Report

	assymbly_b
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1080
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2
Largest contig	750
Total length	1080
Reference length	1000
GC (%)	52.31
Reference GC (%)	52.00
N50	750
NG50	750
N90	330
NG90	330
auN	621.7
auNG	671.4
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	330
Genome fraction (%)	66.800
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	668
Total aligned length	668
NA50	668
NGA50	668
NA90	-
NGA90	-
auNA	413.2
auNGA	446.2
LA50	1
LGA50	1
LA90	-
LGA90	-

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

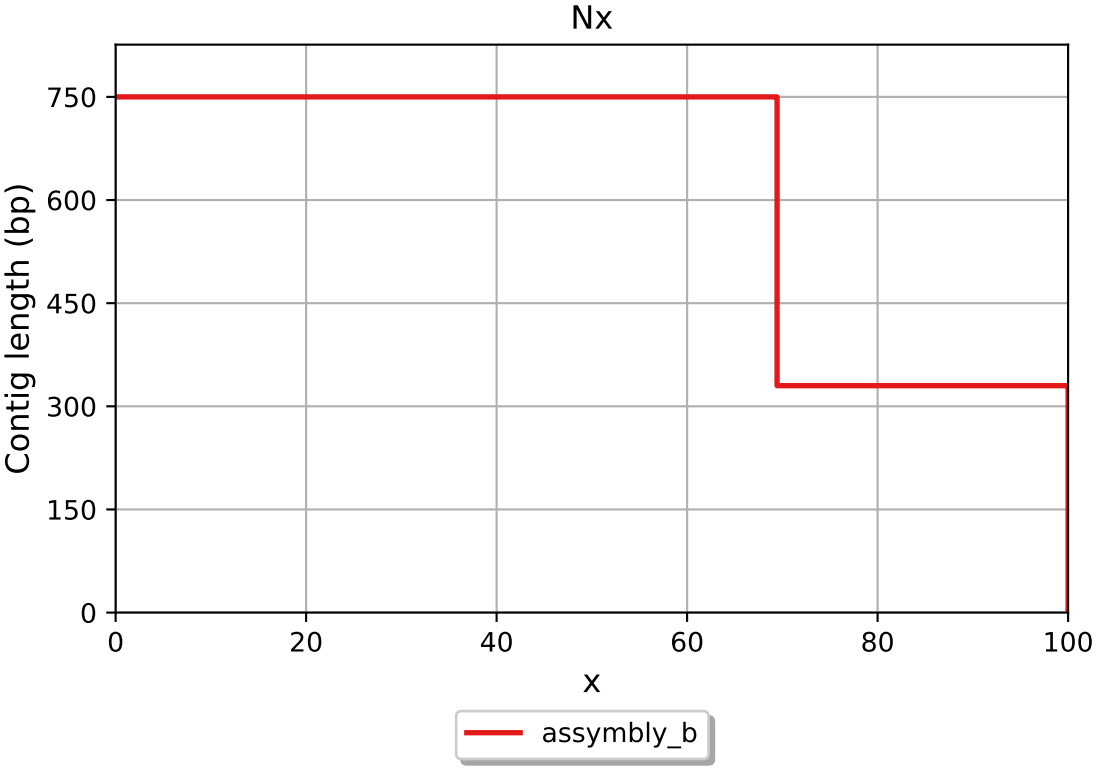
	assymbly_b
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.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

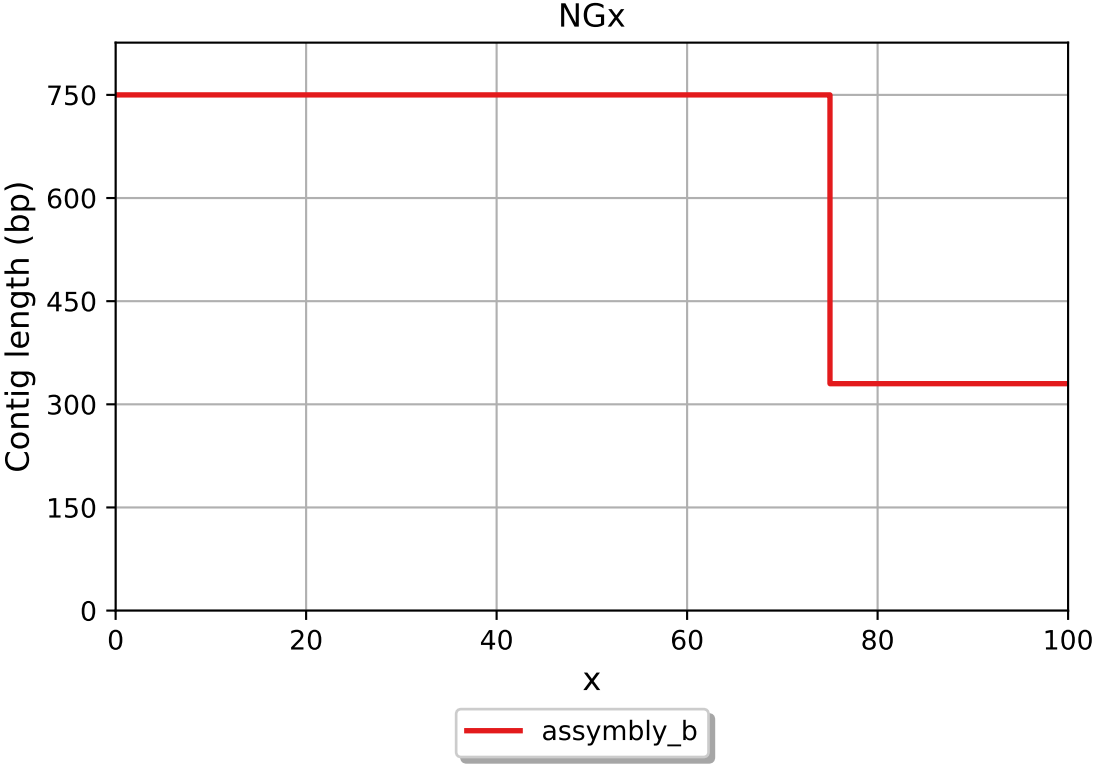
All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

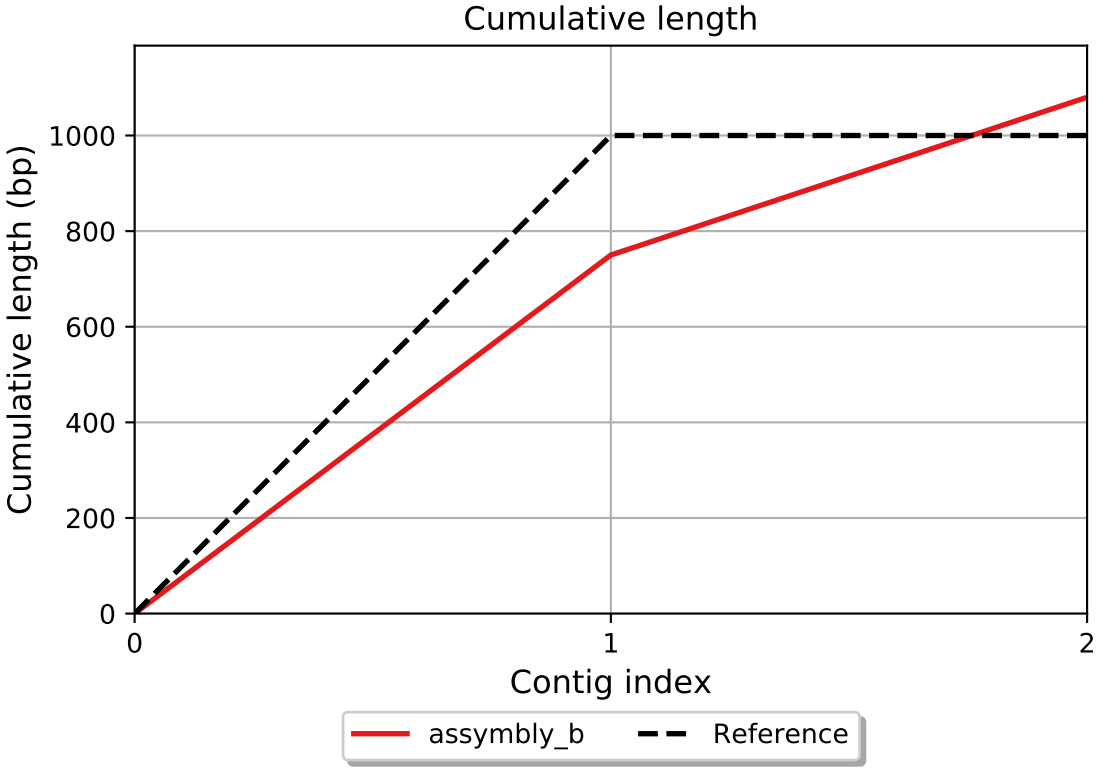
Unaligned report

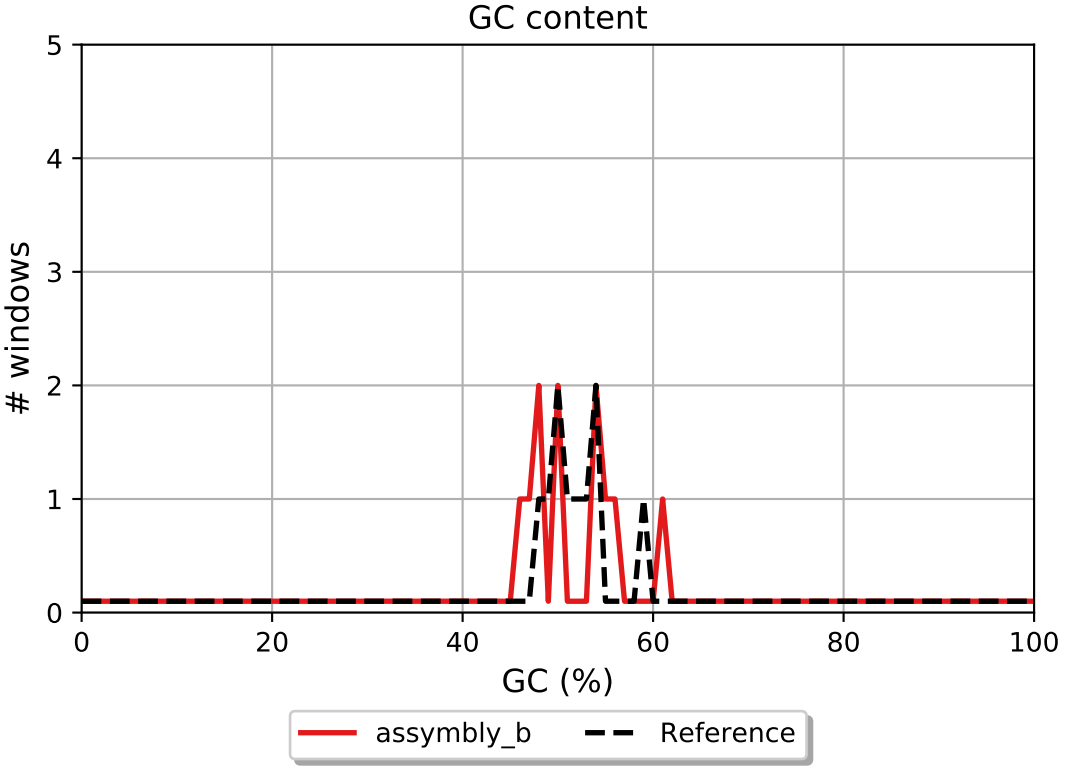
	assymbly_b
# fully unaligned contigs	1
Fully unaligned length	330
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

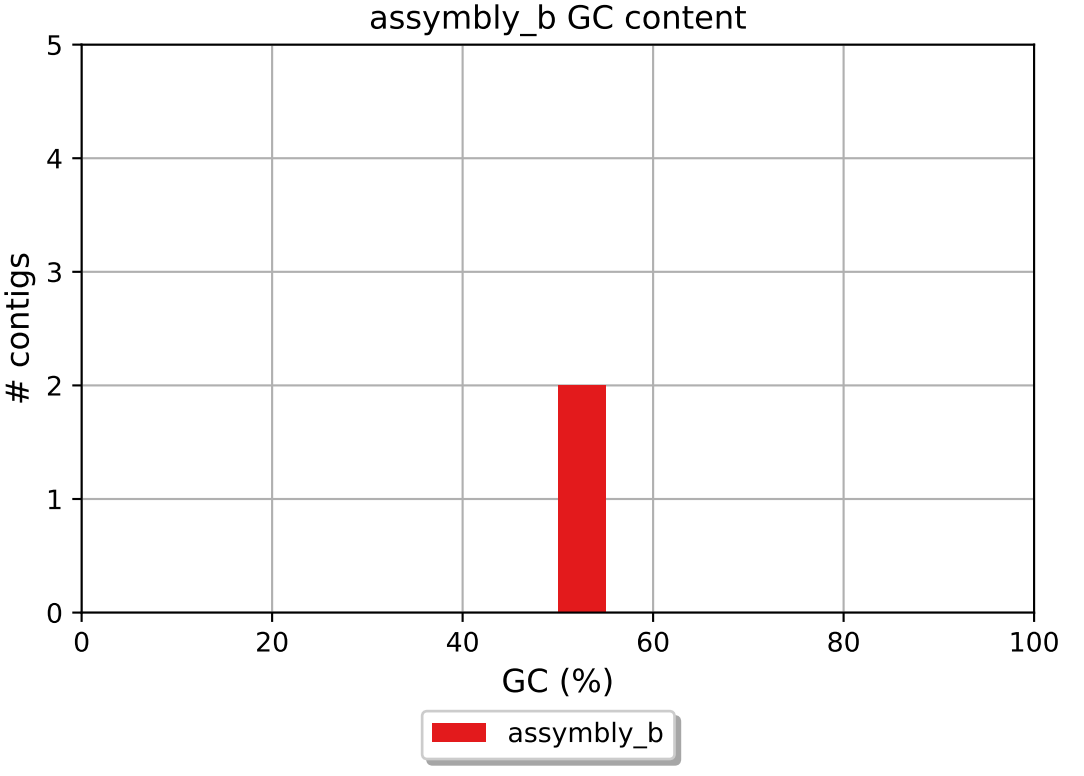
All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

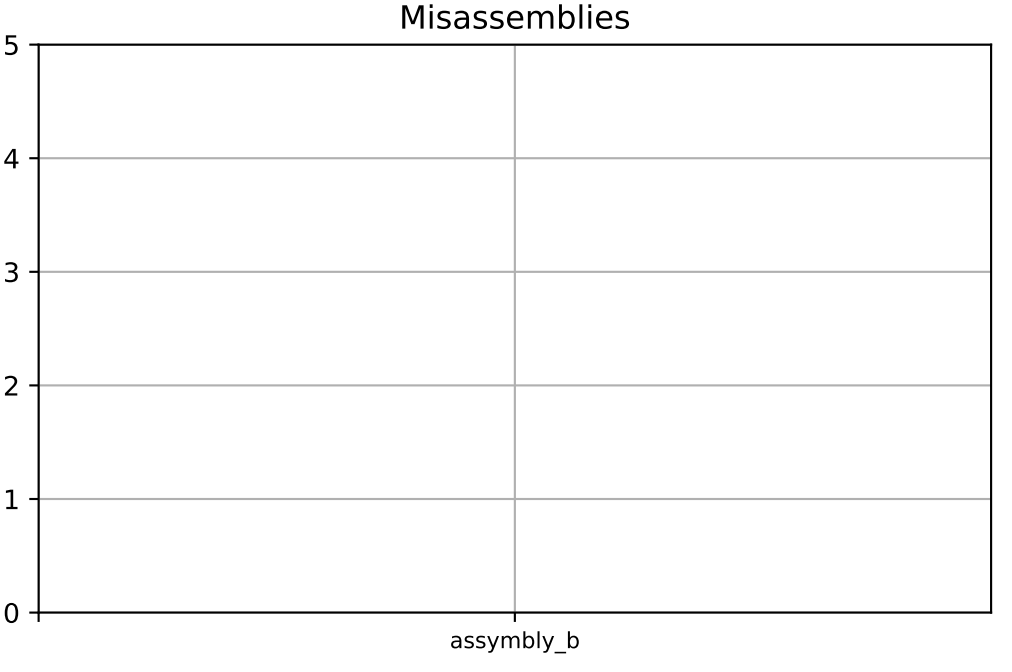

Nx
Contig length (bp)
750
600
450
300
150
0
0
20
40
60
80
100
x
assymbly_b

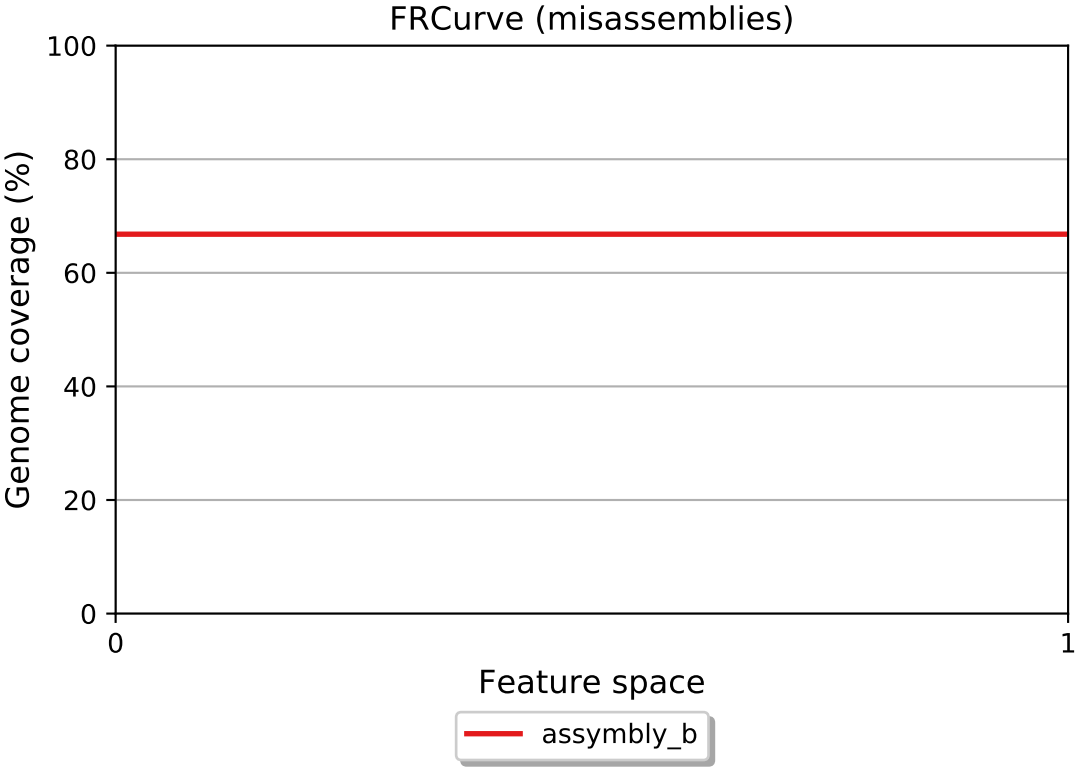

NGx
Contig length (bp)
750
600
450
300
150
0
0
20
40
60
80
100
x
assymbly_b

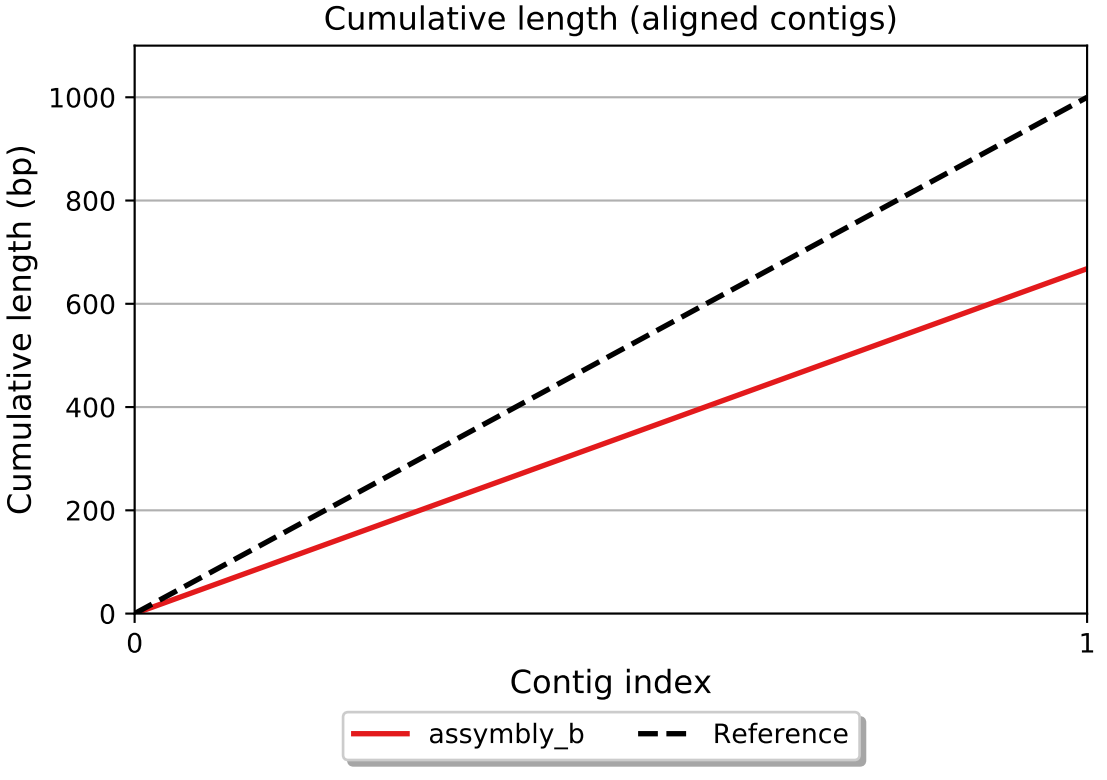

Cumulative length
Cumulative length (bp)
1000
800
600
400
200
0
0
1
2
Contig index
assymbly_b
Reference

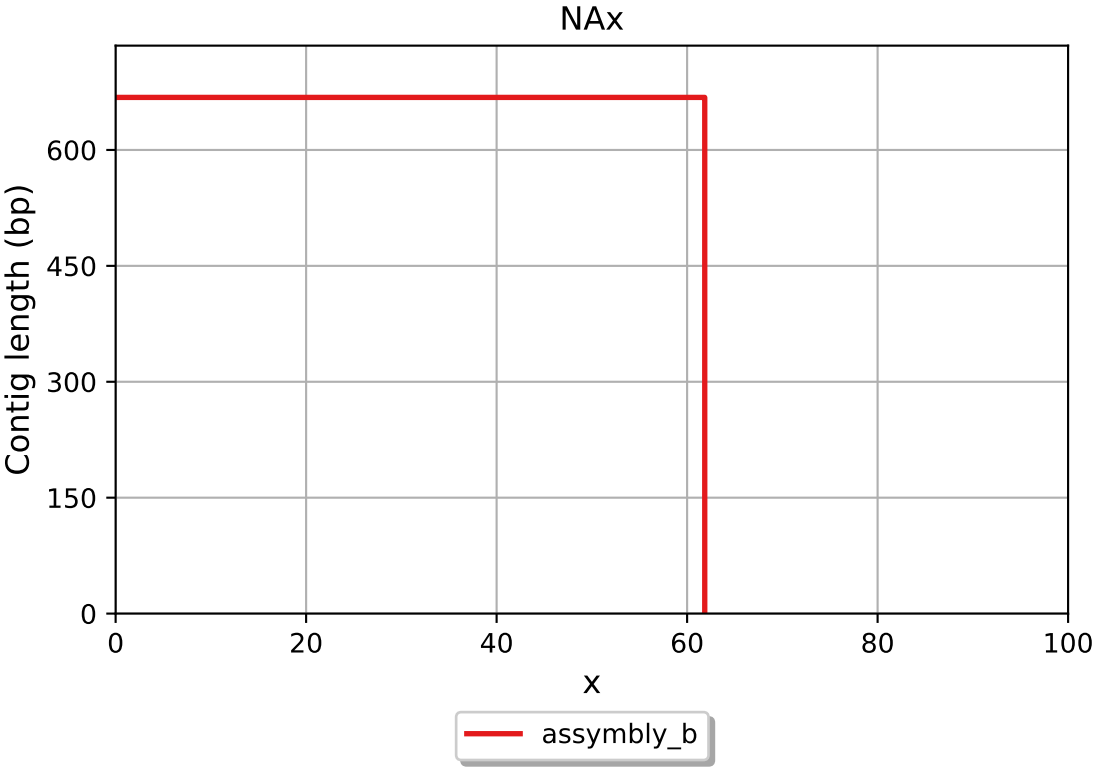

GC content
windows
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
assymbly_b
Reference

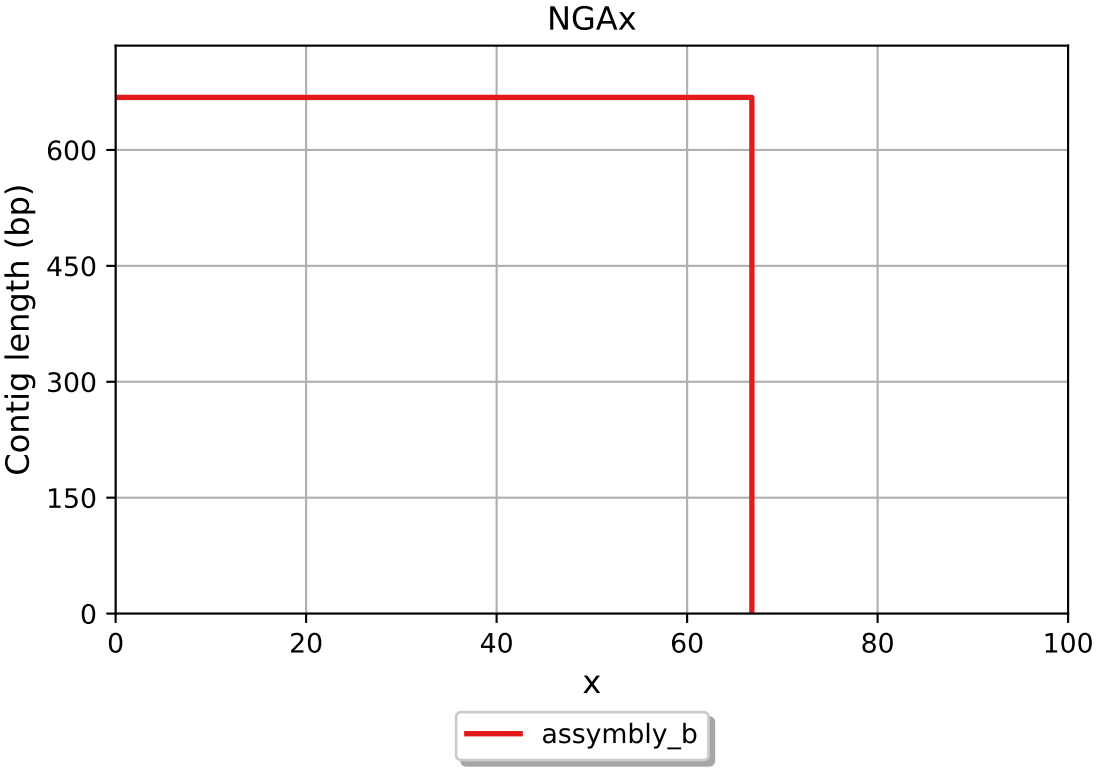

assymbly_b GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
assymbly_b


Misassemblies
5
4
3
2
1
0
assymbly_b


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


Cumulative length (aligned contigs)
Cumulative length (bp)
1000
800
600
400
200
0
0
1
Contig index
assymbly_b
Reference


NAx
Contig length (bp)
600
450
300
150
0
0
20
40
60
80
100
x
assymbly_b


NGAx
Contig length (bp)
600
450
300
150
0
0
20
40
60
80
100
x
assymbly_b