Report

	ERR5770803
# contigs (>= 0 bp)	137
# contigs (>= 1000 bp)	59
# contigs (>= 5000 bp)	46
# contigs (>= 10000 bp)	41
# contigs (>= 25000 bp)	32
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	3970707
Total length (>= 1000 bp)	3950031
Total length (>= 5000 bp)	3912145
Total length (>= 10000 bp)	3870148
Total length (>= 25000 bp)	3713842
Total length (>= 50000 bp)	3567283
# contigs	66
Largest contig	242023
Total length	3954192
Reference length	3981941
GC (%)	38.89
Reference GC (%)	39.17
N50	151234
NG50	151234
N90	50625
NG90	45228
auN	142799.0
auNG	141803.9
L50	10
LG50	10
L90	28
LG90	29
# misassemblies	54
# misassembled contigs	24
Misassembled contigs length	3185773
# local misassemblies	45
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	22 + 35 part
Unaligned length	570695
Genome fraction (%)	84.931
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1756.64
# indels per 100 kbp	37.67
# genomic features	3294 + 96 part
Largest alignment	194762
Total aligned length	3381902
NA50	54448
NGA50	54448
NA90	-
NGA90	-
auNA	71697.4
auNGA	71197.8
LA50	20
LGA50	20
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

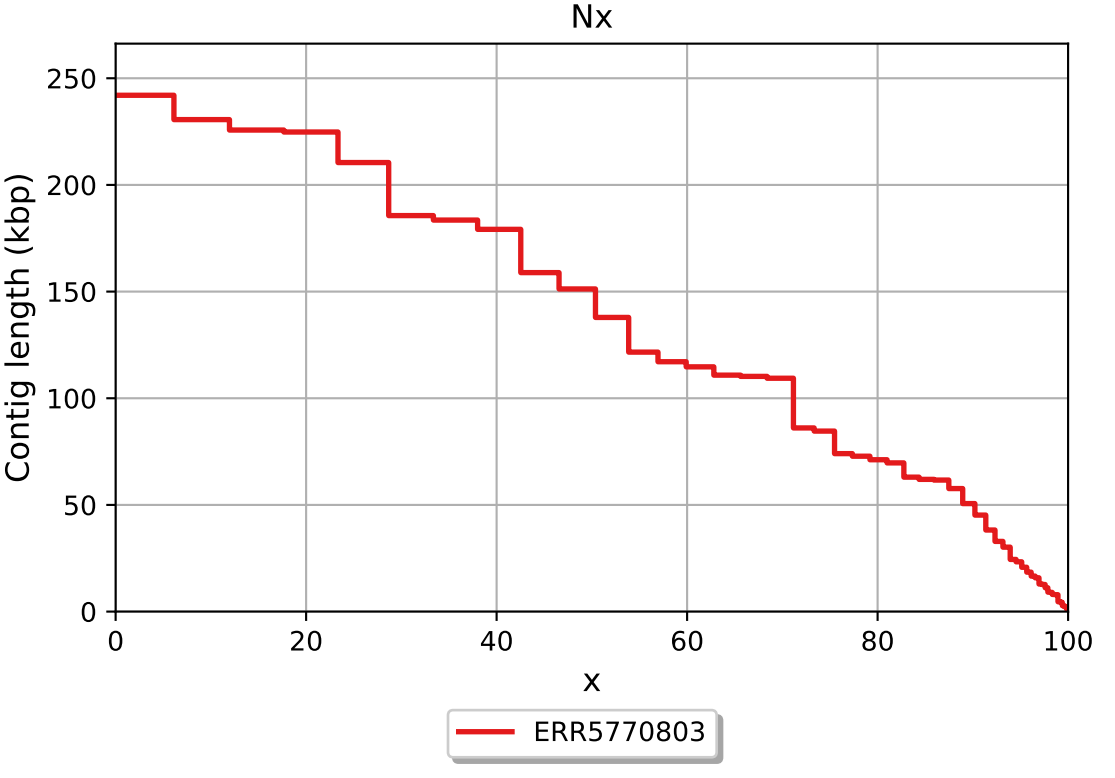
	ERR5770803
# misassemblies	54
# contig misassemblies	54
# c. relocations	54
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	24
Misassembled contigs length	3185773
# local misassemblies	45
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	59408
# indels	1274
# indels (<= 5 bp)	1199
# indels (> 5 bp)	75
Indels length	3774

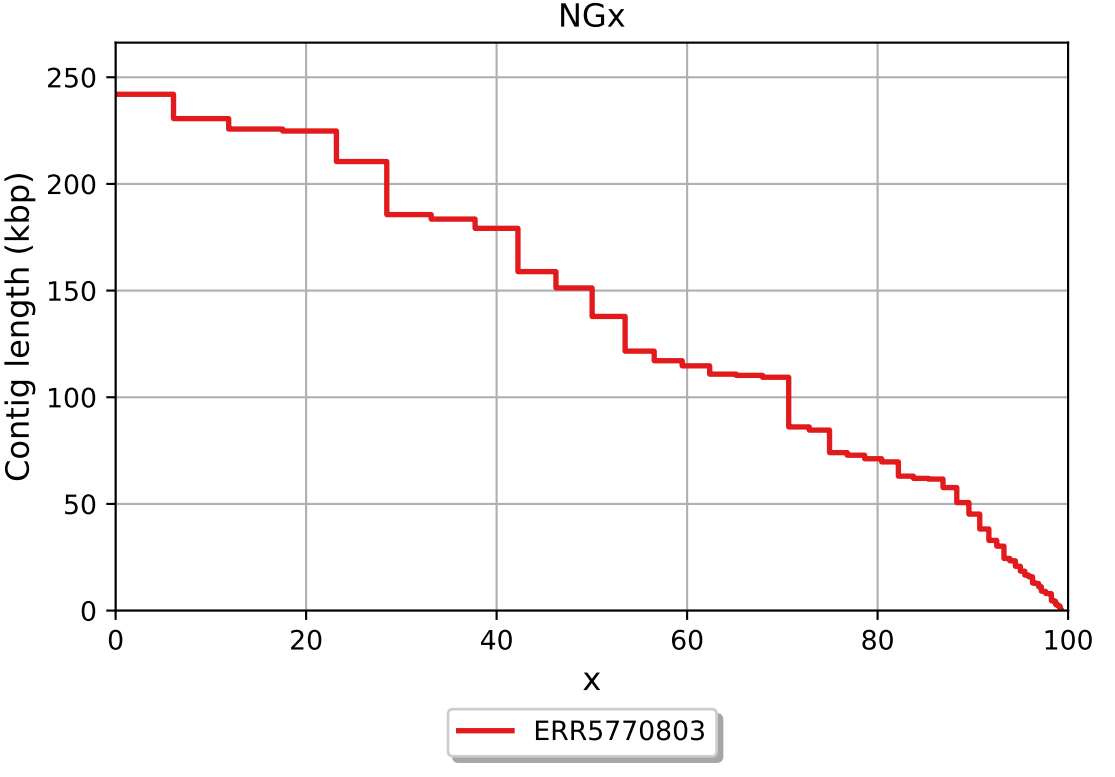
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

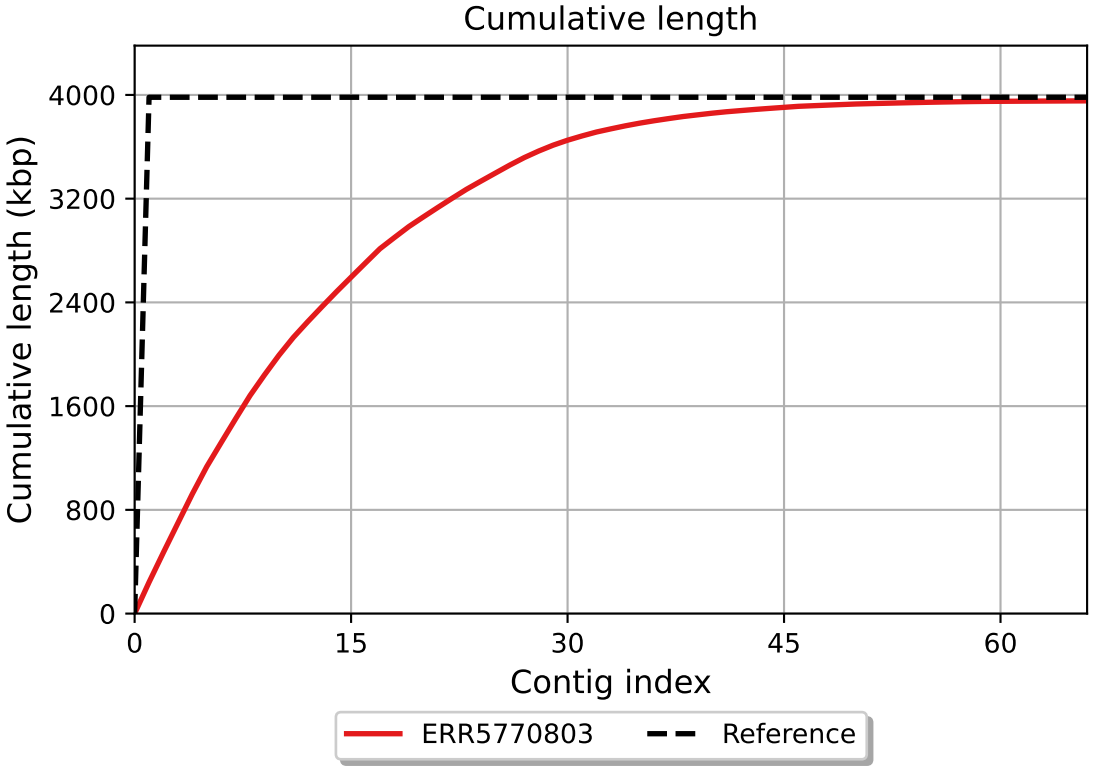
Unaligned report

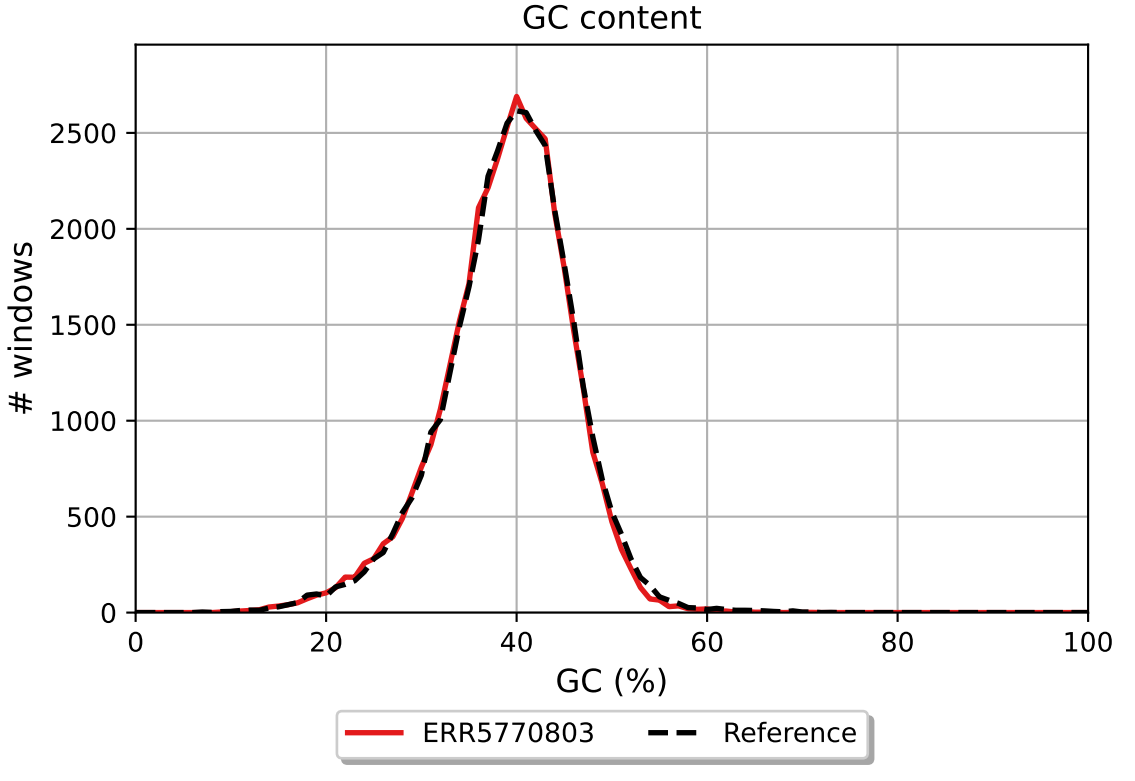
	ERR5770803
# fully unaligned contigs	22
Fully unaligned length	128507
# partially unaligned contigs	35
Partially unaligned length	442188
# N's	0

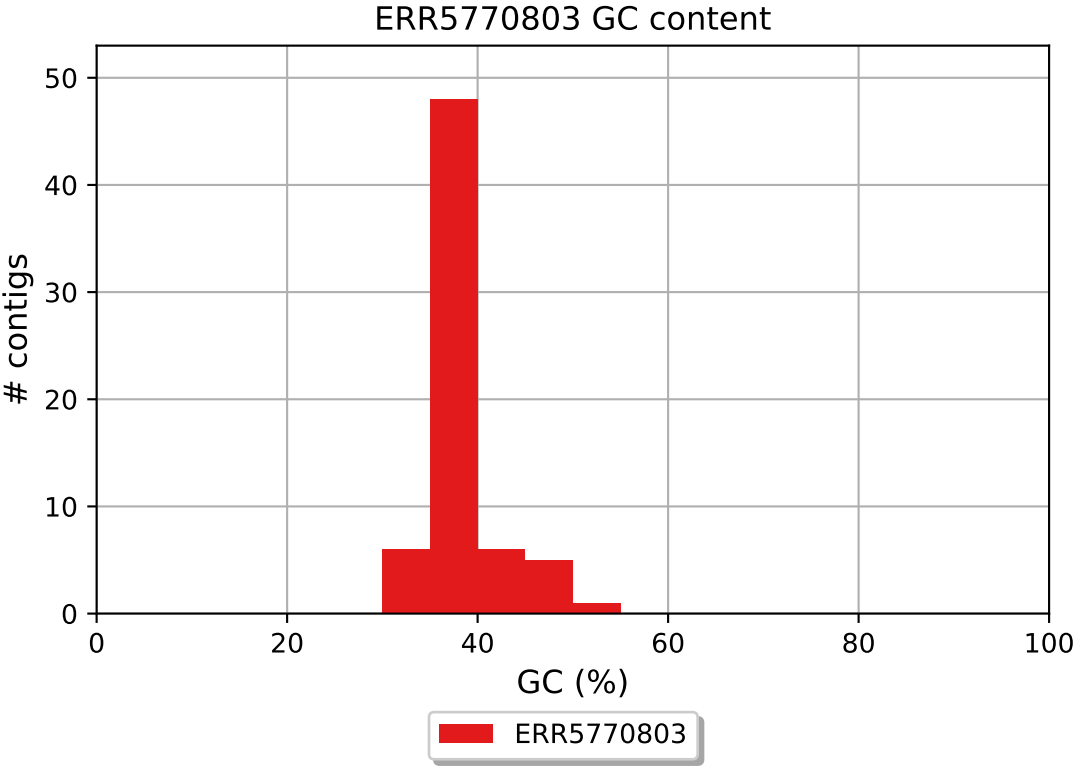
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

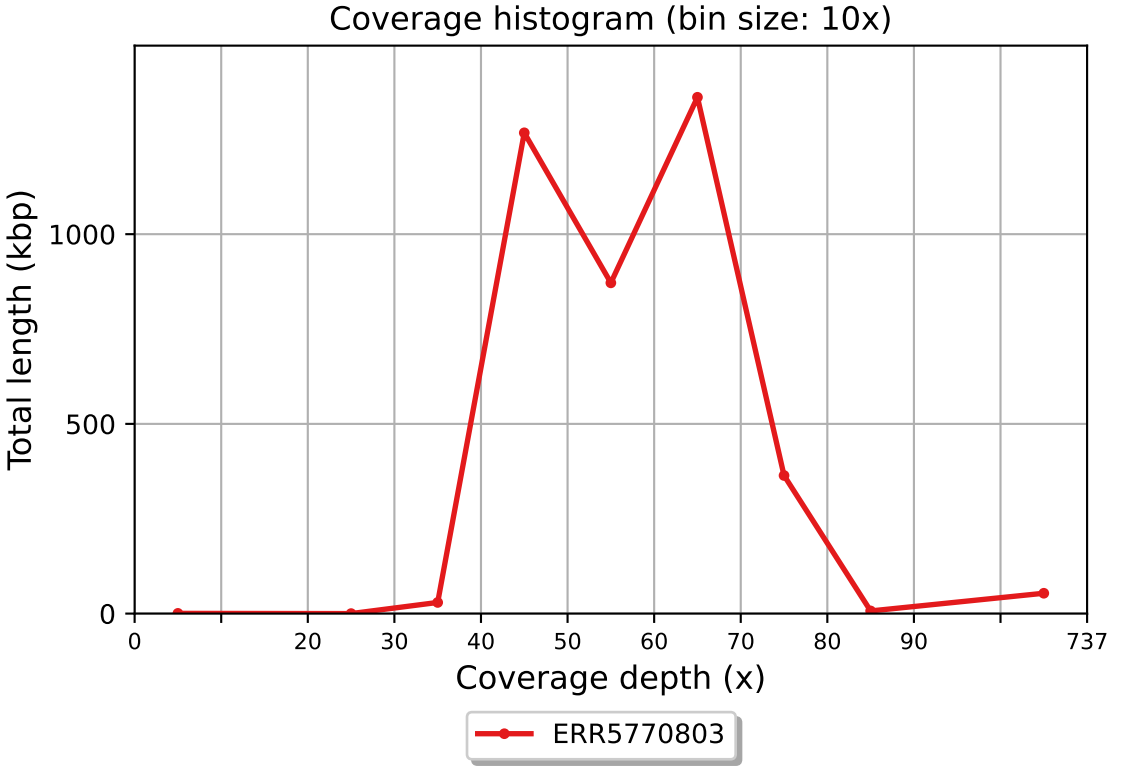

Nx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
ERR5770803

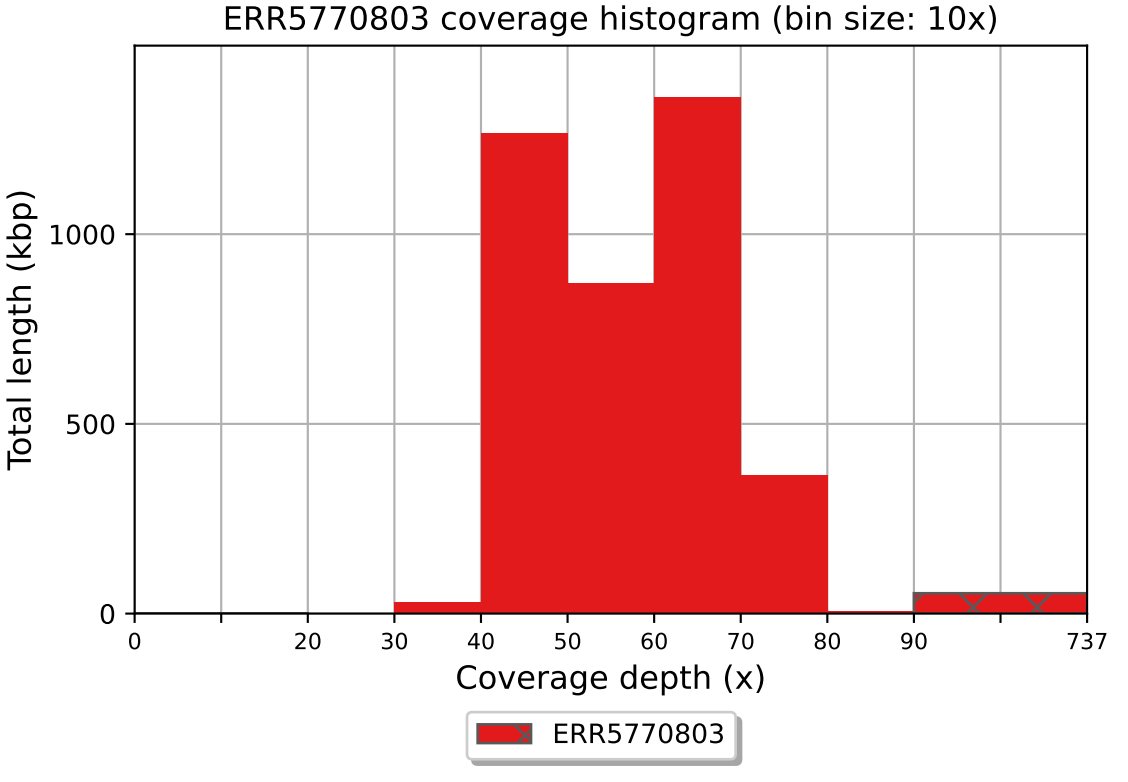

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
ERR5770803

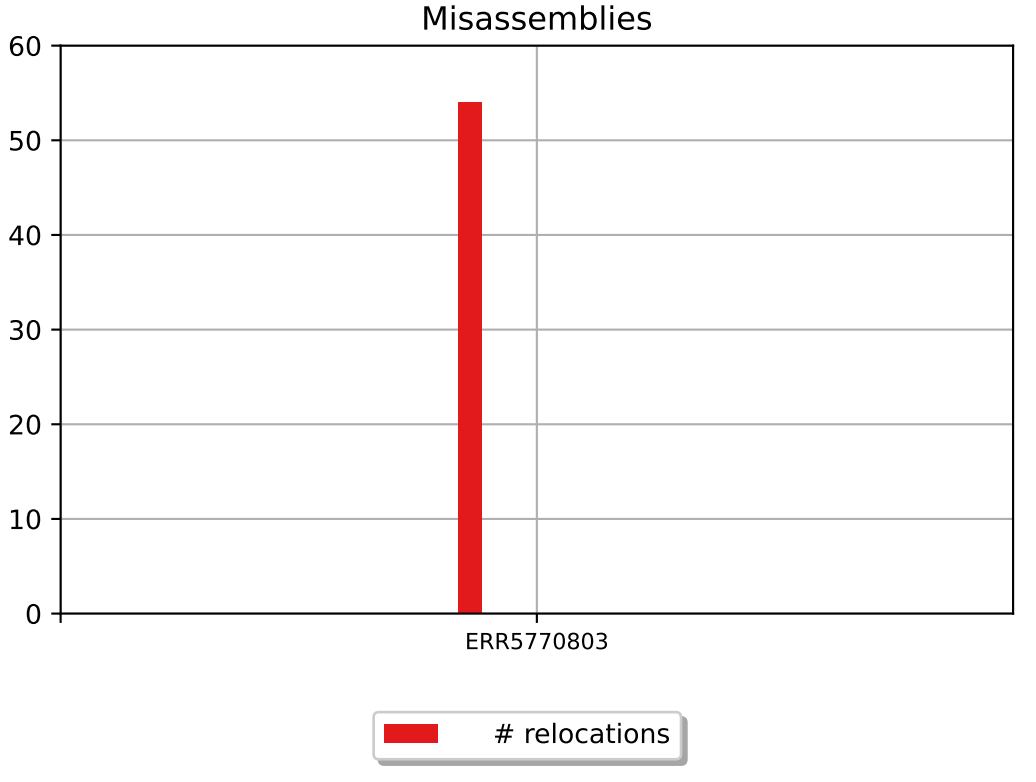

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
15
30
45
60
Contig index
ERR5770803
Reference

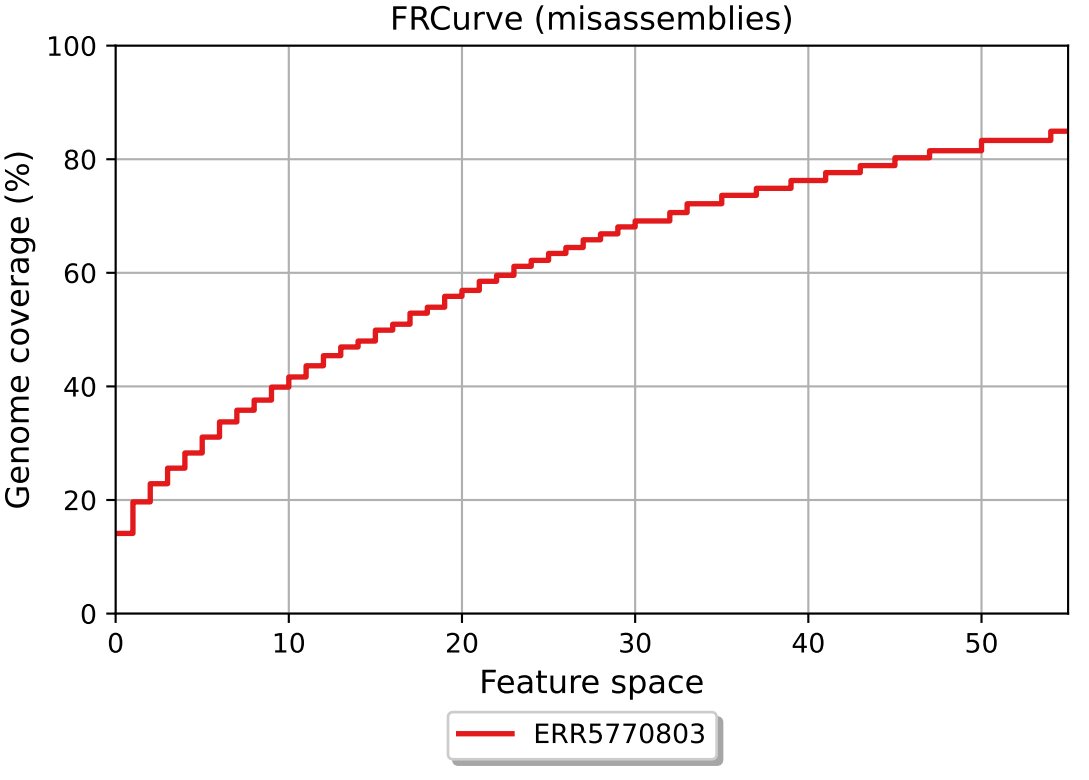

GC content
windows
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
ERR5770803
Reference

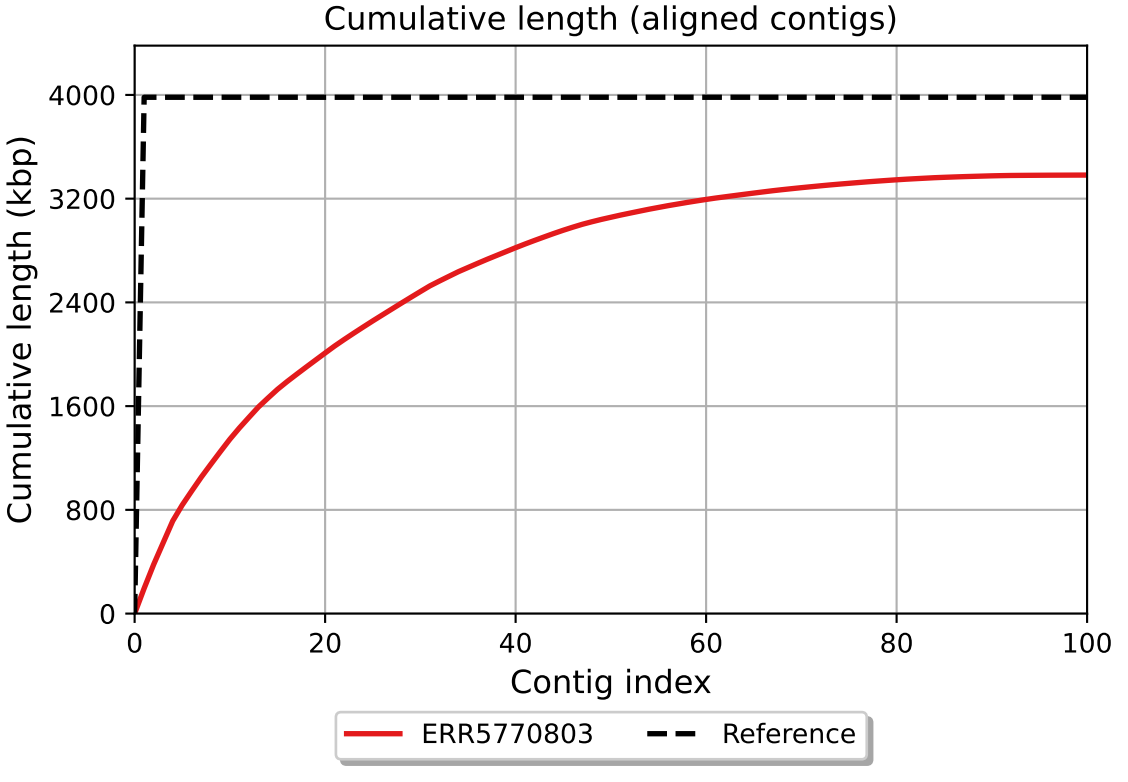

ERR5770803 GC content
contigs
GC (%)
0
10
20
30
40
50
0
20
40
60
80
100
ERR5770803

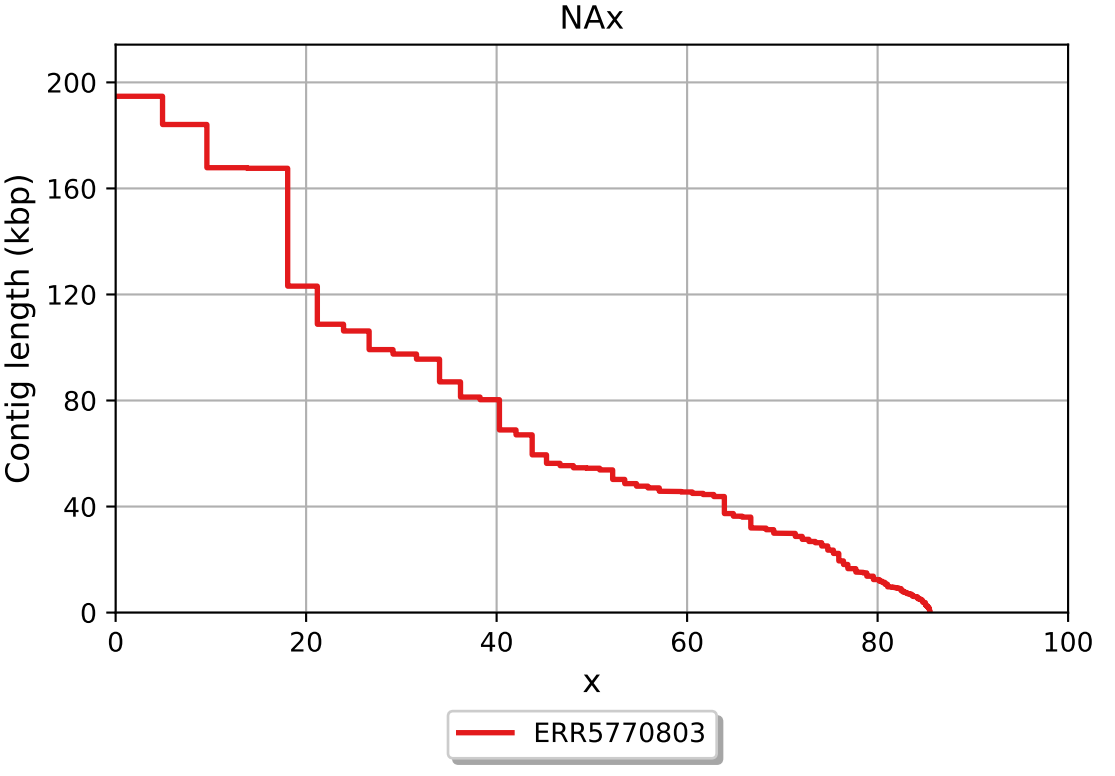

Coverage histogram (bin size: 10x)
Total length (kbp)
1000
500
0
0
20
30
40
50
60
70
80
90
737
Coverage depth (x)
ERR5770803

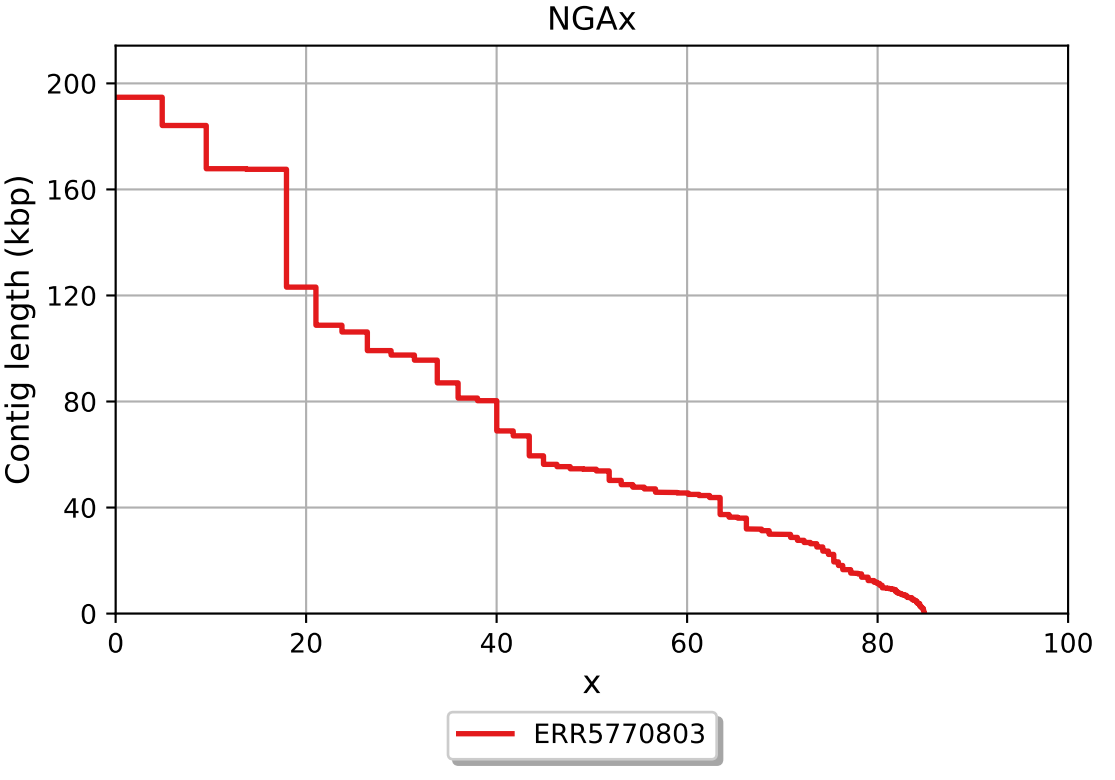

ERR5770803 coverage histogram (bin size: 10x)
Total length (kbp)
1000
500
0
0
20
30
40
50
60
70
80
90
737
Coverage depth (x)
ERR5770803

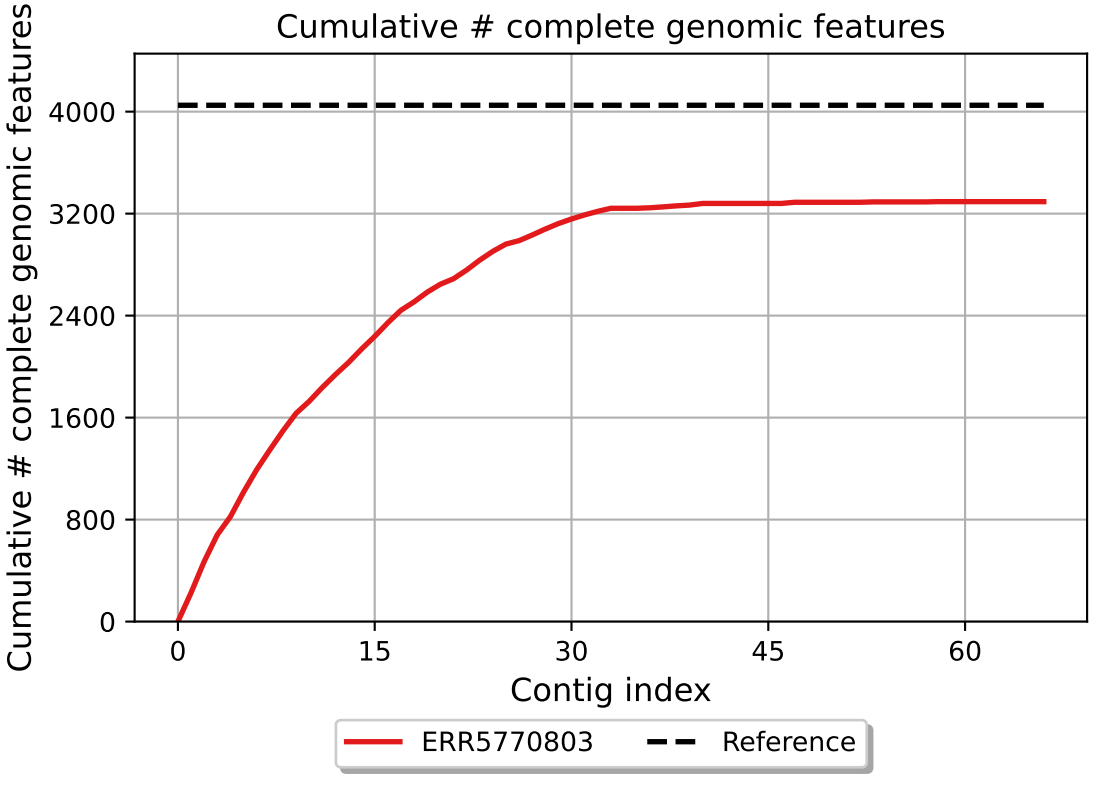

Misassemblies
60
50
40
30
20
10
0
ERR5770803
relocations

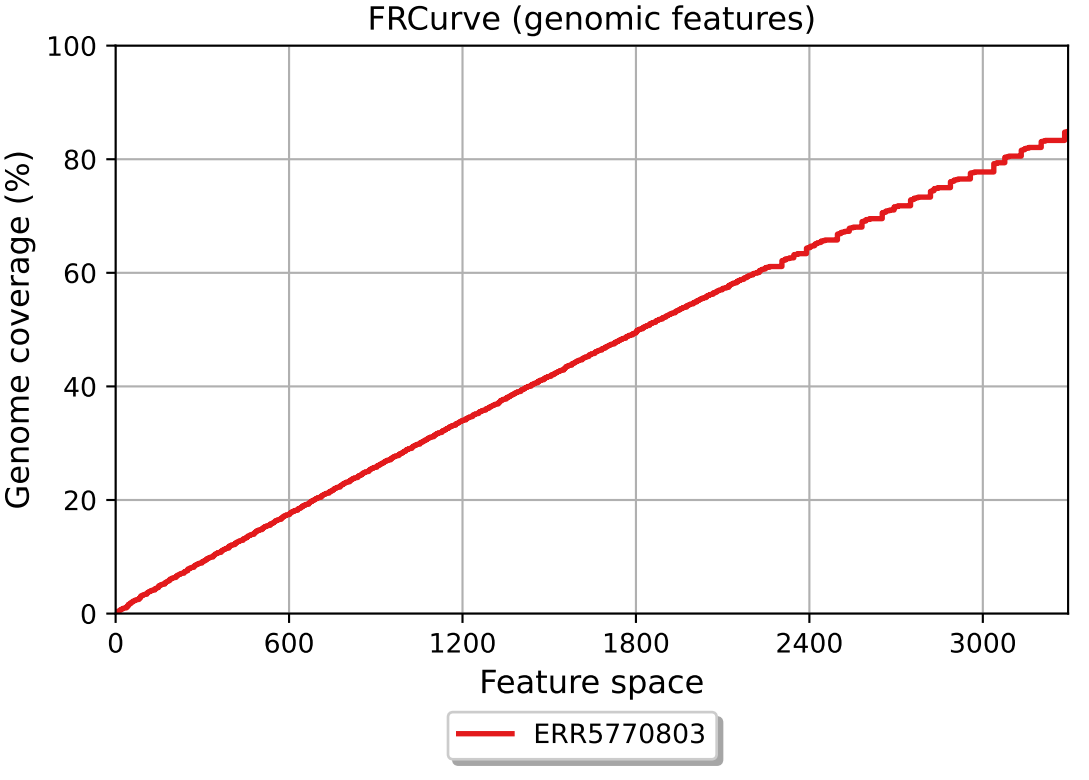

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
10
20
30
40
50
Feature space
ERR5770803


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
Contig index
ERR5770803
Reference


NAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
ERR5770803


NGAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
ERR5770803


Cumulative # complete genomic features
Cumulative # complete genomic features
4000
3200
2400
1600
800
0
0
15
30
45
60
Contig index
ERR5770803
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
600
1200
1800
2400
3000
Feature space
ERR5770803