

Report

	scaffolds
# contigs (≥ 0 bp)	1700
# contigs (≥ 1000 bp)	15
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	489627
Total length (≥ 1000 bp)	28679
Total length (≥ 5000 bp)	7739
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	70
Largest contig	7739
Total length	65992
Reference length	45867
GC (%)	48.83
Reference GC (%)	39.17
N50	882
NG50	1209
N75	664
NG75	865
L50	20
LG50	10
L75	42
LG75	22
# 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	64 + 1 part
Unaligned length	53480
Genome fraction (%)	26.291
Duplication ratio	1.038
# N's per 100 kbp	121.23
# mismatches per 100 kbp	140.97
# indels per 100 kbp	16.59
Largest alignment	7738
Total aligned length	12075
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	17
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	6

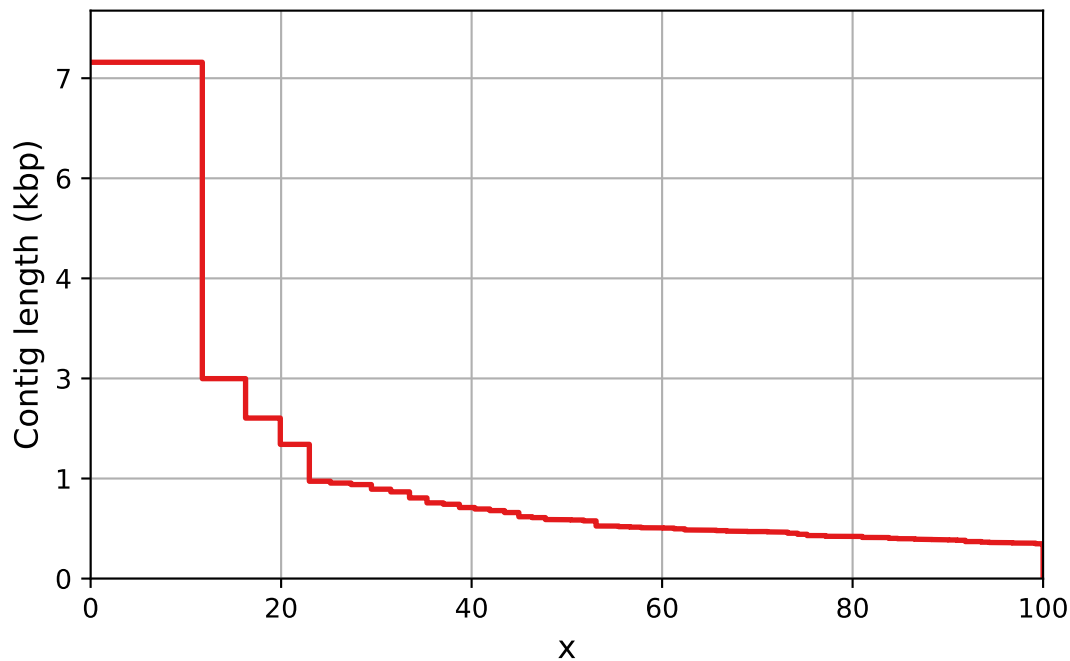
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	64
Fully unaligned length	52954
# partially unaligned contigs	1
Partially unaligned length	526
# N's	80

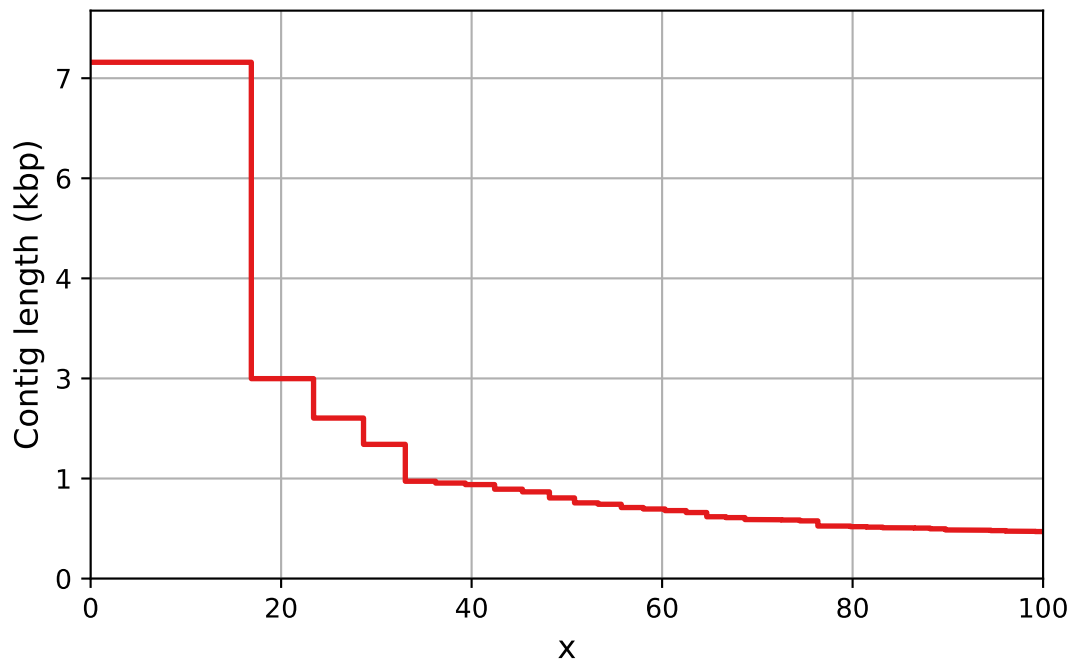
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



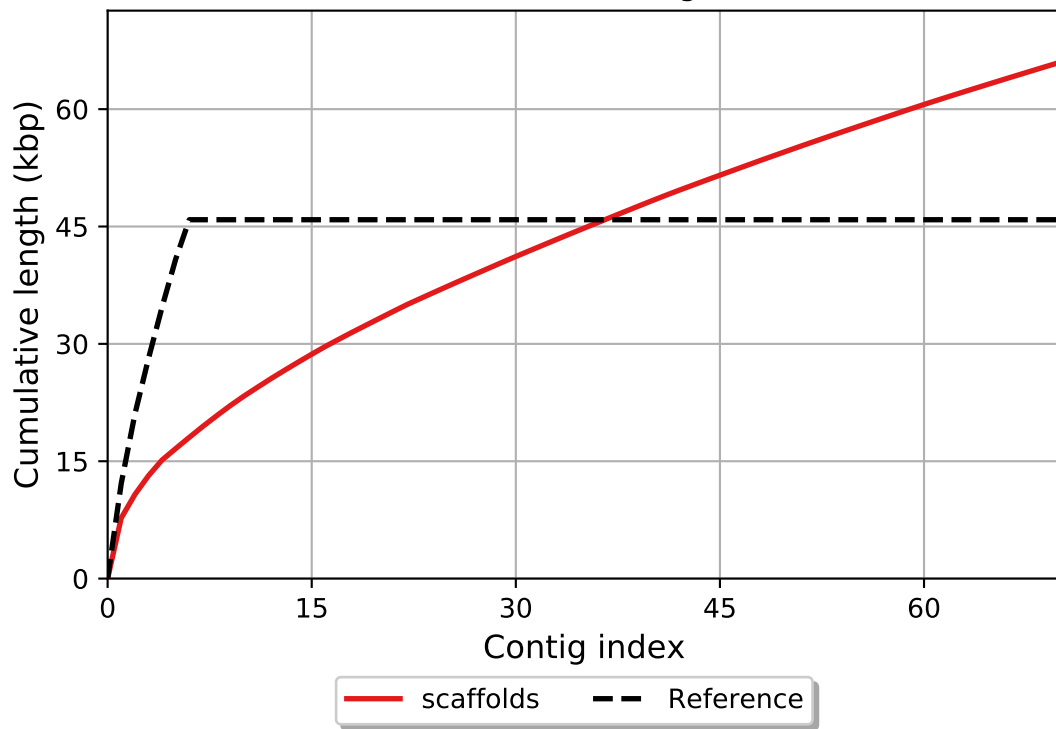
scaffolds

NGx

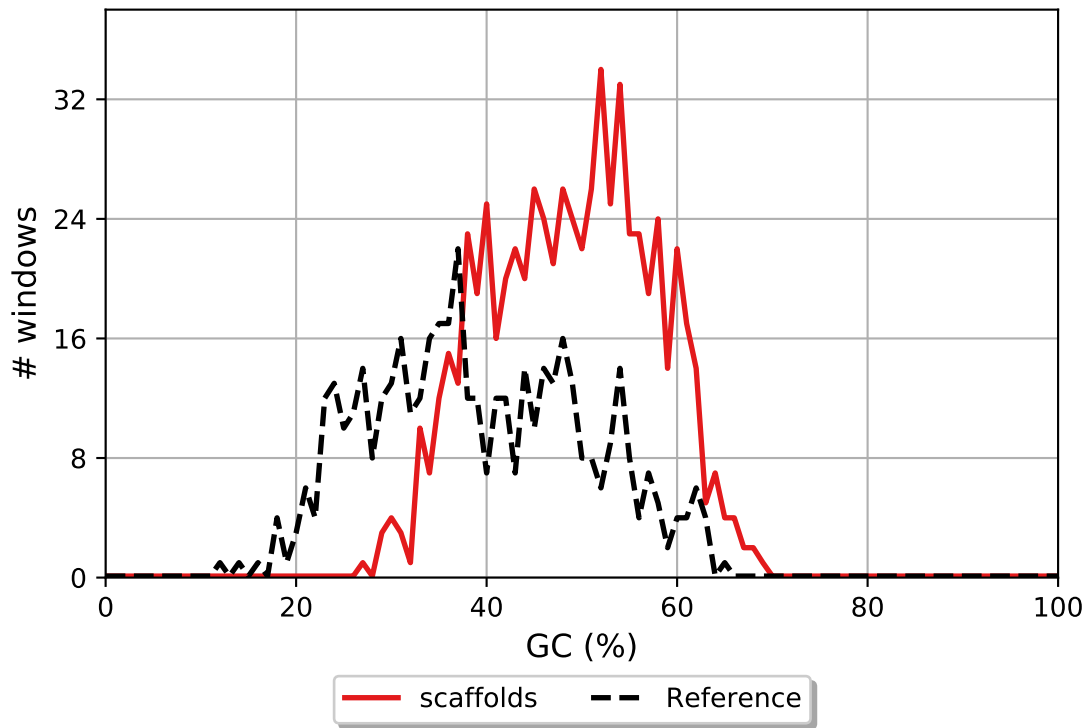


— scaffolds

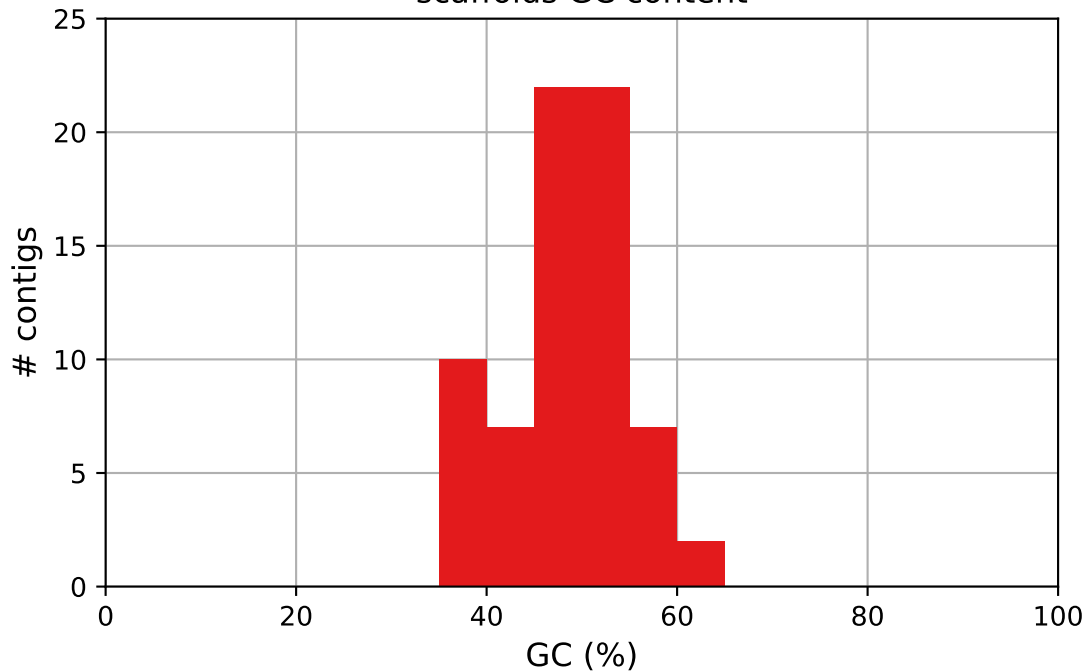
Cumulative length



GC content

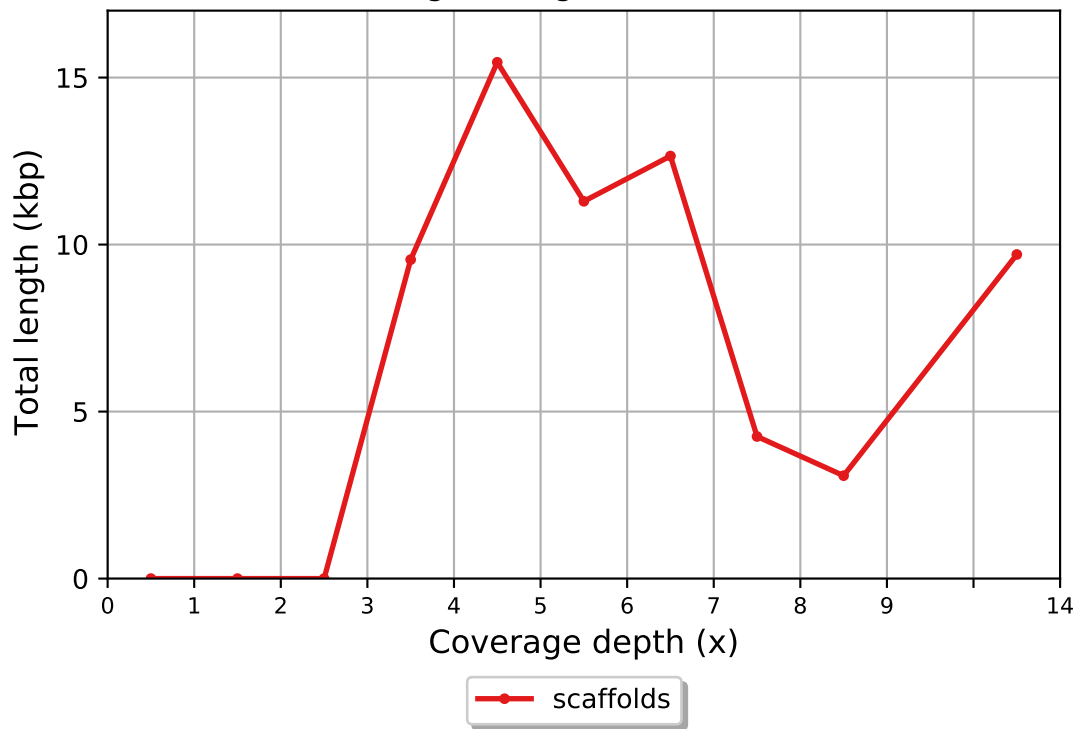


scaffolds GC content

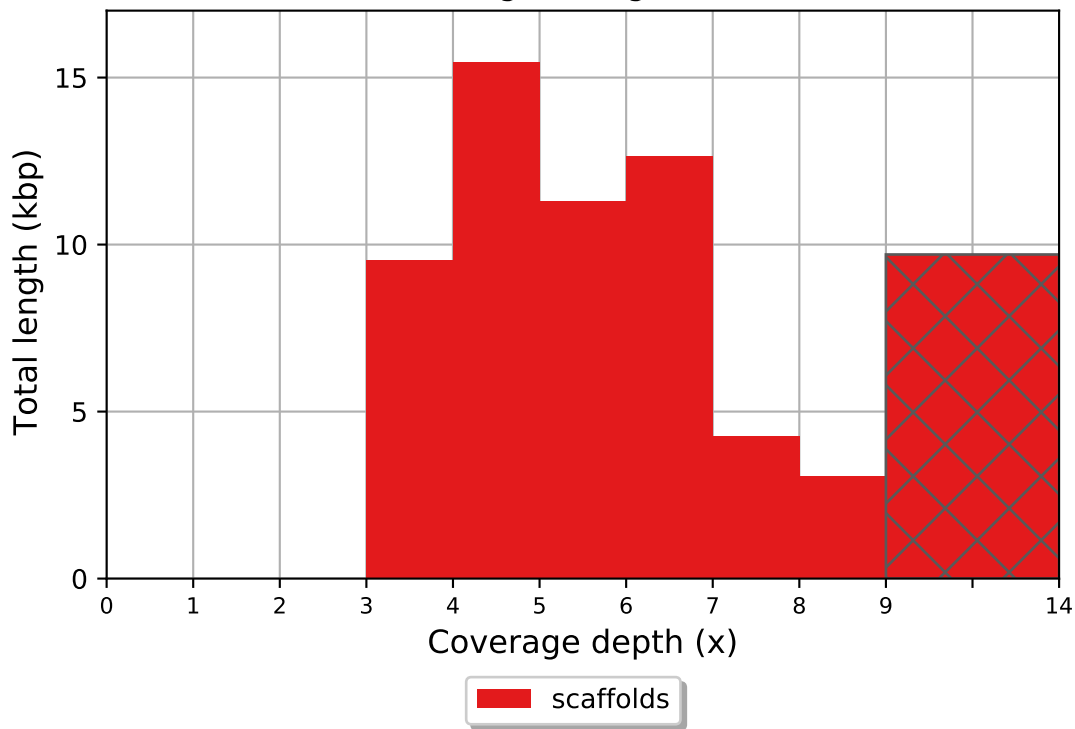


scaffolds

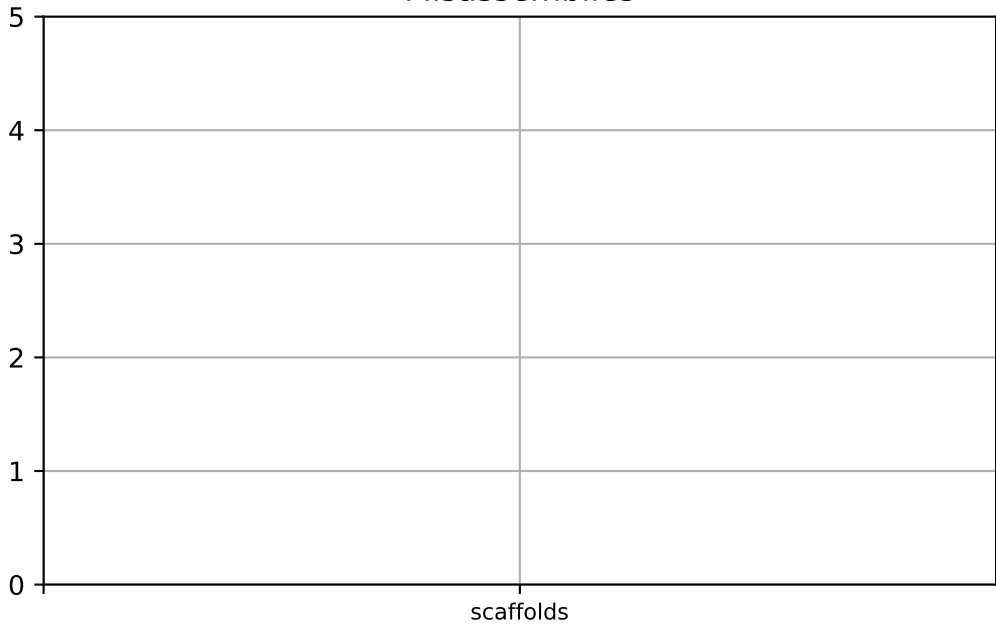
Coverage histogram (bin size: 1x)



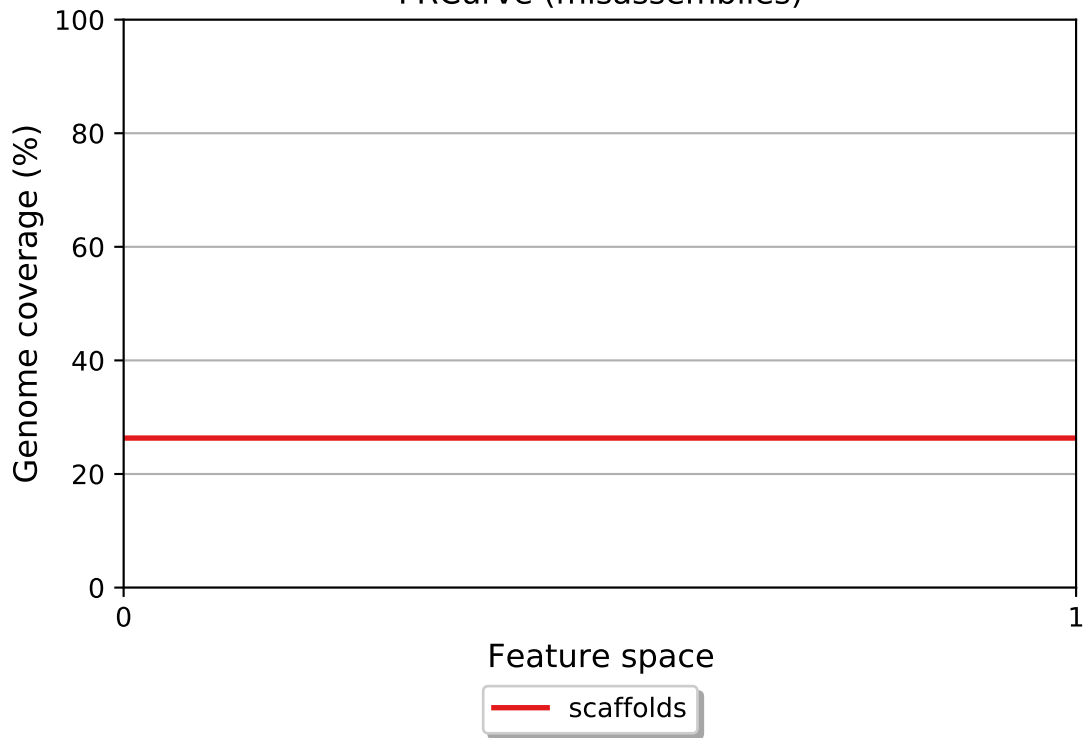
scaffolds coverage histogram (bin size: 1x)



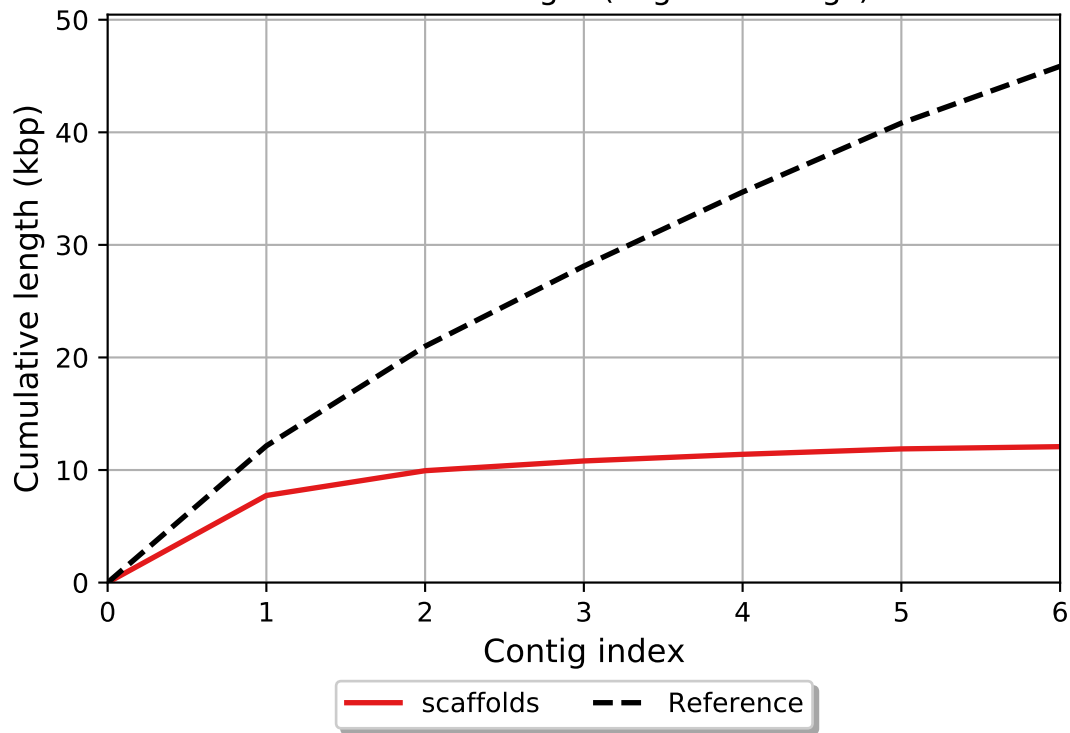
Misassemblies



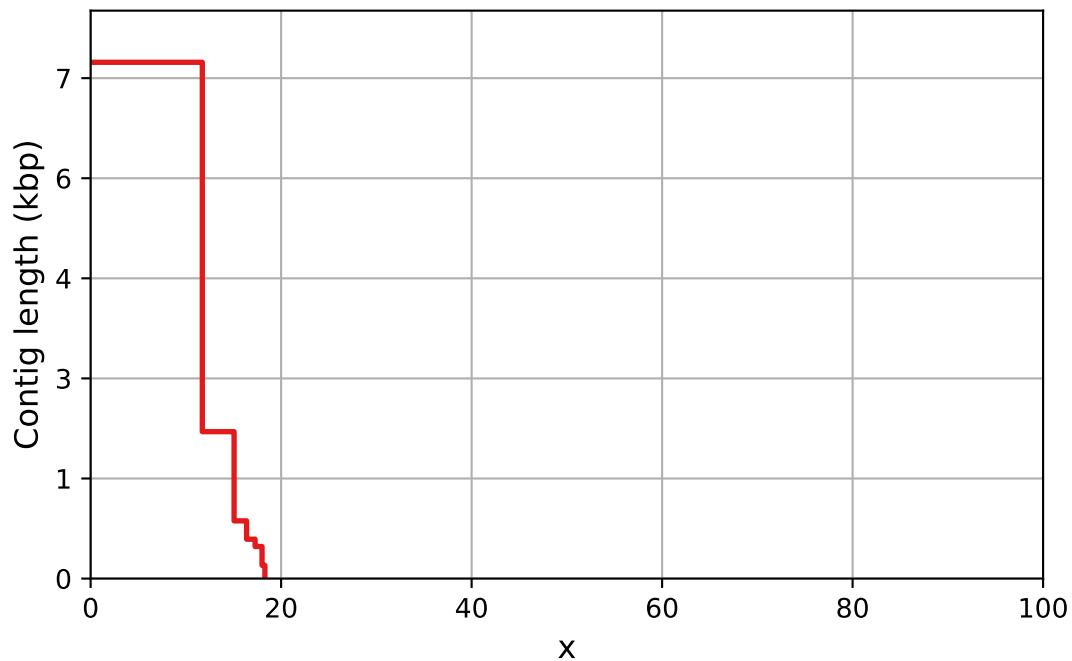
FRCurve (misassemblies)



Cumulative length (aligned contigs)

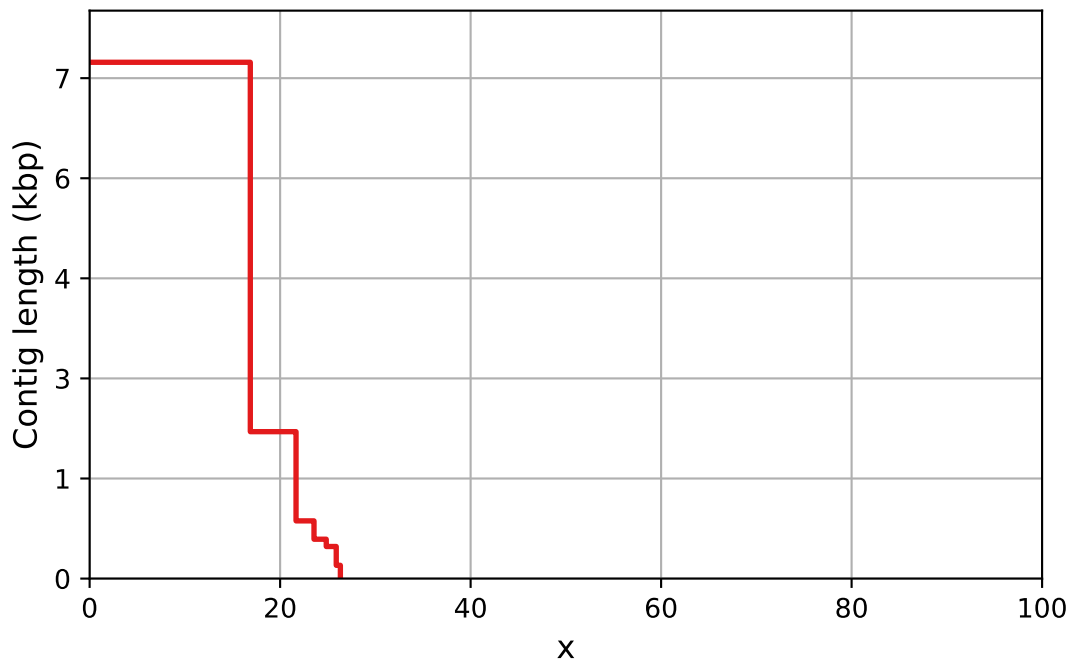


NAx



— scaffolds

NGAx



— scaffolds