

Report

	ERR5770805
# contigs (>= 0 bp)	92
# contigs (>= 1000 bp)	46
# contigs (>= 5000 bp)	33
# contigs (>= 10000 bp)	27
# contigs (>= 25000 bp)	26
# contigs (>= 50000 bp)	21
Total length (>= 0 bp)	3828962
Total length (>= 1000 bp)	3814827
Total length (>= 5000 bp)	3778080
Total length (>= 10000 bp)	3733965
Total length (>= 25000 bp)	3720416
Total length (>= 50000 bp)	3540426
# contigs	52
Largest contig	303777
Total length	3819055
Reference length	3981941
GC (%)	38.88
Reference GC (%)	39.17
N50	232737
NG50	209209
N90	50801
NG90	41756
auN	202106.2
auNG	193838.8
L50	7
LG50	8
L90	19
LG90	23
# misassemblies	53
# misassembled contigs	17
Misassembled contigs length	3200887
# local misassemblies	41
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	14 + 27 part
Unaligned length	484525
Genome fraction (%)	83.615
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1814.22
# indels per 100 kbp	46.74
# genomic features	3244 + 87 part
Largest alignment	273663
Total aligned length	3333109
NA50	69283
NGA50	66468
NA90	-
NGA90	-
auNA	90508.1
auNGA	86805.8
LA50	15
LGA50	16
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

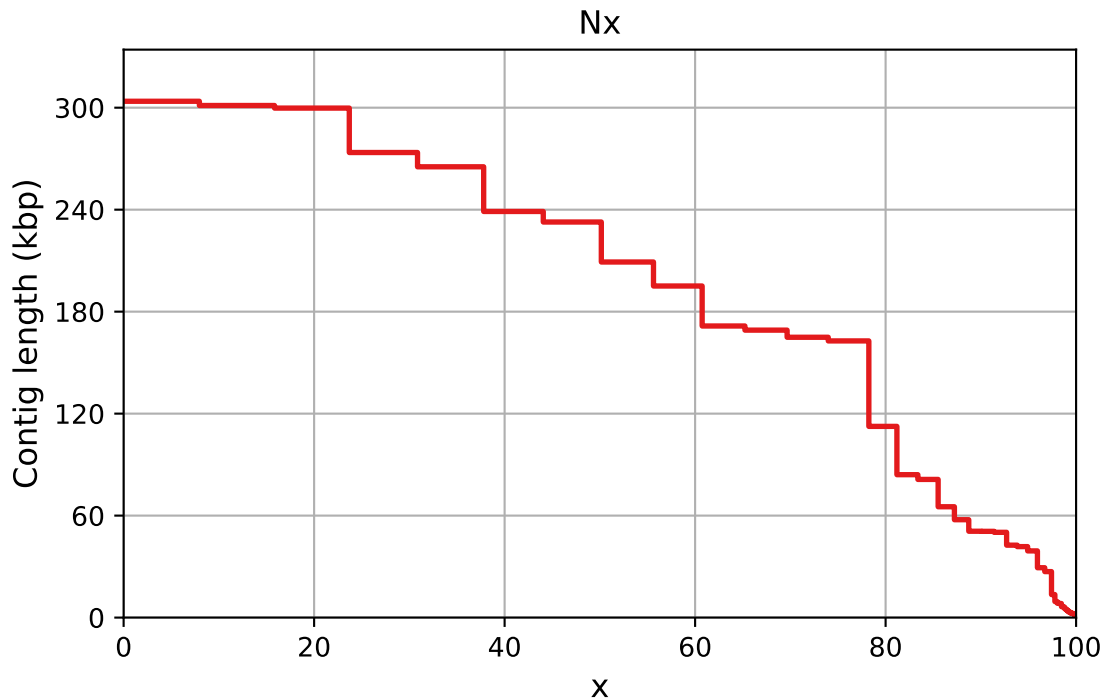
	ERR5770805
# misassemblies	53
# contig misassemblies	53
# c. relocations	53
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	17
Misassembled contigs length	3200887
# local misassemblies	41
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	60470
# indels	1558
# indels (<= 5 bp)	1456
# indels (> 5 bp)	102
Indels length	5082

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

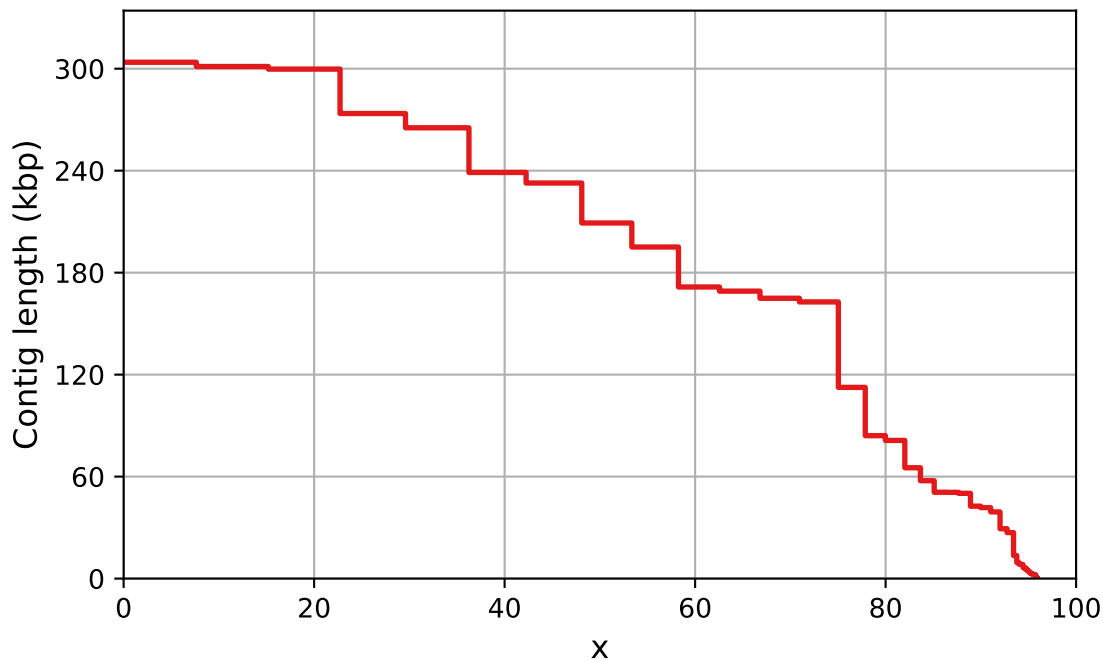
	ERR5770805
# fully unaligned contigs	14
Fully unaligned length	36412
# partially unaligned contigs	27
Partially unaligned length	448113
# N's	0

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).



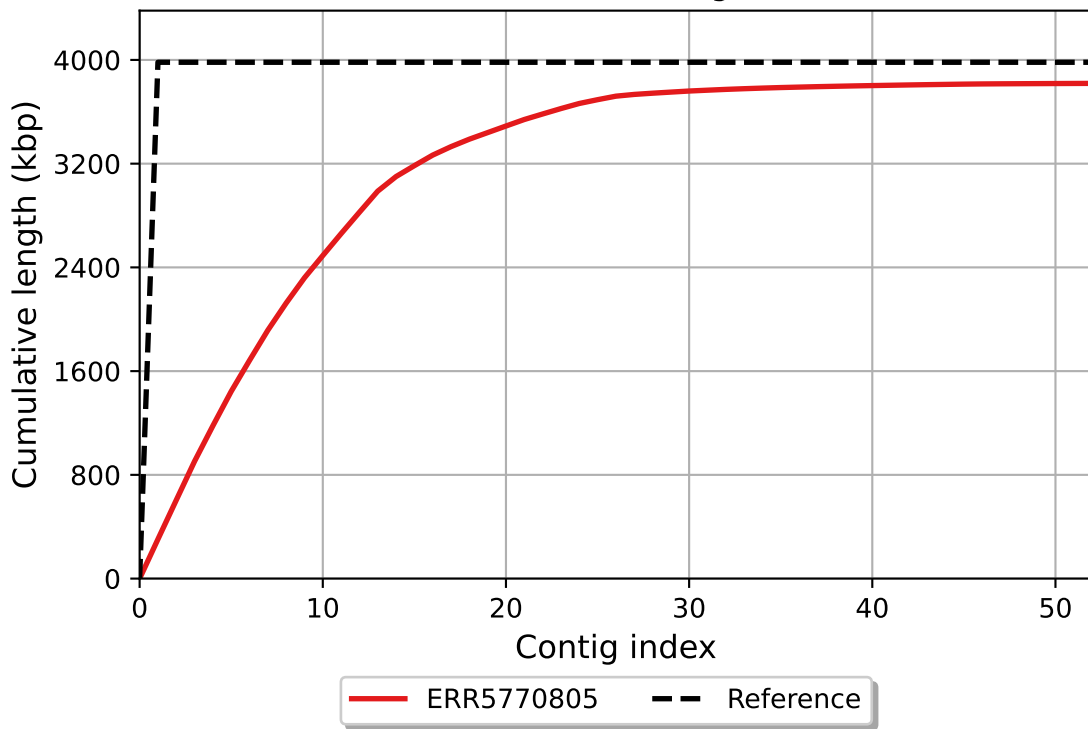
ERR5770805

NGx

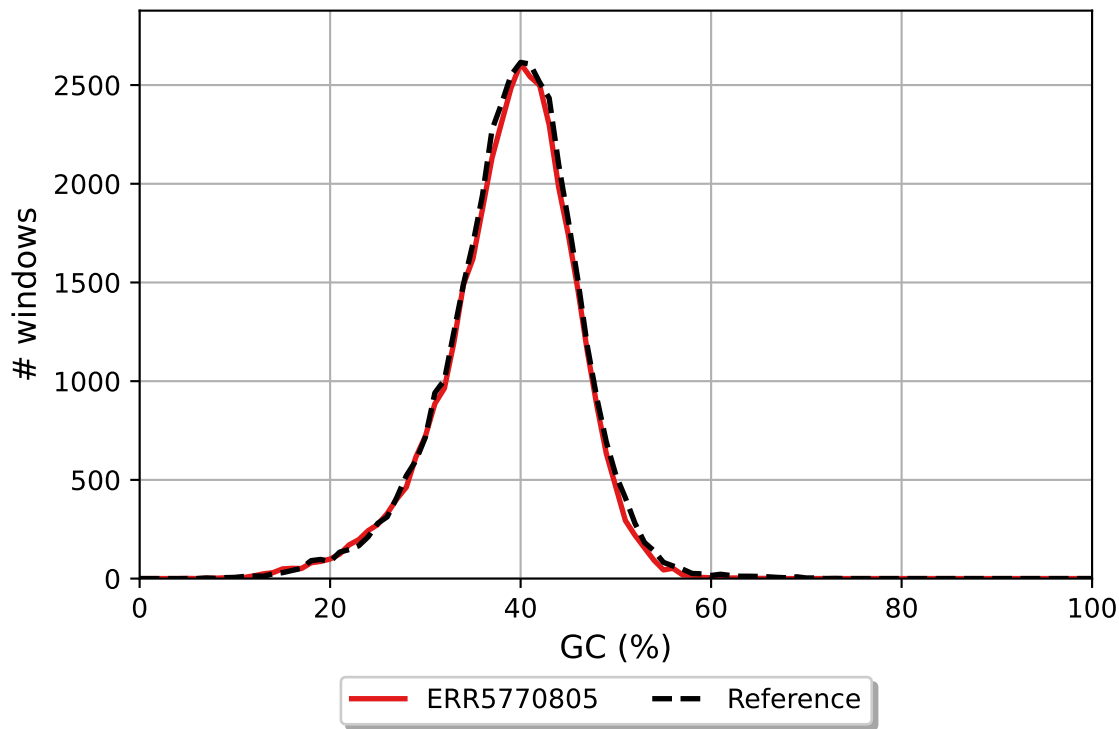


ERR5770805

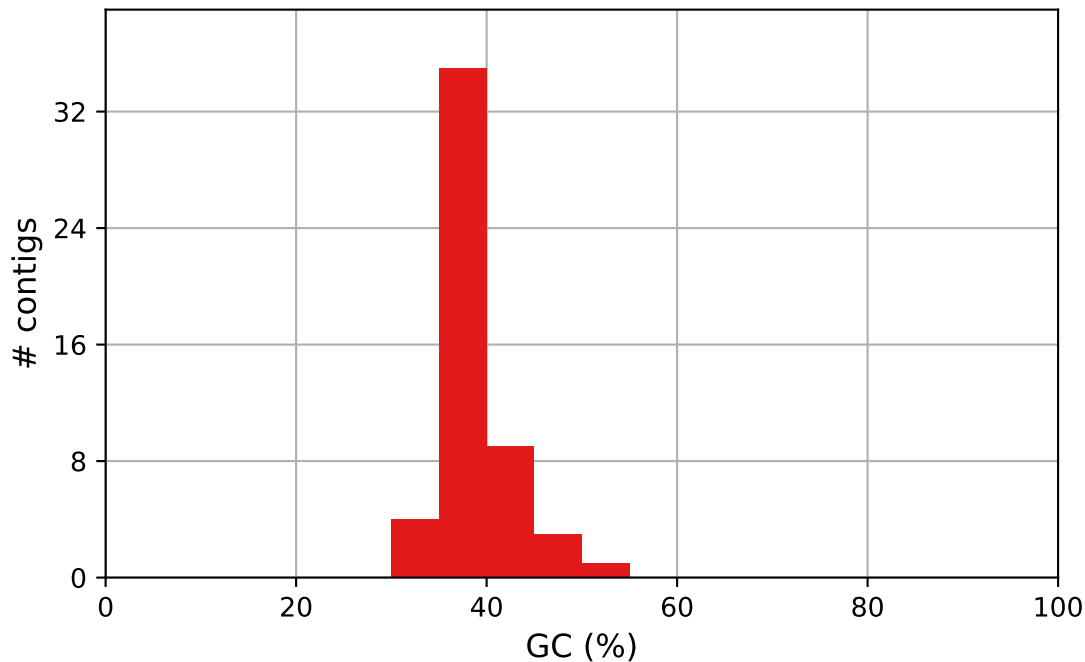
Cumulative length



GC content

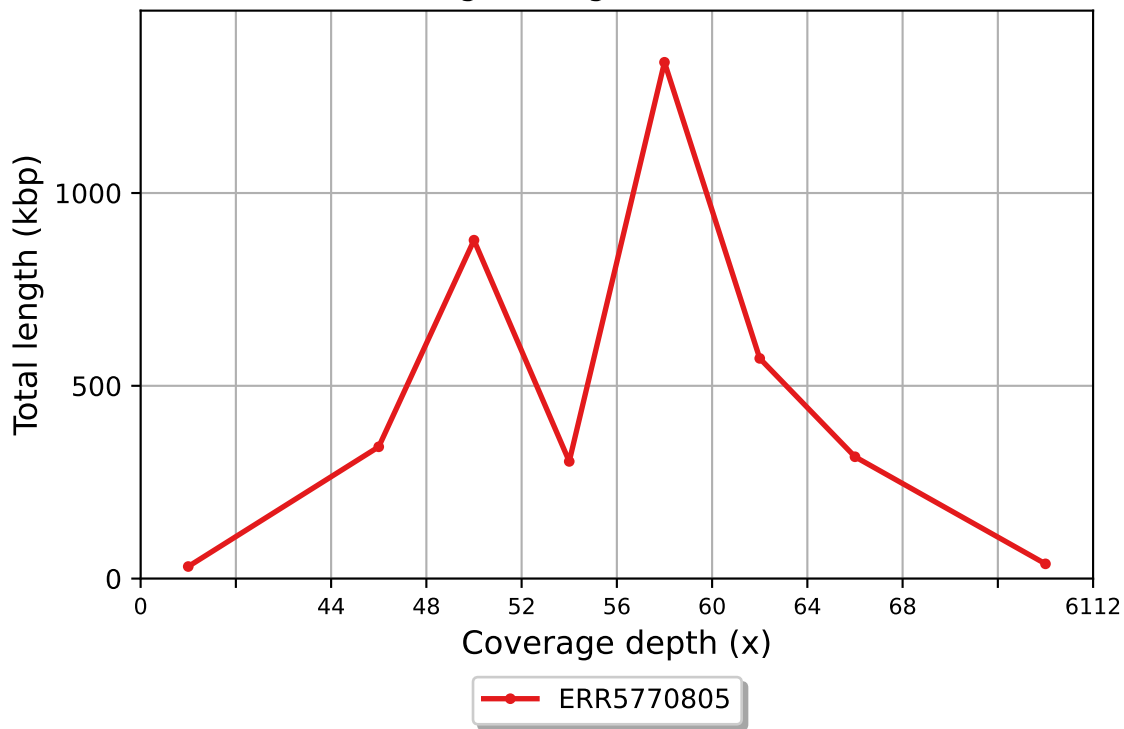


ERR5770805 GC content

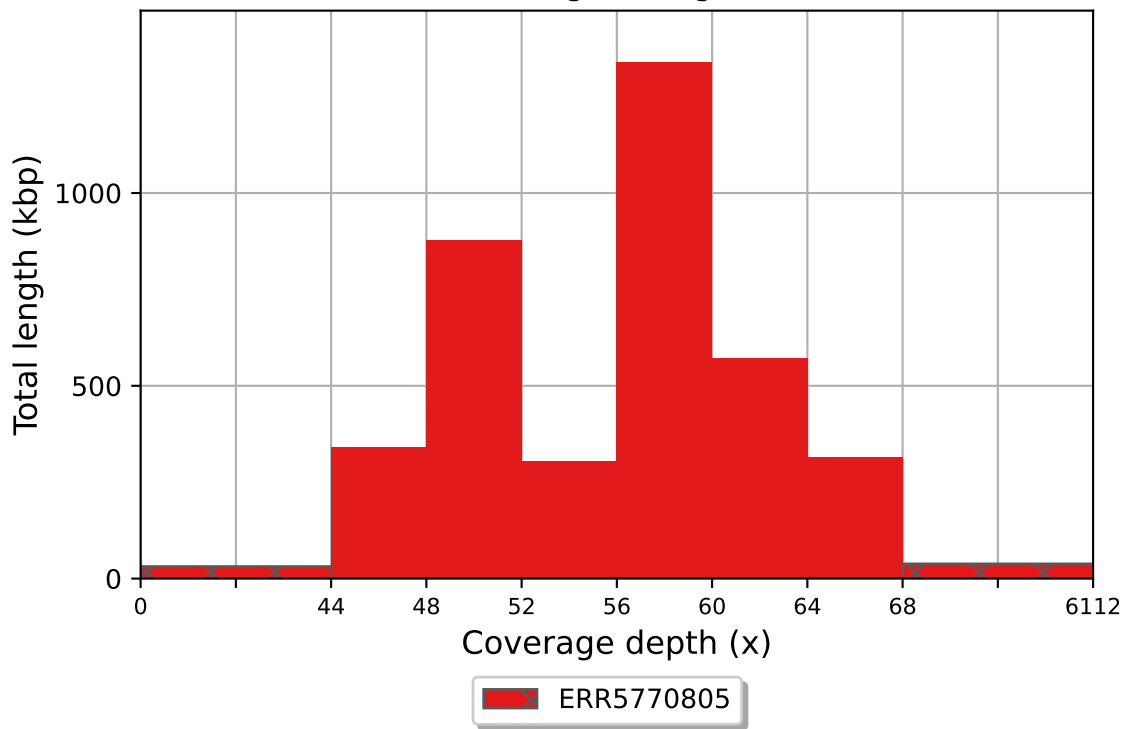


ERR5770805

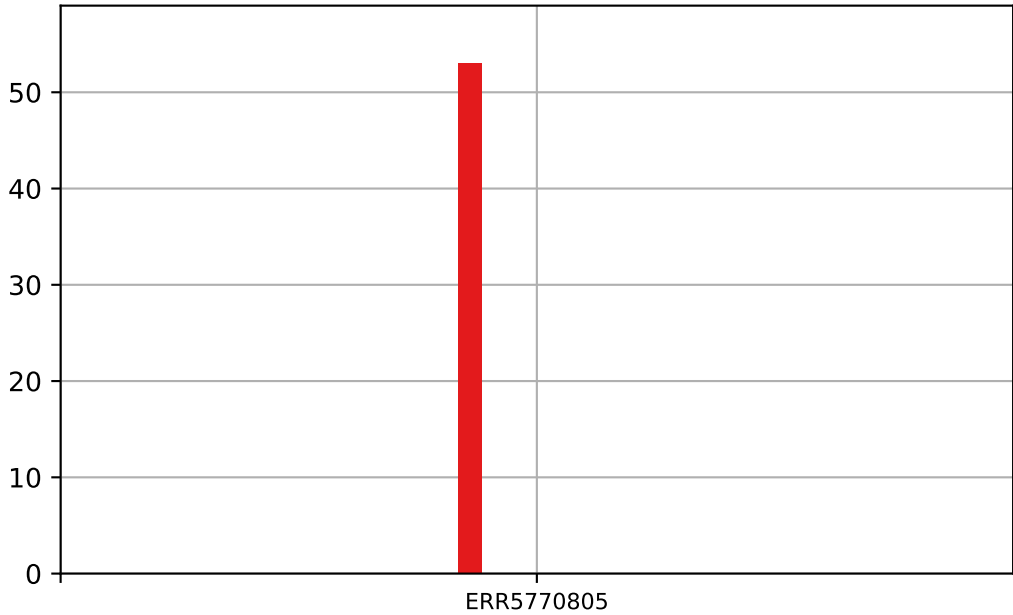
Coverage histogram (bin size: 4x)



ERR5770805 coverage histogram (bin size: 4x)

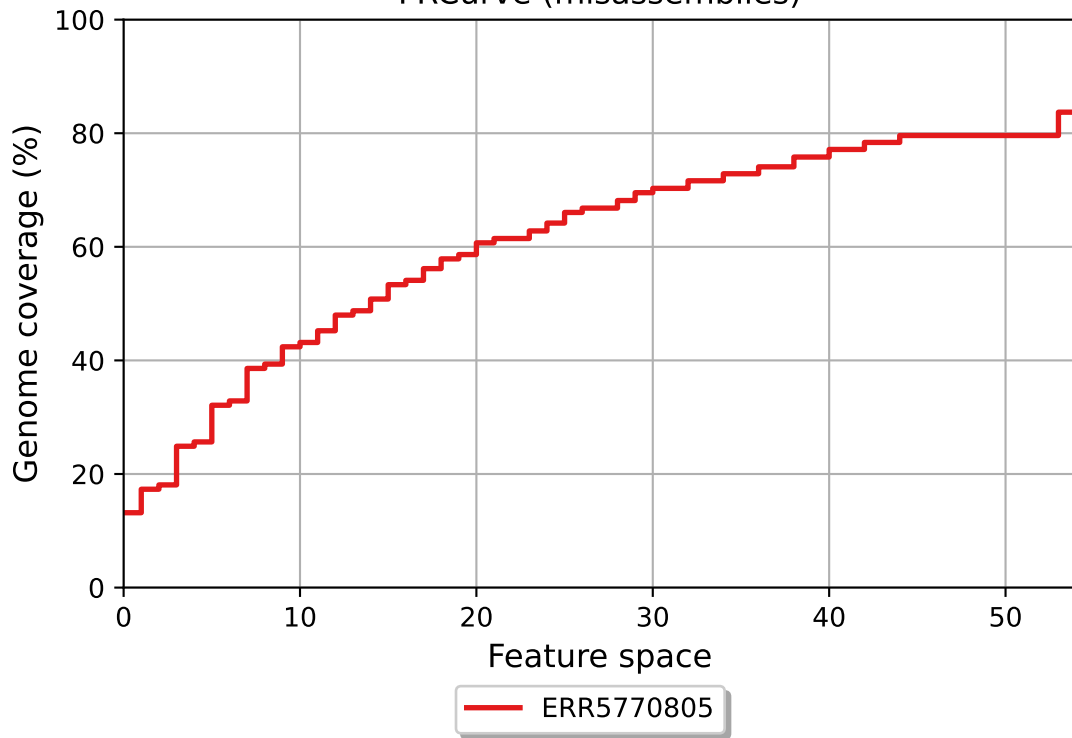


Misassemblies

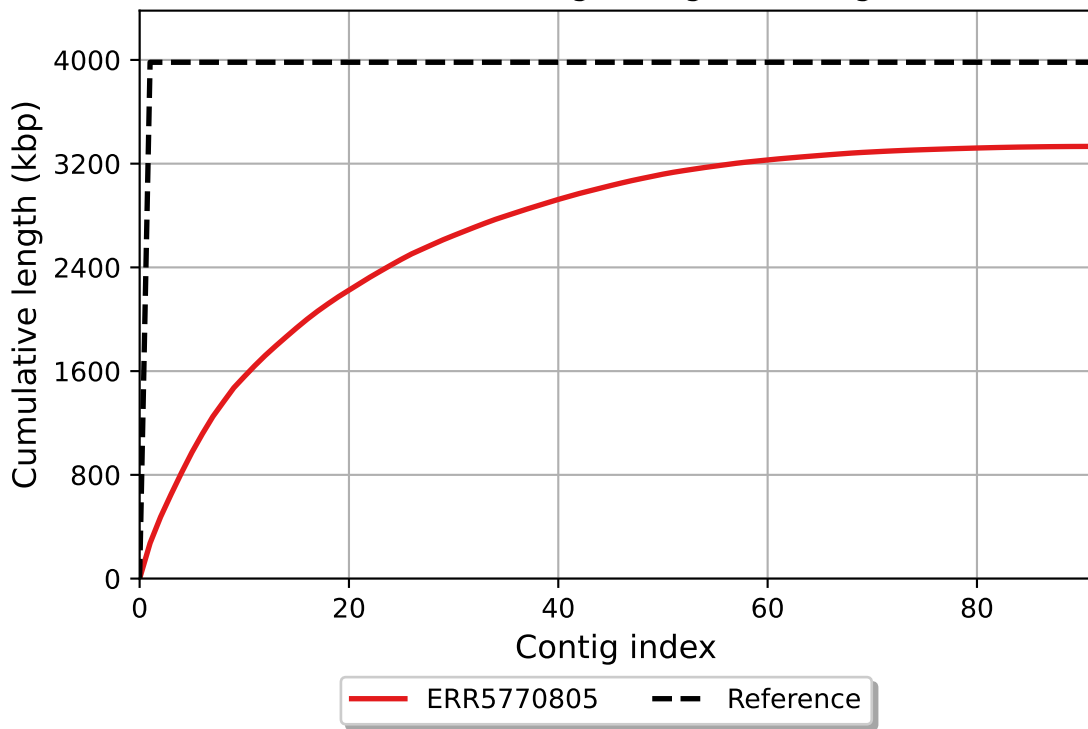


 # relocations

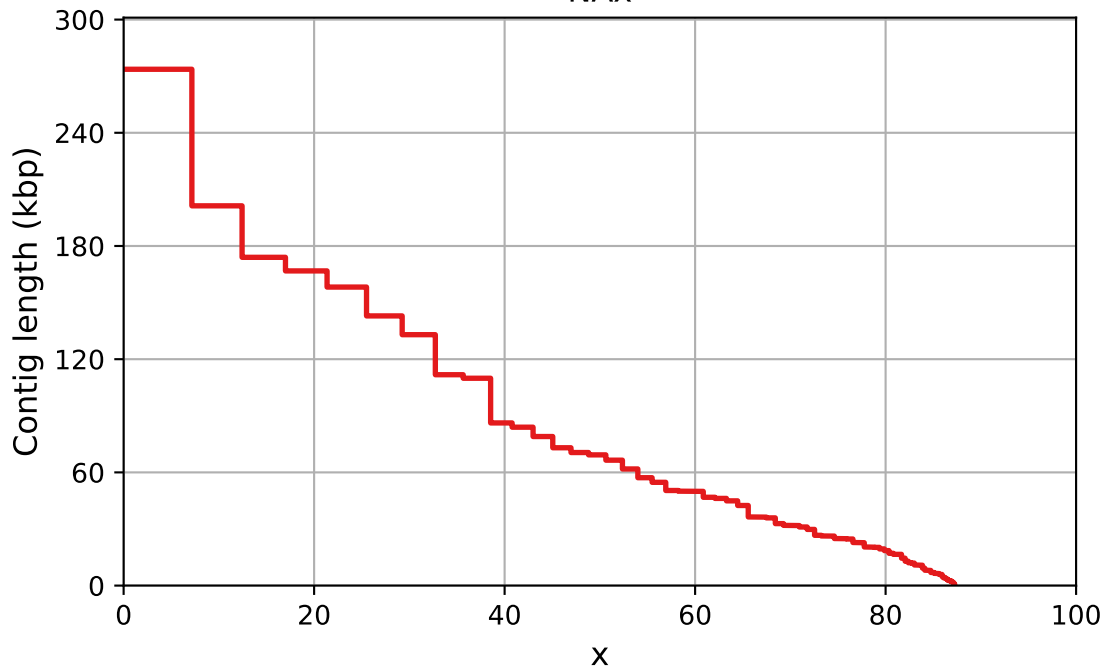
FRCurve (misassemblies)



Cumulative length (aligned contigs)

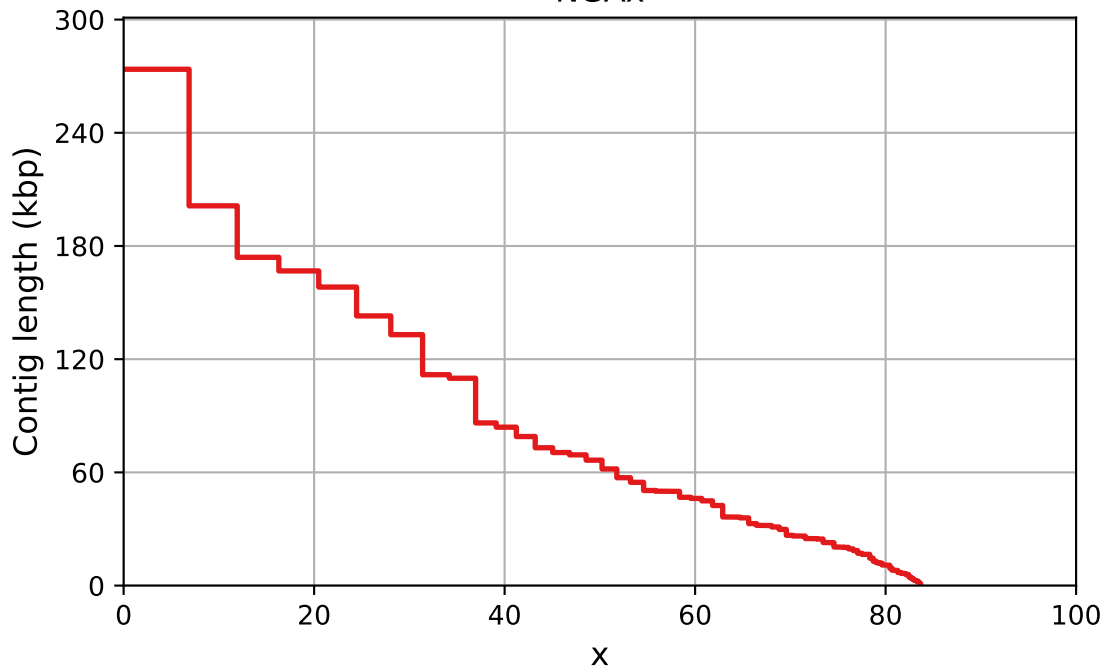


NAx



ERR5770805

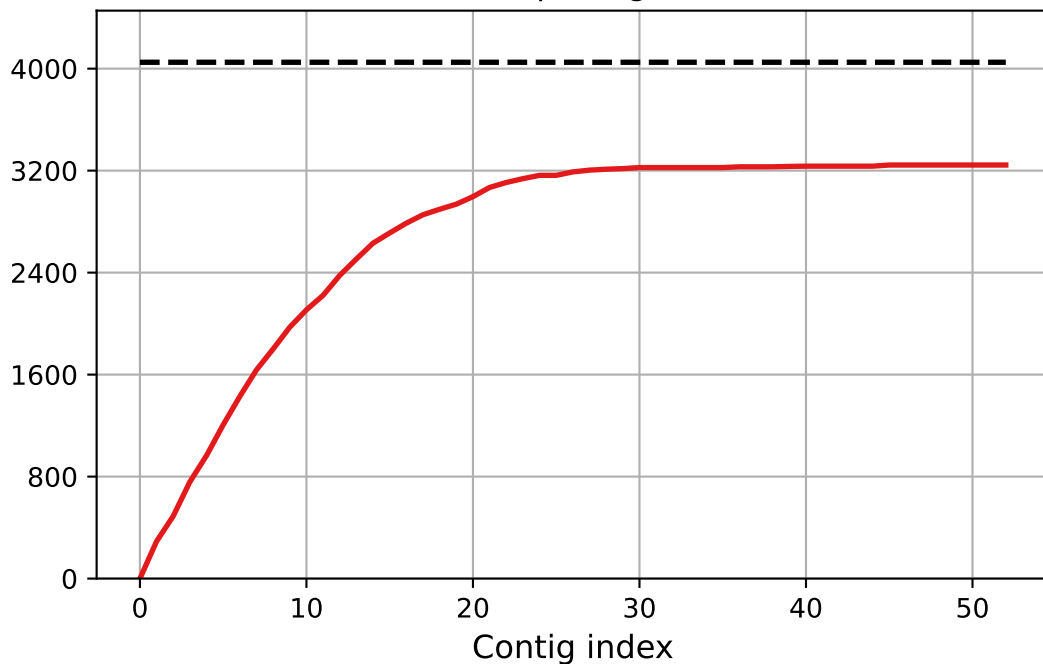
NGAx



ERR5770805

Cumulative # complete genomic features

Cumulative # complete genomic features



ERR5770805 Reference

FRCurve (genomic features)

