

# Report

	ERR5770799
# contigs (>= 0 bp)	198
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	68
# contigs (>= 10000 bp)	60
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4024527
Total length (>= 1000 bp)	3993433
Total length (>= 5000 bp)	3922502
Total length (>= 10000 bp)	3859906
Total length (>= 25000 bp)	3645623
Total length (>= 50000 bp)	2902412
# contigs	111
Largest contig	252629
Total length	4004490
Reference length	3981941
GC (%)	38.89
Reference GC (%)	39.17
N50	82715
NG50	85218
N90	26881
NG90	27851
auN	94826.8
auNG	95363.8
L50	17
LG50	16
L90	47
LG90	46
# misassemblies	45
# misassembled contigs	29
Misassembled contigs length	2253162
# local misassemblies	49
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	35 + 46 part
Unaligned length	639305
Genome fraction (%)	84.225
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1773.07
# indels per 100 kbp	40.72
# genomic features	3271 + 106 part
Largest alignment	172154
Total aligned length	3359545
NA50	43780
NGA50	43780
NA90	-
NGA90	-
auNA	55713.5
auNGA	56029.0
LA50	25
LGA50	25
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

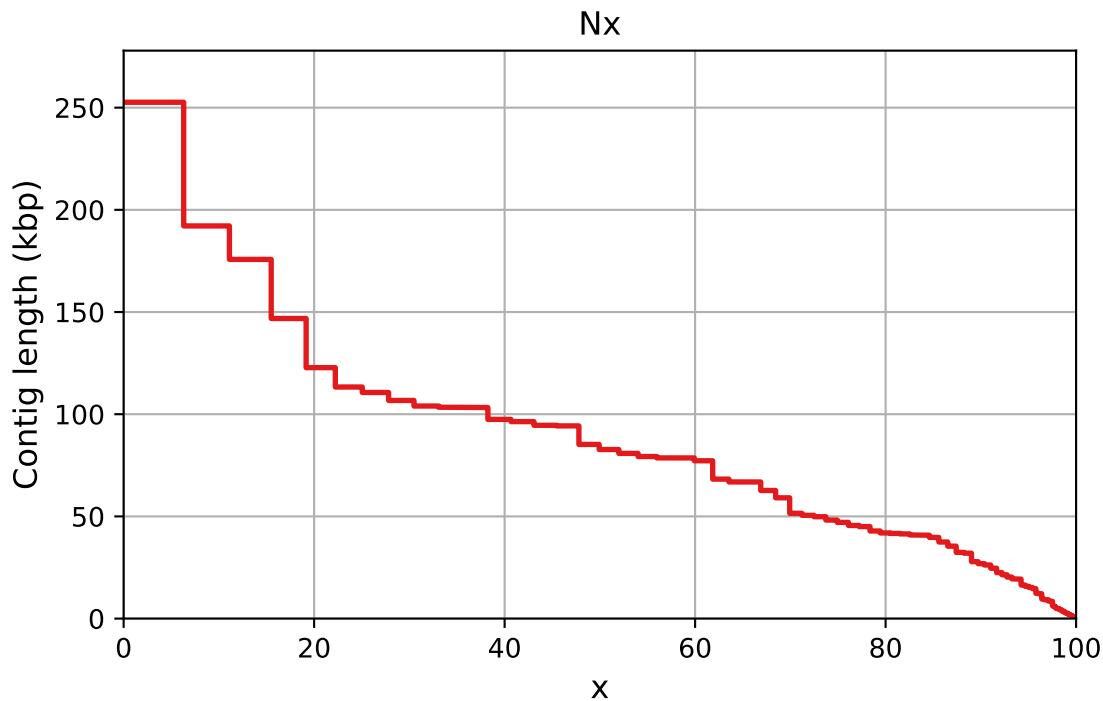
	ERR5770799
# misassemblies	45
# contig misassemblies	45
# c. relocations	45
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	29
Misassembled contigs length	2253162
# local misassemblies	49
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	59567
# indels	1368
# indels (<= 5 bp)	1284
# indels (> 5 bp)	84
Indels length	4113

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

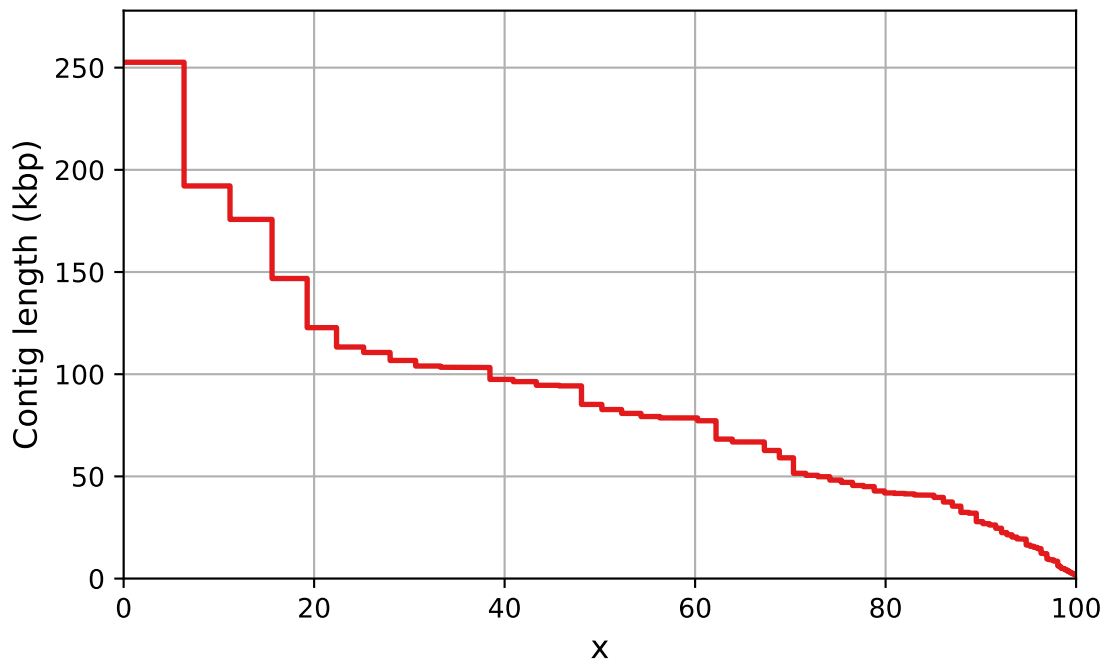
	ERR5770799
# fully unaligned contigs	35
Fully unaligned length	123405
# partially unaligned contigs	46
Partially unaligned length	515900
# N's	0

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).



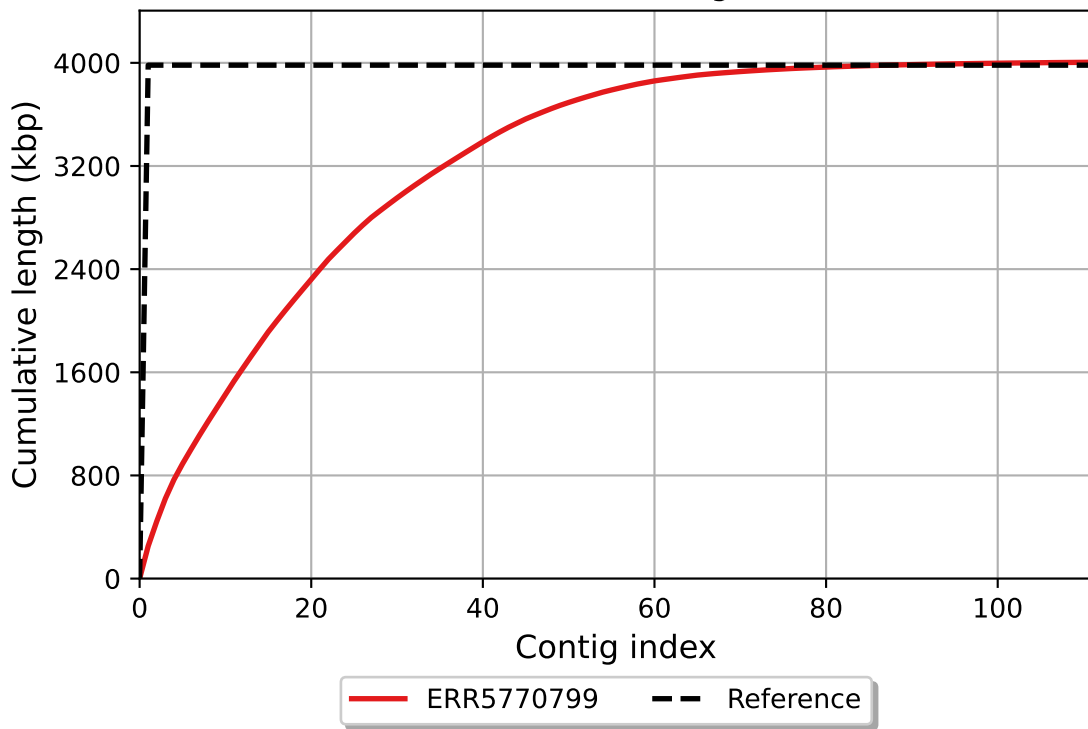
ERR5770799

# NGx

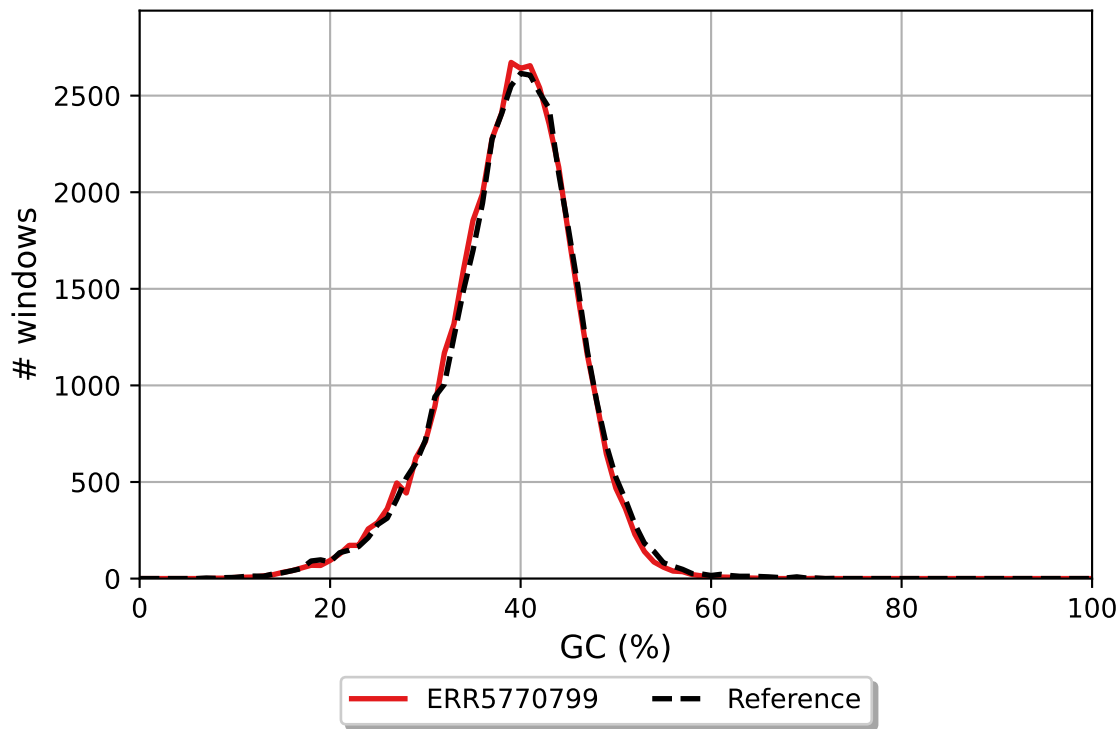


ERR5770799

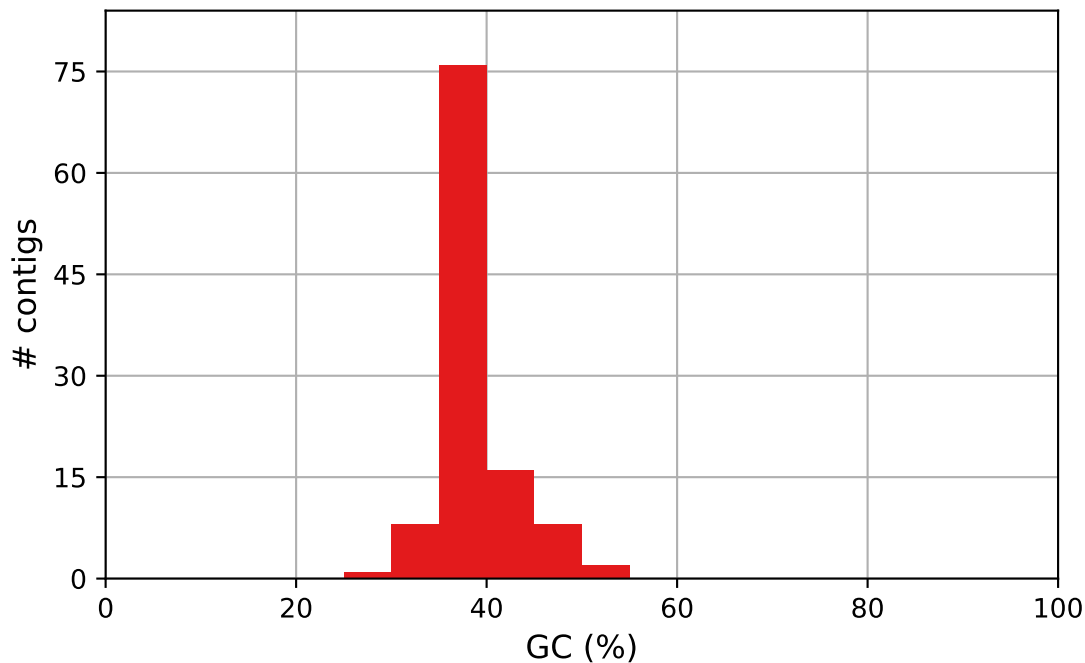
Cumulative length



## GC content



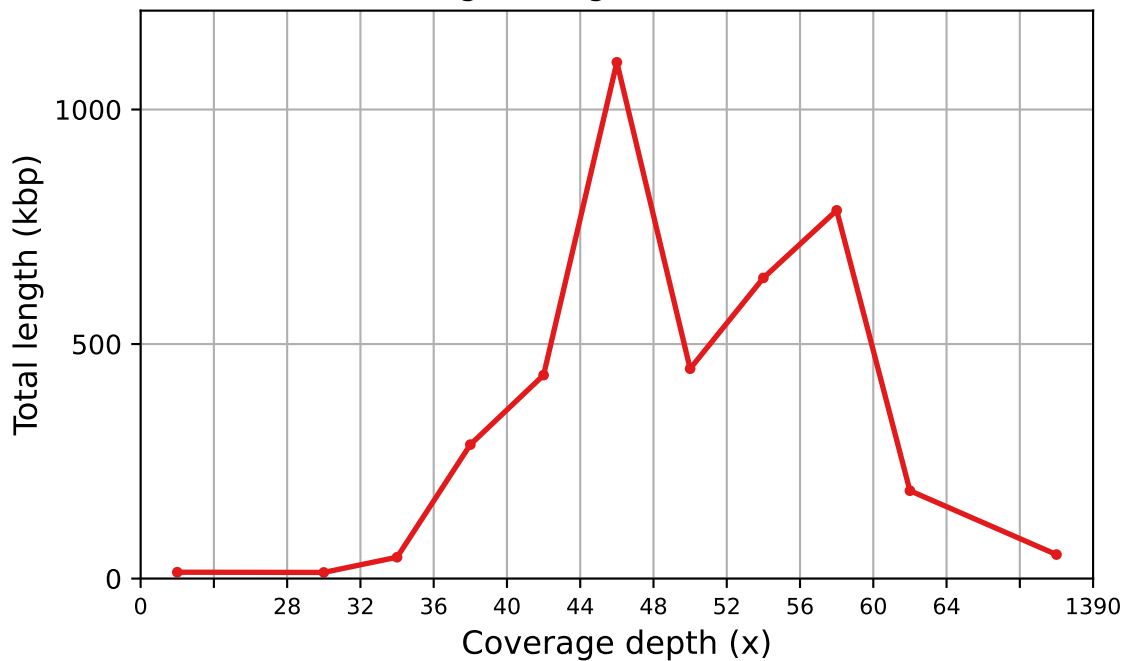
ERR5770799 GC content



ERR5770799

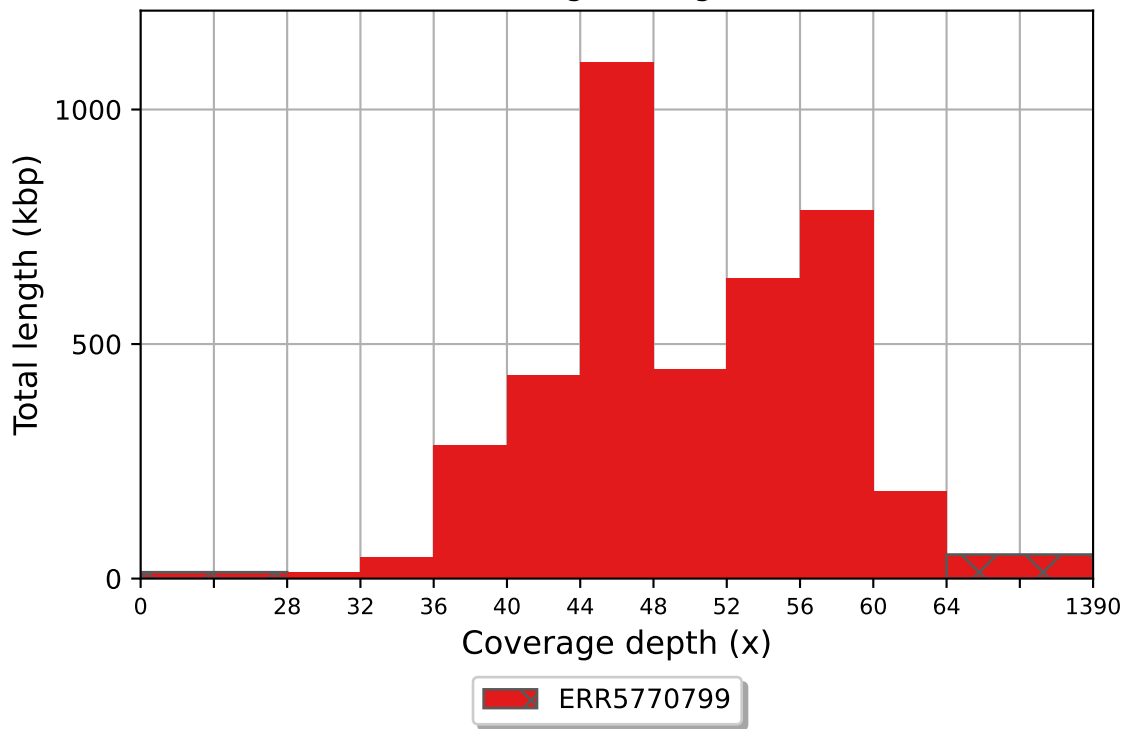


Coverage histogram (bin size: 4x)

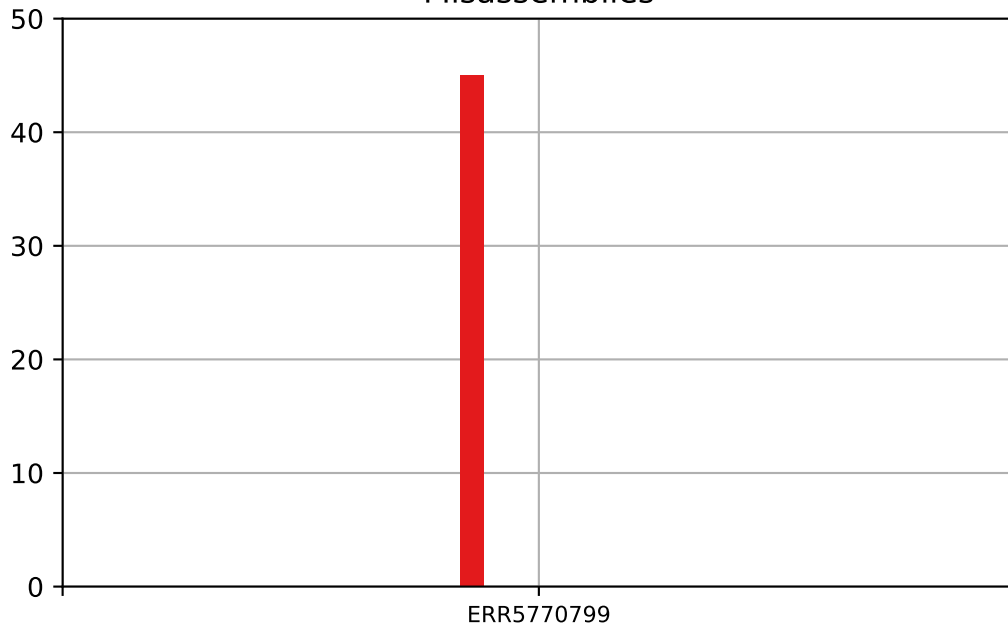


ERR5770799

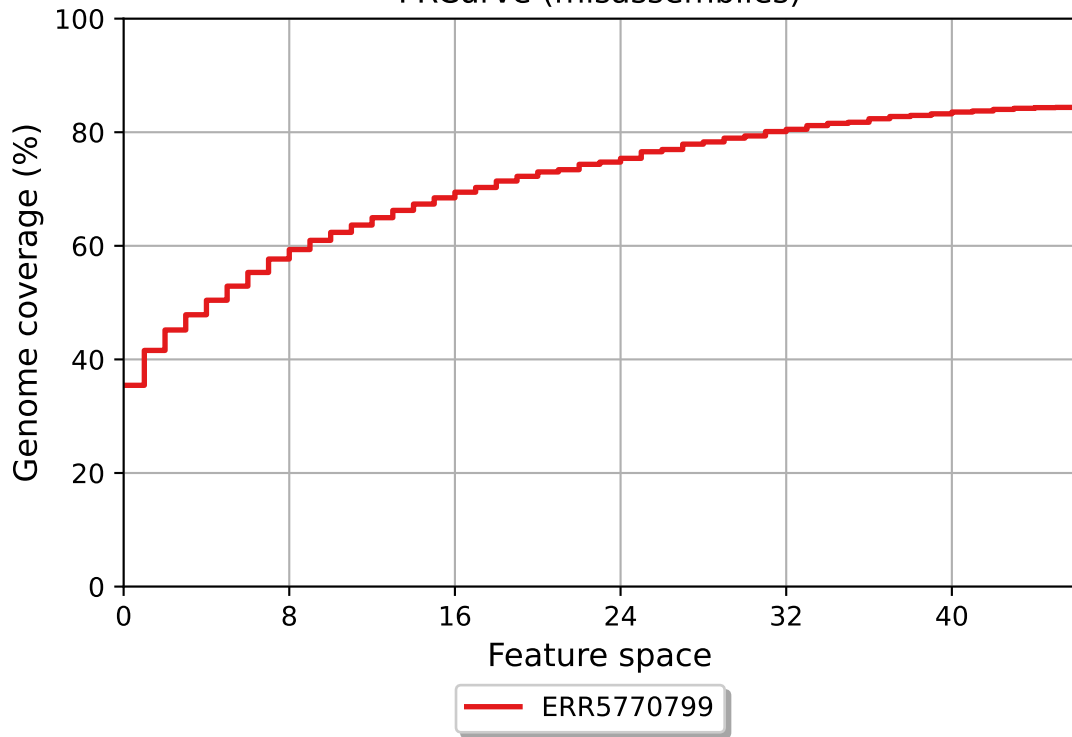
ERR5770799 coverage histogram (bin size: 4x)



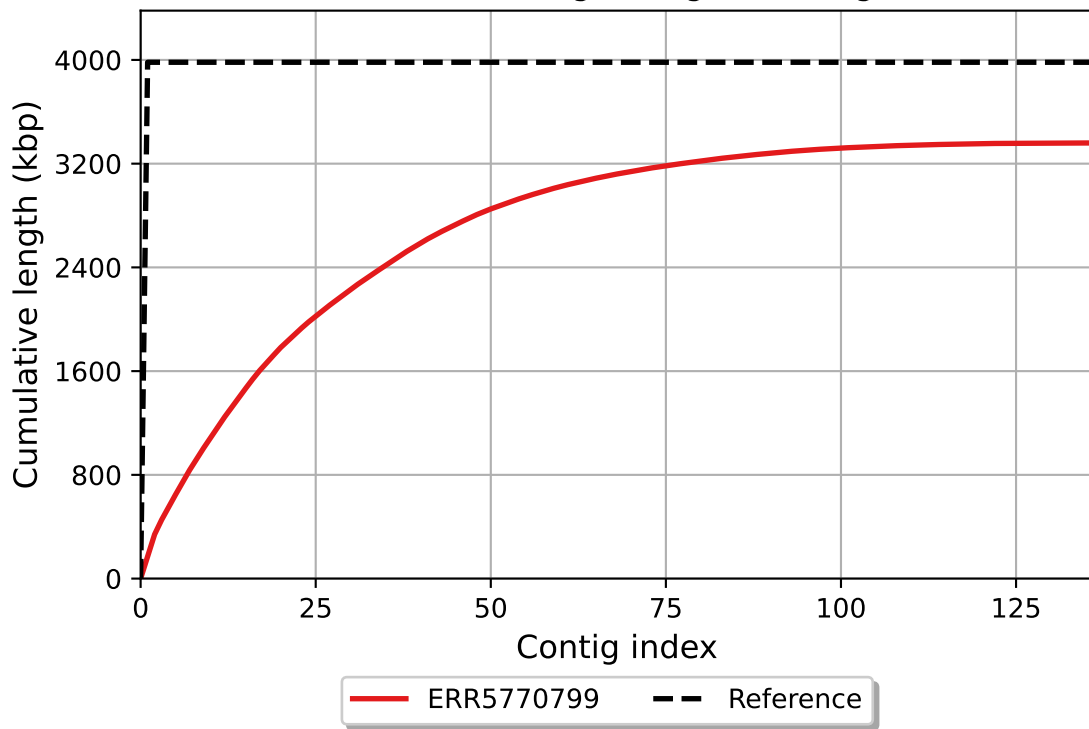
## Misassemblies



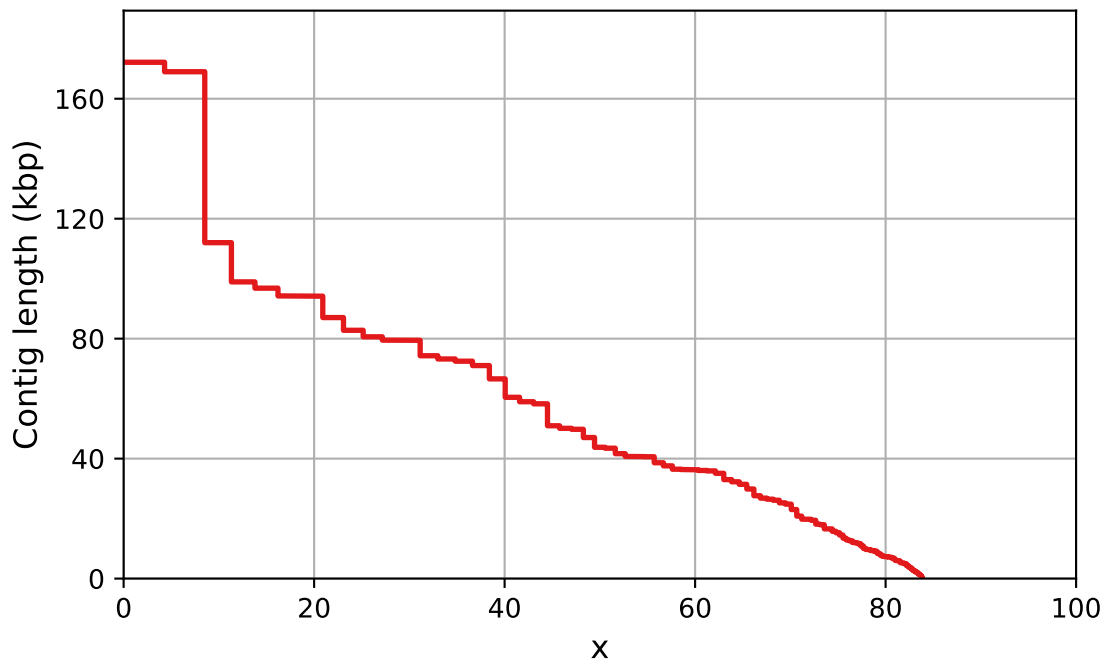
FRCurve (misassemblies)



Cumulative length (aligned contigs)

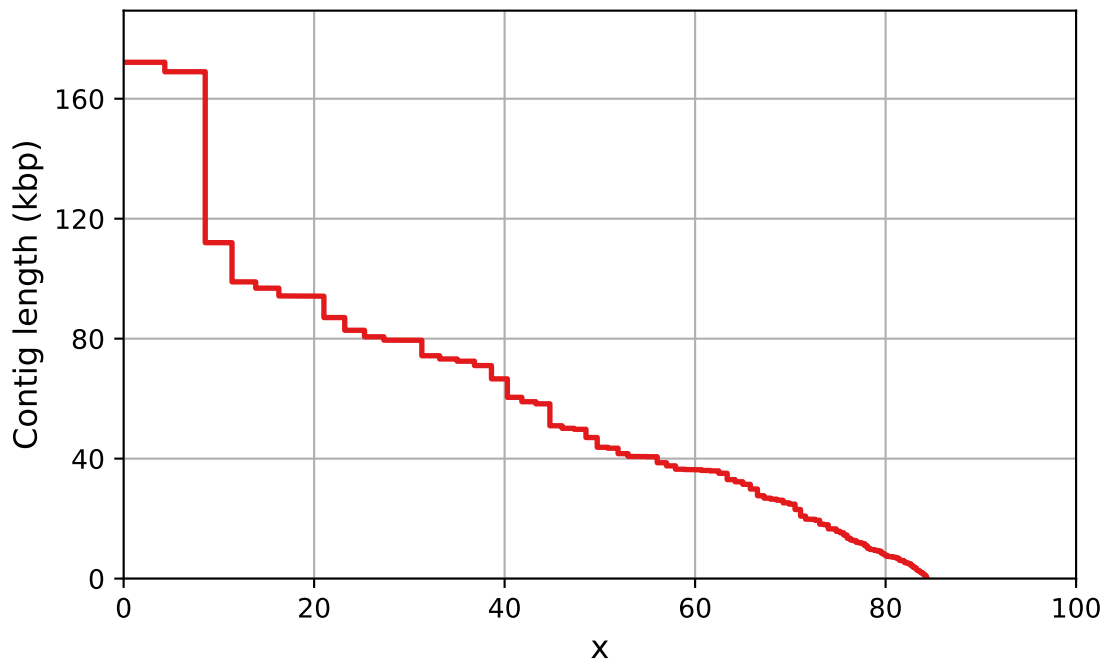


NAx



ERR5770799

# NGAx



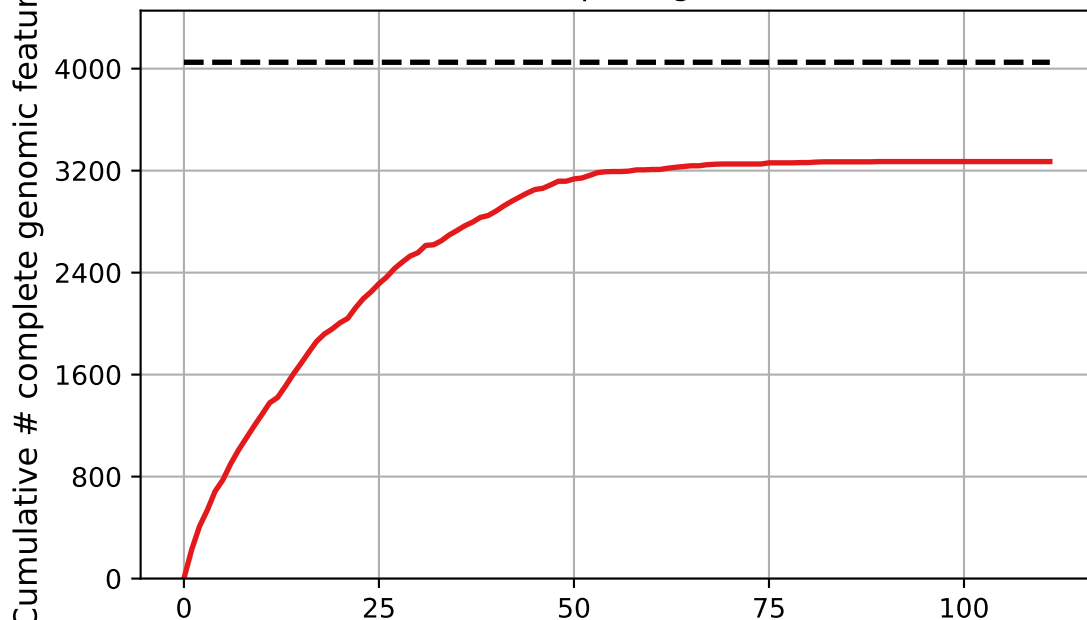
ERR5770799

Cumulative # complete genomic features

Cumulative # complete genomic features

Contig index

ERR5770799      Reference





FRCurve (genomic features)

