Report	out_61
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	7592
Total length (>= 1000 bp)	7592
Total length (>= 5000 bp)	7592
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	7592
Total length	7592
Reference length	10624
GC (%)	43.84
Reference GC (%)	44.14
N50	7592
NG50	7592
N90	7592
NG90	-
auN	7592.0
auNG	5425.3
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	2327
Genome fraction (%)	49.209
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	56.98
# indels per 100 kbp	417.85
Largest alignment	5265
Total aligned length	5265
NA50	5265
NGA50	-
NA90	-
NGA90	-
auNA	3651.2
auNGA	2609.2
LA50	1
LGA50	-
LA90	-
LGA90	-

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

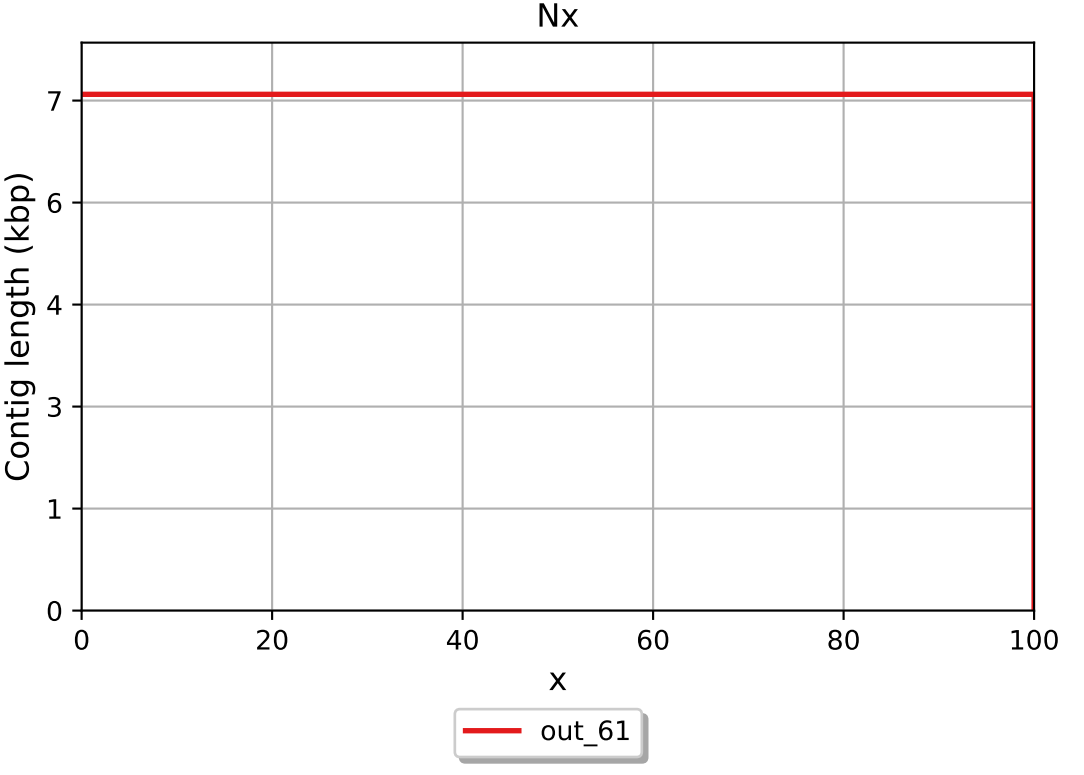
	out_61
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3
# indels	22
# indels (<= 5 bp)	2
# indels (> 5 bp)	20
Indels length	1275

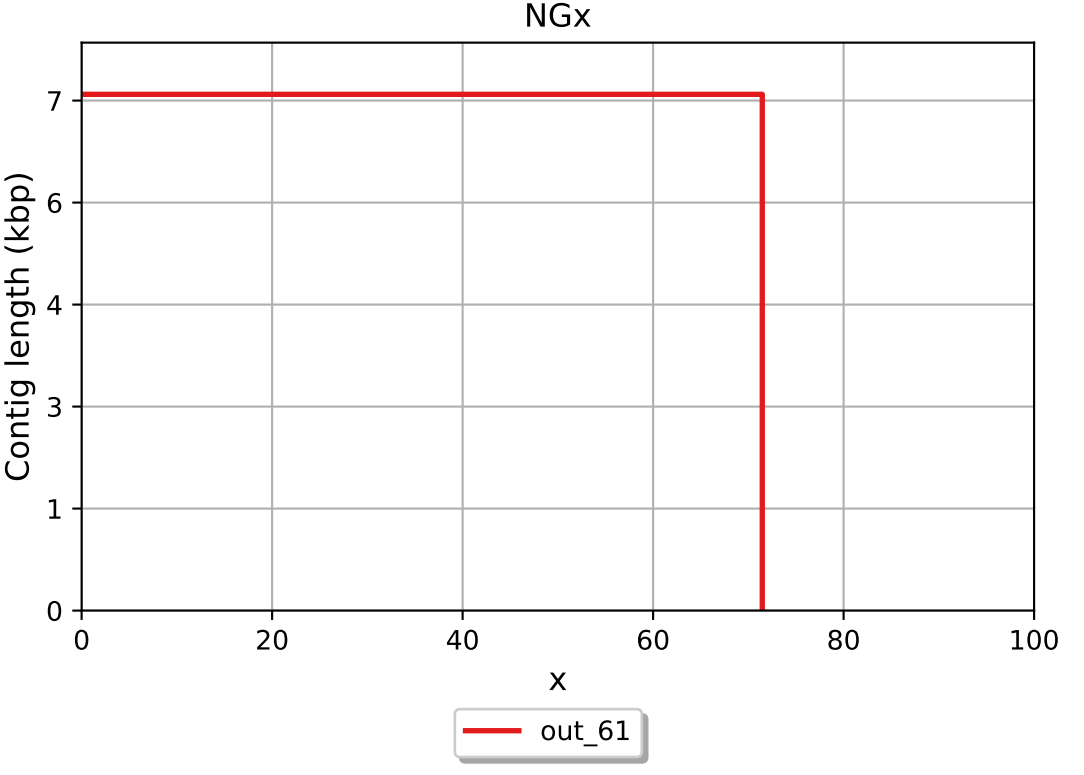
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

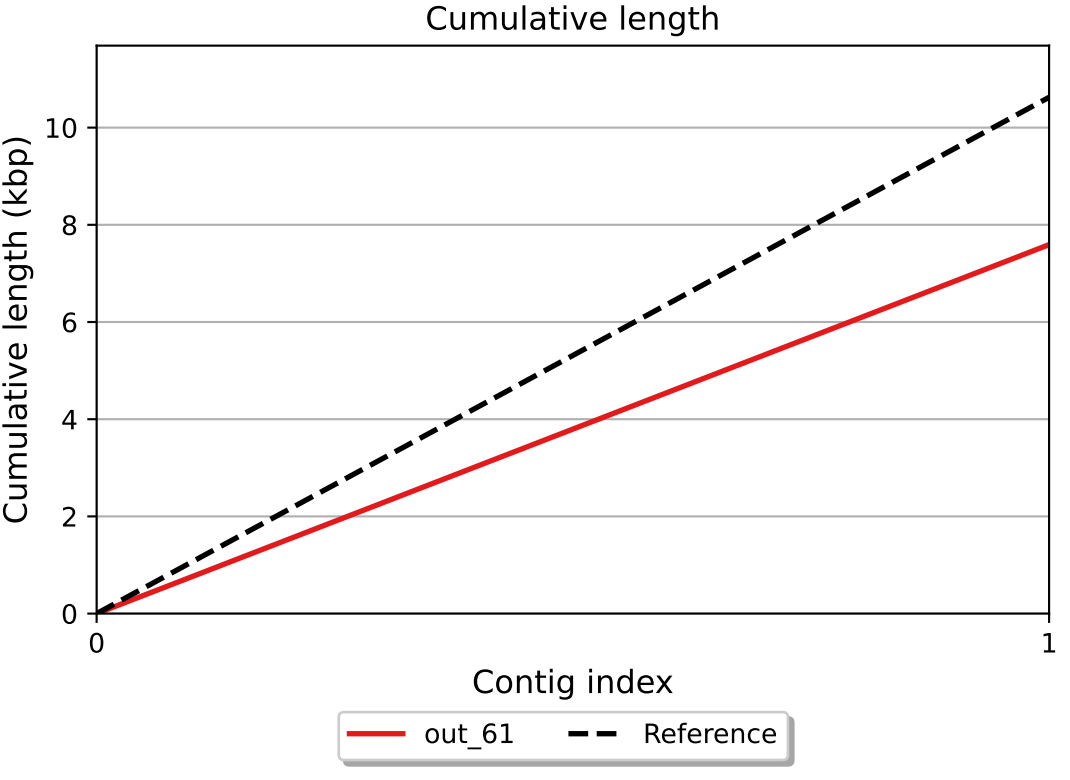
Unaligned report

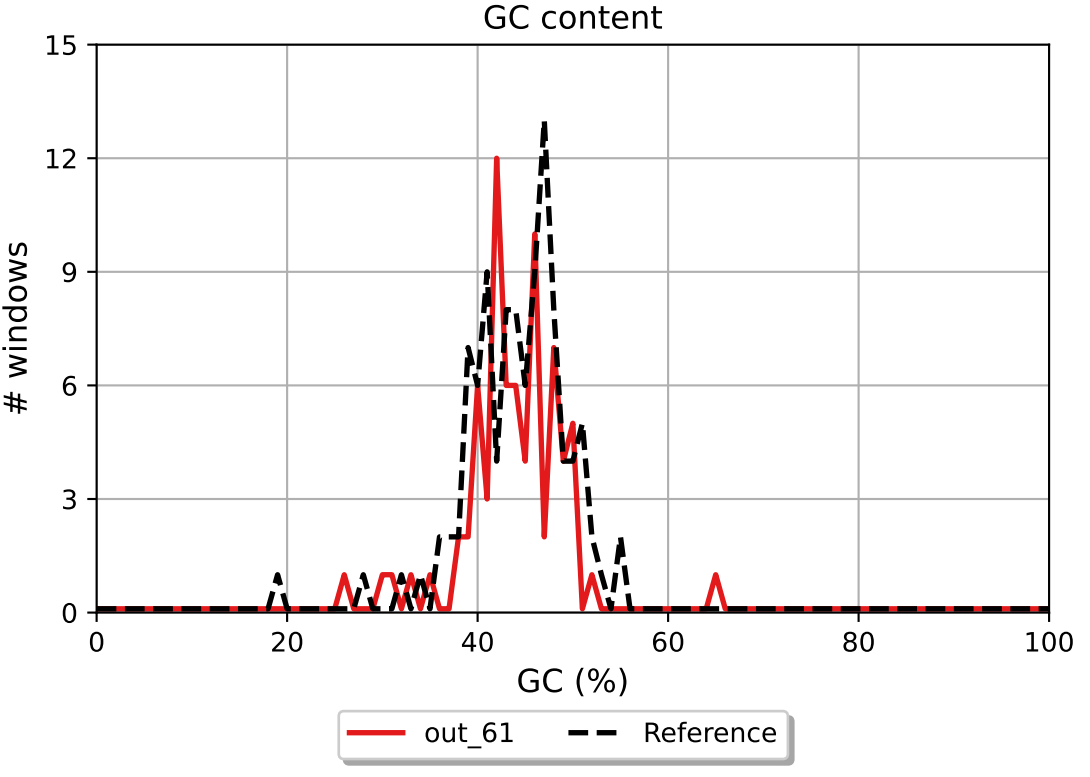
	out_61
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	2327
# N's	0

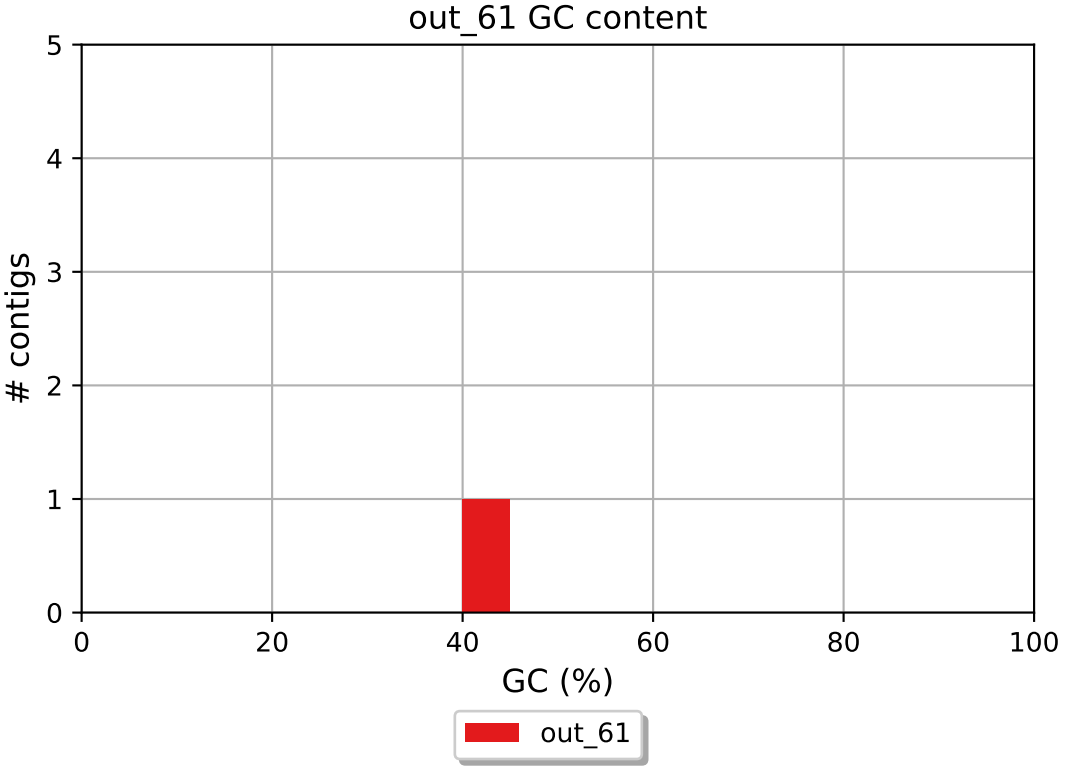
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

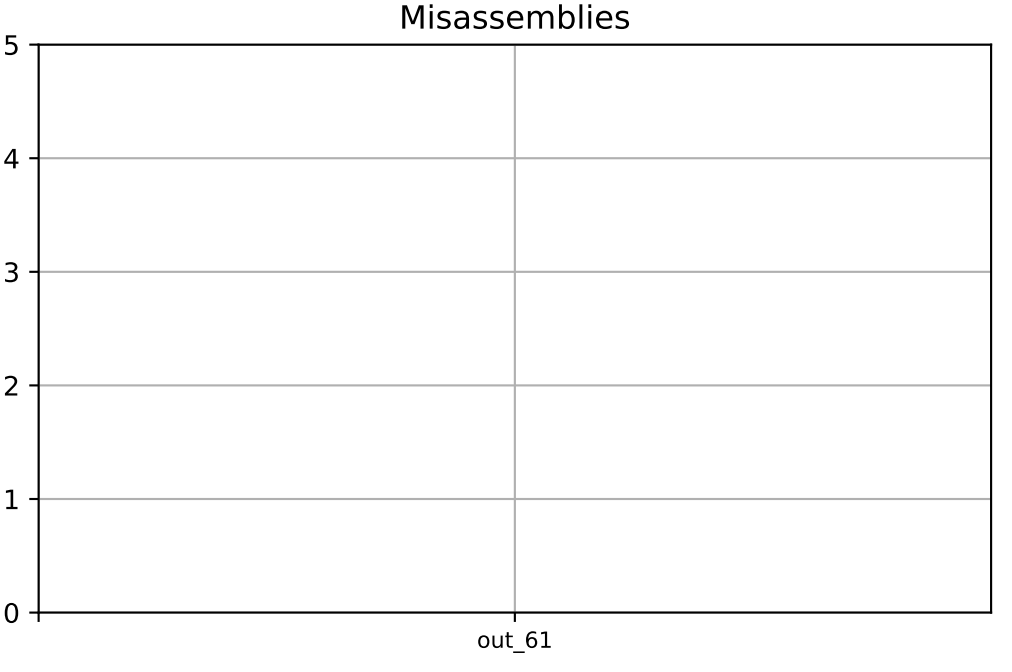

Nx
Contig length (kbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
out_61

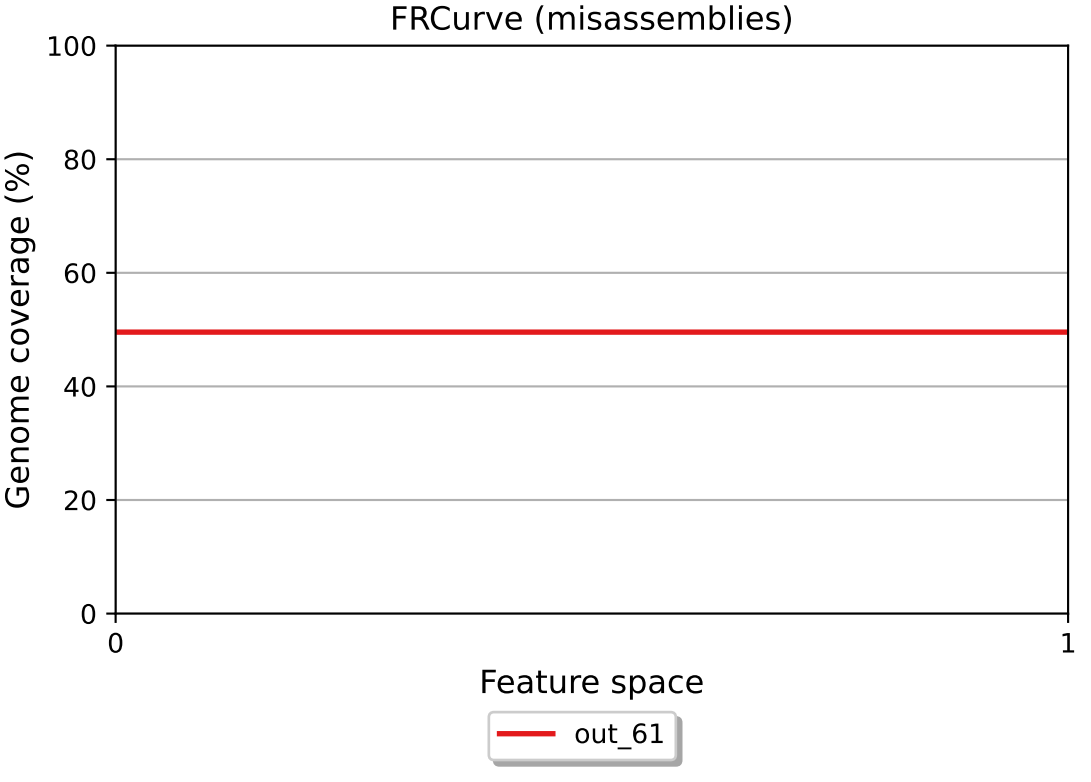

NGx
Contig length (kbp)
0
1
3
4
6
7
0
20
40
60
80
100
x
out_61

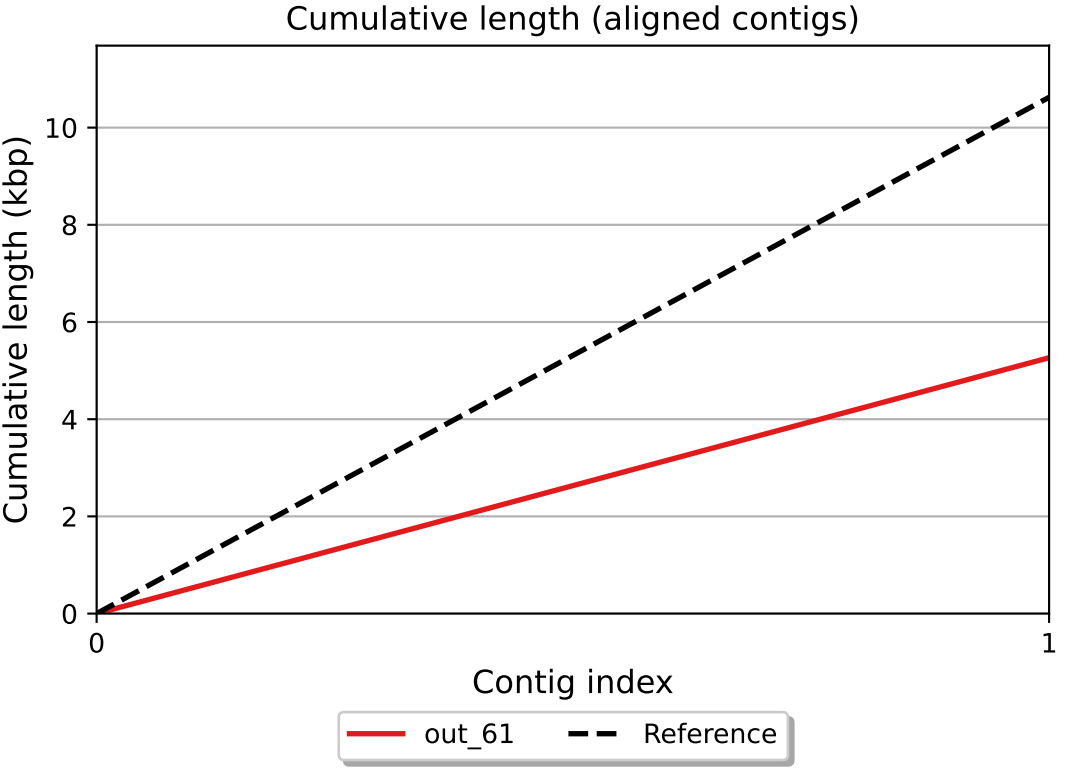

Cumulative length
Cumulative length (kbp)
10
8
6
4
2
0
0
1
Contig index
out_61
Reference

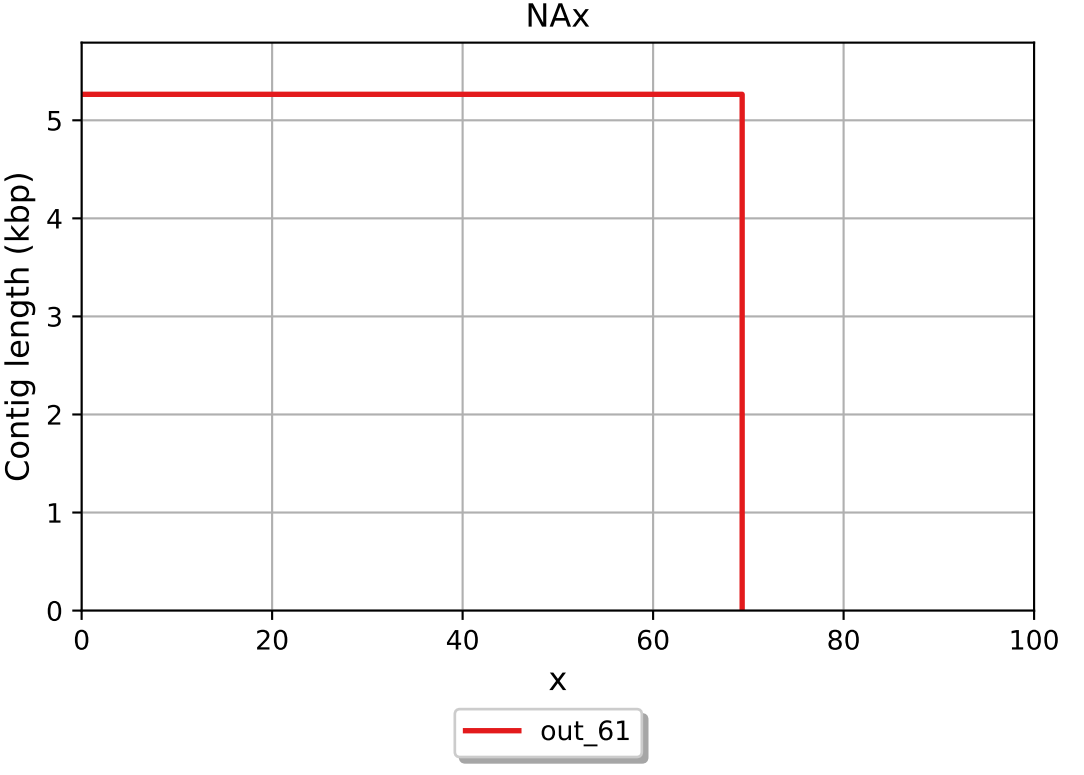

GC content
windows
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
out_61
Reference

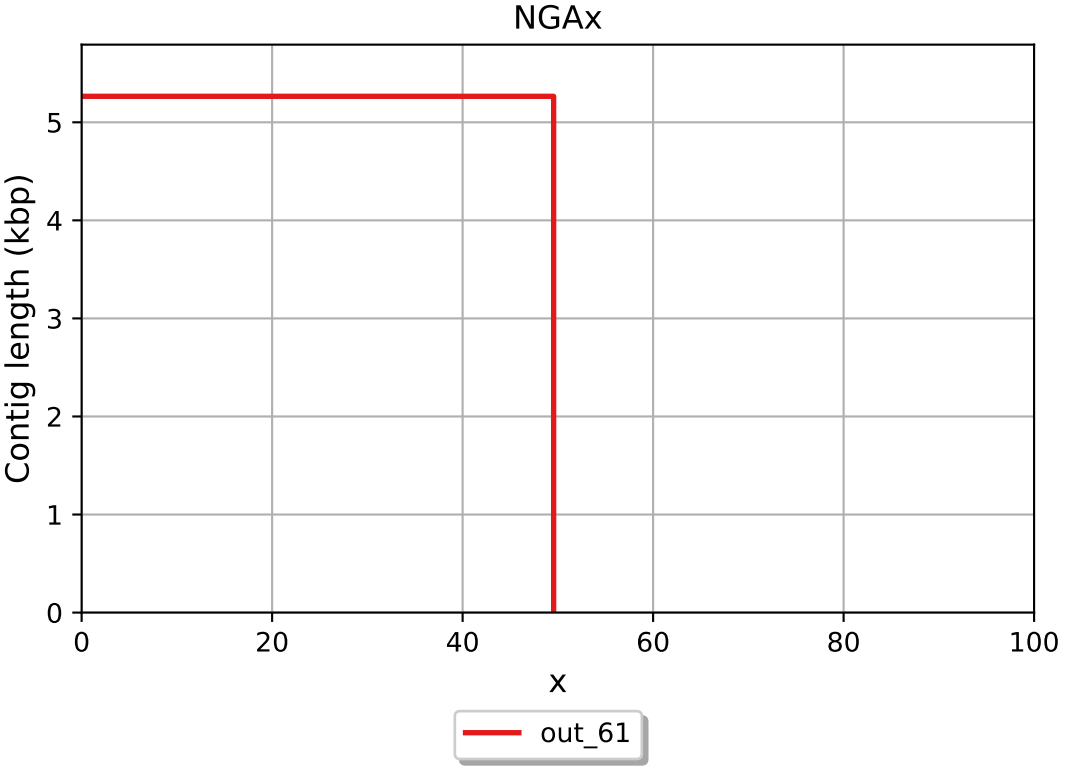

out_61 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
out_61


Misassemblies
5
4
3
2
1
0
out_61


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
out_61


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
2
4
6
8
10
0
1
Contig index
out_61
Reference


NAx
Contig length (kbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
out_61


NGAx
Contig length (kbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
out_61