Report

	no_error_ont_hq_50x_olc
# contigs (>= 0 bp)	8
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	108390
Total length (>= 1000 bp)	108390
Total length (>= 5000 bp)	108390
Total length (>= 10000 bp)	98853
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	8
Largest contig	19213
Total length	108390
Reference length	30119
GC (%)	40.78
Reference GC (%)	41.24
N50	12511
NG50	19213
N90	11469
NG90	16520
auN	14170.2
auNG	50994.5
L50	4
LG50	1
L90	7
LG90	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.663
Duplication ratio	3.723
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	19213
Total aligned length	108390
NA50	12511
NGA50	19213
NA90	11469
NGA90	16520
auNA	14170.2
auNGA	50994.5
LA50	4
LGA50	1
LA90	7
LGA90	2

All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

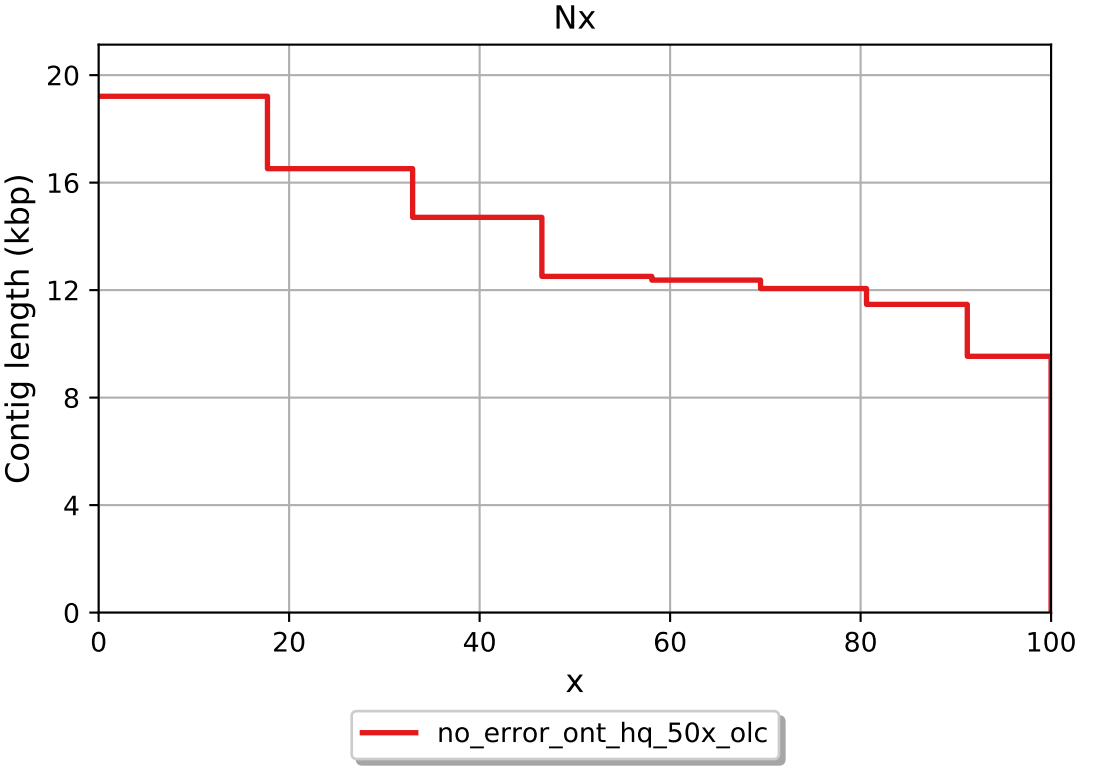
	no_error_ont_hq_50x_olc
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

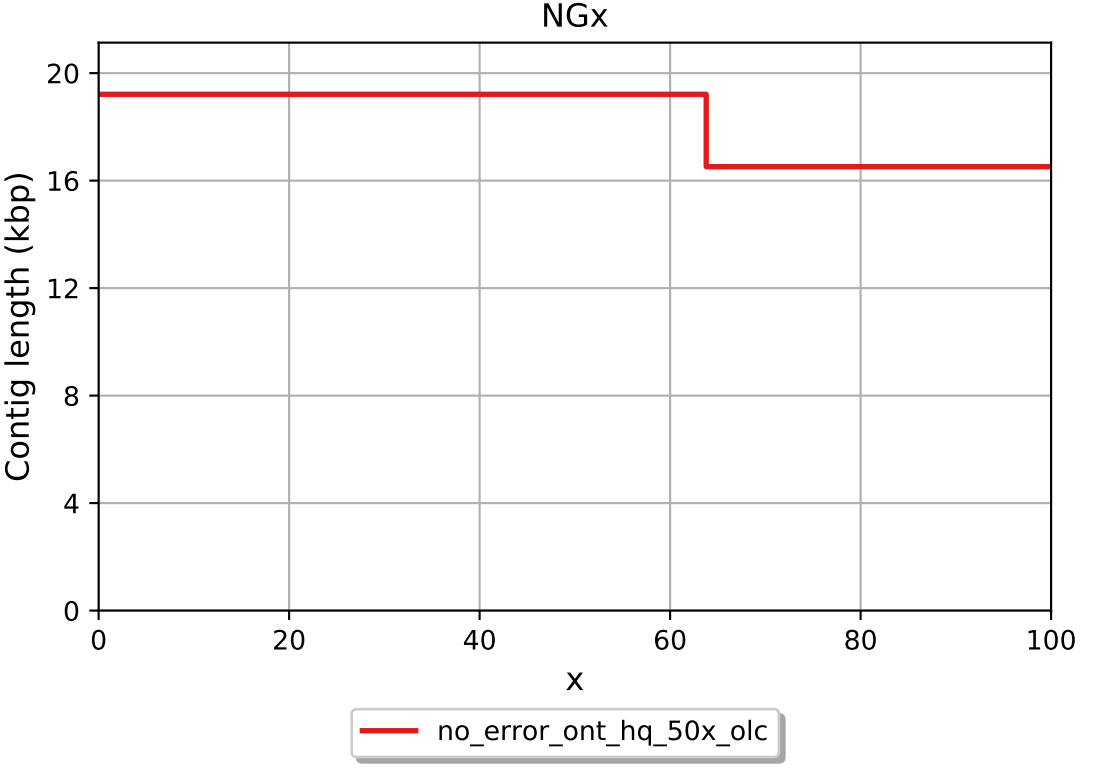
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

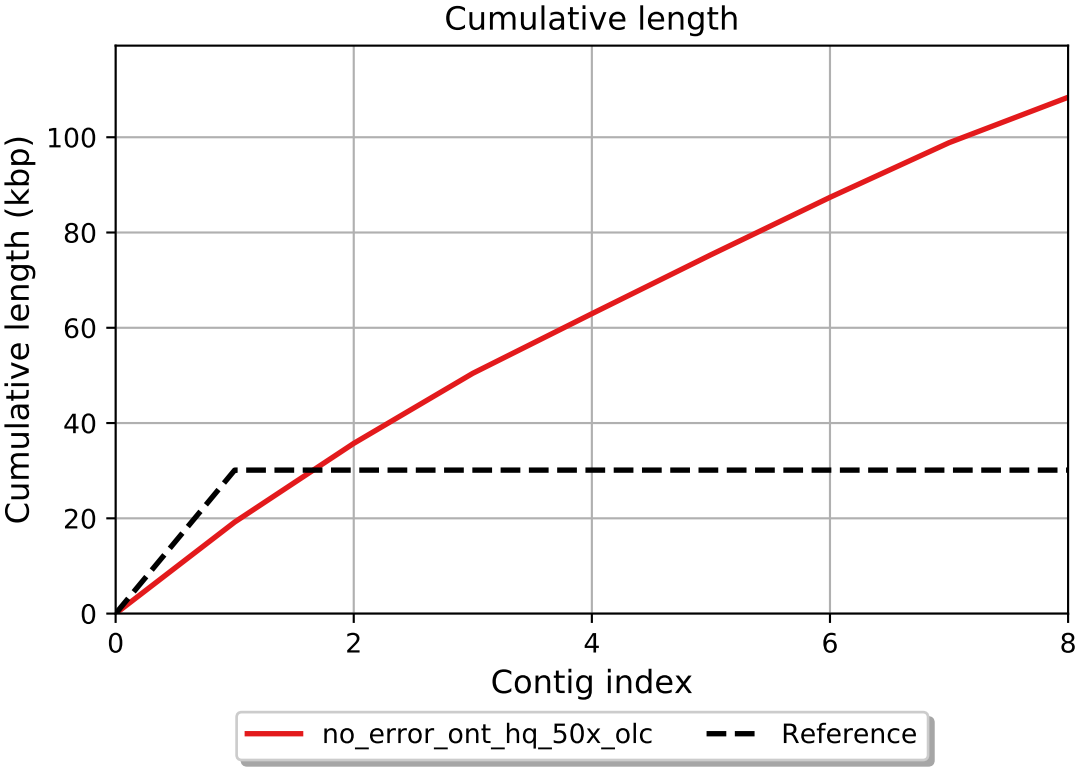
Unaligned report

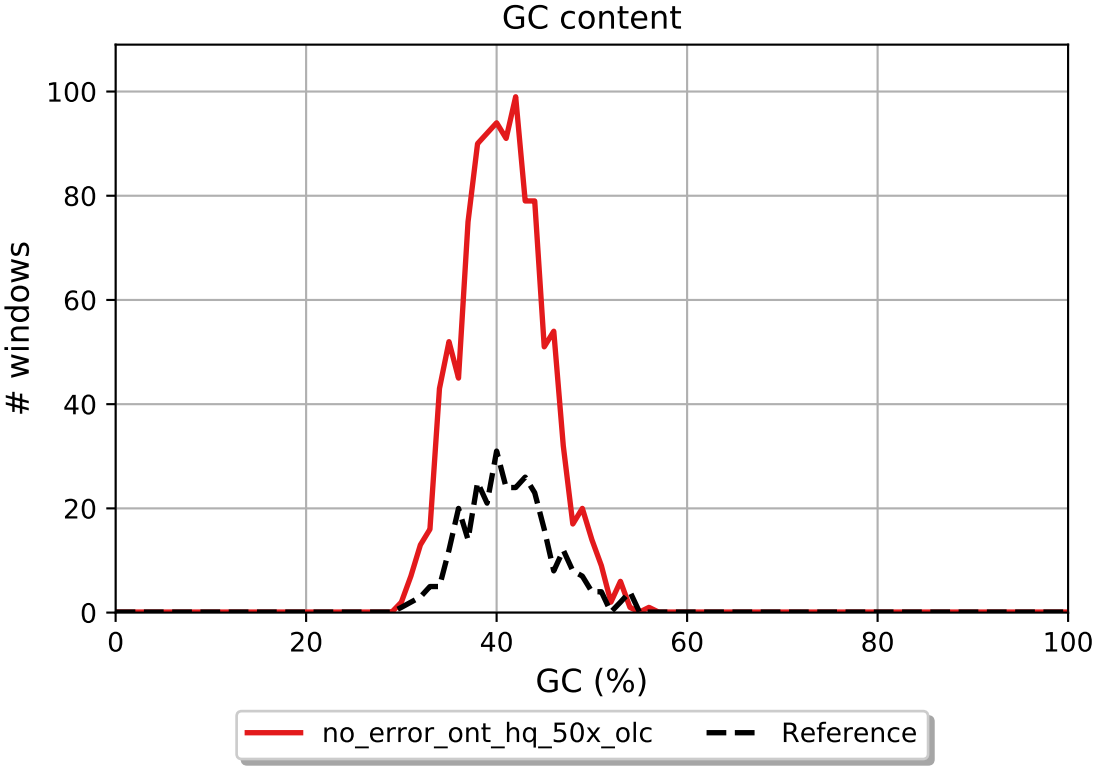
	no_error_ont_hq_50x_olc
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

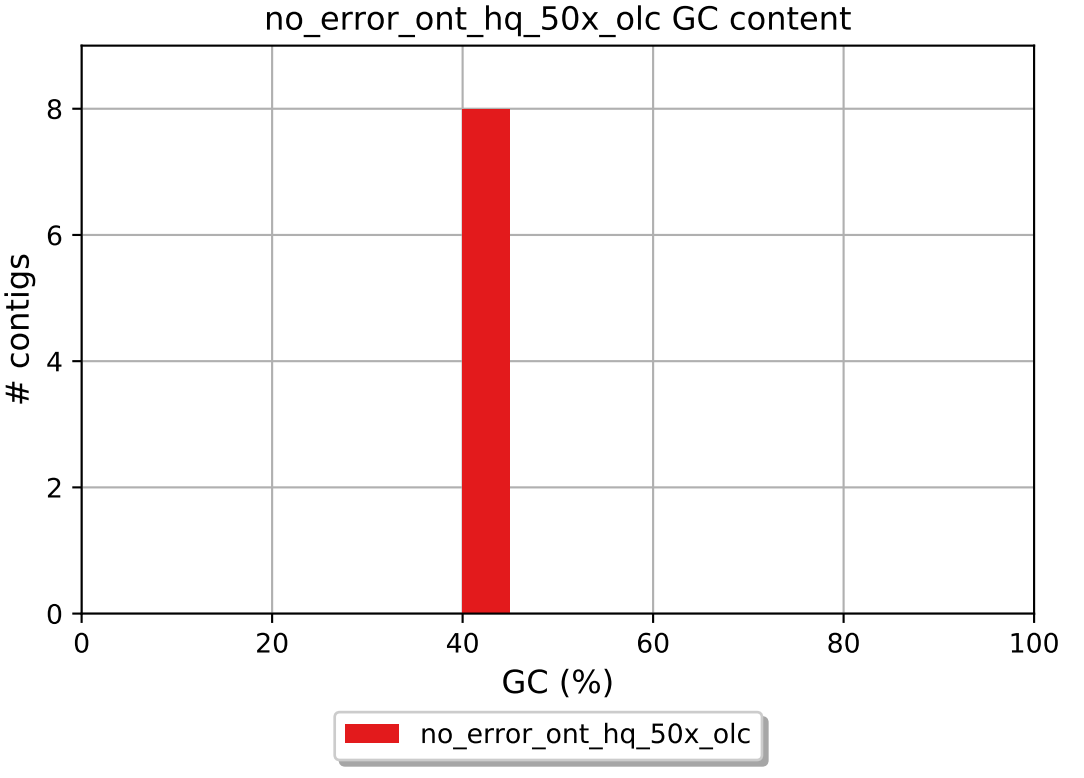
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

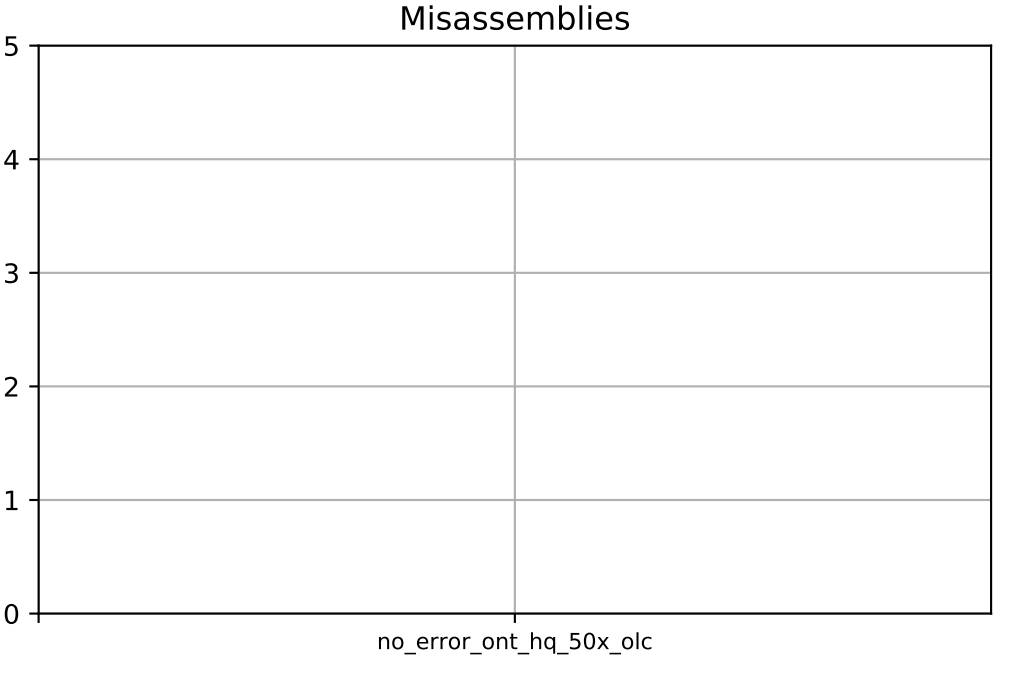

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
no_error_ont_hq_50x_olc

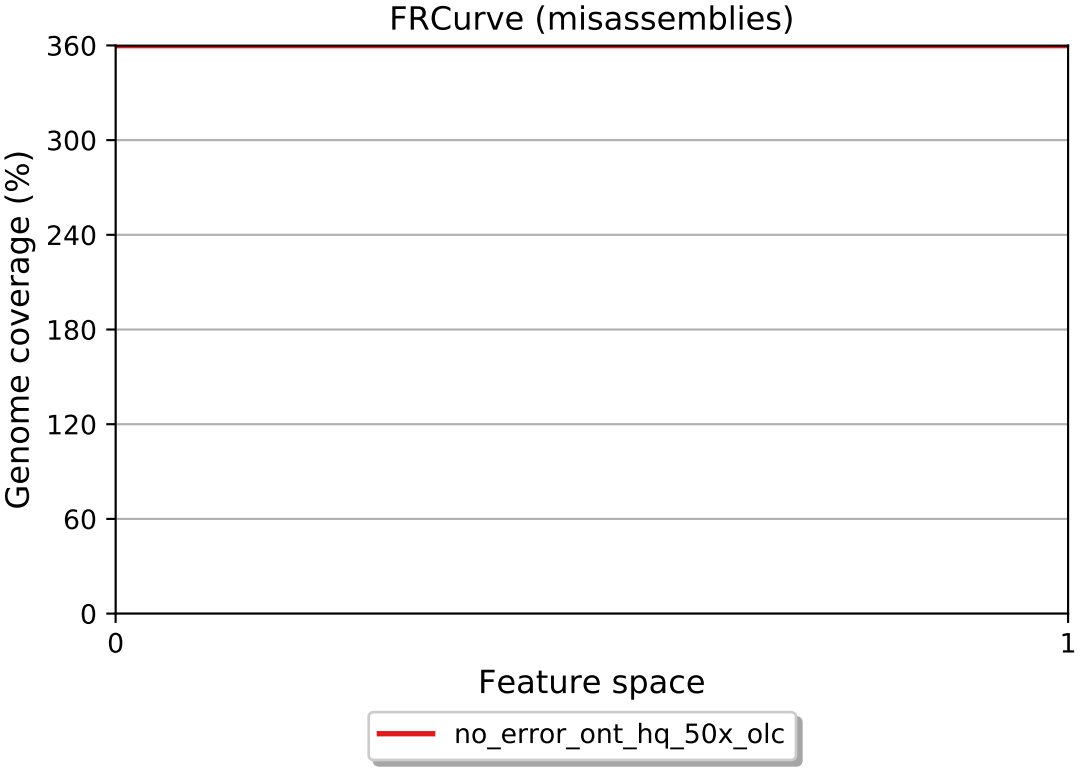

NGx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
no_error_ont_hq_50x_olc

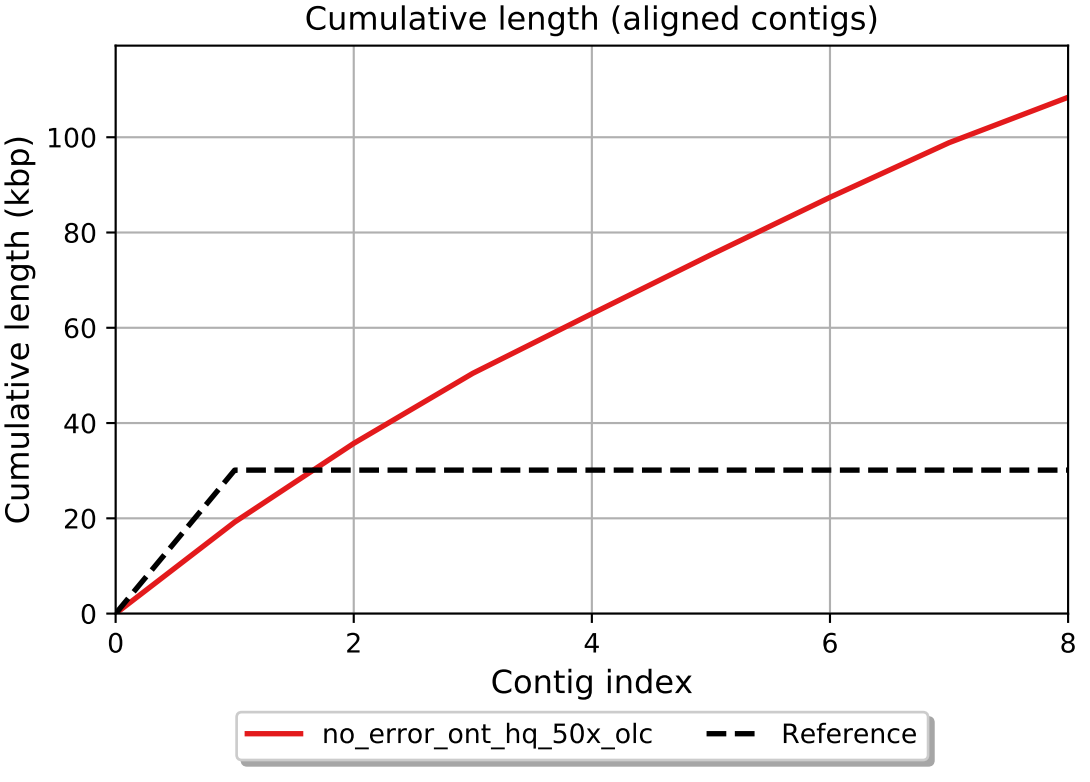

Cumulative length
Cumulative length (kbp)
0
20
40
60
80
100
0
2
4
6
8
Contig index
no_error_ont_hq_50x_olc
Reference

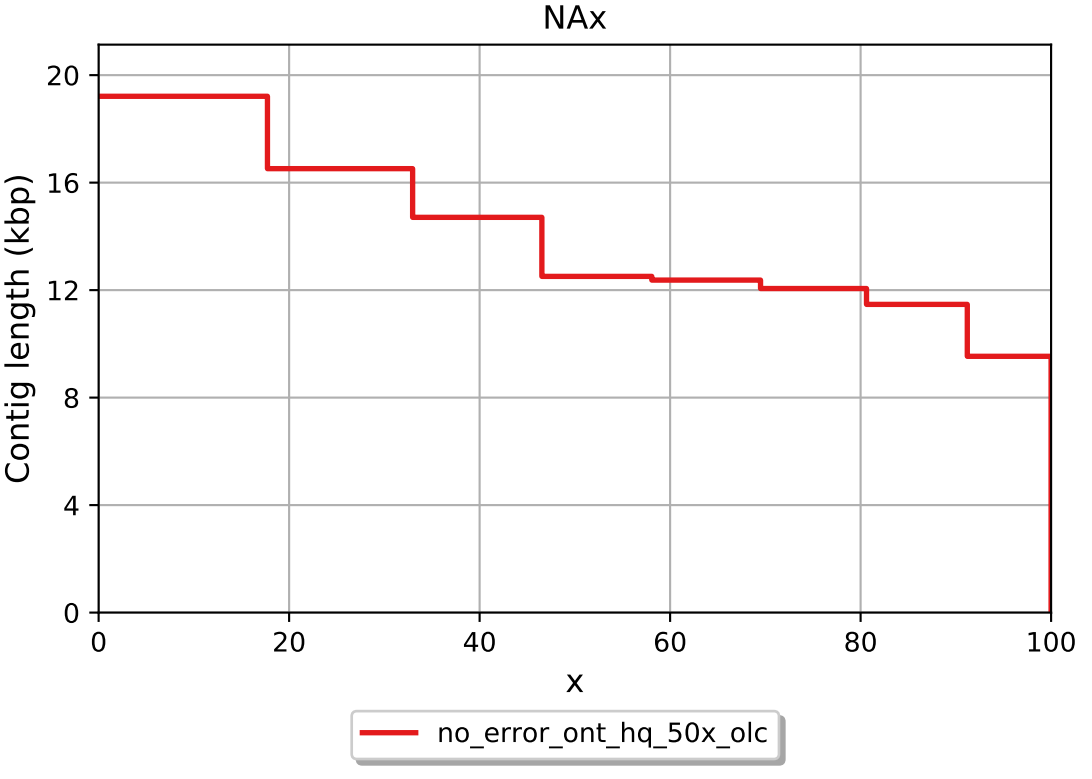

GC content
windows
GC (%)
0
20
40
60
80
100
no_error_ont_hq_50x_olc
Reference

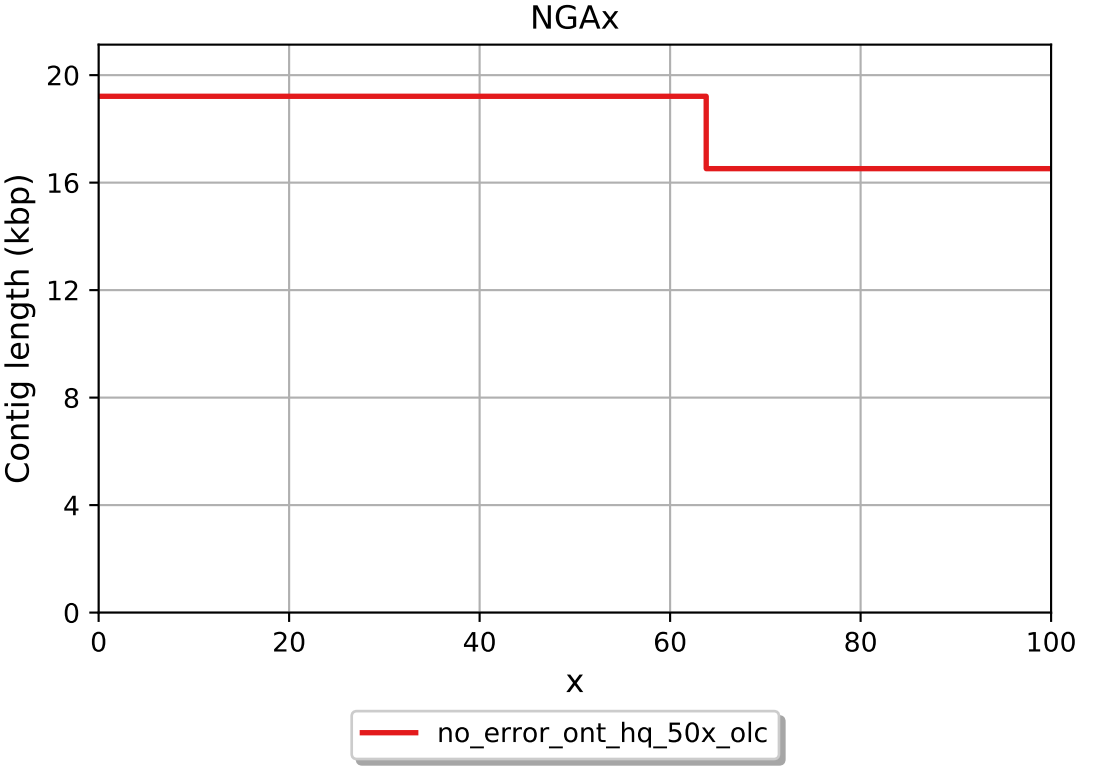

no_error_ont_hq_50x_olc GC content
contigs
0
2
4
6
8
0
20
40
60
80
100
GC (%)
no_error_ont_hq_50x_olc


Misassemblies
5
4
3
2
1
0
no_error_ont_hq_50x_olc


FRCurve (misassemblies)
360
300
240
180
120
60
0
Genome coverage (%)
0
1
Feature space
no_error_ont_hq_50x_olc


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
20
40
60
80
100
0
2
4
6
8
Contig index
no_error_ont_hq_50x_olc
Reference


NAx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
no_error_ont_hq_50x_olc


NGAx
Contig length (kbp)
0
4
8
12
16
20
0
20
40
60
80
100
x
no_error_ont_hq_50x_olc