Report

	scaffolds
# contigs (>= 1000 bp)	800
# contigs (>= 5000 bp)	325
# contigs (>= 10000 bp)	102
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4262469
Total length (>= 5000 bp)	2960601
Total length (>= 10000 bp)	1385446
Total length (>= 25000 bp)	66428
Total length (>= 50000 bp)	0
# contigs	913
Largest contig	37682
Total length	4344540
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	7401
NG50	6859
N75	4242
NG75	3712
L50	195
LG50	216
L75	389
LG75	446
# misassemblies	16
# misassembled contigs	15
Misassembled contigs length	86787
# local misassemblies	10
# unaligned contigs	0 + 2 part
Unaligned length	1528
Genome fraction (%)	93.360
Duplication ratio	1.002
# N's per 100 kbp	481.22
# mismatches per 100 kbp	166.82
# indels per 100 kbp	32.63
Largest alignment	37682
NA50	7226
NGA50	6813
NA75	4149
NGA75	3576
LA50	196
LGA50	217
LA75	395
LGA75	453

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

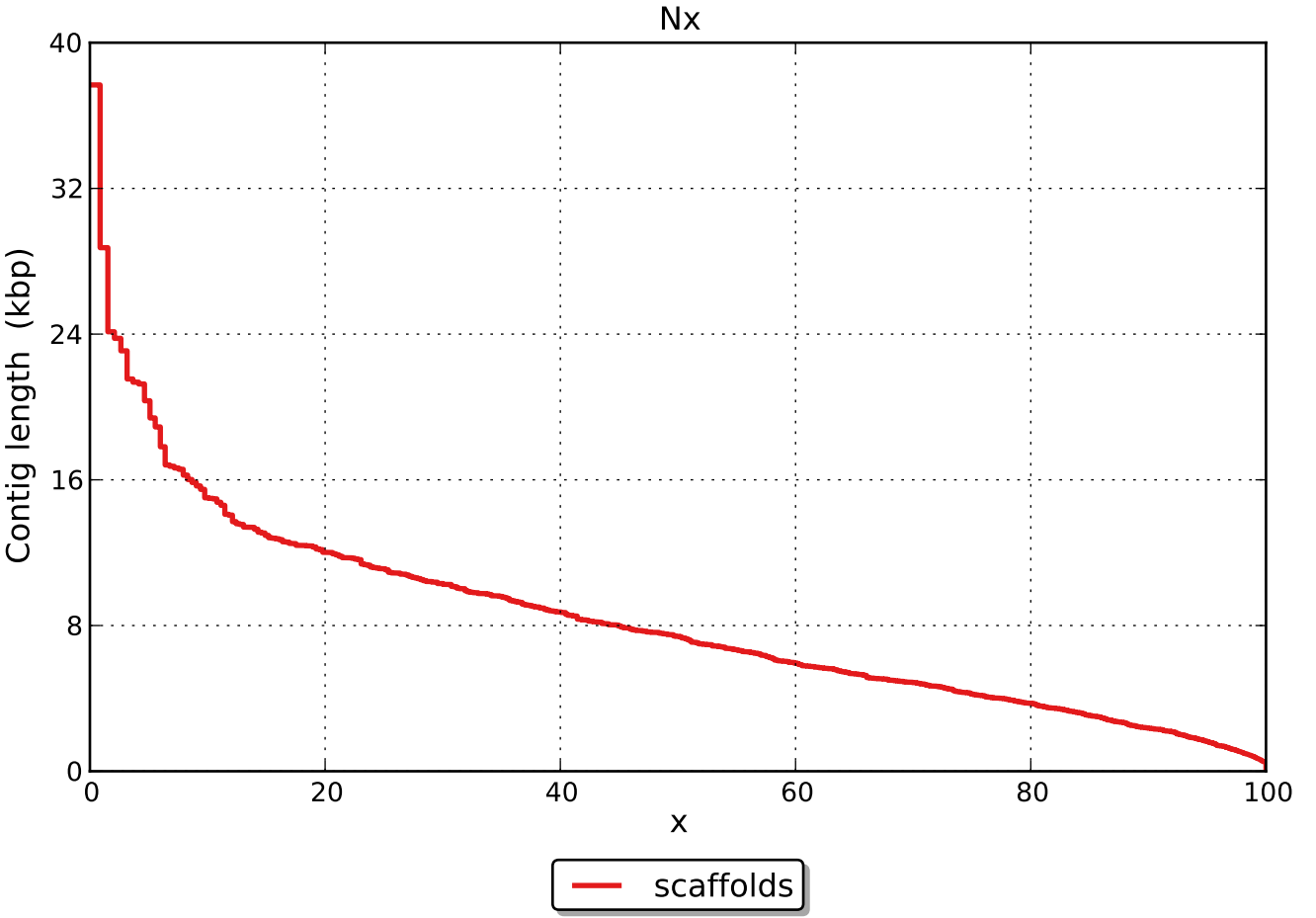
	scaffolds
# misassemblies	16
# relocations	16
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	15
Misassembled contigs length	86787
# local misassemblies	10
# mismatches	7229
# indels	1414
# short indels	738
# long indels	676
Indels length	11527

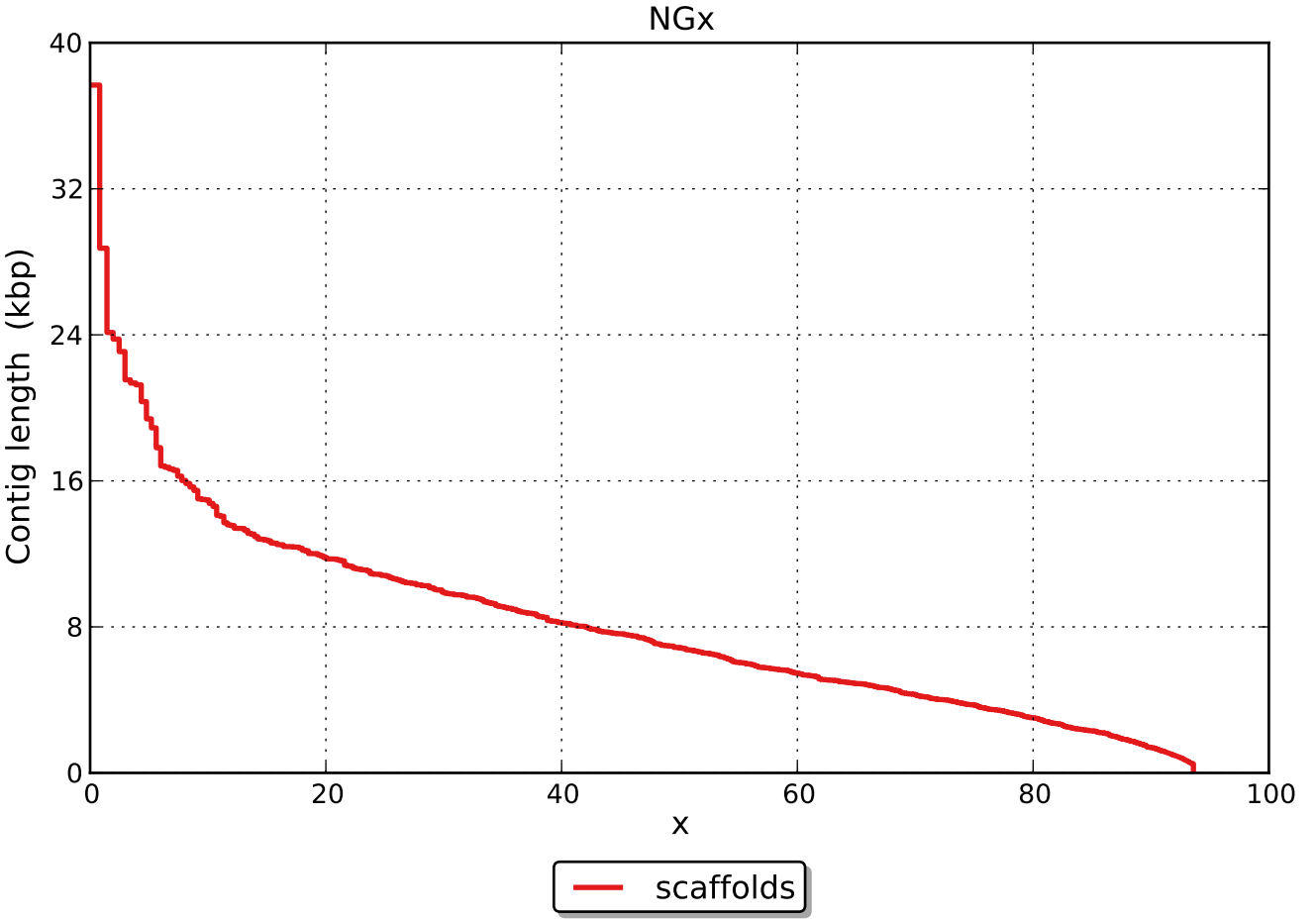
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

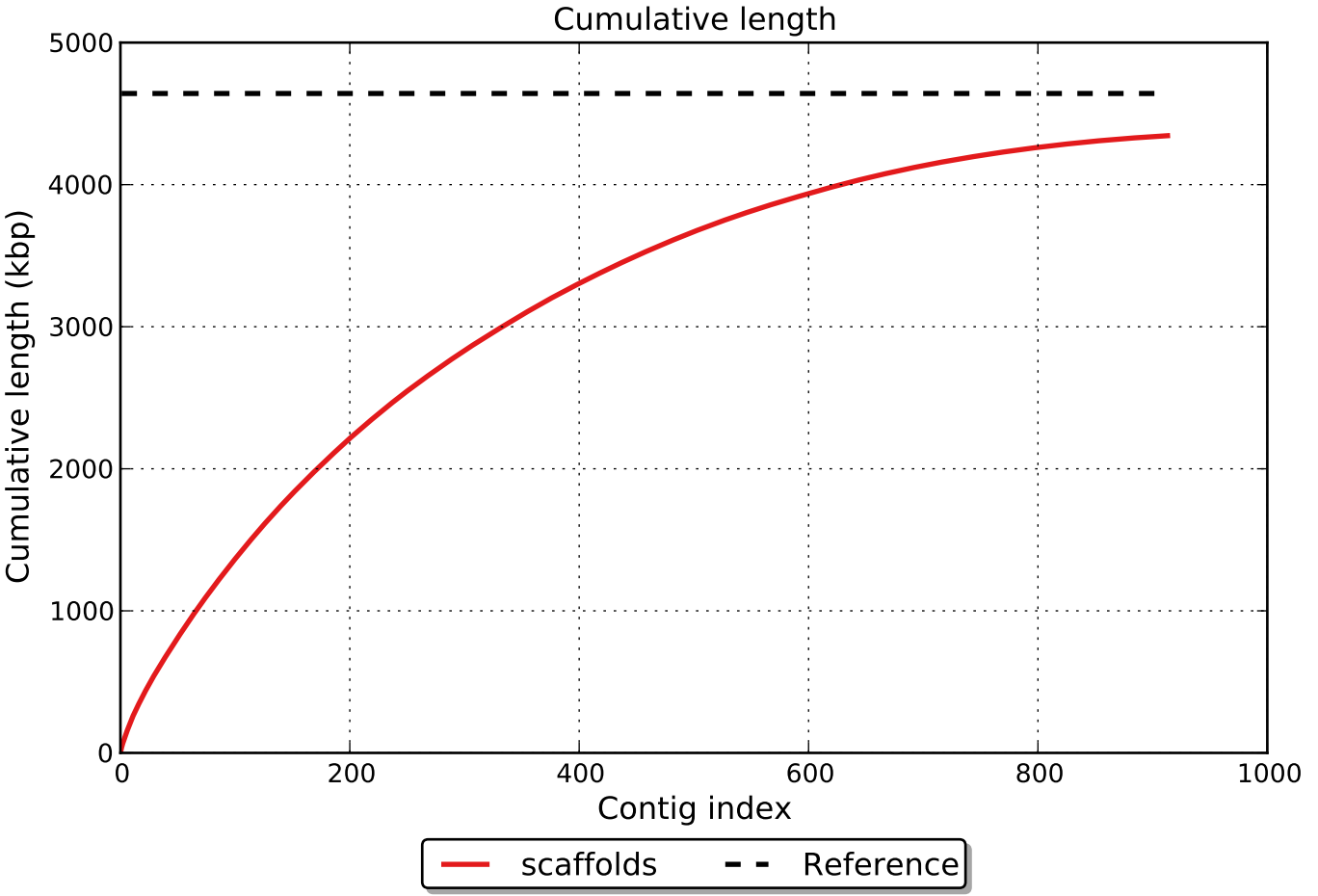
Unaligned report

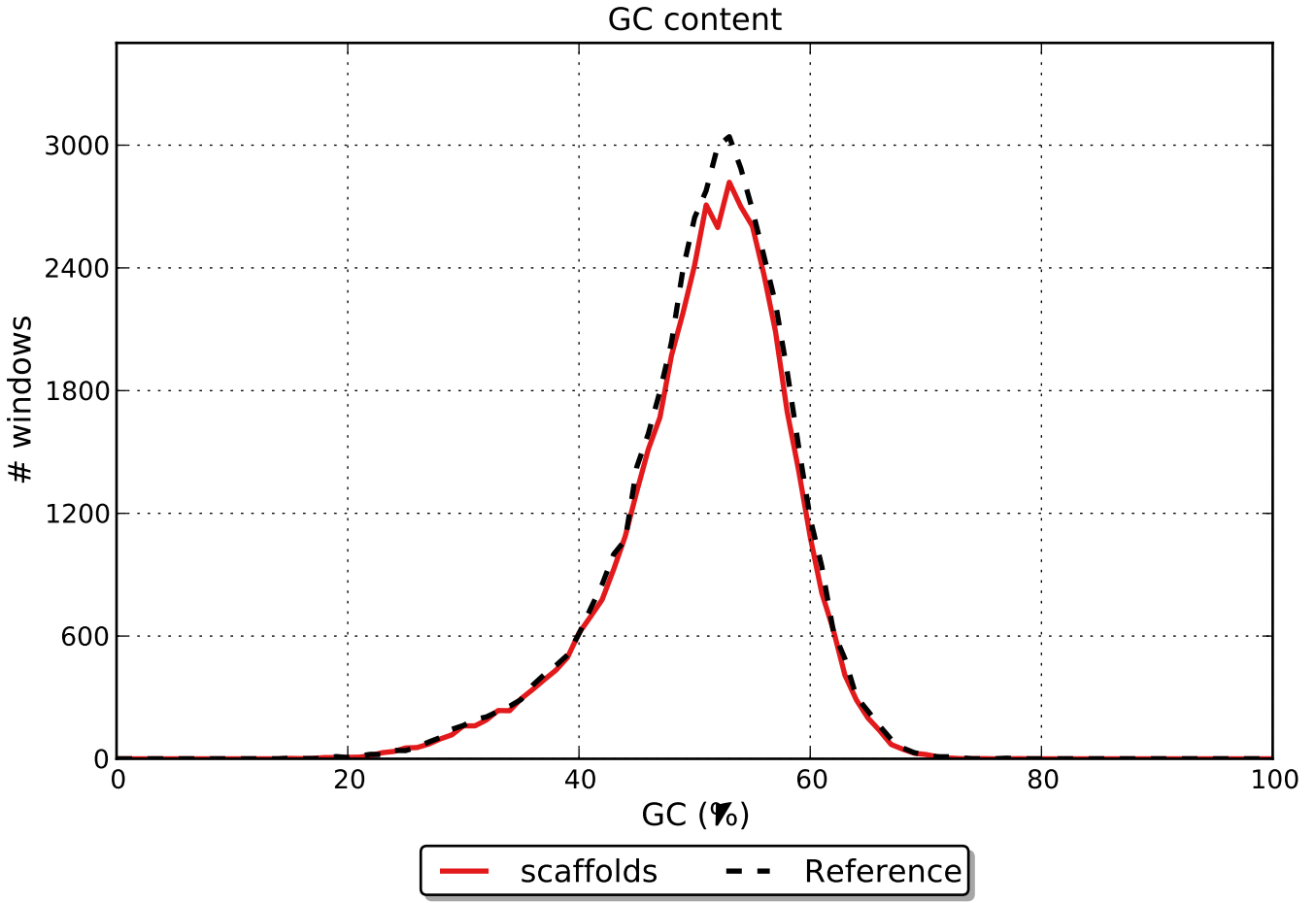
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1528
# N's	20907

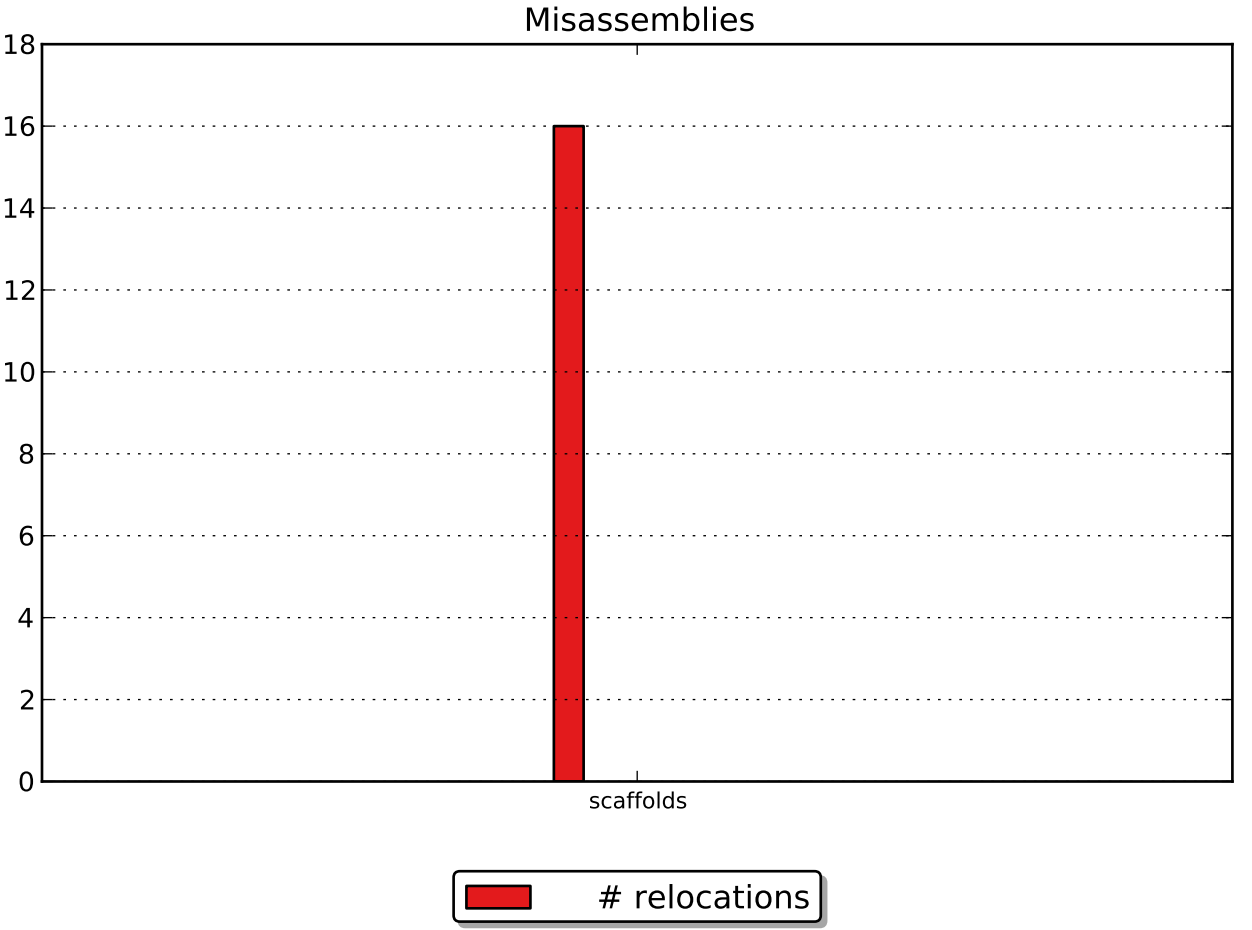
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

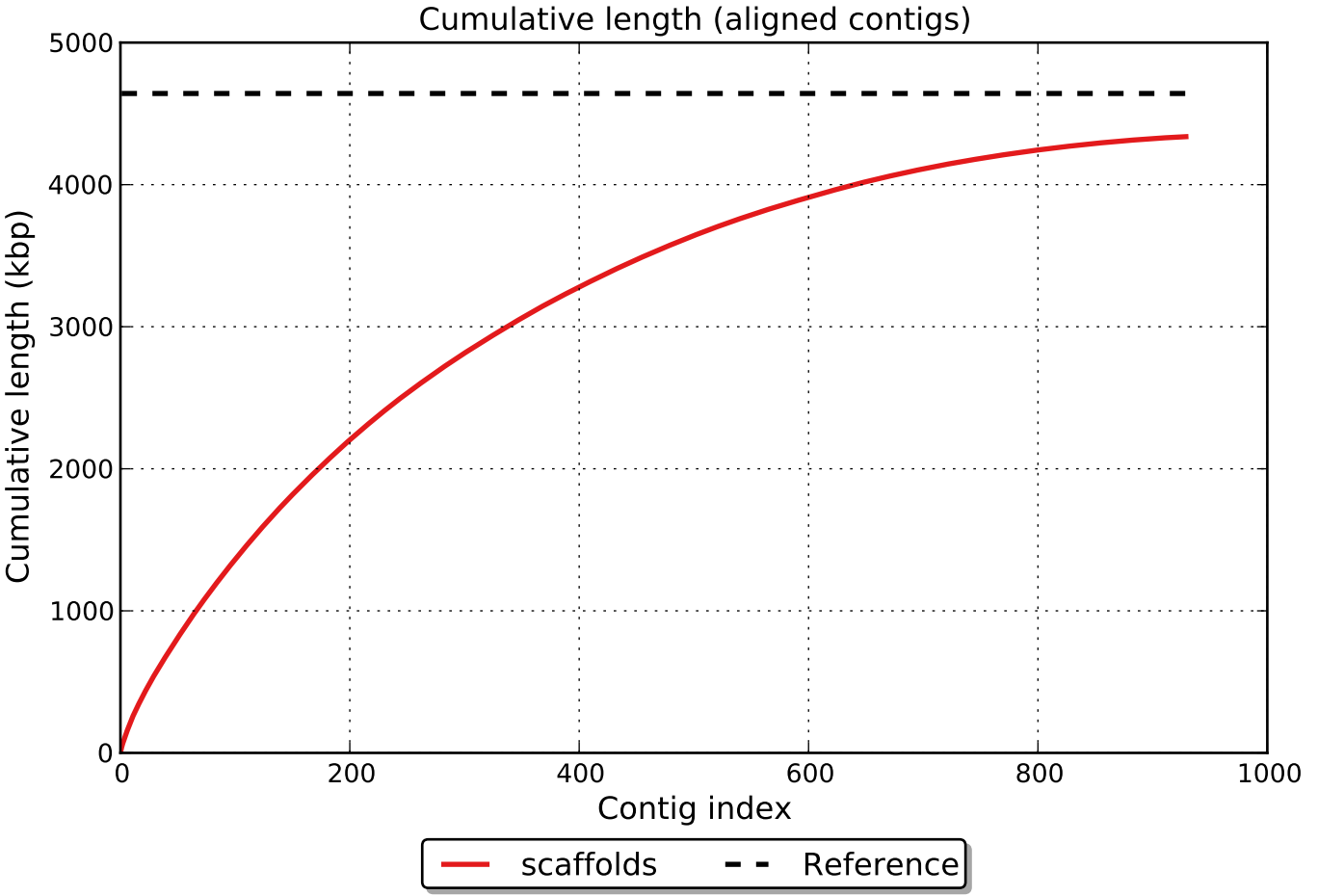

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
scaffolds

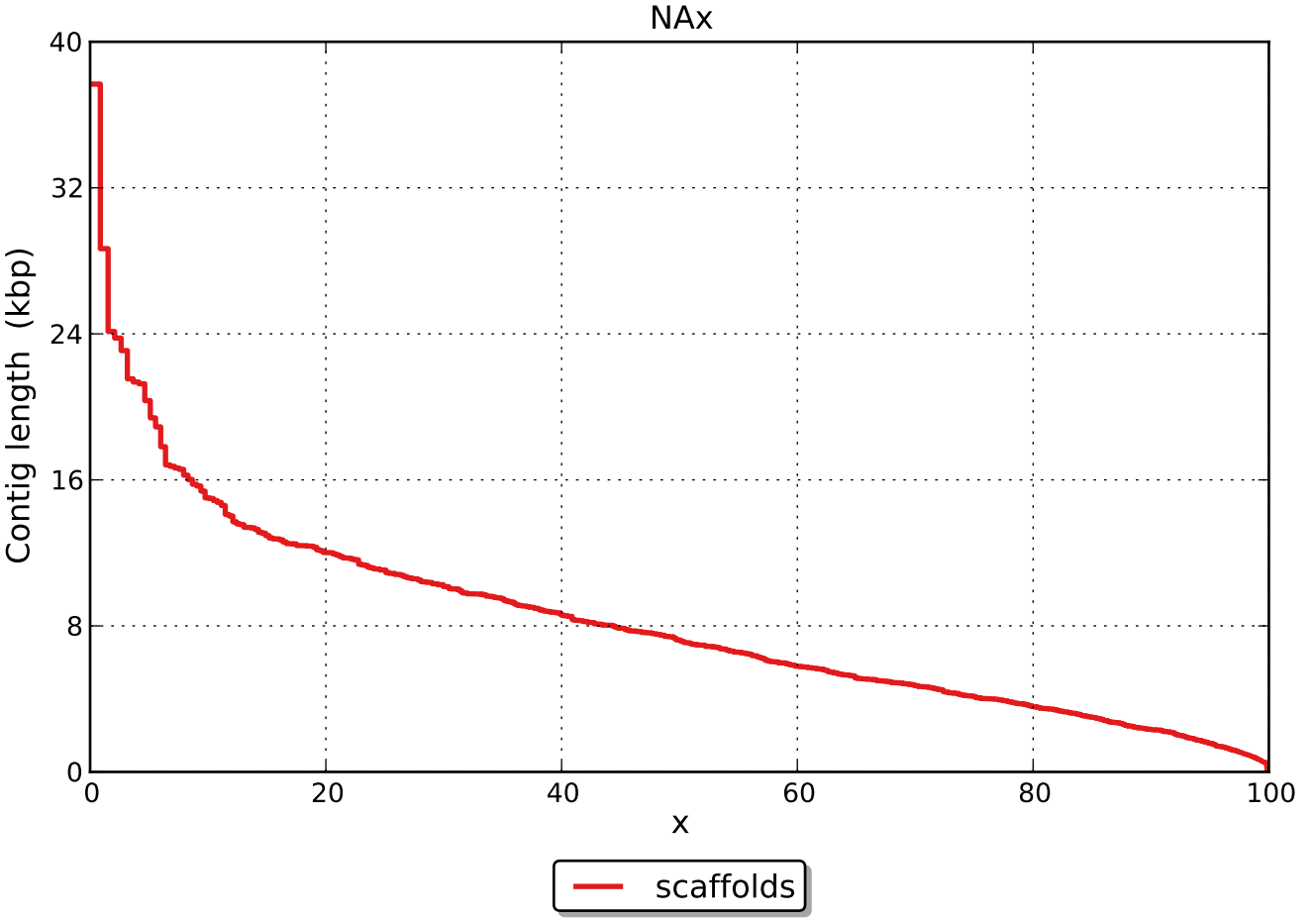

NGx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
scaffolds

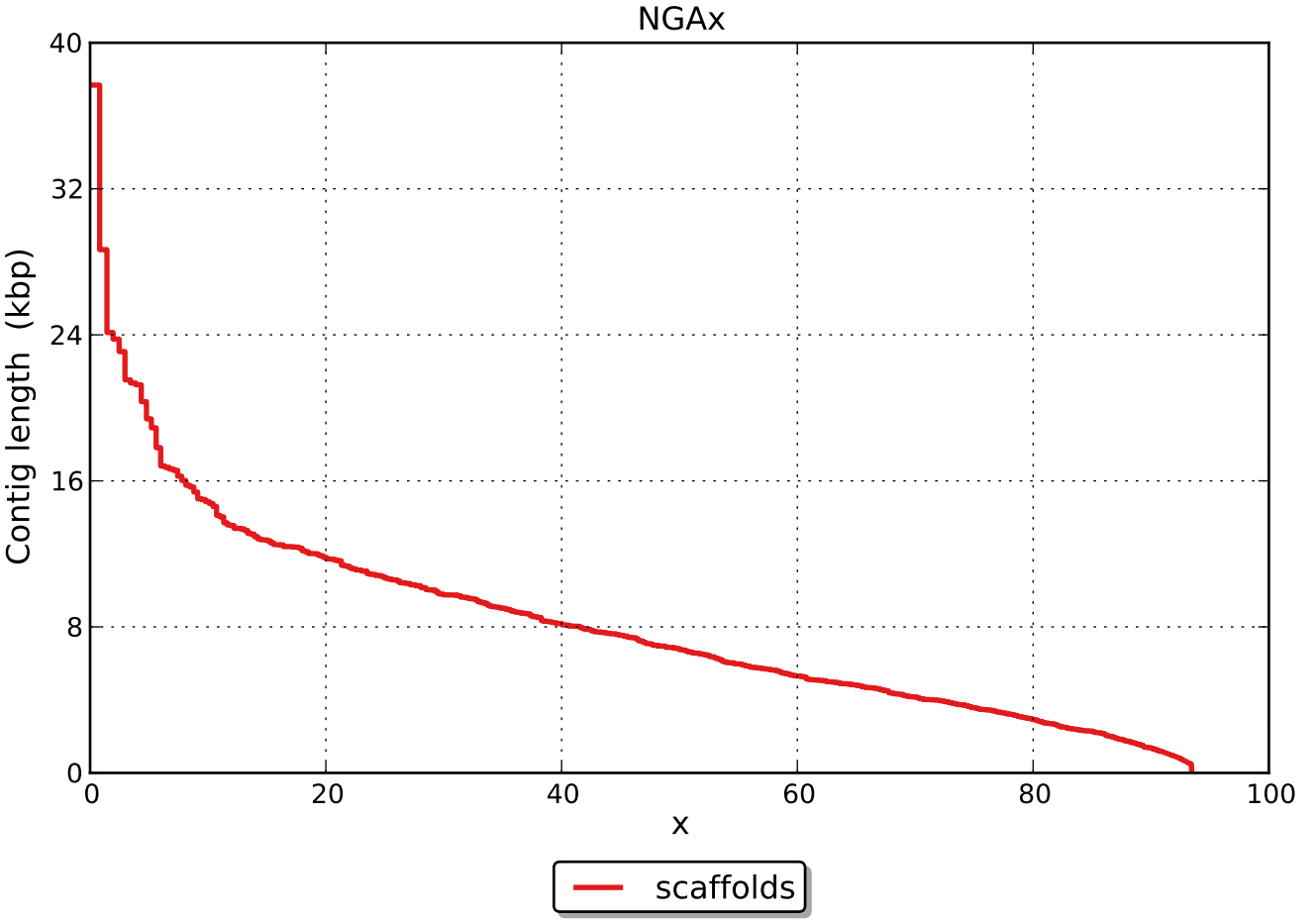

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
1000
Contig index
scaffolds
Reference


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


Misassemblies
18
16
14
12
10
8
6
4
2
0
scaffolds
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
1000
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
scaffolds