

Report

	ragtag.scaffold
# contigs (>= 0 bp)	8406
# contigs (>= 1000 bp)	8406
# contigs (>= 5000 bp)	8402
# contigs (>= 10000 bp)	8365
# contigs (>= 25000 bp)	7053
# contigs (>= 50000 bp)	5021
Total length (>= 0 bp)	1956768660
Total length (>= 1000 bp)	1956768660
Total length (>= 5000 bp)	1956752784
Total length (>= 10000 bp)	1956451036
Total length (>= 25000 bp)	1931022642
Total length (>= 50000 bp)	1859913411
# contigs	8406
Largest contig	38394480
Total length	1956768660
Reference length	1679081592
GC (%)	38.57
Reference GC (%)	38.48
N50	1082552
NG50	12217325
N90	88275
NG90	192111
auN	11586977.9
auNG	13503236.2
L50	56
LG50	36
L90	3559
LG90	1673
# misassemblies	221905
# misassembled contigs	7236
Misassembled contigs length	1901085660
# local misassemblies	77292
# scaffold gap ext. mis.	687
# scaffold gap loc. mis.	219
# unaligned mis. contigs	555
# unaligned contigs	4 + 6880 part
Unaligned length	265787451
Genome fraction (%)	59.243
Duplication ratio	1.680
# N's per 100 kbp	29.74
# mismatches per 100 kbp	1112.46
# indels per 100 kbp	198.57
Largest alignment	1034948
Total aligned length	1650057798
NA50	14294
NGA50	18641
NA90	-
NGA90	2948
auNA	45081.0
auNGA	52536.5
LA50	27277
LGA50	18748
LA90	-
LGA90	105614

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

	ragtag.scaffold
# misassemblies	221905
# contig misassemblies	217051
# c. relocations	29422
# c. translocations	187098
# c. inversions	531
# scaffold misassemblies	4854
# s. relocations	1911
# s. translocations	2942
# s. inversions	1
# misassembled contigs	7236
Misassembled contigs length	1901085660
# local misassemblies	77292
# scaffold gap ext. mis.	687
# scaffold gap loc. mis.	219
# unaligned mis. contigs	555
# mismatches	18356240
# indels	3276499
# indels (<= 5 bp)	2534899
# indels (> 5 bp)	741600
Indels length	25787477

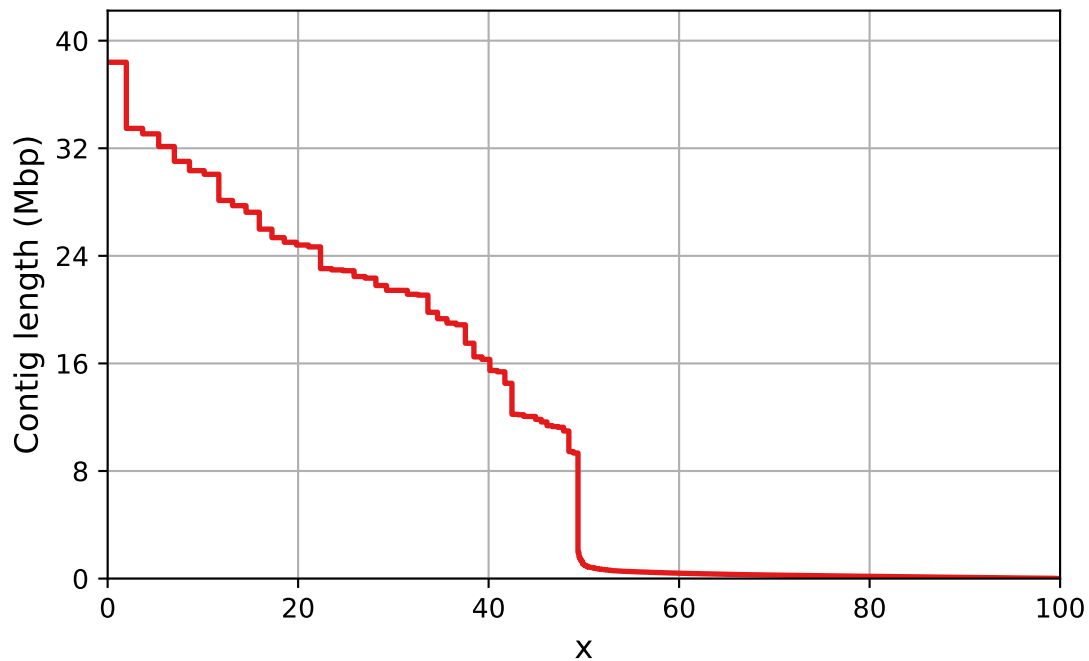
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	ragtag.scaffold
# fully unaligned contigs	4
Fully unaligned length	97228
# partially unaligned contigs	6880
Partially unaligned length	265690223
# N's	582000

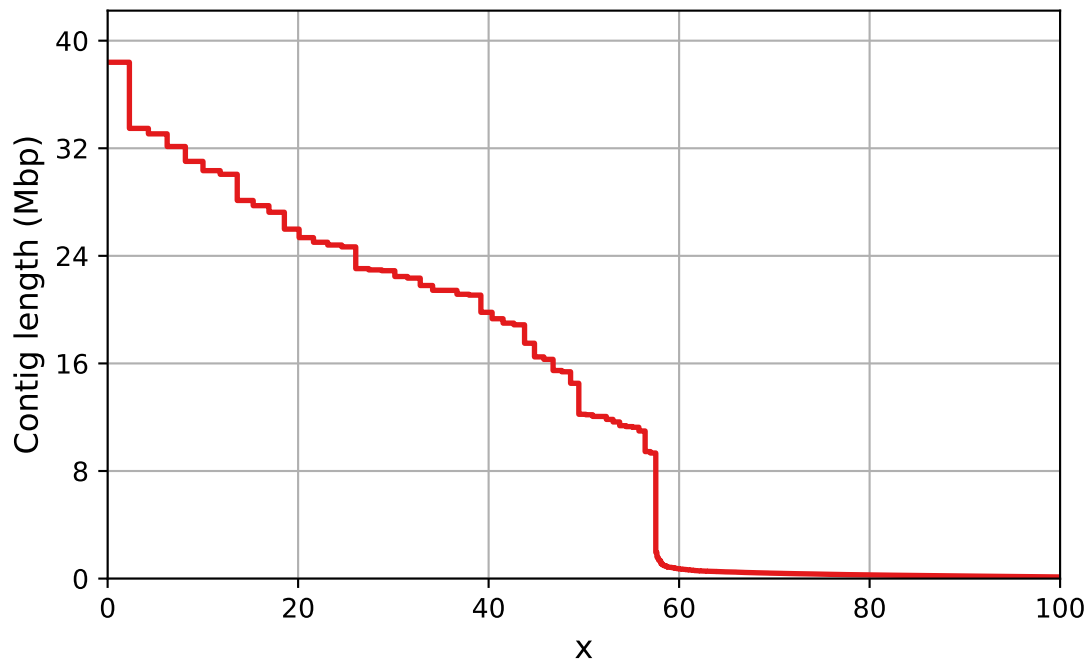
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

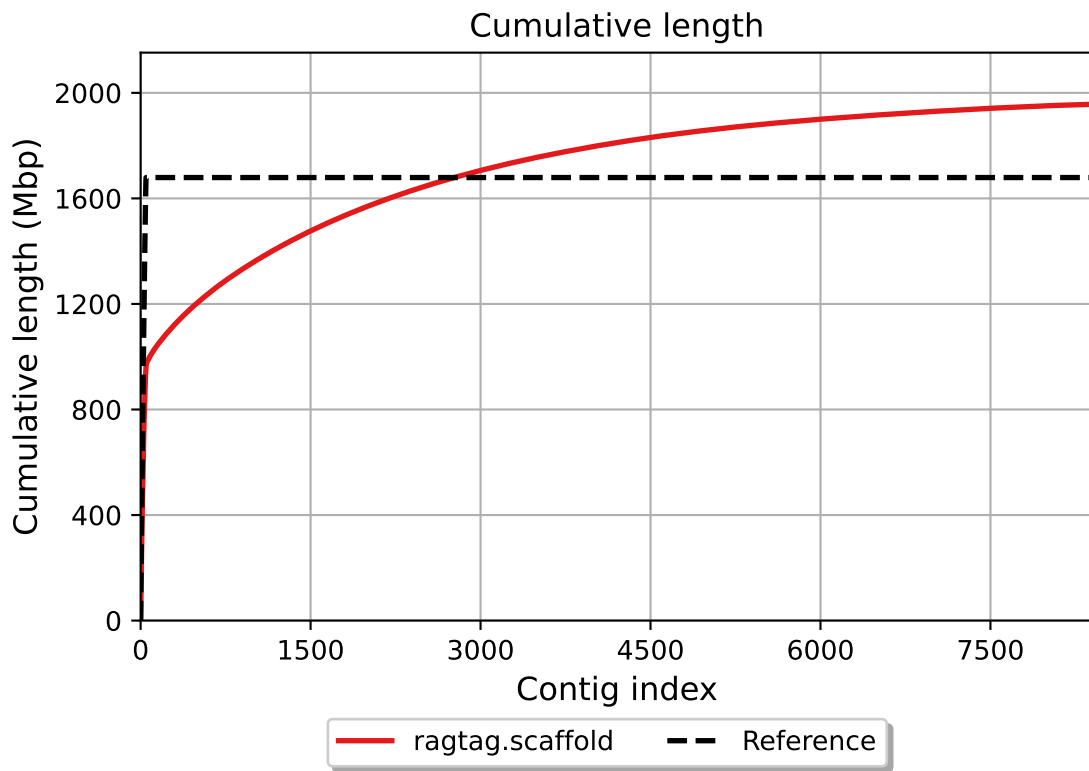


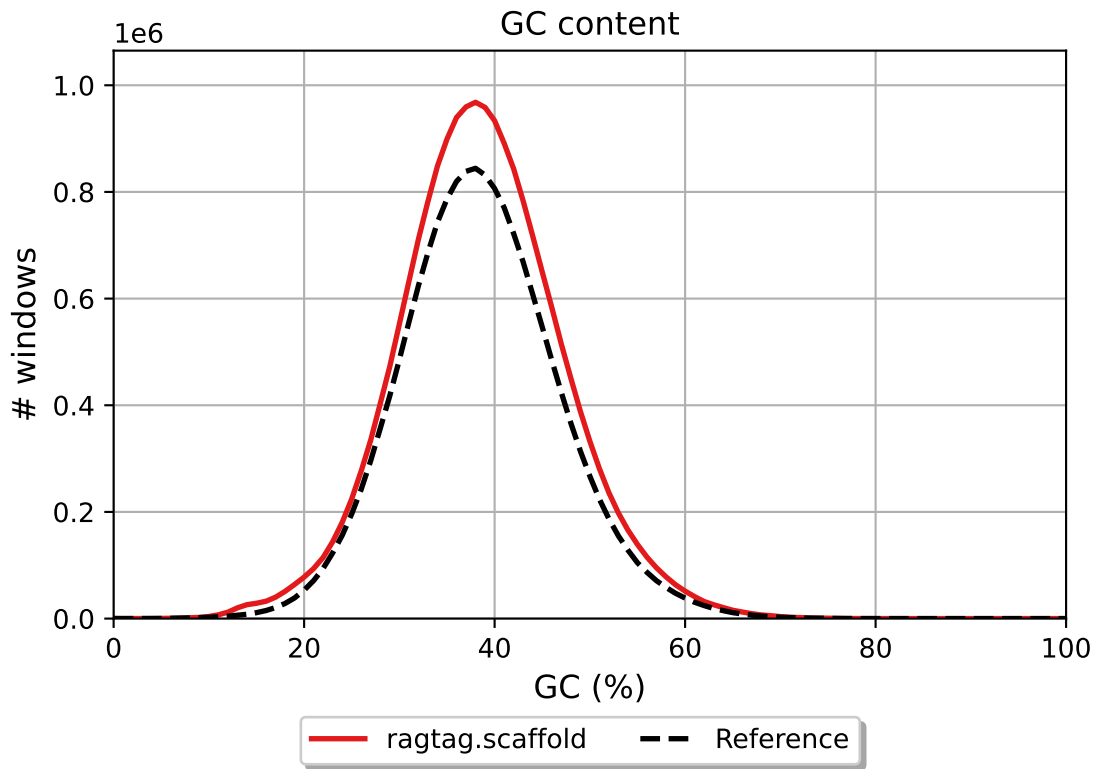
ragtag.scaffold

NGx

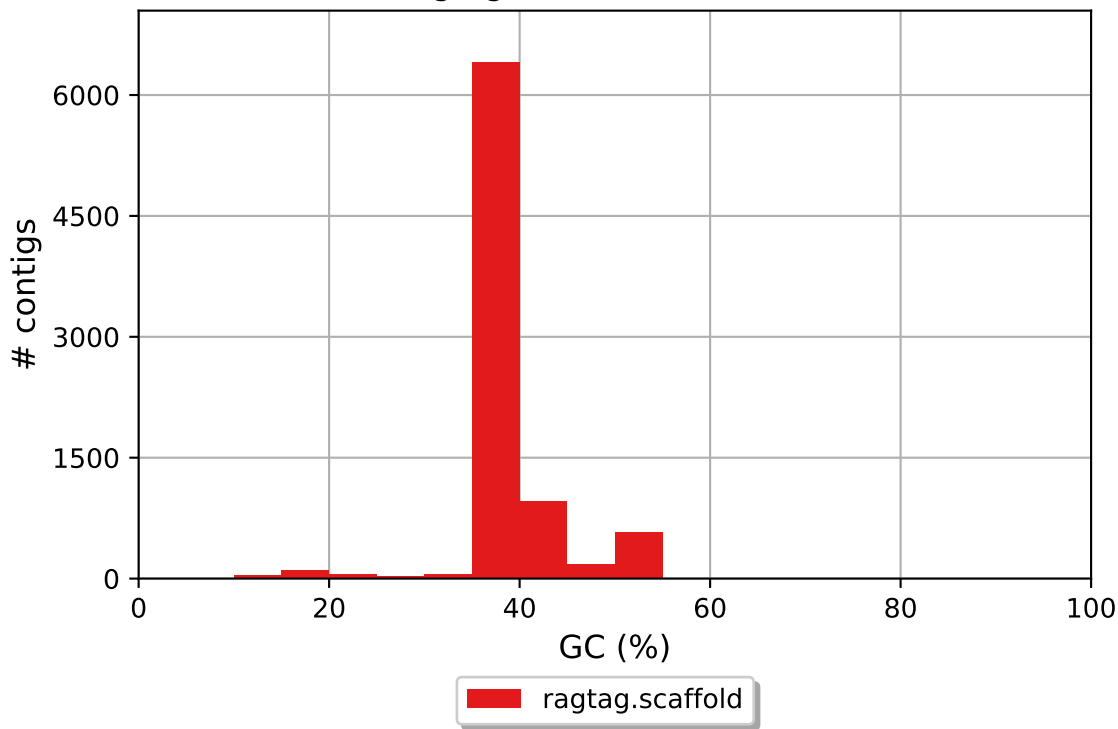


ragtag.scaffold

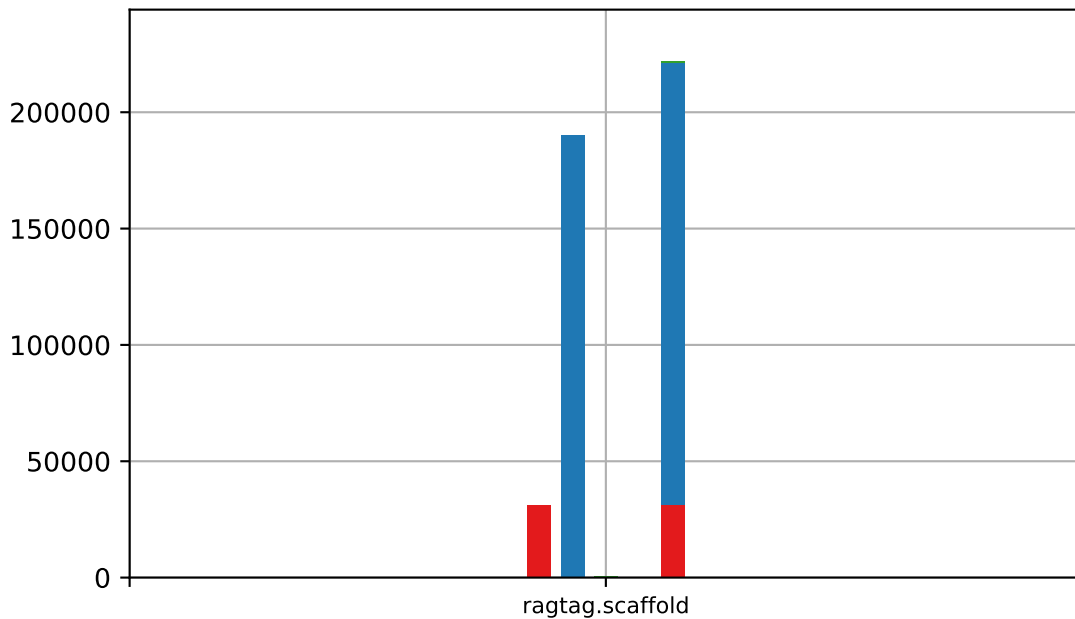




ragtag.scaffold GC content



Misassemblies



relocations

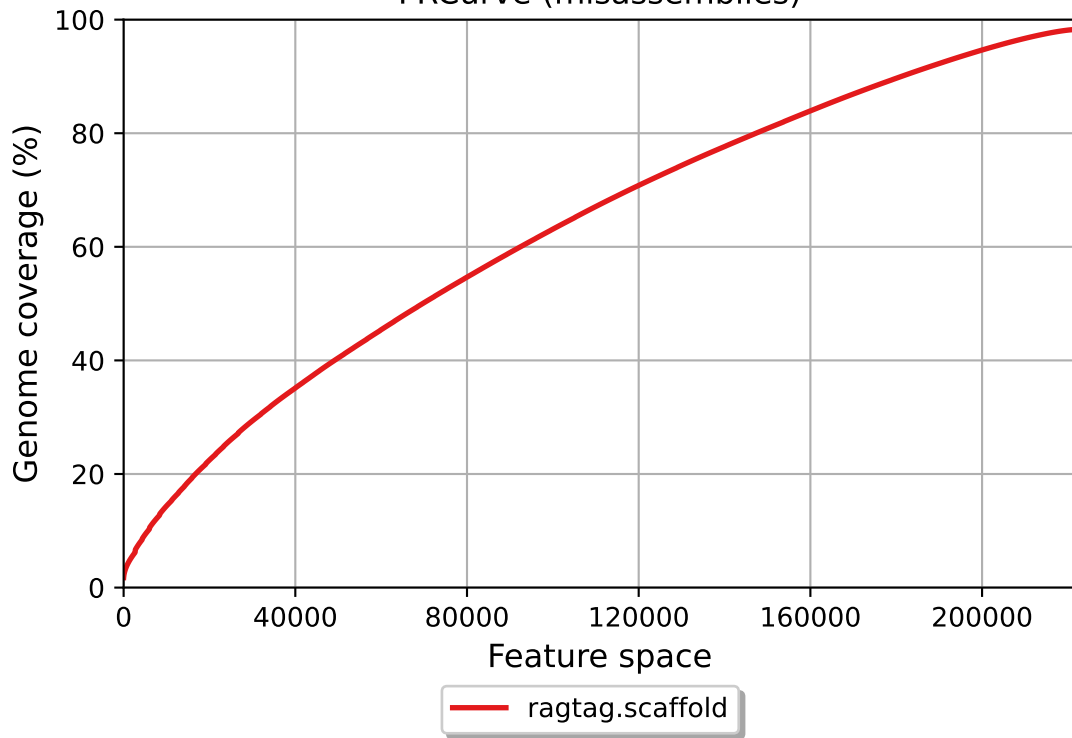


translocations

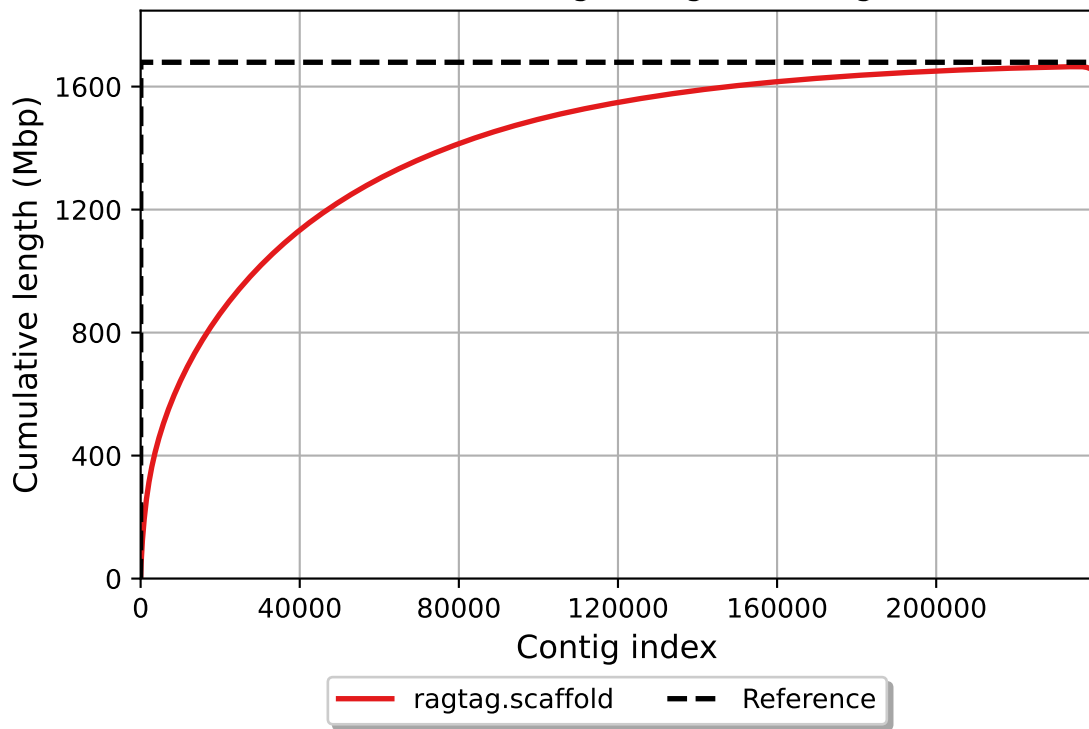


inversions

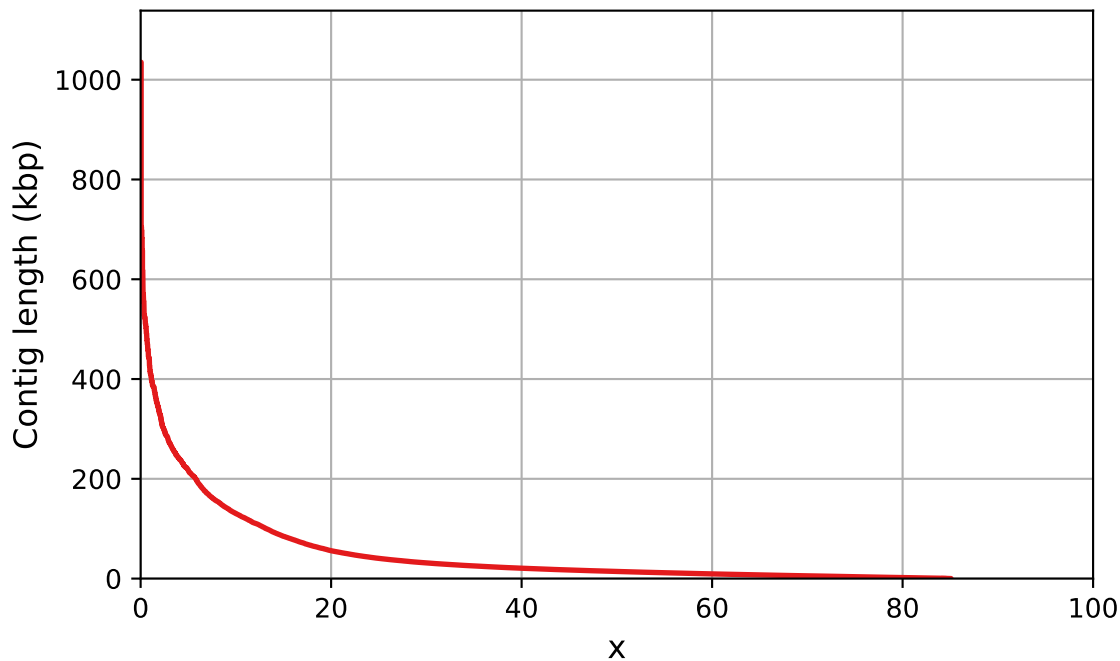
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



ragtag.scaffold

NGAx

