Report

	contigs
# contigs (>= 1000 bp)	175
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	245387
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	704
Largest contig	2698
Total length	610980
Reference length	2391686
GC (%)	36.61
Reference GC (%)	36.78
N50	881
NG50	-
N90	562
NG90	-
auN	1029.8
auNG	263.1
L50	240
LG50	-
L90	588
LG90	-
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	7261
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 5 part
Unaligned length	6280
Genome fraction (%)	25.153
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1904.90
# indels per 100 kbp	44.66
Largest alignment	2584
Total aligned length	602395
NA50	864
NGA50	-
NA90	545
NGA90	-
auNA	984.8
auNGA	251.6
LA50	248
LGA50	-
LA90	606
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

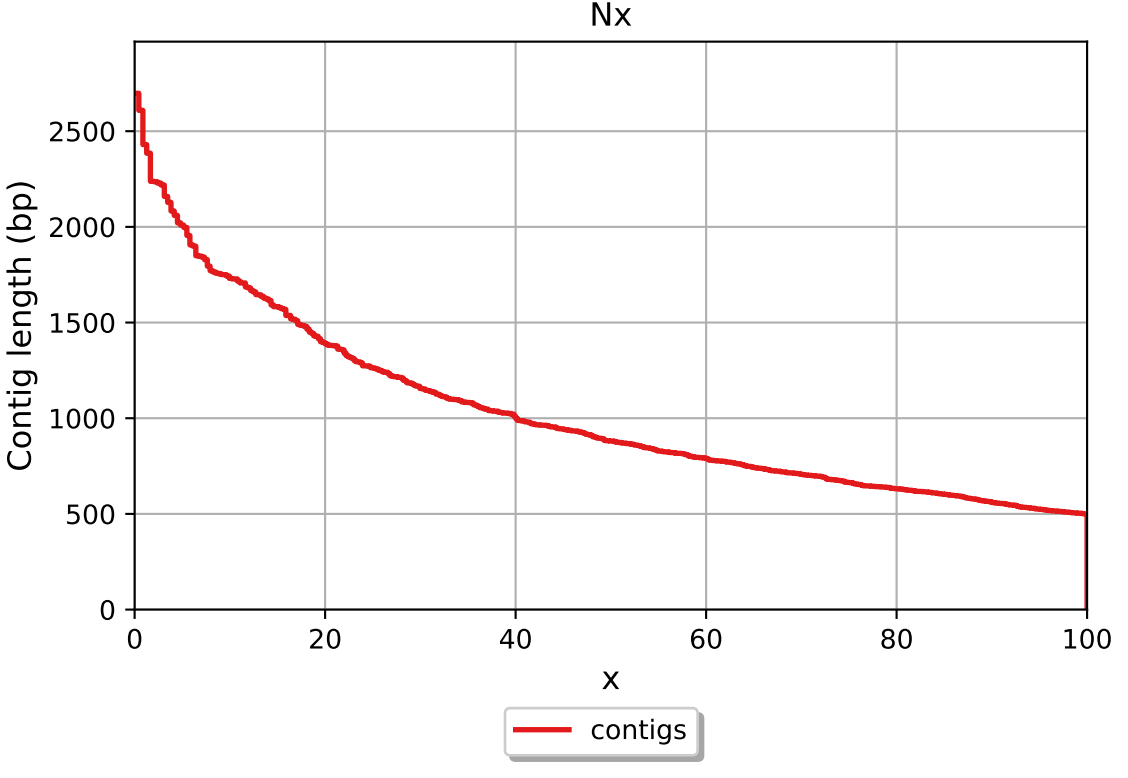
	contigs
# misassemblies	5
# contig misassemblies	5
# c. relocations	1
# c. translocations	4
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	7261
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	11475
# indels	269
# indels (<= 5 bp)	241
# indels (> 5 bp)	28
Indels length	1084

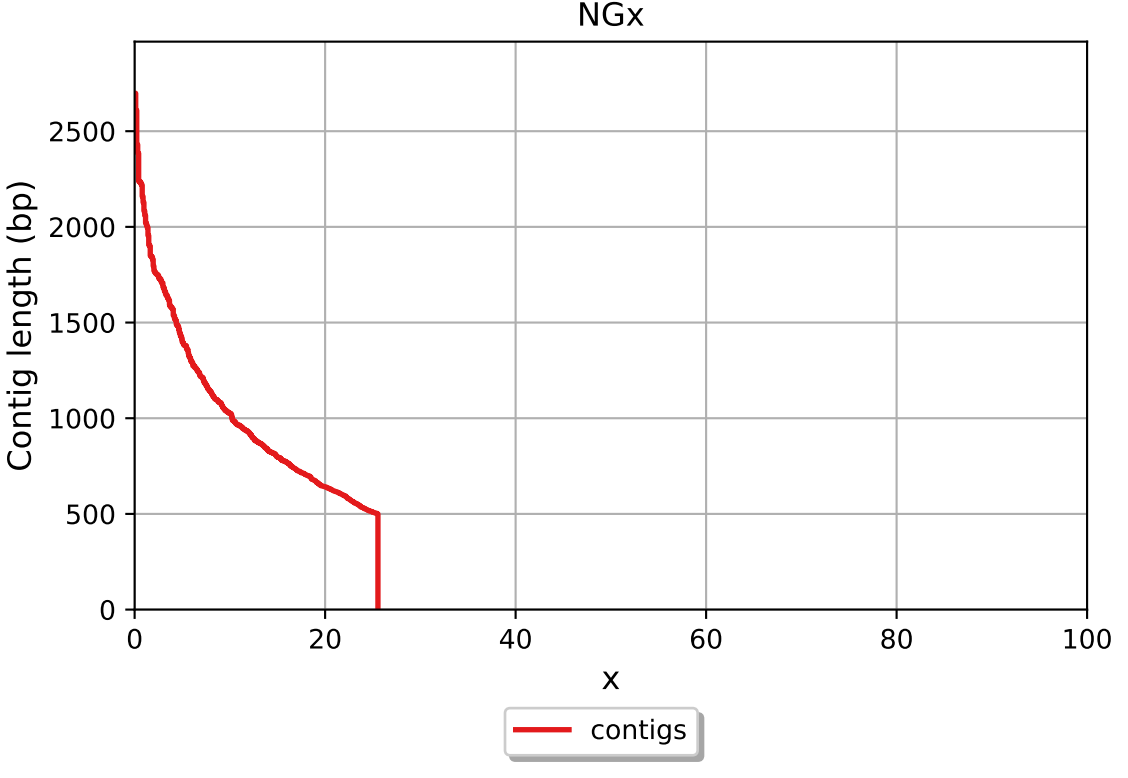
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

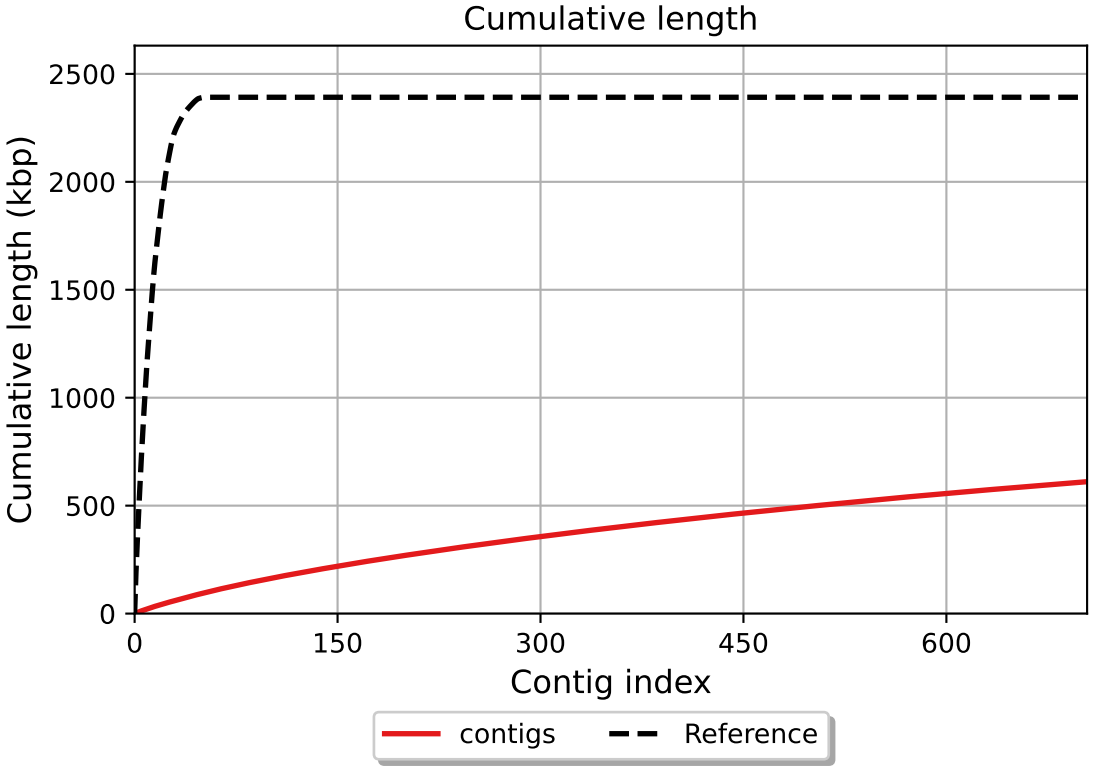
Unaligned report

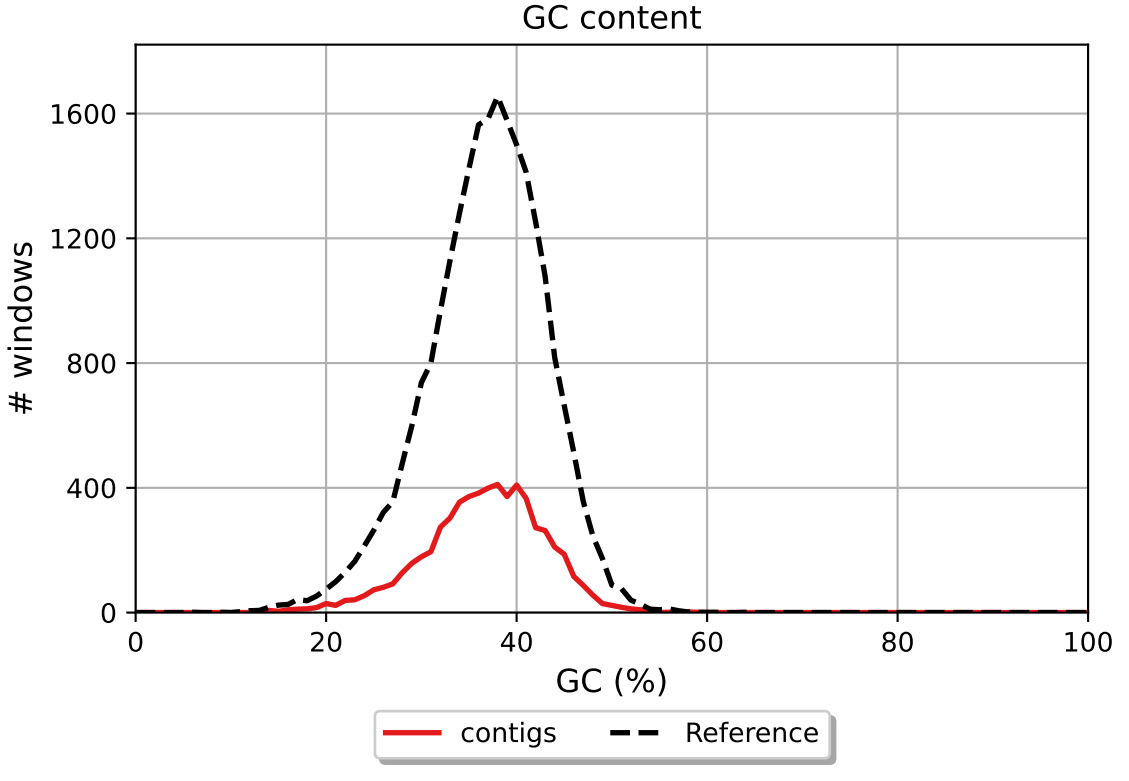
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	6280
# N's	0

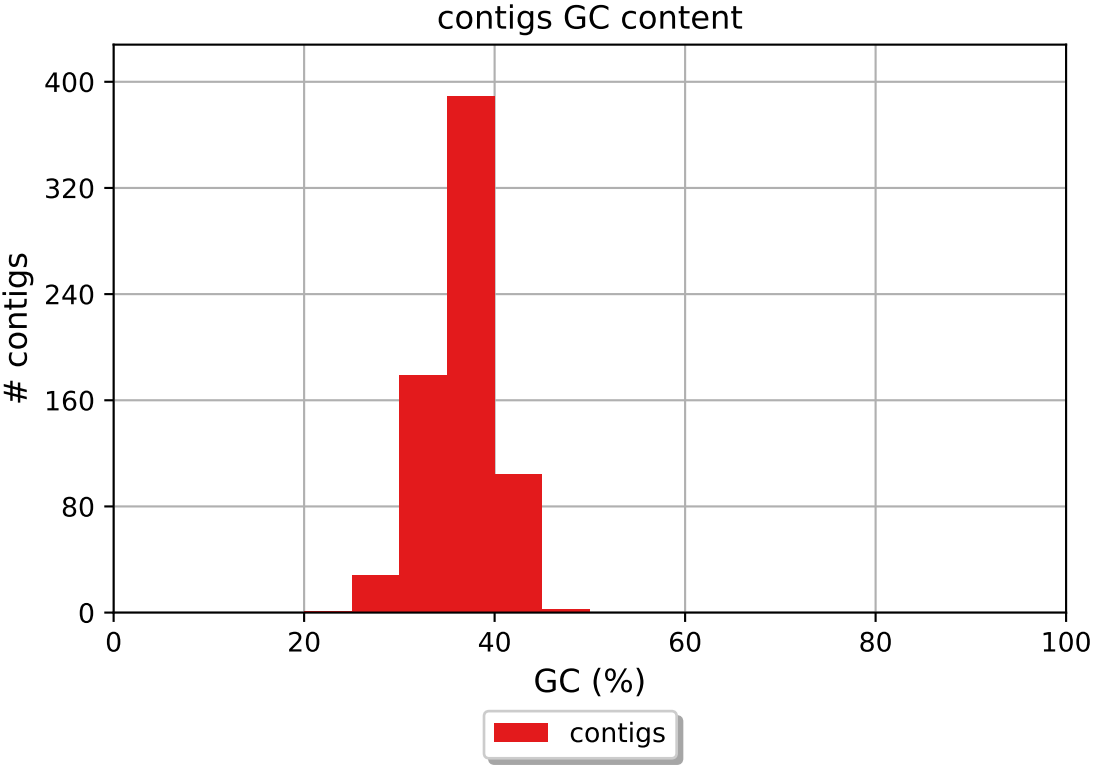
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

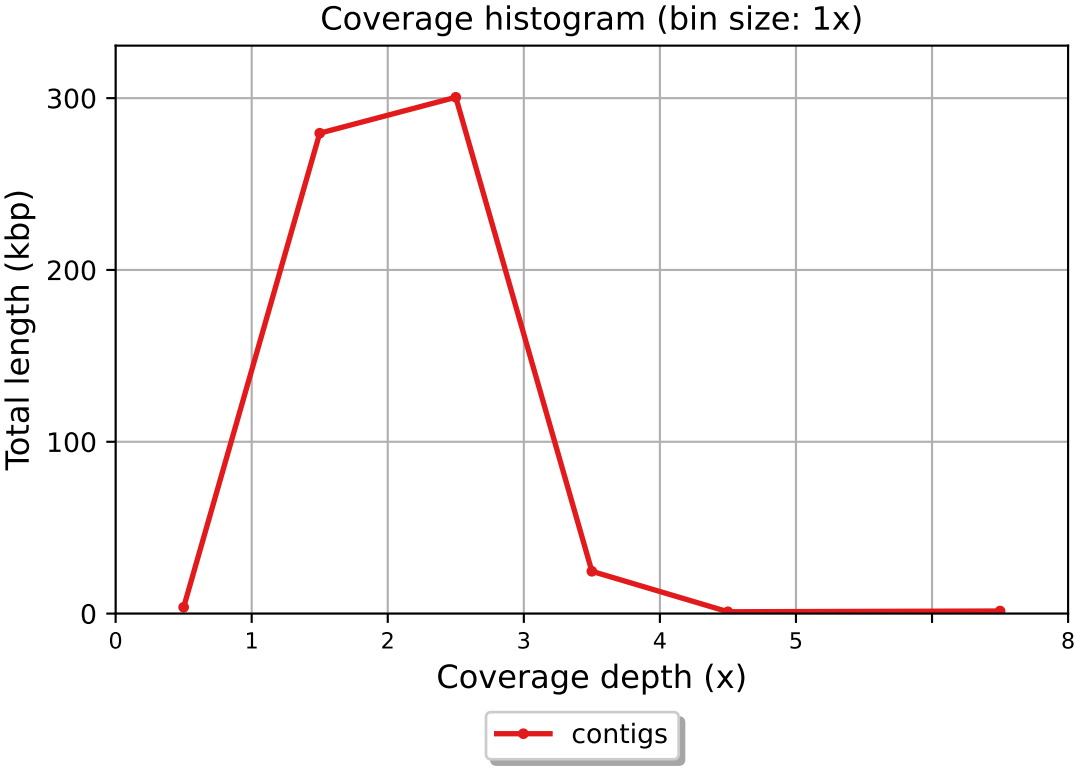

Nx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
contigs

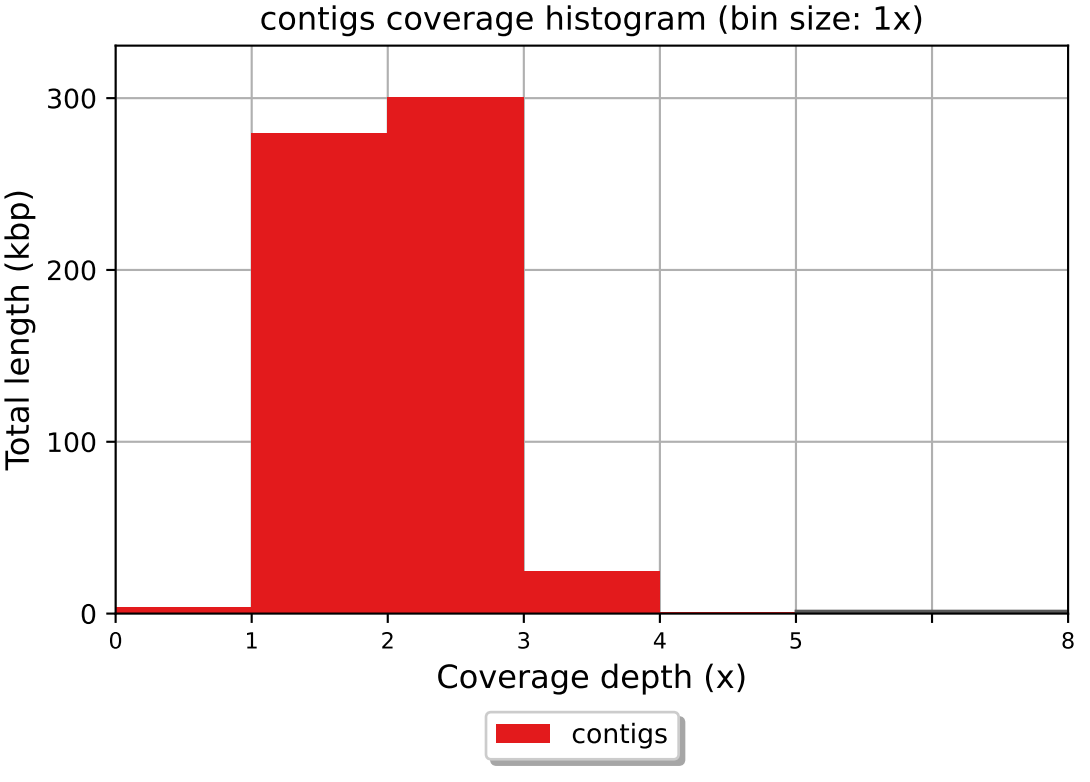

NGx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
contigs

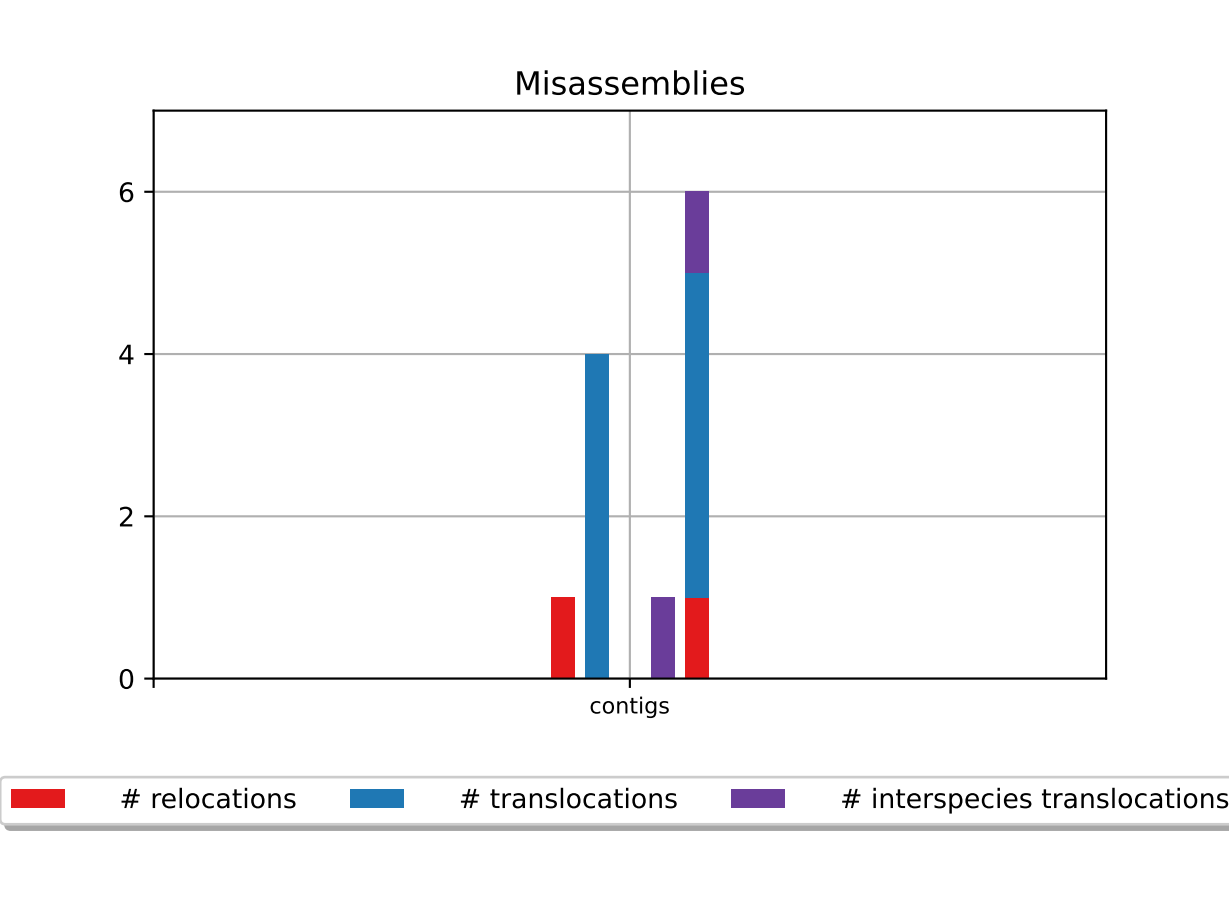

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
150
300
450
600
Contig index
contigs
Reference

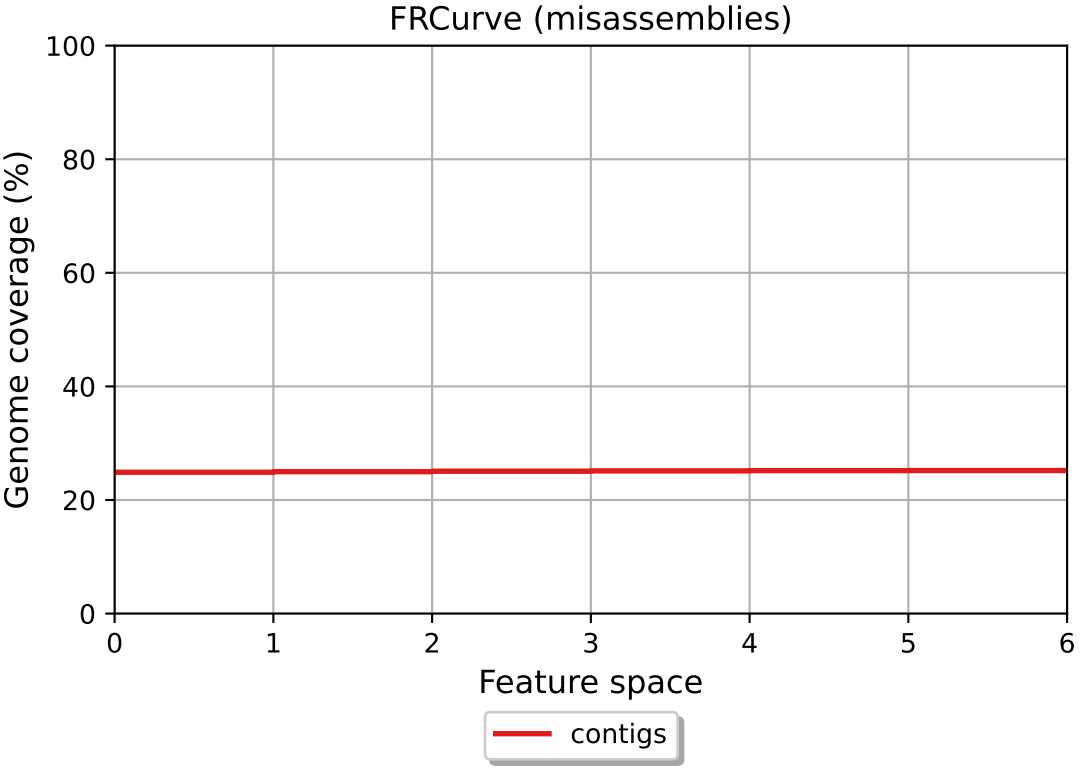

GC content
windows
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
contigs
Reference

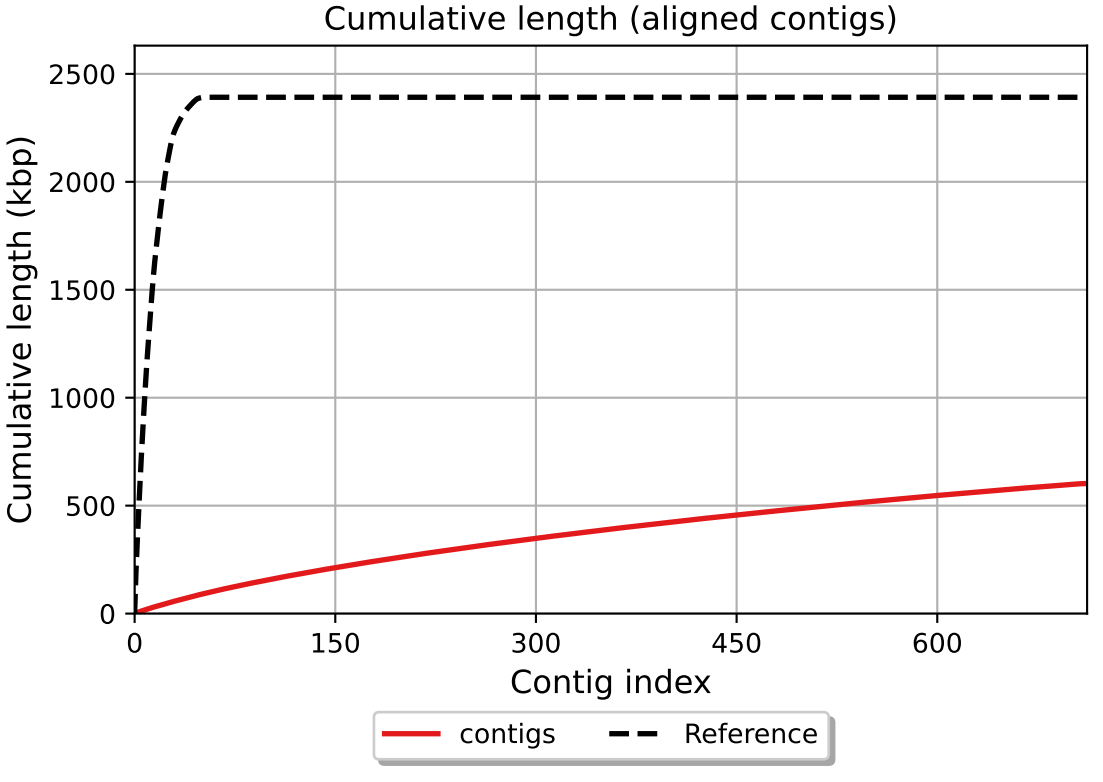

contigs GC content
400
320
240
160
80
0
contigs
0
20
40
60
80
100
GC (%)
contigs

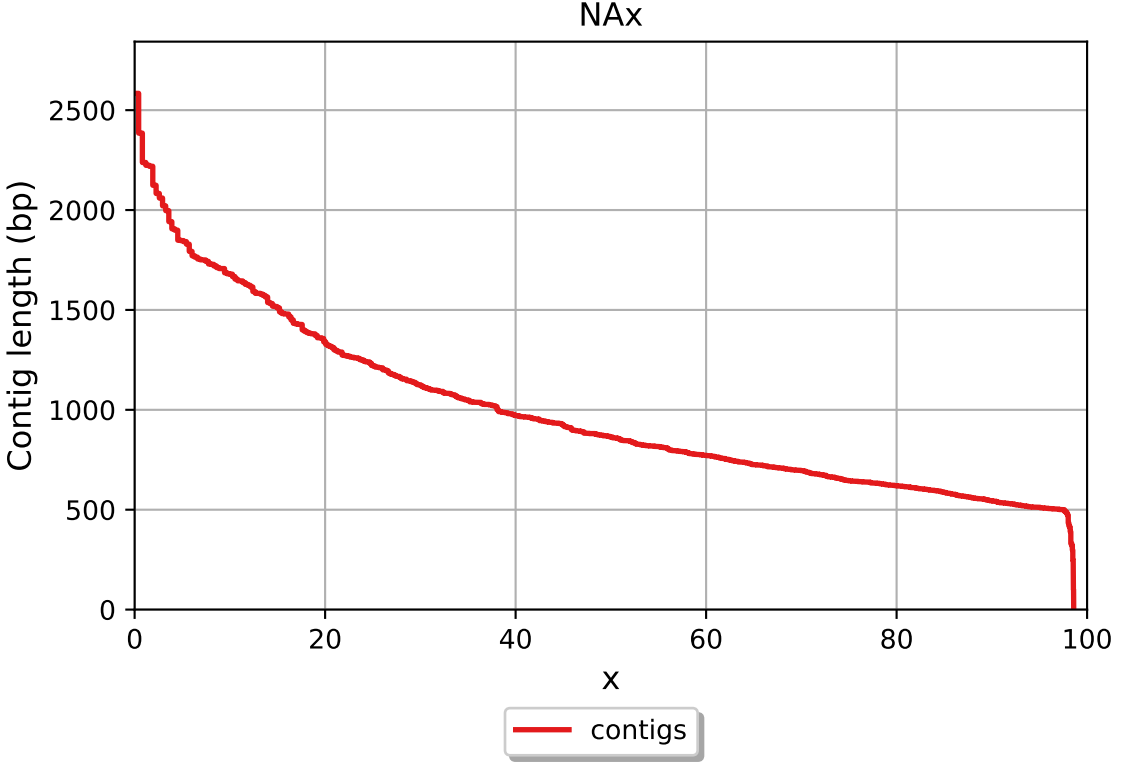

Coverage histogram (bin size: 1x)
Total length (kbp)
300
200
100
0
0
1
2
3
4
5
8
Coverage depth (x)
contigs

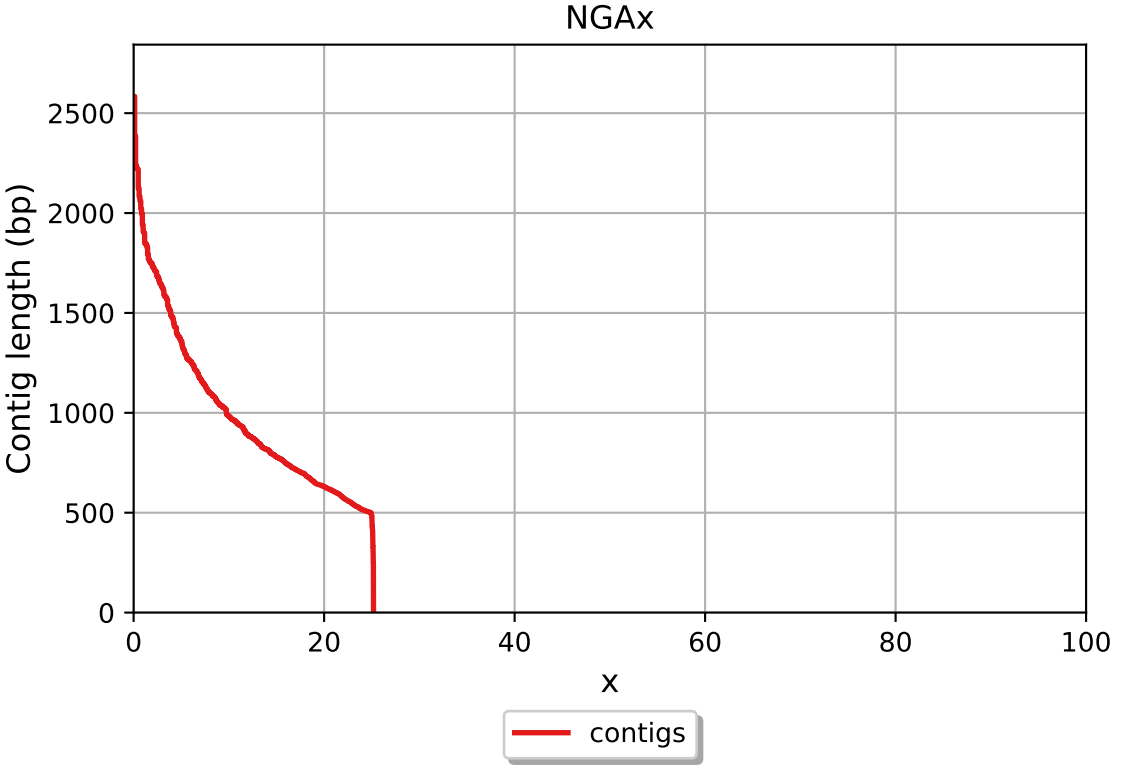

contigs coverage histogram (bin size: 1x)
Total length (kbp)
300
200
100
0
0
1
2
3
4
5
8
Coverage depth (x)
contigs


Misassemblies
6
4
2
0
contigs
relocations
translocations
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
Feature space
contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
150
300
450
600
Contig index
contigs
Reference


NAx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
contigs