

Report

	scaffolds
# contigs (≥ 1000 bp)	9
# contigs (≥ 5000 bp)	9
# contigs (≥ 10000 bp)	8
# contigs (≥ 25000 bp)	8
# contigs (≥ 50000 bp)	5
Total length (≥ 1000 bp)	792574
Total length (≥ 5000 bp)	792574
Total length (≥ 10000 bp)	783136
Total length (≥ 25000 bp)	783136
Total length (≥ 50000 bp)	693095
# contigs	9
Largest contig	201734
Total length	792574
Reference length	4641652
GC (%)	51.09
Reference GC (%)	50.78
N50	132188
N75	109215
L50	3
L75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 9 part
Unaligned length	774330
Genome fraction (%)	0.393
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4483.67
# indels per 100 kbp	0.00
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

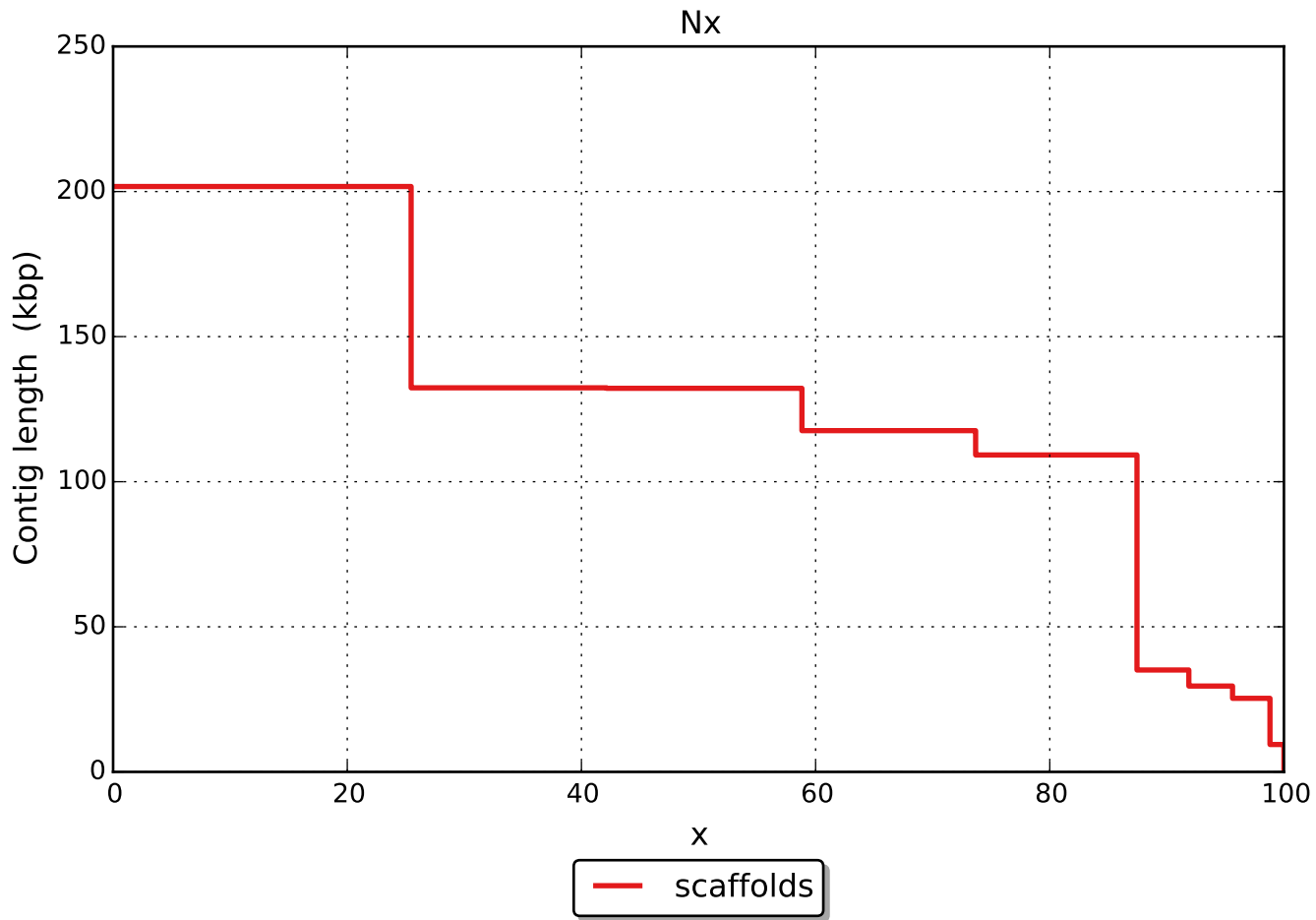
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	8
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	818
# indels	0
# short indels	0
# long indels	0
Indels length	0

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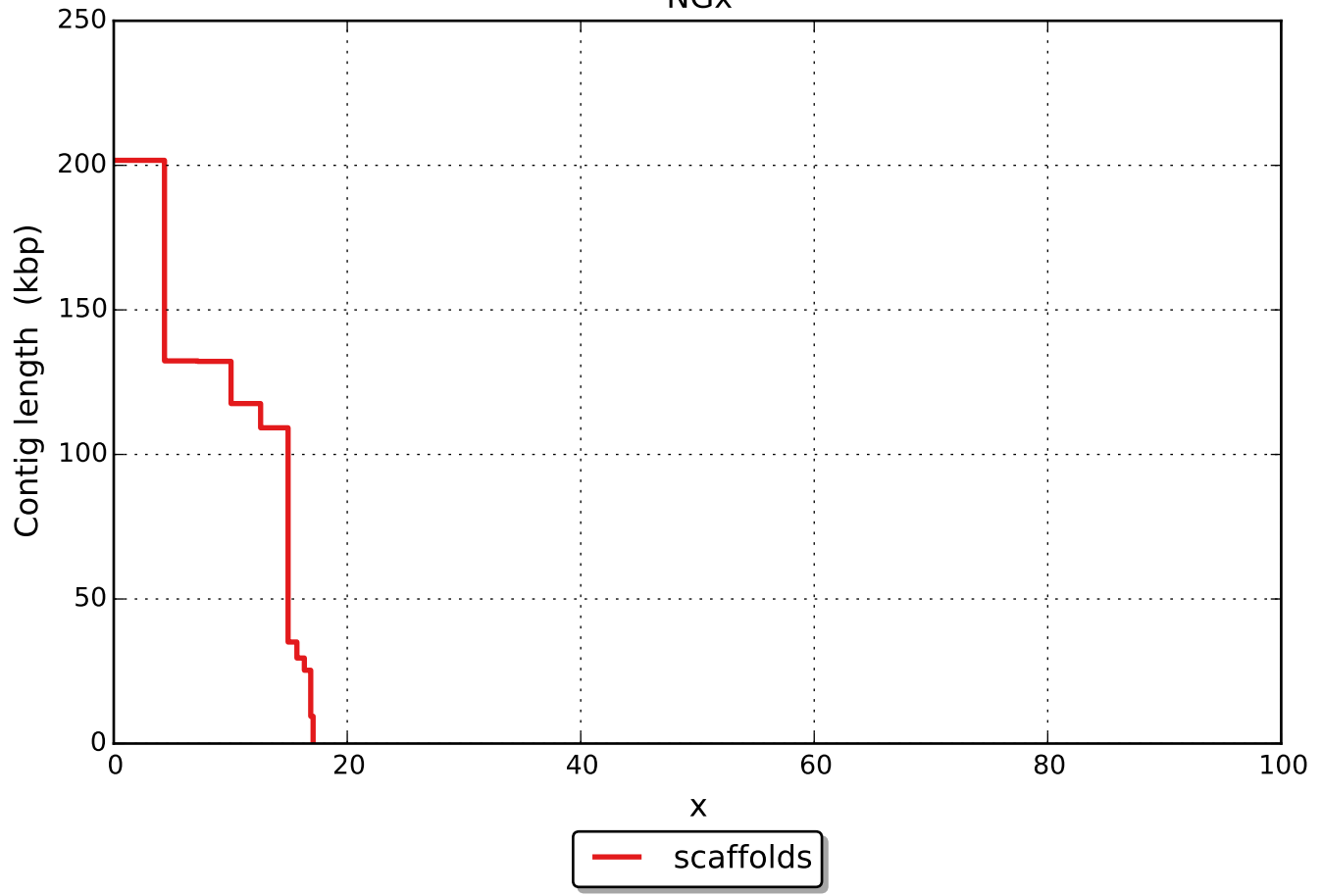
Unaligned report

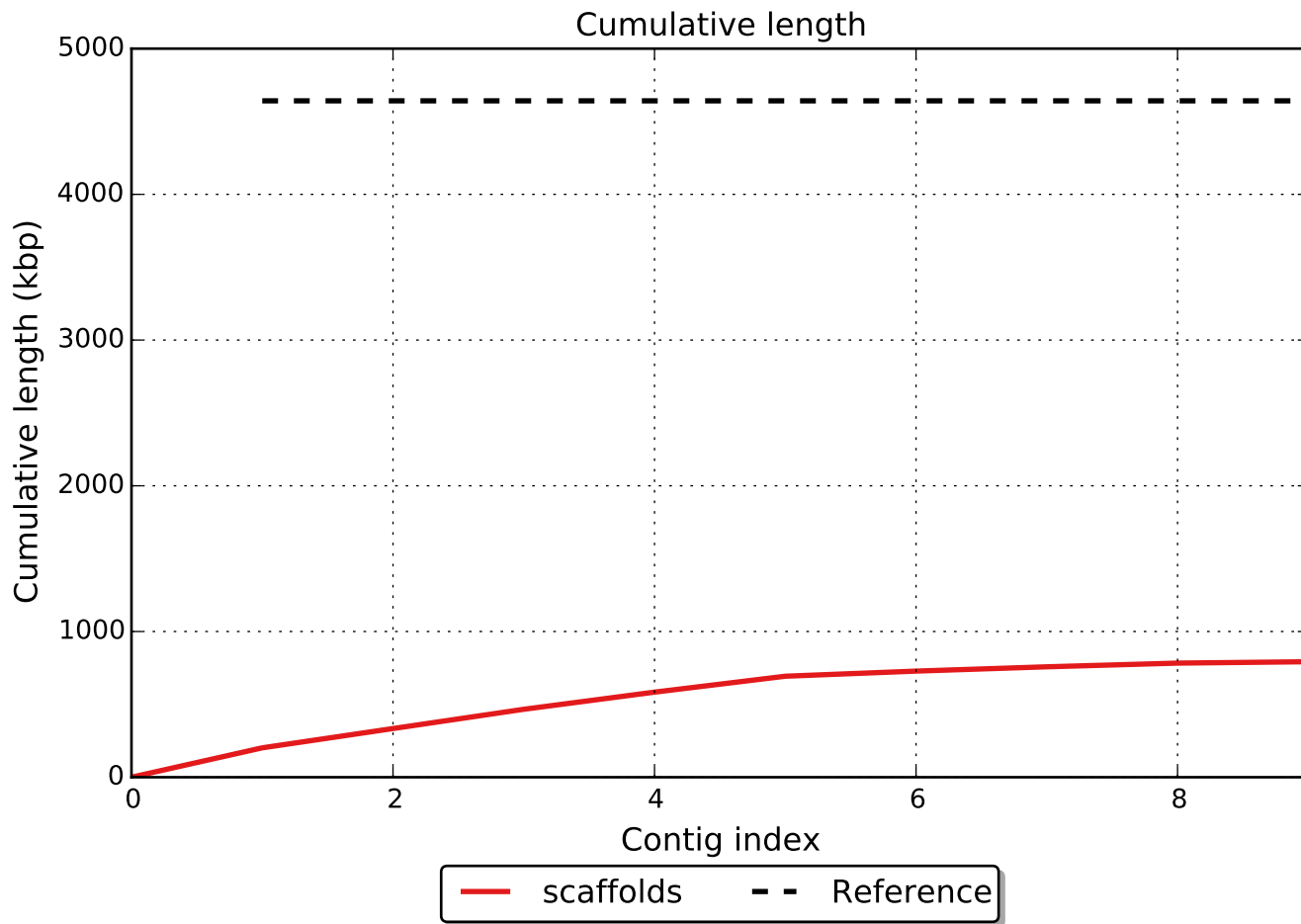
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	9
# with misassembly	3
# both parts are significant	8
Partially unaligned length	774330
# N's	0

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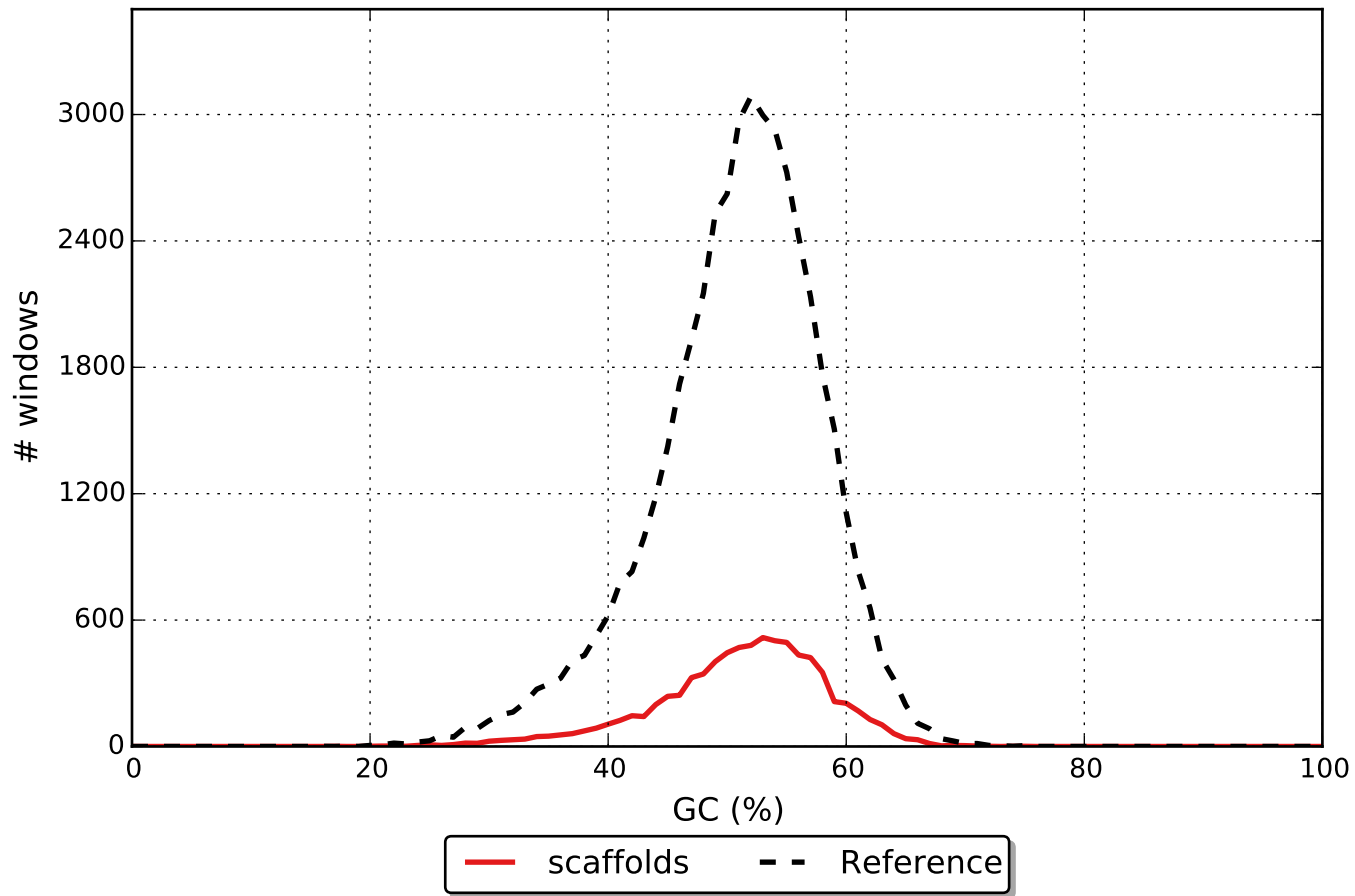


NGx

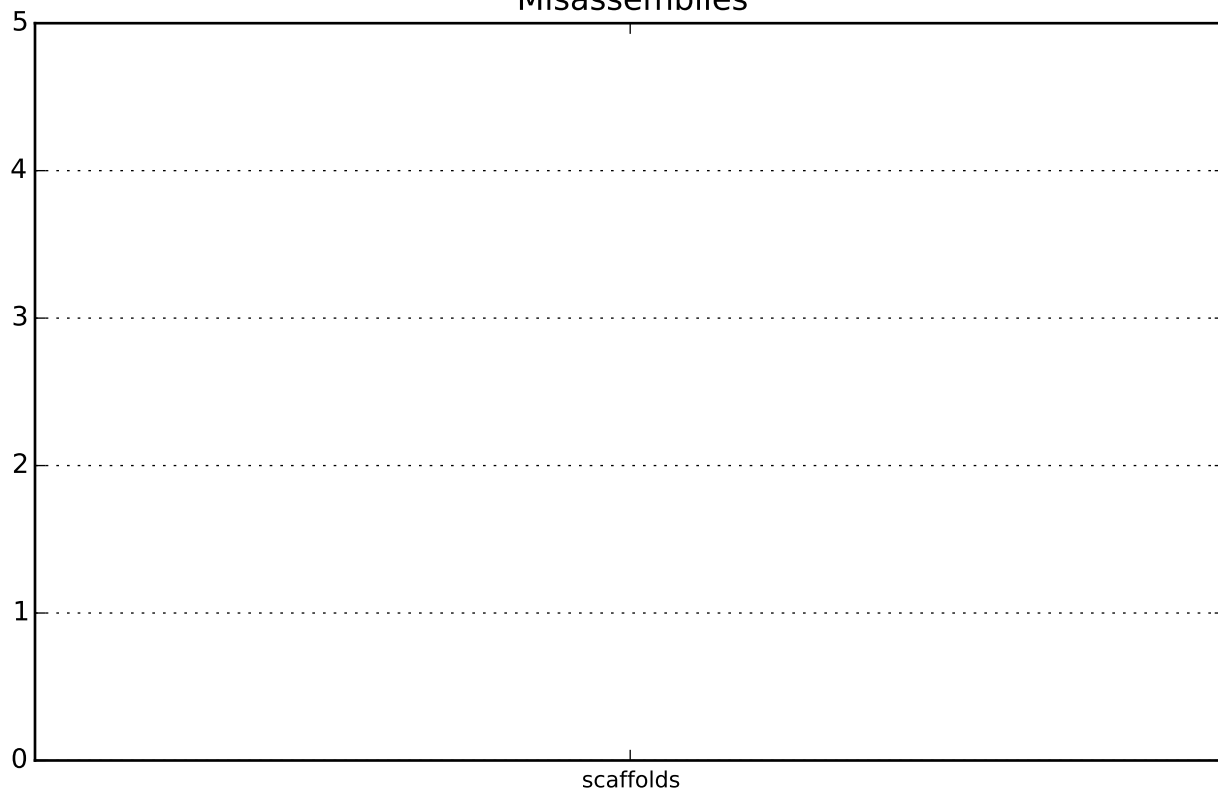




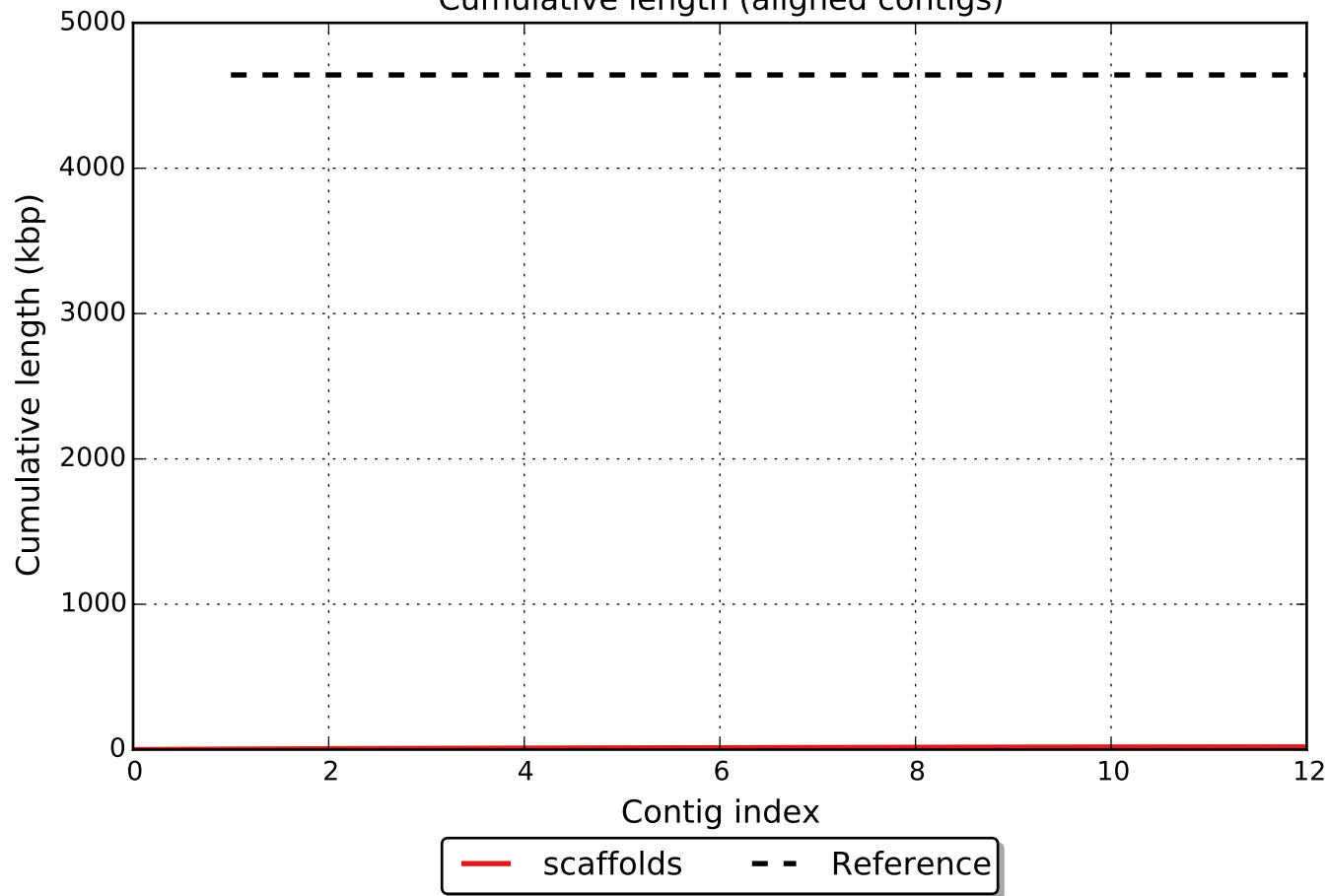
GC content



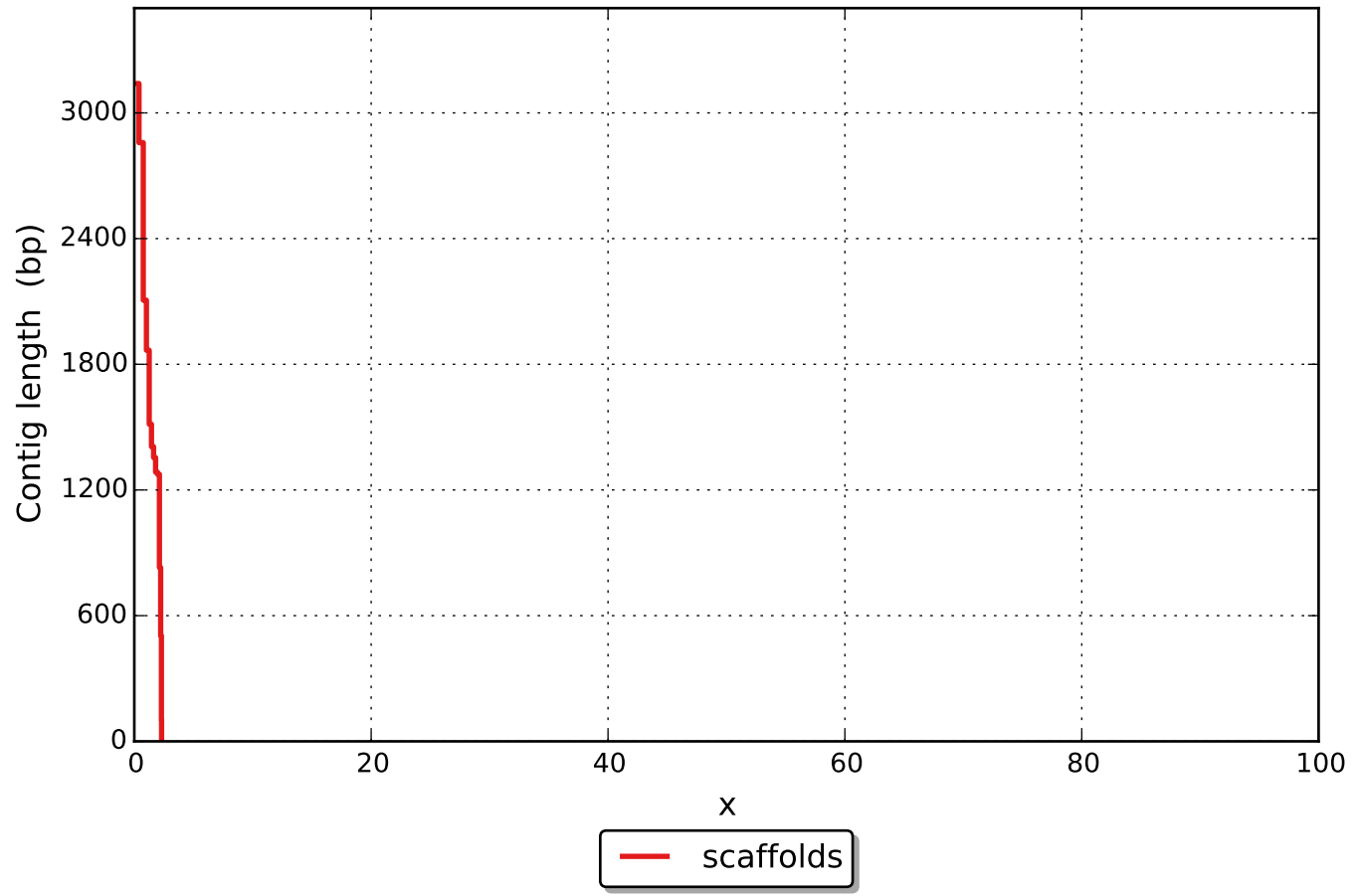
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

