

Report

	scaffolds
# contigs (>= 0 bp)	82
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	4650085
Total length (>= 1000 bp)	4625516
Total length (>= 5000 bp)	4607778
Total length (>= 10000 bp)	4601038
Total length (>= 25000 bp)	4601038
Total length (>= 50000 bp)	4601038
# contigs	18
Largest contig	4601038
Total length	4630354
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	4601038
NG50	4601038
N75	4601038
NG75	4601038
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	4
# misassembled contigs	1
Misassembled contigs length	4601038
# local misassemblies	10
# scaffold gap ext. mis.	5
# scaffold gap loc. mis.	19
# unaligned mis. contigs	0
# unaligned contigs	5 + 1 part
Unaligned length	3442
Genome fraction (%)	99.423
Duplication ratio	1.003
# N's per 100 kbp	205.10
# mismatches per 100 kbp	3.42
# indels per 100 kbp	0.41
Largest alignment	2821658
Total aligned length	4615088
NA50	2821658
NGA50	2821658
NA75	1286505
NGA75	1286505
LA50	1
LGA50	1
LA75	2
LGA75	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).

## Misassemblies report

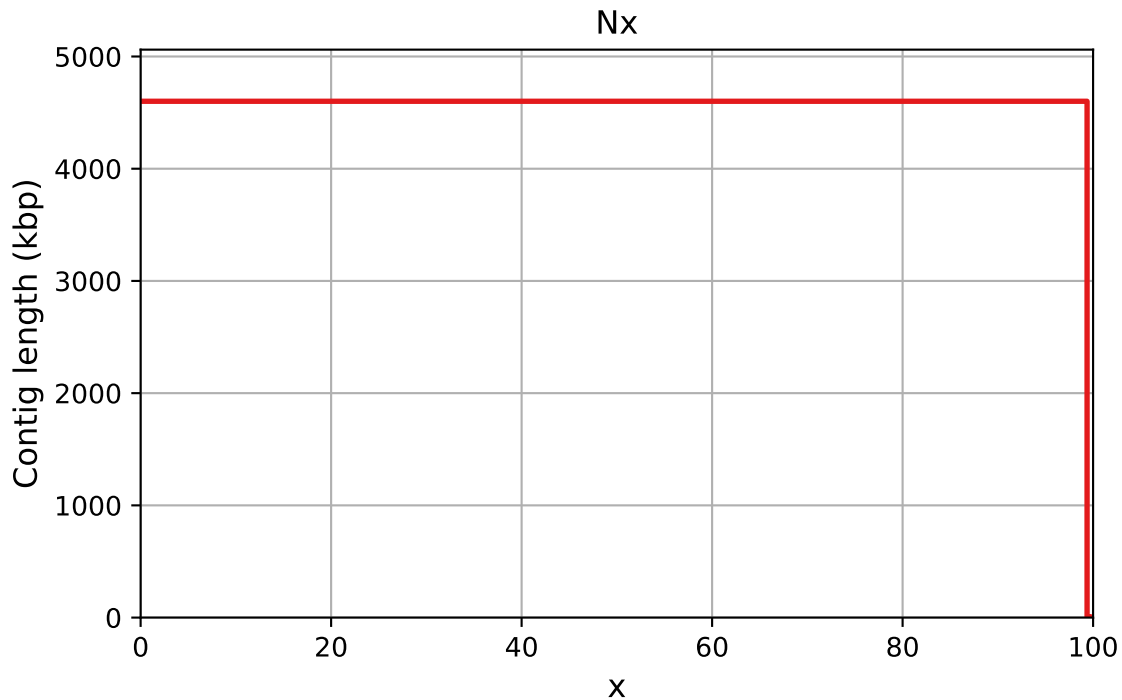
	scaffolds
# misassemblies	4
# contig misassemblies	4
# c. relocations	4
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	4601038
# local misassemblies	10
# scaffold gap ext. mis.	5
# scaffold gap loc. mis.	19
# unaligned mis. contigs	0
# mismatches	158
# indels	19
# indels (<= 5 bp)	12
# indels (> 5 bp)	7
Indels length	575

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

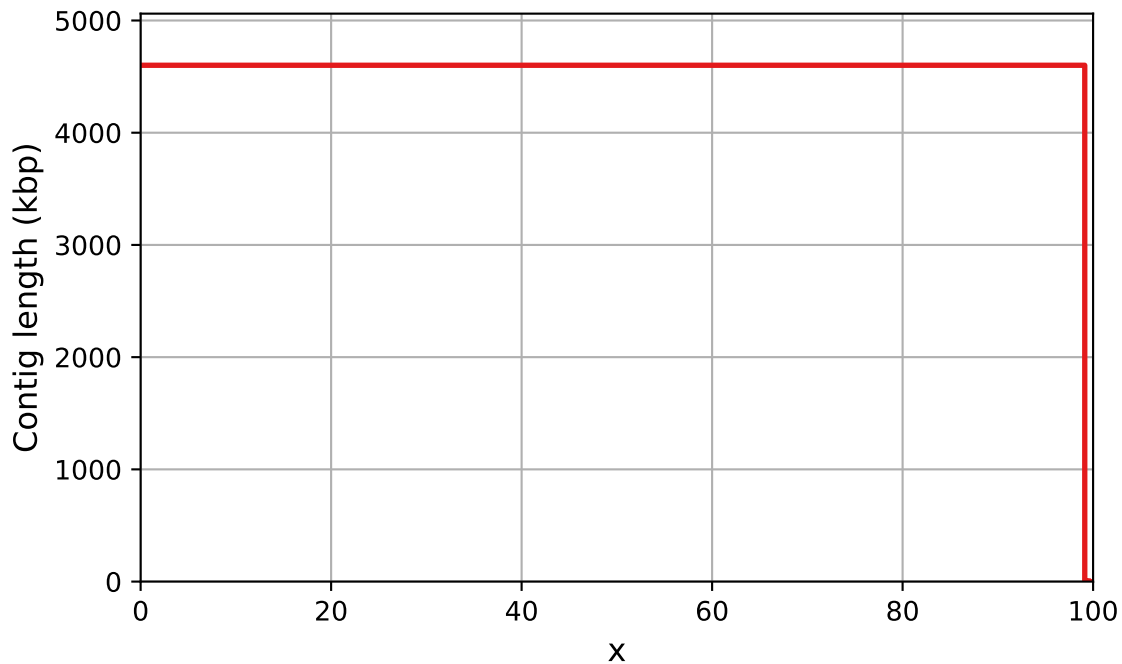
	scaffolds
# fully unaligned contigs	5
Fully unaligned length	2789
# partially unaligned contigs	1
Partially unaligned length	653
# N's	9497

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).

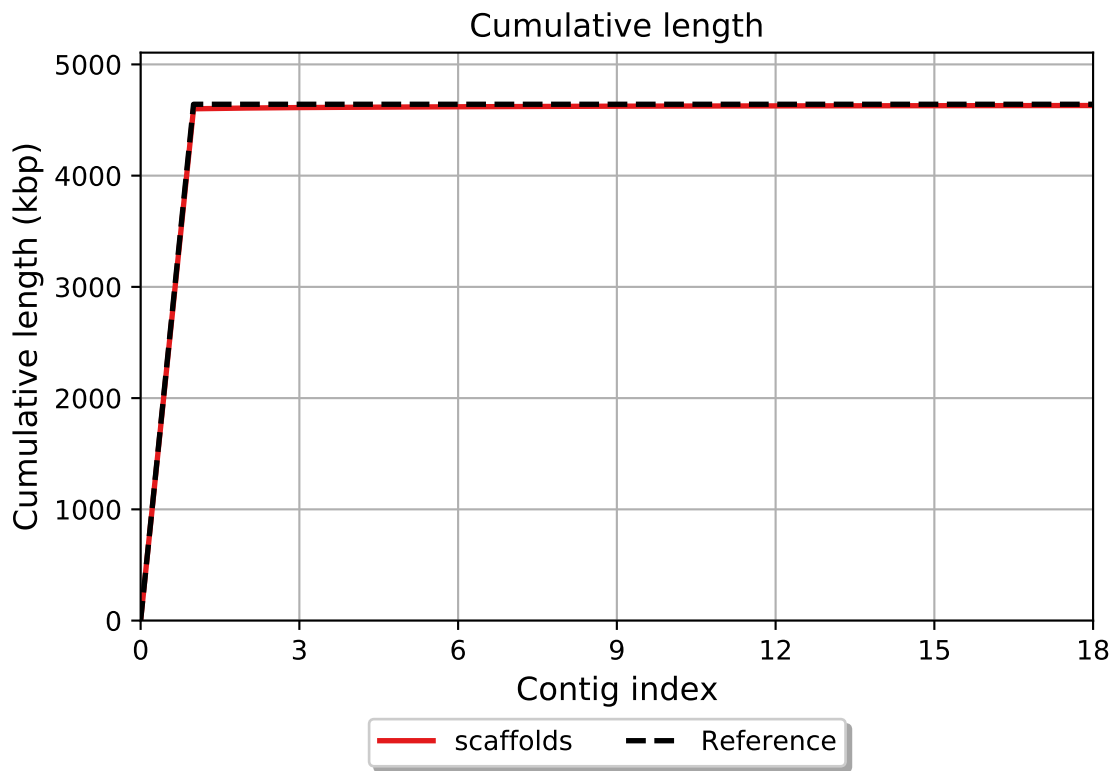


— scaffolds

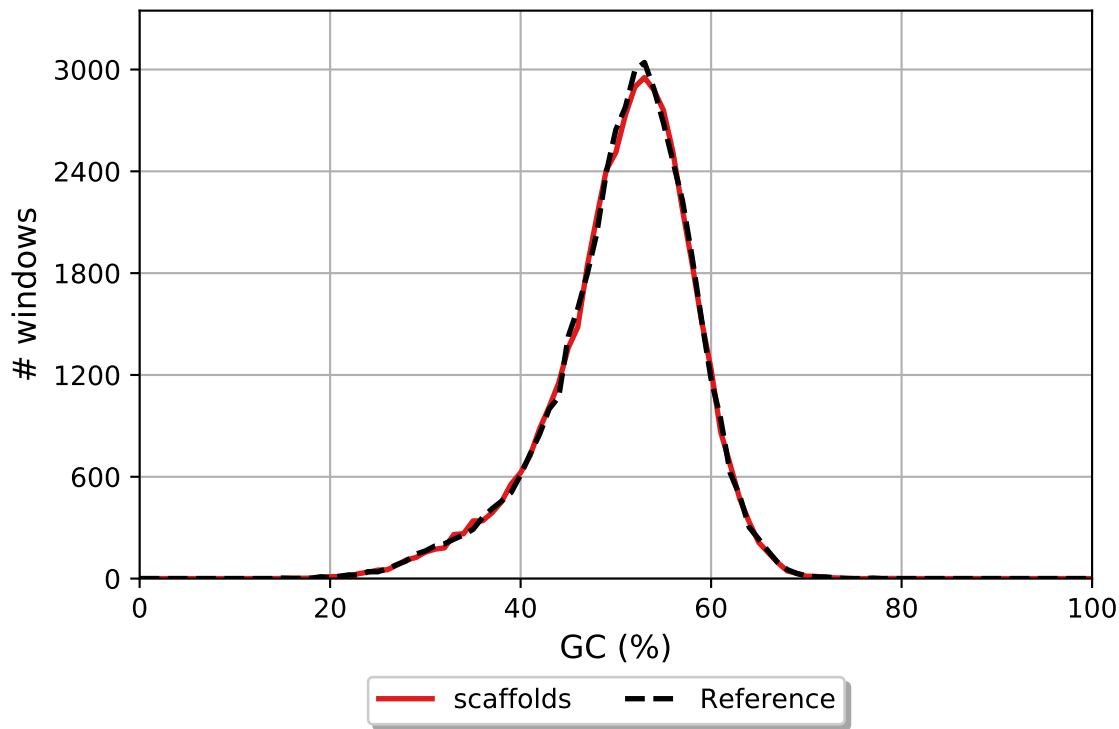
NGx



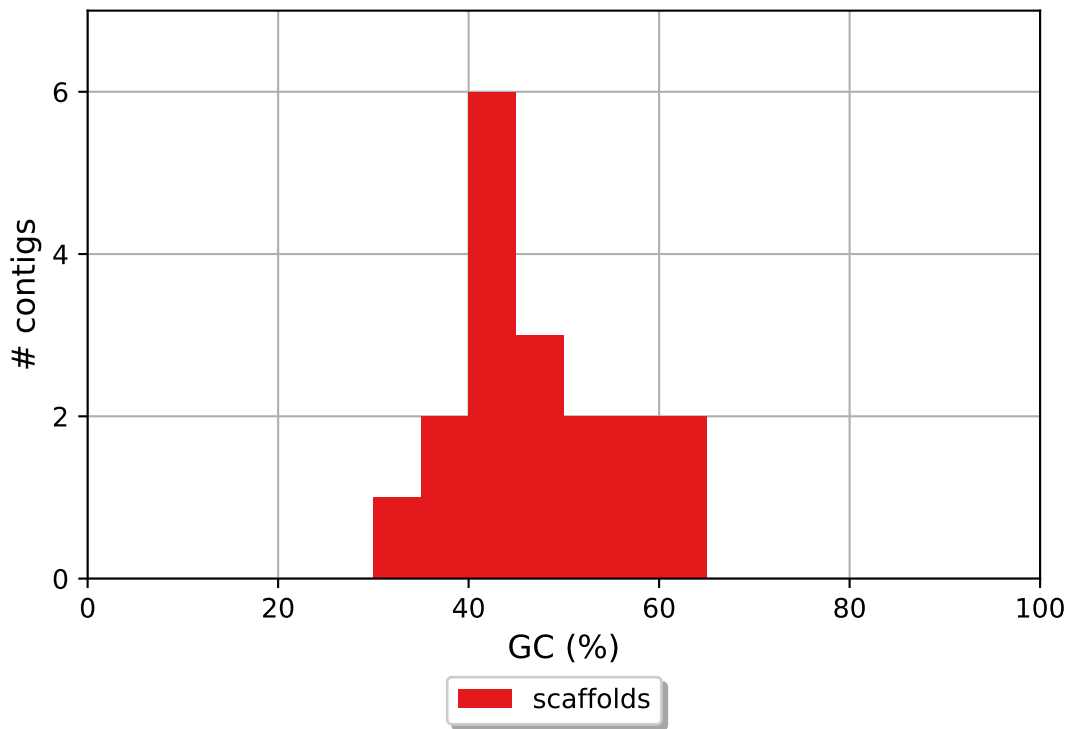
— scaffolds



## GC content

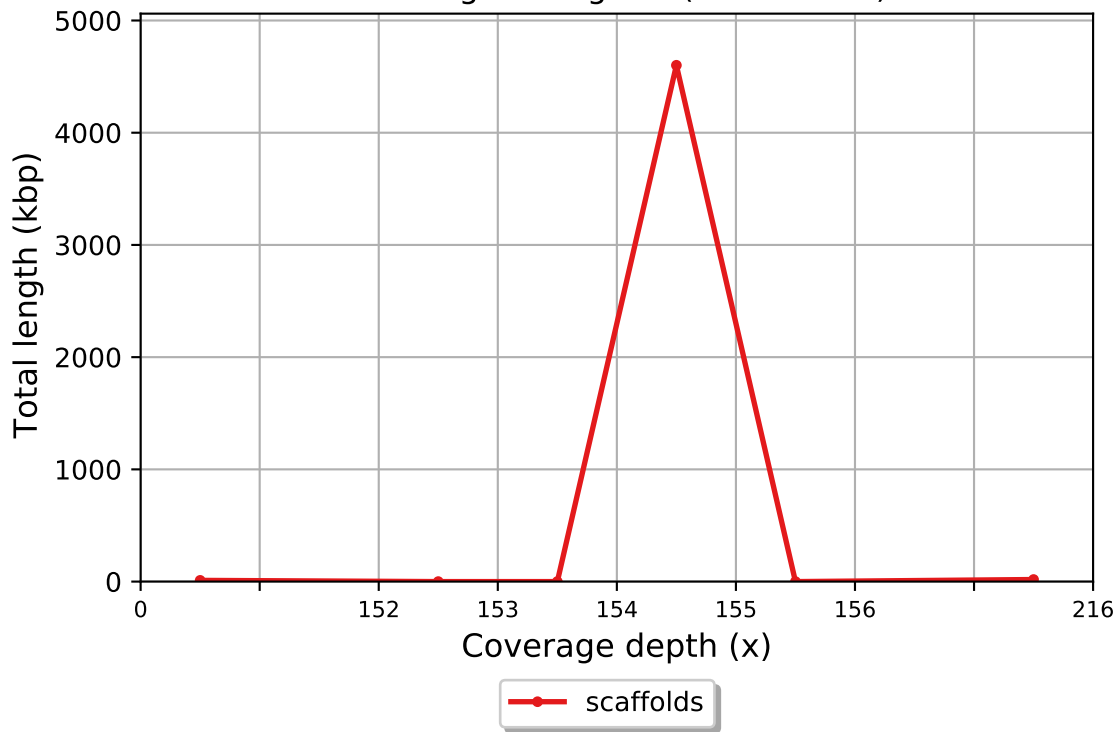


scaffolds GC content

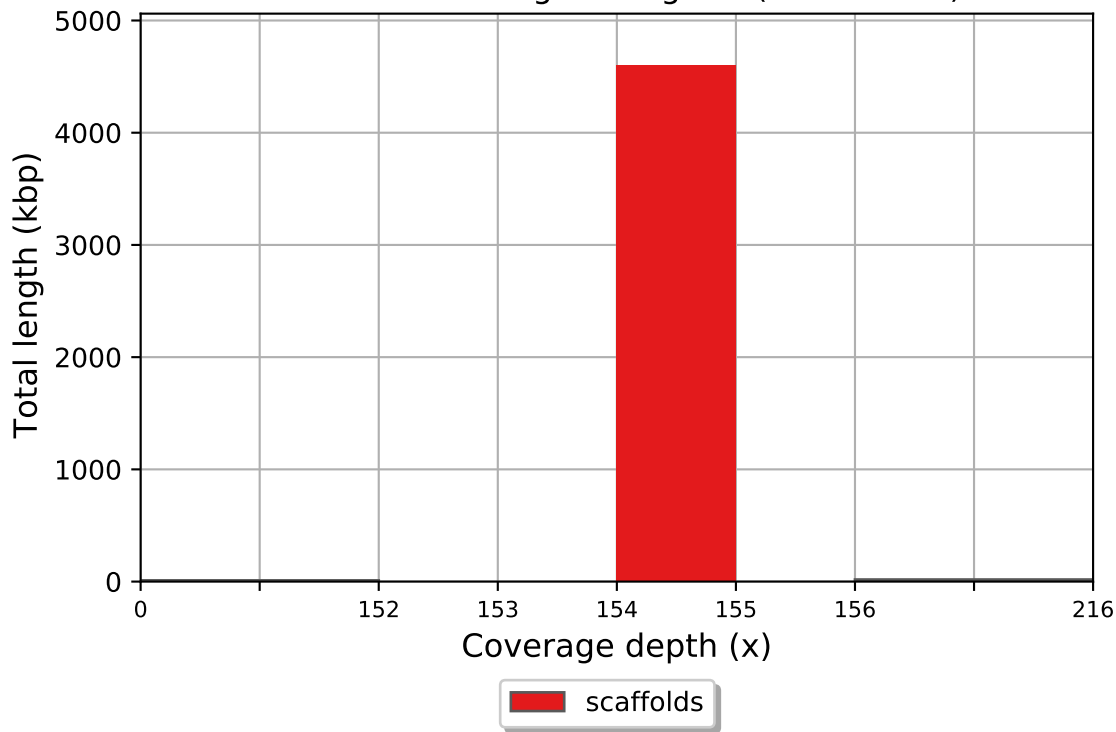




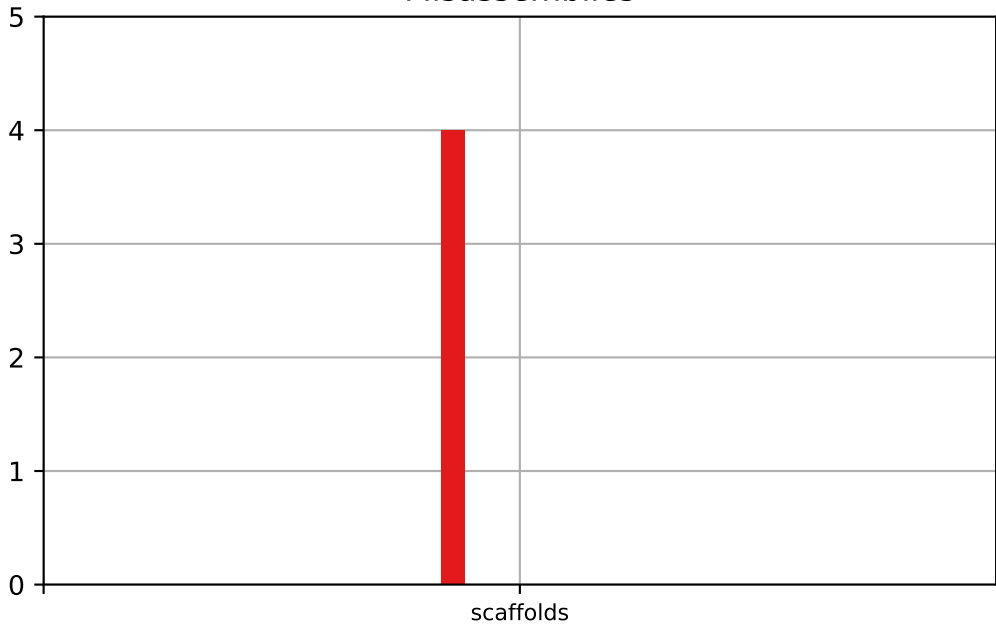
Coverage histogram (bin size: 1x)



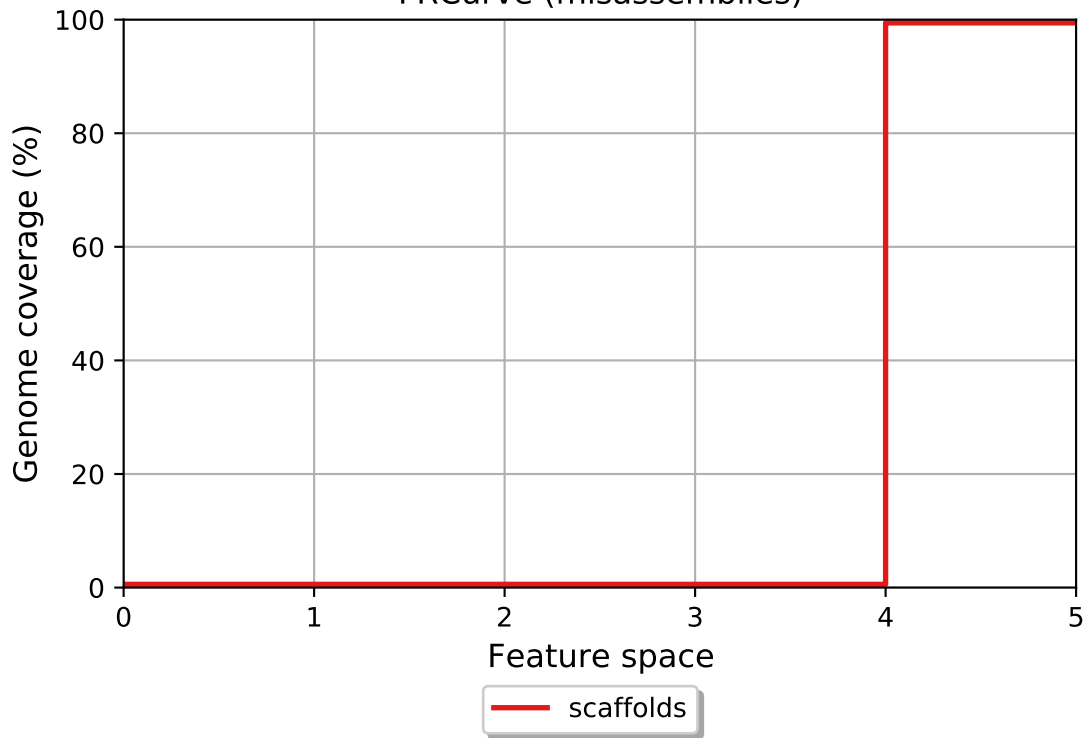
scaffolds coverage histogram (bin size: 1x)

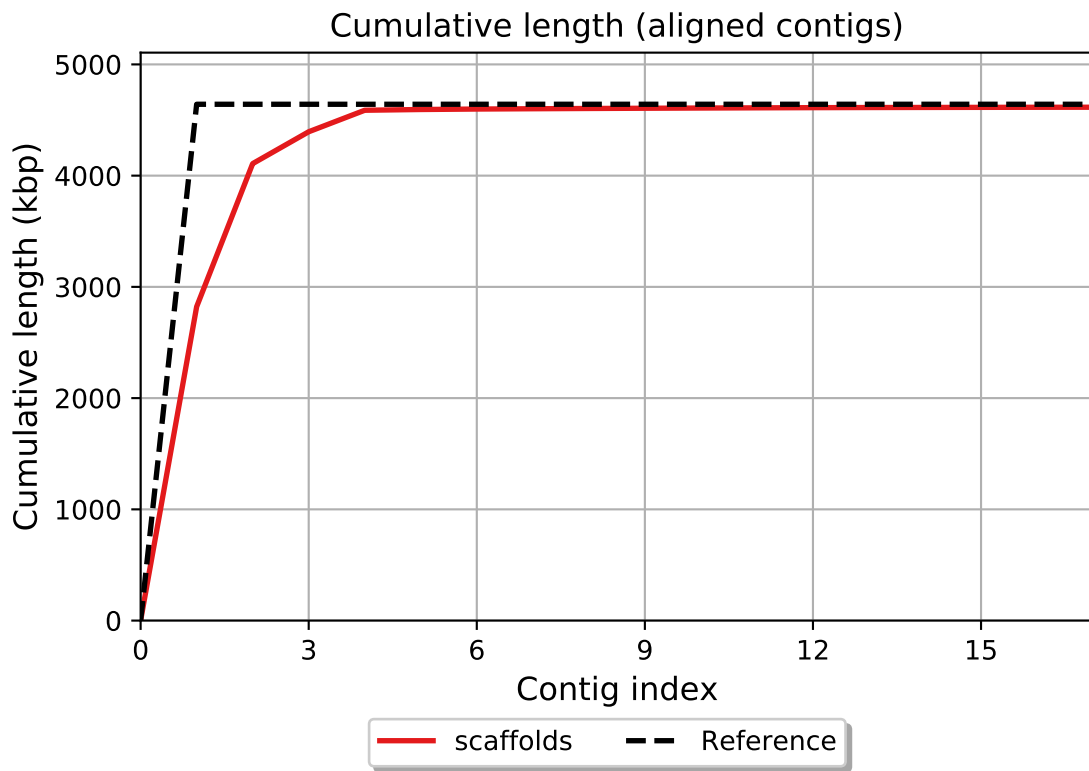


## Misassemblies

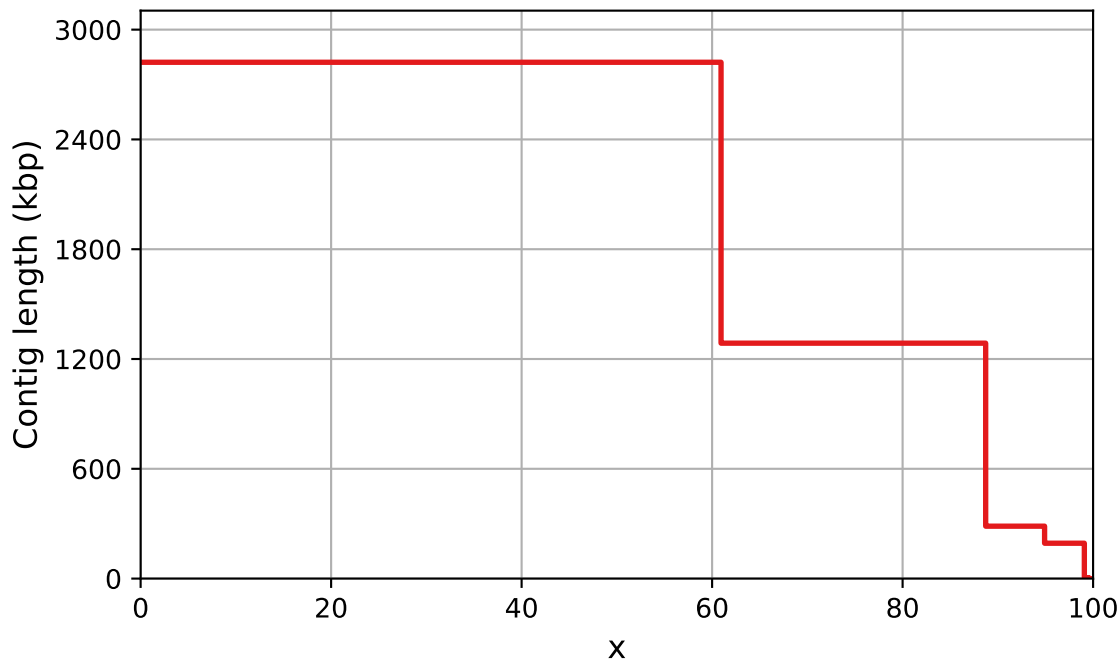


FRCurve (misassemblies)



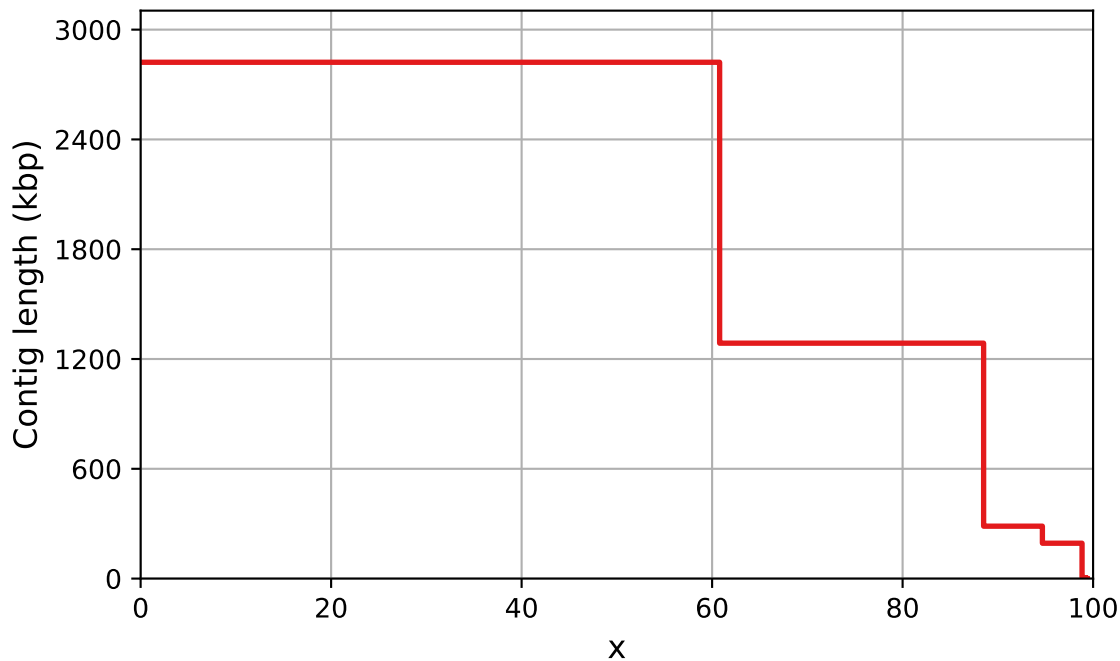


NAx



— scaffolds

# NGAx



— scaffolds