

Report

	URI102H
# contigs (>= 0 bp)	44
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1442774
Total length (>= 1000 bp)	1434568
Total length (>= 5000 bp)	1426403
Total length (>= 10000 bp)	1426403
Total length (>= 25000 bp)	1404462
Total length (>= 50000 bp)	1020730
# contigs	25
Largest contig	910559
Total length	1438278
Reference length	1521208
GC (%)	28.16
Reference GC (%)	28.18
N50	910559
NG50	910559
N90	30222
NG90	27792
auN	589752.8
auNG	557601.9
L50	1
LG50	1
L90	12
LG90	14
# misassemblies	10
# misassembled contigs	9
Misassembled contigs length	273400
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 4 part
Unaligned length	22831
Genome fraction (%)	91.219
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	92.81
# indels per 100 kbp	11.59
# genomic features	1504 + 35 part
Largest alignment	910559
Total aligned length	1414646
NA50	910559
NGA50	910559
NA90	24180
NGA90	15817
auNA	586882.7
auNGA	554888.3
LA50	1
LGA50	1
LA90	13
LGA90	17

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

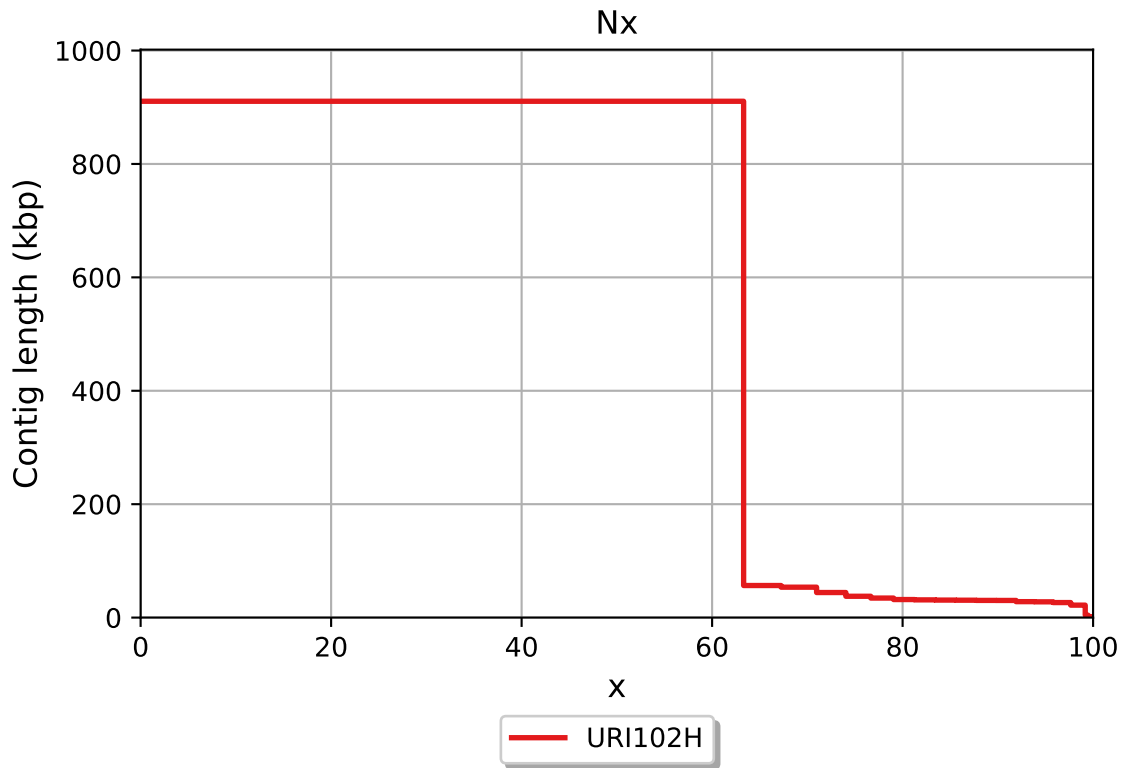
	URI102H
# misassemblies	10
# contig misassemblies	10
# c. relocations	6
# c. translocations	4
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	273400
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1313
# indels	164
# indels (<= 5 bp)	146
# indels (> 5 bp)	18
Indels length	1399

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).

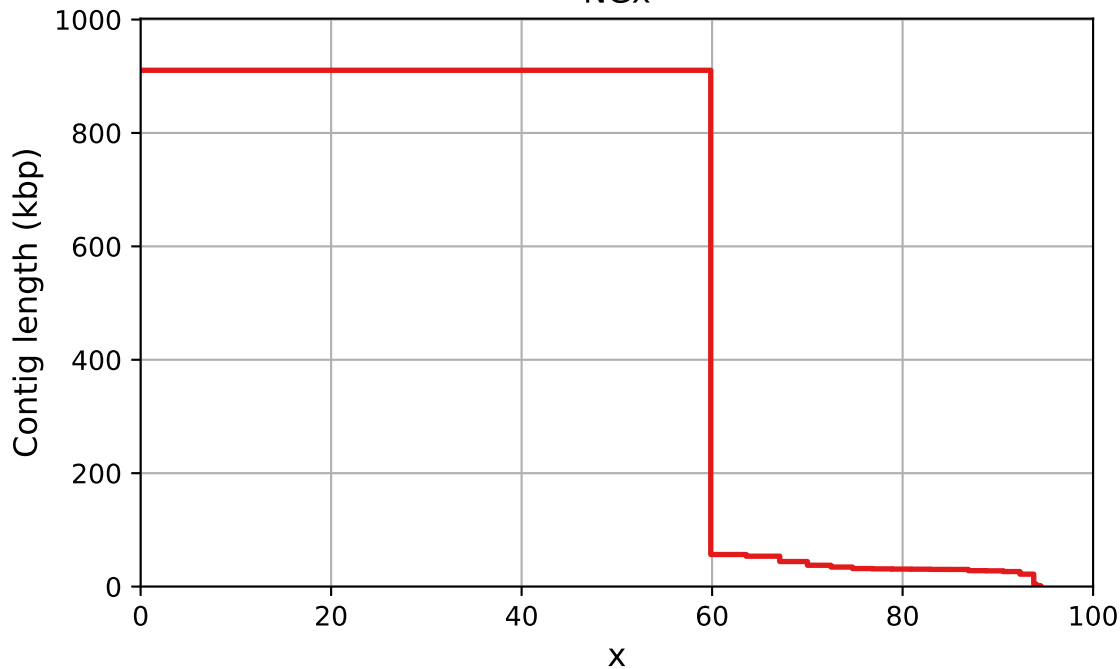
Unaligned report

	URI102H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
Partially unaligned length	22831
# 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).

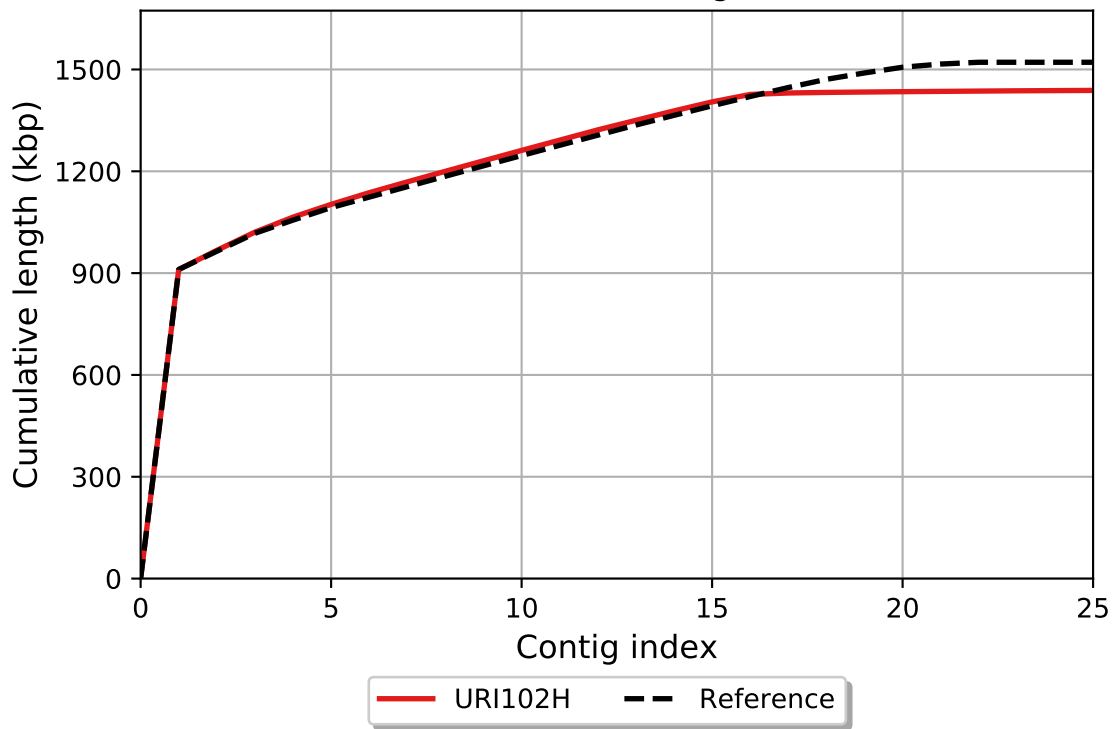


NGx

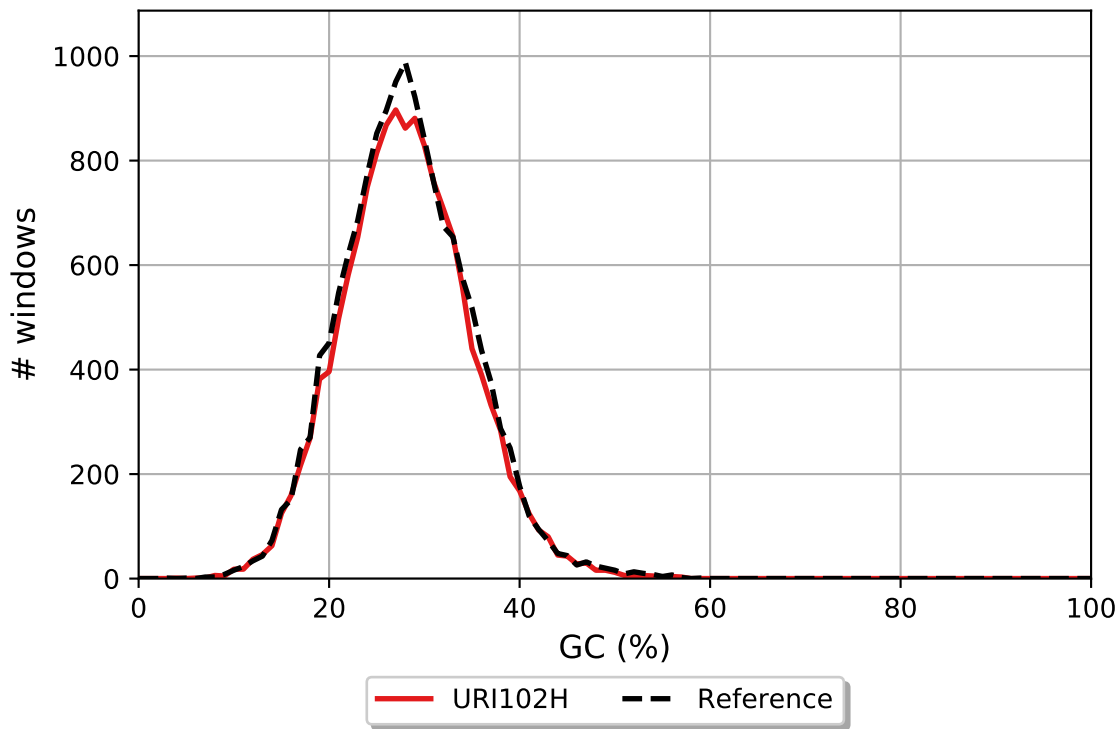


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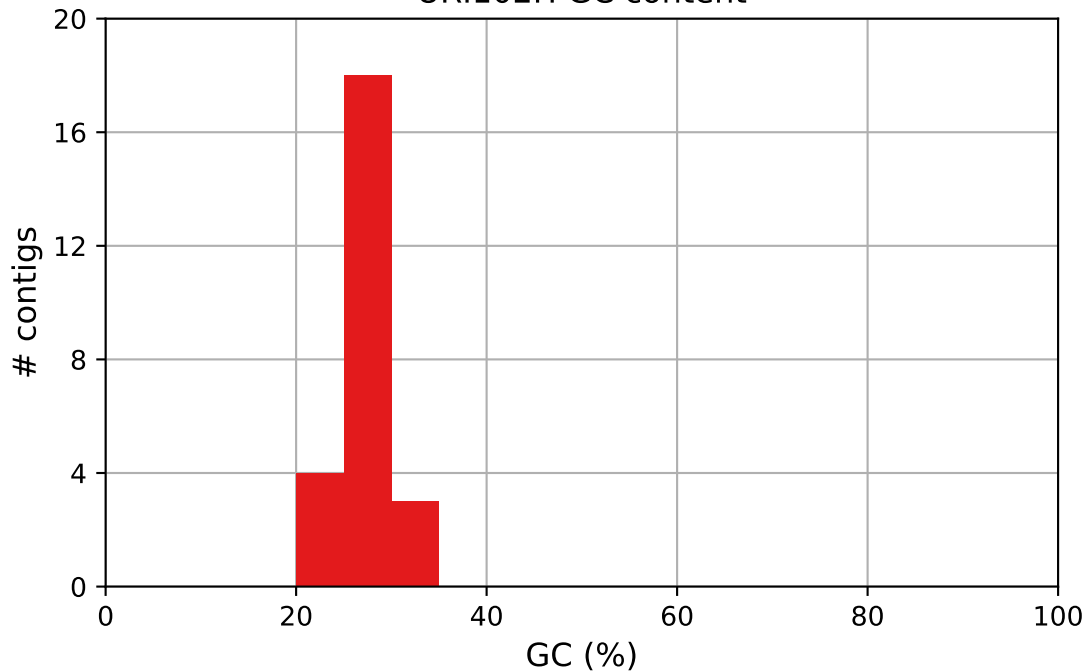
Cumulative length



GC content

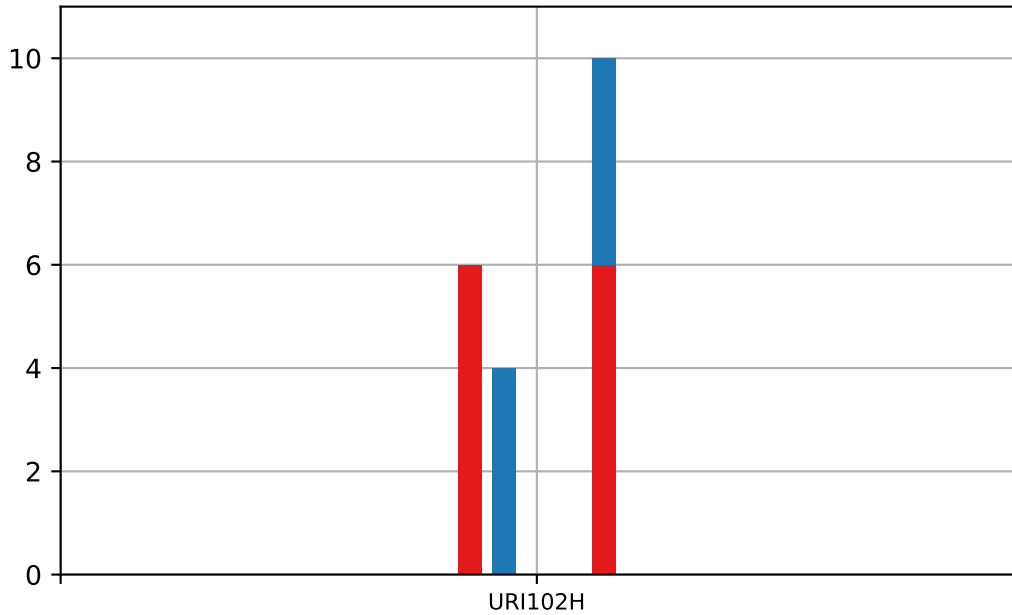


URI102H GC content



URI102H

Misassemblies

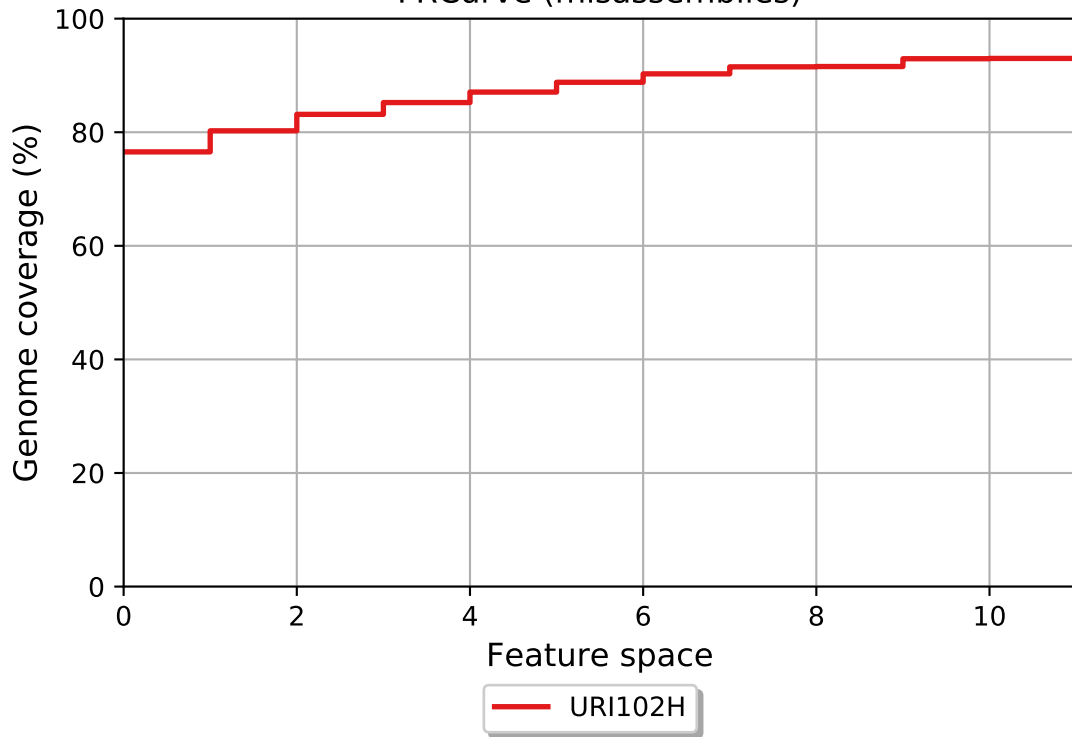


relocations

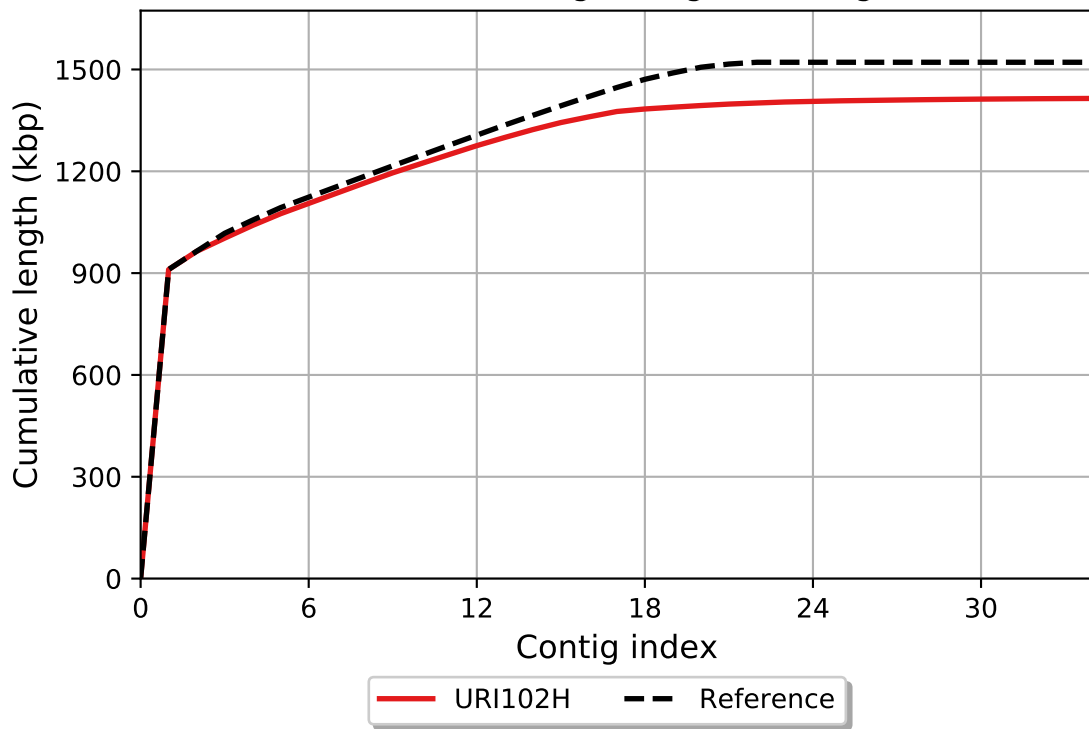


translocations

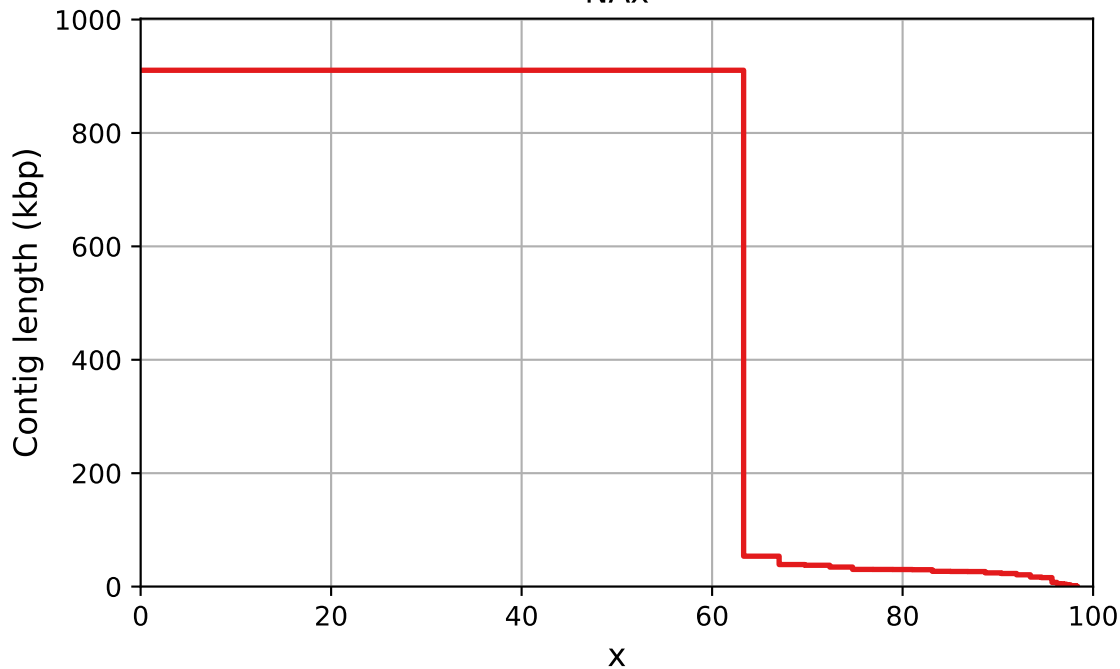
FRCurve (misassemblies)



Cumulative length (aligned contigs)

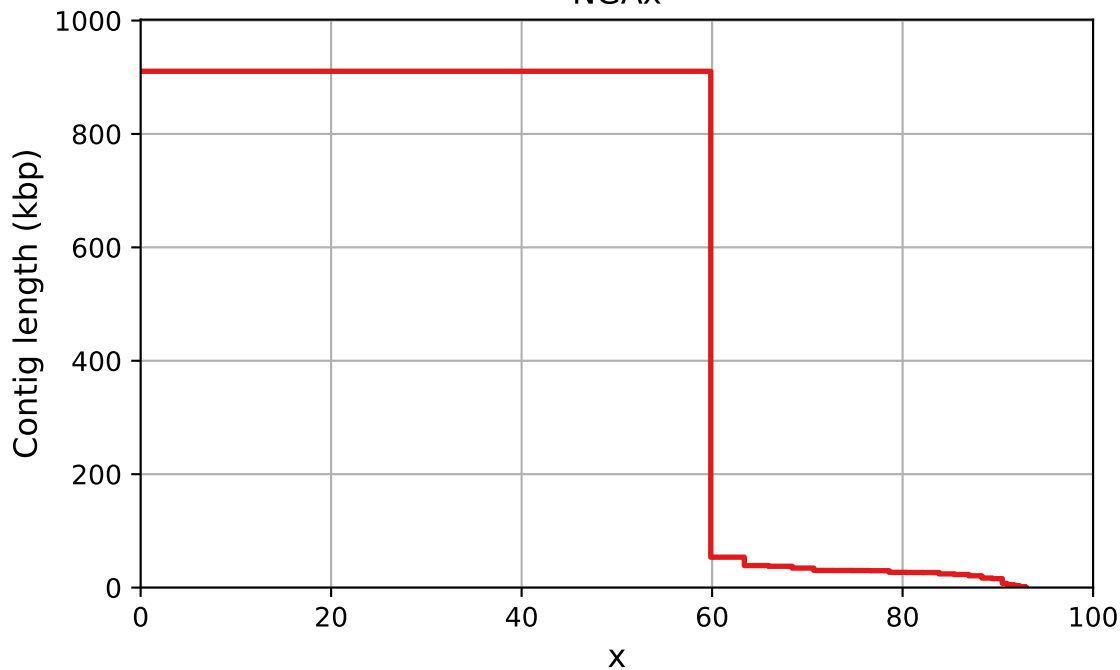


NAx

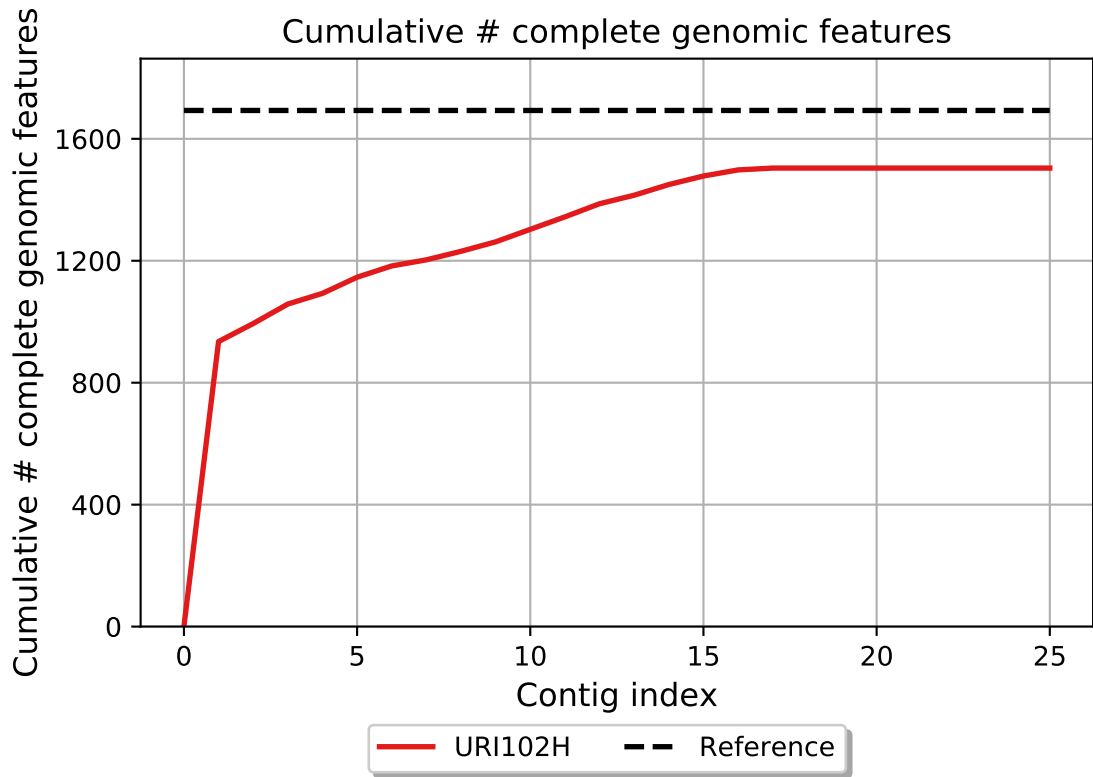


— URI102H

NGAx



— URI102H



FRCurve (genomic features)

