

Report

	URI86H
# contigs (>= 0 bp)	88
# contigs (>= 1000 bp)	25
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1406230
Total length (>= 1000 bp)	1384893
Total length (>= 5000 bp)	1375267
Total length (>= 10000 bp)	1360659
Total length (>= 25000 bp)	1232882
Total length (>= 50000 bp)	1059318
# contigs	39
Largest contig	919077
Total length	1395149
Reference length	1521208
GC (%)	28.07
Reference GC (%)	28.18
N50	919077
NG50	919077
N90	24381
NG90	8673
auN	618587.5
auNG	567326.6
L50	1
LG50	1
L90	10
LG90	16
# misassemblies	24
# misassembled contigs	13
Misassembled contigs length	1227542
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	11 + 15 part
Unaligned length	194419
Genome fraction (%)	78.017
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	763.12
# indels per 100 kbp	43.83
# genomic features	1238 + 51 part
Largest alignment	905419
Total aligned length	1202425
NA50	905419
NGA50	905419
NA90	-
NGA90	-
auNA	591532.4
auNGA	542513.5
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

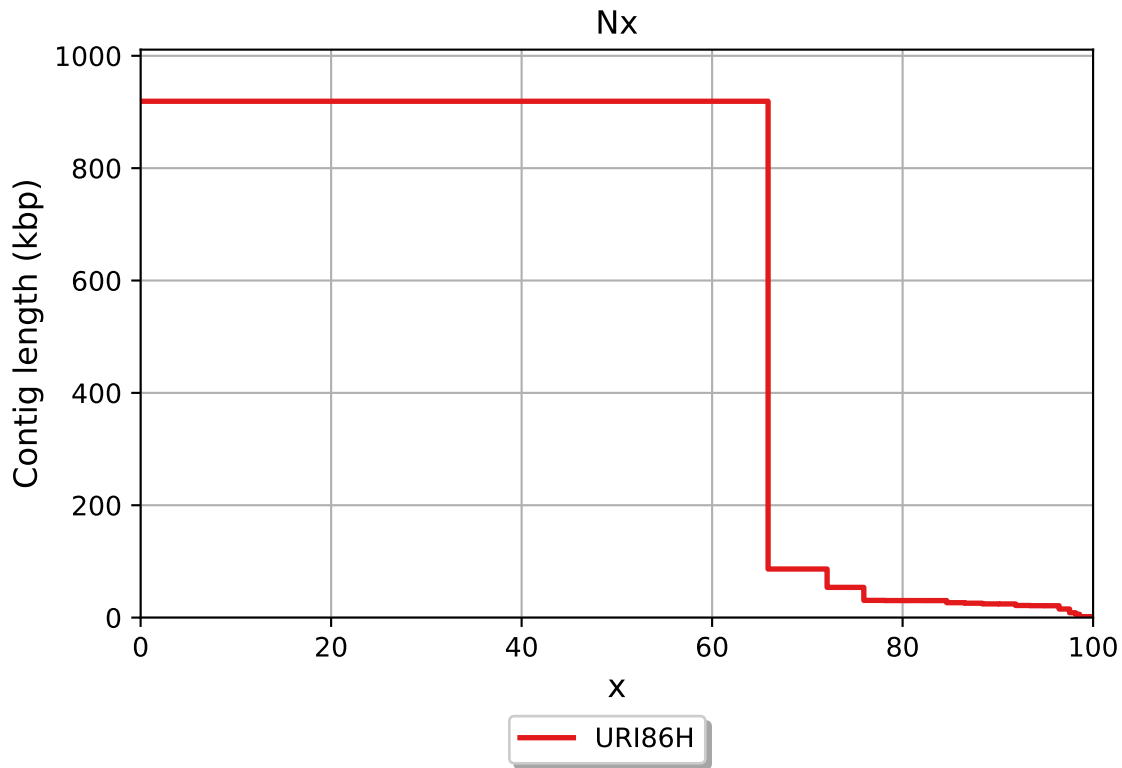
	URI86H
# misassemblies	24
# contig misassemblies	24
# c. relocations	6
# c. translocations	17
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	13
Misassembled contigs length	1227542
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	9176
# indels	527
# indels (<= 5 bp)	472
# indels (> 5 bp)	55
Indels length	3468

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).

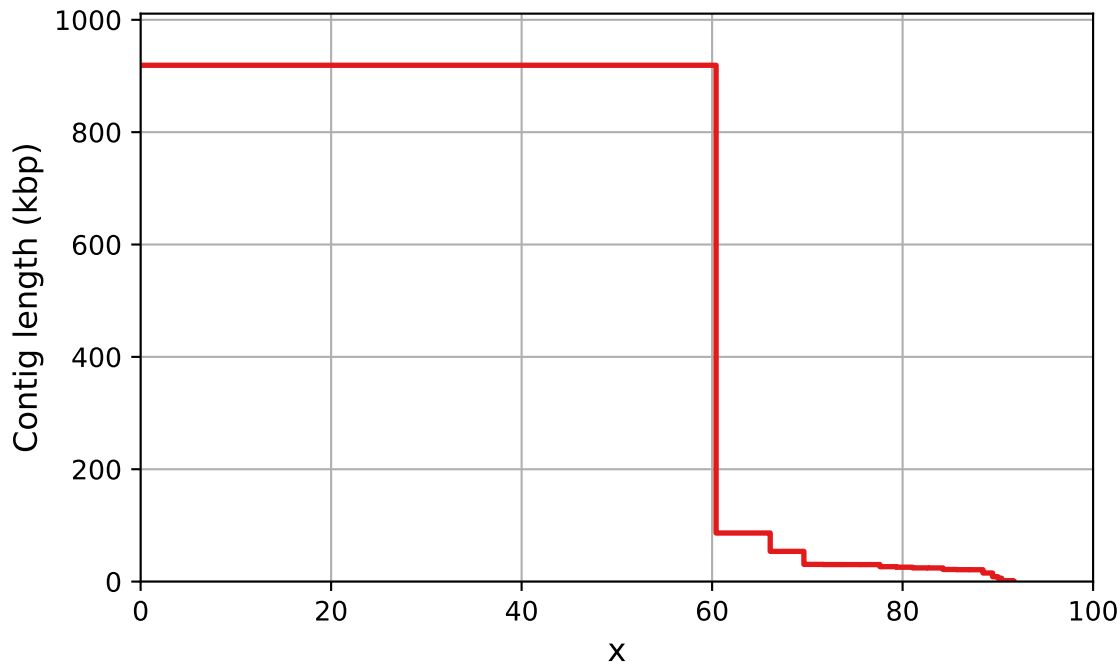
Unaligned report

	URI86H
# fully unaligned contigs	11
Fully unaligned length	15238
# partially unaligned contigs	15
Partially unaligned length	179181
# N's	0

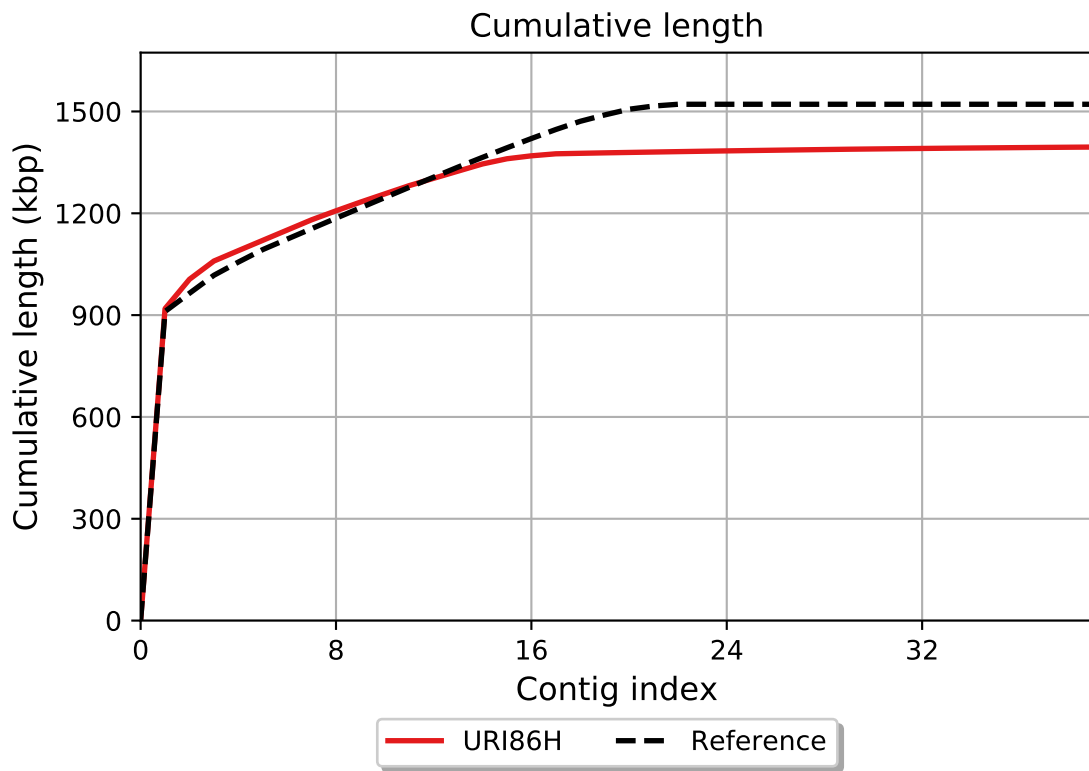
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



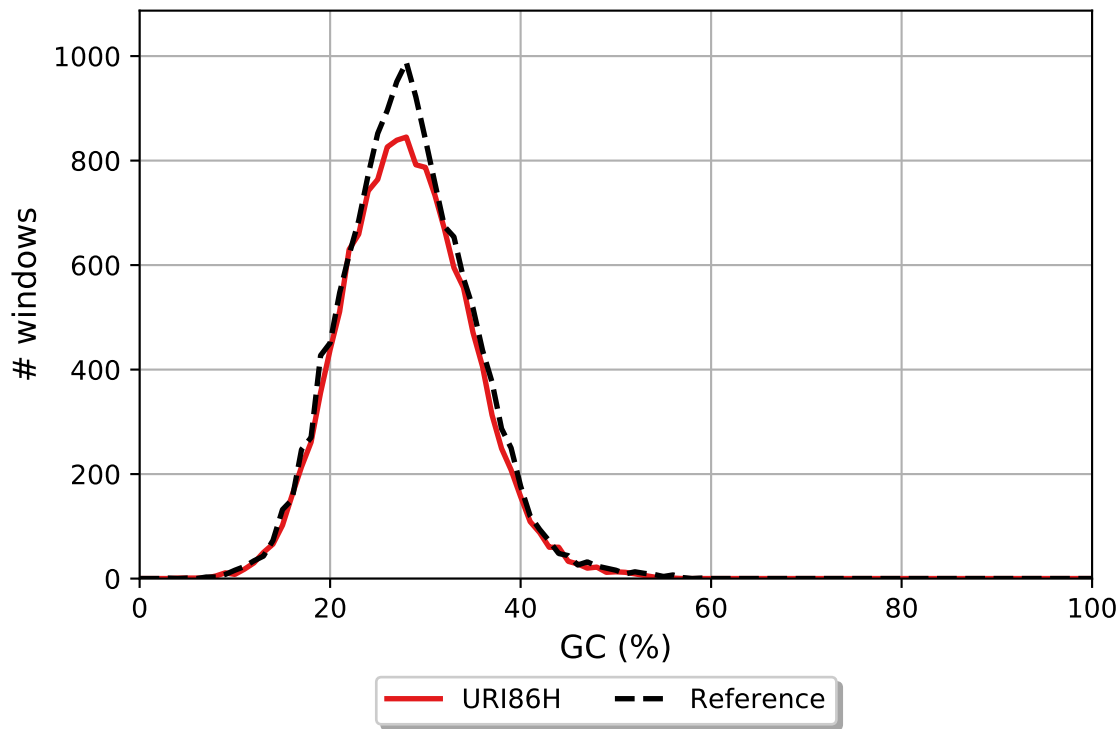
NGx



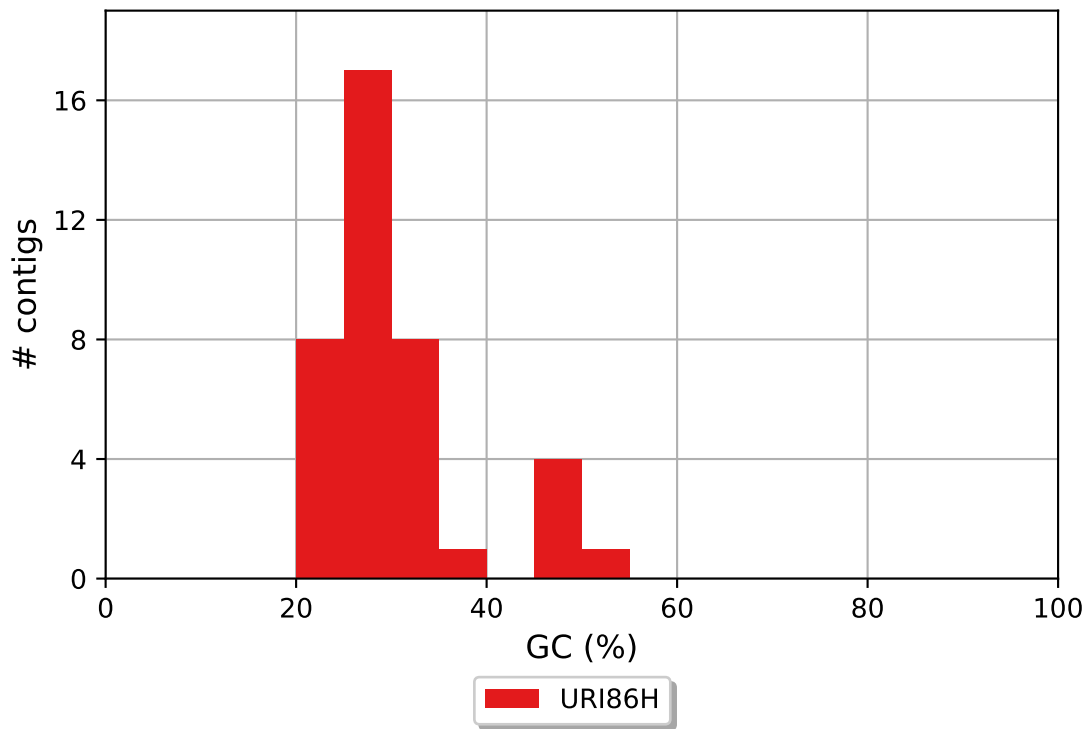
URI86H



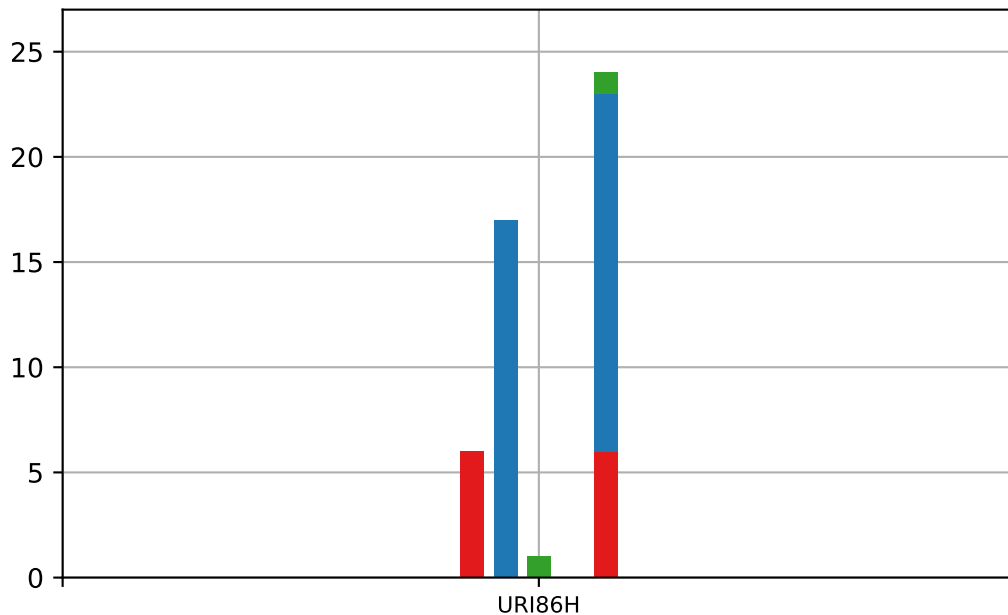
GC content



URI86H GC content



Misassemblies



relocations



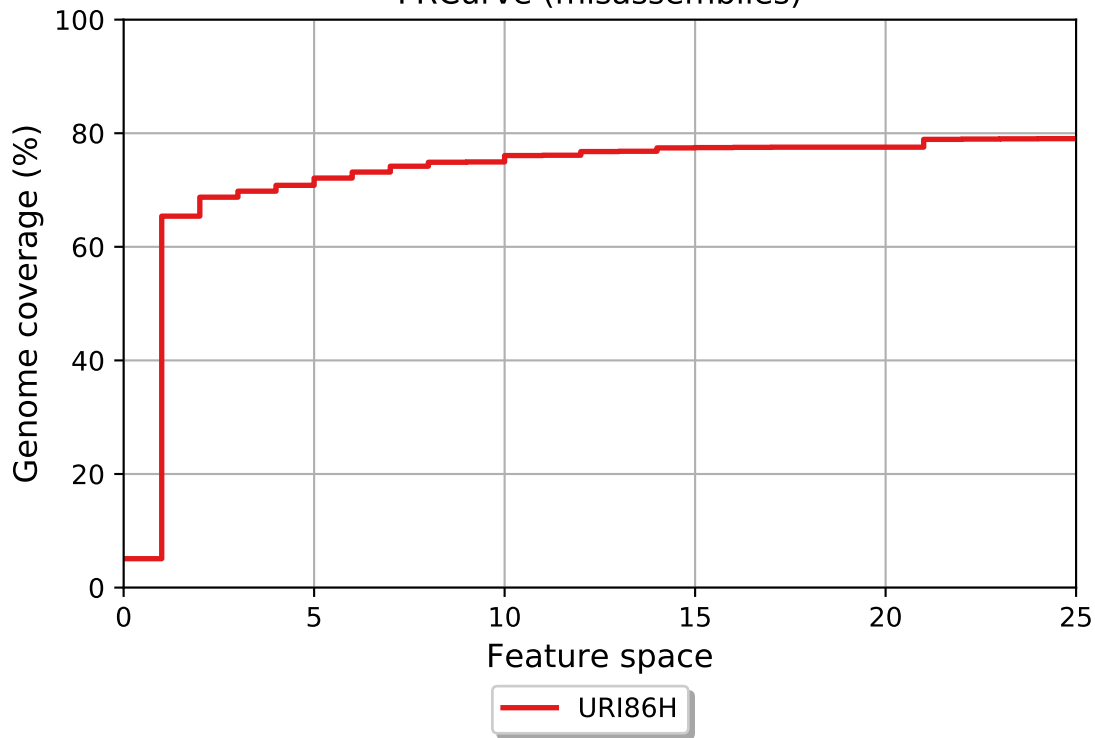
translocations



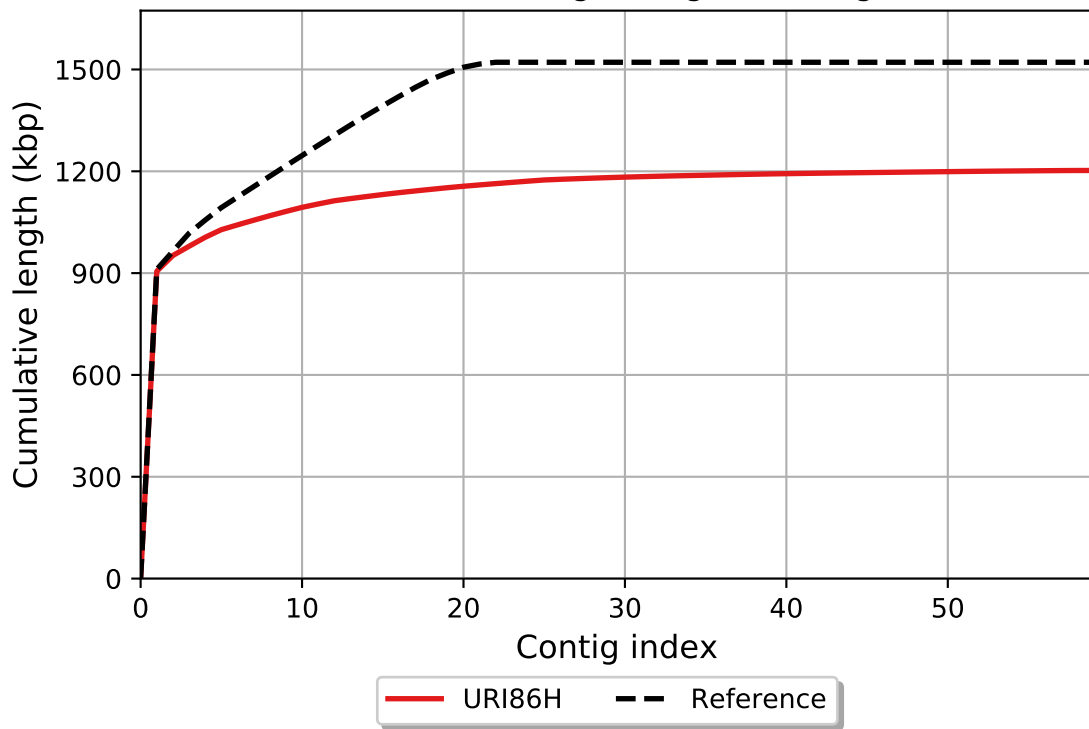
inversions



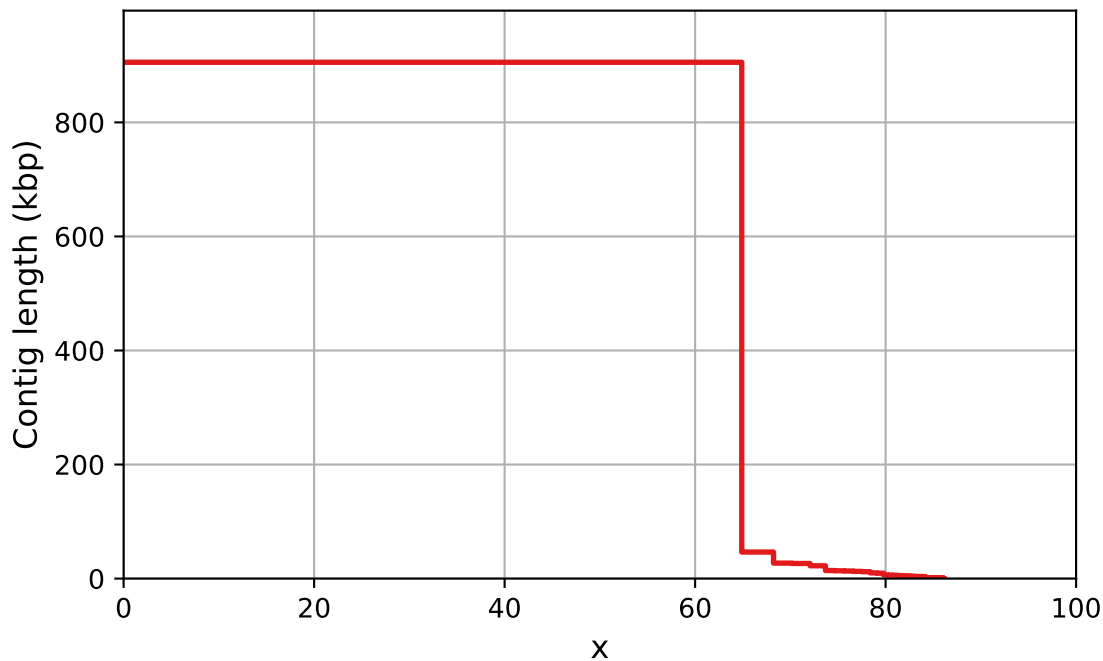
FRCurve (misassemblies)



Cumulative length (aligned contigs)

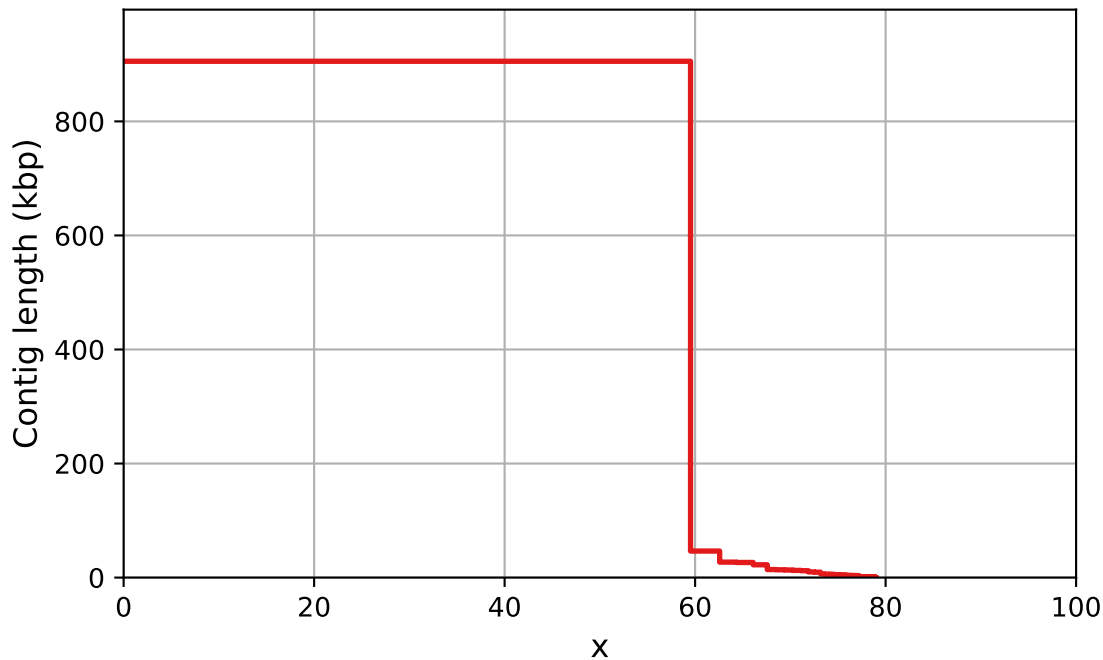


NAx

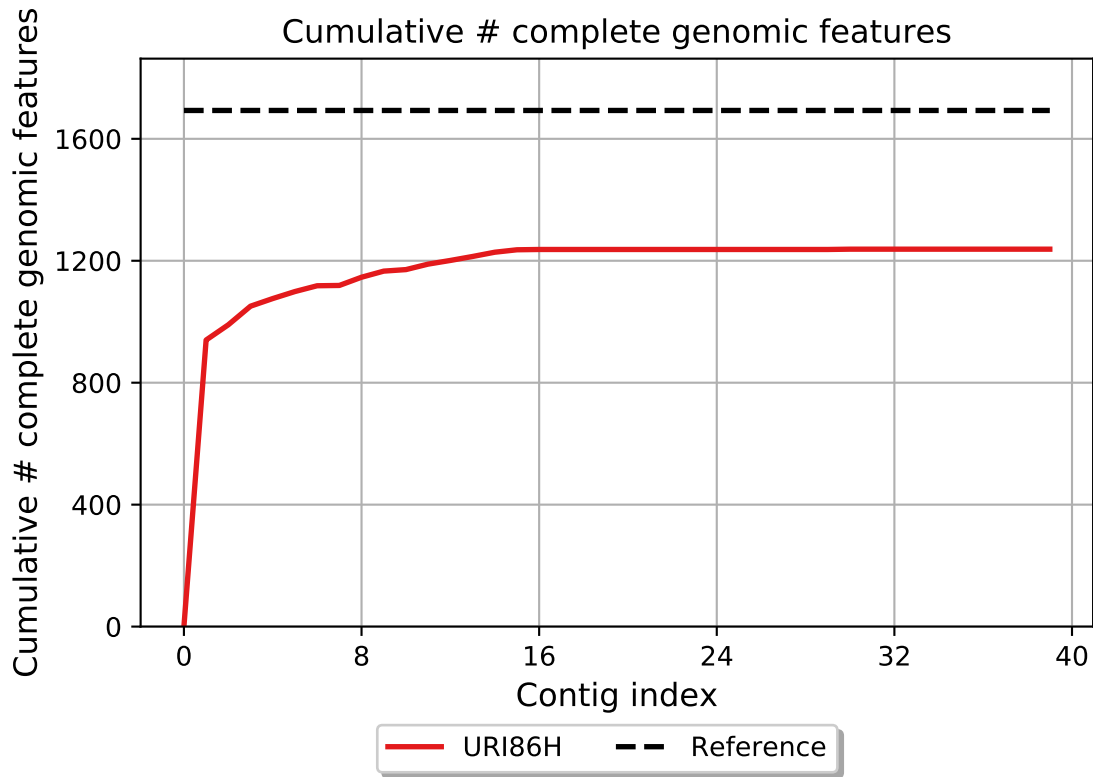


URI86H

NGAx



URI86H



FRCurve (genomic features)

