Report

	scaffolds
# contigs (>= 1000 bp)	77
# contigs (>= 5000 bp)	45
# contigs (>= 10000 bp)	43
# contigs (>= 25000 bp)	36
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	4497034
Total length (>= 5000 bp)	4433281
Total length (>= 10000 bp)	4418811
Total length (>= 25000 bp)	4317692
Total length (>= 50000 bp)	3972370
# contigs	98
Largest contig	475325
Total length	4511491
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	186479
NG50	173165
N75	85499
NG75	78915
L50	8
LG50	9
L75	18
LG75	19
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.149
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	861.73
# indels per 100 kbp	0.78
Largest alignment	475325
NA50	186479
NGA50	173164
NA75	85499
NGA75	78915
LA50	8
LGA50	9
LA75	18
LGA75	19

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

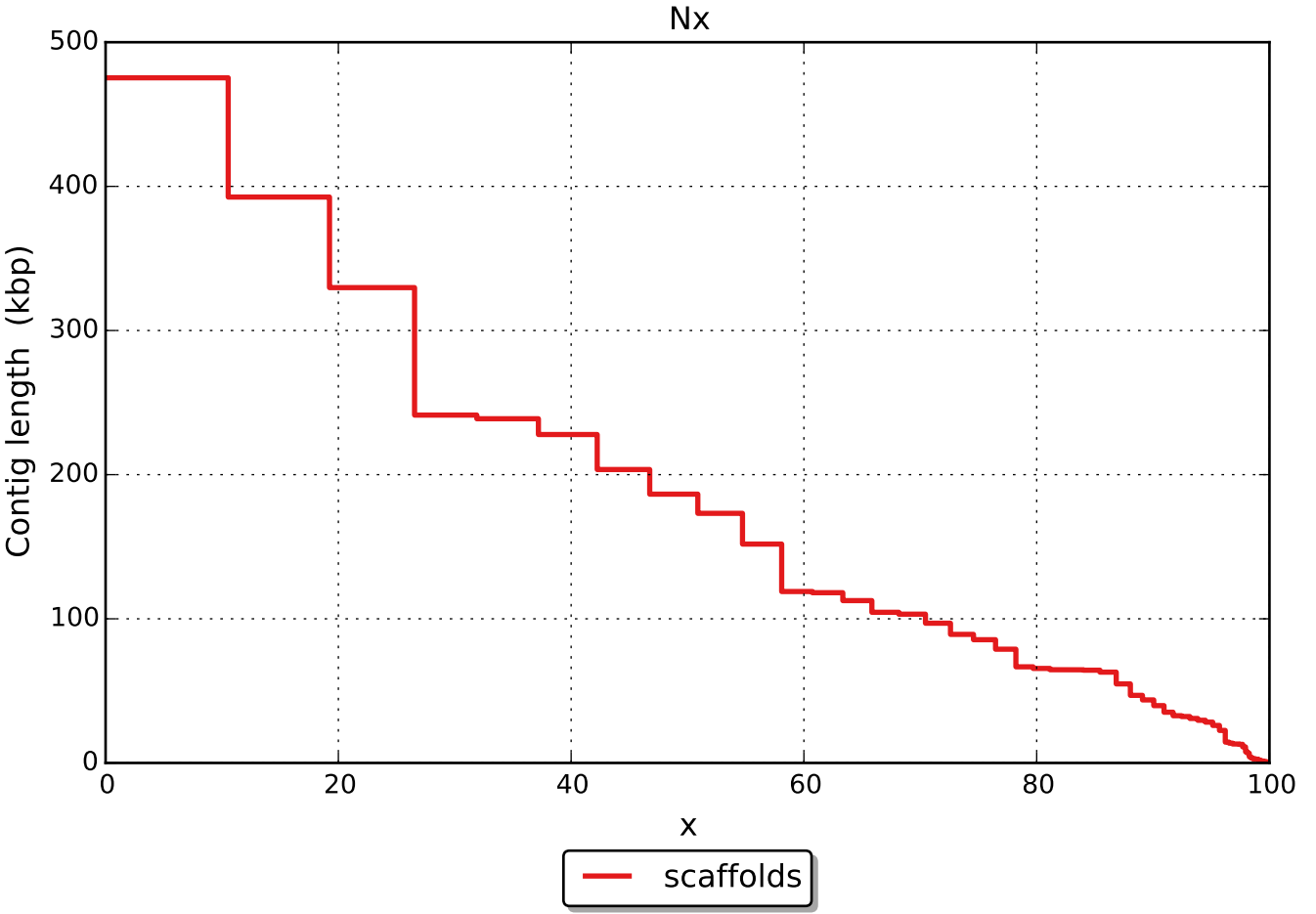
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	38858
# indels	35
# short indels	33
# long indels	2
Indels length	48

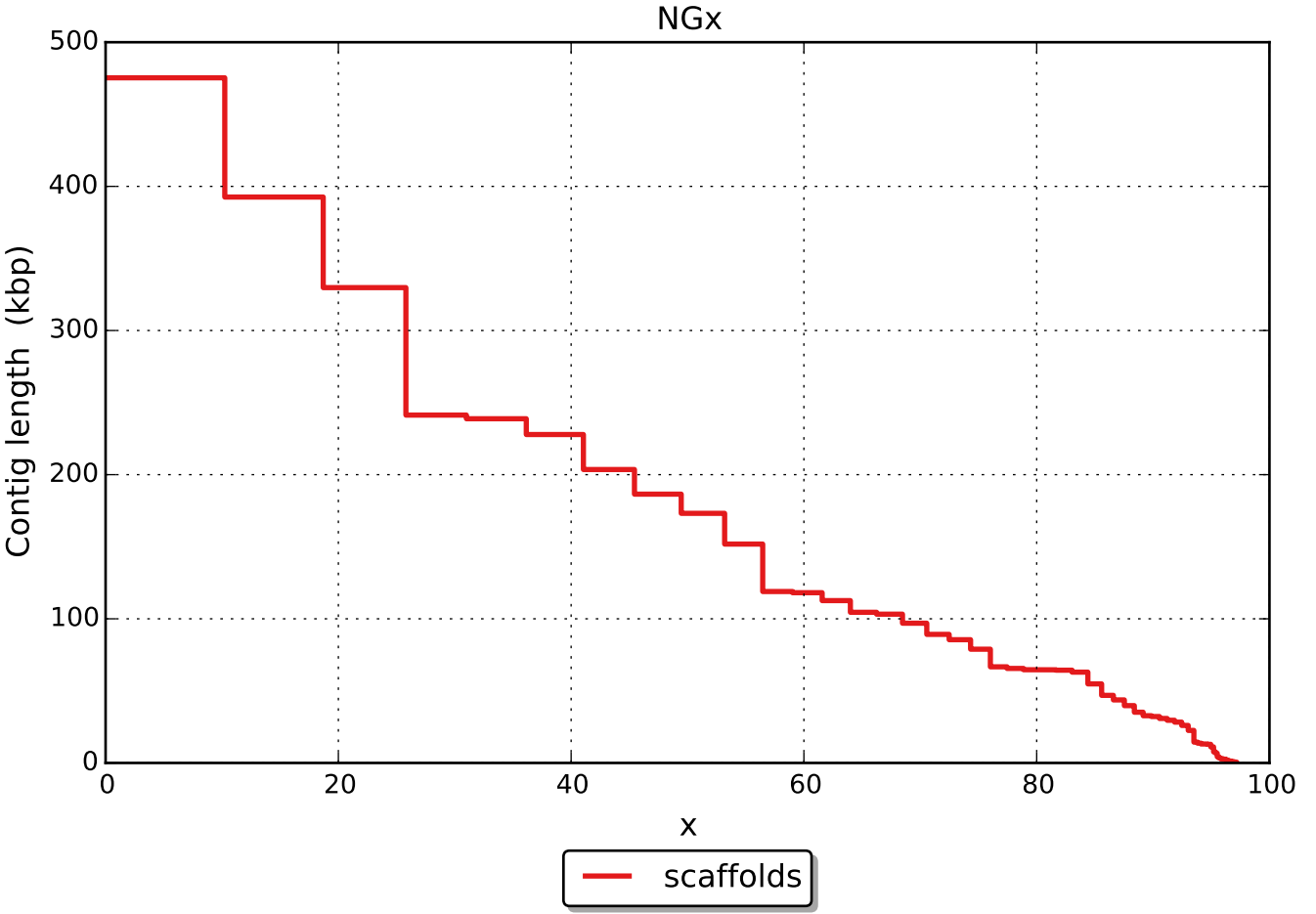
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

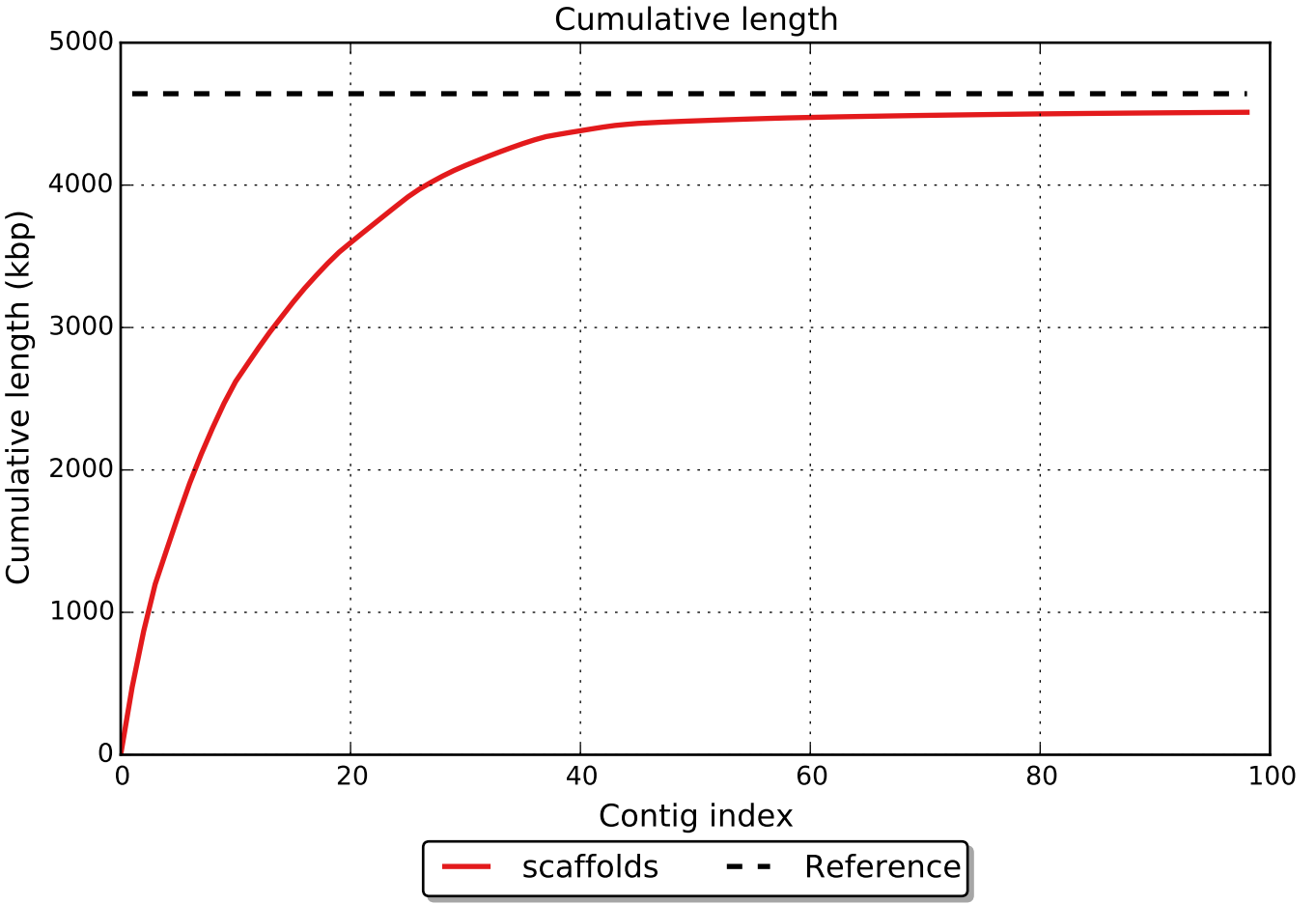
Unaligned report

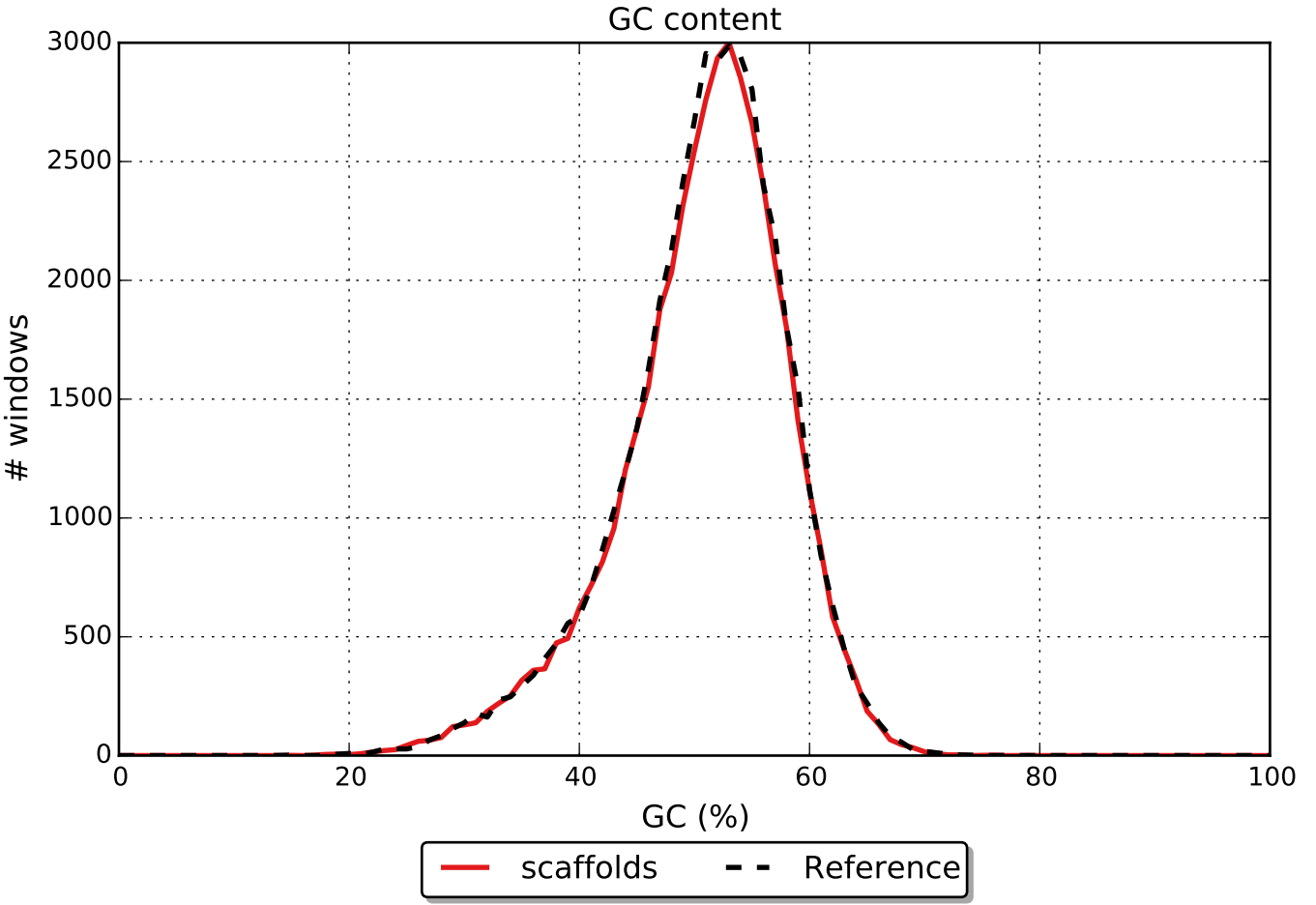
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

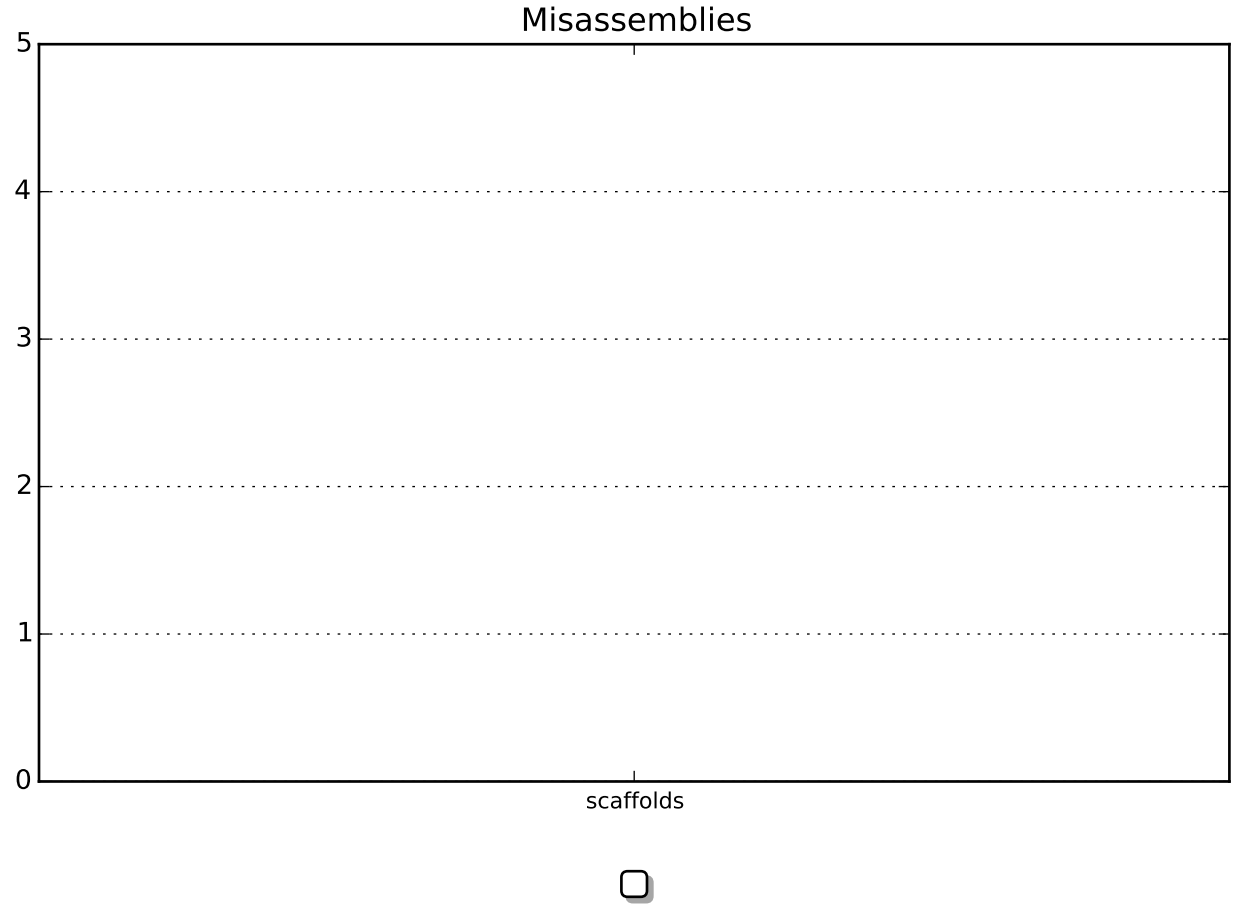
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

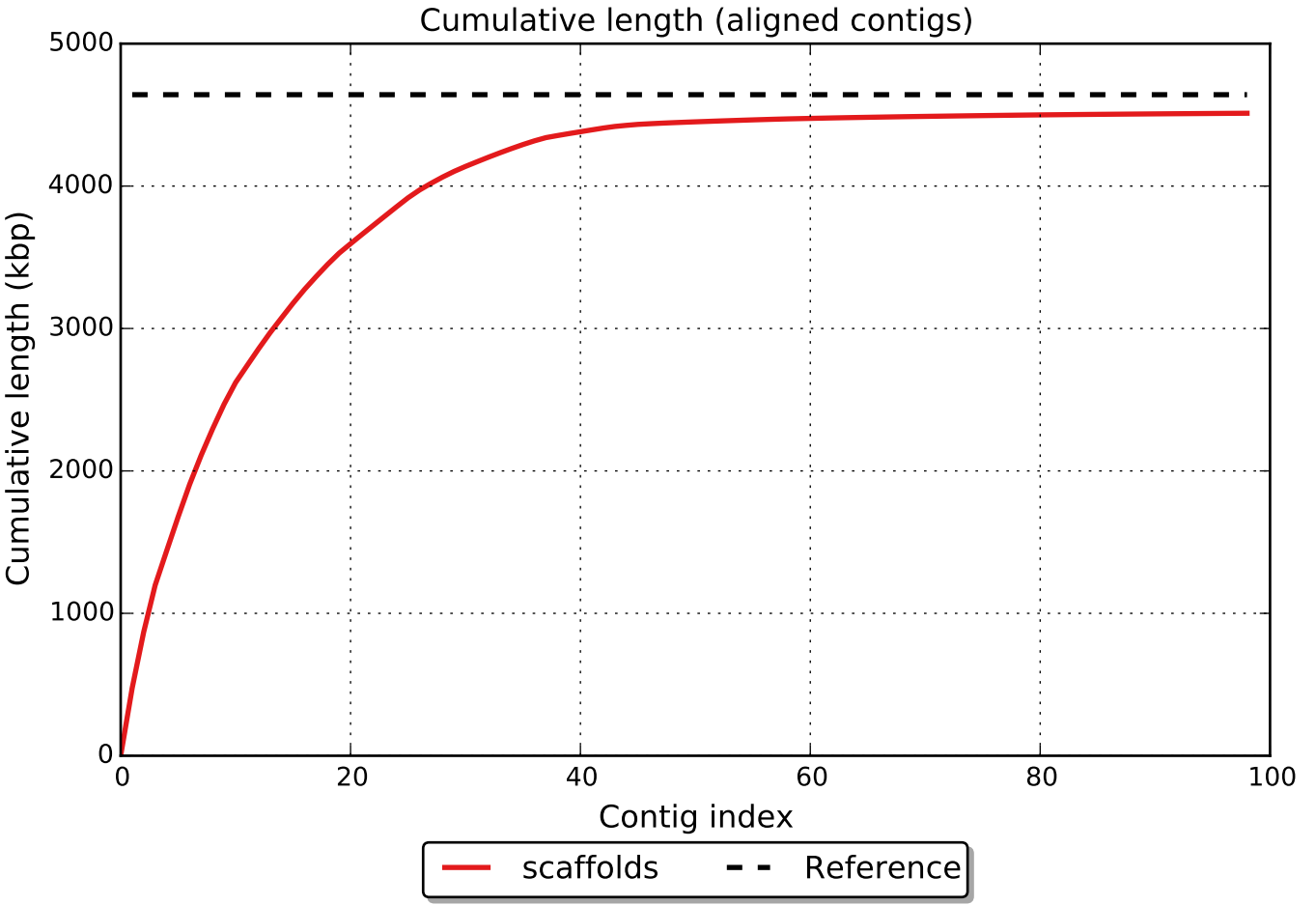

Nx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
scaffolds

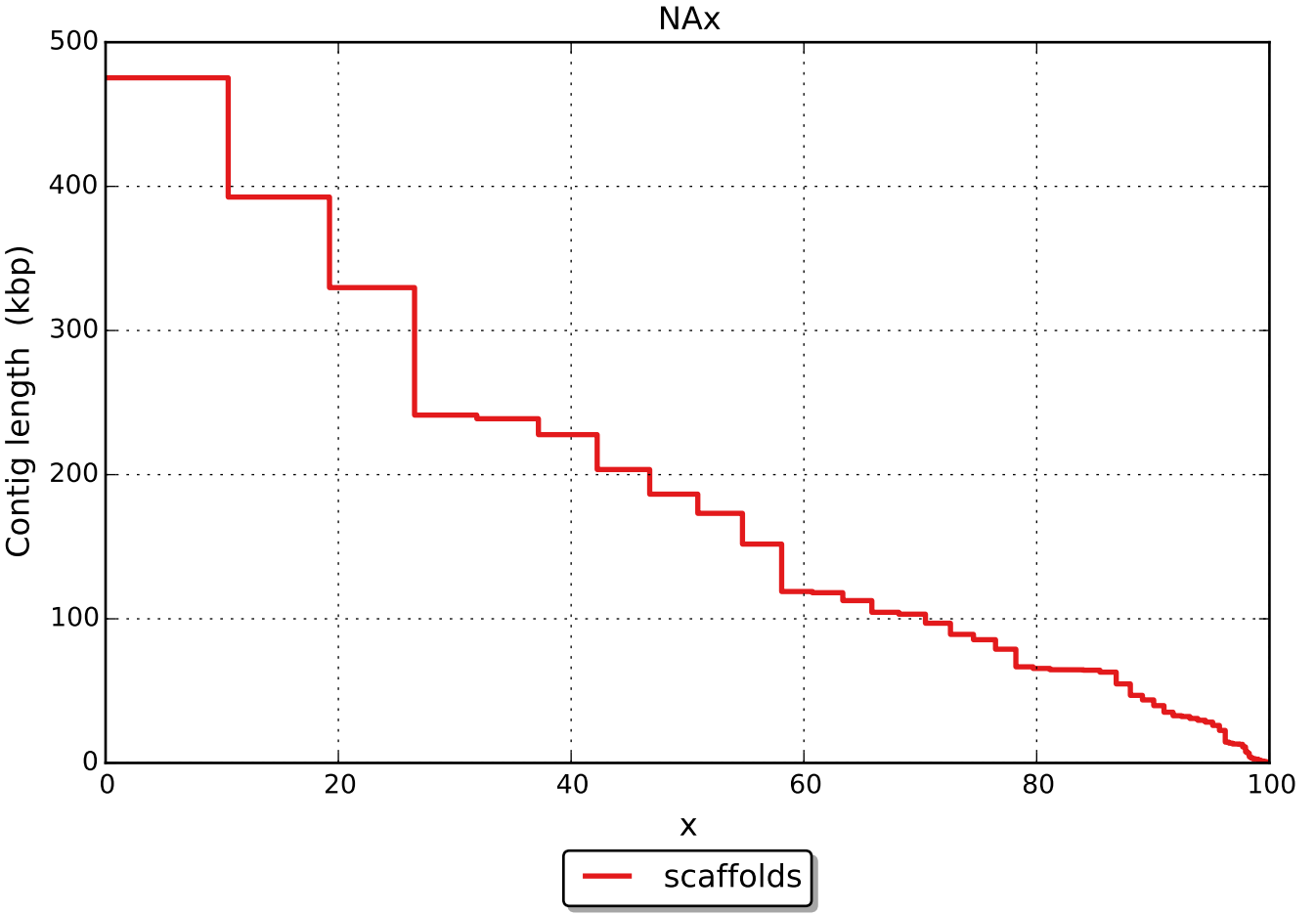

NGx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
scaffolds

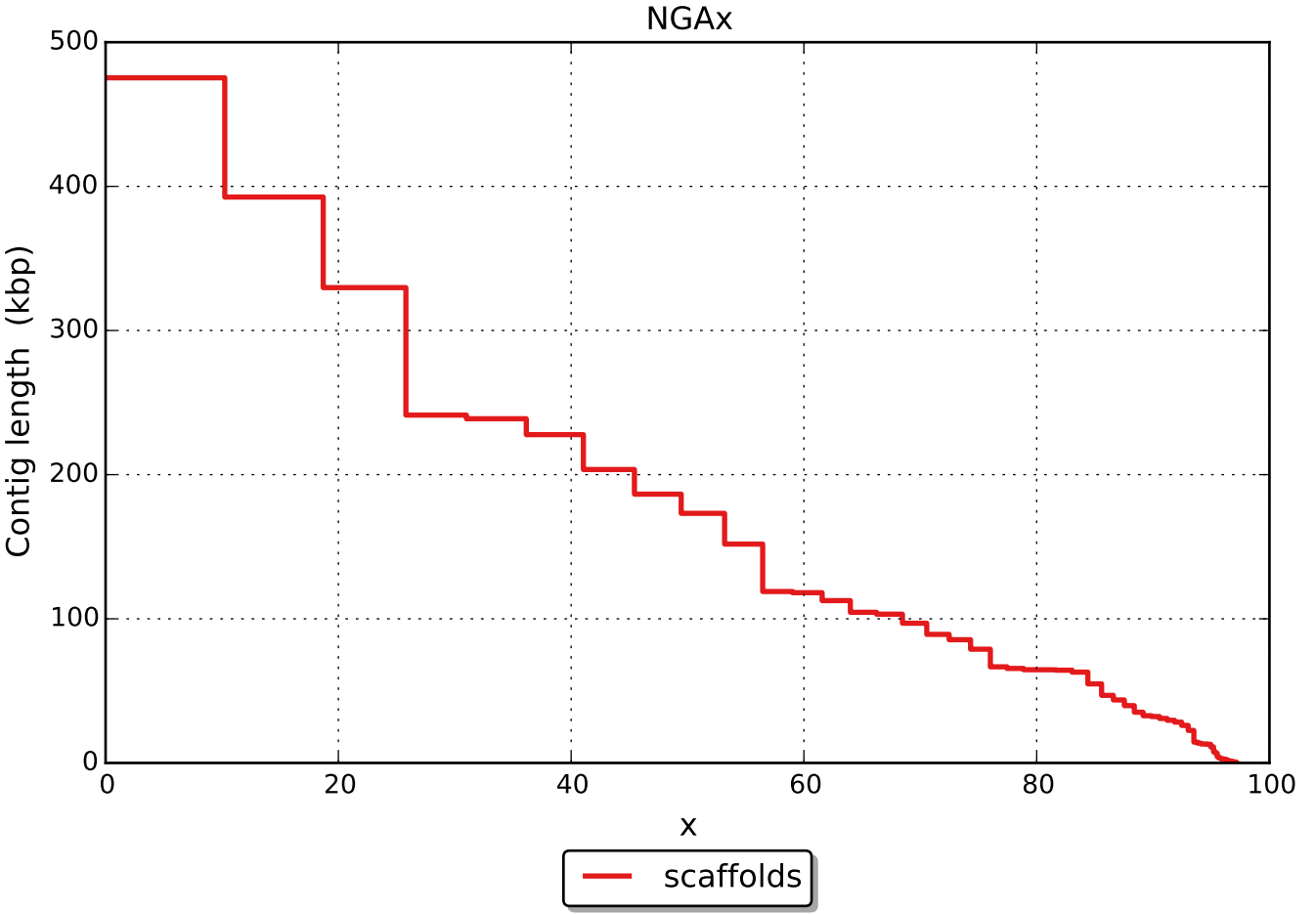

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
Contig index
scaffolds
Reference


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


Misassemblies
5
4
3
2
1
0
scaffolds


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
scaffolds