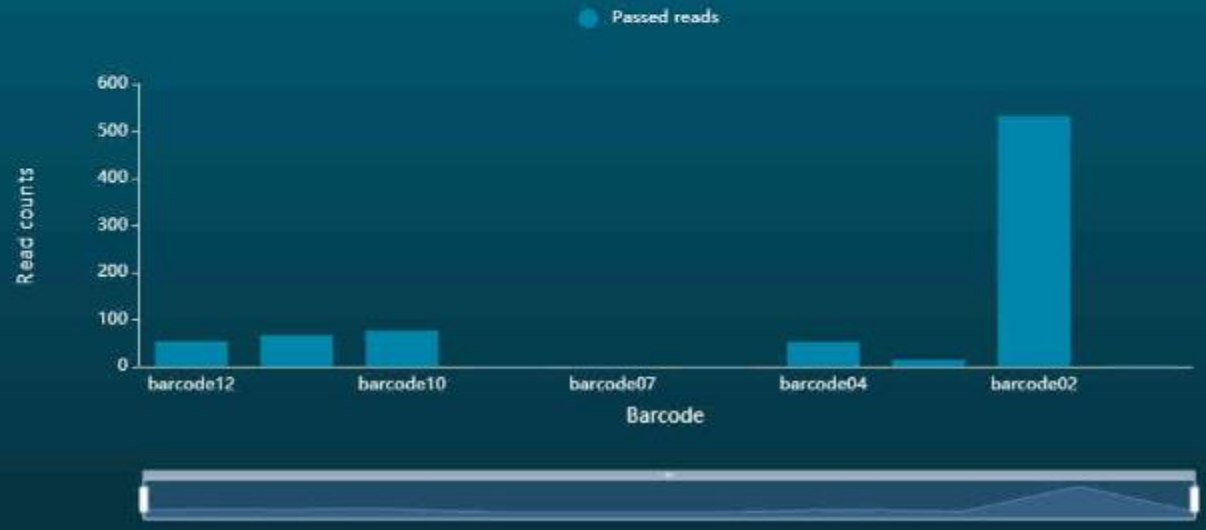
2022-01-18_12samplemethylationtest

Resume | Pause | Stop | Start MUX scan | Export PDF | Experiment group

Position	Flow cell ID	Sample ID	Health	Run time	Run state	Reads	Bases	Basecalled %
MN30914	ACR467 | FA-01378	no_sample	–	1 d 14 h	Complete	8.08 k	34.36 Mb basecalled 31.13 Mb estimated	100%

Scroll right

Barcode hits



Sort

Reads | Bases

Display failed | Display unclassified | Hide zero values | Reset selection