

Report

	scaffolds
# contigs (≥ 1000 bp)	9
# contigs (≥ 5000 bp)	8
# contigs (≥ 10000 bp)	6
# contigs (≥ 25000 bp)	5
# contigs (≥ 50000 bp)	5
Total length (≥ 1000 bp)	809346
Total length (≥ 5000 bp)	808345
Total length (≥ 10000 bp)	792417
Total length (≥ 25000 bp)	778756
Total length (≥ 50000 bp)	778756
# contigs	10
Largest contig	209836
Total length	810282
Reference length	4641652
GC (%)	50.62
Reference GC (%)	50.78
N50	165543
N75	117612
L50	3
L75	4
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 8 part
Unaligned length	796287
Genome fraction (%)	0.297
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4524.33
# indels per 100 kbp	0.00
Largest alignment	2929
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

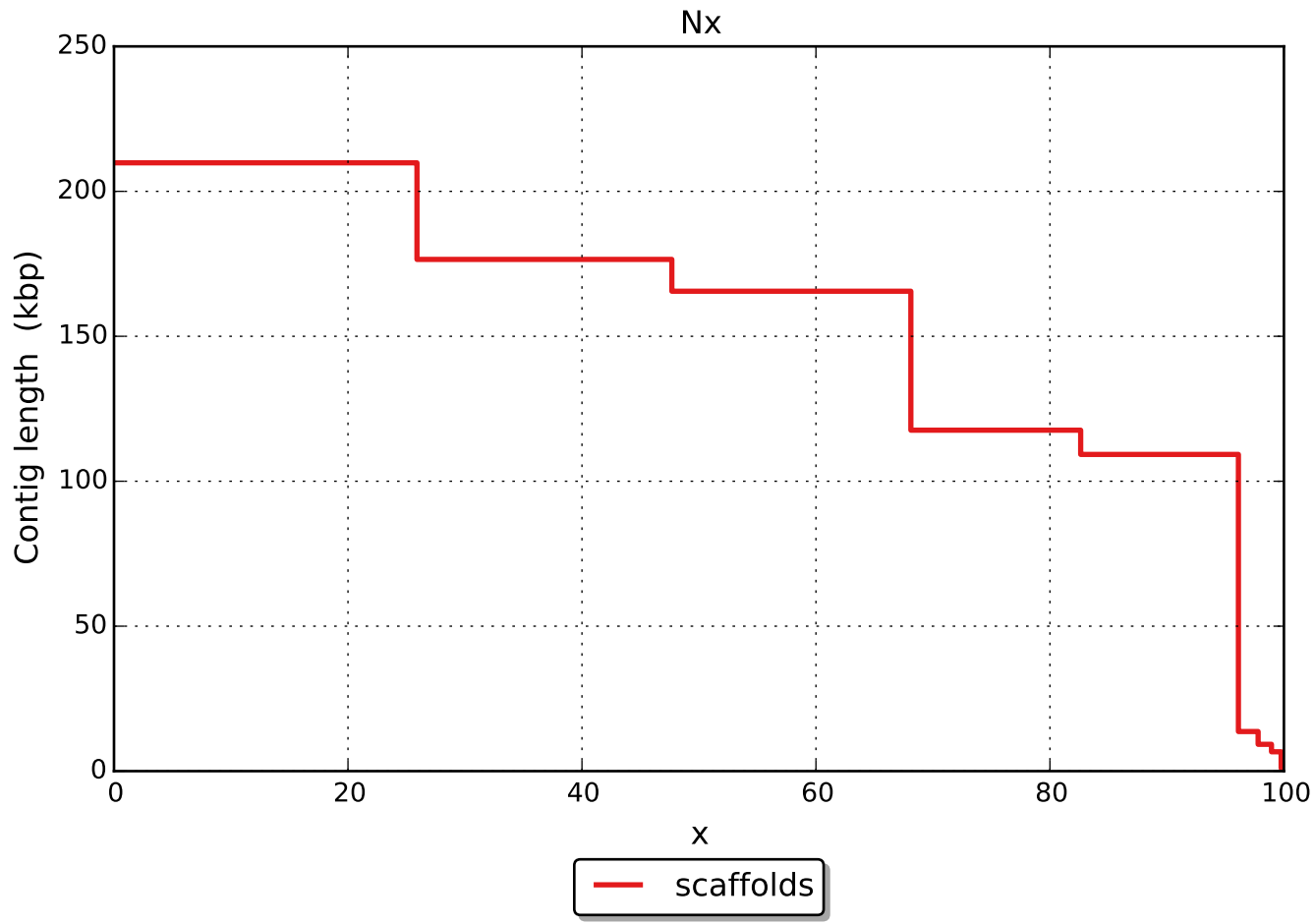
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	5
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	623
# indels	0
# short indels	0
# long indels	0
Indels length	0

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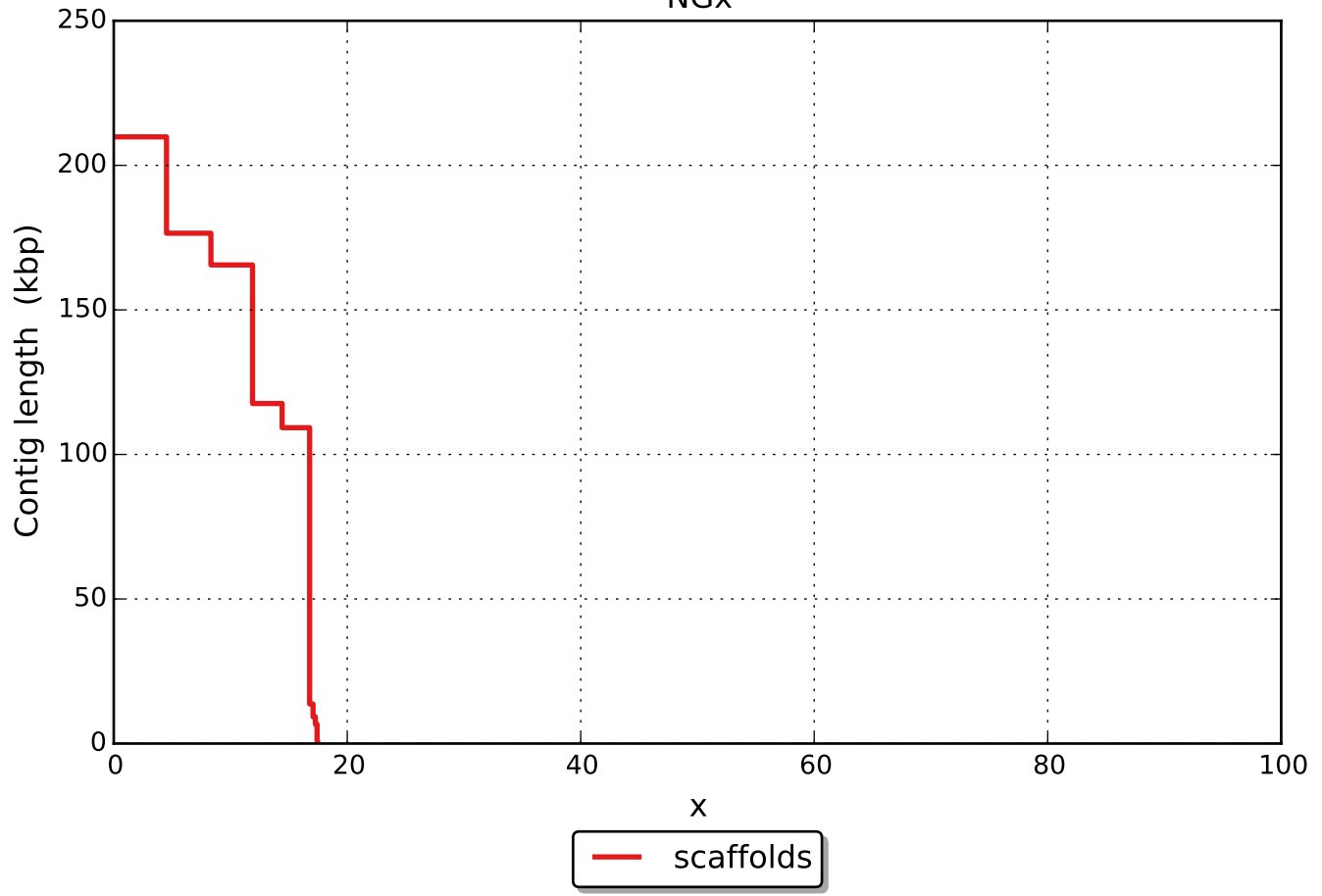
Unaligned report

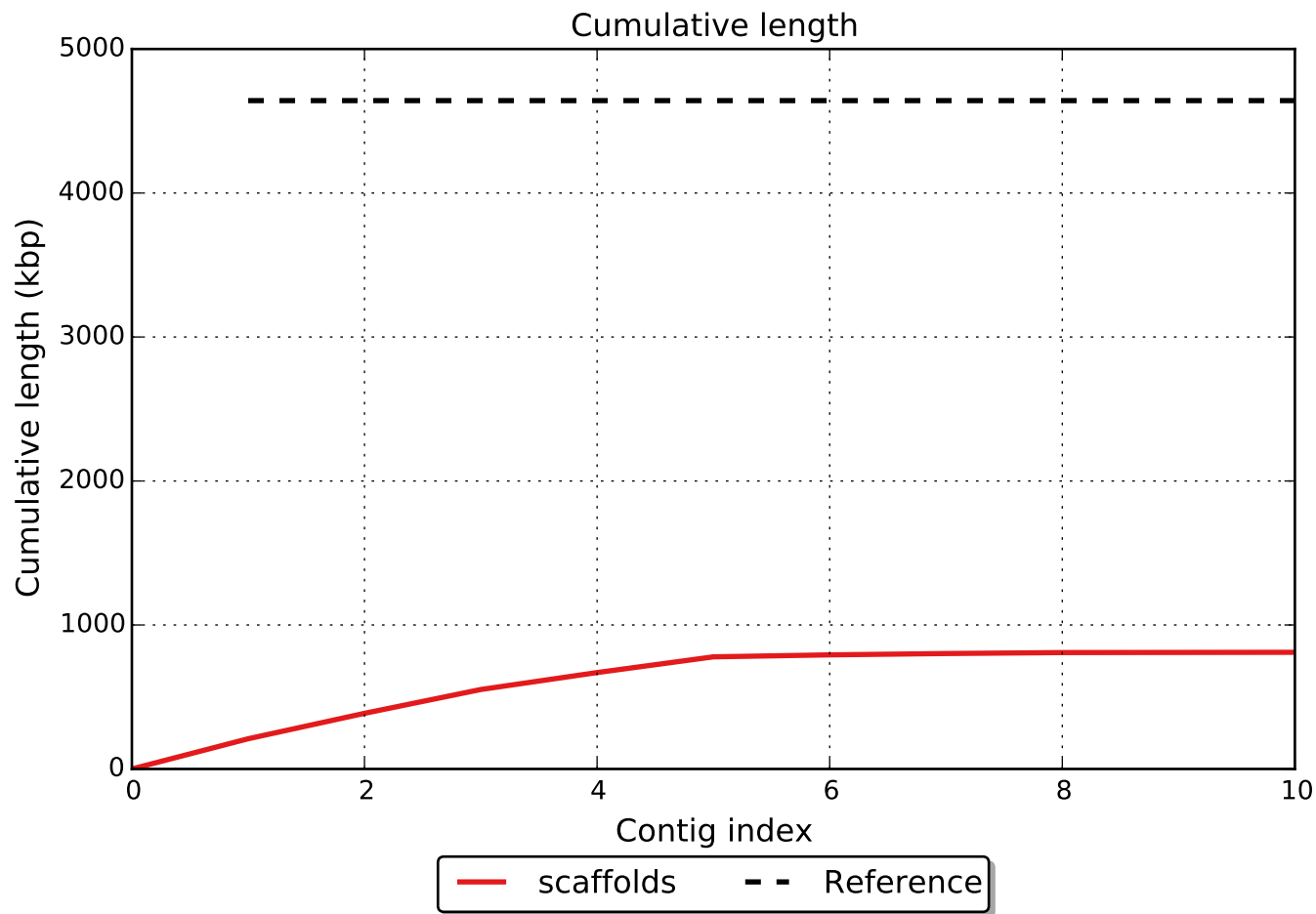
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
# with misassembly	3
# both parts are significant	5
Partially unaligned length	796287
# N's	0

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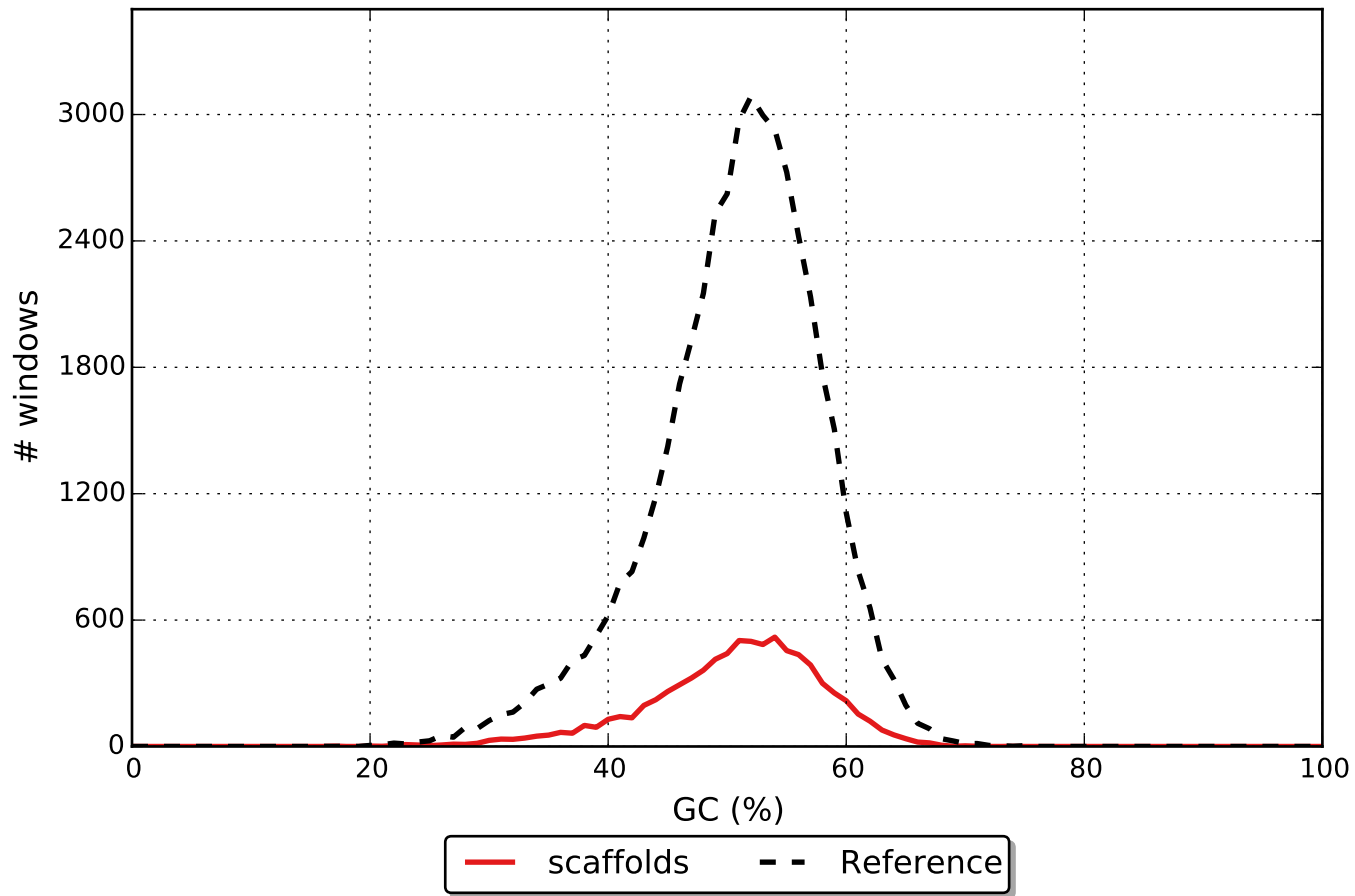


NGx





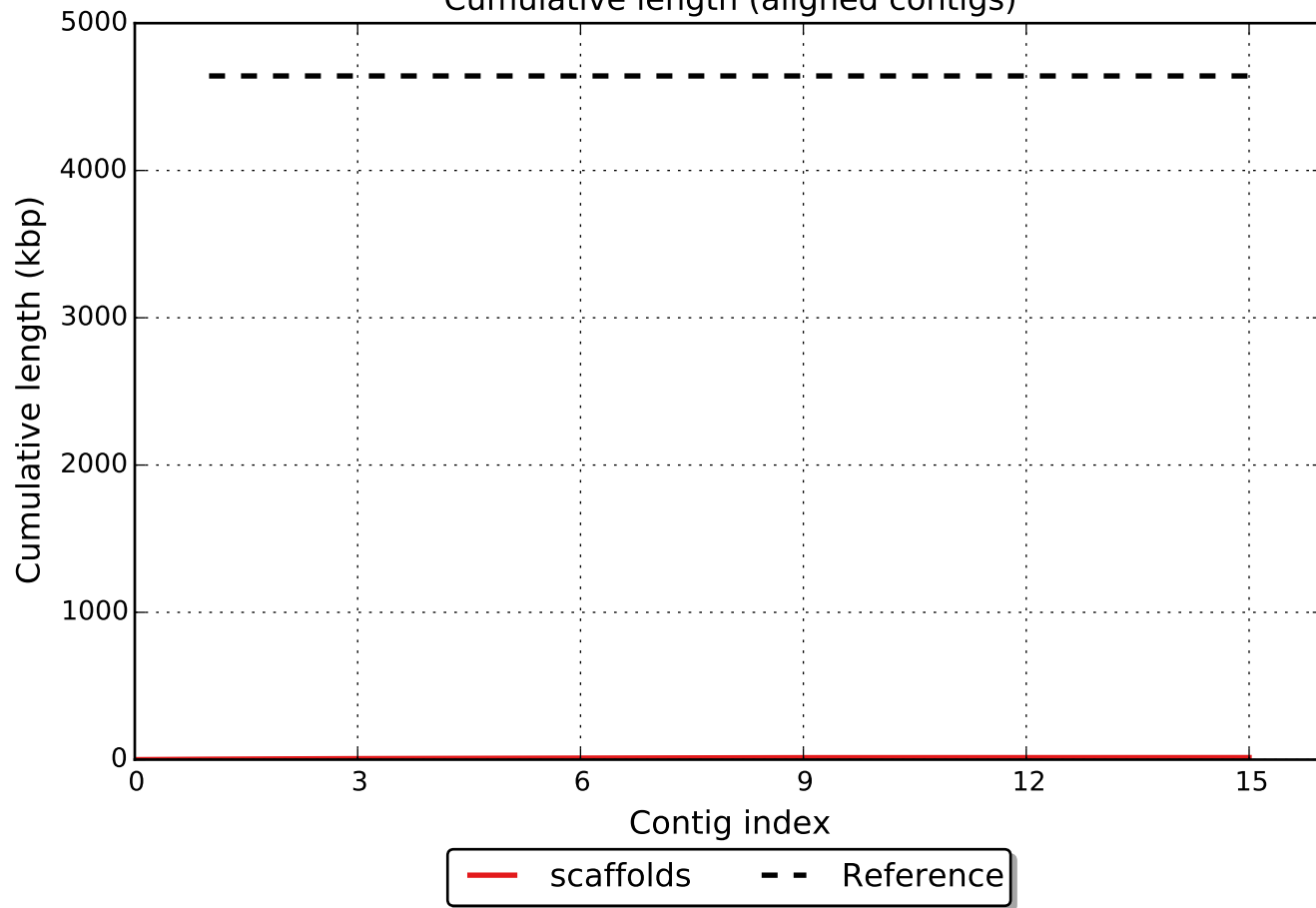
GC content



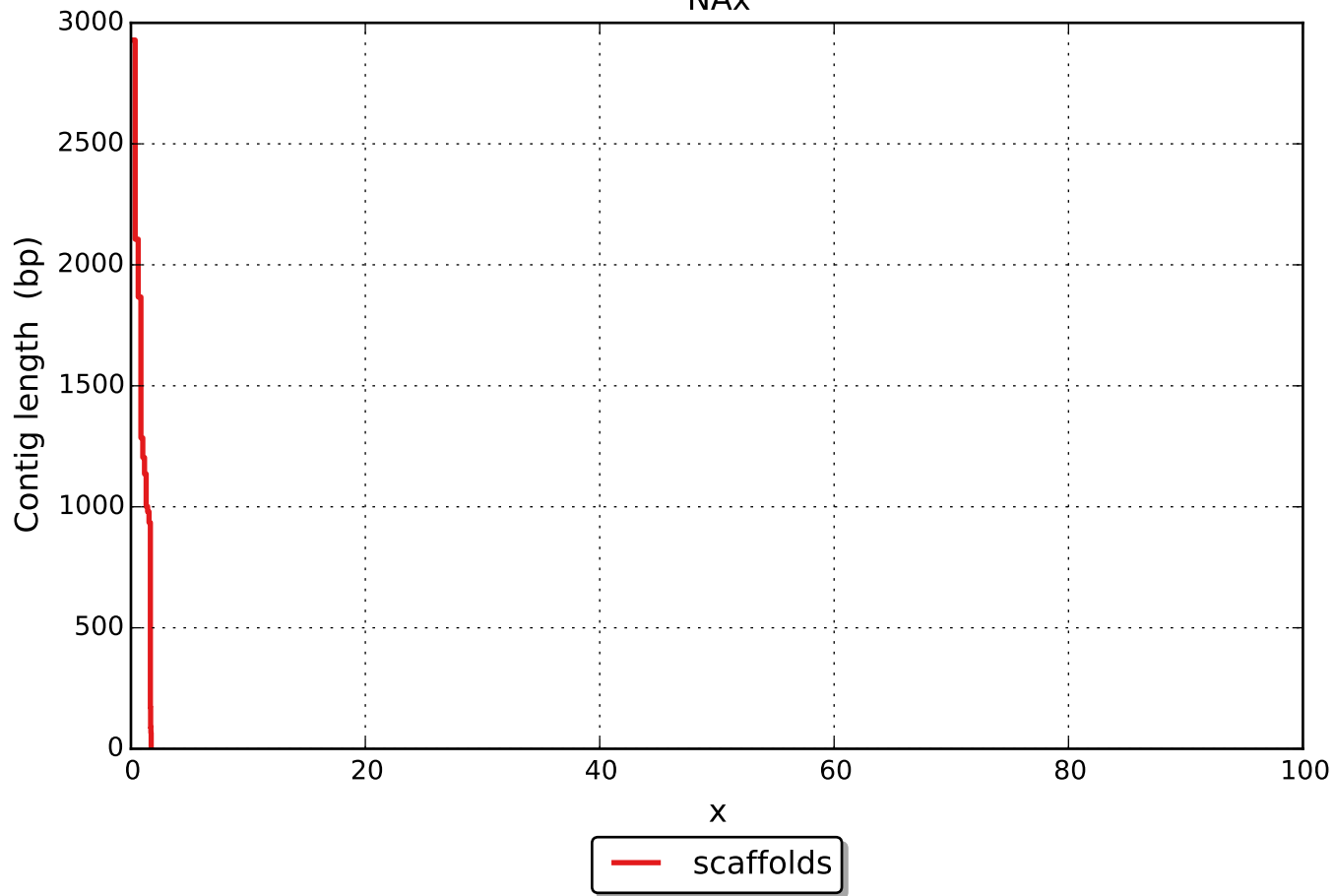
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

