Report

	contigs
# contigs (>= 0 bp)	36
# contigs (>= 1000 bp)	12
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	9
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	3148469
Total length (>= 1000 bp)	3143472
Total length (>= 5000 bp)	3136912
Total length (>= 10000 bp)	3127539
Total length (>= 25000 bp)	3115156
Total length (>= 50000 bp)	3011862
# contigs	12
Largest contig	2027623
Total length	3143472
Reference length	2919198
GC (%)	37.69
Reference GC (%)	37.88
N50	2027623
NG50	2027623
N75	557694
NG75	557694
L50	1
LG50	1
L75	2
LG75	2
# misassemblies	188
# misassembled contigs	4
Misassembled contigs length	2755069
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	3 + 8 part
Unaligned length	564836
Genome fraction (%)	84.837
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	390.66
# indels per 100 kbp	14.78
Largest alignment	137660
Total aligned length	2578294
NA50	24276
NGA50	27356
NA75	4045
NGA75	9933
LA50	32
LGA50	27
LA75	91
LGA75	68

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

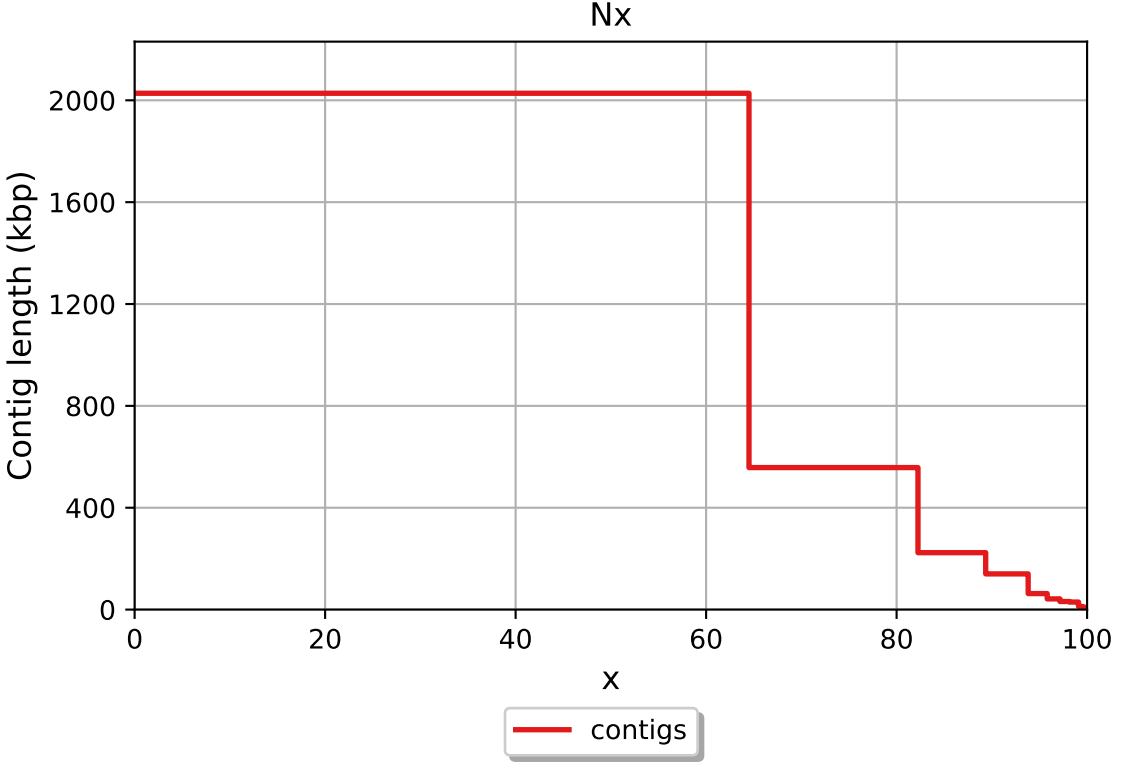
	contigs
# misassemblies	188
# contig misassemblies	188
# c. relocations	171
# c. translocations	14
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	4
Misassembled contigs length	2755069
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	9675
# indels	366
# indels (<= 5 bp)	329
# indels (> 5 bp)	37
Indels length	1453

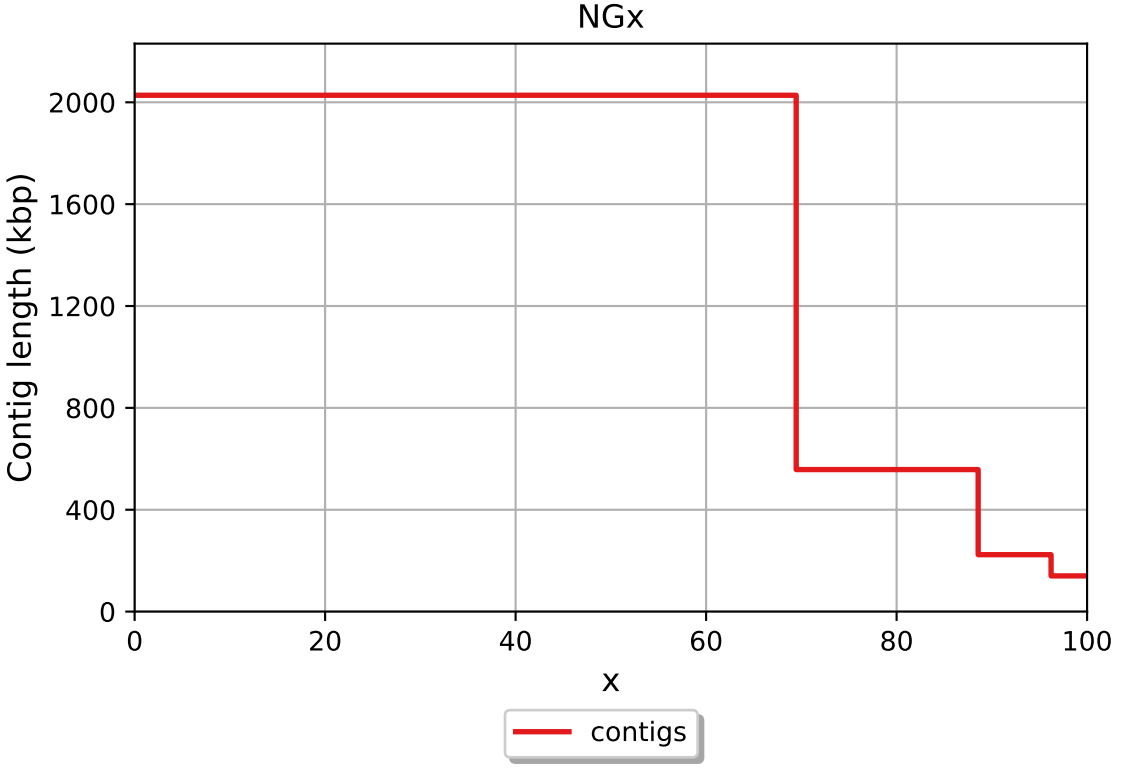
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

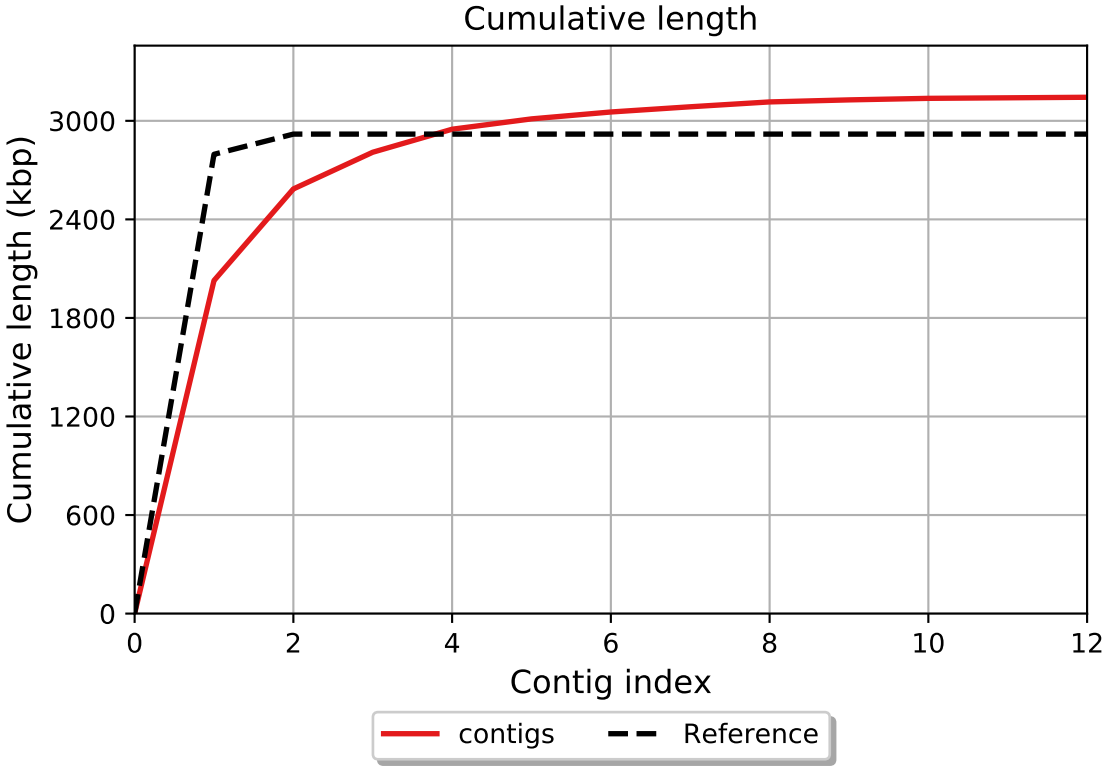
Unaligned report

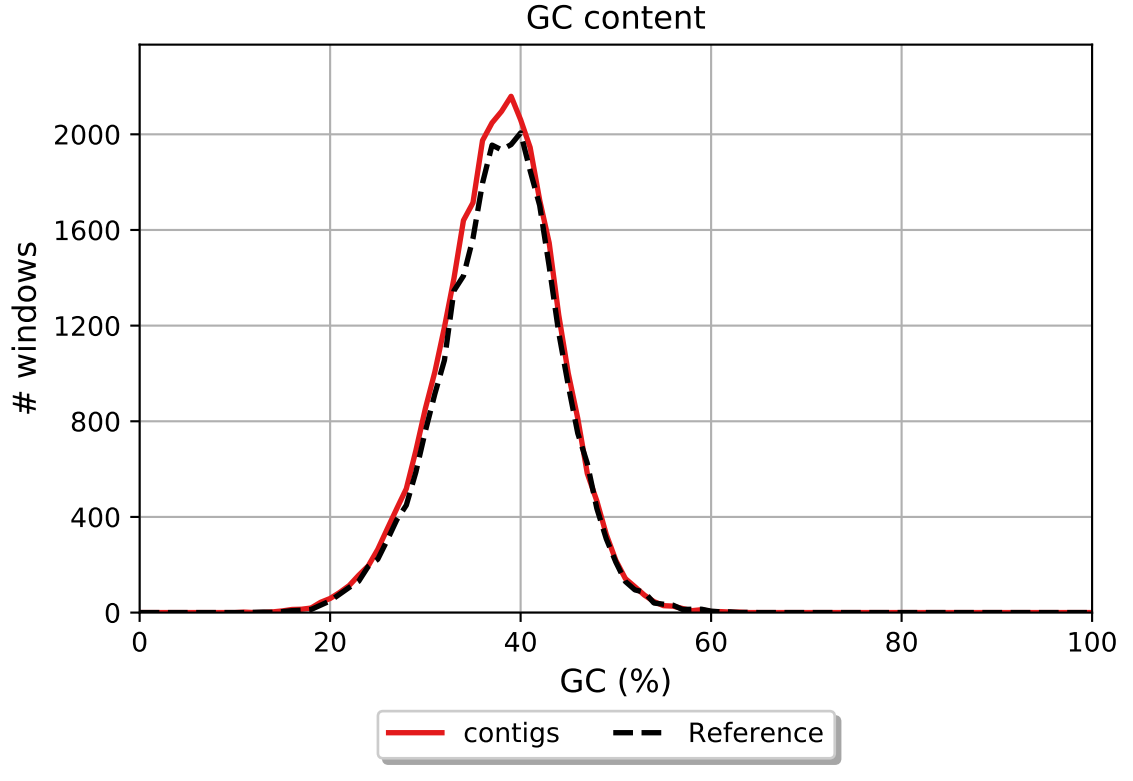
	contigs
# fully unaligned contigs	3
Fully unaligned length	15933
# partially unaligned contigs	8
Partially unaligned length	548903
# N's	0

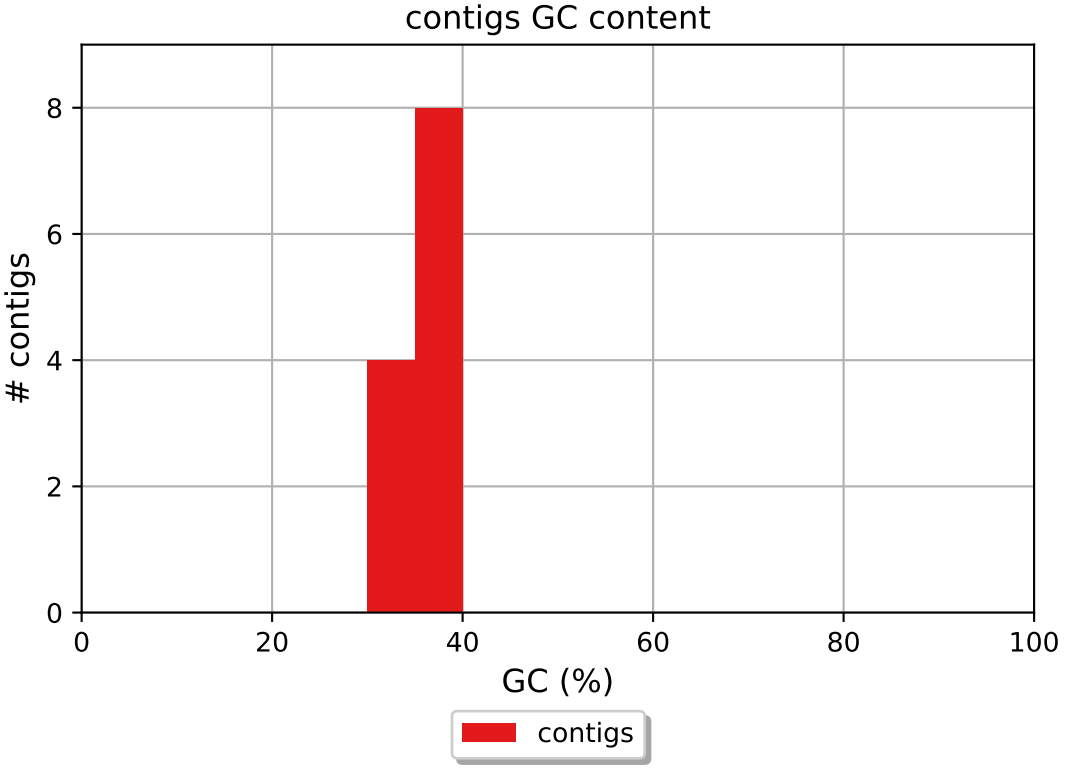
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

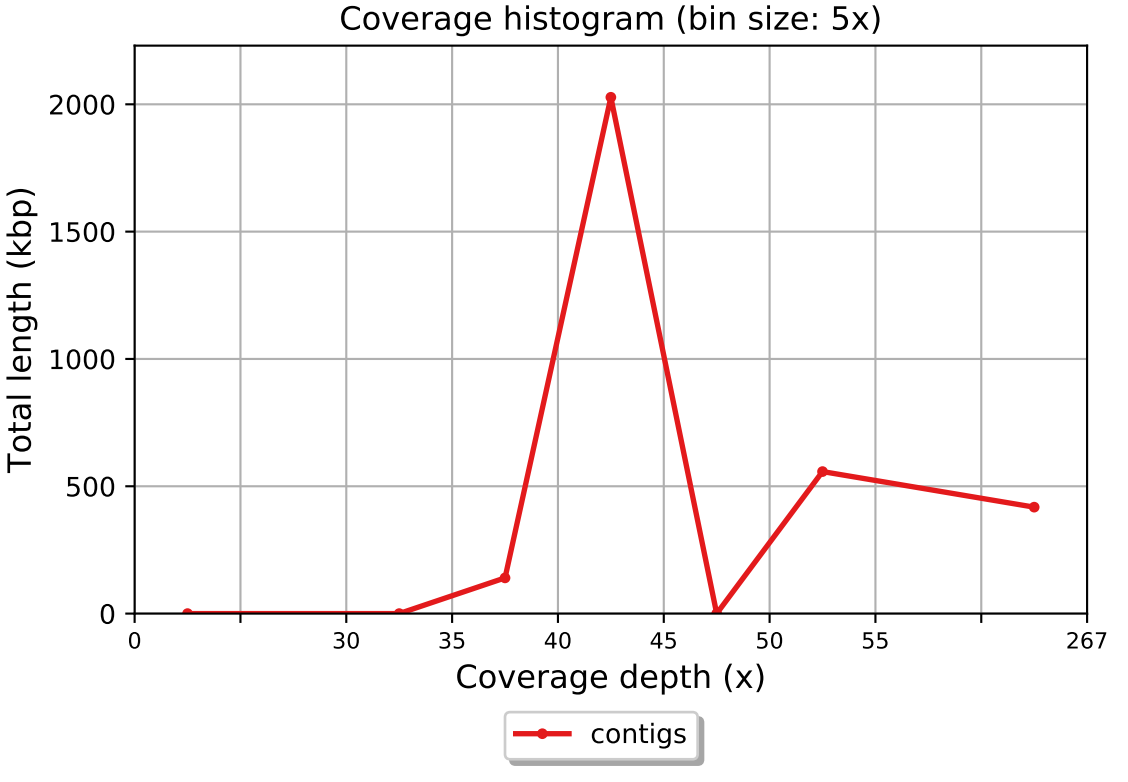

Nx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
contigs

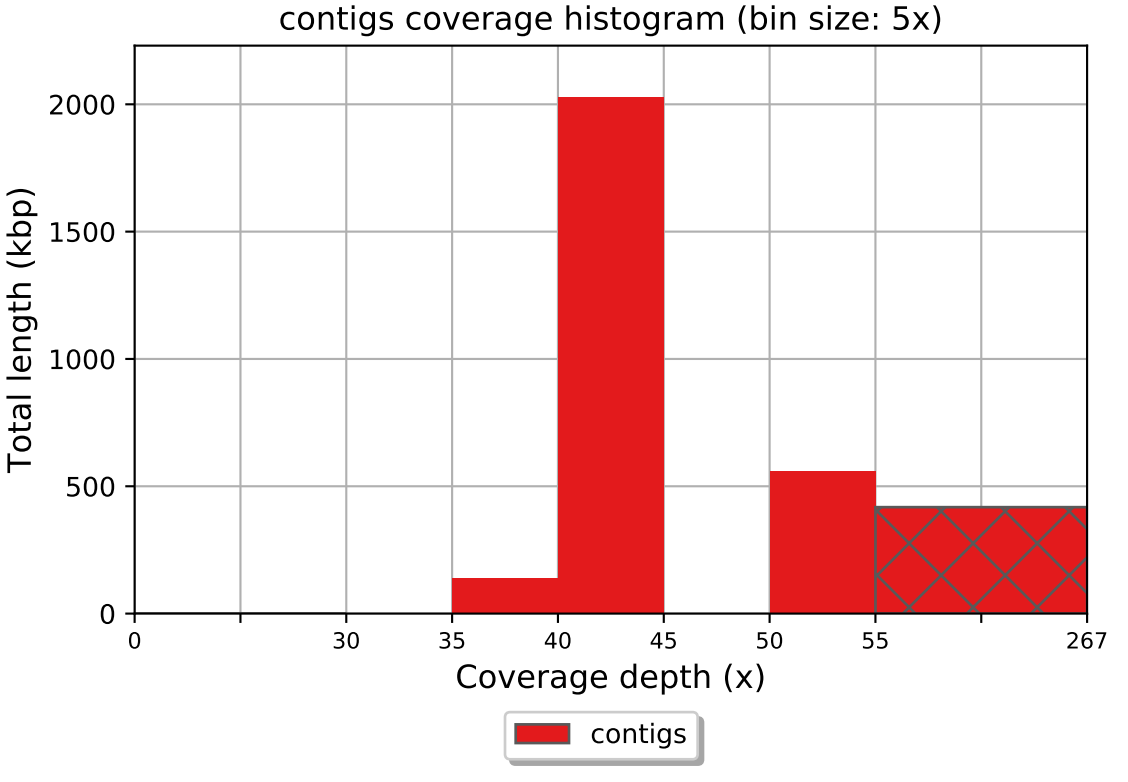

NGx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
contigs


Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
2
4
6
8
10
12
Contig index
contigs
Reference

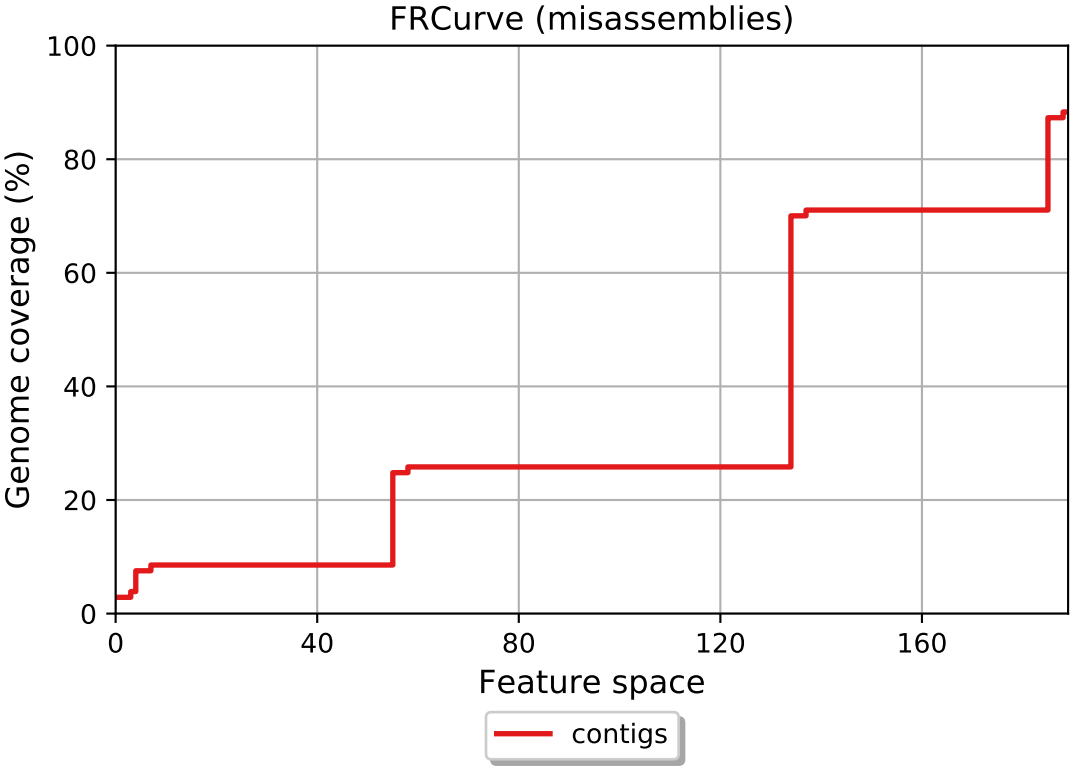

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
contigs
Reference

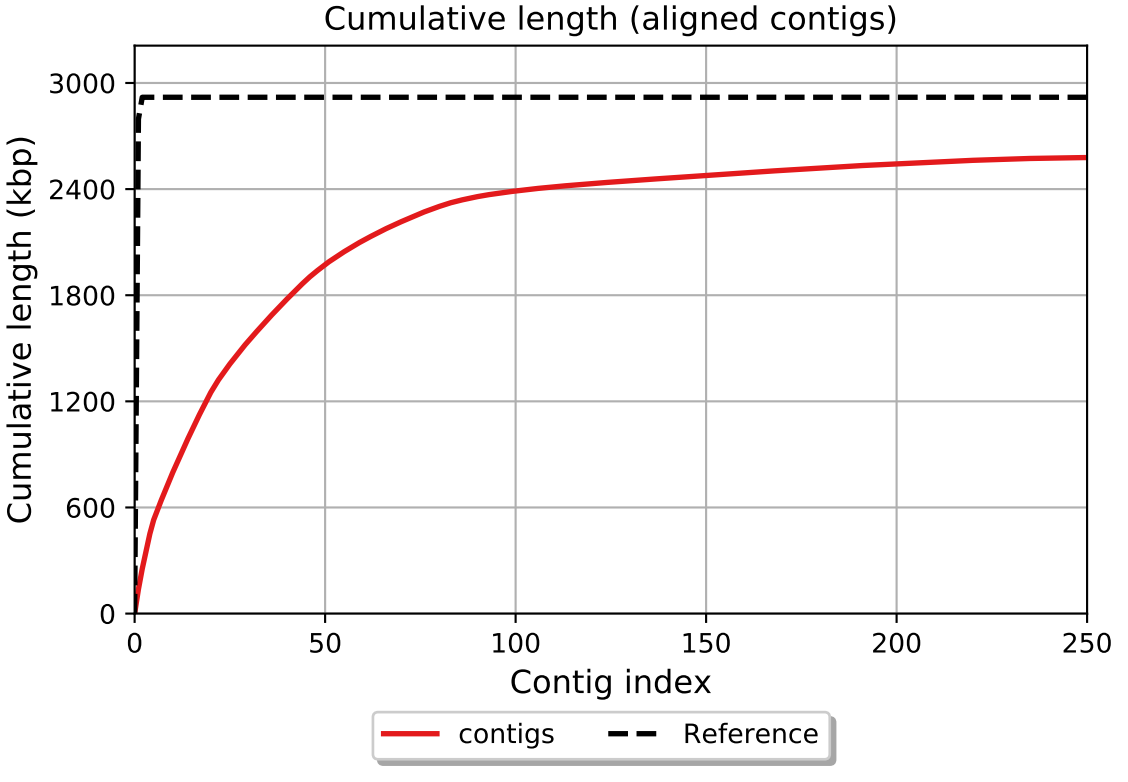

contigs GC content
contigs
0
2
4
6
8
0
20
40
60
80
100
GC (%)
contigs

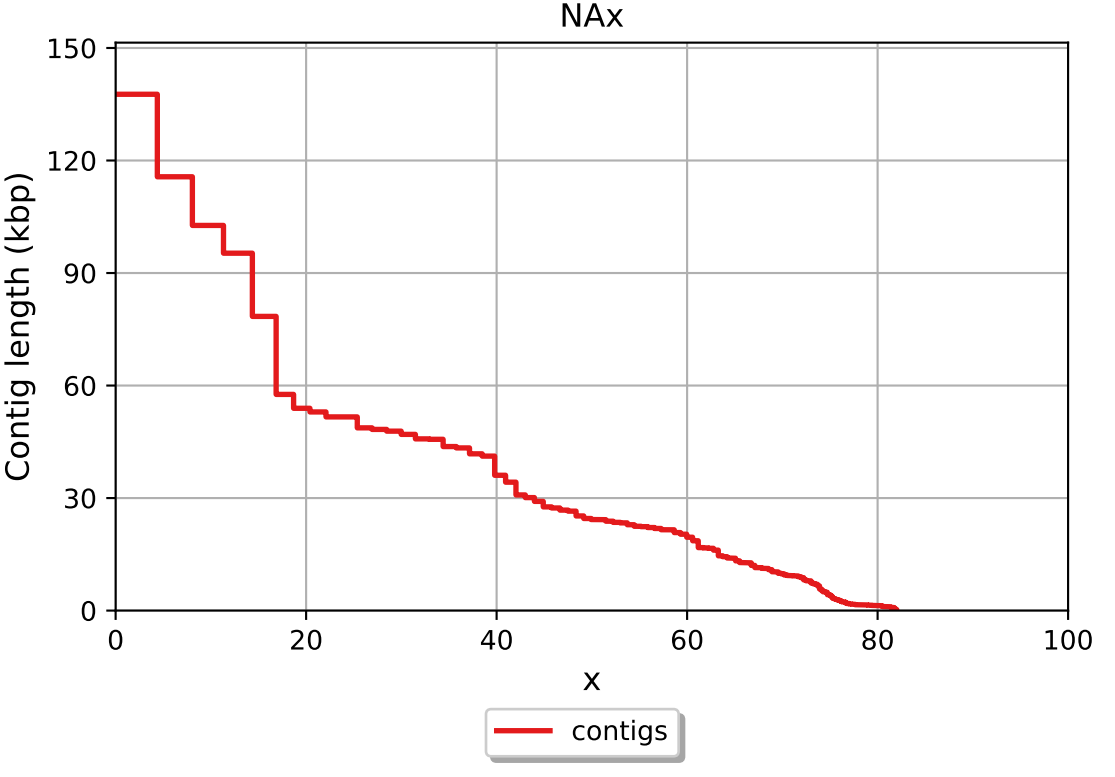

Coverage histogram (bin size: 5x)
Total length (kbp)
2000
1500
1000
500
0
0
30
35
40
45
50
55
267
Coverage depth (x)
contigs

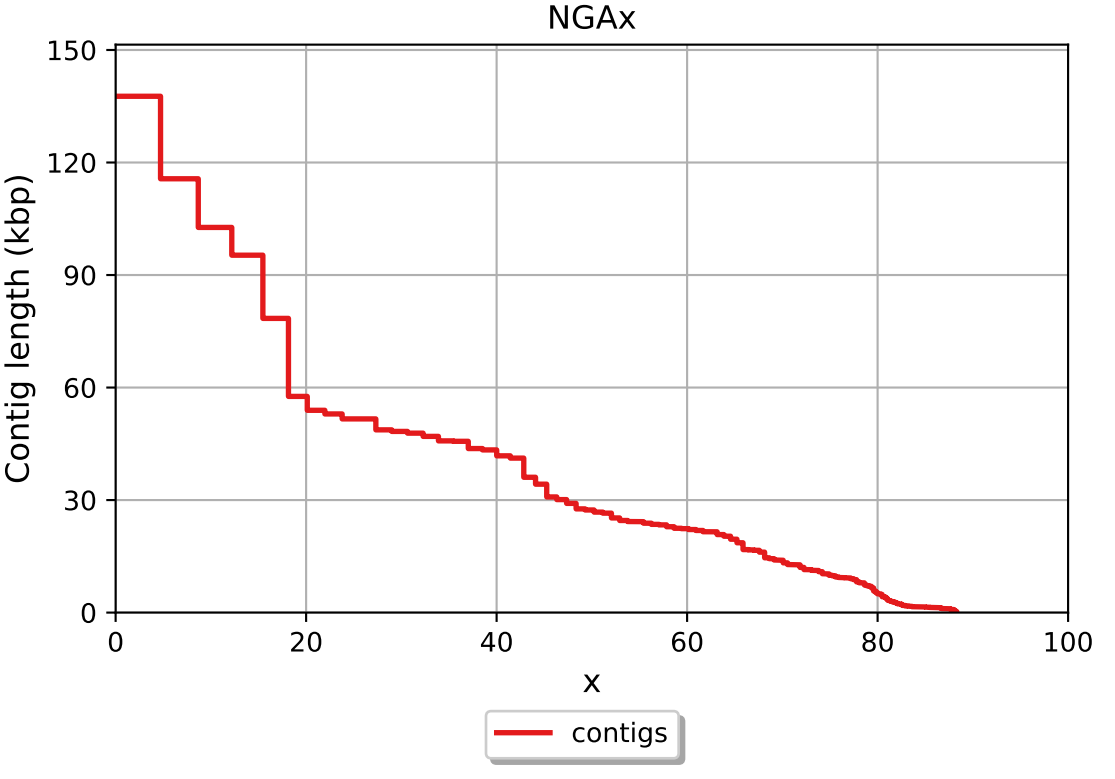

contigs coverage histogram (bin size: 5x)
Total length (kbp)
2000
1500
1000
500
0
0
30
35
40
45
50
55
267
Coverage depth (x)
contigs

Misassemblies
200
160
120
80
40
0
contigs
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
40
80
120
160
Feature space
contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
50
100
150
200
250
Contig index
contigs
Reference


NAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
contigs