

Report

	ERR5770798
# contigs (>= 0 bp)	222
# contigs (>= 1000 bp)	139
# contigs (>= 5000 bp)	97
# contigs (>= 10000 bp)	74
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	3954196
Total length (>= 1000 bp)	3930280
Total length (>= 5000 bp)	3820947
Total length (>= 10000 bp)	3654054
Total length (>= 25000 bp)	3341411
Total length (>= 50000 bp)	2420886
# contigs	152
Largest contig	205597
Total length	3938530
Reference length	3981941
GC (%)	39.01
Reference GC (%)	39.17
N50	61814
NG50	60654
N90	15166
NG90	13569
auN	74005.6
auNG	73198.7
L50	20
LG50	21
L90	66
LG90	69
# misassemblies	37
# misassembled contigs	28
Misassembled contigs length	1916418
# local misassemblies	35
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	27 + 54 part
Unaligned length	521035
Genome fraction (%)	85.527
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1722.10
# indels per 100 kbp	36.00
# genomic features	3319 + 101 part
Largest alignment	176188
Total aligned length	3408563
NA50	37821
NGA50	37821
NA90	-
NGA90	-
auNA	46527.8
auNGA	46020.5
LA50	31
LGA50	31
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

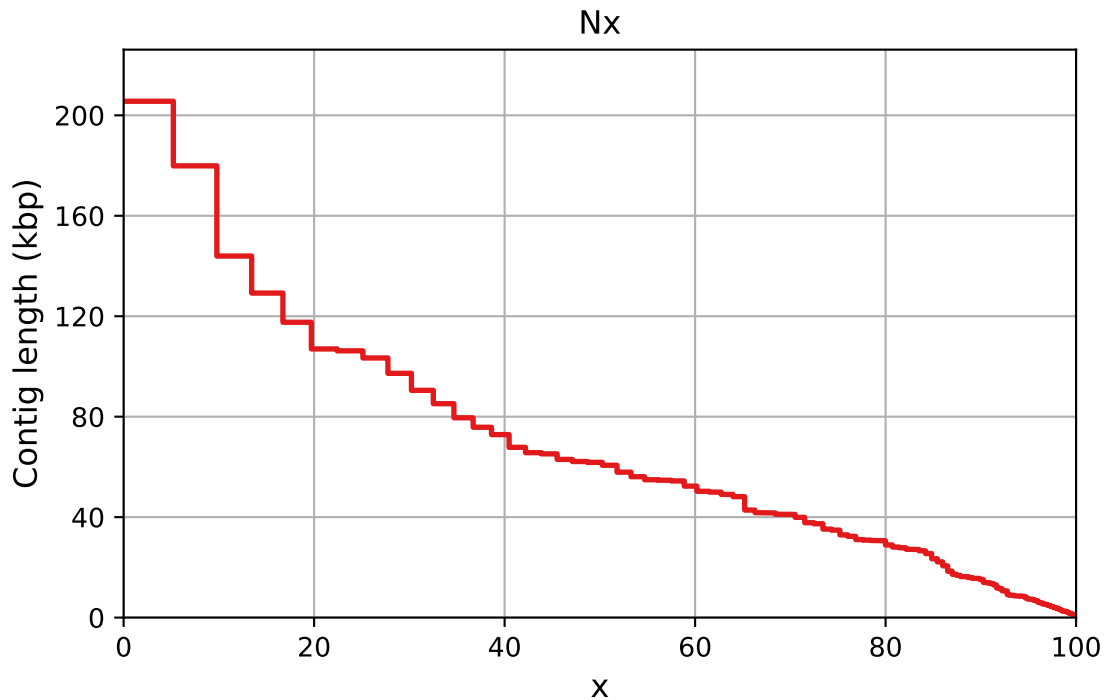
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# misassemblies	37
# contig misassemblies	37
# c. relocations	37
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	28
Misassembled contigs length	1916418
# local misassemblies	35
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	58699
# indels	1227
# indels (<= 5 bp)	1154
# indels (> 5 bp)	73
Indels length	3975

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

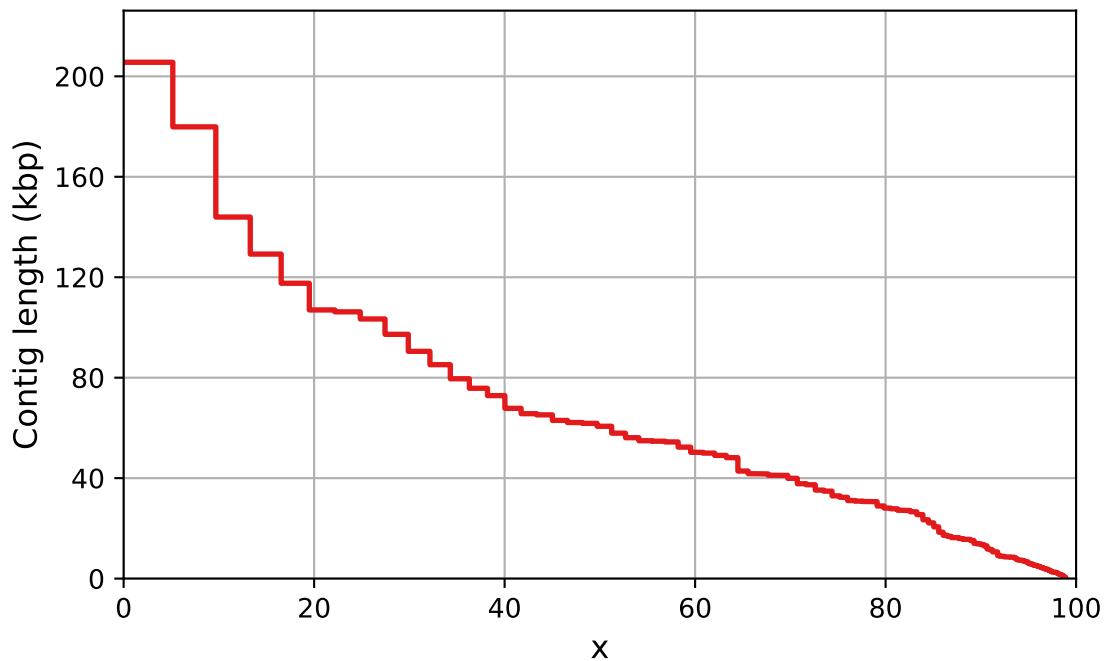
	ERR5770798
# fully unaligned contigs	27
Fully unaligned length	157603
# partially unaligned contigs	54
Partially unaligned length	363432
# N's	0

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).



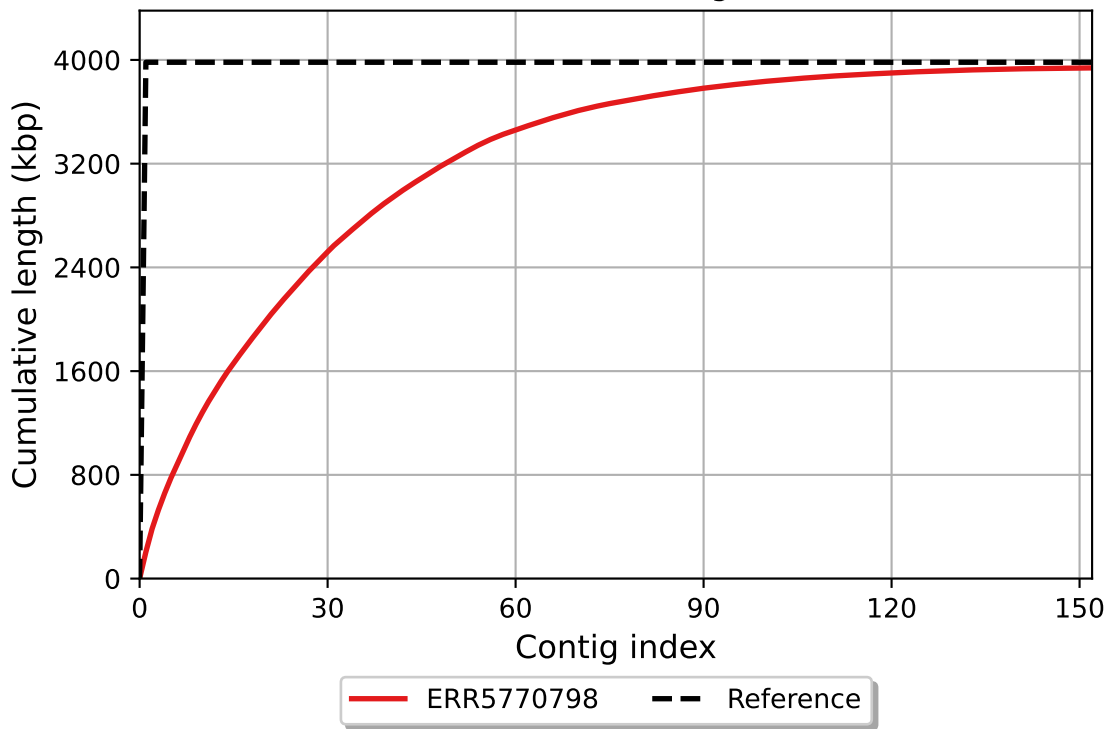
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NGx

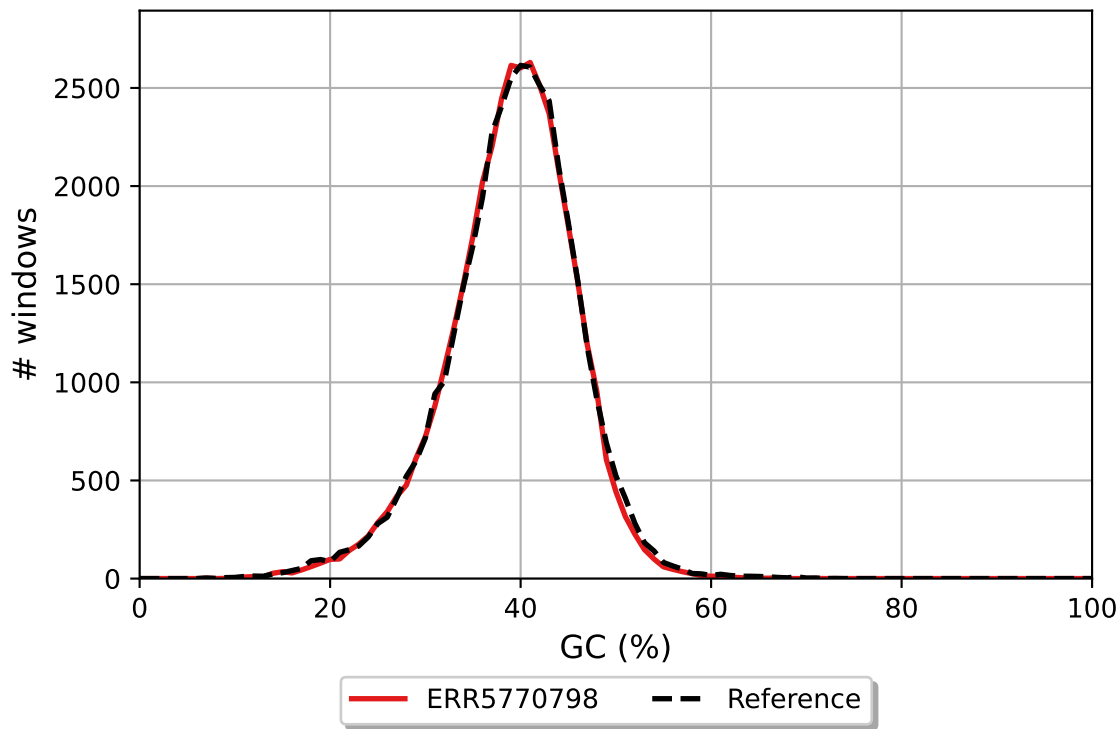


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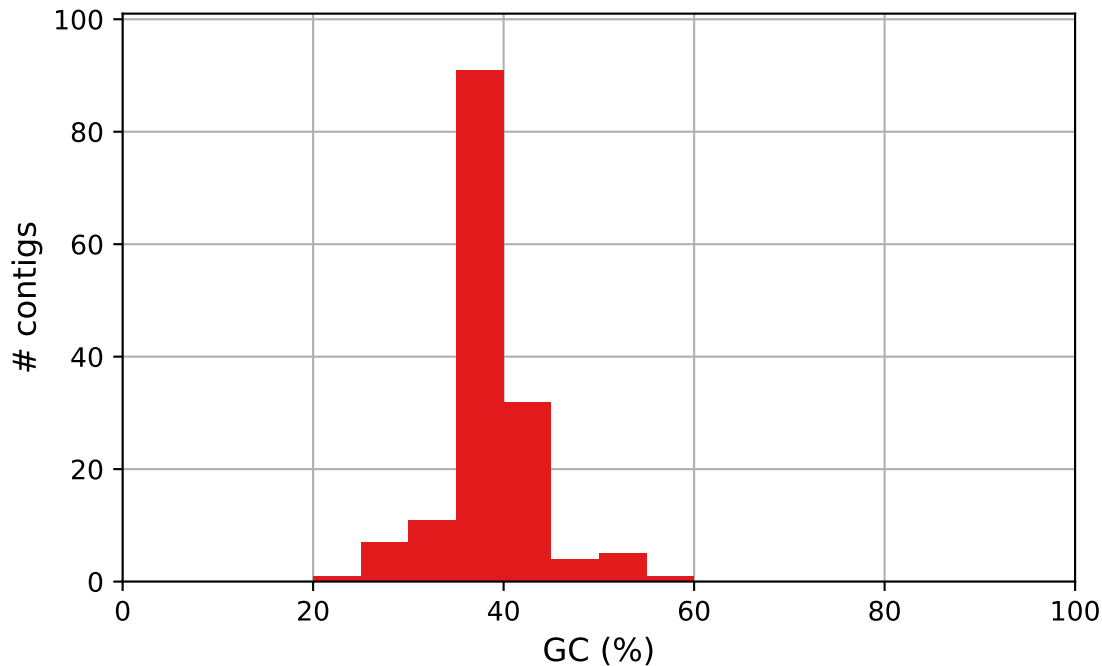
Cumulative length



GC content

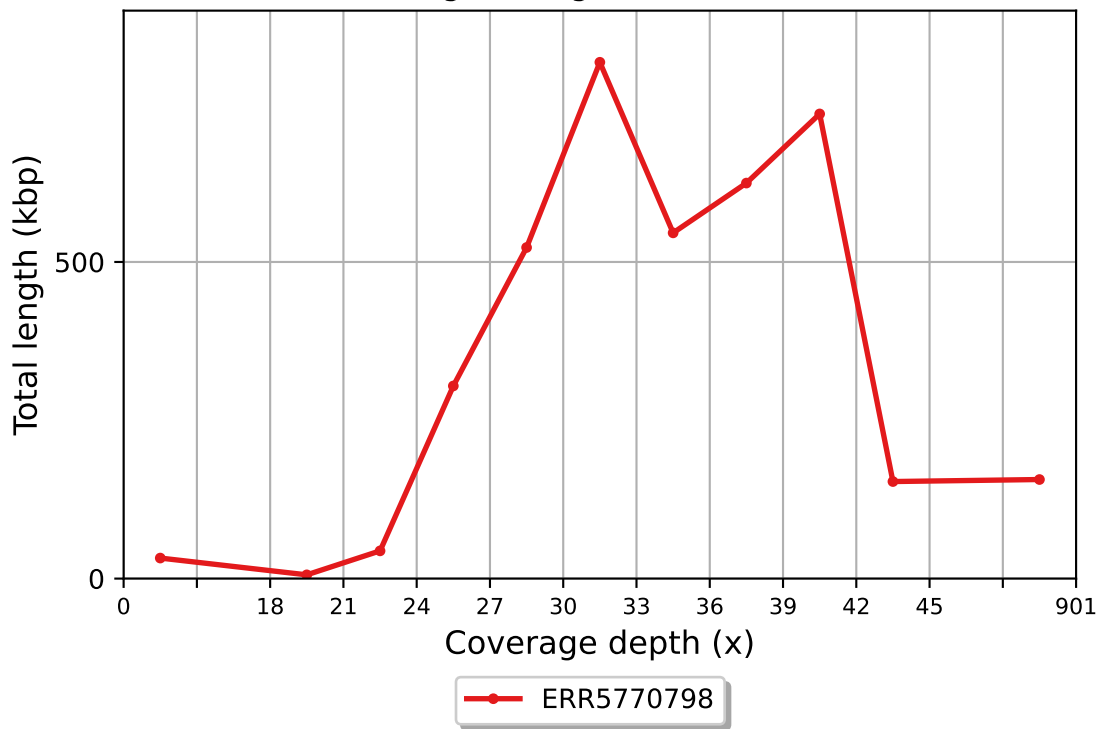


ERR5770798 GC content

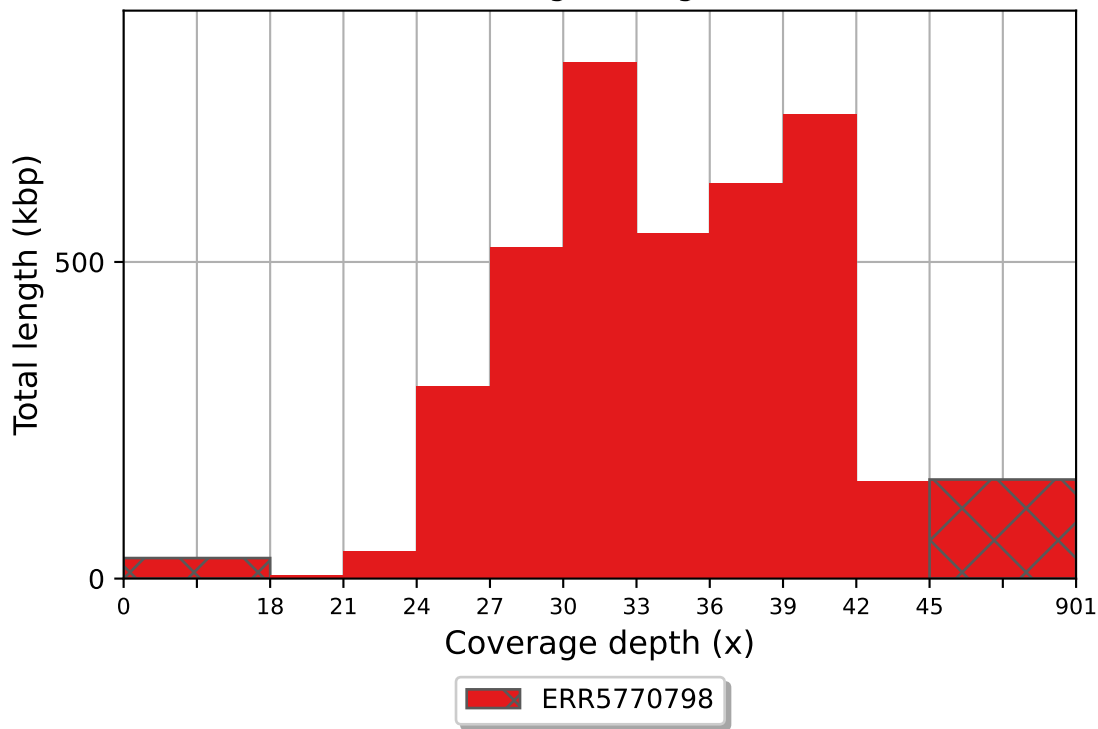


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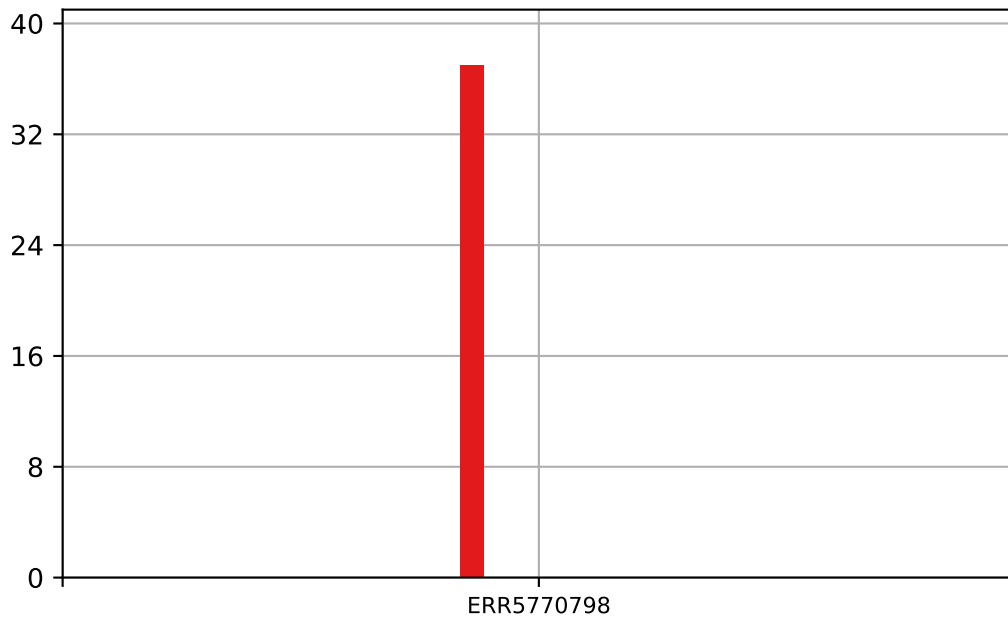
Coverage histogram (bin size: 3x)



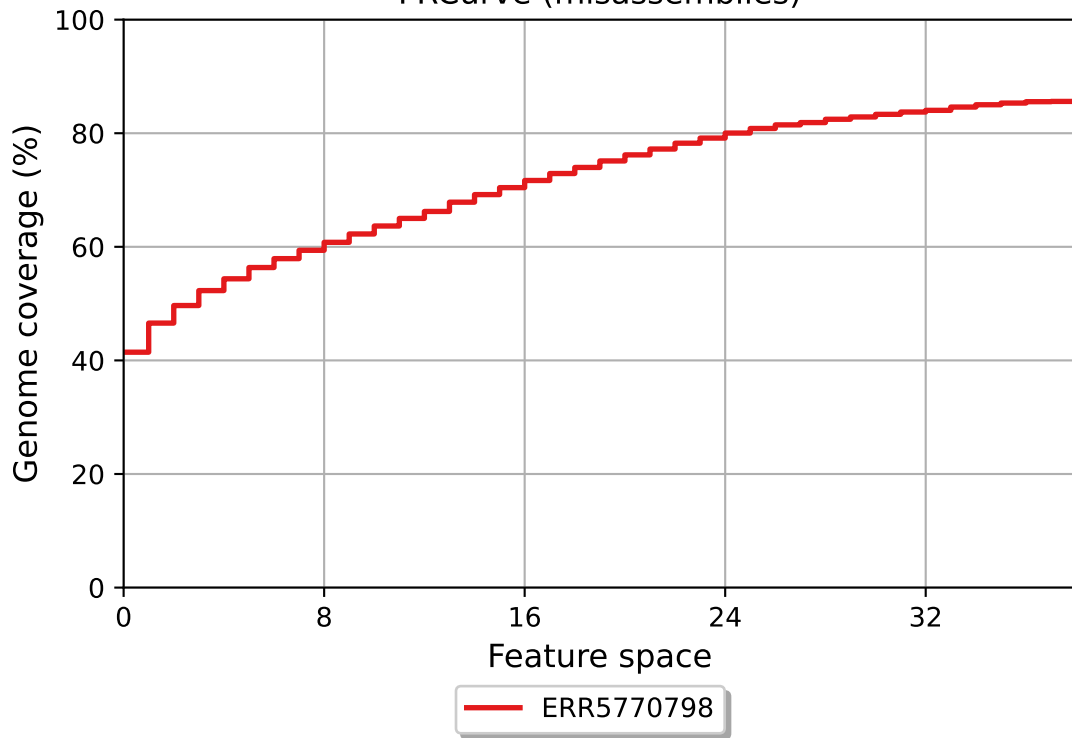
ERR5770798 coverage histogram (bin size: 3x)



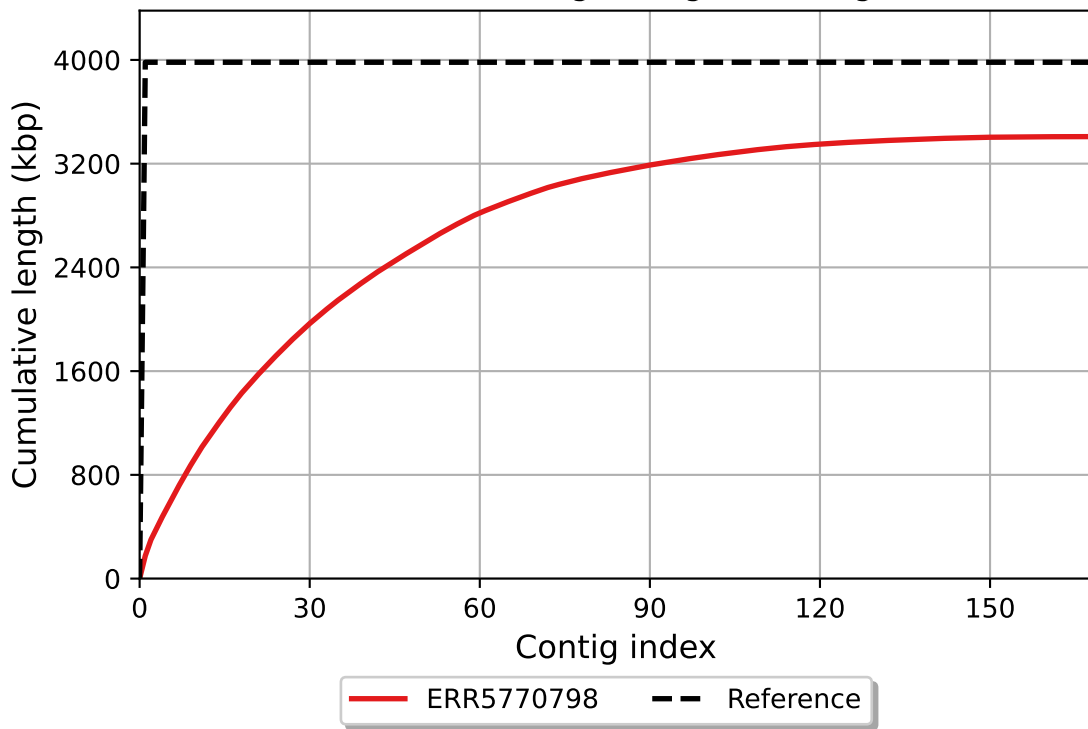
Misassemblies



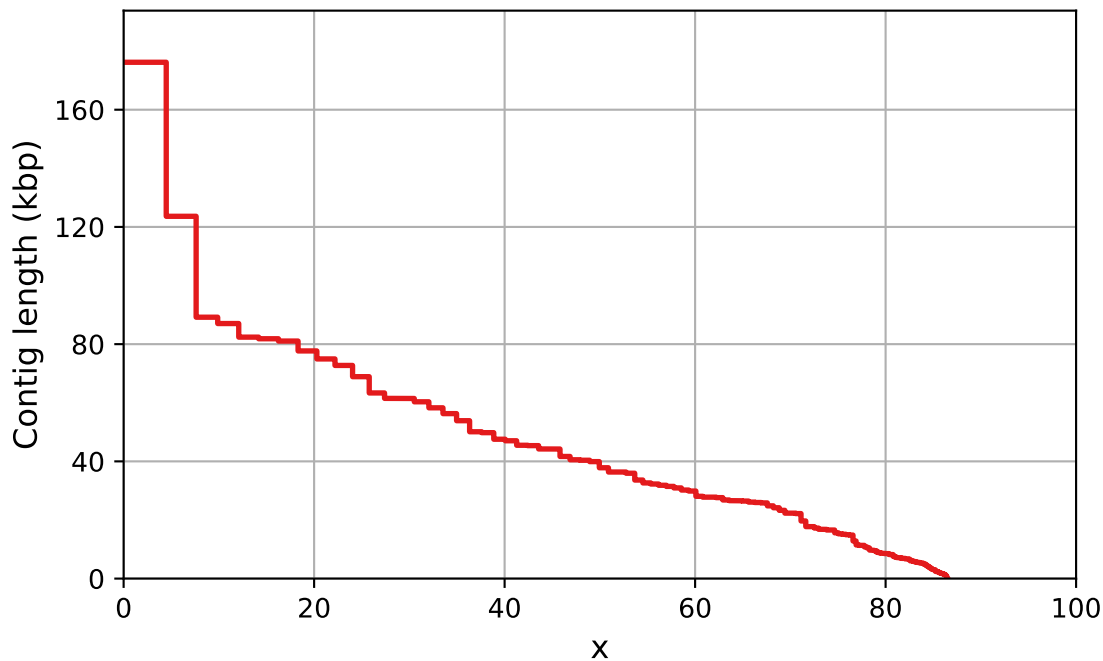
FRCurve (misassemblies)



Cumulative length (aligned contigs)

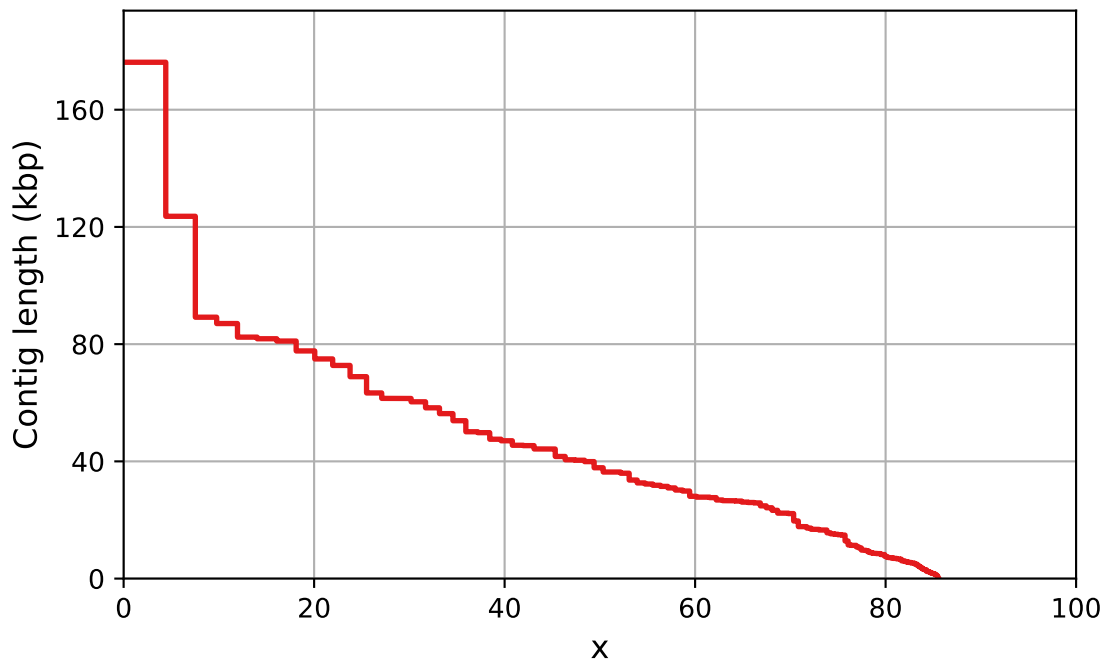


NAx



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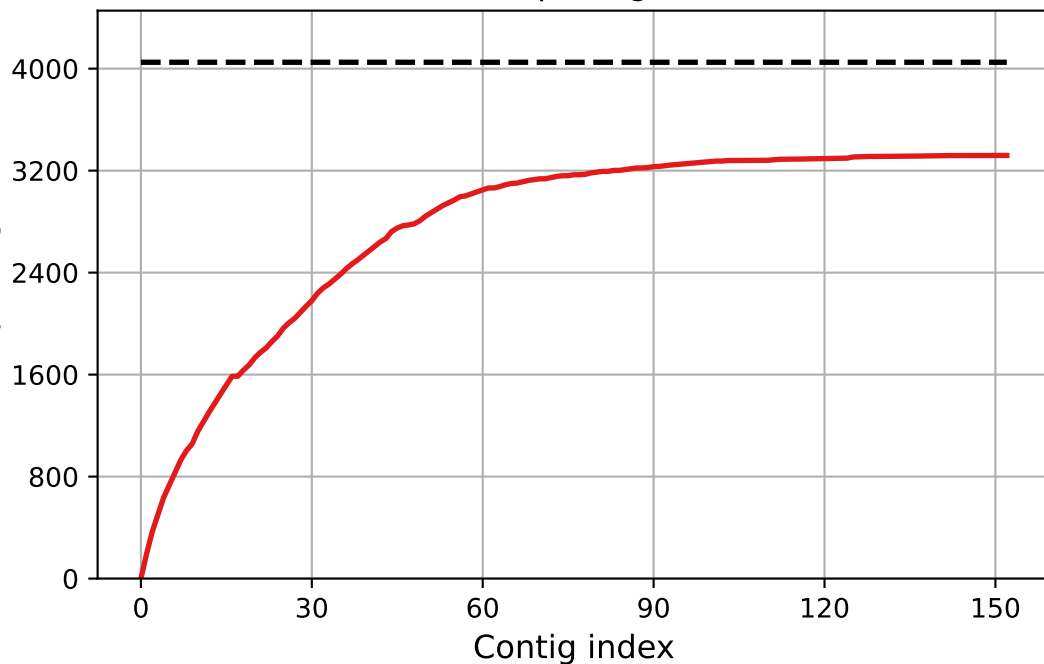
NGAx



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Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)

