Report

	final.contigs
# contigs (>= 1000 bp)	171
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	347969
Total length (>= 5000 bp)	87834
Total length (>= 10000 bp)	74034
Total length (>= 25000 bp)	74034
Total length (>= 50000 bp)	74034
# contigs	541
Largest contig	74034
Total length	603756
Reference length	2177915
GC (%)	54.27
Reference GC (%)	54.54
N50	1164
NG50	-
N90	589
NG90	-
L50	129
LG50	-
L90	430
LG90	-
# misassemblies	6
# misassembled contigs	5
Misassembled contigs length	4337
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 63 part
Unaligned length	158297
Genome fraction (%)	17.363
Duplication ratio	1.033
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7692.45
# indels per 100 kbp	164.13
Largest alignment	3524
Total aligned length	390552
NA50	580
NGA50	-
NA90	-
NGA90	-
LA50	310
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

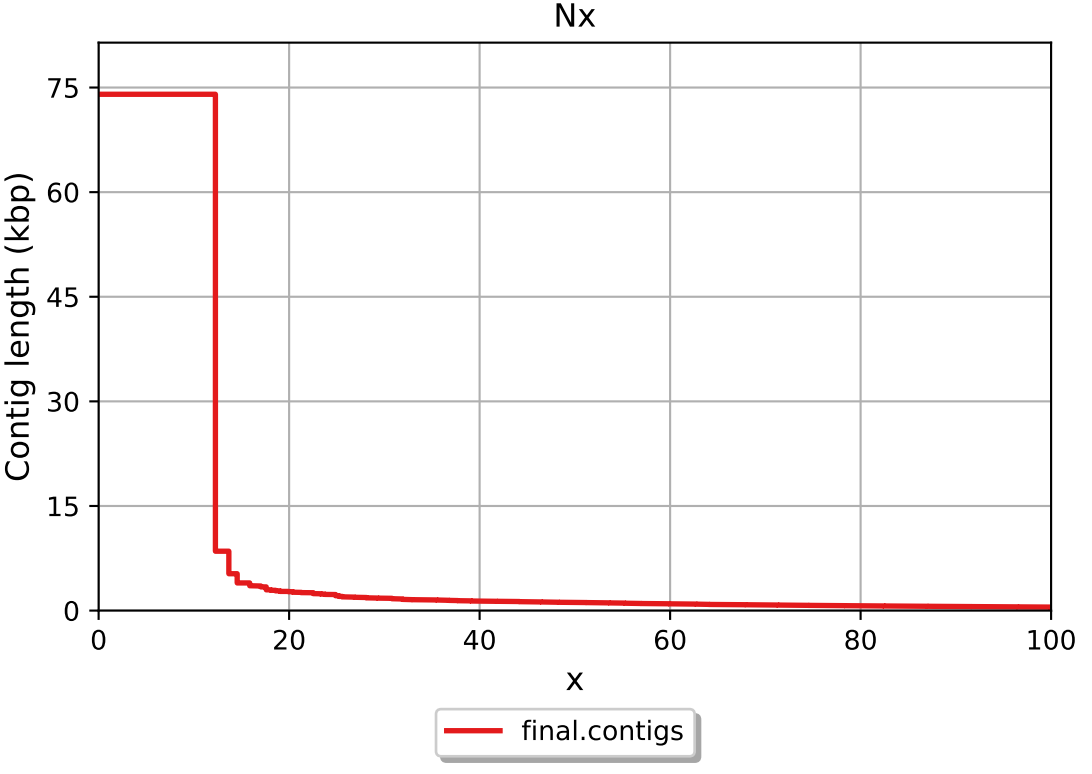
	final.contigs
# misassemblies	6
# contig misassemblies	6
# c. relocations	5
# c. translocations	1
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	4337
# possibly misassembled contigs	62
# possible misassemblies	71
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# misassemblies caused by fragmented reference	0
# unaligned mis. contigs	1
# mismatches	30043
# indels	641
# indels (<= 5 bp)	622
# indels (> 5 bp)	19
Indels length	1217

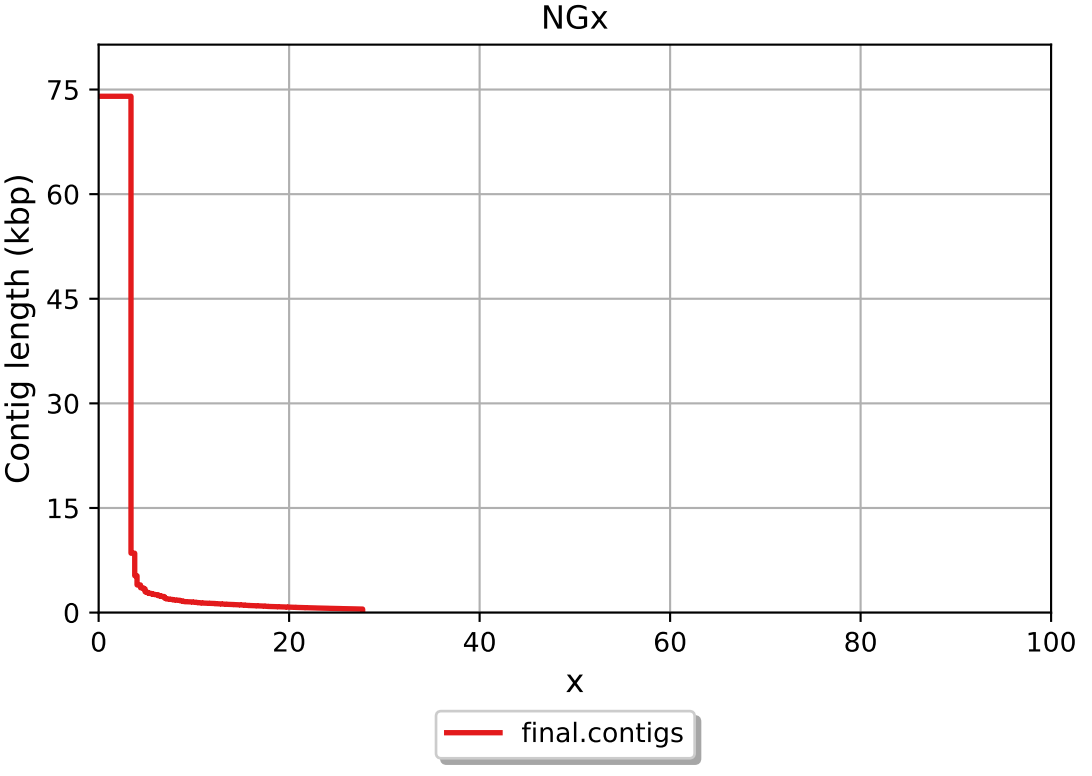
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

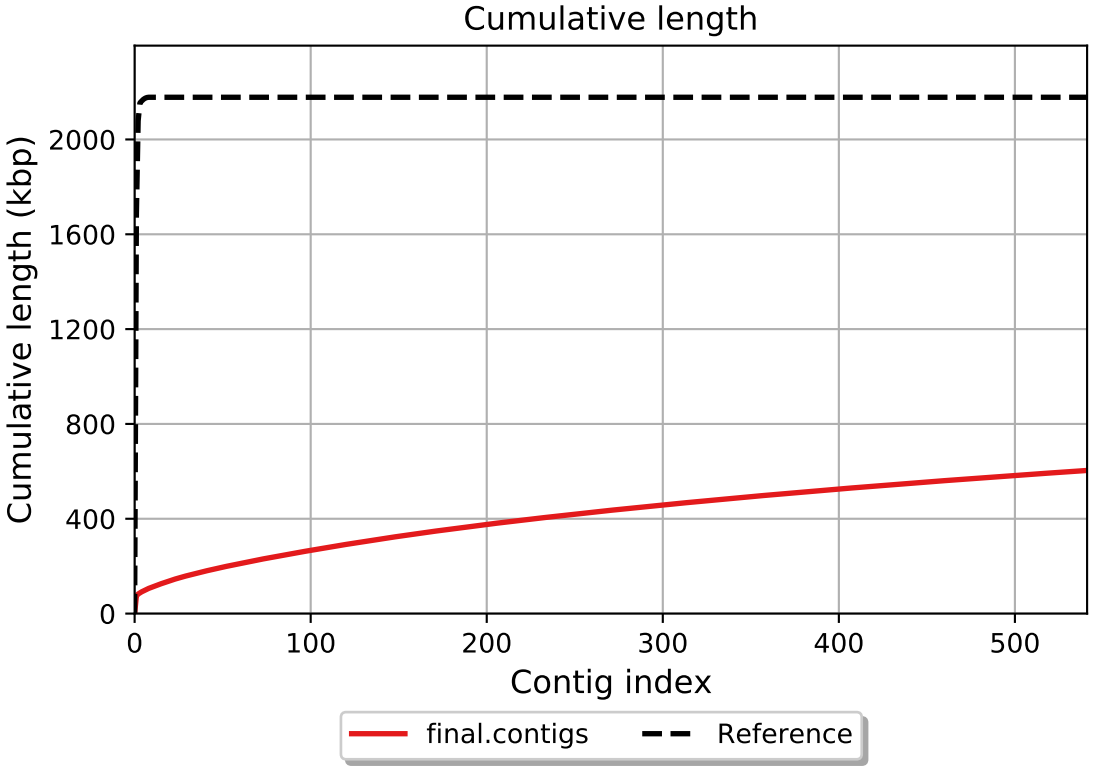
Unaligned report

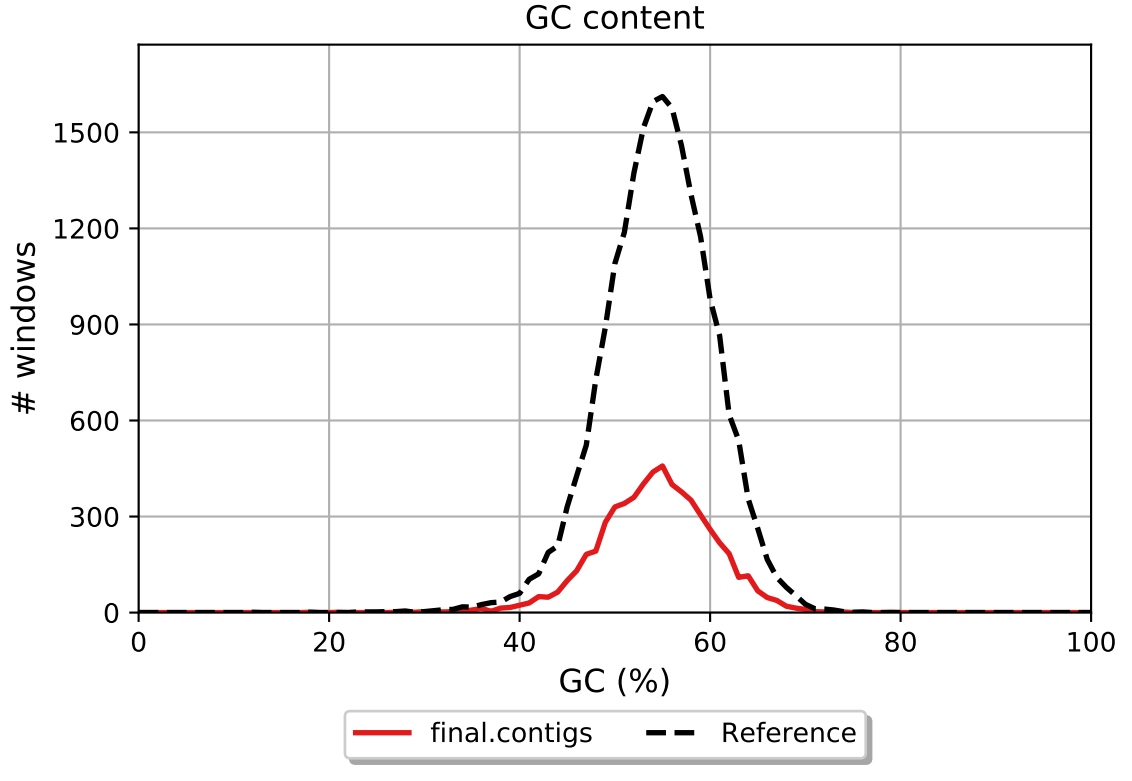
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	63
Partially unaligned length	158297
# N's	0

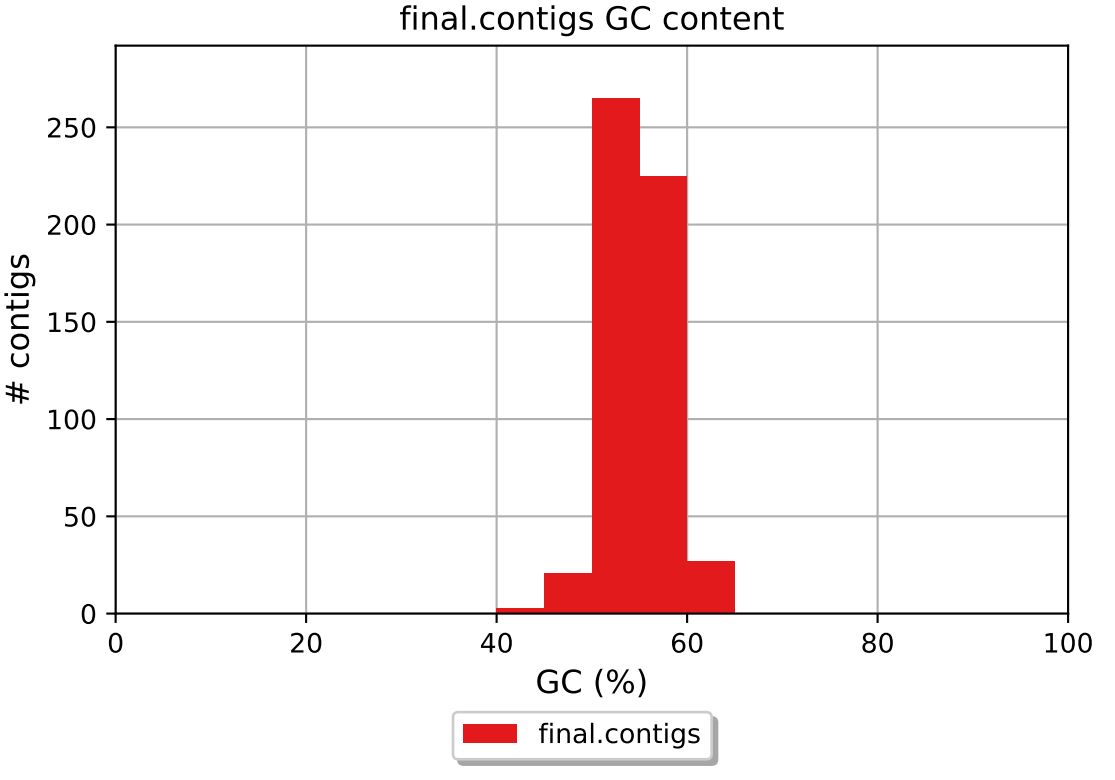
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

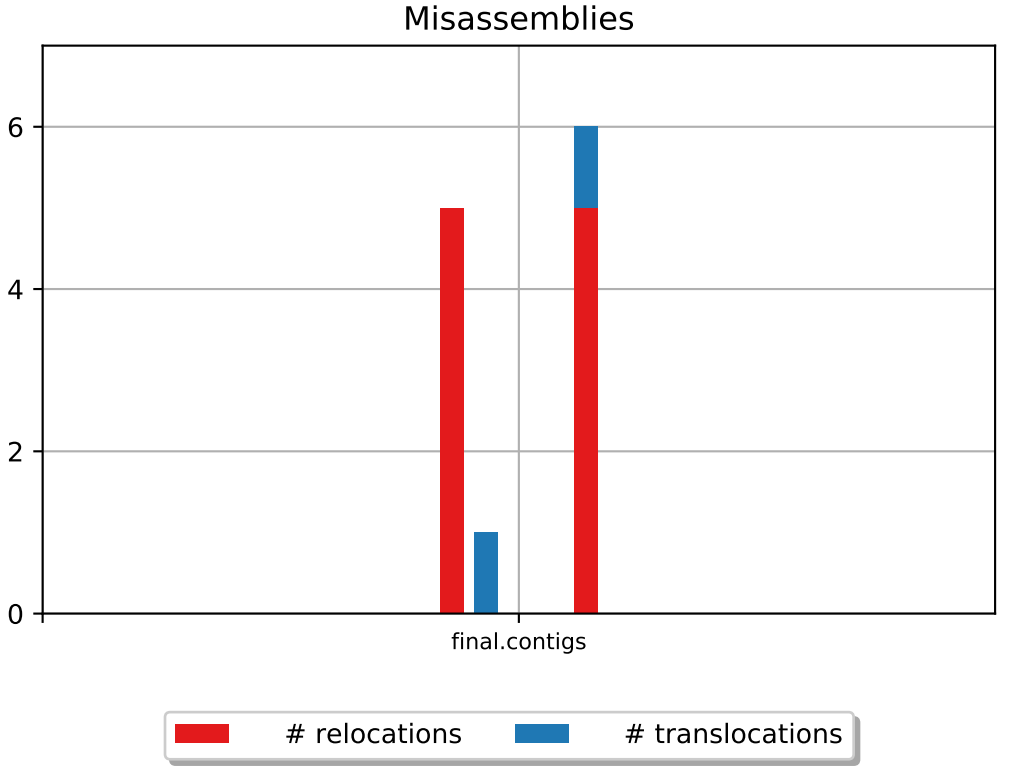

Nx
Contig length (kbp)
75
60
45
30
15
0
0
20
40
60
80
100
x
final.contigs

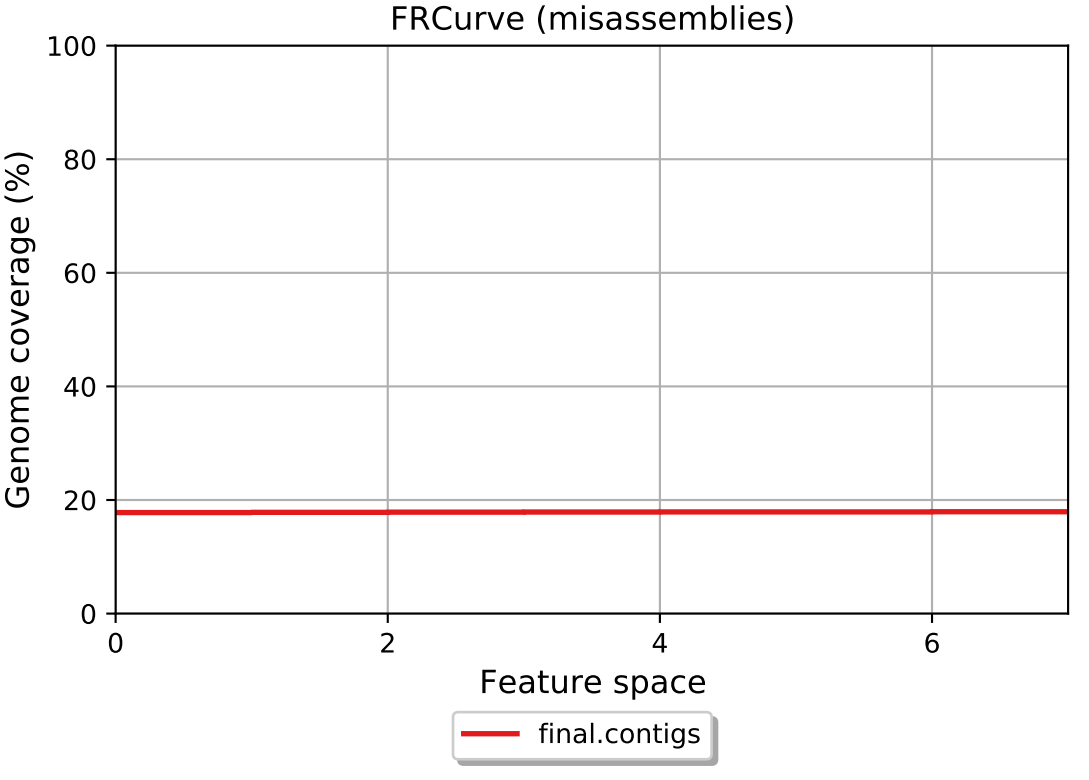

NGx
Contig length (kbp)
75
60
45
30
15
0
0
20
40
60
80
100
x
final.contigs

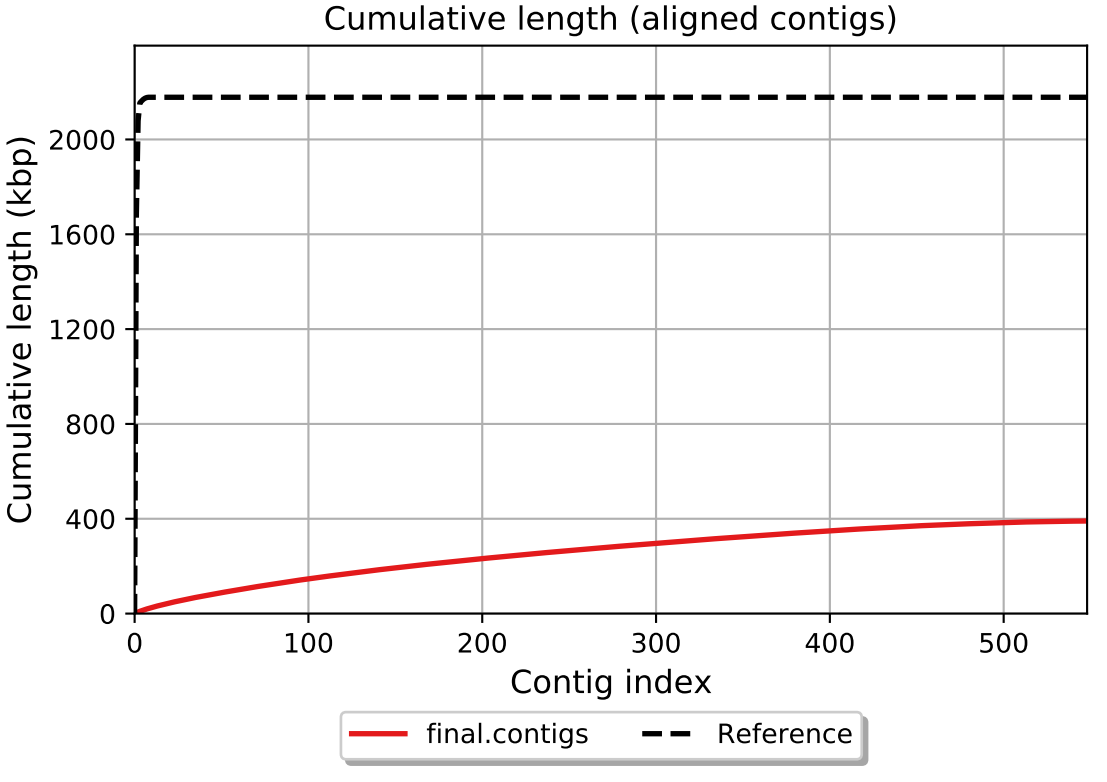

Cumulative length
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
100
200
300
400
500
Contig index
final.contigs
Reference

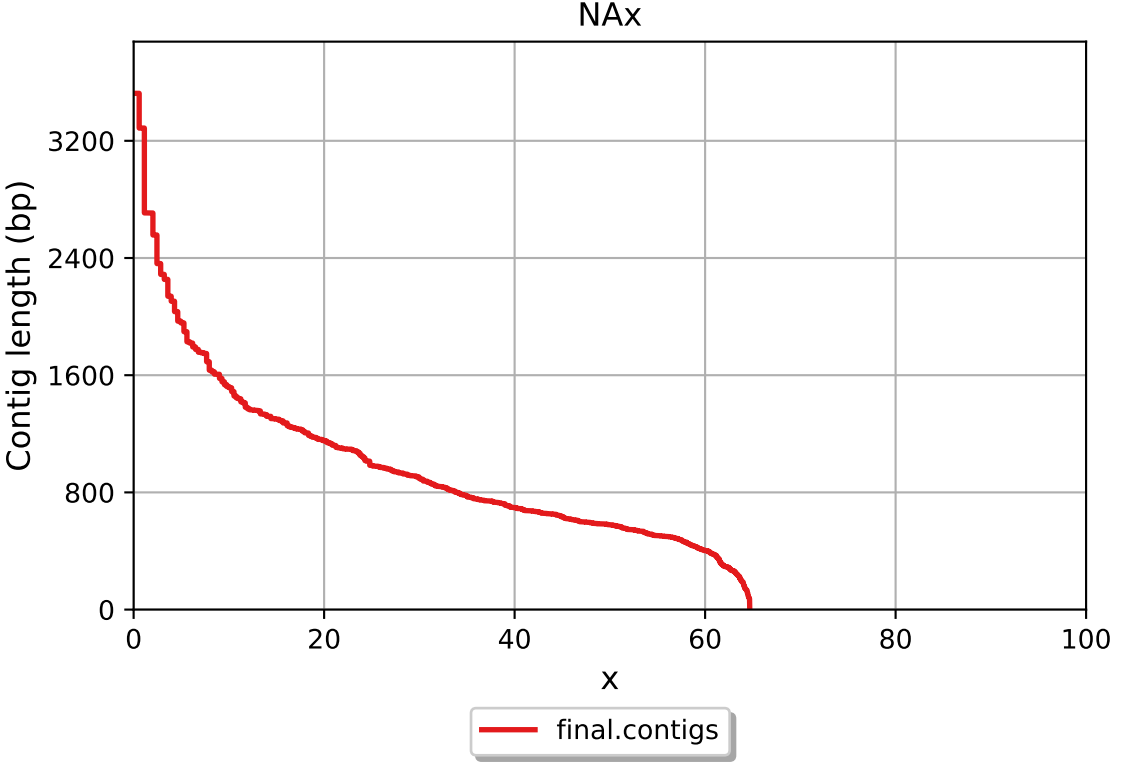

GC content
windows
1500
1200
900
600
300
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

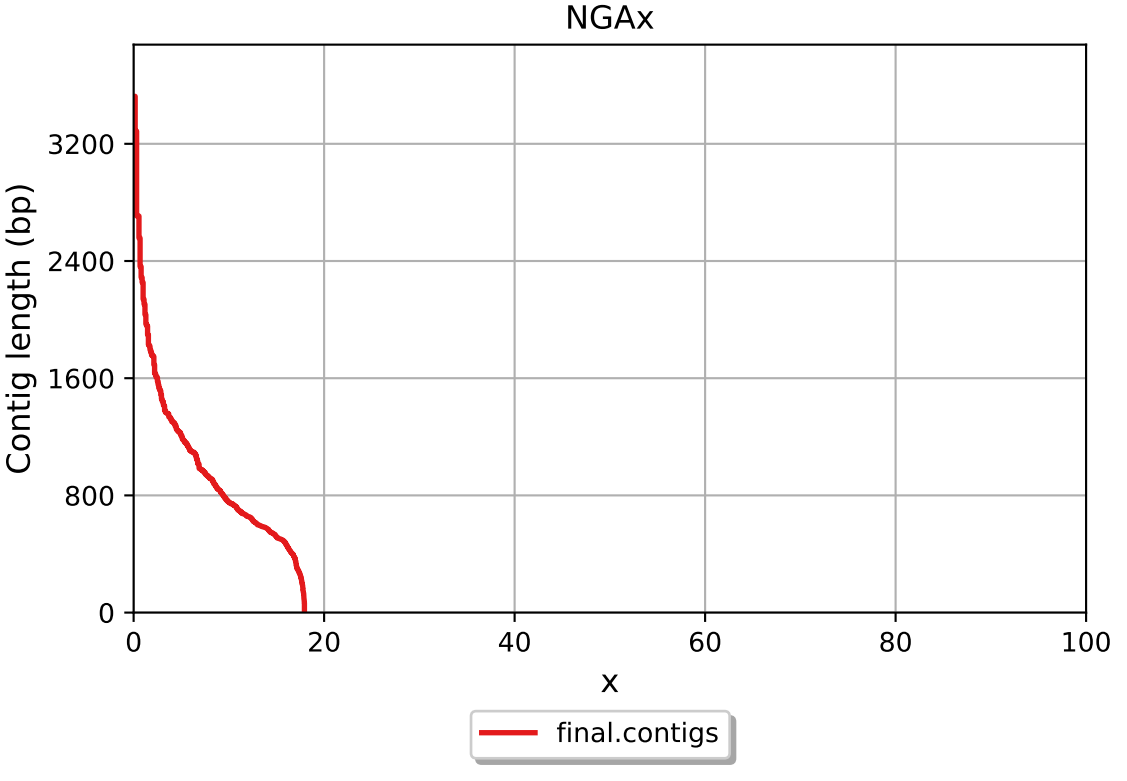

final.contigs GC content
contigs
0
50
100
150
200
250
0
20
40
60
80
100
GC (%)
final.contigs


Misassemblies
6
4
2
0
final.contigs
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
Feature space
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
100
200
300
400
500
Contig index
final.contigs
Reference


NAx
Contig length (bp)
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs