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
N90	55106	54221
NG90	55106	54221
auN	51385.4	50527.6
auNG	50682.3	49207.2
L50	1	1
LG50	1	1
L90	1	1
LG90	1	1
# misassemblies	0	3
# misassembled contigs	0	2
Misassembled contigs length	0	54984
# local misassemblies	0	0
# scaffold gap ext. mis.	1	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	97.797	96.628
Duplication ratio	1.003	1.004
# N's per 100 kbp	35.49	0.00
# mismatches per 100 kbp	47.59	58.40
# indels per 100 kbp	1.70	1.72
Largest alignment	55106	36102
Total aligned length	58842	58220
NA50	55106	36102
NGA50	55106	36102
NA90	55106	18119
NGA90	55106	18119
auNA	51374.2	28129.6
auNGA	50671.3	27394.4
LA50	1	1
LGA50	1	1
LA90	1	2
LGA90	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

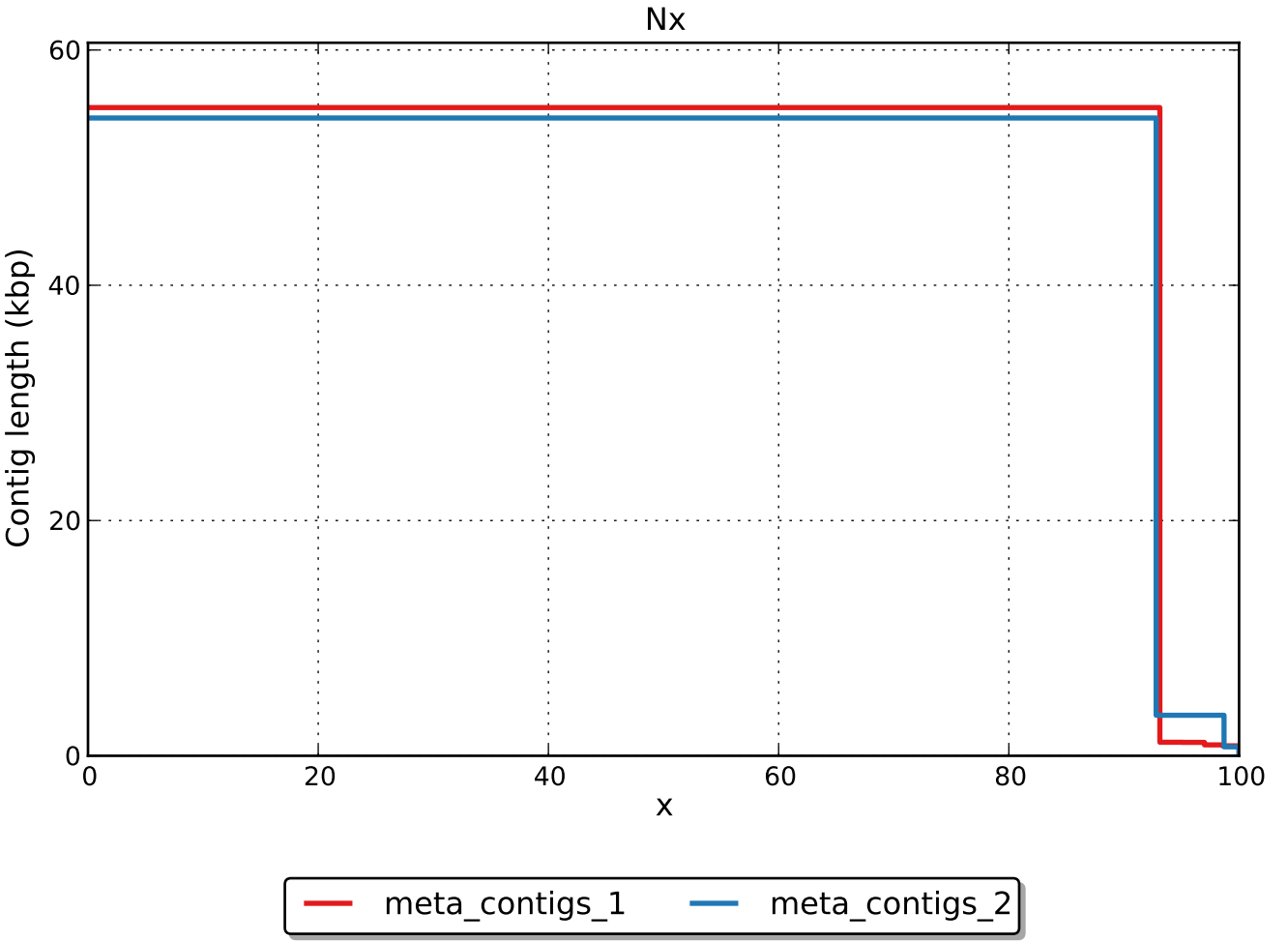
	meta_contigs_1	meta_contigs_2
# misassemblies	0	3
# contig misassemblies	0	3
# c. relocations	0	3
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	2
Misassembled contigs length	0	54984
# possibly misassembled contigs	0	0
# possible misassemblies	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	1	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	28	34
# indels	1	1
# indels (<= 5 bp)	1	1
# indels (> 5 bp)	0	0
Indels length	1	1

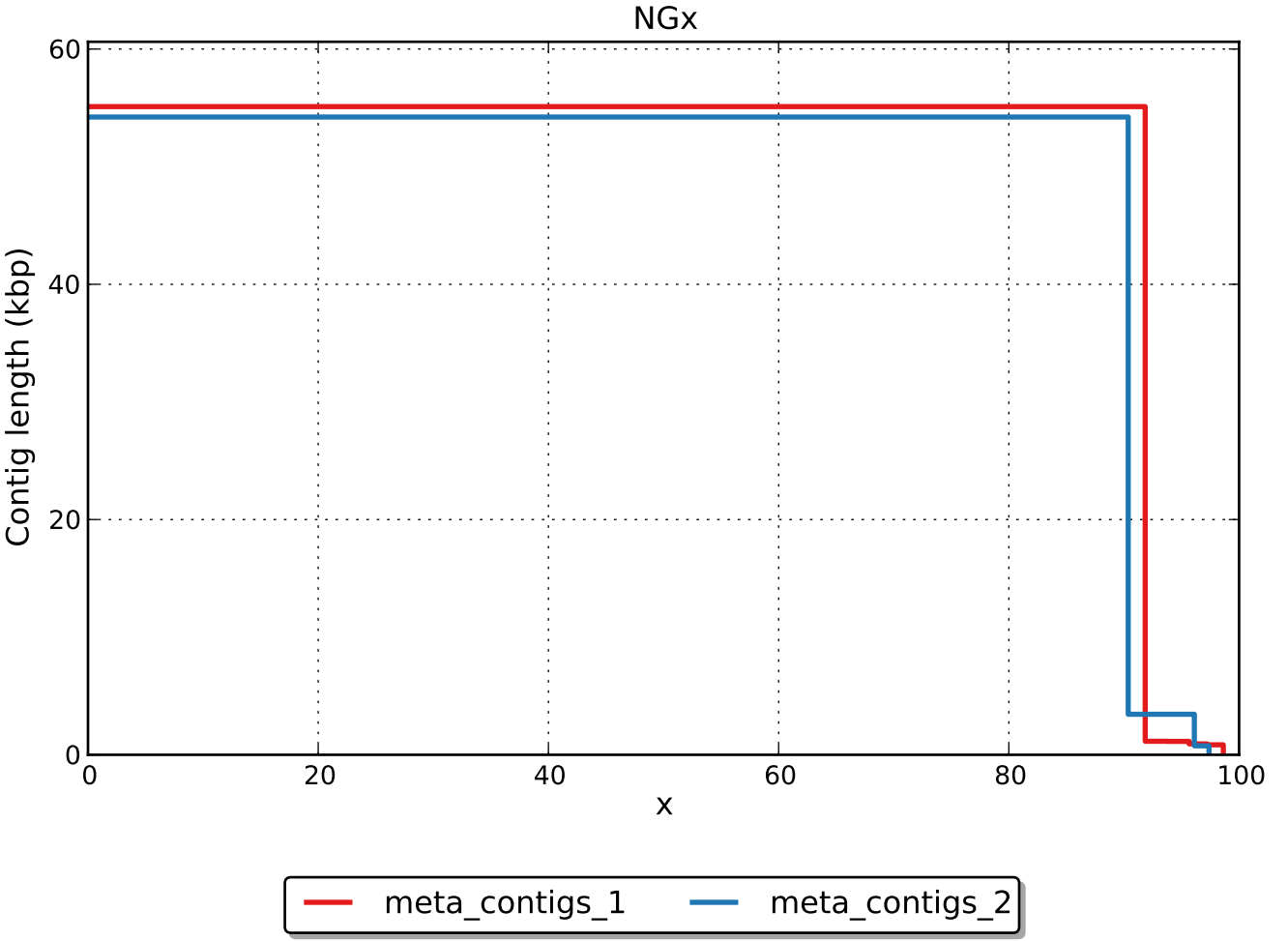
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

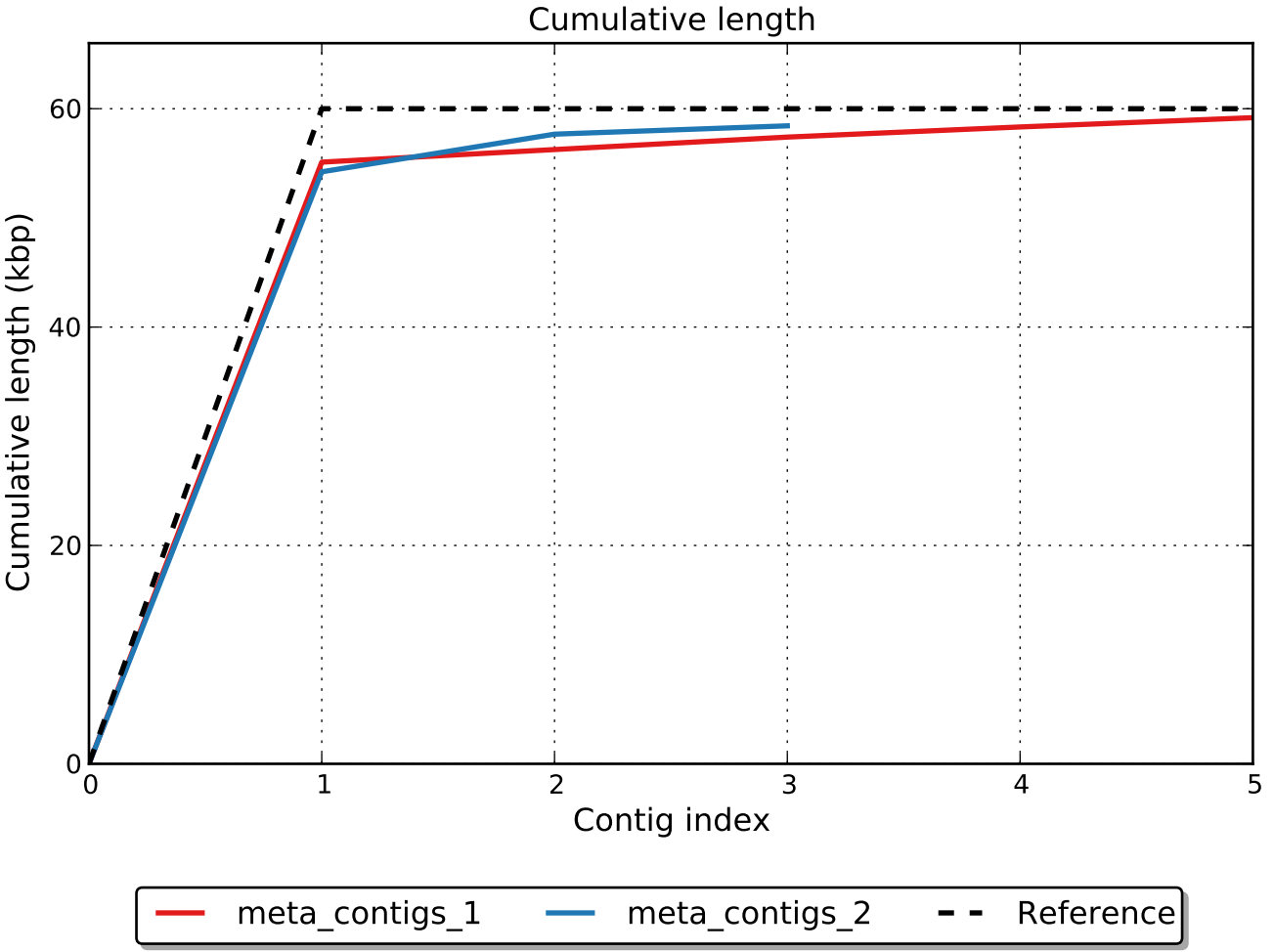
Unaligned report

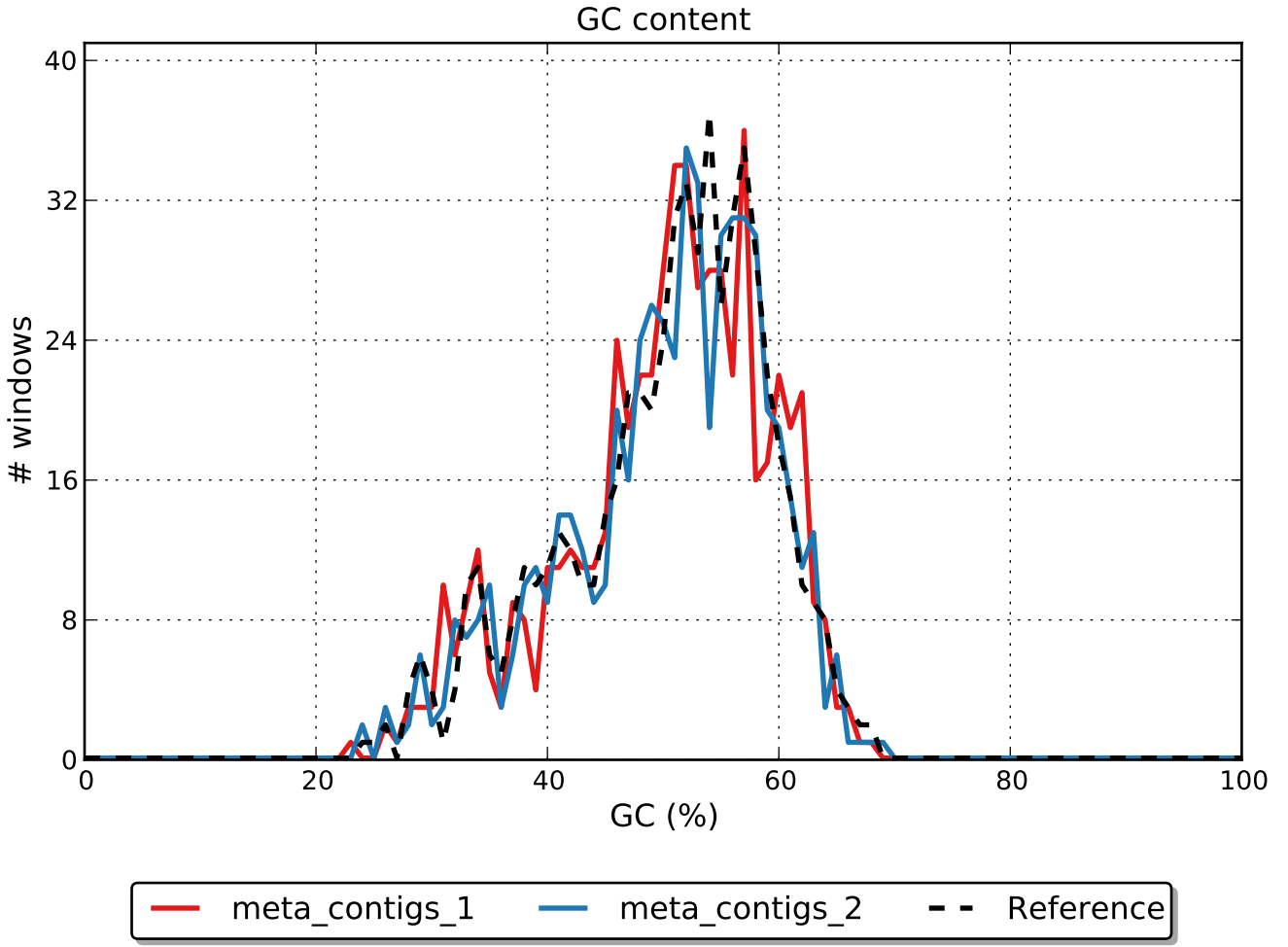
	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	21	0

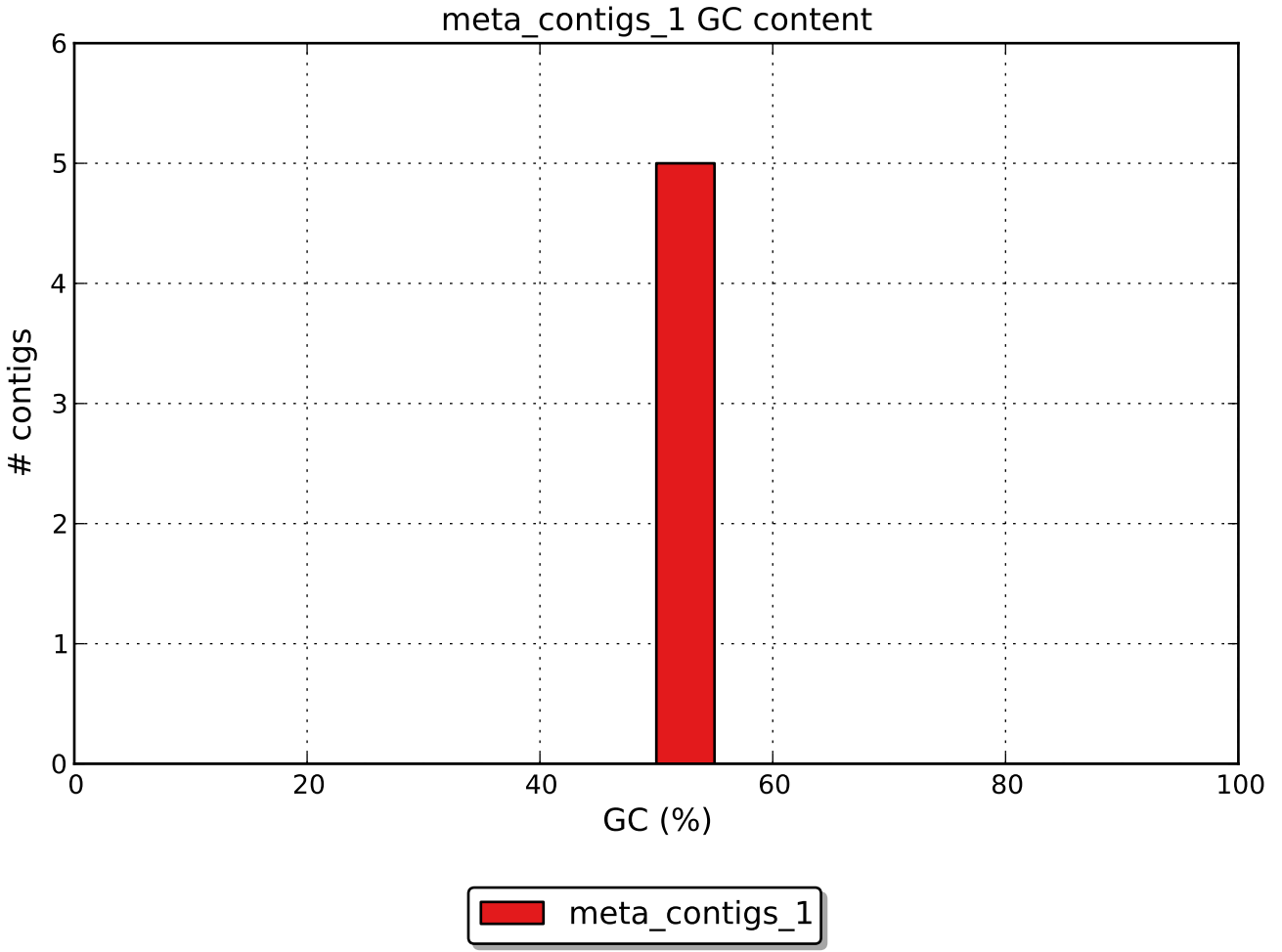
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

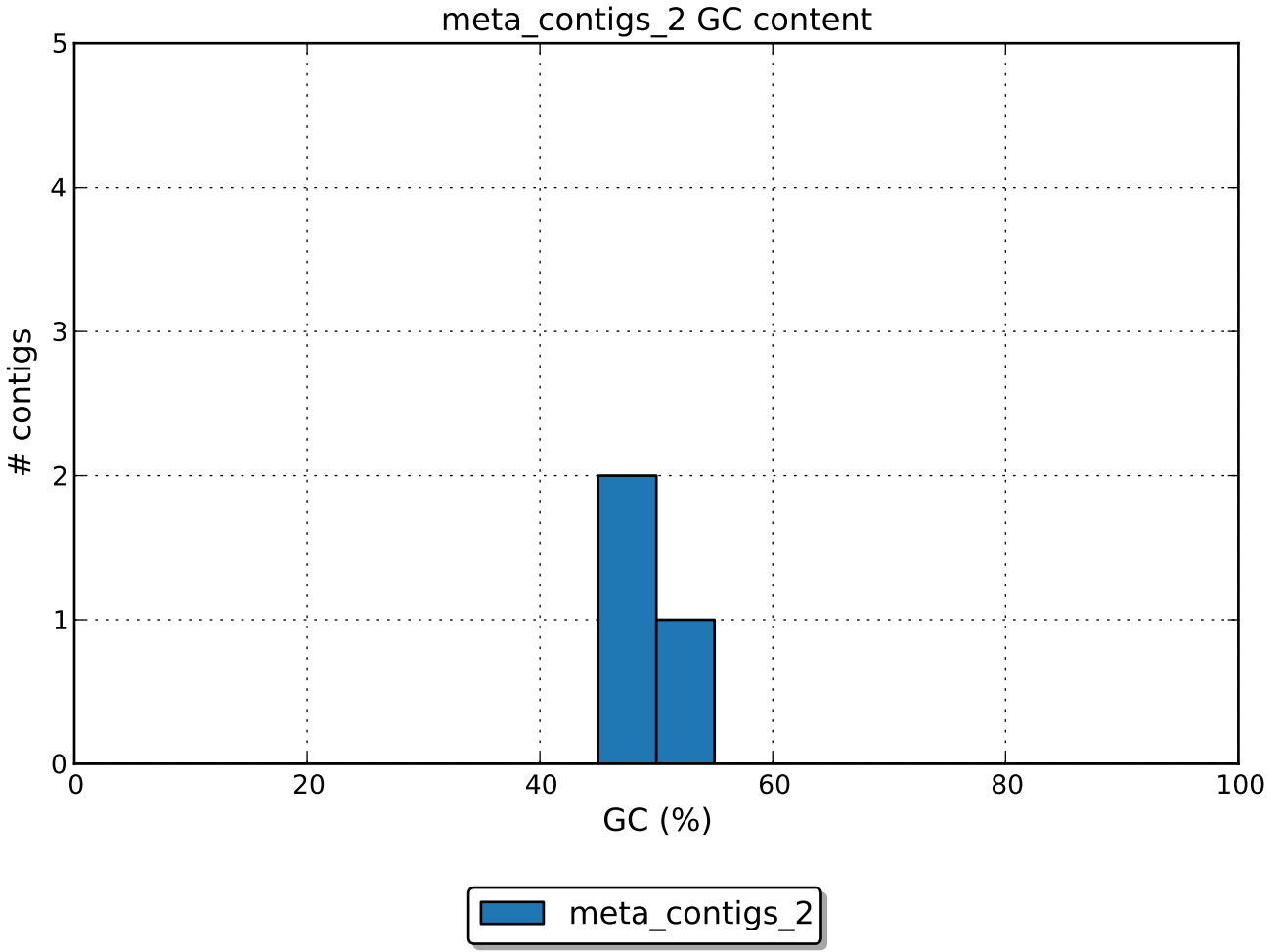

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

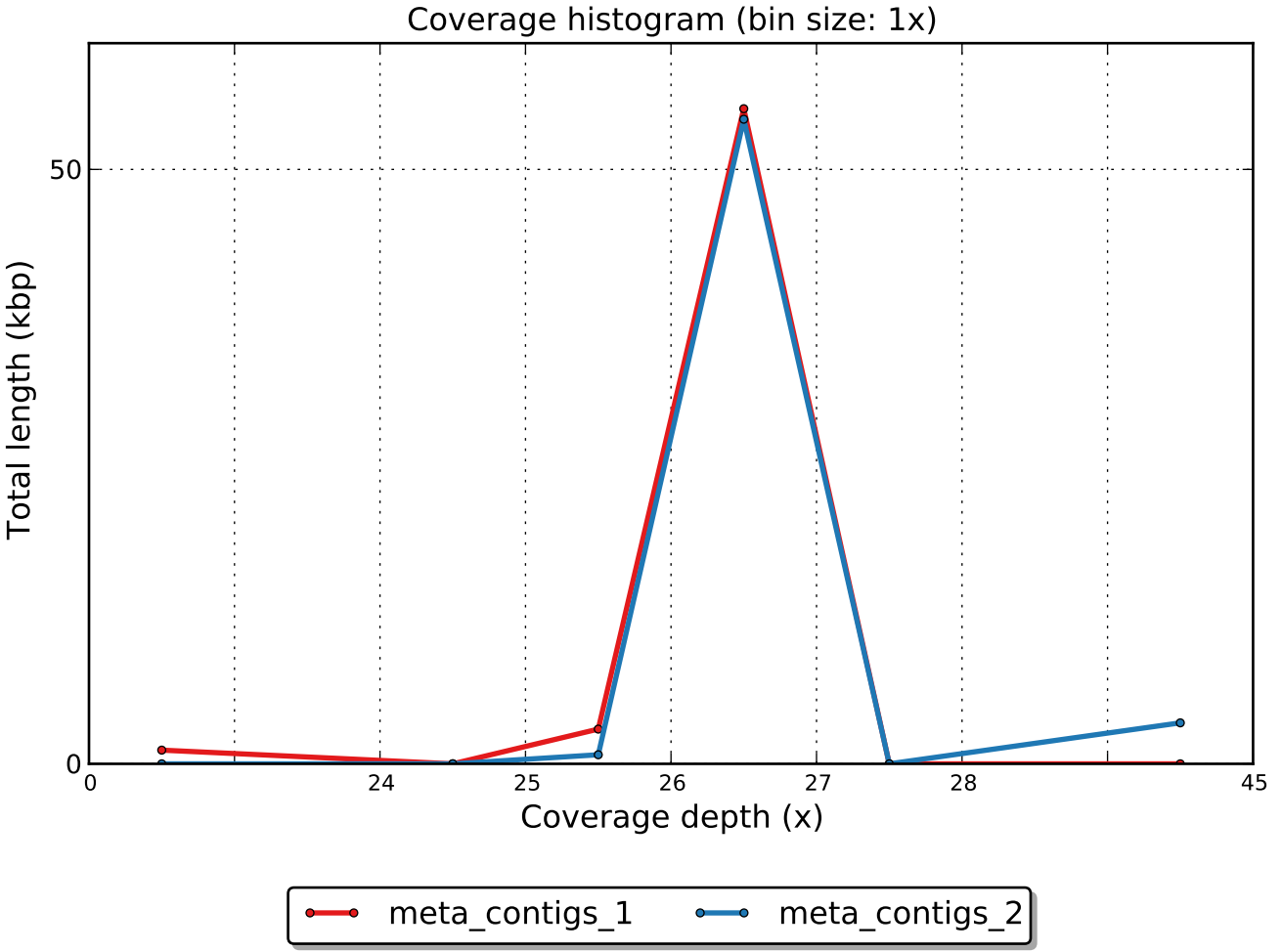

NGx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

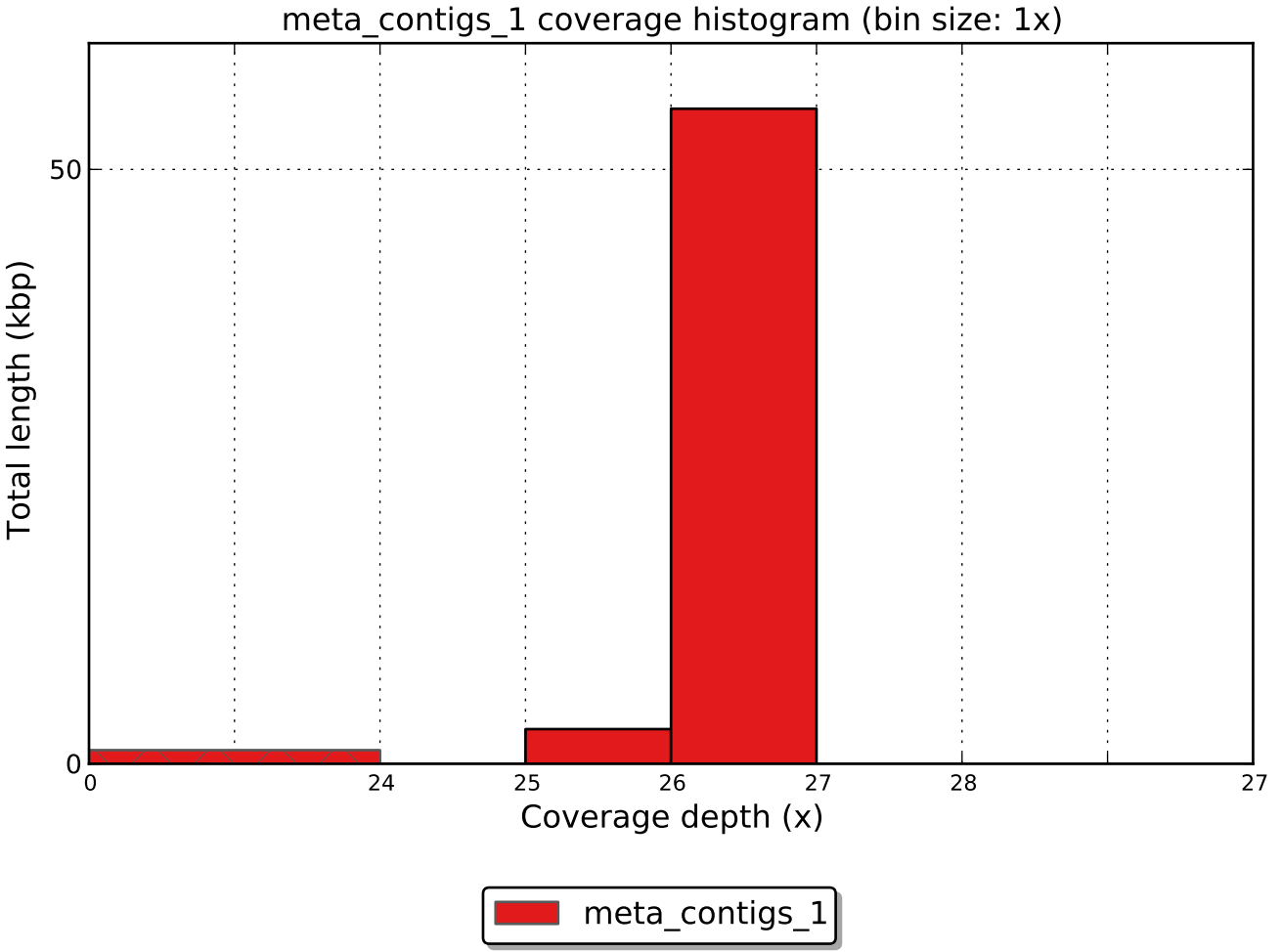

Cumulative length
Cumulative length (kbp)
0
20
40
60
0
1
2
3
4
5
Contig index
meta_contigs_1
meta_contigs_2
Reference

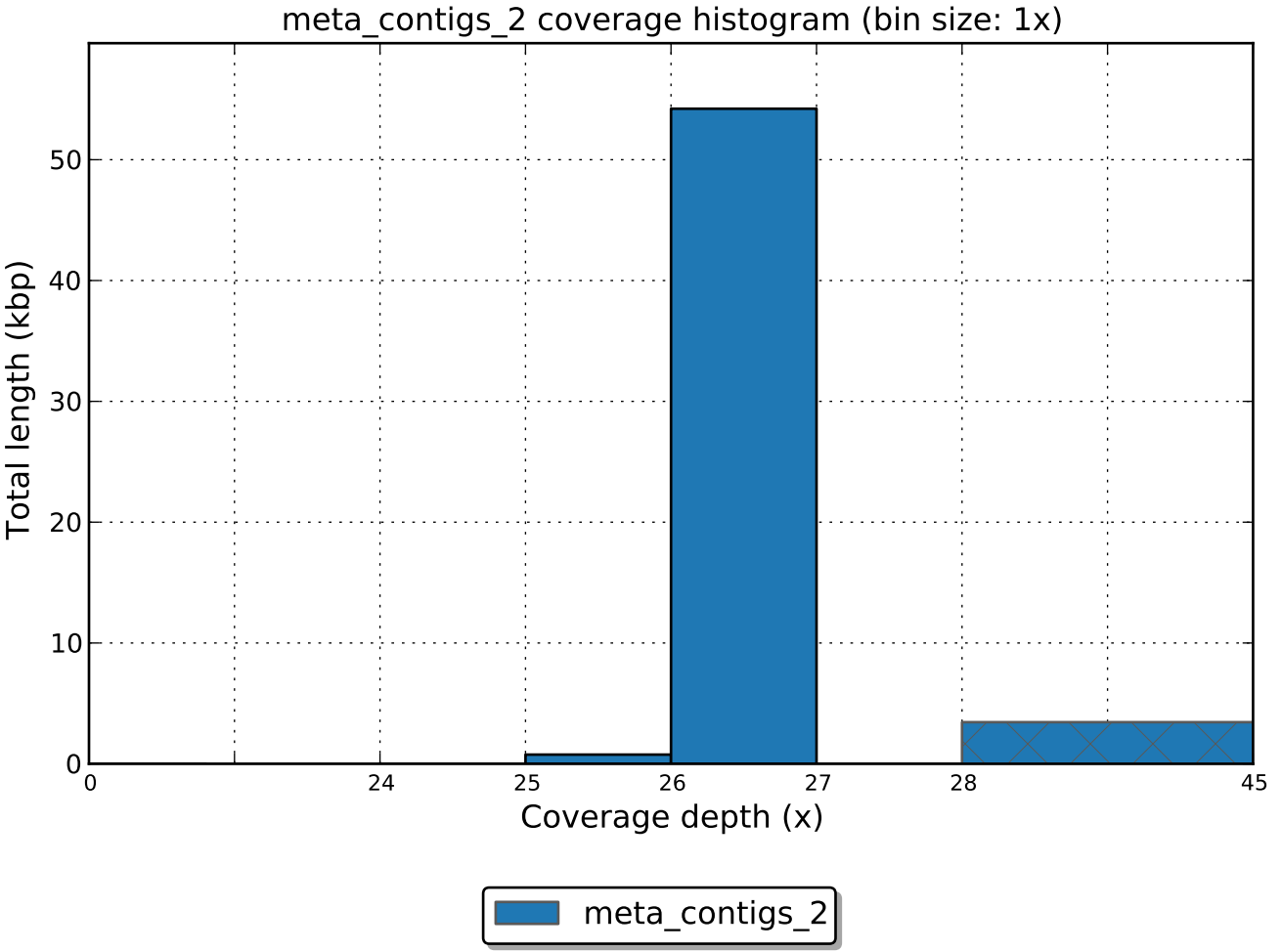

GC content
windows
GC (%)
0
8
16
24
32
40
0
20
40
60
80
100
meta_contigs_1
meta_contigs_2
Reference

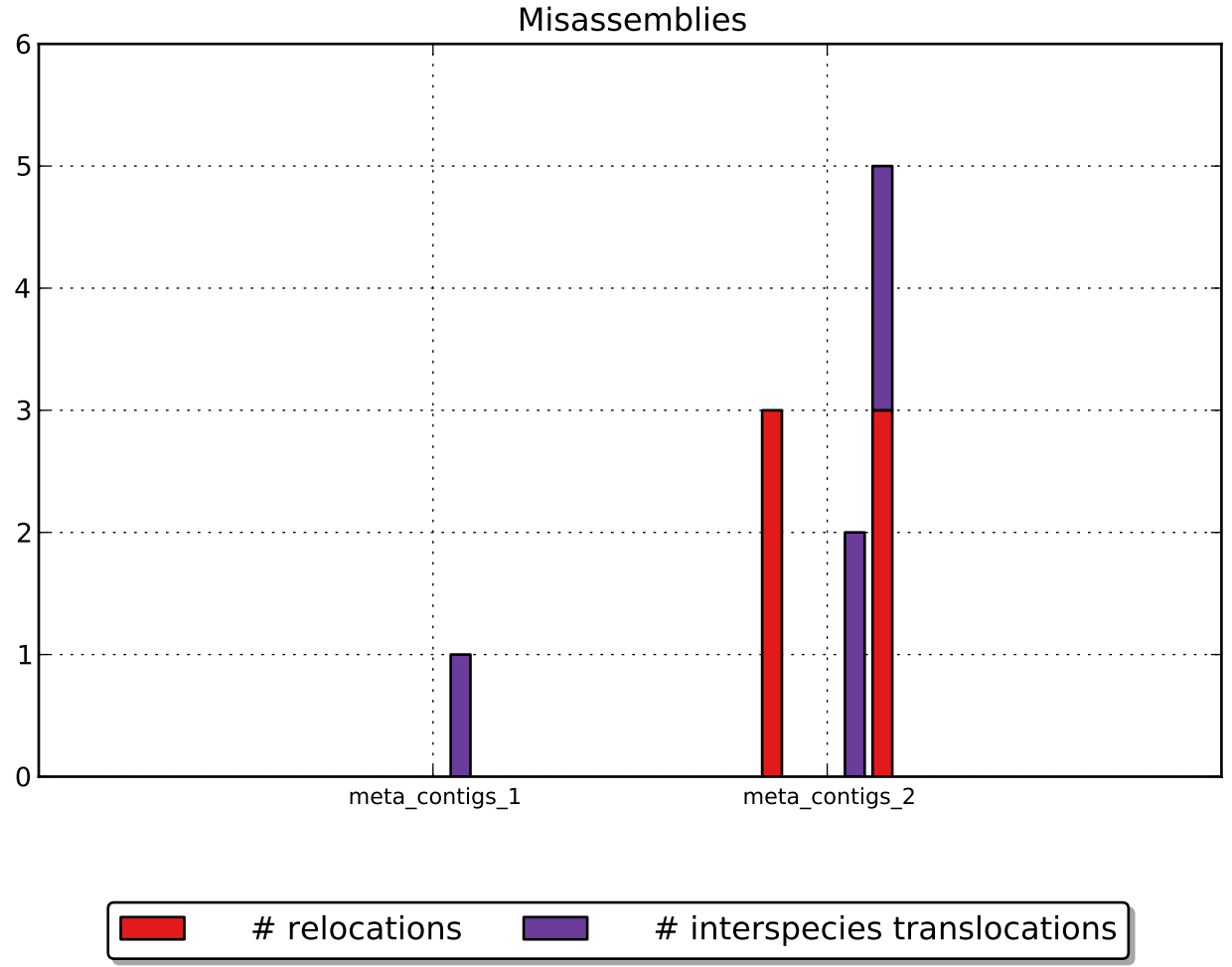

meta_contigs_1 GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
meta_contigs_1

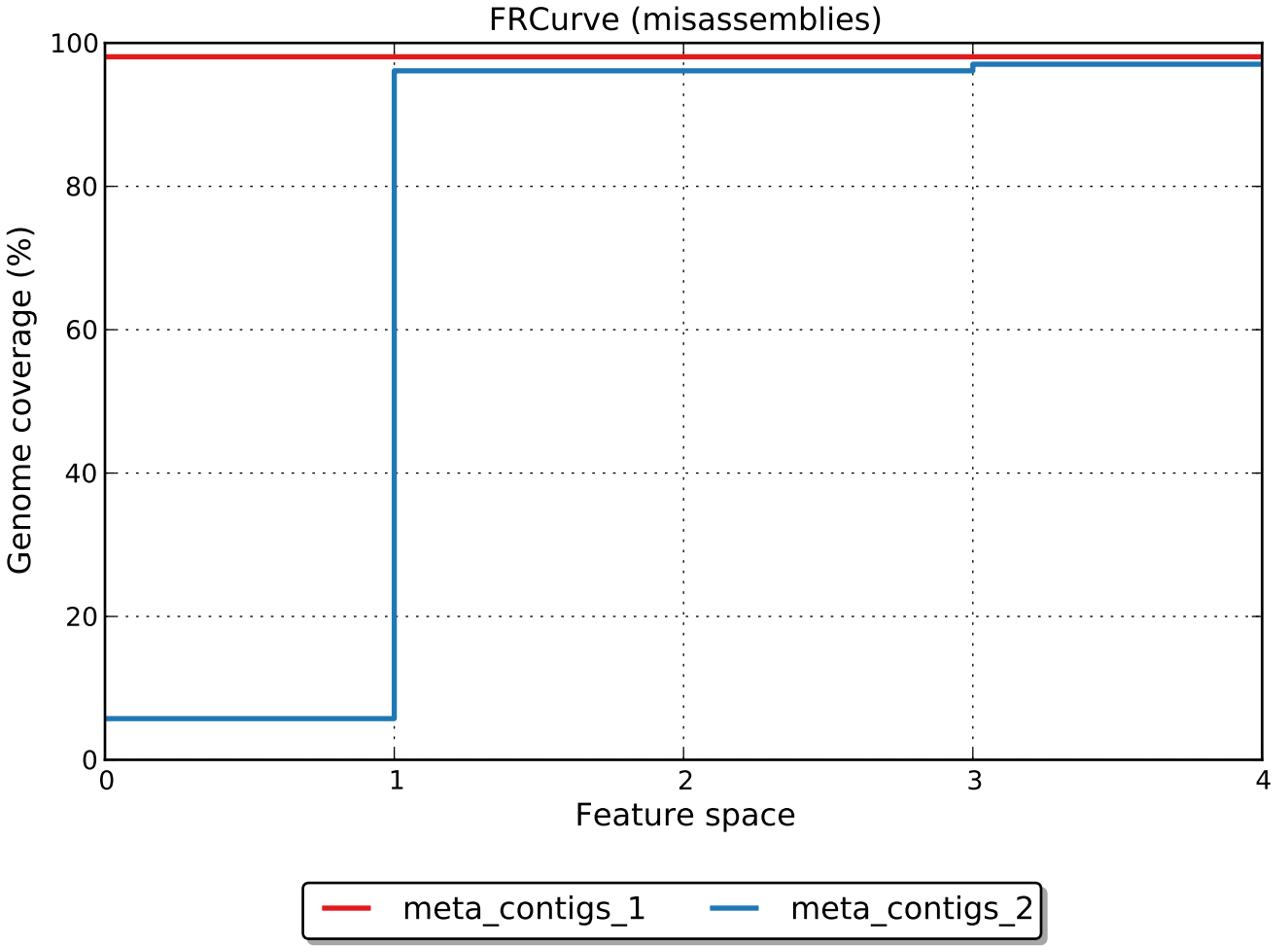

meta_contigs_2 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
meta_contigs_2

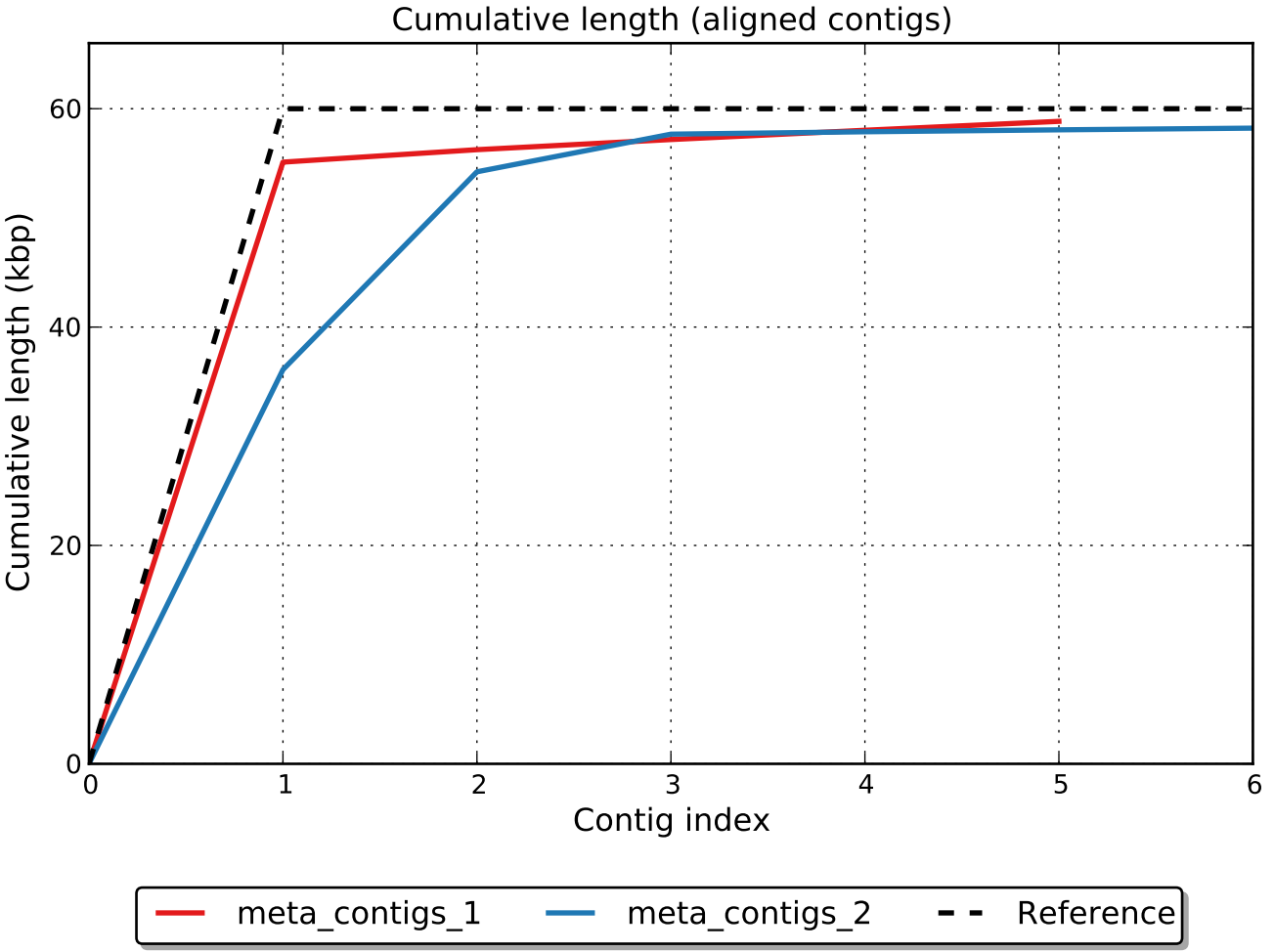

Coverage histogram (bin size: 1x)
Total length (kbp)
50
0
0
24
25
26
27
28
45
Coverage depth (x)
meta_contigs_1
meta_contigs_2

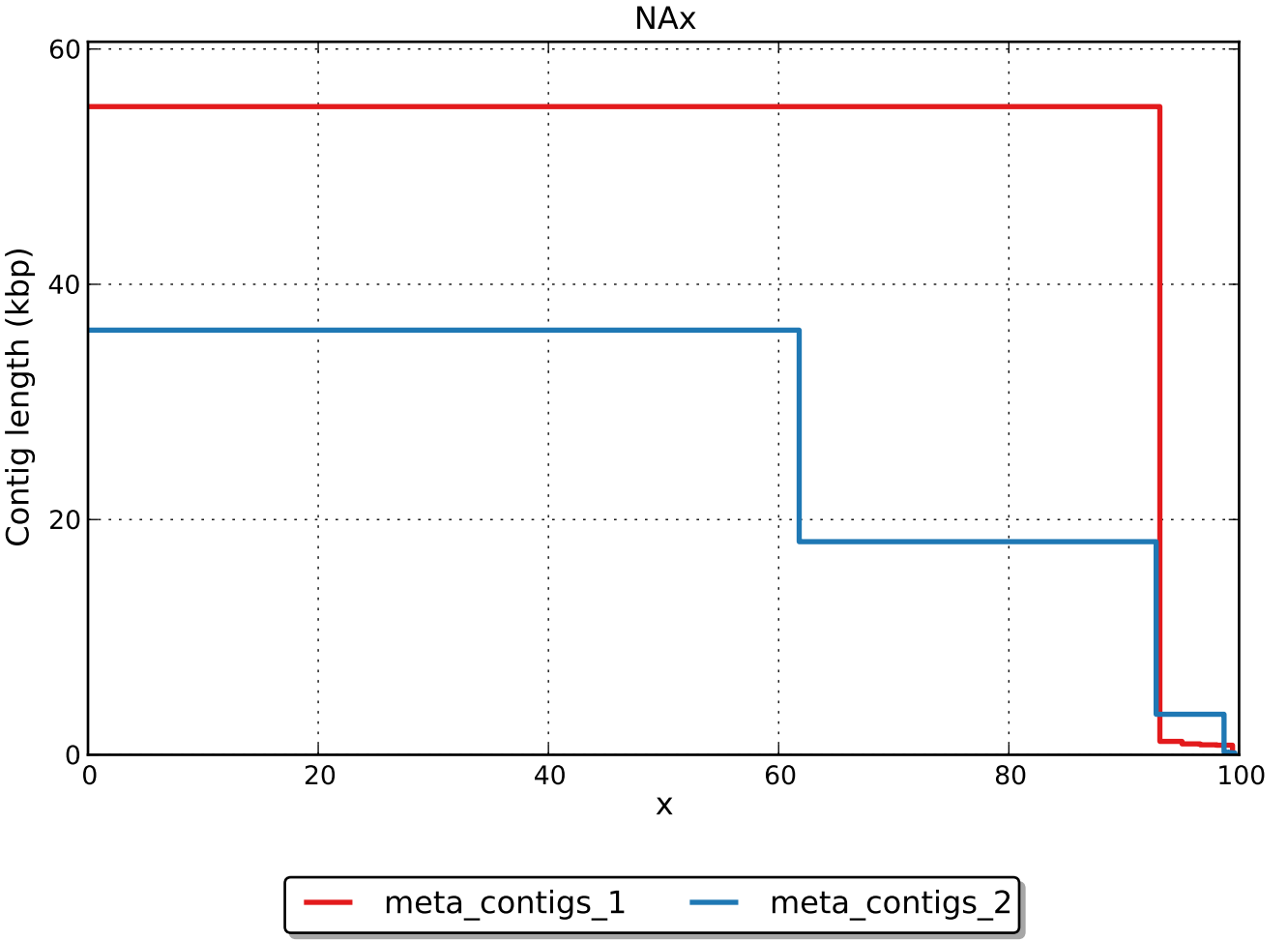

meta_contigs_1 coverage histogram (bin size: 1x)
Total length (kbp)
50
0
0
24
25
26
27
28
27
Coverage depth (x)
meta_contigs_1

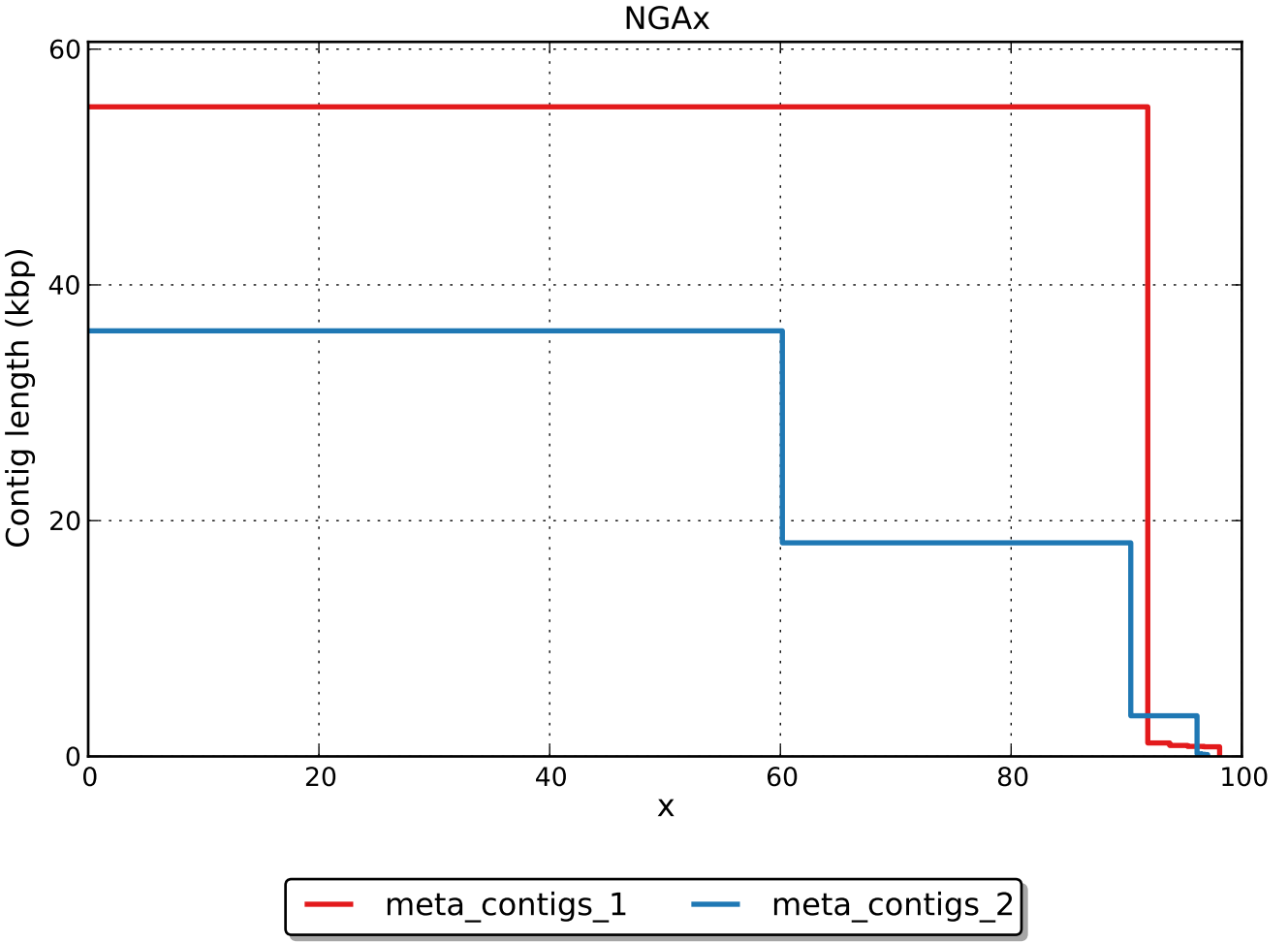

meta_contigs_2 coverage histogram (bin size: 1x)
Total length (kbp)
0
10
20
30
40
50
0
24
25
26
27
28
45
Coverage depth (x)
meta_contigs_2

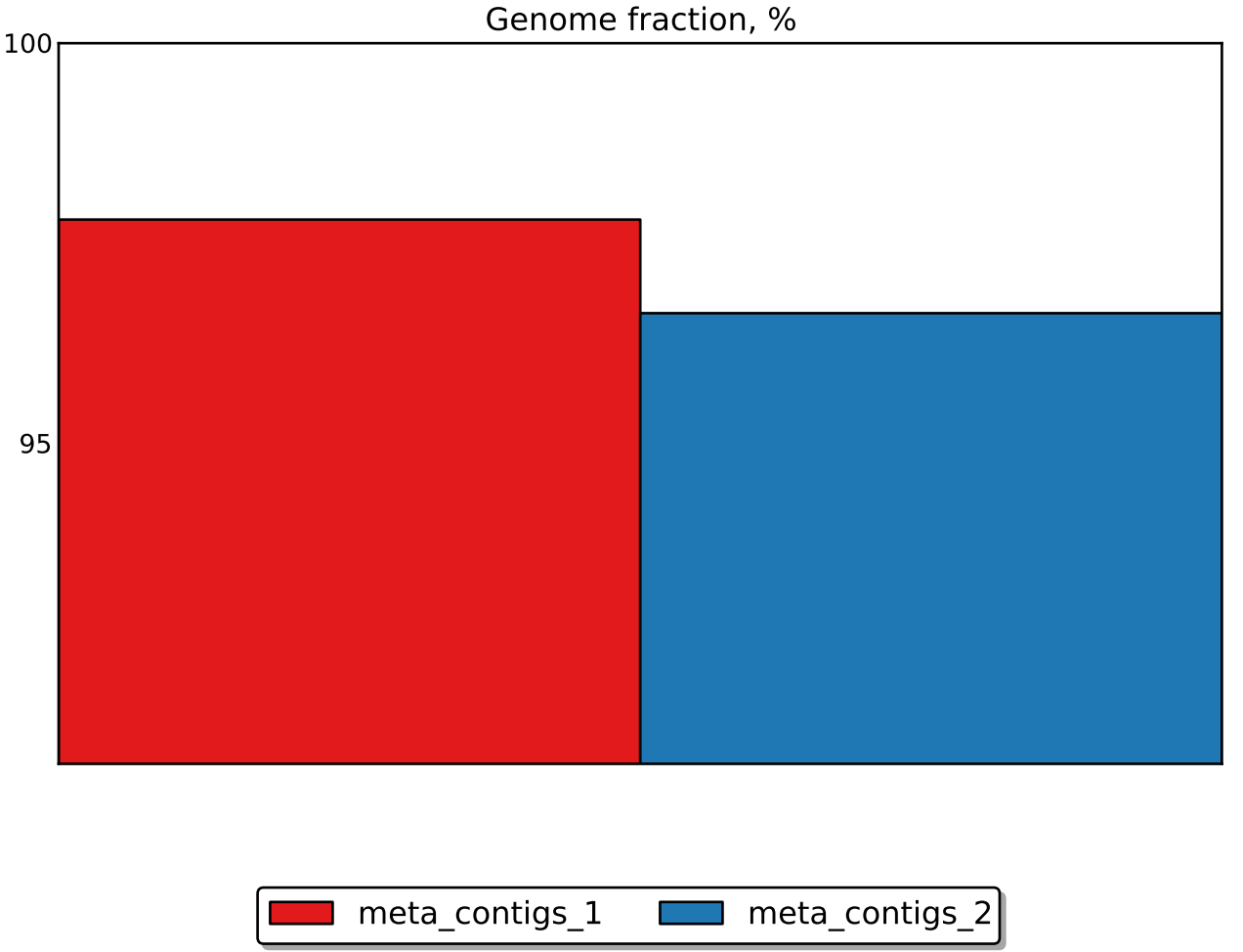

Misassemblies
6
5
4
3
2
1
0
meta_contigs_1
meta_contigs_2
relocations
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
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
6
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