

Report

	URI45H
# contigs (>= 0 bp)	350
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	39
# contigs (>= 10000 bp)	24
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	1585394
Total length (>= 1000 bp)	1502288
Total length (>= 5000 bp)	1367871
Total length (>= 10000 bp)	1264378
Total length (>= 25000 bp)	1143683
Total length (>= 50000 bp)	748610
# contigs	139
Largest contig	254720
Total length	1532603
Reference length	1521208
GC (%)	28.06
Reference GC (%)	28.18
N50	42830
NG50	42830
N90	4696
NG90	4917
auN	114914.3
auNG	115775.1
L50	5
LG50	5
L90	42
LG90	40
# misassemblies	21
# misassembled contigs	15
Misassembled contigs length	273617
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# unaligned contigs	22 + 22 part
Unaligned length	214935
Genome fraction (%)	80.823
Duplication ratio	1.071
# N's per 100 kbp	0.00
# mismatches per 100 kbp	859.07
# indels per 100 kbp	53.87
# genomic features	1233 + 118 part
Largest alignment	254720
Total aligned length	1316192
NA50	38825
NGA50	38825
NA90	-
NGA90	-
auNA	109932.1
auNGA	110755.5
LA50	5
LGA50	5
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

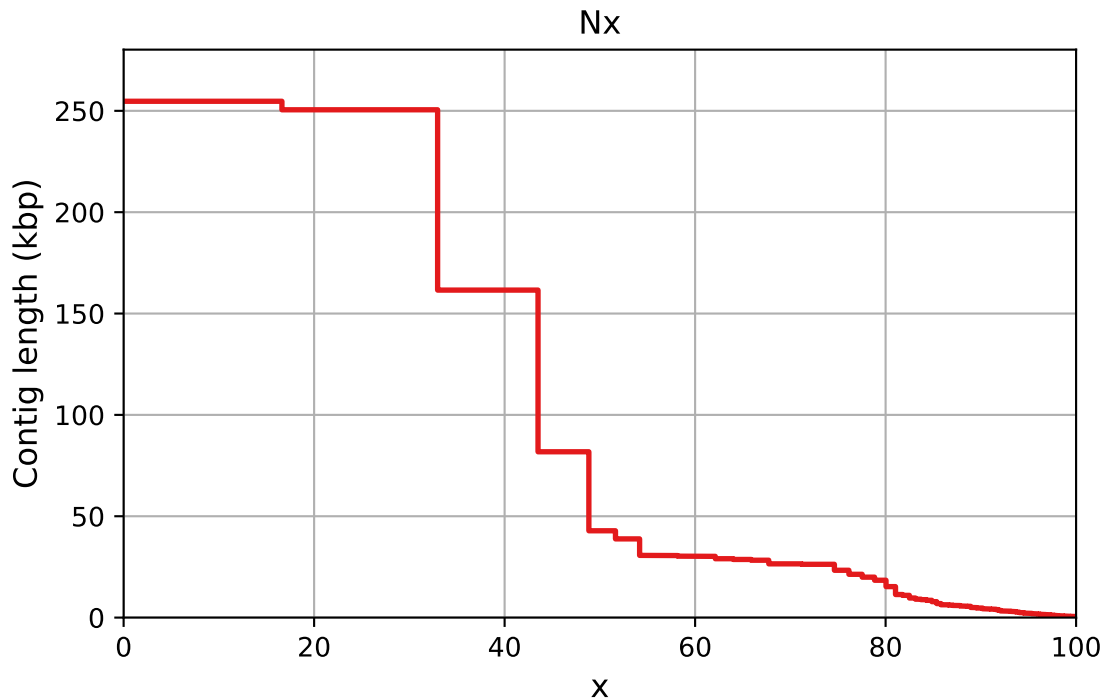
	URI45H
# misassemblies	21
# contig misassemblies	21
# c. relocations	4
# c. translocations	11
# c. inversions	6
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	15
Misassembled contigs length	273617
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	5
# mismatches	11307
# indels	709
# indels (<= 5 bp)	638
# indels (> 5 bp)	71
Indels length	3879

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

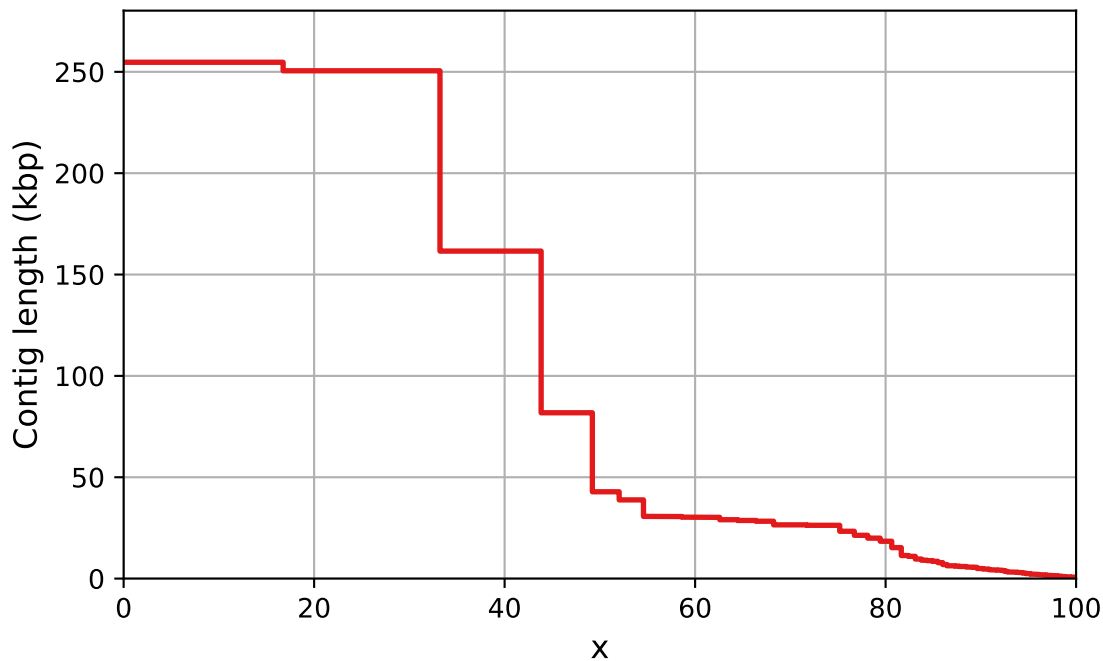
	URI45H
# fully unaligned contigs	22
Fully unaligned length	32506
# partially unaligned contigs	22
Partially unaligned length	182429
# N's	0

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).

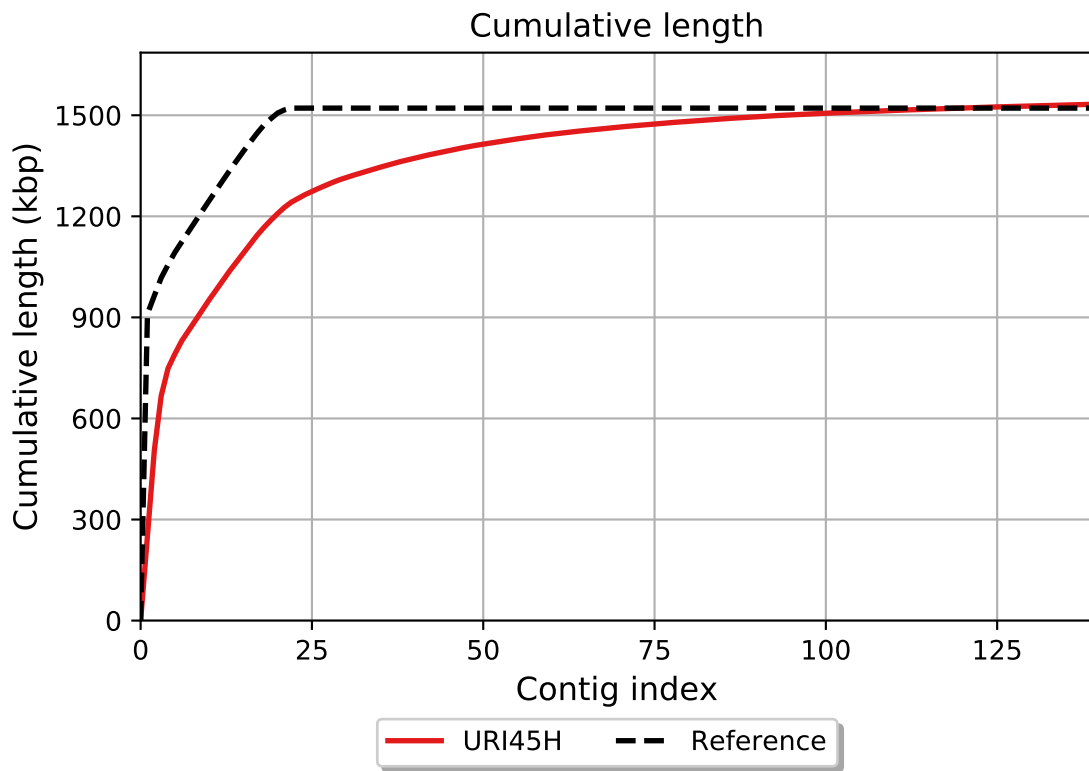


— URI45H

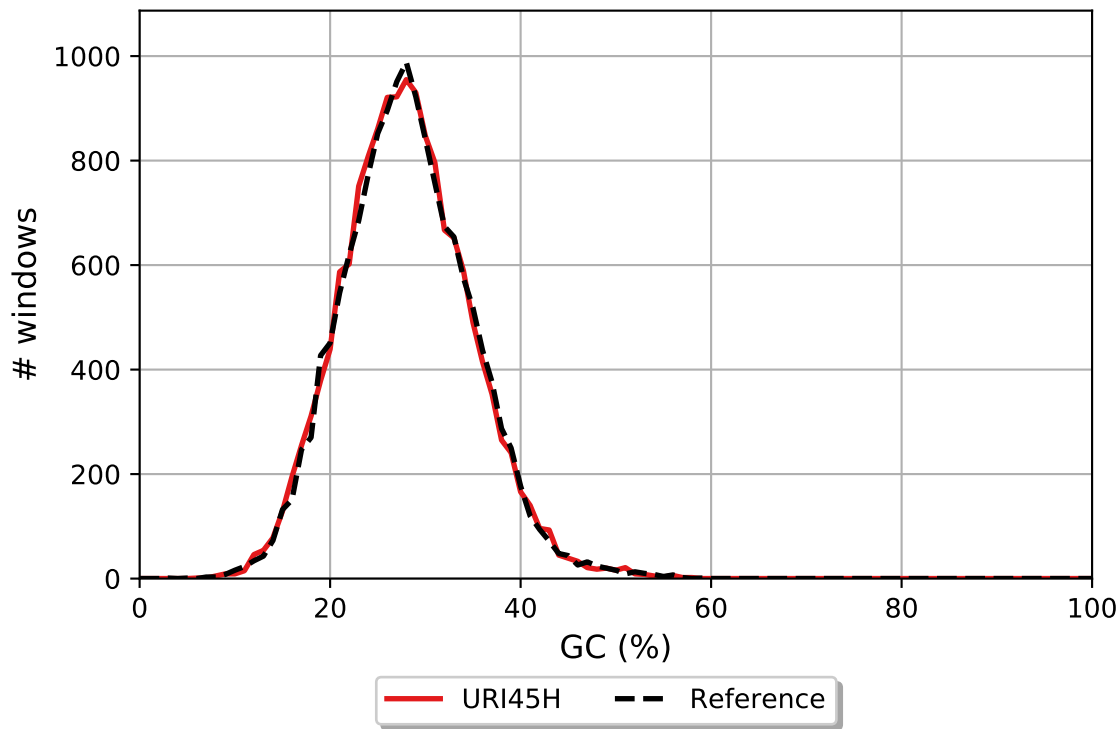
NGx



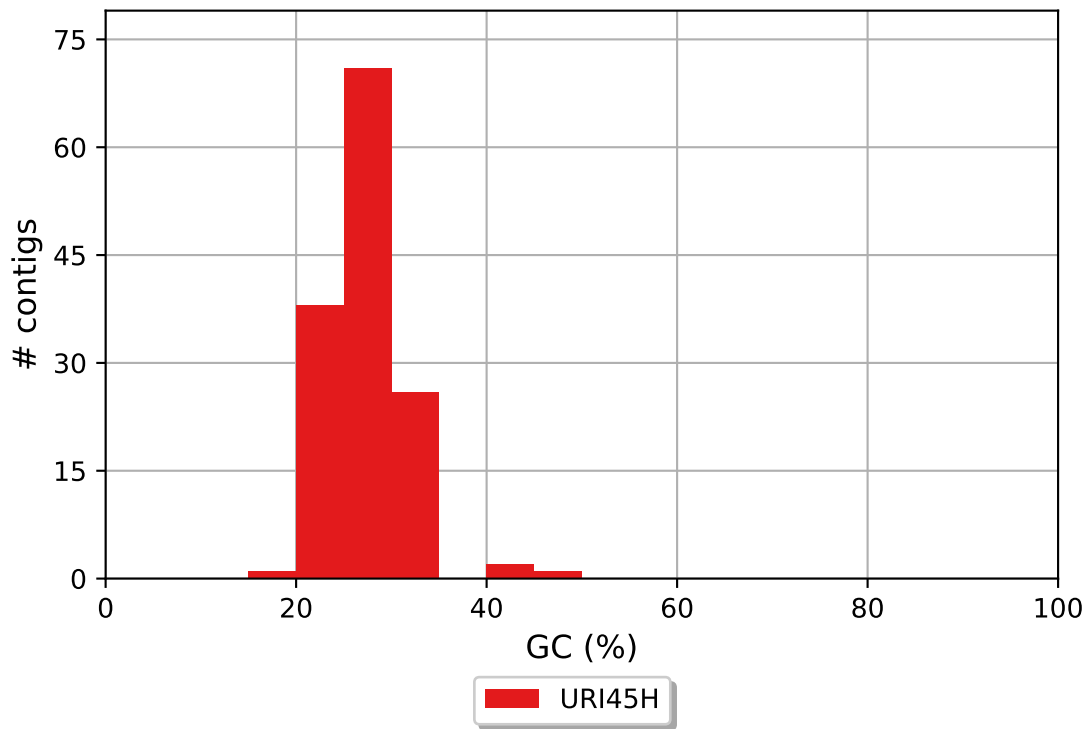
URI45H



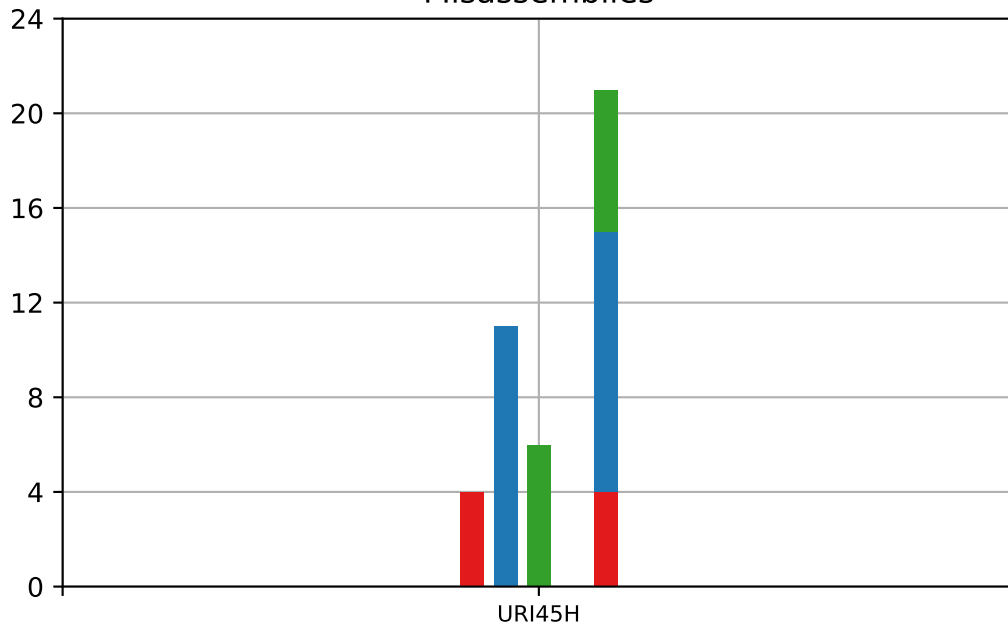
GC content



URI45H GC content



Misassemblies



relocations

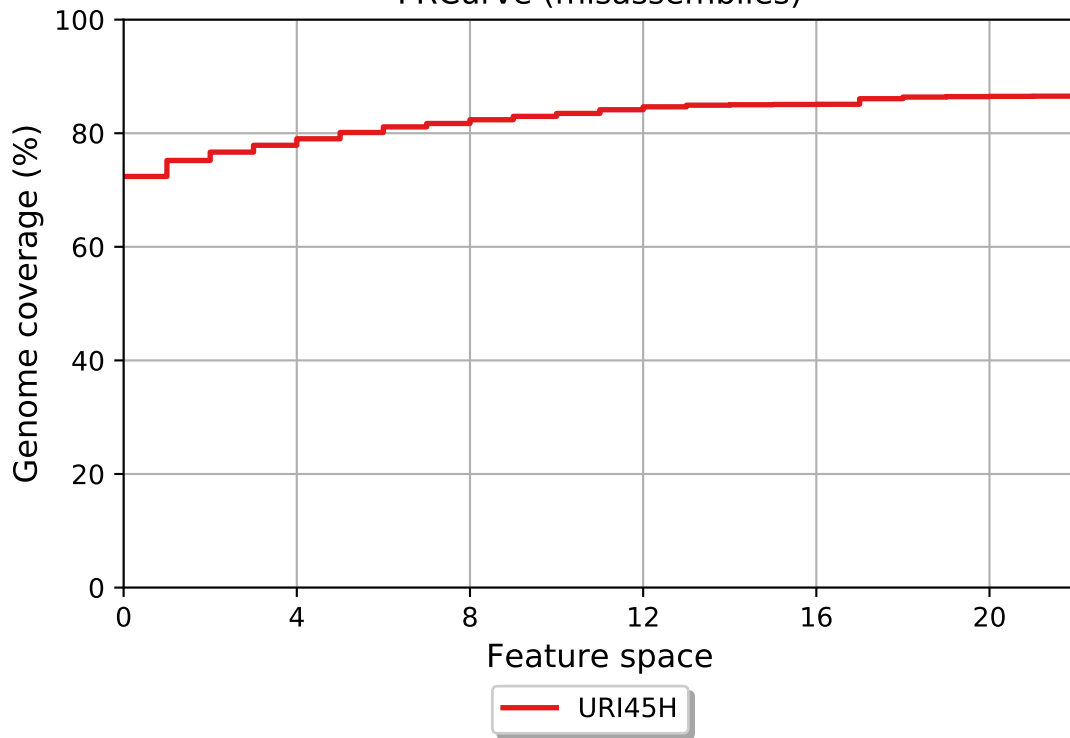


translocations

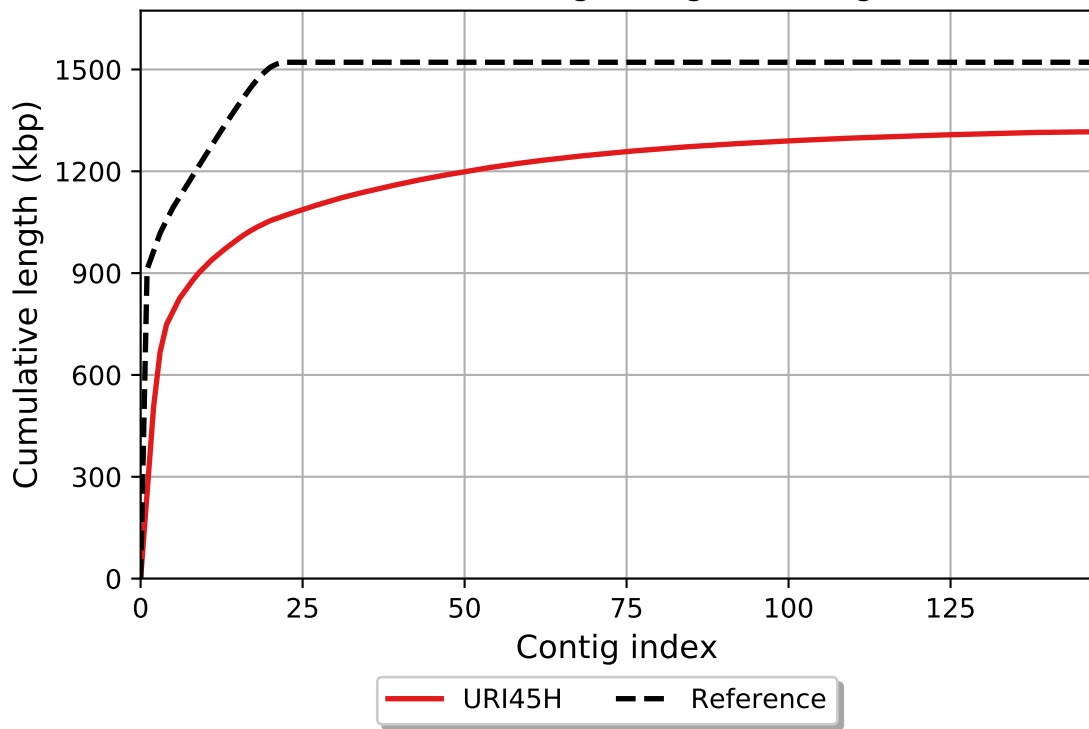


inversions

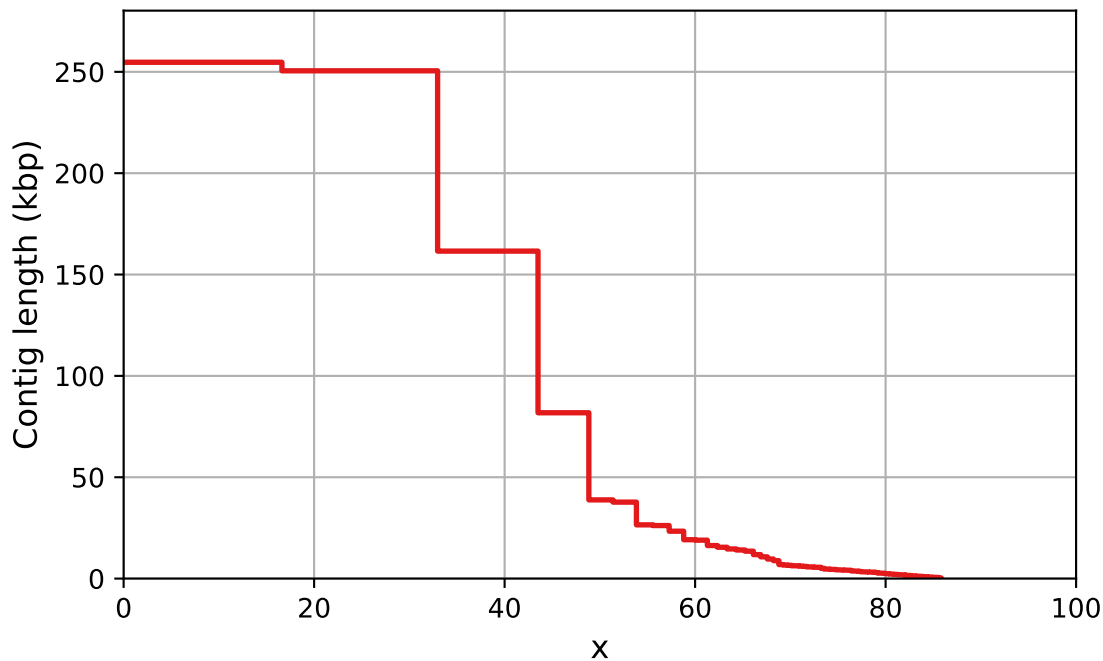
FRCurve (misassemblies)



Cumulative length (aligned contigs)

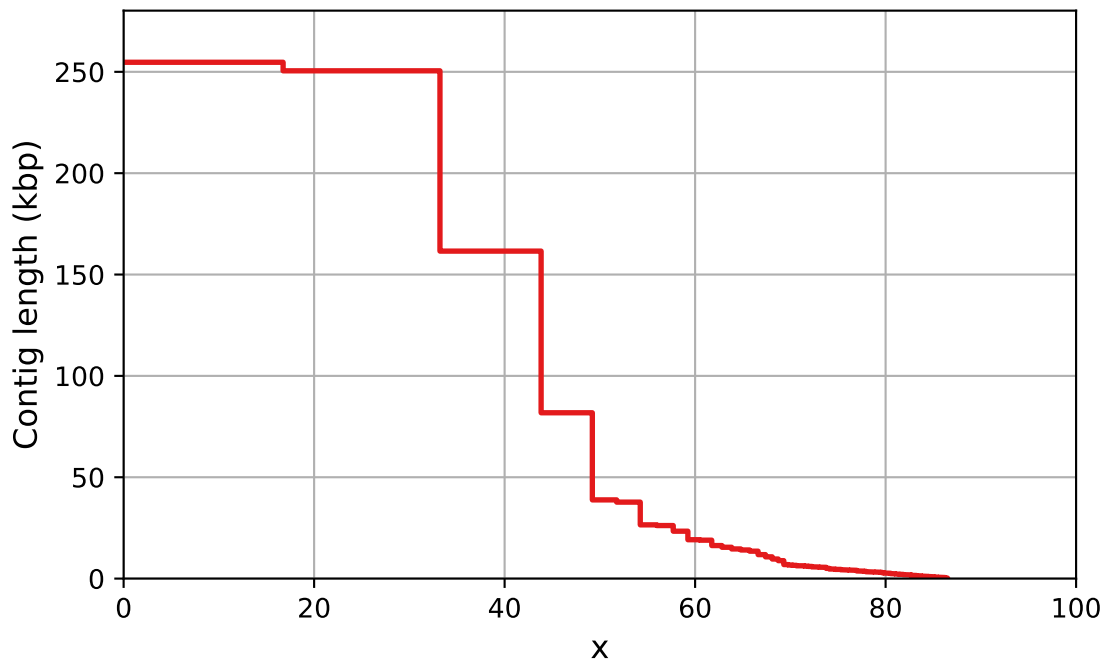


NAx

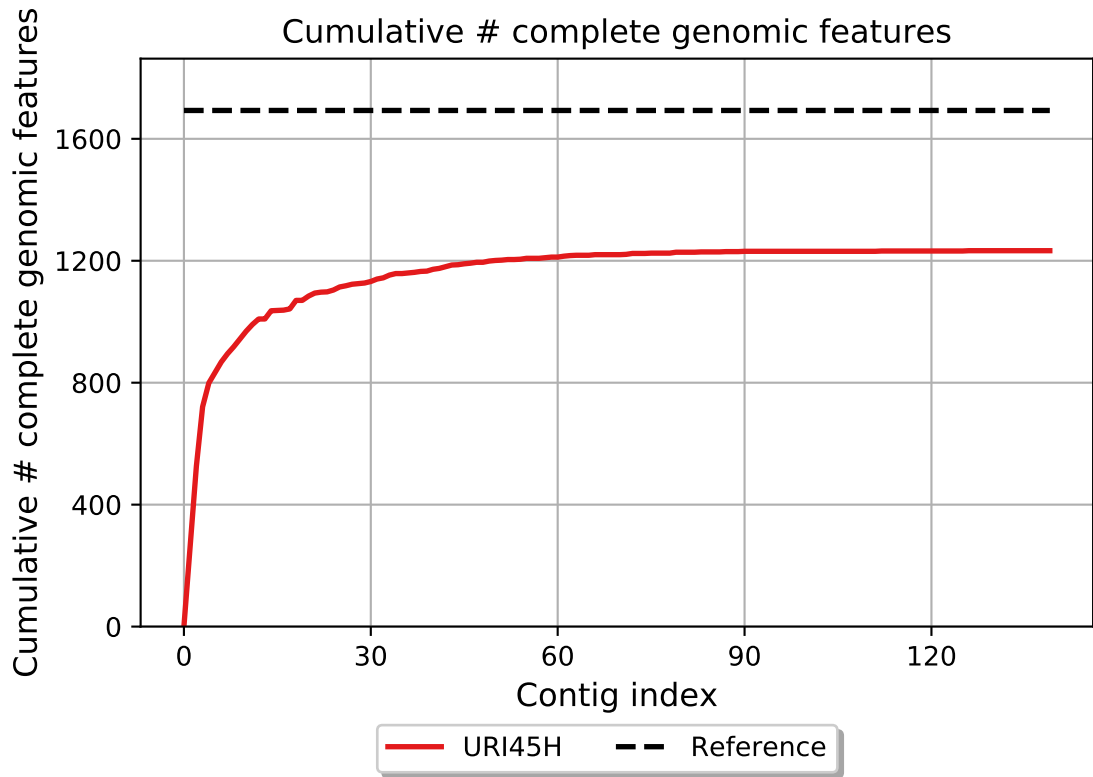


URI45H

NGAx



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FRCurve (genomic features)

