

Report

	URI89H
# contigs (>= 0 bp)	85
# contigs (>= 1000 bp)	26
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1553229
Total length (>= 1000 bp)	1536778
Total length (>= 5000 bp)	1530148
Total length (>= 10000 bp)	1523878
Total length (>= 25000 bp)	1464255
Total length (>= 50000 bp)	964384
# contigs	33
Largest contig	910720
Total length	1541420
Reference length	1521208
GC (%)	28.23
Reference GC (%)	28.18
N50	910720
NG50	910720
N90	28159
NG90	29732
auN	551068.6
auNG	558390.5
L50	1
LG50	1
L90	16
LG90	15
# misassemblies	17
# misassembled contigs	11
Misassembled contigs length	333226
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 6 part
Unaligned length	30796
Genome fraction (%)	94.092
Duplication ratio	1.055
# N's per 100 kbp	0.00
# mismatches per 100 kbp	195.47
# indels per 100 kbp	23.38
# genomic features	1540 + 44 part
Largest alignment	910720
Total aligned length	1509728
NA50	910720
NGA50	910720
NA90	15818
NGA90	16801
auNA	548321.8
auNGA	555607.2
LA50	1
LGA50	1
LA90	18
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

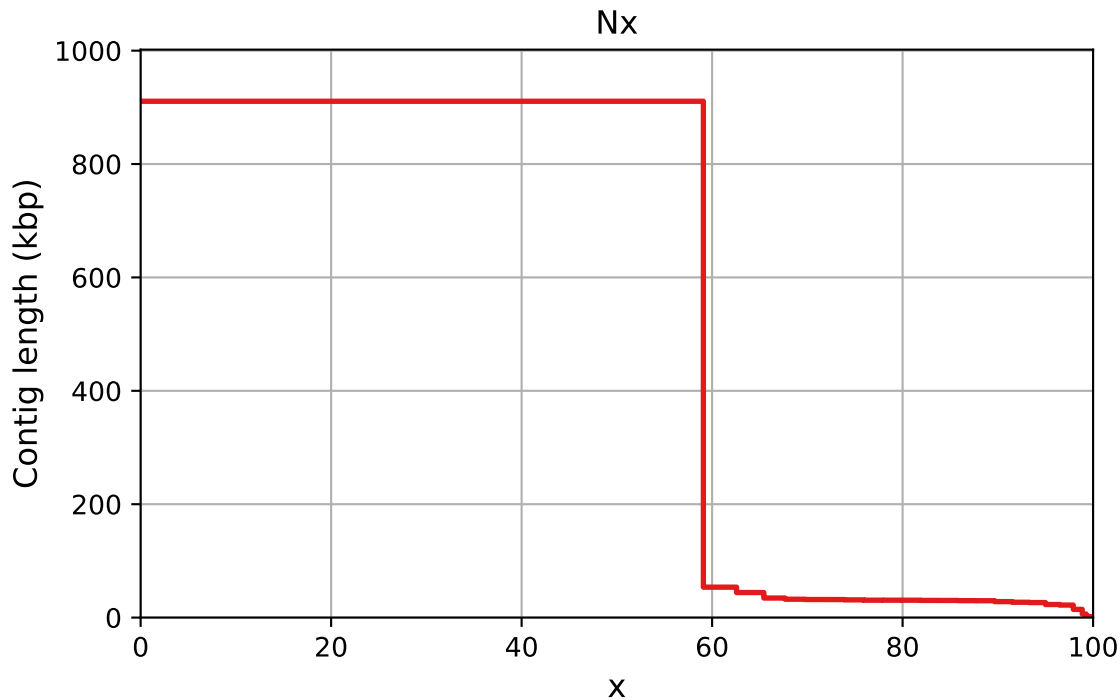
	URI89H
# misassemblies	17
# contig misassemblies	17
# c. relocations	8
# c. translocations	7
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	11
Misassembled contigs length	333226
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	2951
# indels	353
# indels (<= 5 bp)	306
# indels (> 5 bp)	47
Indels length	1725

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

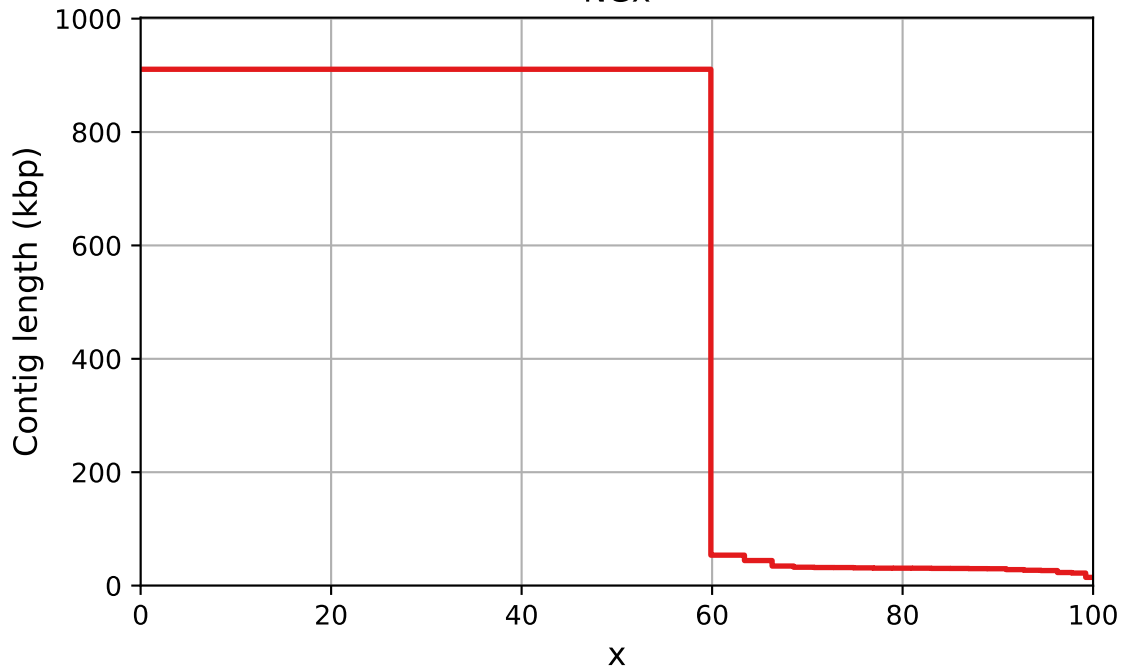
	URI89H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	30796
# N's	0

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).



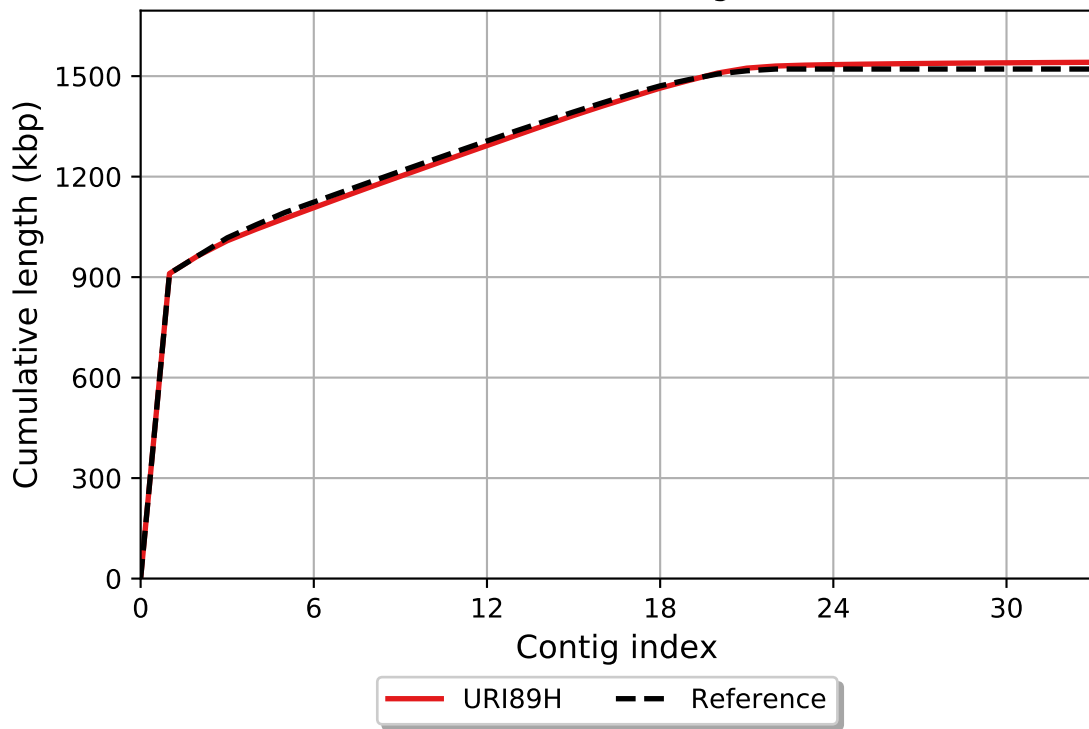
URI89H

NGx

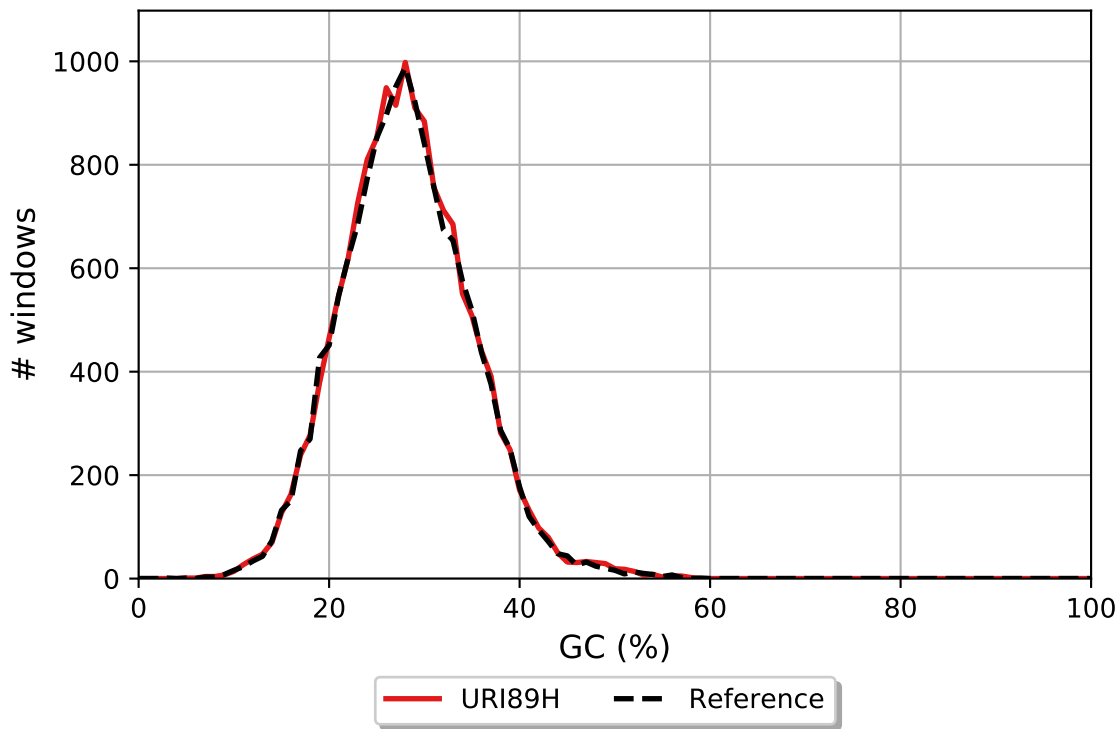


URI89H

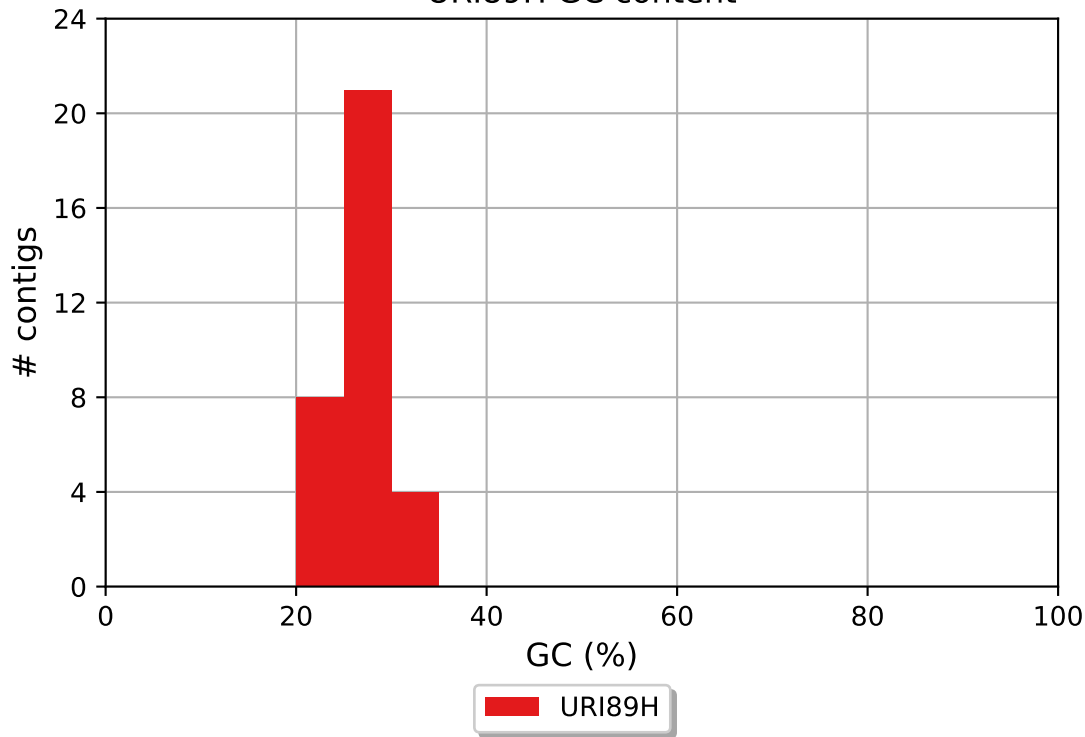
Cumulative length



GC content

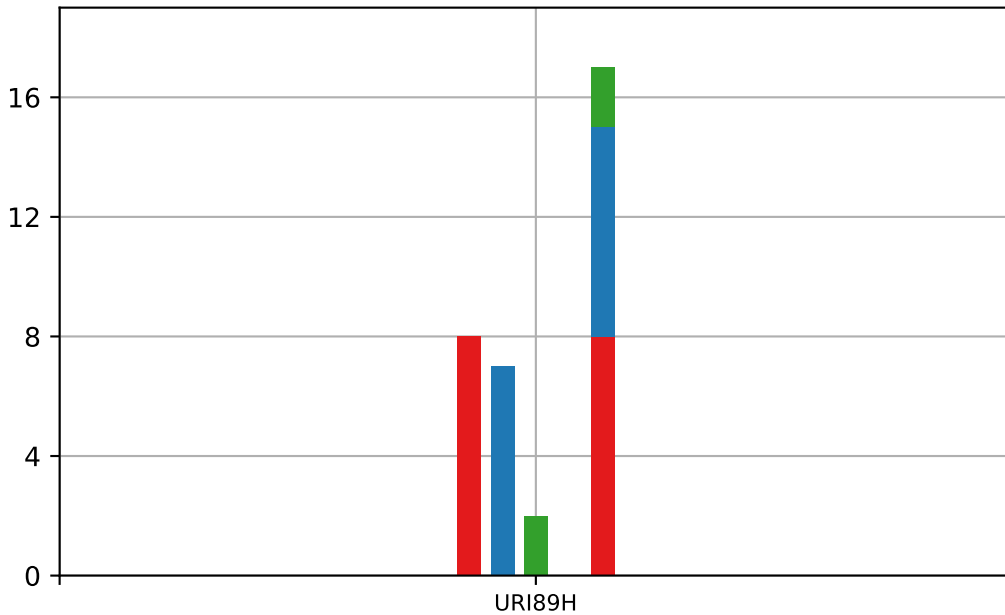


URI89H GC content





## Misassemblies



# relocations

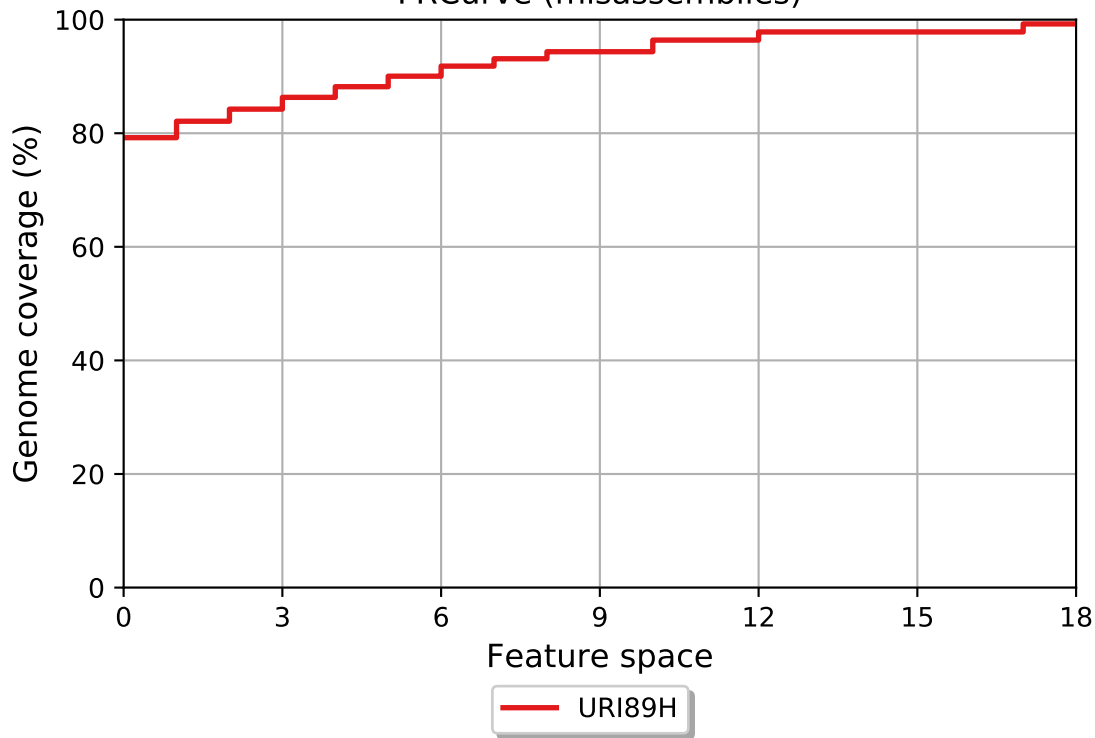


# translocations

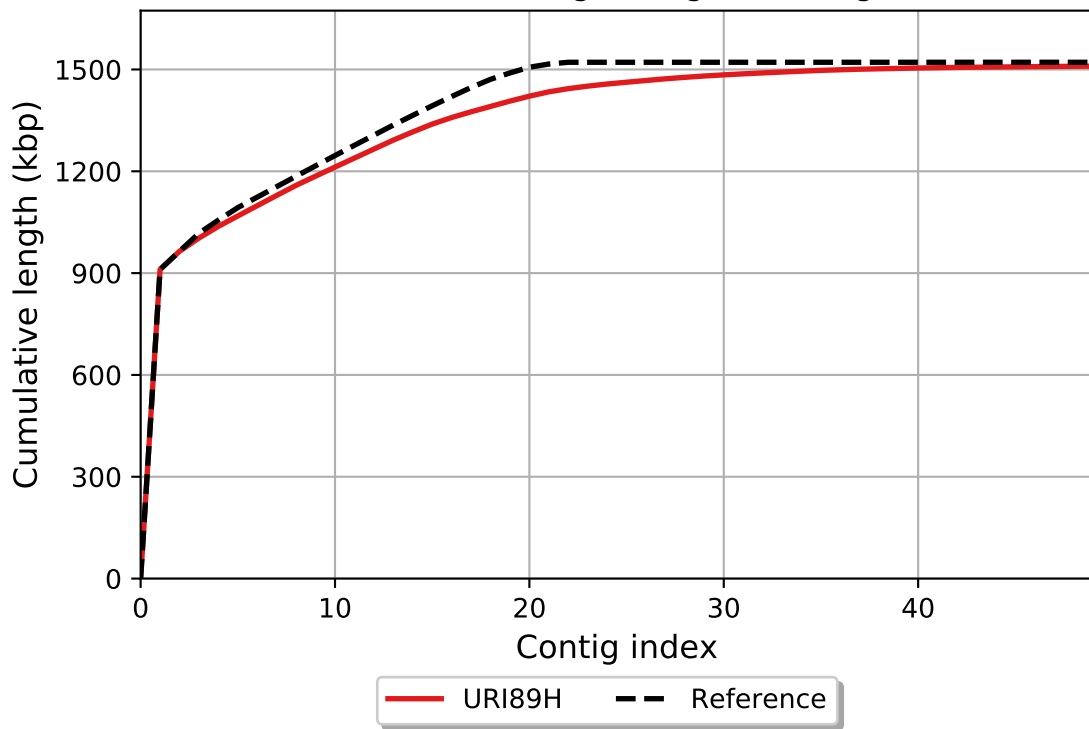


# inversions

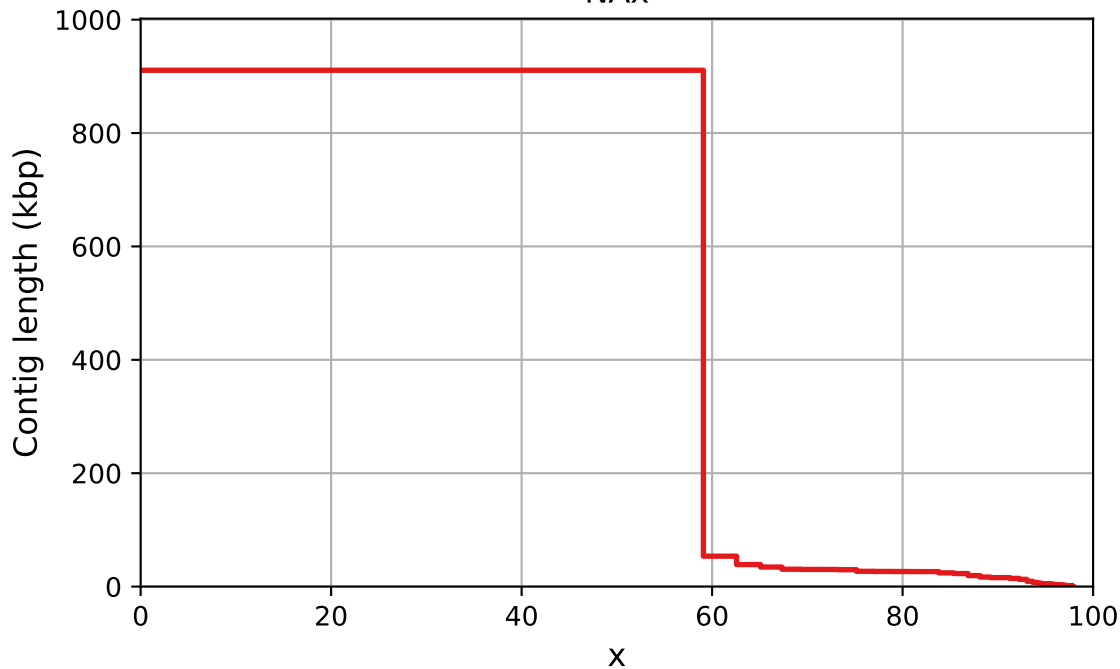
FRCurve (misassemblies)



Cumulative length (aligned contigs)

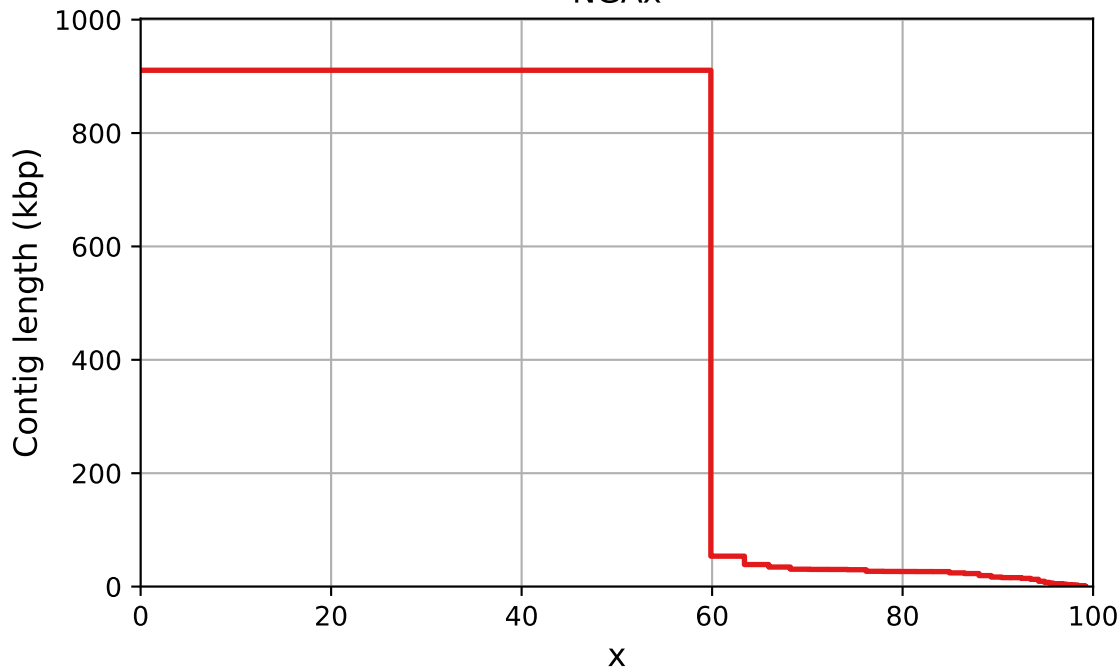


NAx



URI89H

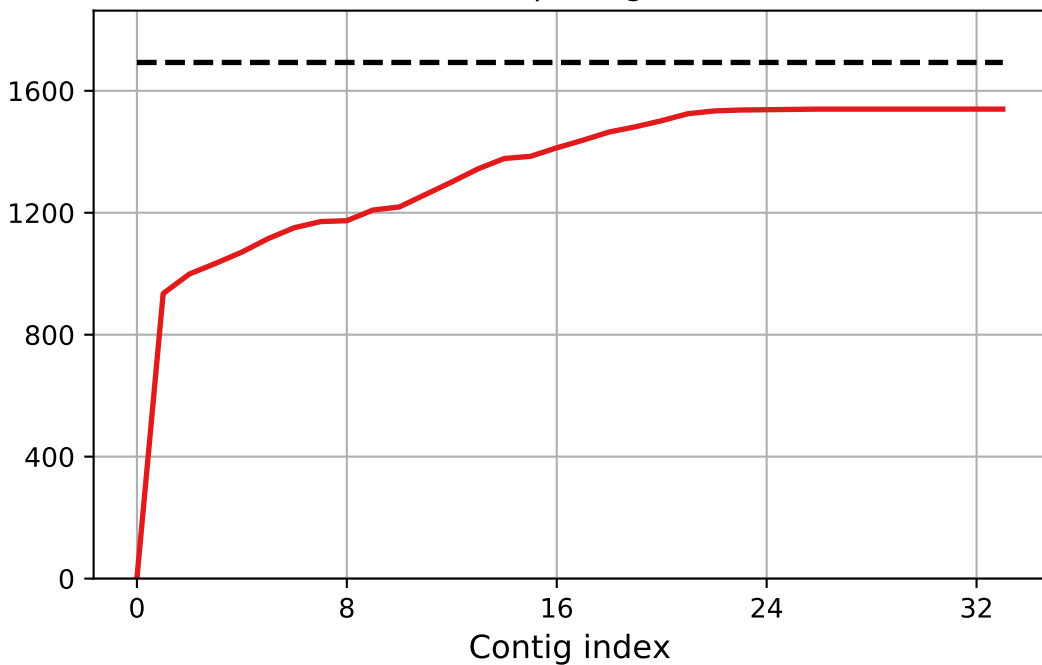
NGAx



URI89H

Cumulative # complete genomic features

Cumulative # complete genomic features



— URI89H    - - Reference

FRCurve (genomic features)

