

Report

	scaffolds
# contigs (≥ 1000 bp)	1
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	1
# contigs (≥ 25000 bp)	1
# contigs (≥ 50000 bp)	1
Total length (≥ 1000 bp)	53559
Total length (≥ 5000 bp)	53559
Total length (≥ 10000 bp)	53559
Total length (≥ 25000 bp)	53559
Total length (≥ 50000 bp)	53559
# contigs	1
Largest contig	53559
Total length	53559
Reference length	4641652
GC (%)	51.40
Reference GC (%)	50.78
N50	53559
N75	53559
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	50701
Genome fraction (%)	0.062
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4933.52
# indels per 100 kbp	0.00
Largest alignment	2858
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

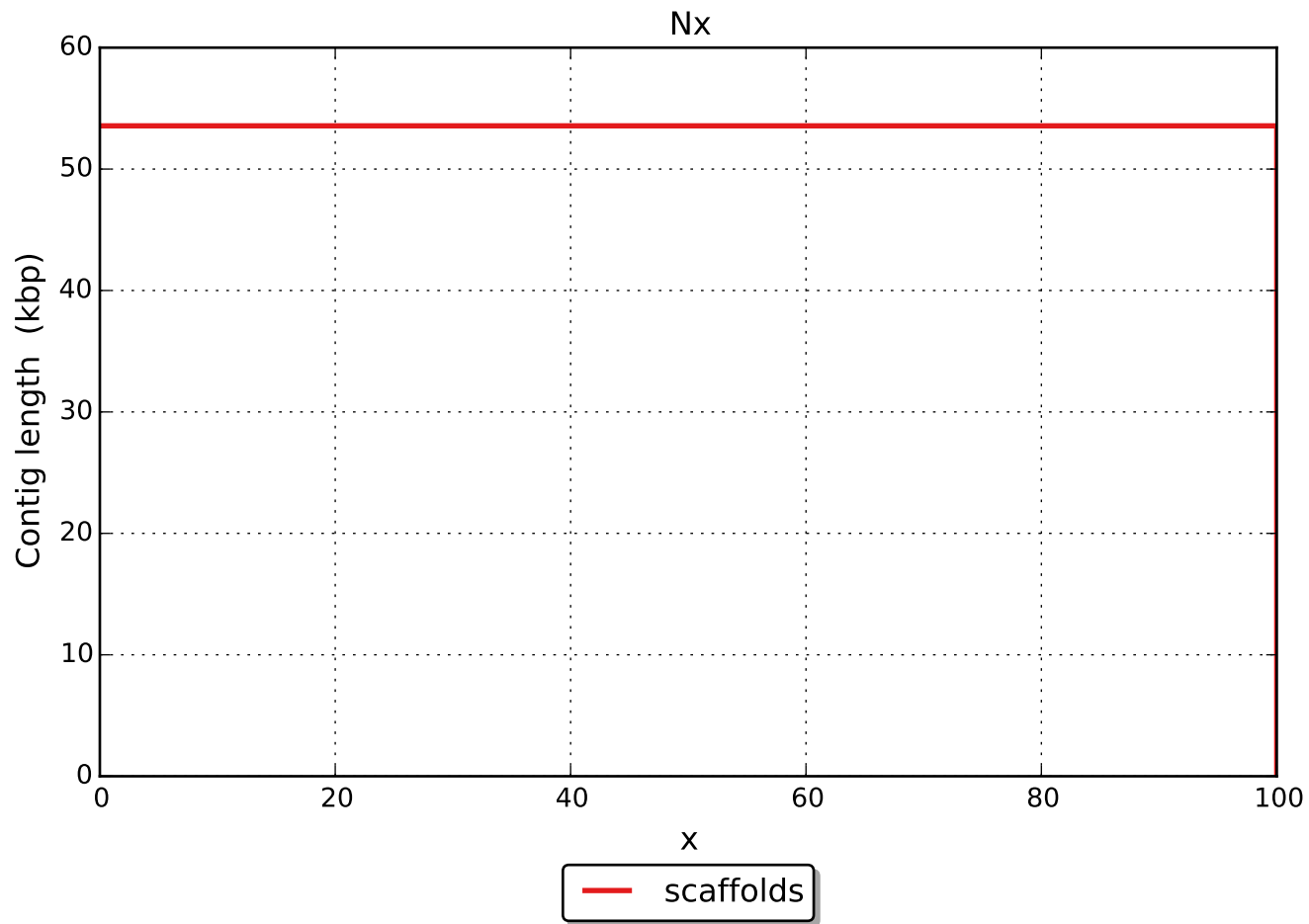
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	141
# indels	0
# short indels	0
# long indels	0
Indels length	0

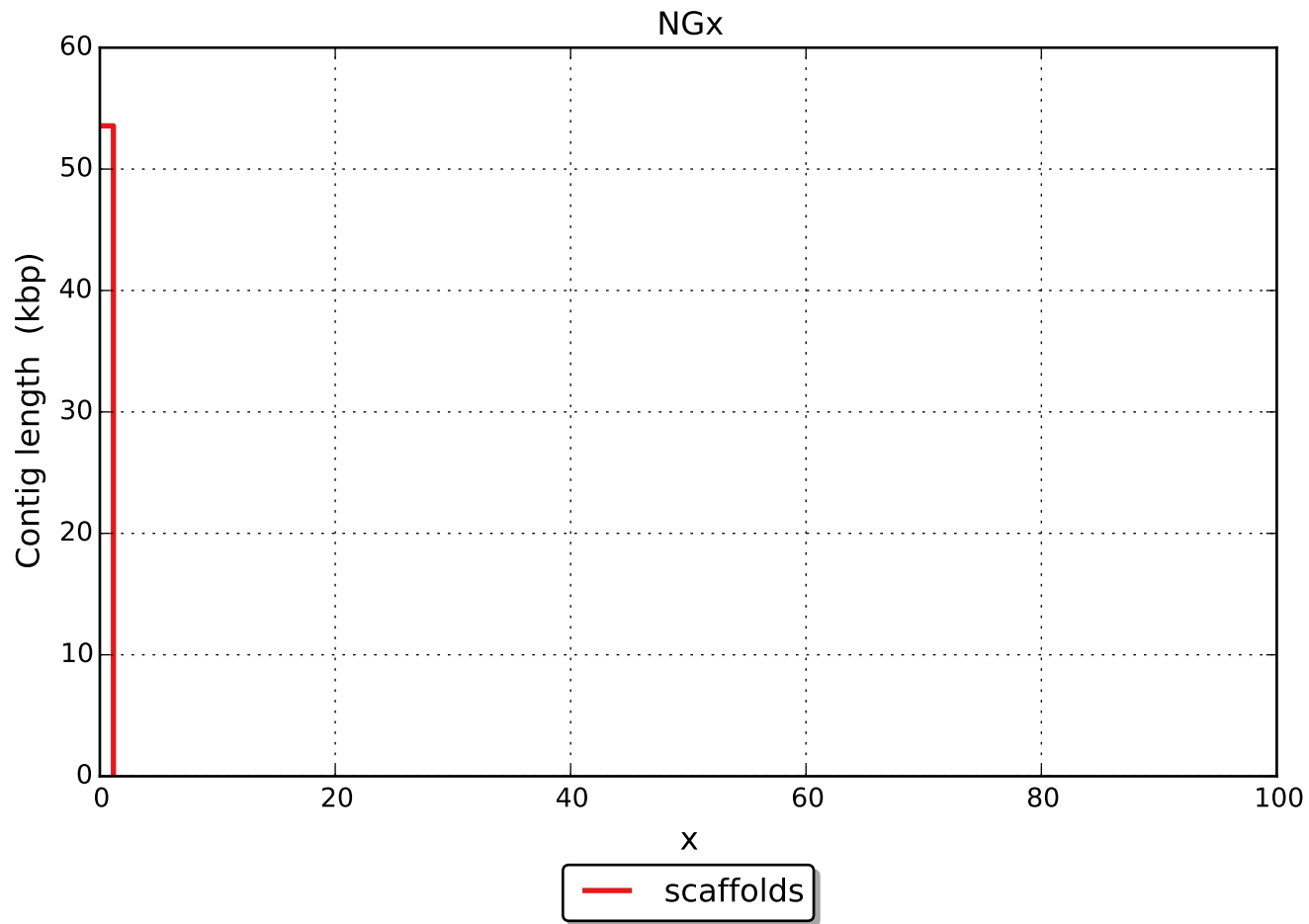
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

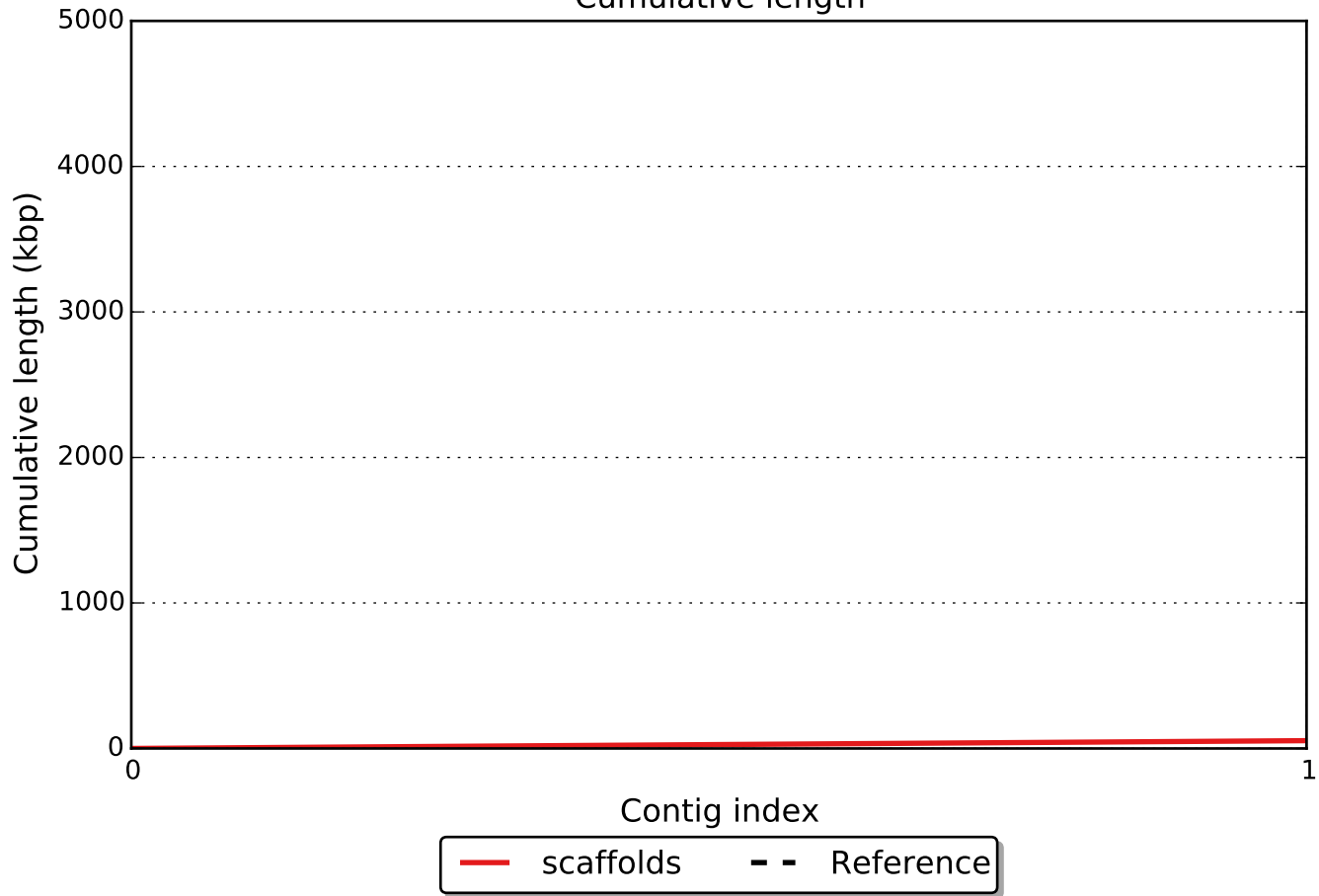
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	50701
# N's	0

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).

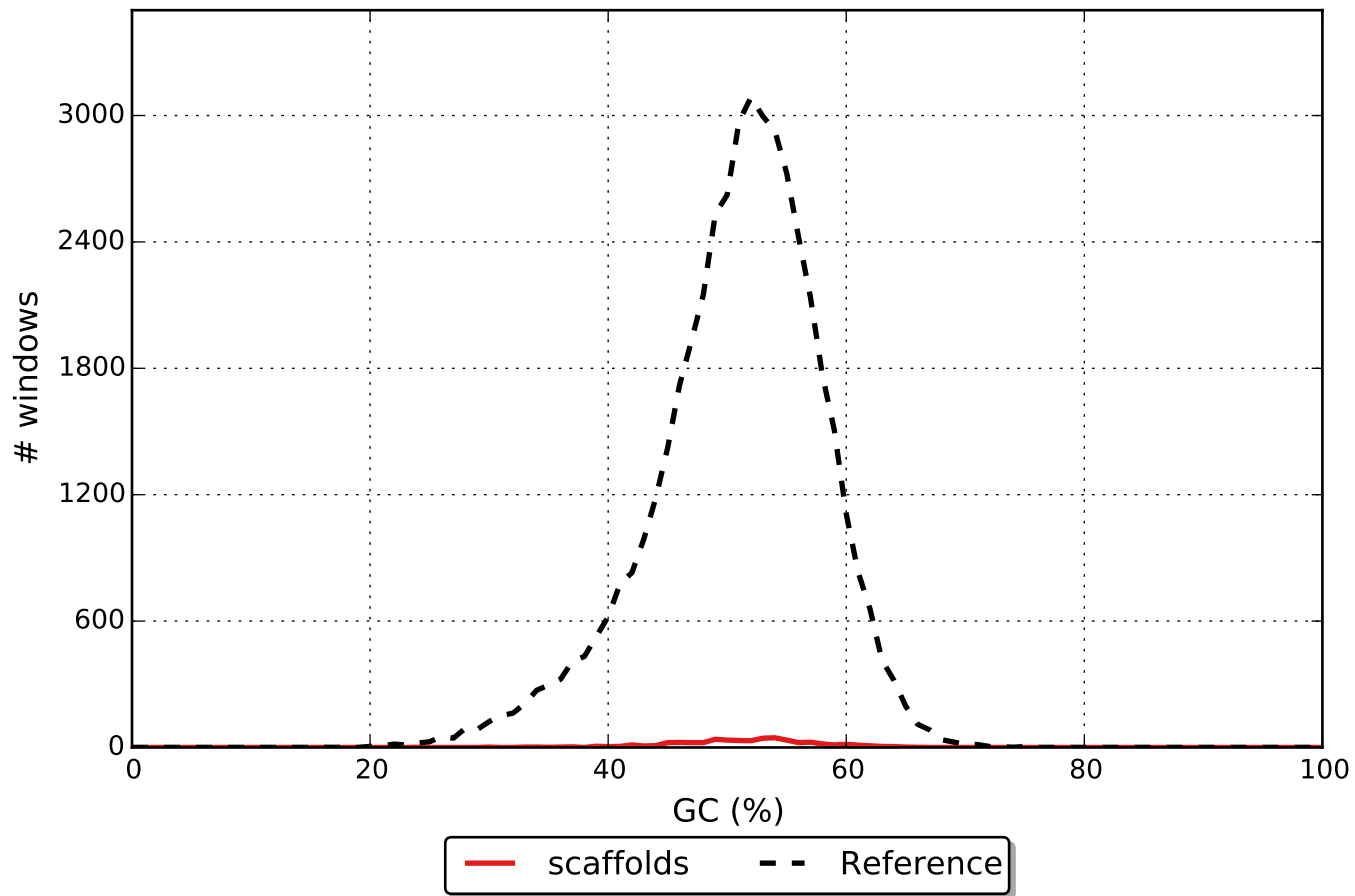




Cumulative length



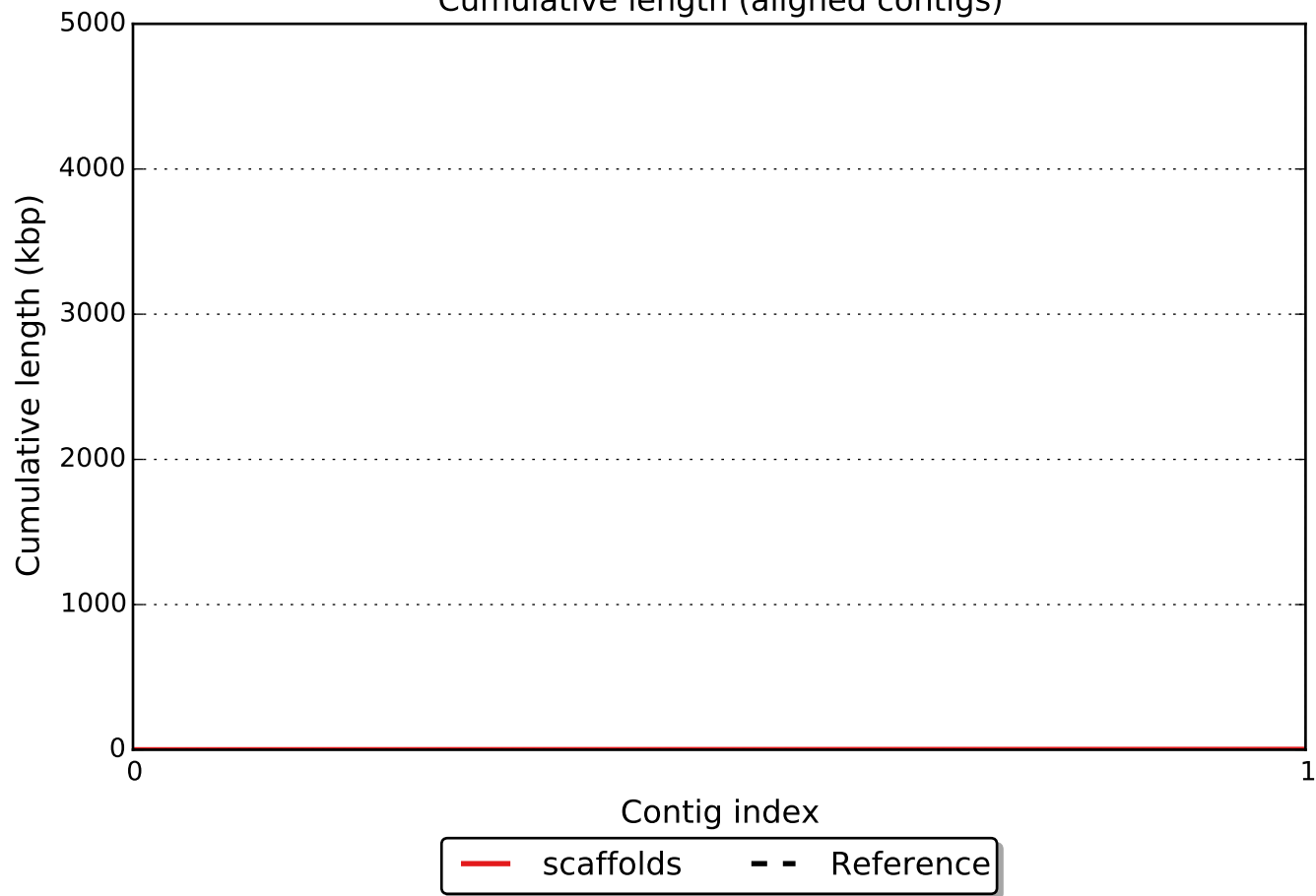
GC content



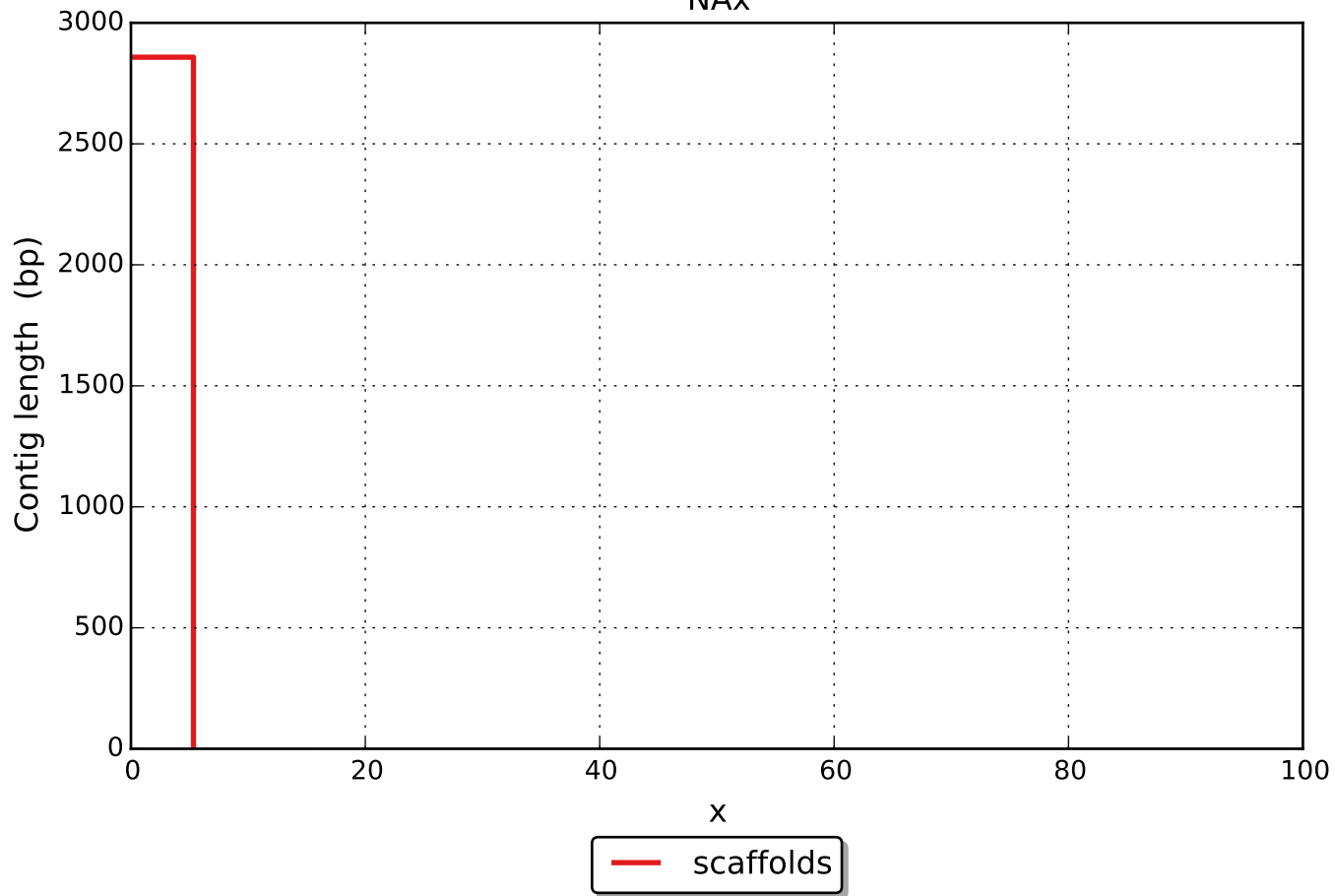
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

