Report

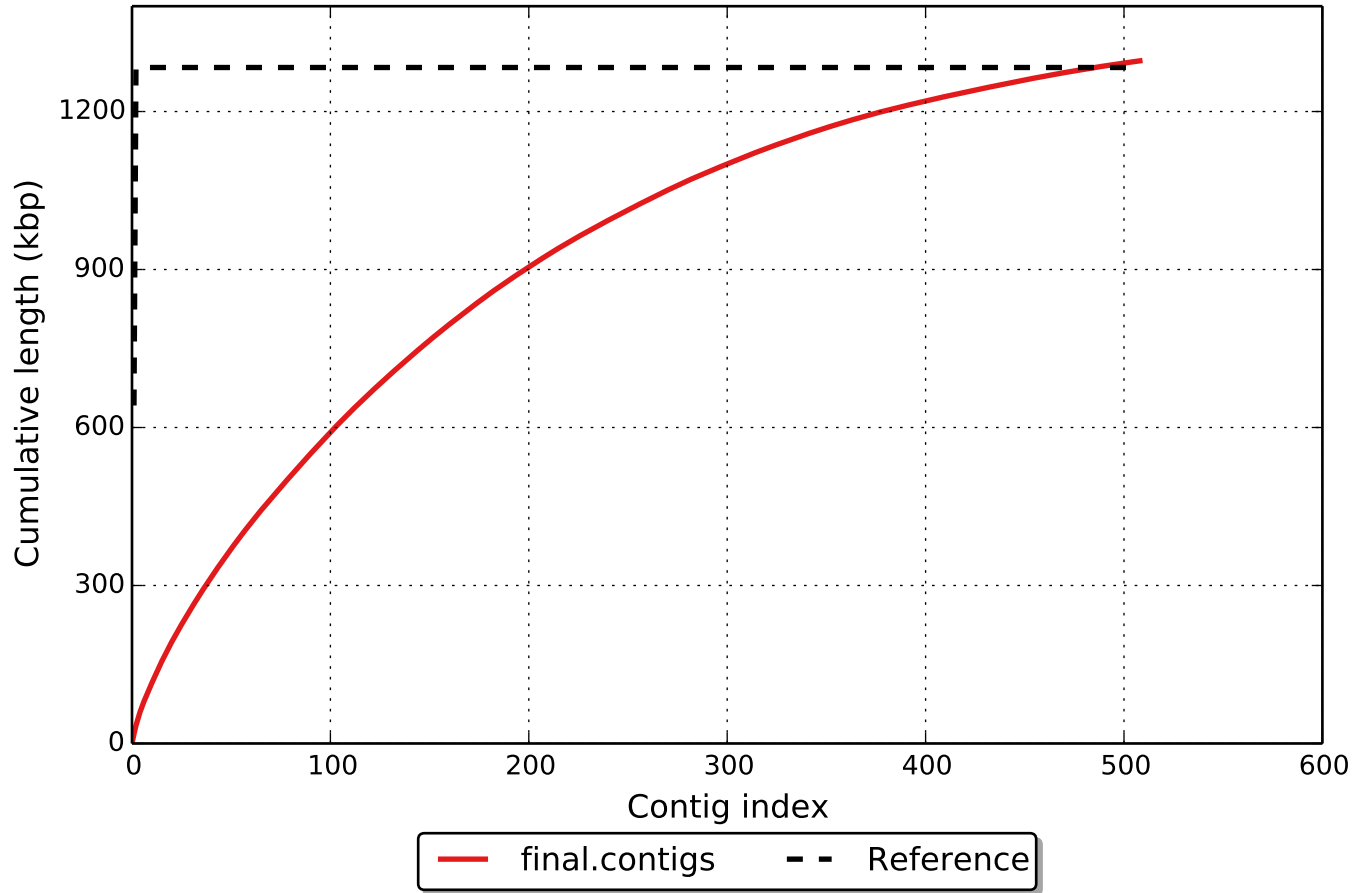|	final.contigs
# contigs (>= 0 bp)	578
# contigs (>= 1000 bp)	377
Total length (>= 0 bp)	1321047
Total length (>= 1000 bp)	1198900
# contigs	508
Largest contig	18135
Total length	1296225
Reference length	1283598
GC (%)	26.29
Reference GC (%)	26.29
N50	3618
NG50	3661
N75	2097
NG75	2137
L50	116
LG50	114
L75	230
LG75	226
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.988
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.28
# indels per 100 kbp	0.00
Largest alignment	18135
NA50	3618
NGA50	3661
NA75	2097
NGA75	2137
LA50	116
LGA50	114
LA75	230
LGA75	226

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

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	79
# indels	0
# short indels	0
# long indels	0
Indels length	0

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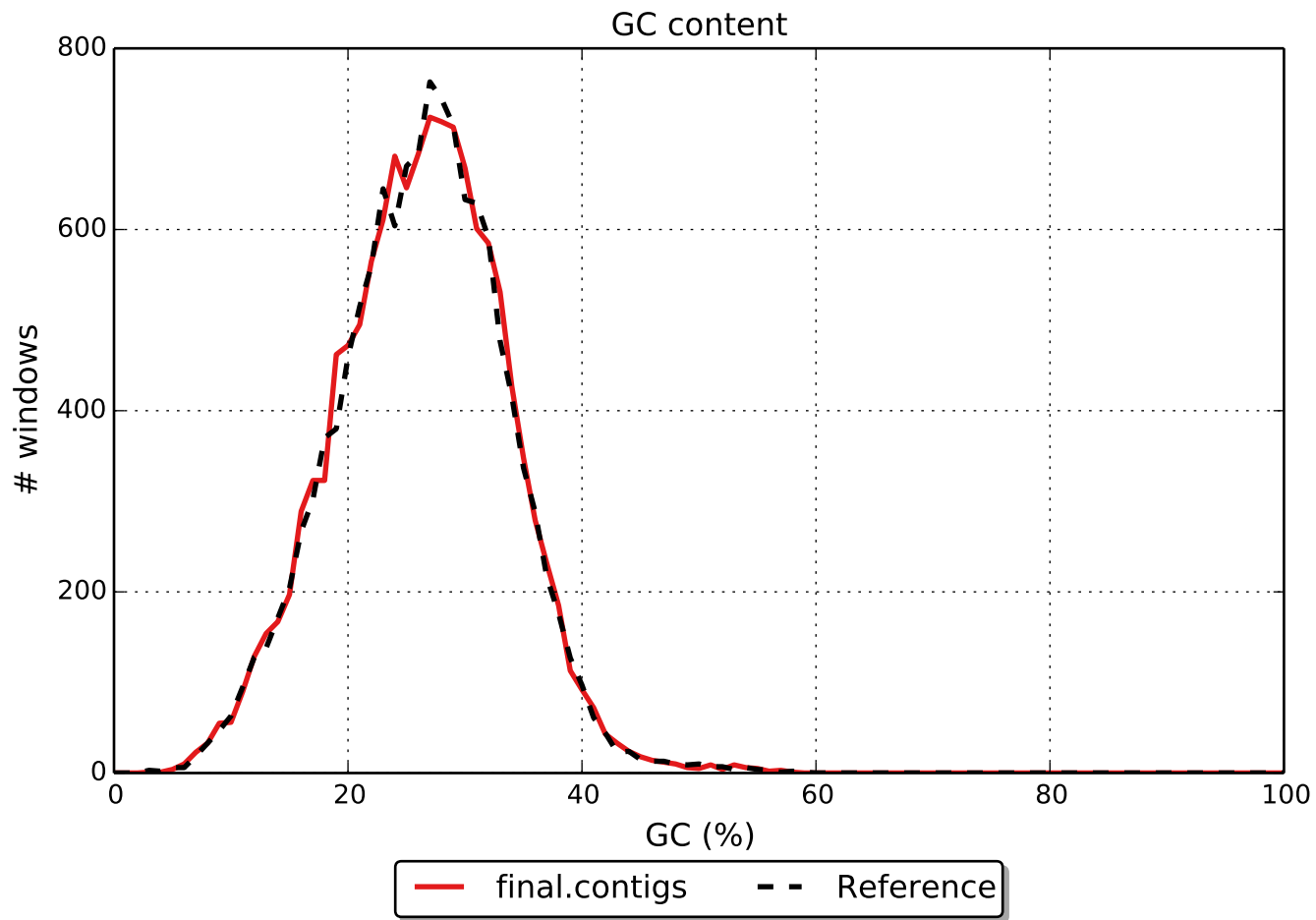(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
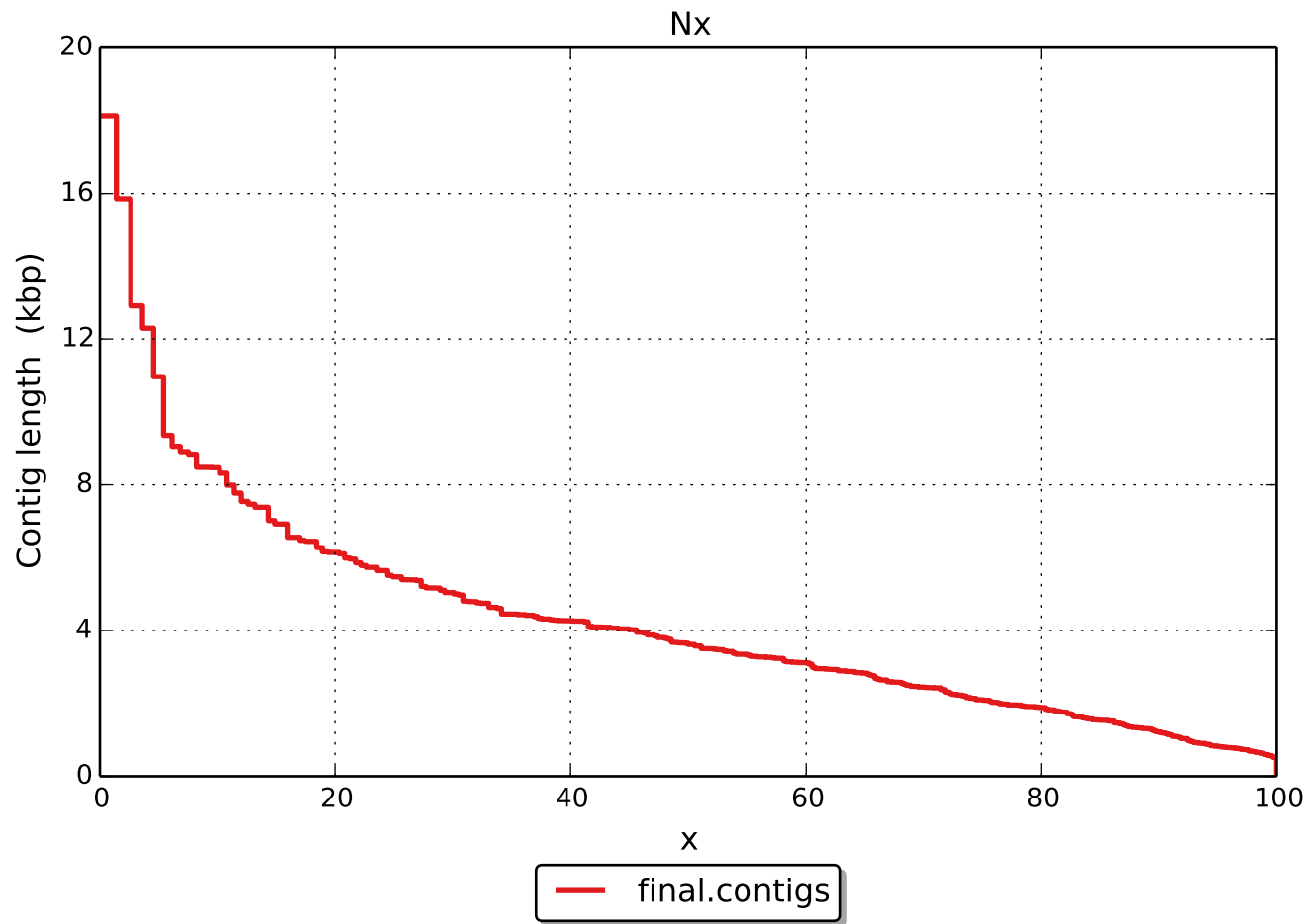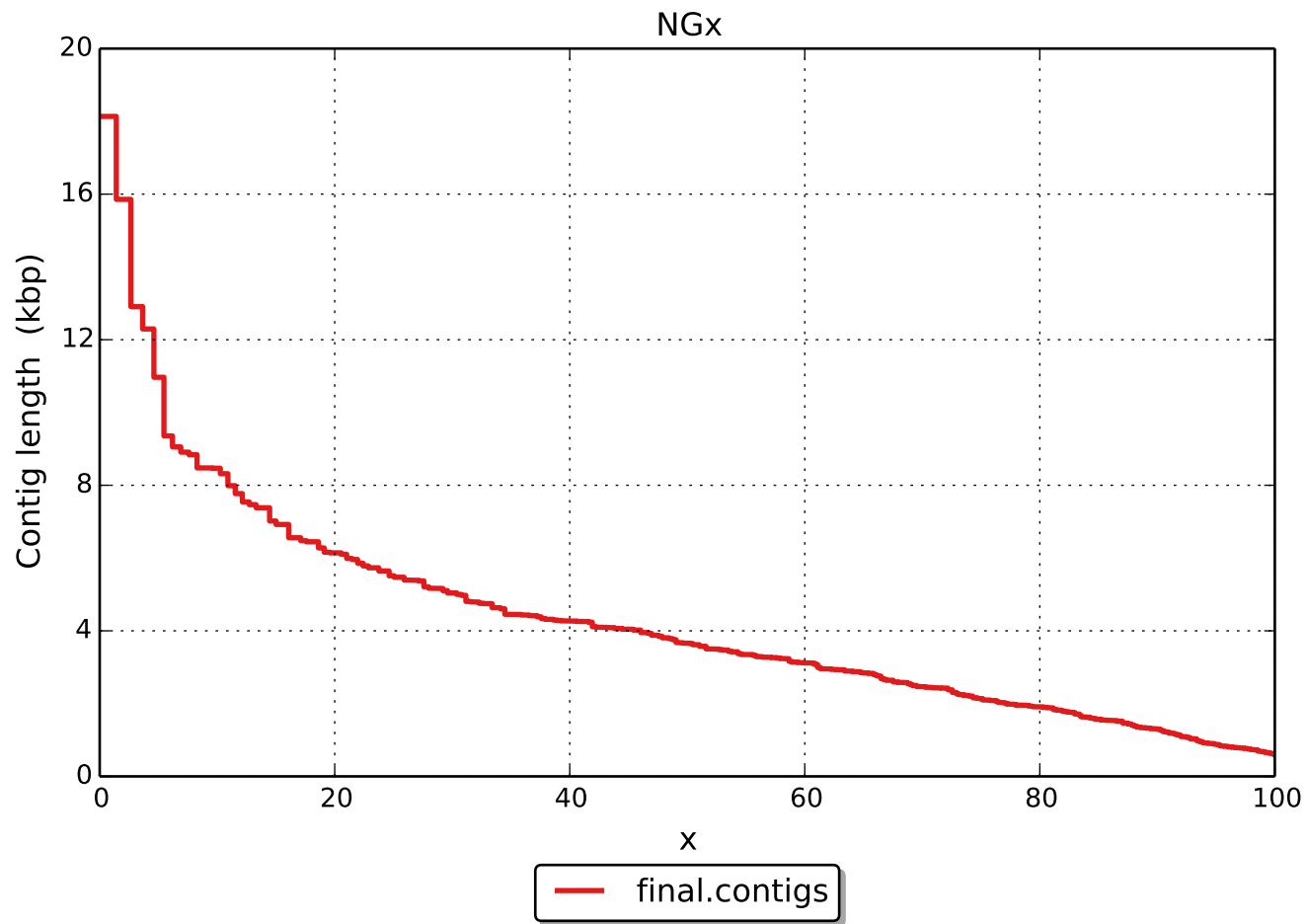
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	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).
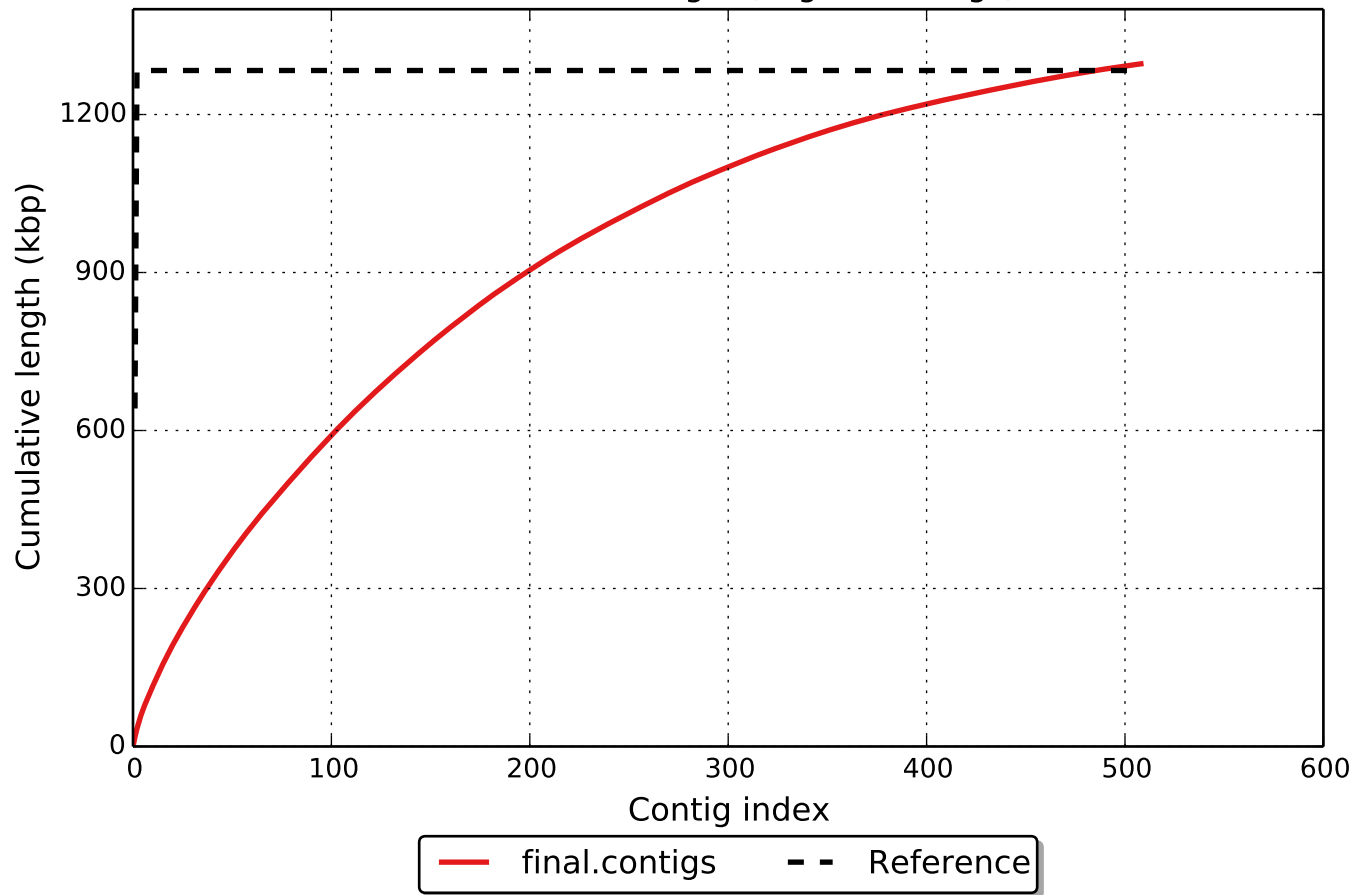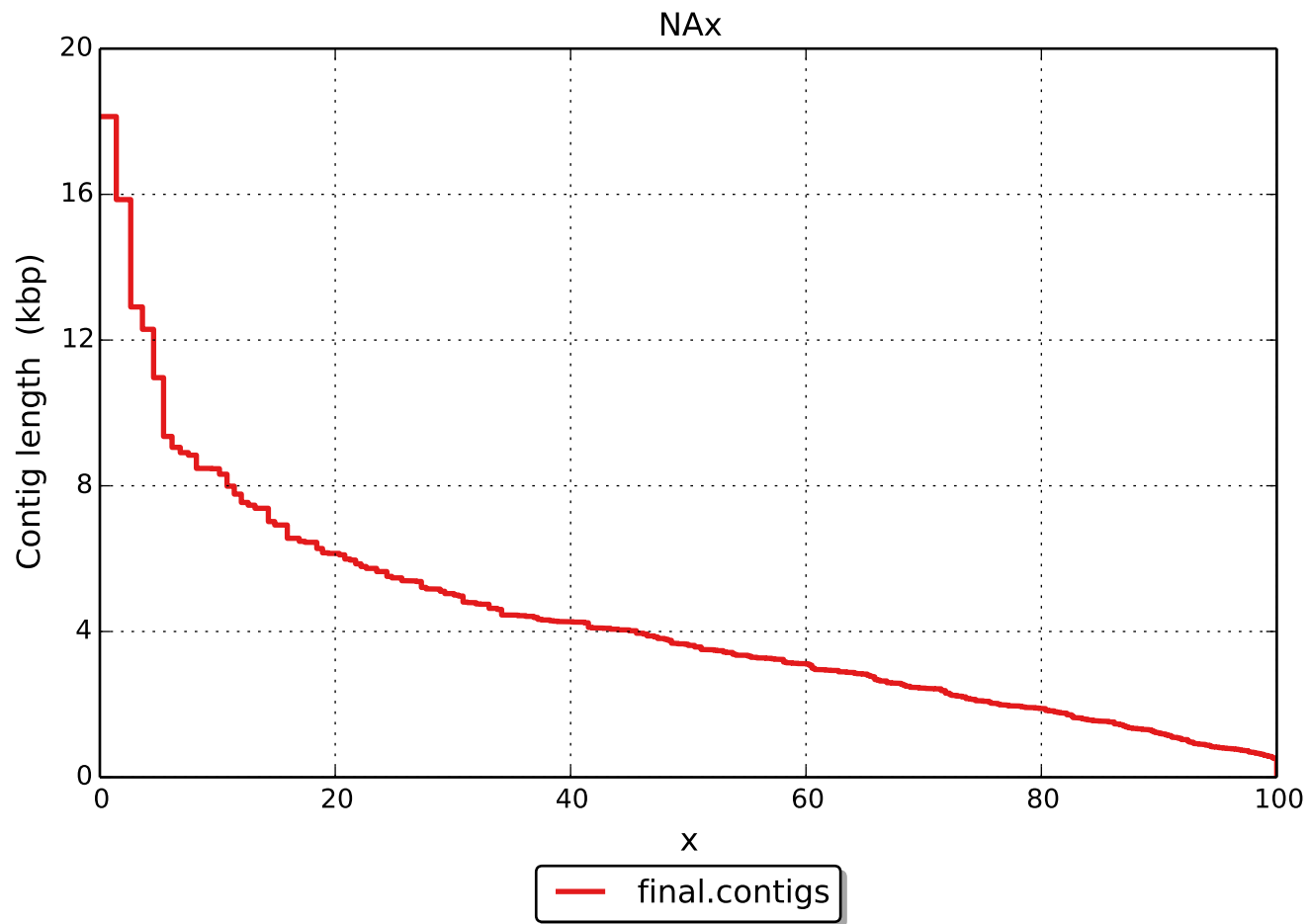
Cumulative length

GC content

windows vs. GC (%)

final.contigs — Reference

Nx

Contig length (kbp) vs x

final.contigs

Misassemblies

final.contigs

Cumulative length (aligned contigs)