

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	31
# contigs ( $\geq 5000$ bp)	27
# contigs ( $\geq 10000$ bp)	26
# contigs ( $\geq 25000$ bp)	25
# contigs ( $\geq 50000$ bp)	22
Total length ( $\geq 1000$ bp)	4696185
Total length ( $\geq 5000$ bp)	4691496
Total length ( $\geq 10000$ bp)	4686030
Total length ( $\geq 25000$ bp)	4672863
Total length ( $\geq 50000$ bp)	4576116
# contigs	39
Largest contig	529644
Total length	4701773
Reference length	4641652
GC (%)	50.82
Reference GC (%)	50.78
N50	305443
NG50	305443
N75	176954
NG75	182223
L50	6
LG50	6
L75	12
LG75	11
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	578950
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.120
Duplication ratio	1.022
# N's per 100 kbp	0.47
# mismatches per 100 kbp	374.98
# indels per 100 kbp	1.00
Largest alignment	529644
NA50	301763
NGA50	301763
NA75	128117
NGA75	128117
LA50	7
LGA50	7
LA75	12
LGA75	12

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	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	2
Misassembled contigs length	578950
# local misassemblies	1
# mismatches	17252
# indels	46
# short indels	45
# long indels	1
Indels length	67

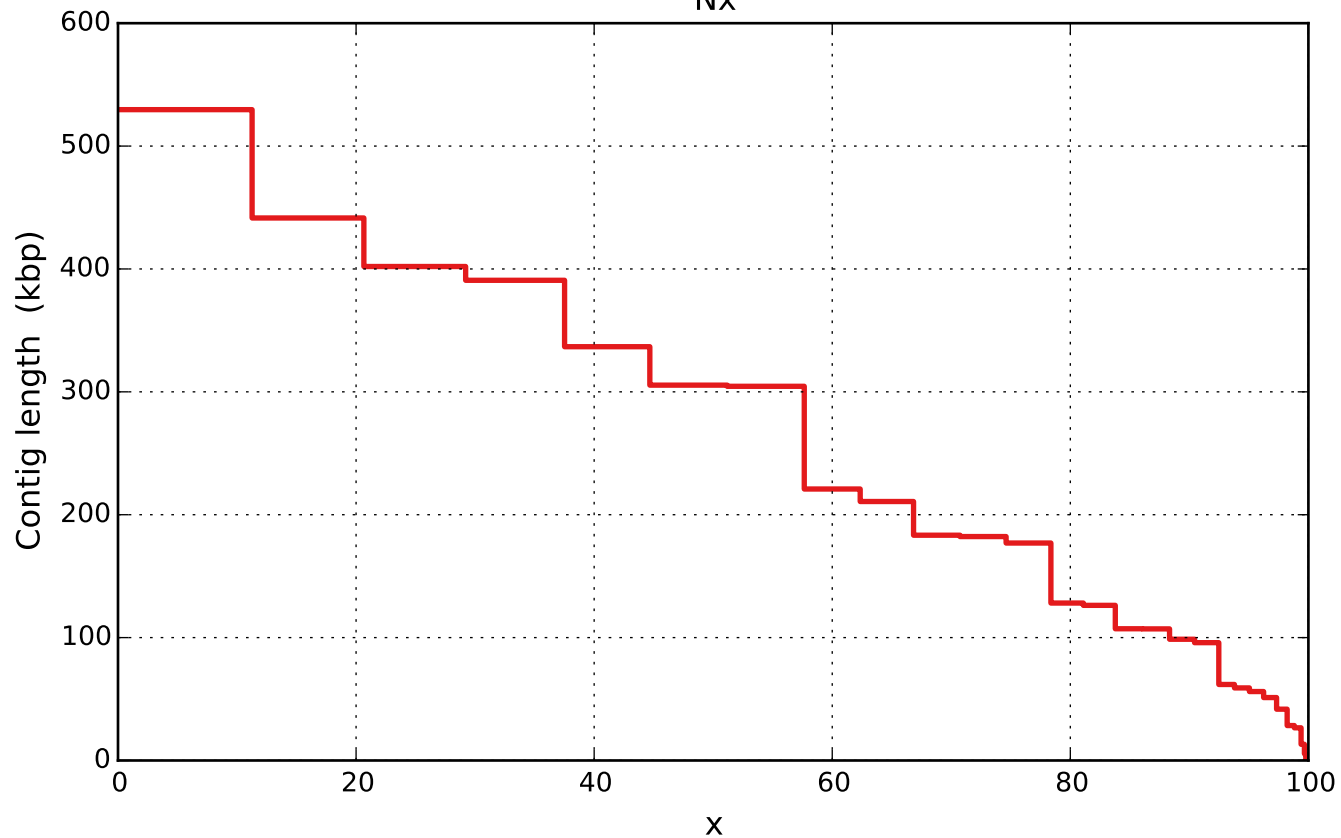
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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	22

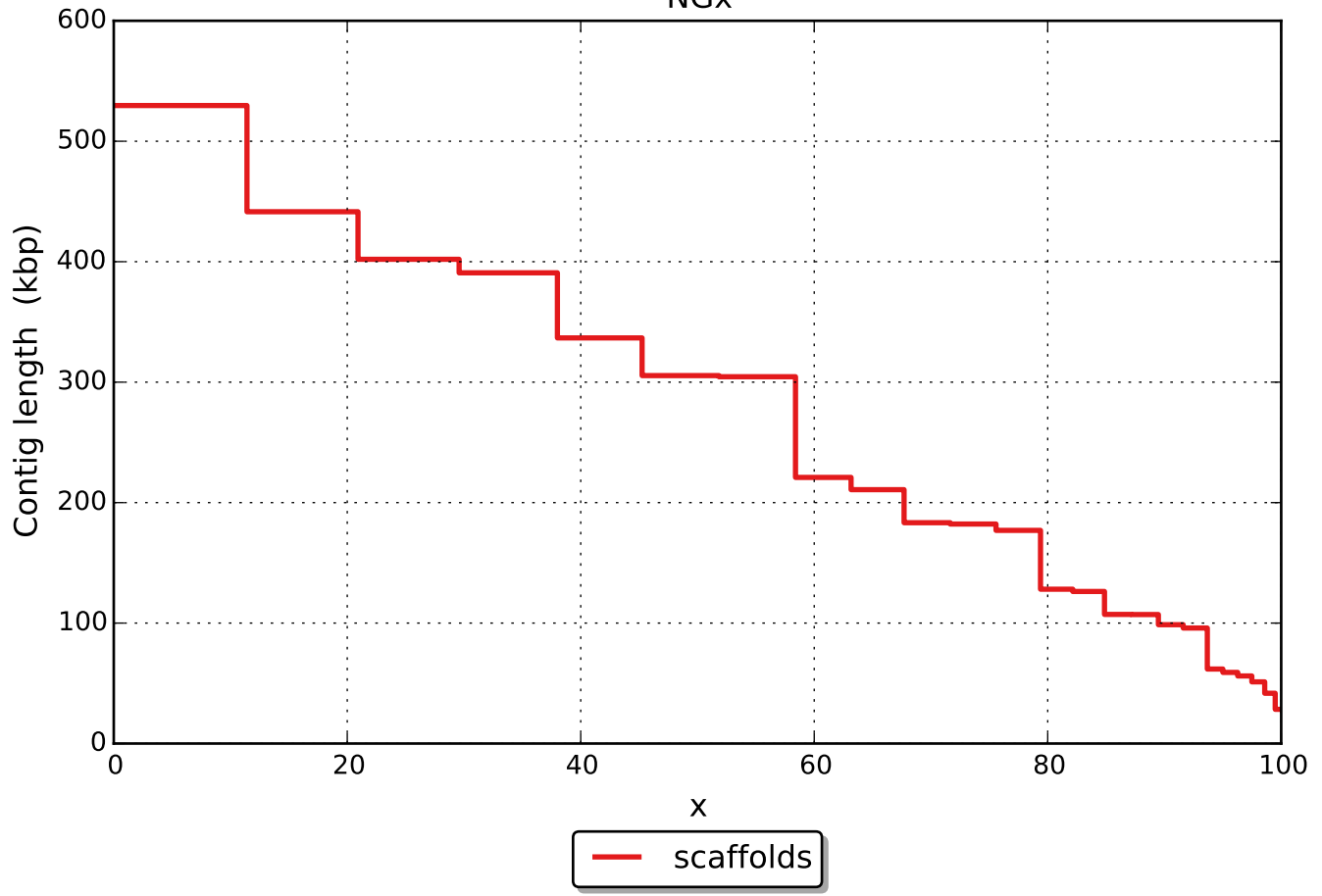
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

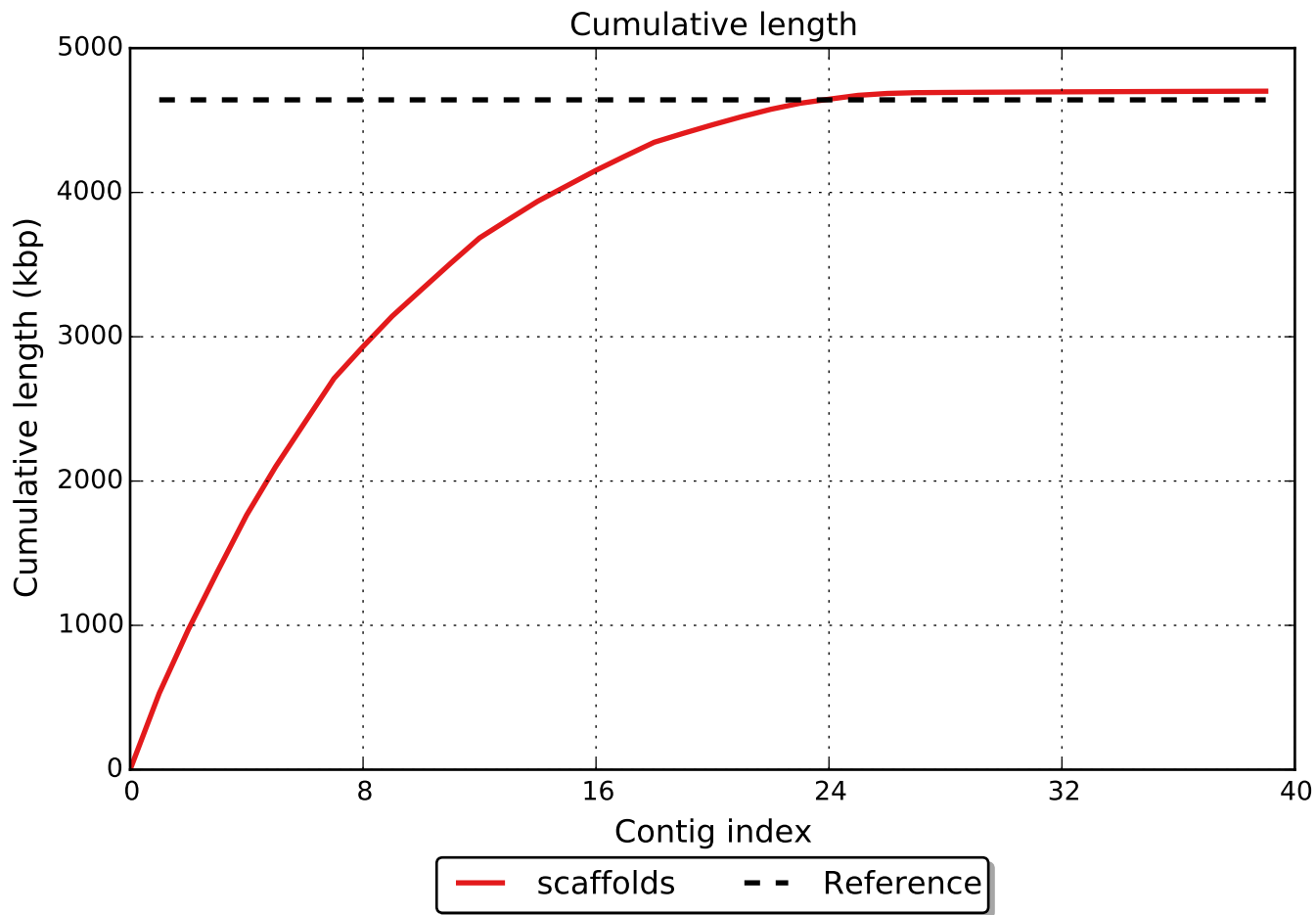
Nx



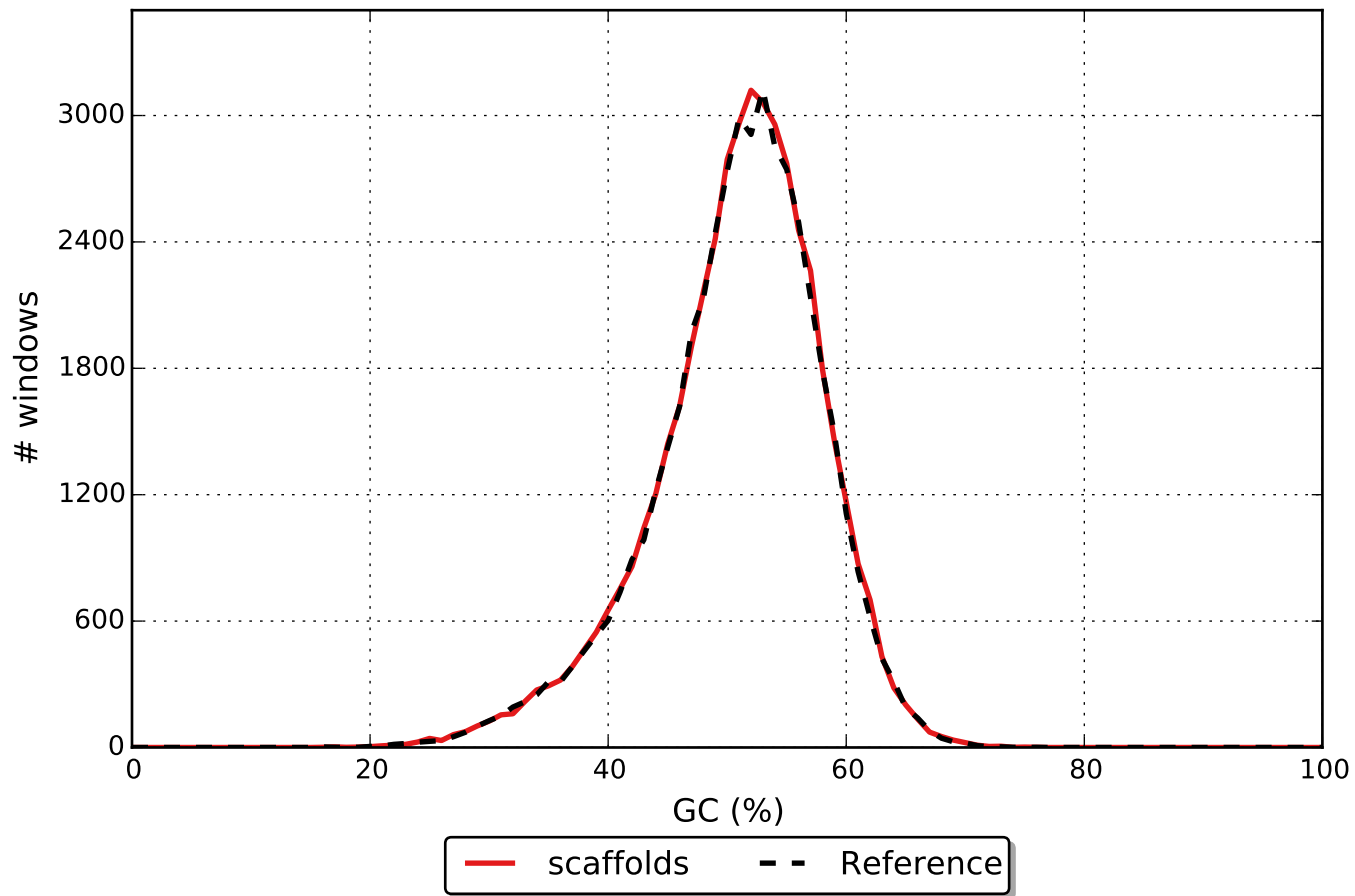
— scaffolds

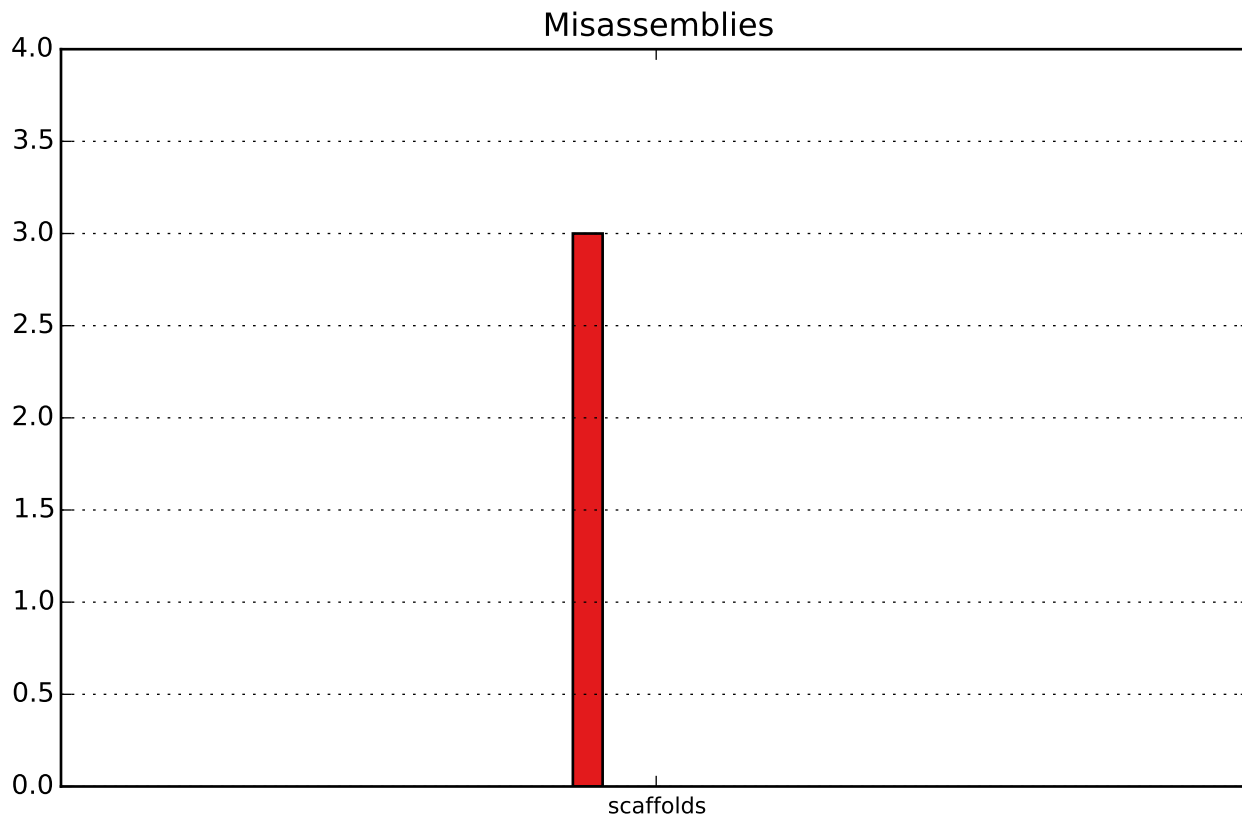
NGx





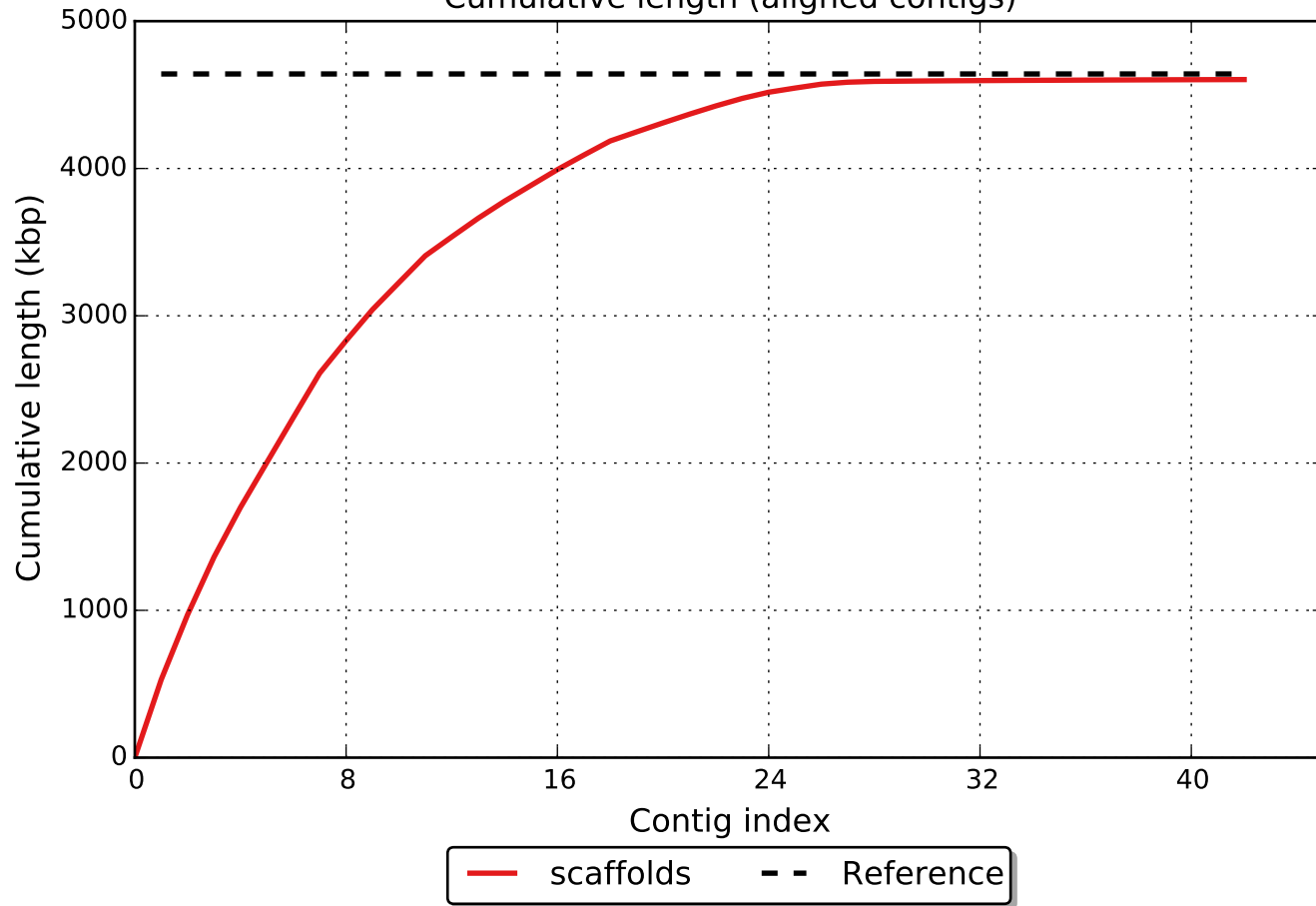
# GC content



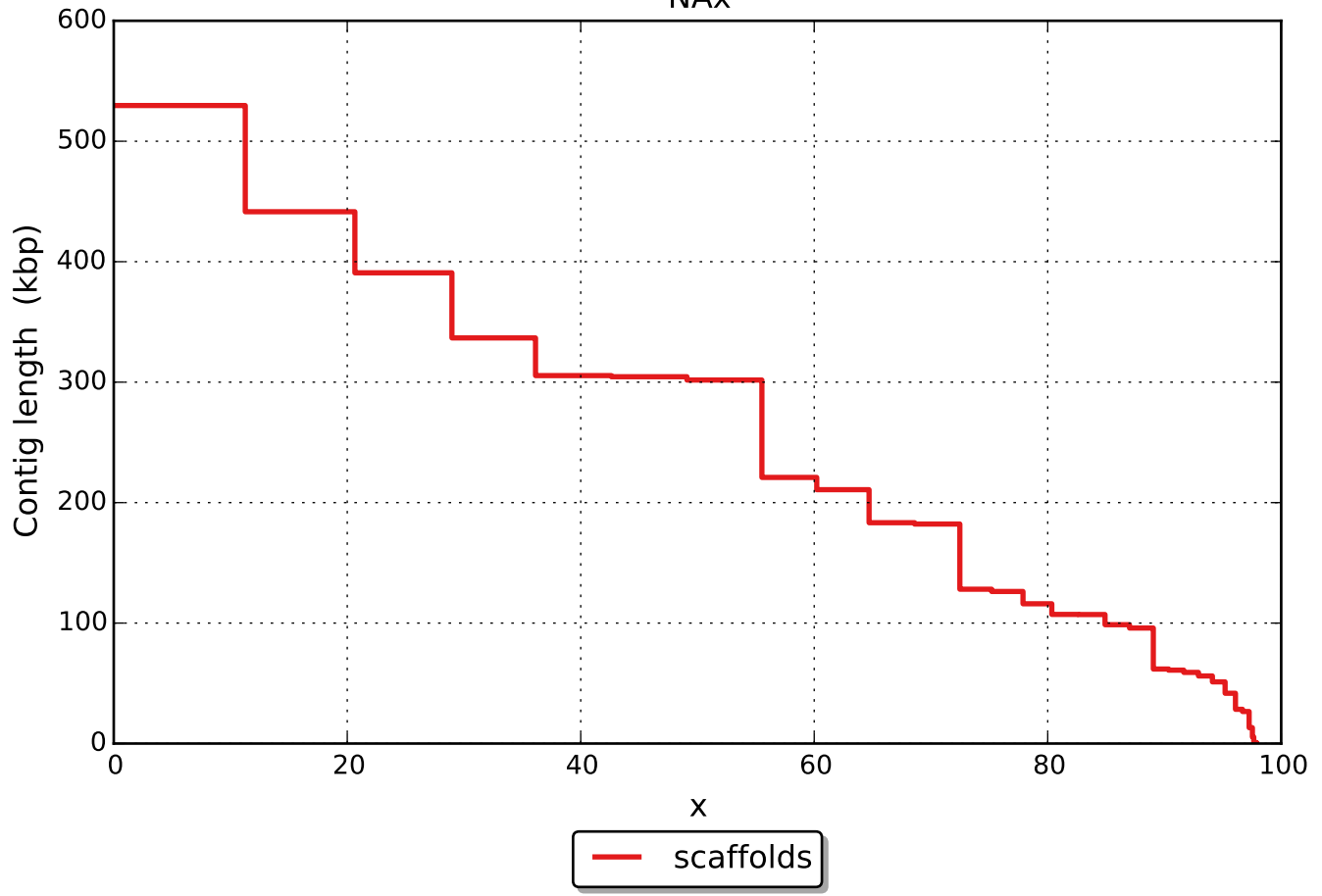




Cumulative length (aligned contigs)



NAx



# NGAx

