Report

	ERR5770797
# contigs (>= 0 bp)	208
# contigs (>= 1000 bp)	123
# contigs (>= 5000 bp)	86
# contigs (>= 10000 bp)	66
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	3955156
Total length (>= 1000 bp)	3929625
Total length (>= 5000 bp)	3826855
Total length (>= 10000 bp)	3679954
Total length (>= 25000 bp)	3410760
Total length (>= 50000 bp)	2649123
# contigs	137
Largest contig	222551
Total length	3938546
Reference length	3981941
GC (%)	38.99
Reference GC (%)	39.17
N50	71836
NG50	70034
N90	15601
NG90	13842
auN	88307.8
auNG	87345.4
L50	16
LG50	17
L90	55
LG90	58
# misassemblies	40
# misassembled contigs	26
Misassembled contigs length	2177706
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	26 + 52 part
Unaligned length	518151
Genome fraction (%)	85.689
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1721.57
# indels per 100 kbp	35.90
# genomic features	3325 + 106 part
Largest alignment	193142
Total aligned length	3414675
NA50	41973
NGA50	40379
NA90	-
NGA90	-
auNA	50964.9
auNGA	50409.5
LA50	27
LGA50	28
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

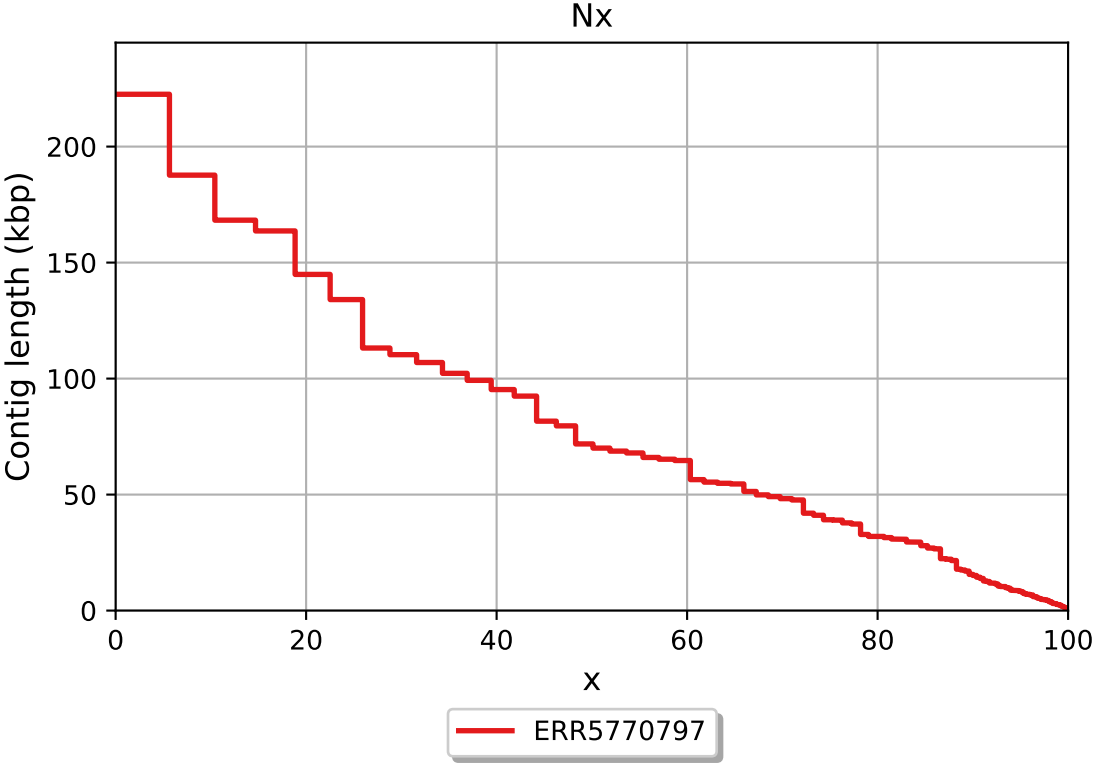
	ERR5770797
# misassemblies	40
# contig misassemblies	40
# c. relocations	40
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	26
Misassembled contigs length	2177706
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	58786
# indels	1226
# indels (<= 5 bp)	1148
# indels (> 5 bp)	78
Indels length	4009

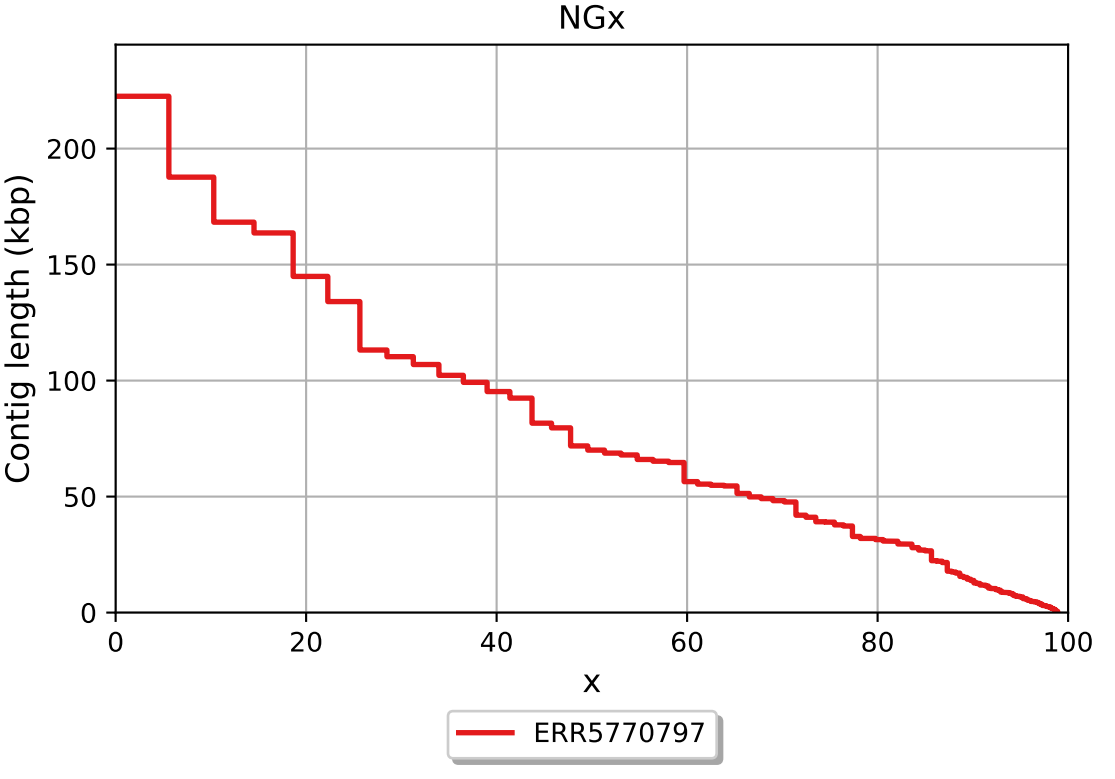
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

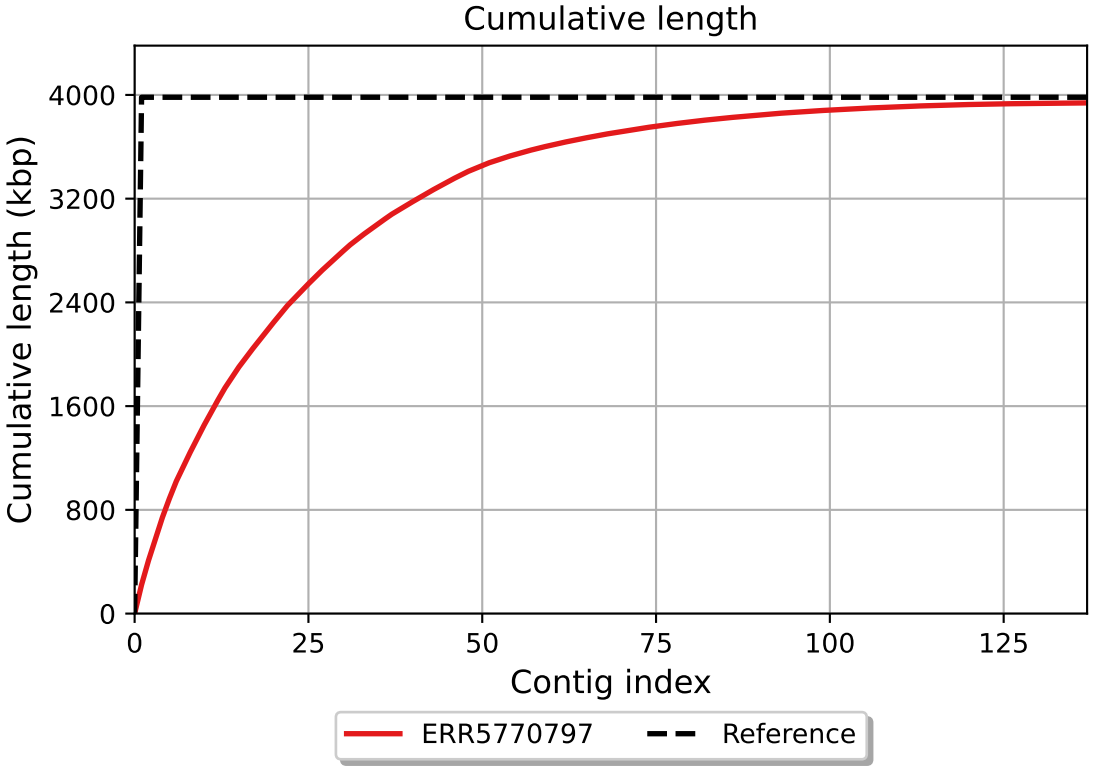
Unaligned report

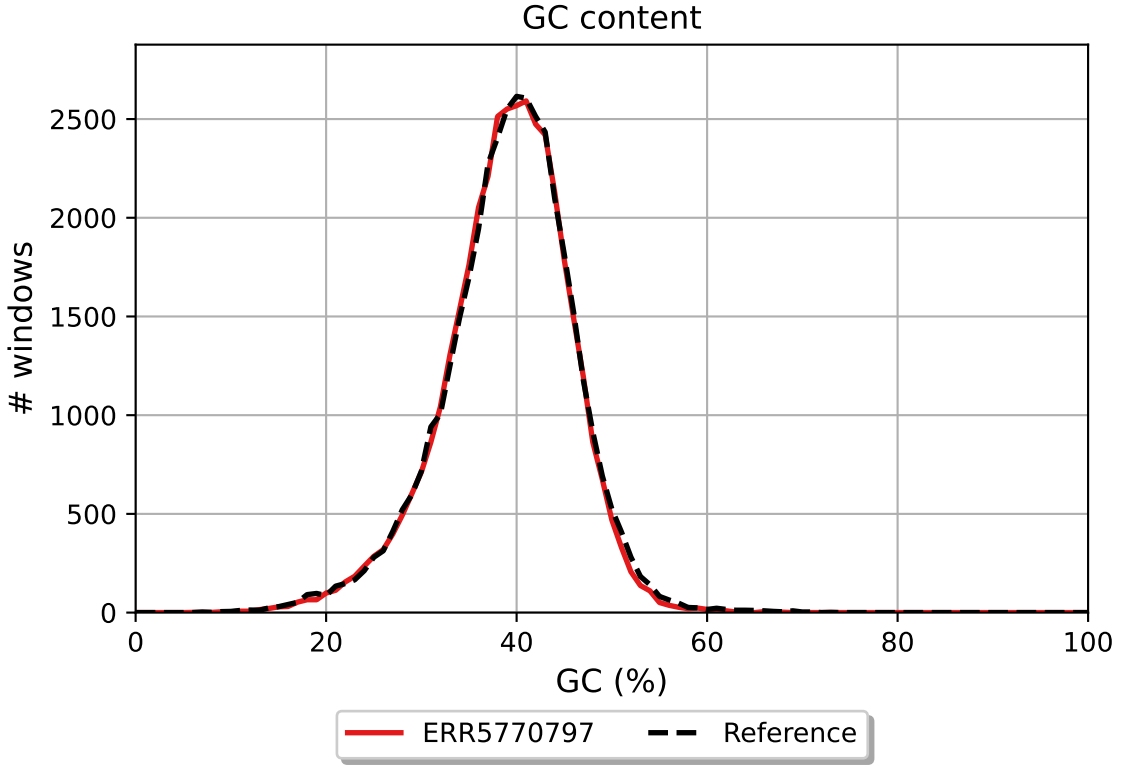
	ERR5770797
# fully unaligned contigs	26
Fully unaligned length	141951
# partially unaligned contigs	52
Partially unaligned length	376200
# N's	0

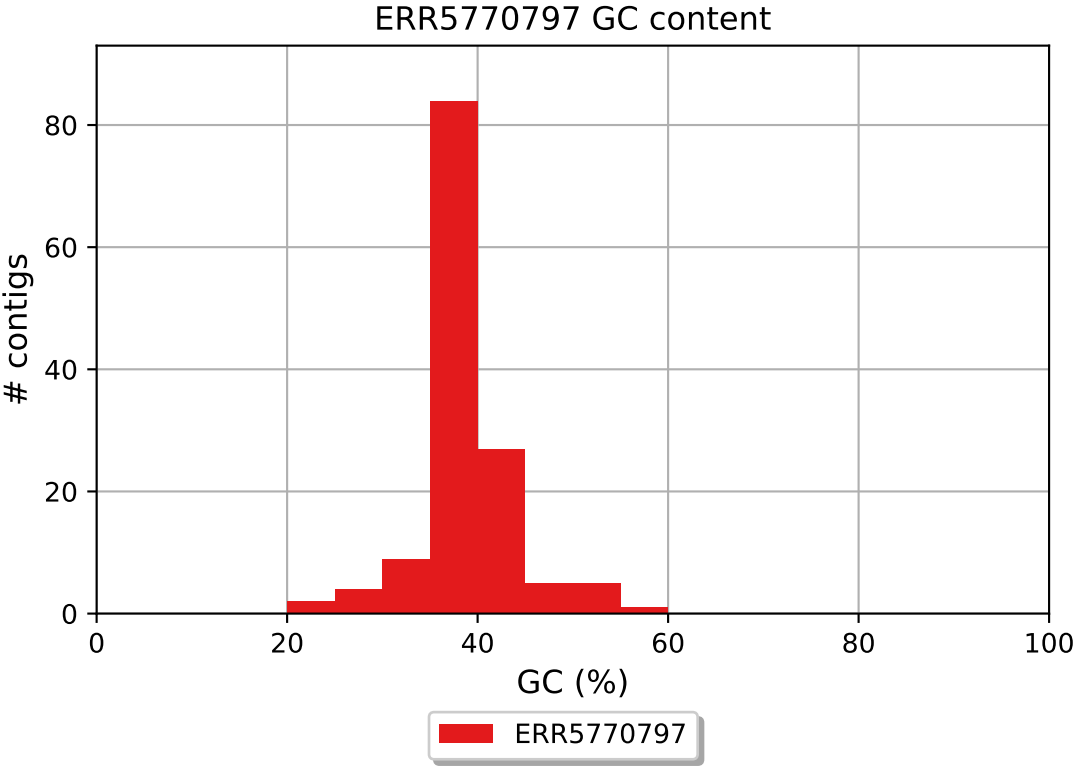
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

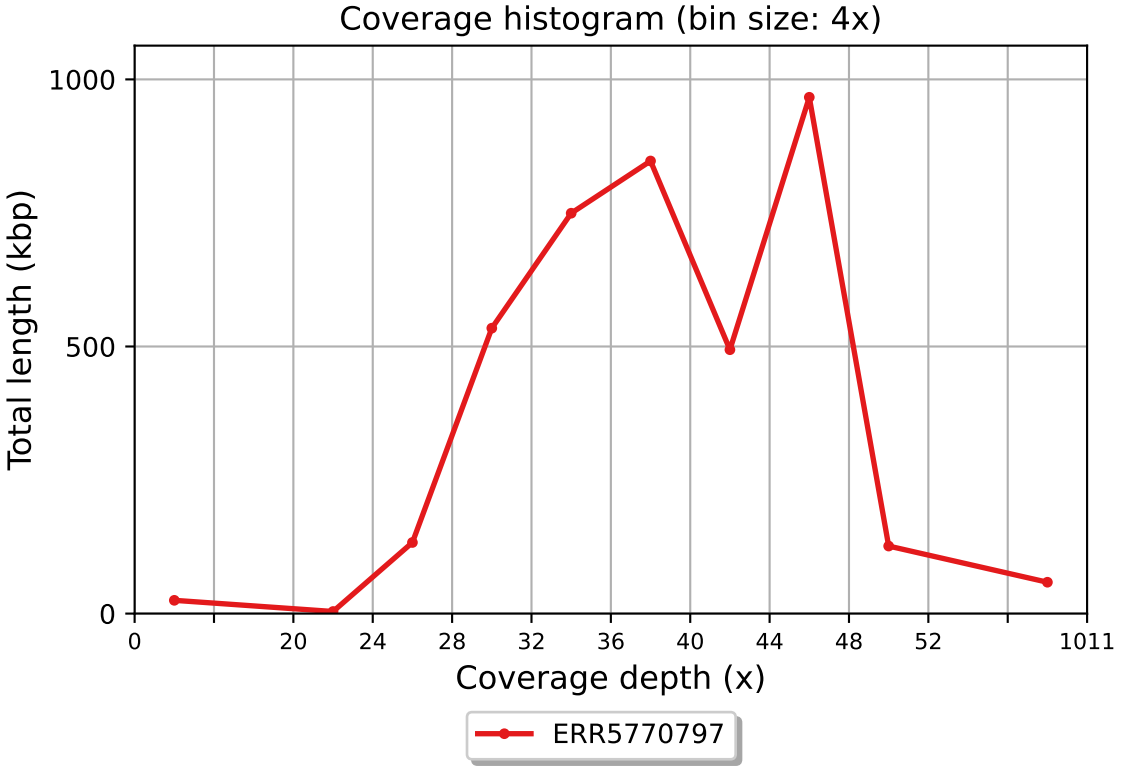

Nx
Contig length (kbp)
200
150
100
50
0
0
20
40
60
80
100
x
ERR5770797

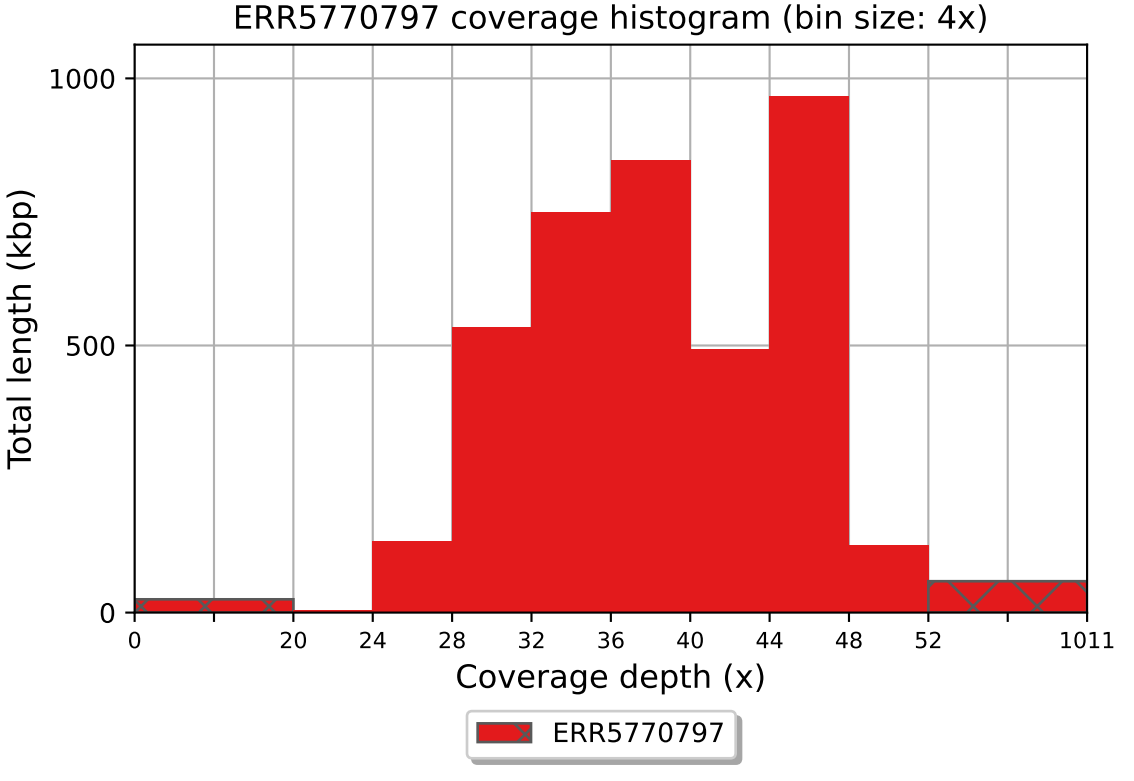

NGx
Contig length (kbp)
200
150
100
50
0
0
20
40
60
80
100
x
ERR5770797

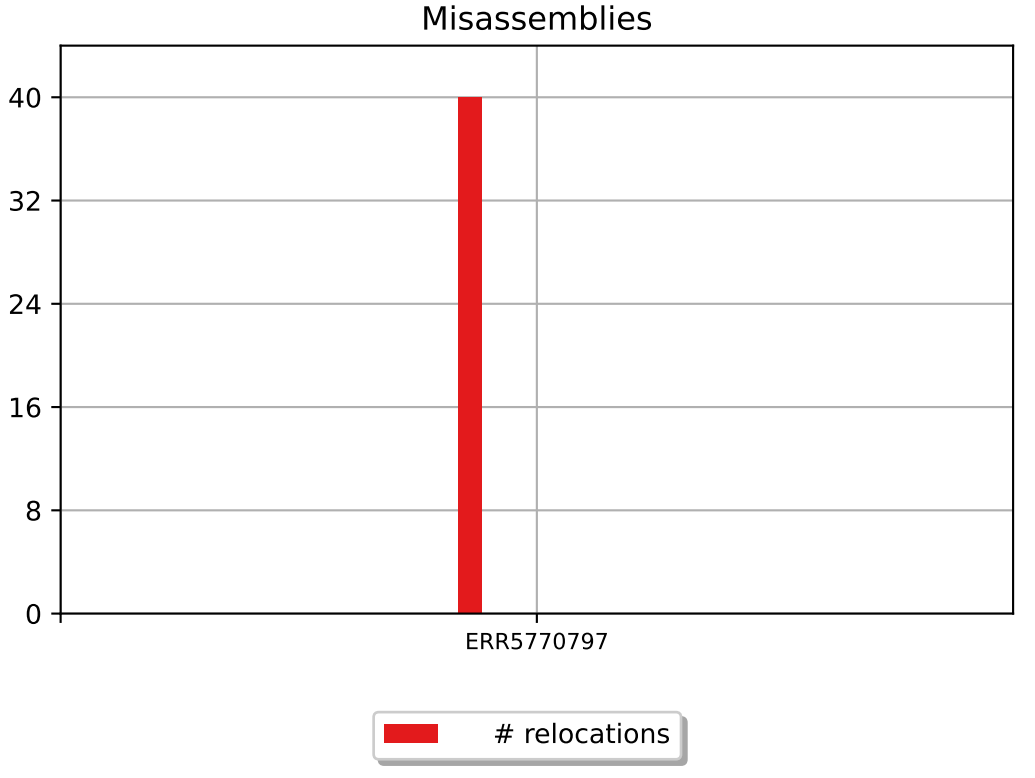

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
25
50
75
100
125
Contig index
ERR5770797
Reference

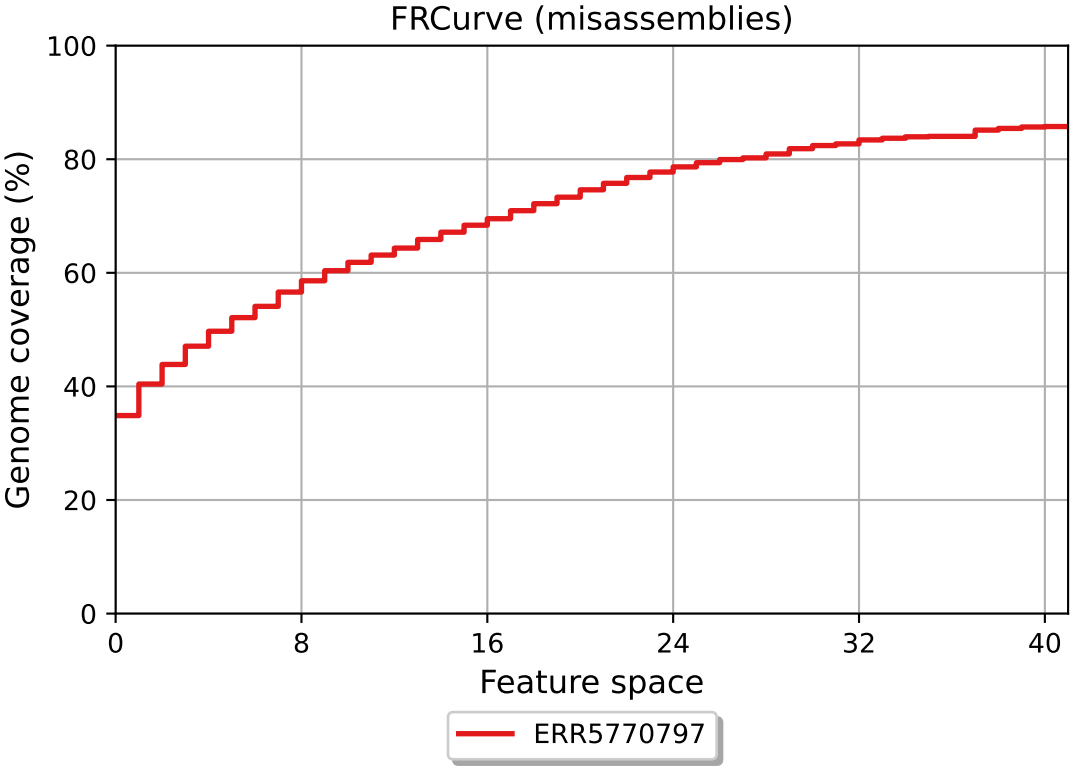

GC content
windows
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
ERR5770797
Reference

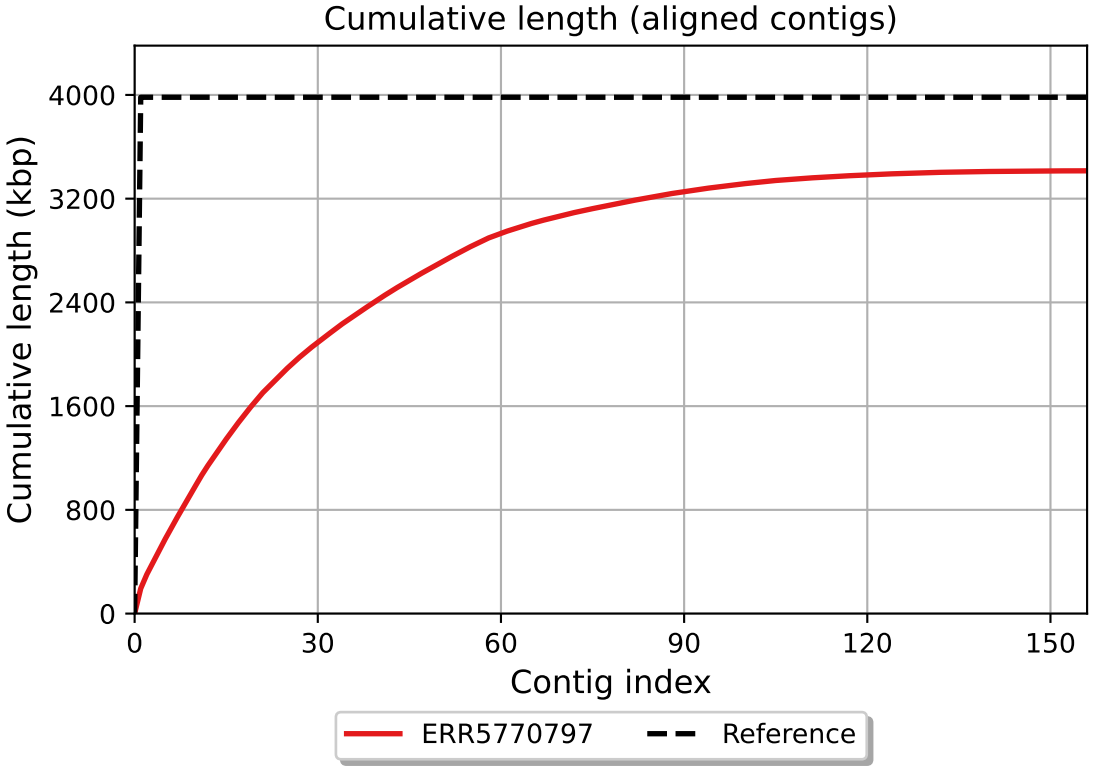

ERR5770797 GC content
contigs
0
20
40
60
80
0
20
40
60
80
100
GC (%)
ERR5770797

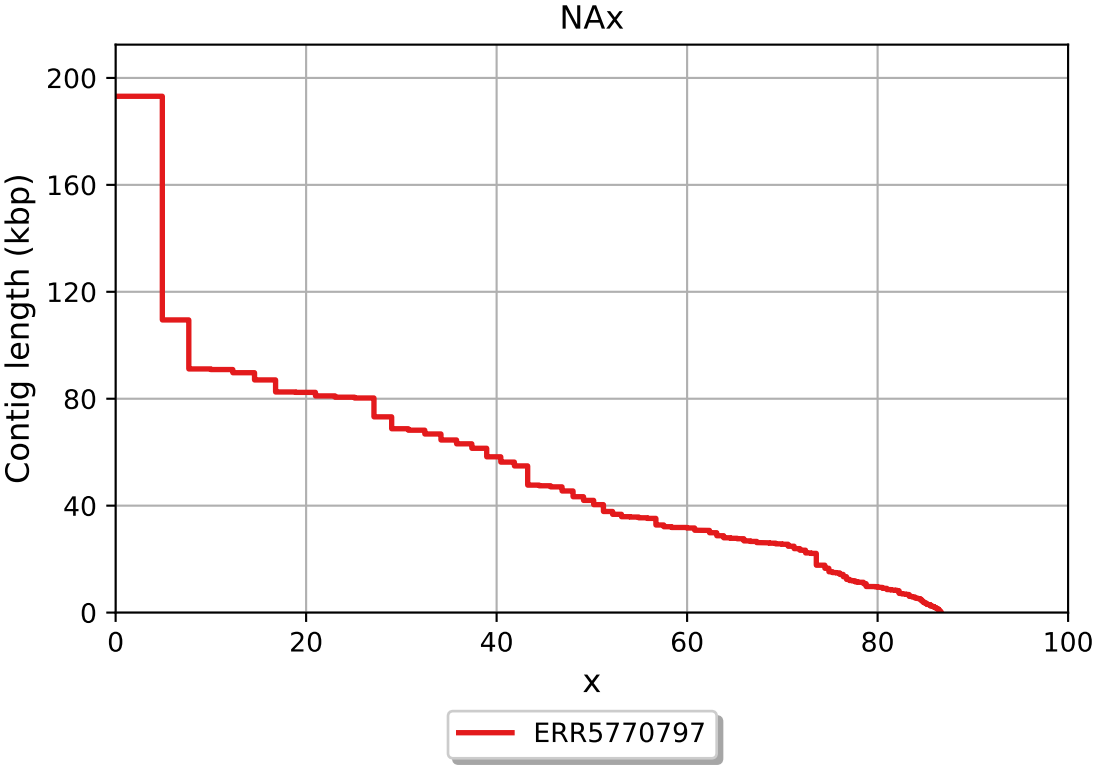

Coverage histogram (bin size: 4x)
Total length (kbp)
1000
500
0
0
20
24
28
32
36
40
44
48
52
1011
Coverage depth (x)
ERR5770797

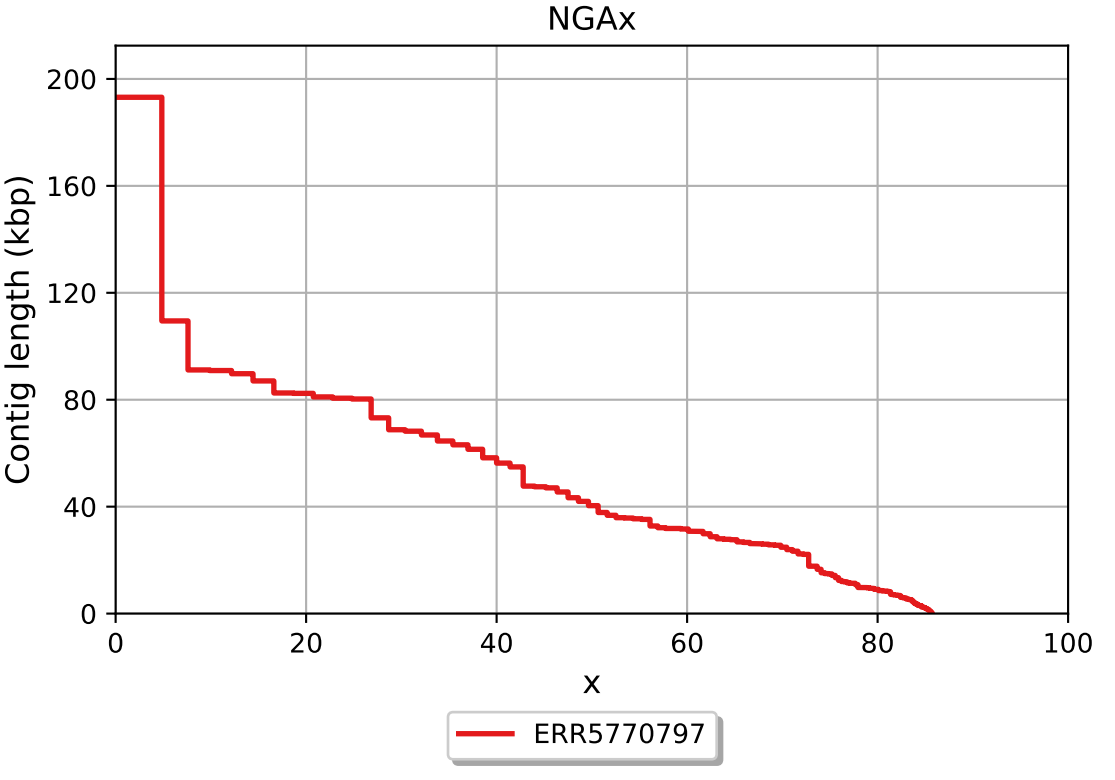

ERR5770797 coverage histogram (bin size: 4x)
Total length (kbp)
1000
500
0
0
20
24
28
32
36
40
44
48
52
1011
Coverage depth (x)
ERR5770797

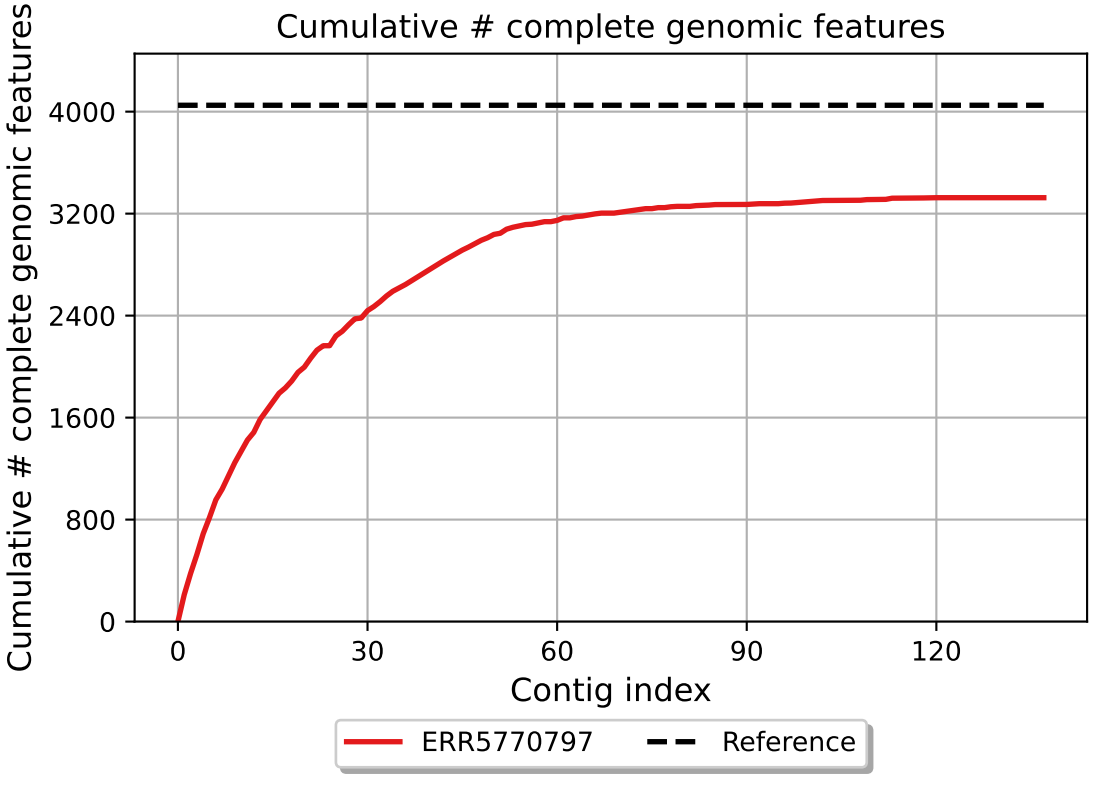

Misassemblies
40
32
24
16
8
0
ERR5770797
relocations

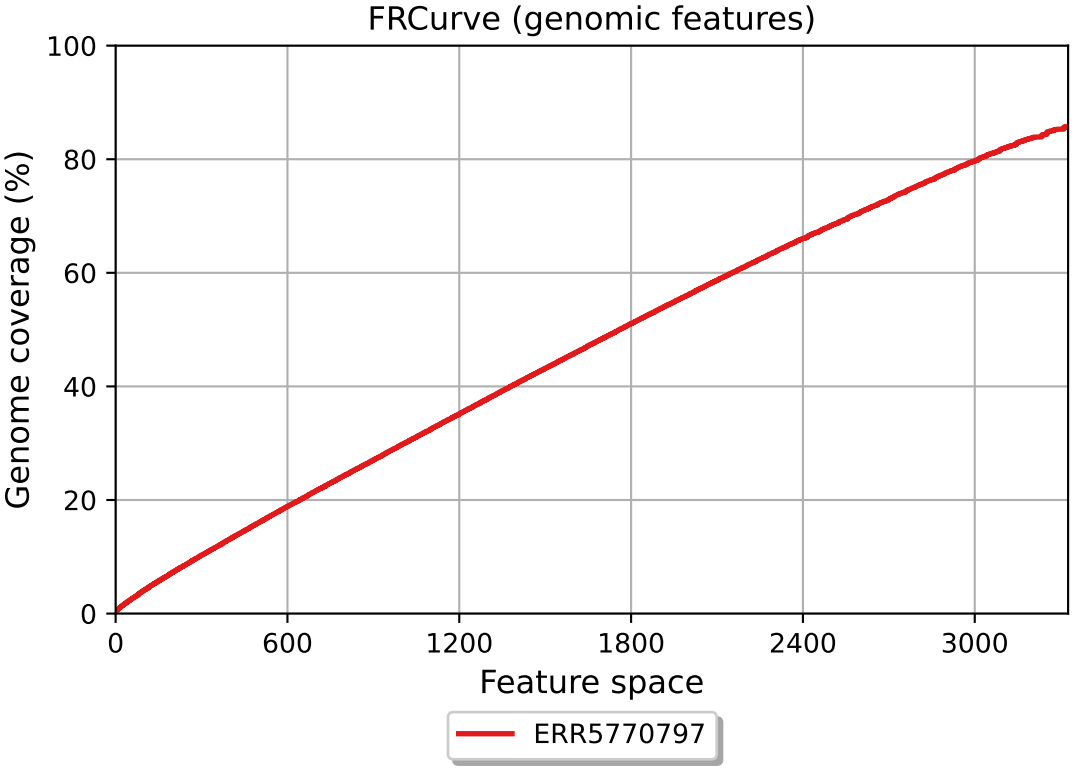

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
8
16
24
32
40
Feature space
ERR5770797


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
30
60
90
120
150
Contig index
ERR5770797
Reference


NAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
ERR5770797


NGAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
ERR5770797


Cumulative # complete genomic features
Cumulative # complete genomic features
4000
3200
2400
1600
800
0
0
30
60
90
120
Contig index
ERR5770797
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
600
1200
1800
2400
3000
Feature space
ERR5770797