

# Report

	ERR5770807
# contigs (>= 0 bp)	219
# contigs (>= 1000 bp)	121
# contigs (>= 5000 bp)	88
# contigs (>= 10000 bp)	70
# contigs (>= 25000 bp)	46
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	3998705
Total length (>= 1000 bp)	3966043
Total length (>= 5000 bp)	3887799
Total length (>= 10000 bp)	3757016
Total length (>= 25000 bp)	3364353
Total length (>= 50000 bp)	2710381
# contigs	140
Largest contig	165239
Total length	3978814
Reference length	3981941
GC (%)	38.90
Reference GC (%)	39.17
N50	81641
NG50	81641
N90	16306
NG90	16306
auN	81465.6
auNG	81401.6
L50	18
LG50	18
L90	57
LG90	57
# misassemblies	45
# misassembled contigs	29
Misassembled contigs length	2201256
# local misassemblies	47
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	44 + 55 part
Unaligned length	638372
Genome fraction (%)	83.611
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1765.17
# indels per 100 kbp	40.78
# genomic features	3246 + 105 part
Largest alignment	123141
Total aligned length	3334867
NA50	48647
NGA50	48647
NA90	-
NGA90	-
auNA	47308.2
auNGA	47271.1
LA50	27
LGA50	27
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

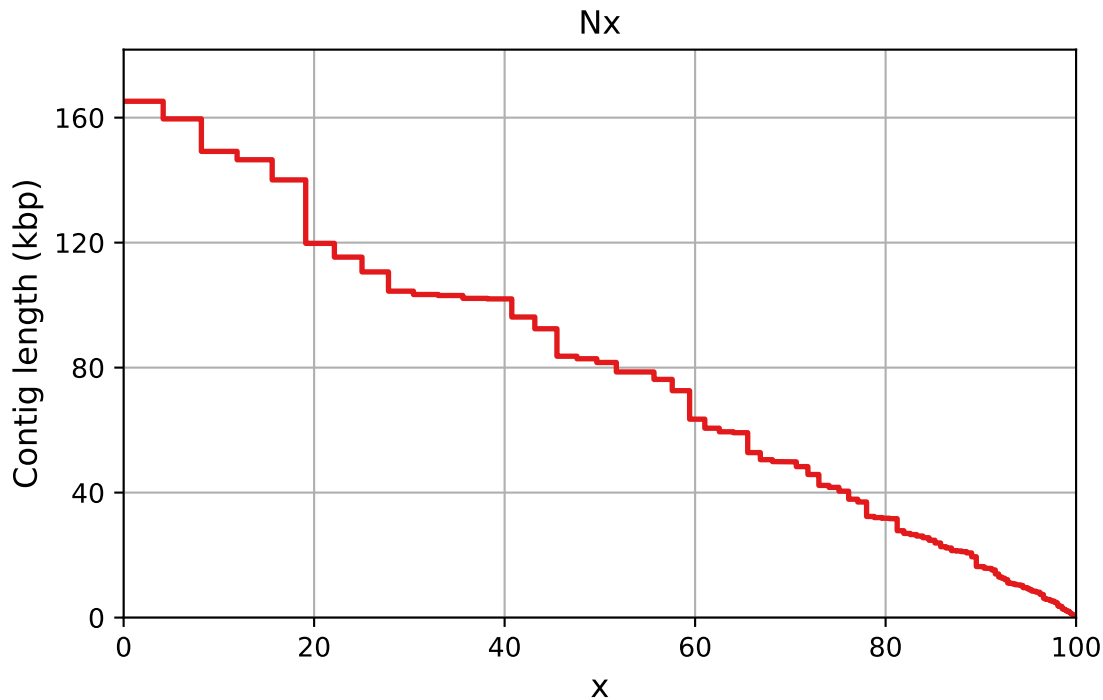
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# misassemblies	45
# contig misassemblies	45
# c. relocations	45
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	29
Misassembled contigs length	2201256
# local misassemblies	47
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	58866
# indels	1360
# indels (<= 5 bp)	1277
# indels (> 5 bp)	83
Indels length	4056

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

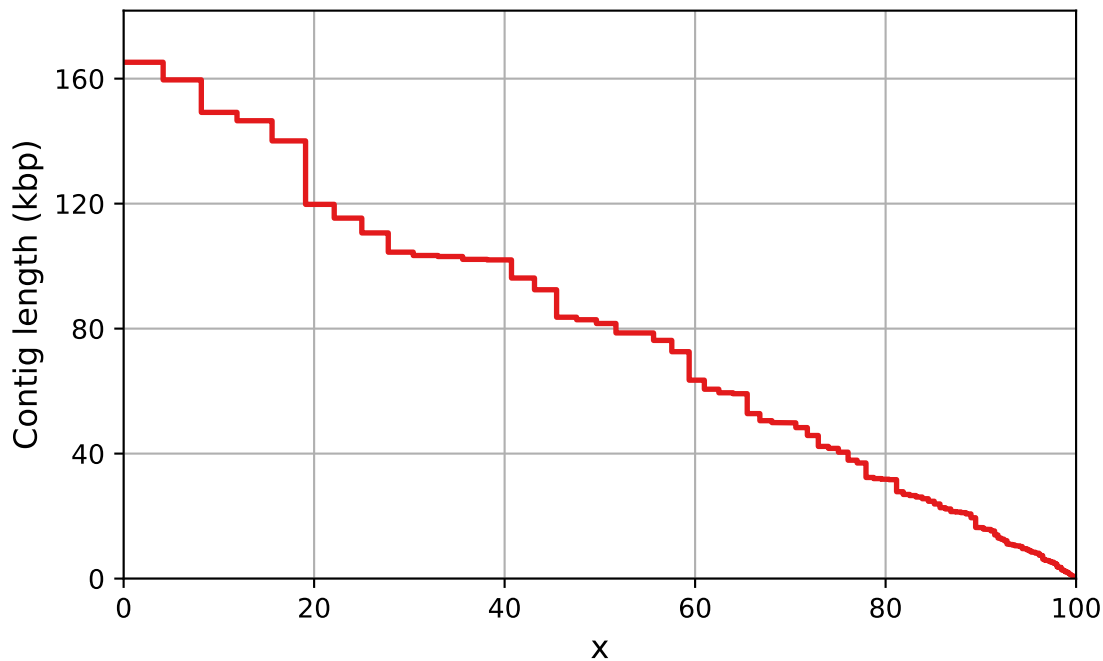
	ERR5770807
# fully unaligned contigs	44
Fully unaligned length	173365
# partially unaligned contigs	55
Partially unaligned length	465007
# N's	0

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).



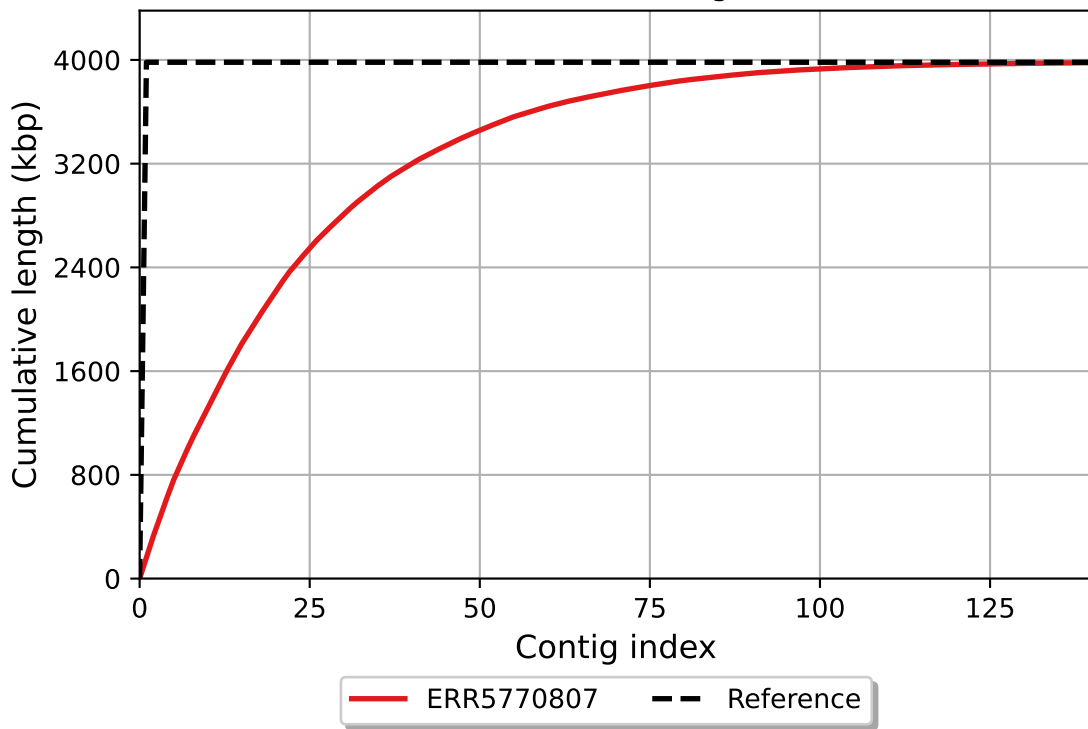
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NGx

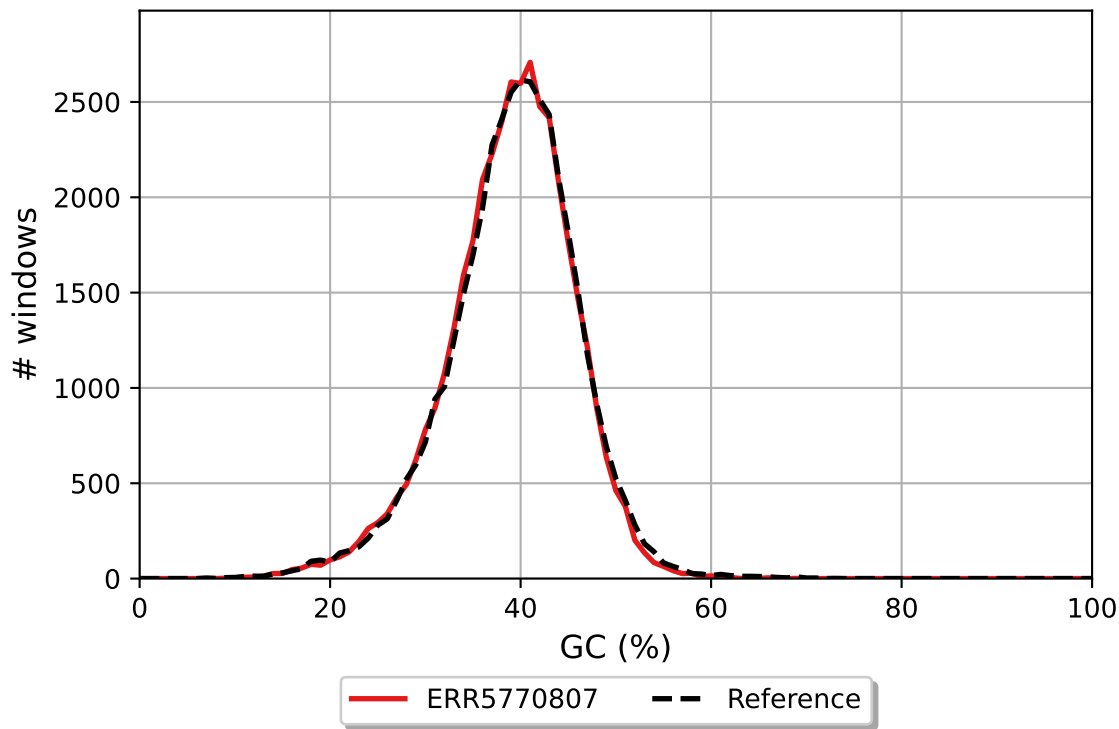


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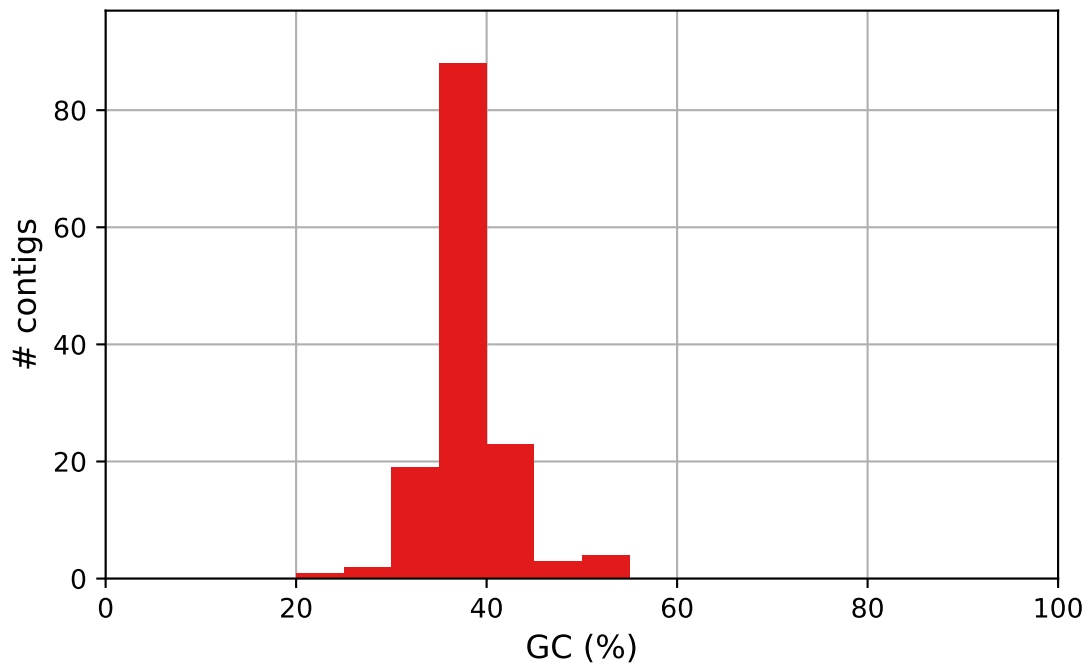
Cumulative length



## GC content



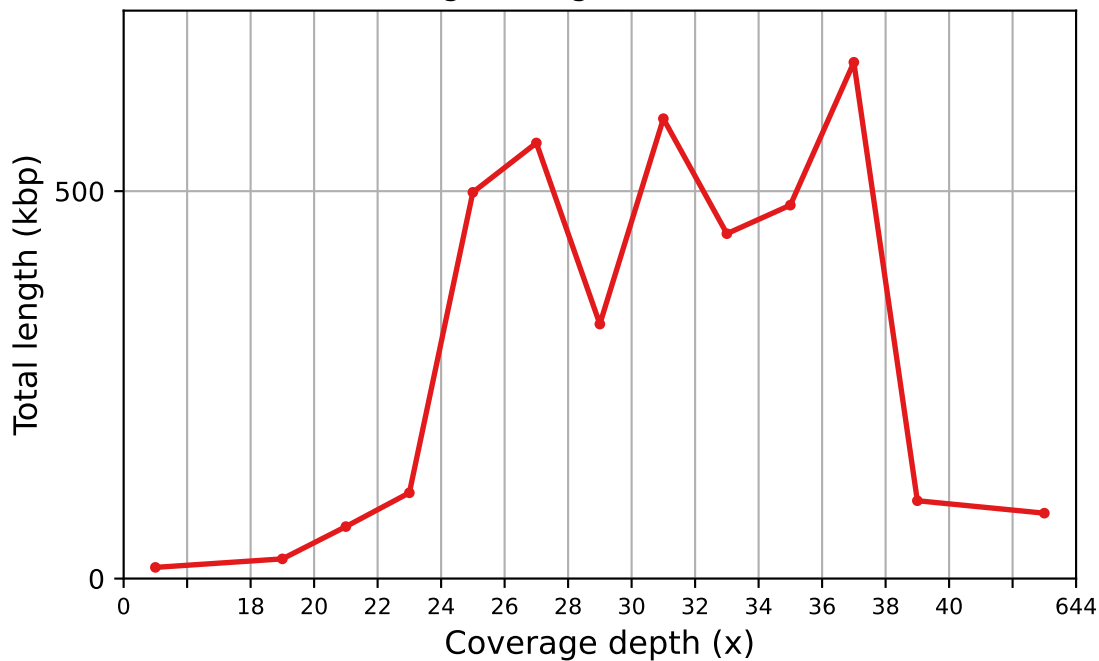
ERR5770807 GC content



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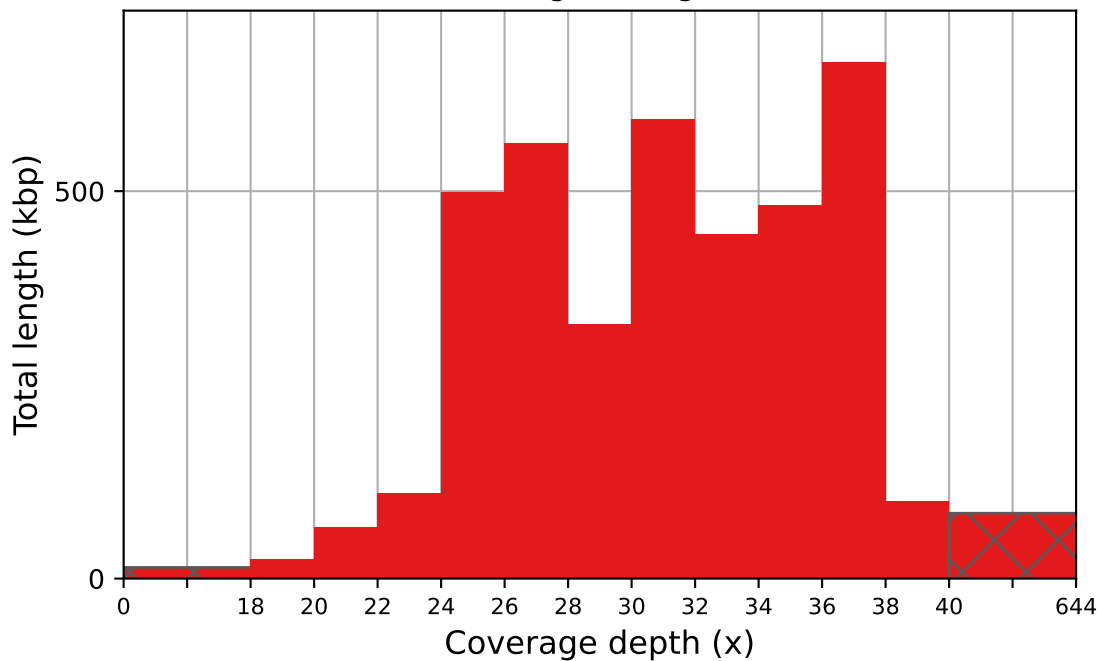


Coverage histogram (bin size: 2x)



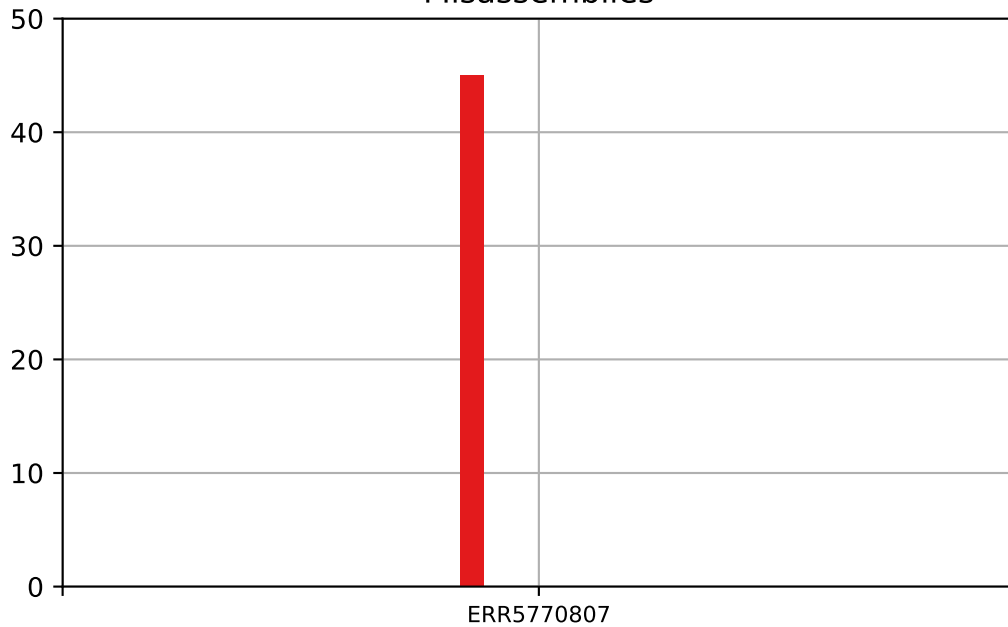
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ERR5770807 coverage histogram (bin size: 2x)

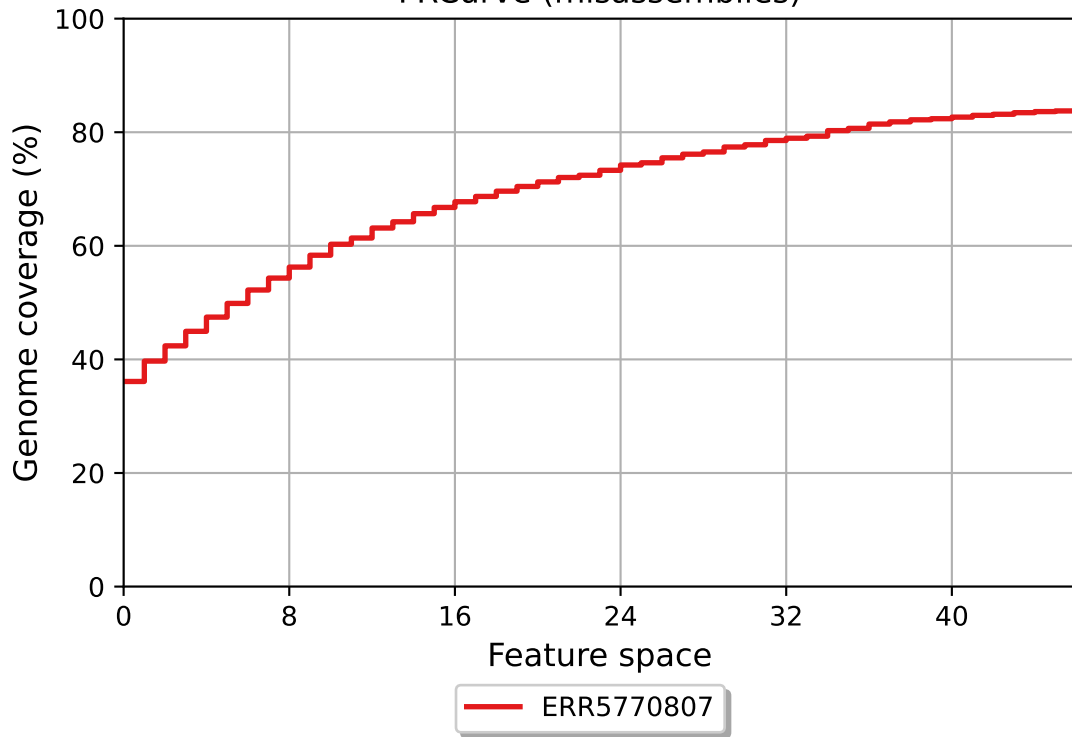


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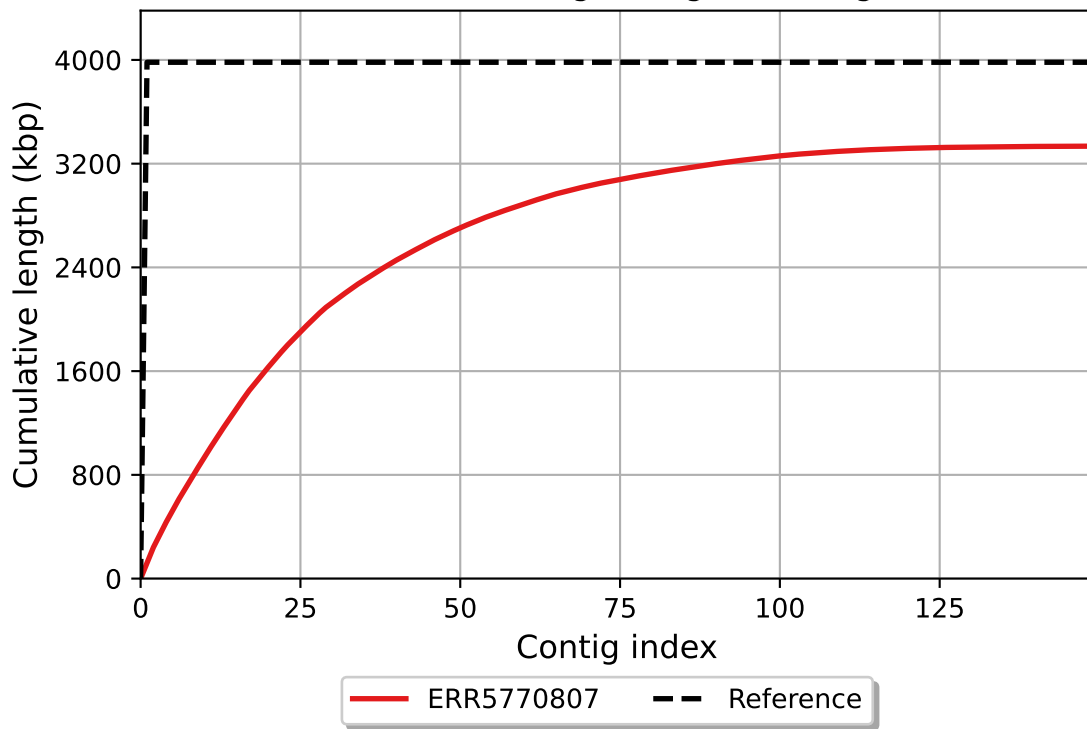
## Misassemblies



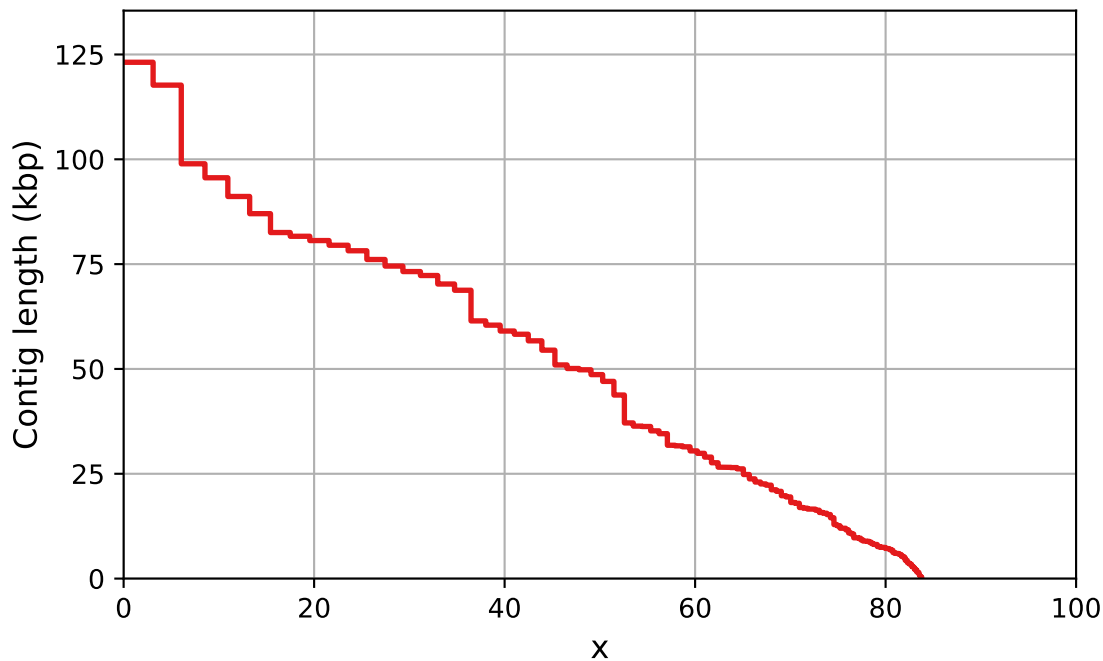
FRCurve (misassemblies)



Cumulative length (aligned contigs)

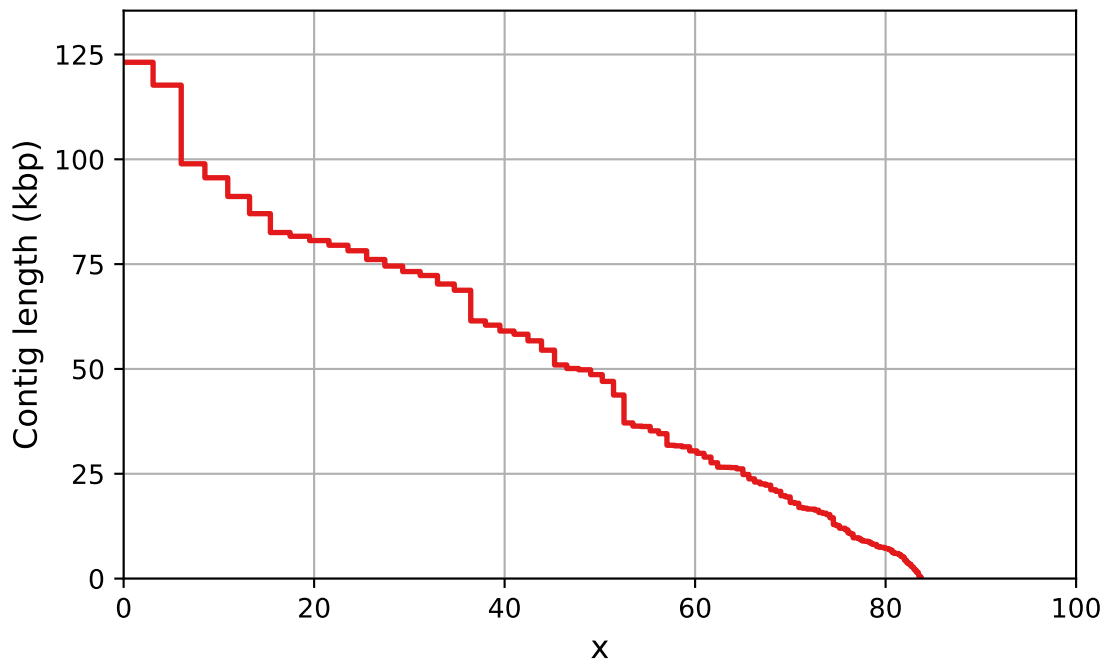


NAx



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# NGAx



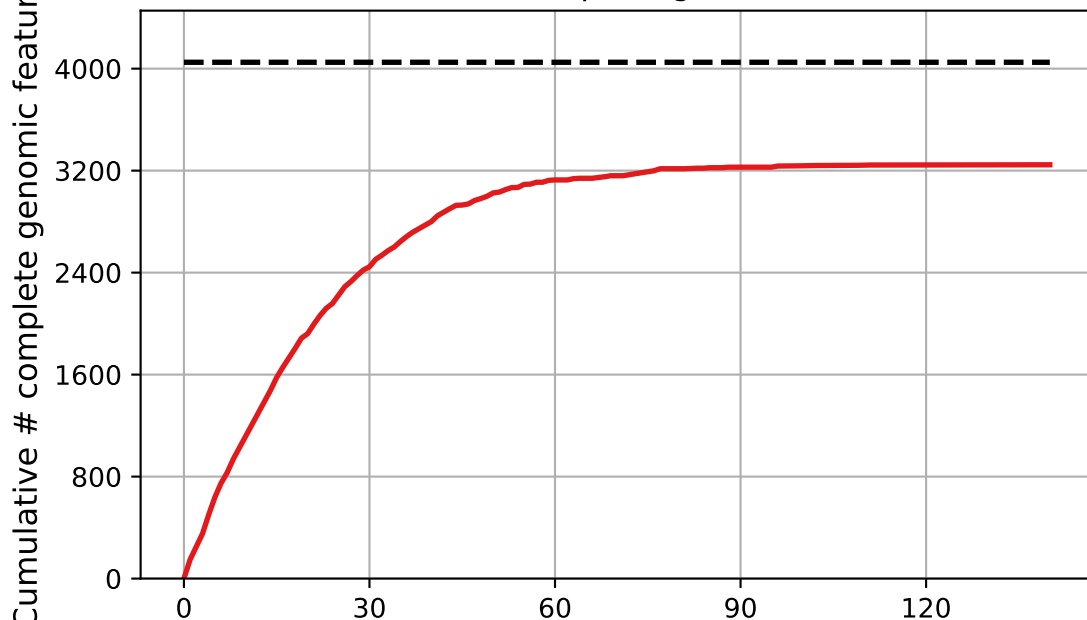
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Cumulative # complete genomic features

Cumulative # complete genomic features

Contig index

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FRCurve (genomic features)

