Report

	GAS.filtered_sequences
# contigs (>= 0 bp)	66
# contigs (>= 1000 bp)	50
# contigs (>= 5000 bp)	37
# contigs (>= 10000 bp)	34
# contigs (>= 25000 bp)	25
# contigs (>= 50000 bp)	15
Total length (>= 0 bp)	1806353
Total length (>= 1000 bp)	1799854
Total length (>= 5000 bp)	1769911
Total length (>= 10000 bp)	1748459
Total length (>= 25000 bp)	1615051
Total length (>= 50000 bp)	1265587
# contigs	53
Largest contig	144239
Total length	1802391
Reference length	1791401
GC (%)	38.36
Reference GC (%)	38.56
N50	66934
NG50	67674
N90	21088
NG90	25476
auN	72861.4
auNG	73308.4
L50	10
LG50	9
L90	26
LG90	25
# misassemblies	18
# misassembled contigs	13
Misassembled contigs length	793688
# local misassemblies	15
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	3 + 19 part
Unaligned length	142656
Genome fraction (%)	92.320
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	875.16
# indels per 100 kbp	34.06
Largest alignment	144239
Total aligned length	1655699
NA50	52362
NGA50	52362
NA90	3609
NGA90	4086
auNA	55881.2
auNGA	56224.0
LA50	12
LGA50	12
LA90	48
LGA90	45

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

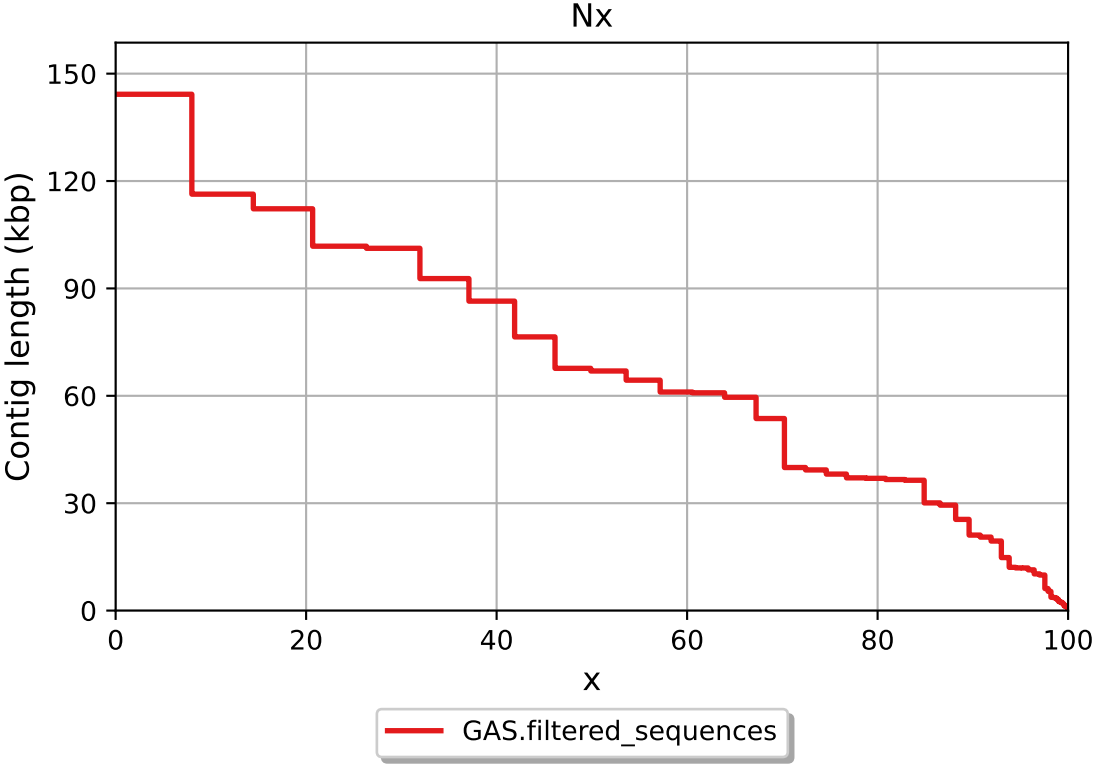
	GAS.filtered_sequences
# misassemblies	18
# contig misassemblies	18
# c. relocations	18
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	13
Misassembled contigs length	793688
# local misassemblies	15
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	14490
# indels	564
# indels (<= 5 bp)	478
# indels (> 5 bp)	86
Indels length	2937

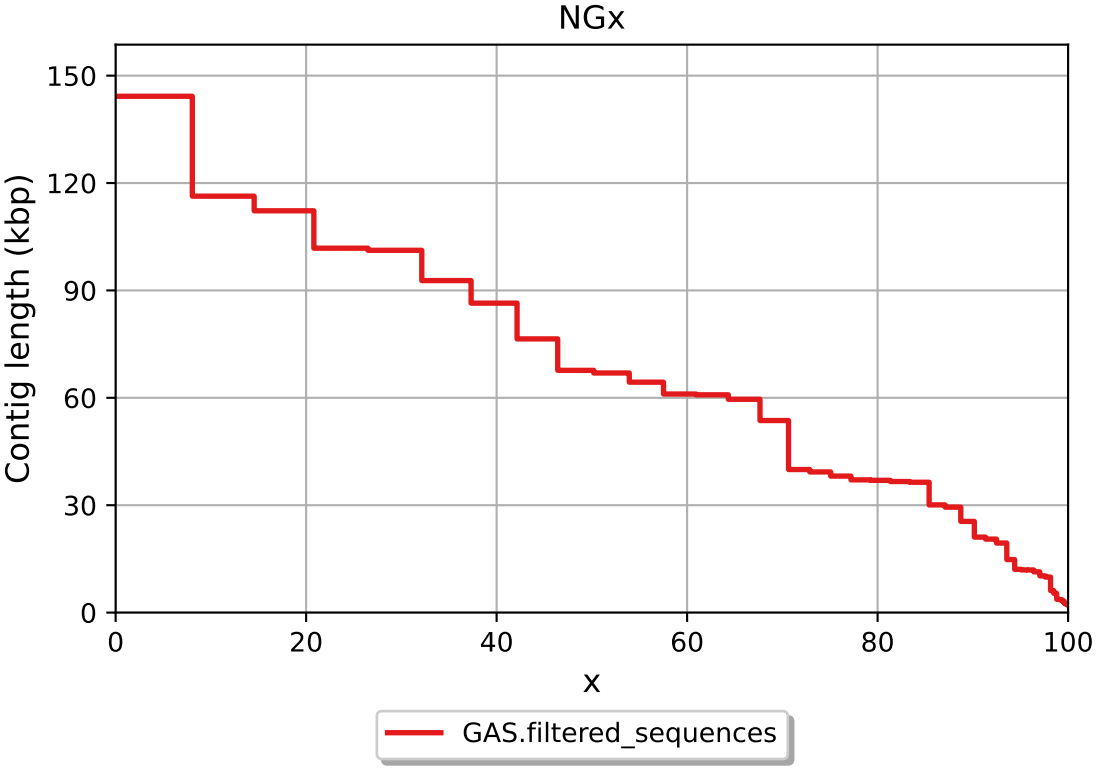
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

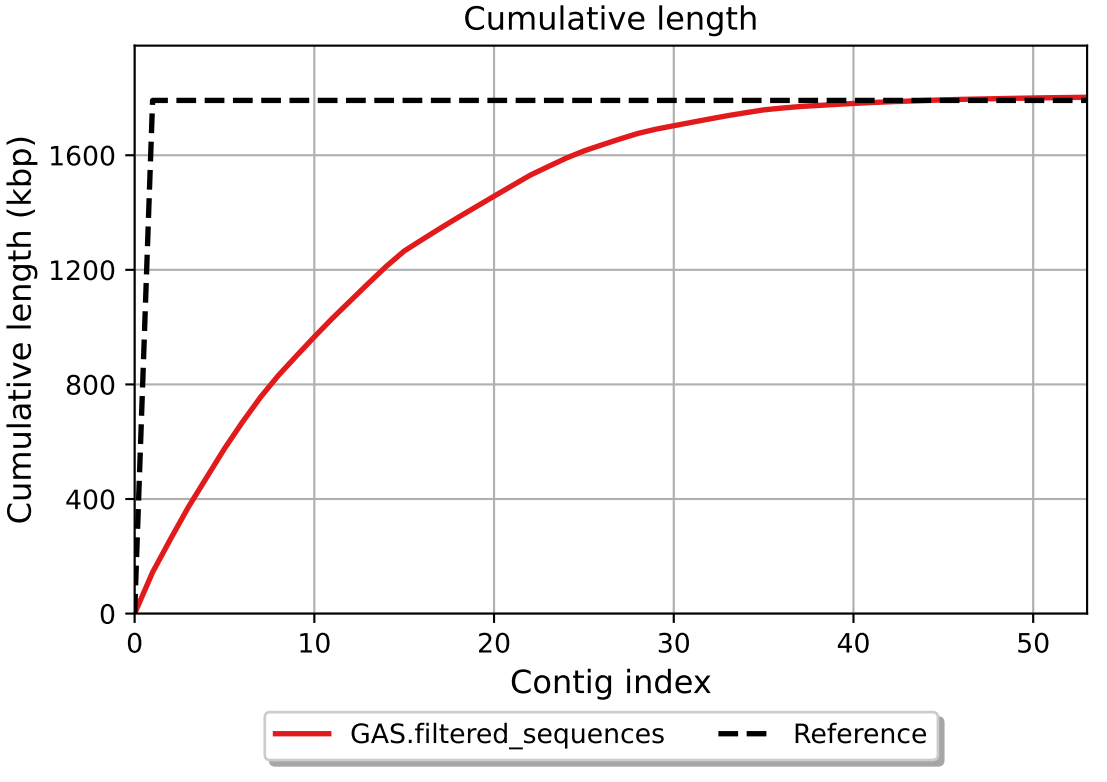
Unaligned report

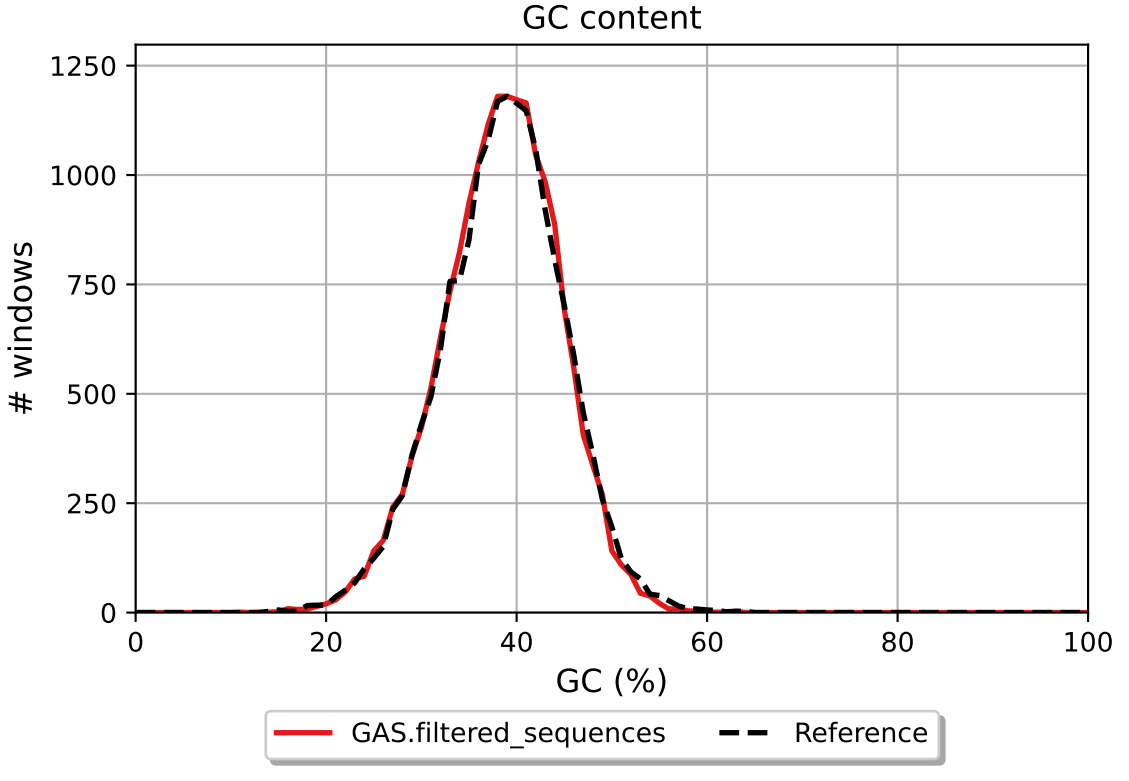
	GAS.filtered_sequences
# fully unaligned contigs	3
Fully unaligned length	8994
# partially unaligned contigs	19
Partially unaligned length	133662
# N's	0

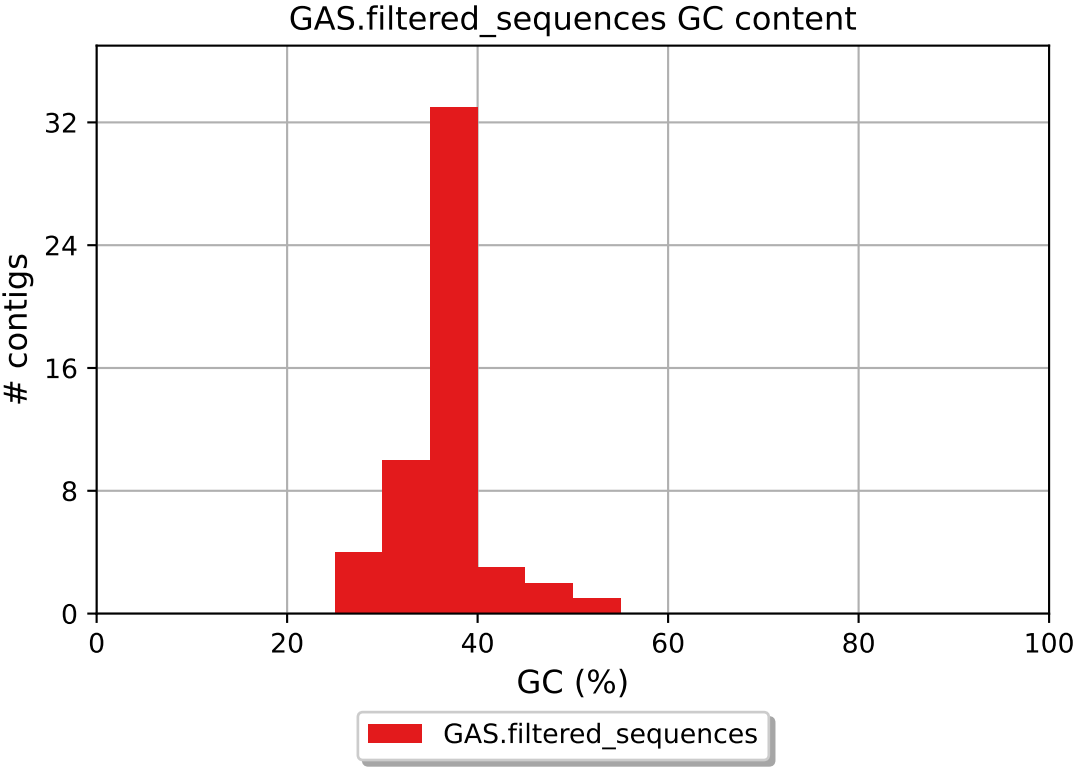
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

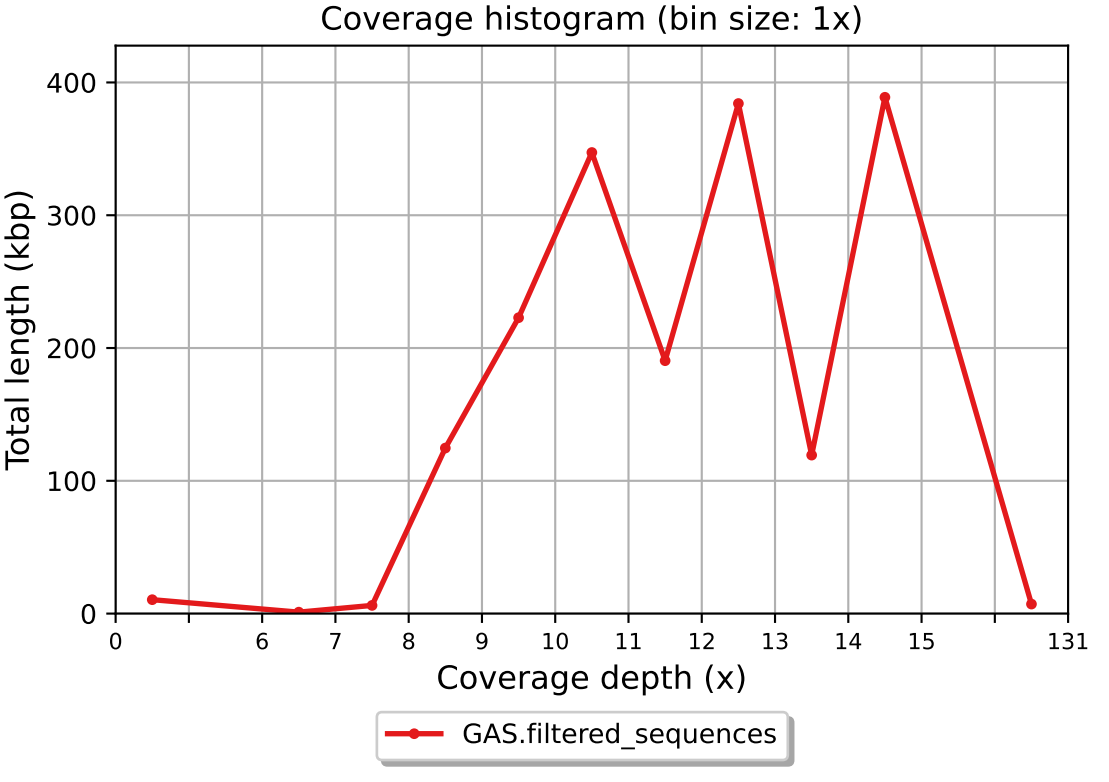

Nx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
GAS.filtered_sequences

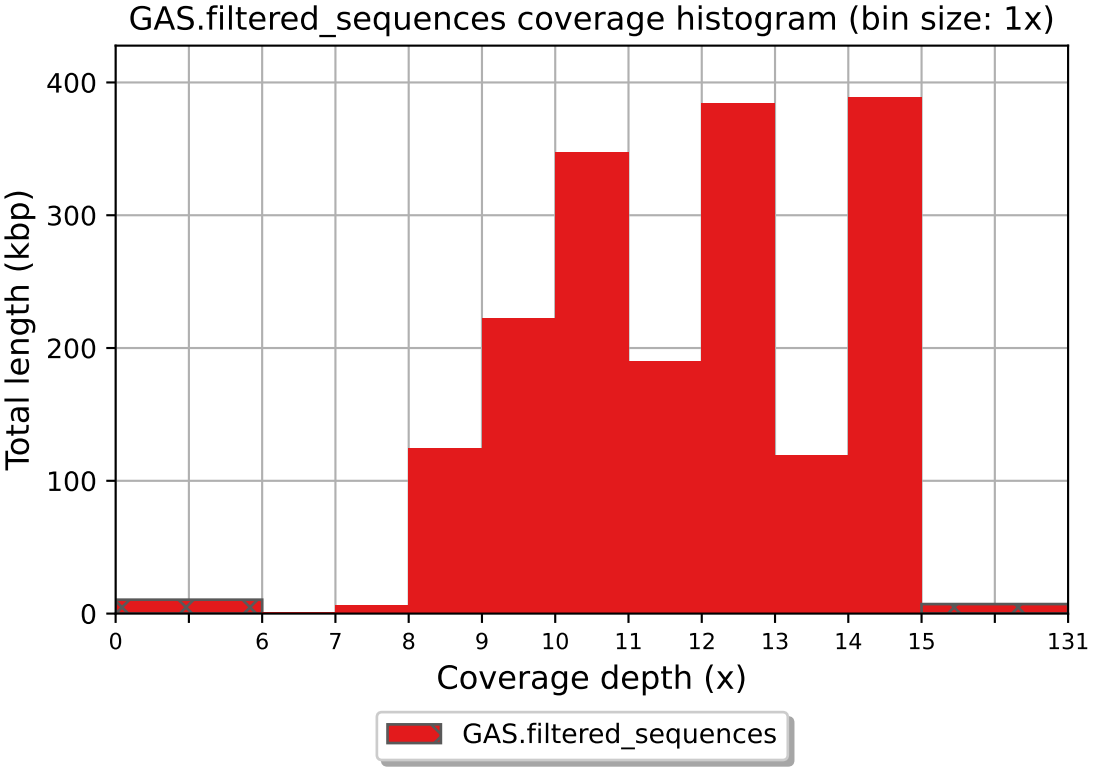

NGx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
GAS.filtered_sequences


Cumulative length
Cumulative length (kbp)
0
400
800
1200
1600
0
10
20
30
40
50
Contig index
GAS.filtered_sequences
Reference

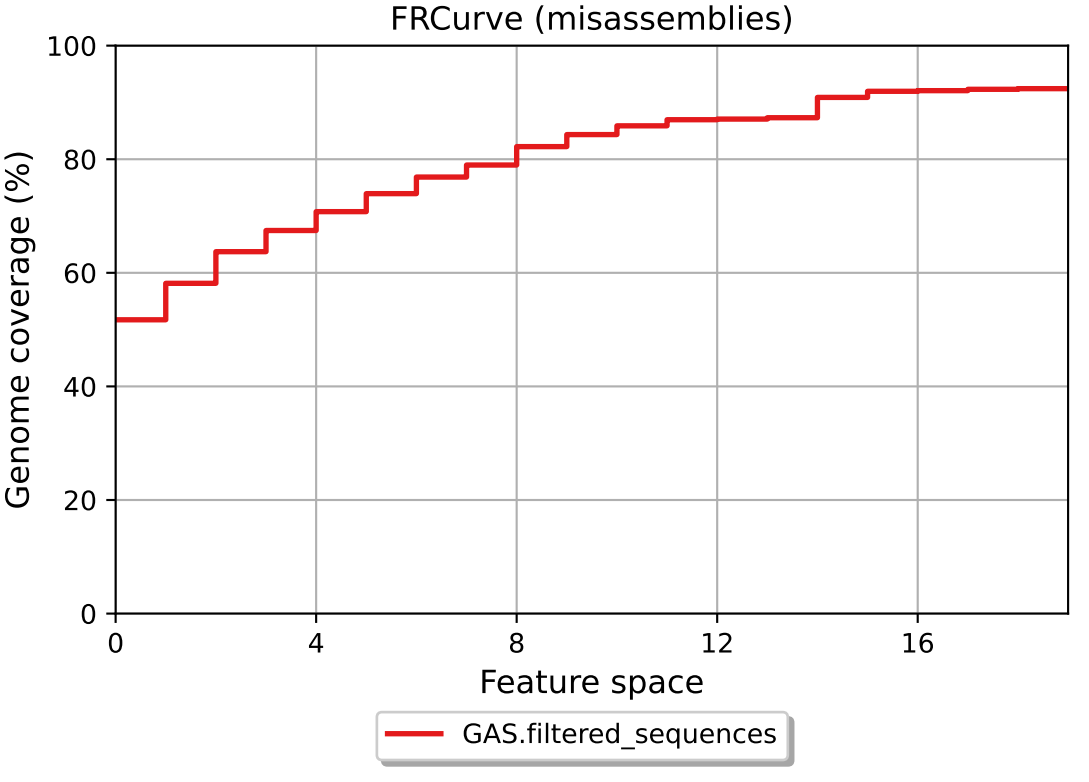

GC content
windows
GC (%)
0
250
500
750
1000
1250
0
20
40
60
80
100
GAS.filtered_sequences
Reference

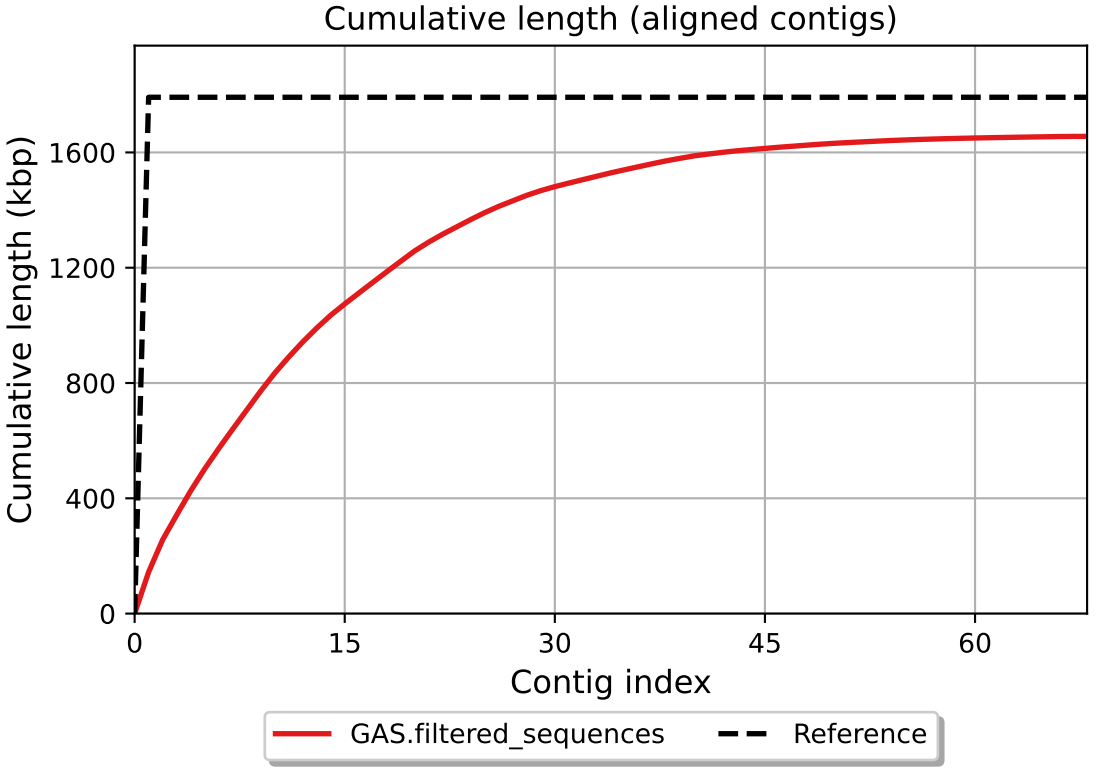

GAS.filtered_sequences GC content
contigs
0
8
16
24
32
0
20
40
60
80
100
GC (%)
GAS.filtered_sequences

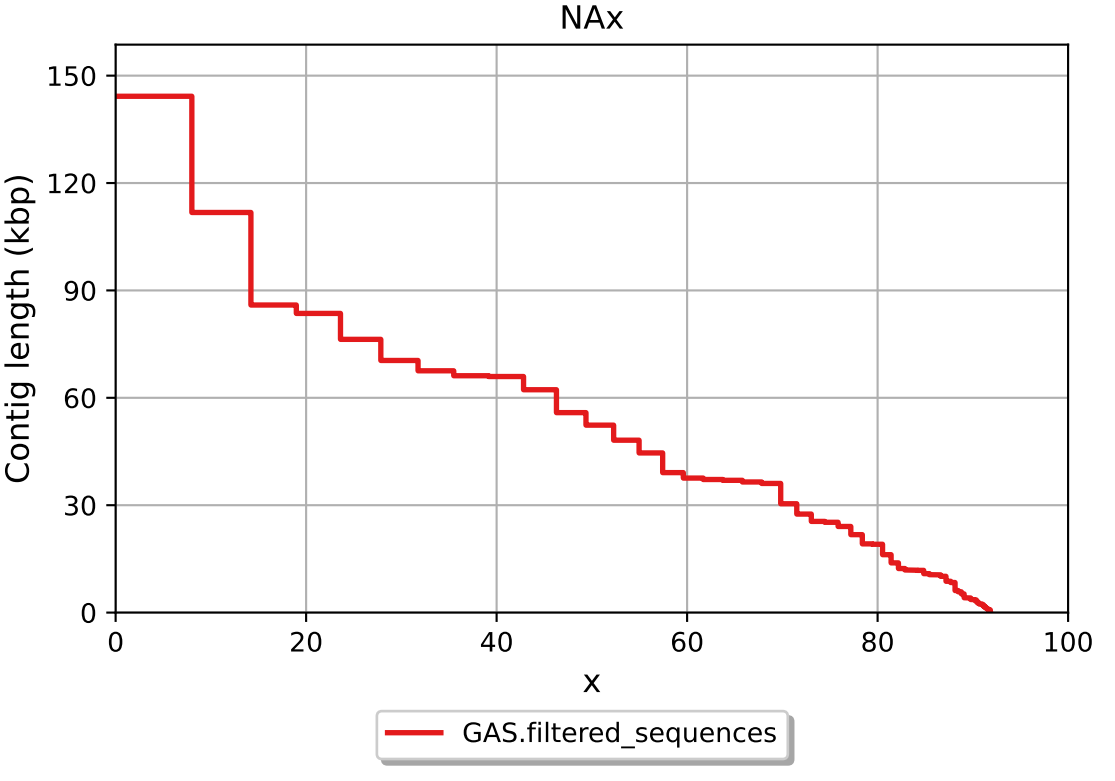

Coverage histogram (bin size: 1x)
Total length (kbp)
400
300
200
100
0
0
6
7
8
9
10
11
12
13
14
15
131
Coverage depth (x)
GAS.filtered_sequences

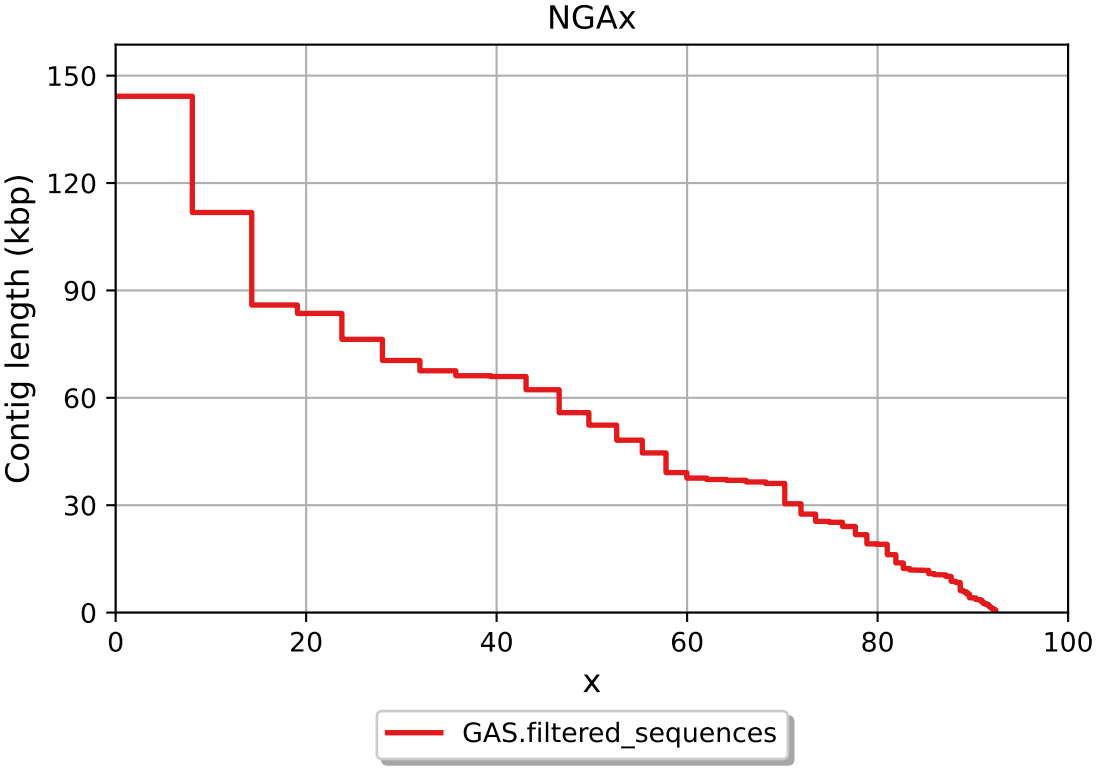

GAS.filtered_sequences coverage histogram (bin size: 1x)
Total length (kbp)
400
300
200
100
0
0
6
7
8
9
10
11
12
13
14
15
131
Coverage depth (x)
GAS.filtered_sequences

Misassemblies
20
16
12
8
4
0
GAS.filtered_sequences
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
Feature space
GAS.filtered_sequences


Cumulative length (aligned contigs)
Cumulative length (kbp)
1600
1200
800
400
0
0
15
30
45
60
Contig index
GAS.filtered_sequences
Reference


NAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
GAS.filtered_sequences


NGAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
GAS.filtered_sequences