Report

	contigs
# contigs (>= 1000 bp)	137
# contigs (>= 5000 bp)	77
# contigs (>= 10000 bp)	60
# contigs (>= 25000 bp)	38
# contigs (>= 50000 bp)	25
Total length (>= 1000 bp)	4222154
Total length (>= 5000 bp)	4079622
Total length (>= 10000 bp)	3960061
Total length (>= 25000 bp)	3595430
Total length (>= 50000 bp)	3155565
# contigs	170
Largest contig	331931
Total length	4242579
Reference length	4641652
GC (%)	50.84
Reference GC (%)	50.79
N50	98590
NG50	92158
N75	47699
NG75	30754
L50	12
LG50	14
L75	26
LG75	34
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.283
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1004.36
# indels per 100 kbp	0.93
Largest alignment	331931
NA50	98590
NGA50	92158
NA75	47699
NGA75	30754
LA50	12
LGA50	14
LA75	26
LGA75	34

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

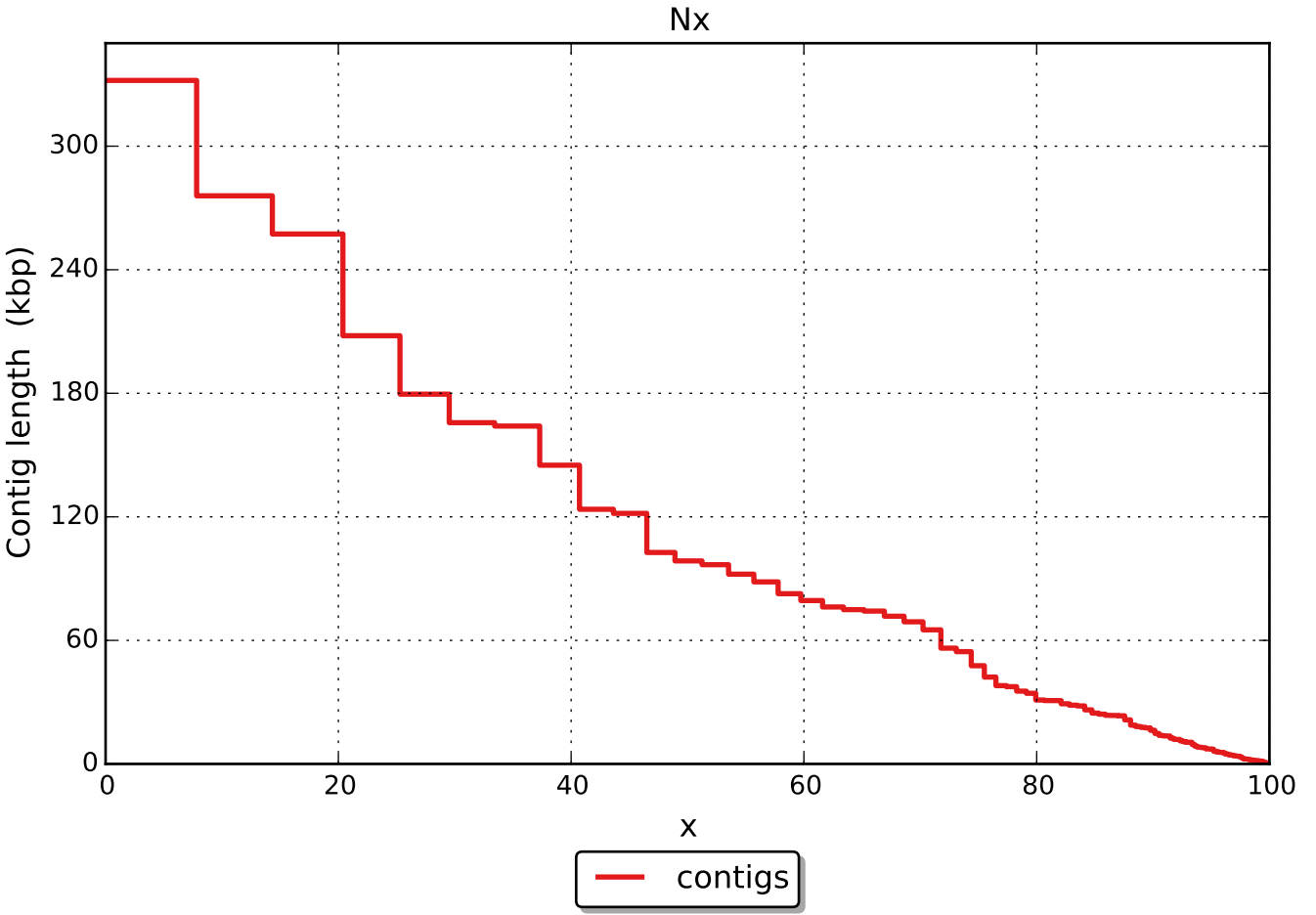
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	42089
# indels	39
# short indels	39
# long indels	0
Indels length	46

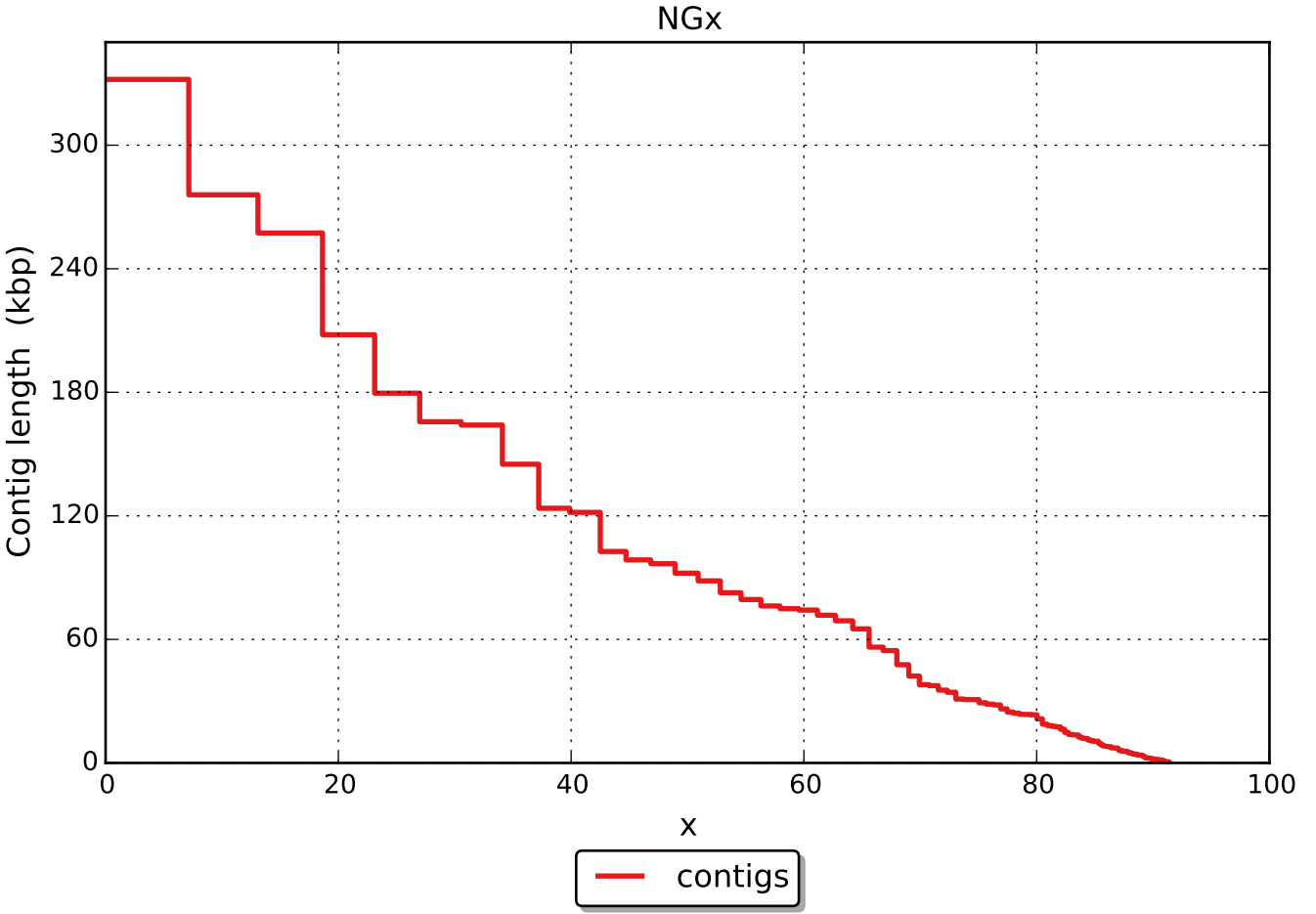
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

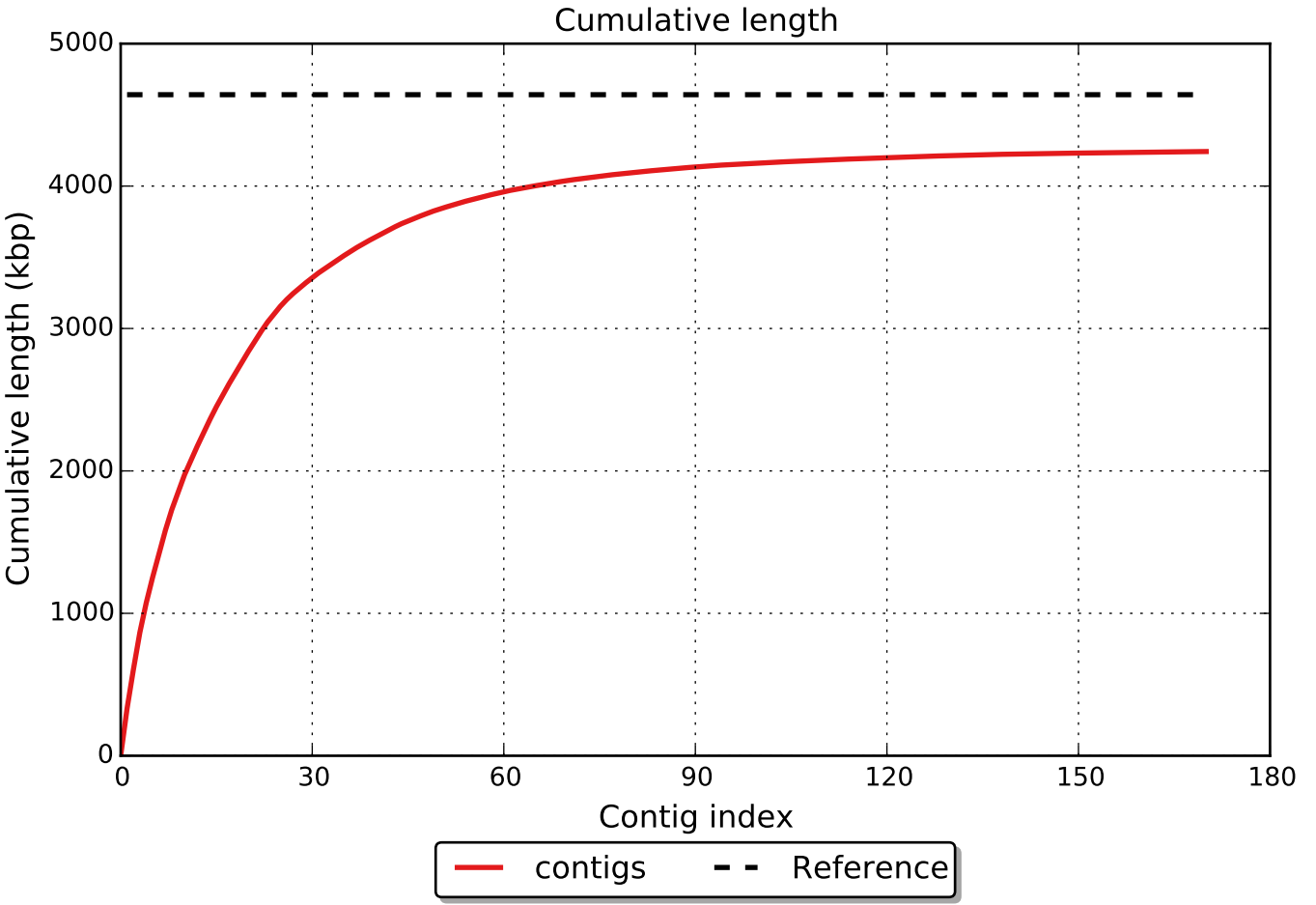
Unaligned report

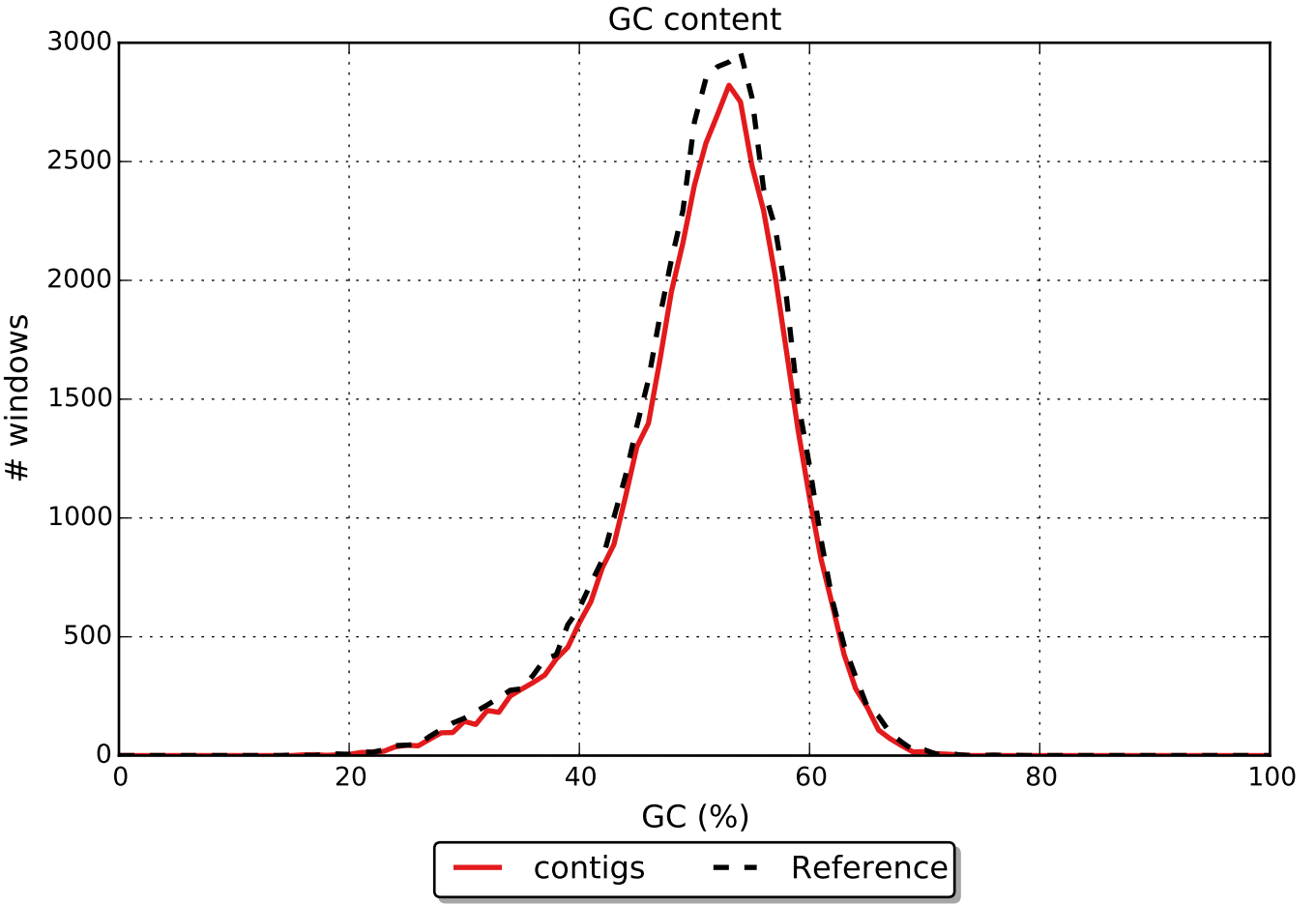
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

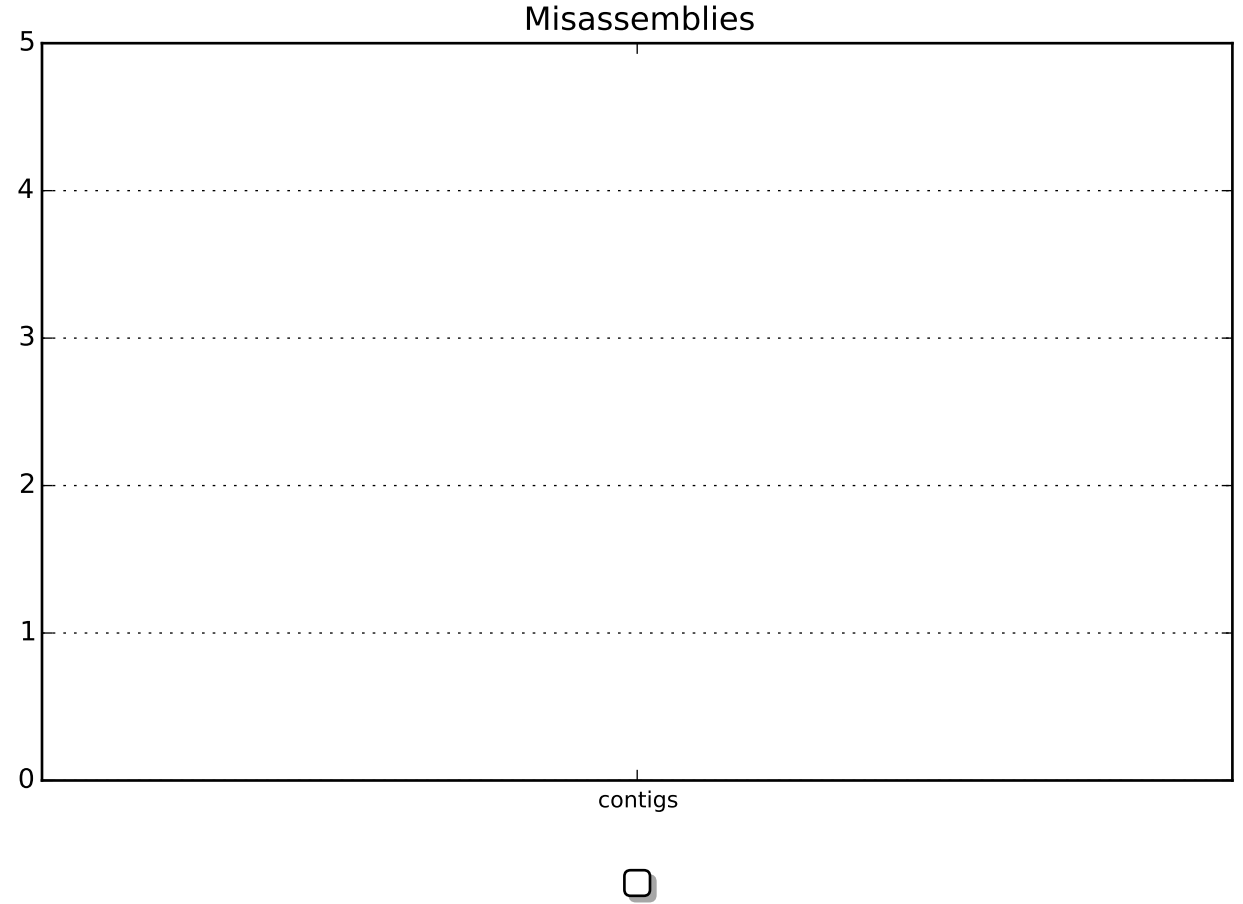
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

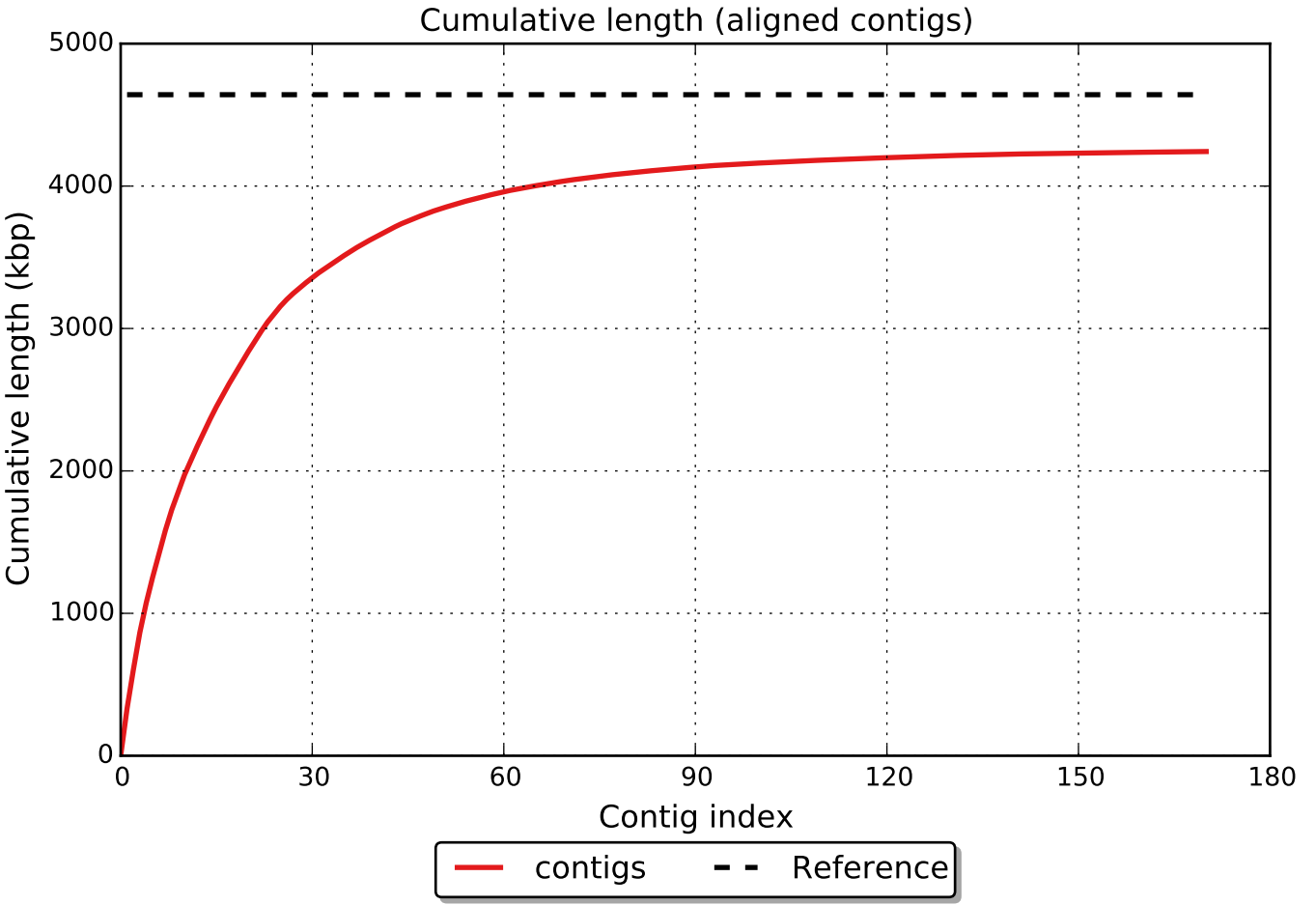

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

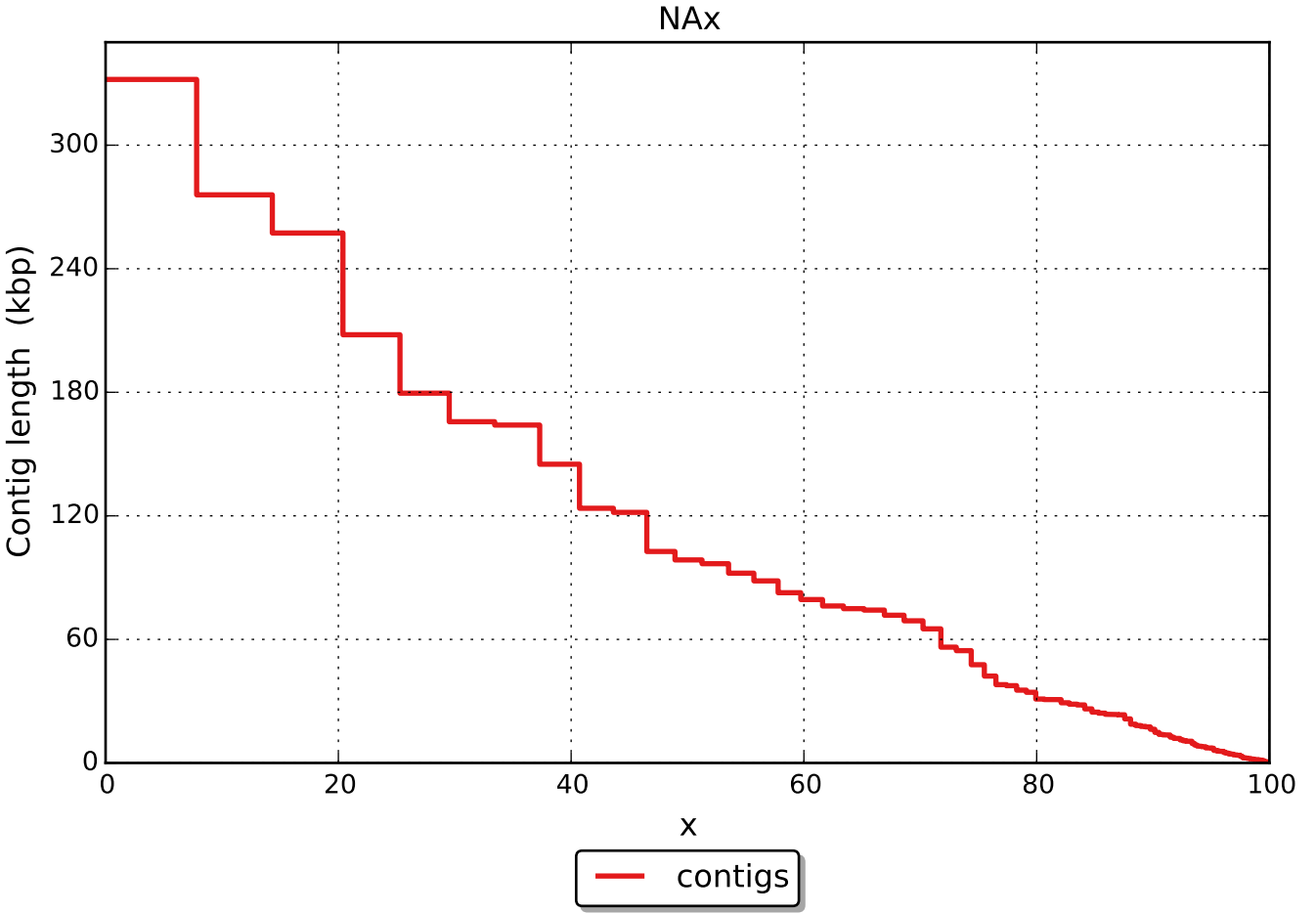

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

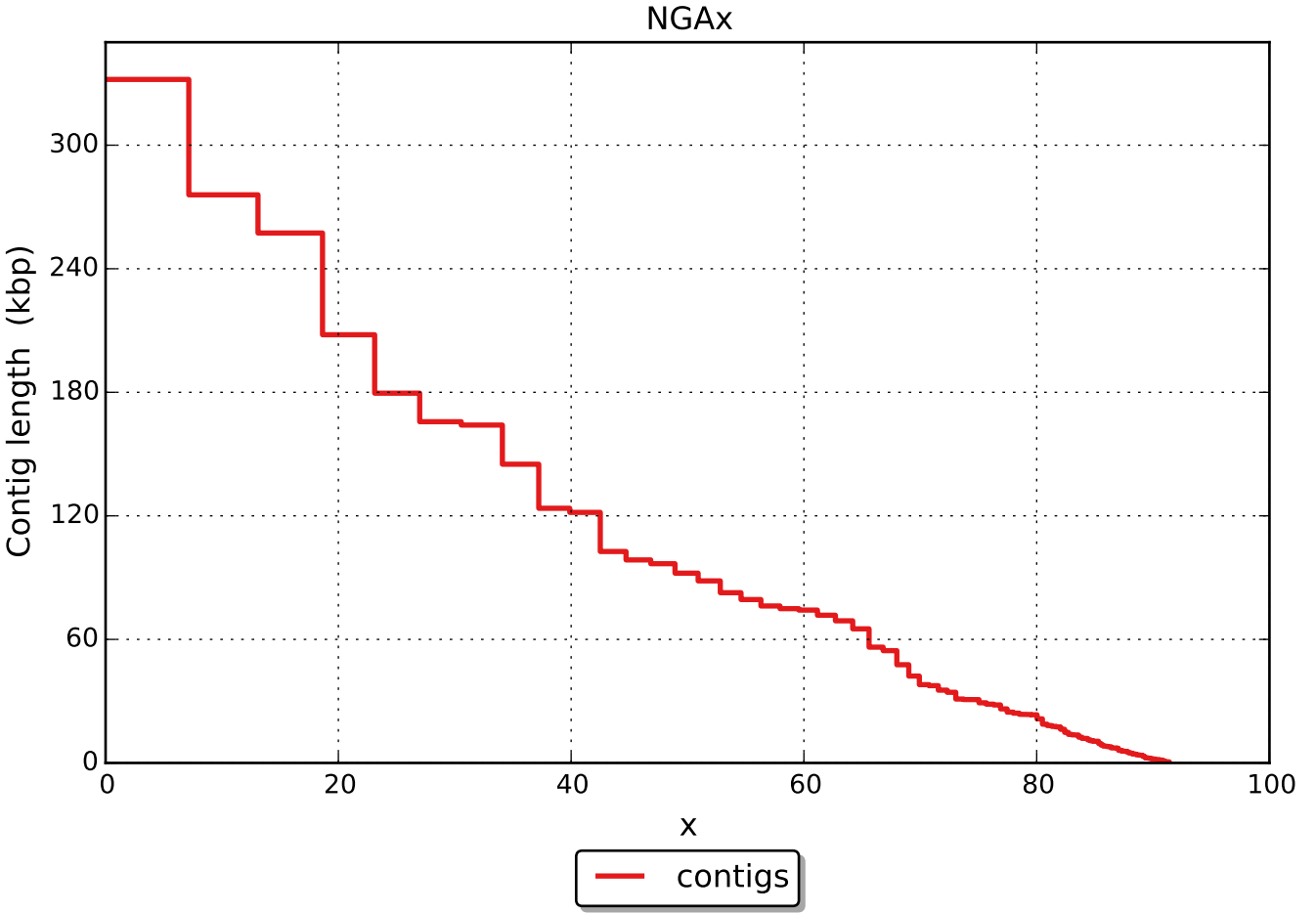

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
180
Contig index
contigs
Reference


GC content
3000
2500
2000
1500
1000
500
0
windows
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
30
60
90
120
150
180
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