Report

	final.contigs
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	33664
Total length (>= 5000 bp)	5625
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	17
Largest contig	5625
Total length	36316
Reference length	3712900
GC (%)	36.38
Reference GC (%)	31.25
N50	4157
N75	1805
L50	4
L75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	3 + 11 part
Unaligned length	32745
Genome fraction (%)	0.056
Duplication ratio	1.722
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3905.50
# indels per 100 kbp	48.22
Largest alignment	619
Total aligned length	2409
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

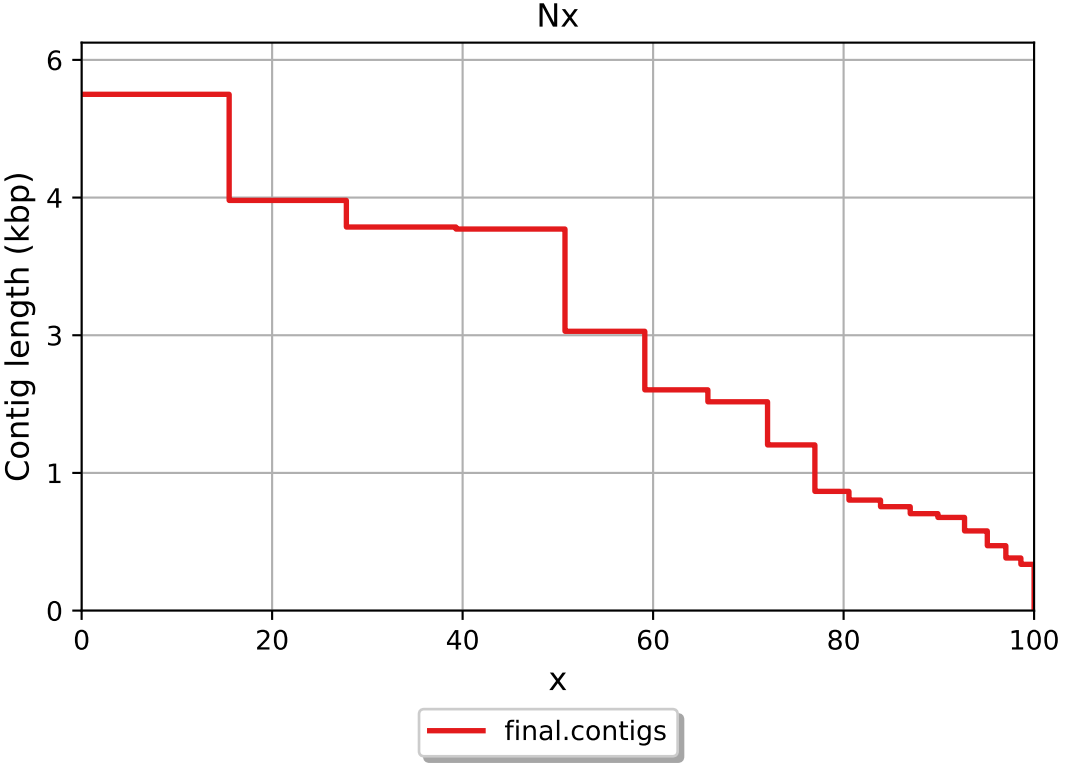
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	7
# possible misassemblies	11
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	81
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

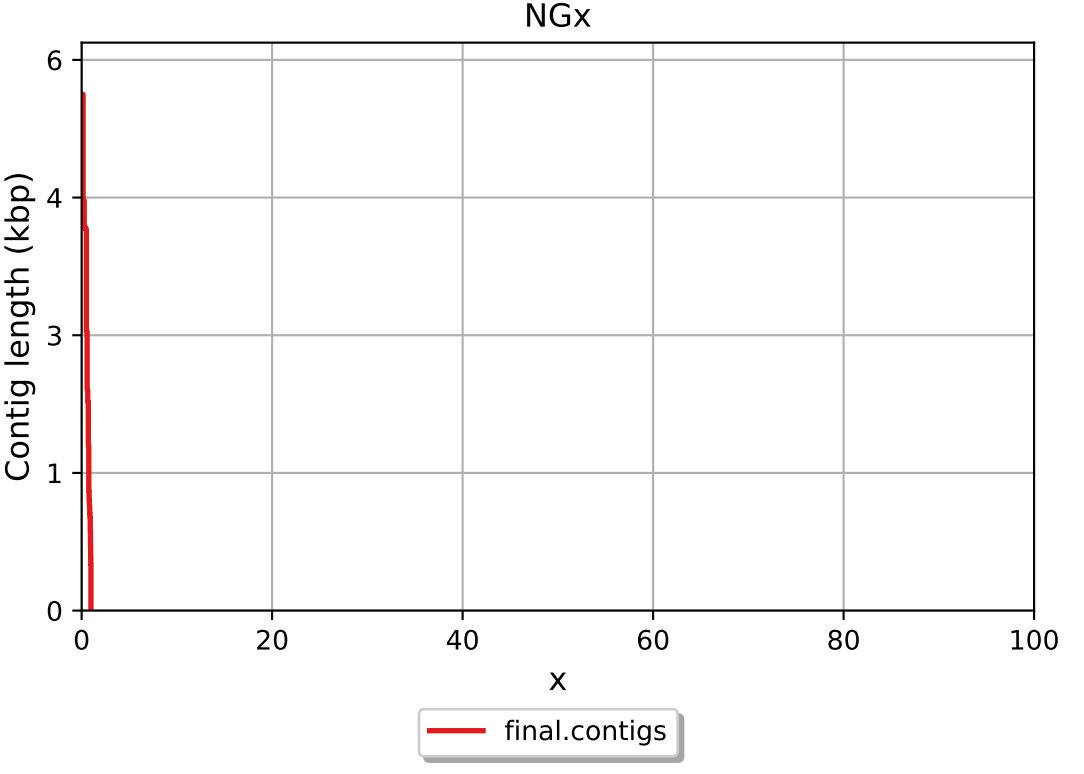
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

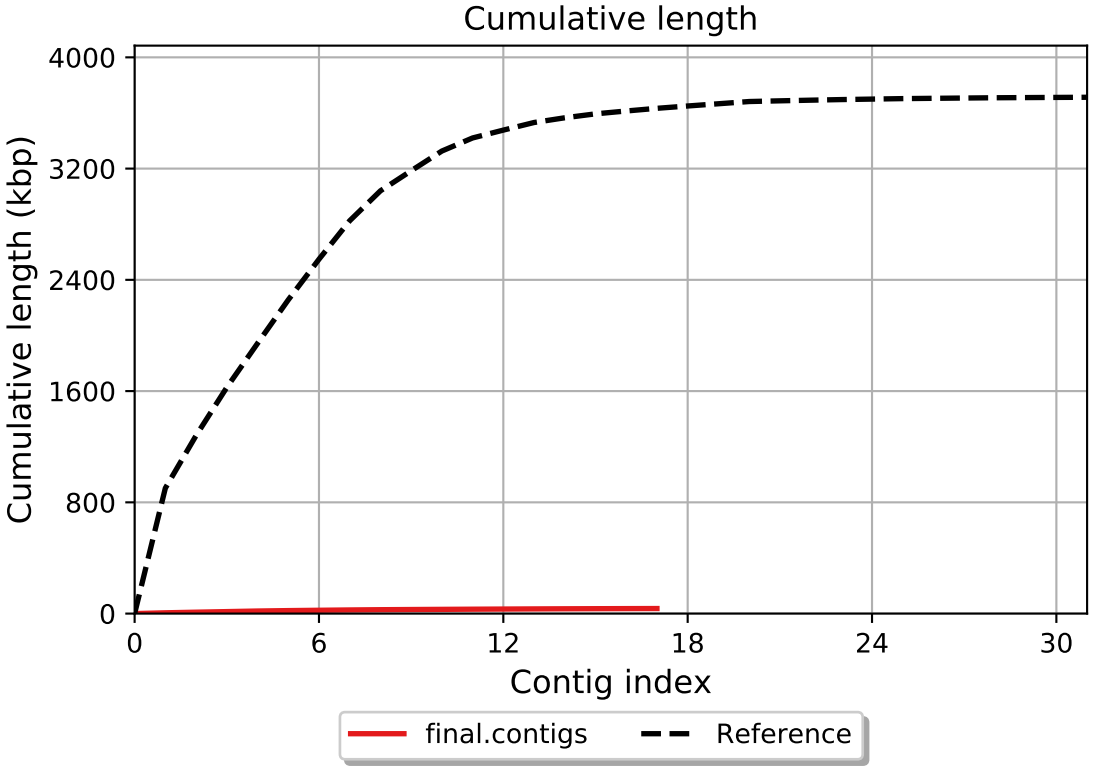
Unaligned report

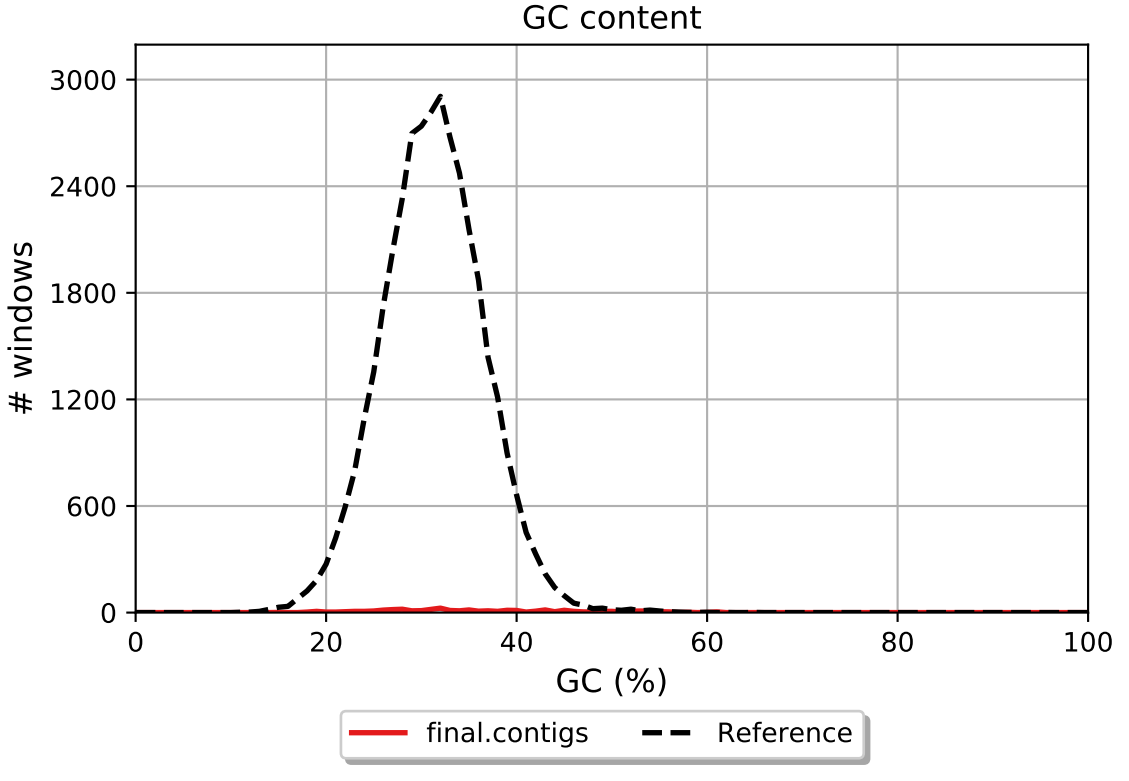
	final.contigs
# fully unaligned contigs	3
Fully unaligned length	3965
# partially unaligned contigs	11
Partially unaligned length	28780
# N's	0

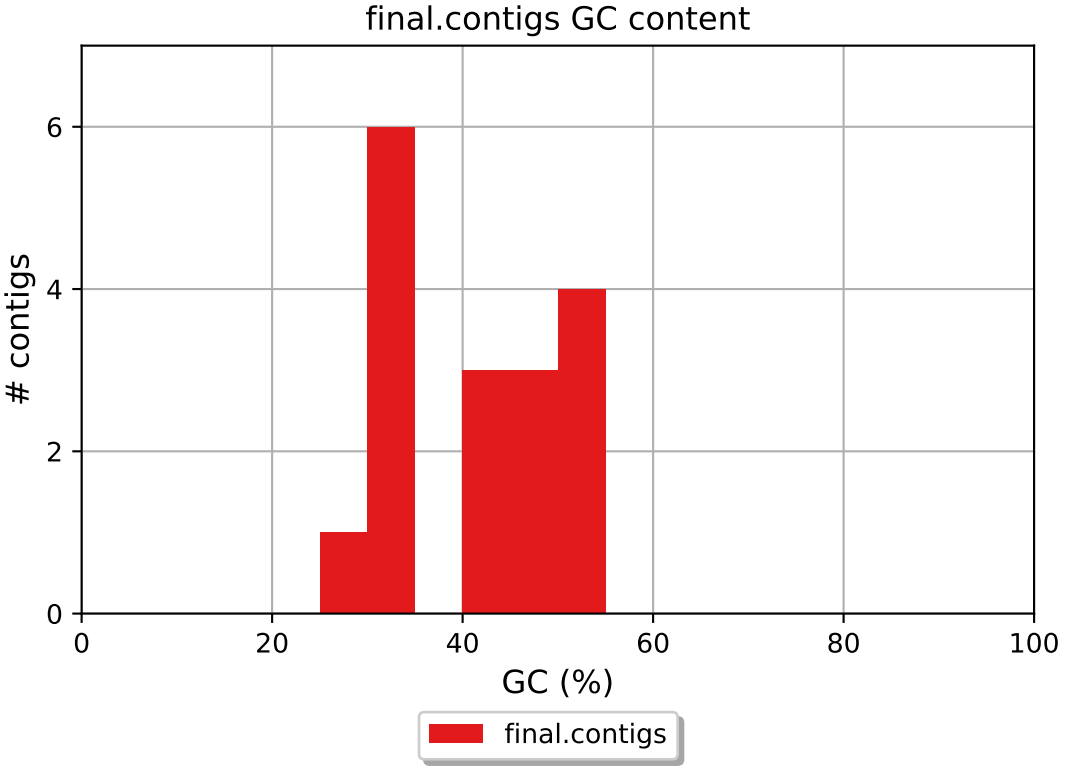
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

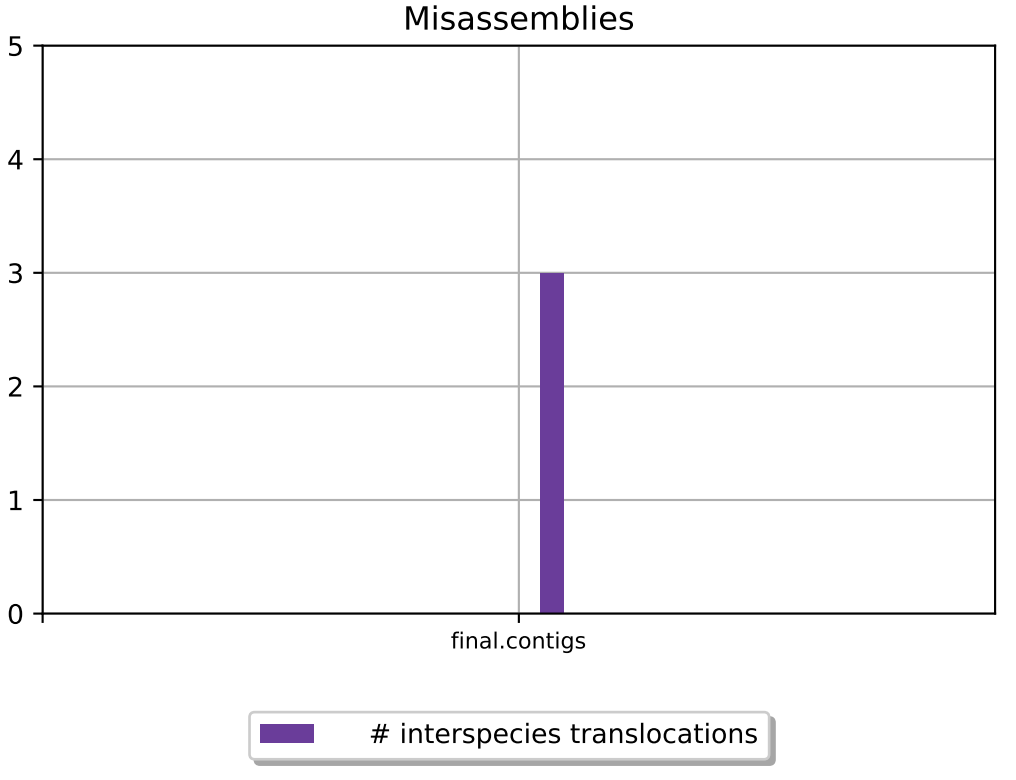

Nx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
final.contigs

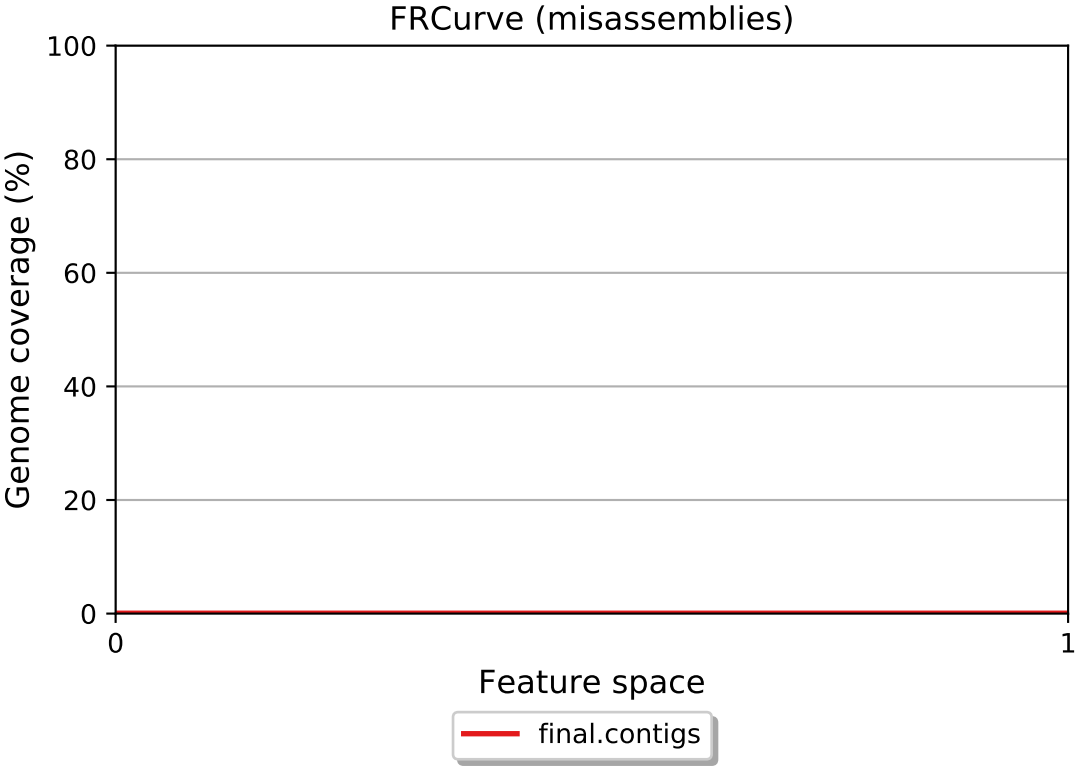

NGx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
final.contigs

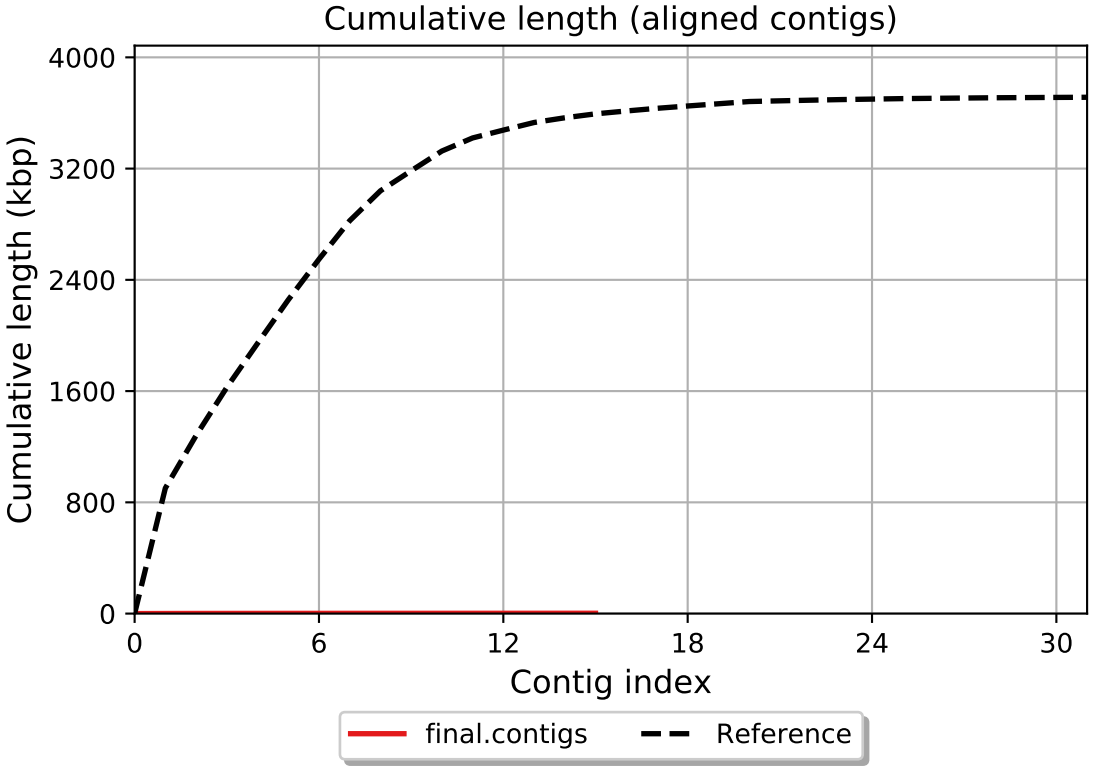

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
6
12
18
24
30
Contig index
final.contigs
Reference

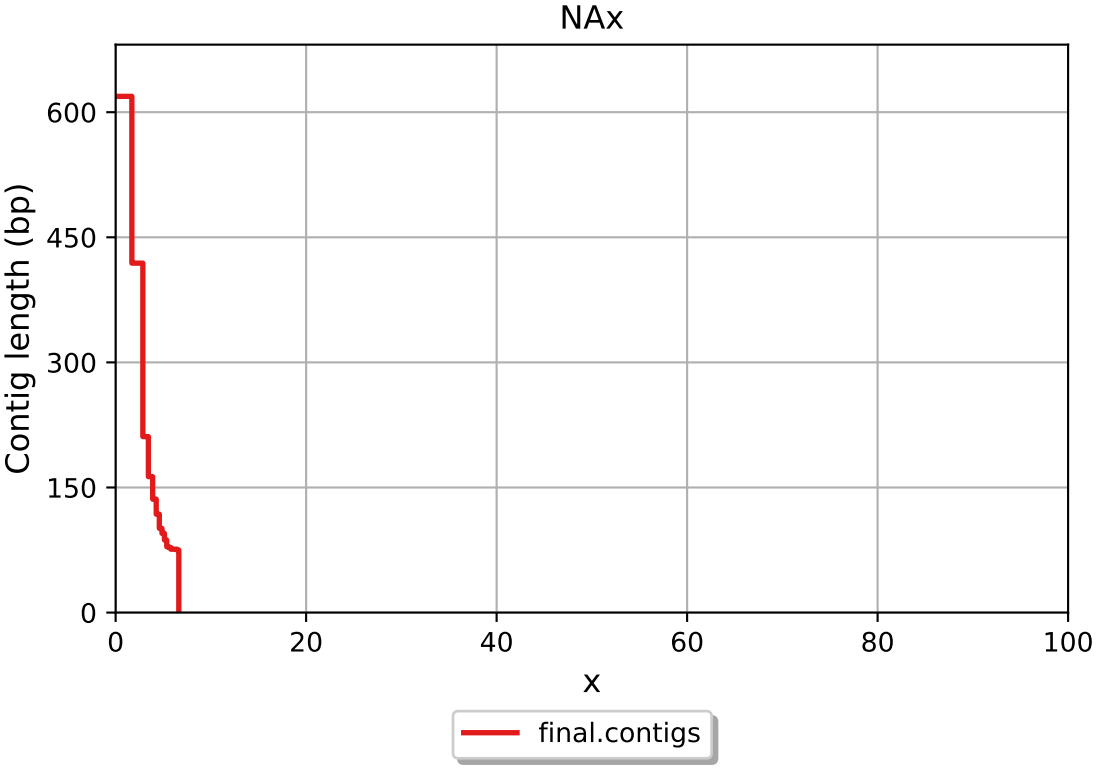

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

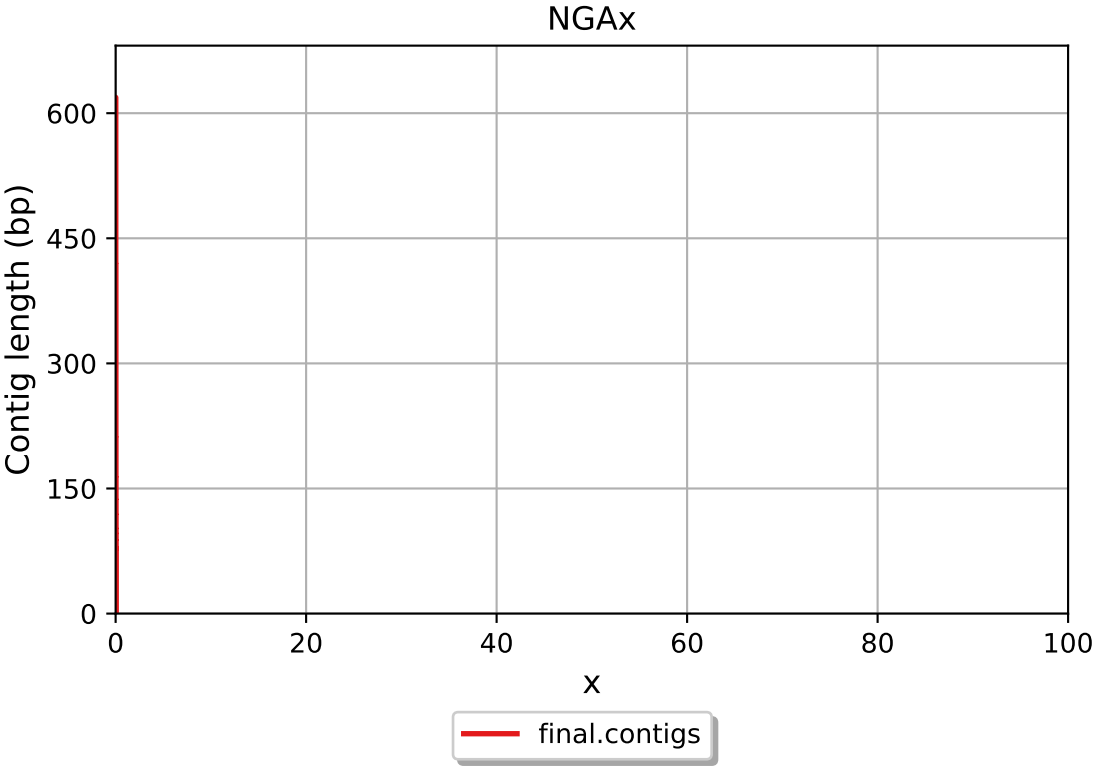

final.contigs GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
final.contigs


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


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
6
12
18
24
30
Contig index
final.contigs
Reference


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


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