

Report

	URI42H
# contigs (>= 0 bp)	74
# contigs (>= 1000 bp)	25
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1460998
Total length (>= 1000 bp)	1444651
Total length (>= 5000 bp)	1434764
Total length (>= 10000 bp)	1427480
Total length (>= 25000 bp)	1389625
Total length (>= 50000 bp)	1021763
# contigs	36
Largest contig	910587
Total length	1452605
Reference length	1521208
GC (%)	28.33
Reference GC (%)	28.18
N50	910587
NG50	910587
N90	29948
NG90	26498
auN	583429.6
auNG	557118.2
L50	1
LG50	1
L90	13
LG90	15
# misassemblies	12
# misassembled contigs	8
Misassembled contigs length	242305
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	3 + 5 part
Unaligned length	34240
Genome fraction (%)	90.328
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	153.47
# indels per 100 kbp	20.25
# genomic features	1499 + 28 part
Largest alignment	910587
Total aligned length	1417187
NA50	910587
NGA50	910587
NA90	17431
NGA90	7399
auNA	580220.8
auNGA	554054.2
LA50	1
LGA50	1
LA90	15
LGA90	19

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

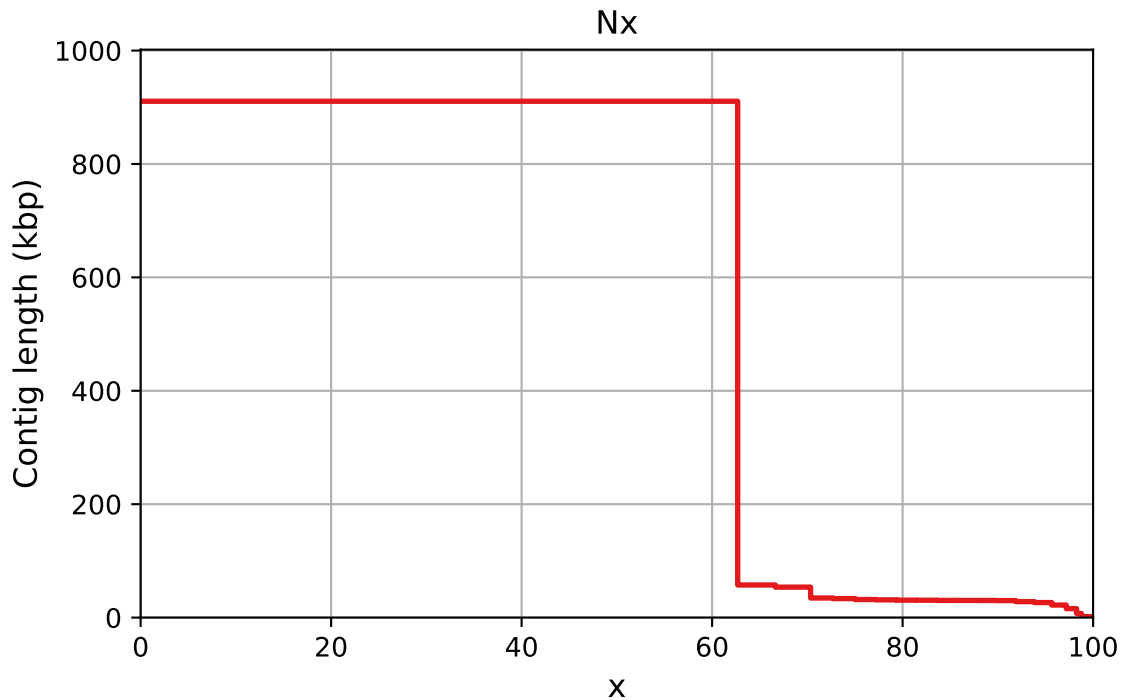
	URI42H
# misassemblies	12
# contig misassemblies	12
# c. relocations	6
# c. translocations	6
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	242305
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	2175
# indels	287
# indels (<= 5 bp)	250
# indels (> 5 bp)	37
Indels length	1340

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

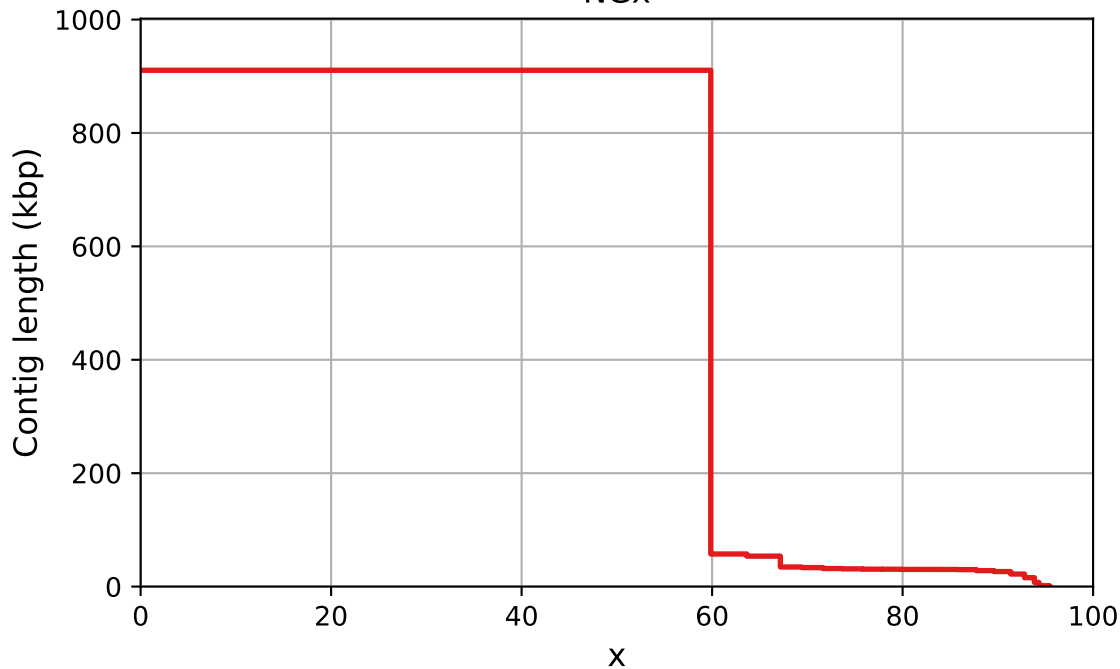
	URI42H
# fully unaligned contigs	3
Fully unaligned length	3708
# partially unaligned contigs	5
Partially unaligned length	30532
# N's	0

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).

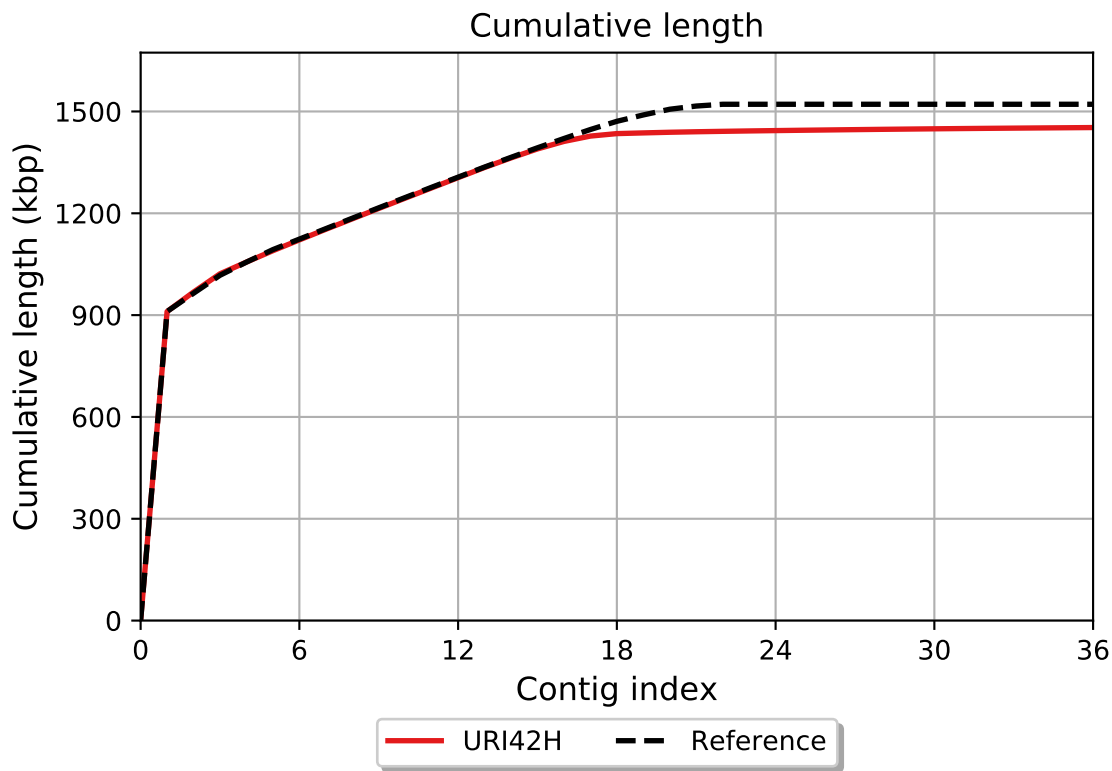


URI42H

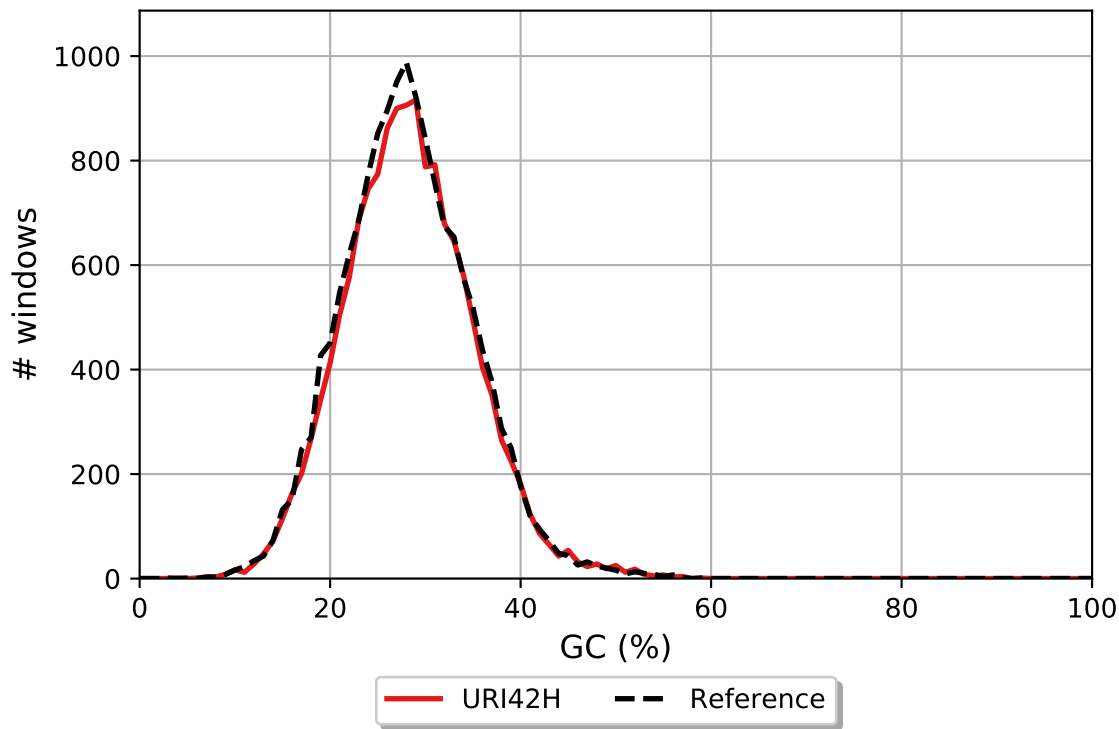
NGx



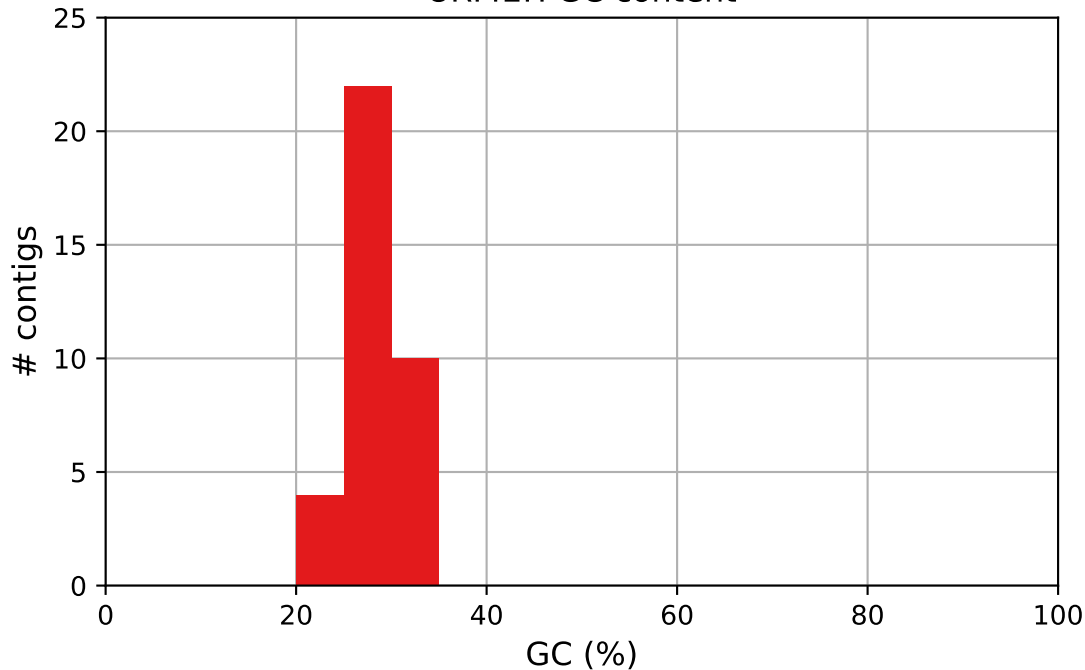
URI42H



GC content

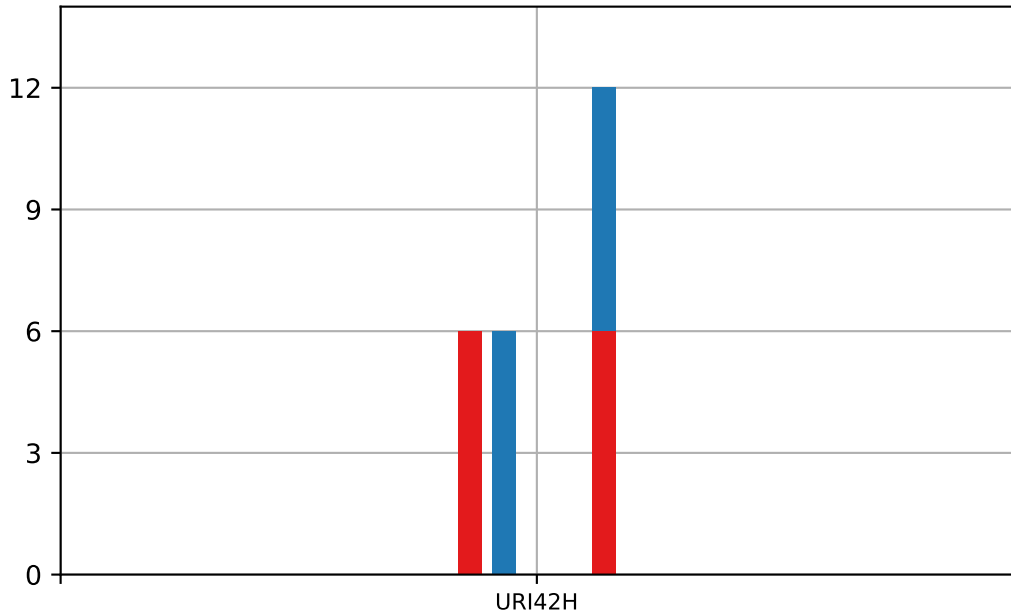


URI42H GC content



URI42H

Misassemblies

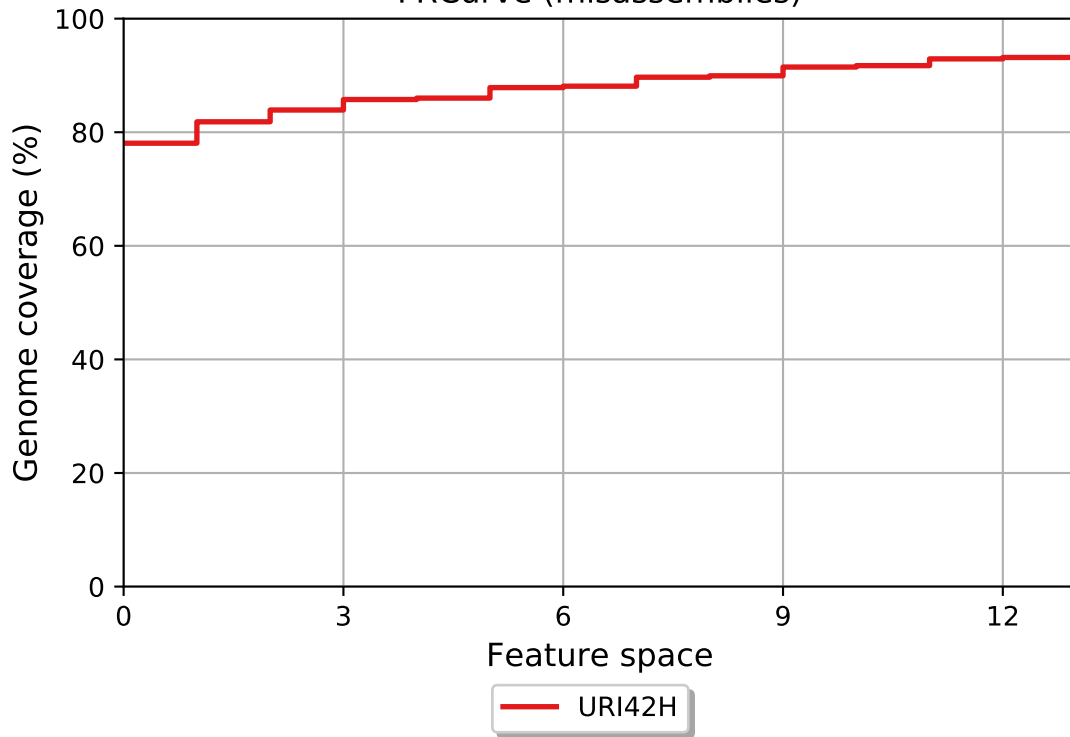


relocations

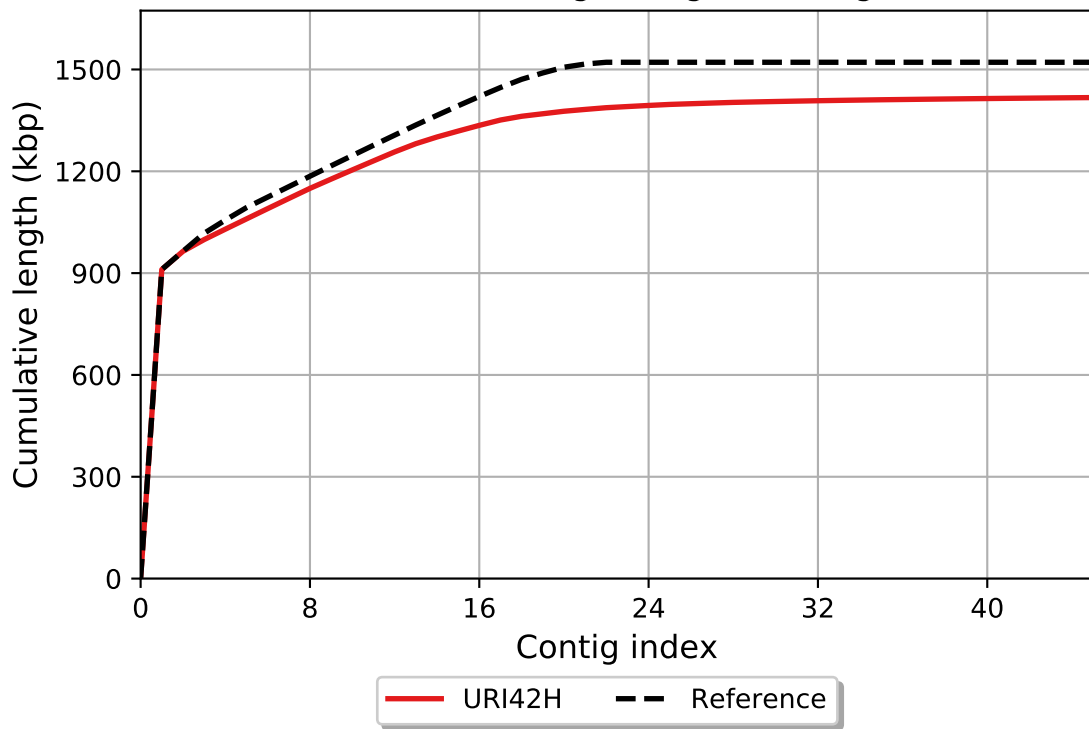


translocations

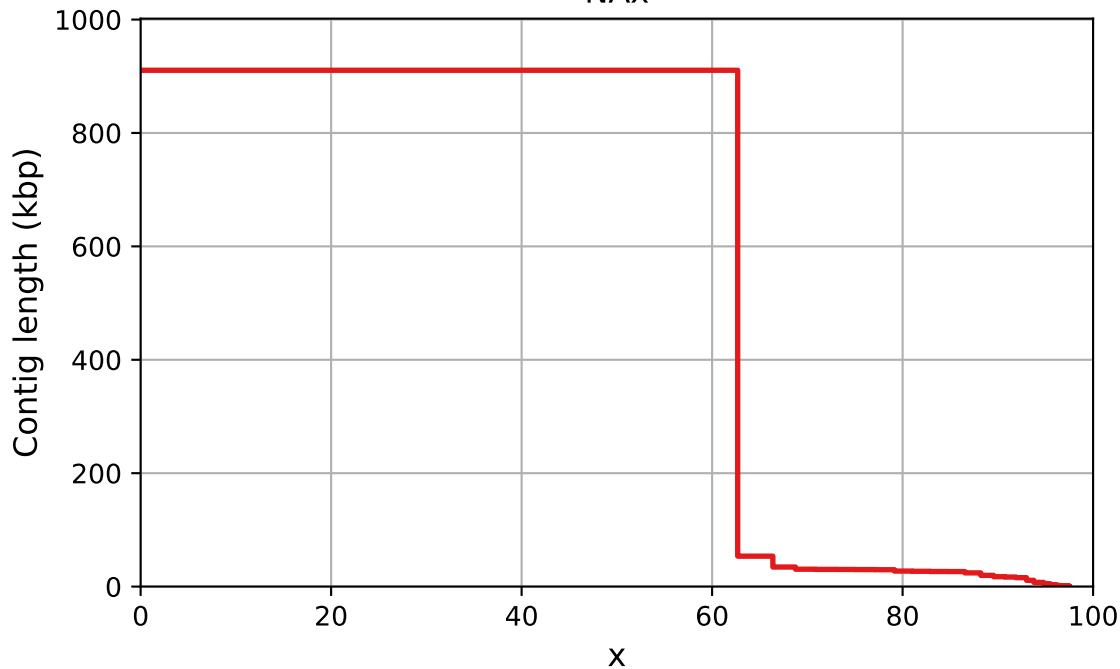
FRCurve (misassemblies)



Cumulative length (aligned contigs)

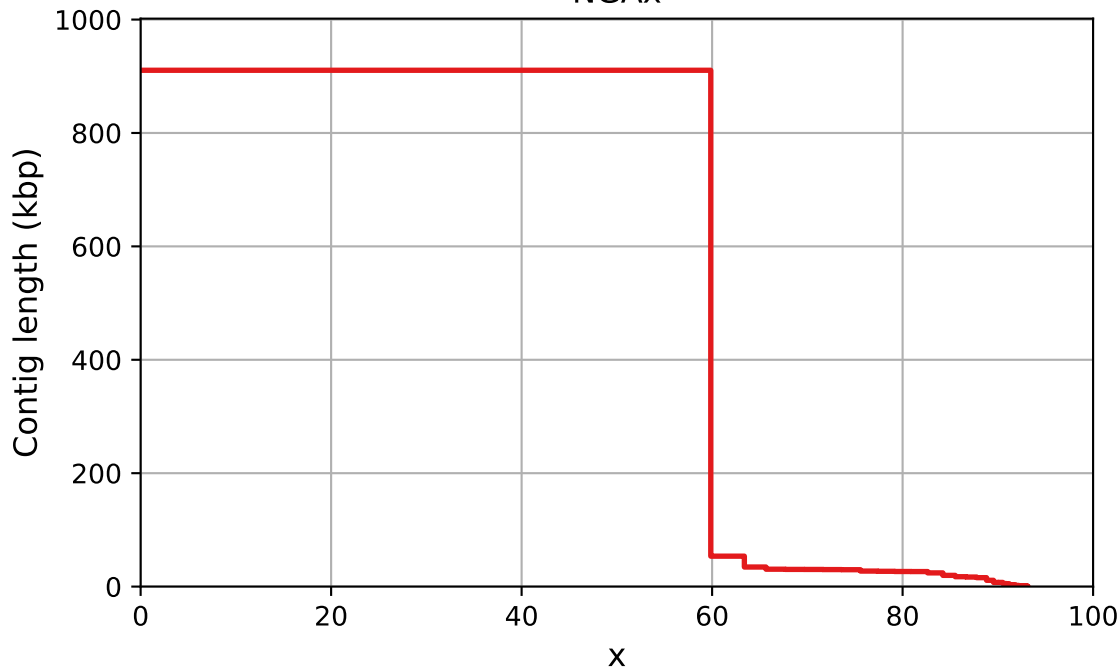


NAx

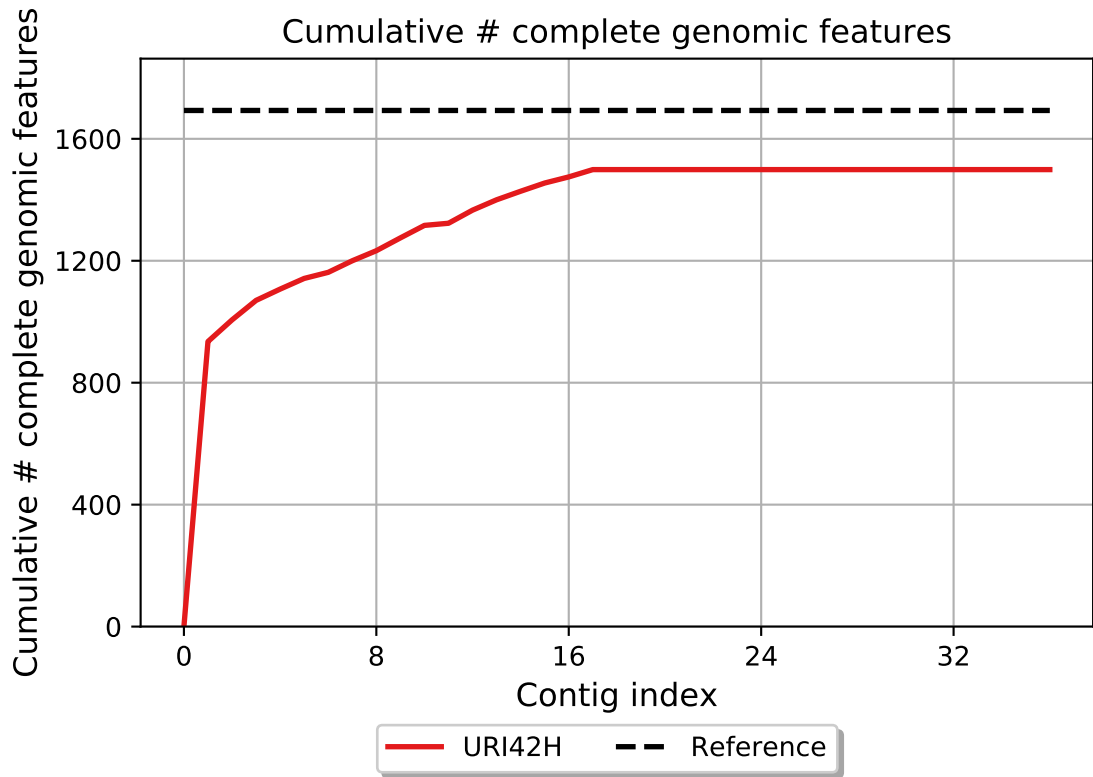


URI42H

NGAx



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FRCurve (genomic features)

