Report

	pos_sorted_bam_filtered.long
# contigs (>= 0 bp)	9508
# contigs (>= 1000 bp)	67
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	2783972
Total length (>= 1000 bp)	86587
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2513
Largest contig	3116
Total length	1160941
Reference length	1556
GC (%)	43.83
Reference GC (%)	50.90
N50	447
NG50	3116
N75	355
NG75	3116
L50	882
LG50	1
L75	1619
LG75	1
# 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	2511 + 0 part
Unaligned length	1160229
Genome fraction (%)	37.082
Duplication ratio	1.234
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1039.86
# indels per 100 kbp	346.62
Largest alignment	365
Total aligned length	571
NGA50	-

All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

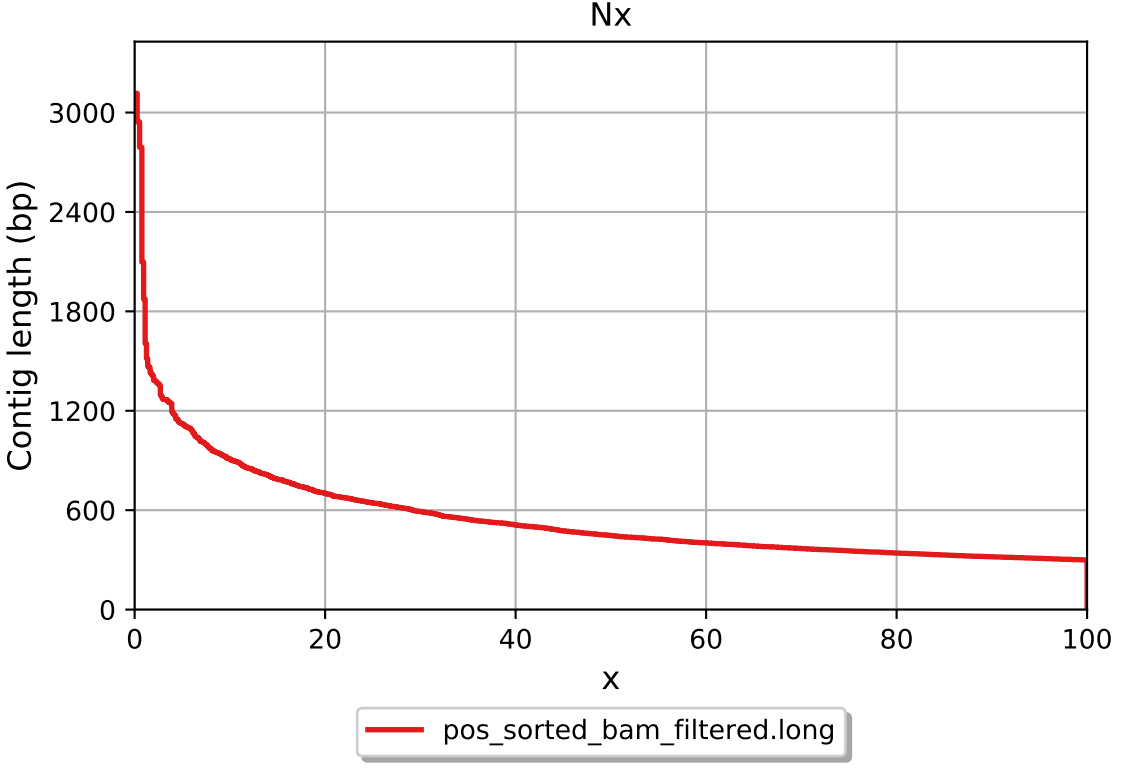
	pos_sorted_bam_filtered.long
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	6
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	6

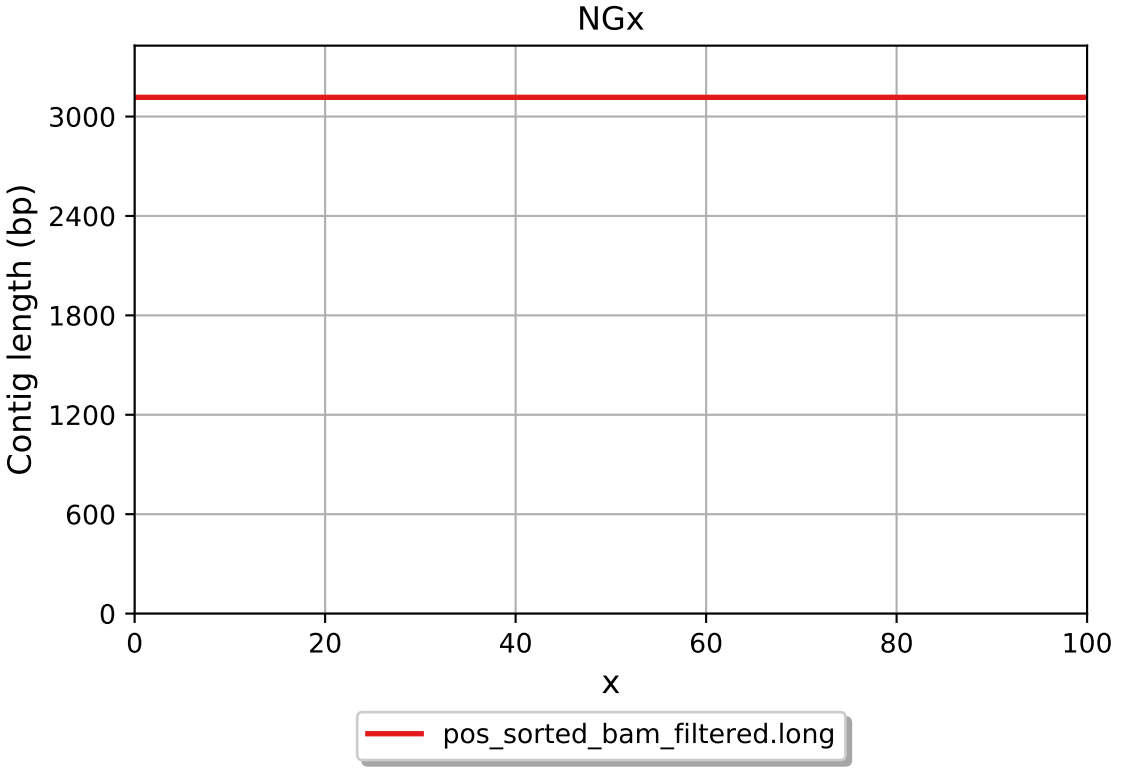
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

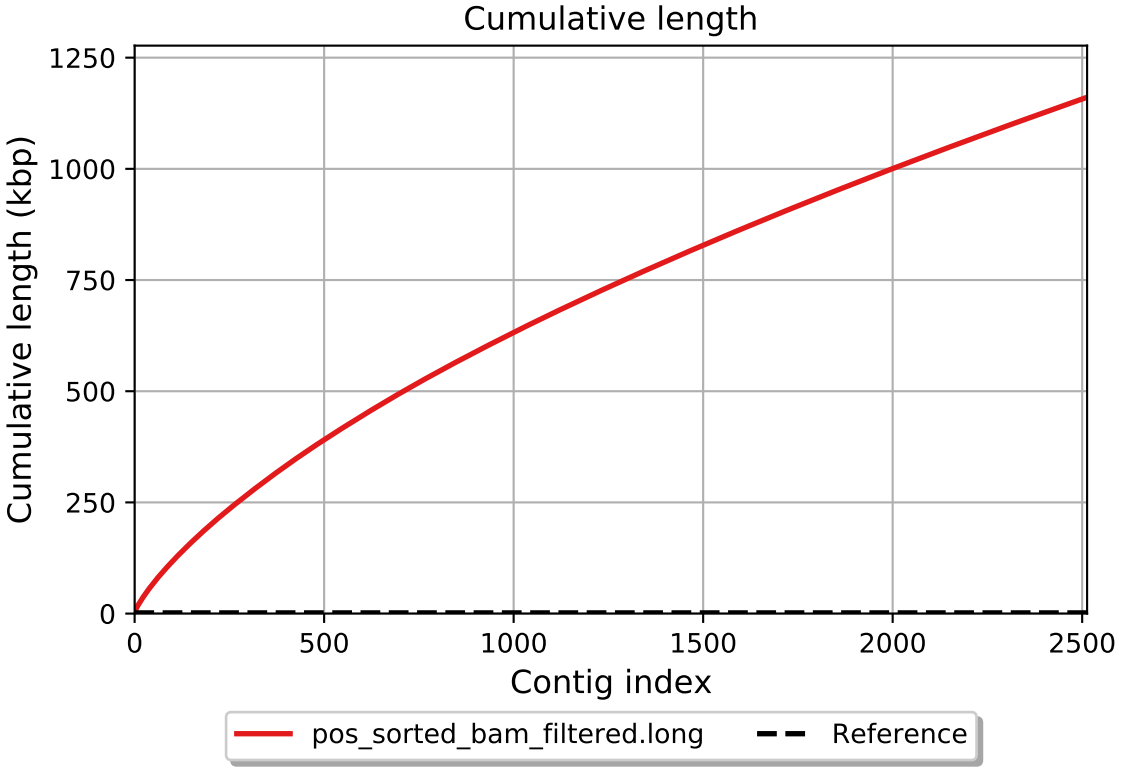
Unaligned report

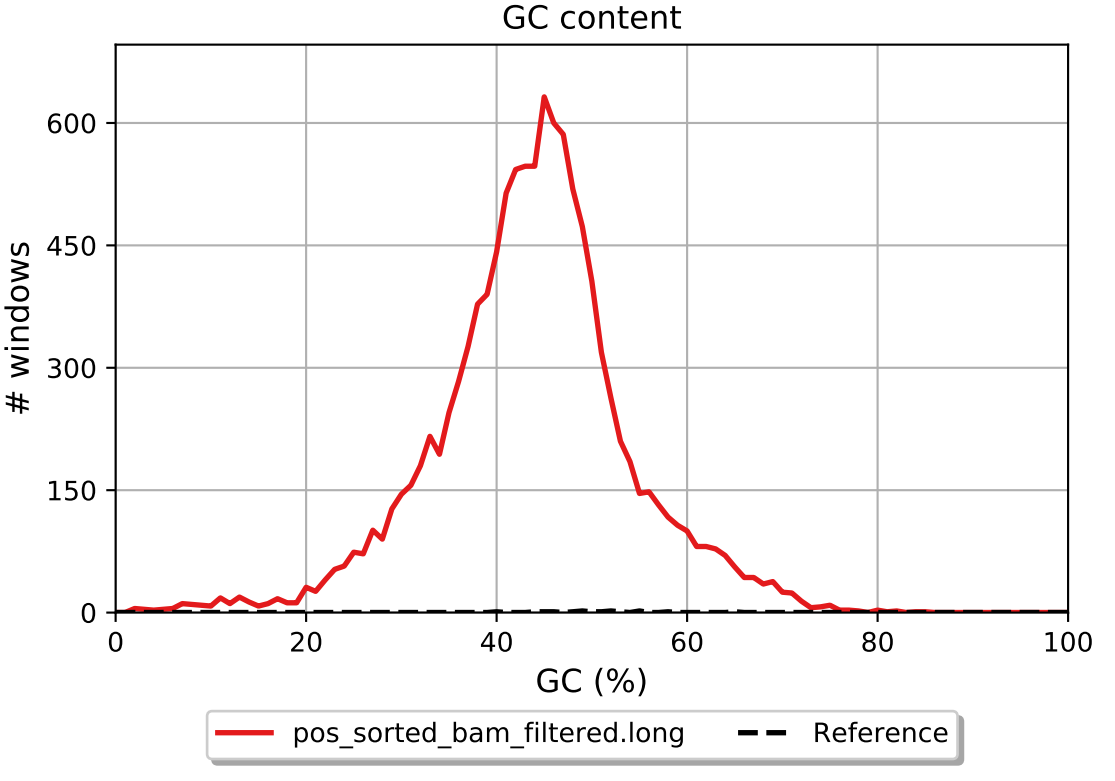
	pos_sorted_bam_filtered.long
# fully unaligned contigs	2511
Fully unaligned length	1160229
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

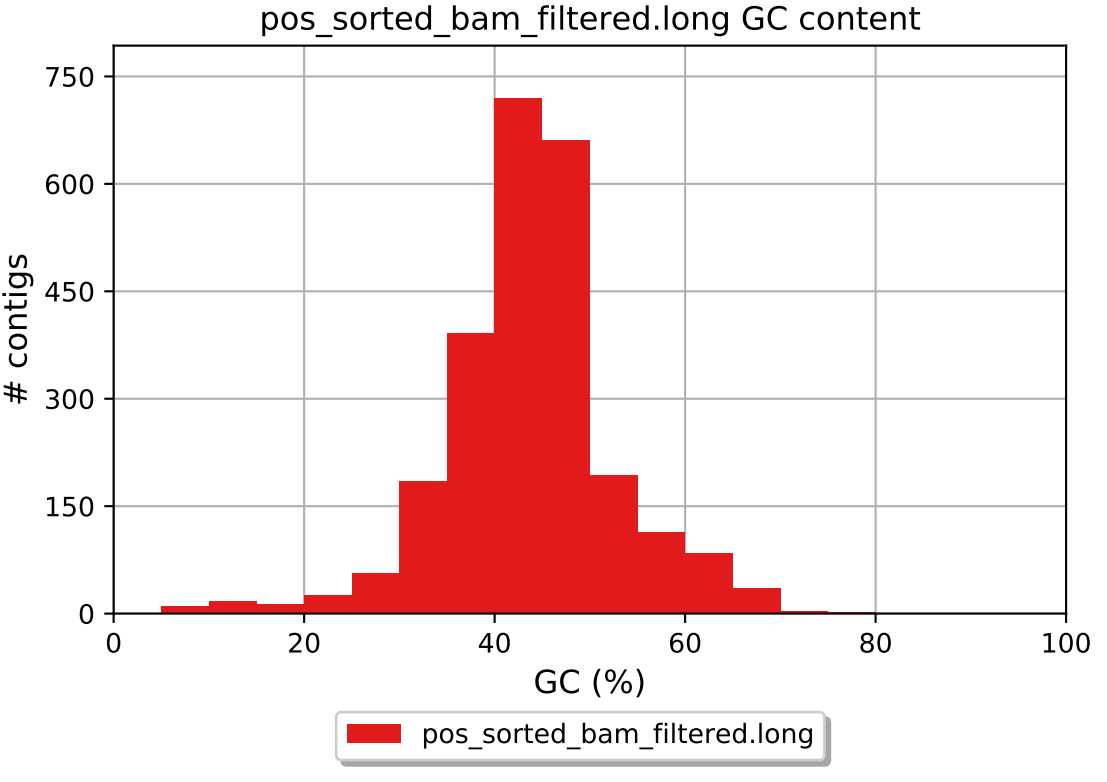
All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

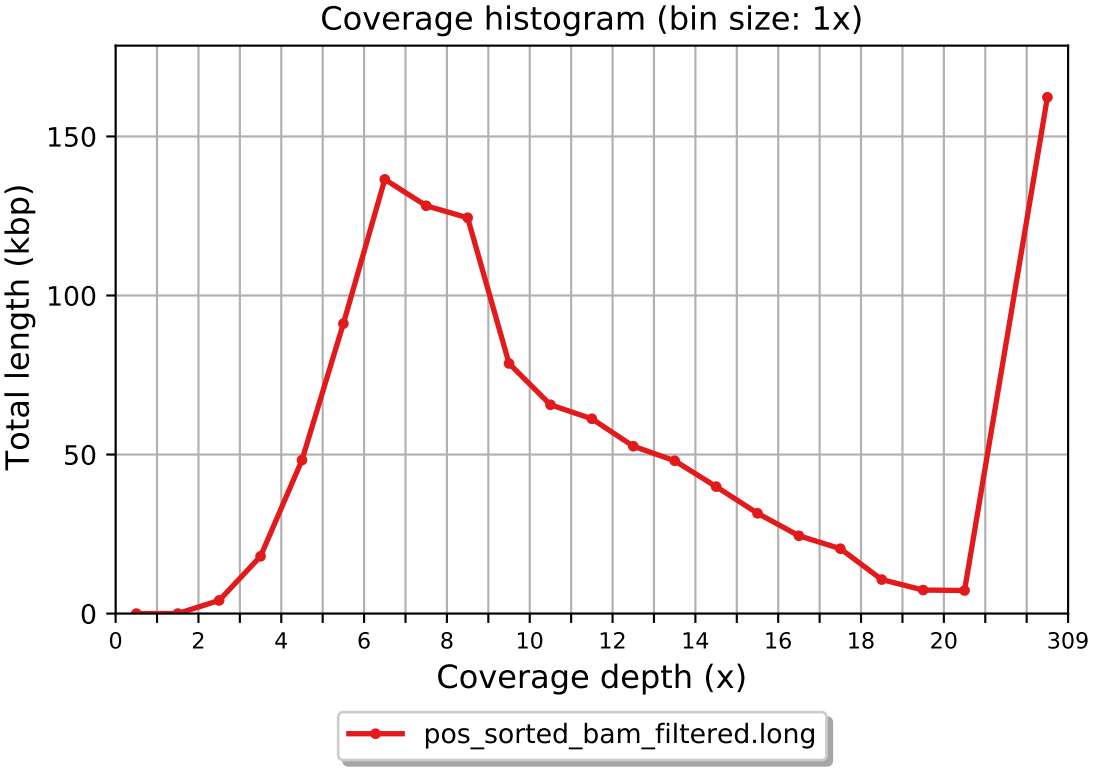

Nx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
pos_sorted_bam_filtered.long

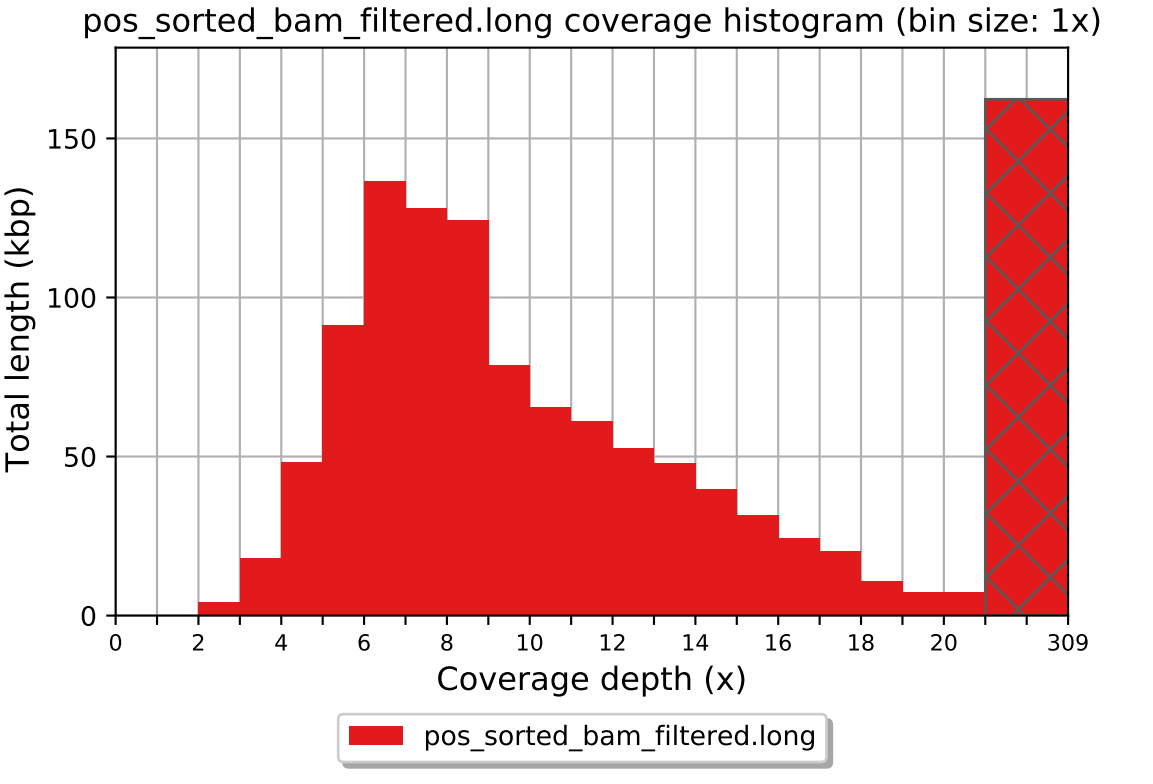

NGx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
pos_sorted_bam_filtered.long

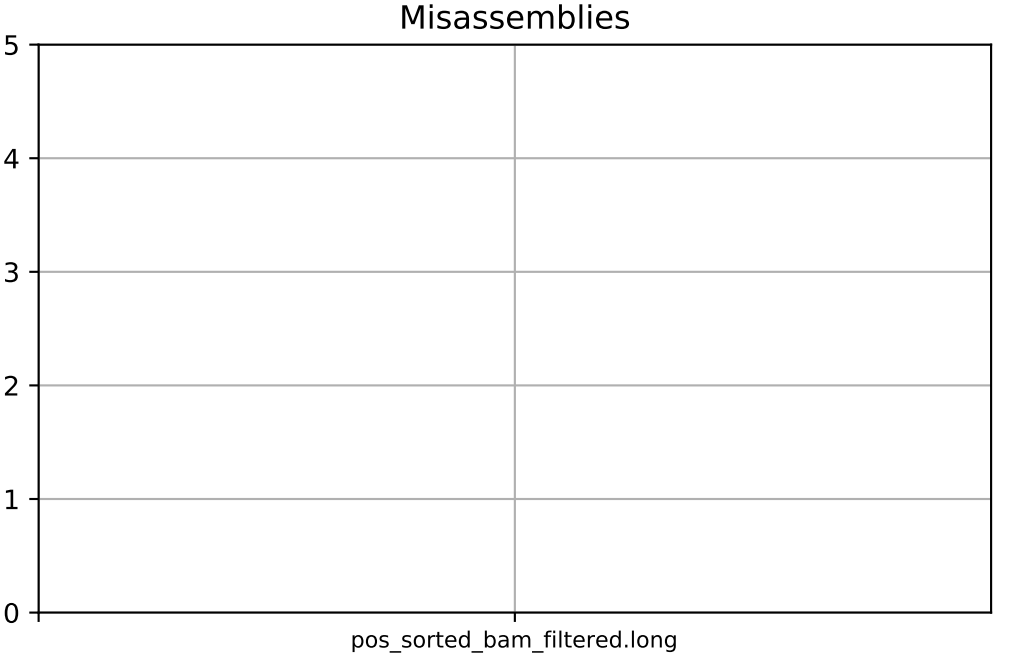

Cumulative length
Cumulative length (kbp)
1250
1000
750
500
250
0
0
500
1000
1500
2000
2500
Contig index
pos_sorted_bam_filtered.long
Reference

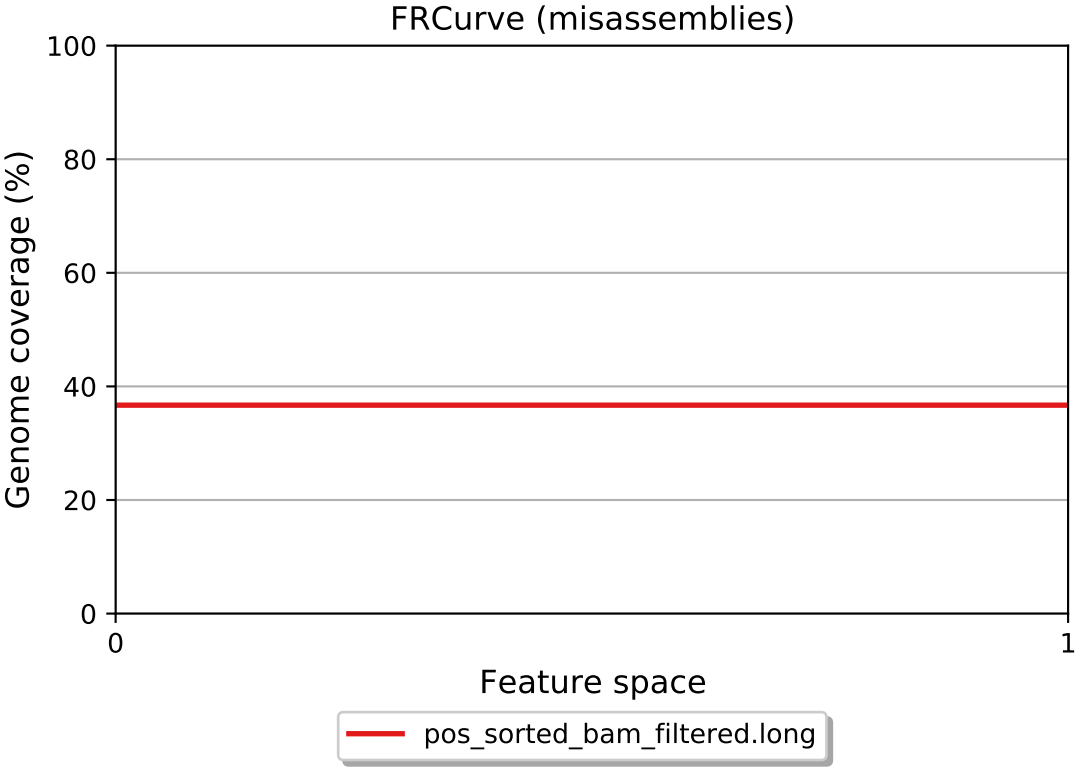

GC content
windows
600
450
300
150
0
0
20
40
60
80
100
GC (%)
pos_sorted_bam_filtered.long
Reference

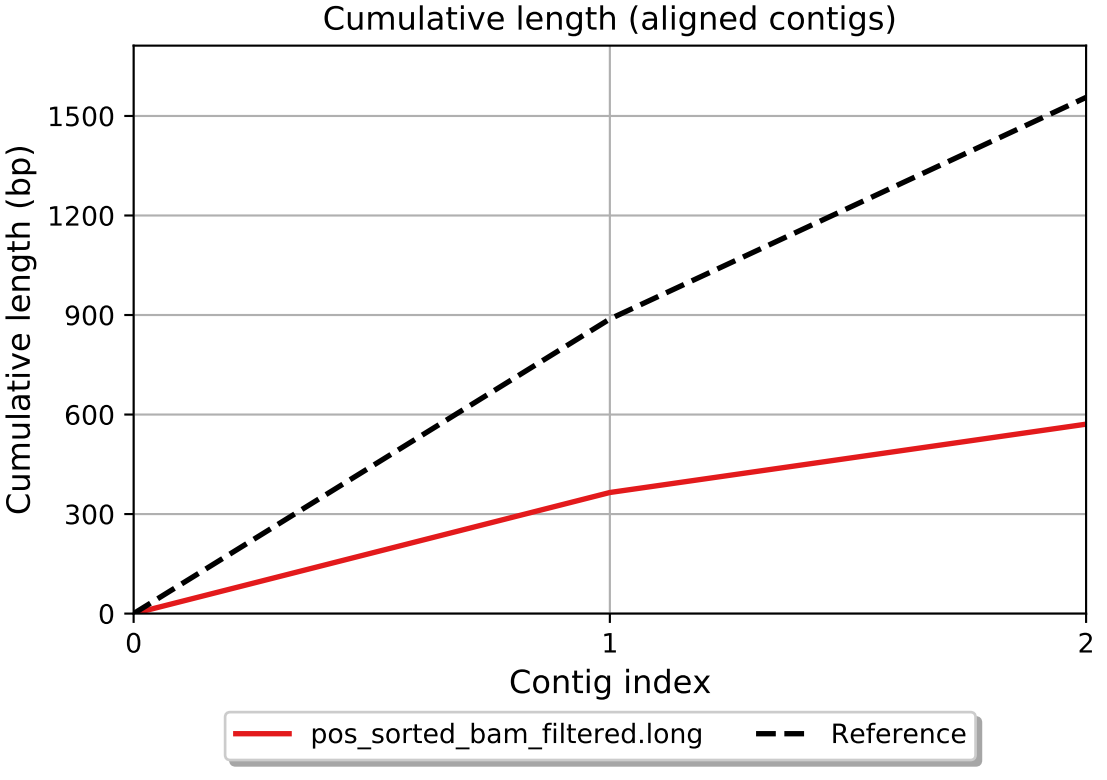

pos_sorted_bam_filtered.long GC content
contigs
GC (%)
0
150
300
450
600
750
0
20
40
60
80
100
pos_sorted_bam_filtered.long

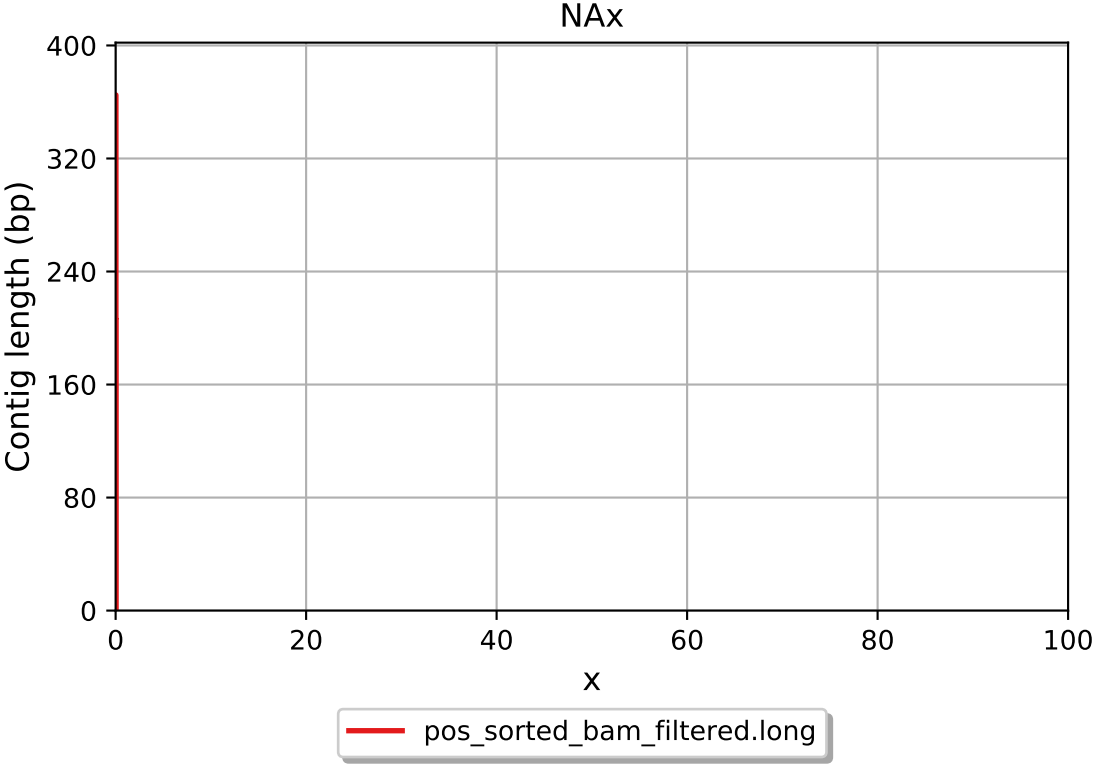

Coverage histogram (bin size: 1x)
Total length (kbp)
150
100
50
0
0
2
4
6
8
10
12
14
16
18
20
309
Coverage depth (x)
pos_sorted_bam_filtered.long

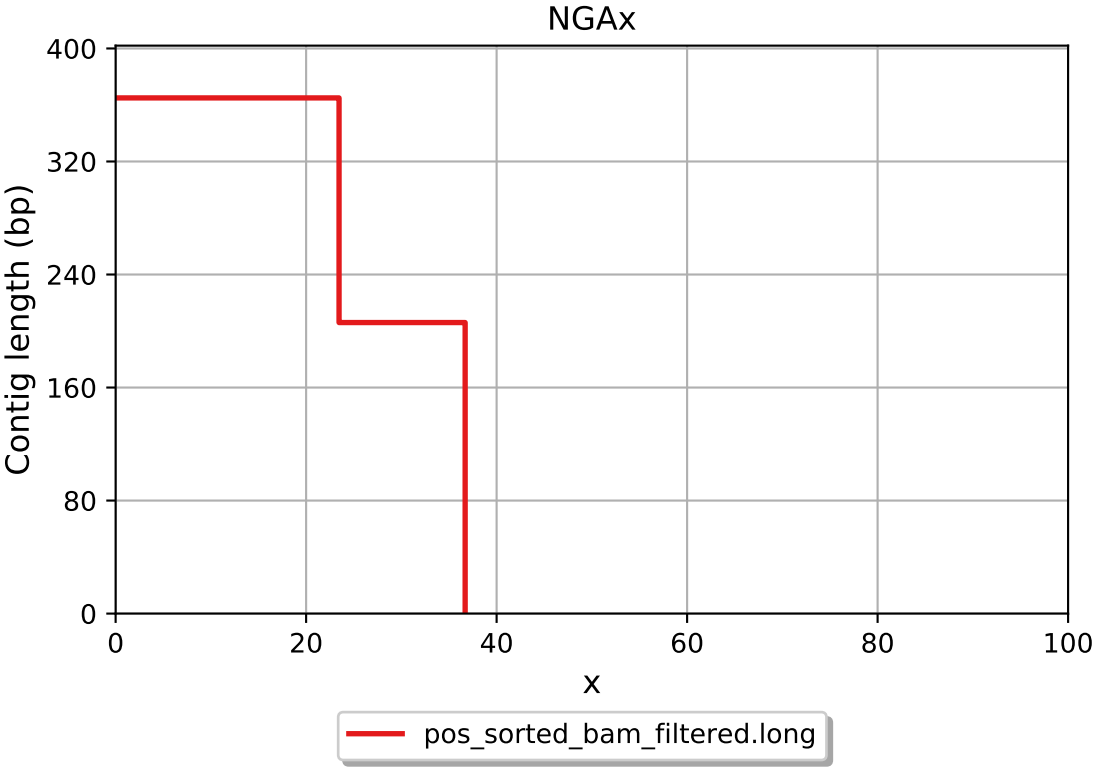

pos_sorted_bam_filtered.long coverage histogram (bin size: 1x)
Total length (kbp)
150
100
50
0
0
2
4
6
8
10
12
14
16
18
20
309
Coverage depth (x)
pos_sorted_bam_filtered.long


Misassemblies
5
4
3
2
1
0
pos_sorted_bam_filtered.long


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


Cumulative length (aligned contigs)
Cumulative length (bp)
1500
1200
900
600
300
0
0
1
2
Contig index
pos_sorted_bam_filtered.long
Reference


NAx
400
320
240
160
80
0
Contig length (bp)
0
20
40
60
80
100
x
pos_sorted_bam_filtered.long


NGAx
400
320
240
160
80
0
Contig length (bp)
0
20
40
60
80
100
x
pos_sorted_bam_filtered.long