Report

	final.contigs
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	37222
Total length (>= 5000 bp)	19114
Total length (>= 10000 bp)	13792
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	21
Largest contig	13792
Total length	45534
Reference length	2077614
GC (%)	47.22
Reference GC (%)	39.47
N50	4587
N75	1238
L50	3
L75	7
# 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	3
# unaligned contigs	3 + 11 part
Unaligned length	39804
Genome fraction (%)	0.098
Duplication ratio	2.809
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4166.67
# indels per 100 kbp	539.22
Largest alignment	558
Total aligned length	3168
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

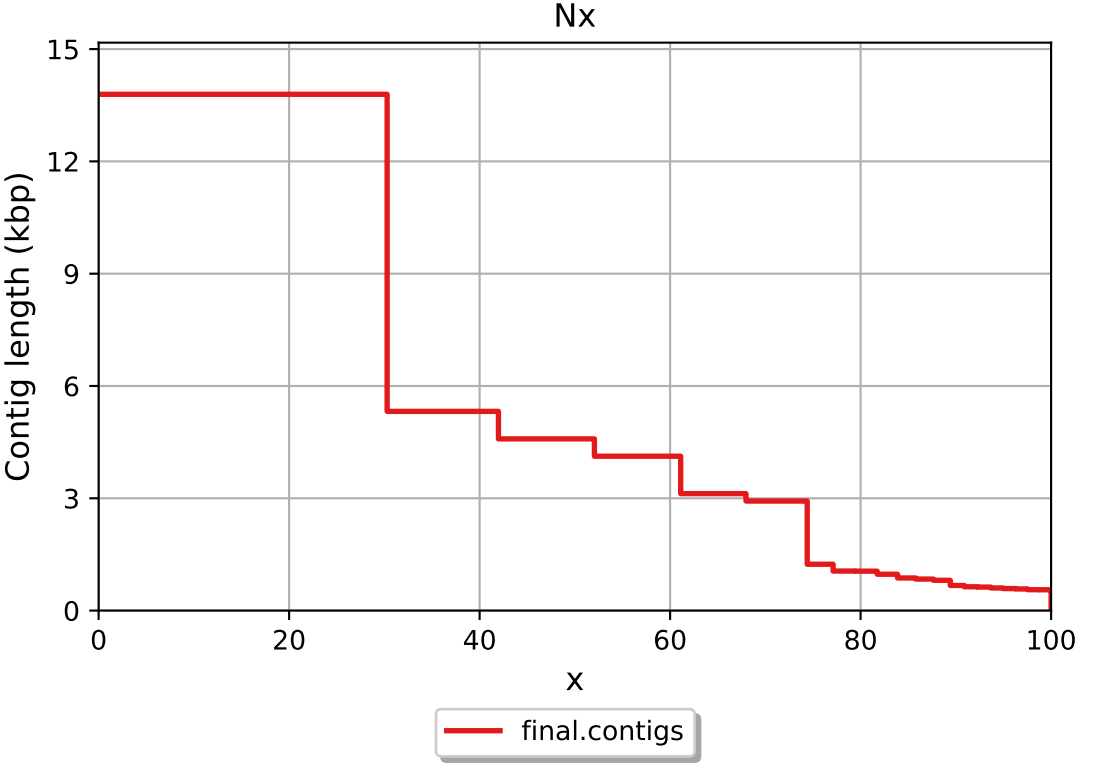
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	7
# possible misassemblies	11
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	85
# indels	11
# indels (<= 5 bp)	11
# indels (> 5 bp)	0
Indels length	12

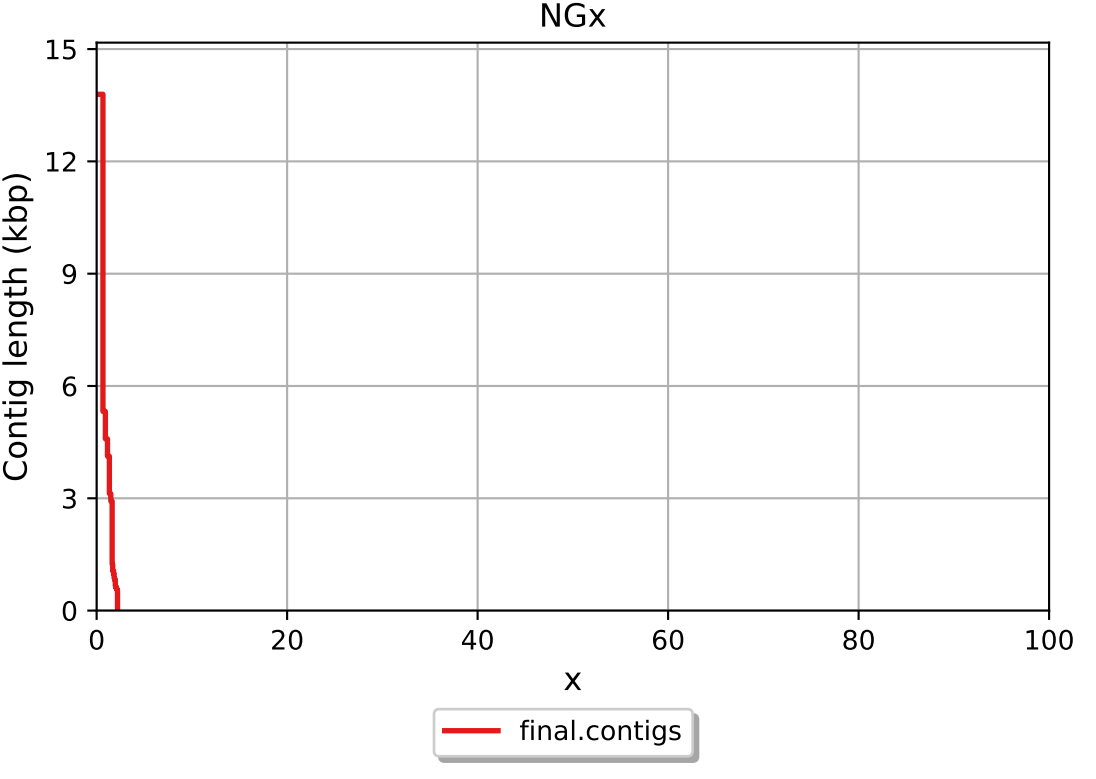
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

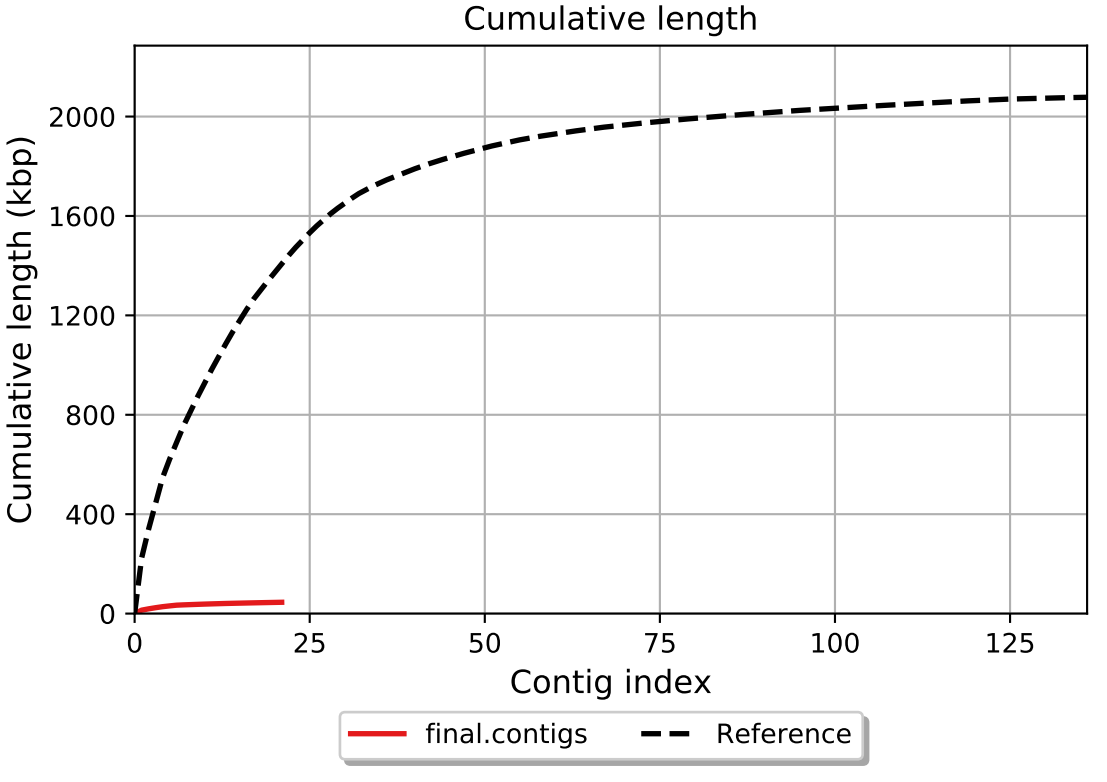
Unaligned report

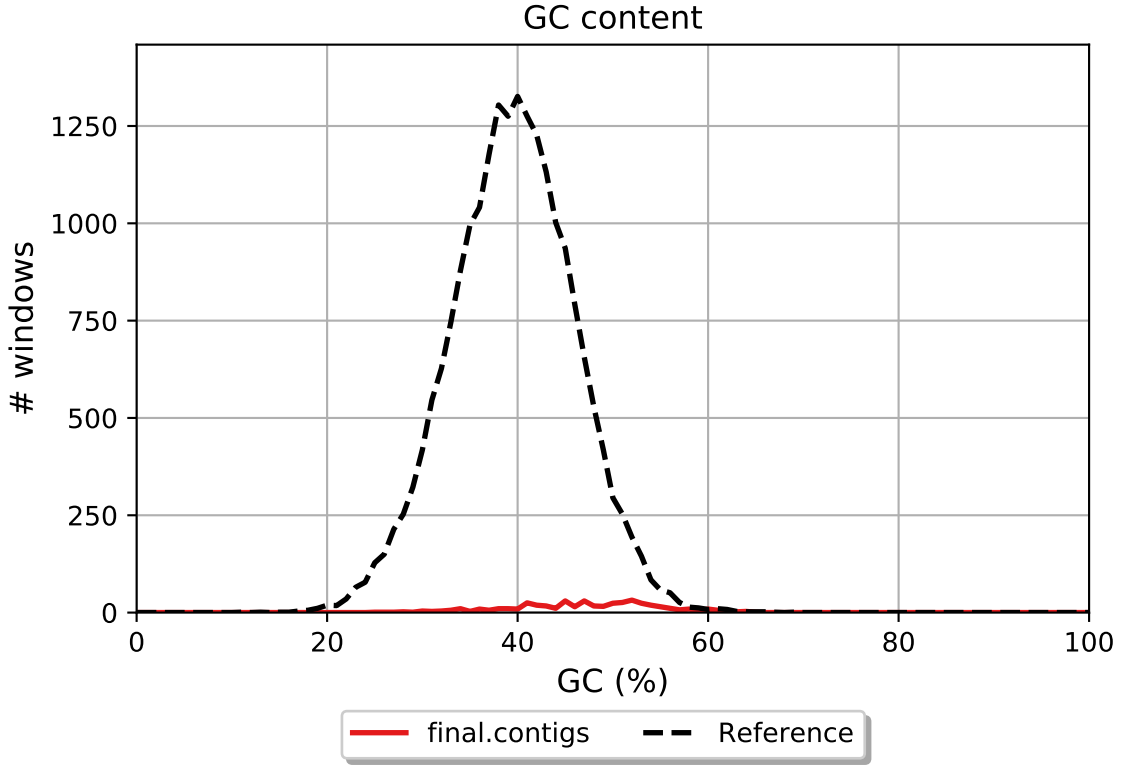
	final.contigs
# fully unaligned contigs	3
Fully unaligned length	2272
# partially unaligned contigs	11
Partially unaligned length	37532
# N's	0

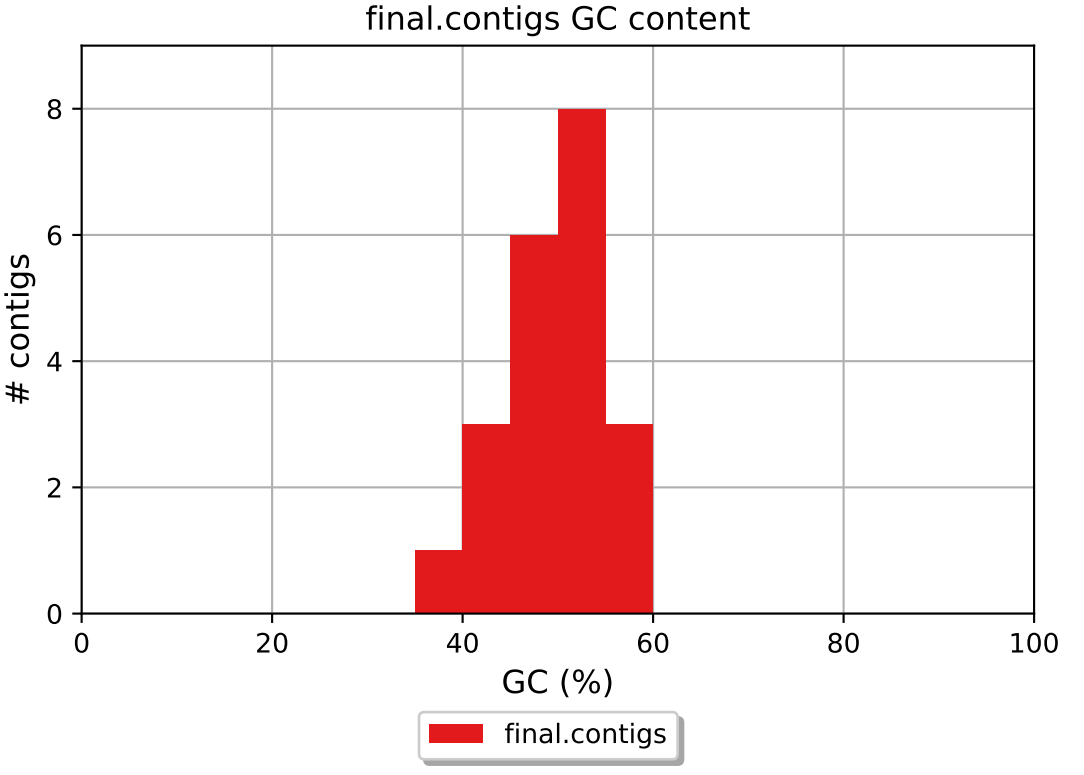
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

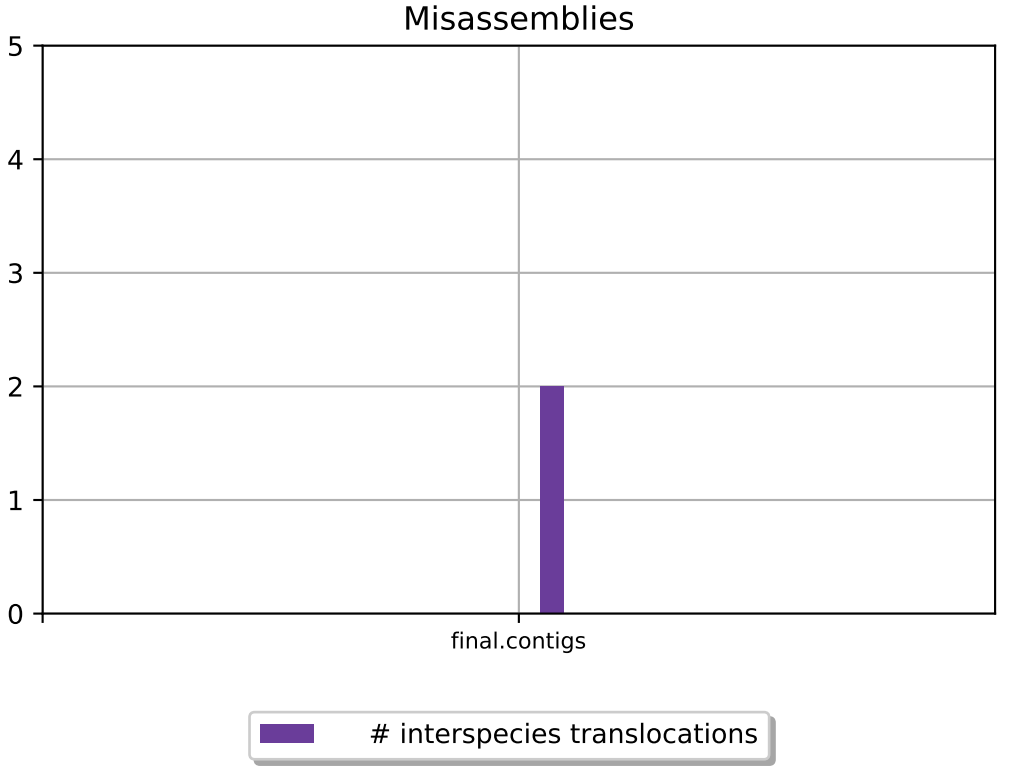

Nx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

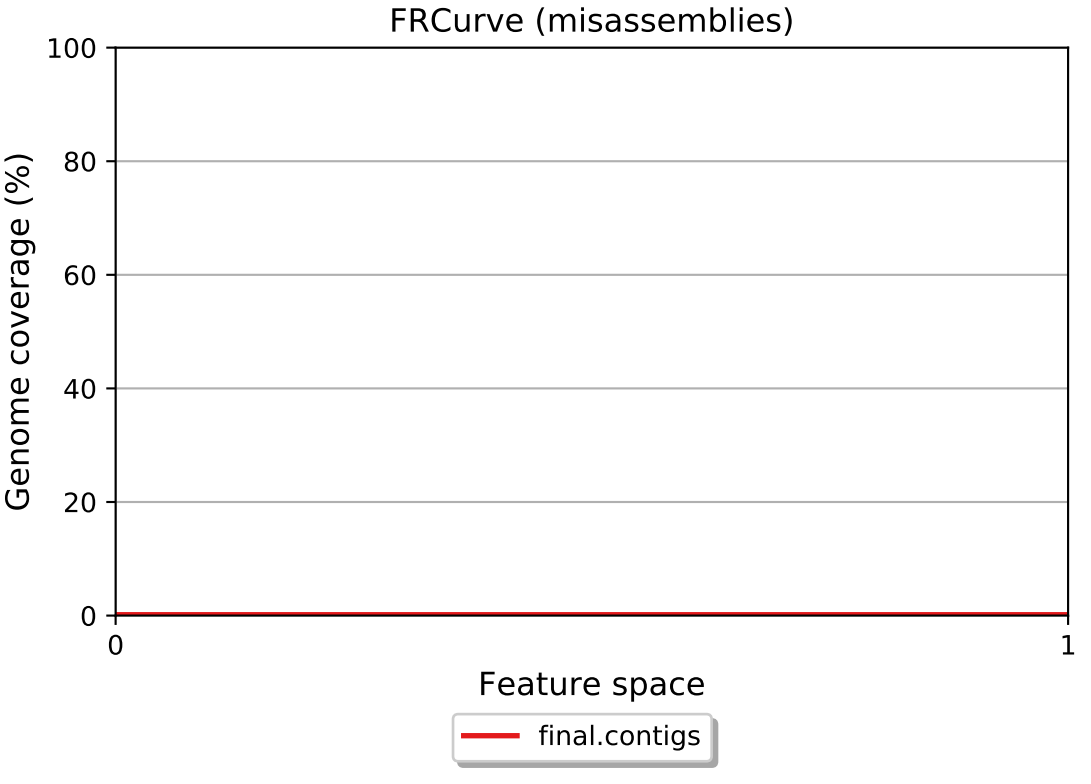

NGx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

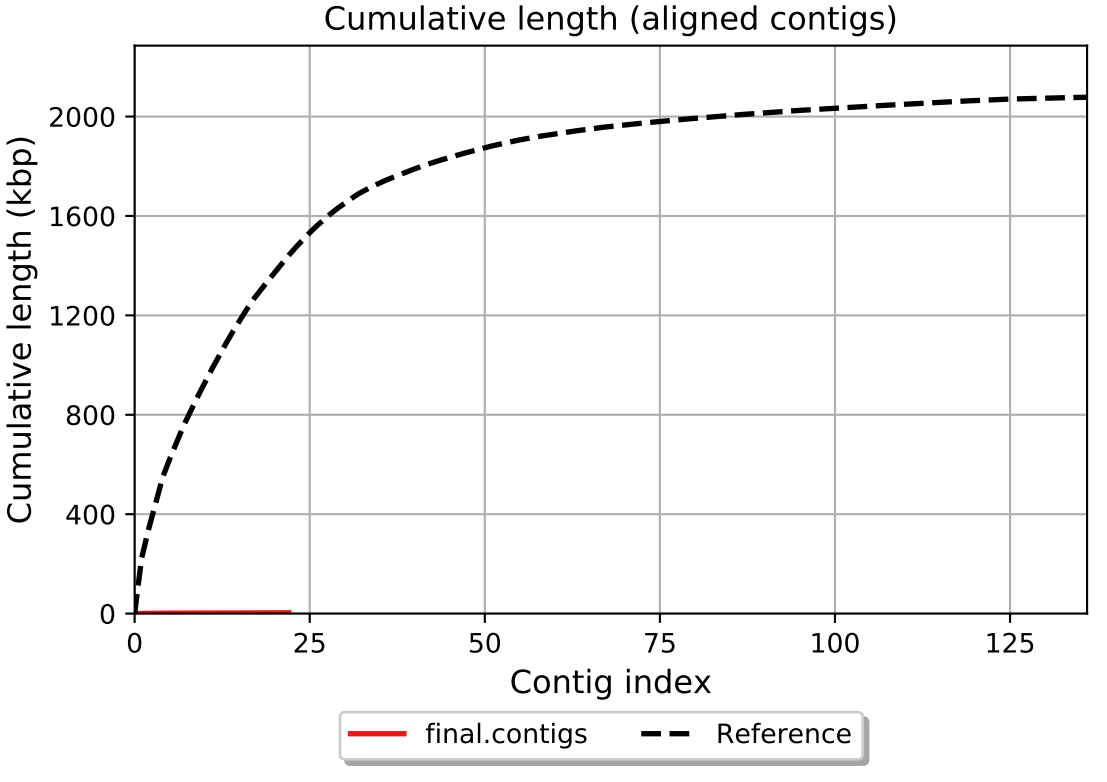

Cumulative length
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
25
50
75
100
125
Contig index
final.contigs
Reference

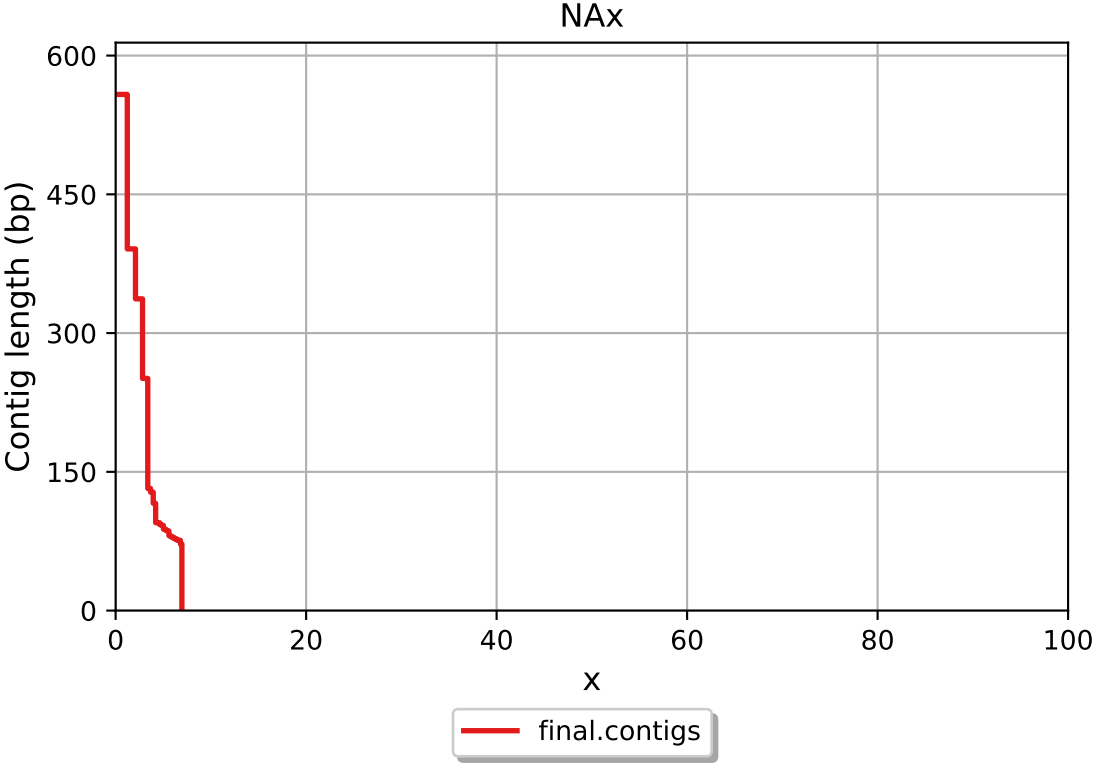

GC content
windows
1250
1000
750
500
250
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

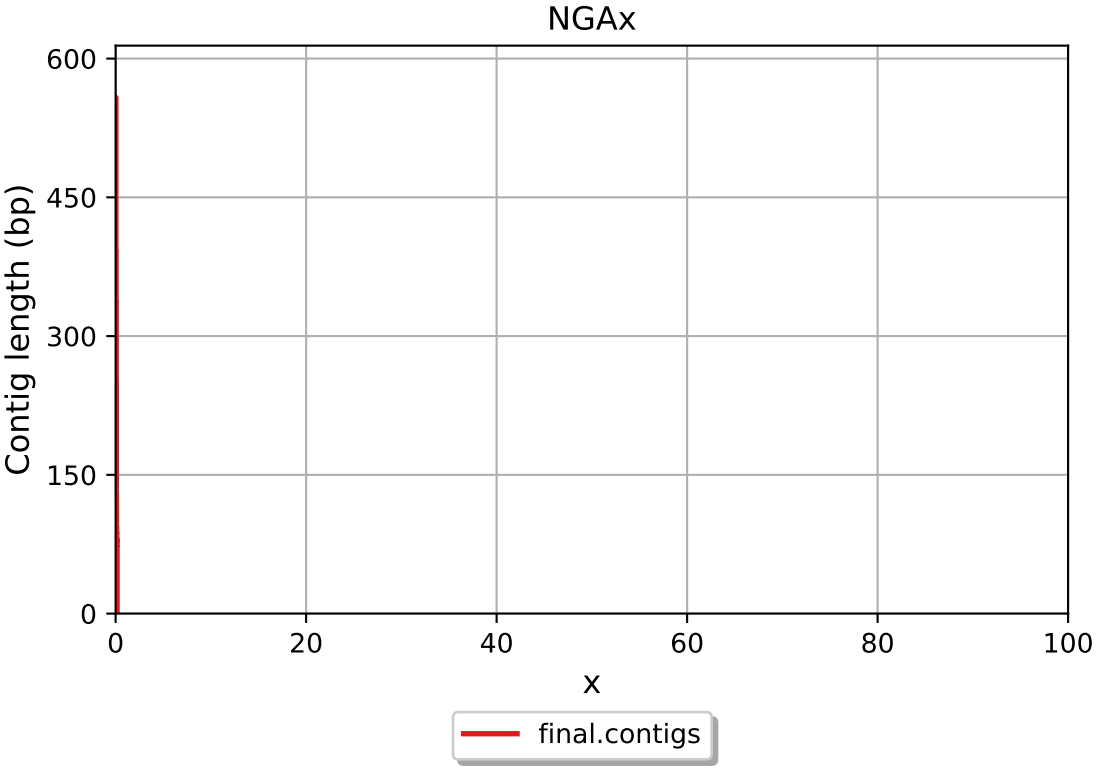

final.contigs GC content
contigs
0
2
4
6
8
0
20
40
60
80
100
GC (%)
final.contigs


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


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
25
50
75
100
125
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