

Report

	scaffolds
# contigs (≥ 1000 bp)	7
# contigs (≥ 5000 bp)	5
# contigs (≥ 10000 bp)	5
# contigs (≥ 25000 bp)	5
# contigs (≥ 50000 bp)	4
Total length (≥ 1000 bp)	618900
Total length (≥ 5000 bp)	616744
Total length (≥ 10000 bp)	616744
Total length (≥ 25000 bp)	616744
Total length (≥ 50000 bp)	591579
# contigs	9
Largest contig	283870
Total length	620595
Reference length	4641652
GC (%)	50.98
Reference GC (%)	50.78
N50	132188
N75	108452
L50	2
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 5 part
Unaligned length	596151
Genome fraction (%)	0.524
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4591.79
# indels per 100 kbp	24.66
Largest alignment	5186
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

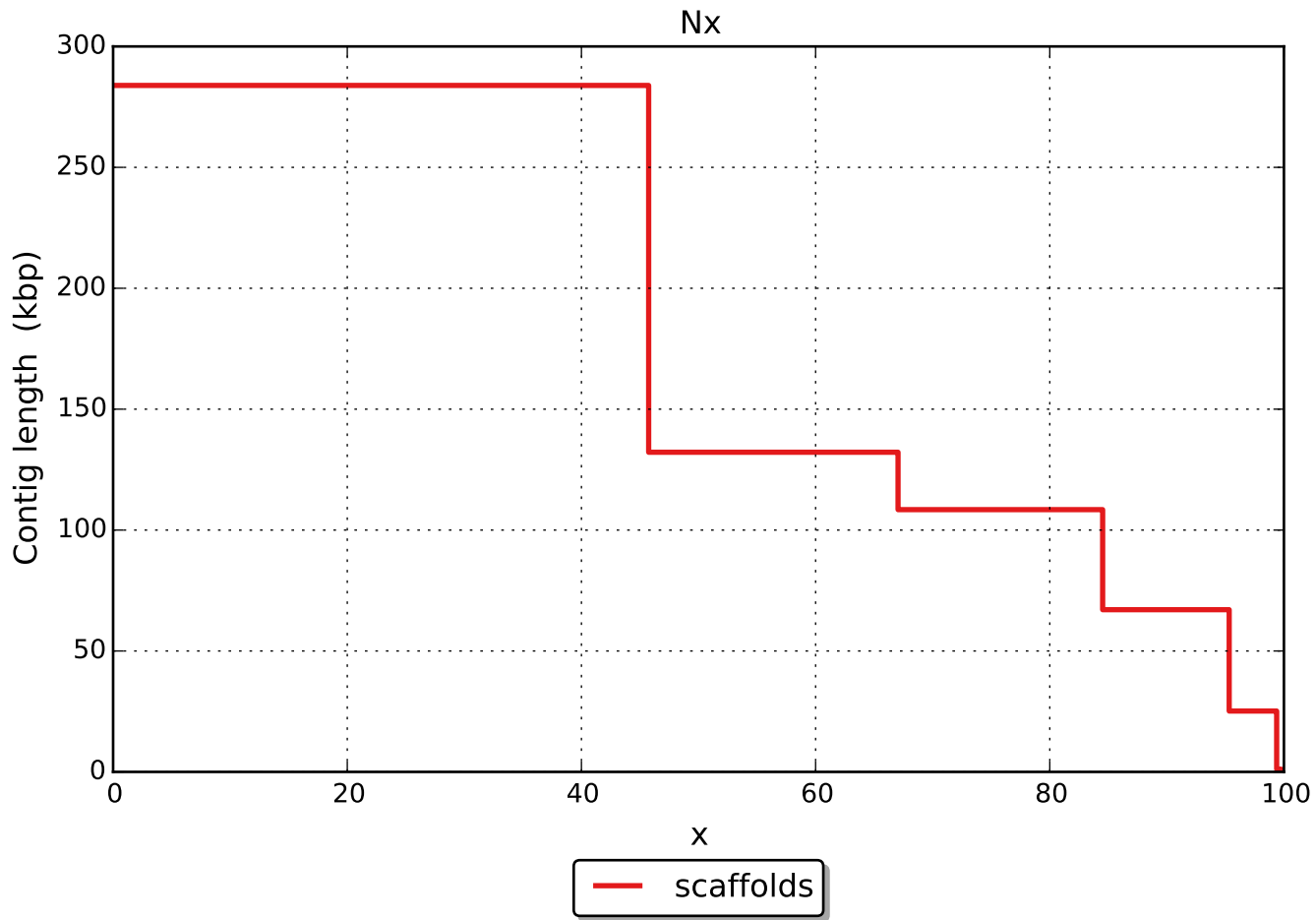
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	4
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1117
# indels	6
# short indels	6
# long indels	0
Indels length	6

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).

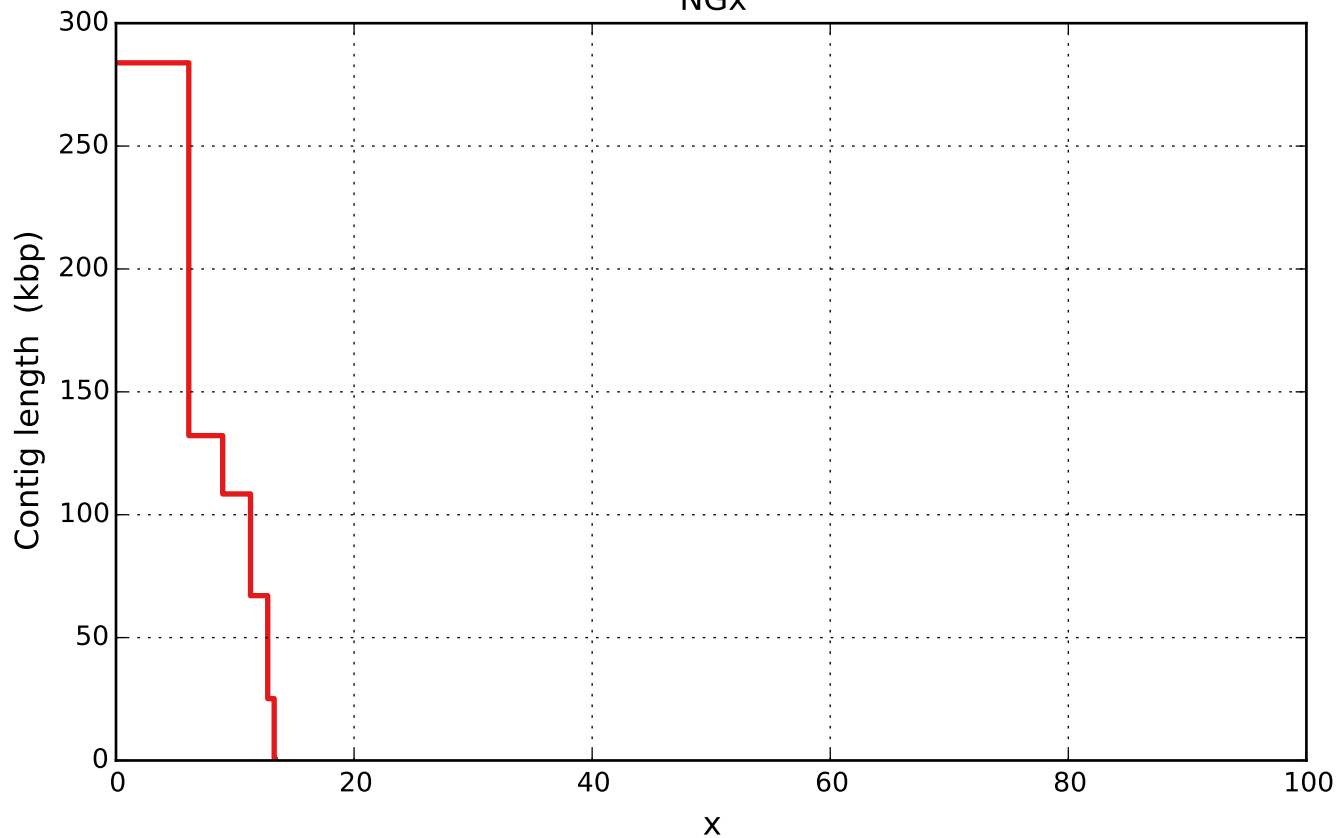
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
# with misassembly	3
# both parts are significant	4
Partially unaligned length	596151
# N's	0

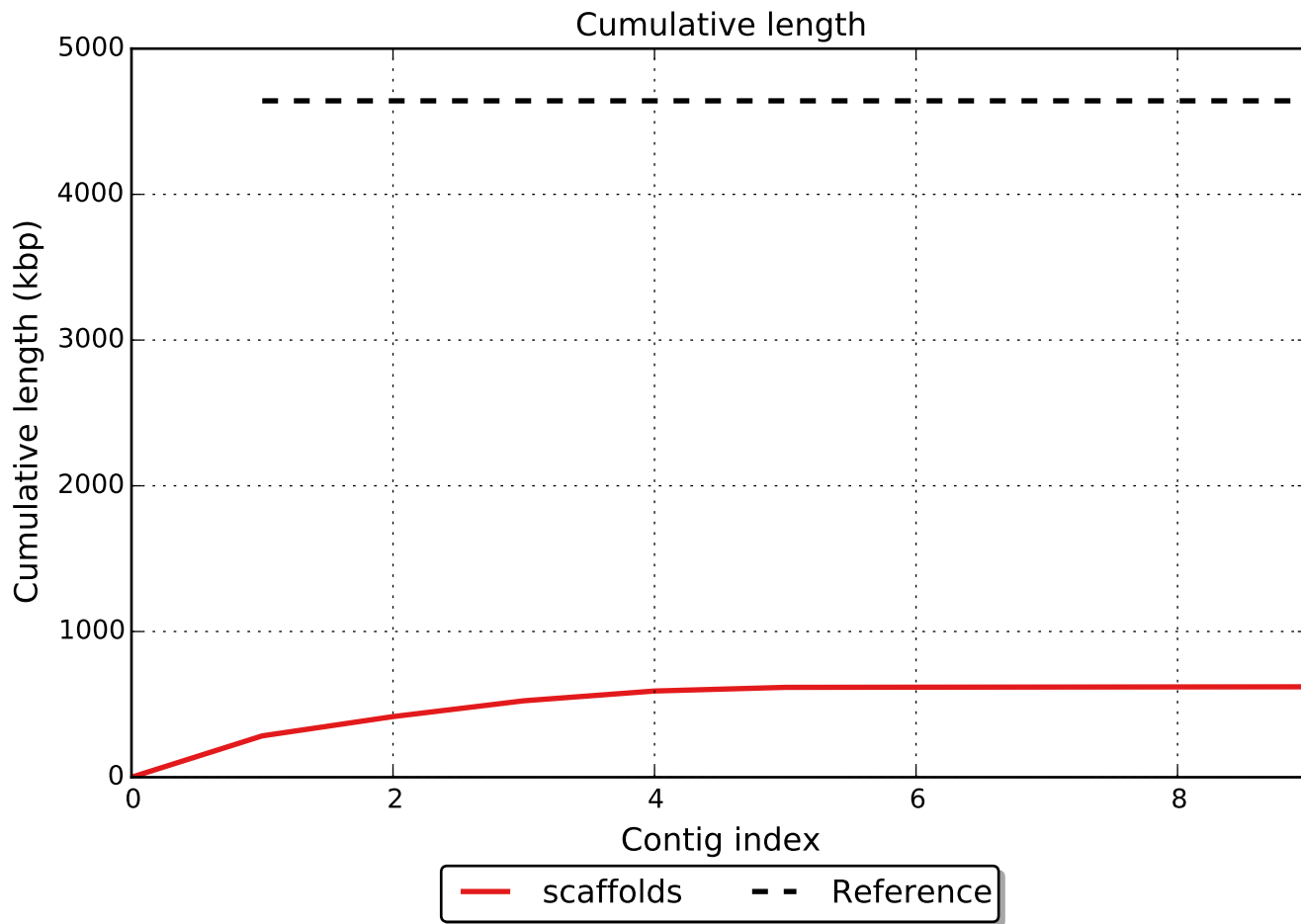
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



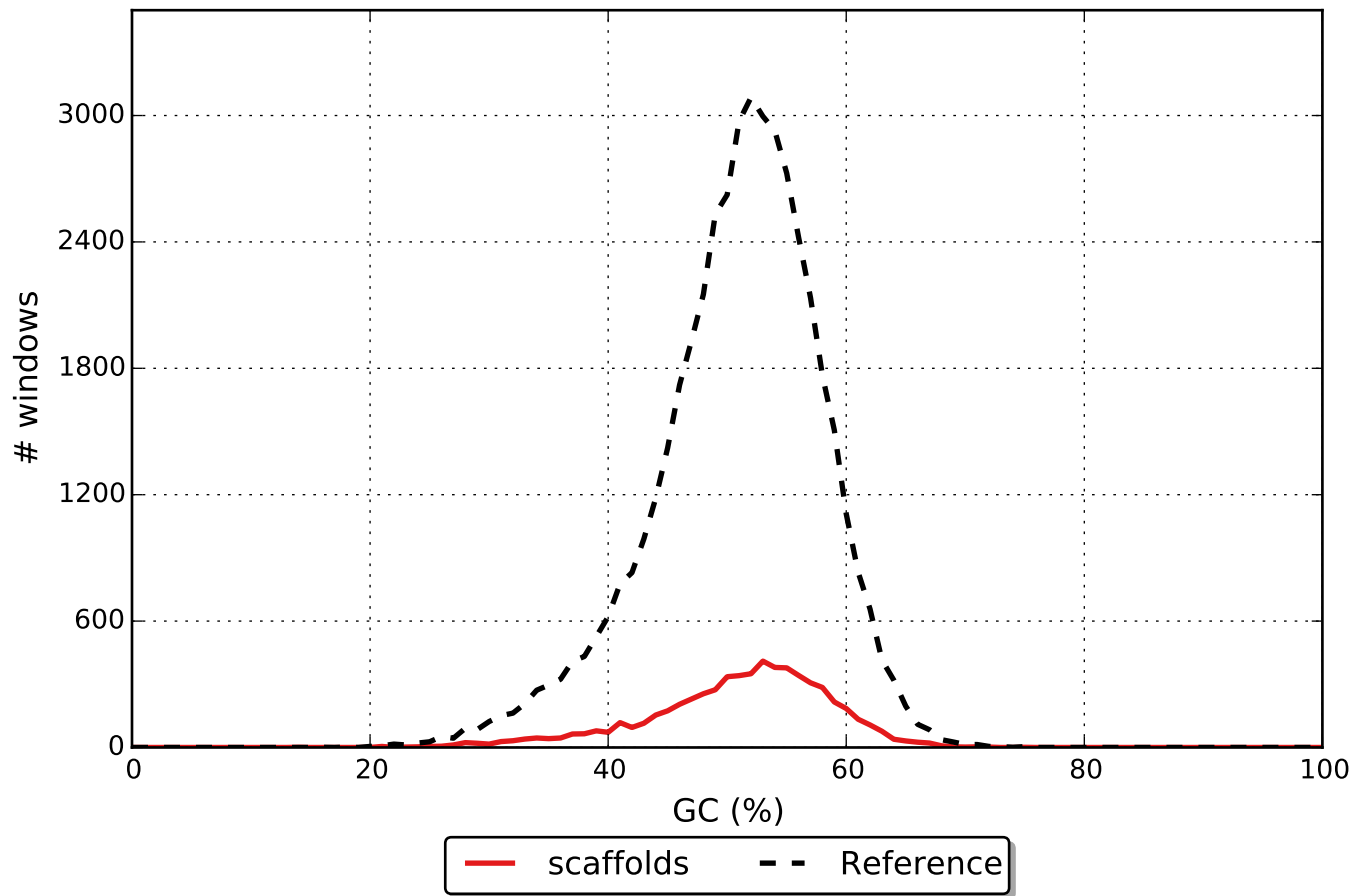
NGx



— scaffolds



GC content



Misassemblies



Cumulative length (aligned contigs)

