

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	170
# contigs ( $\geq 5000$ bp)	133
# contigs ( $\geq 10000$ bp)	108
# contigs ( $\geq 25000$ bp)	68
# contigs ( $\geq 50000$ bp)	33
Total length ( $\geq 1000$ bp)	4628660
Total length ( $\geq 5000$ bp)	4538215
Total length ( $\geq 10000$ bp)	4360771
Total length ( $\geq 25000$ bp)	3737309
Total length ( $\geq 50000$ bp)	2476487
# contigs	184
Largest contig	148188
Total length	4638300
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.78
N50	54079
NG50	53894
N75	32460
NG75	32460
L50	30
LG50	31
L75	59
LG75	59
# misassemblies	21
# misassembled contigs	19
Misassembled contigs length	1112114
# local misassemblies	6
# unaligned contigs	0 + 5 part
Unaligned length	1089
Genome fraction (%)	98.069
Duplication ratio	1.019
# N's per 100 kbp	79.53
# mismatches per 100 kbp	742.94
# indels per 100 kbp	0.83
Largest alignment	122264
NA50	45250
NGA50	45250
NA75	28482
NGA75	28463
LA50	35
LGA50	35
LA75	67
LGA75	68

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	21
# relocations	17
# translocations	0
# inversions	4
# possibly misassembled contigs	3
# misassembled contigs	19
Misassembled contigs length	1112114
# local misassemblies	6
# mismatches	33819
# indels	38
# short indels	27
# long indels	11
Indels length	639

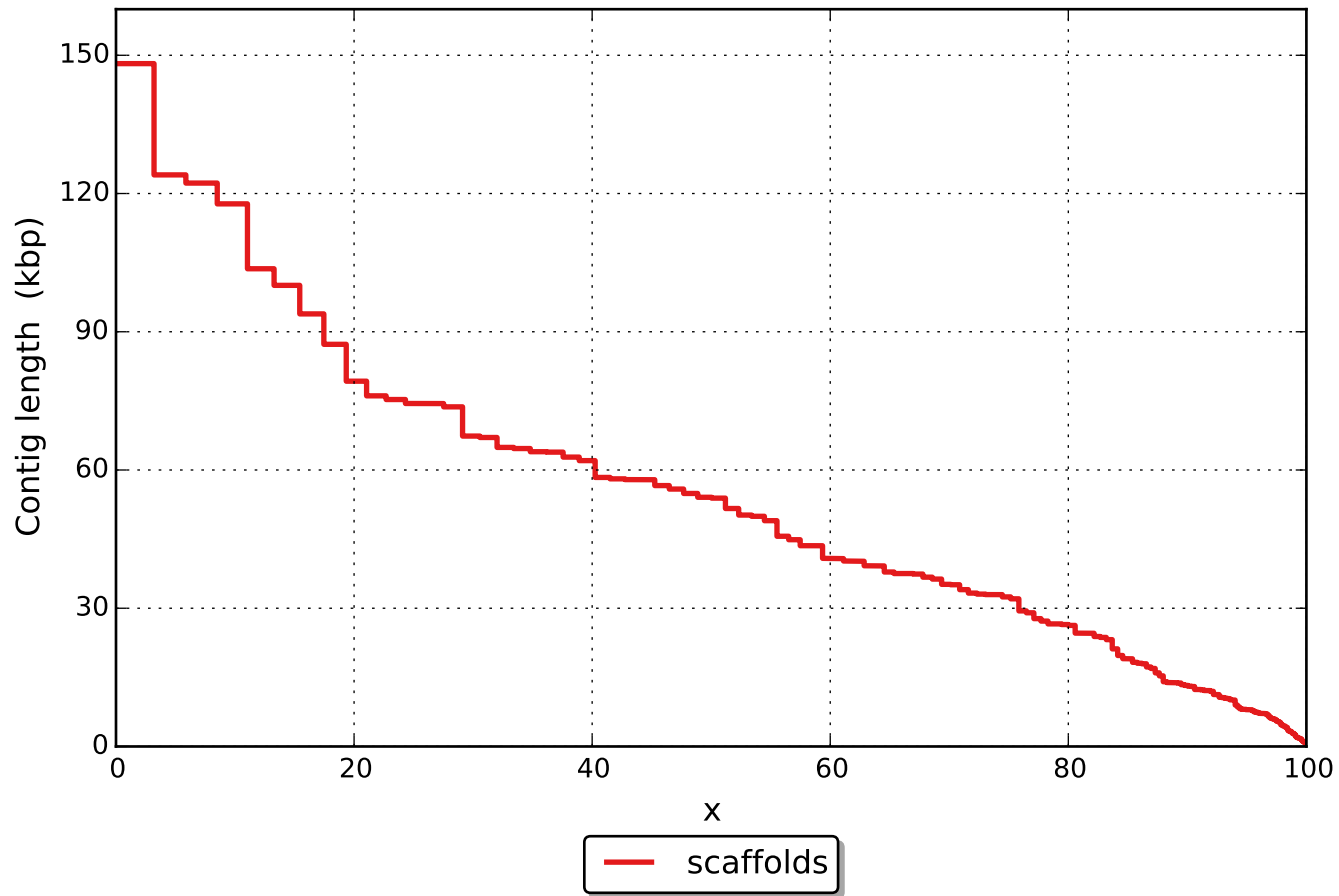
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

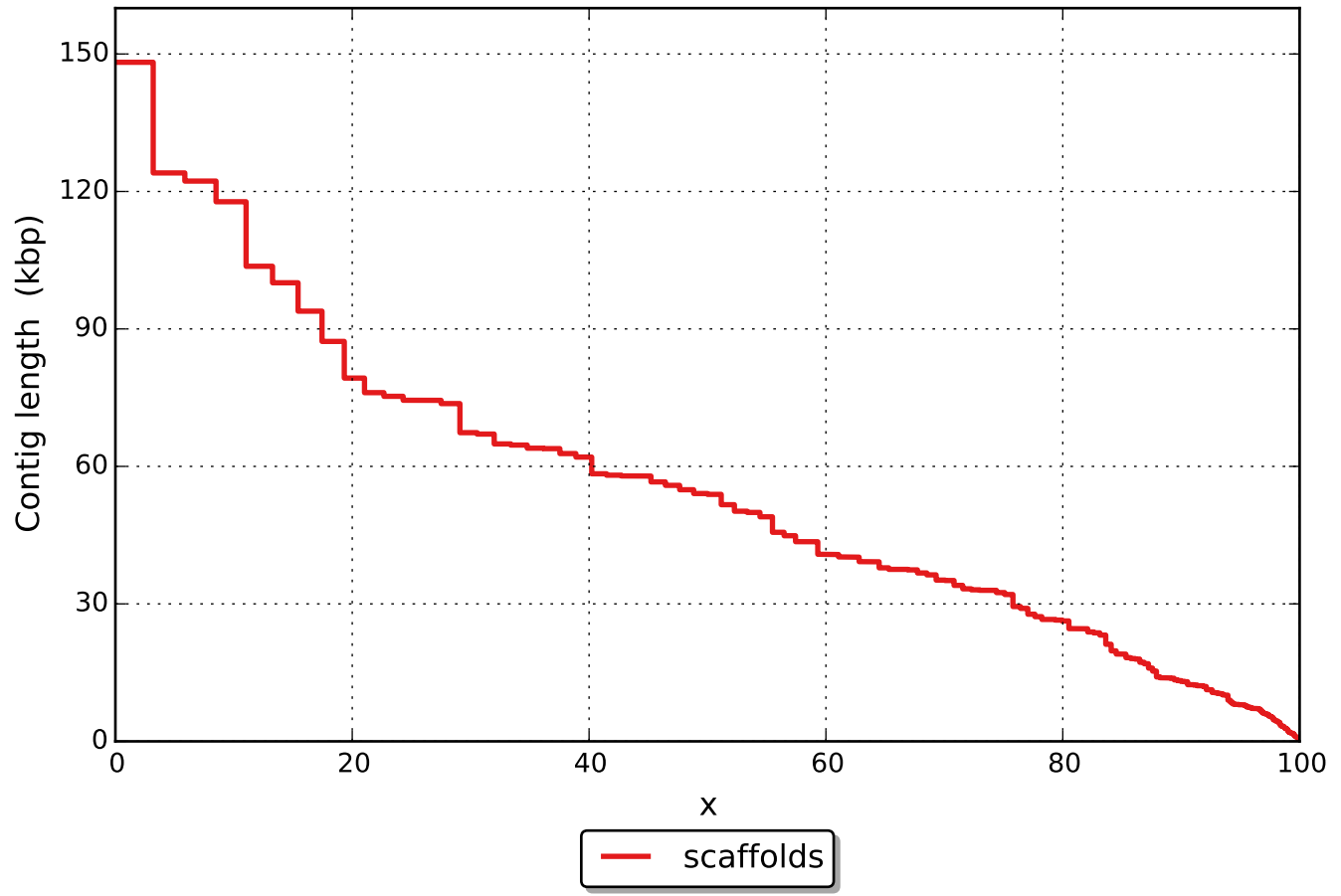
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1089
# N's	3689

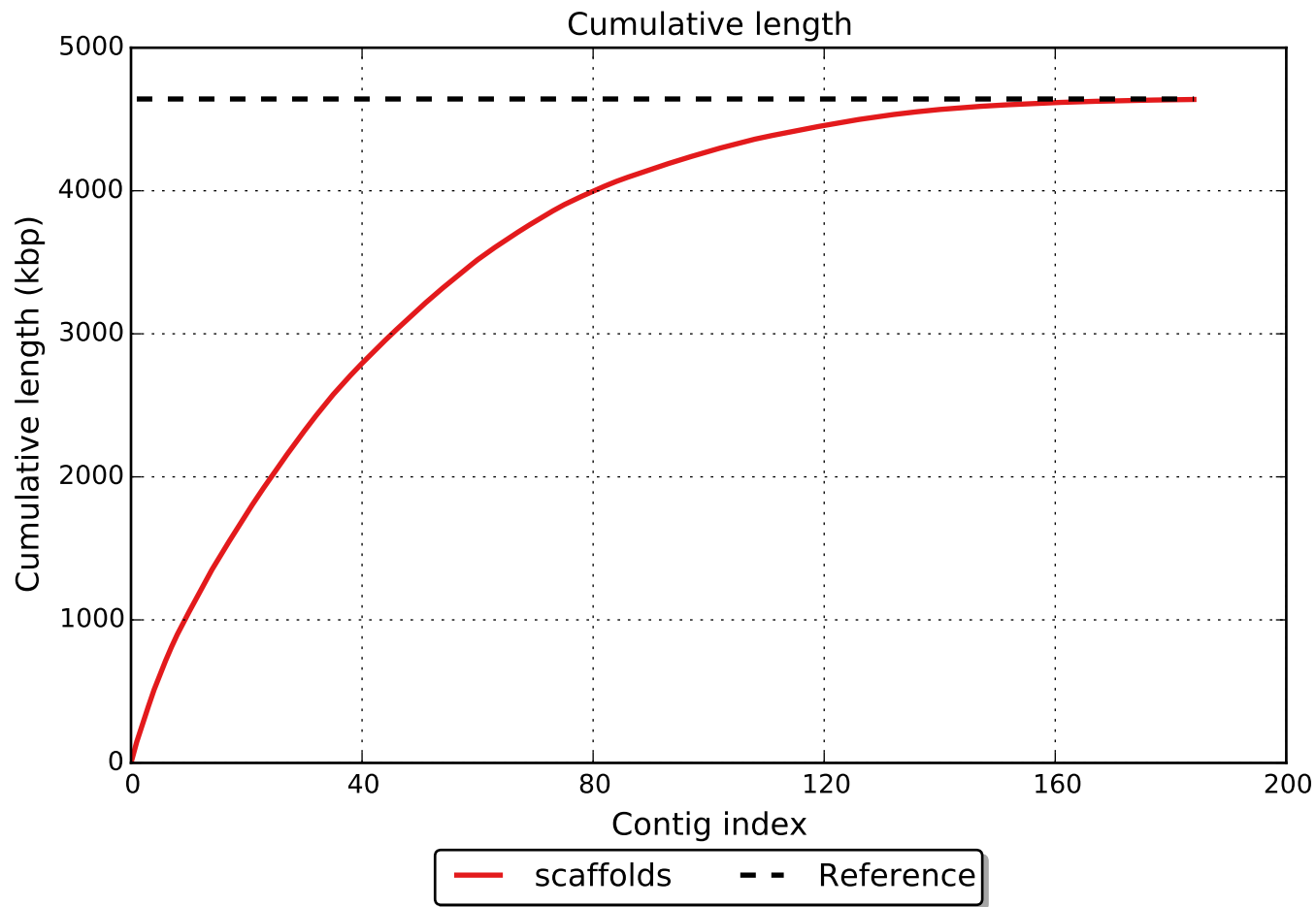
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

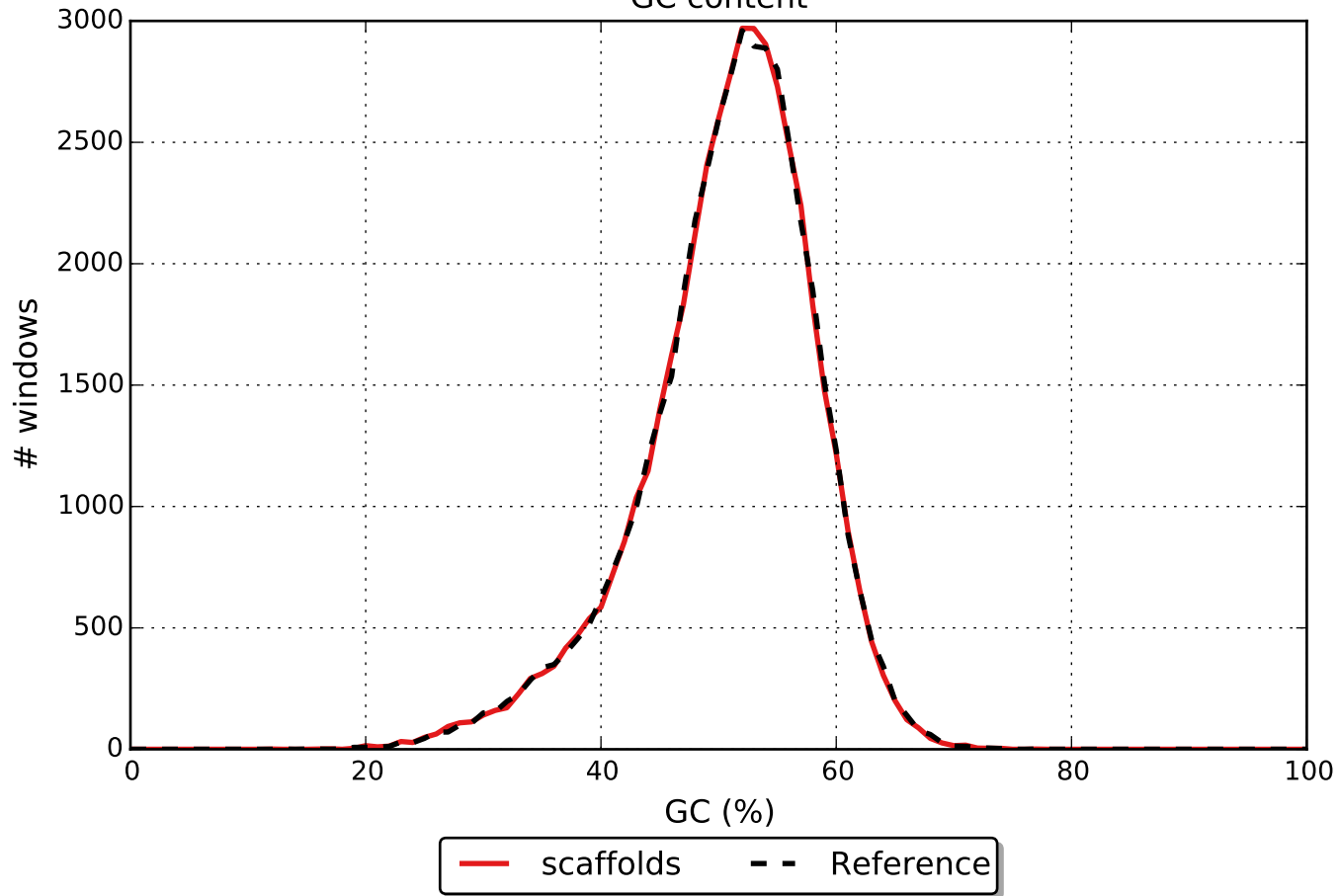


NGx

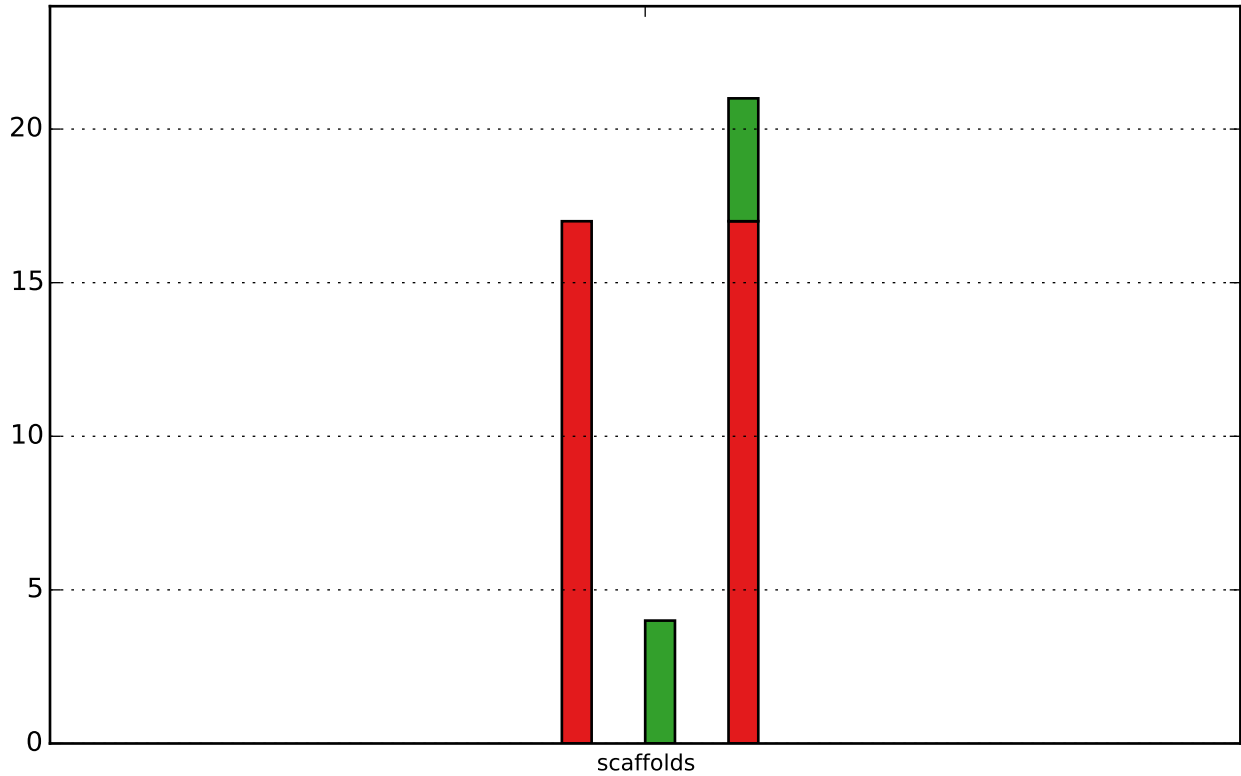




GC content

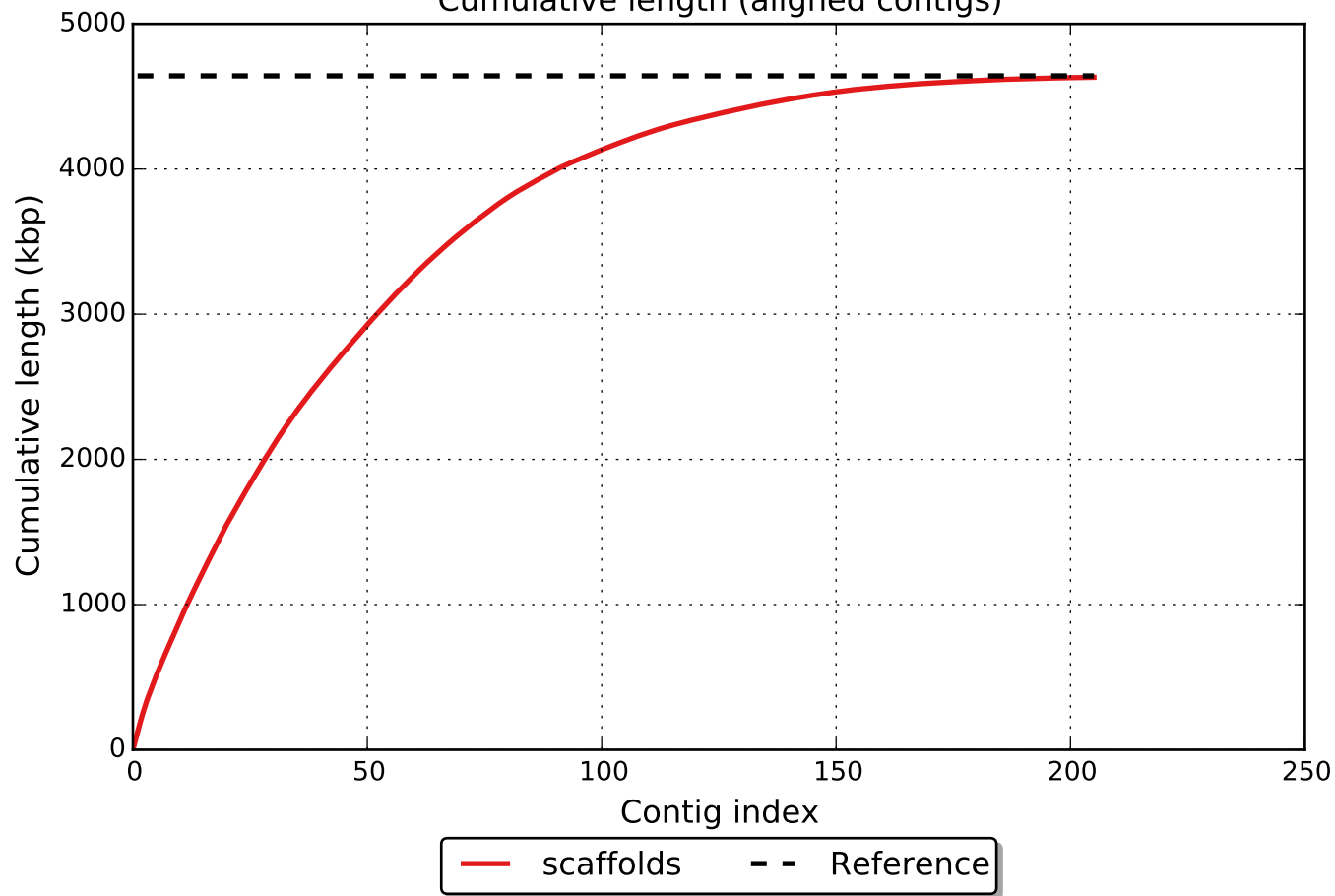


# Misassemblies

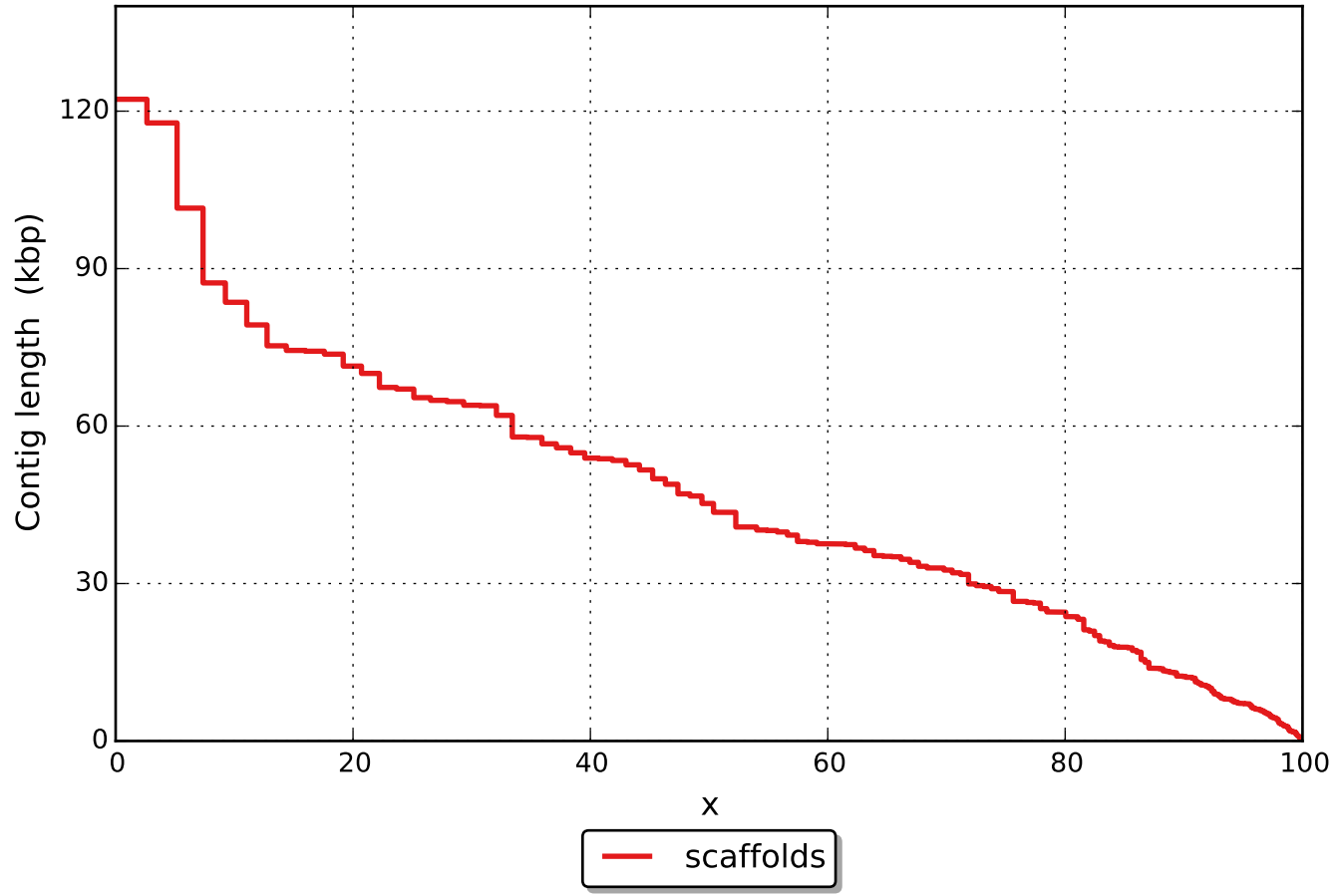




Cumulative length (aligned contigs)



NAx



# NGAx

