

Report

	scaffolds
# contigs (≥ 1000 bp)	9
# contigs (≥ 5000 bp)	8
# contigs (≥ 10000 bp)	8
# contigs (≥ 25000 bp)	7
# contigs (≥ 50000 bp)	7
Total length (≥ 1000 bp)	1321565
Total length (≥ 5000 bp)	1320131
Total length (≥ 10000 bp)	1320131
Total length (≥ 25000 bp)	1304742
Total length (≥ 50000 bp)	1304742
# contigs	9
Largest contig	284062
Total length	1321565
Reference length	4641652
GC (%)	50.86
Reference GC (%)	50.78
N50	210555
N75	166049
L50	3
L75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 8 part
Unaligned length	1308077
Genome fraction (%)	0.291
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4544.78
# 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	6
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	613
# indels	0
# short indels	0
# long indels	0
Indels length	0

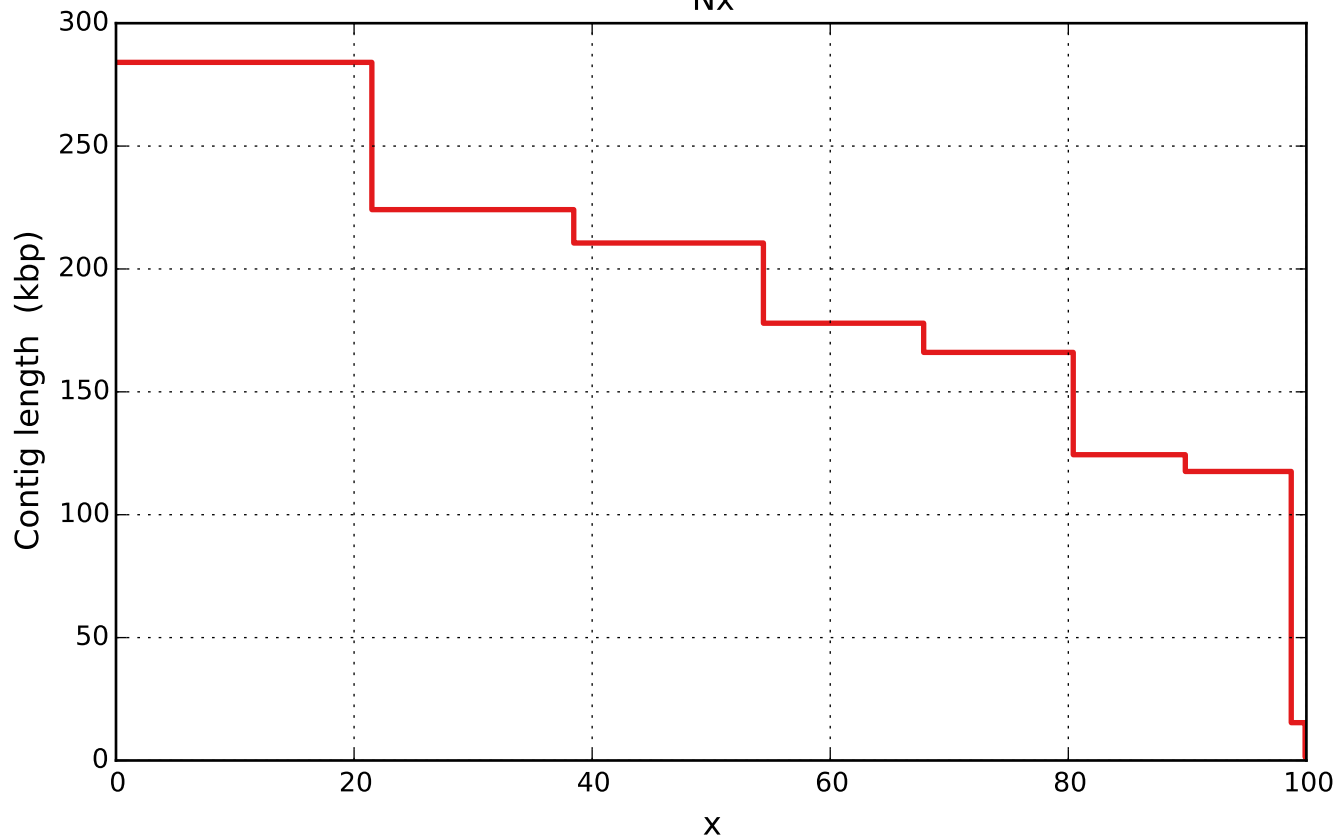
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
# with misassembly	3
# both parts are significant	6
Partially unaligned length	1308077
# 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).

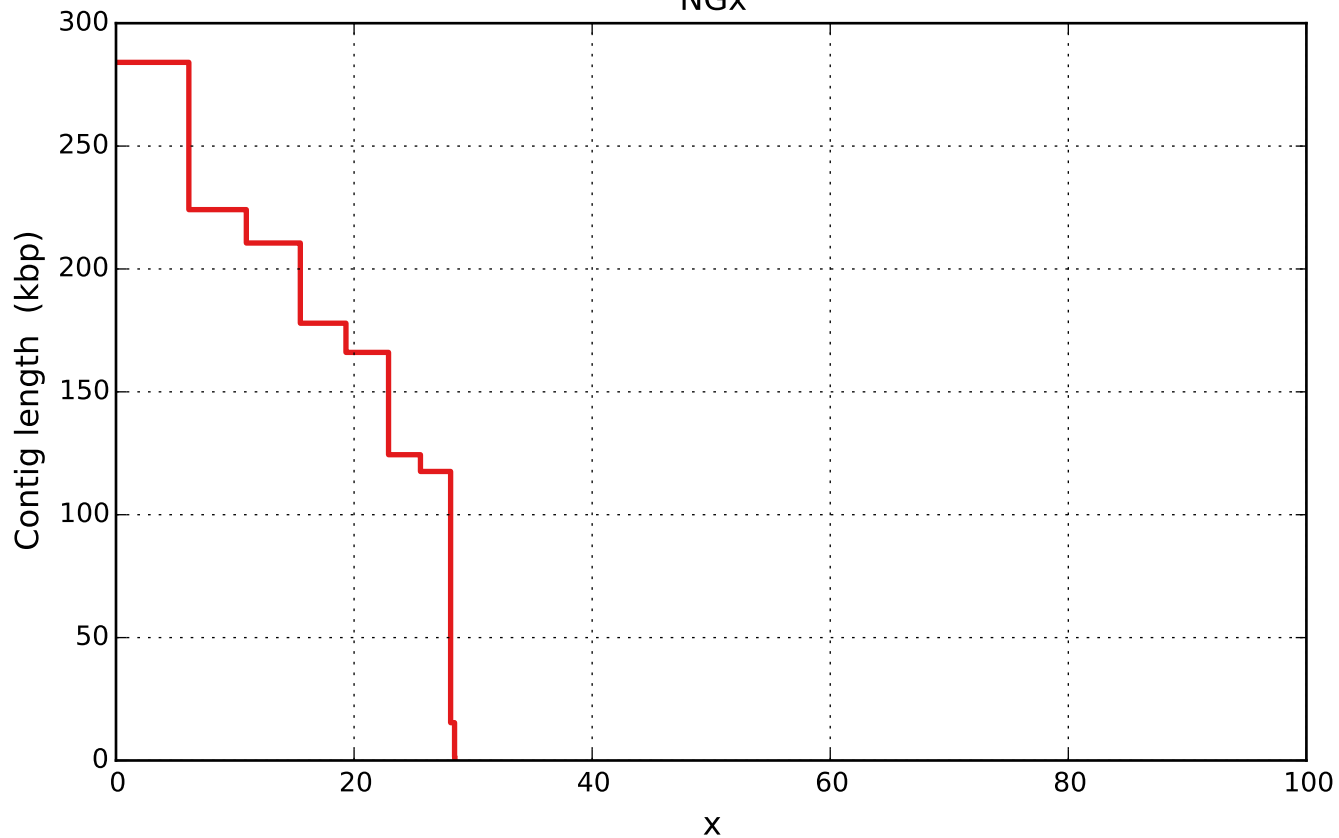
Nx



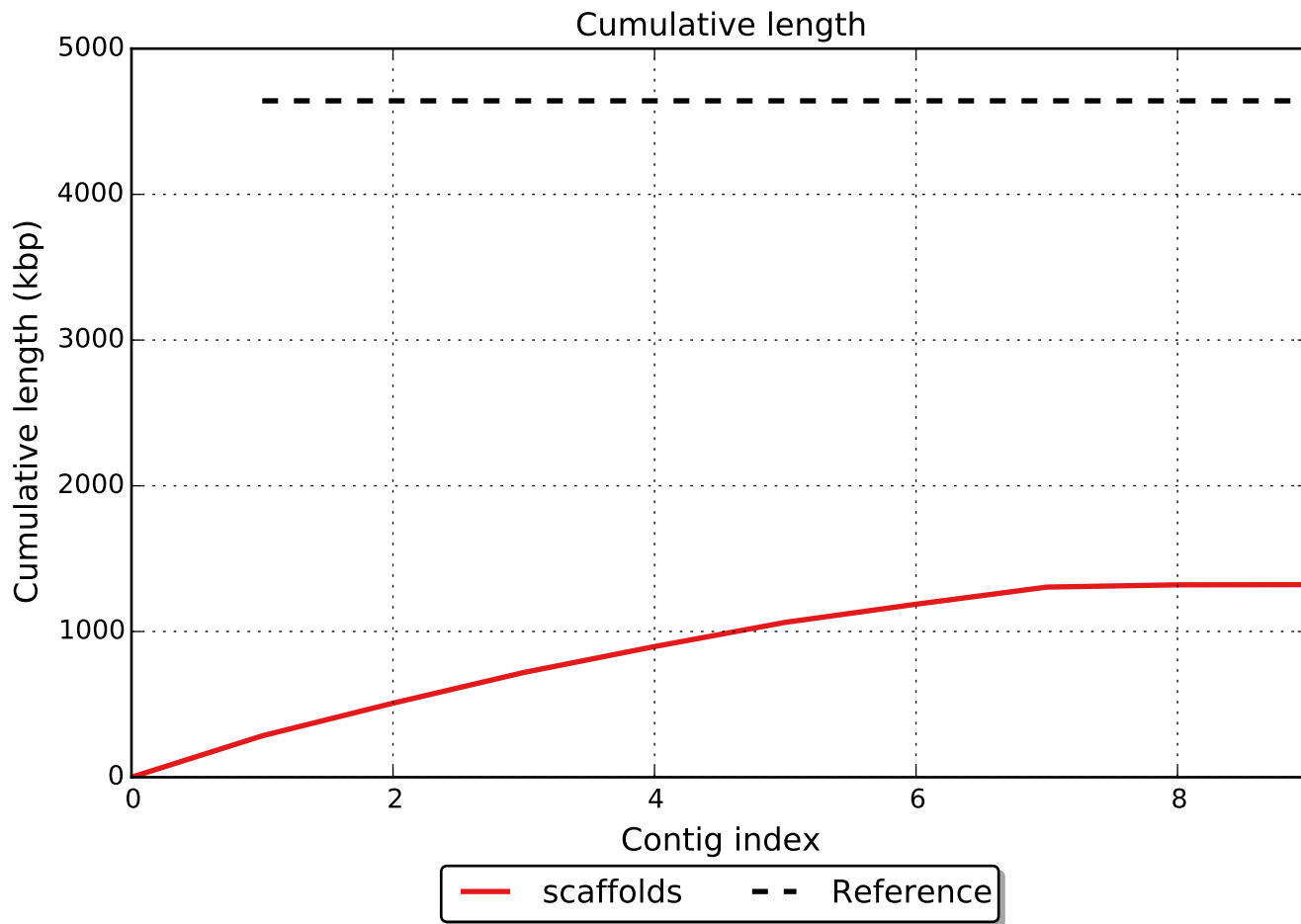
—

scaffolds

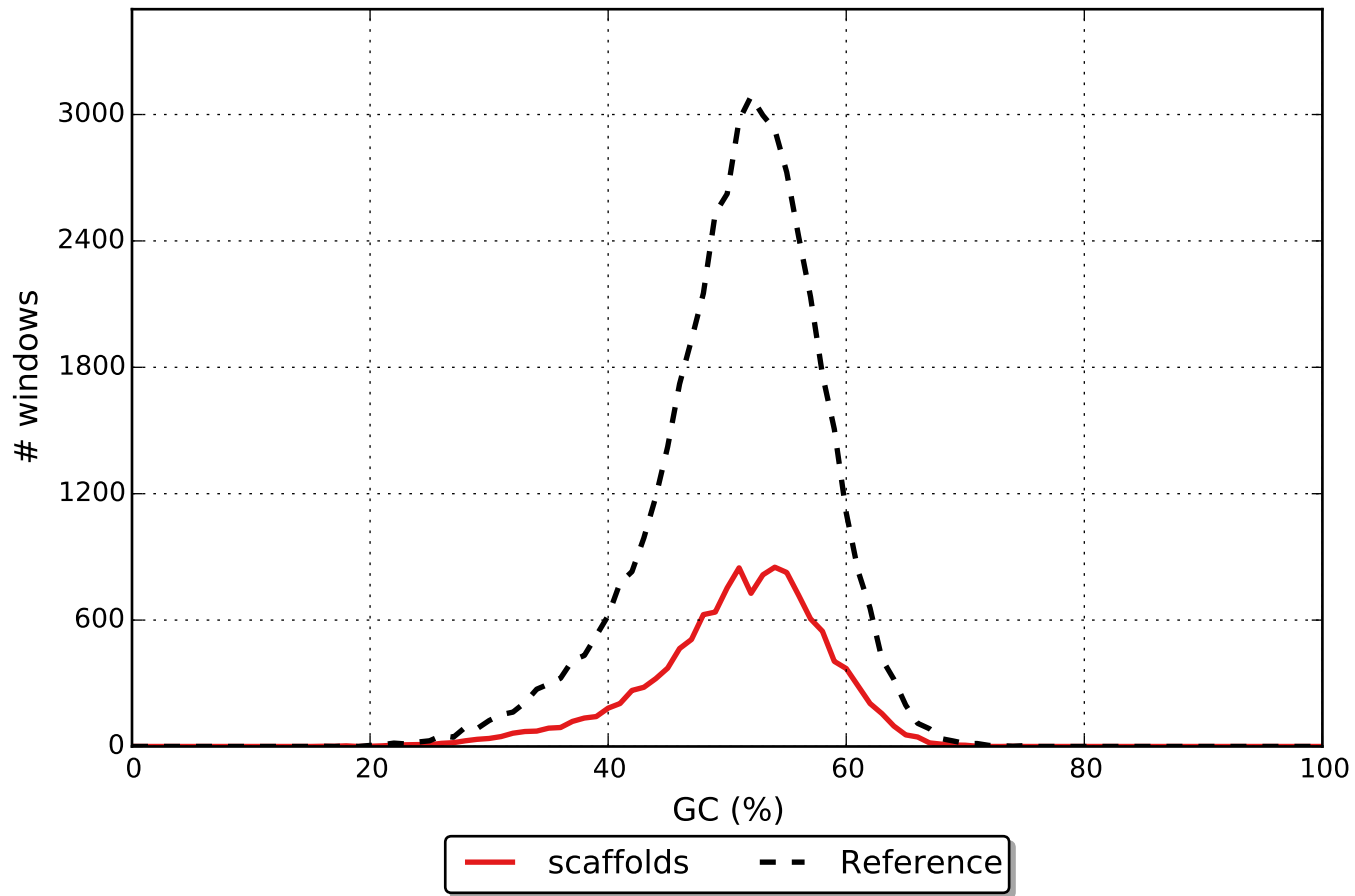
NGx



— scaffolds



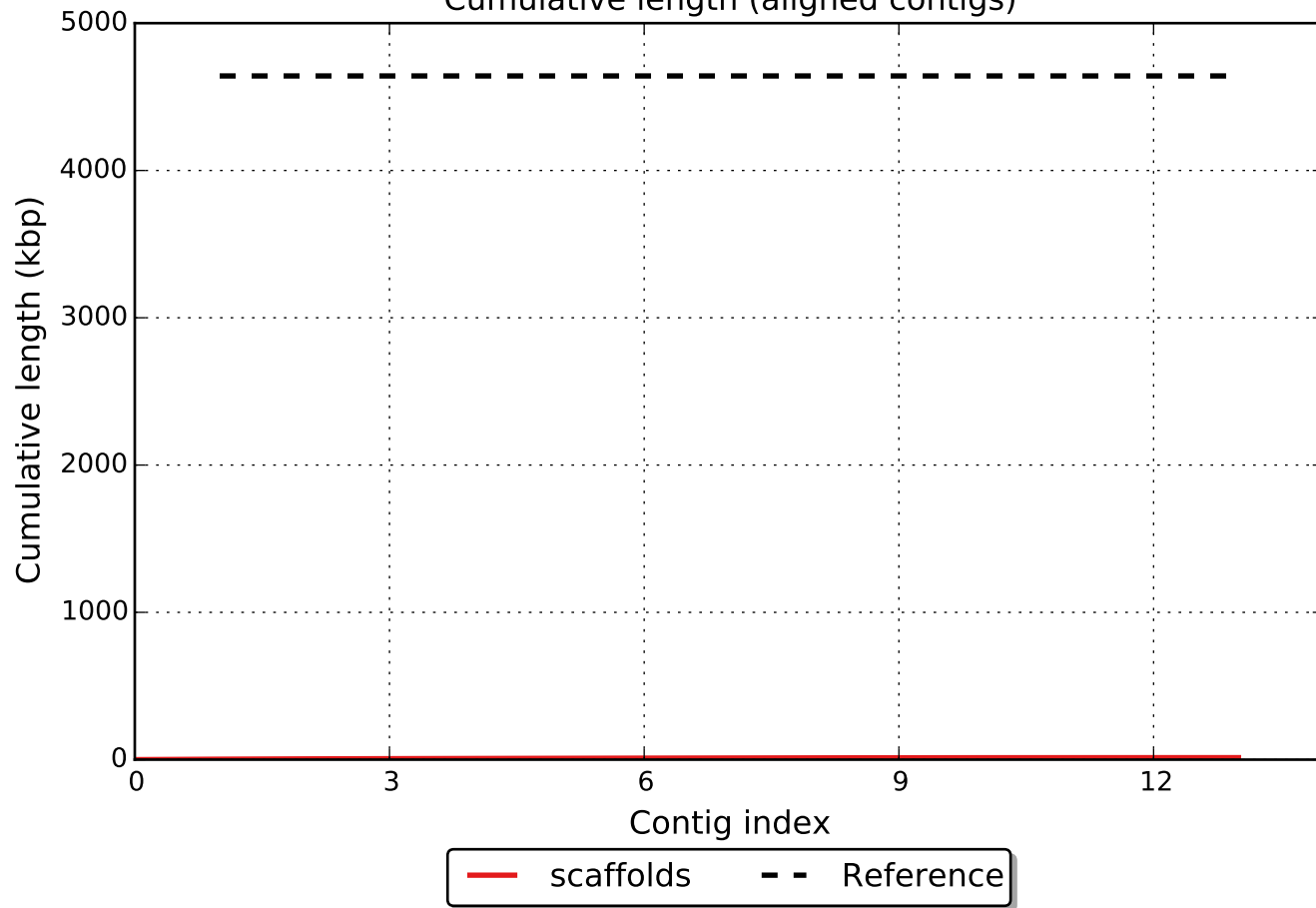
GC content



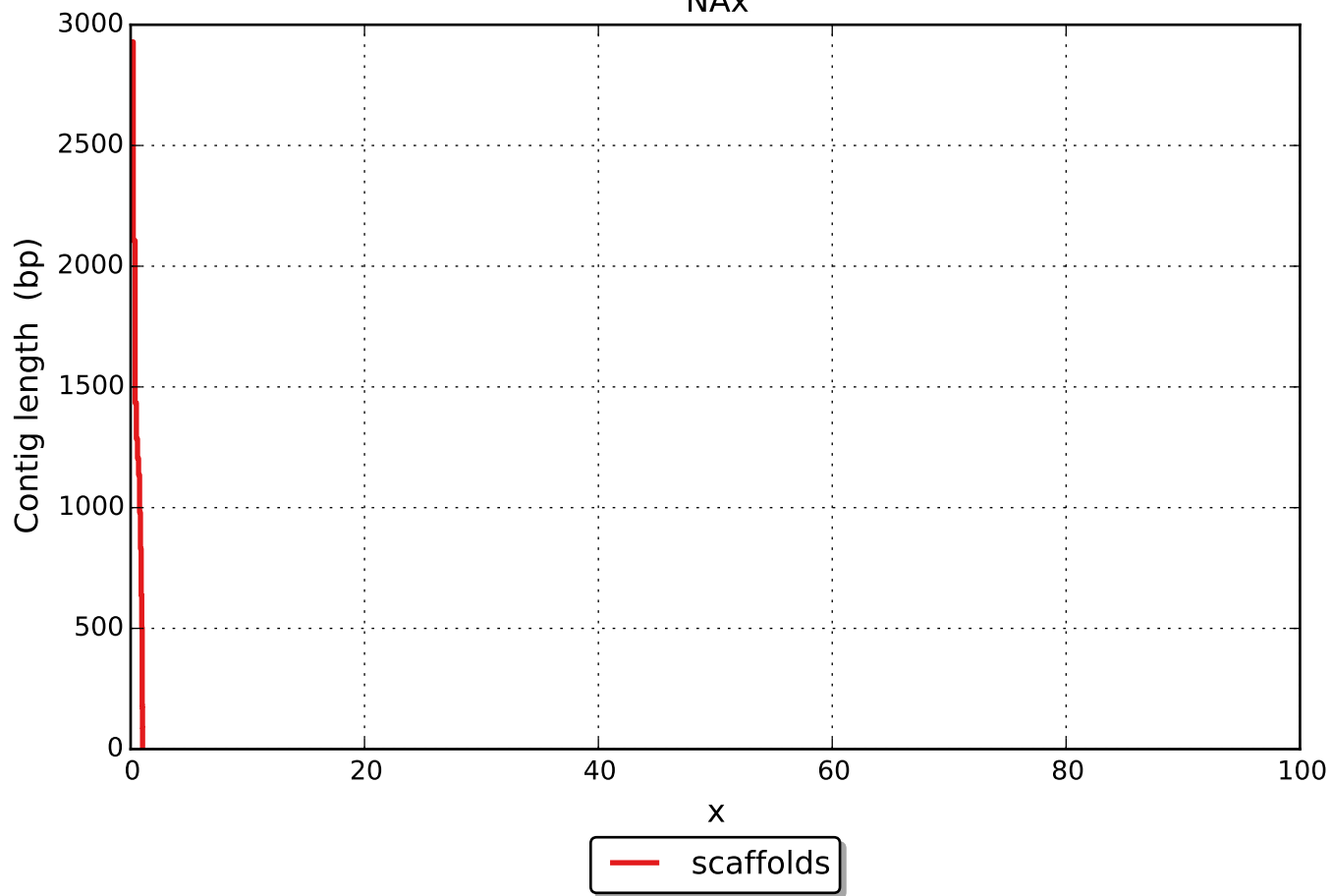
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

