Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 1000 bp)	3	2
# contigs (>= 5000 bp)	1	1
# contigs (>= 10000 bp)	1	1
# contigs (>= 25000 bp)	1	1
# contigs (>= 50000 bp)	1	1
Total length (>= 1000 bp)	57399	57668
Total length (>= 5000 bp)	55106	54221
Total length (>= 10000 bp)	55106	54221
Total length (>= 25000 bp)	55106	54221
Total length (>= 50000 bp)	55106	54221
# contigs	5	3
Largest contig	55106	54221
Total length	59178	58431
Reference length	59999	59999
GC (%)	50.17	50.11
Reference GC (%)	50.25	50.25
N50	55106	54221
NG50	55106	54221
N75	55106	54221
NG75	55106	54221
L50	1	1
LG50	1	1
L75	1	1
LG75	1	1
# misassemblies	0	1
# misassembled contigs	0	1
Misassembled contigs length	0	54221
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	1
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	97.575	96.422
Duplication ratio	1.011	1.010
# N's per 100 kbp	35.49	0.00
# mismatches per 100 kbp	23.91	34.57
# indels per 100 kbp	0.00	0.00
Largest alignment	55106	36102
Total aligned length	58664	58042
NA50	55106	36102
NGA50	55106	36102
NA75	55106	18119
NGA75	55106	18119
LA50	1	1
LGA50	1	1
LA75	1	2
LGA75	1	2

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

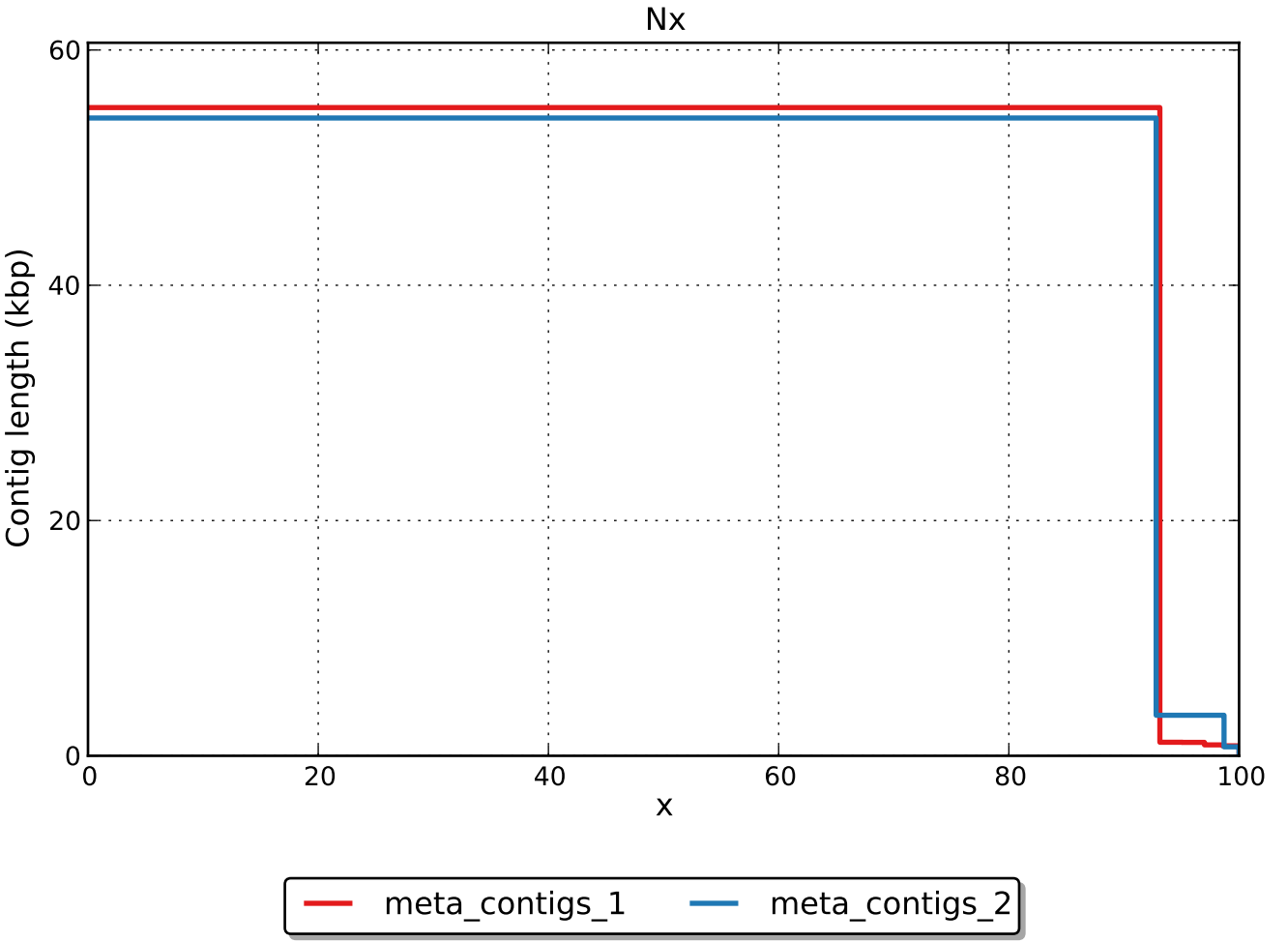
	meta_contigs_1	meta_contigs_2
# misassemblies	0	1
# contig misassemblies	0	1
# c. relocations	0	1
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	1
Misassembled contigs length	0	54221
# possibly misassembled contigs	0	0
# possible misassemblies	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	1
# mismatches	14	20
# indels	0	0
# indels (<= 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	0	0

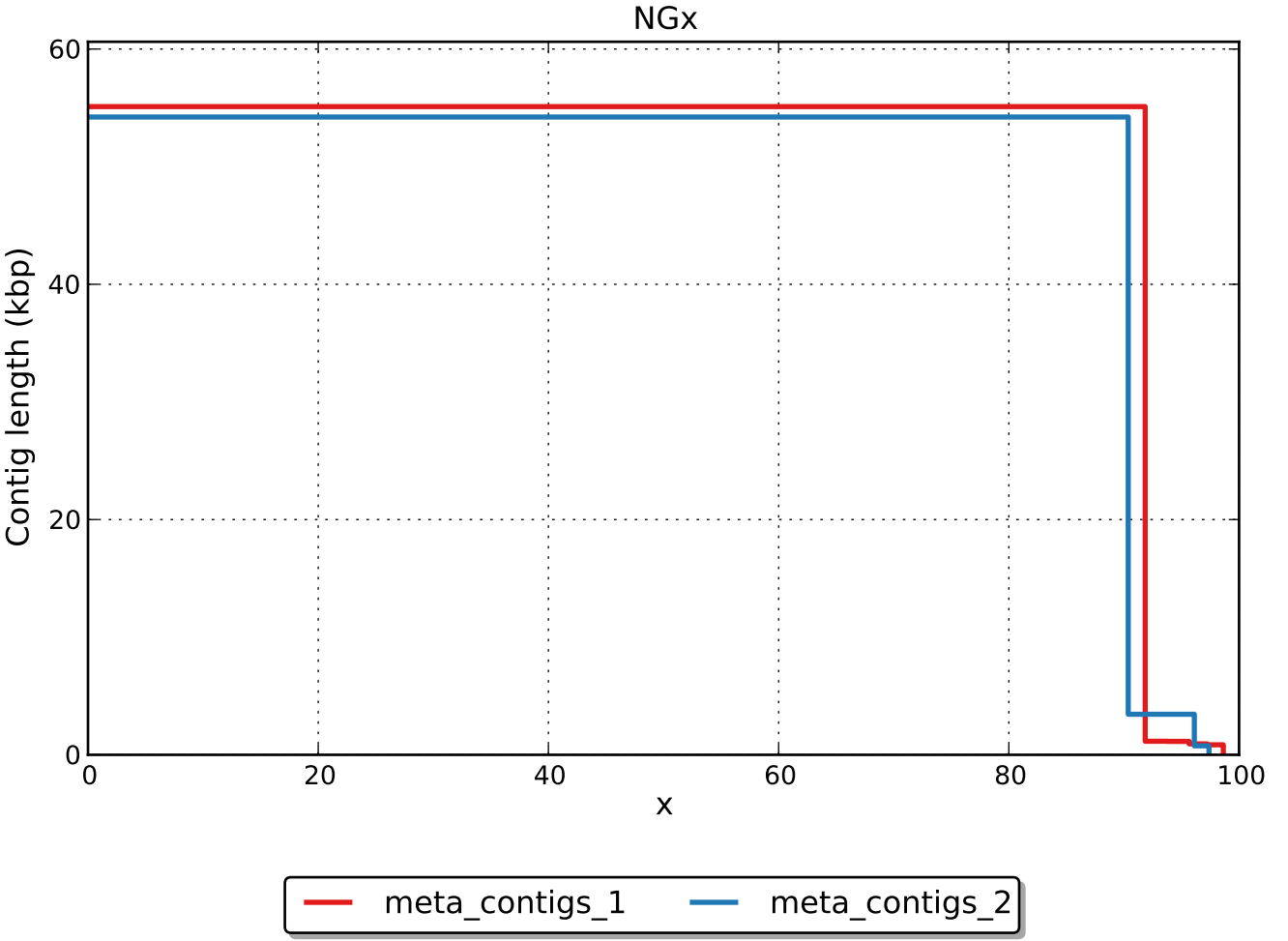
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

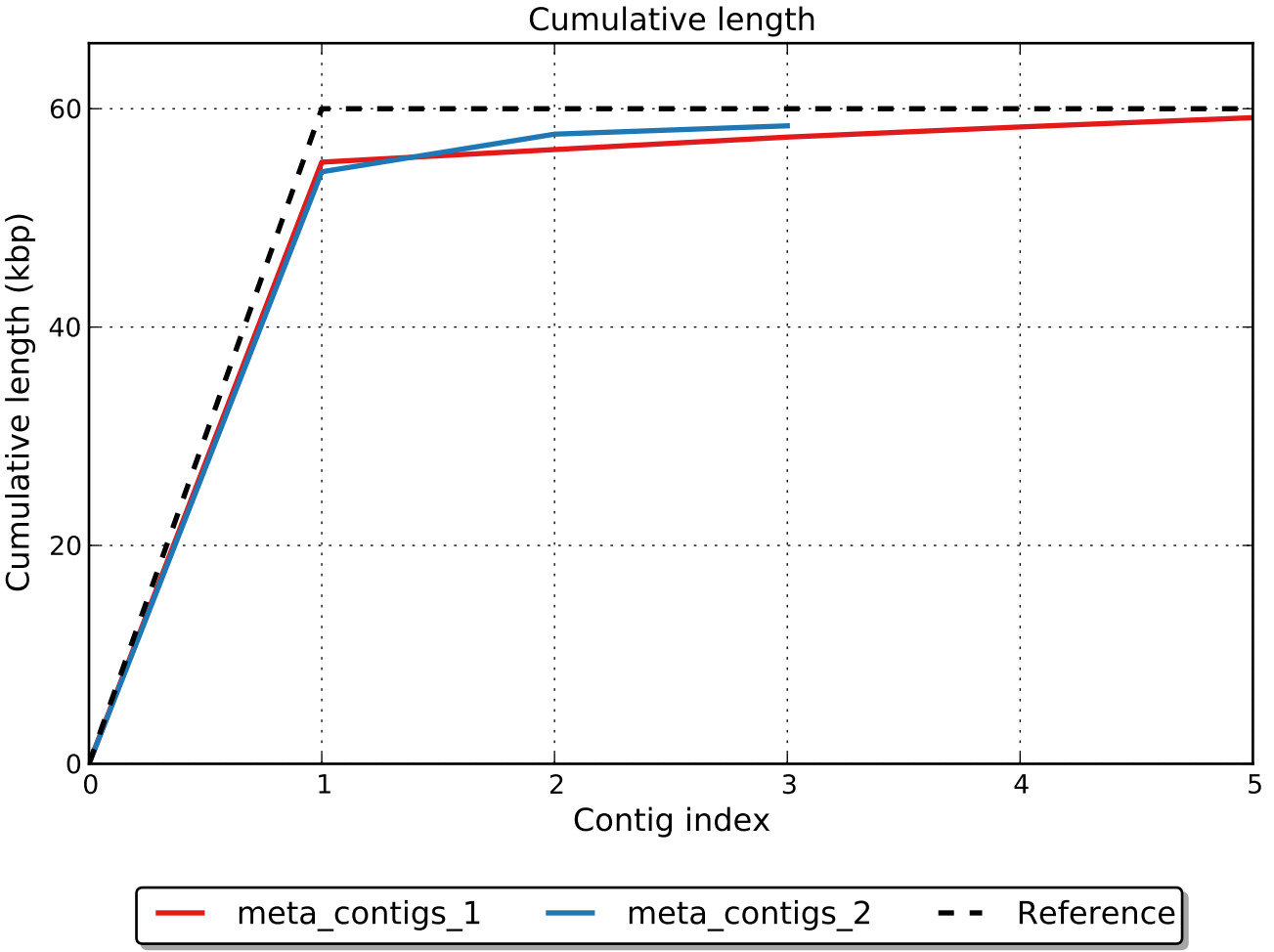
Unaligned report

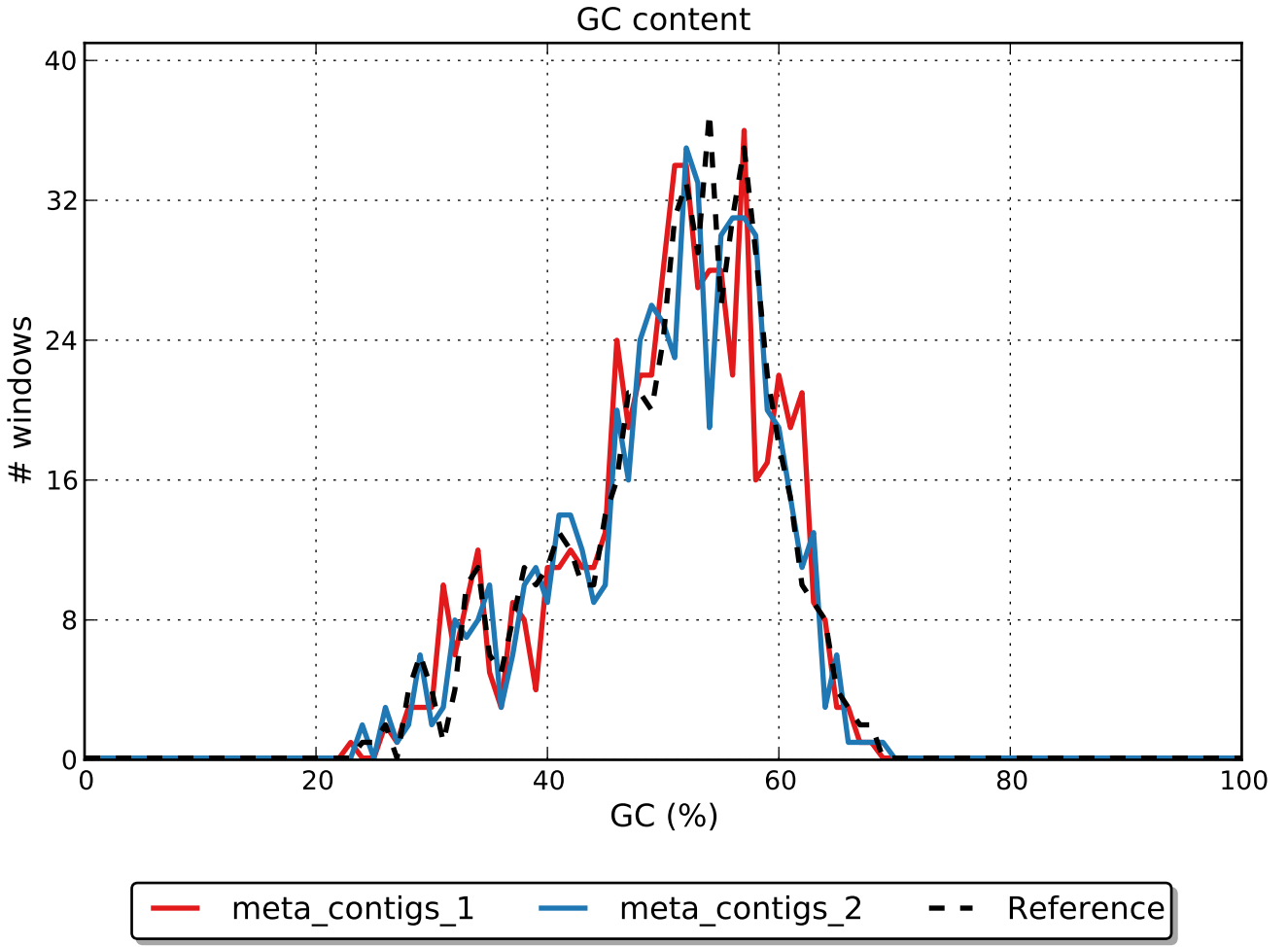
	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	21	0

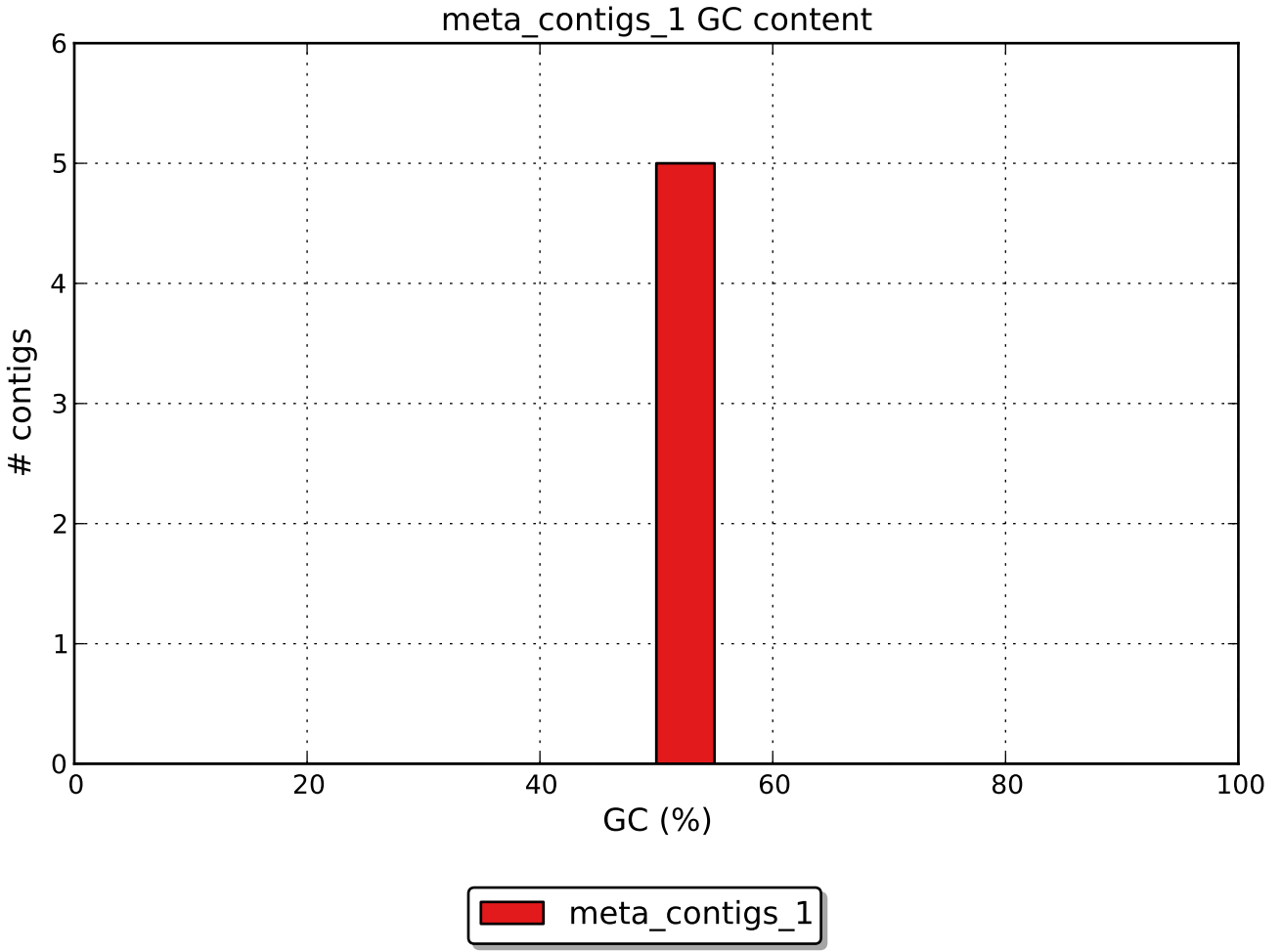
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

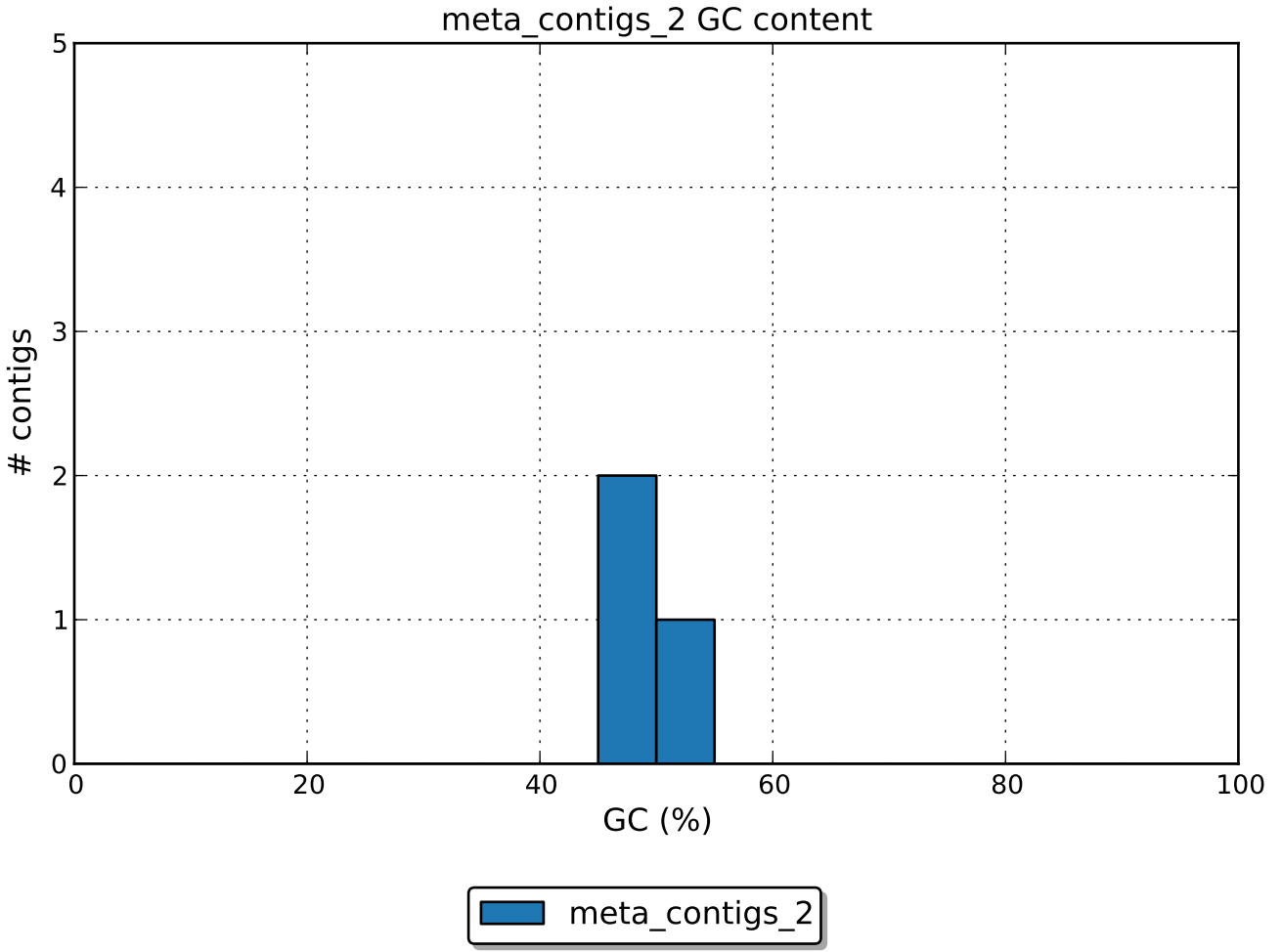

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

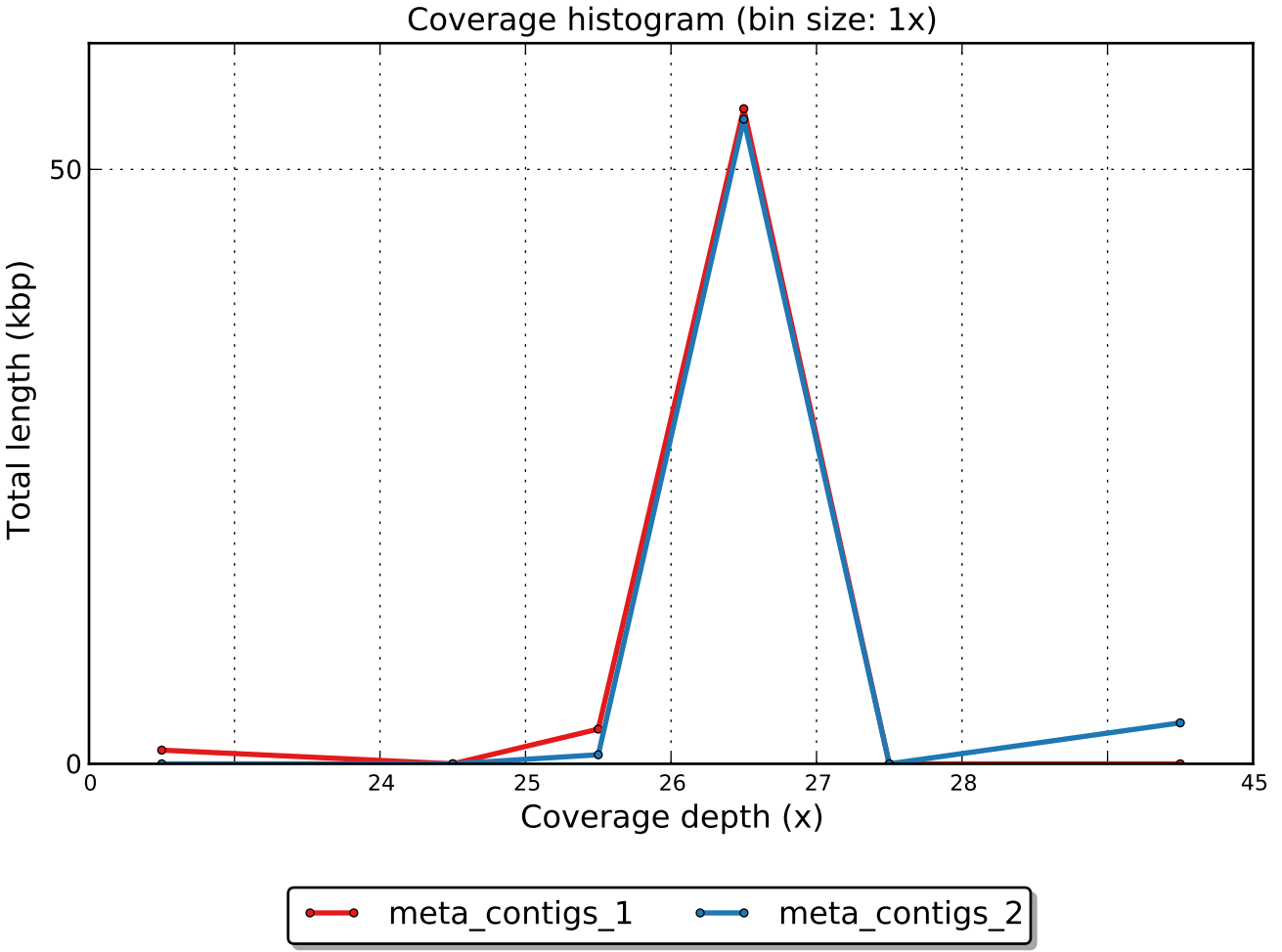

NGx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

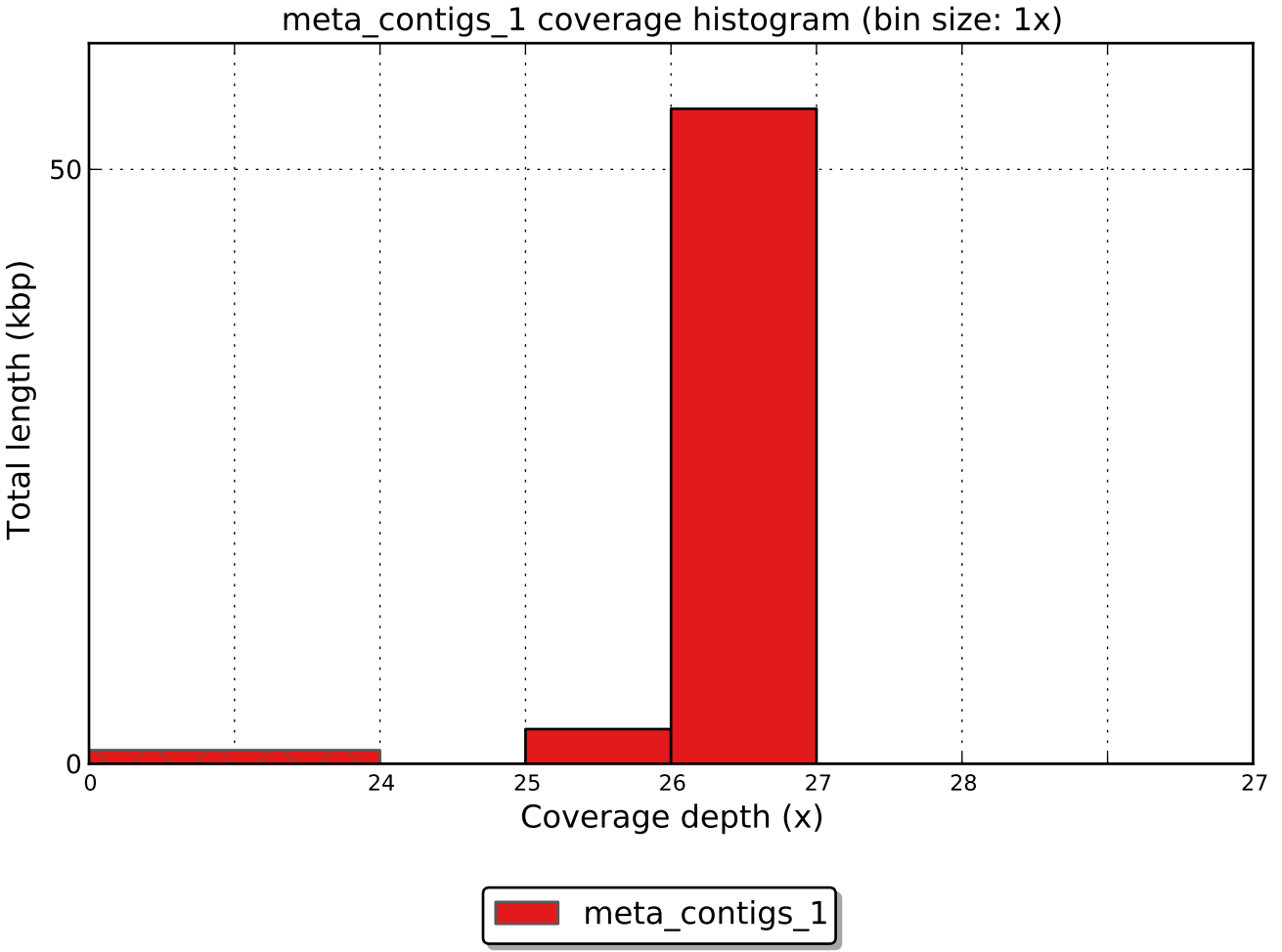

Cumulative length
Cumulative length (kbp)
0
20
40
60
0
1
2
3
4
5
Contig index
meta_contigs_1
meta_contigs_2
Reference

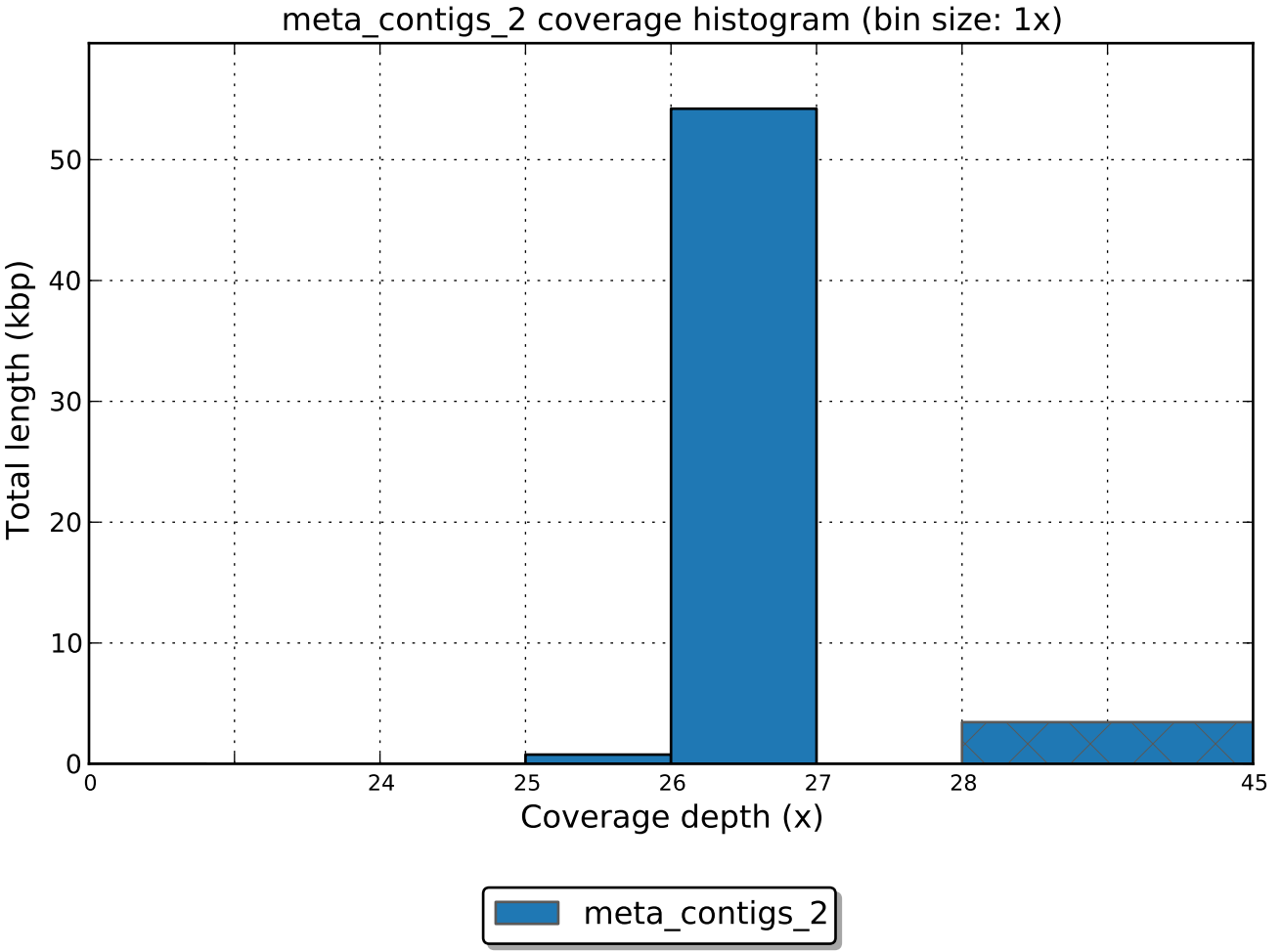

GC content
windows
GC (%)
0
8
16
24
32
40
0
20
40
60
80
100
meta_contigs_1
meta_contigs_2
Reference

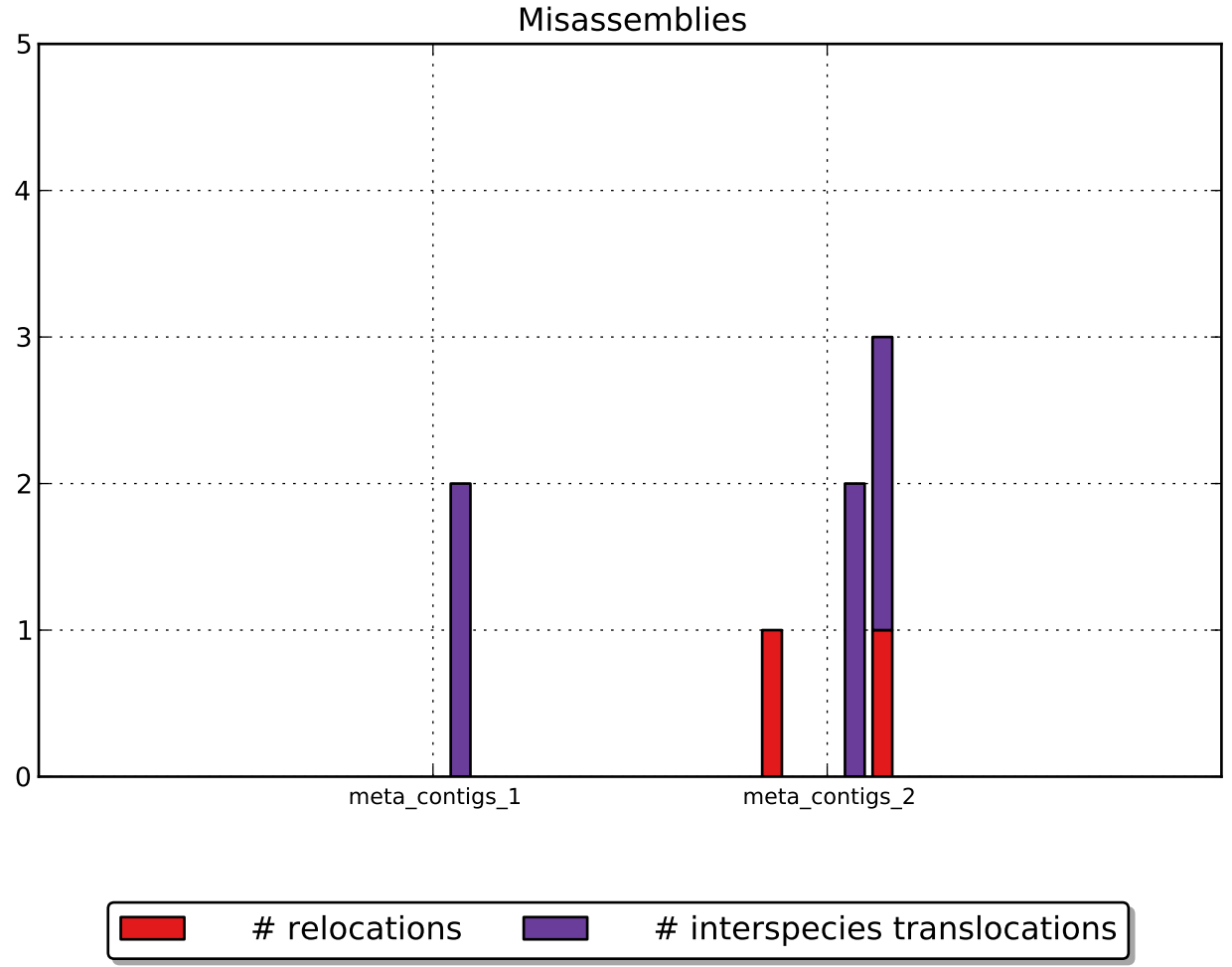

meta_contigs_1 GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
meta_contigs_1

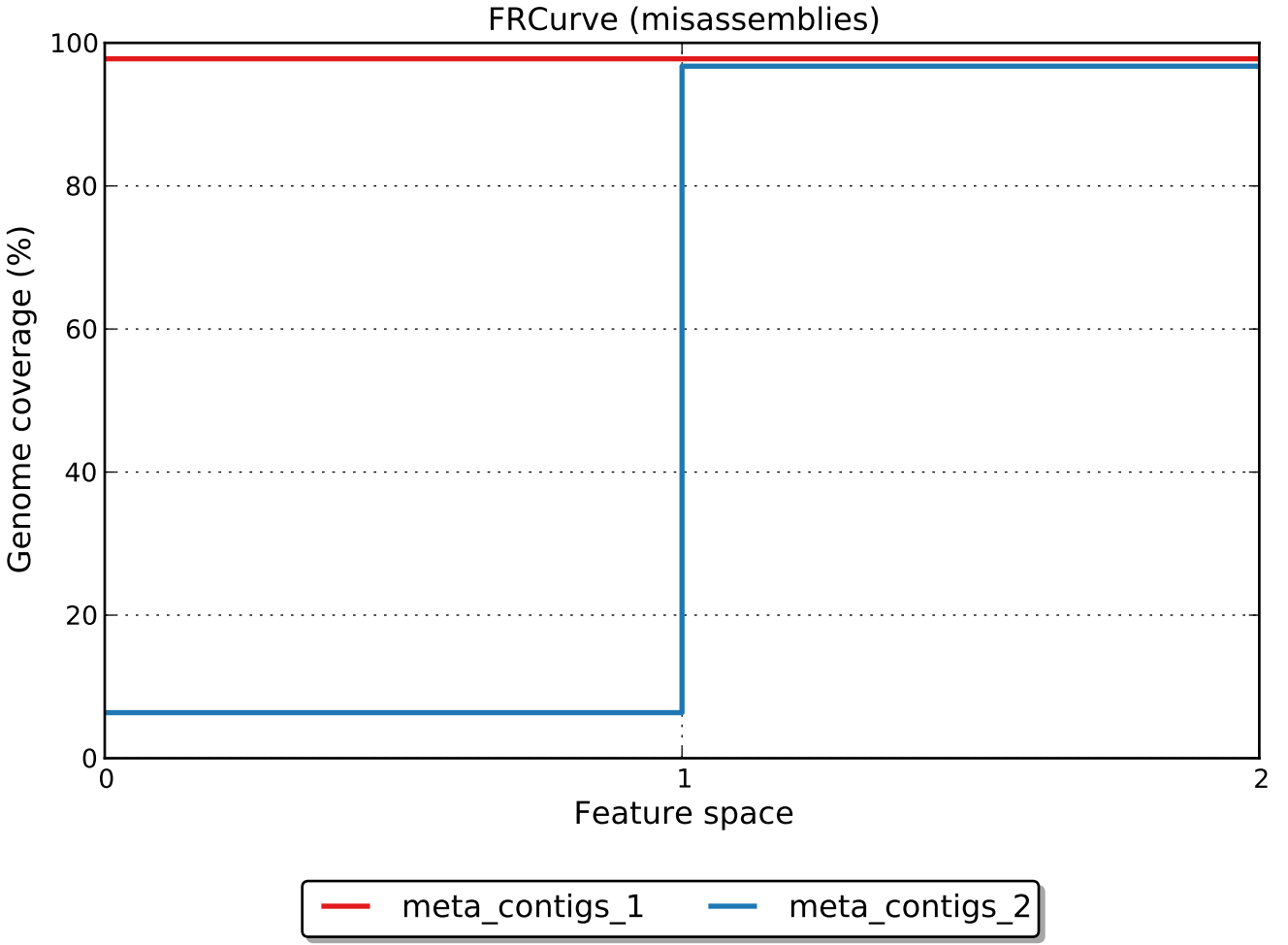

meta_contigs_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
meta_contigs_2

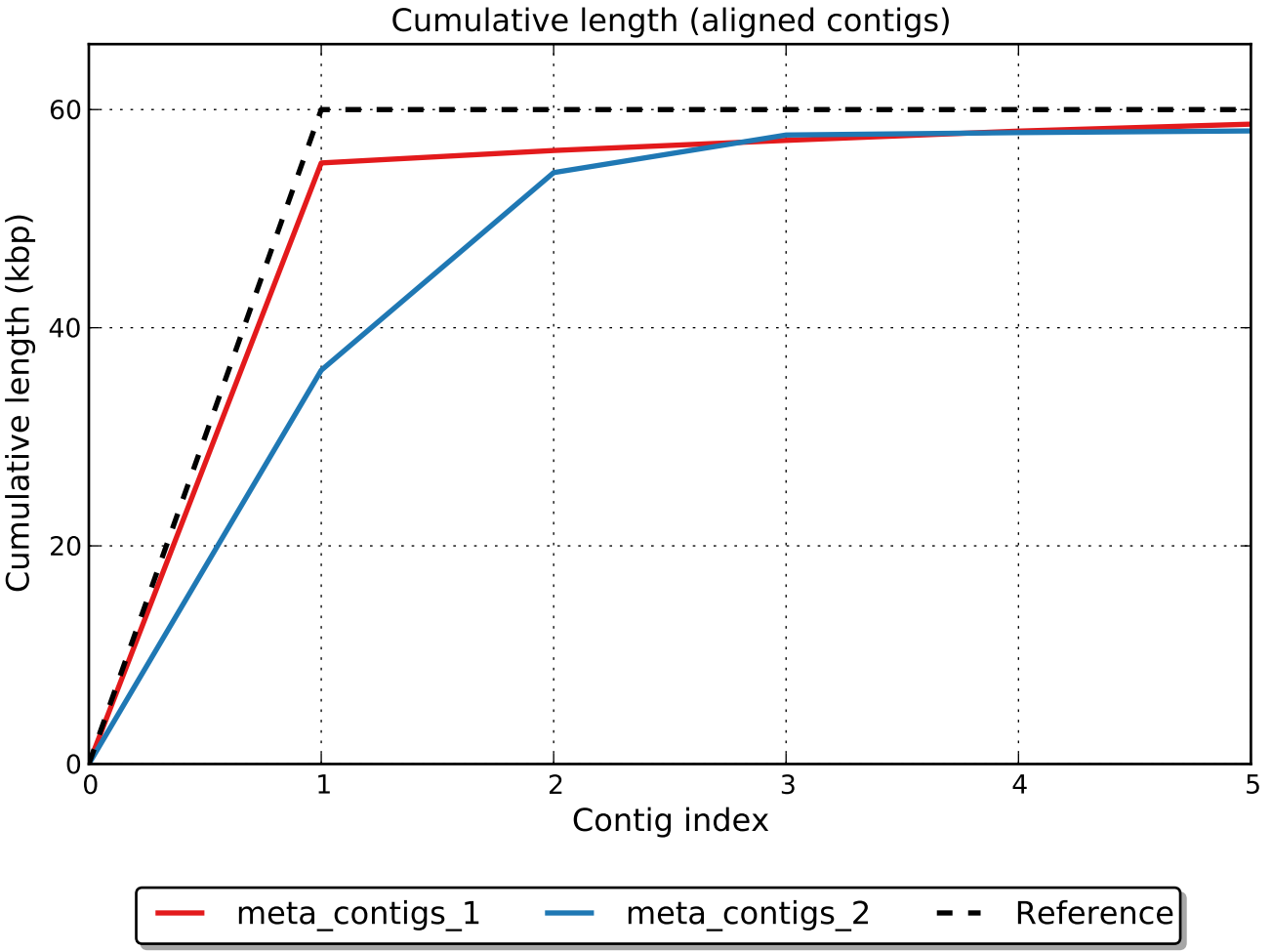

Coverage histogram (bin size: 1x)
Total length (kbp)
50
0
0
24
25
26
27
28
45
Coverage depth (x)
meta_contigs_1
meta_contigs_2

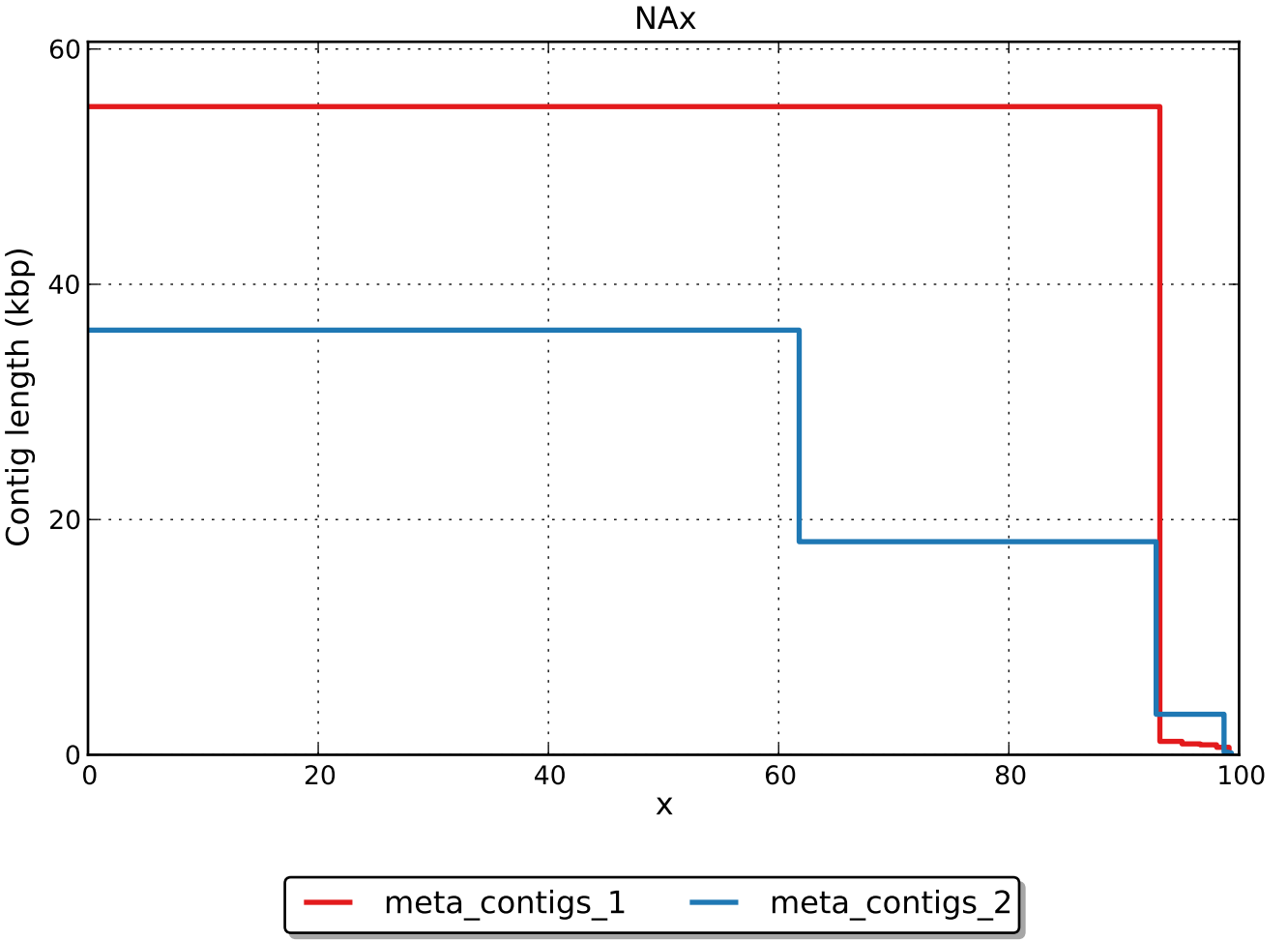

meta_contigs_1 coverage histogram (bin size: 1x)
Total length (kbp)
50
0
0
24
25
26
27
28
27
Coverage depth (x)
meta_contigs_1

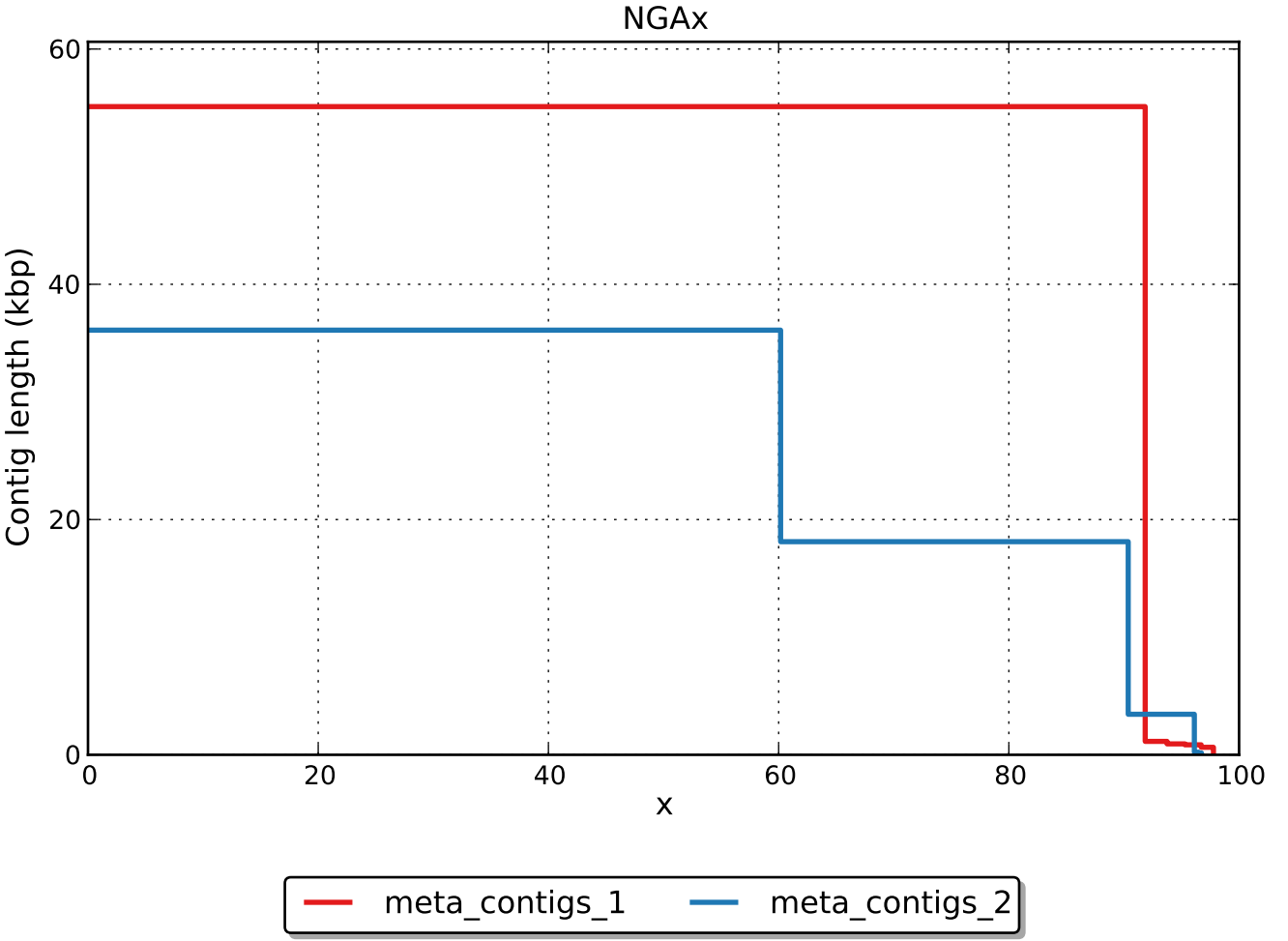

meta_contigs_2 coverage histogram (bin size: 1x)
Total length (kbp)
0
10
20
30
40
50
0
24
25
26
27
28
45
Coverage depth (x)
meta_contigs_2

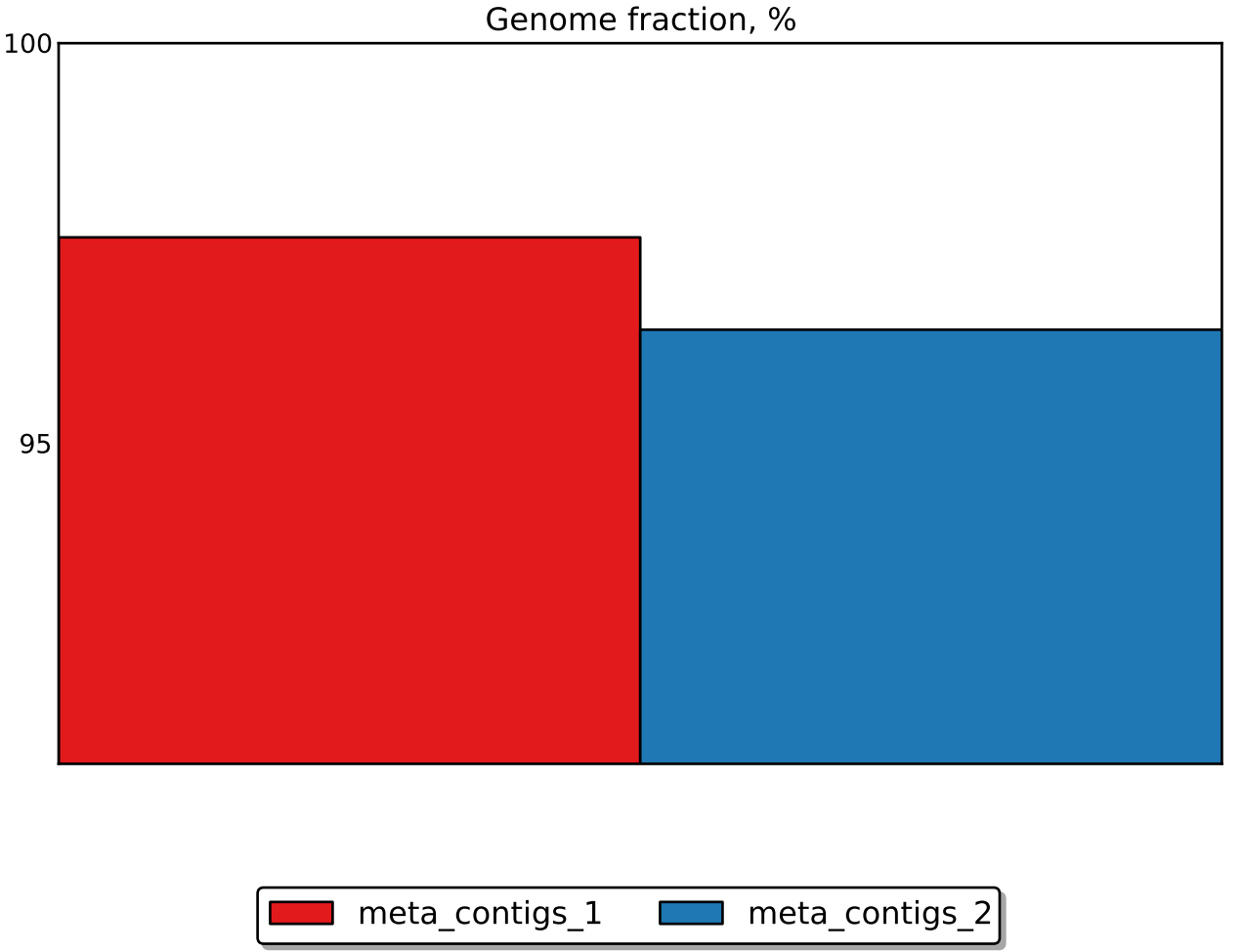

Misassemblies
5
4
3
2
1
0
meta_contigs_1
meta_contigs_2
relocations
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
meta_contigs_1
meta_contigs_2


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
20
40
60
0
1
2
3
4
5
Contig index
meta_contigs_1
meta_contigs_2
Reference


NAx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2


NGAx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2


Genome fraction, %
100
95
meta_contigs_1
meta_contigs_2