

Report

	smart_nanopore_30
# contigs (>= 0 bp)	308
# contigs (>= 1000 bp)	308
# contigs (>= 5000 bp)	308
# contigs (>= 10000 bp)	219
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	5332227
Total length (>= 1000 bp)	5332227
Total length (>= 5000 bp)	5332227
Total length (>= 10000 bp)	4675126
Total length (>= 25000 bp)	1950595
Total length (>= 50000 bp)	259379
# contigs	308
Largest contig	89962
Total length	5332227
Reference length	335799
GC (%)	34.70
Reference GC (%)	35.65
N50	21175
NG50	54819
N75	14113
NG75	51335
L50	85
LG50	3
L75	162
LG75	4
# misassemblies	249
# misassembled contigs	113
Misassembled contigs length	2141882
# local misassemblies	147
# unaligned contigs	84 + 67 part
Unaligned length	2389683
Genome fraction (%)	65.890
Duplication ratio	13.800
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1175.10
# indels per 100 kbp	2232.24
Largest alignment	32082
NGA50	24998
NGA75	20185
LGA50	6
LGA75	10

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_30
# misassemblies	249
# relocations	249
# translocations	0
# inversions	0
# misassembled contigs	113
Misassembled contigs length	2141882
# local misassemblies	147
# mismatches	2600
# indels	4939
# short indels	4870
# long indels	69
Indels length	6633

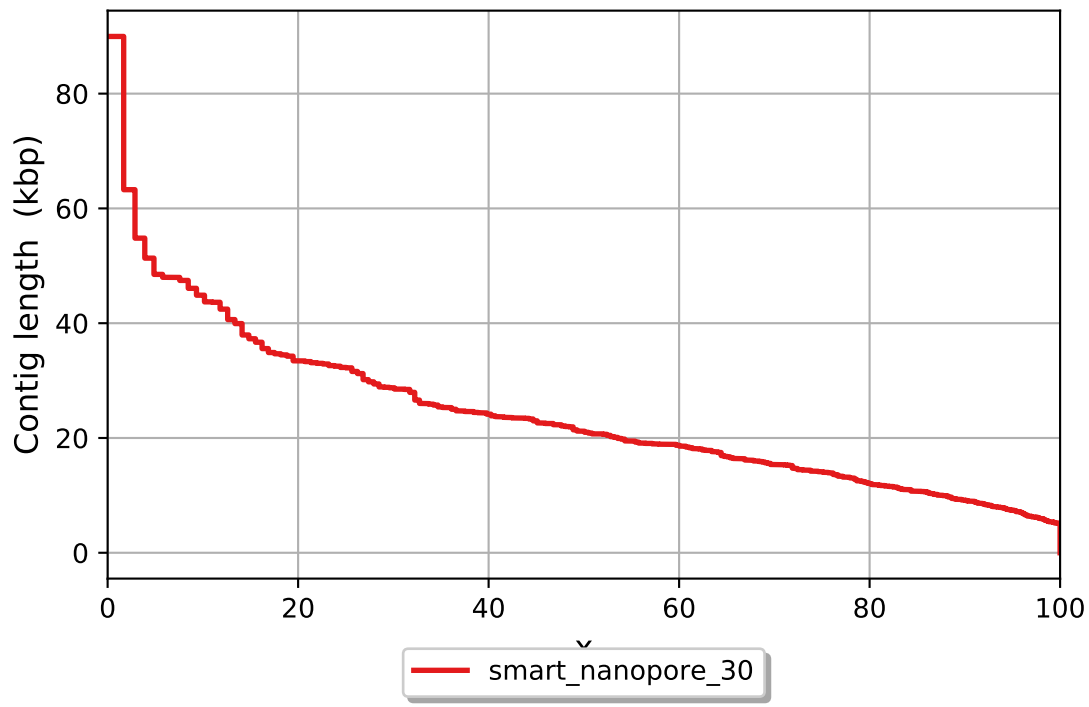
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

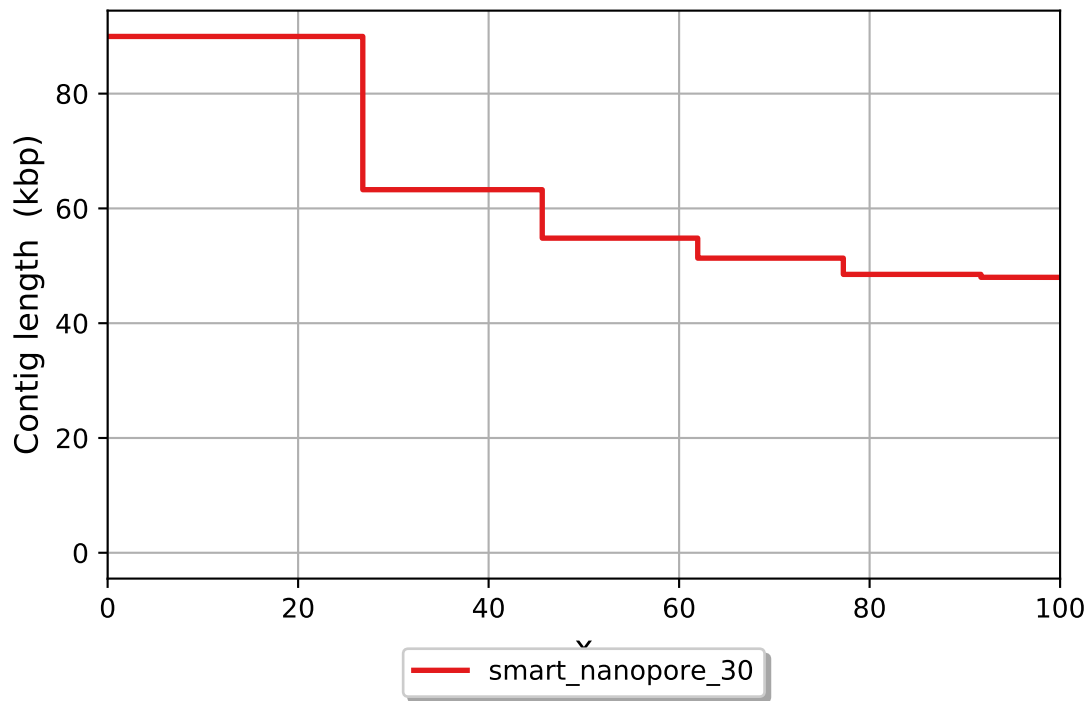
	smart_nanopore_30
# fully unaligned contigs	84
Fully unaligned length	1482493
# partially unaligned contigs	67
# with misassembly	20
# both parts are significant	46
Partially unaligned length	907190
# N's	0

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).

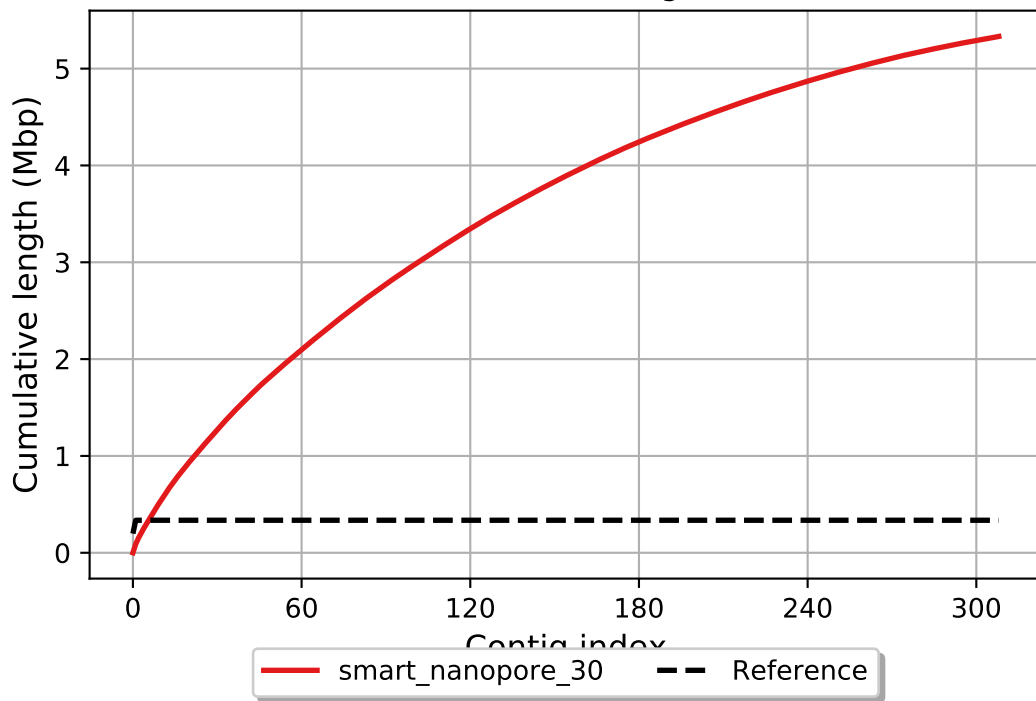
Nx



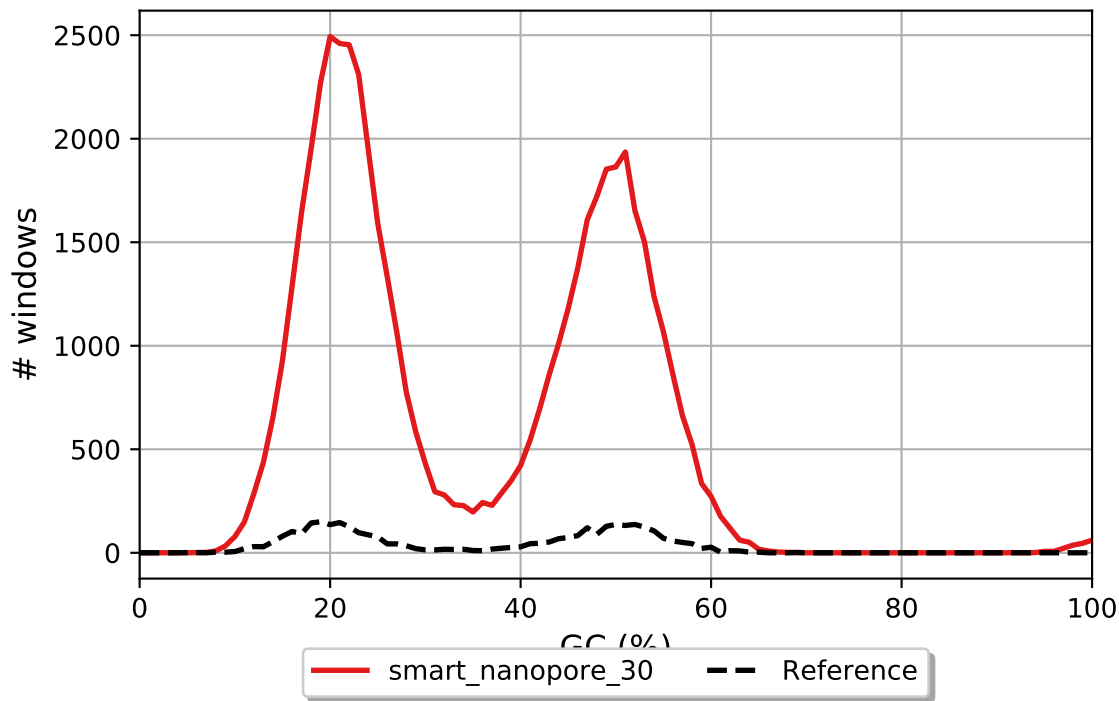
NGx



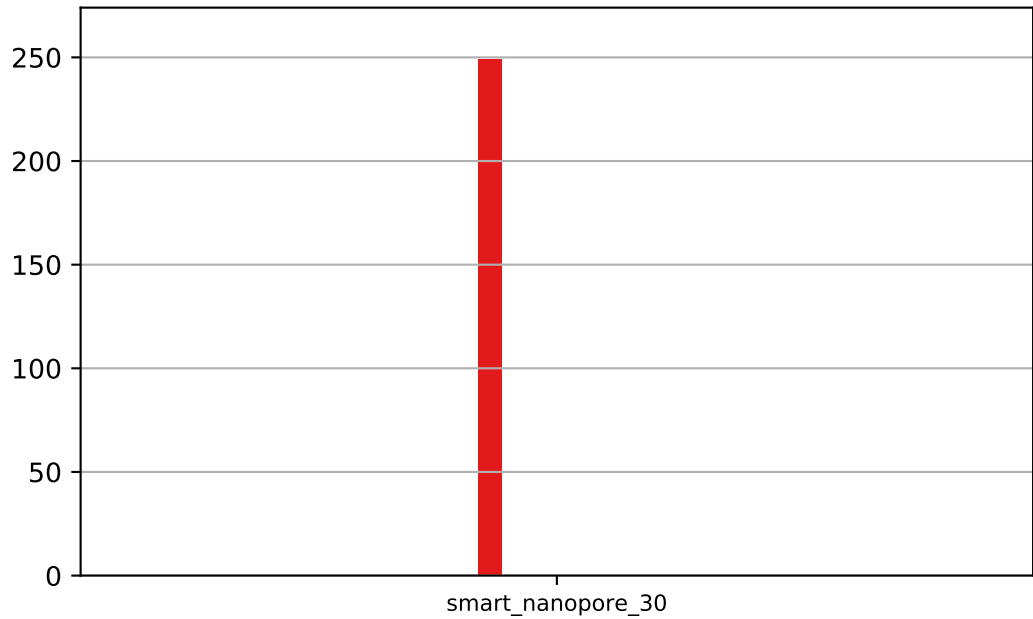
Cumulative length



GC content

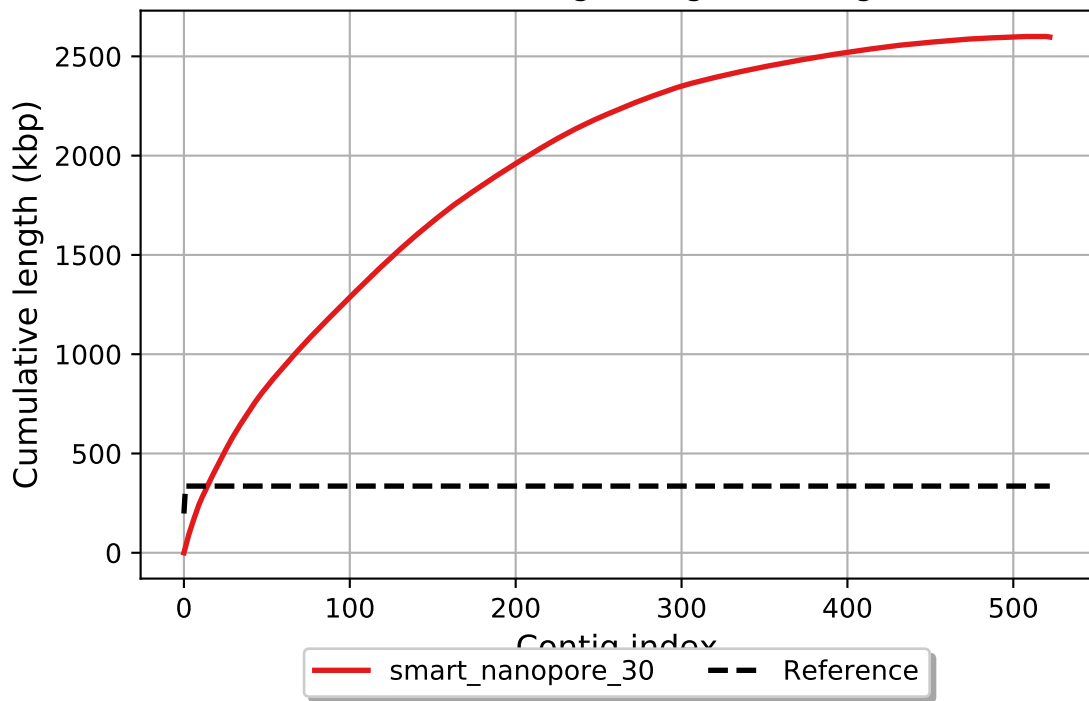


Misassemblies

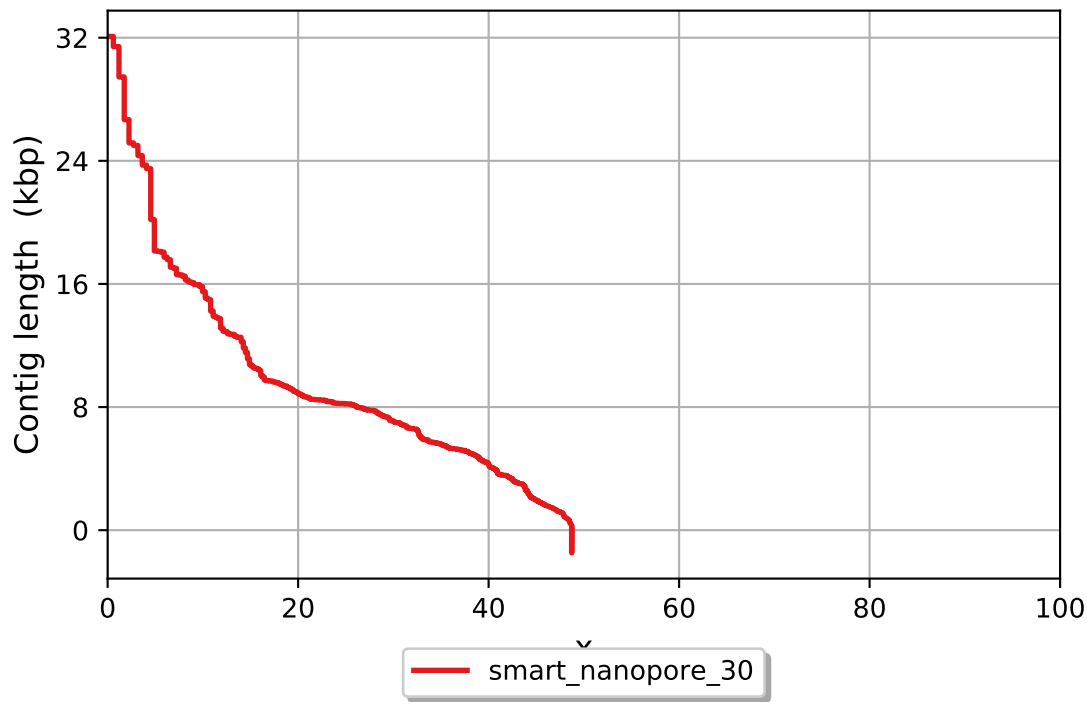


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

