Report

	final.contigs
# contigs (>= 1000 bp)	345
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	483160
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1222
Largest contig	3095
Total length	1099599
Reference length	4869432
GC (%)	51.80
Reference GC (%)	51.08
N50	929
NG50	-
N90	578
NG90	-
auN	1069.2
auNG	241.4
L50	415
LG50	-
L90	1017
LG90	-
# misassemblies	17
# misassembled contigs	16
Misassembled contigs length	16601
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	3 + 74 part
Unaligned length	66364
Genome fraction (%)	18.995
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7460.28
# indels per 100 kbp	172.43
Largest alignment	2958
Total aligned length	938369
NA50	767
NGA50	-
NA90	-
NGA90	-
auNA	828.2
auNGA	187.0
LA50	480
LGA50	-
LA90	-
LGA90	-

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

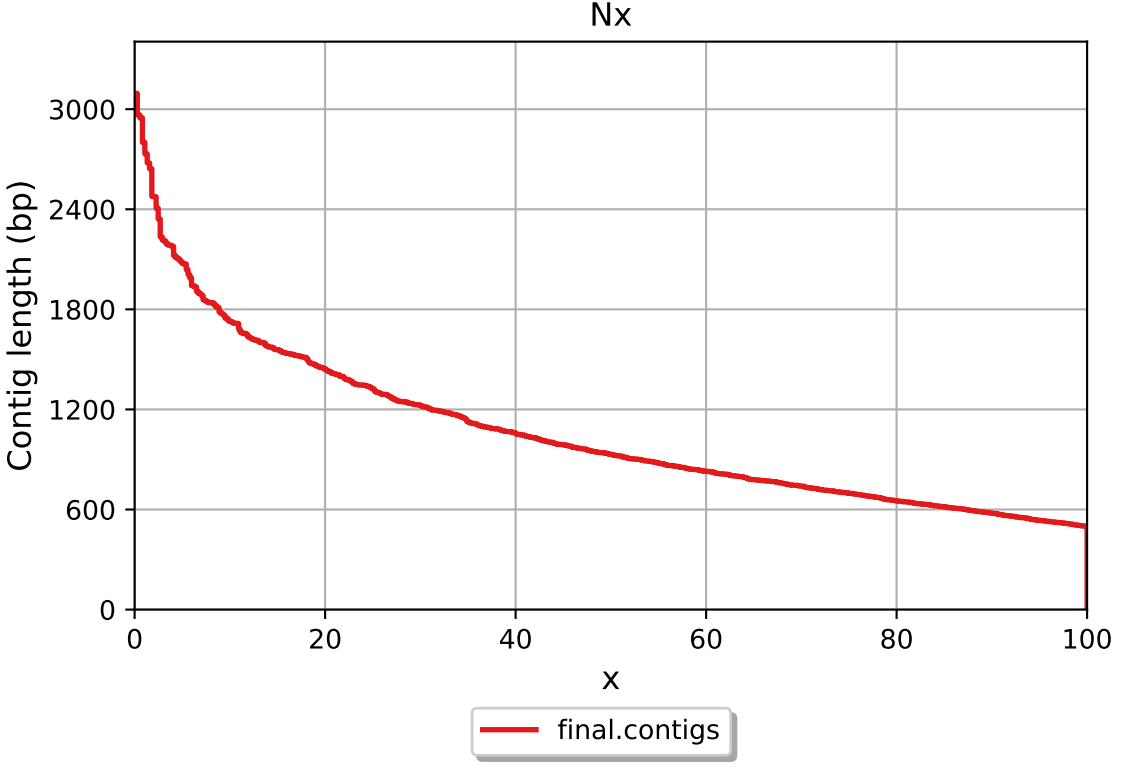
	final.contigs
# misassemblies	17
# contig misassemblies	17
# c. relocations	14
# c. translocations	2
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	16
Misassembled contigs length	16601
# possibly misassembled contigs	55
# possible misassemblies	58
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	70005
# indels	1618
# indels (<= 5 bp)	1524
# indels (> 5 bp)	94
Indels length	4601

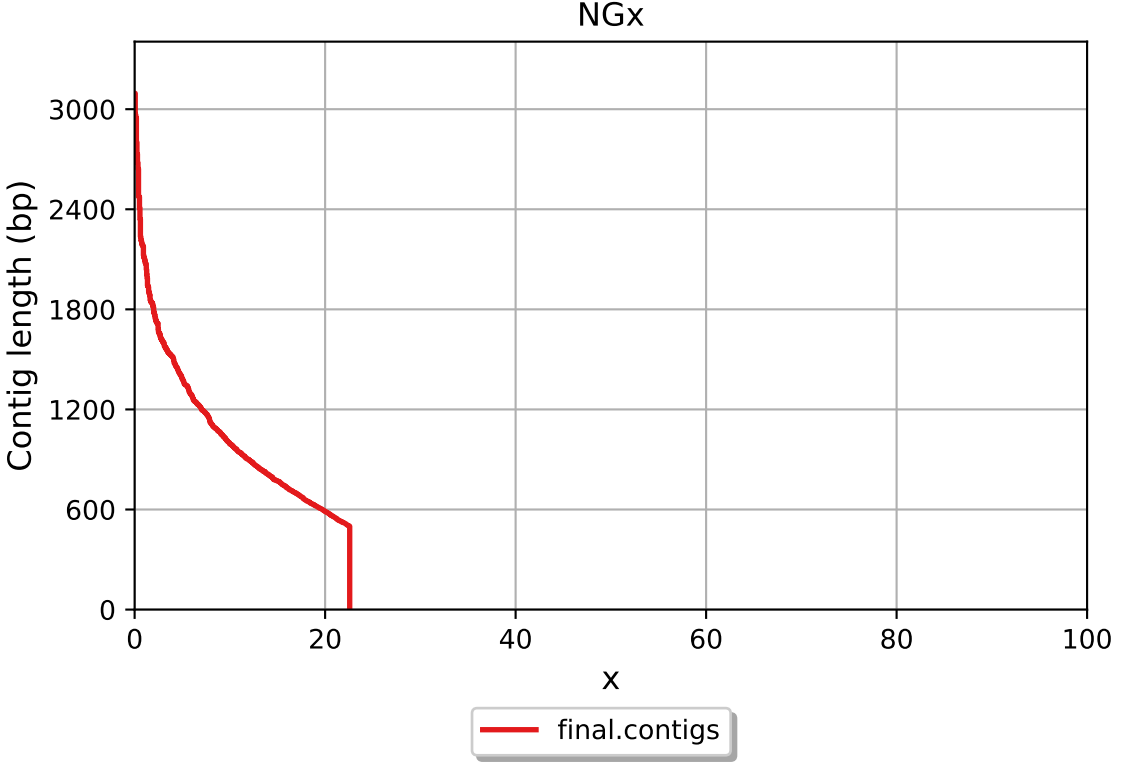
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

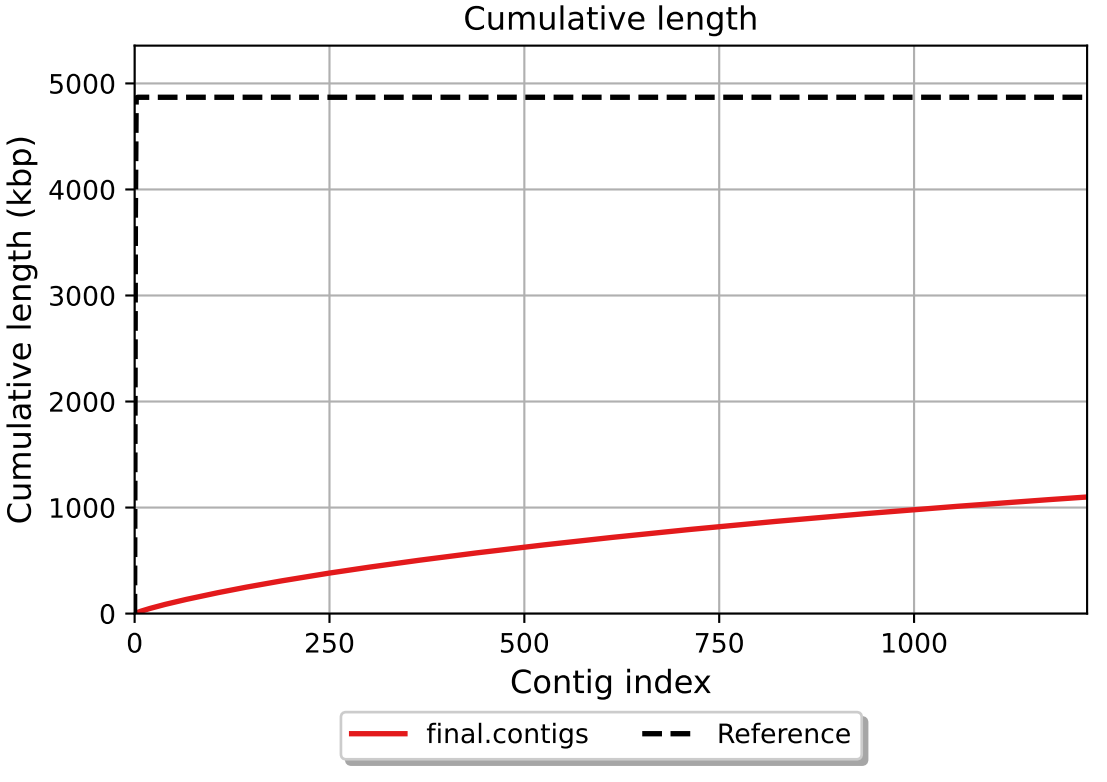
Unaligned report

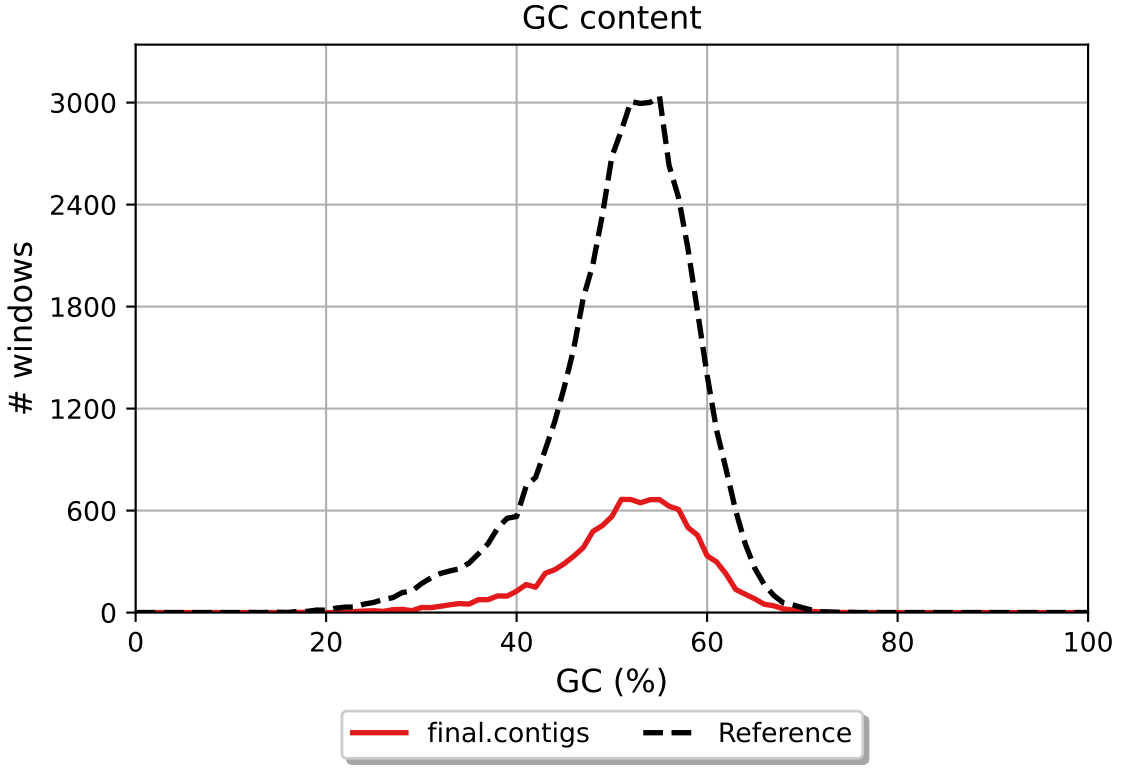
	final.contigs
# fully unaligned contigs	3
Fully unaligned length	4108
# partially unaligned contigs	74
Partially unaligned length	62256
# N's	0

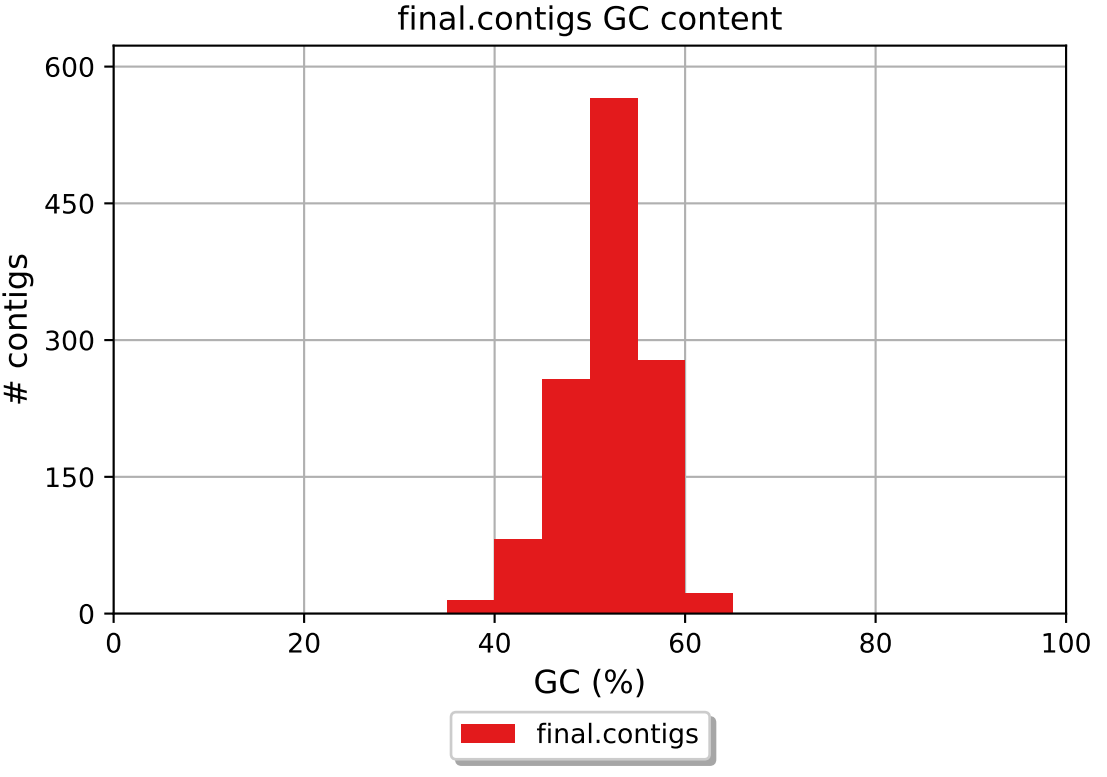
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

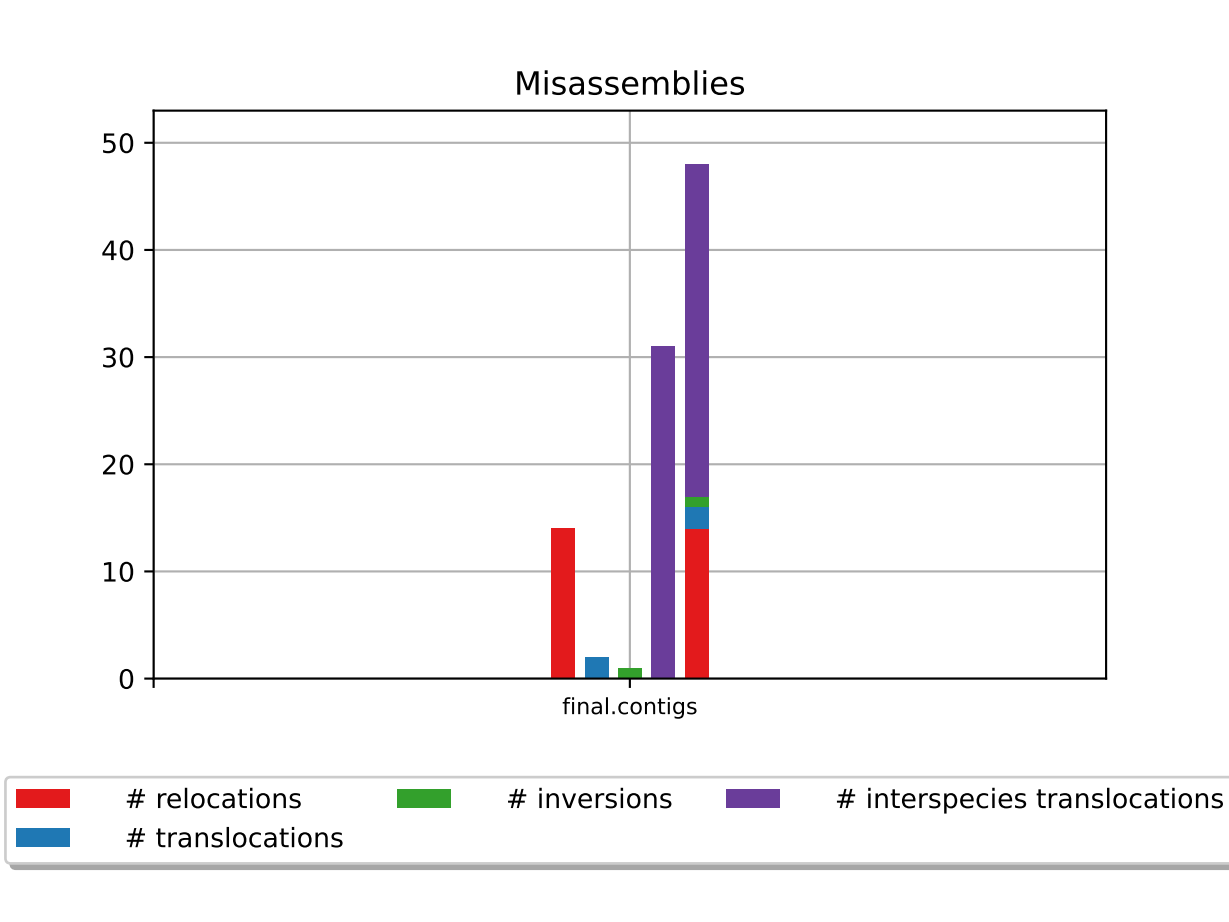

Nx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs

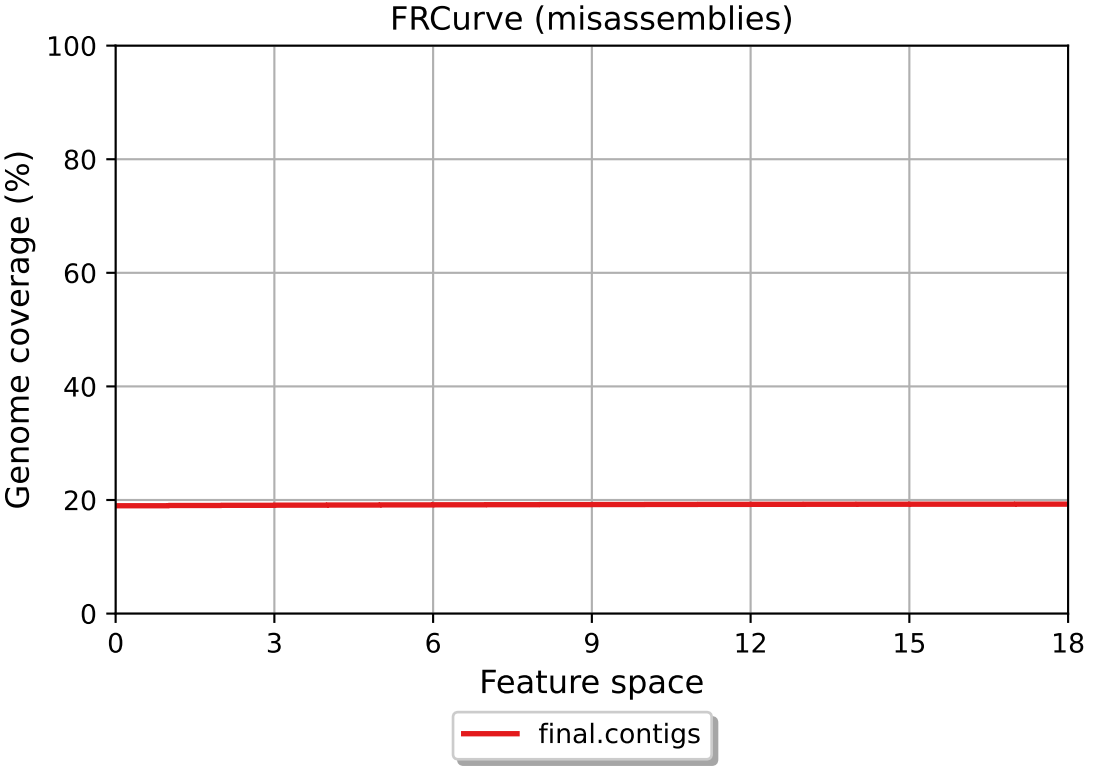

NGx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs

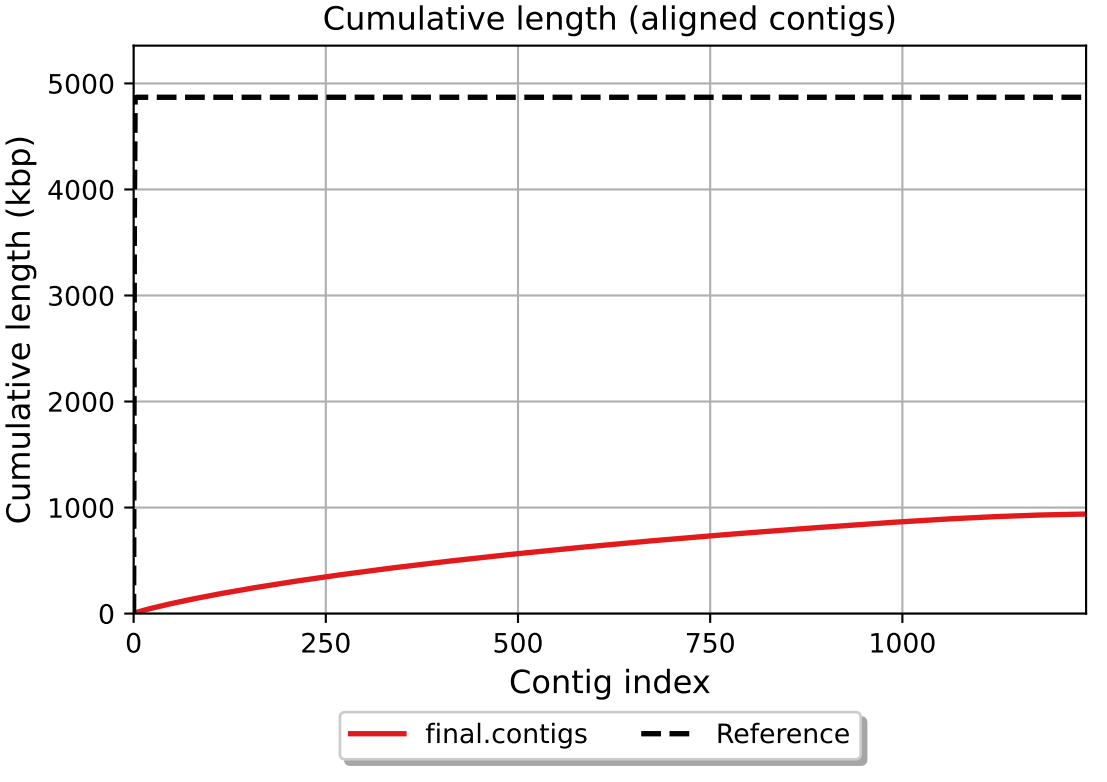

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
250
500
750
1000
Contig index
final.contigs
Reference

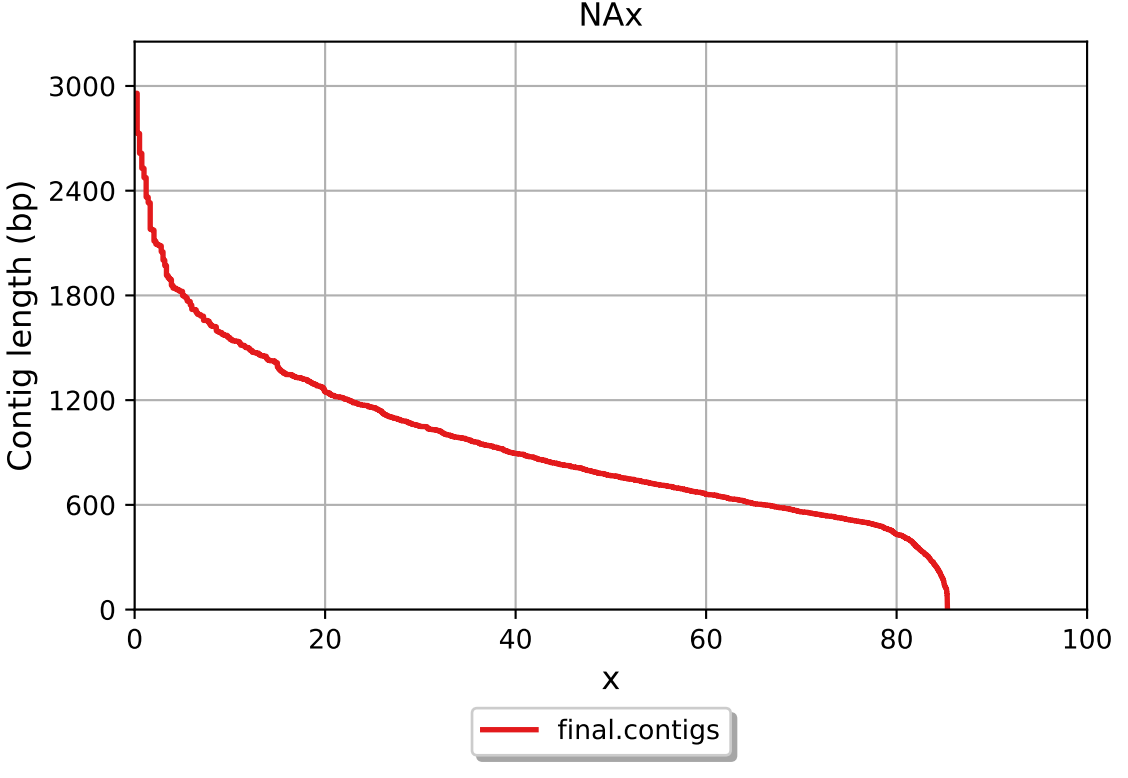

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

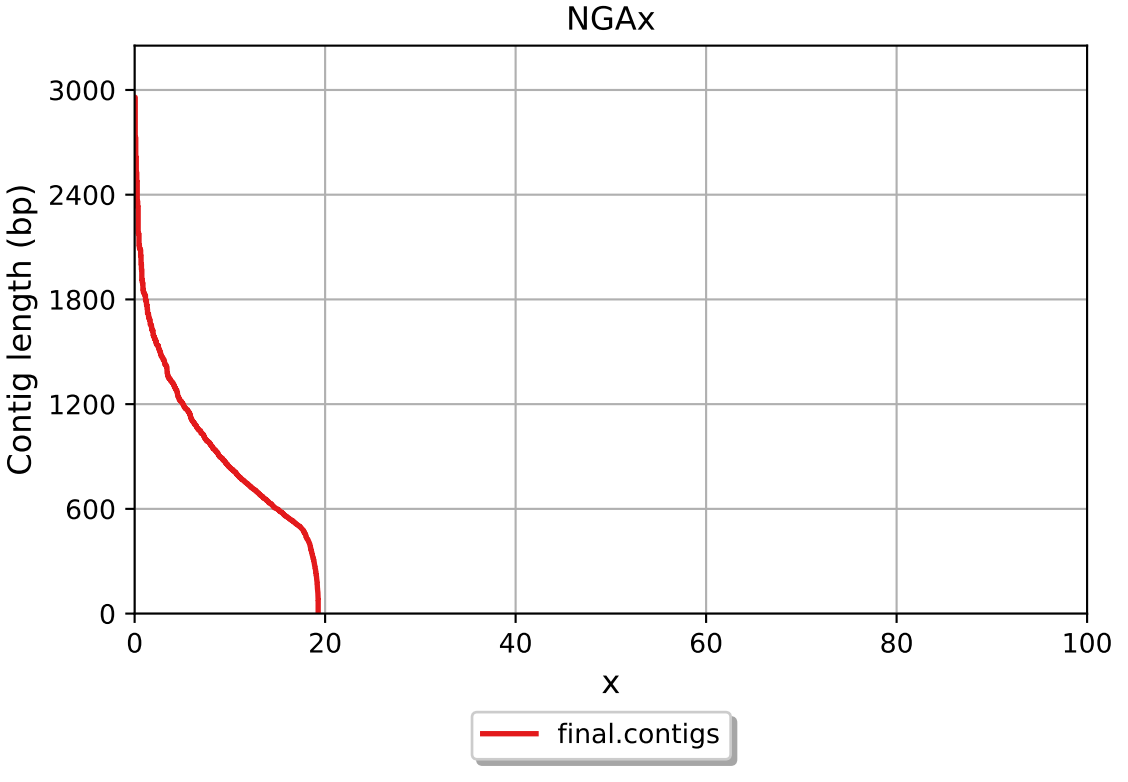

final.contigs GC content
600
450
300
150
0
contigs
0
20
40
60
80
100
GC (%)
final.contigs


Misassemblies
50
40
30
20
10
0
final.contigs
relocations
translocations
inversions
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
18
Feature space
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
250
500
750
1000
Contig index
final.contigs
Reference


NAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs