

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	3044678	3044678
GC (%)	45.67	45.67
Reference GC (%)	44.74	44.74
N50	49658	49658
N75	49658	49658
L50	1	1
L75	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 (%)	1.654	1.654
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	375.36	375.36
# indels per 100 kbp	17.87	17.87
Largest alignment	49639	49639
NA50	49639	49639
NGA50	-	-
NA75	49639	49639
LA50	1	1
LA75	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

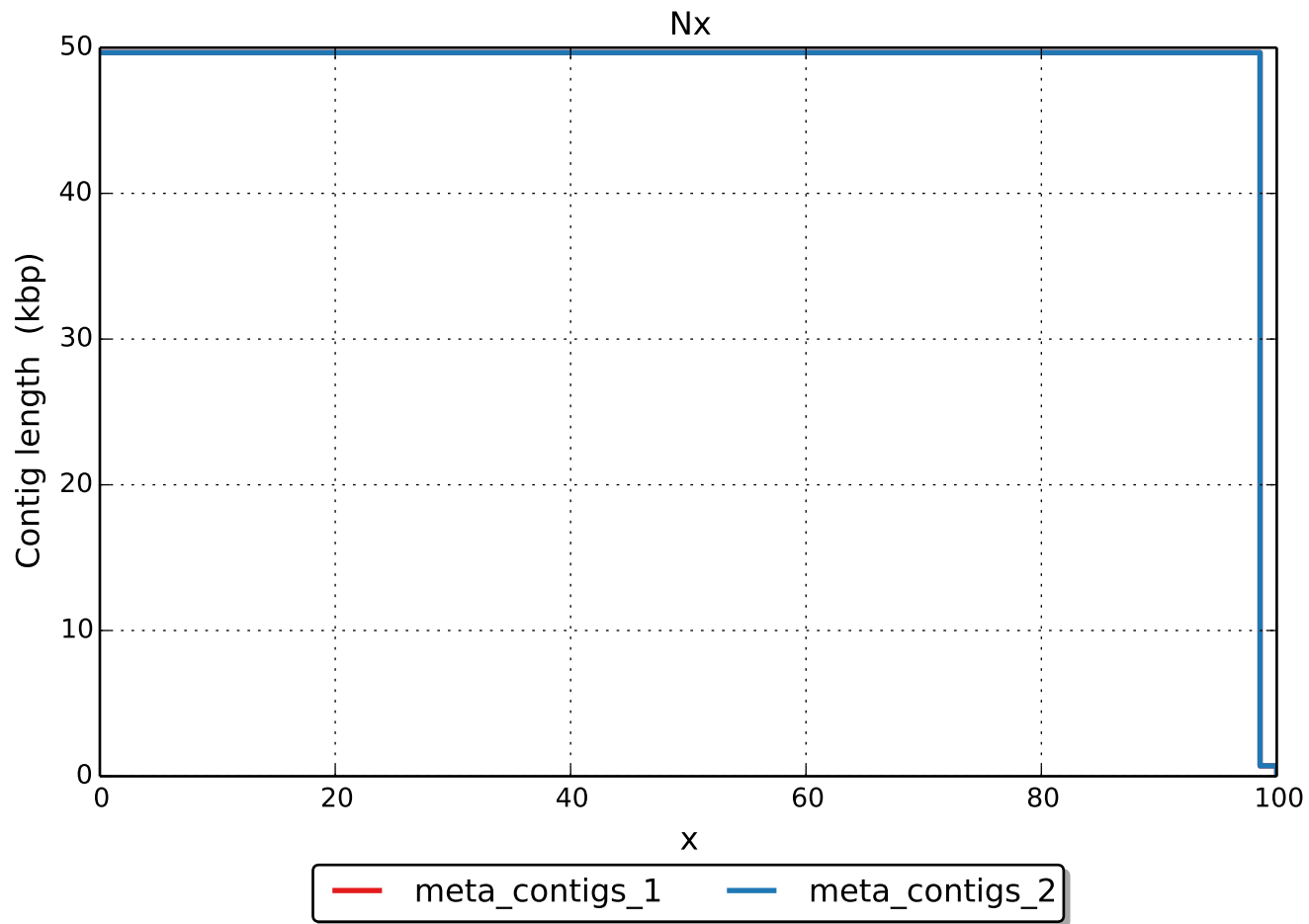
	meta_contigs_1	meta_contigs_2
# misassemblies	0	0
# relocations	0	0
# translocations	0	0
# inversions	0	0
# possibly misassembled contigs	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# mismatches	189	189
# indels	9	9
# short indels	7	7
# long indels	2	2
Indels length	30	30

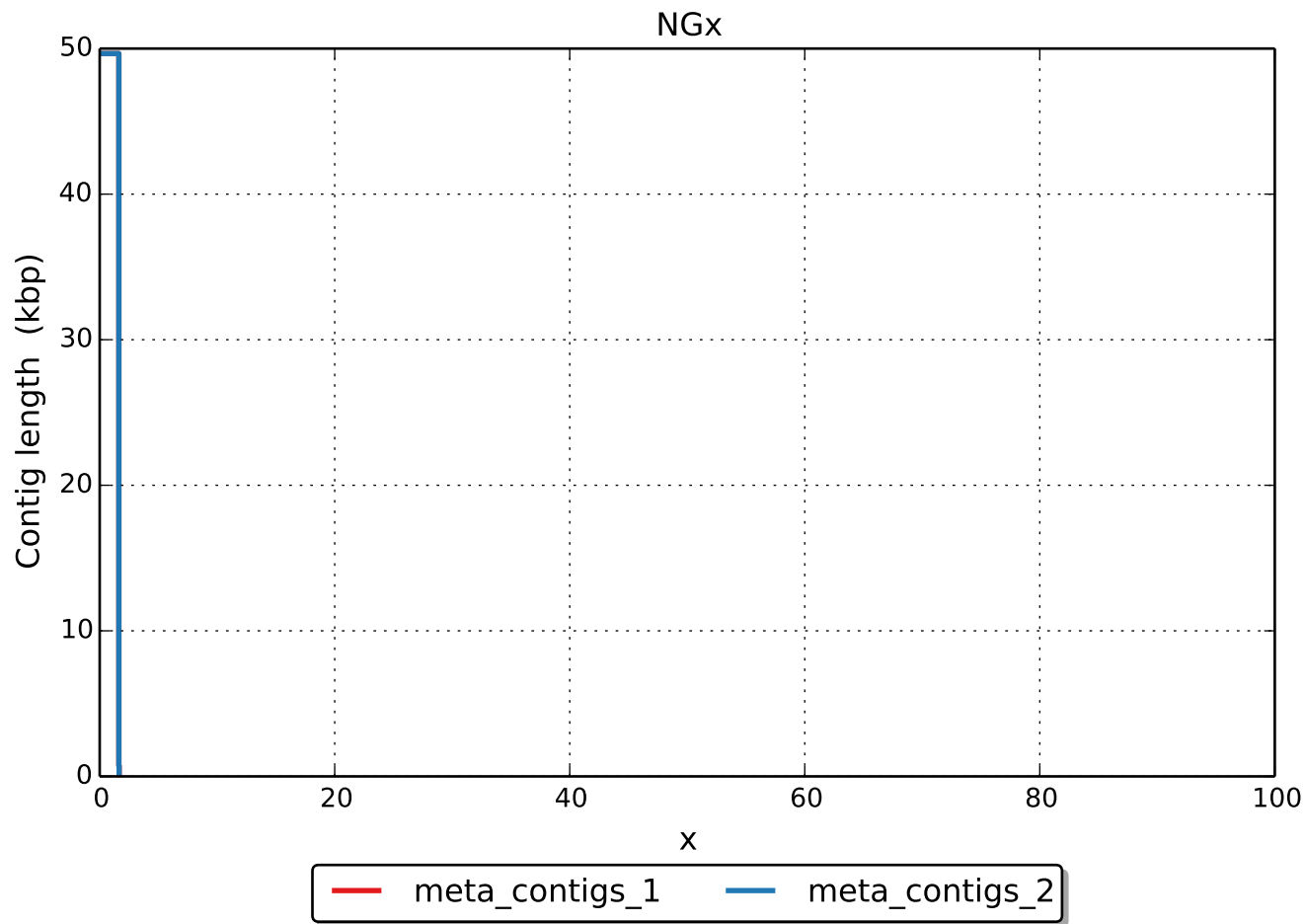
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

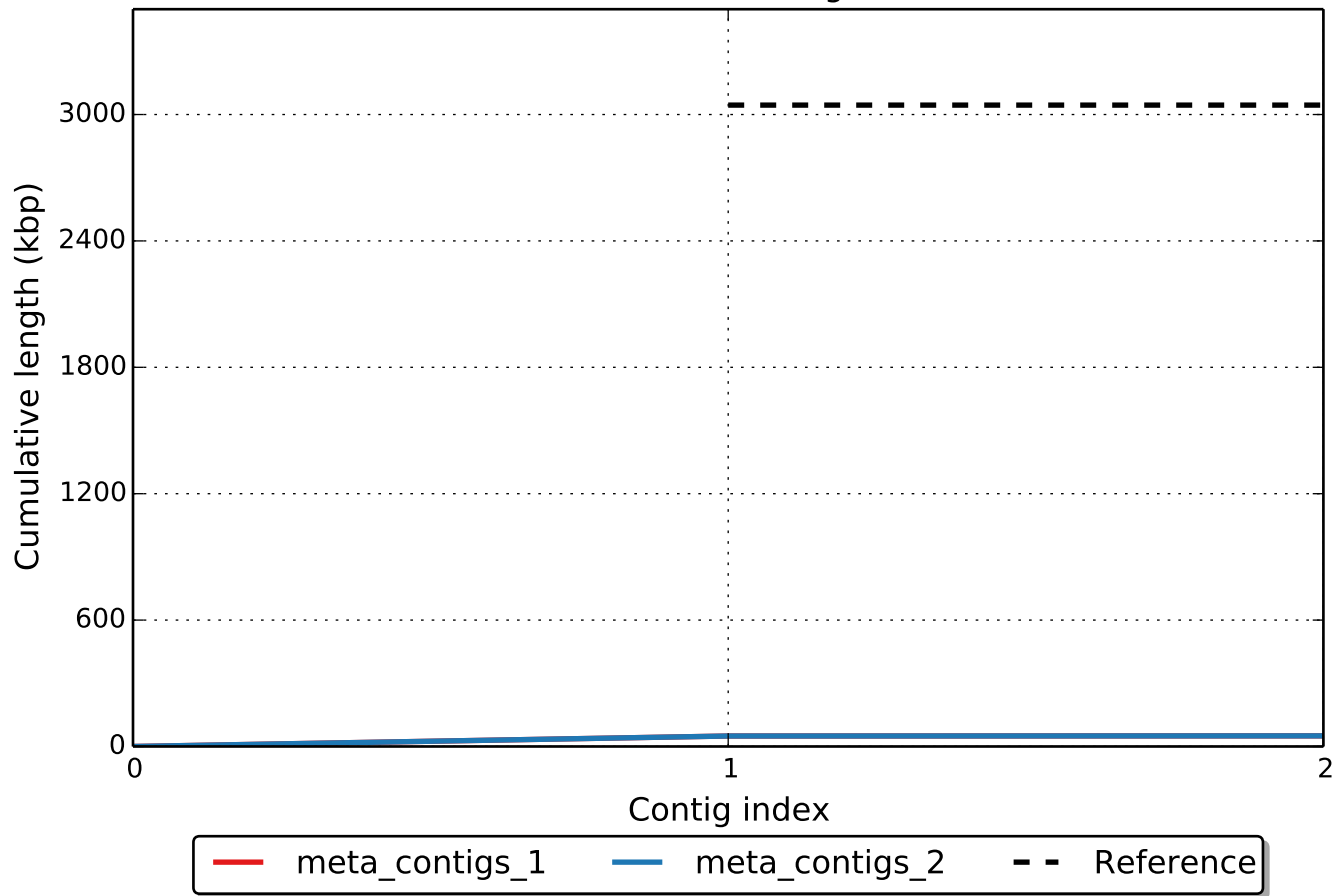
	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	0	0
# N's	0	0

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).

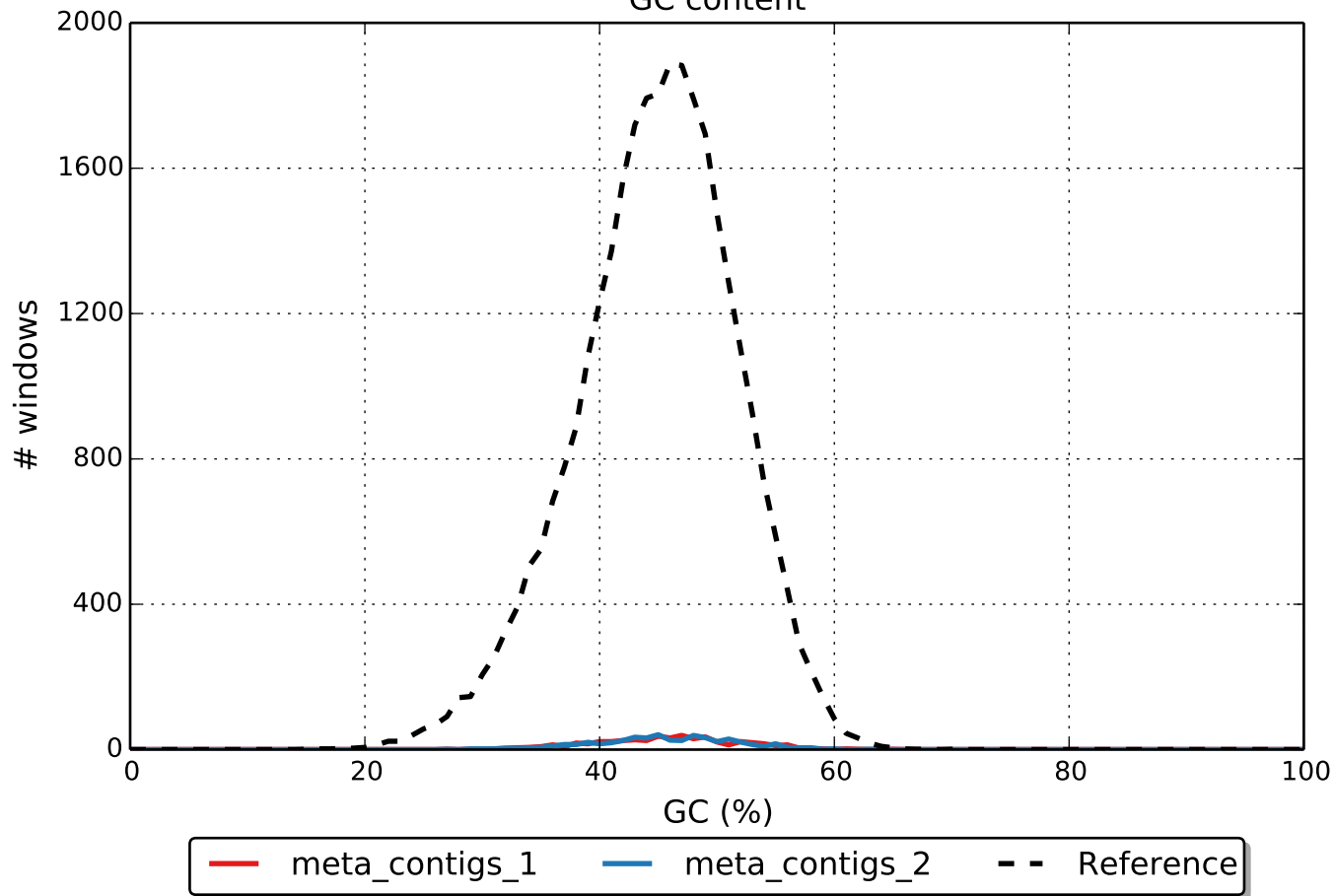


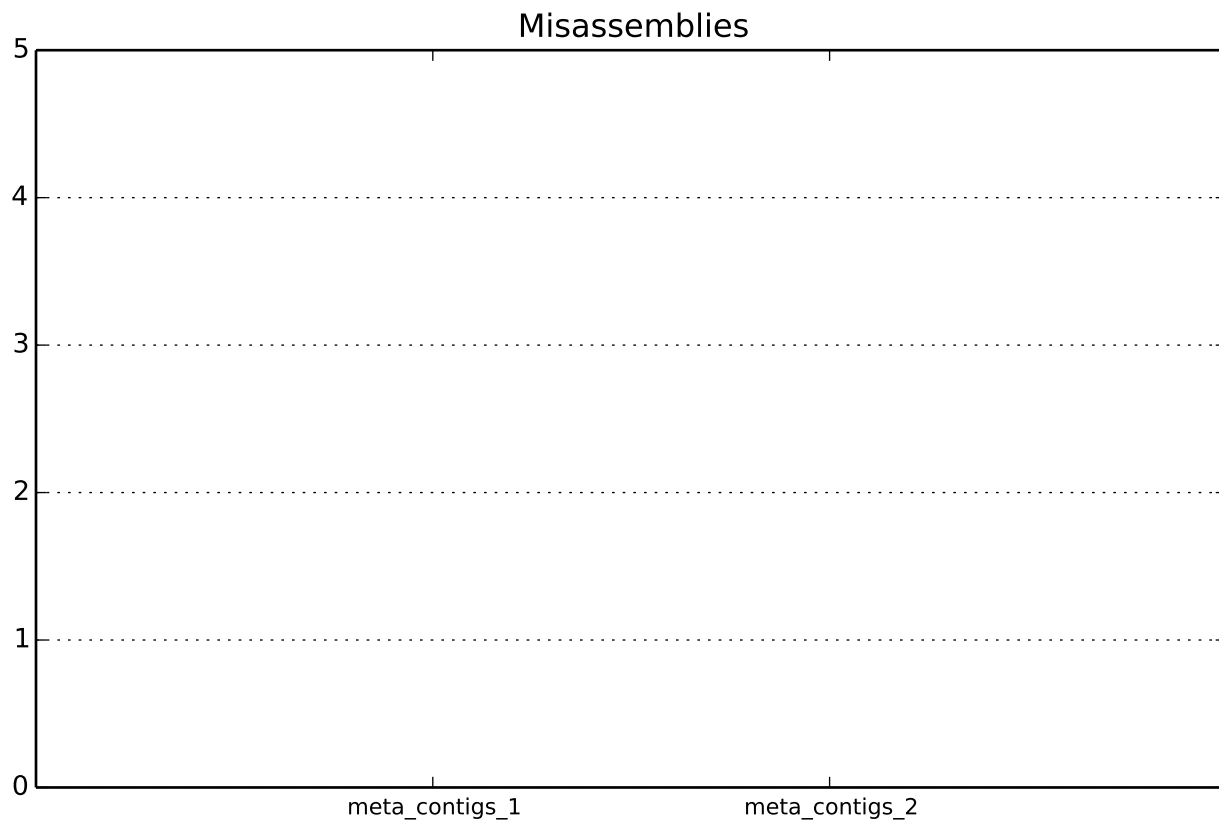


Cumulative length



GC content





Cumulative length (aligned contigs)

