

Report

	smart_nanopore_50
# contigs (>= 0 bp)	503
# contigs (>= 1000 bp)	503
# contigs (>= 5000 bp)	503
# contigs (>= 10000 bp)	364
# contigs (>= 25000 bp)	92
# contigs (>= 50000 bp)	10
Total length (>= 0 bp)	8884368
Total length (>= 1000 bp)	8884368
Total length (>= 5000 bp)	8884368
Total length (>= 10000 bp)	7837288
Total length (>= 25000 bp)	3462562
Total length (>= 50000 bp)	636906
# contigs	503
Largest contig	99953
Total length	8884368
Reference length	335799
GC (%)	33.97
Reference GC (%)	35.65
N50	20880
NG50	81167
N75	14071
NG75	58310
L50	135
LG50	2
L75	266
LG75	4
# misassemblies	353
# misassembled contigs	161
Misassembled contigs length	3331351
# local misassemblies	294
# unaligned contigs	145 + 118 part
Unaligned length	4013273
Genome fraction (%)	67.690
Duplication ratio	22.180
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1061.14
# indels per 100 kbp	2026.38
Largest alignment	39702
NGA50	34078
NGA75	30436
LGA50	5
LGA75	8

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

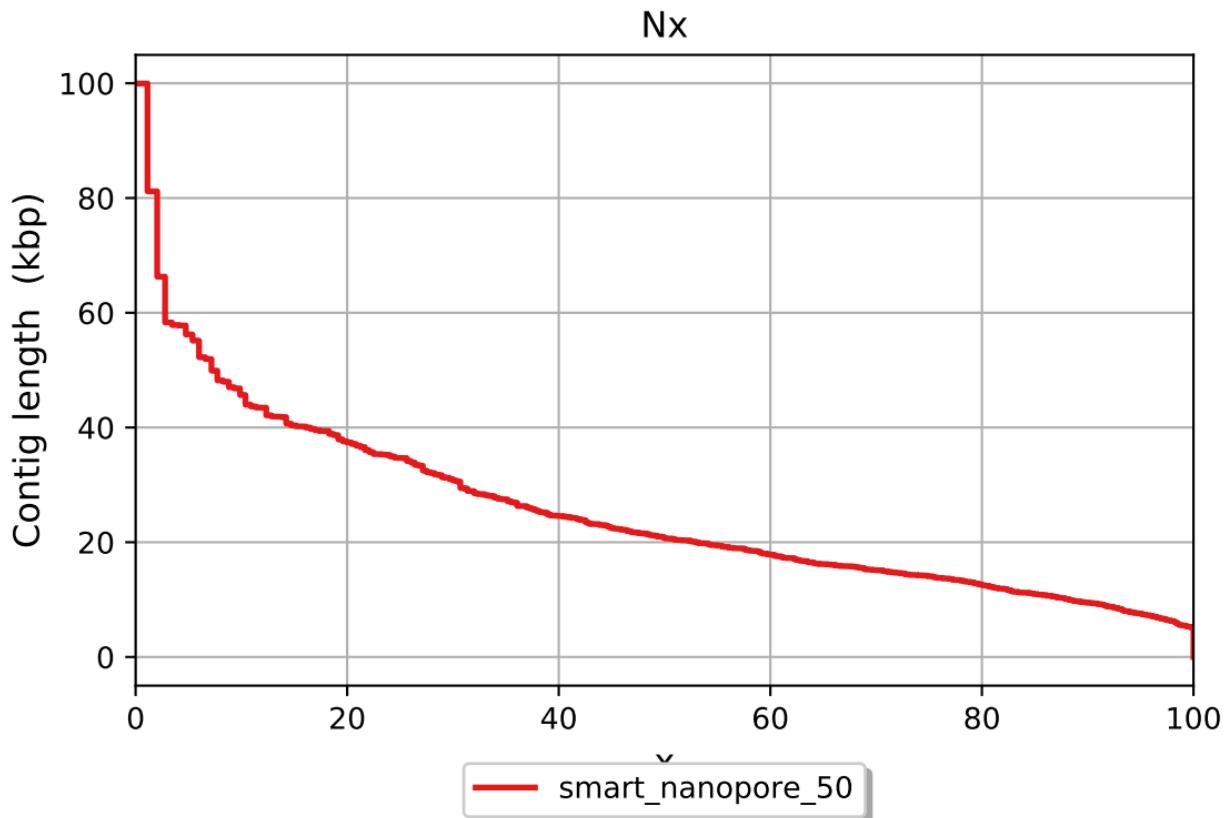
	smart_nanopore_50
# misassemblies	353
# relocations	351
# translocations	2
# inversions	0
# misassembled contigs	161
Misassembled contigs length	3331351
# local misassemblies	294
# mismatches	2412
# indels	4606
# short indels	4533
# long indels	73
Indels length	6536

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).

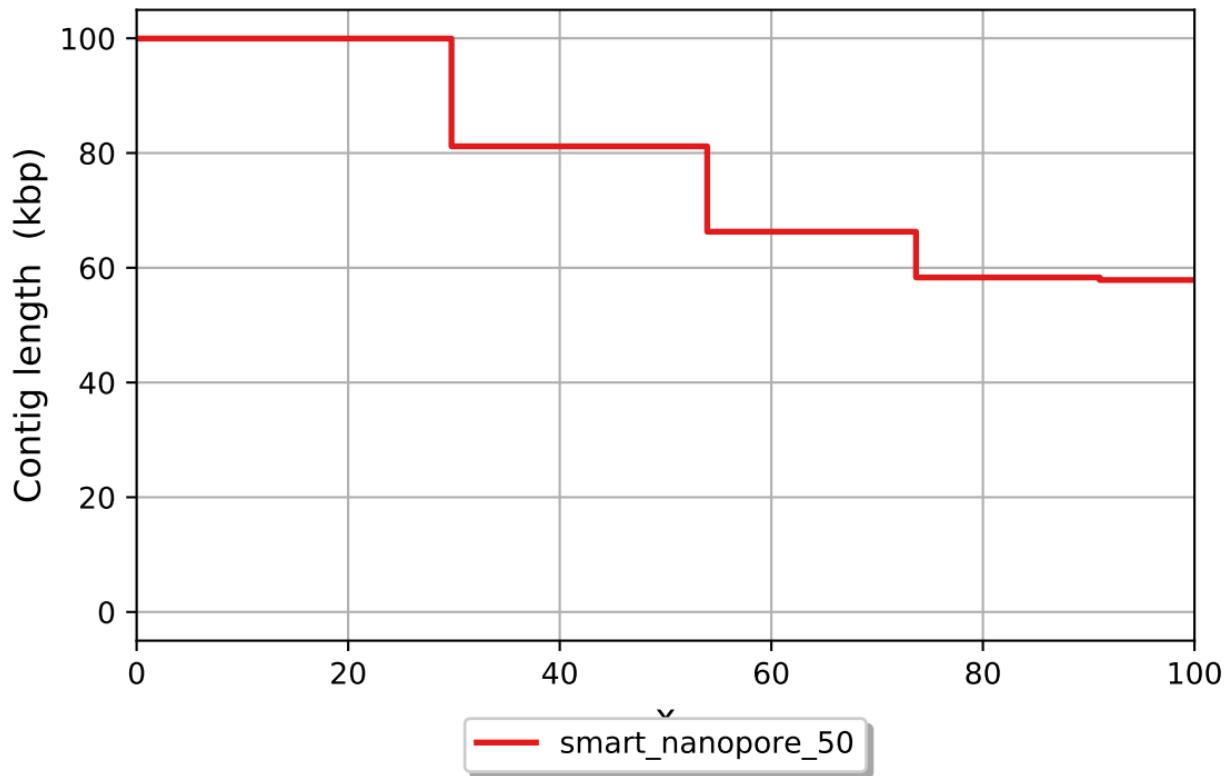
Unaligned report

	smart_nanopore_50
# fully unaligned contigs	145
Fully unaligned length	2277898
# partially unaligned contigs	118
# with misassembly	49
# both parts are significant	95
Partially unaligned length	1735375
# N's	0

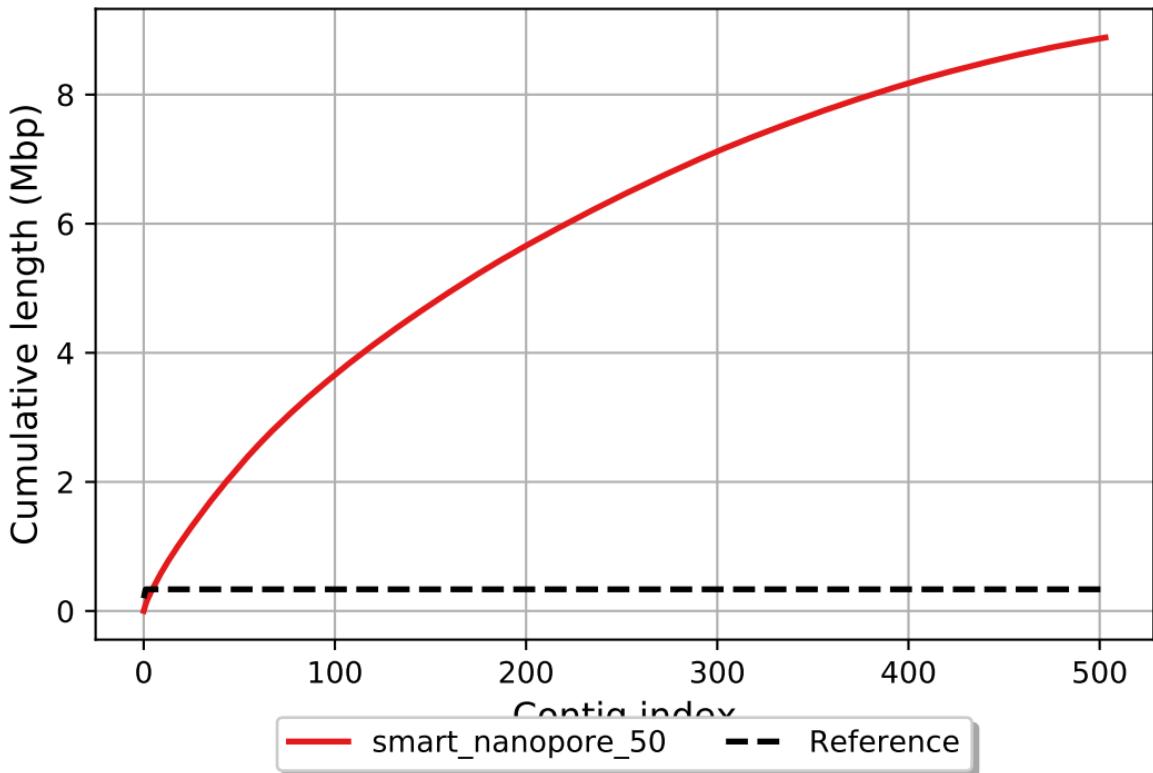
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



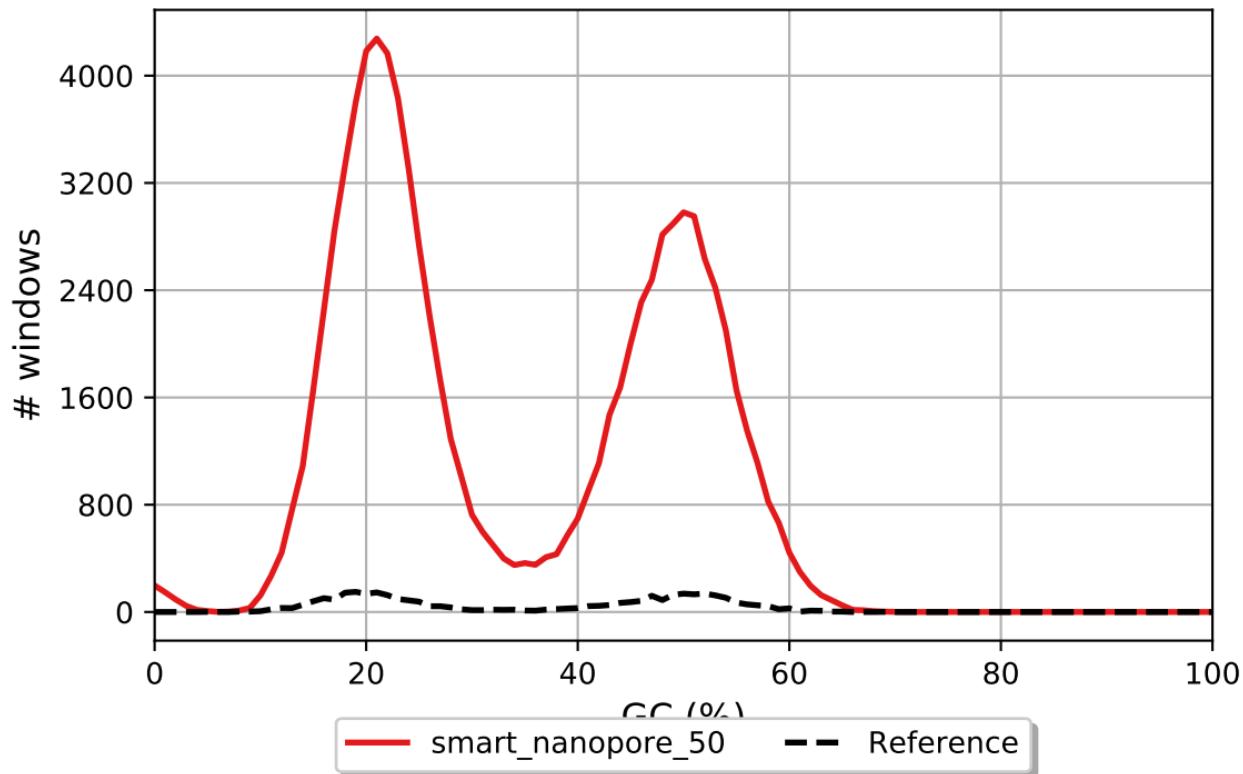
NGx



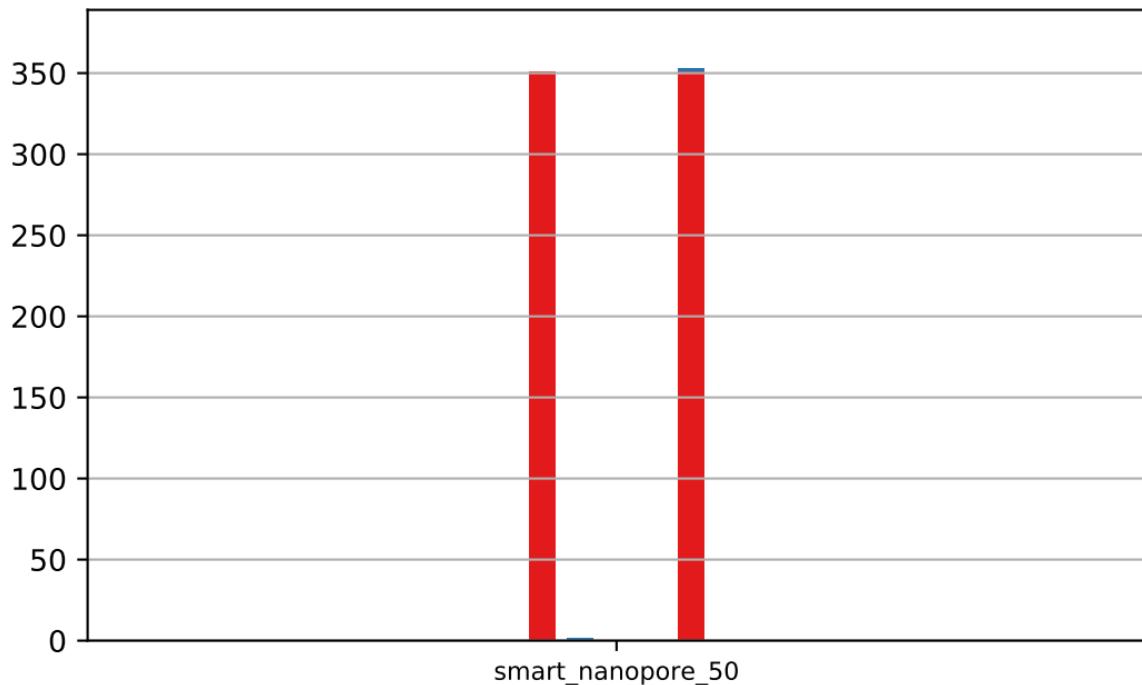
Cumulative length



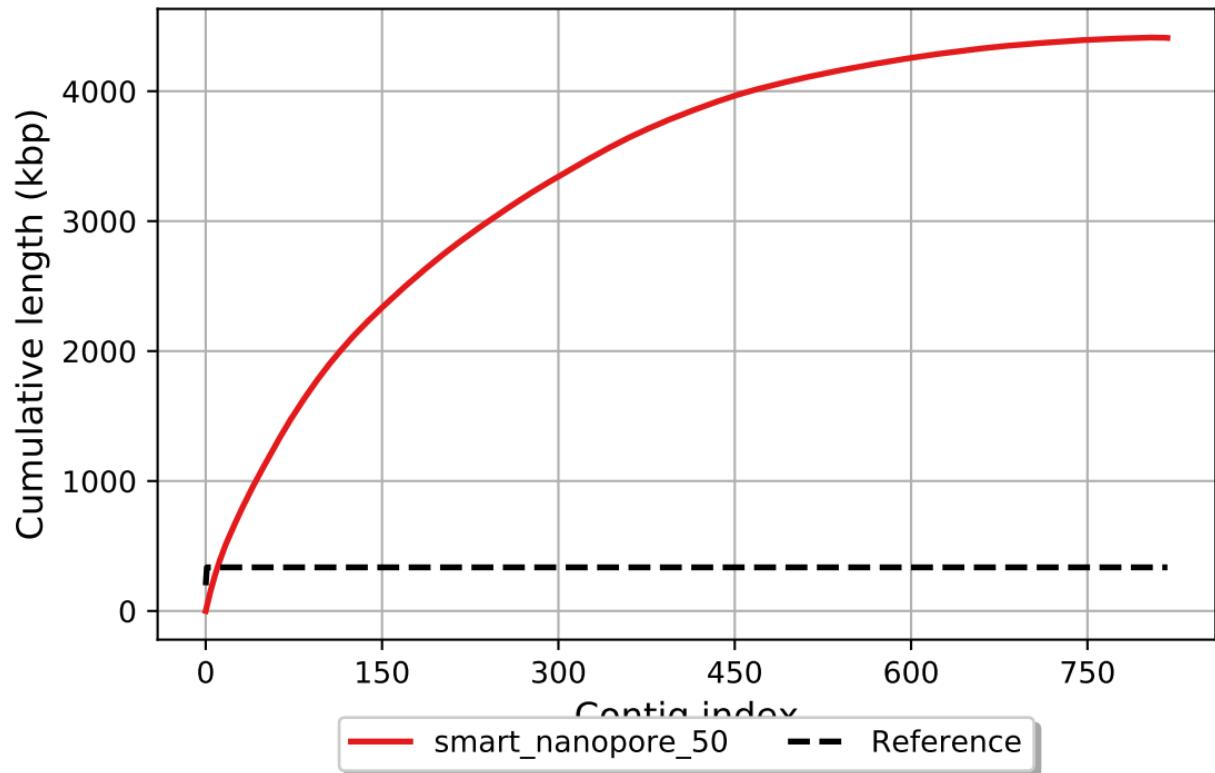
GC content



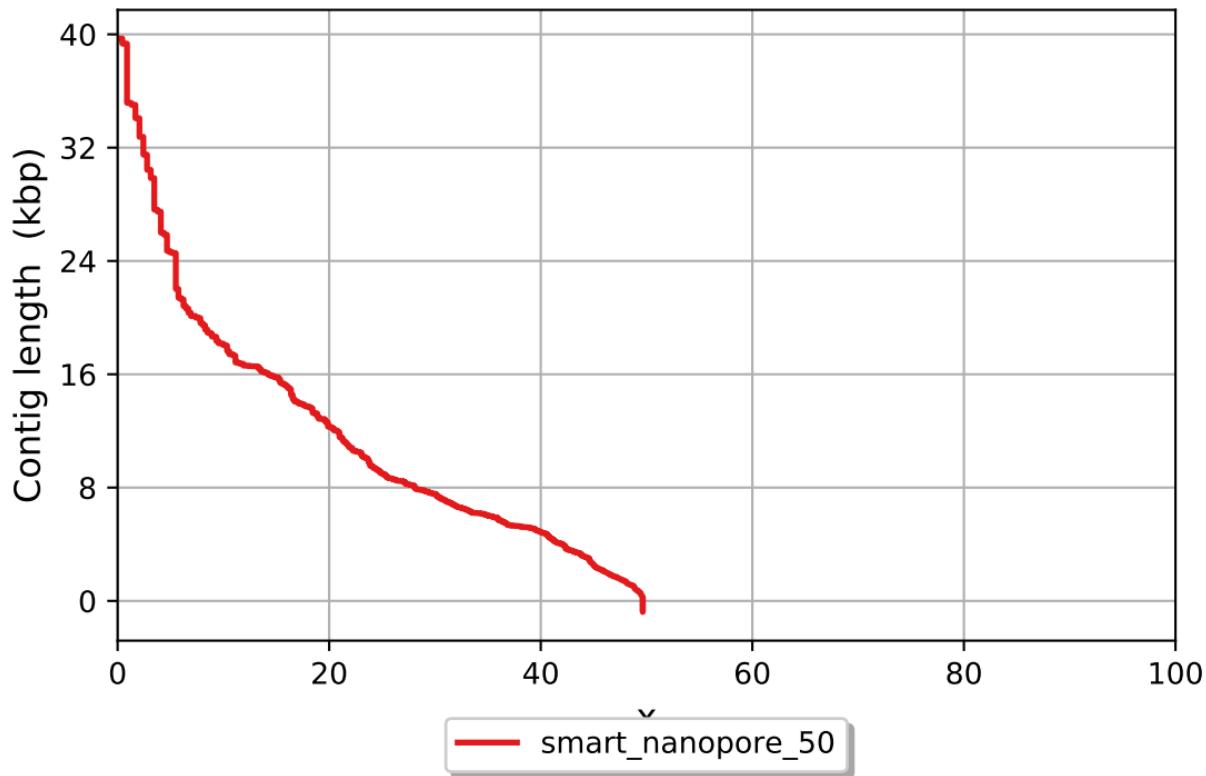
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

