

Report

	scaffolds
# contigs (≥ 1000 bp)	7
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	14460
Total length (≥ 5000 bp)	5687
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	26
Largest contig	5687
Total length	25592
Reference length	4641652
GC (▼)	53.12
Reference GC (▼)	50.79
N50	1268
N75	604
L50	6
L75	14
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	8583
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	40
Genome fraction (▼)	0.544
Duplication ratio	1.013
# N's per 100 kbp	1137.07
# mismatches per 100 kbp	435.99
# indels per 100 kbp	67.38
Largest alignment	5494
NA50	1039
NGA50	-
NA75	564
LA50	7
LA75	16

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

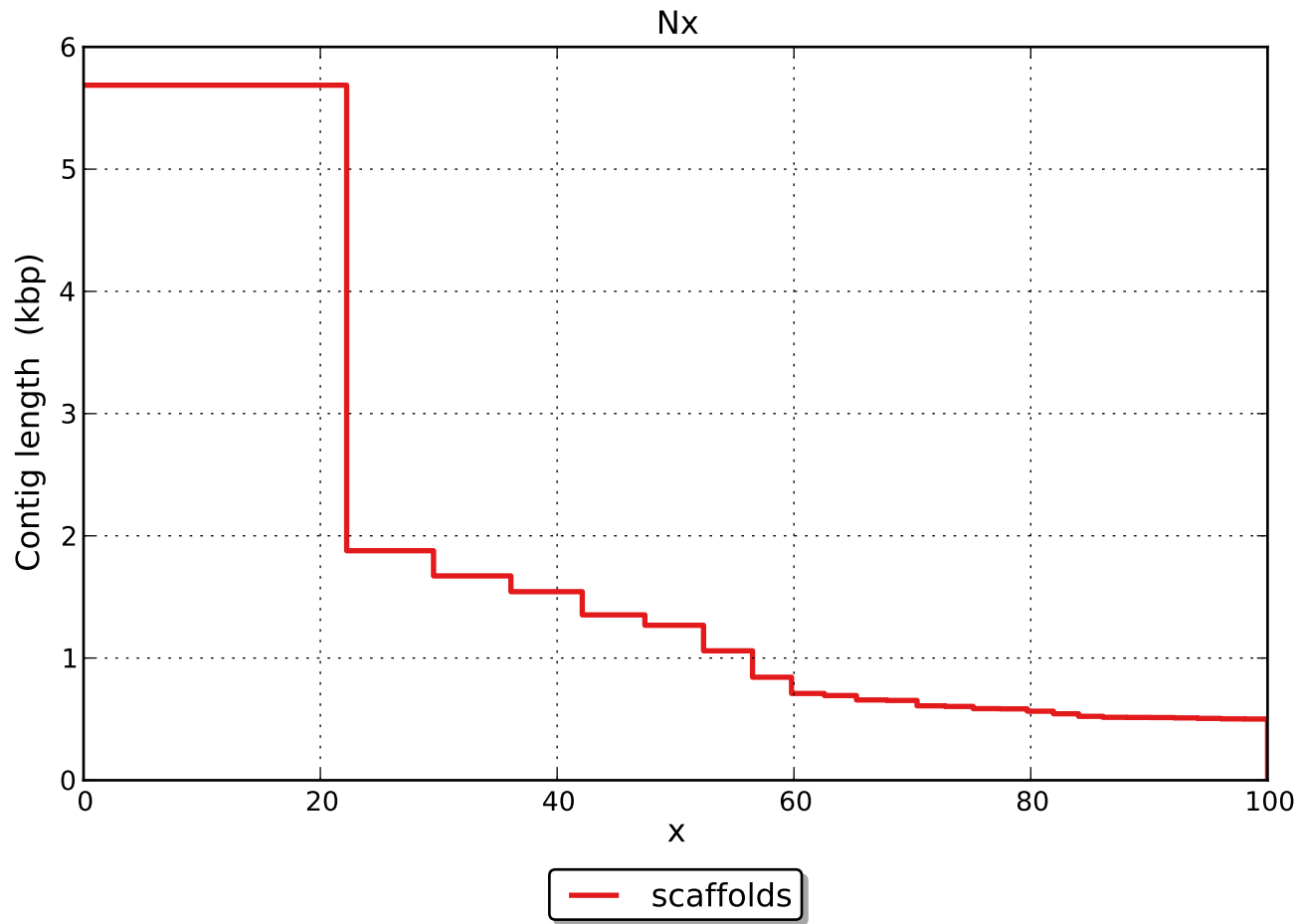
	scaffolds
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	8583
# local misassemblies	0
# mismatches	110
# indels	17
# short indels	12
# long indels	5
Indels length	104

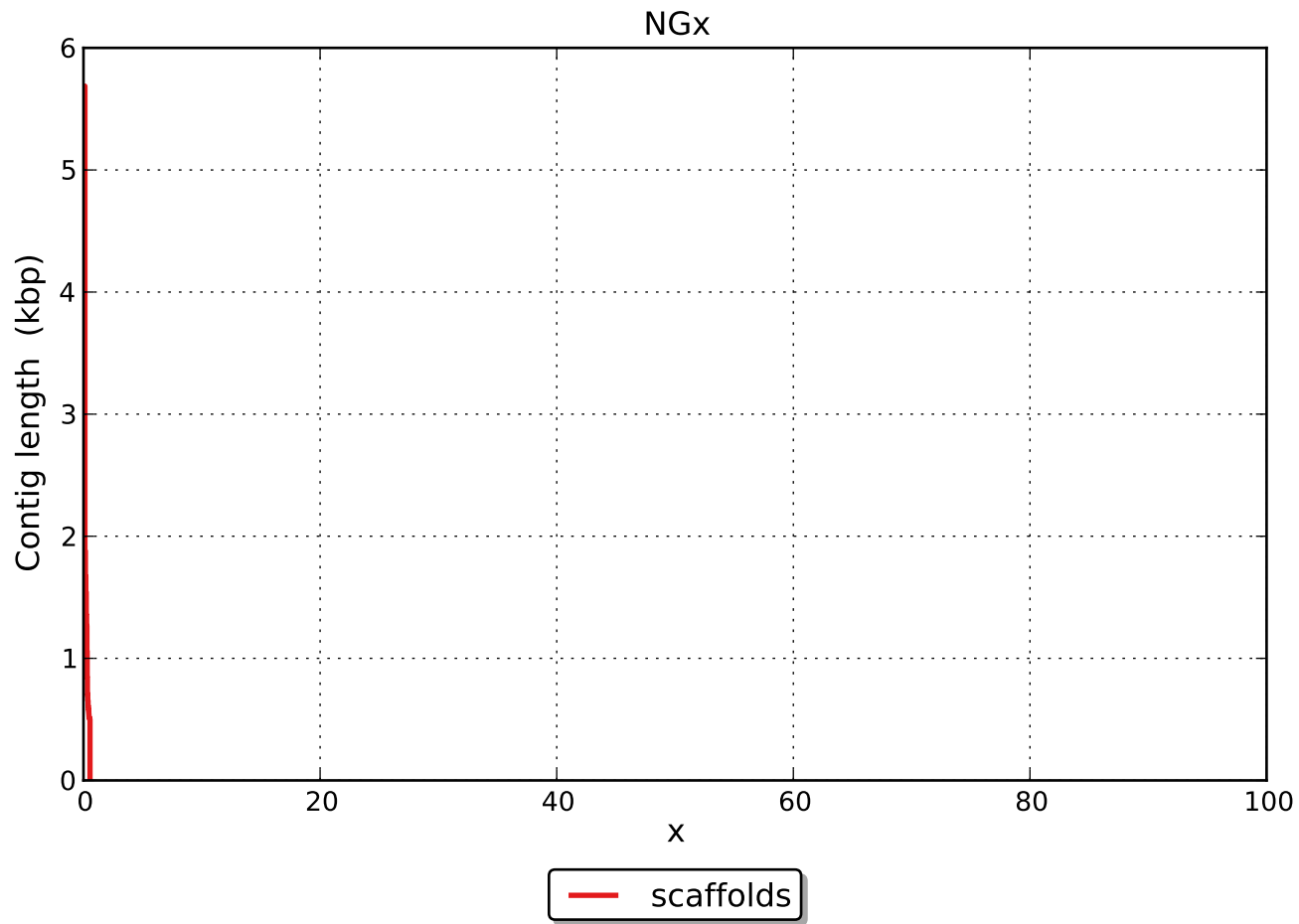
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

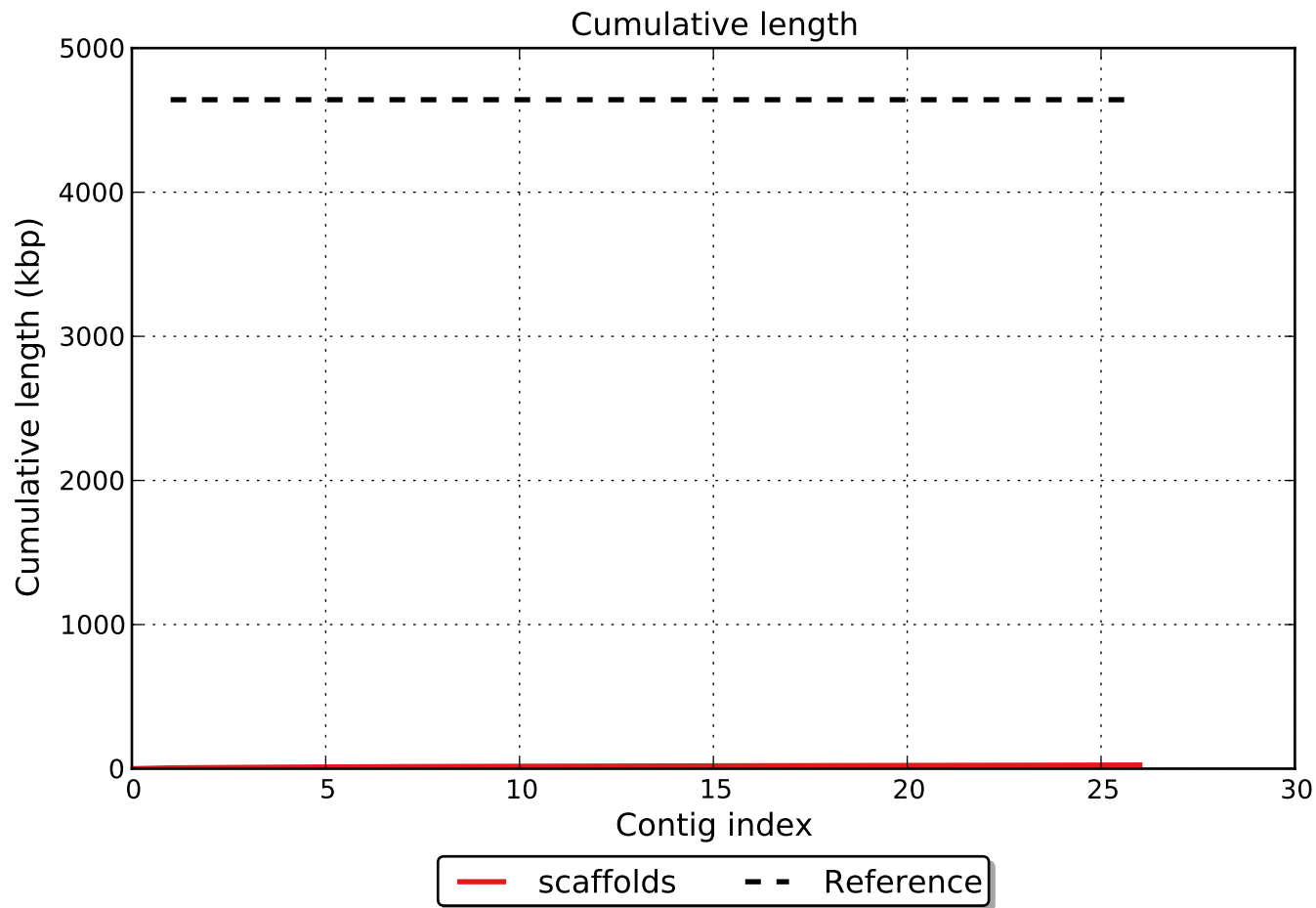
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	40
# N's	291

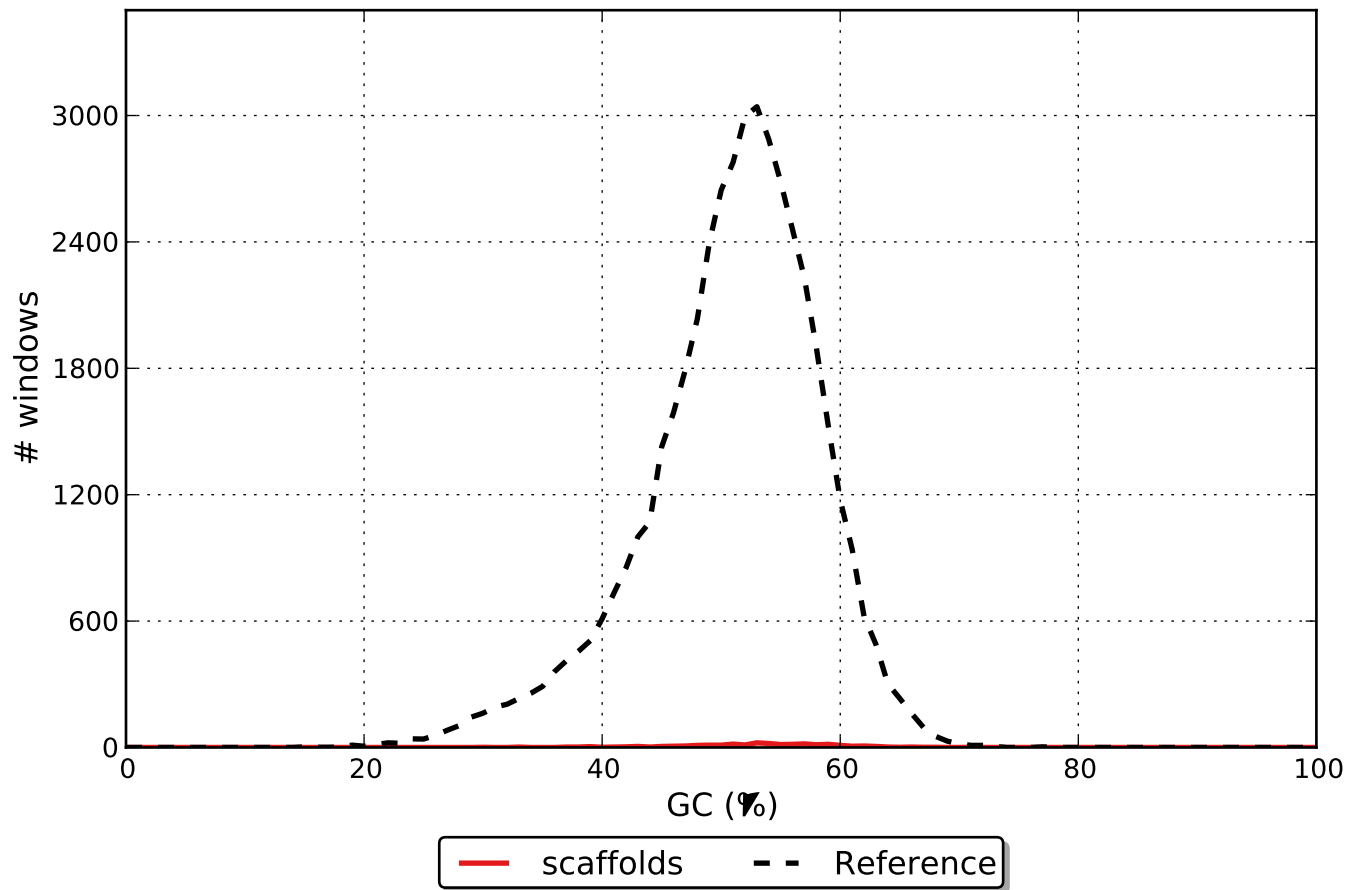
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



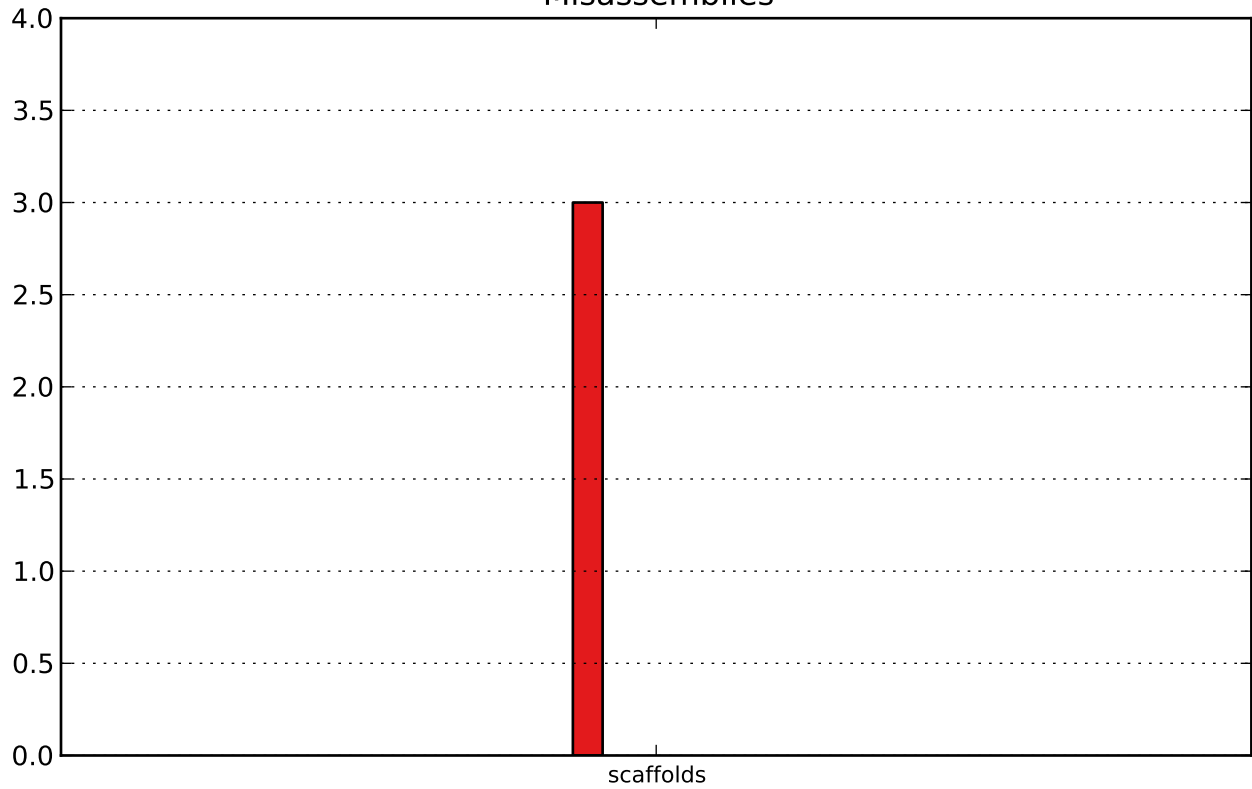




GC content

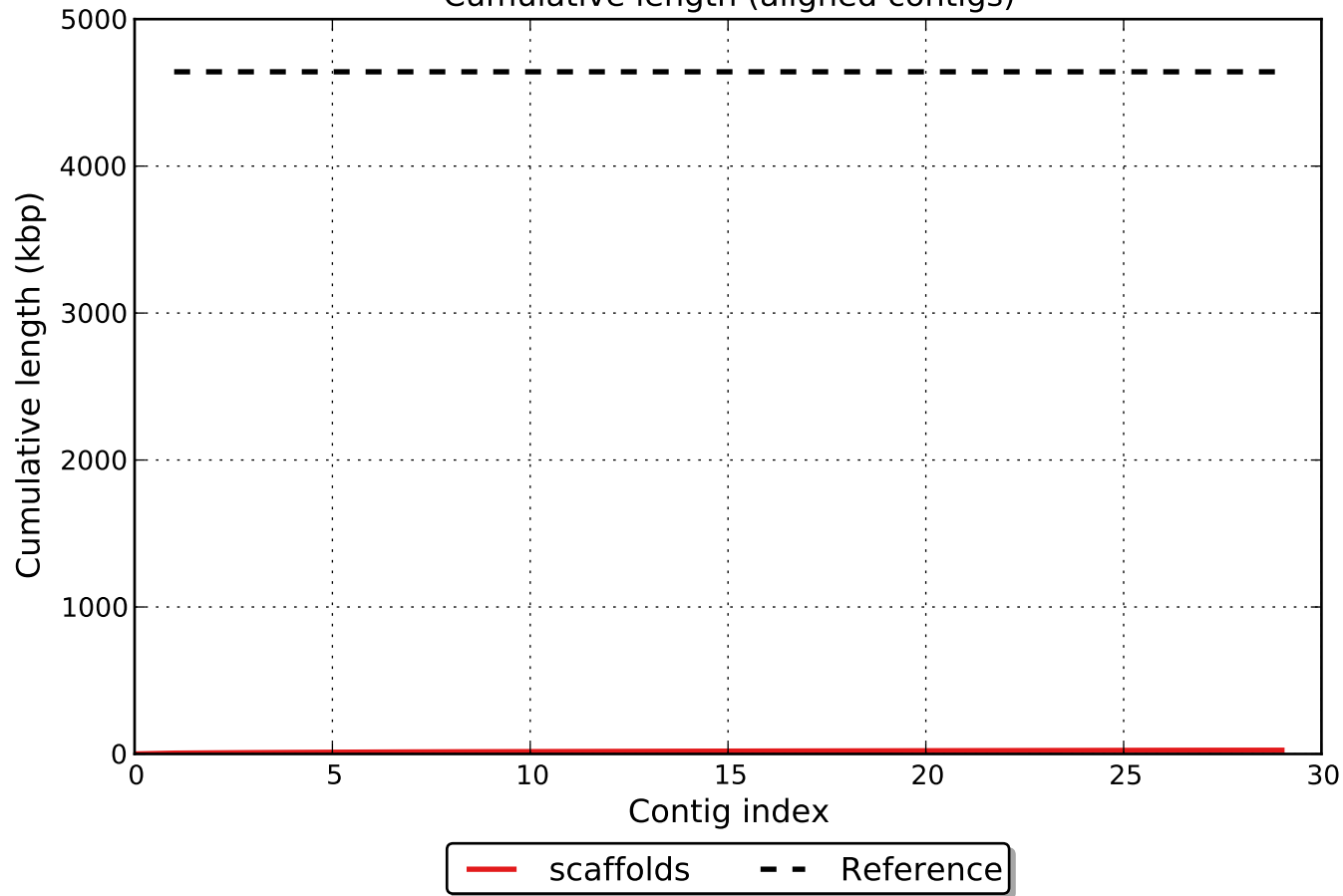


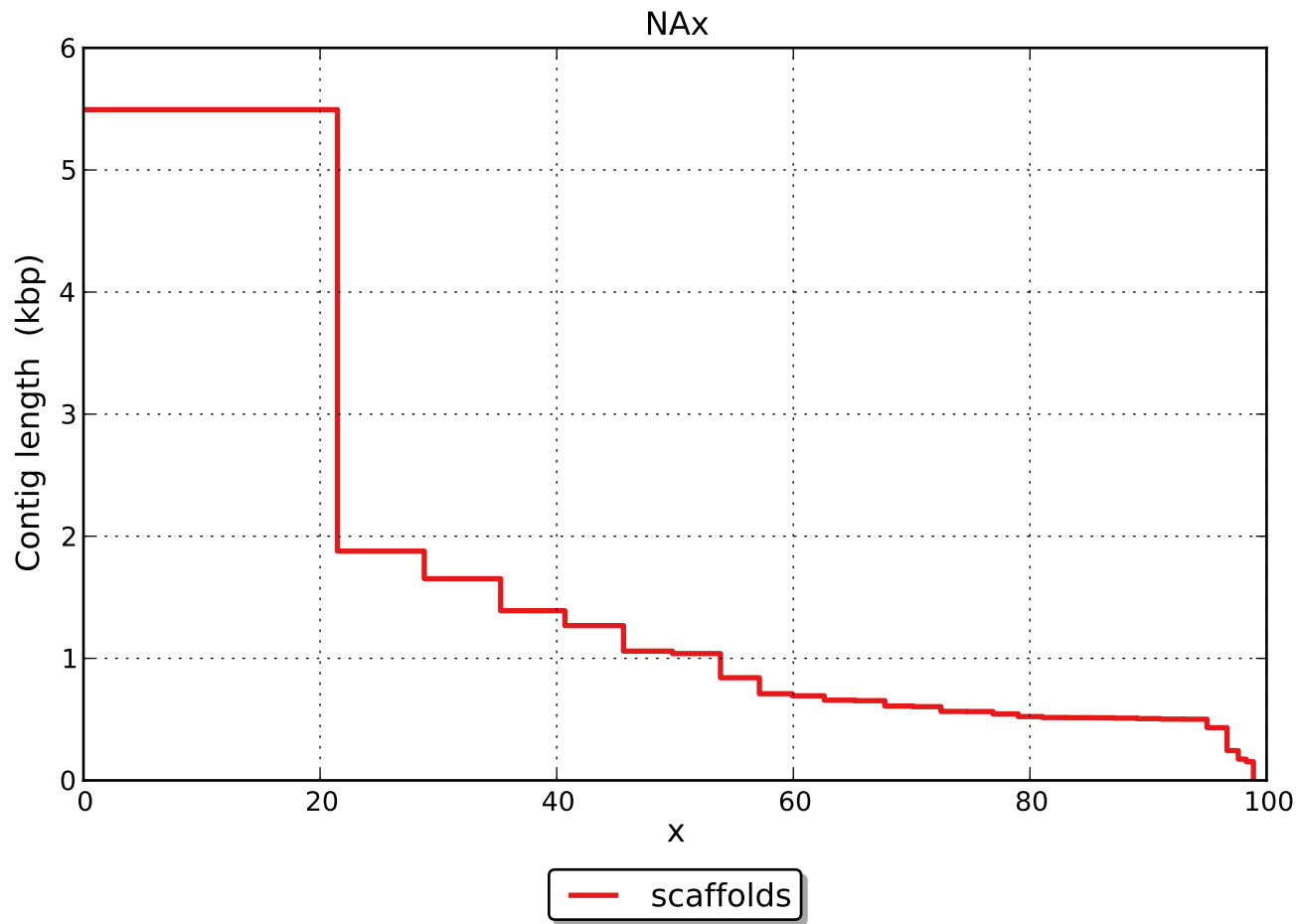
Misassemblies



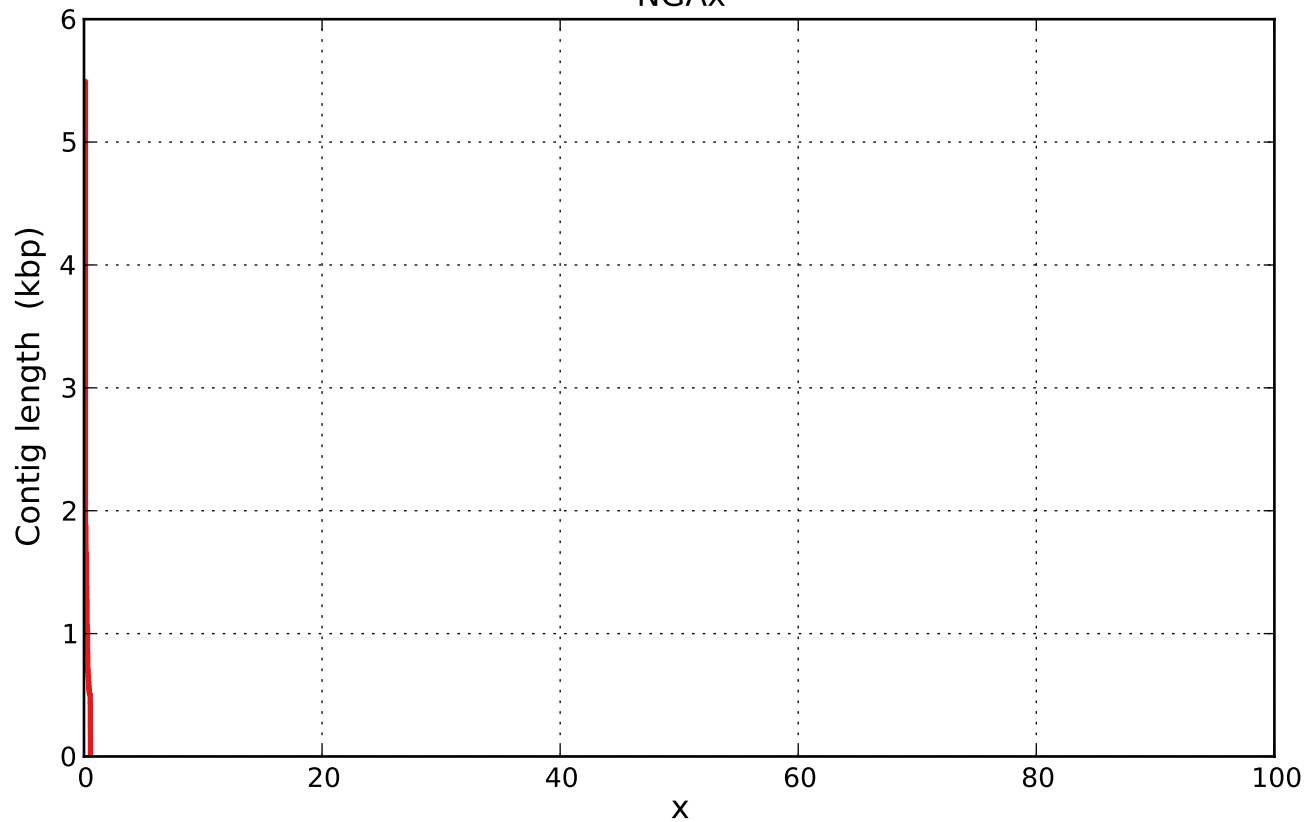
relocations

Cumulative length (aligned contigs)





NGAx



— scaffolds