Report

	uniq-contigs-contigs-contigs-contigs-contigs
# contigs (>= 0 bp)	74
# contigs (>= 1000 bp)	26
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	574064
Total length (>= 1000 bp)	538909
Total length (>= 5000 bp)	529919
Total length (>= 10000 bp)	508846
Total length (>= 25000 bp)	390096
Total length (>= 50000 bp)	52011
# contigs	74
Largest contig	52011
Total length	574064
Reference length	599940
GC (%)	51.02
Reference GC (%)	51.01
N50	35246
NG50	35246
N75	22525
NG75	12991
L50	7
LG50	7
L75	12
LG75	14
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.901
Duplication ratio	1.064
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.19
Largest alignment	52011
Total aligned length	574064
NA50	35246
NGA50	35246
NA75	22525
NGA75	12991
LA50	7
LGA50	7
LA75	12
LGA75	14

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

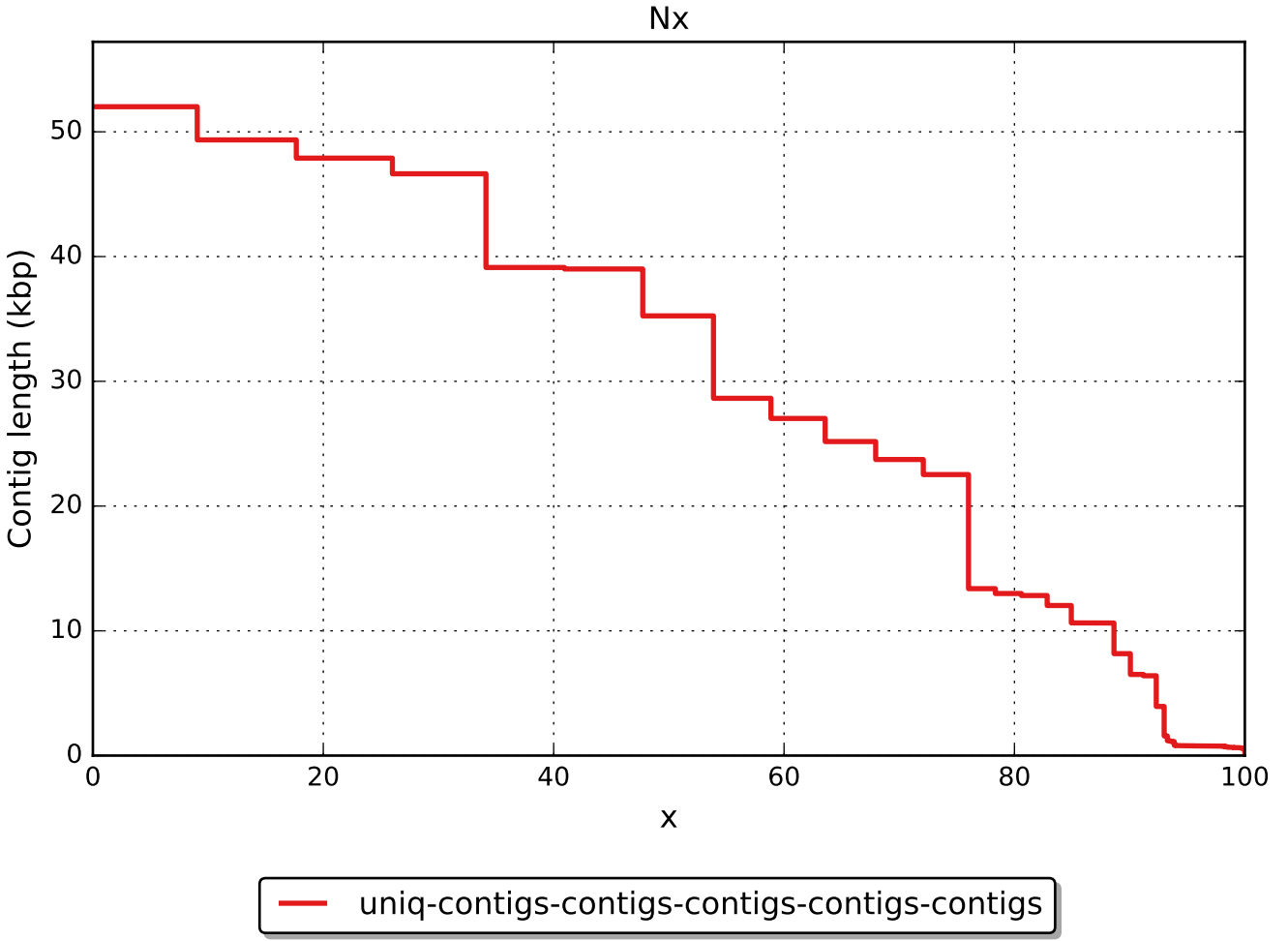
	uniq-contigs-contigs-contigs-contigs-contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

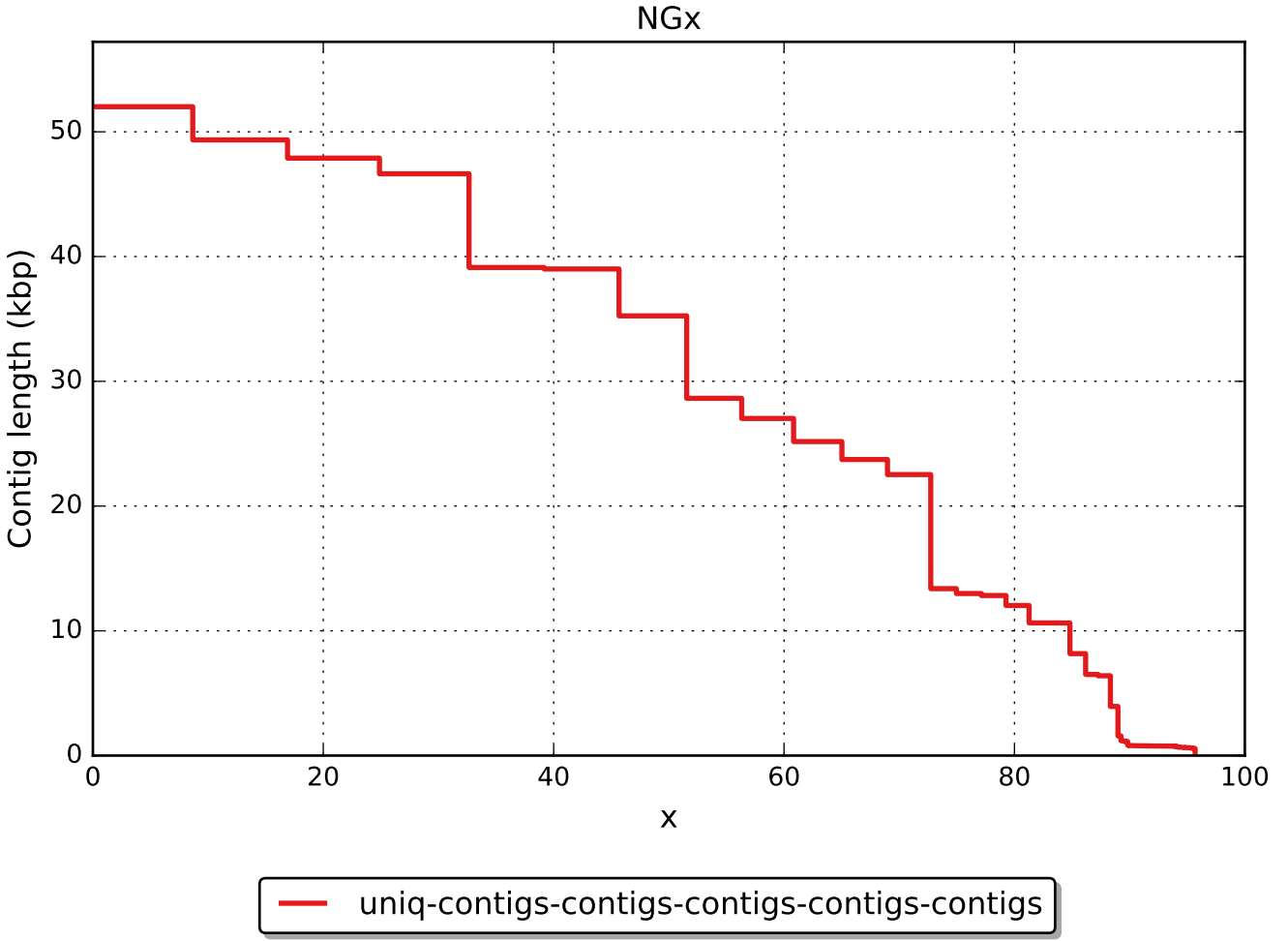
All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

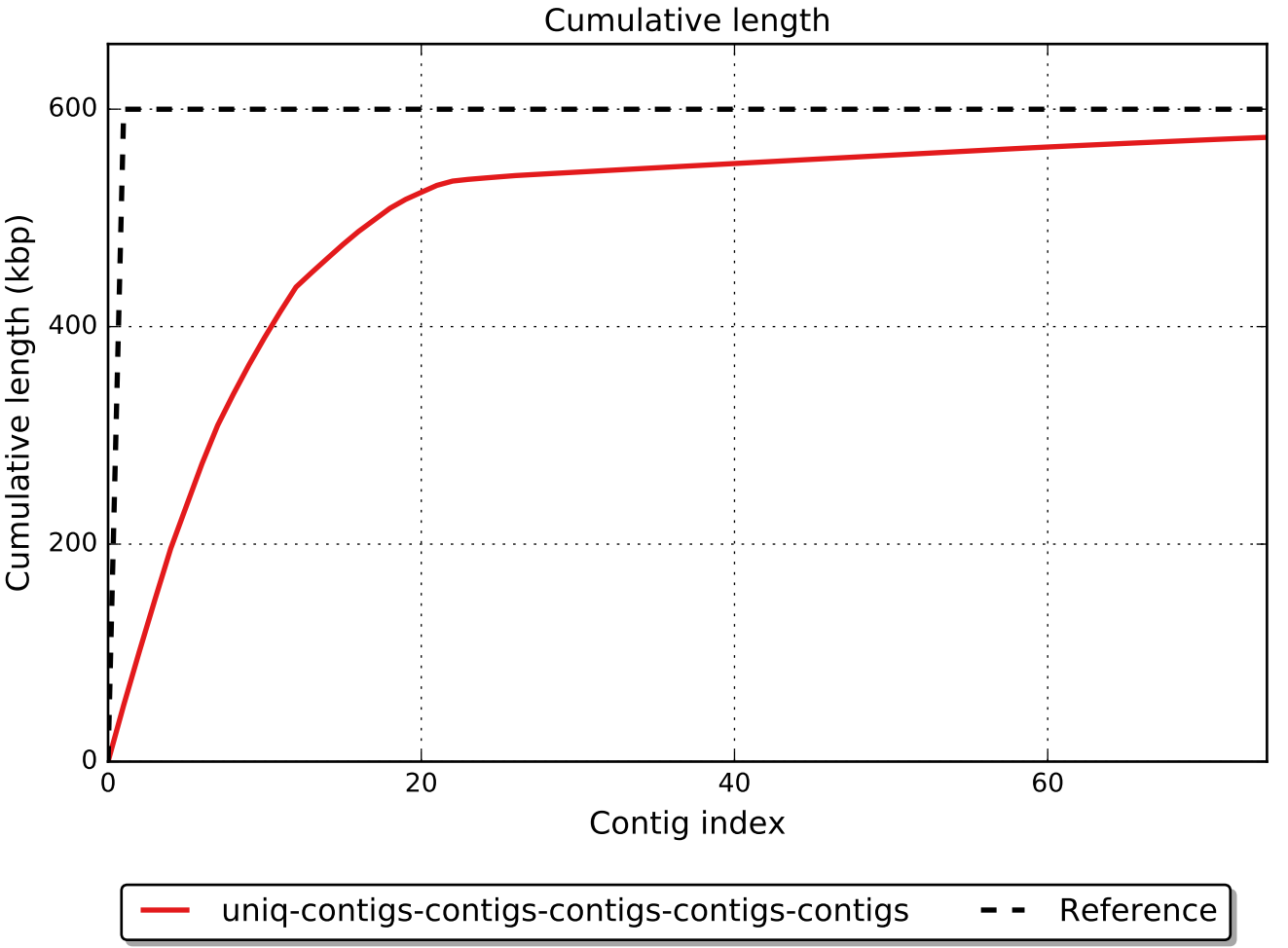
Unaligned report

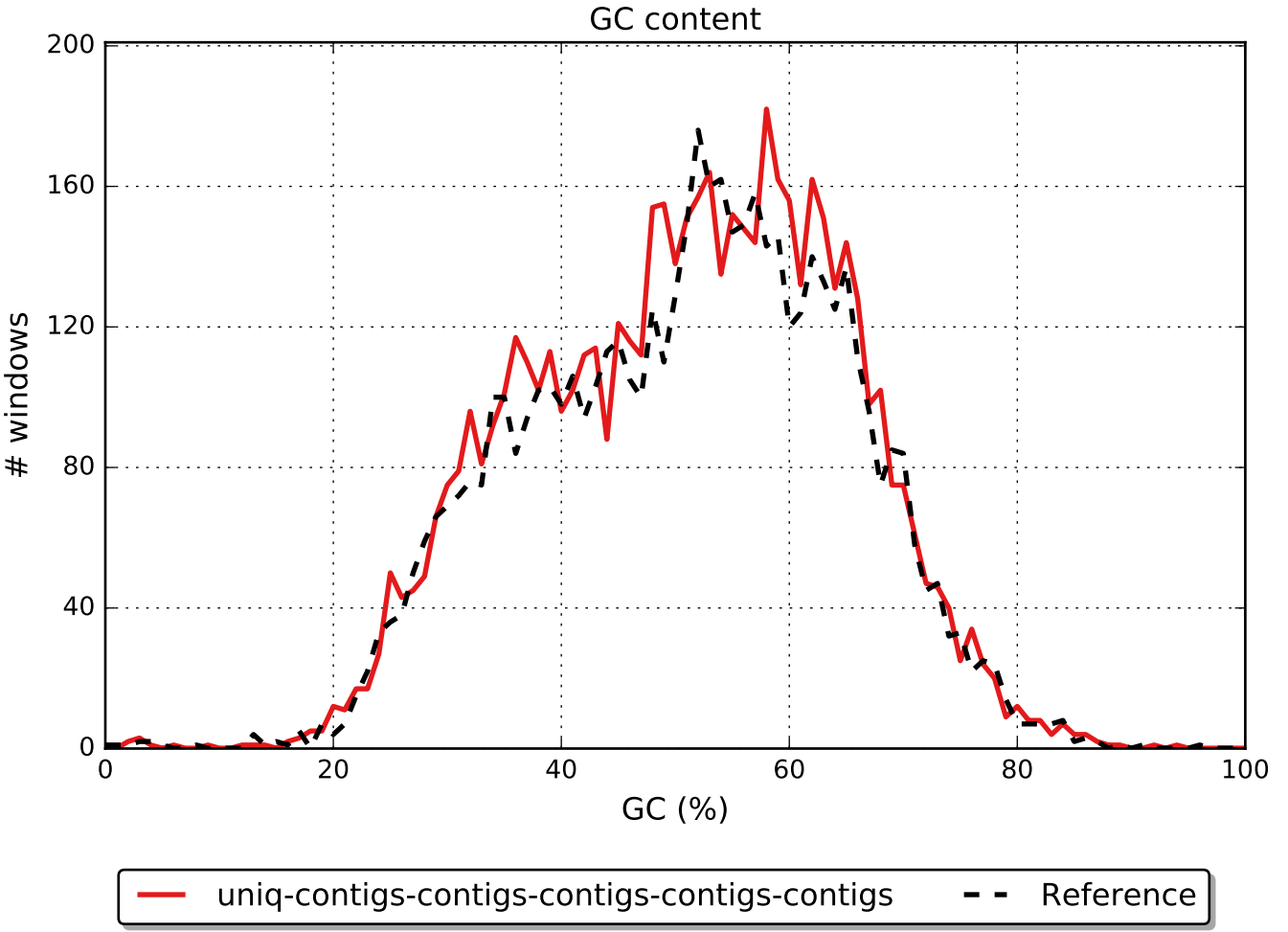
	uniq-contigs-contigs-contigs-contigs-contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

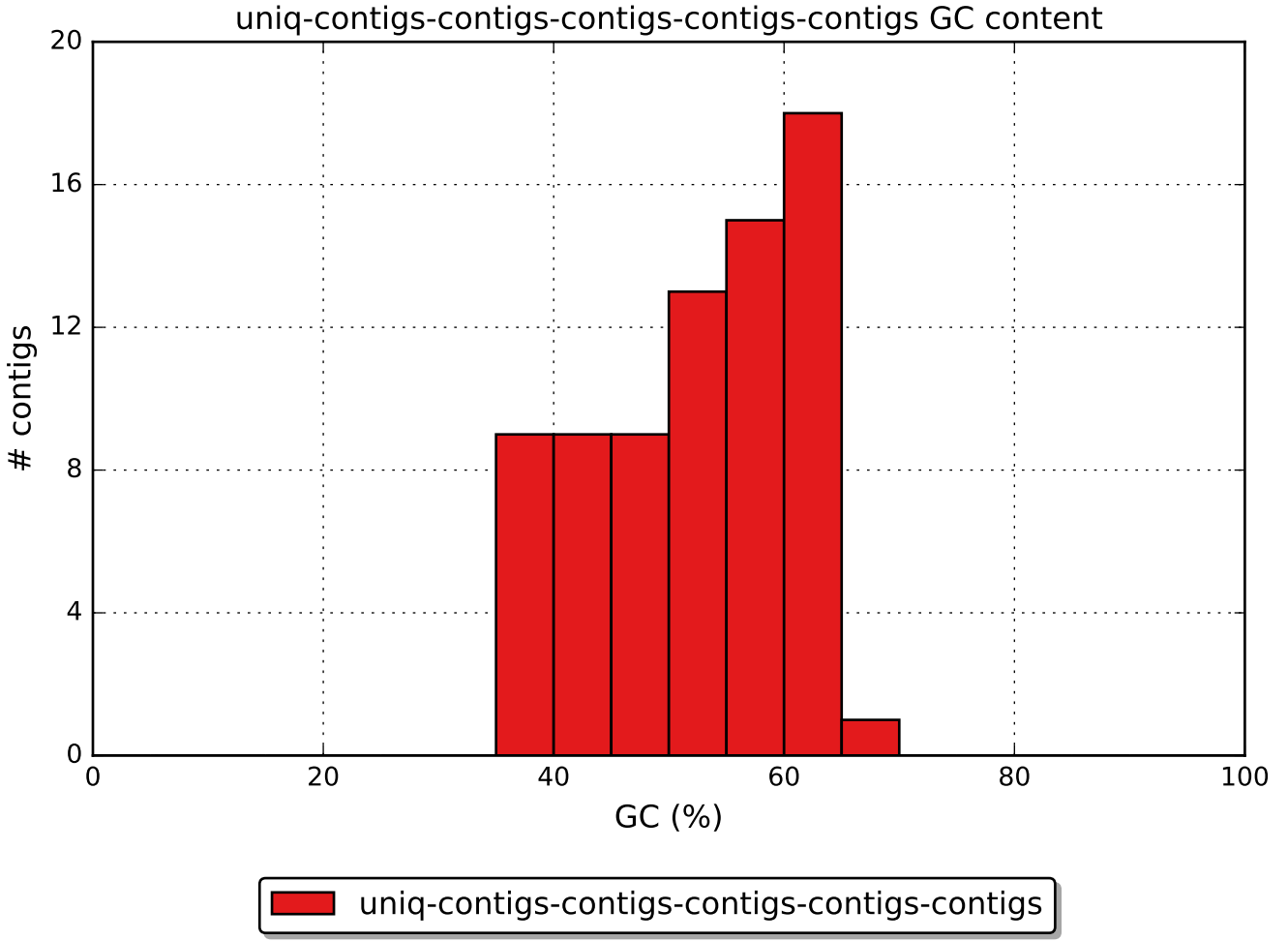
All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

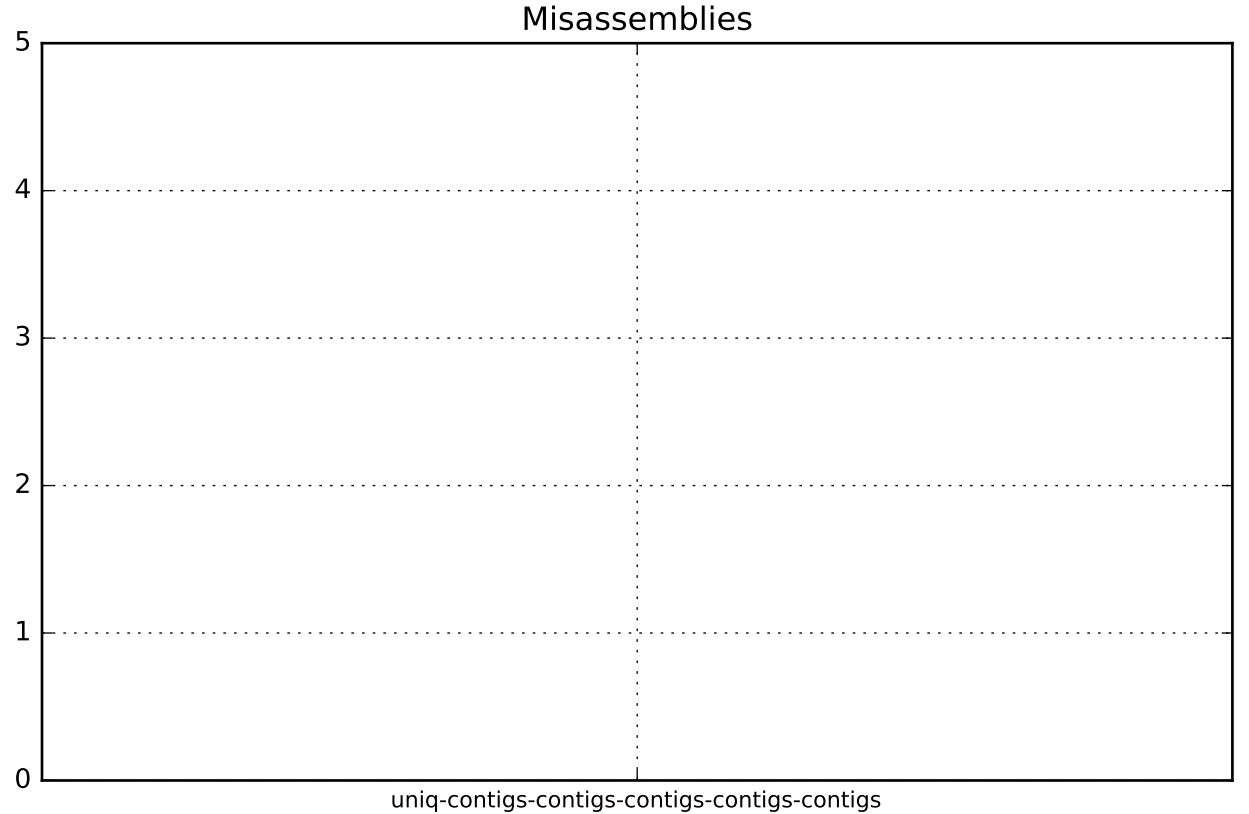

Nx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
uniq-contigs-contigs-contigs-contigs-contigs

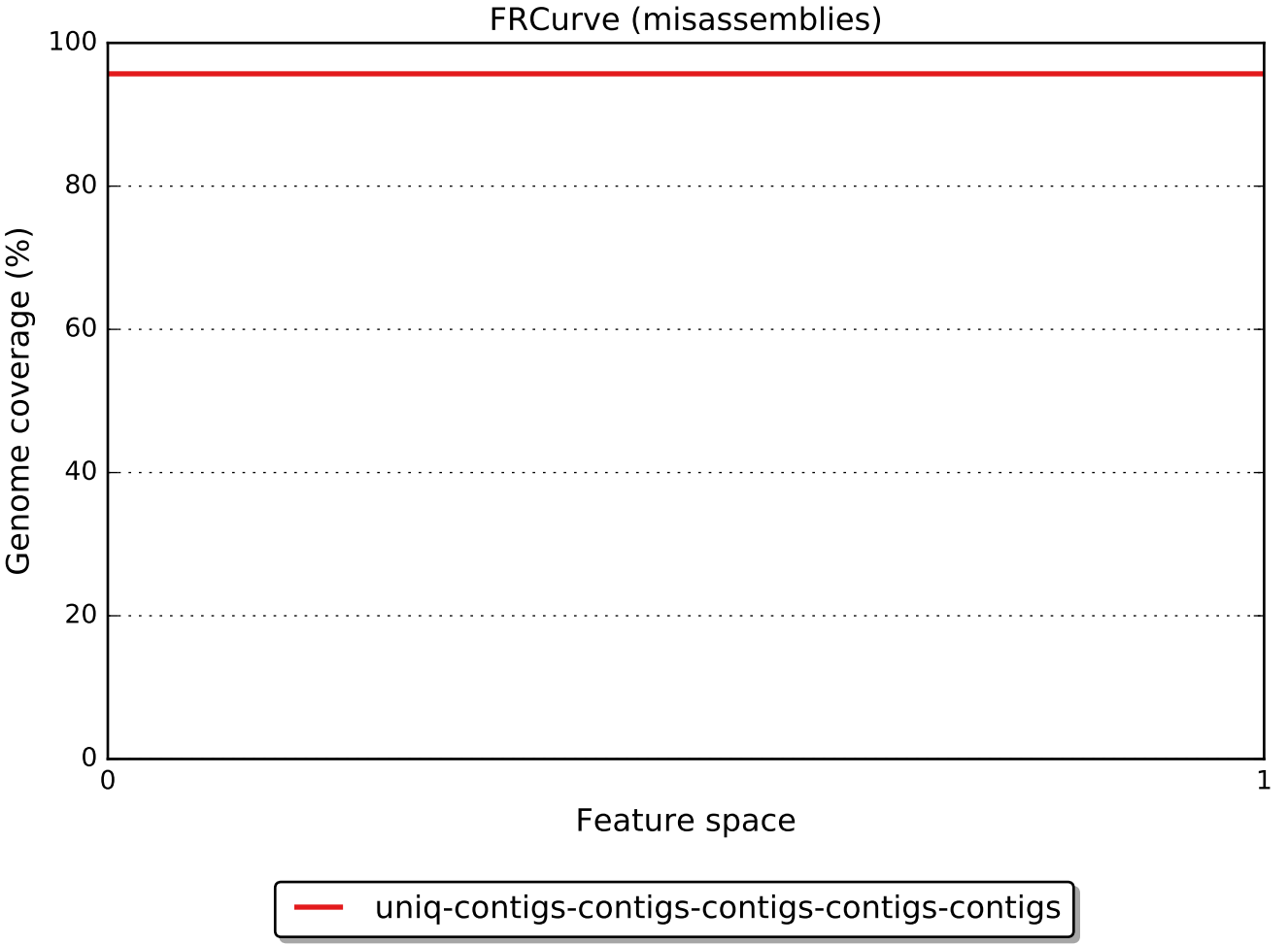

NGx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
uniq-contigs-contigs-contigs-contigs-contigs

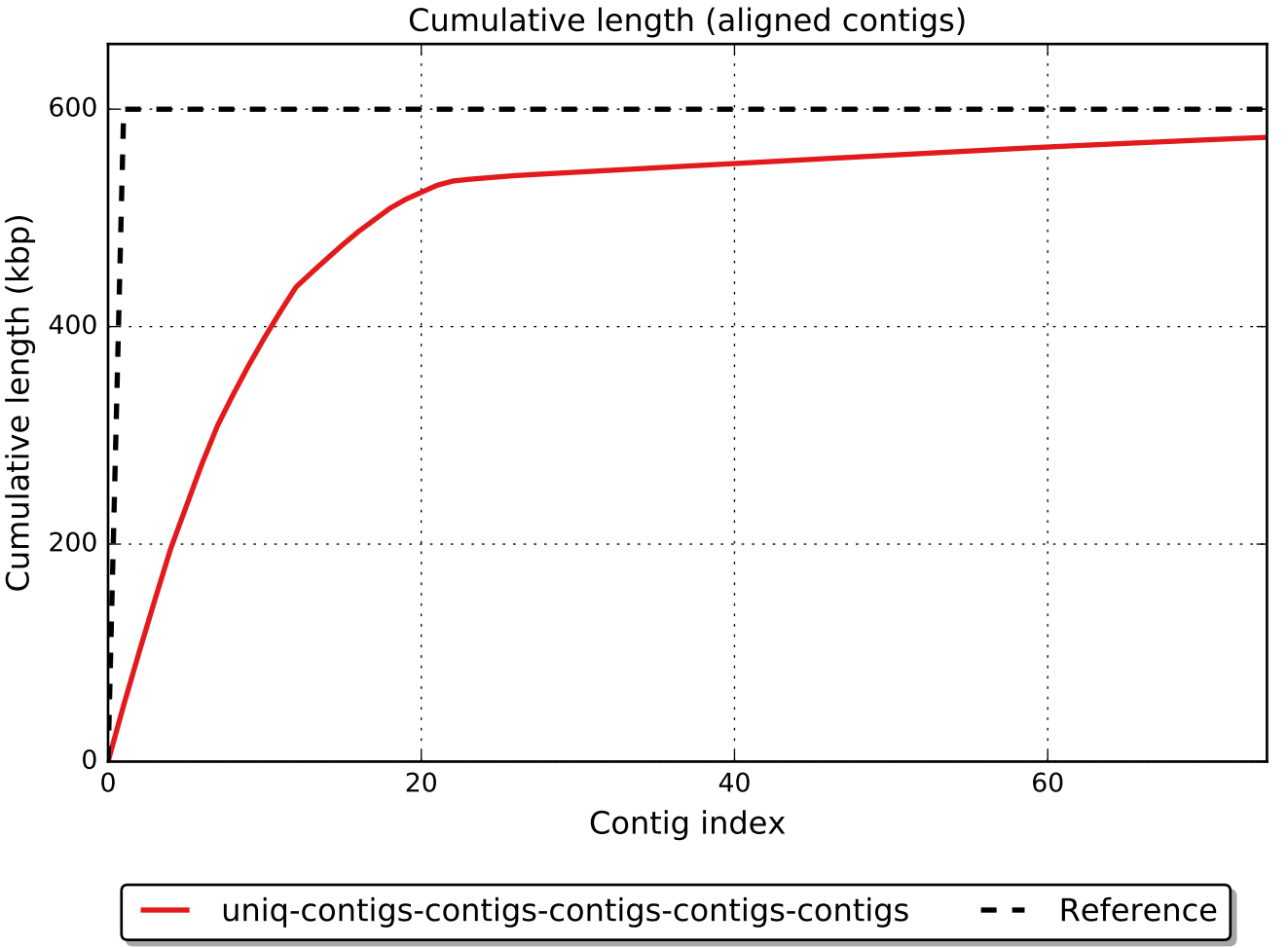

Cumulative length
Cumulative length (kbp)
600
400
200
0
0
20
40
60
Contig index
uniq-contigs-contigs-contigs-contigs-contigs
Reference

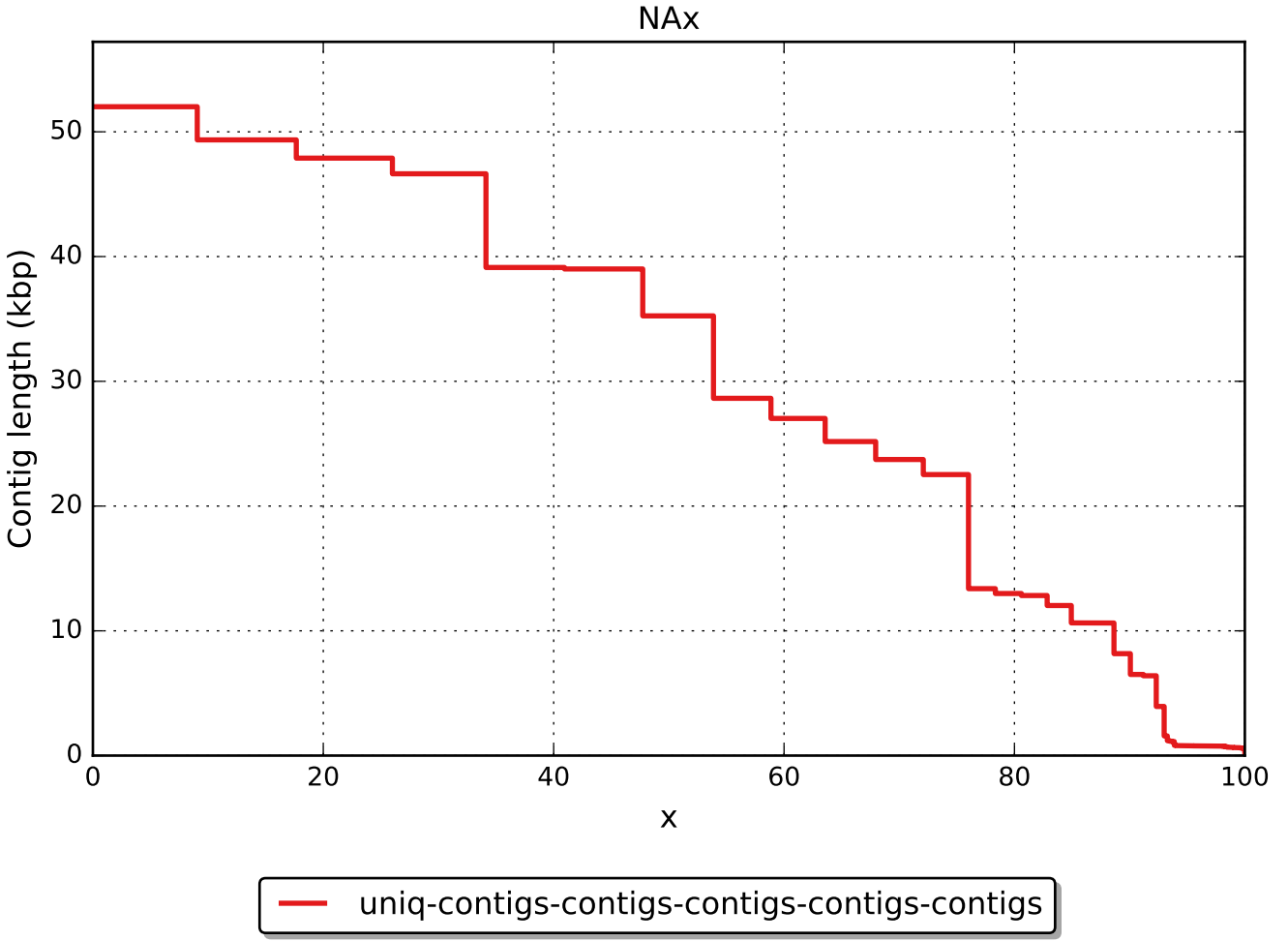

GC content
windows
GC (%)
0
40
80
120
160
200
0
20
40
60
80
100
uniq-contigs-contigs-contigs-contigs-contigs
Reference

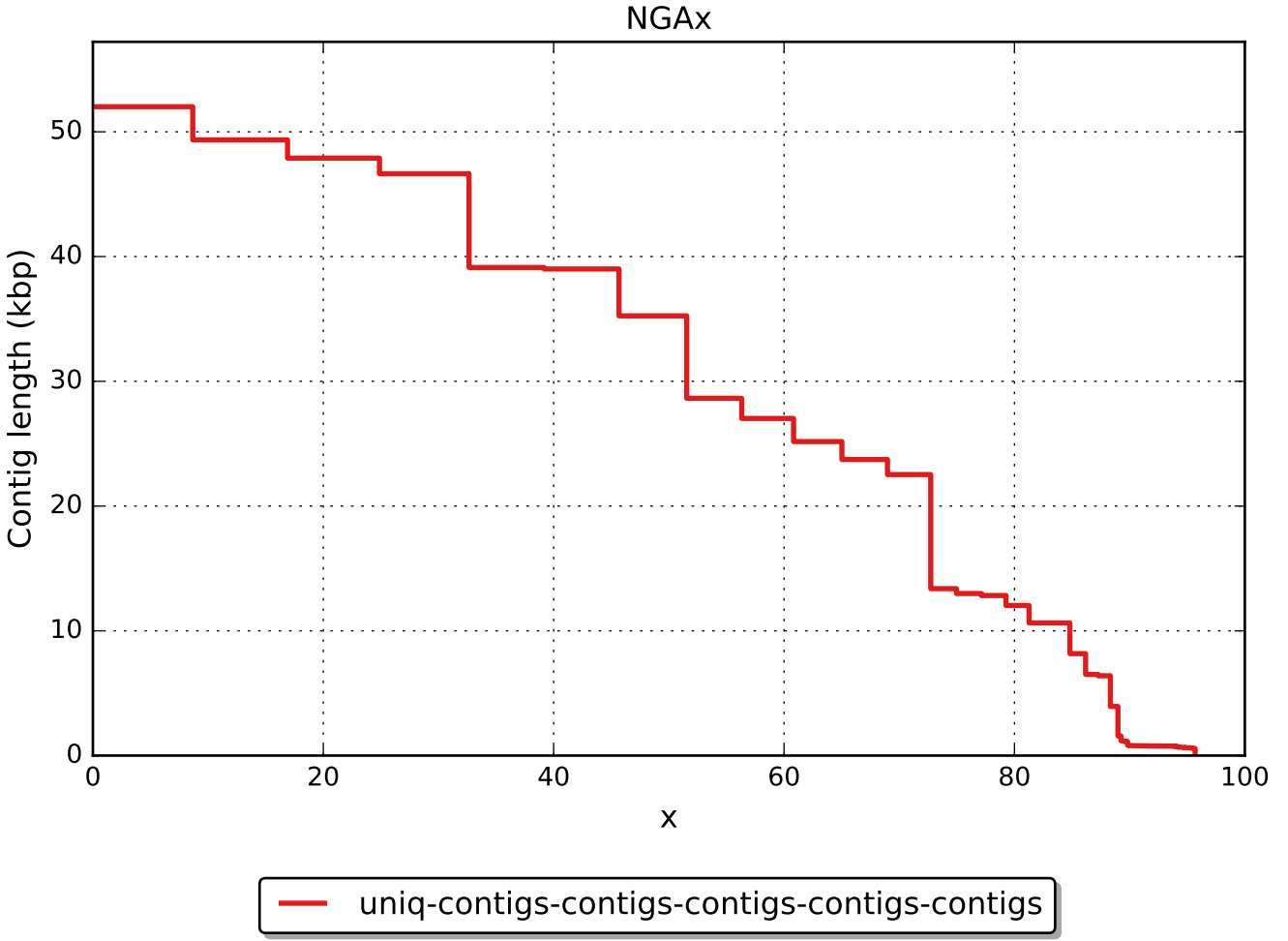

uniq-contigs-contigs-contigs-contigs-contigs GC content
contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
uniq-contigs-contigs-contigs-contigs-contigs


Misassemblies
5
4
3
2
1
0
uniq-contigs-contigs-contigs-contigs-contigs


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
600
400
200
0
0
20
40
60
Contig index
uniq-contigs-contigs-contigs-contigs-contigs
Reference


NAx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
uniq-contigs-contigs-contigs-contigs-contigs


NGAx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
uniq-contigs-contigs-contigs-contigs-contigs