

# Report

	scaffolds	scaffolds_broken
# contigs (>= 0 bp)	404	-
# contigs (>= 1000 bp)	270	285
# contigs (>= 5000 bp)	190	201
# contigs (>= 10000 bp)	141	148
# contigs (>= 25000 bp)	59	54
# contigs (>= 50000 bp)	13	13
Total length (>= 0 bp)	4555635	-
Total length (>= 1000 bp)	4504725	4503165
Total length (>= 5000 bp)	4294132	4278360
Total length (>= 10000 bp)	3933416	3884184
Total length (>= 25000 bp)	2579412	2363848
Total length (>= 50000 bp)	1013179	1002058
# contigs	307	323
Largest contig	104244	104244
Total length	4531725	4530997
Reference length	4602977	4602977
GC (%)	68.80	68.80
Reference GC (%)	68.79	68.79
N50	27657	25496
NG50	27495	25362
N75	15782	14493
NG75	15507	13822
L50	48	51
LG50	49	52
L75	100	109
LG75	103	112
# misassemblies	7	7
# misassembled contigs	7	7
Misassembled contigs length	141261	141261
# local misassemblies	7	5
# scaffold gap size misassemblies	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	98.317	98.317
Duplication ratio	1.001	1.001
# N's per 100 kbp	16.06	0.00
# mismatches per 100 kbp	13.30	13.32
# indels per 100 kbp	2.21	1.79
# predicted genes (unique)	4471	4476
# predicted genes (>= 0 bp)	4471	4476
# predicted genes (>= 300 bp)	3891	3895
# predicted genes (>= 1500 bp)	505	504
# predicted genes (>= 3000 bp)	36	35
Largest alignment	104244	104244
Total aligned length	4530867	4530707
NA50	27657	25496
NGA50	27458	25362
NA75	15617	14211
NGA75	15442	13692
LA50	48	51
LGA50	49	52
LA75	101	109
LGA75	104	113

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

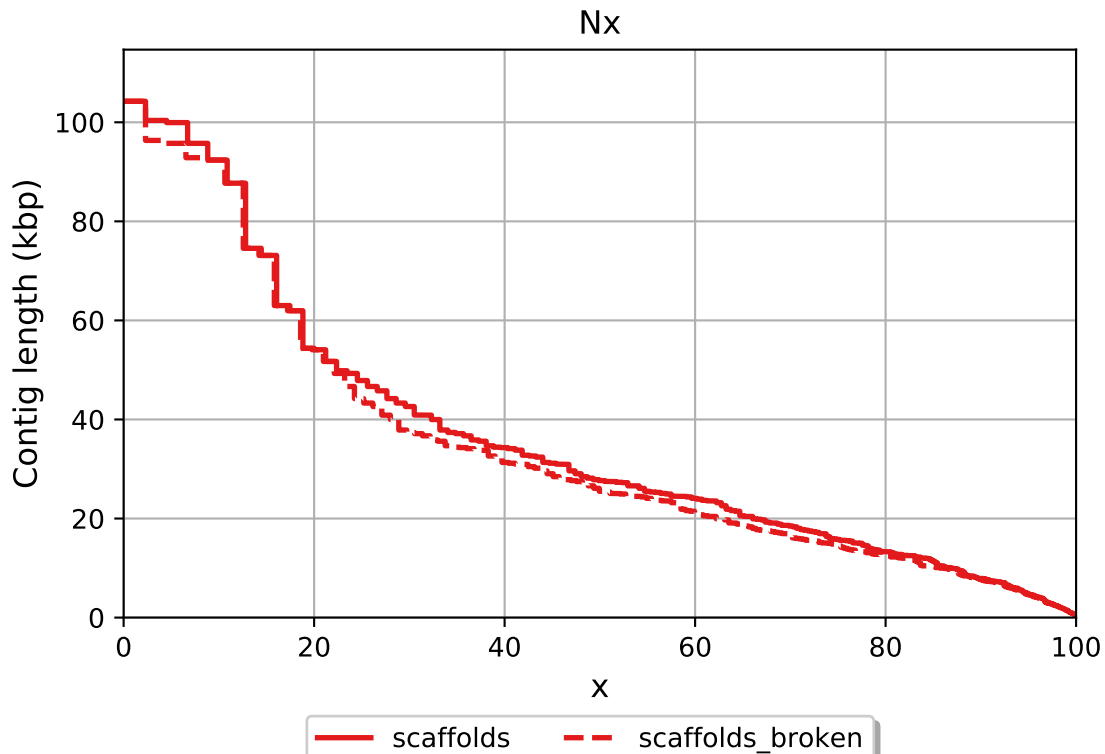
	scaffolds	scaffolds_broken
# misassemblies	7	7
# relocations	2	2
# translocations	5	5
# inversions	0	0
# misassembled contigs	7	7
Misassembled contigs length	141261	141261
# local misassemblies	7	5
# scaffold gap size misassemblies	0	-
# unaligned mis. contigs	0	0
# mismatches	602	603
# indels	100	81
# indels (<= 5 bp)	64	63
# indels (> 5 bp)	36	18
Indels length	857	443

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).

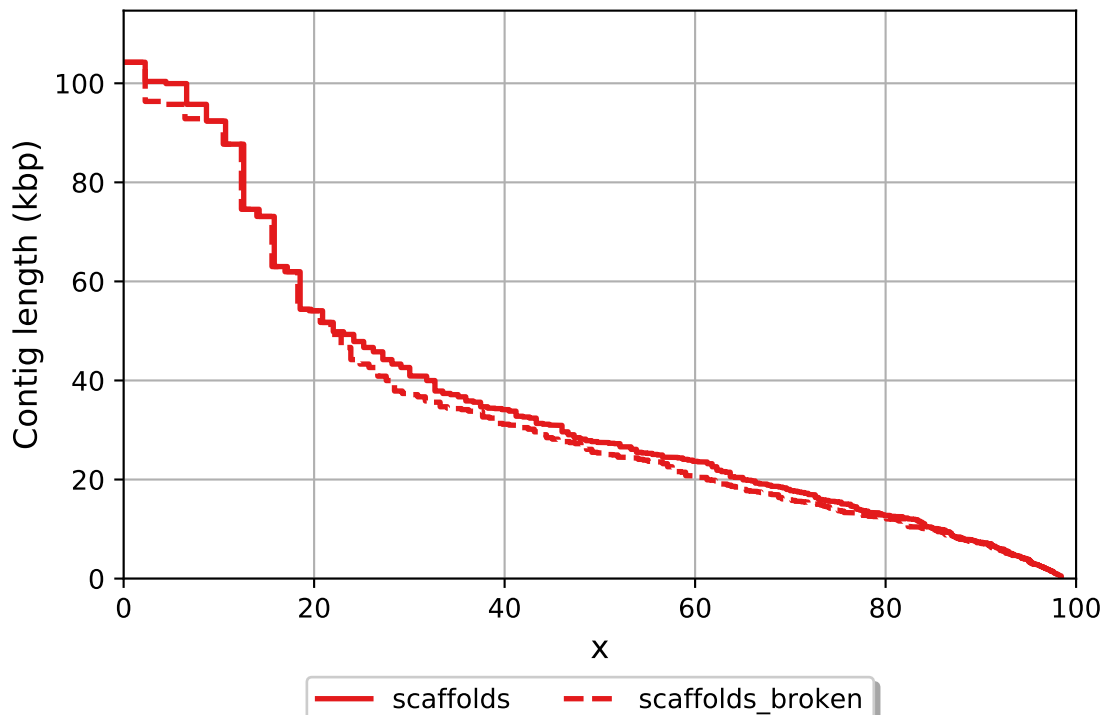
## Unaligned report

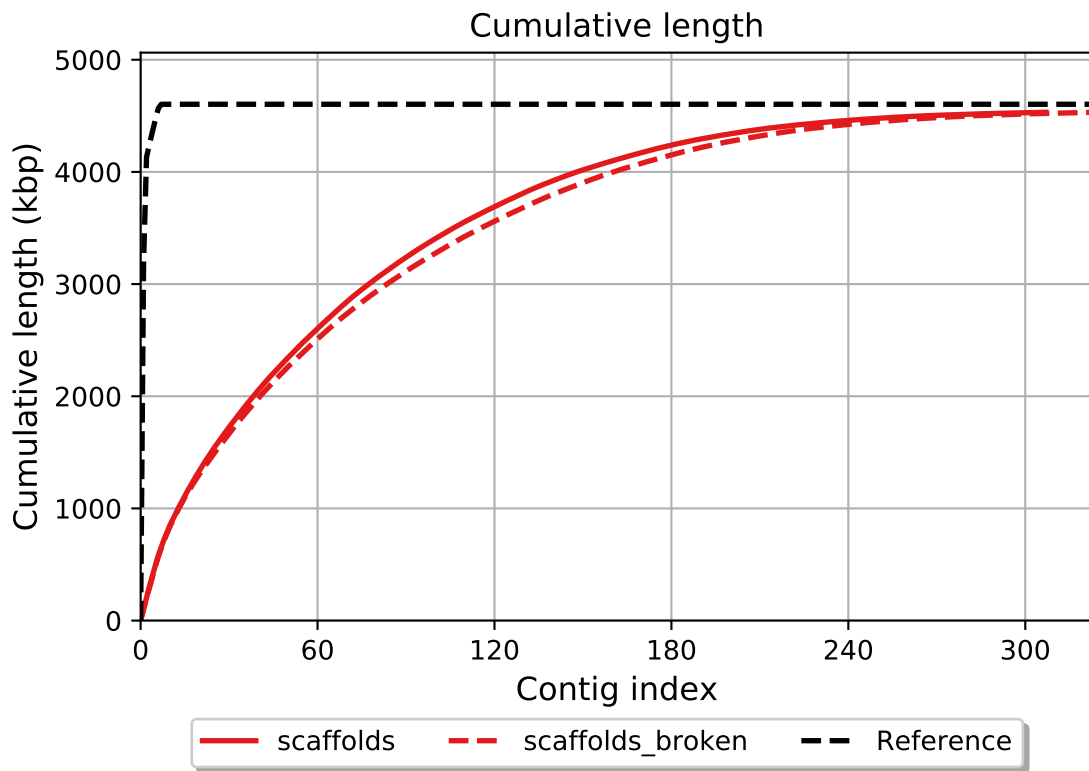
	scaffolds	scaffolds_broken
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	728	0

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).

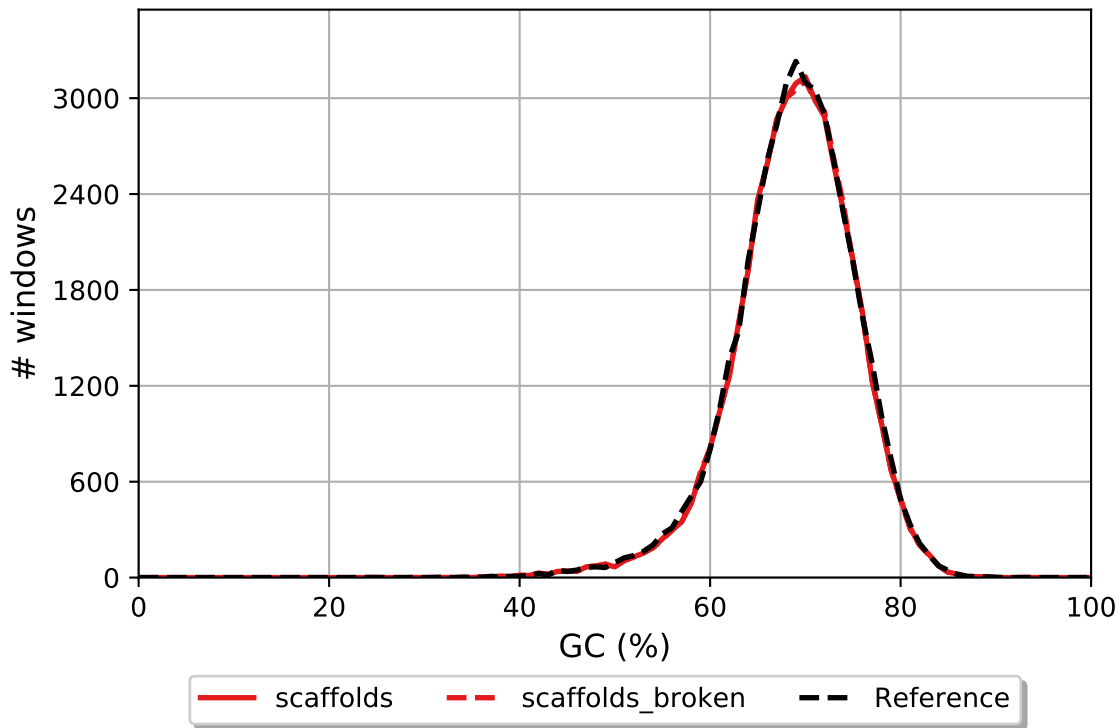


# NGx

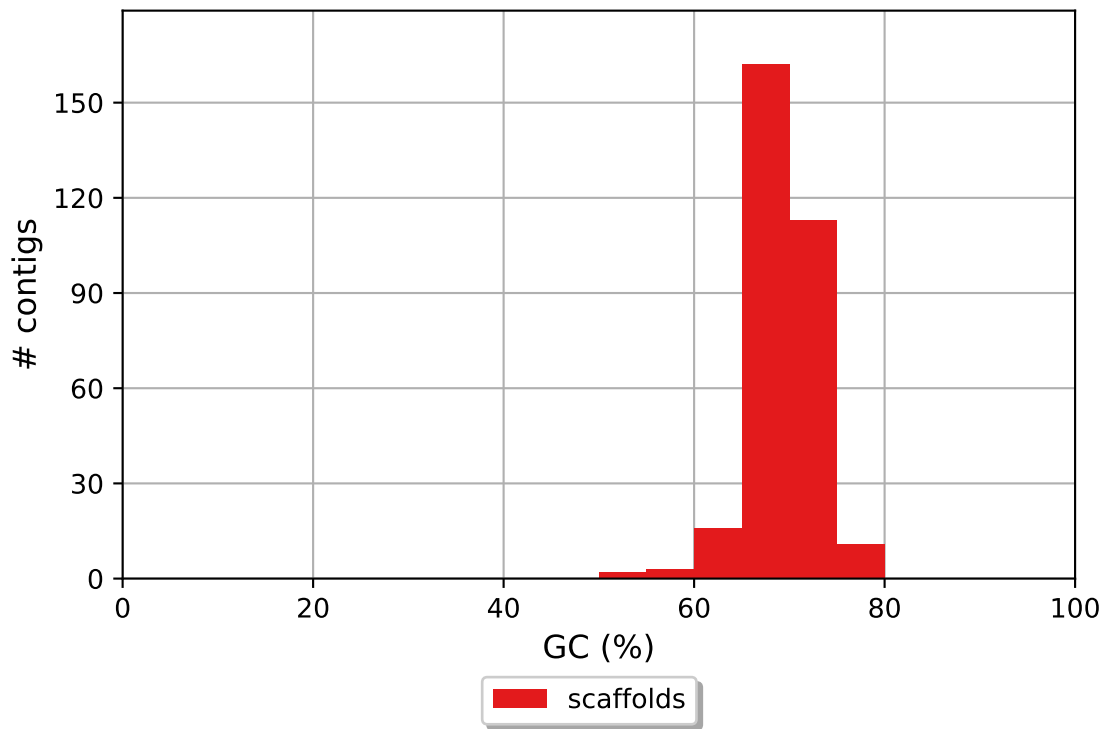




GC content

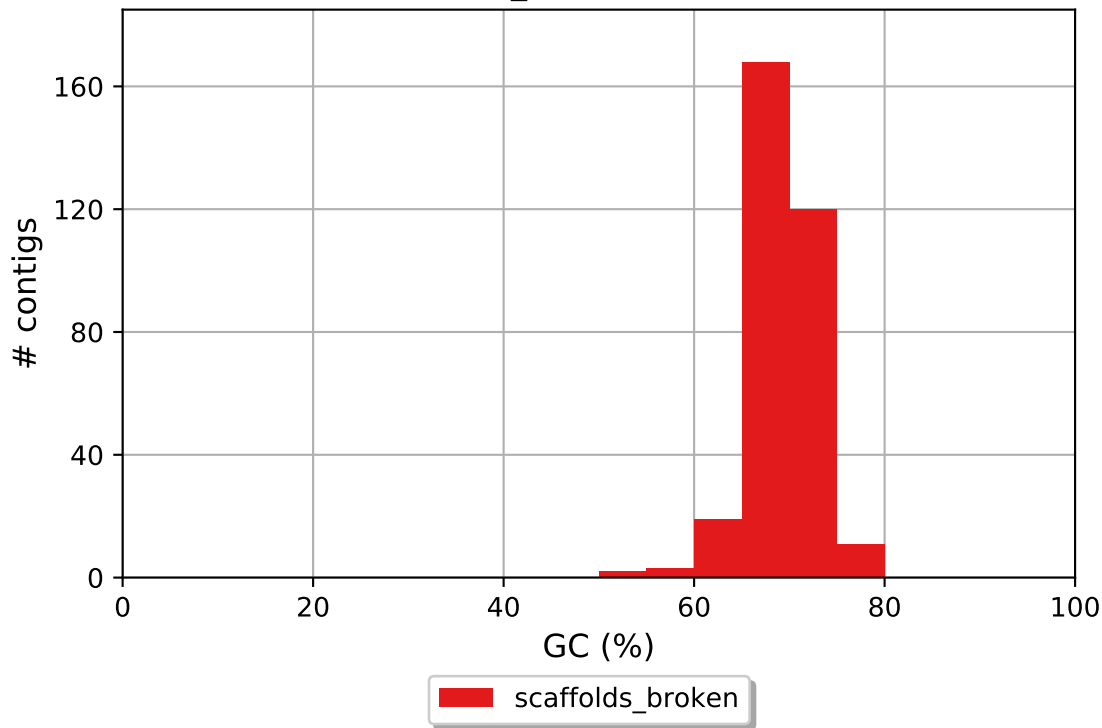


scaffolds GC content

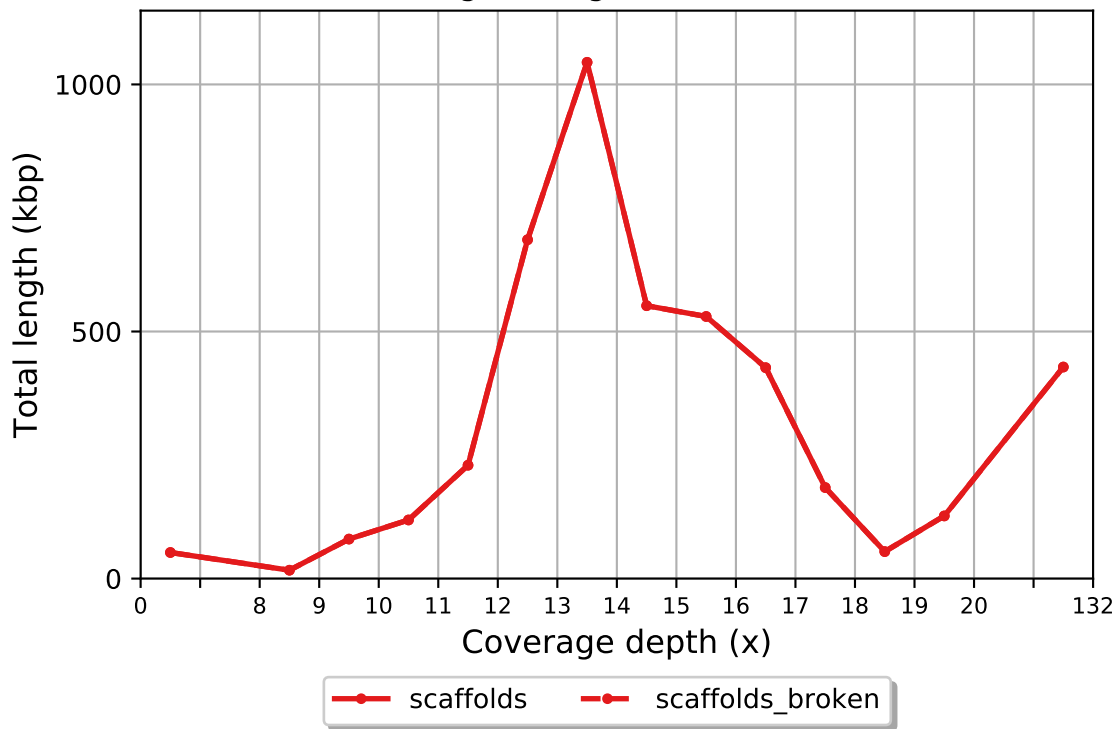




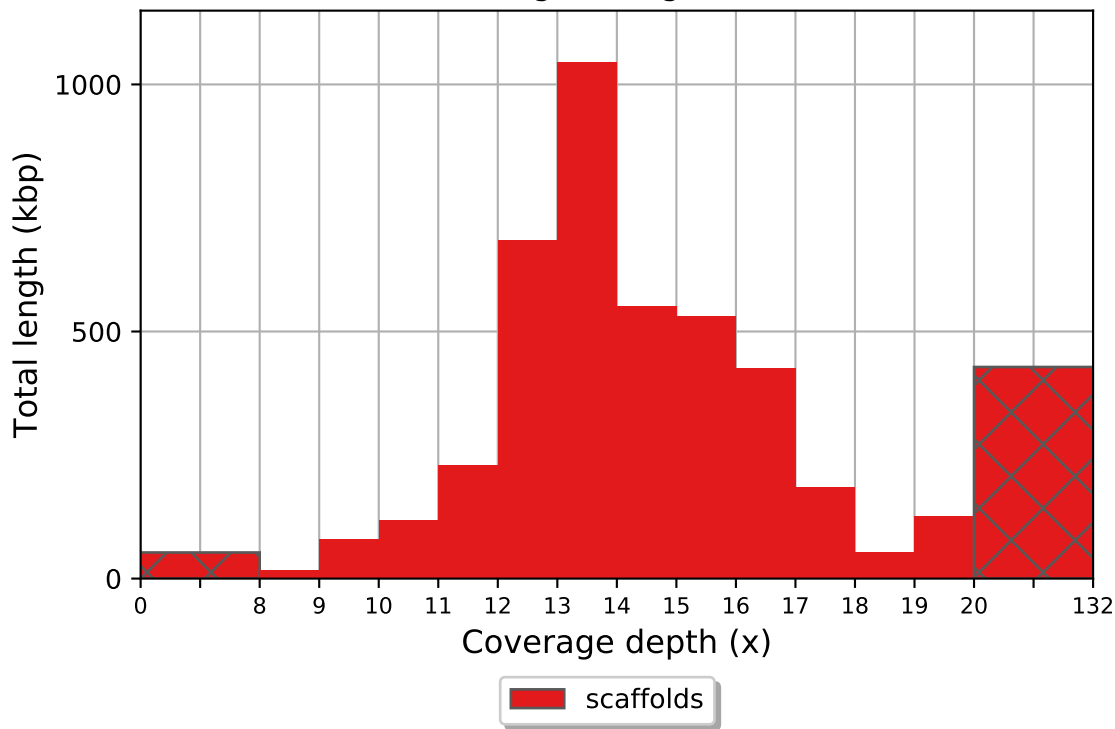
scaffolds\_broken GC content



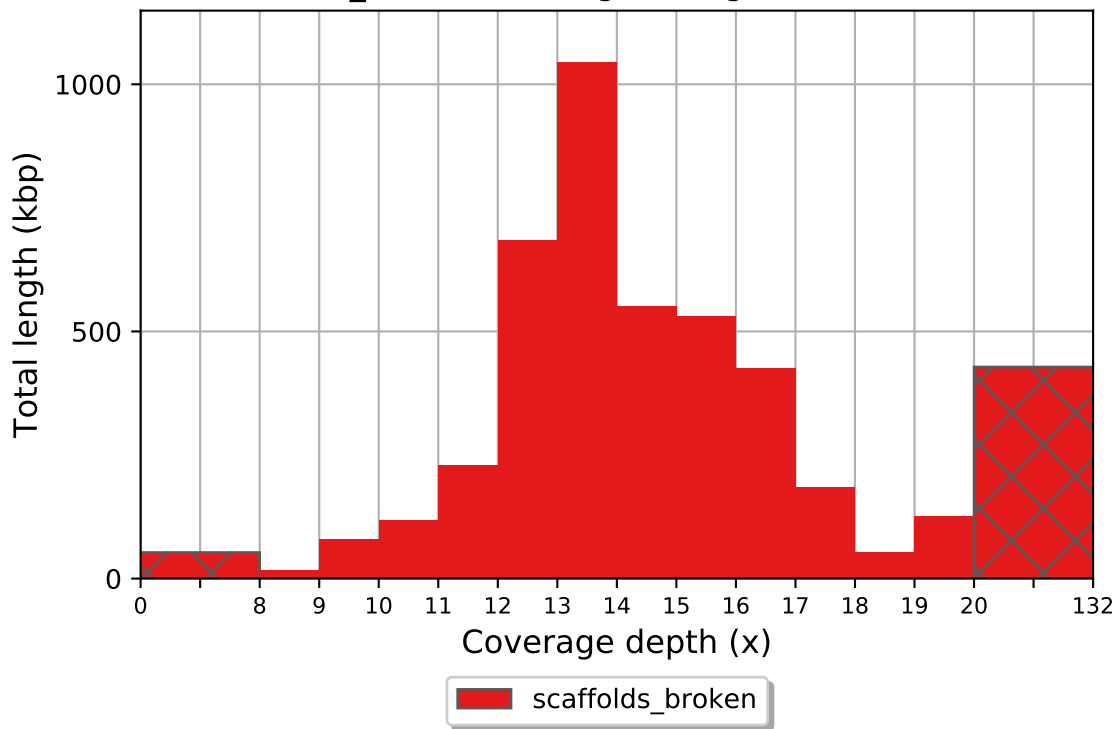
Coverage histogram (bin size: 1x)



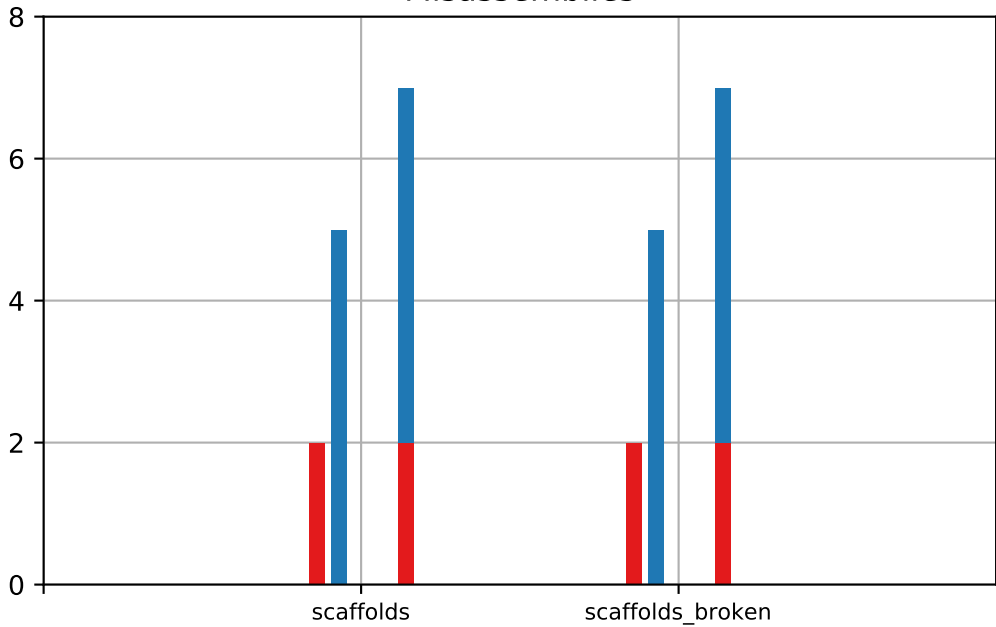
scaffolds coverage histogram (bin size: 1x)



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



## Misassemblies

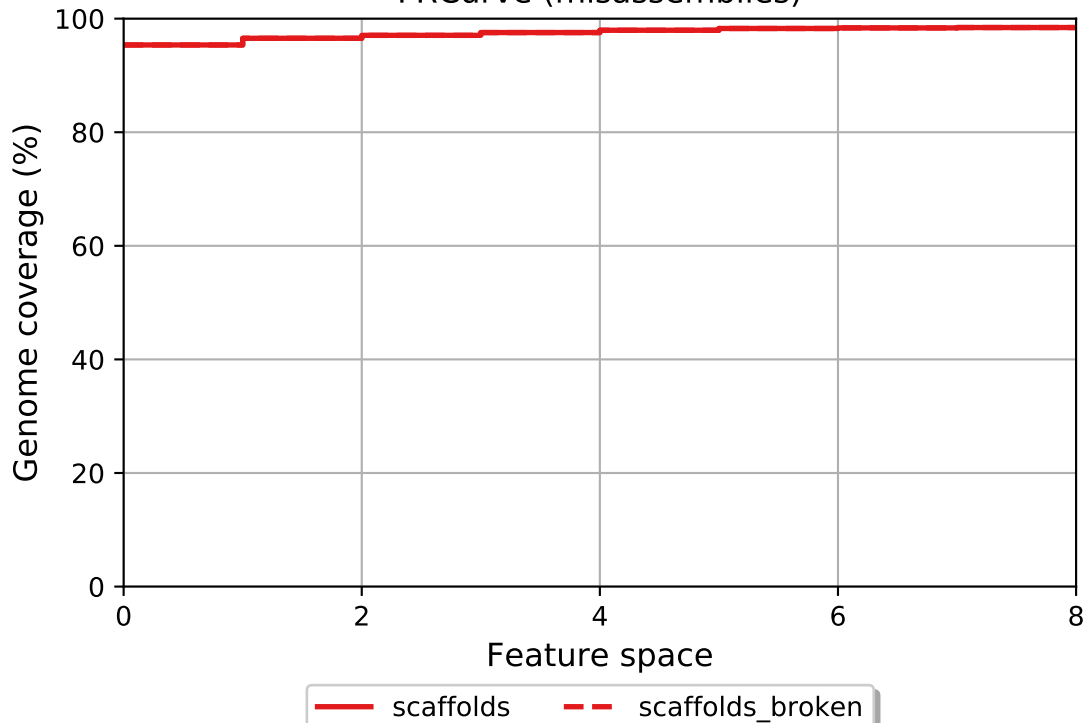


# relocations

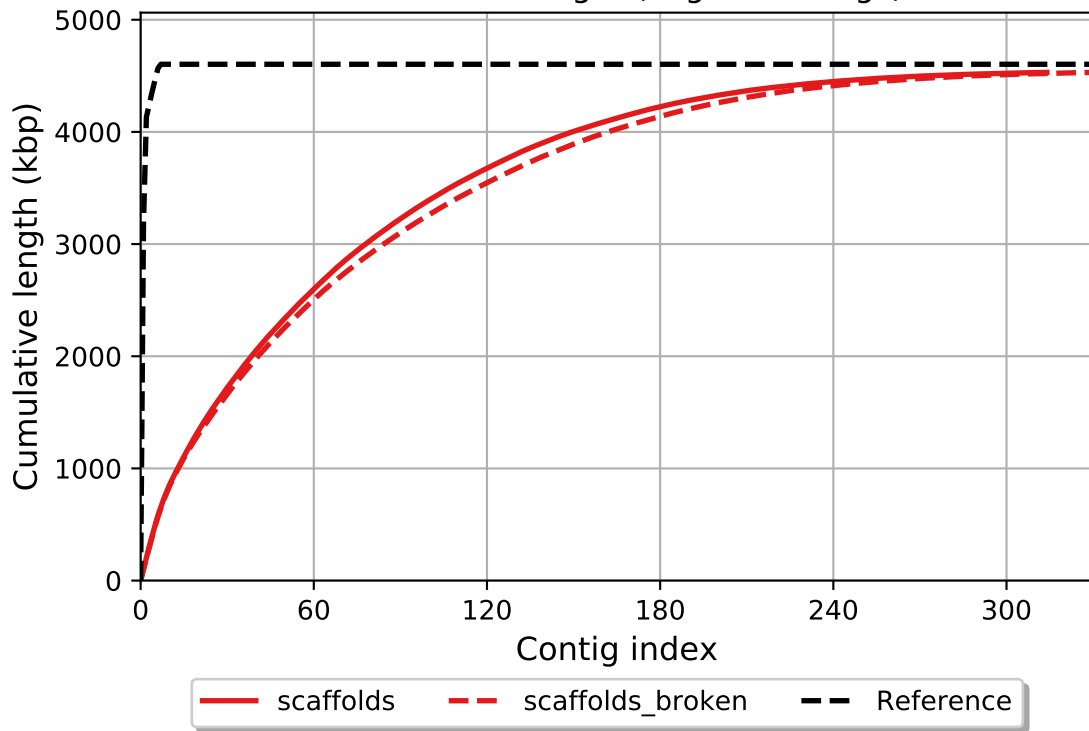


# translocations

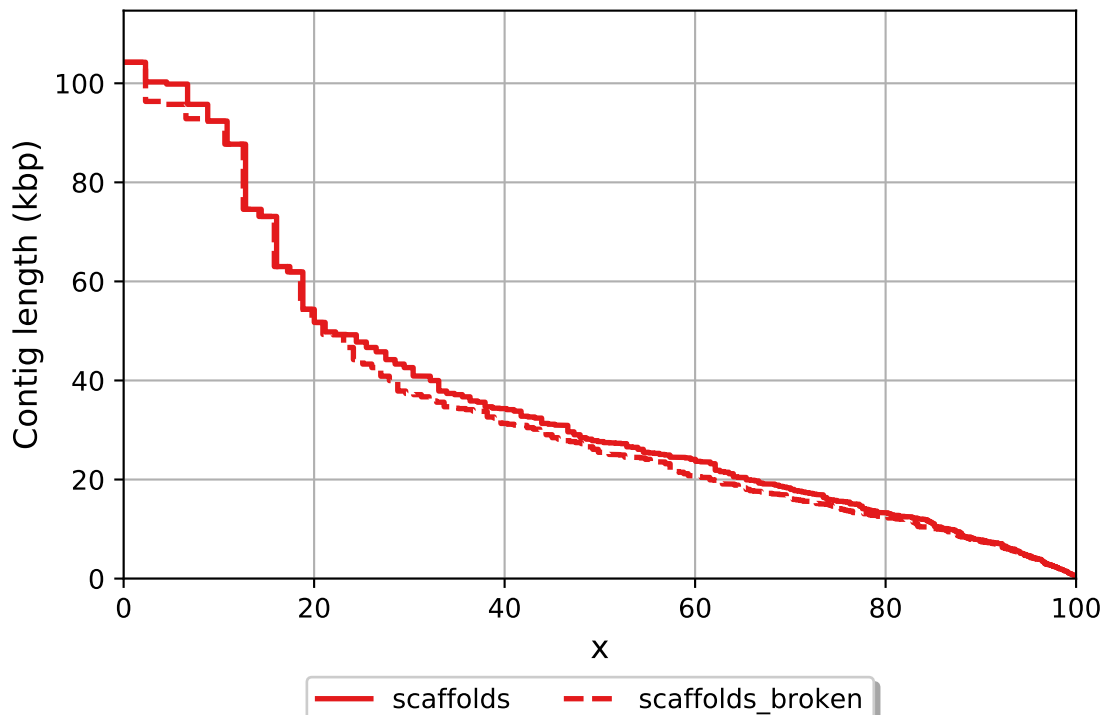
FRCurve (misassemblies)



Cumulative length (aligned contigs)

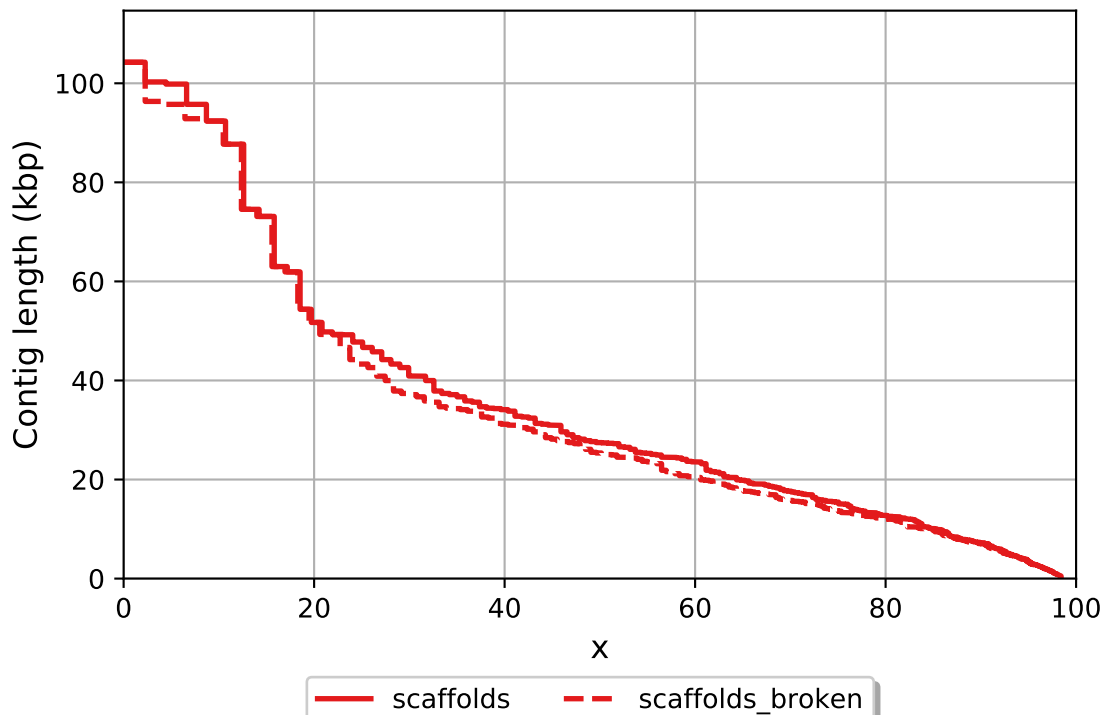


NAx





# NGAx



# Genome fraction, %

100

99



scaffolds



scaffolds\_broken