

	Report	
	scaffolds_fasta_fasta	scaffolds_fasta_fasta_broken
# contigs (>= 0 bp)	212	-
# contigs (>= 1000 bp)	65	76
Total length (>= 0 bp)	5514153	-
Total length (>= 1000 bp)	5481110	5480100
# contigs	75	86
Largest contig	465286	390830
Total length	5487655	5486645
Reference length	5682322	5682322
GC (%)	57.21	57.21
Reference GC (%)	57.12	57.12
N50	195186	172642
NG50	195186	172642
N90	77460	61419
NG90	73398	56140
auN	226003.0	167915.0
auNG	218260.5	162132.6
L50	10	13
LG50	10	13
L90	26	34
LG90	28	37
# misassemblies	76	76
# misassembled contigs	27	32
Misassembled contigs length	4615337	4263738
# local misassemblies	30	29
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	4	-
# unaligned mis. contigs	1	1
# unaligned contigs	21 + 31 part	21 + 35 part
Unaligned length	688558	687338
Genome fraction (%)	85.323	85.318
Duplication ratio	1.002	1.002
# N's per 100 kbp	18.40	0.00
# mismatches per 100 kbp	688.20	688.49
# indels per 100 kbp	20.01	19.81
# genomic features	9717 + 186 part	9690 + 210 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	4 + 0 part	3 + 0 part
Largest alignment	205341	205341
Total aligned length	4796579	4796618
NA50	71923	64682
NGA50	69622	60726
NA90	-	-
NGA90	-	-
auNA	83119.8	75269.8
auNGA	80272.3	72677.8
LA50	23	26
LGA50	25	28
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).

## Misassemblies report

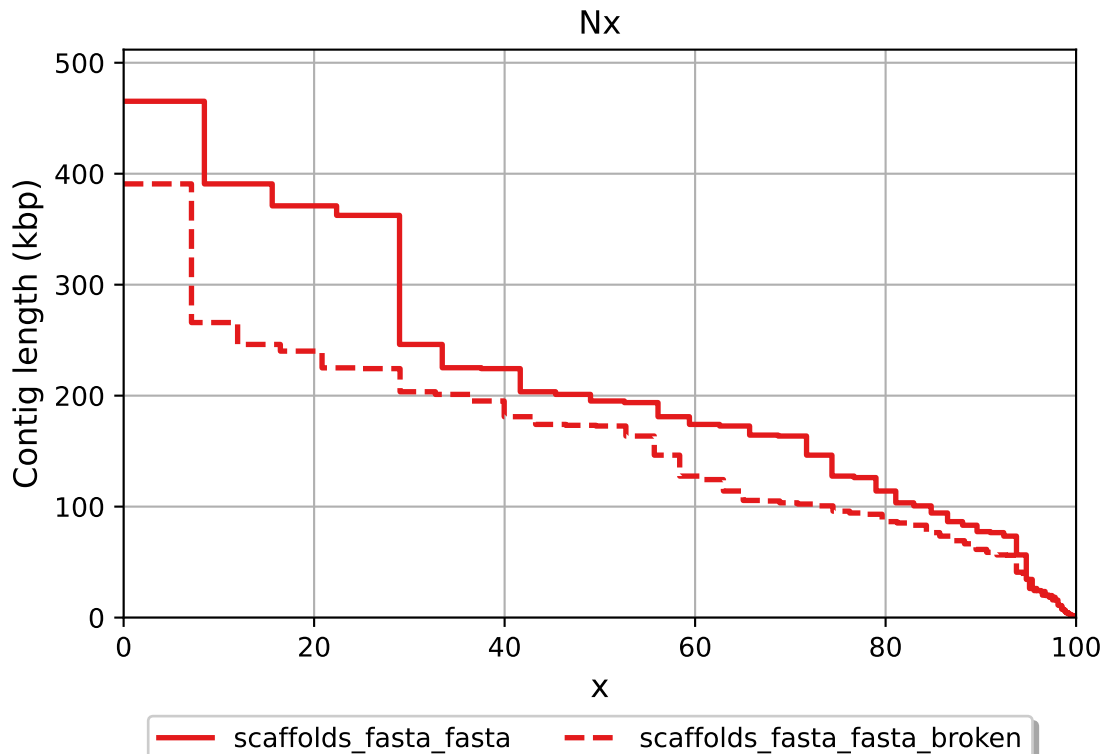
	scaffolds_fasta_fasta	scaffolds_fasta_fasta_broken
# misassemblies	76	76
# contig misassemblies	75	76
# c. relocations	72	73
# c. translocations	3	3
# c. inversions	0	0
# scaffold misassemblies	1	0
# s. relocations	1	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	27	32
Misassembled contigs length	4615337	4263738
# local misassemblies	30	29
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	4	-
# unaligned mis. contigs	1	1
# mismatches	33010	33024
# indels	960	950
# indels (<= 5 bp)	862	865
# indels (> 5 bp)	98	85
Indels length	8046	6320

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).

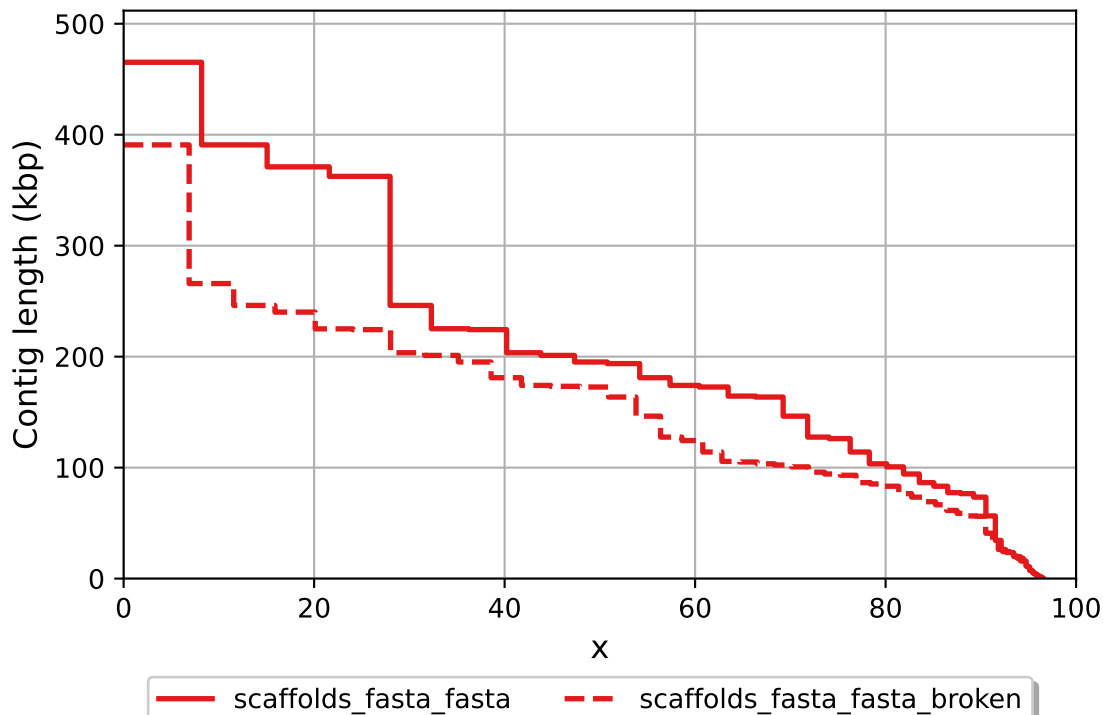
## Unaligned report

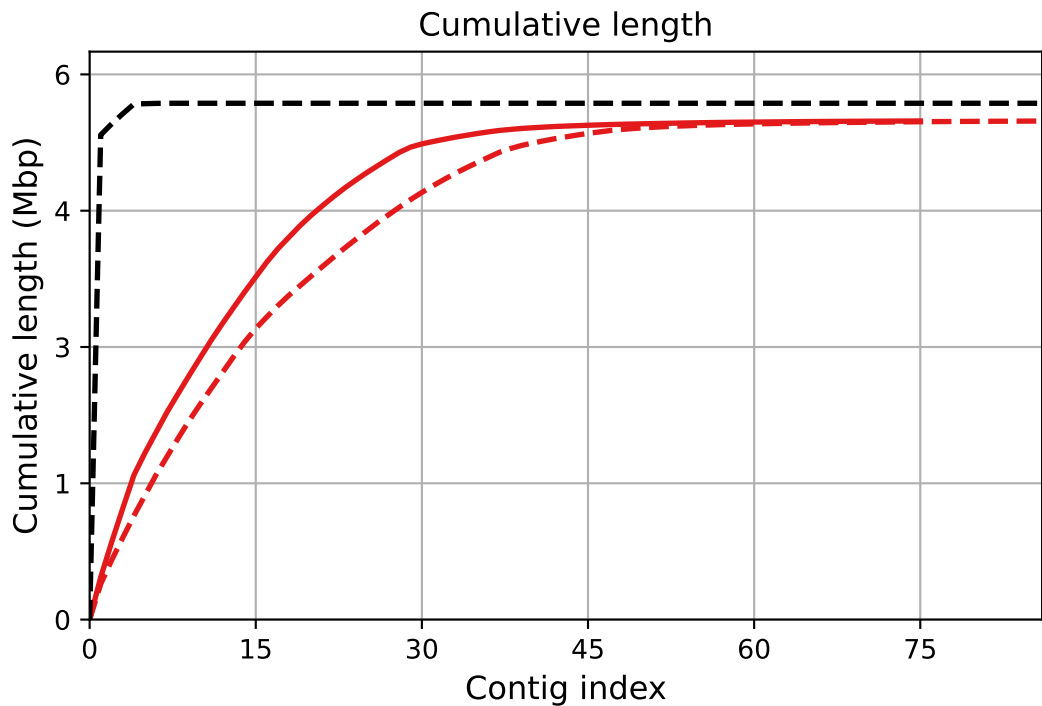
	scaffolds_fasta_fasta	scaffolds_fasta_fasta_broken
# fully unaligned contigs	21	21
Fully unaligned length	80604	80604
# partially unaligned contigs	31	35
Partially unaligned length	607954	606734
# N's	1010	0

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).



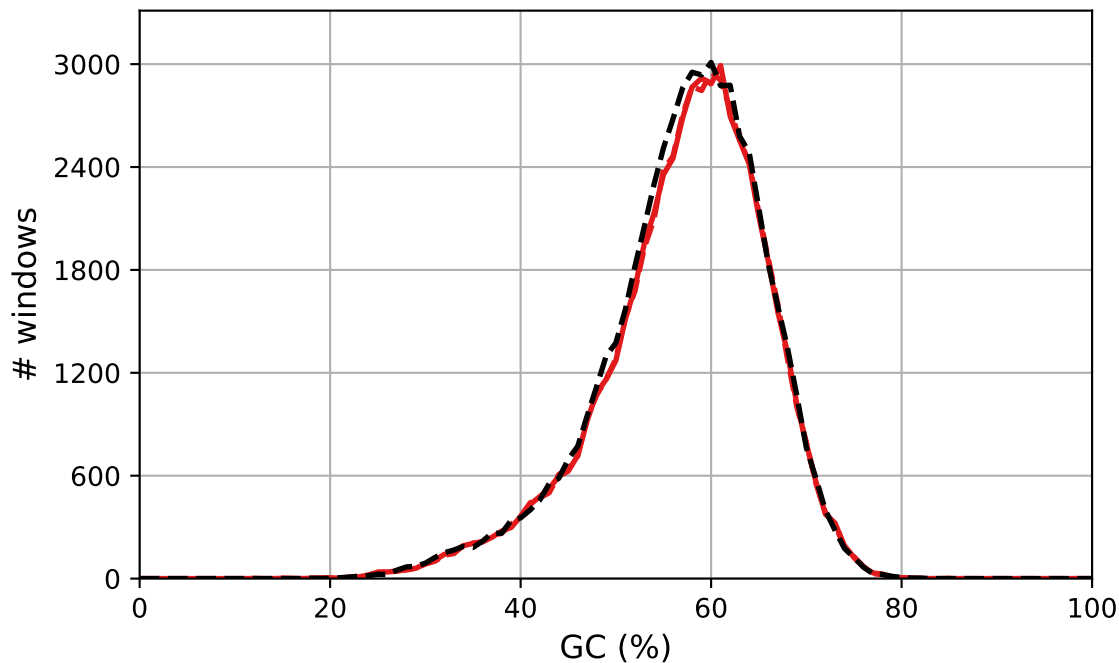
# NGx





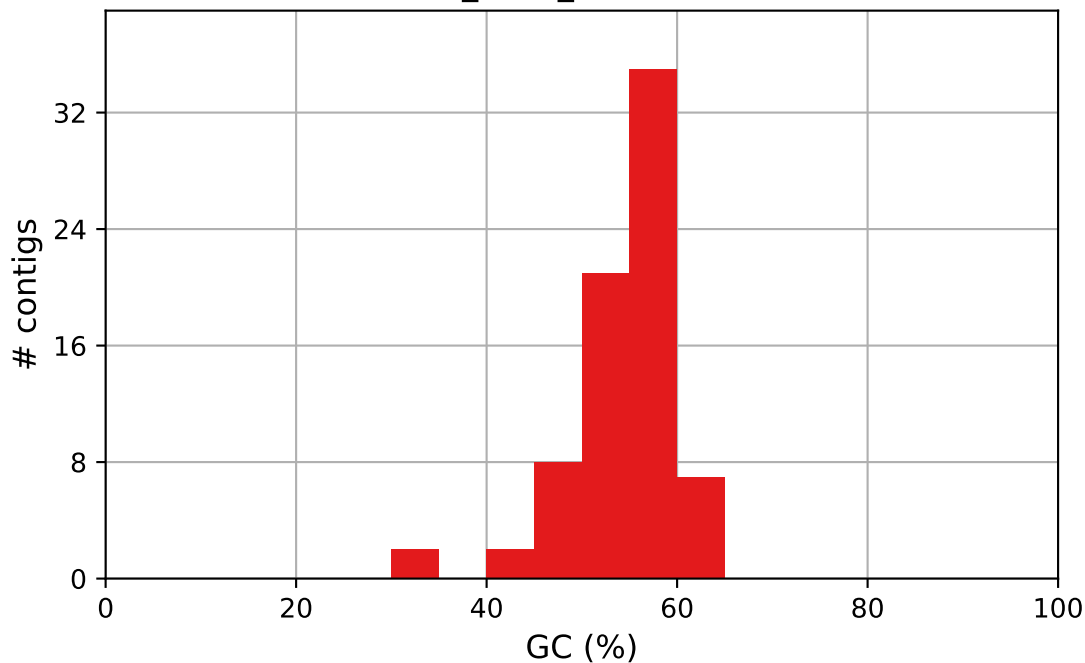
— scaffolds\_fasta\_fasta    - - scaffolds\_fasta\_fasta\_broken    - - Reference

GC content



— scaffolds\_fasta\_fasta    - - scaffolds\_fasta\_fasta\_broken    - - Reference

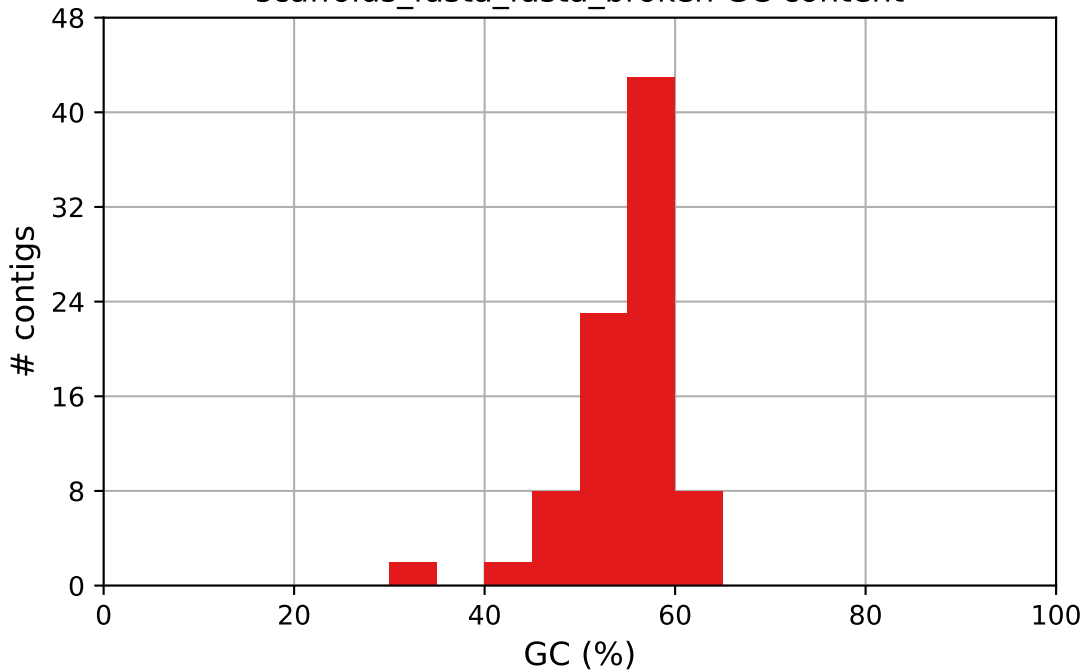
scaffolds\_fasta\_fasta GC content



scaffolds\_fasta\_fasta

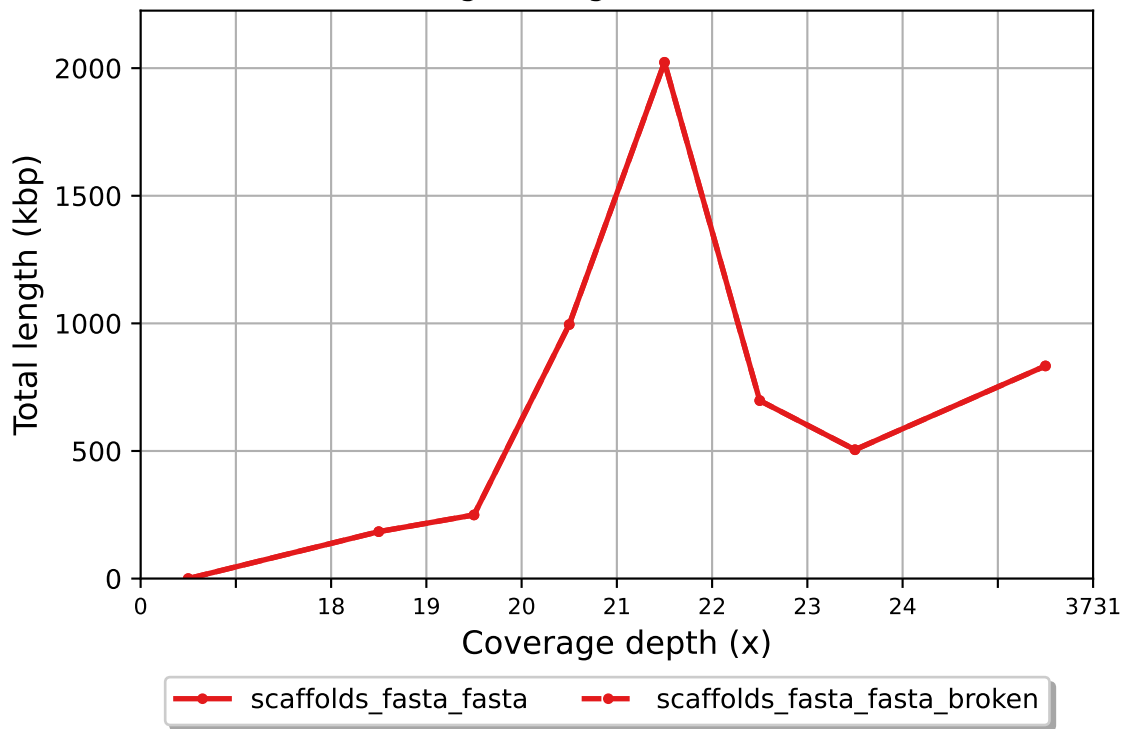


scaffolds\_fasta\_fasta\_broken GC content

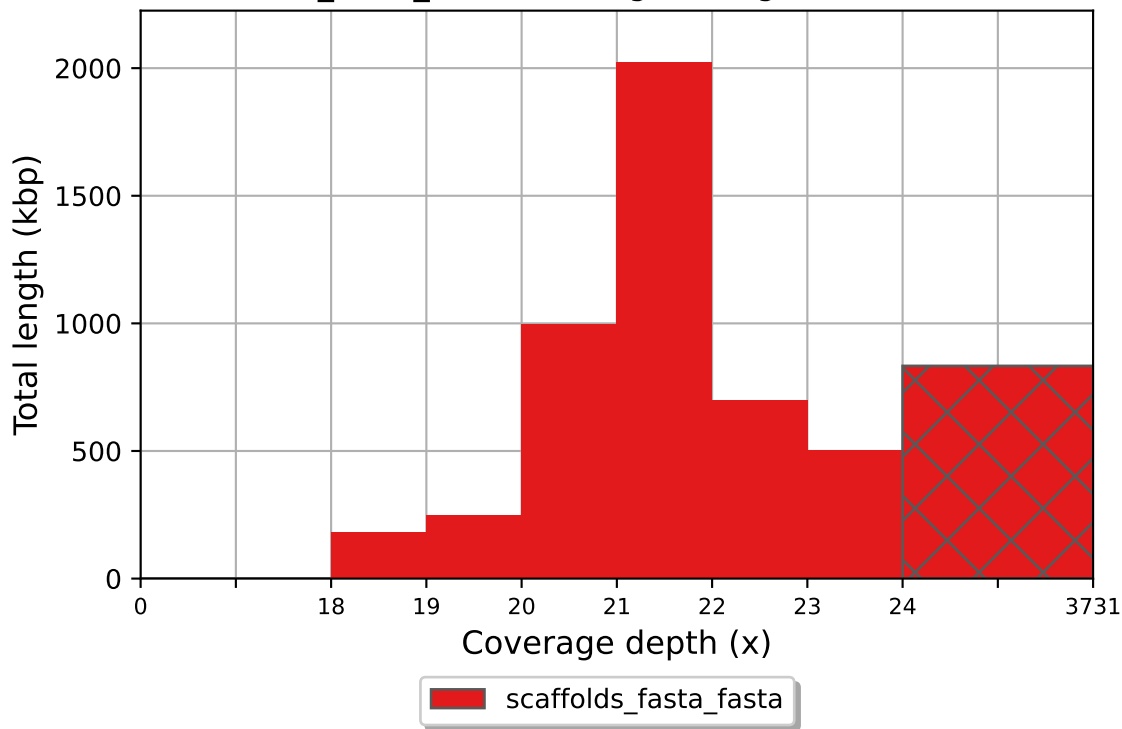


scaffolds\_fasta\_fasta\_broken

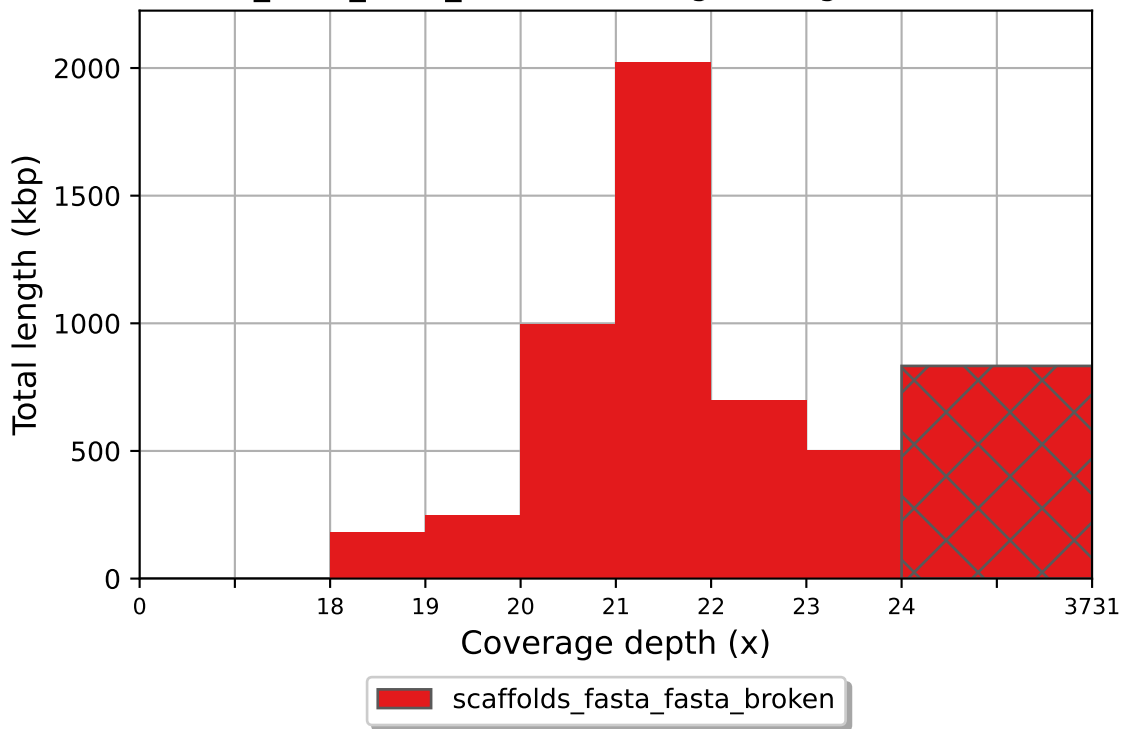
Coverage histogram (bin size: 1x)



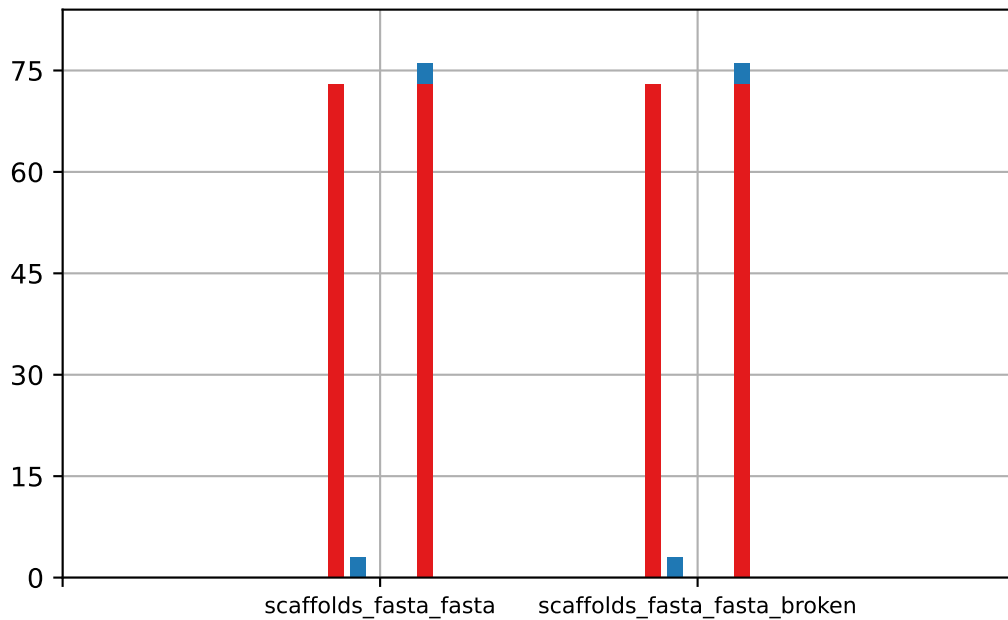
scaffolds\_fasta\_fasta coverage histogram (bin size: 1x)



scaffolds\_fasta\_fasta\_broken coverage histogram (bin size: 1x)



## Misassemblies

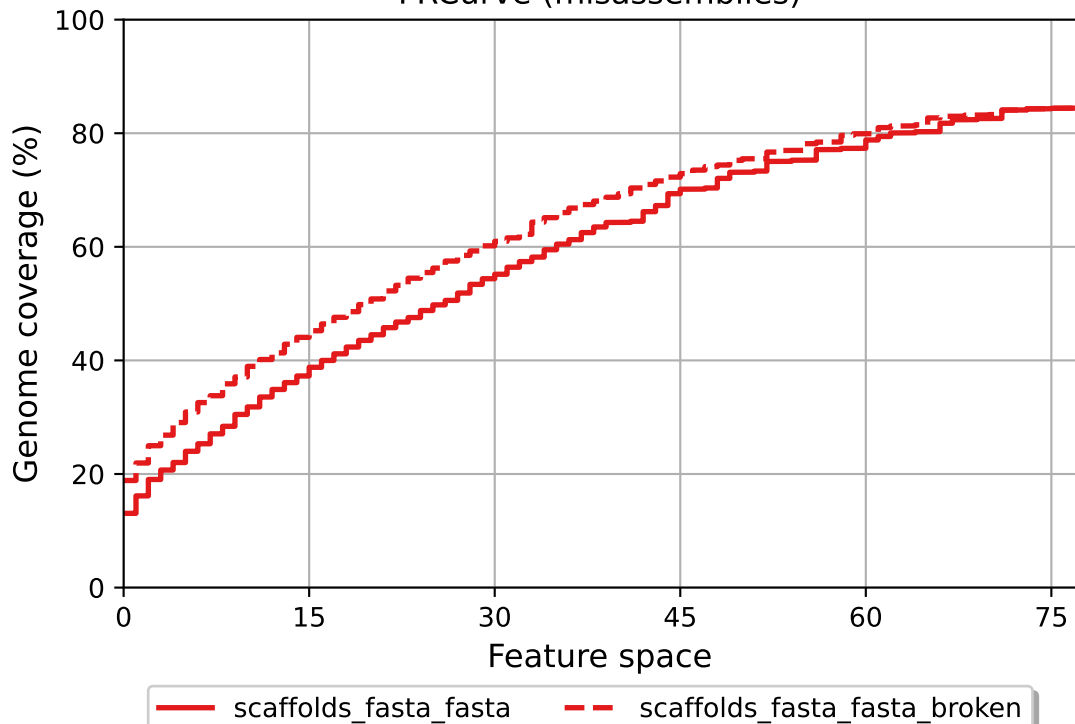


# relocations

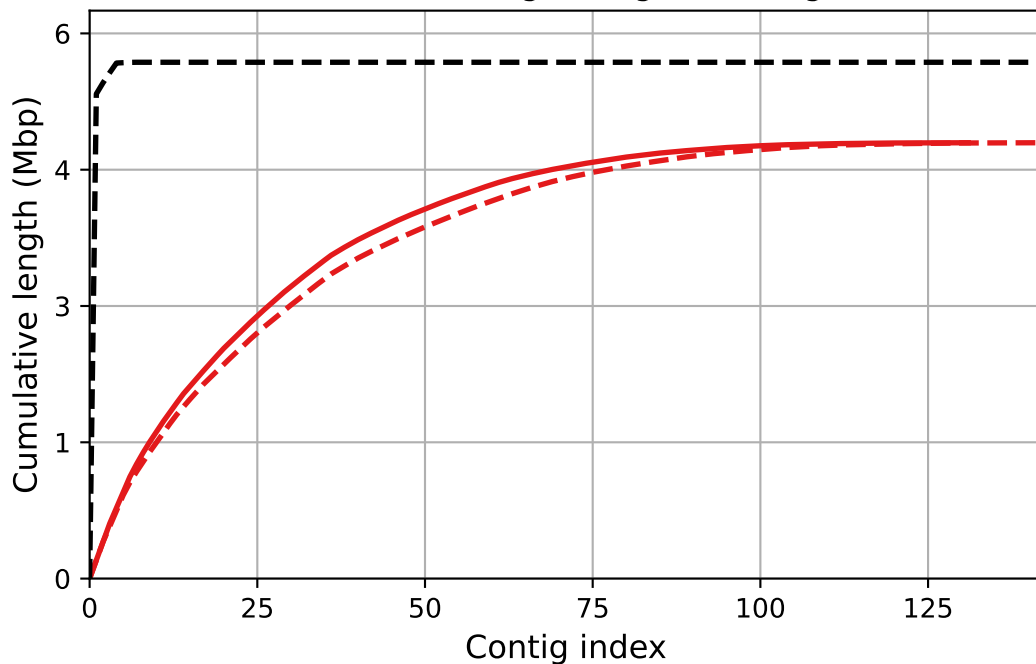


# translocations

FRCurve (misassemblies)

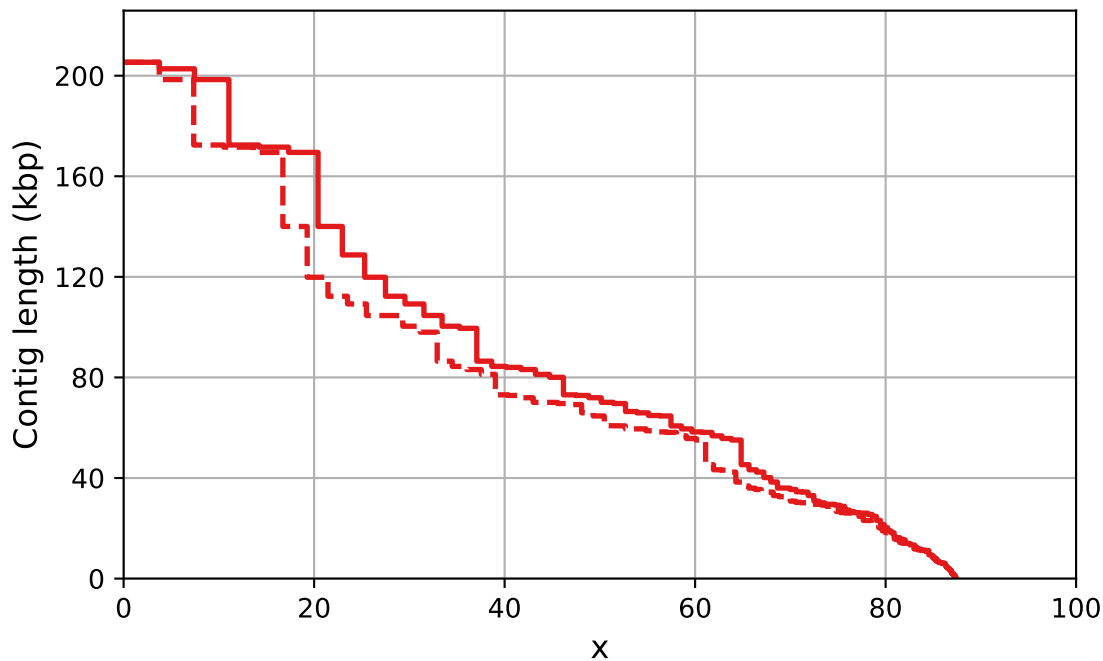


Cumulative length (aligned contigs)



— scaffolds\_fasta\_fasta    - - scaffolds\_fasta\_fasta\_broken    - - Reference

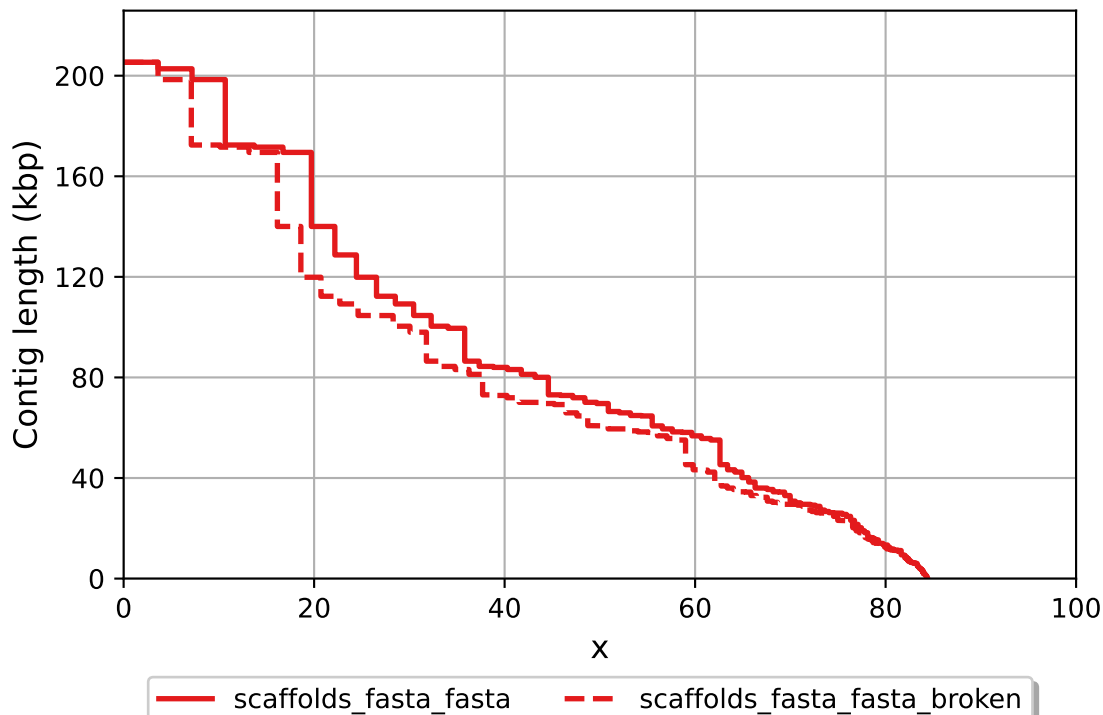
NAx



— scaffolds\_fasta\_fasta      - - scaffolds\_fasta\_fasta\_broken

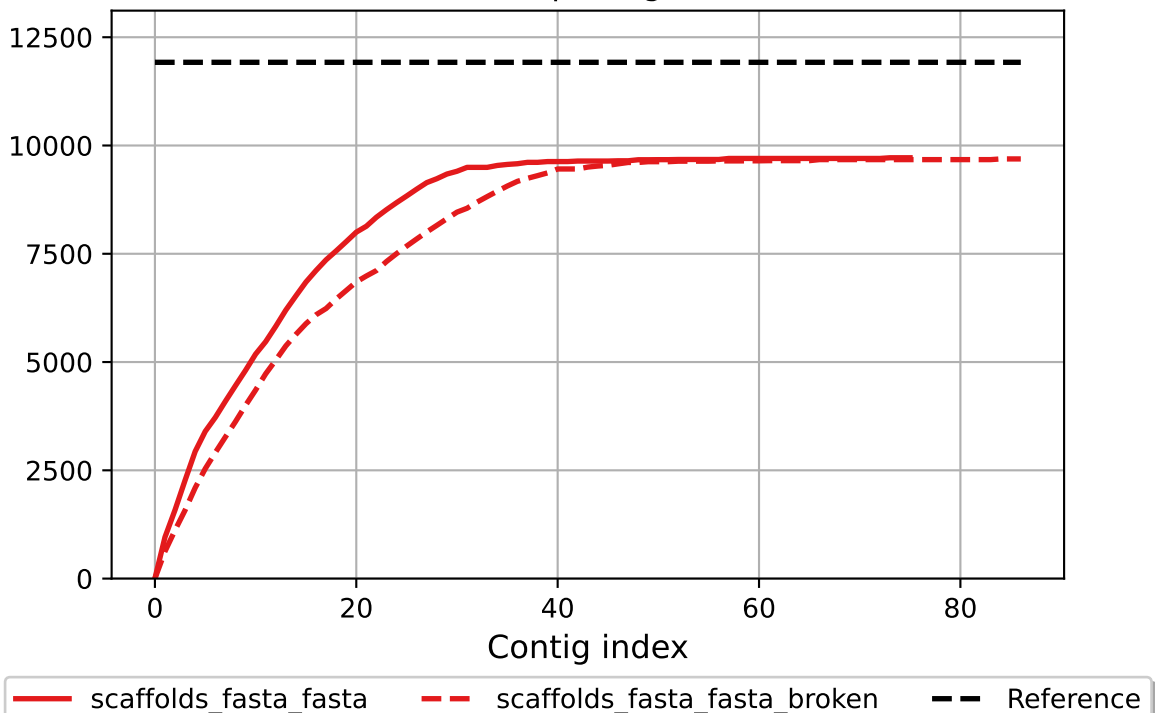


## NGAx

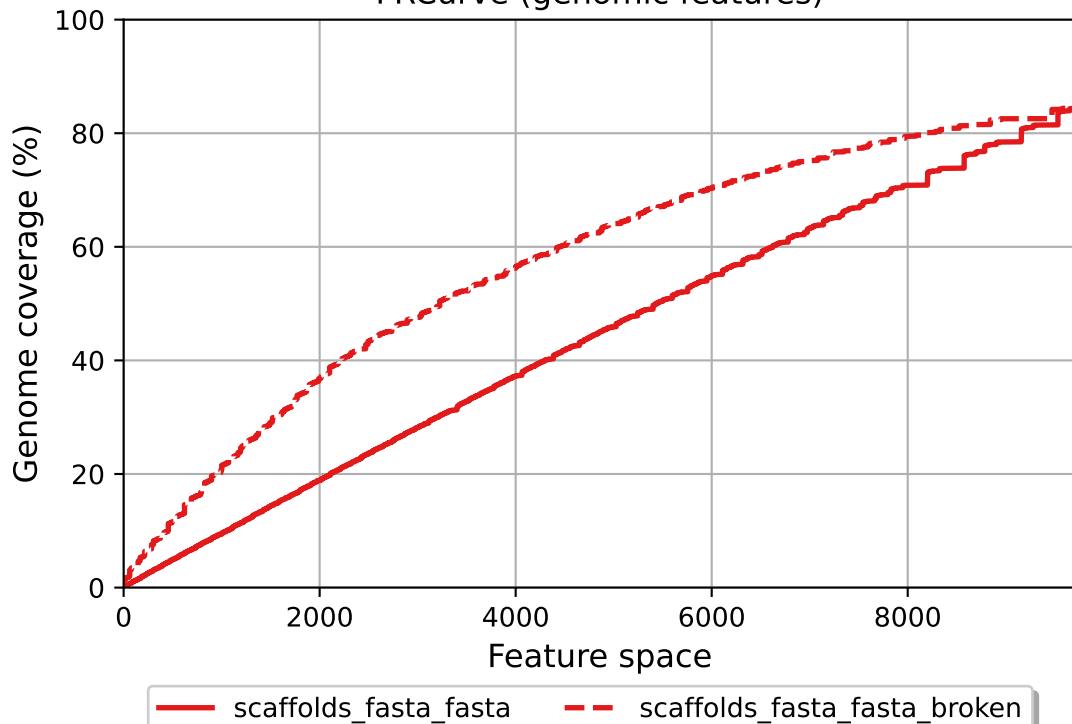


Cumulative # complete genomic features

Cumulative # complete genomic features



FRCurve (genomic features)



# complete genomic features



scaffolds\_fasta\_fasta

scaffolds\_fasta\_fasta\_broken

# Genome fraction, %



scaffolds\_fasta\_fasta



scaffolds\_fasta\_fasta\_broken