Report

	assembly
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	4644123
Total length (>= 1000 bp)	4644123
Total length (>= 5000 bp)	4640495
Total length (>= 10000 bp)	4640495
Total length (>= 25000 bp)	4640495
Total length (>= 50000 bp)	4640495
# contigs	3
Largest contig	4640495
Total length	4644123
Reference length	4639675
GC (%)	50.79
Reference GC (%)	50.79
N50	4640495
NG50	4640495
N75	4640495
NG75	4640495
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	6
# misassembled contigs	1
Misassembled contigs length	4640495
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	914
Genome fraction (%)	99.979
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.41
# indels per 100 kbp	5.20
Largest alignment	3022566
Total aligned length	4640369
NA50	3022566
NGA50	3022566
NA75	949242
NGA75	949242
LA50	1
LGA50	1
LA75	2
LGA75	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

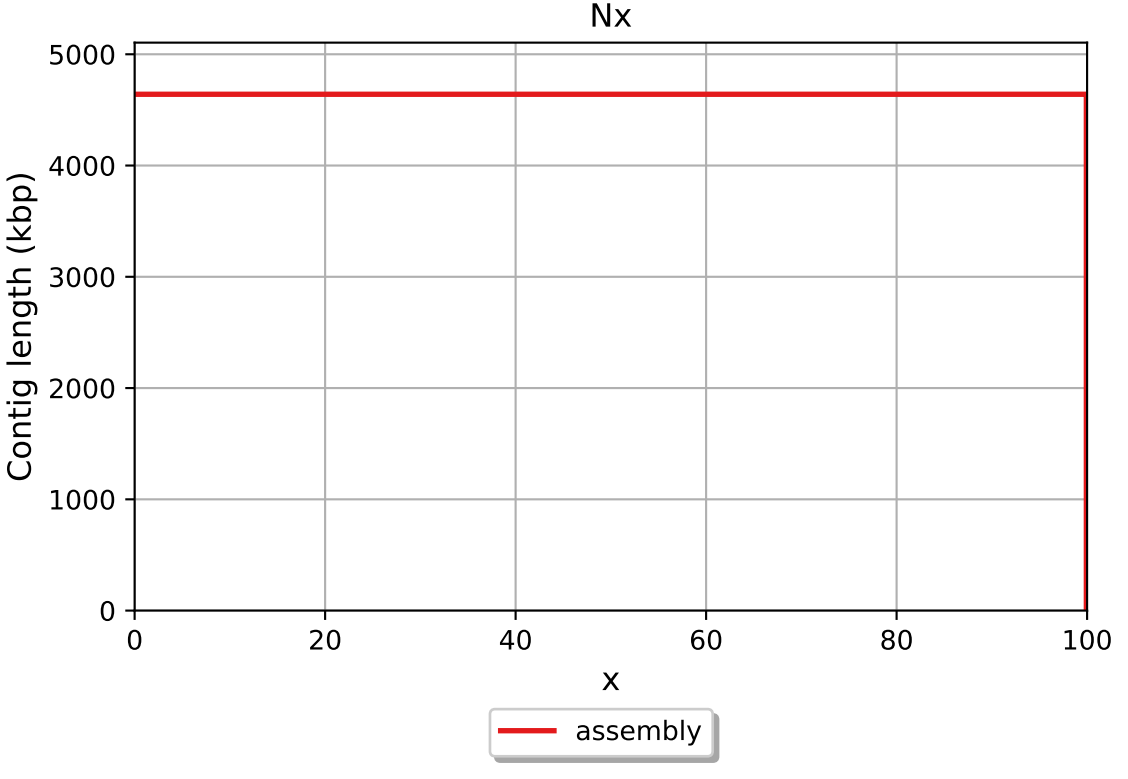
	assembly
# misassemblies	6
# contig misassemblies	6
# c. relocations	6
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	4640495
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	19
# indels	241
# indels (<= 5 bp)	241
# indels (> 5 bp)	0
Indels length	242

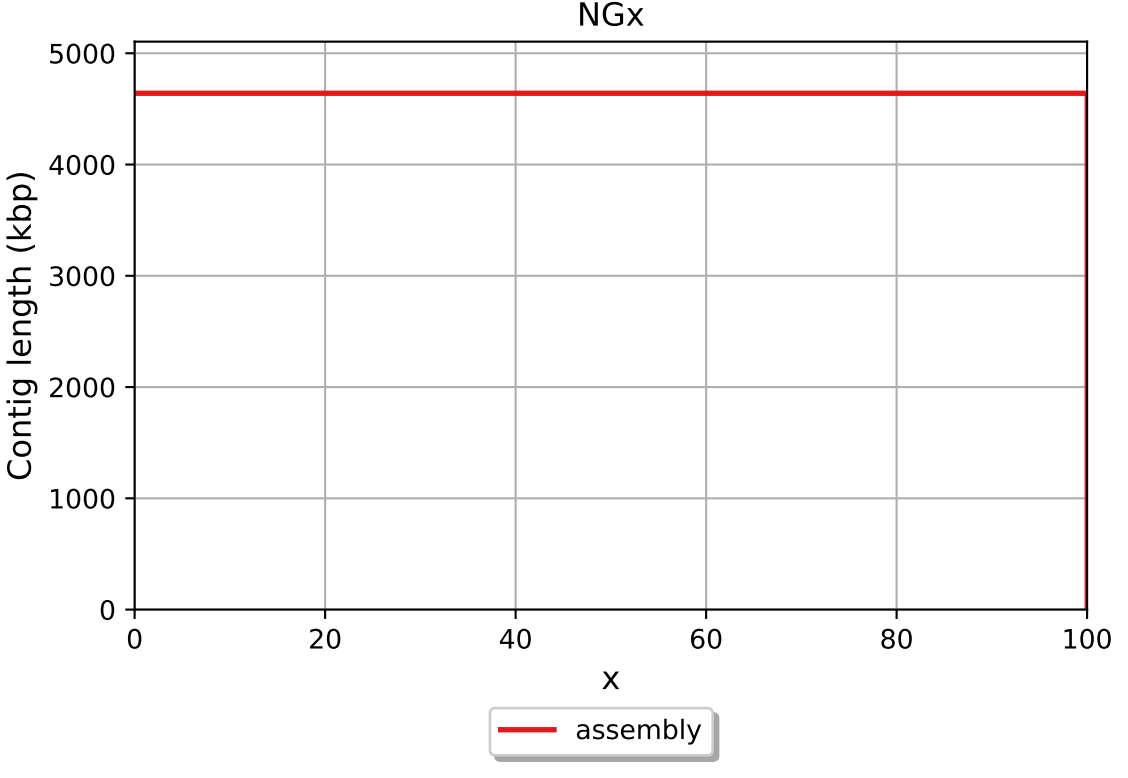
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

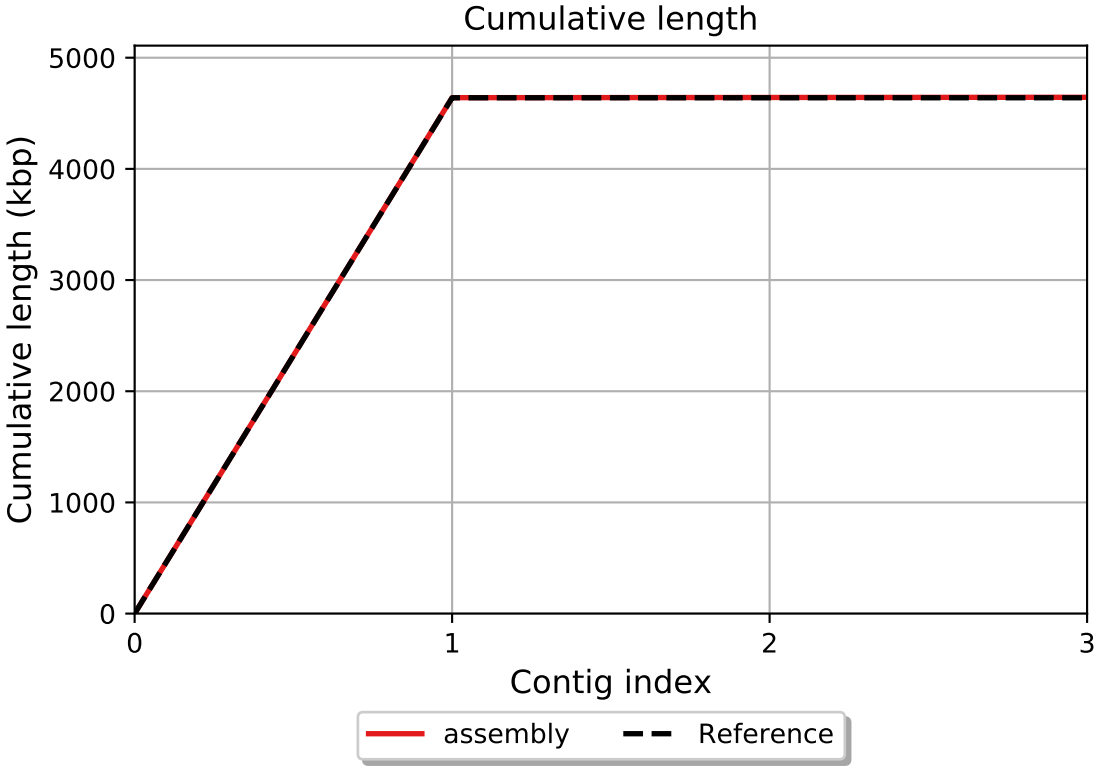
Unaligned report

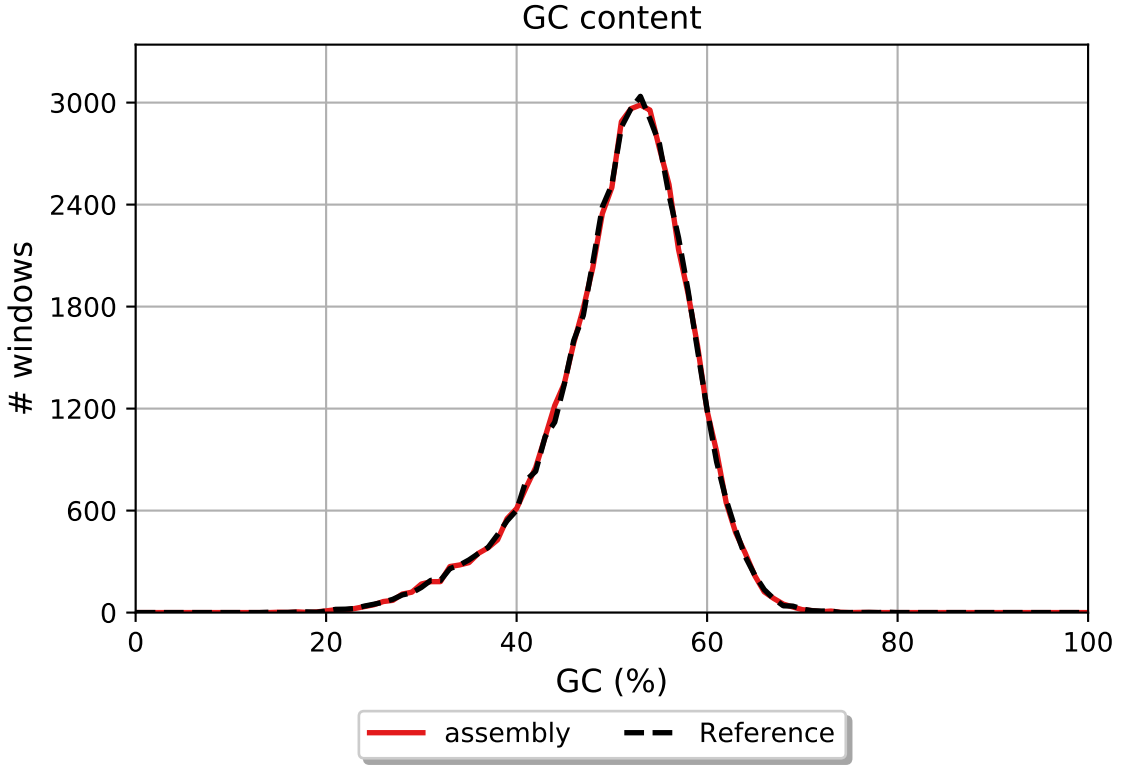
	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	914
# N's	0

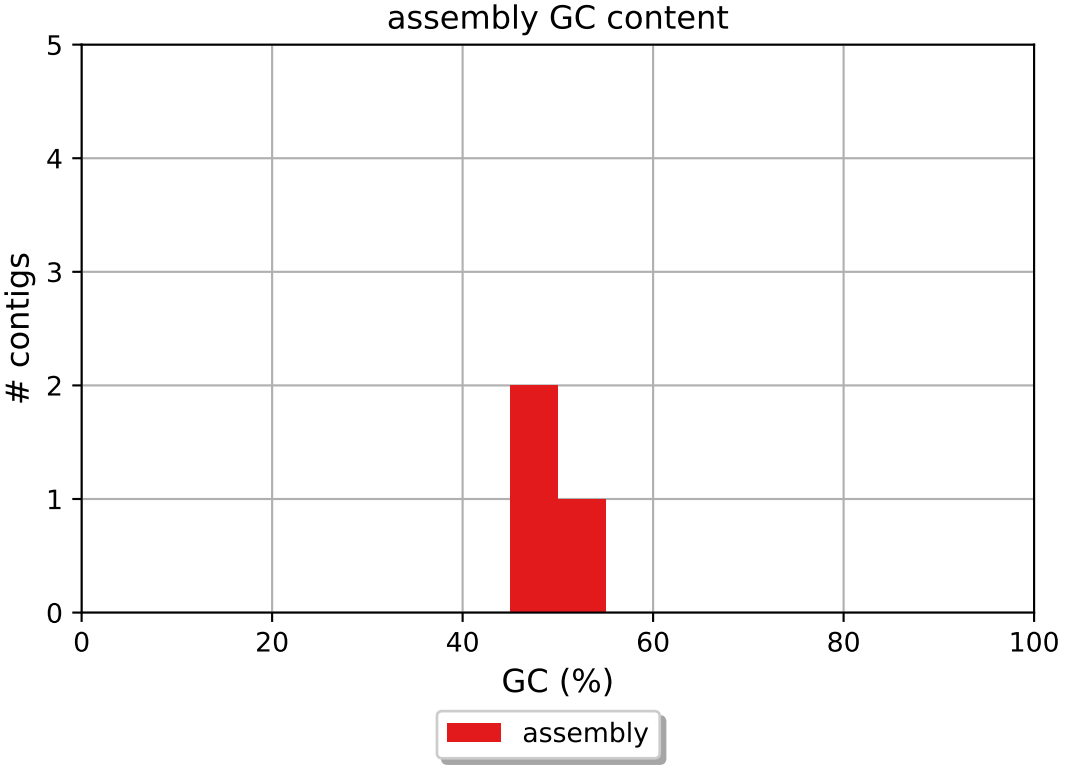
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

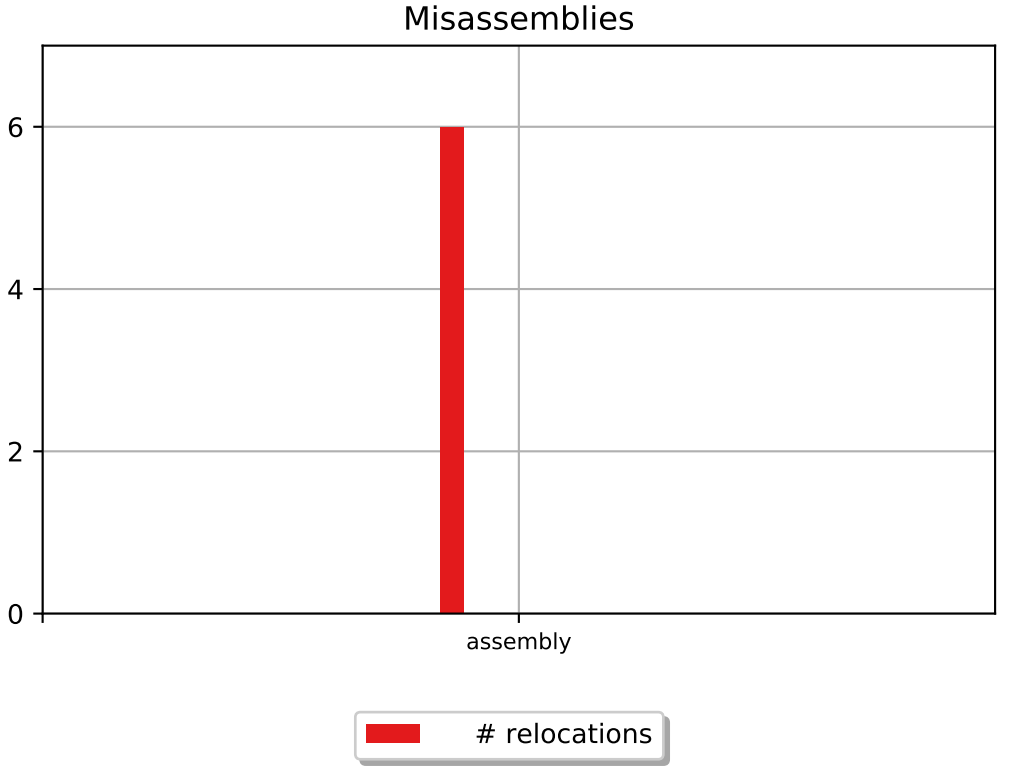

Nx
5000
4000
3000
2000
1000
0
Contig length (kbp)
0
20
40
60
80
100
x
assembly

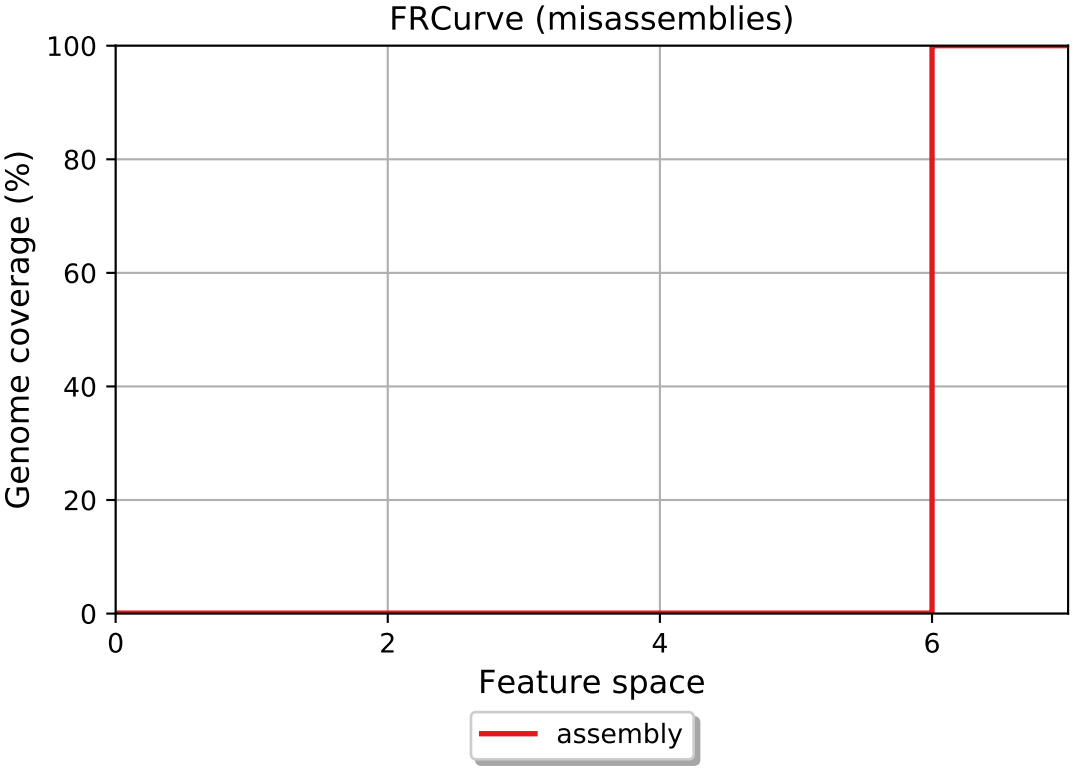

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
assembly

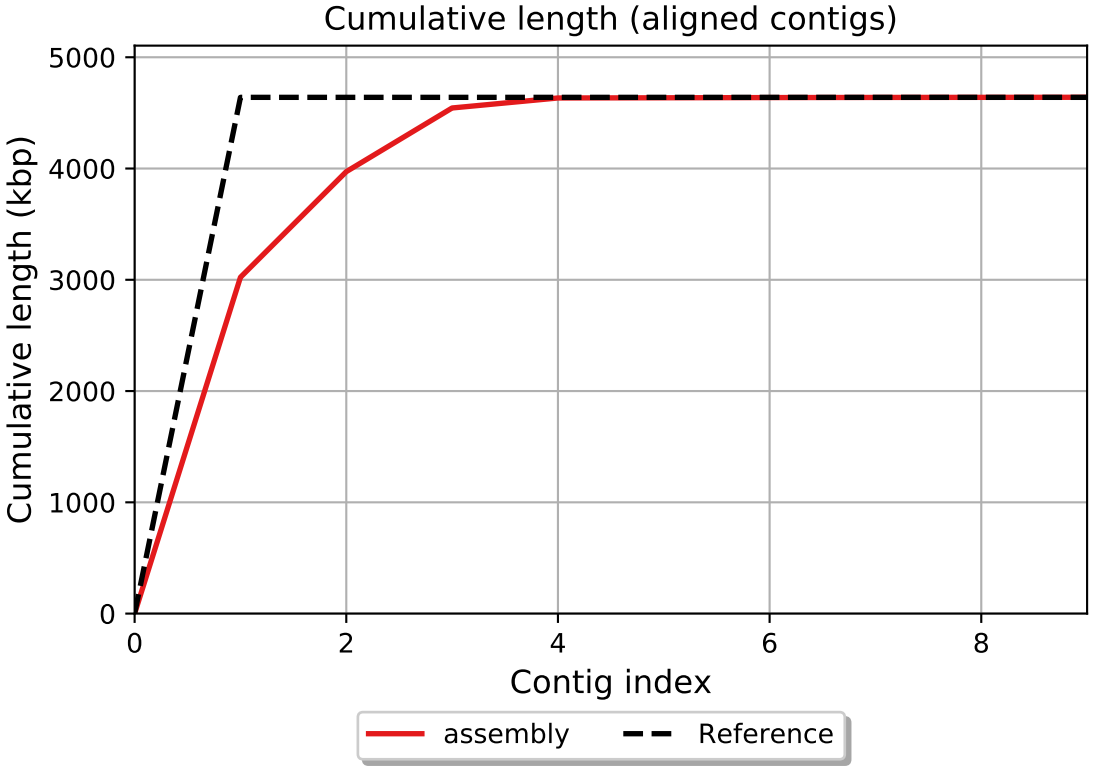

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
3
Contig index
assembly
Reference

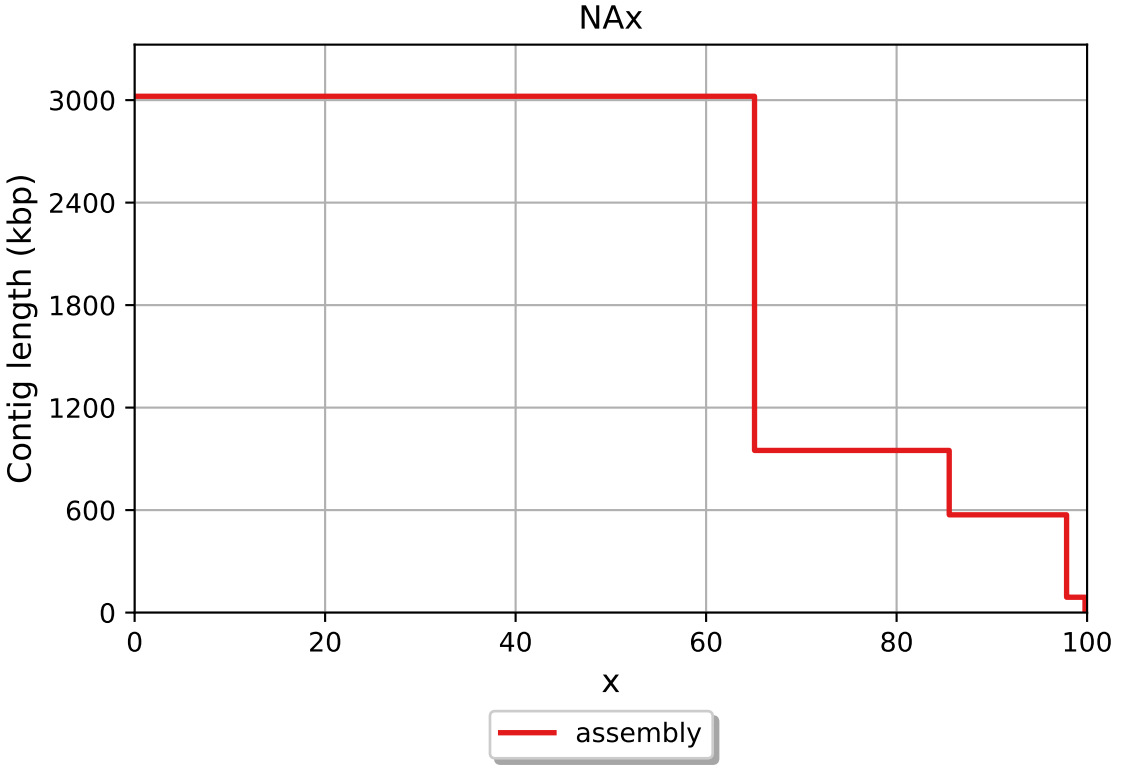

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
assembly
Reference

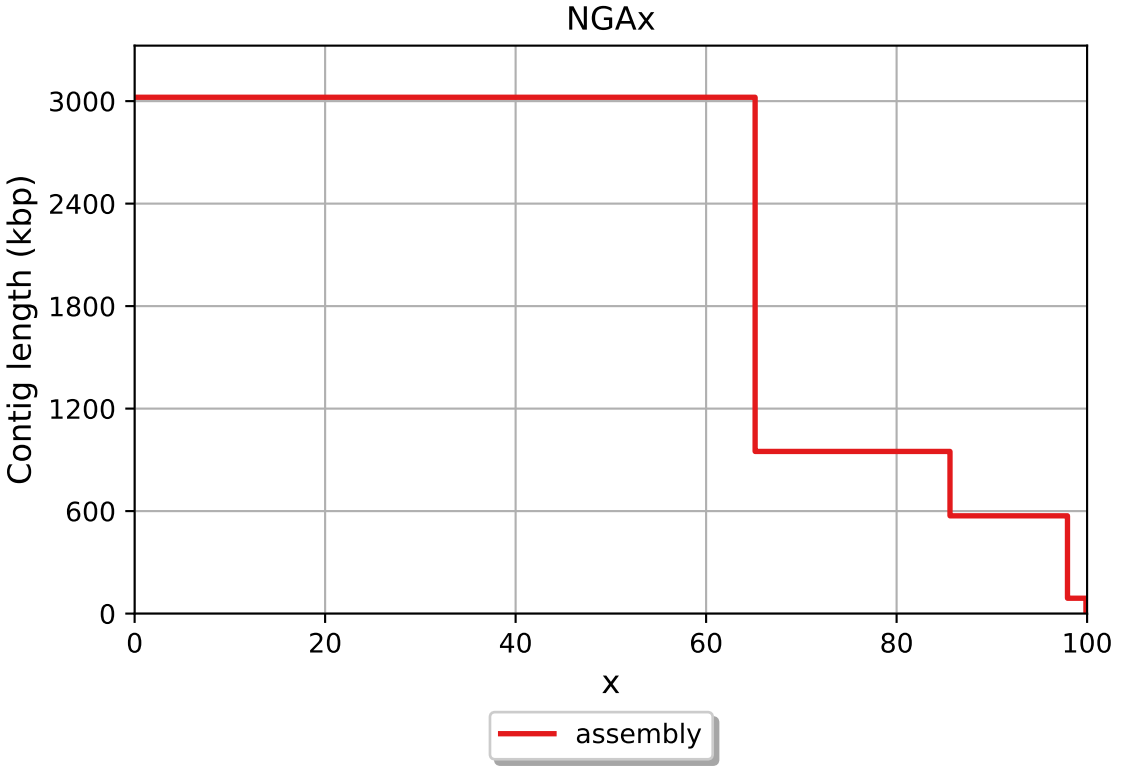

assembly GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
assembly


Misassemblies
6
4
2
0
assembly
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
Feature space
assembly


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
2
4
6
8
Contig index
assembly
Reference


NAx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
assembly


NGAx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
assembly