Report

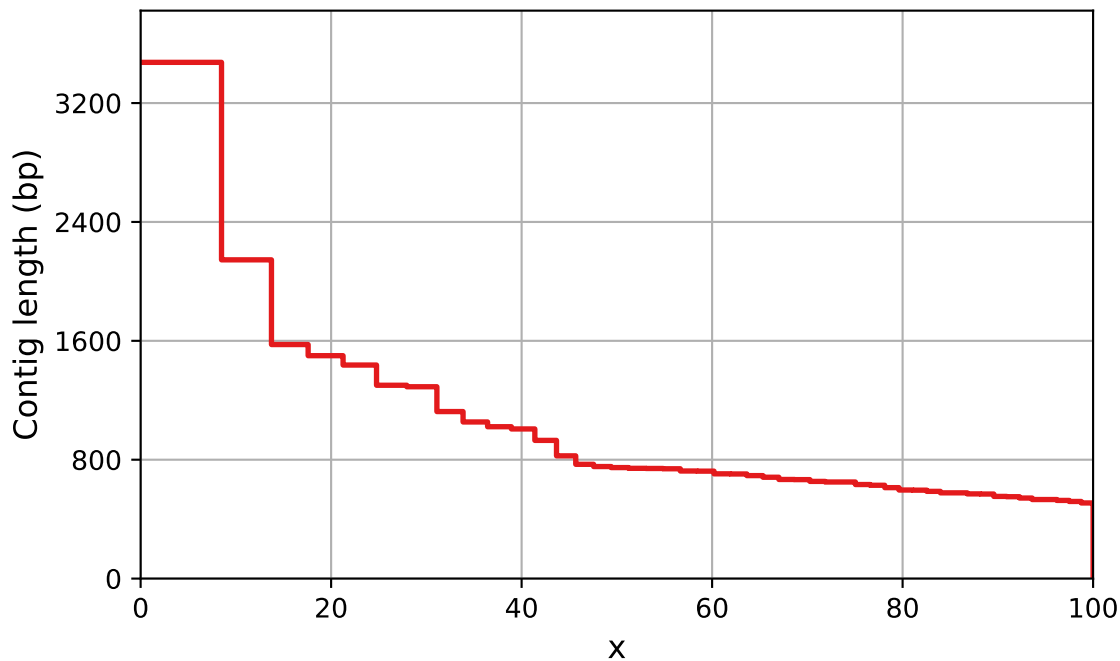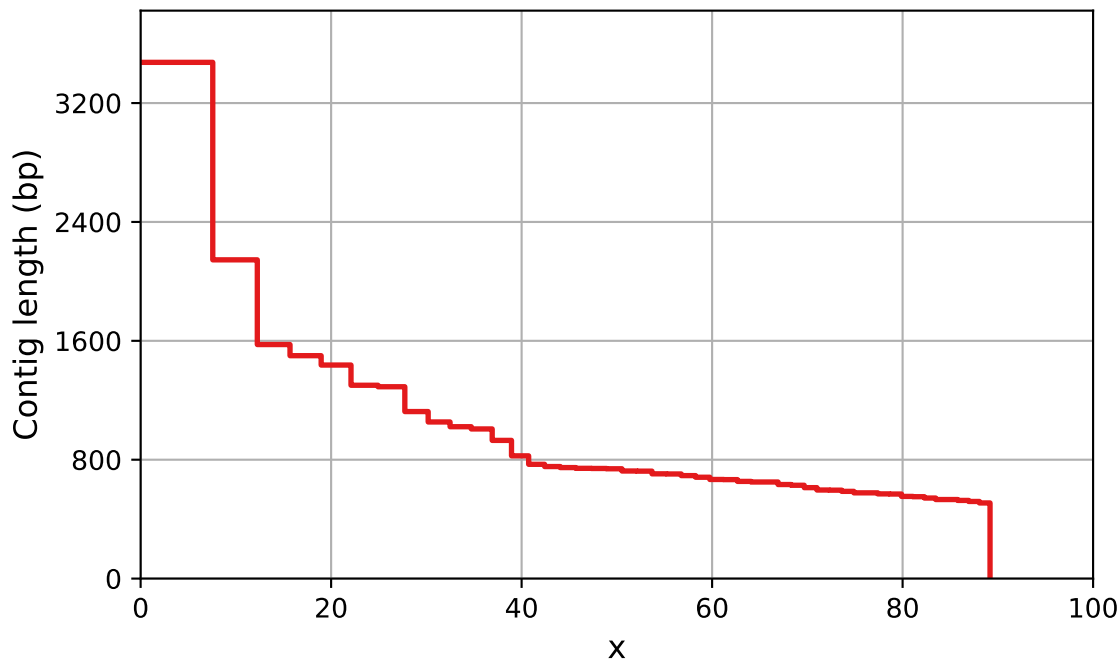|	scaffolds
# contigs (>= 0 bp)	1158
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	332643
Total length (>= 1000 bp)	16930
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	48
Largest contig	3474
Total length	40904
Reference length	45867
GC (%)	34.80
Reference GC (%)	39.17
N50	747
NG50	739
N75	650
NG75	577
L50	16
LG50	19
L75	30
LG75	37
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	46 + 1 part
Unaligned length	36979
Genome fraction (%)	8.444
Duplication ratio	1.013
# N's per 100 kbp	122.24
# mismatches per 100 kbp	103.28
# indels per 100 kbp	25.82
Largest alignment	3474
Total aligned length	3875
NGA50	-

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
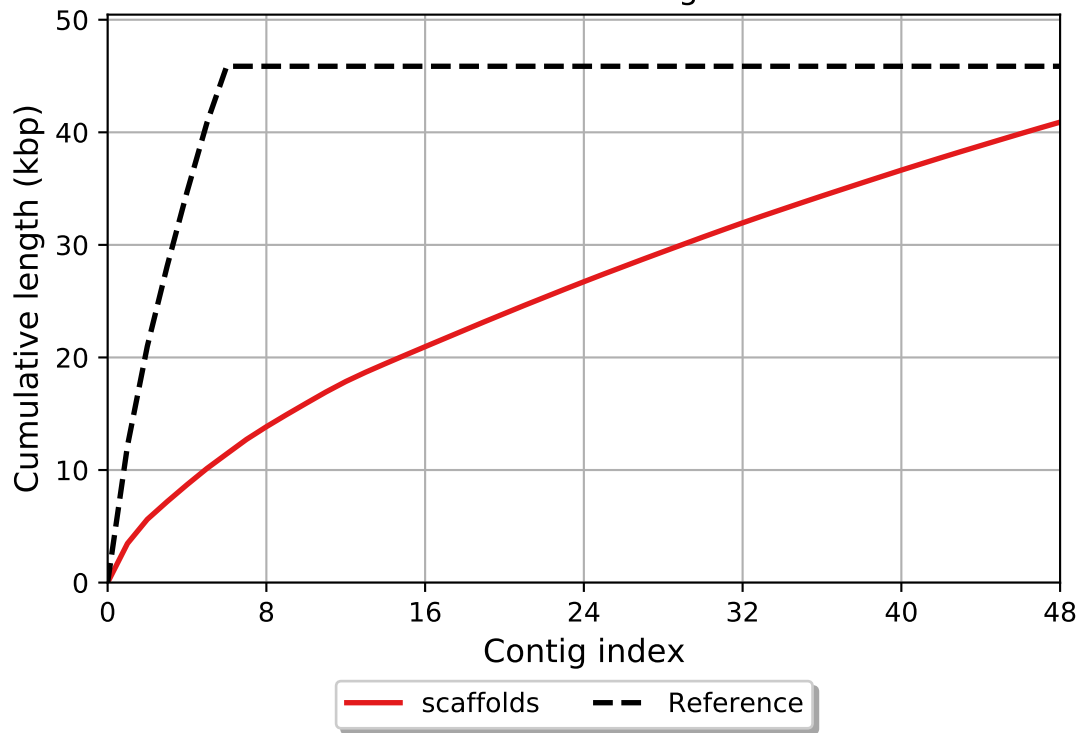
	scaffolds
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	4
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

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).

Unaligned report

	scaffolds
# fully unaligned contigs	46
Fully unaligned length	36326
# partially unaligned contigs	1
Partially unaligned length	653
# N's	50

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).
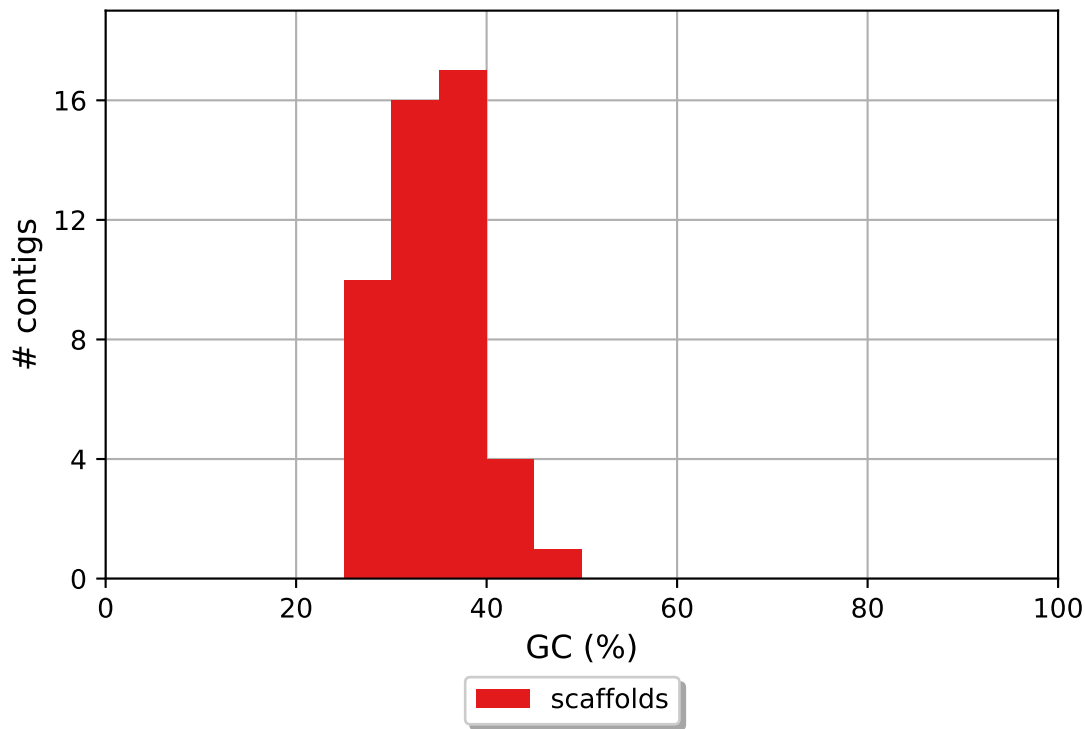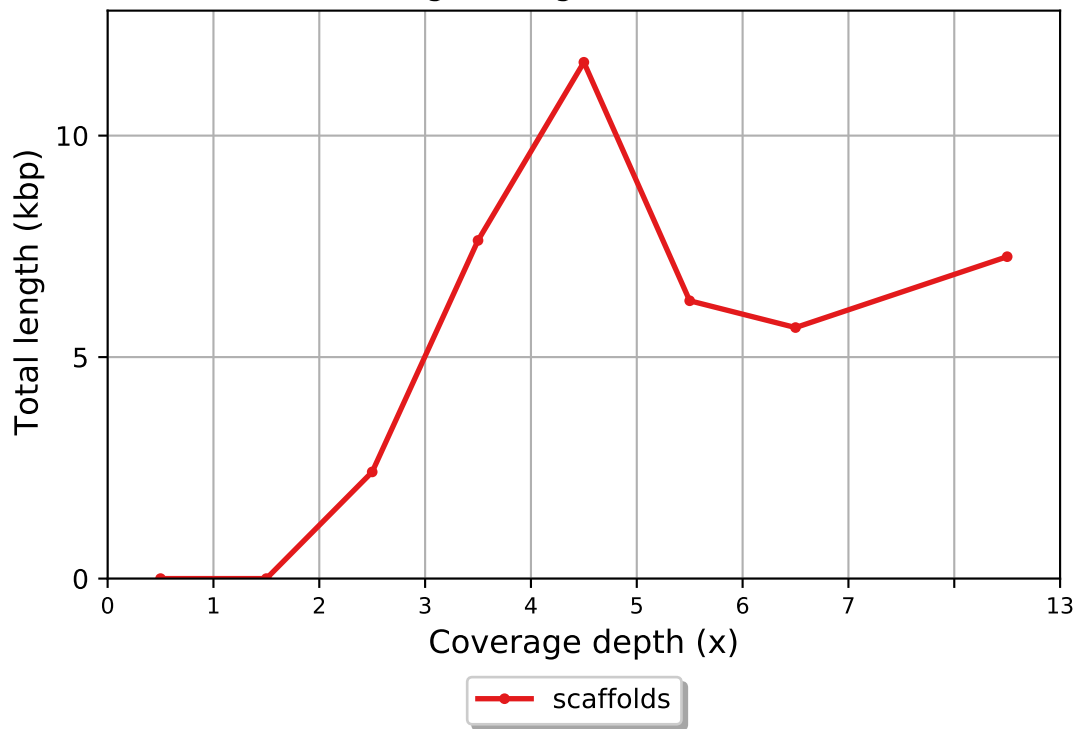
Nx

NGx

Cumulative length

GC content
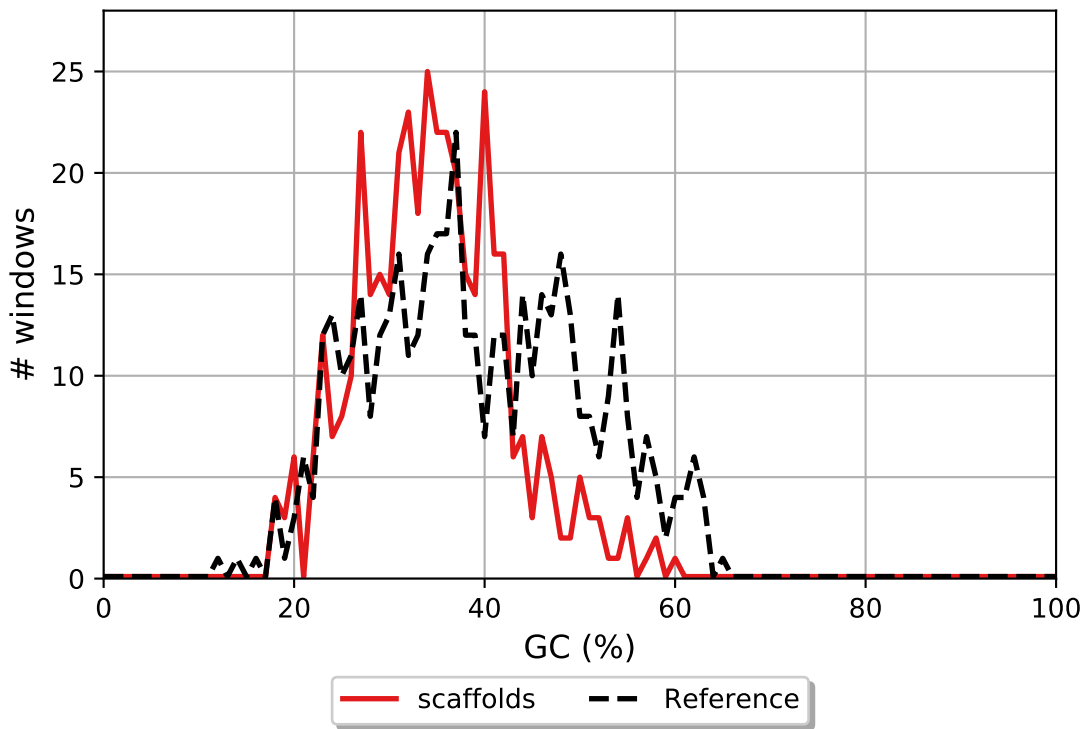
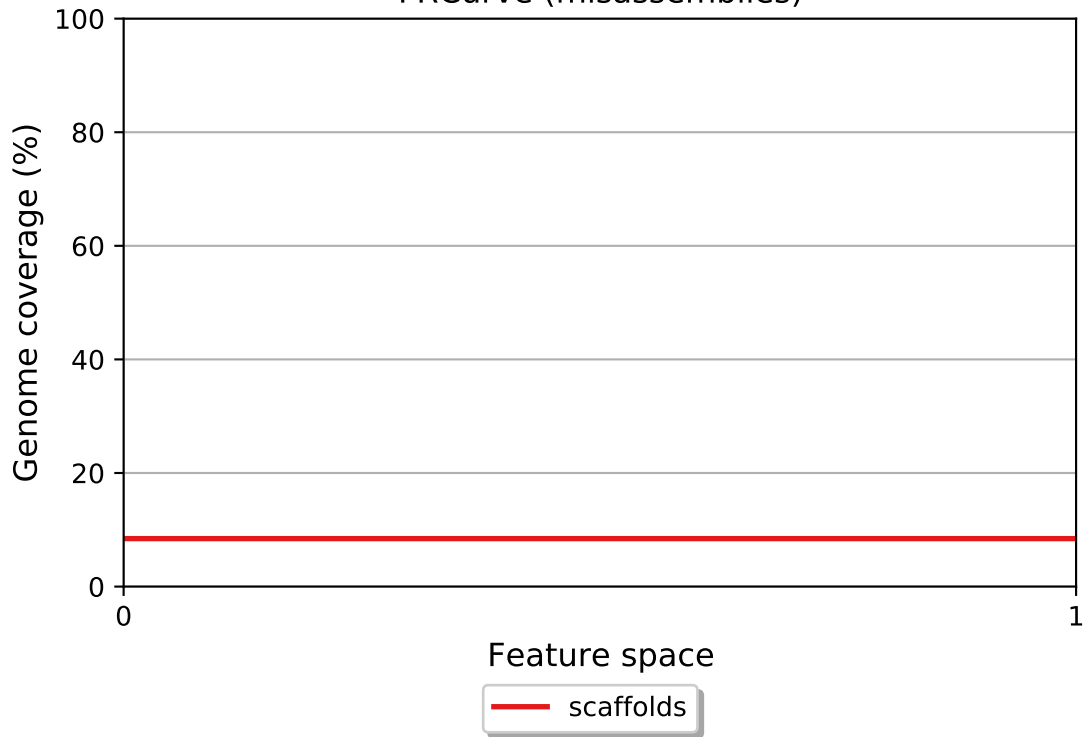scaffolds GC content

Coverage histogram (bin size: 1x)
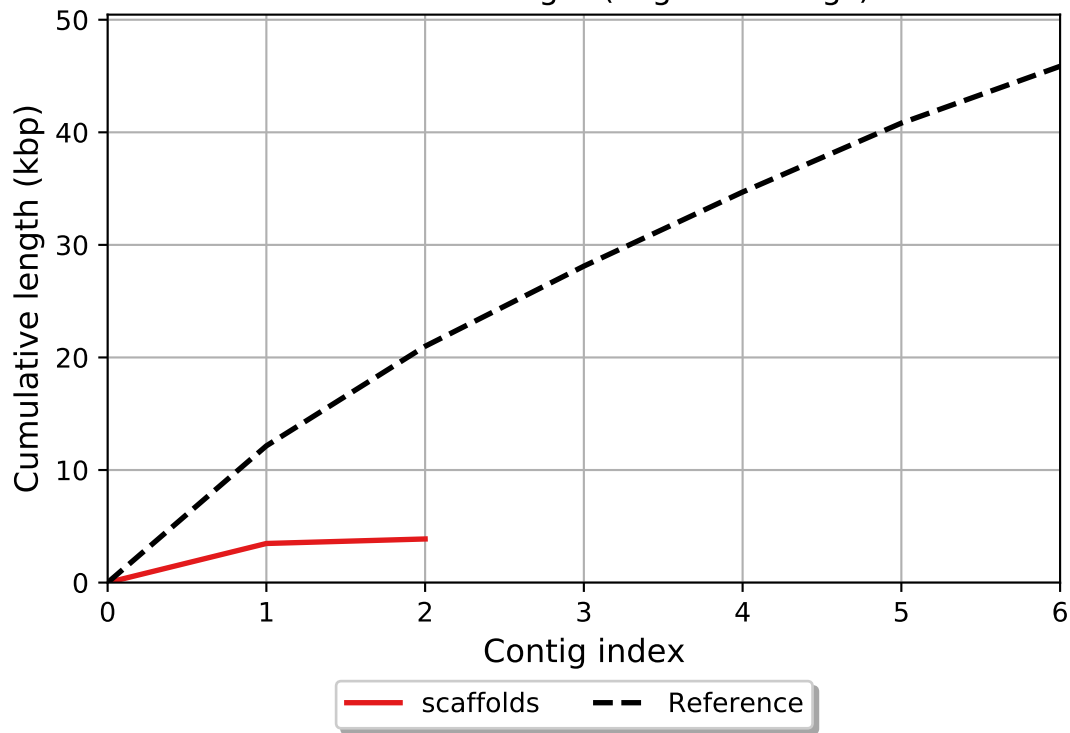
scaffolds coverage histogram (bin size: 1x)
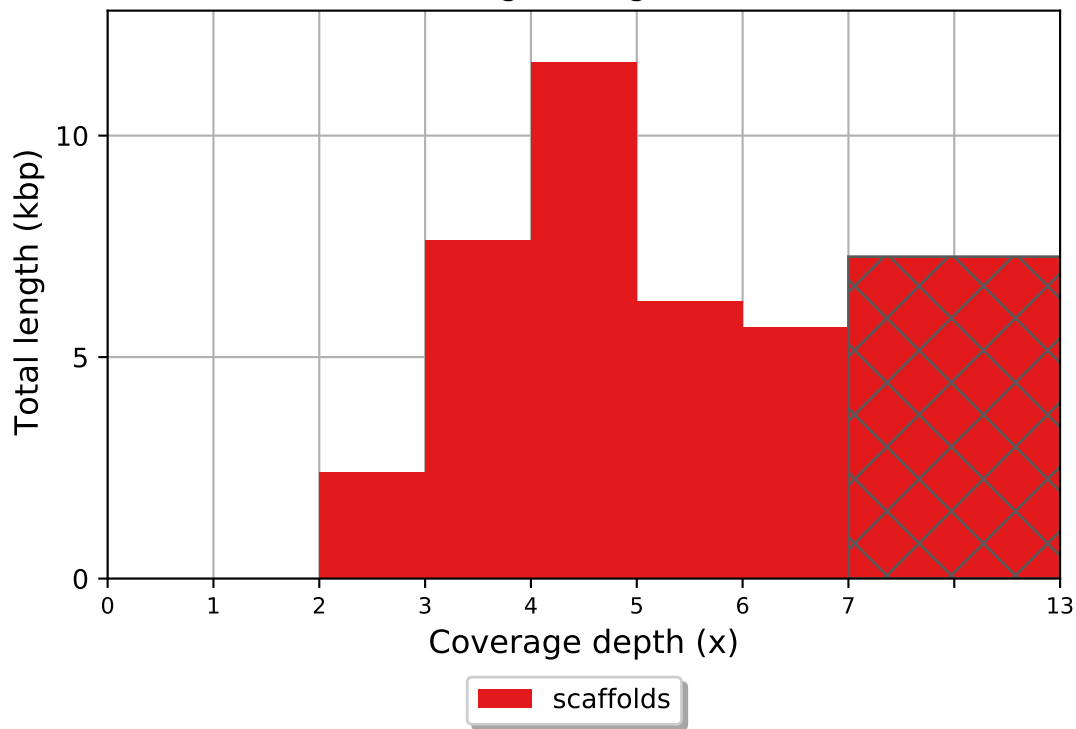
Misassemblies
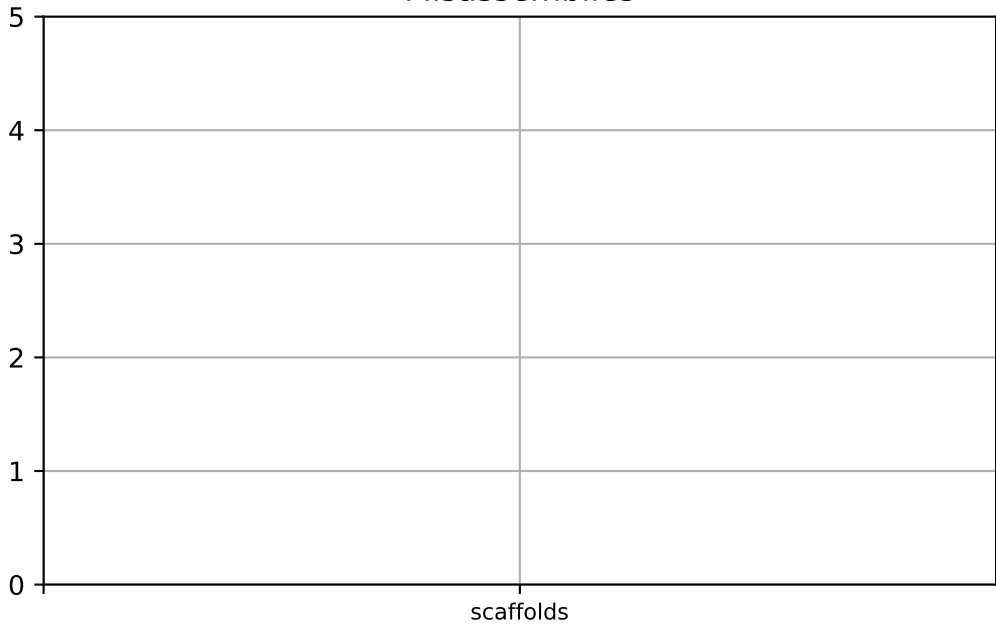
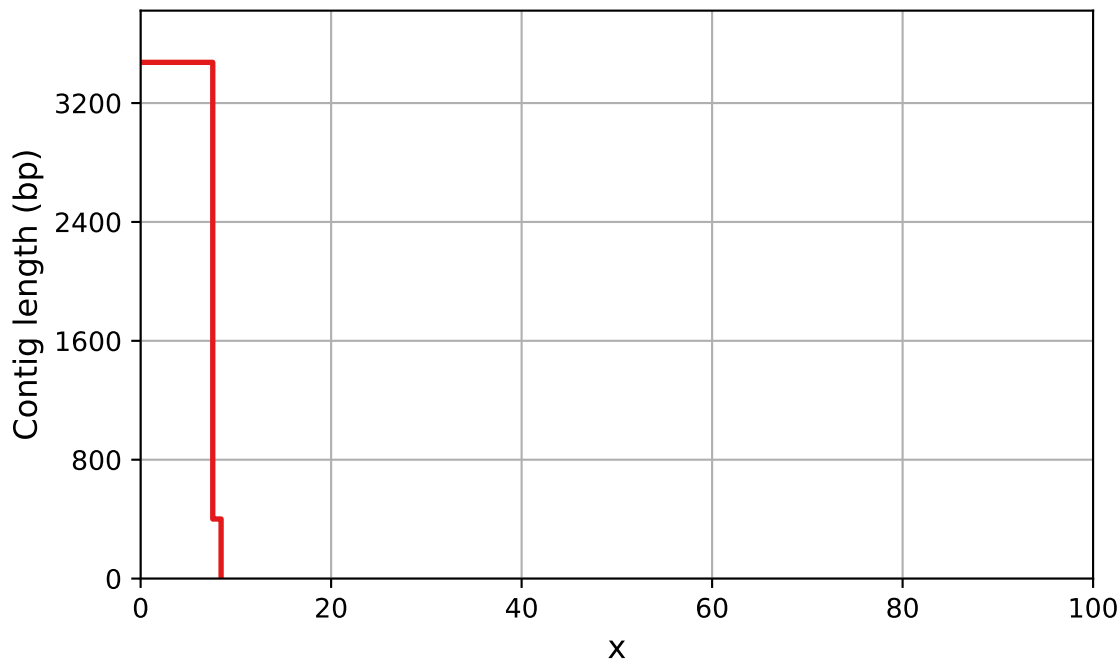FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

NGAx