Report

	scaffolds
# contigs (>= 1000 bp)	982
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1547021
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2345
Largest contig	4985
Total length	2520187
Reference length	4641652
GC (%)	50.69
Reference GC (%)	50.79
N50	1180
NG50	594
N75	819
L50	718
LG50	1978
L75	1362
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	17085
# local misassemblies	1
# unaligned contigs	0 + 22 part
Unaligned length	12184
Genome fraction (%)	53.792
Duplication ratio	1.004
# N's per 100 kbp	734.99
# mismatches per 100 kbp	416.36
# indels per 100 kbp	47.18
Largest alignment	4985
NA50	1162
NGA50	581
NA75	802
LA50	729
LGA50	2013
LA75	1385

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

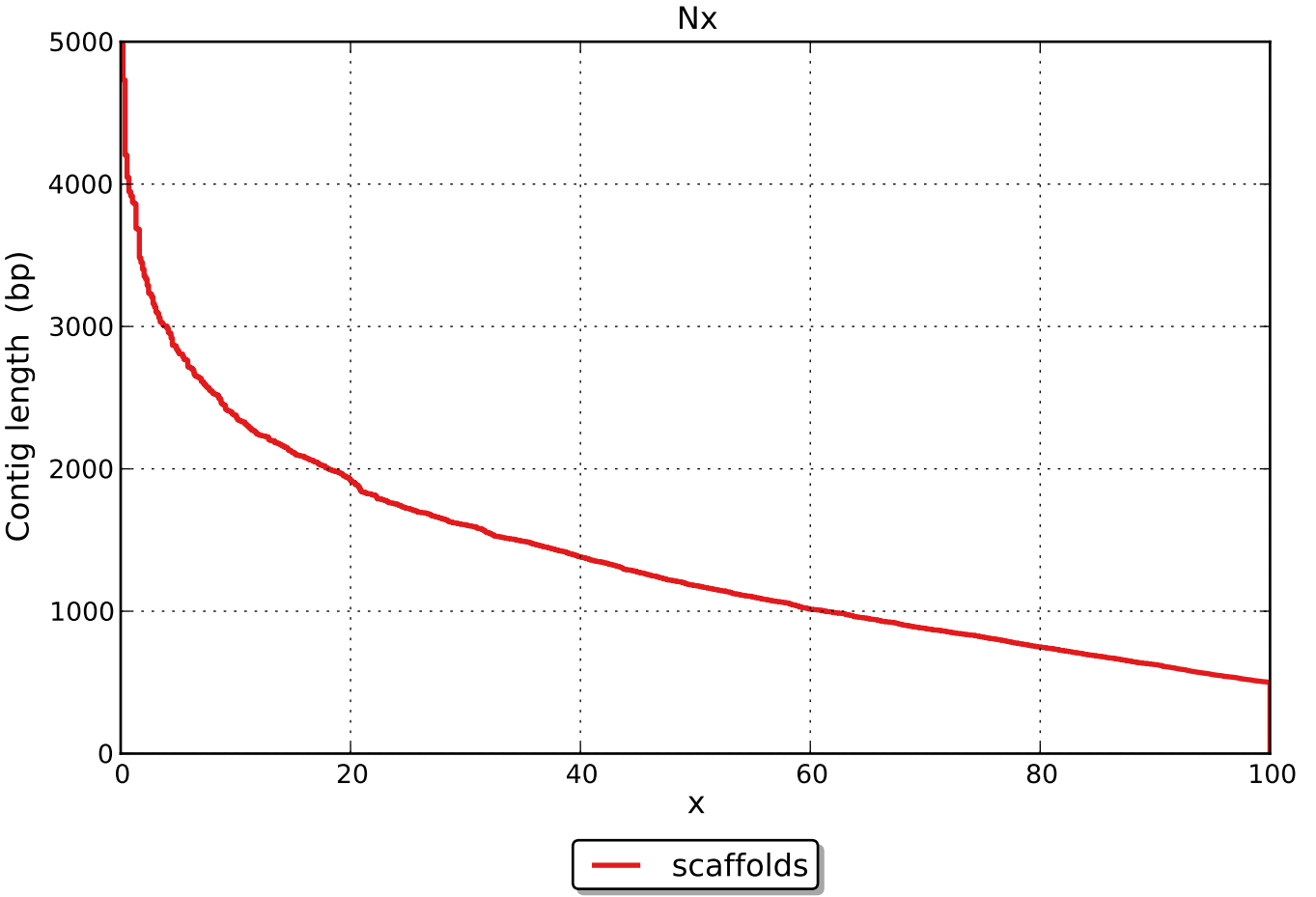
	scaffolds
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# possibly misassembled contigs	6
# misassembled contigs	8
Misassembled contigs length	17085
# local misassemblies	1
# mismatches	10396
# indels	1178
# short indels	601
# long indels	577
Indels length	9743

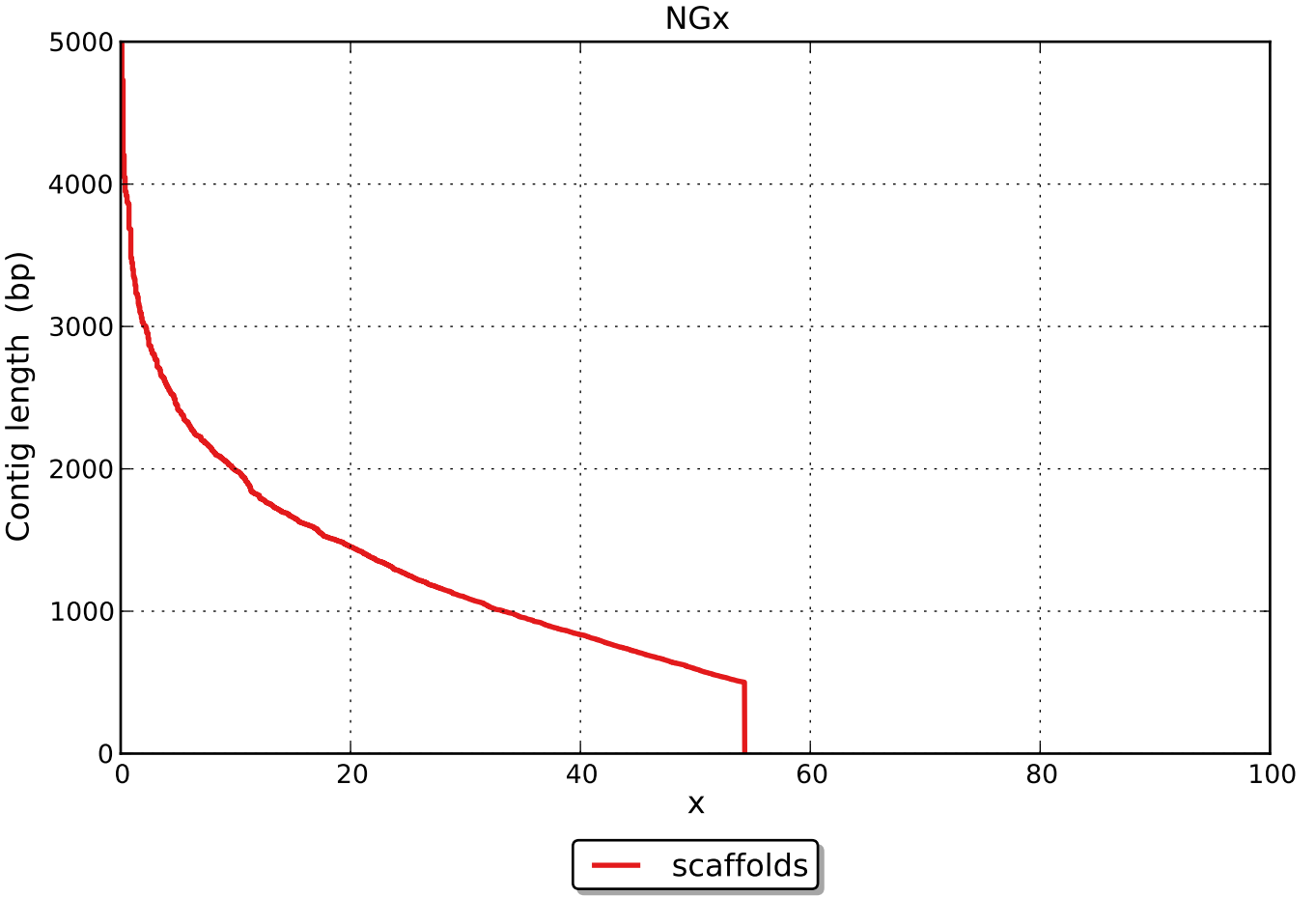
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

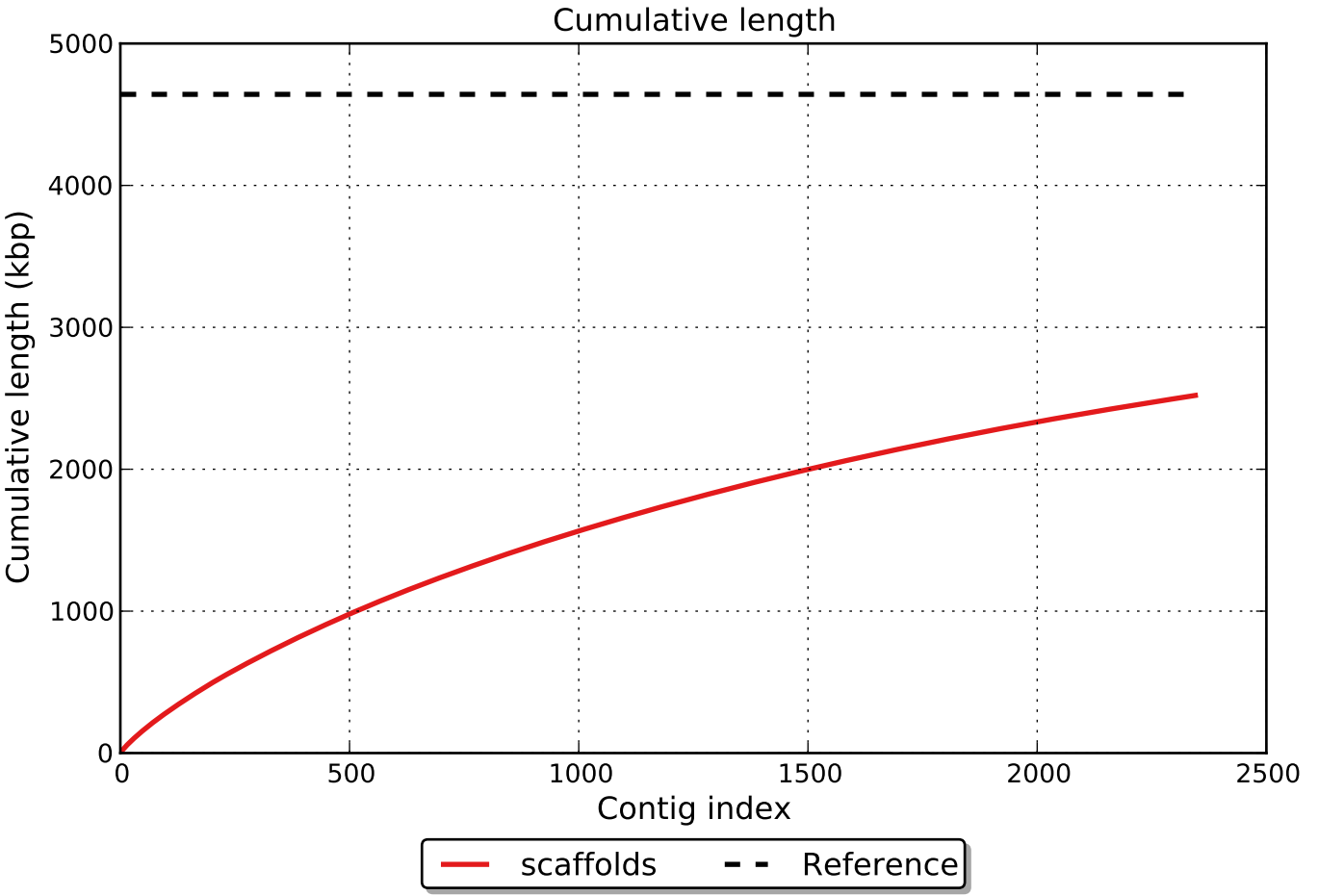
Unaligned report

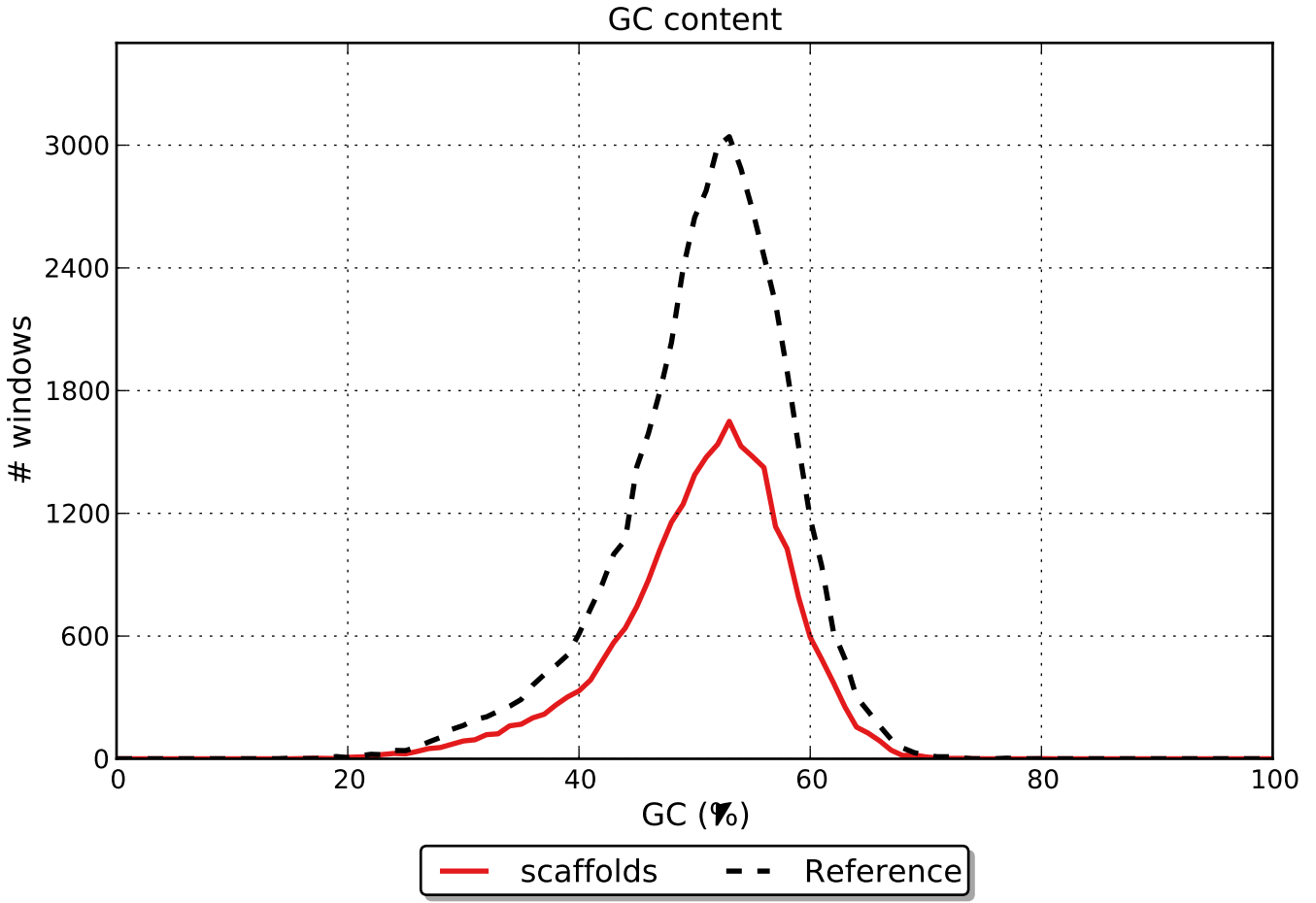
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	22
# with misassembly	0
# both parts are significant	6
Partially unaligned length	12184
# N's	18523

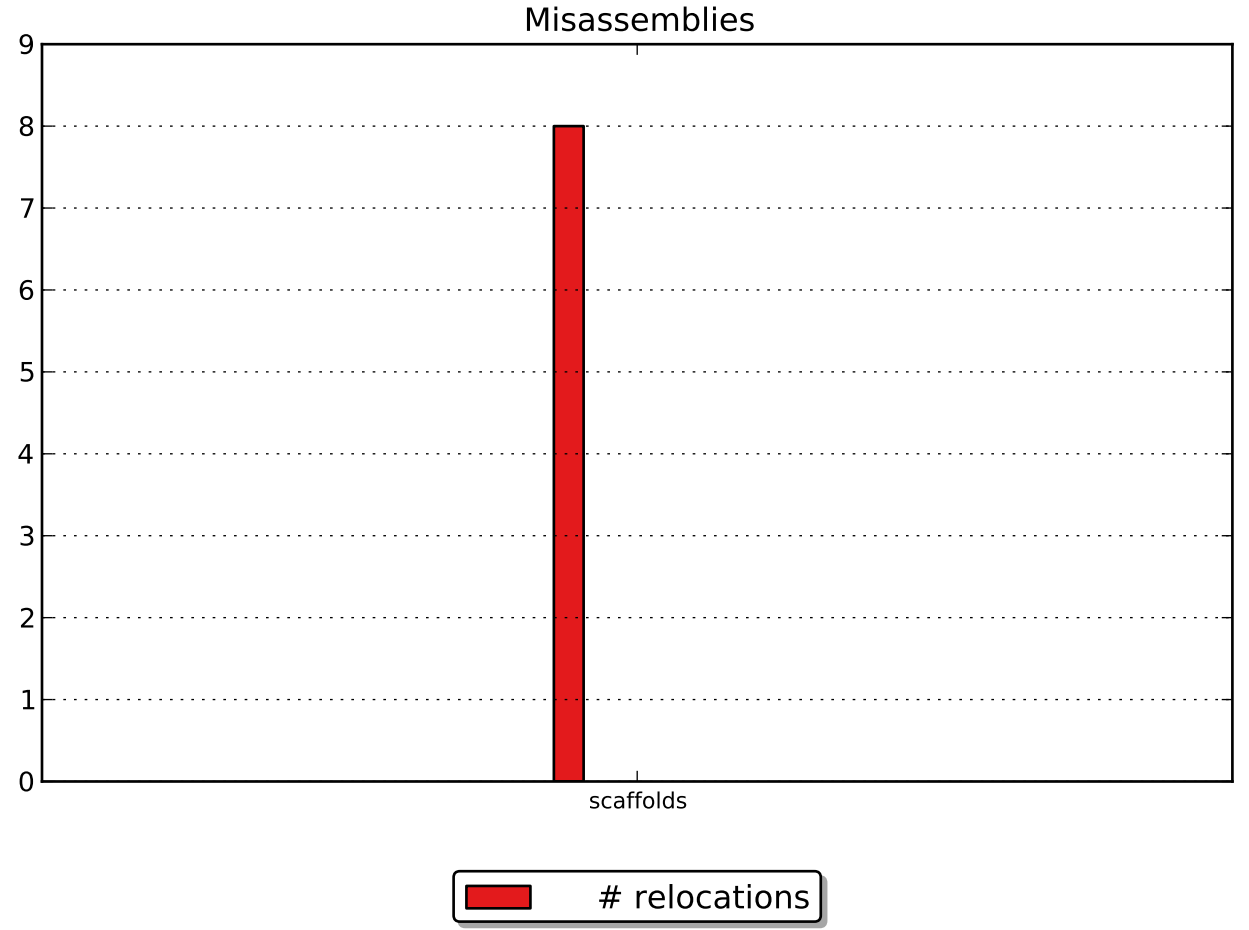
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

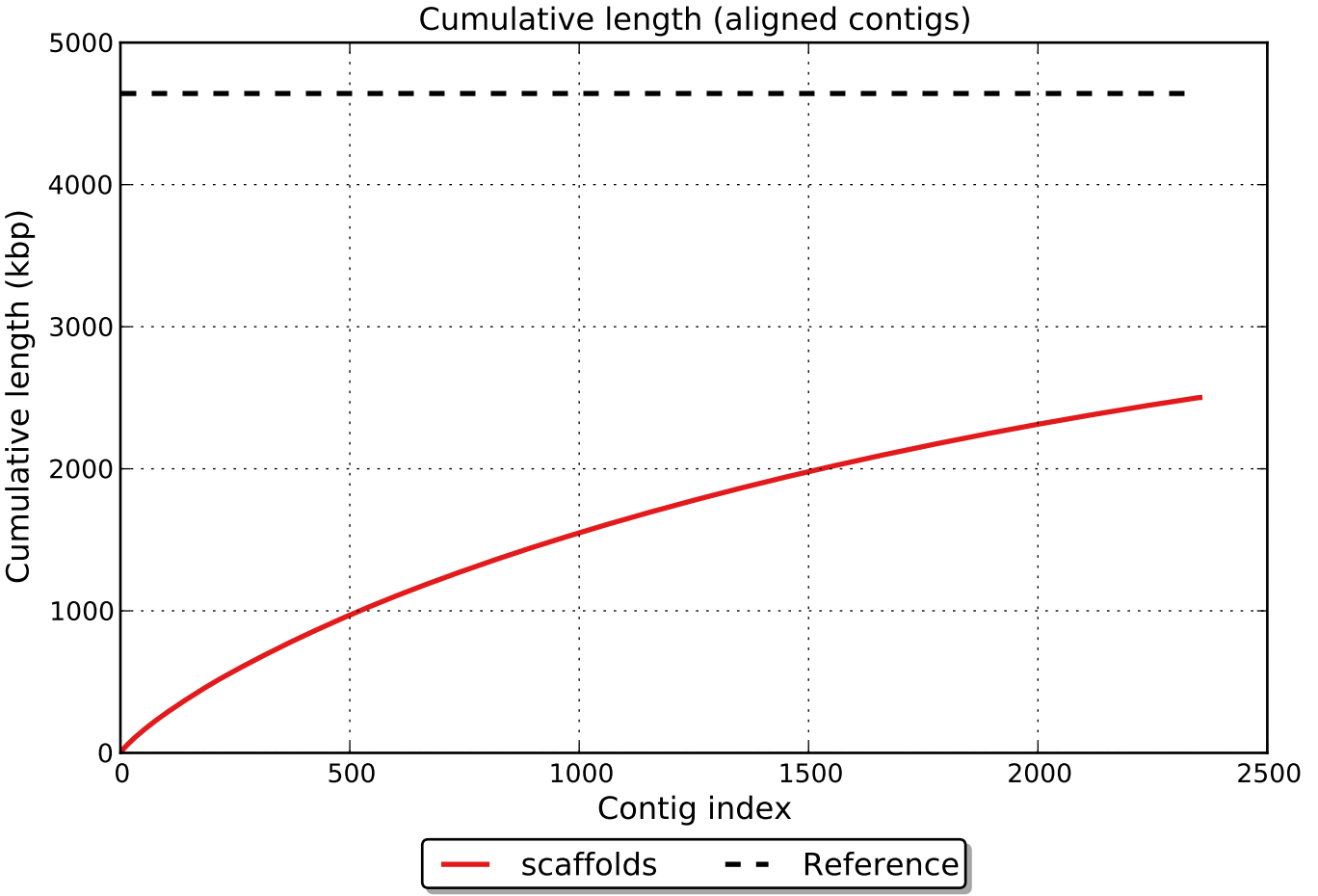

Nx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
scaffolds

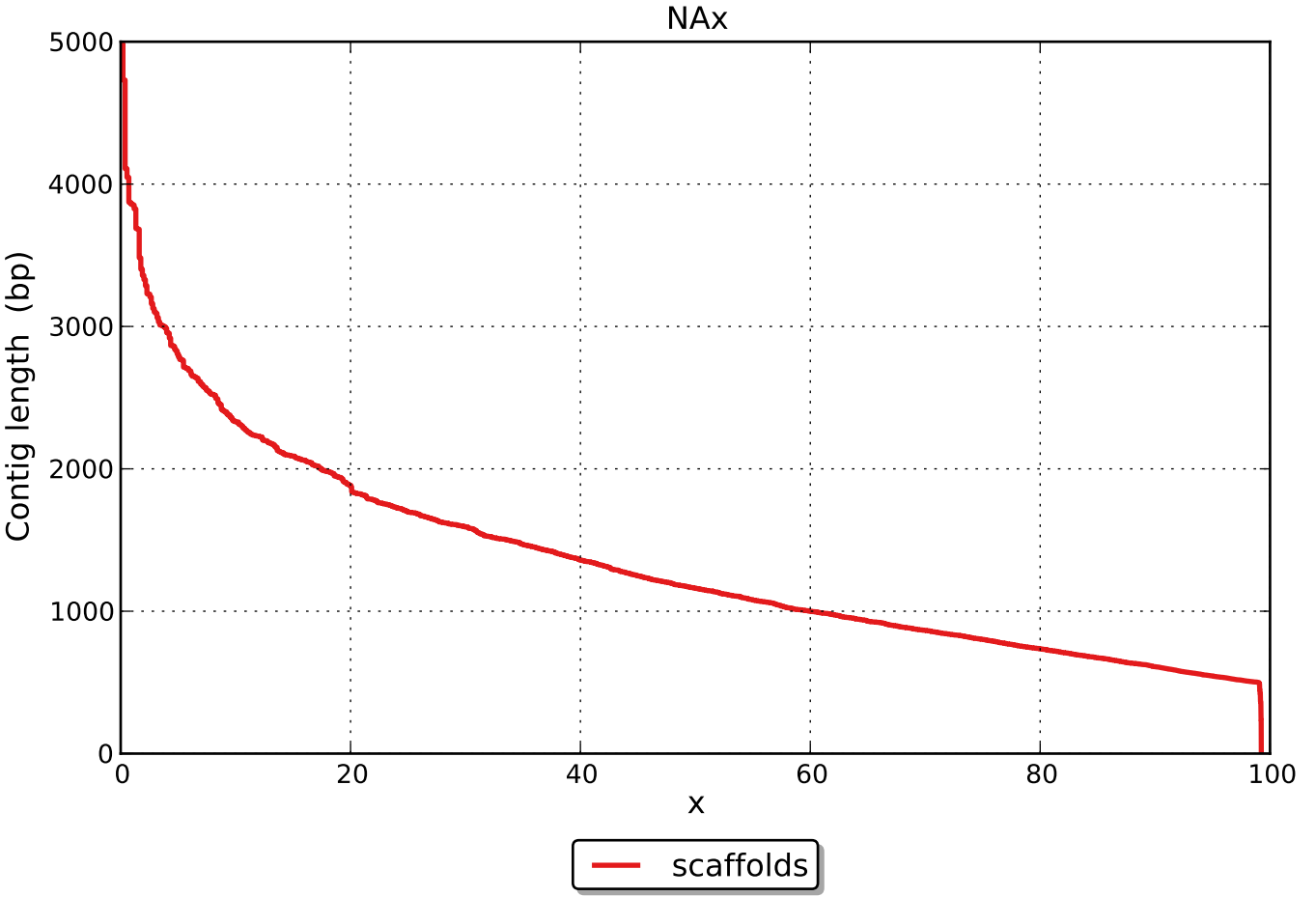

NGx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
scaffolds

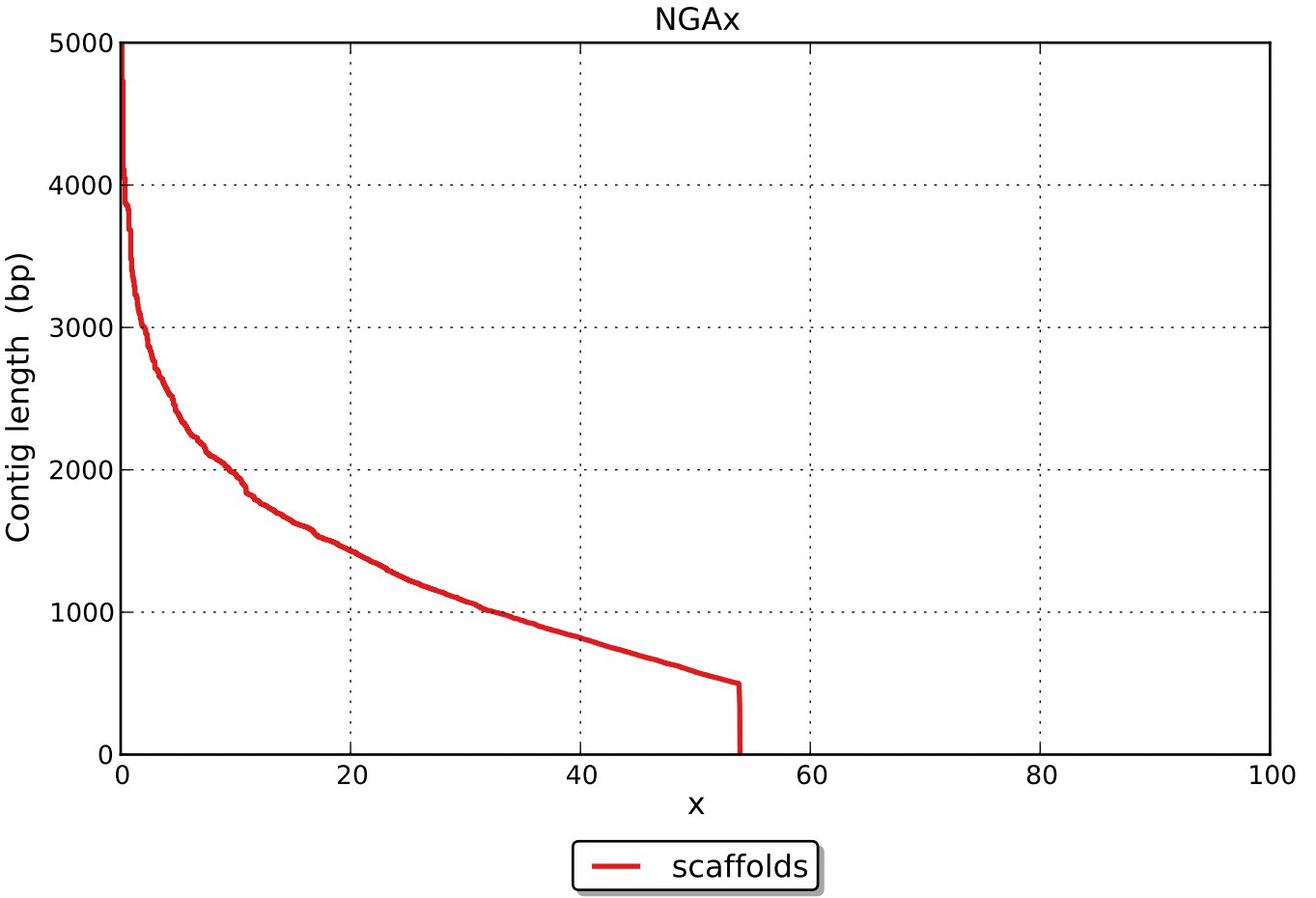

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
scaffolds
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
scaffolds
Reference


Misassemblies
9
8
7
6
5
4
3
2
1
0
scaffolds
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
scaffolds
Reference


NAx
Contig length (bp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (bp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
scaffolds