Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 1000 bp)	2	1
# contigs (>= 5000 bp)	1	1
# contigs (>= 10000 bp)	1	1
# contigs (>= 25000 bp)	1	1
# contigs (>= 50000 bp)	0	0
Total length (>= 1000 bp)	49610	49658
Total length (>= 5000 bp)	48458	49658
Total length (>= 10000 bp)	48458	49658
Total length (>= 25000 bp)	48458	49658
Total length (>= 50000 bp)	0	0
# contigs	3	3
Largest contig	48458	49658
Total length	50324	51135
Reference length	54999	54999
GC (%)	45.77	45.73
Reference GC (%)	45.96	45.96
N50	48458	49658
NG50	48458	49658
N90	48458	49658
NG90	1152	49658
auN	46697.7	48245.0
auNG	42728.3	44855.5
L50	1	1
LG50	1	1
L90	1	1
LG90	2	1
# misassemblies	1	1
# misassembled contigs	1	1
Misassembled contigs length	48458	763
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	1	0
# unaligned contigs	0 + 1 part	0 + 0 part
Unaligned length	665	0
Genome fraction (%)	90.254	92.318
Duplication ratio	1.000	1.000
# N's per 100 kbp	39.74	0.00
# mismatches per 100 kbp	26.19	53.18
# indels per 100 kbp	0.00	9.85
Largest alignment	37178	49658
Total aligned length	49639	50774
NA50	37178	49658
NGA50	37178	49658
NA90	11280	49658
NGA90	182	49658
auNA	30006.9	48235.2
auNGA	27456.2	44846.4
LA50	1	1
LGA50	1	1
LA90	2	1
LGA90	5	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).

Misassemblies report

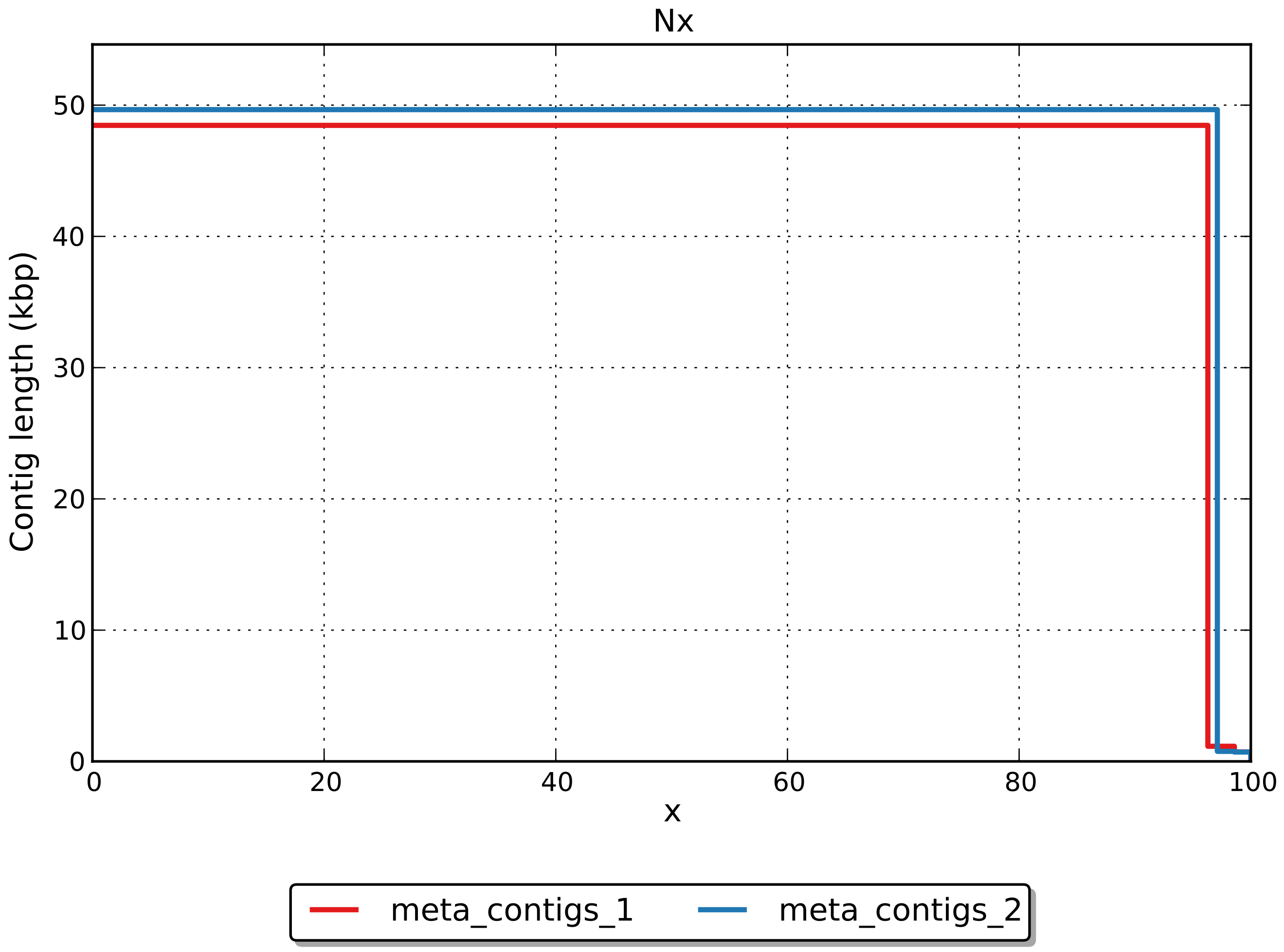
	meta_contigs_1	meta_contigs_2
# misassemblies	1	1
# contig misassemblies	1	1
# c. relocations	1	1
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	1	1
Misassembled contigs length	48458	763
# 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	1	0
# mismatches	13	27
# indels	0	5
# indels (<= 5 bp)	0	5
# indels (> 5 bp)	0	0
Indels length	0	8

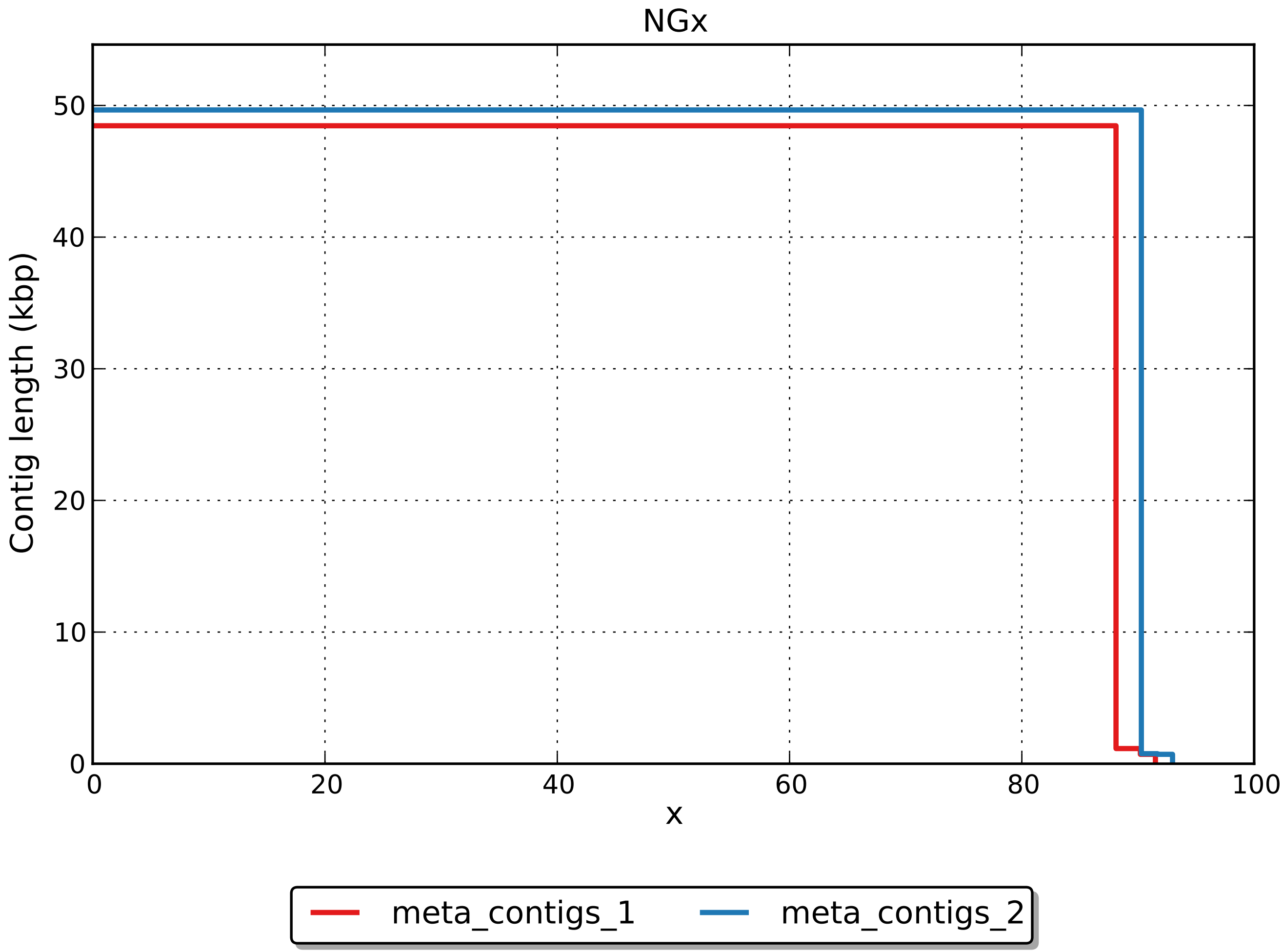
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

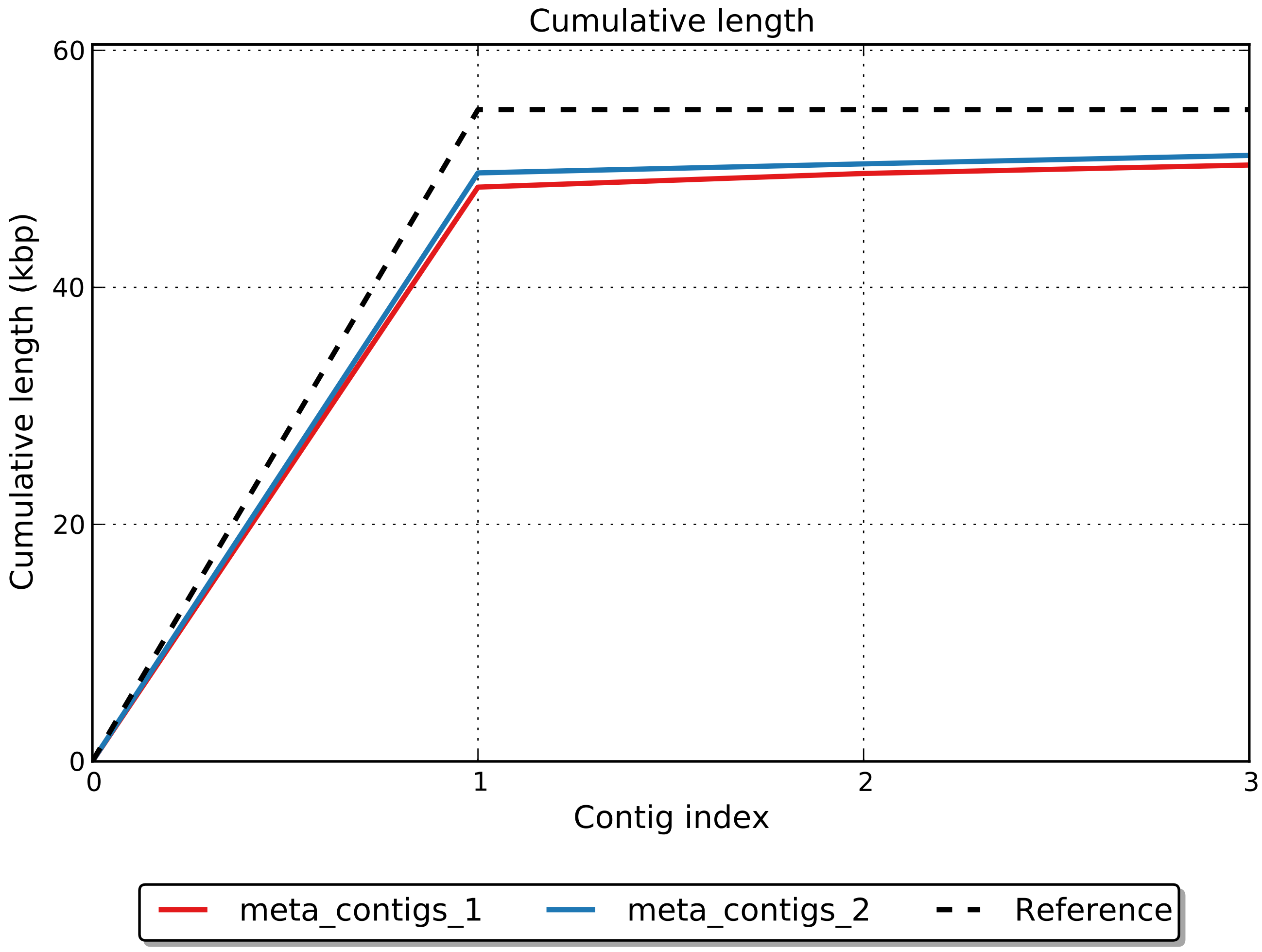
Unaligned report

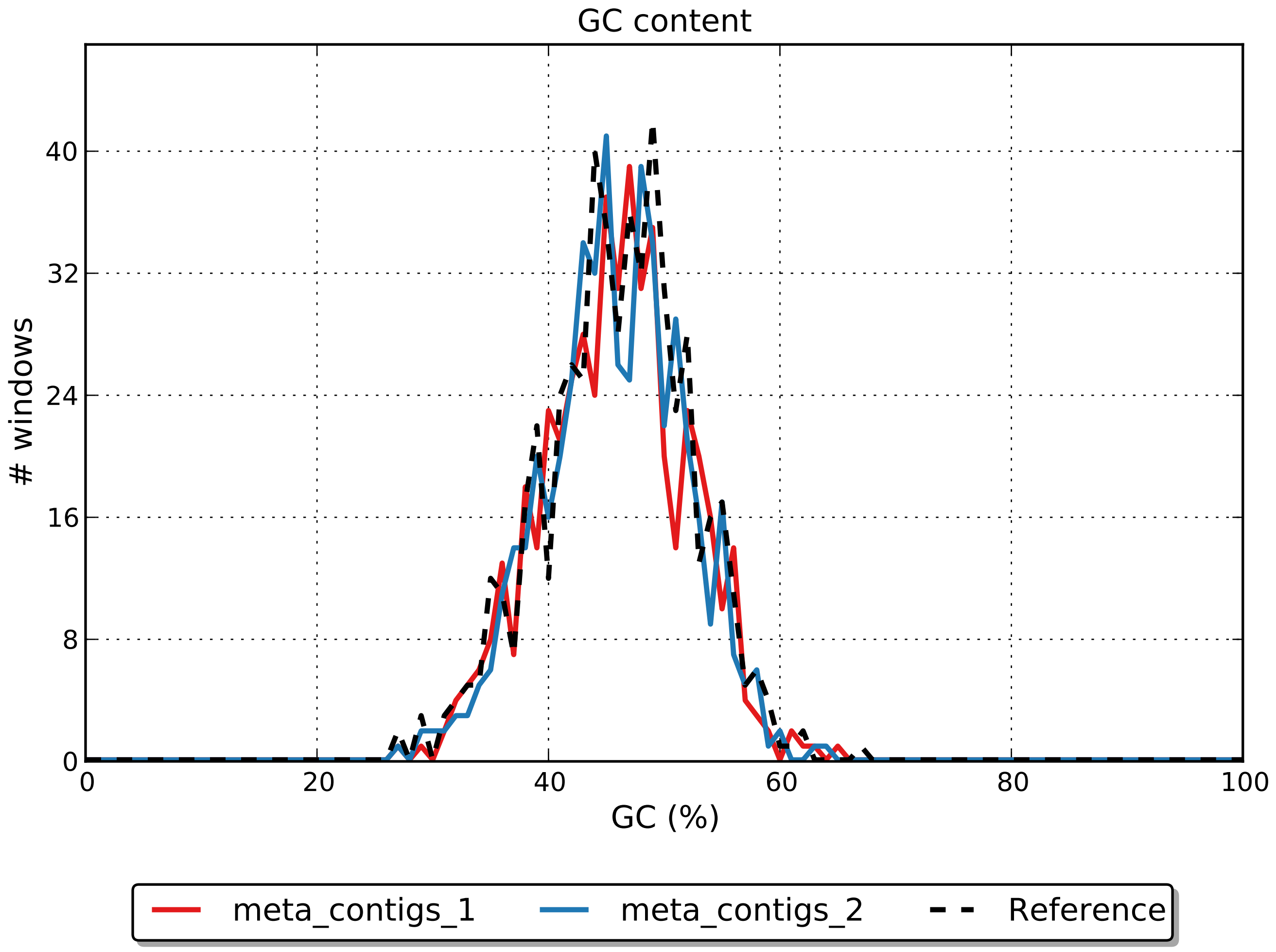
	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	1	0
Partially unaligned length	665	0
# N's	20	0

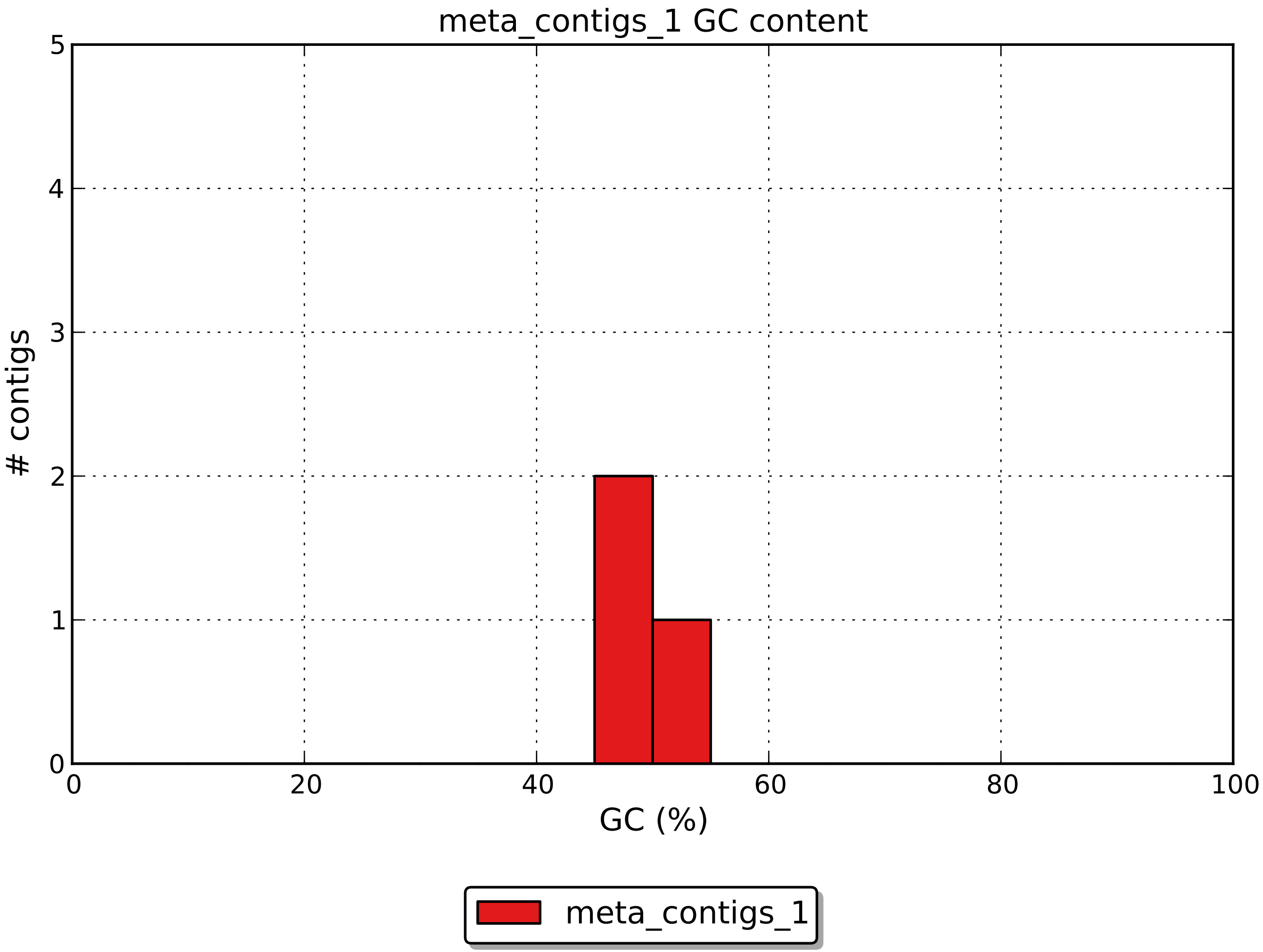
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

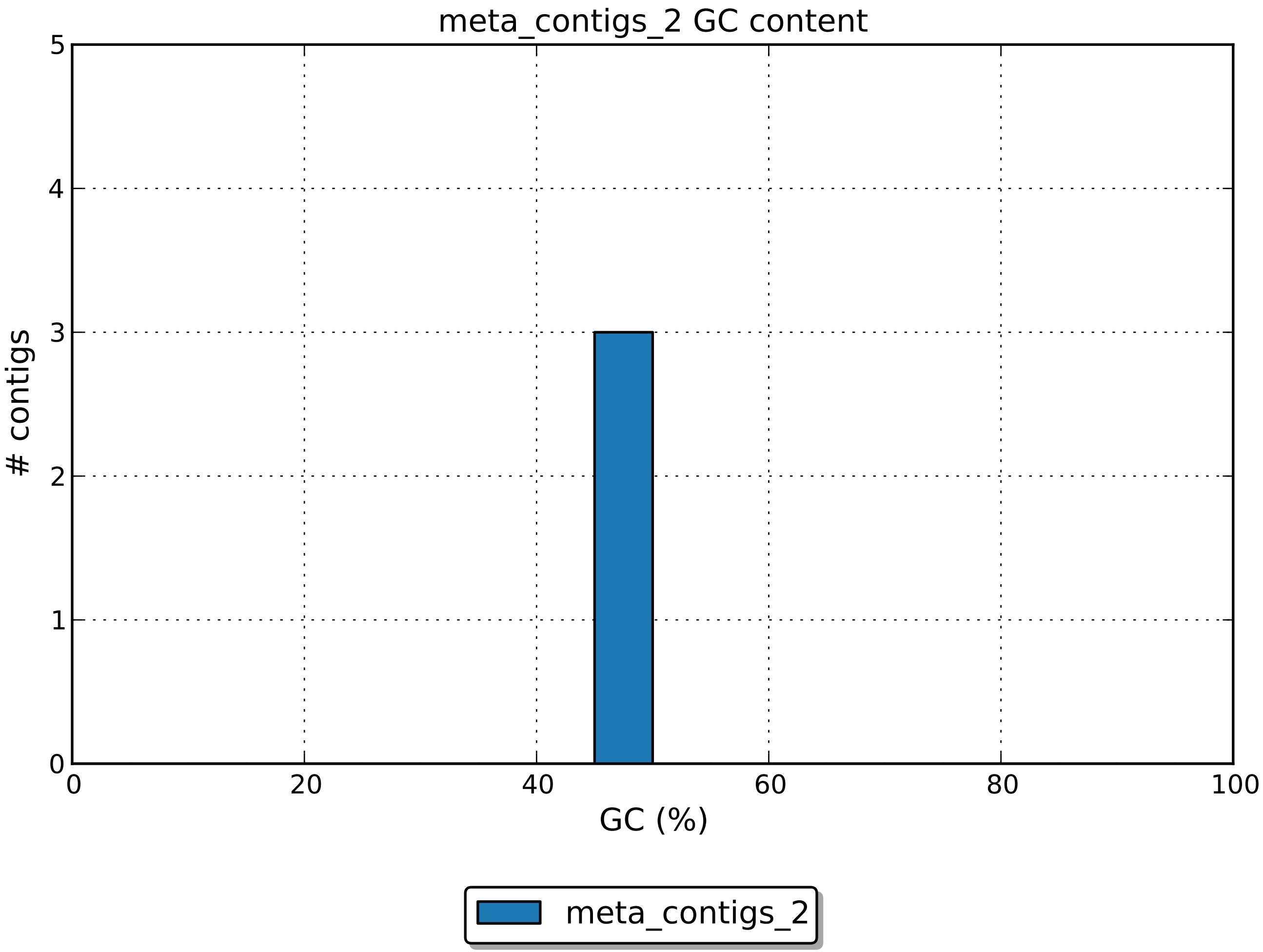

Nx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

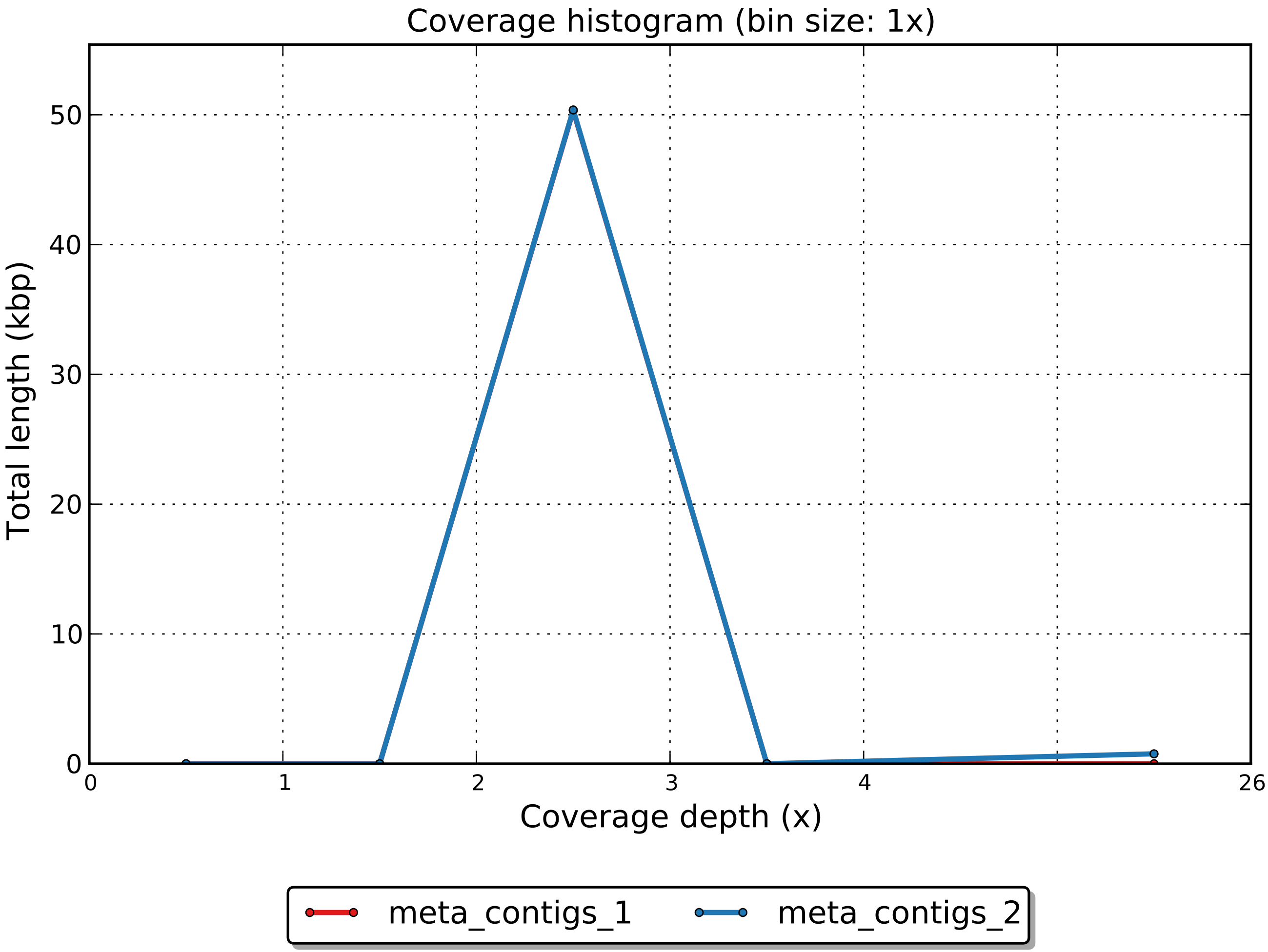

NGx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

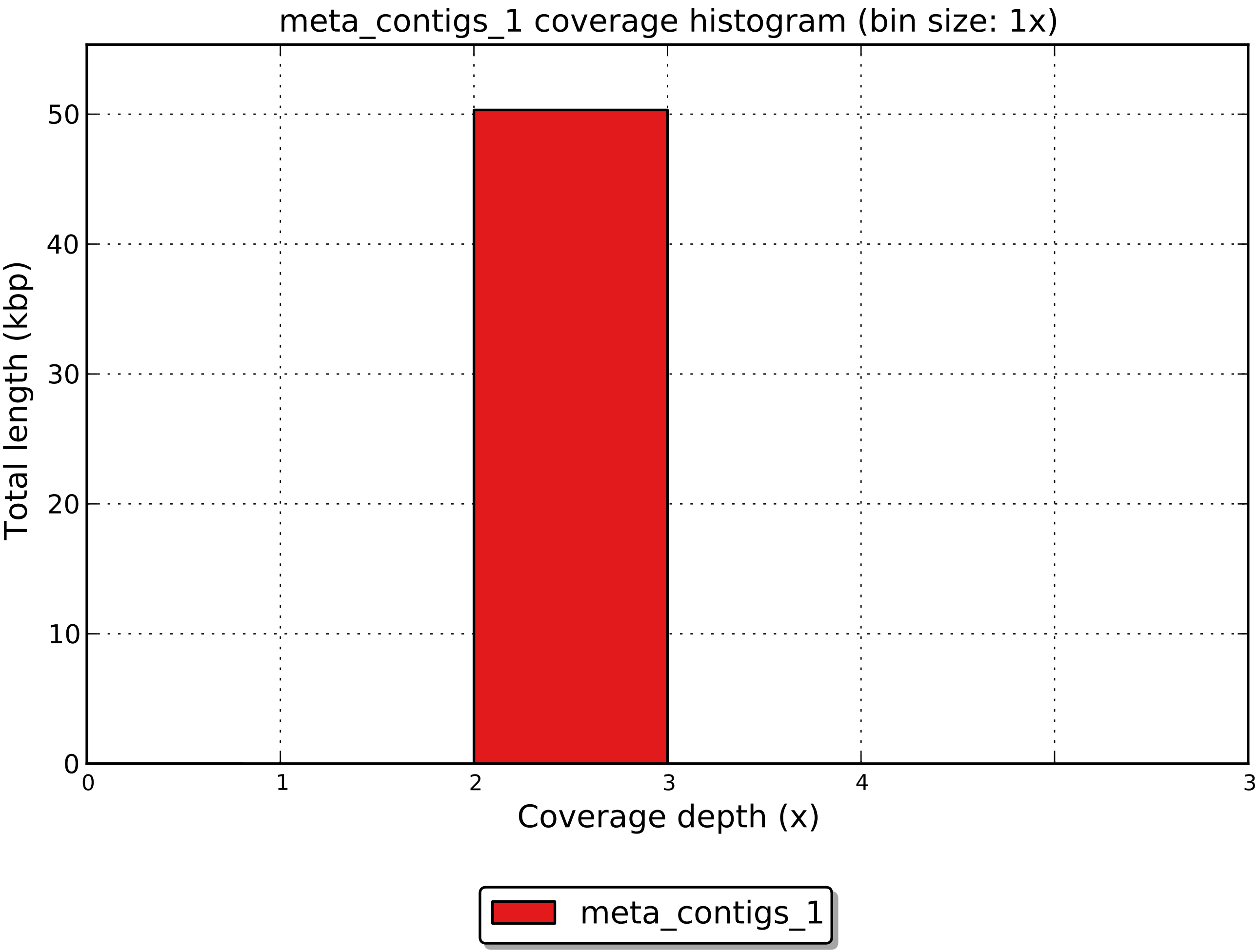

Cumulative length
Cumulative length (kbp)
0
20
40
60
0
1
2
3
Contig index
meta_contigs_1
meta_contigs_2
Reference

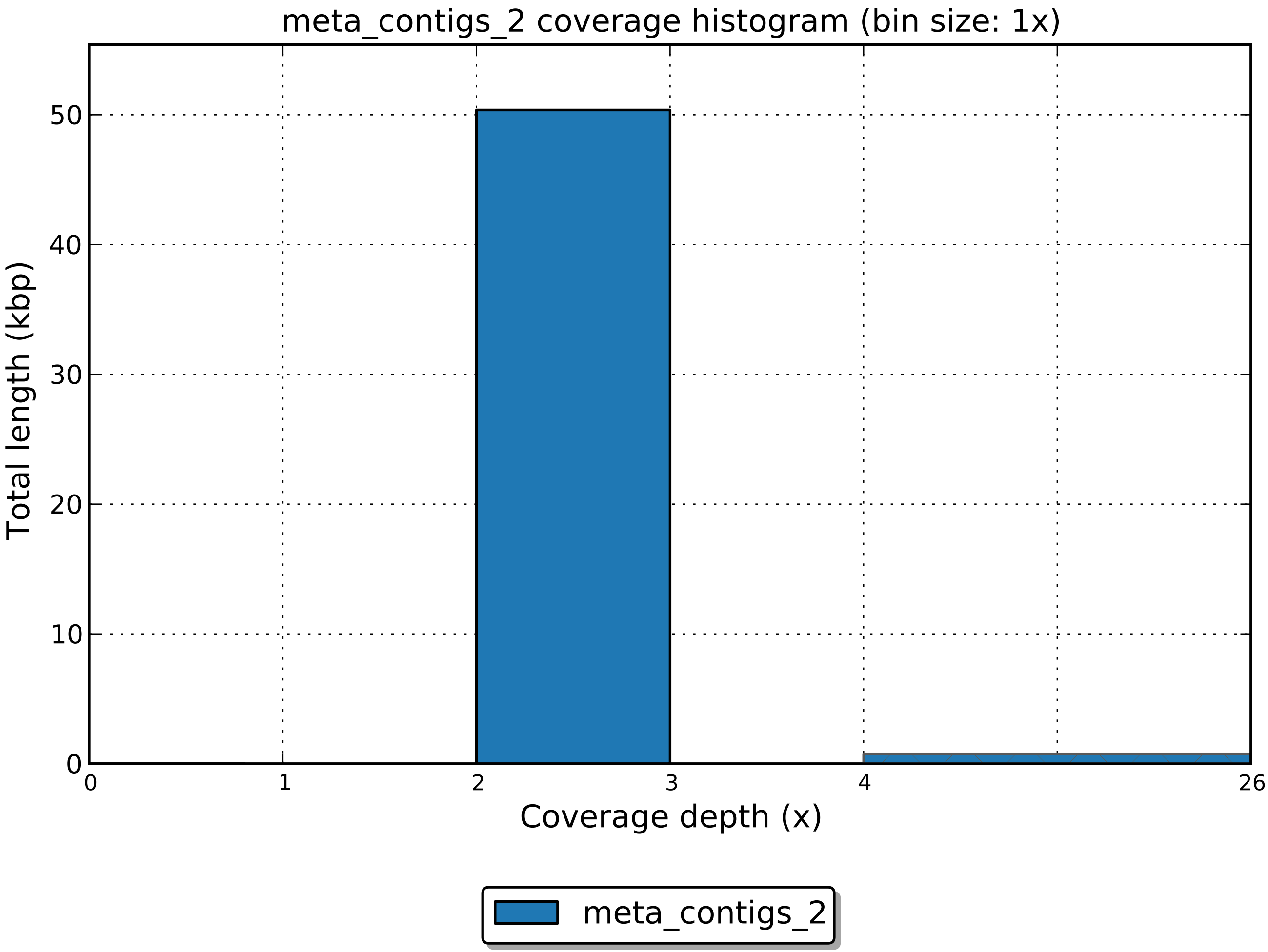

GC content
windows
0
8
16
24
32
40
0
20
40
60
80
100
GC (%)
meta_contigs_1
meta_contigs_2
Reference

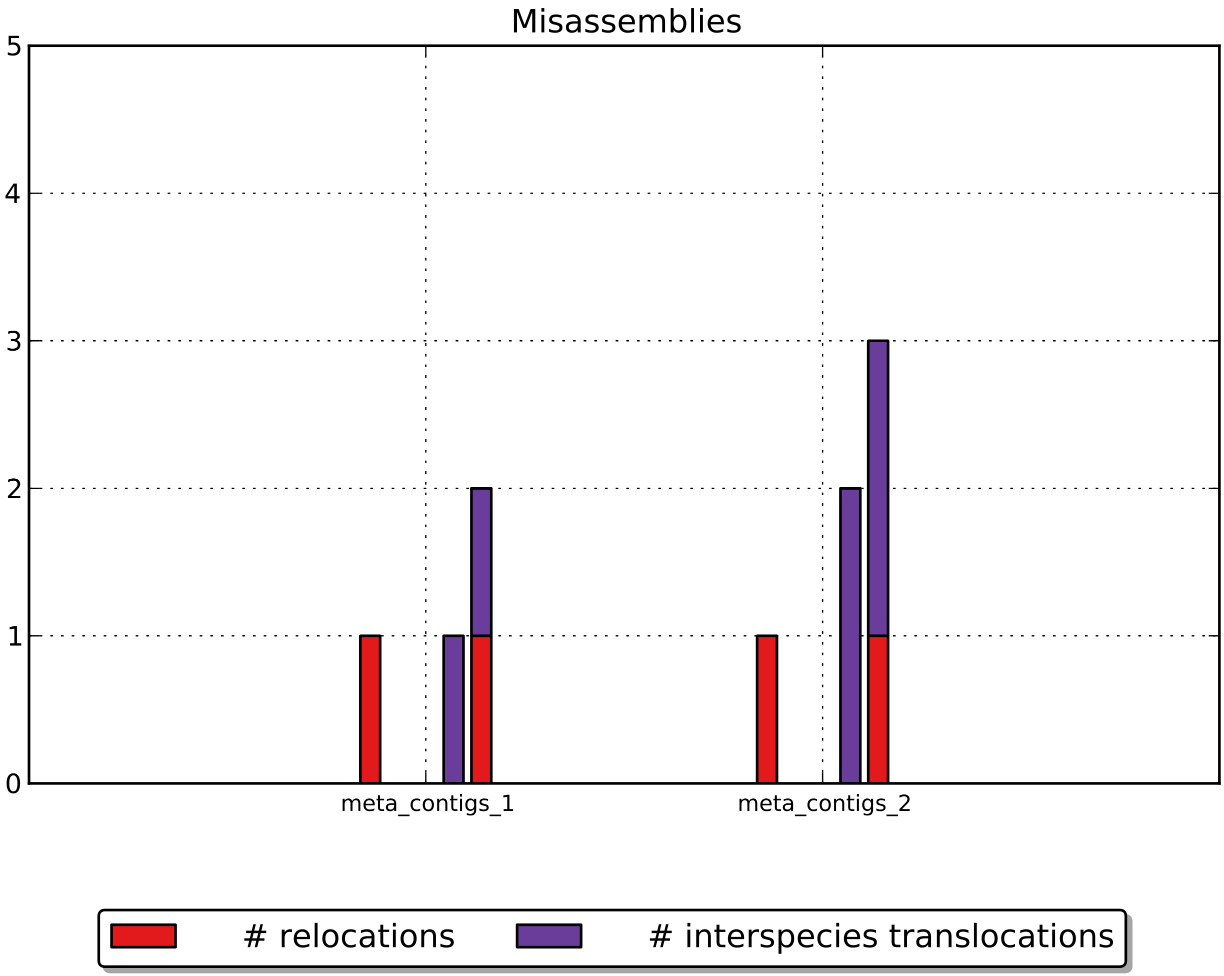

meta_contigs_1 GC content
contigs
0
1
2
3
4
5
0
20
40
60
80
100
GC (%)
meta_contigs_1

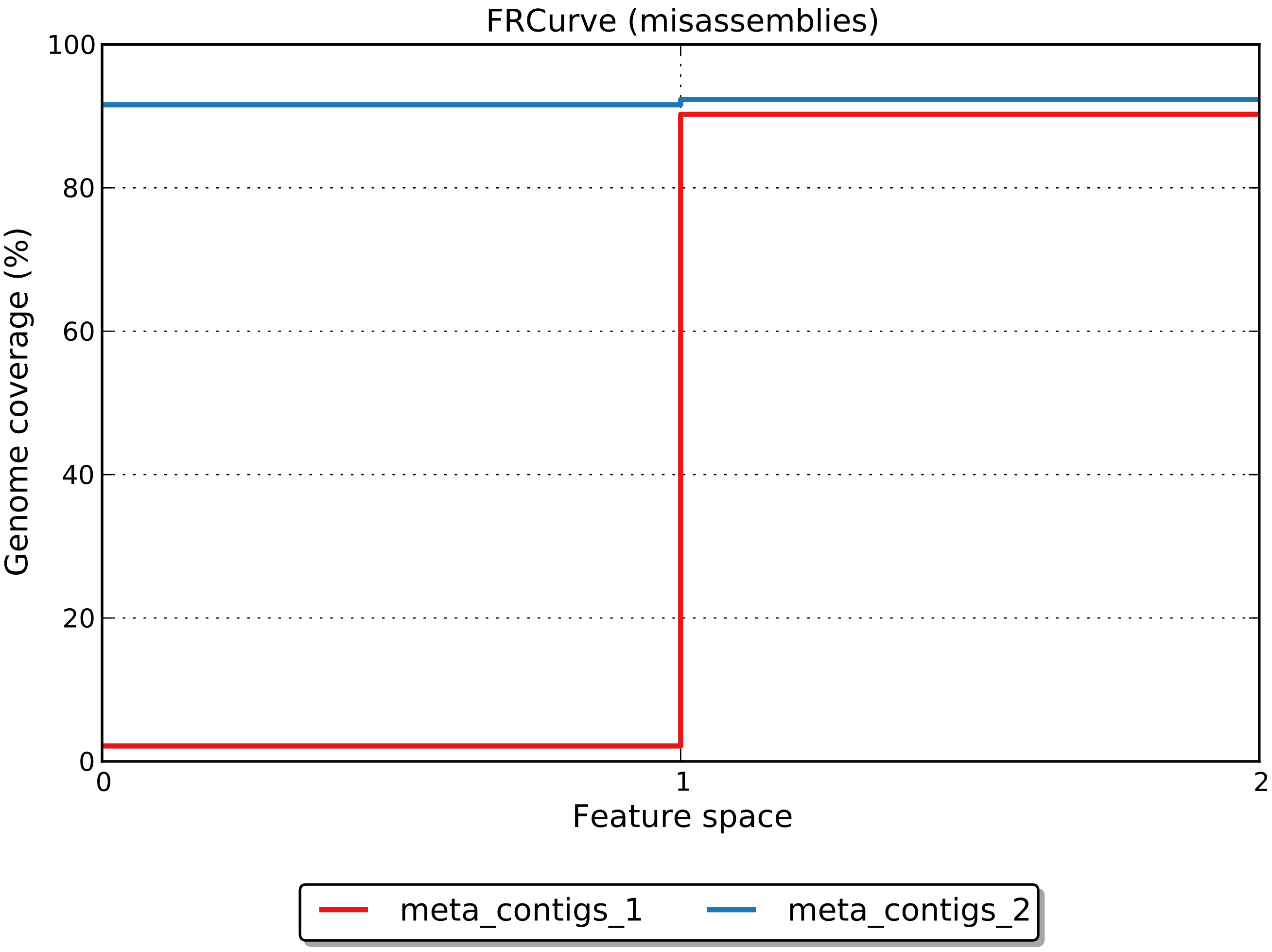

meta_contigs_2 GC content
contigs
0
1
2
3
4
5
0
20
40
60
80
100
GC (%)
meta_contigs_2

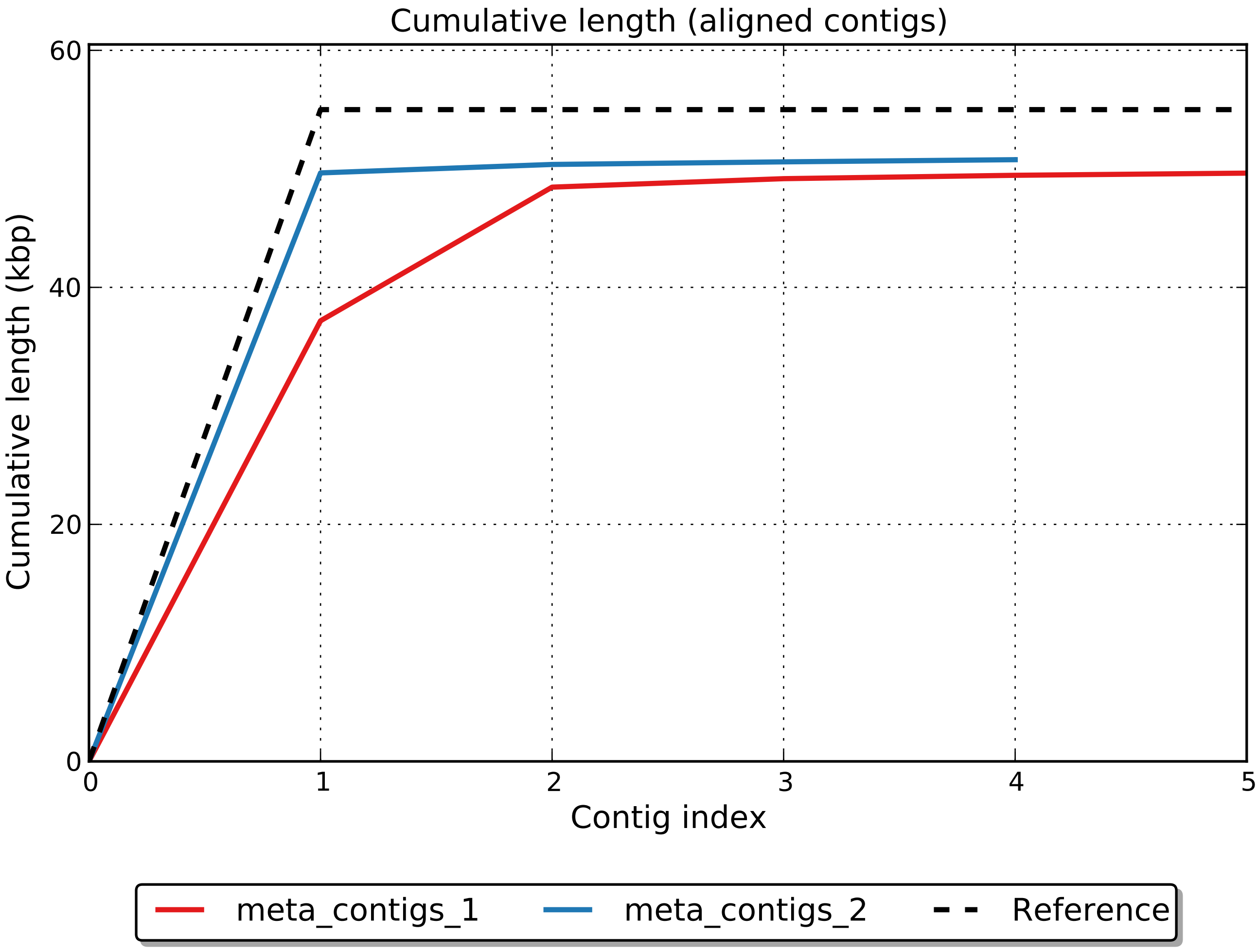
Coverage histogram (bin size: 1x)
Total length (kbp)
0
10
20
30
40
50
0
1
2
3
4
26
Coverage depth (x)
meta_contigs_1
meta_contigs_2

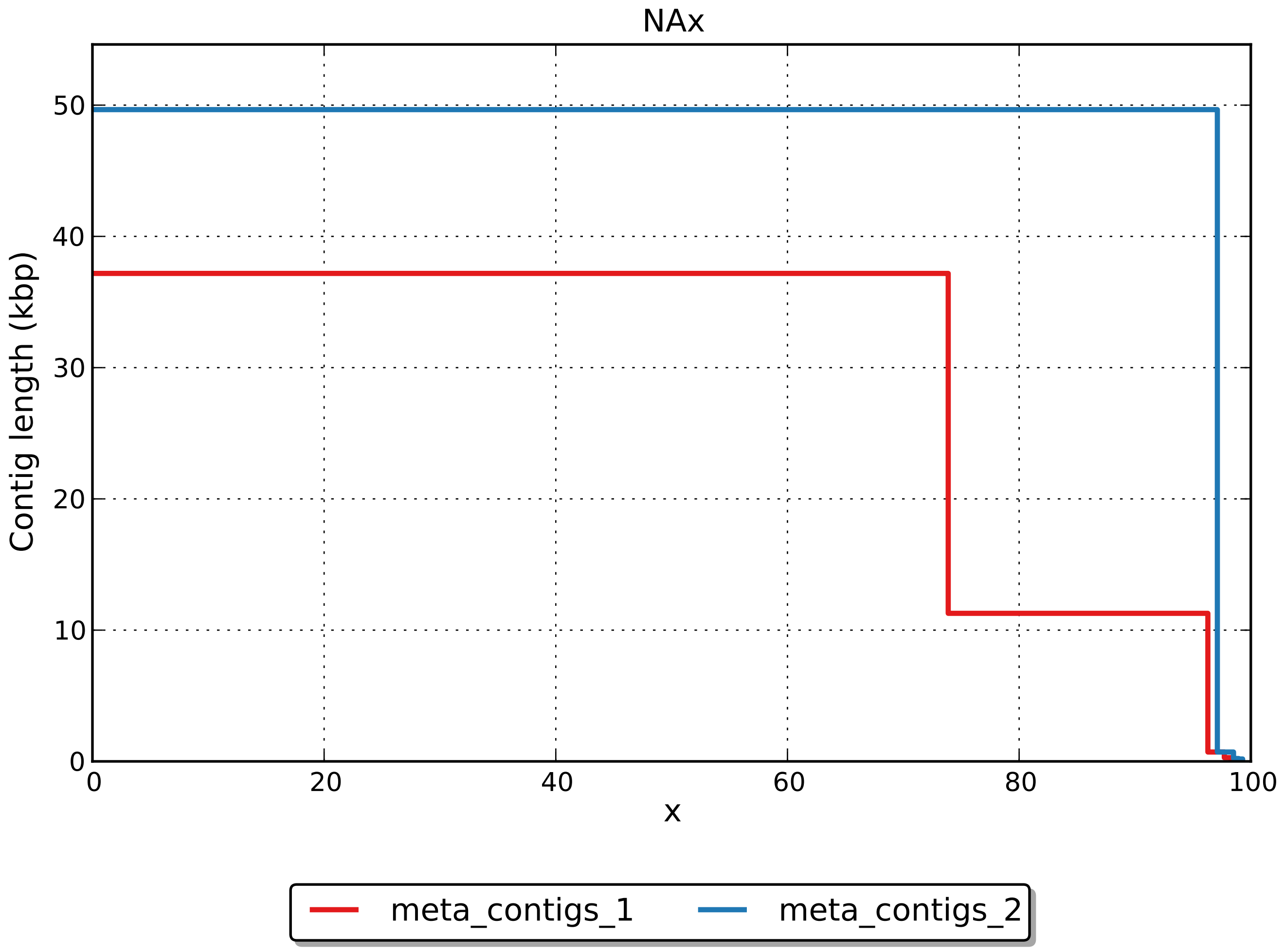

meta_contigs_1 coverage histogram (bin size: 1x)
Total length (kbp)
0
10
20
30
40
50
0
1
2
3
4
3
Coverage depth (x)
meta_contigs_1

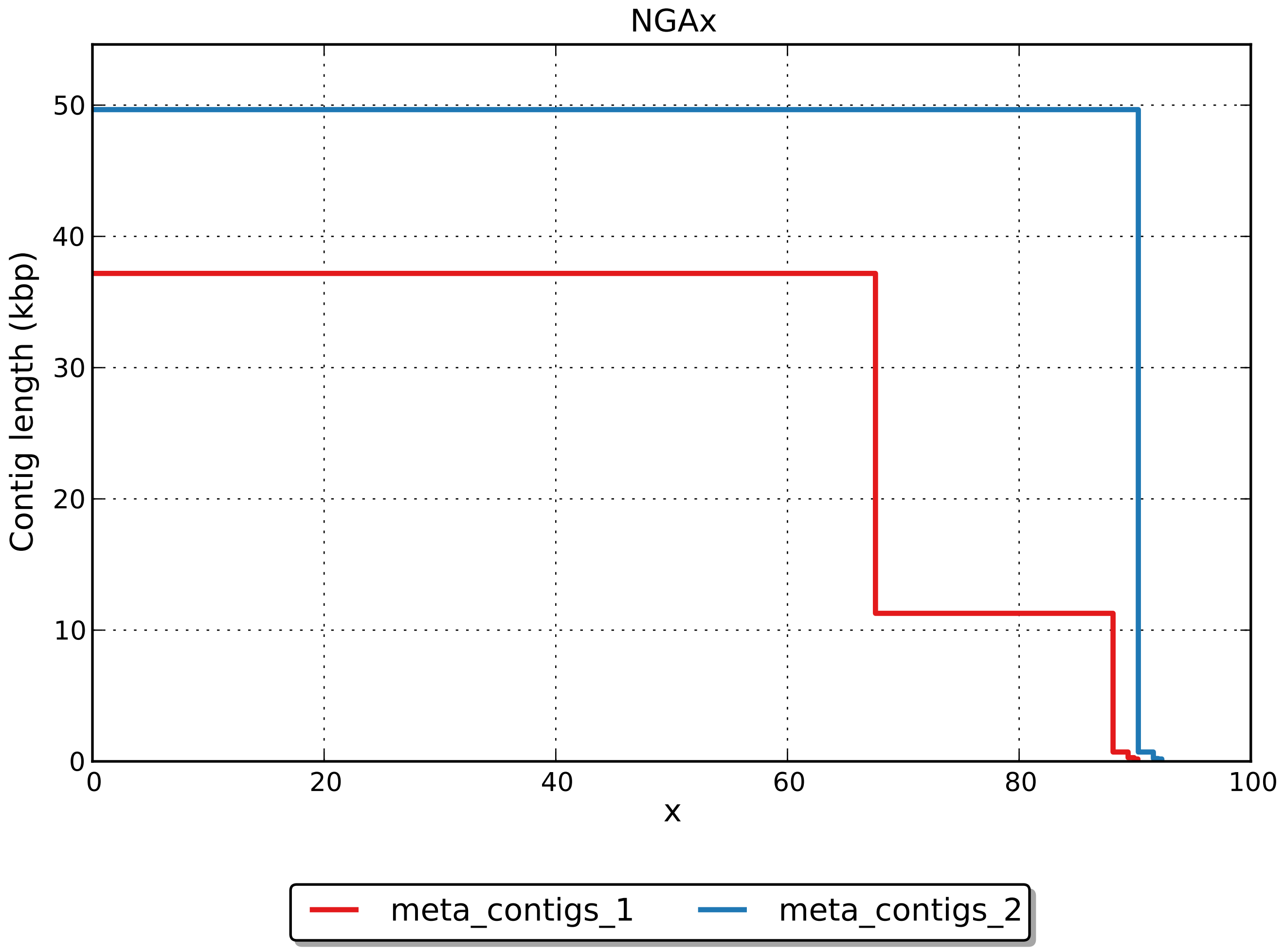

meta_contigs_2 coverage histogram (bin size: 1x)
Total length (kbp)
50
40
30
20
10
0
0
1
2
3
4
26
Coverage depth (x)
meta_contigs_2

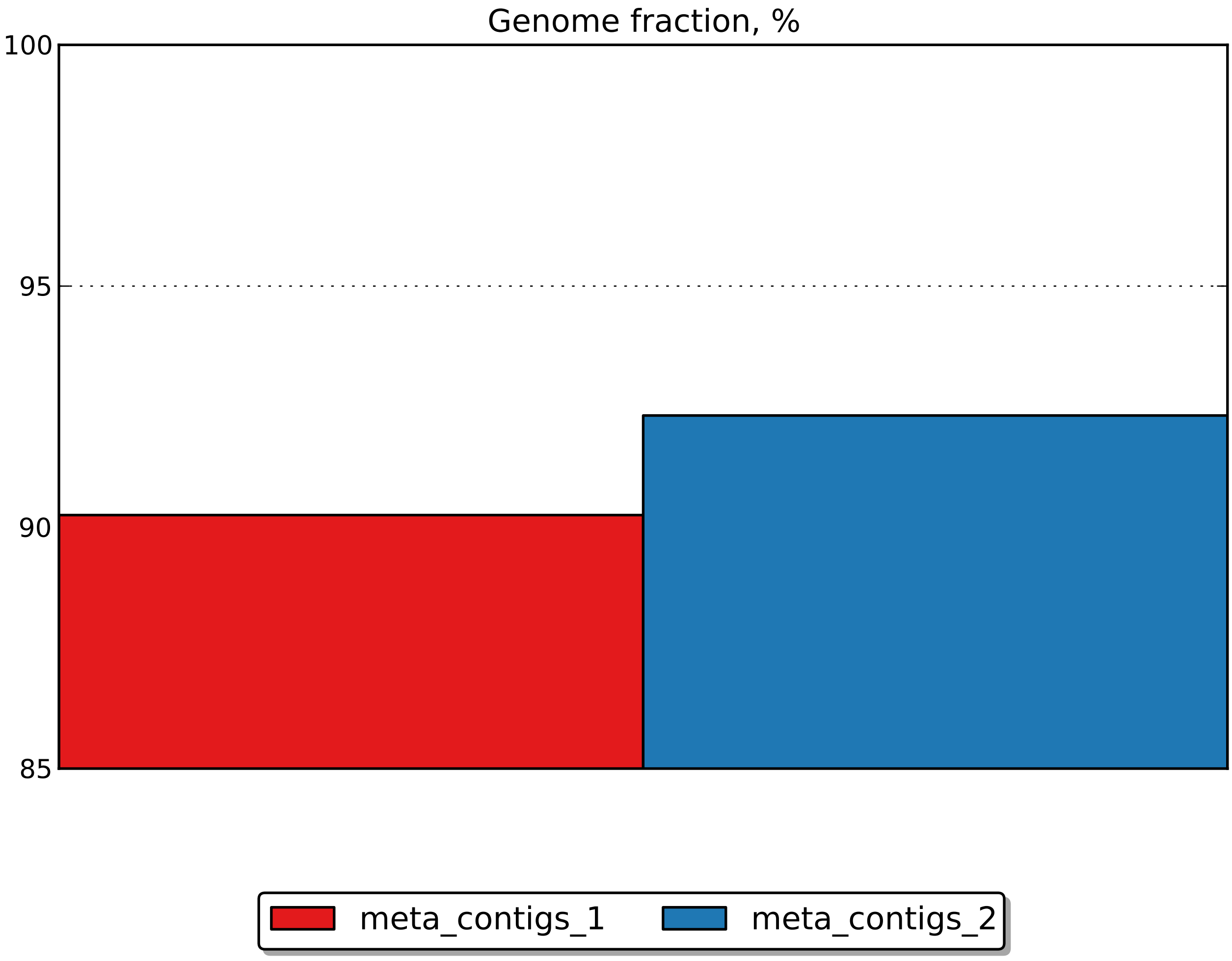

Misassemblies
5
4
3
2
1
0
meta_contigs_1
meta_contigs_2
relocations
interspecies translocations


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)
60
40
20
0
0
1
2
3
4
5
Contig index
meta_contigs_1
meta_contigs_2
Reference


NAx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2


NGAx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2


Genome fraction, %
100
95
90
85
meta_contigs_1
meta_contigs_2