

Report

	URI34H
# contigs (>= 0 bp)	79
# contigs (>= 1000 bp)	29
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1376021
Total length (>= 1000 bp)	1352700
Total length (>= 5000 bp)	1335437
Total length (>= 10000 bp)	1317270
Total length (>= 25000 bp)	1191974
Total length (>= 50000 bp)	964064
# contigs	53
Largest contig	910082
Total length	1369133
Reference length	1521208
GC (%)	28.26
Reference GC (%)	28.18
N50	910082
NG50	910082
N90	24444
NG90	517
auN	613972.7
auNG	552593.9
L50	1
LG50	1
L90	12
LG90	53
# misassemblies	9
# misassembled contigs	4
Misassembled contigs length	117675
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	11 + 12 part
Unaligned length	185898
Genome fraction (%)	75.937
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	704.15
# indels per 100 kbp	41.21
# genomic features	1186 + 61 part
Largest alignment	904883
Total aligned length	1174458
NA50	904883
NGA50	904883
NA90	-
NGA90	-
auNA	602436.3
auNGA	542210.8
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

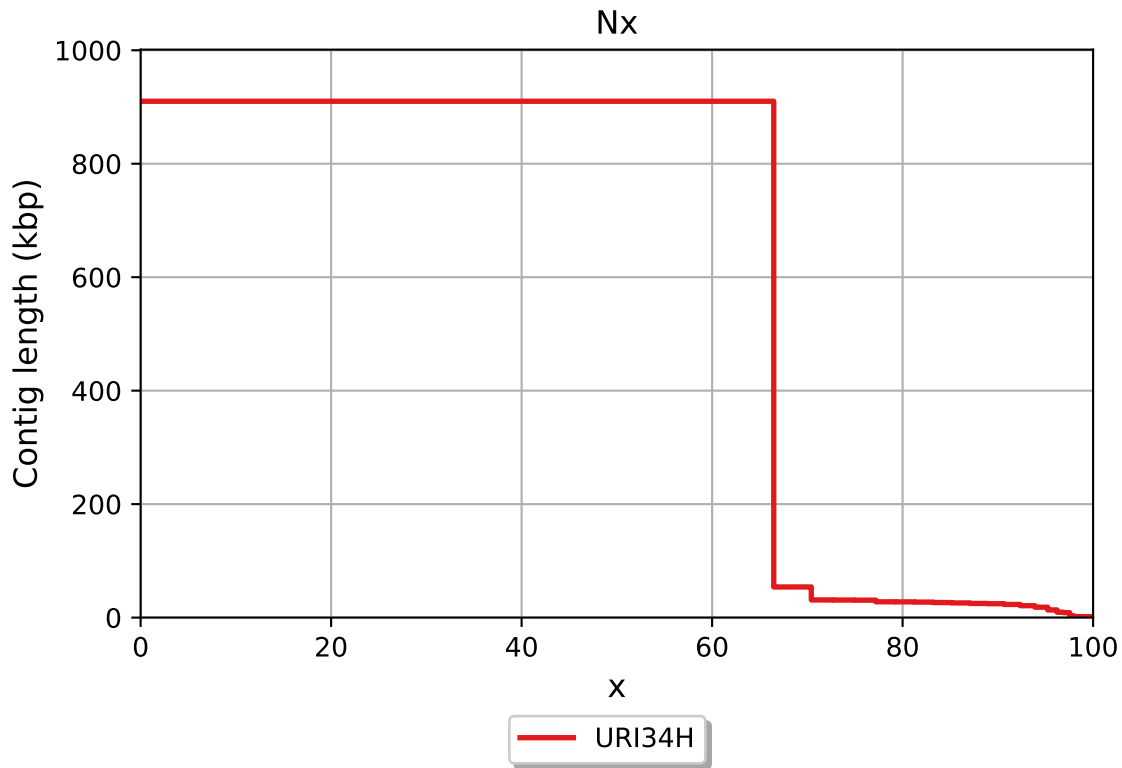
	URI34H
# misassemblies	9
# contig misassemblies	9
# c. relocations	1
# c. translocations	8
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	4
Misassembled contigs length	117675
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	8270
# indels	484
# indels (<= 5 bp)	446
# indels (> 5 bp)	38
Indels length	1787

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

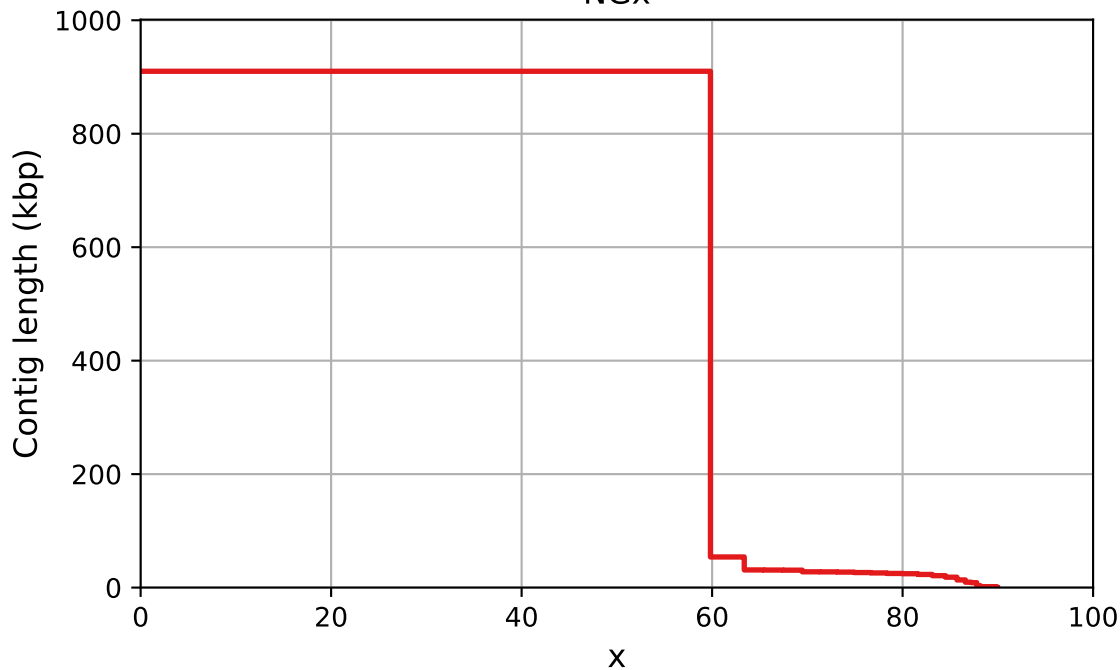
## Unaligned report

	URI34H
# fully unaligned contigs	11
Fully unaligned length	62202
# partially unaligned contigs	12
Partially unaligned length	123696
# N's	0

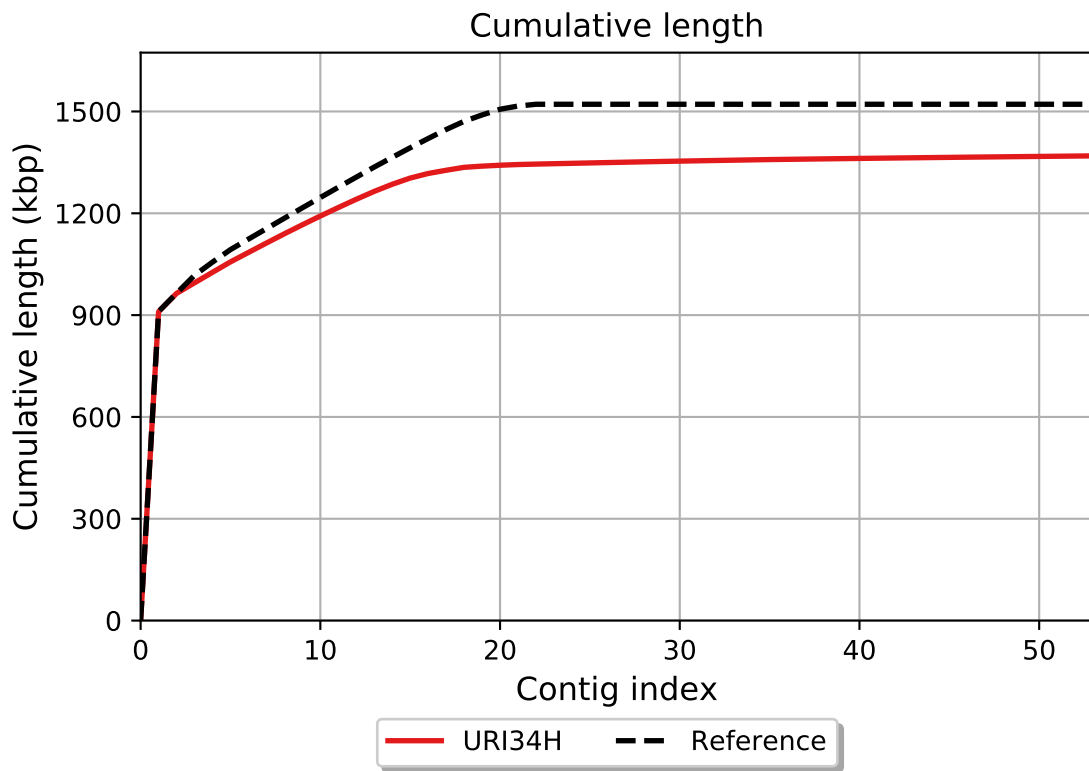
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



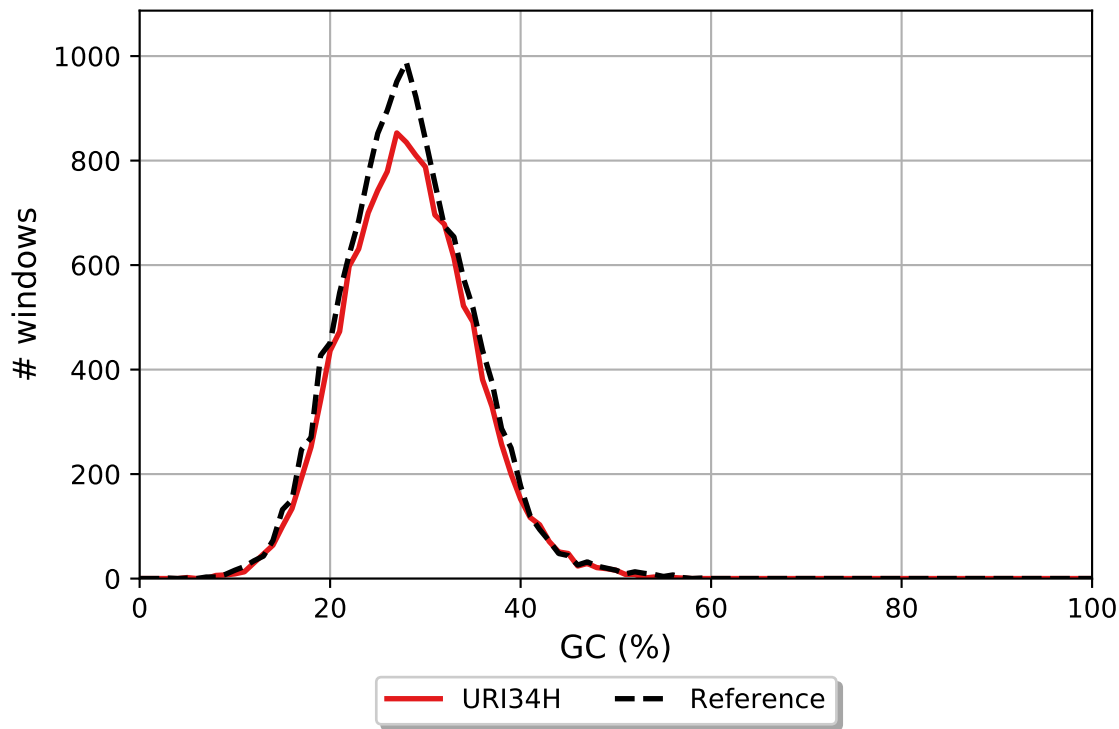
NGx



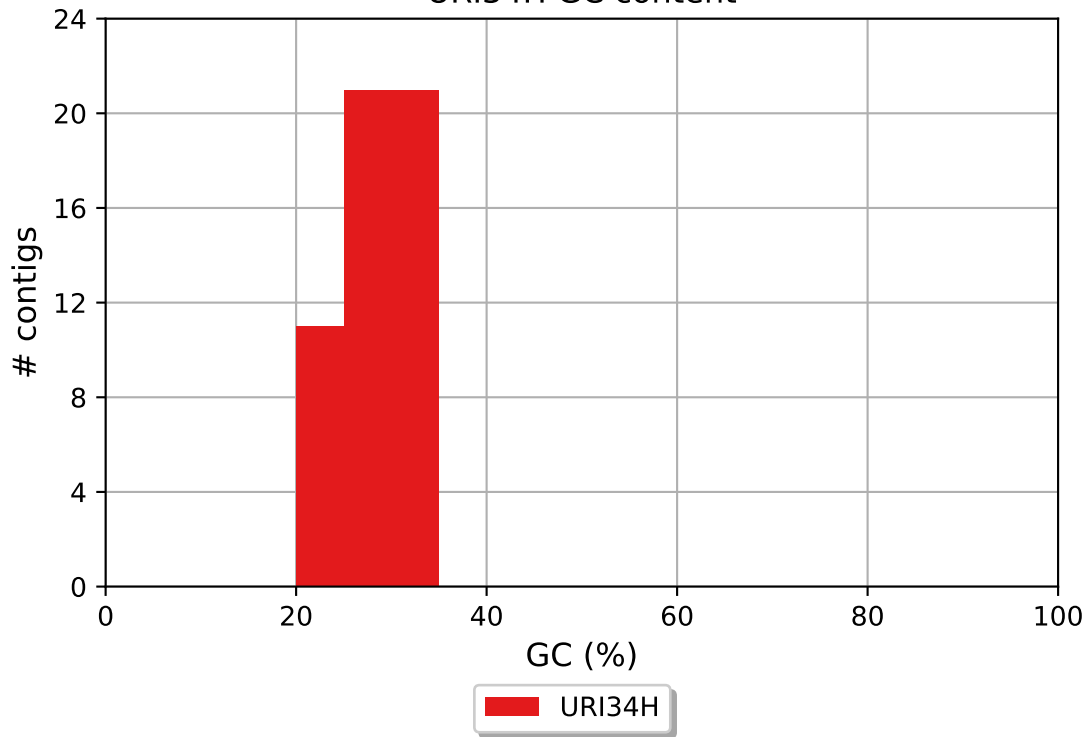
URI34H



GC content

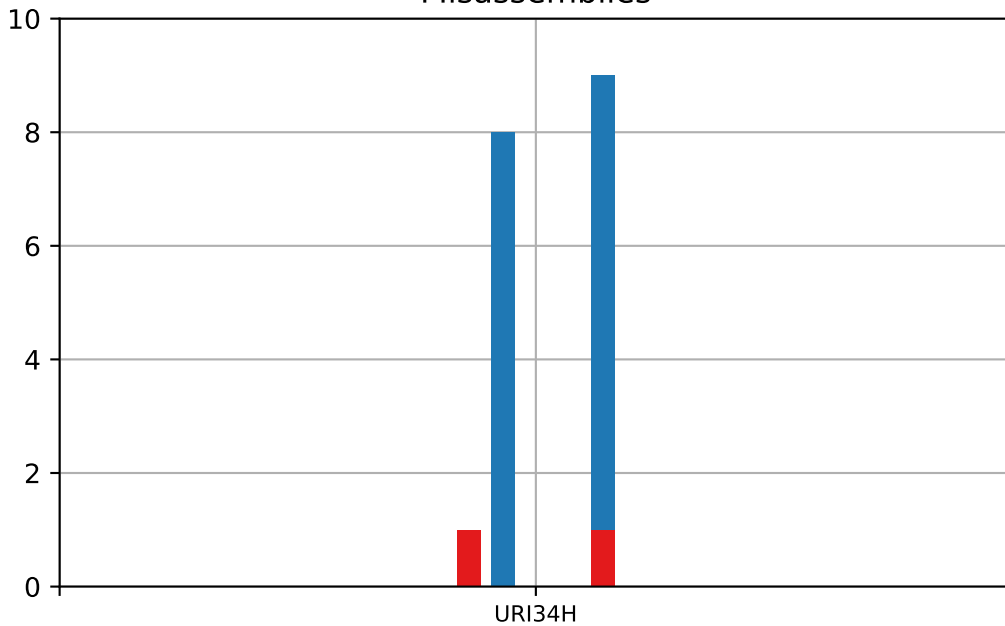


URI34H GC content





## Misassemblies

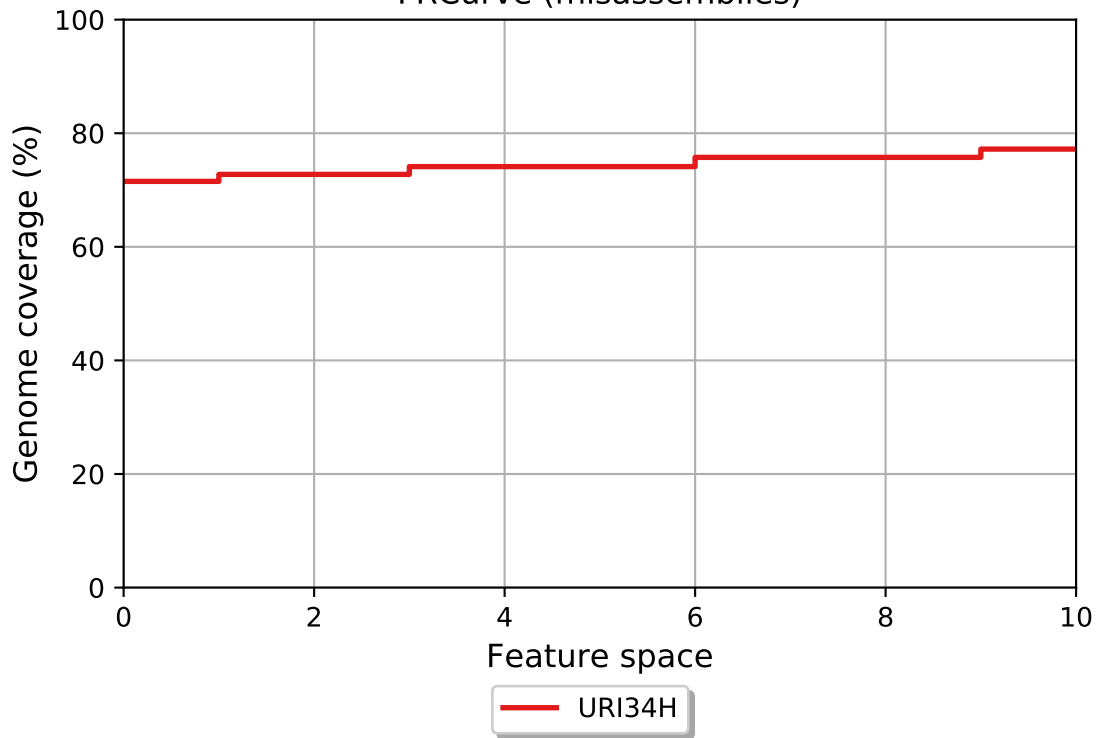


# relocations

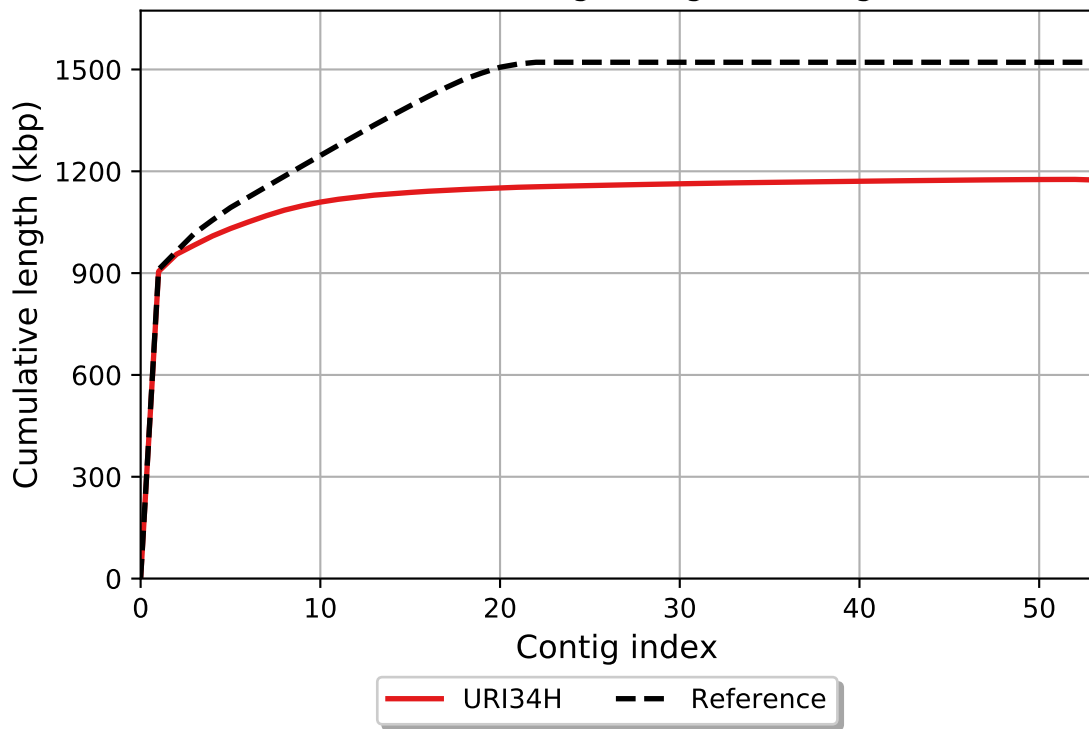


# translocations

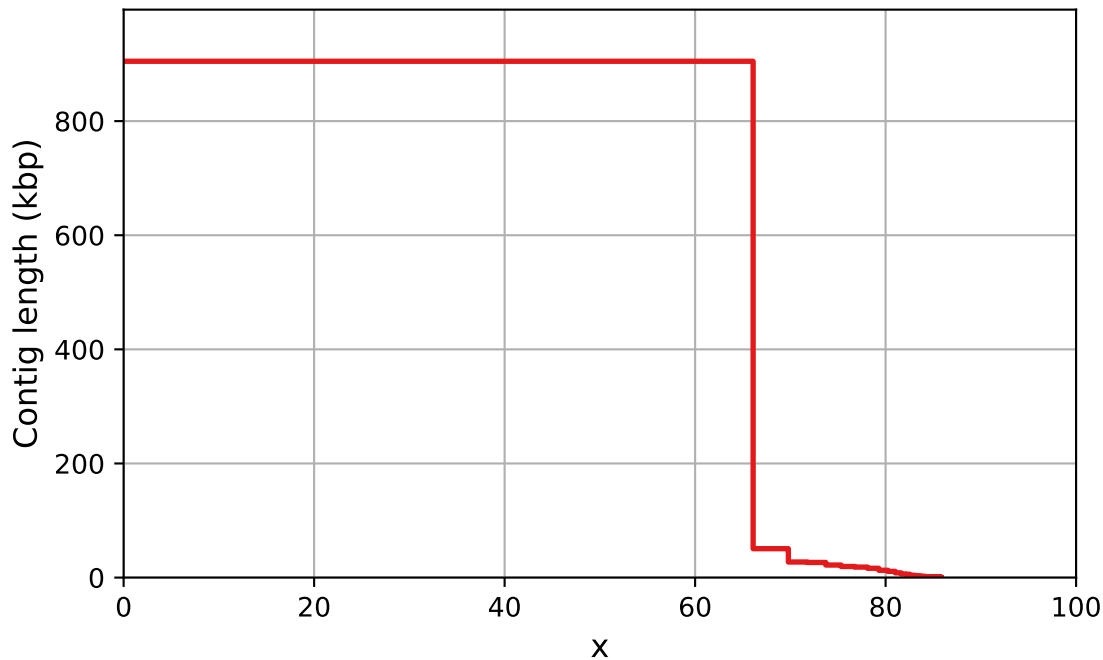
FRCurve (misassemblies)



Cumulative length (aligned contigs)

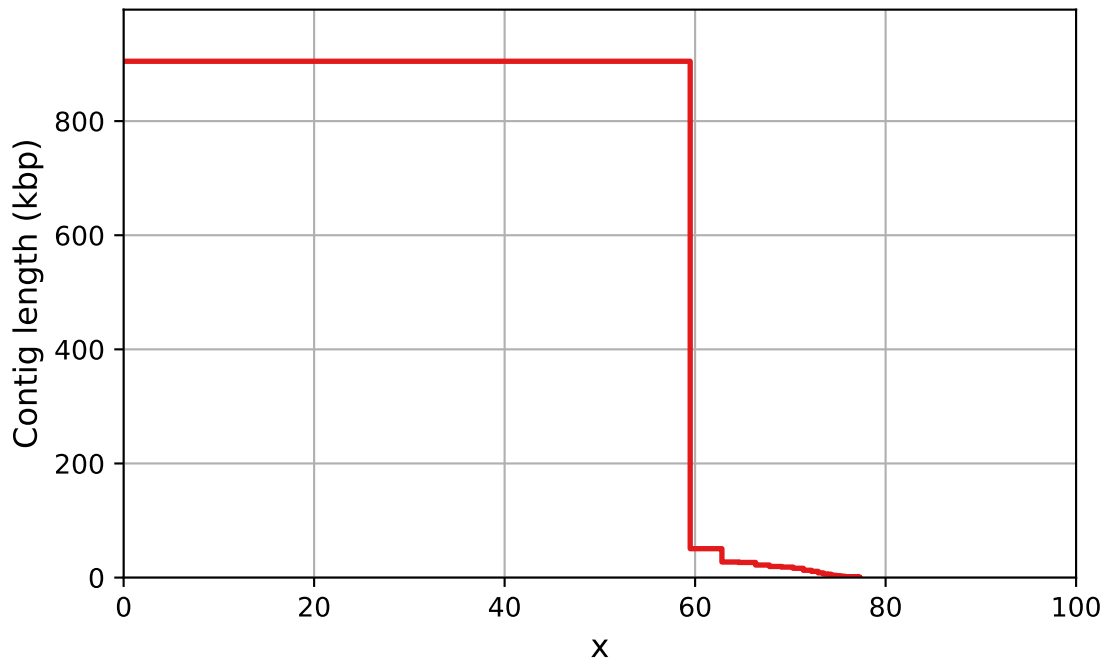


NAx

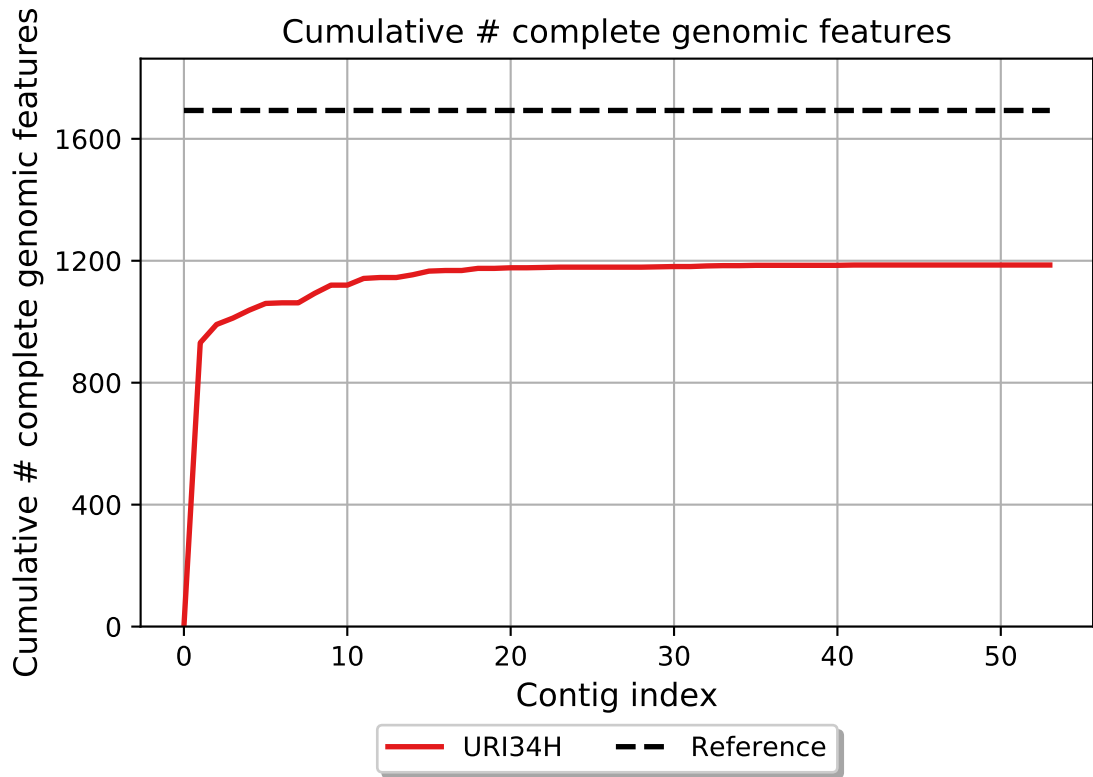


URI34H

NGAx



URI34H



FRCurve (genomic features)

