

Report

	RagTag_Flye
# contigs (>= 0 bp)	11
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	8
Total length (>= 0 bp)	34875698
Total length (>= 1000 bp)	34875698
Total length (>= 5000 bp)	34871541
Total length (>= 10000 bp)	34871541
Total length (>= 25000 bp)	34871541
Total length (>= 50000 bp)	34792138
# contigs	11
Largest contig	12202900
Total length	34875698
Reference length	34204973
GC (%)	22.73
Reference GC (%)	22.44
N50	8062995
NG50	8062995
N90	4041305
NG90	4041305
auN	8120809.9
auNG	8280050.8
L50	2
LG50	2
L90	5
LG90	5
# misassemblies	675
# misassembled contigs	9
Misassembled contigs length	34816006
# local misassemblies	165
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 9 part
Unaligned length	424840
Genome fraction (%)	97.158
Duplication ratio	1.036
# N's per 100 kbp	1.43
# mismatches per 100 kbp	142.23
# indels per 100 kbp	211.18
Largest alignment	1455203
Total aligned length	34390152
NA50	404377
NGA50	405183
NA90	78836
NGA90	94458
auNA	476707.3
auNGA	486055.0
LA50	27
LGA50	26
LA90	94
LGA90	87

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_Flye
# misassemblies	675
# contig misassemblies	672
# c. relocations	276
# c. translocations	384
# c. inversions	12
# scaffold misassemblies	3
# s. relocations	2
# s. translocations	1
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	34816006
# local misassemblies	165
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	48913
# indels	72624
# indels (<= 5 bp)	68542
# indels (> 5 bp)	4082
Indels length	168977

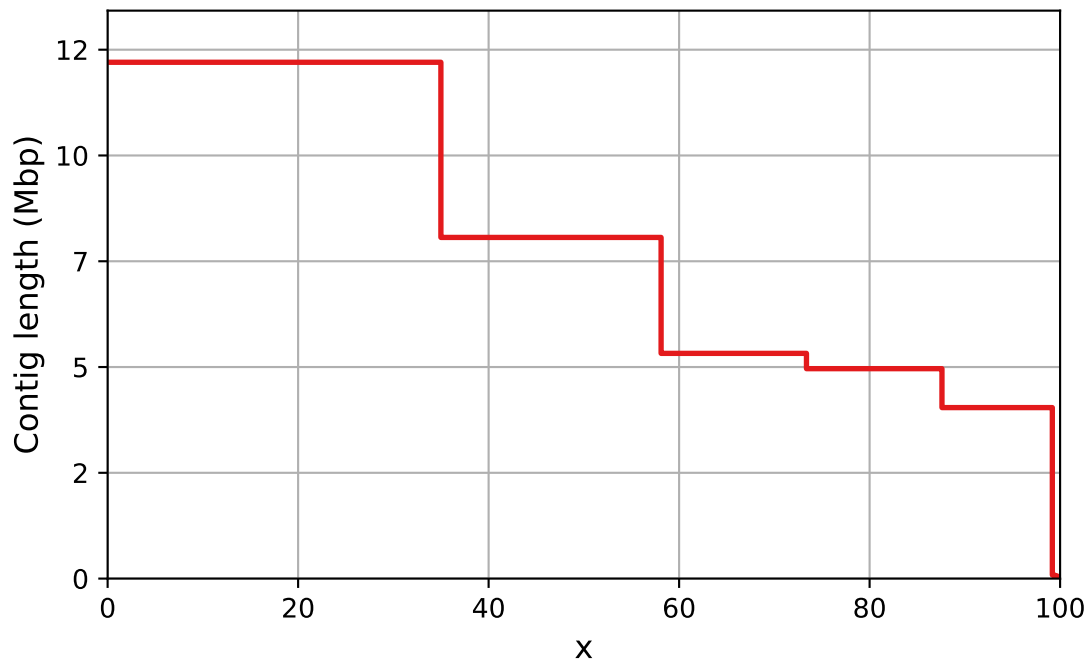
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	RagTag_Flye
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	9
Partially unaligned length	424840
# N's	500

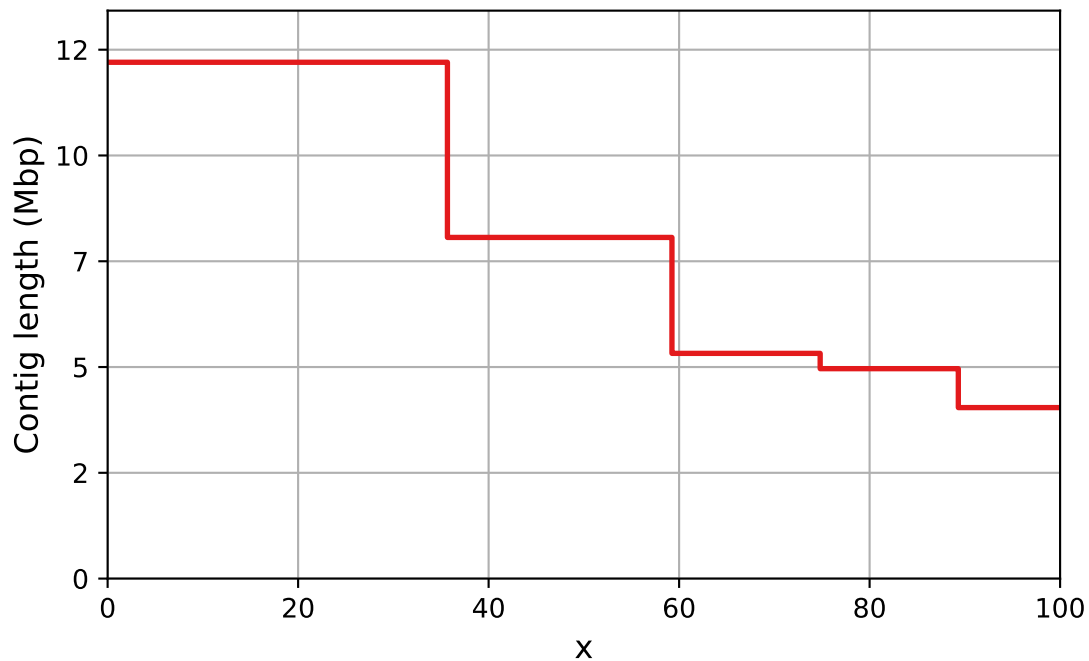
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



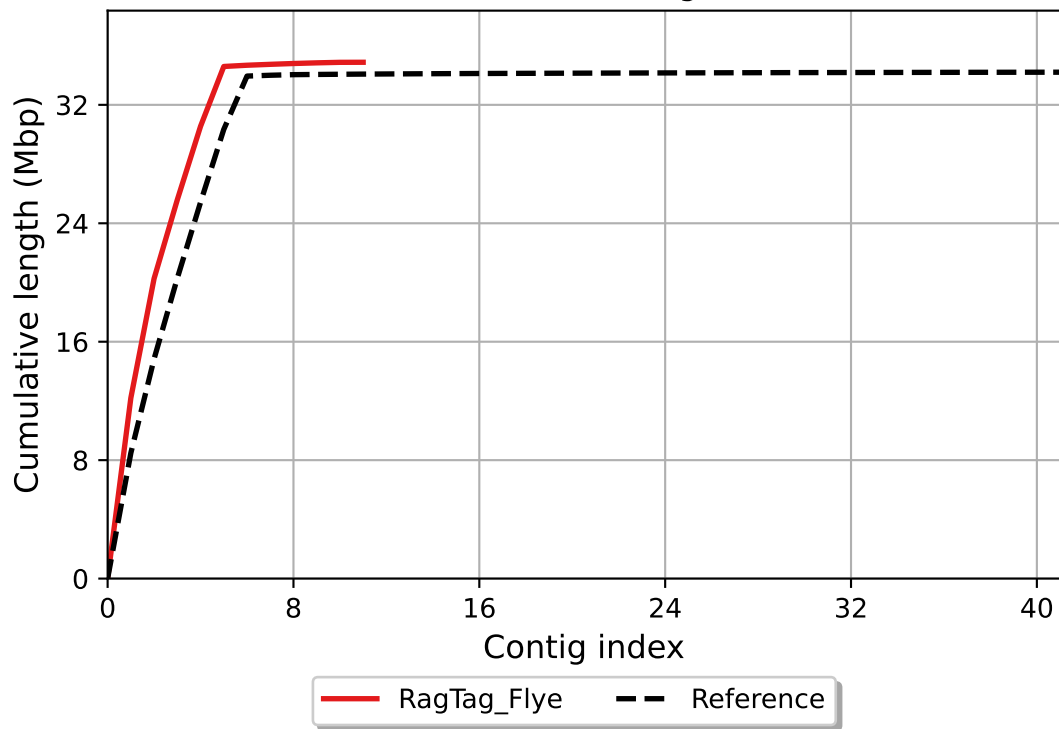
RagTag\_Flye

NGx

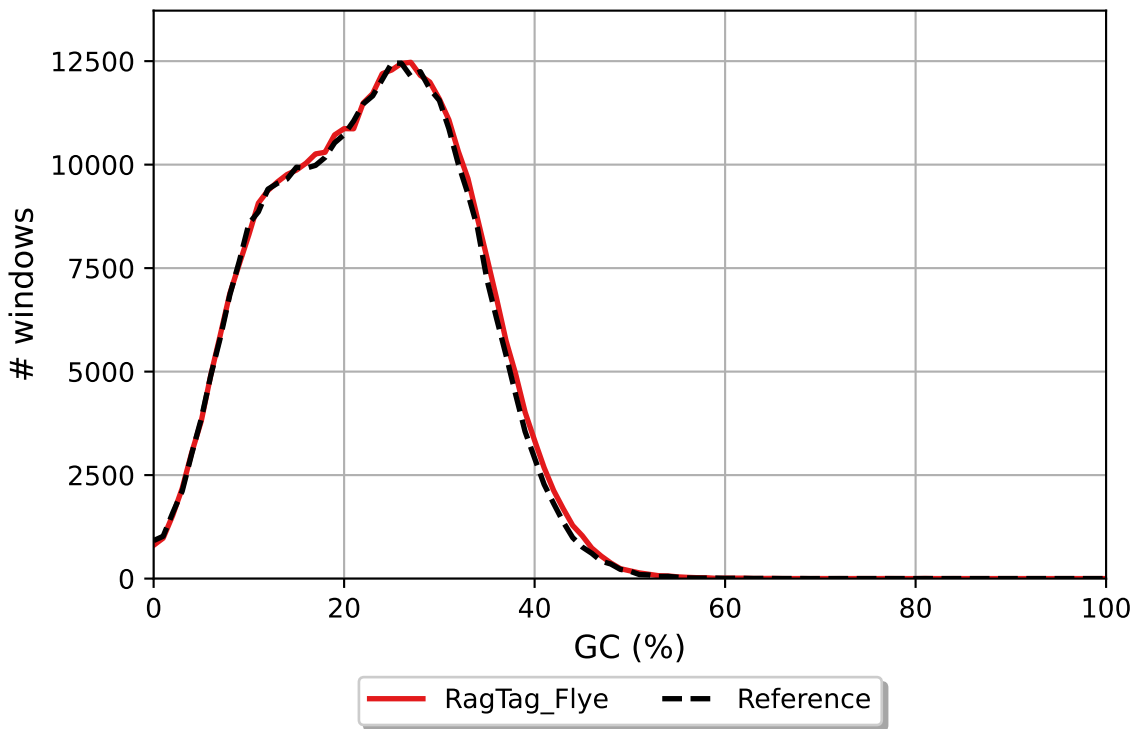


RagTag\_Flye

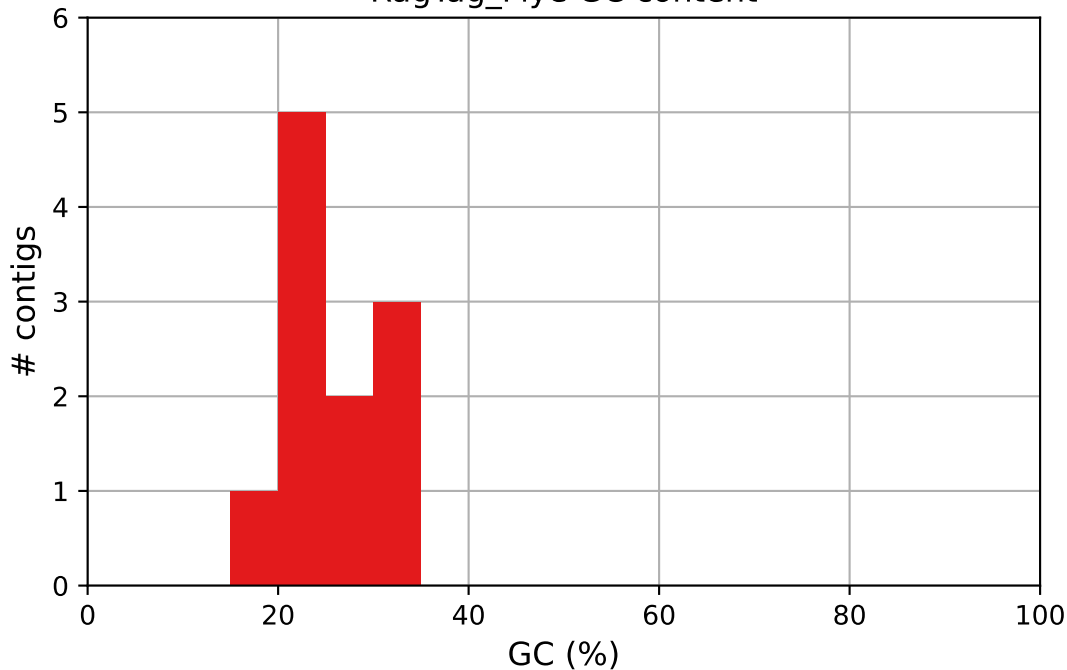
Cumulative length



GC content



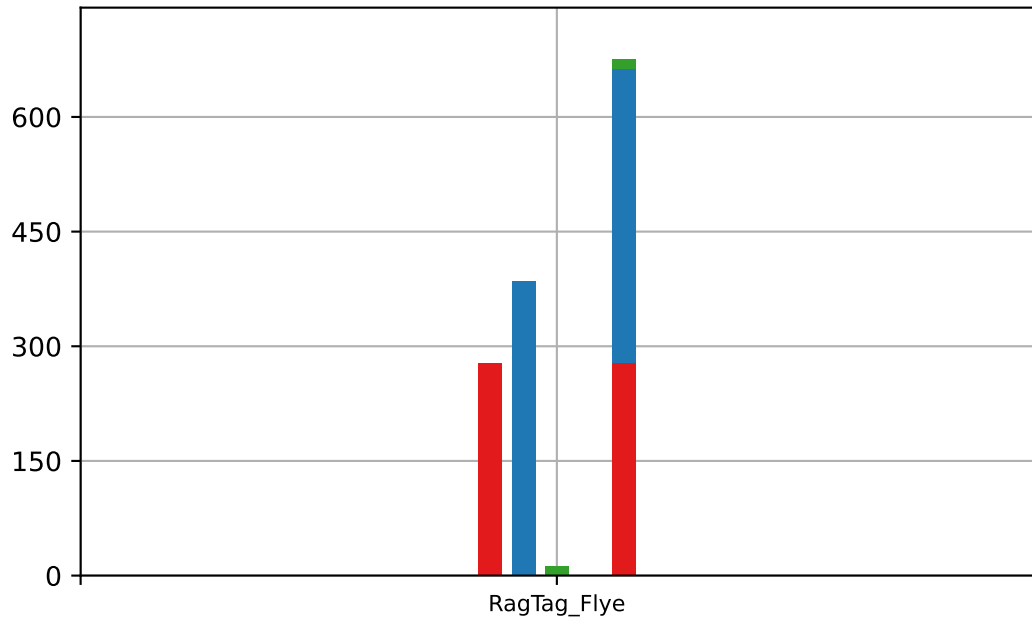
RagTag\_Flye GC content



RagTag\_Flye



## Misassemblies



# relocations

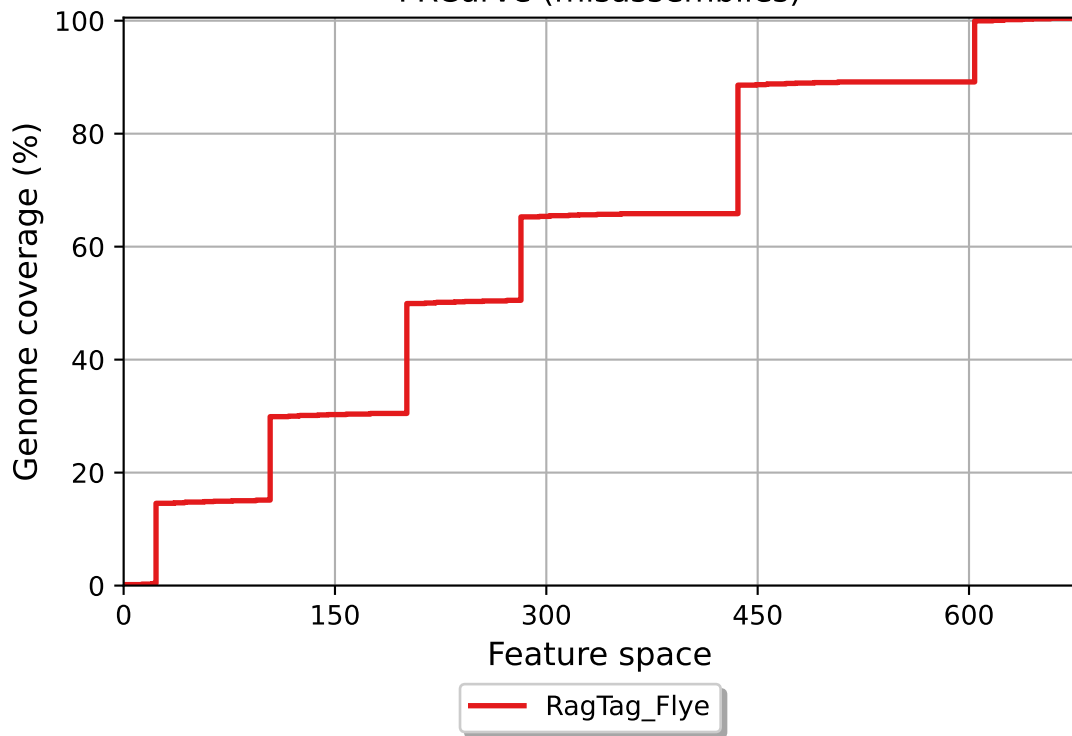


# translocations

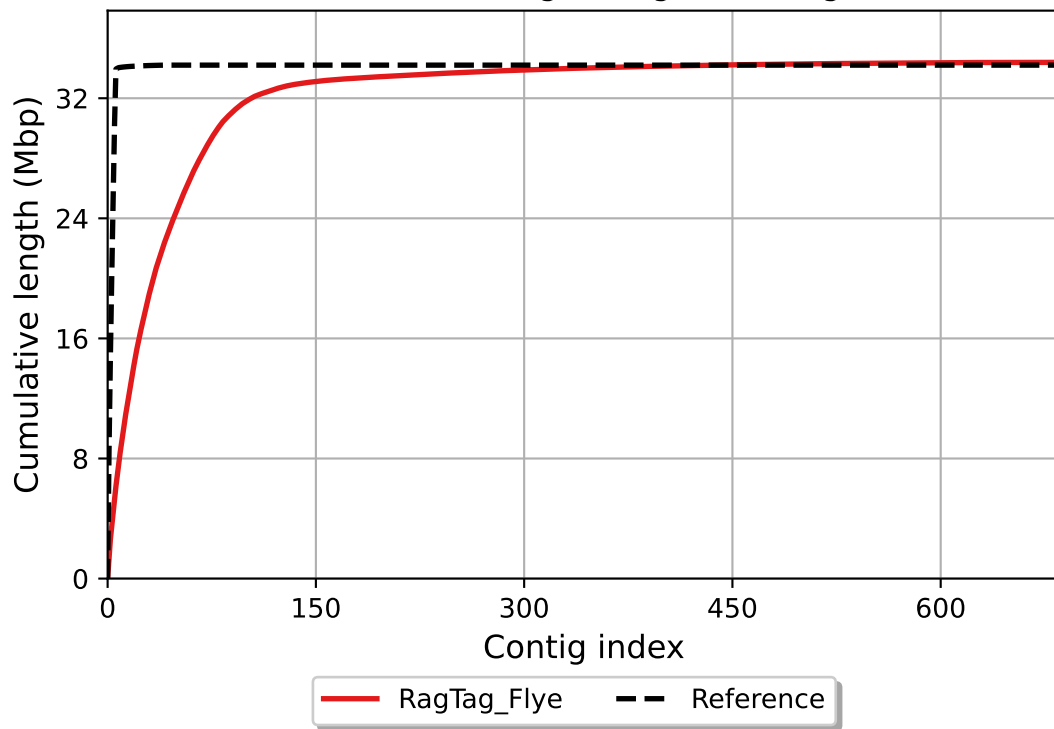


# inversions

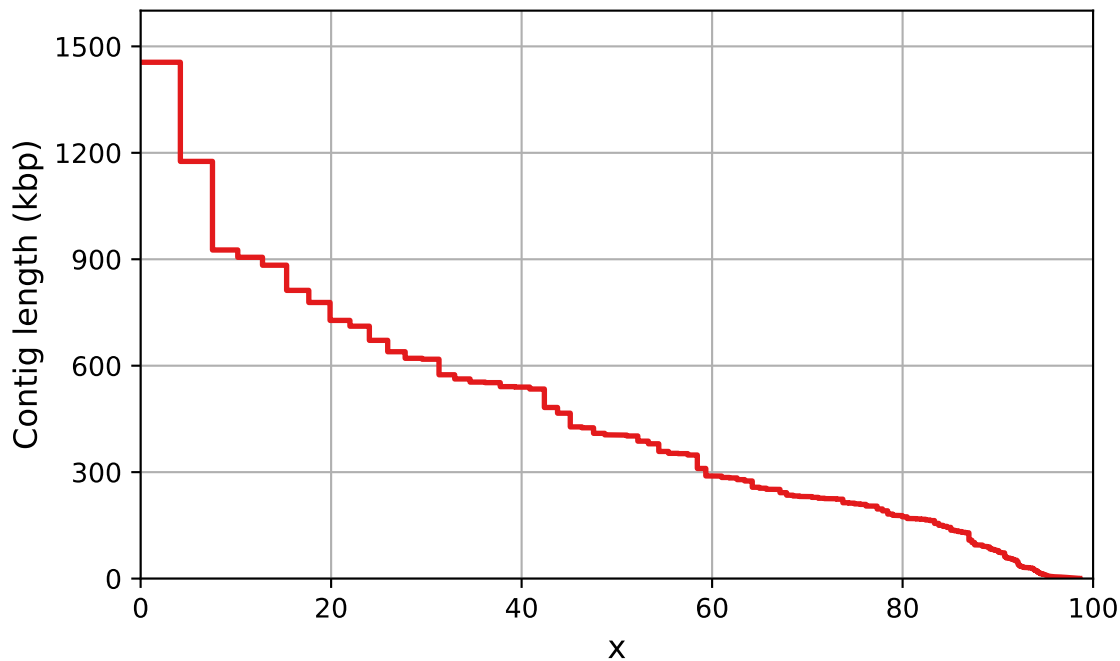
FRCurve (misassemblies)



Cumulative length (aligned contigs)

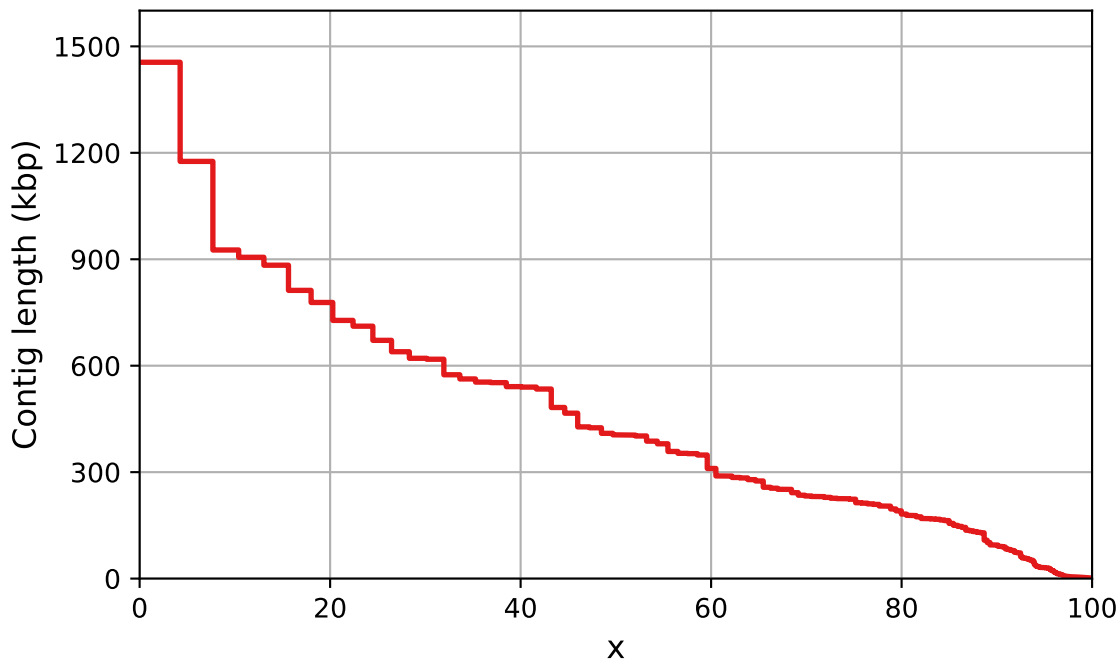


# NAx



RagTag\_Flye

# NGAx



RagTag\_Flye