

# Report

	ERR5770804
# contigs (>= 0 bp)	153
# contigs (>= 1000 bp)	94
# contigs (>= 5000 bp)	69
# contigs (>= 10000 bp)	61
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	25
Total length (>= 0 bp)	3806489
Total length (>= 1000 bp)	3787030
Total length (>= 5000 bp)	3714156
Total length (>= 10000 bp)	3655621
Total length (>= 25000 bp)	3431476
Total length (>= 50000 bp)	2605483
# contigs	105
Largest contig	238912
Total length	3794620
Reference length	3981941
GC (%)	39.08
Reference GC (%)	39.17
N50	76541
NG50	75413
N90	25775
NG90	14632
auN	97878.5
auNG	93274.1
L50	15
LG50	16
L90	48
LG90	56
# misassemblies	62
# misassembled contigs	35
Misassembled contigs length	2669387
# local misassemblies	34
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	26 + 46 part
Unaligned length	619976
Genome fraction (%)	79.523
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1831.71
# indels per 100 kbp	47.81
# genomic features	3085 + 124 part
Largest alignment	116656
Total aligned length	3166884
NA50	36064
NGA50	32691
NA90	-
NGA90	-
auNA	42992.9
auNGA	40970.4
LA50	31
LGA50	34
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

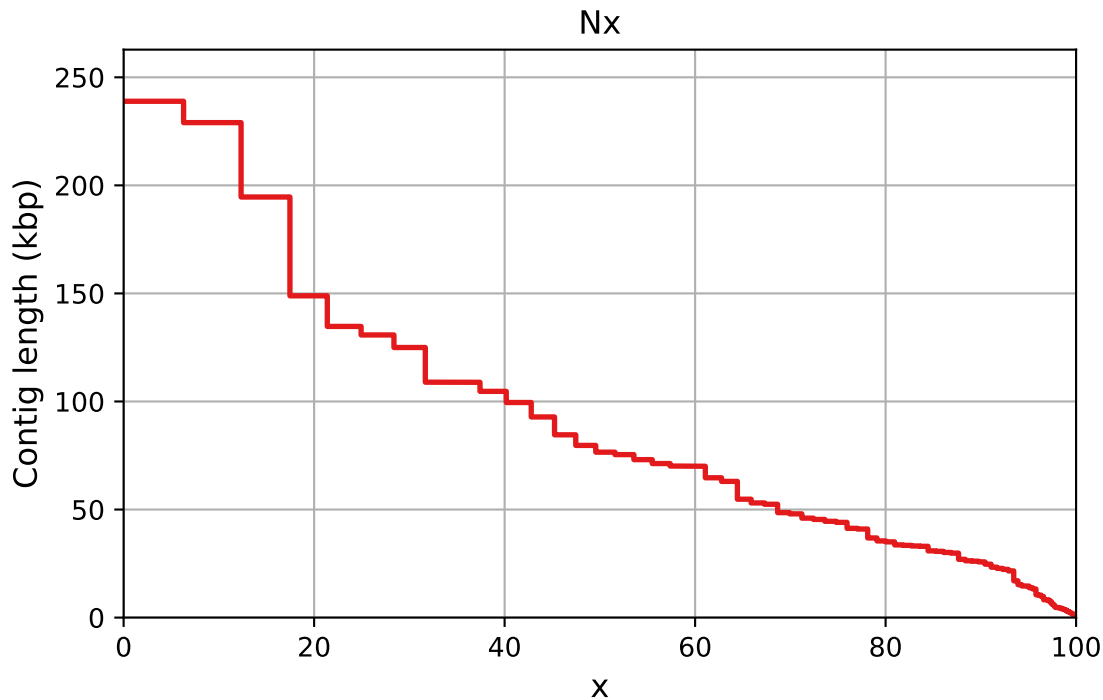
	ERR5770804
# misassemblies	62
# contig misassemblies	62
# c. relocations	62
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	35
Misassembled contigs length	2669387
# local misassemblies	34
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	58008
# indels	1514
# indels (<= 5 bp)	1429
# indels (> 5 bp)	85
Indels length	4447

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

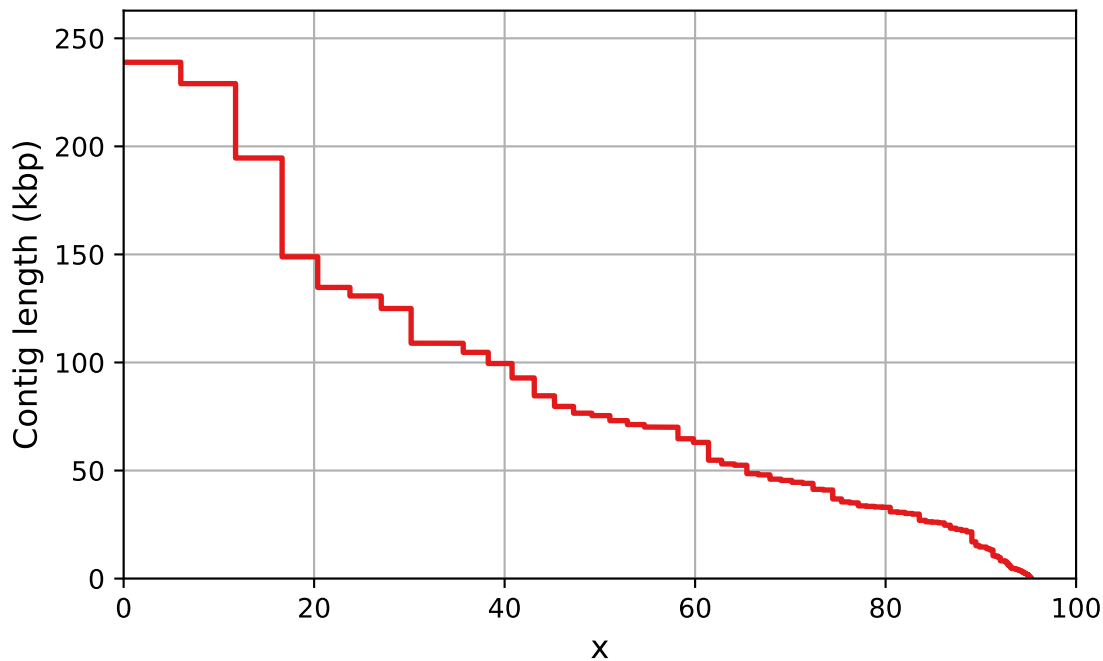
	ERR5770804
# fully unaligned contigs	26
Fully unaligned length	131103
# partially unaligned contigs	46
Partially unaligned length	488873
# N's	0

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).



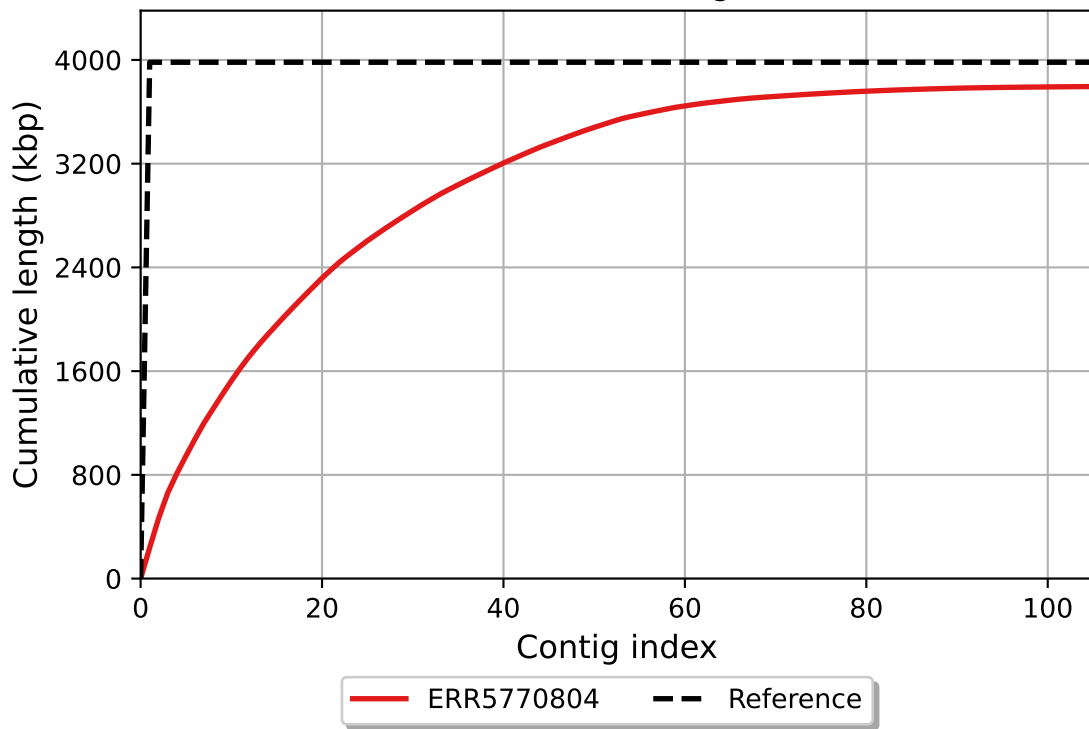
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# NGx

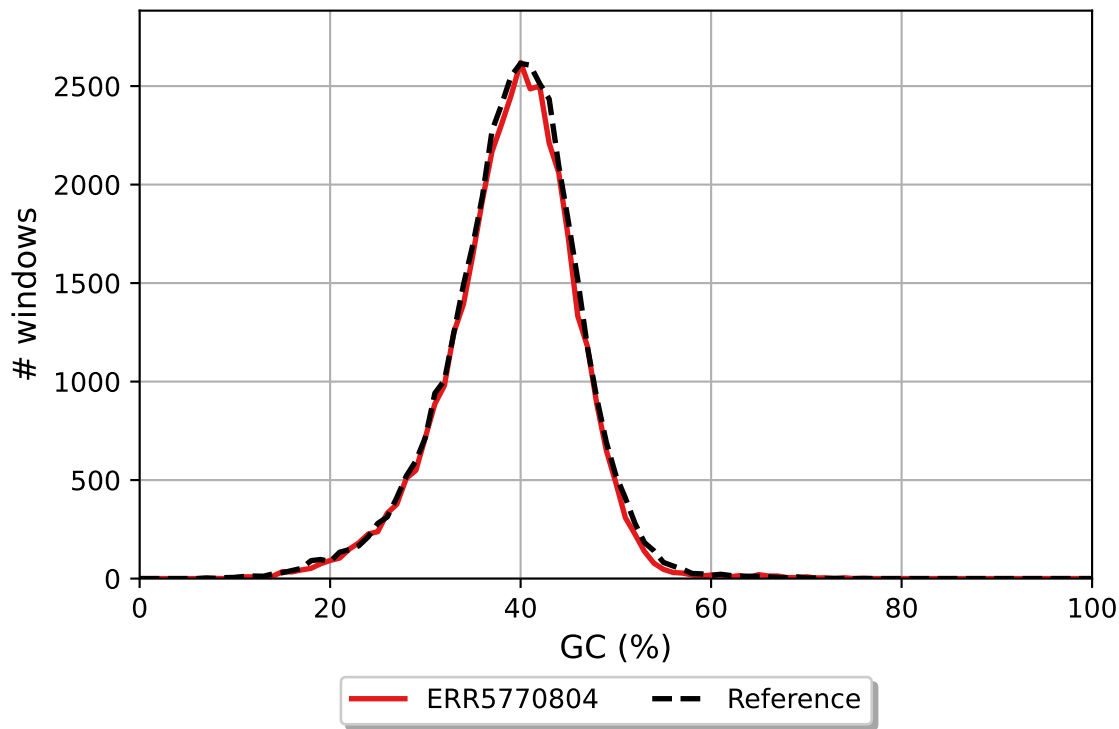


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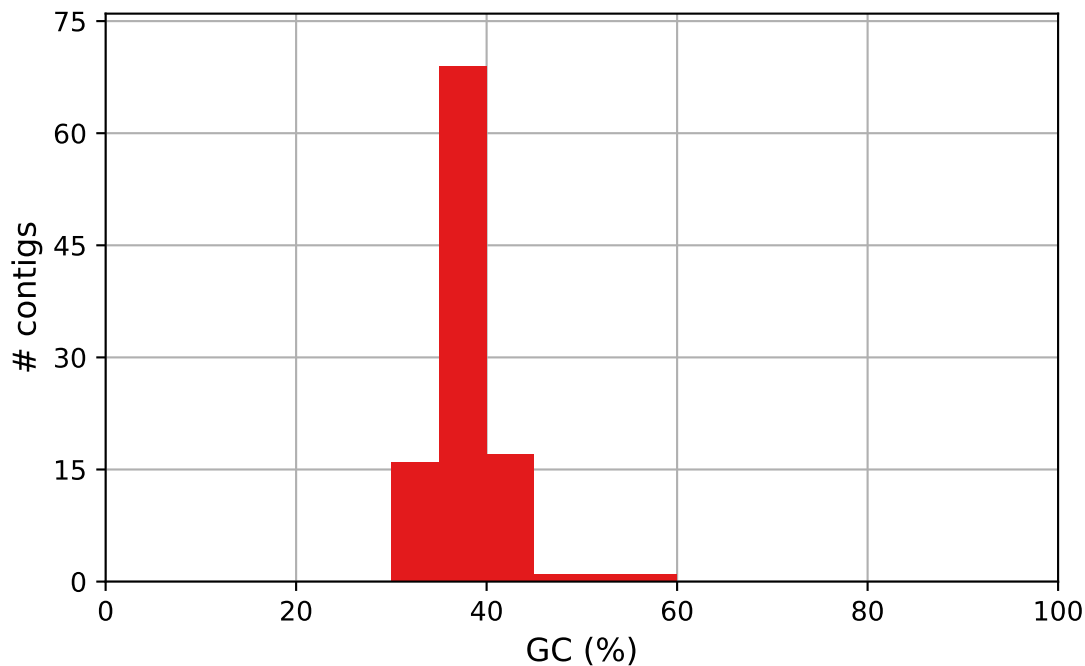
Cumulative length



## GC content



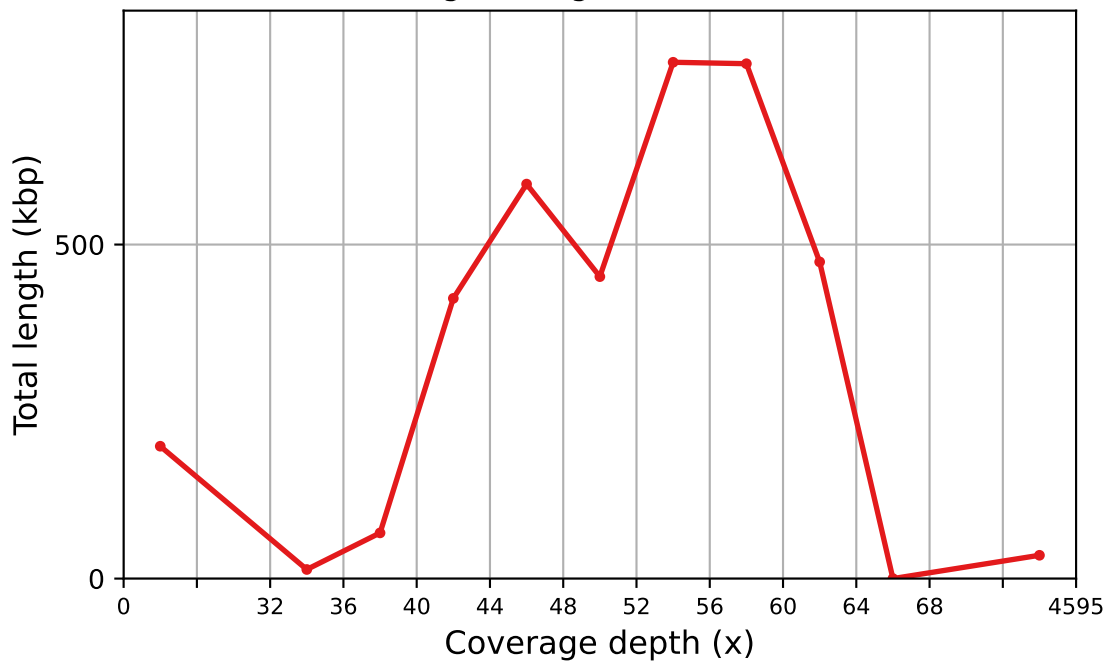
ERR5770804 GC content



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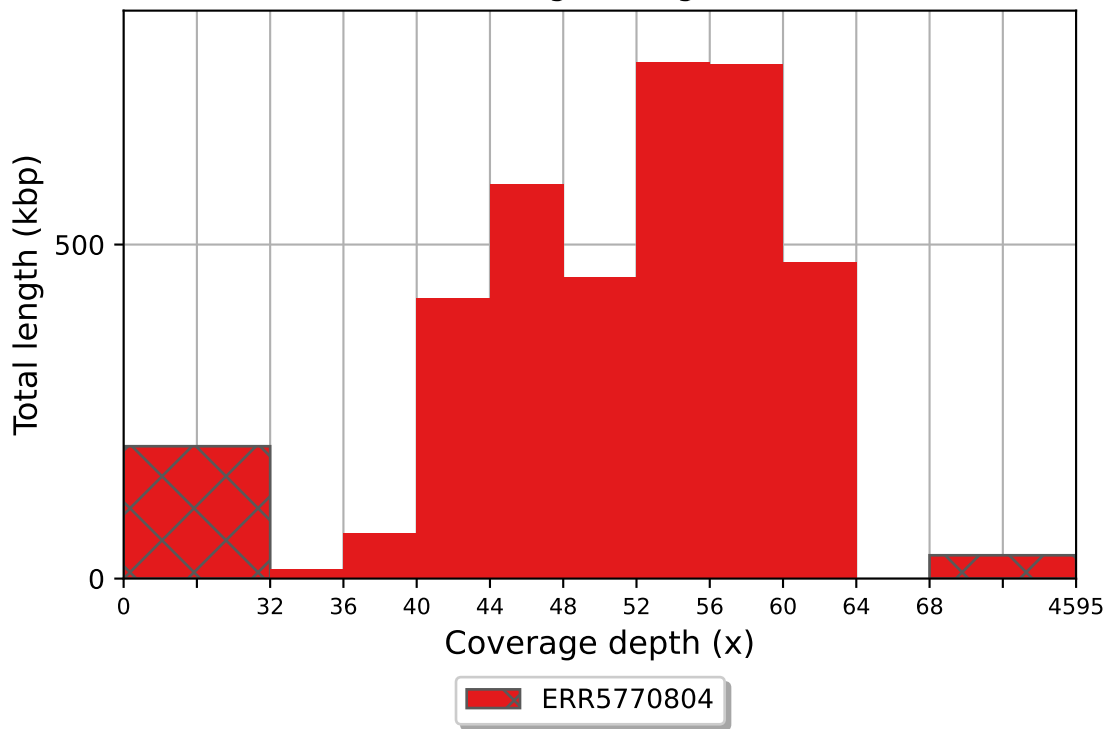


Coverage histogram (bin size: 4x)

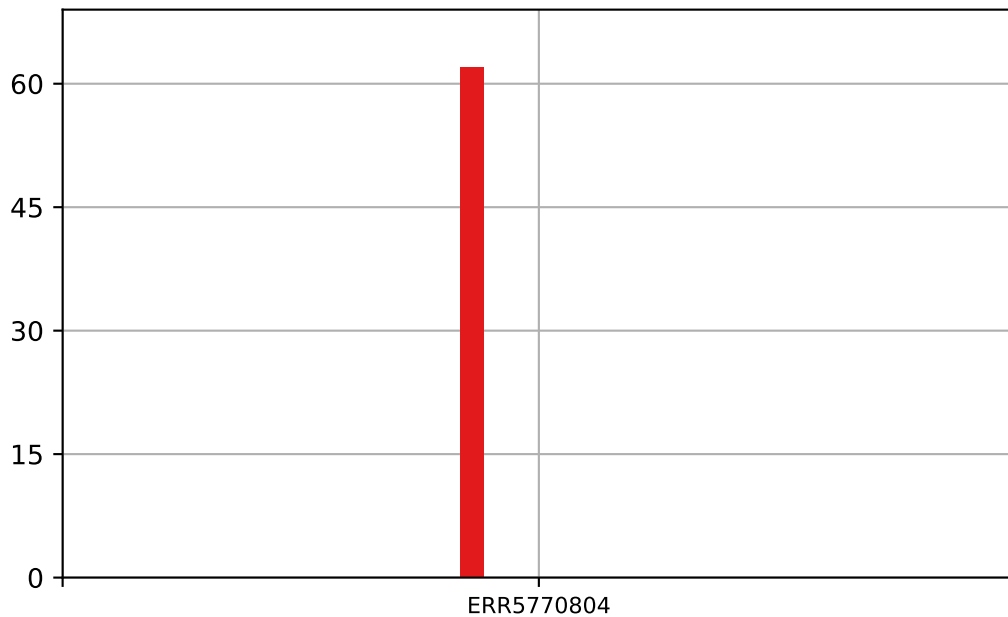


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ERR5770804 coverage histogram (bin size: 4x)

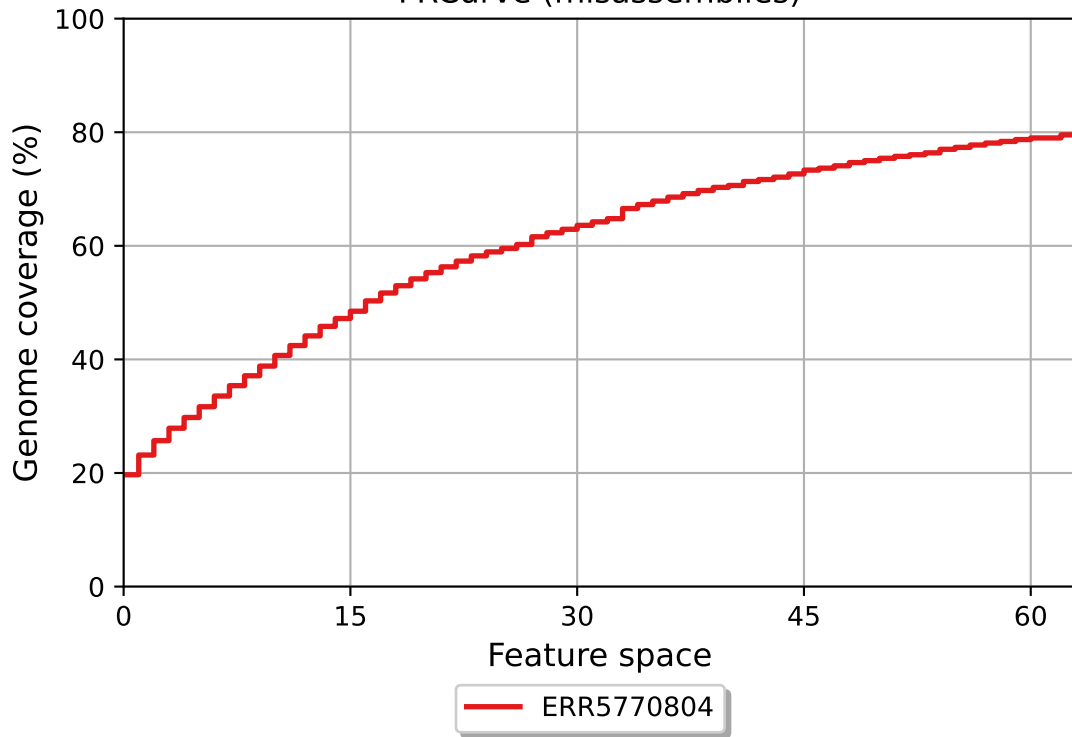


## Misassemblies

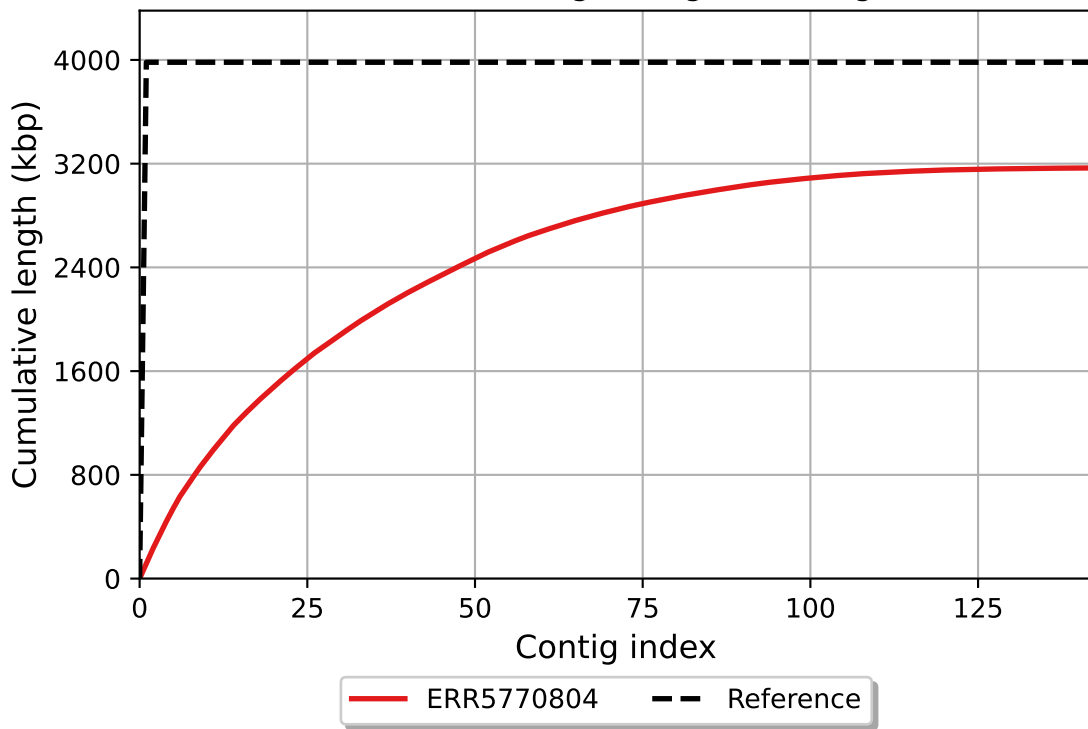


 # relocations

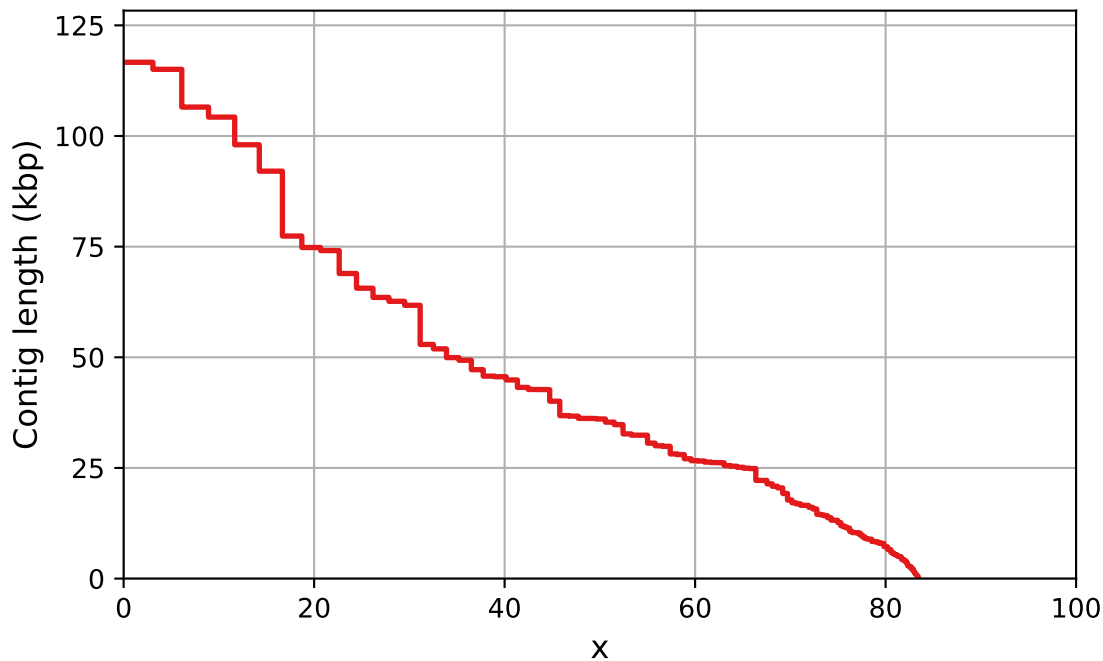
FRCurve (misassemblies)



Cumulative length (aligned contigs)

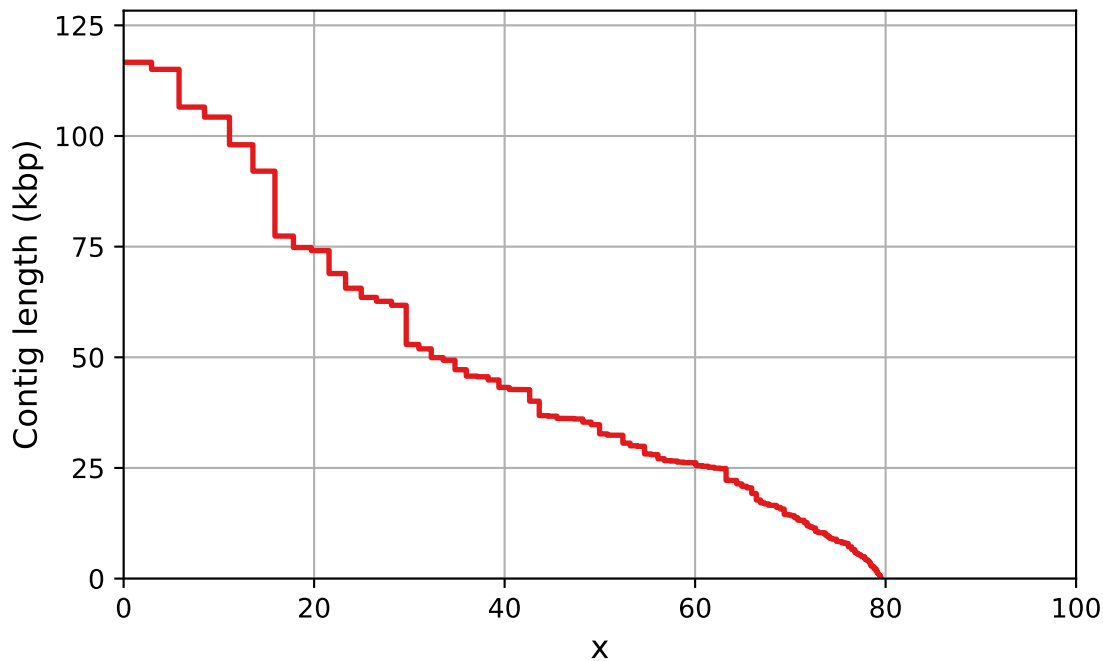


NAx



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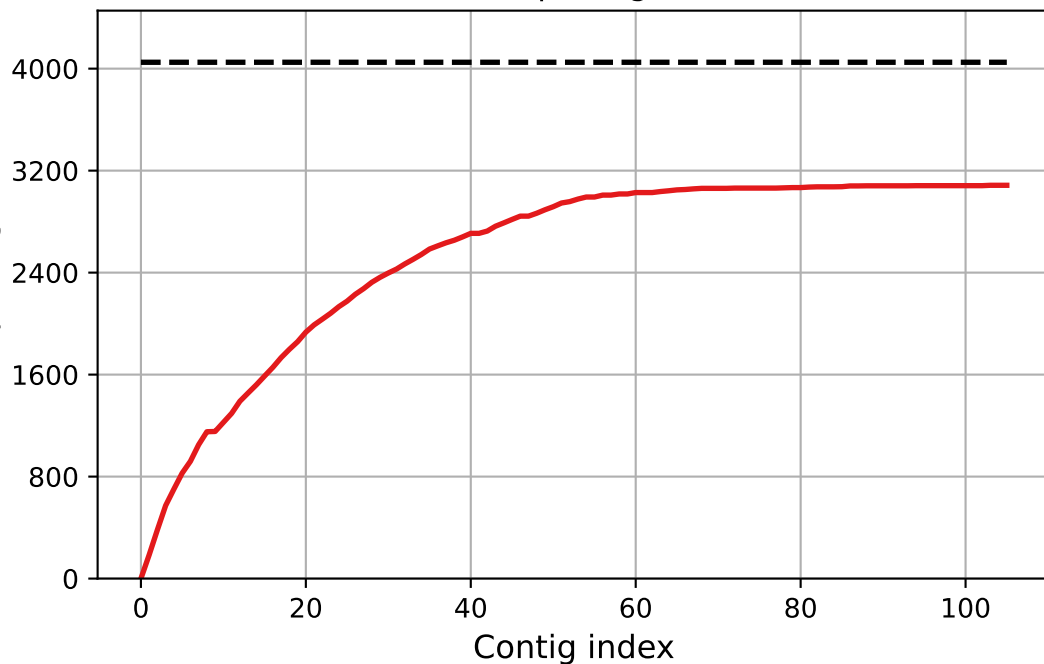
# NGAx



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Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)

