

Report	scaffolds
# contigs (>= 0 bp)	242
# contigs (>= 1000 bp)	100
# contigs (>= 5000 bp)	74
# contigs (>= 10000 bp)	65
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	34
Total length (>= 0 bp)	4786811
Total length (>= 1000 bp)	4759154
Total length (>= 5000 bp)	4702347
Total length (>= 10000 bp)	4631468
Total length (>= 25000 bp)	4309484
Total length (>= 50000 bp)	3752099
# contigs	111
Largest contig	230283
Total length	4767084
Reference length	4987882
GC (%)	50.79
Reference GC (%)	50.71
N50	101316
NG50	96924
N90	26183
NG90	21843
auN	112255.8
auNG	107286.6
L50	15
LG50	17
L90	49
LG90	57
# total reads	1883136
# left	941568
# right	941568
Mapped (%)	99.76
Reference mapped (%)	94.74
Properly paired (%)	98.27
Reference properly paired (%)	93.58
Avg. coverage depth	44
Reference avg. coverage depth	40
Coverage >= 1x (%)	99.98
Reference coverage >= 1x (%)	91.21
# misassemblies	21
# misassembled contigs	13
Misassembled contigs length	1512161
# local misassemblies	19
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	4
# structural variations	3
# unaligned mis. contigs	3
# unaligned contigs	9 + 24 part
Unaligned length	316936
Genome fraction (%)	89.153
Duplication ratio	1.000
# N's per 100 kbp	18.88
# mismatches per 100 kbp	106.00
# indels per 100 kbp	2.97
Largest alignment	194298
Total aligned length	4447092
NA50	81034
NGA50	77202
NA90	9703
NGA90	-
auNA	83128.0
auNGA	79448.2
LA50	20
LGA50	22
LA90	72
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

	scaffolds
# total reads	1883136
# left	941568
# right	941568
# mapped	1878651
Mapped (%)	99.76
# properly paired	1850632
Properly paired (%)	98.27
# singletons	3286
Singletons (%)	0.17
# misjoint mates	22960
Misjoint mates (%)	1.22
Avg. coverage depth	44
Coverage >= 1x (%)	99.98
Coverage >= 5x (%)	99.98
Coverage >= 10x (%)	99.89
# reference mapped	1784102
Reference mapped (%)	94.74
# reference properly paired	1762160
Reference properly paired (%)	93.58
# reference singletons	8181
Reference singletons (%)	0.43
# reference misjoint mates	386
Reference misjoint mates (%)	0.02
Reference avg. coverage depth	40
Reference coverage >= 1x (%)	91.21
Reference coverage >= 5x (%)	91.14
Reference coverage >= 10x (%)	91.04

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

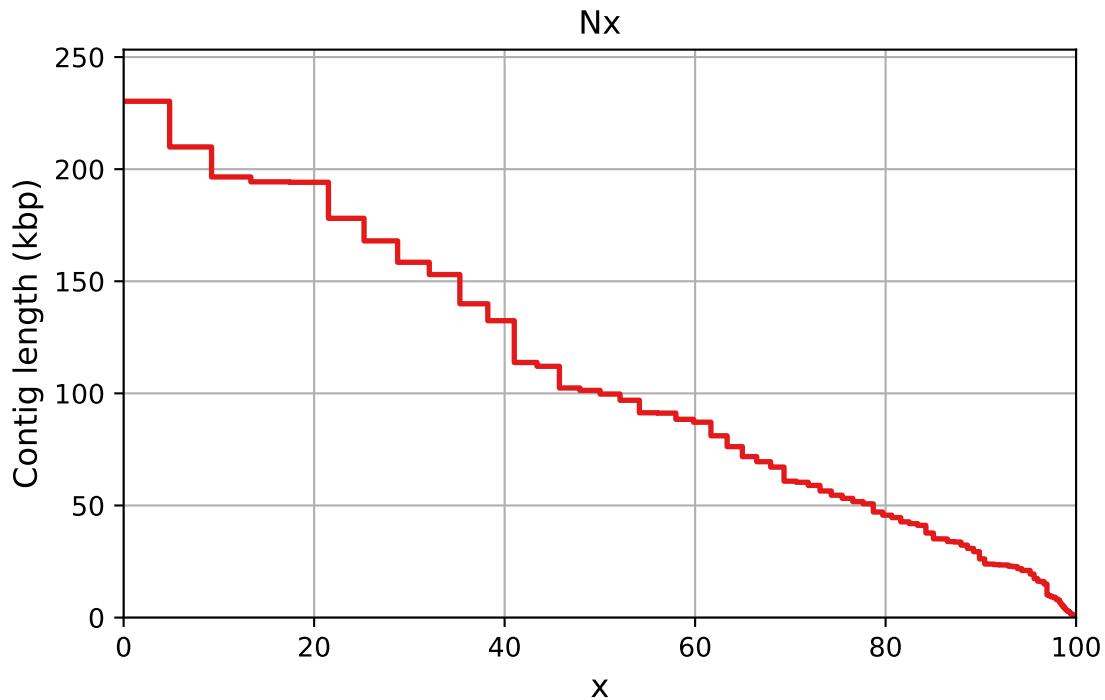
	scaffolds
# misassemblies	21
# contig misassemblies	21
# c. relocations	21
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	13
Misassembled contigs length	1512161
# local misassemblies	19
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	4
# structural variations	3
# unaligned mis. contigs	3
# mismatches	4714
# indels	132
# indels ( $\leq 5$ bp)	99
# indels ( $> 5$ bp)	33
Indels length	4481

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

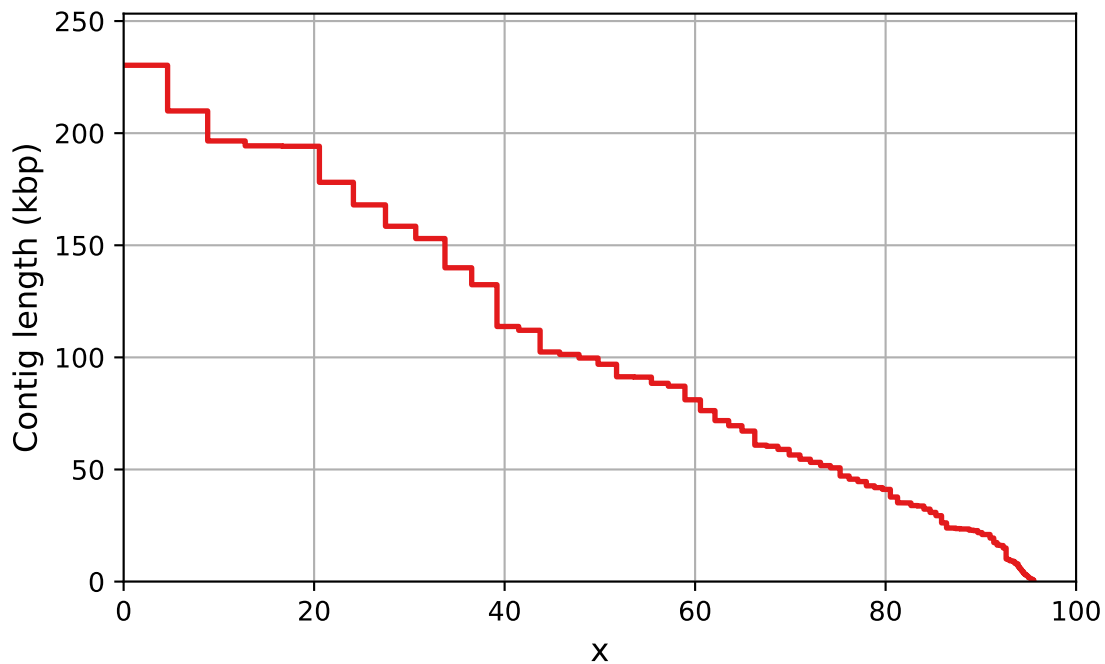
	scaffolds
# fully unaligned contigs	9
Fully unaligned length	53949
# partially unaligned contigs	24
Partially unaligned length	262987
# N's	900

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).



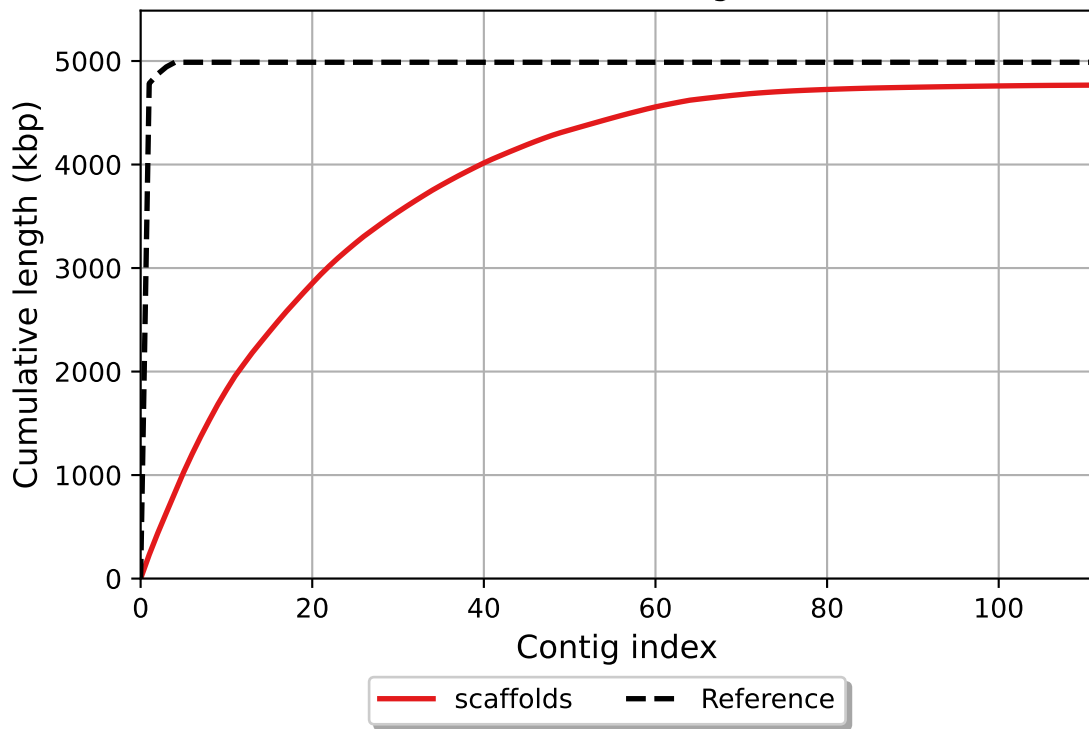
— scaffolds

# NGx

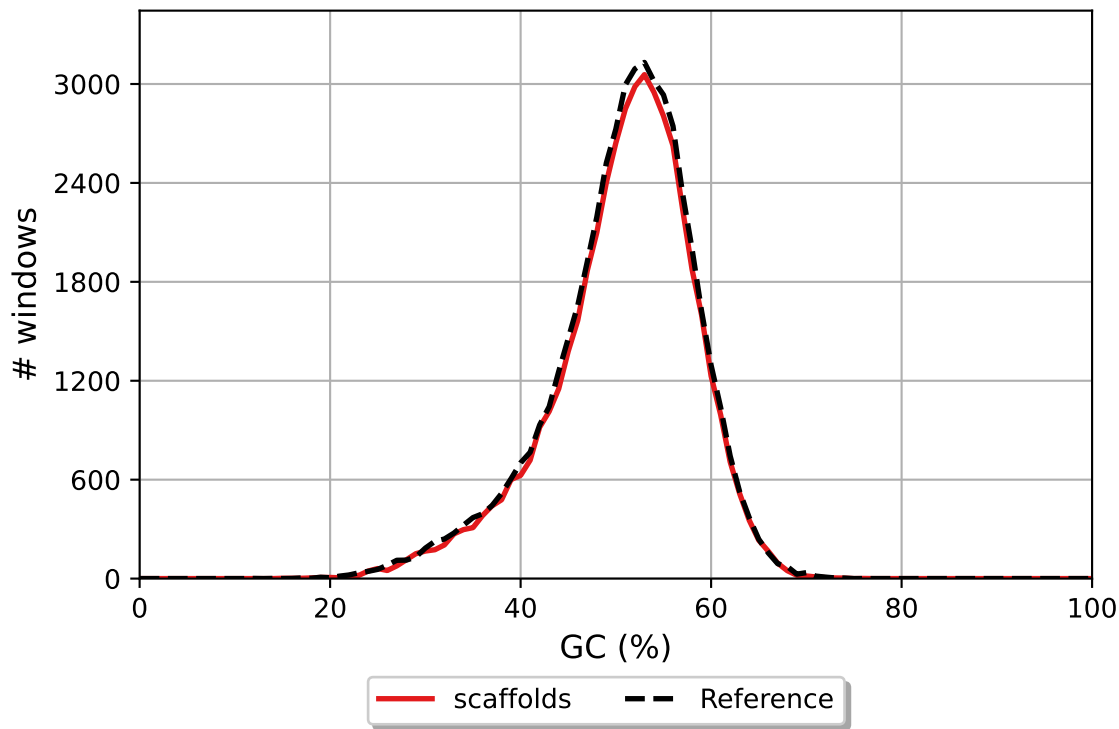


— scaffolds

Cumulative length

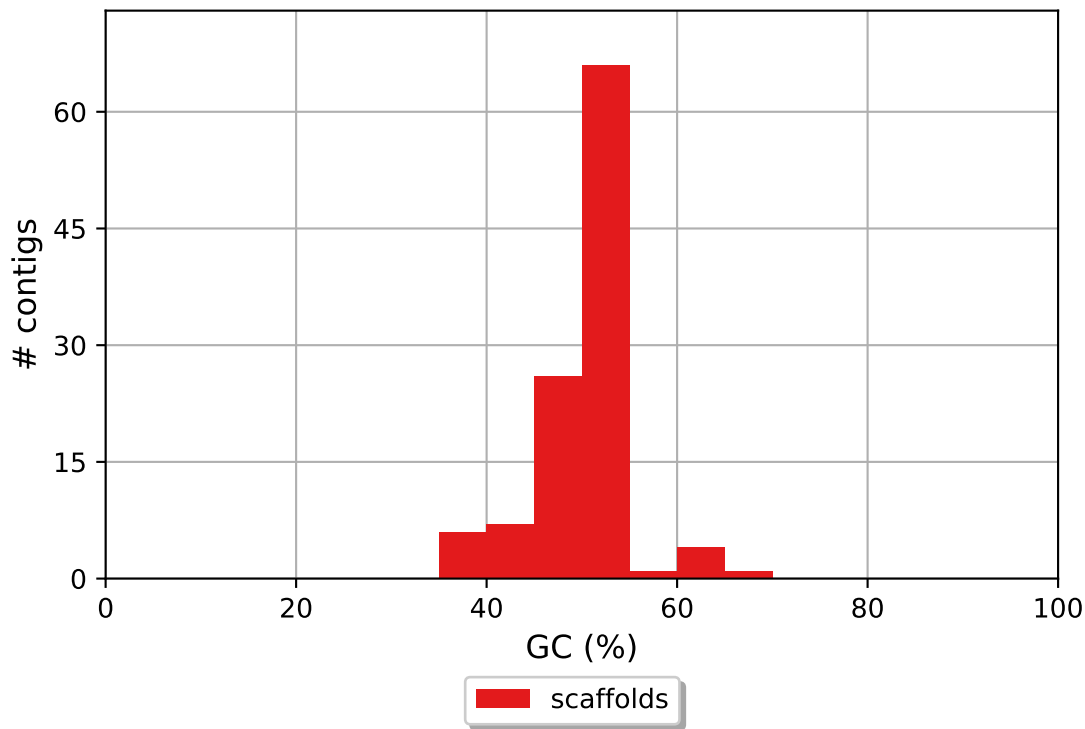


## GC content

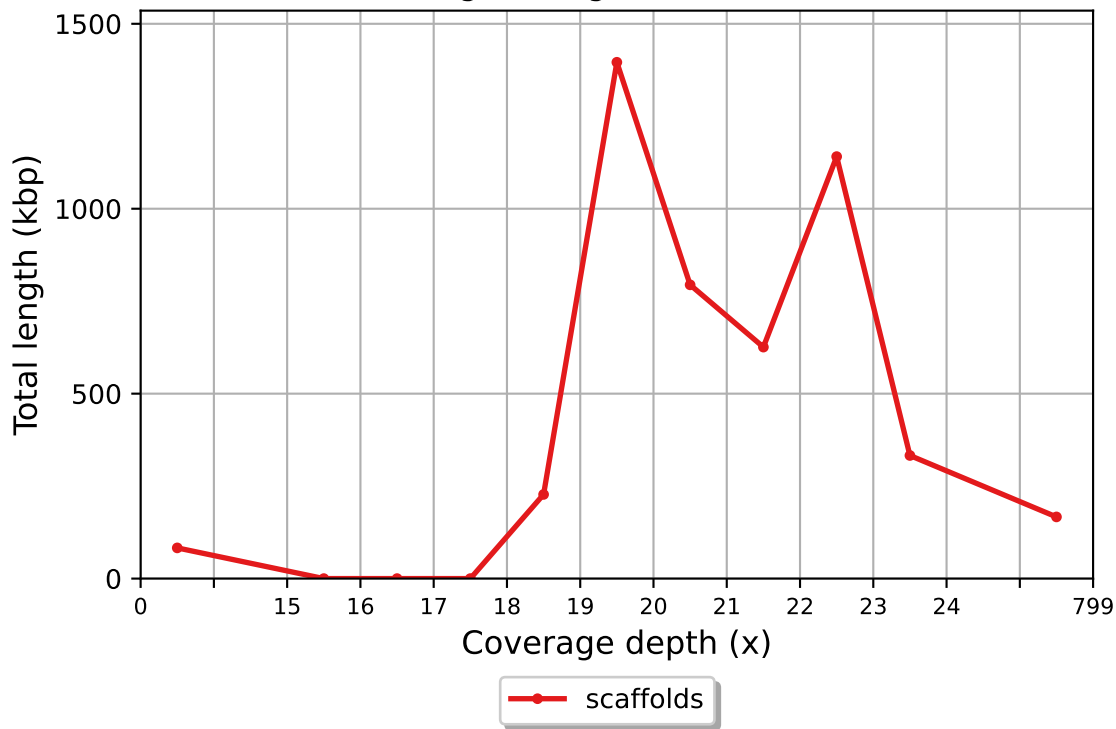




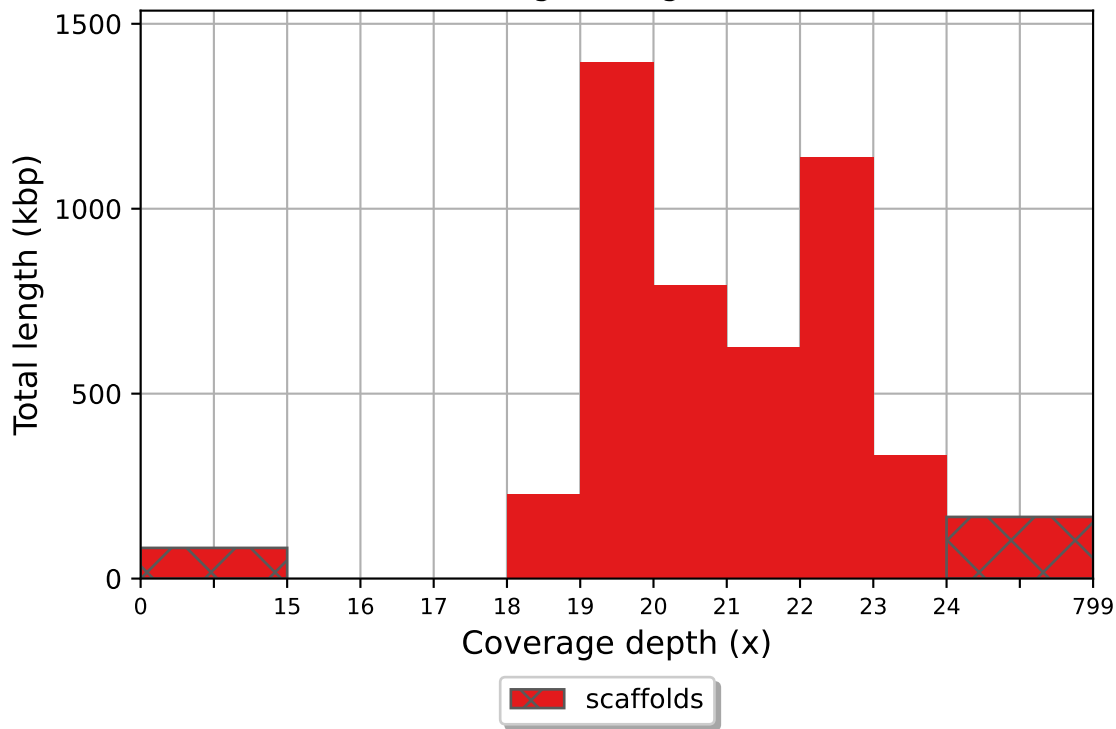
scaffolds GC content



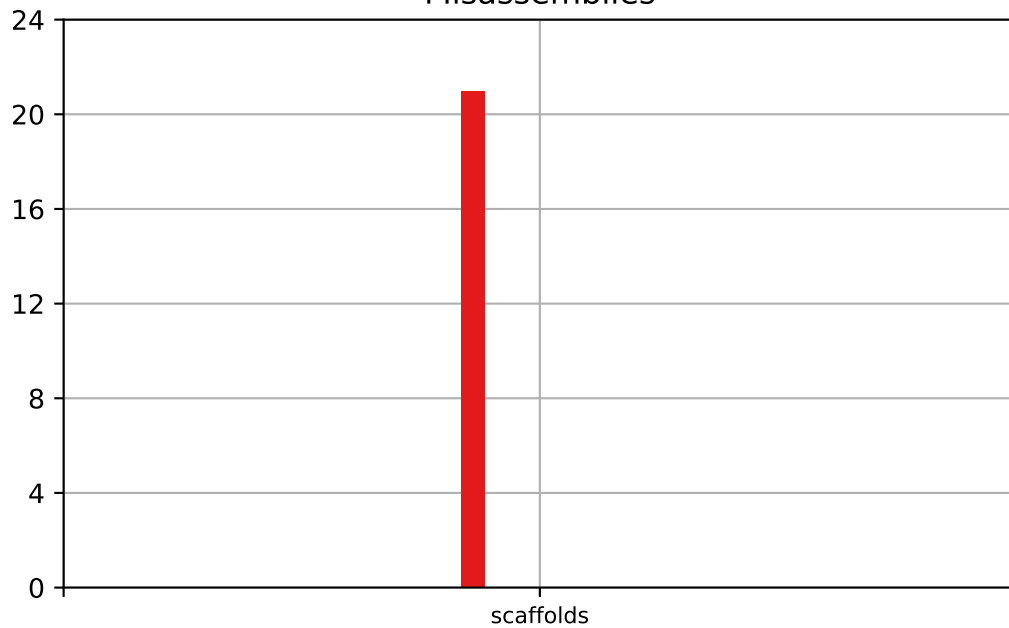
Coverage histogram (bin size: 1x)



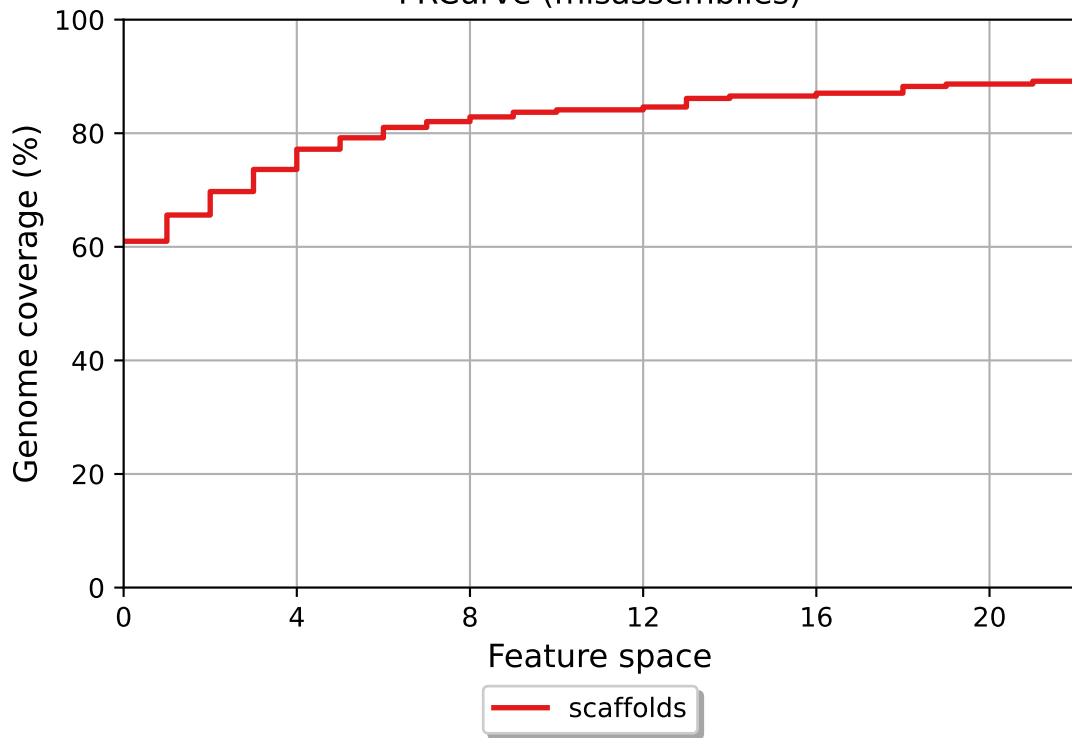
scaffolds coverage histogram (bin size: 1x)



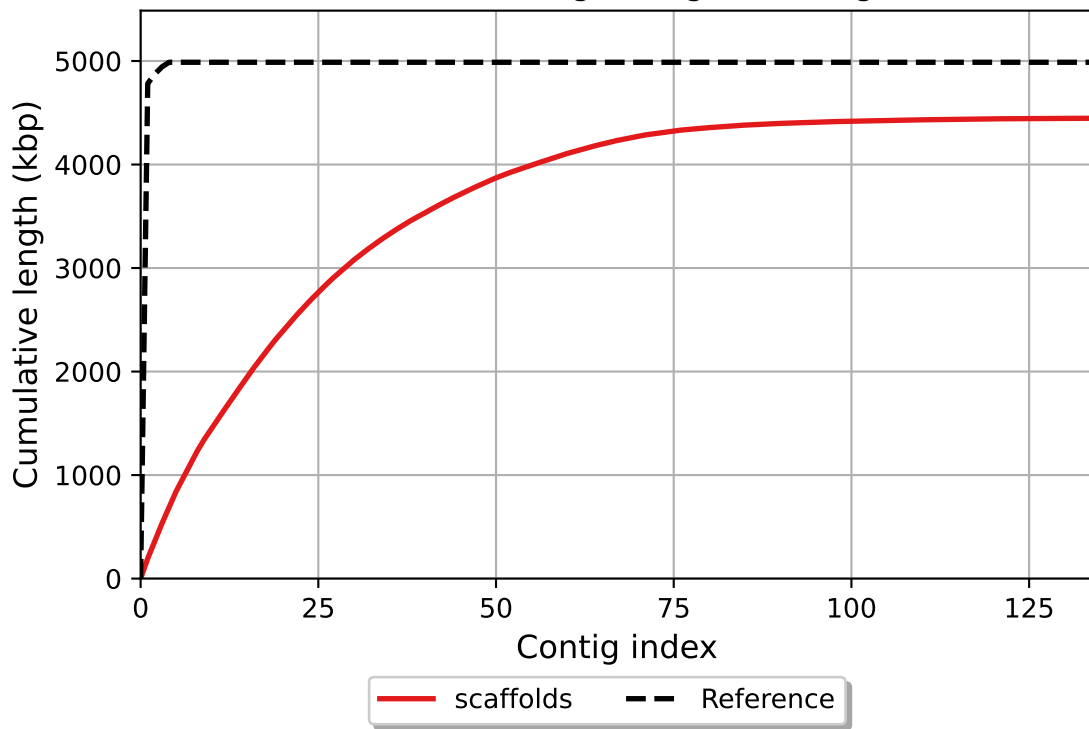
## Misassemblies



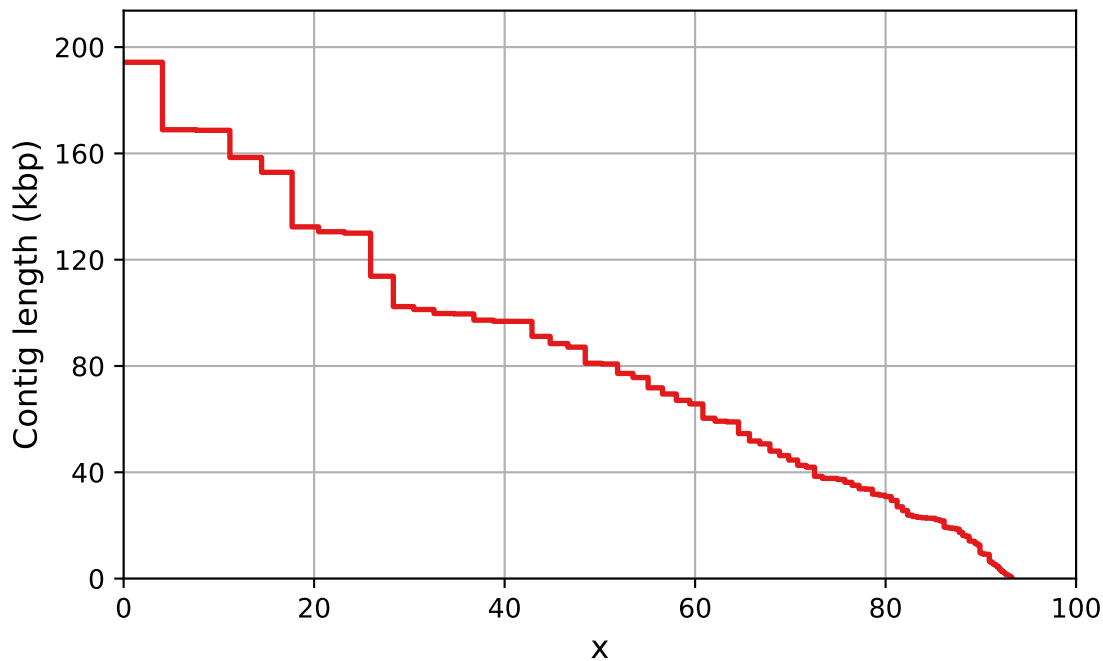
FRCurve (misassemblies)



Cumulative length (aligned contigs)

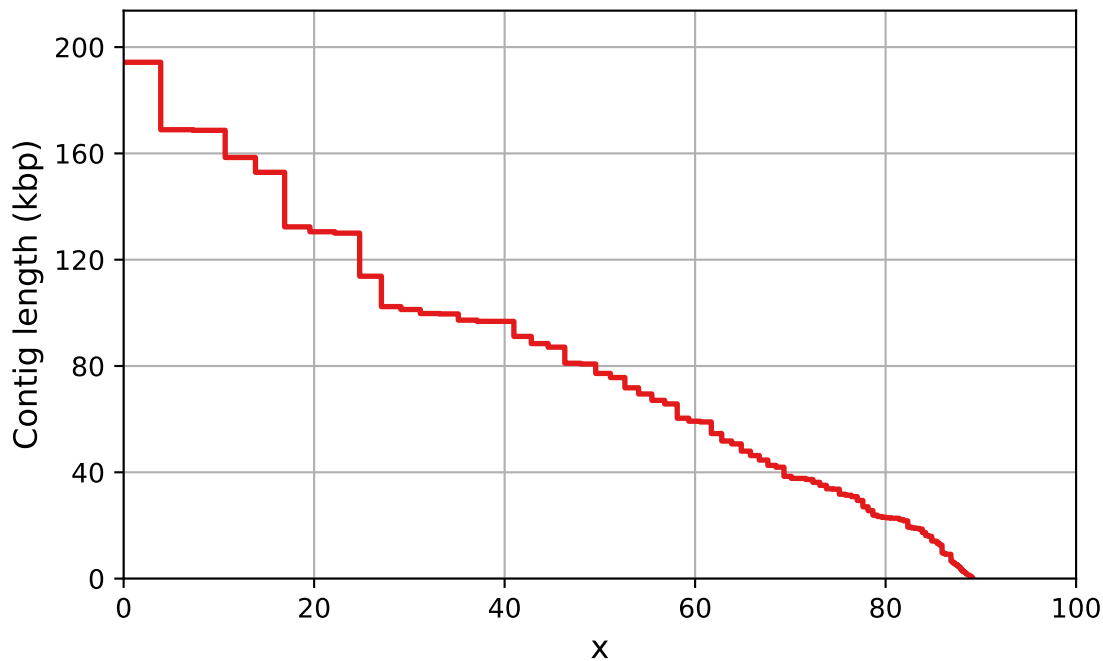


NAx



— scaffolds

# NGAx



— scaffolds