Report

	final.contigs
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	49761
Total length (>= 5000 bp)	23066
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	37
Largest contig	8796
Total length	64491
Reference length	3576081
GC (%)	55.95
Reference GC (%)	51.82
N50	2823
N75	1085
L50	6
L75	16
# 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	1 + 24 part
Unaligned length	50973
Genome fraction (%)	0.186
Duplication ratio	2.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3615.00
# indels per 100 kbp	135.56
Largest alignment	1743
Total aligned length	8319
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

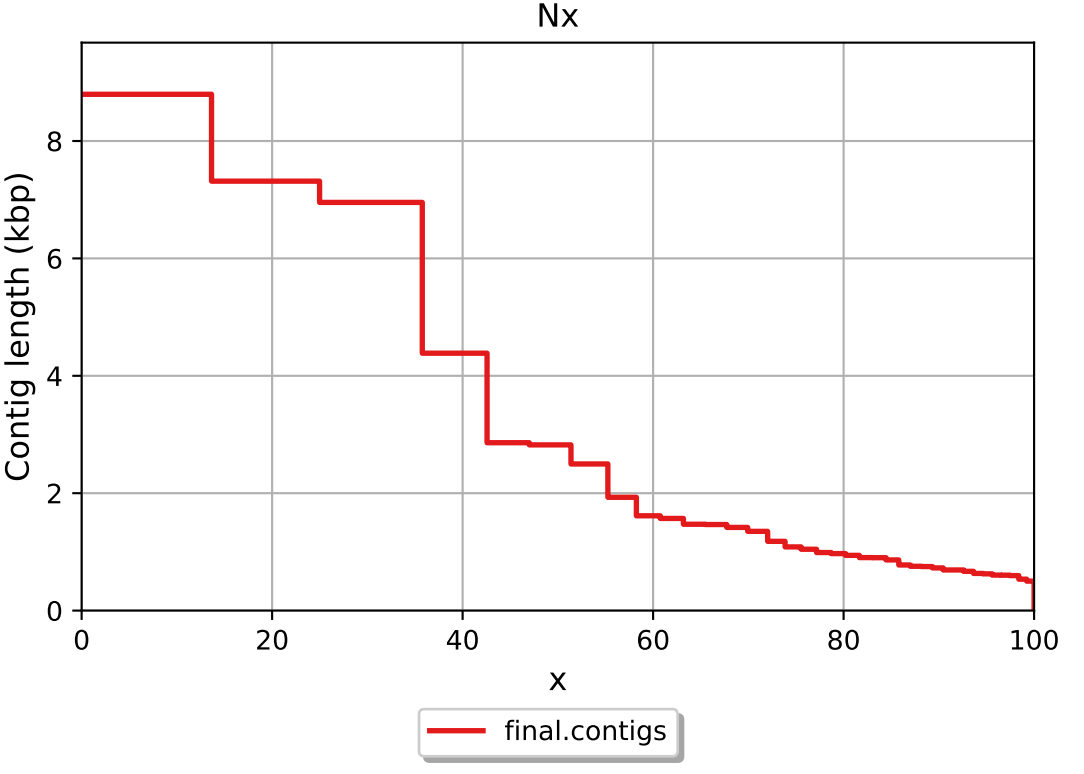
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	20
# possible misassemblies	25
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	240
# indels	9
# indels (<= 5 bp)	9
# indels (> 5 bp)	0
Indels length	10

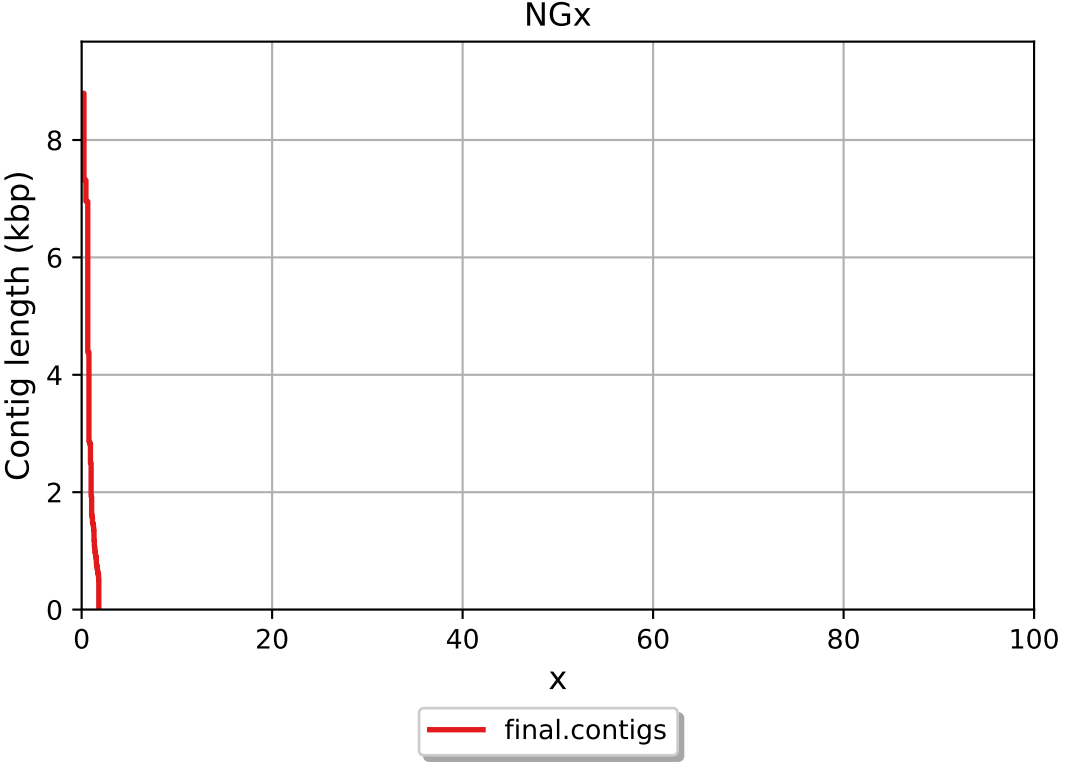
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

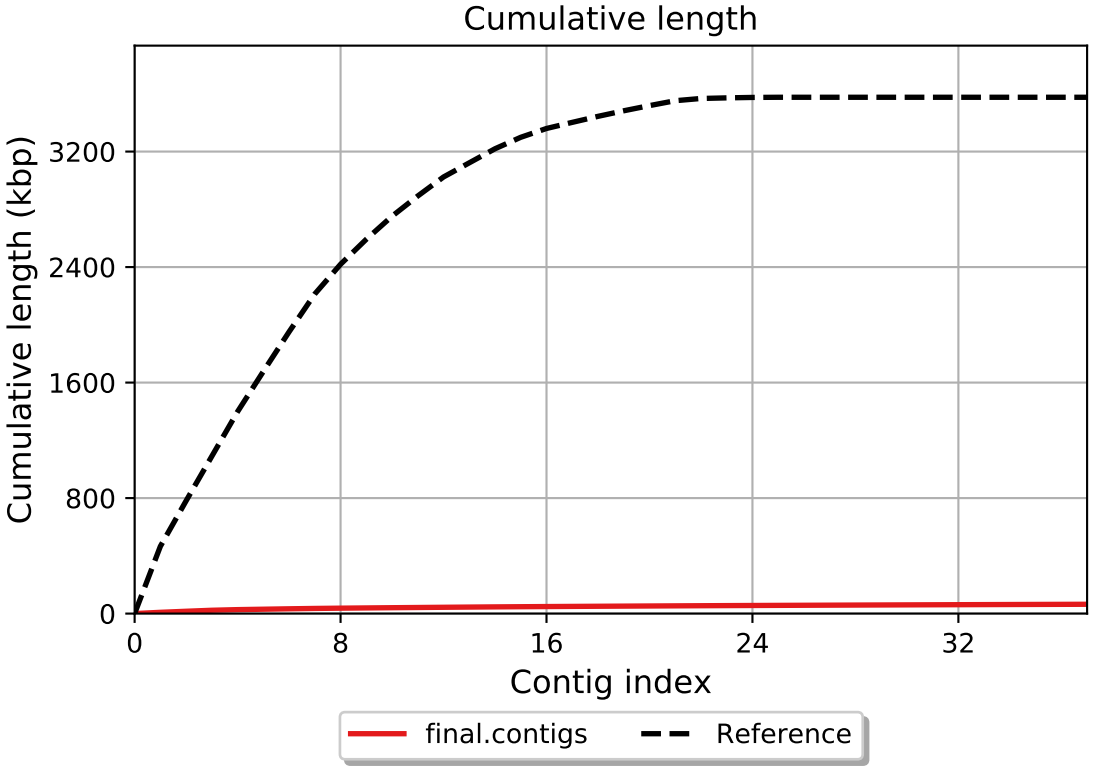
Unaligned report

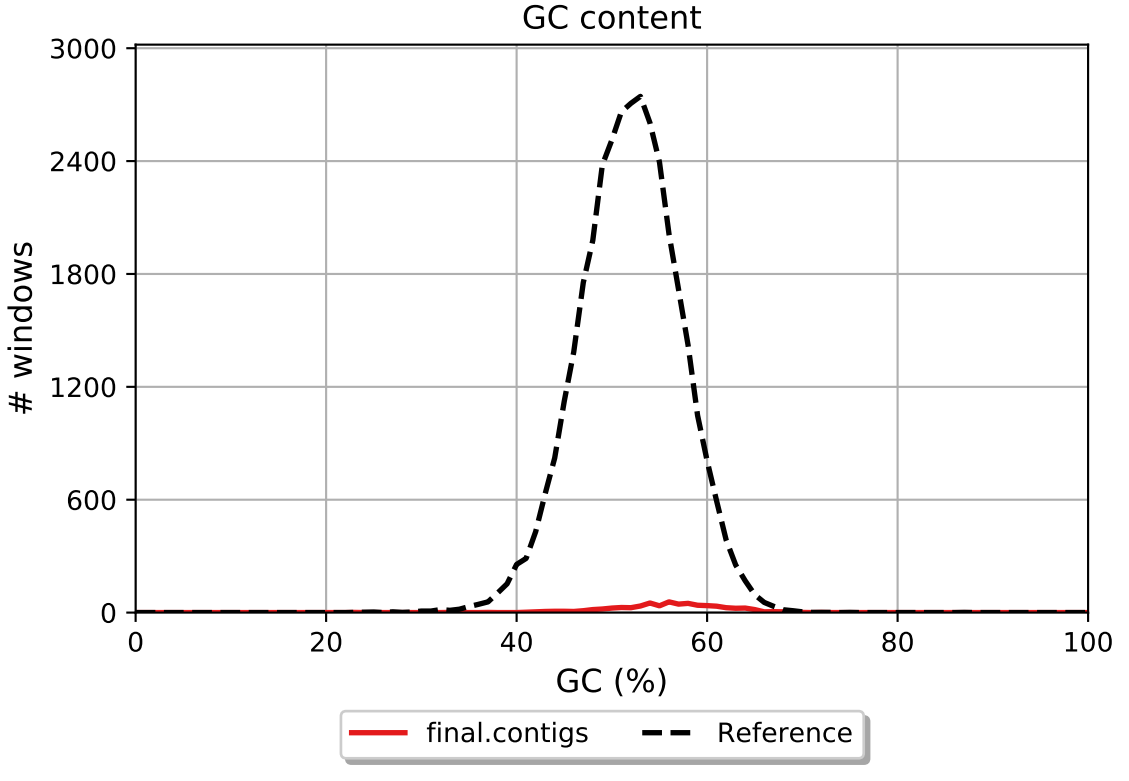
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	901
# partially unaligned contigs	24
Partially unaligned length	50072
# N's	0

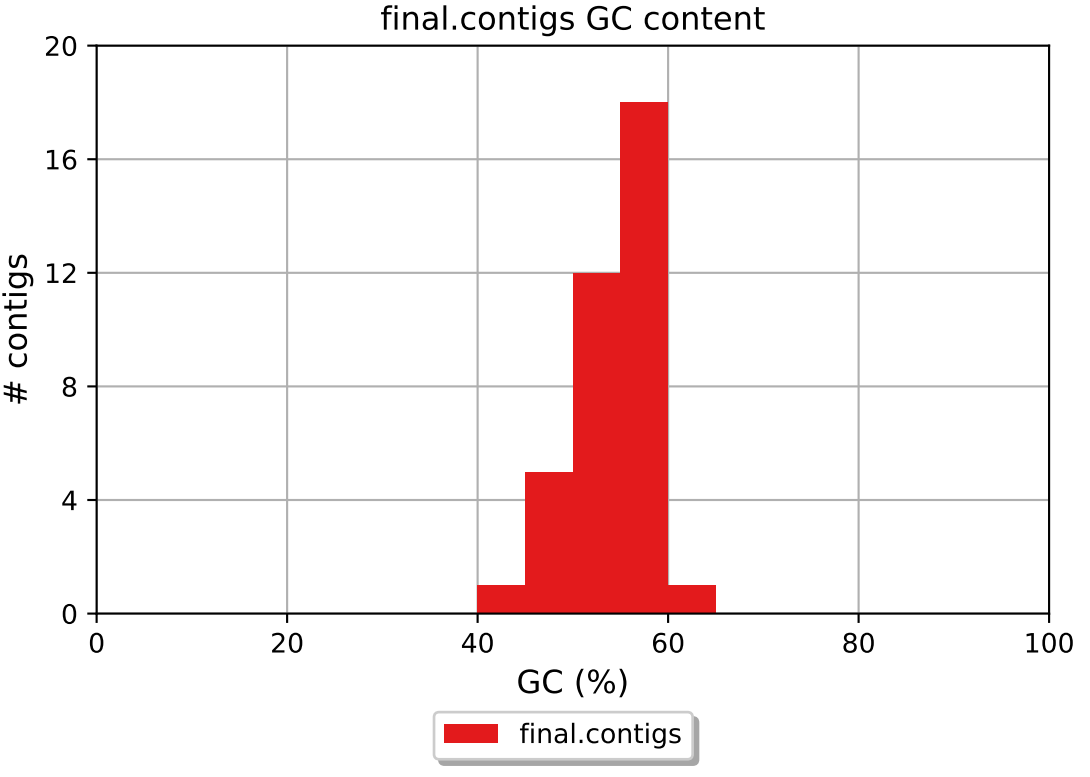
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

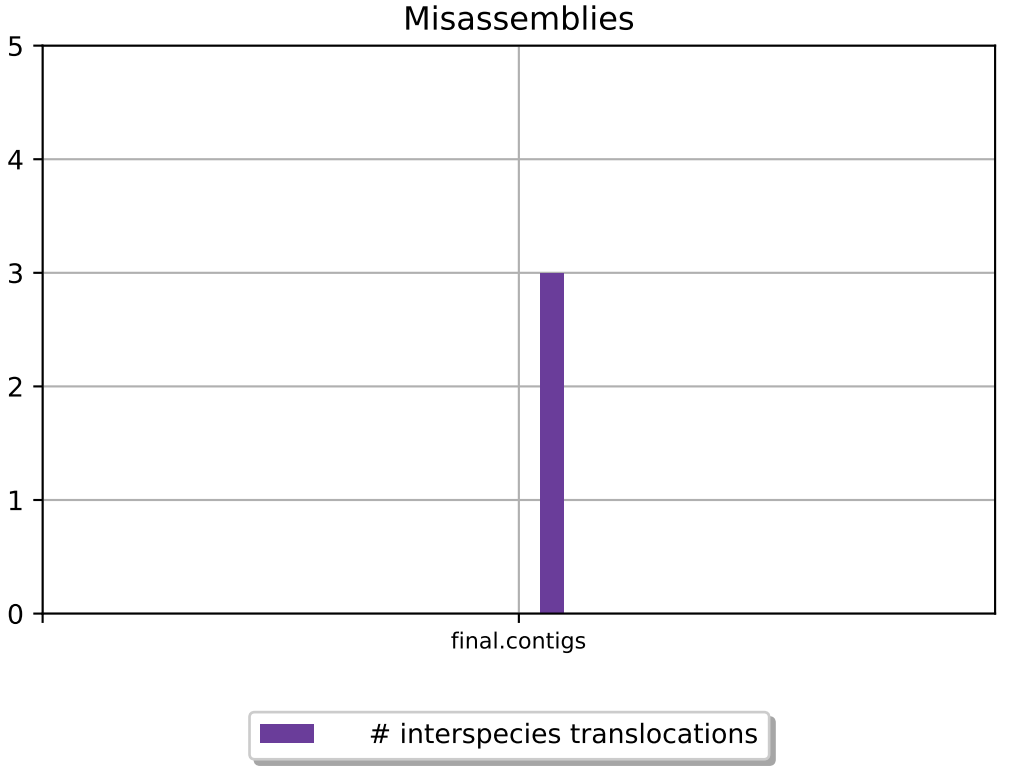

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

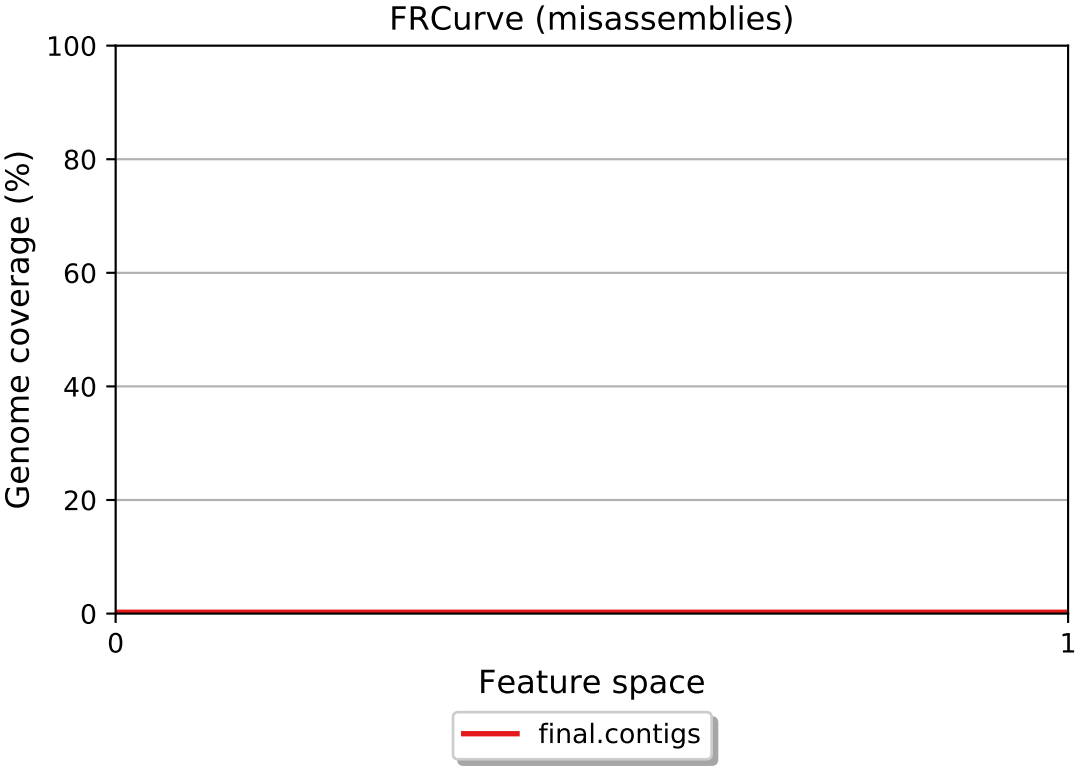

NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

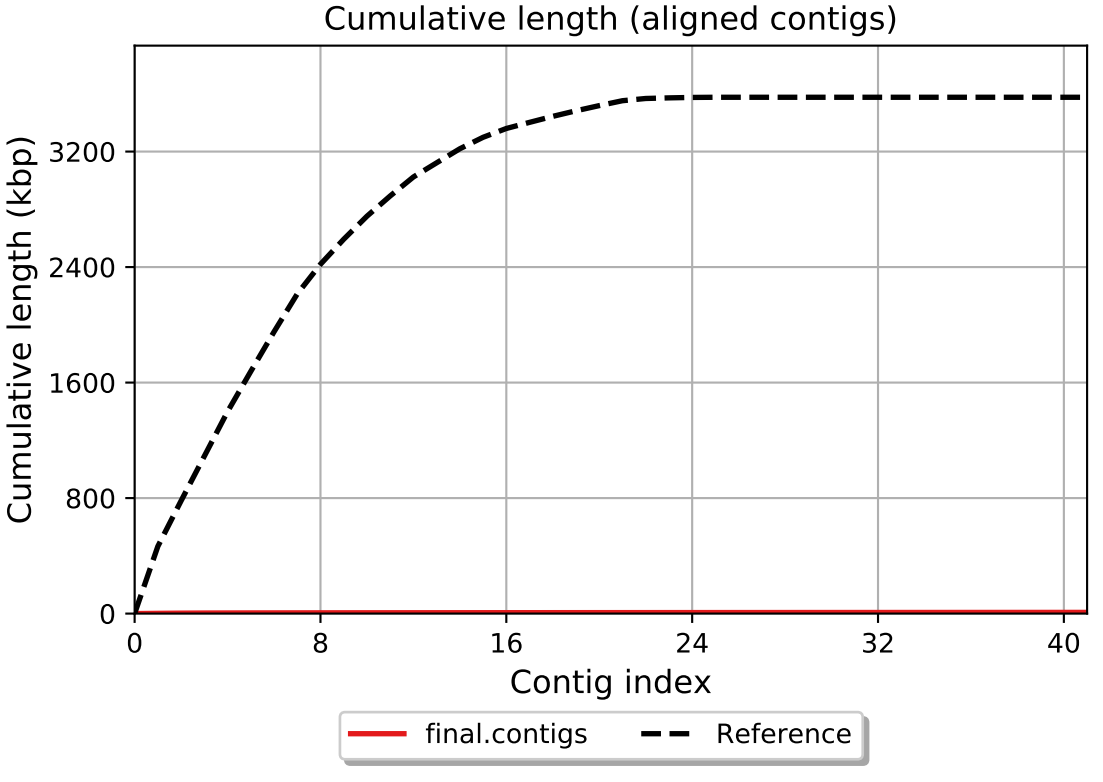

Cumulative length
Cumulative length (kbp)
3200
2400
1600
800
0
0
8
16
24
32
Contig index
final.contigs
Reference

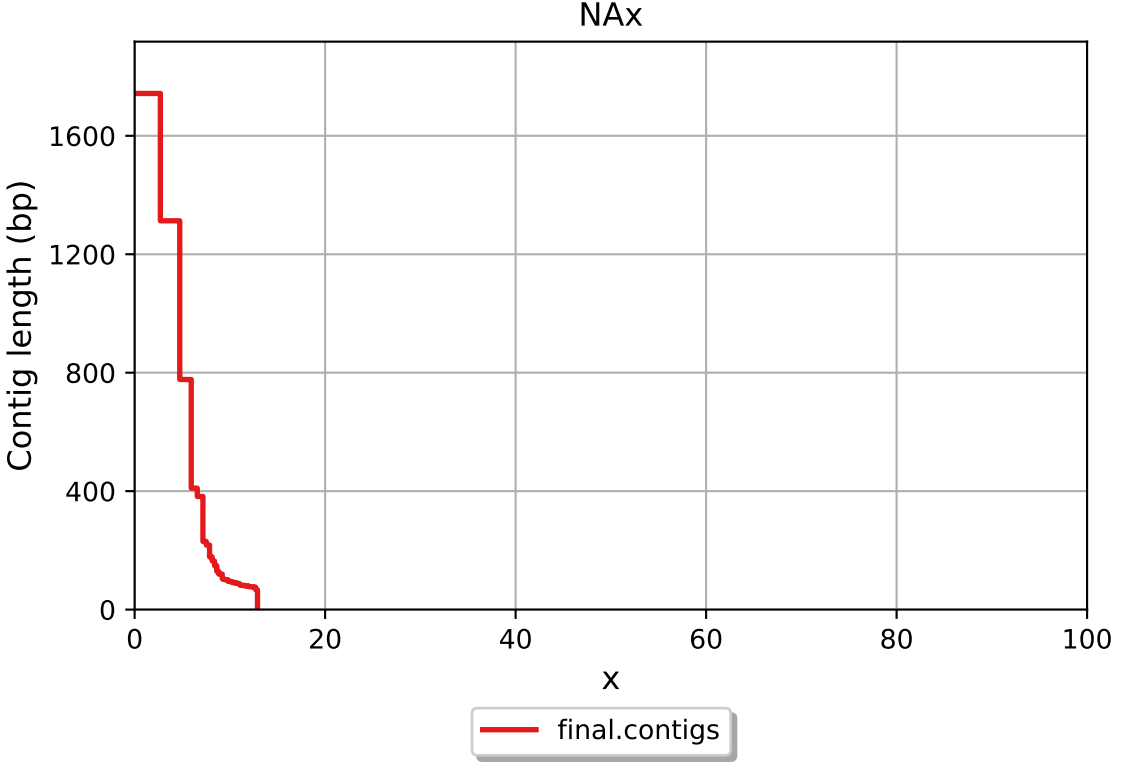

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

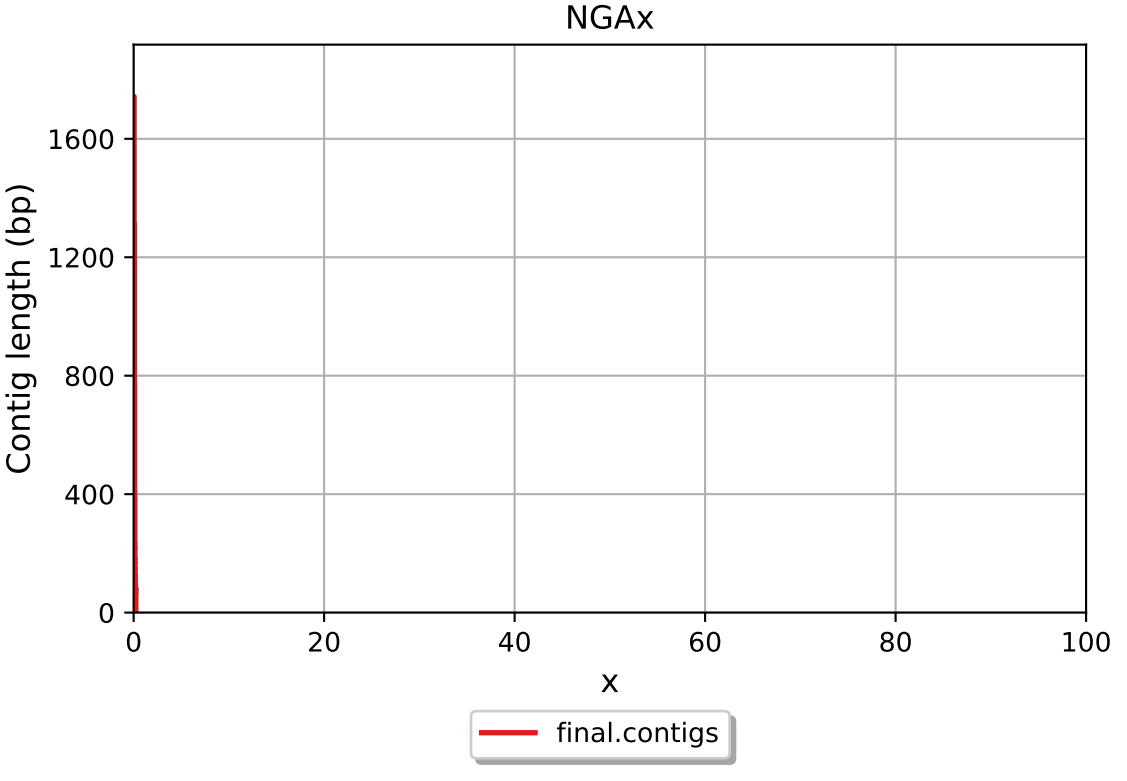

final.contigs GC content
20
16
12
8
4
0
contigs
0
20
40
60
80
100
GC (%)
final.contigs


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)
3200
2400
1600
800
0
0
8
16
24
32
40
Contig index
final.contigs
Reference


NAx
Contig length (bp)
1600
1200
800
400
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
1600
1200
800
400
0
0
20
40
60
80
100
x
final.contigs