Report

	scaffolds
# contigs (>= 1000 bp)	42
# contigs (>= 5000 bp)	32
# contigs (>= 10000 bp)	32
# contigs (>= 25000 bp)	28
# contigs (>= 50000 bp)	22
Total length (>= 1000 bp)	4568710
Total length (>= 5000 bp)	4554211
Total length (>= 10000 bp)	4554211
Total length (>= 25000 bp)	4482201
Total length (>= 50000 bp)	4258569
# contigs	51
Largest contig	600951
Total length	4574764
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.78
N50	239444
NG50	239444
N75	116014
NG75	116014
L50	7
LG50	7
L75	13
LG75	13
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.532
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	576.18
# indels per 100 kbp	0.90
Largest alignment	600951
NA50	239444
NGA50	239444
NA75	116014
NGA75	116014
LA50	7
LGA50	7
LA75	13
LGA75	13

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

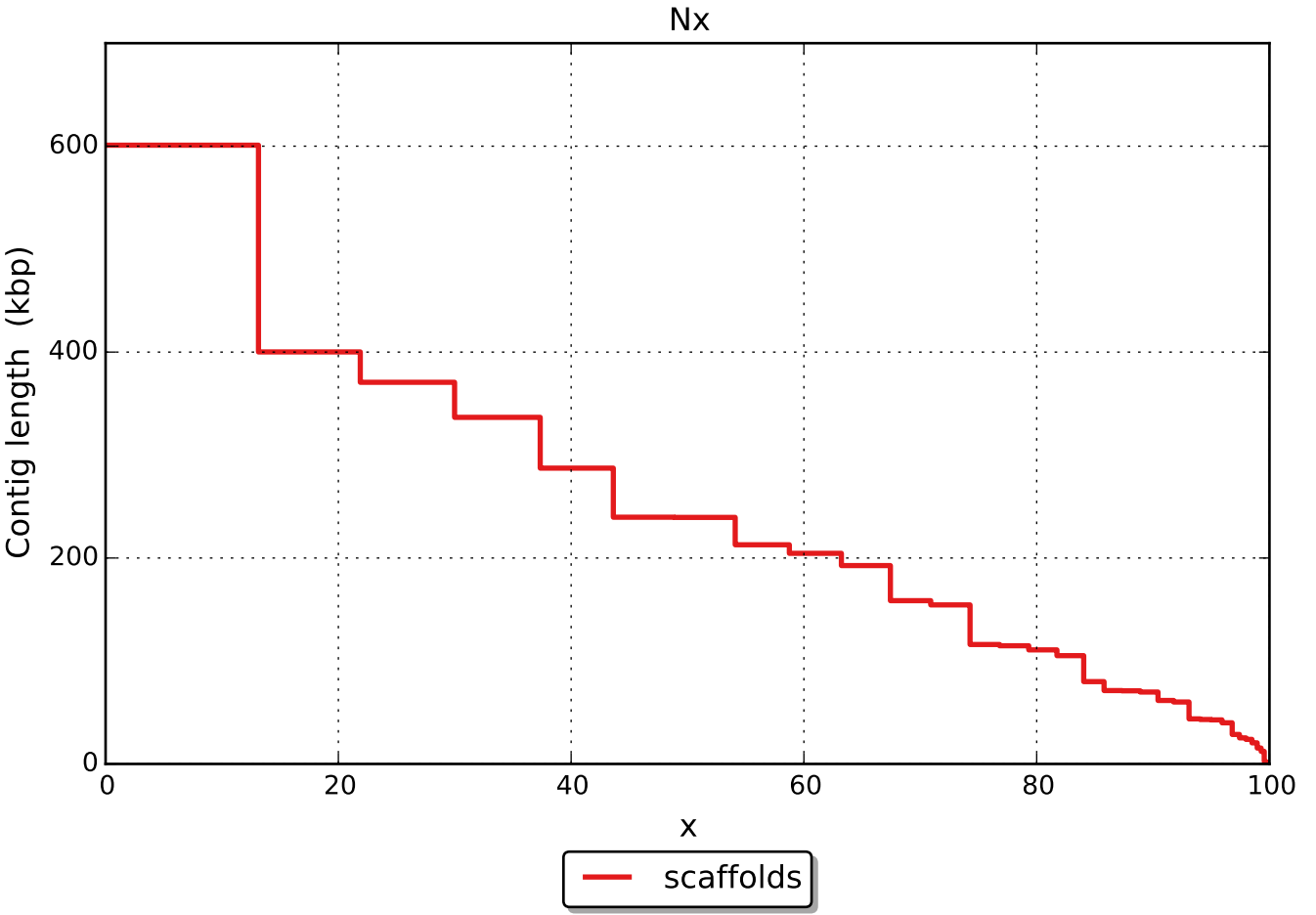
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	26352
# indels	41
# short indels	41
# long indels	0
Indels length	41

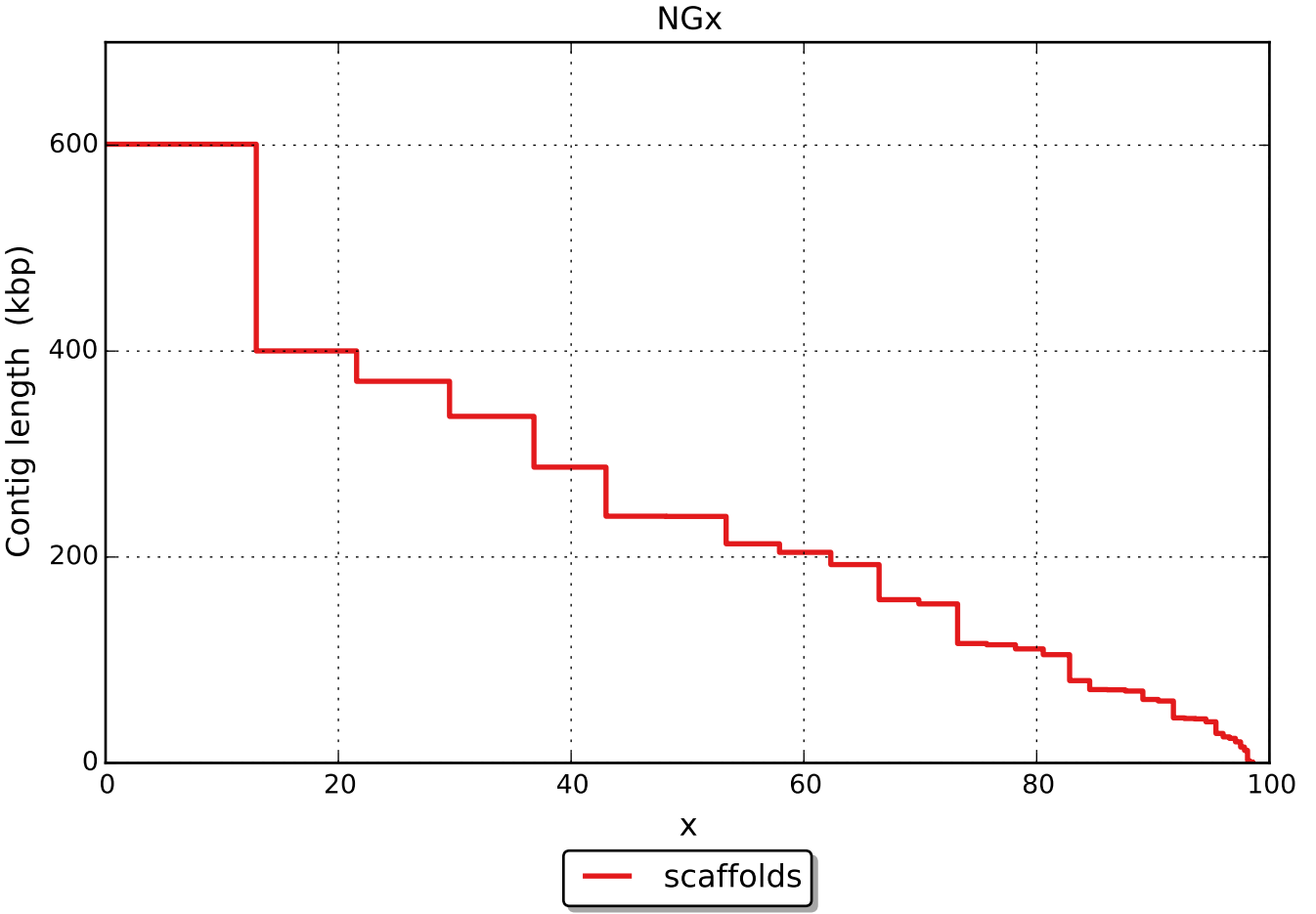
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

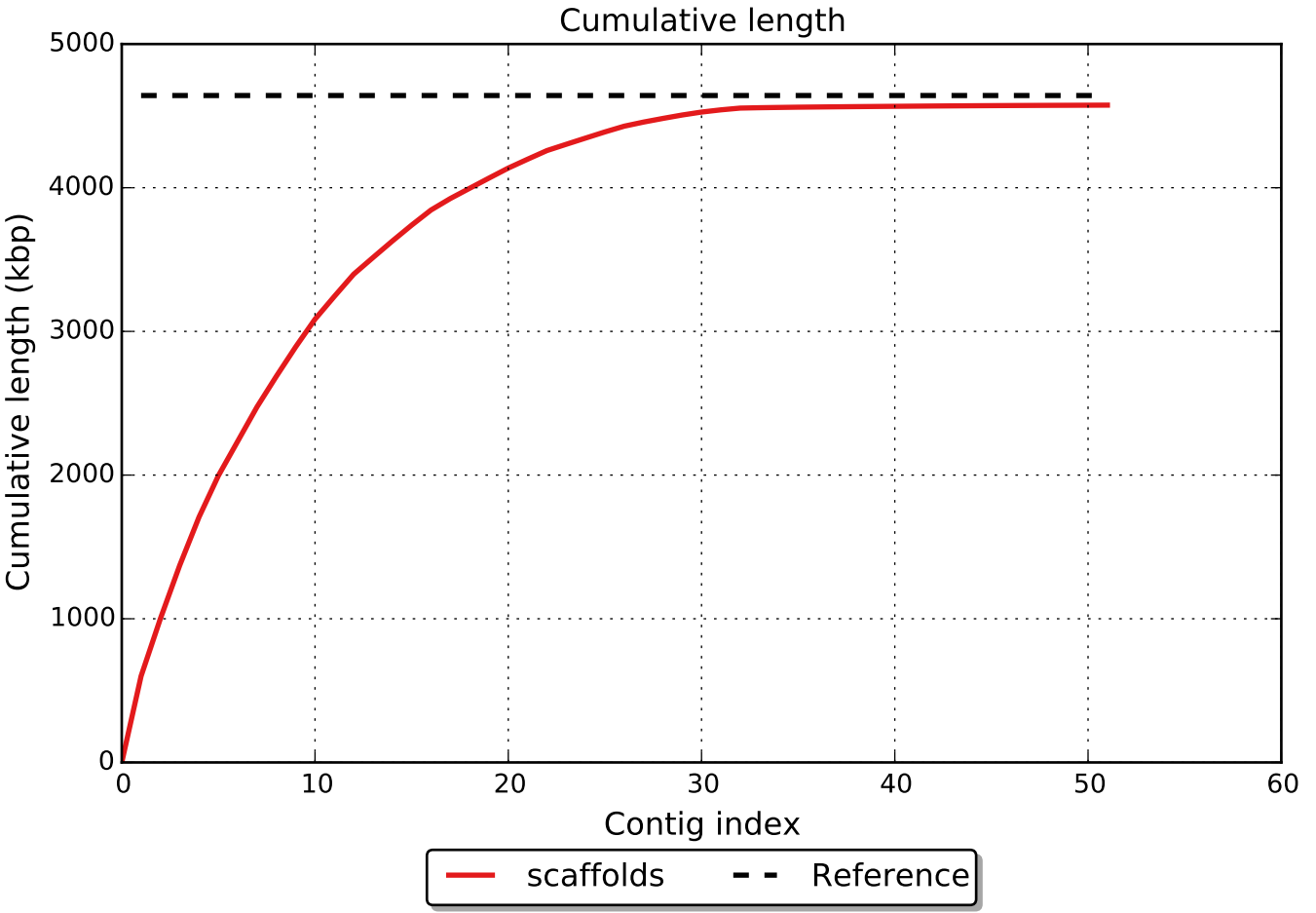
Unaligned report

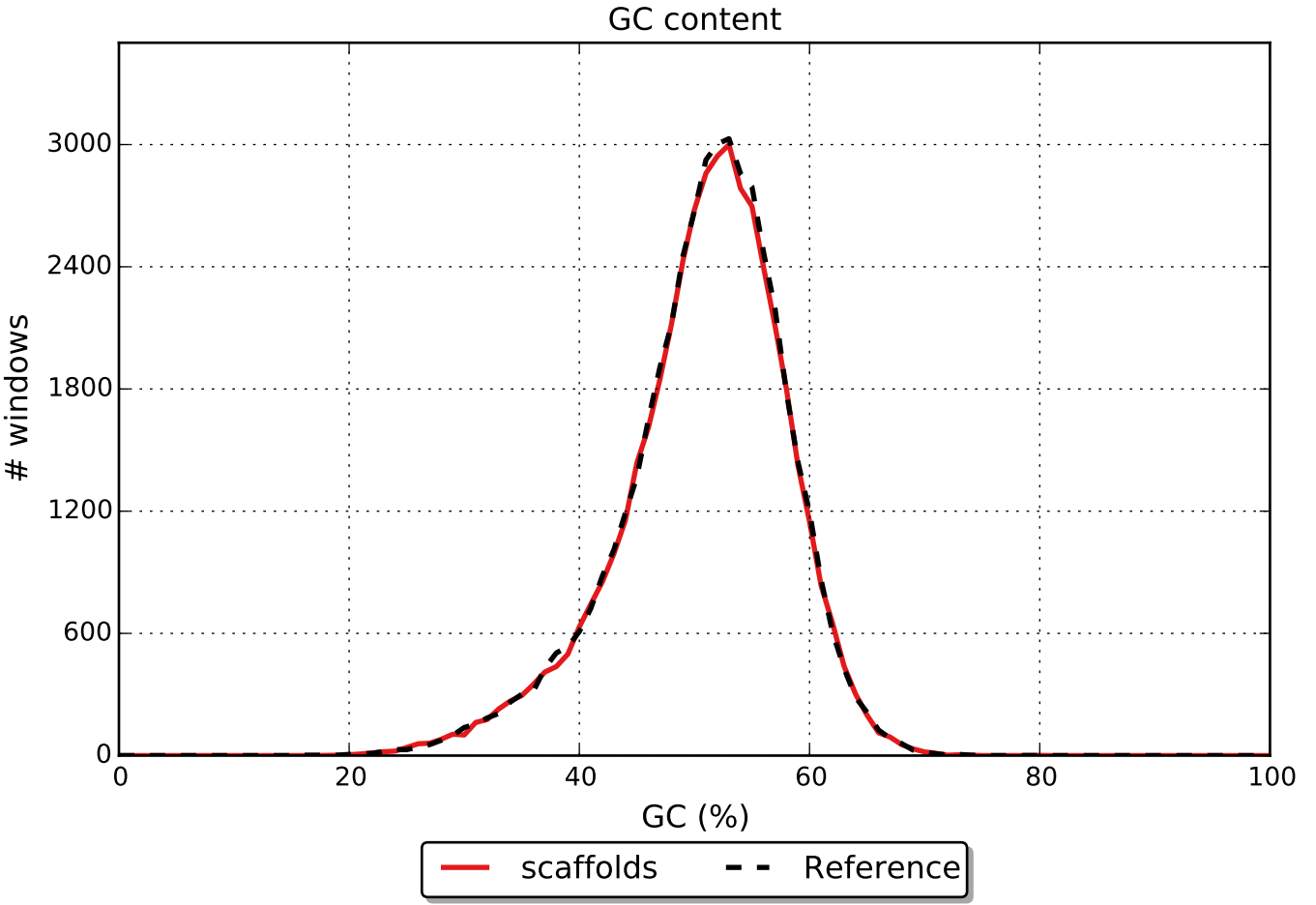
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

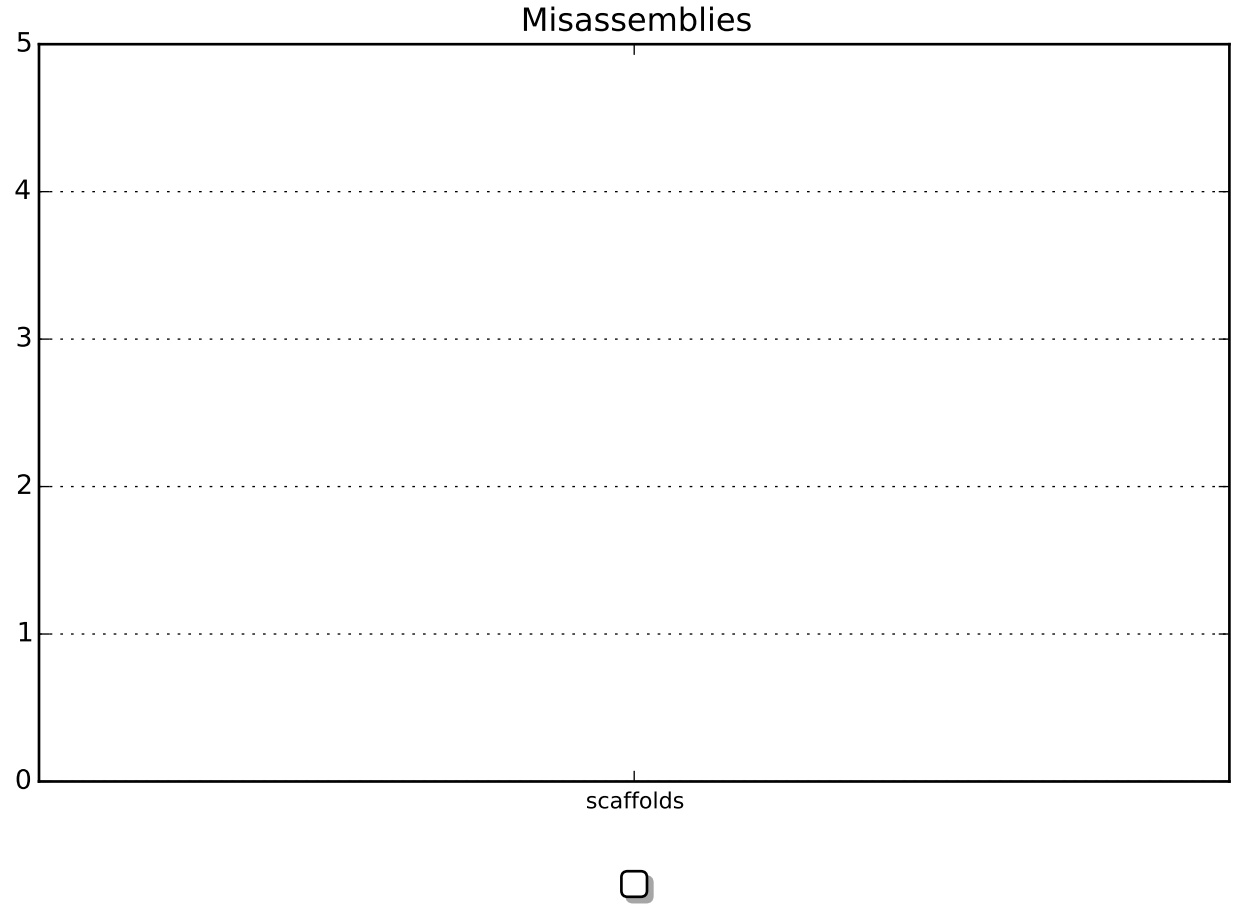
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

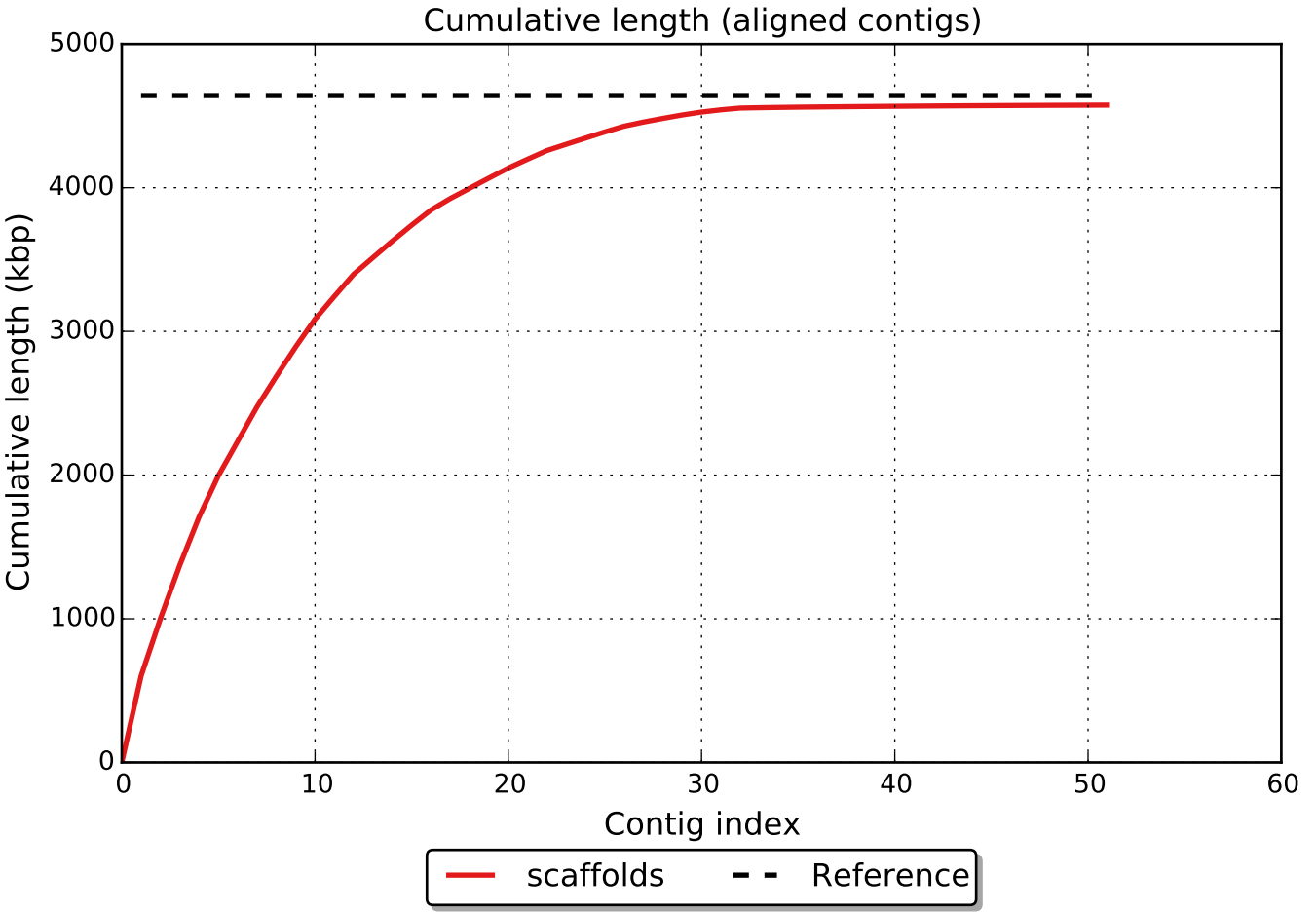

Nx
Contig length (kbp)
600
400
200
0
0
20
40
60
80
100
x
scaffolds

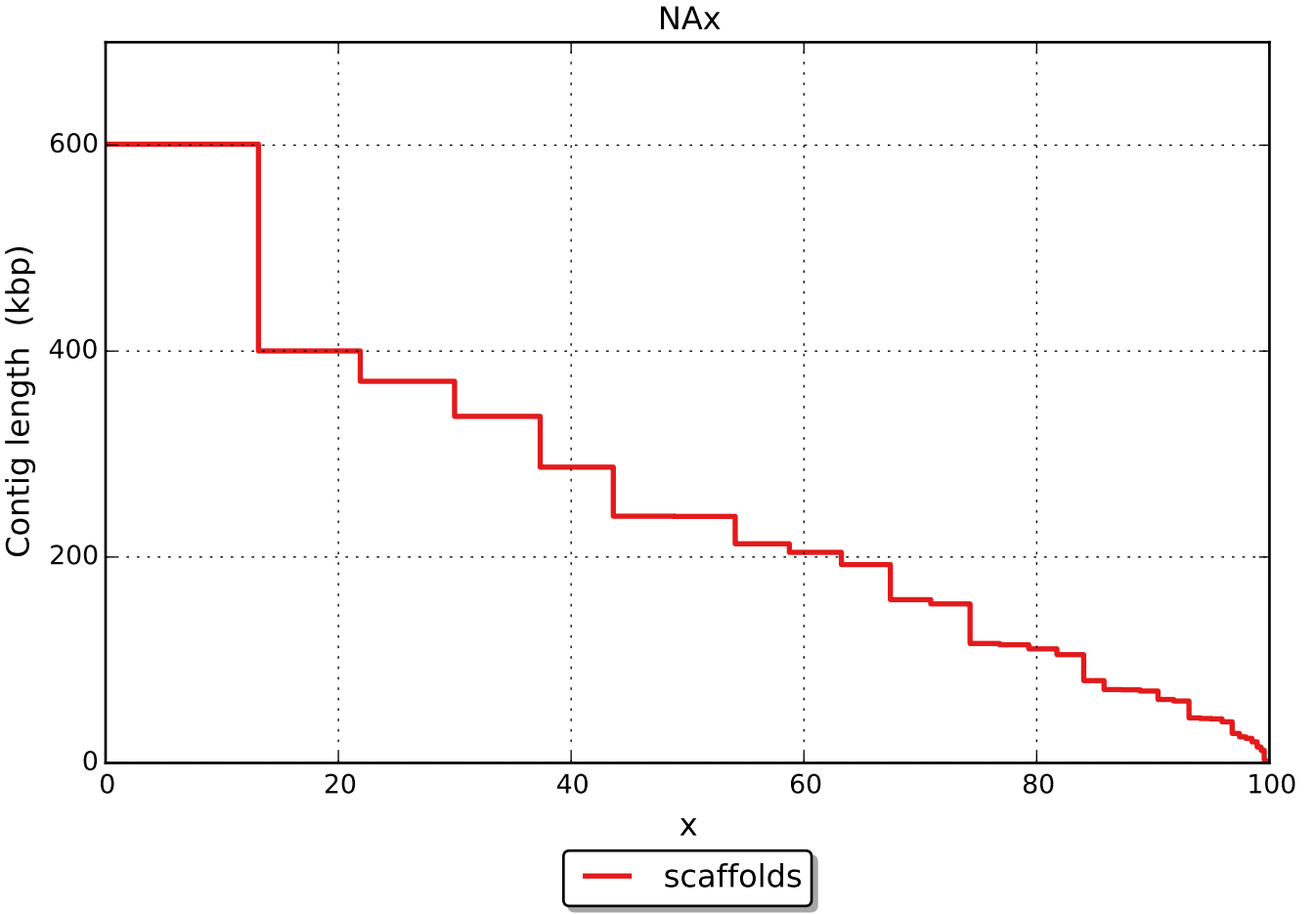

NGx
Contig length (kbp)
600
400
200
0
0
20
40
60
80
100
x
scaffolds

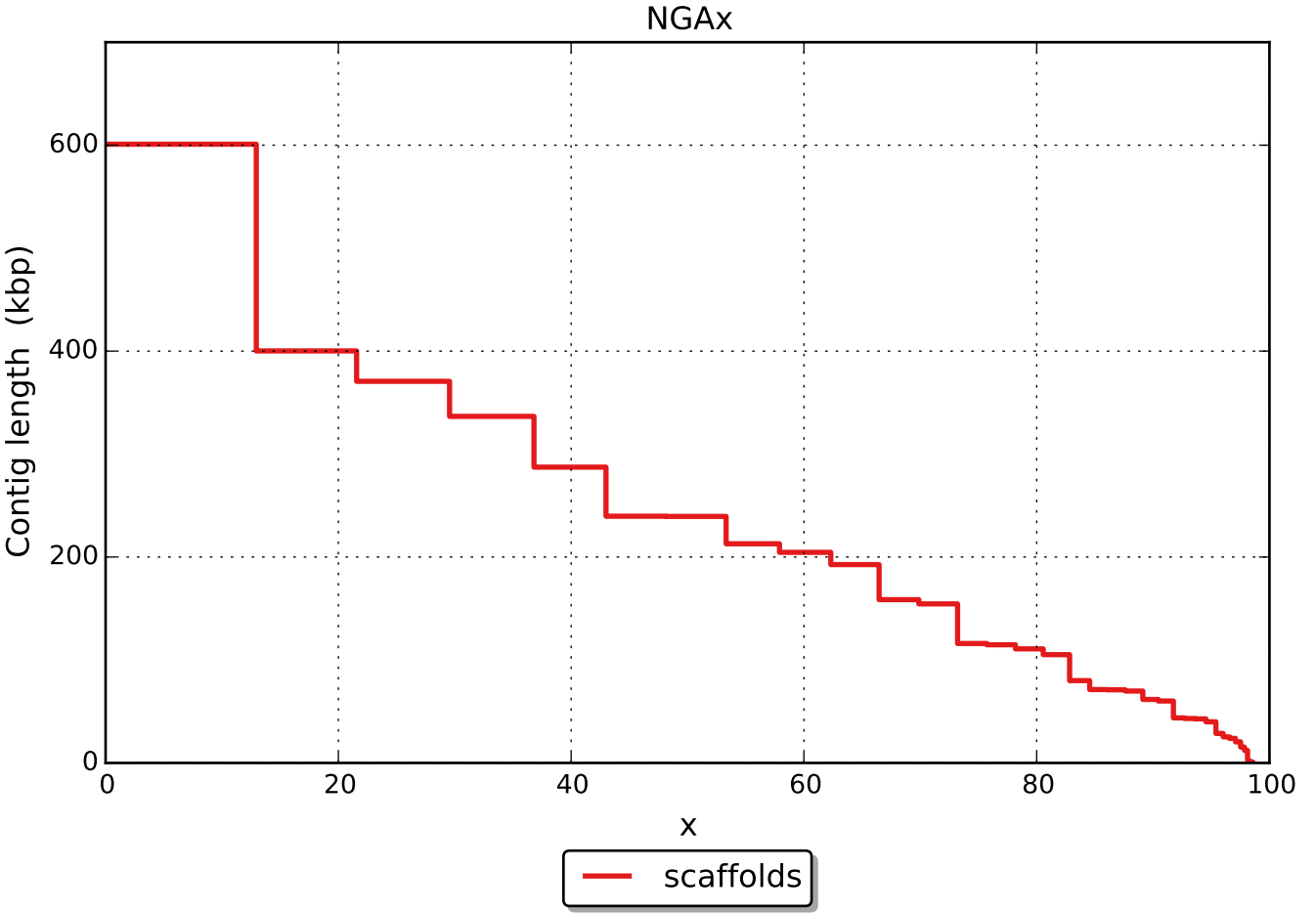

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
10
20
30
40
50
60
Contig index
scaffolds
Reference


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
10
20
30
40
50
60
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
600
400
200
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
600
400
200
0
0
20
40
60
80
100
x
scaffolds