Report

	contigs
# contigs (>= 0 bp)	87
# contigs (>= 1000 bp)	67
# contigs (>= 5000 bp)	50
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	26
Total length (>= 0 bp)	4569917
Total length (>= 1000 bp)	4564666
Total length (>= 5000 bp)	4525197
Total length (>= 10000 bp)	4501229
Total length (>= 25000 bp)	4410038
Total length (>= 50000 bp)	3892765
# contigs	70
Largest contig	327064
Total length	4567081
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	174013
NG50	174013
N75	87065
NG75	87065
L50	10
LG50	10
L75	20
LG75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.333
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.04
# indels per 100 kbp	0.39
Largest alignment	327064
NA50	174013
NGA50	174013
NA75	87065
NGA75	87065
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

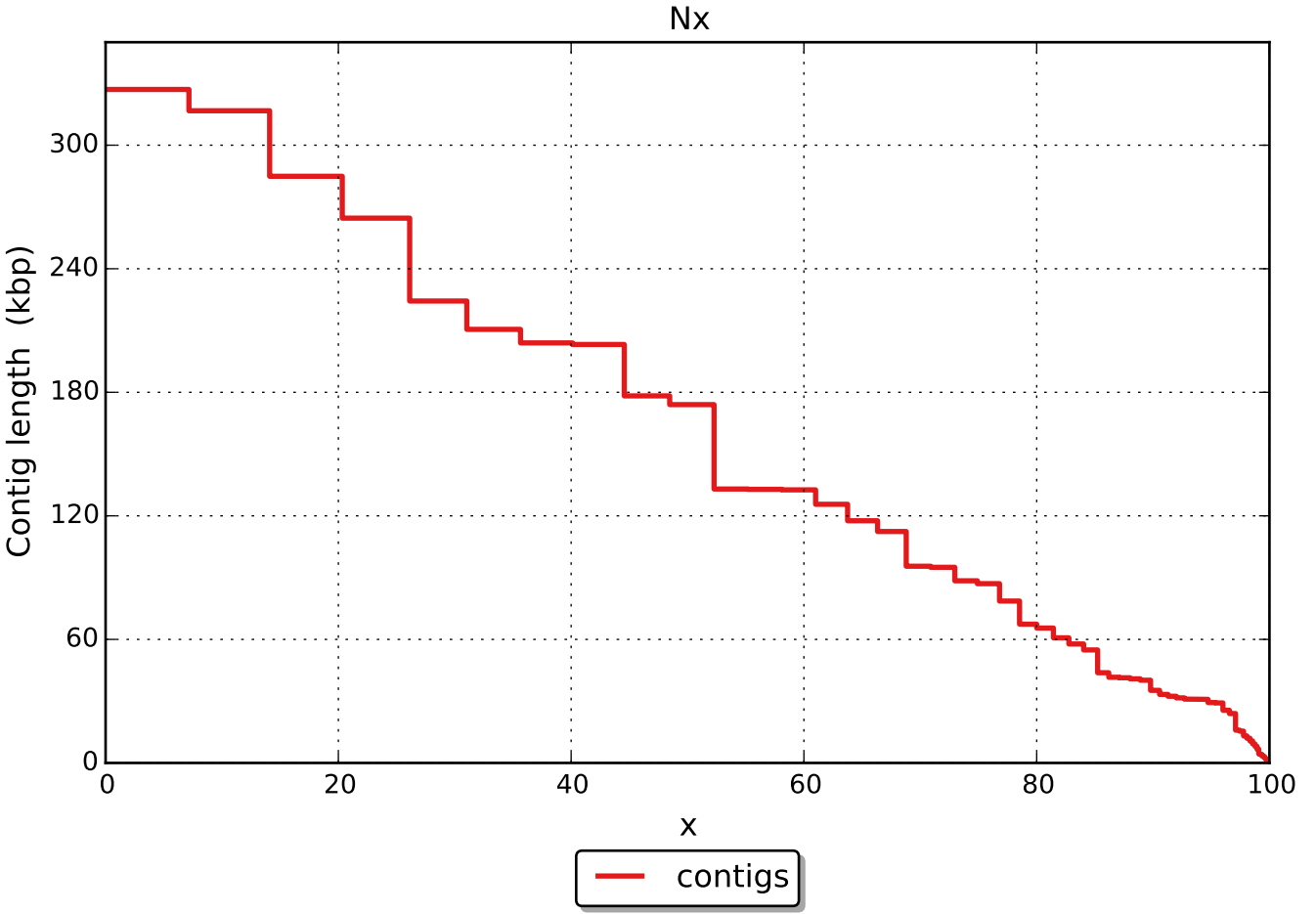
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	230
# indels	18
# short indels	18
# long indels	0
Indels length	25

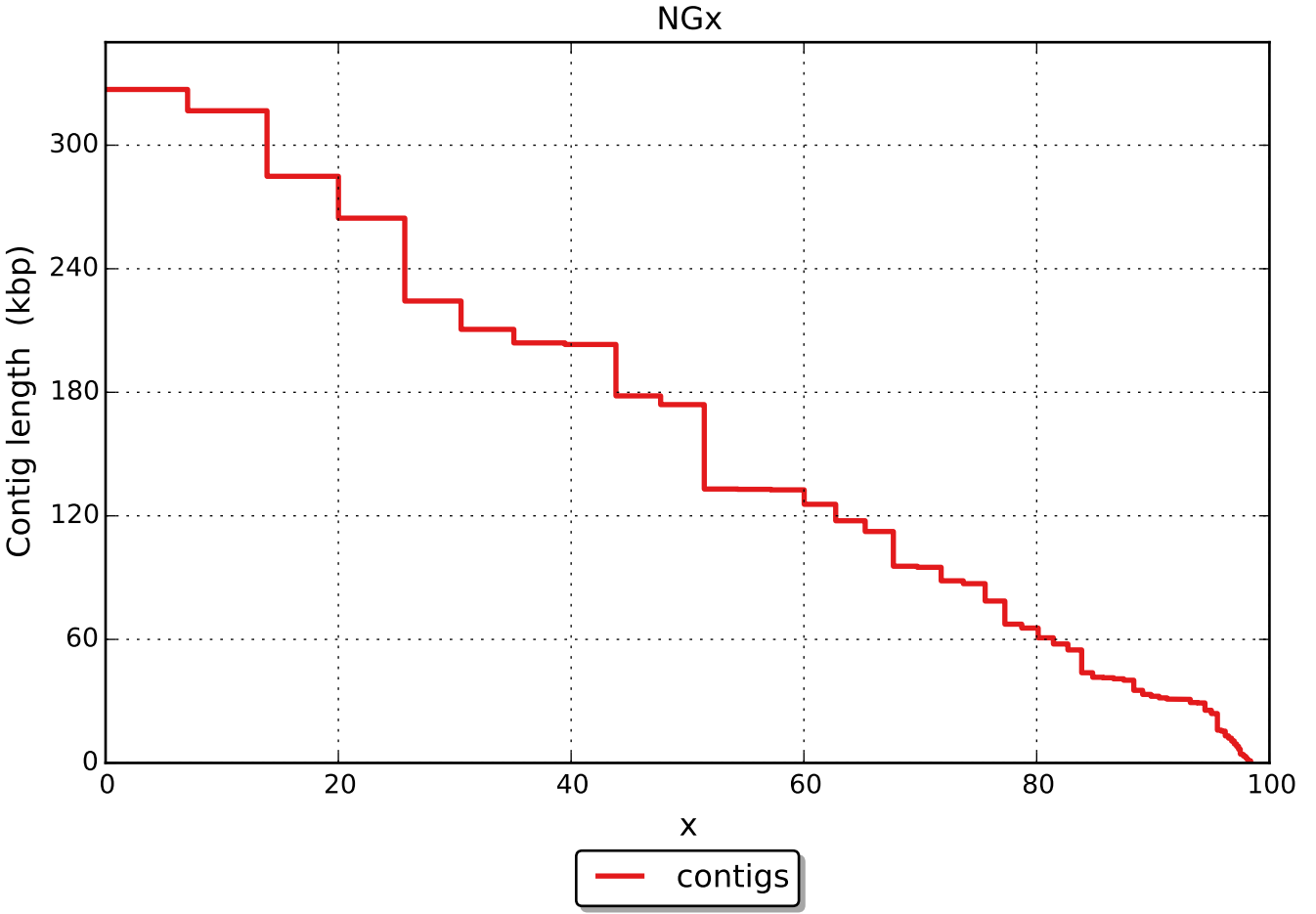
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

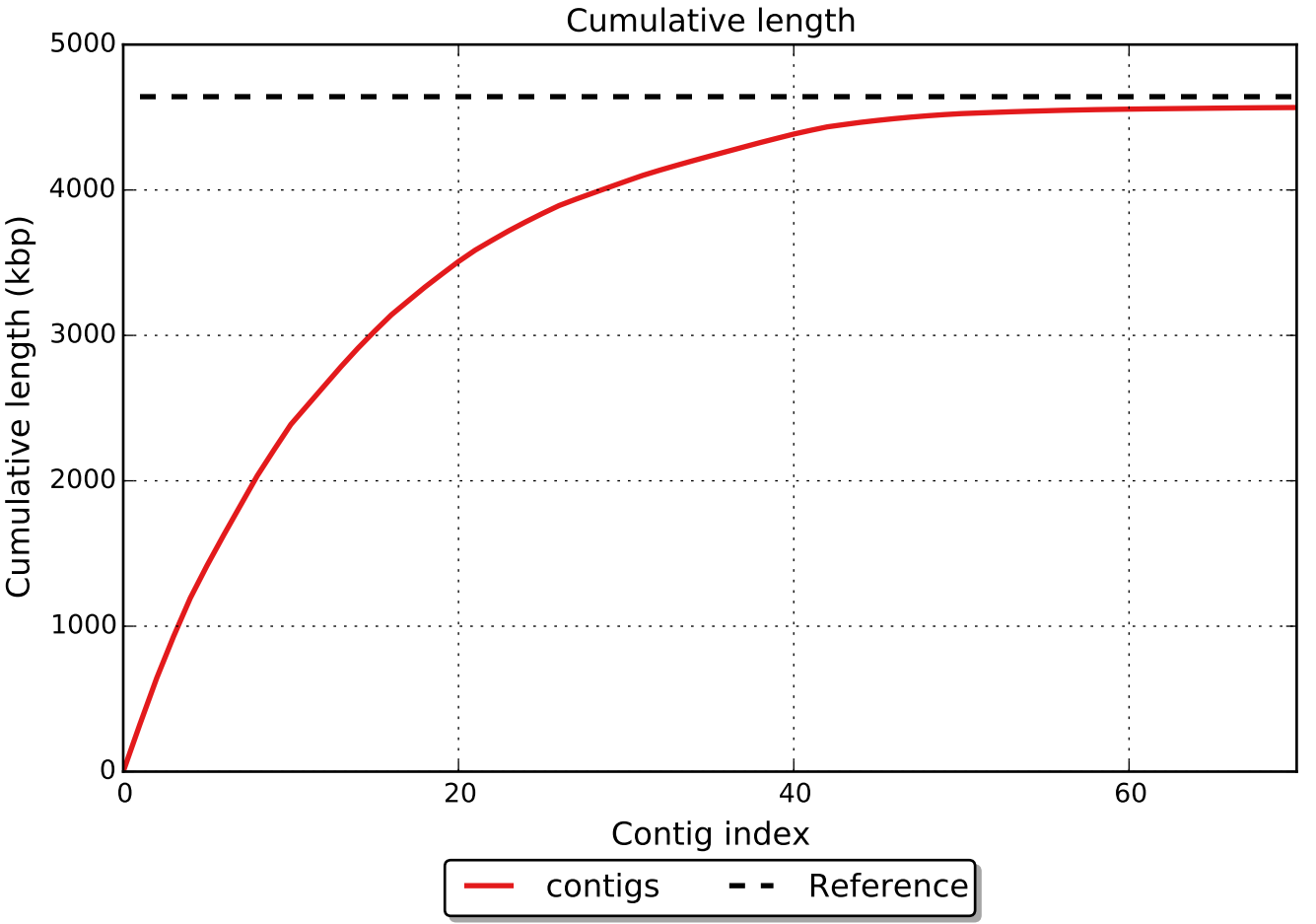
Unaligned report

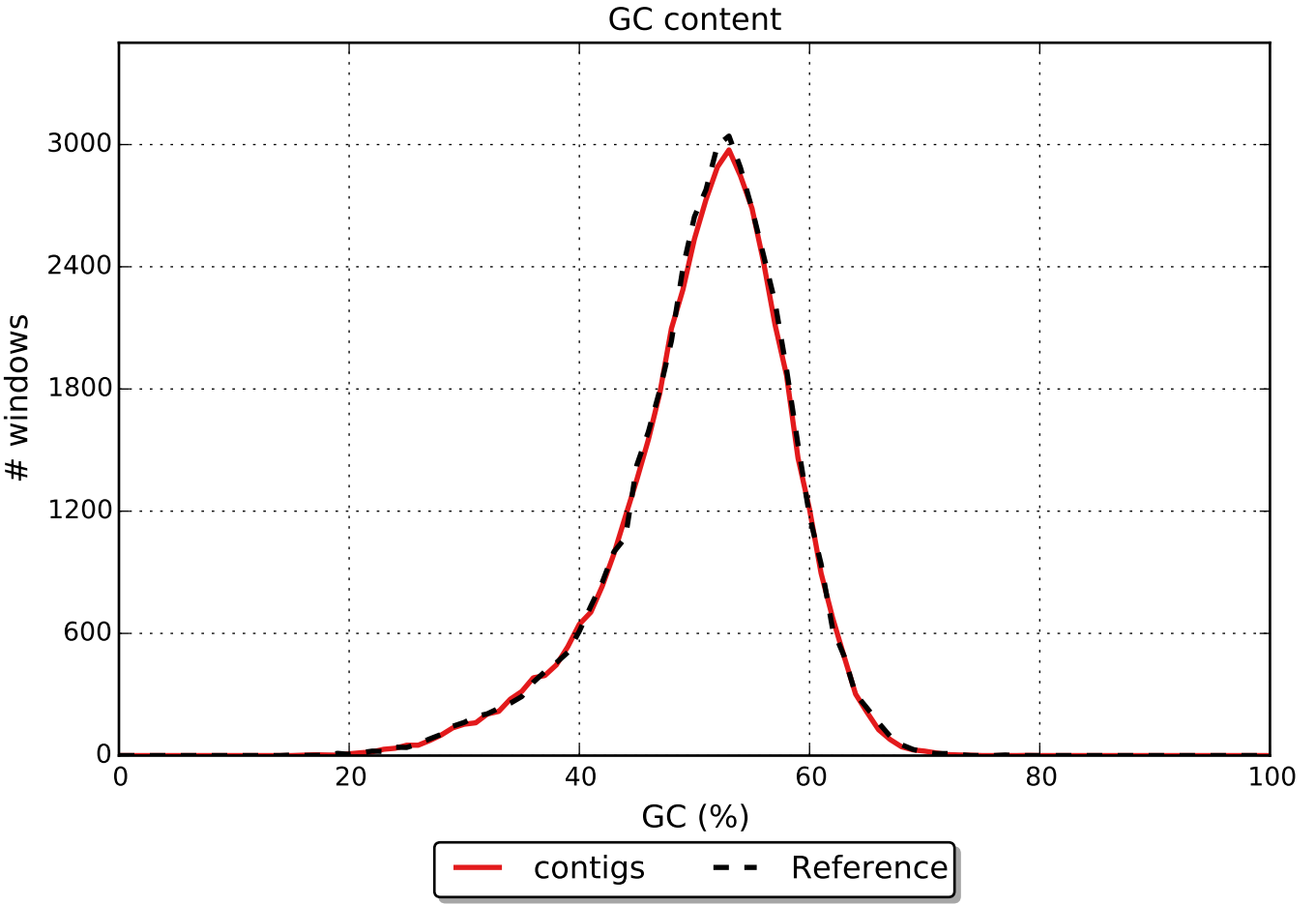
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

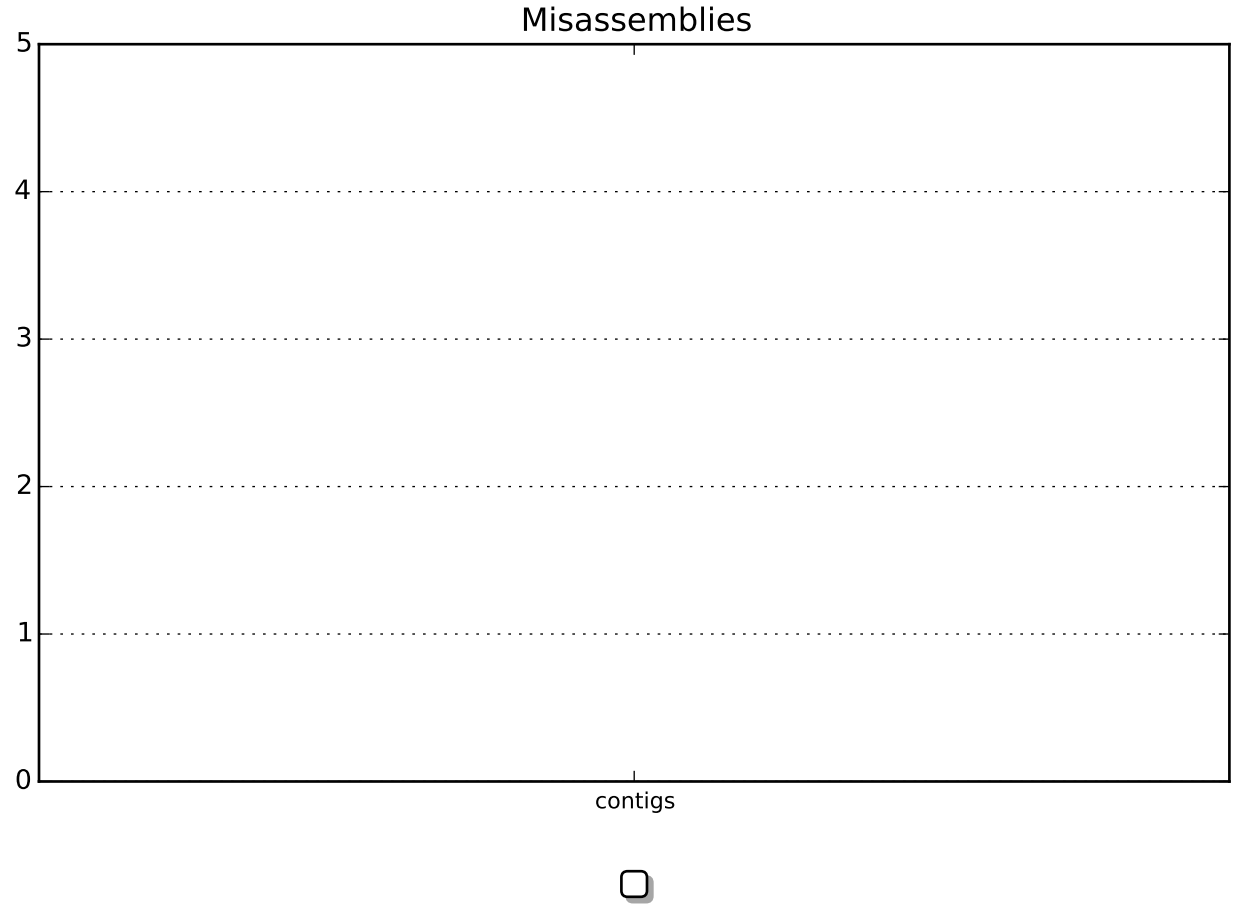
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

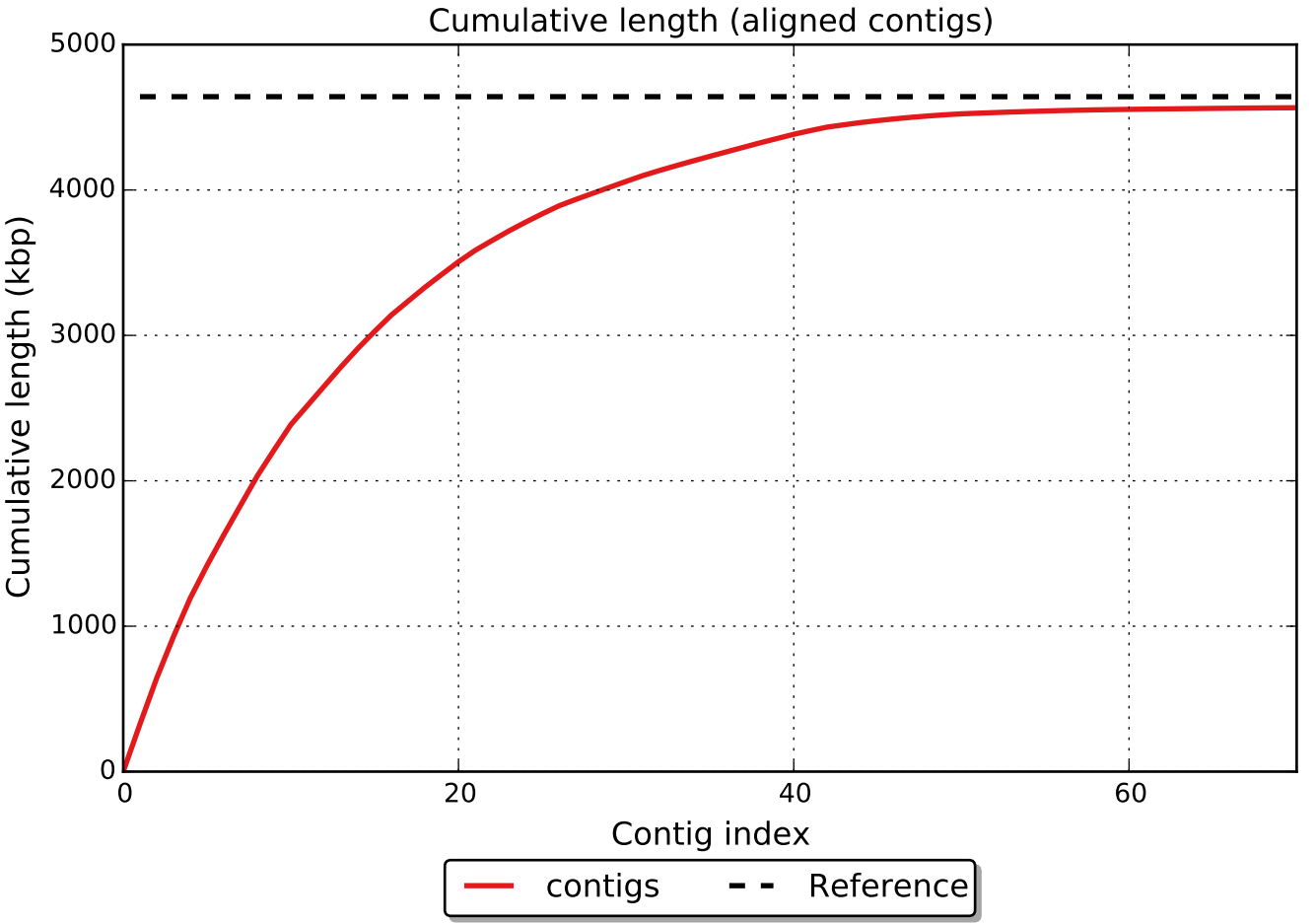

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

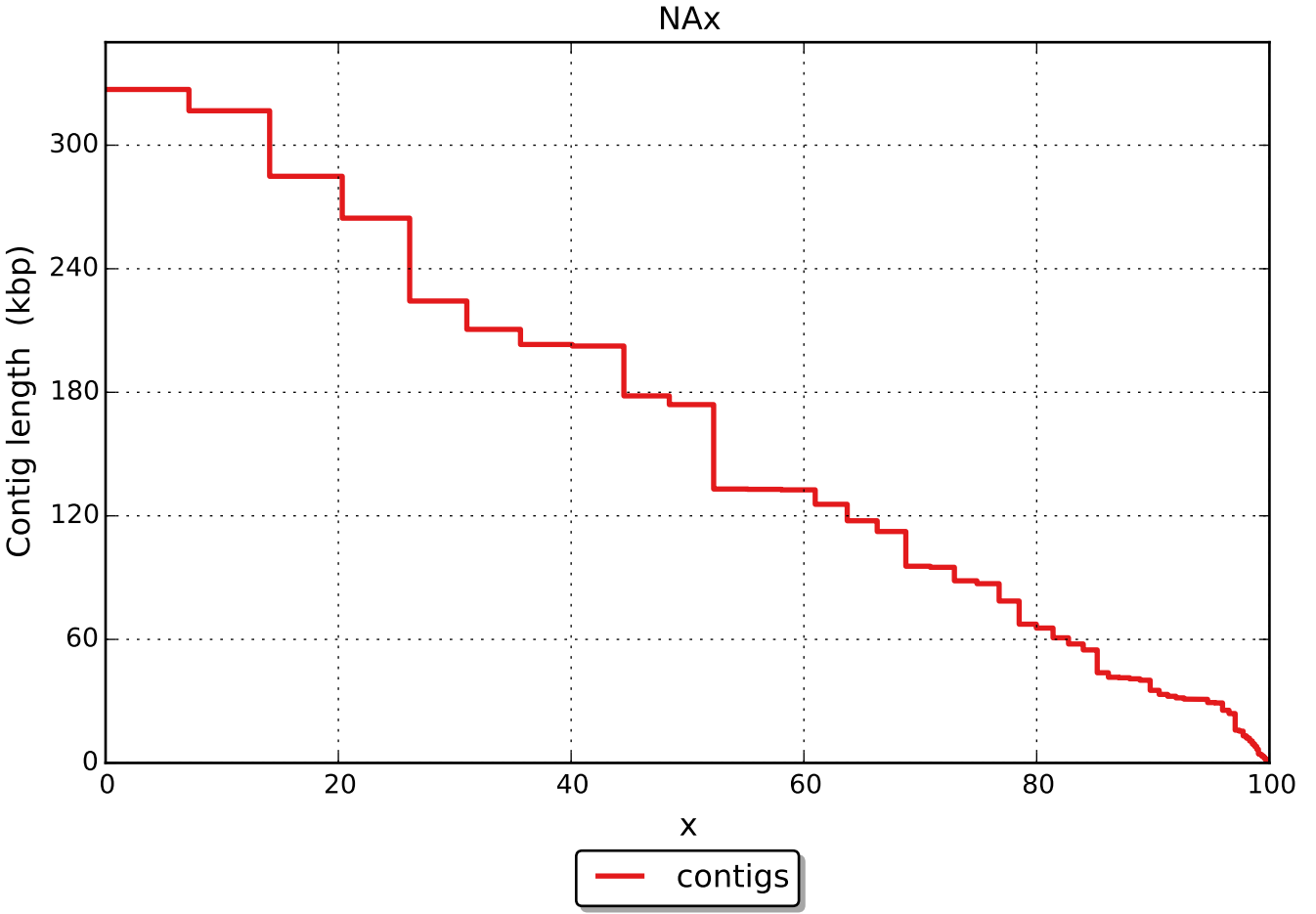

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

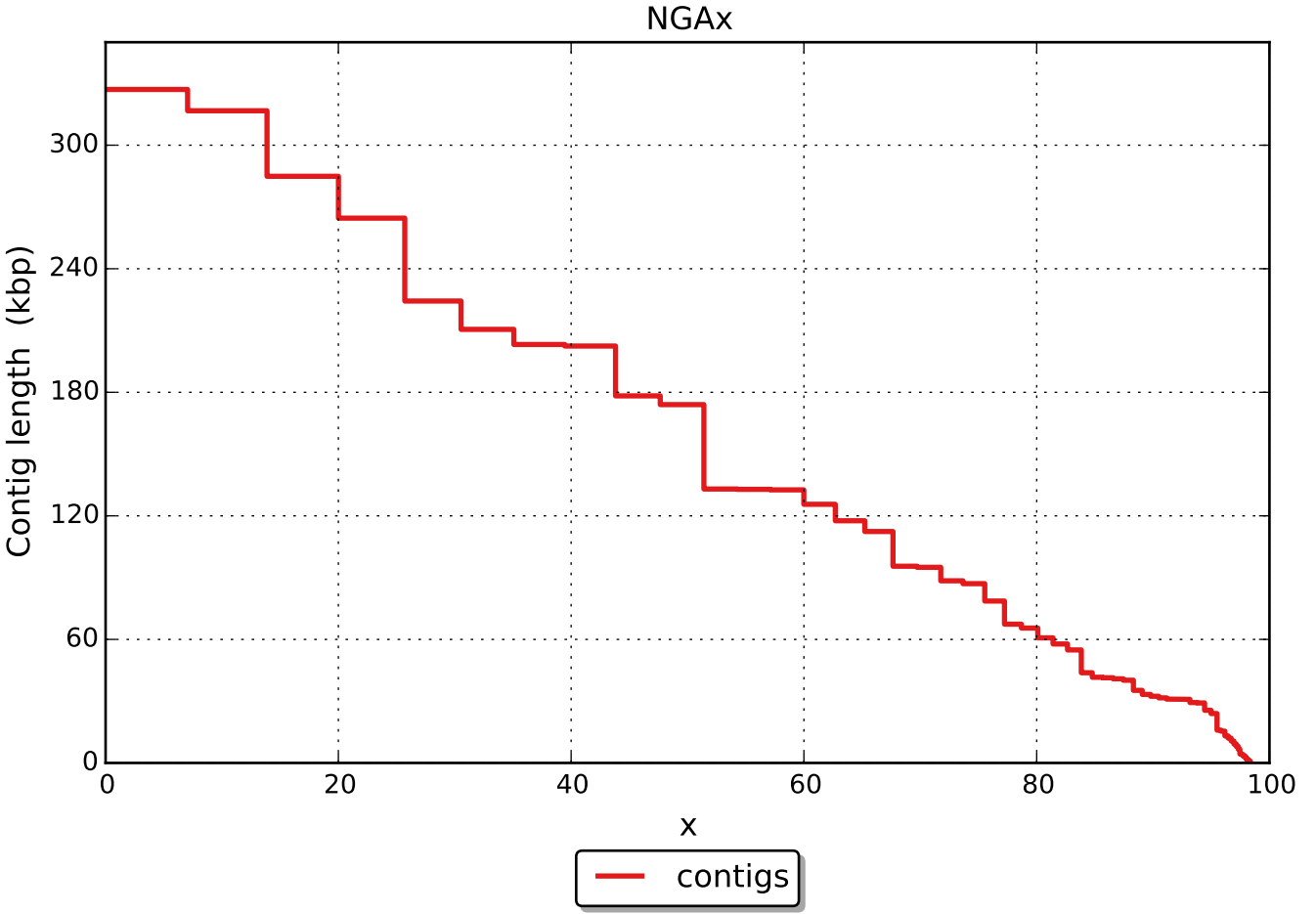

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
20
40
60
Contig index
contigs
Reference


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
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