

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	179
# contigs ( $\geq 5000$ bp)	140
# contigs ( $\geq 10000$ bp)	102
# contigs ( $\geq 25000$ bp)	62
# contigs ( $\geq 50000$ bp)	24
Total length ( $\geq 1000$ bp)	4537084
Total length ( $\geq 5000$ bp)	4425493
Total length ( $\geq 10000$ bp)	4123960
Total length ( $\geq 25000$ bp)	3462834
Total length ( $\geq 50000$ bp)	2085767
# contigs	187
Largest contig	255476
Total length	4542889
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	46912
NG50	46674
N75	26834
NG75	24332
L50	28
LG50	29
L75	60
LG75	63
# misassemblies	14
# misassembled contigs	13
Misassembled contigs length	613325
# local misassemblies	7
# unaligned contigs	0 + 2 part
Unaligned length	113
Genome fraction (%)	97.767
Duplication ratio	1.001
# N's per 100 kbp	15.47
# mismatches per 100 kbp	88.63
# indels per 100 kbp	10.36
Largest alignment	255473
NA50	46087
NGA50	45277
NA75	23452
NGA75	22766
LA50	30
LGA50	31
LA75	65
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	14
# relocations	14
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	13
Misassembled contigs length	613325
# local misassemblies	7
# mismatches	4022
# indels	470
# short indels	431
# long indels	39
Indels length	1216

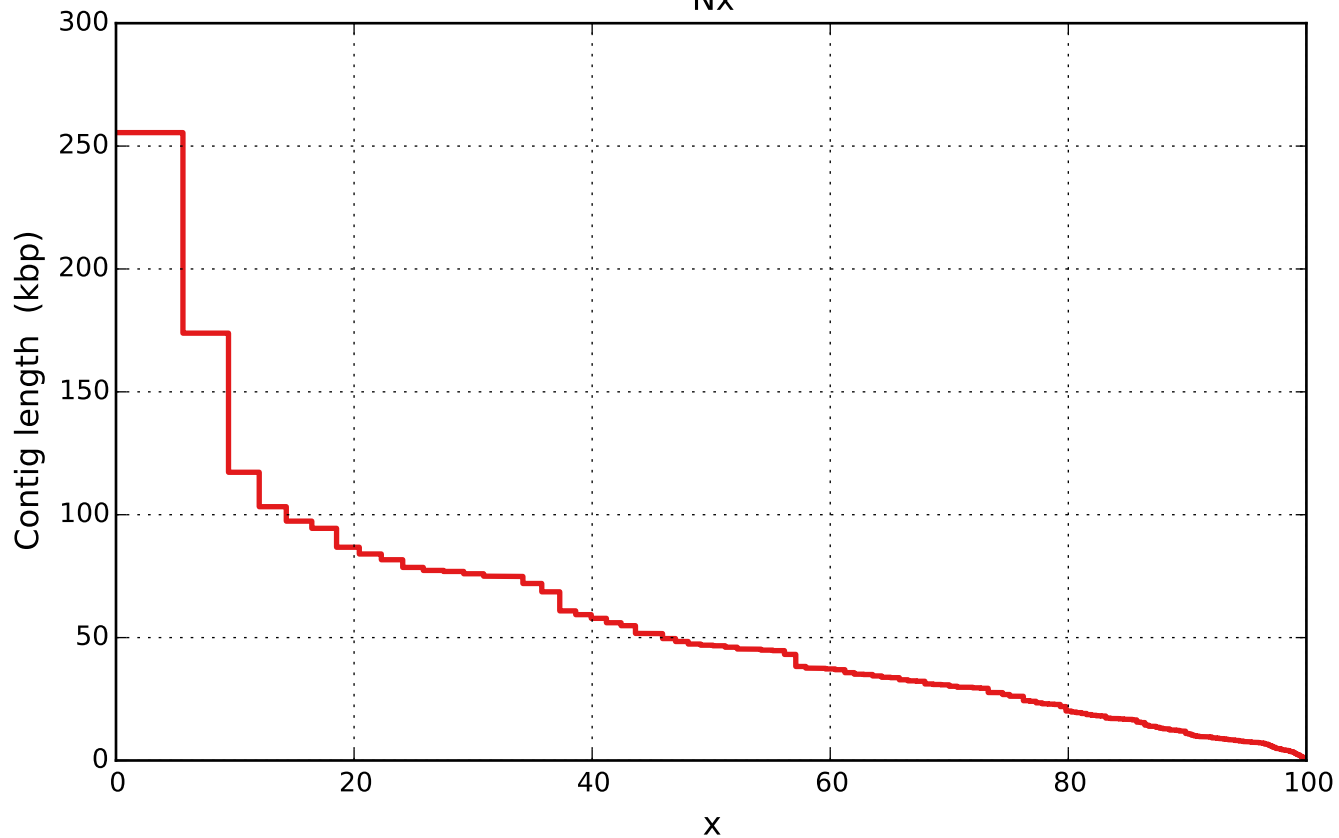
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	113
# N's	703

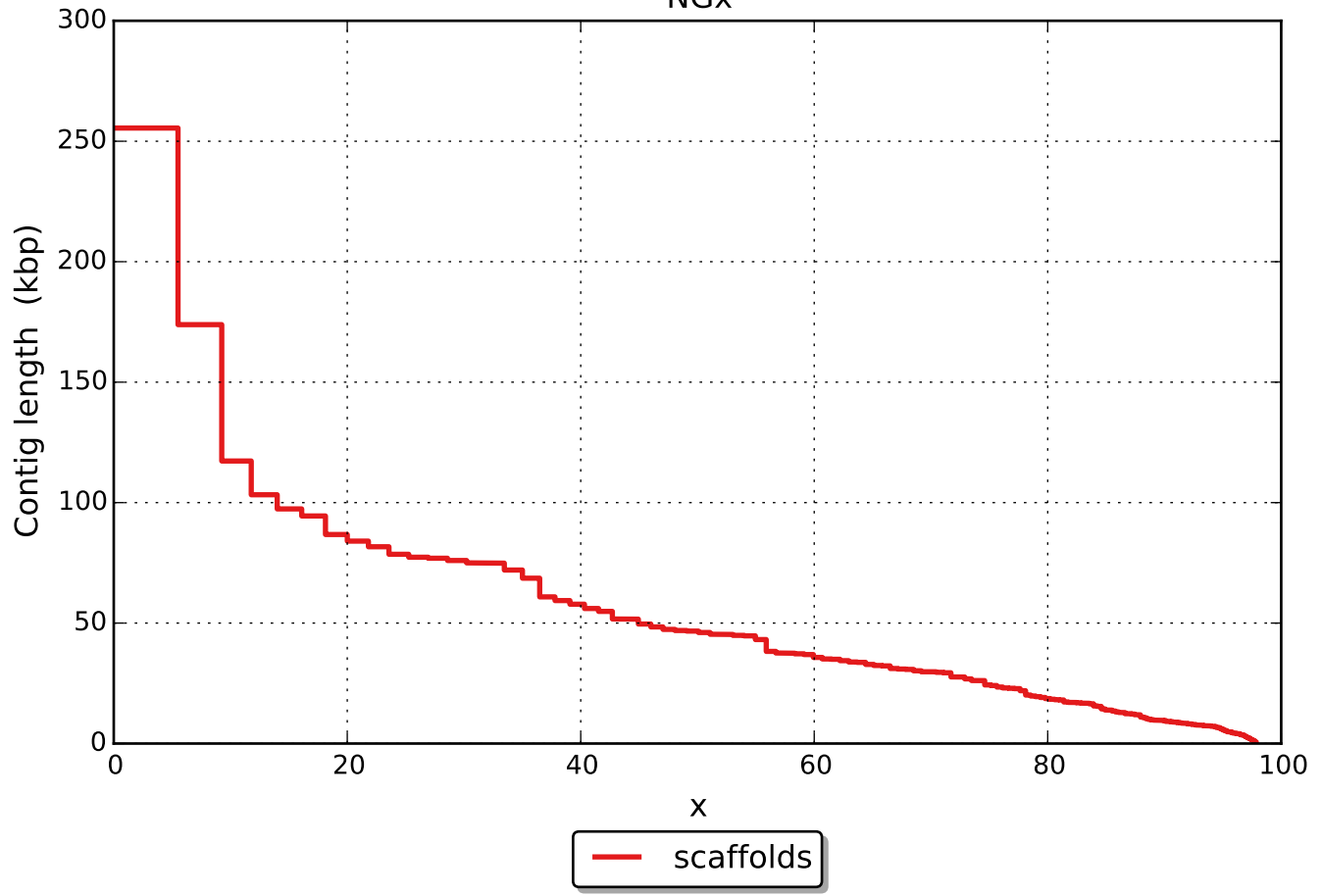
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

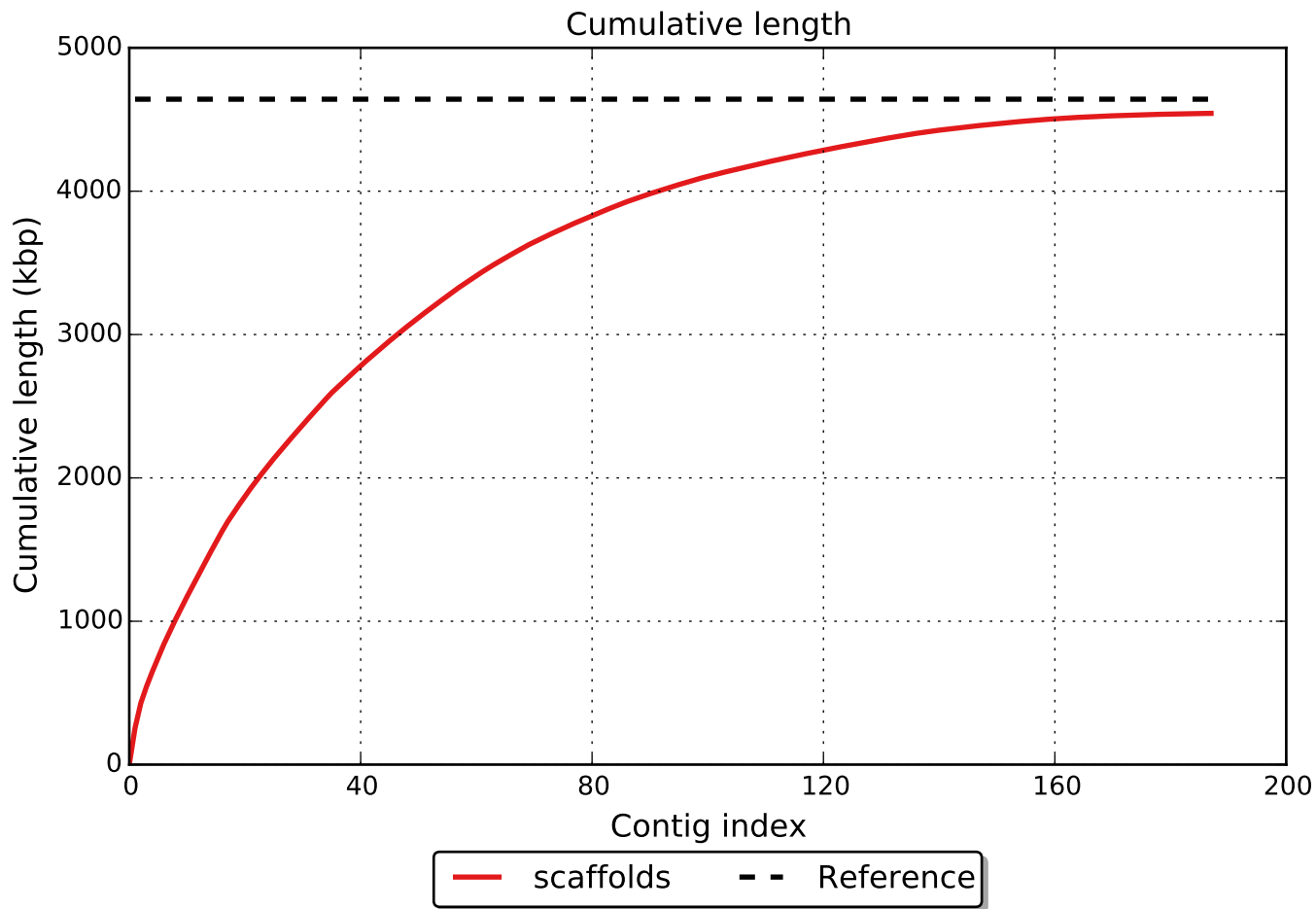
Nx



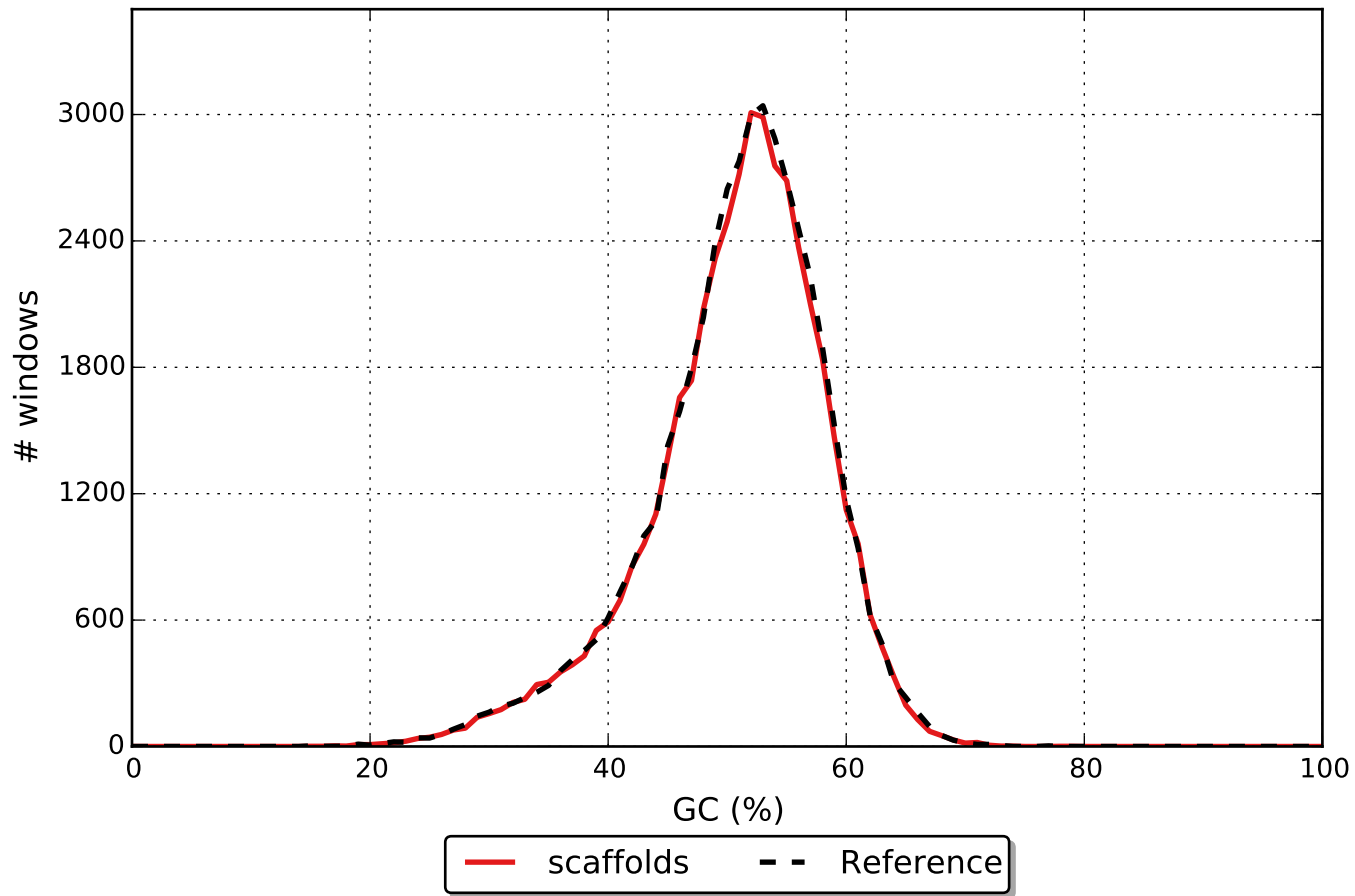
— scaffolds

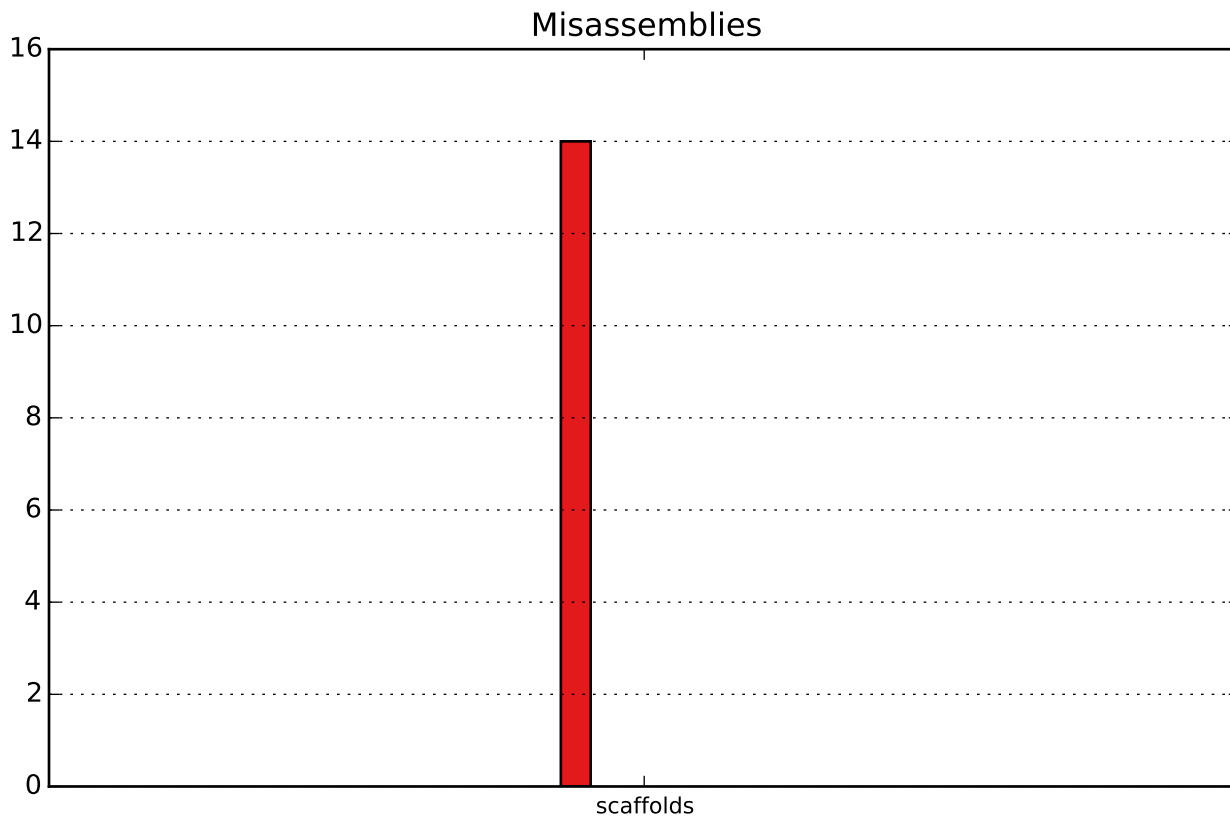
NGx





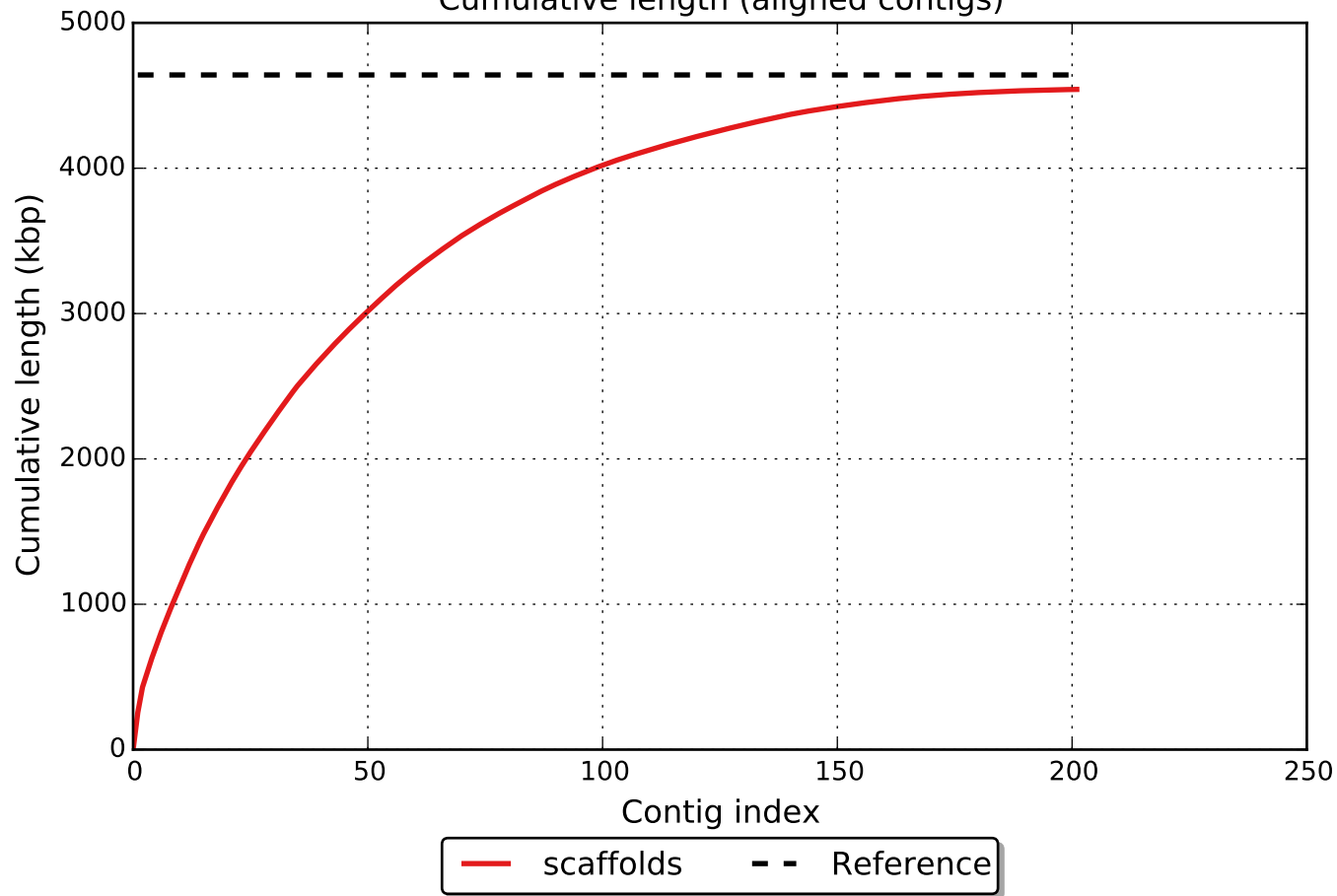
# GC content



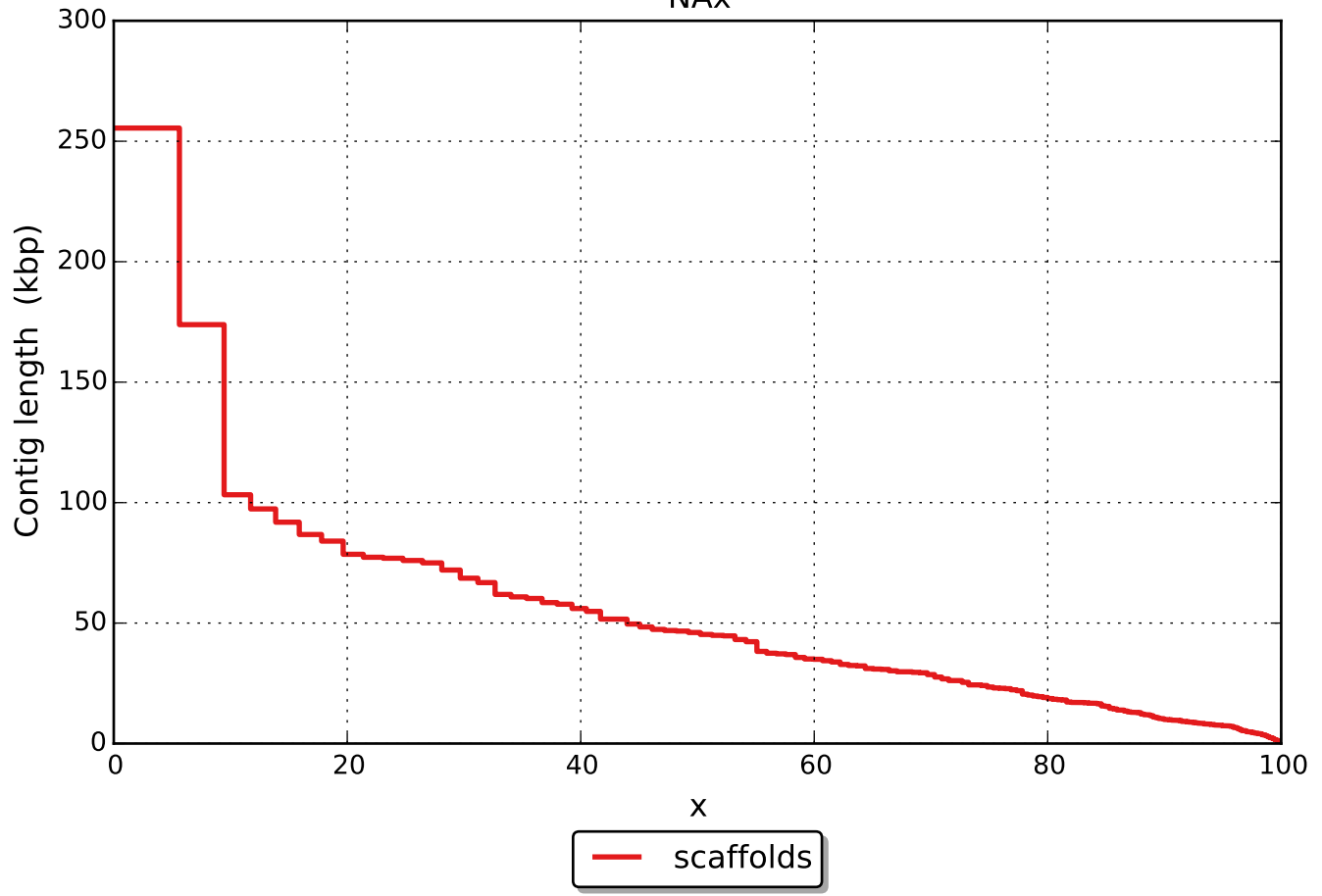




Cumulative length (aligned contigs)



NAx



# NGAx

