Report

	final.contigs
# contigs (>= 1000 bp)	875
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1253807
Total length (>= 5000 bp)	6306
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2959
Largest contig	6306
Total length	2714231
Reference length	4413398
GC (%)	49.93
Reference GC (%)	49.98
N50	945
NG50	656
N90	576
NG90	-
auN	1117.5
auNG	687.3
L50	982
LG50	2070
L90	2453
LG90	-
# misassemblies	19
# misassembled contigs	19
Misassembled contigs length	22573
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	0 + 62 part
Unaligned length	53132
Genome fraction (%)	53.583
Duplication ratio	1.076
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4166.04
# indels per 100 kbp	92.07
Largest alignment	4227
Total aligned length	2544863
NA50	873
NGA50	577
NA90	501
NGA90	-
auNA	1004.0
auNGA	617.5
LA50	1046
LGA50	2243
LA90	2683
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

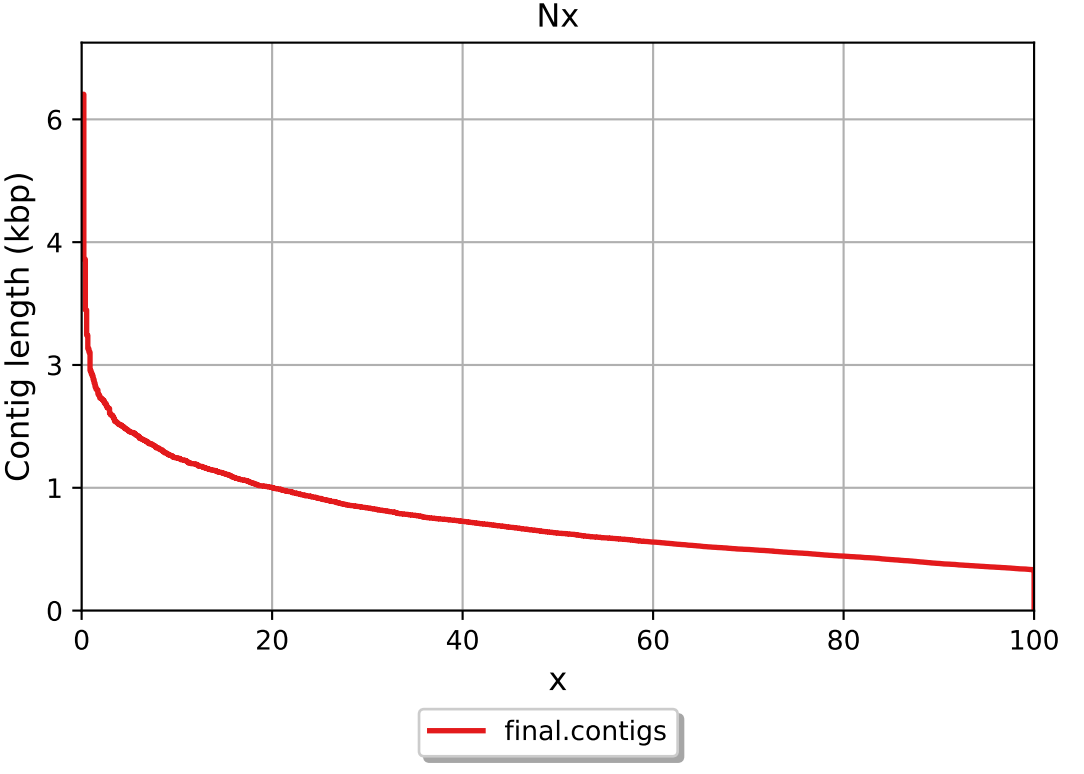
	final.contigs
# misassemblies	19
# contig misassemblies	19
# c. relocations	16
# c. translocations	1
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	19
Misassembled contigs length	22573
# possibly misassembled contigs	52
# possible misassemblies	55
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	106020
# indels	2343
# indels (<= 5 bp)	2262
# indels (> 5 bp)	81
Indels length	4661

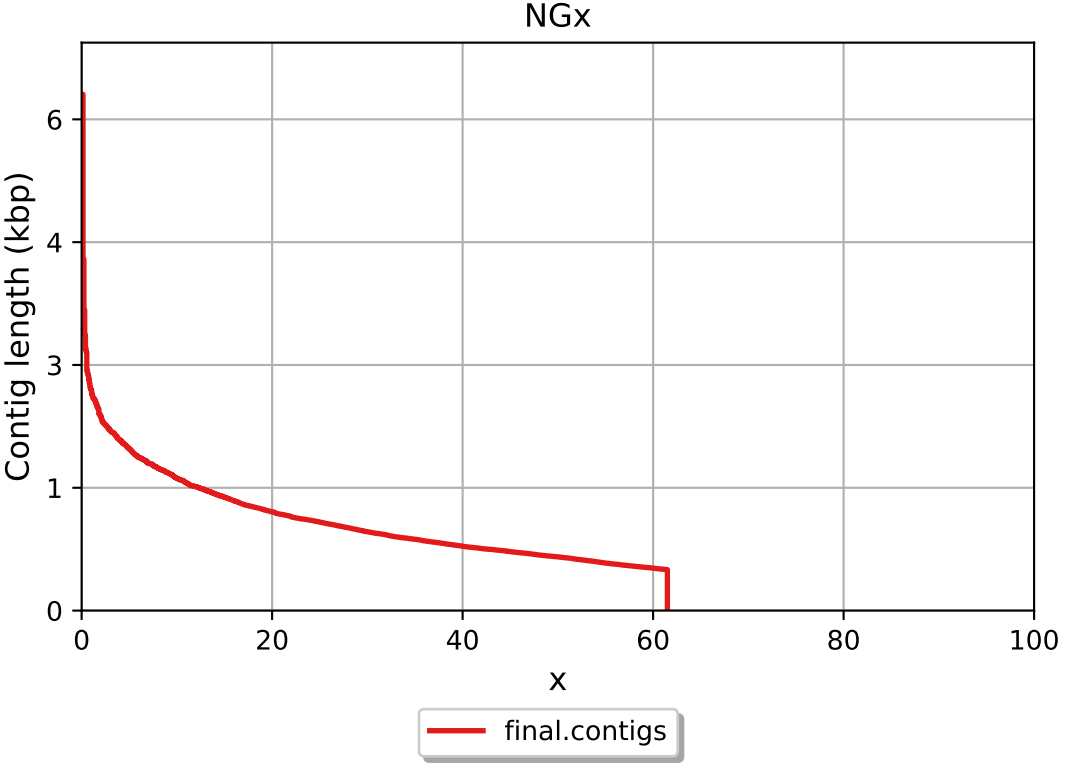
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

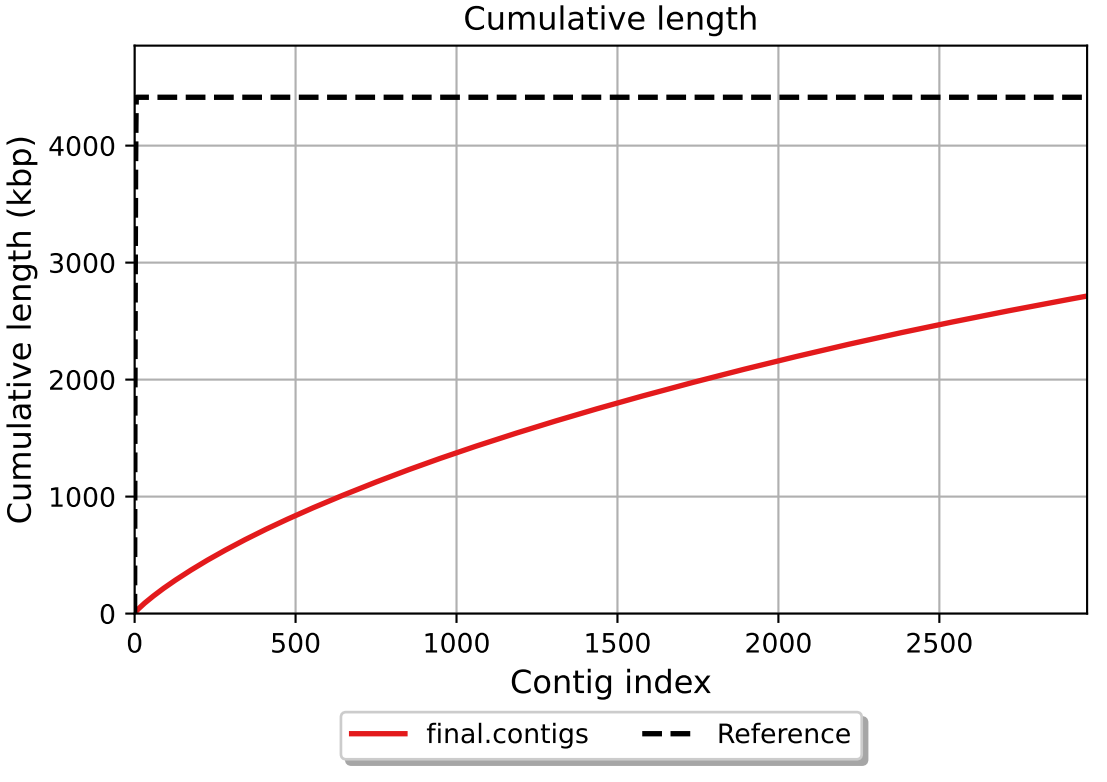
Unaligned report

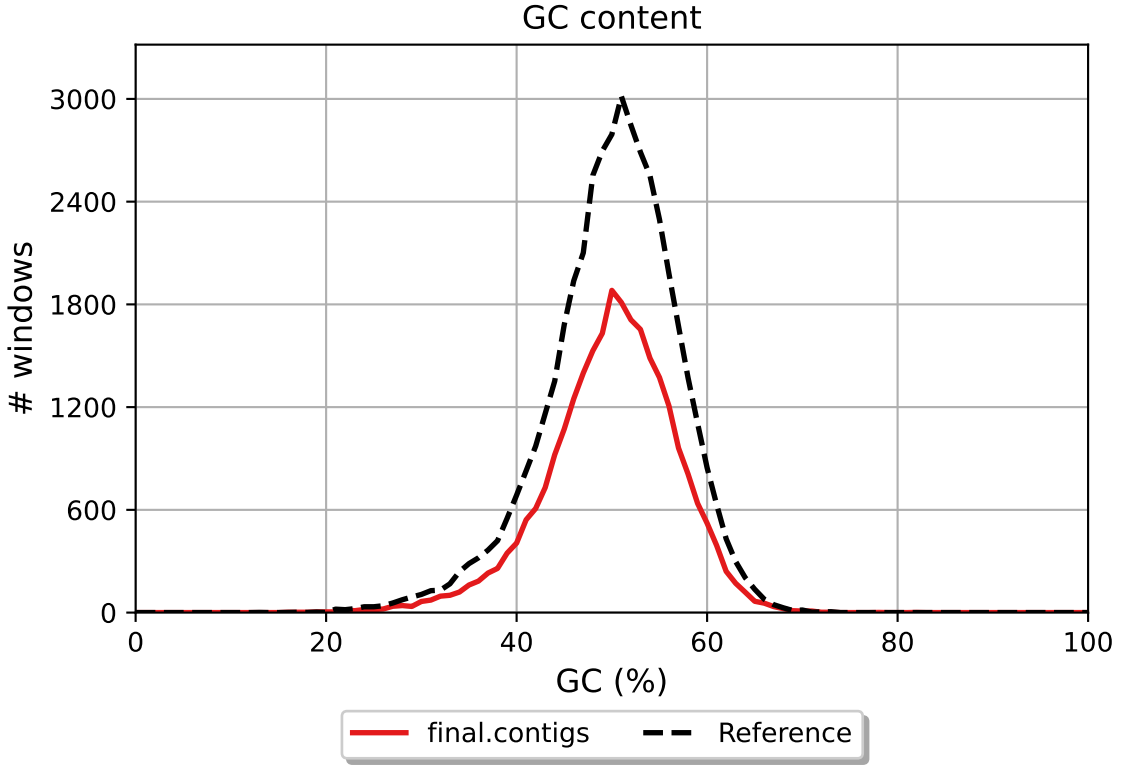
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	62
Partially unaligned length	53132
# N's	0

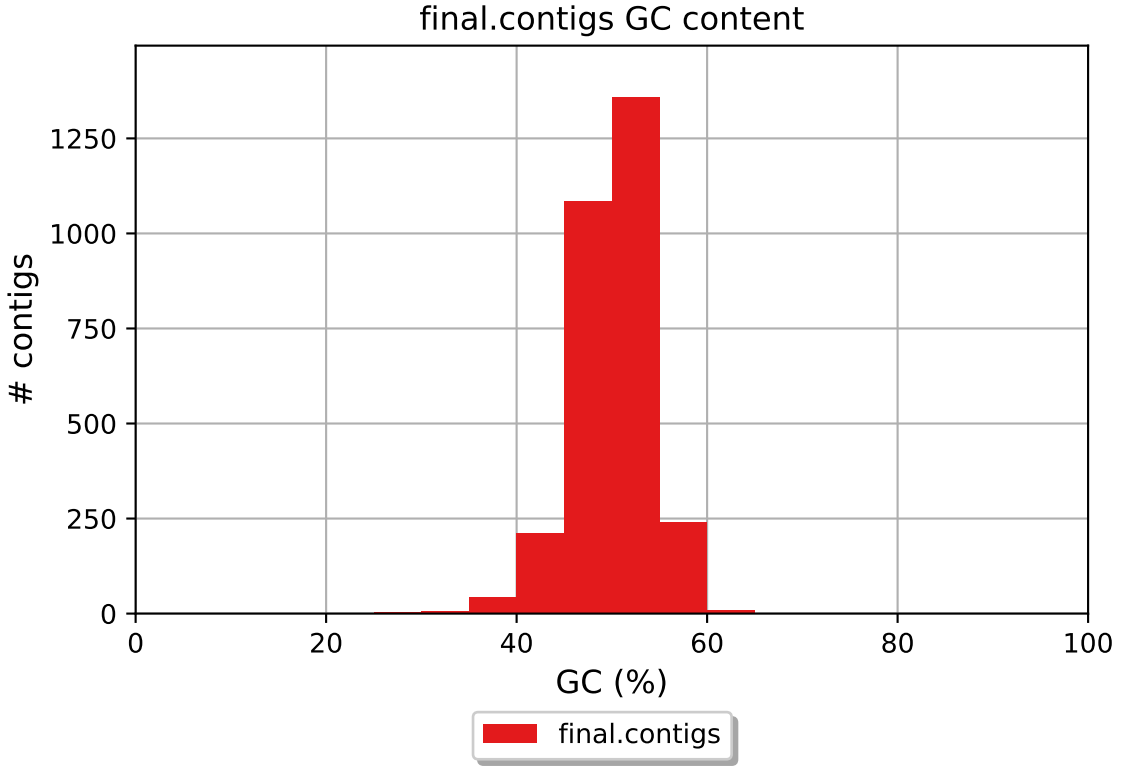
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

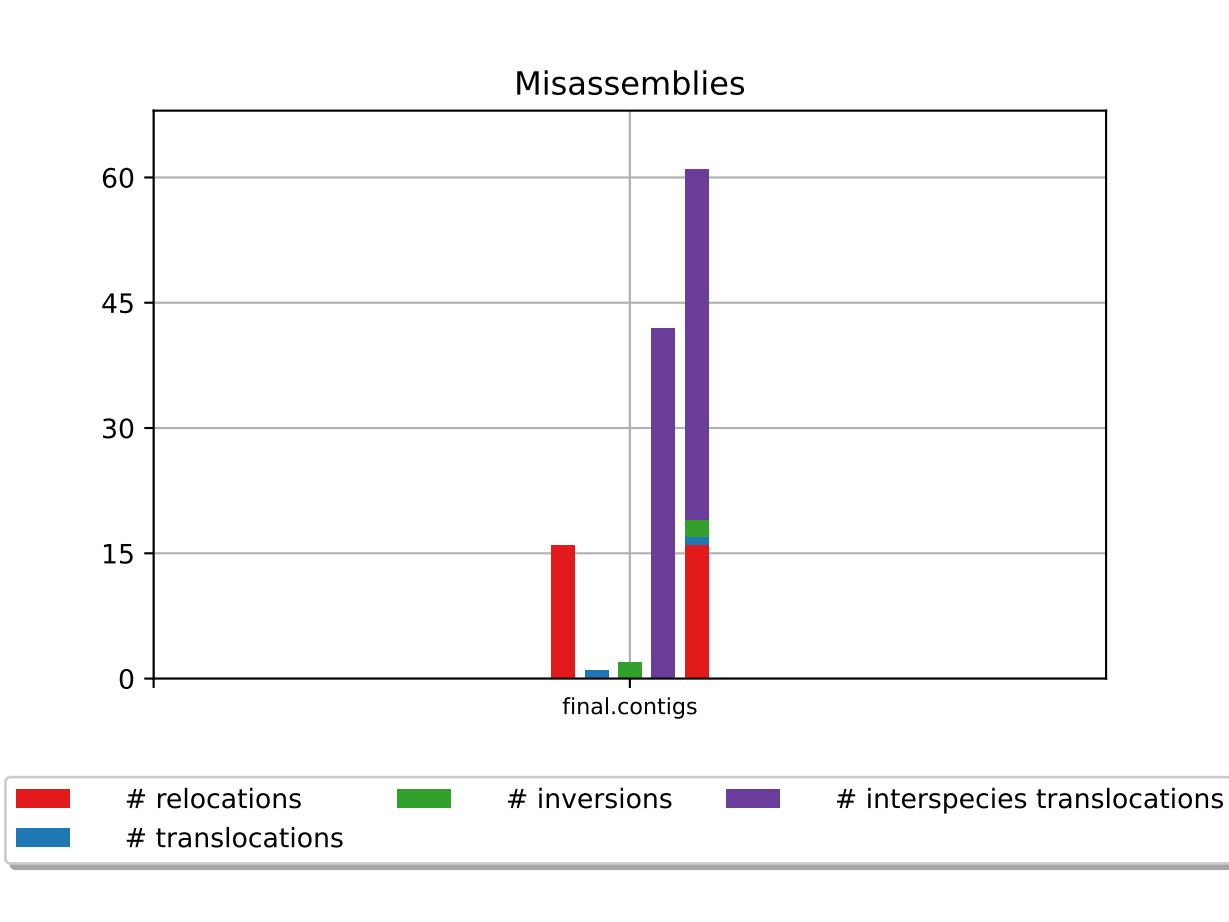

Nx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
final.contigs

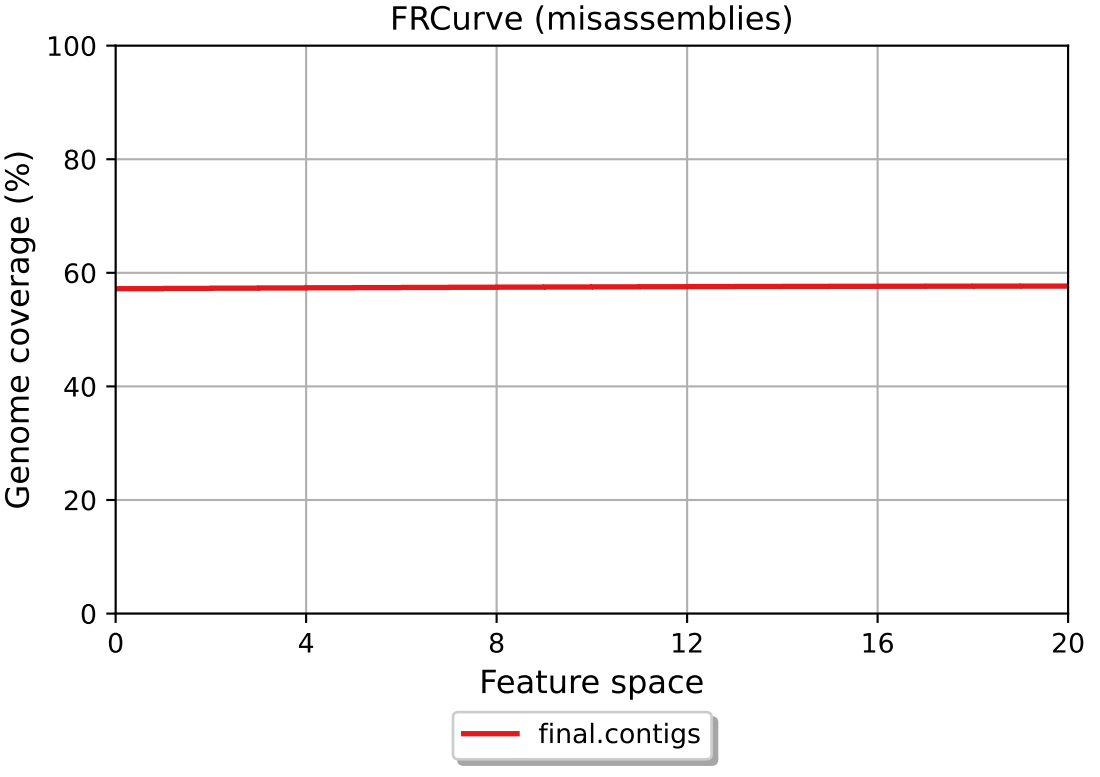

NGx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
final.contigs

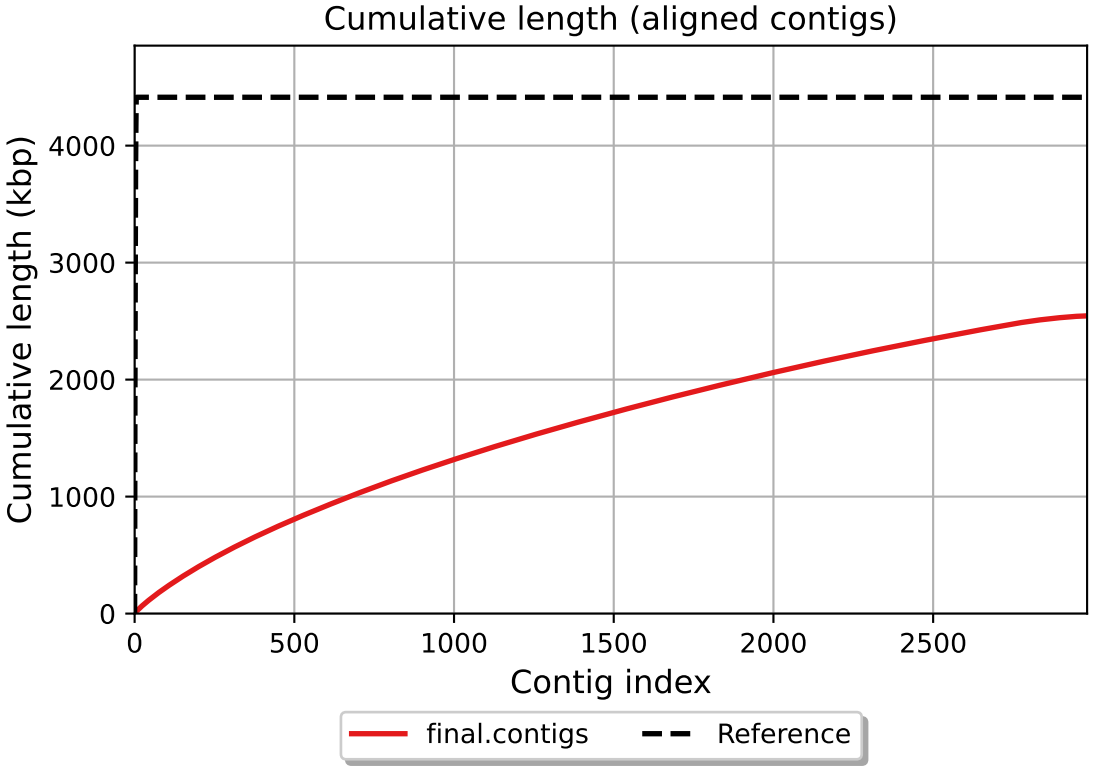

Cumulative length
Cumulative length (kbp)
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference

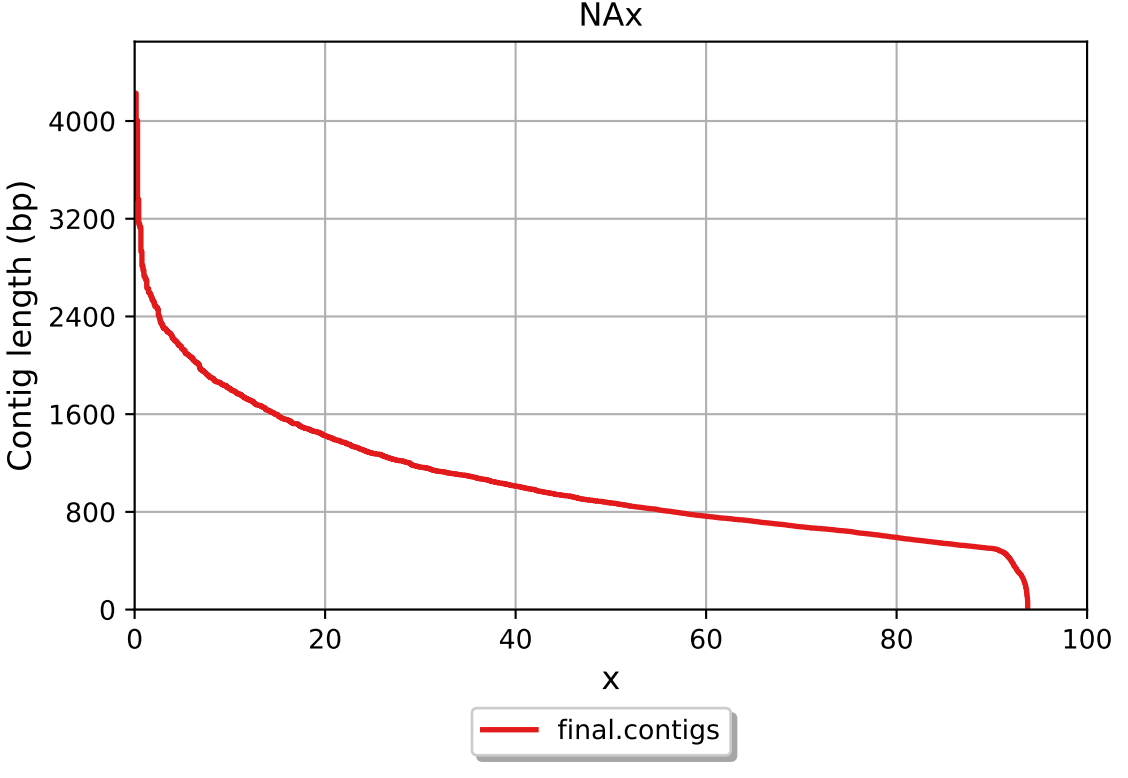

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

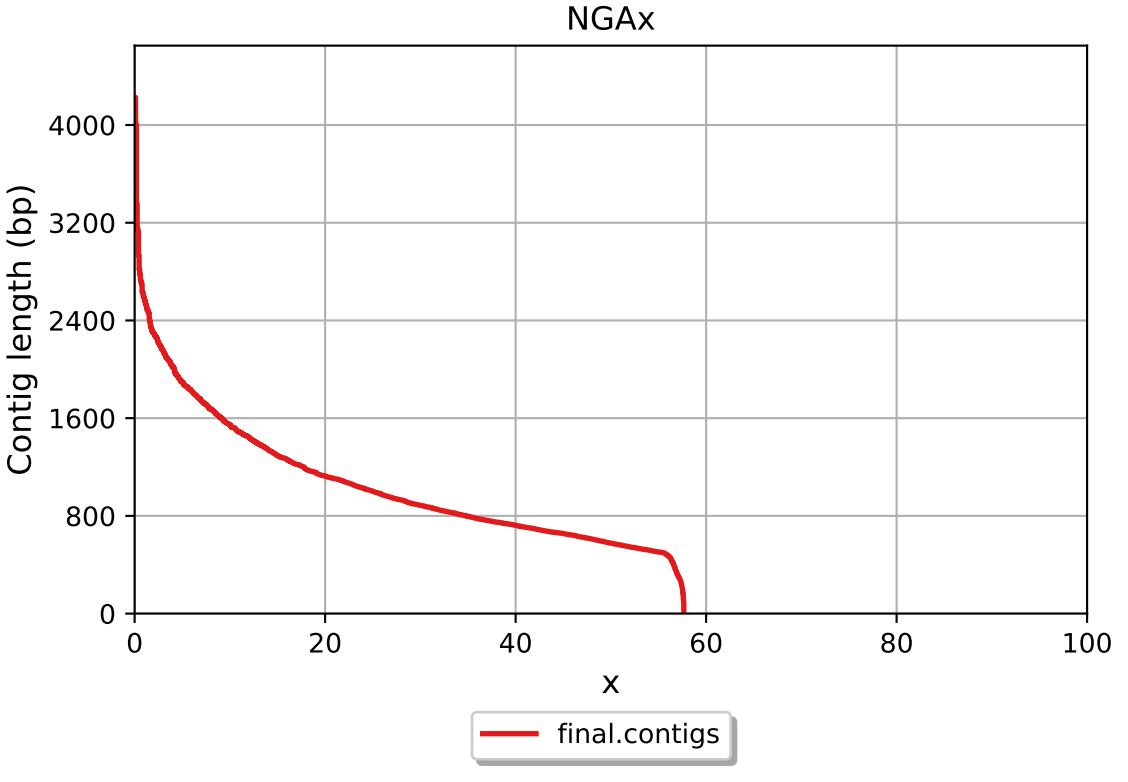

final.contigs GC content
contigs
1250
1000
750
500
250
0
0
20
40
60
80
100
GC (%)
final.contigs


Misassemblies
60
45
30
15
0
final.contigs
relocations
translocations
inversions
interspecies 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)
0
1000
2000
3000
4000
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


NAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs