Report

	final.contigs
# contigs (>= 1000 bp)	23
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	12
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	5
Total length (>= 1000 bp)	958452
Total length (>= 5000 bp)	939022
Total length (>= 10000 bp)	915925
Total length (>= 25000 bp)	850849
Total length (>= 50000 bp)	736182
# contigs	34
Largest contig	255300
Total length	966365
Reference length	3442017
GC (%)	59.02
Reference GC (%)	58.88
N50	124997
N75	74884
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	5
# unaligned contigs	3 + 25 part
Unaligned length	958598
Genome fraction (%)	0.110
Duplication ratio	2.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4551.43
# indels per 100 kbp	236.78
Largest alignment	608
Total aligned length	5589
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

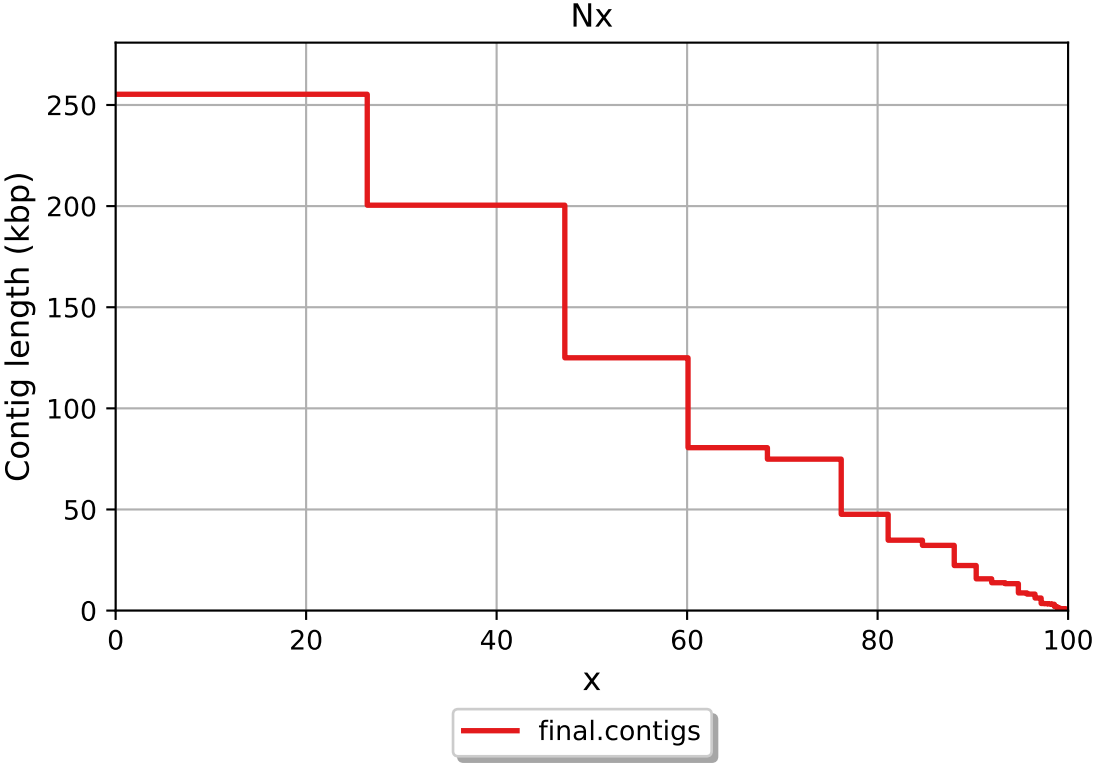
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	17
# possible misassemblies	27
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	173
# indels	9
# indels (<= 5 bp)	9
# indels (> 5 bp)	0
Indels length	13

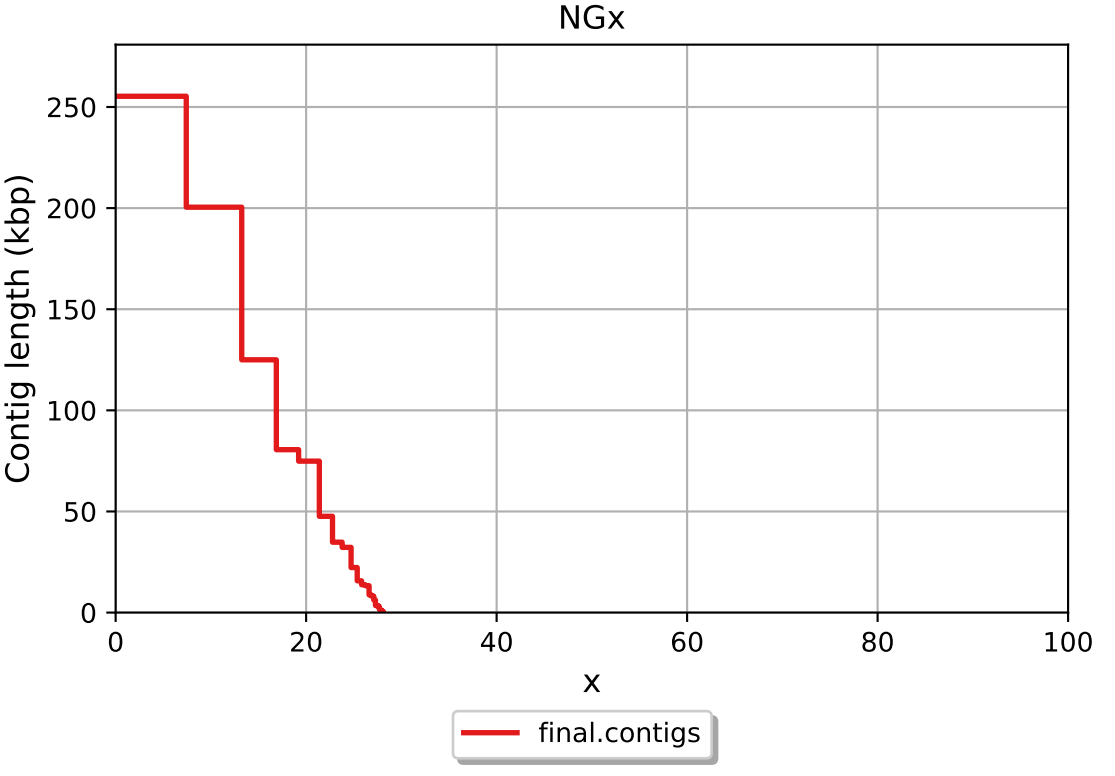
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

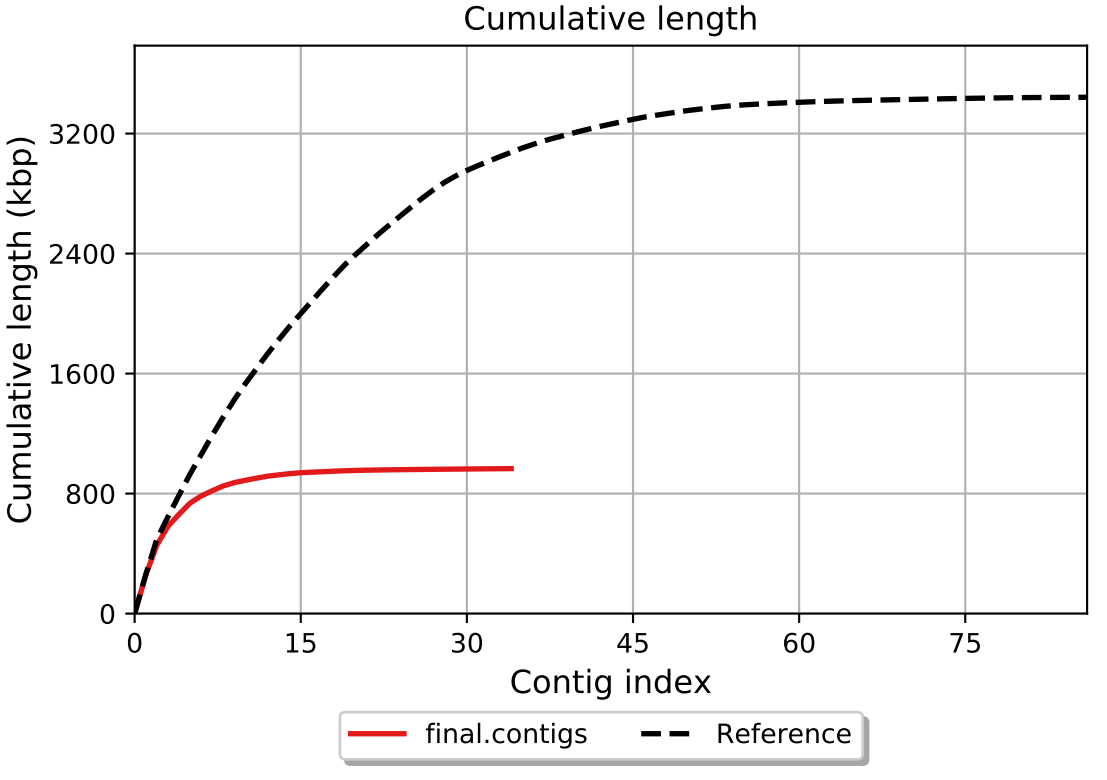
Unaligned report

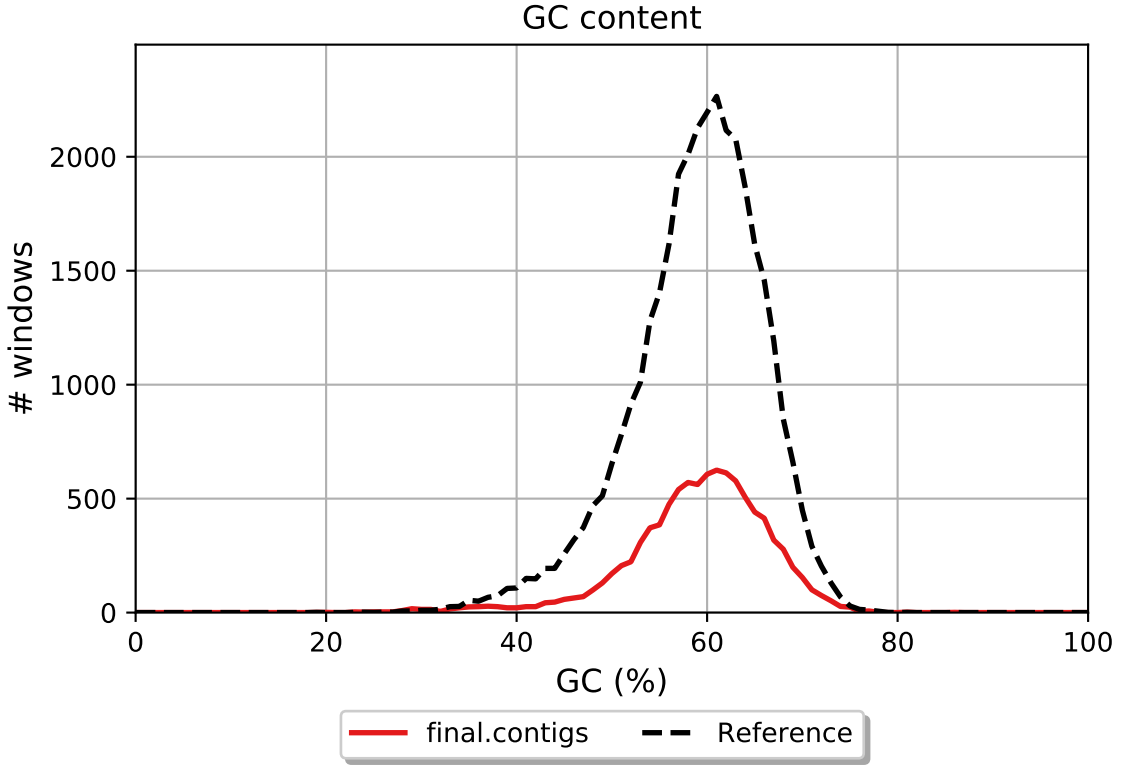
	final.contigs
# fully unaligned contigs	3
Fully unaligned length	3257
# partially unaligned contigs	25
Partially unaligned length	955341
# N's	0

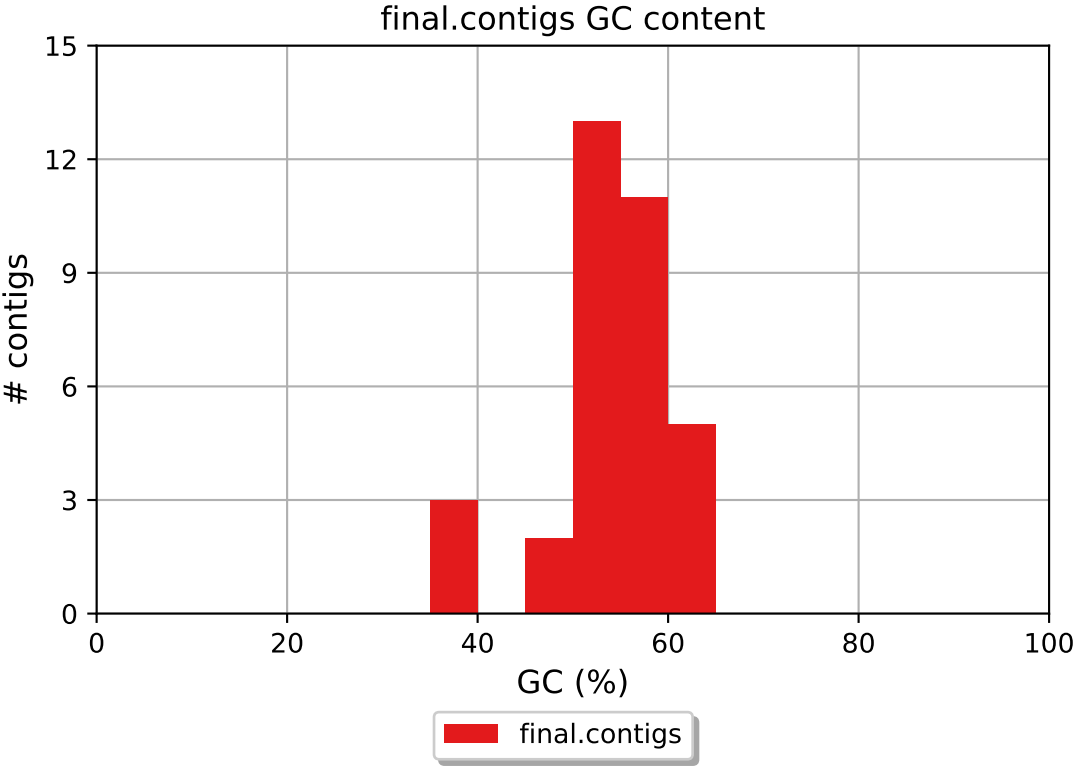
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

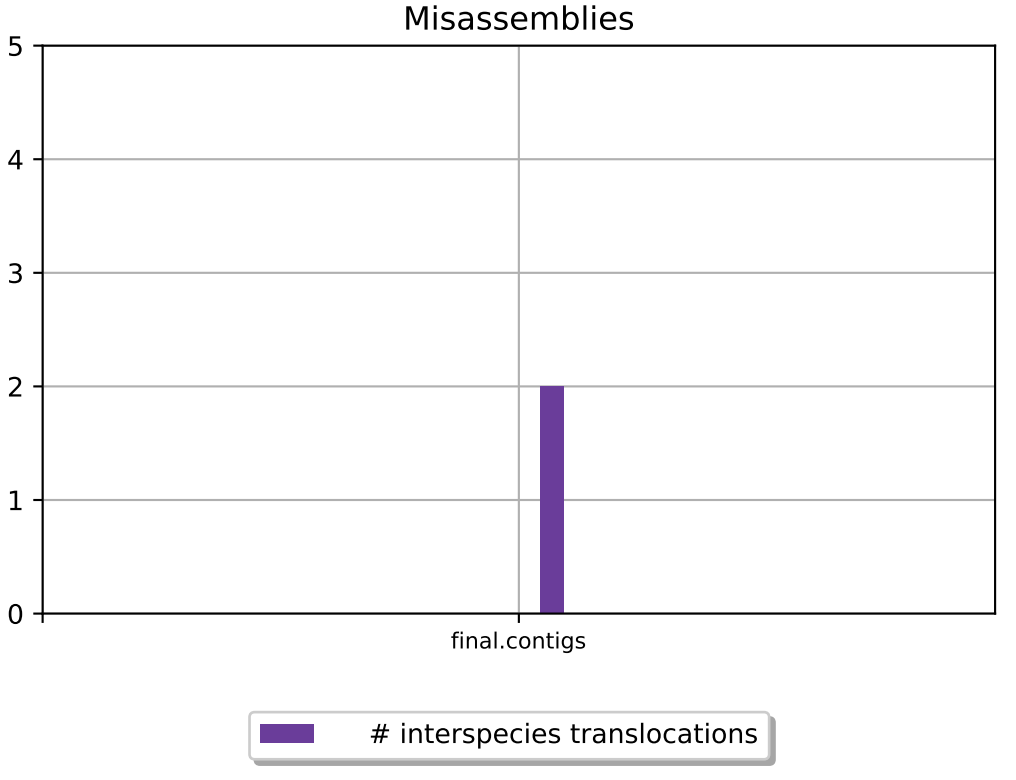

Nx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

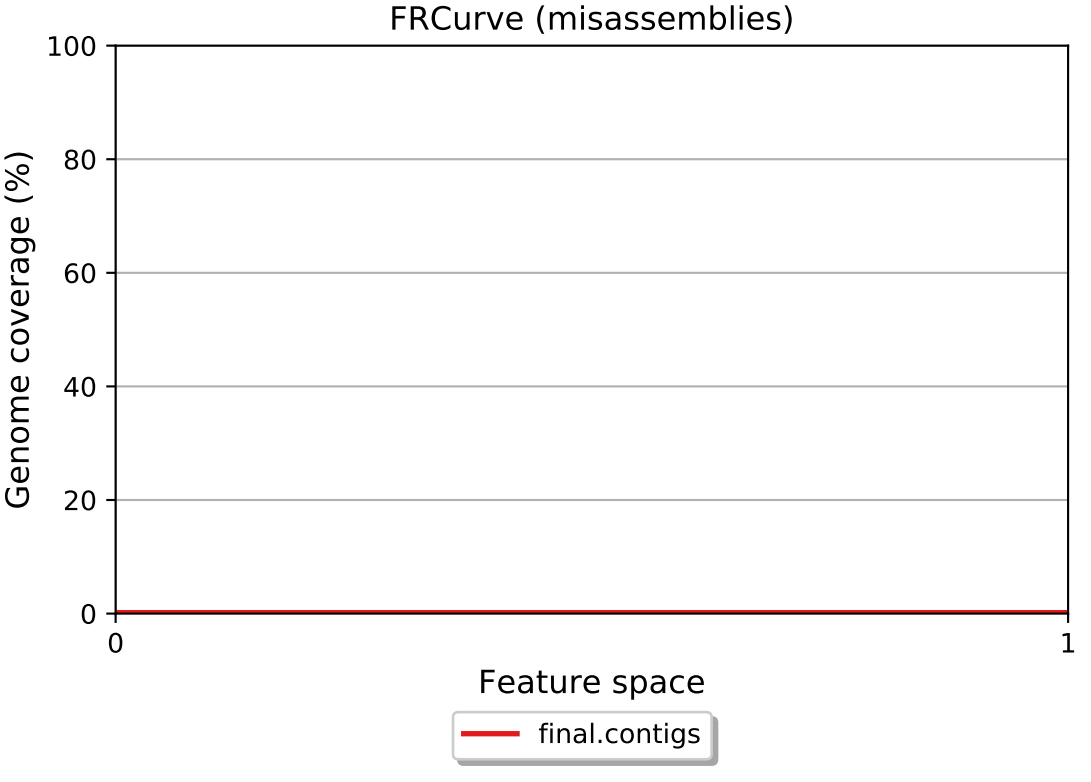

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

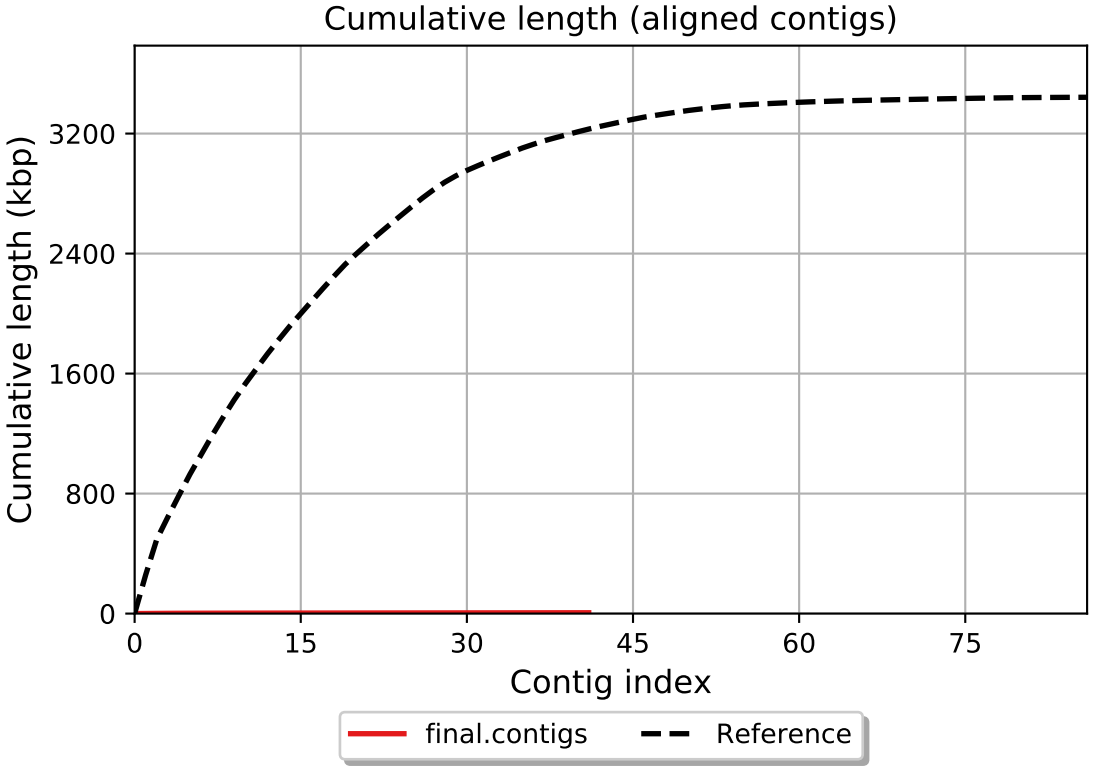

Cumulative length
Cumulative length (kbp)
3200
2400
1600
800
0
0
15
30
45
60
75
Contig index
final.contigs
Reference

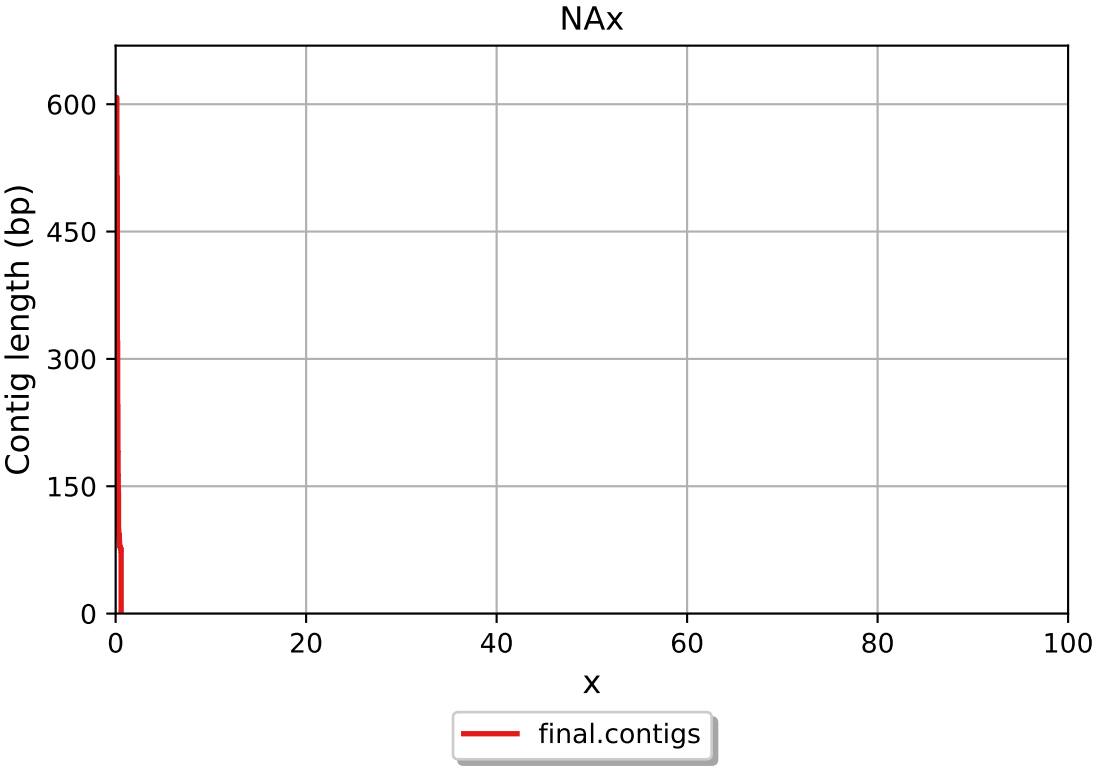

GC content
windows
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

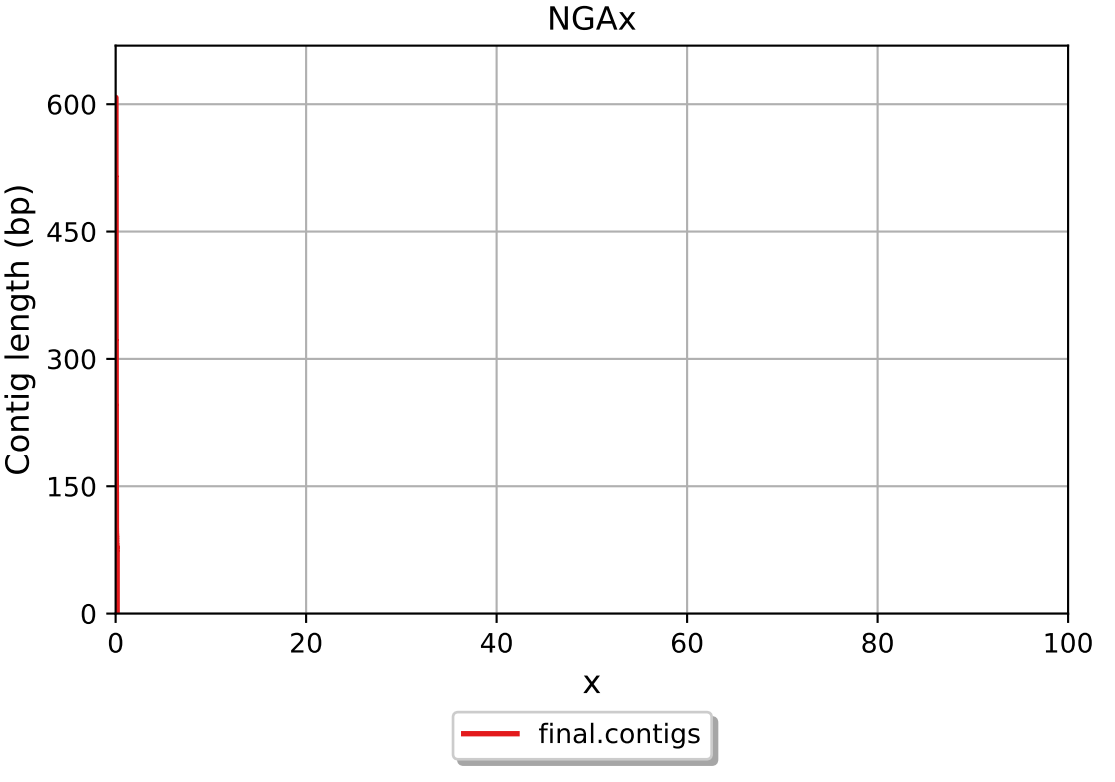

final.contigs GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
final.contigs


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 (kbp)
3200
2400
1600
800
0
0
15
30
45
60
75
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