

Report

	scaffolds
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	5
Total length (>= 1000 bp)	810856
Total length (>= 5000 bp)	808345
Total length (>= 10000 bp)	792417
Total length (>= 25000 bp)	778756
Total length (>= 50000 bp)	778756
# contigs	12
Largest contig	209836
Total length	812642
Reference length	4641652
GC (%)	50.61
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 (%)	0.348
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4283.94
# 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

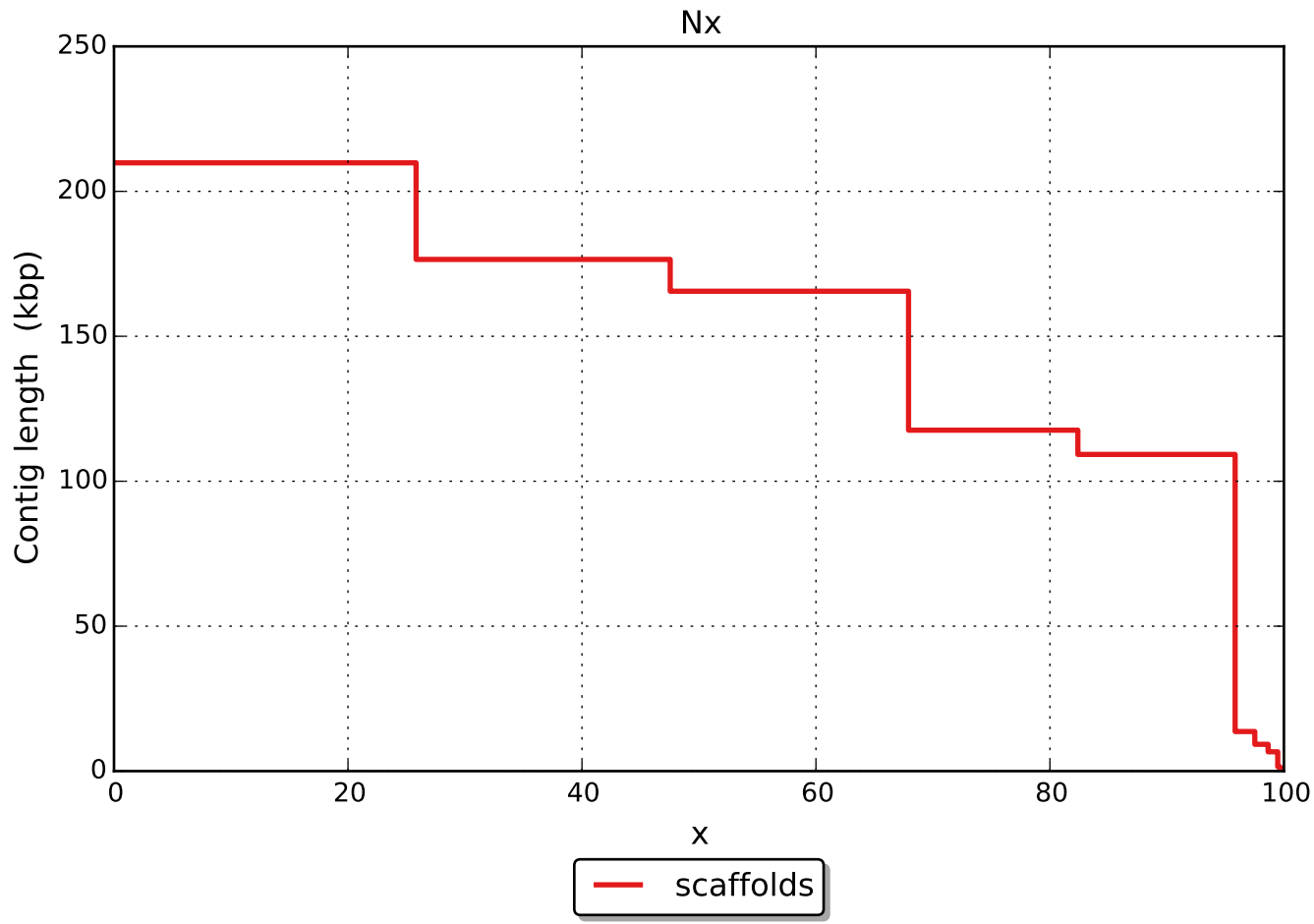
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	5
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	691
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

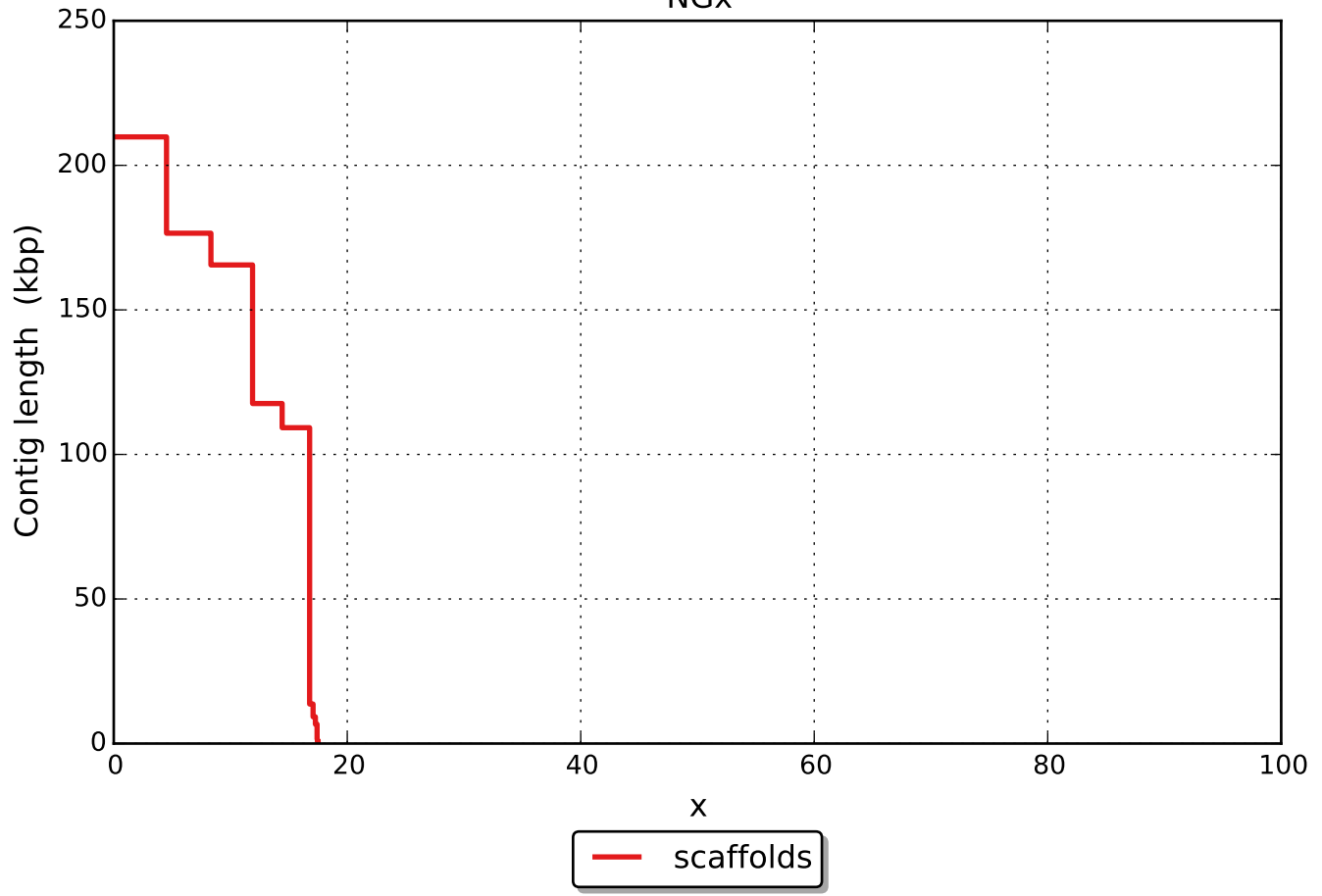
Unaligned report

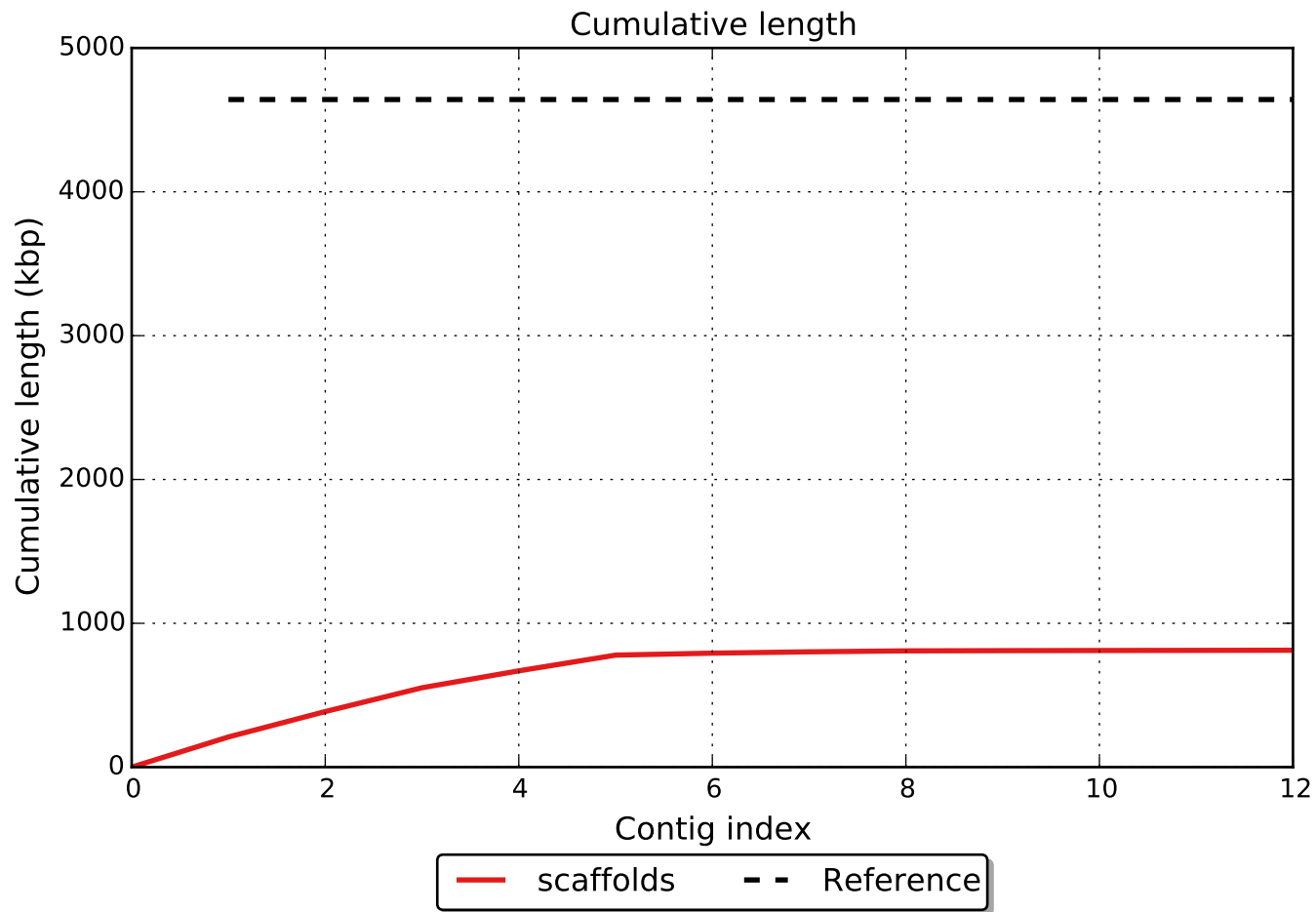
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
# with misassembly	3
# both parts are significant	5
Partially unaligned length	796287
# N's	0

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).

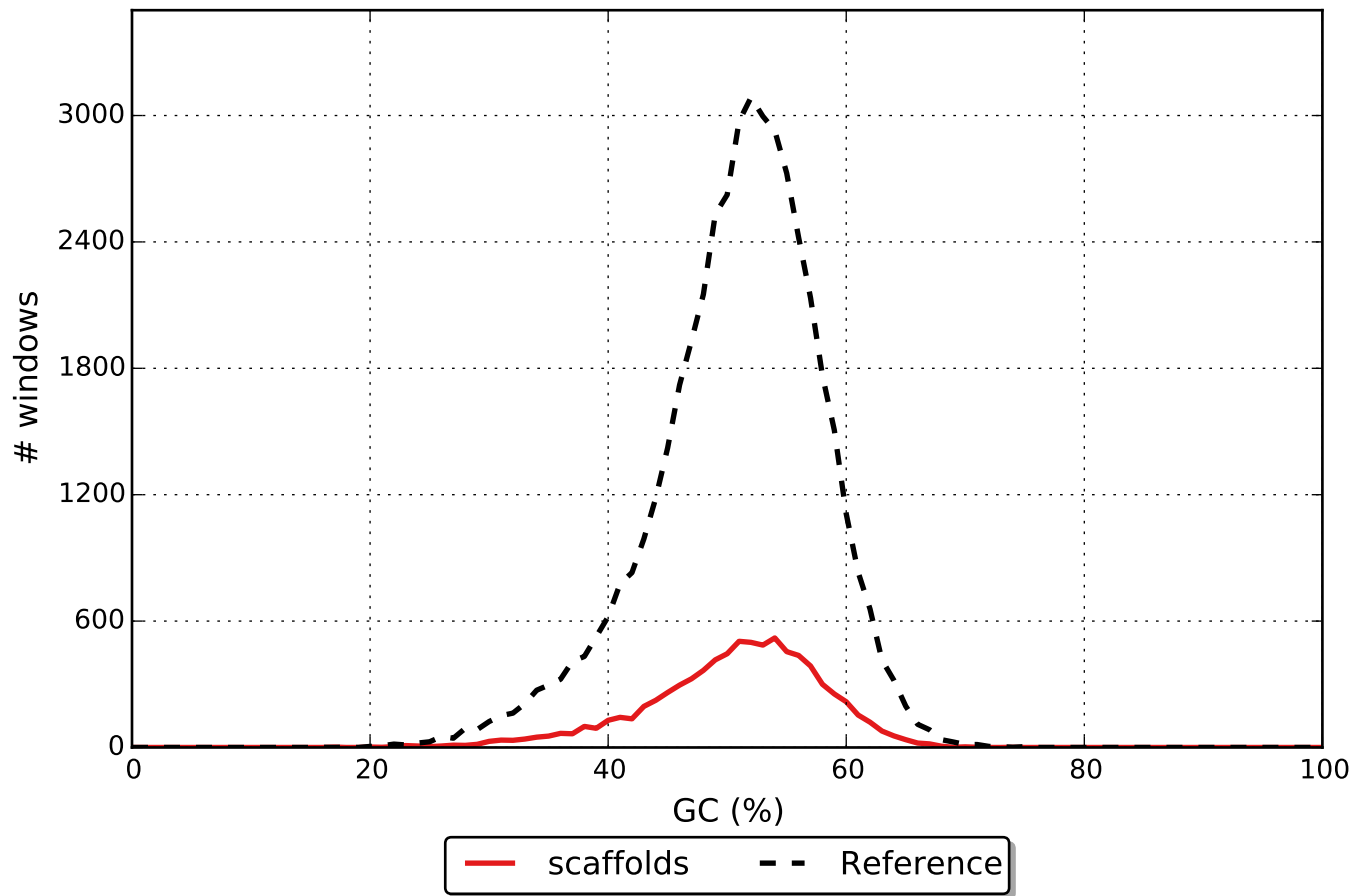


NGx





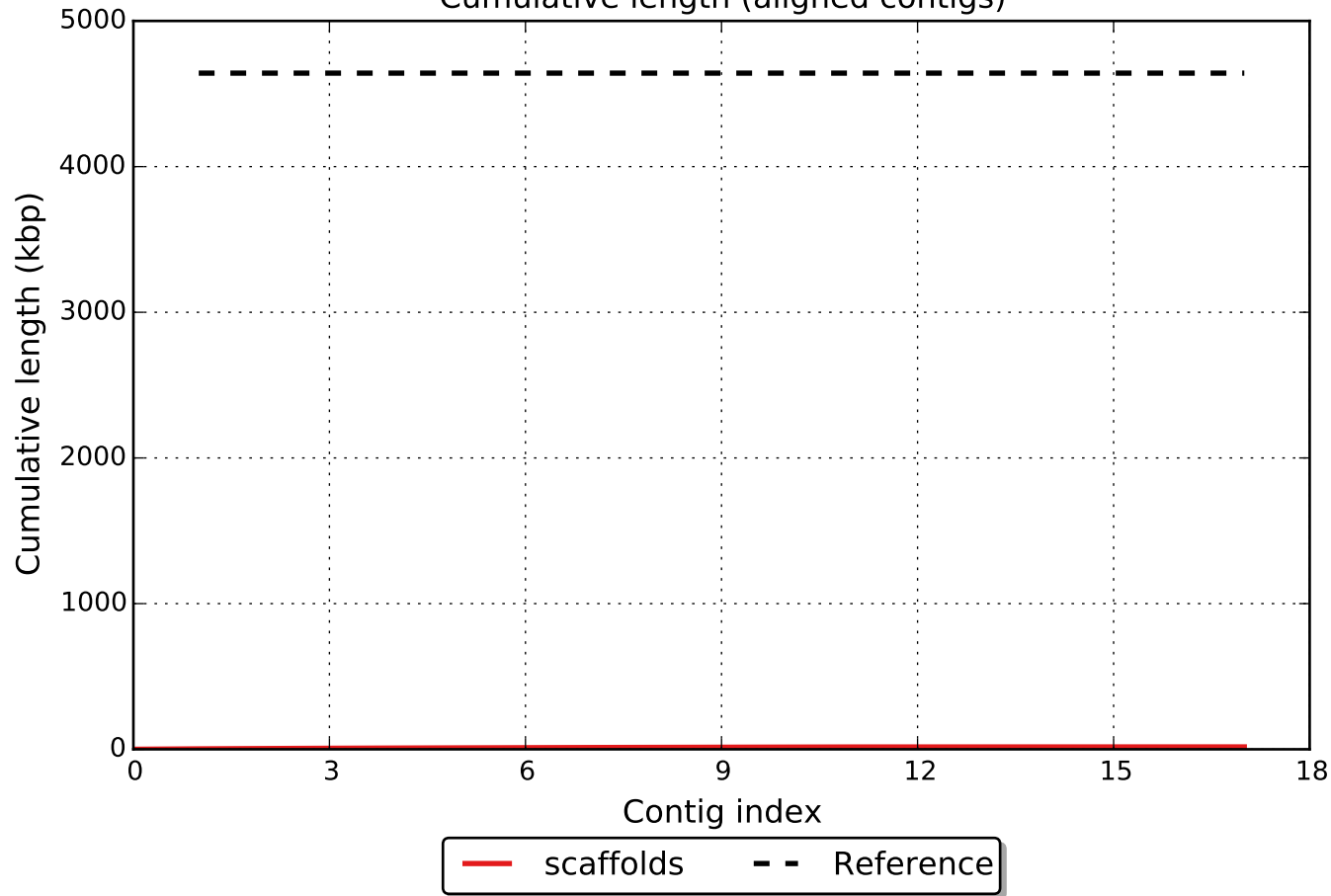
GC content



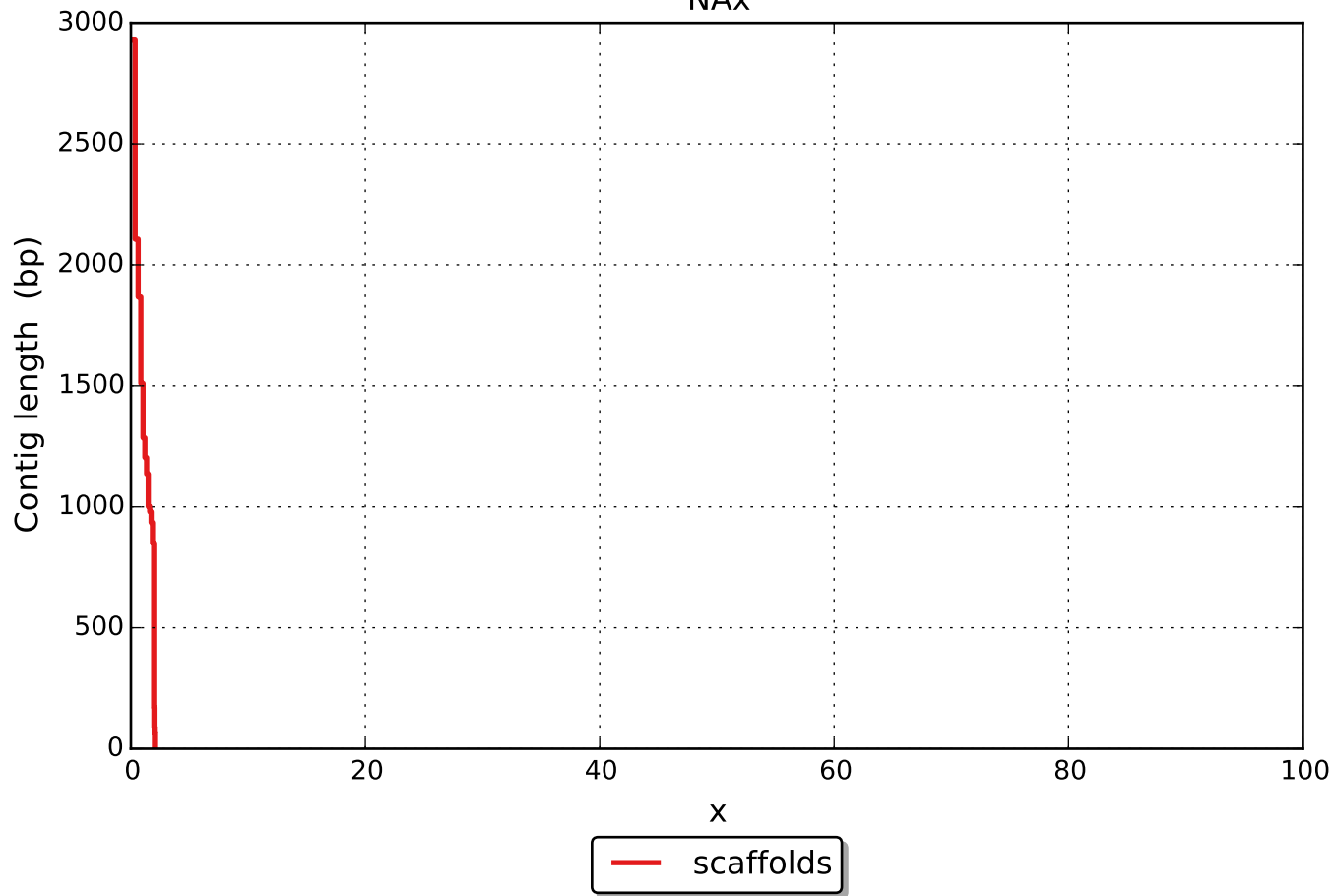
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

