Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 1000 bp)	1	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)	49658	49658
Total length (>= 5000 bp)	49658	49658
Total length (>= 10000 bp)	49658	49658
Total length (>= 25000 bp)	49658	49658
Total length (>= 50000 bp)	0	0
# contigs	2	2
Largest contig	49658	49658
Total length	50372	50372
Reference length	54999	54999
GC (%)	45.67	45.67
Reference GC (%)	45.96	45.96
N50	49658	49658
NG50	49658	49658
N75	49658	49658
NG75	49658	49658
L50	1	1
LG50	1	1
L75	1	1
LG75	1	1
# 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 (%)	91.587	91.587
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	25.81	25.81
# indels per 100 kbp	0.00	0.00
Largest alignment	49658	49658
NA50	49658	49658
NGA50	49658	49658
NA75	49658	49658
NGA75	49658	49658
LA50	1	1
LGA50	1	1
LA75	1	1
LGA75	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).
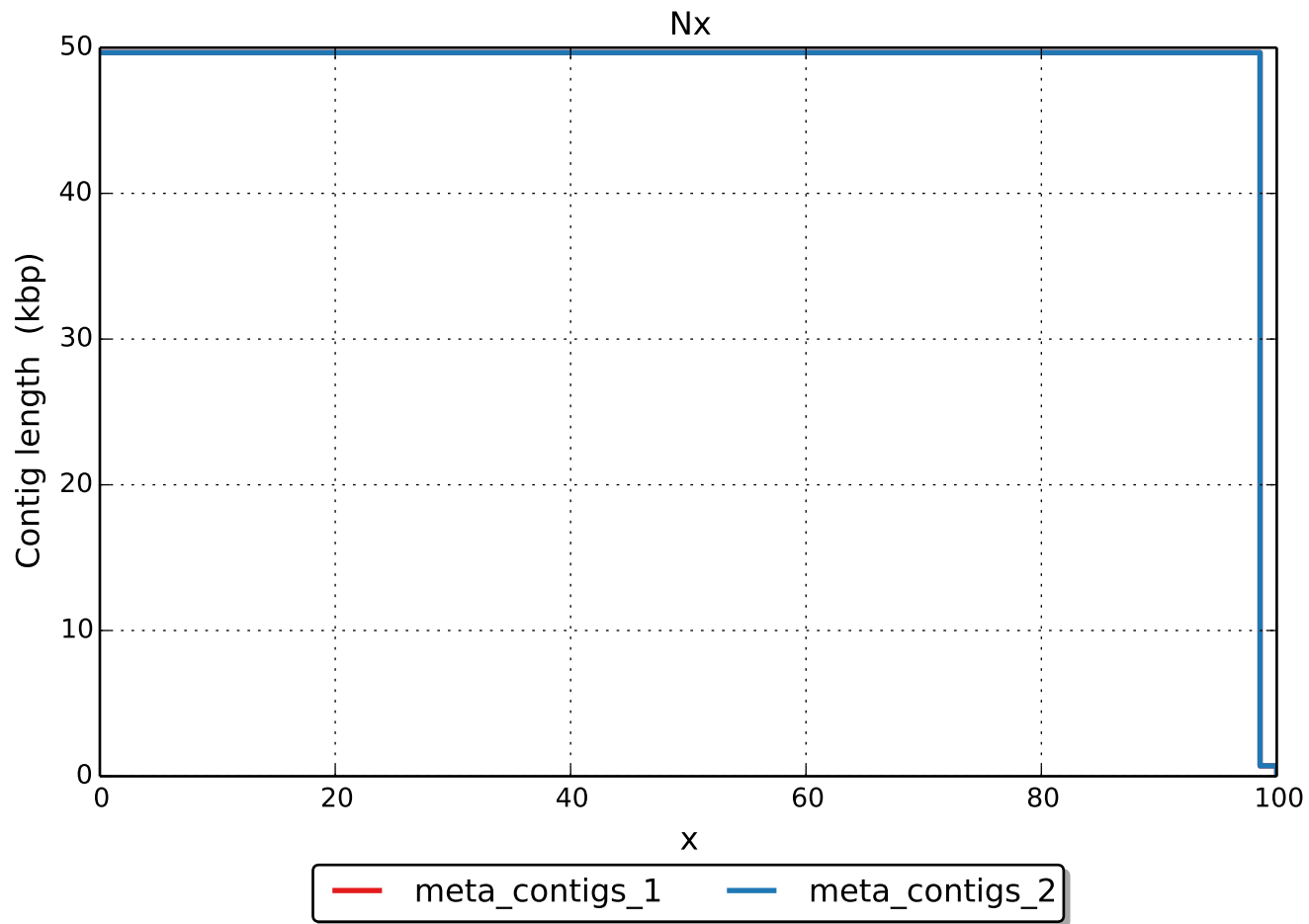
Misassemblies report

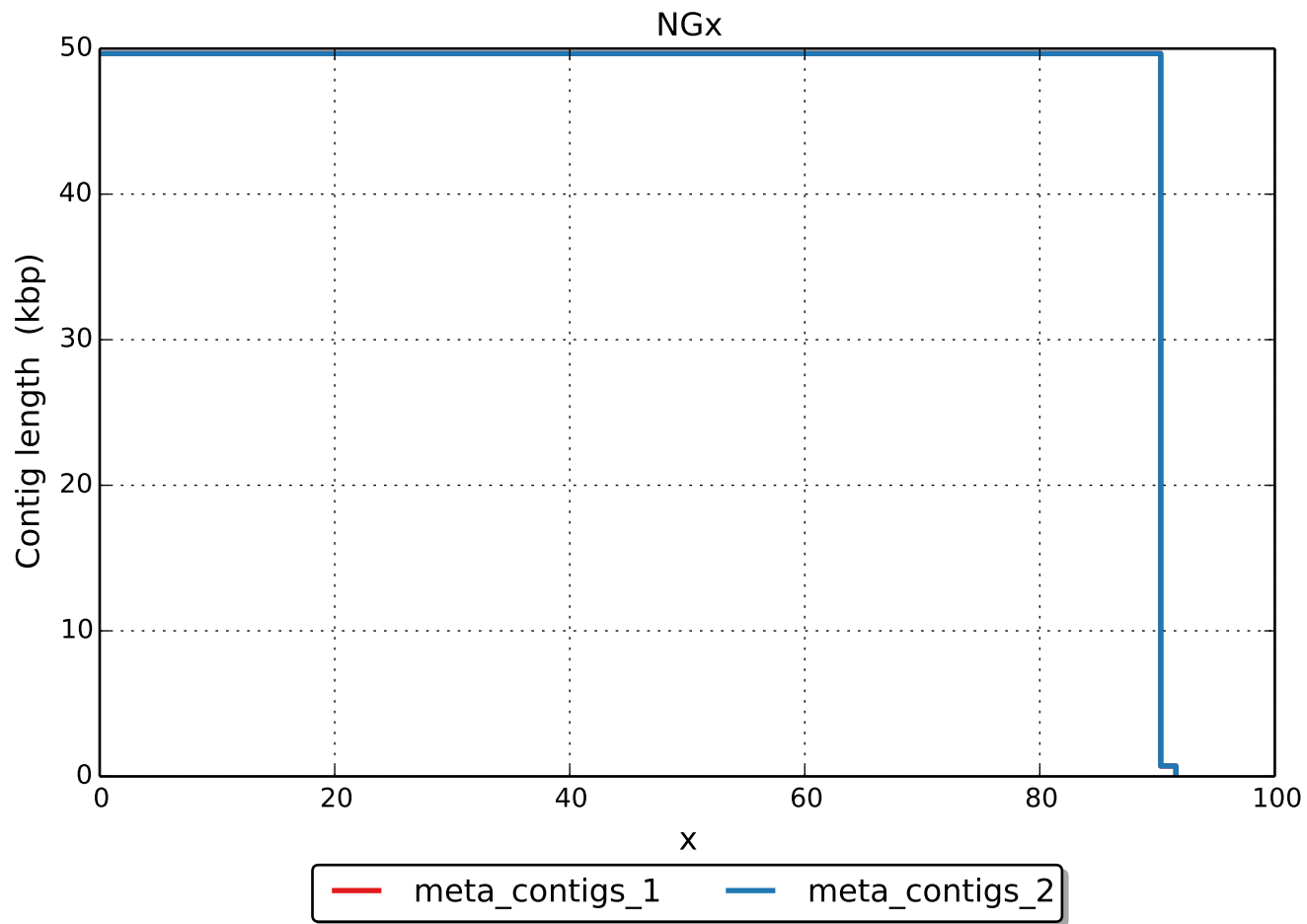|	meta_contigs_1	meta_contigs_2
# misassemblies	0	0
# relocations	0	0
# translocations	0	0
# inversions	0	0
# possibly misassembled contigs	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# mismatches	13	13
# indels	0	0
# short indels	0	0
# long indels	0	0
Indels length	0	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).
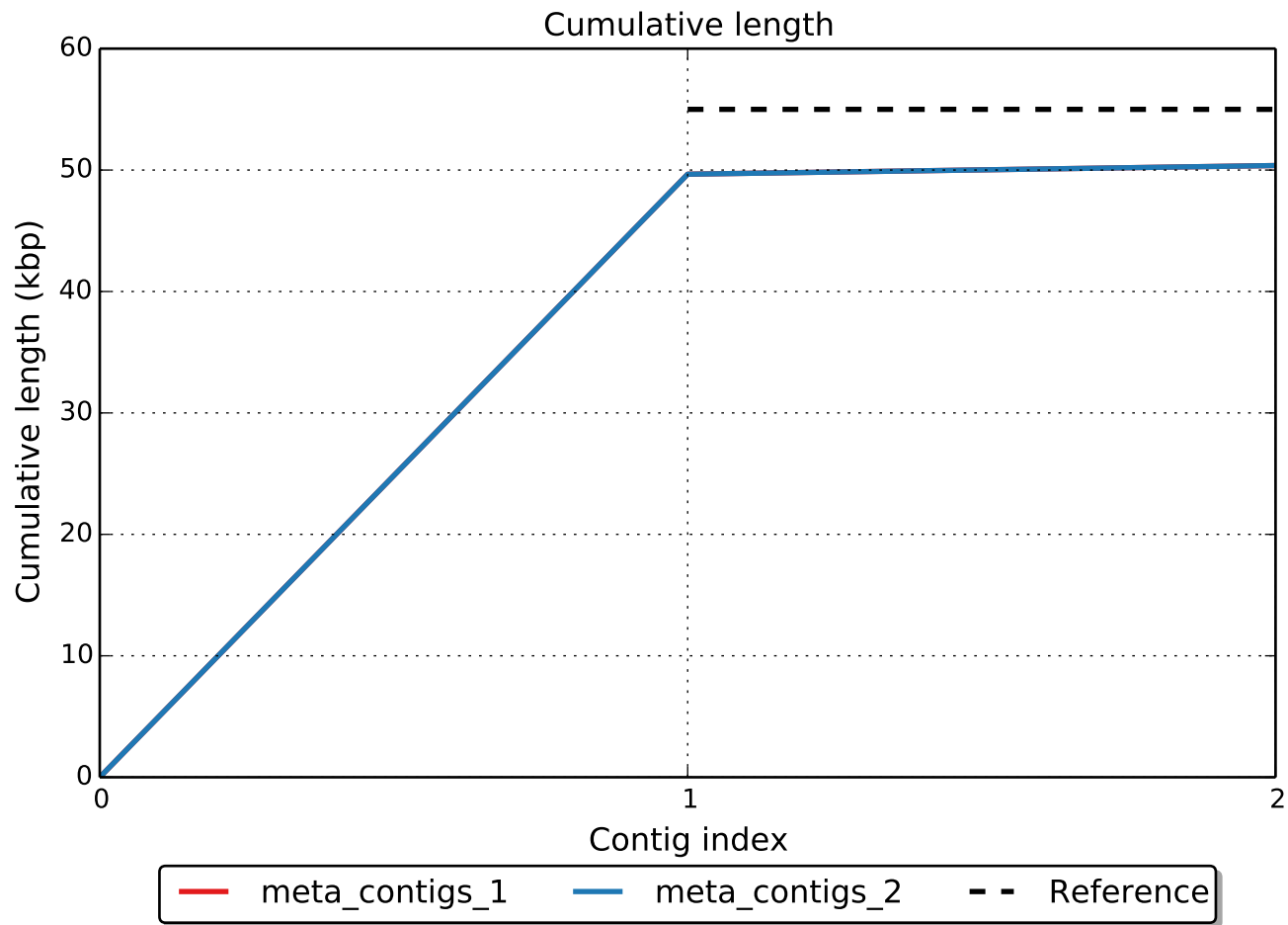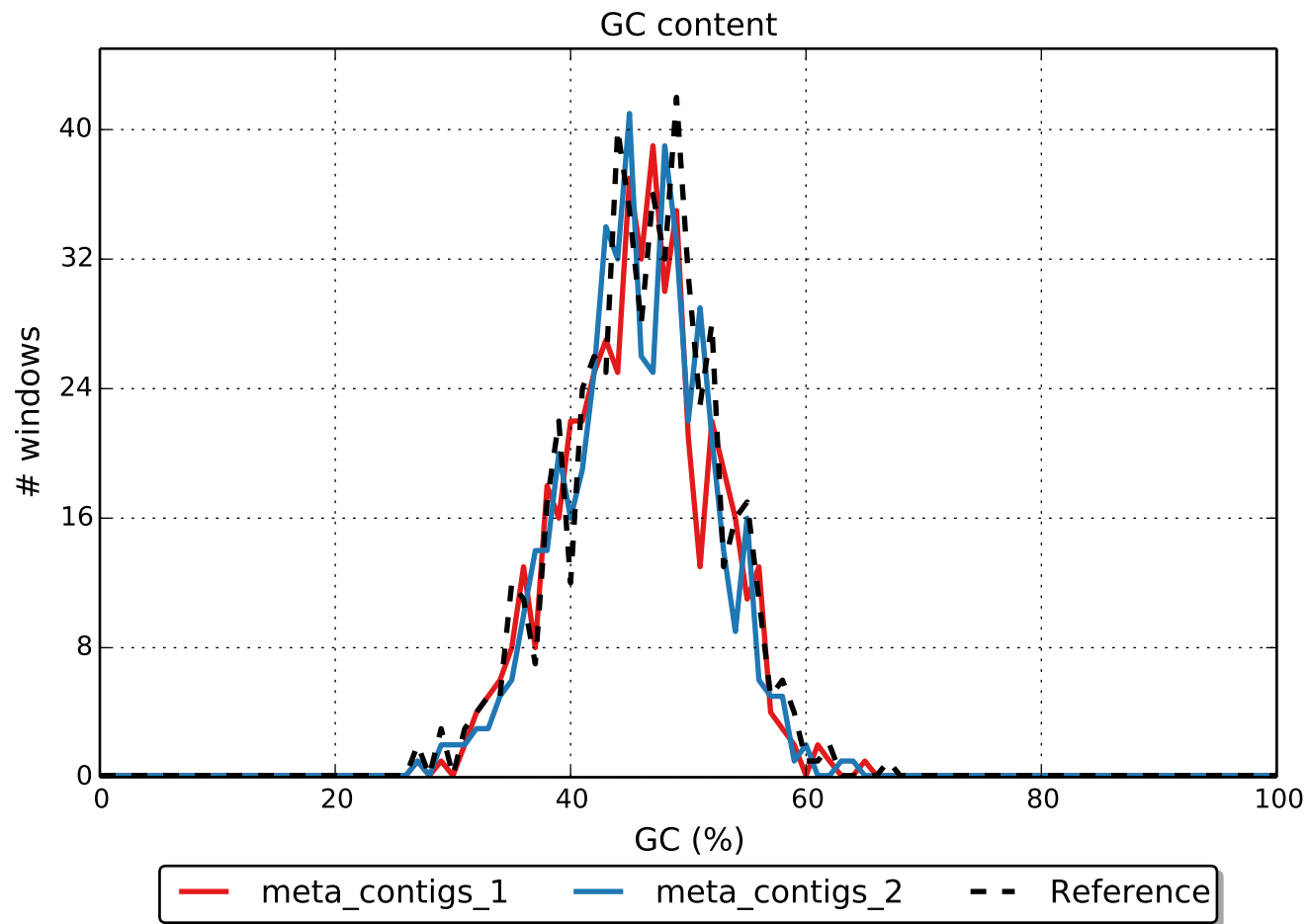
Unaligned report

	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	0	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).

NGx

Contig length (kbp)

x

meta_contigs_1   meta_contigs_2

Cumulative length

GC content

windows

GC (%)

meta_contigs_1   meta_contigs_2   - - - Reference

Misassemblies

	meta_contigs_1	meta_contigs_2

Cumulative length (aligned contigs)

Genome fraction, %