Report

	contigs_ERR204044_spades_fasta
# contigs (>= 0 bp)	676
# contigs (>= 1000 bp)	141
Total length (>= 0 bp)	2046030
Total length (>= 1000 bp)	1970061
# contigs	157
Largest contig	103473
Total length	1981480
Reference length	2191149
GC (%)	36.50
Reference GC (%)	37.07
N50	29703
NG50	24960
N90	6389
NG90	895
auN	34268.8
auNG	30989.7
L50	22
LG50	26
L90	80
LG90	144
# misassemblies	124
# misassembled contigs	55
Misassembled contigs length	1376119
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# unaligned contigs	22 + 73 part
Unaligned length	442842
Genome fraction (%)	77.022
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1171.70
# indels per 100 kbp	79.01
Largest alignment	51210
Total aligned length	1531453
NA50	8165
NGA50	6433
NA90	-
NGA90	-
auNA	10891.4
auNGA	9849.2
LA50	65
LGA50	80
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

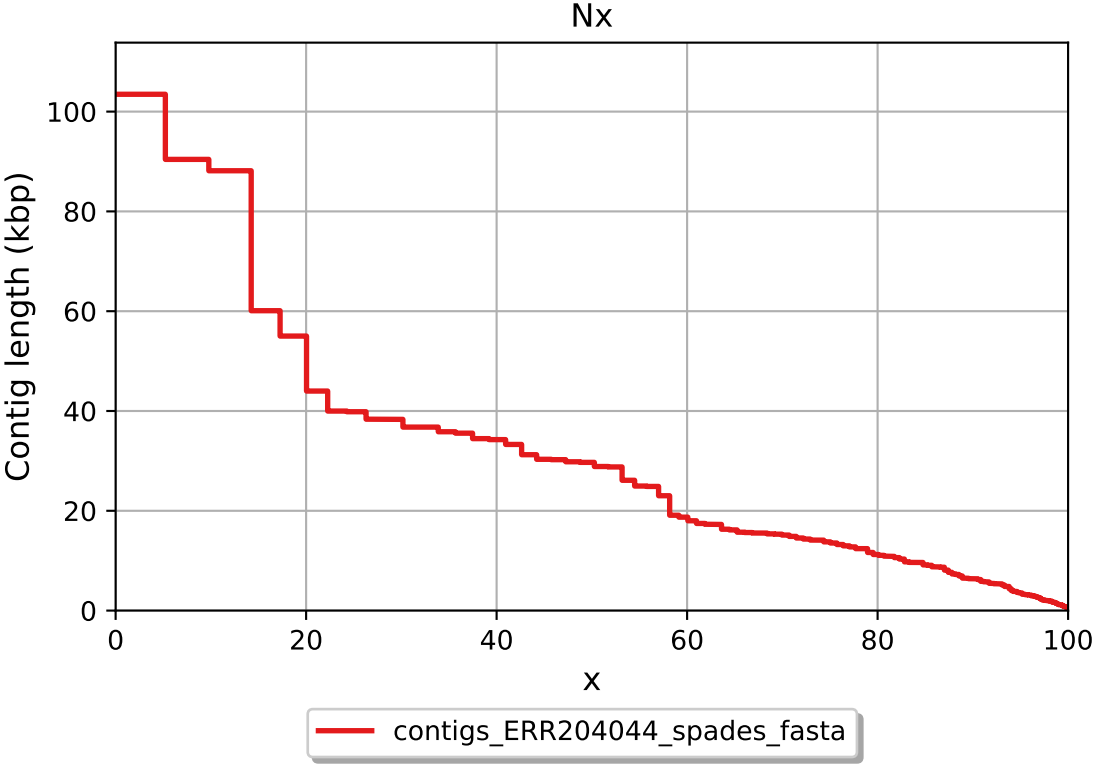
	contigs_ERR204044_spades_fasta
# misassemblies	124
# contig misassemblies	124
# c. relocations	124
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	55
Misassembled contigs length	1376119
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	17944
# indels	1210
# indels (<= 5 bp)	923
# indels (> 5 bp)	287
Indels length	8290

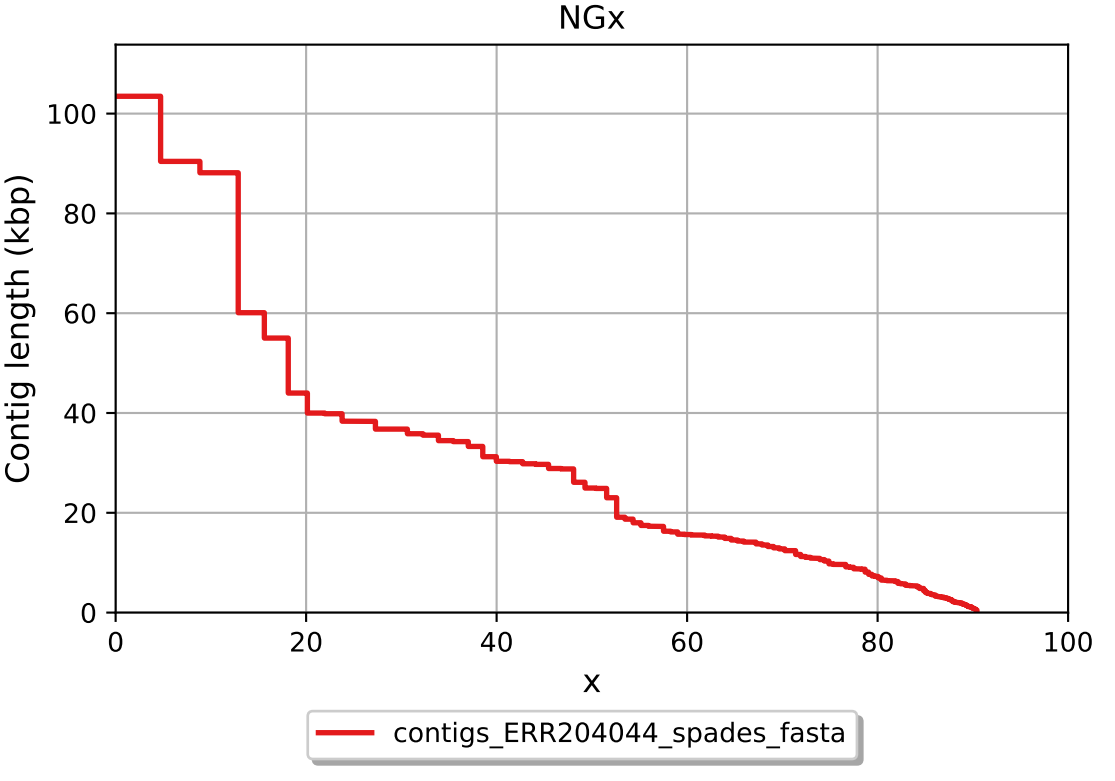
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

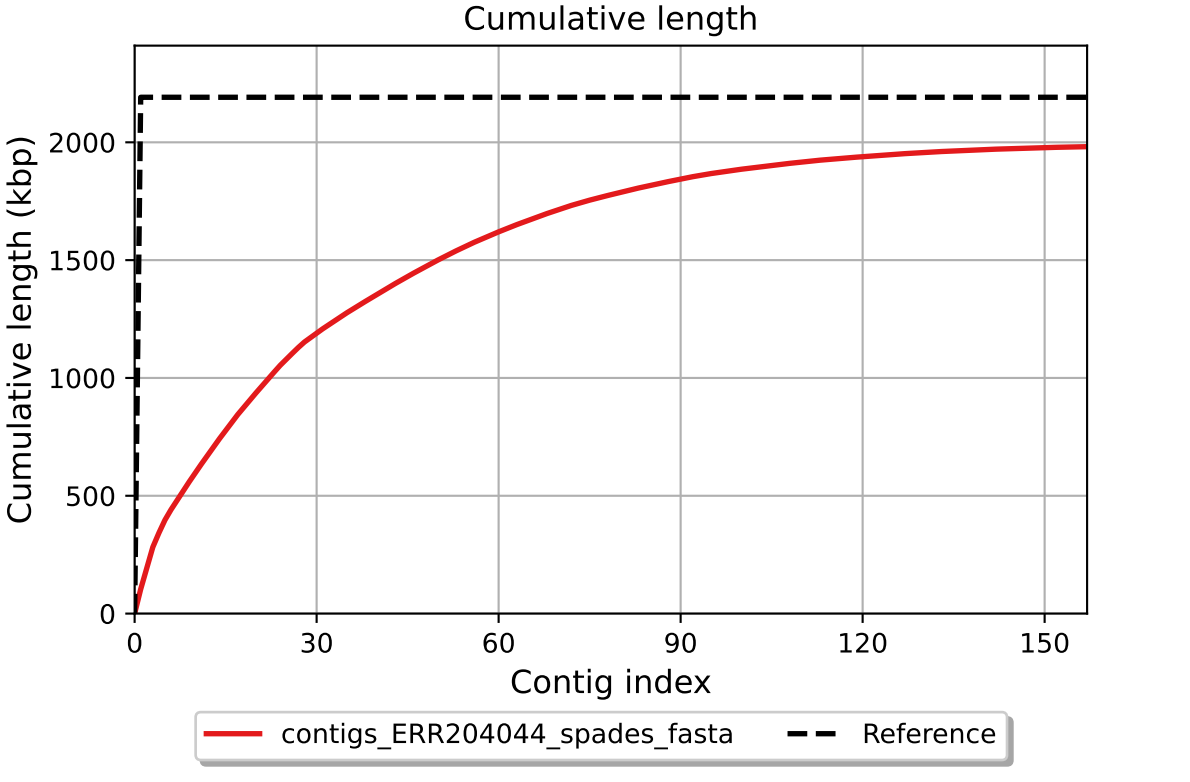
Unaligned report

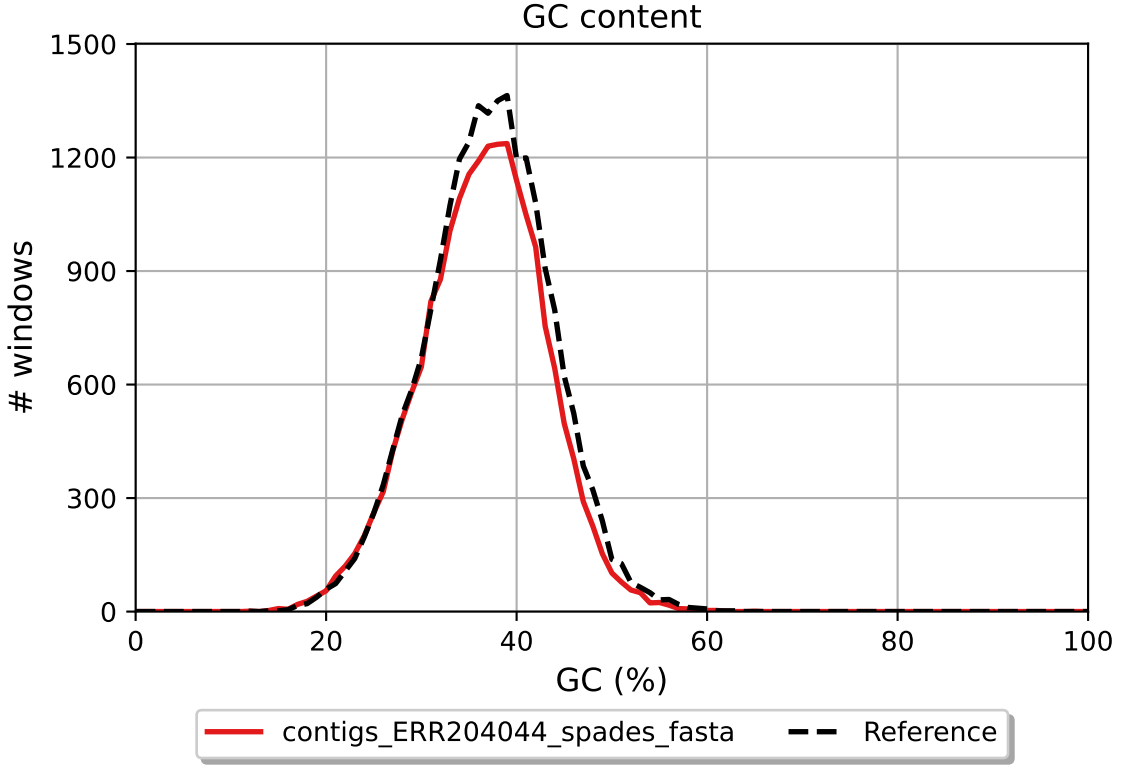
	contigs_ERR204044_spades_fasta
# fully unaligned contigs	22
Fully unaligned length	61359
# partially unaligned contigs	73
Partially unaligned length	381483
# N's	0

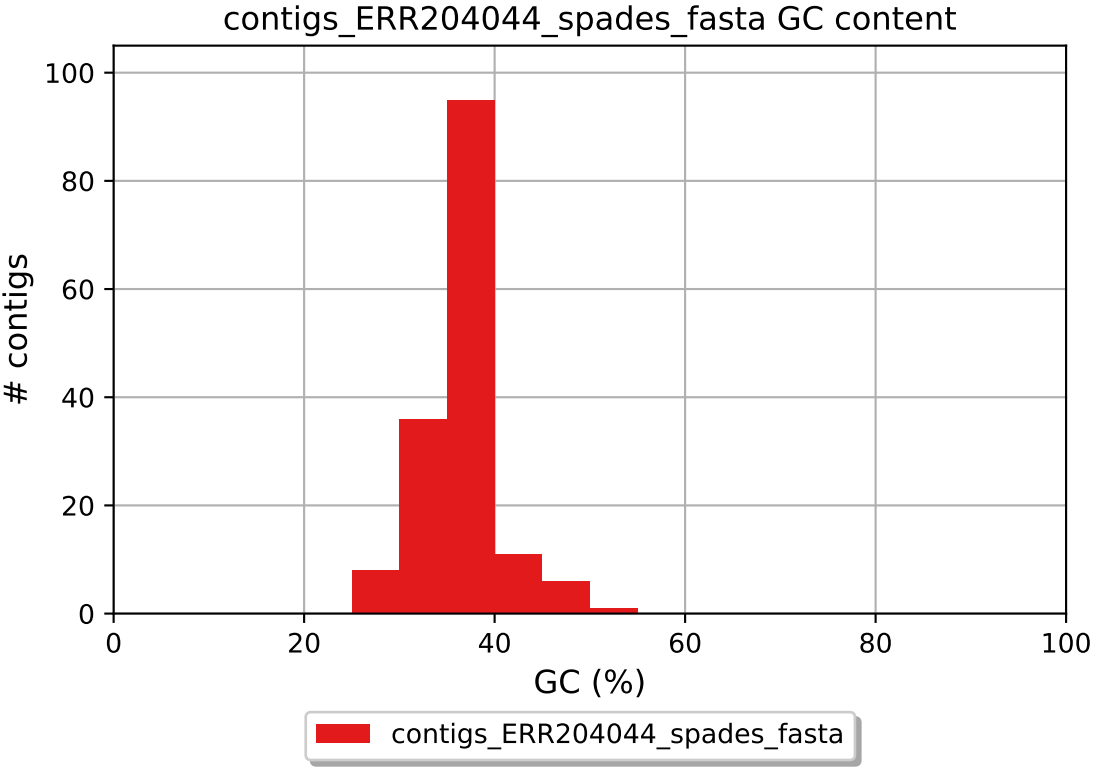
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

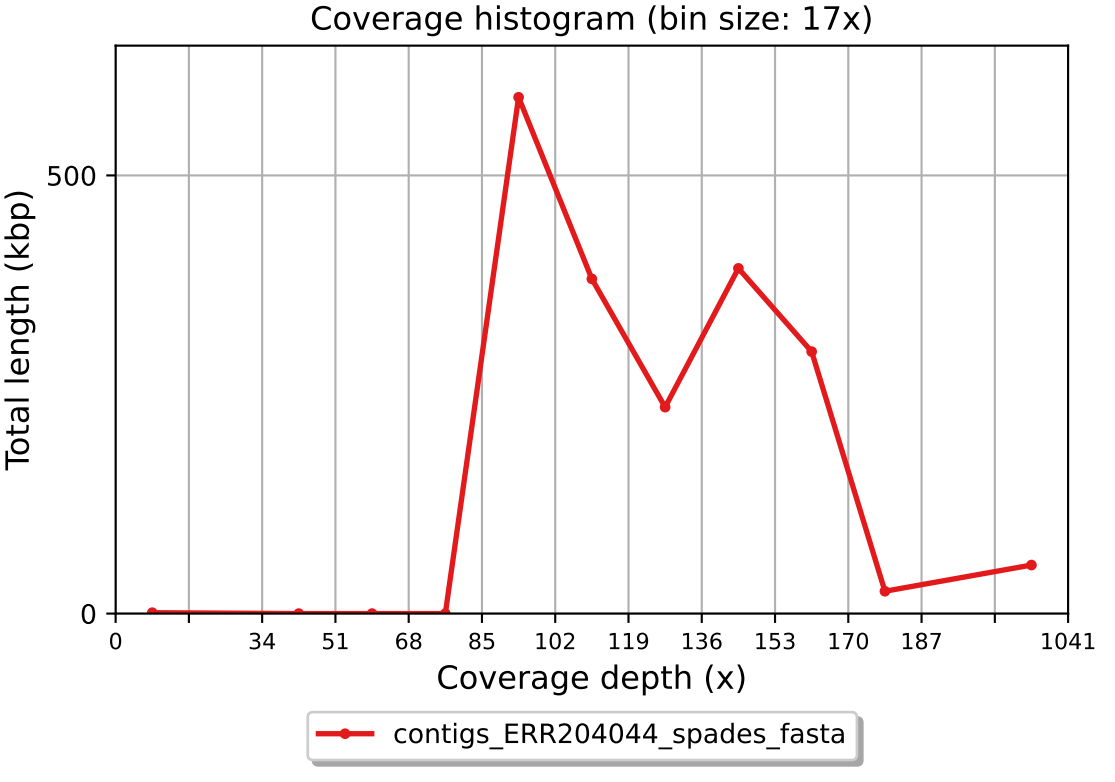

Nx
Contig length (kbp)
0
20
40
60
80
100
0
20
40
60
80
100
x
contigs_ERR204044_spades_fasta

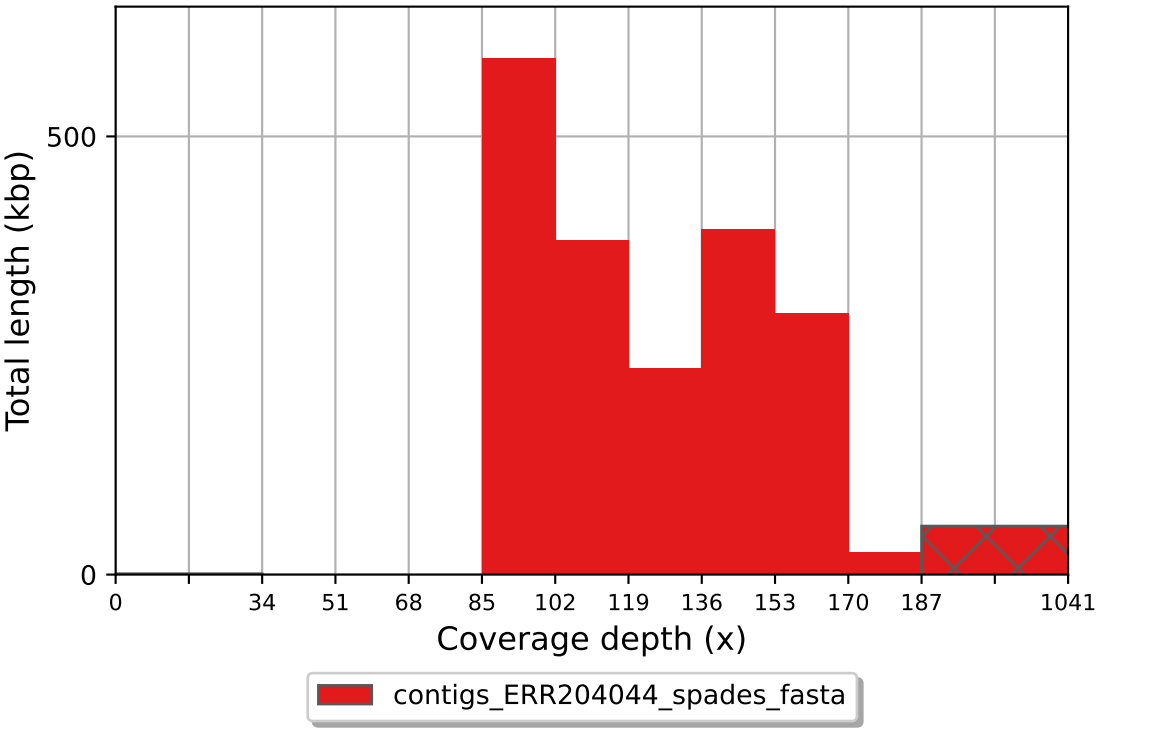

NGx
Contig length (kbp)
0
20
40
60
80
100
0
20
40
60
80
100
x
contigs_ERR204044_spades_fasta

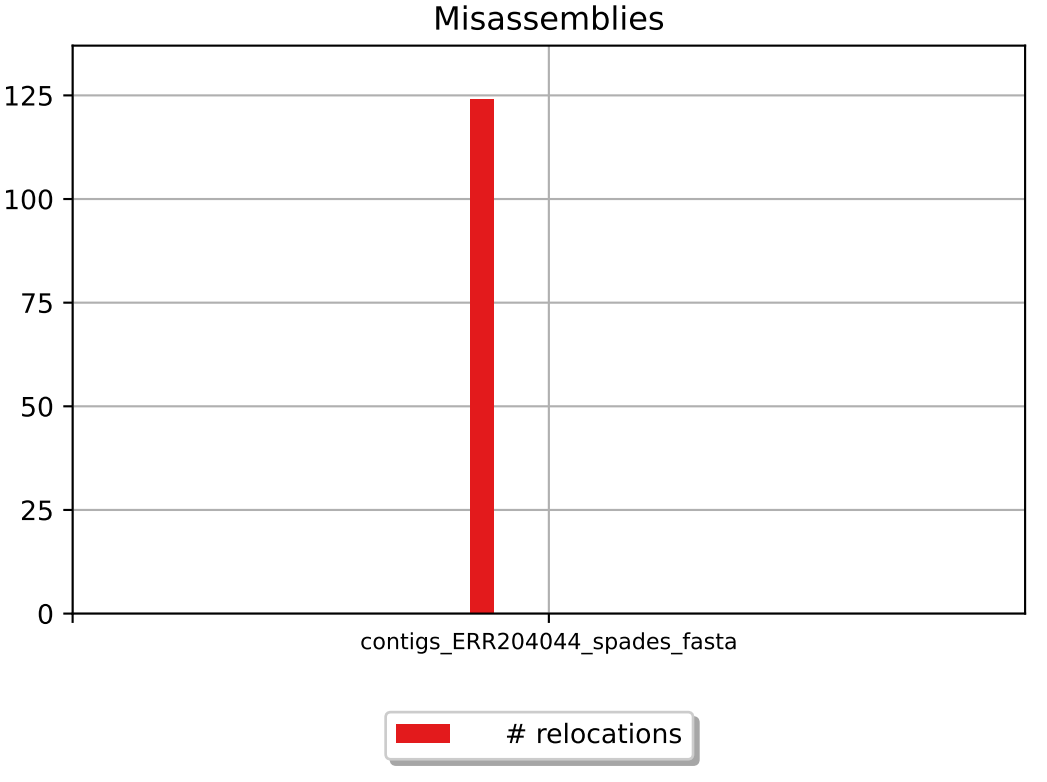

Cumulative length
Cumulative length (kbp)
2000
1500
1000
500
0
0
30
60
90
120
150
Contig index
contigs_ERR204044_spades_fasta
Reference

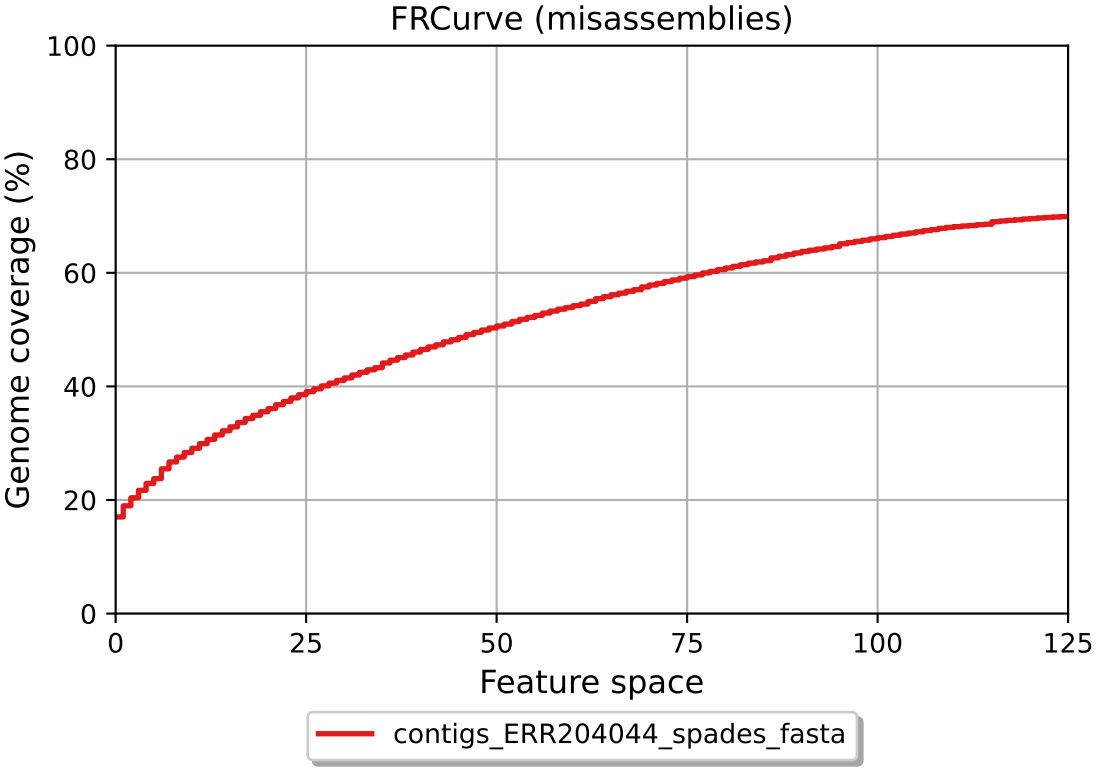

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
contigs_ERR204044_spades_fasta
Reference

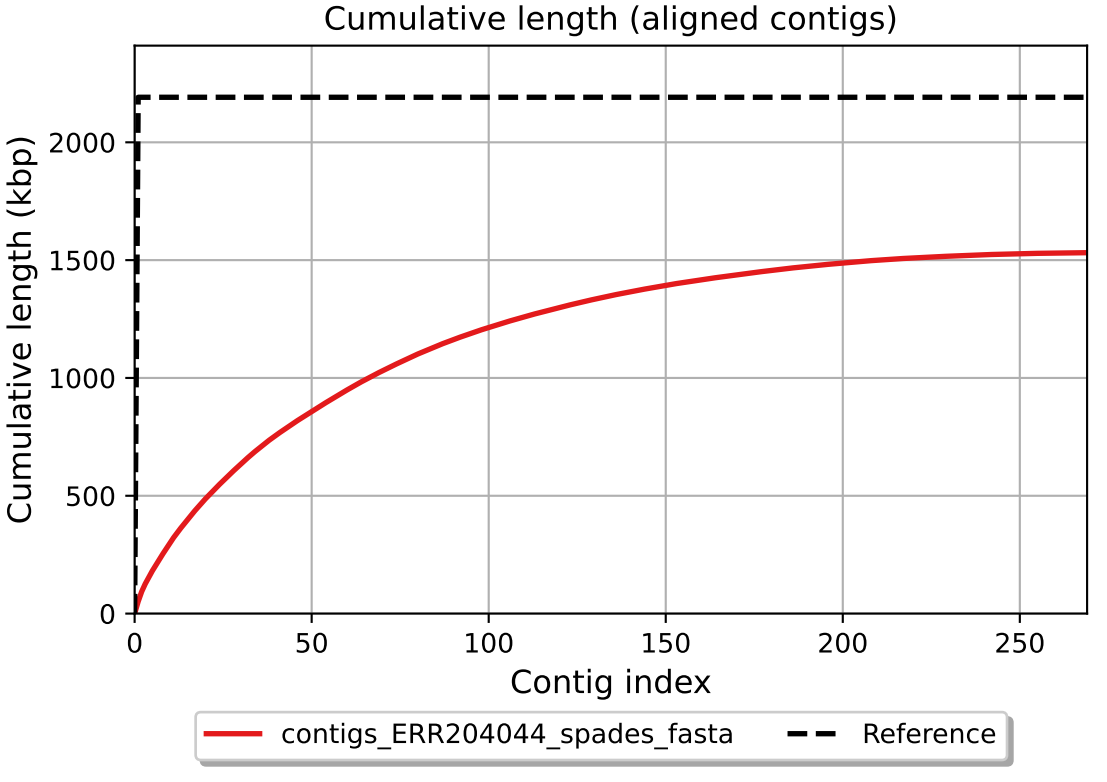

contigs_ERR204044_spades_fasta GC content
contigs
GC (%)
0
20
40
60
80
100
contigs_ERR204044_spades_fasta

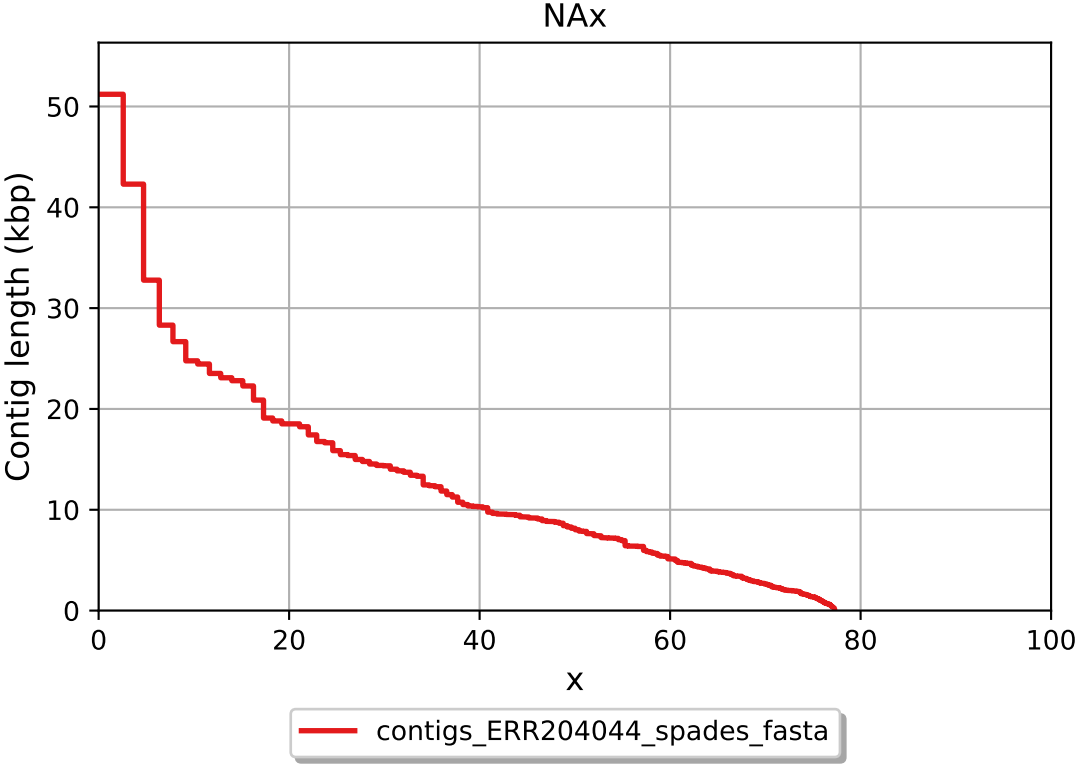

Coverage histogram (bin size: 17x)
Total length (kbp)
500
0
0
34
51
68
85
102
119
136
153
170
187
1041
Coverage depth (x)
contigs_ERR204044_spades_fasta

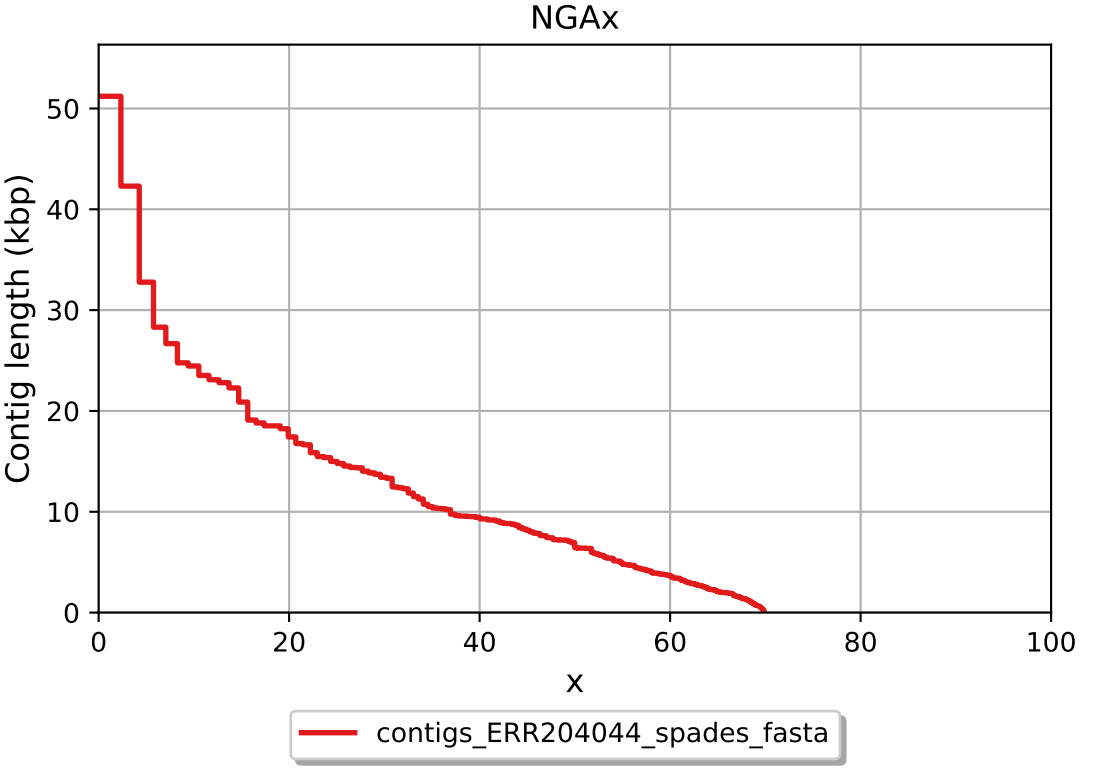

contigs_ERR204044_spades_fasta coverage histogram (bin size: 17x)
Total length (kbp)
500
0
0
34
51
68
85
102
119
136
153
170
187
1041
Coverage depth (x)
contigs_ERR204044_spades_fasta


Misassemblies
125
100
75
50
25
0
contigs_ERR204044_spades_fasta
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
25
50
75
100
125
Feature space
contigs_ERR204044_spades_fasta


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1500
1000
500
0
0
50
100
150
200
250
Contig index
contigs_ERR204044_spades_fasta
Reference


NAx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
contigs_ERR204044_spades_fasta


NGAx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
contigs_ERR204044_spades_fasta