

Report

	URI39H
# contigs (>= 0 bp)	28
# contigs (>= 1000 bp)	25
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1557202
Total length (>= 1000 bp)	1556617
Total length (>= 5000 bp)	1550714
Total length (>= 10000 bp)	1550714
Total length (>= 25000 bp)	1491460
Total length (>= 50000 bp)	974342
# contigs	25
Largest contig	920673
Total length	1556617
Reference length	1521208
GC (%)	28.18
Reference GC (%)	28.18
N50	920673
NG50	920673
N90	29922
NG90	29953
auN	558251.9
auNG	571246.3
L50	1
LG50	1
L90	15
LG90	14
# misassemblies	15
# misassembled contigs	9
Misassembled contigs length	1145996
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 5 part
Unaligned length	33225
Genome fraction (%)	96.519
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	216.20
# indels per 100 kbp	22.67
# genomic features	1592 + 35 part
Largest alignment	910664
Total aligned length	1521753
NA50	910664
NGA50	910664
NA90	17053
NGA90	24180
auNA	544132.2
auNGA	556797.9
LA50	1
LGA50	1
LA90	17
LGA90	15

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

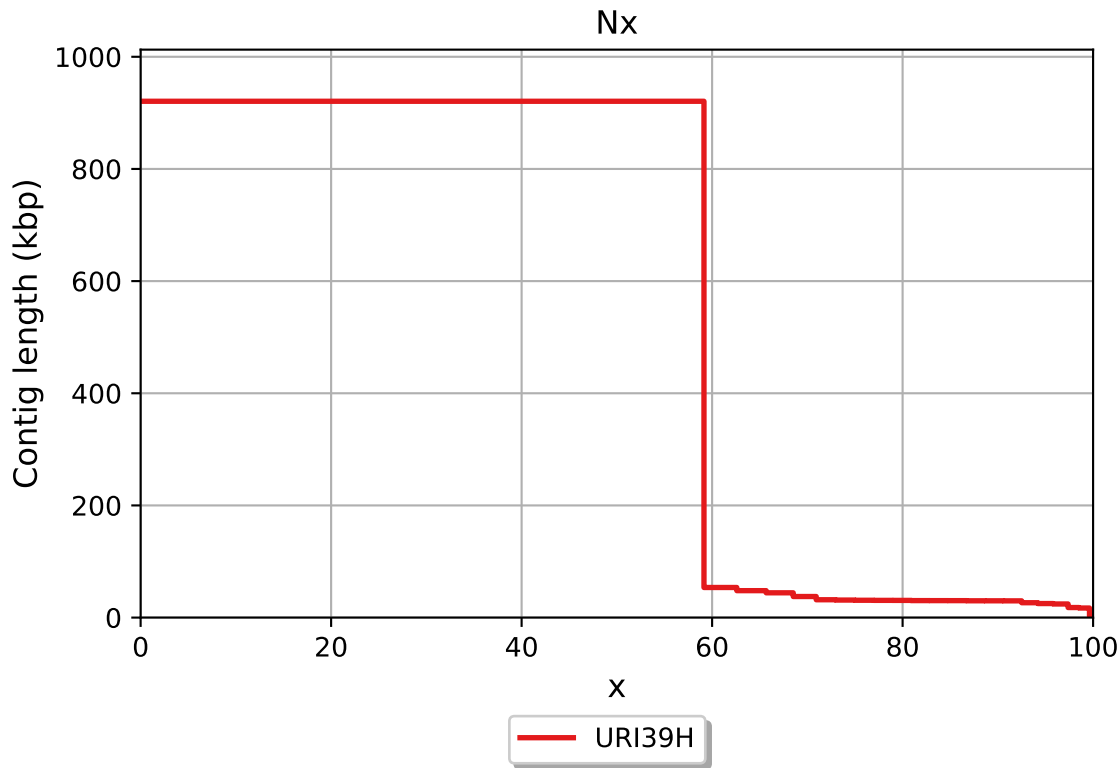
	URI39H
# misassemblies	15
# contig misassemblies	15
# c. relocations	5
# c. translocations	8
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	1145996
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3290
# indels	345
# indels (<= 5 bp)	294
# indels (> 5 bp)	51
Indels length	3178

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).

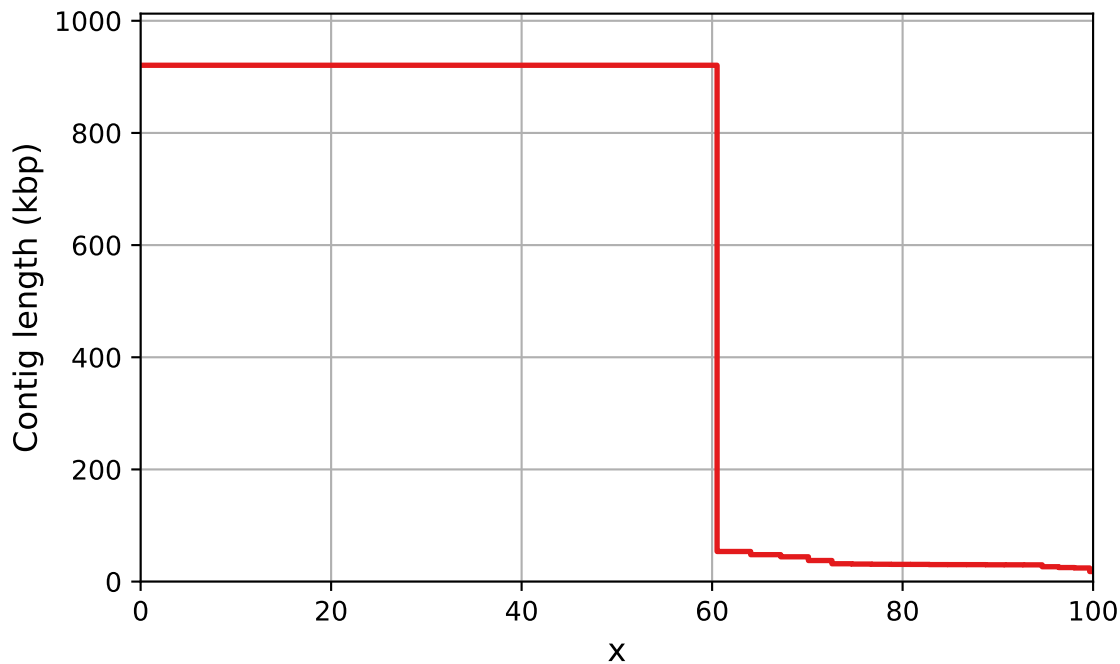
Unaligned report

	URI39H
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	33225
# 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).

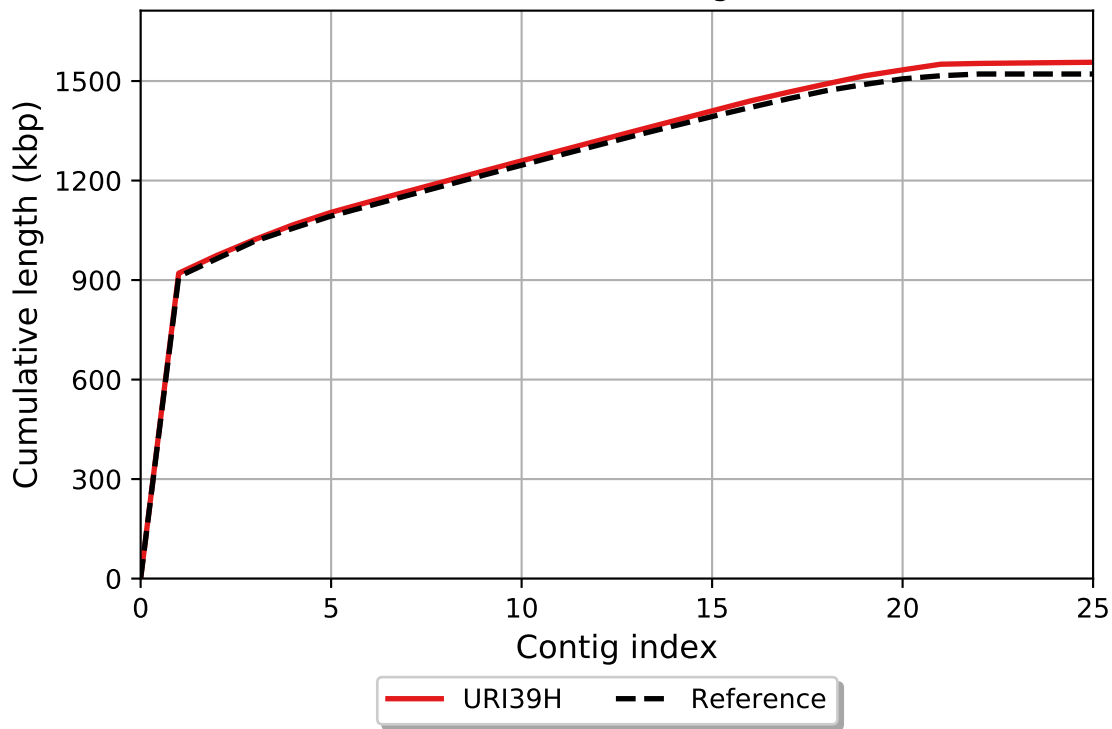


NGx

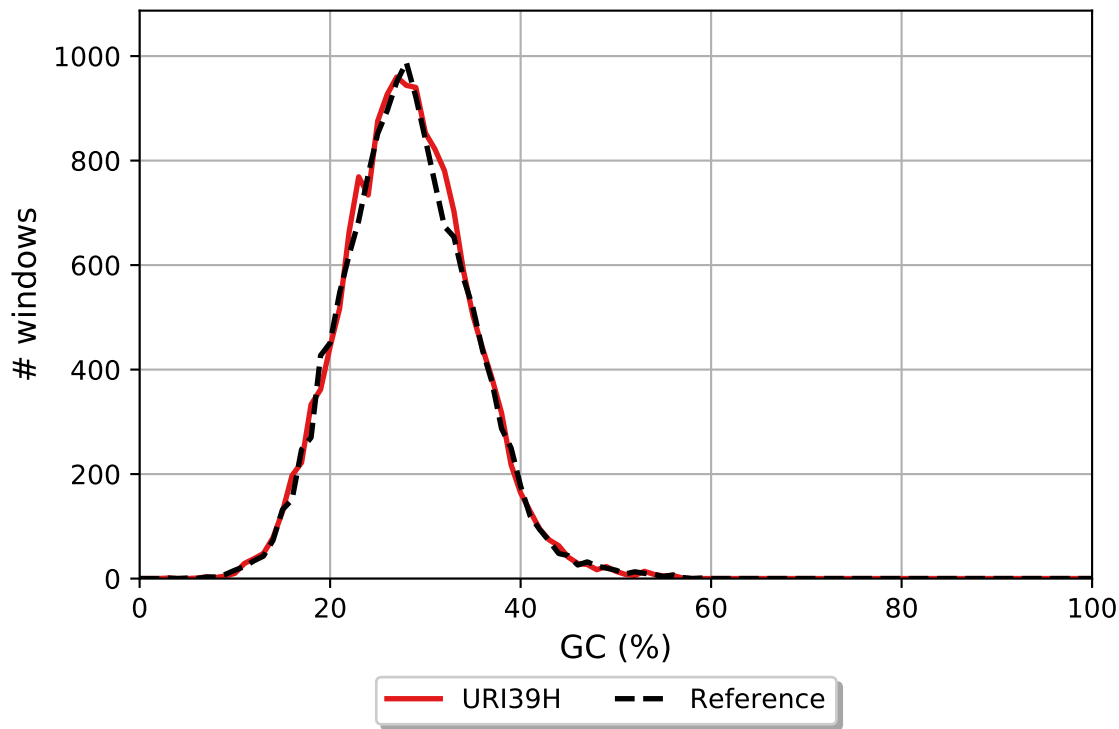


URI39H

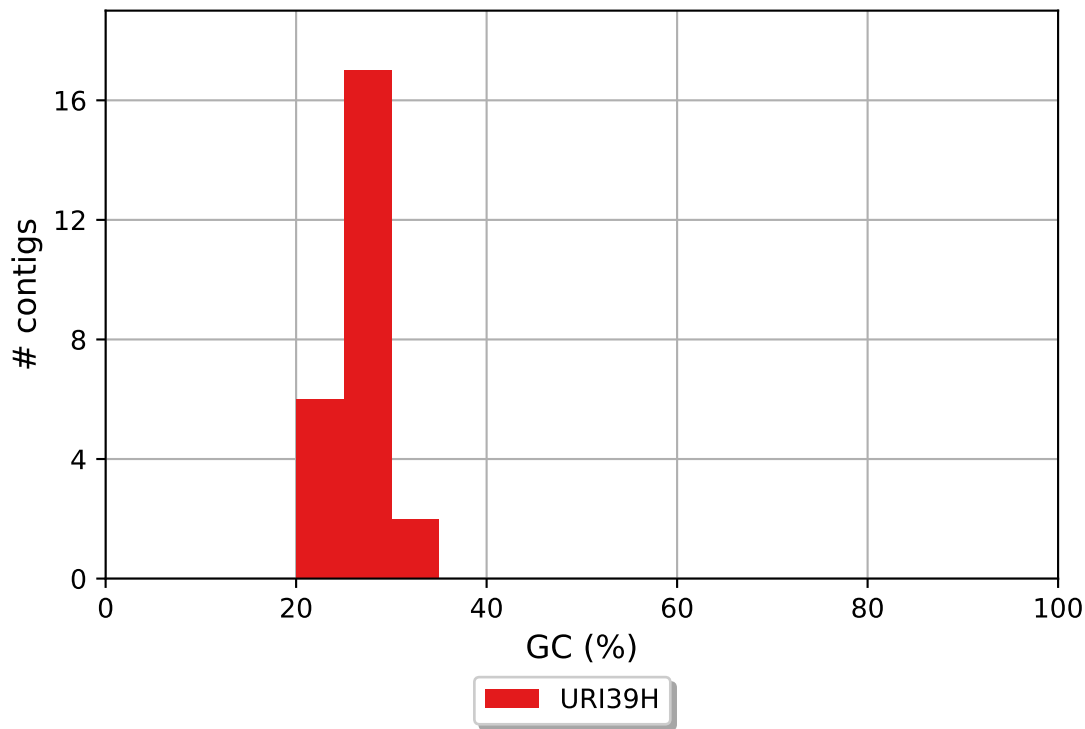
Cumulative length



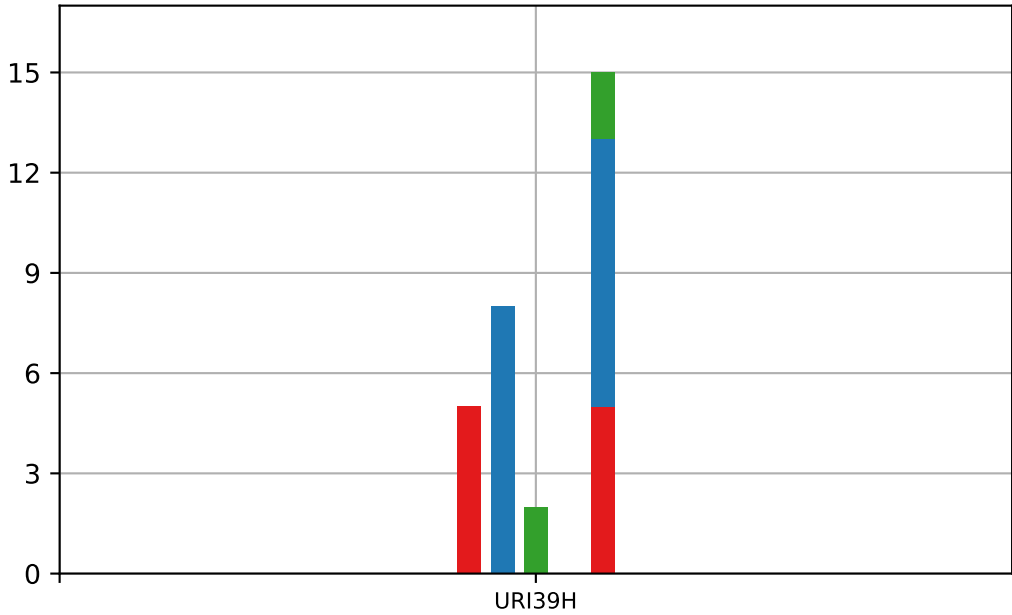
GC content



URI39H GC content



Misassemblies



relocations

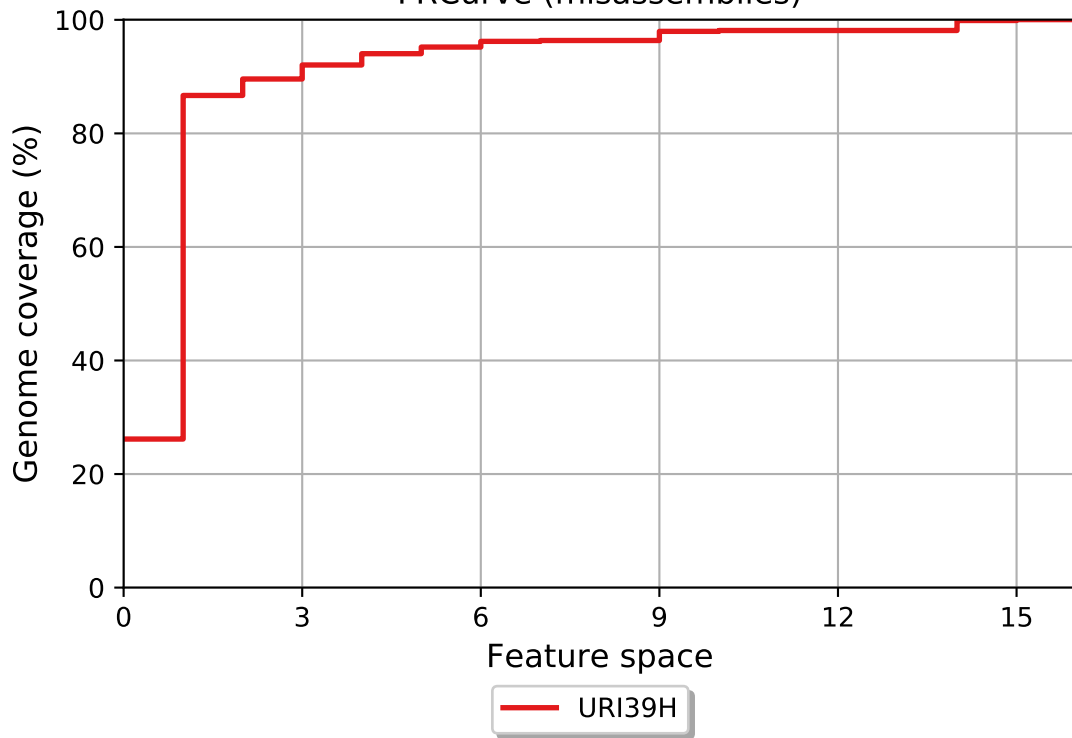


translocations

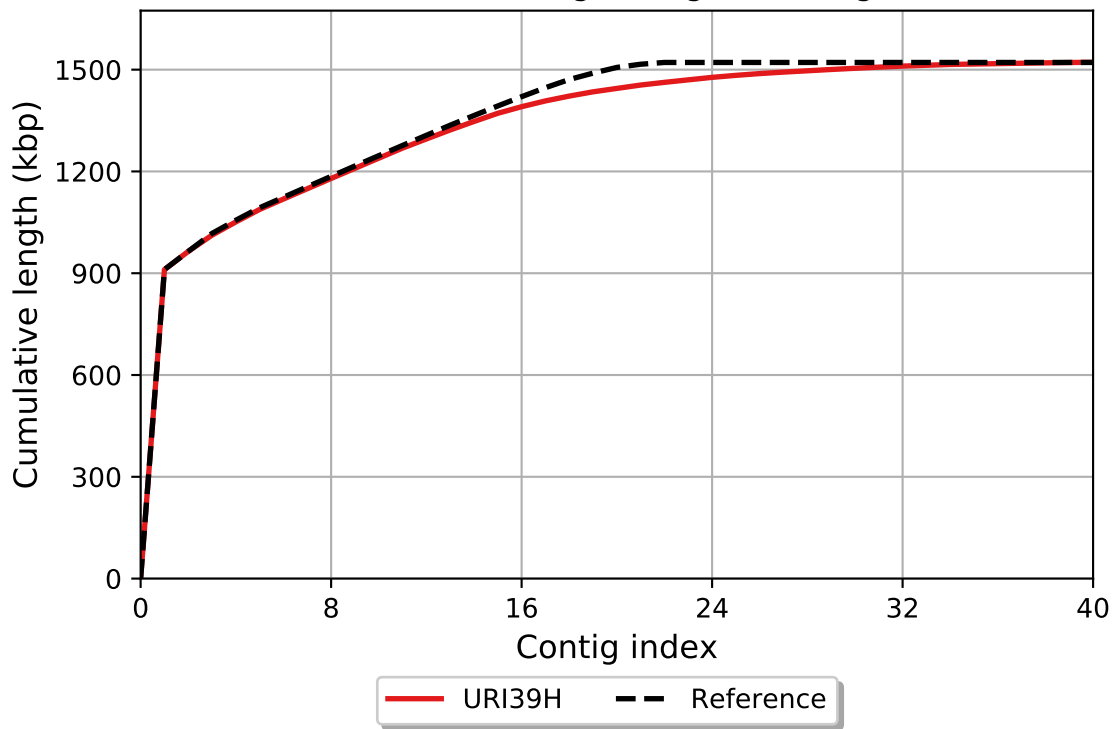


inversions

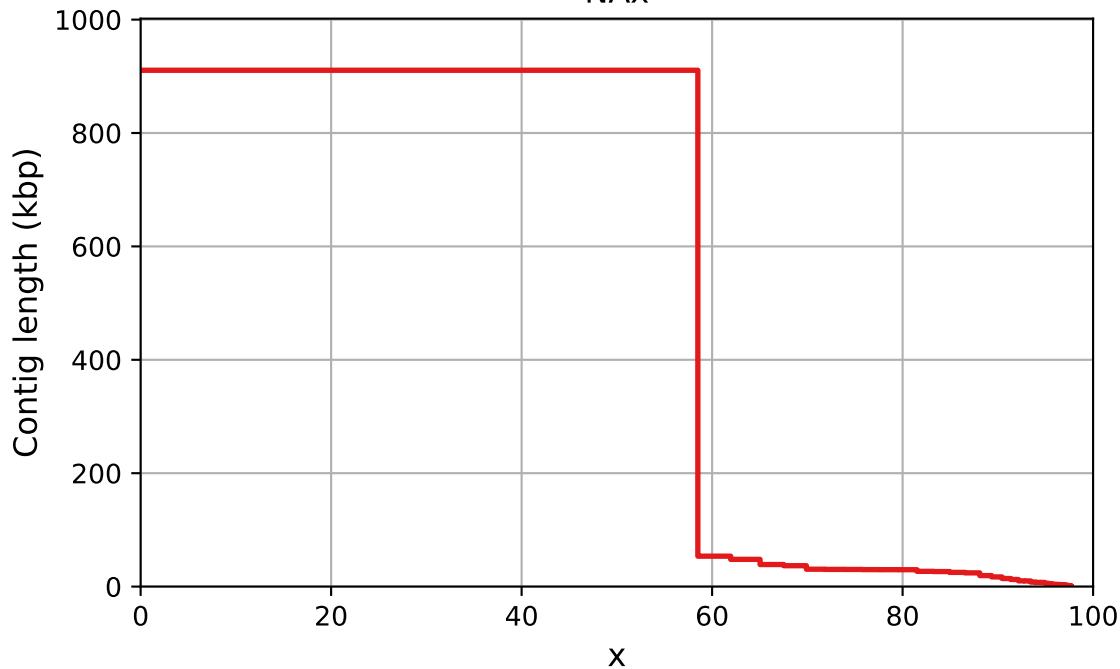
FRCurve (misassemblies)



Cumulative length (aligned contigs)

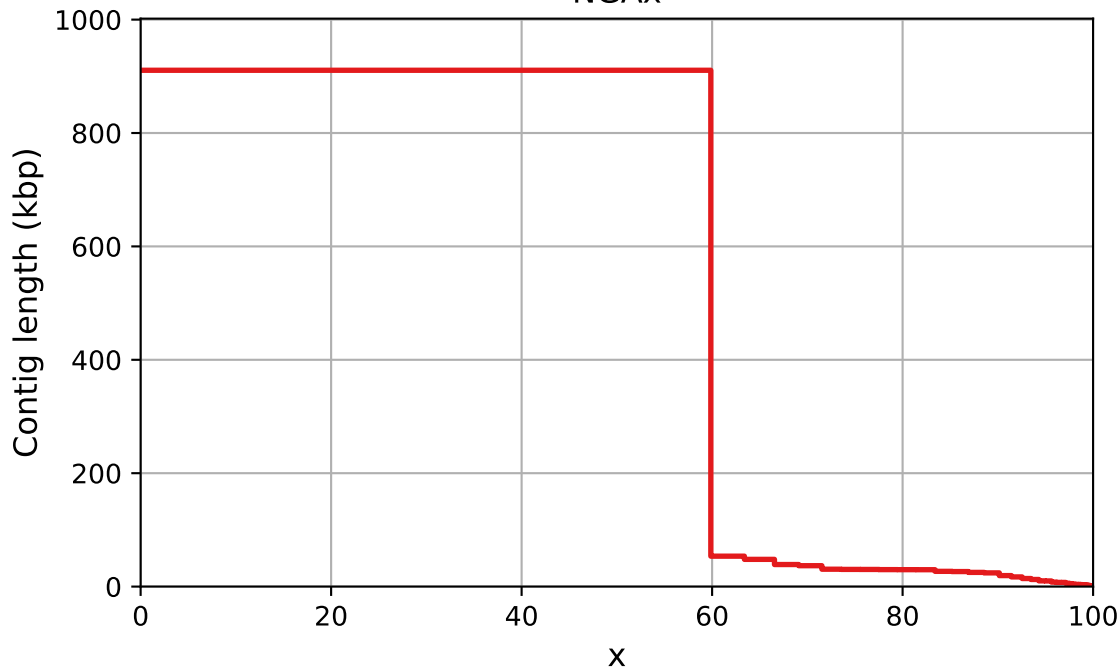


NAx

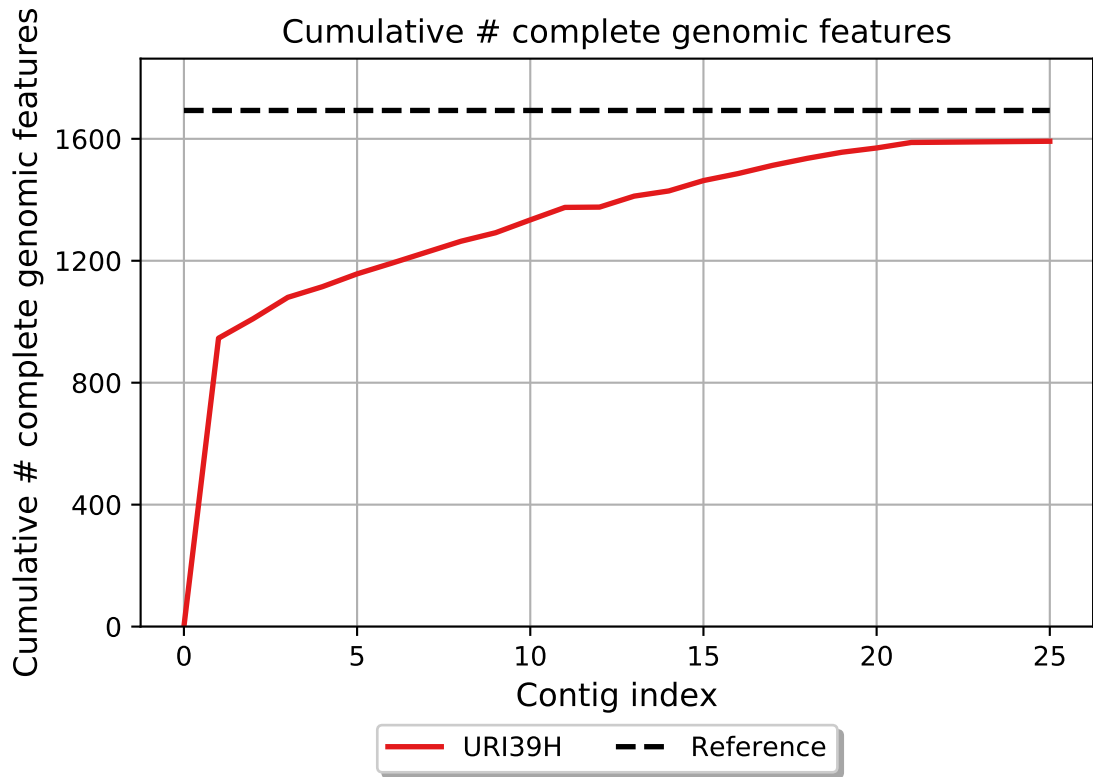


URI39H

NGAx



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FRCurve (genomic features)

