

Report

	scaffolds
# contigs (≥ 1000 bp)	2
# contigs (≥ 5000 bp)	2
# contigs (≥ 10000 bp)	2
# contigs (≥ 25000 bp)	2
# contigs (≥ 50000 bp)	2
Total length (≥ 1000 bp)	176091
Total length (≥ 5000 bp)	176091
Total length (≥ 10000 bp)	176091
Total length (≥ 25000 bp)	176091
Total length (≥ 50000 bp)	176091
# contigs	4
Largest contig	109022
Total length	177420
Reference length	4641652
GC (%)	50.35
Reference GC (%)	50.78
N50	109022
N75	67069
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	173998
Genome fraction (%)	0.071
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3927.49
# indels per 100 kbp	0.00
Largest alignment	1867
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

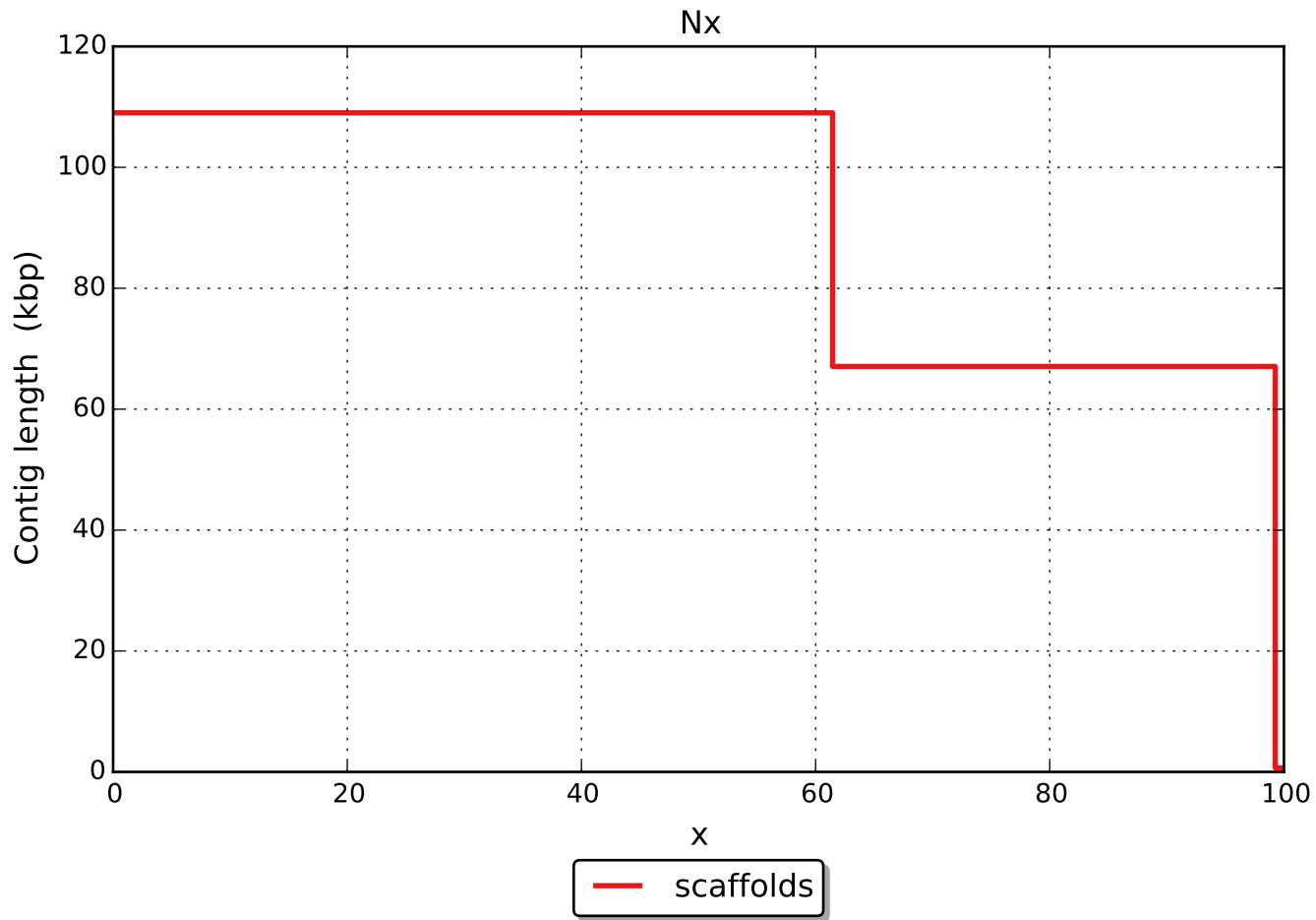
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	130
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

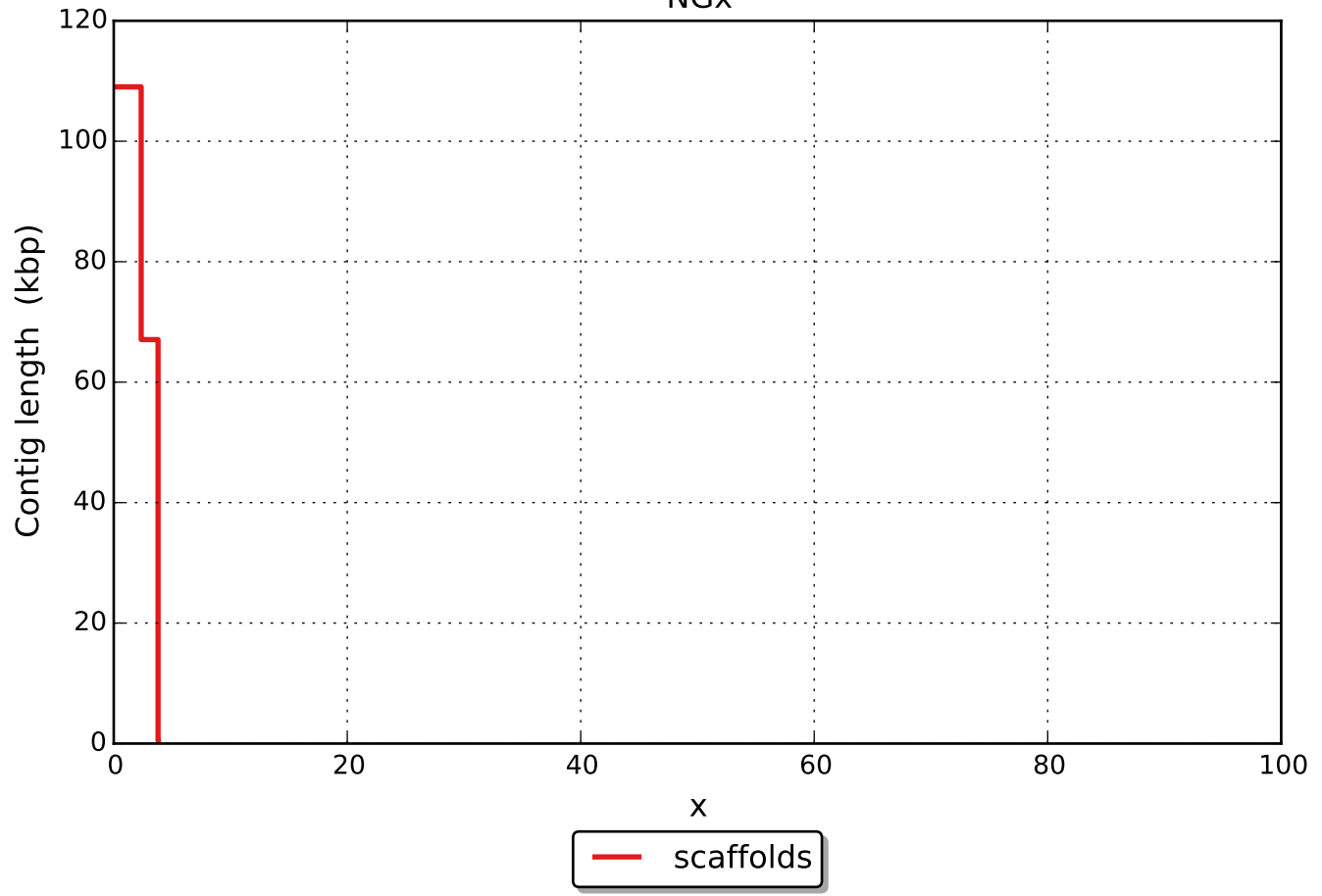
Unaligned report

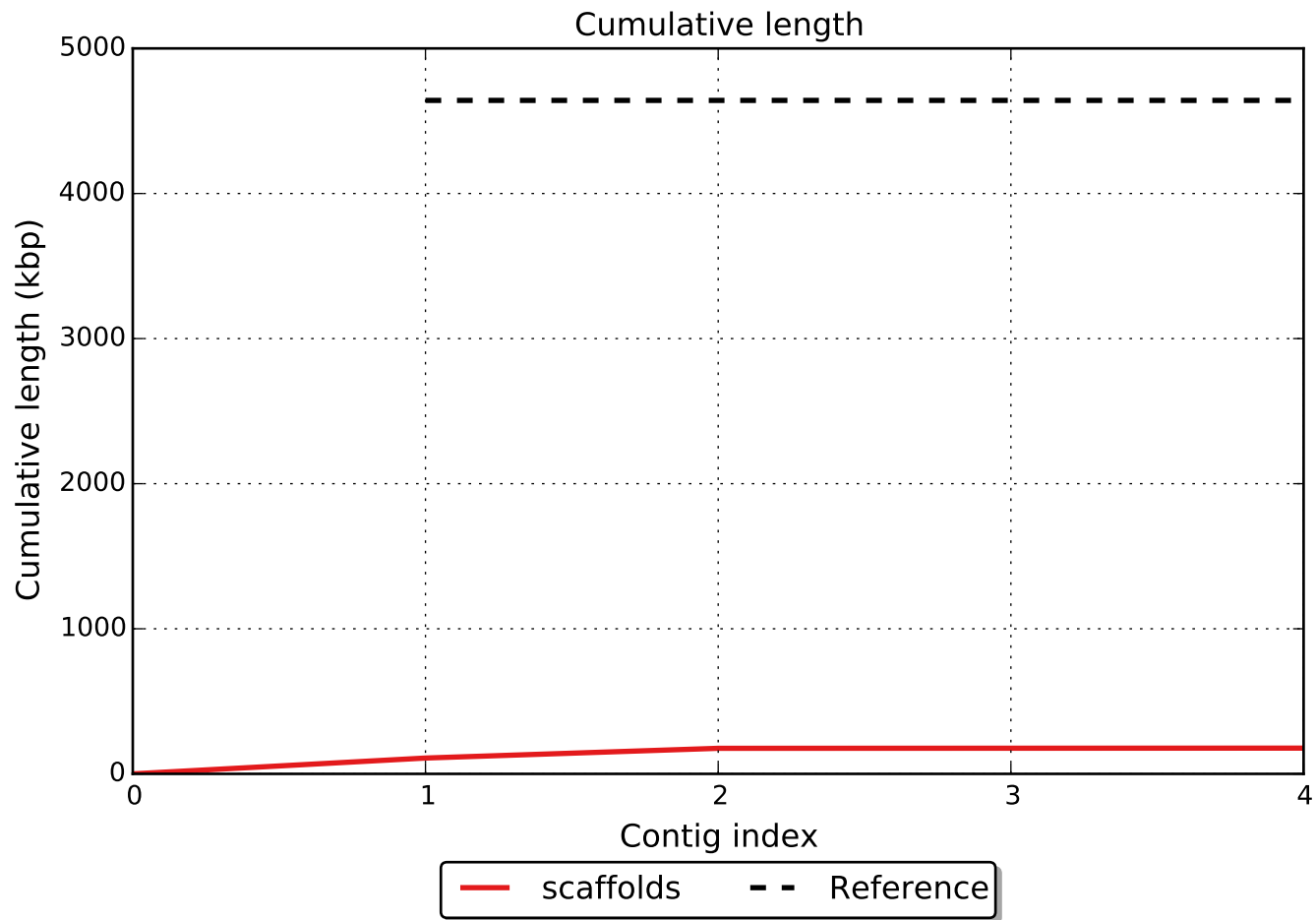
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	1
# both parts are significant	1
Partially unaligned length	173998
# N's	0

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).

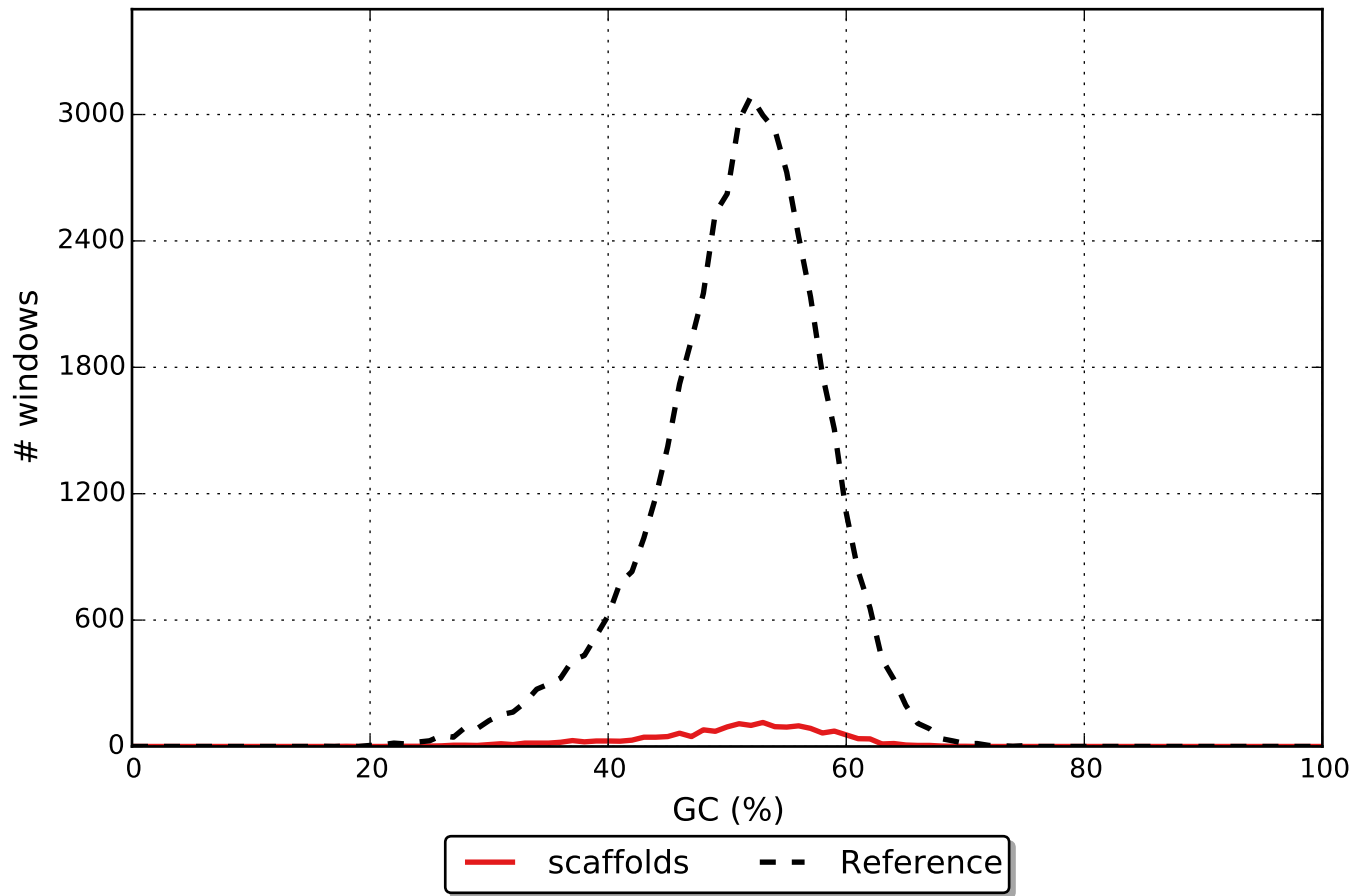


NGx





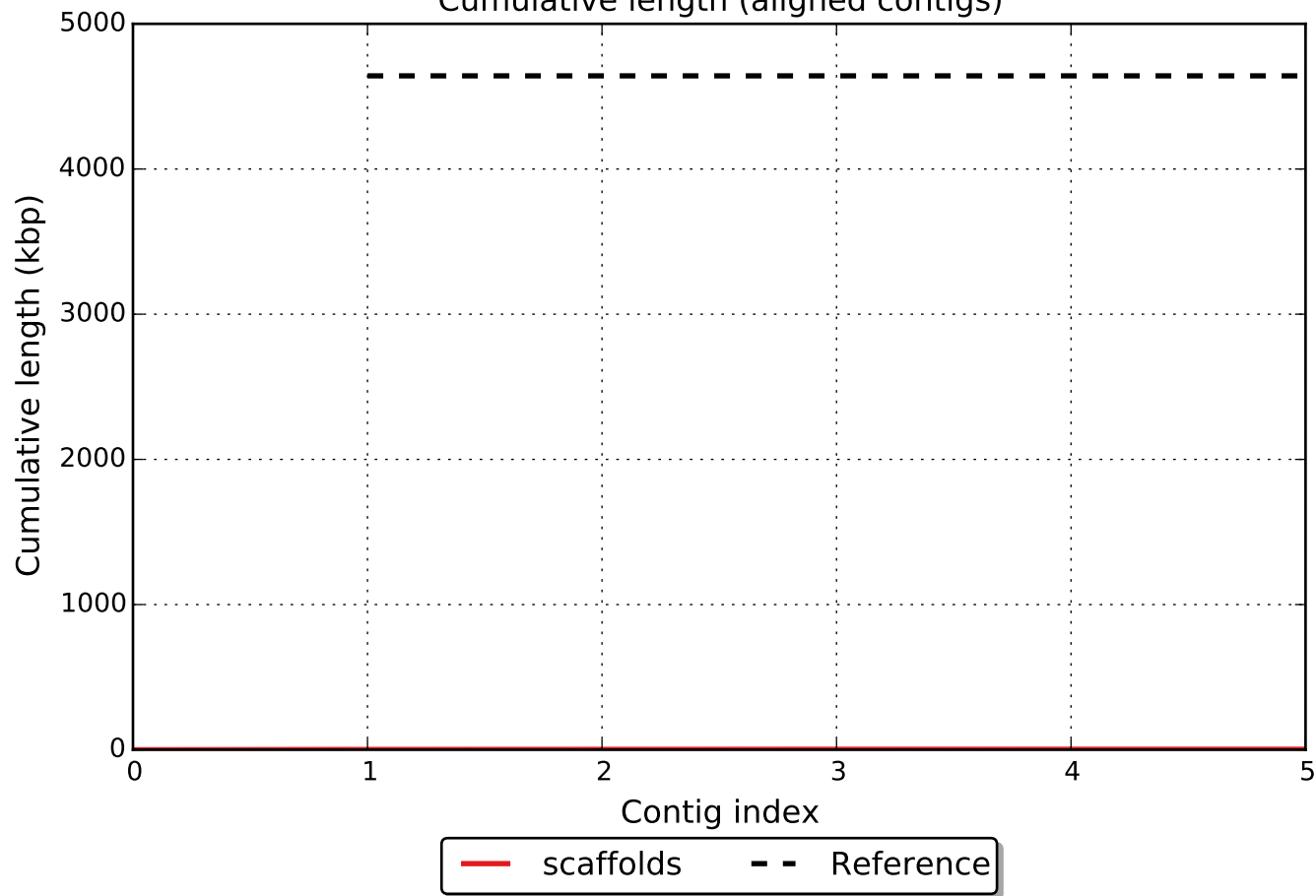
GC content



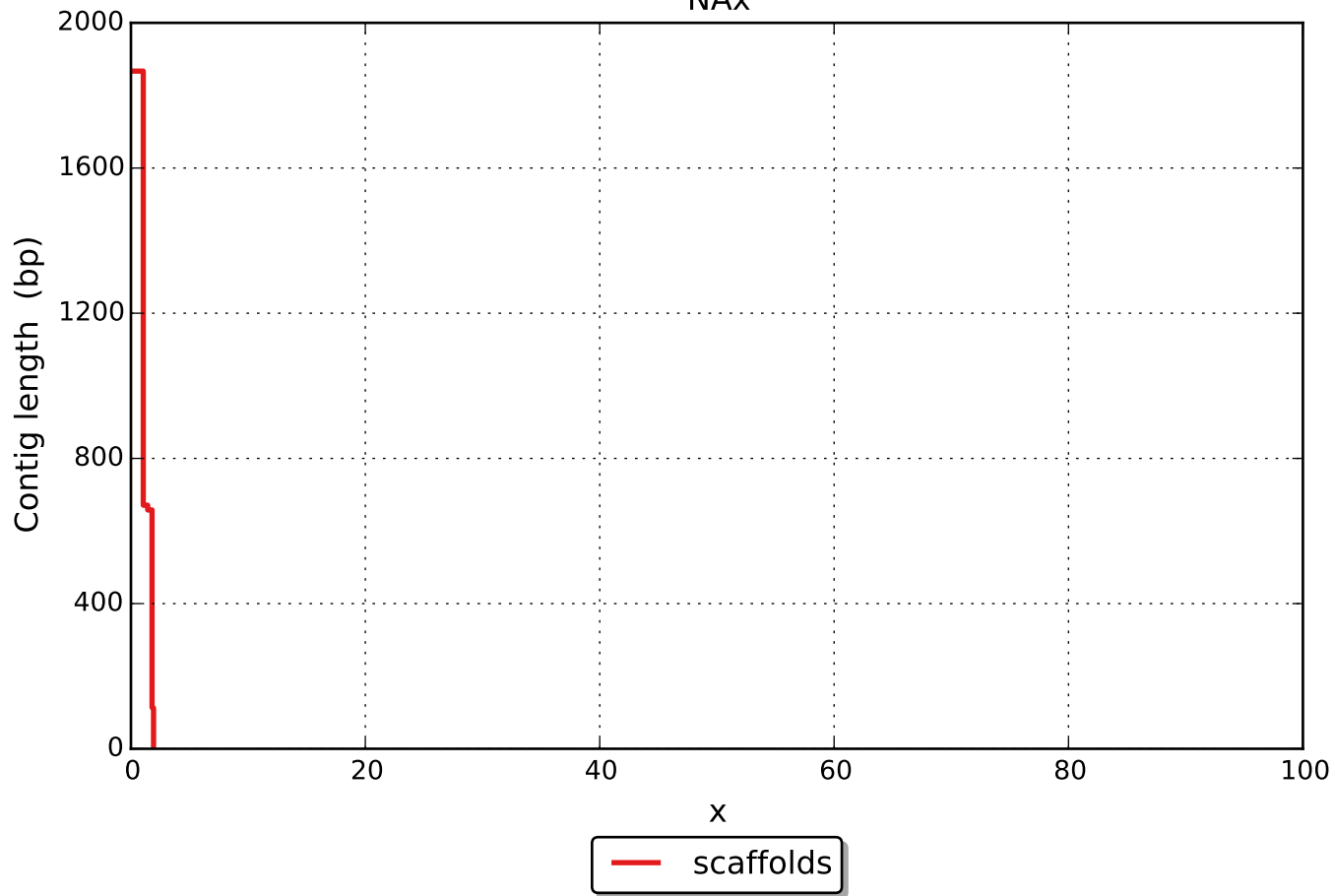
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

