Report

	uniq_contigs_contigs_contigs_contigs
# contigs (>= 0 bp)	29466
# contigs (>= 1000 bp)	5825
# contigs (>= 5000 bp)	1459
# contigs (>= 10000 bp)	1080
# contigs (>= 25000 bp)	690
# contigs (>= 50000 bp)	494
Total length (>= 0 bp)	144471712
Total length (>= 1000 bp)	130854837
Total length (>= 5000 bp)	123372406
Total length (>= 10000 bp)	120745939
Total length (>= 25000 bp)	114612642
Total length (>= 50000 bp)	107592493
# contigs	29466
Largest contig	1624746
Total length	144471712
Reference length	140687039
GC (%)	41.92
Reference GC (%)	41.93
N50	205057
NG50	212648
N75	46592
NG75	59524
L50	186
LG50	177
L75	510
LG75	457
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	0
# unaligned mis. contigs	0
# unaligned contigs	11471 + 0 part
Unaligned length	4973740
Genome fraction (%)	96.377
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.01
# indels per 100 kbp	0.01
Largest alignment	1624746
Total aligned length	139497669
NA50	205057
NGA50	212648
NA75	46592
NGA75	59524
LA50	186
LGA50	177
LA75	510
LGA75	457

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

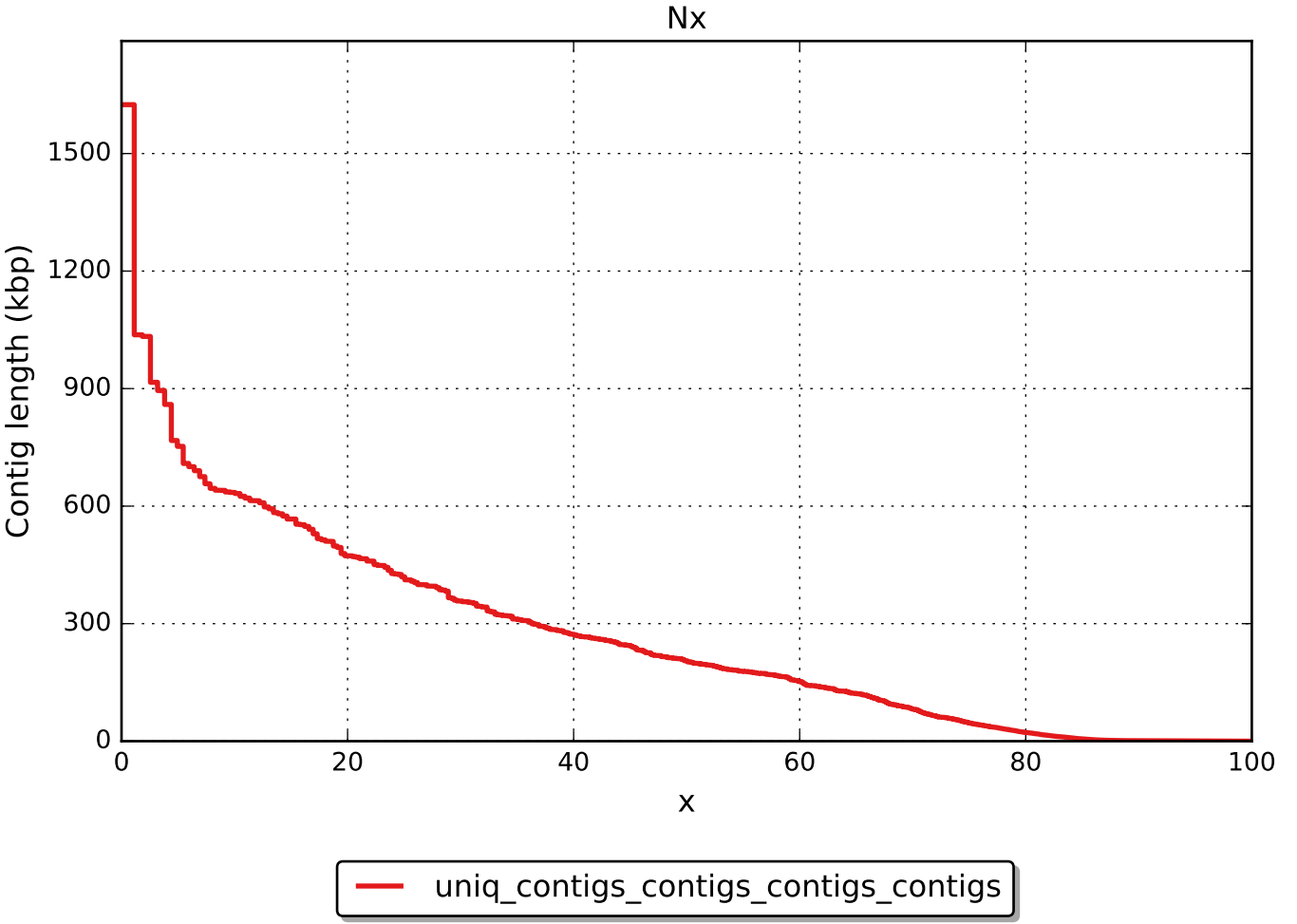
	uniq_contigs_contigs_contigs_contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	0
# unaligned mis. contigs	0
# mismatches	13
# indels	19
# indels (<= 5 bp)	6
# indels (> 5 bp)	13
Indels length	2213

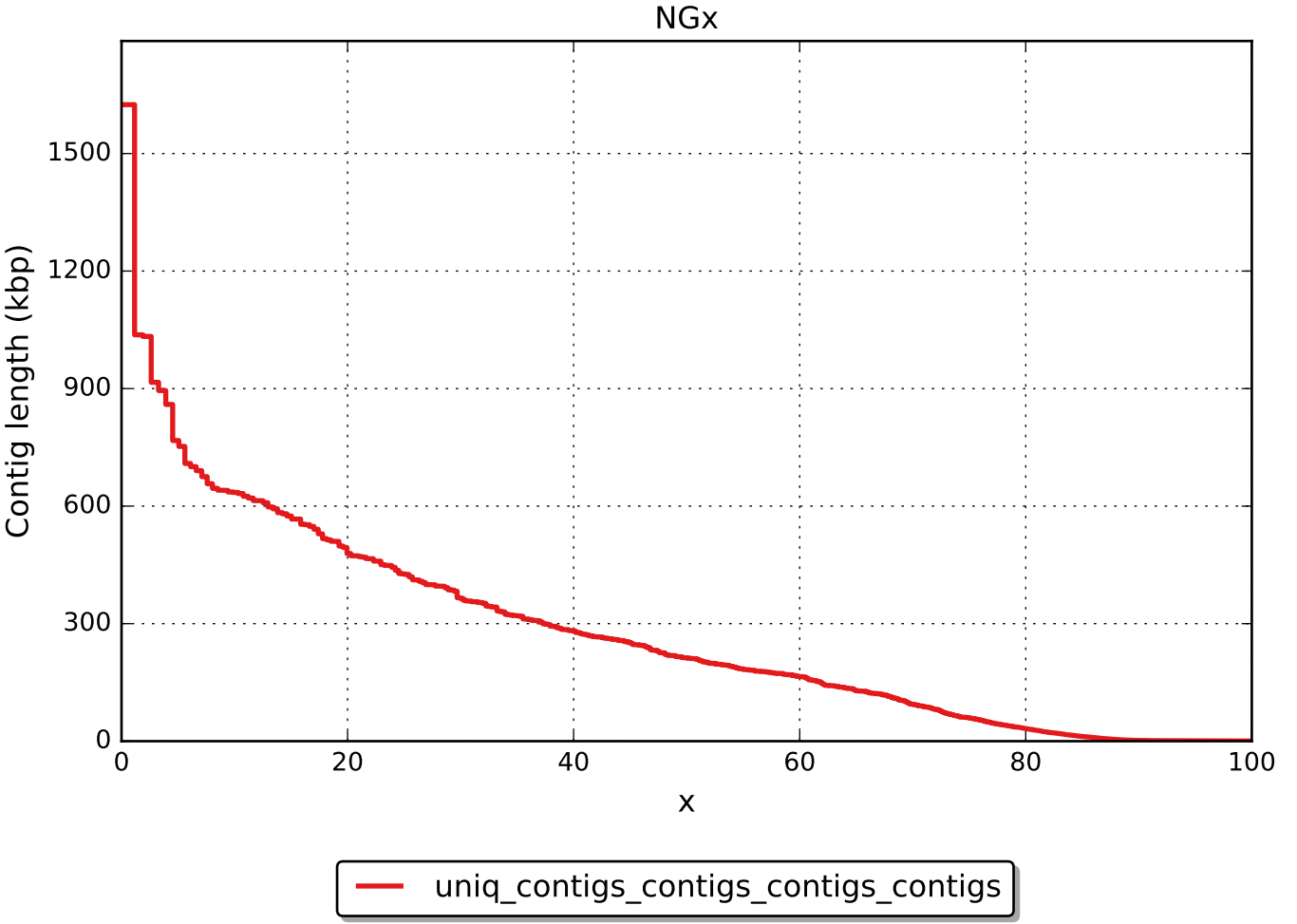
All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

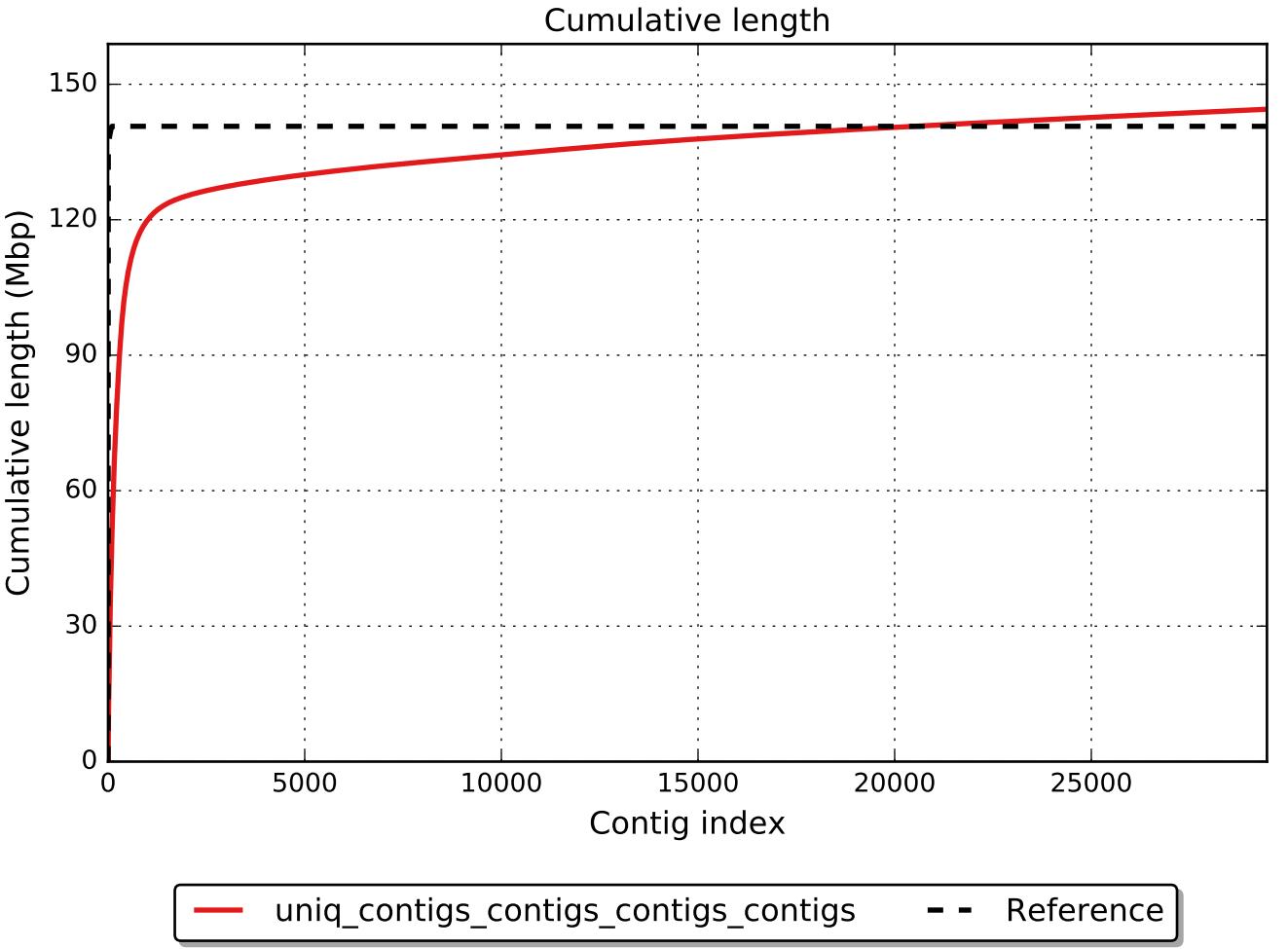
Unaligned report

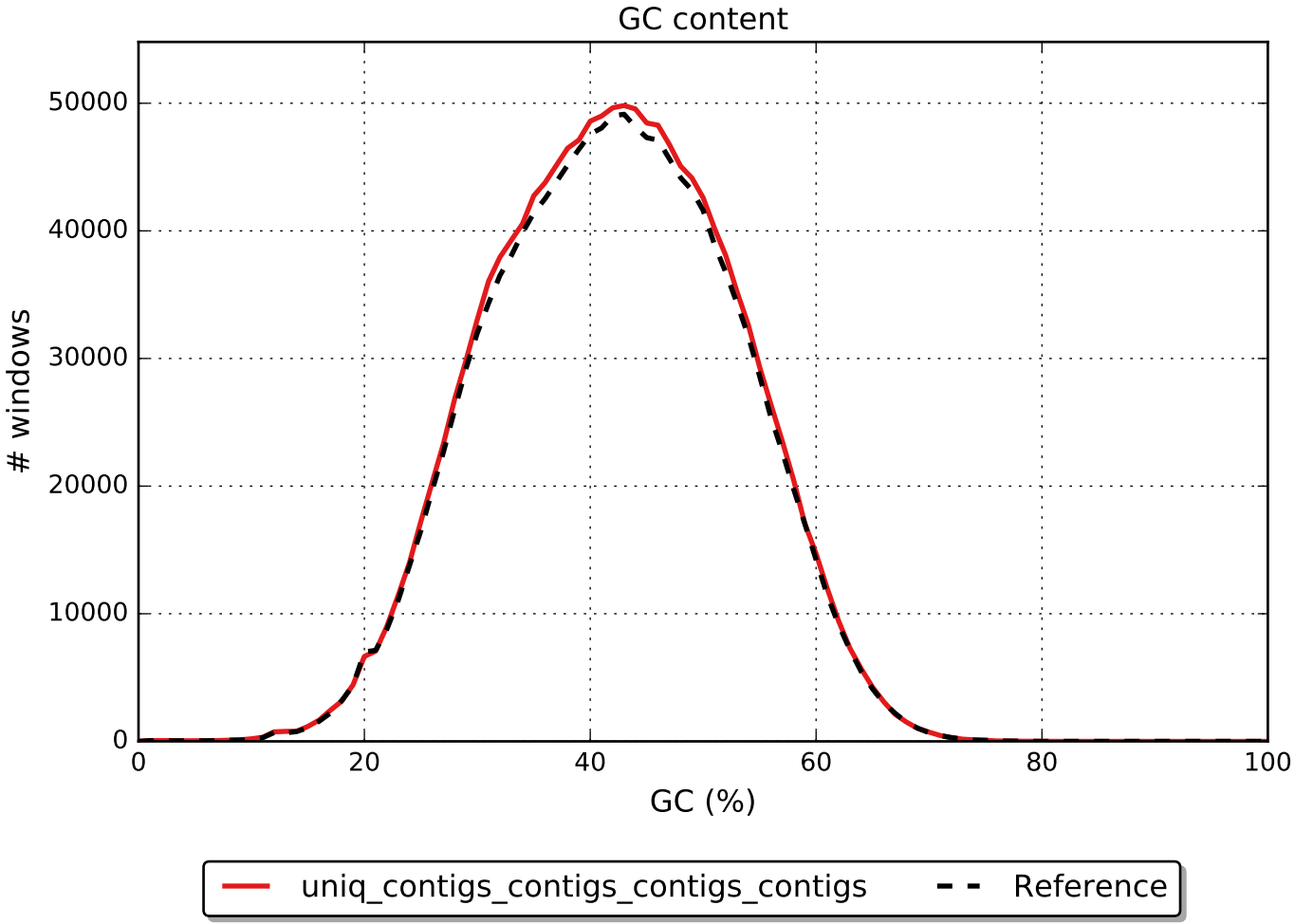
	uniq_contigs_contigs_contigs_contigs
# fully unaligned contigs	11471
Fully unaligned length	4973740
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

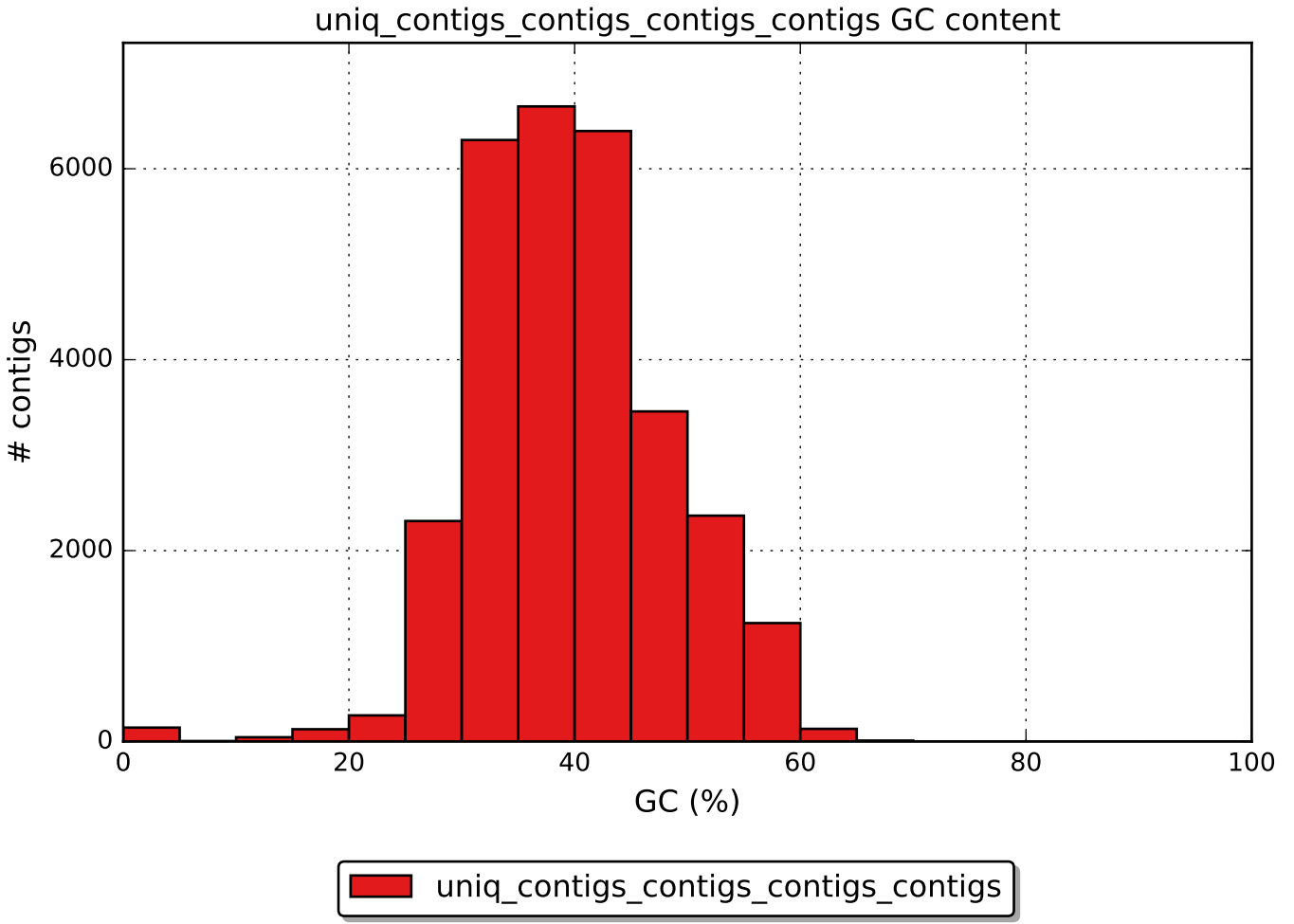
All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

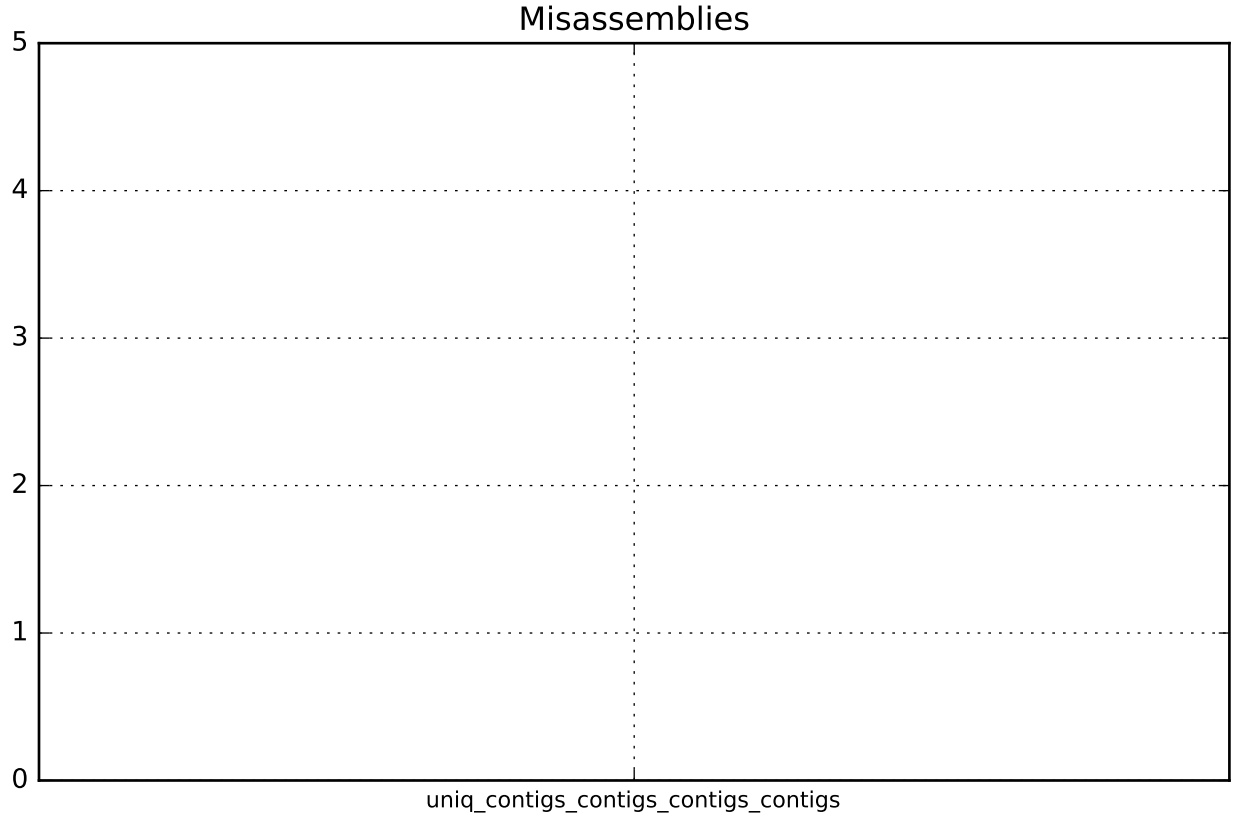

Nx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
uniq_contigs_contigs_contigs_contigs

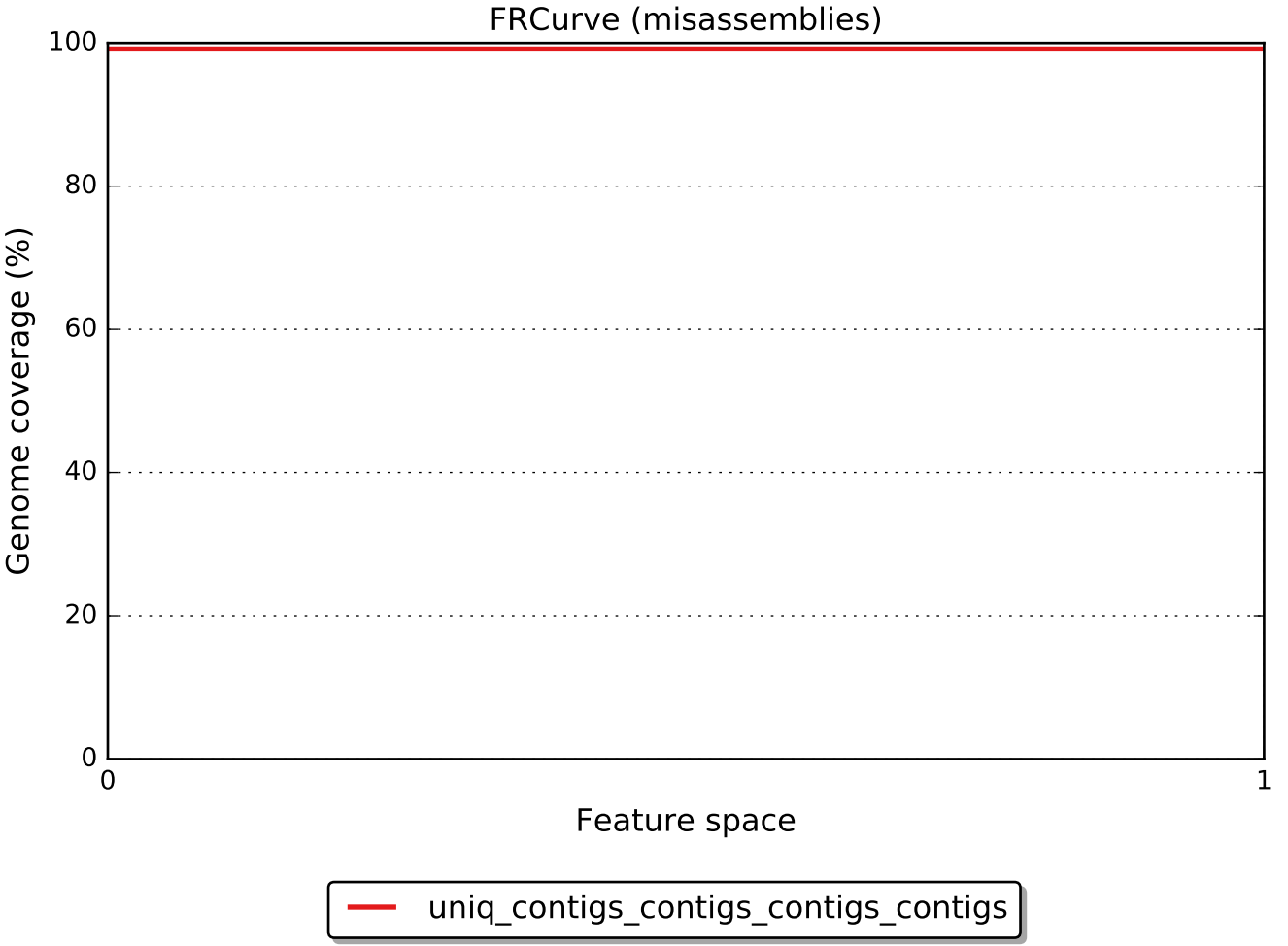

NGx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
uniq_contigs_contigs_contigs_contigs

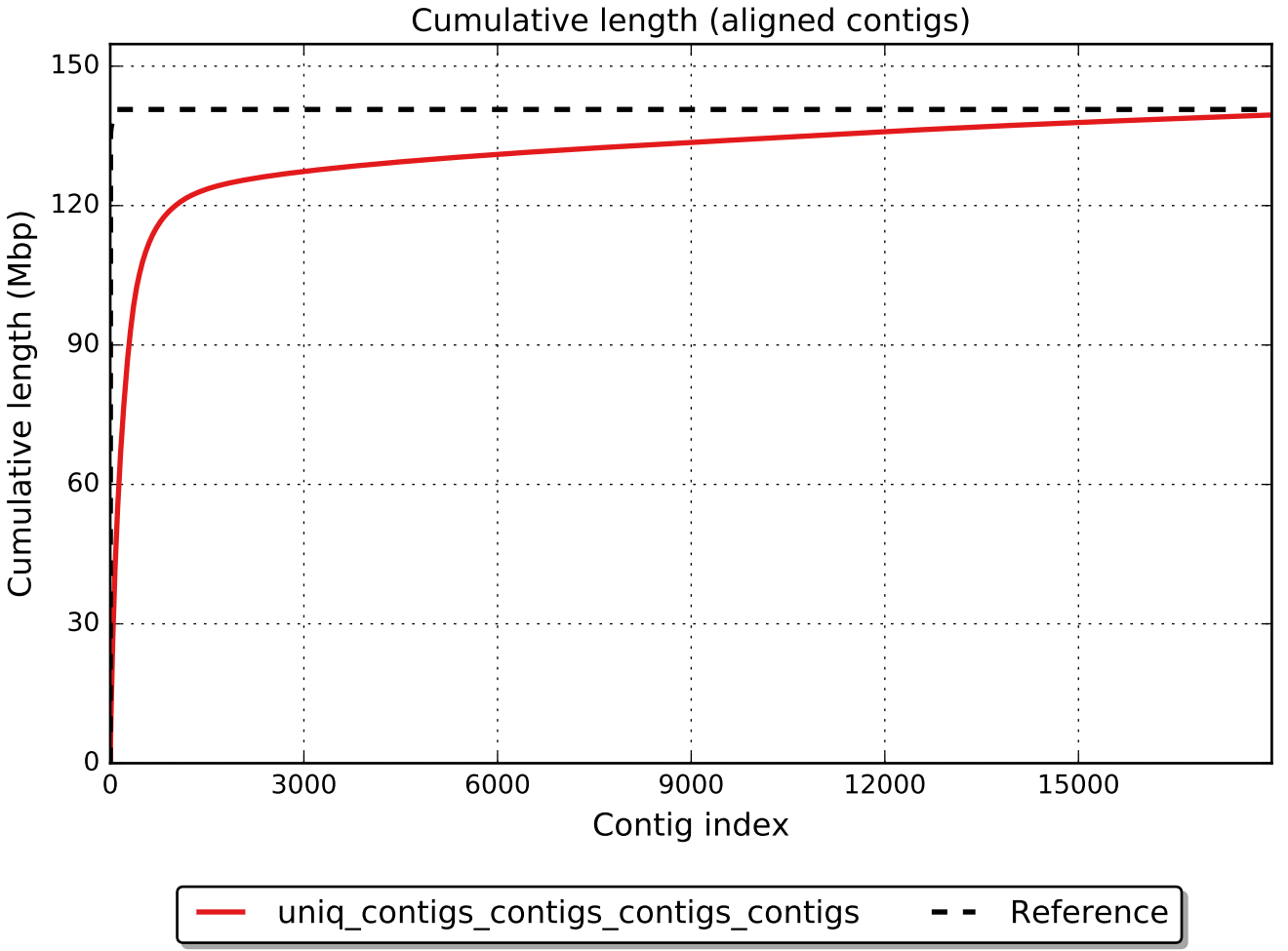

Cumulative length
Cumulative length (Mbp)
150
120
90
60
30
0
0
5000
10000
15000
20000
25000
Contig index
uniq_contigs_contigs_contigs_contigs
Reference

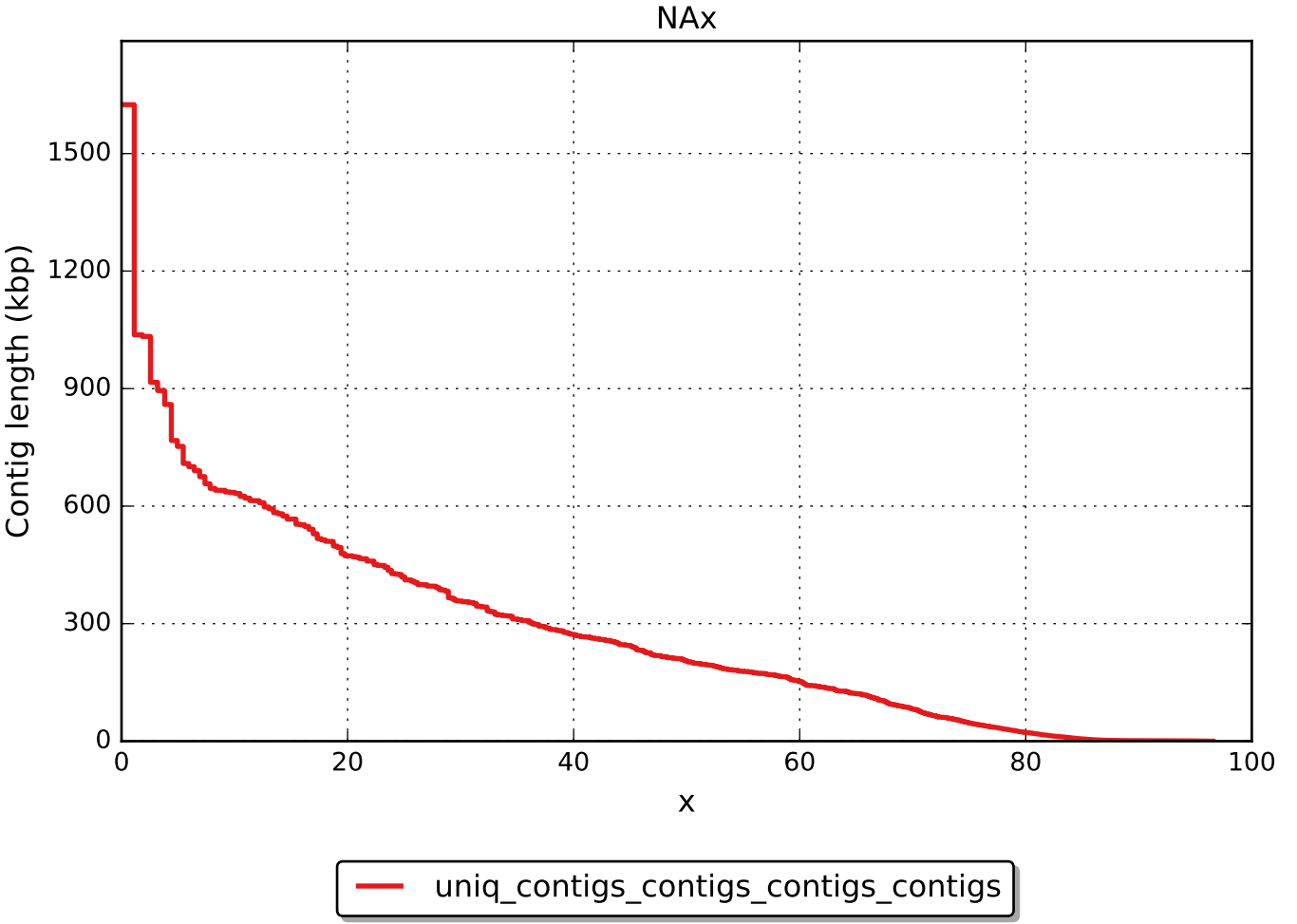

GC content
windows
GC (%)
0
10000
20000
30000
40000
50000
0
20
40
60
80
100
uniq_contigs_contigs_contigs_contigs
Reference

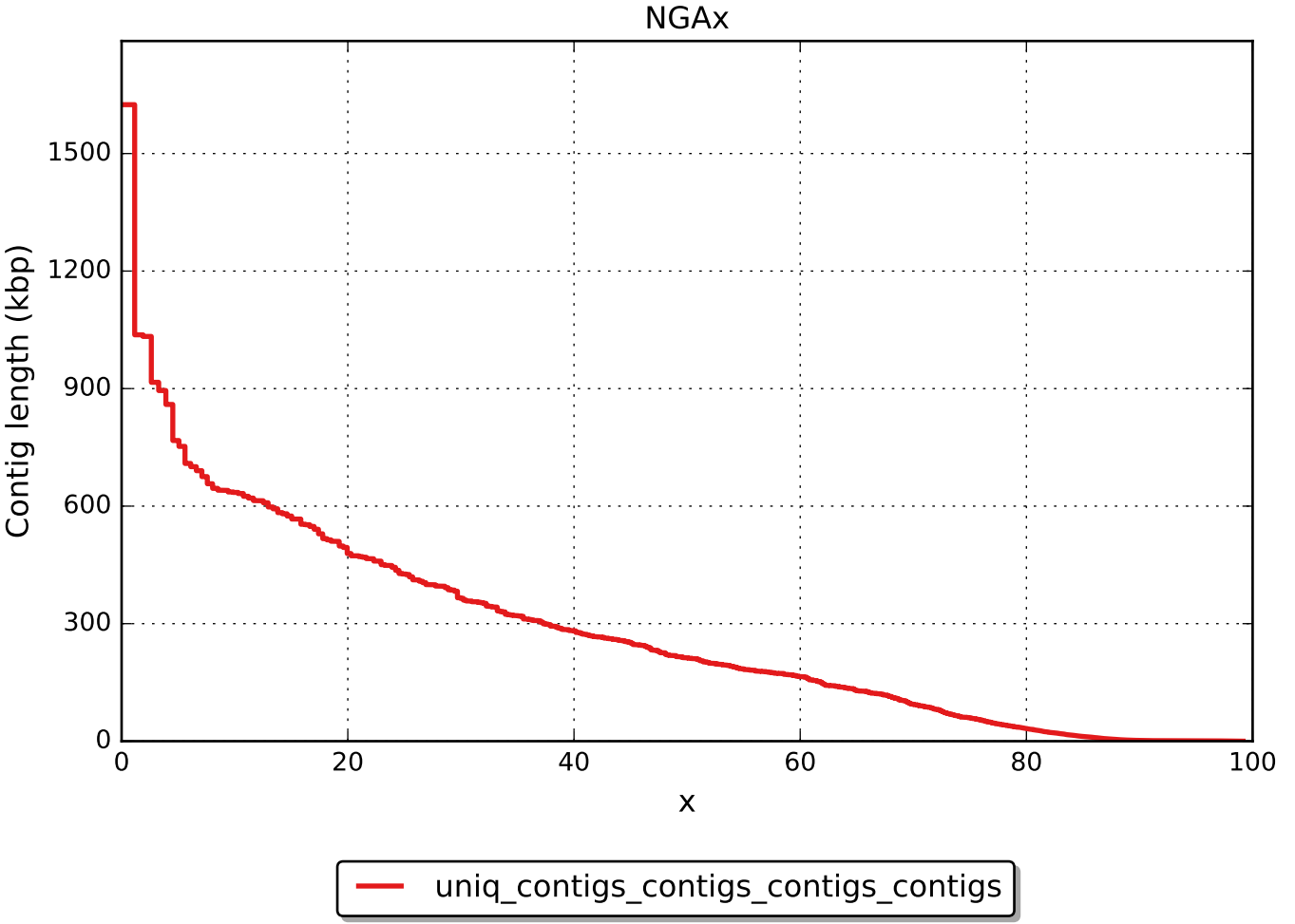

uniq_contigs_contigs_contigs_contigs GC content
contigs
0
2000
4000
6000
0
20
40
60
80
100
GC (%)
uniq_contigs_contigs_contigs_contigs


Misassemblies
5
4
3
2
1
0
uniq_contigs_contigs_contigs_contigs


FRCurve (misassemblies)
100
80
60
40
20
0
Genome coverage (%)
0
1
Feature space
uniq_contigs_contigs_contigs_contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
150
120
90
60
30
0
0
3000
6000
9000
12000
15000
Contig index
uniq_contigs_contigs_contigs_contigs
Reference


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
uniq_contigs_contigs_contigs_contigs


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
uniq_contigs_contigs_contigs_contigs