Report

	final.contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	117721
Total length (>= 5000 bp)	109736
Total length (>= 10000 bp)	109736
Total length (>= 25000 bp)	109736
Total length (>= 50000 bp)	109736
# contigs	19
Largest contig	56925
Total length	125204
Reference length	3691014
GC (%)	58.44
Reference GC (%)	66.65
N50	52811
N75	52811
L50	2
L75	2
# 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	3
# unaligned contigs	5 + 9 part
Unaligned length	120730
Genome fraction (%)	0.066
Duplication ratio	1.849
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3388.43
# indels per 100 kbp	0.00
Largest alignment	513
Total aligned length	3070
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

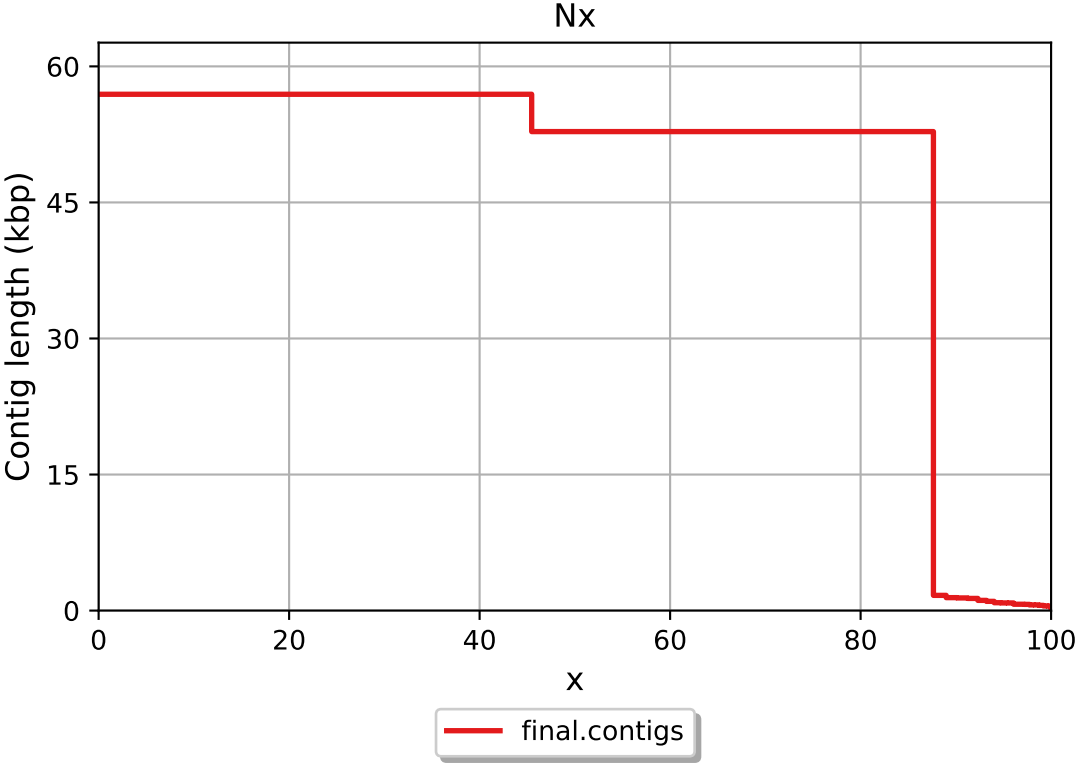
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	6
# possible misassemblies	6
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	82
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

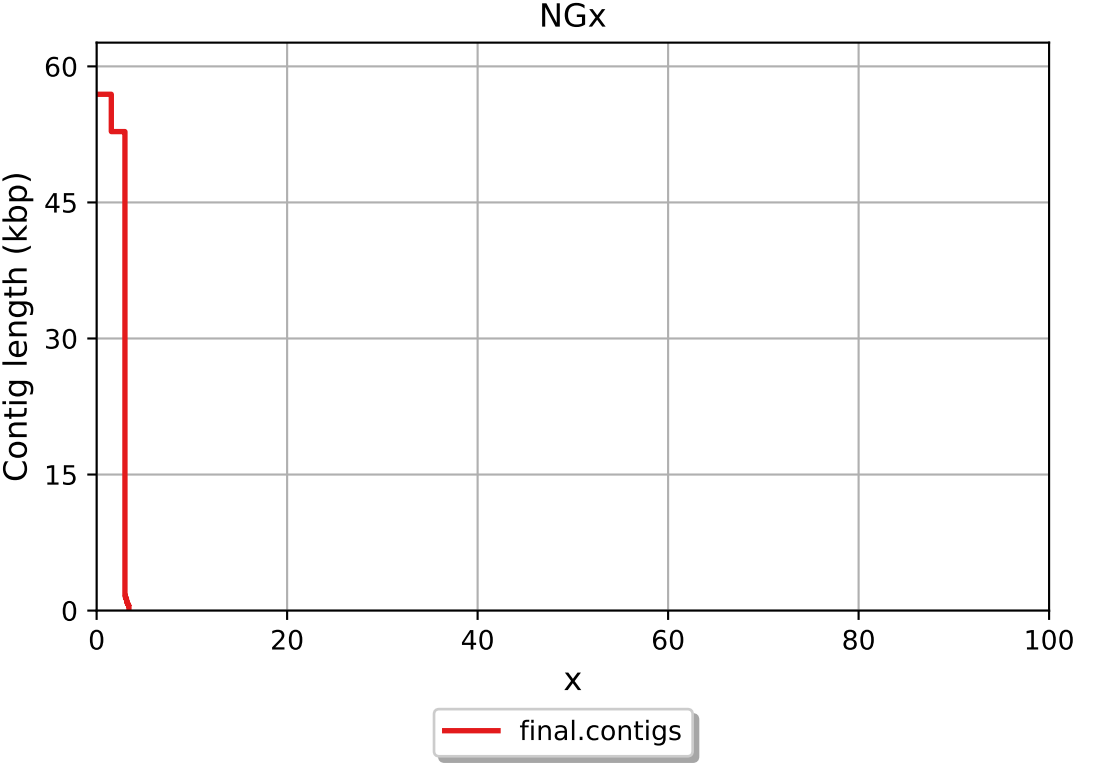
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

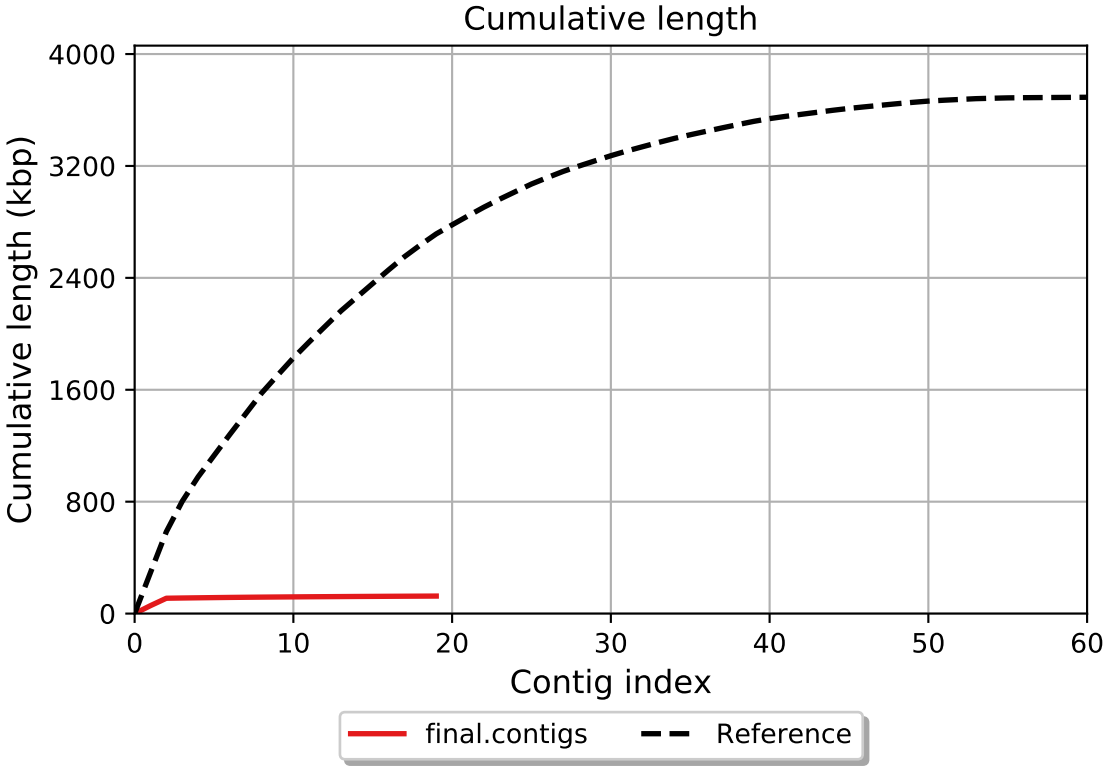
Unaligned report

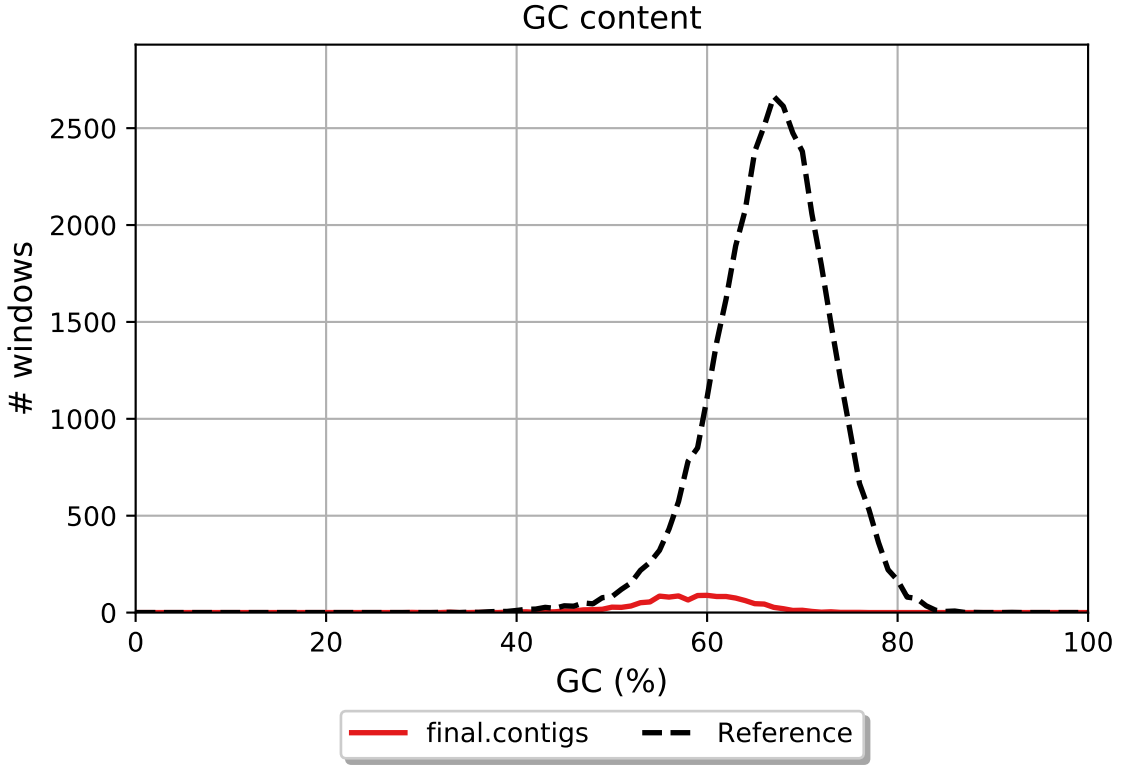
	final.contigs
# fully unaligned contigs	5
Fully unaligned length	4367
# partially unaligned contigs	9
Partially unaligned length	116363
# N's	0

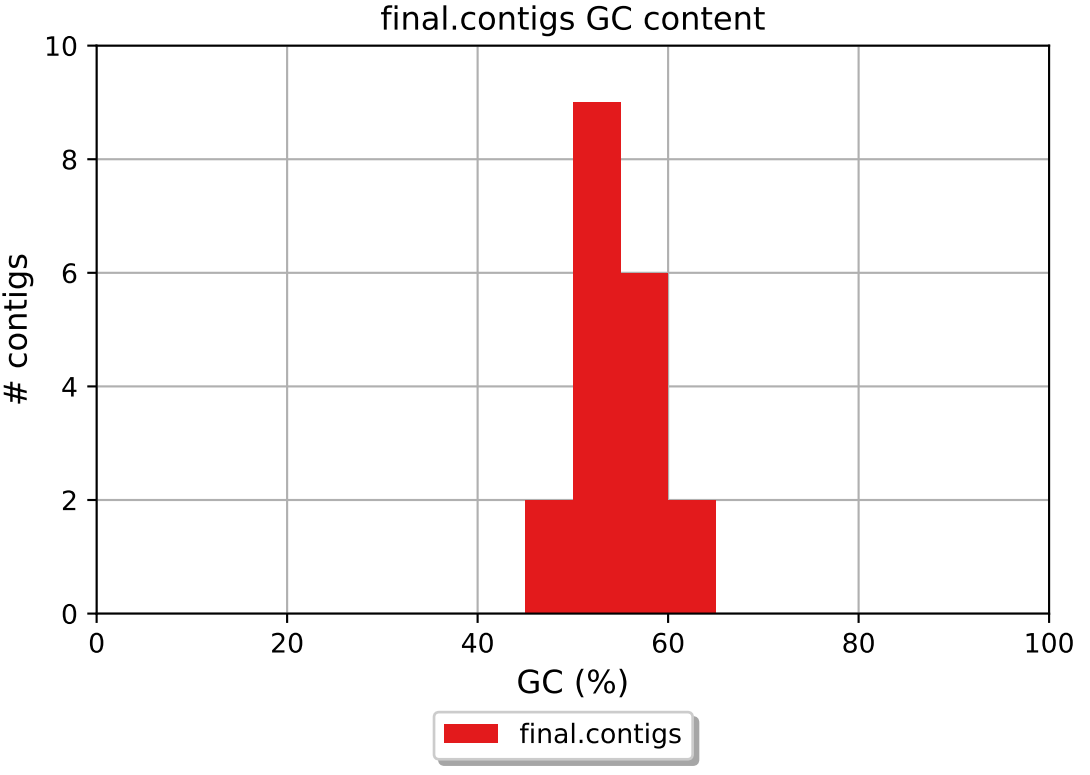
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

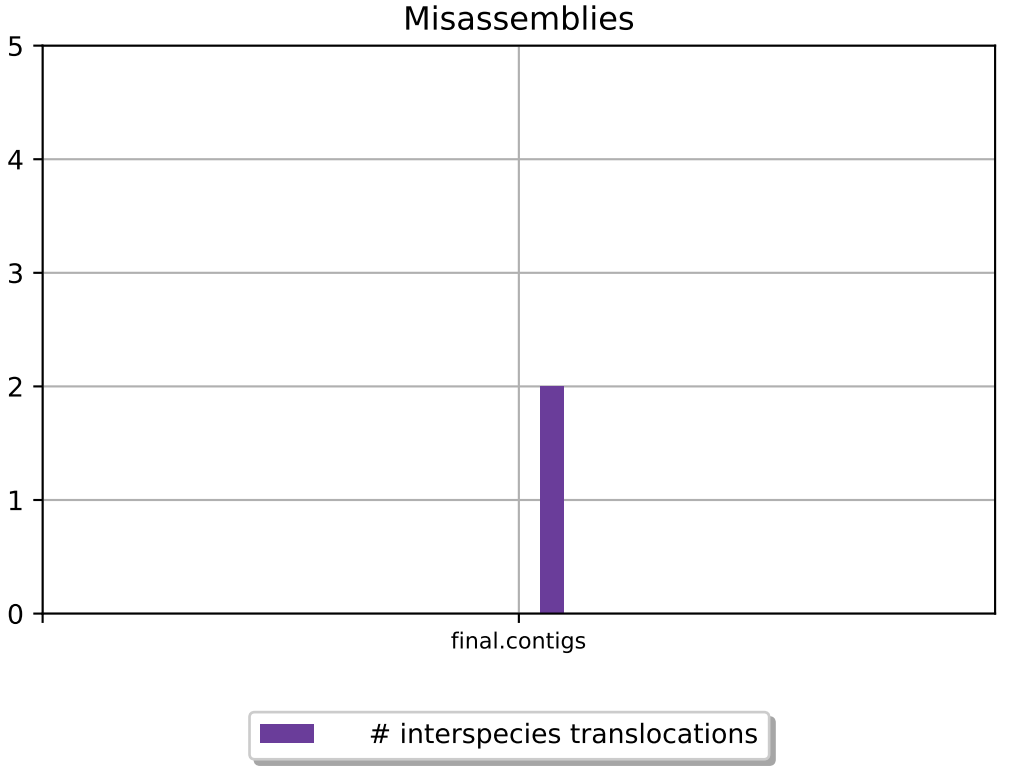

Nx
Contig length (kbp)
60
45
30
15
0
0
20
40
60
80
100
x
final.contigs

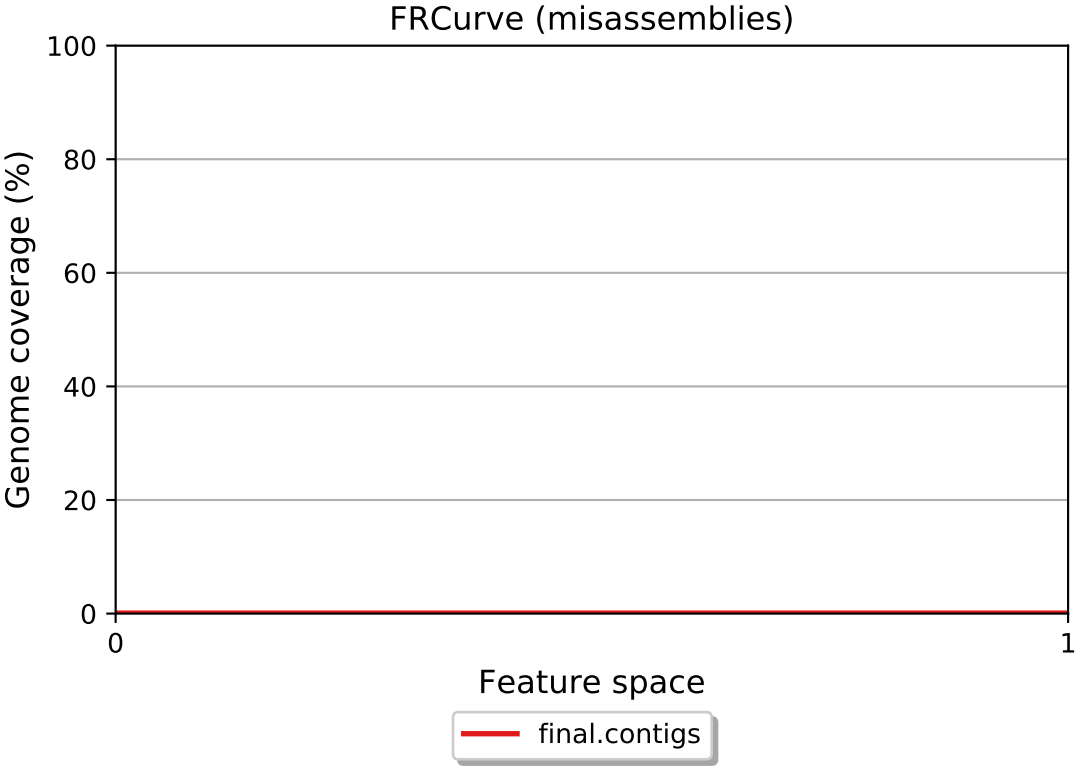

NGx
Contig length (kbp)
60
45
30
15
0
0
20
40
60
80
100
x
final.contigs

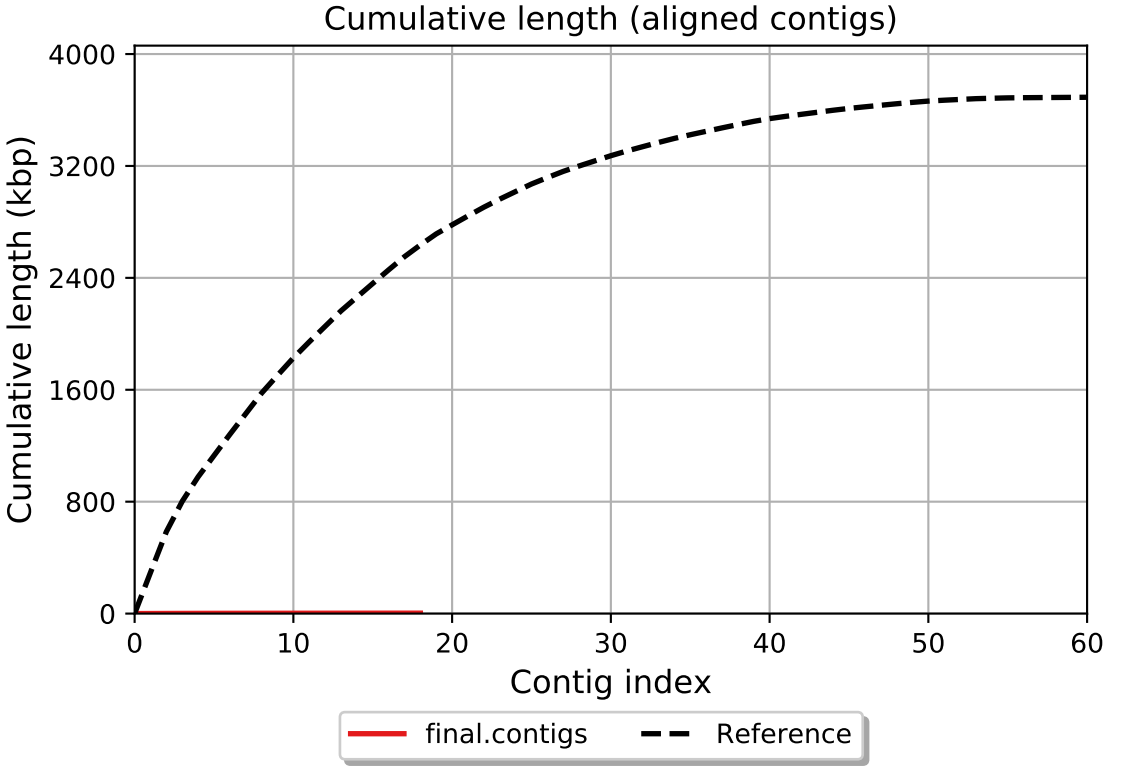

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
10
20
30
40
50
60
Contig index
final.contigs
Reference

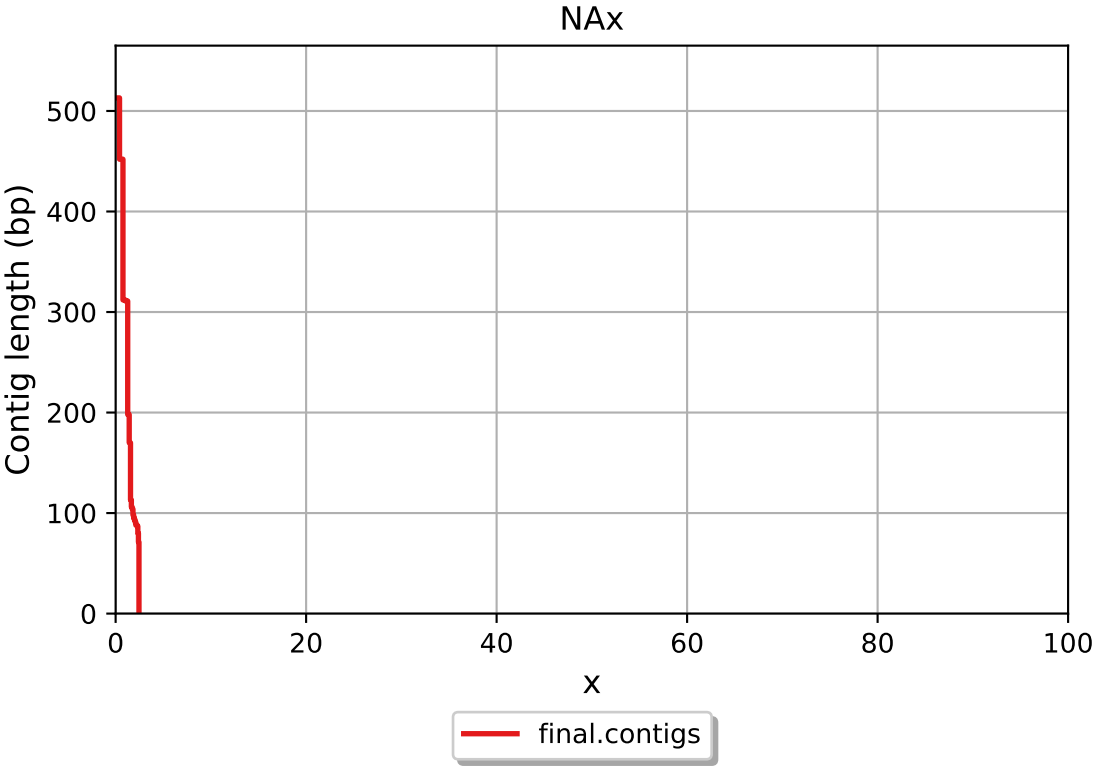

GC content
windows
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

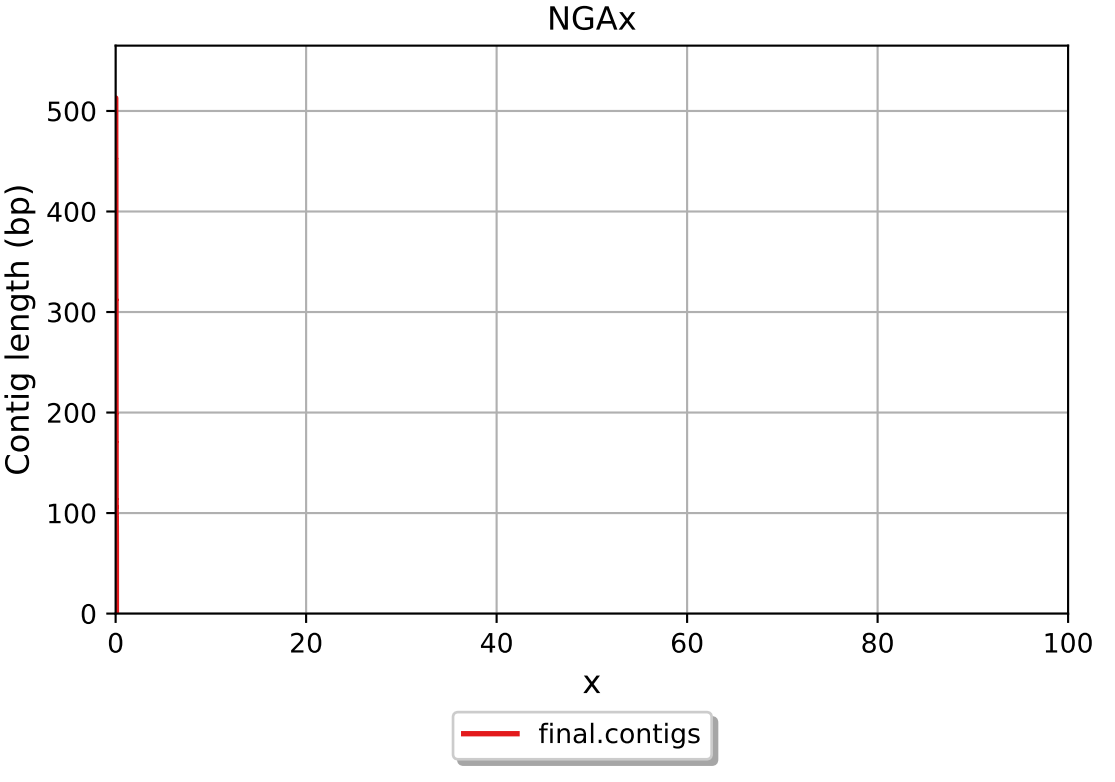

final.contigs GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
final.contigs


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)
4000
3200
2400
1600
800
0
0
10
20
30
40
50
60
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)
0
100
200
300
400
500
0
20
40
60
80
100
x
final.contigs