

Report

	ERR5770800
# contigs (>= 0 bp)	1259
# contigs (>= 1000 bp)	396
# contigs (>= 5000 bp)	145
# contigs (>= 10000 bp)	103
# contigs (>= 25000 bp)	55
# contigs (>= 50000 bp)	16
Total length (>= 0 bp)	4523746
Total length (>= 1000 bp)	4160238
Total length (>= 5000 bp)	3636017
Total length (>= 10000 bp)	3348652
Total length (>= 25000 bp)	2608462
Total length (>= 50000 bp)	1266327
# contigs	648
Largest contig	126919
Total length	4337258
Reference length	3981941
GC (%)	39.03
Reference GC (%)	39.17
N50	30671
NG50	33237
N90	2239
NG90	5743
auN	40481.4
auNG	44093.6
L50	40
LG50	34
L90	228
LG90	135
# misassemblies	33
# misassembled contigs	29
Misassembled contigs length	1012992
# local misassemblies	34
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# unaligned contigs	71 + 80 part
Unaligned length	733076
Genome fraction (%)	85.544
Duplication ratio	1.055
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1734.75
# indels per 100 kbp	35.15
# genomic features	3090 + 338 part
Largest alignment	126376
Total aligned length	3593363
NA50	20518
NGA50	24495
NA90	-
NGA90	514
auNA	29327.9
auNGA	31944.9
LA50	53
LGA50	45
LA90	-
LGA90	591

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

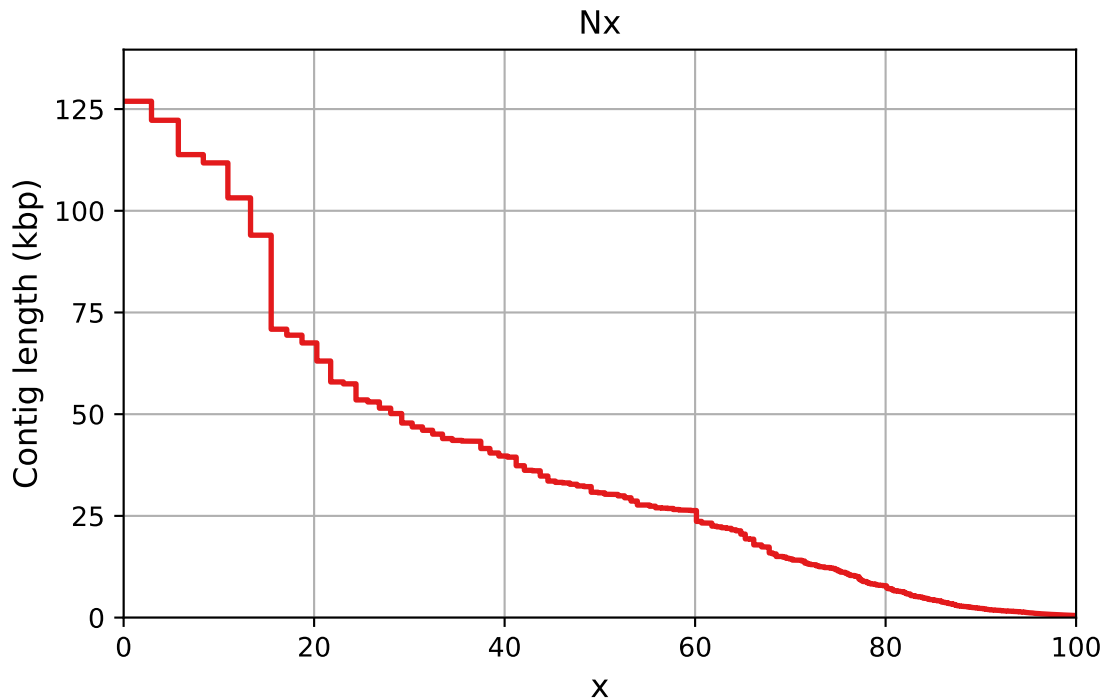
	ERR5770800
# misassemblies	33
# contig misassemblies	33
# c. relocations	33
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	29
Misassembled contigs length	1012992
# local misassemblies	34
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# mismatches	62336
# indels	1263
# indels (<= 5 bp)	1184
# indels (> 5 bp)	79
Indels length	3996

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

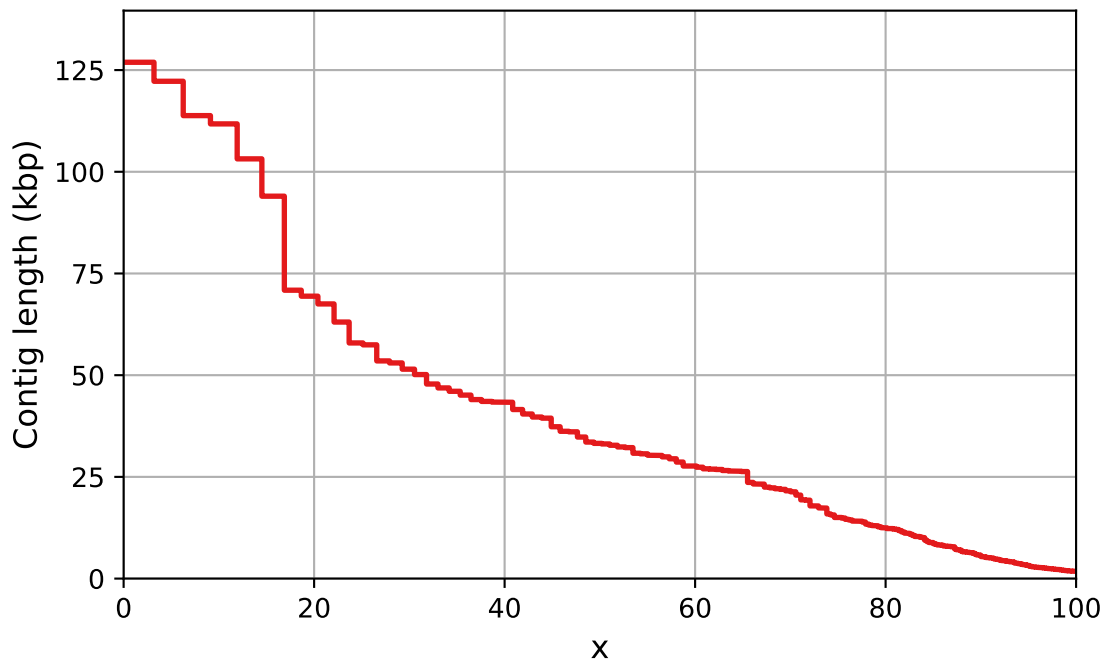
	ERR5770800
# fully unaligned contigs	71
Fully unaligned length	326076
# partially unaligned contigs	80
Partially unaligned length	407000
# N's	0

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).



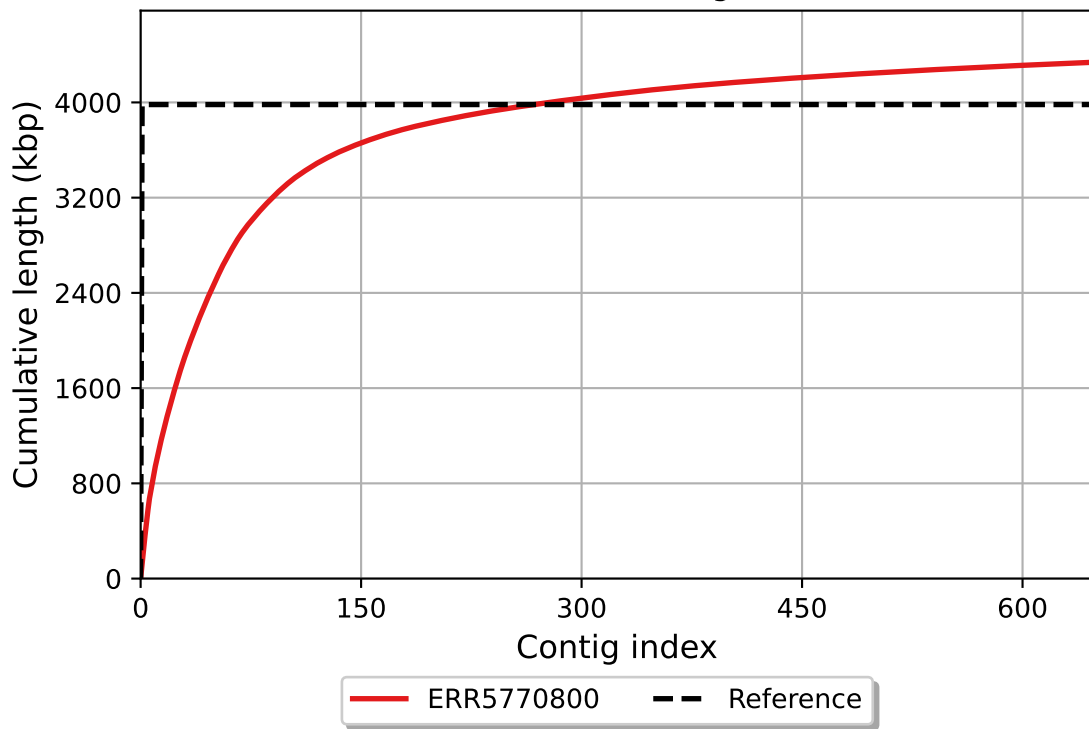
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NGx

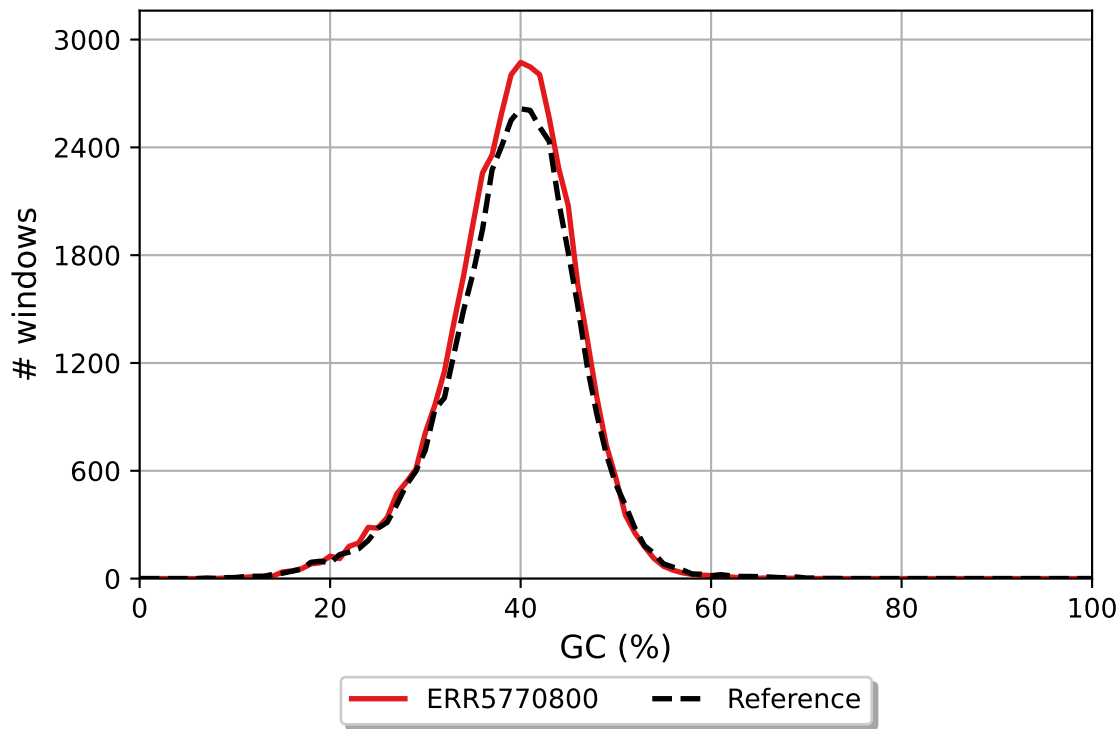


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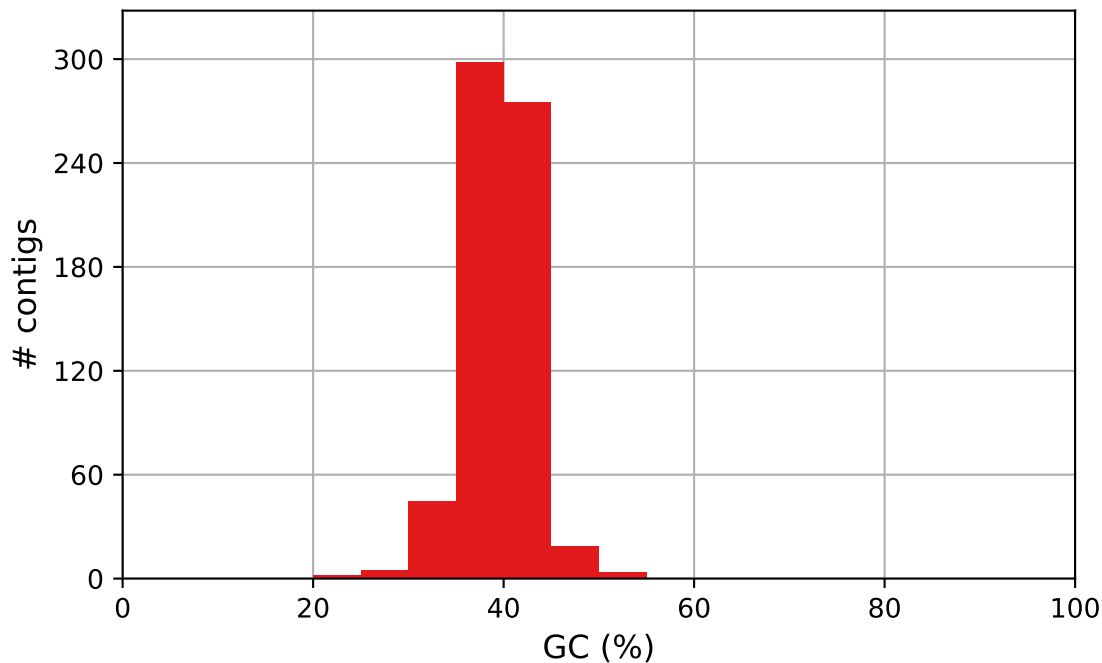
Cumulative length



GC content

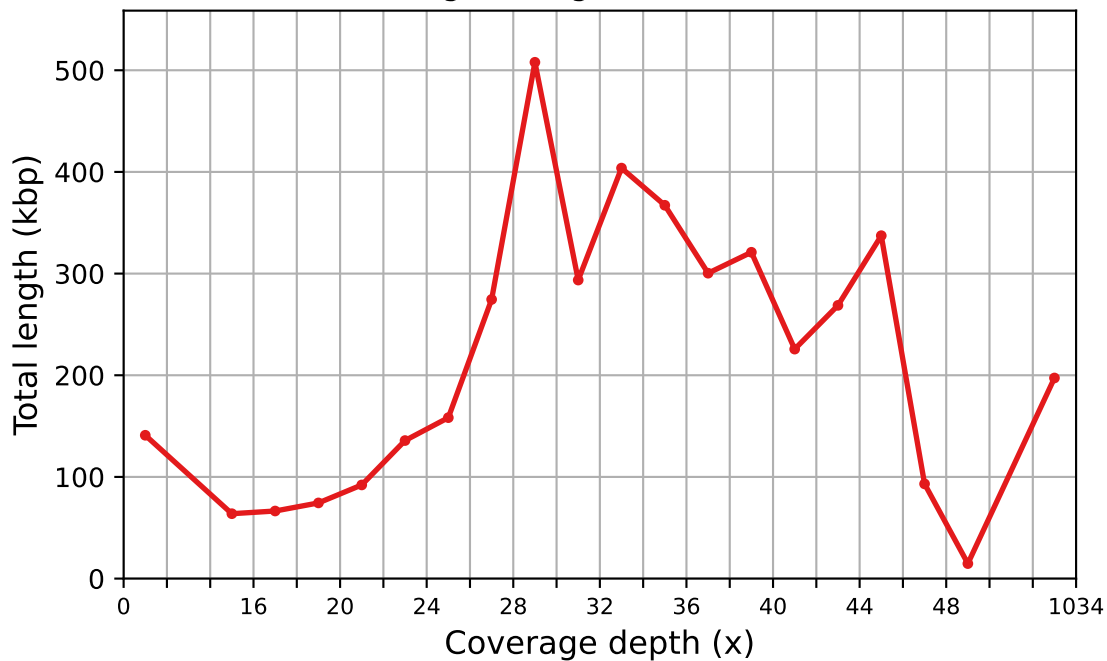


ERR5770800 GC content



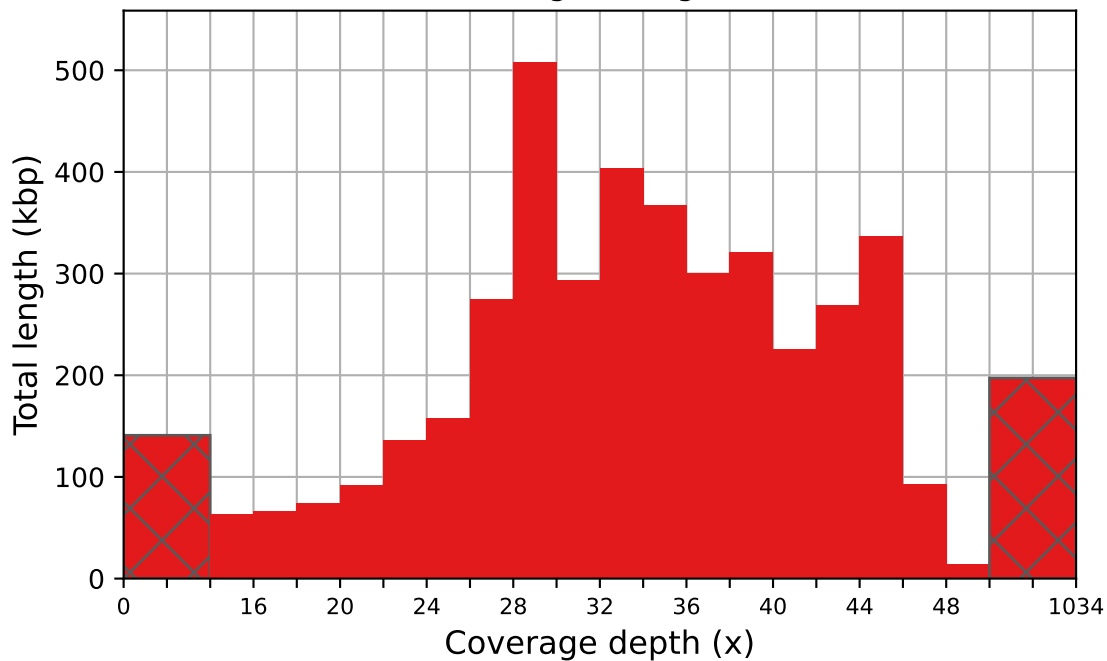
ERR5770800

Coverage histogram (bin size: 2x)



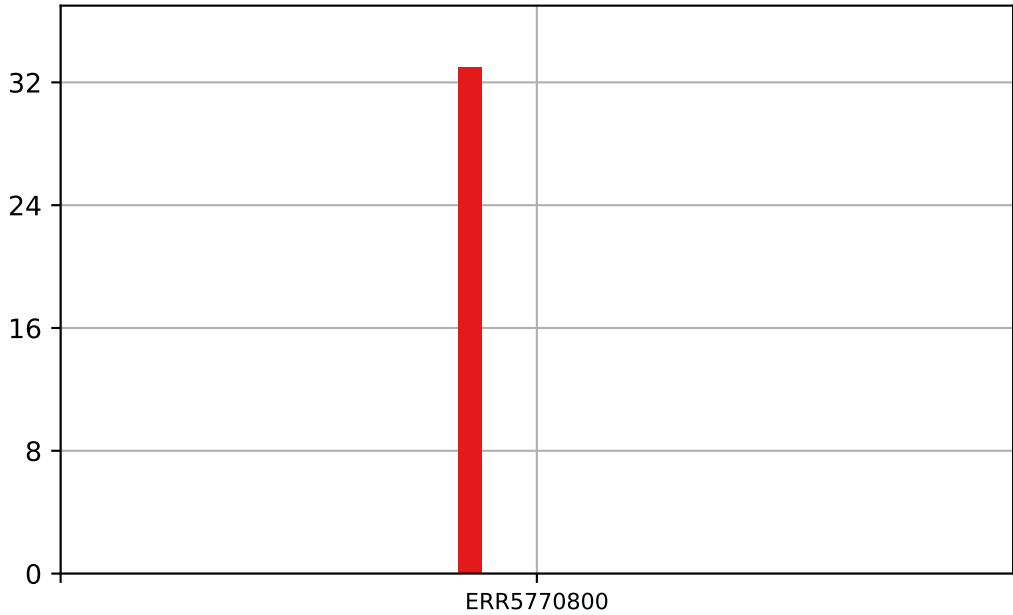
ERR5770800

ERR5770800 coverage histogram (bin size: 2x)

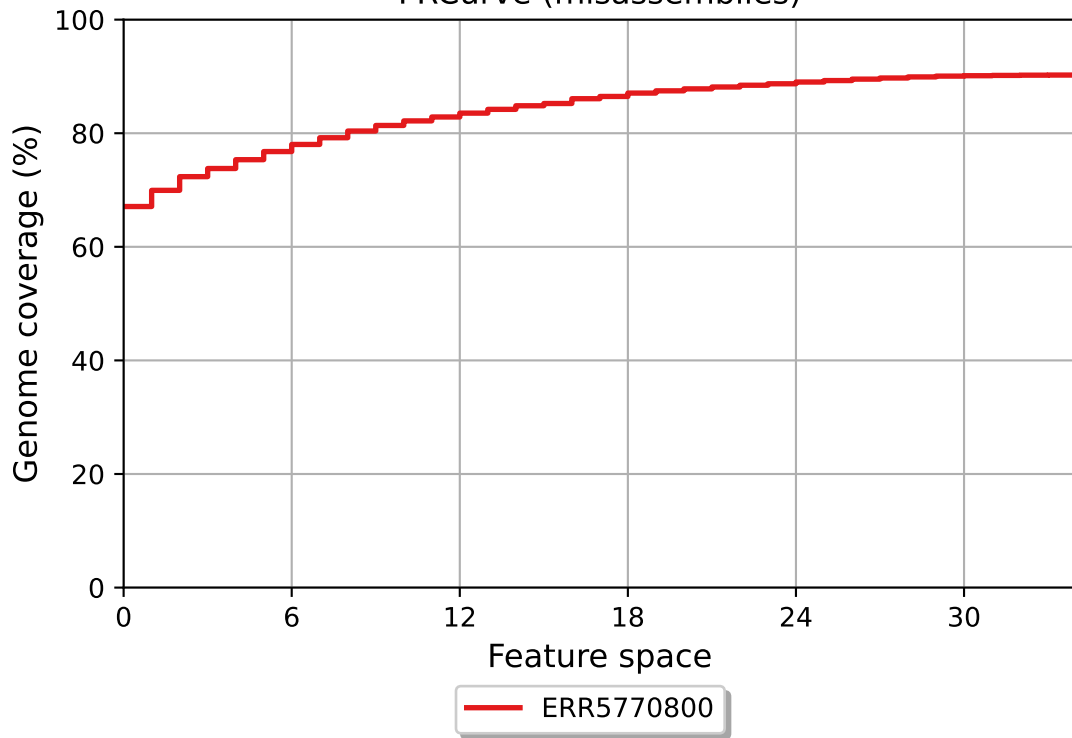


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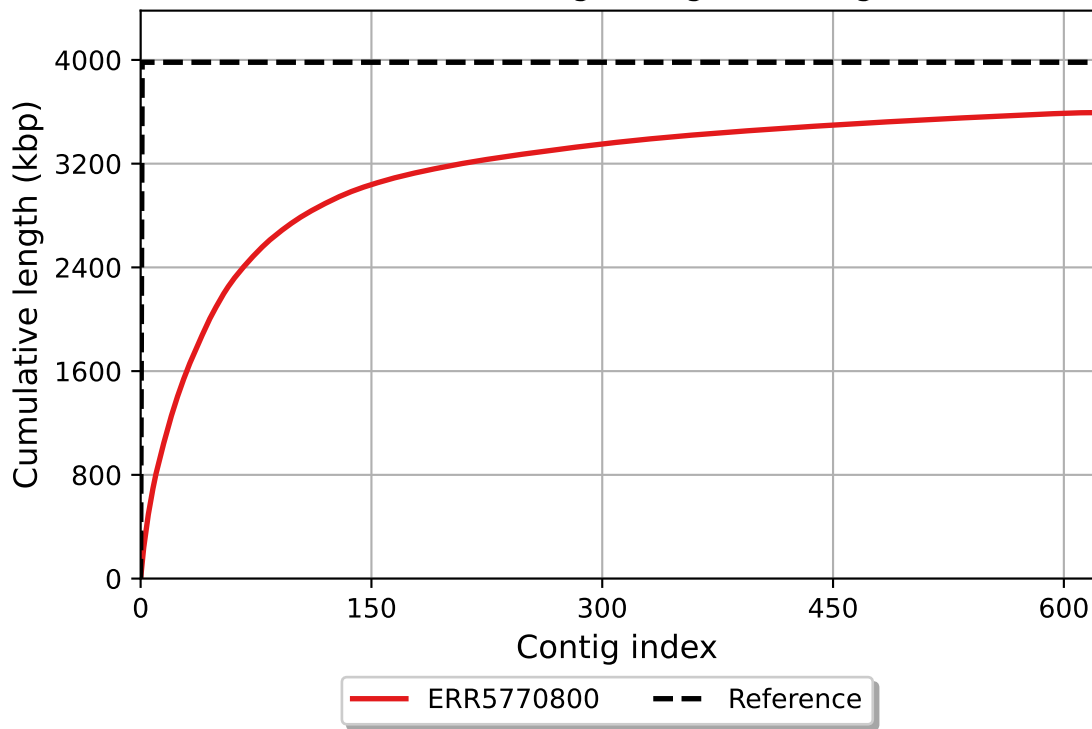
Misassemblies



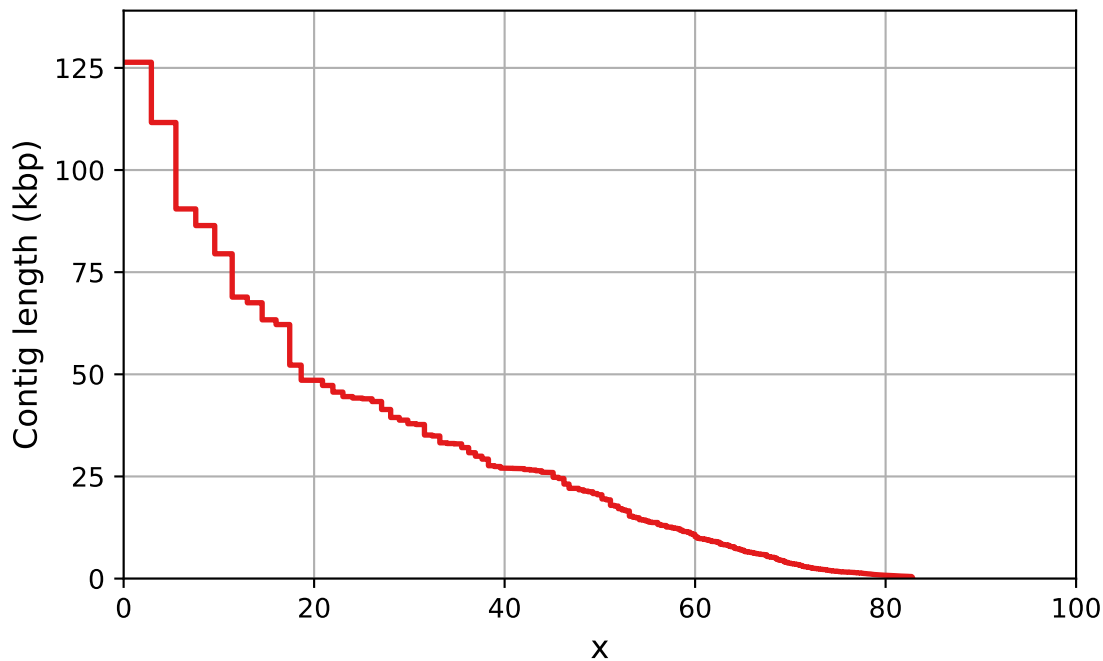
FRCurve (misassemblies)



Cumulative length (aligned contigs)

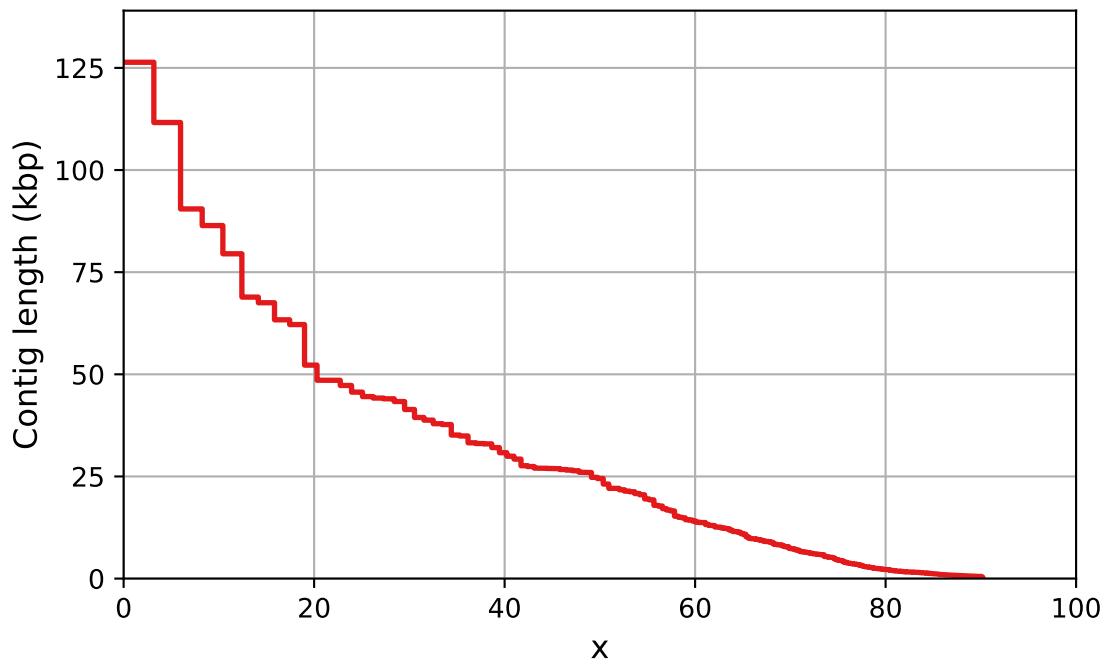


NAx

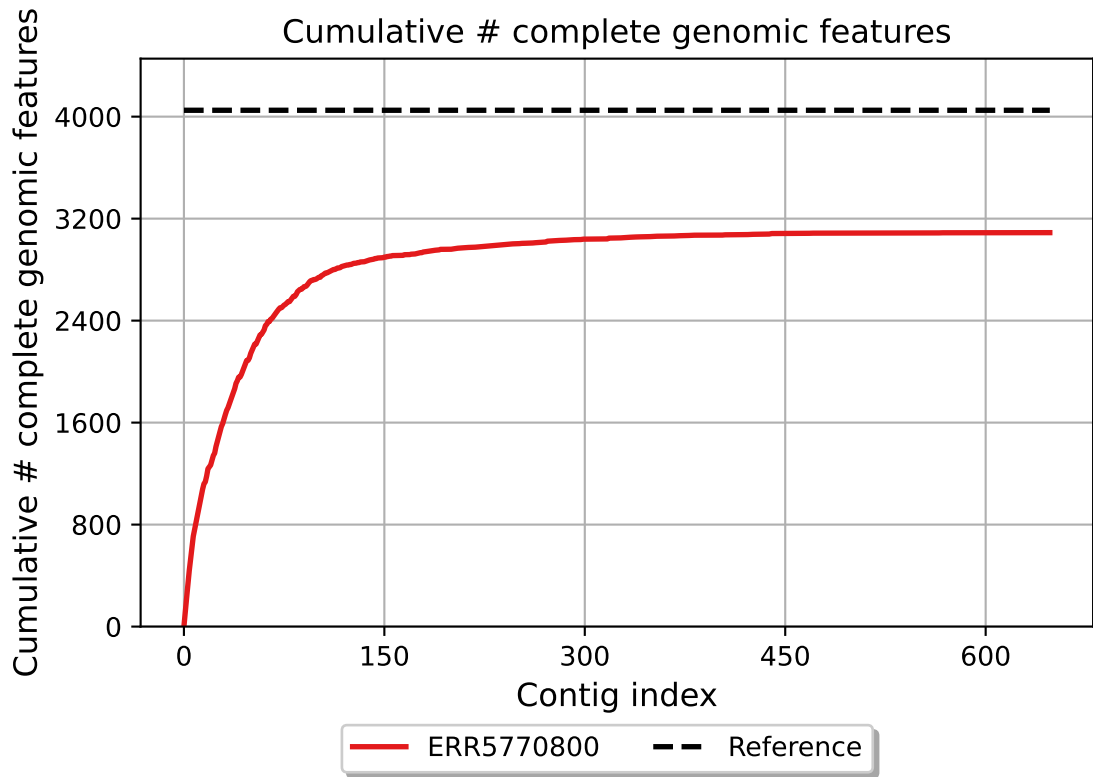


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NGAx



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FRCurve (genomic features)

