Report

	contigs
# contigs (>= 1000 bp)	74
# contigs (>= 5000 bp)	62
# contigs (>= 10000 bp)	49
# contigs (>= 25000 bp)	32
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	2906895
Total length (>= 5000 bp)	2866579
Total length (>= 10000 bp)	2772196
Total length (>= 25000 bp)	2501222
Total length (>= 50000 bp)	2303503
# contigs	78
Largest contig	161420
Total length	2909563
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.78
N50	87964
NG50	43987
N75	54897
L50	13
LG50	27
L75	24
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	62.605
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	541.41
# indels per 100 kbp	0.21
Largest alignment	142244
NA50	87964
NGA50	33561
NA75	43878
LA50	13
LGA50	29
LA75	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).

Misassemblies report

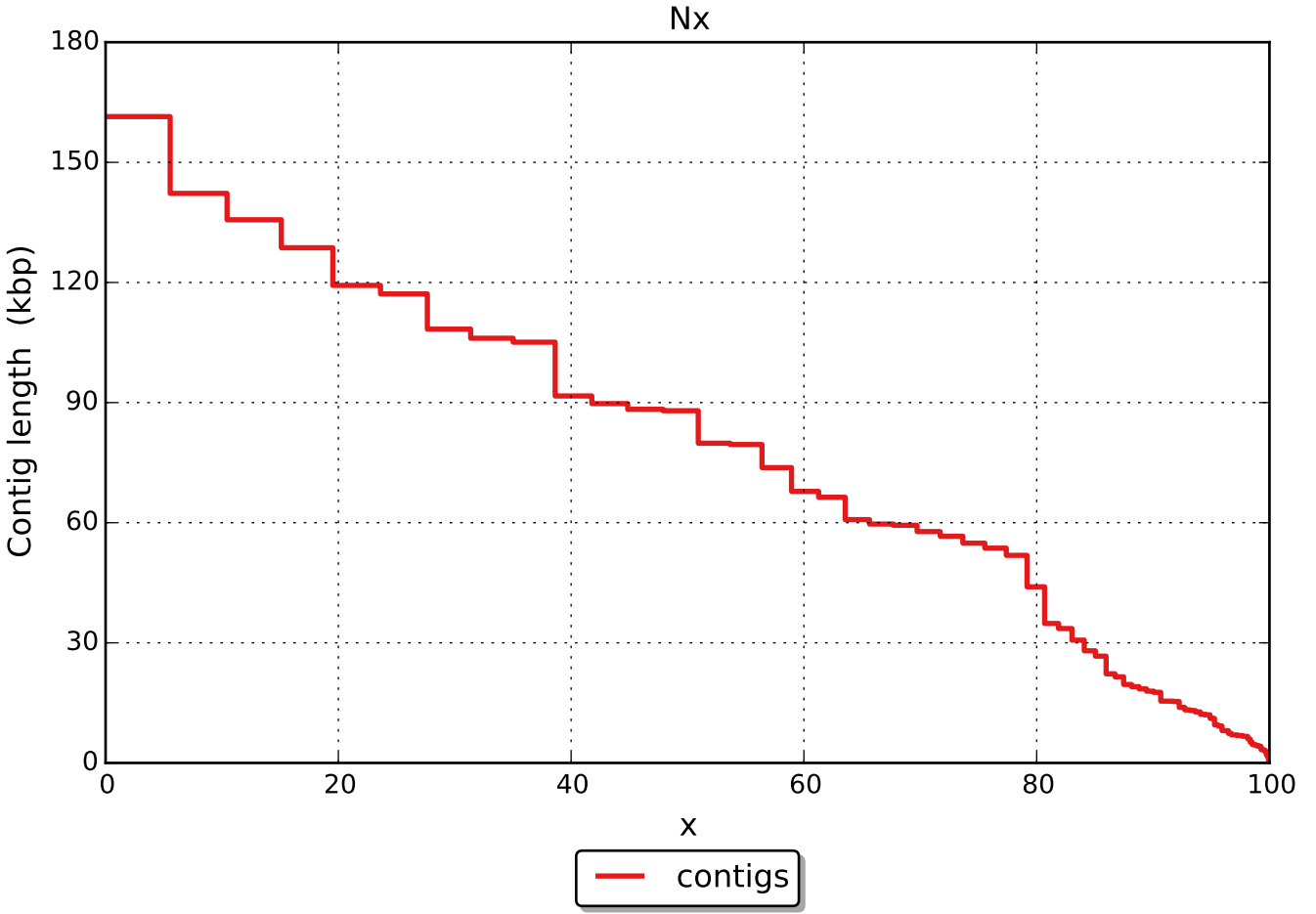
	contigs
# misassemblies	5
# relocations	4
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	2
# mismatches	15733
# indels	6
# short indels	6
# long indels	0
Indels length	7

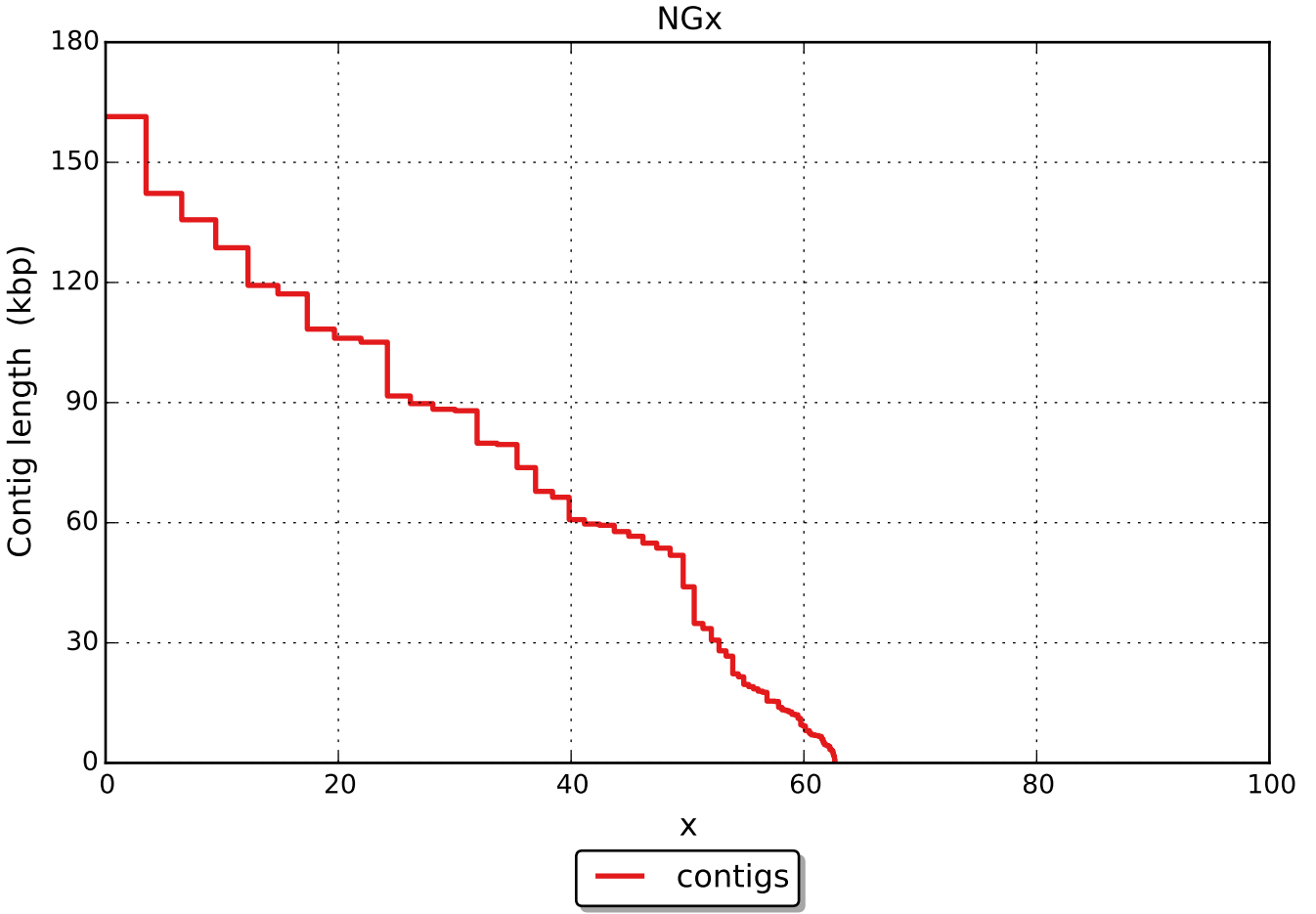
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

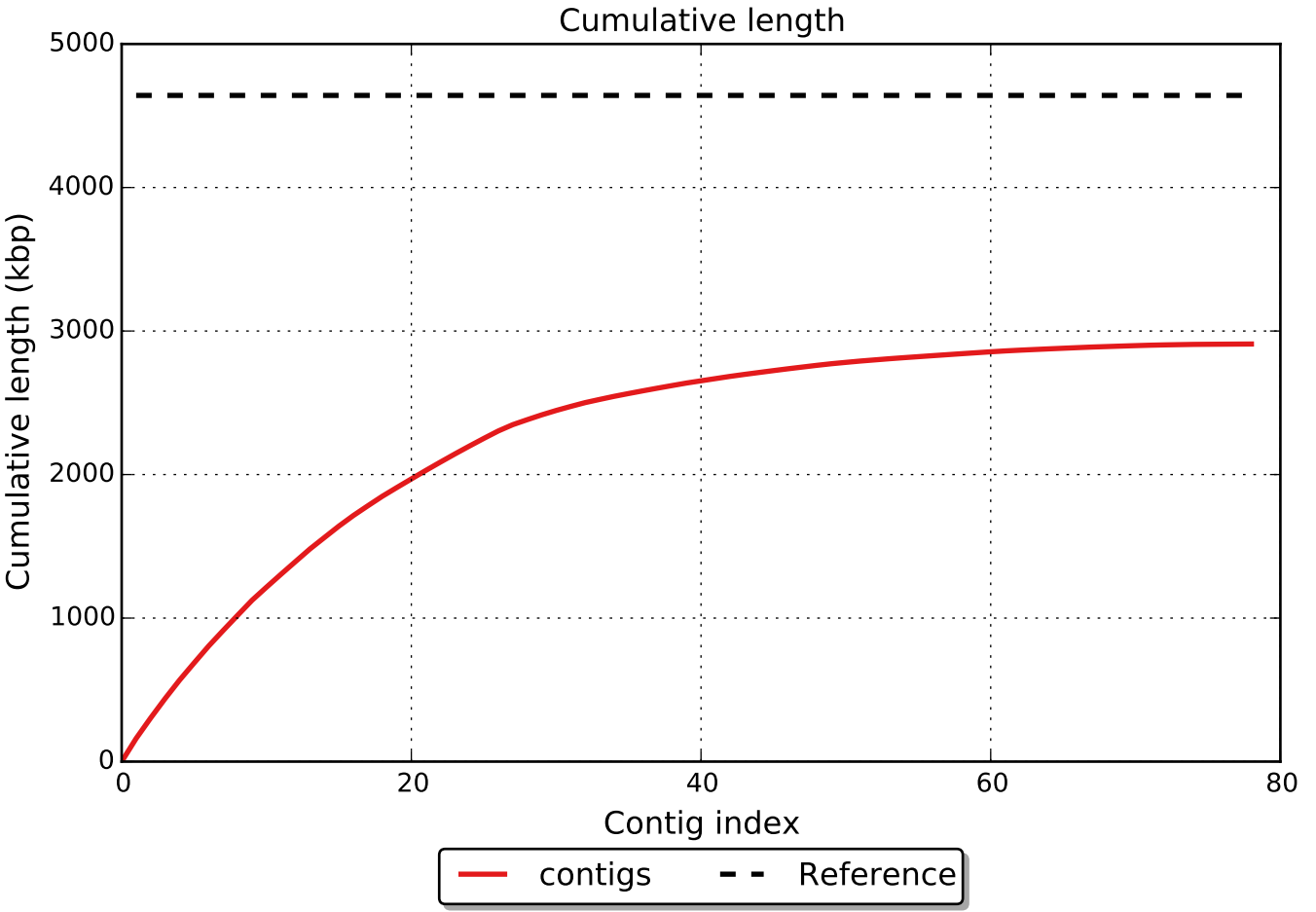
Unaligned report

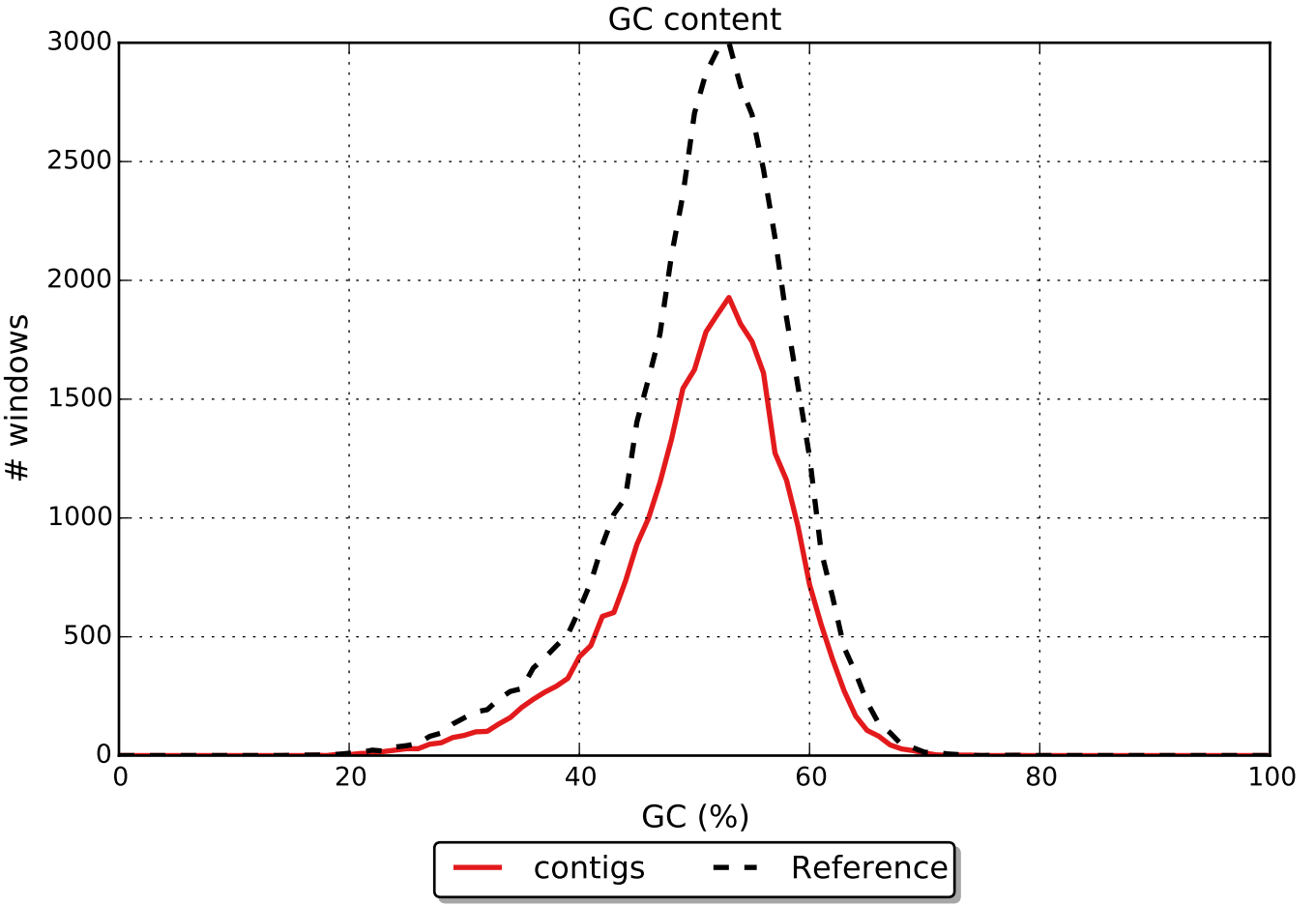
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

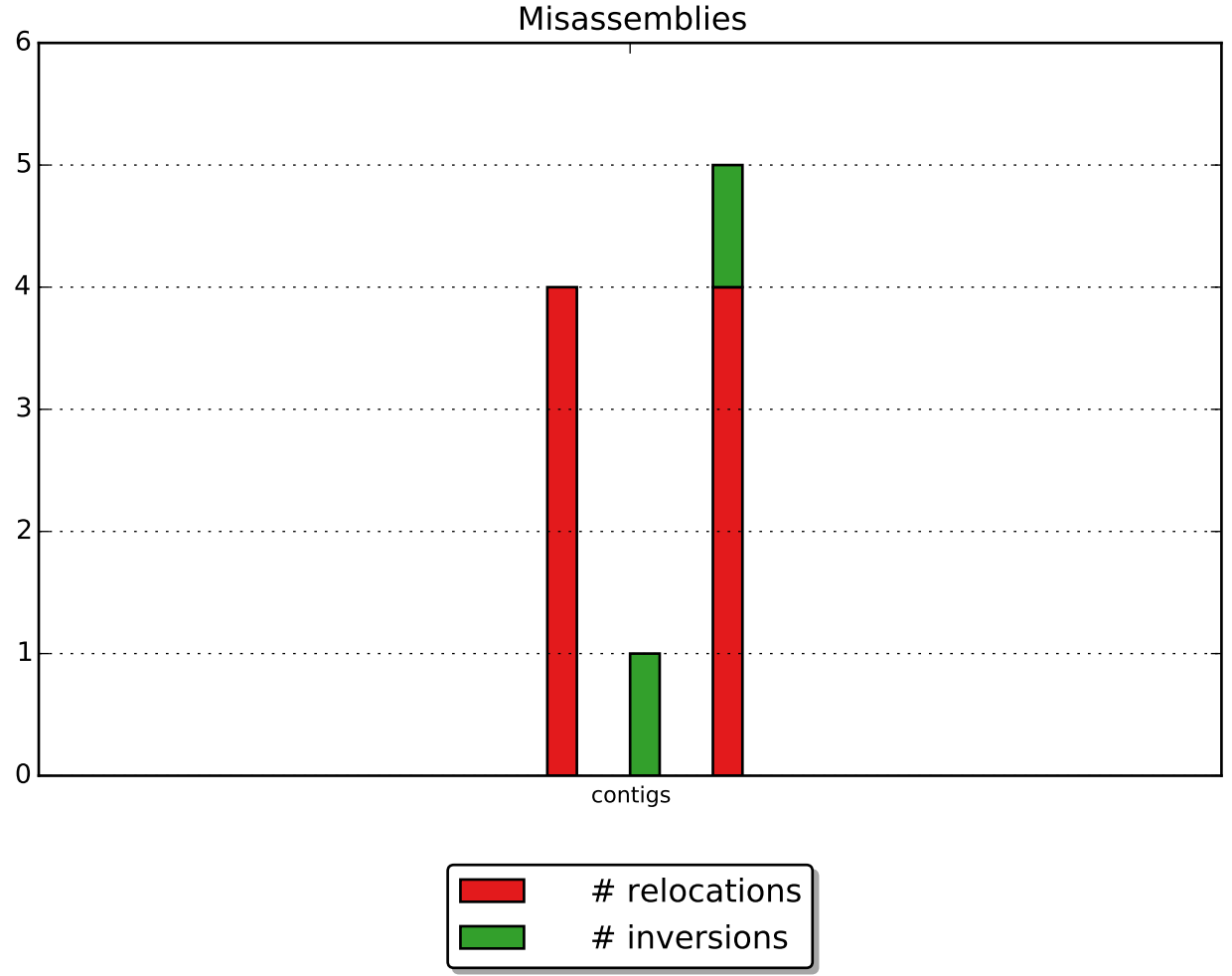
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

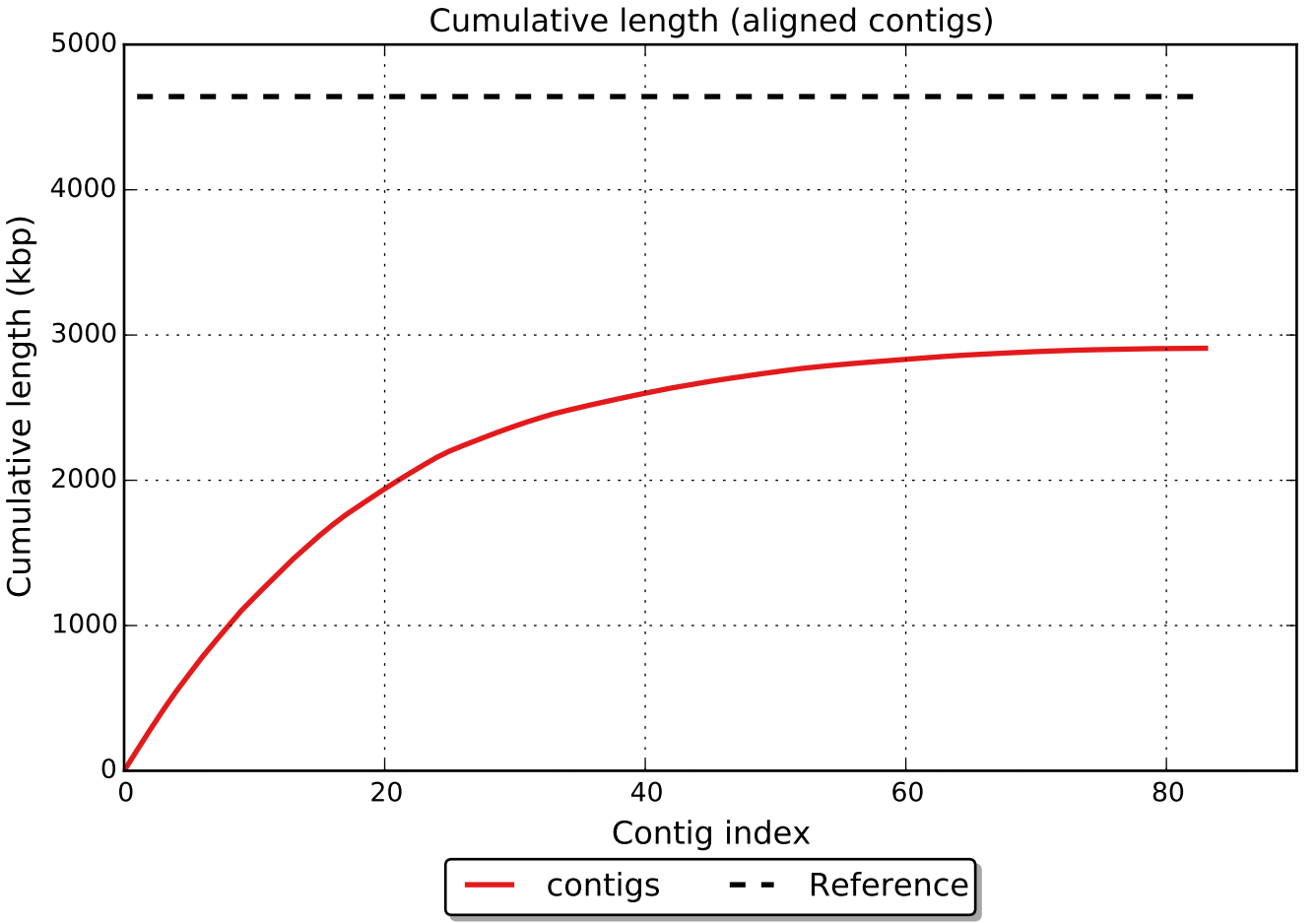

Nx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
contigs

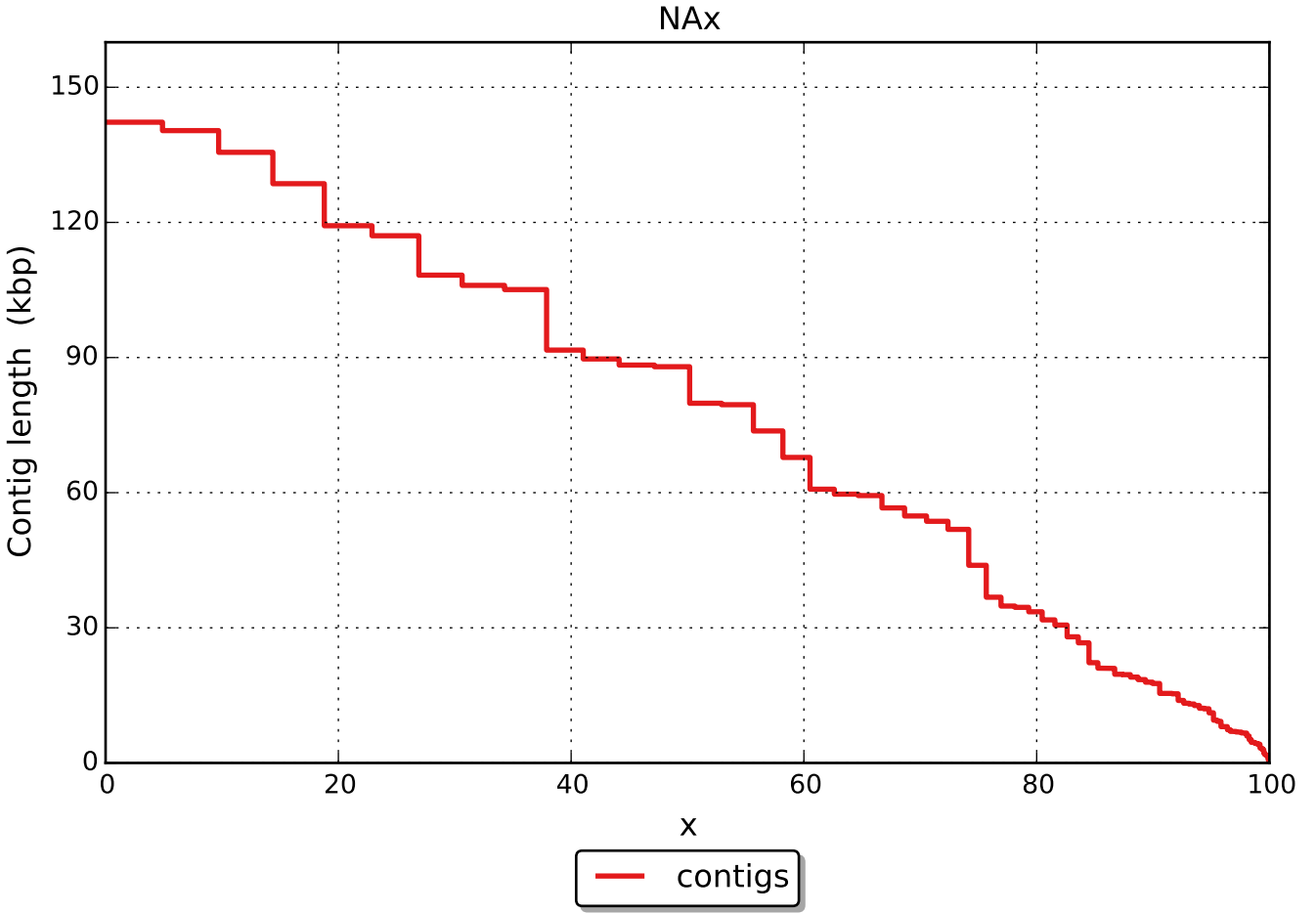

NGx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
contigs

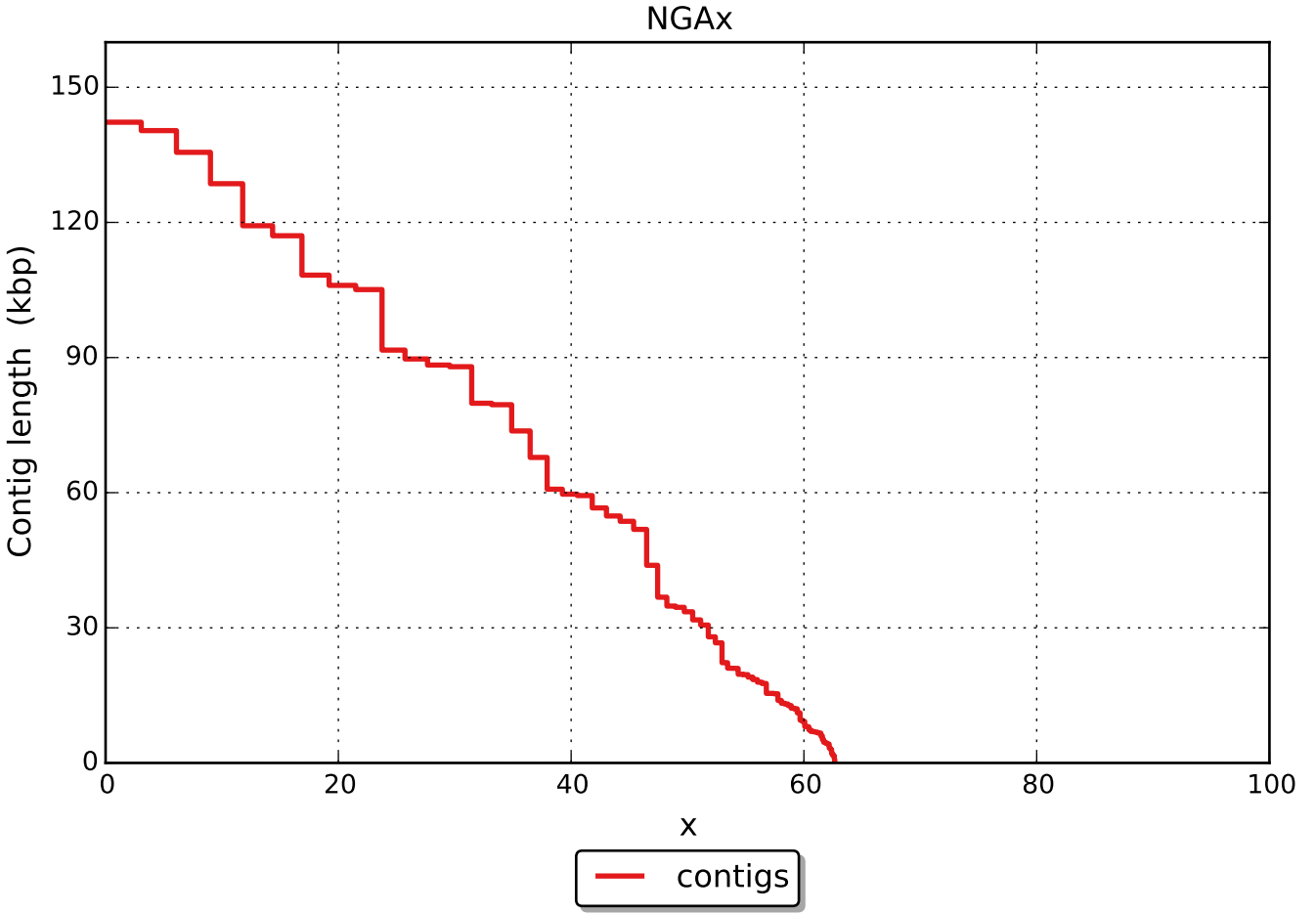

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
20
40
60
80
Contig index
contigs
Reference


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


Misassemblies
6
5
4
3
2
1
0
contigs
relocations
inversions


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)
150
120
90
60
30
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
contigs