Report

| | ERR5770801 |
|---|---|
| # contigs (>= 0 bp) | 129 |
| # contigs (>= 1000 bp) | 60 |
| # contigs (>= 5000 bp) | 46 |
| # contigs (>= 10000 bp) | 44 |
| # contigs (>= 25000 bp) | 38 |
| # contigs (>= 50000 bp) | 28 |
| Total length (>= 0 bp) | 4000645 |
| Total length (>= 1000 bp) | 3981245 |
| Total length (>= 5000 bp) | 3949741 |
| Total length (>= 10000 bp) | 3935741 |
| Total length (>= 25000 bp) | 3834760 |
| Total length (>= 50000 bp) | 3464316 |
| # contigs | 70 |
| Largest contig | 250755 |
| Total length | 3988045 |
| Reference length | 3981941 |
| GC (%) | 38.96 |
| Reference GC (%) | 39.17 |
| N50 | 131109 |
| NG50 | 131109 |
| N90 | 43340 |
| NG90 | 43340 |
| auN | 132421.6 |
| auNG | 132624.6 |
| L50 | 12 |
| LG50 | 12 |
| L90 | 31 |
| LG90 | 31 |
| # misassemblies | 58 |
| # misassembled contigs | 28 |
| Misassembled contigs length | 3262626 |
| # local misassemblies | 39 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 12 + 38 part |
| Unaligned length | 582974 |
| Genome fraction (%) | 85.404 |
| Duplication ratio | 1.000 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1727.15 |
| # indels per 100 kbp | 36.84 |
| # genomic features | 3310 + 98 part |
| Largest alignment | 193142 |
| Total aligned length | 3401556 |
| NA50 | 46557 |
| NGA50 | 46557 |
| NA90 | - |
| NGA90 | - |
| auNA | 58244.9 |
| auNGA | 58334.2 |
| LA50 | 25 |
| LGA50 | 25 |
| 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

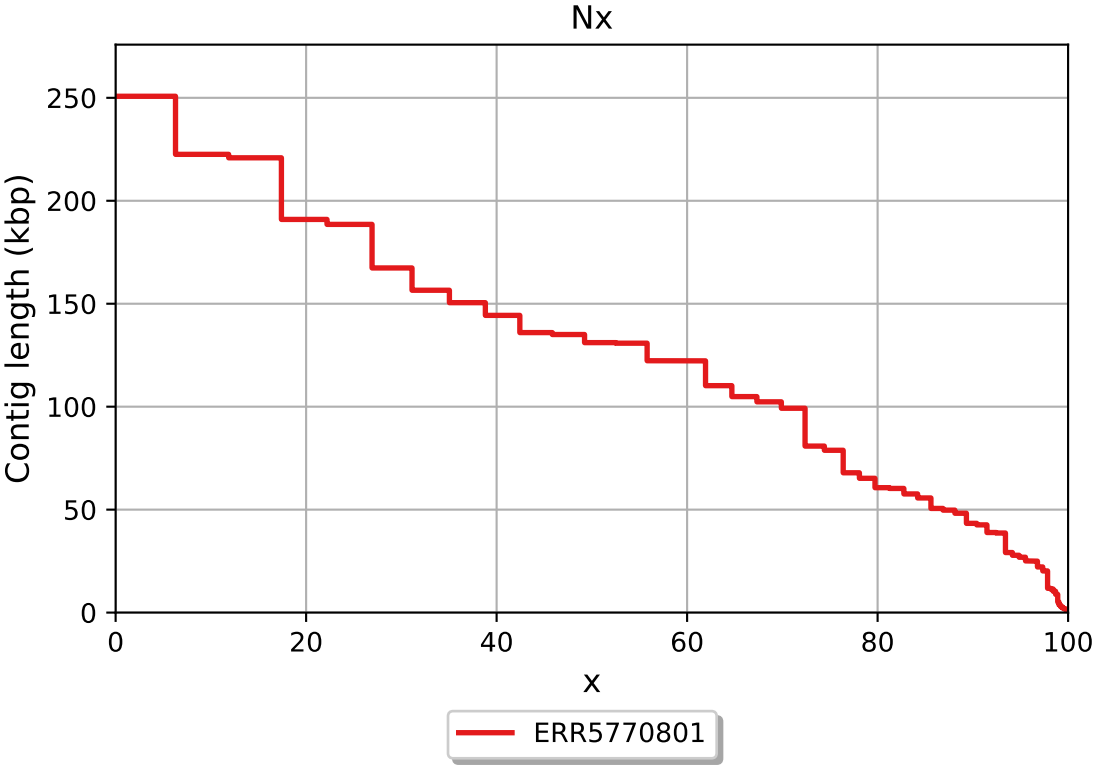
| | ERR5770801 |
|---|---|
| # misassemblies | 58 |
| # contig misassemblies | 58 |
| # c. relocations | 58 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 28 |
| Misassembled contigs length | 3262626 |
| # local misassemblies | 39 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 58750 |
| # indels | 1253 |
| # indels (<= 5 bp) | 1168 |
| # indels (> 5 bp) | 85 |
| Indels length | 4267 |

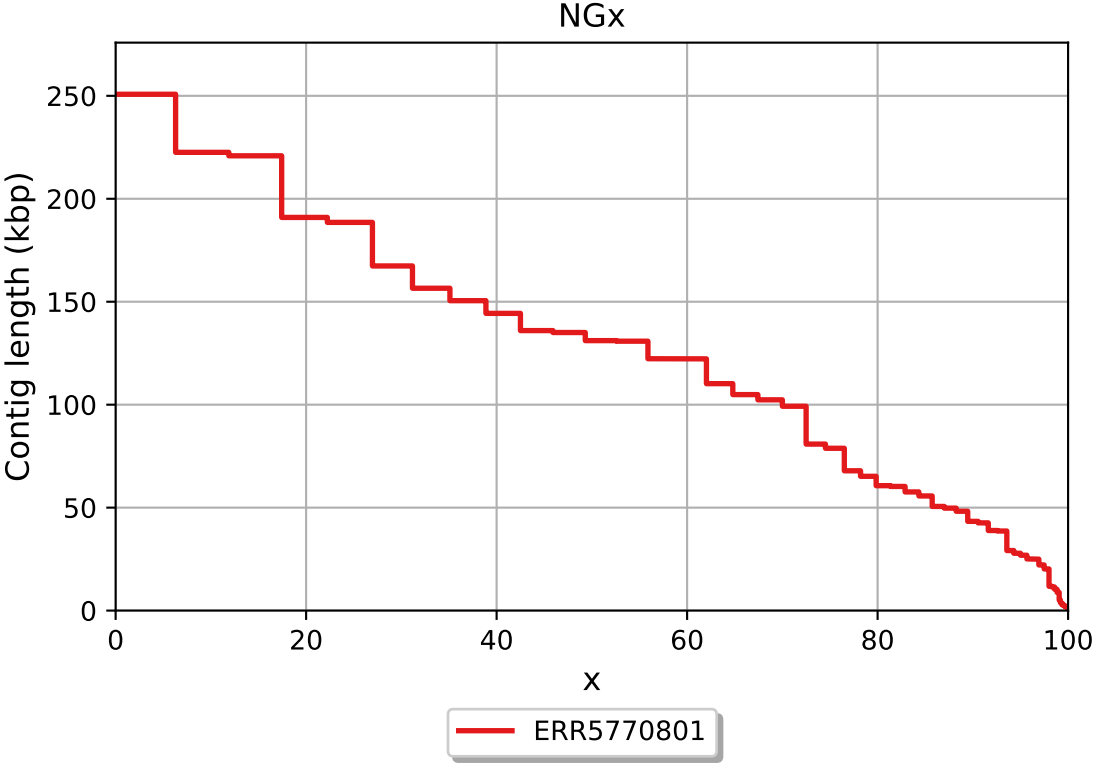
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

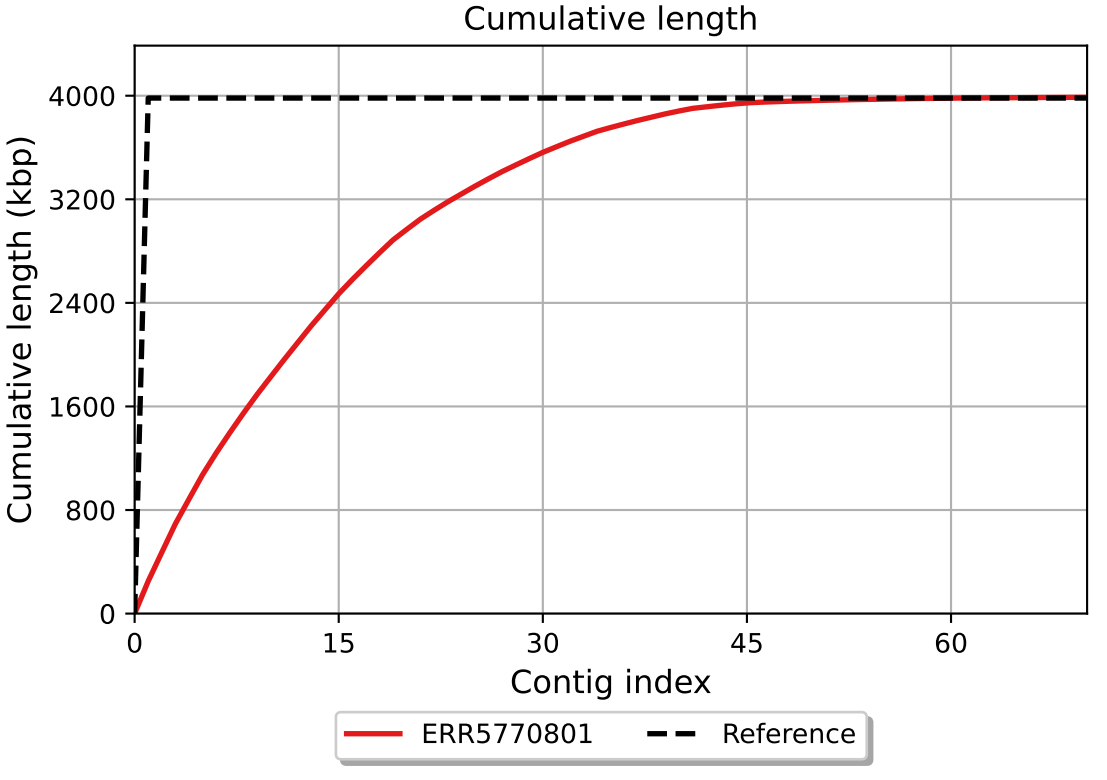
## Unaligned report

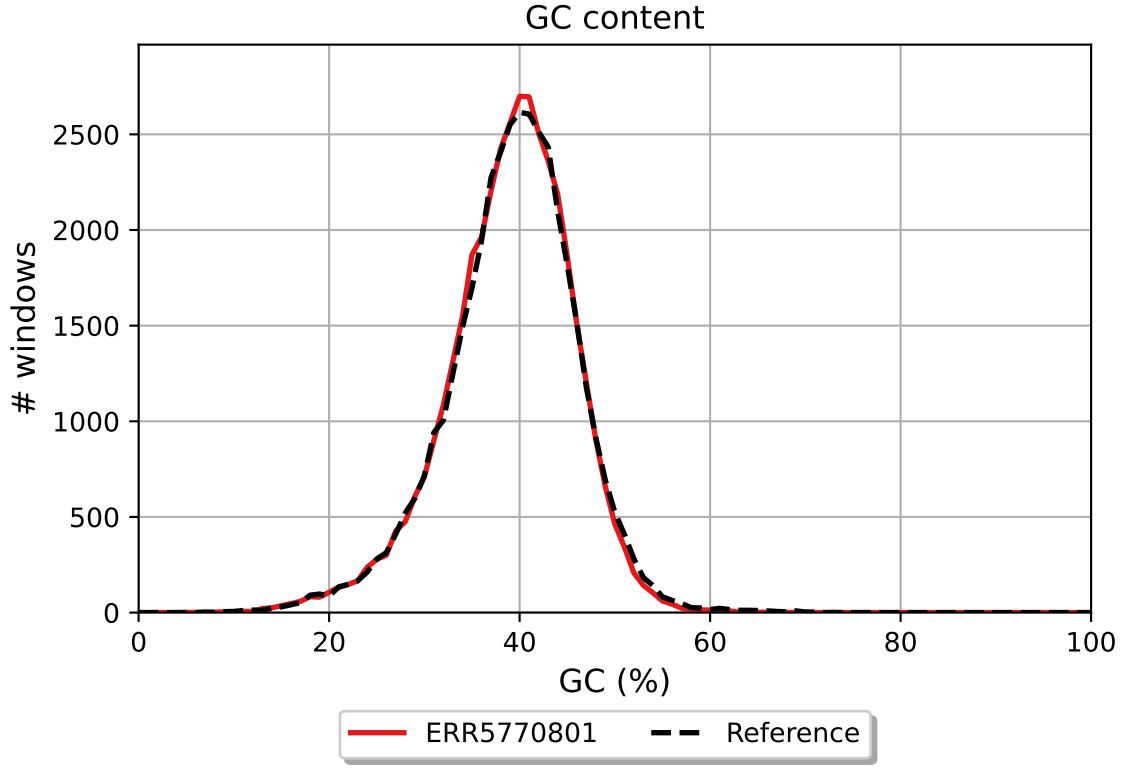
| | ERR5770801 |
|---|---|
| # fully unaligned contigs | 12 |
| Fully unaligned length | 26029 |
| # partially unaligned contigs | 38 |
| Partially unaligned length | 556945 |
| # N's | 0 |

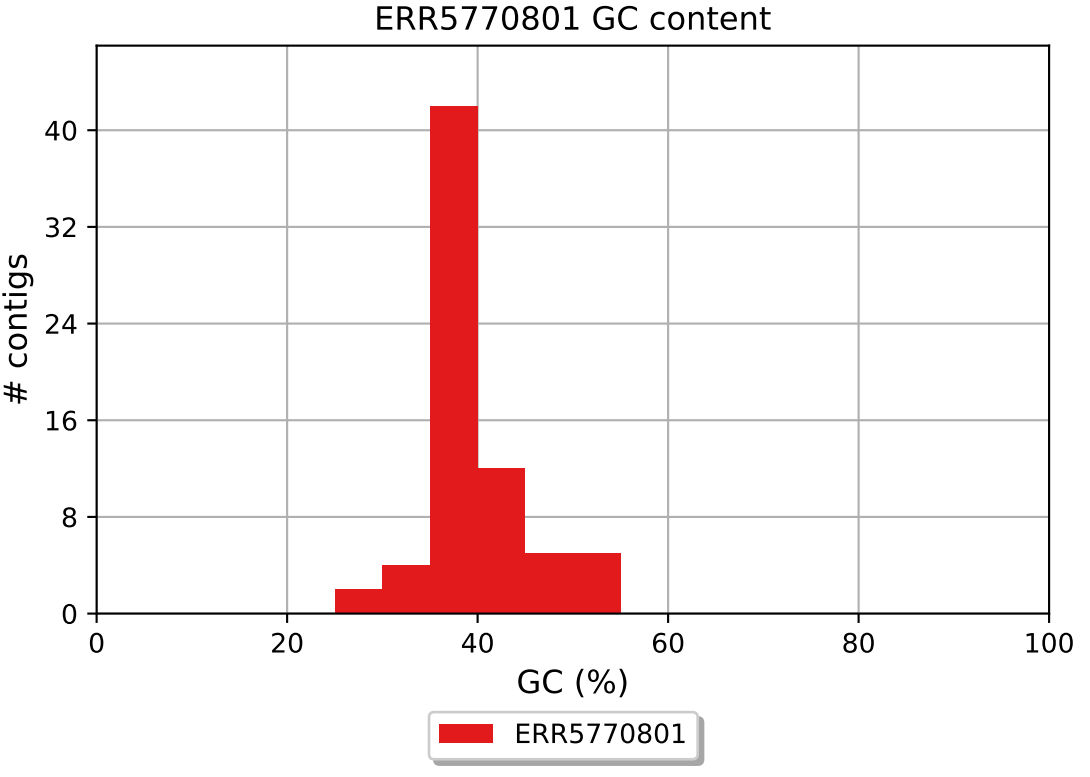
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

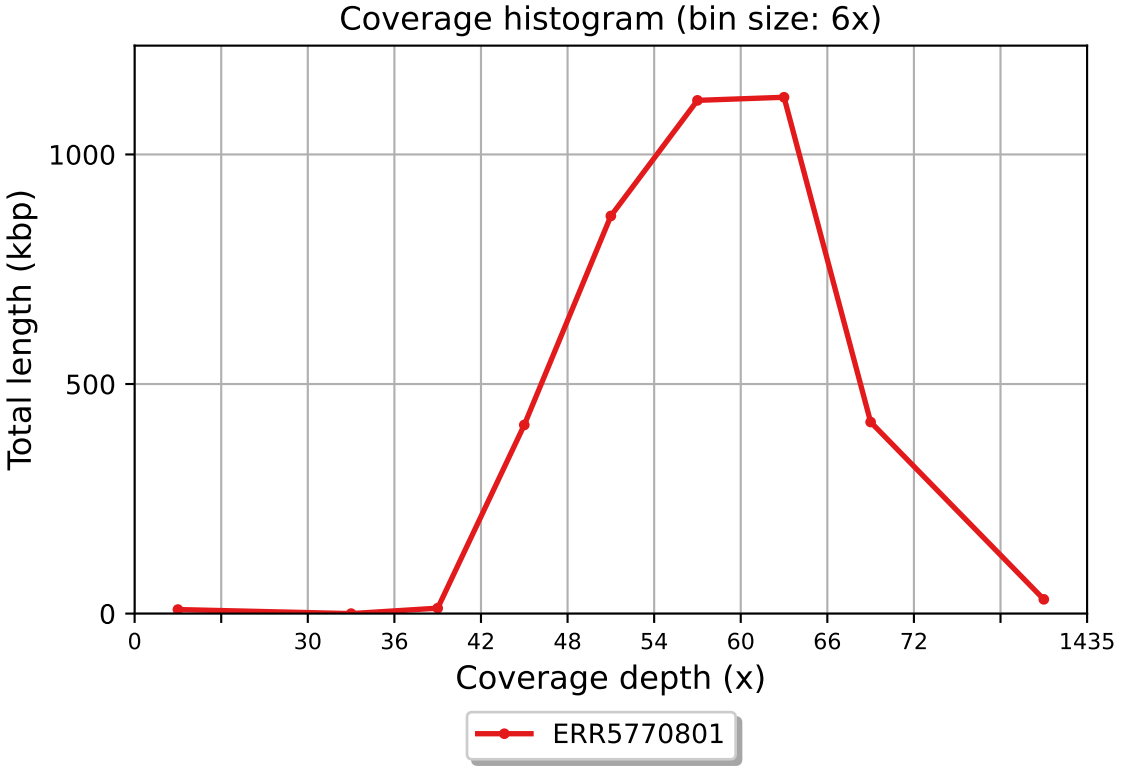

Nx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
ERR5770801

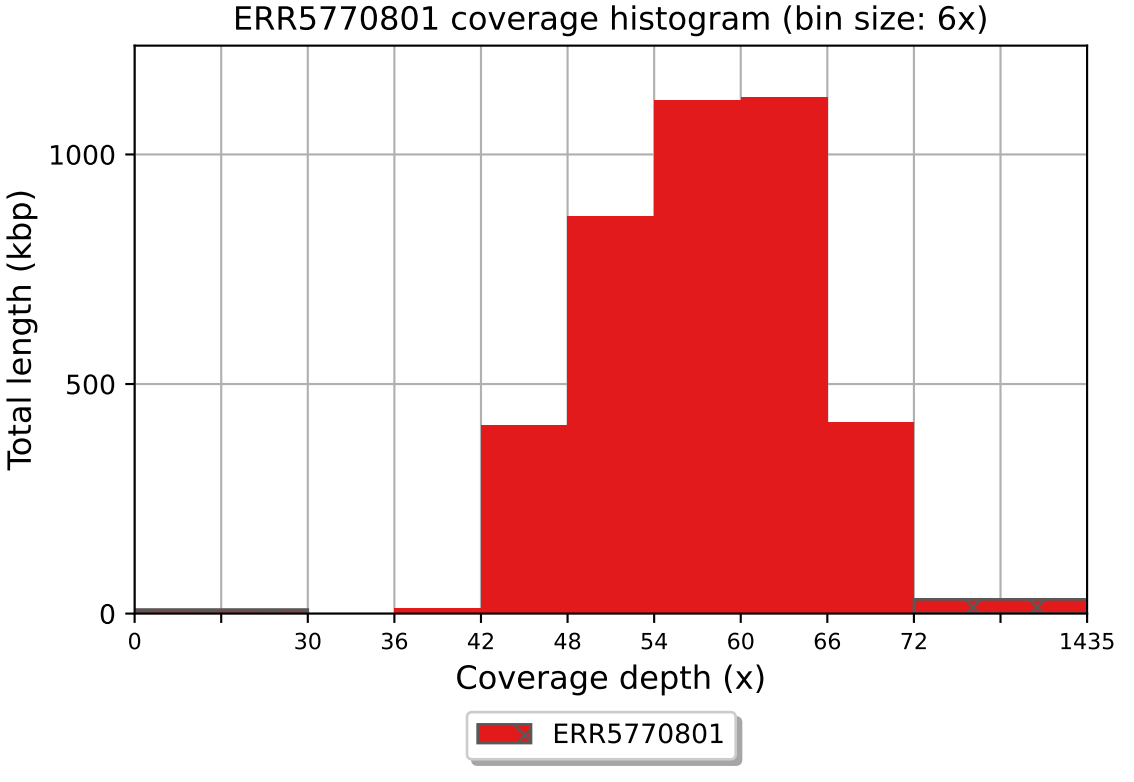

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
ERR5770801

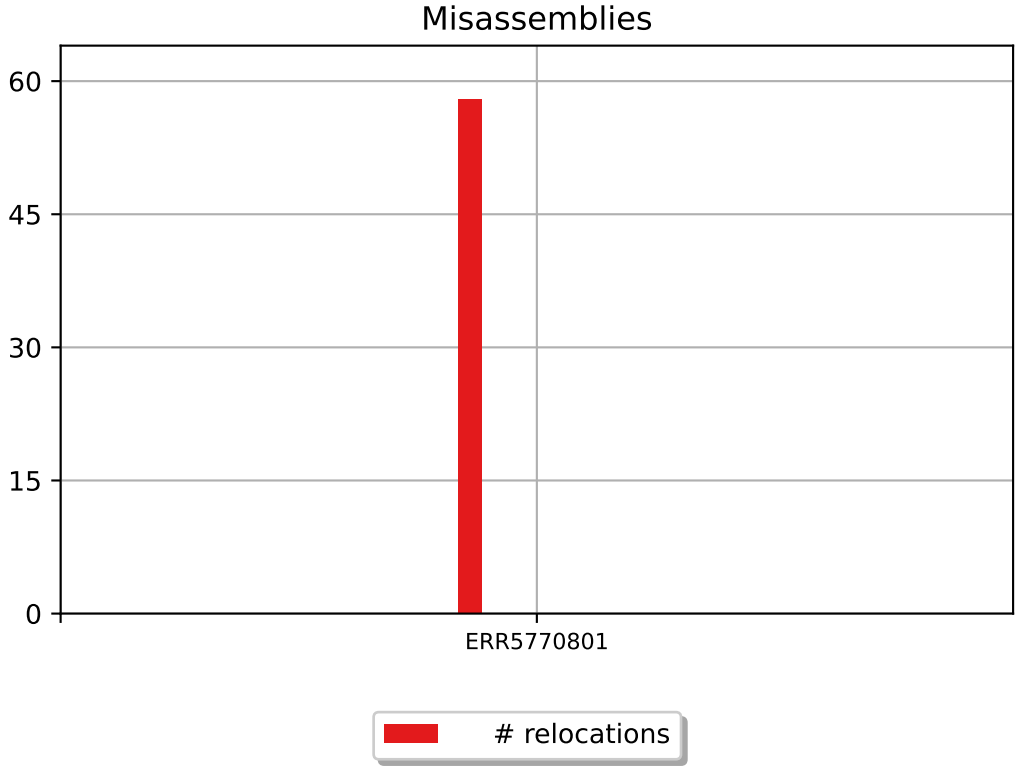

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
15
30
45
60
Contig index
ERR5770801
Reference

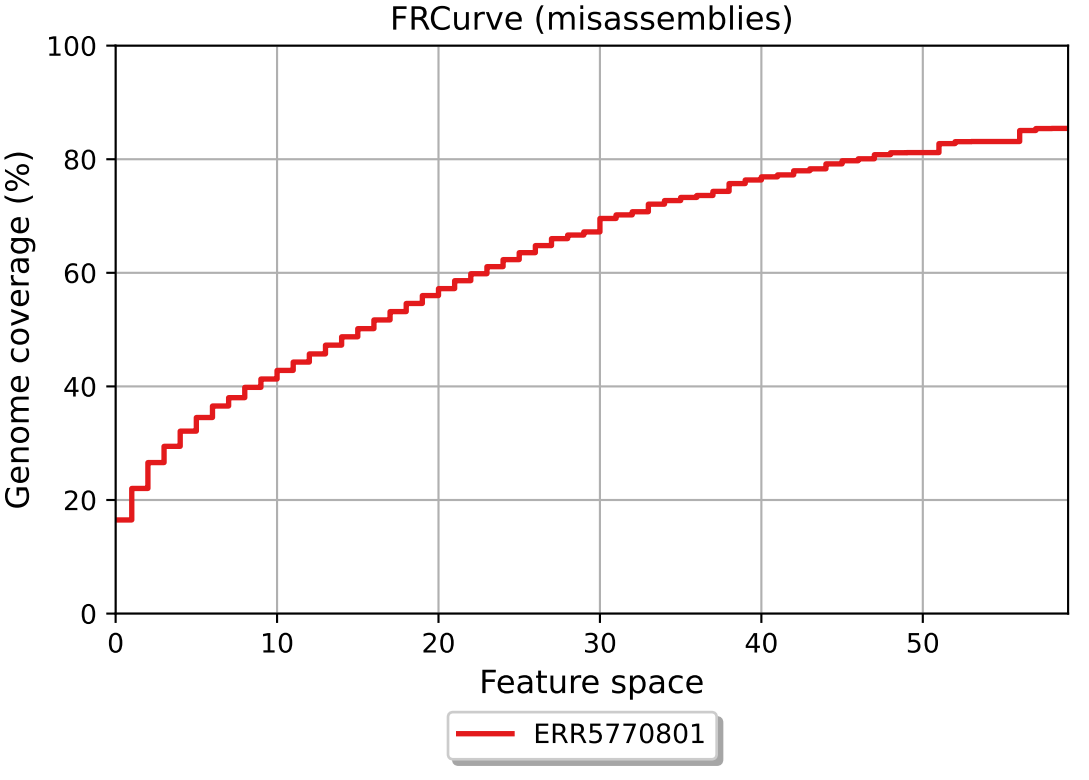

GC content
# windows
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
ERR5770801
Reference

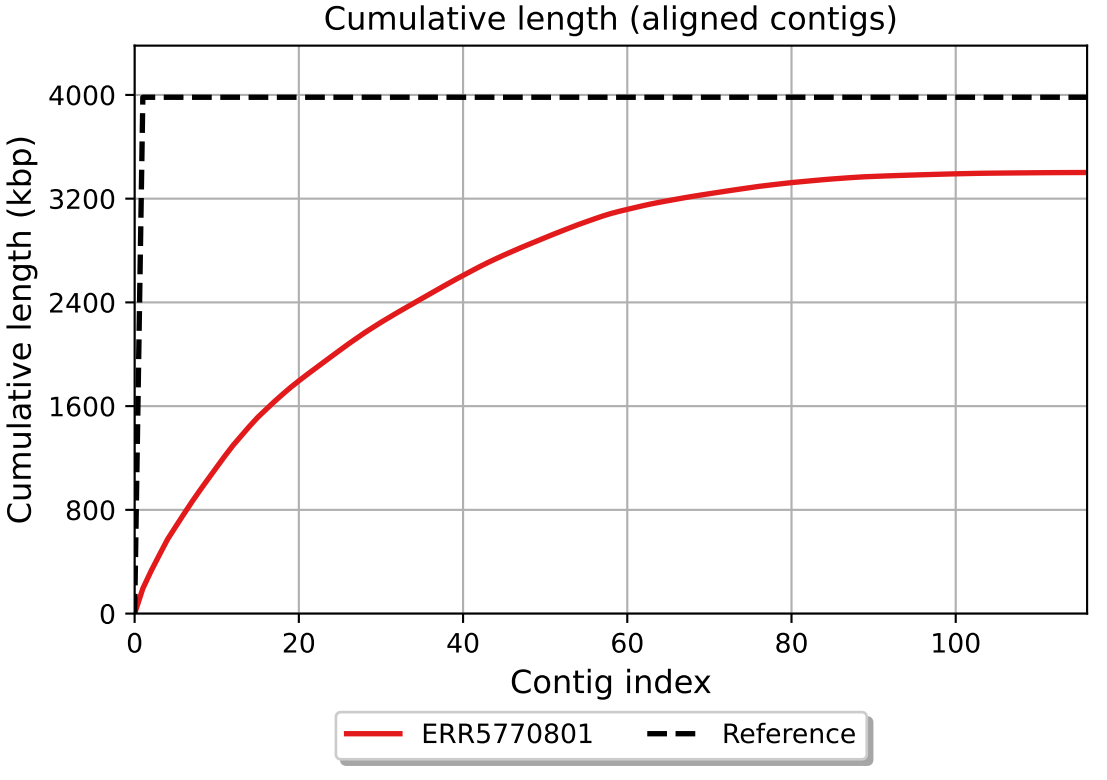

ERR5770801 GC content
# contigs
0
8
16
24
32
40
0
20
40
60
80
100
GC (%)
ERR5770801

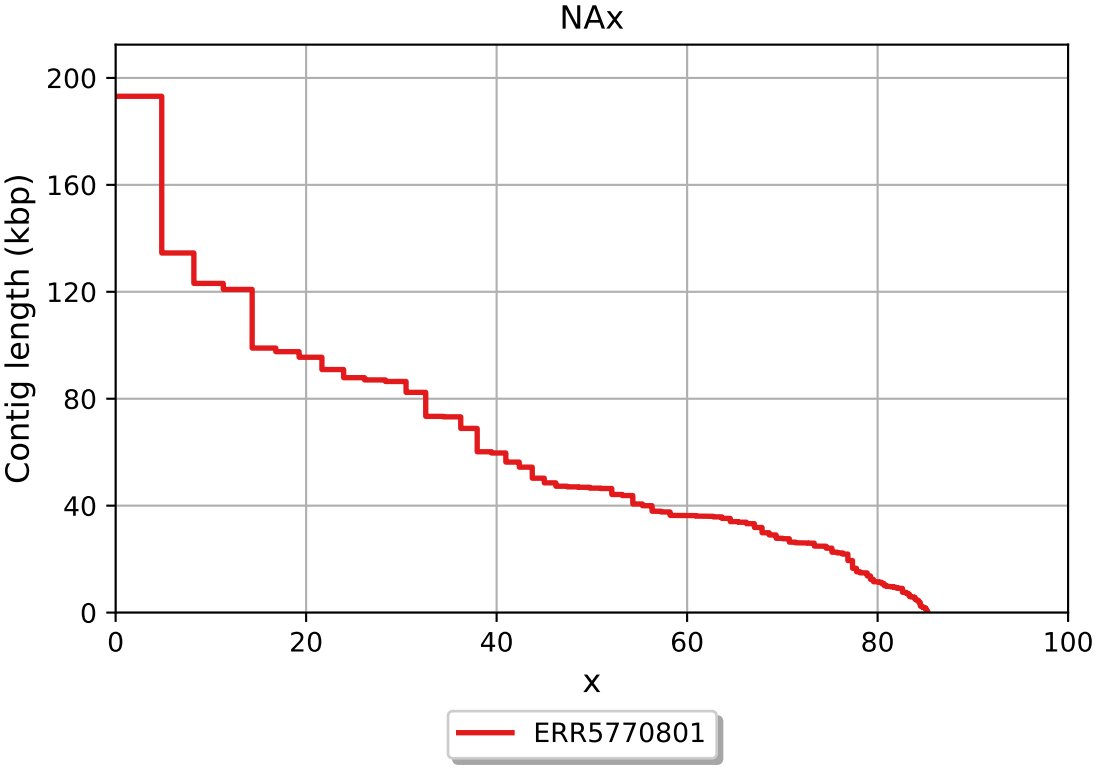

Coverage histogram (bin size: 6x)
Total length (kbp)
1000
500
0
0
30
36
42
48
54
60
66
72
1435
Coverage depth (x)
ERR5770801

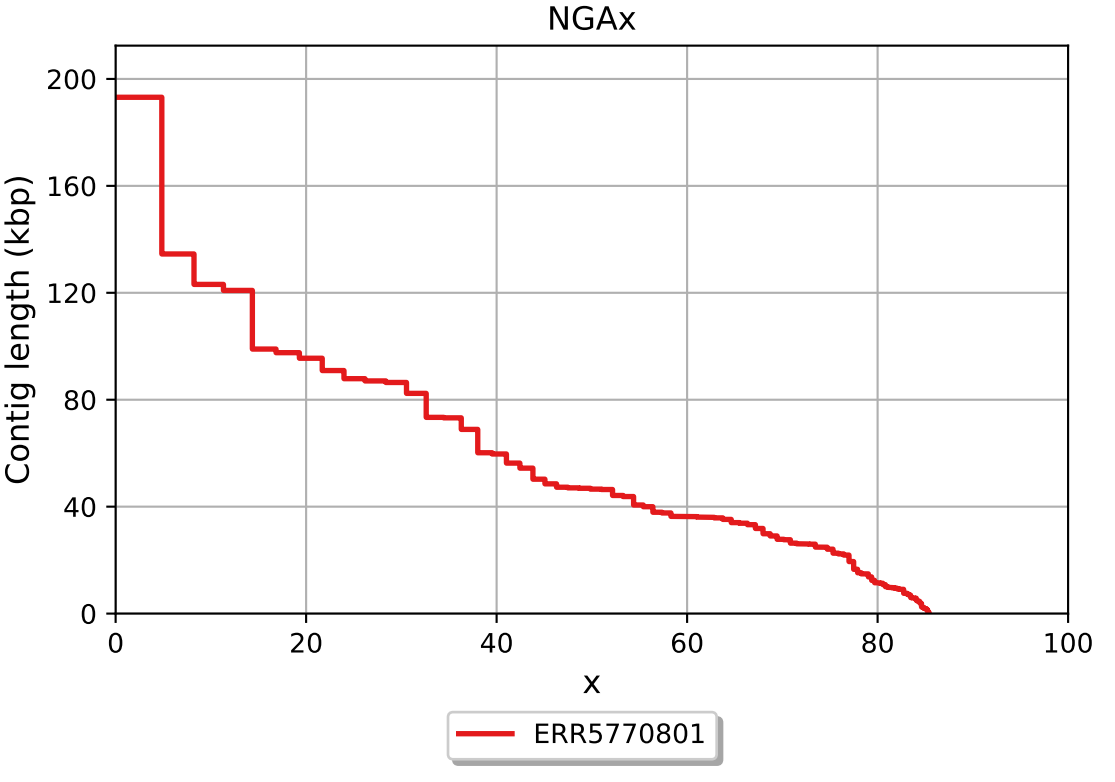

ERR5770801 coverage histogram (bin size: 6x)
Total length (kbp)
1000
500
0
0
30
36
42
48
54
60
66
72
1435
Coverage depth (x)
ERR5770801

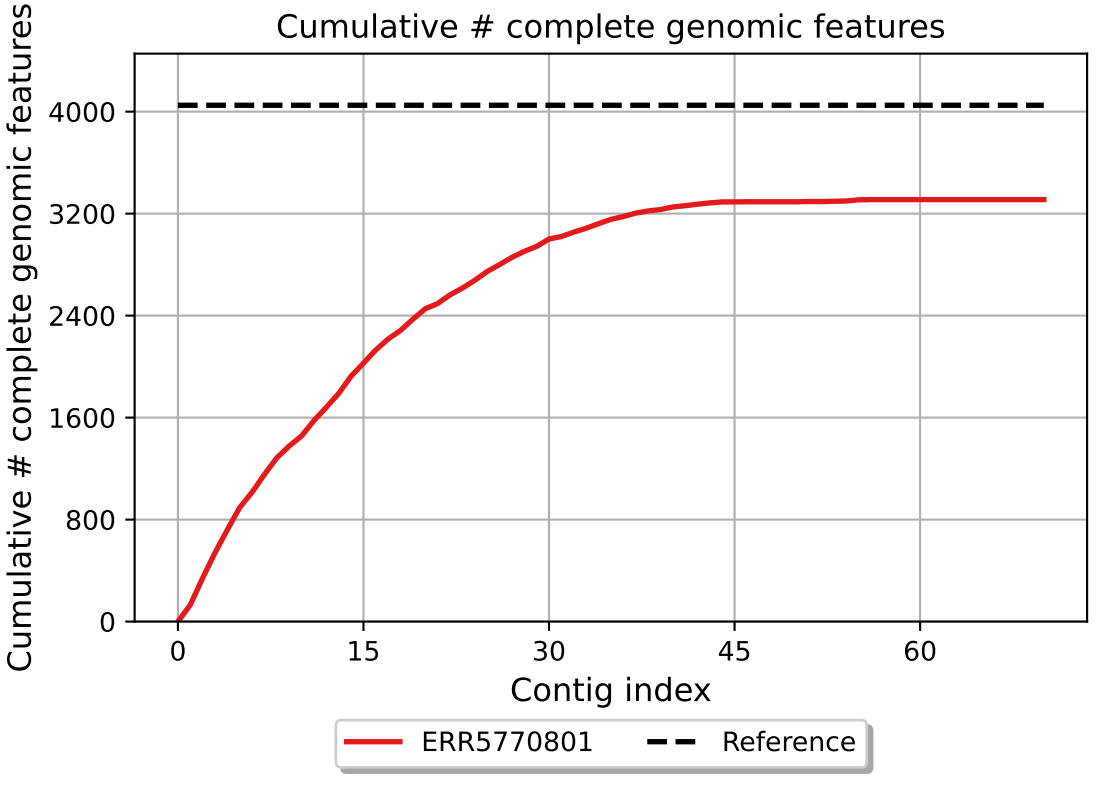

Misassemblies
60
45
30
15
0
ERR5770801
# relocations

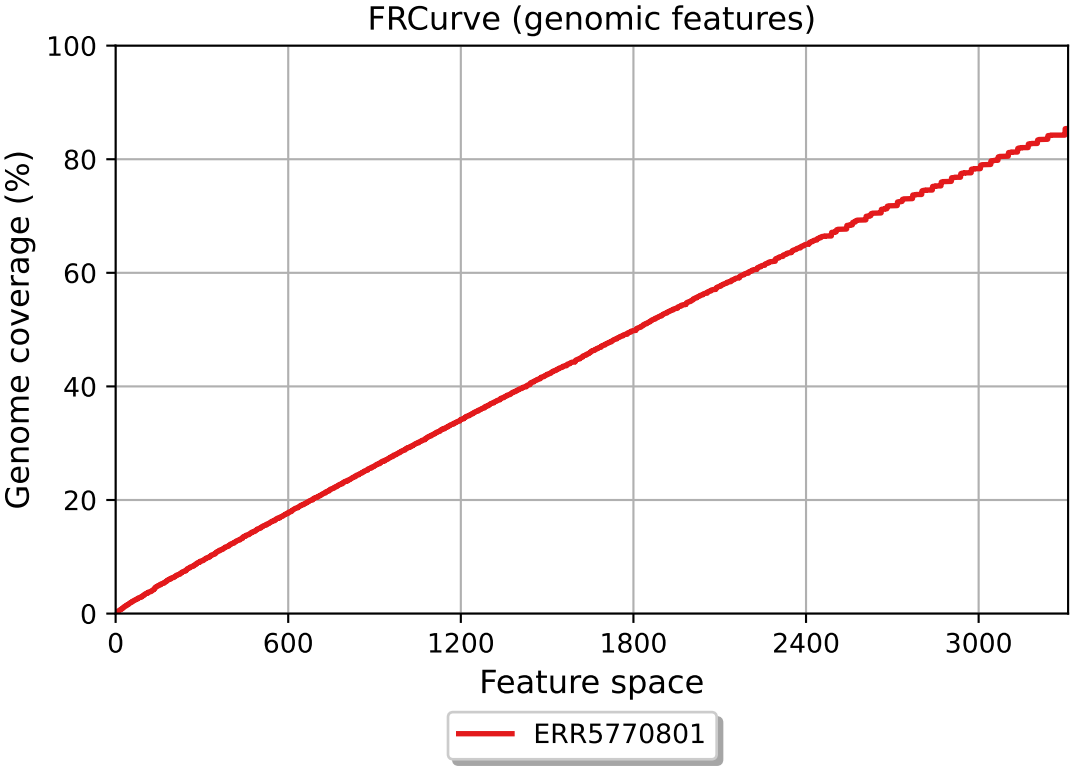

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
10
20
30
40
50
Feature space
ERR5770801


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
Contig index
ERR5770801
Reference


NAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
ERR5770801


NGAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
ERR5770801


Cumulative # complete genomic features
Cumulative # complete genomic features
4000
3200
2400
1600
800
0
0
15
30
45
60
Contig index
ERR5770801
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
600
1200
1800
2400
3000
Feature space
ERR5770801