

Report

	scaffolds
# contigs (≥ 1000 bp)	10
# contigs (≥ 5000 bp)	9
# contigs (≥ 10000 bp)	9
# contigs (≥ 25000 bp)	9
# contigs (≥ 50000 bp)	6
Total length (≥ 1000 bp)	923243
Total length (≥ 5000 bp)	921551
Total length (≥ 10000 bp)	921551
Total length (≥ 25000 bp)	921551
Total length (≥ 50000 bp)	826631
# contigs	11
Largest contig	208409
Total length	924179
Reference length	4641652
GC (%)	50.66
Reference GC (%)	50.78
N50	131825
N75	109022
L50	3
L75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 10 part
Unaligned length	908493
Genome fraction (%)	0.336
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4514.22
# indels per 100 kbp	12.84
Largest alignment	3140
NGA50	-

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

Misassemblies report

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	8
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	703
# indels	2
# short indels	2
# long indels	0
Indels length	2

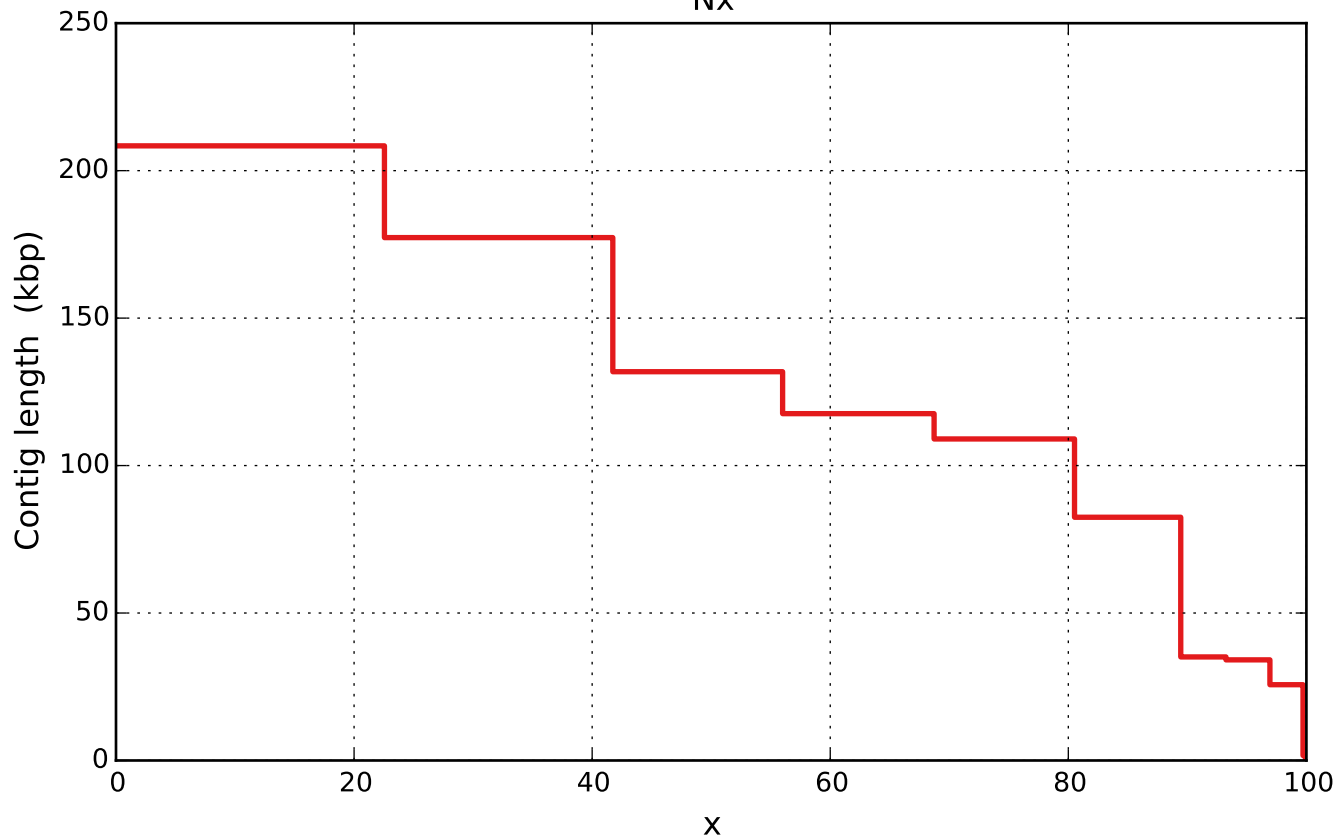
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	10
# with misassembly	1
# both parts are significant	8
Partially unaligned length	908493
# N's	0

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

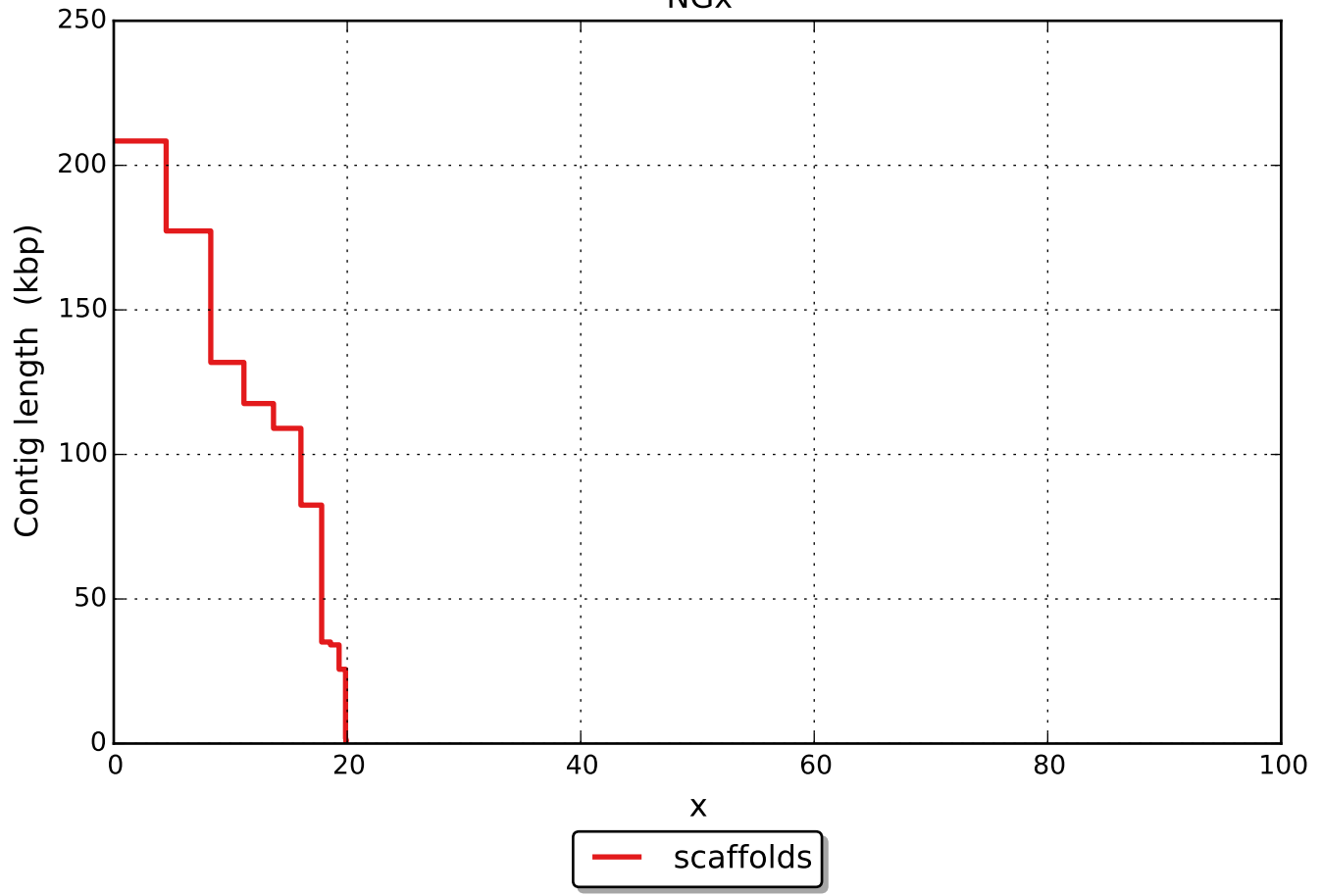
Nx

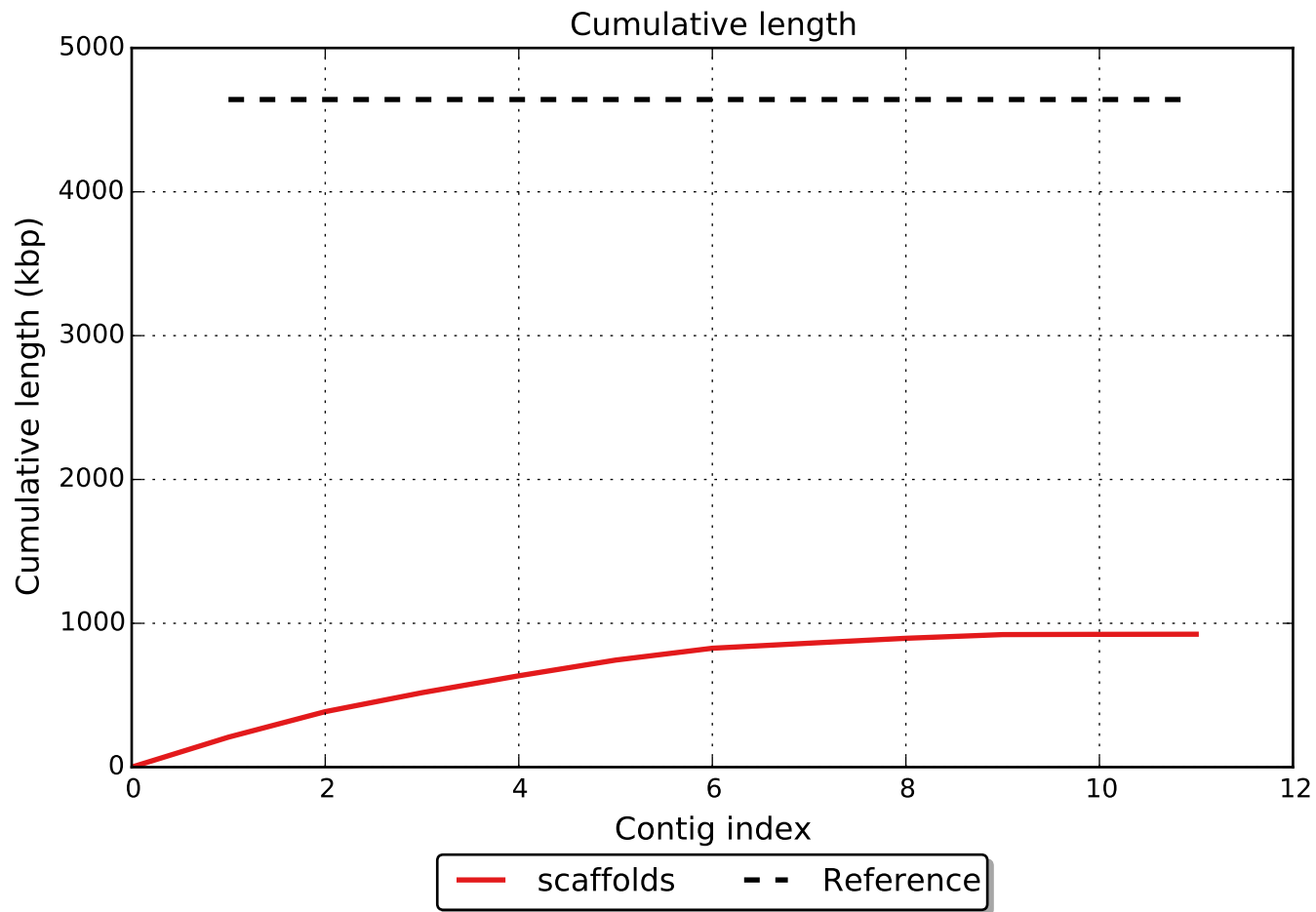


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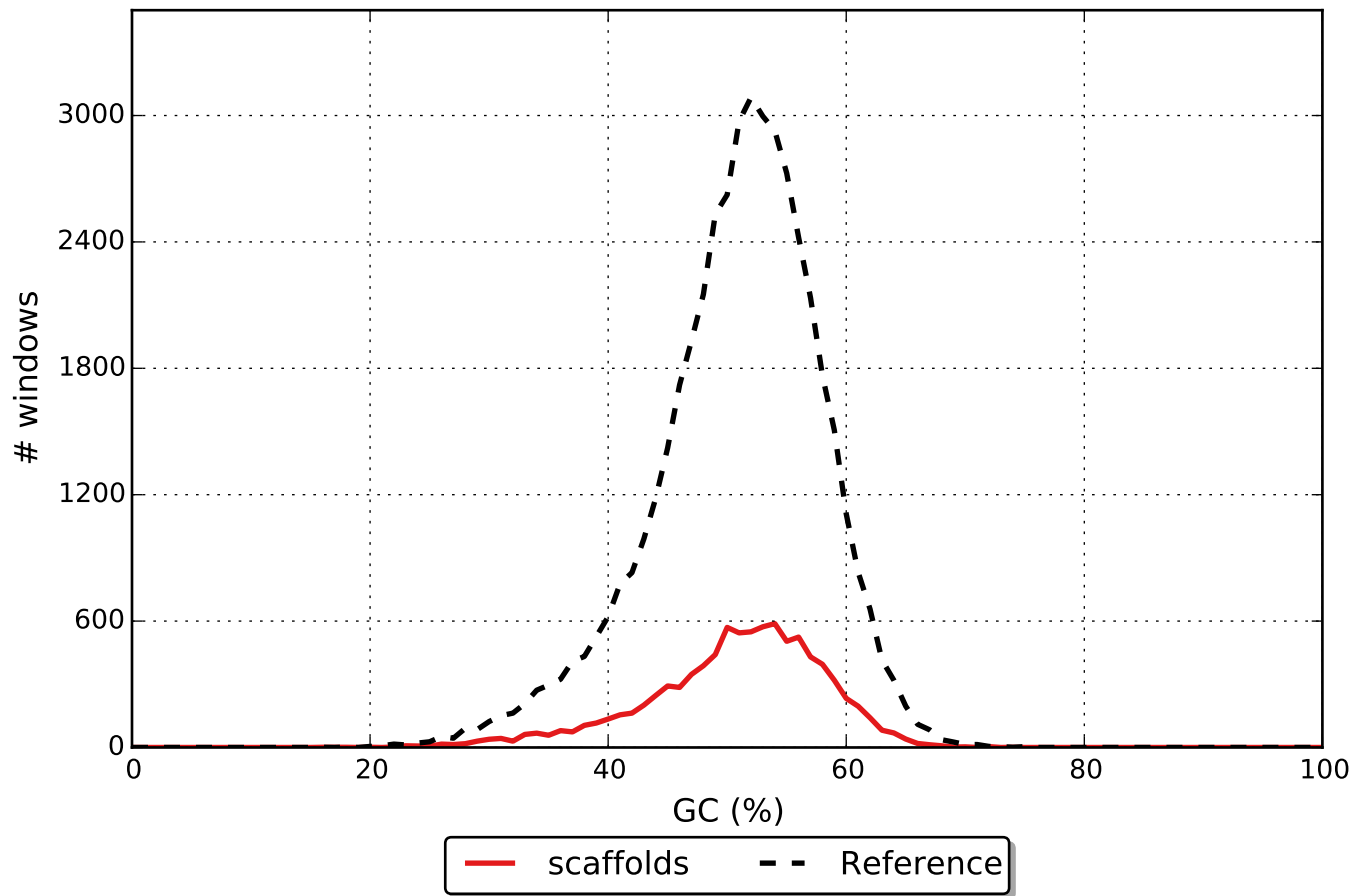
scaffolds

NGx





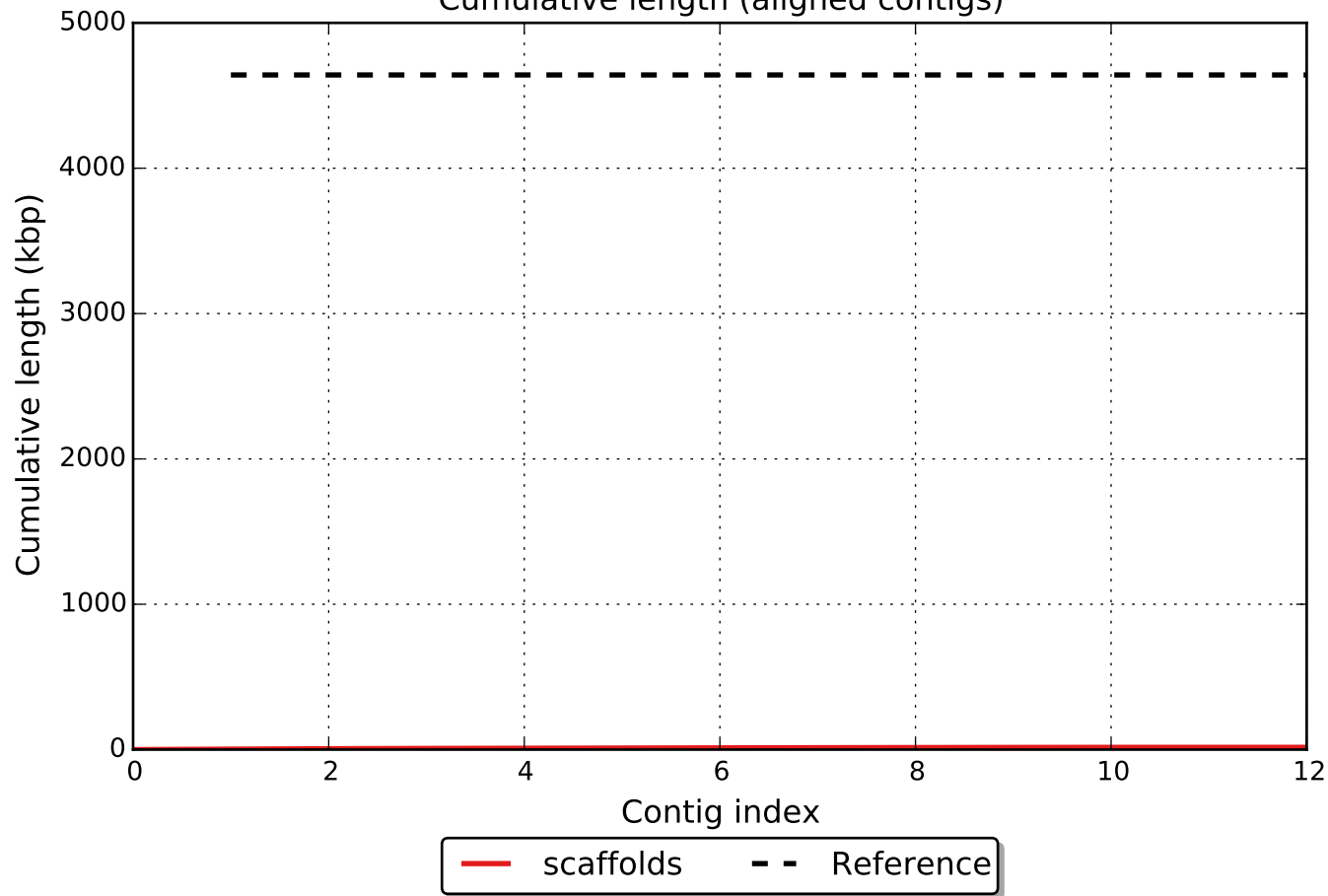
GC content



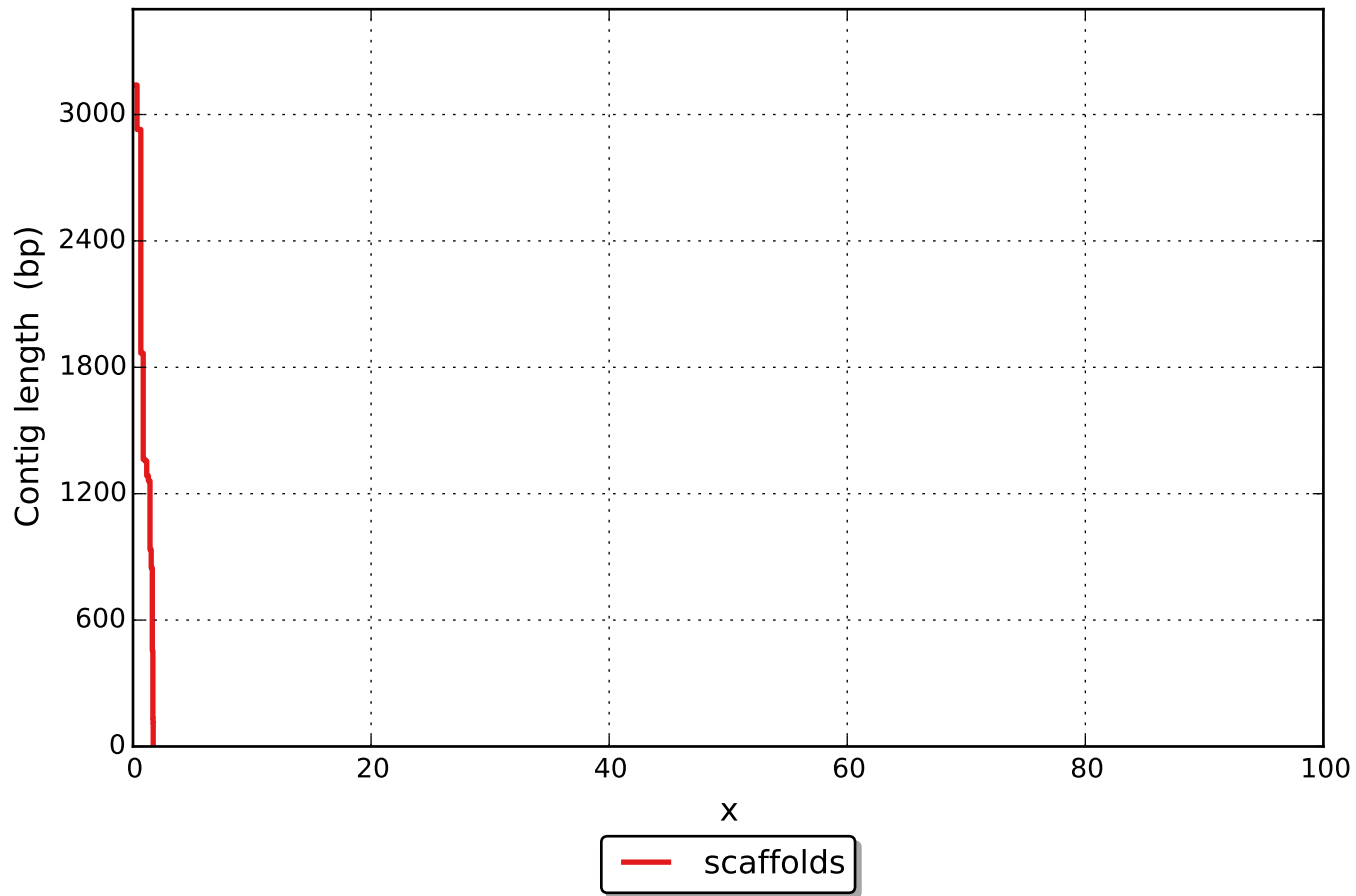
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

