Report

	scaffolds
# contigs (>= 1000 bp)	77
# contigs (>= 5000 bp)	63
# contigs (>= 10000 bp)	50
# contigs (>= 25000 bp)	32
# contigs (>= 50000 bp)	15
Total length (>= 1000 bp)	2250698
Total length (>= 5000 bp)	2211315
Total length (>= 10000 bp)	2120359
Total length (>= 25000 bp)	1849970
Total length (>= 50000 bp)	1206404
# contigs	83
Largest contig	148188
Total length	2255004
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.78
N50	54079
N75	34034
L50	14
L75	27
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	475557
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	47.138
Duplication ratio	1.031
# N's per 100 kbp	163.59
# mismatches per 100 kbp	714.85
# indels per 100 kbp	1.19
Largest alignment	122264
NA50	48914
NGA50	-
NA75	32963
LA50	17
LA75	31

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

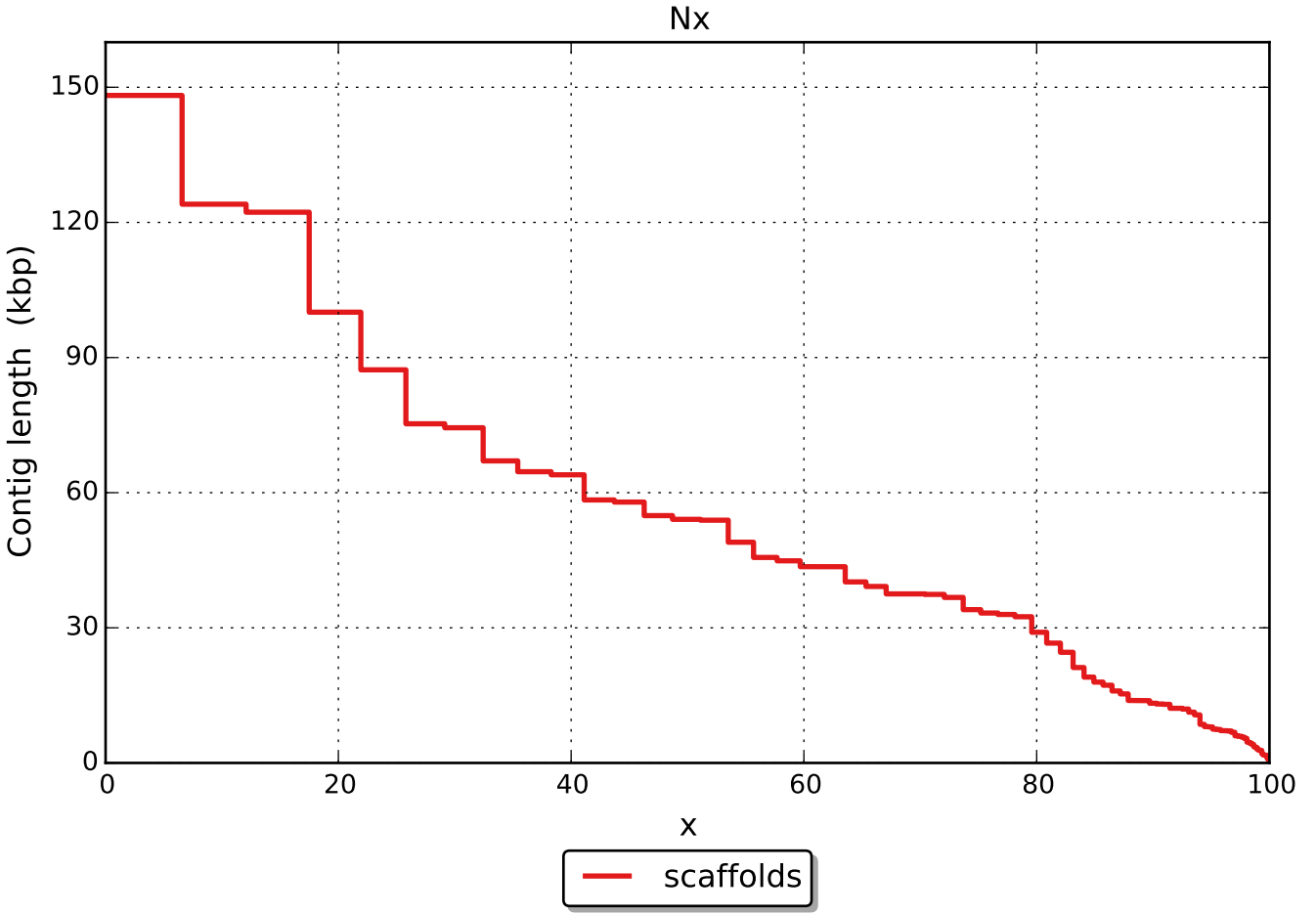
	scaffolds
# misassemblies	5
# relocations	4
# translocations	0
# inversions	1
# possibly misassembled contigs	2
# misassembled contigs	5
Misassembled contigs length	475557
# local misassemblies	4
# mismatches	15641
# indels	26
# short indels	15
# long indels	11
Indels length	626

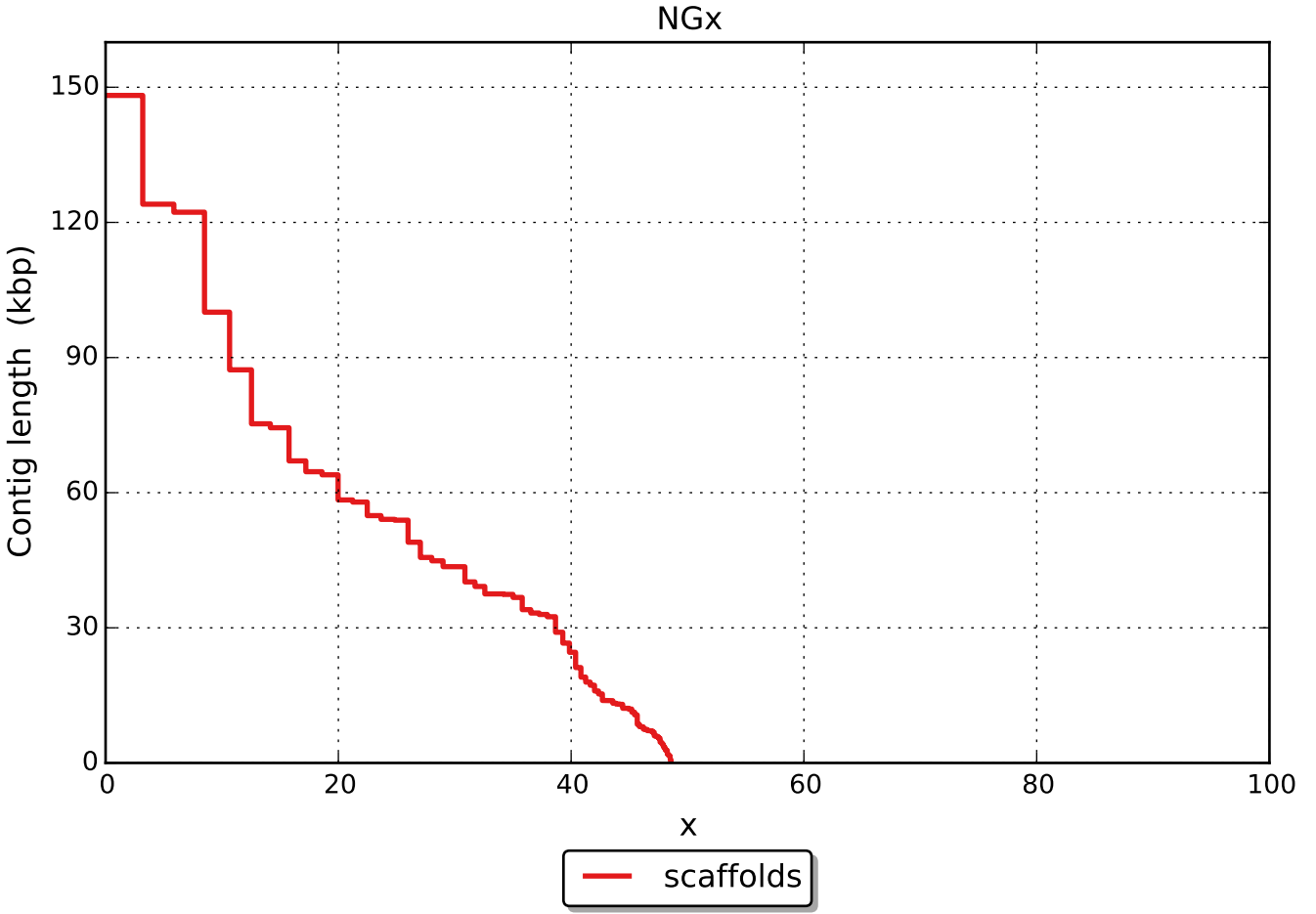
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

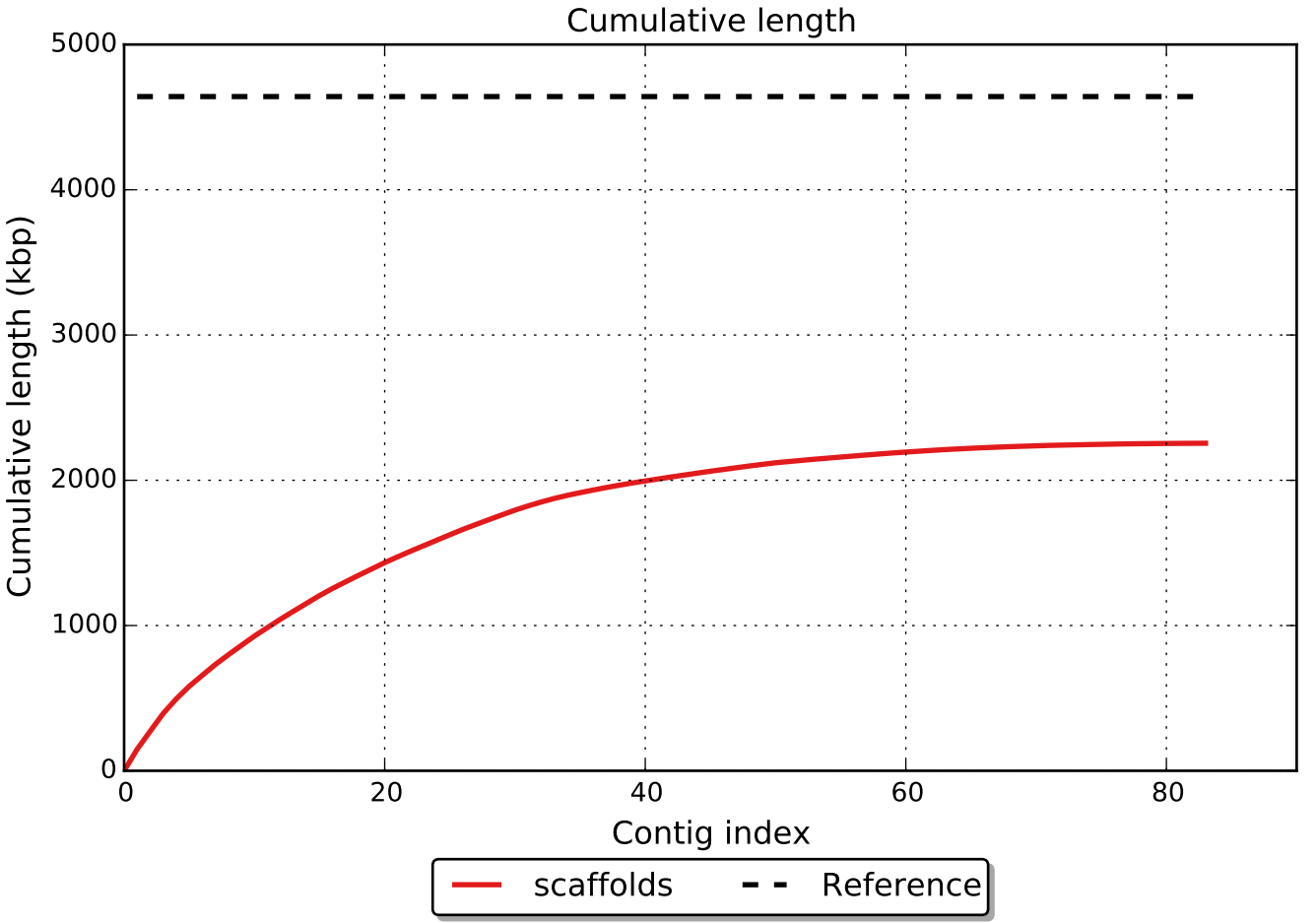
Unaligned report

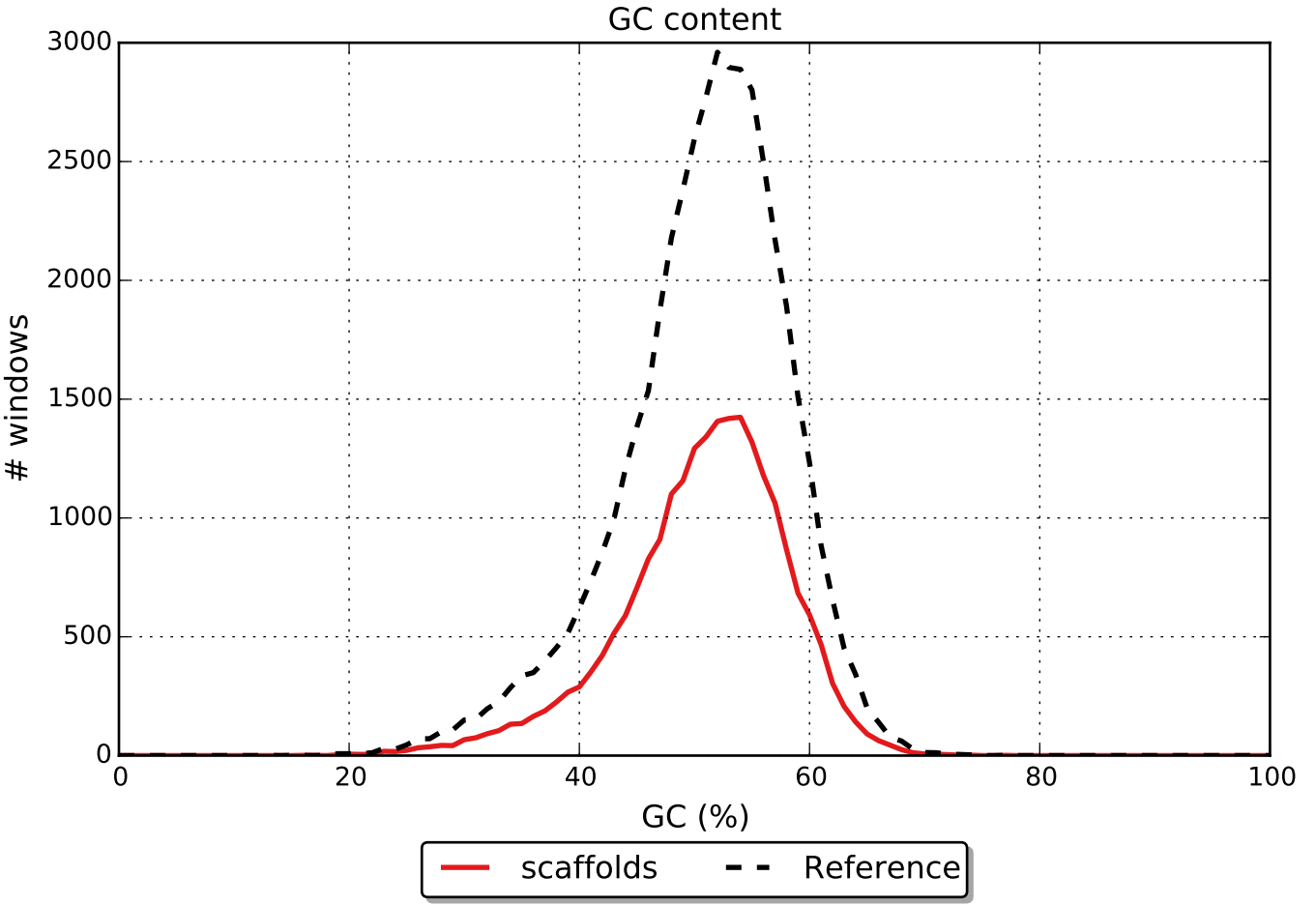
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	3689

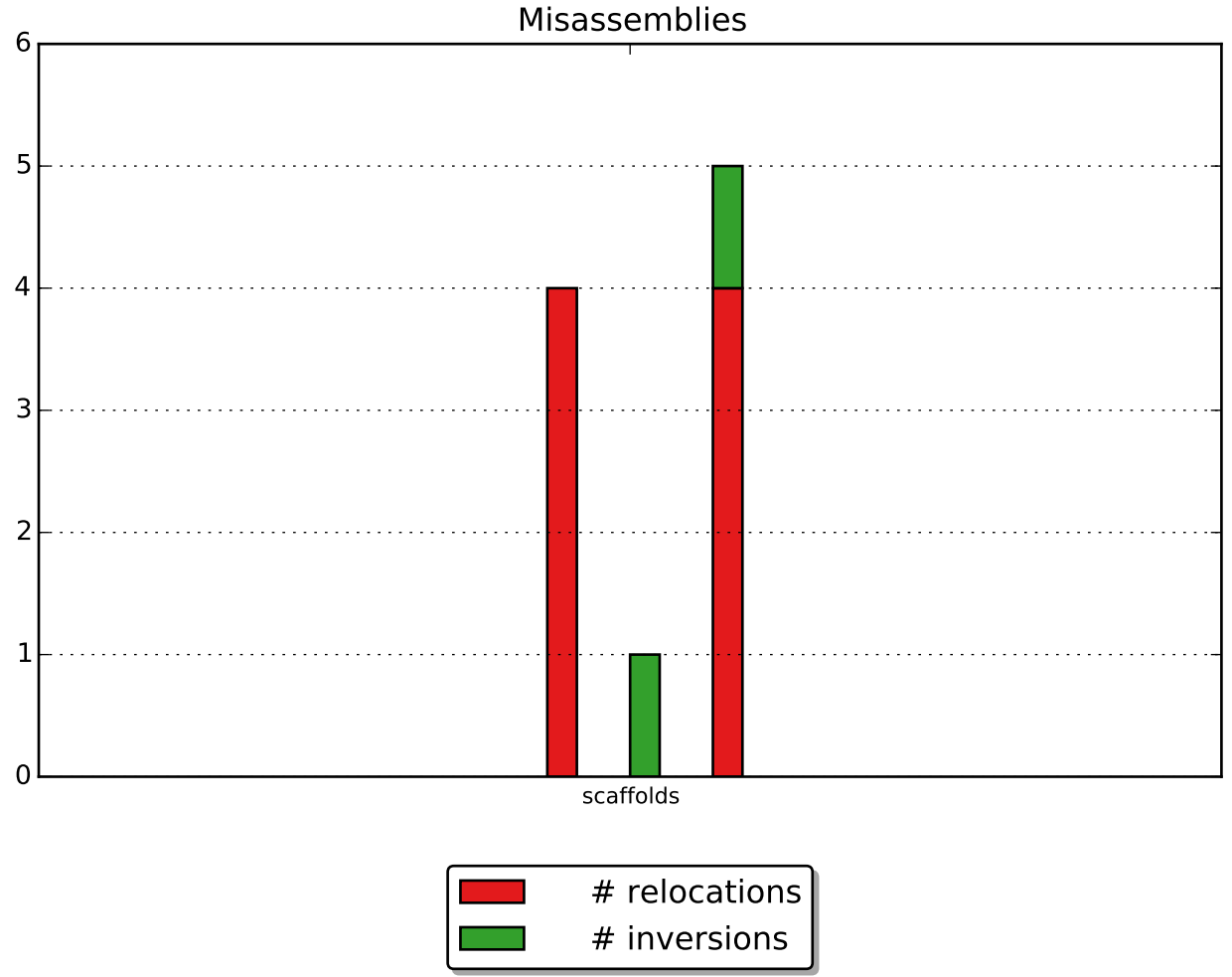
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

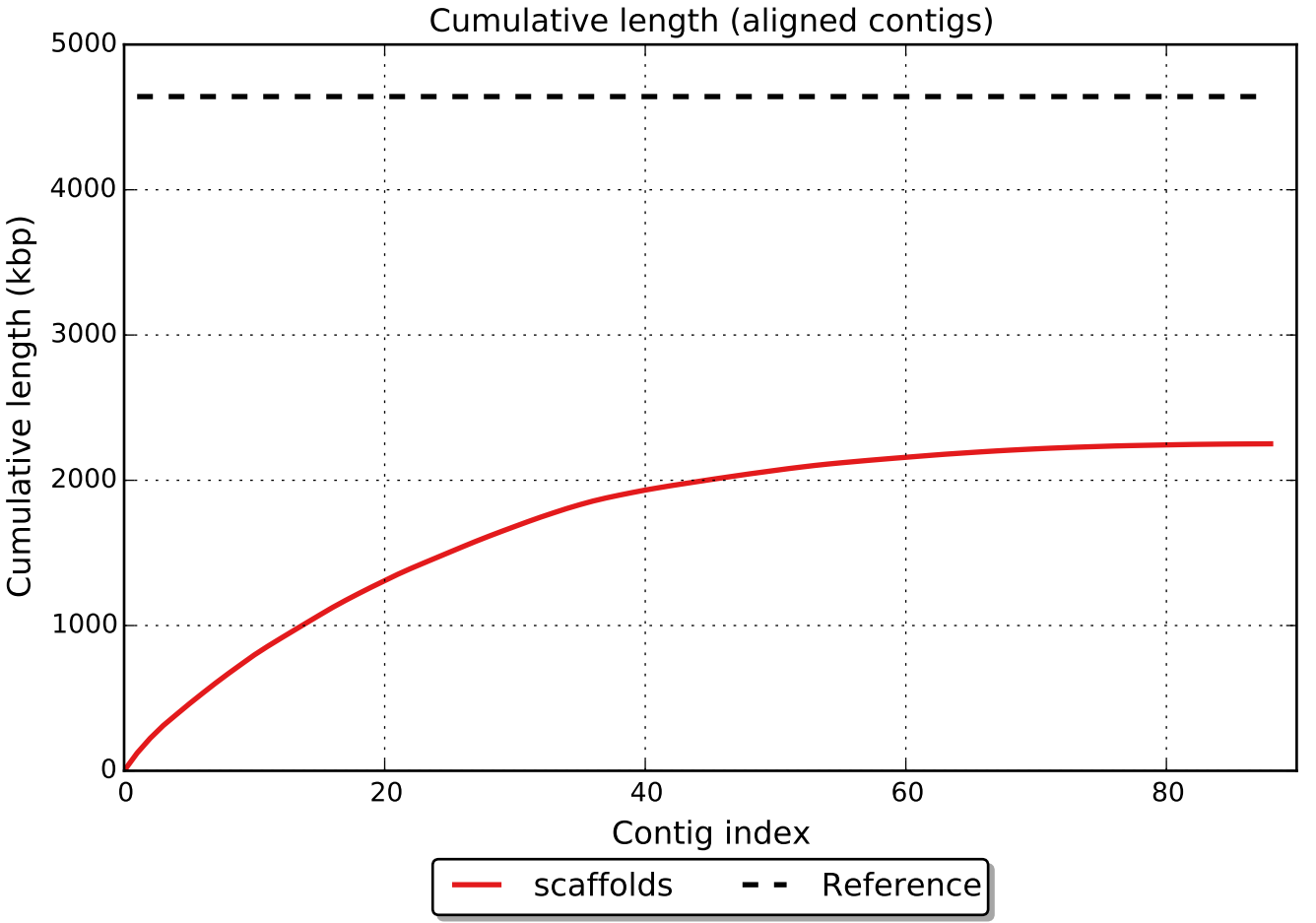

Nx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds

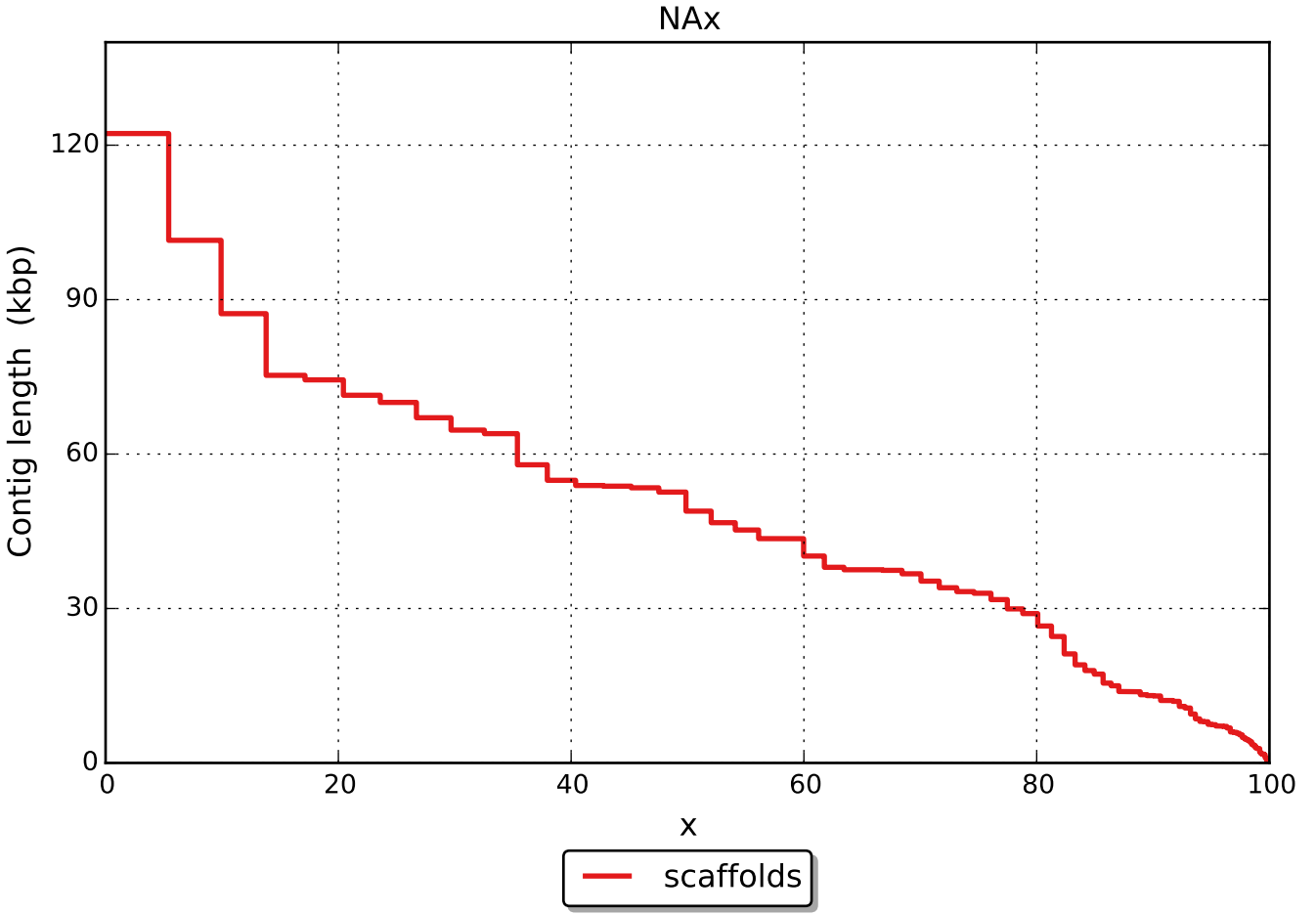

NGx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds

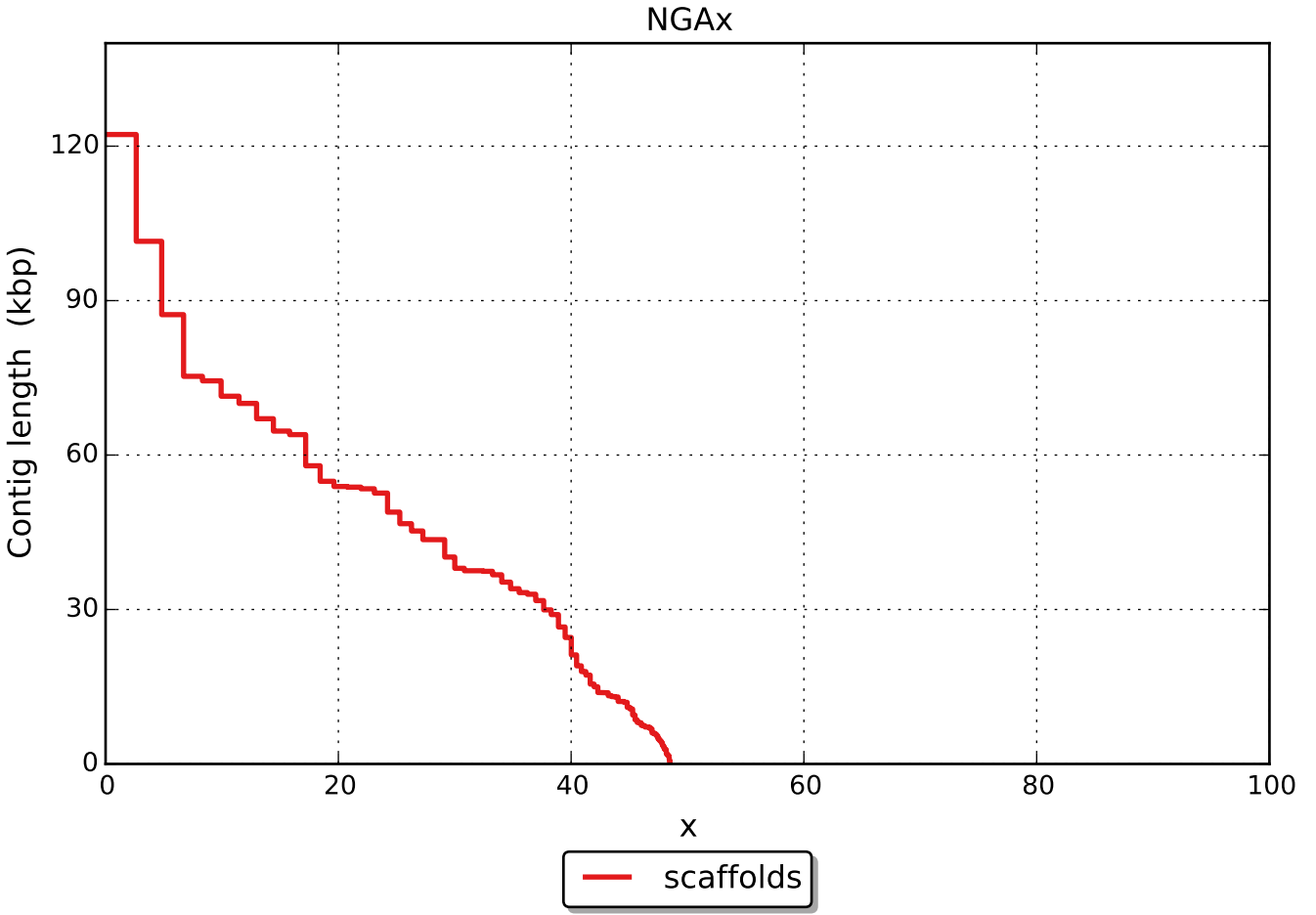

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
20
40
60
80
Contig index
scaffolds
Reference


GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
scaffolds
Reference


Misassemblies
6
5
4
3
2
1
0
scaffolds
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds