Report

	contig1	contig2
# contigs (>= 0 bp)	3	1
# contigs (>= 1000 bp)	3	1
Total length (>= 0 bp)	6710	6650
Total length (>= 1000 bp)	6710	6650
# contigs	3	1
Largest contig	3980	6650
Total length	6710	6650
Reference length	6650	6650
GC (%)	51.28	52.00
Reference GC (%)	52.00	52.00
N50	3980	6650
NG50	3980	6650
N90	1120	6650
NG90	1120	6650
auN	2934.0	6650.0
auNG	2960.4	6650.0
L50	1	1
LG50	1	1
L90	3	1
LG90	3	1
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 1 part	0 + 0 part
Unaligned length	1950	0
Genome fraction (%)	71.579	100.000
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	0.00	0.00
# indels per 100 kbp	0.00	0.00
# genomic features	7 + 7 part	13 + 1 part
Largest alignment	2030	6650
Total aligned length	4760	6650
NA50	1610	6650
NGA50	1610	6650
NA90	-	6650
NGA90	-	6650
auNA	1187.4	6650.0
auNGA	1198.1	6650.0
LA50	2	1
LGA50	2	1
LA90	-	1
LGA90	-	1
K-mer-based compl. (%)	68.09	100.00
K-mer-based cor. length (%)	100.00	100.00
K-mer-based mis. length (%)	0.00	0.00
# k-mer-based misjoins	0	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).

Kmers report

	contig1	contig2
K-mer-based compl. (%)	68.09	100.00
K-mer-based cor. length (%)	100.00	100.00
K-mer-based mis. length (%)	0.00	0.00
K-mer-based undef. length (%)	0.00	0.00
# k-mer-based misjoins	0	0
# k-mer-based translocations	0	0
# k-mer-based 100kbp relocations	0	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).

Misassemblies report

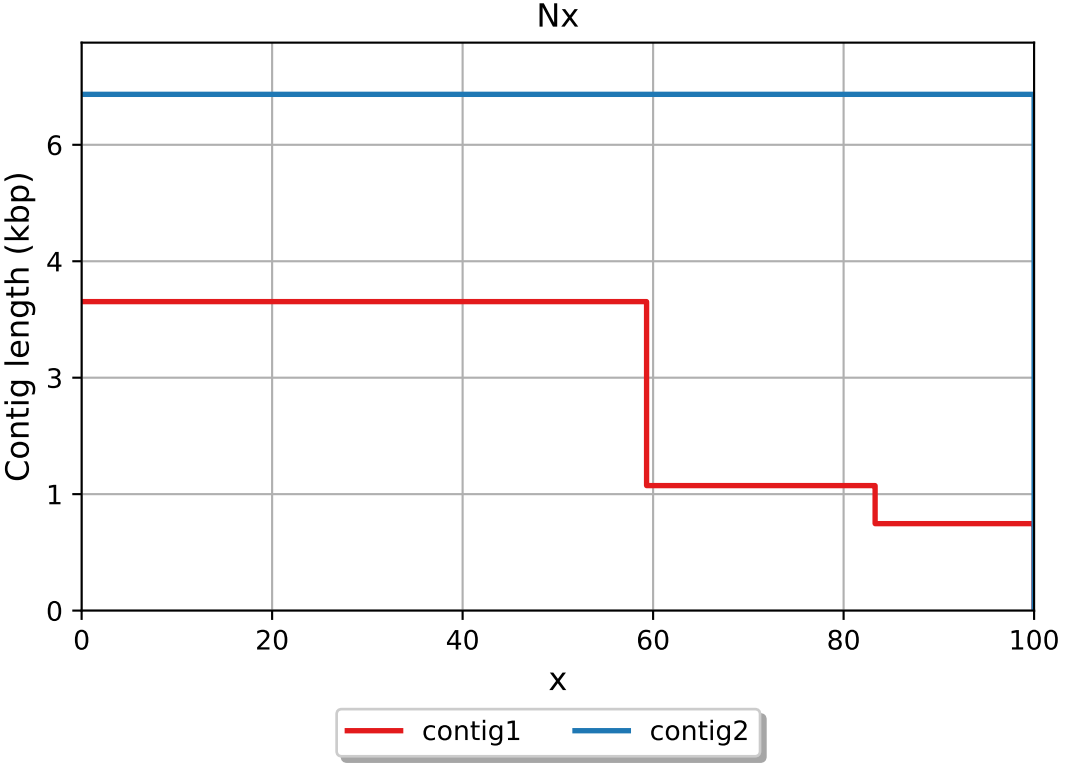
	contig1	contig2
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	0	0
# indels	0	0
# indels (<= 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	0	0

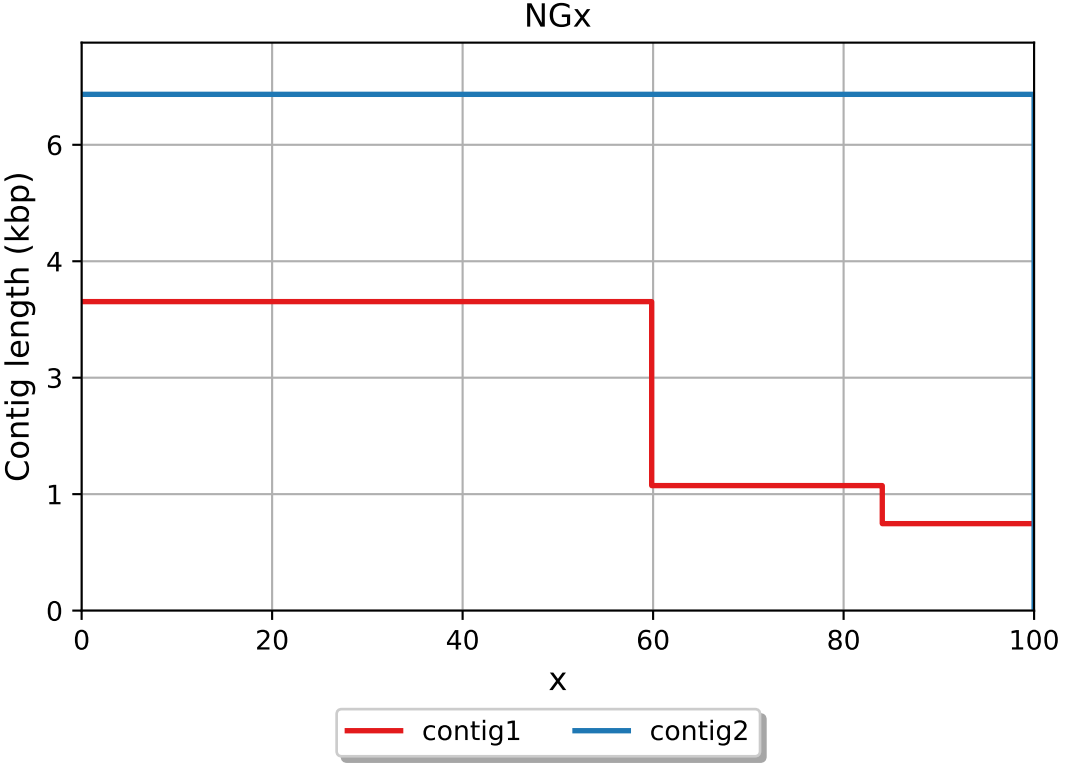
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

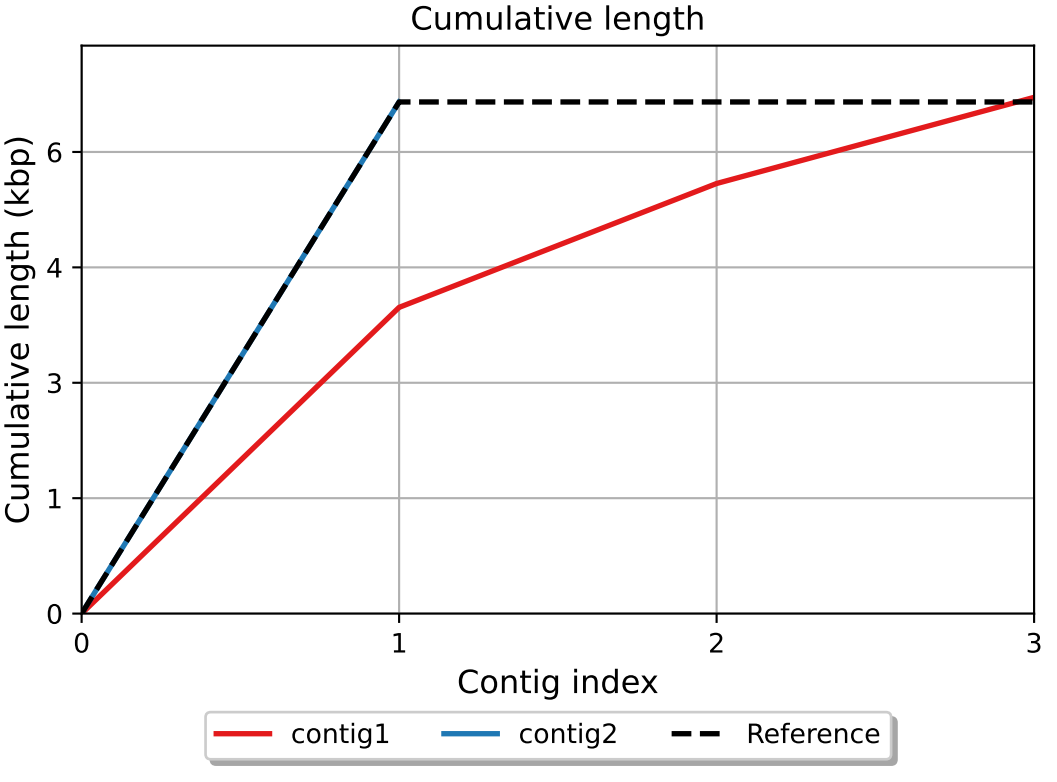
Unaligned report

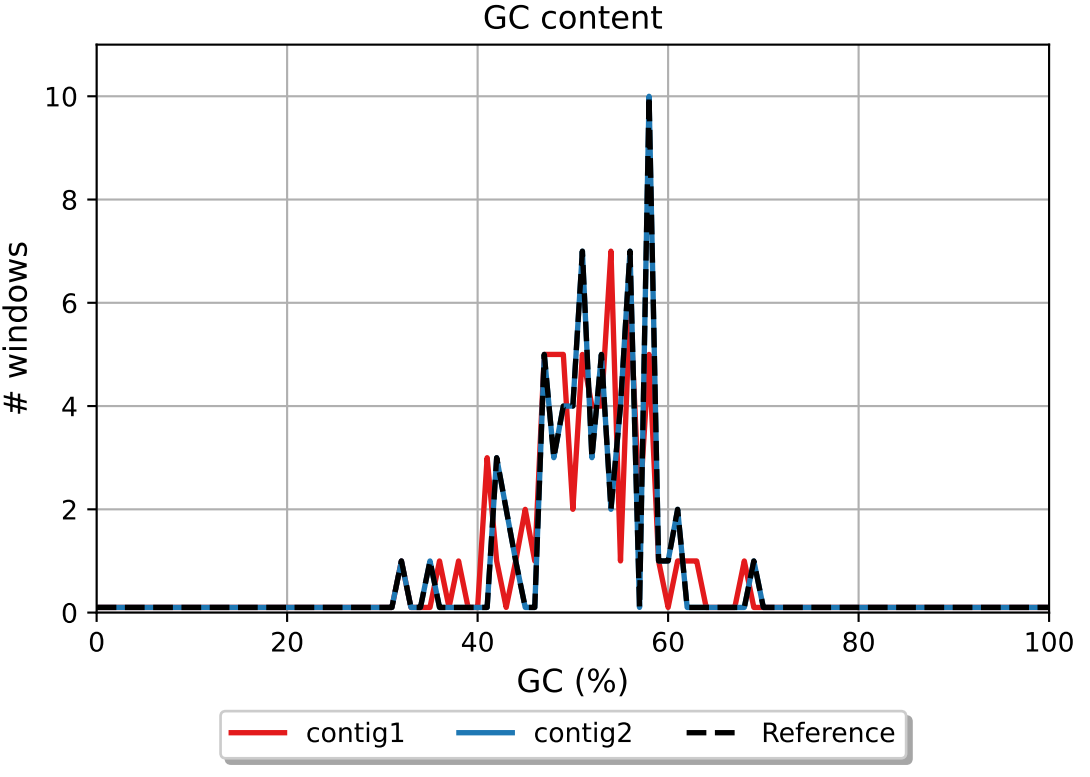
	contig1	contig2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	1	0
Partially unaligned length	1950	0
# N's	0	0

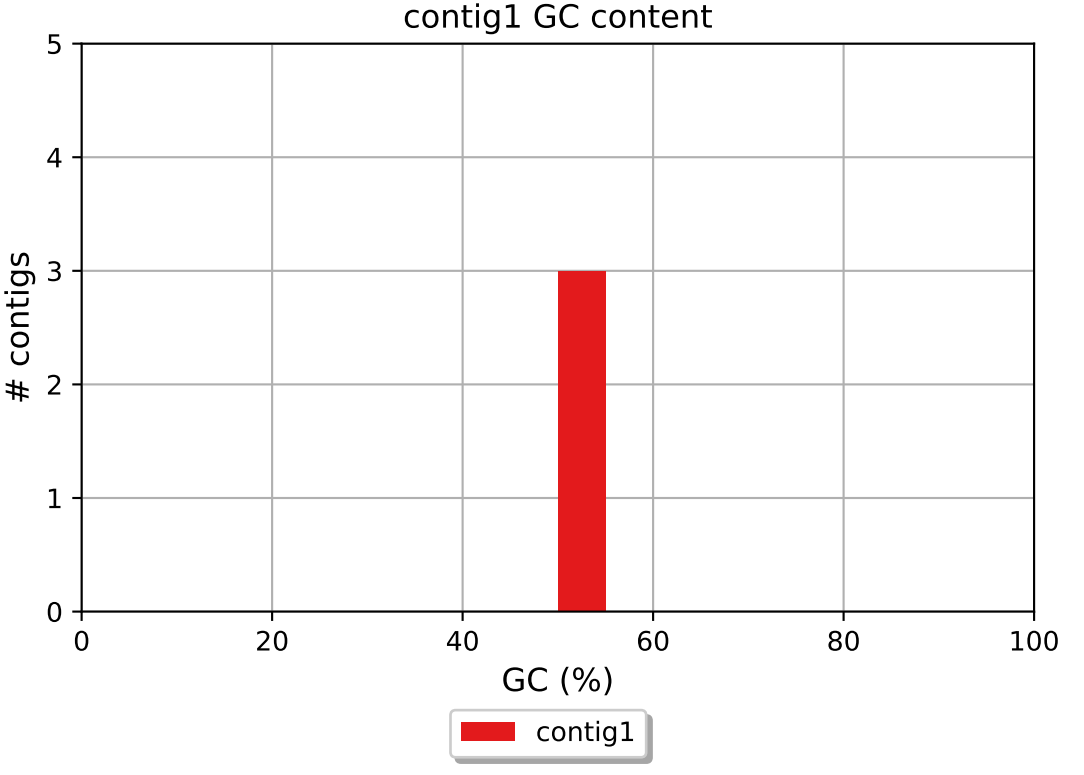
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

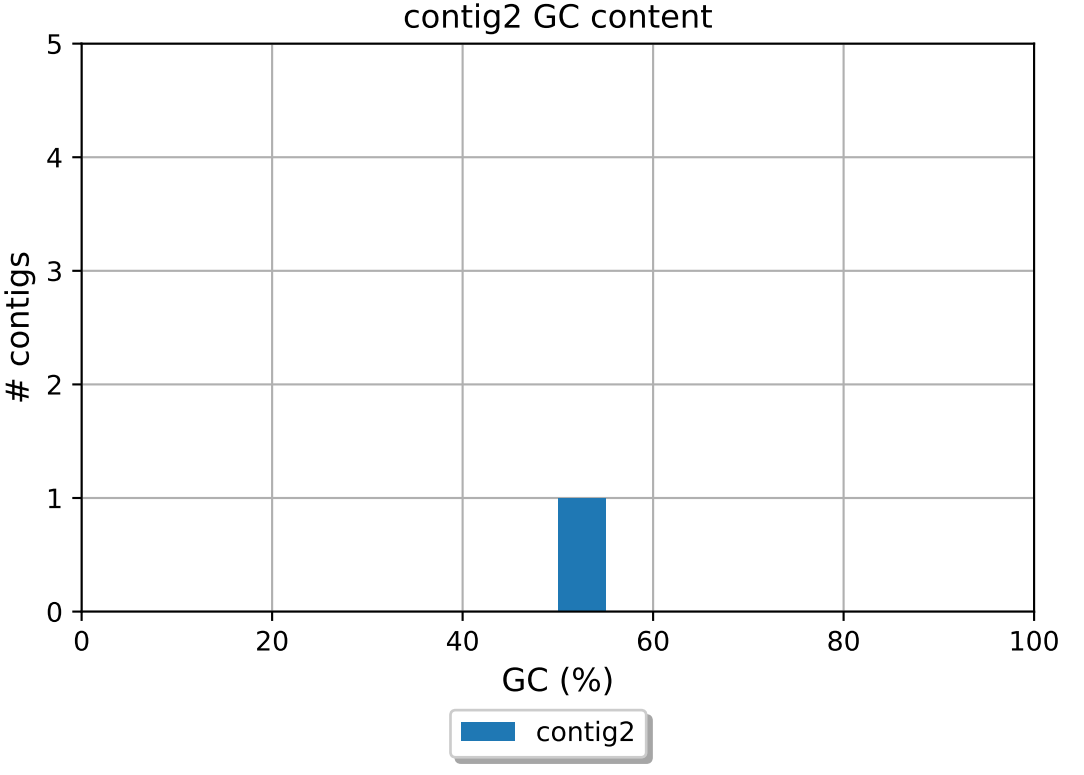

Nx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
contig1
contig2

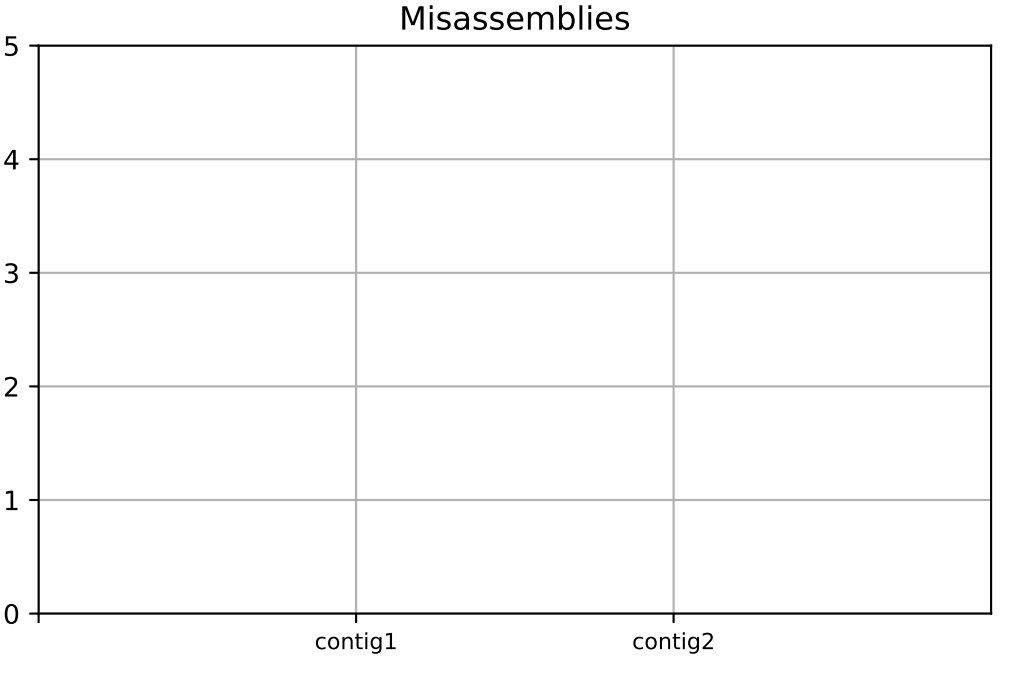

NGx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
contig1
contig2

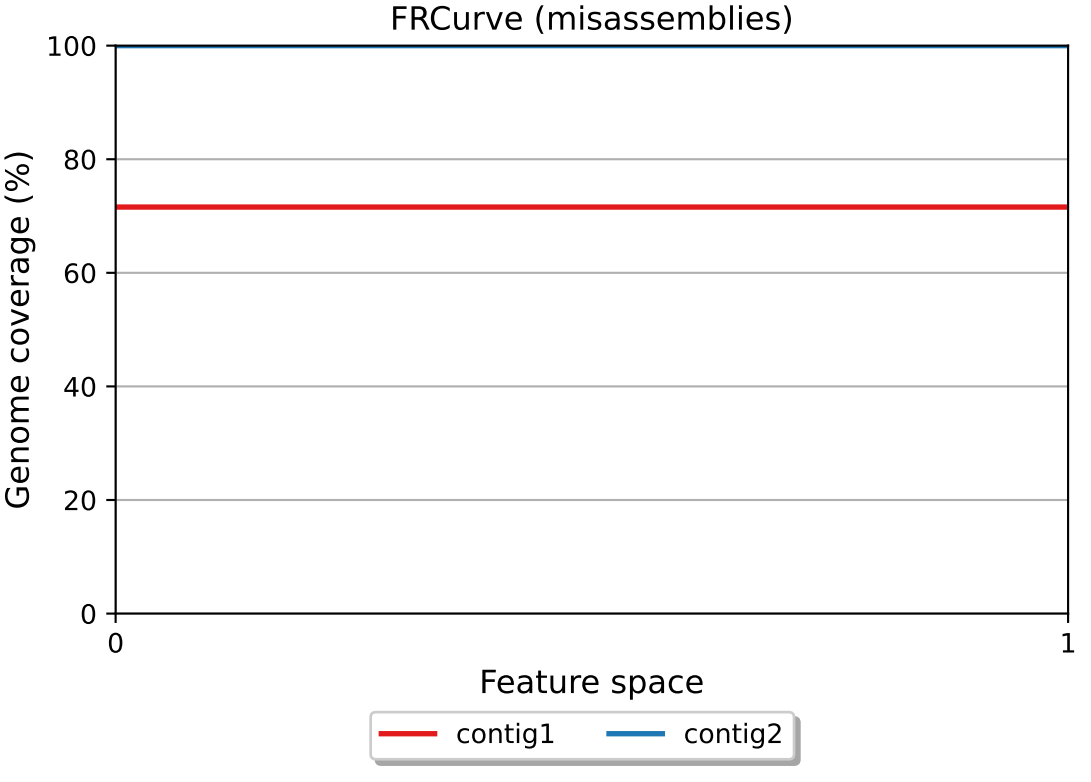

Cumulative length
Cumulative length (kbp)
0
1
3
4
6
0
1
2
3
Contig index
contig1
contig2
Reference

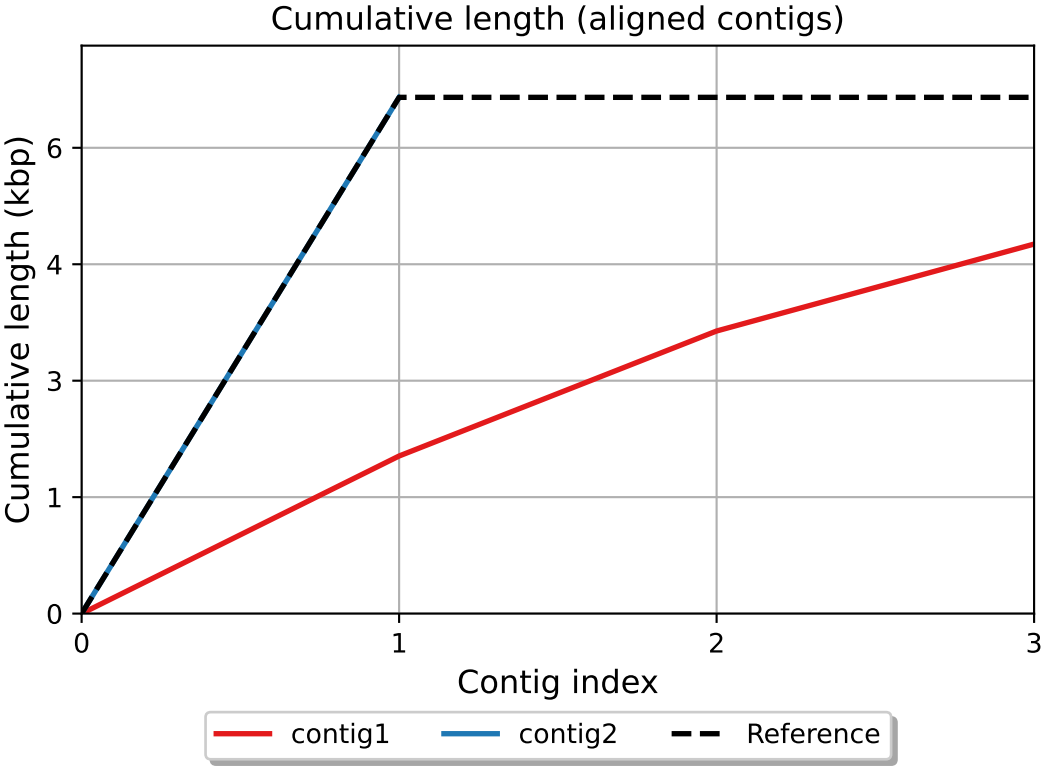

GC content
windows
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
contig1
contig2
Reference

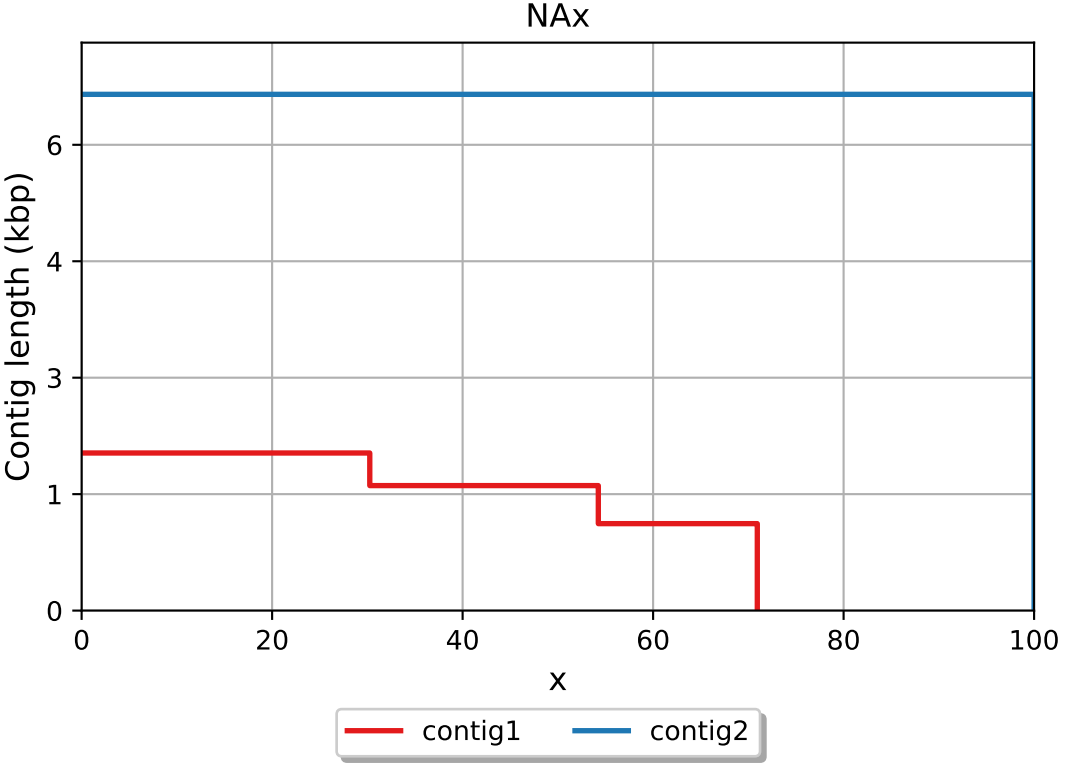

contig1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contig1

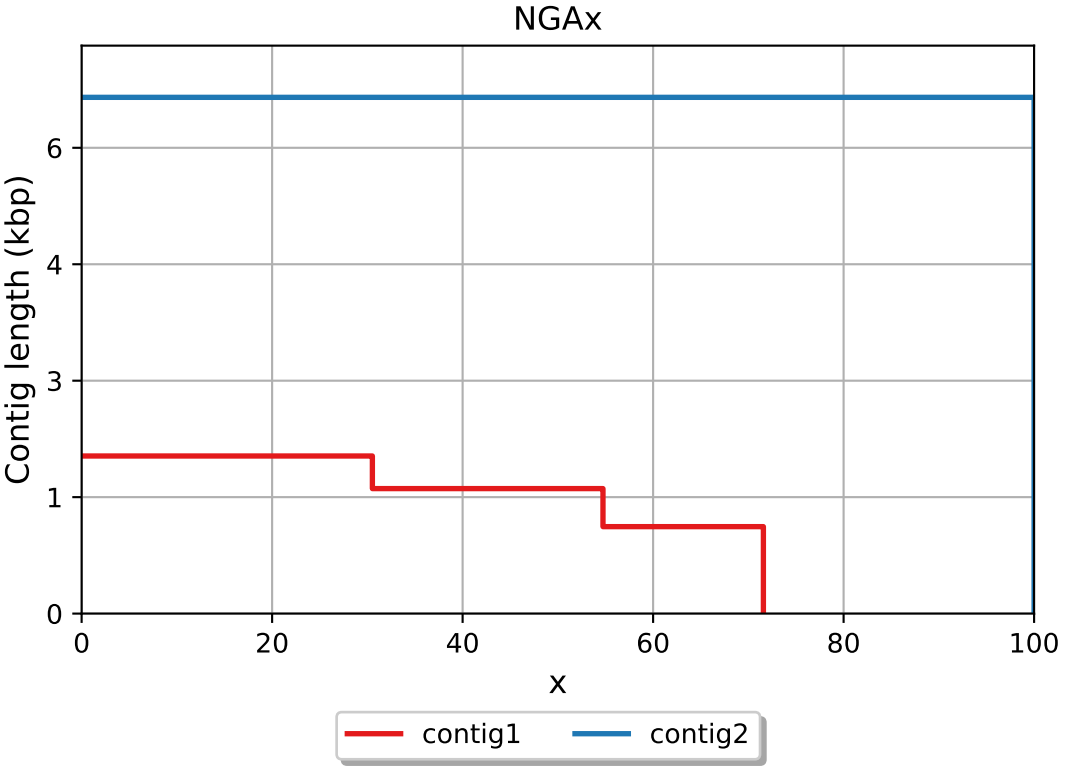

contig2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contig2

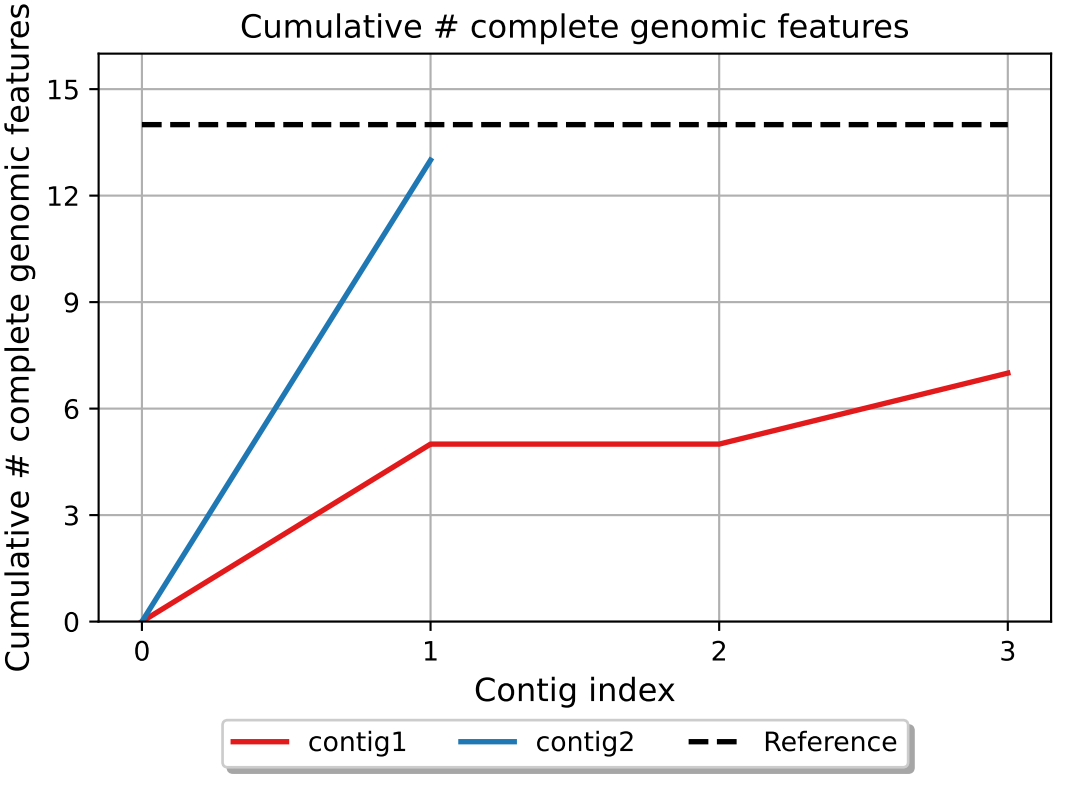

Misassemblies
5
4
3
2
1
0
contig1
contig2

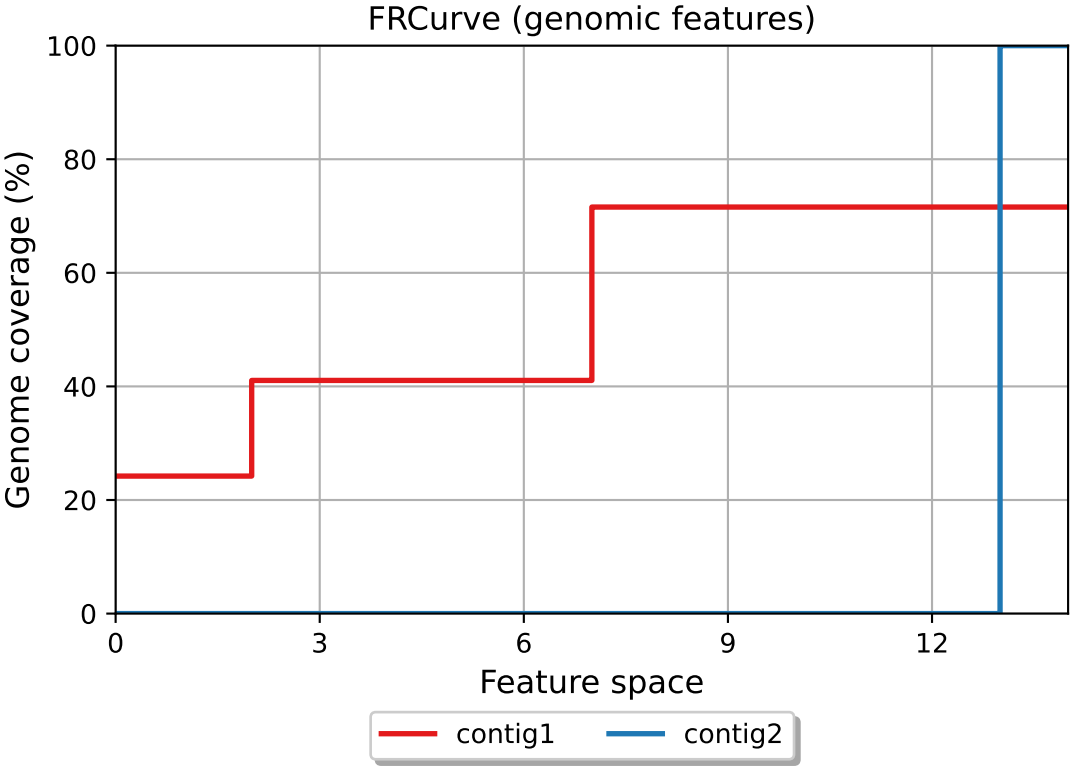

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
contig1
contig2

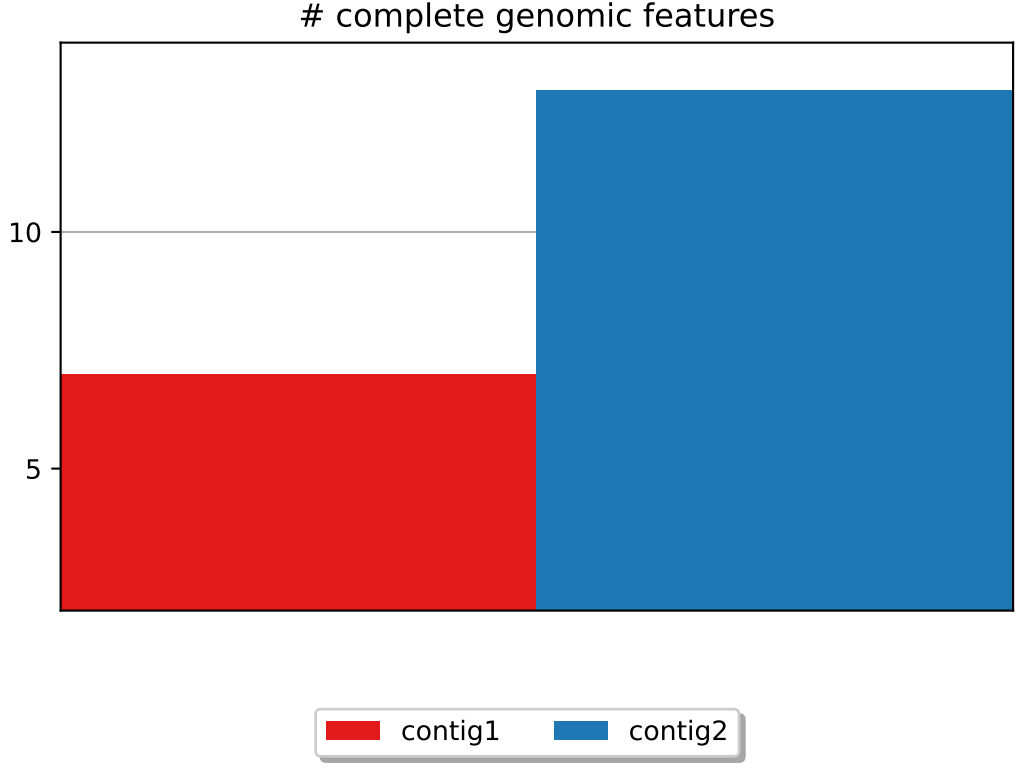

Cumulative length (aligned contigs)
Cumulative length (kbp)
0
1
3
4
6
0
1
2
3
Contig index
contig1
contig2
Reference

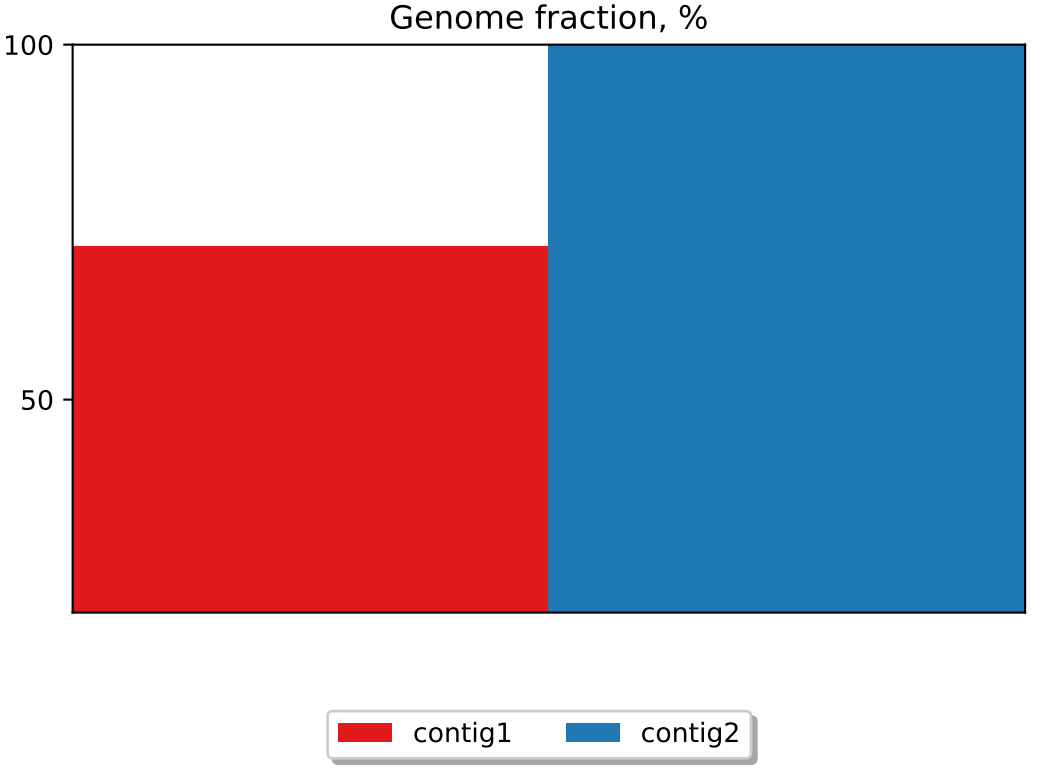

NAx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
contig1
contig2


NGAx
Contig length (kbp)
0
1
3
4
6
0
20
40
60
80
100
x
contig1
contig2


Cumulative # complete genomic features
Cumulative # complete genomic features
0
3
6
9
12
15
0
1
2
3
Contig index
contig1
contig2
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
Feature space
contig1
contig2


complete genomic features
10
5
contig1
contig2


Genome fraction, %
100
50
contig1
contig2