

# Report

	smart_nanopore_10
# contigs (>= 0 bp)	92
# contigs (>= 1000 bp)	92
# contigs (>= 5000 bp)	92
# contigs (>= 10000 bp)	66
# contigs (>= 25000 bp)	25
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	1761492
Total length (>= 1000 bp)	1761492
Total length (>= 5000 bp)	1761492
Total length (>= 10000 bp)	1553402
Total length (>= 25000 bp)	918680
Total length (>= 50000 bp)	288986
# contigs	92
Largest contig	66786
Total length	1761492
Reference length	335799
GC (%)	35.14
Reference GC (%)	35.65
N50	25643
NG50	58478
N75	14243
NG75	51134
L50	24
LG50	3
L75	47
LG75	5
# misassemblies	95
# misassembled contigs	39
Misassembled contigs length	900541
# local misassemblies	62
# unaligned contigs	22 + 16 part
Unaligned length	589399
Genome fraction (%)	62.174
Duplication ratio	5.853
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1072.90
# indels per 100 kbp	2093.60
Largest alignment	35448
NA50	4979
NGA50	17534
NGA75	16614
LA50	89
LGA50	7
LGA75	12

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

	smart_nanopore_10
# misassemblies	95
# relocations	95
# translocations	0
# inversions	0
# misassembled contigs	39
Misassembled contigs length	900541
# local misassemblies	62
# mismatches	2240
# indels	4371
# short indels	4303
# long indels	68
Indels length	6013

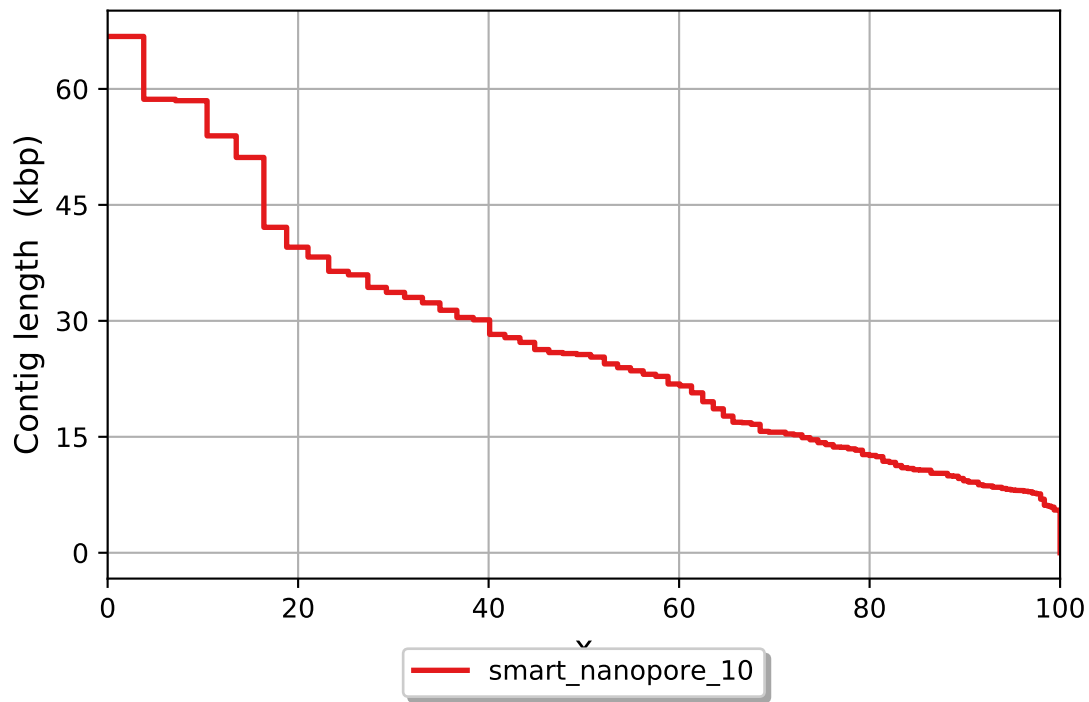
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

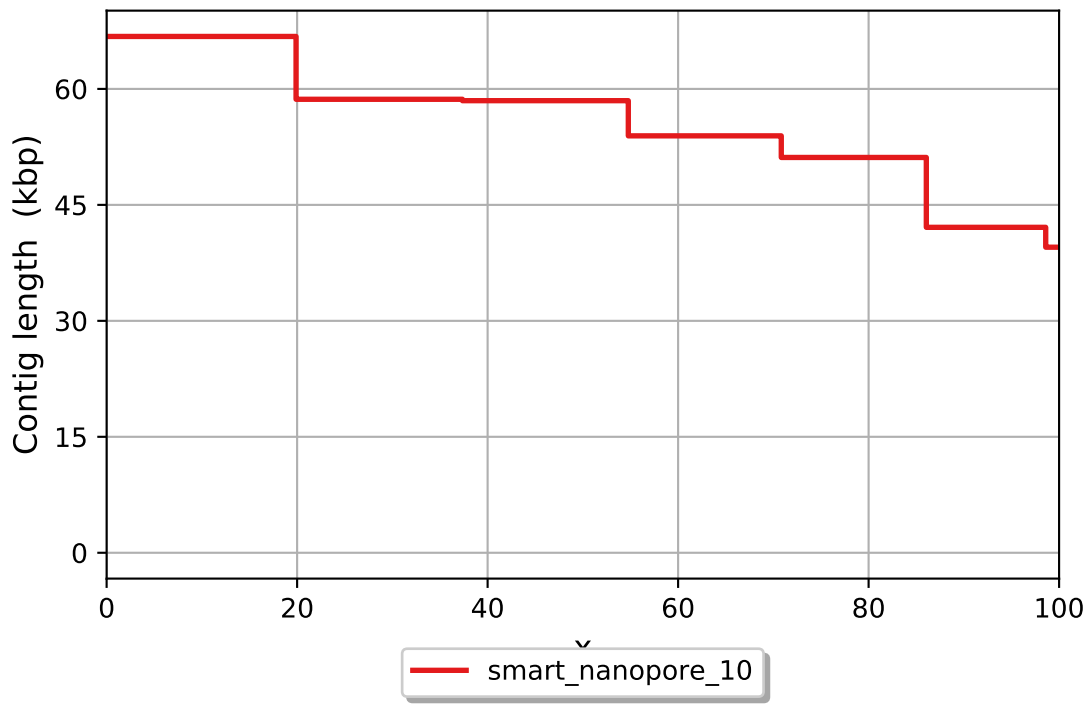
	smart_nanopore_10
# fully unaligned contigs	22
Fully unaligned length	407187
# partially unaligned contigs	16
# with misassembly	5
# both parts are significant	15
Partially unaligned length	182212
# N's	0

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

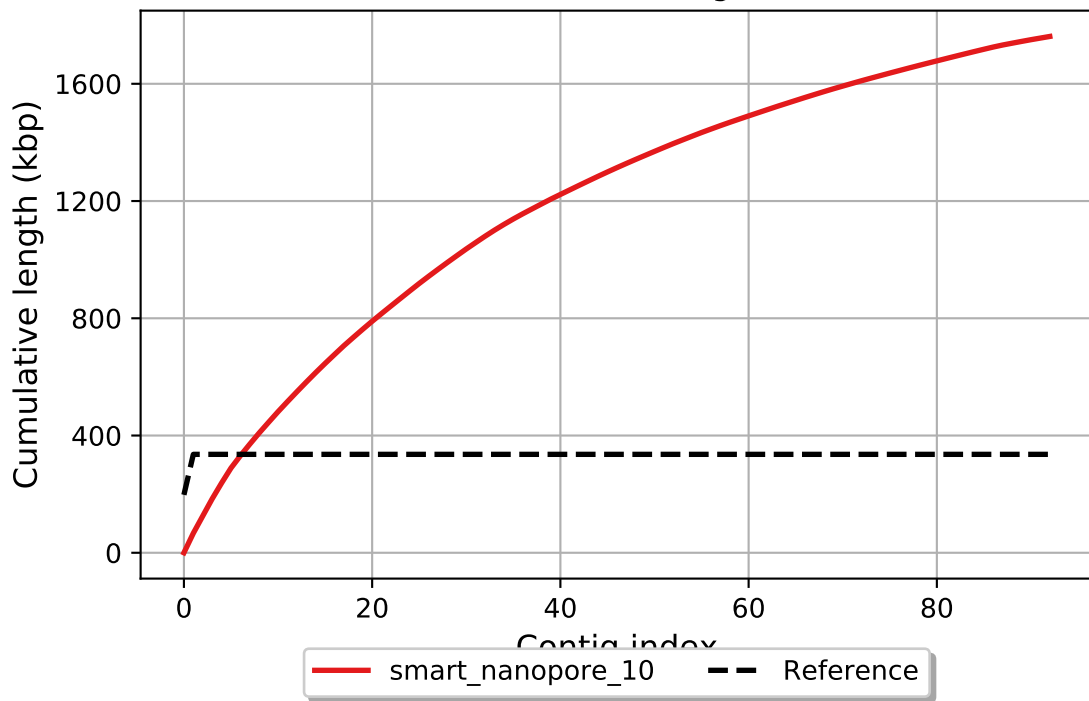
Nx



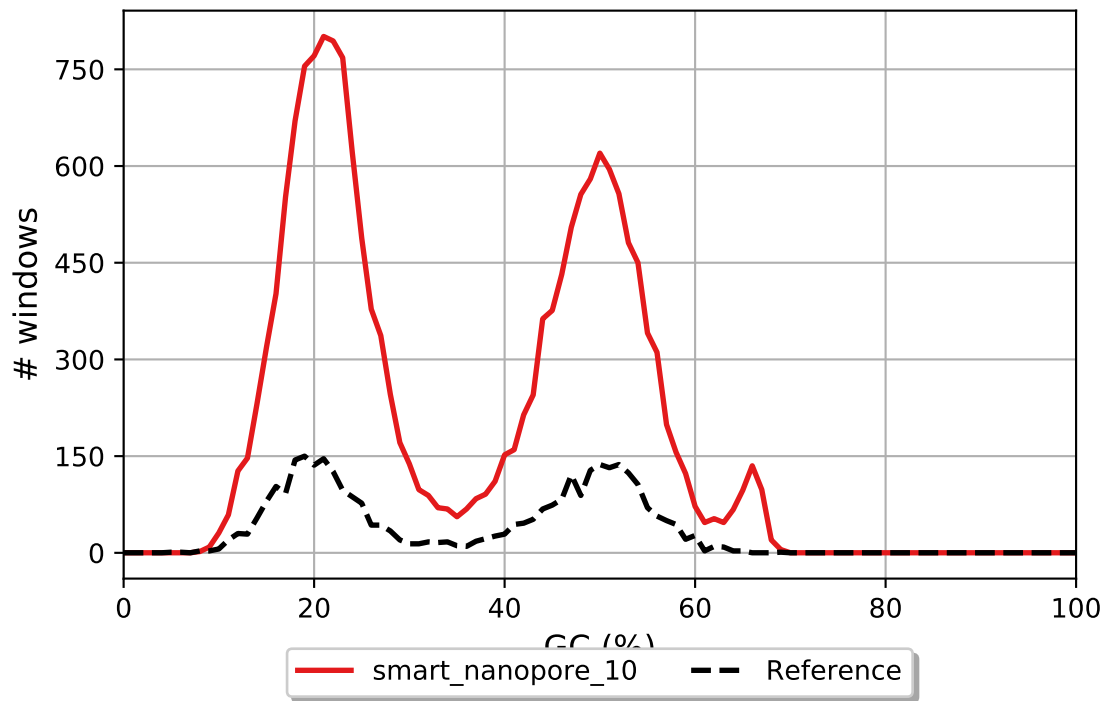
NGx



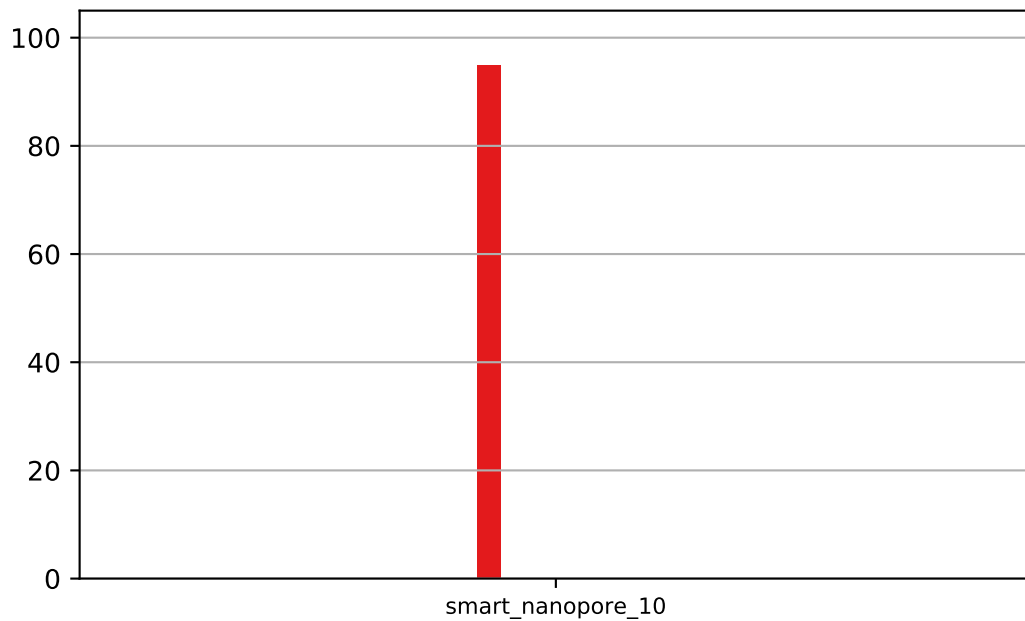
Cumulative length



## GC content

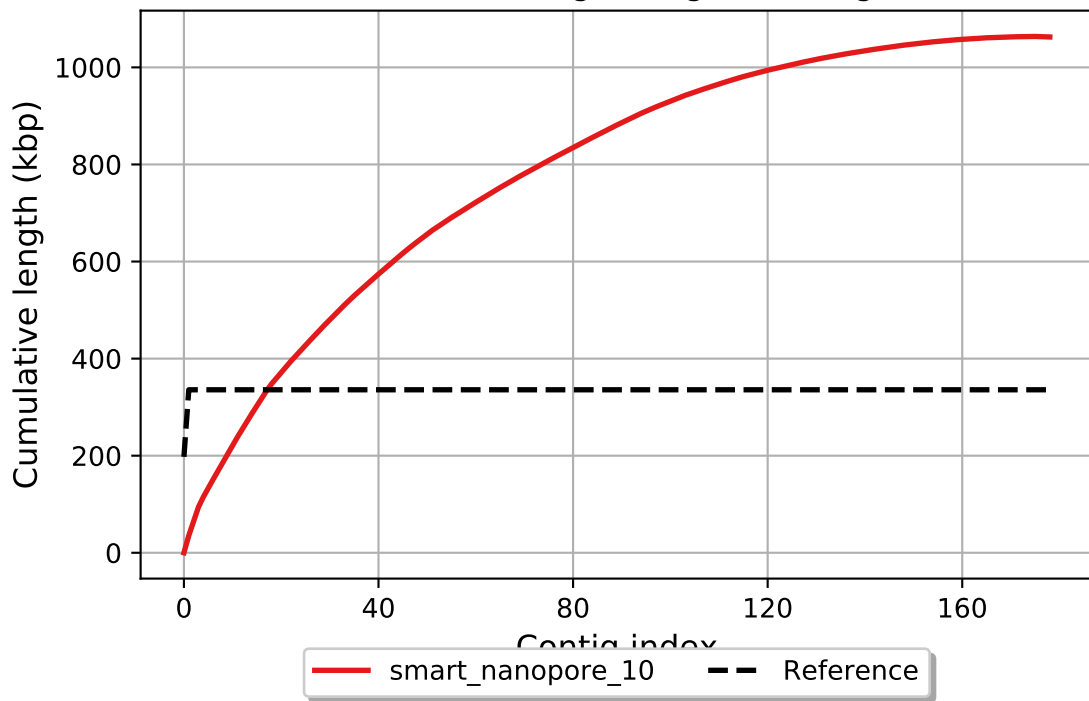


## Misassemblies

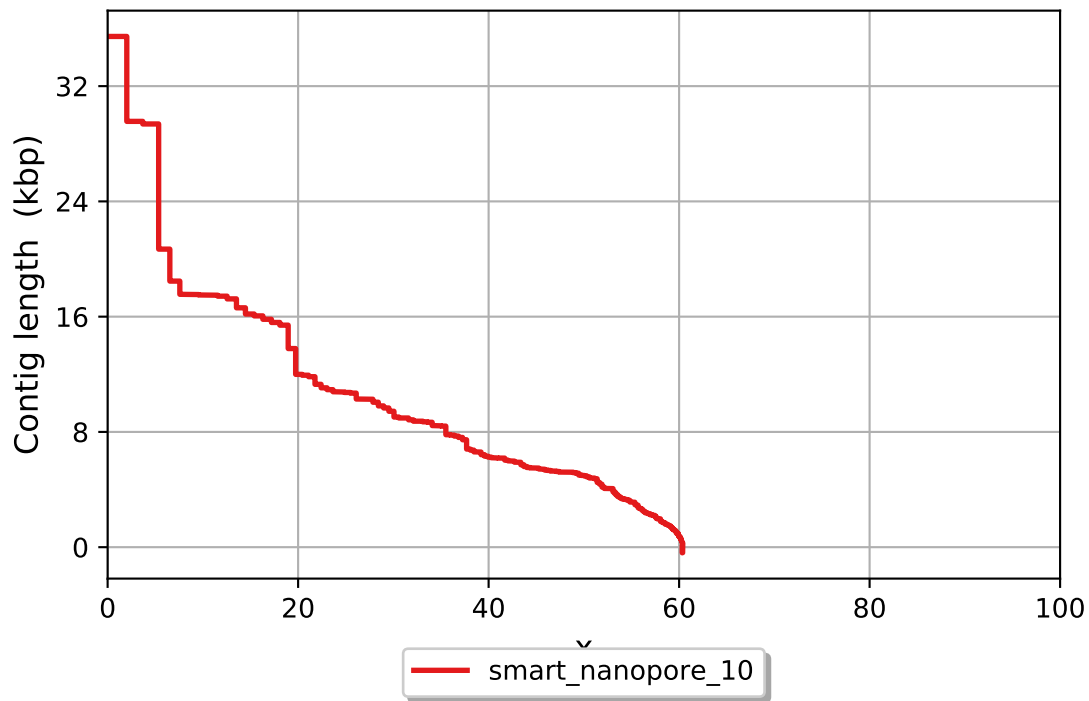


 # relocations

Cumulative length (aligned contigs)



NAx



# NGAx

