Report

	Results
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	31
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5
Largest contig	26654
Total length	48605
Reference length	48576
GC (%)	49.85
Reference GC (%)	49.87
N50	26654
NG50	26654
N75	18481
NG75	18481
L50	1
LG50	1
L75	2
LG75	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	2 + 0 part
Unaligned length	62
Genome fraction (%)	99.870
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	26654
Total aligned length	48543
NA50	26654
NGA50	26654
NA75	18481
NGA75	18481
LA50	1
LGA50	1
LA75	2
LGA75	2

All statistics are based on contigs of size >= 31 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

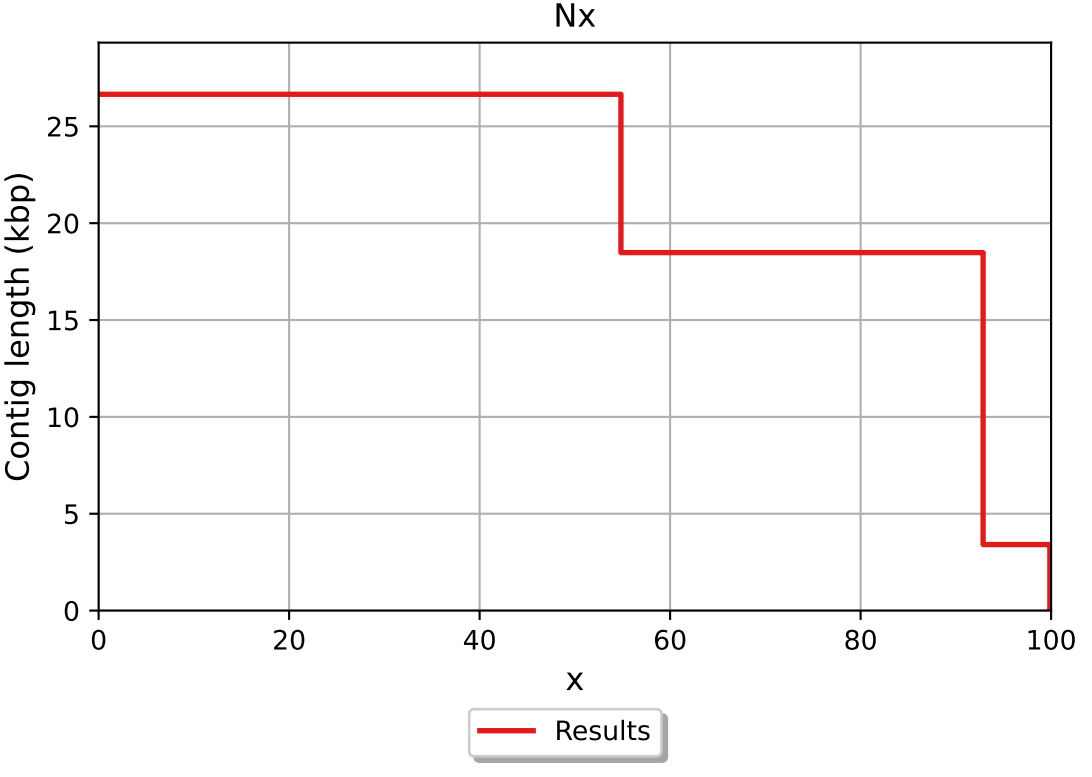
	Results
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0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

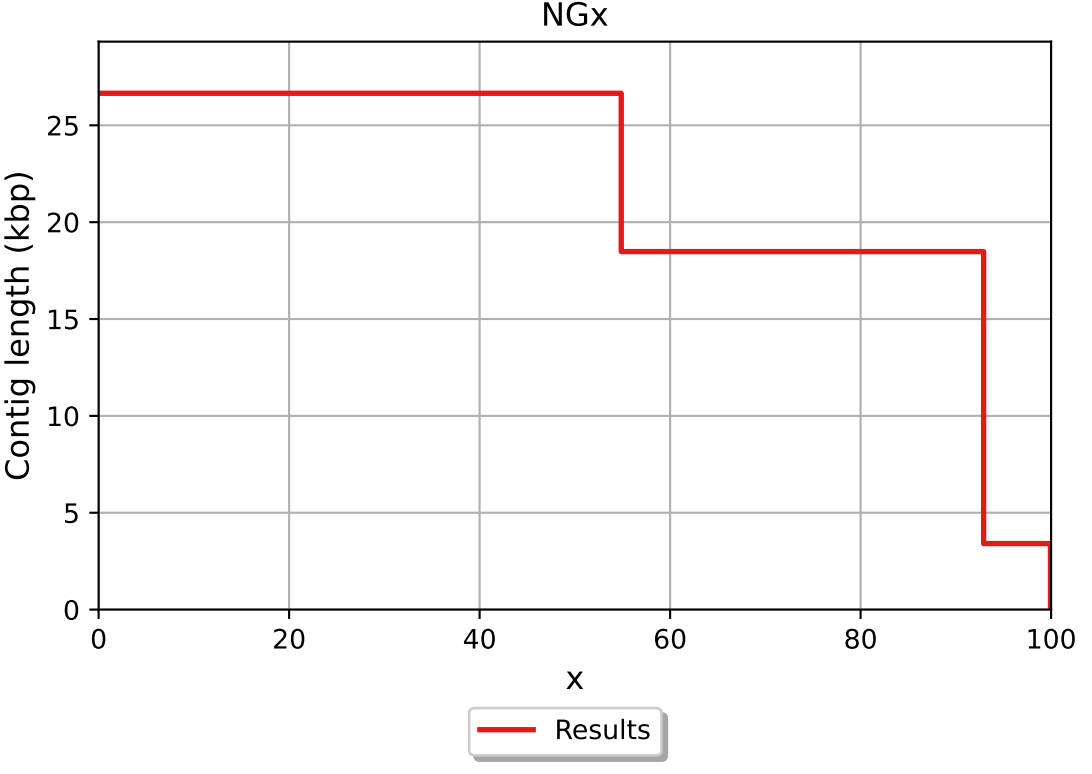
All statistics are based on contigs of size >= 31 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

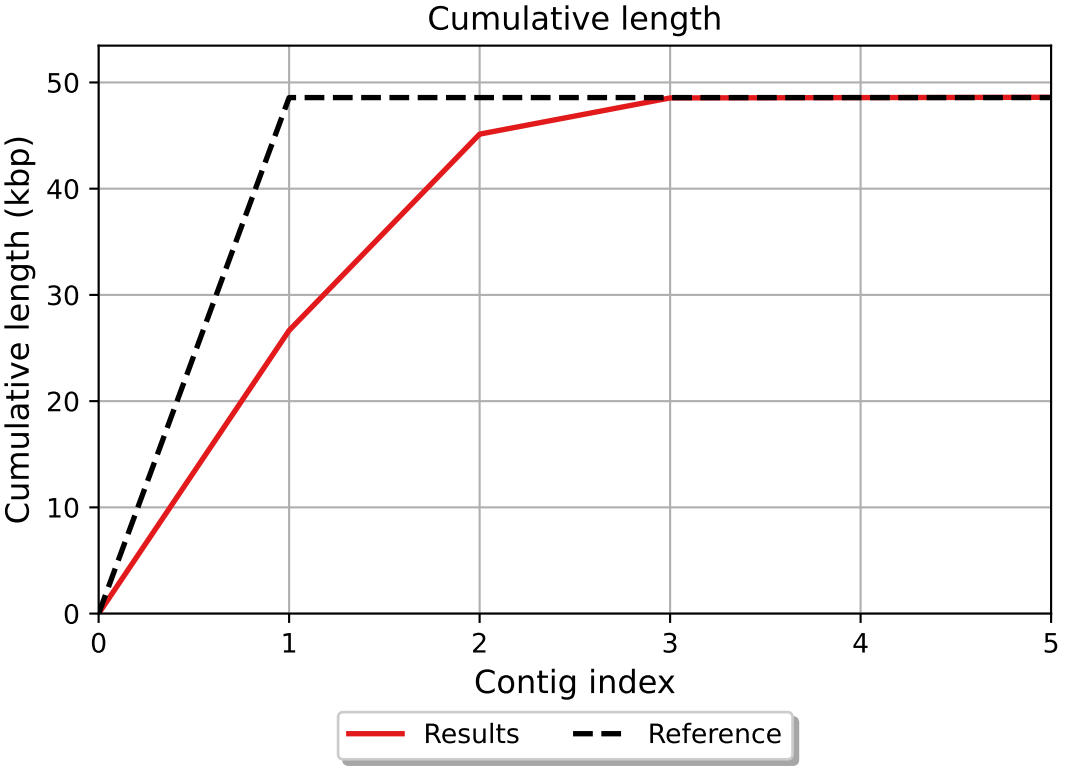
Unaligned report

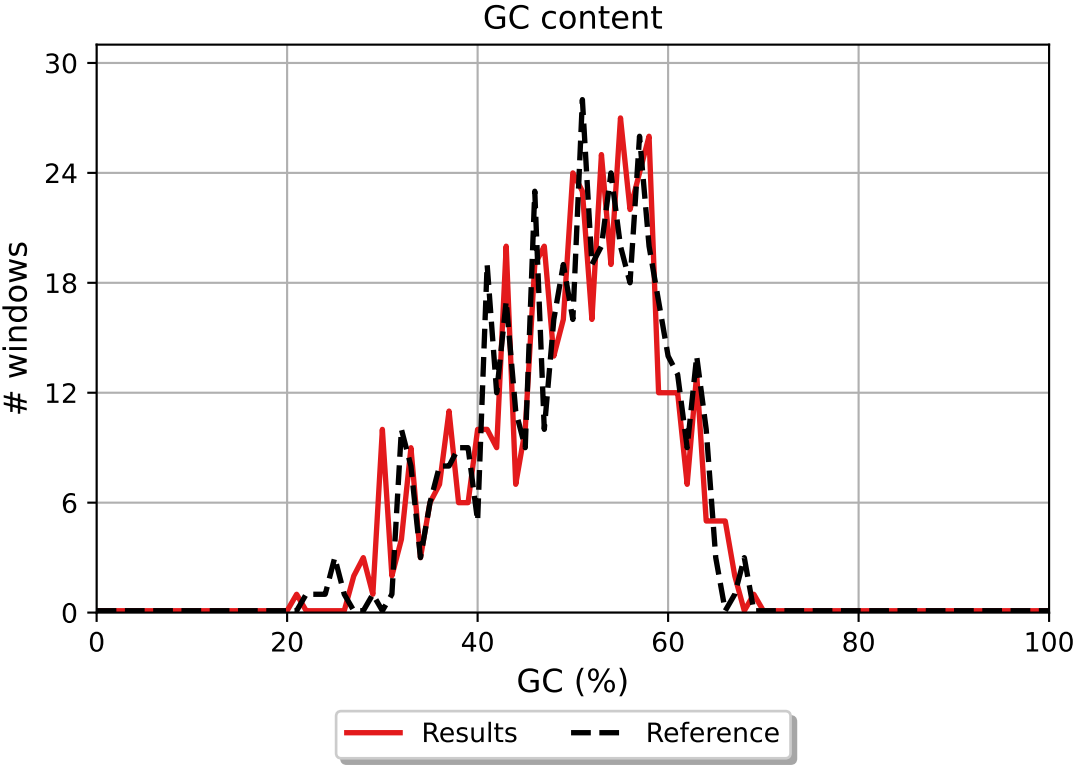
	Results
# fully unaligned contigs	2
Fully unaligned length	62
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

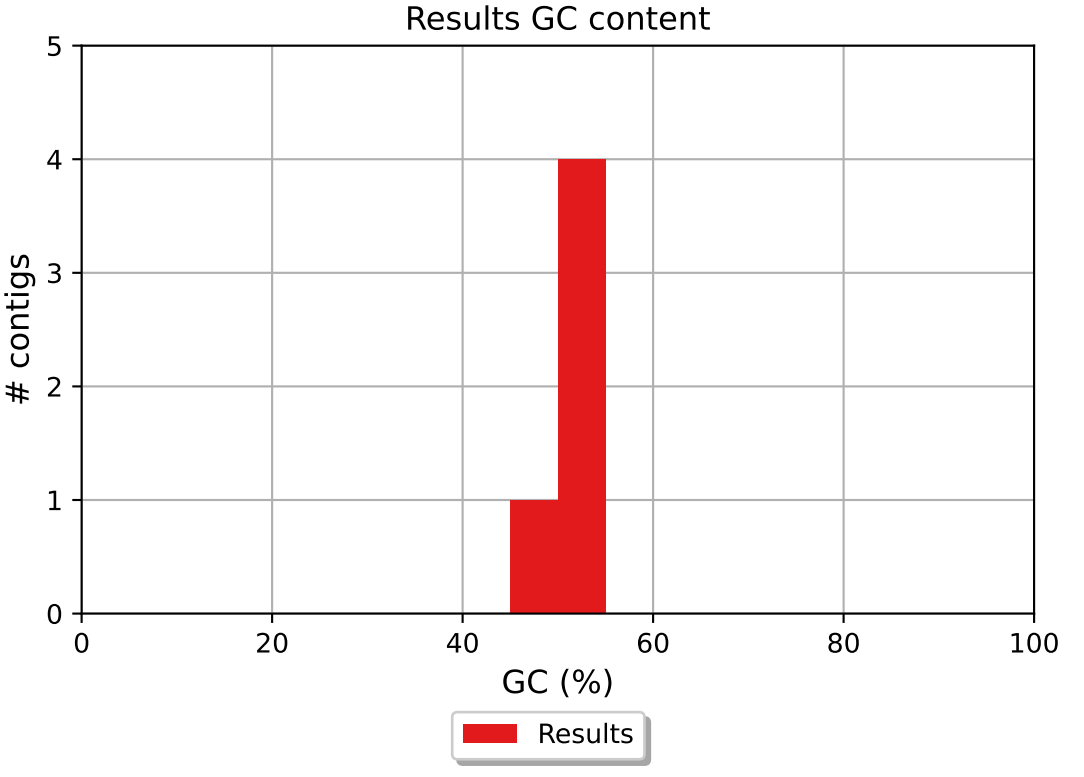
All statistics are based on contigs of size >= 31 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

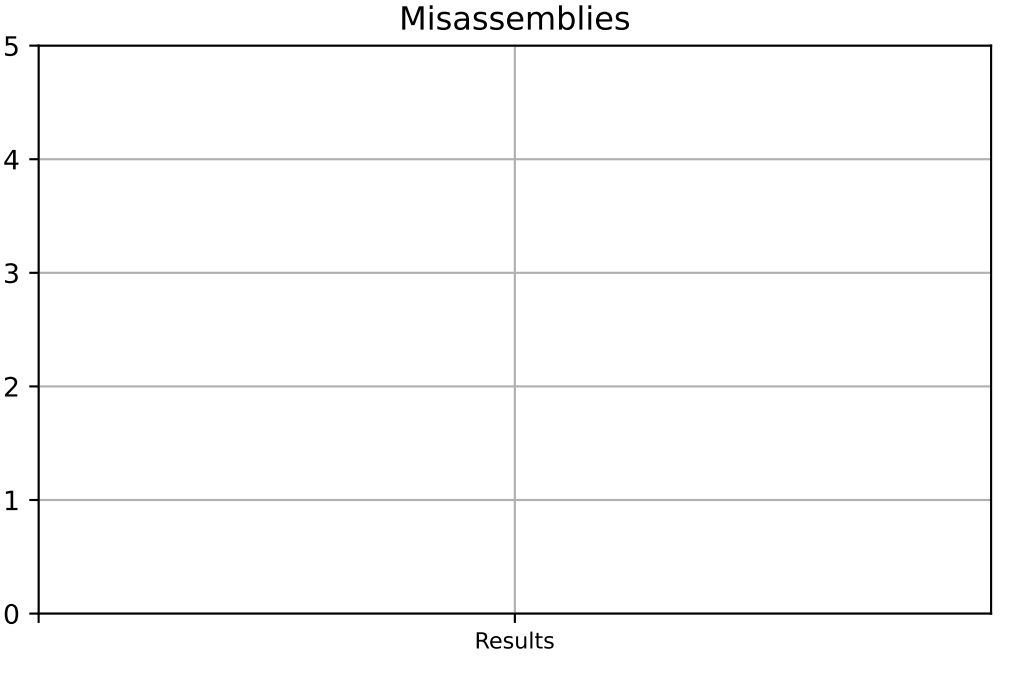

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
Results

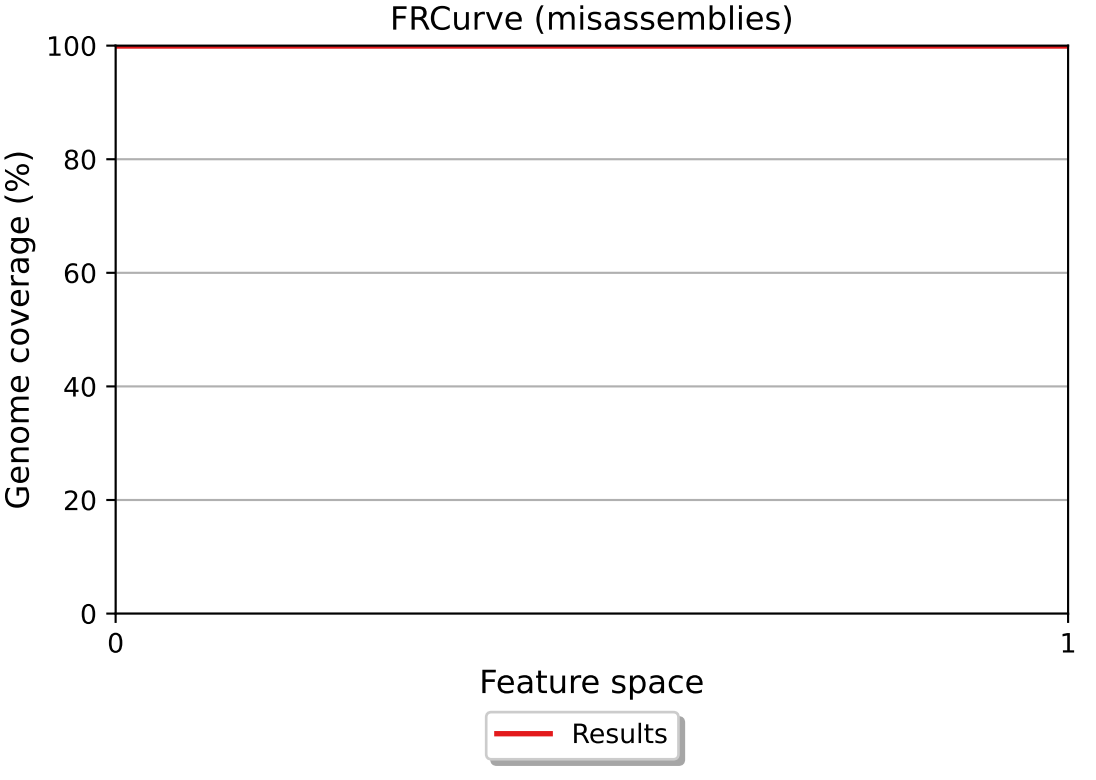

NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
Results

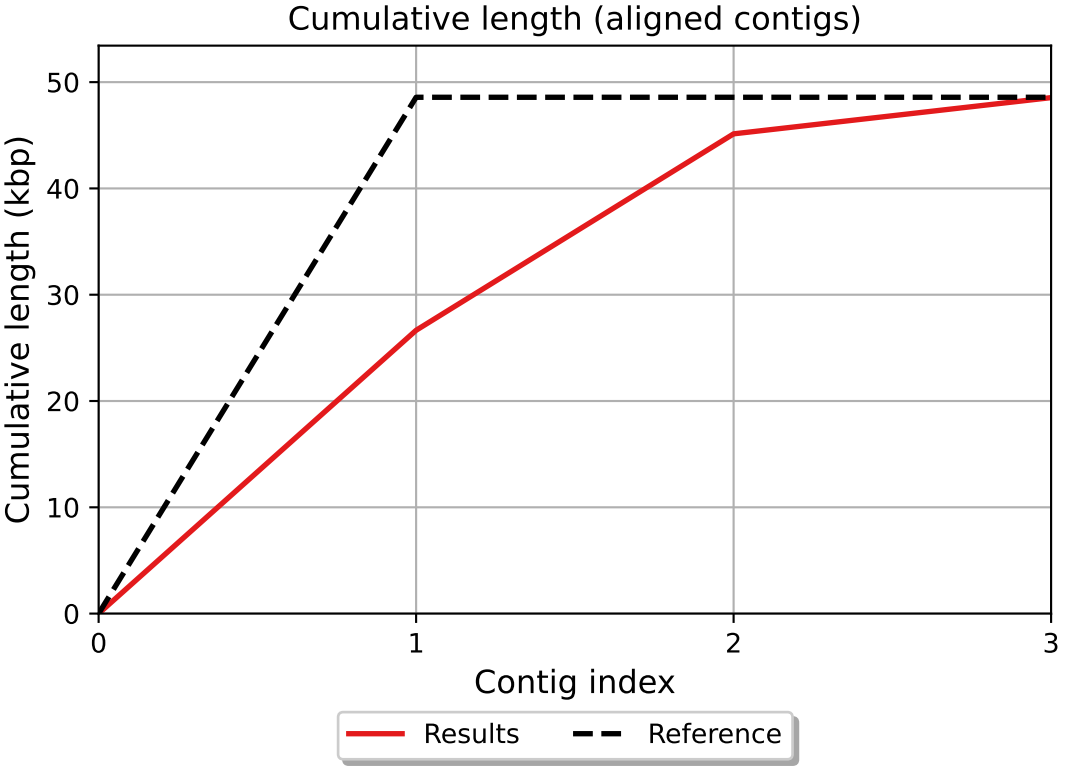

Cumulative length
Cumulative length (kbp)
0
10
20
30
40
50
0
1
2
3
4
5
Contig index
Results
Reference

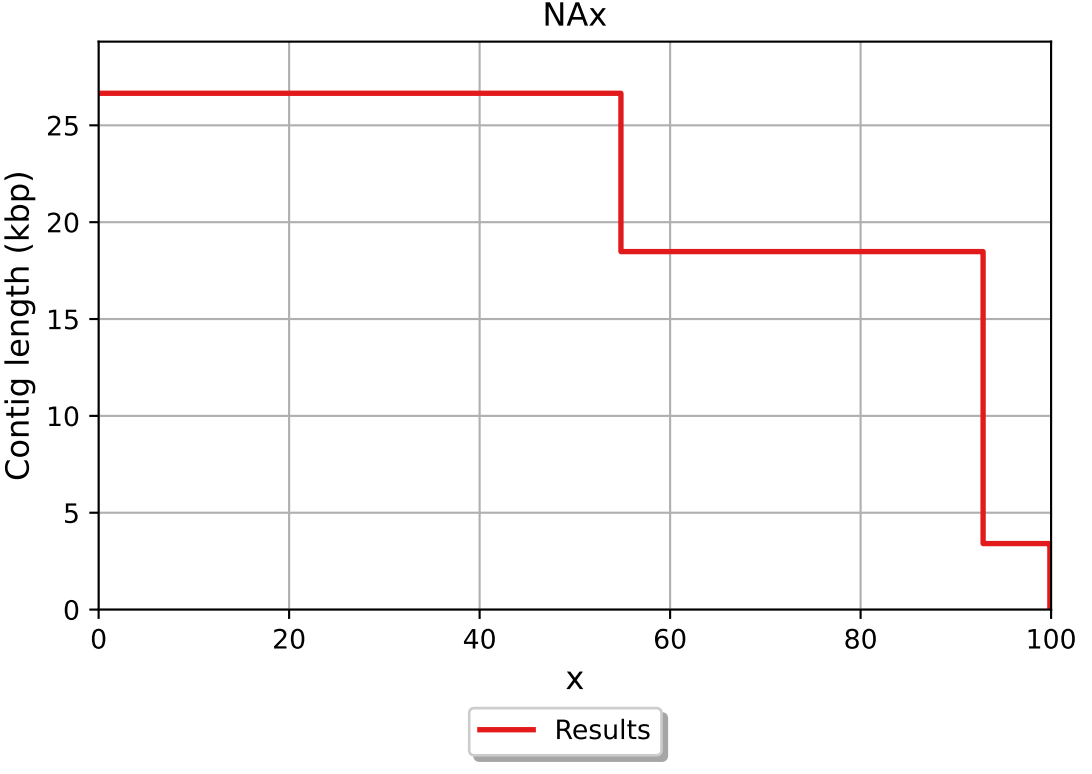

GC content
windows
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
Results
Reference

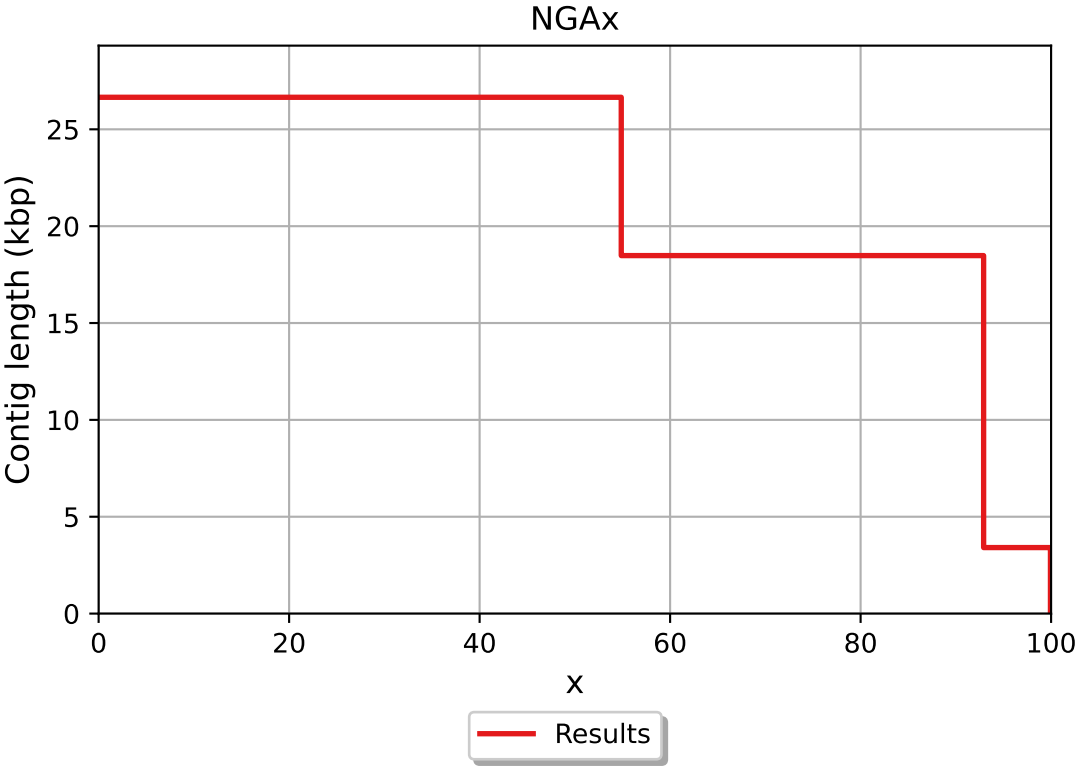

Results GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
Results


Misassemblies
5
4
3
2
1
0
Results


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
Results


Cumulative length (aligned contigs)
Cumulative length (kbp)
50
40
30
20
10
0
0
1
2
3
Contig index
Results
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
Results


NGAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
Results