

Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 1000 bp)	2	2
# 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	58868
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	2
Largest contig	55106	55421
Total length	58663	58868
Reference length	59999	59999
GC (%)	50.17	50.19
Reference GC (%)	50.25	50.25
N50	55106	55421
NG50	55106	55421
N75	55106	55421
NG75	55106	55421
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 (%)	97.575	98.115
Duplication ratio	1.002	1.000
# N's per 100 kbp	1.70	0.00
# mismatches per 100 kbp	23.91	25.48
# indels per 100 kbp	0.00	0.00
Largest alignment	55106	55421
NA50	55106	55421
NGA50	55106	55421
NA75	55106	55421
NGA75	55106	55421
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

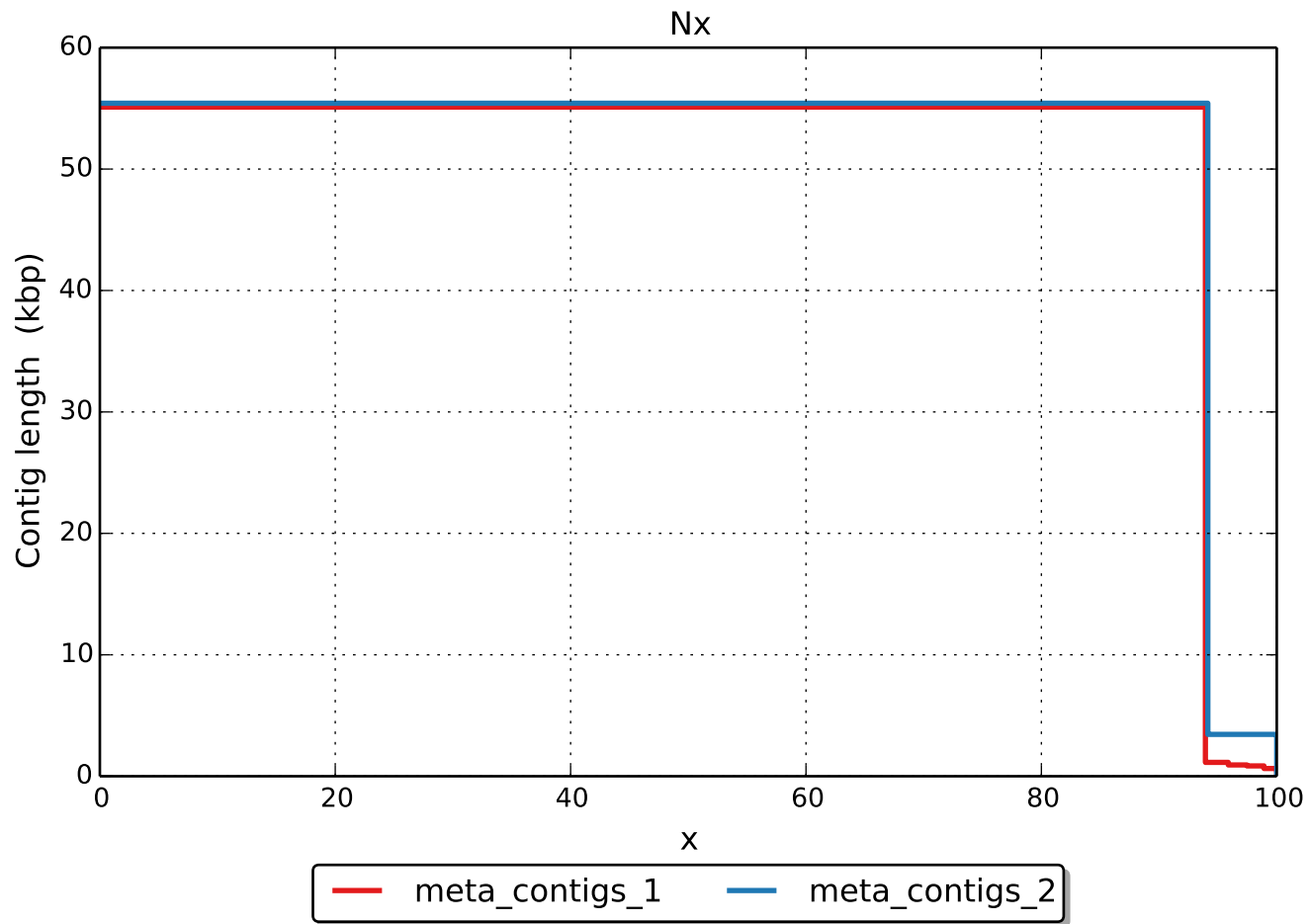
	meta_contigs_1	meta_contigs_2
# misassemblies	0	0
# relocations	0	0
# translocations	0	0
# inversions	0	0
# possibly misassembled contigs	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# mismatches	14	15
# indels	0	0
# short indels	0	0
# long indels	0	0
Indels length	0	0

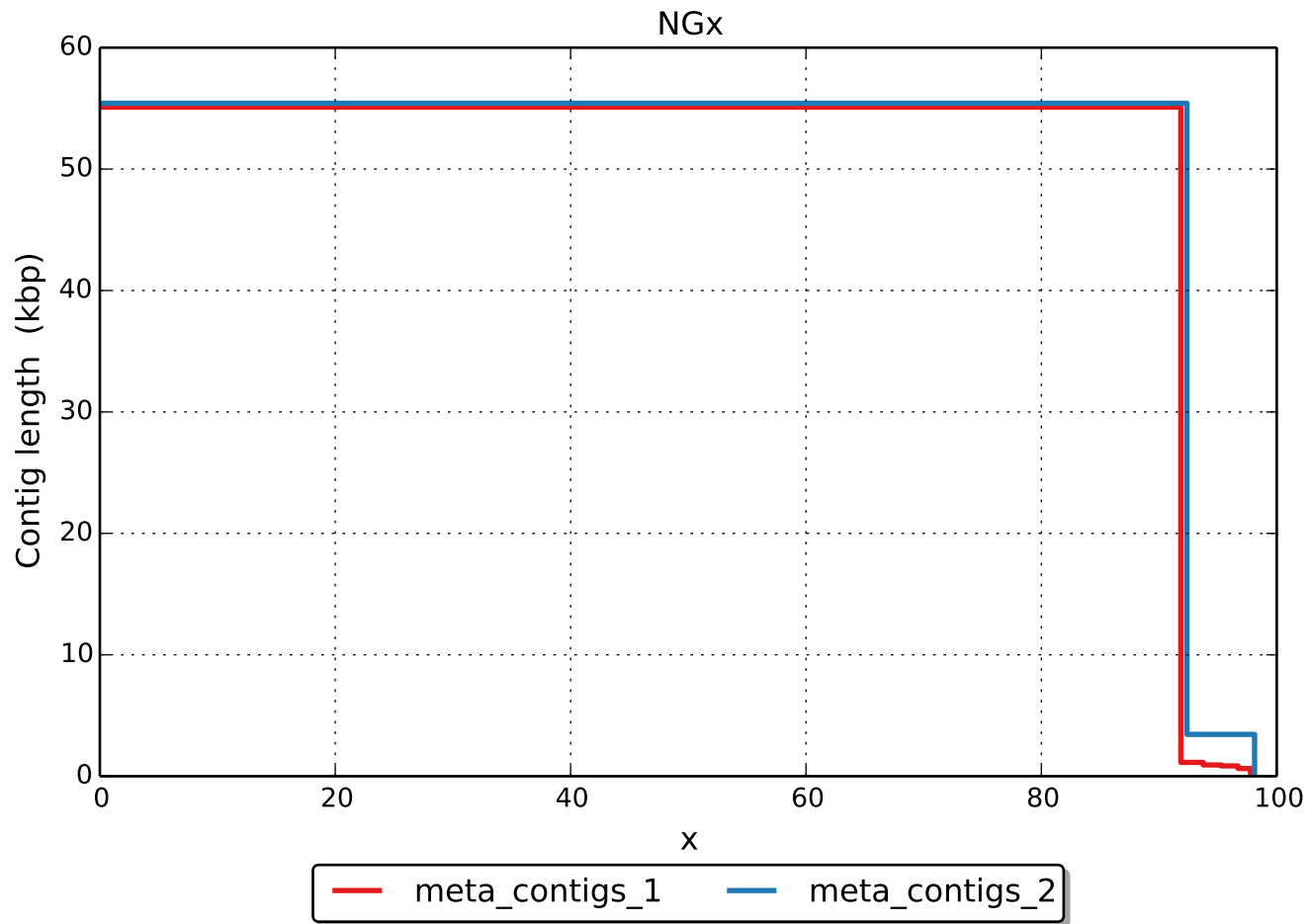
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

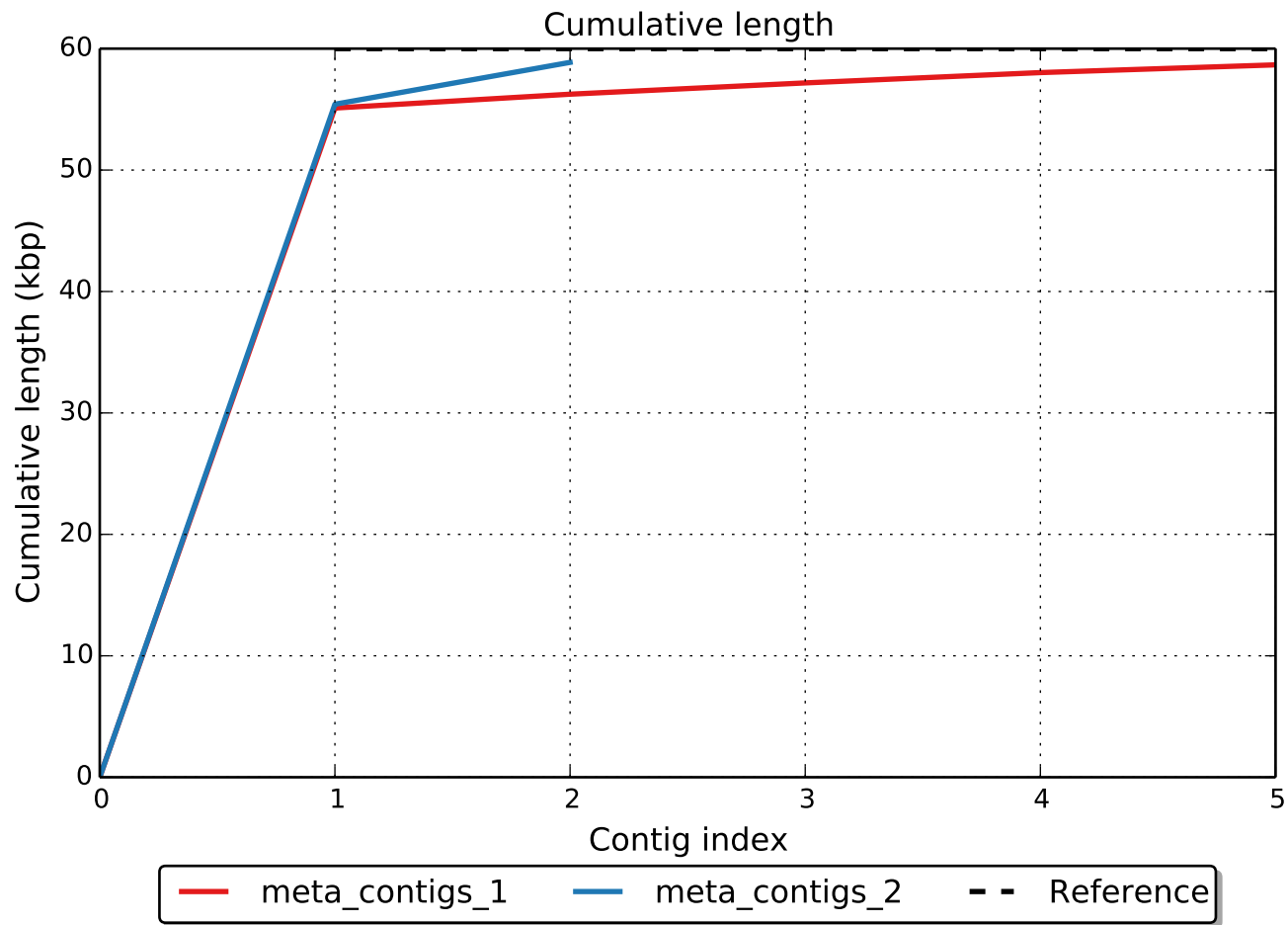
Unaligned report

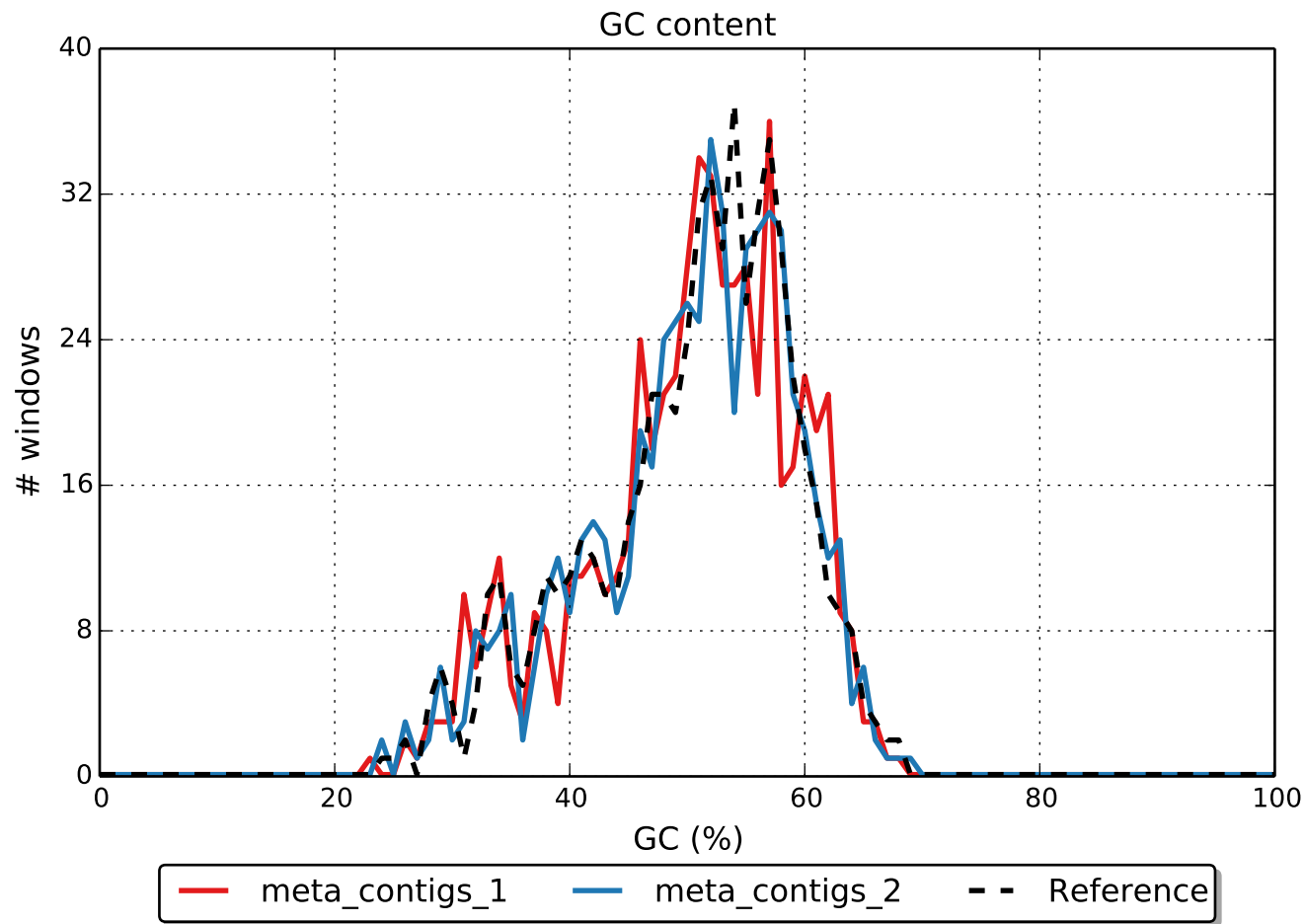
	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	1	0

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).









Misassemblies

