Report

	final.contigs
# contigs (>= 0 bp)	418752
# contigs (>= 1000 bp)	46585
# contigs (>= 5000 bp)	2179
# contigs (>= 10000 bp)	556
# contigs (>= 25000 bp)	116
# contigs (>= 50000 bp)	33
Total length (>= 0 bp)	271395163
Total length (>= 1000 bp)	97440115
Total length (>= 5000 bp)	22537302
Total length (>= 10000 bp)	11760892
Total length (>= 25000 bp)	5297797
Total length (>= 50000 bp)	2500061
# contigs	171623
Largest contig	168358
Total length	181406758
Reference length	4000479
N50	1080
N90	566
L50	40098
L90	137470
# misassemblies	22
# misassembled contigs	19
Misassembled contigs length	61808
# local misassemblies	31
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	9
# unaligned contigs	170414 + 238 part
Unaligned length	179831430
Genome fraction (%)	34.496
Duplication ratio	1.061
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7651.14
# indels per 100 kbp	249.77
Largest alignment	18187
Total aligned length	1462136
NA50	-
NA90	-
LA50	-
LA90	-

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

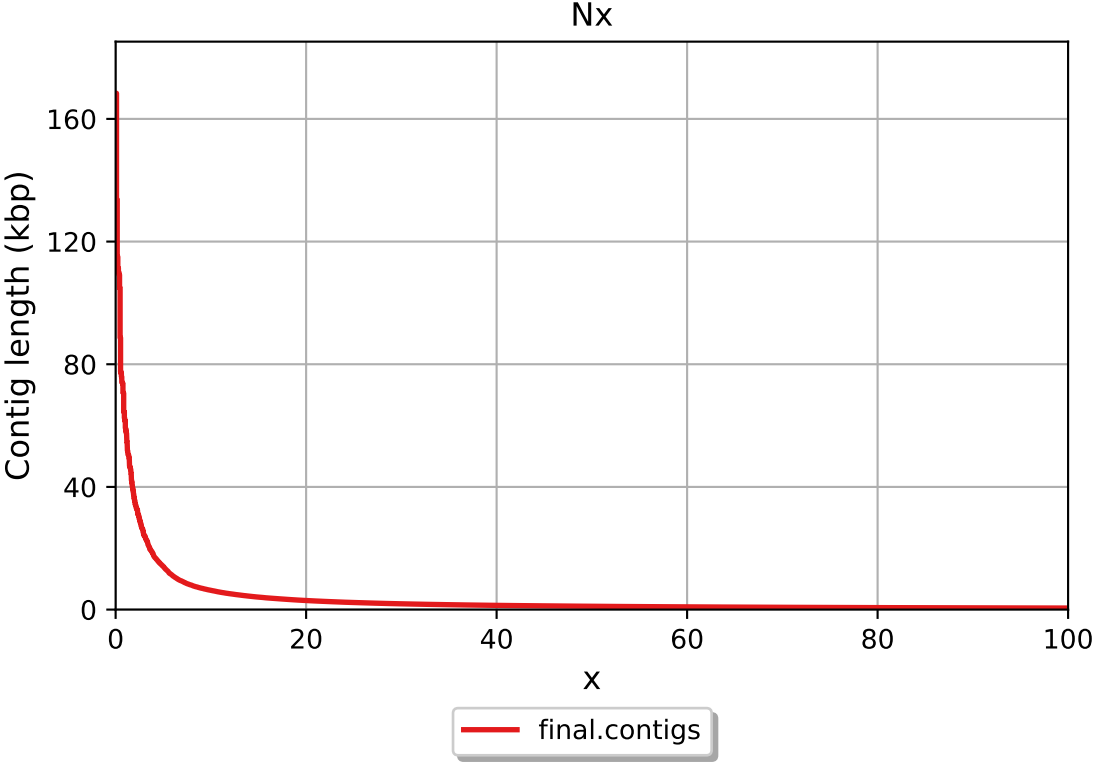
	final.contigs
# misassemblies	22
# contig misassemblies	22
# c. relocations	16
# c. translocations	6
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	19
Misassembled contigs length	61808
# possibly misassembled contigs	229
# possible misassemblies	260
# local misassemblies	31
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# misassemblies caused by fragmented reference	1
# unaligned mis. contigs	9
# mismatches	111870
# indels	3652
# indels (<= 5 bp)	3403
# indels (> 5 bp)	249
Indels length	11111

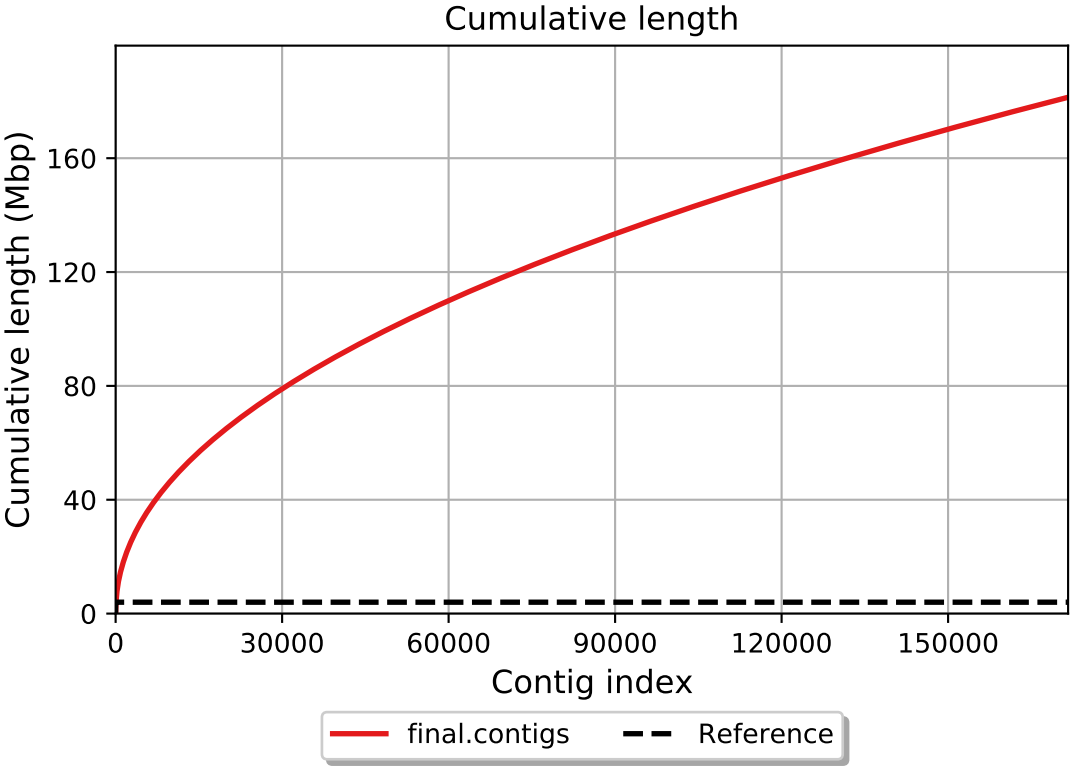
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

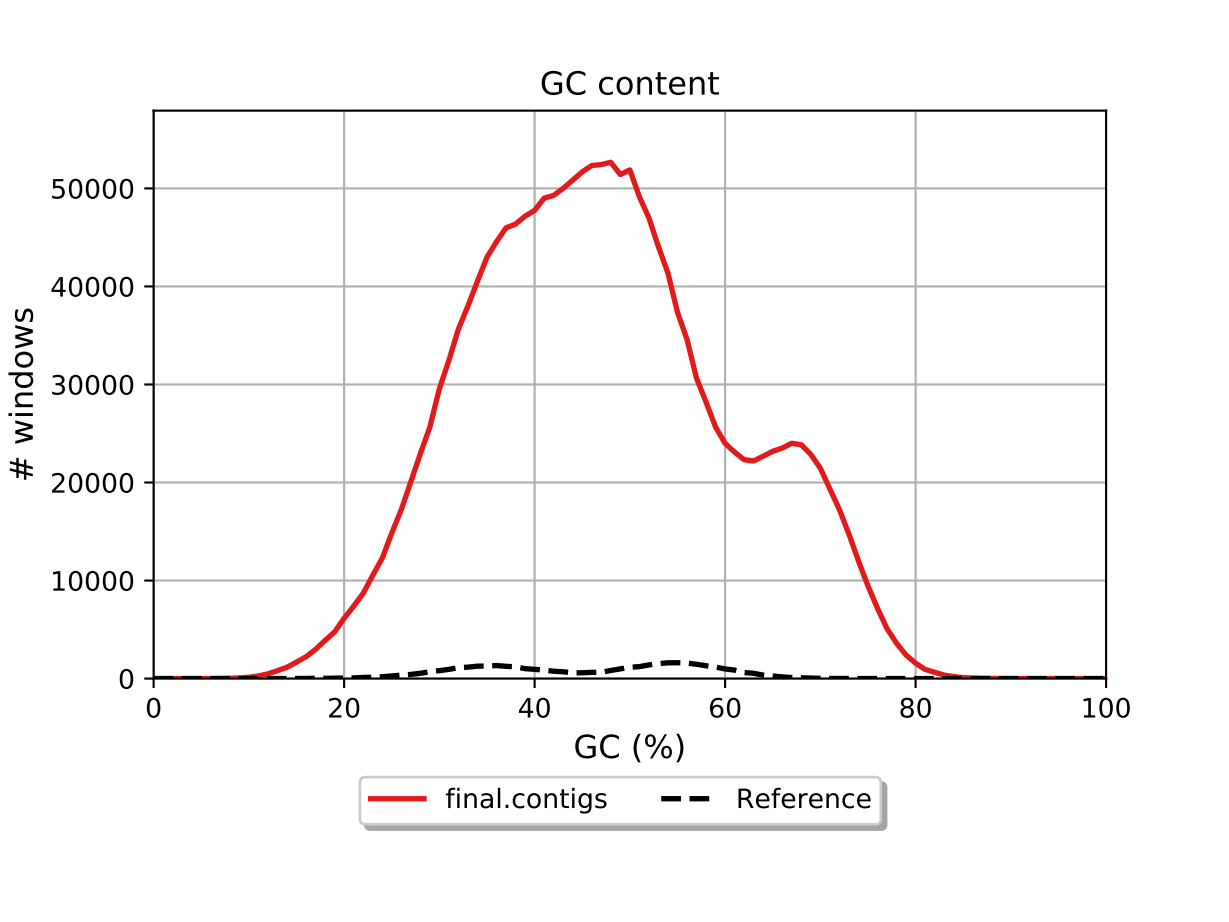
Unaligned report

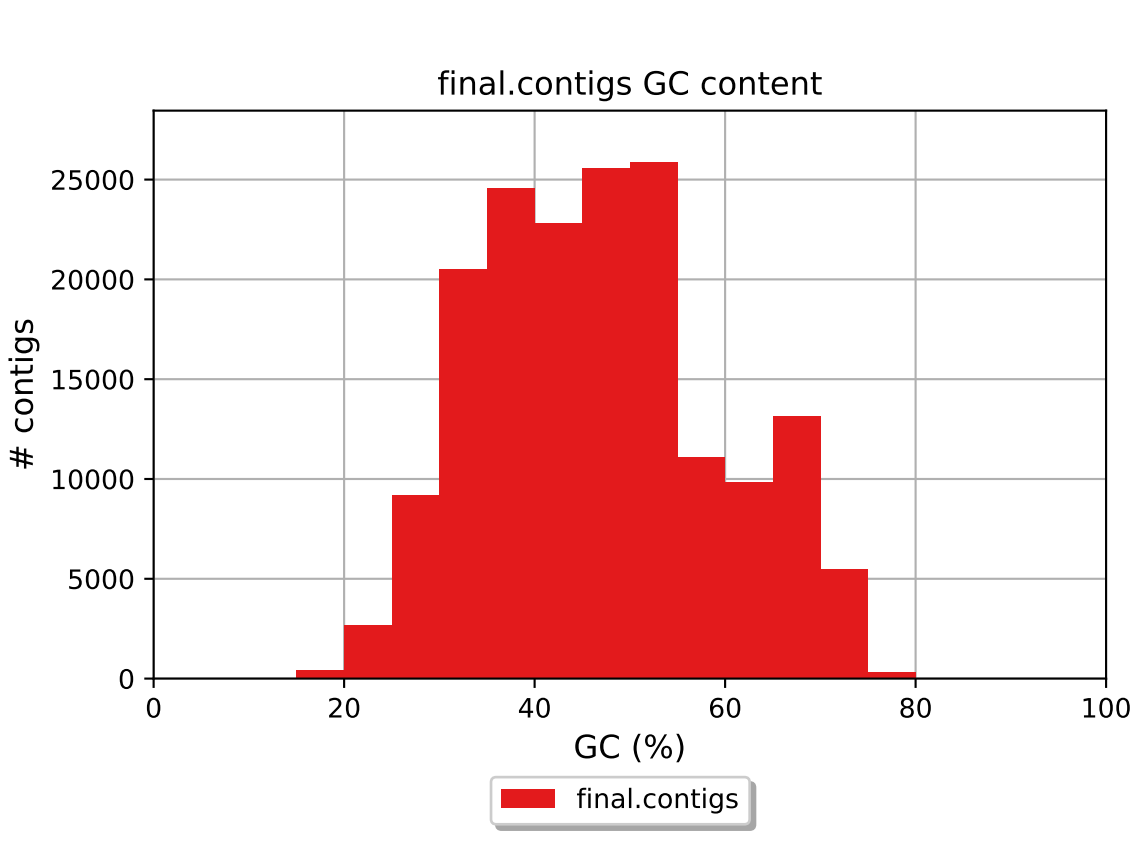
	final.contigs
# fully unaligned contigs	170414
Fully unaligned length	179346006
# partially unaligned contigs	238
Partially unaligned length	485424
# N's	0

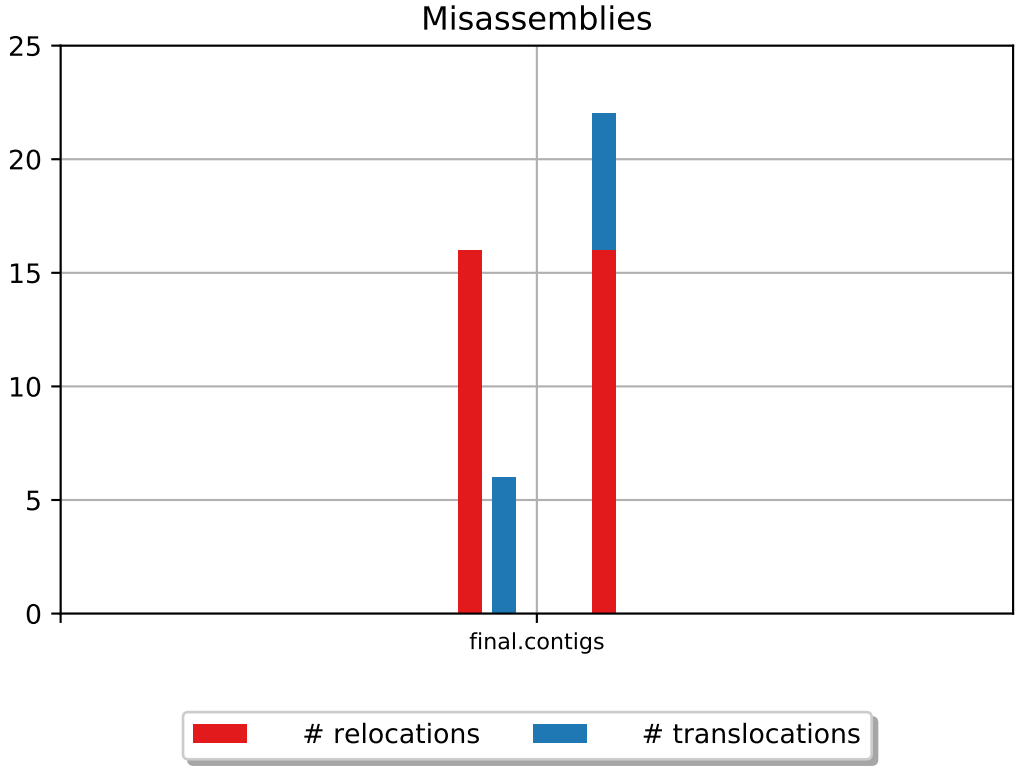
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

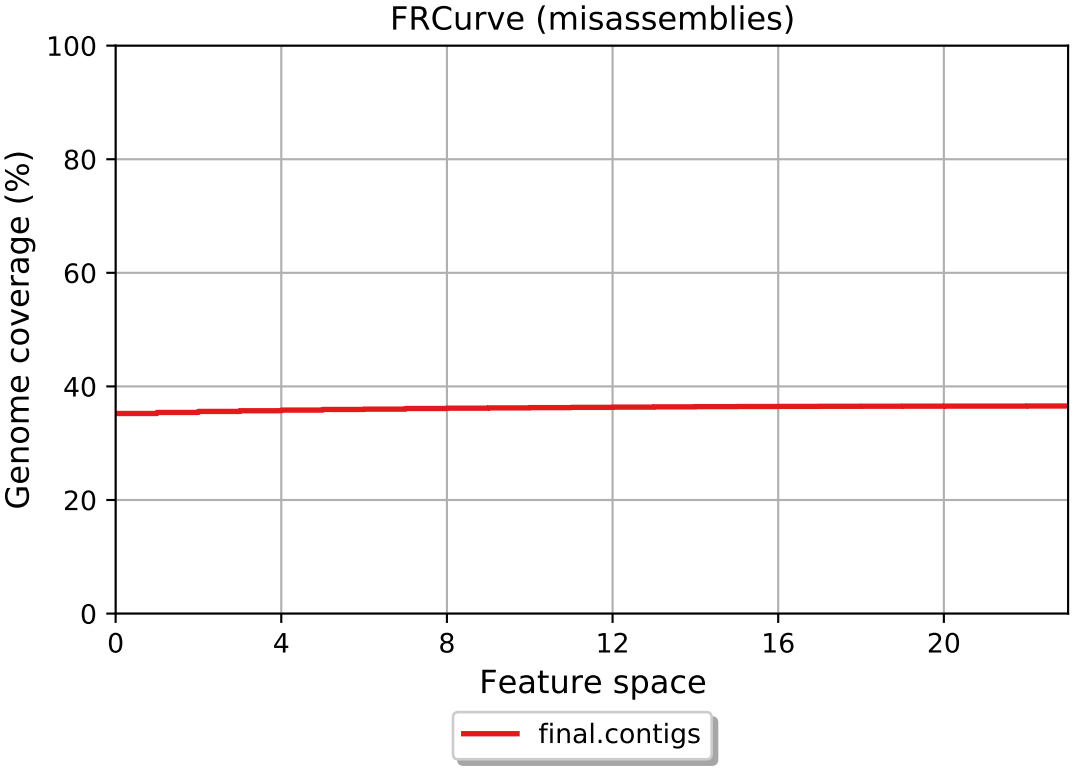

Nx
Contig length (kbp)
160
120
80
40
0
0
20
40
60
80
100
x
final.contigs

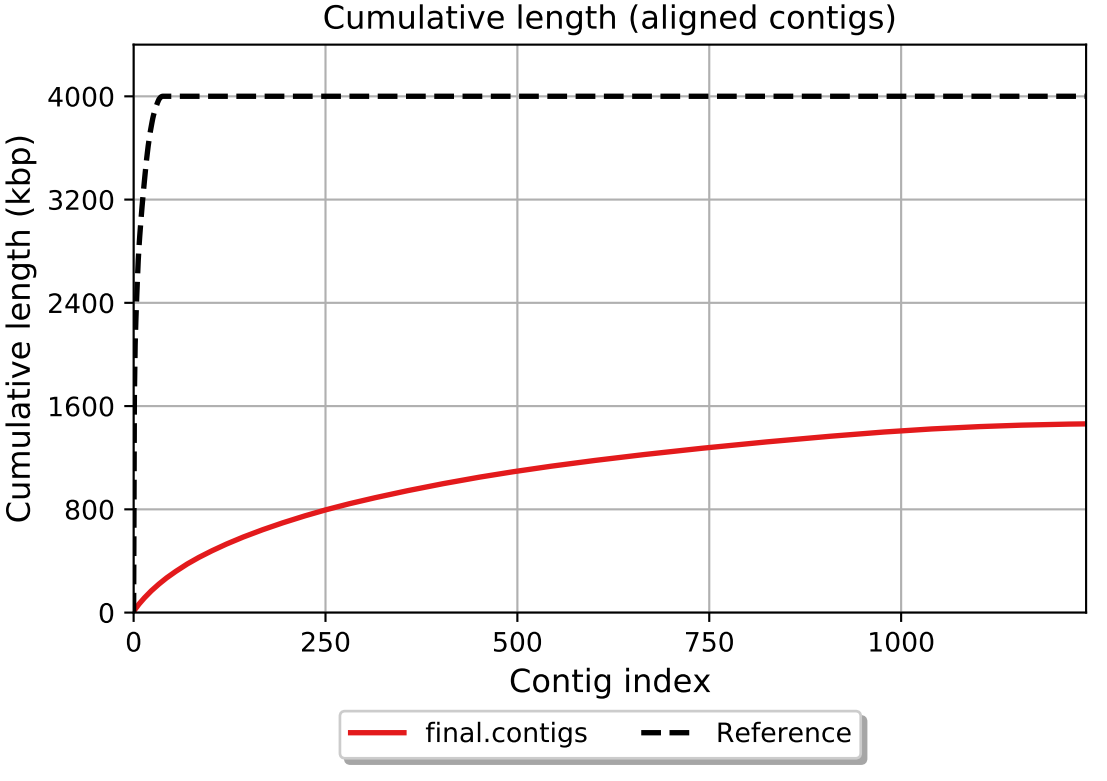

Cumulative length
Cumulative length (Mbp)
160
120
80
40
0
0
30000
60000
90000
120000
150000
Contig index
final.contigs
Reference

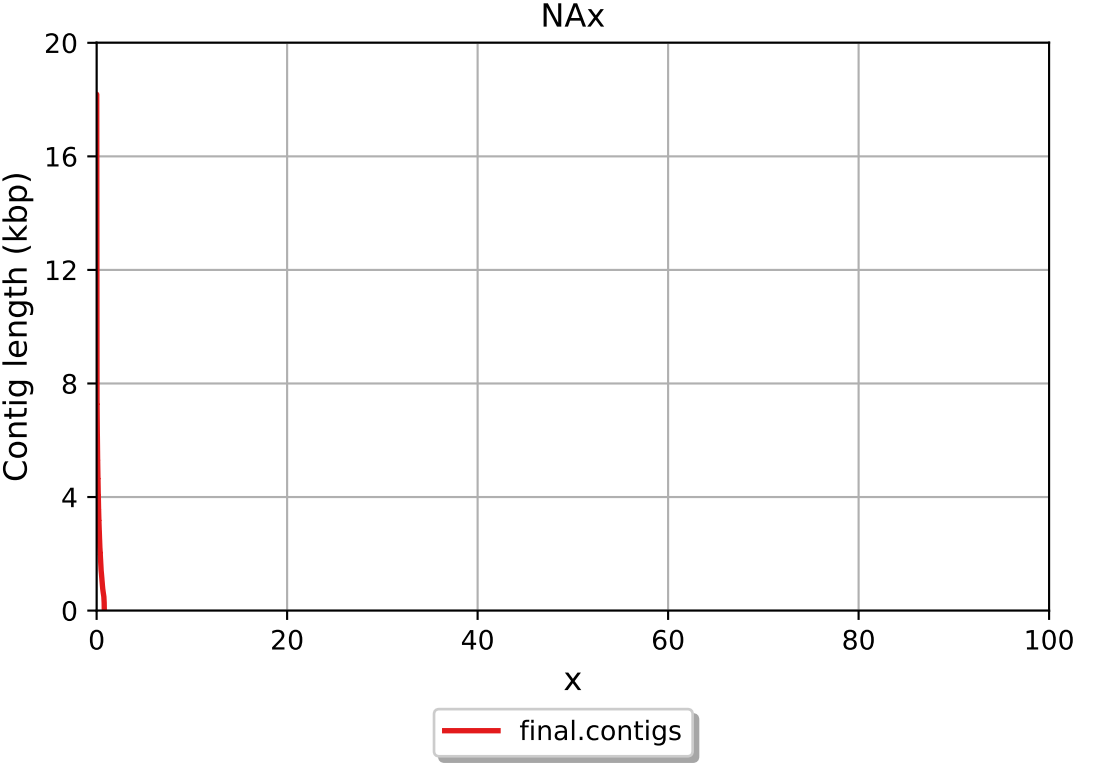

GC content
windows
50000
40000
30000
20000
10000
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference


final.contigs GC content
contigs
25000
20000
15000
10000
5000
0
0
20
40
60
80
100
GC (%)
final.contigs


Misassemblies
25
20
15
10
5
0
final.contigs
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
250
500
750
1000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs