Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 1000 bp)	1	0
# contigs (>= 5000 bp)	0	0
# contigs (>= 10000 bp)	0	0
# contigs (>= 25000 bp)	0	0
# contigs (>= 50000 bp)	0	0
Total length (>= 1000 bp)	1057	0
Total length (>= 5000 bp)	0	0
Total length (>= 10000 bp)	0	0
Total length (>= 25000 bp)	0	0
Total length (>= 50000 bp)	0	0
# contigs	6	2
Largest contig	1057	729
Total length	5179	1423
Reference length	2145445	2145445
GC (%)	52.45	49.33
Reference GC (%)	38.78	38.78
N50	862	729
N75	747	694
L50	3	1
L75	5	2
# 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 (%)	0.174	0.066
Duplication ratio	1.388	1.001
# N's per 100 kbp	154.47	0.00
# mismatches per 100 kbp	294.83	562.98
# indels per 100 kbp	80.41	70.37
Largest alignment	1057	728
NA50	862	728
NGA50	-	-
NA75	747	694
LA50	3	1
LA75	5	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

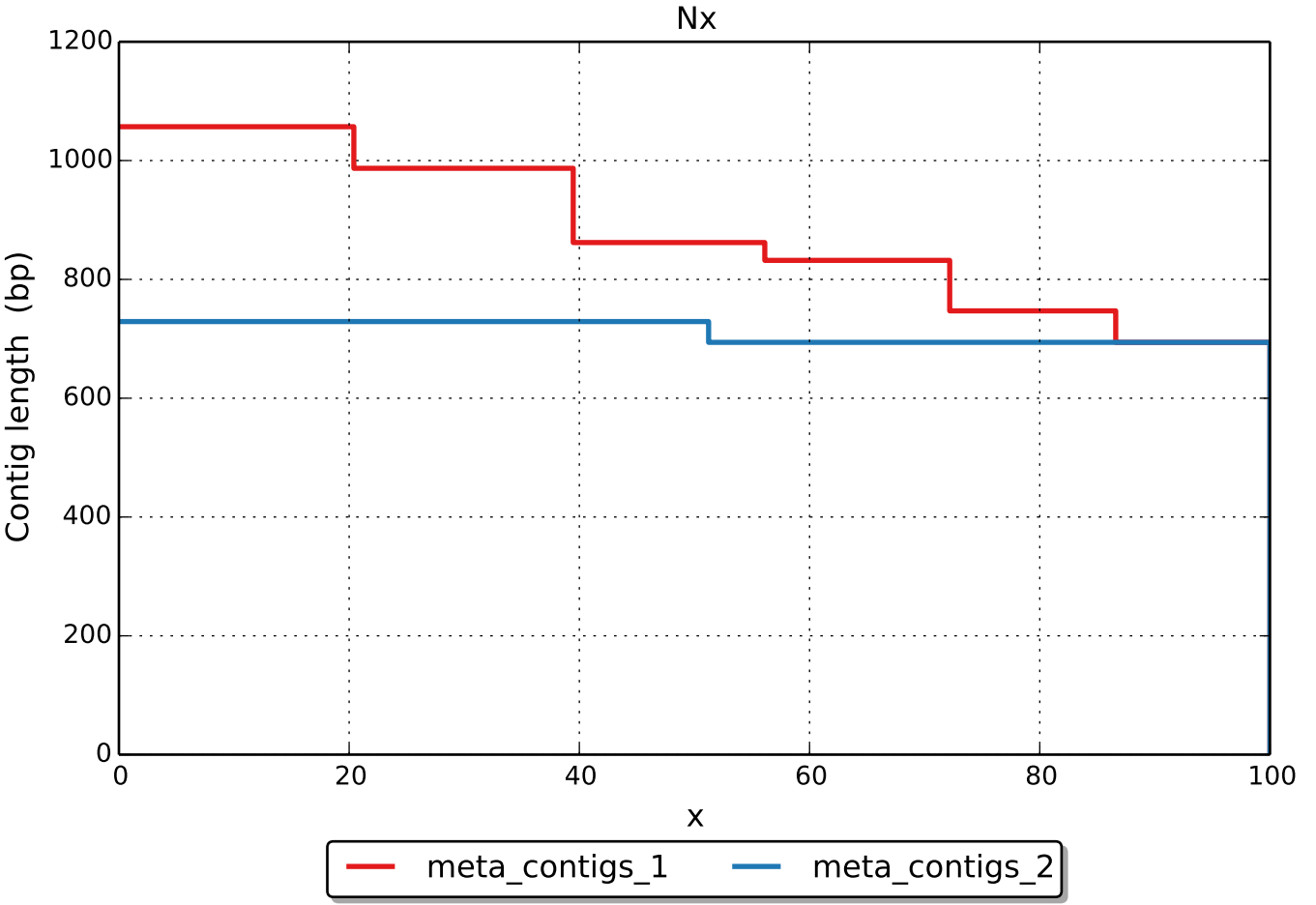
	meta_contigs_1	meta_contigs_2
# misassemblies	0	0
# relocations	0	0
# translocations	0	0
# inversions	0	0
# possibly misassembled contigs	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# mismatches	11	8
# indels	3	1
# short indels	3	1
# long indels	0	0
Indels length	6	1

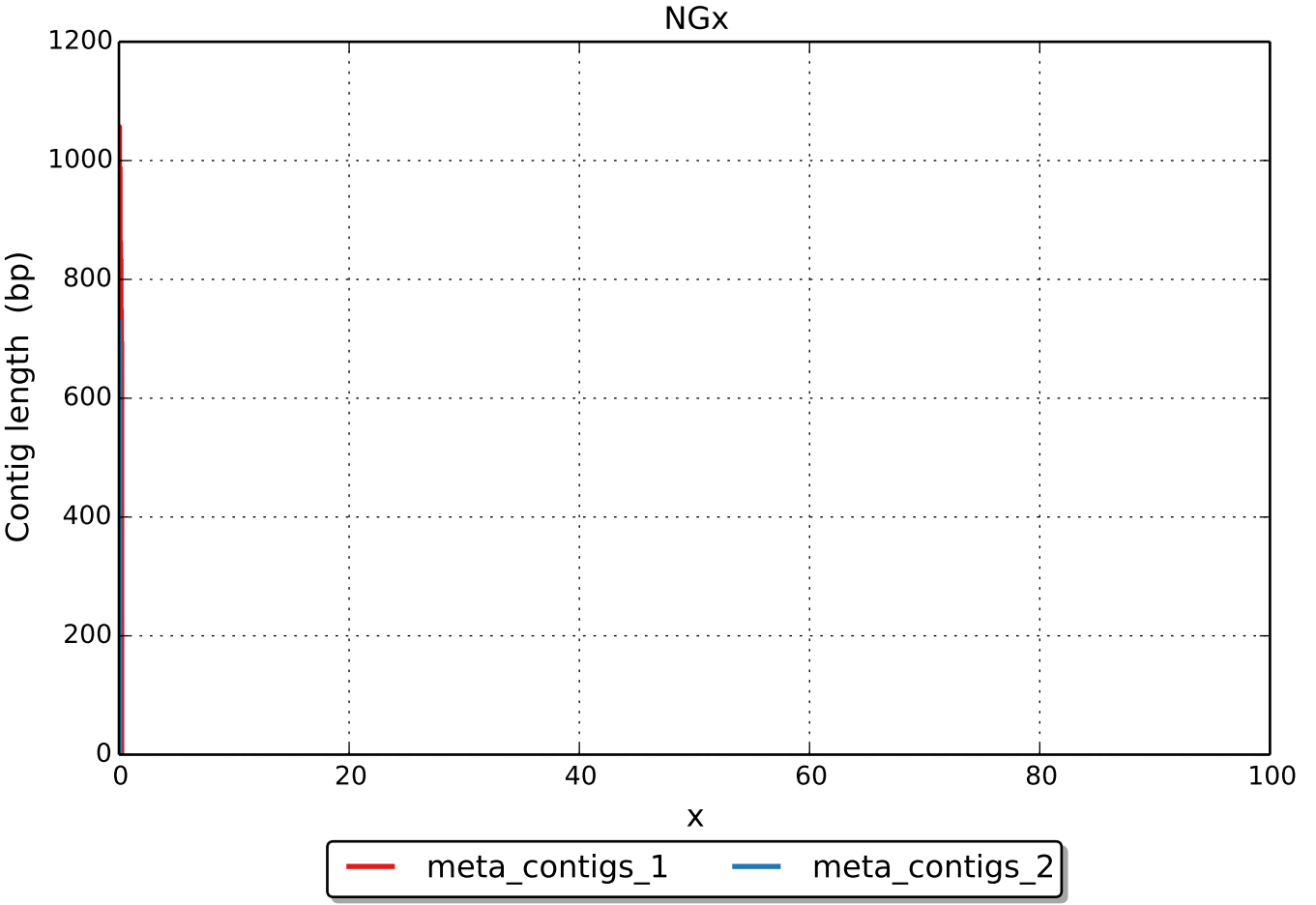
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

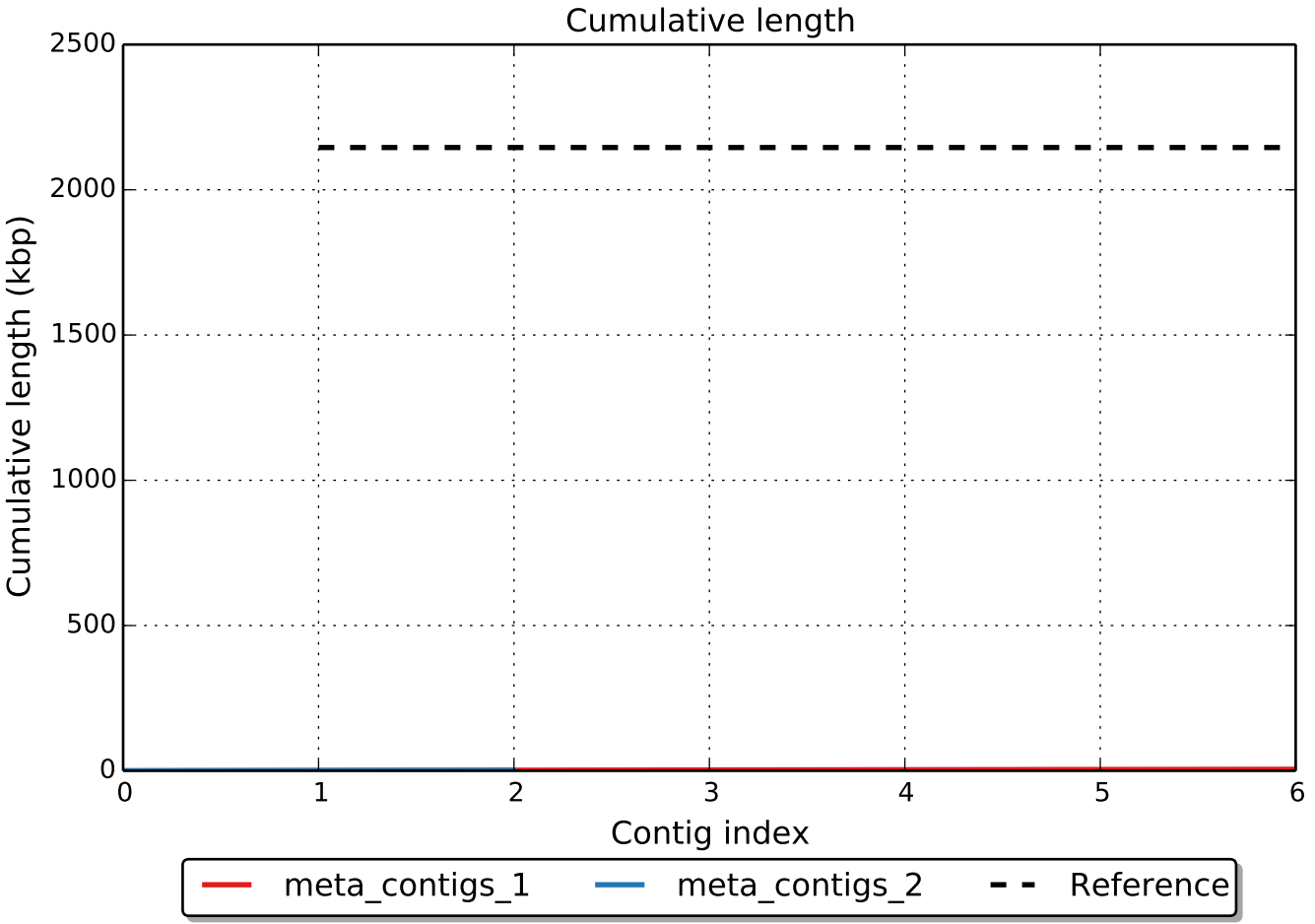
Unaligned report

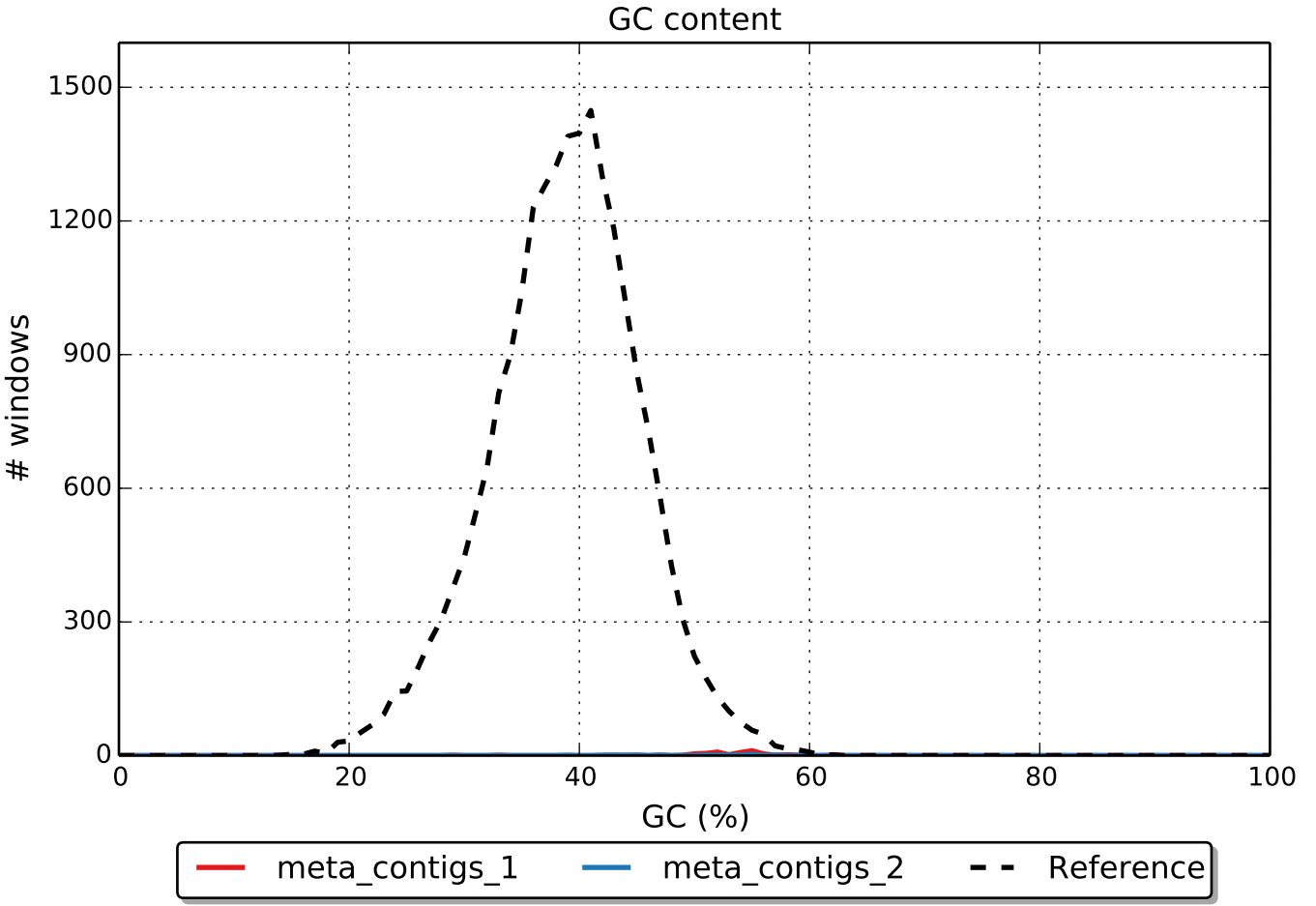
	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	8	0

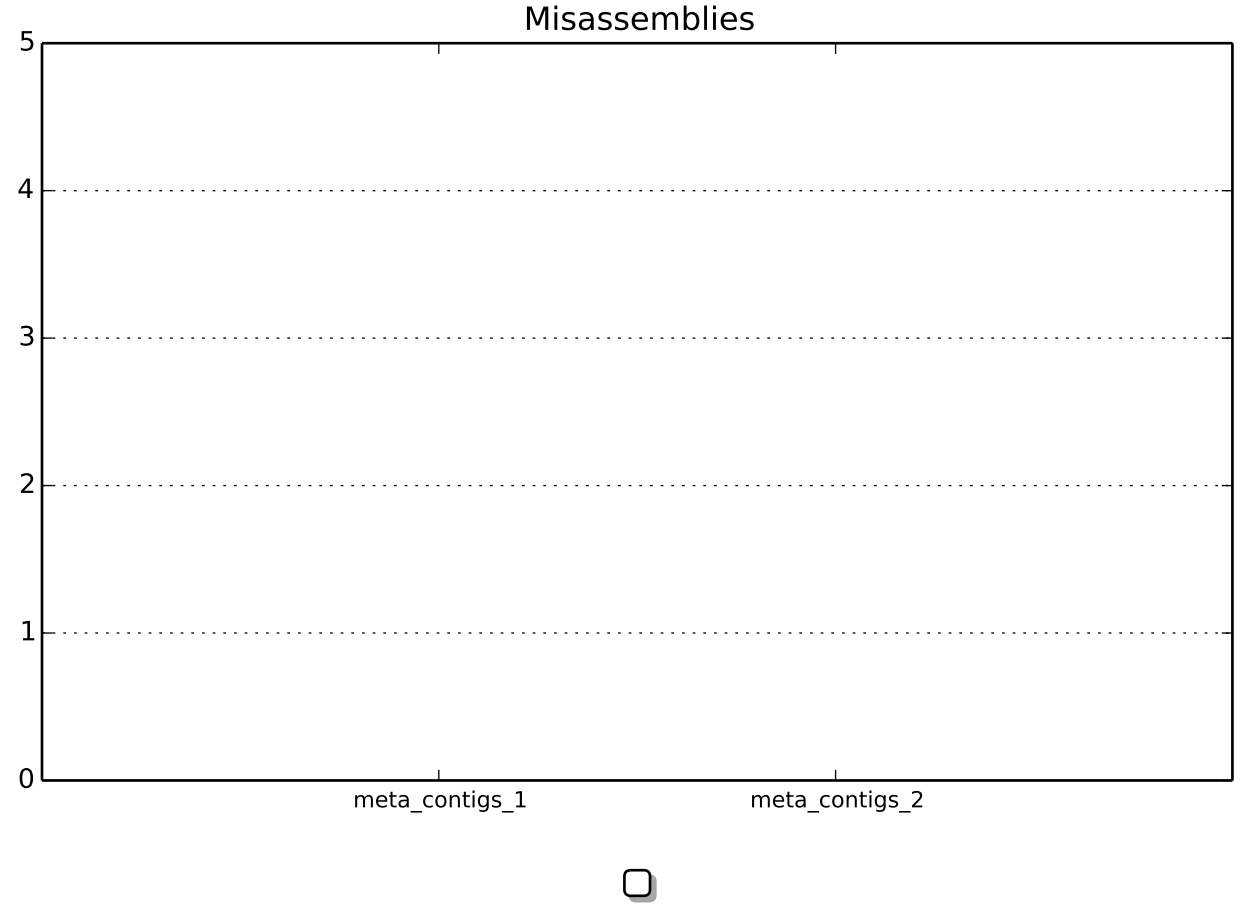
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

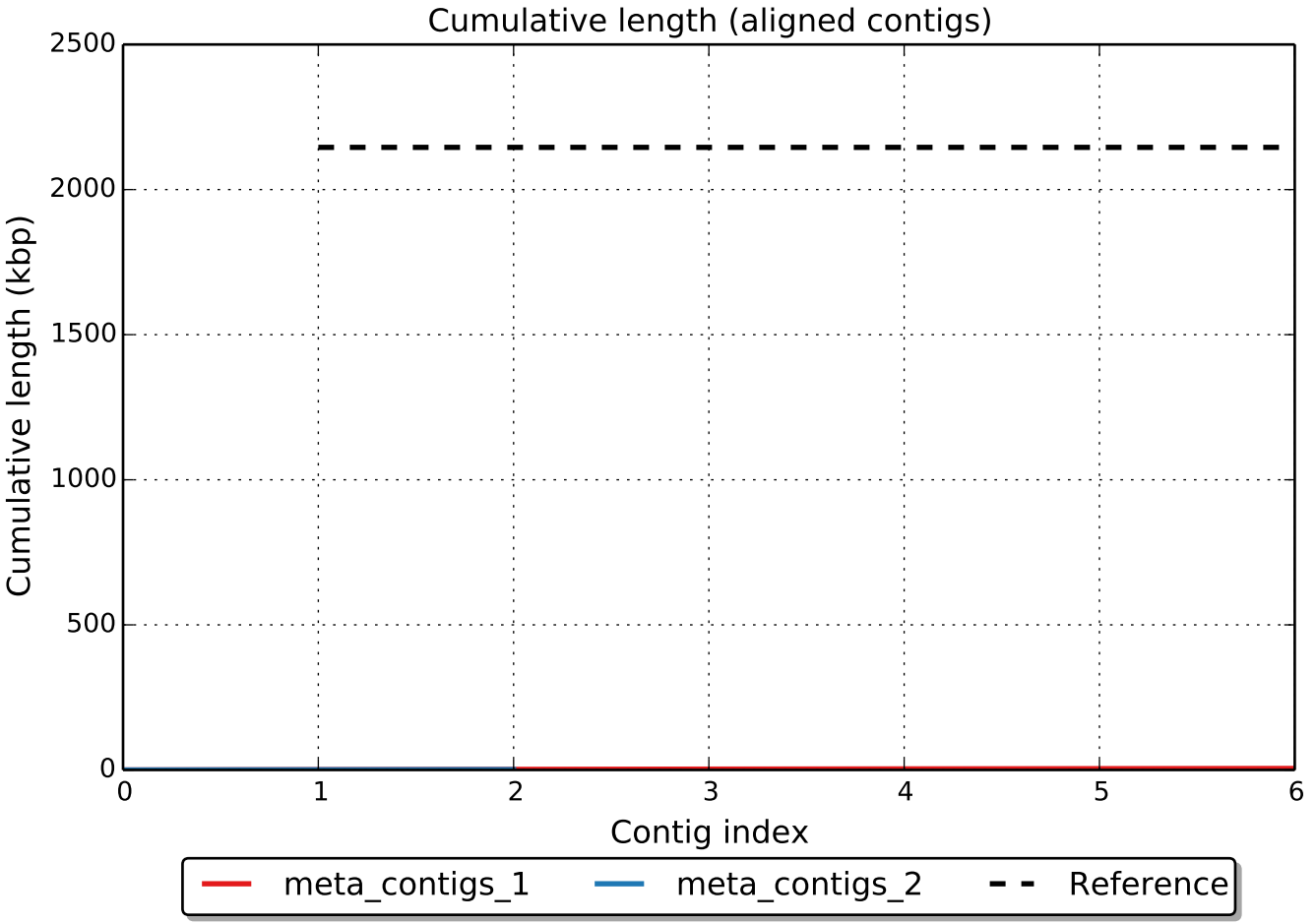

Nx
Contig length (bp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

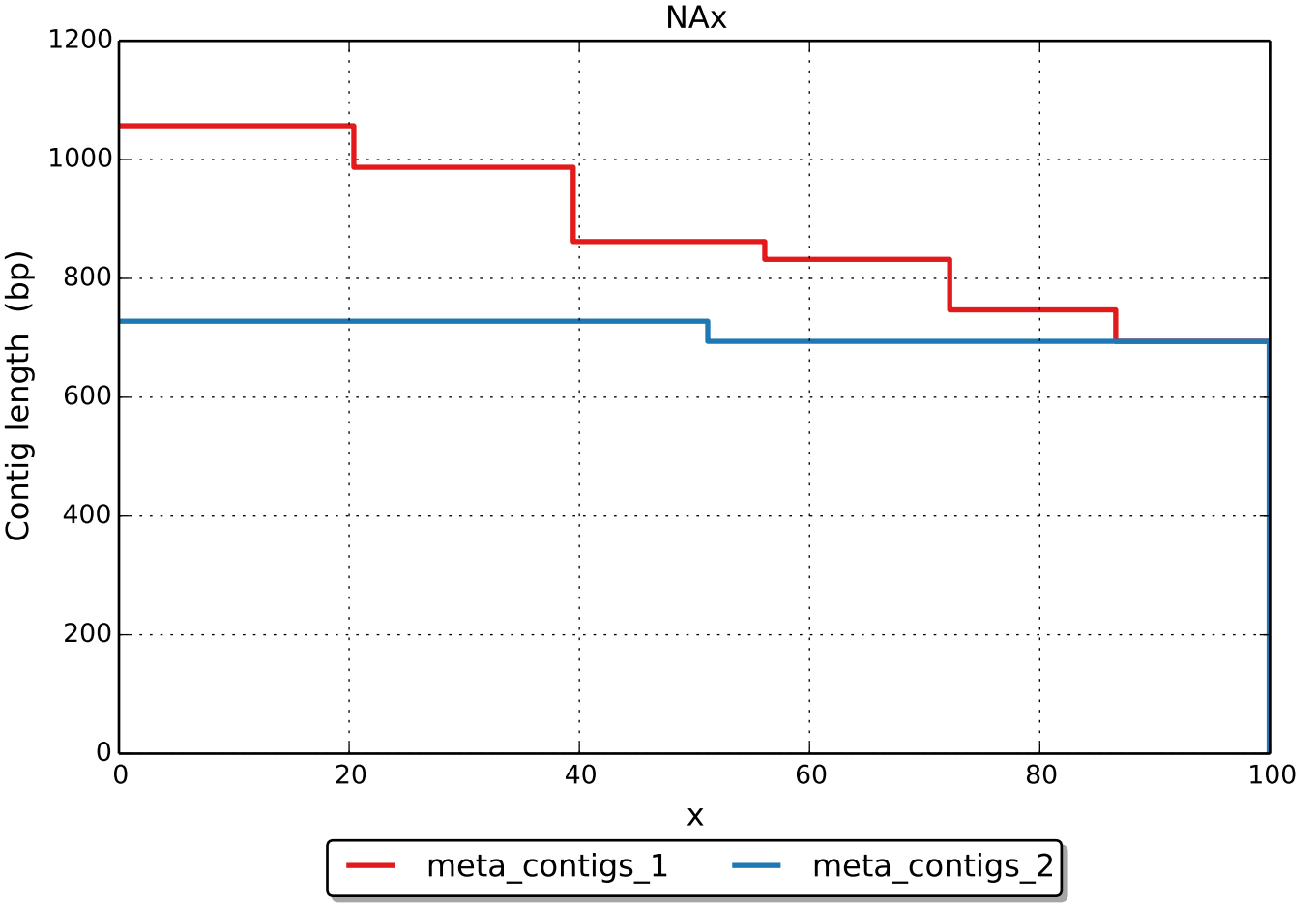

NGx
Contig length (bp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2

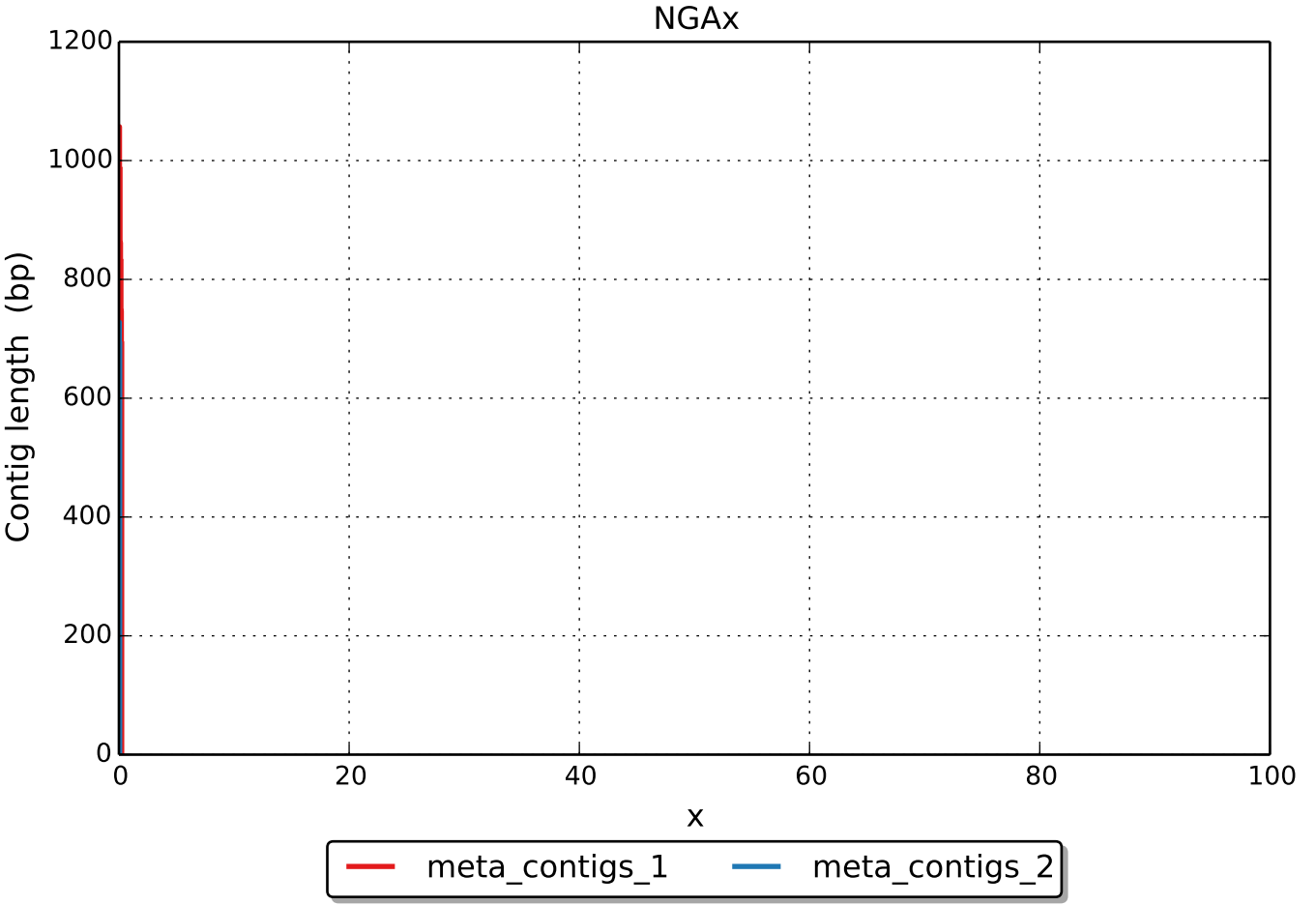

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
3
4
5
6
Contig index
meta_contigs_1
meta_contigs_2
Reference

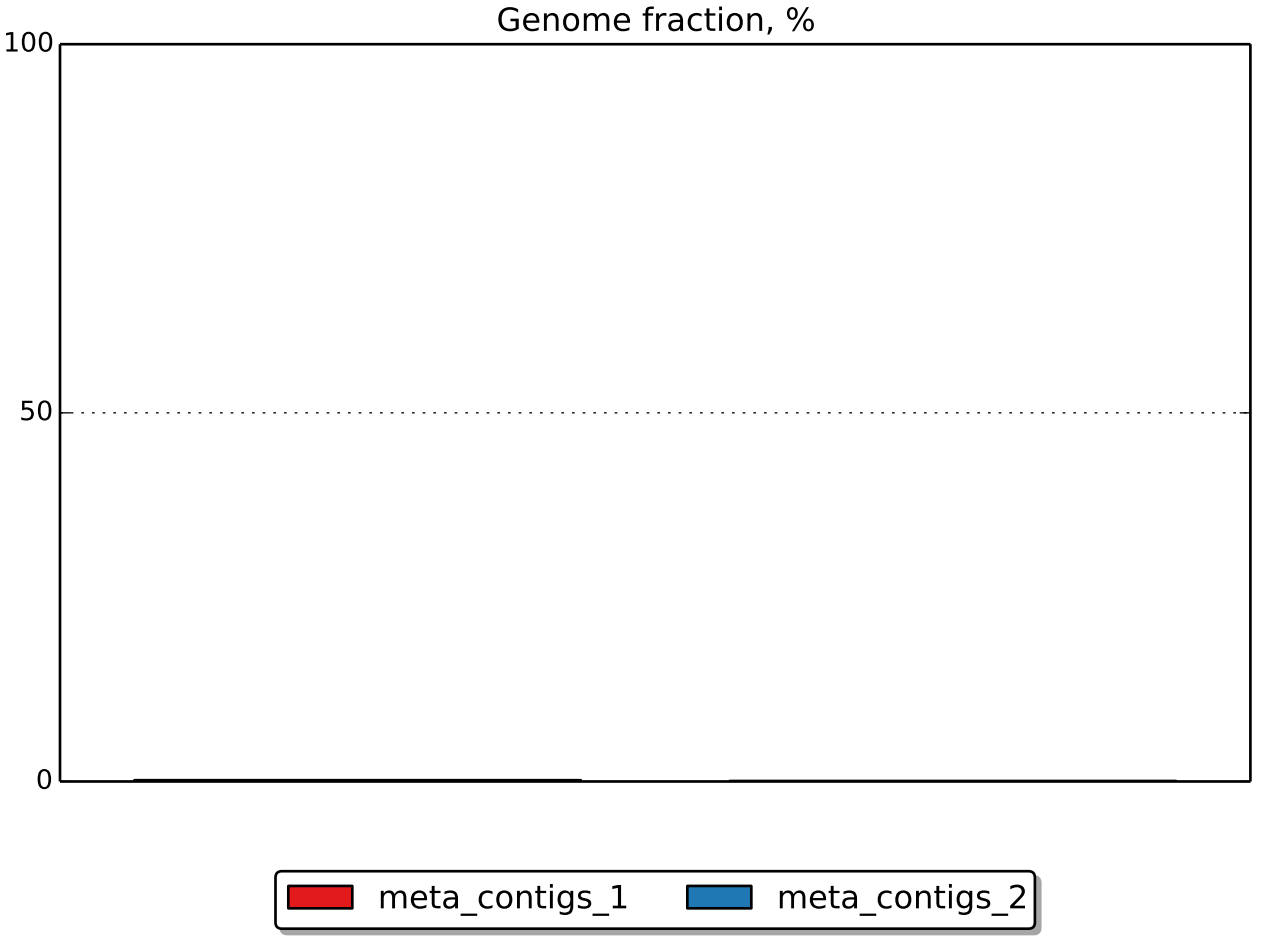

GC content
1500
1200
900
600
300
0
windows
0
20
40
60
80
100
GC (%)
meta_contigs_1
meta_contigs_2
Reference


Misassemblies
5
4
3
2
1
0
meta_contigs_1
meta_contigs_2


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
1
2
3
4
5
6
Contig index
meta_contigs_1
meta_contigs_2
Reference


NAx
Contig length (bp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2


NGAx
Contig length (bp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
meta_contigs_1
meta_contigs_2


Genome fraction, %
100
50
0
meta_contigs_1
meta_contigs_2