

# Report

	scaffolds
# contigs ( $\geq 1000$ bp)	311
# contigs ( $\geq 5000$ bp)	112
# contigs ( $\geq 10000$ bp)	43
# contigs ( $\geq 25000$ bp)	7
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	1756559
Total length ( $\geq 5000$ bp)	1309929
Total length ( $\geq 10000$ bp)	807107
Total length ( $\geq 25000$ bp)	242832
Total length ( $\geq 50000$ bp)	0
# contigs	465
Largest contig	46453
Total length	1862573
Reference length	4641652
GC (%)	50.60
Reference GC (%)	50.79
N50	8742
N75	3980
L50	57
L75	132
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 1 part
Unaligned length	55
Genome fraction (%)	39.403
Duplication ratio	1.018
# N's per 100 kbp	389.57
# mismatches per 100 kbp	1012.99
# indels per 100 kbp	2.24
Largest alignment	43816
NA50	8425
NGA50	-
NA75	3970
LA50	58
LA75	134

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

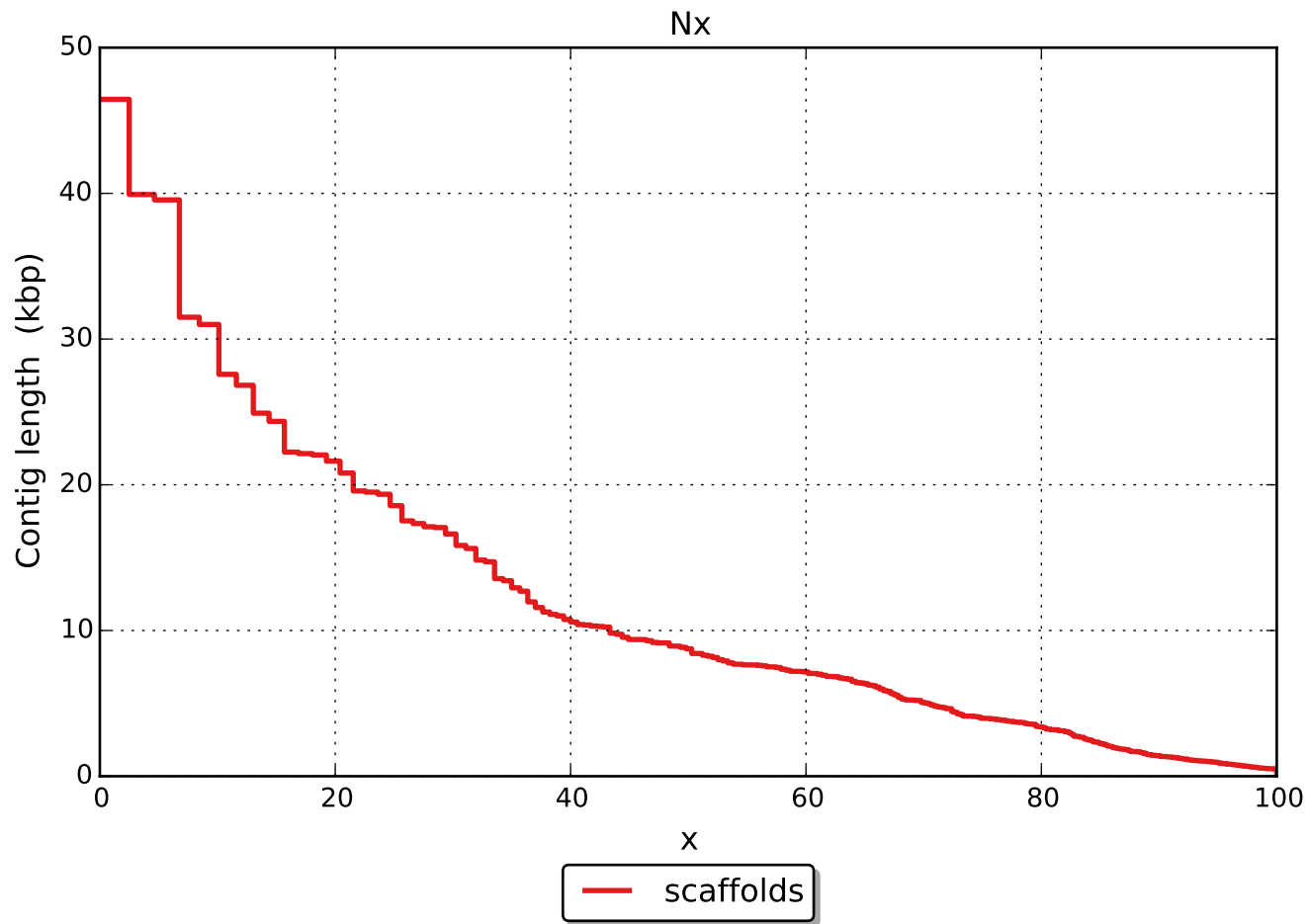
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	5
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	18527
# indels	41
# short indels	21
# long indels	20
Indels length	1122

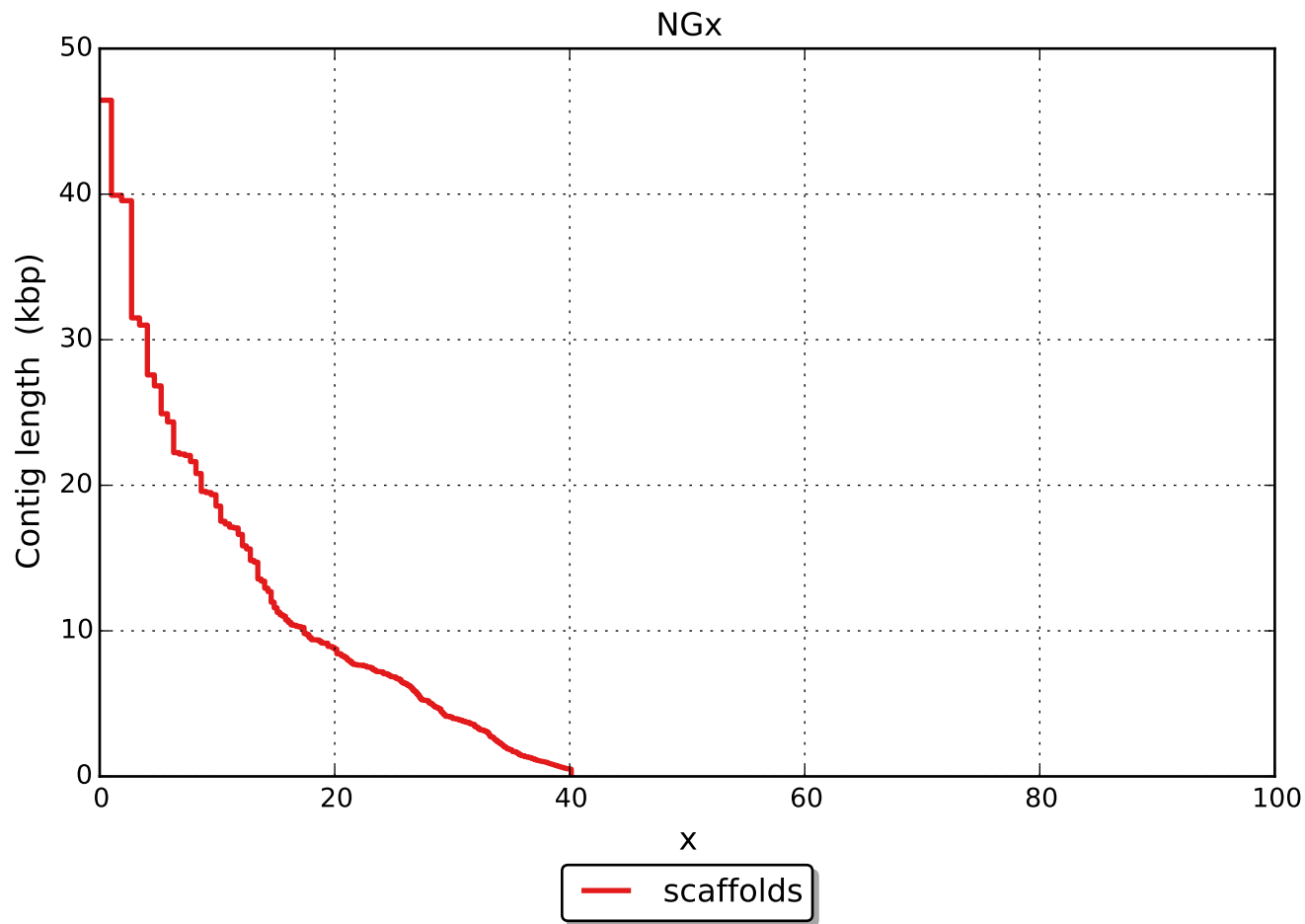
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

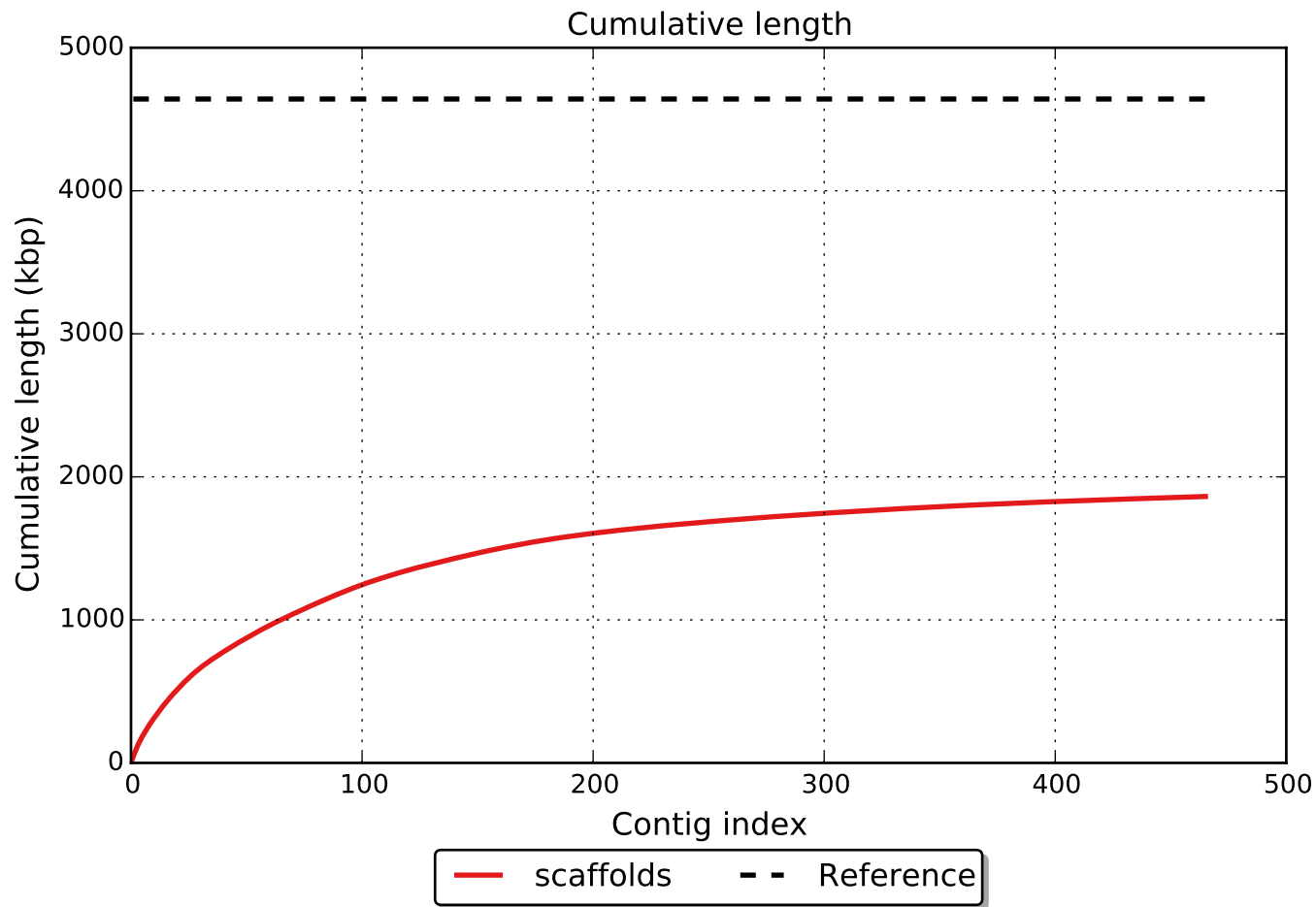
## Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	55
# N's	7256

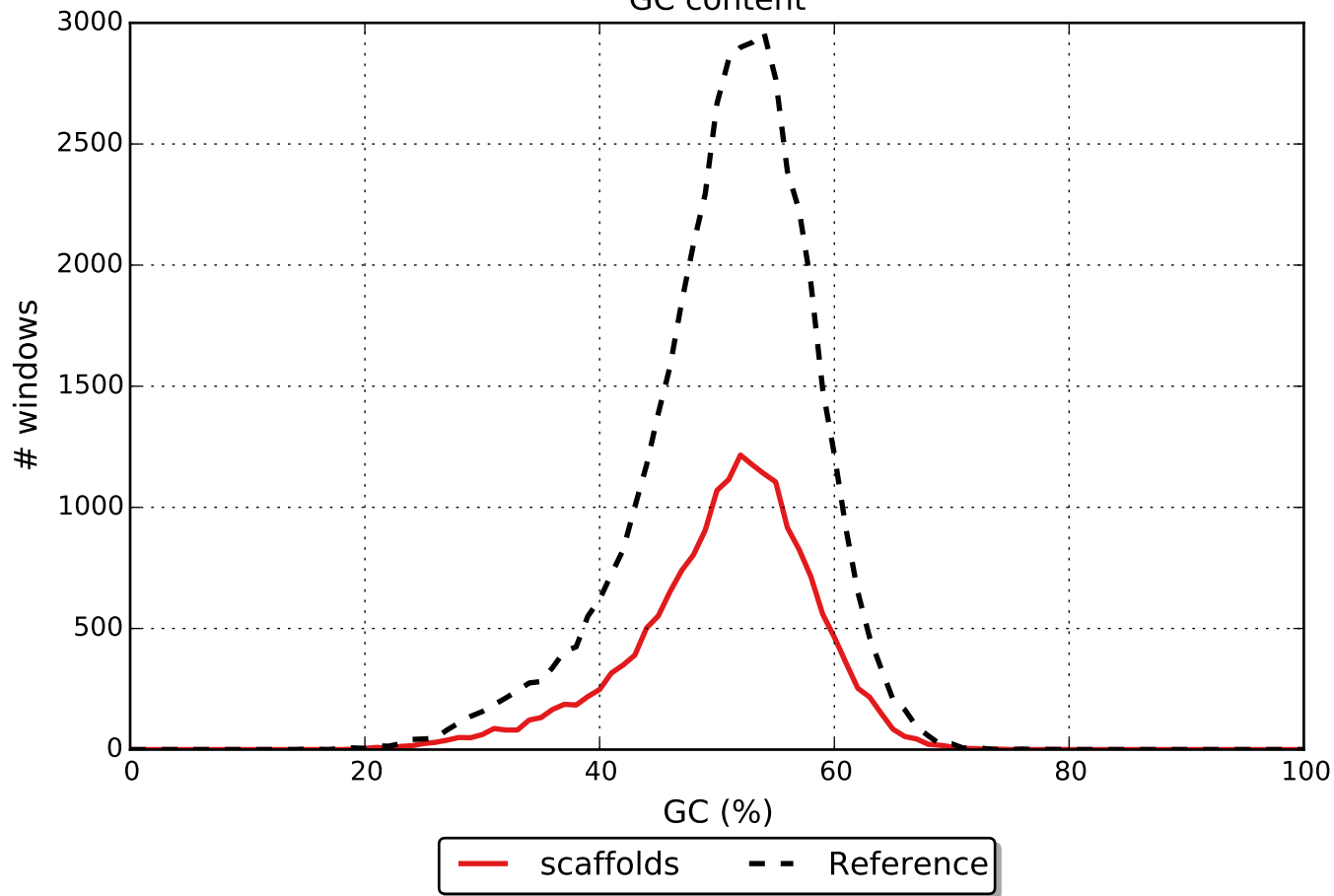
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

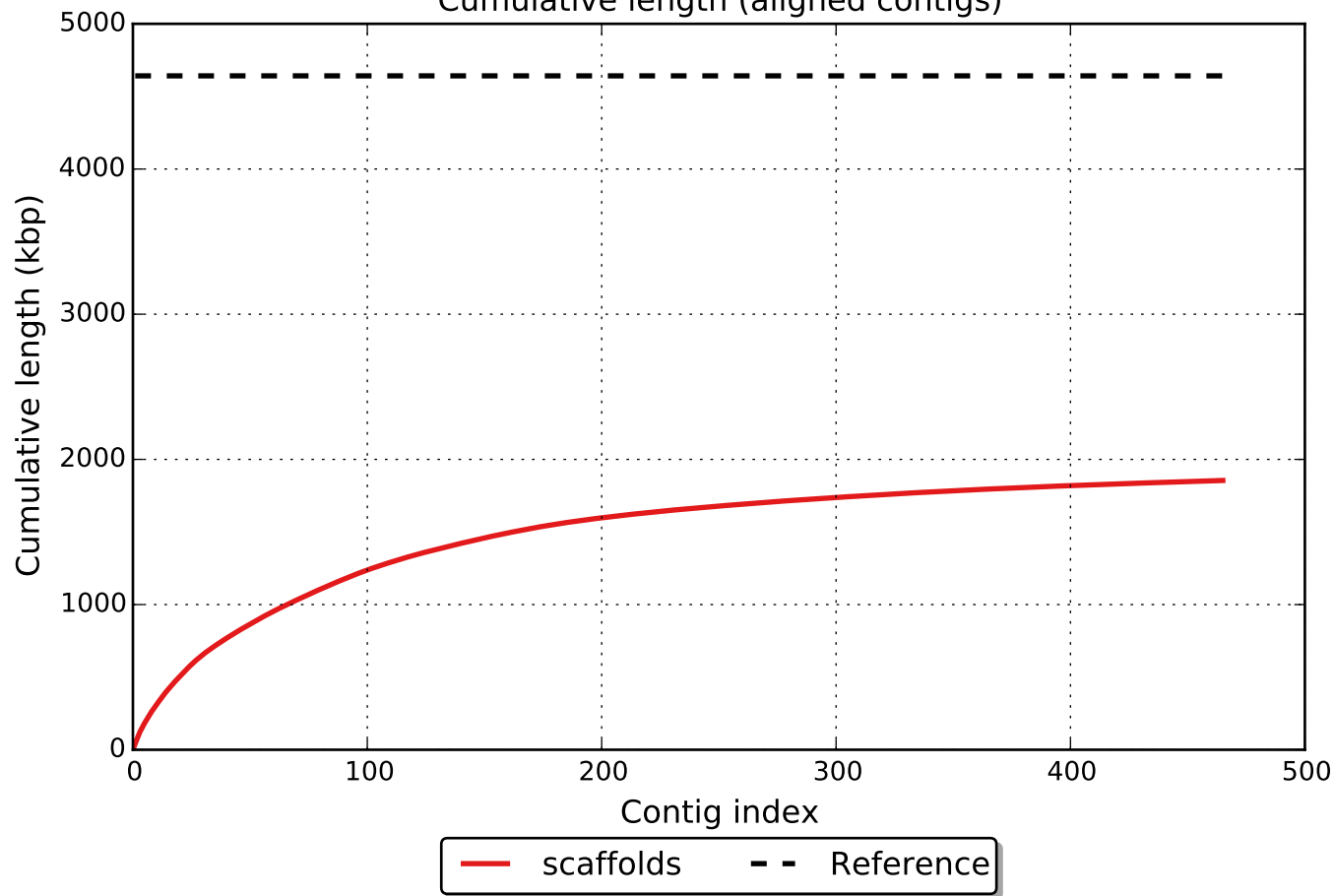


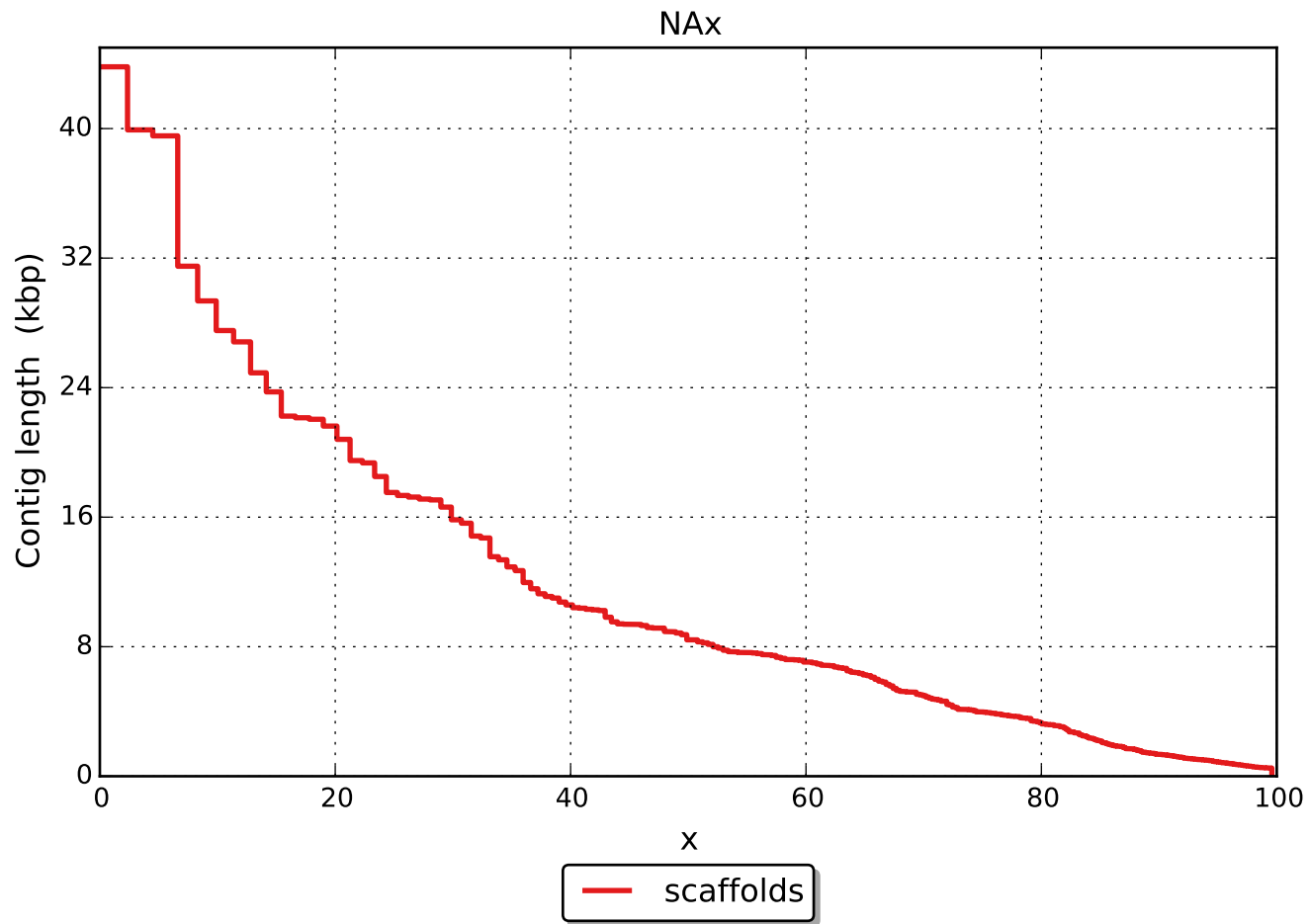
# Misassemblies





Cumulative length (aligned contigs)





NGAx

