Report

	contigs
# contigs (>= 0 bp)	7
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	4642799
Total length (>= 1000 bp)	4641722
Total length (>= 5000 bp)	4641722
Total length (>= 10000 bp)	4641722
Total length (>= 25000 bp)	4641722
Total length (>= 50000 bp)	4641722
# contigs	2
Largest contig	4641722
Total length	4642264
Reference length	4639675
GC (%)	50.79
Reference GC (%)	50.79
N50	4641722
NG50	4641722
N75	4641722
NG75	4641722
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	6
# misassembled contigs	1
Misassembled contigs length	4641722
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	542
Genome fraction (%)	99.983
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.32
# indels per 100 kbp	0.86
Largest alignment	3023578
Total aligned length	4638936
NA50	3023578
NGA50	3023578
NA75	572346
NGA75	572346
LA50	1
LGA50	1
LA75	2
LGA75	2

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

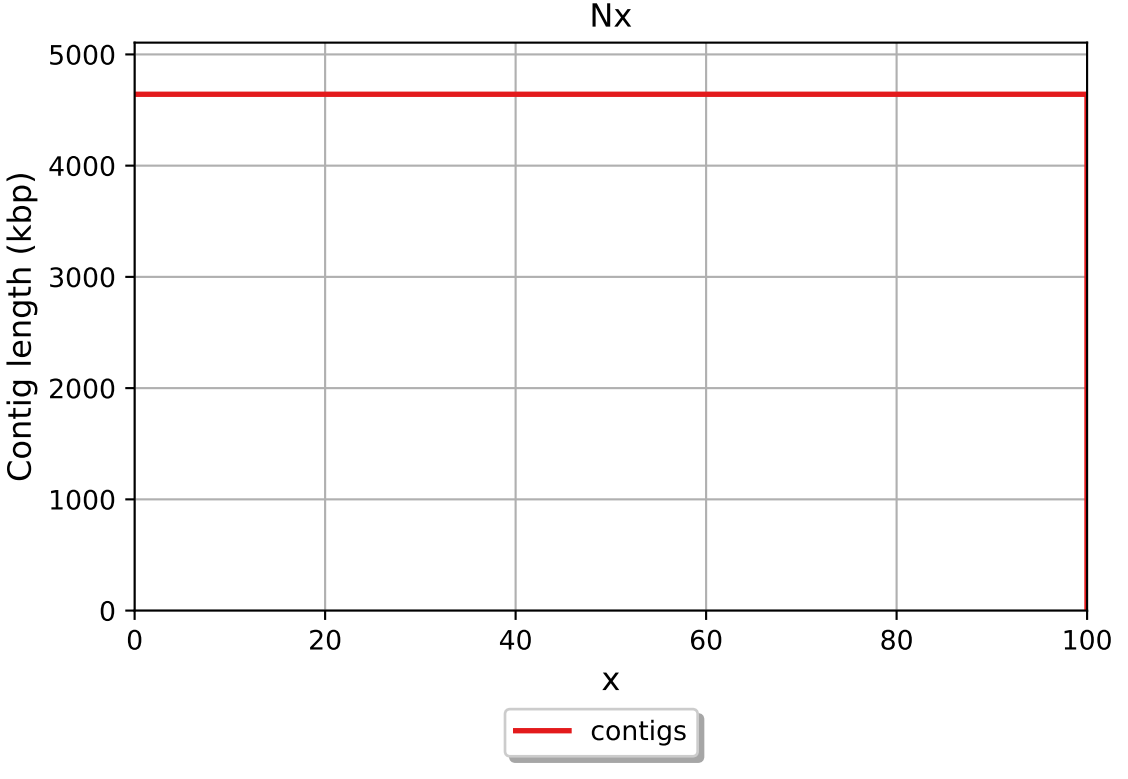
	contigs
# misassemblies	6
# contig misassemblies	6
# c. relocations	6
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	4641722
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	386
# indels	40
# indels (<= 5 bp)	37
# indels (> 5 bp)	3
Indels length	183

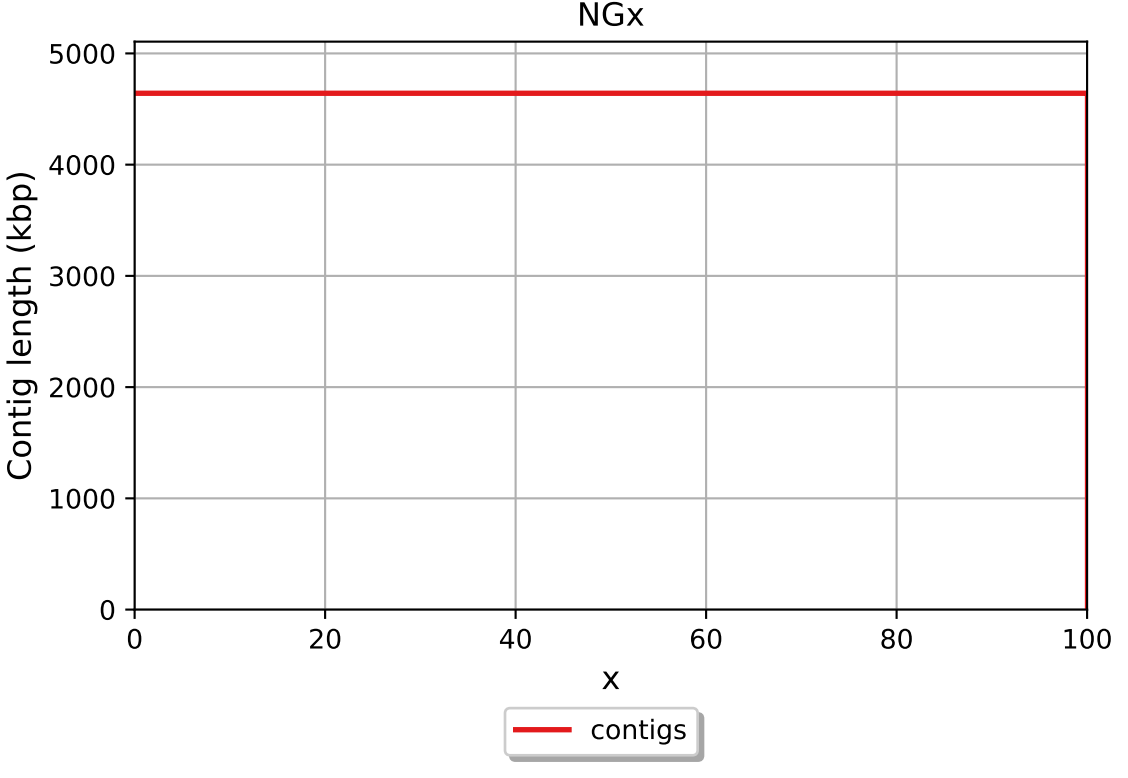
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

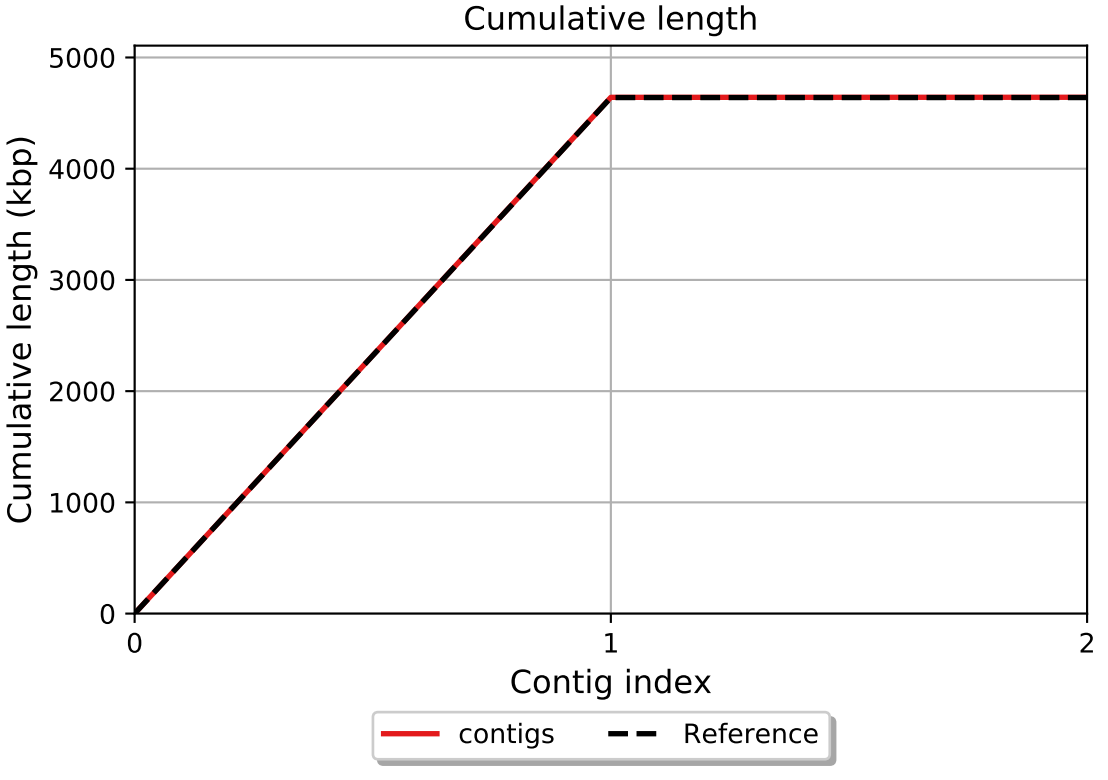
Unaligned report

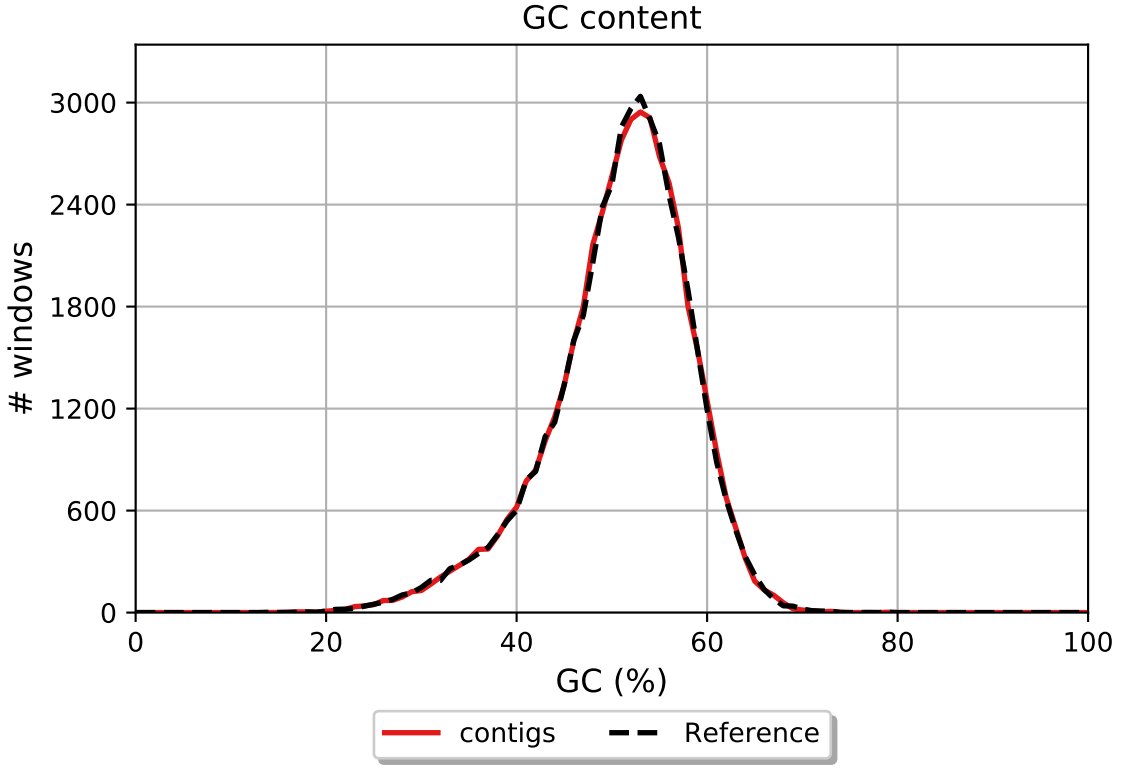
	contigs
# fully unaligned contigs	1
Fully unaligned length	542
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

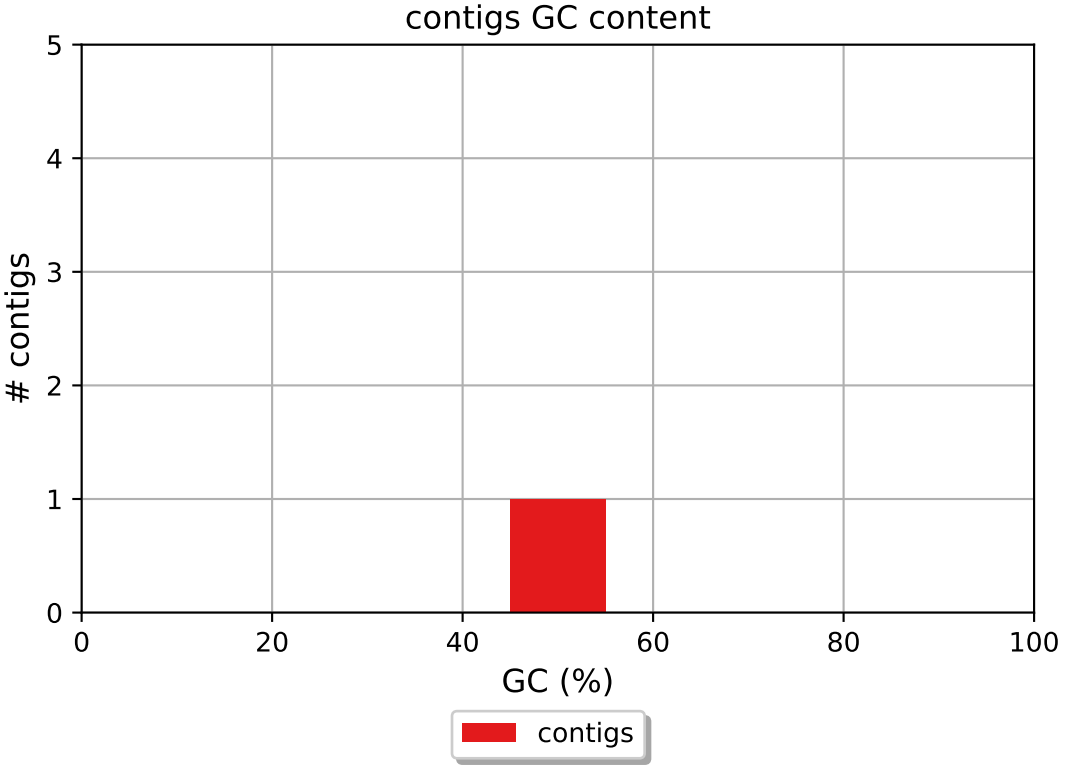
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

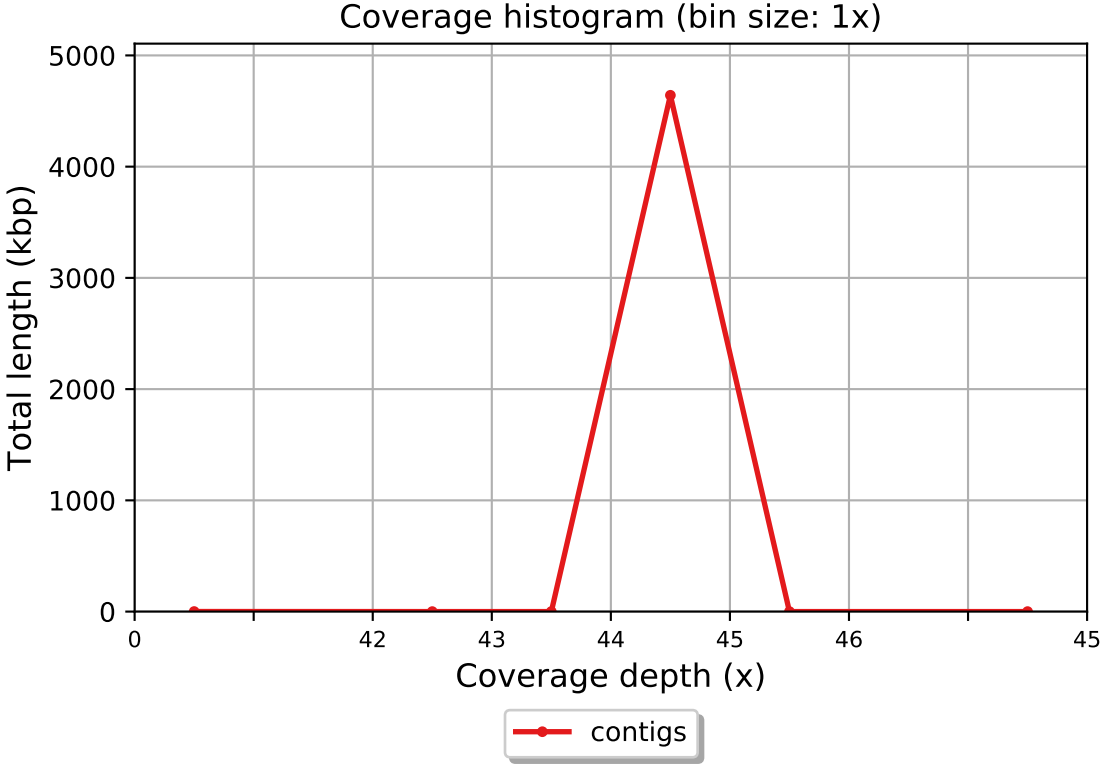

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
contigs

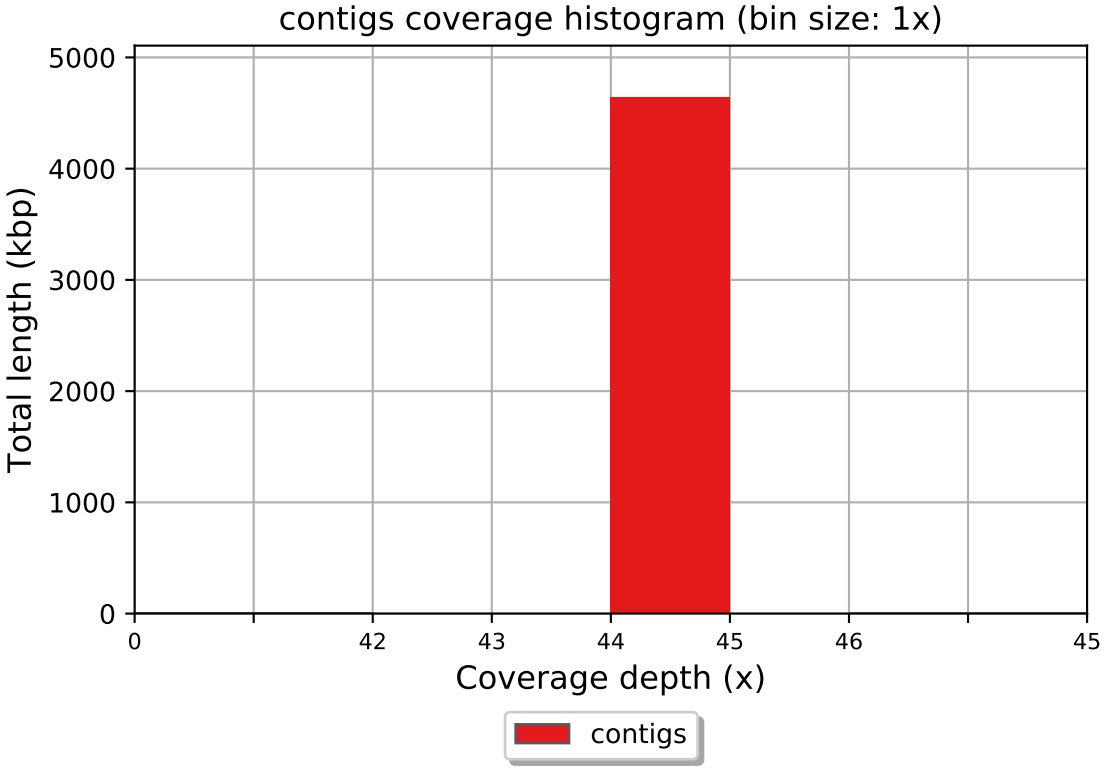

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
contigs

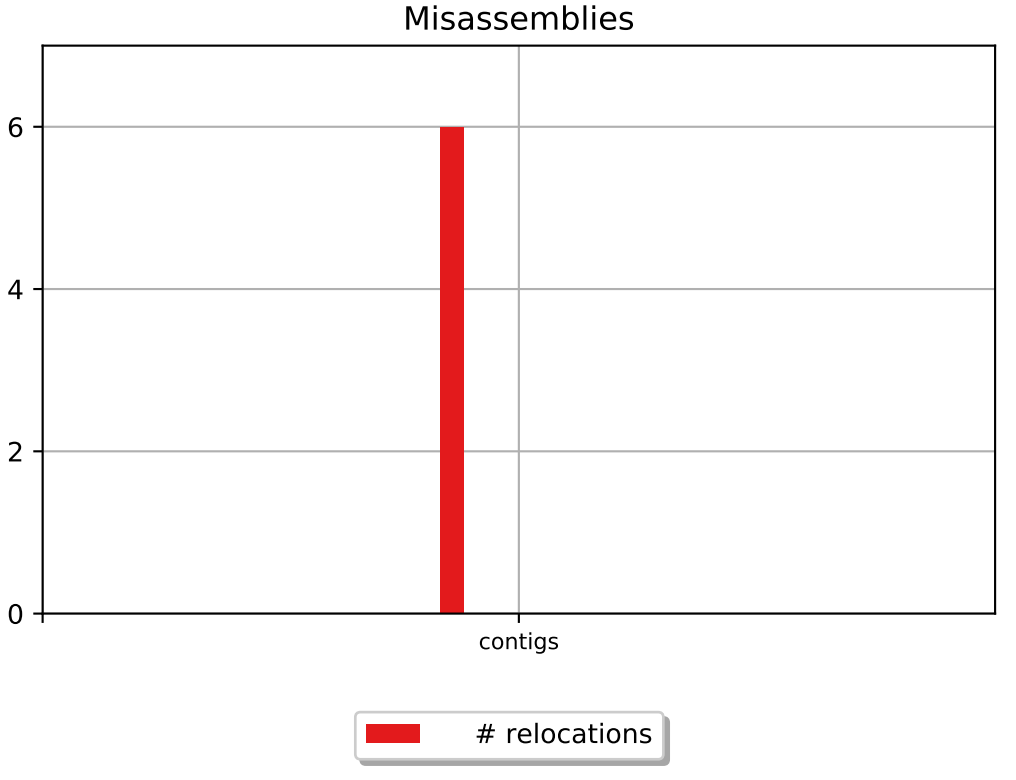

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
Contig index
contigs
Reference

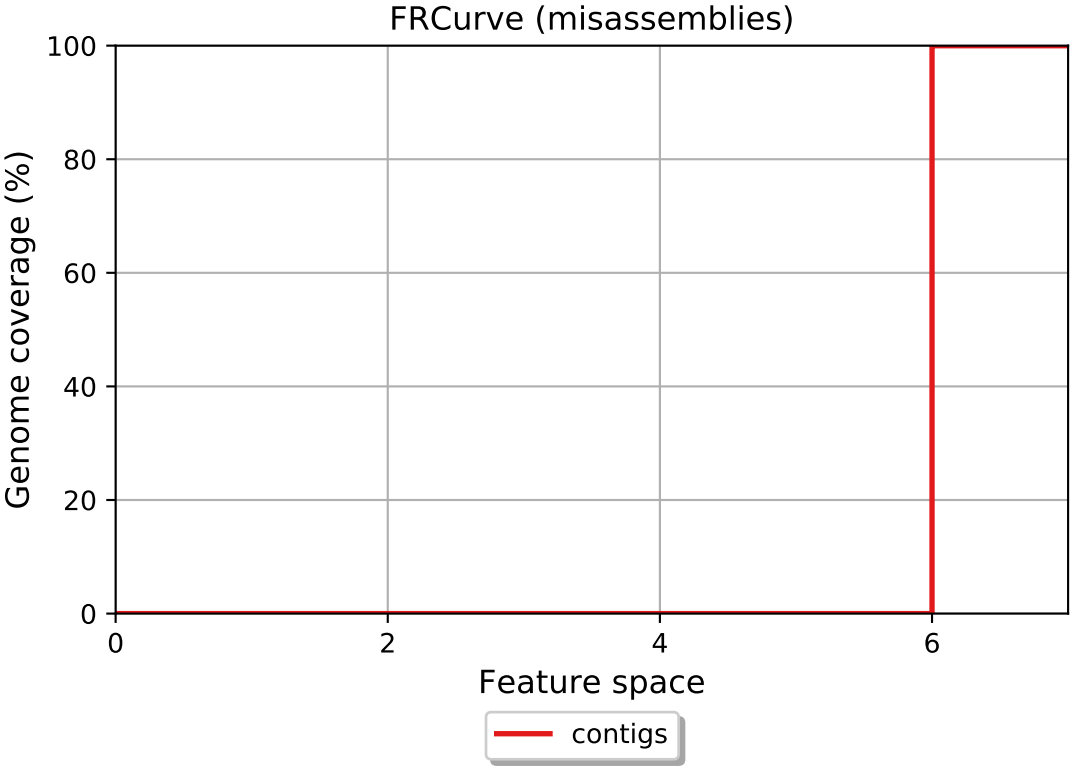

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
contigs
Reference

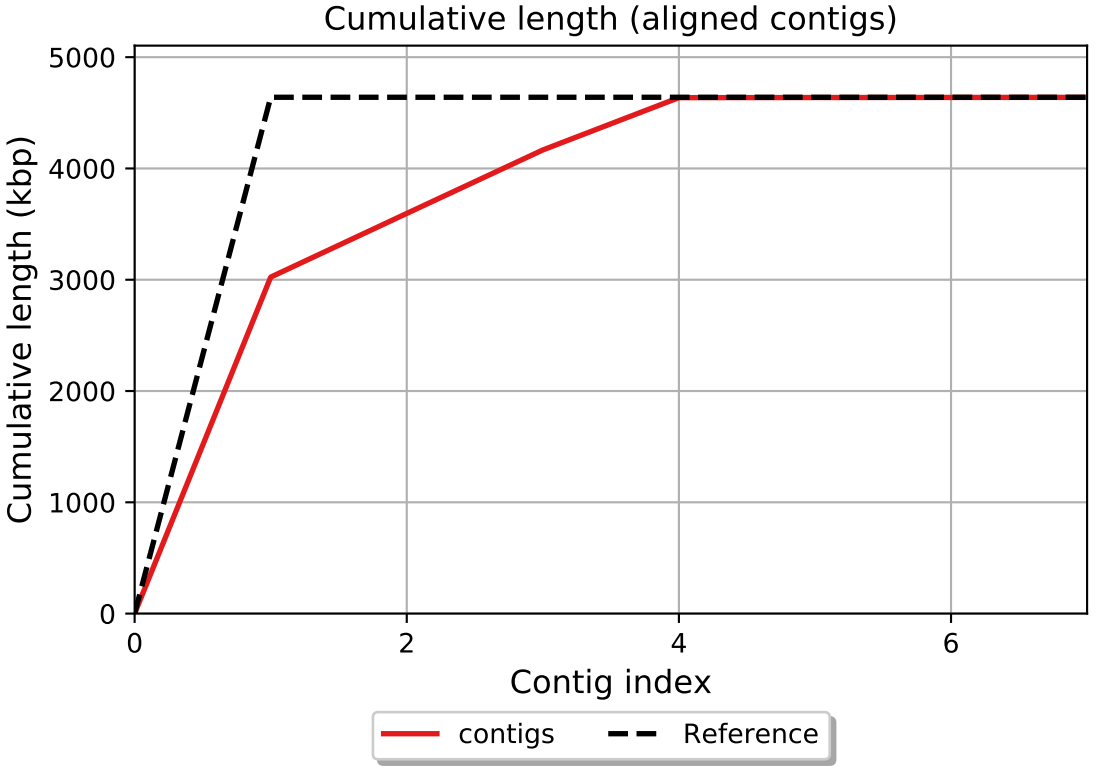

contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contigs

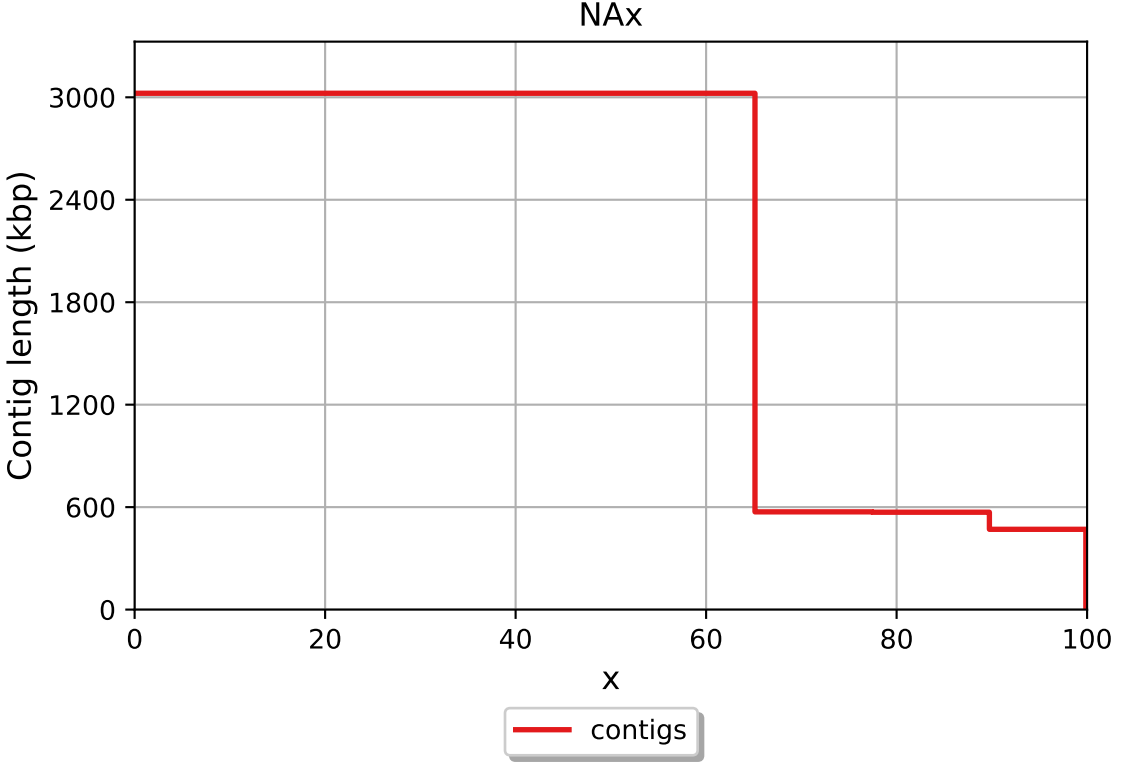

Coverage histogram (bin size: 1x)
Total length (kbp)
5000
4000
3000
2000
1000
0
0
42
43
44
45
46
45
Coverage depth (x)
contigs

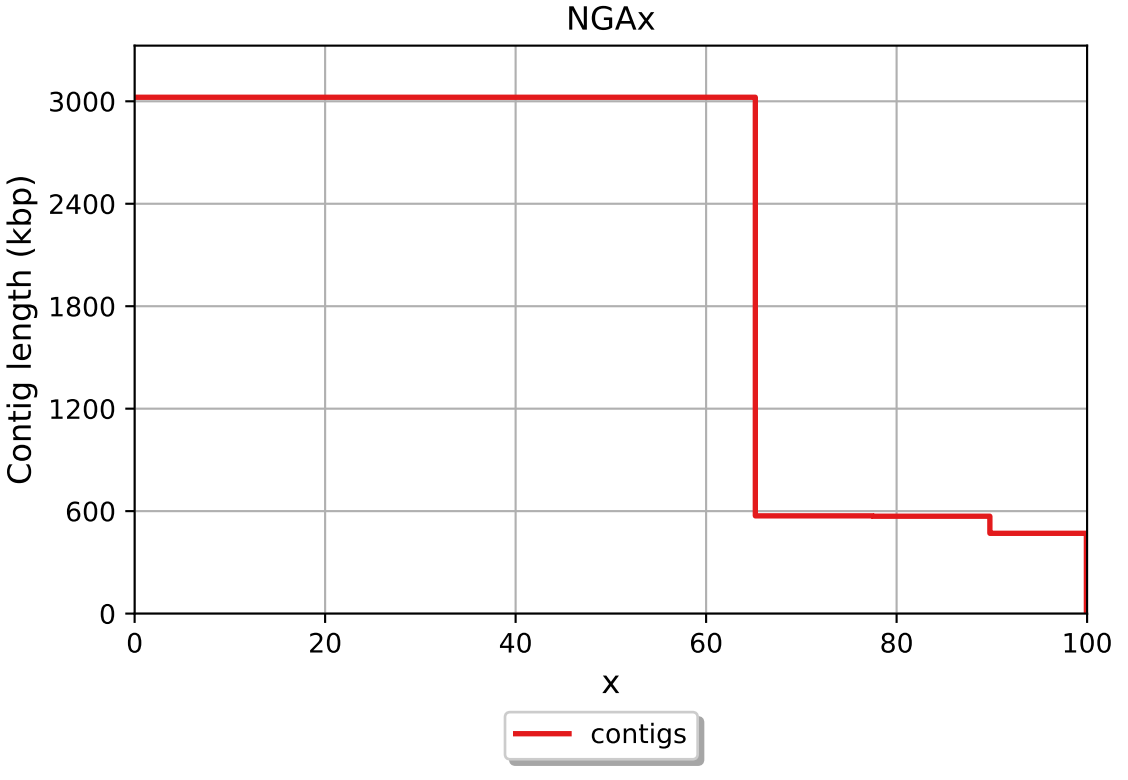

contigs coverage histogram (bin size: 1x)
Total length (kbp)
5000
4000
3000
2000
1000
0
0
42
43
44
45
46
45
Coverage depth (x)
contigs


Misassemblies
6
4
2
0
contigs
relocations


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
2
4
6
Contig index
contigs
Reference


NAx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
contigs