Report

	ont_hq_50x_dbg_k40
# contigs (>= 0 bp)	475
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	78295
Total length (>= 1000 bp)	55090
Total length (>= 5000 bp)	51737
Total length (>= 10000 bp)	37995
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	10
Largest contig	14599
Total length	56670
Reference length	30119
GC (%)	40.84
Reference GC (%)	41.24
N50	11109
NG50	12287
N90	5721
NG90	11109
auN	10433.0
auNG	19630.1
L50	3
LG50	2
L90	5
LG90	3
# 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	2 + 0 part
Unaligned length	824
Genome fraction (%)	91.587
Duplication ratio	1.974
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	119.38
Largest alignment	14170
Total aligned length	54450
NA50	10739
NGA50	11984
NA90	1921
NGA90	10739
auNA	9871.5
auNGA	18573.6
LA50	3
LGA50	2
LA90	6
LGA90	3

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

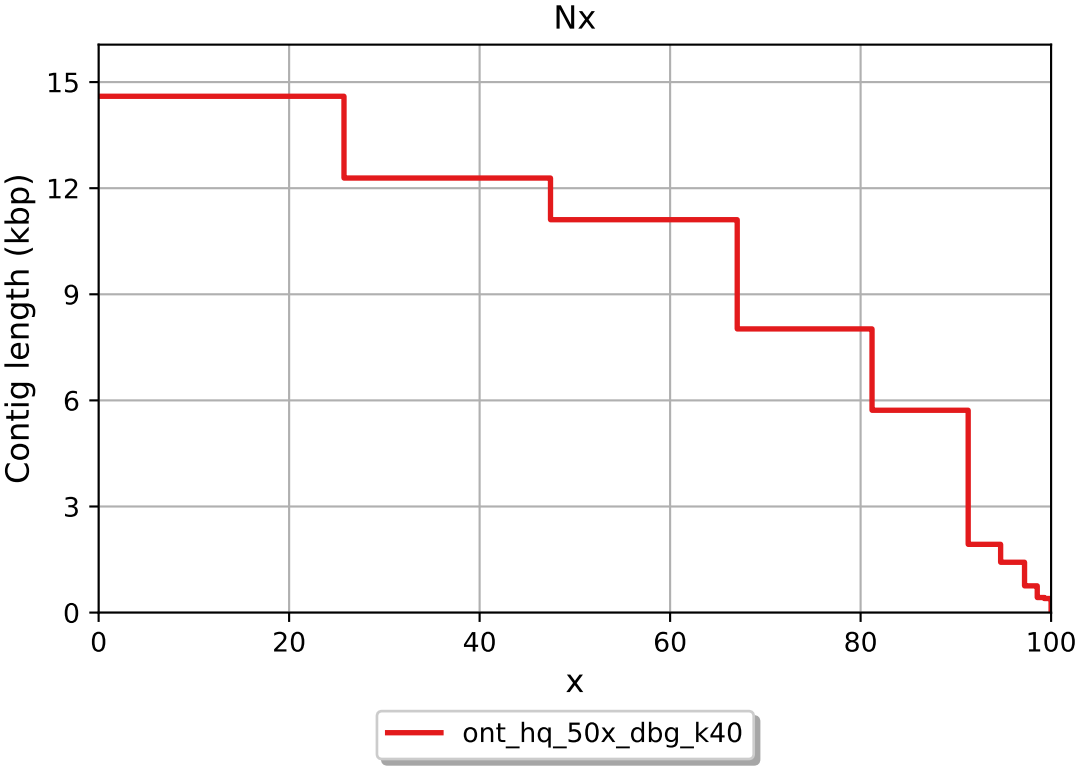
	ont_hq_50x_dbg_k40
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	65
# indels (<= 5 bp)	25
# indels (> 5 bp)	40
Indels length	1245

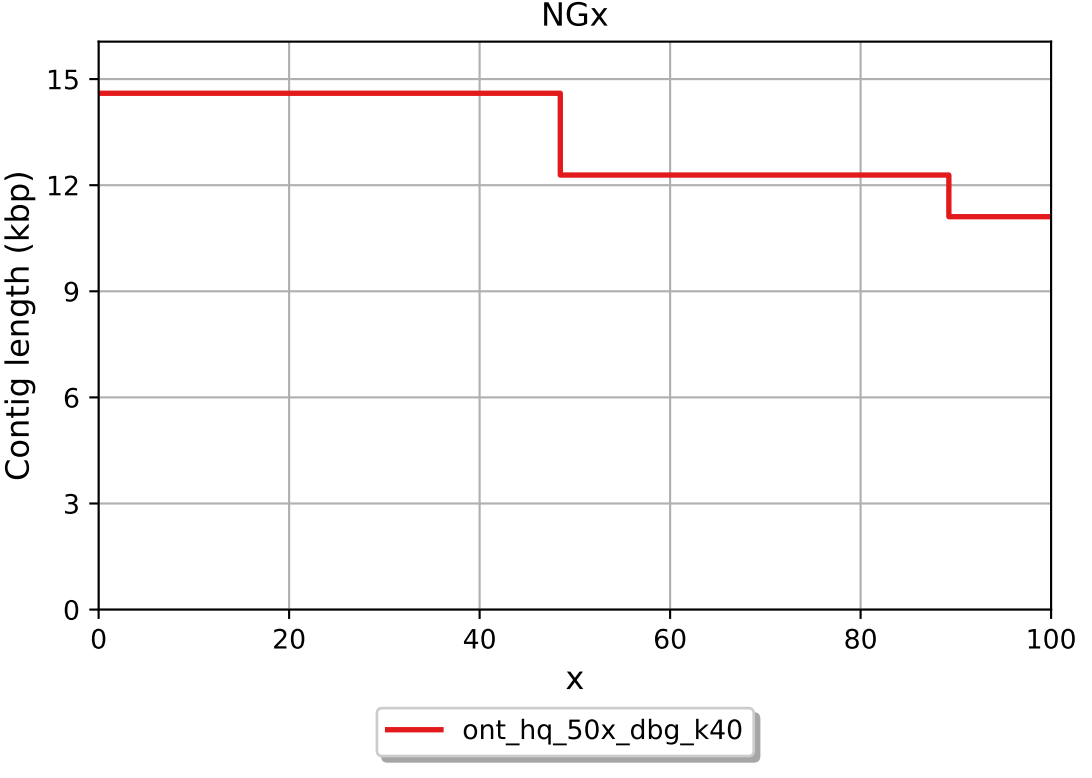
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

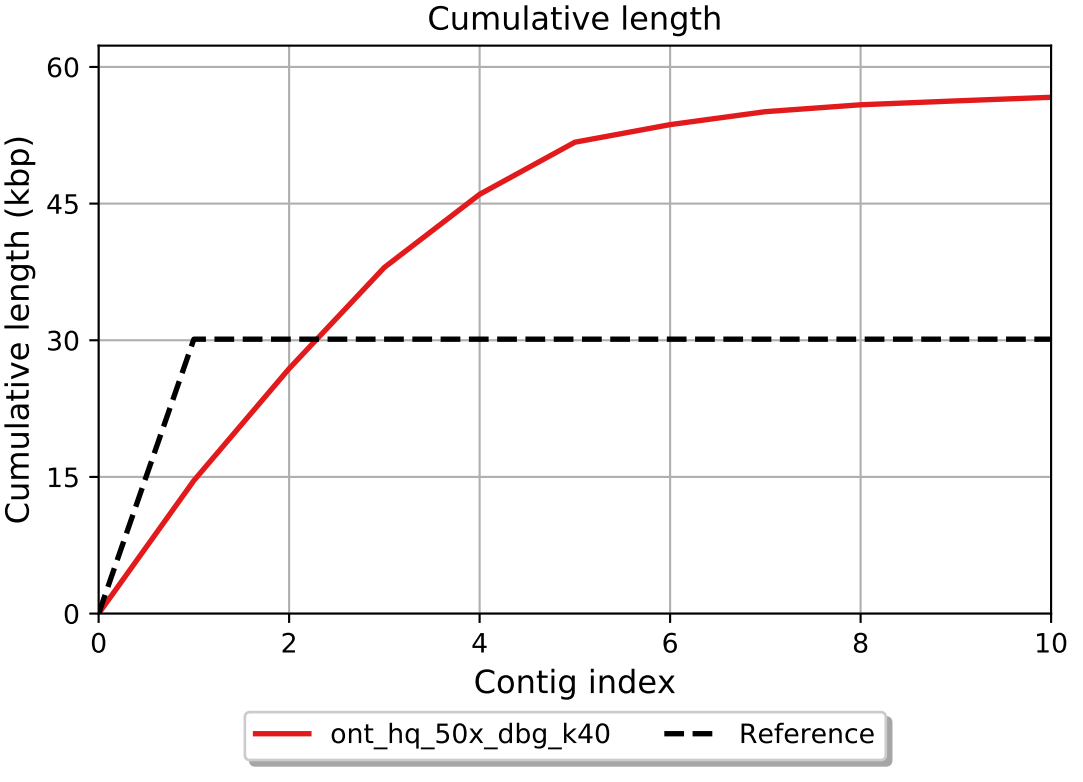
Unaligned report

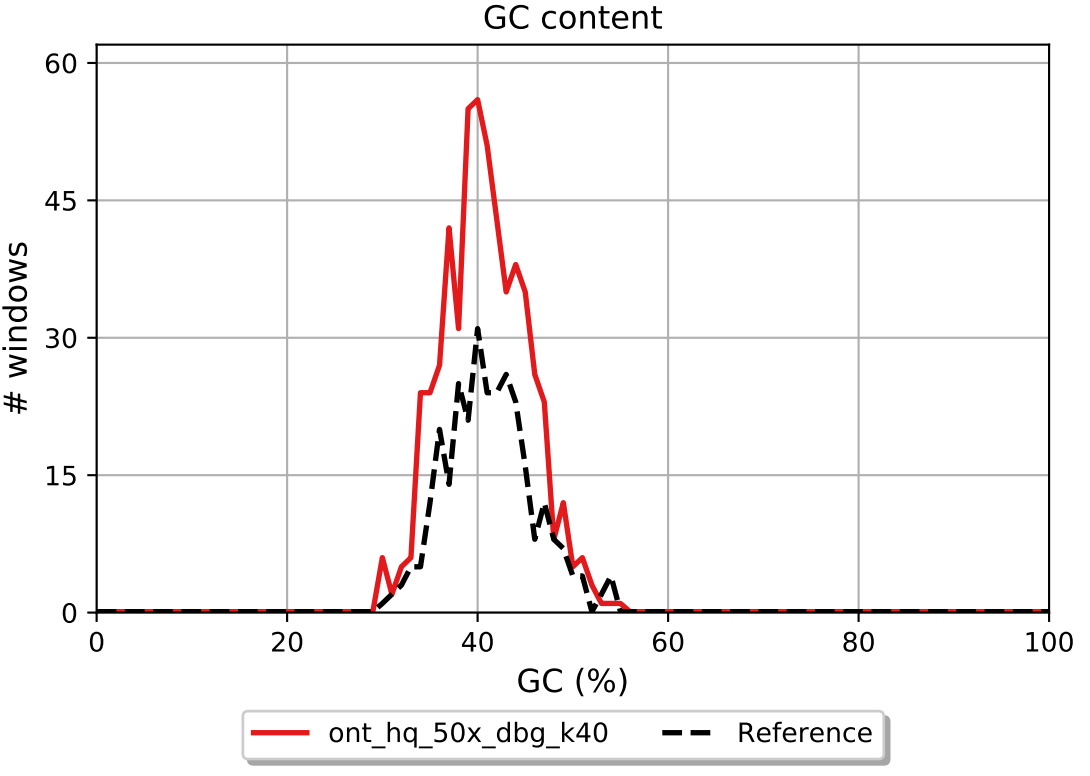
	ont_hq_50x_dbg_k40
# fully unaligned contigs	2
Fully unaligned length	824
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

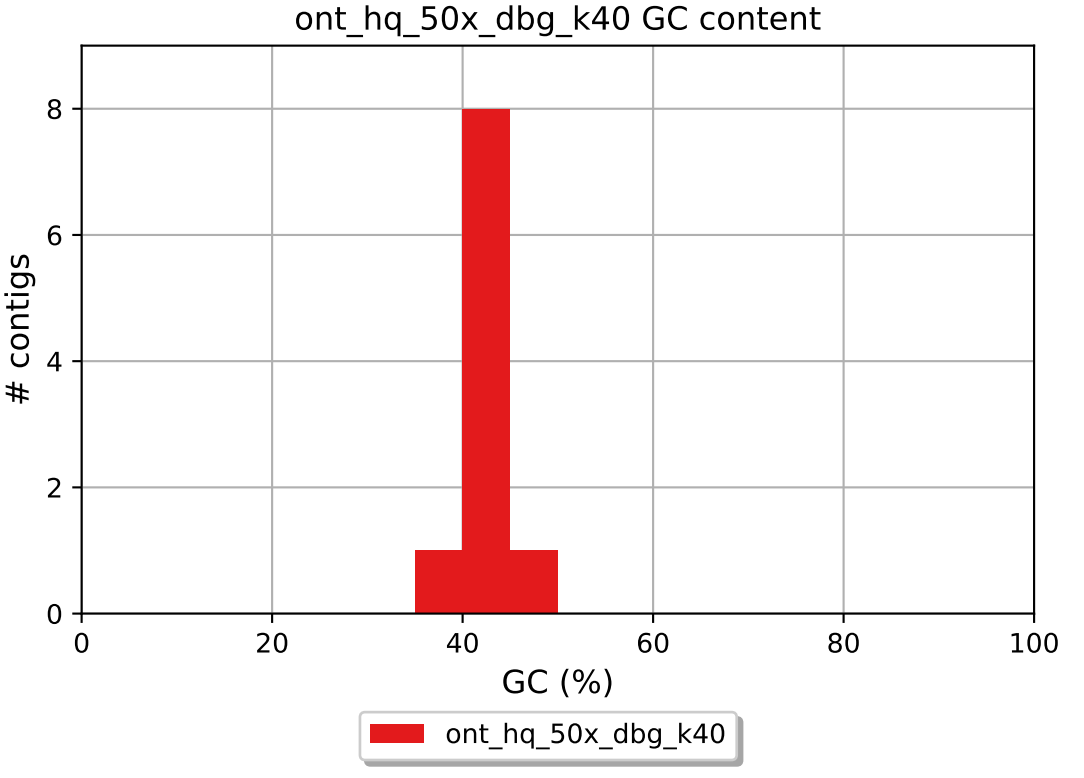
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

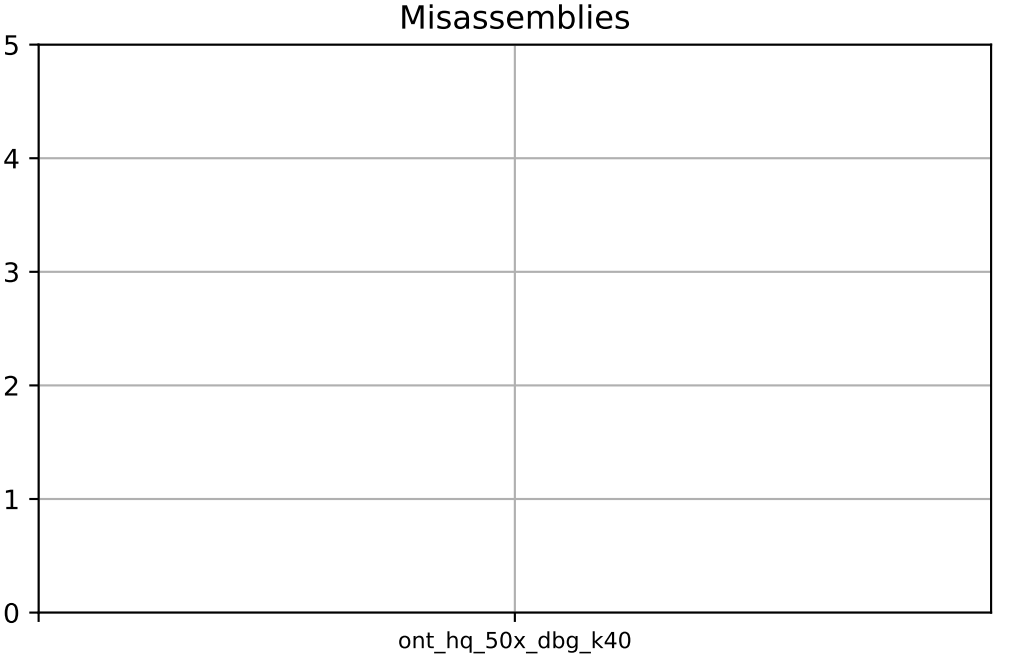

Nx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
ont_hq_50x_dbg_k40

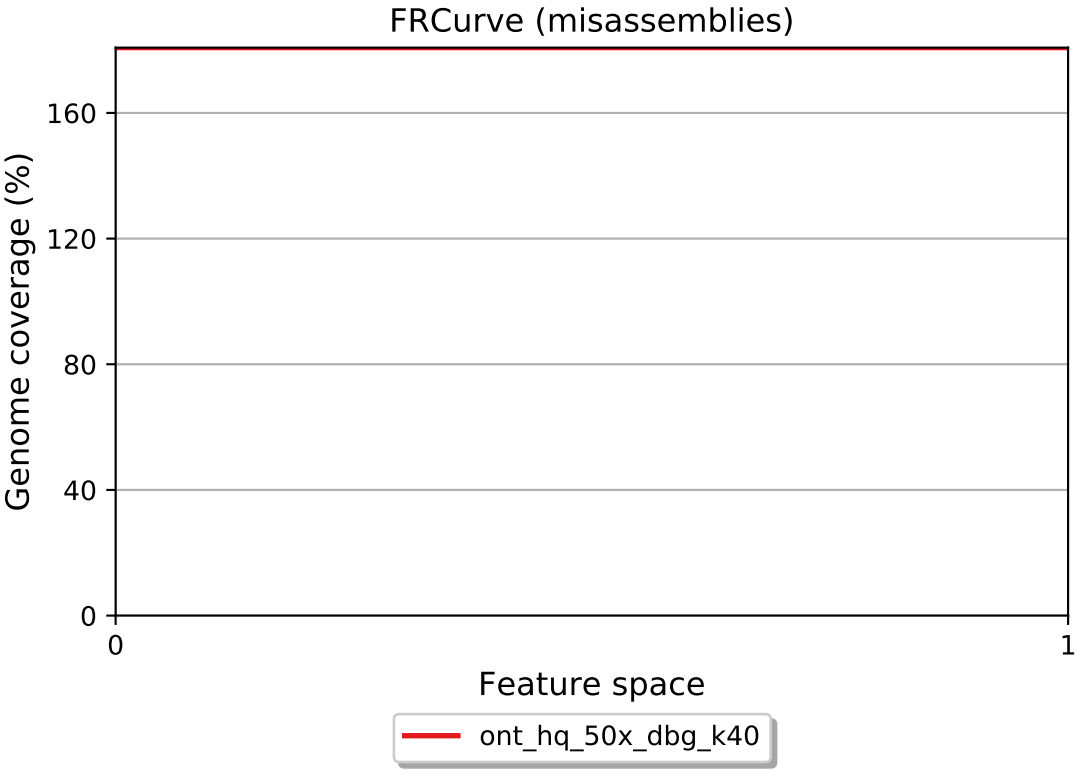

NGx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
ont_hq_50x_dbg_k40

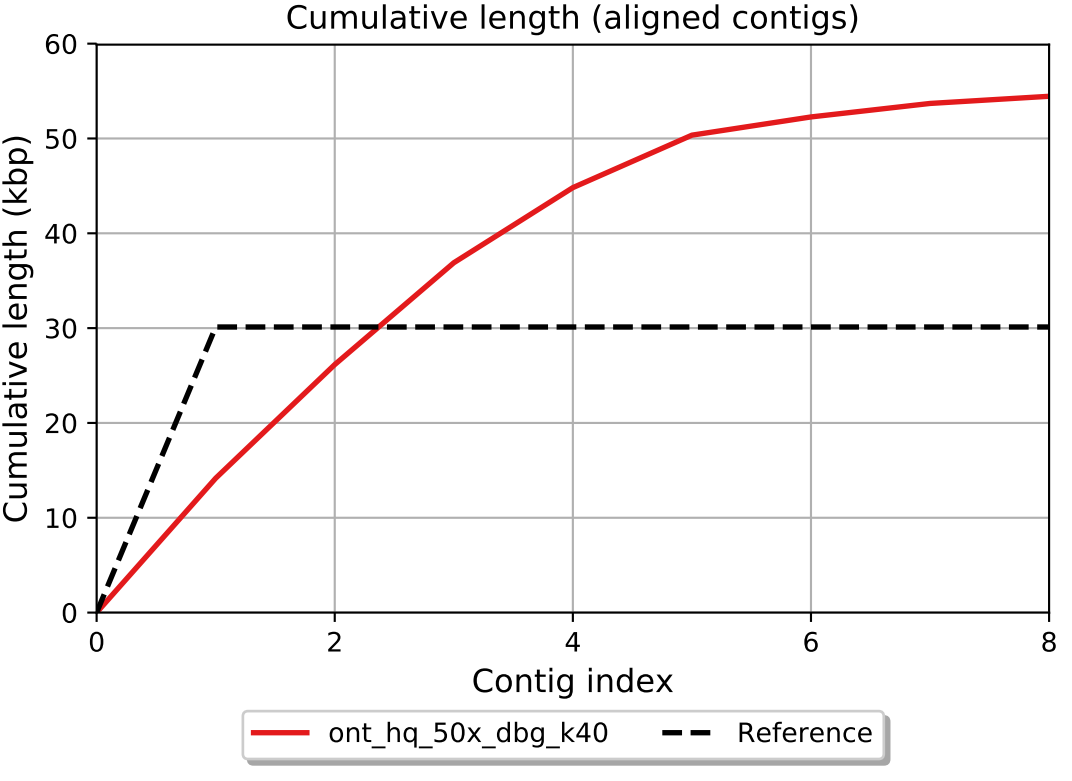

Cumulative length
Cumulative length (kbp)
60
45
30
15
0
0
2
4
6
8
10
Contig index
ont_hq_50x_dbg_k40
Reference

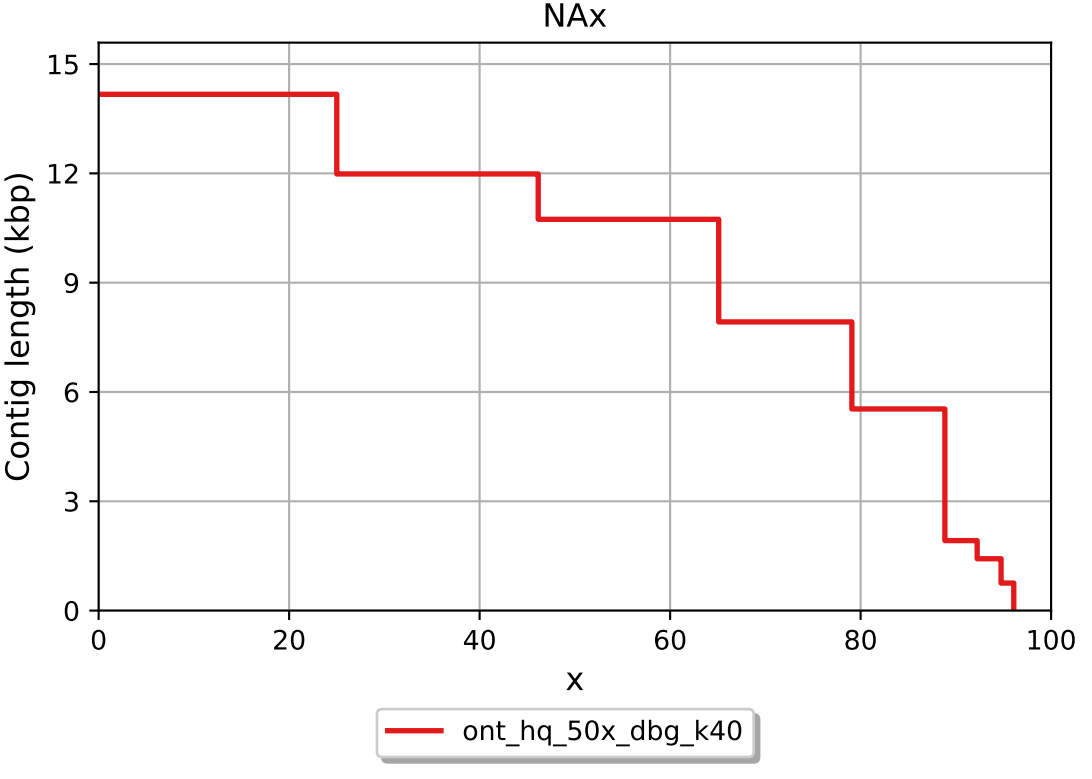

GC content
windows
GC (%)
0
15
30
45
60
0
20
40
60
80
100
ont_hq_50x_dbg_k40
Reference

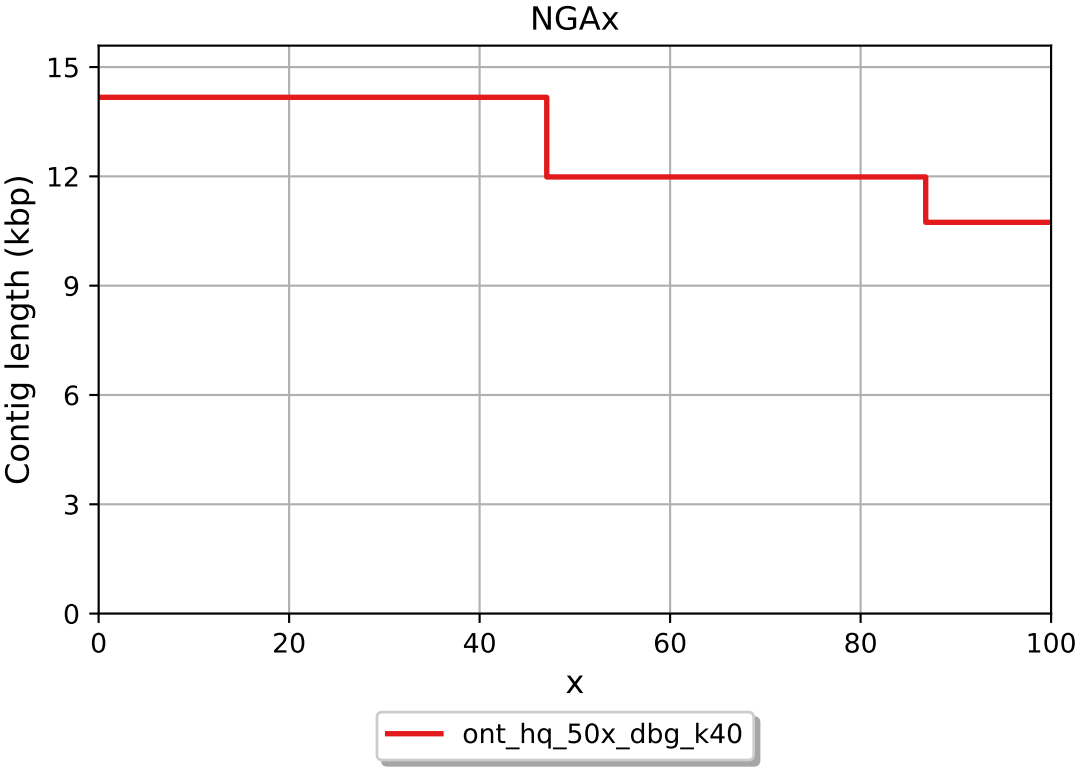

ont_hq_50x_dbg_k40 GC content
contigs
0
2
4
6
8
0
20
40
60
80
100
GC (%)
ont_hq_50x_dbg_k40


Misassemblies
5
4
3
2
1
0
ont_hq_50x_dbg_k40


FRCurve (misassemblies)
Genome coverage (%)
160
120
80
40
0
0
1
Feature space
ont_hq_50x_dbg_k40


Cumulative length (aligned contigs)
Cumulative length (kbp)
60
50
40
30
20
10
0
0
2
4
6
8
Contig index
ont_hq_50x_dbg_k40
Reference


NAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
ont_hq_50x_dbg_k40


NGAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
ont_hq_50x_dbg_k40