Report

	final.contigs
# contigs (>= 1000 bp)	14
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	4
Total length (>= 1000 bp)	503230
Total length (>= 5000 bp)	481269
Total length (>= 10000 bp)	481269
Total length (>= 25000 bp)	481269
Total length (>= 50000 bp)	481269
# contigs	27
Largest contig	172953
Total length	513054
Reference length	3299615
GC (%)	59.73
Reference GC (%)	63.89
N50	134279
N75	87077
L50	2
L75	3
# 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	4
# unaligned contigs	1 + 20 part
Unaligned length	506277
Genome fraction (%)	0.070
Duplication ratio	2.941
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4904.51
# indels per 100 kbp	86.81
Largest alignment	284
Total aligned length	3600
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

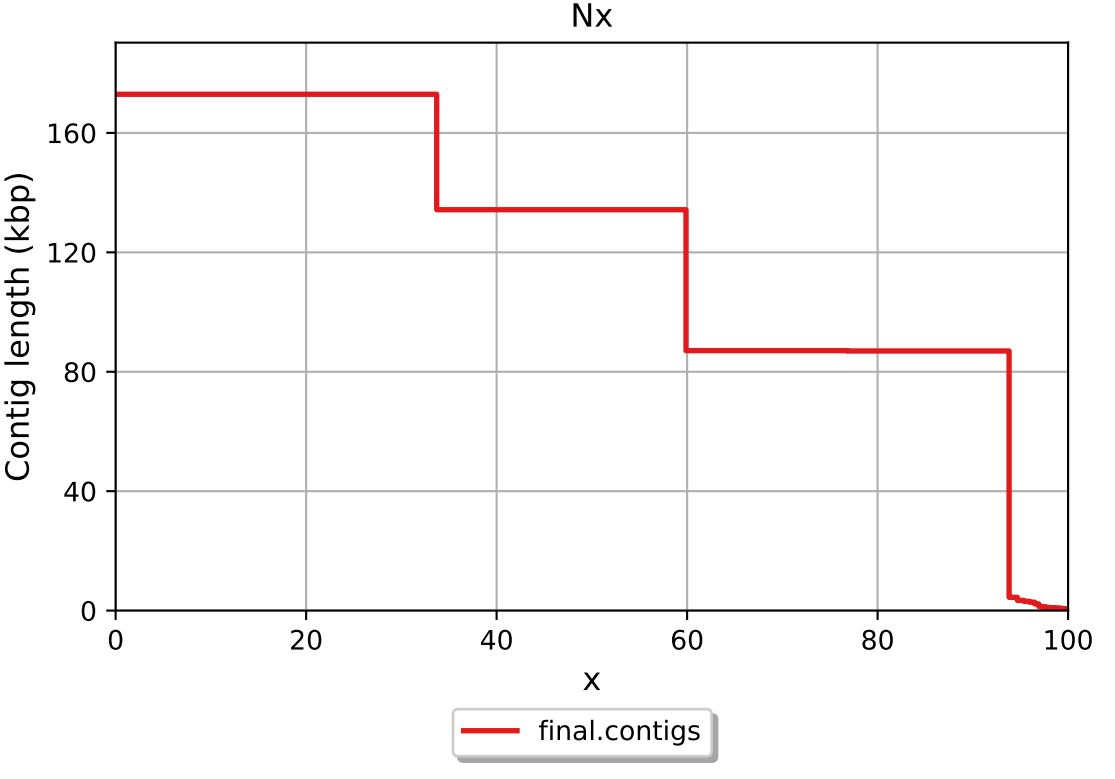
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	9
# possible misassemblies	15
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	113
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

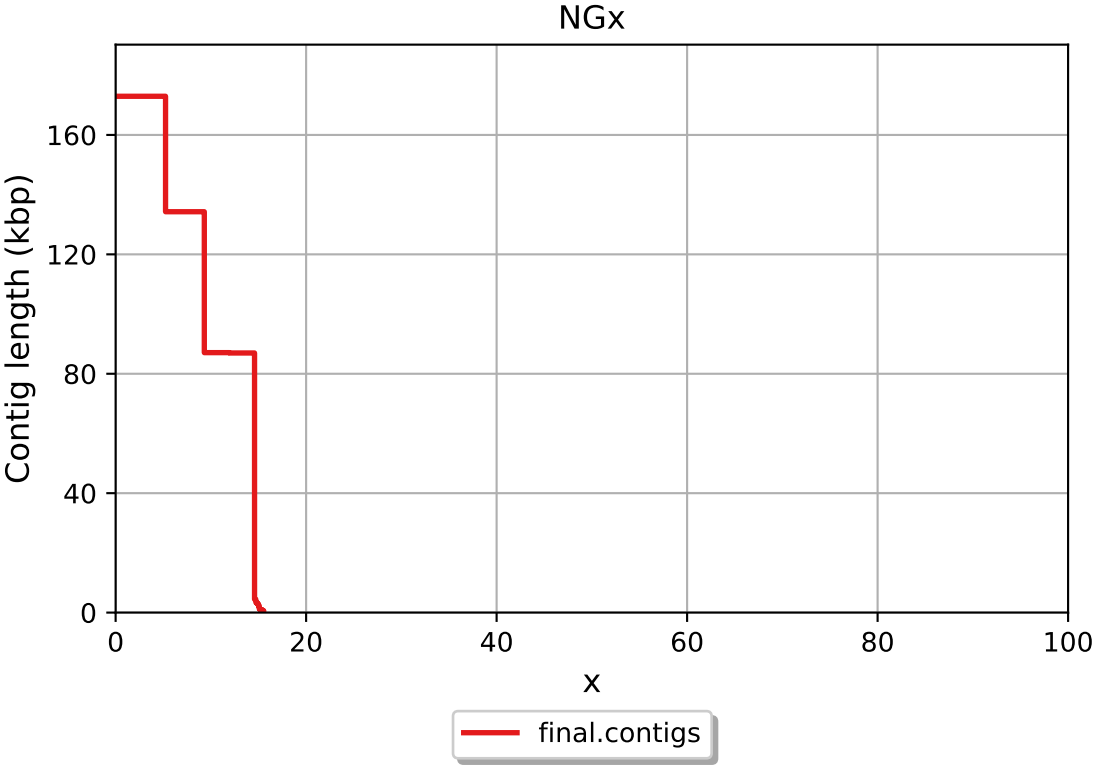
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

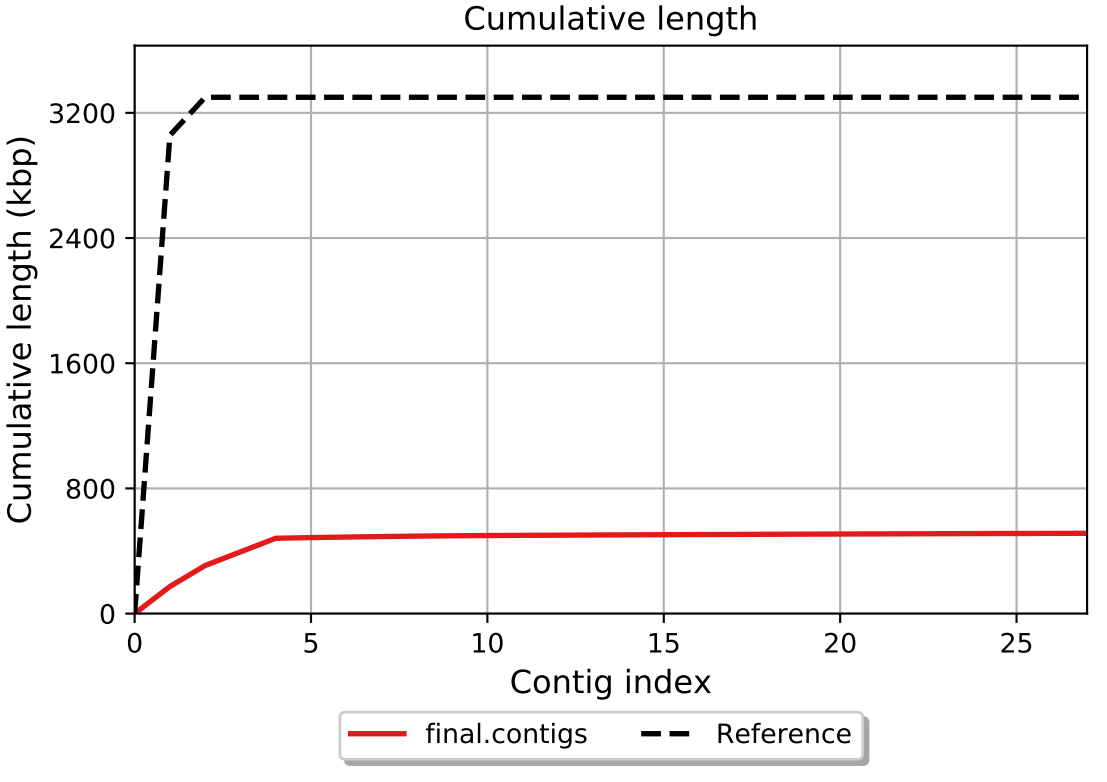
Unaligned report

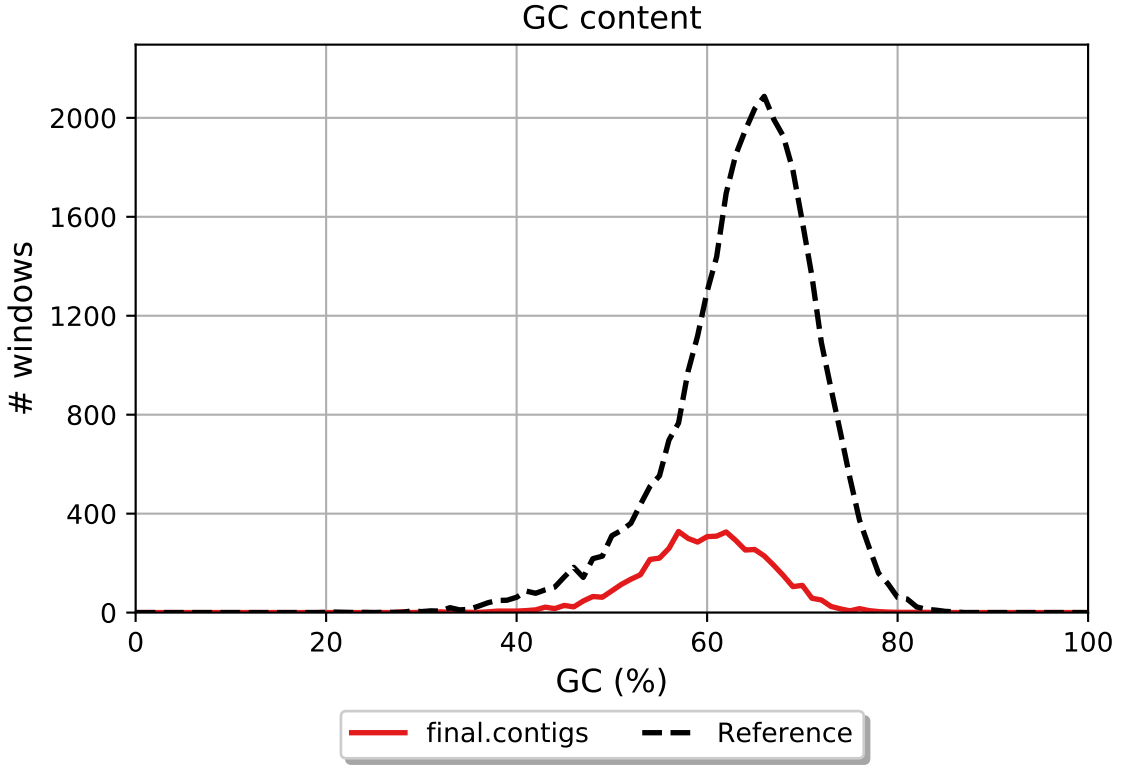
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	691
# partially unaligned contigs	20
Partially unaligned length	505586
# N's	0

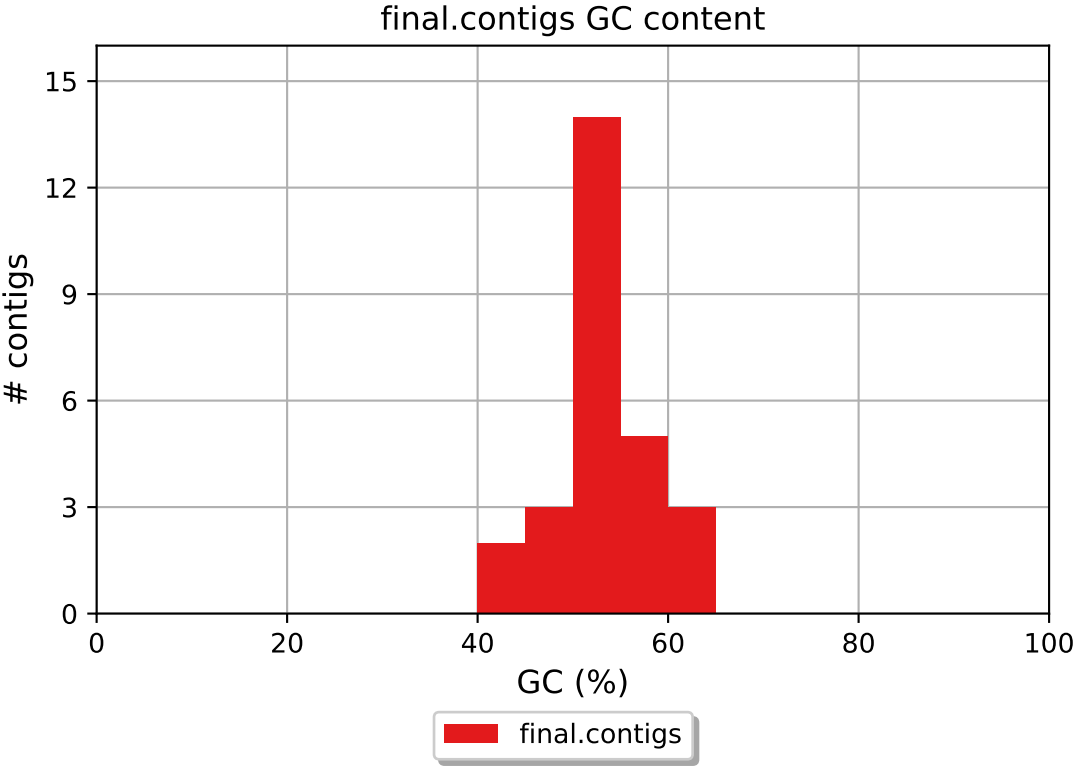
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

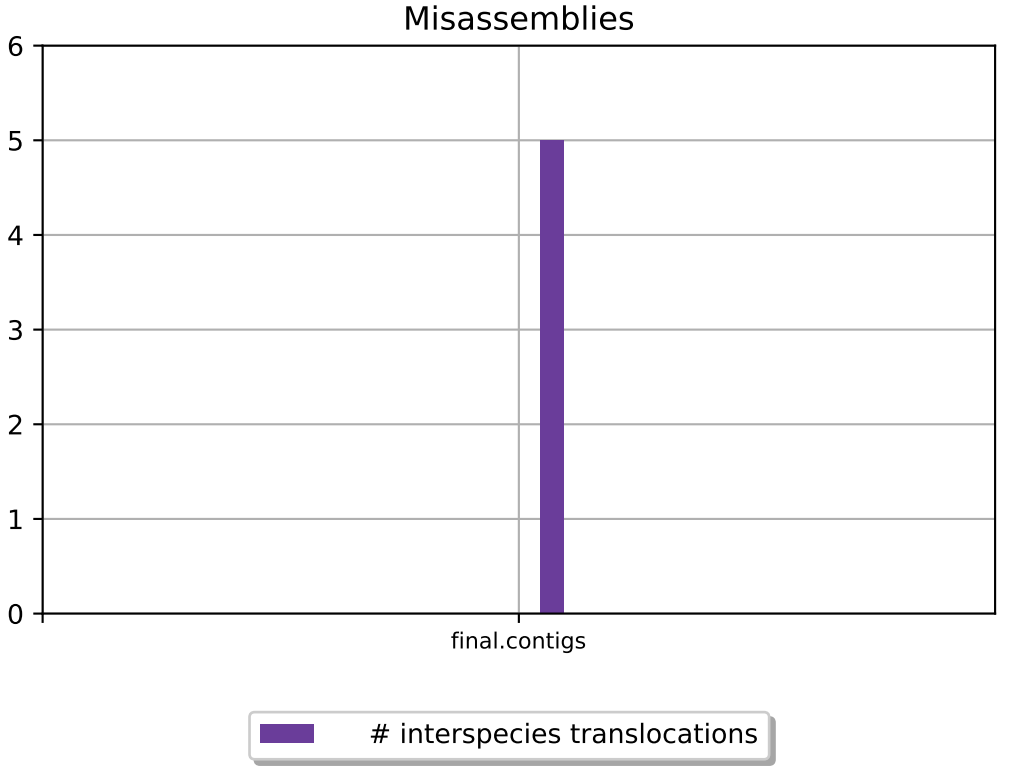

Nx
Contig length (kbp)
160
120
80
40
0
0
20
40
60
80
100
x
final.contigs

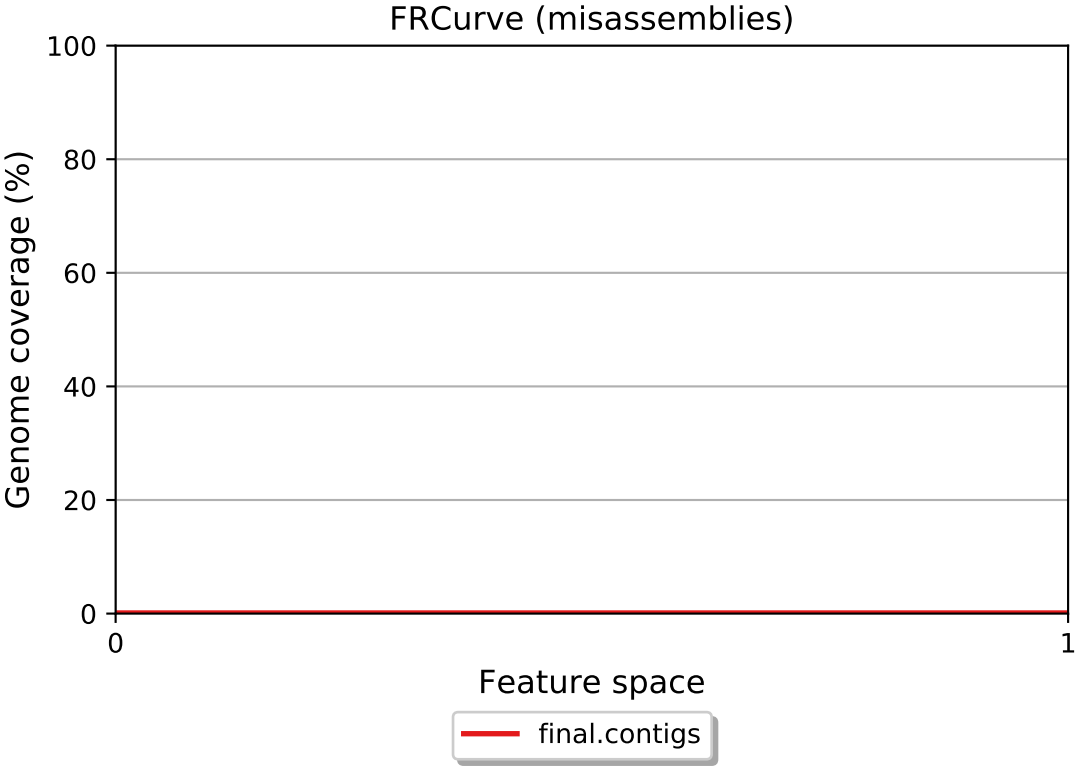

NGx
Contig length (kbp)
160
120
80
40
0
0
20
40
60
80
100
x
final.contigs

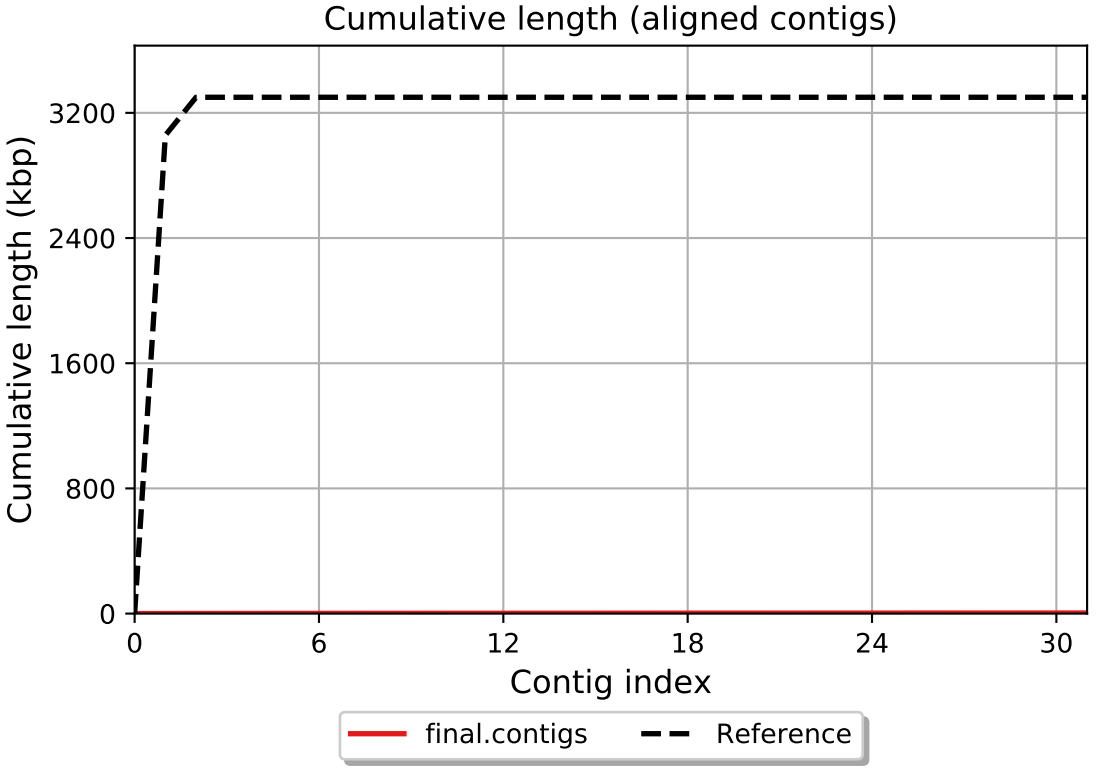

Cumulative length
Cumulative length (kbp)
3200
2400
1600
800
0
0
5
10
15
20
25
Contig index
final.contigs
Reference

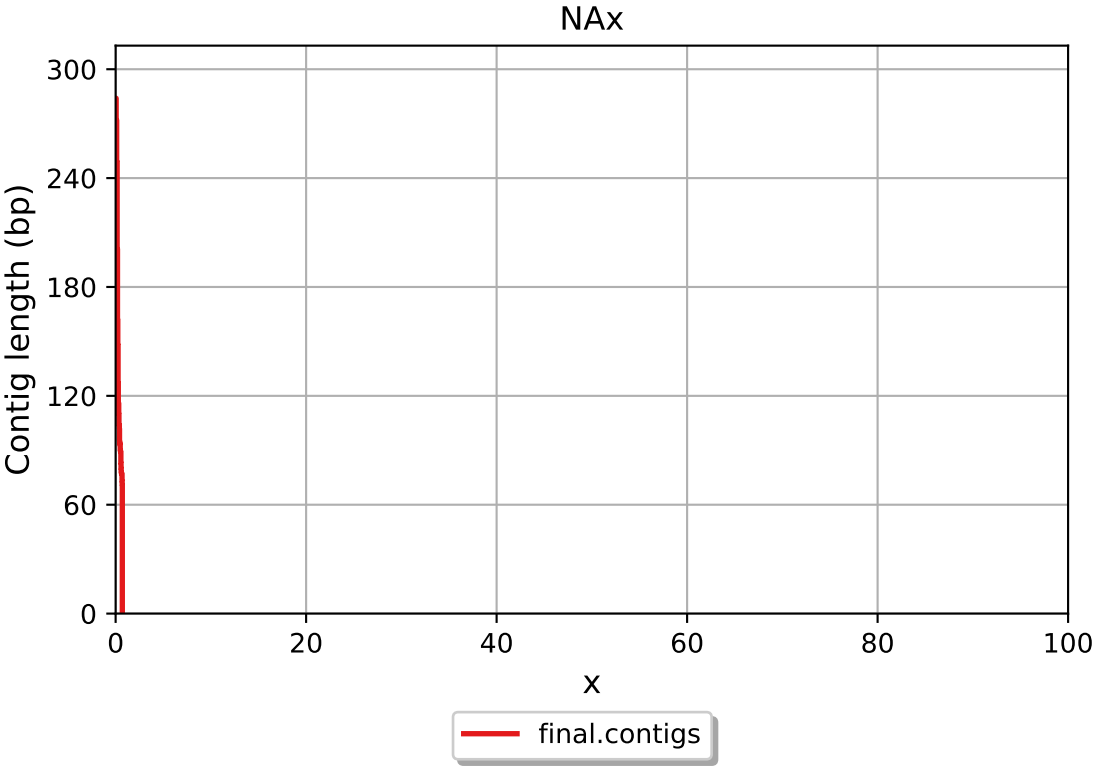

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

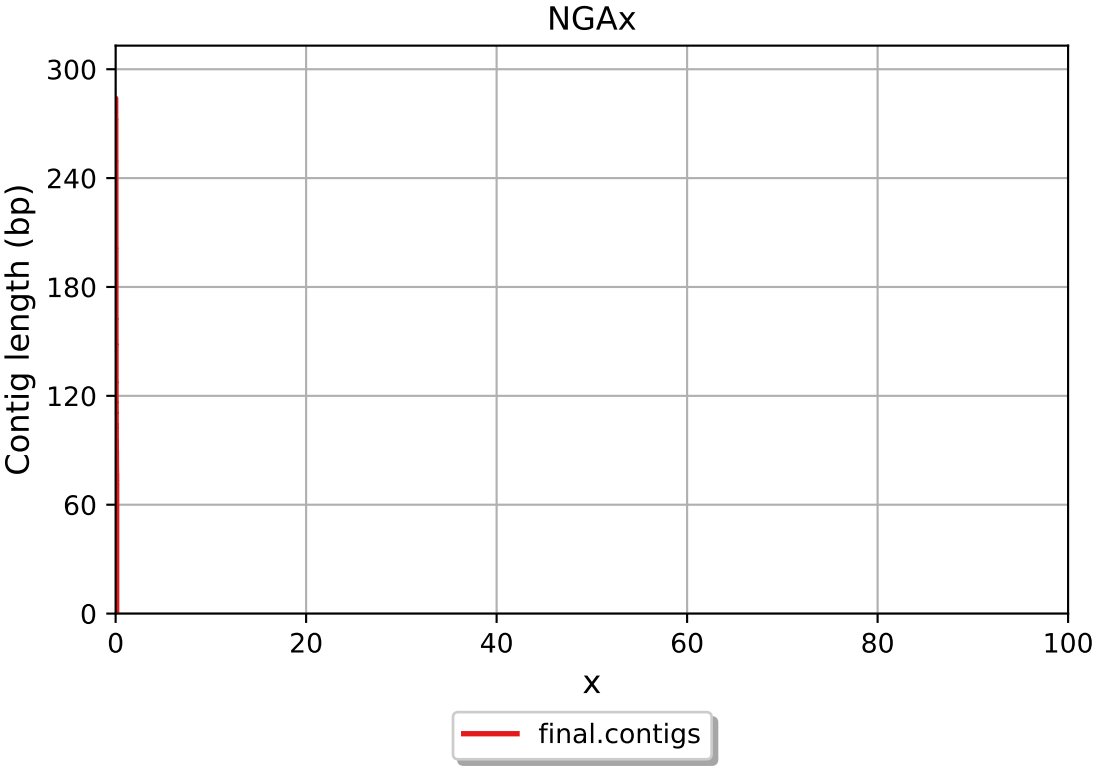

final.contigs GC content
contigs
0
3
6
9
12
15
0
20
40
60
80
100
GC (%)
final.contigs


Misassemblies
6
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
6
12
18
24
30
Contig index
final.contigs
Reference


NAx
Contig length (bp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs


NGAx
300
240
180
120
60
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs