

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)	239239
Total length (≥ 5000 bp)	239239
Total length (≥ 10000 bp)	239239
Total length (≥ 25000 bp)	239239
Total length (≥ 50000 bp)	239239
# contigs	3
Largest contig	132163
Total length	239986
Reference length	4641652
GC (%)	51.37
Reference GC (%)	50.78
N50	132163
N75	107076
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	231676
Genome fraction (%)	0.177
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4794.44
# indels per 100 kbp	12.20
Largest alignment	5170
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

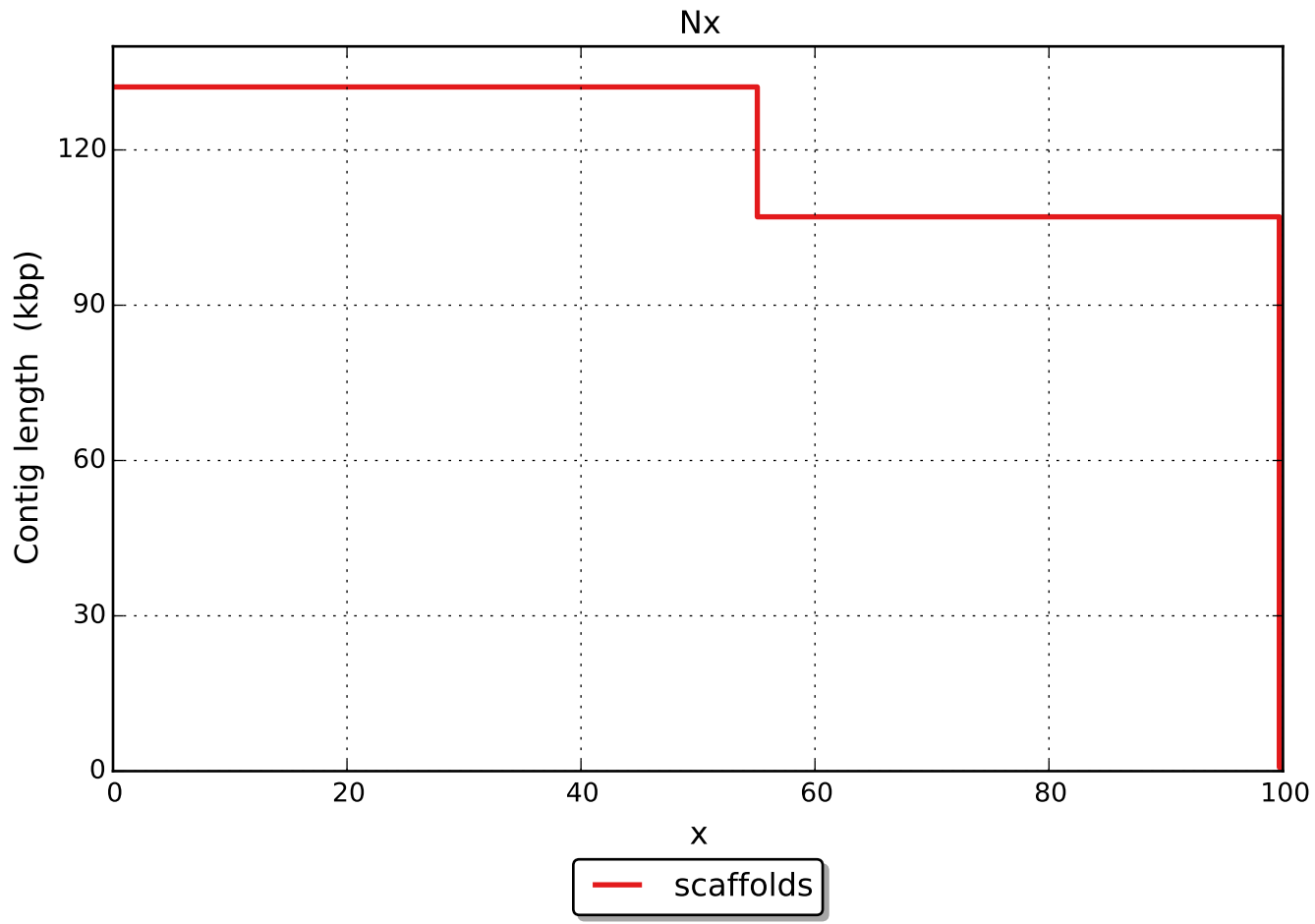
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	393
# indels	1
# short indels	1
# long indels	0
Indels length	1

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).

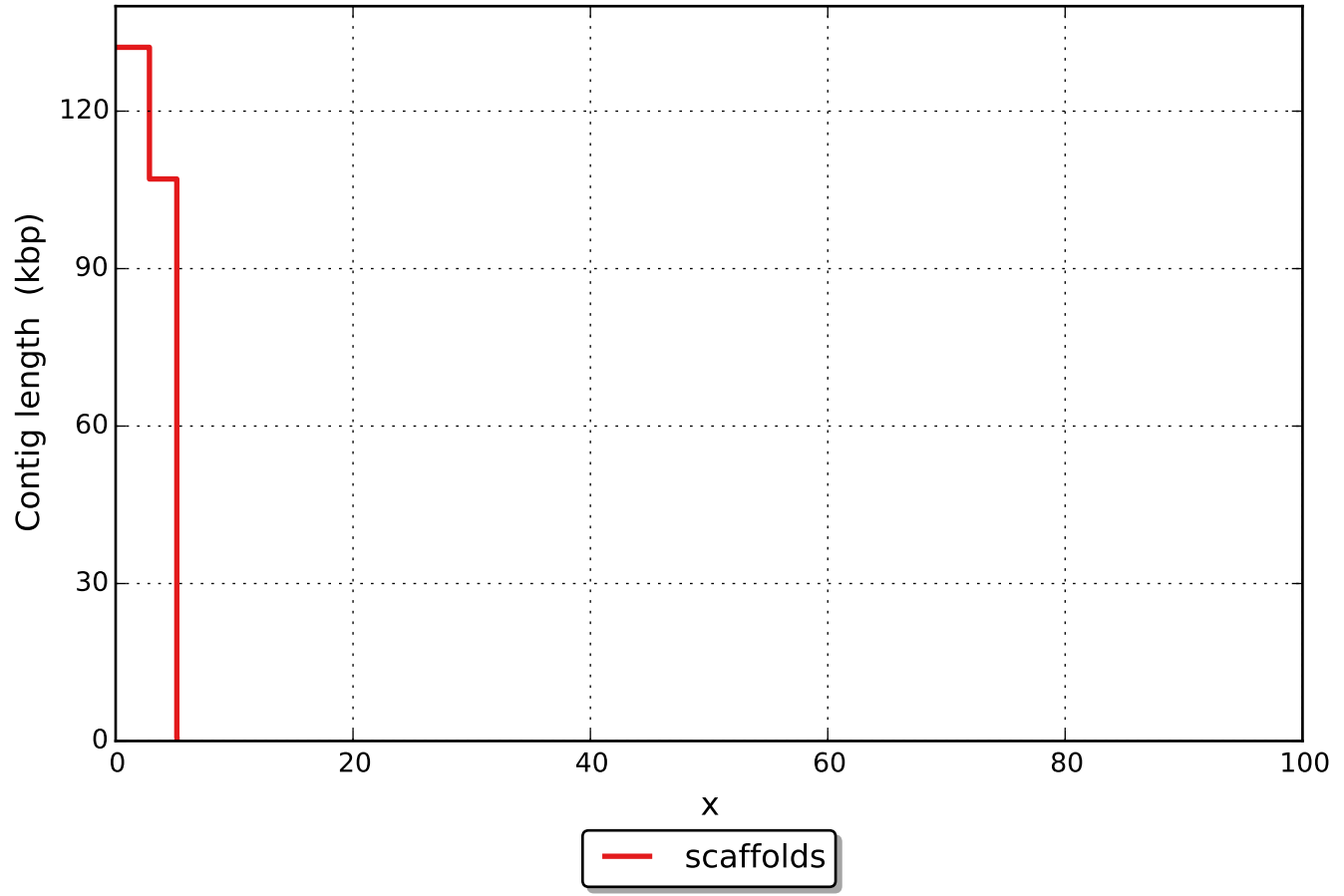
Unaligned report

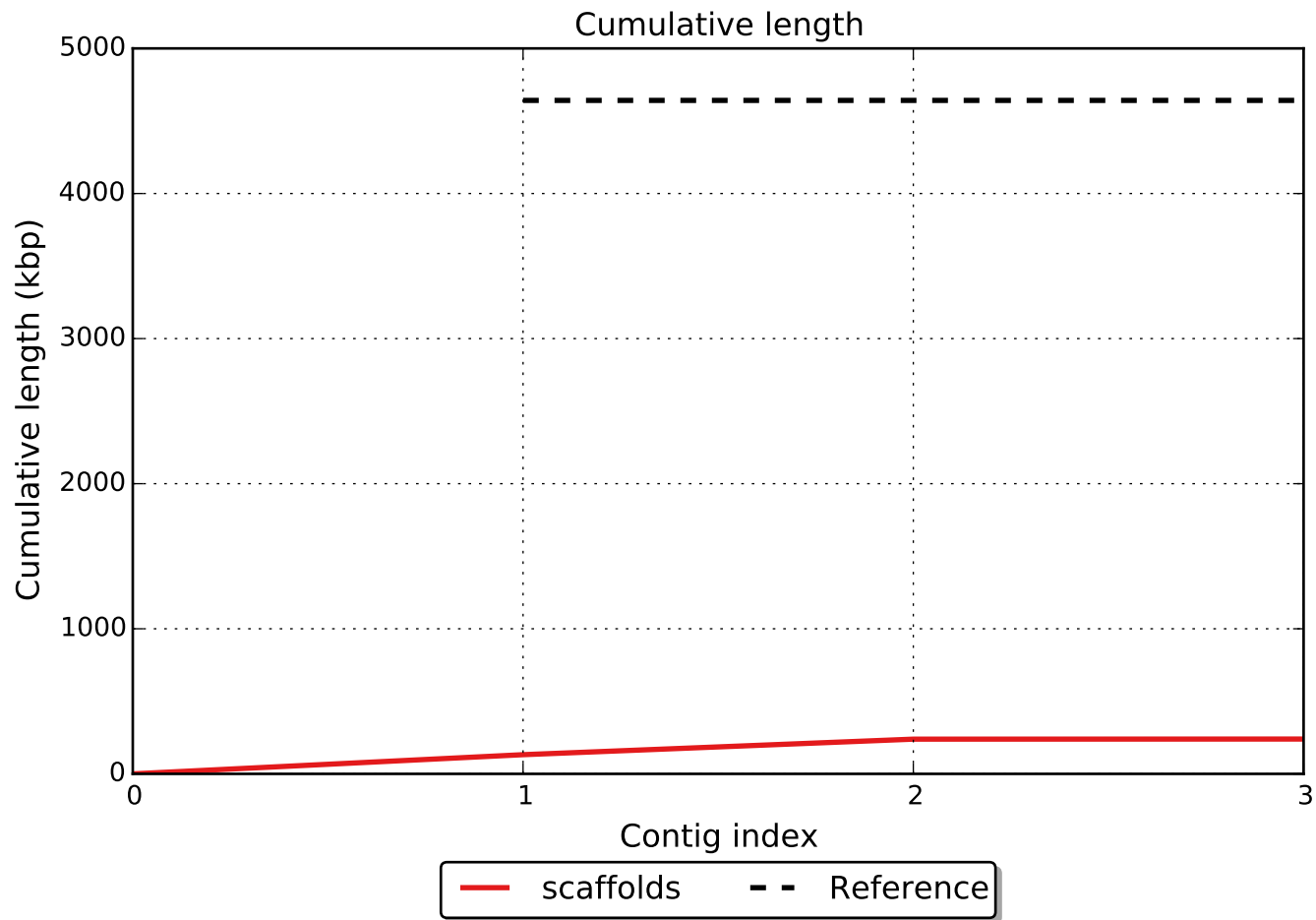
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	2
# both parts are significant	2
Partially unaligned length	231676
# N's	0

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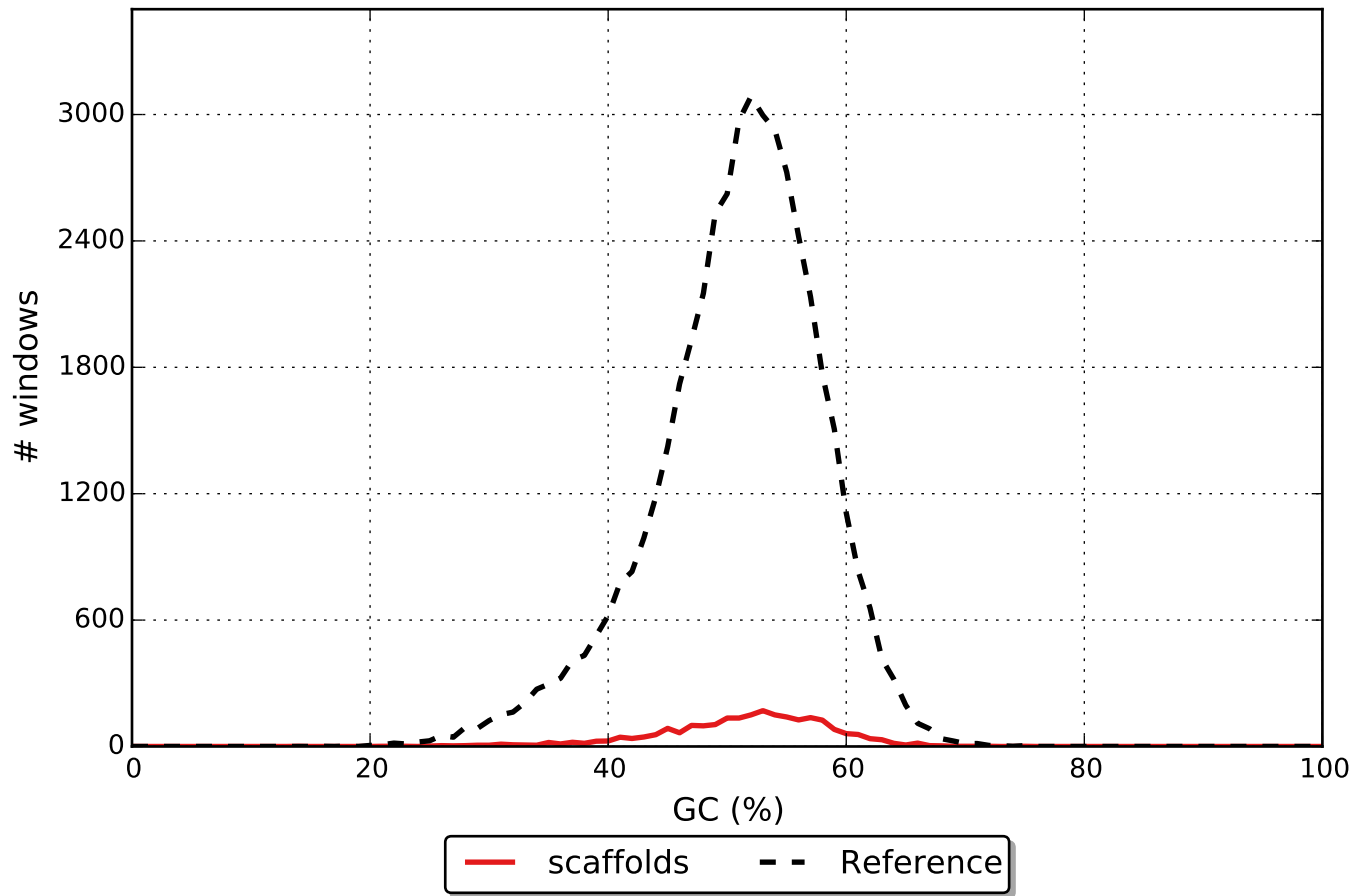


NGx





GC content



Misassemblies



Cumulative length (aligned contigs)

