

Report

	URI117H
# contigs (>= 0 bp)	160
# contigs (>= 1000 bp)	38
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1384478
Total length (>= 1000 bp)	1339171
Total length (>= 5000 bp)	1303375
Total length (>= 10000 bp)	1261701
Total length (>= 25000 bp)	1088008
Total length (>= 50000 bp)	896727
# contigs	73
Largest contig	461794
Total length	1364256
Reference length	1521208
GC (%)	28.01
Reference GC (%)	28.18
N50	434933
NG50	434933
N90	20991
NG90	-
auN	302730.6
auNG	271496.1
L50	2
LG50	2
L90	15
LG90	-
# misassemblies	16
# misassembled contigs	10
Misassembled contigs length	176992
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	16 + 20 part
Unaligned length	170076
Genome fraction (%)	76.743
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	738.38
# indels per 100 kbp	49.21
# genomic features	1206 + 63 part
Largest alignment	461794
Total aligned length	1190713
NA50	434864
NGA50	434864
NA90	-
NGA90	-
auNA	298606.7
auNGA	267797.7
LA50	2
LGA50	2
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

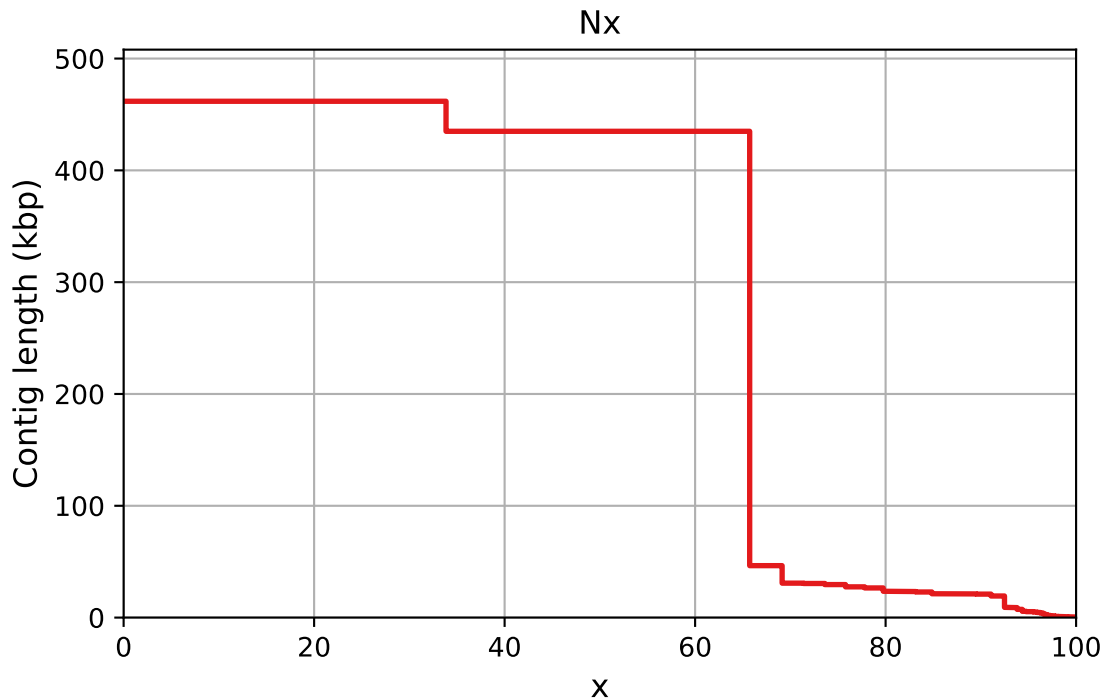
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# misassemblies	16
# contig misassemblies	16
# c. relocations	4
# c. translocations	11
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	10
Misassembled contigs length	176992
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	8792
# indels	586
# indels (<= 5 bp)	531
# indels (> 5 bp)	55
Indels length	2496

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

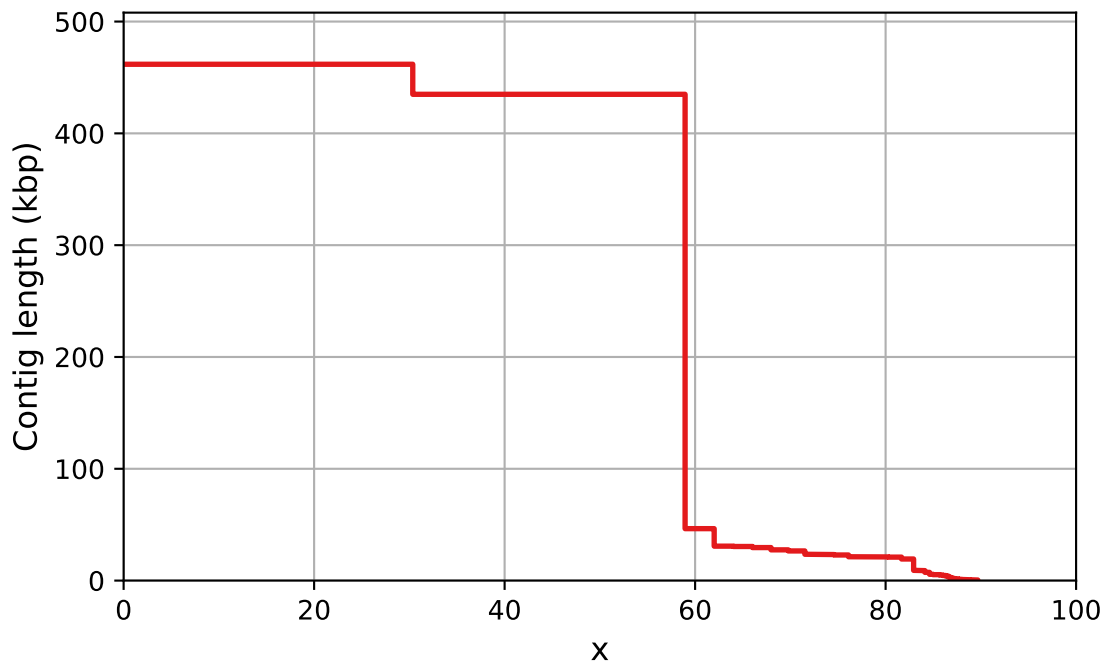
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# fully unaligned contigs	16
Fully unaligned length	20426
# partially unaligned contigs	20
Partially unaligned length	149650
# N's	0

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).

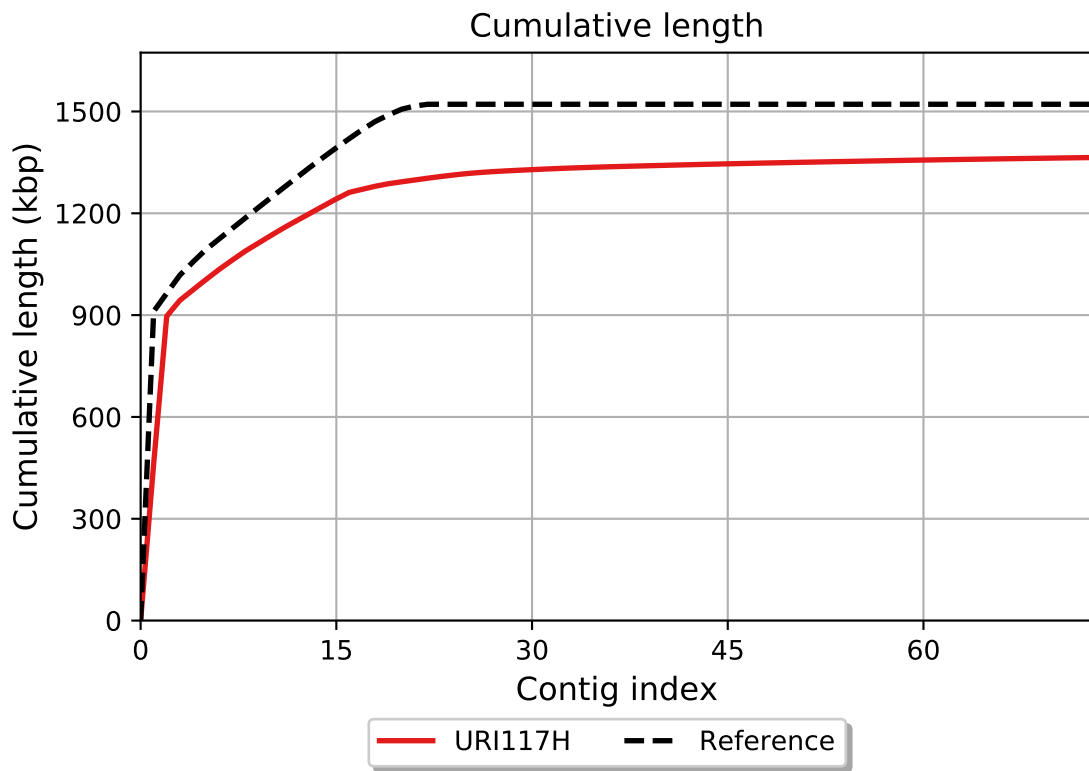


— URI117H

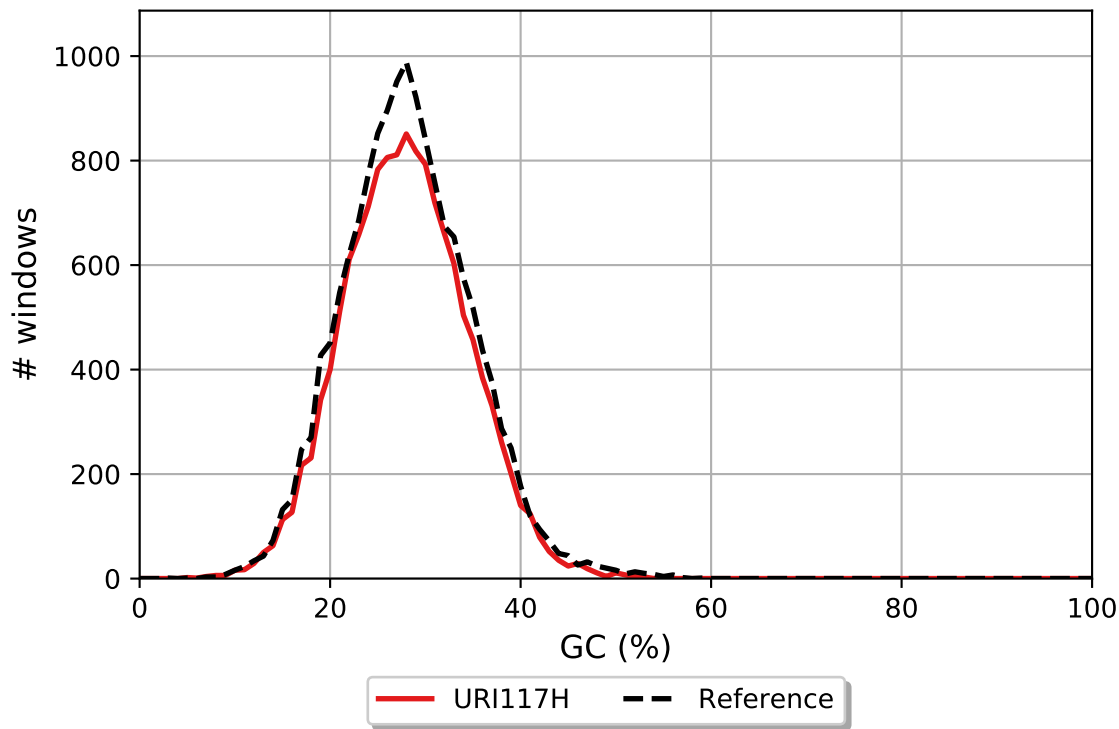
NGx



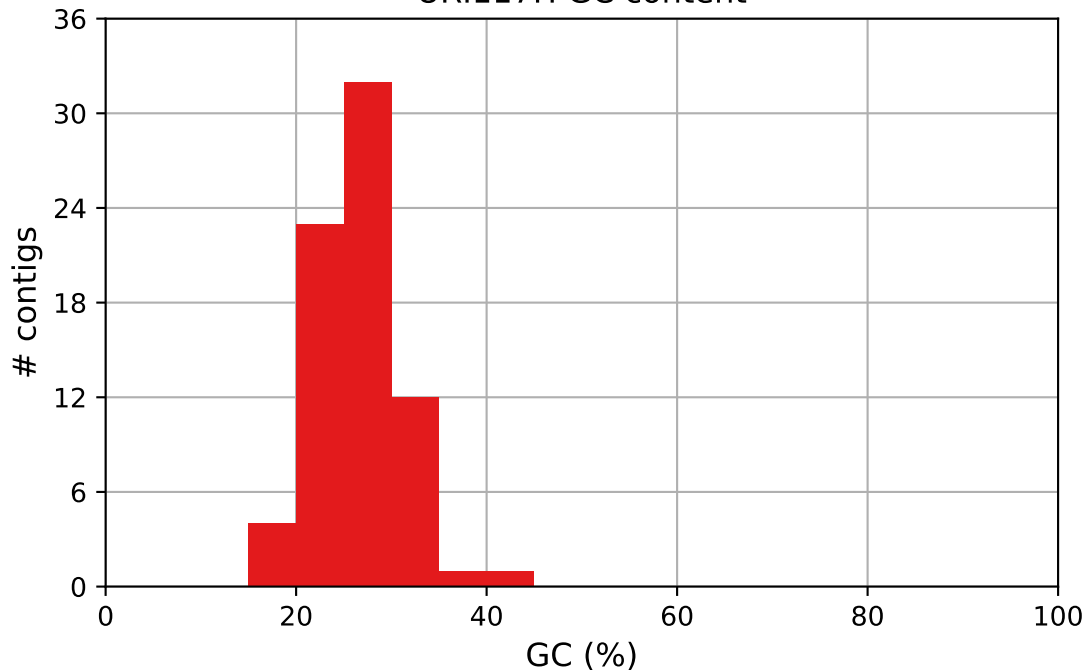
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GC content

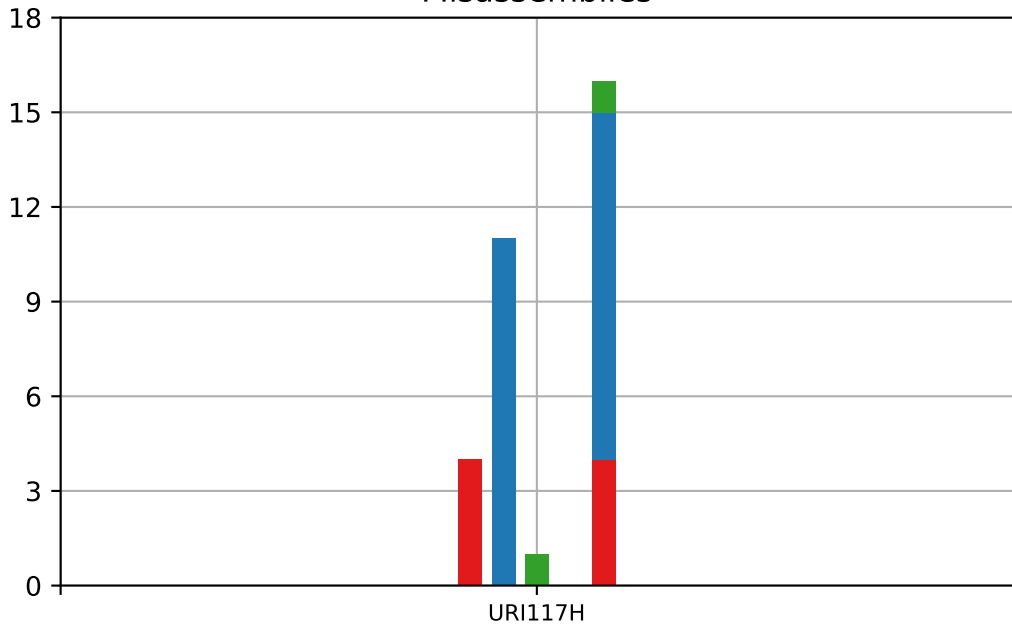


URI117H GC content



URI117H

Misassemblies



relocations

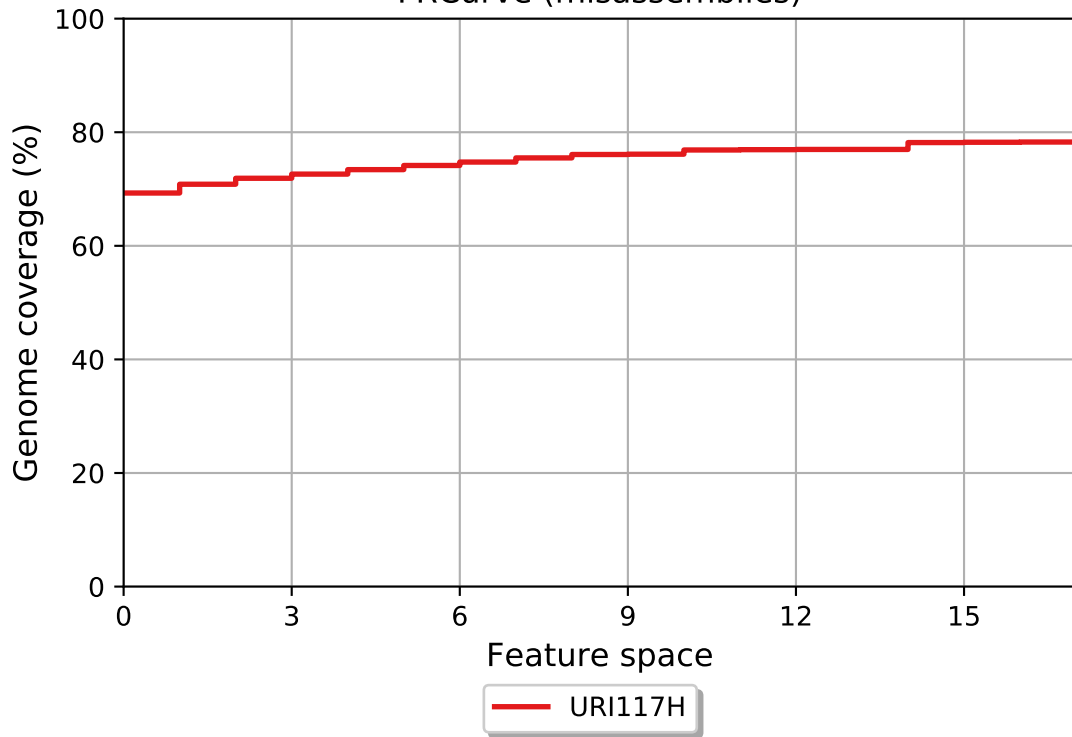


translocations

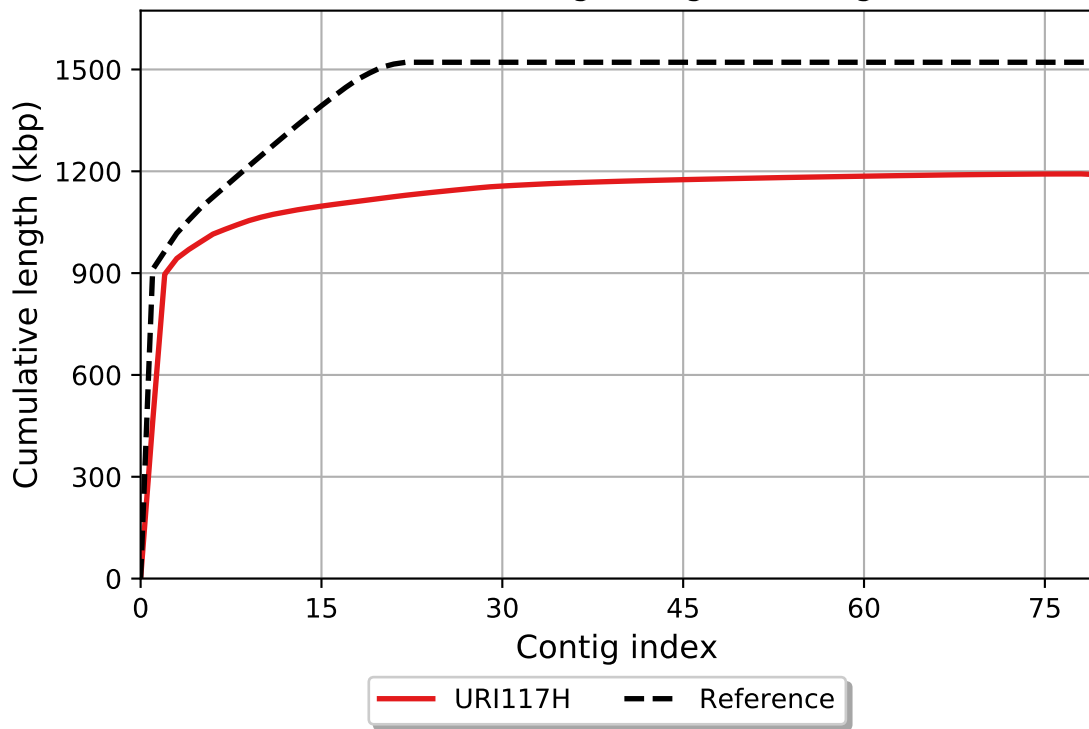


inversions

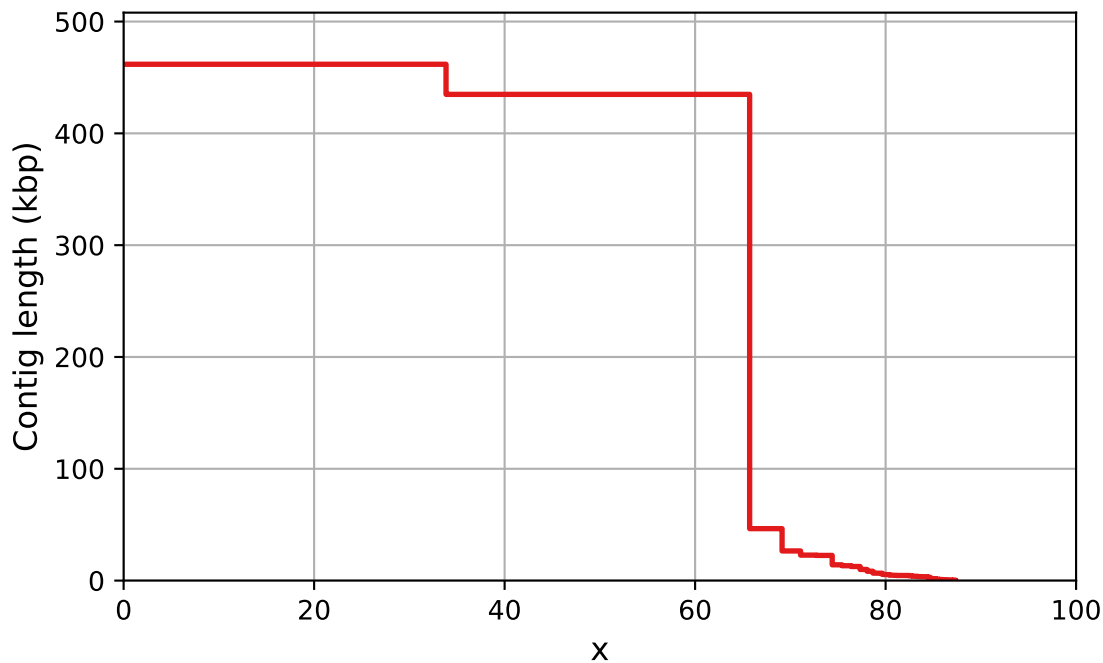
FRCurve (misassemblies)



Cumulative length (aligned contigs)

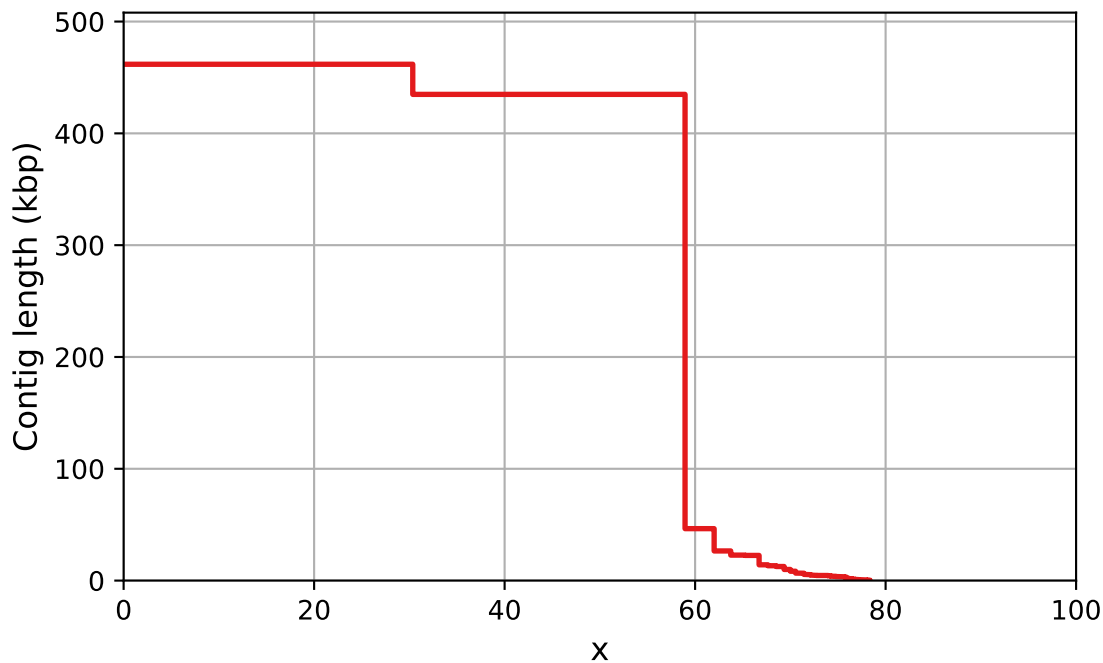


NAx

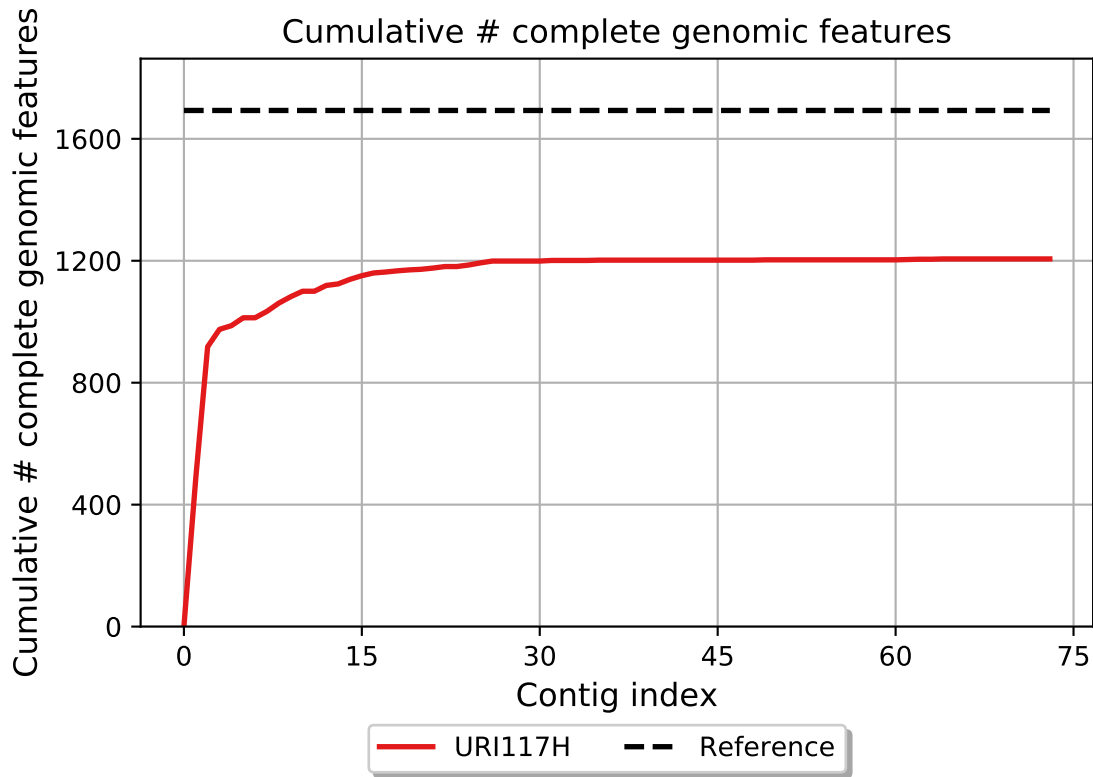


— URI117H

NGAx



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FRCurve (genomic features)

