Report

	contigs
# contigs (>= 1000 bp)	62
# contigs (>= 5000 bp)	48
# contigs (>= 10000 bp)	44
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4510277
Total length (>= 5000 bp)	4488206
Total length (>= 10000 bp)	4455421
Total length (>= 25000 bp)	4374190
Total length (>= 50000 bp)	3975624
# contigs	88
Largest contig	333181
Total length	4527412
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	165569
NG50	165569
N75	88482
NG75	82473
L50	11
LG50	11
L75	20
LG75	21
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	20404
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.505
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	356.69
# indels per 100 kbp	0.62
Largest alignment	333181
NA50	165569
NGA50	165569
NA75	88482
NGA75	82473
LA50	11
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

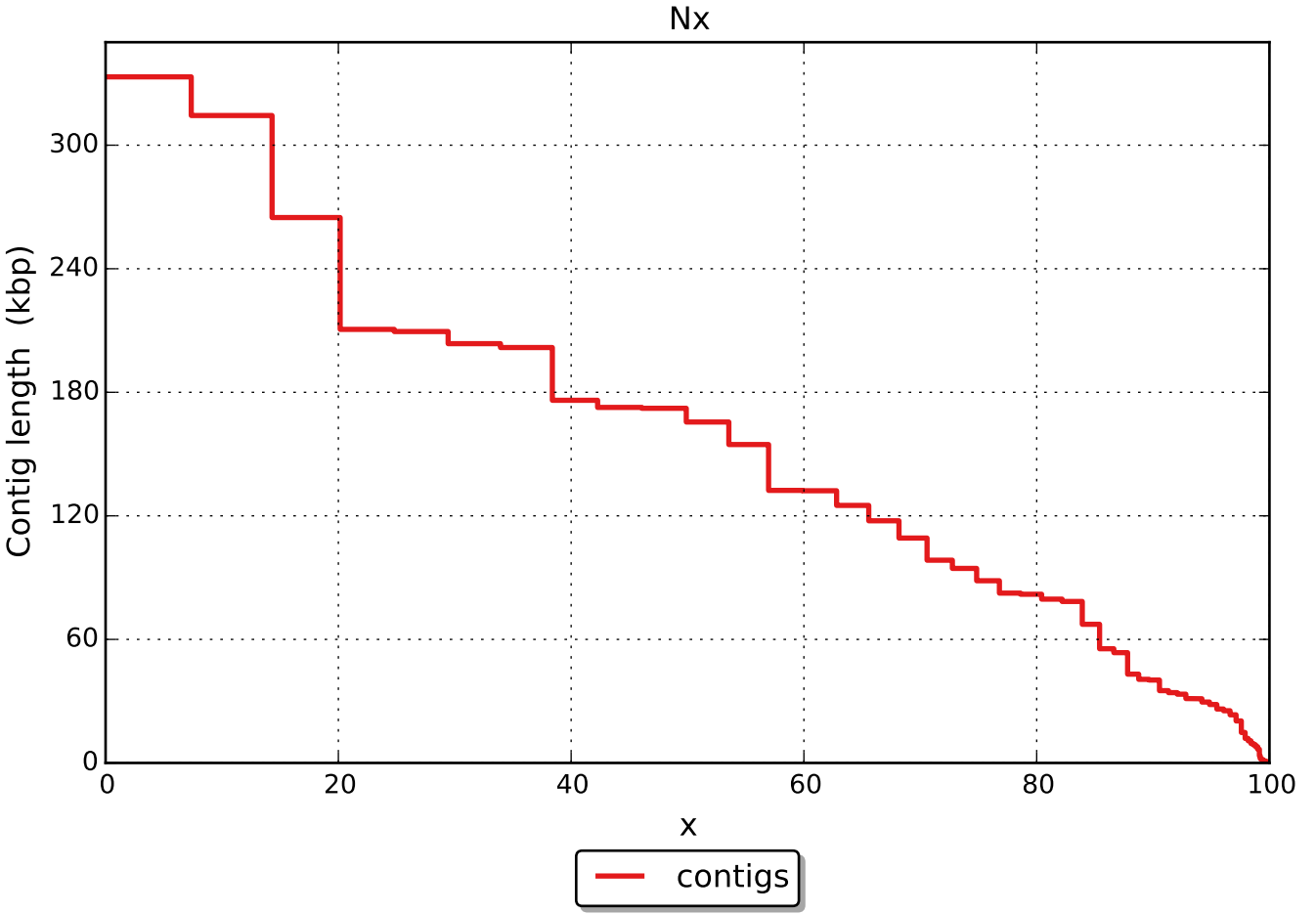
	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	20404
# local misassemblies	0
# mismatches	16143
# indels	28
# short indels	28
# long indels	0
Indels length	28

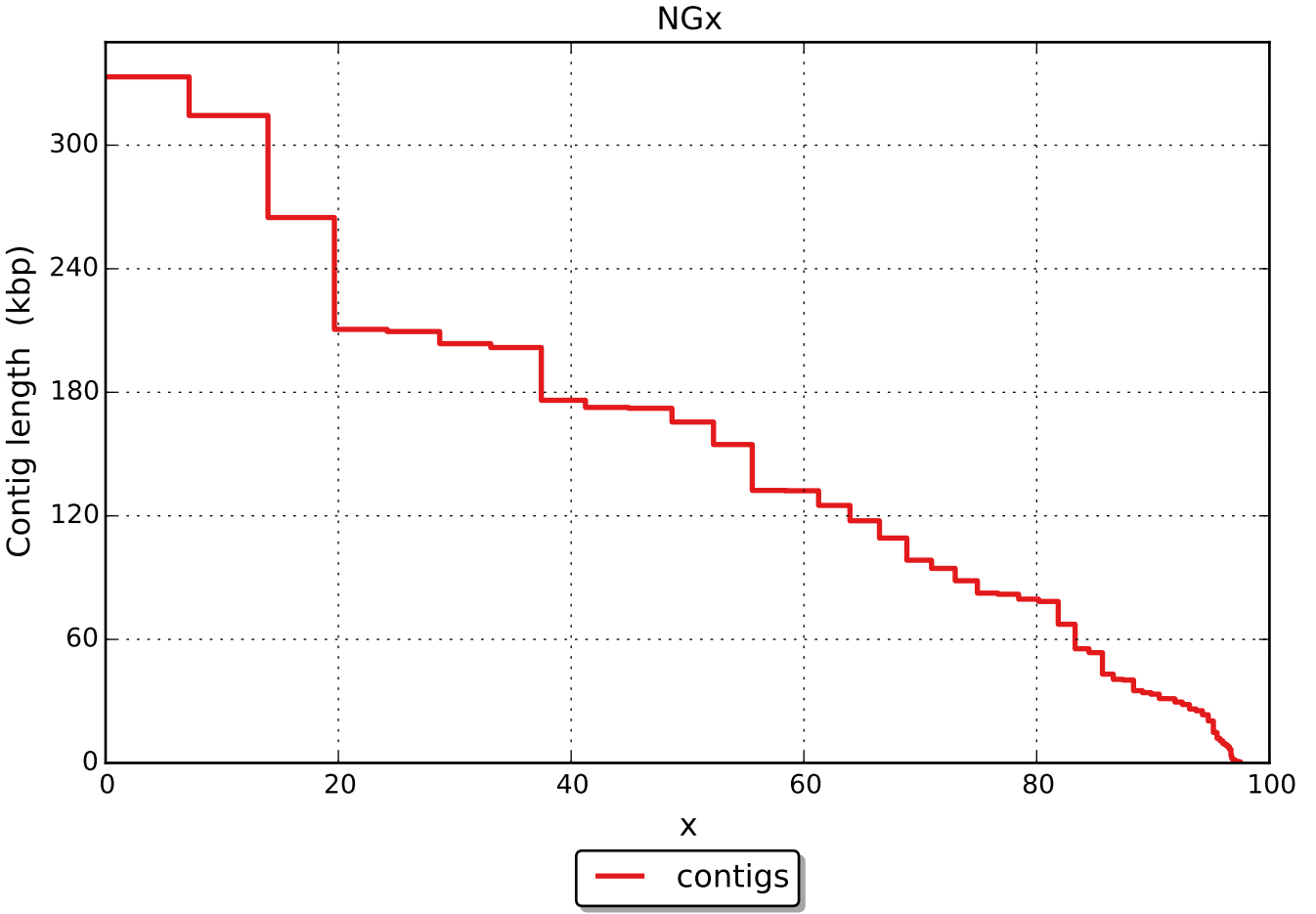
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

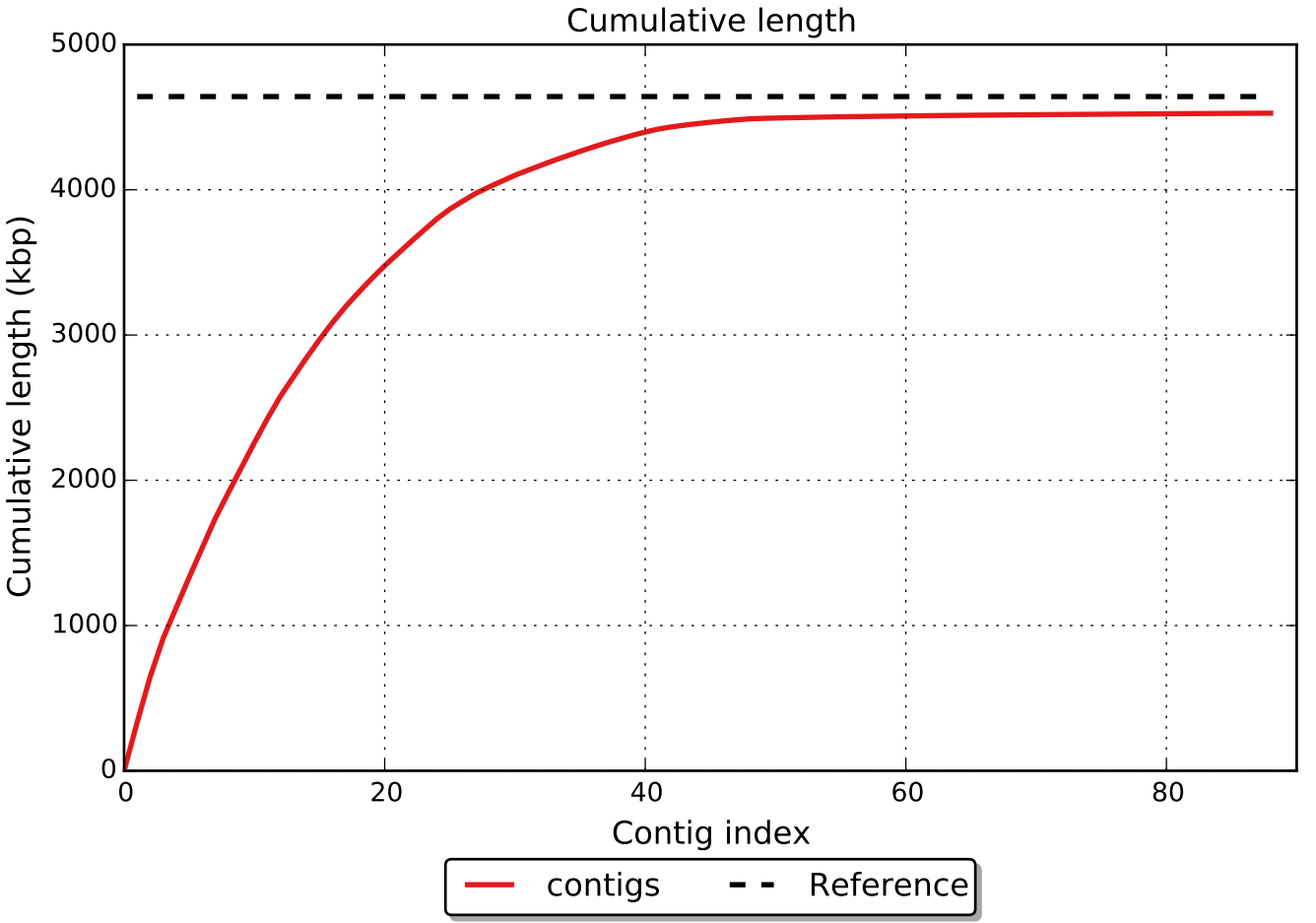
Unaligned report

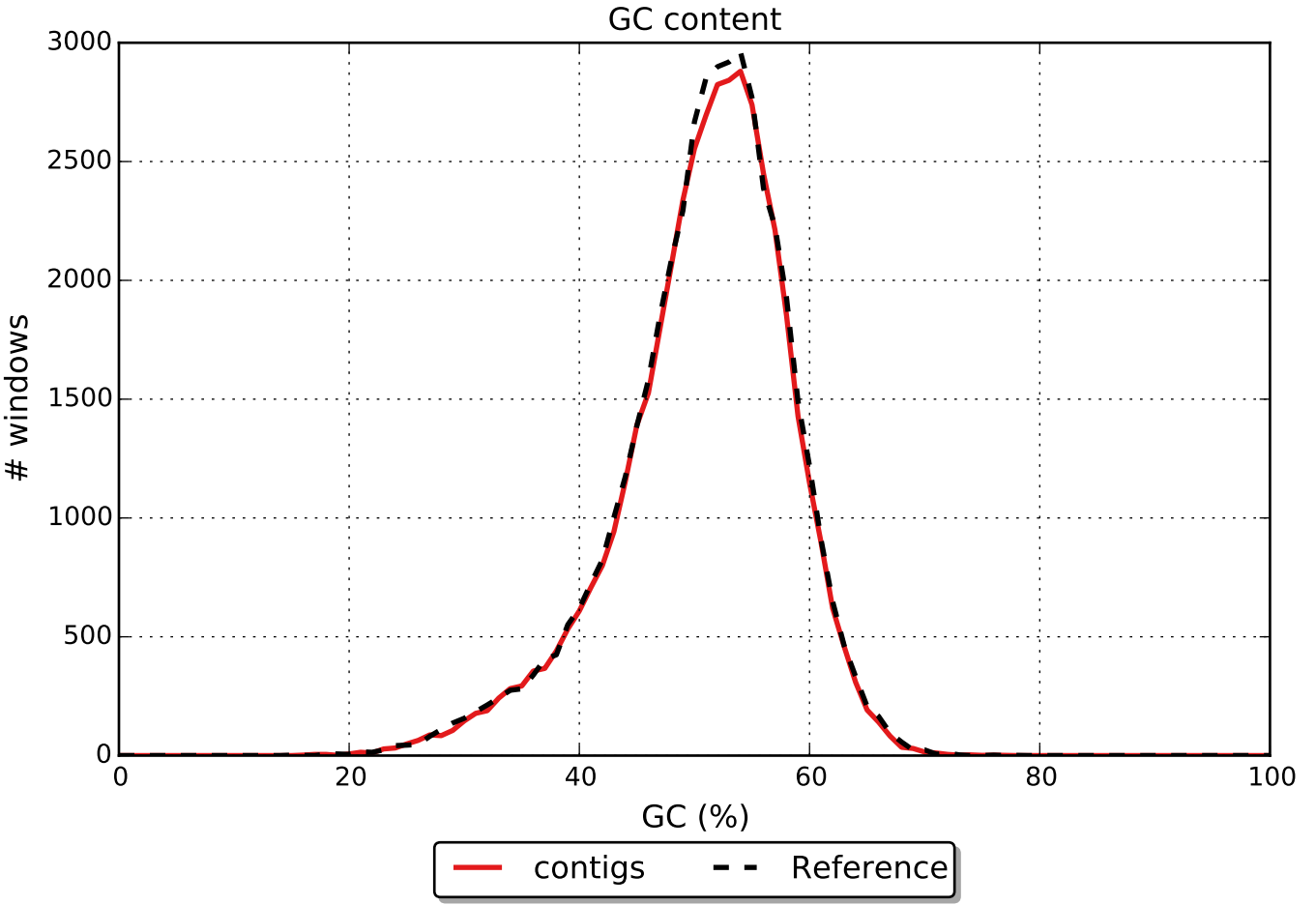
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

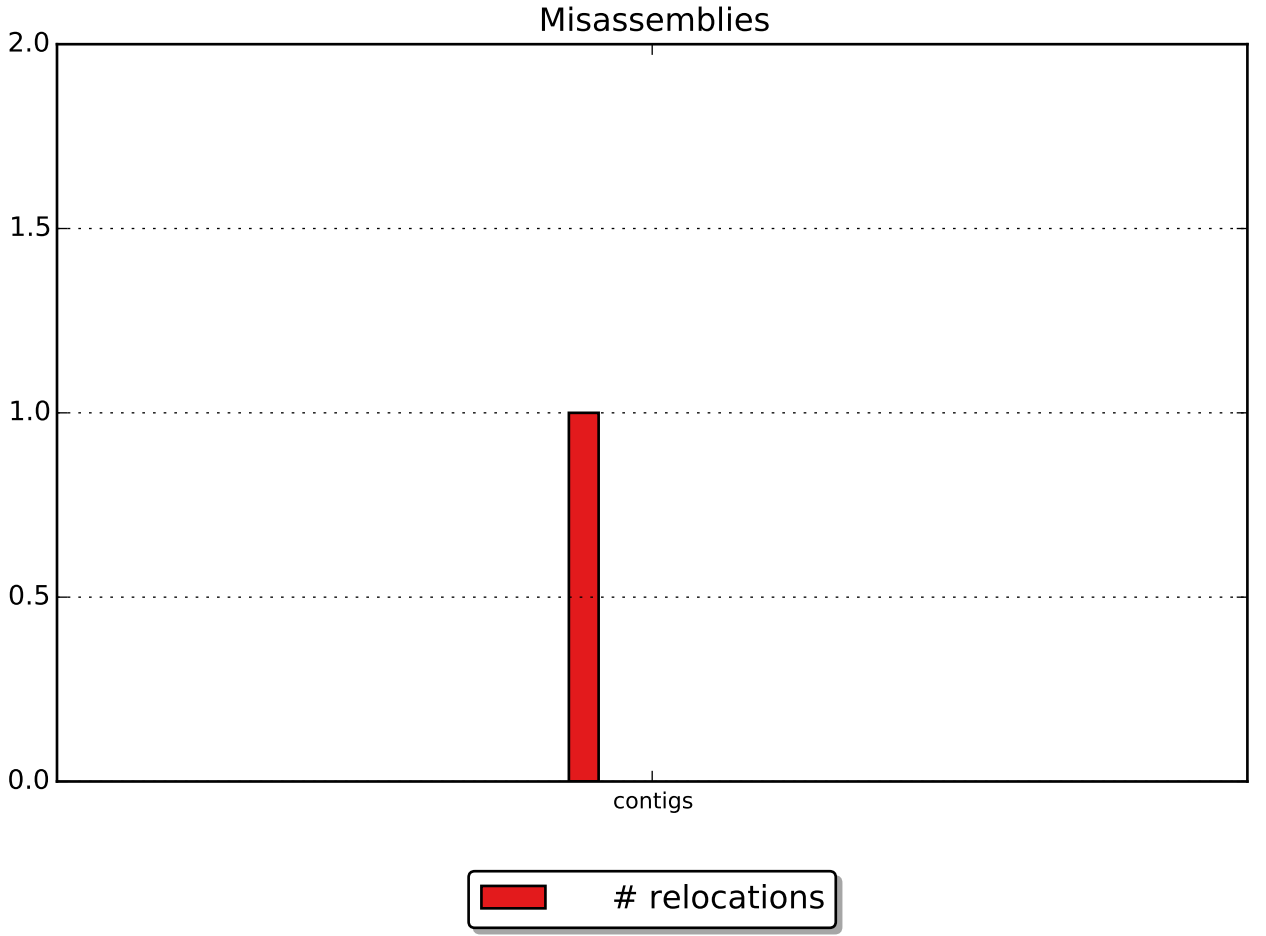
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

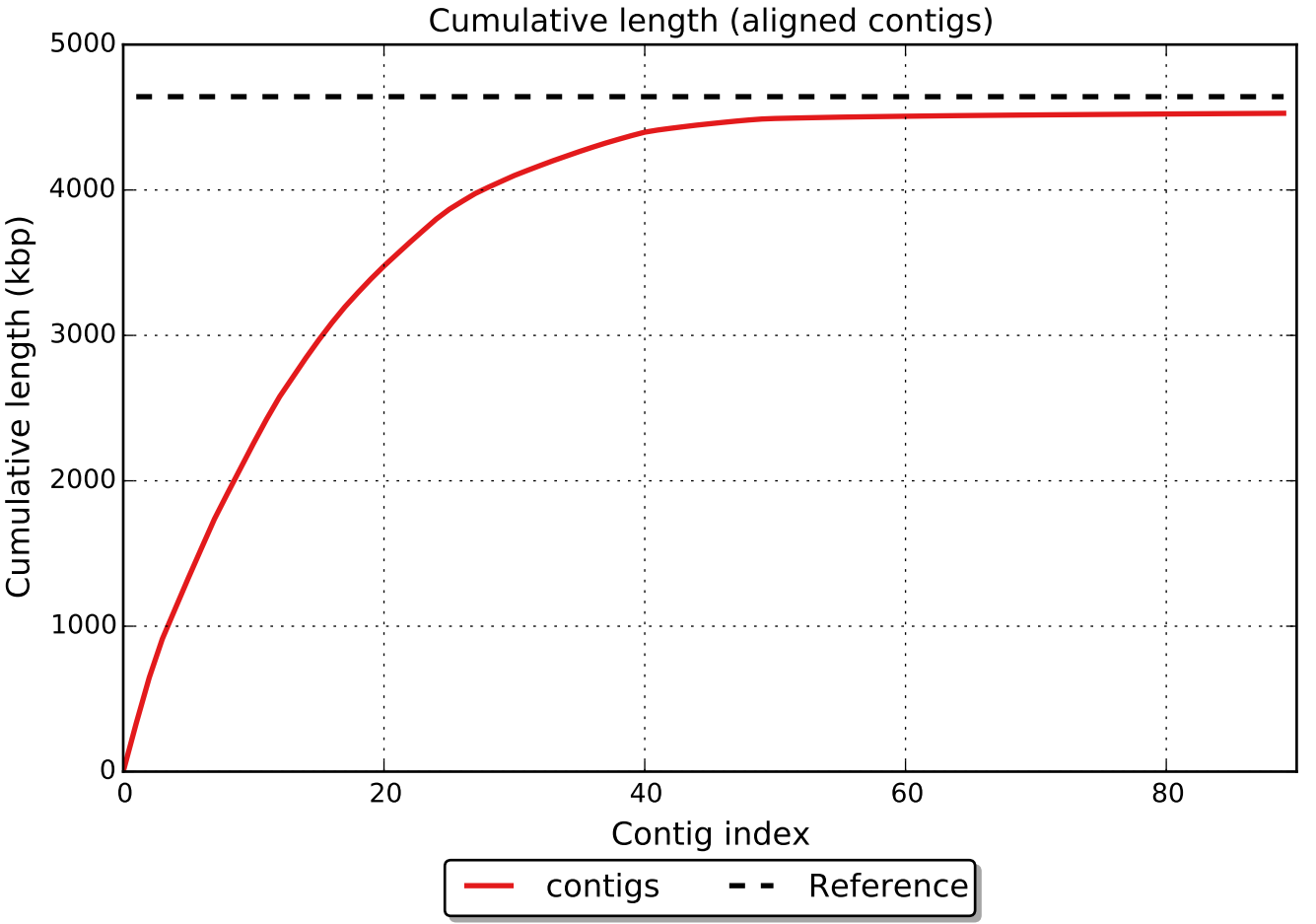

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

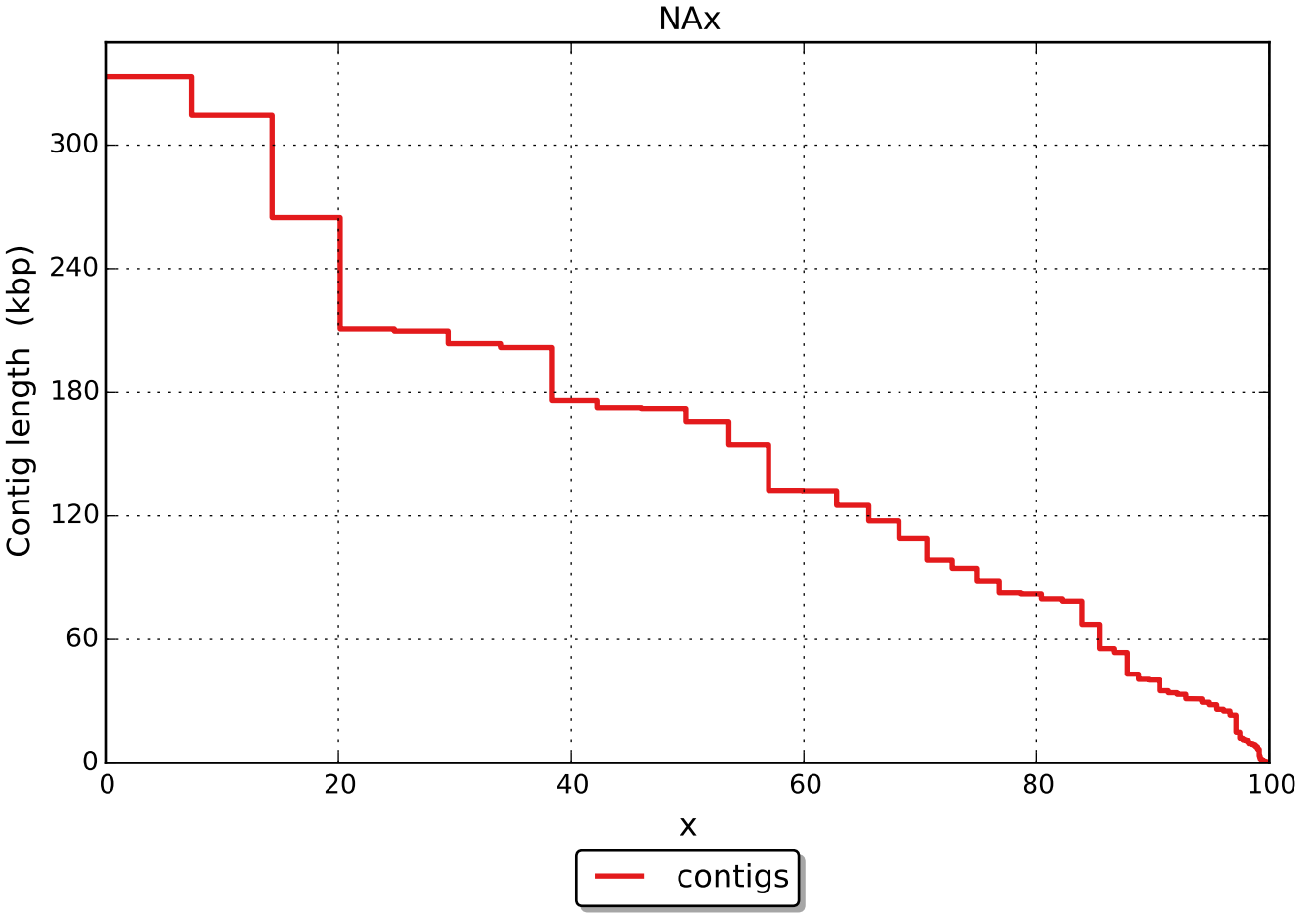

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

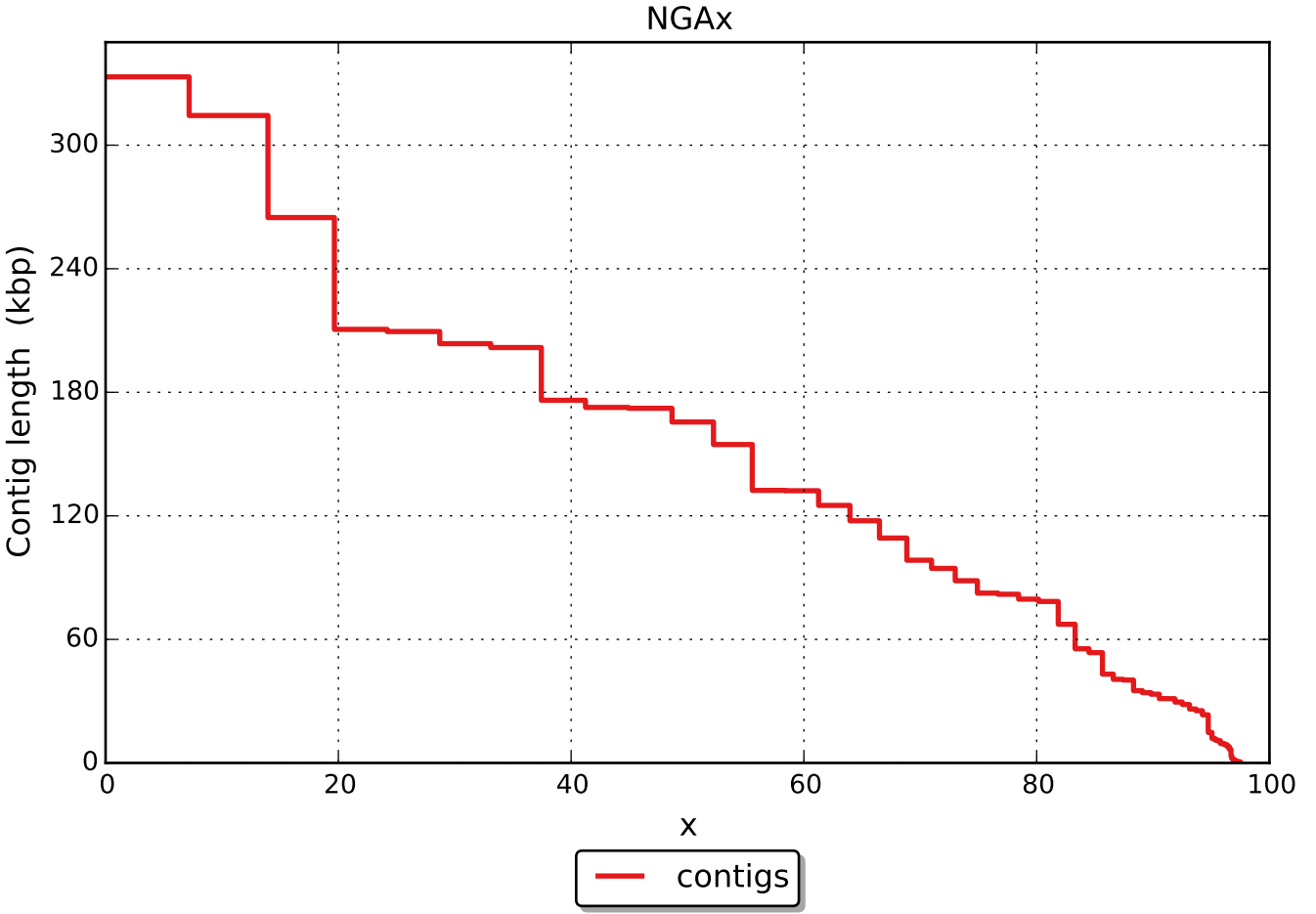

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
contigs
Reference


GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
contigs
Reference


Misassemblies
2.0
1.5
1.0
0.5
0.0
contigs
relocations


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