Report

	contigs
# contigs (>= 0 bp)	114
# contigs (>= 1000 bp)	72
# contigs (>= 5000 bp)	53
# contigs (>= 10000 bp)	48
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	4573774
Total length (>= 1000 bp)	4559272
Total length (>= 5000 bp)	4516140
Total length (>= 10000 bp)	4478999
Total length (>= 25000 bp)	4388736
Total length (>= 50000 bp)	3917454
# contigs	84
Largest contig	327173
Total length	4567347
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	133063
NG50	133063
N75	86633
NG75	78649
L50	11
LG50	11
L75	21
LG75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.325
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.17
# indels per 100 kbp	0.33
Largest alignment	327173
NA50	133063
NGA50	133063
NA75	86633
NGA75	78649
LA50	11
LGA50	11
LA75	21
LGA75	22

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

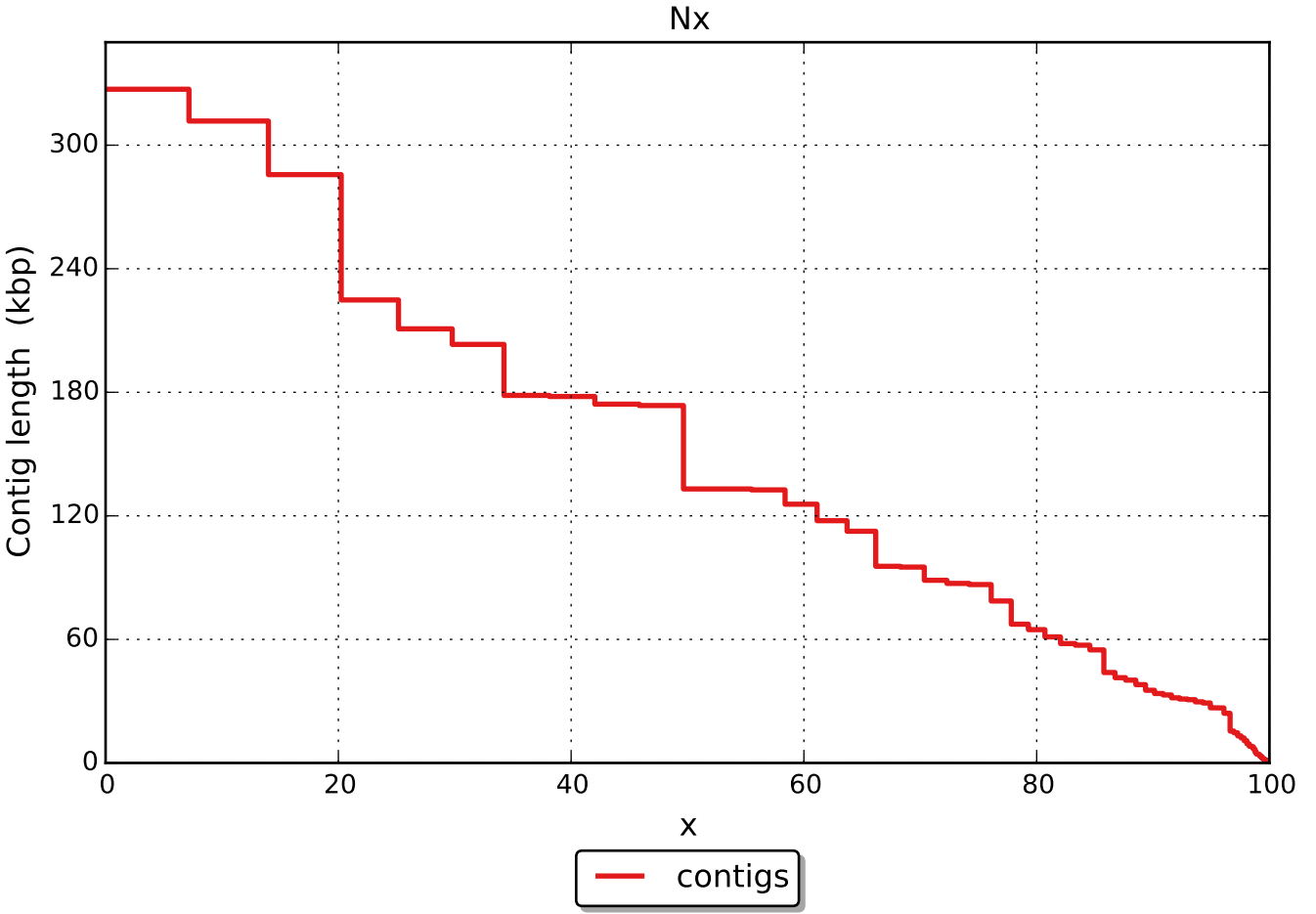
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# mismatches	99
# indels	15
# short indels	14
# long indels	1
Indels length	101

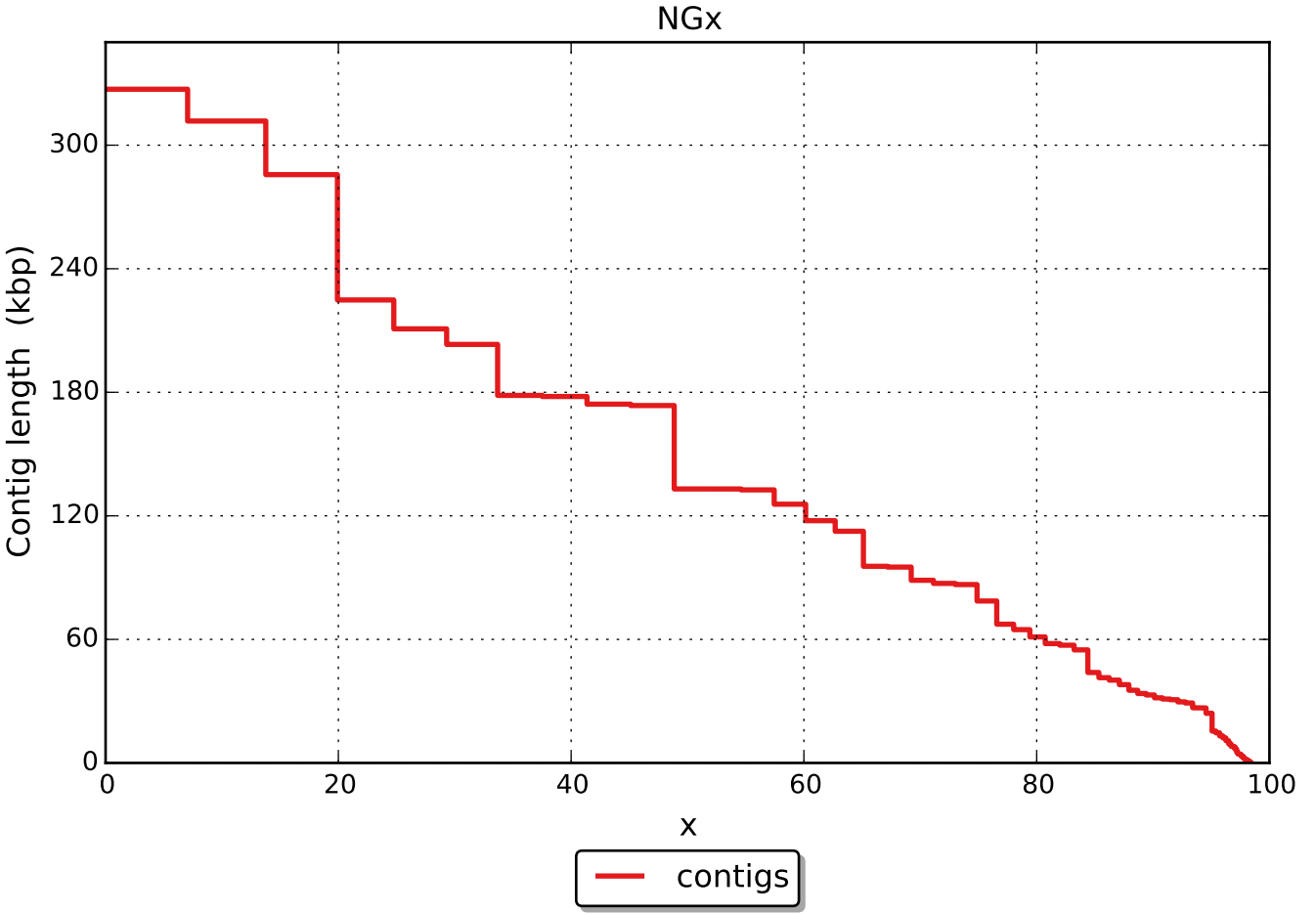
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

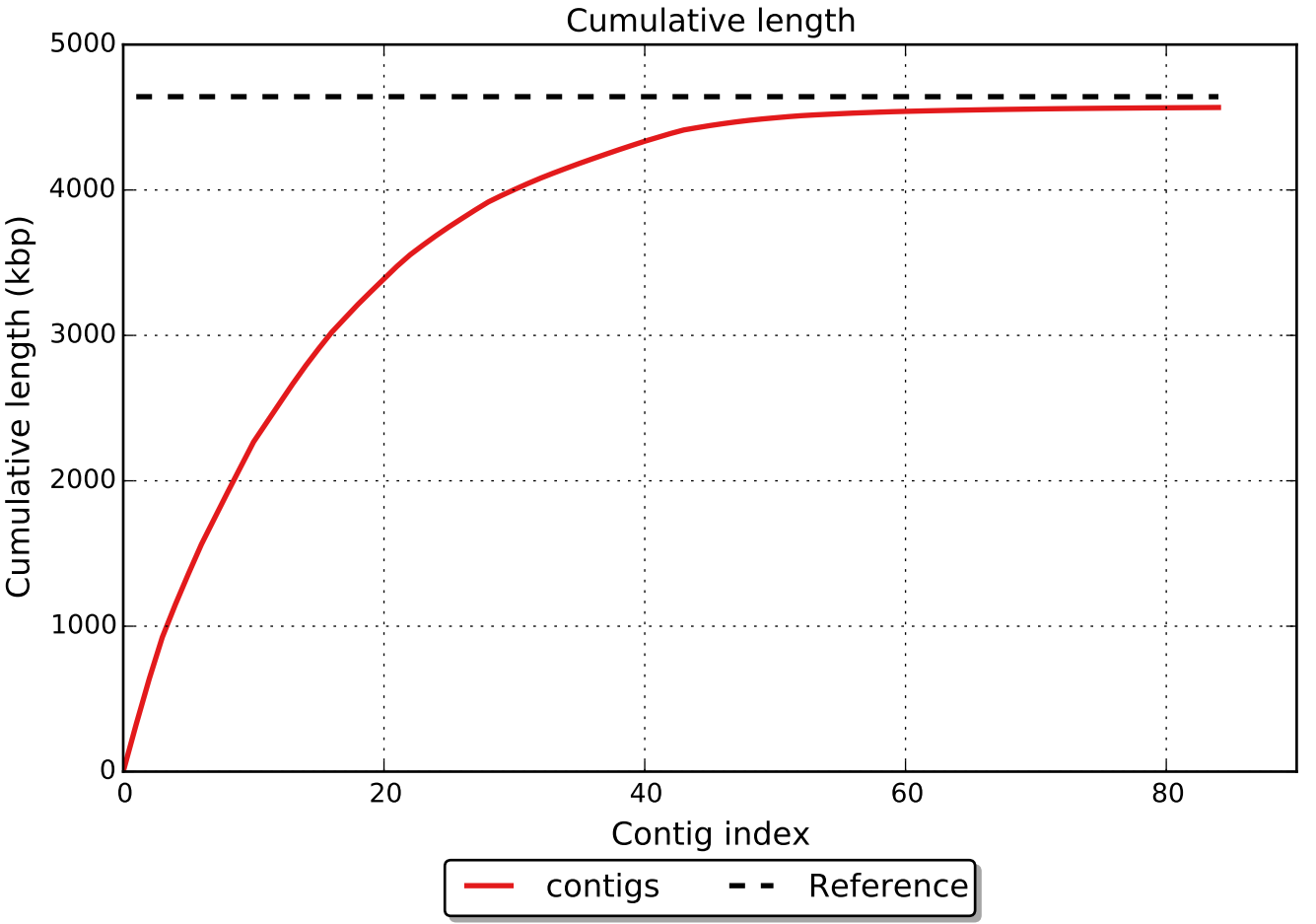
Unaligned report

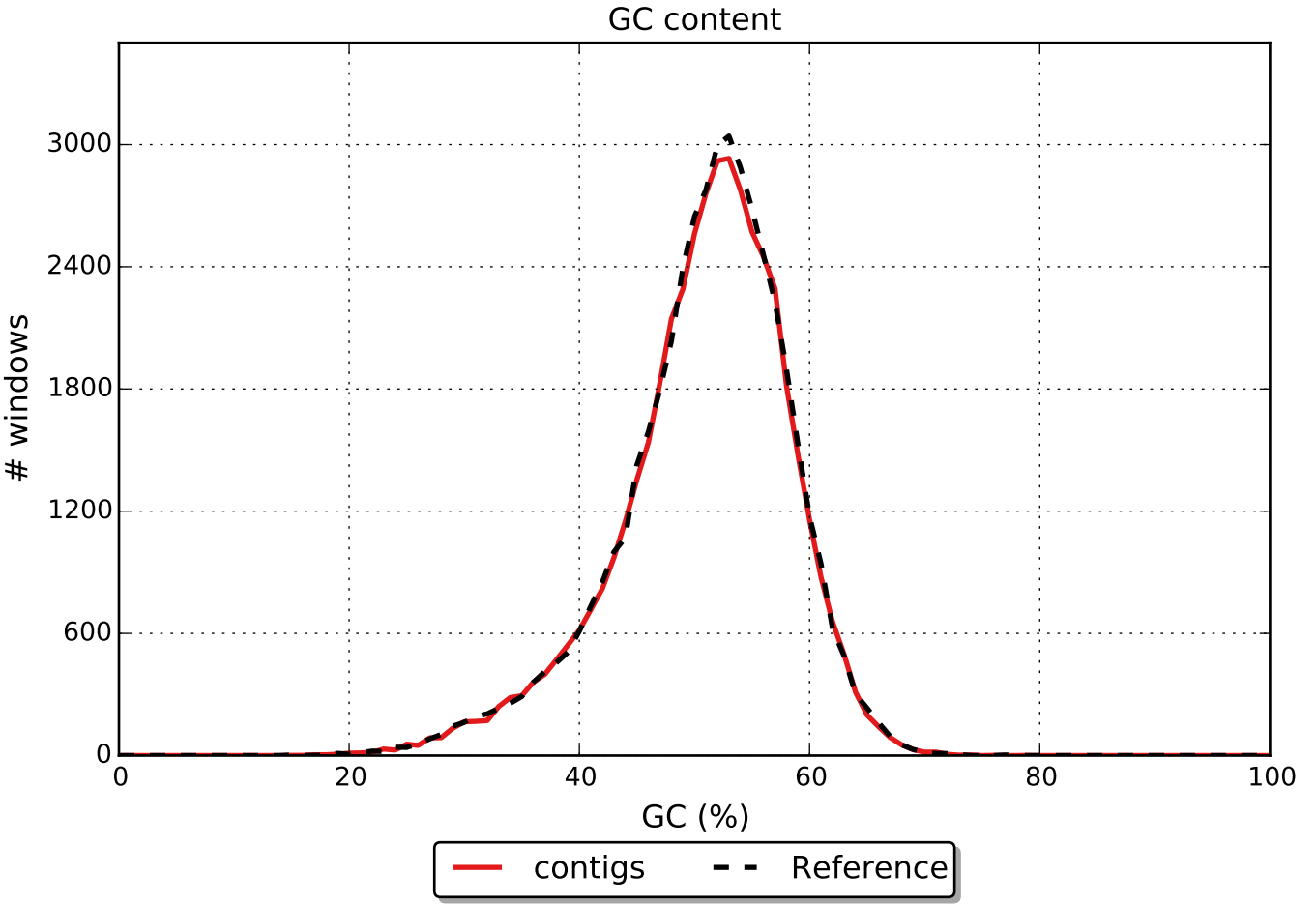
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

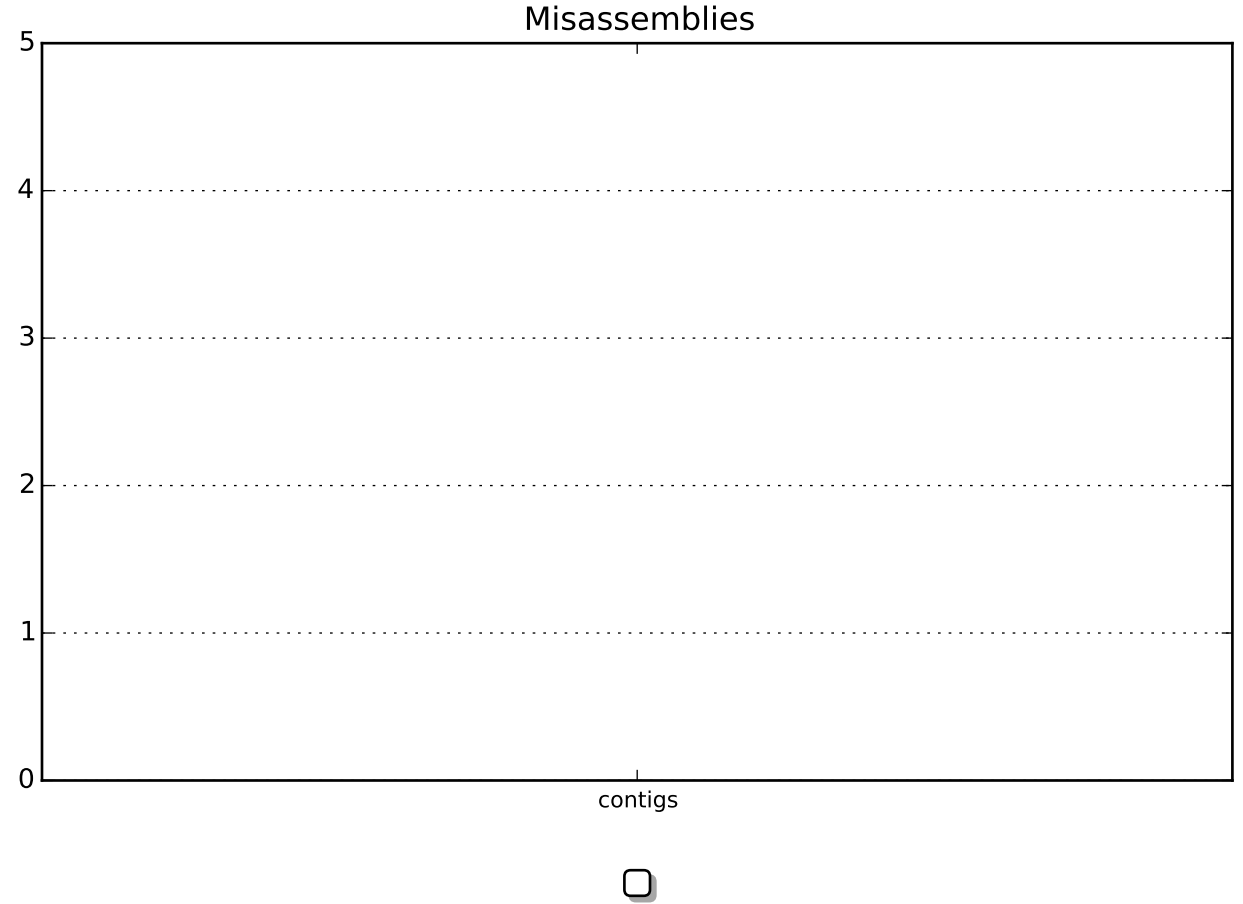
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

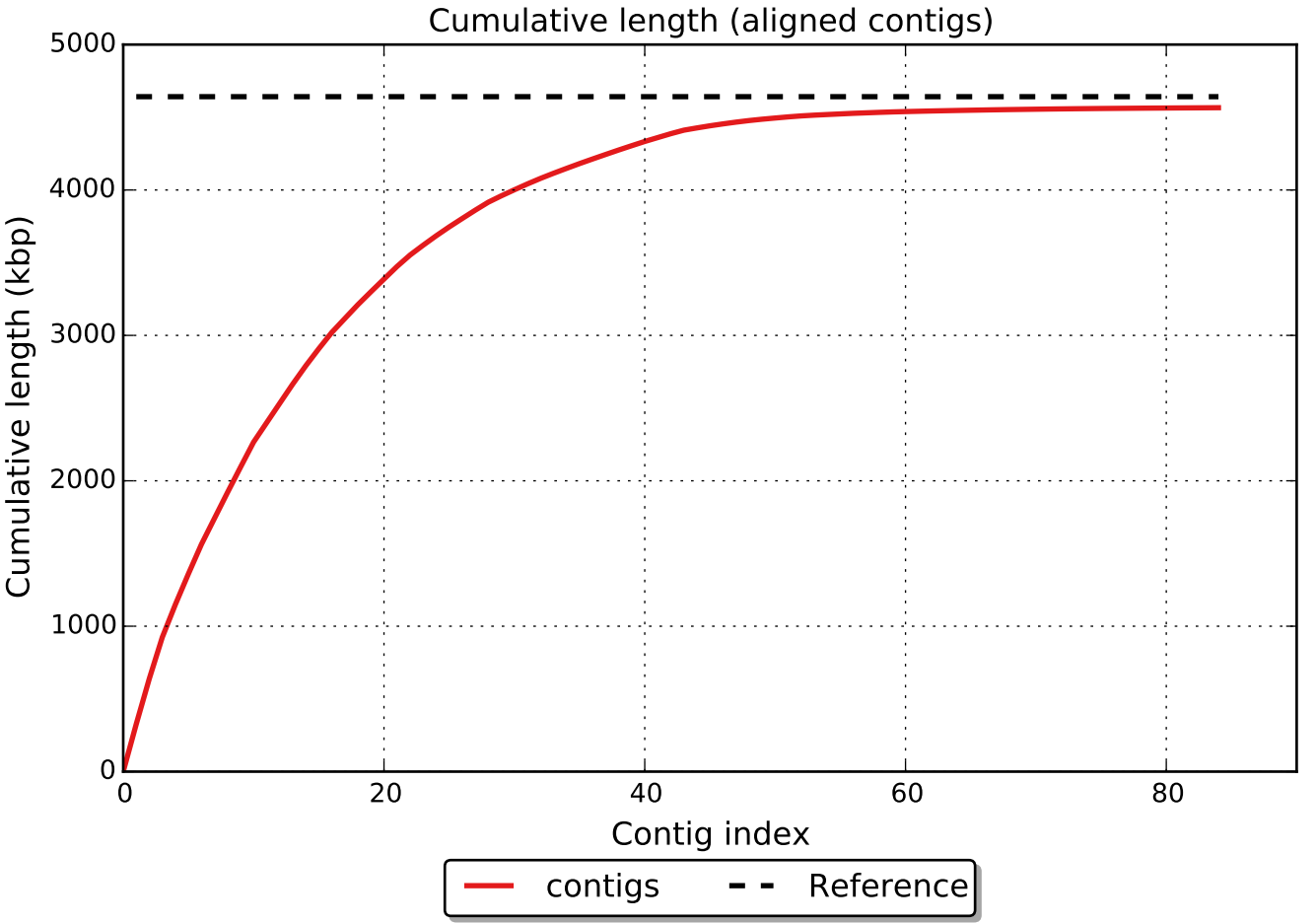

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

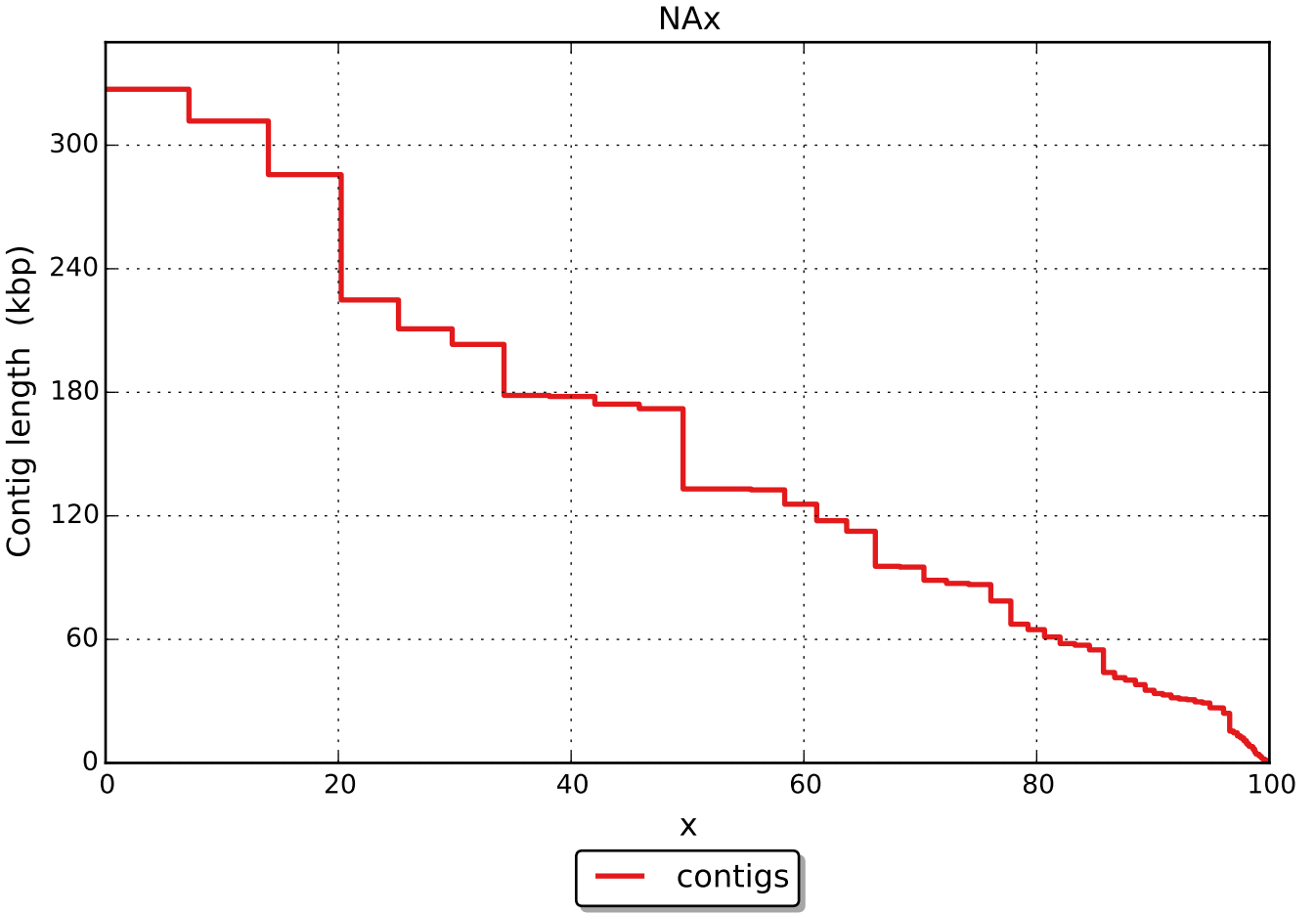

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

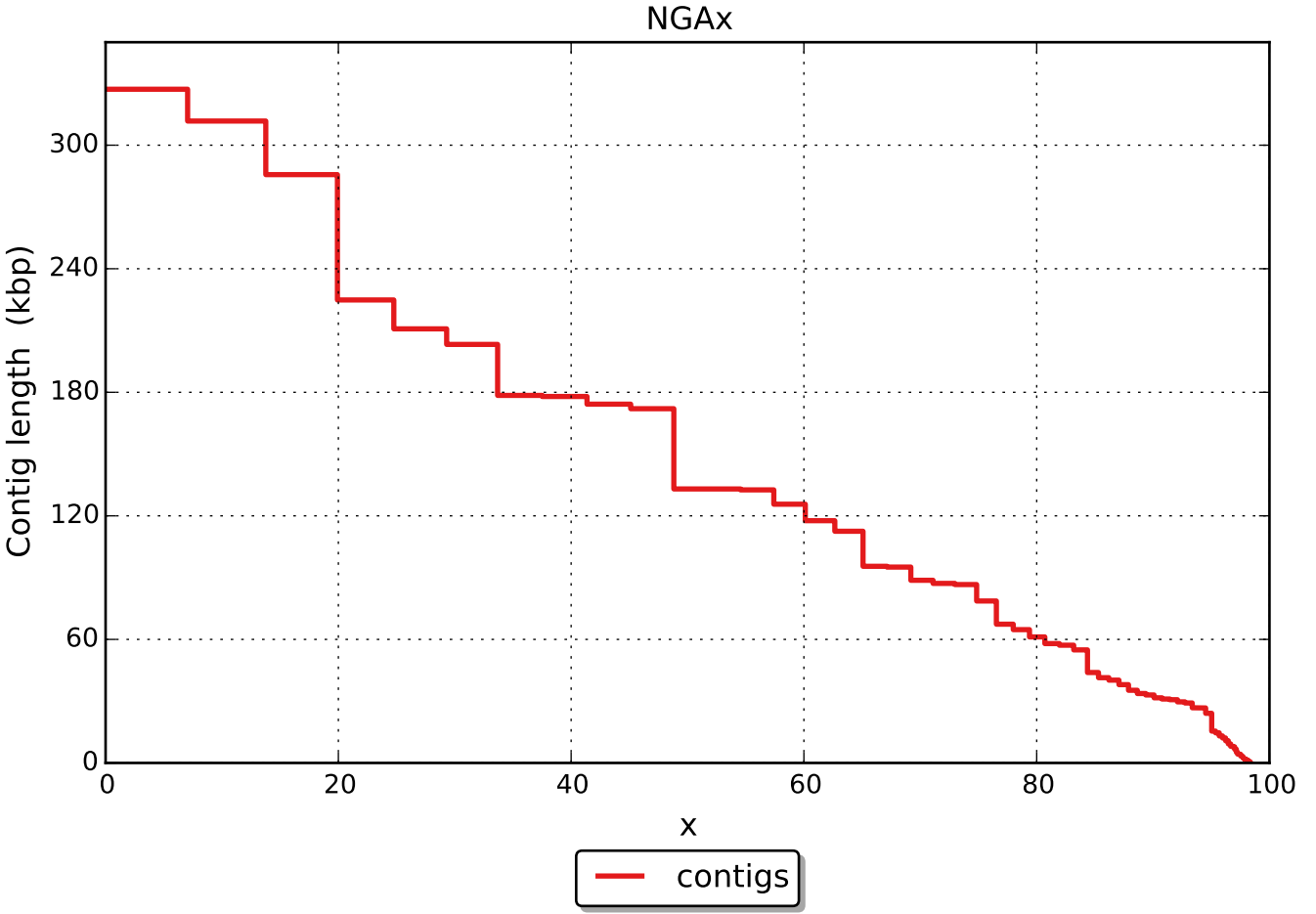

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
contigs
Reference


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