Report

	contigs
# contigs (>= 0 bp)	380
# contigs (>= 1000 bp)	168
# contigs (>= 5000 bp)	91
# contigs (>= 10000 bp)	65
# contigs (>= 25000 bp)	33
# contigs (>= 50000 bp)	16
Total length (>= 0 bp)	2962703
Total length (>= 1000 bp)	2903953
Total length (>= 5000 bp)	2717618
Total length (>= 10000 bp)	2527261
Total length (>= 25000 bp)	2004365
Total length (>= 50000 bp)	1407167
# contigs	203
Largest contig	114283
Total length	2928787
Reference length	2919198
GC (%)	37.64
Reference GC (%)	37.88
N50	49306
NG50	49306
N75	19664
NG75	19664
L50	18
LG50	18
L75	42
LG75	42
# misassemblies	65
# misassembled contigs	40
Misassembled contigs length	1873016
# local misassemblies	29
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	69 + 42 part
Unaligned length	536194
Genome fraction (%)	81.635
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	361.76
# indels per 100 kbp	14.18
Largest alignment	95273
Total aligned length	2385761
NA50	23387
NGA50	23522
NA75	7350
NGA75	7355
LA50	35
LGA50	34
LA75	87
LGA75	86

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

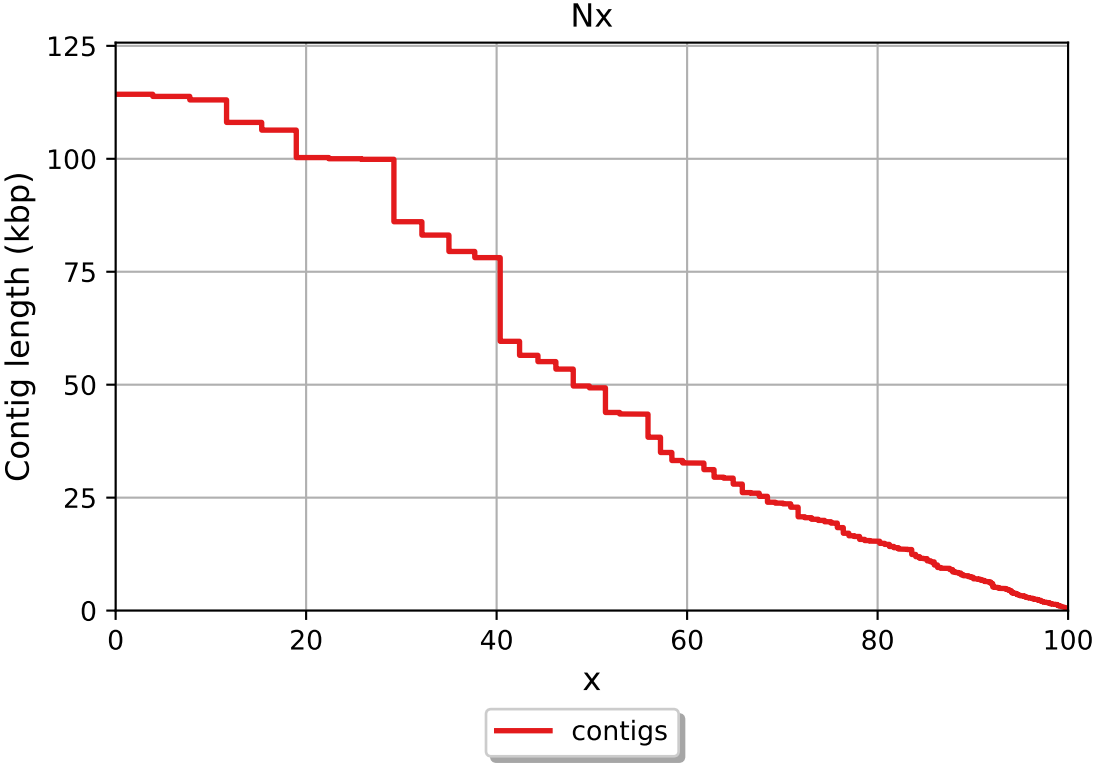
	contigs
# misassemblies	65
# contig misassemblies	65
# c. relocations	64
# c. translocations	0
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	40
Misassembled contigs length	1873016
# local misassemblies	29
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	8621
# indels	338
# indels (<= 5 bp)	306
# indels (> 5 bp)	32
Indels length	1278

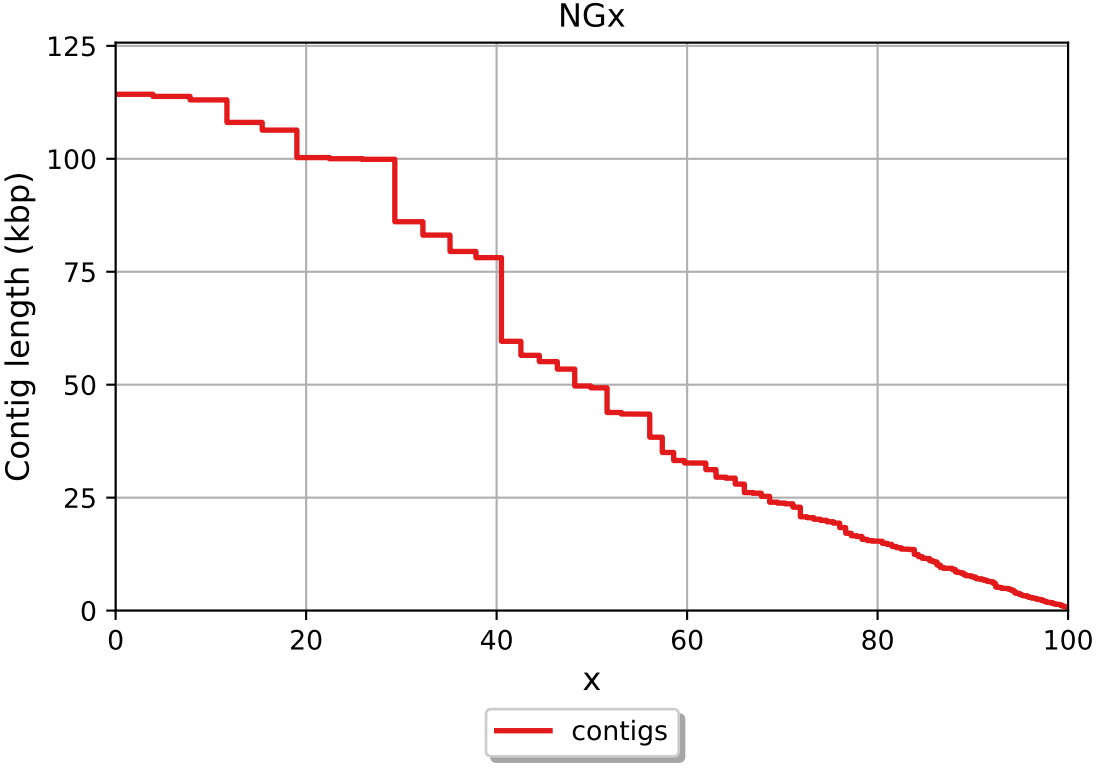
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

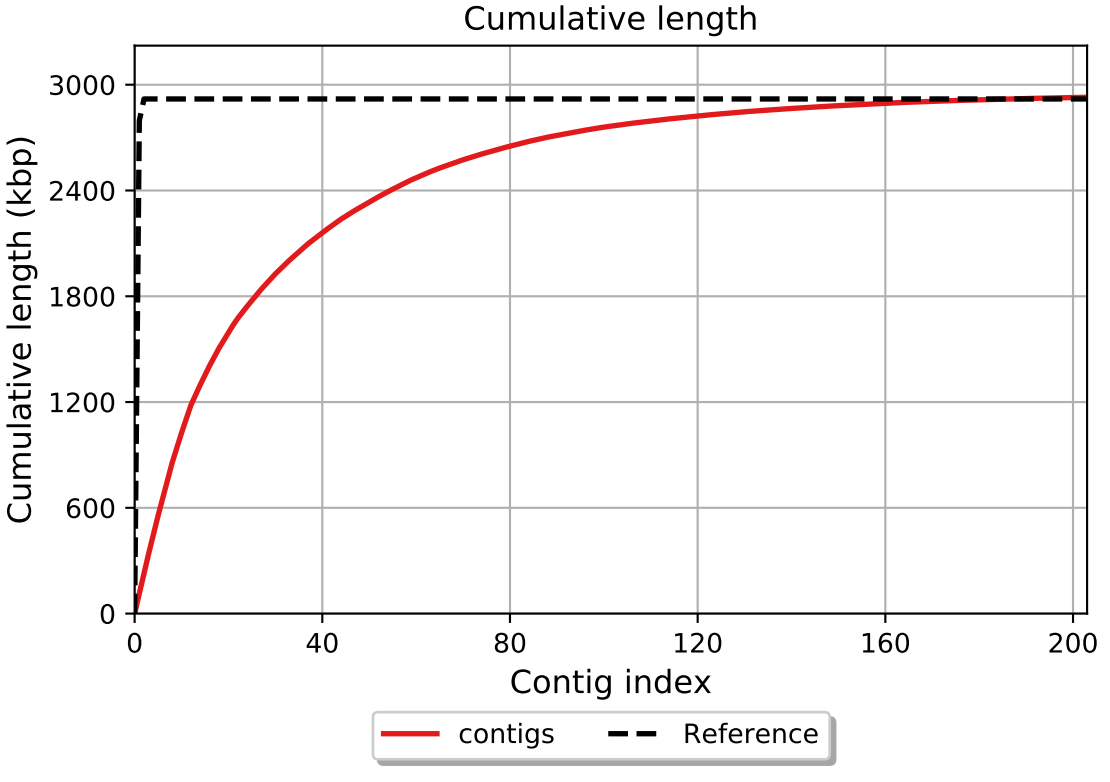
Unaligned report

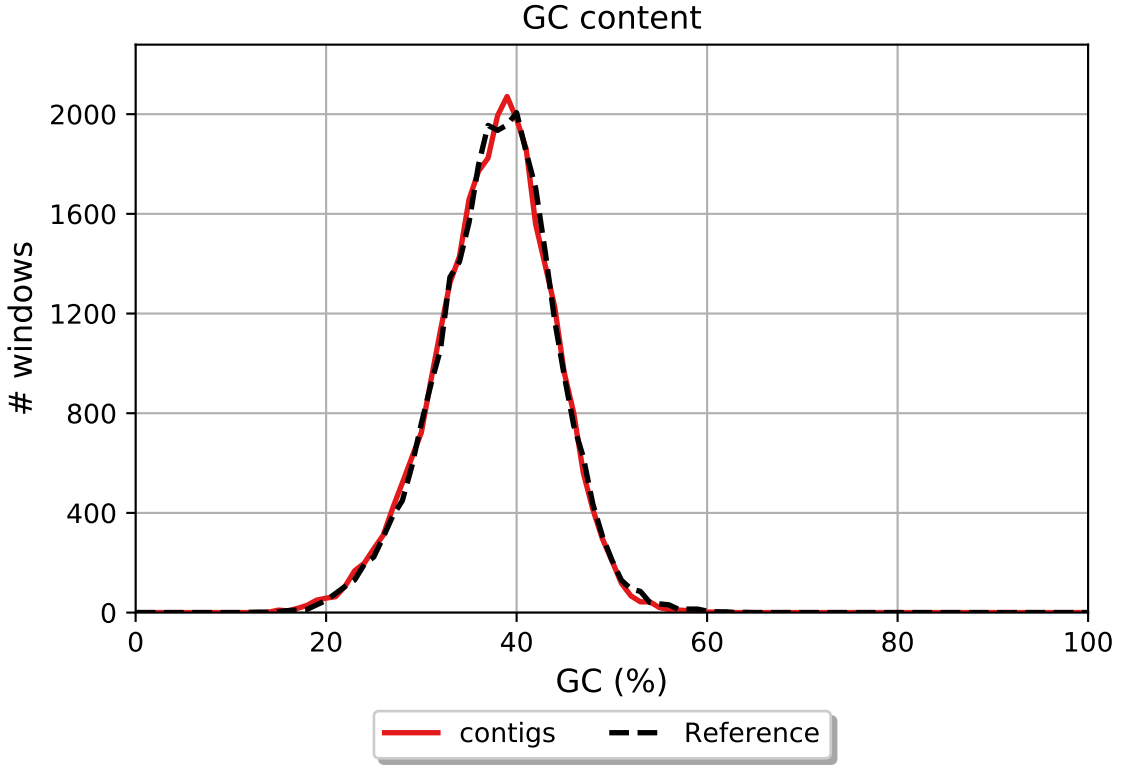
	contigs
# fully unaligned contigs	69
Fully unaligned length	278430
# partially unaligned contigs	42
Partially unaligned length	257764
# N's	0

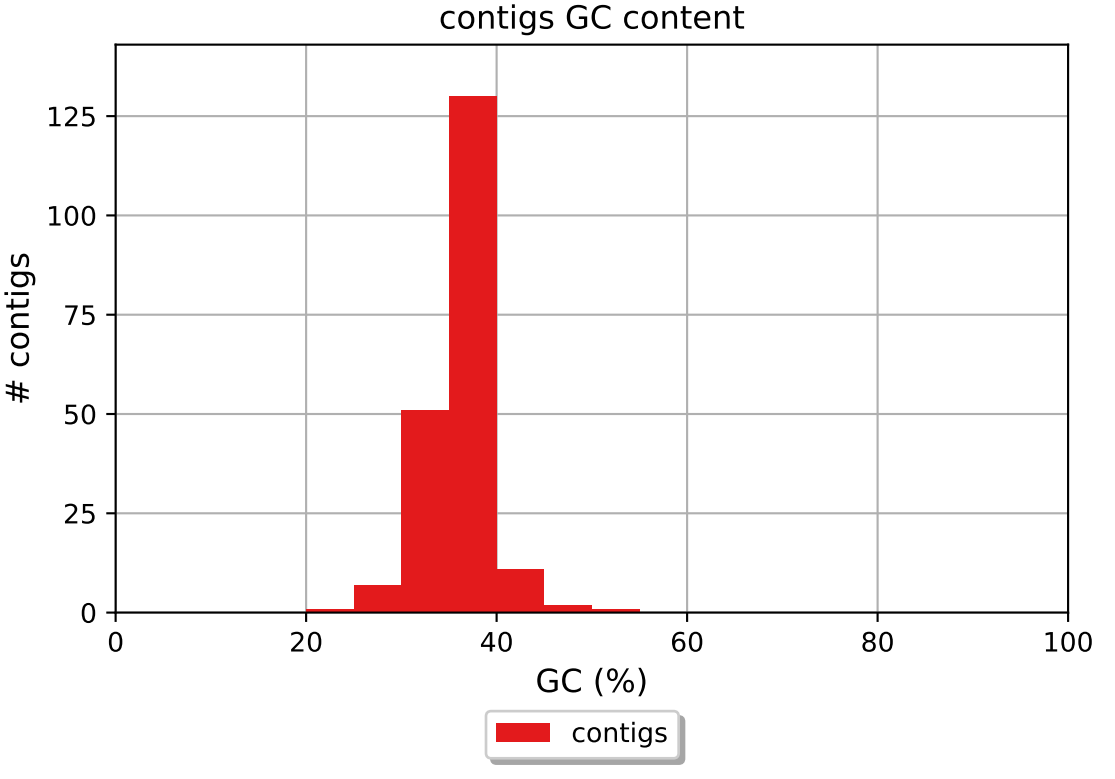
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

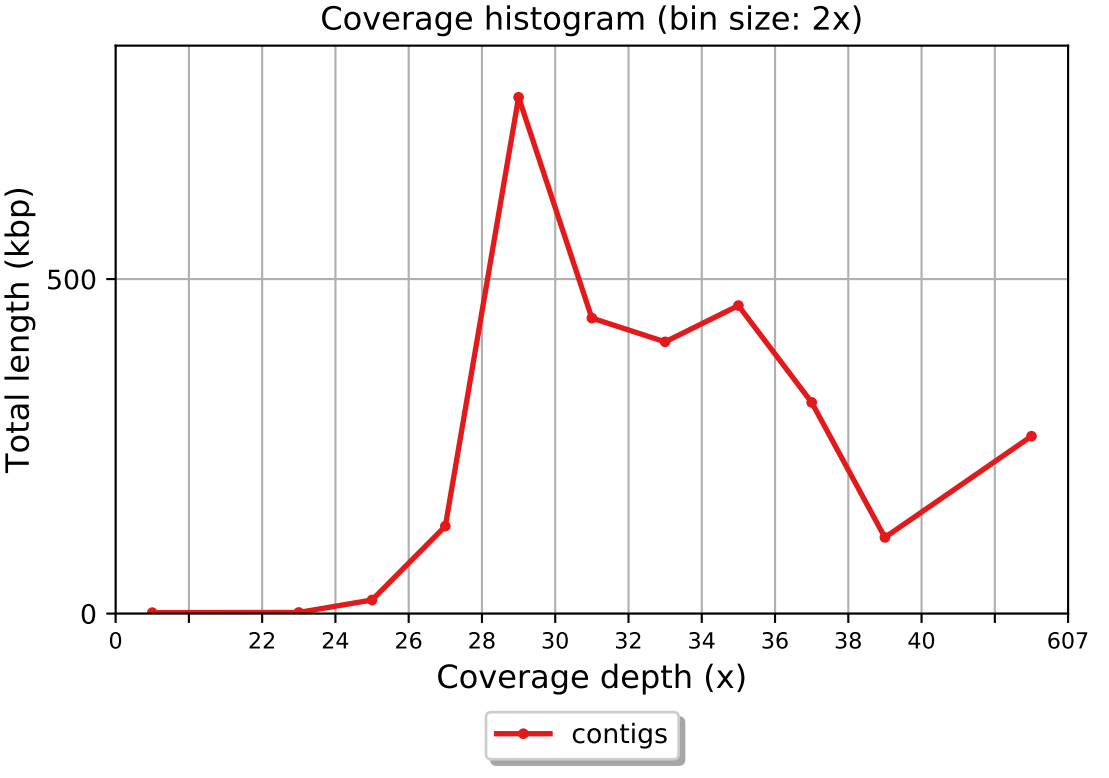

Nx
Contig length (kbp)
125
100
75
50
25
0
0
20
40
60
80
100
x
contigs

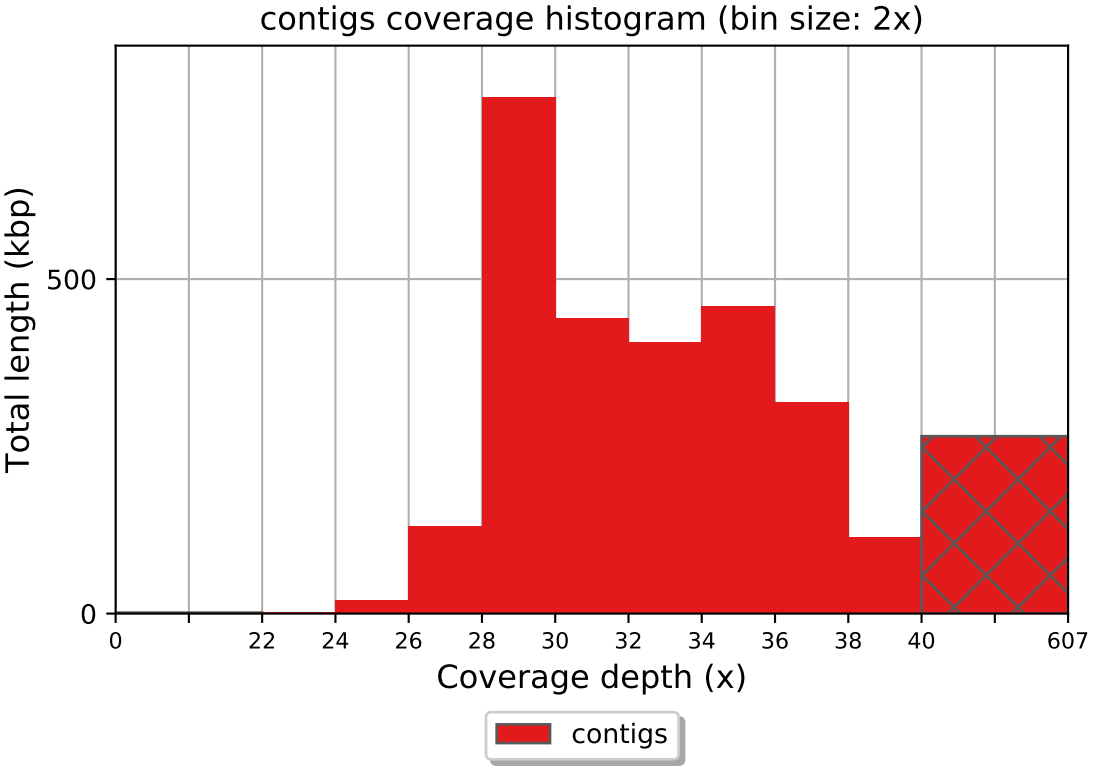

NGx
Contig length (kbp)
125
100
75
50
25
0
0
20
40
60
80
100
x
contigs

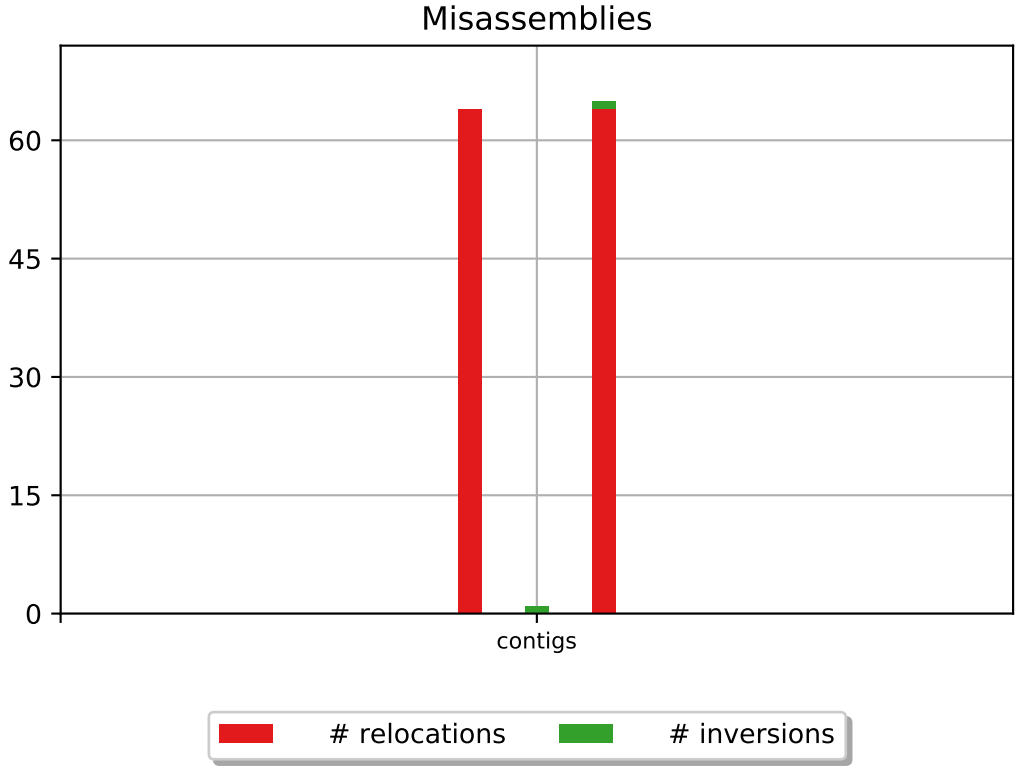

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
40
80
120
160
200
Contig index
contigs
Reference

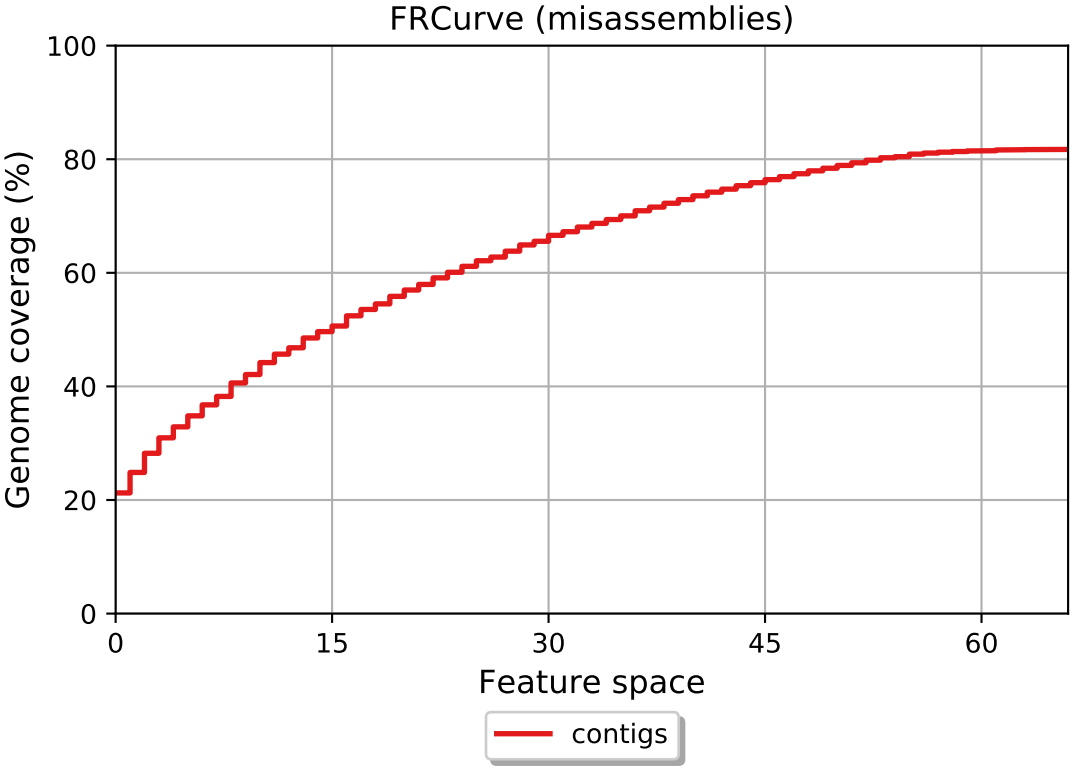

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
contigs
Reference

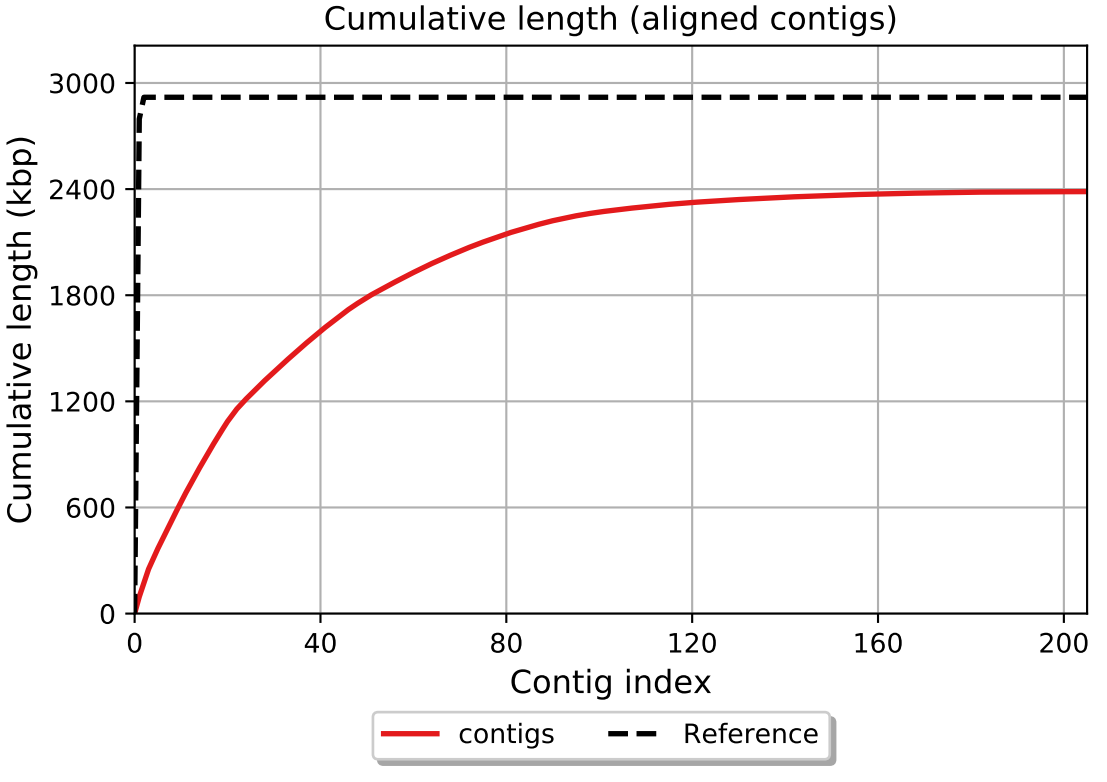

contigs GC content
contigs
125
100
75
50
25
0
0
20
40
60
80
100
GC (%)
contigs

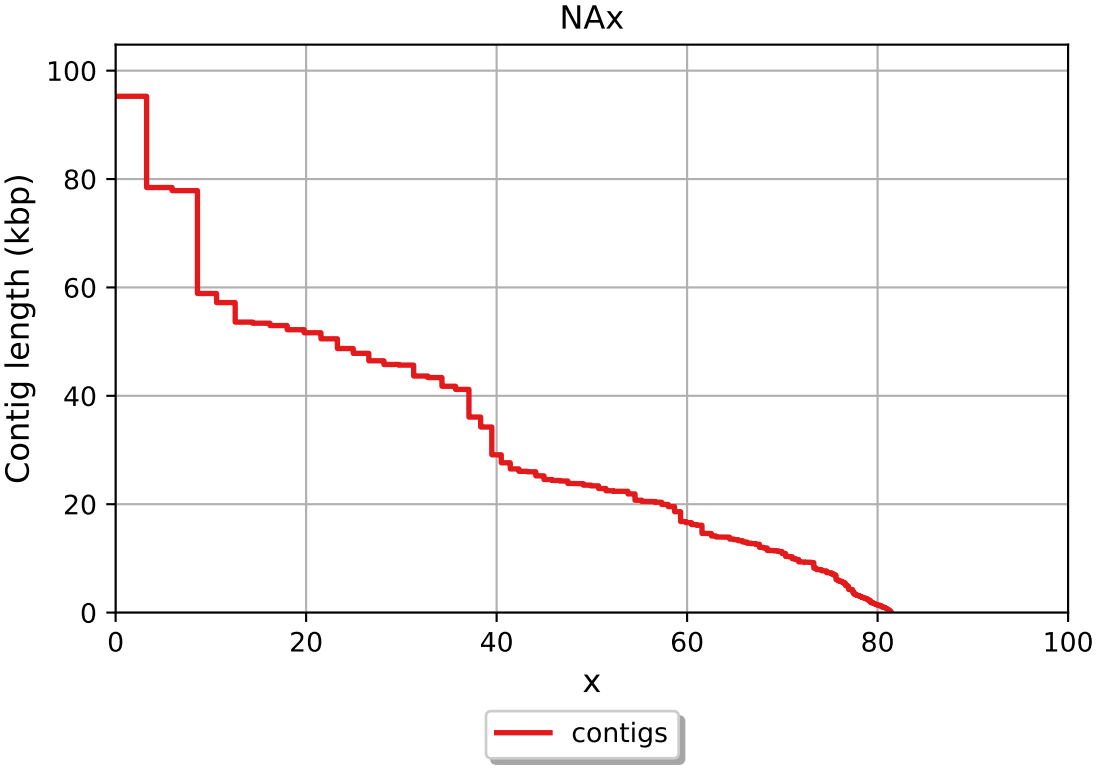

Coverage histogram (bin size: 2x)
Total length (kbp)
500
0
0
22
24
26
28
30
32
34
36
38
40
607
Coverage depth (x)
contigs

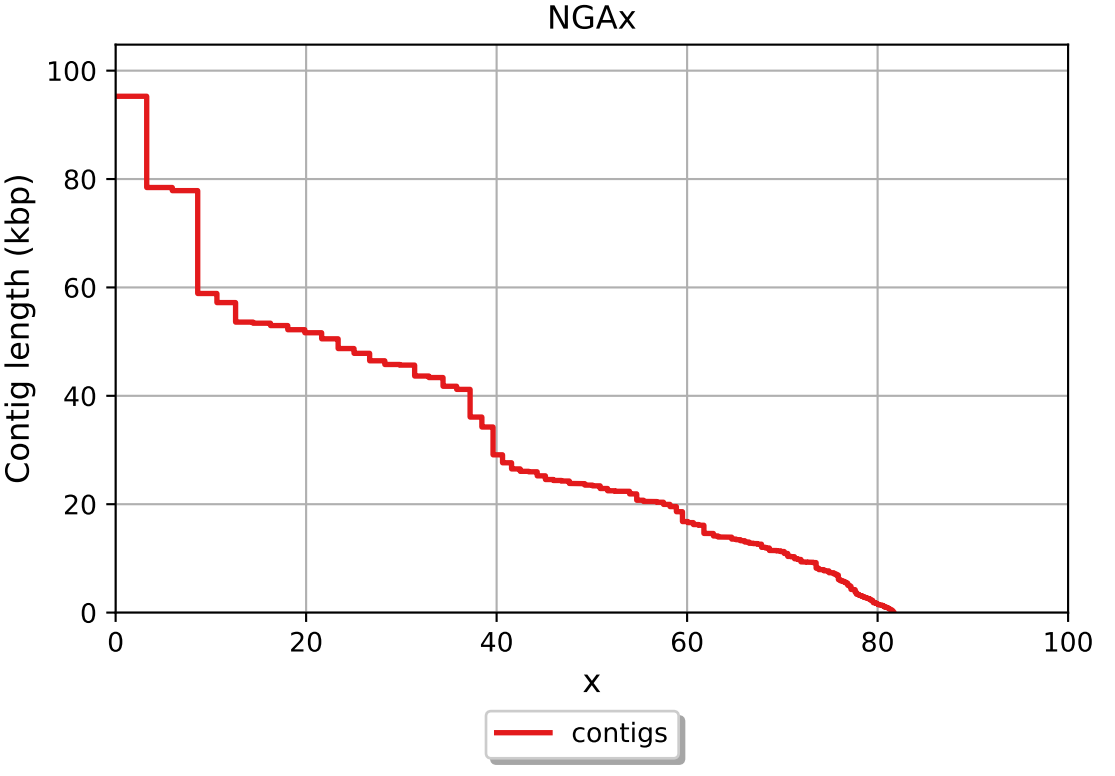

contigs coverage histogram (bin size: 2x)
Total length (kbp)
500
0
0
22
24
26
28
30
32
34
36
38
40
607
Coverage depth (x)
contigs


Misassemblies
60
45
30
15
0
contigs
relocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
15
30
45
60
Feature space
contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
40
80
120
160
200
Contig index
contigs
Reference


NAx
Contig length (kbp)
0
20
40
60
80
100
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
0
20
40
60
80
100
0
20
40
60
80
100
x
contigs