Report

	mini-ava-ont_10
# contigs (>= 0 bp)	17
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	4241309
Total length (>= 1000 bp)	4241309
Total length (>= 5000 bp)	4241309
Total length (>= 10000 bp)	4241309
Total length (>= 25000 bp)	4241309
Total length (>= 50000 bp)	4241309
# contigs	17
Largest contig	897424
Total length	4241309
Reference length	4686137
GC (%)	50.79
Reference GC (%)	50.78
N50	309905
NG50	303248
N90	98810
NG90	58227
auN	448312.7
auNG	405757.0
L50	4
LG50	5
L90	12
LG90	17
# 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 (%)	89.171
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	897424
Total aligned length	4241309
NA50	309905
NGA50	303248
NA90	98810
NGA90	58227
auNA	448312.7
auNGA	405757.0
LA50	4
LGA50	5
LA90	12
LGA90	17

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

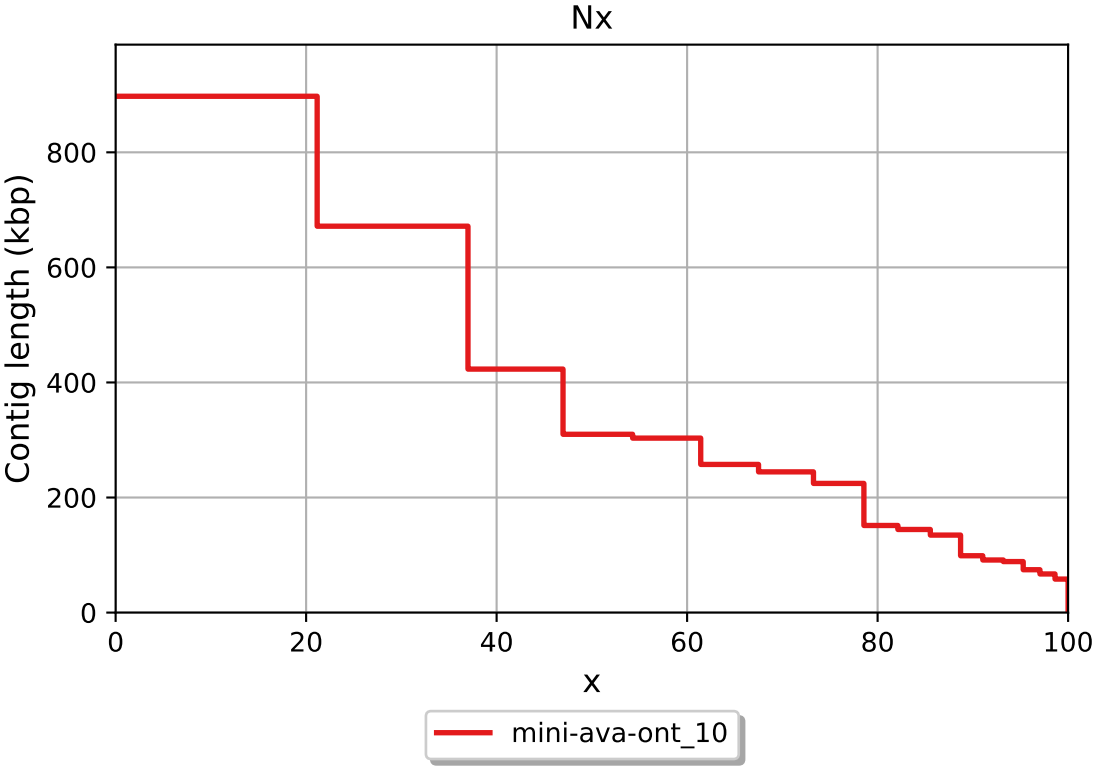
	mini-ava-ont_10
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. 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

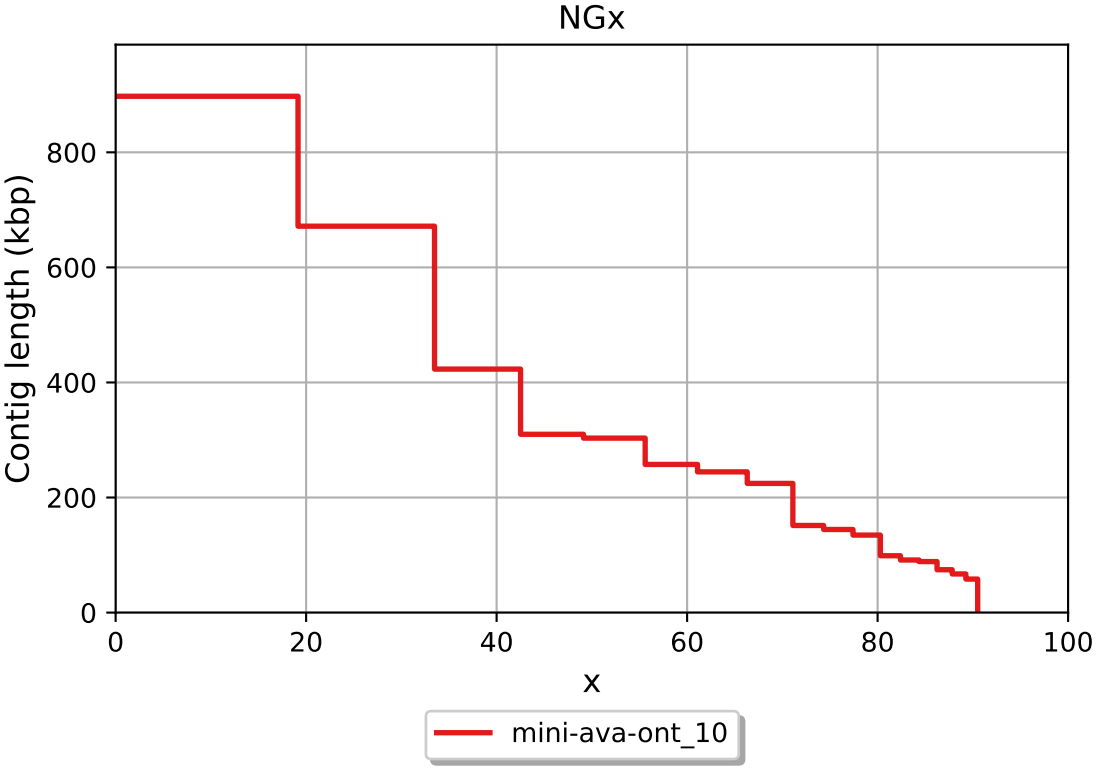
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

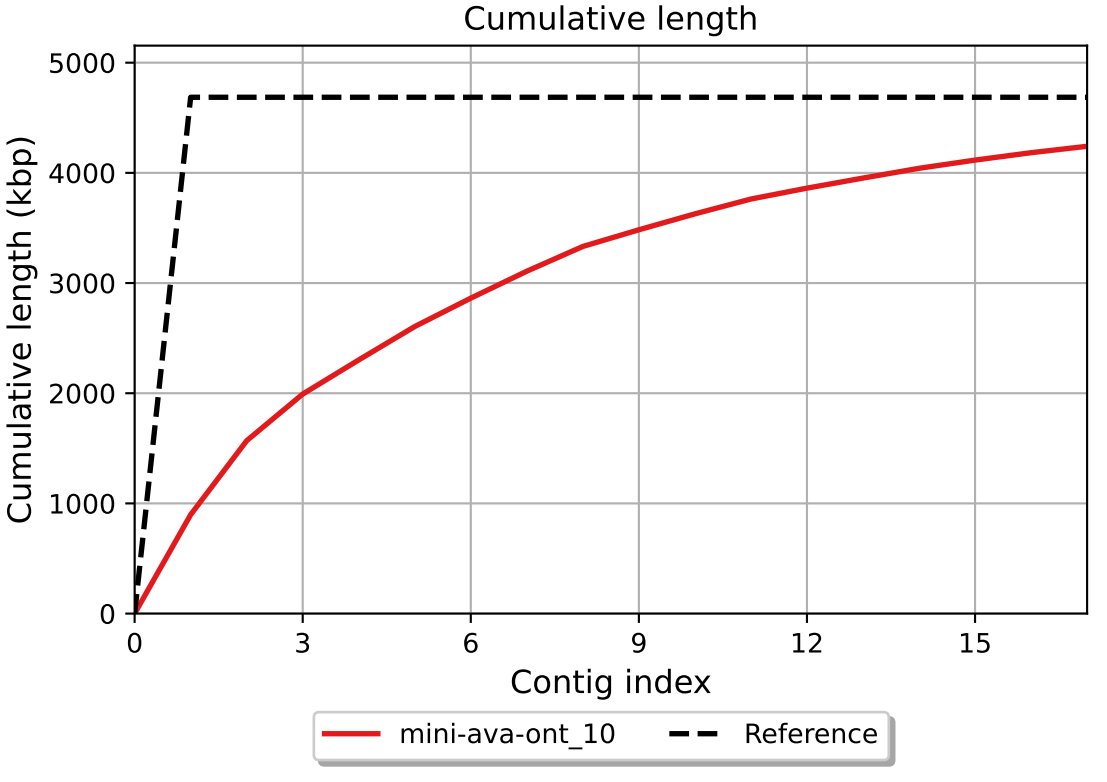
Unaligned report

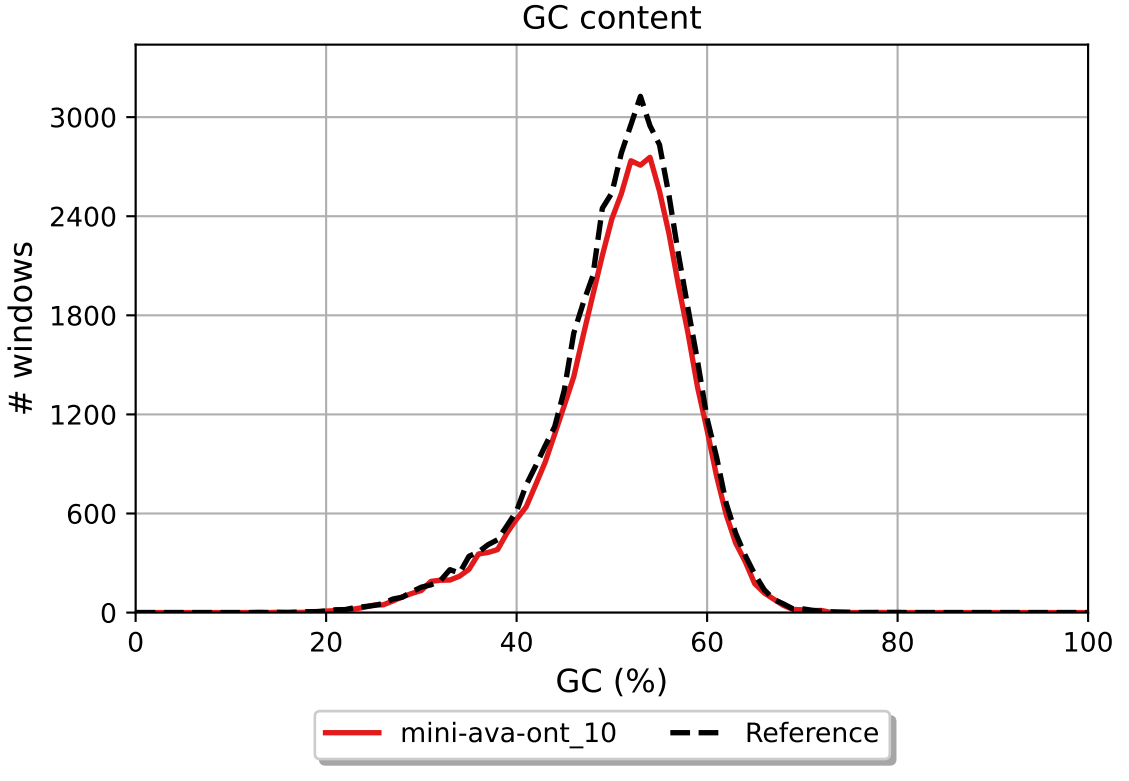
	mini-ava-ont_10
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

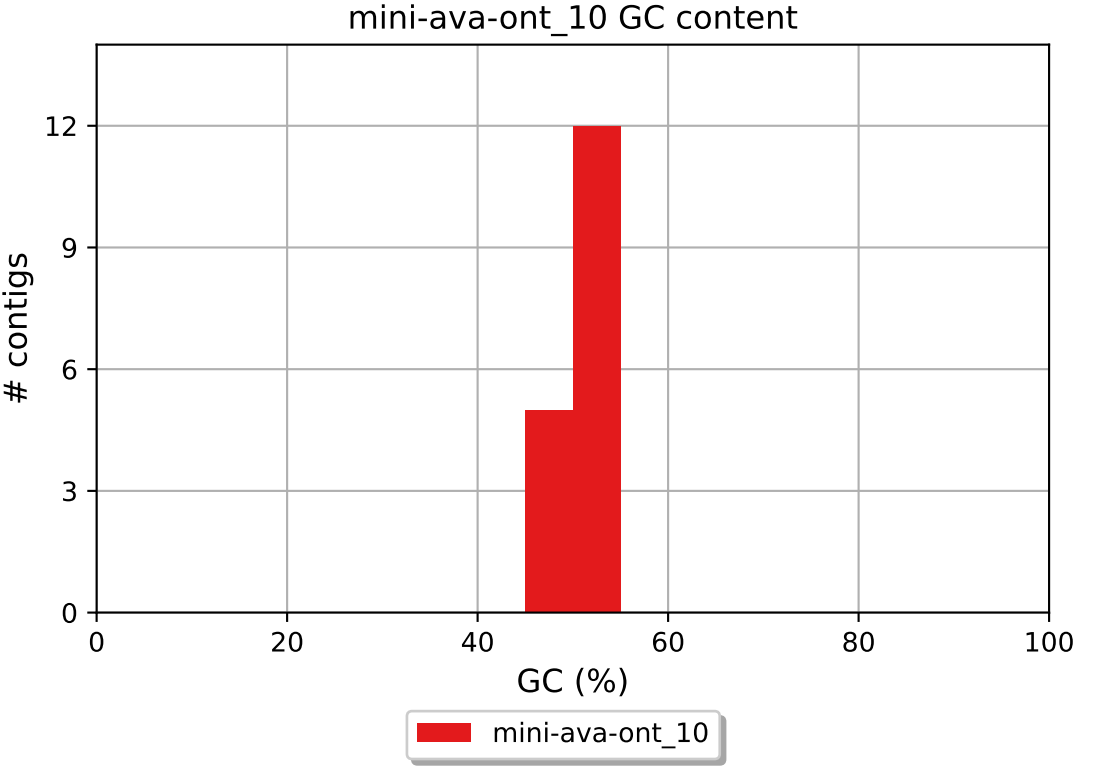
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

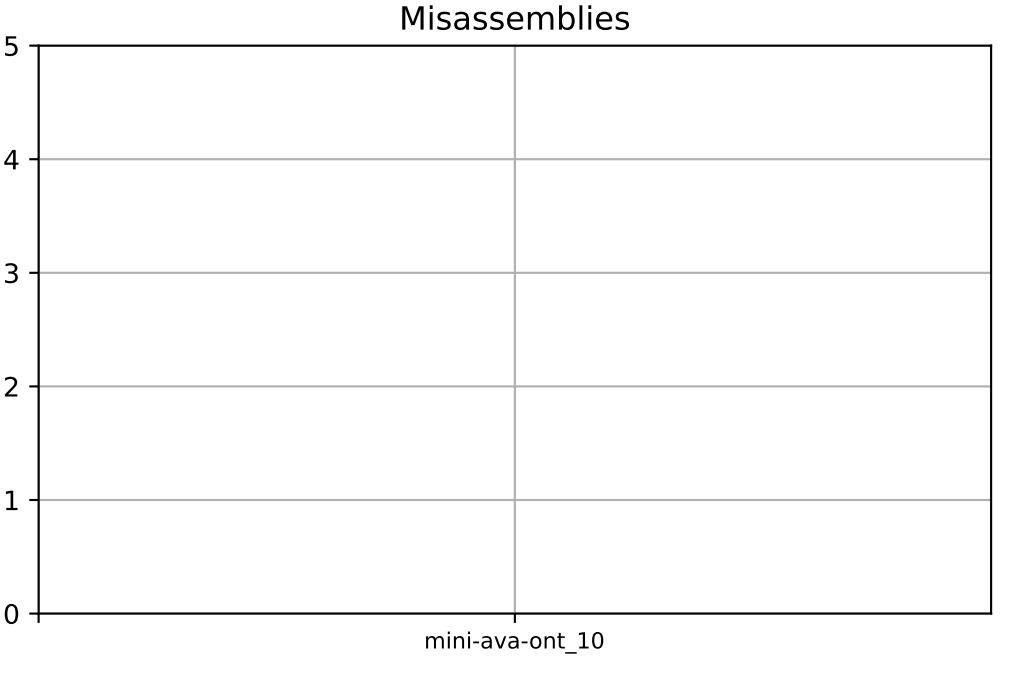

Nx
Contig length (kbp)
0
200
400
600
800
0
20
40
60
80
100
x
mini-ava-ont_10

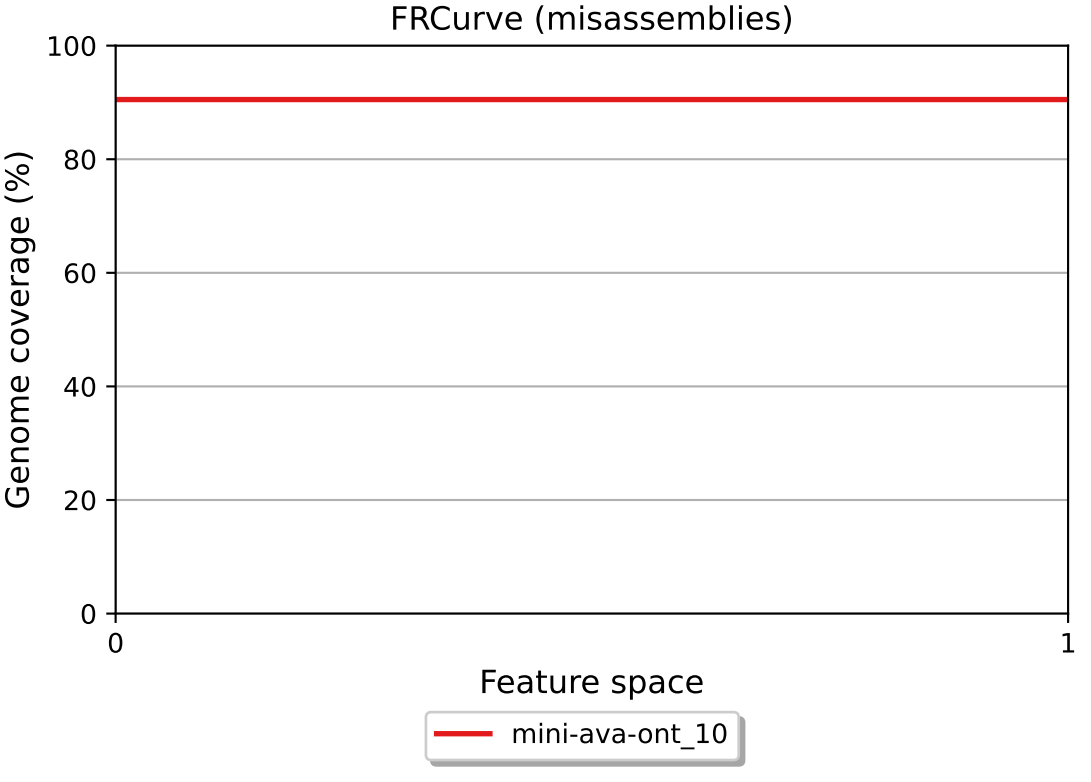

NGx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
mini-ava-ont_10

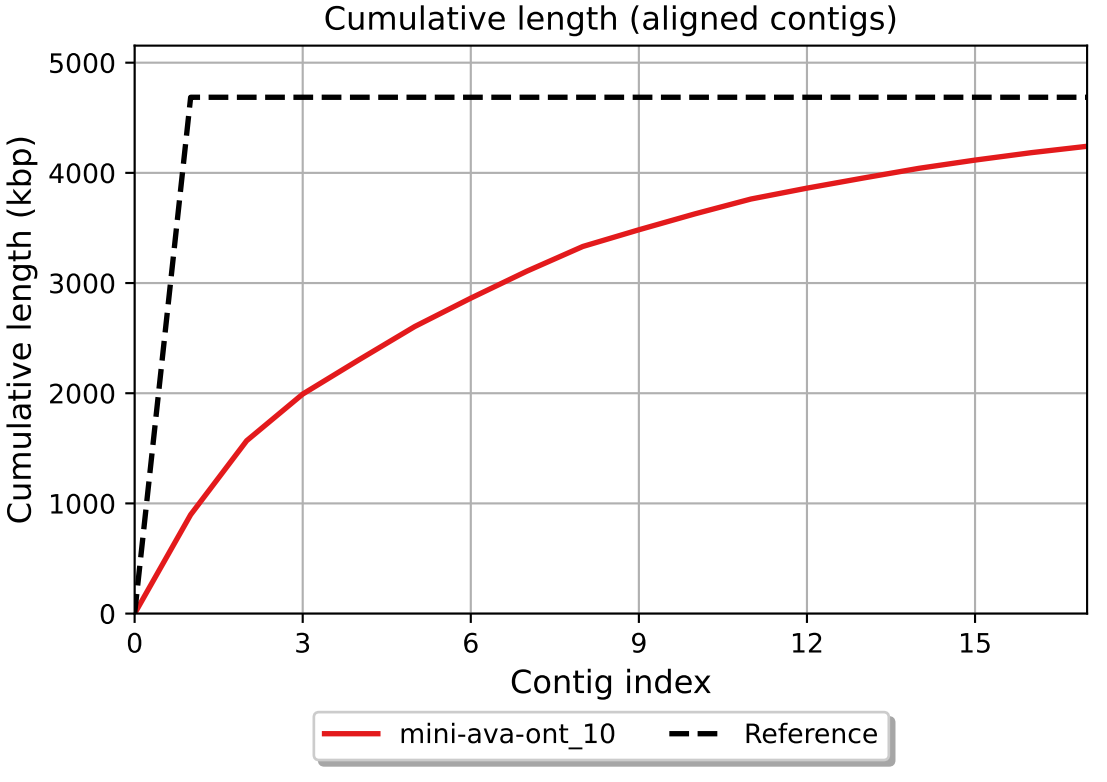

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
15
Contig index
mini-ava-ont_10
Reference

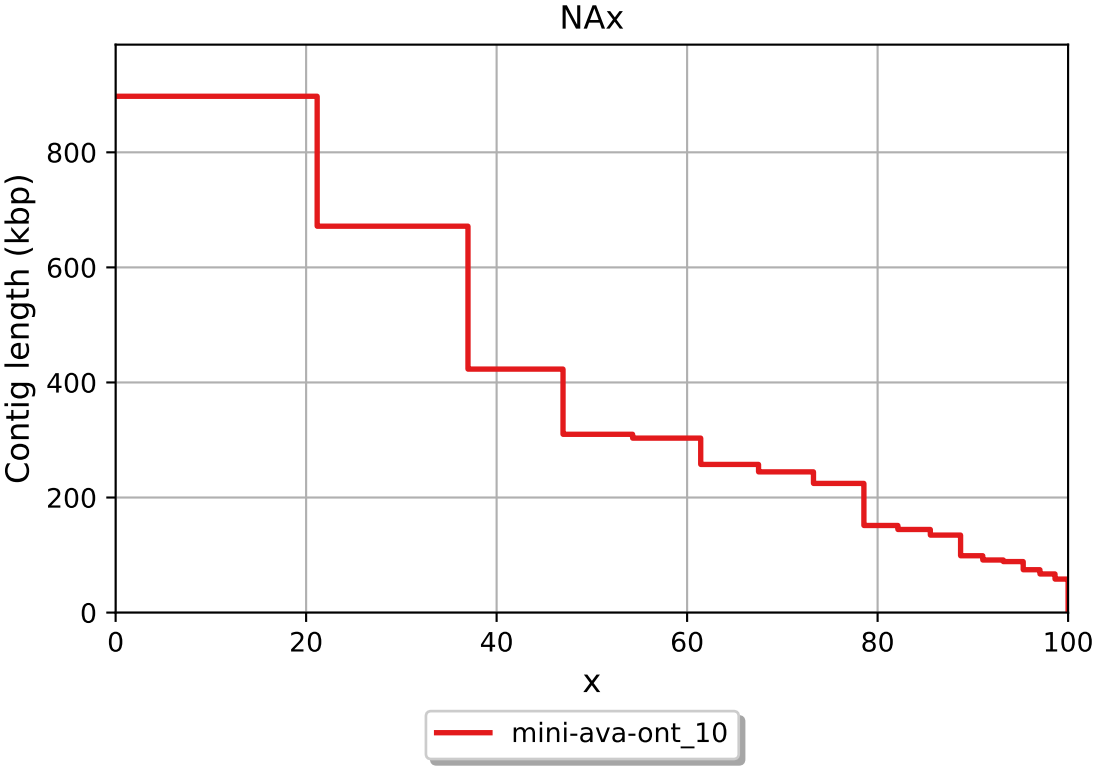

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
mini-ava-ont_10
Reference

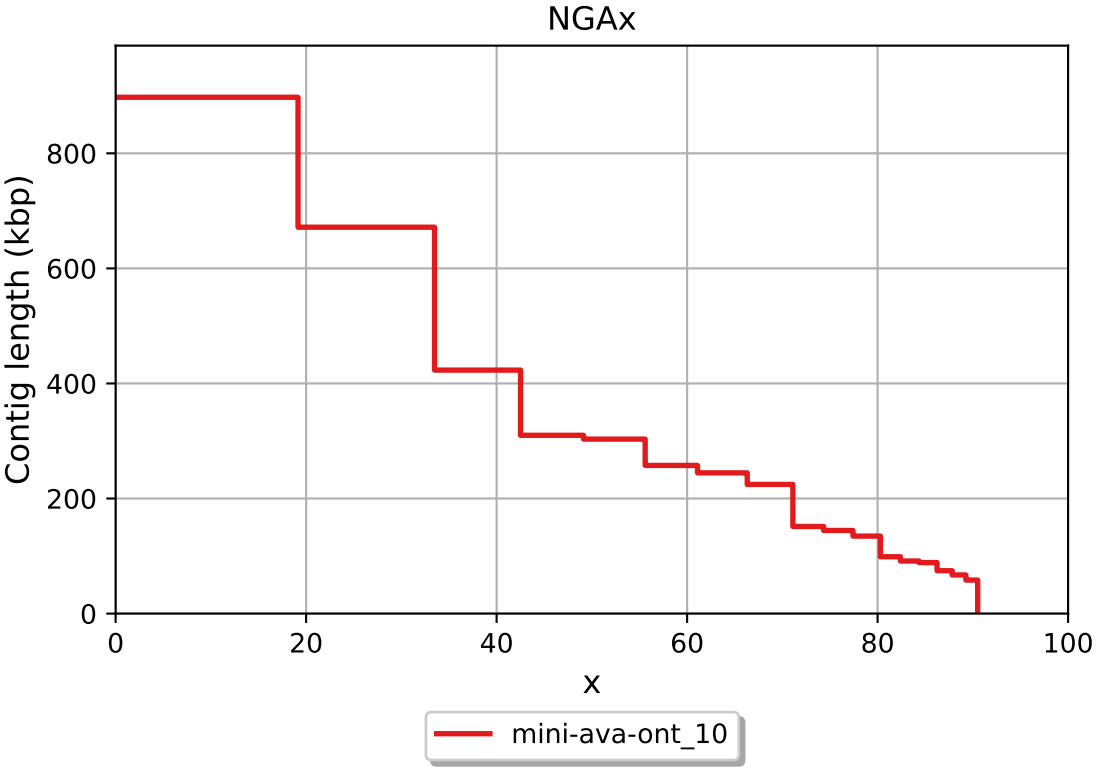

mini-ava-ont_10 GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
mini-ava-ont_10


Misassemblies
5
4
3
2
1
0
mini-ava-ont_10


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
mini-ava-ont_10


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
15
Contig index
mini-ava-ont_10
Reference


NAx
Contig length (kbp)
0
200
400
600
800
0
20
40
60
80
100
x
mini-ava-ont_10


NGAx
Contig length (kbp)
0
200
400
600
800
0
20
40
60
80
100
x
mini-ava-ont_10