Report

	ERR5770806
# contigs (>= 0 bp)	741
# contigs (>= 1000 bp)	485
# contigs (>= 5000 bp)	183
# contigs (>= 10000 bp)	117
# contigs (>= 25000 bp)	64
# contigs (>= 50000 bp)	18
Total length (>= 0 bp)	4985157
Total length (>= 1000 bp)	4860298
Total length (>= 5000 bp)	4168014
Total length (>= 10000 bp)	3710284
Total length (>= 25000 bp)	2911113
Total length (>= 50000 bp)	1322666
# contigs	605
Largest contig	138505
Total length	4941043
Reference length	3981941
GC (%)	38.91
Reference GC (%)	39.17
N50	29991
NG50	36485
N90	2801
NG90	11424
auN	36423.9
auNG	45197.1
L50	49
LG50	34
L90	257
LG90	106
# misassemblies	43
# misassembled contigs	33
Misassembled contigs length	1015759
# local misassemblies	33
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	10
# unaligned contigs	251 + 105 part
Unaligned length	1496339
Genome fraction (%)	83.679
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1835.60
# indels per 100 kbp	45.01
# genomic features	3127 + 235 part
Largest alignment	95012
Total aligned length	3428251
NA50	14517
NGA50	25714
NA90	-
NGA90	-
auNA	22324.5
auNGA	27701.6
LA50	75
LGA50	49
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

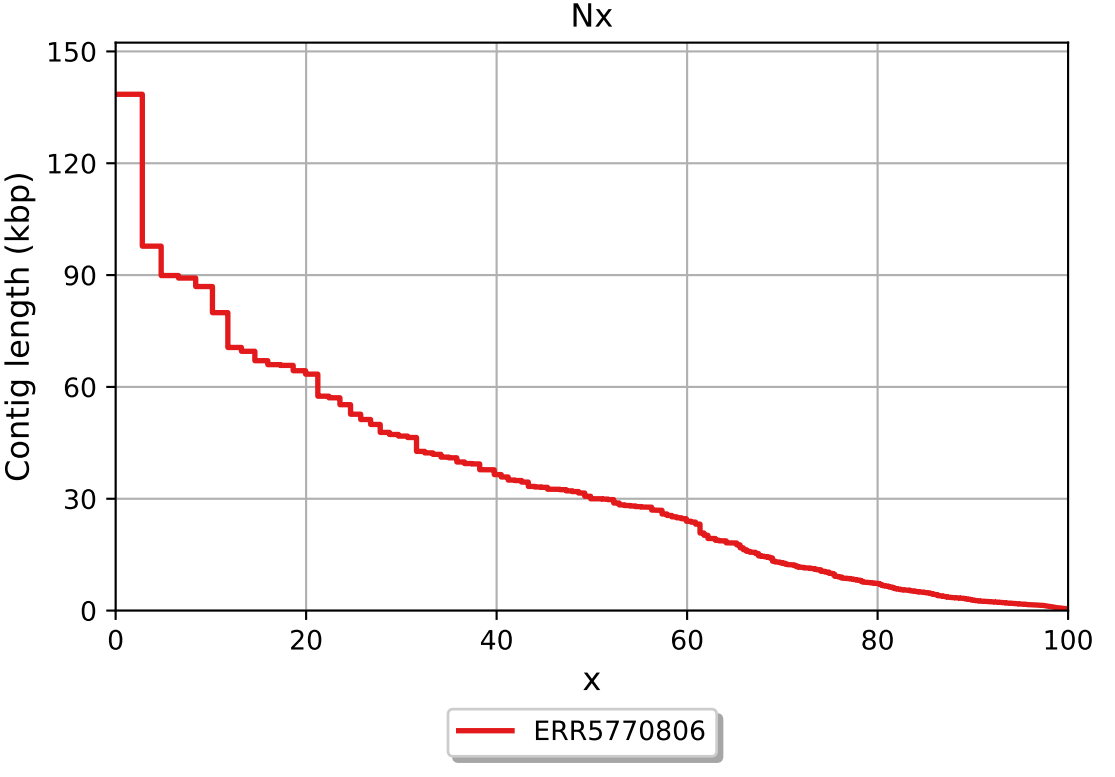
	ERR5770806
# misassemblies	43
# contig misassemblies	43
# c. relocations	43
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	33
Misassembled contigs length	1015759
# local misassemblies	33
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	10
# mismatches	62929
# indels	1543
# indels (<= 5 bp)	1448
# indels (> 5 bp)	95
Indels length	4707

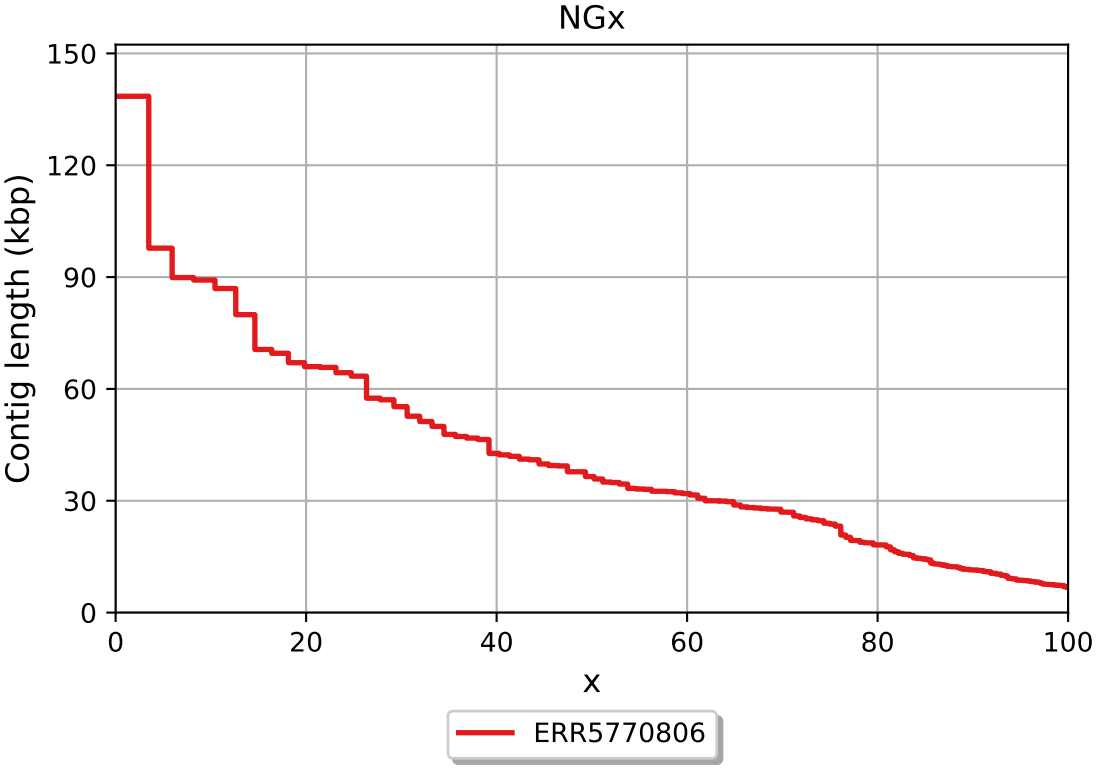
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

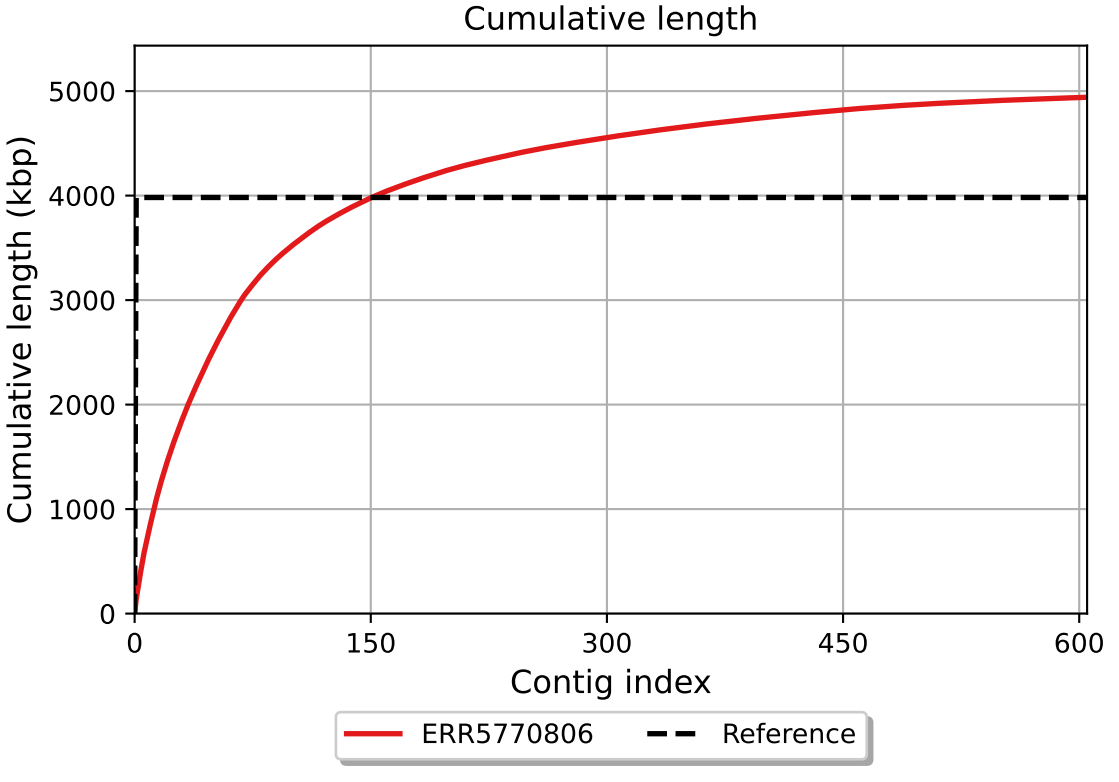
Unaligned report

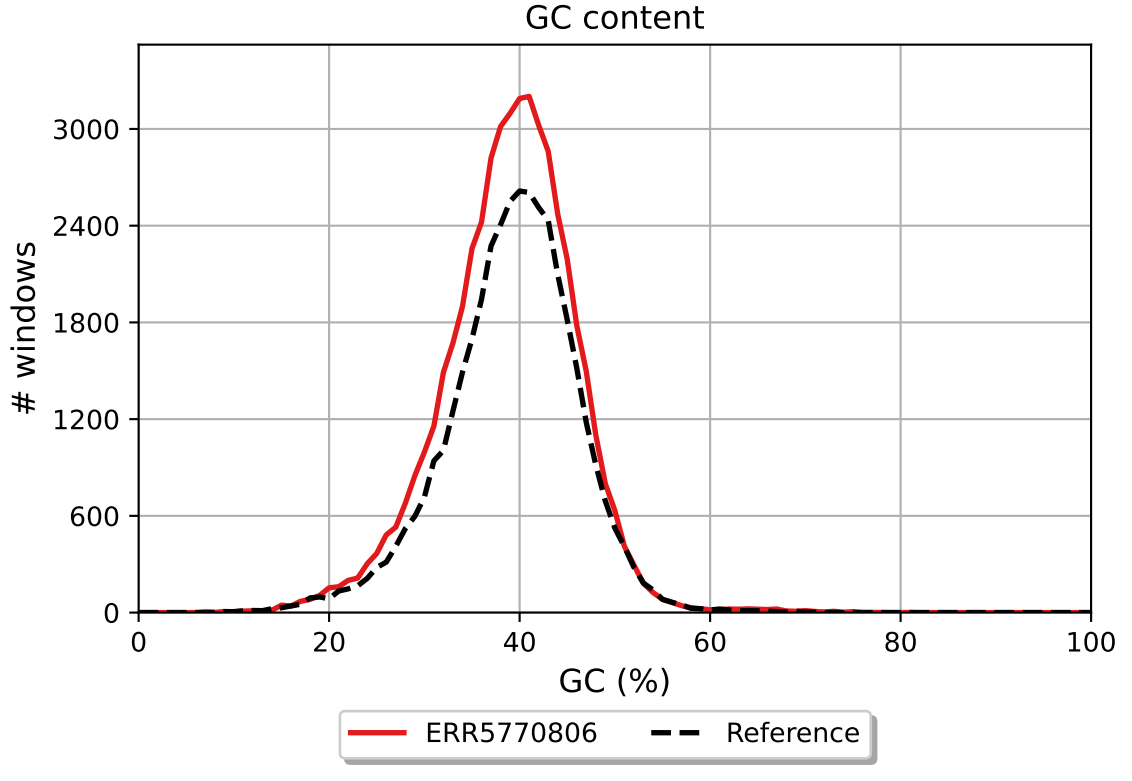
	ERR5770806
# fully unaligned contigs	251
Fully unaligned length	880995
# partially unaligned contigs	105
Partially unaligned length	615344
# N's	0

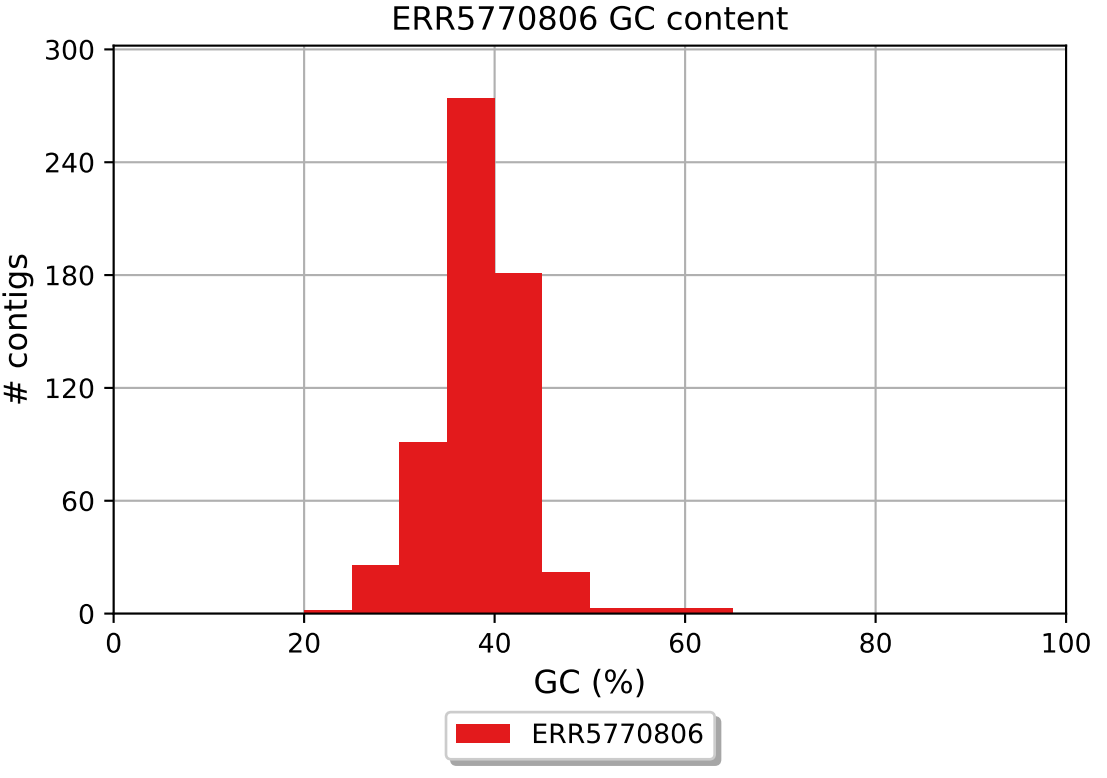
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

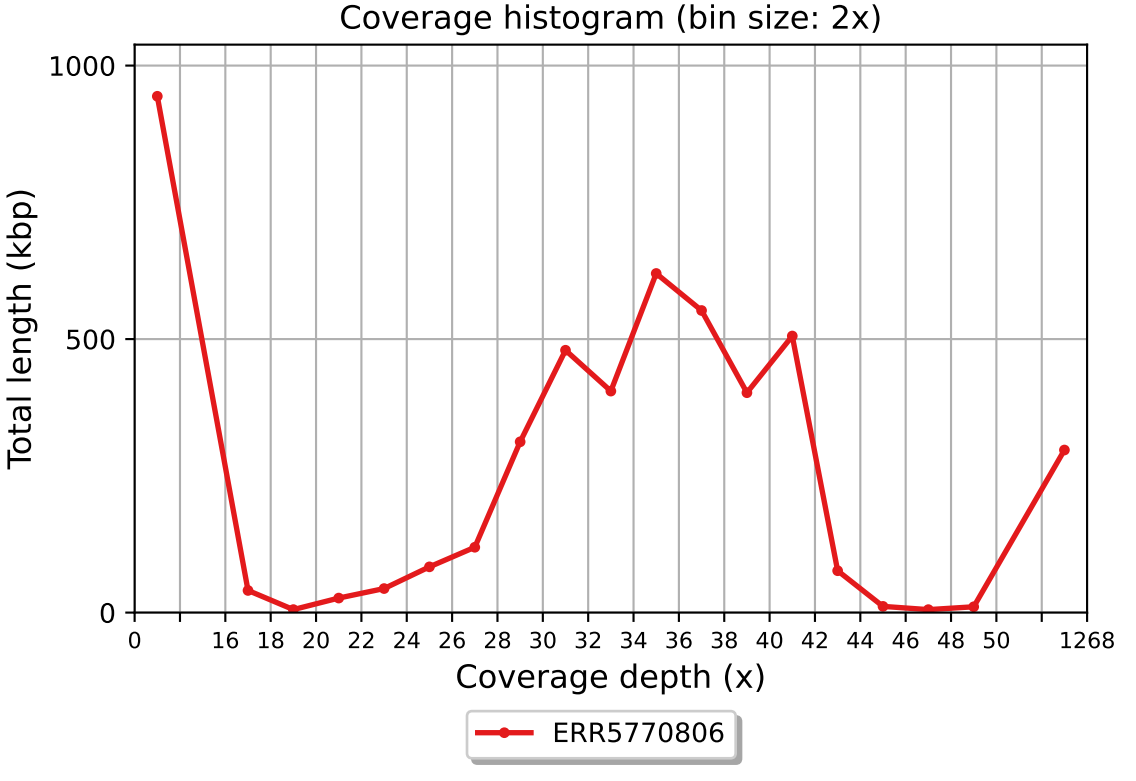

Nx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
ERR5770806

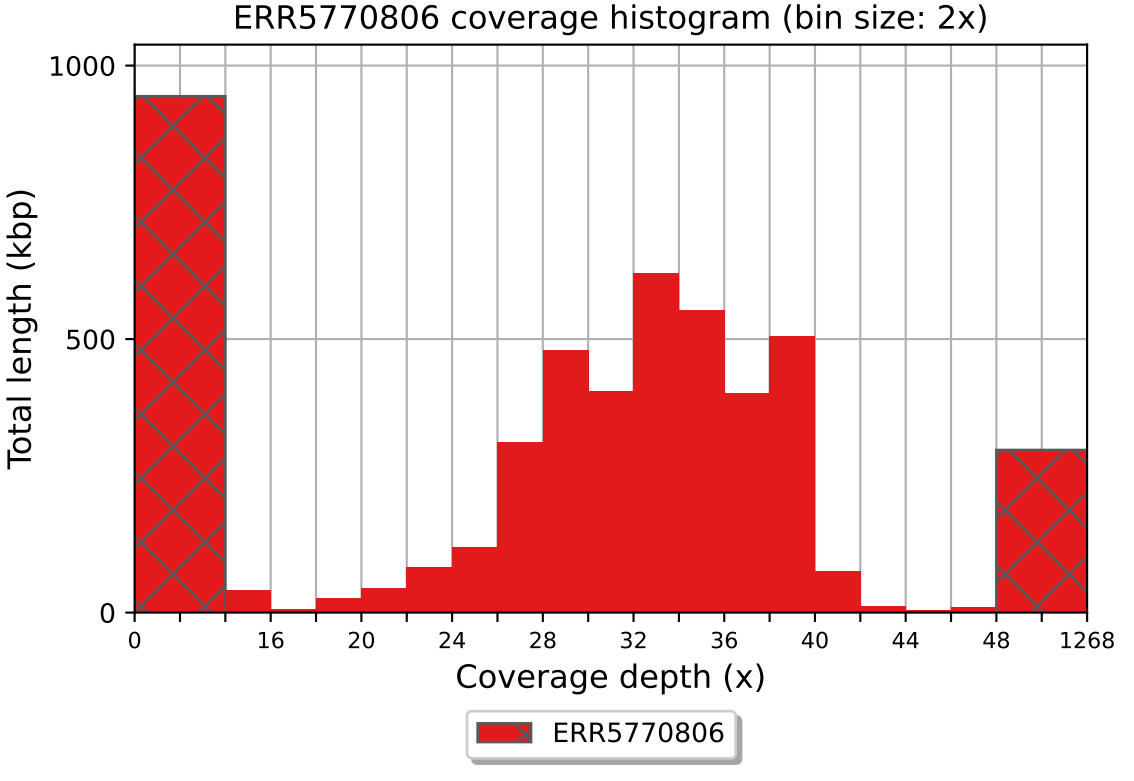

NGx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
ERR5770806

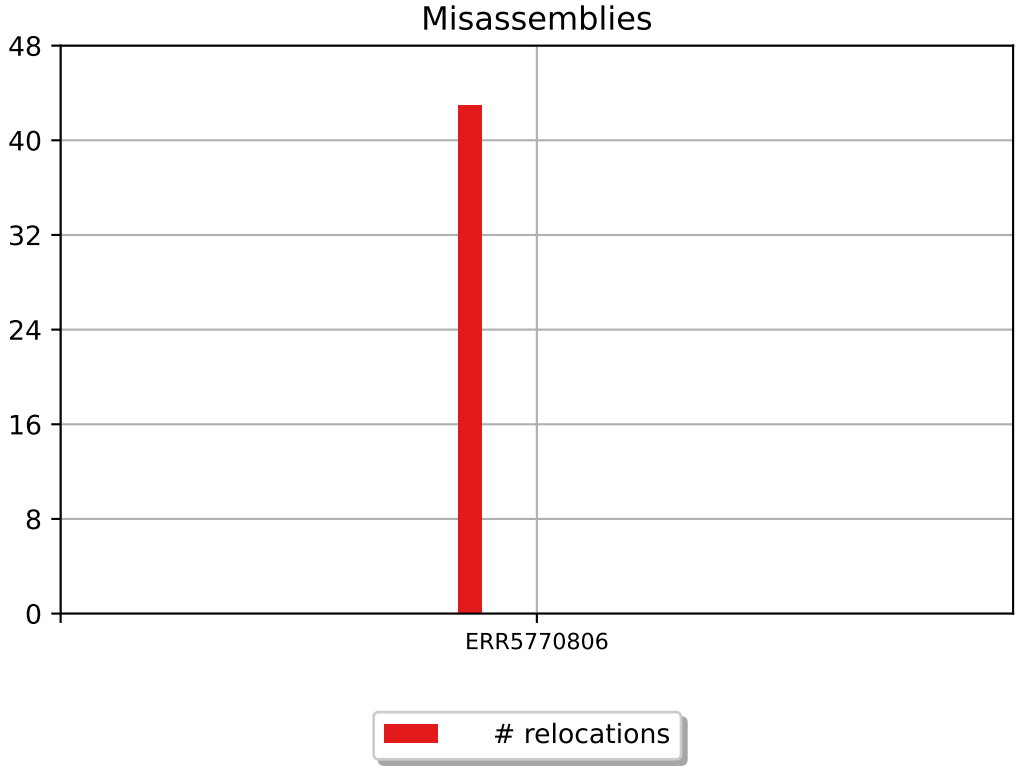

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
150
300
450
600
Contig index
ERR5770806
Reference

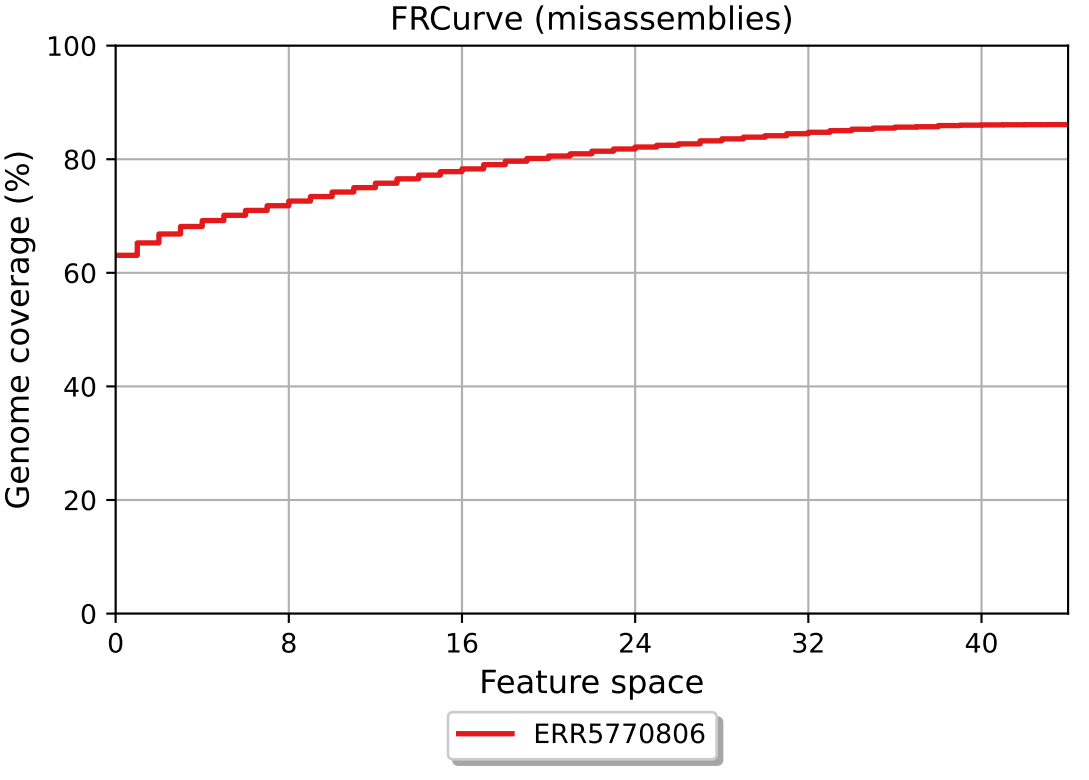

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
ERR5770806
Reference

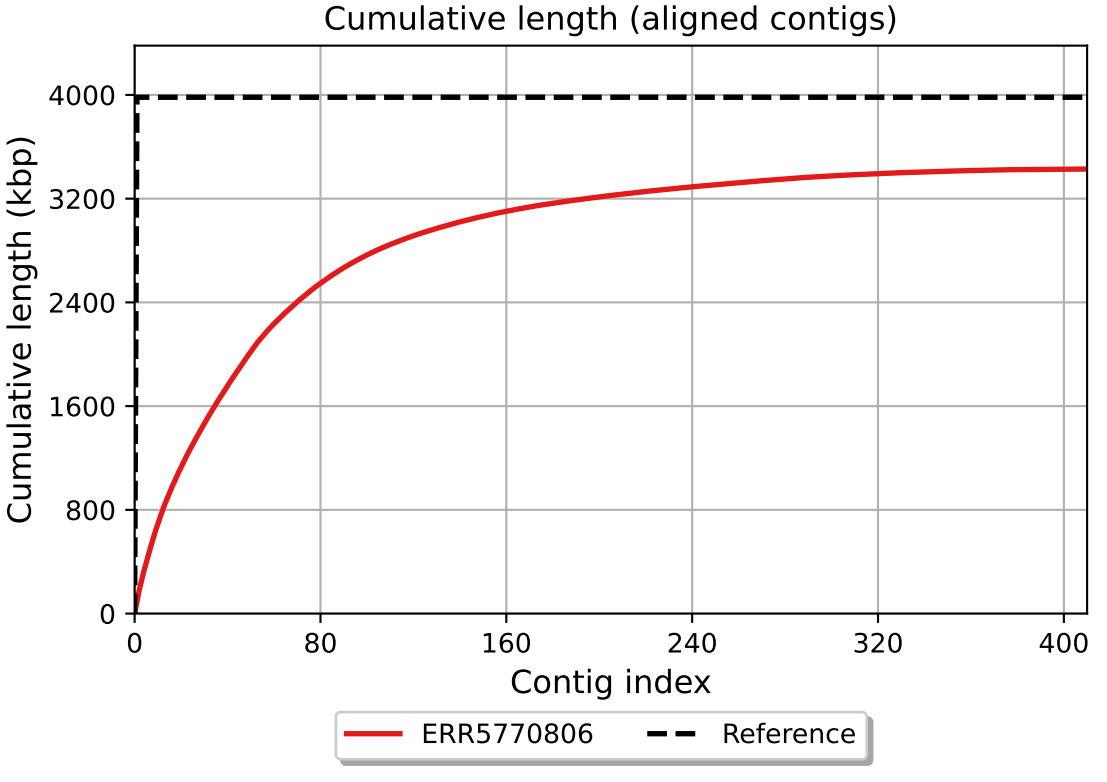

ERR5770806 GC content
300
240
180
120
60
0
contigs
0
20
40
60
80
100
GC (%)
ERR5770806

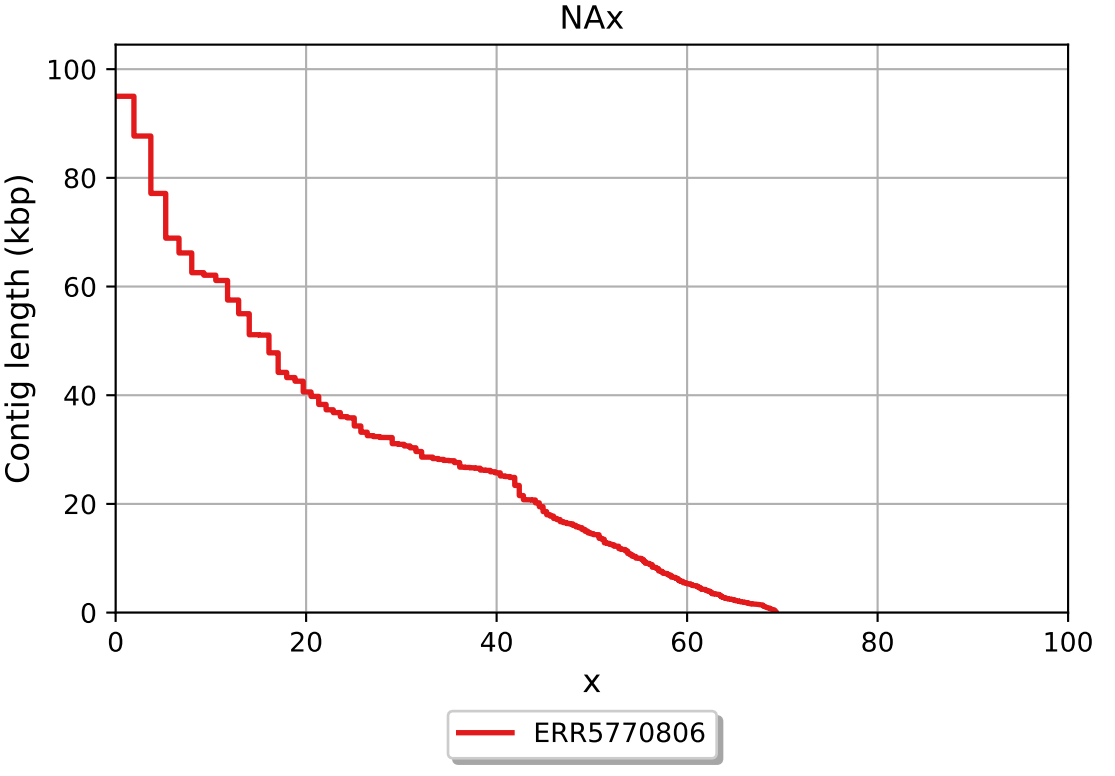

Coverage histogram (bin size: 2x)
Total length (kbp)
1000
500
0
0
16
18
20
22
24
26
28
30
32
34
36
38
40
42
44
46
48
50
1268
Coverage depth (x)
ERR5770806

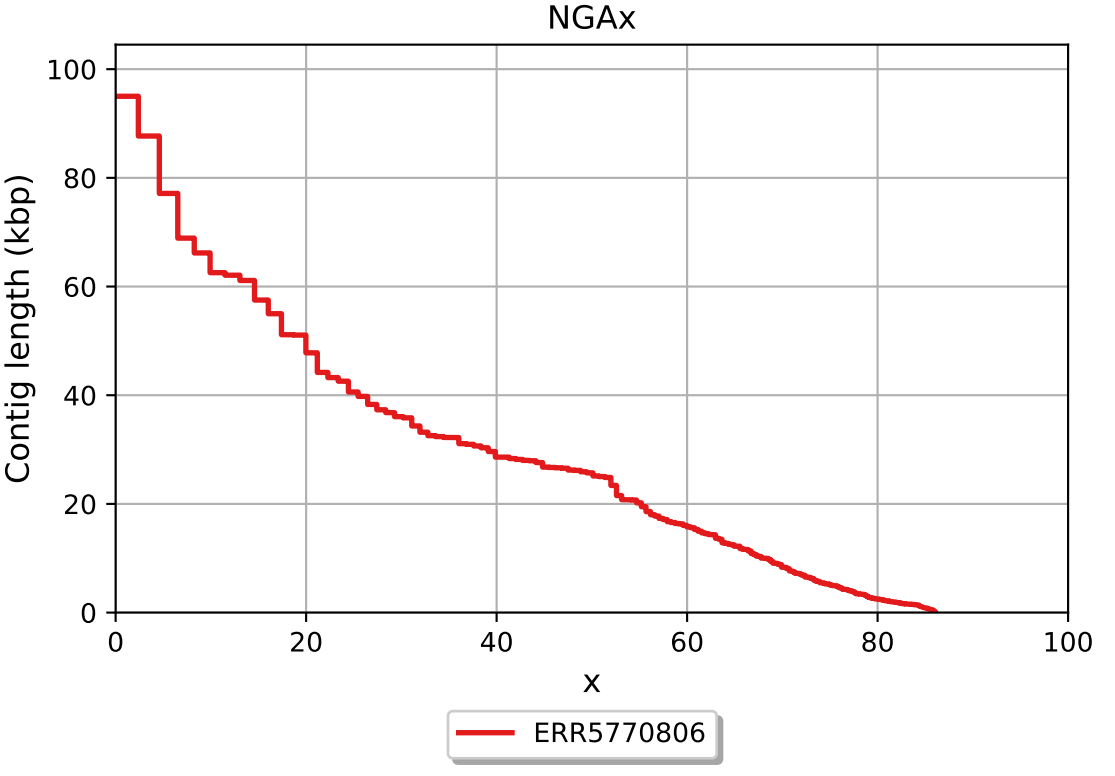

ERR5770806 coverage histogram (bin size: 2x)
Total length (kbp)
1000
500
0
0
16
20
24
28
32
36
40
44
48
1268
Coverage depth (x)
ERR5770806

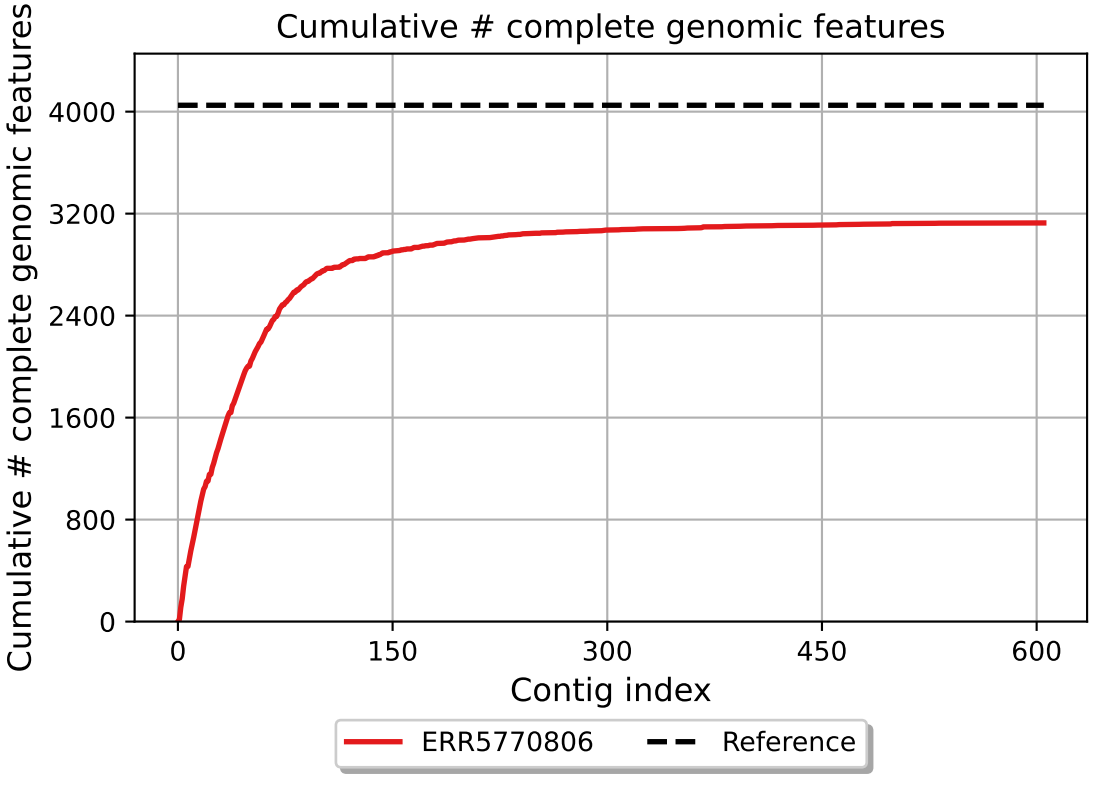

Misassemblies
48
40
32
24
16
8
0
ERR5770806
relocations

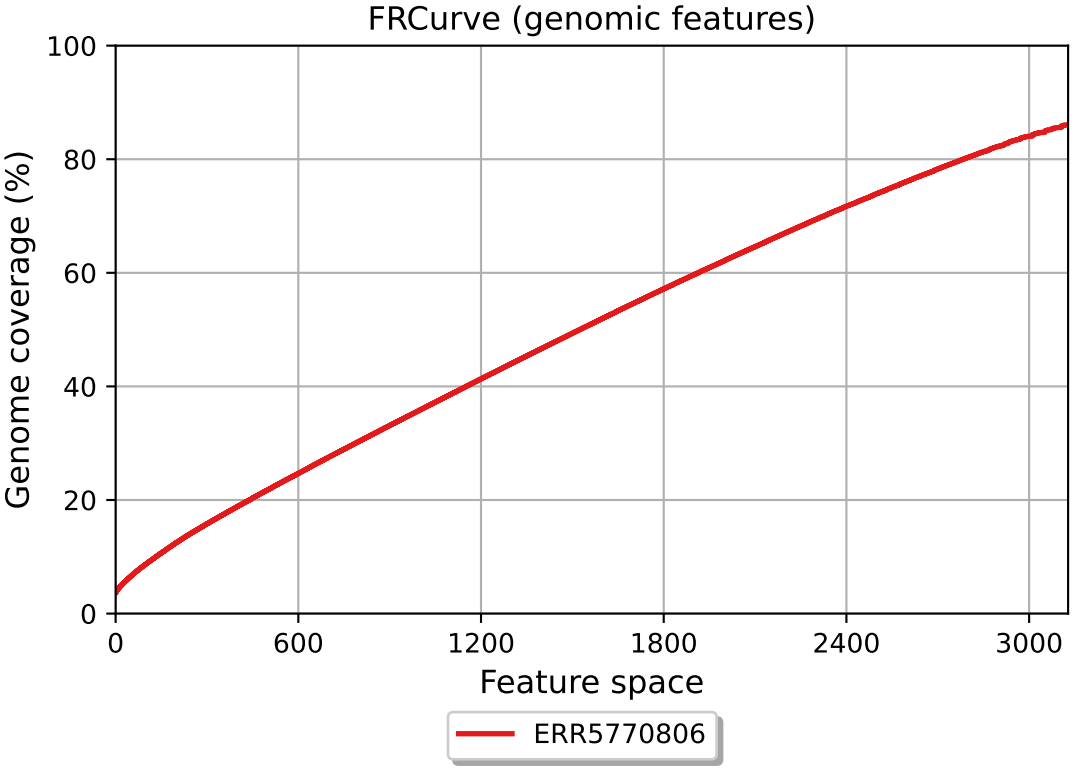

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
8
16
24
32
40
Feature space
ERR5770806


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
80
160
240
320
400
Contig index
ERR5770806
Reference


NAx
Contig length (kbp)
0
20
40
60
80
100
0
20
40
60
80
100
x
ERR5770806


NGAx
Contig length (kbp)
0
20
40
60
80
100
0
20
40
60
80
100
x
ERR5770806


Cumulative # complete genomic features
Cumulative # complete genomic features
4000
3200
2400
1600
800
0
0
150
300
450
600
Contig index
ERR5770806
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
600
1200
1800
2400
3000
Feature space
ERR5770806