Report

	assembly
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	4627920
Total length (>= 1000 bp)	4627920
Total length (>= 5000 bp)	4627920
Total length (>= 10000 bp)	4627920
Total length (>= 25000 bp)	4627920
Total length (>= 50000 bp)	4627920
# contigs	1
Largest contig	4627920
Total length	4627920
Reference length	4653851
GC (%)	44.70
Reference GC (%)	44.71
N50	4627920
NG50	4627920
N90	4627920
NG90	4627920
auN	4627920.0
auNG	4602133.5
L50	1
LG50	1
L90	1
LG90	1
# misassemblies	19
# misassembled contigs	1
Misassembled contigs length	4627920
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	29290
Genome fraction (%)	98.429
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	18.33
# indels per 100 kbp	6.13
Largest alignment	861465
Total aligned length	4583177
NA50	569118
NGA50	569118
NA90	219466
NGA90	219466
auNA	567955.0
auNGA	564790.4
LA50	4
LGA50	4
LA90	8
LGA90	8

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

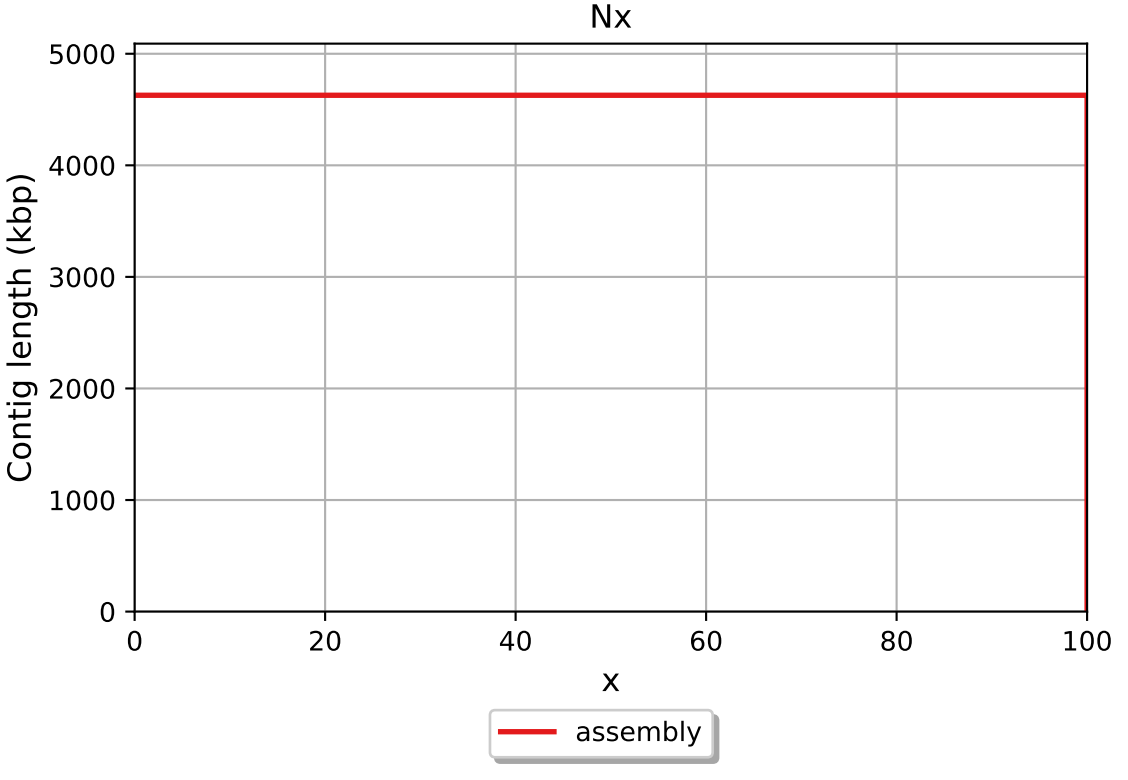
	assembly
# misassemblies	19
# contig misassemblies	19
# c. relocations	19
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	4627920
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	840
# indels	281
# indels (<= 5 bp)	238
# indels (> 5 bp)	43
Indels length	4973

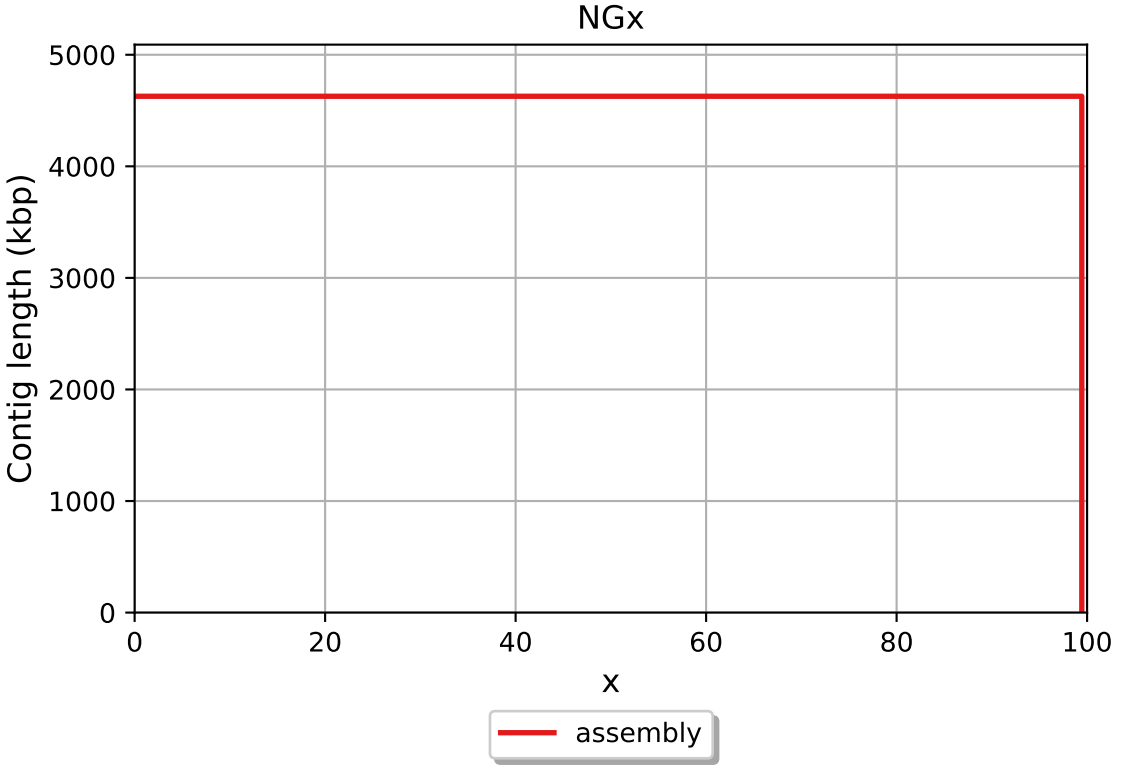
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

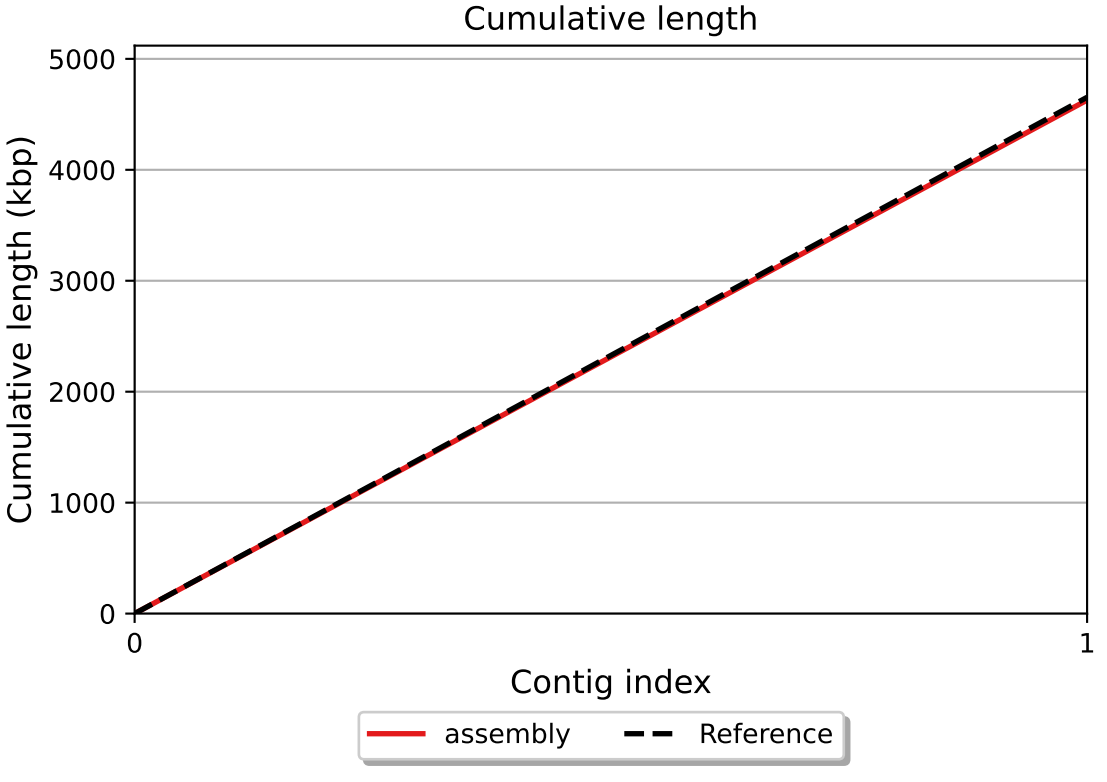
Unaligned report

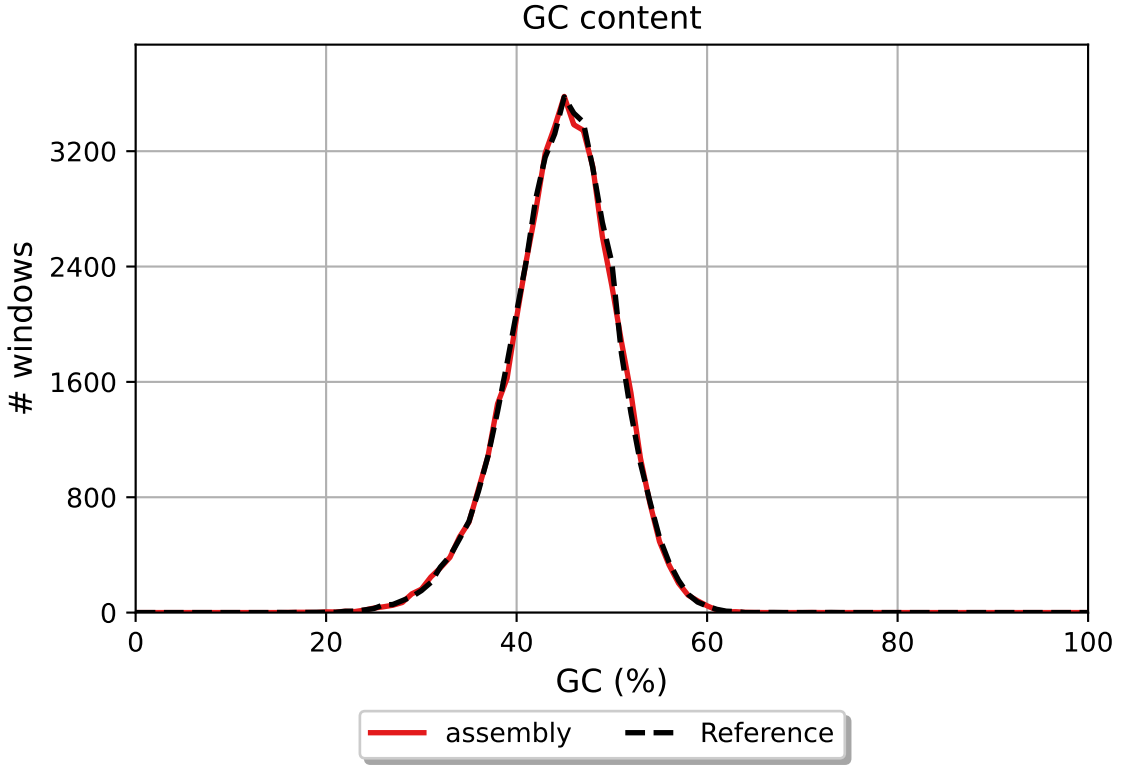
	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	29290
# N's	0

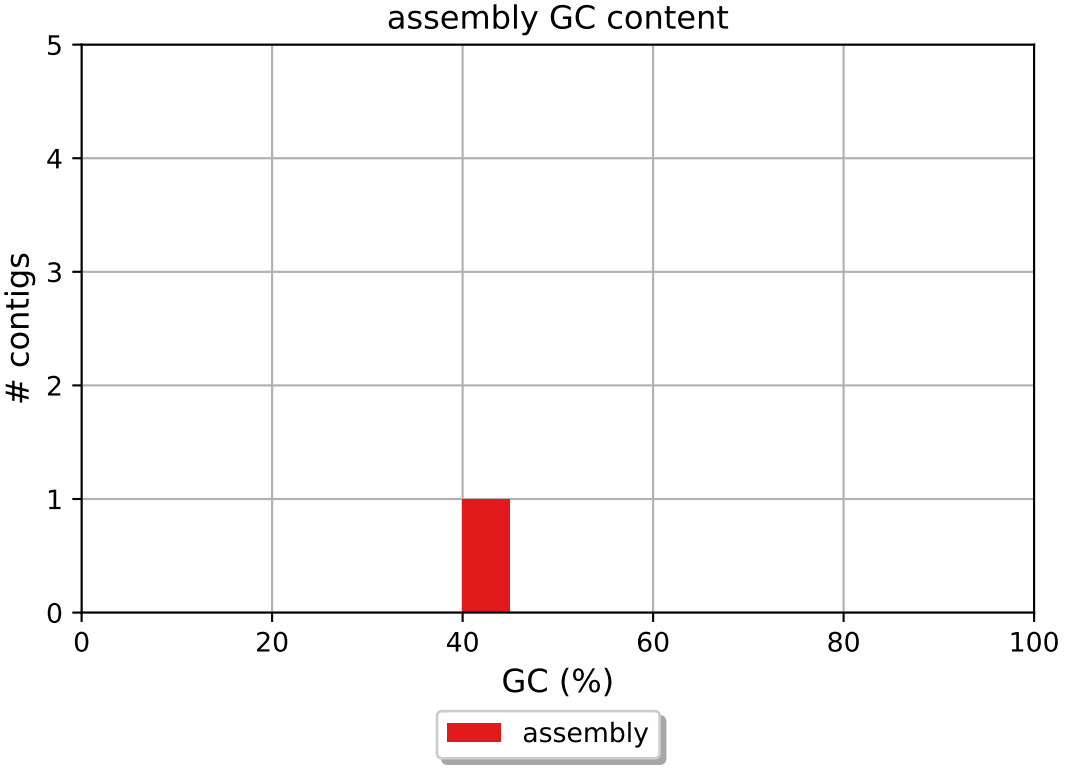
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
5000
4000
3000
2000
1000
0
Contig length (kbp)
0
20
40
60
80
100
x
assembly

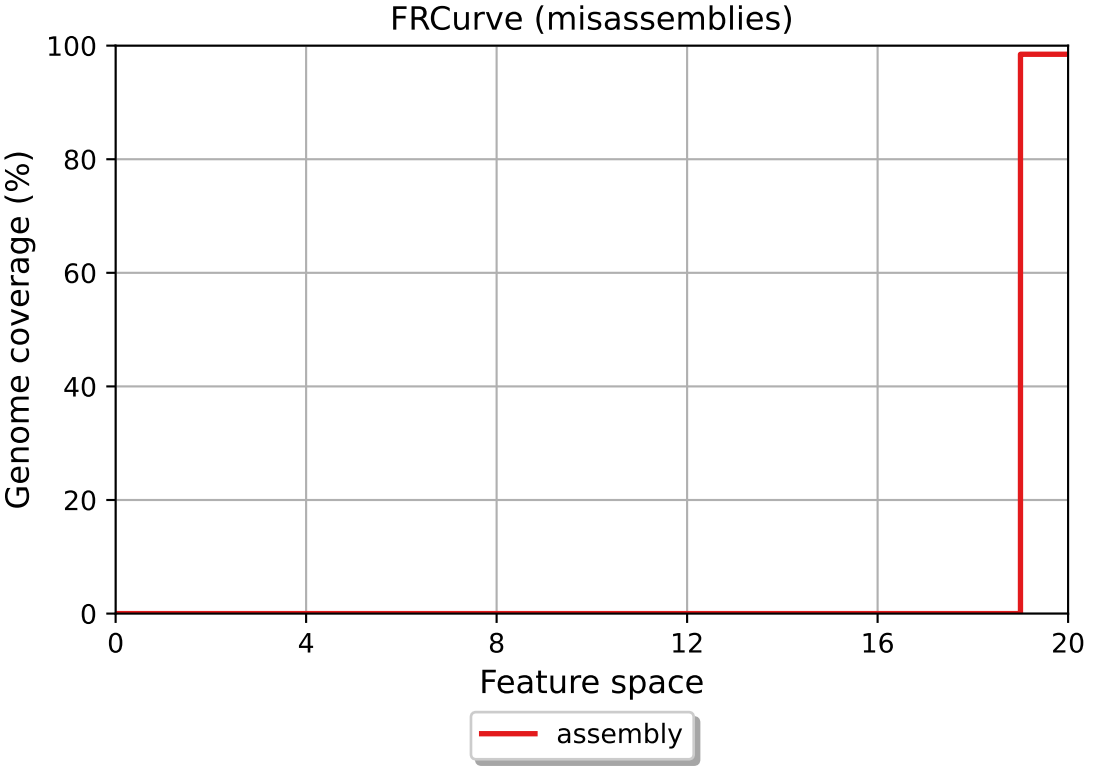

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
assembly

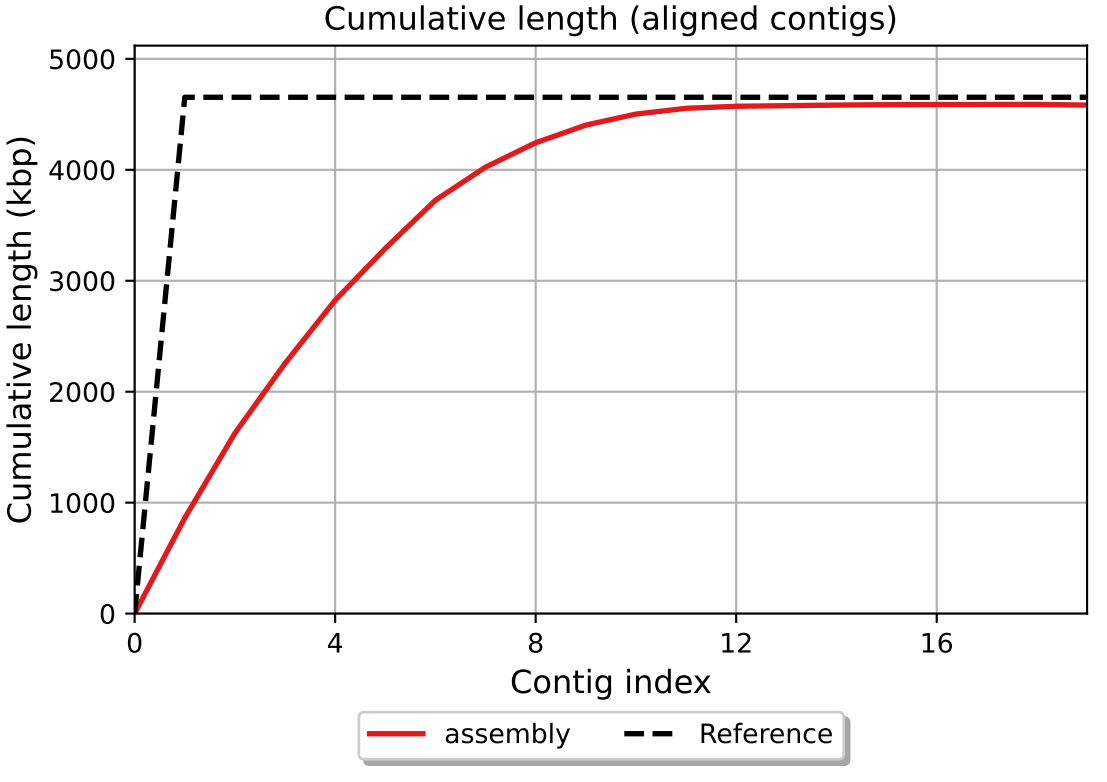

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
Contig index
assembly
Reference

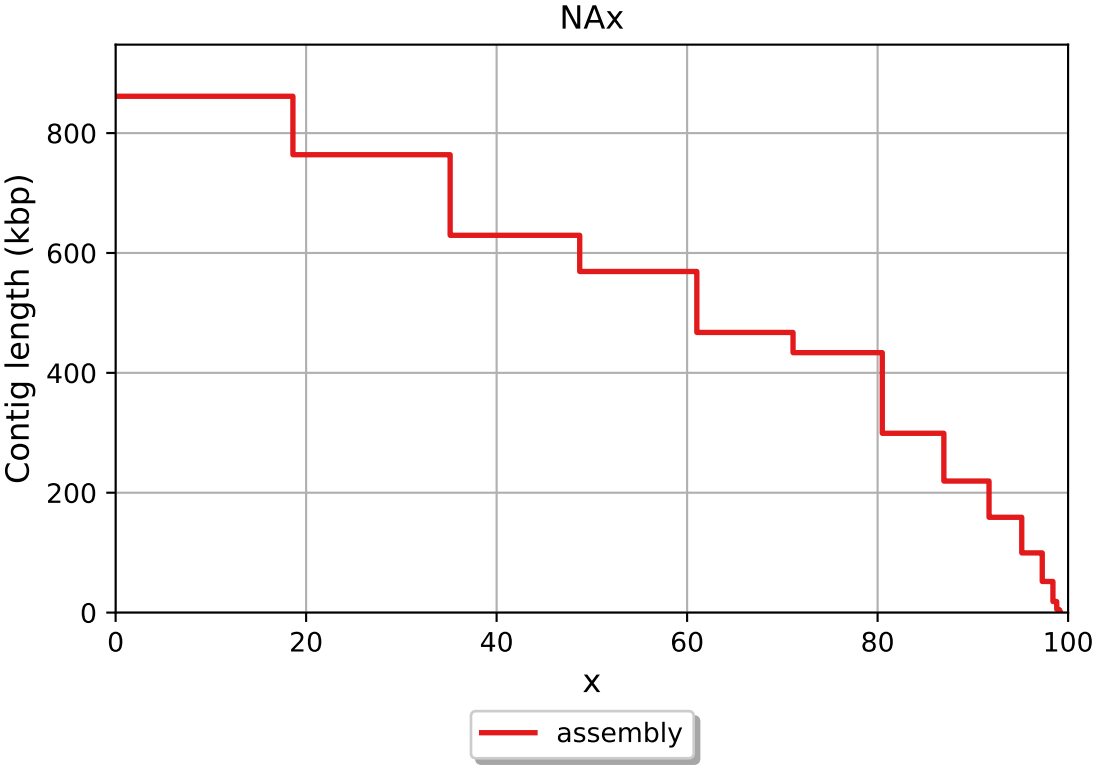

GC content
windows
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
assembly
Reference

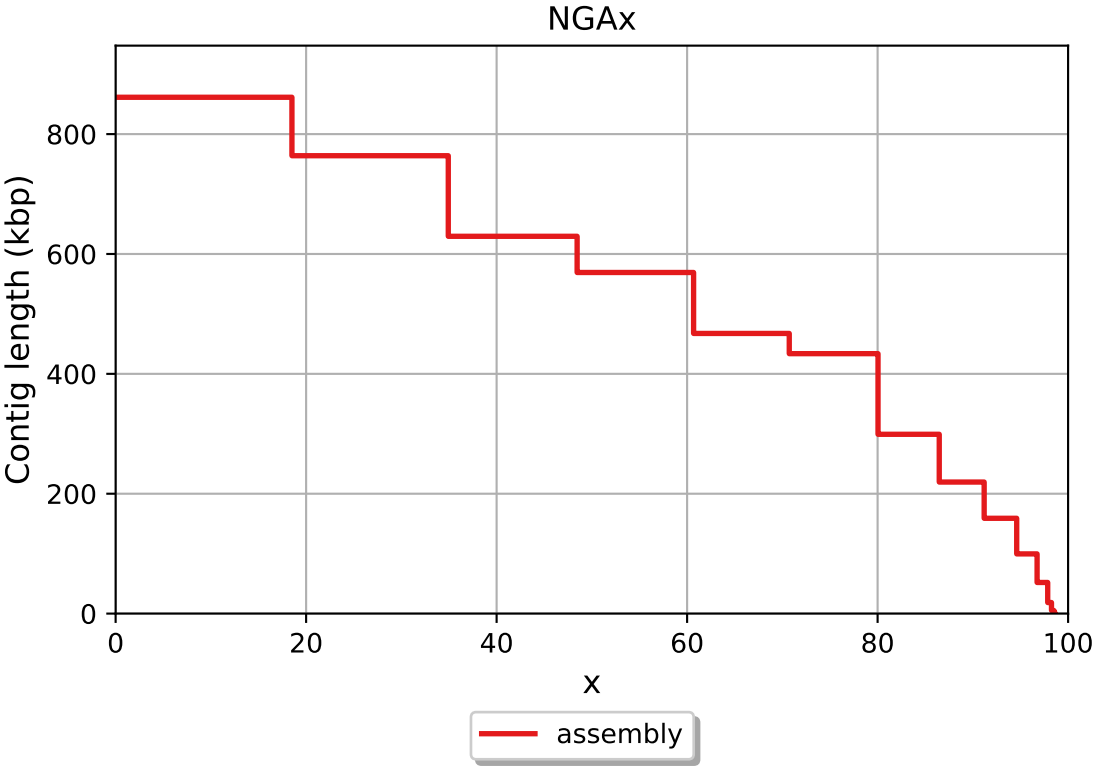

assembly GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
assembly

Misassemblies
20
16
12
8
4
0
assembly
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
assembly


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
Contig index
assembly
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
assembly


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
assembly