

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	57
# contigs ( $\geq 5000$ bp)	44
# contigs ( $\geq 10000$ bp)	44
# contigs ( $\geq 25000$ bp)	38
# contigs ( $\geq 50000$ bp)	33
Total length ( $\geq 1000$ bp)	4750508
Total length ( $\geq 5000$ bp)	4722723
Total length ( $\geq 10000$ bp)	4722723
Total length ( $\geq 25000$ bp)	4634350
Total length ( $\geq 50000$ bp)	4474495
# contigs	75
Largest contig	300358
Total length	4762136
Reference length	4641652
GC (%)	50.83
Reference GC (%)	50.79
N50	167276
NG50	167276
N75	92493
NG75	104699
L50	11
LG50	11
L75	20
LG75	19
# misassemblies	20
# misassembled contigs	1
Misassembled contigs length	210680
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.041
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	785.31
# indels per 100 kbp	1.10
Largest alignment	300358
NA50	159904
NGA50	159904
NA75	79751
NGA75	87060
LA50	11
LGA50	11
LA75	22
LGA75	21

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).

## Misassemblies report

	scaffolds
# misassemblies	20
# relocations	18
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	210680
# local misassemblies	2
# mismatches	35737
# indels	50
# short indels	49
# long indels	1
Indels length	58

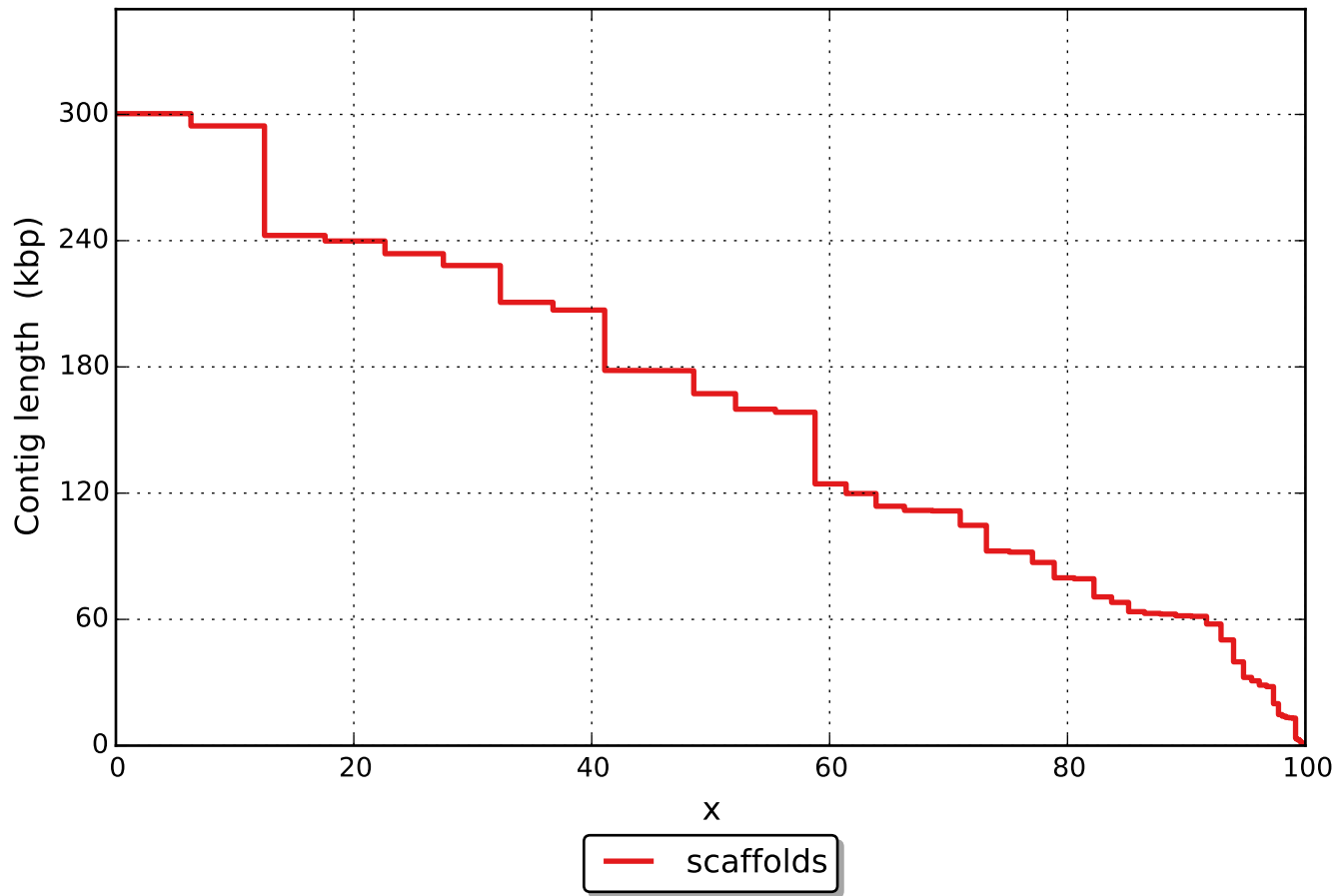
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

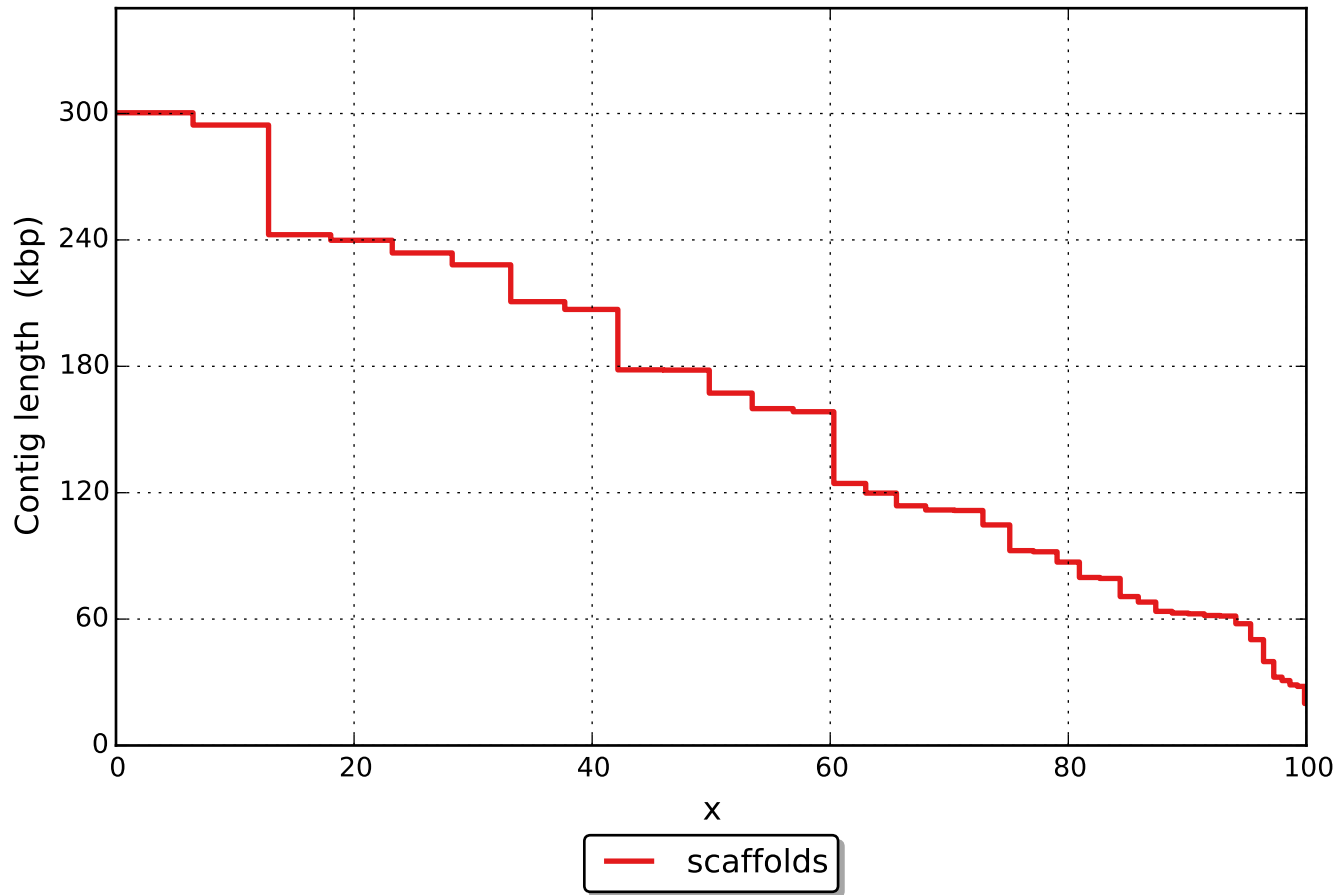
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

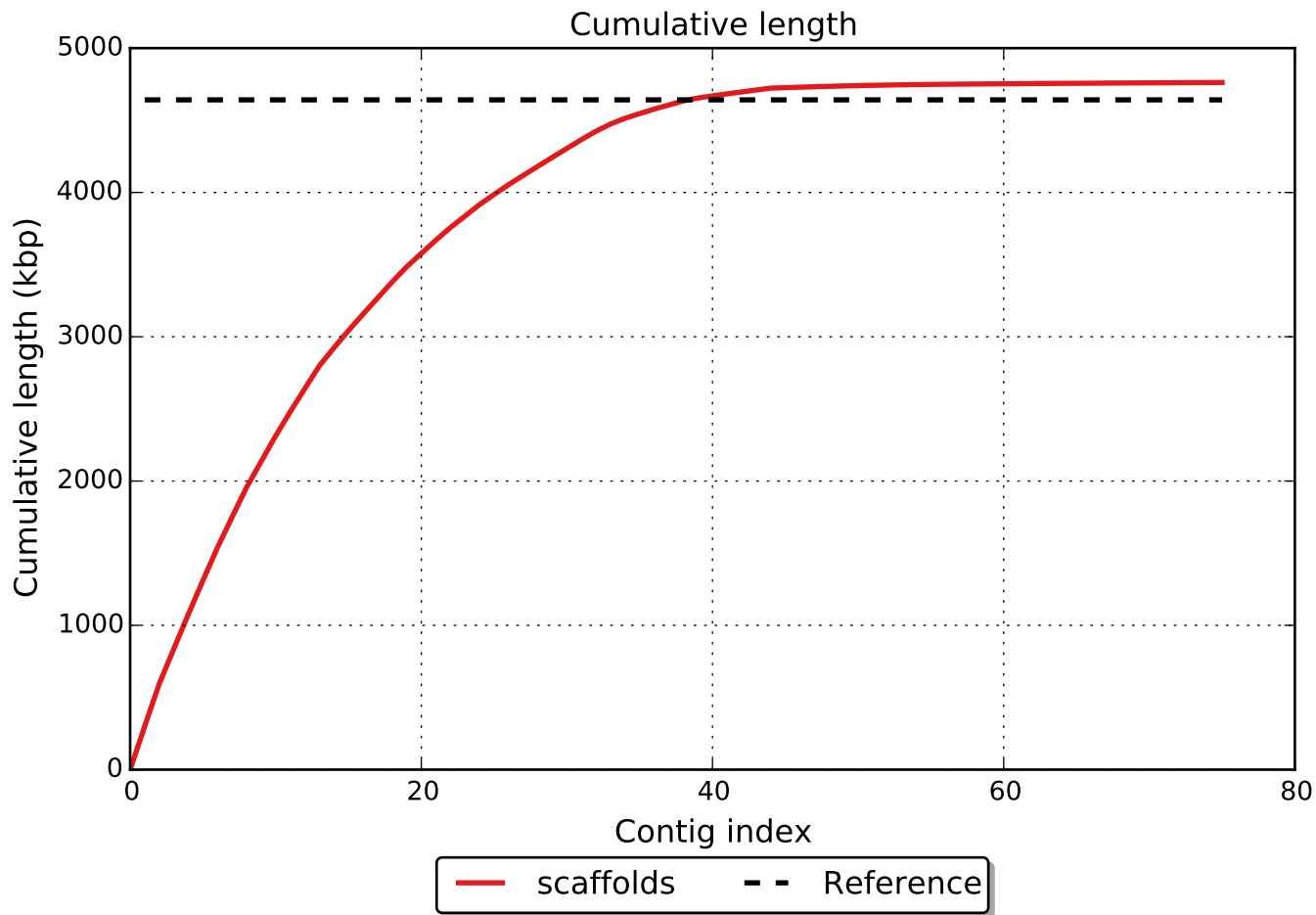
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

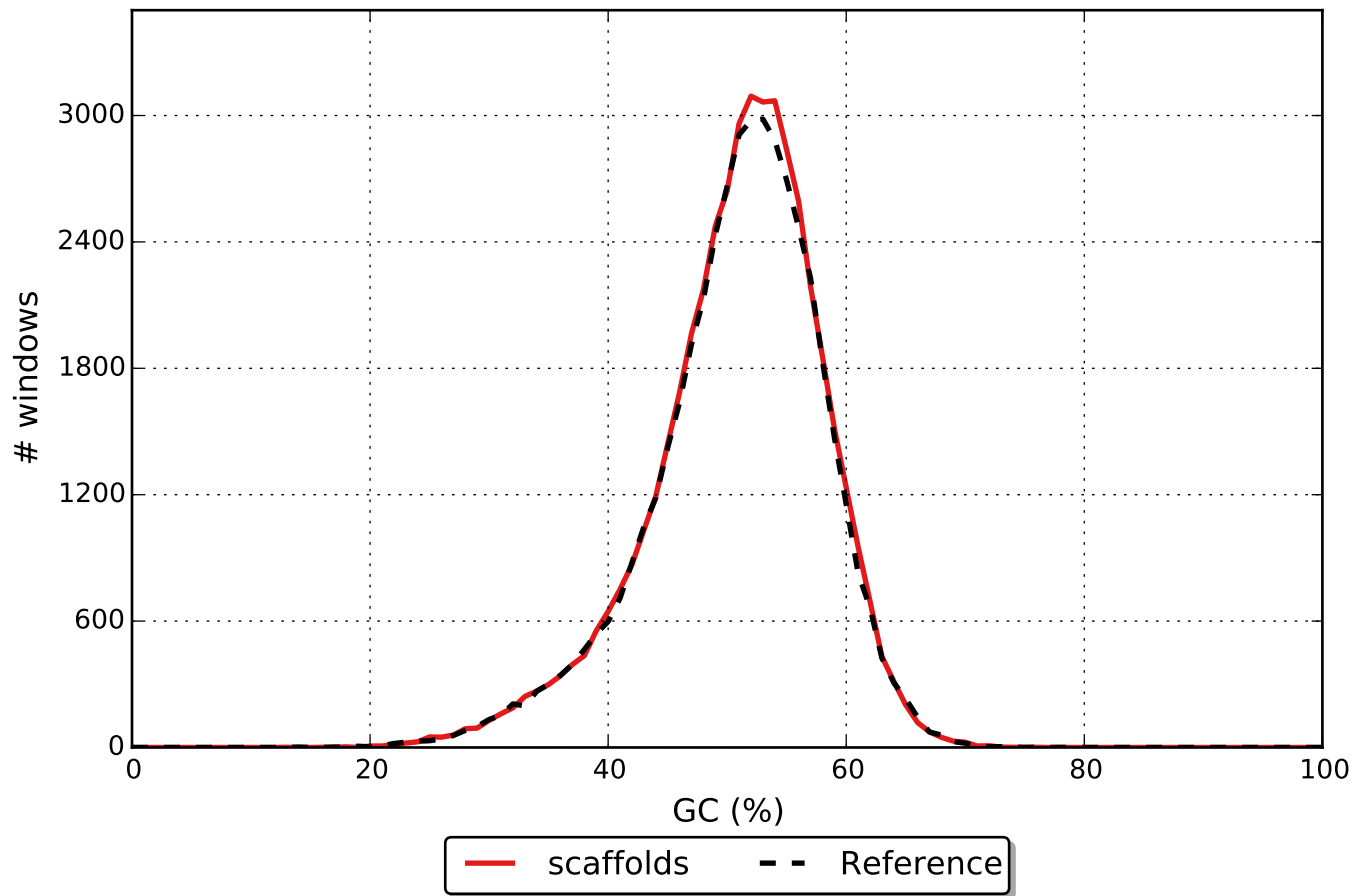


NGx

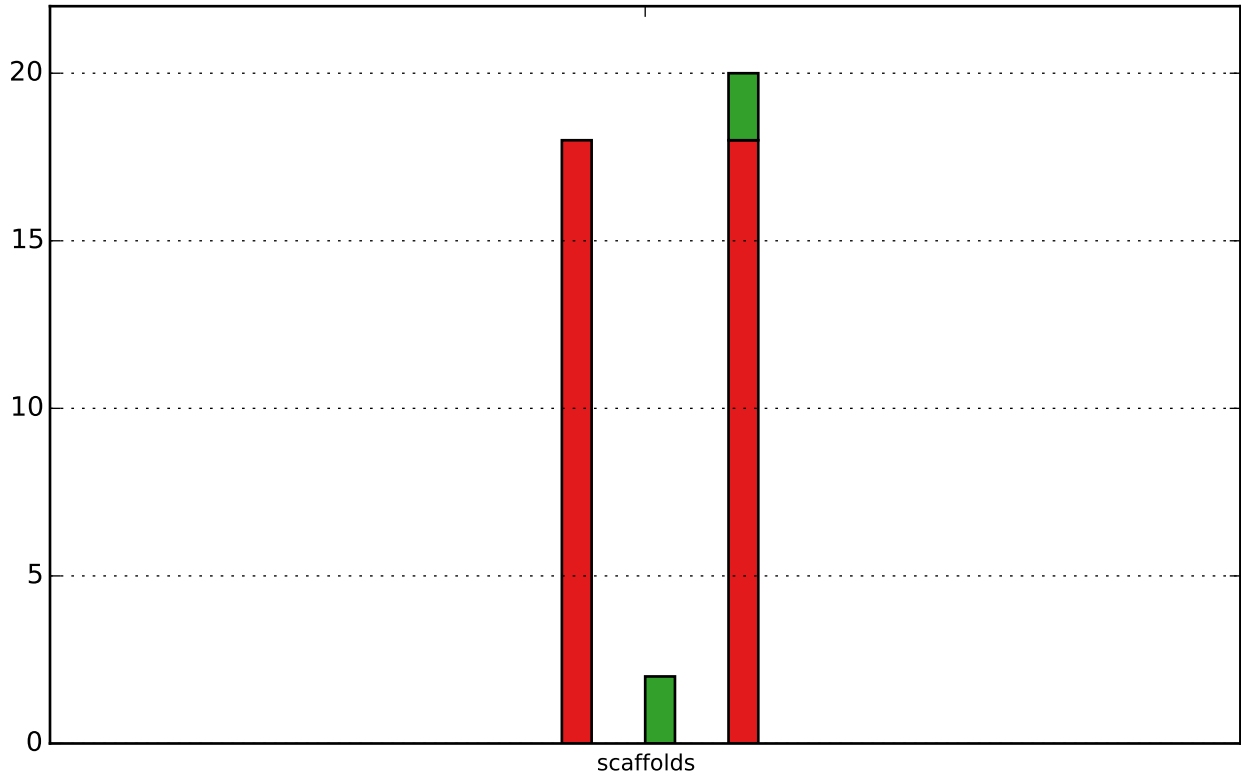




GC content



# Misassemblies



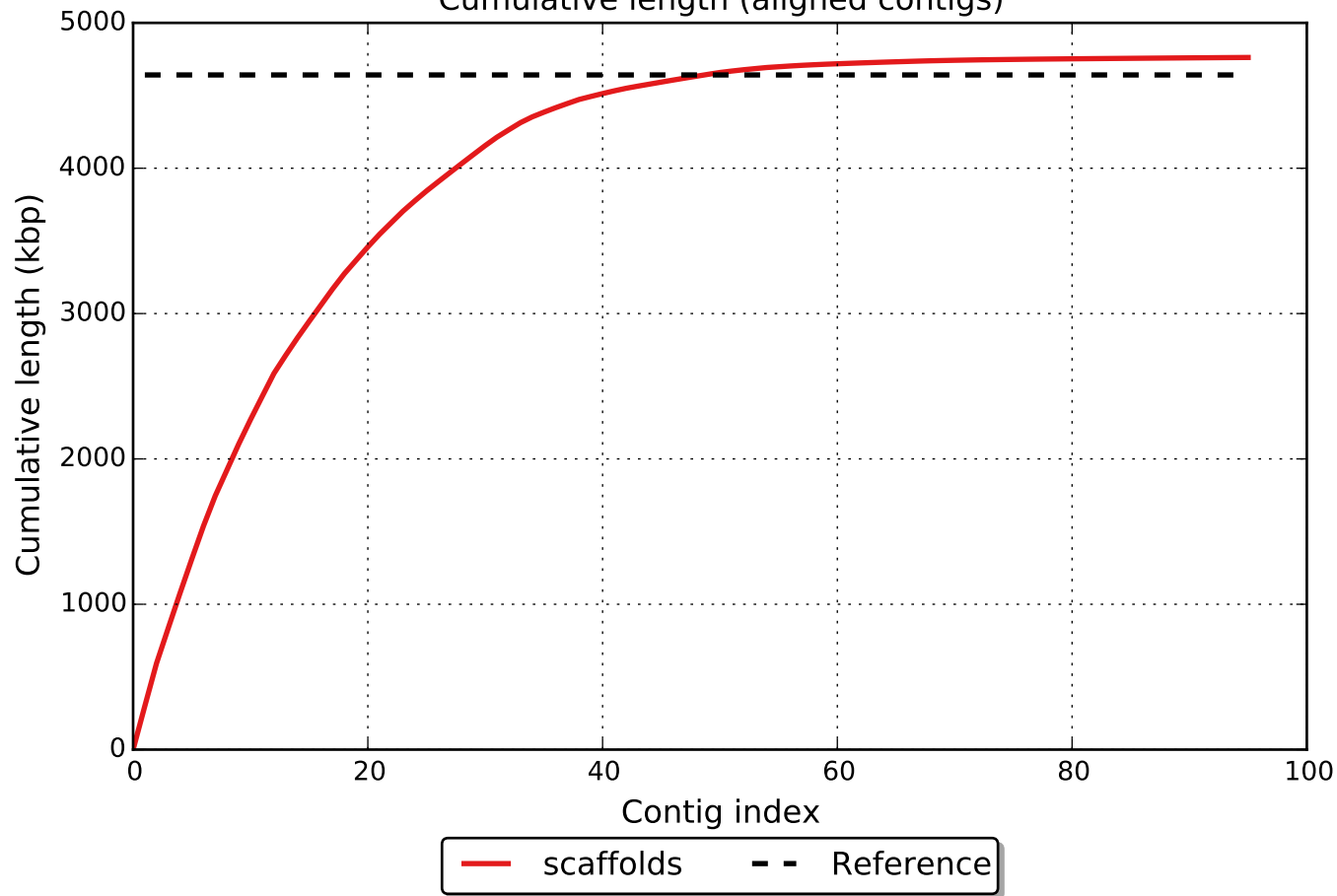
# relocations



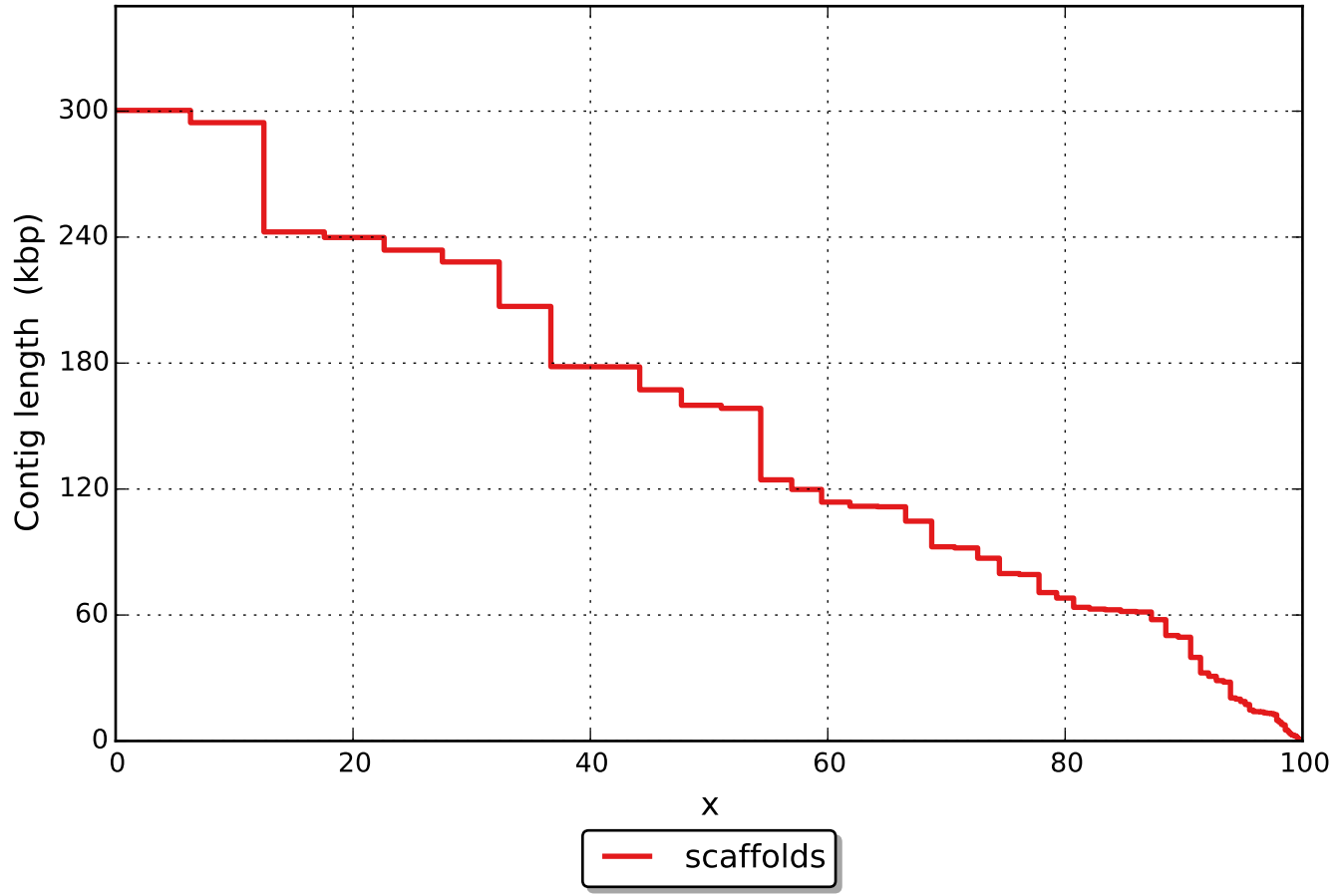
# inversions



Cumulative length (aligned contigs)



NAx



# NGAx

