

# Report

	ERR5770802
# contigs (>= 0 bp)	260
# contigs (>= 1000 bp)	105
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	43
# contigs (>= 25000 bp)	33
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4113950
Total length (>= 1000 bp)	4036050
Total length (>= 5000 bp)	3918029
Total length (>= 10000 bp)	3870231
Total length (>= 25000 bp)	3701815
Total length (>= 50000 bp)	3473193
# contigs	183
Largest contig	242150
Total length	4092012
Reference length	3981941
GC (%)	38.92
Reference GC (%)	39.17
N50	137884
NG50	137884
N90	28458
NG90	44397
auN	134647.0
auNG	138369.0
L50	11
LG50	11
L90	33
LG90	30
# misassemblies	54
# misassembled contigs	25
Misassembled contigs length	3177807
# local misassemblies	45
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	119 + 40 part
Unaligned length	688569
Genome fraction (%)	85.375
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1758.83
# indels per 100 kbp	37.45
# genomic features	3303 + 109 part
Largest alignment	194382
Total aligned length	3399474
NA50	53815
NGA50	54448
NA90	-
NGA90	-
auNA	66911.3
auNGA	68760.9
LA50	22
LGA50	21
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

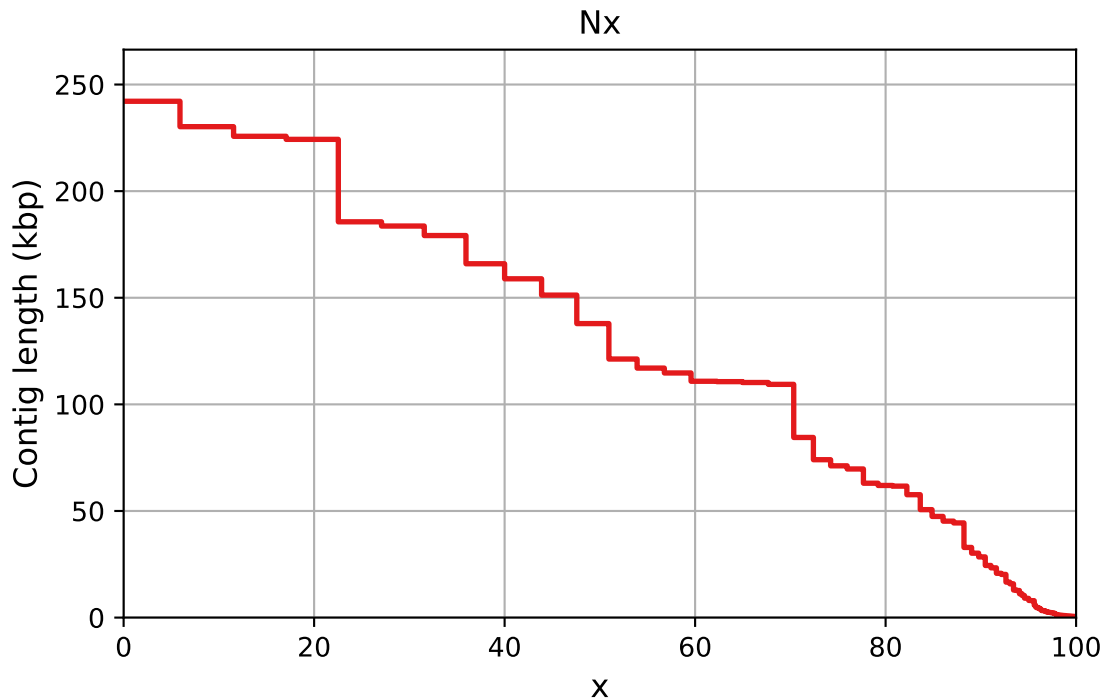
	ERR5770802
# misassemblies	54
# contig misassemblies	54
# c. relocations	54
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	25
Misassembled contigs length	3177807
# local misassemblies	45
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	59791
# indels	1273
# indels (<= 5 bp)	1198
# indels (> 5 bp)	75
Indels length	3770

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

## Unaligned report

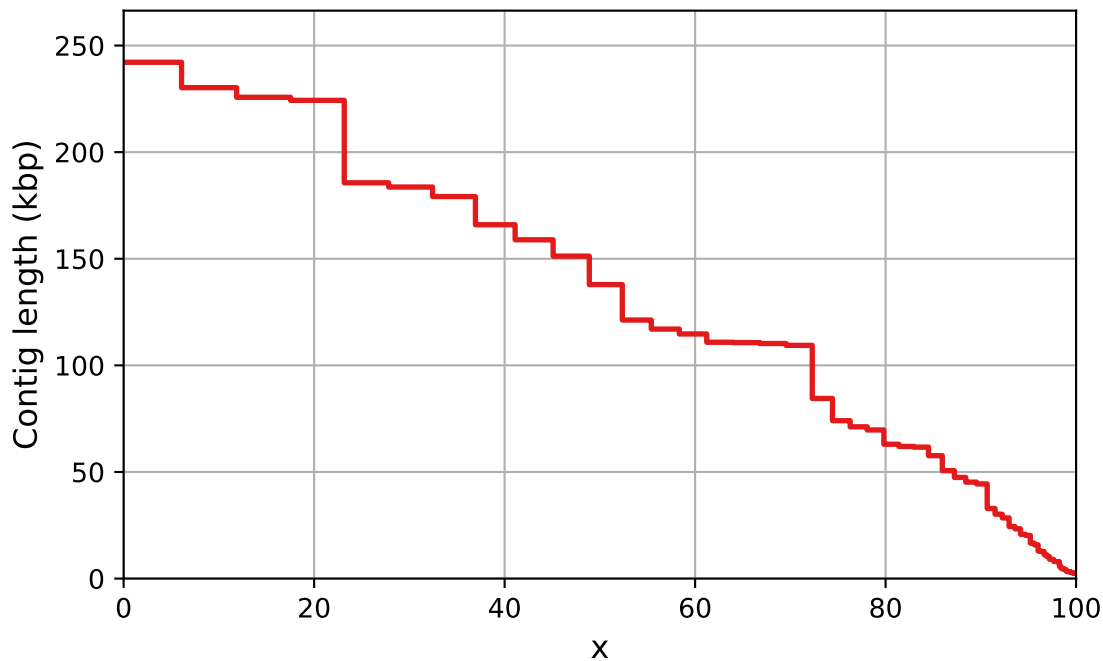
	ERR5770802
# fully unaligned contigs	119
Fully unaligned length	240441
# partially unaligned contigs	40
Partially unaligned length	448128
# N's	0

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



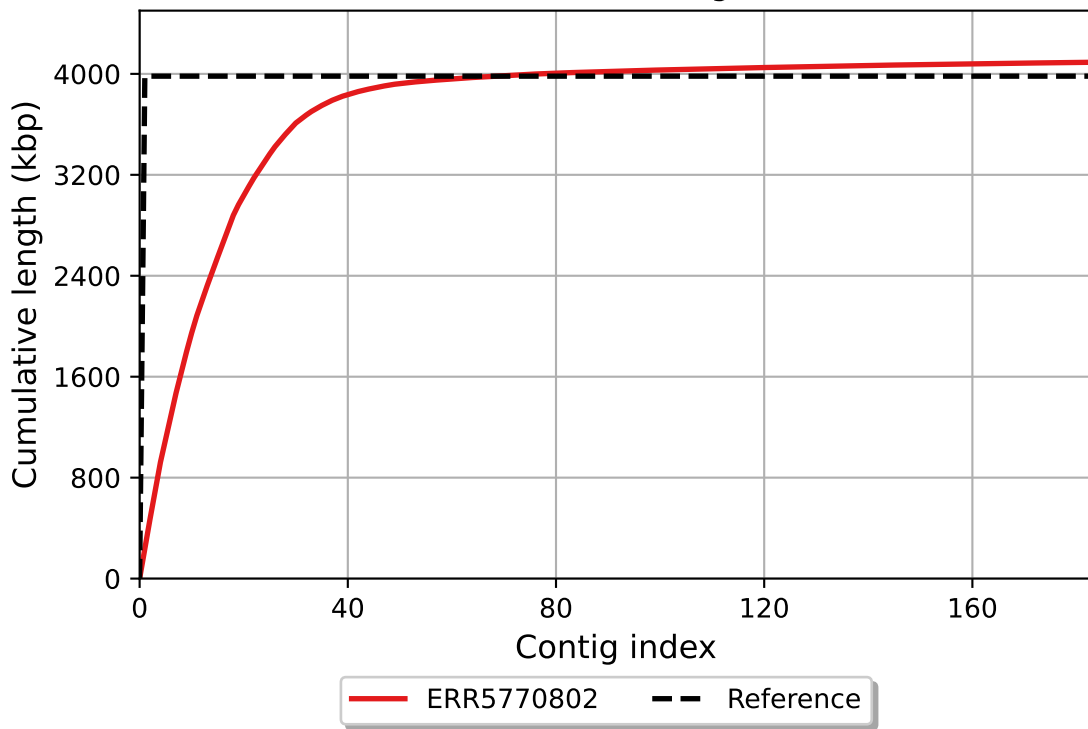
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NGx

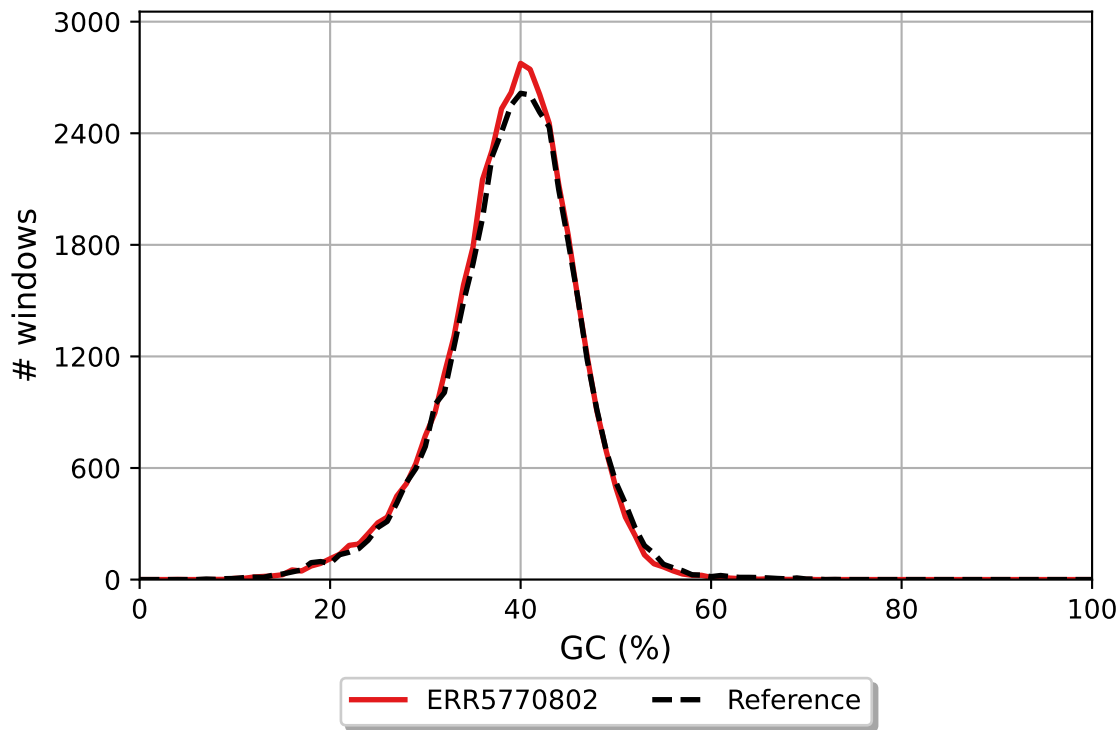


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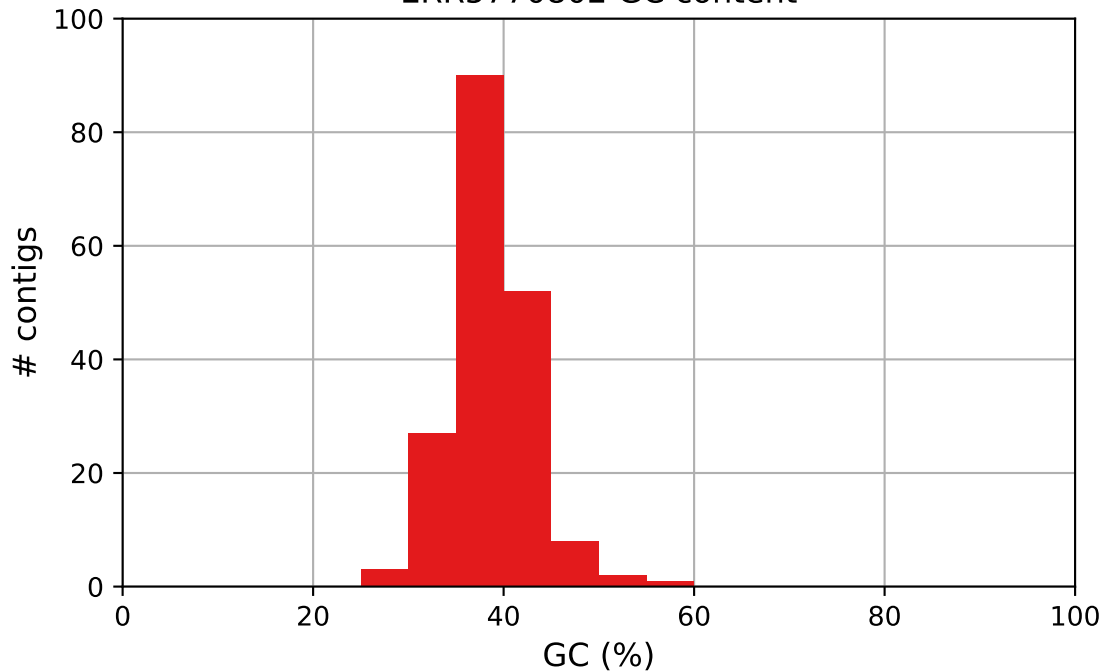
Cumulative length



# GC content



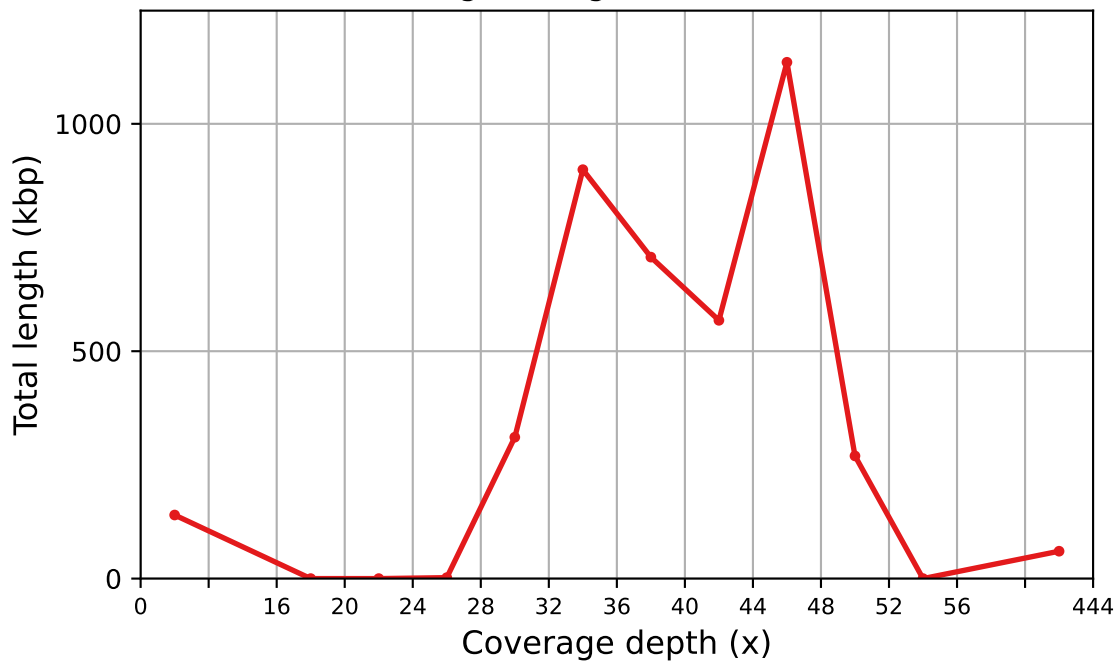
ERR5770802 GC content



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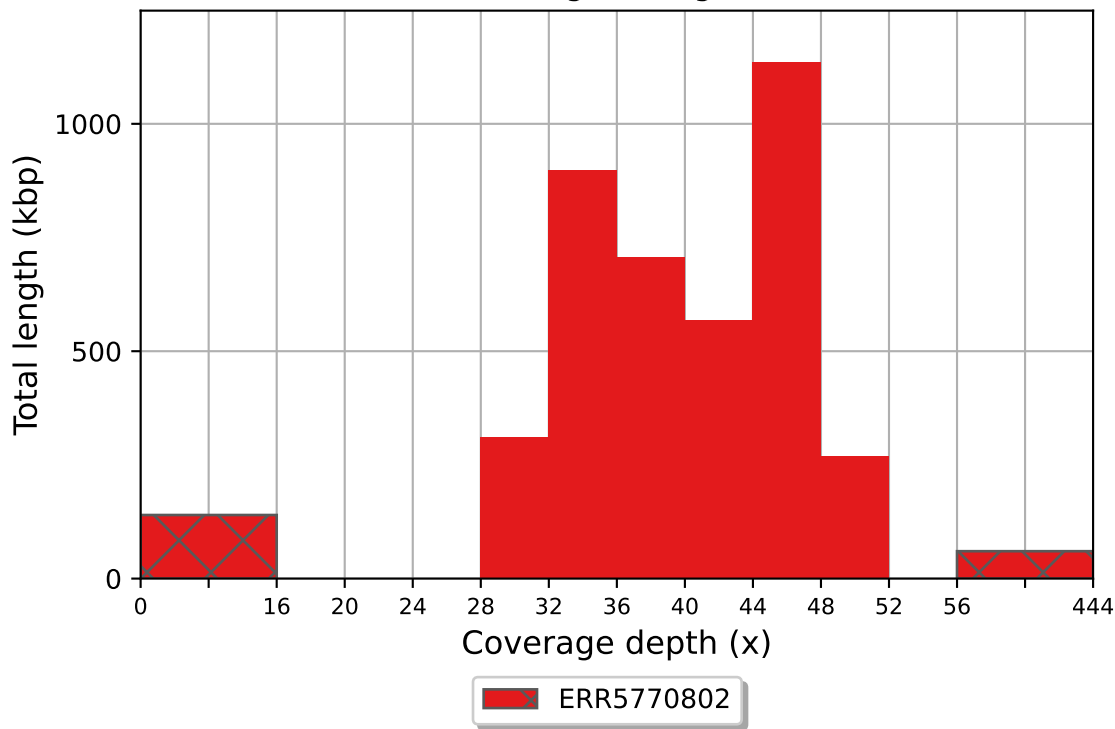


Coverage histogram (bin size: 4x)

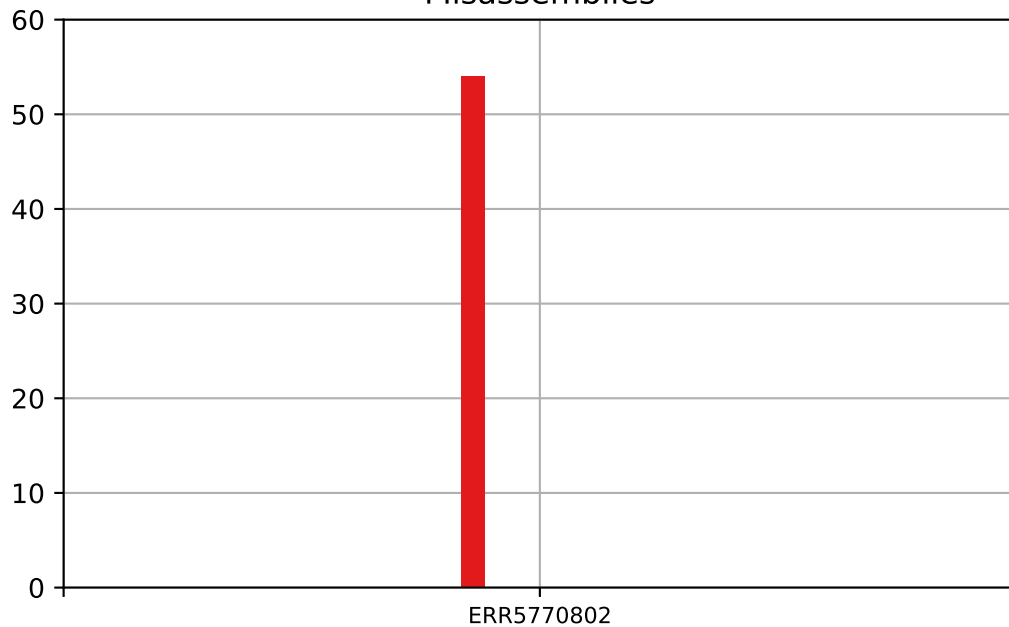


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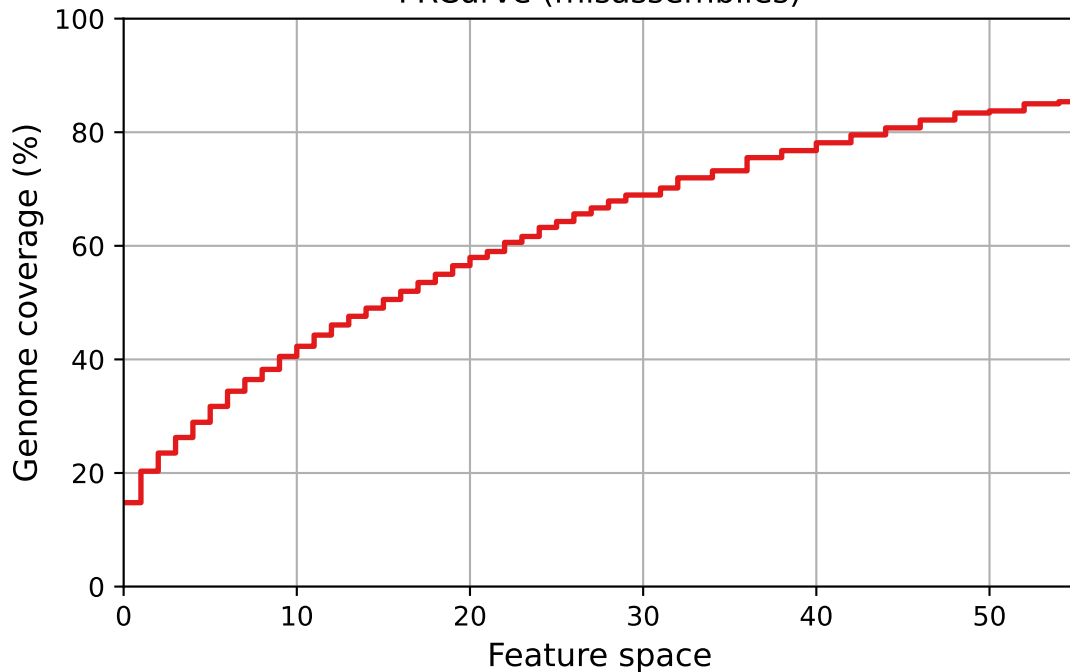
ERR5770802 coverage histogram (bin size: 4x)



## Misassemblies

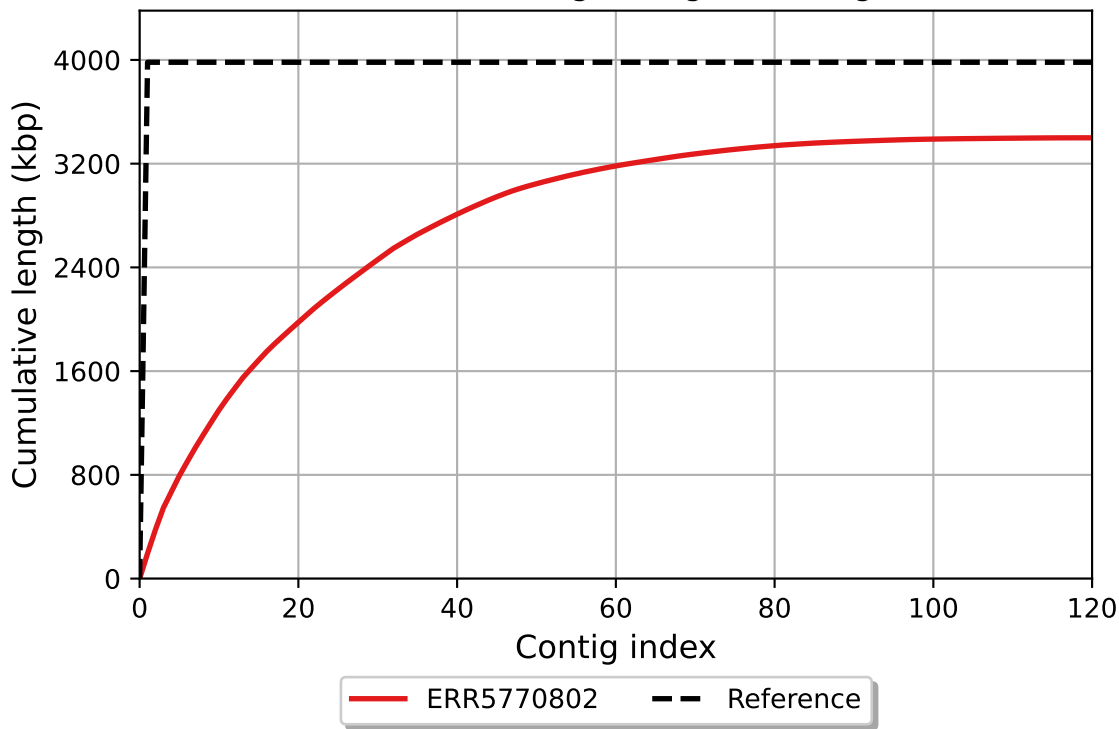


FRCurve (misassemblies)

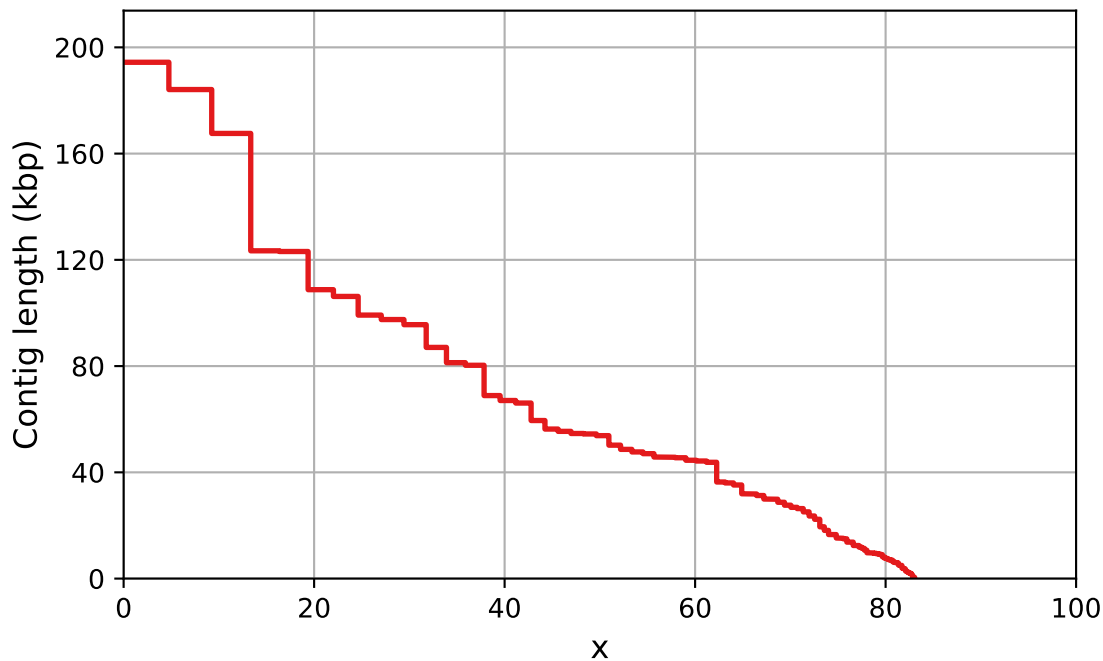


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Cumulative length (aligned contigs)

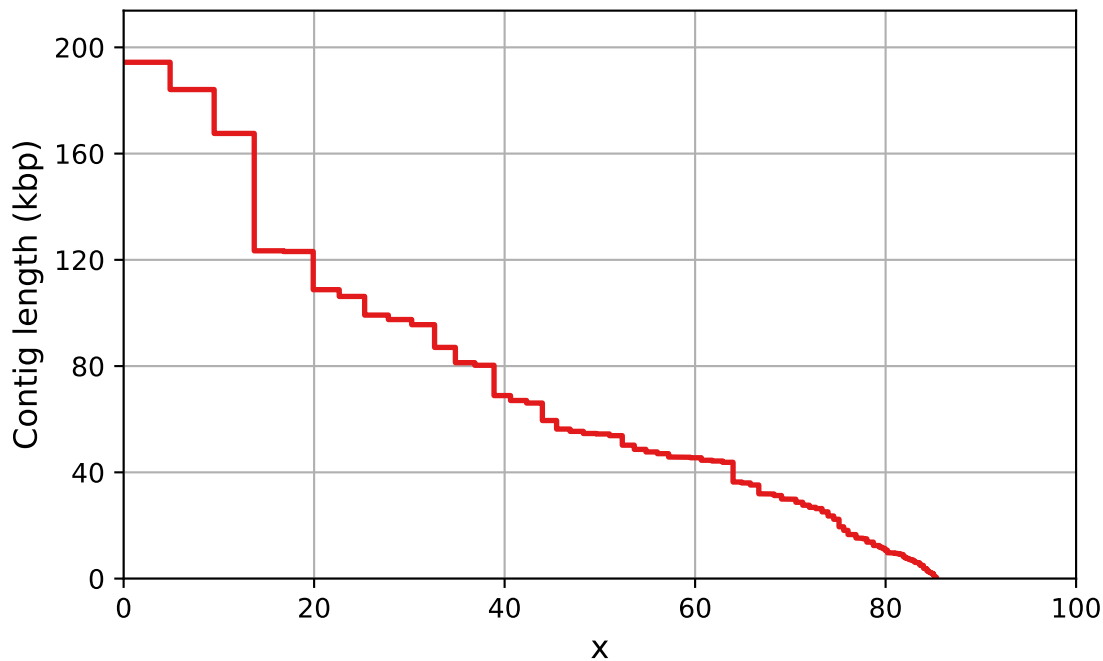


NAx



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# NGAx



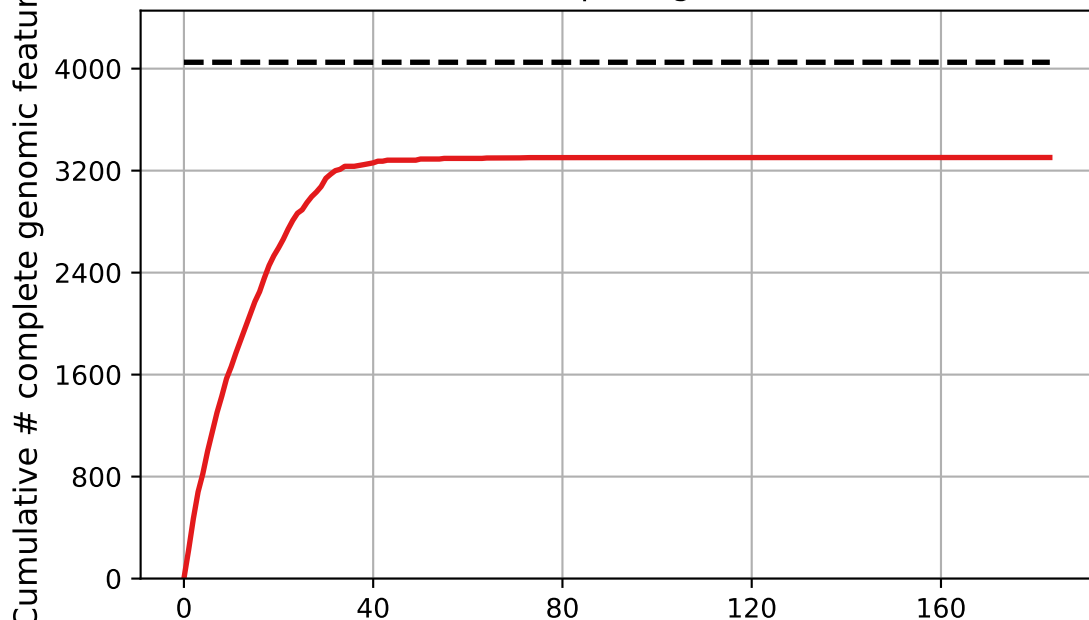
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Cumulative # complete genomic features

Cumulative # complete genomic features

Contig index

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FRCurve (genomic features)

