Report

	final.contigs
# contigs (>= 1000 bp)	381
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	507664
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2231
Largest contig	3389
Total length	1777094
Reference length	4621502
GC (%)	55.40
Reference GC (%)	56.54
N50	799
NG50	-
N90	548
NG90	-
auN	916.2
auNG	352.3
L50	814
LG50	-
L90	1891
LG90	-
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	7466
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 61 part
Unaligned length	47033
Genome fraction (%)	33.288
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2726.01
# indels per 100 kbp	62.77
Largest alignment	3389
Total aligned length	1599407
NA50	714
NGA50	-
NA90	69
NGA90	-
auNA	775.8
auNGA	298.3
LA50	887
LGA50	-
LA90	2237
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

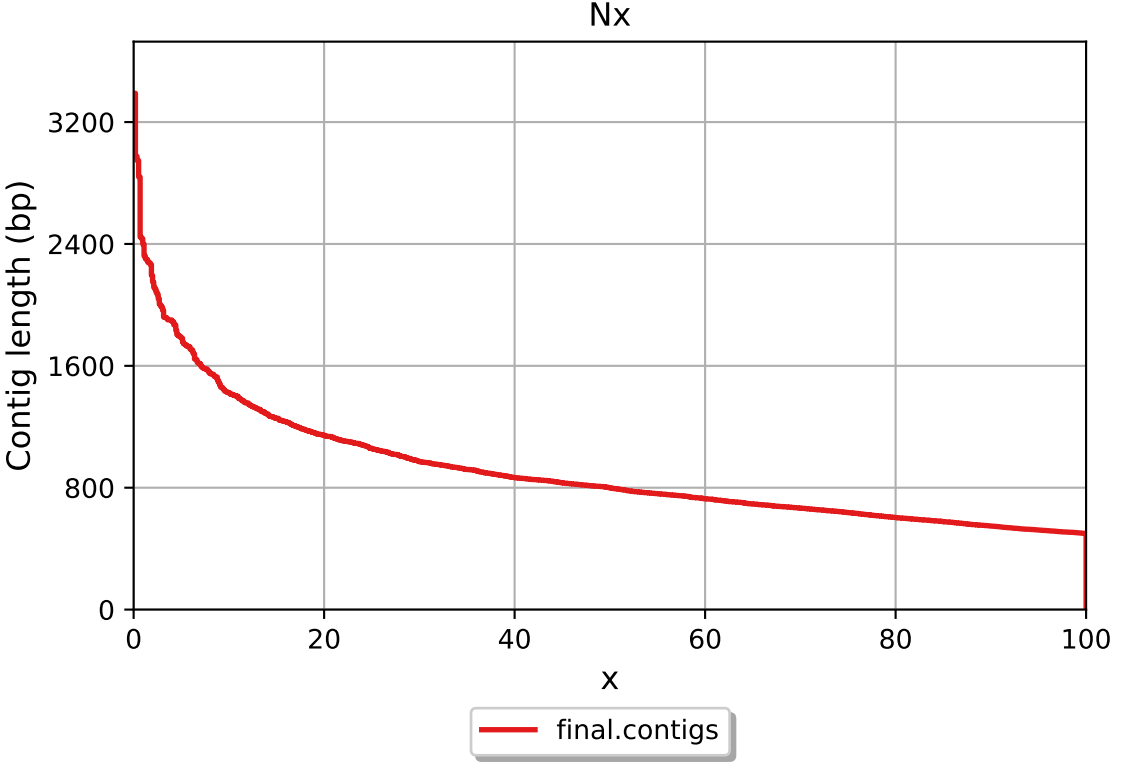
	final.contigs
# misassemblies	7
# contig misassemblies	7
# c. relocations	7
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	7
Misassembled contigs length	7466
# possibly misassembled contigs	45
# possible misassemblies	46
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	43600
# indels	1004
# indels (<= 5 bp)	963
# indels (> 5 bp)	41
Indels length	2764

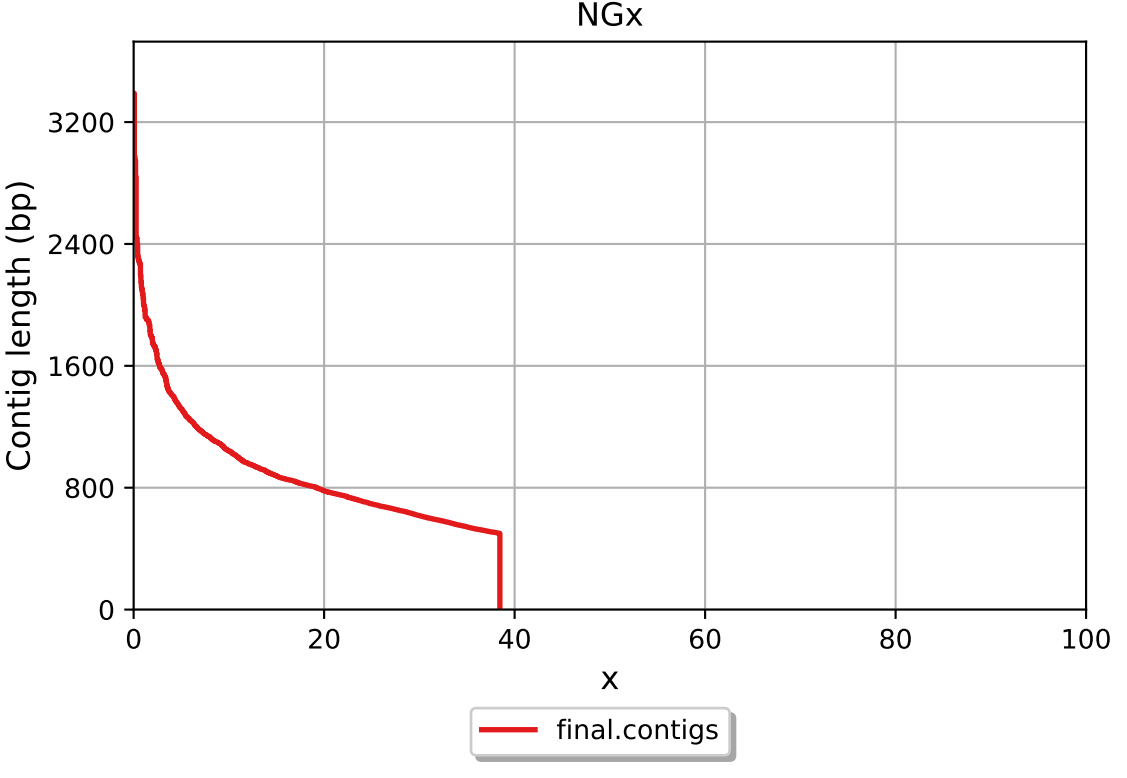
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

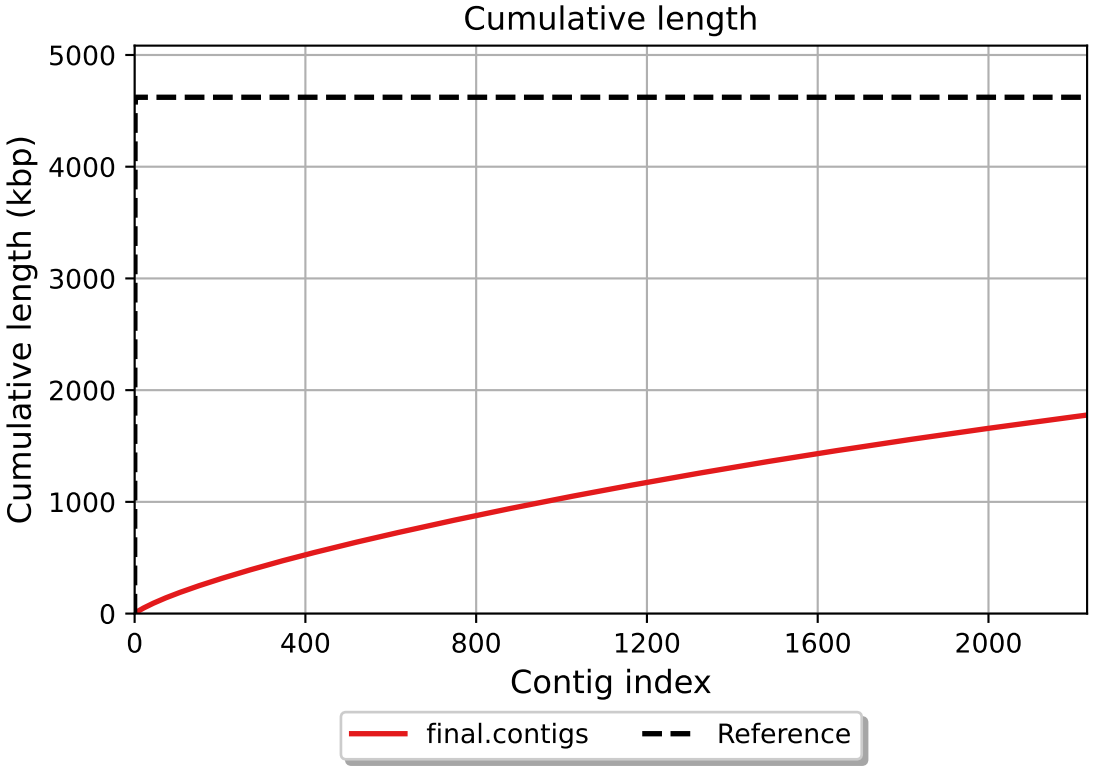
Unaligned report

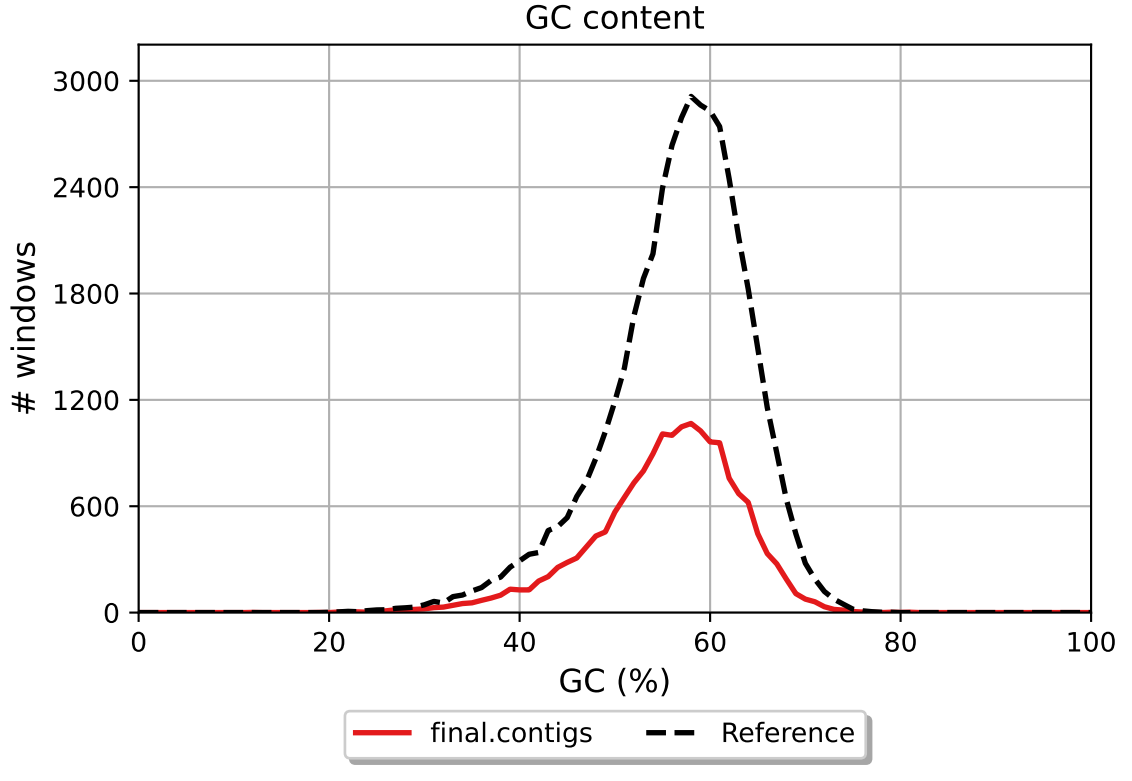
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	1086
# partially unaligned contigs	61
Partially unaligned length	45947
# N's	0

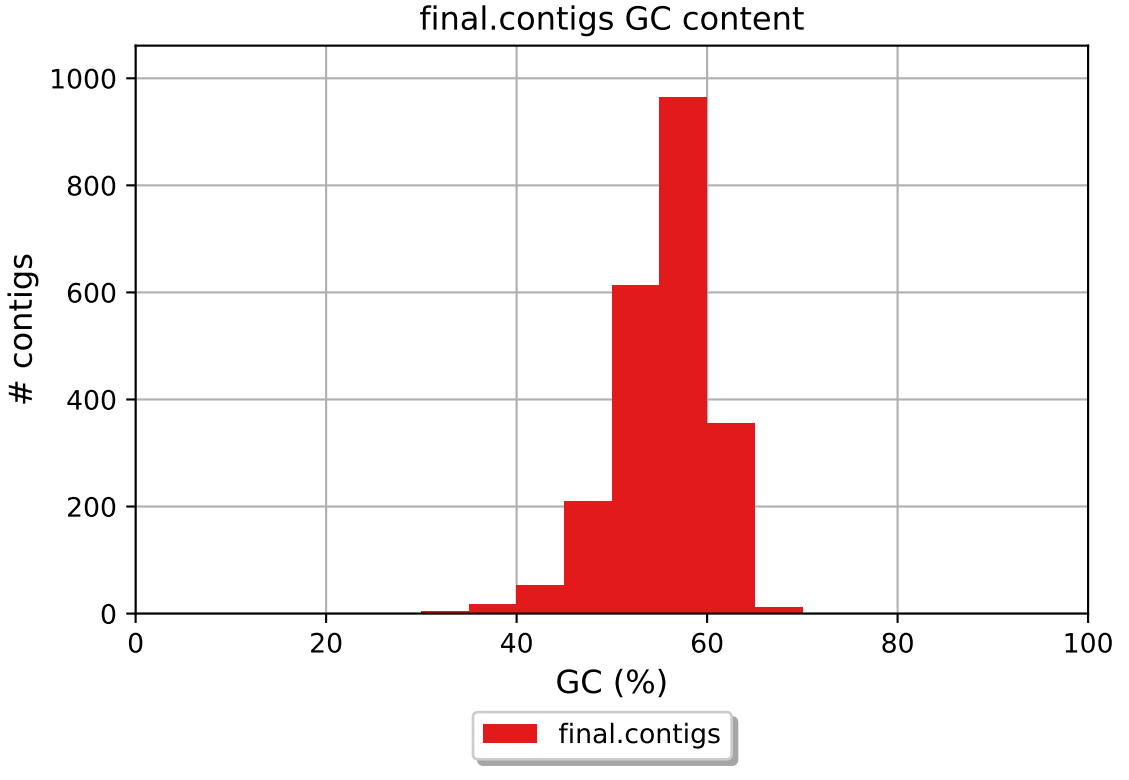
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


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

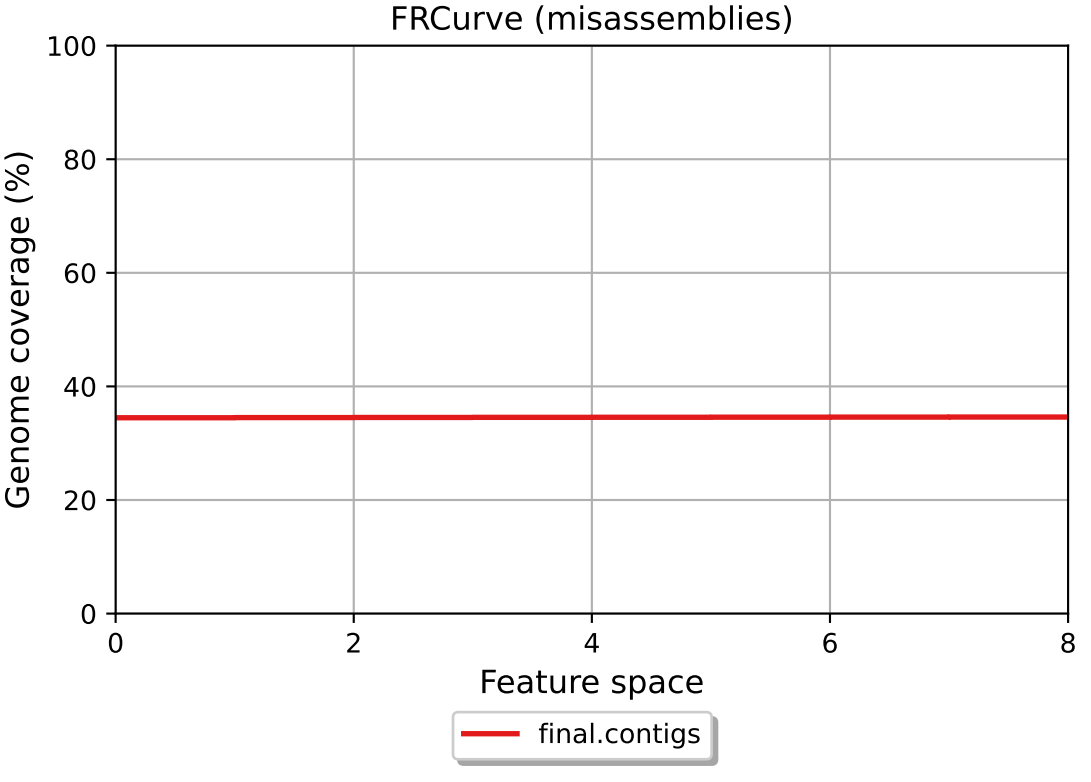

NGx
Contig length (bp)
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

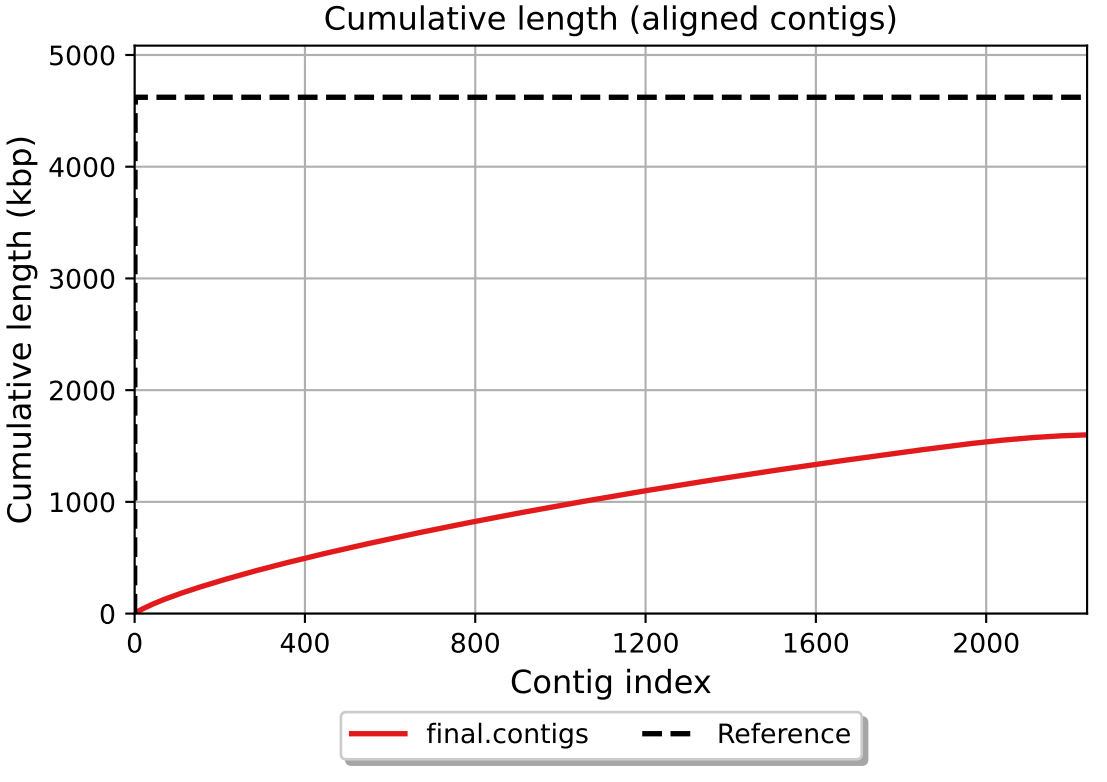

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
400
800
1200
1600
2000
Contig index
final.contigs
Reference

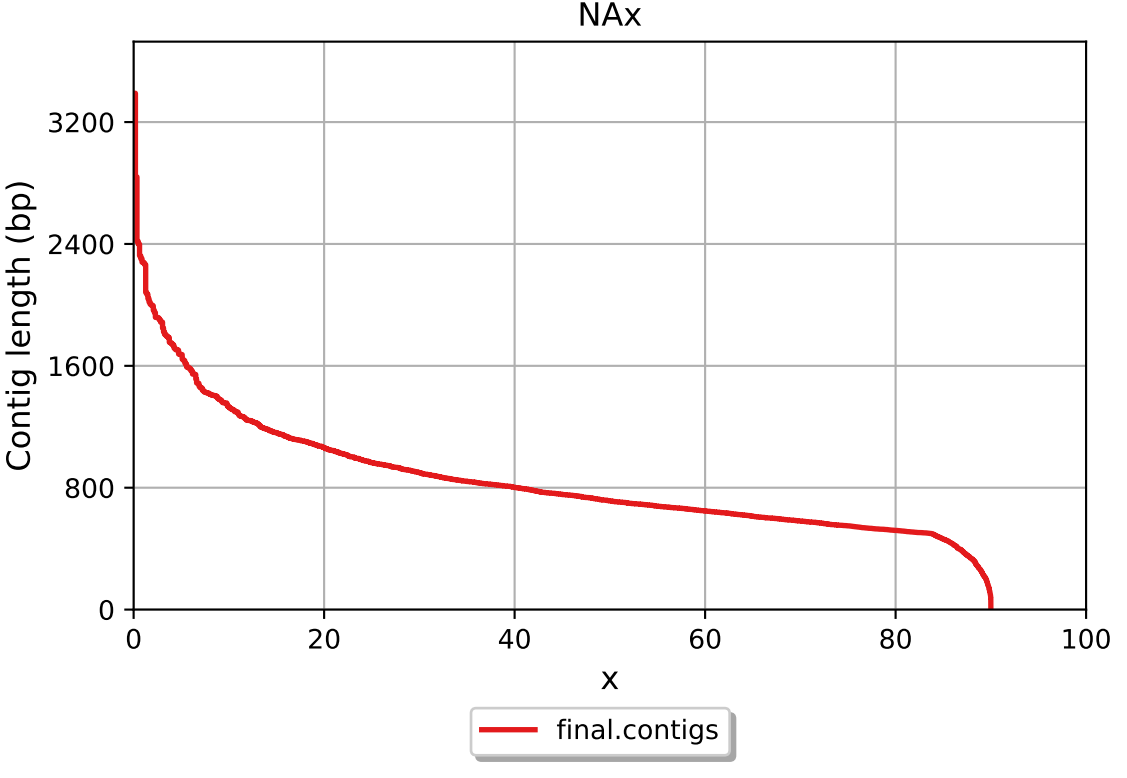

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

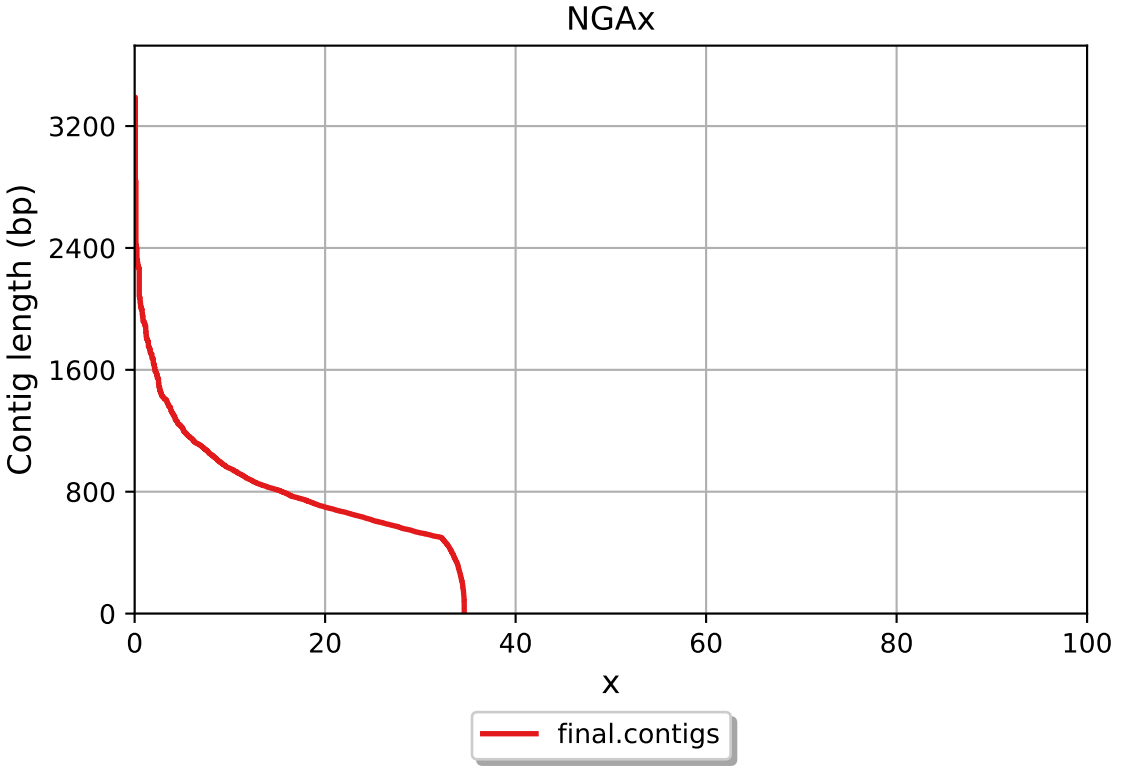

final.contigs GC content
contigs
1000
800
600
400
200
0
0
20
40
60
80
100
GC (%)
final.contigs

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


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
Feature space
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
400
800
1200
1600
2000
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