Report

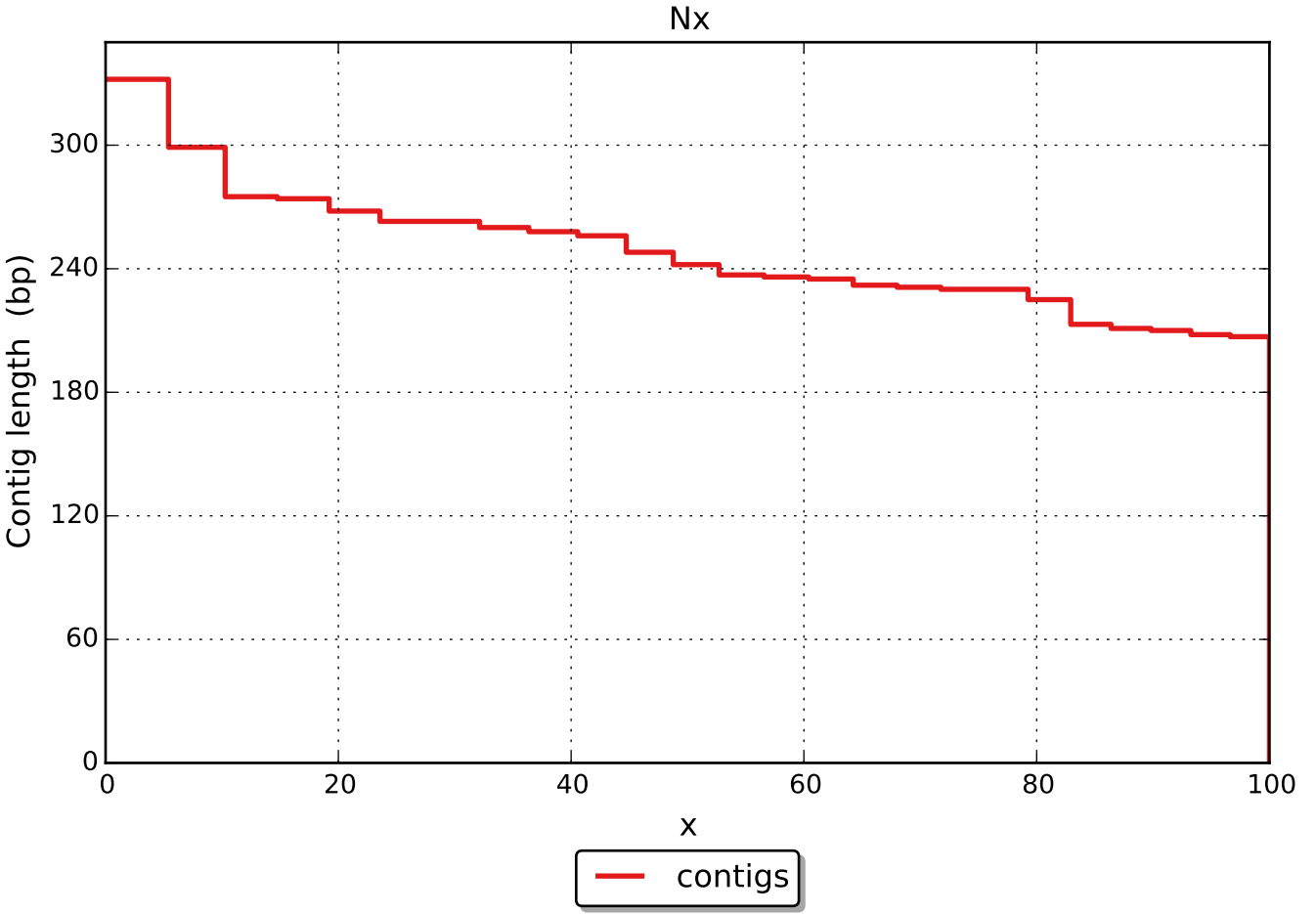
	contigs
# contigs (>= 0 bp)	25
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6143
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	25
Largest contig	332
Total length	6143
Reference length	4641652
GC (%)	53.04
Reference GC (%)	50.79
N50	242
N75	230
L50	12
L75	18
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	9 + 1 part
Unaligned length	2267
Genome fraction (%)	0.080
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2780.03
# indels per 100 kbp	53.98
Largest alignment	332
NA50	211
NGA50	-
LA50	12

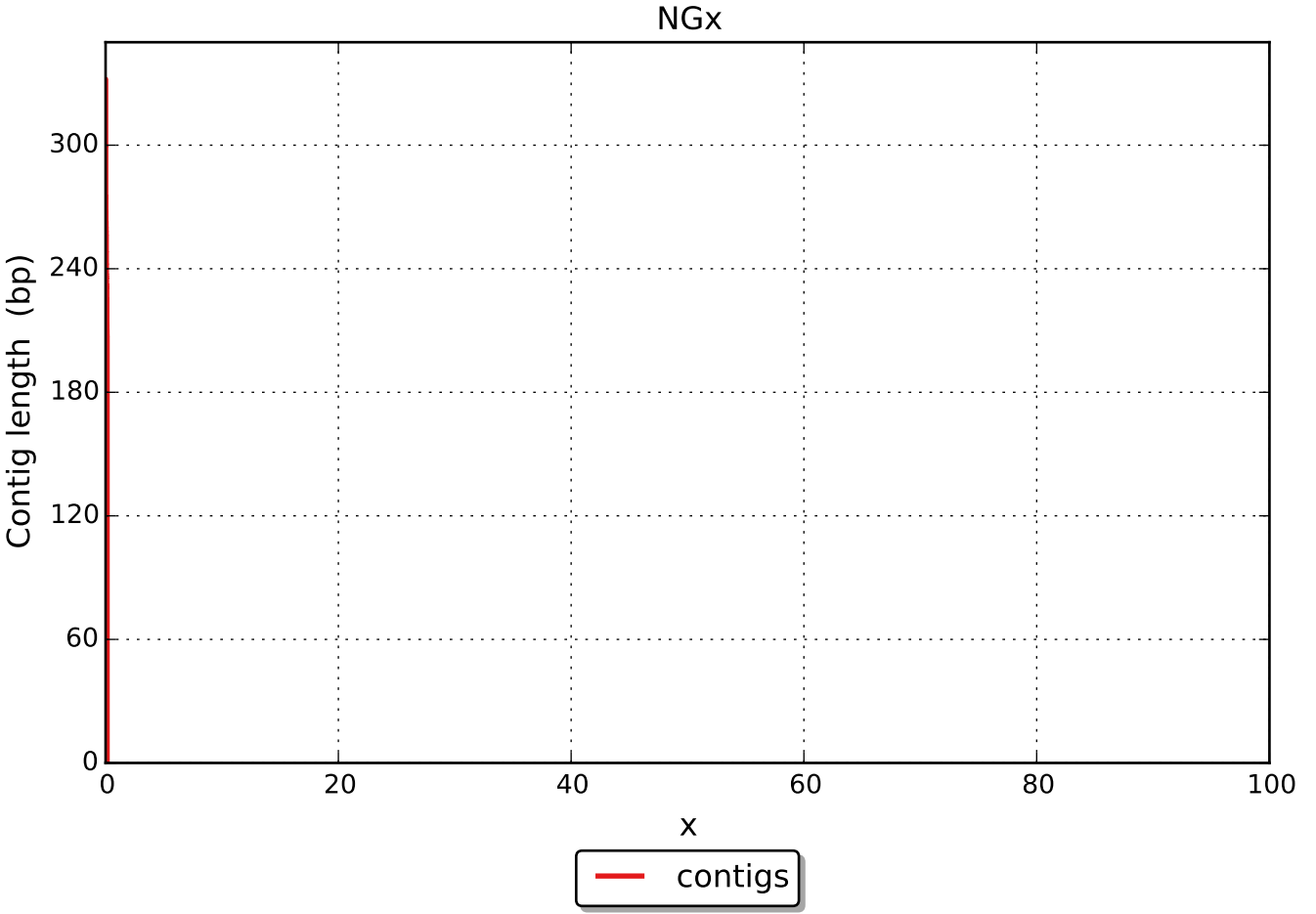
Misassemblies report

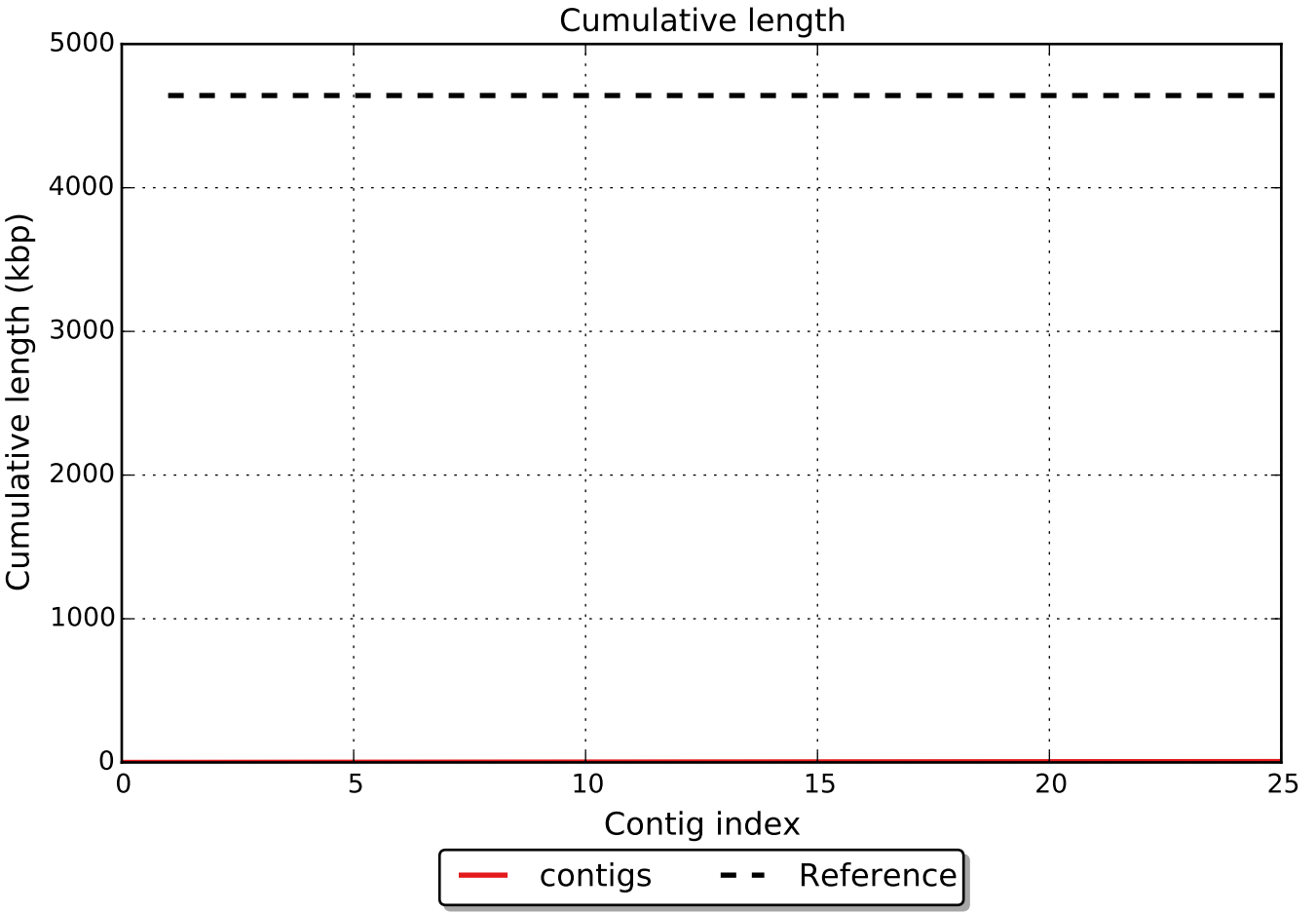
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	103
# indels	2
# short indels	2
# long indels	0
Indels length	2

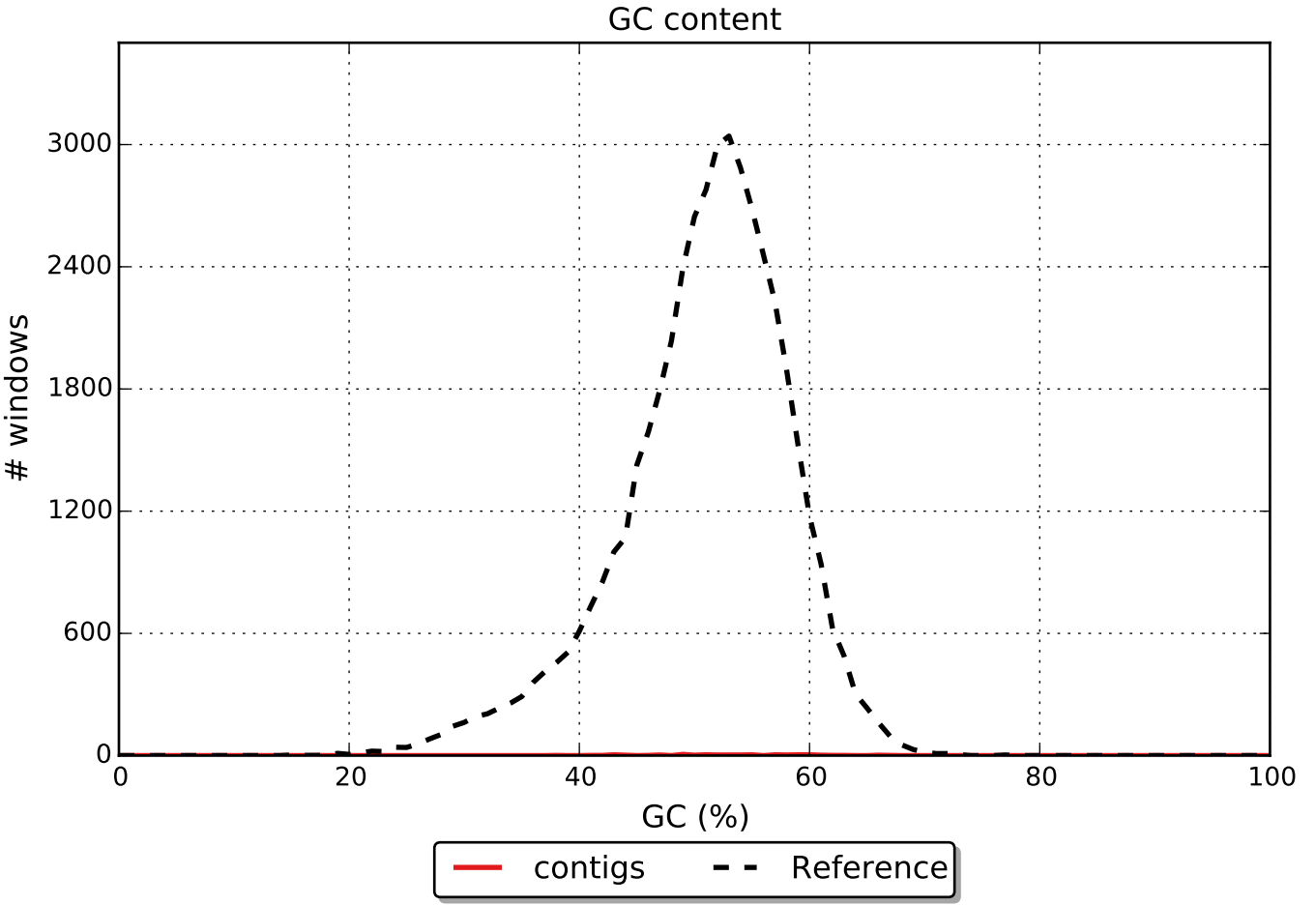
Unaligned report

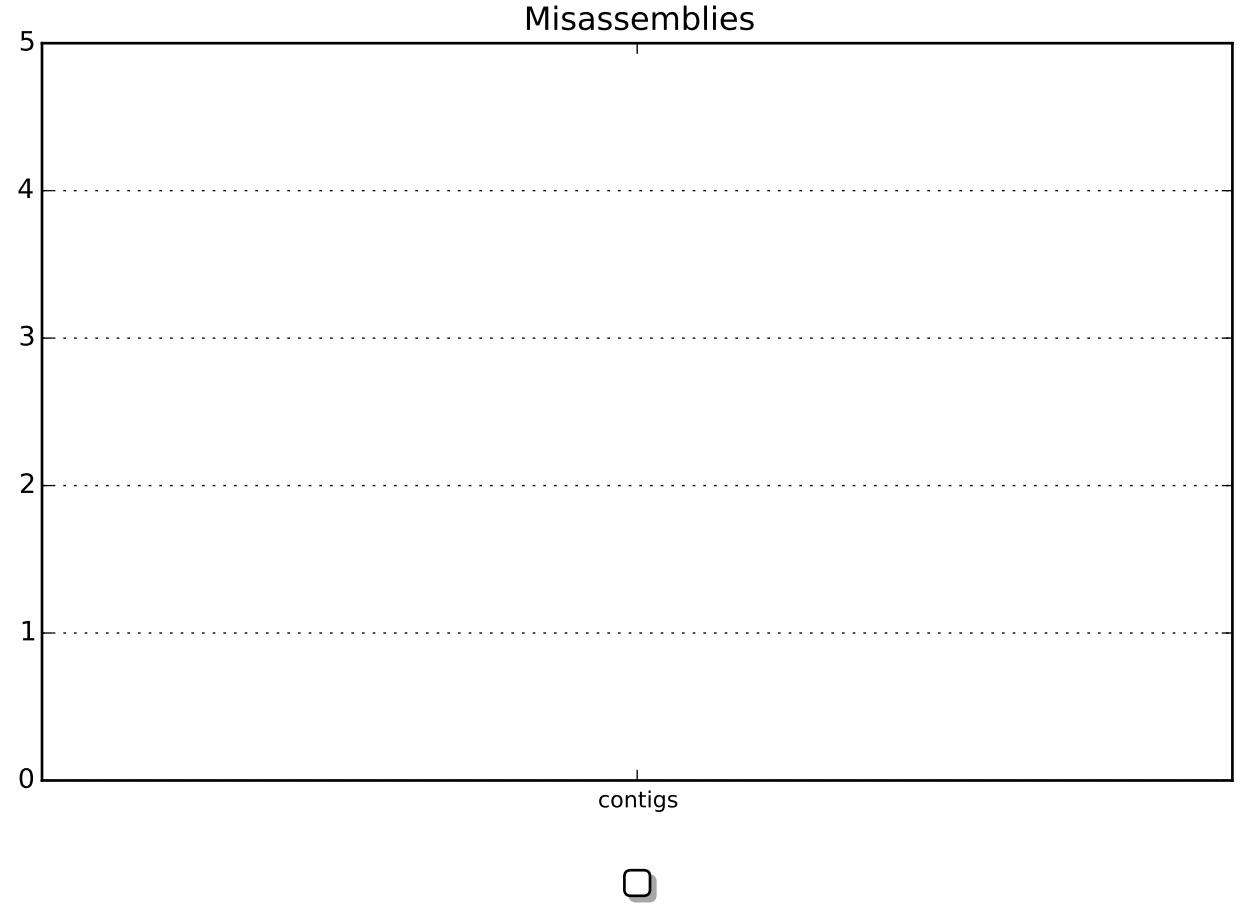
	contigs
# fully unaligned contigs	9
Fully unaligned length	2207
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	60
# N's	0

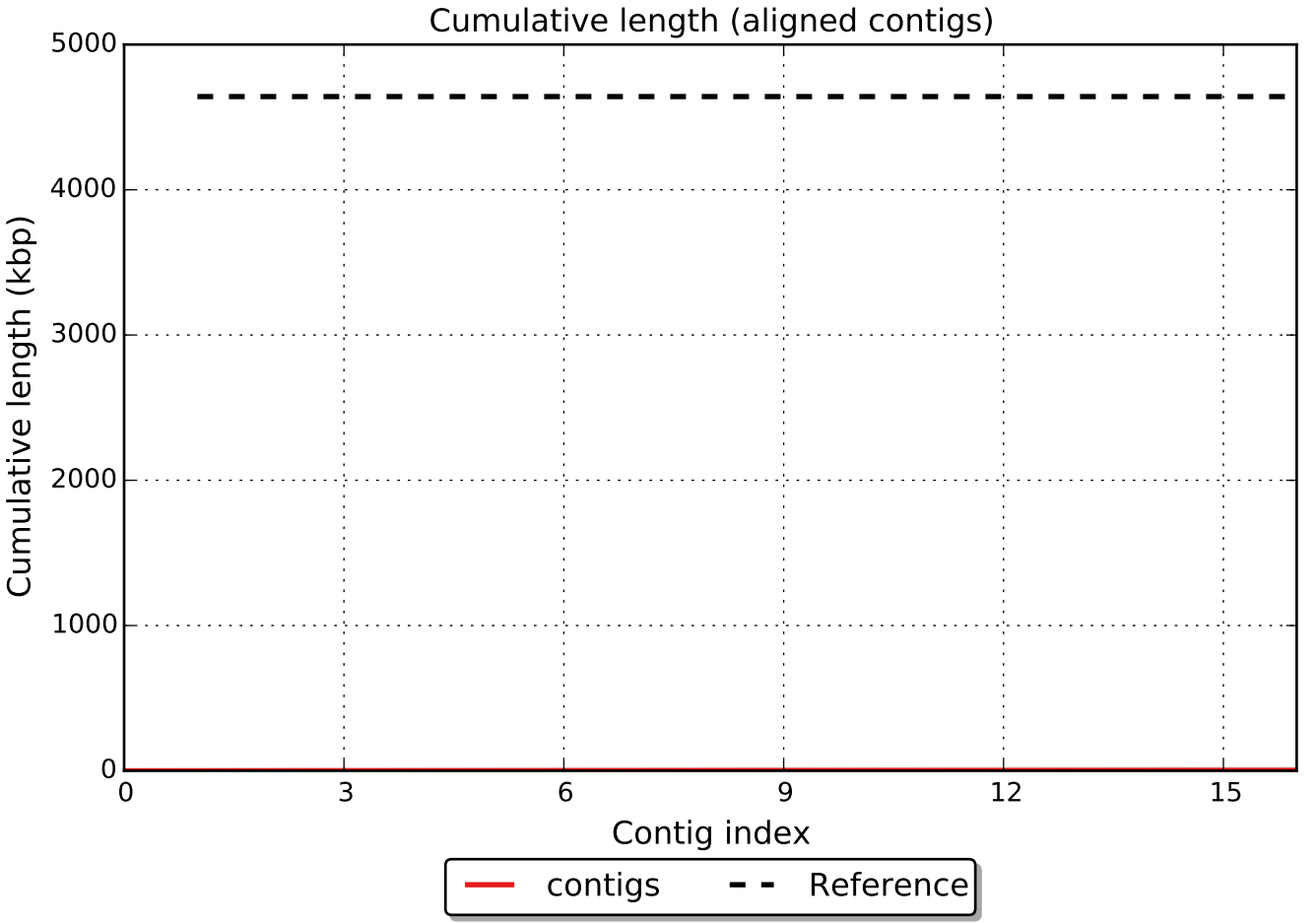

Nx
Contig length (bp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

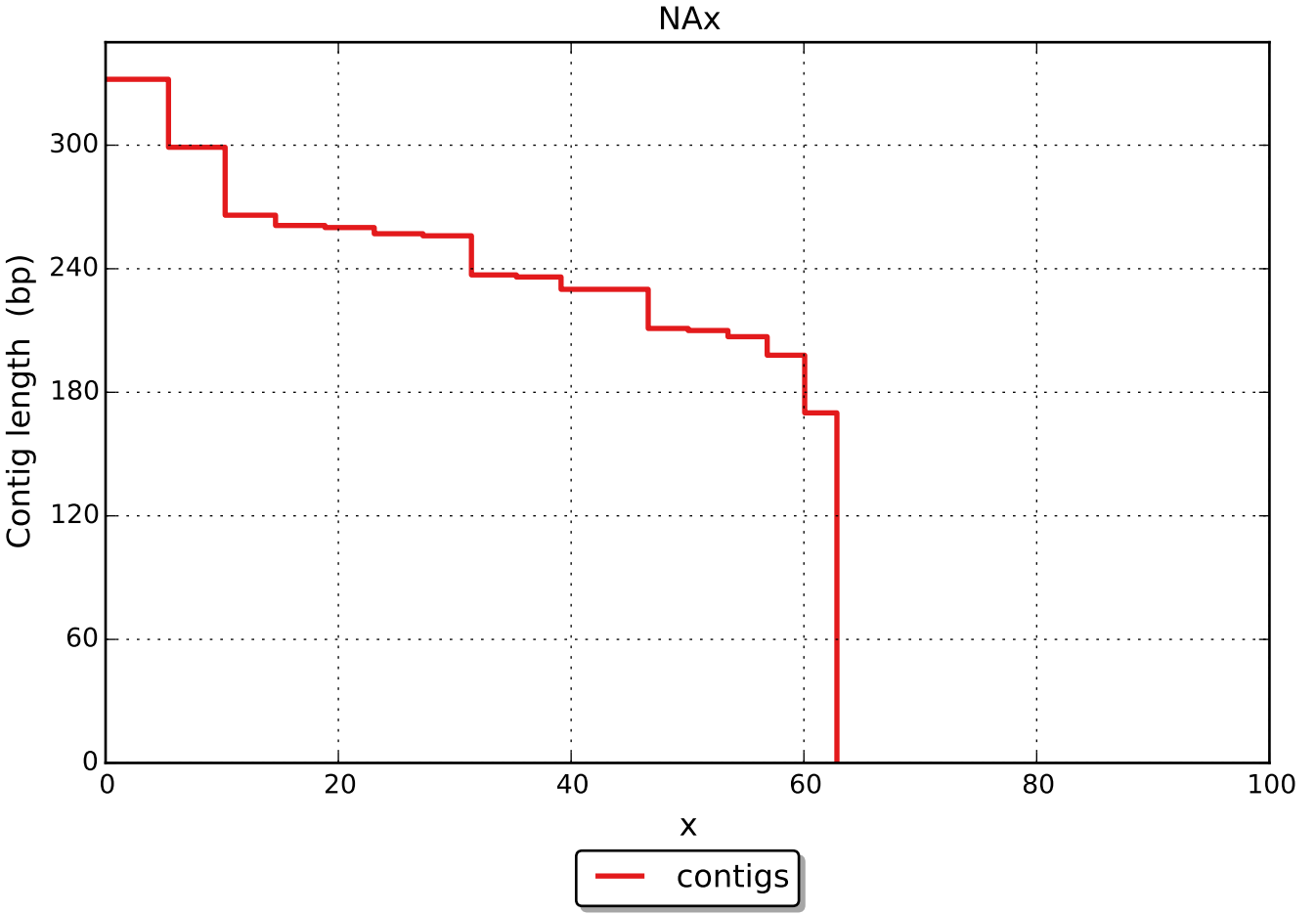

NGx
Contig length (bp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

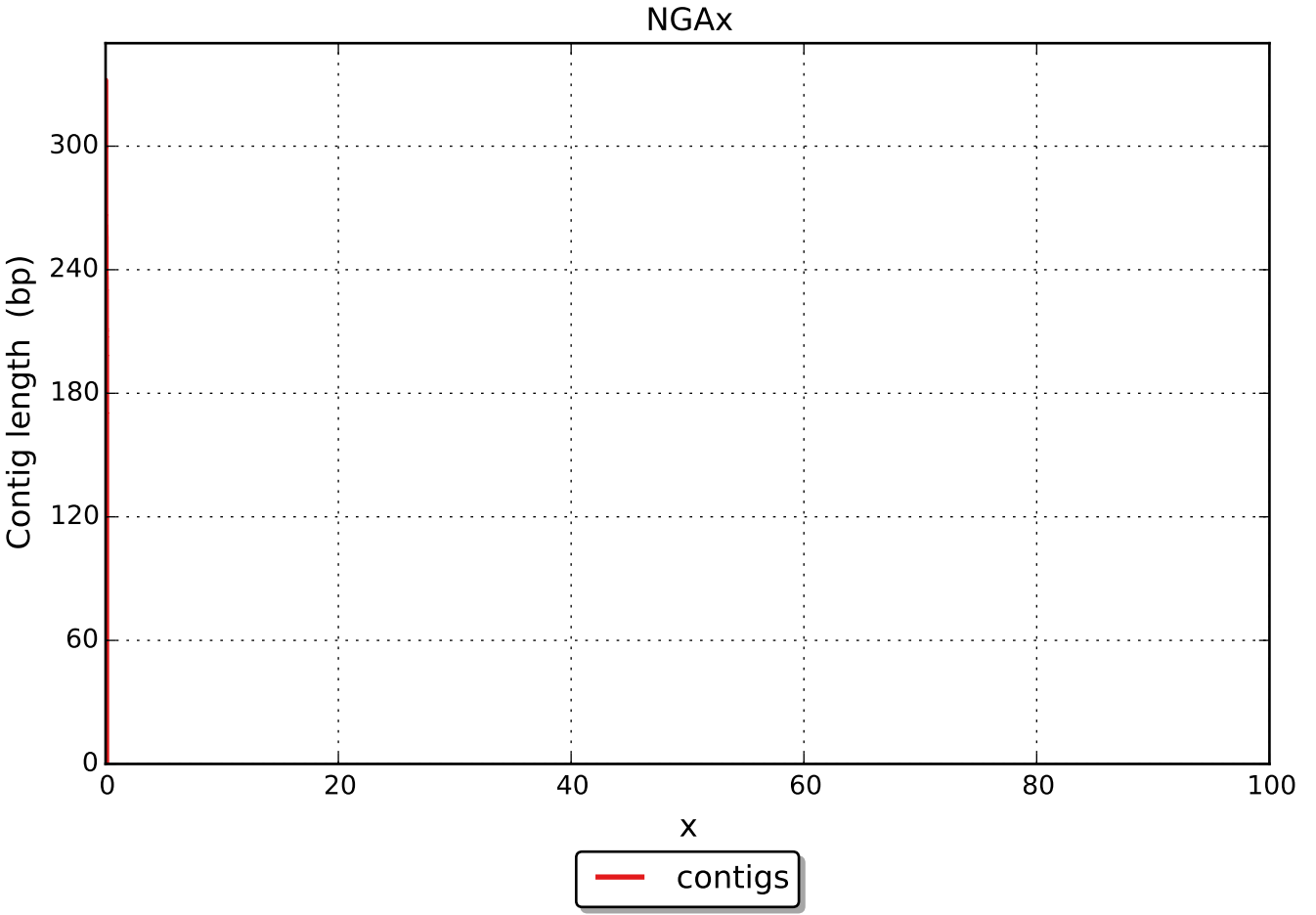

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Contig index
contigs
Reference


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
3
6
9
12
15
Contig index
contigs
Reference


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


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