Report

	Galaxy13_fna
# contigs (>= 0 bp)	449
# contigs (>= 1000 bp)	23
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	13
Total length (>= 0 bp)	3116159
Total length (>= 1000 bp)	2998937
Total length (>= 5000 bp)	2991520
Total length (>= 10000 bp)	2986339
Total length (>= 25000 bp)	2970749
Total length (>= 50000 bp)	2805918
# contigs	449
Largest contig	805683
Total length	3116159
Reference length	2952961
GC (%)	48.38
Reference GC (%)	47.88
N50	234751
NG50	234751
N75	171100
NG75	171100
L50	4
LG50	4
L75	8
LG75	8
# misassemblies	76
# misassembled contigs	13
Misassembled contigs length	1836736
# local misassemblies	114
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	412 + 16 part
Unaligned length	1122755
Genome fraction (%)	67.271
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3437.73
# indels per 100 kbp	61.16
Largest alignment	115106
Total aligned length	1990885
NA50	6503
NGA50	8823
LA50	71
LGA50	60

All statistics are based on contigs of size >= 10 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

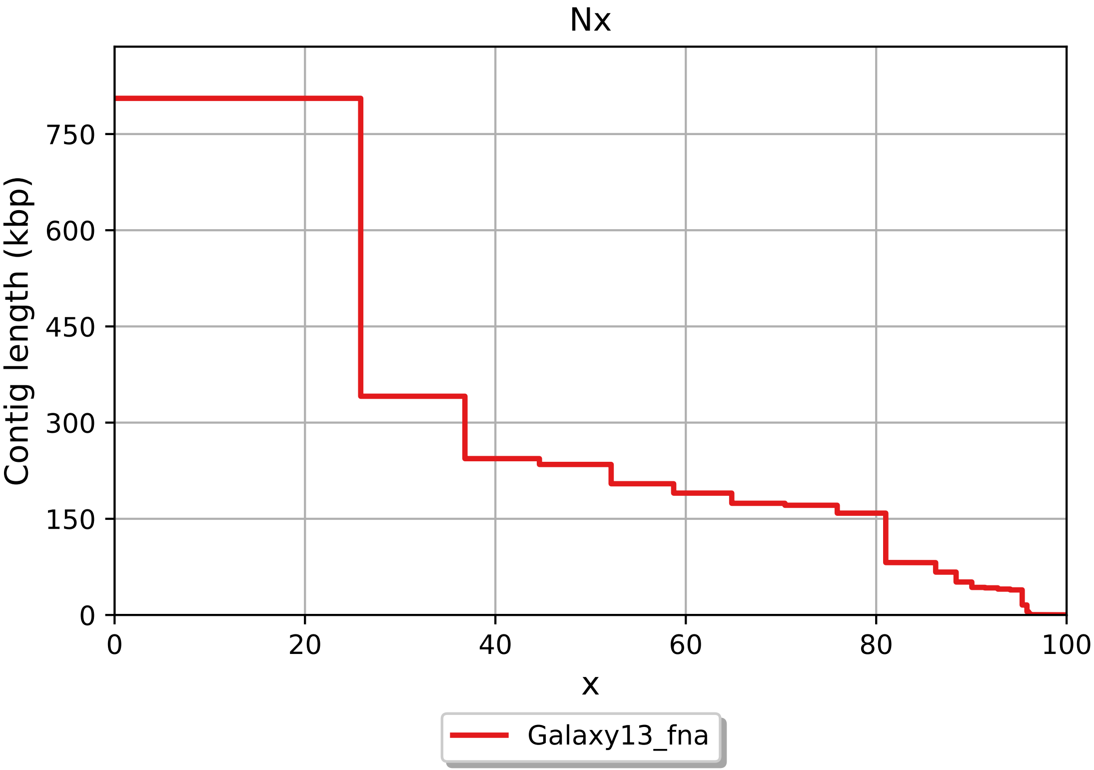
	Galaxy13_fna
# misassemblies	76
# contig misassemblies	76
# c. relocations	76
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	13
Misassembled contigs length	1836736
# local misassemblies	114
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	68290
# indels	1215
# indels (<= 5 bp)	1092
# indels (> 5 bp)	123
Indels length	4905

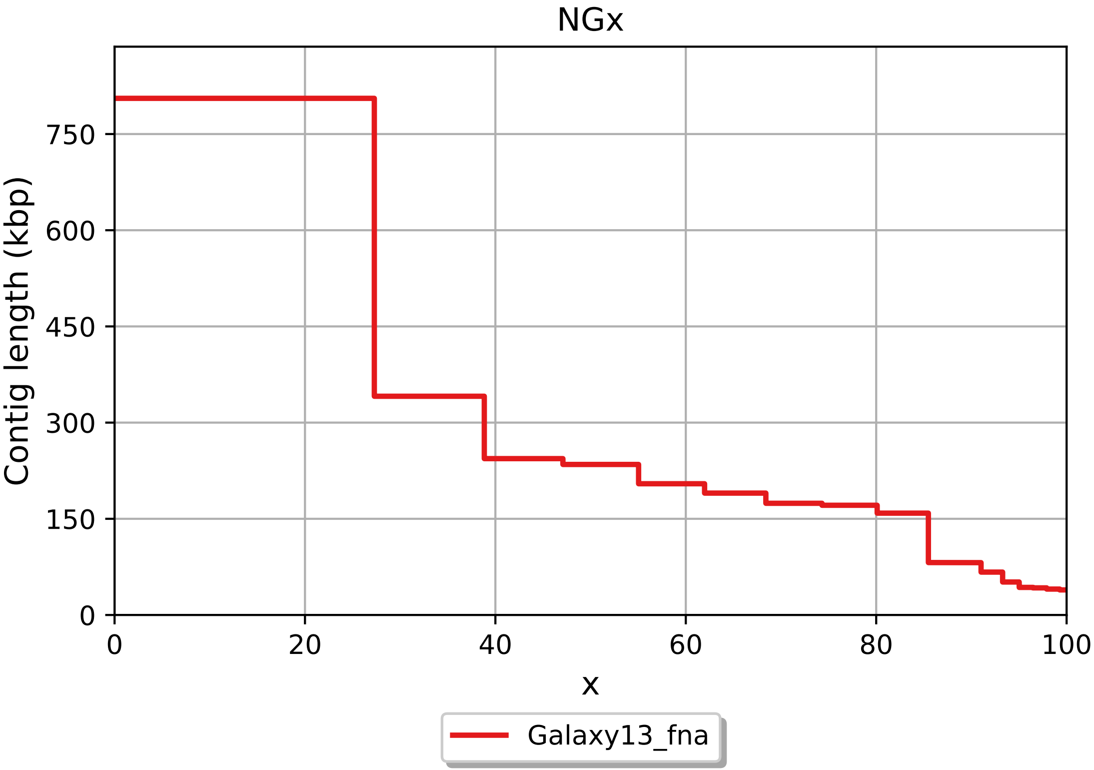
All statistics are based on contigs of size >= 10 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

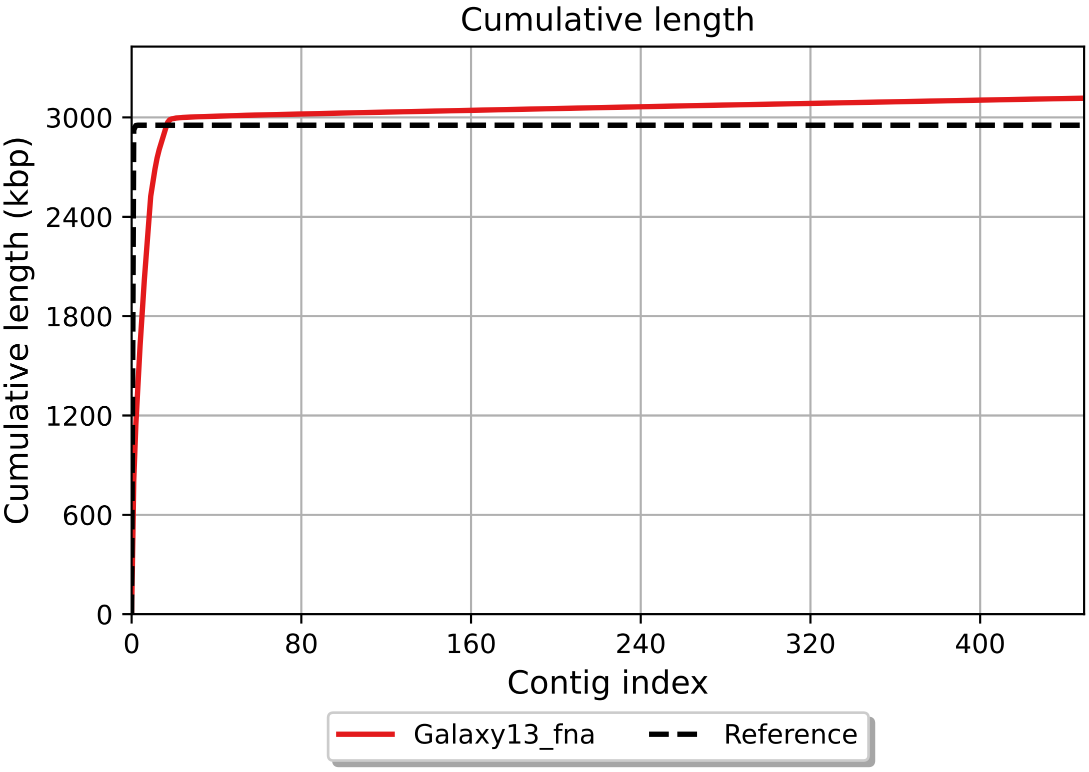
Unaligned report

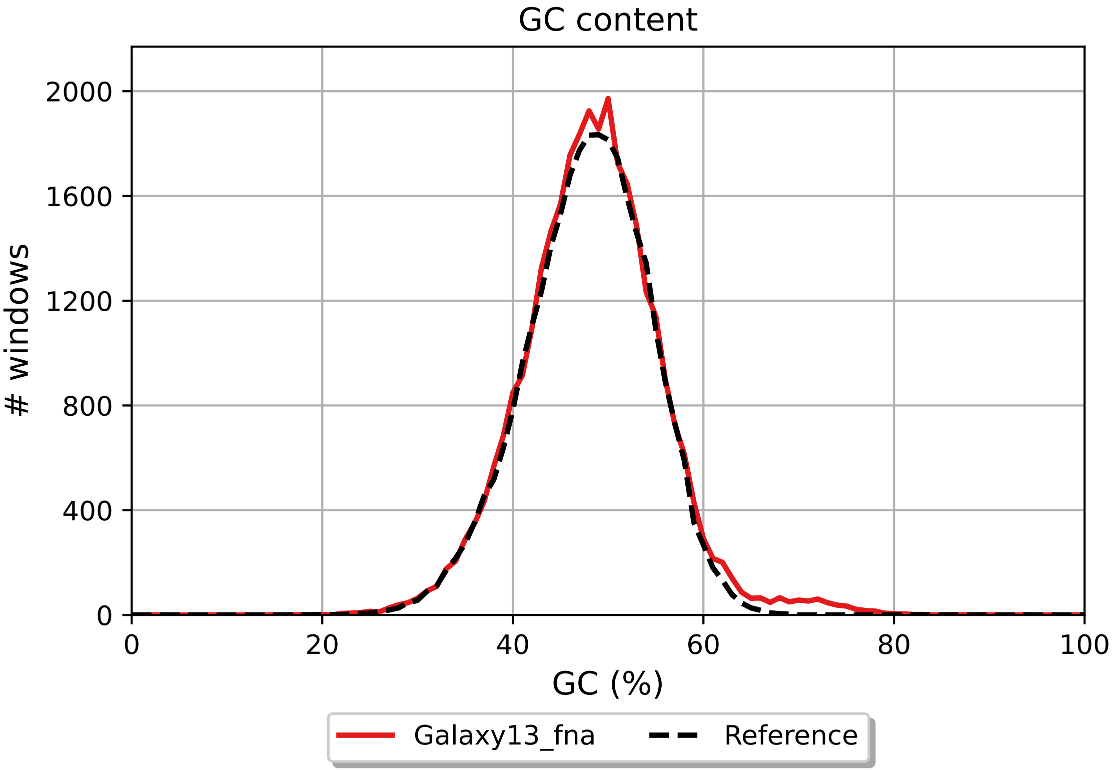
	Galaxy13_fna
# fully unaligned contigs	412
Fully unaligned length	112546
# partially unaligned contigs	16
Partially unaligned length	1010209
# N's	0

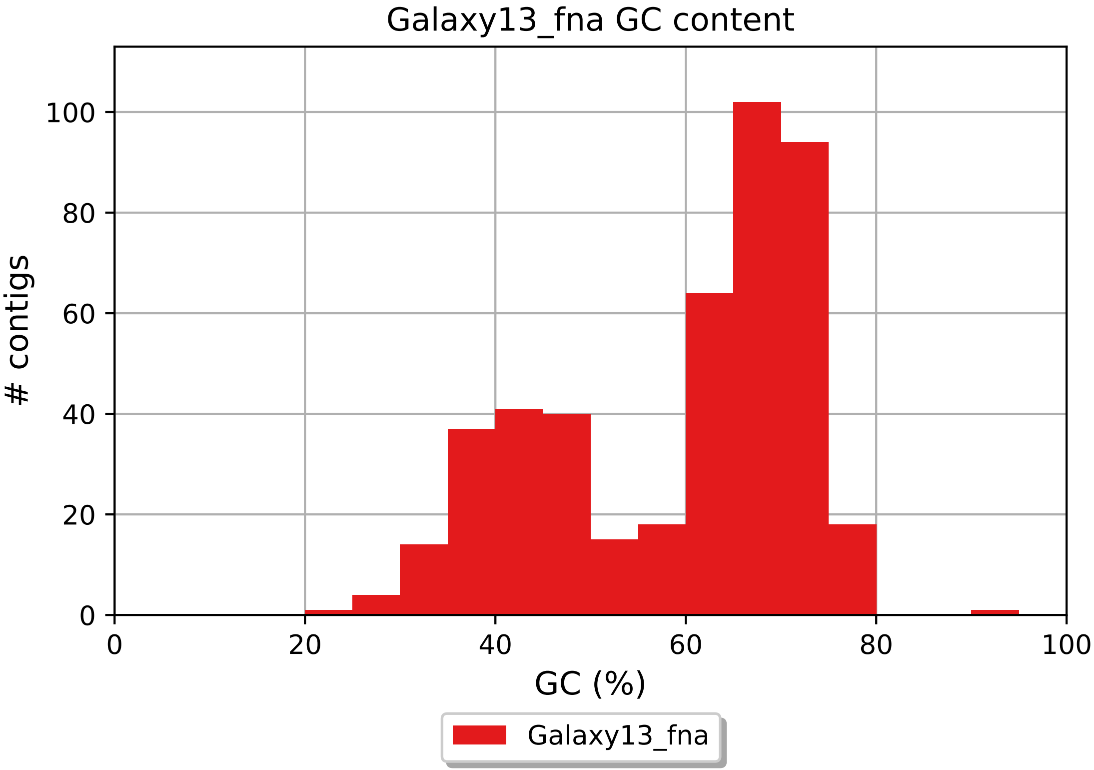
All statistics are based on contigs of size >= 10 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

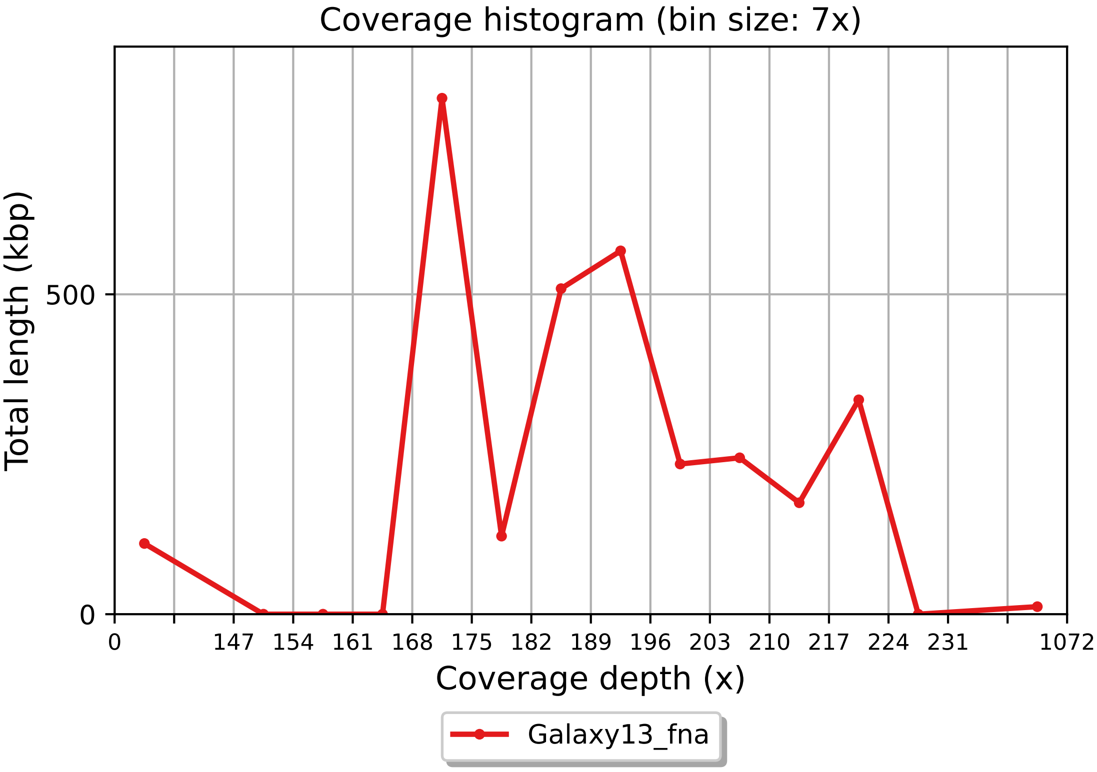

Nx
Contig length (kbp)
750
600
450
300
150
0
0
20
40
60
80
100
x
Galaxy13_fna

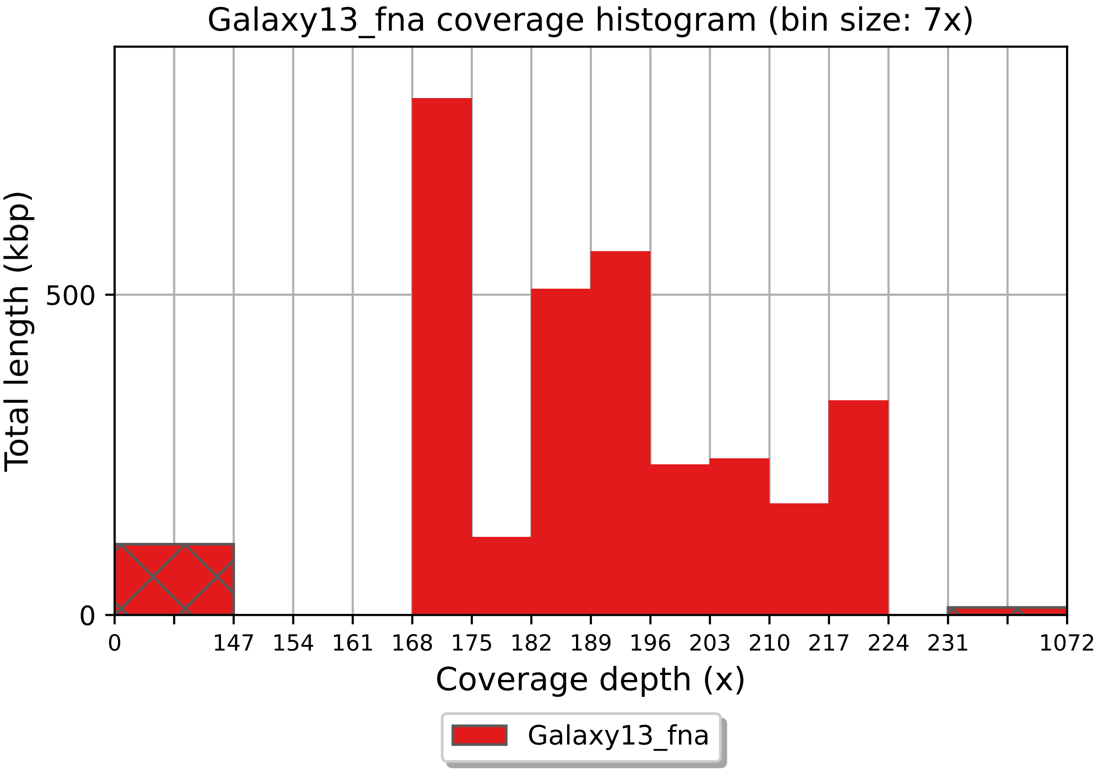

NGx
Contig length (kbp)
0
150
300
450
600
750
0
20
40
60
80
100
x
Galaxy13_fna

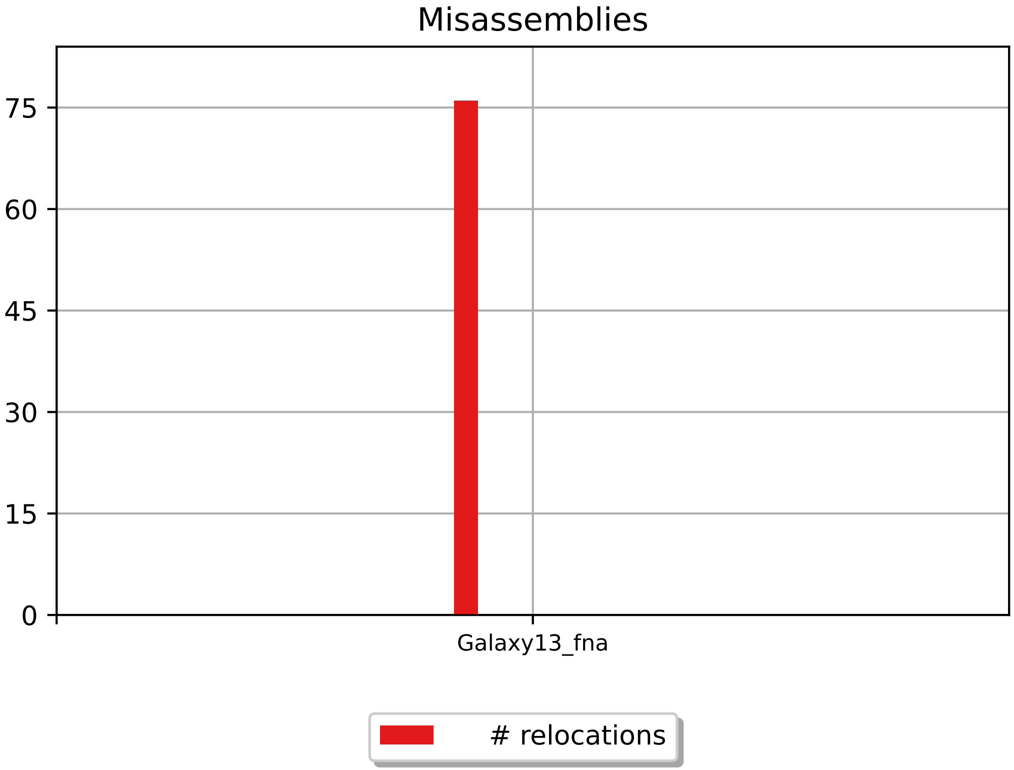

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
80
160
240
320
400
Contig index
Galaxy13_fna
Reference

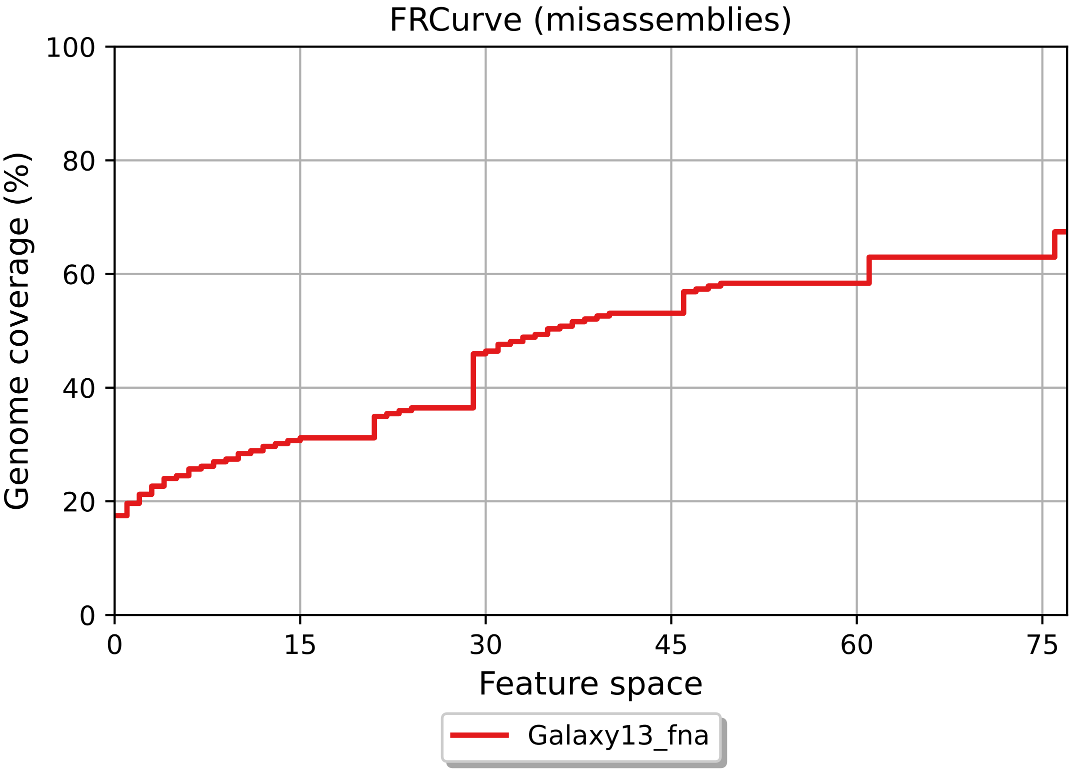

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
Galaxy13_fna
Reference

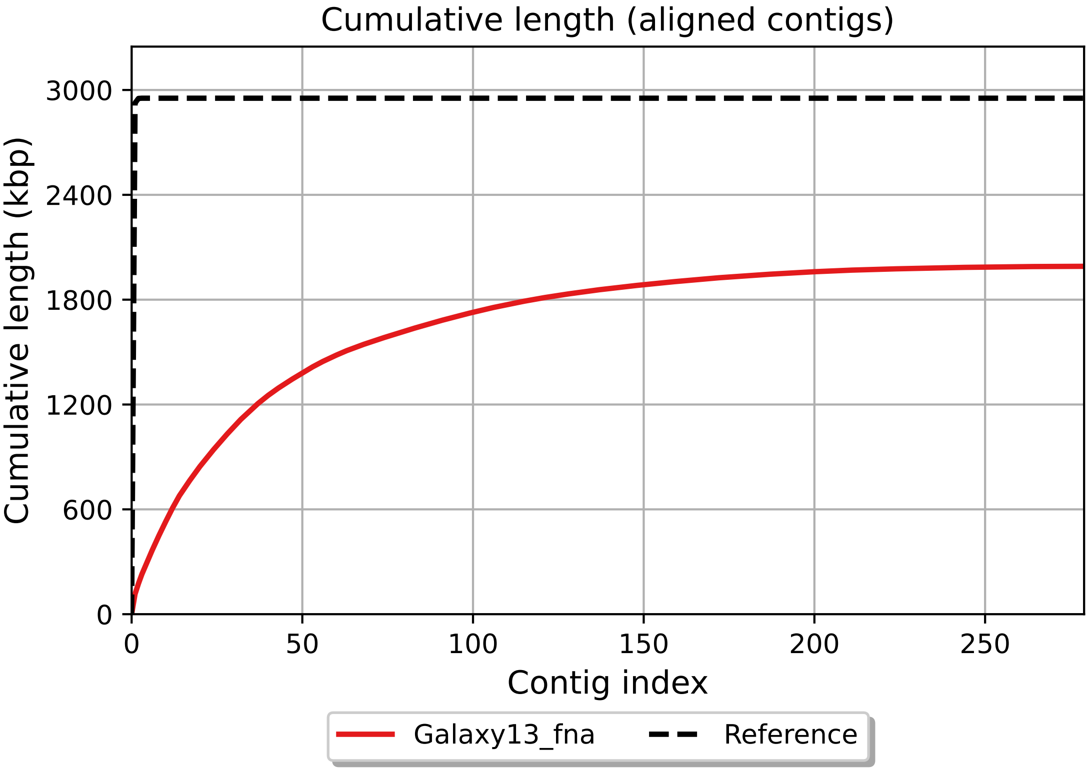

Galaxy13_fna GC content
contigs
0
20
40
60
80
100
0
20
40
60
80
100
GC (%)
Galaxy13_fna

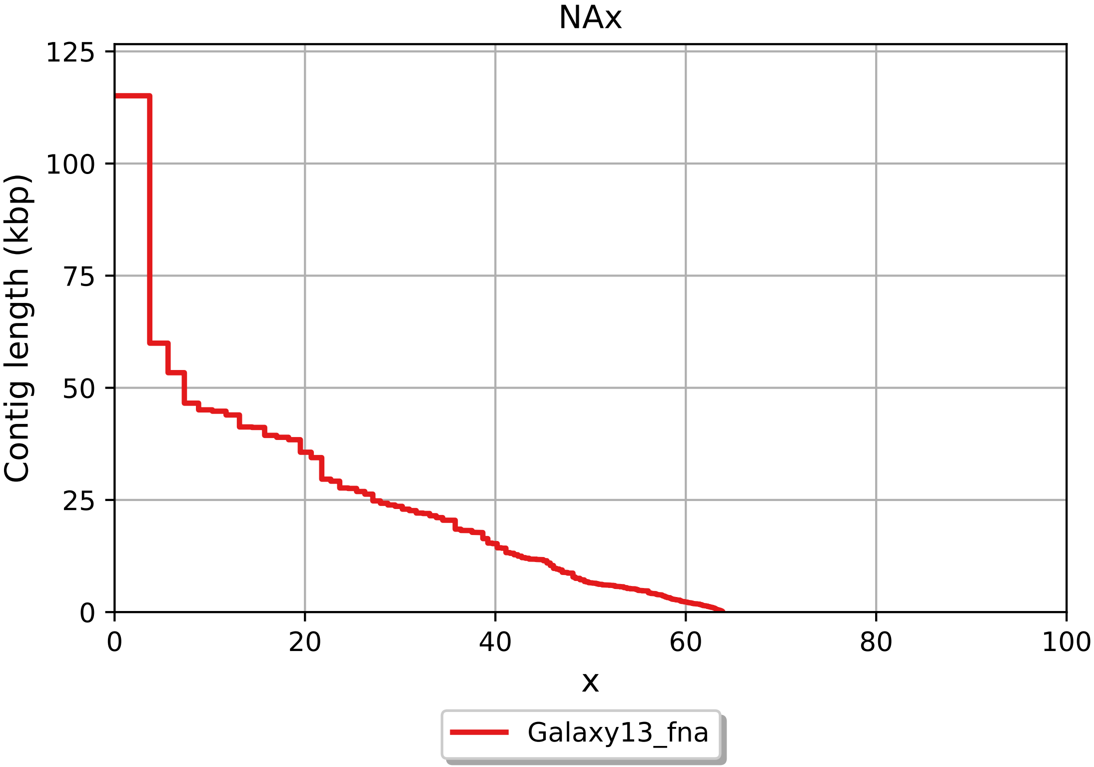

Coverage histogram (bin size: 7x)
Total length (kbp)
500
0
0
147
154
161
168
175
182
189
196
203
210
217
224
231
1072
Coverage depth (x)
Galaxy13_fna

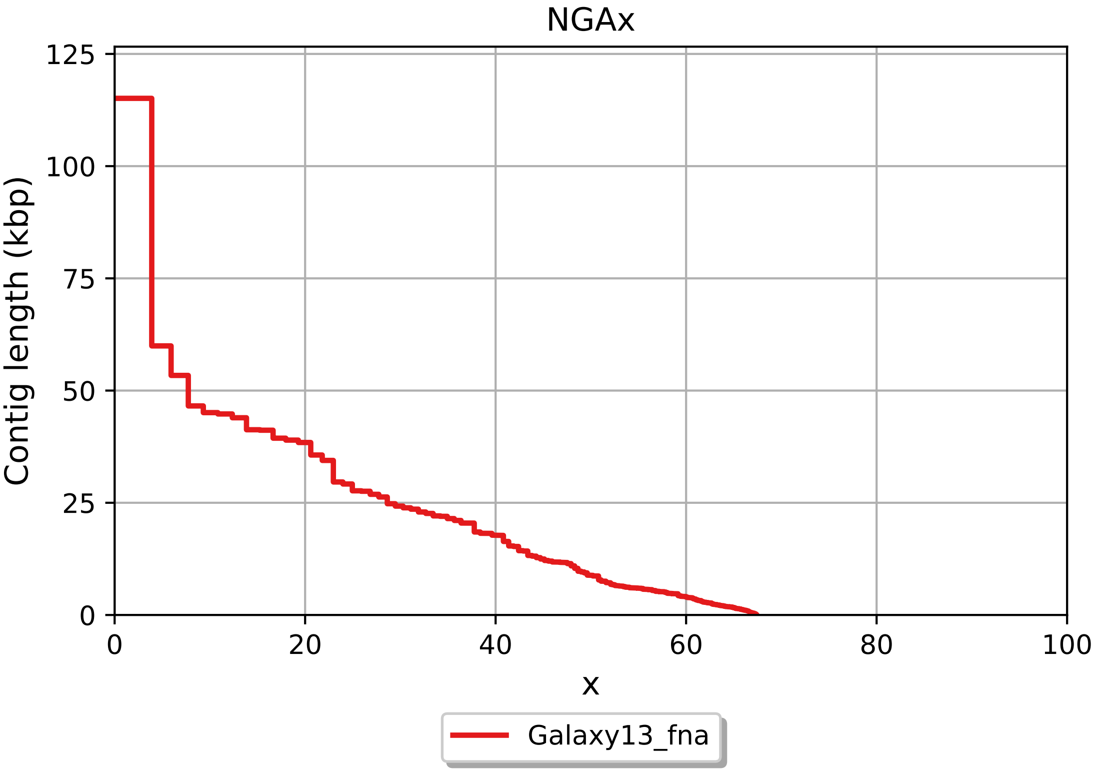

Galaxy13_fna coverage histogram (bin size: 7x)
Total length (kbp)
500
0
0
147
154
161
168
175
182
189
196
203
210
217
224
231
1072
Coverage depth (x)
Galaxy13_fna


Misassemblies
75
60
45
30
15
0
Galaxy13_fna
relocations


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
15
30
45
60
75
Feature space
Galaxy13_fna


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
50
100
150
200
250
Contig index
Galaxy13_fna
Reference


NAx
Contig length (kbp)
0
25
50
75
100
125
0
20
40
60
80
100
x
Galaxy13_fna


NGAx
Contig length (kbp)
125
100
75
50
25
0
0
20
40
60
80
100
x
Galaxy13_fna