Report

	final.contigs
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	63269
Total length (>= 5000 bp)	39648
Total length (>= 10000 bp)	39648
Total length (>= 25000 bp)	39648
Total length (>= 50000 bp)	0
# contigs	27
Largest contig	39648
Total length	74444
Reference length	3069626
GC (%)	48.24
Reference GC (%)	57.43
N50	39648
N75	1690
L50	1
L75	7
# 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	2
# unaligned contigs	2 + 14 part
Unaligned length	65307
Genome fraction (%)	0.076
Duplication ratio	3.921
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5579.40
# indels per 100 kbp	0.00
Largest alignment	506
Total aligned length	3783
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

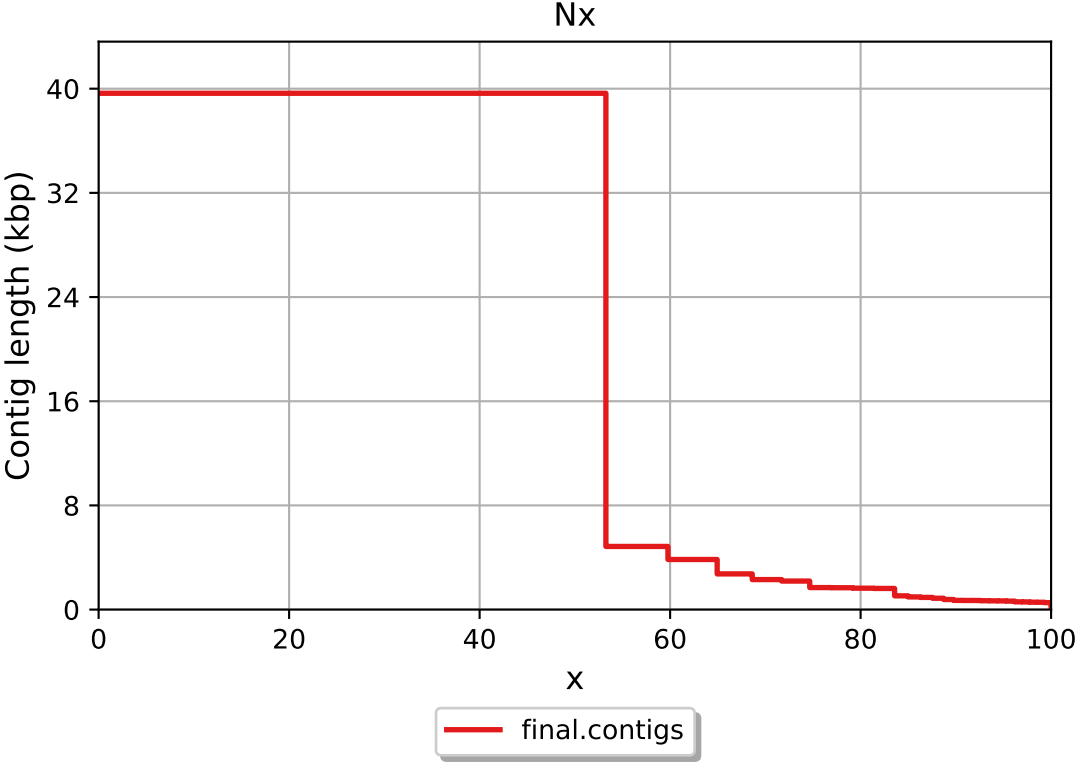
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	7
# possible misassemblies	10
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	130
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

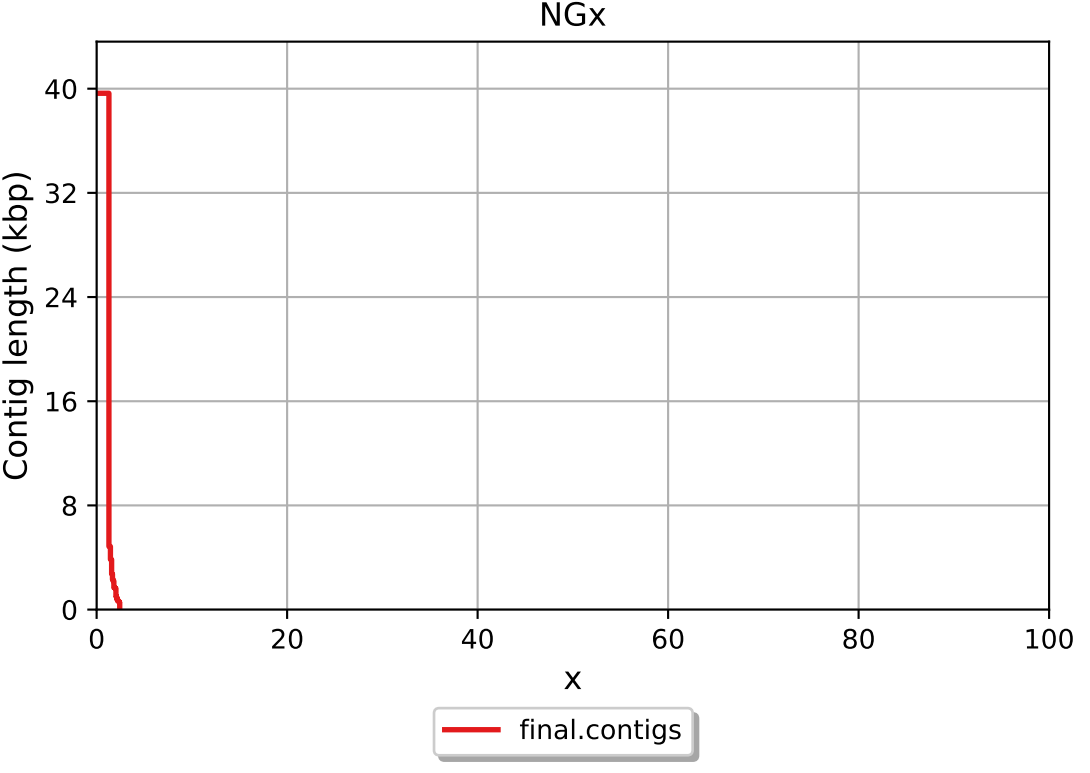
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

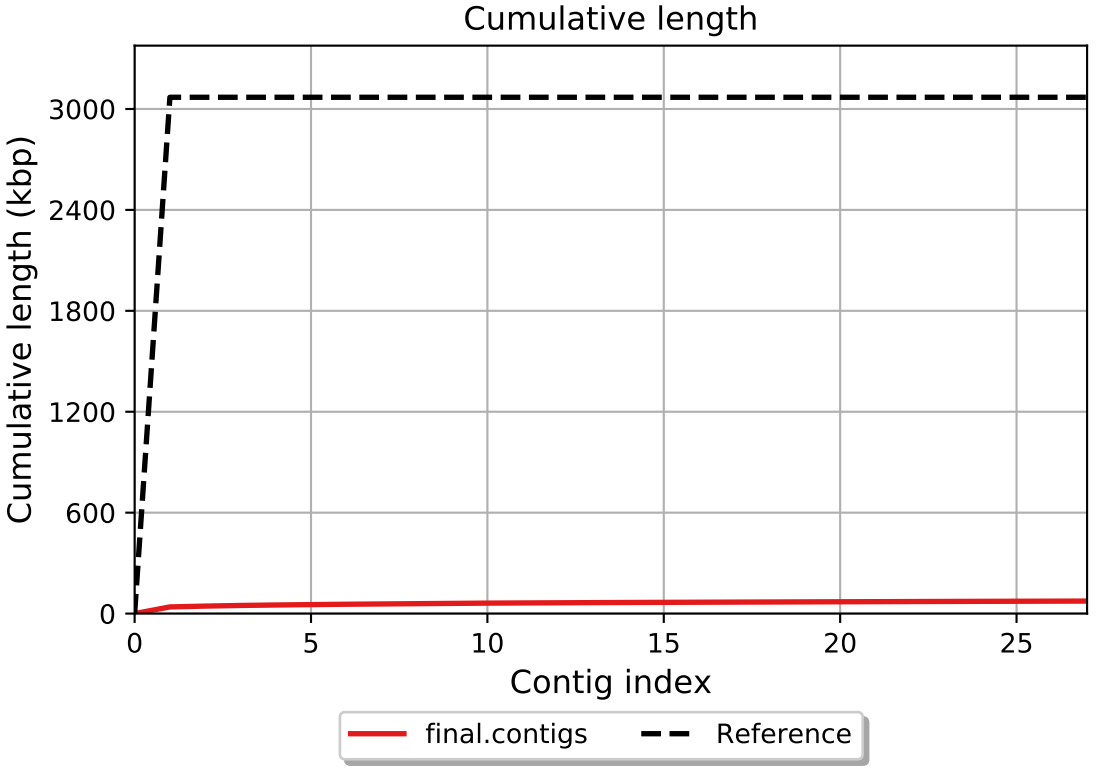
Unaligned report

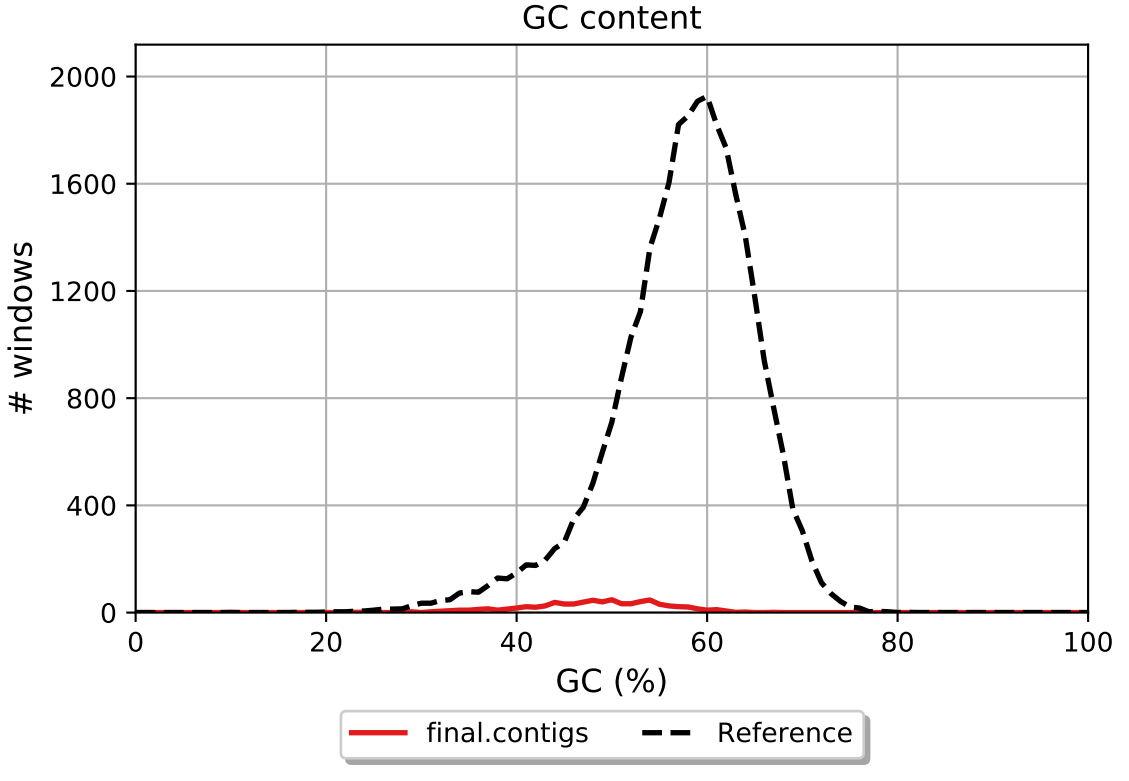
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1735
# partially unaligned contigs	14
Partially unaligned length	63572
# N's	0

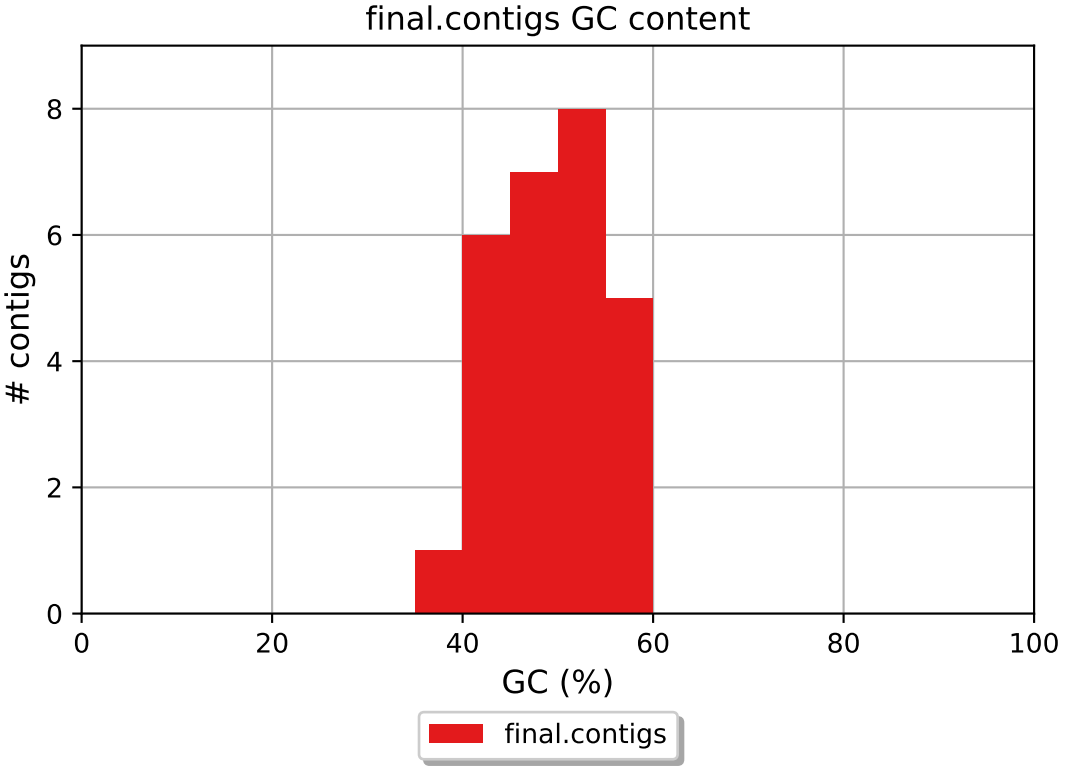
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

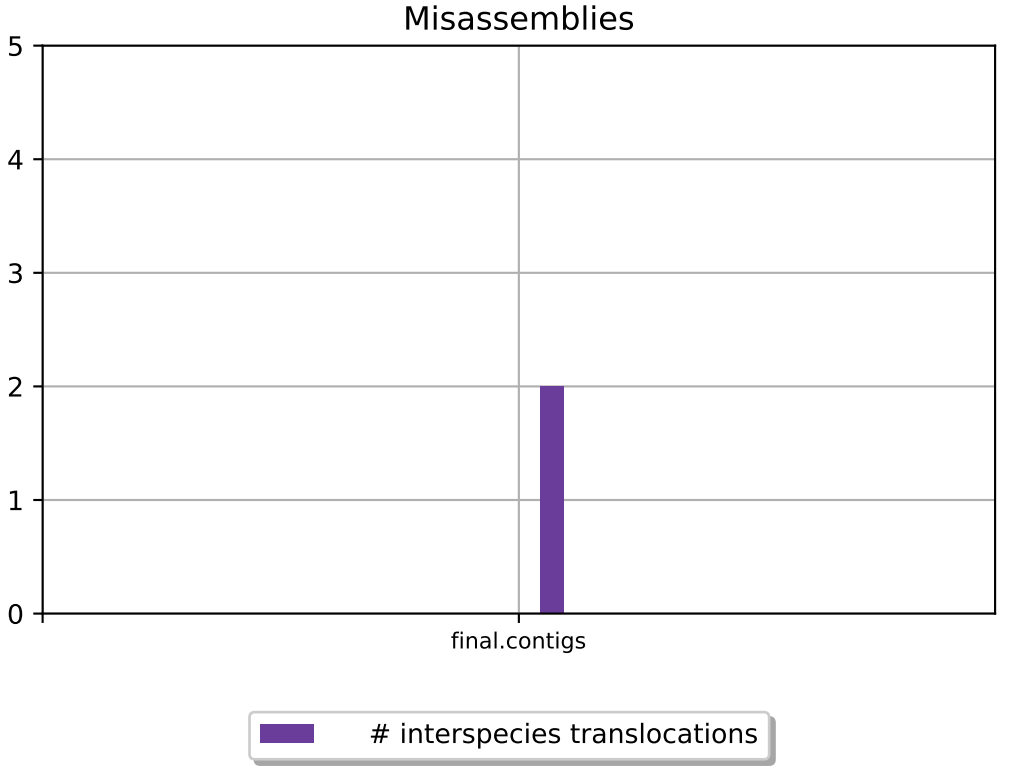

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs

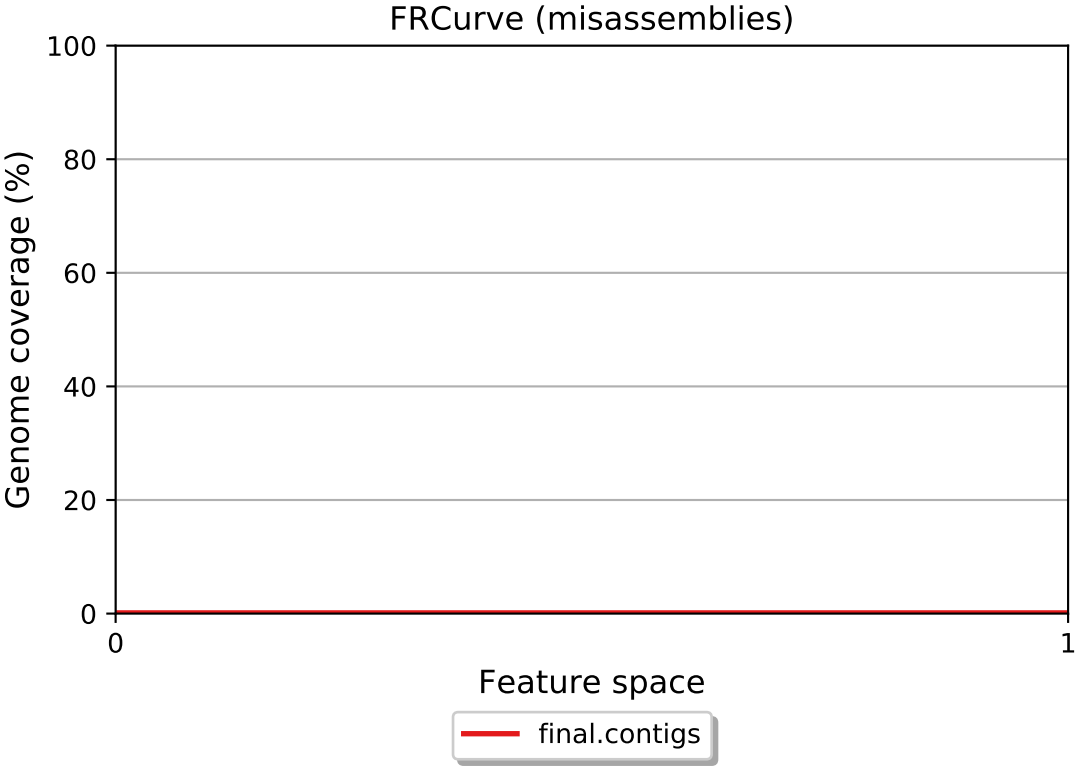

NGx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs

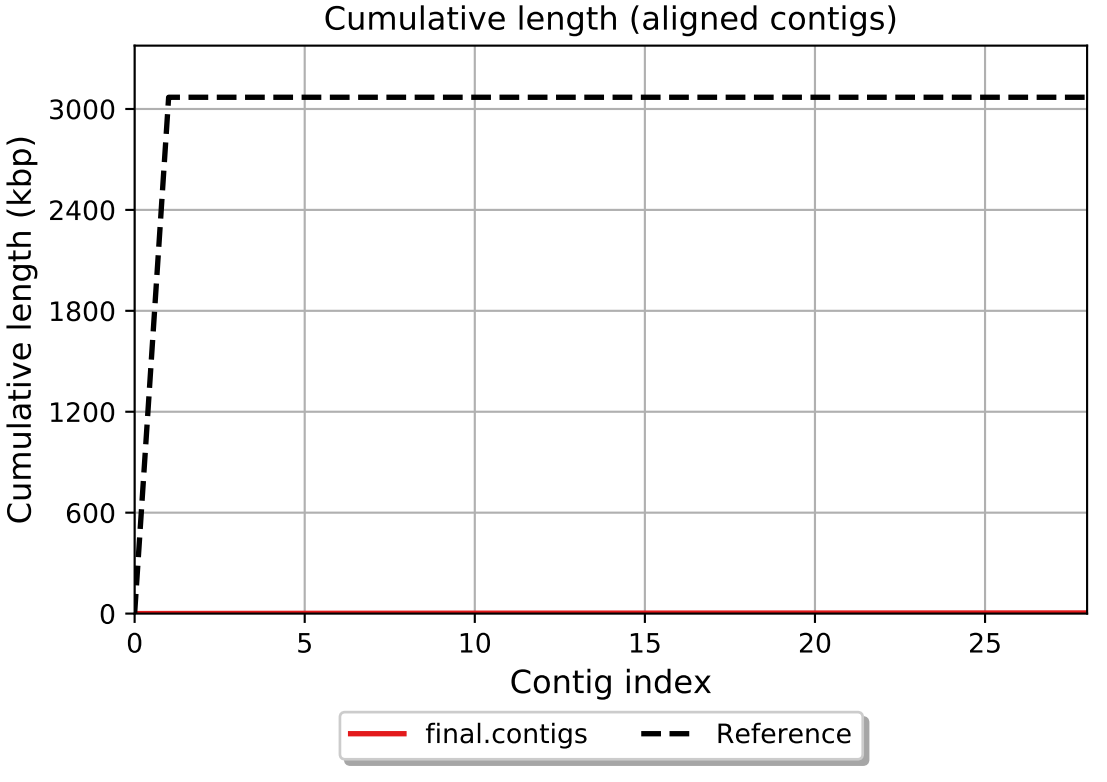

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
5
10
15
20
25
Contig index
final.contigs
Reference

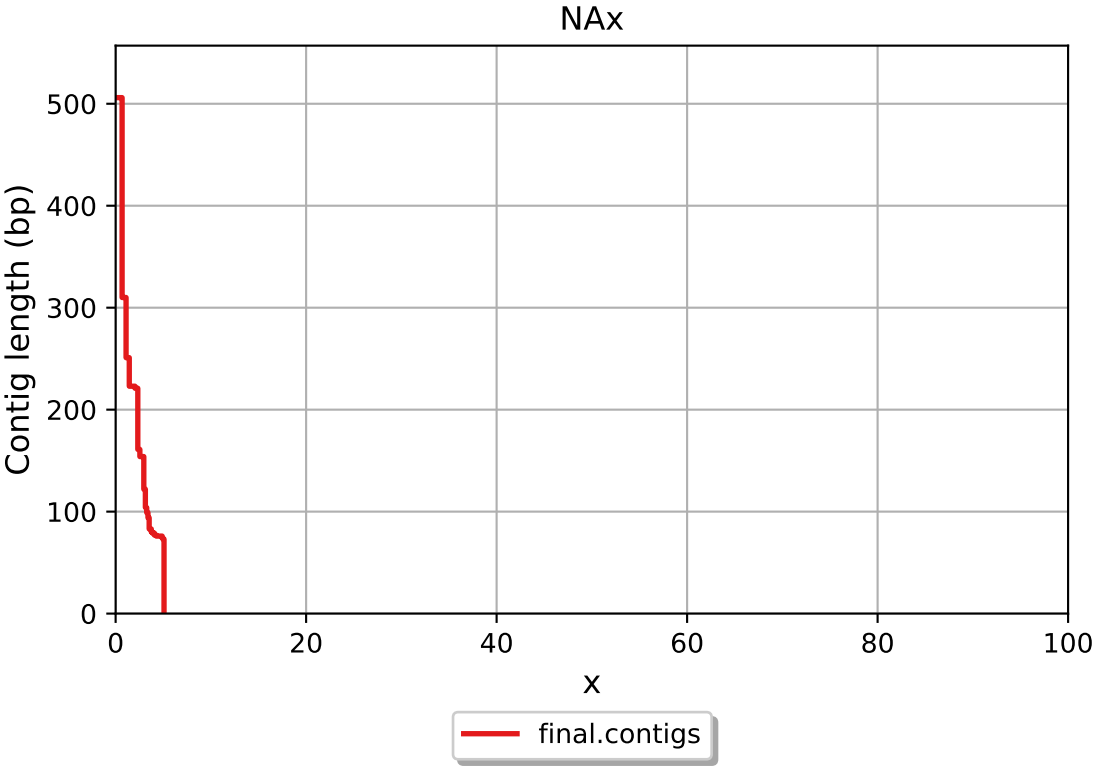

GC content
2000
1600
1200
800
400
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

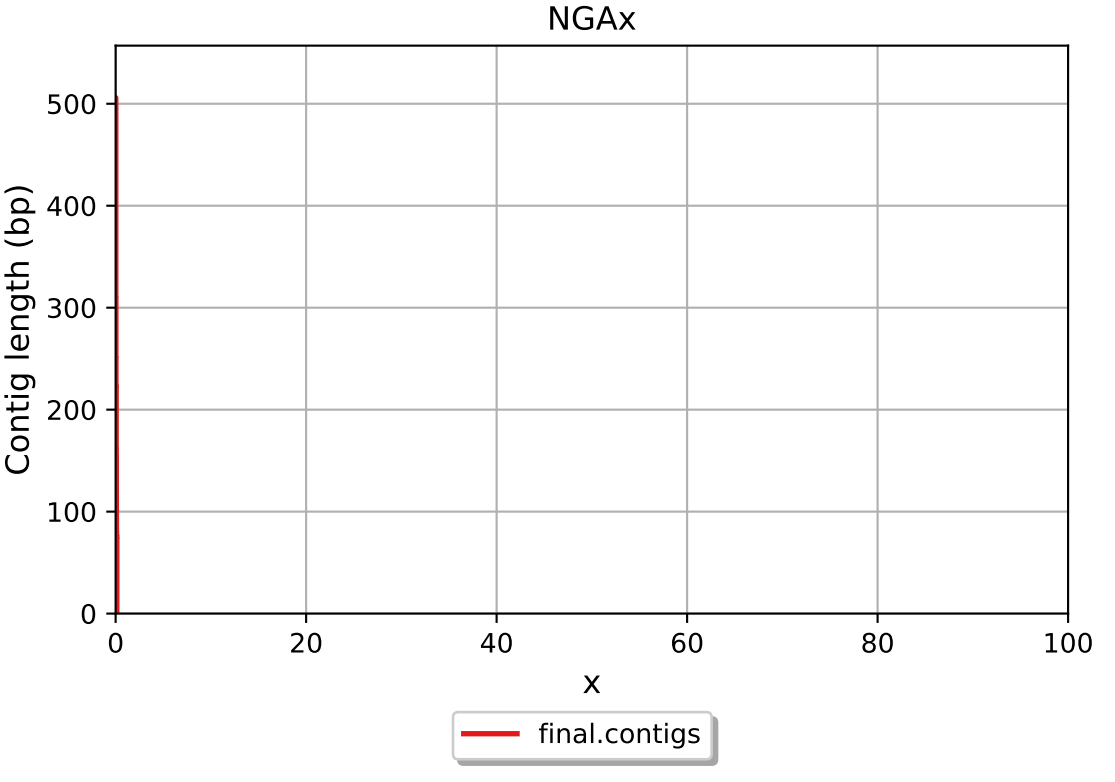

final.contigs GC content
contigs
0
2
4
6
8
0
20
40
60
80
100
GC (%)
final.contigs


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 (kbp)
3000
2400
1800
1200
600
0
0
5
10
15
20
25
Contig index
final.contigs
Reference


NAx
Contig length (bp)
500
400
300
200
100
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
500
400
300
200
100
0
0
20
40
60
80
100
x
final.contigs