

Report

	URI88H
# contigs (>= 0 bp)	33
# contigs (>= 1000 bp)	21
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	20
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	1540602
Total length (>= 1000 bp)	1536809
Total length (>= 5000 bp)	1533641
Total length (>= 10000 bp)	1533641
Total length (>= 25000 bp)	1459031
Total length (>= 50000 bp)	1128755
# contigs	23
Largest contig	906672
Total length	1538319
Reference length	1521208
GC (%)	28.23
Reference GC (%)	28.18
N50	906672
NG50	906672
N90	29970
NG90	30258
auN	549806.3
auNG	555990.7
L50	1
LG50	1
L90	14
LG90	13
# misassemblies	34
# misassembled contigs	12
Misassembled contigs length	441972
# local misassemblies	24
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	2 + 18 part
Unaligned length	215944
Genome fraction (%)	81.483
Duplication ratio	1.065
# N's per 100 kbp	0.00
# mismatches per 100 kbp	919.68
# indels per 100 kbp	56.37
# genomic features	1300 + 45 part
Largest alignment	904981
Total aligned length	1319922
NA50	904981
NGA50	904981
NA90	-
NGA90	-
auNA	537221.6
auNGA	543264.4
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

	URI88H
# misassemblies	34
# contig misassemblies	34
# c. relocations	8
# c. translocations	24
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	441972
# local misassemblies	24
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	12139
# indels	744
# indels (<= 5 bp)	666
# indels (> 5 bp)	78
Indels length	4151

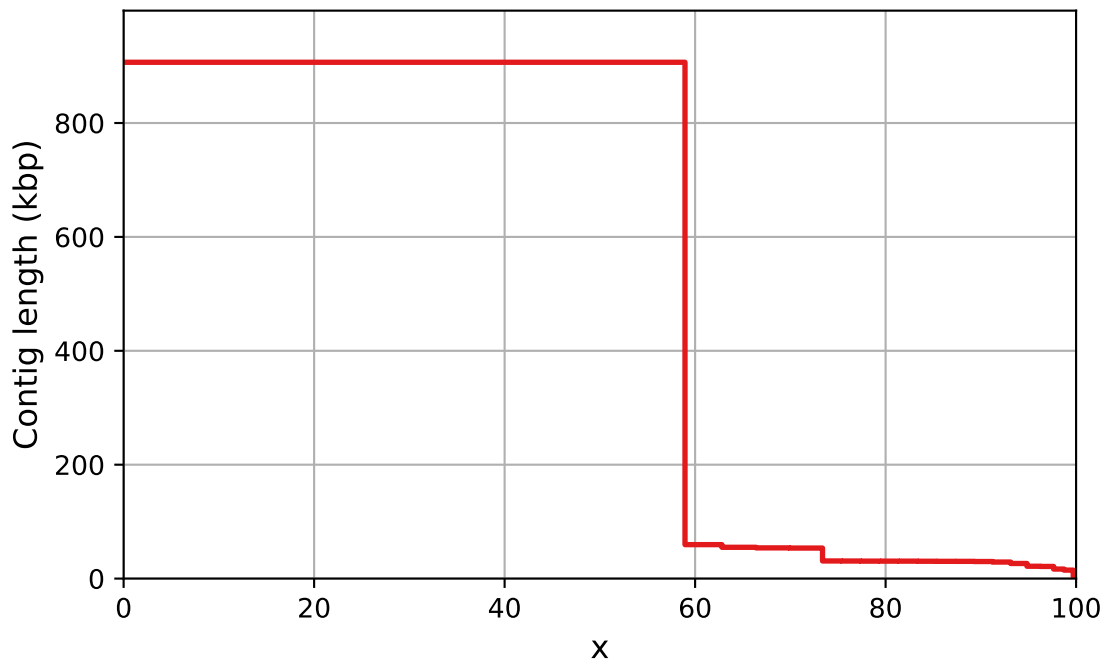
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	URI88H
# fully unaligned contigs	2
Fully unaligned length	1510
# partially unaligned contigs	18
Partially unaligned length	214434
# N's	0

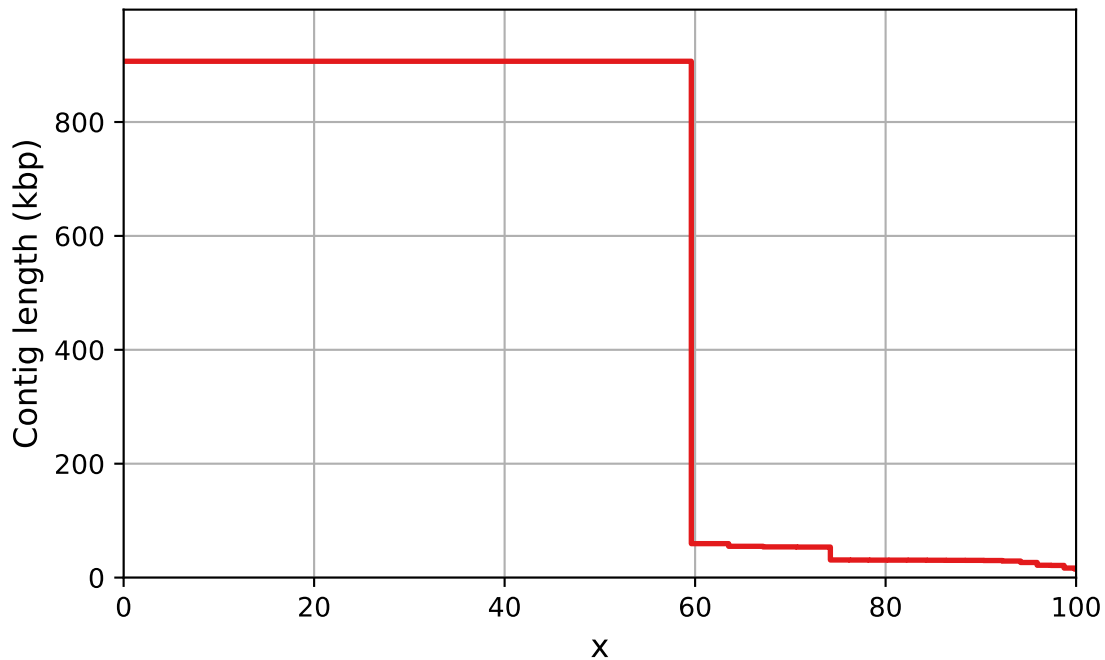
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

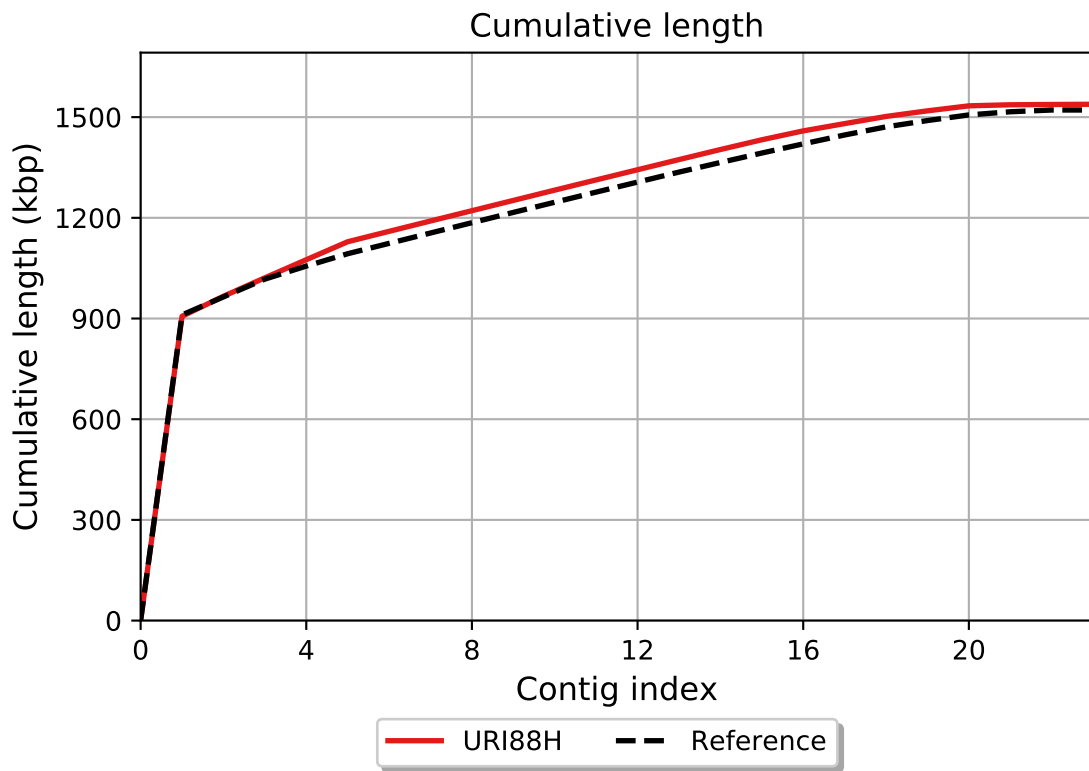


URI88H

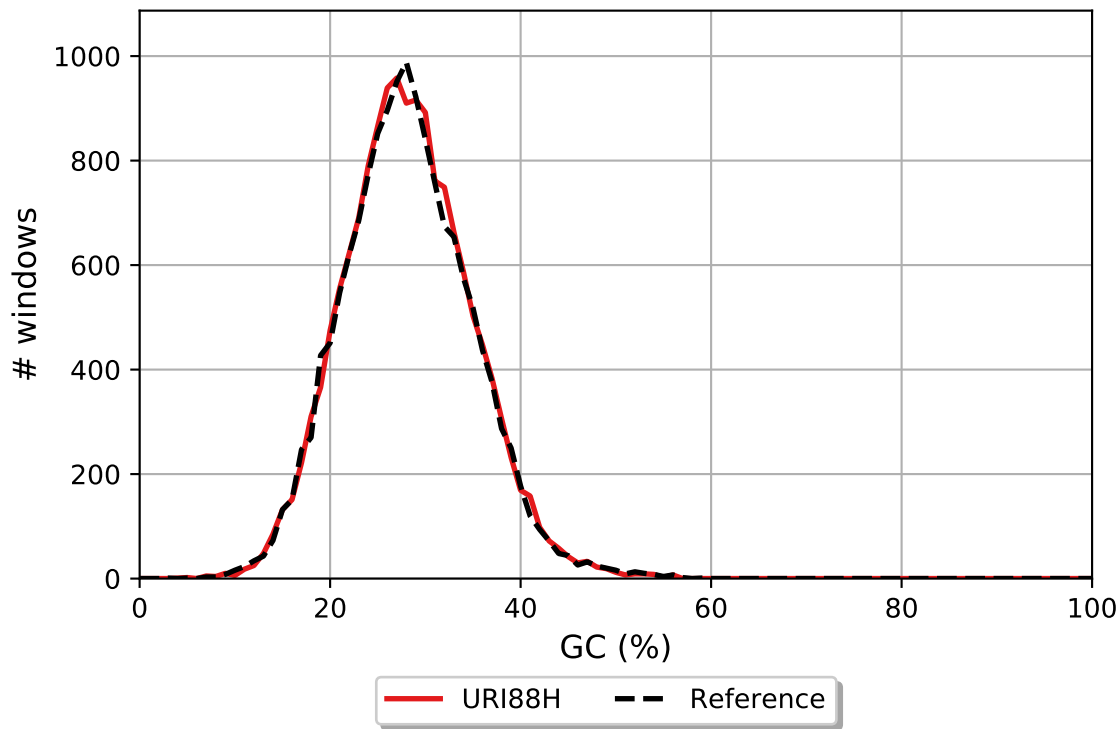
NGx



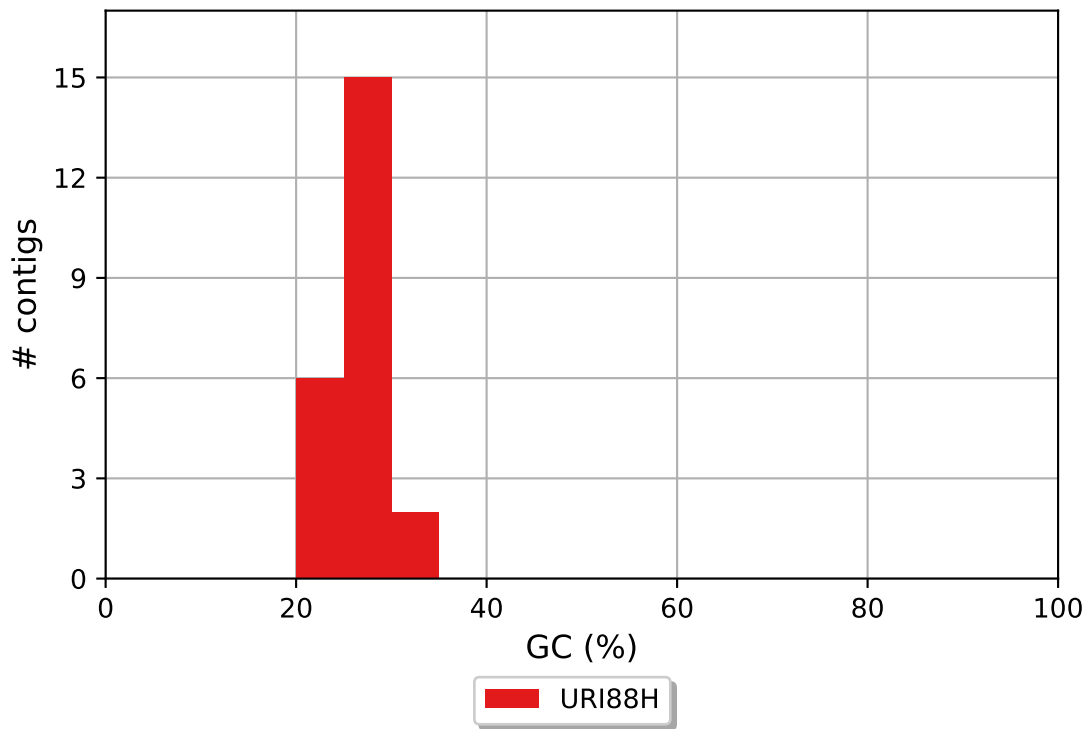
URI88H



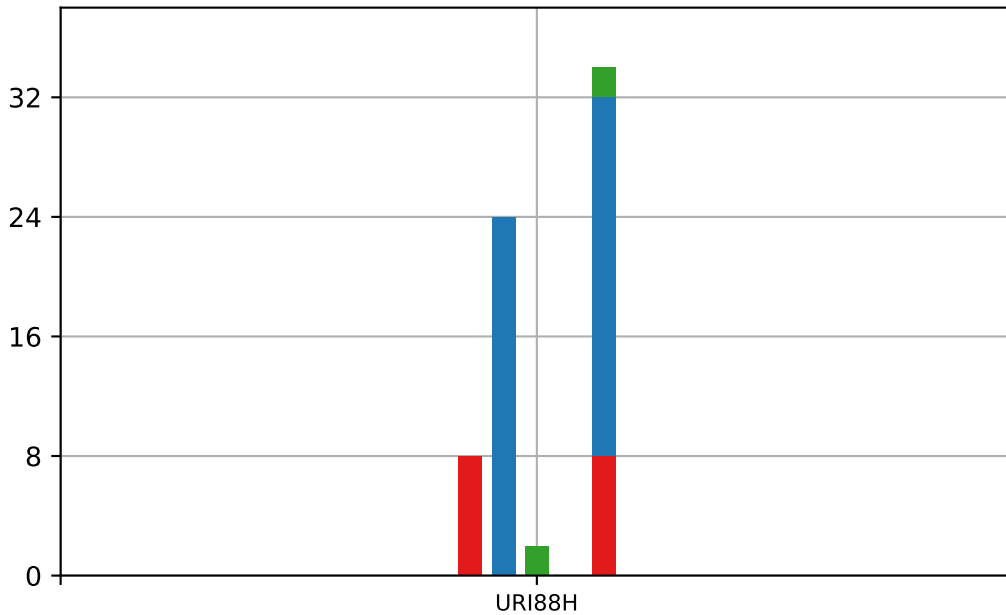
GC content



URI88H GC content



Misassemblies



relocations

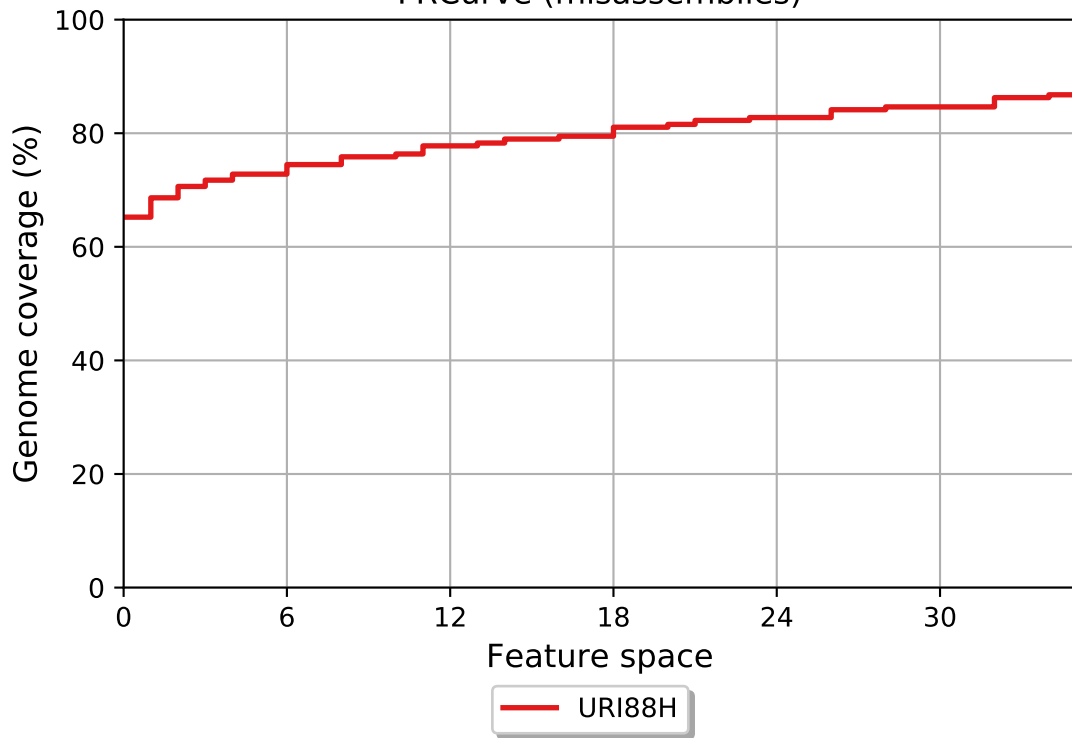


translocations

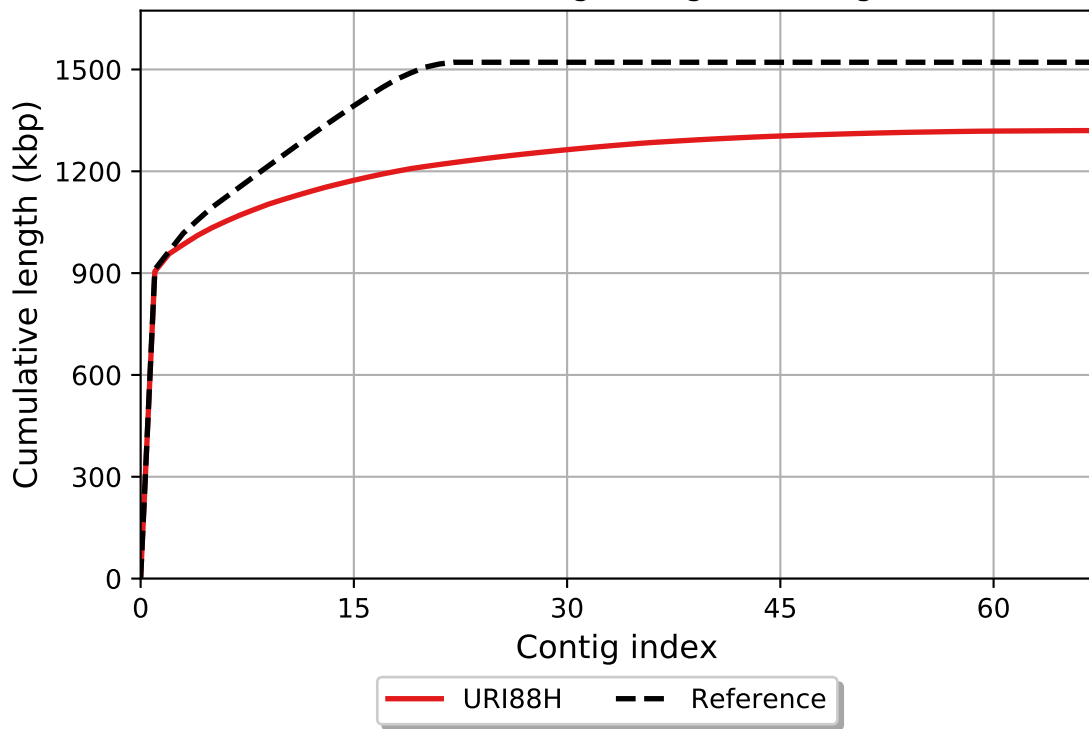


inversions

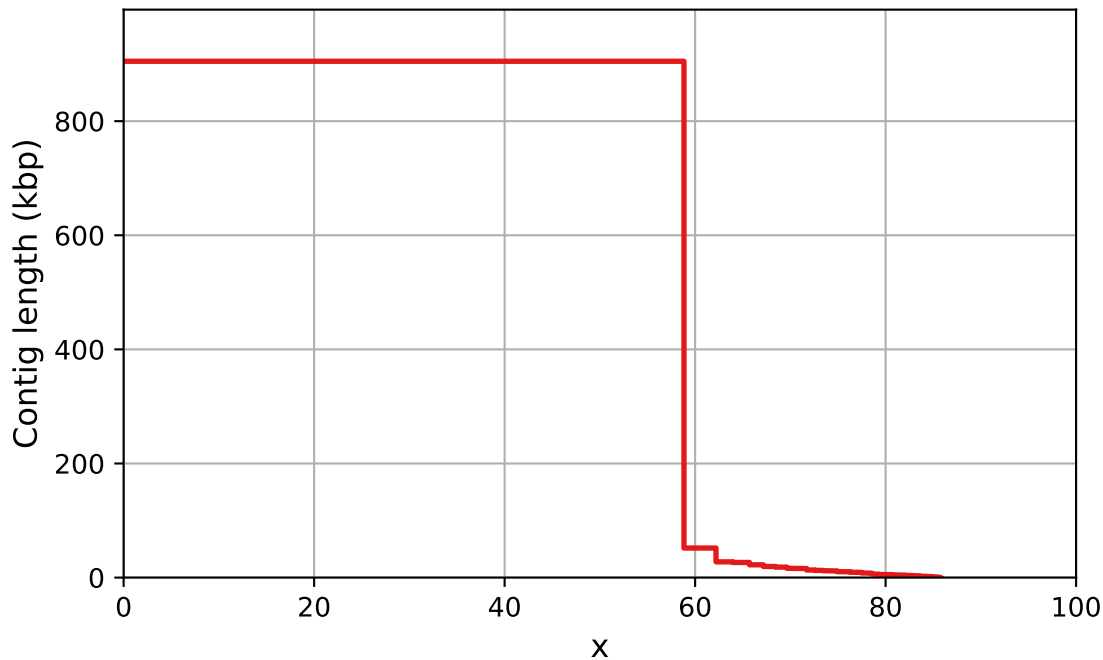
FRCurve (misassemblies)



Cumulative length (aligned contigs)

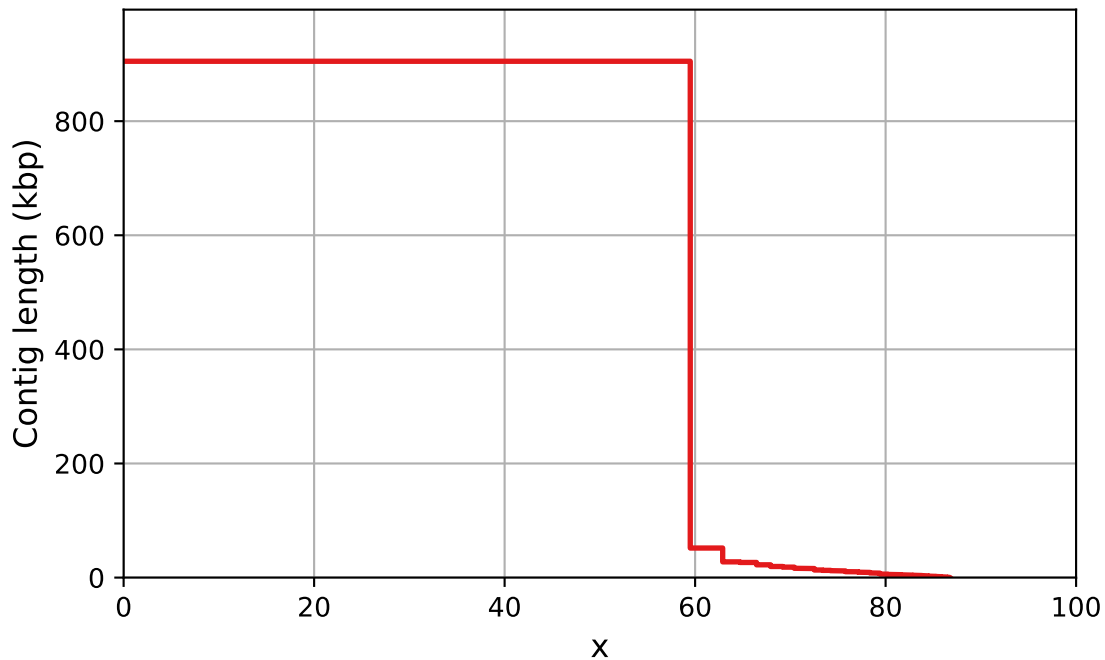


NAx



URI88H

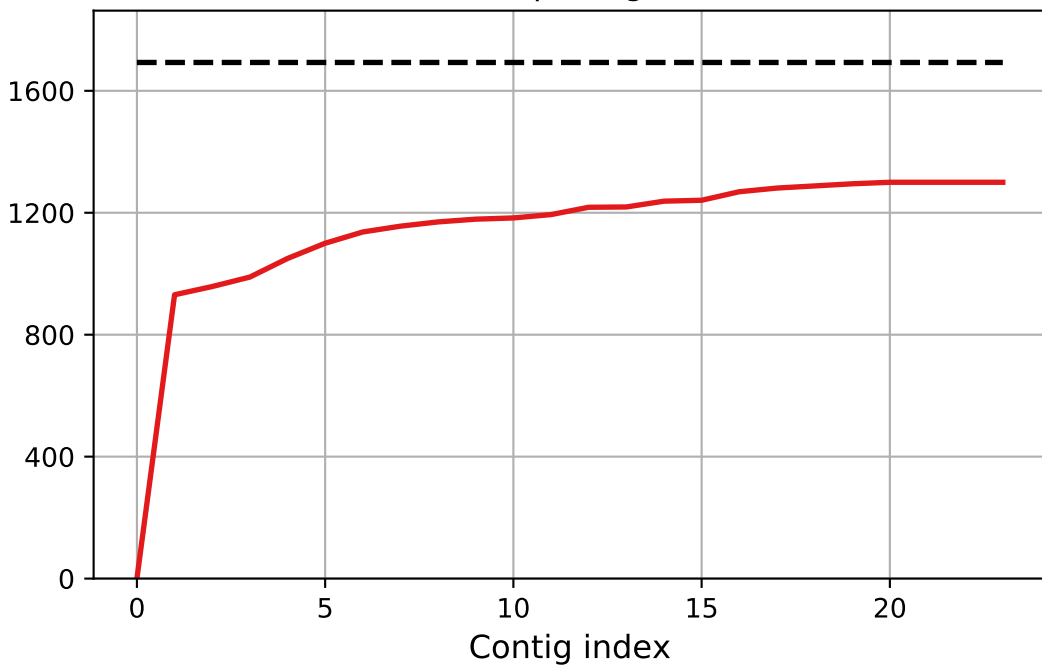
NGAx



URI88H

Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)

