Report

	contigs
# contigs (>= 1000 bp)	67
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	48
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4656709
Total length (>= 5000 bp)	4628608
Total length (>= 10000 bp)	4606921
Total length (>= 25000 bp)	4530167
Total length (>= 50000 bp)	4016121
# contigs	85
Largest contig	332104
Total length	4669840
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	167862
NG50	167862
N75	85064
NG75	85064
L50	10
LG50	10
L75	21
LG75	21
# misassemblies	3
# misassembled contigs	1
Misassembled contigs length	308025
# local misassemblies	3
# unaligned contigs	0 + 2 part
Unaligned length	23786
Genome fraction (%)	97.762
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	475.48
# indels per 100 kbp	0.95
Largest alignment	332104
NA50	132902
NGA50	132902
NA75	79547
NGA75	79547
LA50	11
LGA50	11
LA75	22
LGA75	22

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

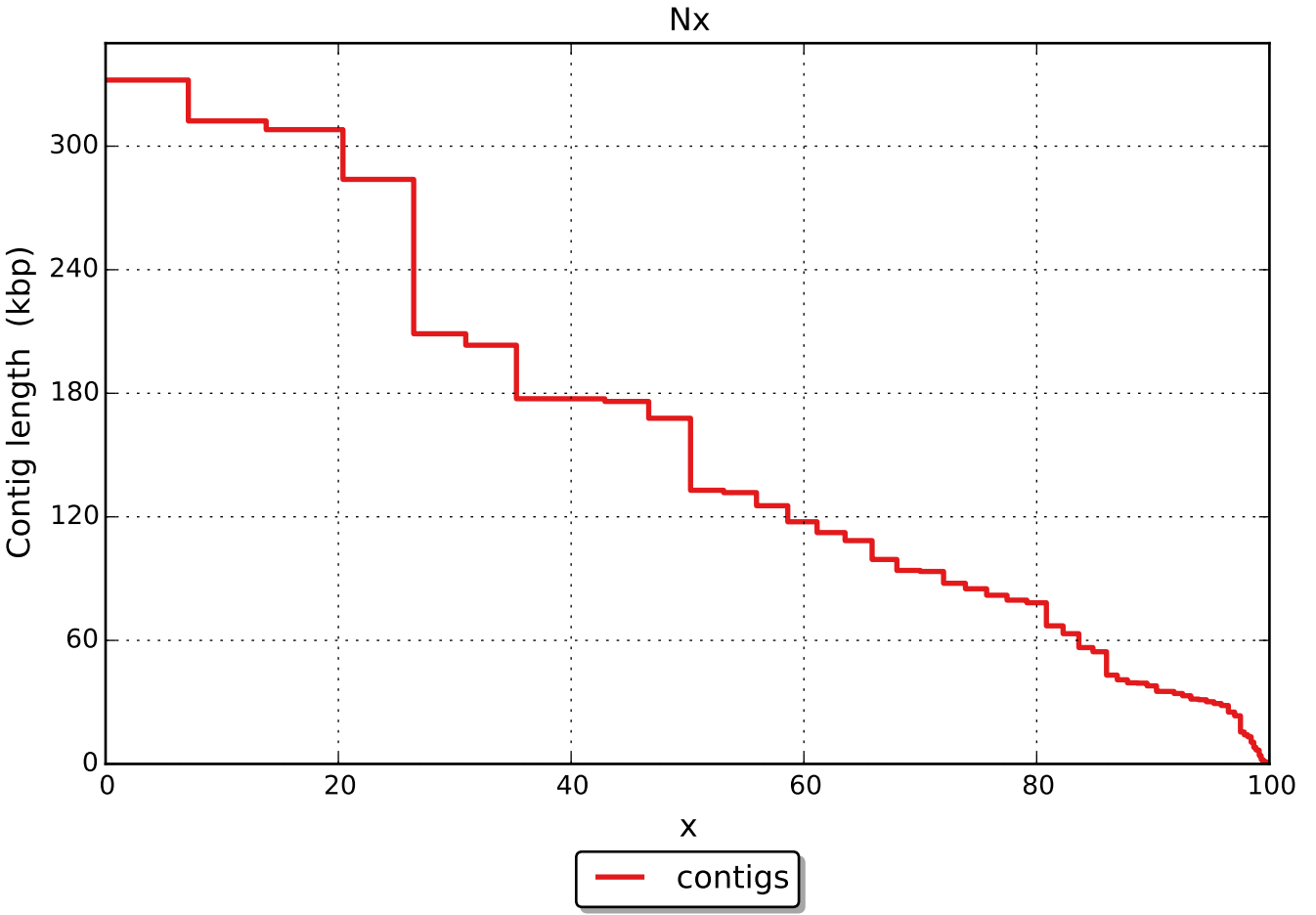
	contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	3
# misassembled contigs	1
Misassembled contigs length	308025
# local misassemblies	3
# mismatches	21576
# indels	43
# short indels	38
# long indels	5
Indels length	119

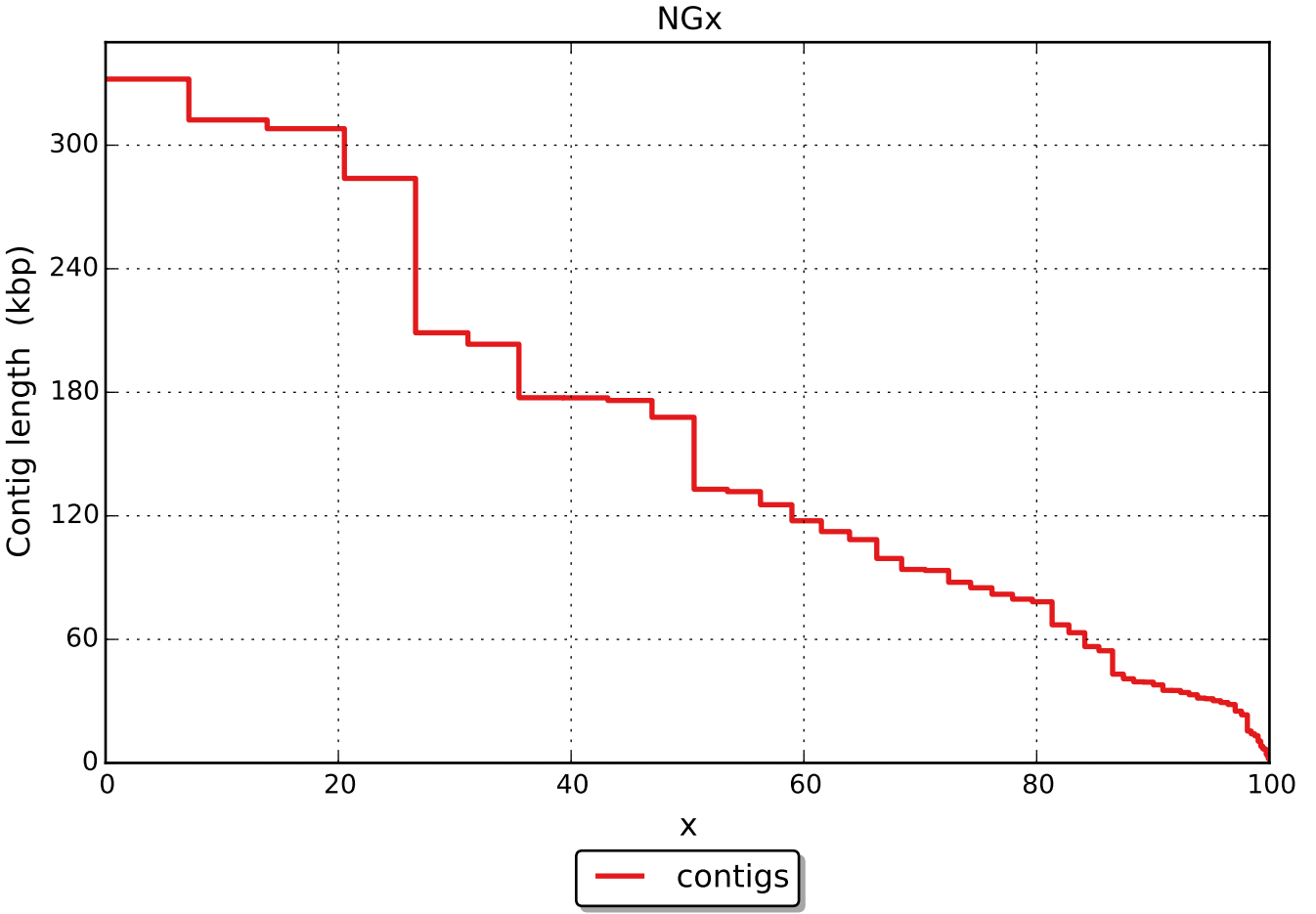
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

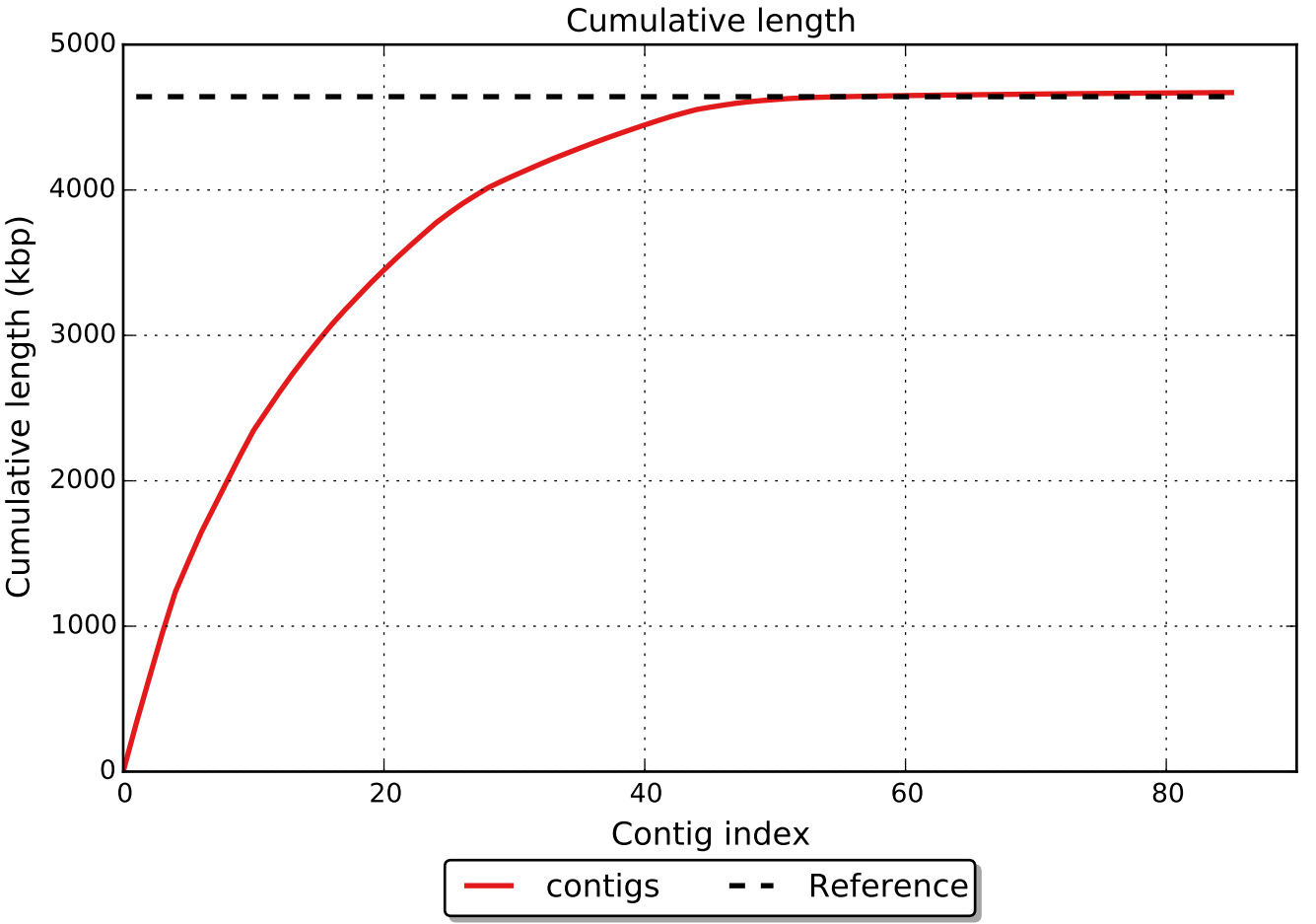
Unaligned report

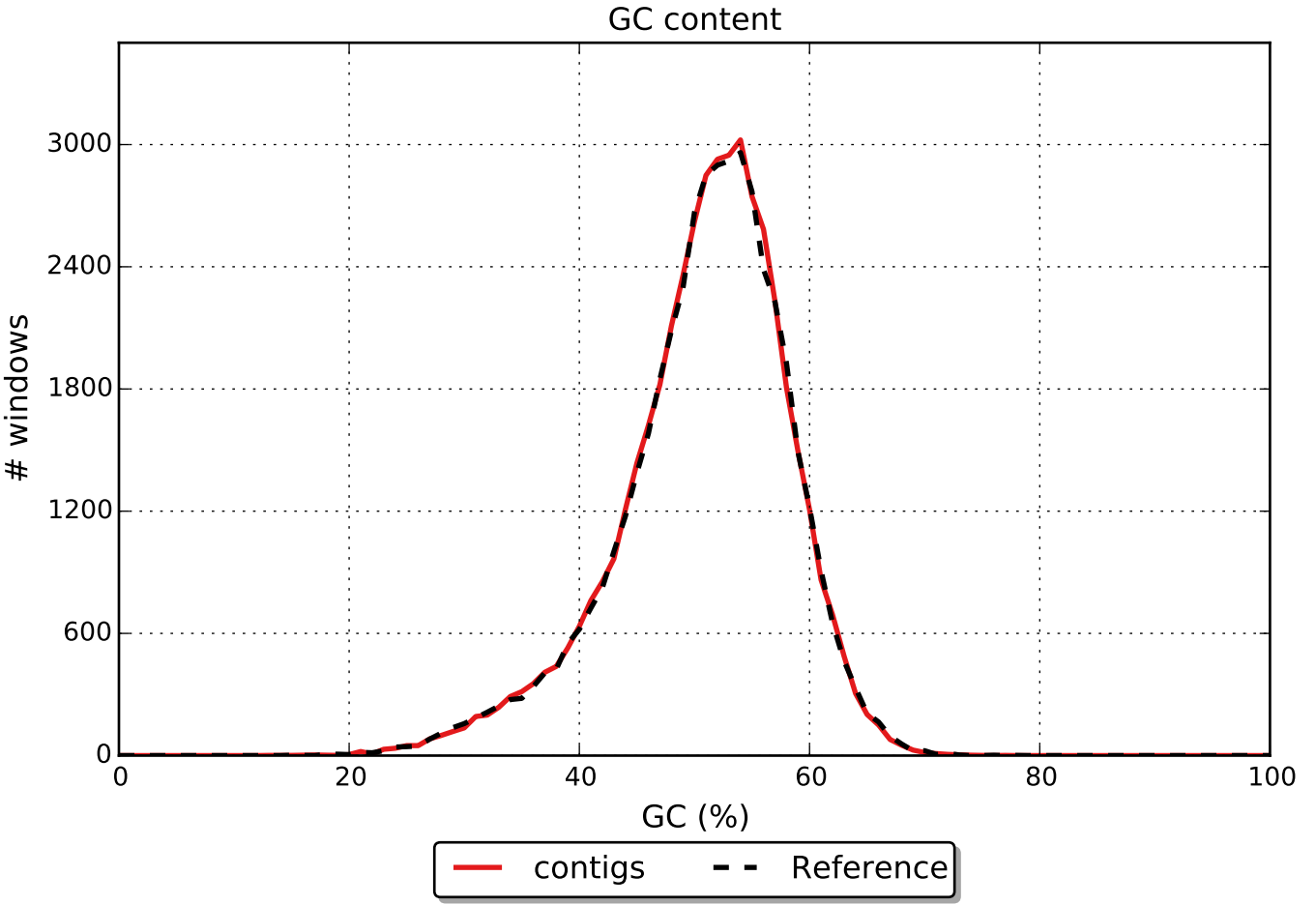
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	23786
# N's	0

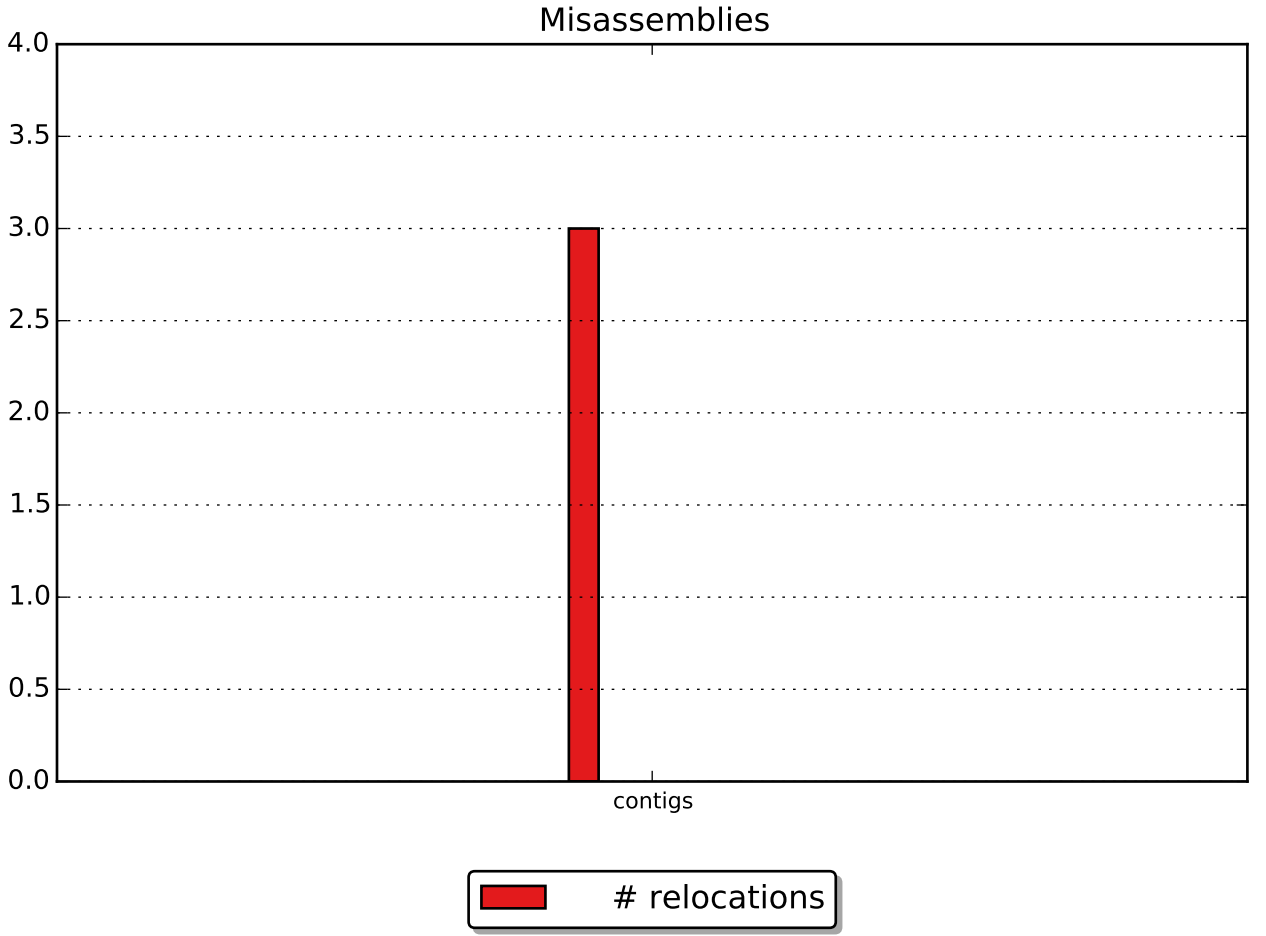
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

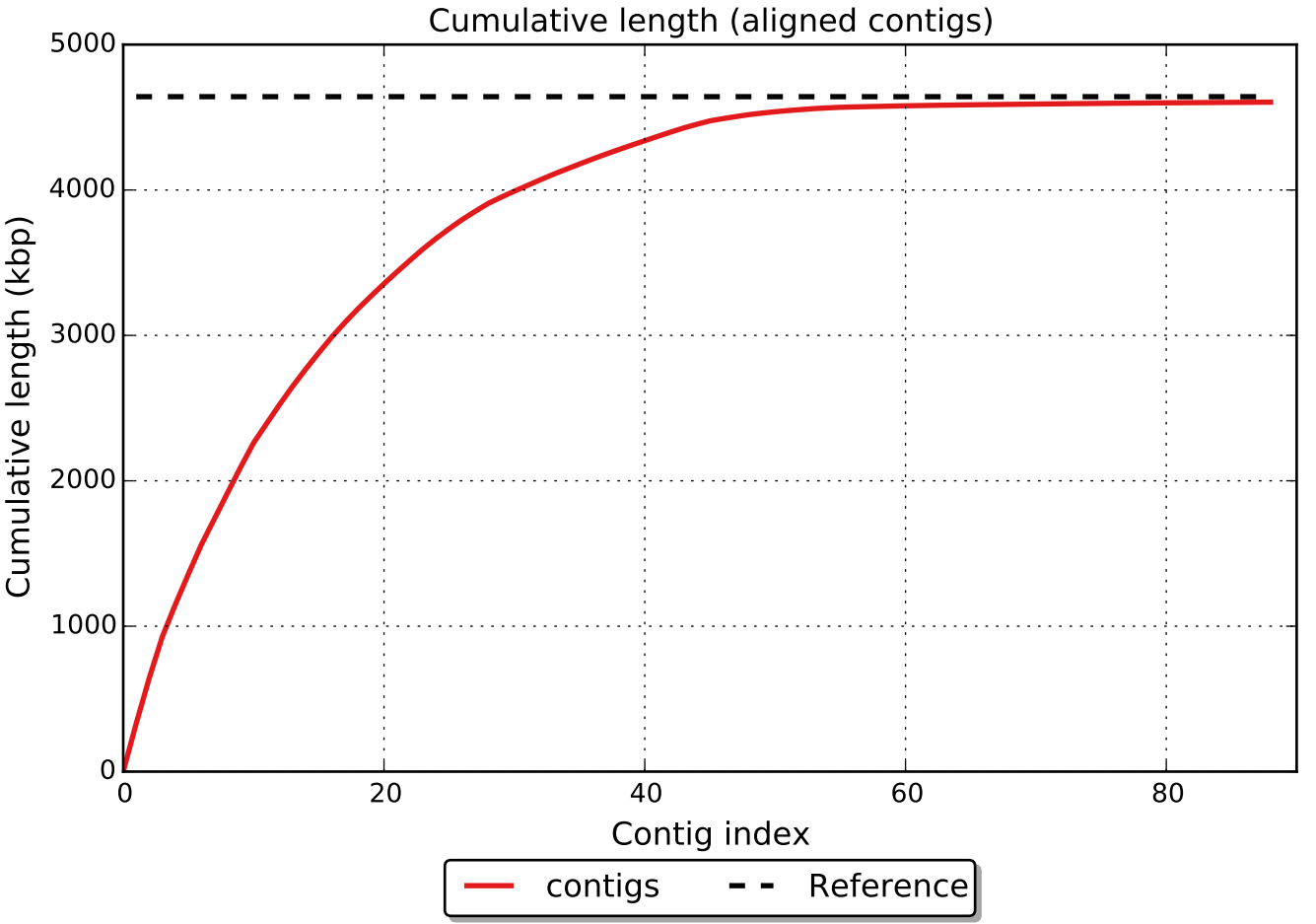

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

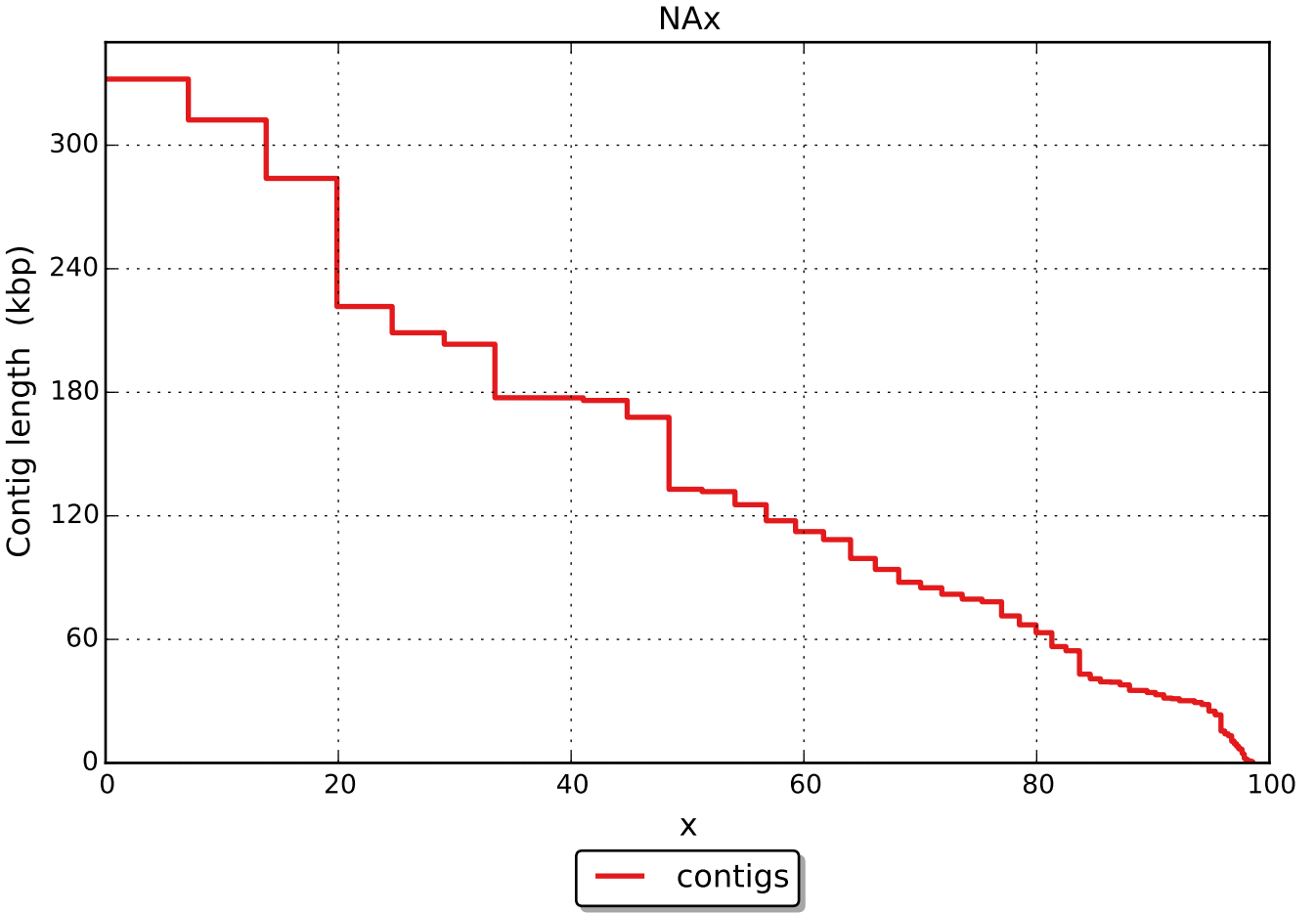

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

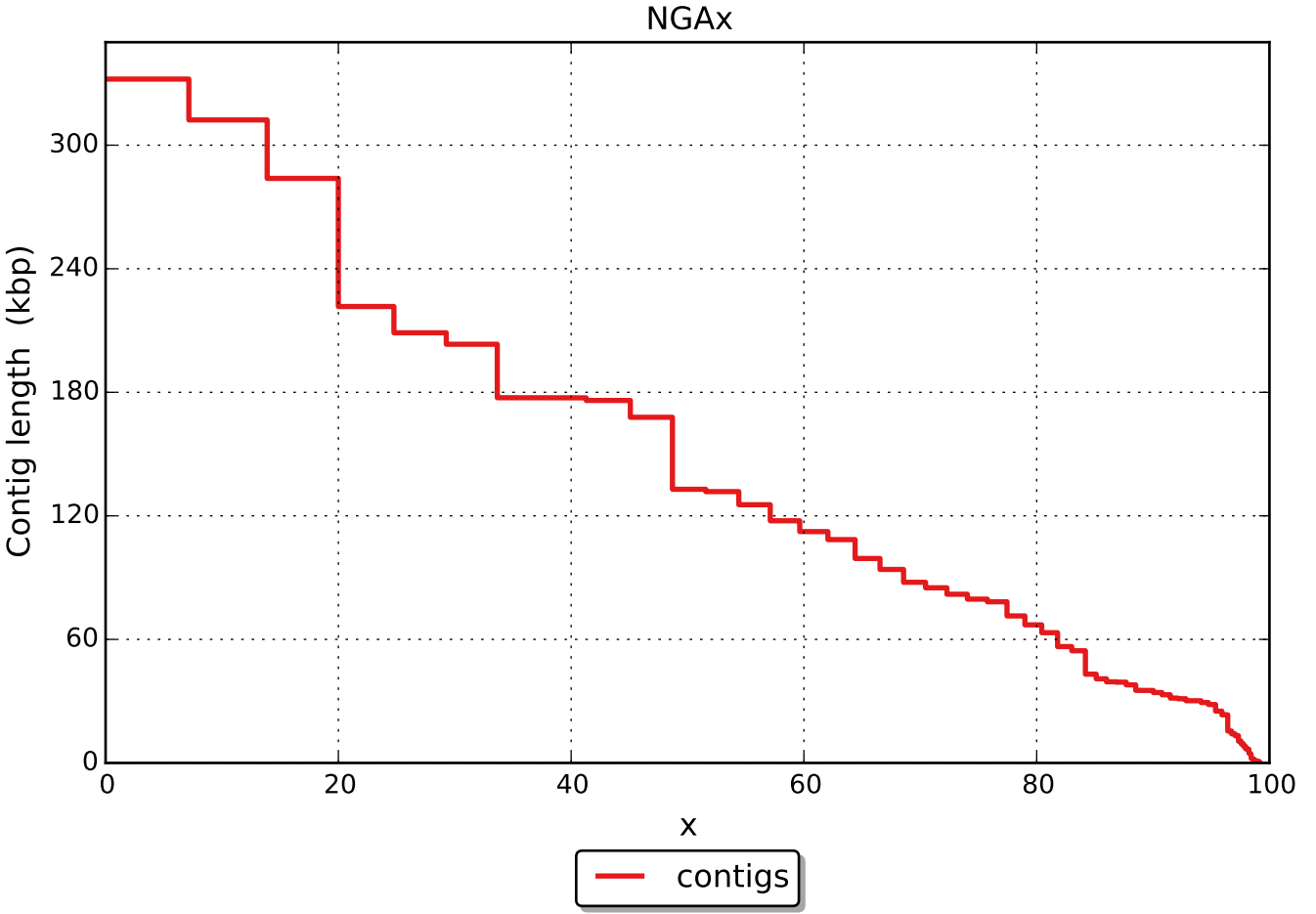

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
20
40
60
80
Contig index
contigs
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
contigs
Reference


Misassemblies
4.0
3.5
3.0
2.5
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