Report

	canu_L_Ferri_combined.contigs
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2571206
Total length (>= 1000 bp)	2571206
Total length (>= 5000 bp)	2568586
Total length (>= 10000 bp)	2568586
Total length (>= 25000 bp)	2568586
Total length (>= 50000 bp)	2568586
# contigs	2
Largest contig	2568586
Total length	2571206
Reference length	2610531
GC (%)	54.22
Reference GC (%)	54.14
N50	2568586
NG50	2568586
N75	2568586
NG75	2568586
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2568586
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	2620
Genome fraction (%)	97.566
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.08
# indels per 100 kbp	13.27
Largest alignment	1831715
Total aligned length	2568586
NA50	1831715
NGA50	1831715
NA75	736871
NGA75	736871
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

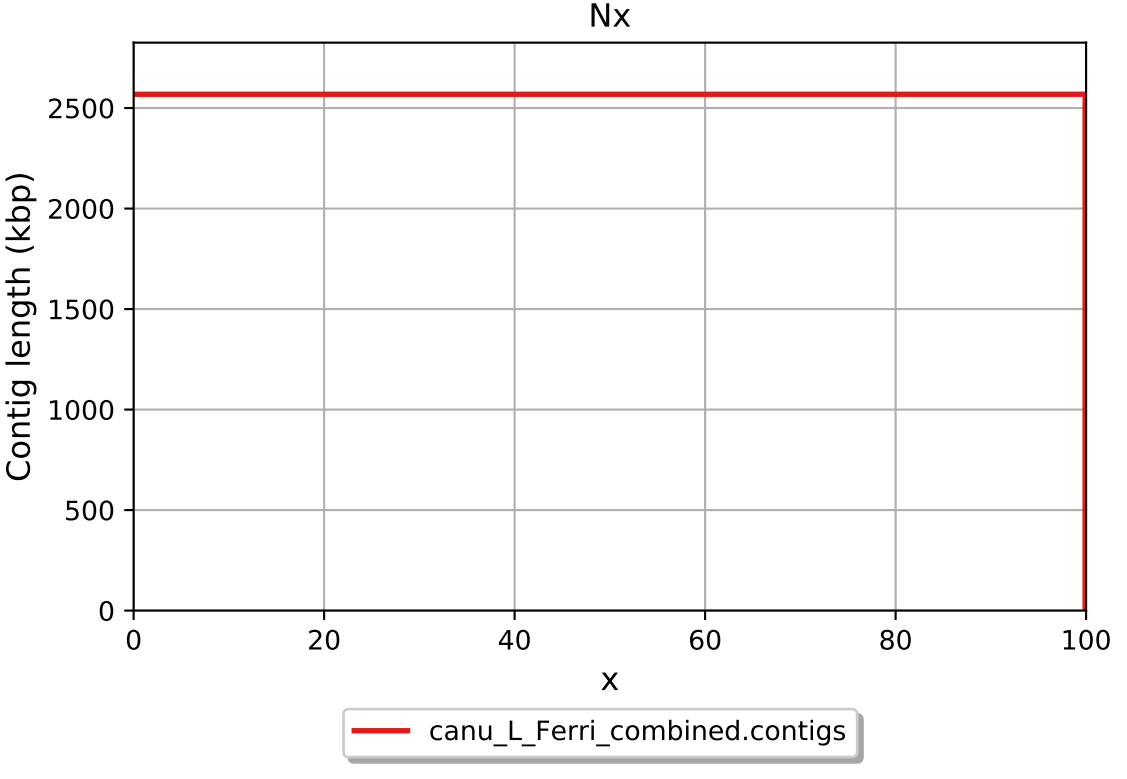
	canu_L_Ferri_combined.contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2568586
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	2
# indels	338
# indels (<= 5 bp)	338
# indels (> 5 bp)	0
Indels length	343

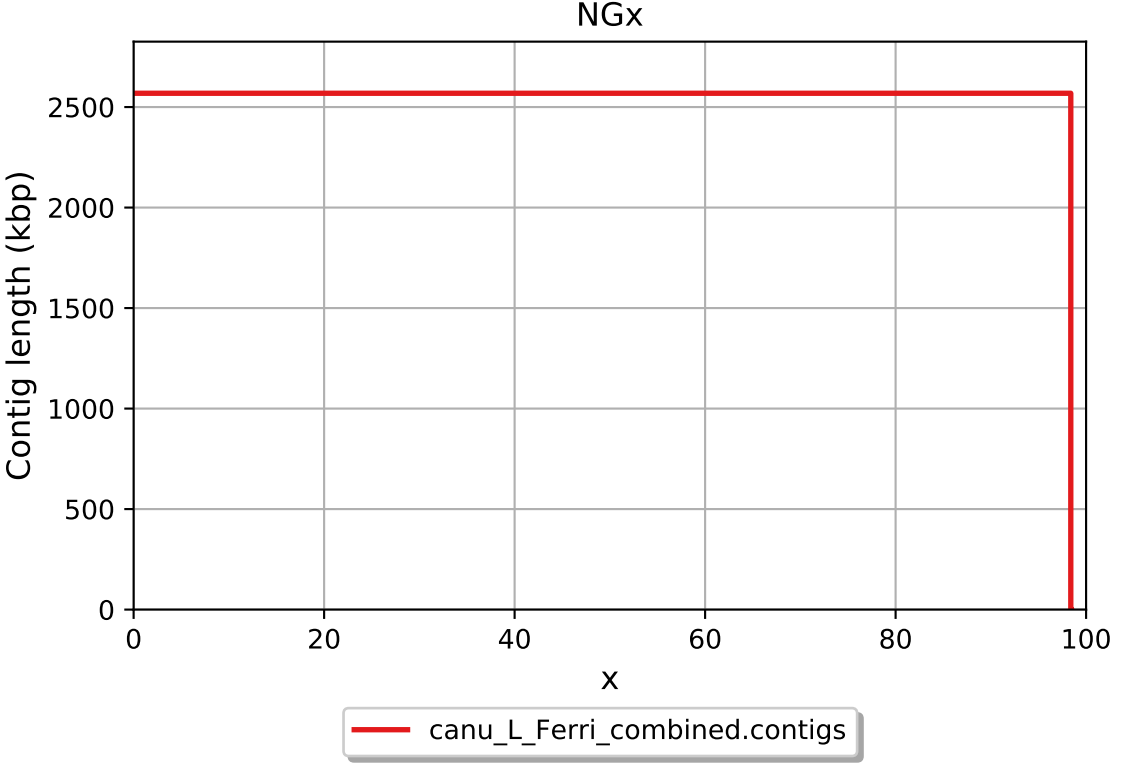
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

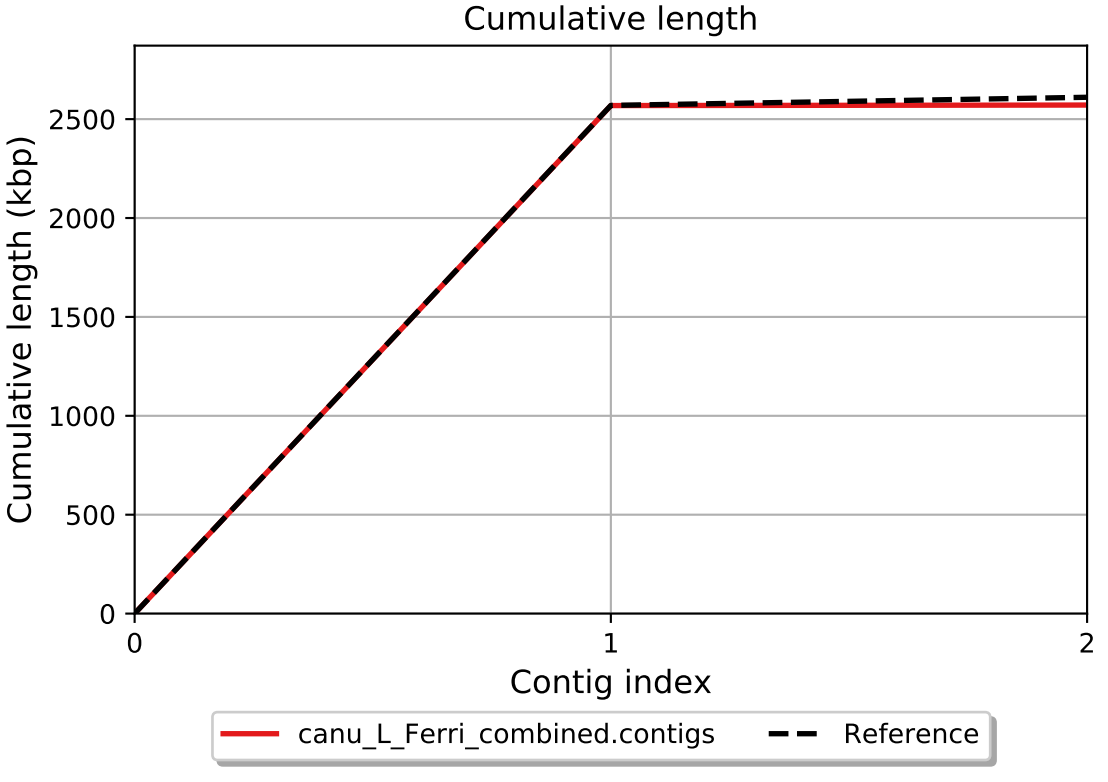
Unaligned report

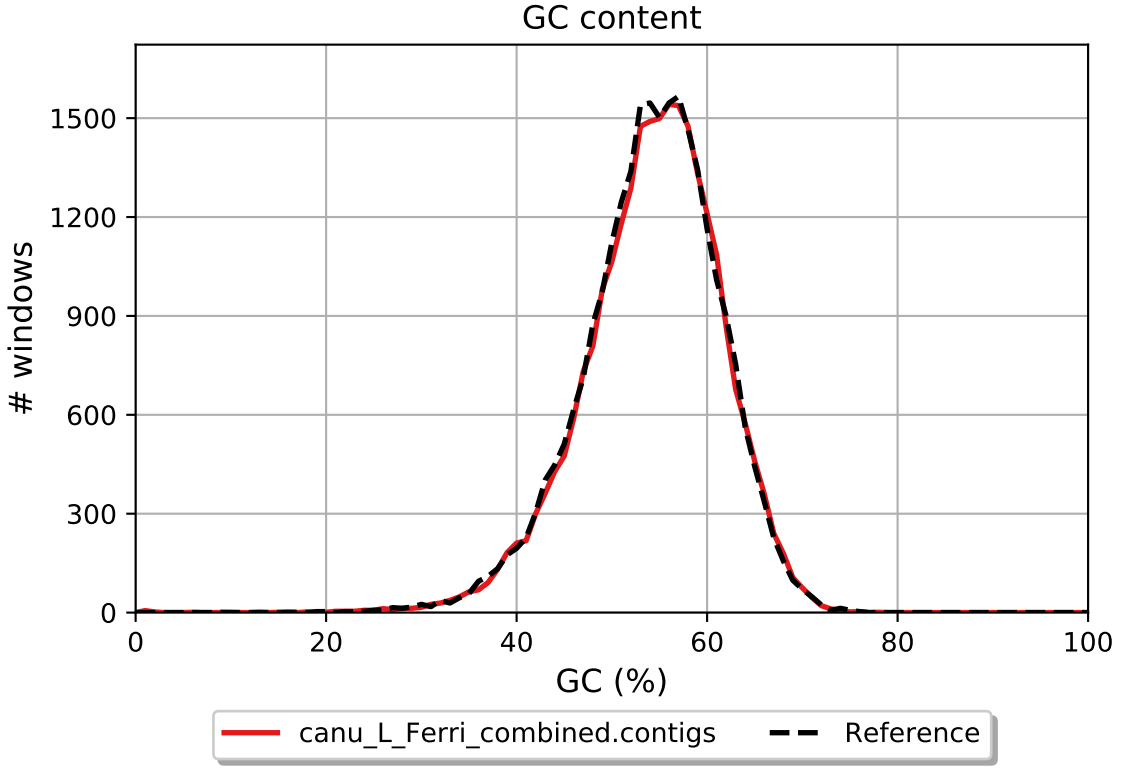
	canu_L_Ferri_combined.contigs
# fully unaligned contigs	1
Fully unaligned length	2620
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

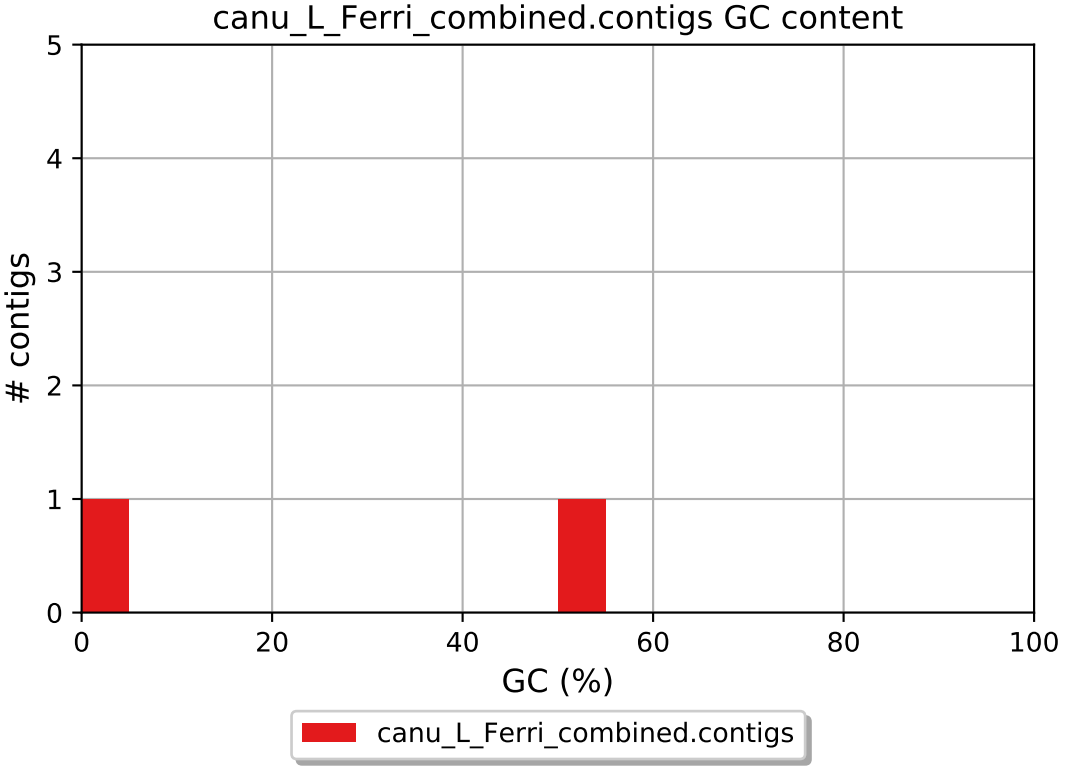
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

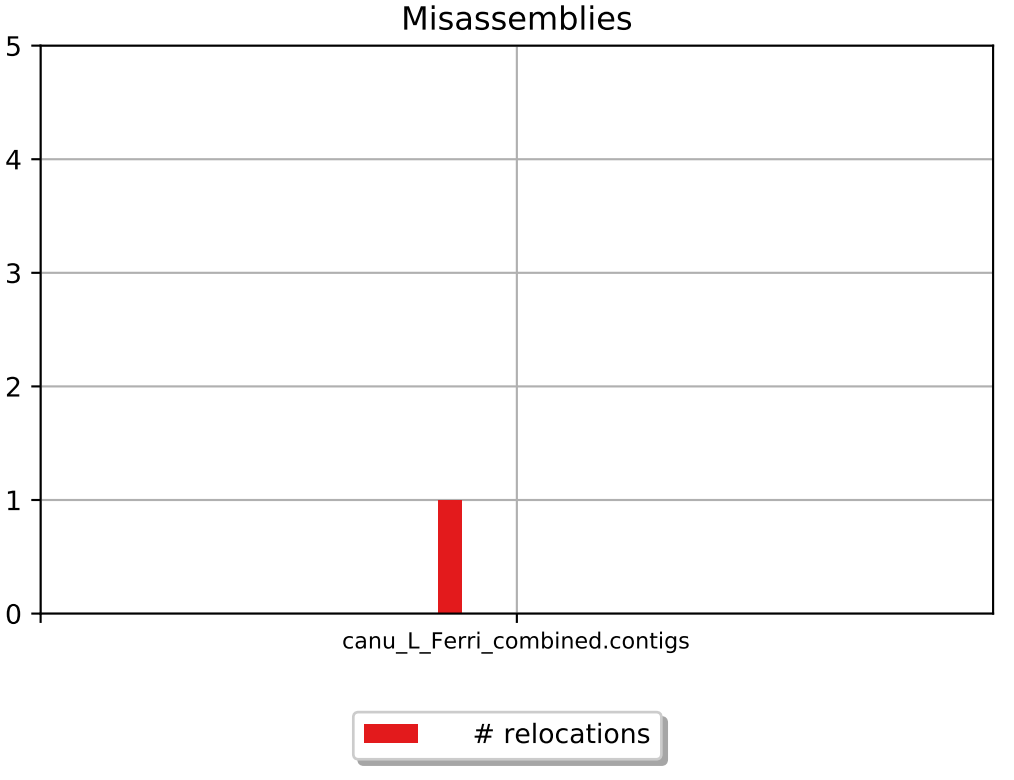

Nx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
canu_L_Ferri_combined.contigs

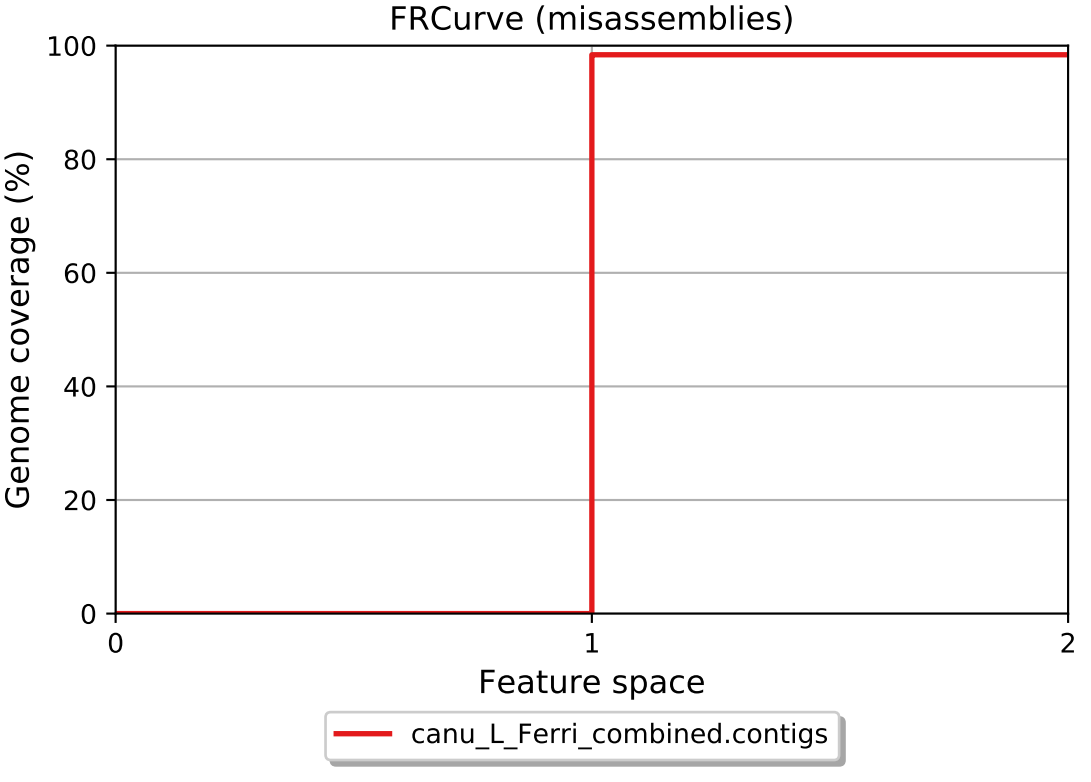

NGx
Contig length (kbp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
canu_L_Ferri_combined.contigs

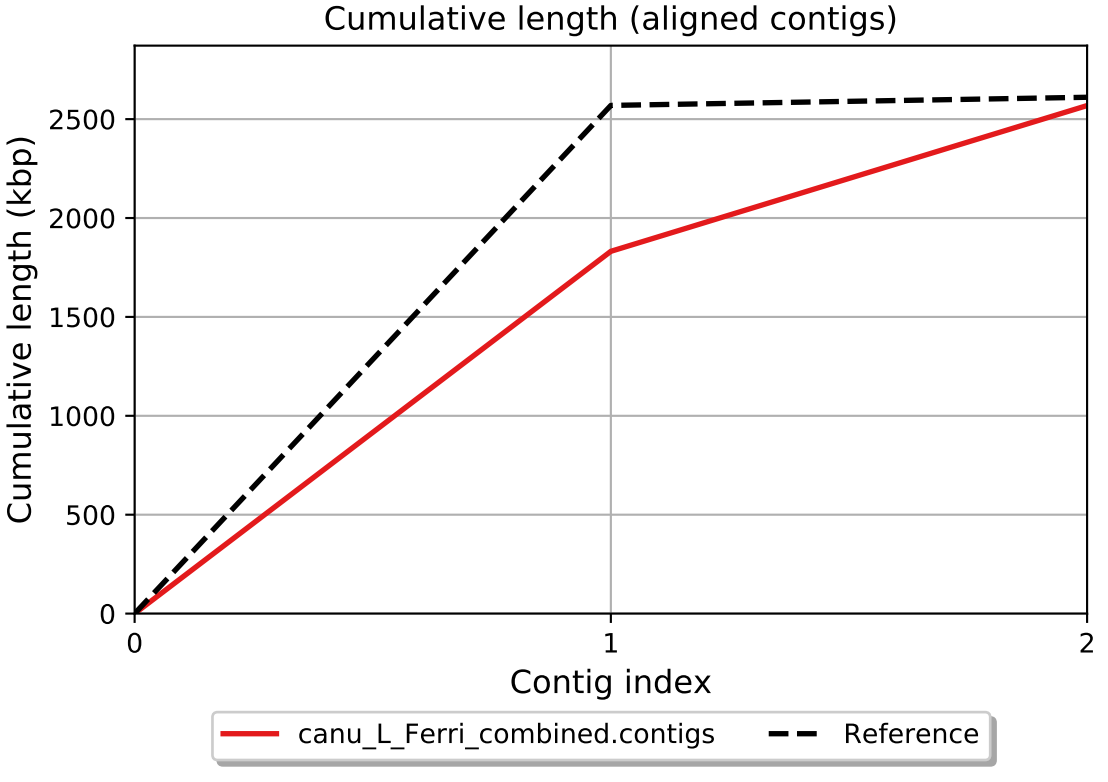

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
Contig index
canu_L_Ferri_combined.contigs
Reference

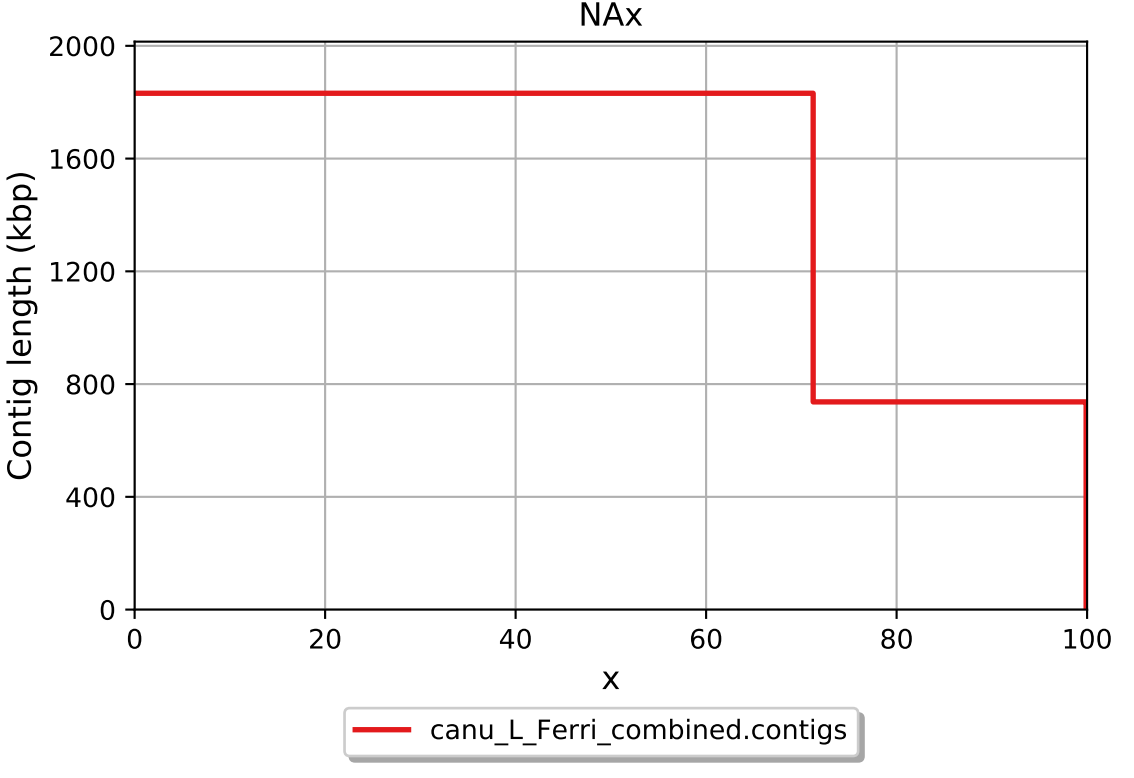

GC content
windows
1500
1200
900
600
300
0
0
20
40
60
80
100
GC (%)
canu_L_Ferri_combined.contigs
Reference

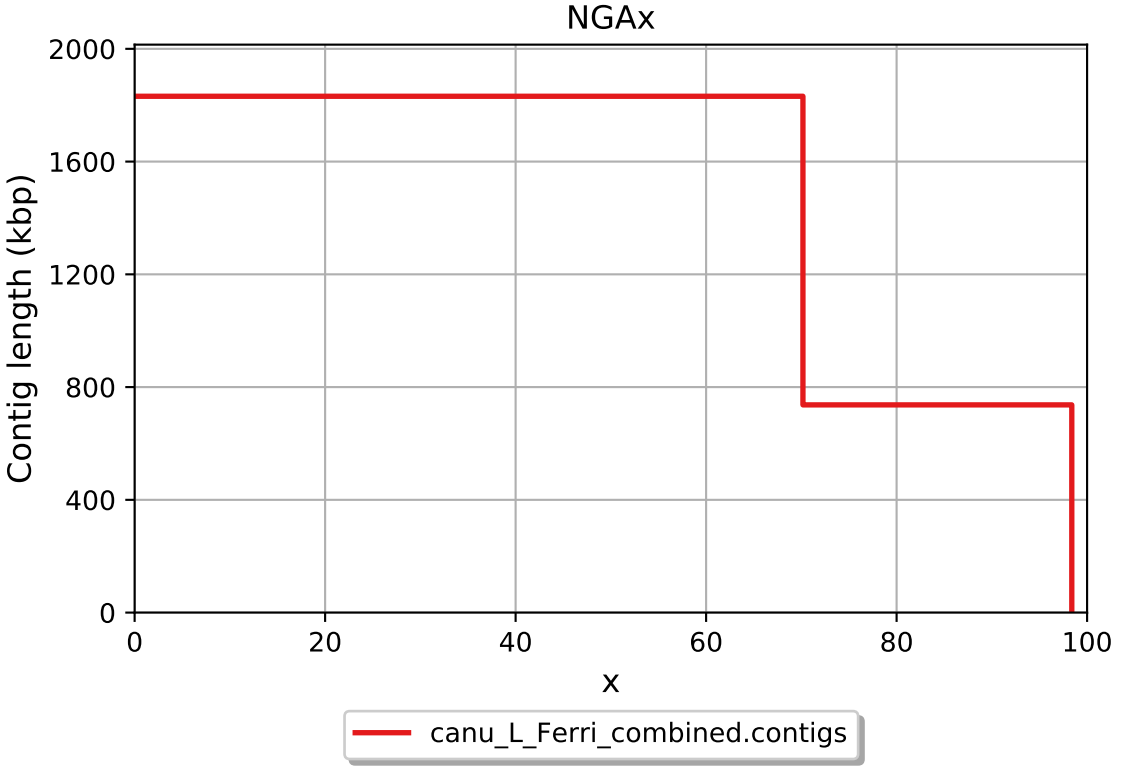

canu_L_Ferri_combined.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
canu_L_Ferri_combined.contigs


Misassemblies
5
4
3
2
1
0
canu_L_Ferri_combined.contigs
relocations


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


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


NAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
canu_L_Ferri_combined.contigs


NGAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
canu_L_Ferri_combined.contigs