Report

	contigs
# contigs (>= 0 bp)	124
# contigs (>= 1000 bp)	75
# contigs (>= 5000 bp)	53
# contigs (>= 10000 bp)	48
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4572763
Total length (>= 1000 bp)	4558778
Total length (>= 5000 bp)	4509616
Total length (>= 10000 bp)	4472290
Total length (>= 25000 bp)	4382553
Total length (>= 50000 bp)	3868982
# contigs	83
Largest contig	327173
Total length	4564538
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	173566
NG50	133063
N75	87186
NG75	78649
L50	10
LG50	11
L75	20
LG75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.272
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.19
# indels per 100 kbp	0.15
Largest alignment	327173
NA50	172028
NGA50	133063
NA75	87186
NGA75	78649
LA50	10
LGA50	11
LA75	20
LGA75	21

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

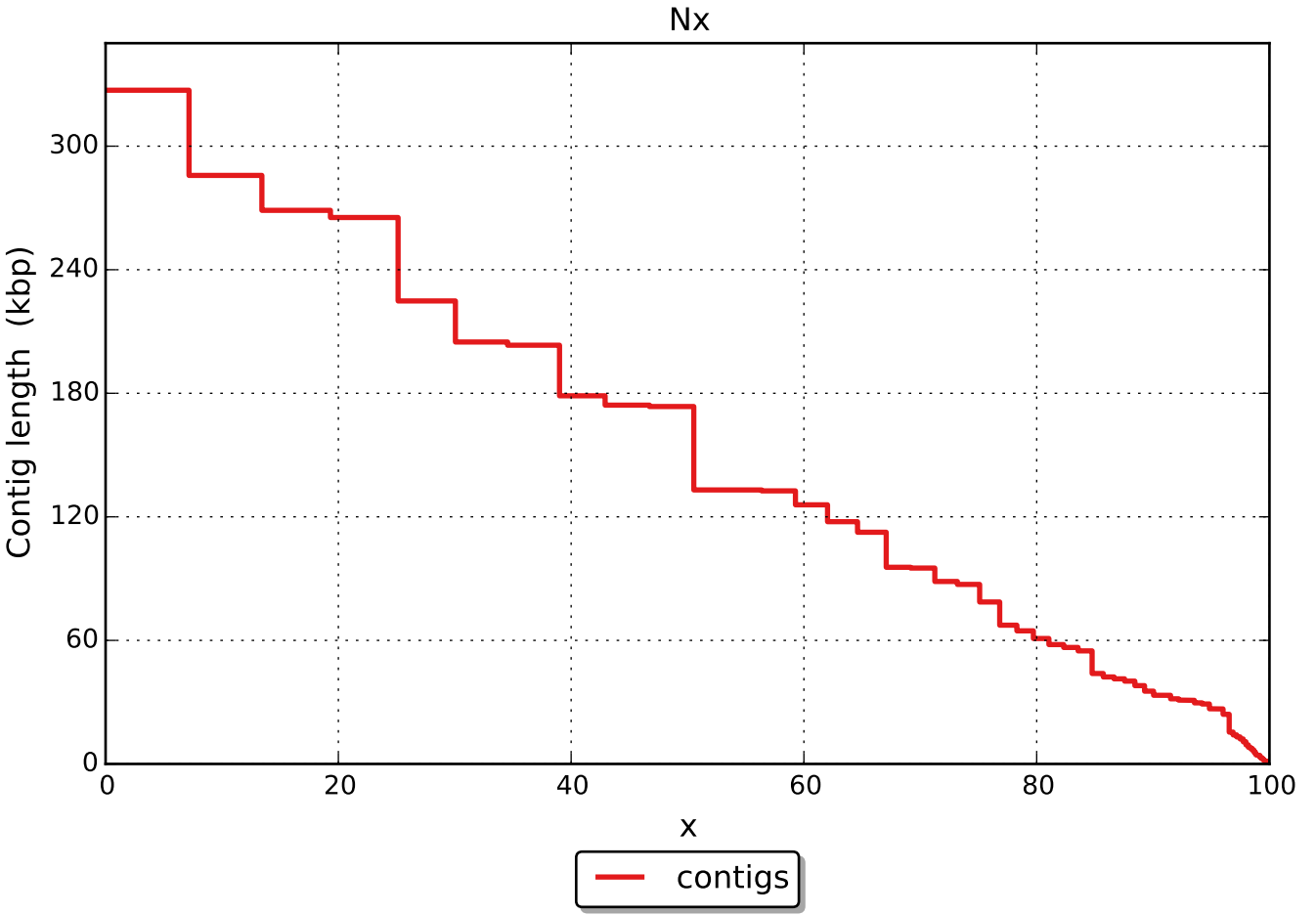
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# mismatches	100
# indels	7
# short indels	7
# long indels	0
Indels length	8

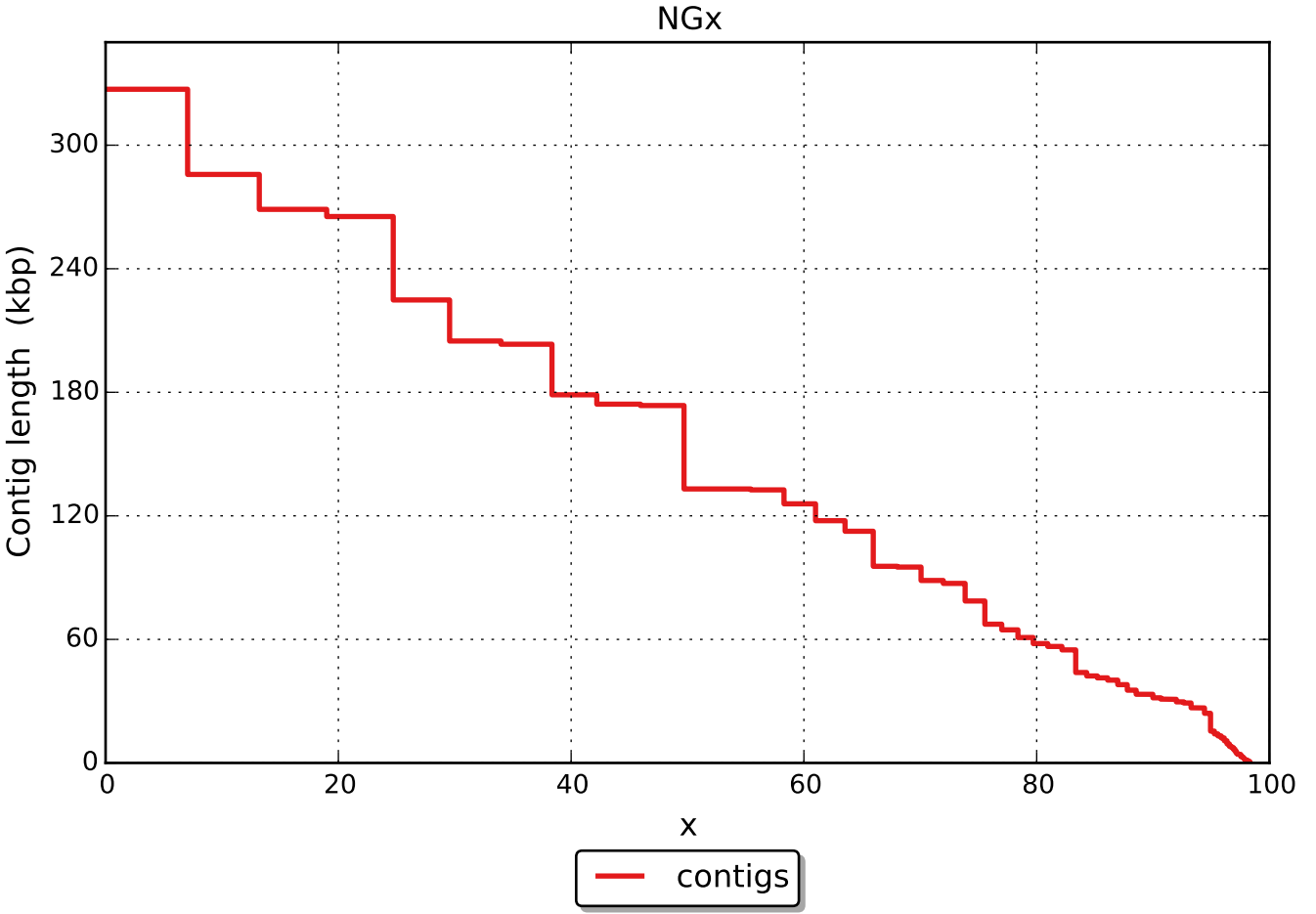
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

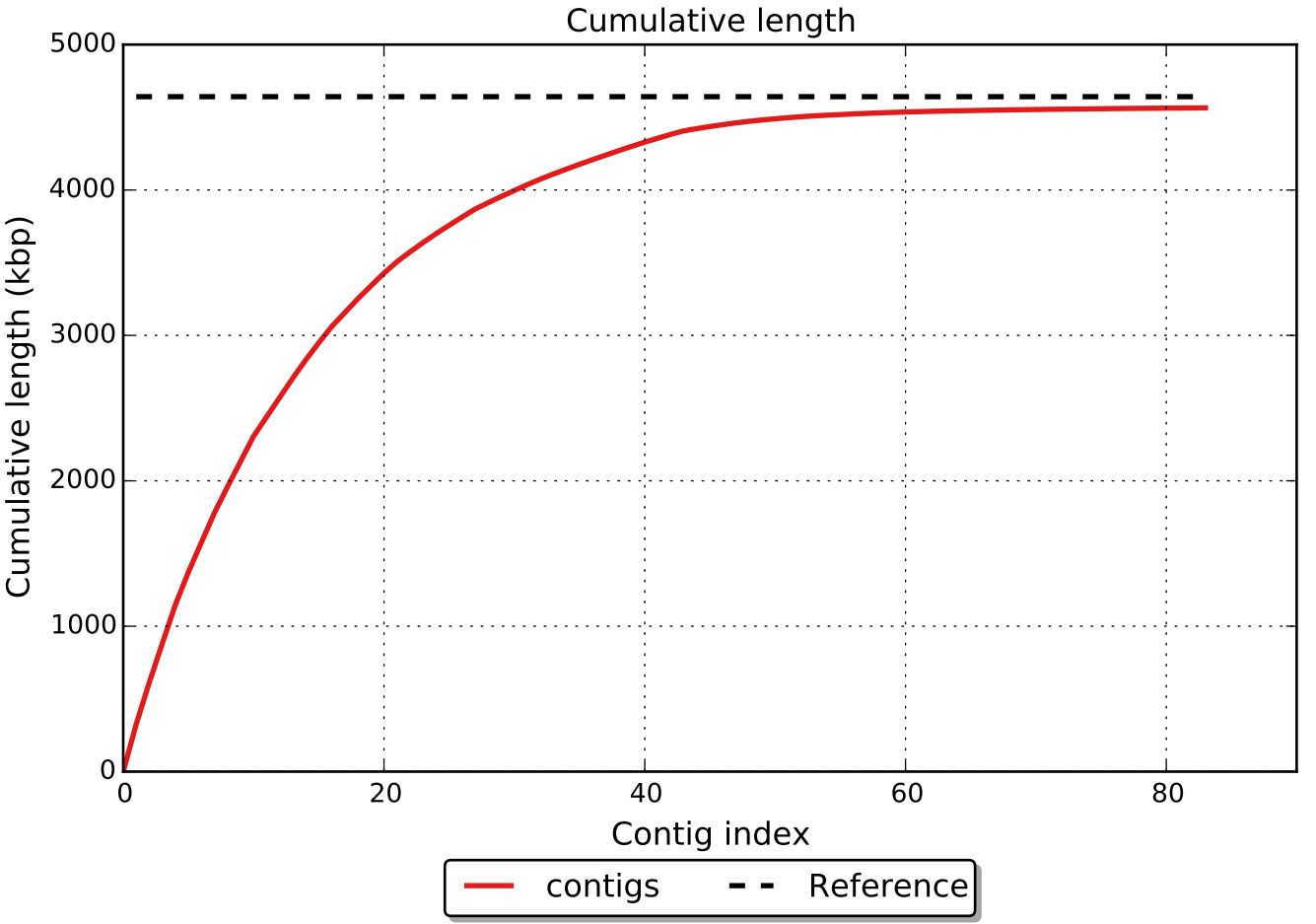
Unaligned report

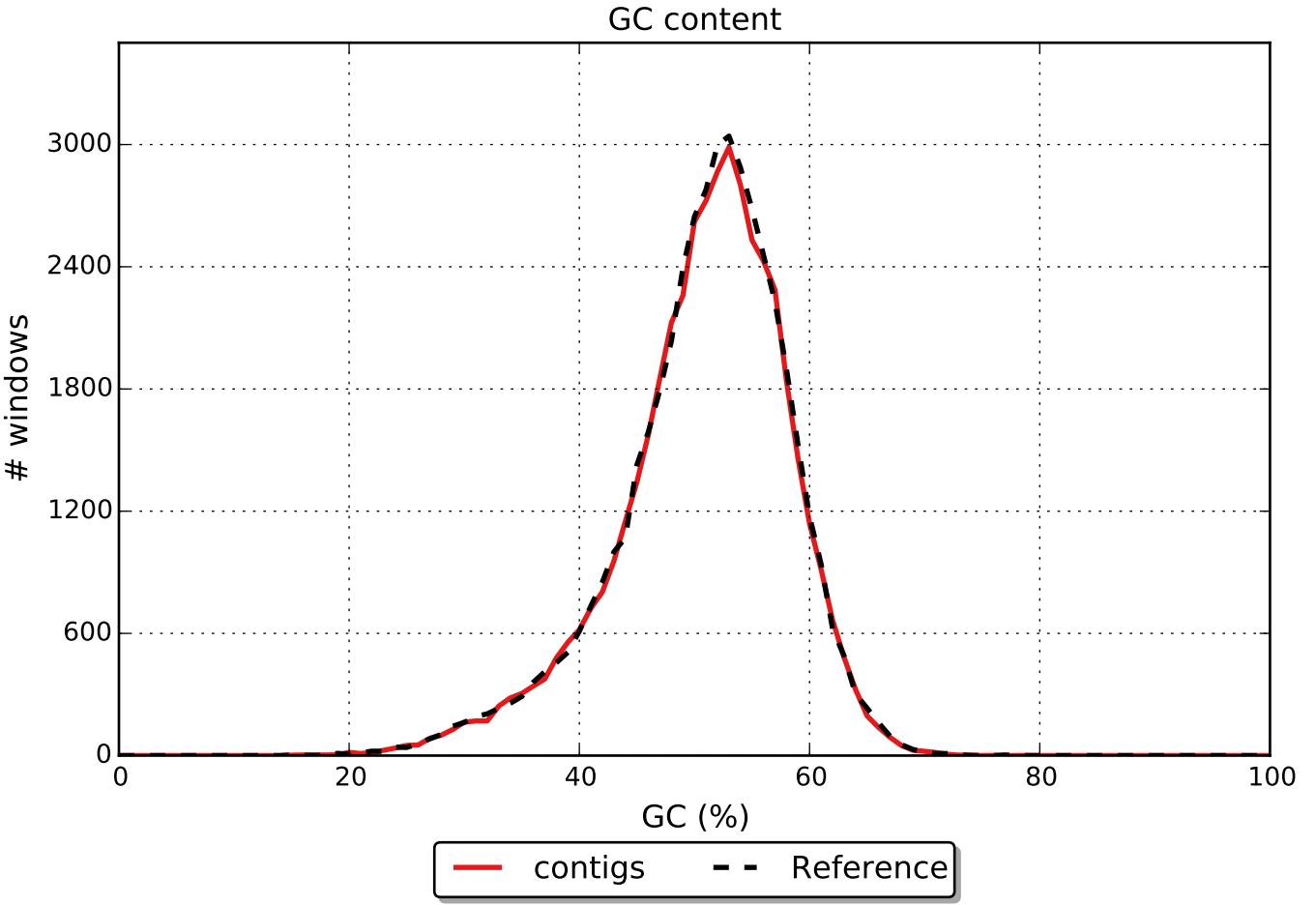
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

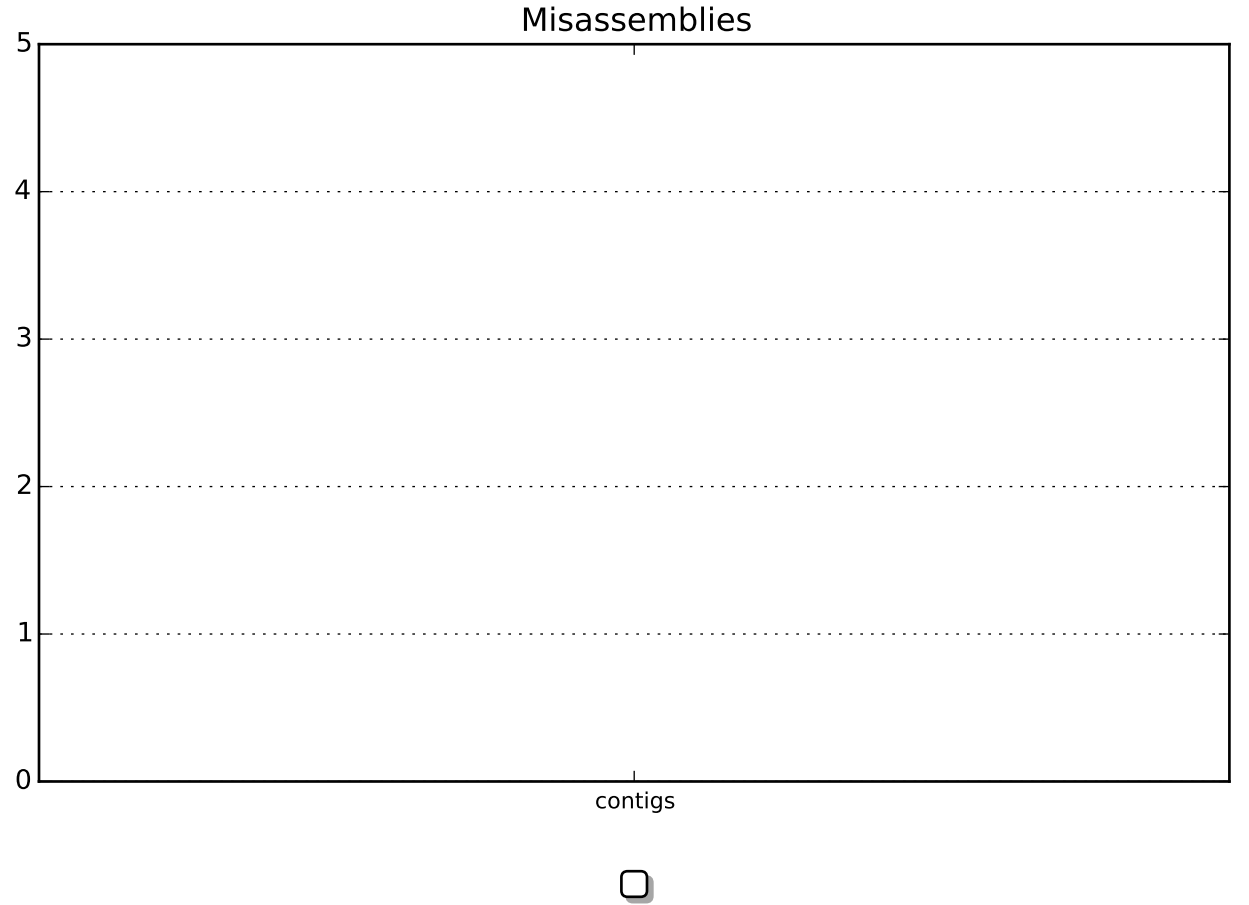
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

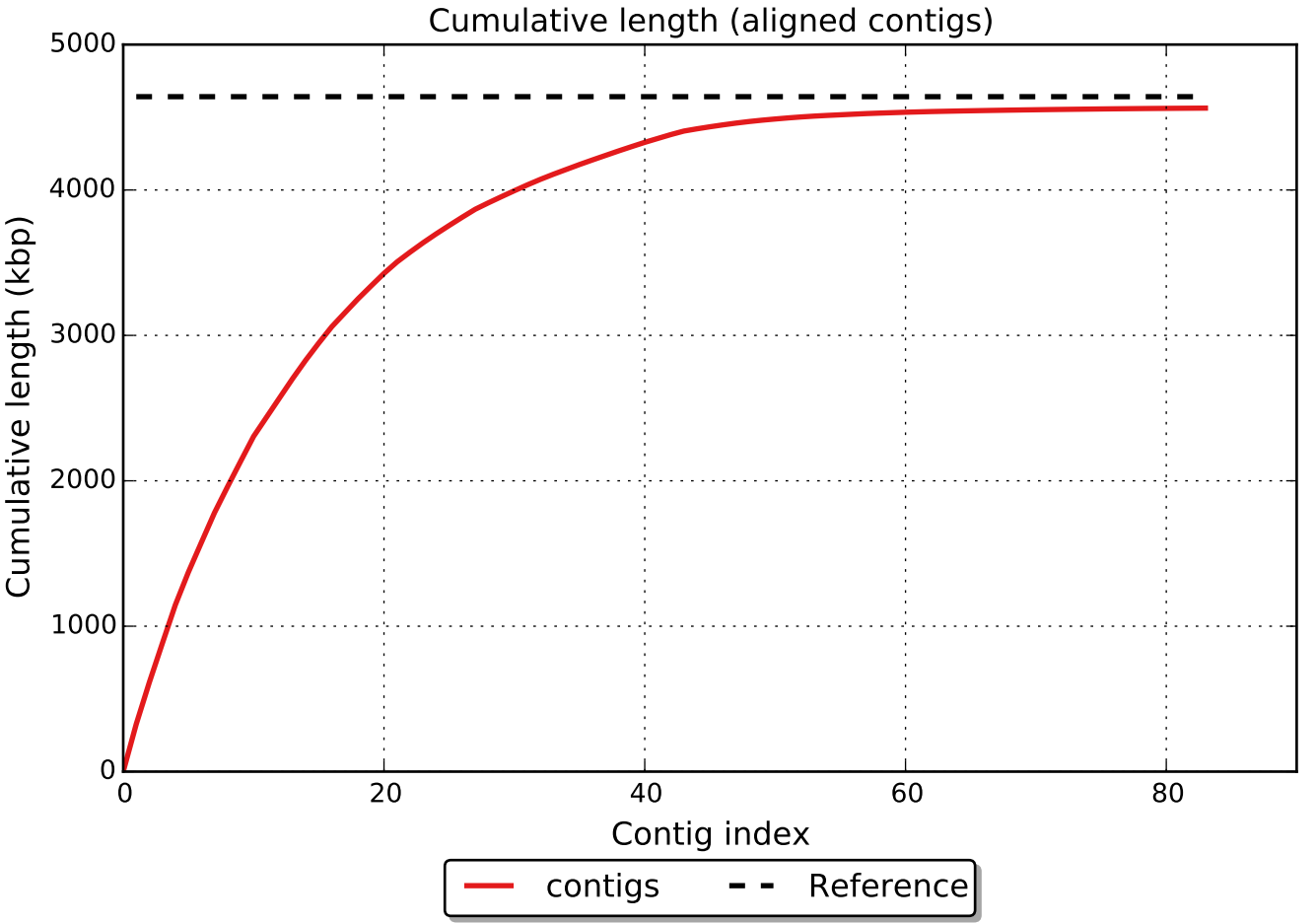

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

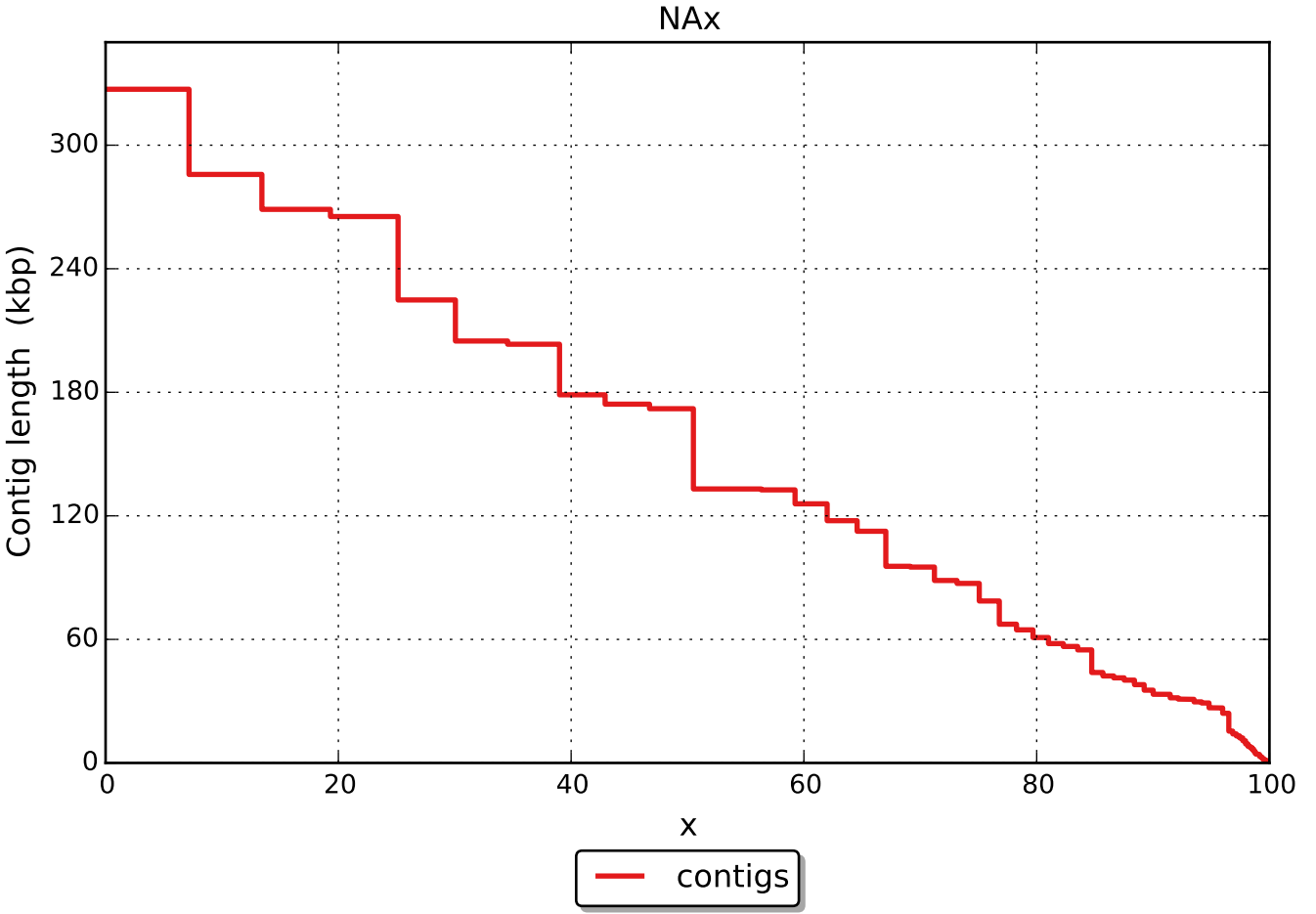

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

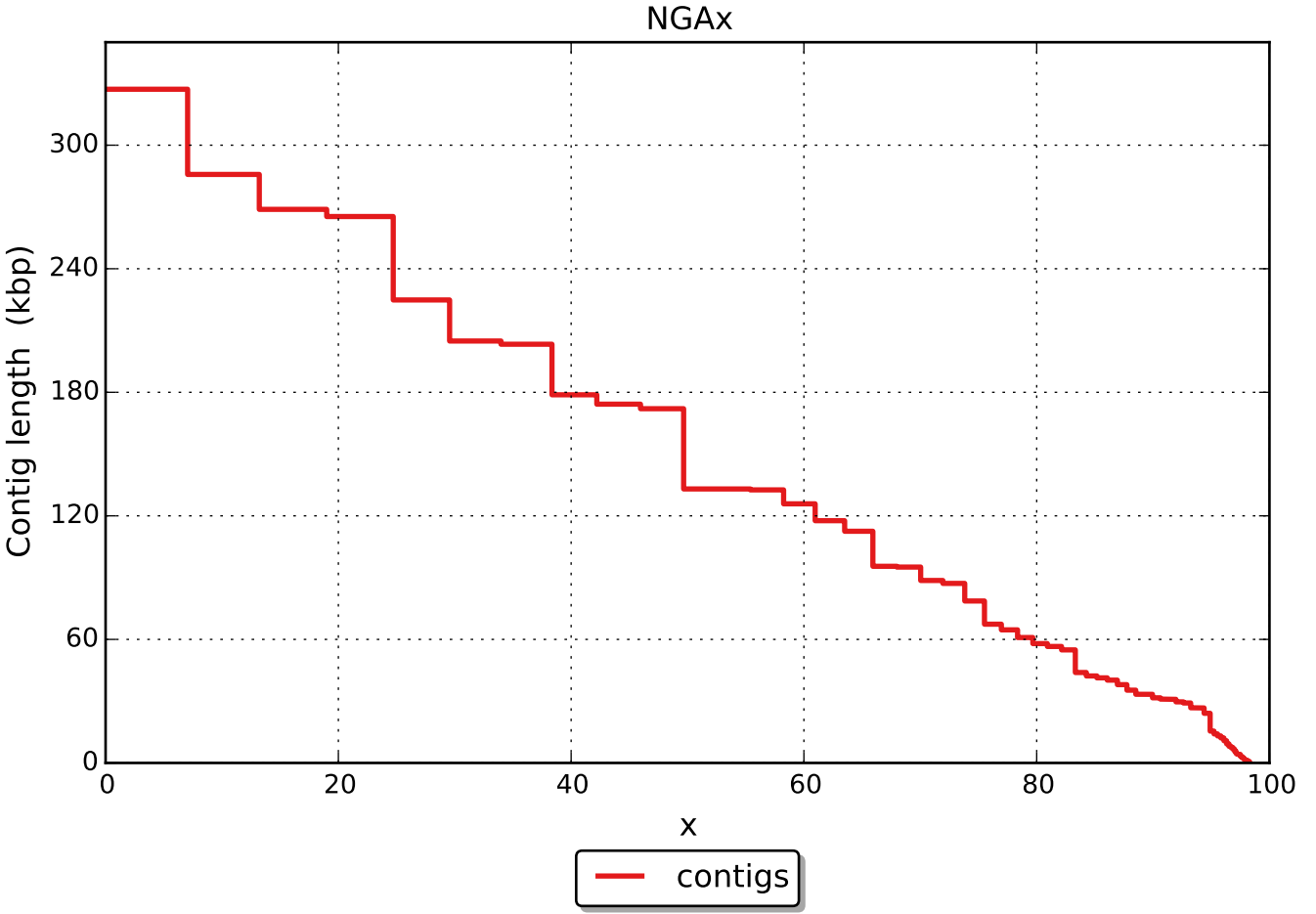

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
contigs
Reference


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