

Report

	URI48H
# contigs (>= 0 bp)	22
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1377993
Total length (>= 1000 bp)	1375278
Total length (>= 5000 bp)	1375278
Total length (>= 10000 bp)	1366758
Total length (>= 25000 bp)	1350631
Total length (>= 50000 bp)	957485
# contigs	18
Largest contig	902776
Total length	1377107
Reference length	1521208
GC (%)	28.30
Reference GC (%)	28.18
N50	902776
NG50	902776
N90	29586
NG90	8520
auN	603907.5
auNG	546700.5
L50	1
LG50	1
L90	11
LG90	16
# misassemblies	18
# misassembled contigs	8
Misassembled contigs length	257775
# local misassemblies	12
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	1 + 13 part
Unaligned length	135317
Genome fraction (%)	79.659
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	854.78
# indels per 100 kbp	48.47
# genomic features	1261 + 56 part
Largest alignment	902586
Total aligned length	1237857
NA50	902586
NGA50	902586
NA90	-
NGA90	-
auNA	597531.8
auNGA	540928.8
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

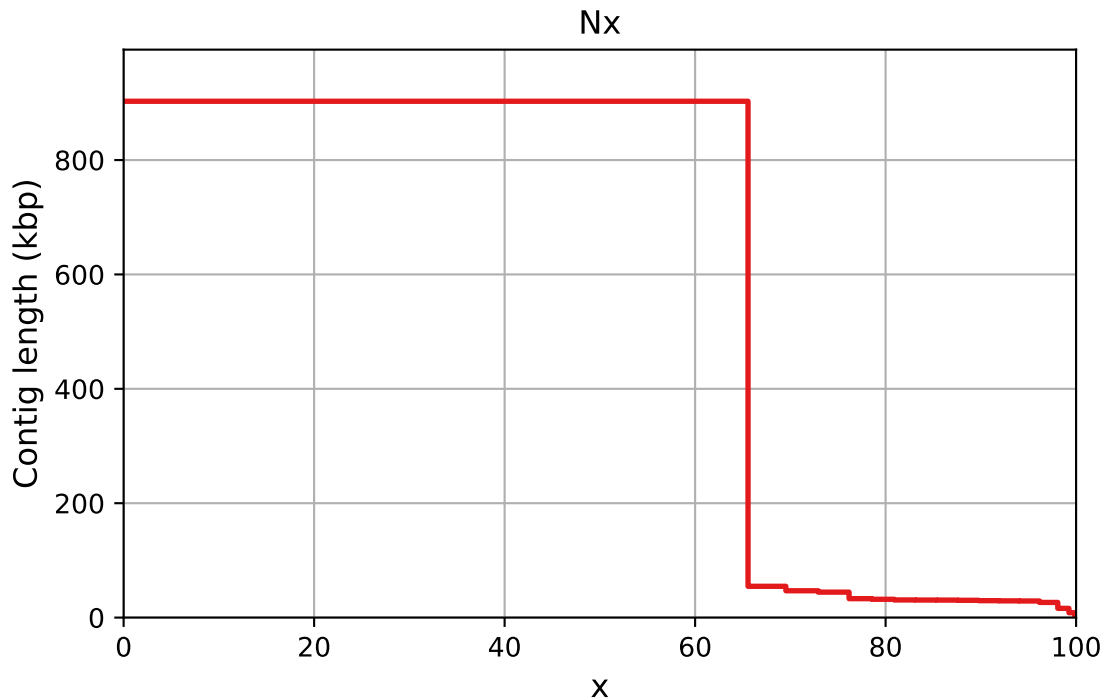
	URI48H
# misassemblies	18
# contig misassemblies	18
# c. relocations	7
# c. translocations	11
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	257775
# local misassemblies	12
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	10581
# indels	600
# indels (<= 5 bp)	534
# indels (> 5 bp)	66
Indels length	3988

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

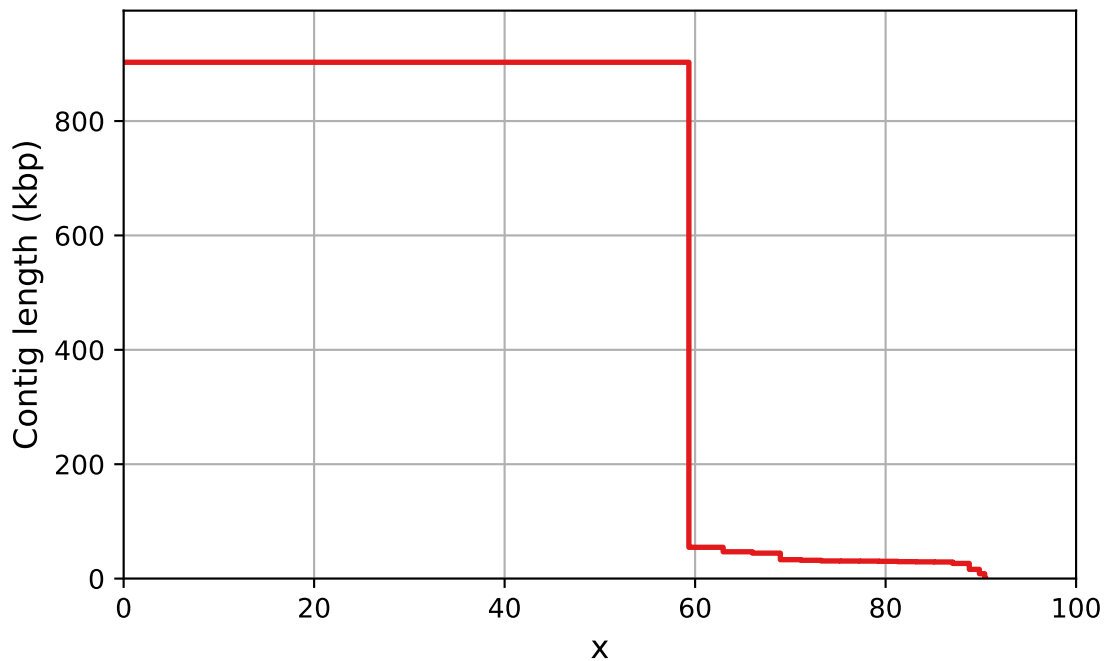
	URI48H
# fully unaligned contigs	1
Fully unaligned length	940
# partially unaligned contigs	13
Partially unaligned length	134377
# N's	0

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).

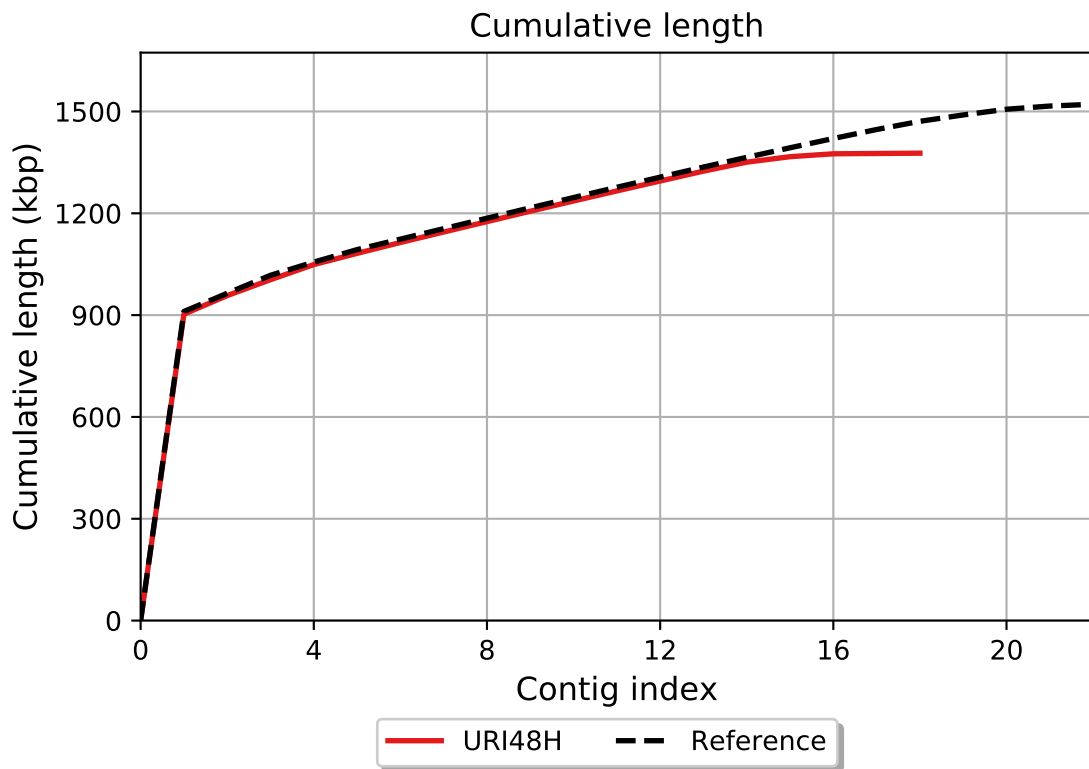


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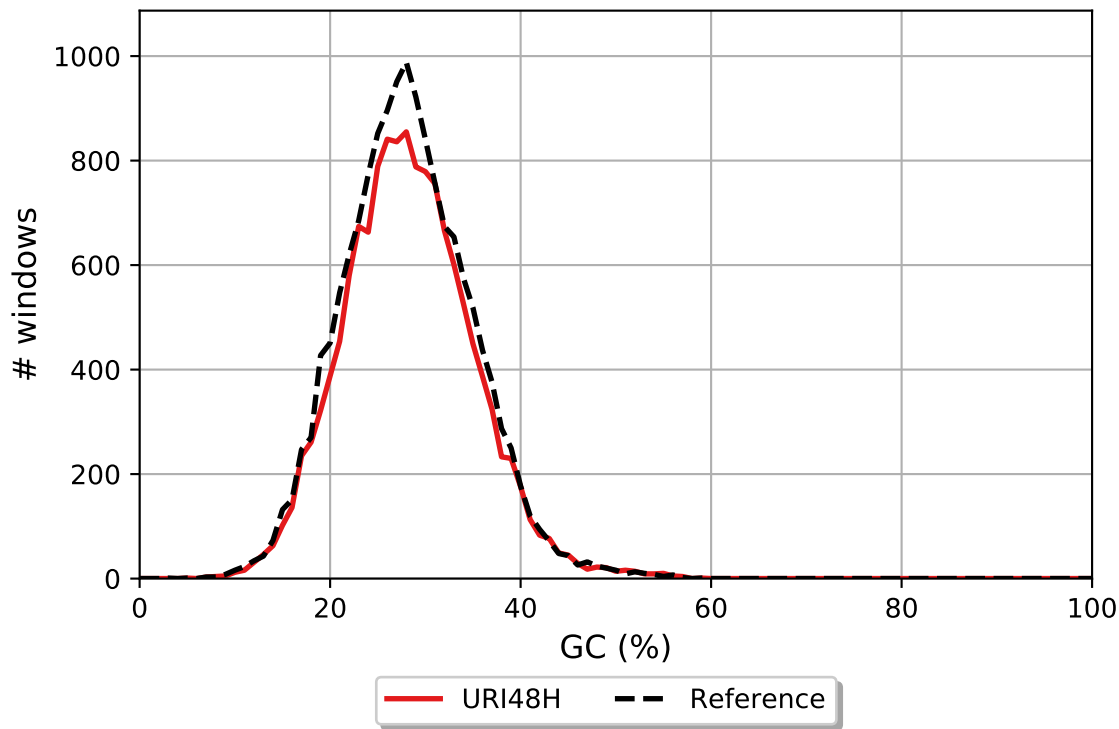
NGx



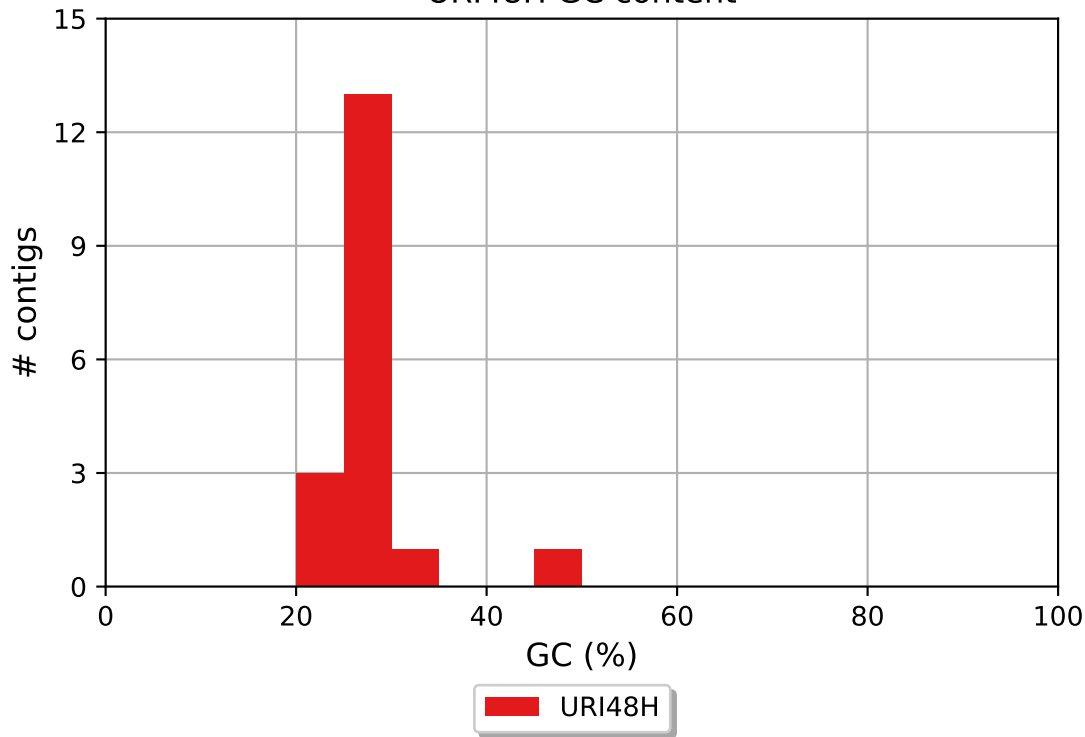
URI48H



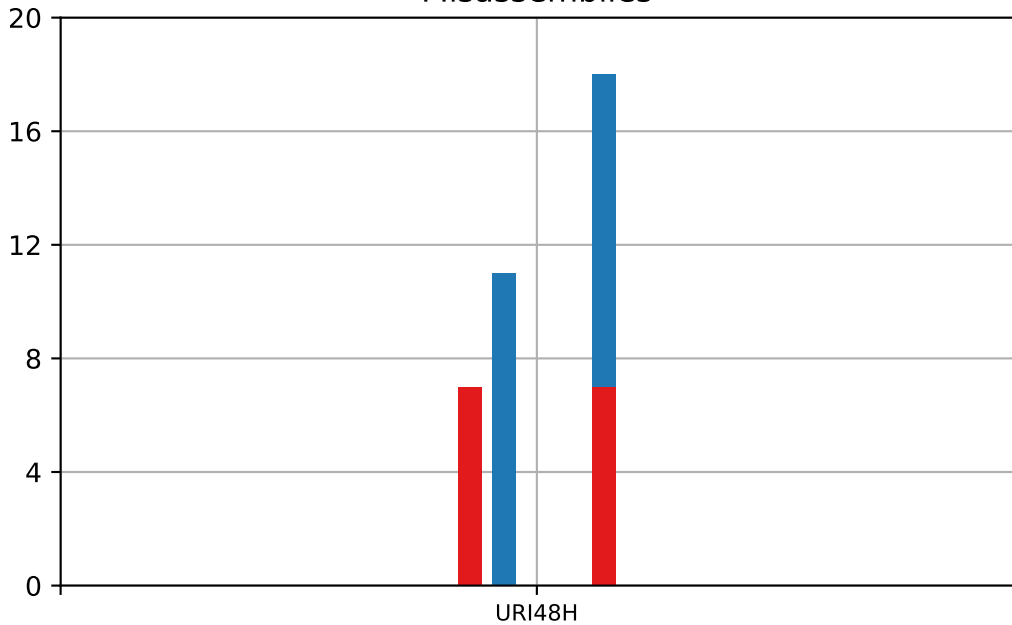
GC content



URI48H GC content



Misassemblies

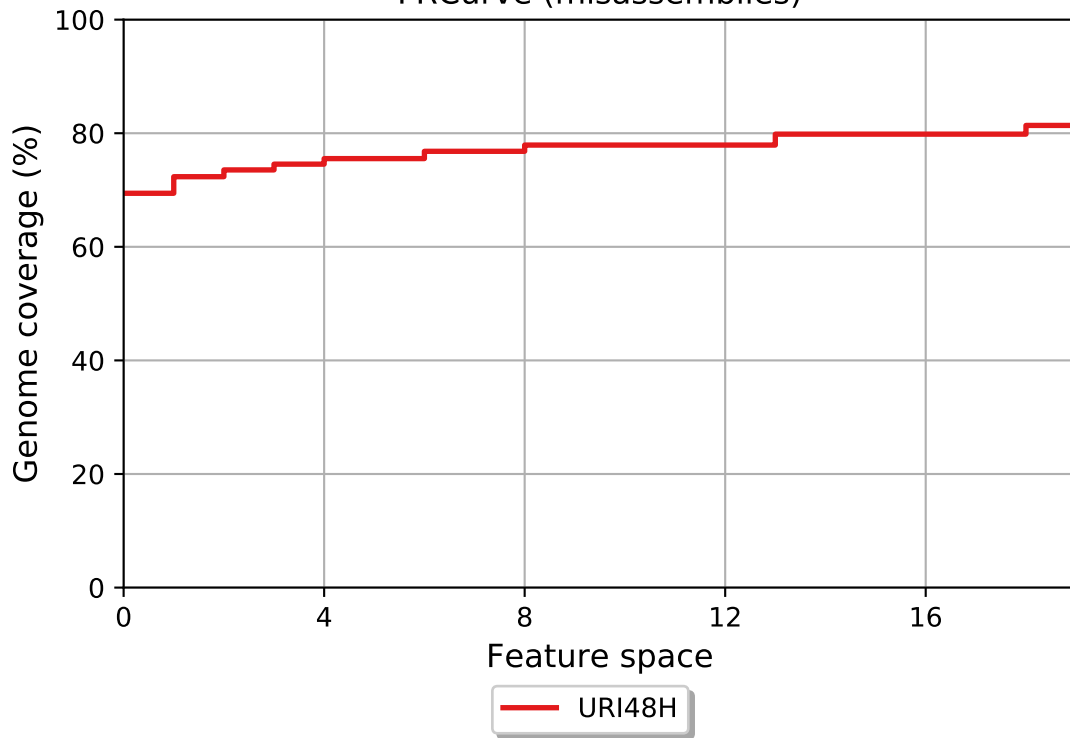


relocations

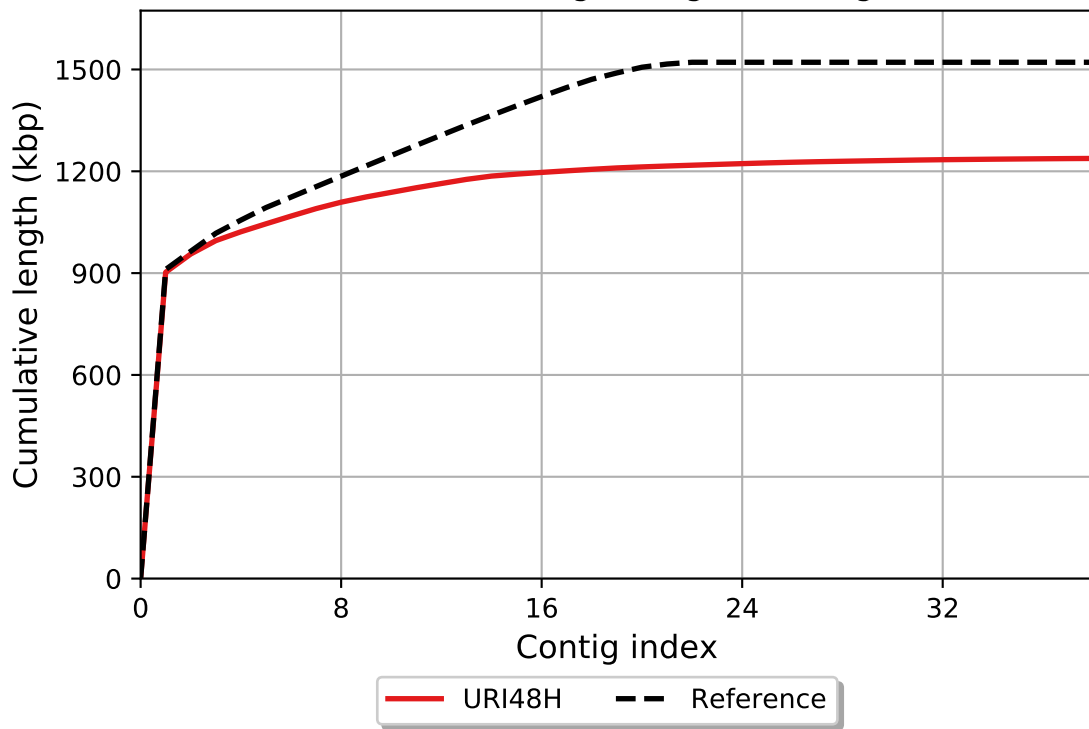


translocations

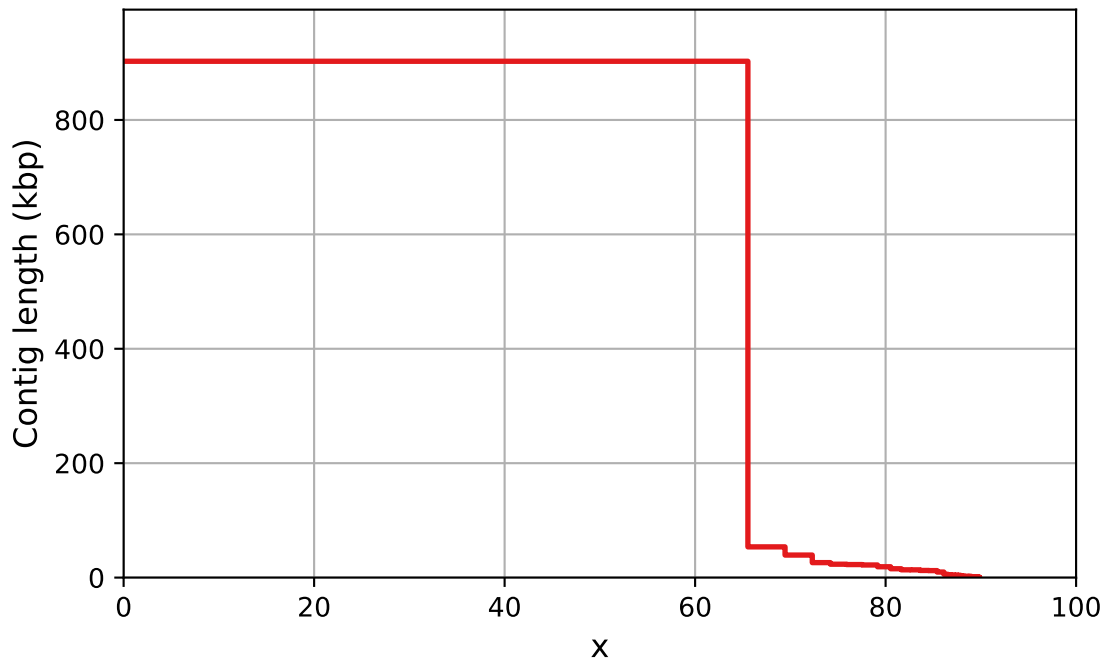
FRCurve (misassemblies)



Cumulative length (aligned contigs)

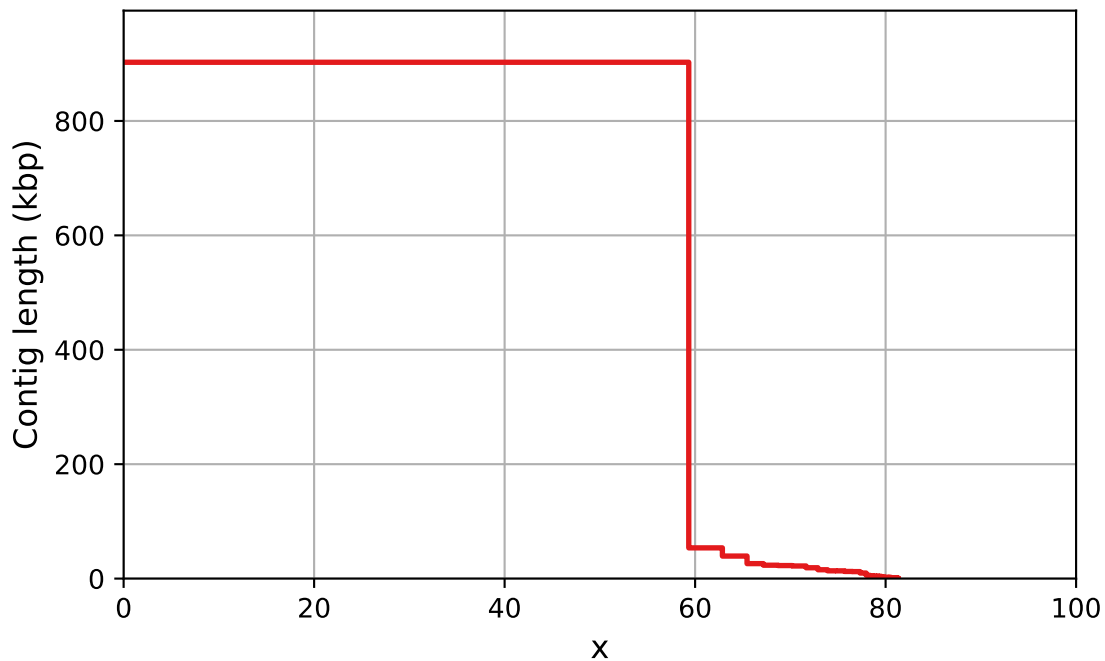


NAx

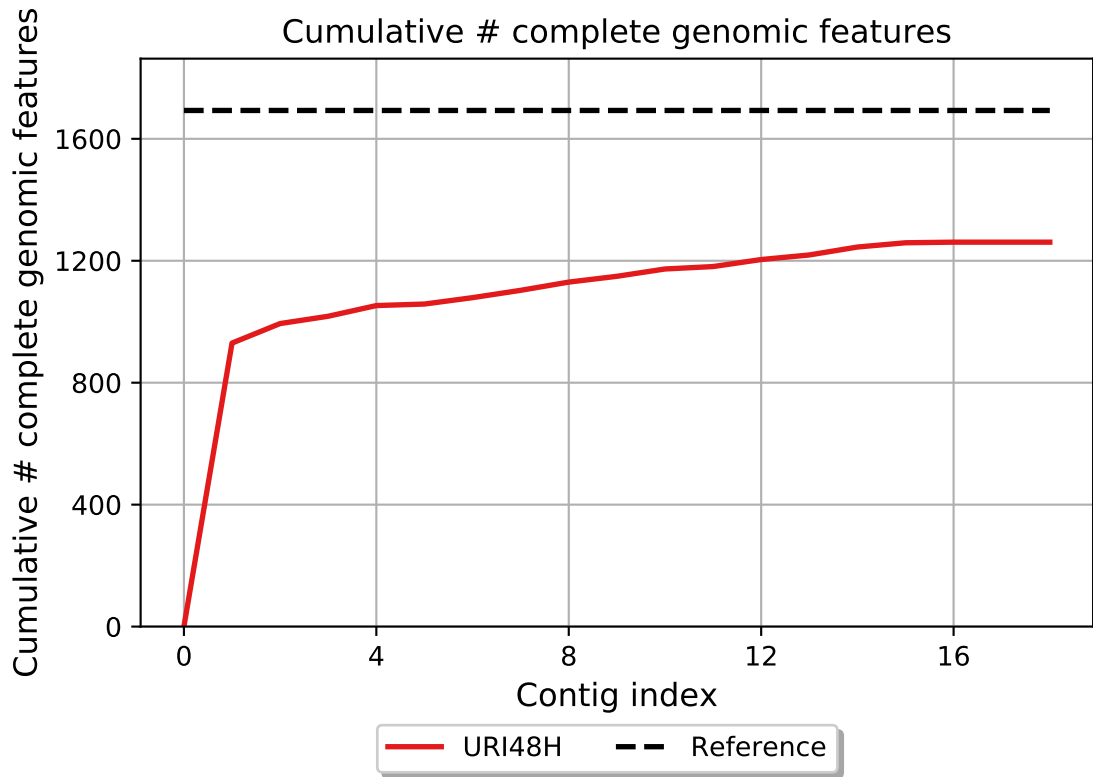


URI48H

NGAx



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FRCurve (genomic features)

