Report

	contigs
# contigs (>= 0 bp)	145
# contigs (>= 1000 bp)	79
# contigs (>= 5000 bp)	59
# contigs (>= 10000 bp)	51
# contigs (>= 25000 bp)	47
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4574593
Total length (>= 1000 bp)	4555397
Total length (>= 5000 bp)	4511772
Total length (>= 10000 bp)	4451665
Total length (>= 25000 bp)	4388125
Total length (>= 50000 bp)	3757635
# contigs	89
Largest contig	327173
Total length	4562285
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	132662
NG50	132662
N75	59713
NG75	57882
L50	12
LG50	12
L75	24
LG75	25
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.221
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.92
# indels per 100 kbp	0.26
Largest alignment	327173
NA50	132662
NGA50	132662
NA75	59713
NGA75	57882
LA50	12
LGA50	12
LA75	24
LGA75	25

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

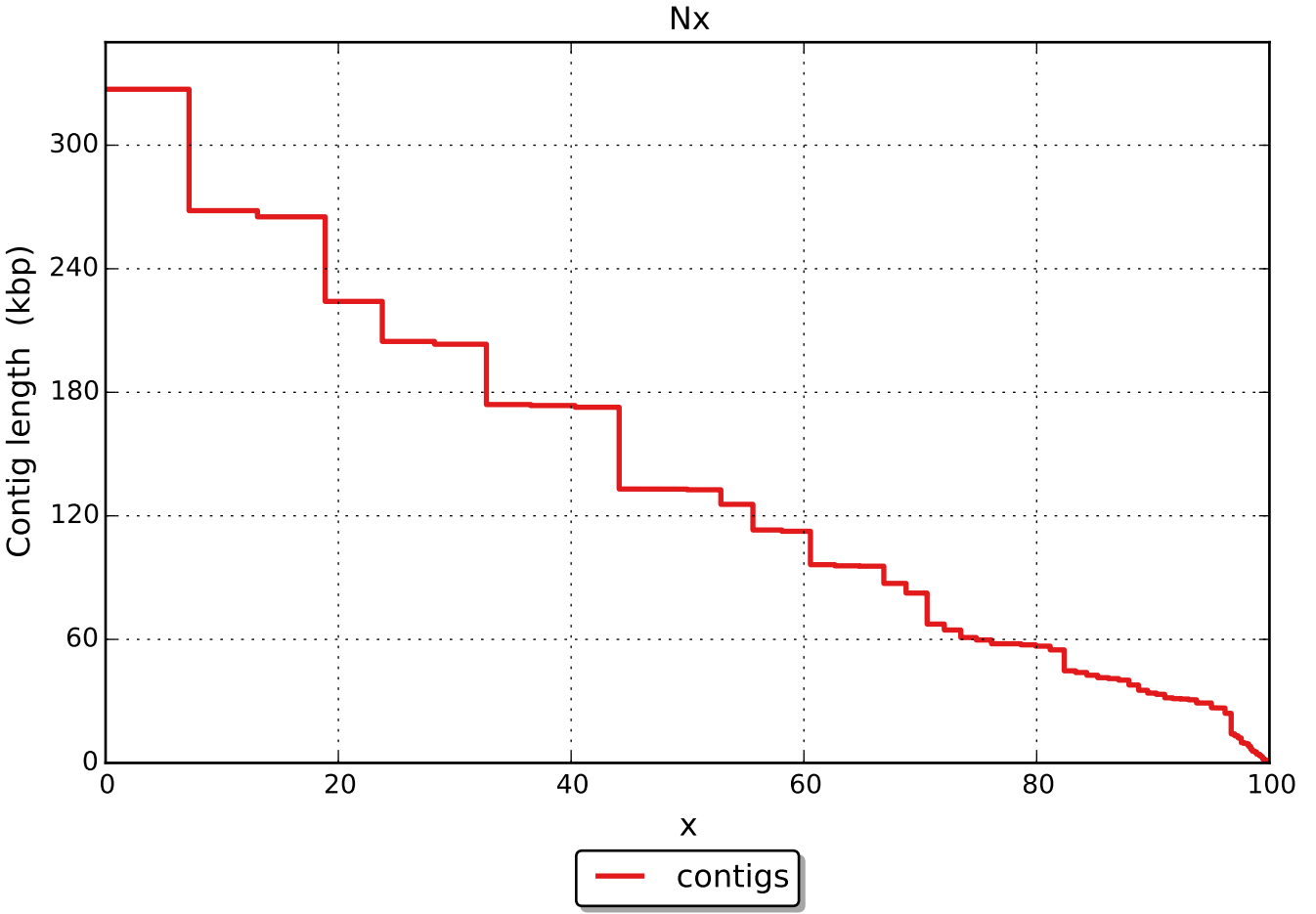
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# mismatches	270
# indels	12
# short indels	12
# long indels	0
Indels length	14

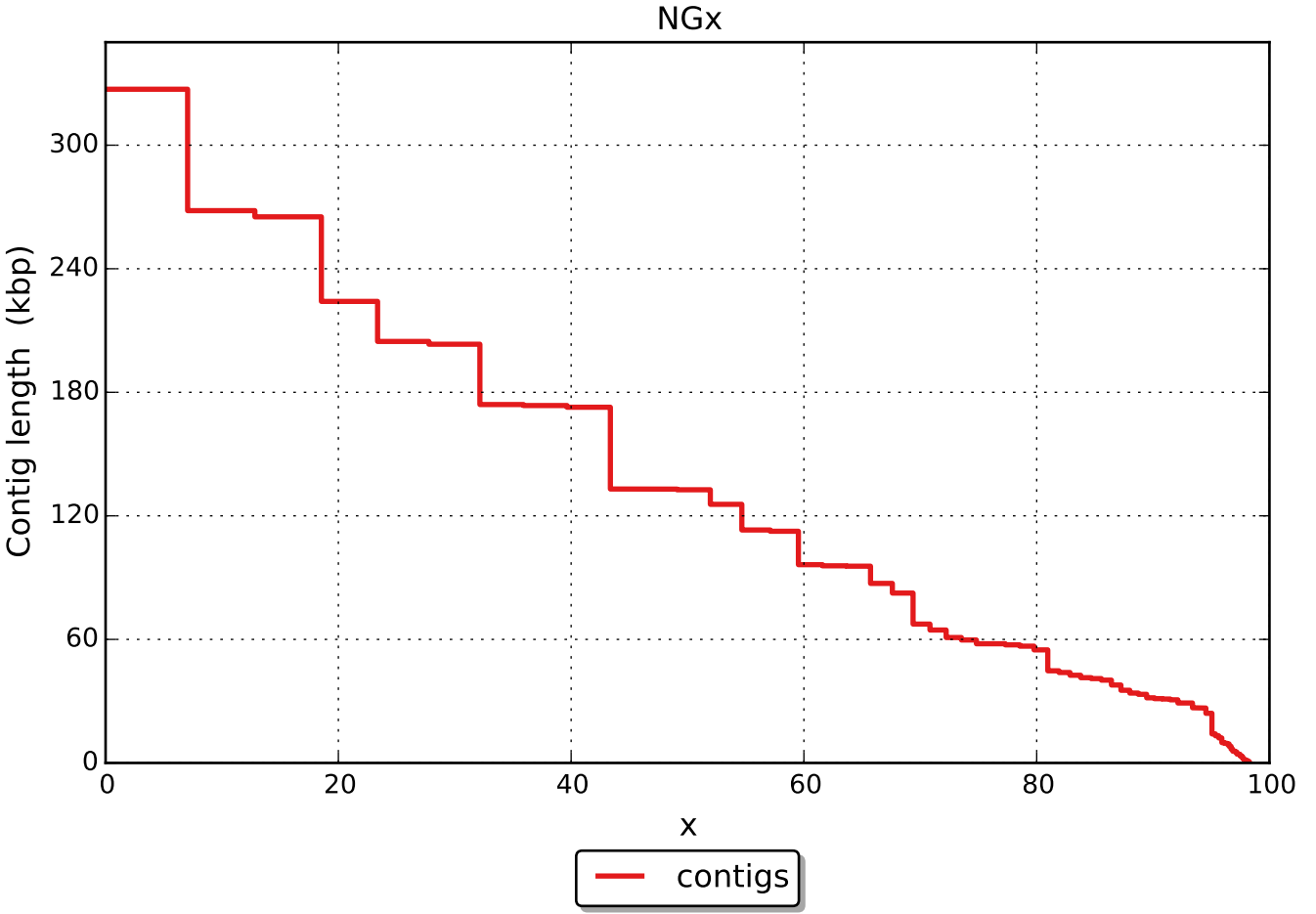
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

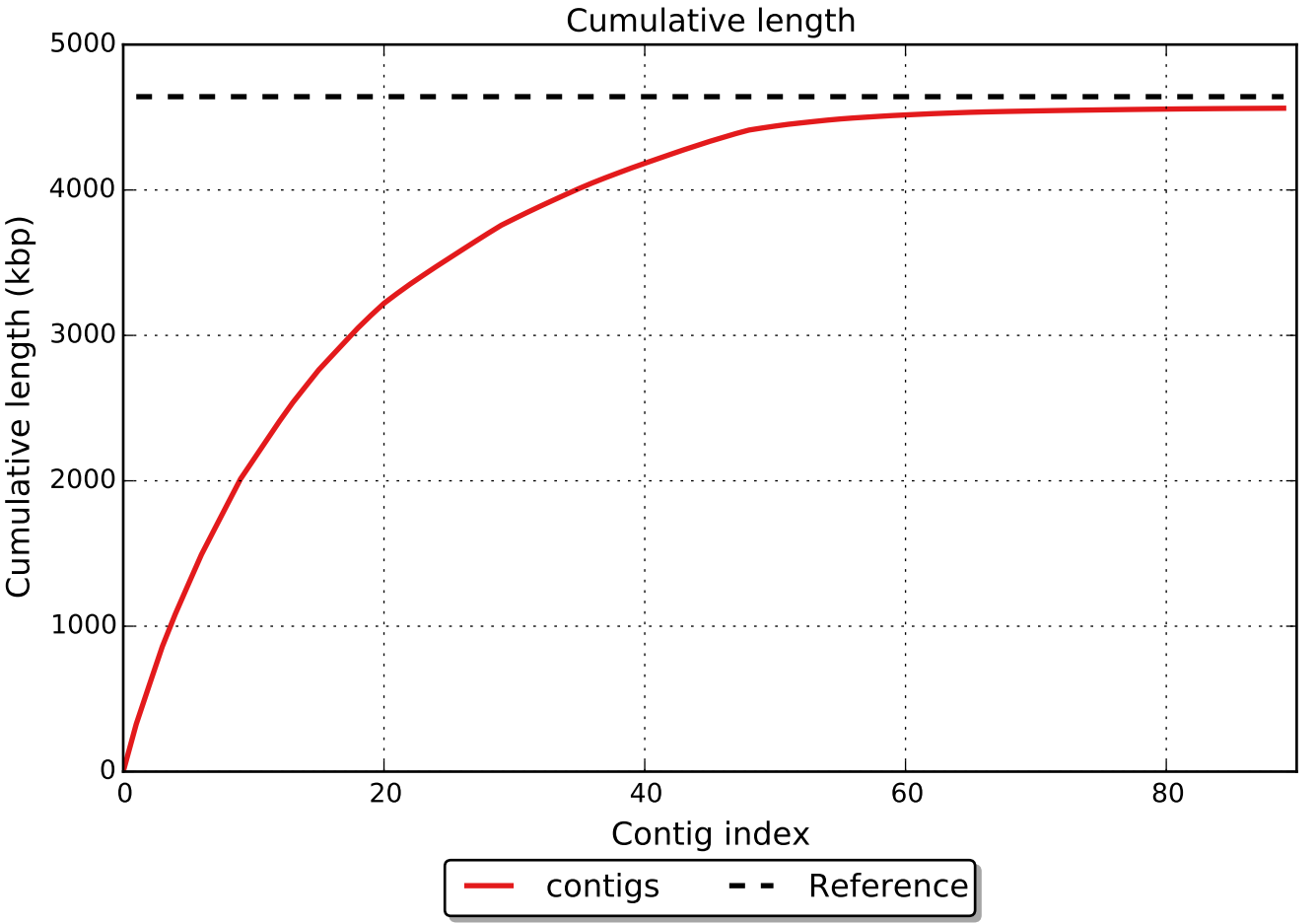
Unaligned report

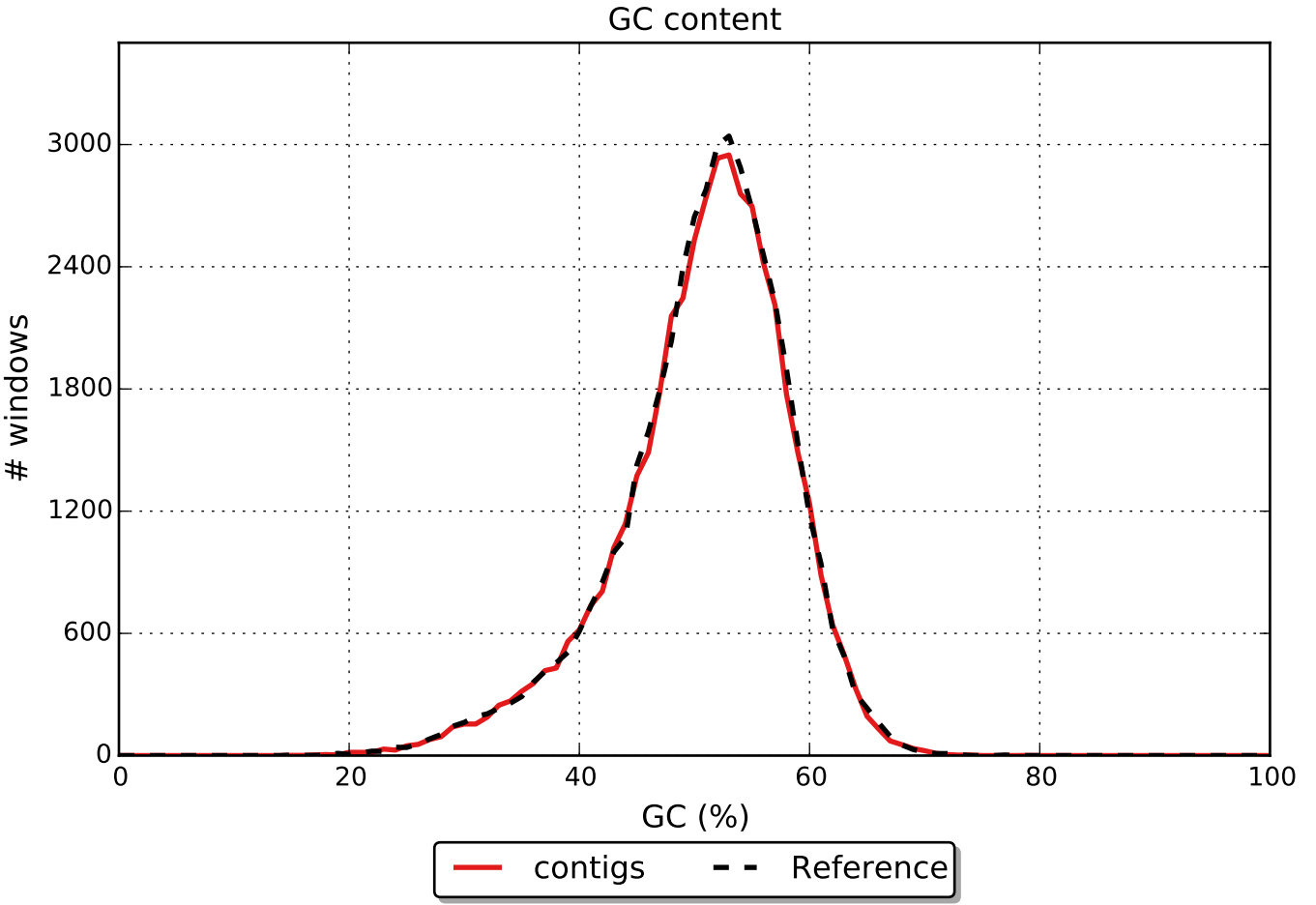
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

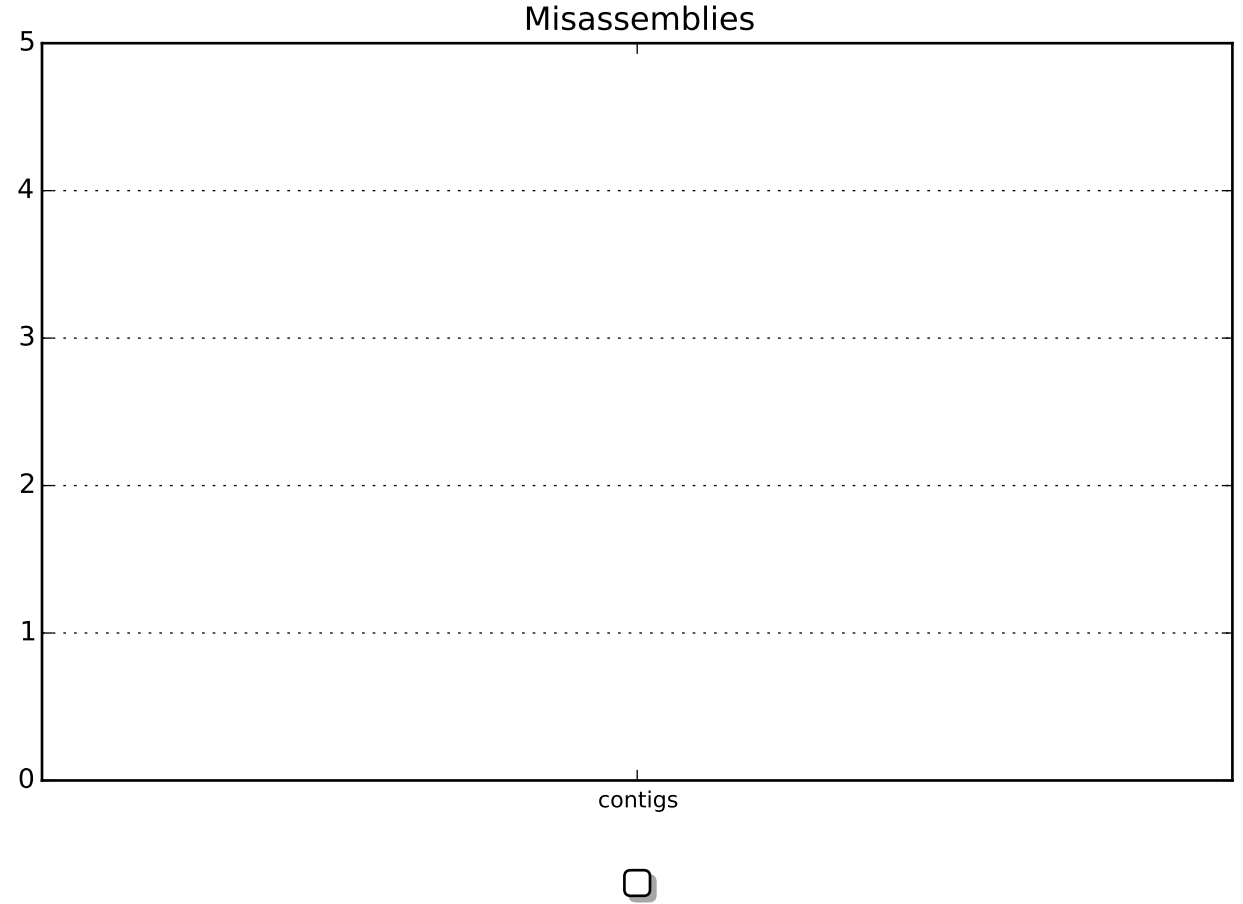
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

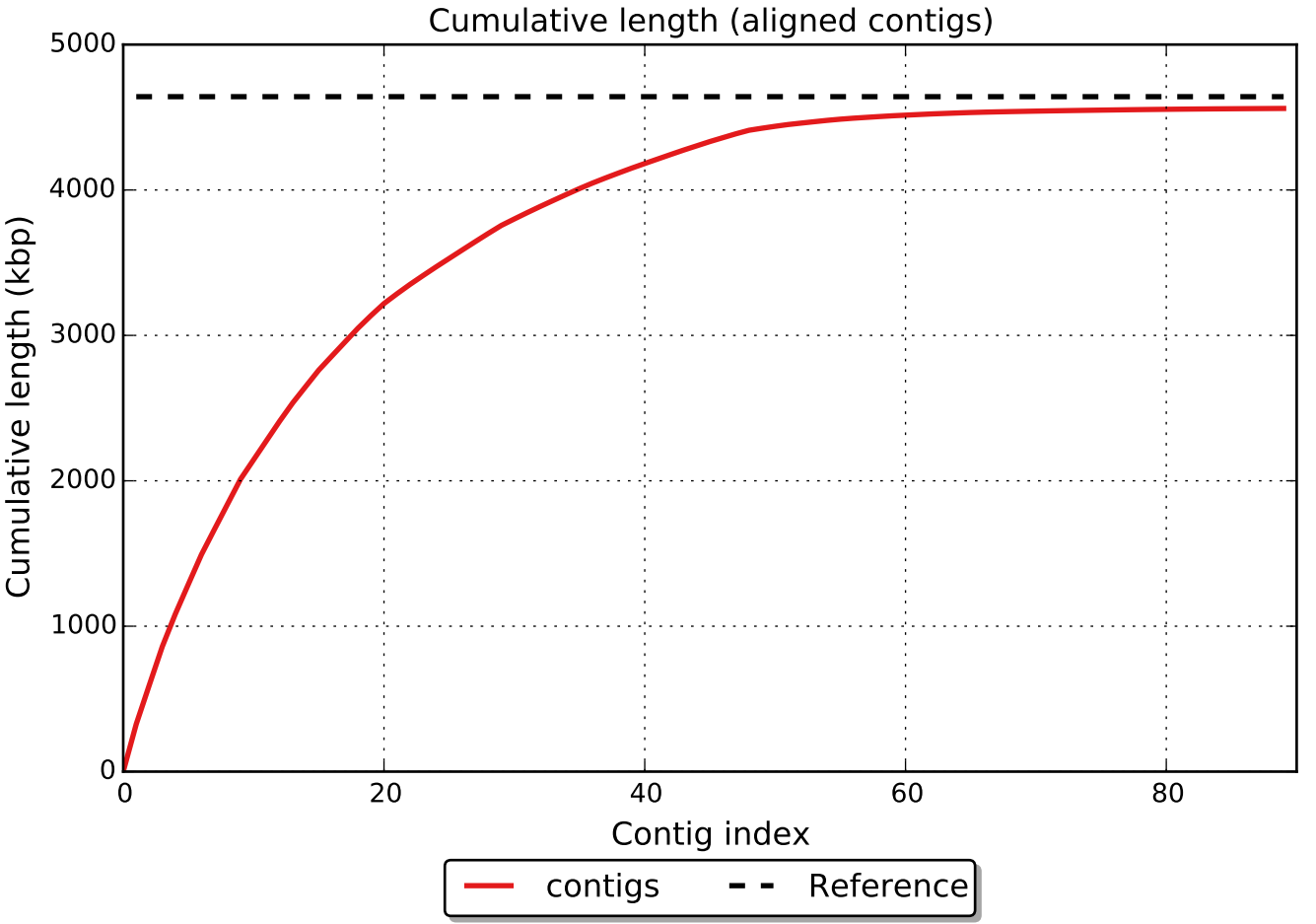

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

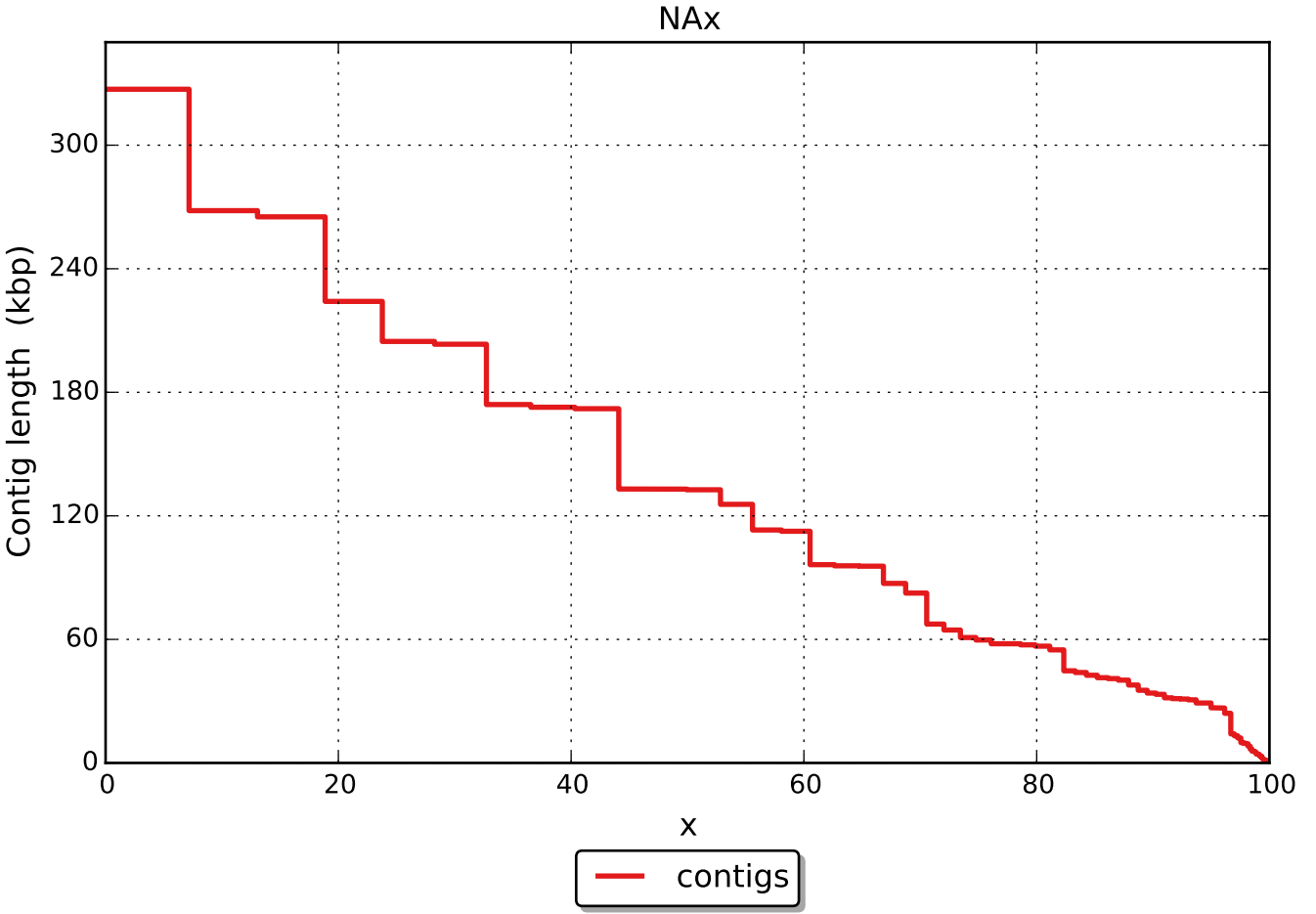

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

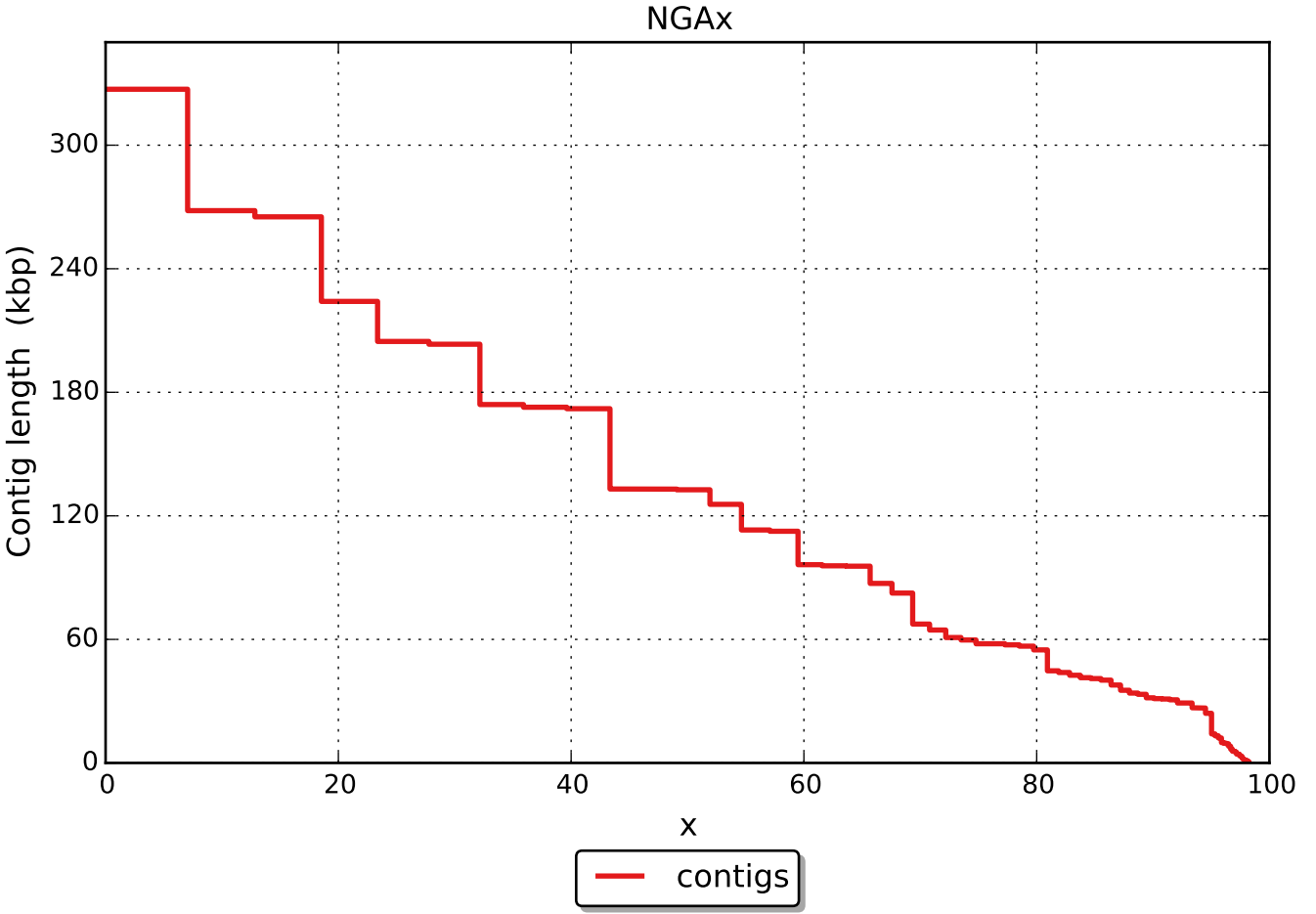

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
20
40
60
80
Contig index
contigs
Reference


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


Misassemblies
5
4
3
2
1
0
contigs


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


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


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