Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 1000 bp)	6	4
# contigs (>= 5000 bp)	3	4
# contigs (>= 10000 bp)	3	3
# contigs (>= 25000 bp)	1	1
# contigs (>= 50000 bp)	0	0
Total length (>= 1000 bp)	64988	60775
Total length (>= 5000 bp)	56606	60775
Total length (>= 10000 bp)	56606	53787
Total length (>= 25000 bp)	27969	27260
Total length (>= 50000 bp)	0	0
# contigs	11	7
Largest contig	27969	27260
Total length	69110	63015
Reference length	1999618	1999618
GC (%)	40.75	40.67
Reference GC (%)	38.87	38.87
N50	17535	16099
N75	11102	10428
L50	2	2
L75	3	3
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	3.212	3.146
Duplication ratio	1.076	1.002
# N's per 100 kbp	18.81	0.00
# mismatches per 100 kbp	70.05	20.67
# indels per 100 kbp	7.78	4.77
Largest alignment	27969	27260
NA50	17534	16099
NGA50	-	-
NA75	11101	10428
LA50	2	2
LA75	3	3

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

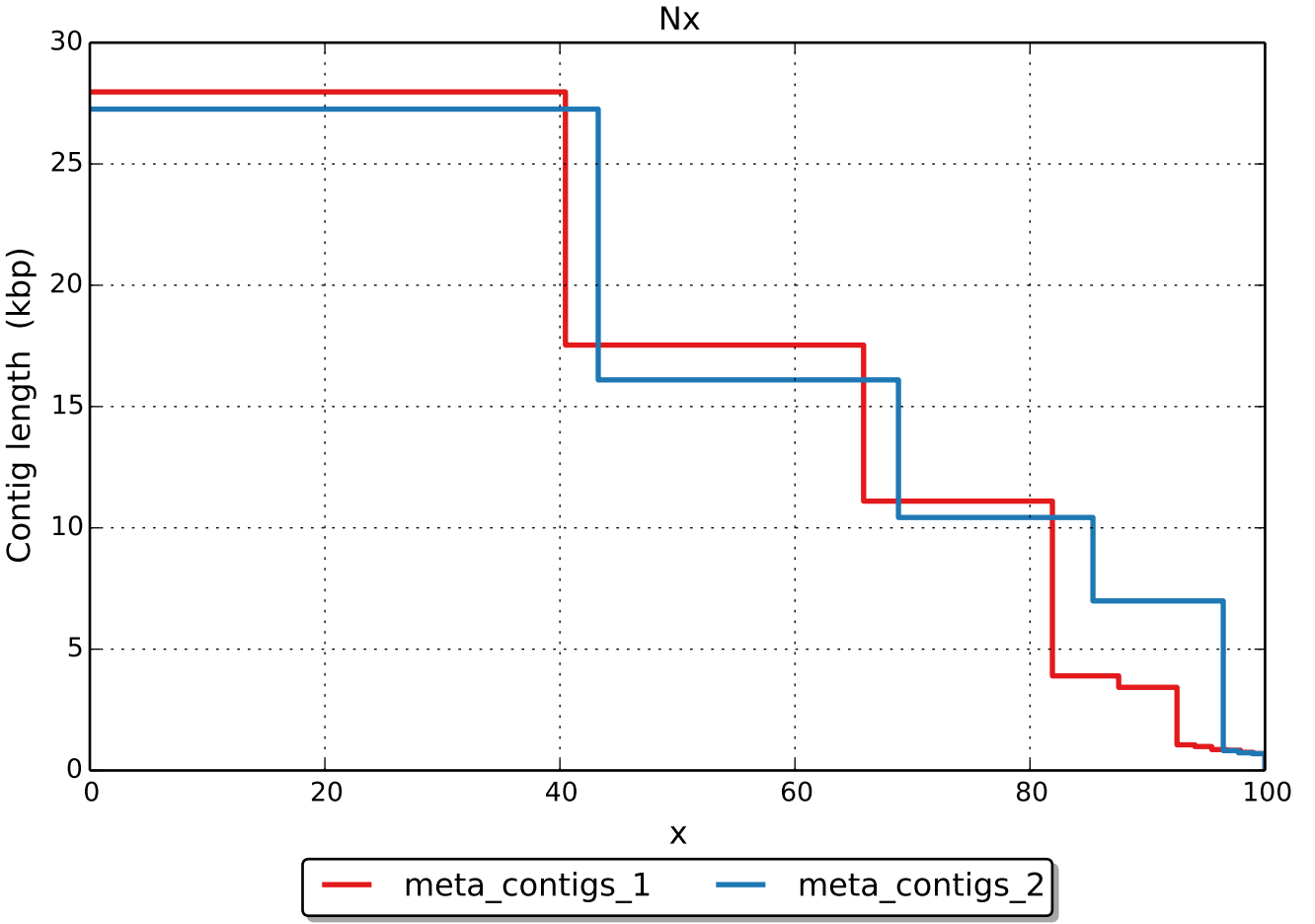
	meta_contigs_1	meta_contigs_2
# misassemblies	0	0
# relocations	0	0
# translocations	0	0
# inversions	0	0
# possibly misassembled contigs	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# mismatches	45	13
# indels	5	3
# short indels	5	3
# long indels	0	0
Indels length	8	6

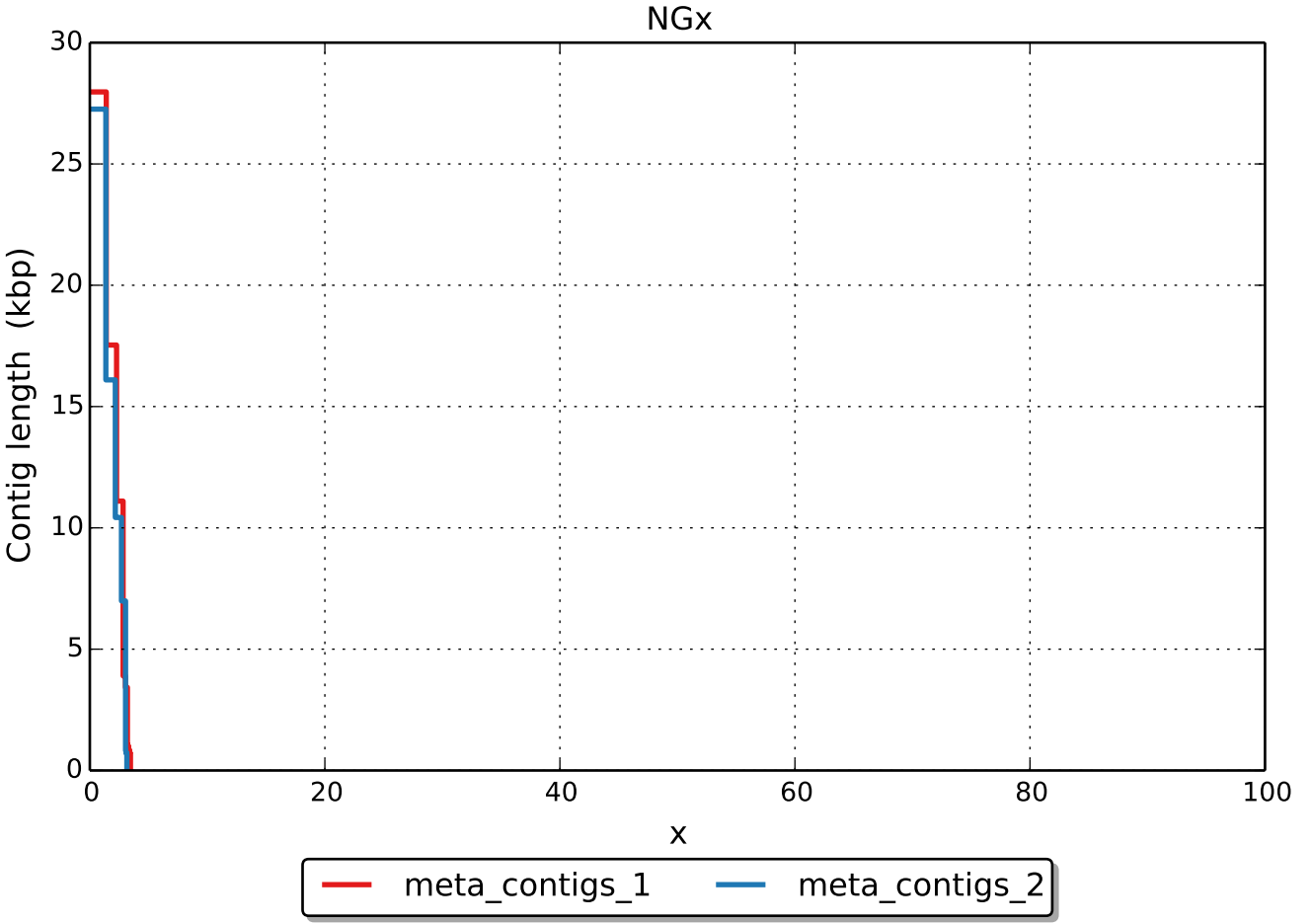
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

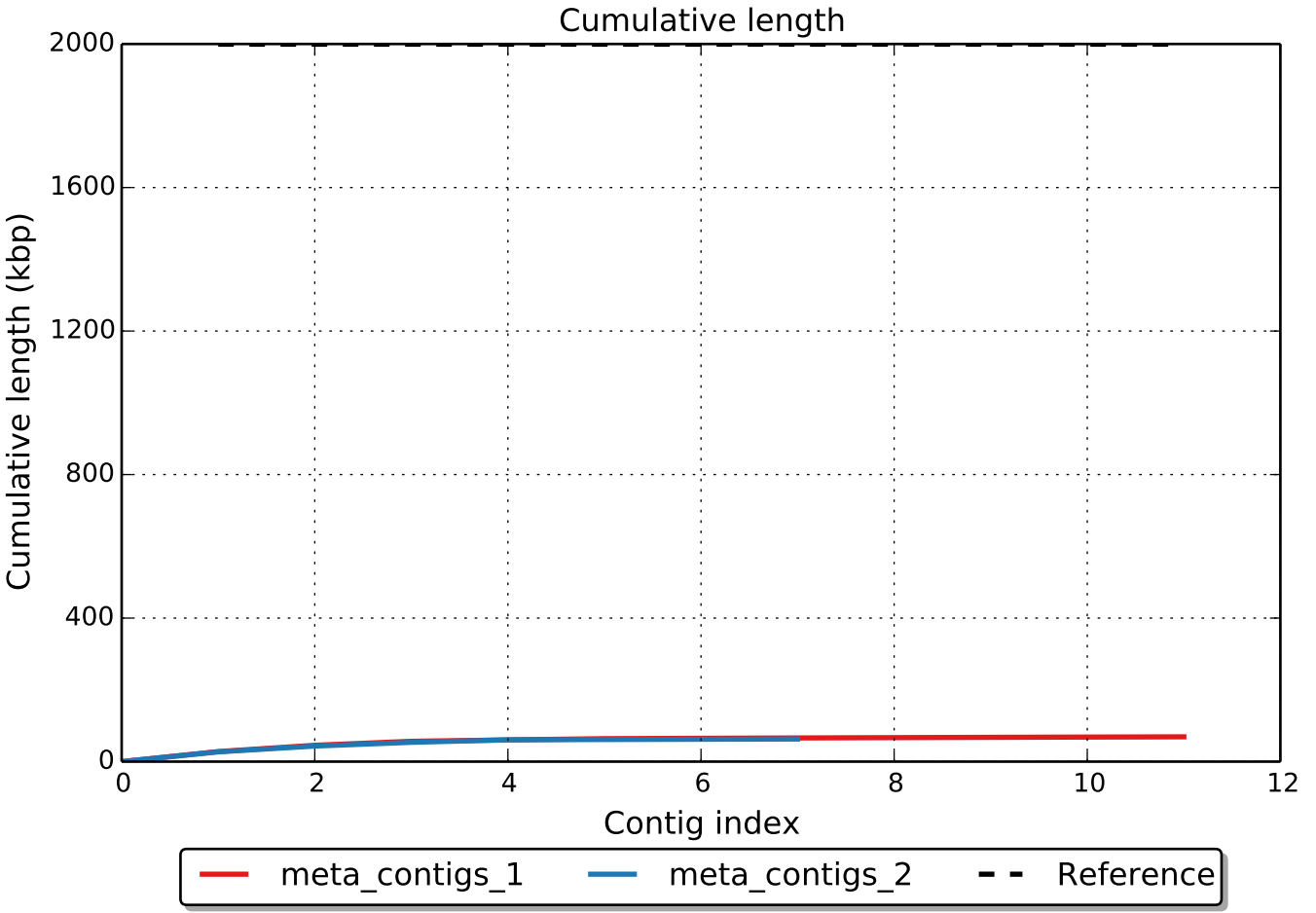
Unaligned report

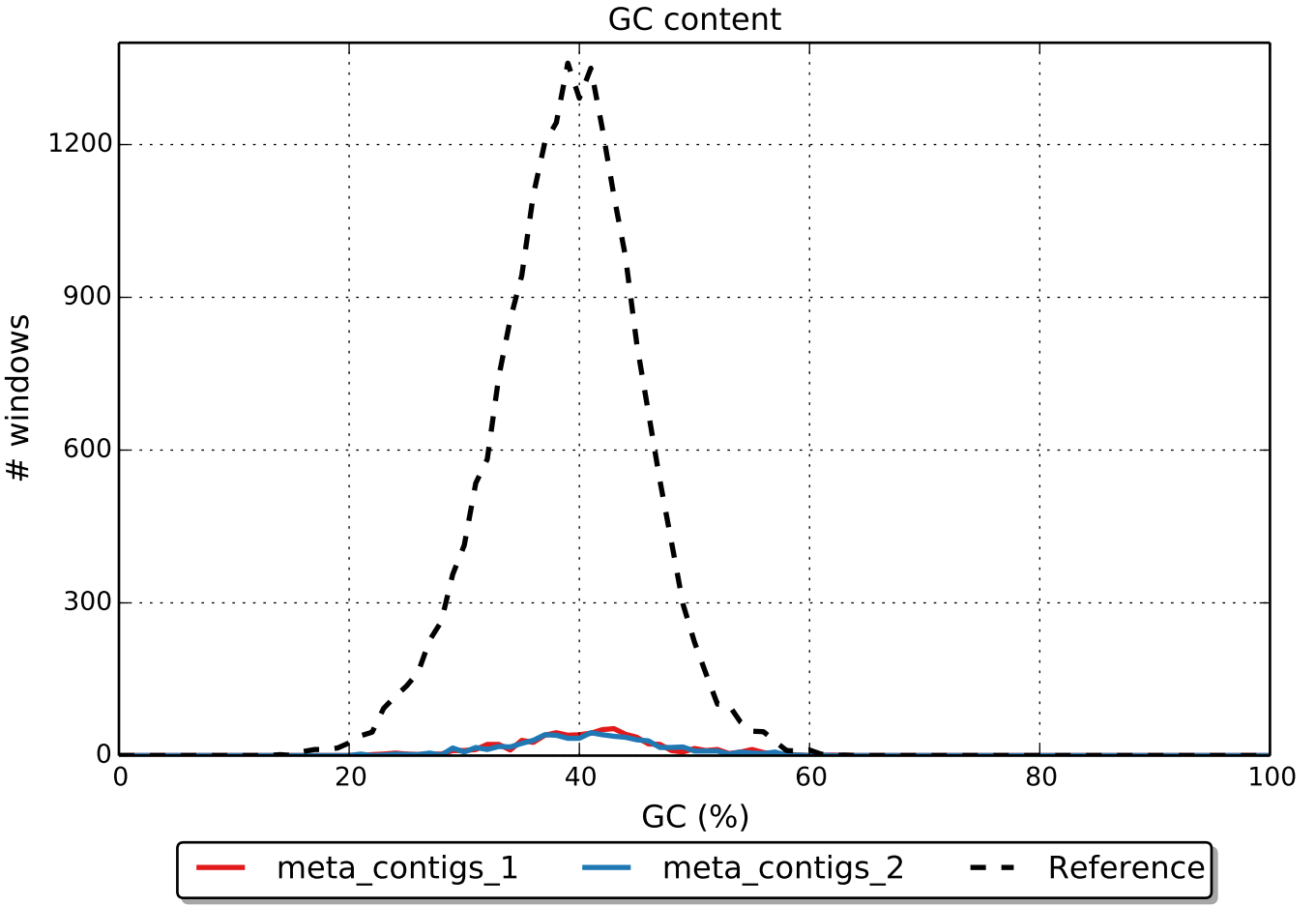
	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	13	0

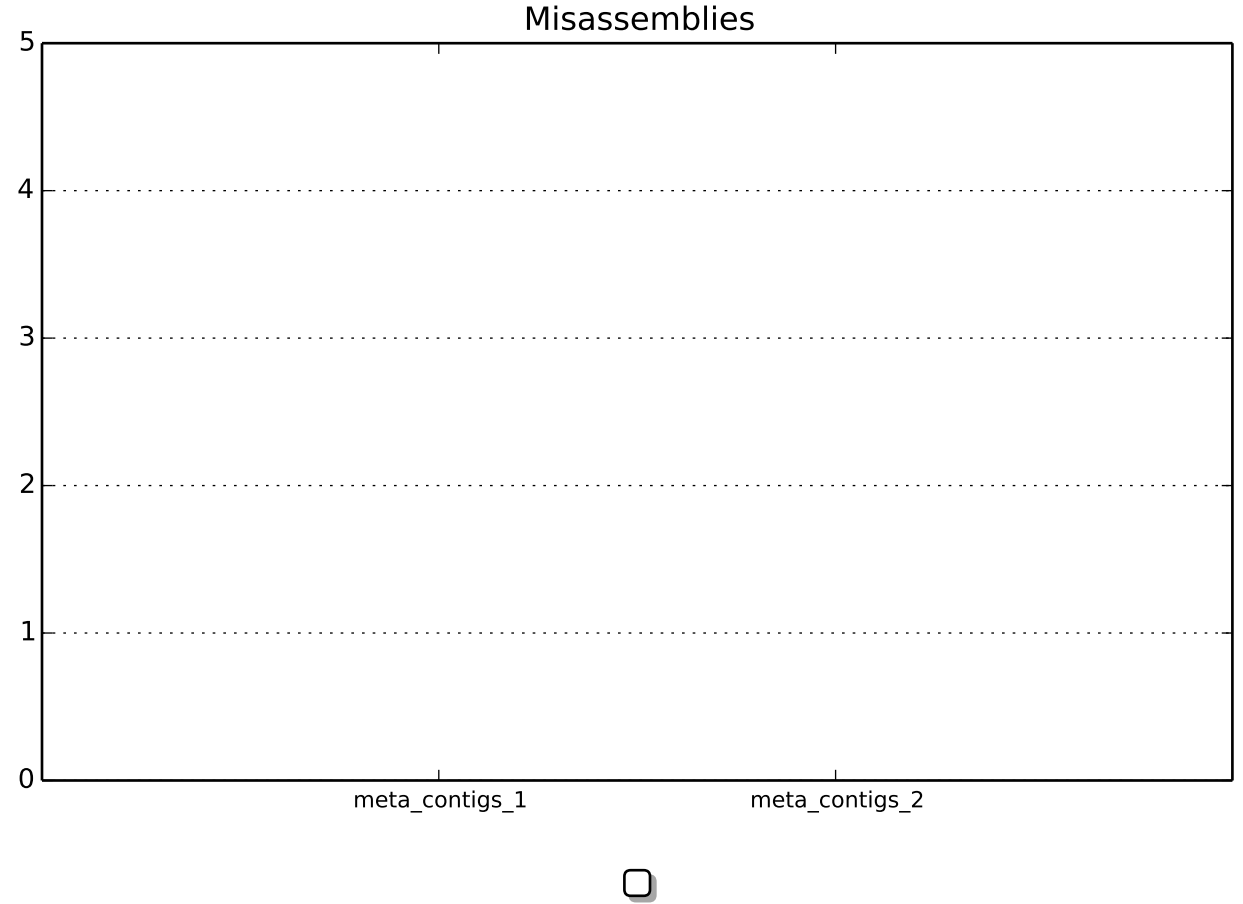
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

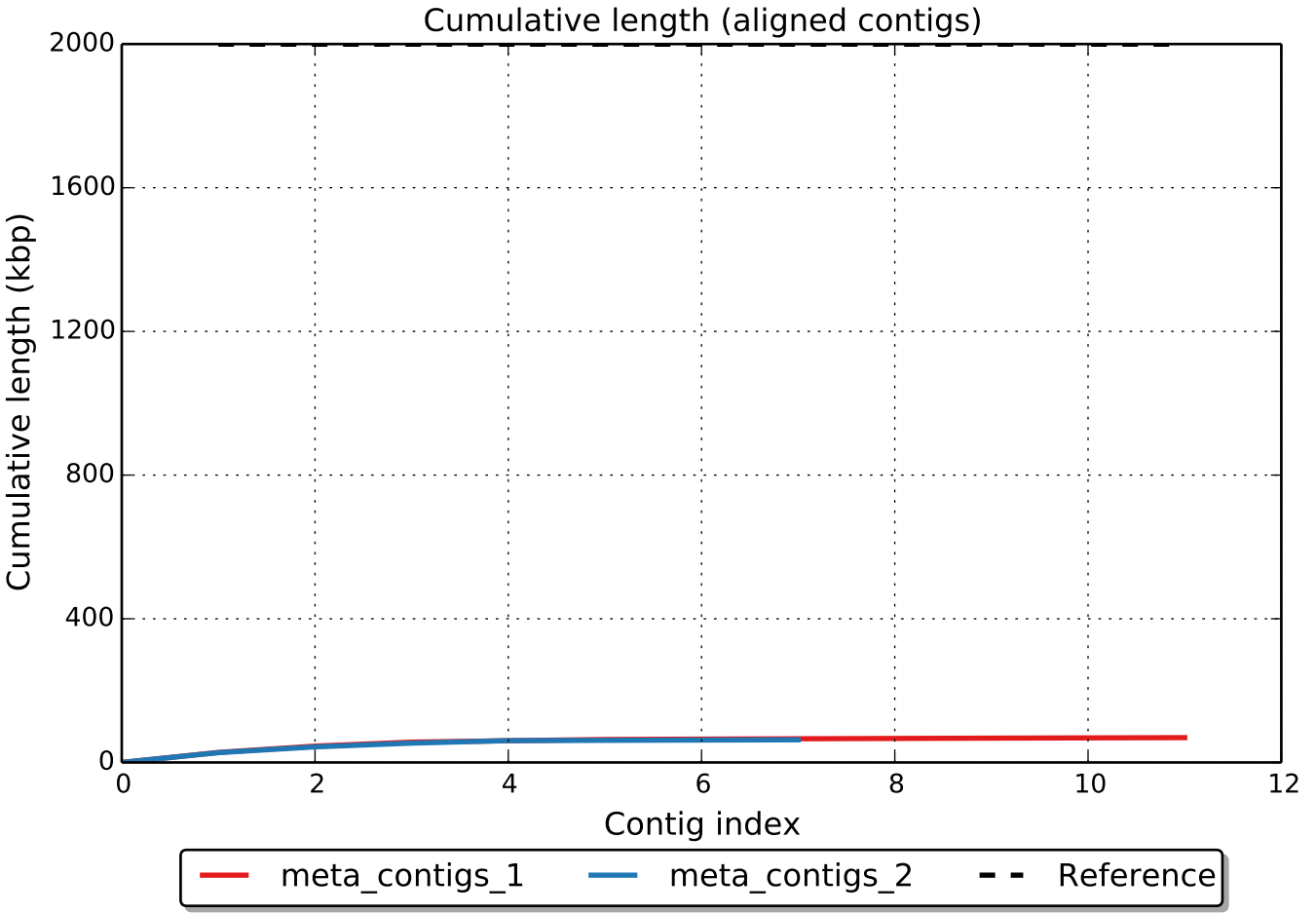

Nx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

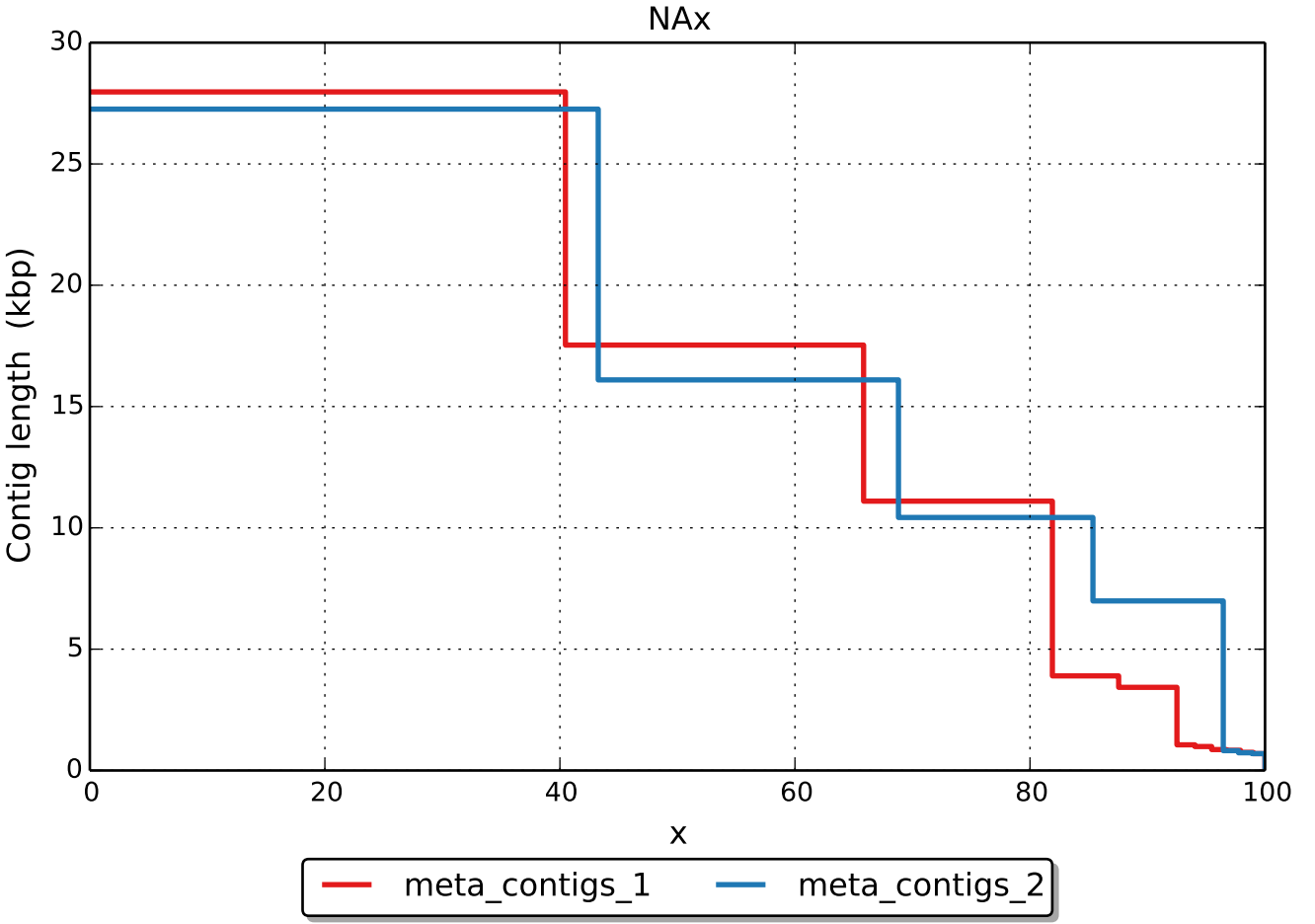

NGx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

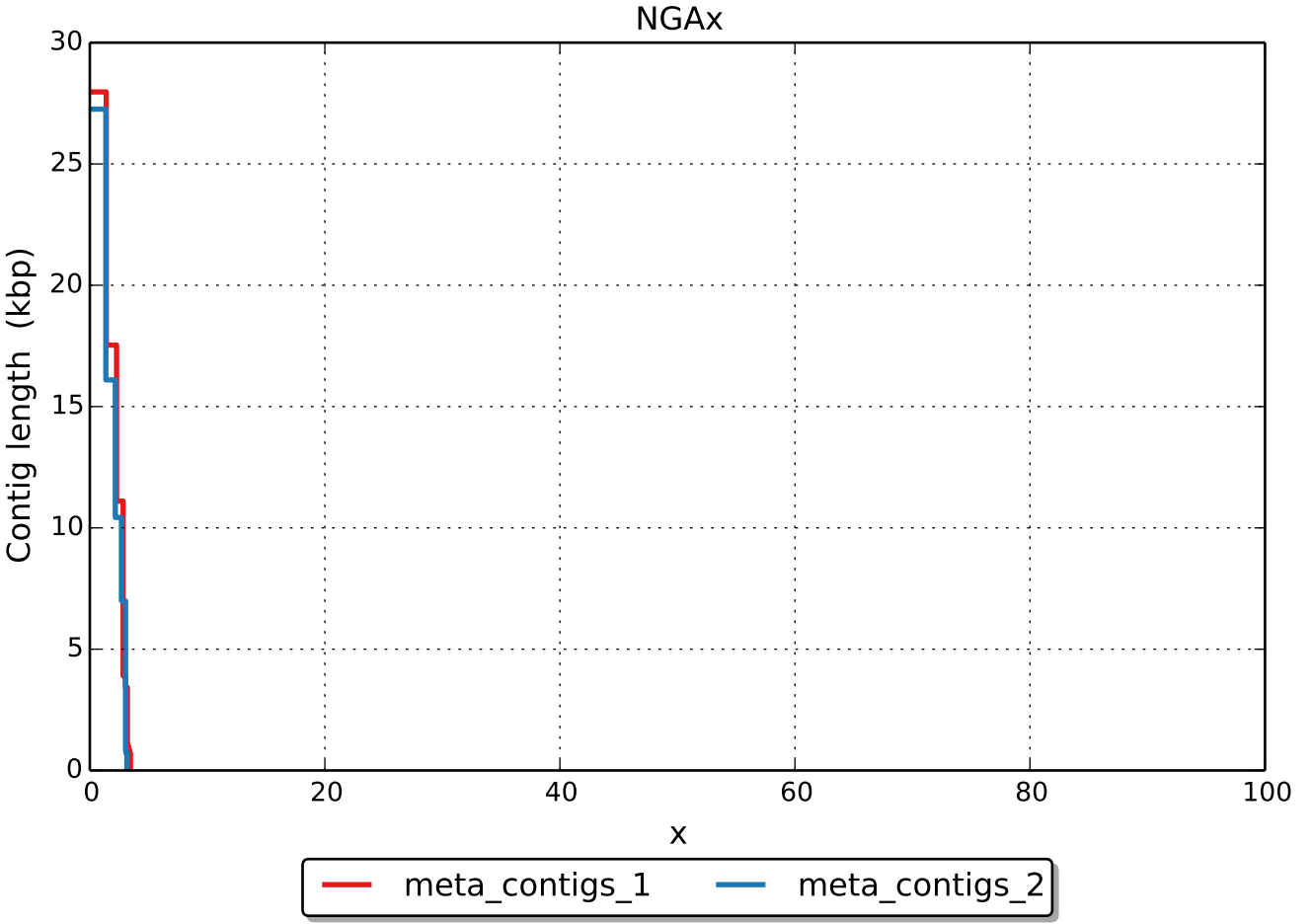

Cumulative length
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
2
4
6
8
10
12
Contig index
meta_contigs_1
meta_contigs_2
Reference

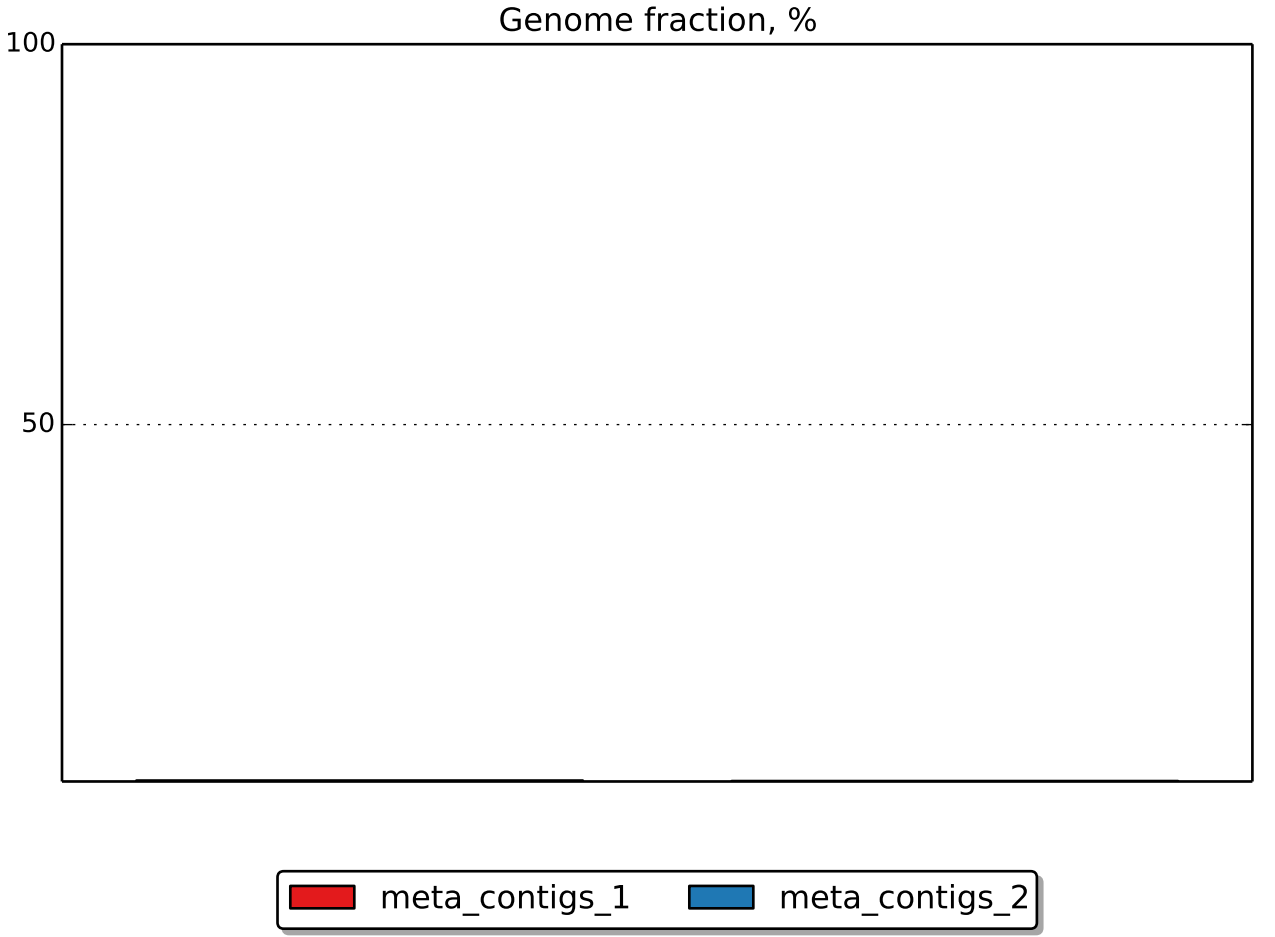

GC content
windows
GC (%)
0
300
600
900
1200
0
20
40
60
80
100
meta_contigs_1
meta_contigs_2
Reference


Misassemblies
5
4
3
2
1
0
meta_contigs_1
meta_contigs_2


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
2
4
6
8
10
12
Contig index
meta_contigs_1
meta_contigs_2
Reference


NAx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2


NGAx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2


Genome fraction, %
100
50
meta_contigs_1
meta_contigs_2