Report

	01_01_assembly_canu.contigs
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	2675032
Total length (>= 1000 bp)	2675032
Total length (>= 5000 bp)	2675032
Total length (>= 10000 bp)	2675032
Total length (>= 25000 bp)	2675032
Total length (>= 50000 bp)	2640962
# contigs	3
Largest contig	2581413
Total length	2675032
Reference length	2610531
GC (%)	54.05
Reference GC (%)	54.14
N50	2581413
NG50	2581413
N75	2581413
NG75	2581413
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	2581413
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	2 + 0 part
Unaligned length	93619
Genome fraction (%)	97.566
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.43
# indels per 100 kbp	16.29
Largest alignment	1471245
Total aligned length	2581383
NA50	1471245
NGA50	1471245
NA75	1097517
NGA75	1097517
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

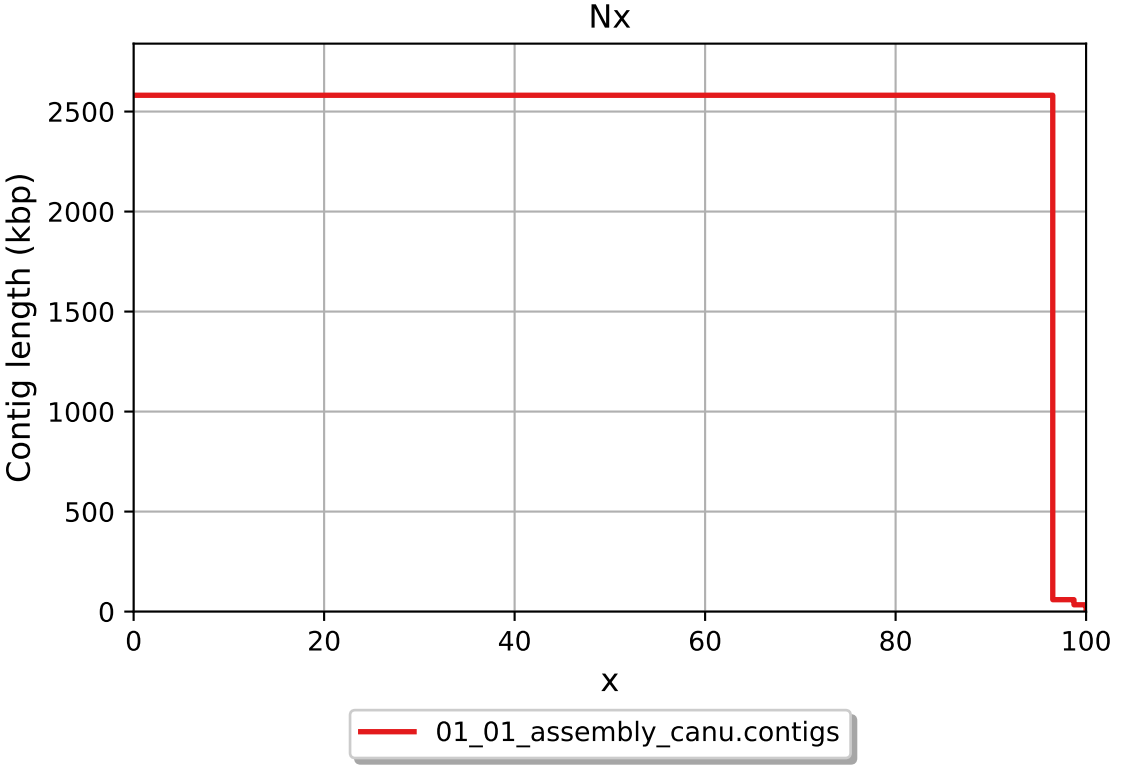
	01_01_assembly_canu.contigs
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2581413
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	11
# indels	415
# indels (<= 5 bp)	415
# indels (> 5 bp)	0
Indels length	430

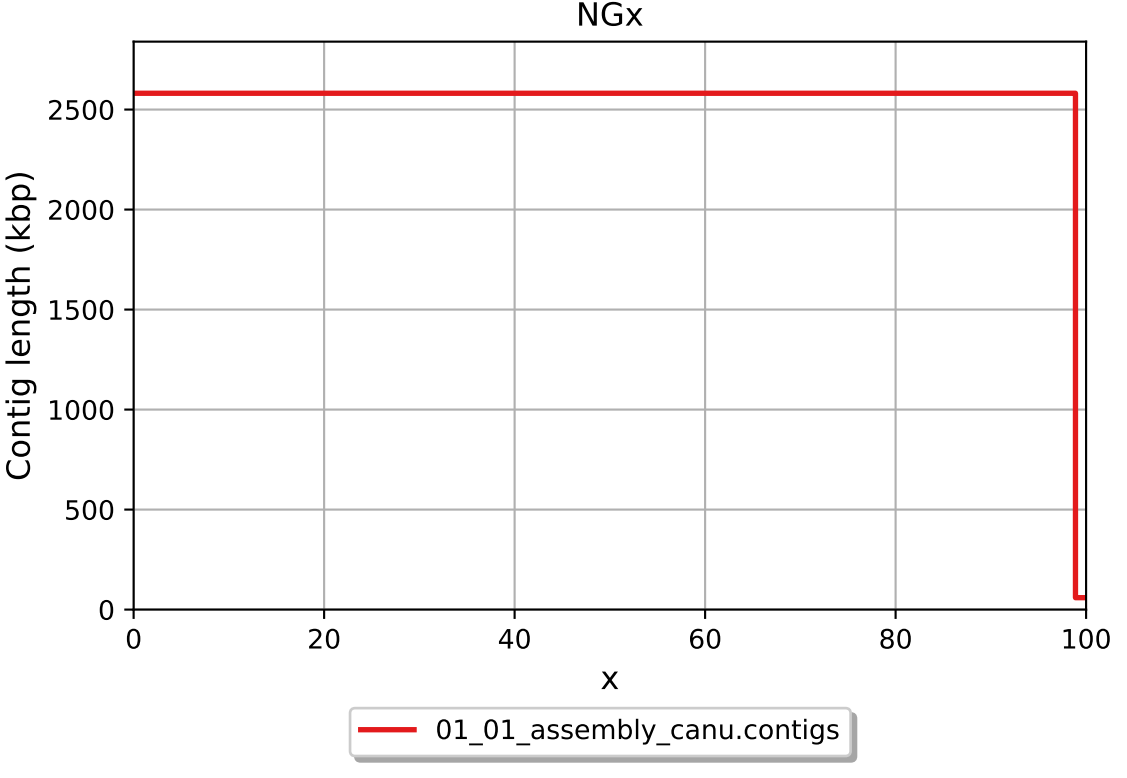
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

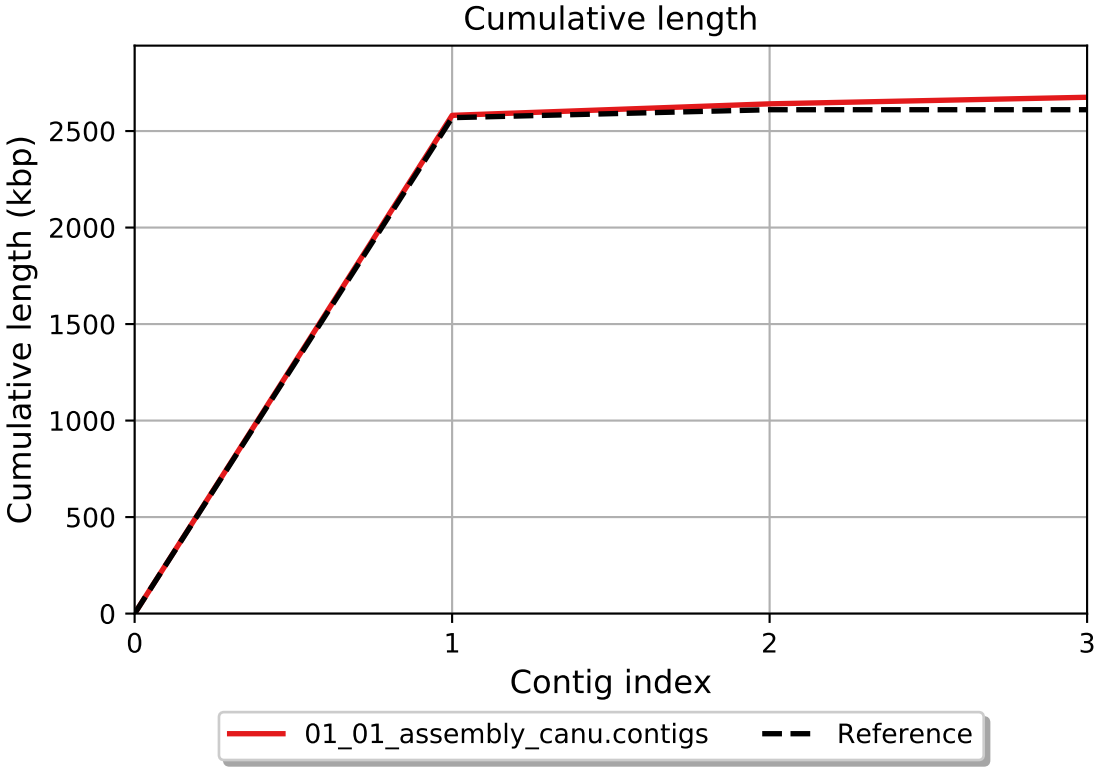
Unaligned report

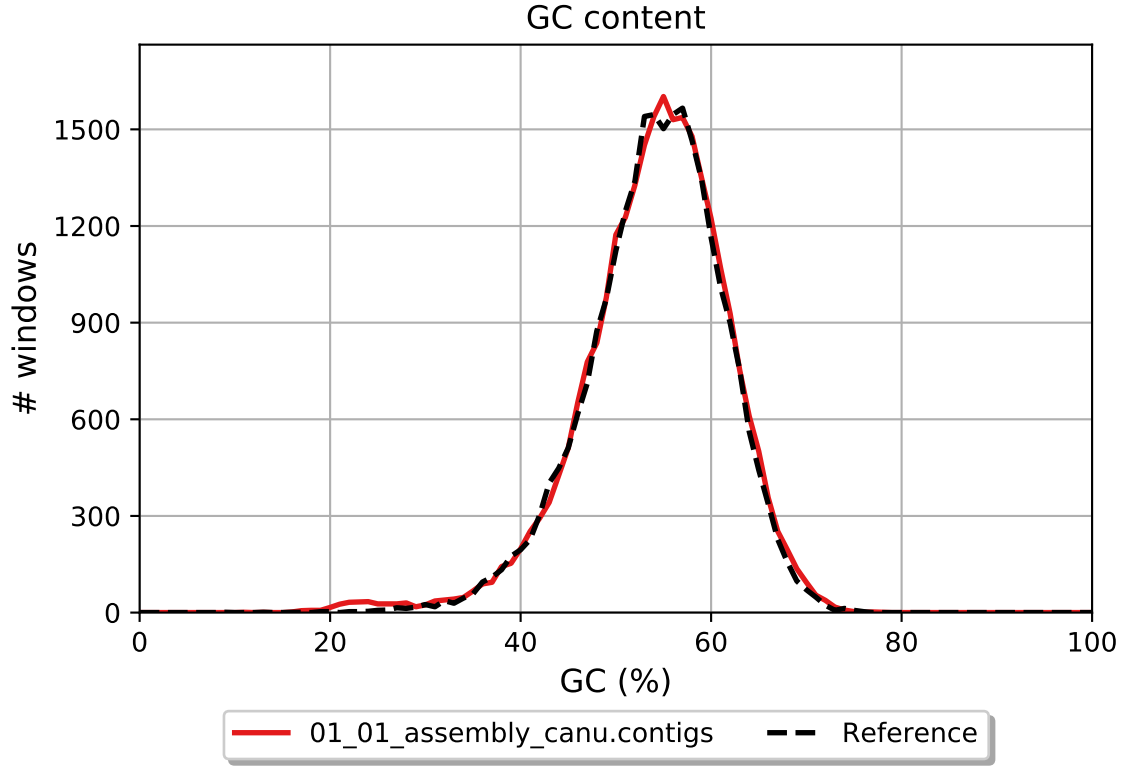
	01_01_assembly_canu.contigs
# fully unaligned contigs	2
Fully unaligned length	93619
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

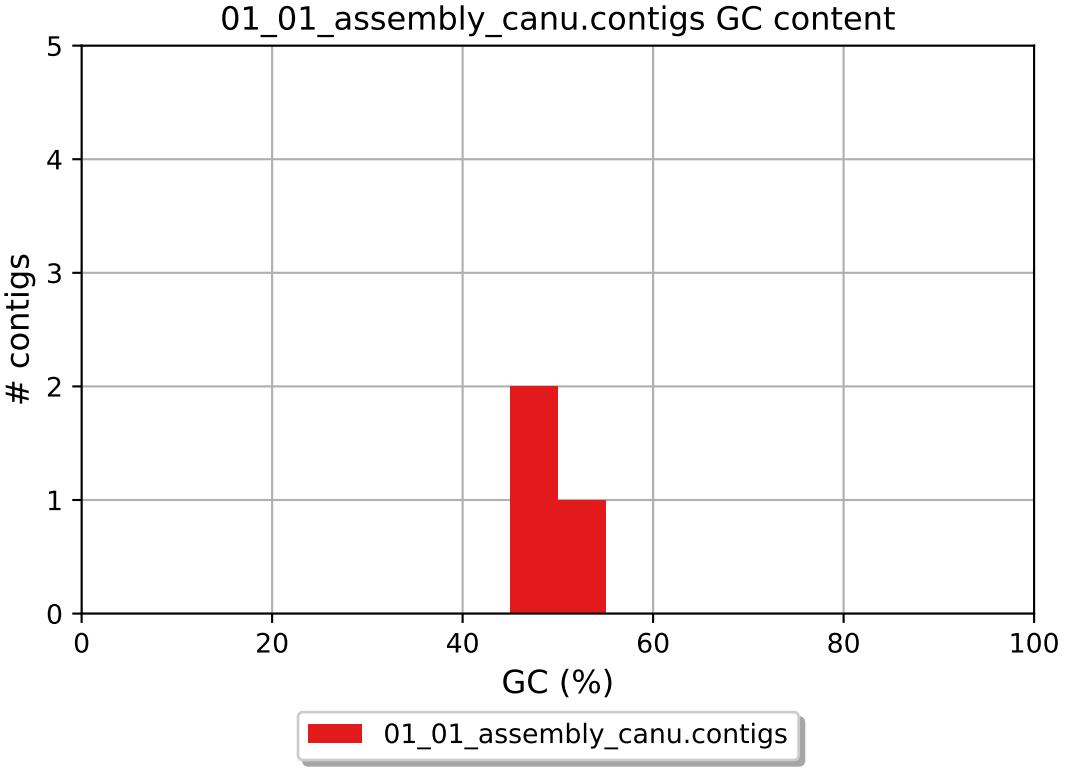
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

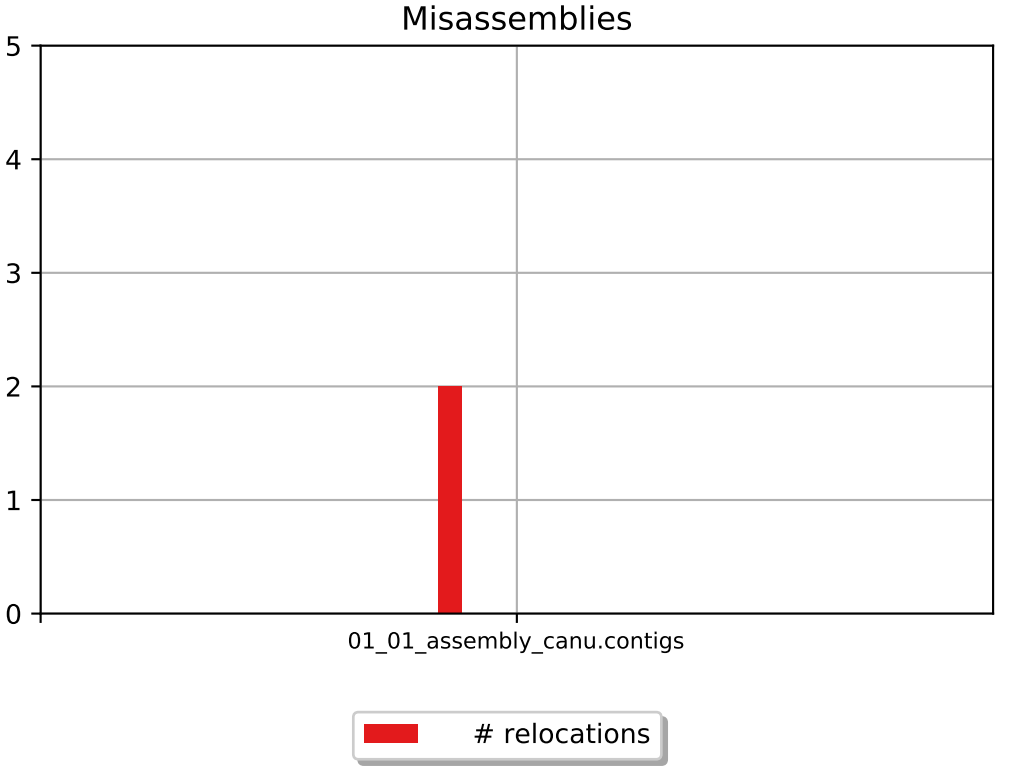

Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
01_01_assembly_canu.contigs

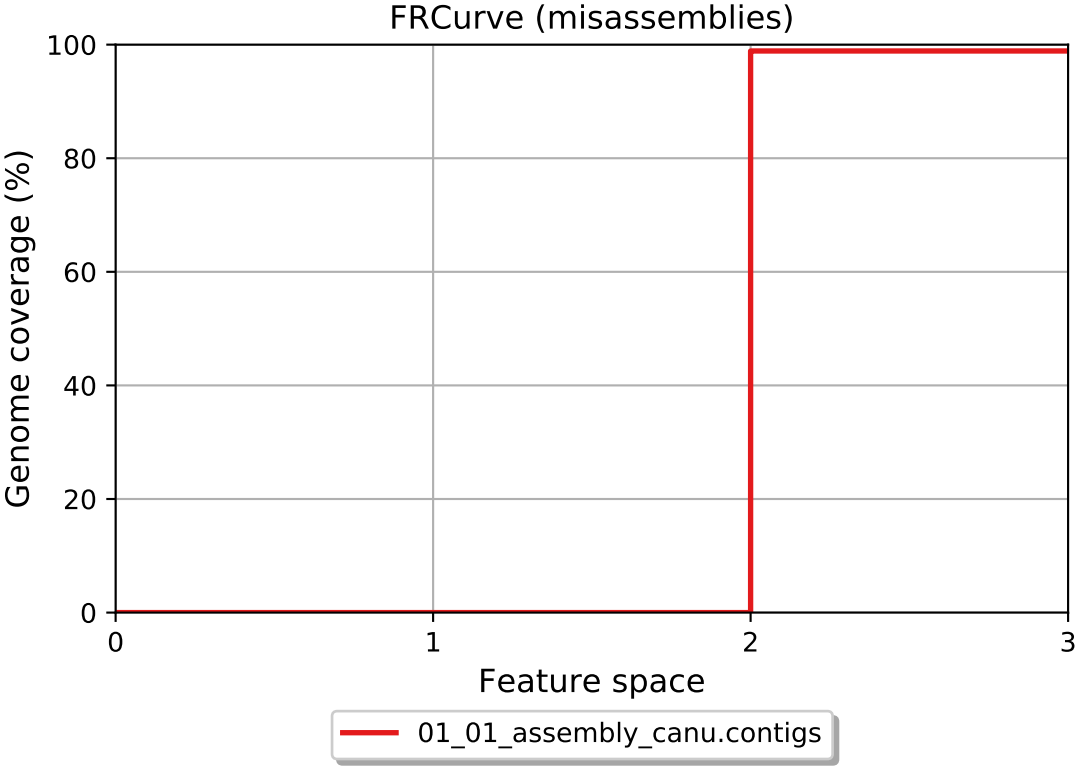

NGx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
01_01_assembly_canu.contigs

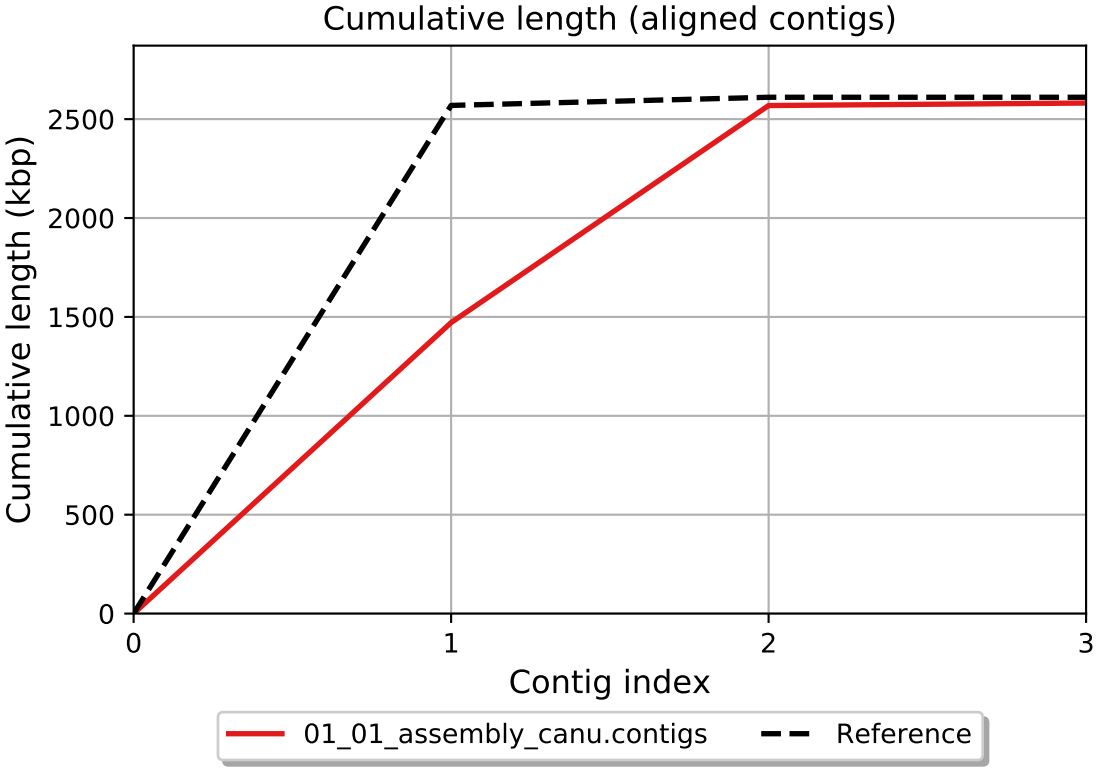

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
3
Contig index
01_01_assembly_canu.contigs
Reference

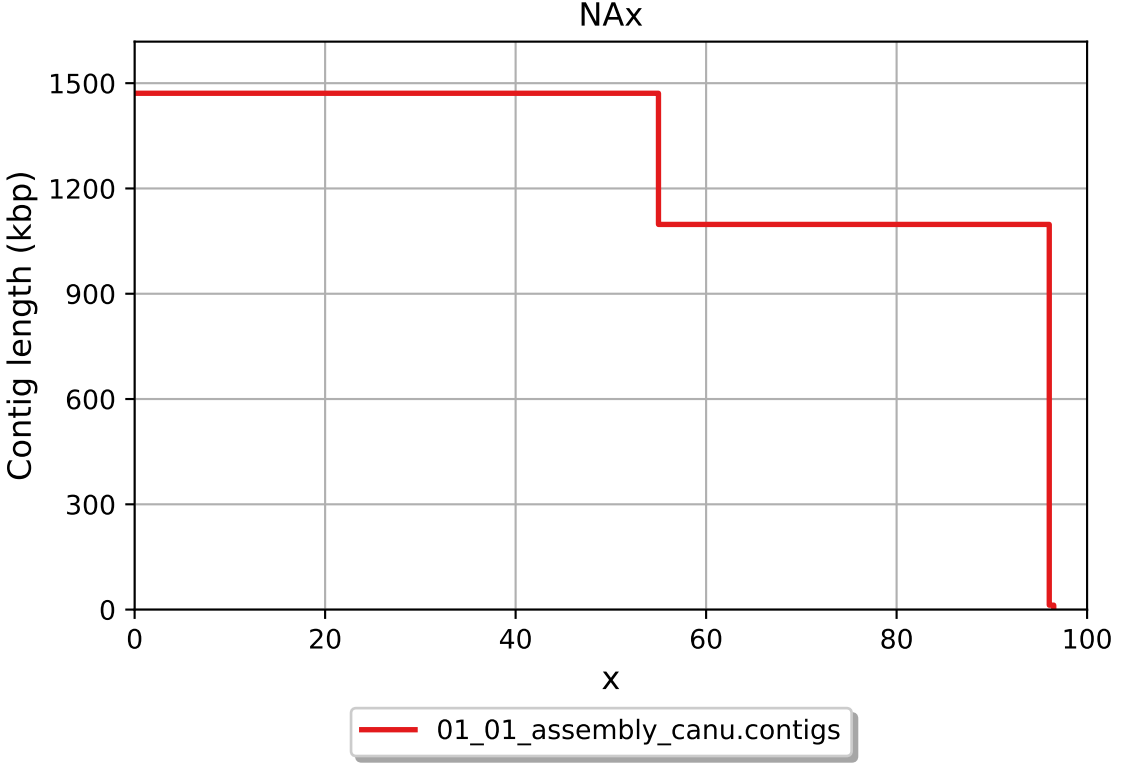

GC content
windows
1500
1200
900
600
300
0
0
20
40
60
80
100
GC (%)
01_01_assembly_canu.contigs
Reference

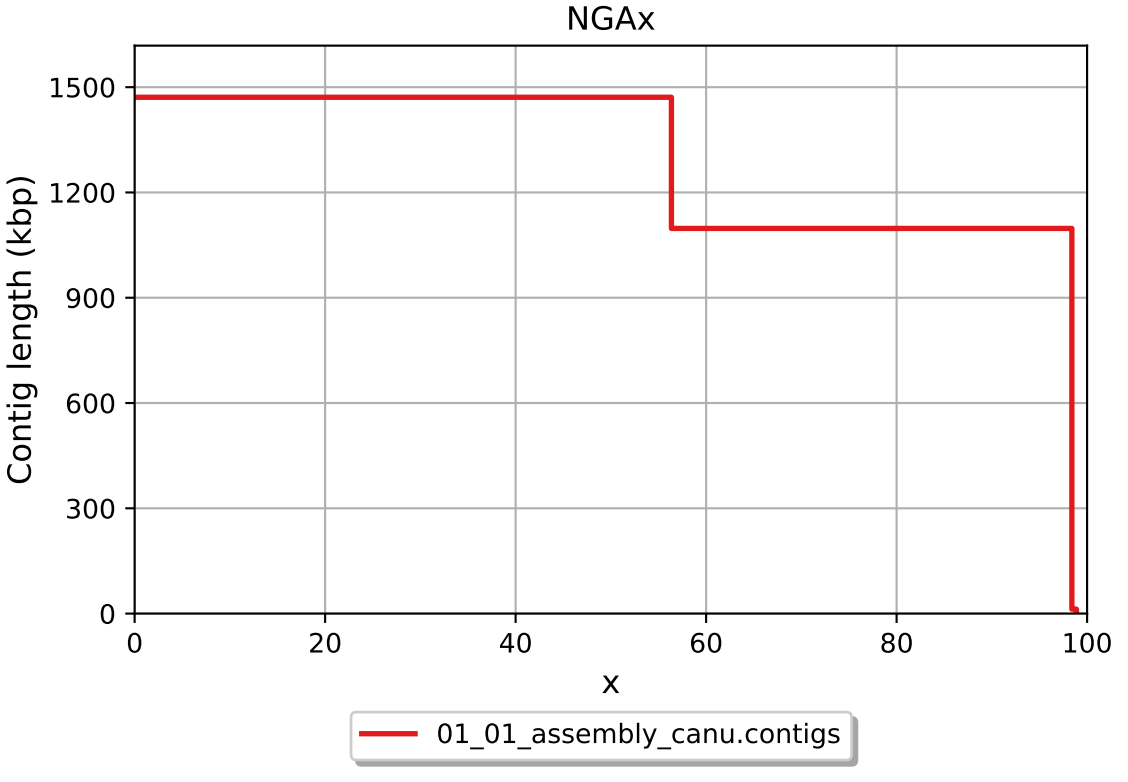

01_01_assembly_canu.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
01_01_assembly_canu.contigs


Misassemblies
5
4
3
2
1
0
01_01_assembly_canu.contigs
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
Feature space
01_01_assembly_canu.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
3
Contig index
01_01_assembly_canu.contigs
Reference


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
01_01_assembly_canu.contigs


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
01_01_assembly_canu.contigs