Report

	genome_assembly_canu.contigs
# contigs (>= 0 bp)	9
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3154995
Total length (>= 1000 bp)	3154995
Total length (>= 5000 bp)	3154995
Total length (>= 10000 bp)	3145708
Total length (>= 25000 bp)	3096150
Total length (>= 50000 bp)	2982128
# contigs	9
Largest contig	2775620
Total length	3154995
Reference length	2919198
GC (%)	37.75
Reference GC (%)	37.88
N50	2775620
NG50	2775620
N75	2775620
NG75	2775620
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	190
# misassembled contigs	1
Misassembled contigs length	2775620
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	3 + 6 part
Unaligned length	557350
Genome fraction (%)	85.051
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	392.94
# indels per 100 kbp	19.01
Largest alignment	115726
Total aligned length	2592243
NA50	24553
NGA50	30127
NA75	4951
NGA75	10362
LA50	32
LGA50	27
LA75	88
LGA75	66

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

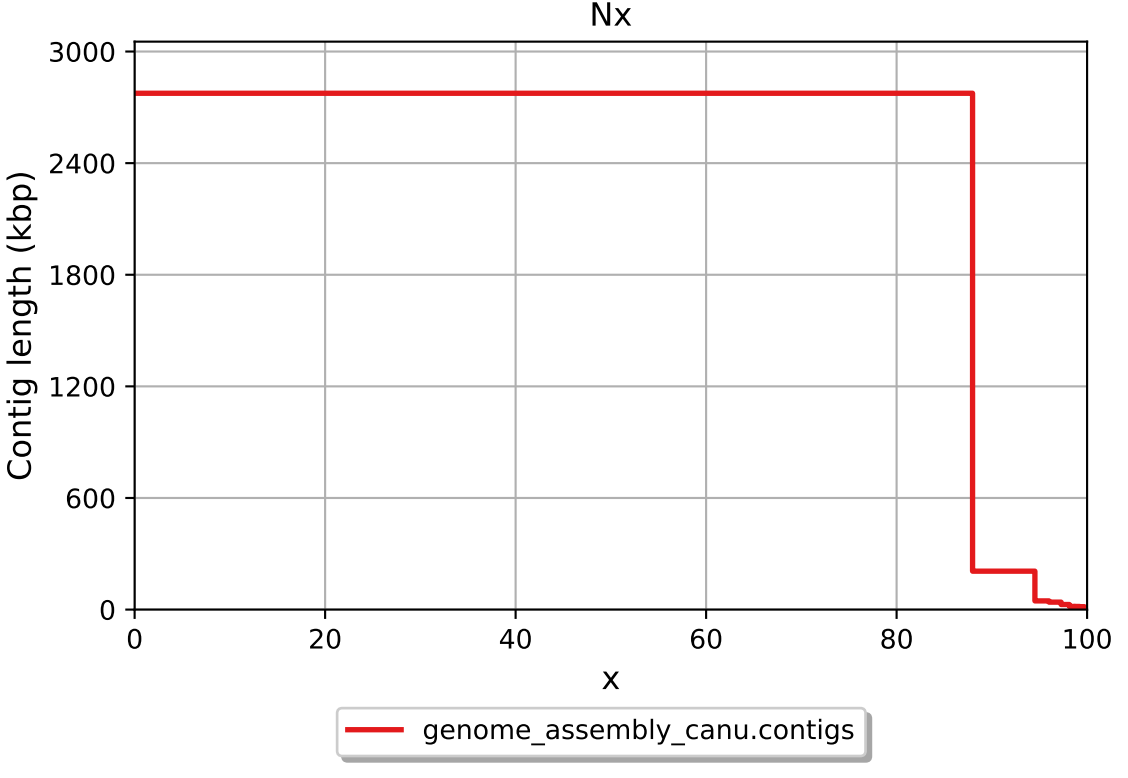
	genome_assembly_canu.contigs
# misassemblies	190
# contig misassemblies	190
# c. relocations	176
# c. translocations	12
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2775620
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	9756
# indels	472
# indels (<= 5 bp)	434
# indels (> 5 bp)	38
Indels length	1661

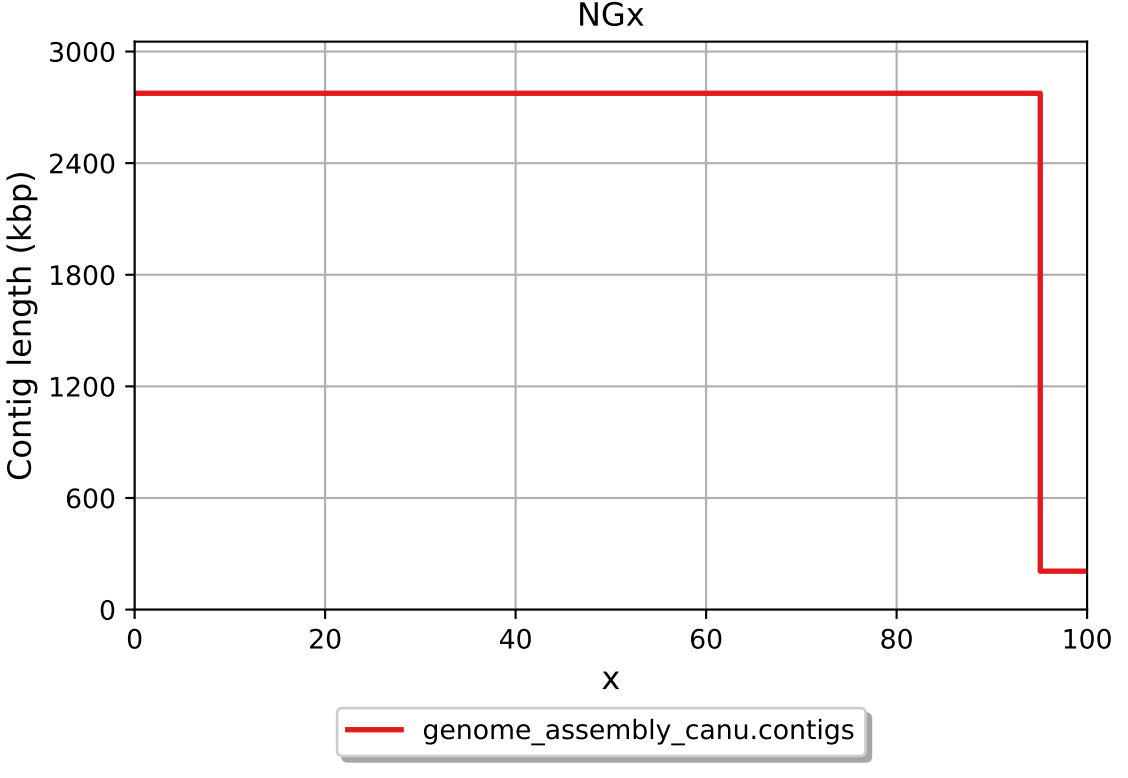
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

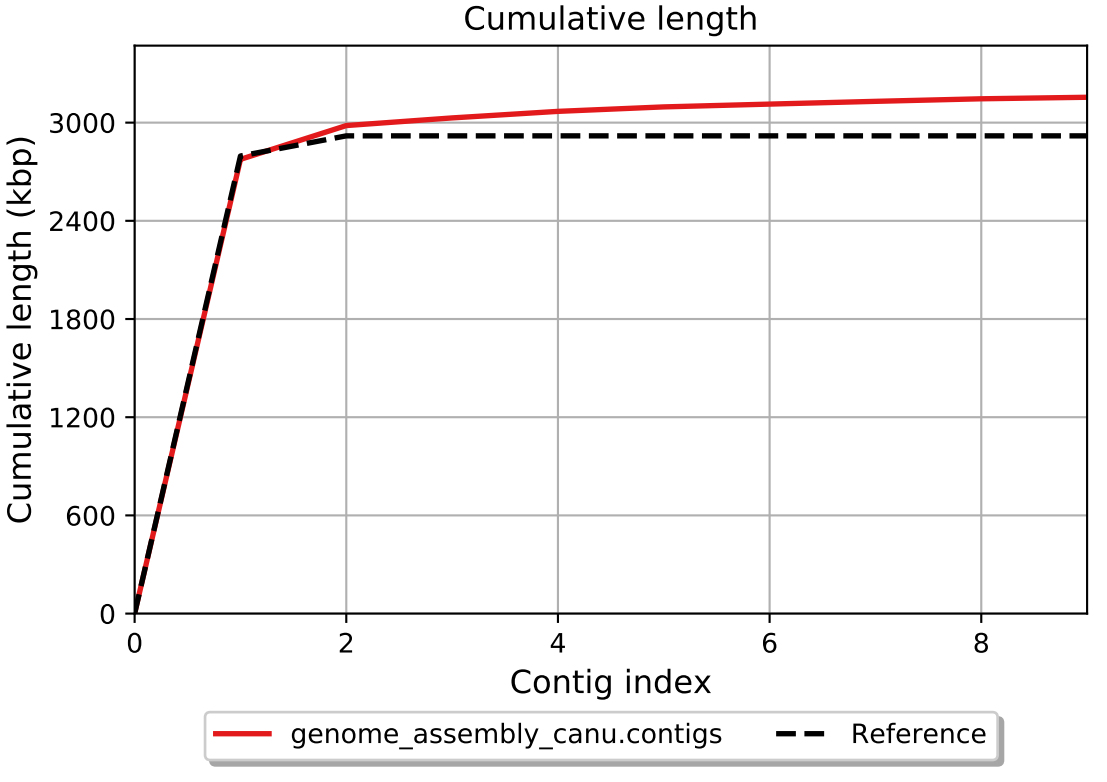
Unaligned report

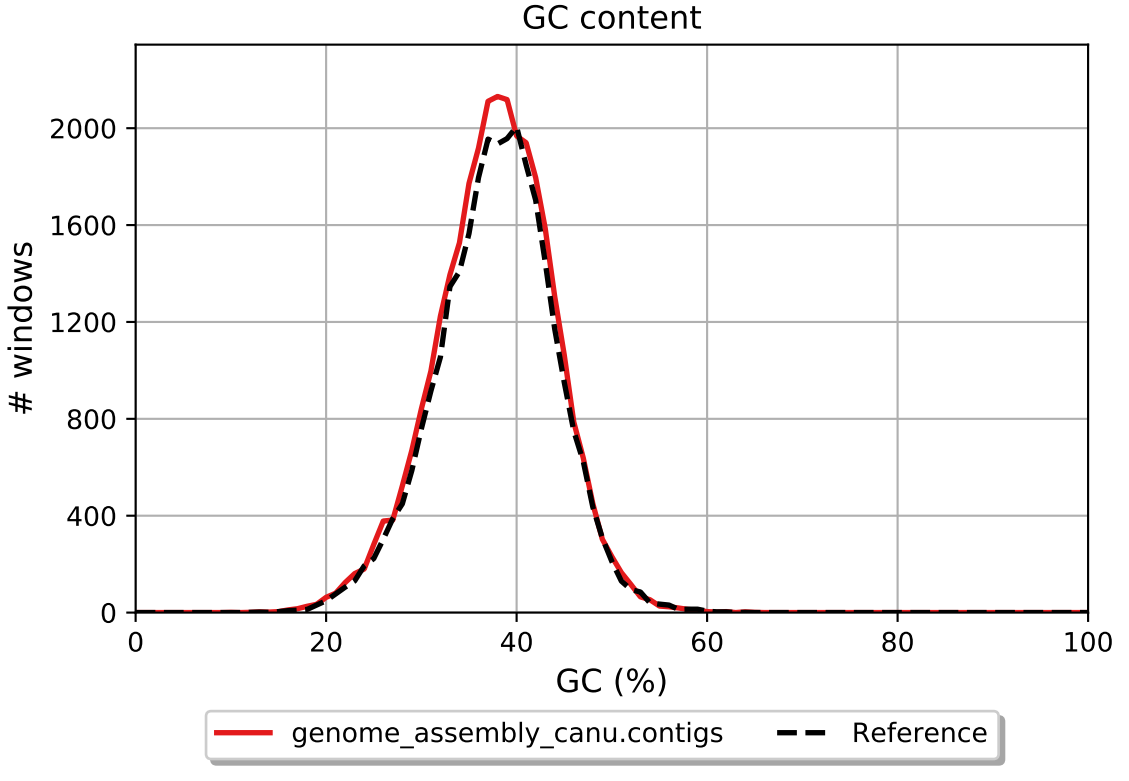
	genome_assembly_canu.contigs
# fully unaligned contigs	3
Fully unaligned length	52191
# partially unaligned contigs	6
Partially unaligned length	505159
# N's	0

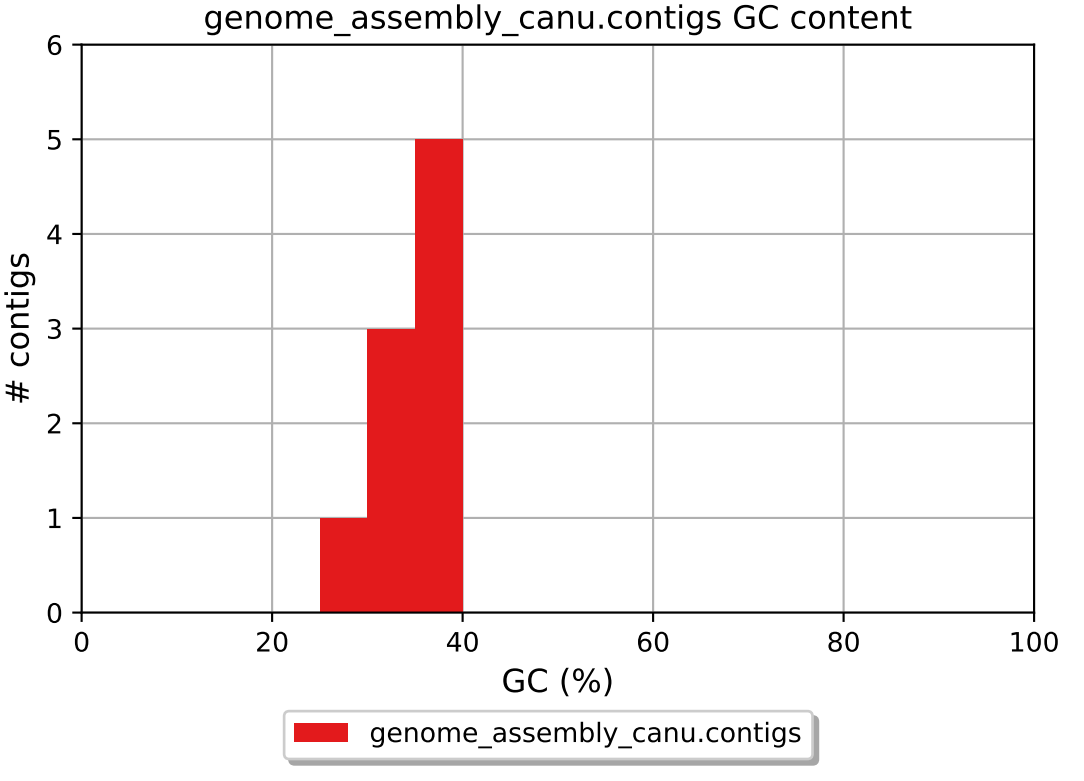
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

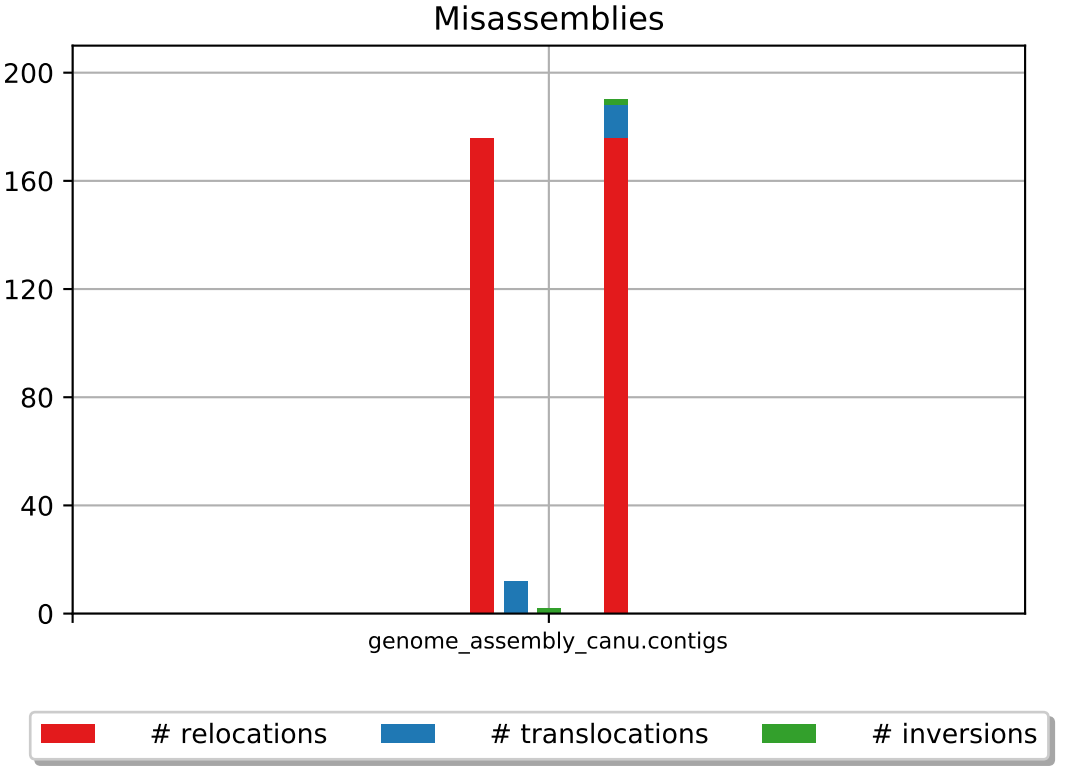

Nx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
genome_assembly_canu.contigs

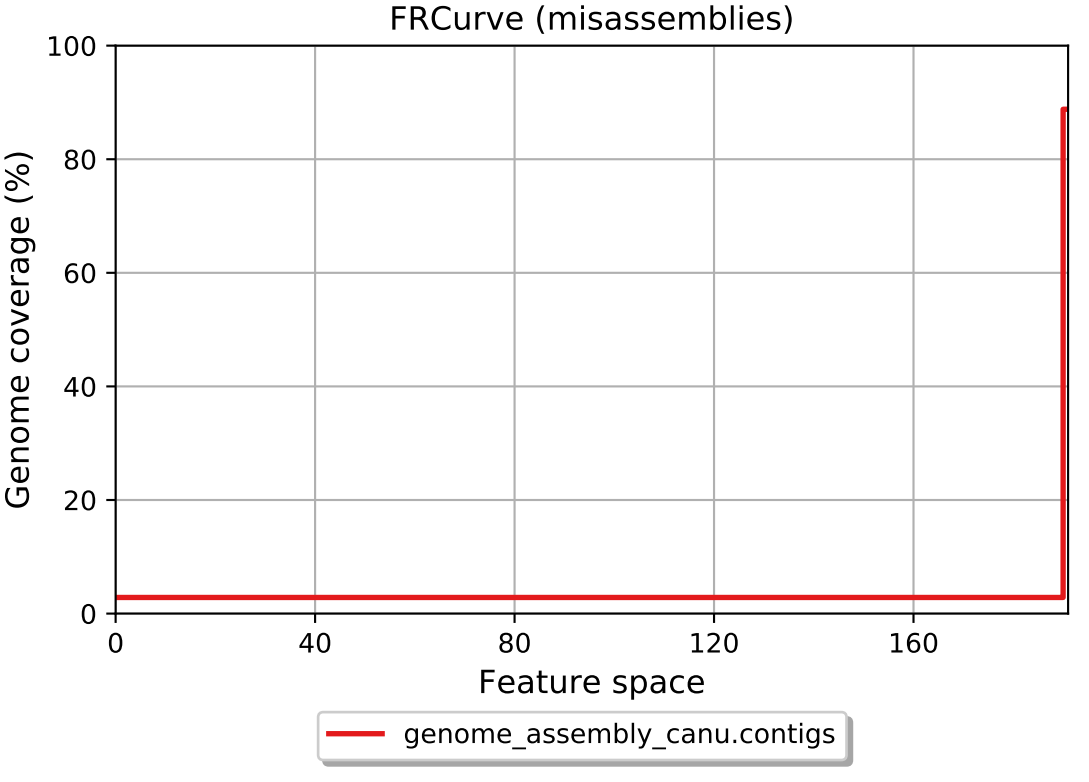

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
genome_assembly_canu.contigs

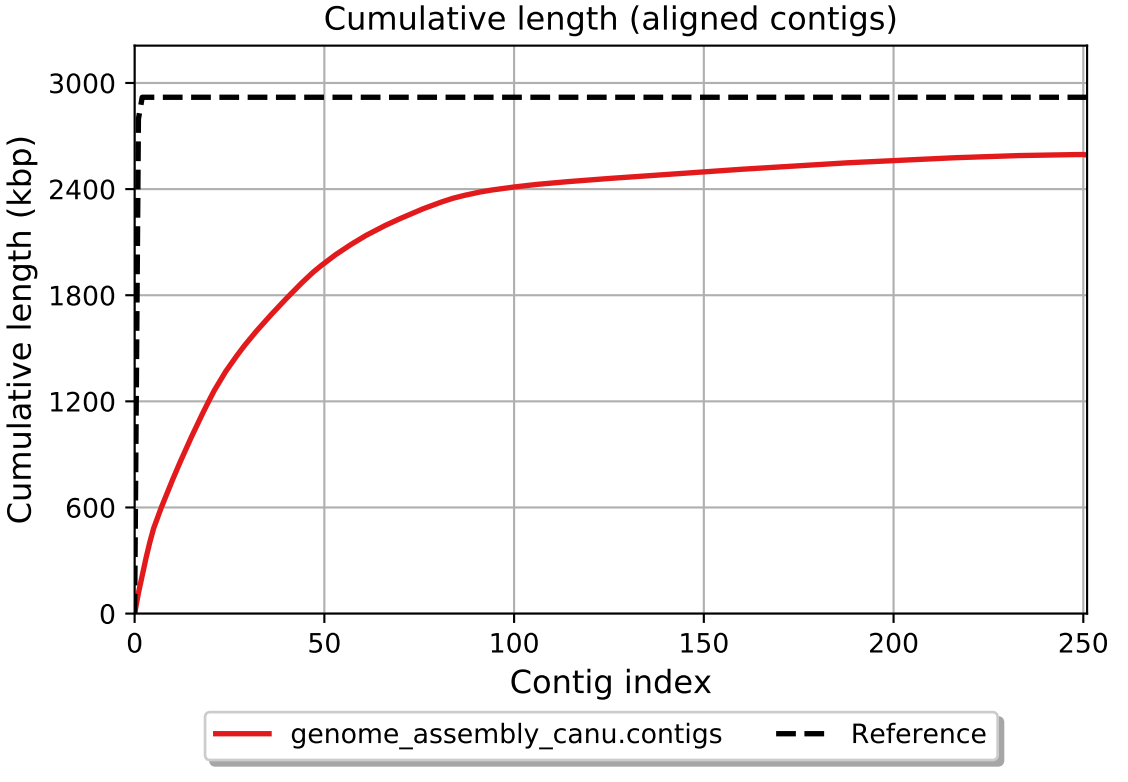

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
2
4
6
8
Contig index
genome_assembly_canu.contigs
Reference

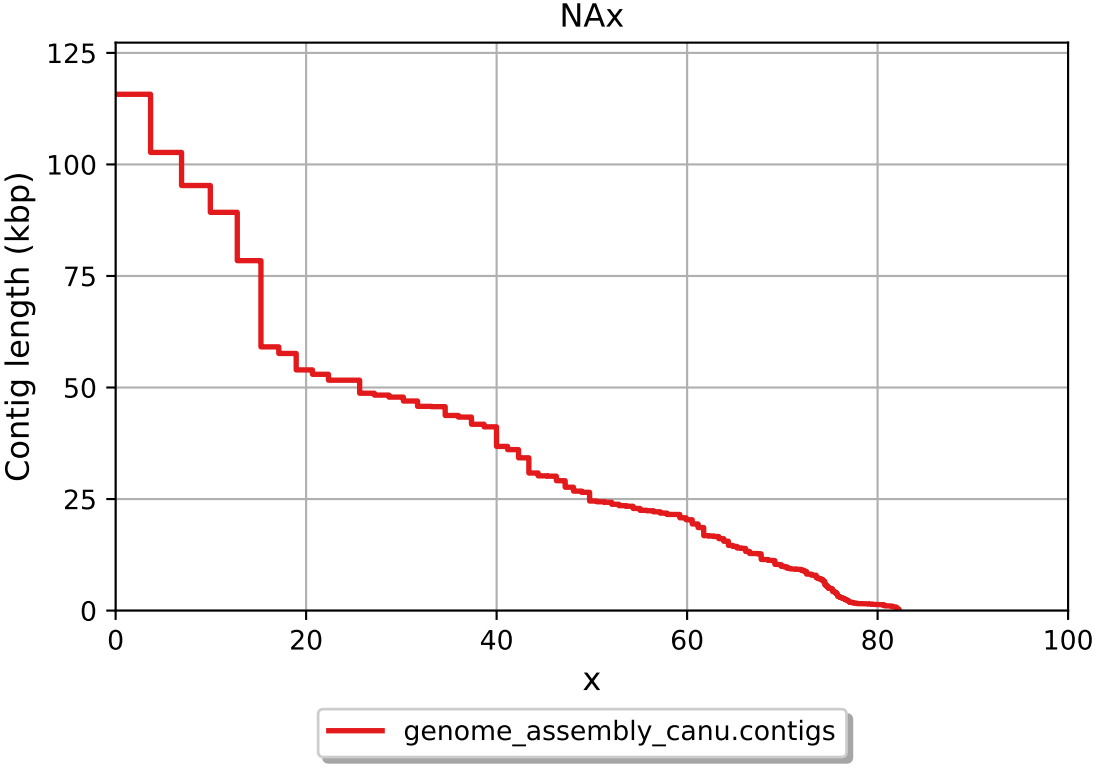

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
genome_assembly_canu.contigs
Reference

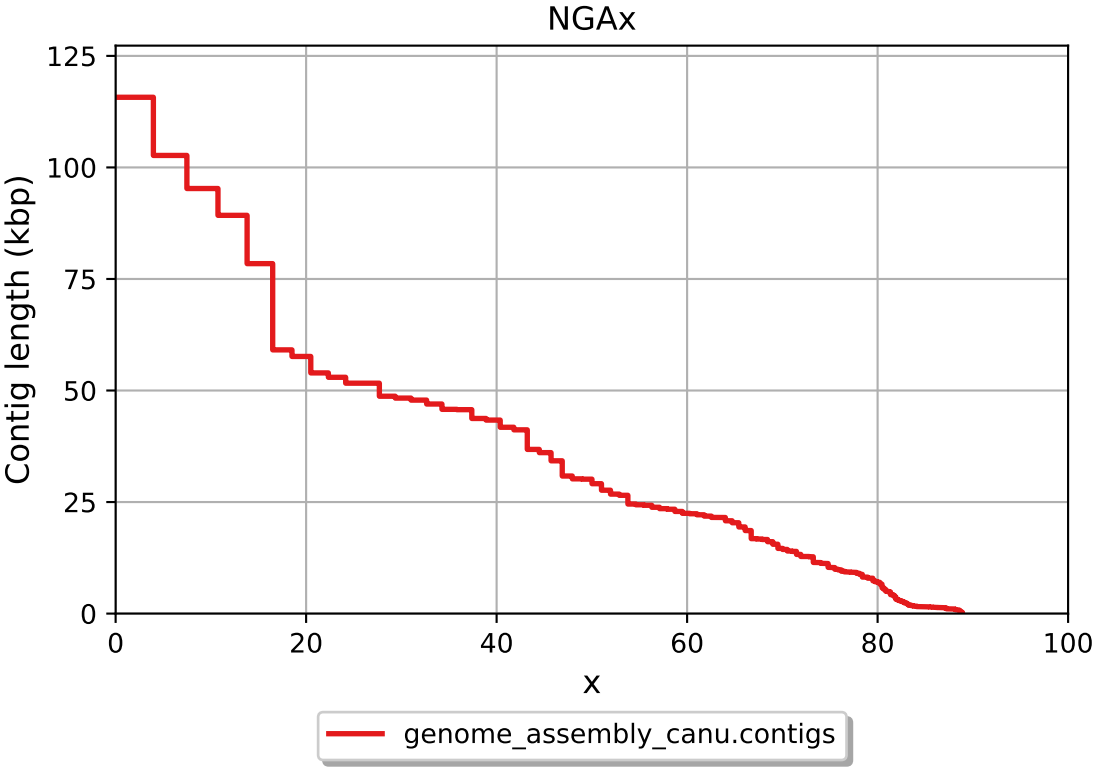

genome_assembly_canu.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
genome_assembly_canu.contigs


Misassemblies
200
160
120
80
40
0
genome_assembly_canu.contigs
relocations
translocations
inversions


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


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


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


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