Report

	mini-ava-pb_100
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	4779043
Total length (>= 1000 bp)	4779043
Total length (>= 5000 bp)	4779043
Total length (>= 10000 bp)	4779043
Total length (>= 25000 bp)	4779043
Total length (>= 50000 bp)	4779043
# contigs	4
Largest contig	3997703
Total length	4779043
Reference length	4686137
GC (%)	50.76
Reference GC (%)	50.78
N50	3997703
NG50	3997703
N90	561927
NG90	561927
auN	3415221.0
auNG	3482930.2
L50	1
LG50	1
L90	2
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 (%)	99.944
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.25
Largest alignment	3997703
Total aligned length	4779043
NA50	3997703
NGA50	3997703
NA90	561927
NGA90	561927
auNA	3415221.0
auNGA	3482930.2
LA50	1
LGA50	1
LA90	2
LGA90	2

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

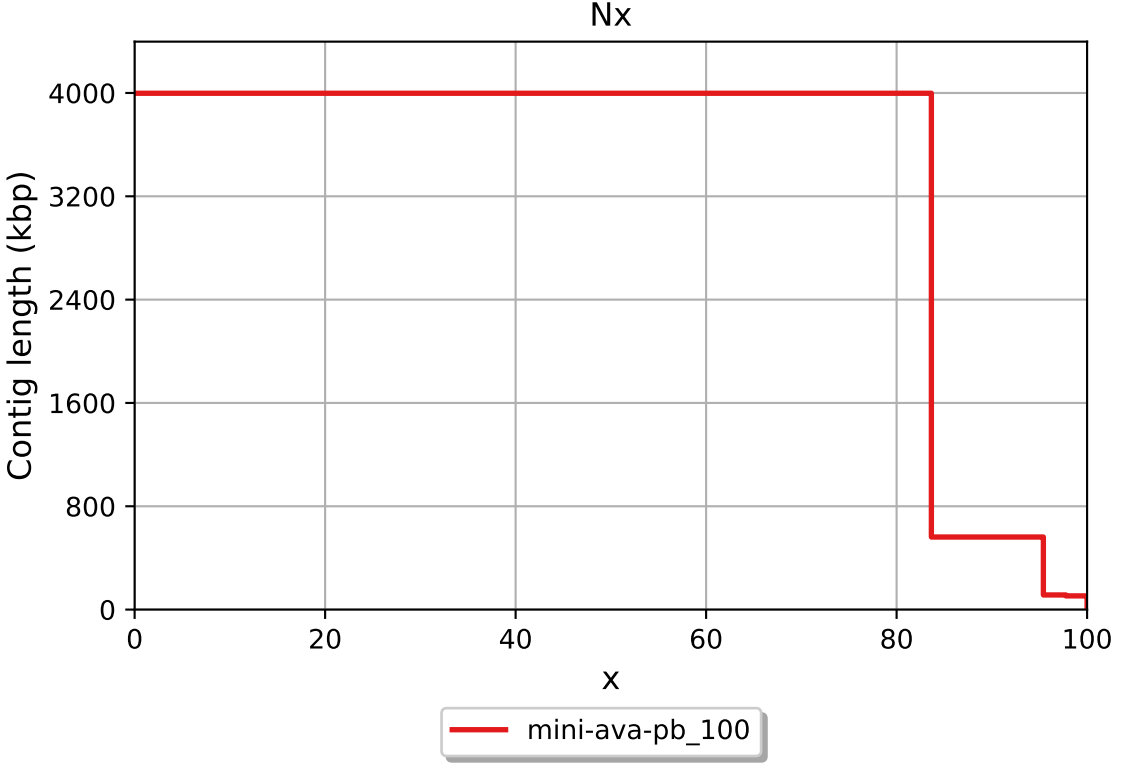
	mini-ava-pb_100
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	12
# indels (<= 5 bp)	12
# indels (> 5 bp)	0
Indels length	13

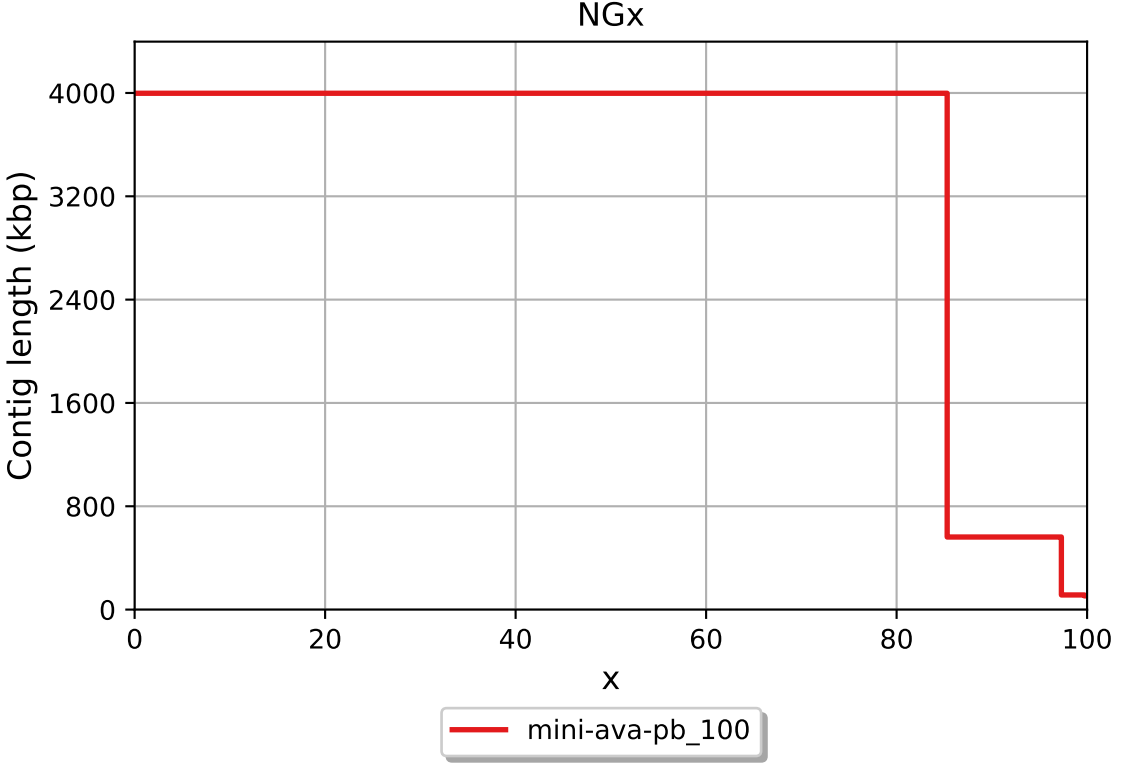
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

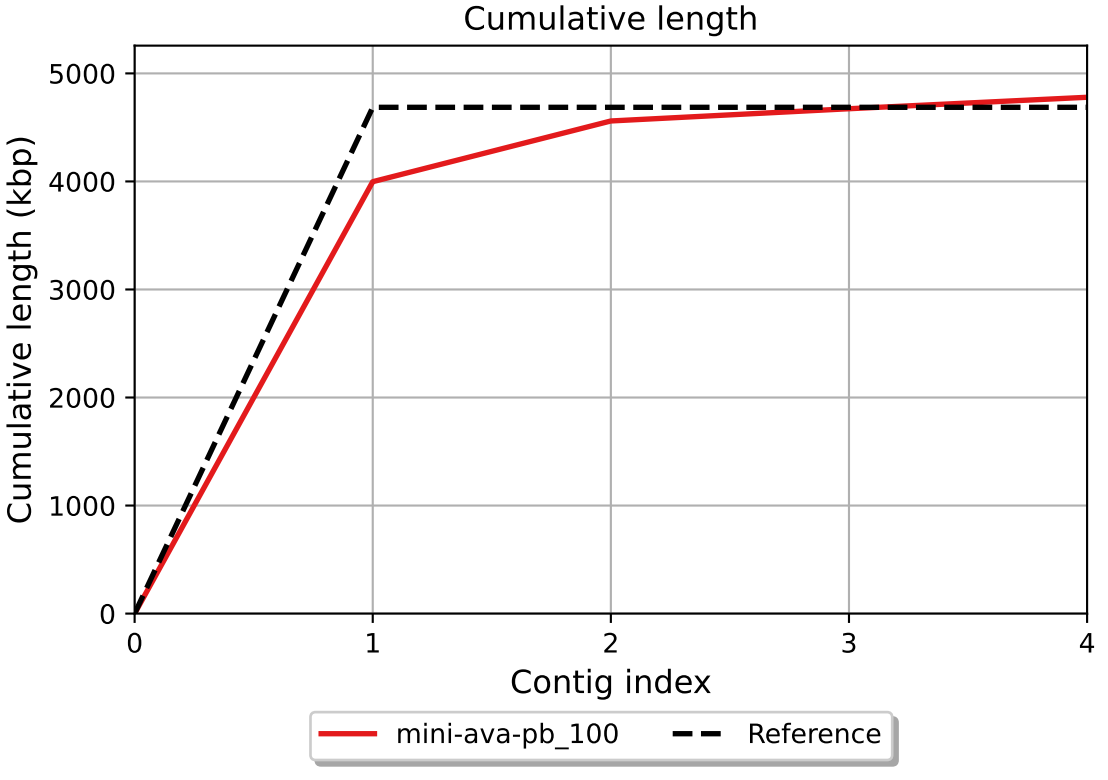
Unaligned report

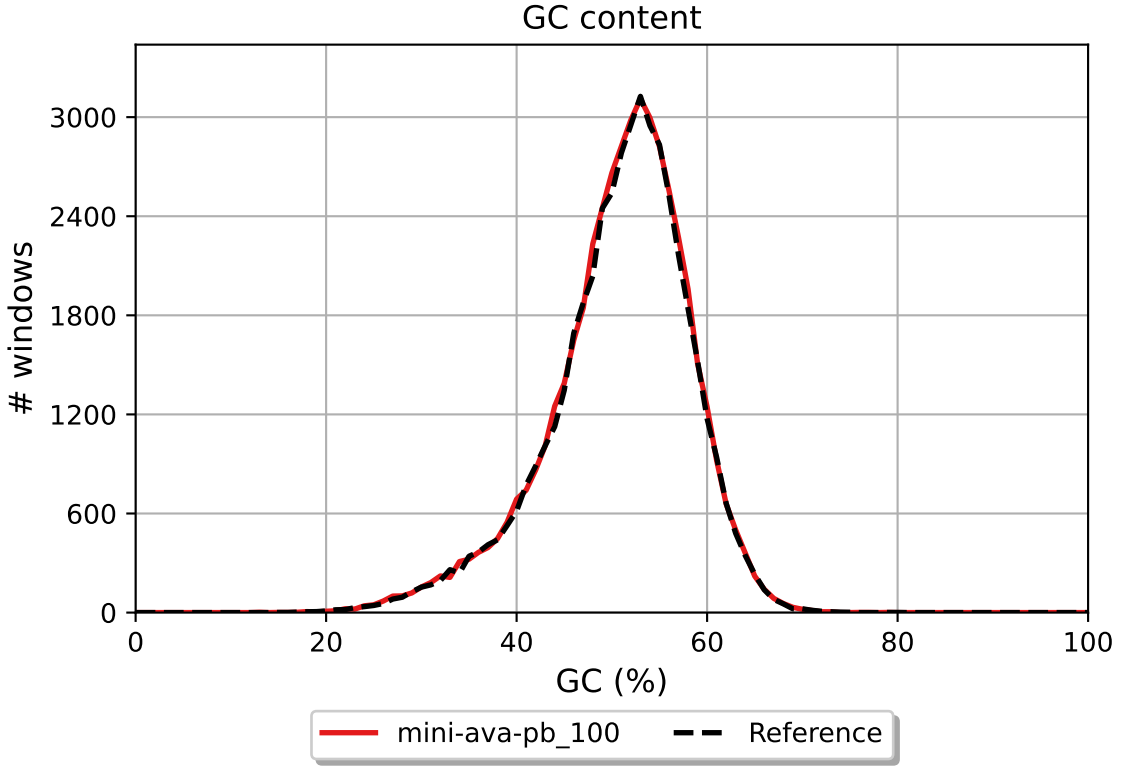
	mini-ava-pb_100
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

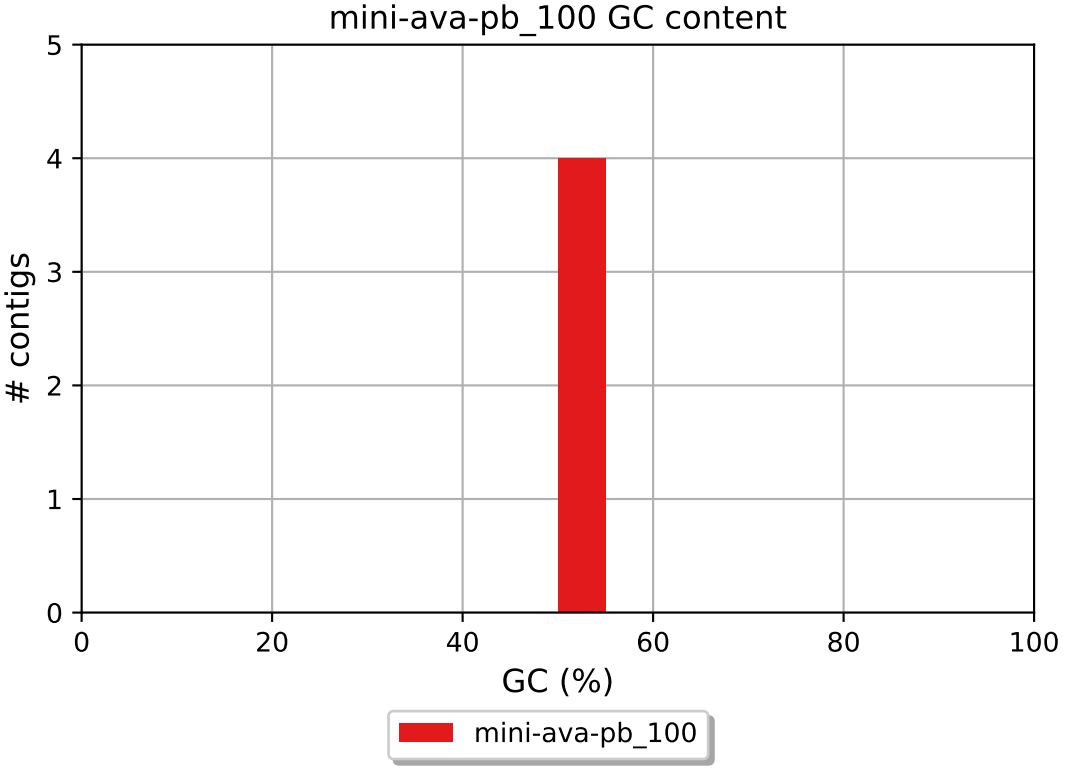
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

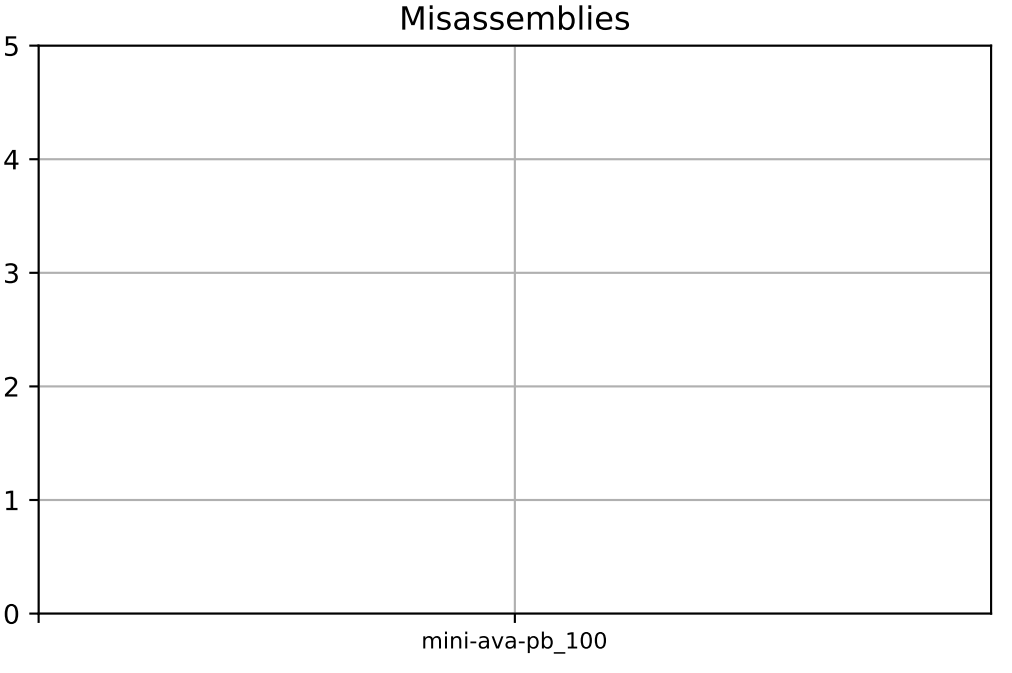

Nx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
mini-ava-pb_100

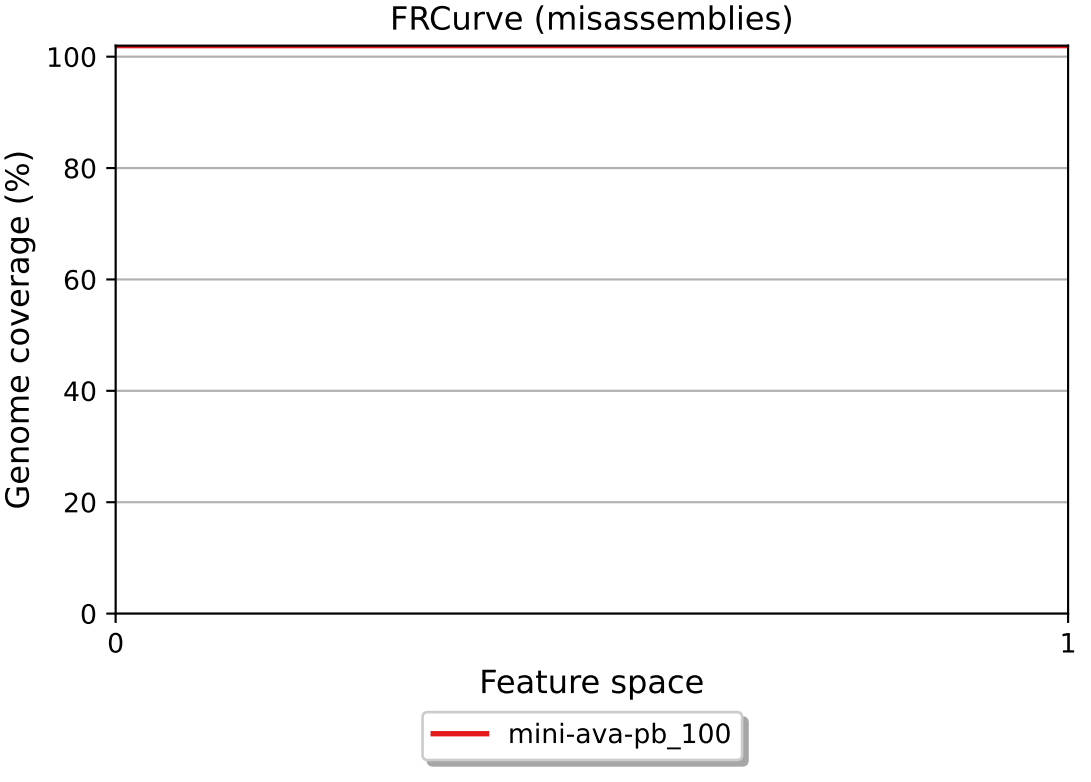

NGx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
mini-ava-pb_100

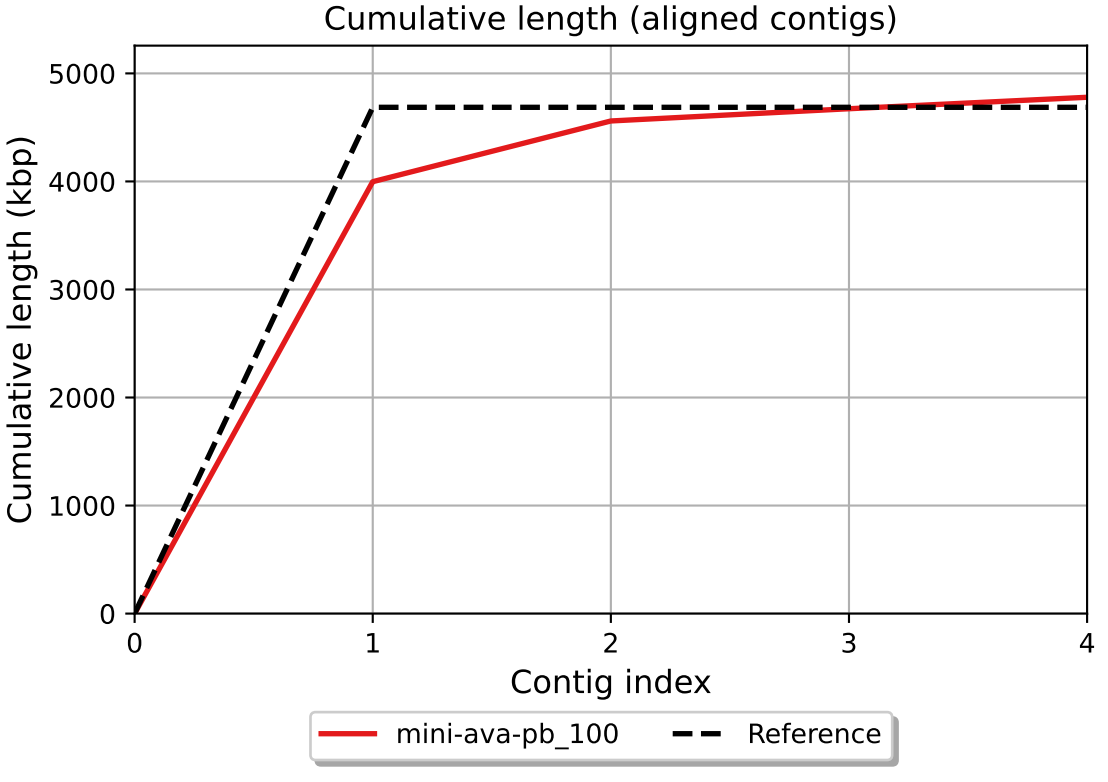

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
3
4
Contig index
mini-ava-pb_100
Reference

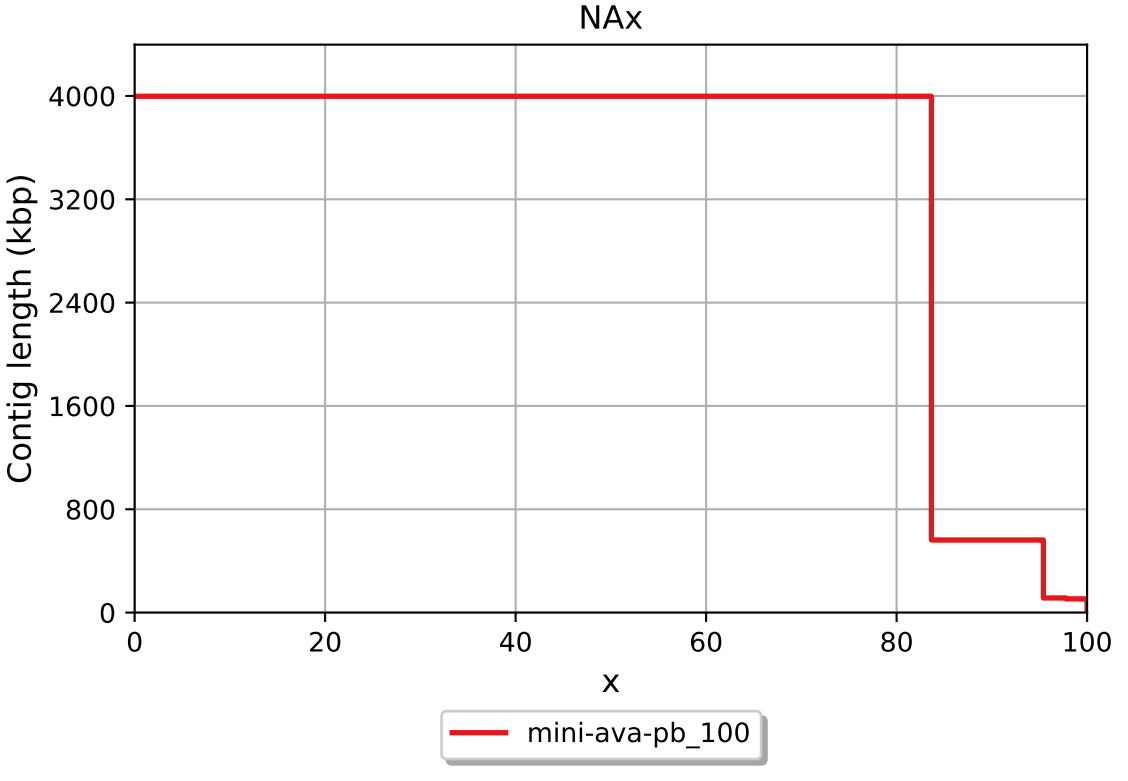

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
mini-ava-pb_100
Reference

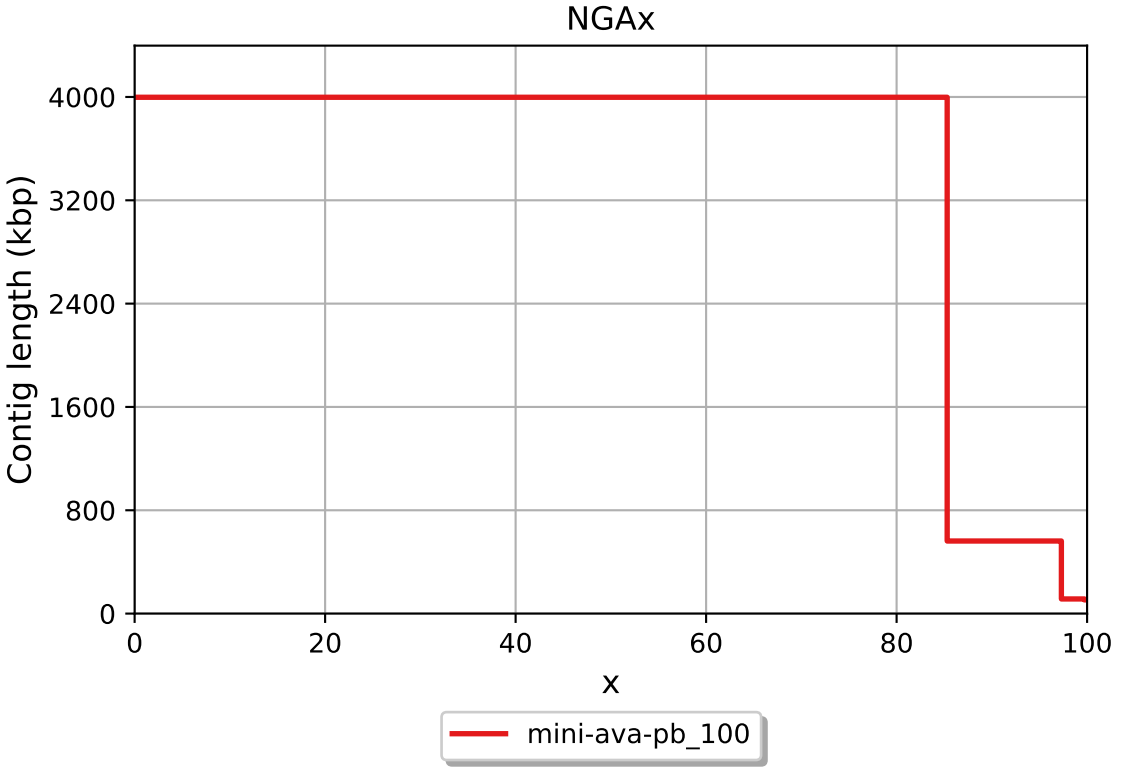

mini-ava-pb_100 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
mini-ava-pb_100


Misassemblies
5
4
3
2
1
0
mini-ava-pb_100


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
mini-ava-pb_100


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
3
4
Contig index
mini-ava-pb_100
Reference


NAx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
mini-ava-pb_100


NGAx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
mini-ava-pb_100