

Report

	unknown-8_fa
# contigs (>= 0 bp)	71
# contigs (>= 1000 bp)	26
Total length (>= 0 bp)	4266401
Total length (>= 1000 bp)	4256033
# contigs	30
Largest contig	1046978
Total length	4258661
Reference length	4299846
GC (%)	43.26
Reference GC (%)	43.35
N50	478305
NG50	478305
N90	66811
NG90	66811
auN	559059.5
auNG	553704.7
L50	3
LG50	3
L90	12
LG90	12
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	23182
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.849
Duplication ratio	1.002
# N's per 100 kbp	1.17
# mismatches per 100 kbp	3.27
# indels per 100 kbp	0.31
Largest alignment	1037503
Total aligned length	4249181
NA50	478305
NGA50	478305
NA90	66811
NGA90	66811
auNA	554360.1
auNGA	549050.3
LA50	3
LGA50	3
LA90	12
LGA90	12

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

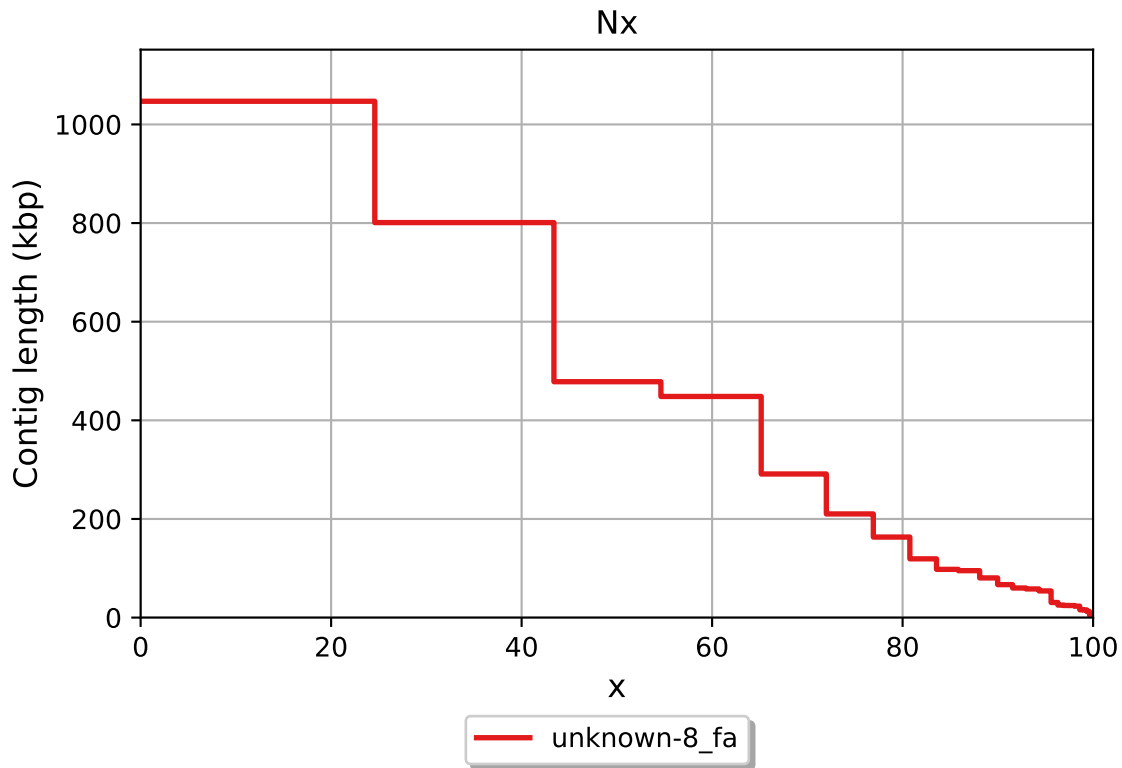
	unknown-8_fa
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	23182
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	139
# indels	13
# indels (<= 5 bp)	10
# indels (> 5 bp)	3
Indels length	215

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).

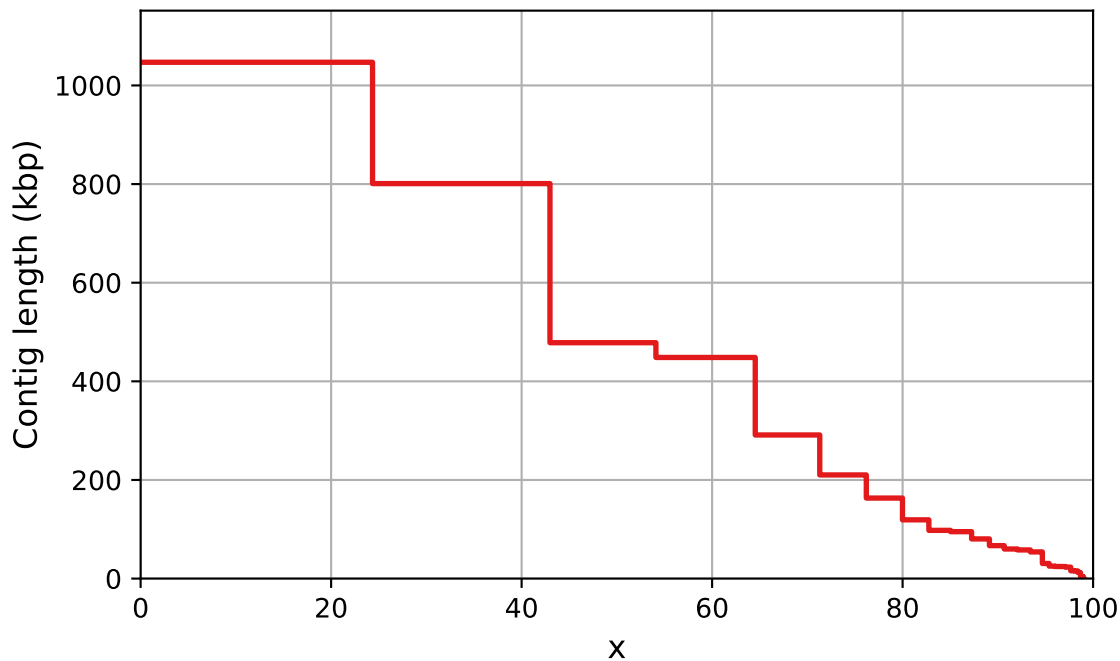
Unaligned report

	unknown-8_fa
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	50

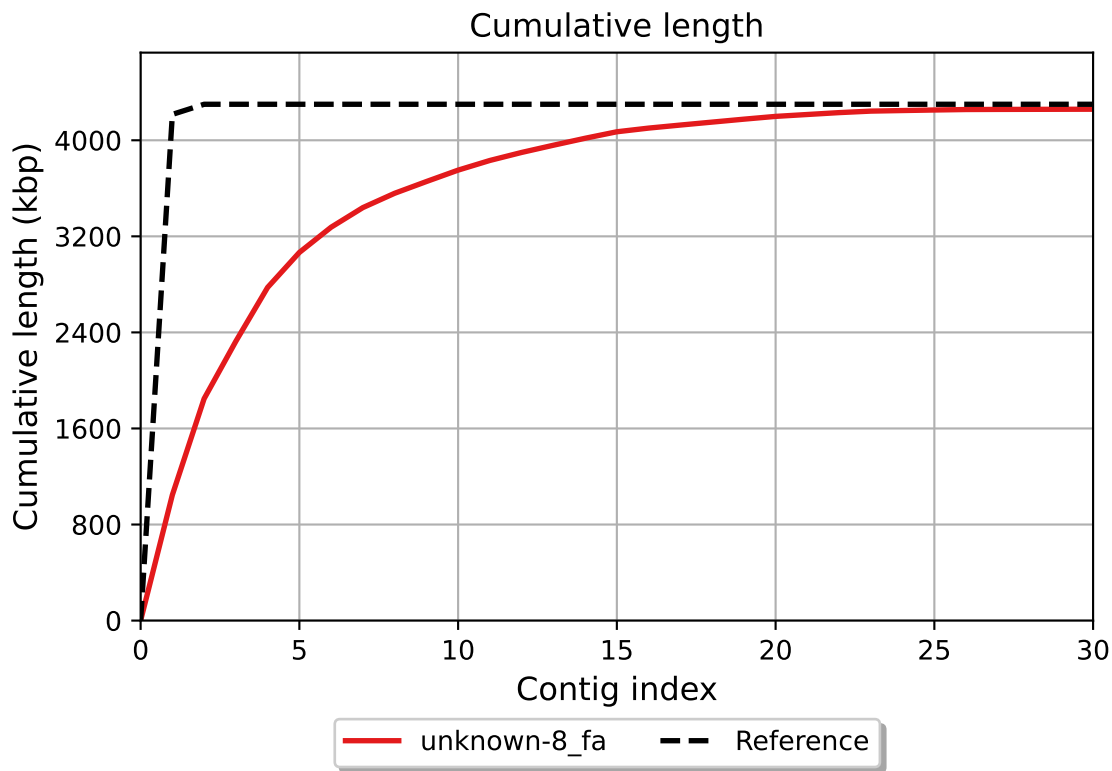
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



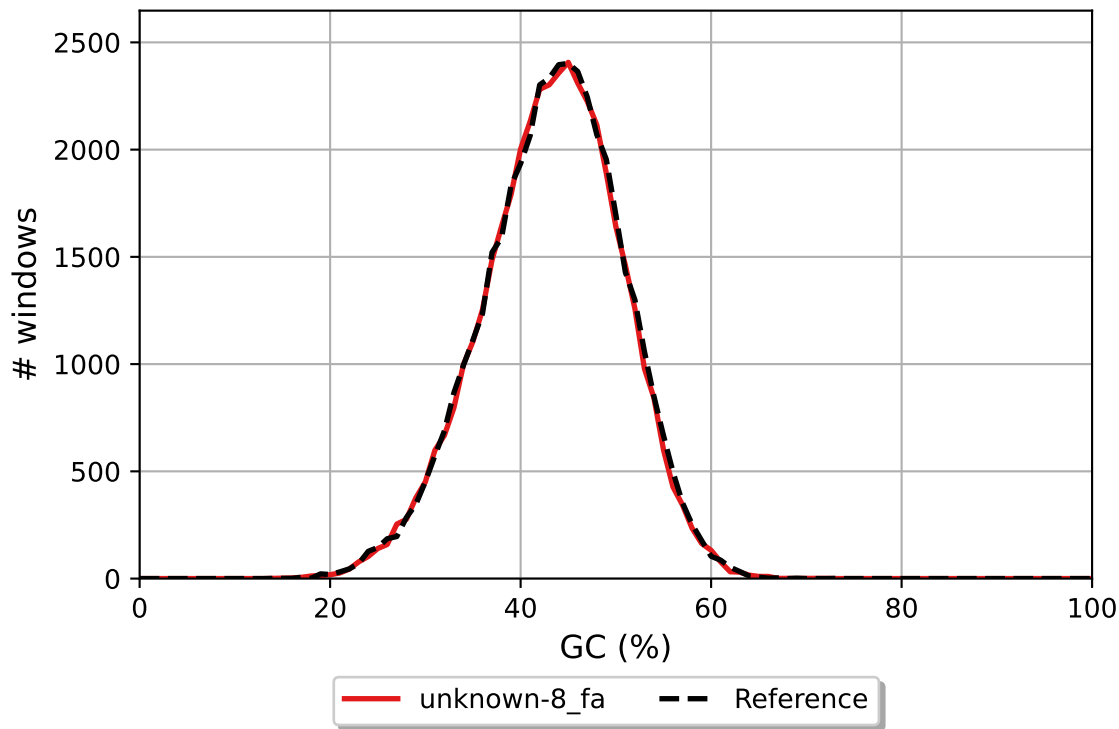
NGx



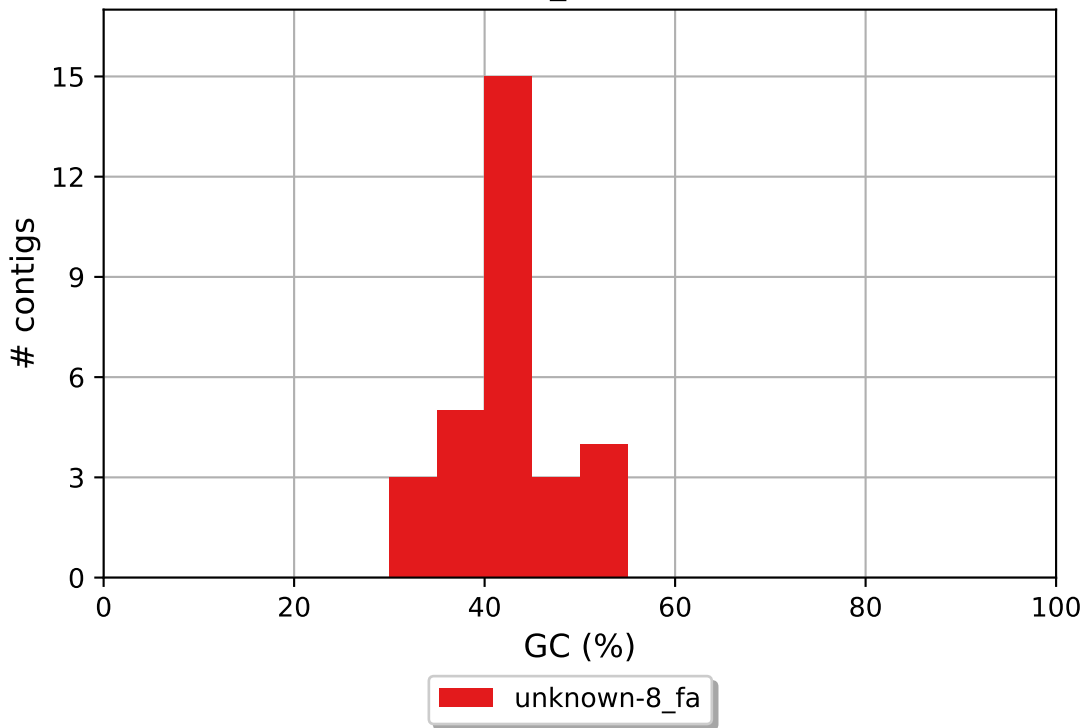
unknown-8_fa



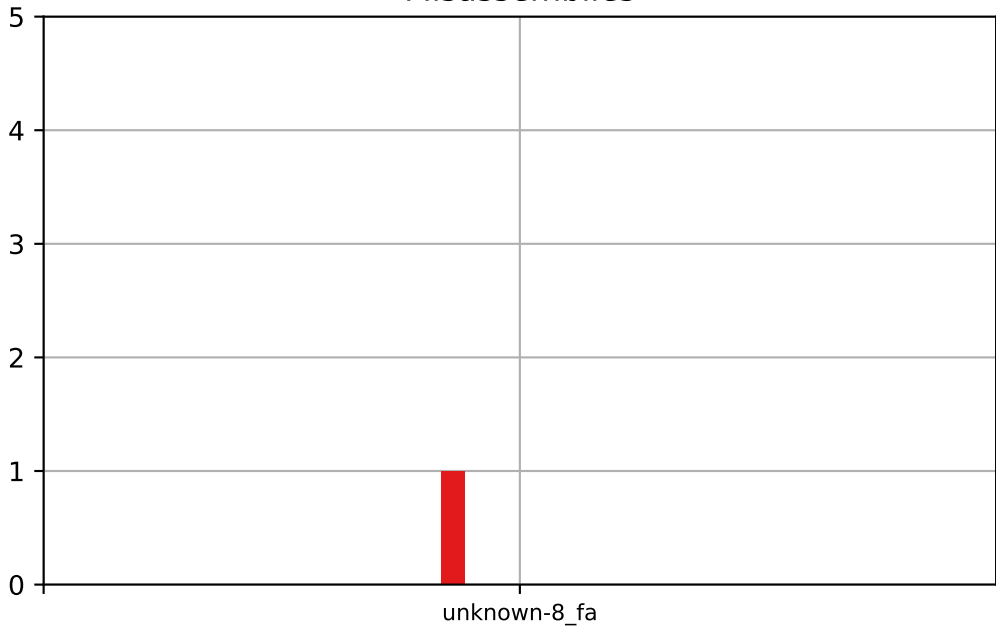
GC content



unknown-8_fa GC content

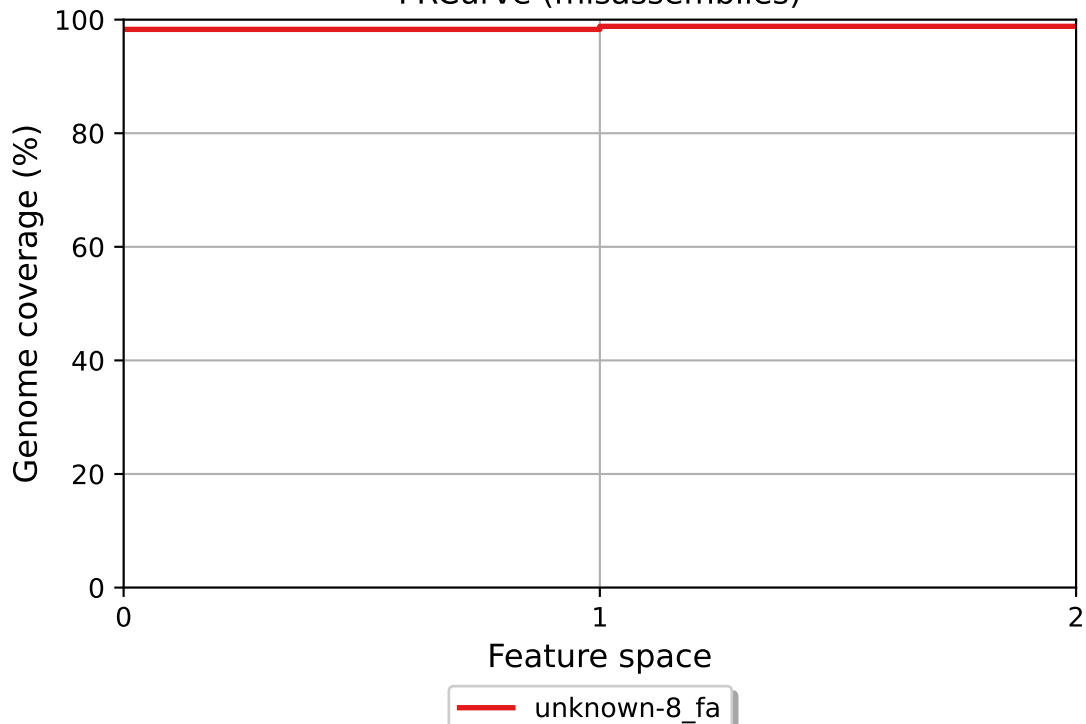


Misassemblies

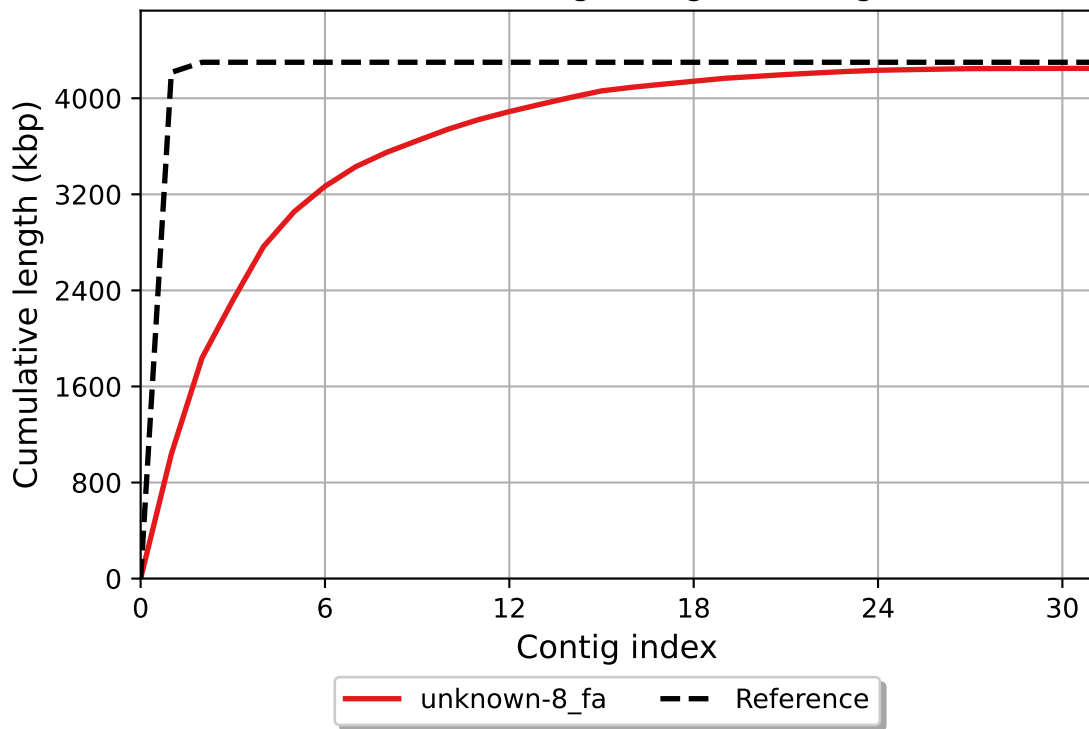


 # relocations

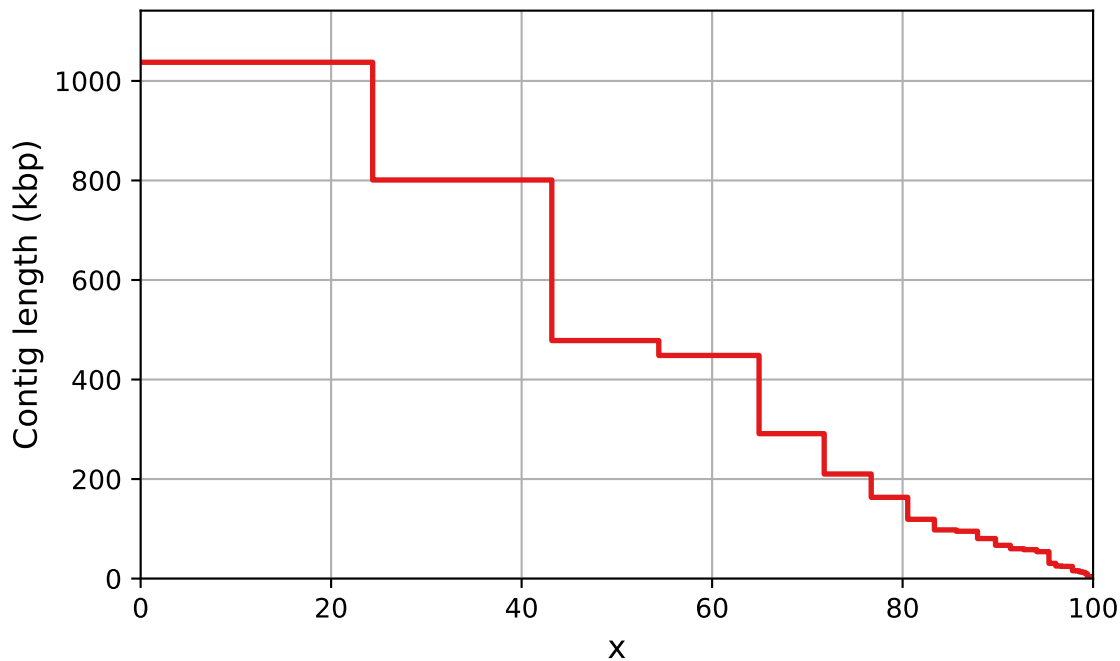
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



unknown-8_fa

NGAx

