

Report

	URI46H
# contigs (>= 0 bp)	95
# contigs (>= 1000 bp)	27
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	1437550
Total length (>= 1000 bp)	1414866
Total length (>= 5000 bp)	1405423
Total length (>= 10000 bp)	1383984
Total length (>= 25000 bp)	1253795
Total length (>= 50000 bp)	1077575
# contigs	41
Largest contig	906762
Total length	1425069
Reference length	1521208
GC (%)	28.00
Reference GC (%)	28.18
N50	906762
NG50	906762
N90	24565
NG90	17119
auN	589625.5
auNG	552361.7
L50	1
LG50	1
L90	12
LG90	16
# misassemblies	29
# misassembled contigs	15
Misassembled contigs length	342002
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	8 + 18 part
Unaligned length	180297
Genome fraction (%)	79.301
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	817.66
# indels per 100 kbp	52.04
# genomic features	1248 + 62 part
Largest alignment	904647
Total aligned length	1239384
NA50	904647
NGA50	904647
NA90	-
NGA90	-
auNA	578233.1
auNGA	541689.3
LA50	1
LGA50	1
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

	URI46H
# misassemblies	29
# contig misassemblies	29
# c. relocations	6
# c. translocations	21
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	15
Misassembled contigs length	342002
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	10134
# indels	645
# indels (<= 5 bp)	592
# indels (> 5 bp)	53
Indels length	2724

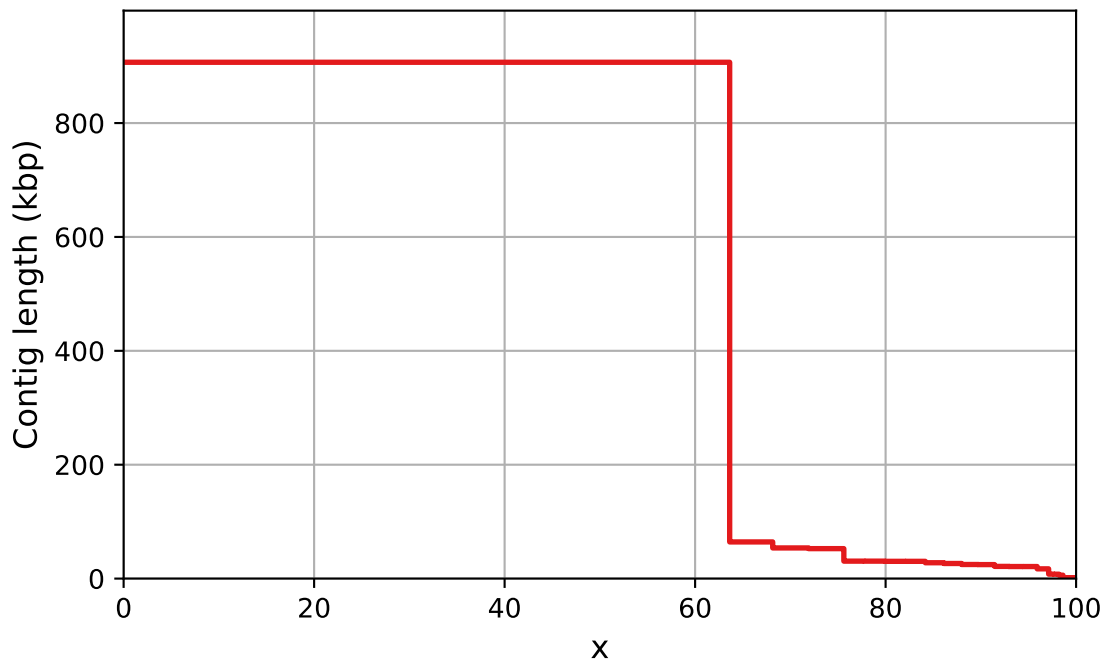
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	URI46H
# fully unaligned contigs	8
Fully unaligned length	12656
# partially unaligned contigs	18
Partially unaligned length	167641
# N's	0

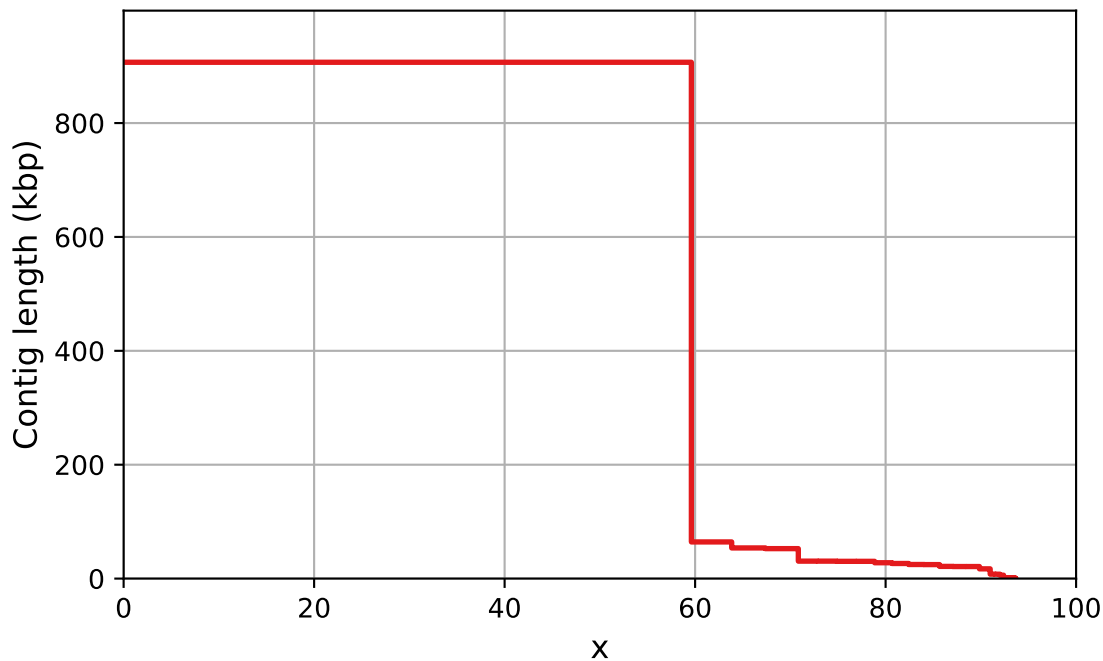
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

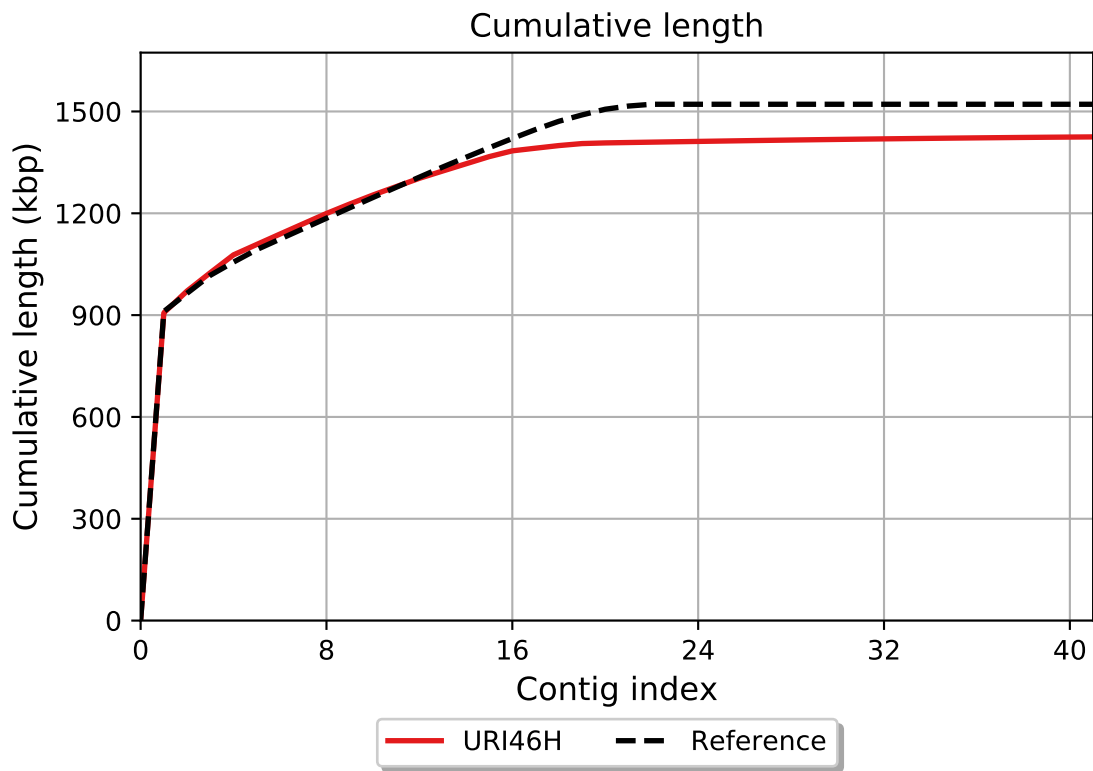


URI46H

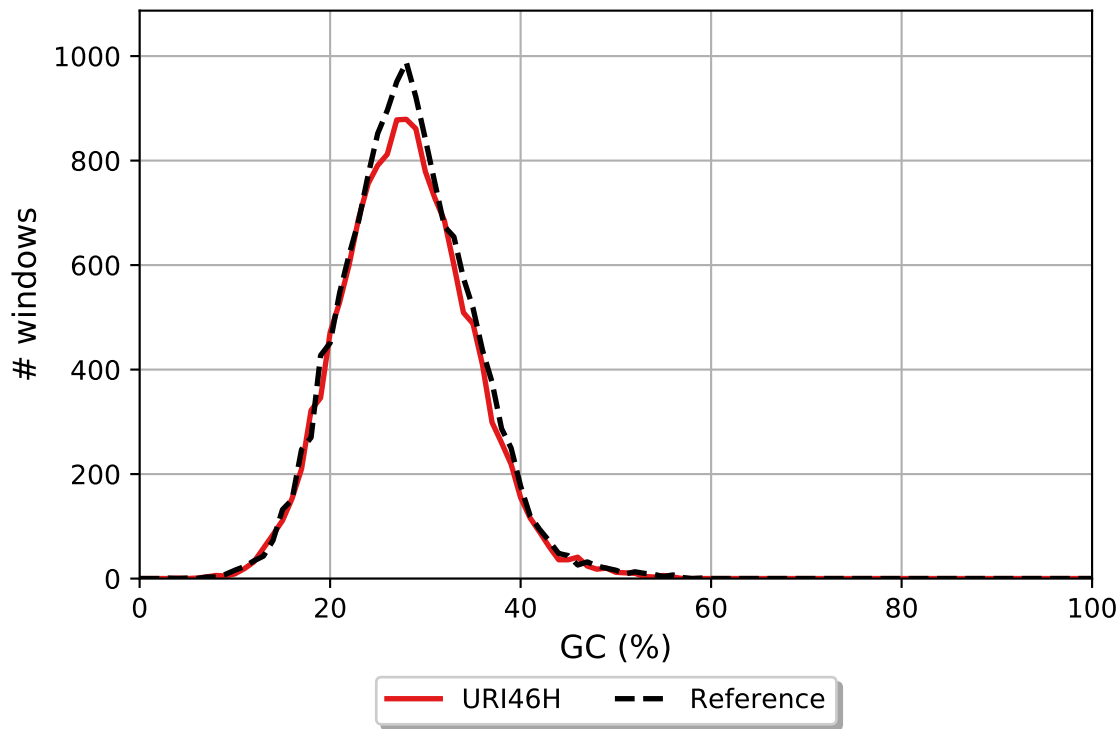
NGx



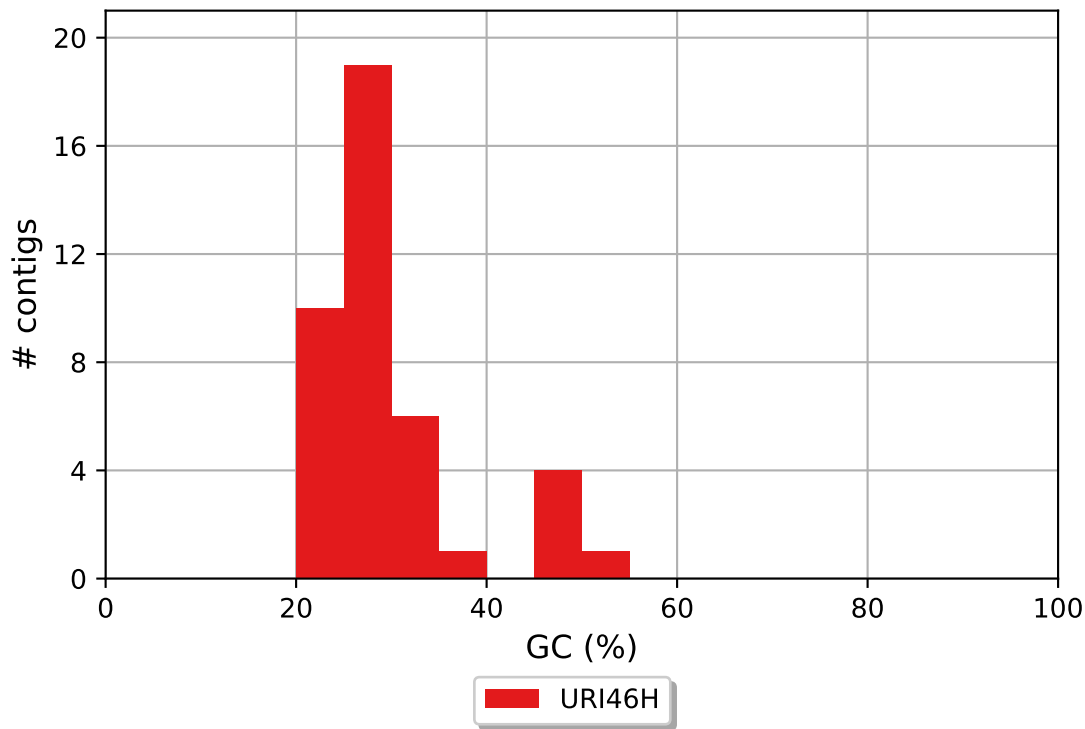
URI46H



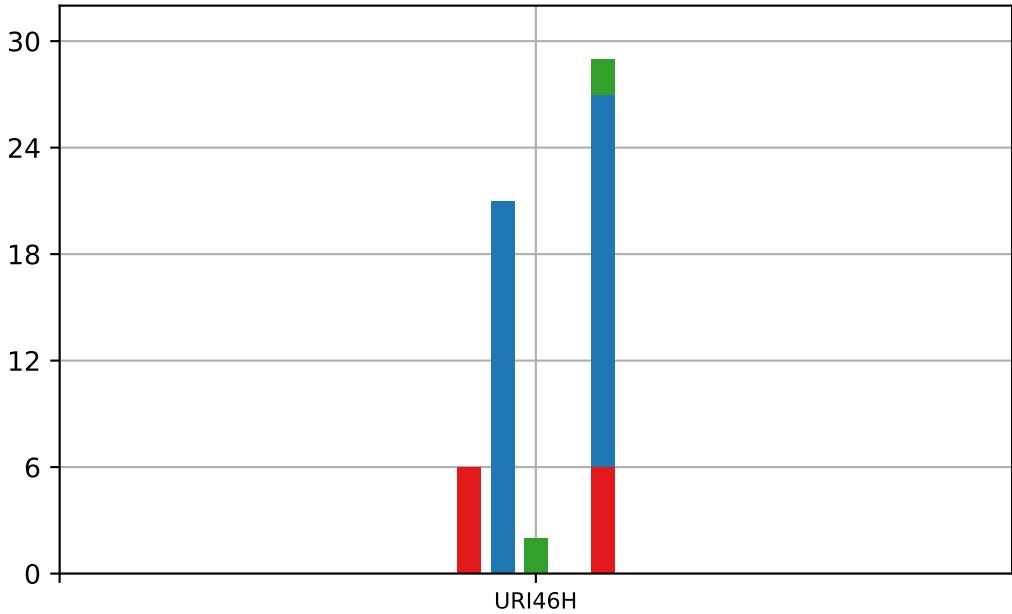
GC content



URI46H GC content



Misassemblies



relocations

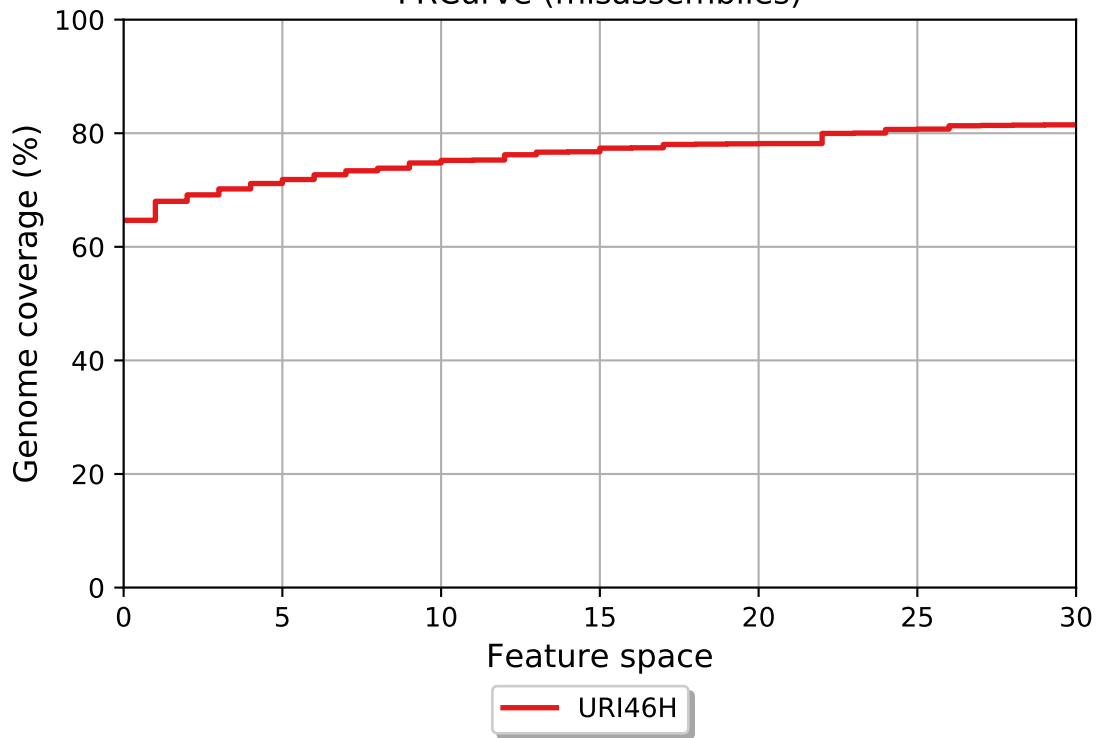


translocations

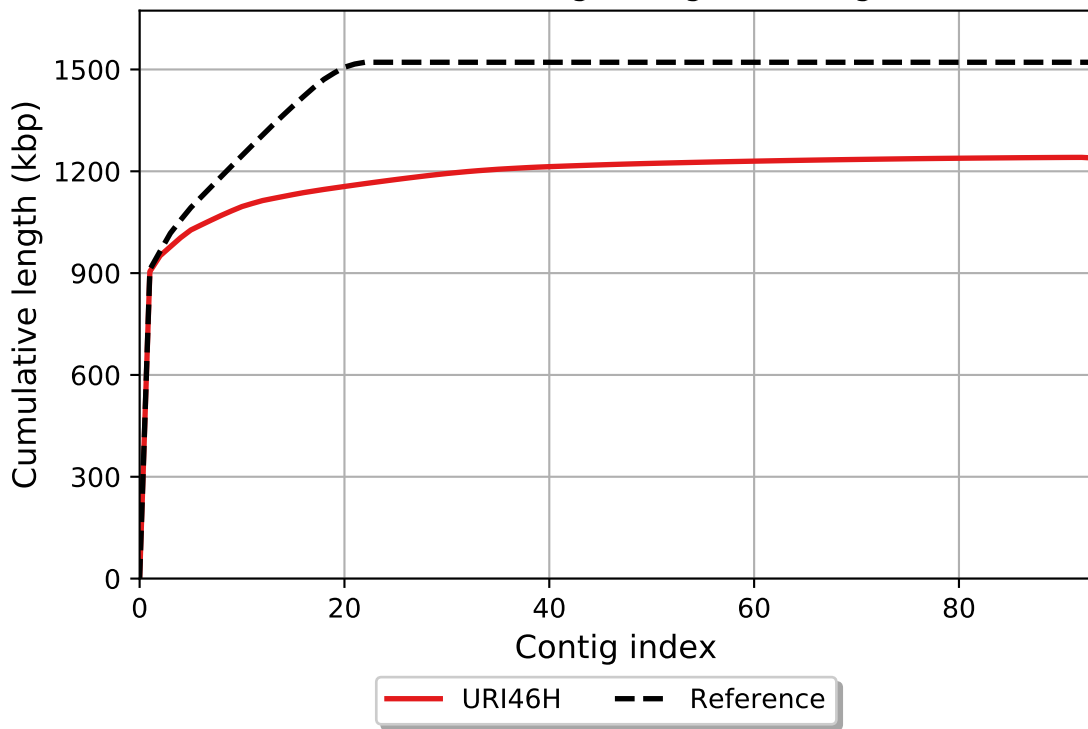


inversions

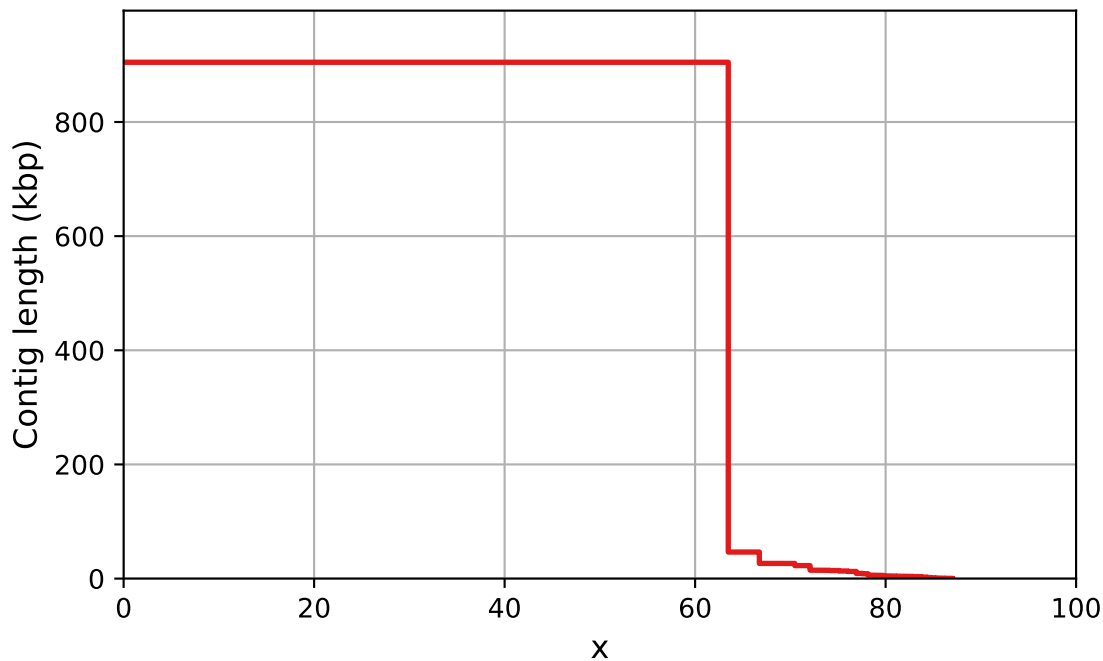
FRCurve (misassemblies)



Cumulative length (aligned contigs)

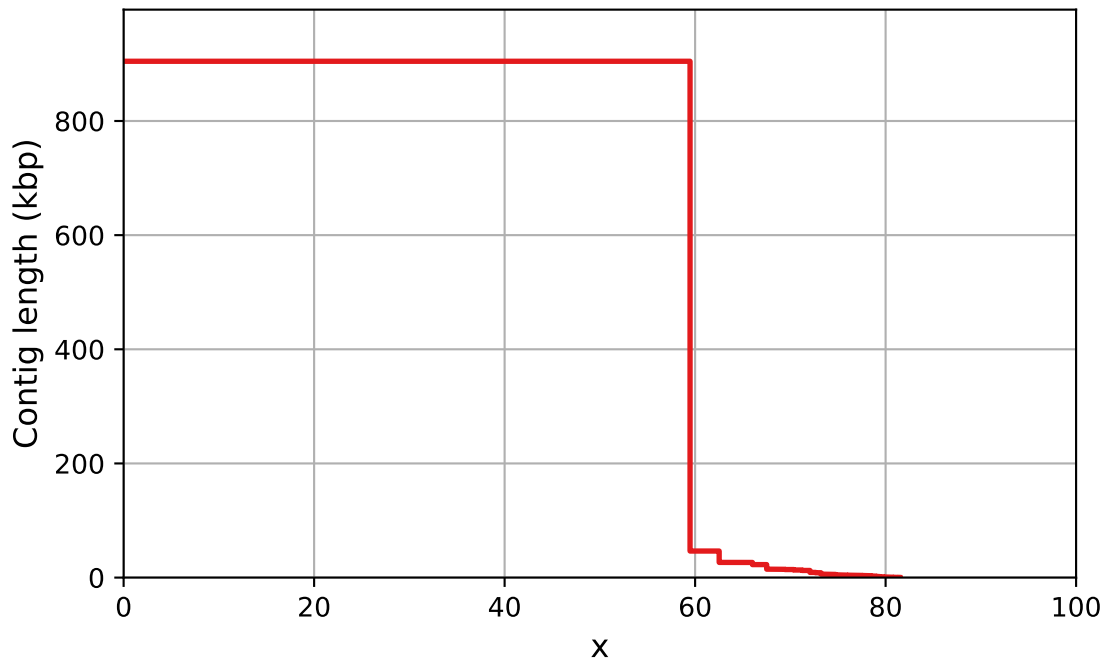


NAx



URI46H

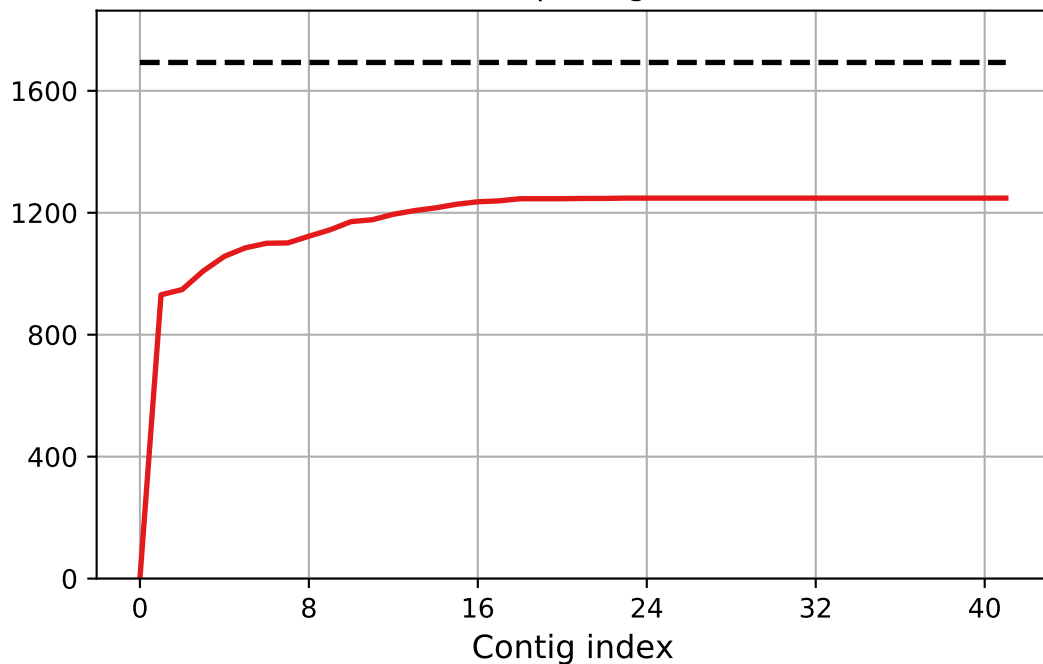
NGAx



URI46H

Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)

