Report

	final.contigs
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	333849
Total length (>= 5000 bp)	324228
Total length (>= 10000 bp)	324228
Total length (>= 25000 bp)	299823
Total length (>= 50000 bp)	266140
# contigs	20
Largest contig	266140
Total length	341974
Reference length	3464554
GC (%)	59.47
Reference GC (%)	65.06
N50	266140
N75	266140
L50	1
L75	1
# 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	1 + 11 part
Unaligned length	335384
Genome fraction (%)	0.058
Duplication ratio	3.275
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3677.93
# indels per 100 kbp	49.70
Largest alignment	561
Total aligned length	2265
NGA50	-

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

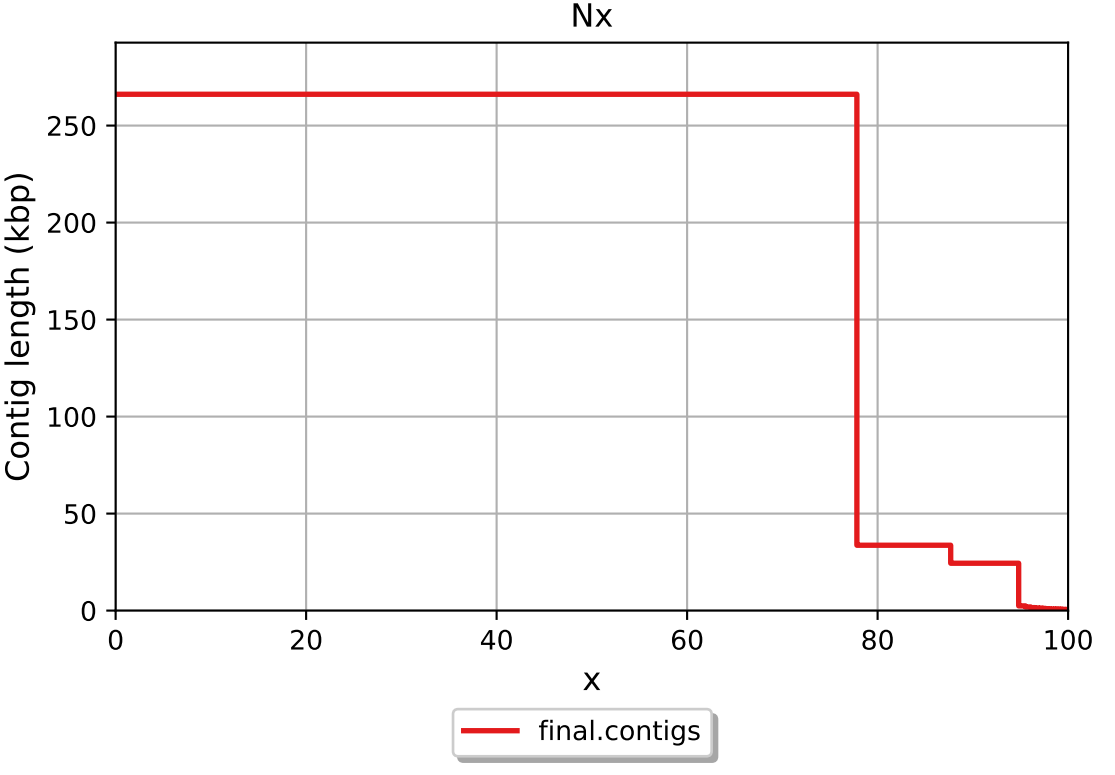
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	6
# possible misassemblies	10
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	74
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

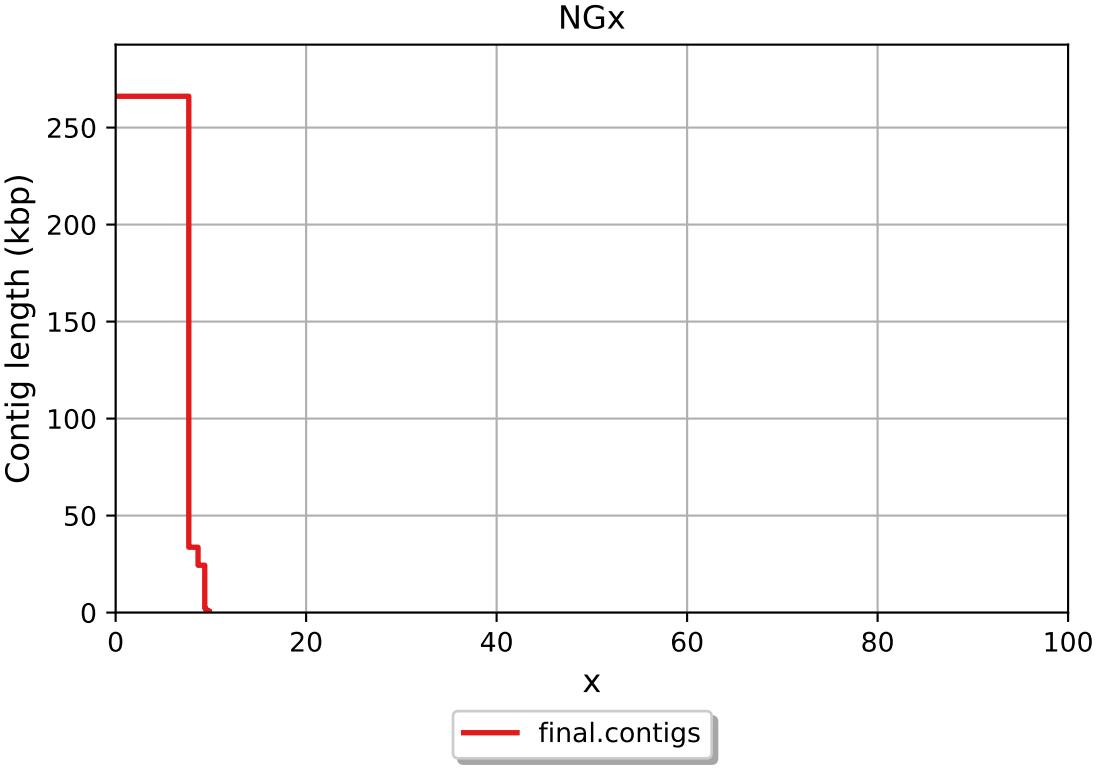
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

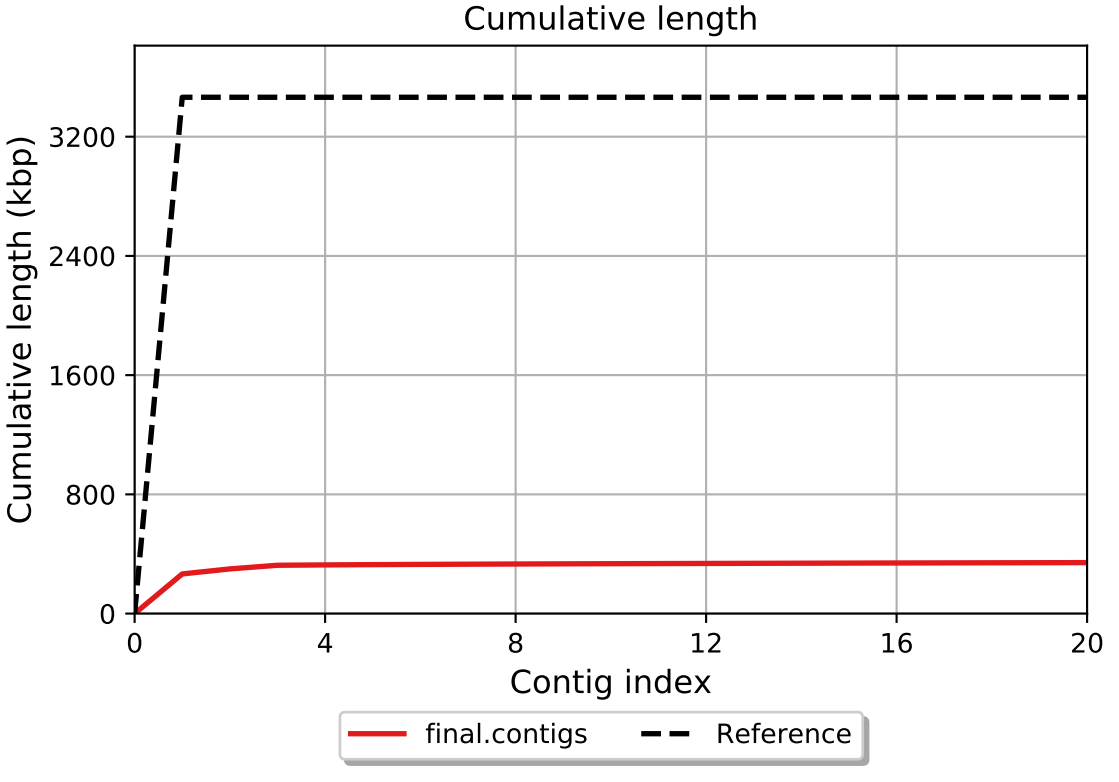
Unaligned report

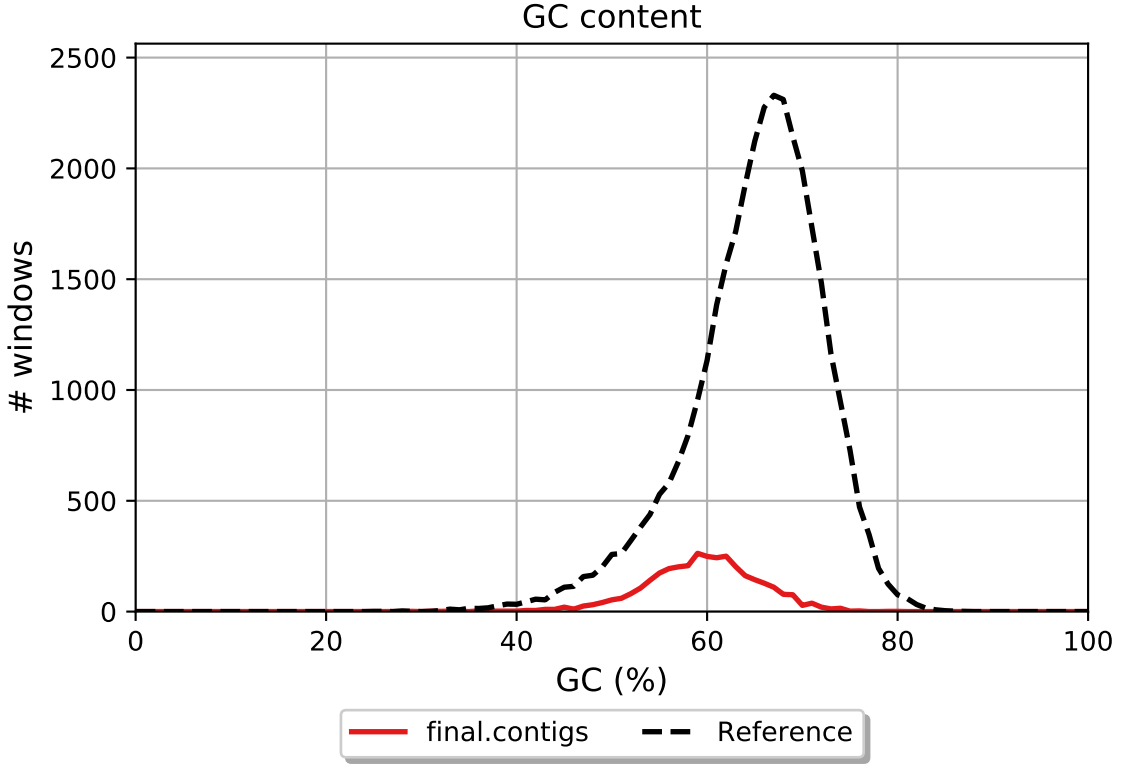
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	871
# partially unaligned contigs	11
Partially unaligned length	334513
# N's	0

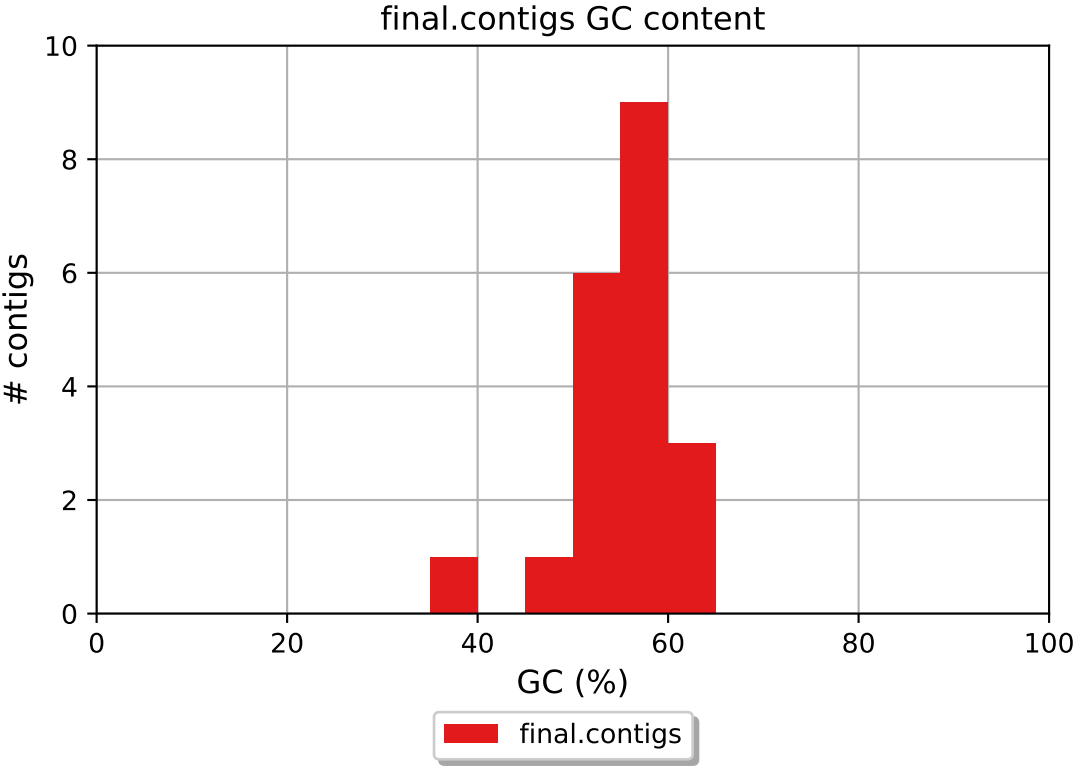
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

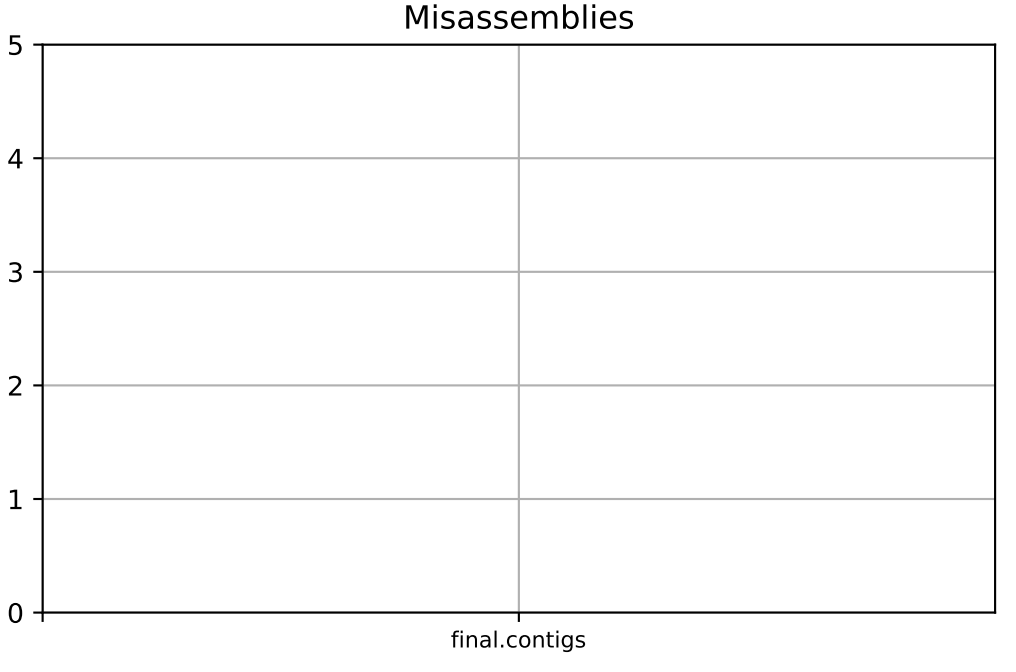

Nx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

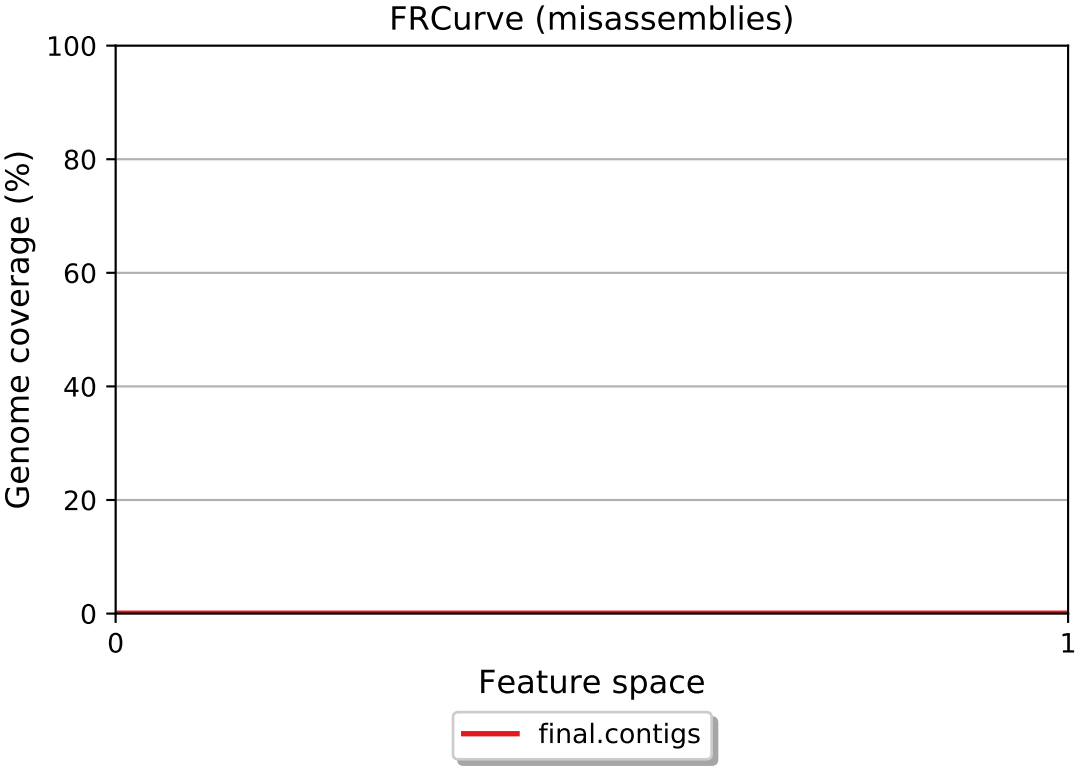

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

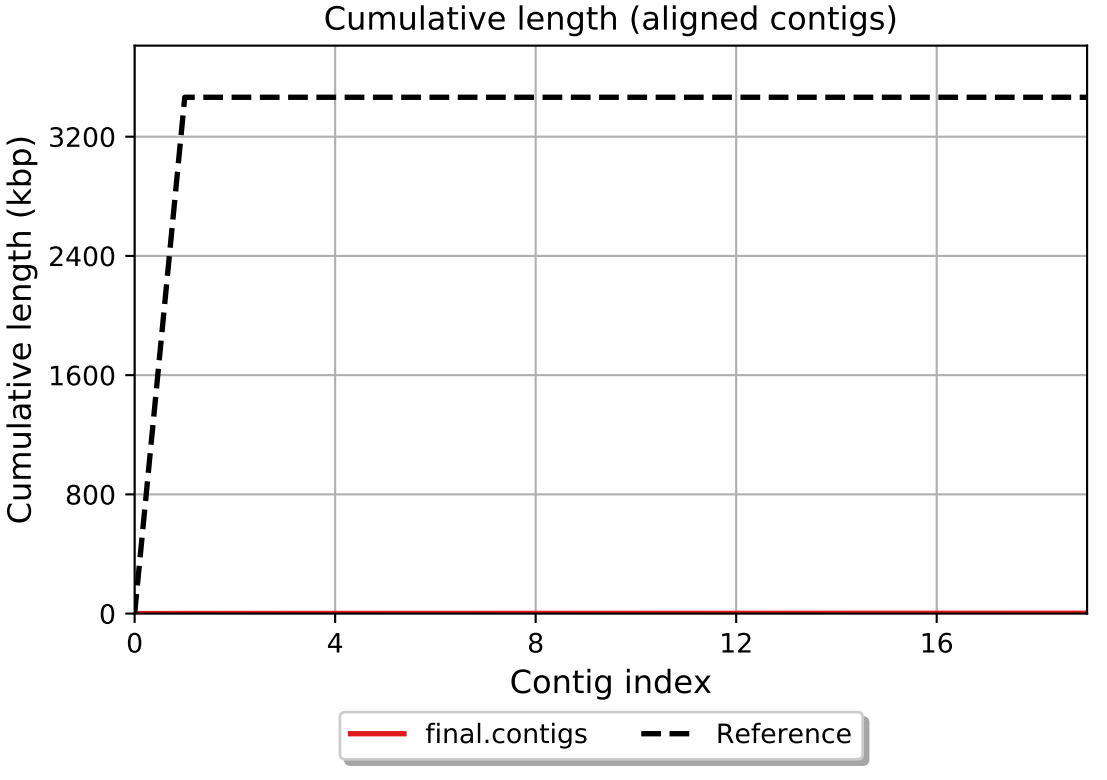

Cumulative length
Cumulative length (kbp)
3200
2400
1600
800
0
0
4
8
12
16
20
Contig index
final.contigs
Reference

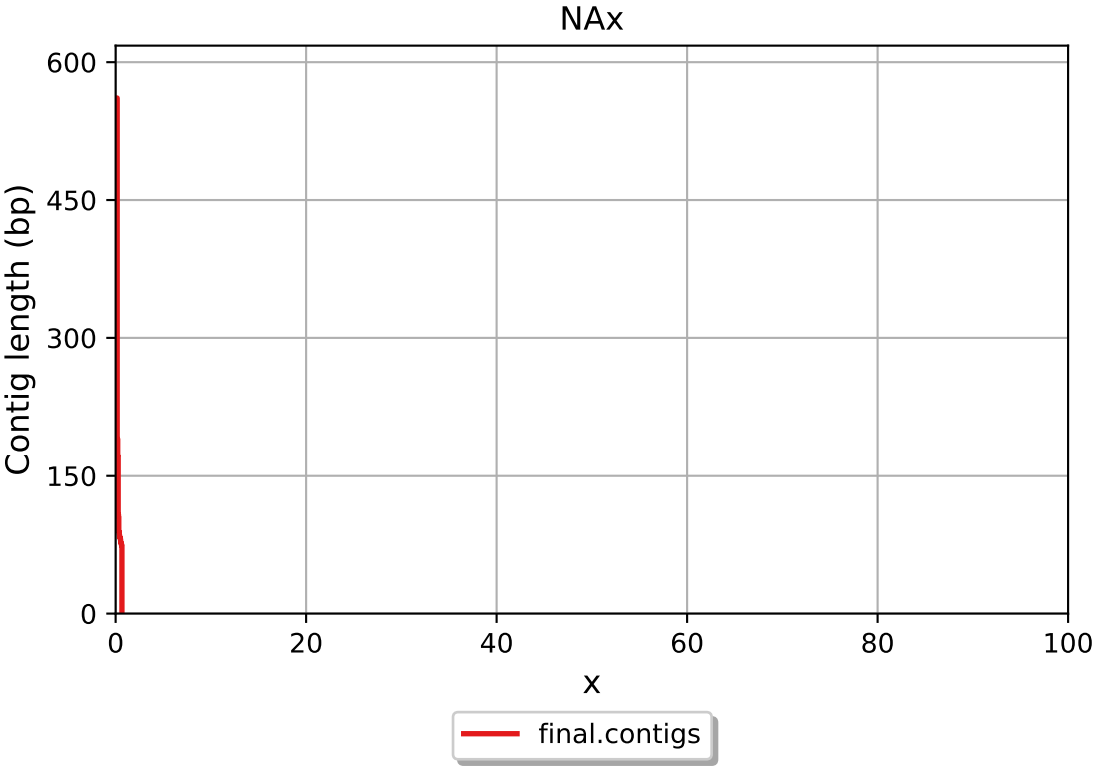

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

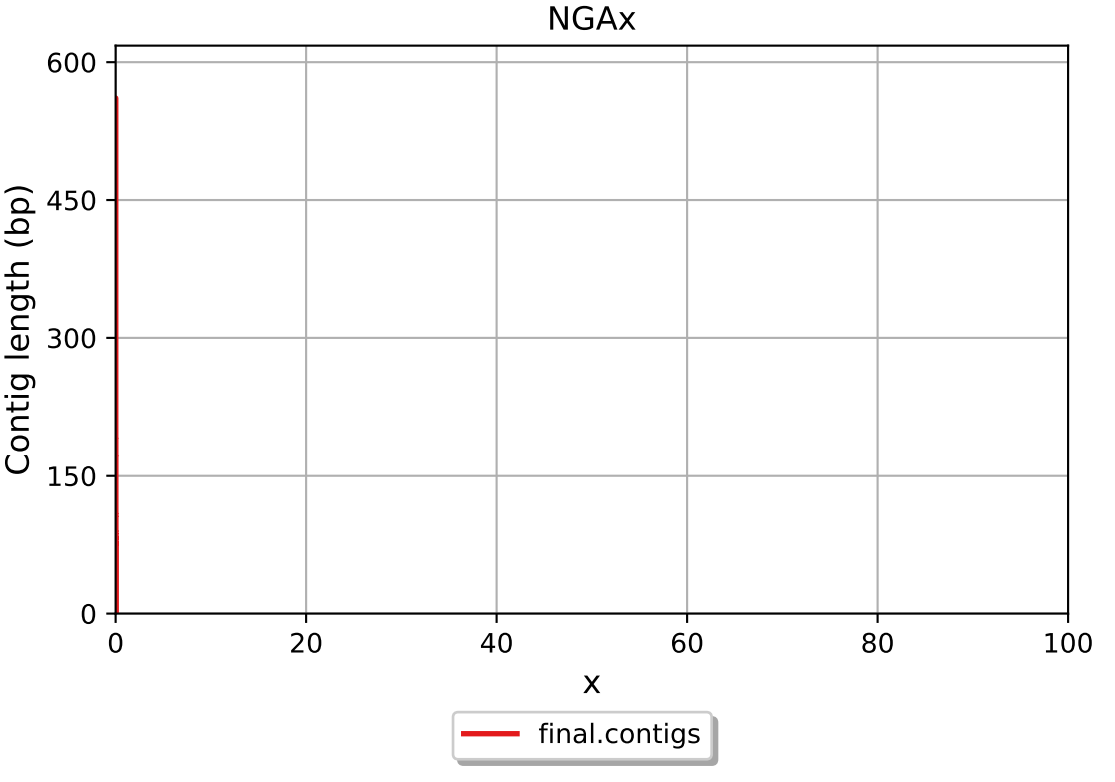

final.contigs GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
3200
2400
1600
800
0
0
4
8
12
16
Contig index
final.contigs
Reference


NAx
600
450
300
150
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
600
450
300
150
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs