Report

	final.contigs
# contigs (>= 1000 bp)	469
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	720335
Total length (>= 5000 bp)	12565
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1369
Largest contig	7528
Total length	1358321
Reference length	2224914
GC (%)	61.38
Reference GC (%)	60.84
N50	1040
NG50	670
N75	737
L50	429
LG50	953
L75	820
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	7320
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	6 + 41 part
Unaligned length	61780
Genome fraction (%)	55.804
Duplication ratio	1.044
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1155.45
# indels per 100 kbp	5.64
Largest alignment	3896
Total aligned length	1279761
NA50	981
NGA50	621
NA75	680
LA50	457
LGA50	1020
LA75	876

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

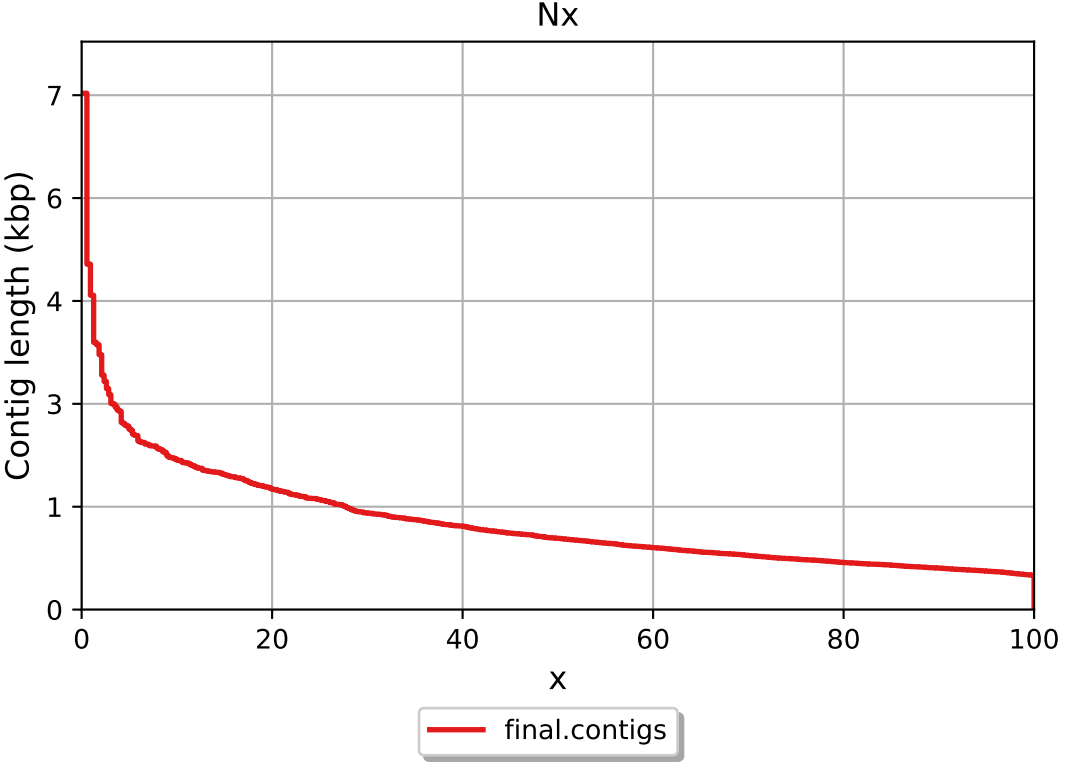
	final.contigs
# misassemblies	6
# contig misassemblies	6
# c. relocations	6
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	7320
# possibly misassembled contigs	46
# possible misassemblies	55
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	14346
# indels	70
# indels (<= 5 bp)	62
# indels (> 5 bp)	8
Indels length	266

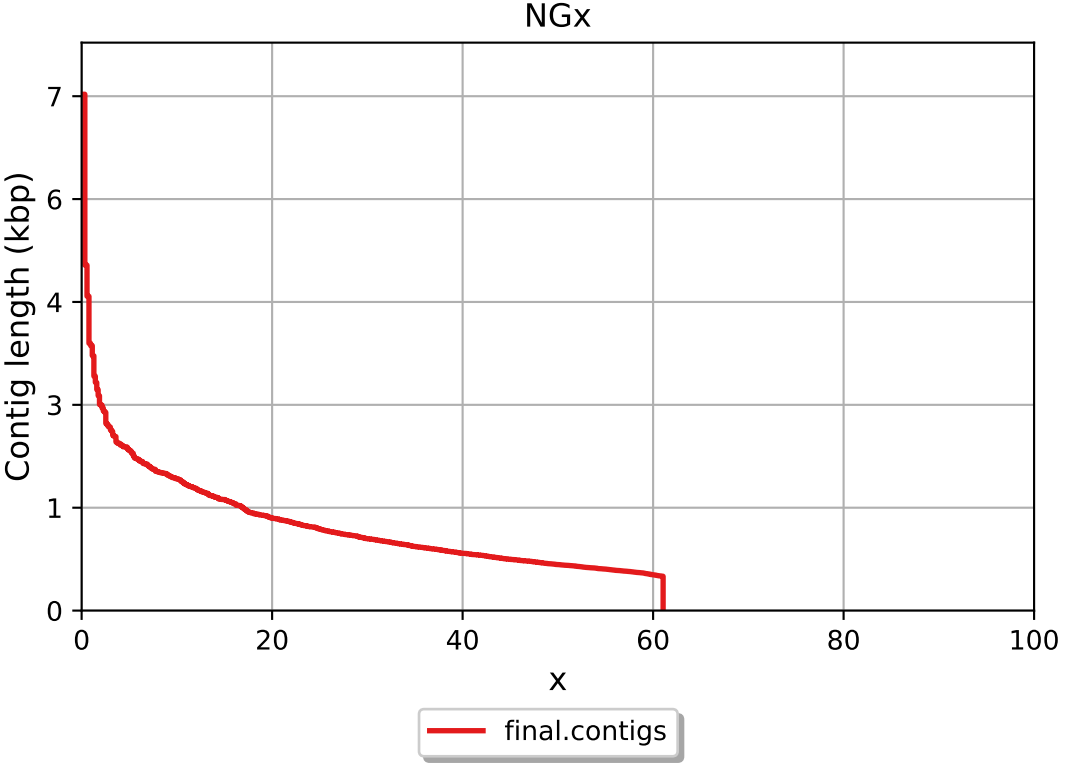
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

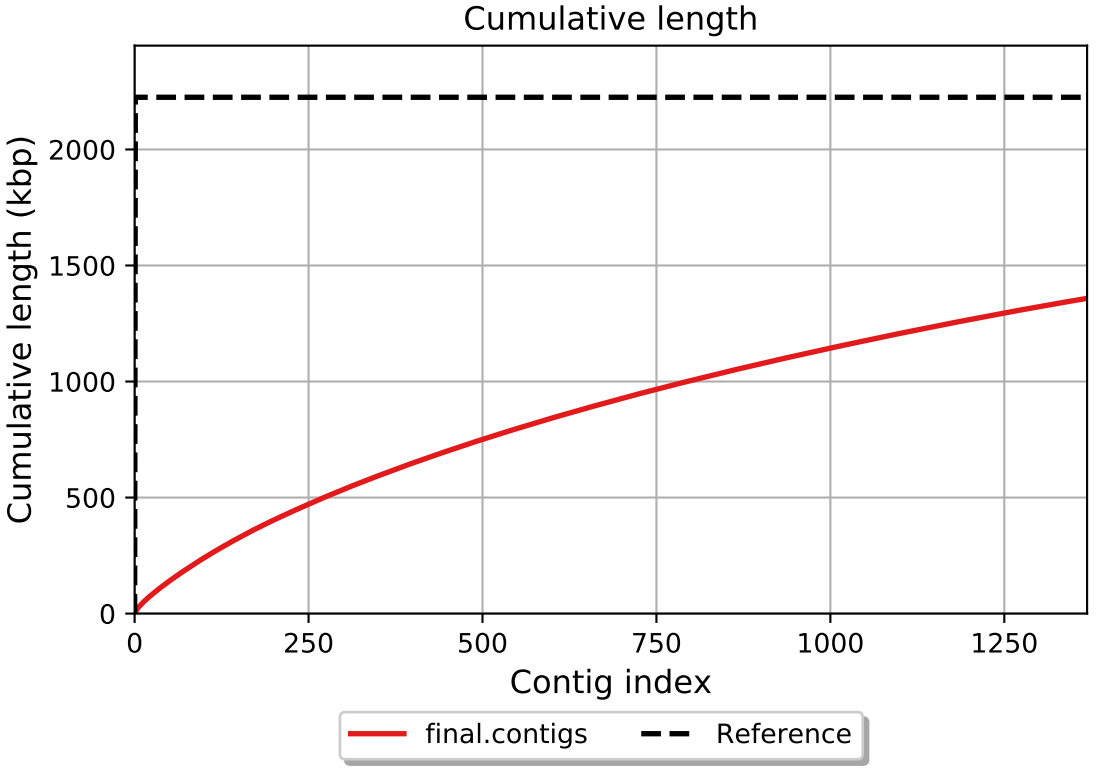
Unaligned report

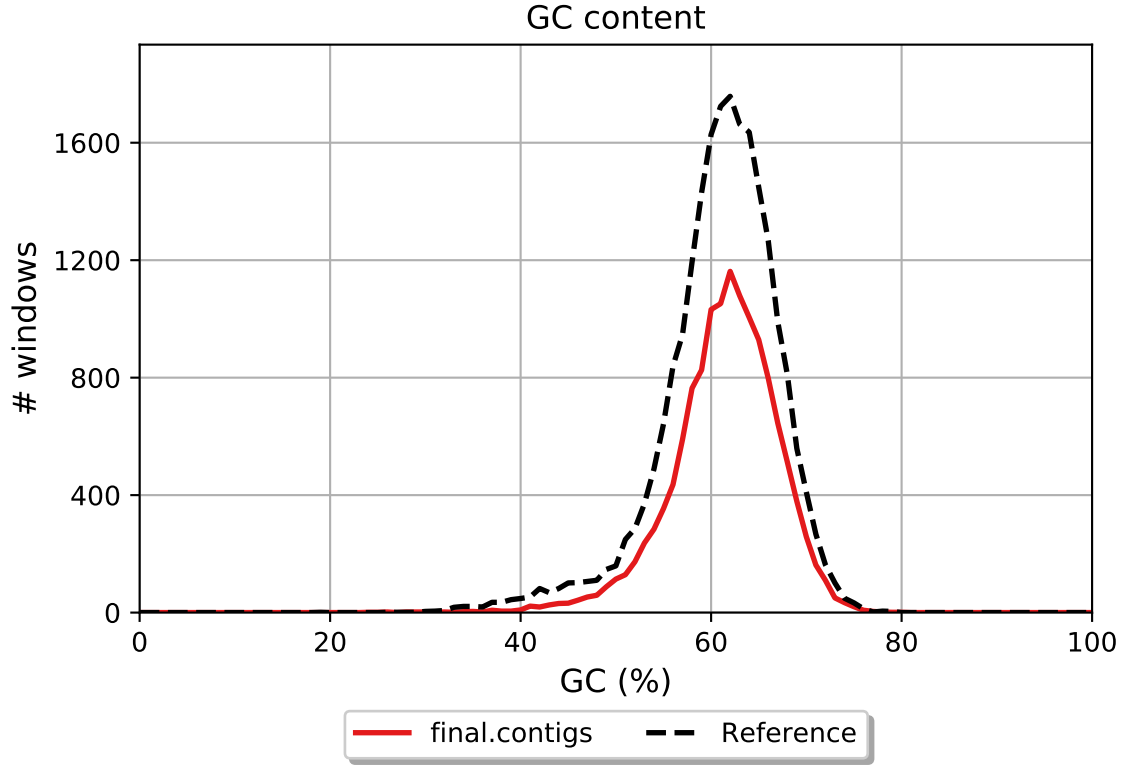
	final.contigs
# fully unaligned contigs	6
Fully unaligned length	6805
# partially unaligned contigs	41
Partially unaligned length	54975
# N's	0

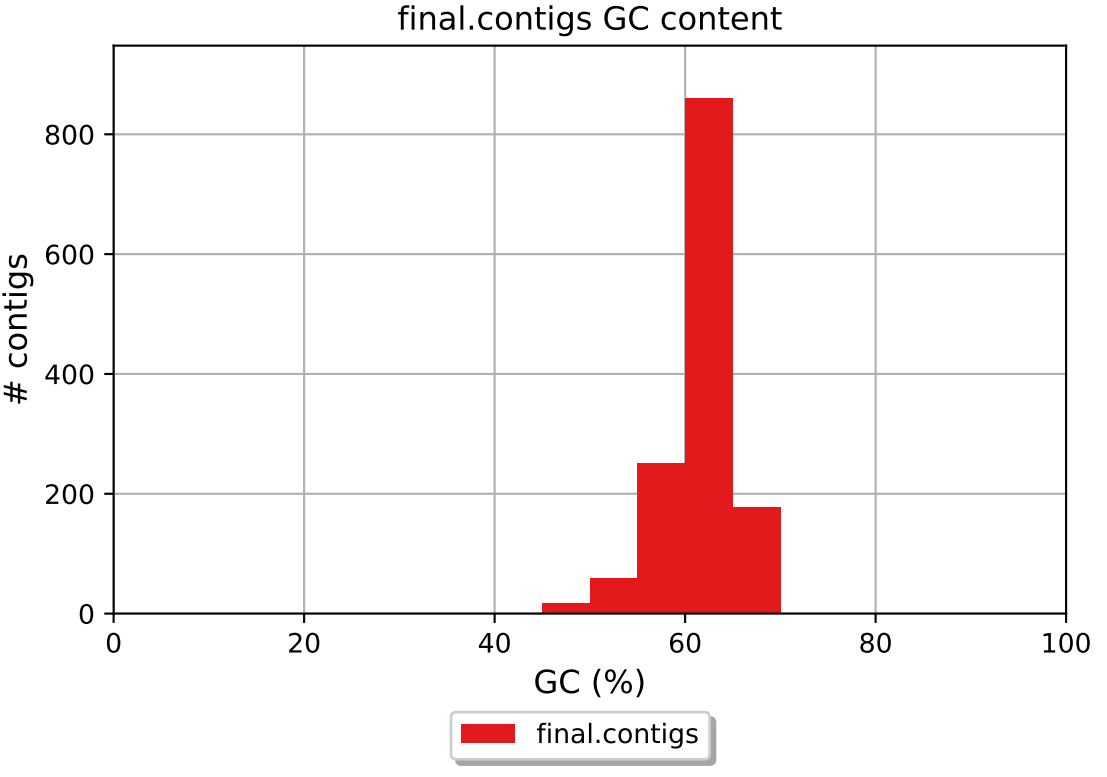
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

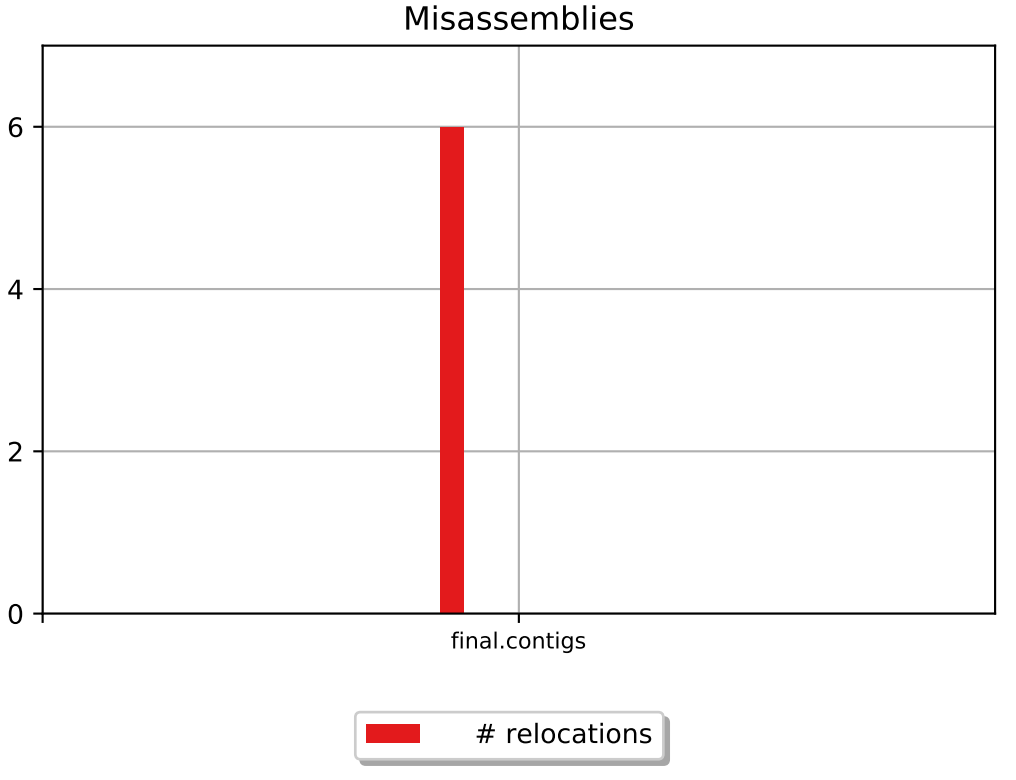

Nx
Contig length (kbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
final.contigs

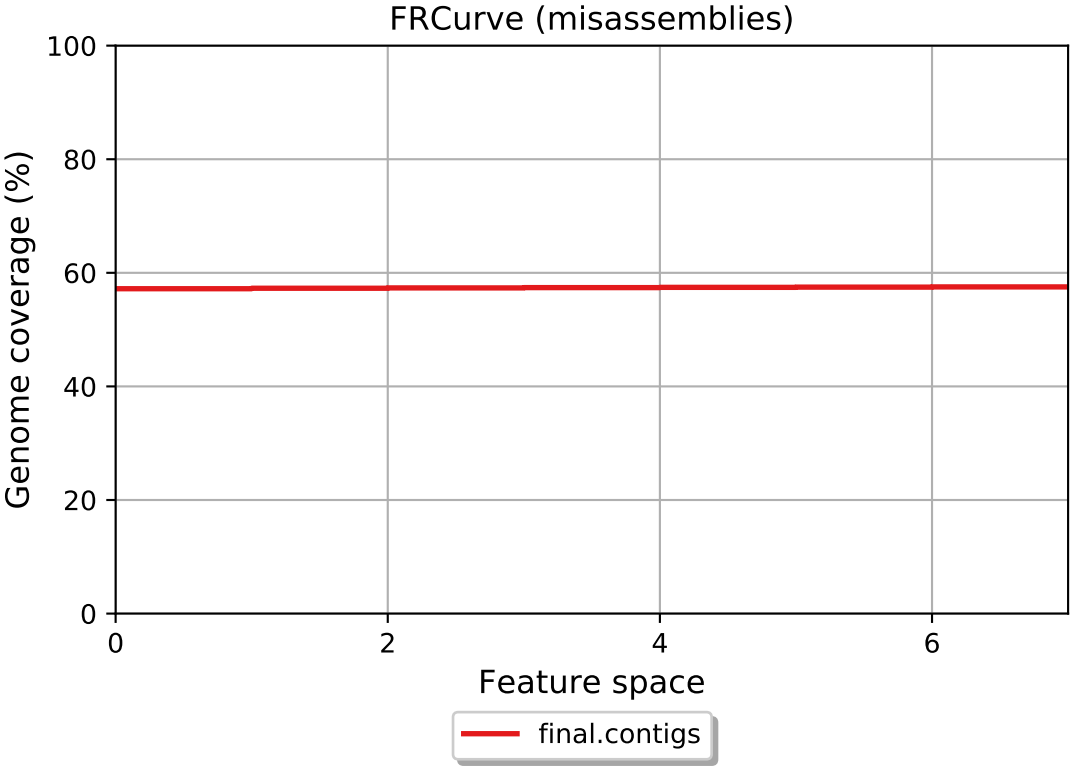

NGx
Contig length (kbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
final.contigs

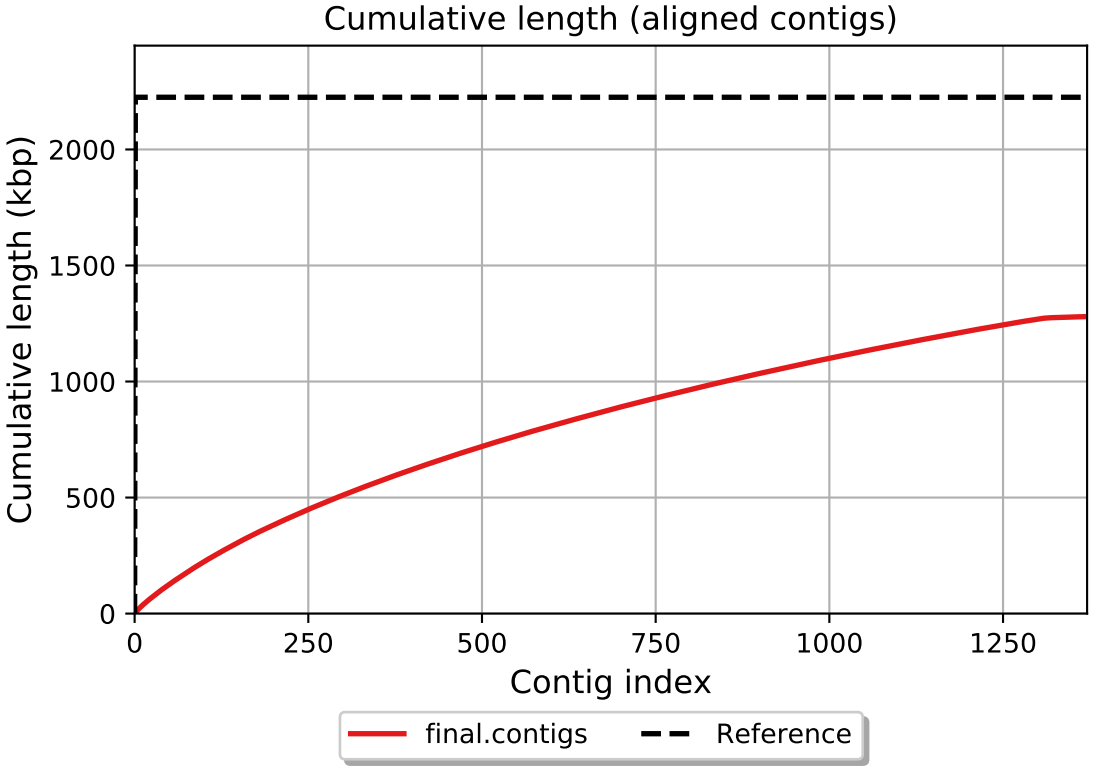

Cumulative length
Cumulative length (kbp)
2000
1500
1000
500
0
0
250
500
750
1000
1250
Contig index
final.contigs
Reference

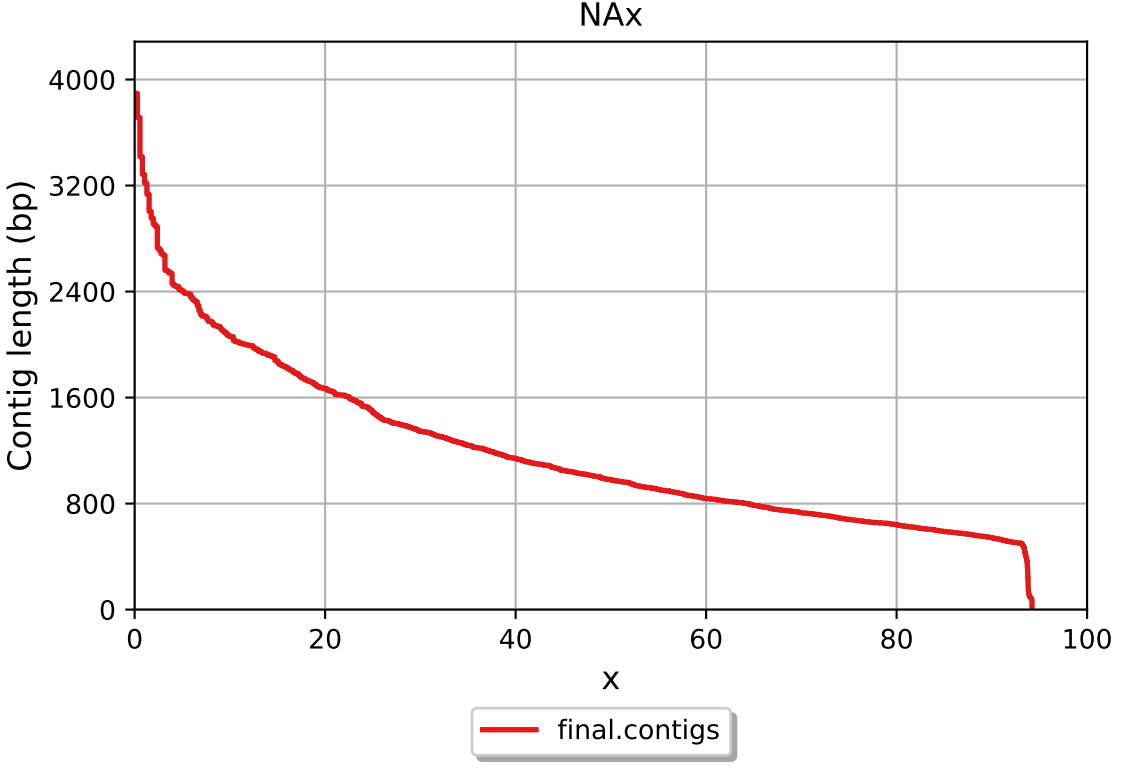

GC content
windows
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

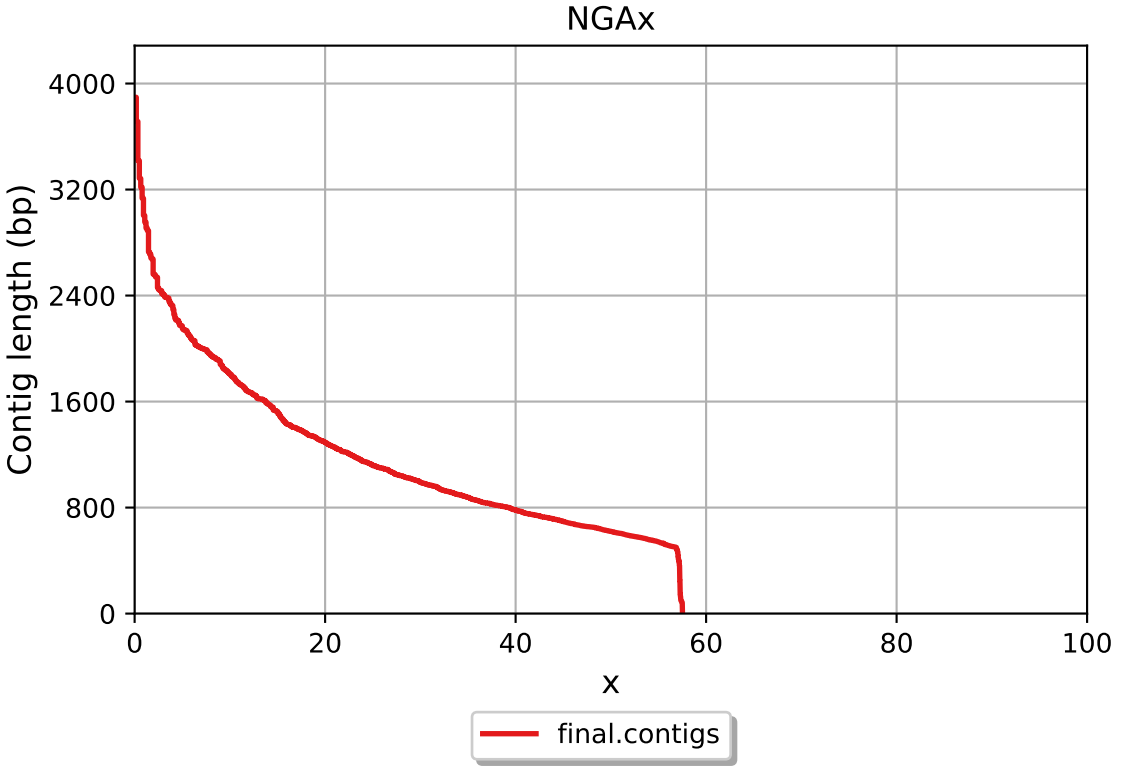

final.contigs GC content
contigs
0
200
400
600
800
0
20
40
60
80
100
GC (%)
final.contigs


Misassemblies
6
4
2
0
final.contigs
relocations


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
1500
1000
500
0
0
250
500
750
1000
1250
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