Report

	final.contigs
# contigs (>= 1000 bp)	12
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	67554
Total length (>= 5000 bp)	50462
Total length (>= 10000 bp)	32298
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	19
Largest contig	18858
Total length	71998
Reference length	6102701
GC (%)	44.90
Reference GC (%)	65.02
N50	9851
N75	4157
L50	3
L75	5
# 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	1
# unaligned contigs	2 + 13 part
Unaligned length	68001
Genome fraction (%)	0.020
Duplication ratio	3.274
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4832.10
# indels per 100 kbp	0.00
Largest alignment	254
Total aligned length	2059
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

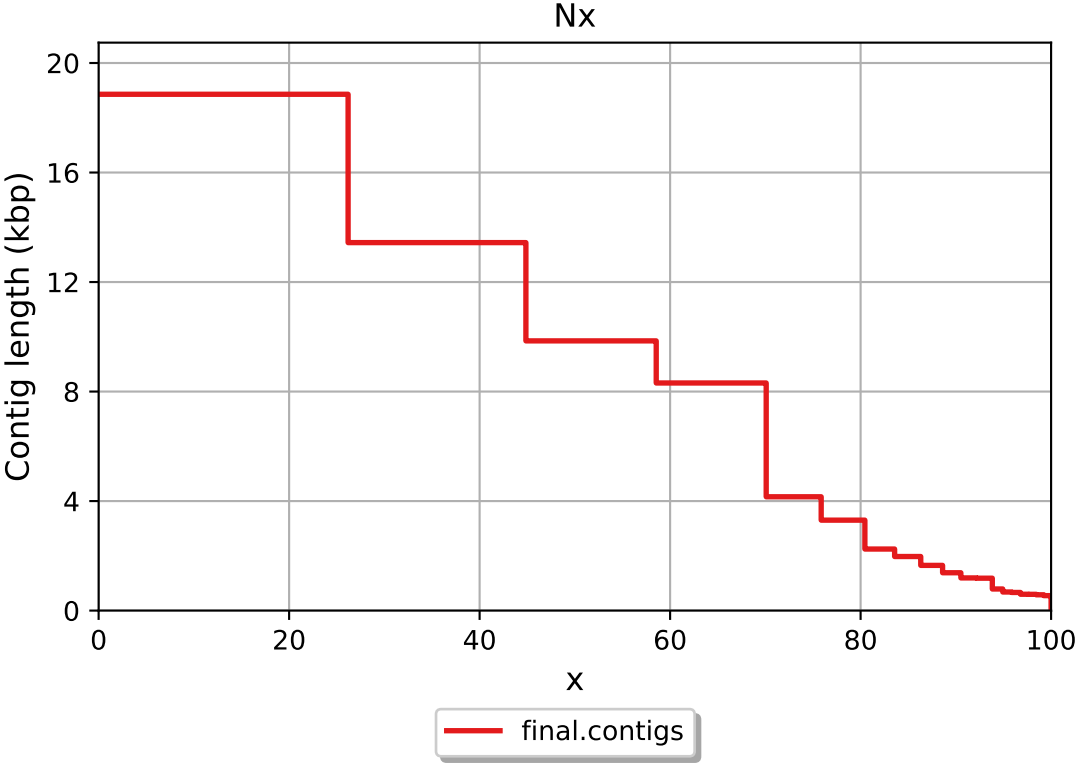
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	10
# possible misassemblies	14
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	59
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

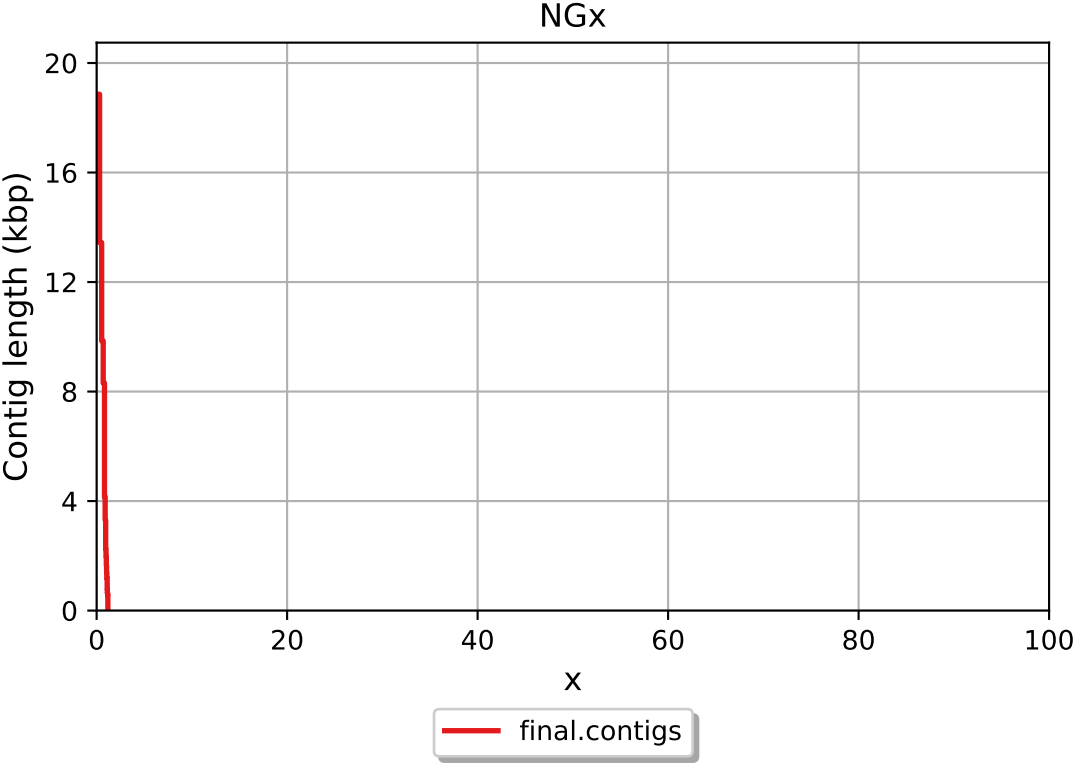
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

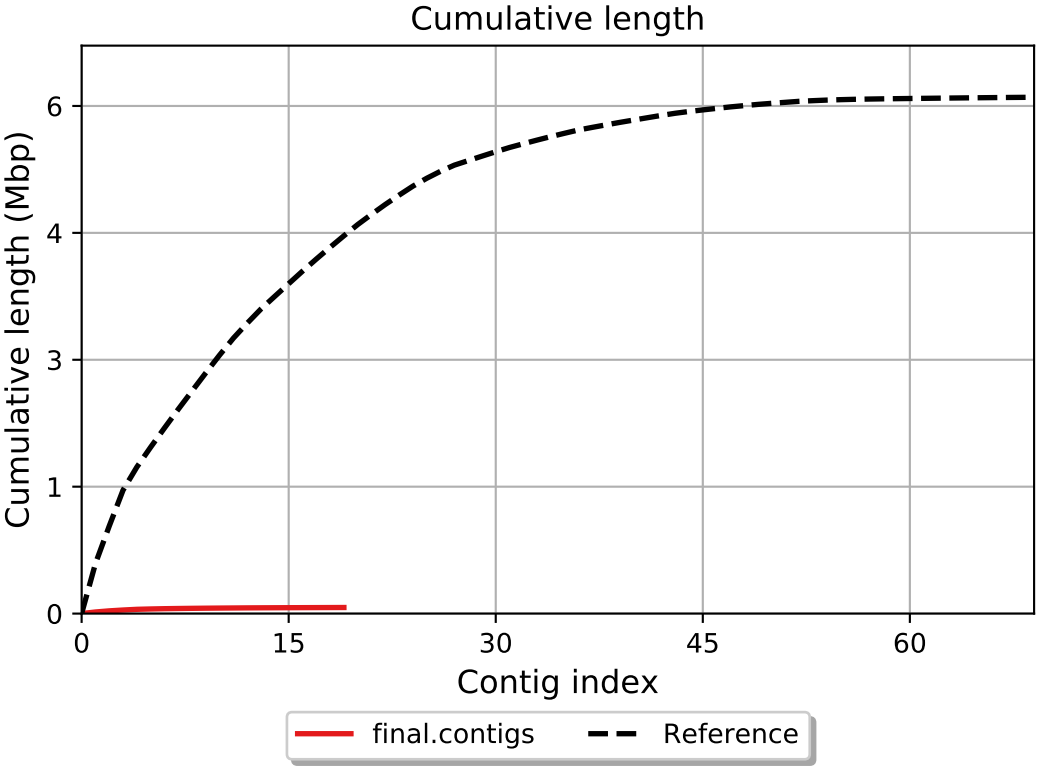
Unaligned report

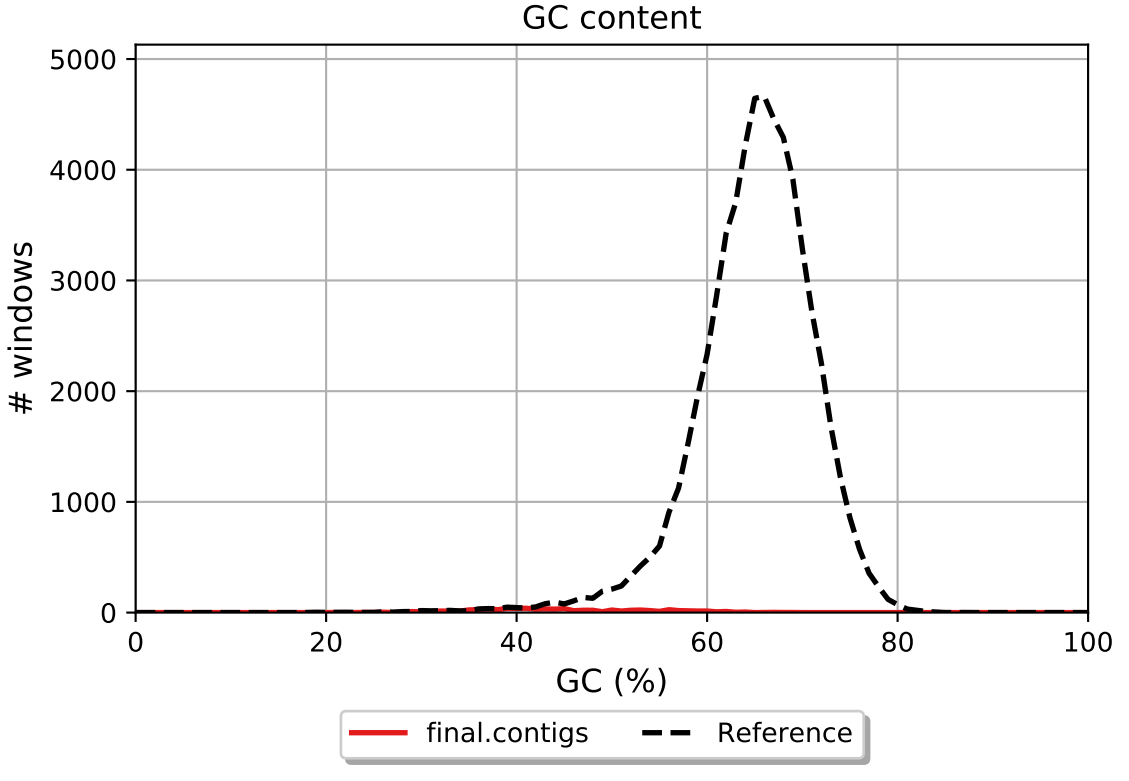
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1140
# partially unaligned contigs	13
Partially unaligned length	66861
# N's	0

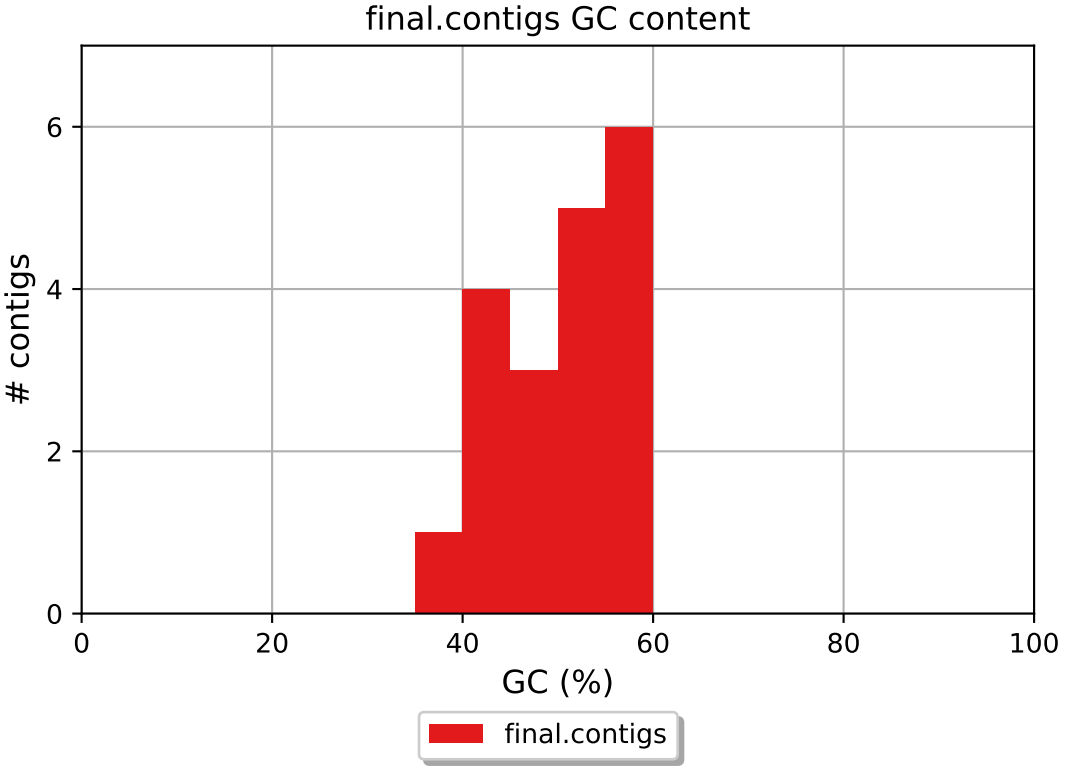
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

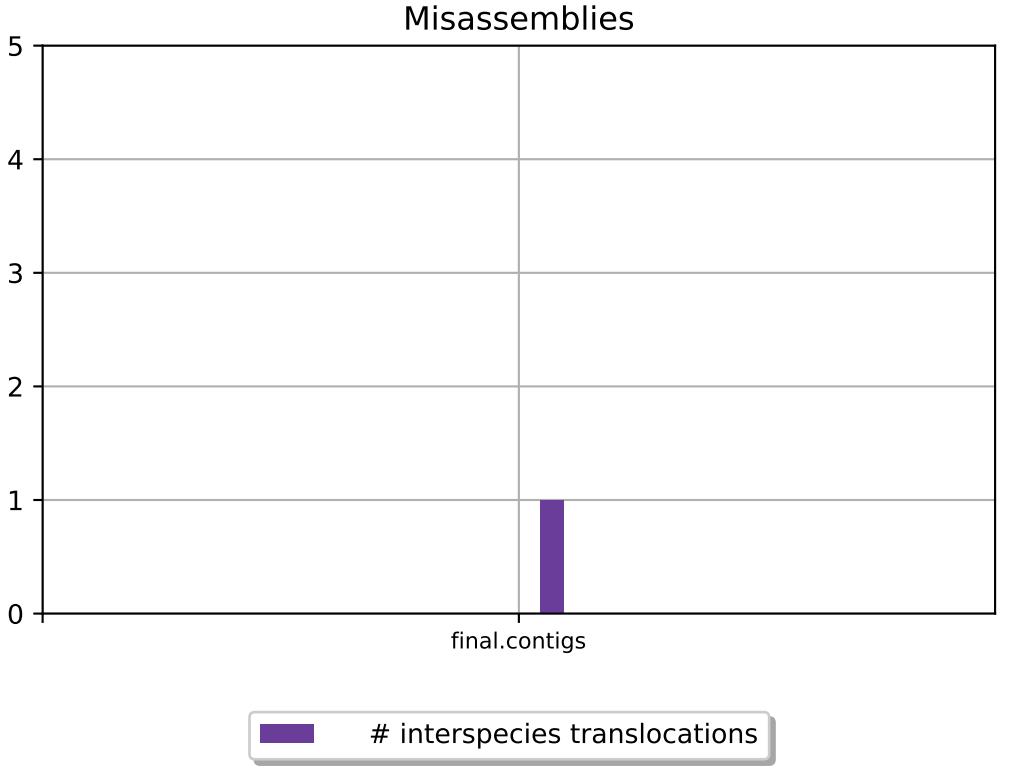

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs

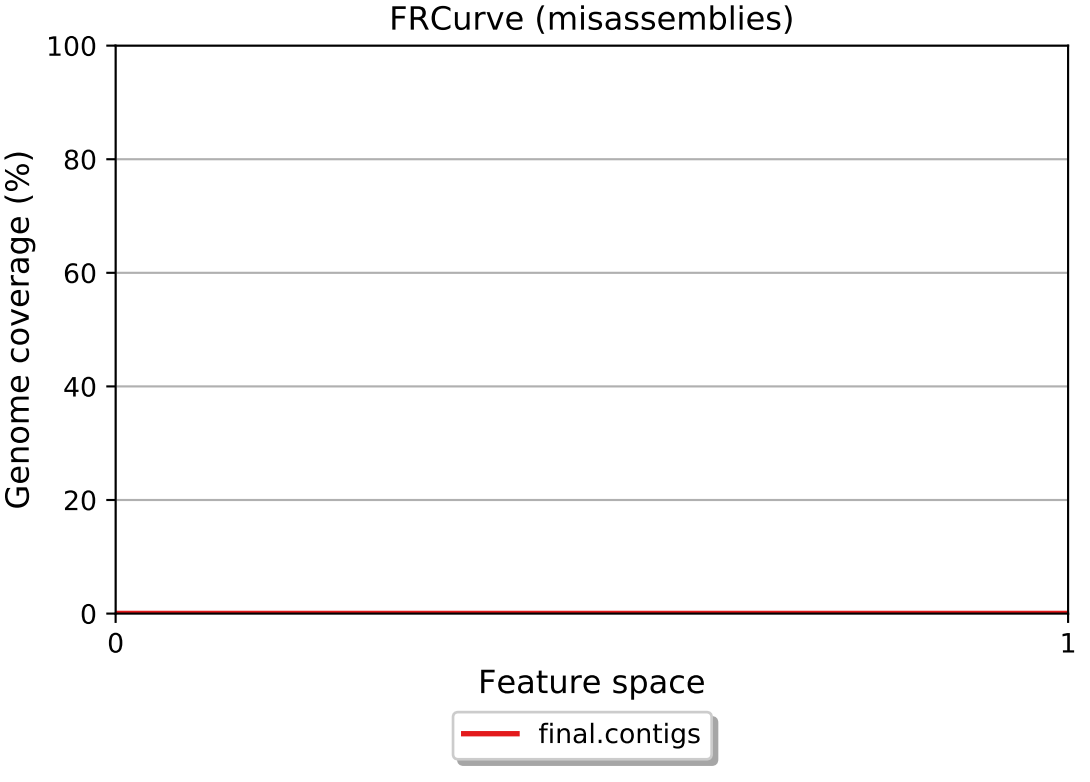

NGx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs

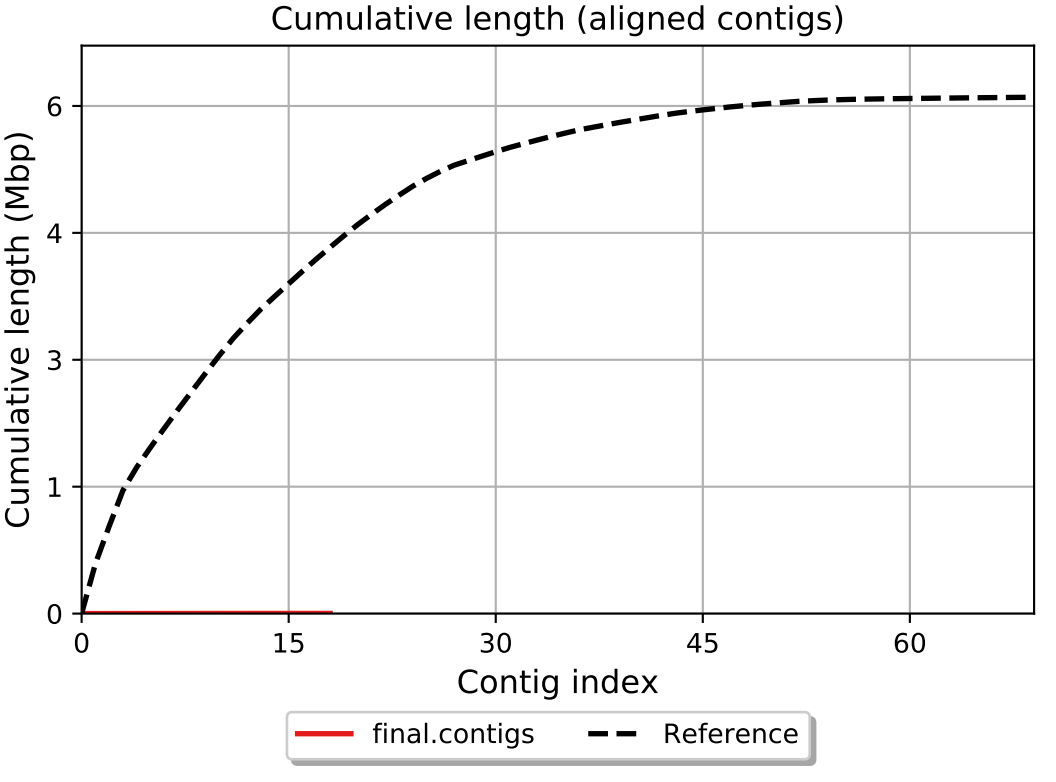

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
15
30
45
60
Contig index
final.contigs
Reference

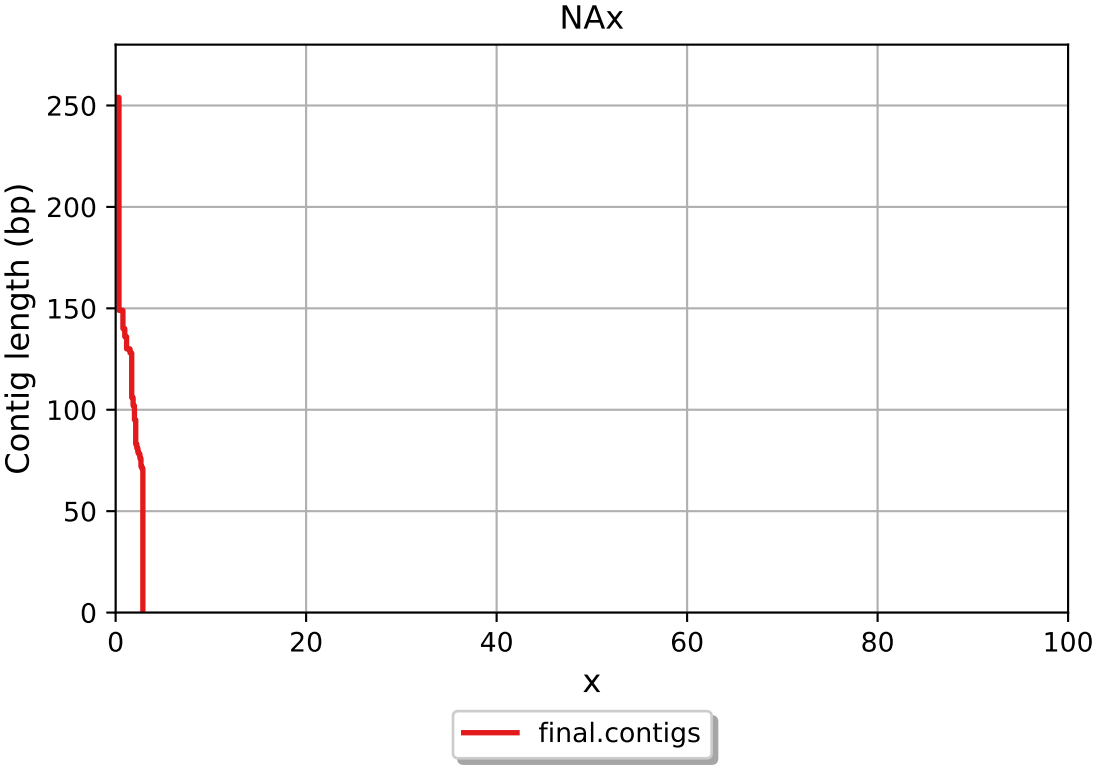

GC content
5000
4000
3000
2000
1000
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

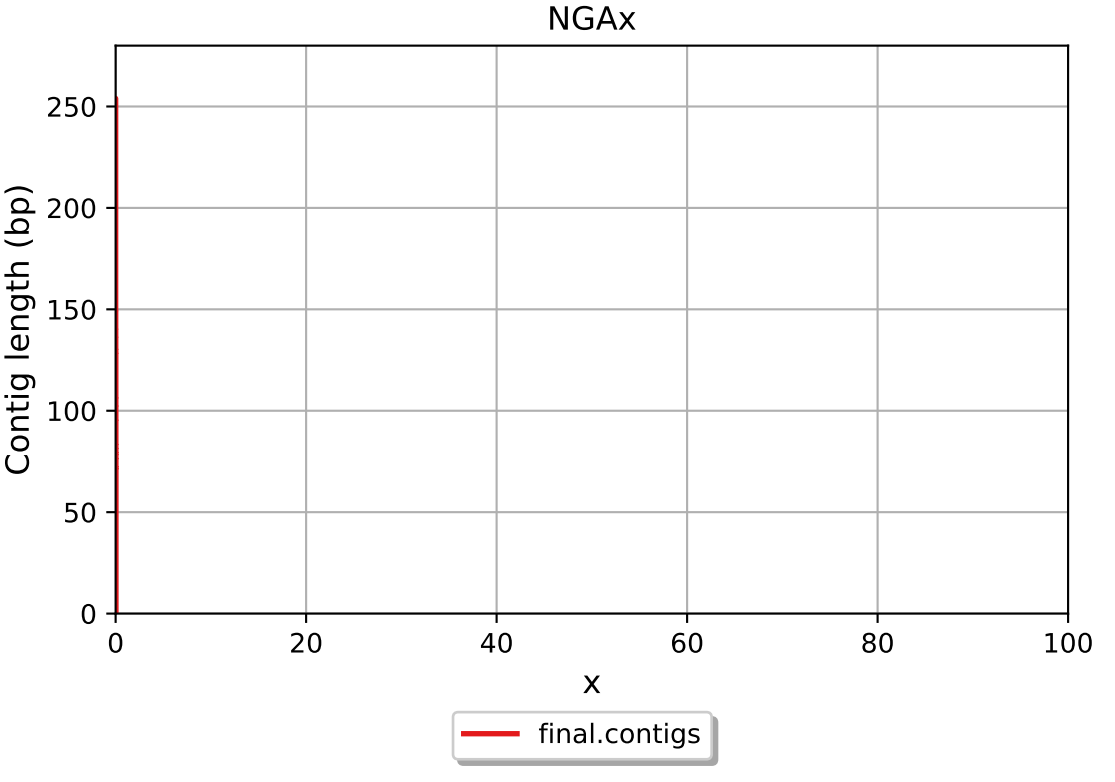

final.contigs GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs
interspecies translocations


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
15
30
45
60
Contig index
final.contigs
Reference


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


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