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)	1	1
Total length (>= 1000 bp)	56247	55421
Total length (>= 5000 bp)	55106	55421
Total length (>= 10000 bp)	55106	55421
Total length (>= 25000 bp)	55106	55421
Total length (>= 50000 bp)	55106	55421
# contigs	5	1
Largest contig	55106	55421
Total length	58663	55421
Reference length	1864998	1864998
GC (%)	50.17	50.07
Reference GC (%)	49.72	49.72
N50	55106	55421
N75	55106	55421
L50	1	1
L75	1	1
# misassemblies	2	2
# misassembled contigs	1	1
Misassembled contigs length	55106	55421
# local misassemblies	3	3
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	3.085	2.911
Duplication ratio	1.020	1.021
# N's per 100 kbp	1.70	0.00
# mismatches per 100 kbp	493.57	488.06
# indels per 100 kbp	33.02	33.15
Largest alignment	31432	31432
NA50	31432	31432
NGA50	-	-
NA75	11261	11575
LA50	1	1
LA75	3	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

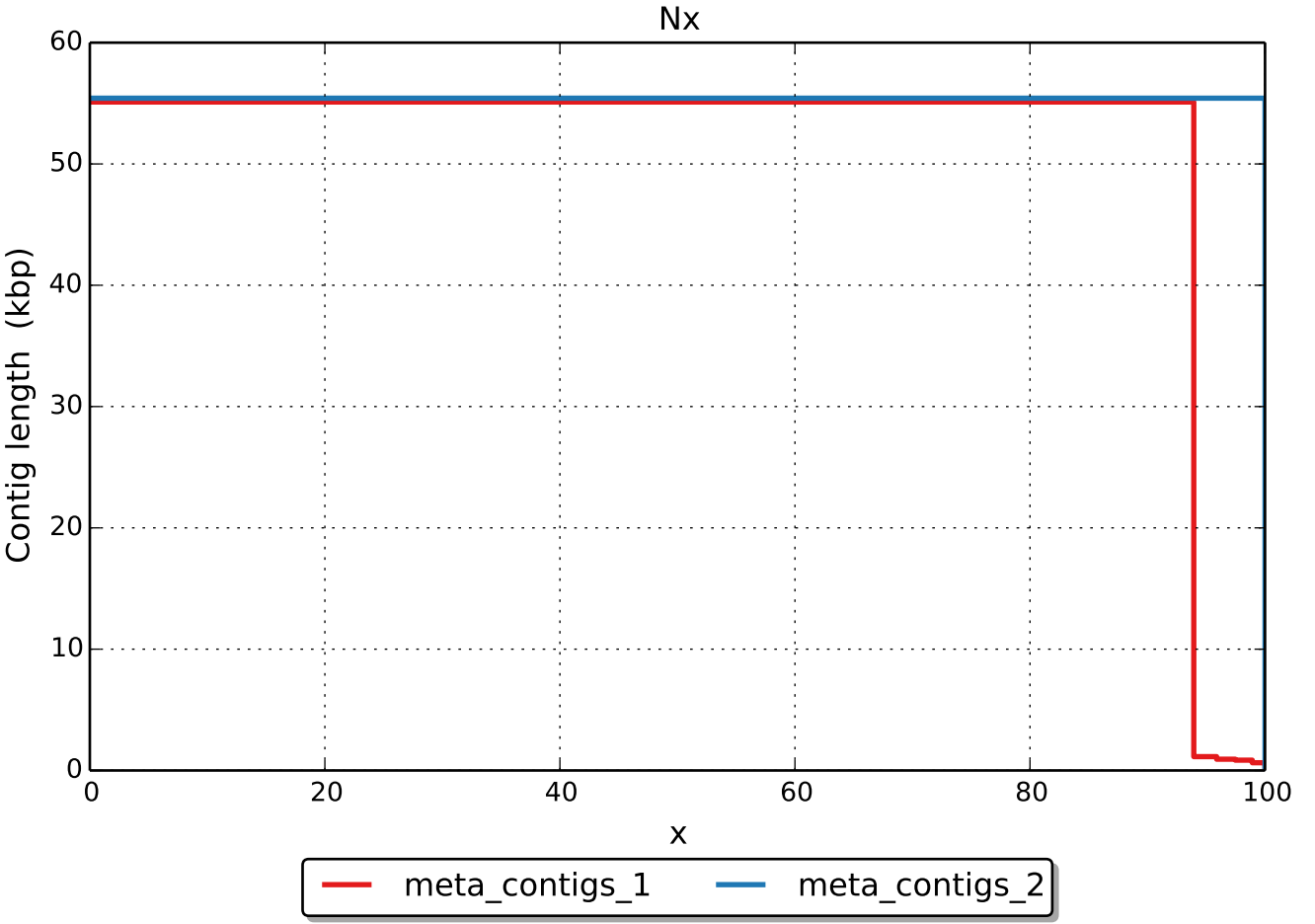
	meta_contigs_1	meta_contigs_2
# misassemblies	2	2
# relocations	2	2
# translocations	0	0
# inversions	0	0
# possibly misassembled contigs	1	1
# misassembled contigs	1	1
Misassembled contigs length	55106	55421
# local misassemblies	3	3
# mismatches	284	265
# indels	19	18
# short indels	18	17
# long indels	1	1
Indels length	32	31

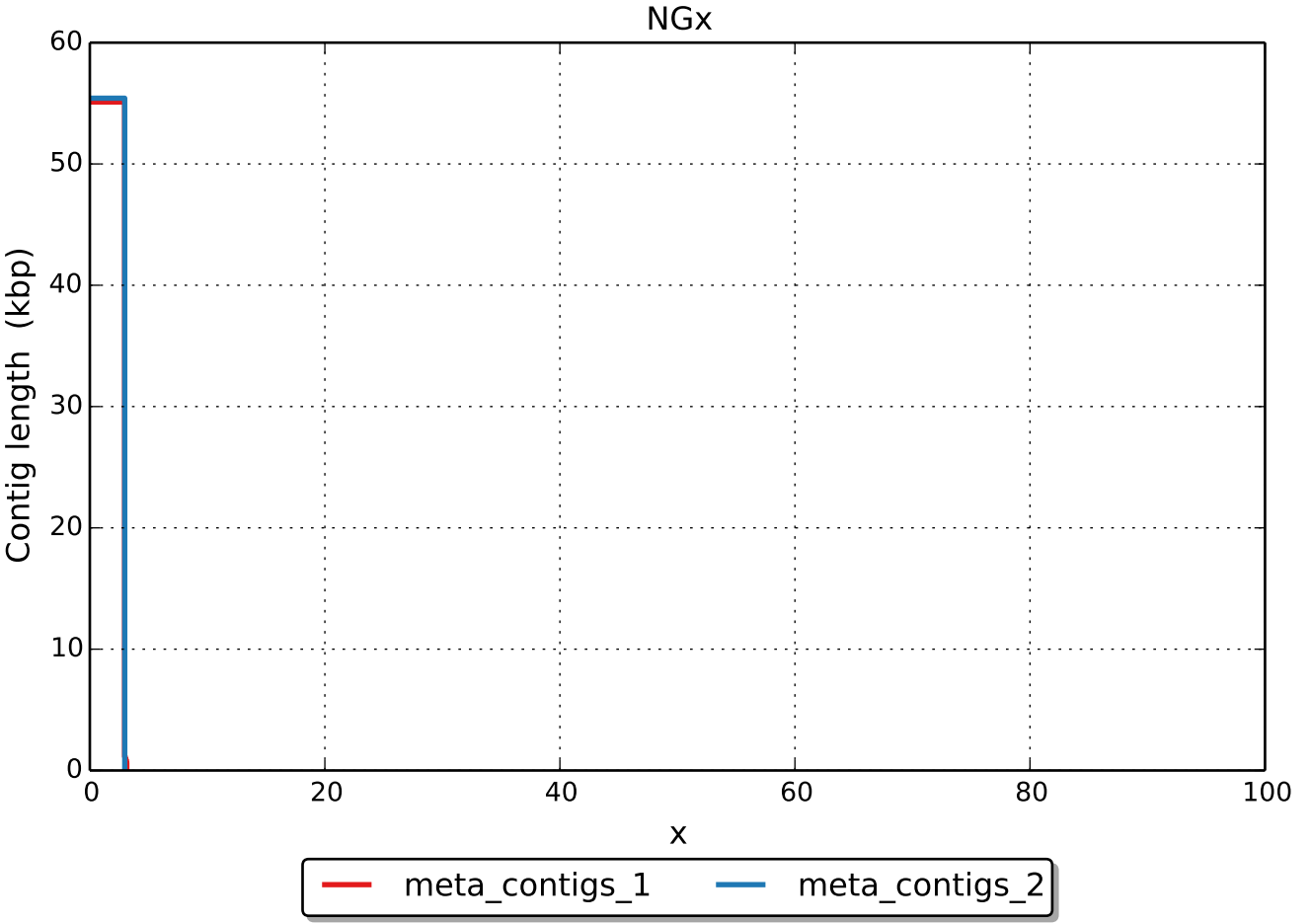
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

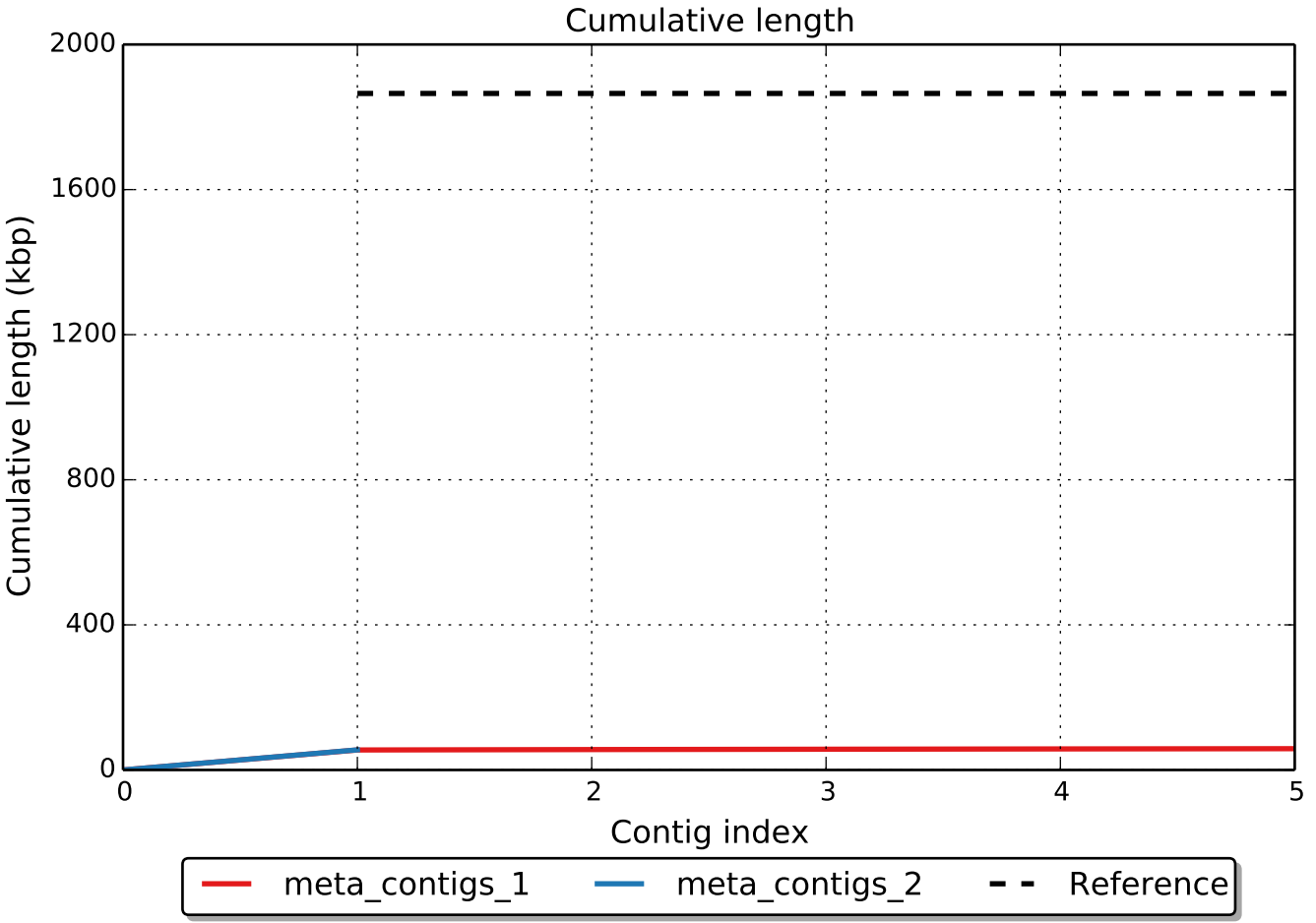
Unaligned report

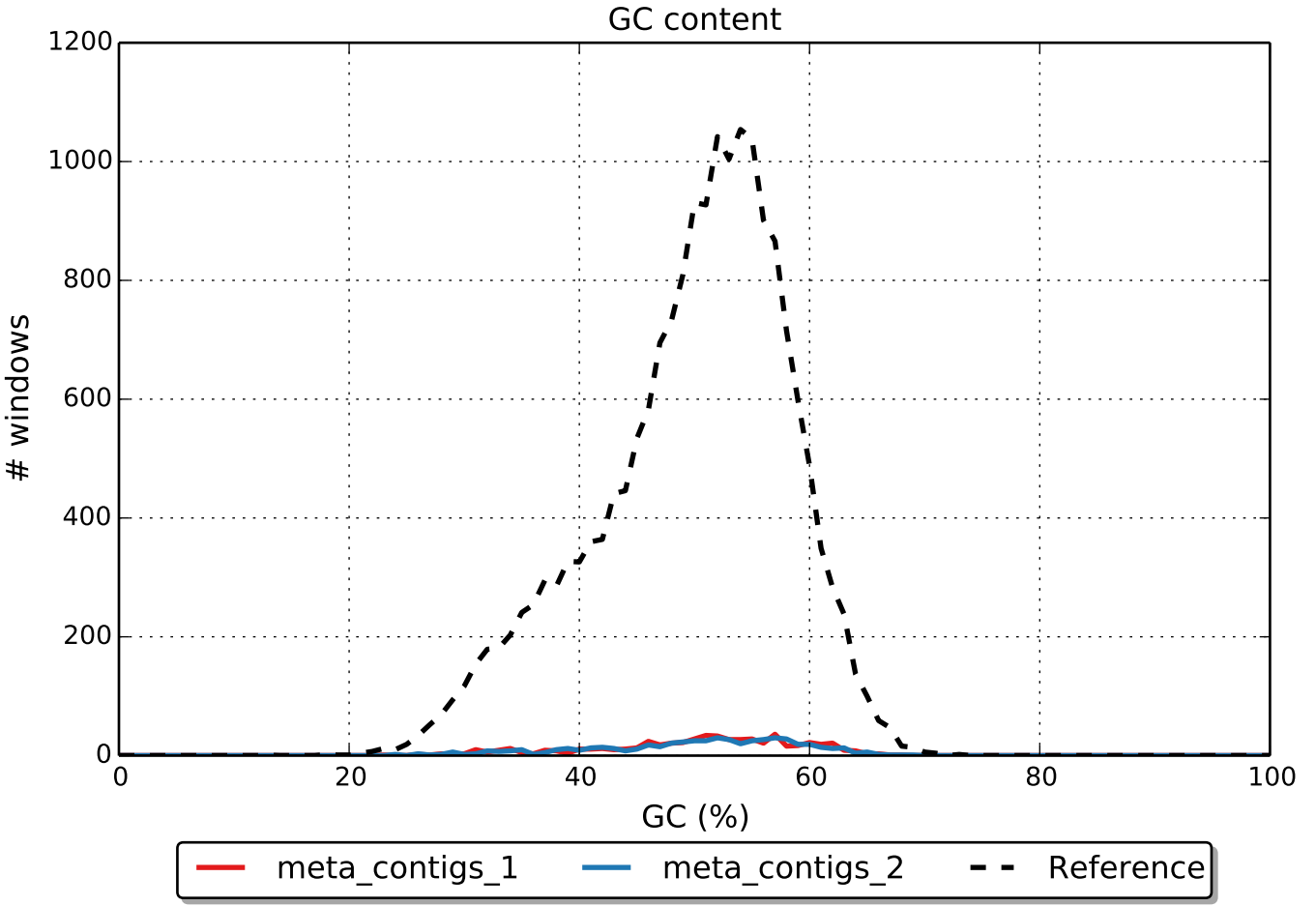
	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	1	0

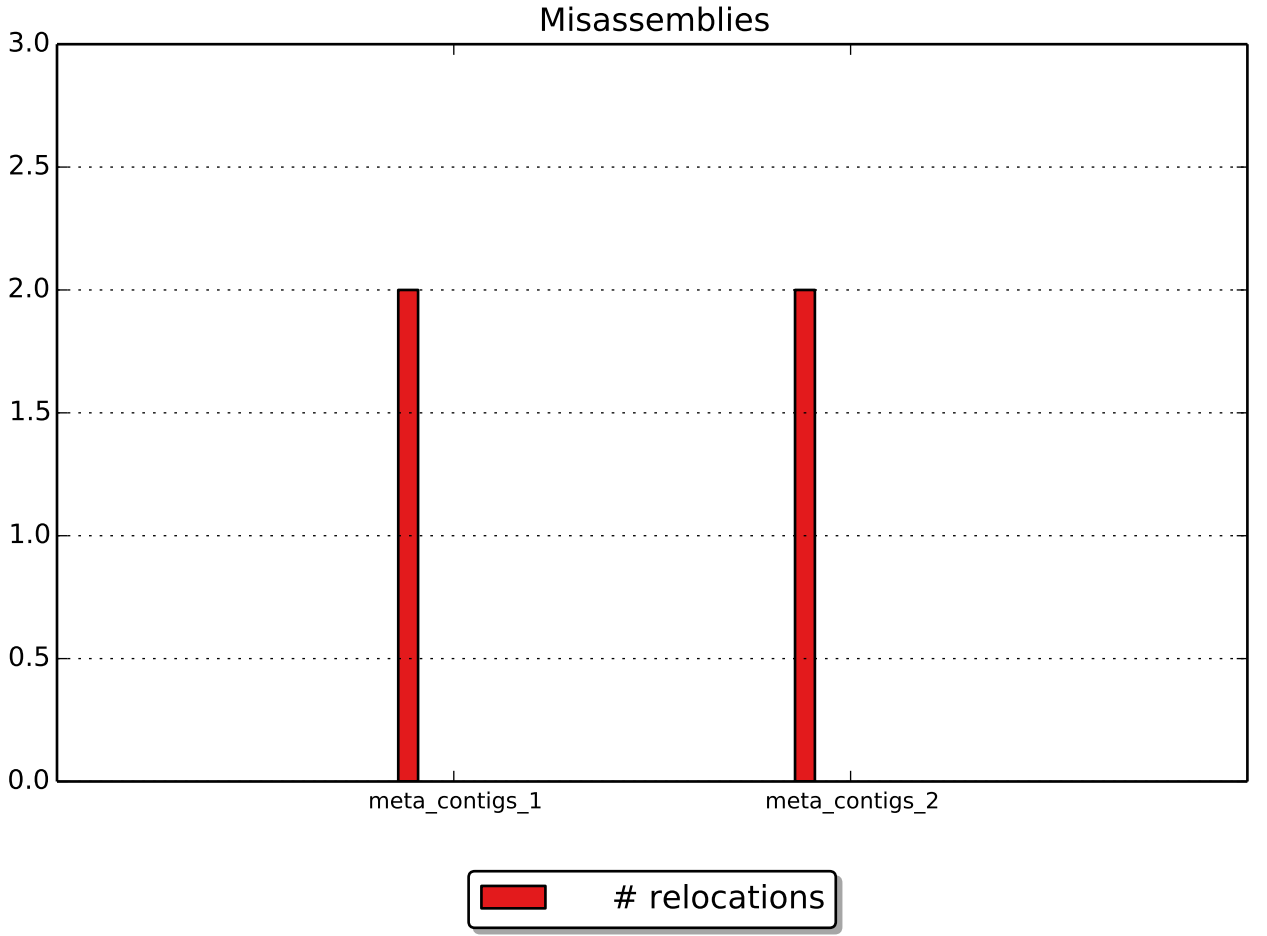
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

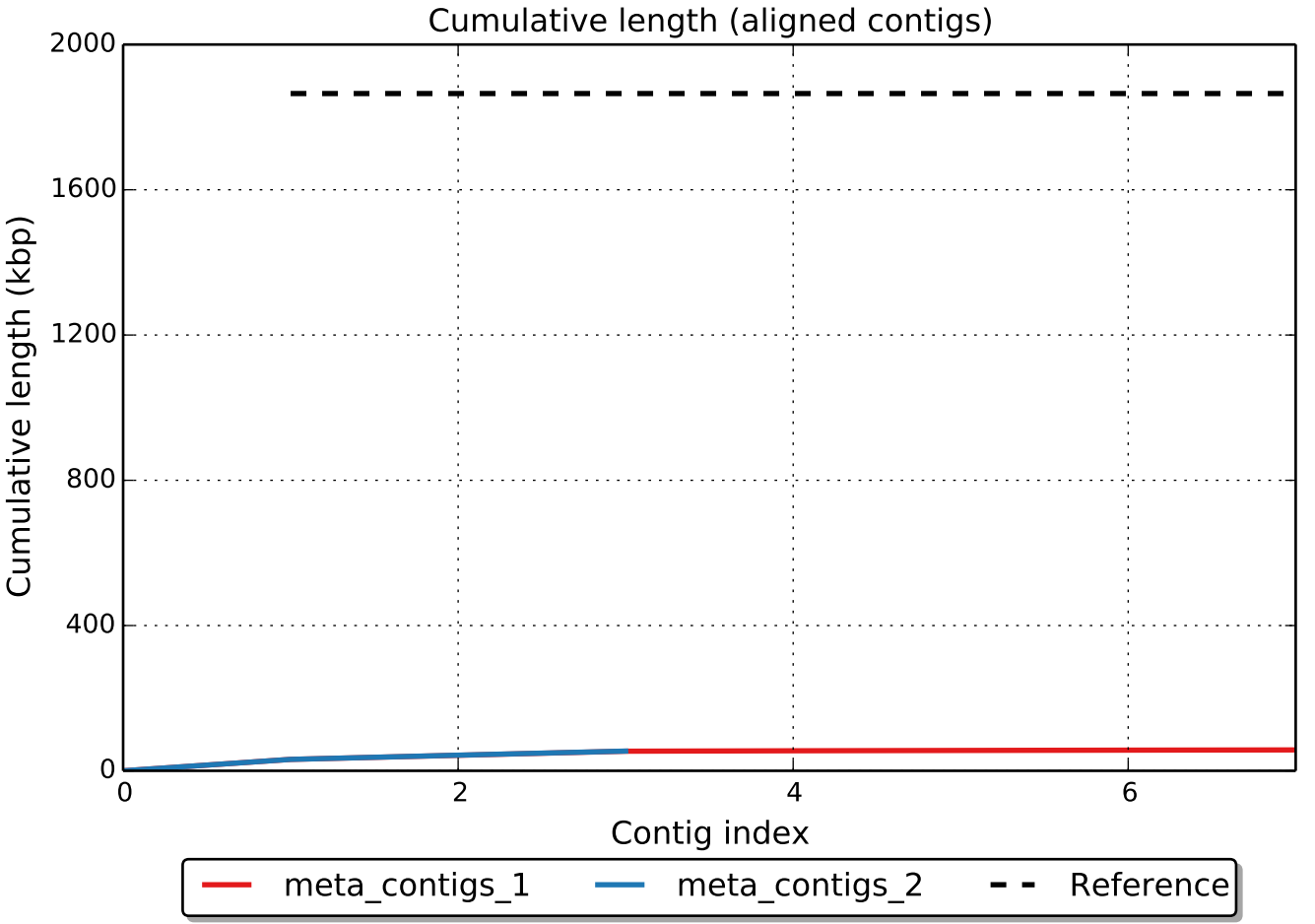

Nx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

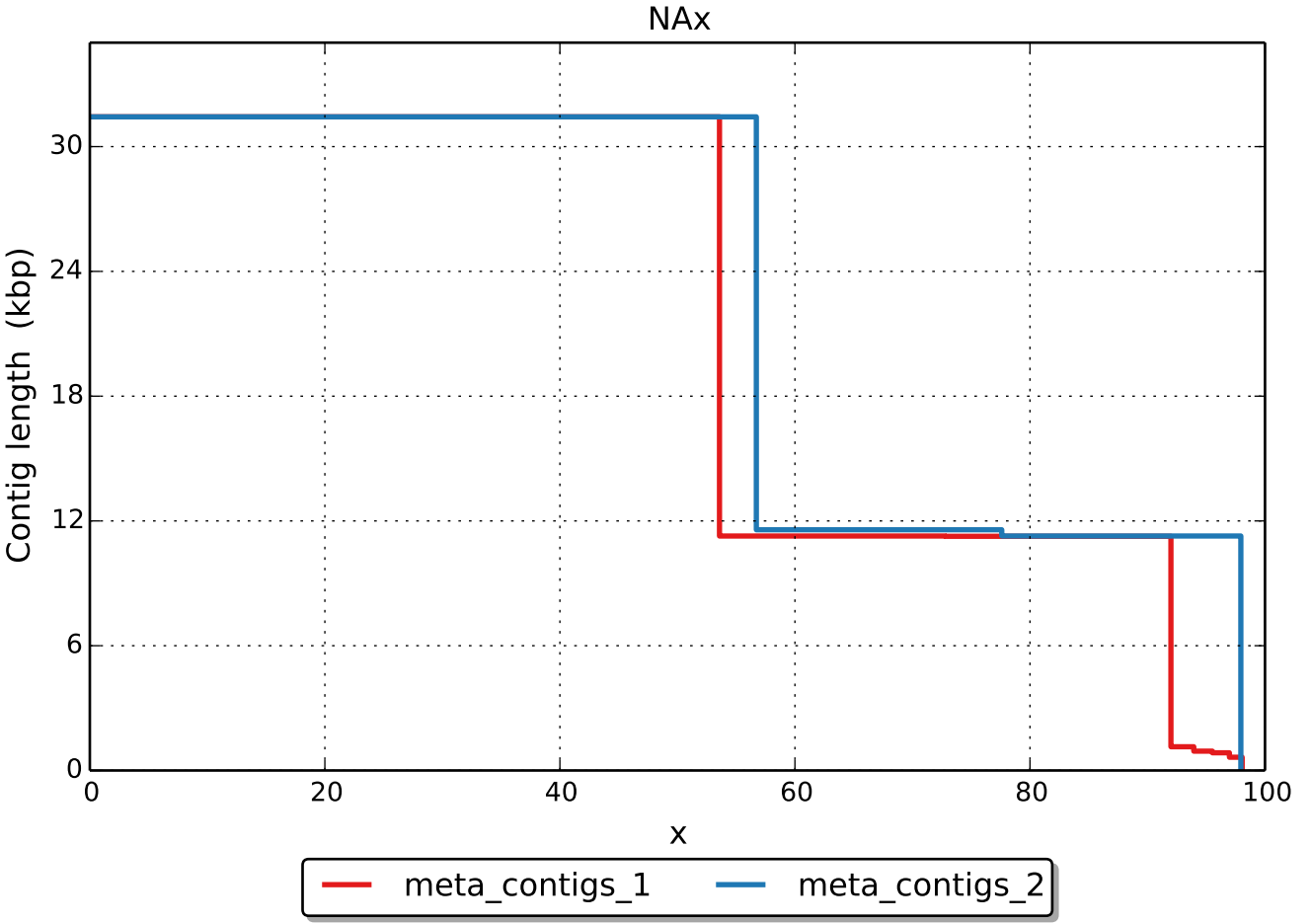

NGx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

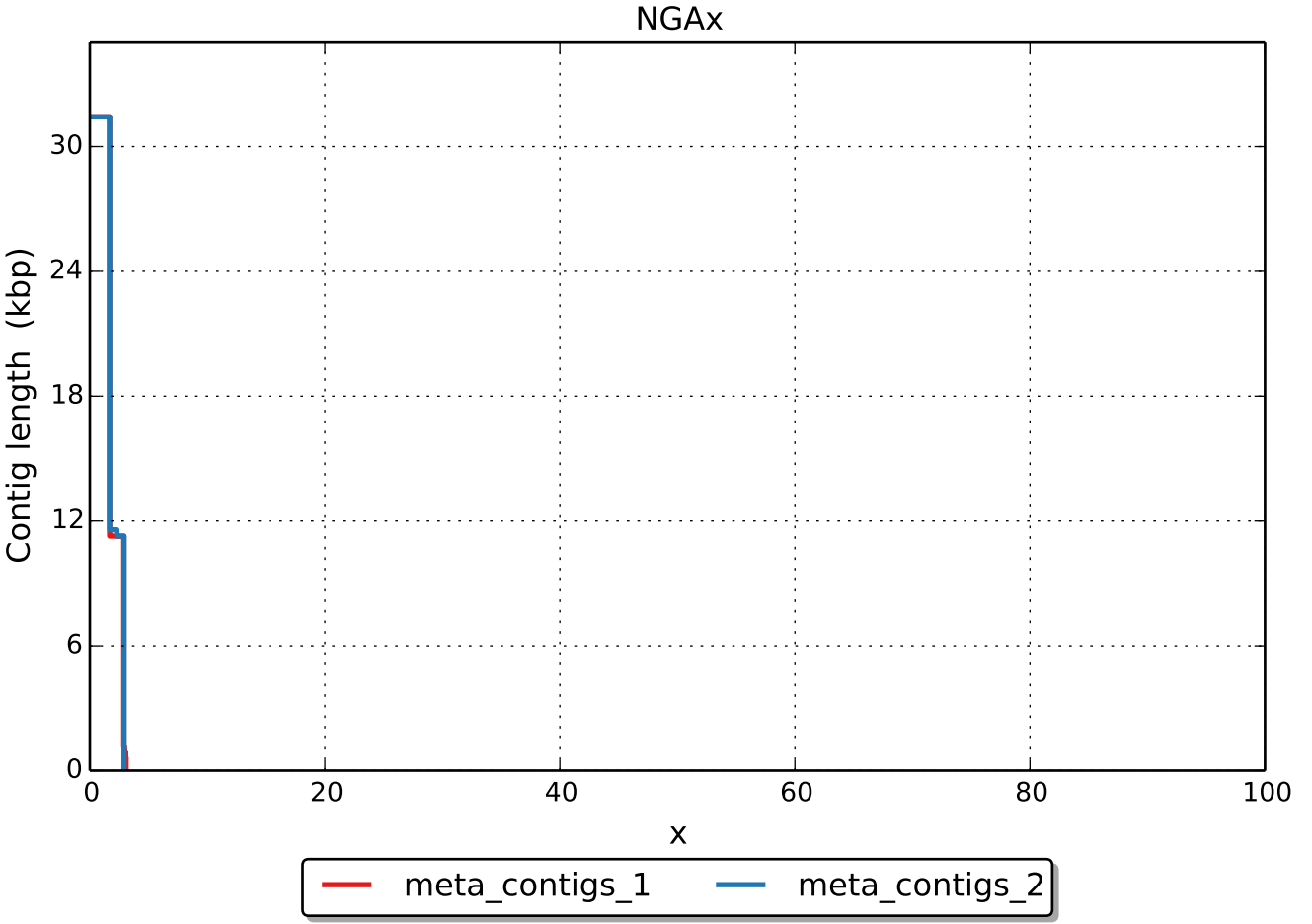

Cumulative length
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
1
2
3
4
5
Contig index
meta_contigs_1
meta_contigs_2
Reference

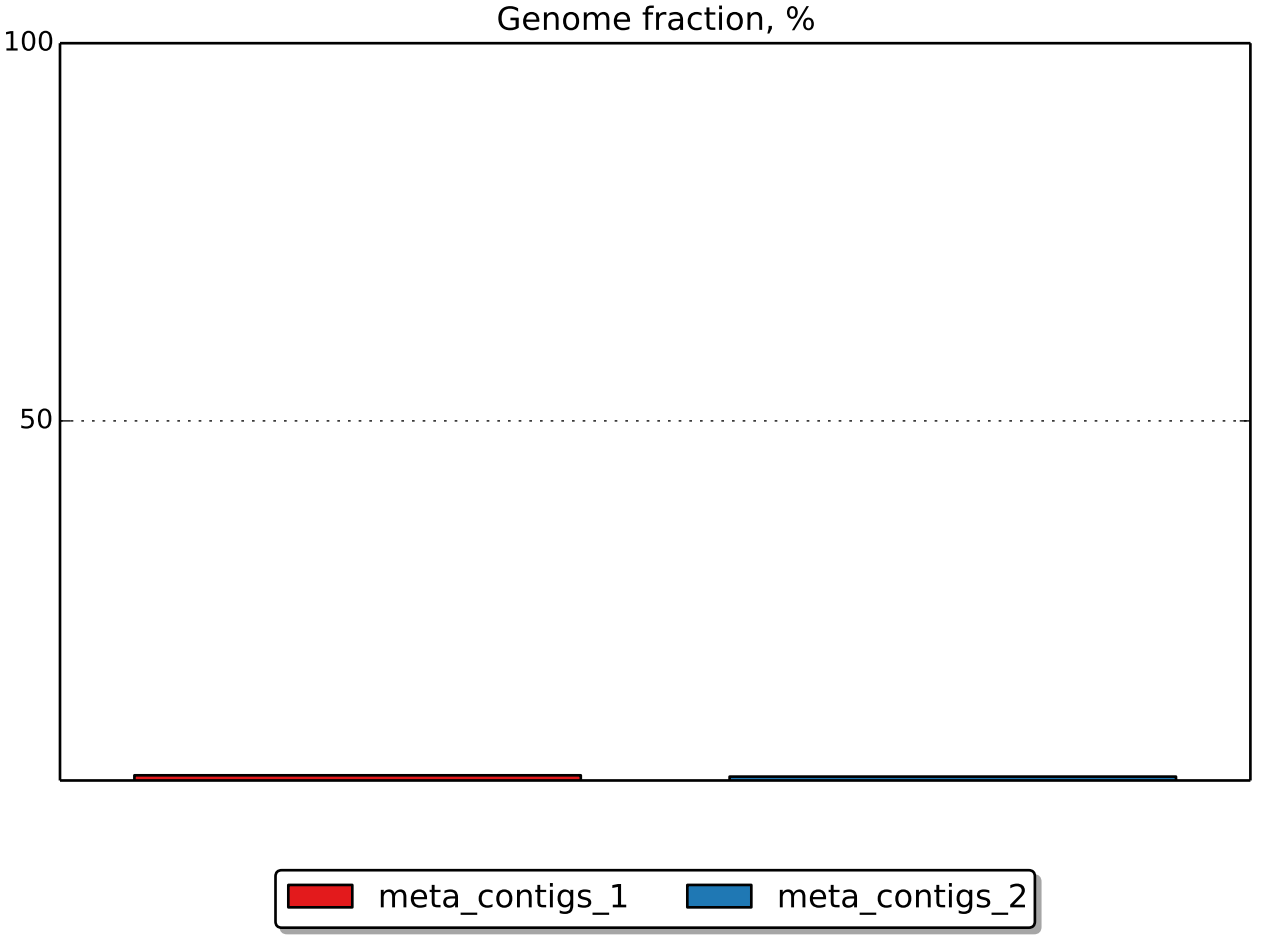

GC content
1200
1000
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
meta_contigs_1
meta_contigs_2
Reference


Misassemblies
3.0
2.5
2.0
1.5
1.0
0.5
0.0
meta_contigs_1
meta_contigs_2
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
2
4
6
Contig index
meta_contigs_1
meta_contigs_2
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2


Genome fraction, %
100
50
meta_contigs_1
meta_contigs_2