

Report	ragtag.scaffold
# contigs (>= 0 bp)	9
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	3534564
Total length (>= 1000 bp)	3534564
Total length (>= 5000 bp)	3520142
Total length (>= 10000 bp)	3520142
Total length (>= 25000 bp)	3520142
Total length (>= 50000 bp)	3520142
# contigs	9
Largest contig	3520142
Total length	3534564
Reference length	3409143
GC (%)	38.26
Reference GC (%)	38.33
N50	3520142
NG50	3520142
N90	3520142
NG90	3520142
auN	3505787.2
auNG	3634763.7
L50	1
LG50	1
L90	1
LG90	1
# total reads	17888536
# left	8944268
# right	8944268
Mapped (%)	98.85
Reference mapped (%)	83.29
Properly paired (%)	96.98
Reference properly paired (%)	80.31
Avg. coverage depth	748
Reference avg. coverage depth	638
Coverage >= 1x (%)	99.95
Reference coverage >= 1x (%)	88.57
# misassemblies	79
# misassembled contigs	1
Misassembled contigs length	3520142
# local misassemblies	48
# scaffold gap ext. mis.	5
# scaffold gap loc. mis.	3
# structural variations	6
# unaligned mis. contigs	0
# unaligned contigs	5 + 1 part
Unaligned length	813315
Genome fraction (%)	79.725
Duplication ratio	1.001
# N's per 100 kbp	50.93
# mismatches per 100 kbp	2507.94
# indels per 100 kbp	66.91
# genomic features	0 + 0 part
Largest alignment	222123
Total aligned length	2720006
NA50	51709
NGA50	54220
NA90	-
NGA90	-
auNA	68830.7
auNGA	71362.9
LA50	18
LGA50	17
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).

## Reads report

	ragtag.scaffold
# total reads	17888536
# left	8944268
# right	8944268
# mapped	17683150
Mapped (%)	98.85
# properly paired	17348180
Properly paired (%)	96.98
# singletons	154035
Singletons (%)	0.86
# misjoint mates	38640
Misjoint mates (%)	0.22
Avg. coverage depth	748
Coverage >= 1x (%)	99.95
Coverage >= 5x (%)	99.95
Coverage >= 10x (%)	99.95
# reference mapped	14898857
Reference mapped (%)	83.29
# reference properly paired	14366862
Reference properly paired (%)	80.31
# reference singletons	316564
Reference singletons (%)	1.77
# reference misjoint mates	0
Reference misjoint mates (%)	0.0
Reference avg. coverage depth	638
Reference coverage >= 1x (%)	88.57
Reference coverage >= 5x (%)	88.46
Reference coverage >= 10x (%)	88.39

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

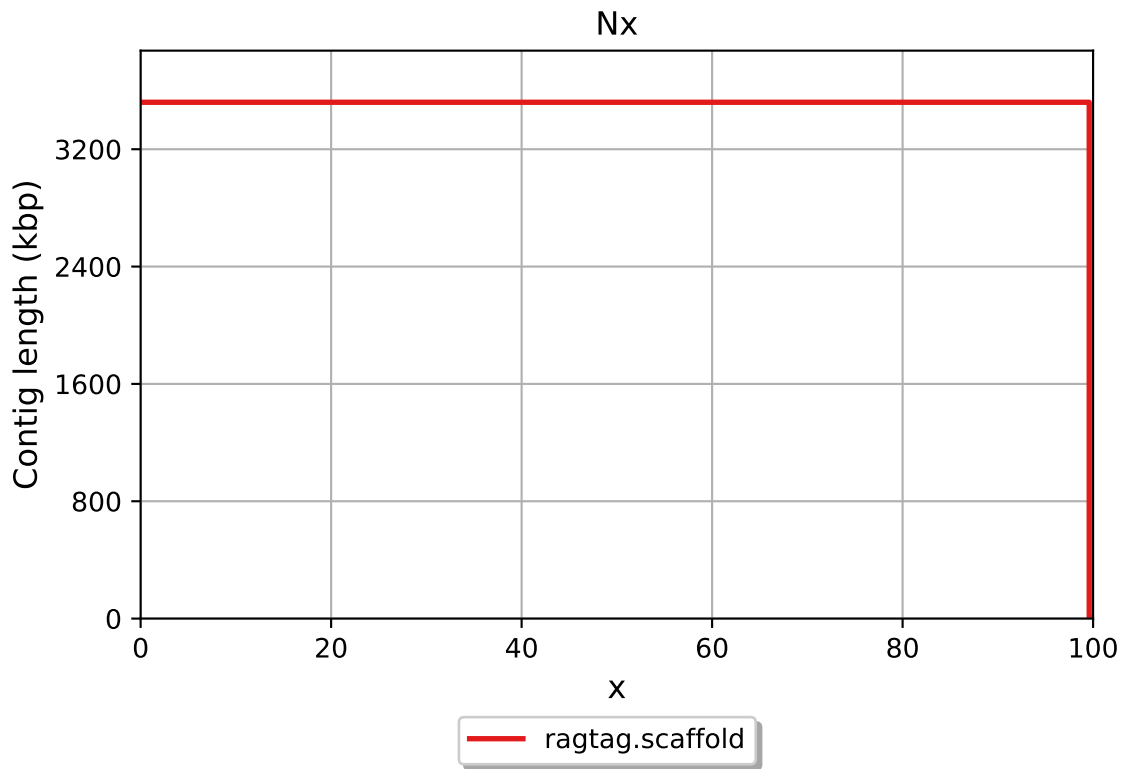
	ragtag.scaffold
# misassemblies	79
# contig misassemblies	76
# c. relocations	76
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	3
# s. relocations	3
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	3520142
# local misassemblies	48
# scaffold gap ext. mis.	5
# scaffold gap loc. mis.	3
# structural variations	6
# unaligned mis. contigs	0
# mismatches	68216
# indels	1820
# indels (<= 5 bp)	1592
# indels (> 5 bp)	228
Indels length	11707

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).

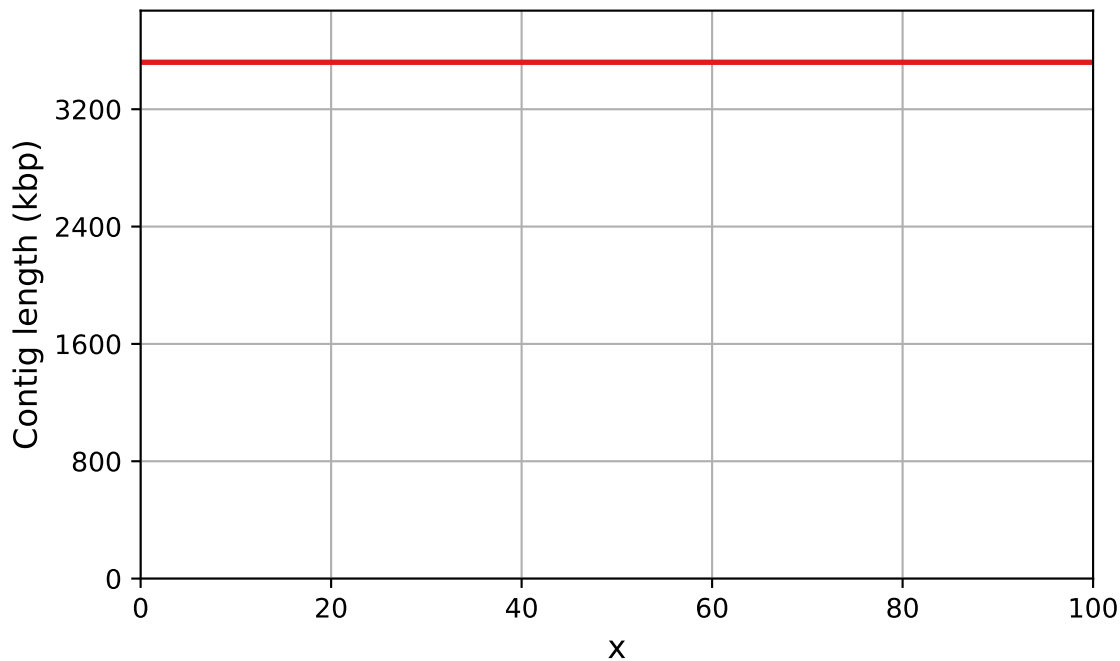
## Unaligned report

	ragtag.scaffold
# fully unaligned contigs	5
Fully unaligned length	8592
# partially unaligned contigs	1
Partially unaligned length	804723
# N's	1800

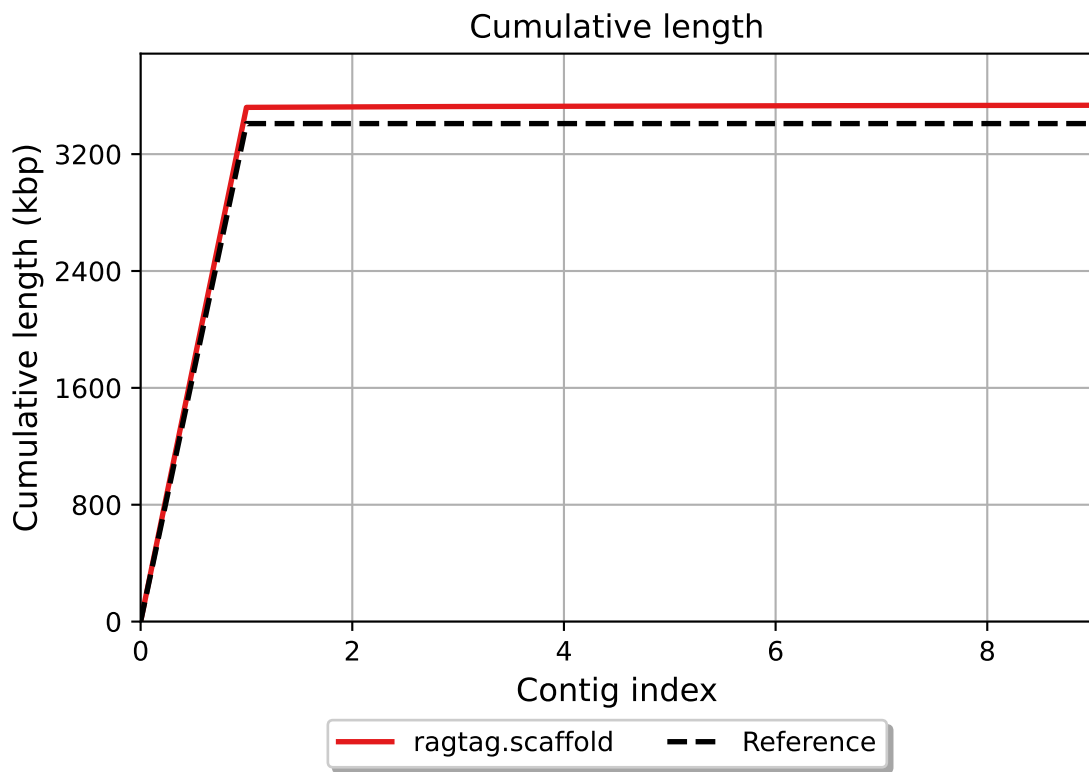
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

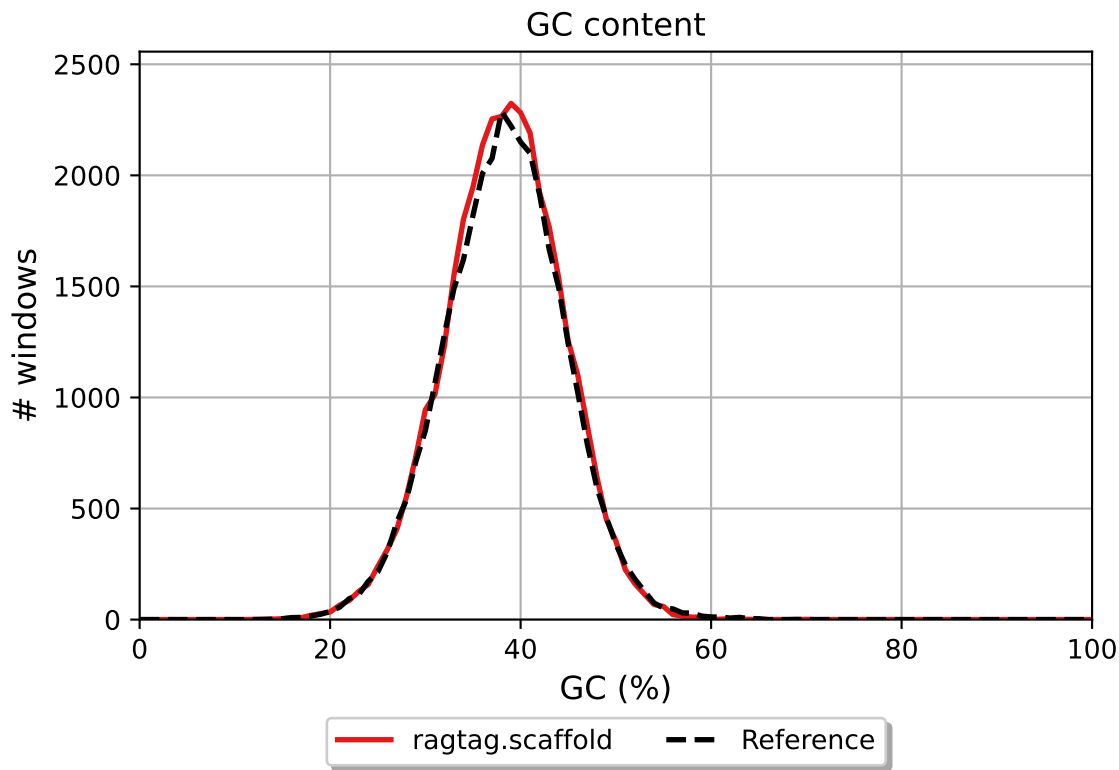


NGx



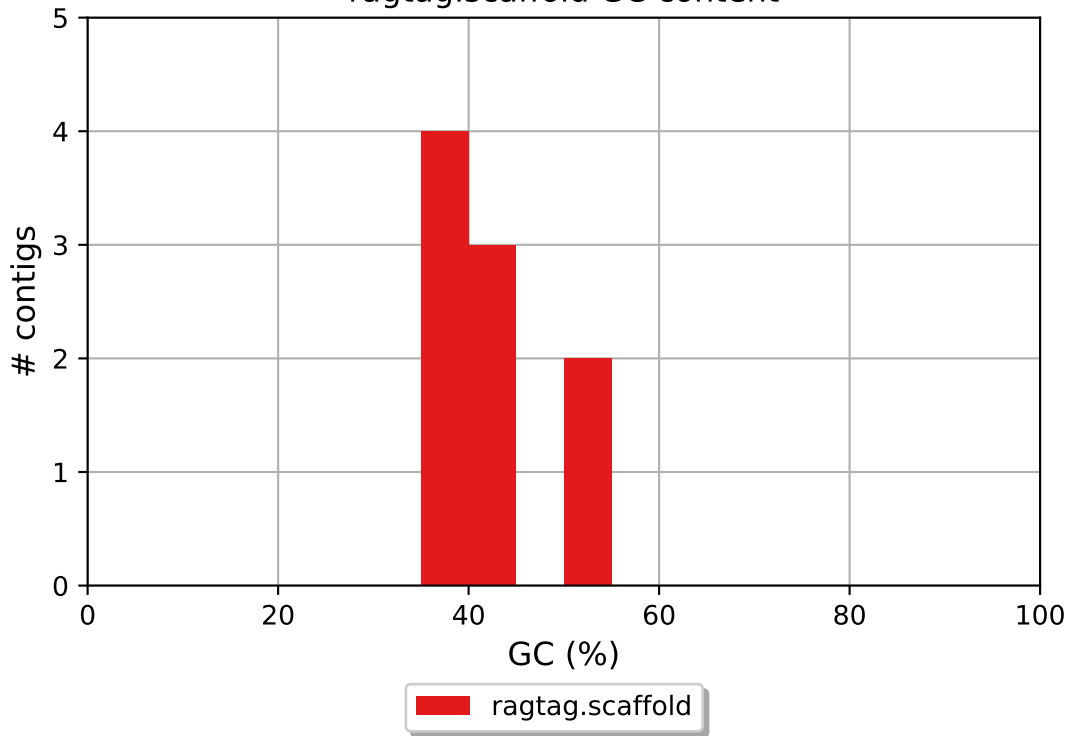
ragtag.scaffold



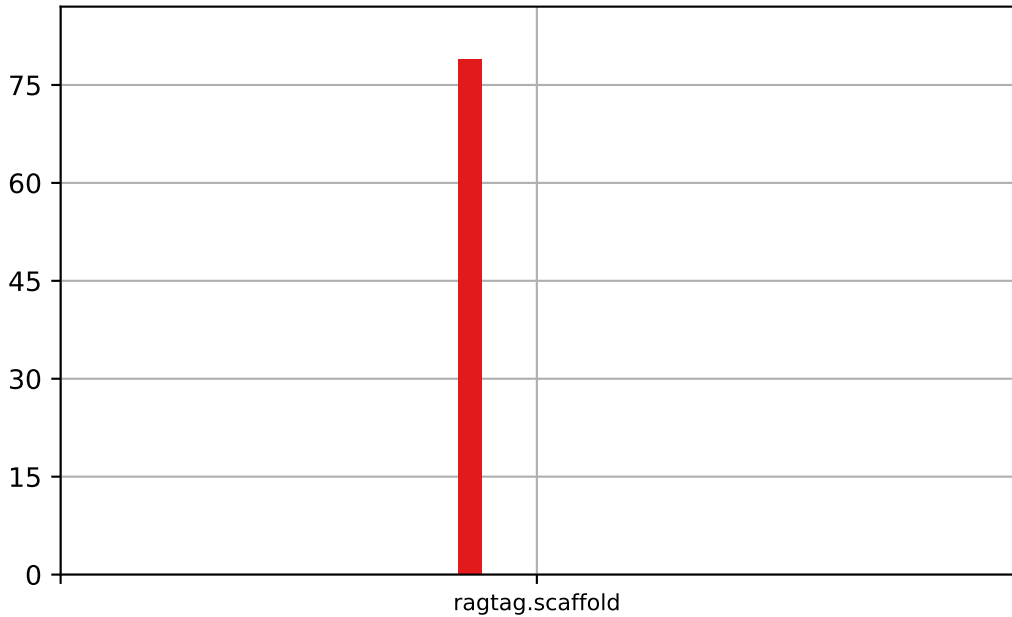




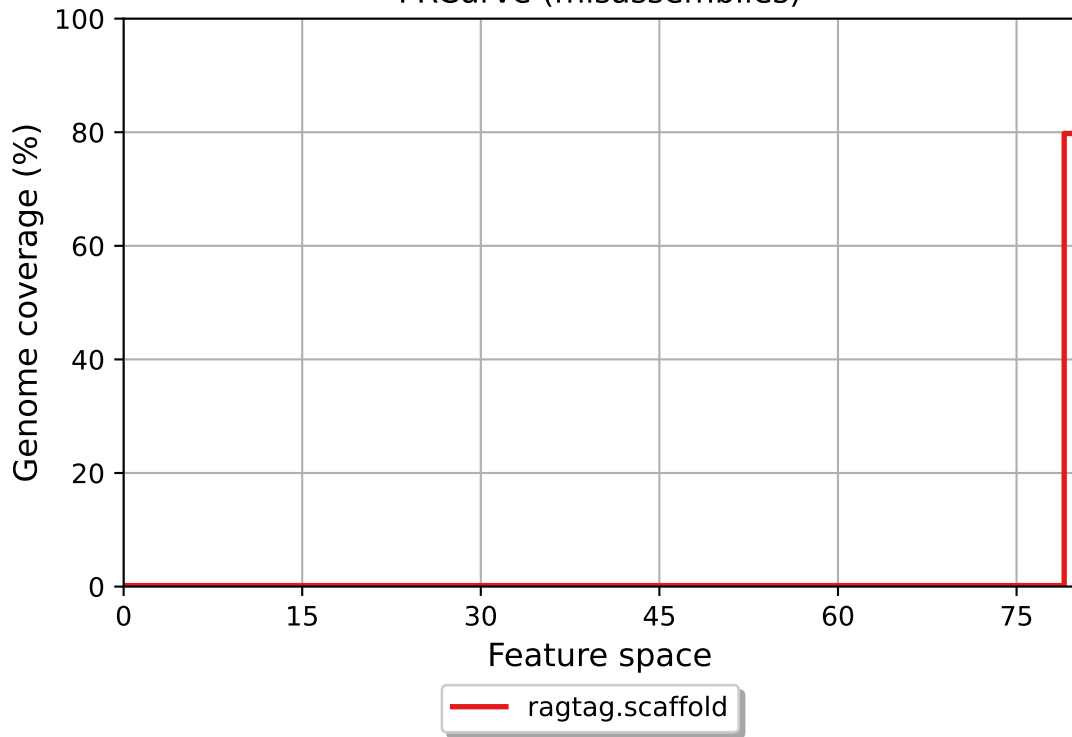
ragtag.scaffold GC content



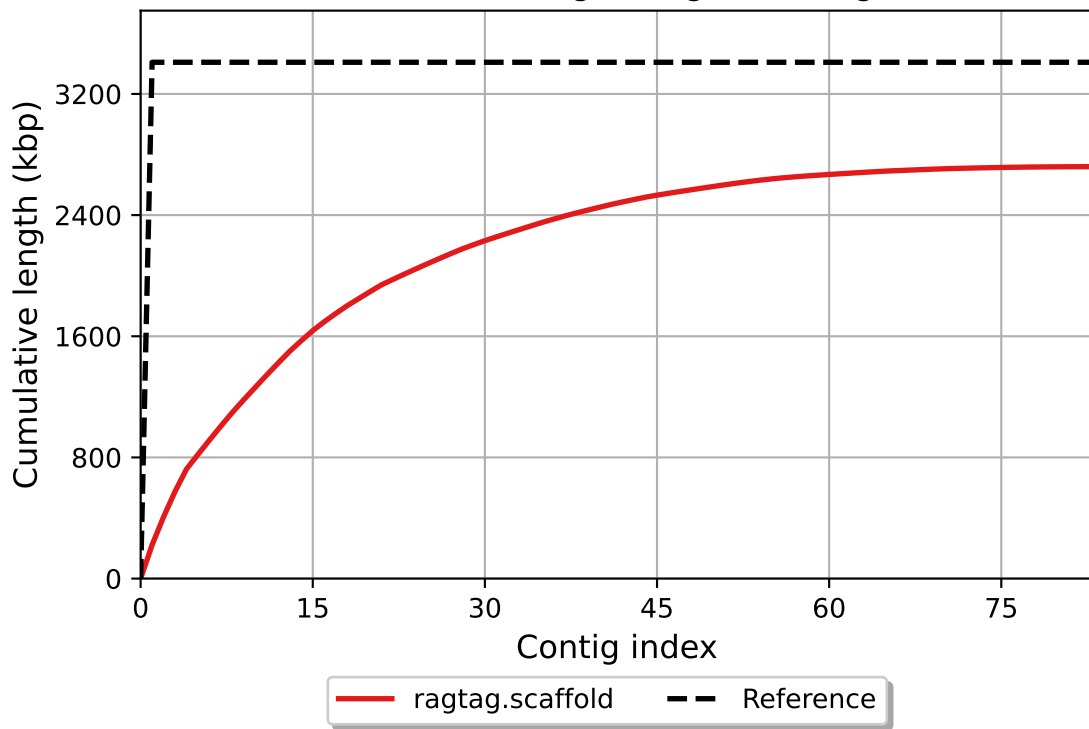
## Misassemblies



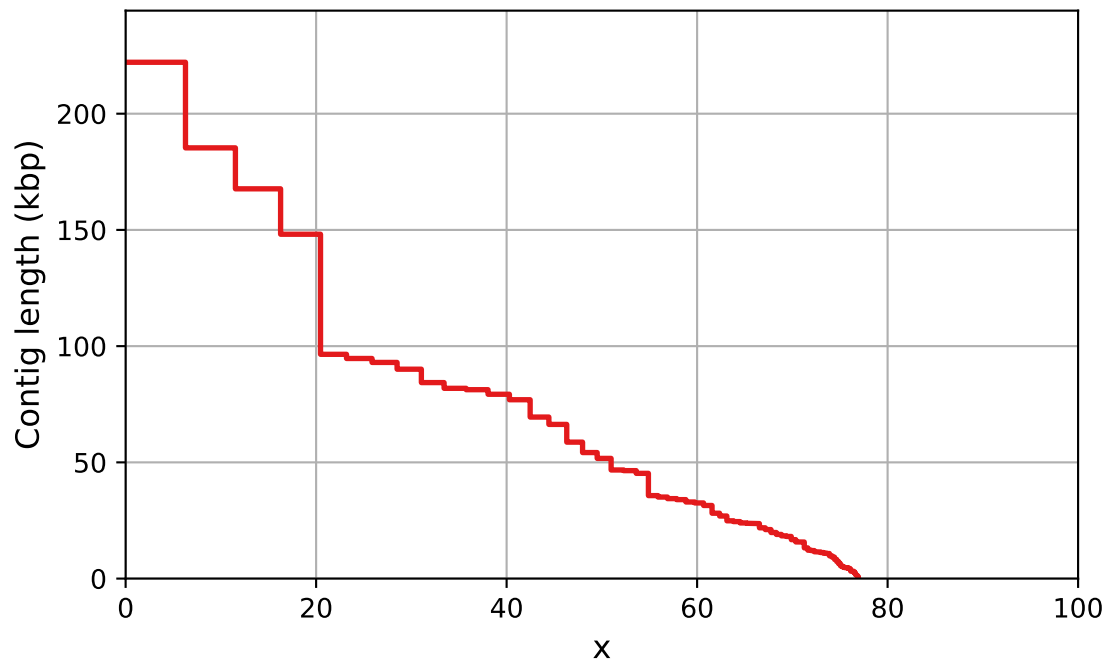
FRCurve (misassemblies)



Cumulative length (aligned contigs)

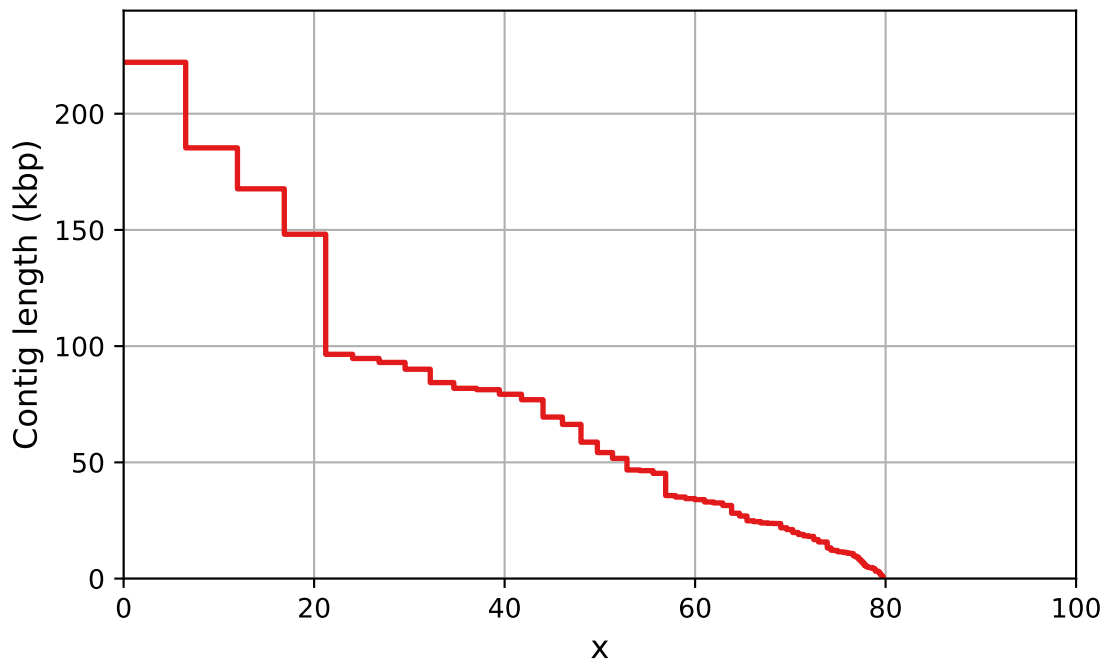


NAx

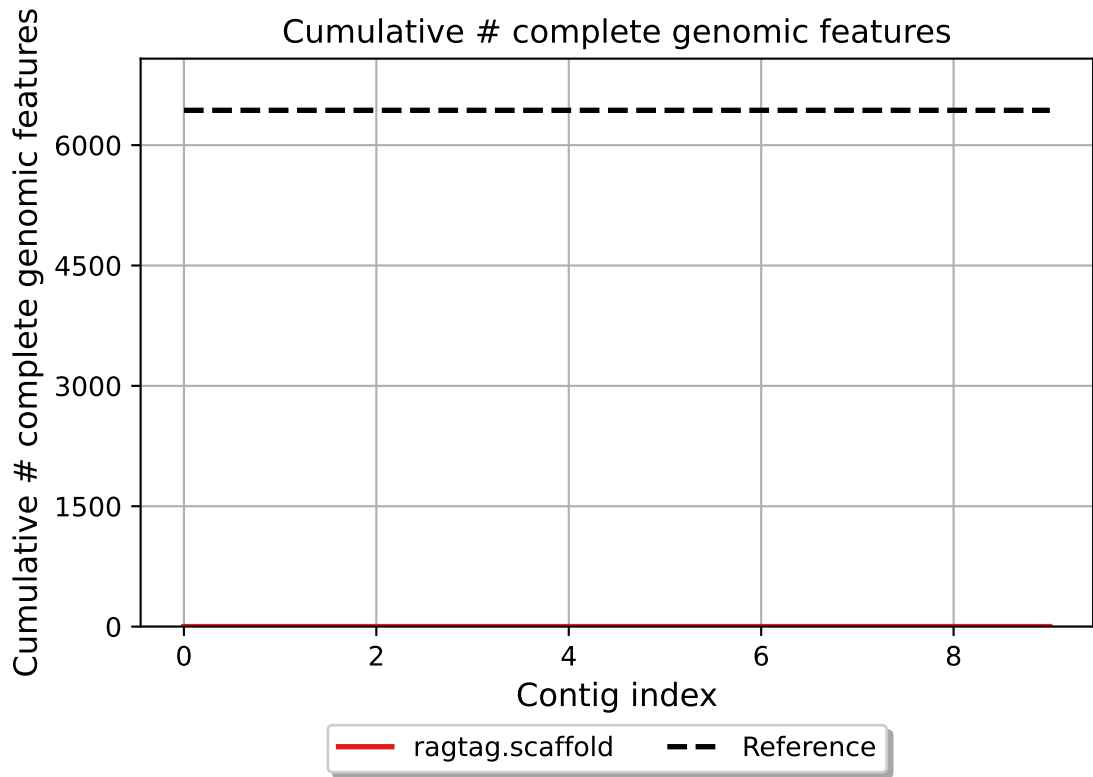


ragtag.scaffold

# NGAx



ragtag.scaffold



FRCurve (genomic features)

