

Report

	URI33H
# contigs (>= 0 bp)	44
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1353948
Total length (>= 1000 bp)	1344529
Total length (>= 5000 bp)	1342007
Total length (>= 10000 bp)	1334990
Total length (>= 25000 bp)	1307570
Total length (>= 50000 bp)	957555
# contigs	25
Largest contig	902844
Total length	1349420
Reference length	1521208
GC (%)	28.05
Reference GC (%)	28.18
N50	902844
NG50	902844
N90	30583
NG90	-
auN	615027.7
auNG	545573.4
L50	1
LG50	1
L90	10
LG90	-
# misassemblies	18
# misassembled contigs	7
Misassembled contigs length	213190
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	7 + 12 part
Unaligned length	115663
Genome fraction (%)	79.791
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	777.30
# indels per 100 kbp	49.44
# genomic features	1255 + 47 part
Largest alignment	902630
Total aligned length	1229764
NA50	902630
NGA50	902630
NA90	2376
NGA90	-
auNA	609741.7
auNGA	540884.3
LA50	1
LGA50	1
LA90	24
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

	URI33H
# misassemblies	18
# contig misassemblies	18
# c. relocations	5
# c. translocations	11
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	7
Misassembled contigs length	213190
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	9559
# indels	608
# indels (<= 5 bp)	527
# indels (> 5 bp)	81
Indels length	5663

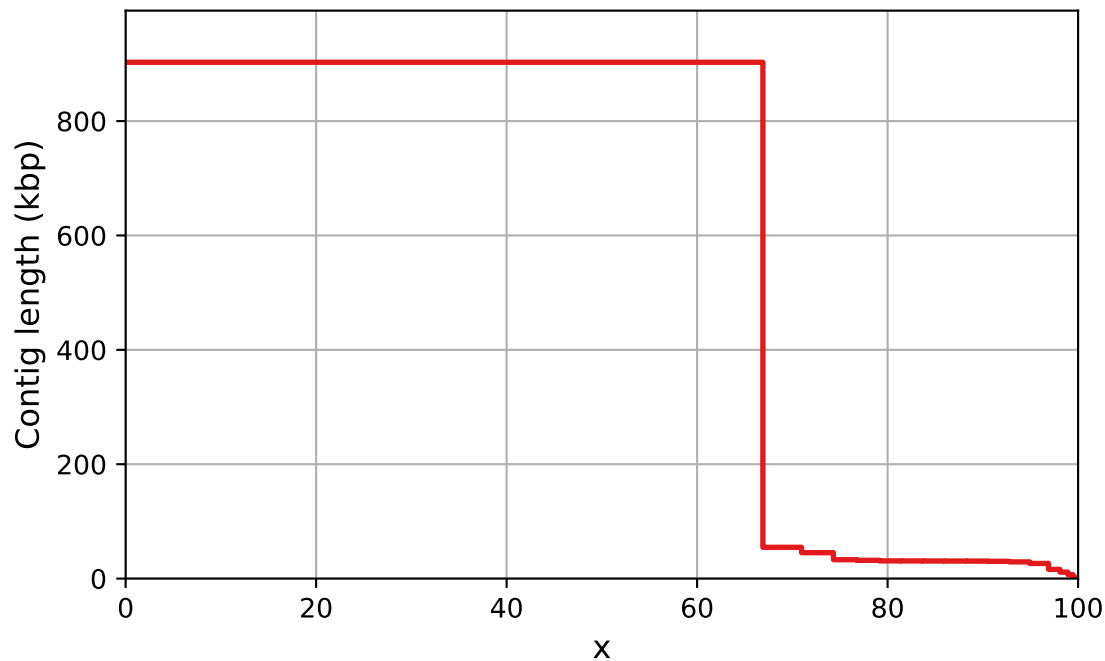
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	URI33H
# fully unaligned contigs	7
Fully unaligned length	6020
# partially unaligned contigs	12
Partially unaligned length	109643
# N's	0

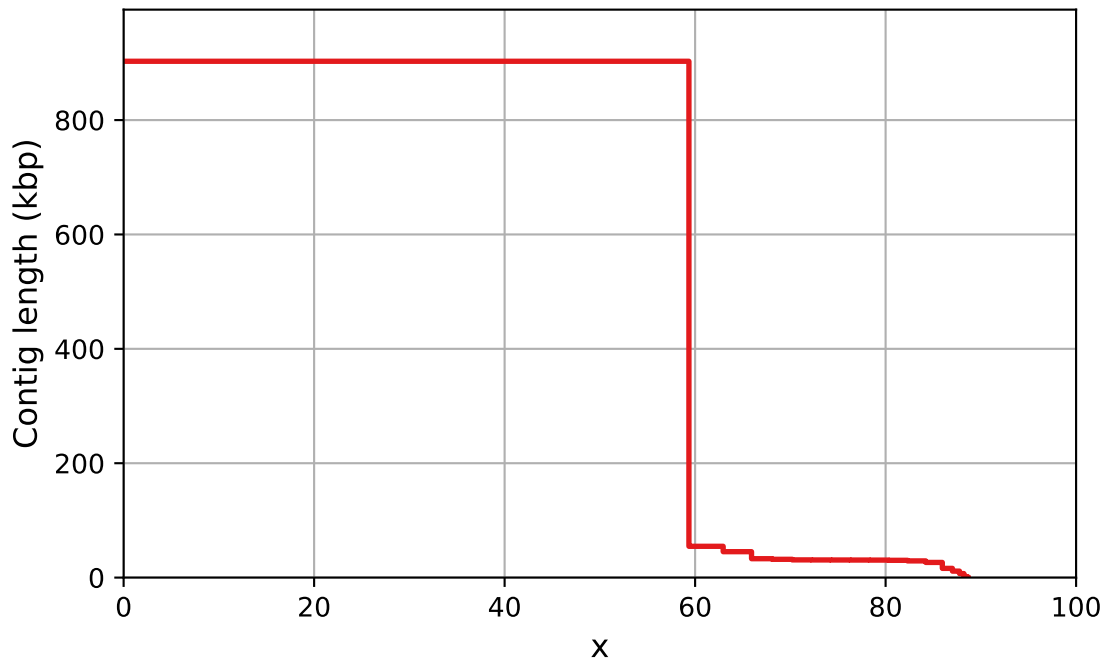
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

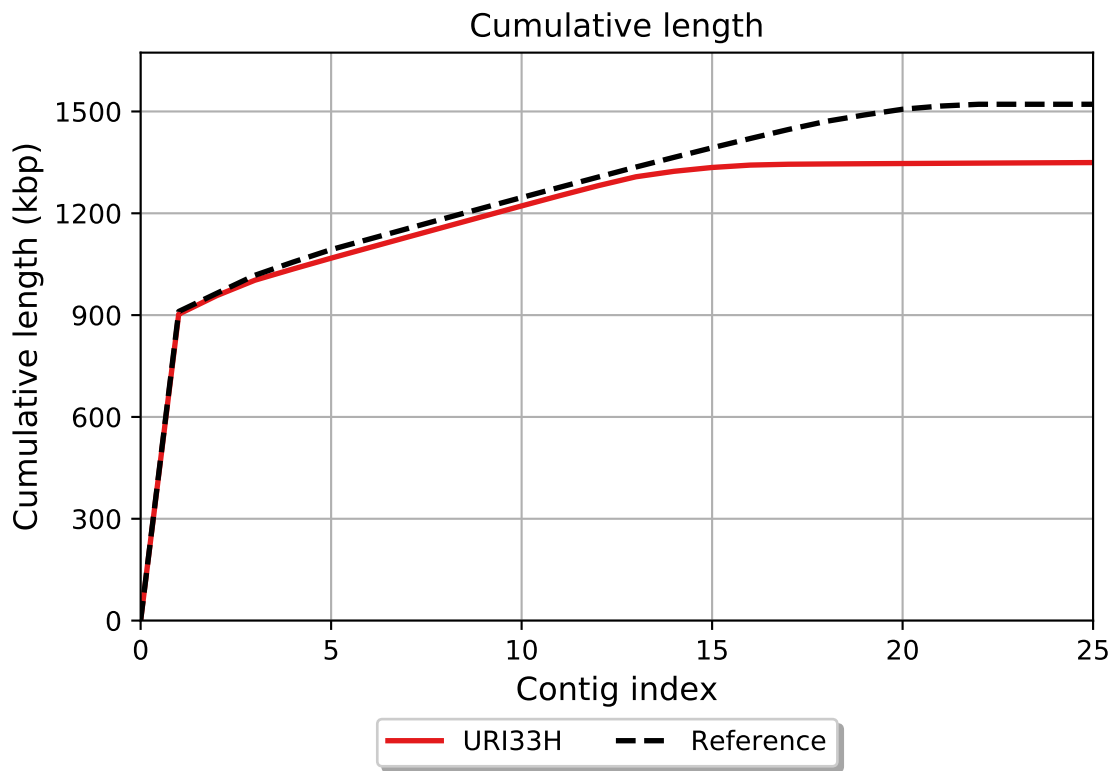


URI33H

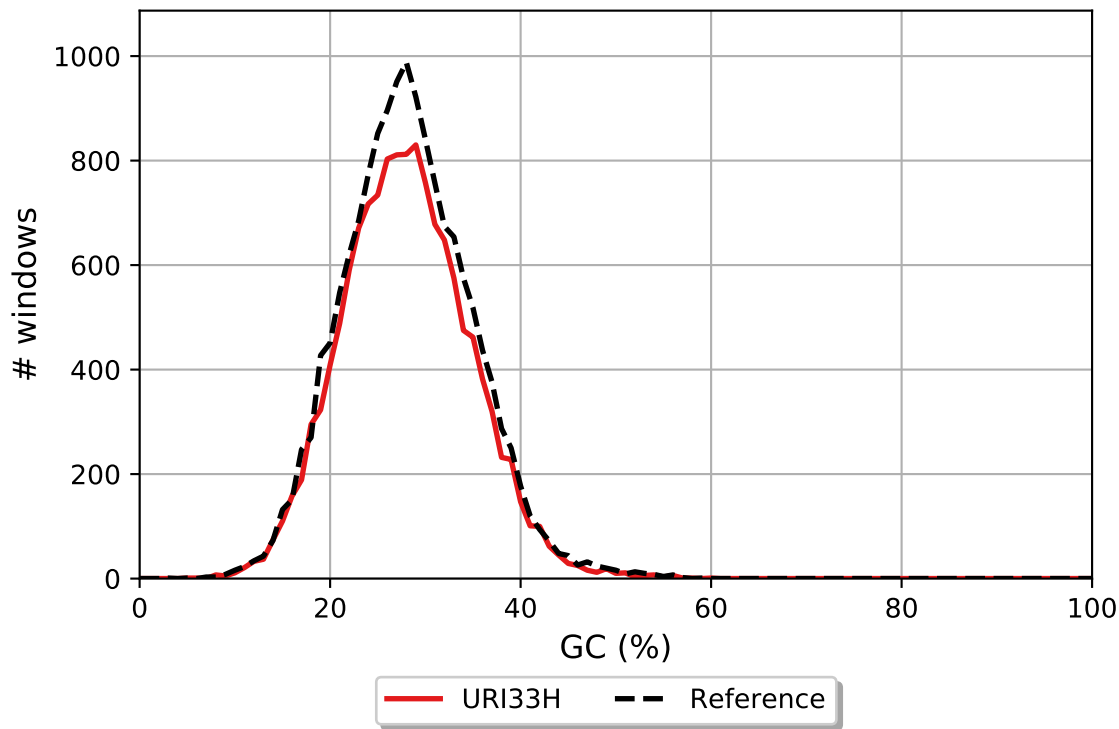
NGx



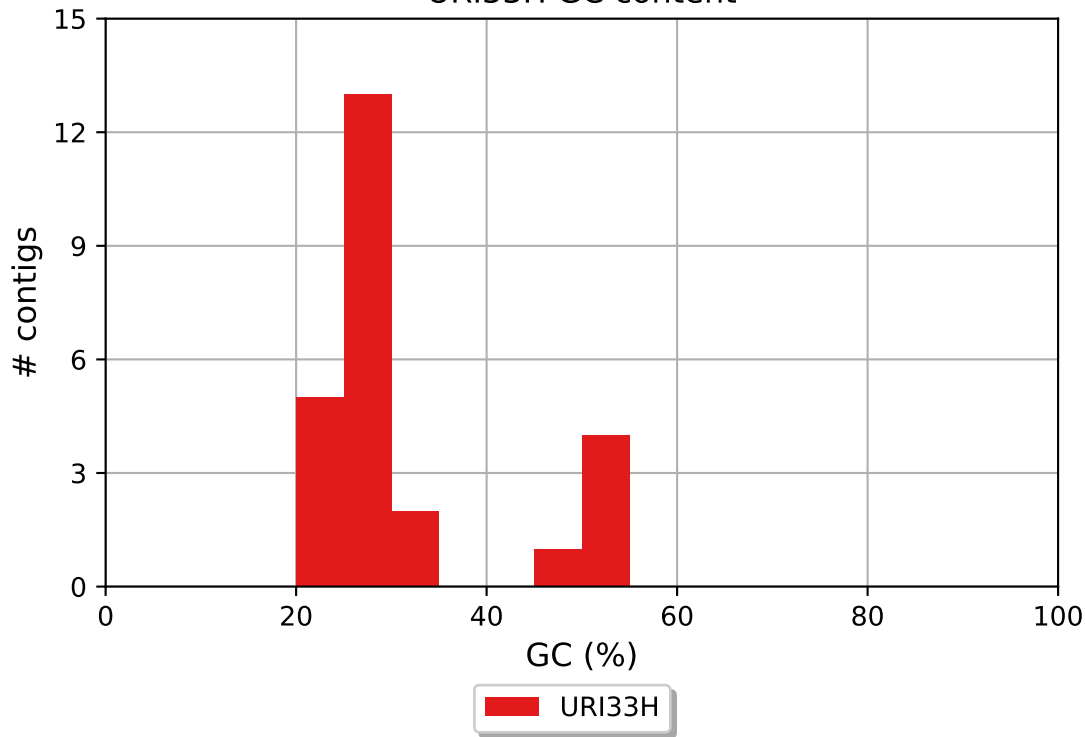
URI33H



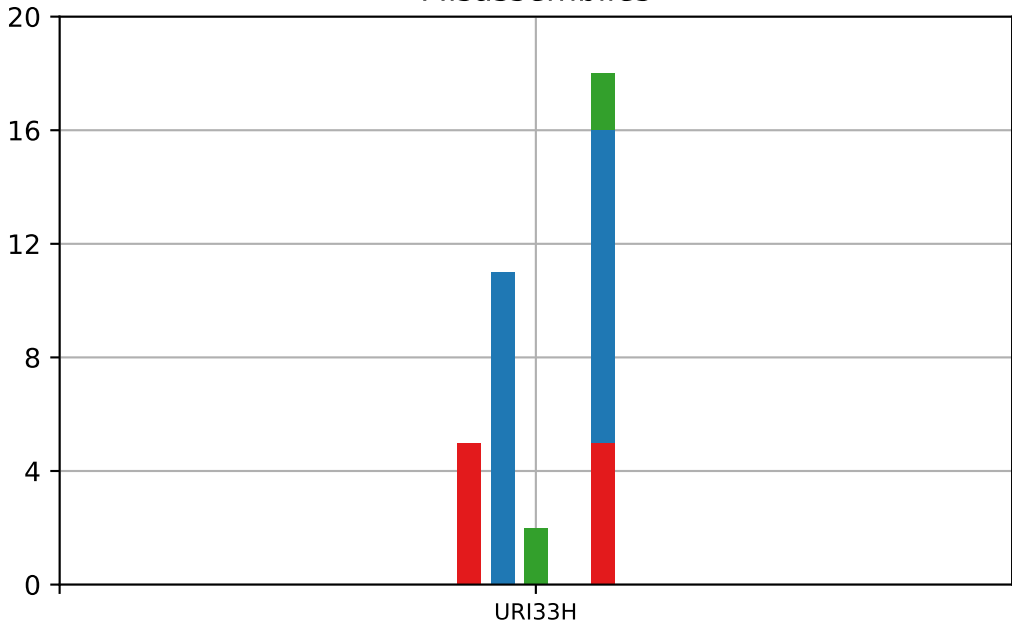
GC content



URI33H GC content



Misassemblies



relocations

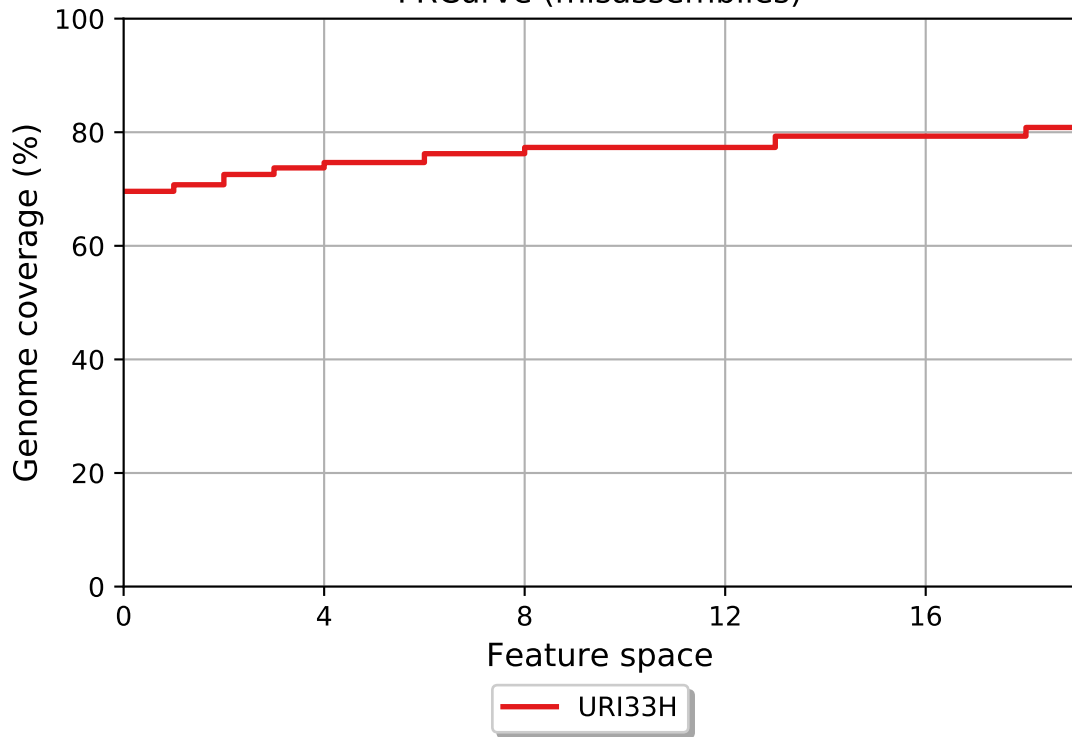


translocations

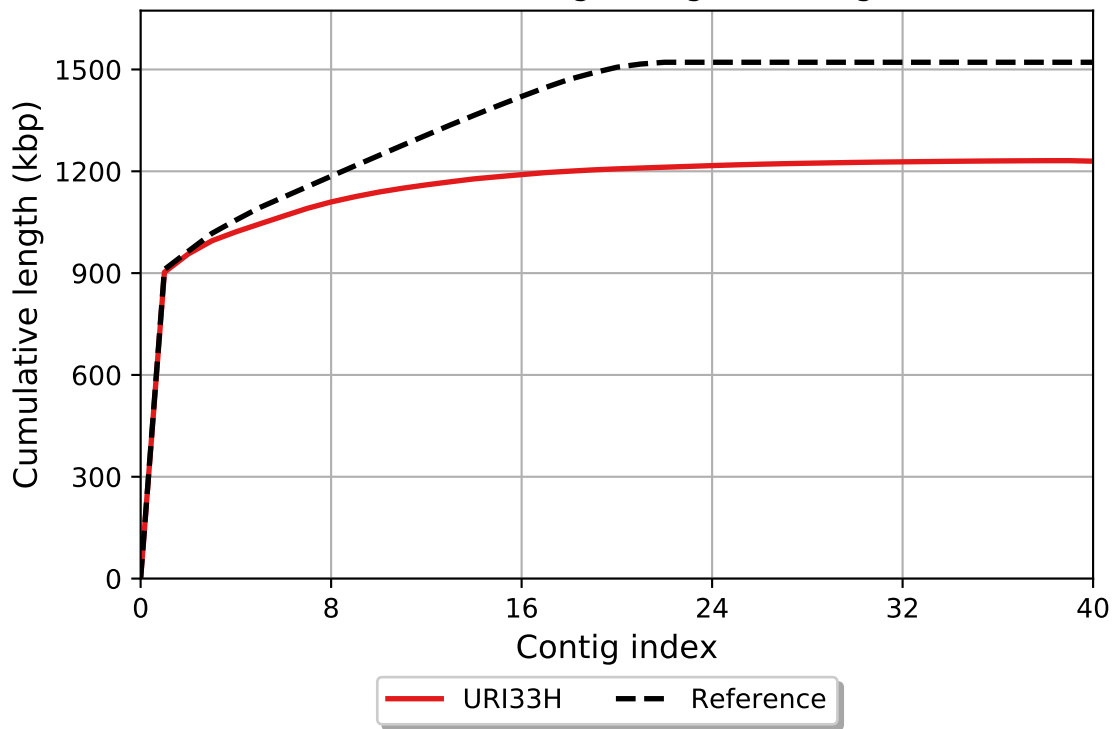


inversions

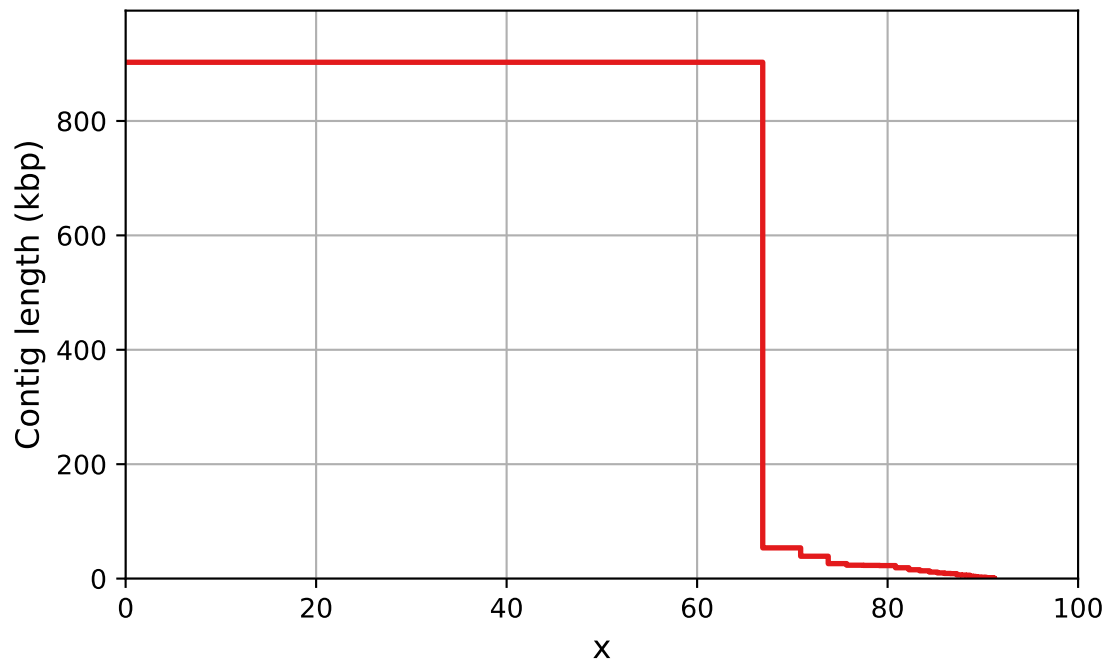
FRCurve (misassemblies)



Cumulative length (aligned contigs)

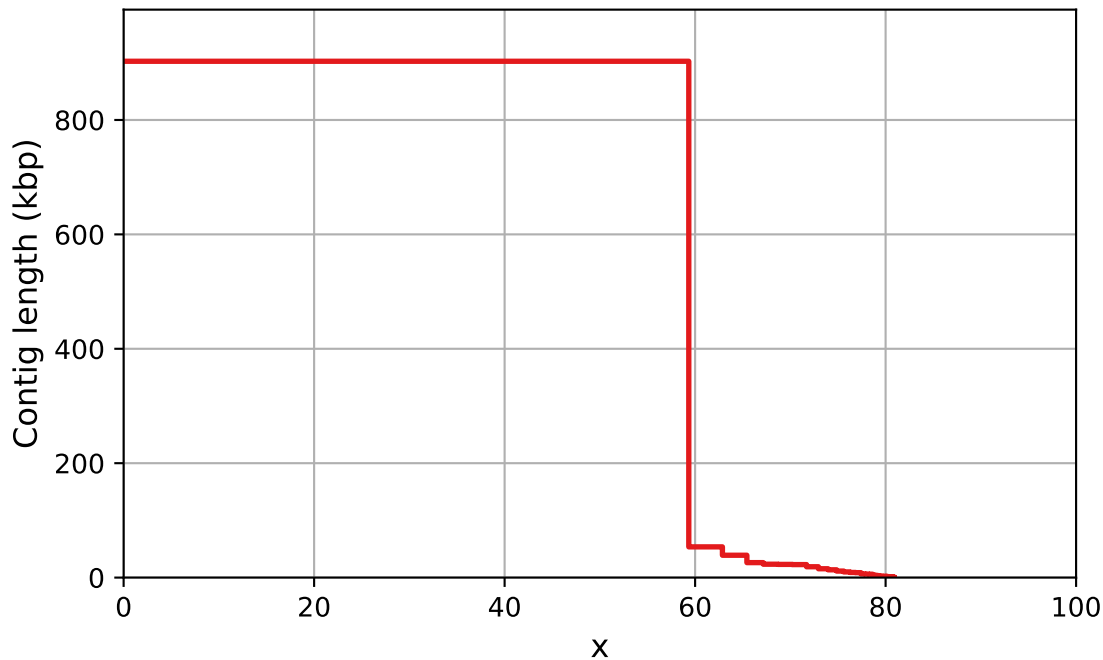


NAx



URI33H

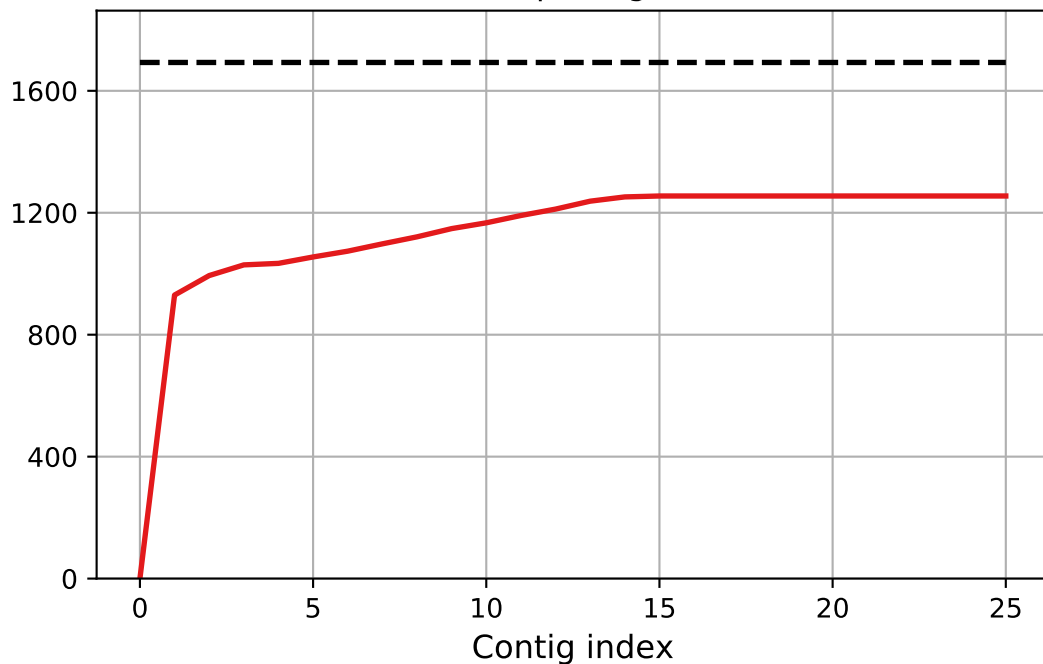
NGAx



URI33H

Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)

