Report

	scaffolds
# contigs (>= 1000 bp)	67
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	46
# contigs (>= 25000 bp)	40
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4561512
Total length (>= 5000 bp)	4522537
Total length (>= 10000 bp)	4498467
Total length (>= 25000 bp)	4409098
Total length (>= 50000 bp)	3947942
# contigs	72
Largest contig	327055
Total length	4565287
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	173973
NG50	173973
N75	87062
NG75	87062
L50	10
LG50	10
L75	20
LG75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.302
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.50
# indels per 100 kbp	8.20
Largest alignment	327055
NA50	173973
NGA50	173973
NA75	87062
NGA75	87062
LA50	10
LGA50	10
LA75	20
LGA75	20

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

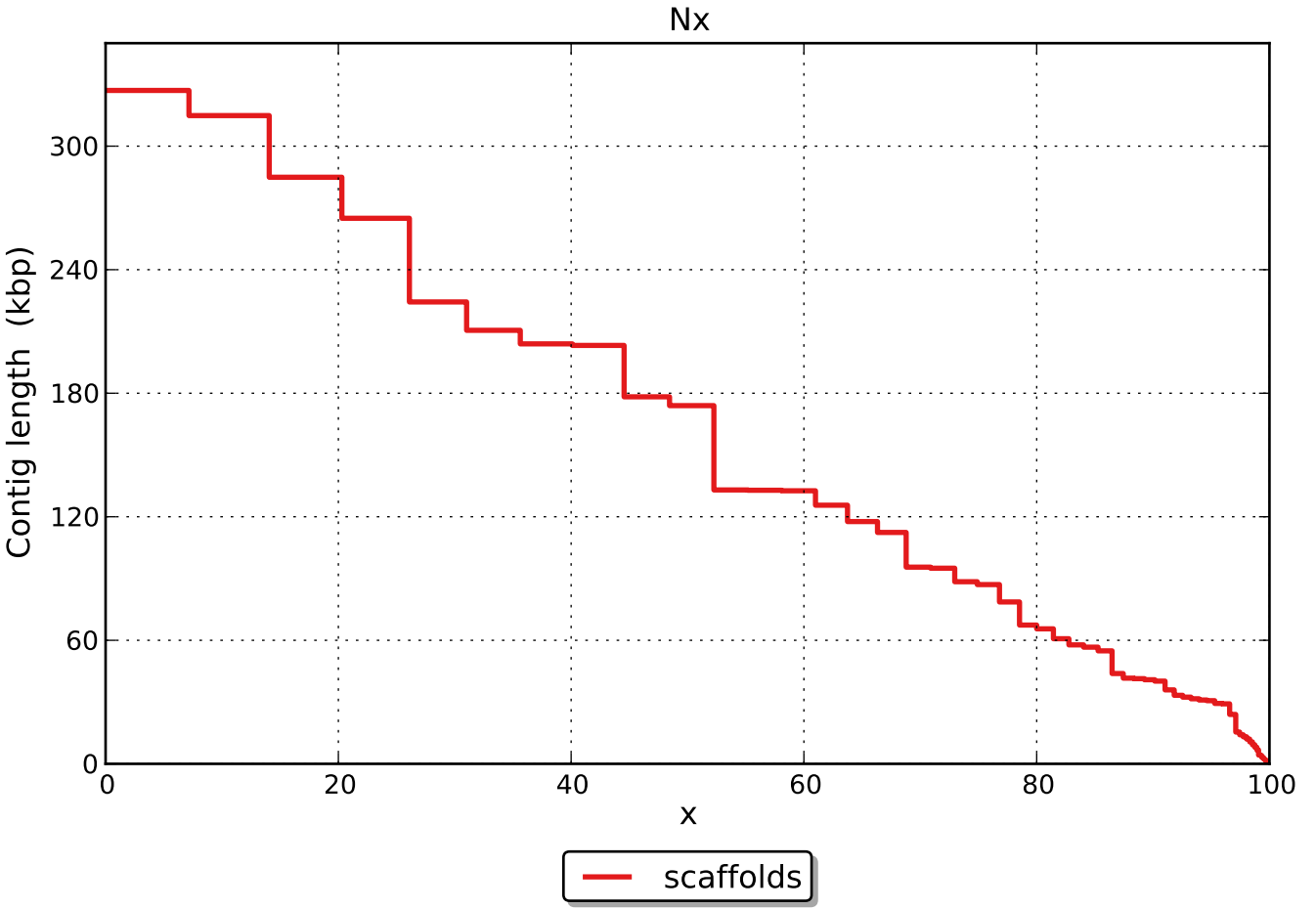
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	2806
# indels	374
# short indels	374
# long indels	0
Indels length	538

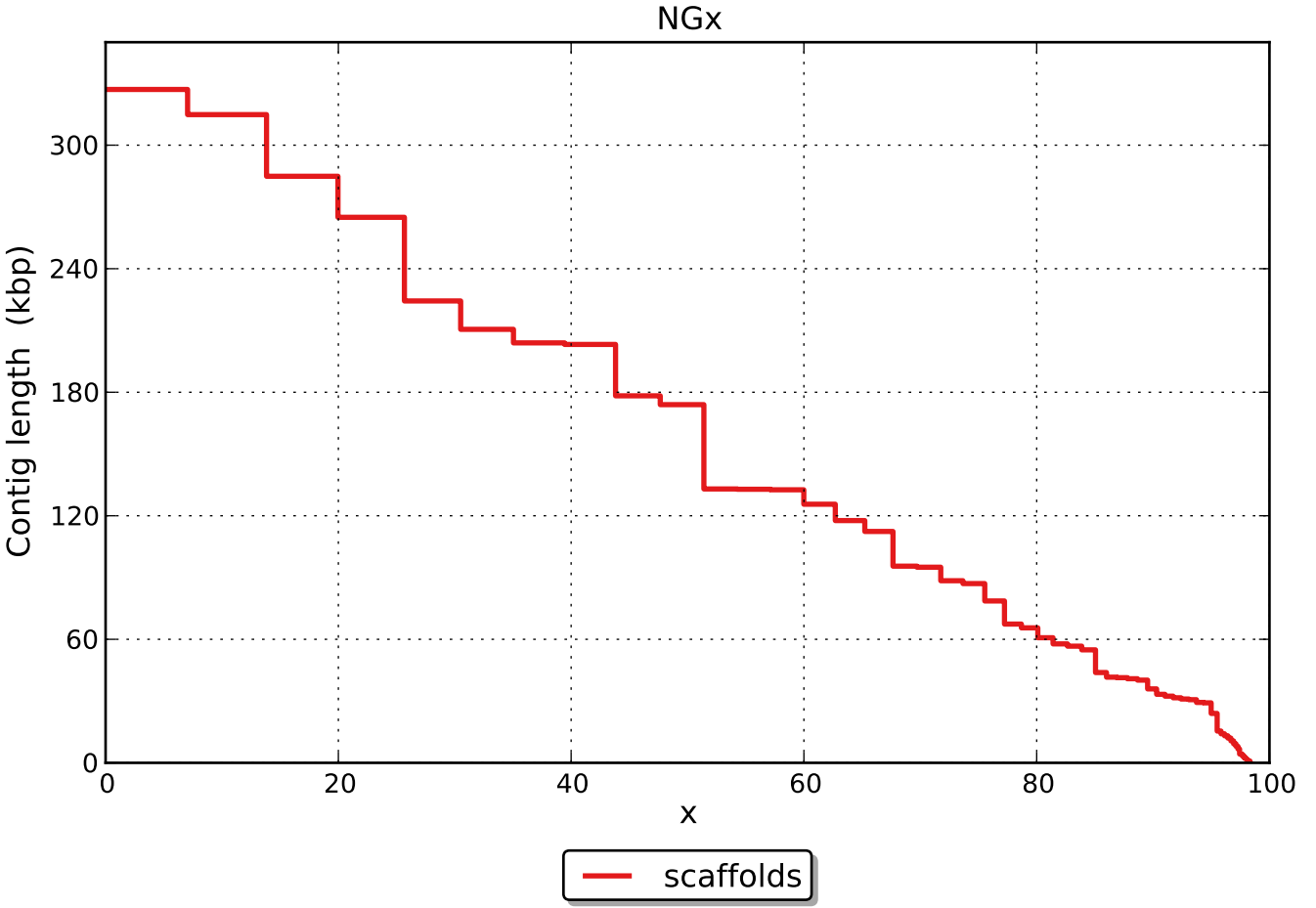
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

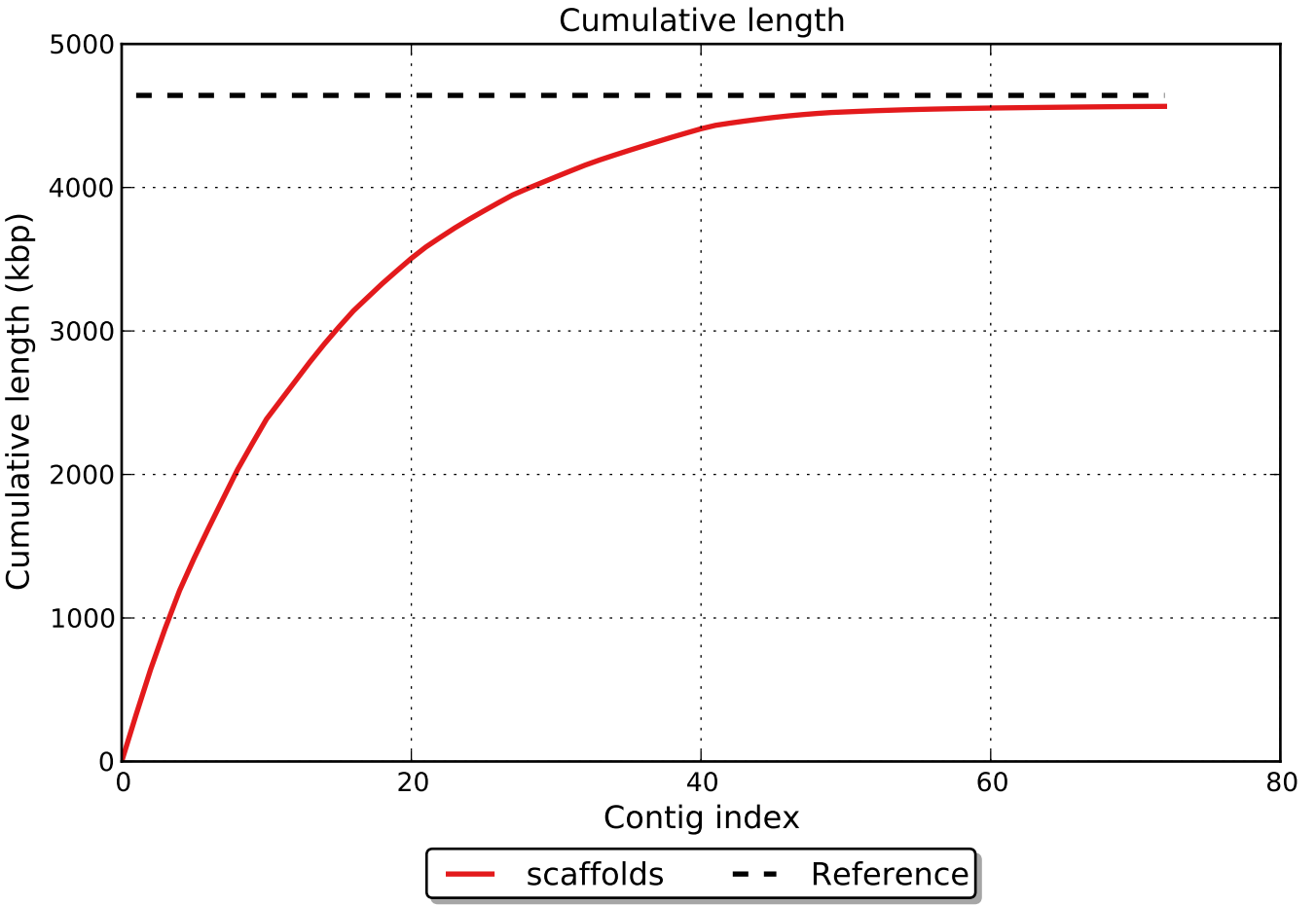
Unaligned report

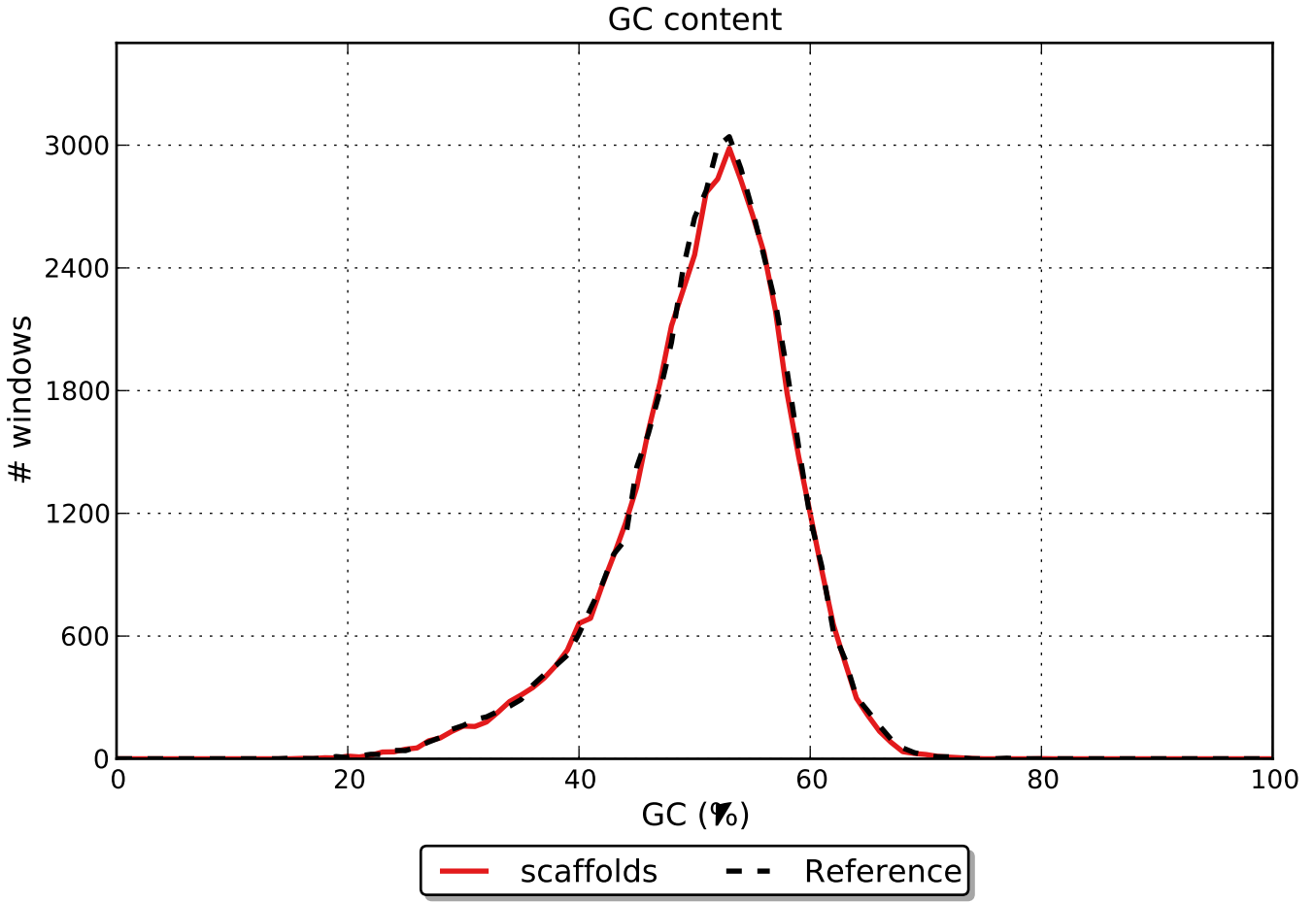
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

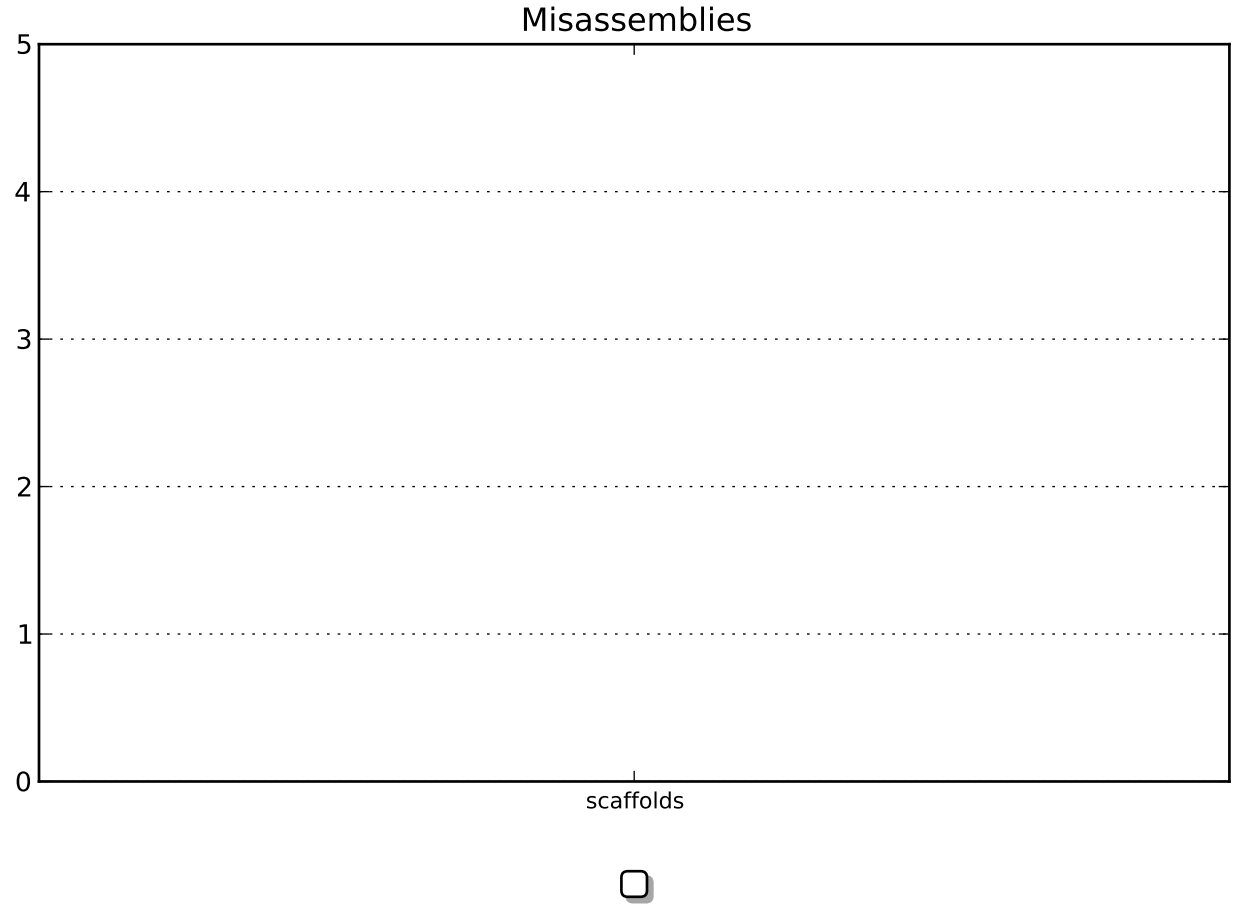
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

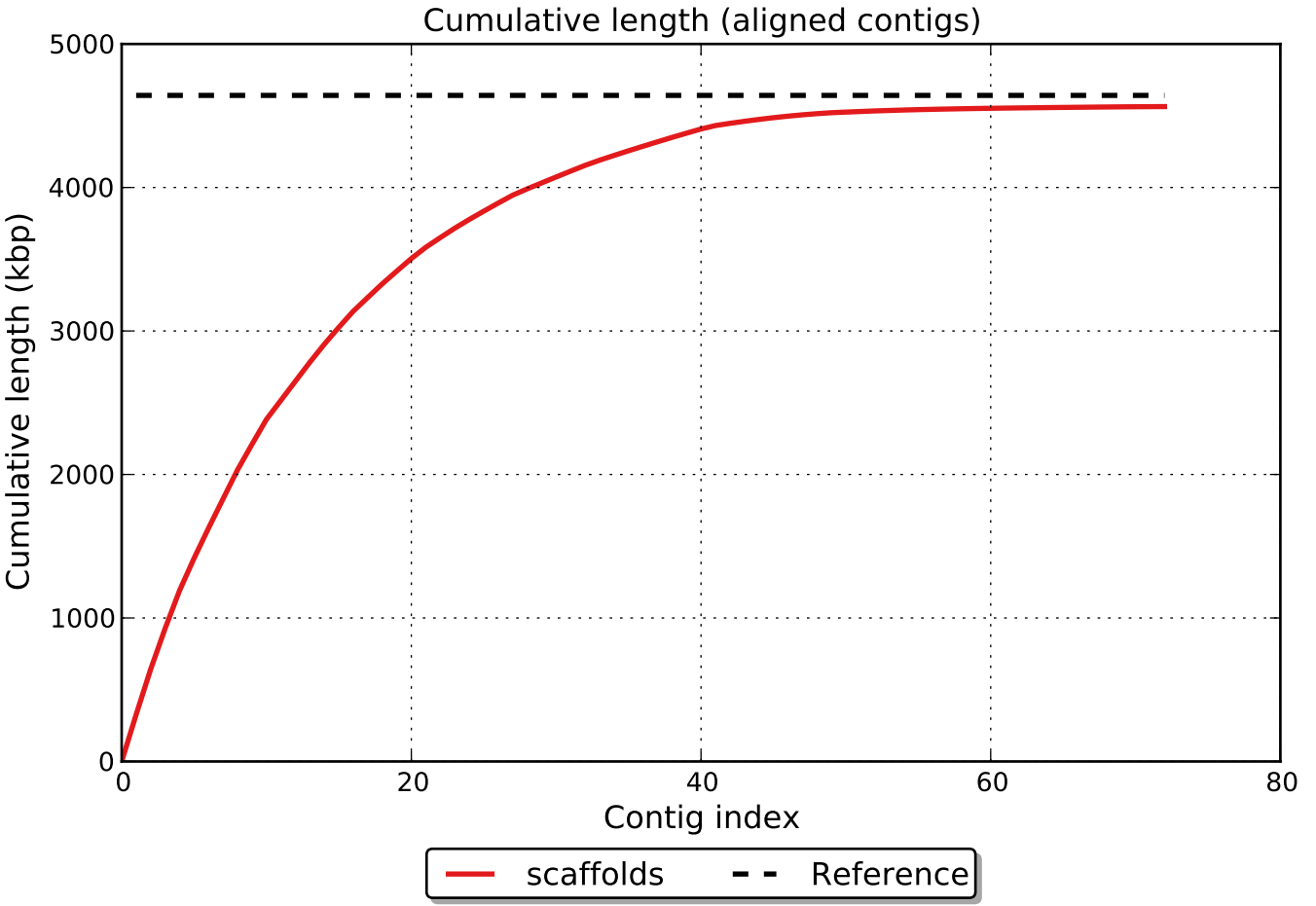

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

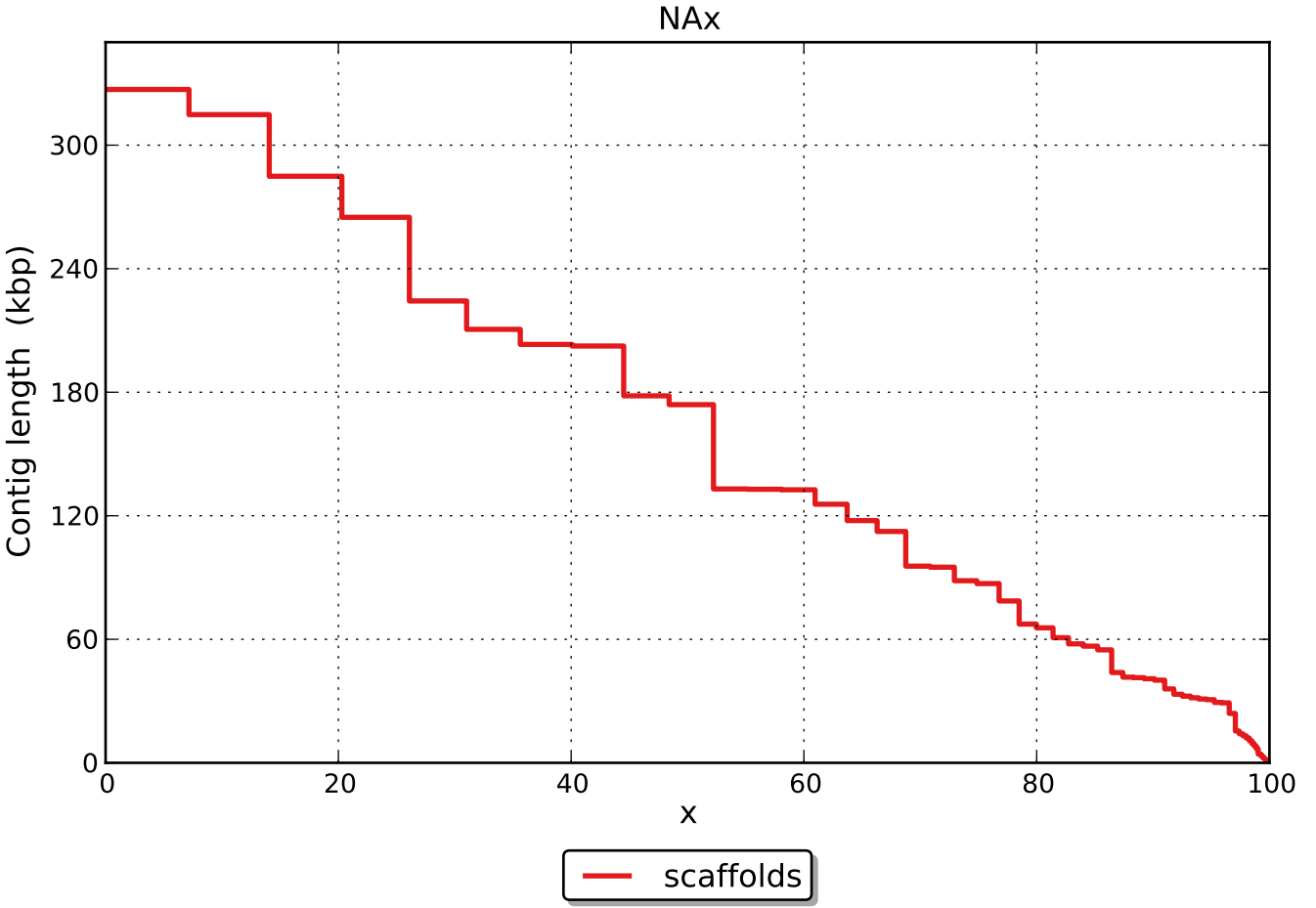

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

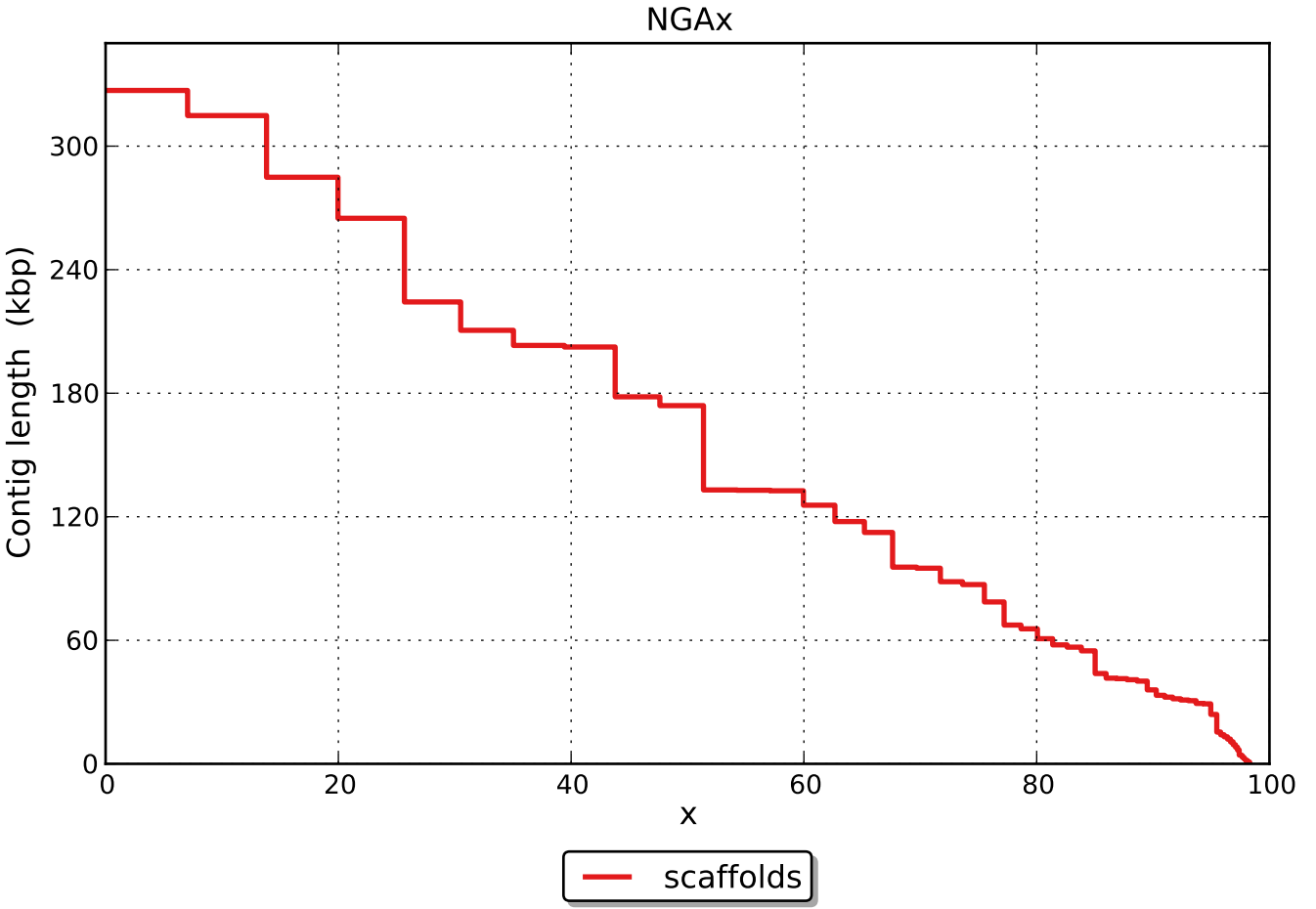

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
scaffolds
Reference


GC content
windows
3000
2400
1800
1200
600
0
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
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds