

Report

	URI107H
# contigs (>= 0 bp)	49
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1505434
Total length (>= 1000 bp)	1495807
Total length (>= 5000 bp)	1495807
Total length (>= 10000 bp)	1495807
Total length (>= 25000 bp)	1473869
Total length (>= 50000 bp)	964183
# contigs	26
Largest contig	910570
Total length	1501264
Reference length	1521208
GC (%)	28.22
Reference GC (%)	28.18
N50	910570
NG50	910570
N90	29727
NG90	28108
auN	565721.6
auNG	558304.7
L50	1
LG50	1
L90	14
LG90	15
# misassemblies	12
# misassembled contigs	9
Misassembled contigs length	245415
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 4 part
Unaligned length	20832
Genome fraction (%)	92.989
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	127.59
# indels per 100 kbp	12.91
# genomic features	1537 + 30 part
Largest alignment	910570
Total aligned length	1479733
NA50	910570
NGA50	910570
NA90	21987
NGA90	21614
auNA	563750.1
auNGA	556358.9
LA50	1
LGA50	1
LA90	15
LGA90	16

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

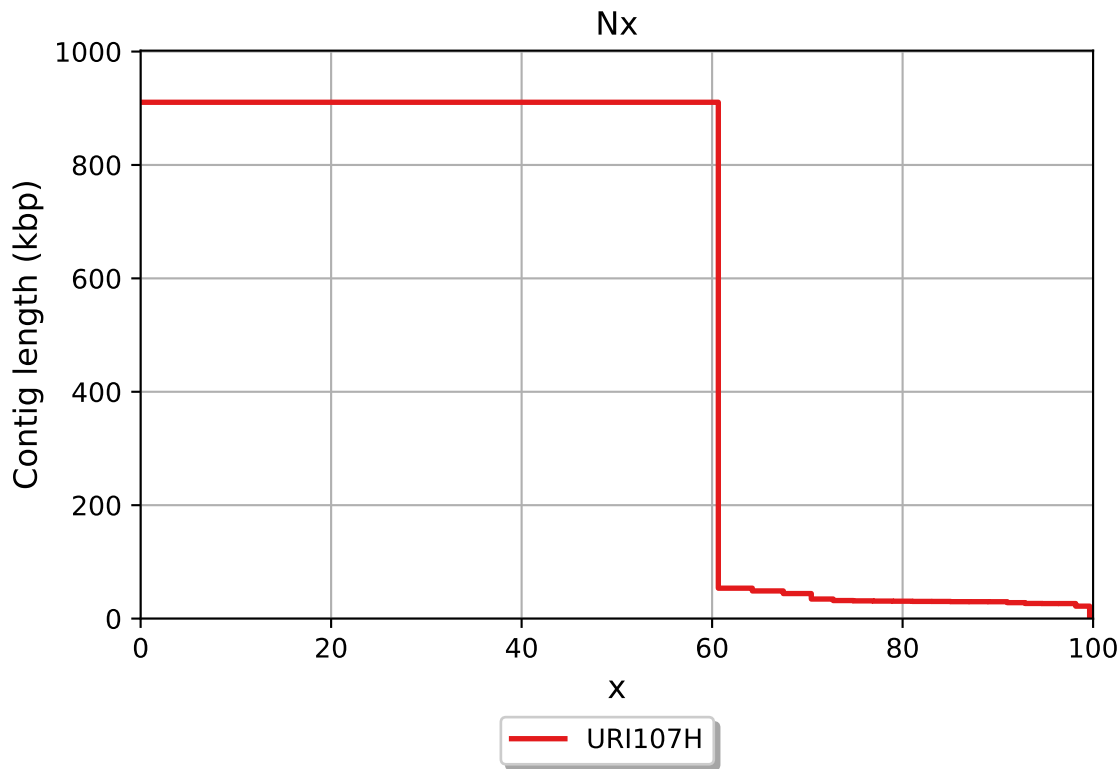
	URI107H
# misassemblies	12
# contig misassemblies	12
# c. relocations	6
# c. translocations	6
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	245415
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1888
# indels	191
# indels (<= 5 bp)	170
# indels (> 5 bp)	21
Indels length	1344

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).

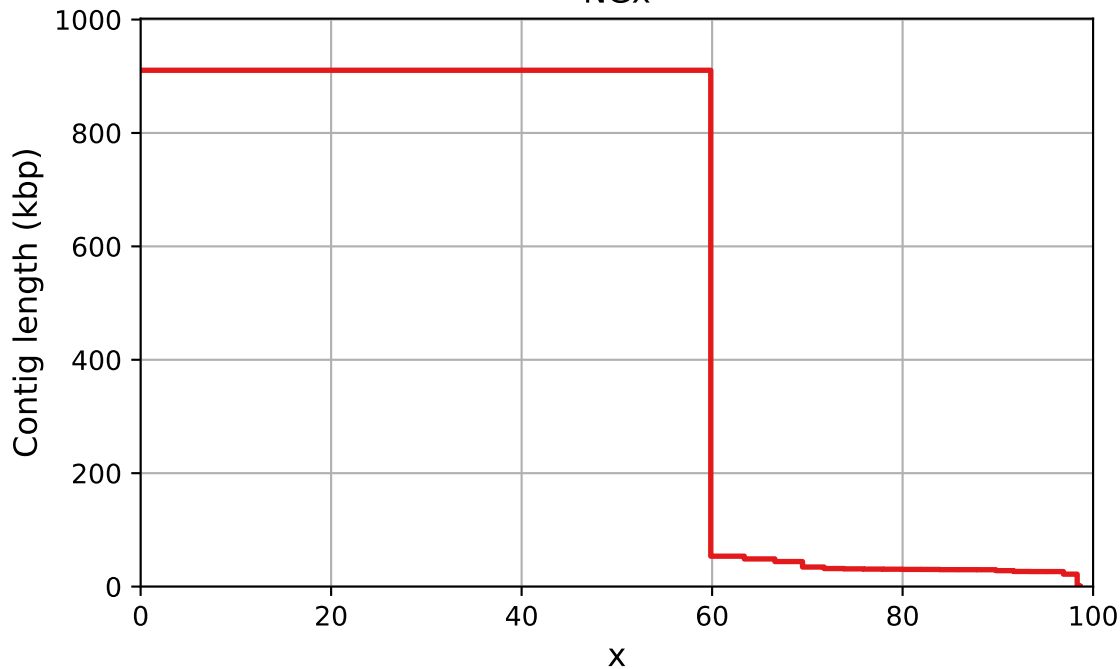
Unaligned report

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# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
Partially unaligned length	20832
# 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).

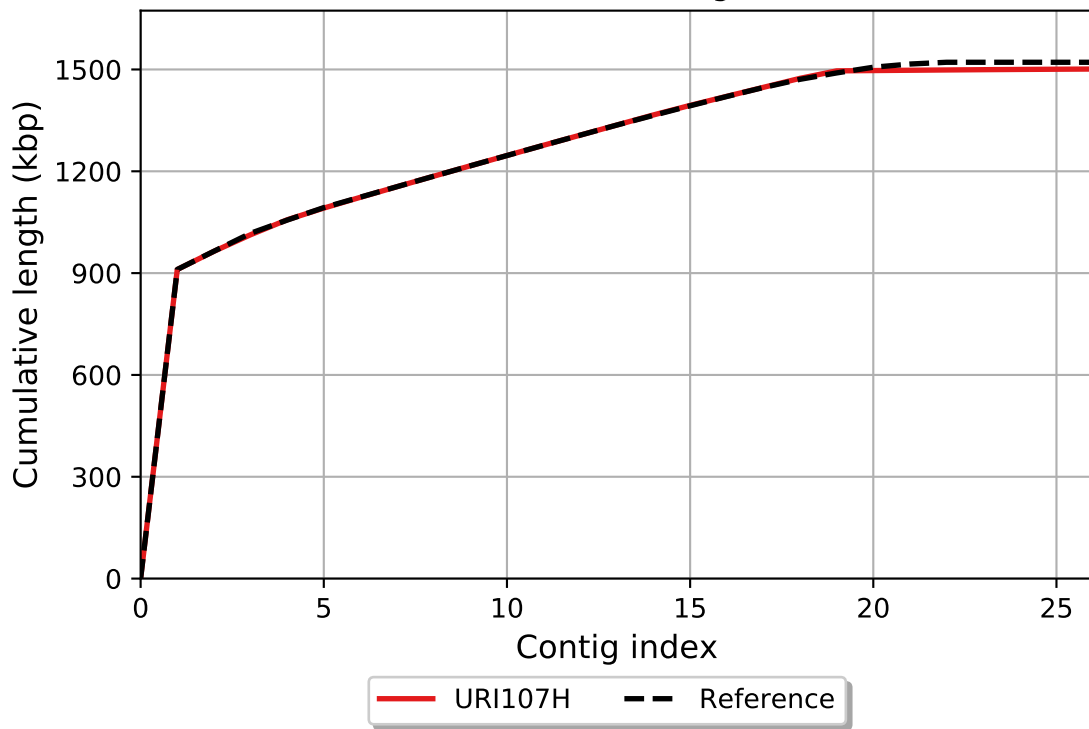


NGx

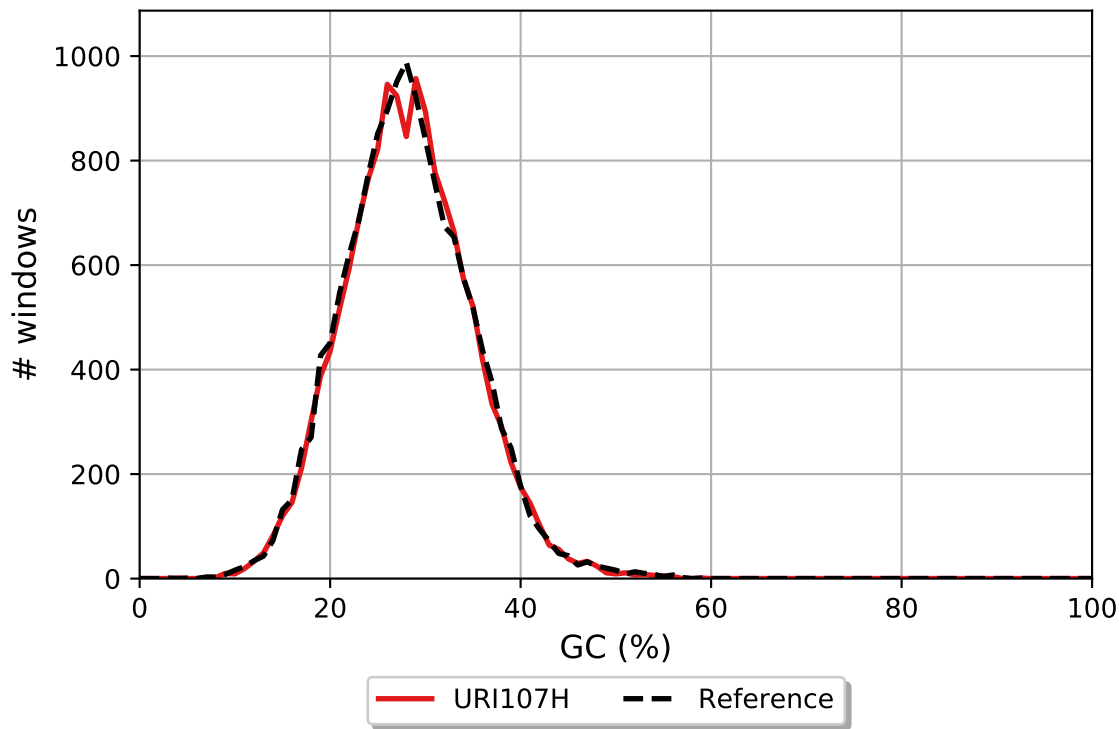


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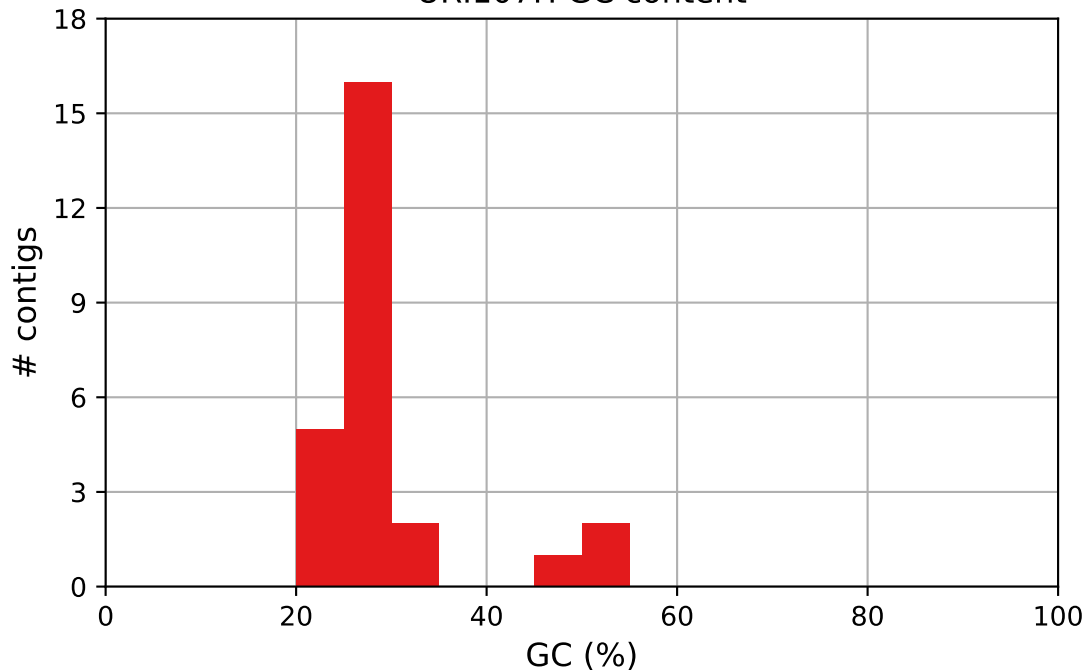
Cumulative length



GC content

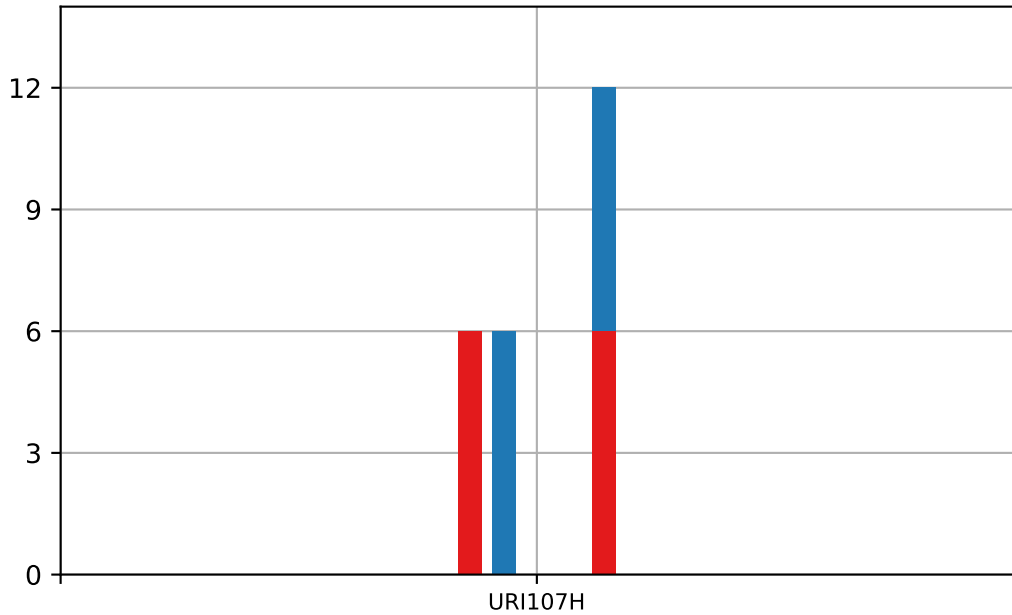


URI107H GC content



URI107H

Misassemblies

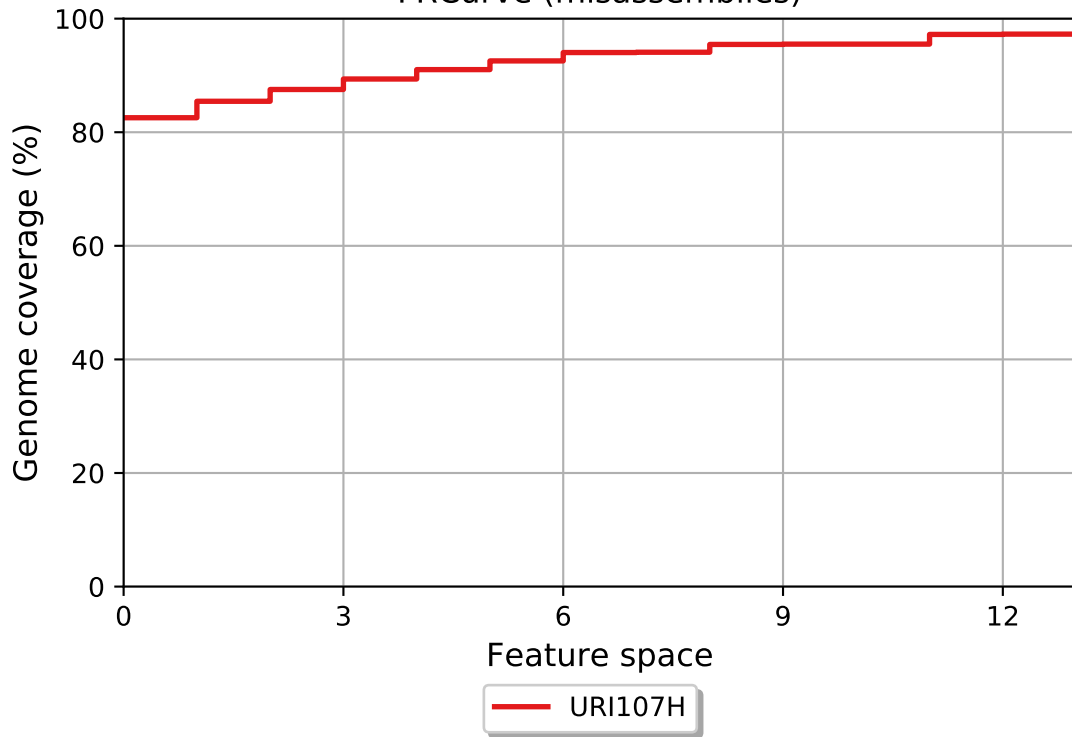


relocations

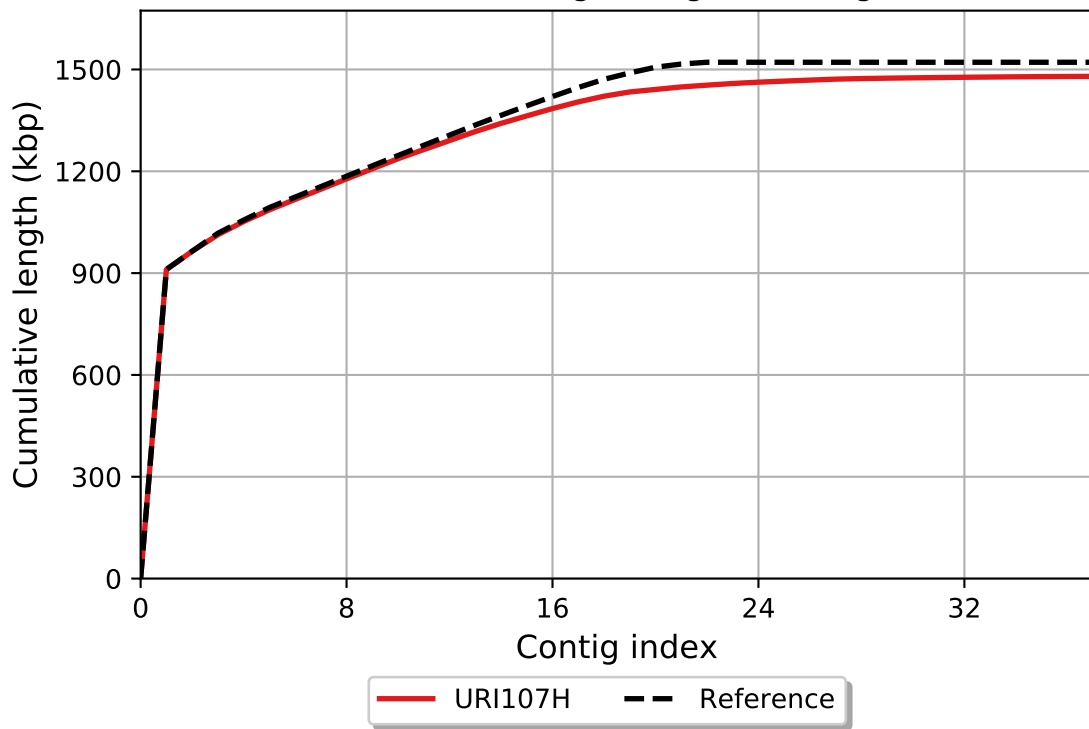


translocations

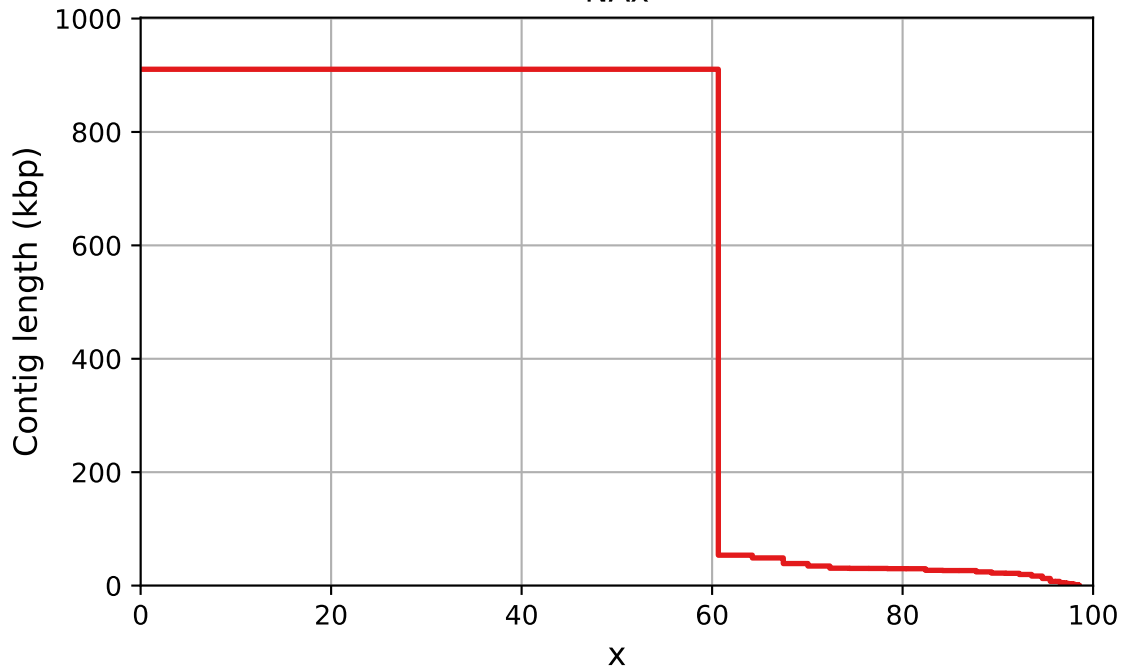
FRCurve (misassemblies)



Cumulative length (aligned contigs)

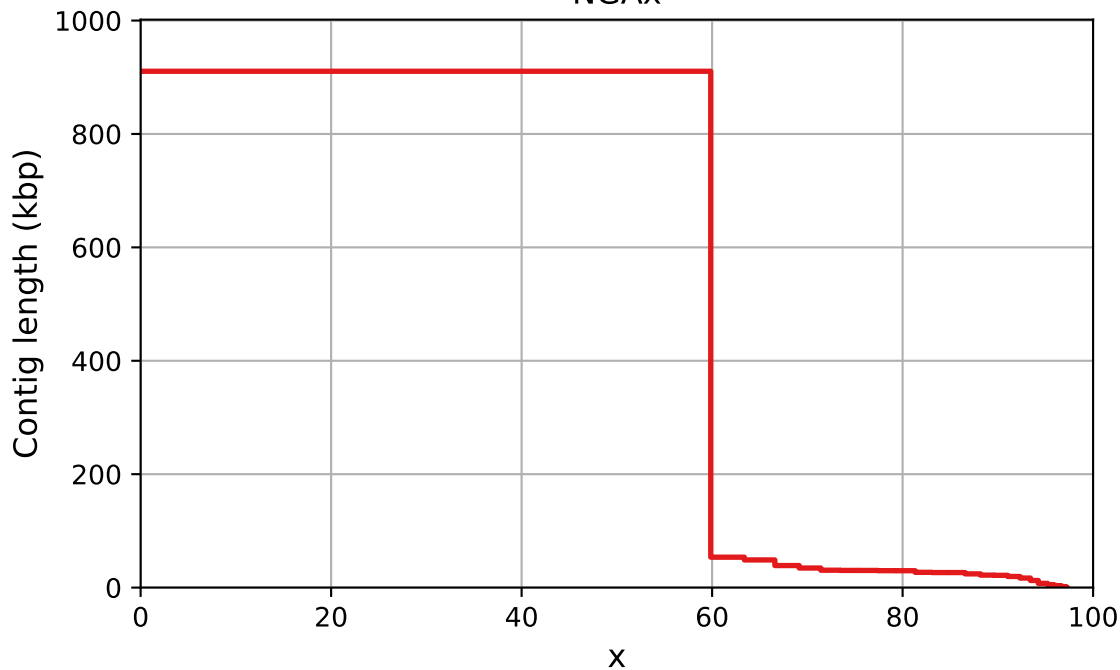


NAx

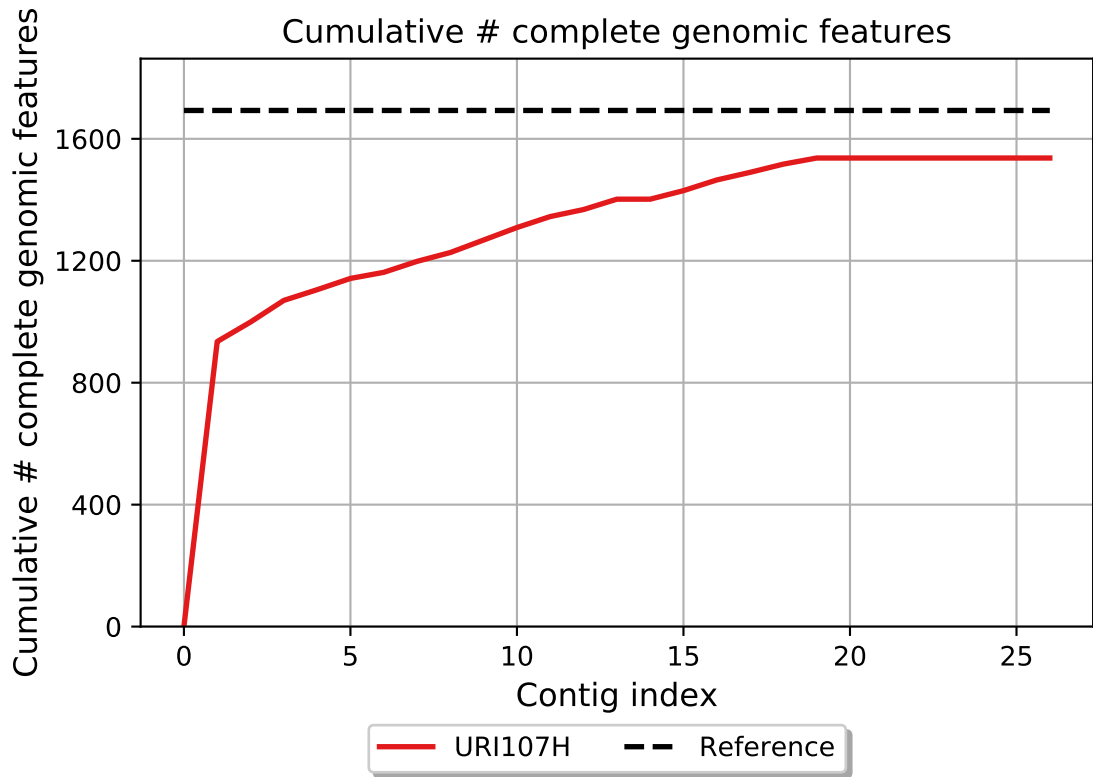


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NGAx



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FRCurve (genomic features)

