

Report

	scaffolds
# contigs (≥ 1000 bp)	9
# contigs (≥ 5000 bp)	8
# contigs (≥ 10000 bp)	7
# contigs (≥ 25000 bp)	6
# contigs (≥ 50000 bp)	5
Total length (≥ 1000 bp)	1380172
Total length (≥ 5000 bp)	1378579
Total length (≥ 10000 bp)	1368823
Total length (≥ 25000 bp)	1354351
Total length (≥ 50000 bp)	1325023
# contigs	10
Largest contig	478751
Total length	1380981
Reference length	4641652
GC (%)	50.32
Reference GC (%)	50.78
N50	284387
N75	176518
L50	2
L75	4
# misassemblies	14
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	0
# unaligned contigs	0 + 7 part
Unaligned length	886674
Genome fraction (%)	7.192
Duplication ratio	1.481
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2118.55
# indels per 100 kbp	2.10
Largest alignment	46257
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	14
# relocations	12
# translocations	0
# inversions	2
# possibly misassembled contigs	6
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	0
# mismatches	7072
# indels	7
# short indels	6
# long indels	1
Indels length	18

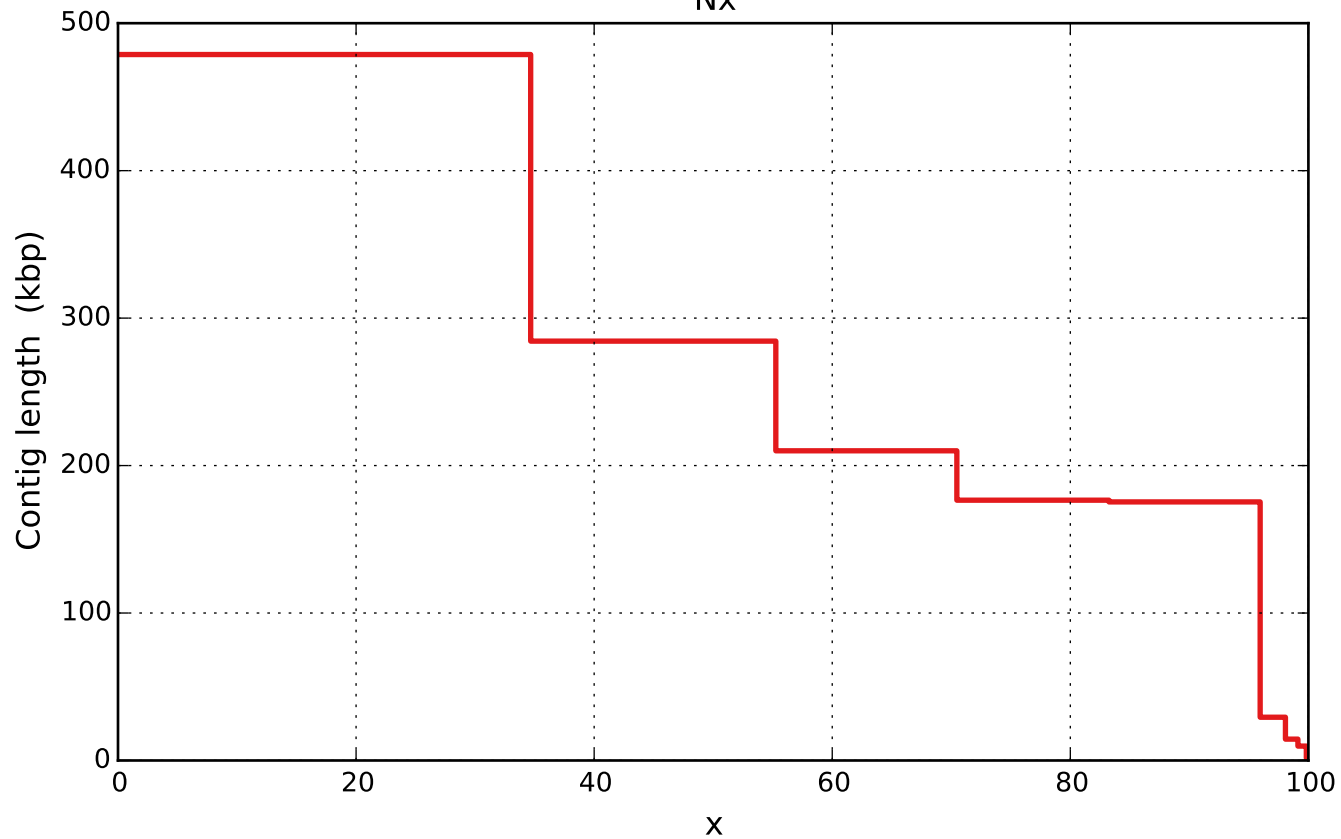
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
# with misassembly	2
# both parts are significant	5
Partially unaligned length	886674
# N's	0

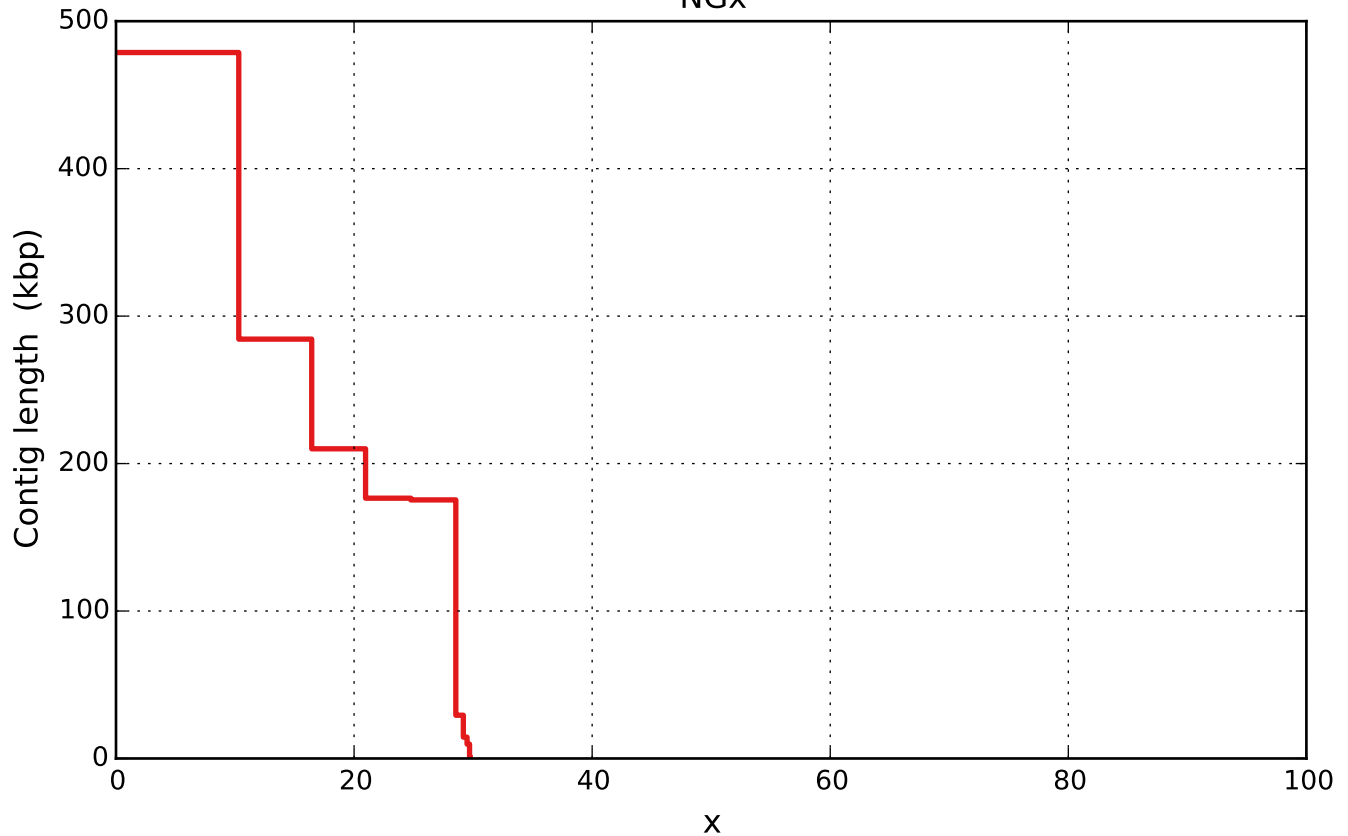
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

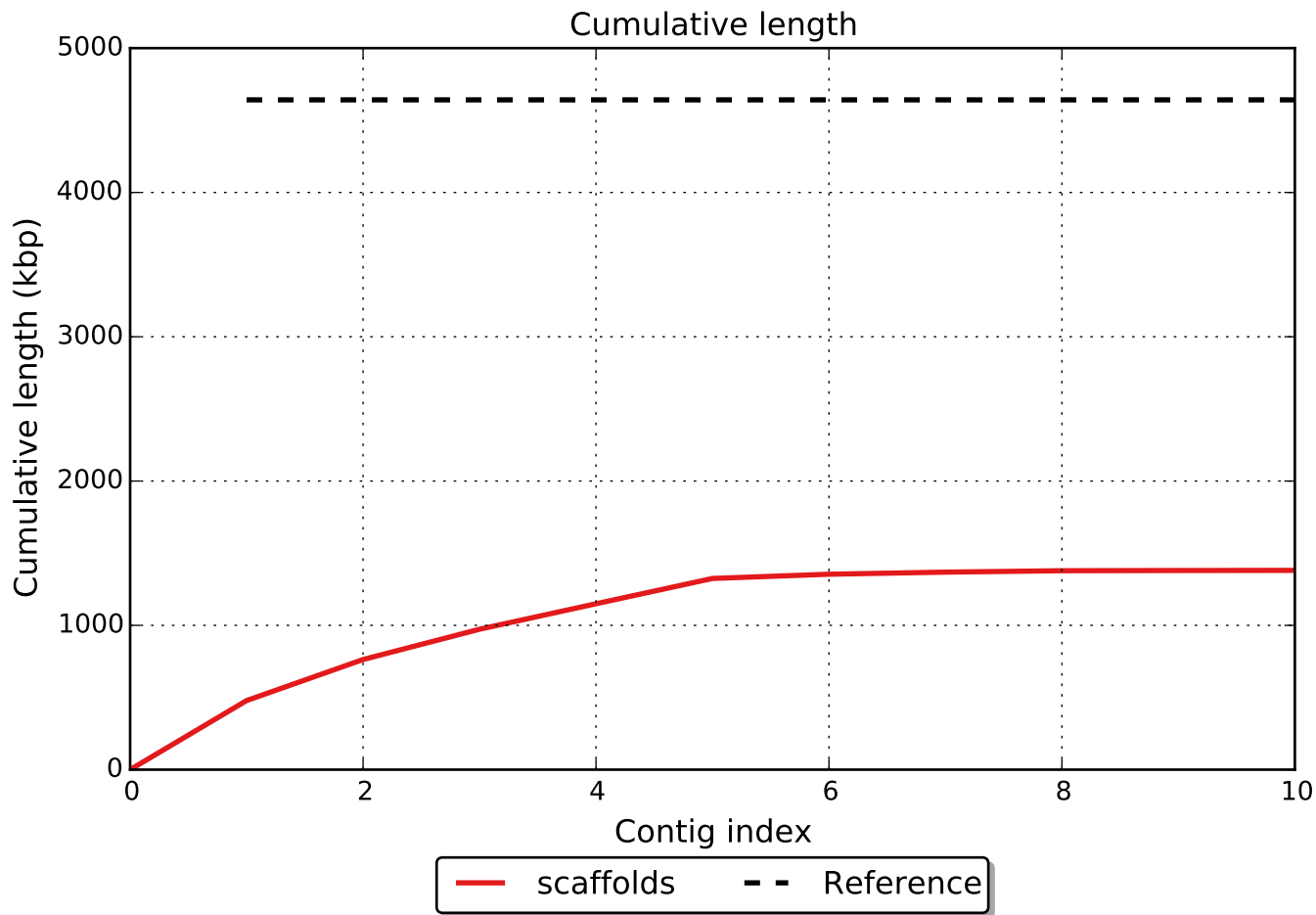


— scaffolds

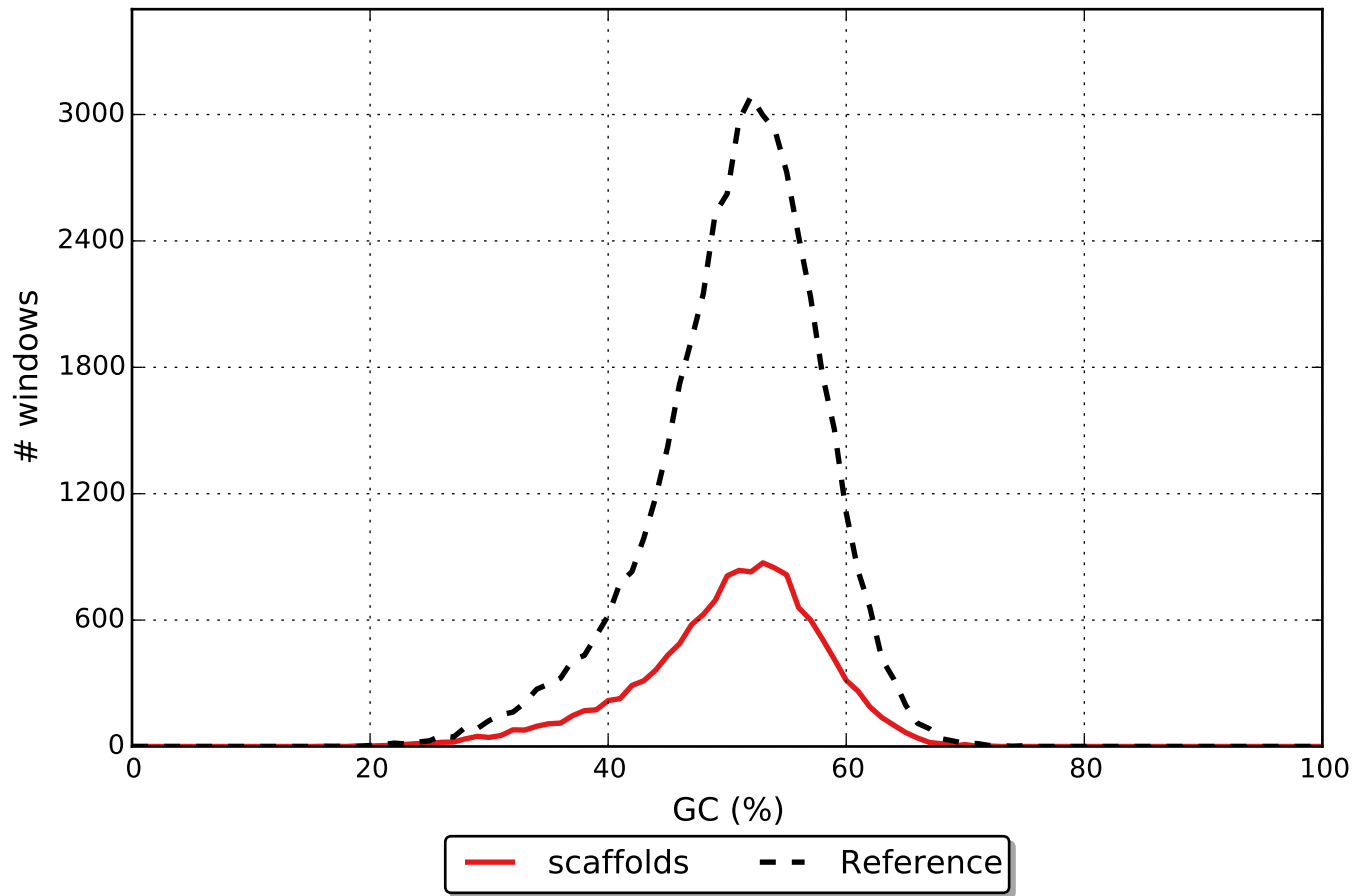
NGx

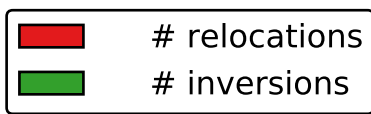
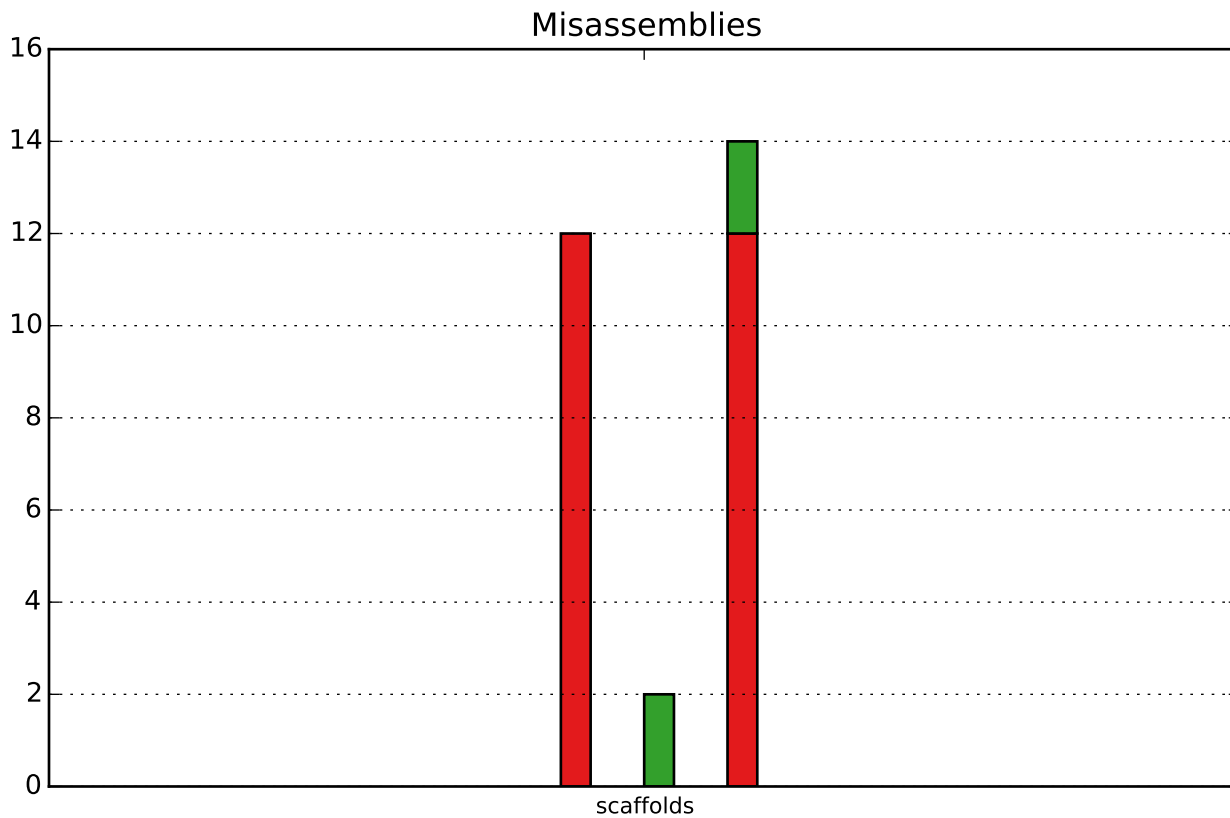


— scaffolds

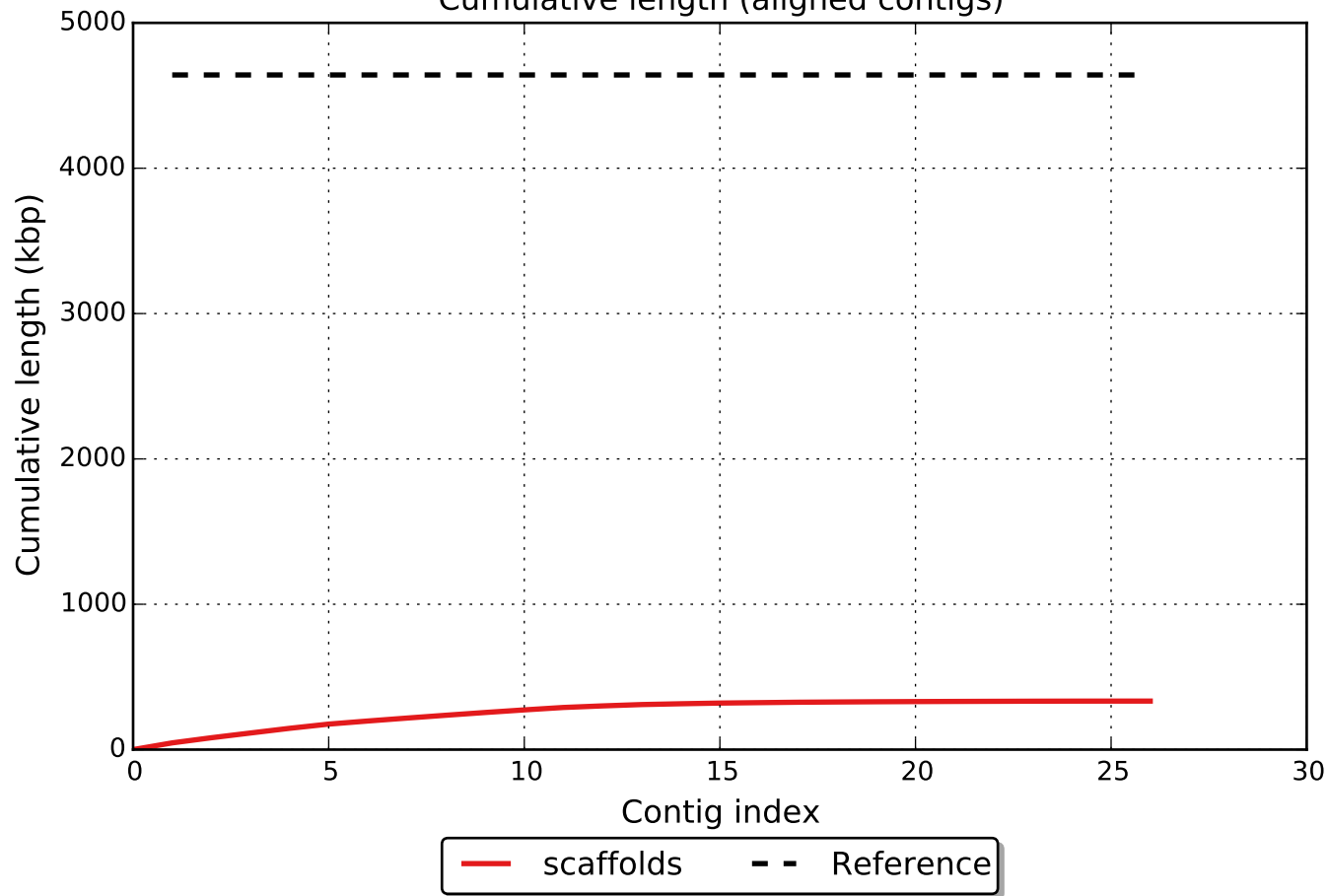


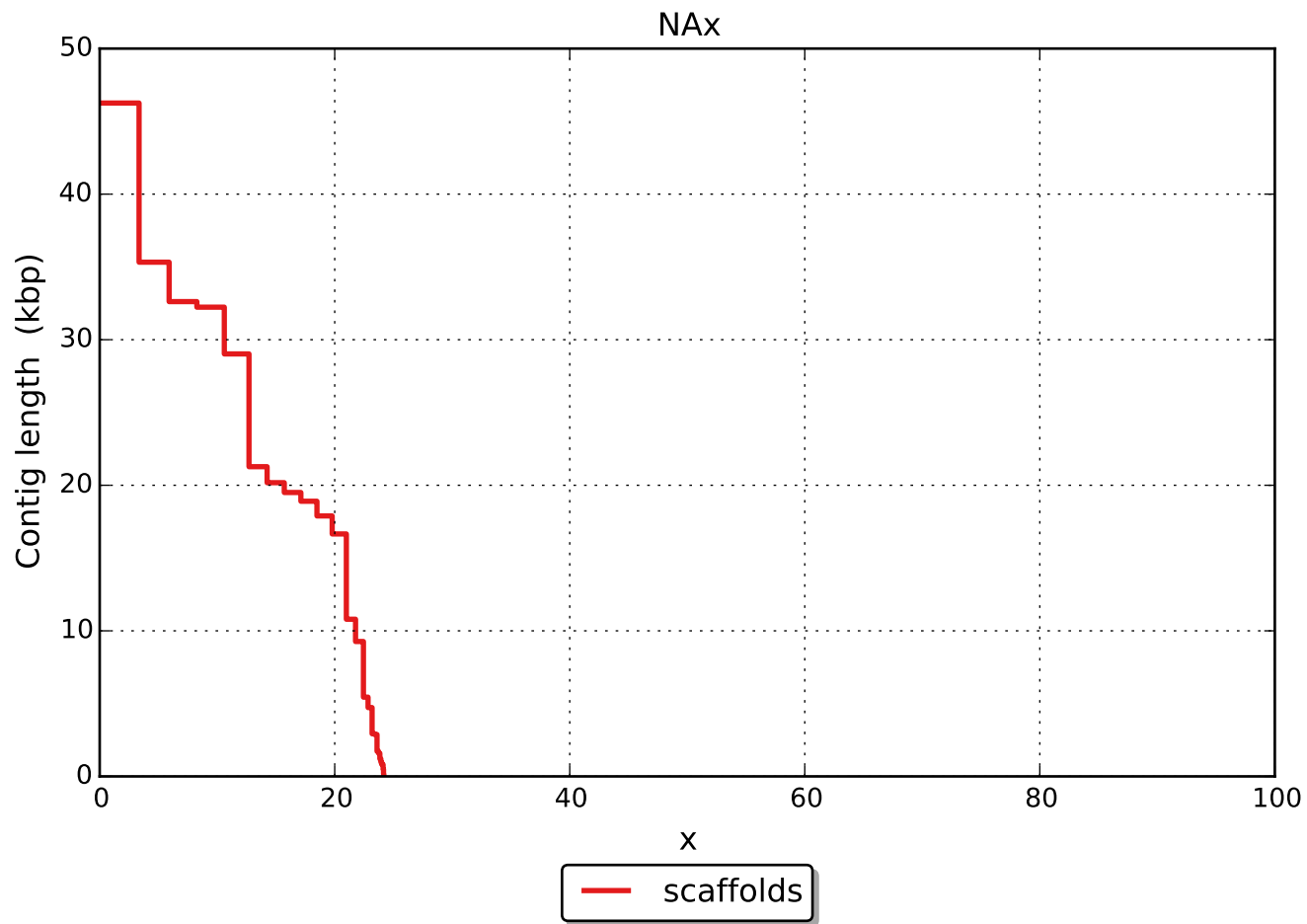
GC content





Cumulative length (aligned contigs)





NGAx

