Report

	scaffolds
# contigs (>= 1000 bp)	539
# contigs (>= 5000 bp)	269
# contigs (>= 10000 bp)	149
# contigs (>= 25000 bp)	36
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	4490880
Total length (>= 5000 bp)	3899587
Total length (>= 10000 bp)	3011827
Total length (>= 25000 bp)	1258049
Total length (>= 50000 bp)	61819
# contigs	737
Largest contig	61819
Total length	4631011
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	14997
NG50	14997
N75	7576
NG75	7511
L50	93
LG50	93
L75	202
LG75	203
# misassemblies	13
# misassembled contigs	13
Misassembled contigs length	131374
# local misassemblies	8
# unaligned contigs	0 + 14 part
Unaligned length	2451
Genome fraction (%)	94.446
Duplication ratio	1.056
# N's per 100 kbp	3277.19
# mismatches per 100 kbp	1061.12
# indels per 100 kbp	9.92
Largest alignment	59611
NA50	13558
NGA50	13558
NA75	6713
NGA75	6696
LA50	101
LGA50	101
LA75	224
LGA75	225

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

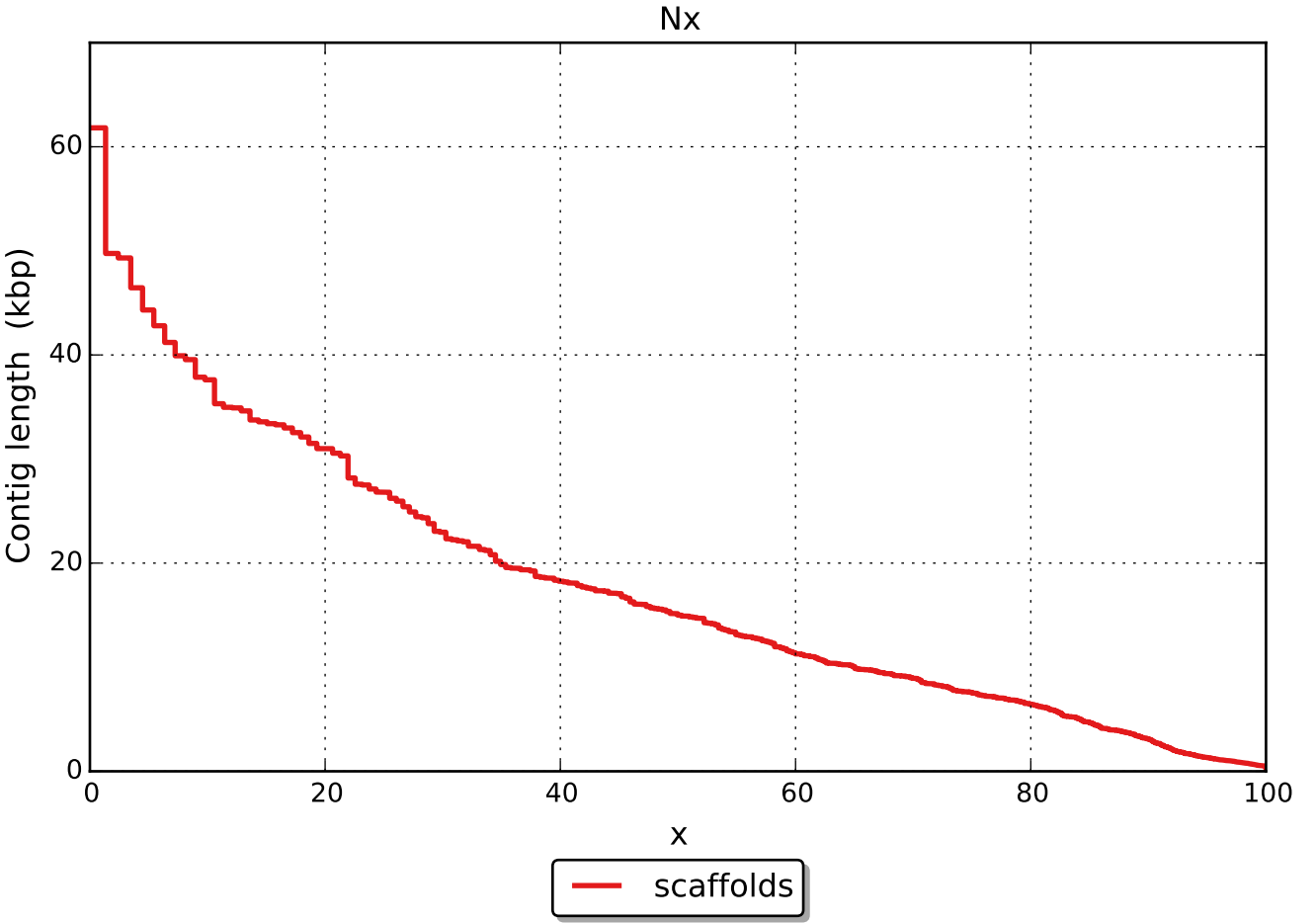
	scaffolds
# misassemblies	13
# relocations	13
# translocations	0
# inversions	0
# possibly misassembled contigs	103
# misassembled contigs	13
Misassembled contigs length	131374
# local misassemblies	8
# mismatches	46518
# indels	435
# short indels	35
# long indels	400
Indels length	22028

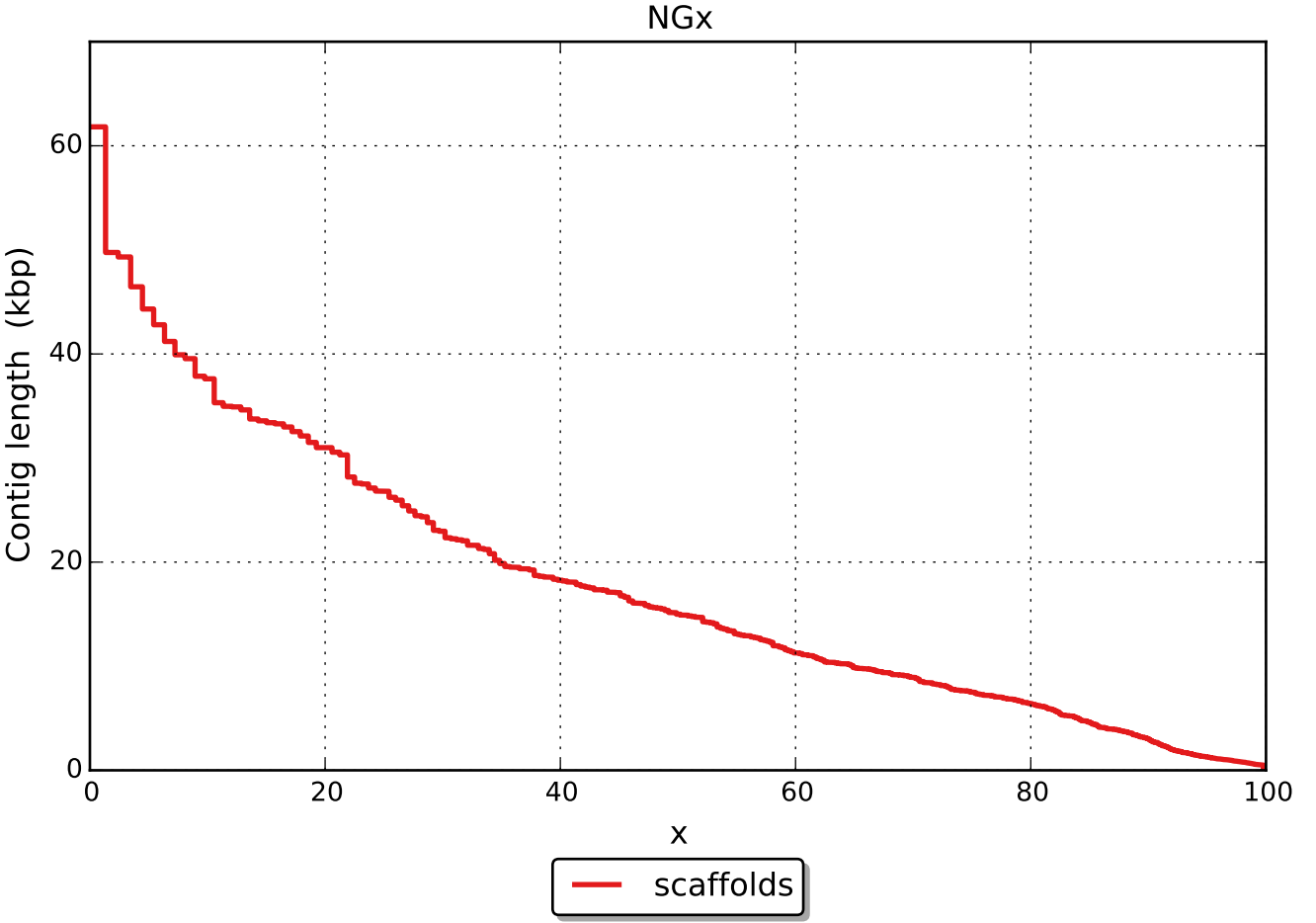
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

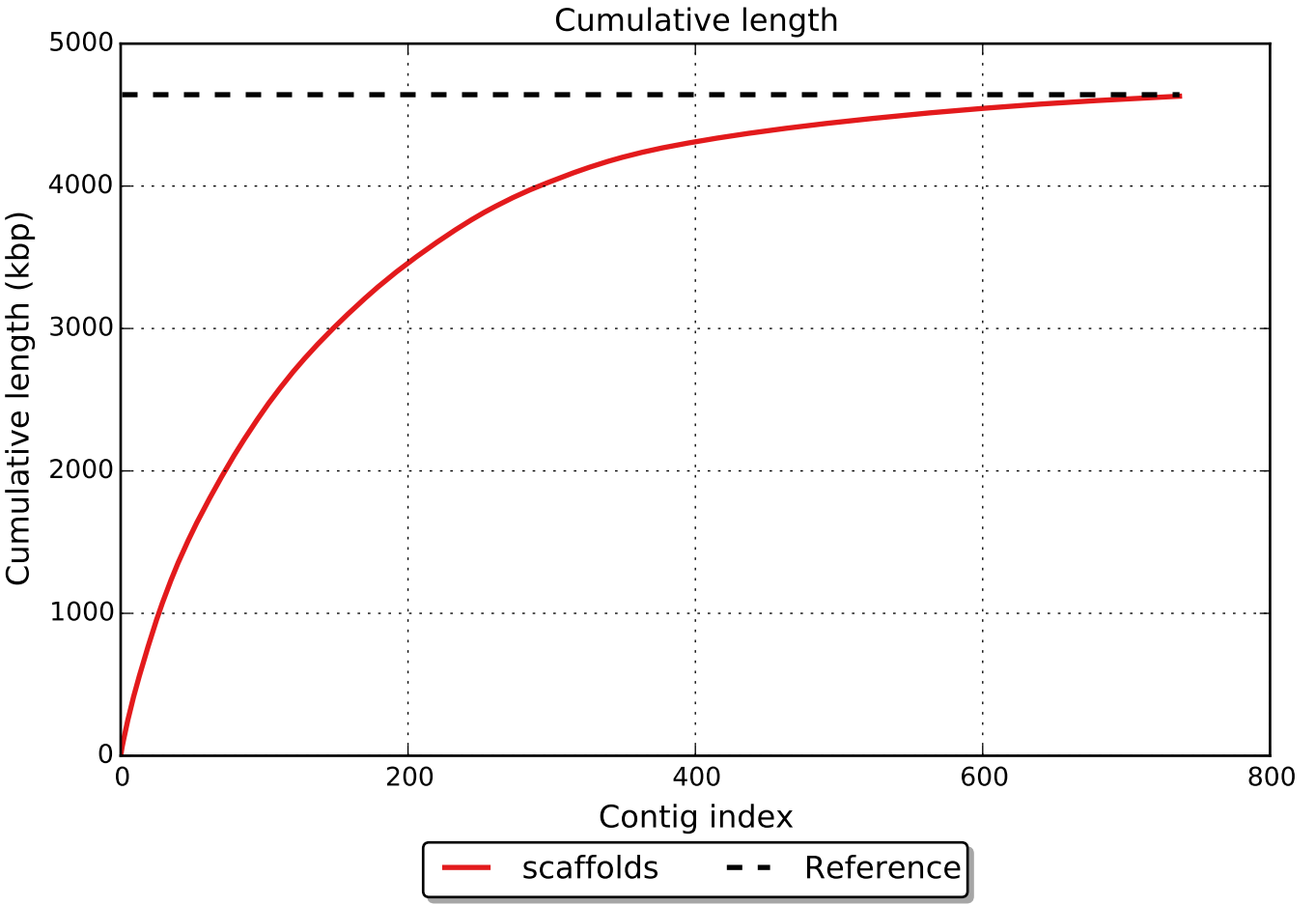
Unaligned report

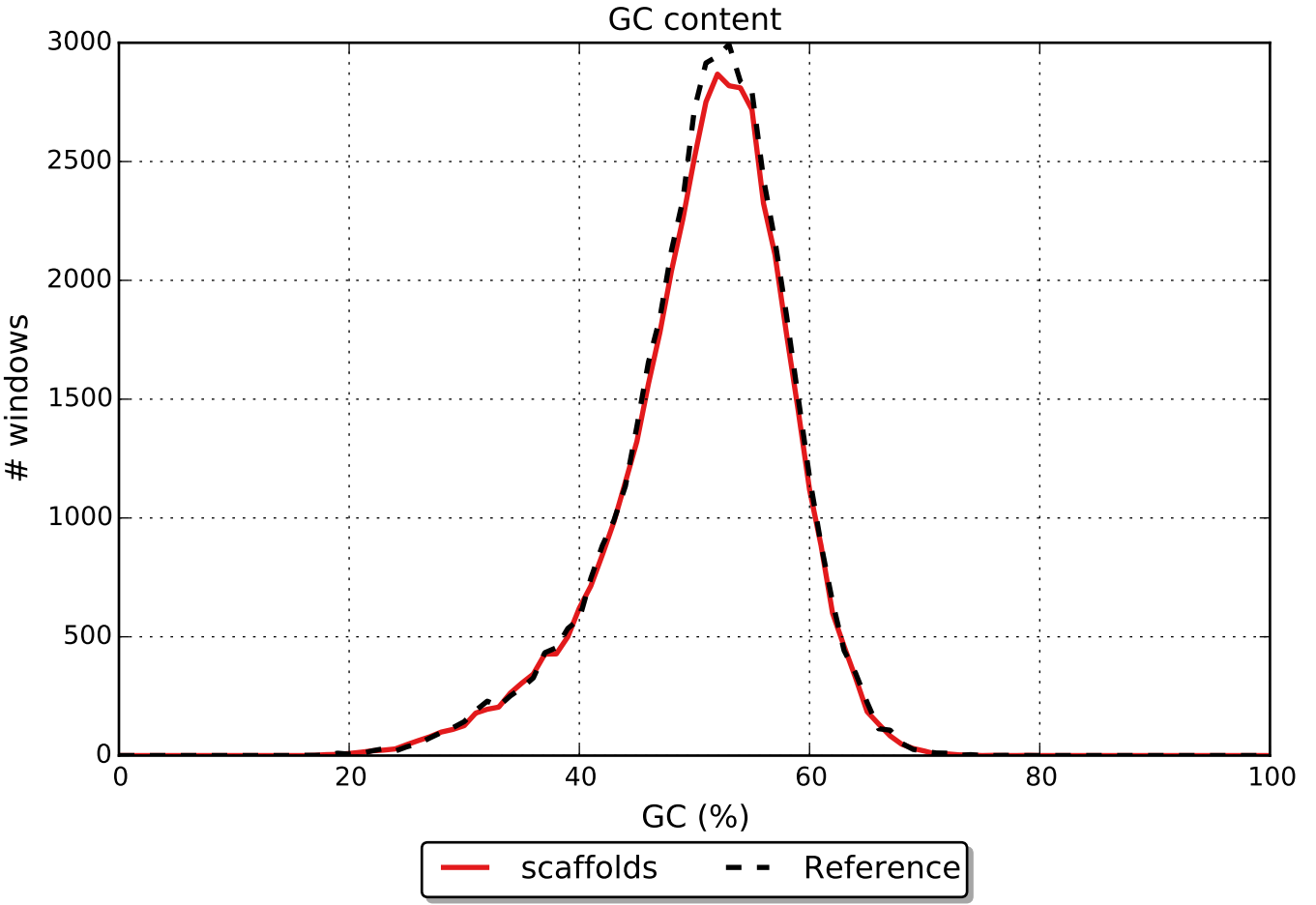
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	14
# with misassembly	0
# both parts are significant	0
Partially unaligned length	2451
# N's	151767

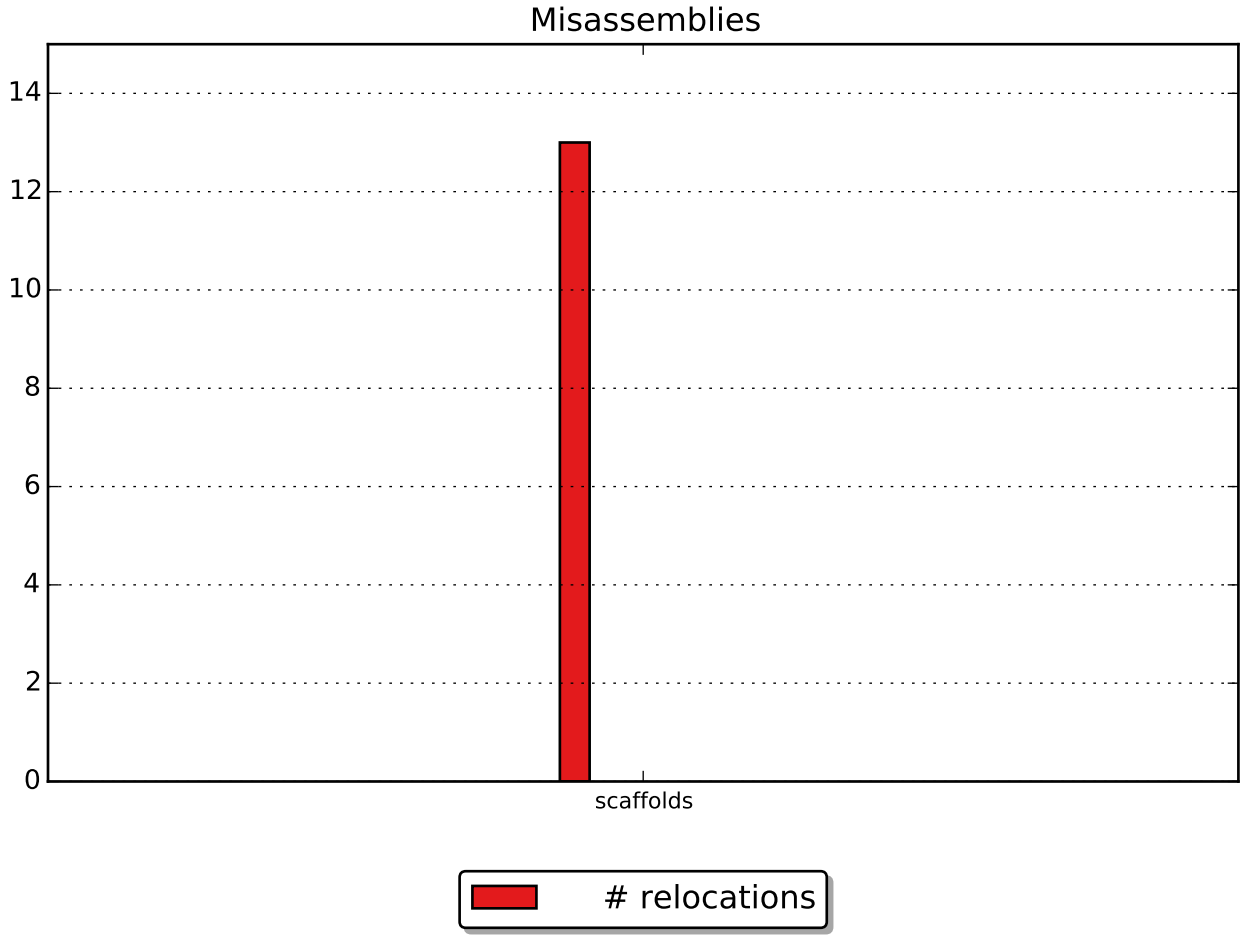
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

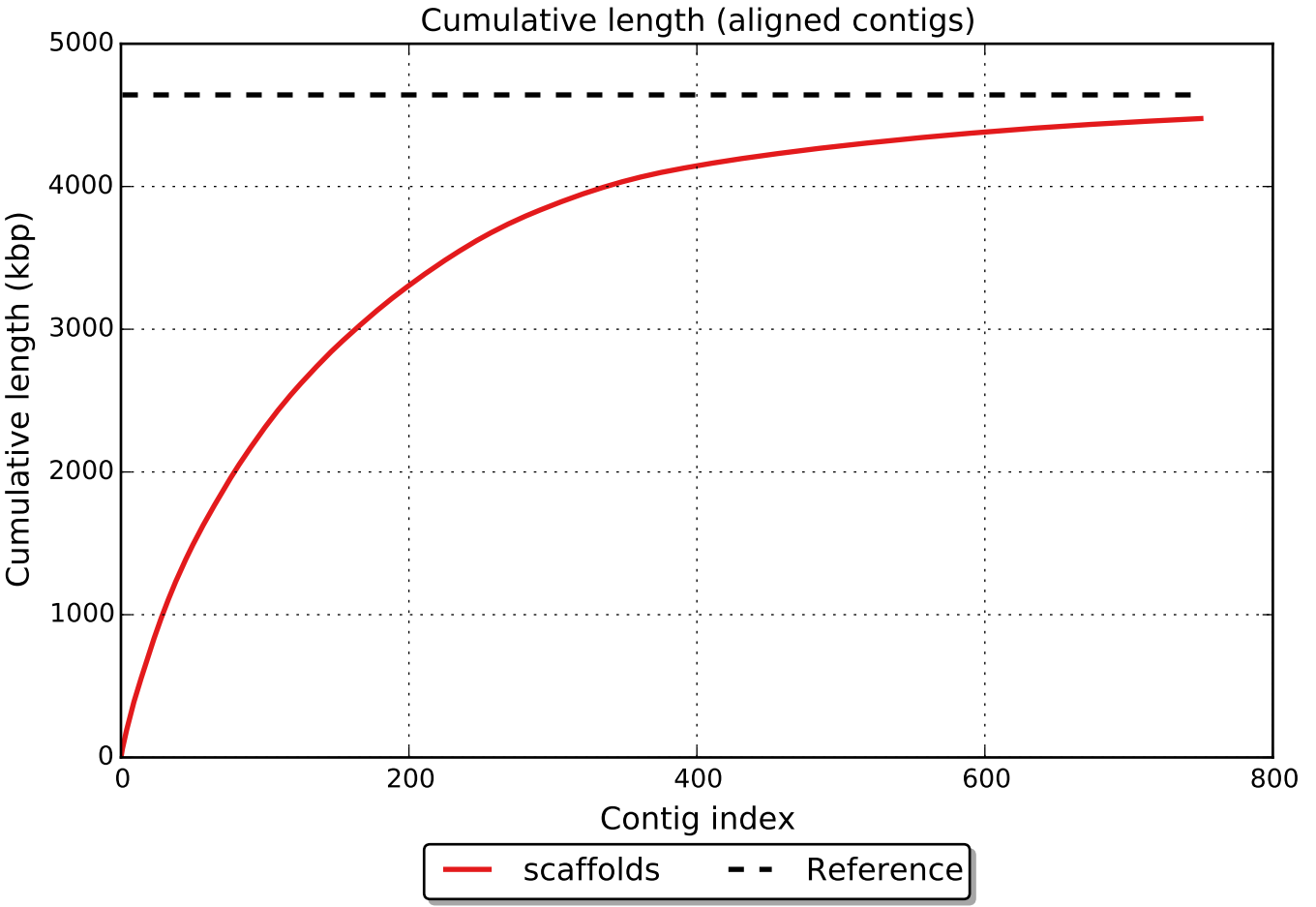

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
scaffolds

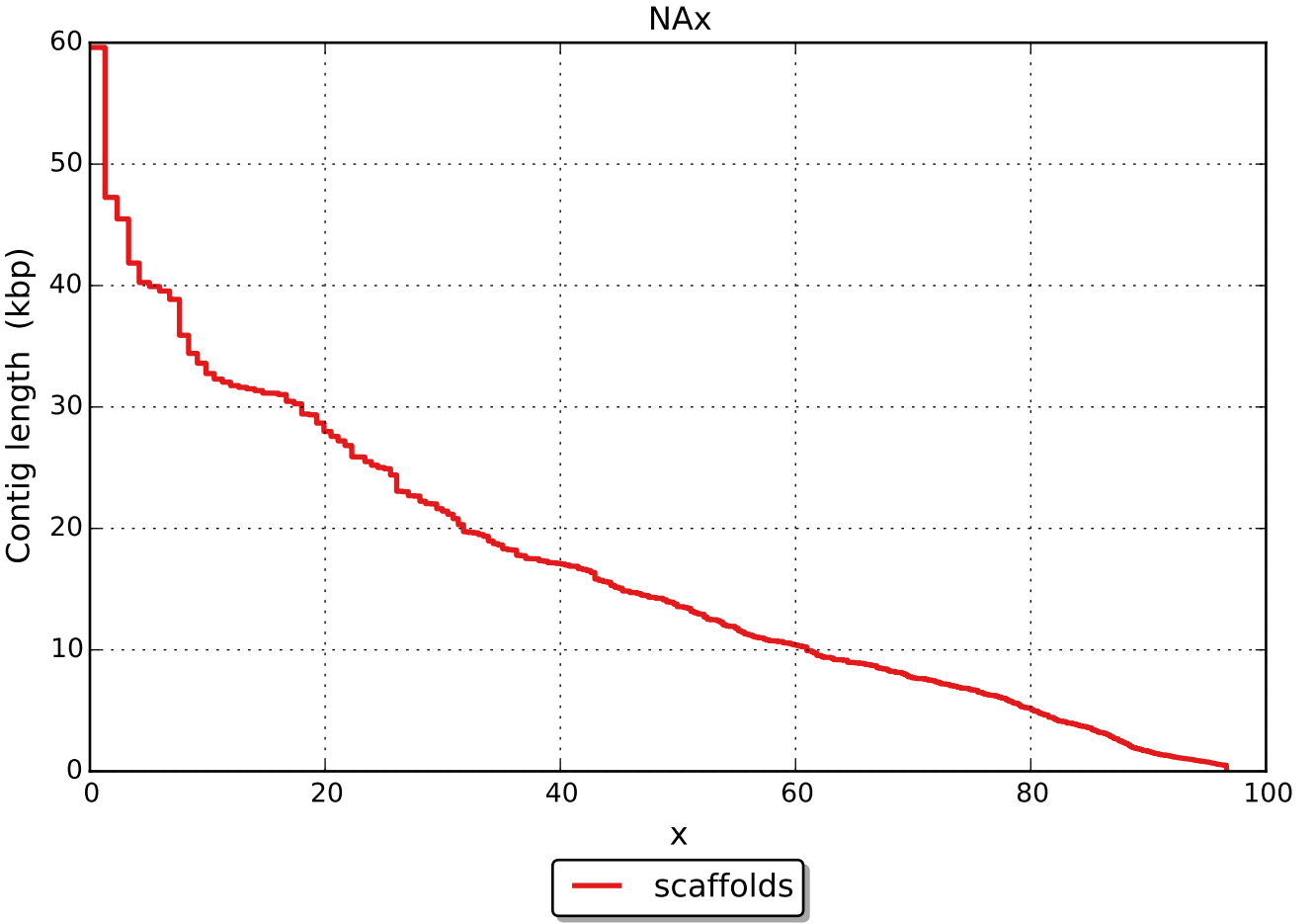

NGx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
scaffolds

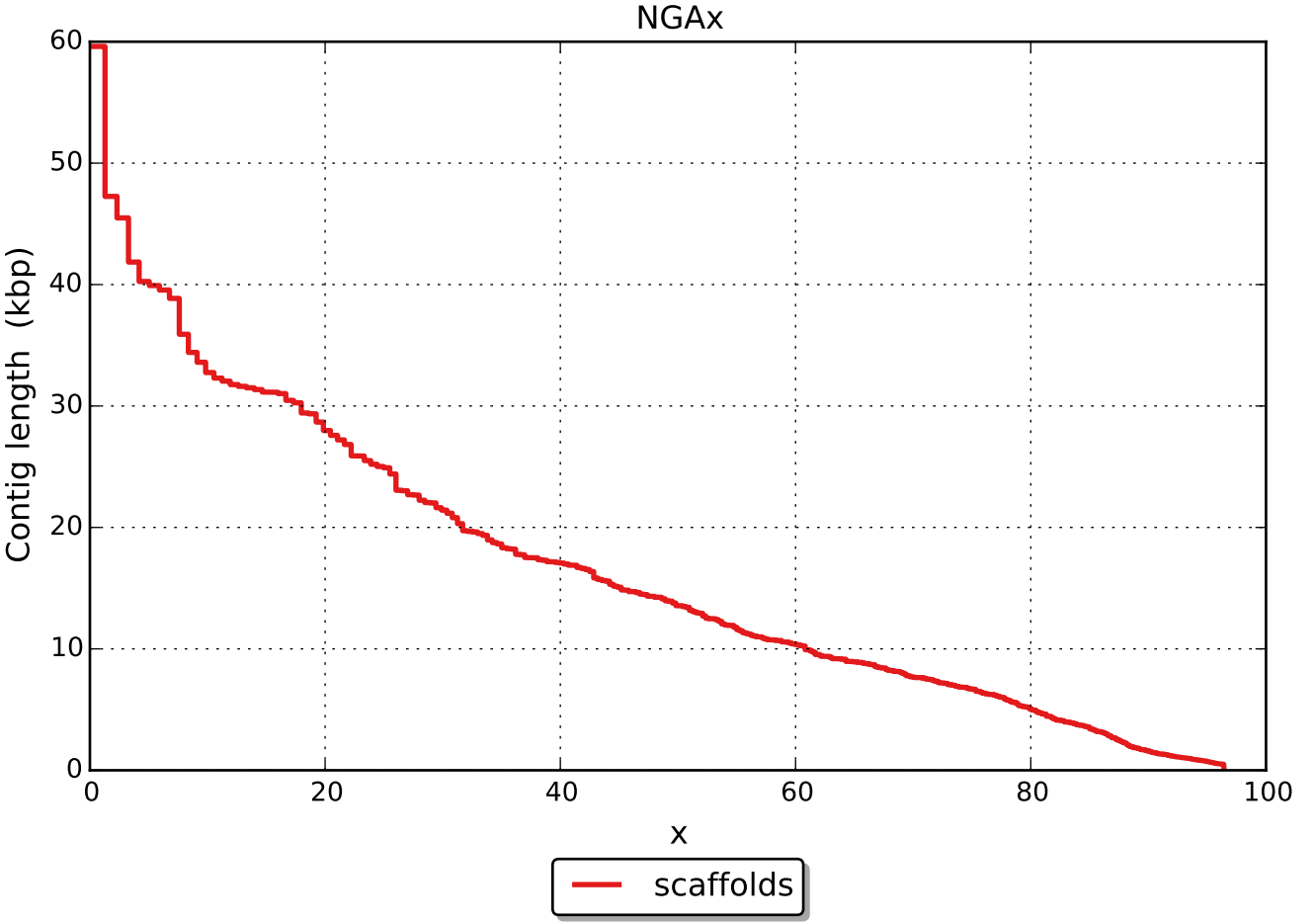

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
Contig index
scaffolds
Reference


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


Misassemblies
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
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
scaffolds