

Report

	scaffolds_fasta
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
Total length (>= 0 bp)	190004
Total length (>= 1000 bp)	190004
# contigs	2
Largest contig	174093
Total length	190004
Reference length	190733
GC (%)	23.81
Reference GC (%)	24.00
N50	174093
NG50	174093
N75	174093
NG75	174093
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	174093
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.907
Duplication ratio	1.007
# N's per 100 kbp	26.32
# mismatches per 100 kbp	1227.15
# indels per 100 kbp	243.84
Largest alignment	129587
Total aligned length	189690
NA50	129587
NGA50	129587
NA75	44277
NGA75	44277
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

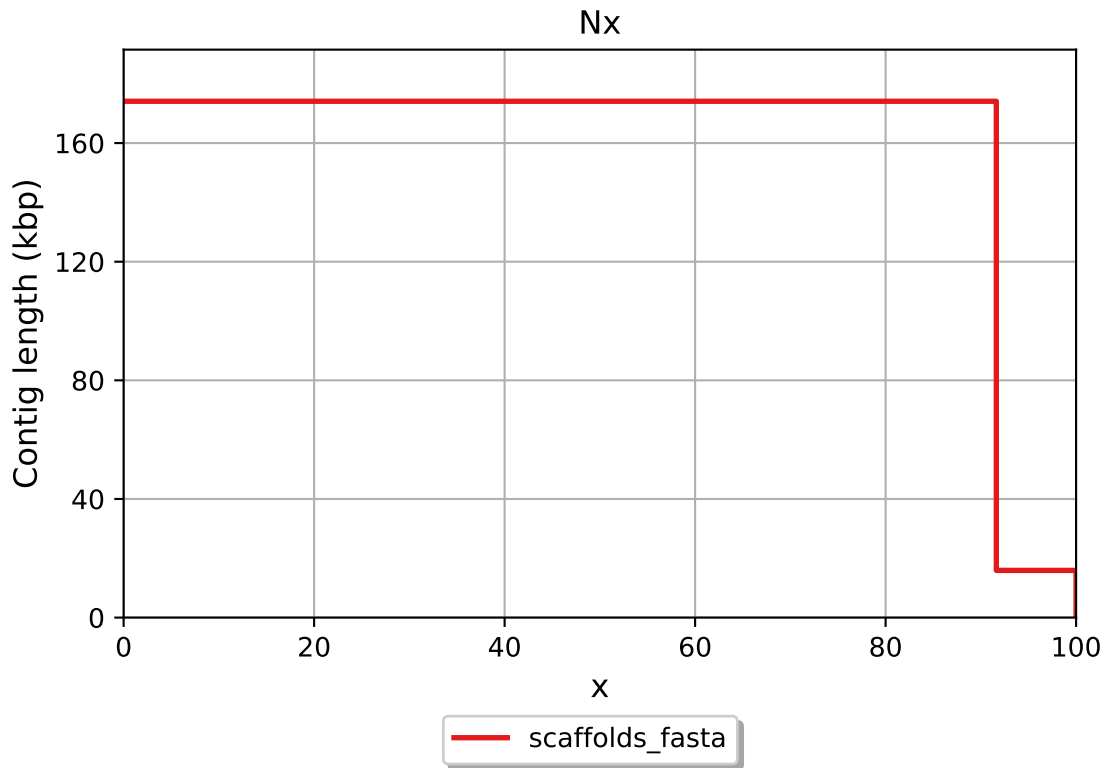
	scaffolds_fasta
# misassemblies	1
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	1
# s. relocations	1
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	174093
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	1
# unaligned mis. contigs	0
# mismatches	2315
# indels	460
# indels (<= 5 bp)	226
# indels (> 5 bp)	234
Indels length	3180

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).

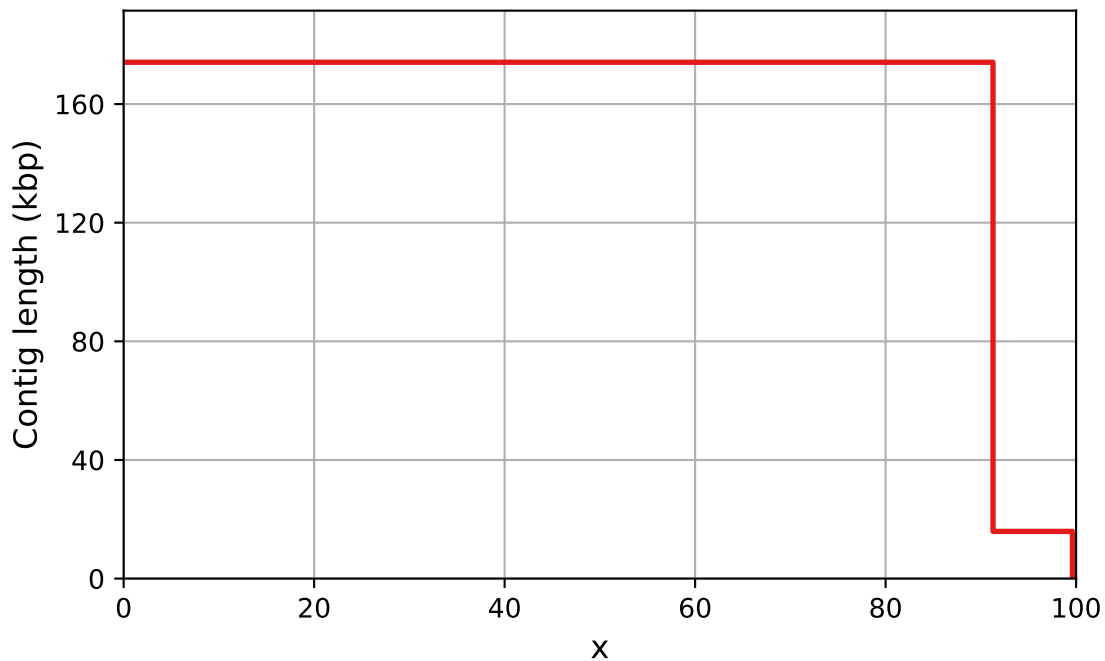
Unaligned report

	scaffolds_fasta
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	50

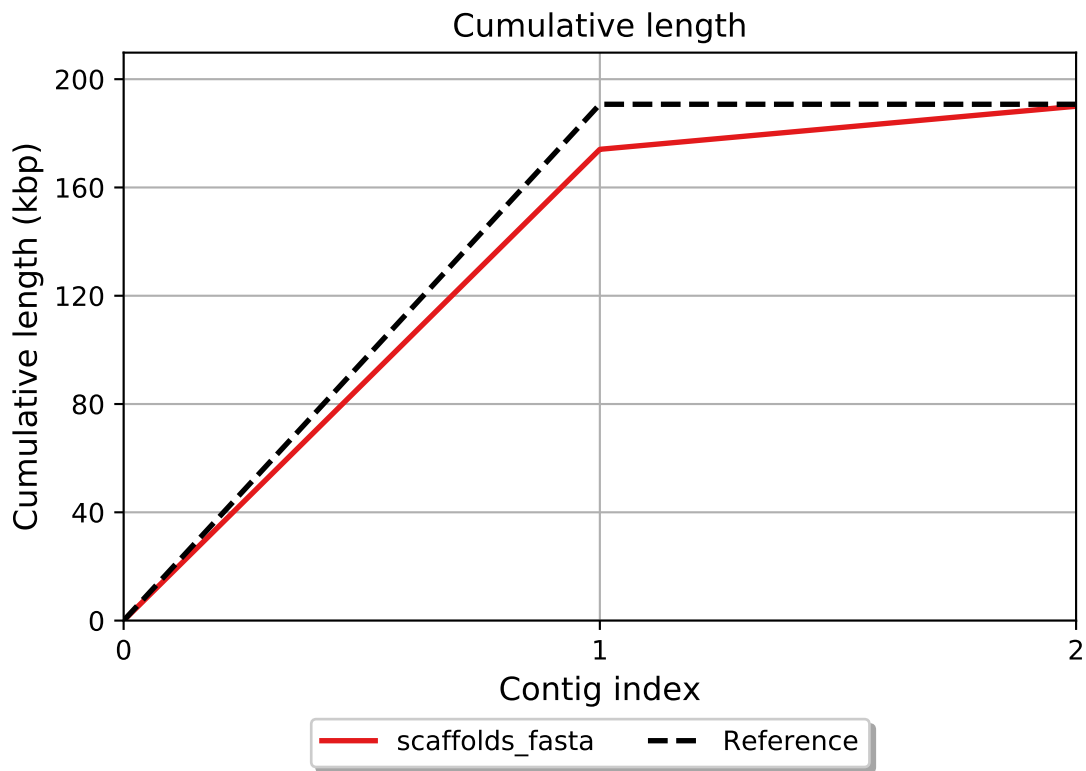
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



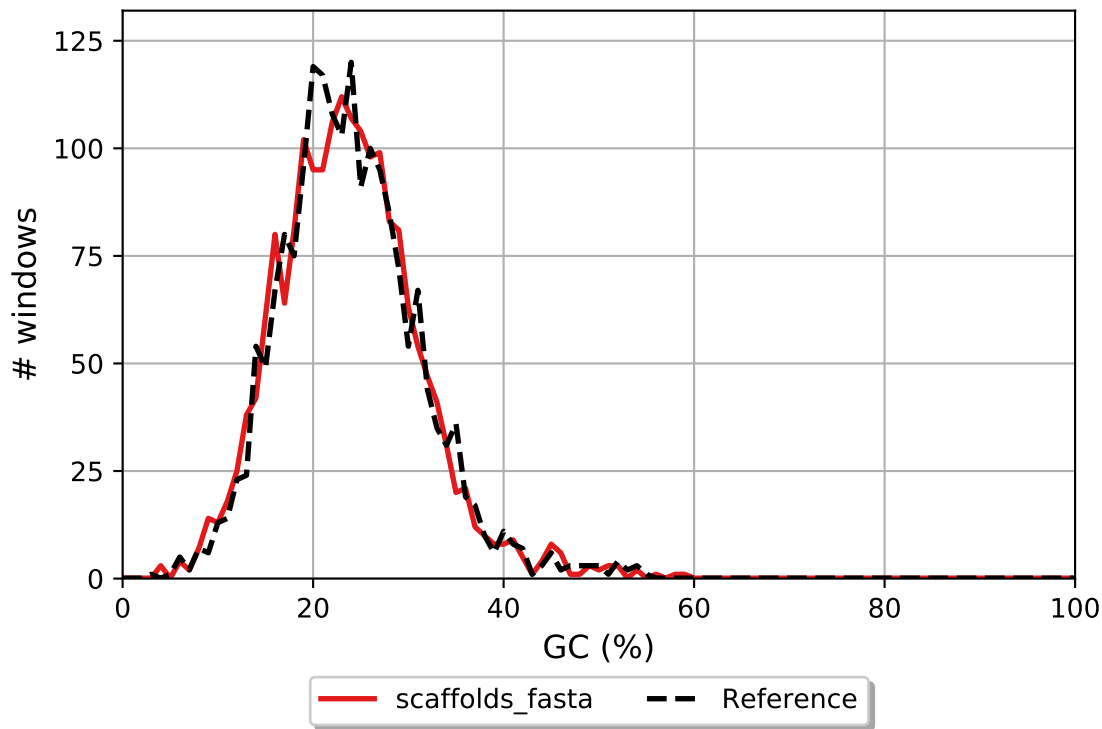
NGx



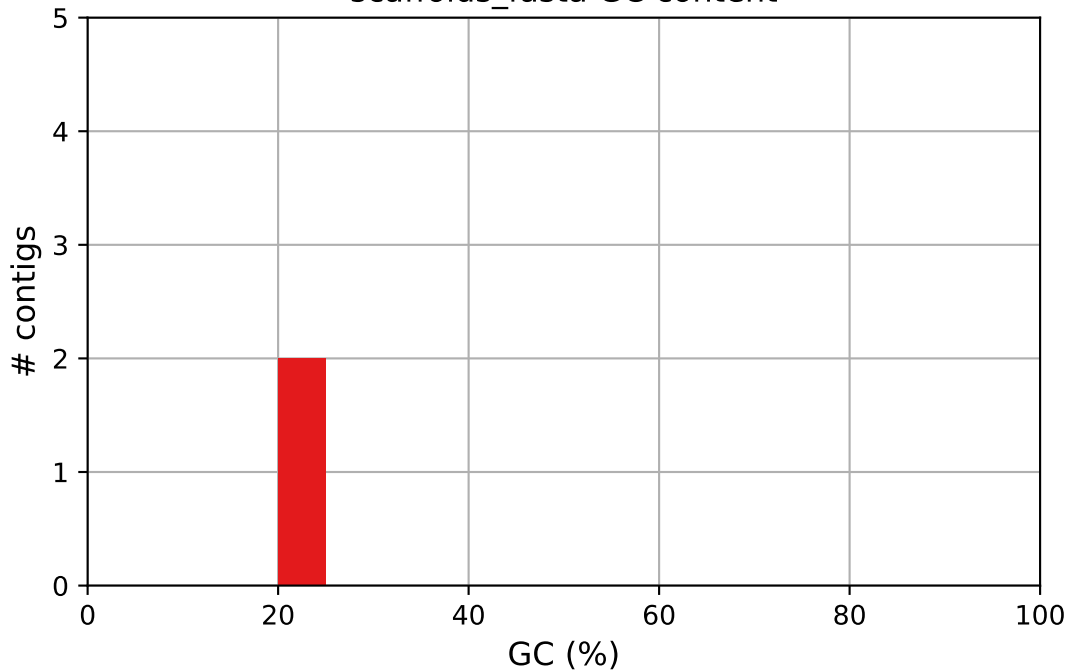
scaffolds_fasta



GC content

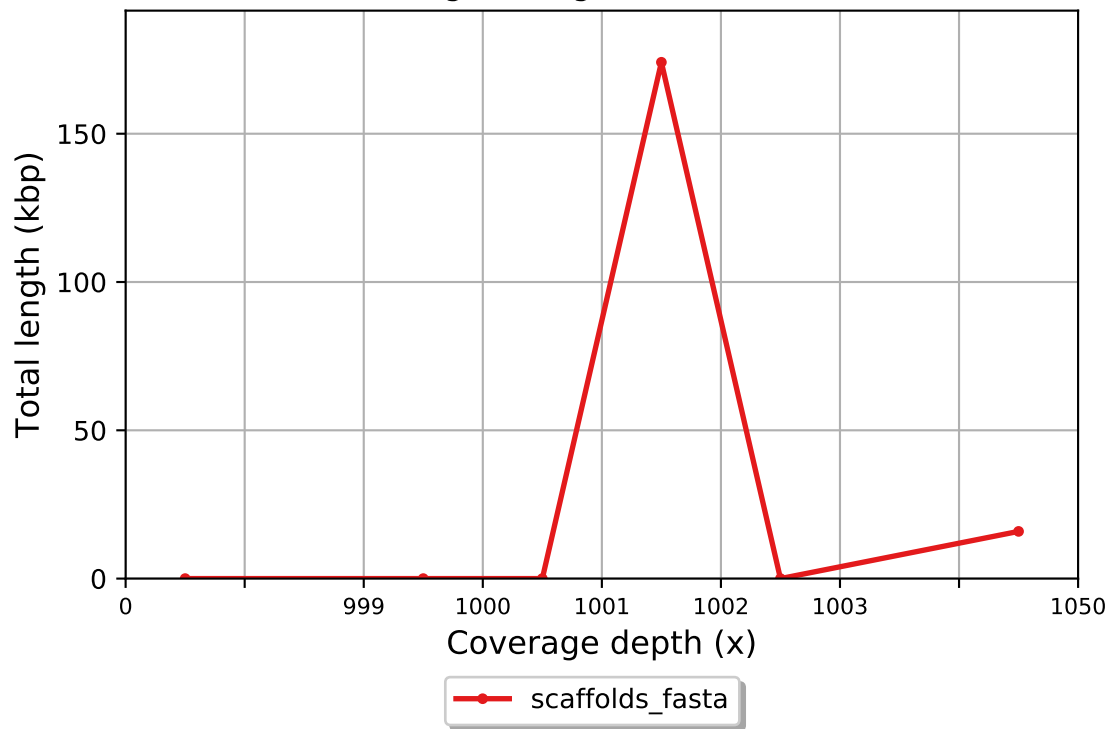


scaffolds_fasta GC content

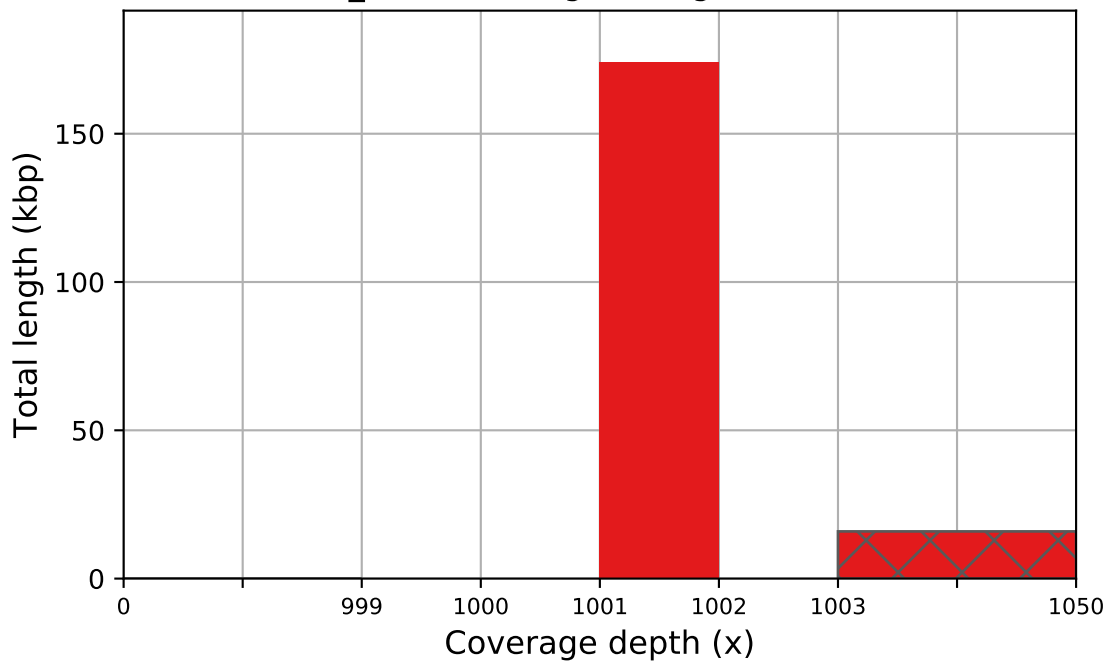


scaffolds_fasta

Coverage histogram (bin size: 1x)

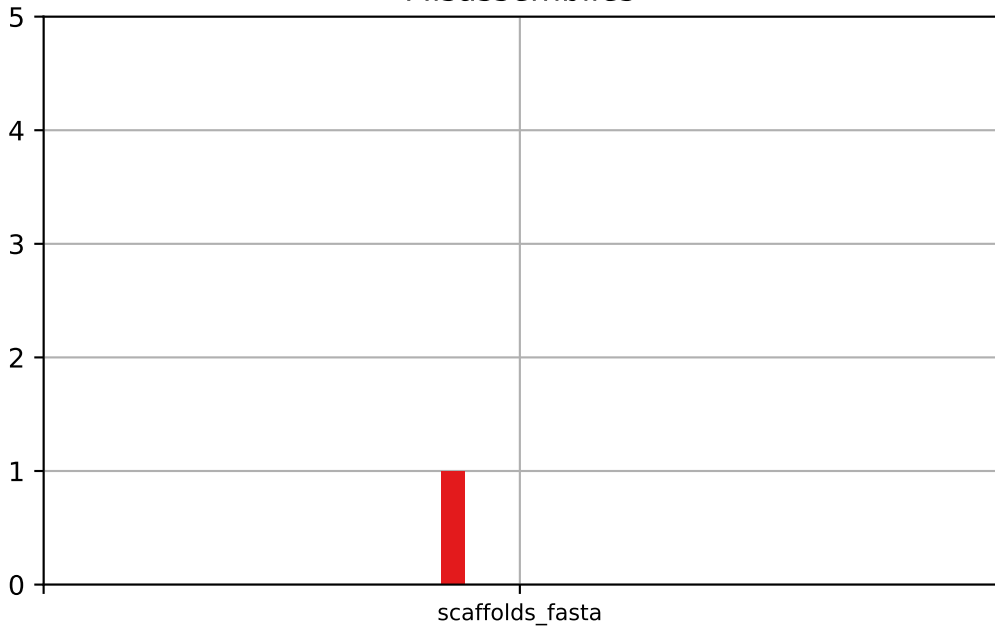


scaffolds_fasta coverage histogram (bin size: 1x)

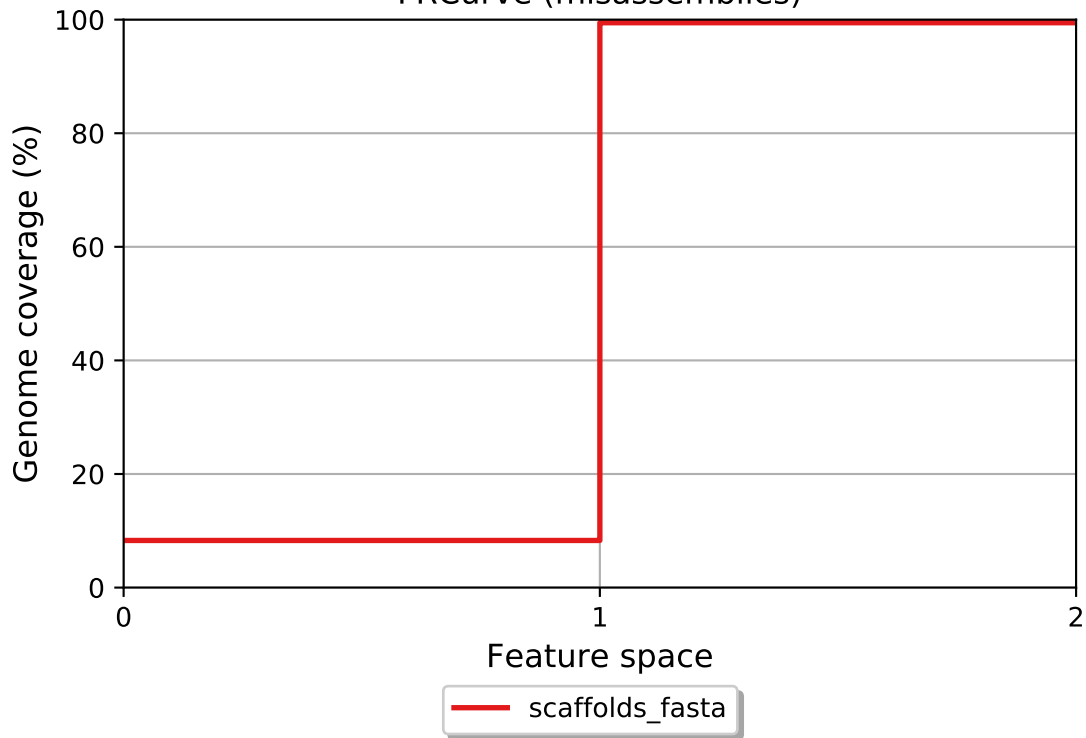


scaffolds_fasta

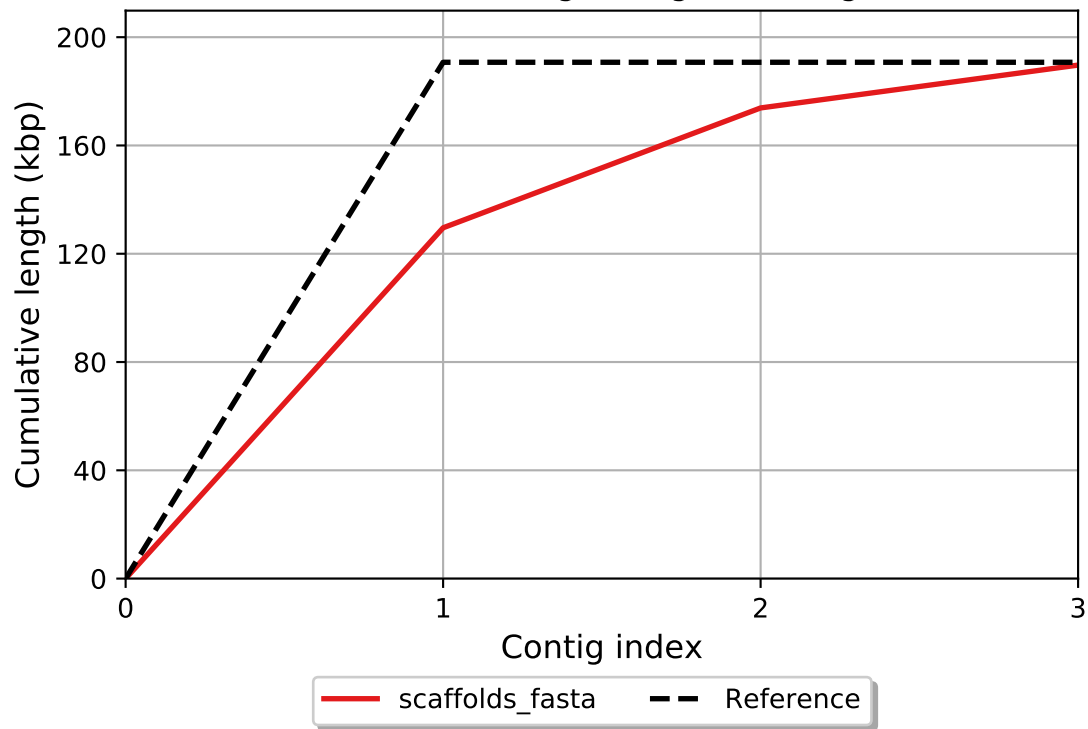
Misassemblies



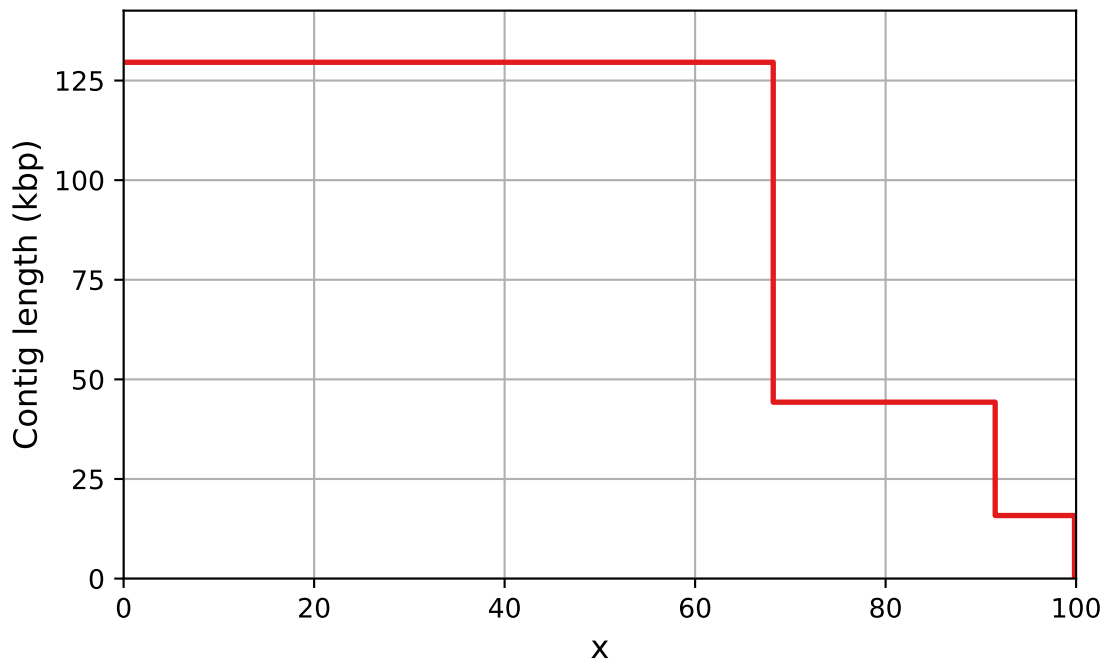
FRCurve (misassemblies)



Cumulative length (aligned contigs)

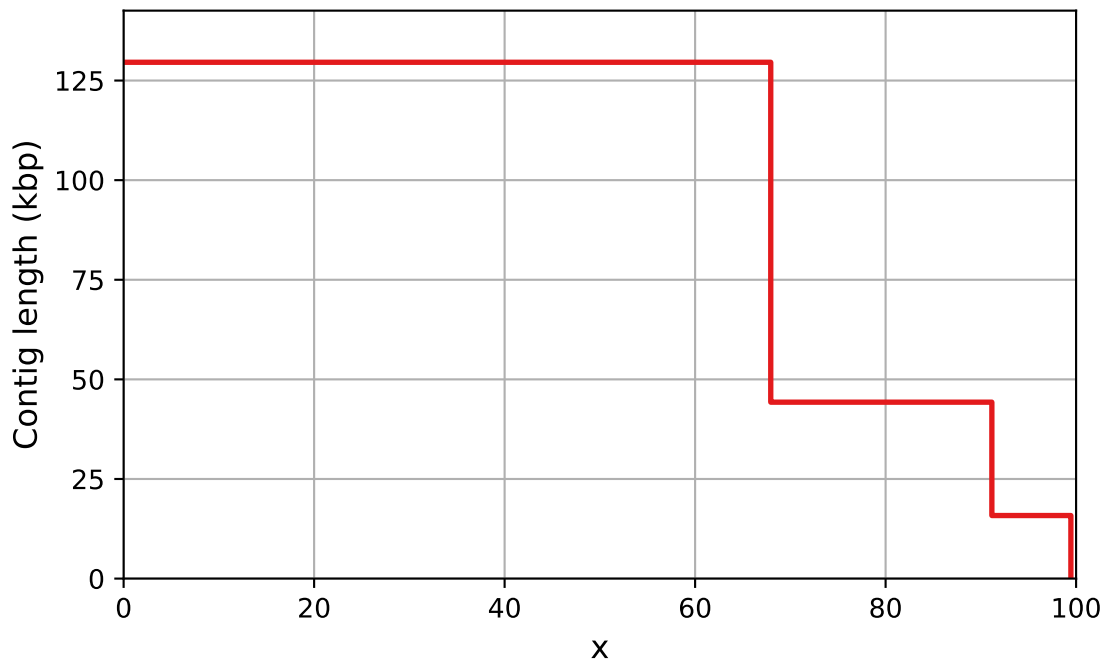


NAx



scaffolds_fasta

NGAx



scaffolds_fasta