Report

	final.contigs
# contigs (>= 0 bp)	6861
# contigs (>= 1000 bp)	3821
Total length (>= 0 bp)	11217884
Total length (>= 1000 bp)	9576202
# contigs	5380
Largest contig	12599
Total length	10721602
Reference length	11094646
GC (%)	50.38
Reference GC (%)	50.48
N50	2606
NG50	2534
N75	1575
NG75	1471
L50	1287
LG50	1360
L75	2606
LG75	2790
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1135
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.282
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	43.78
# indels per 100 kbp	0.16
Largest alignment	12599
NA50	2606
NGA50	2534
NA75	1575
NGA75	1471
LA50	1287
LGA50	1360
LA75	2606
LGA75	2790

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).
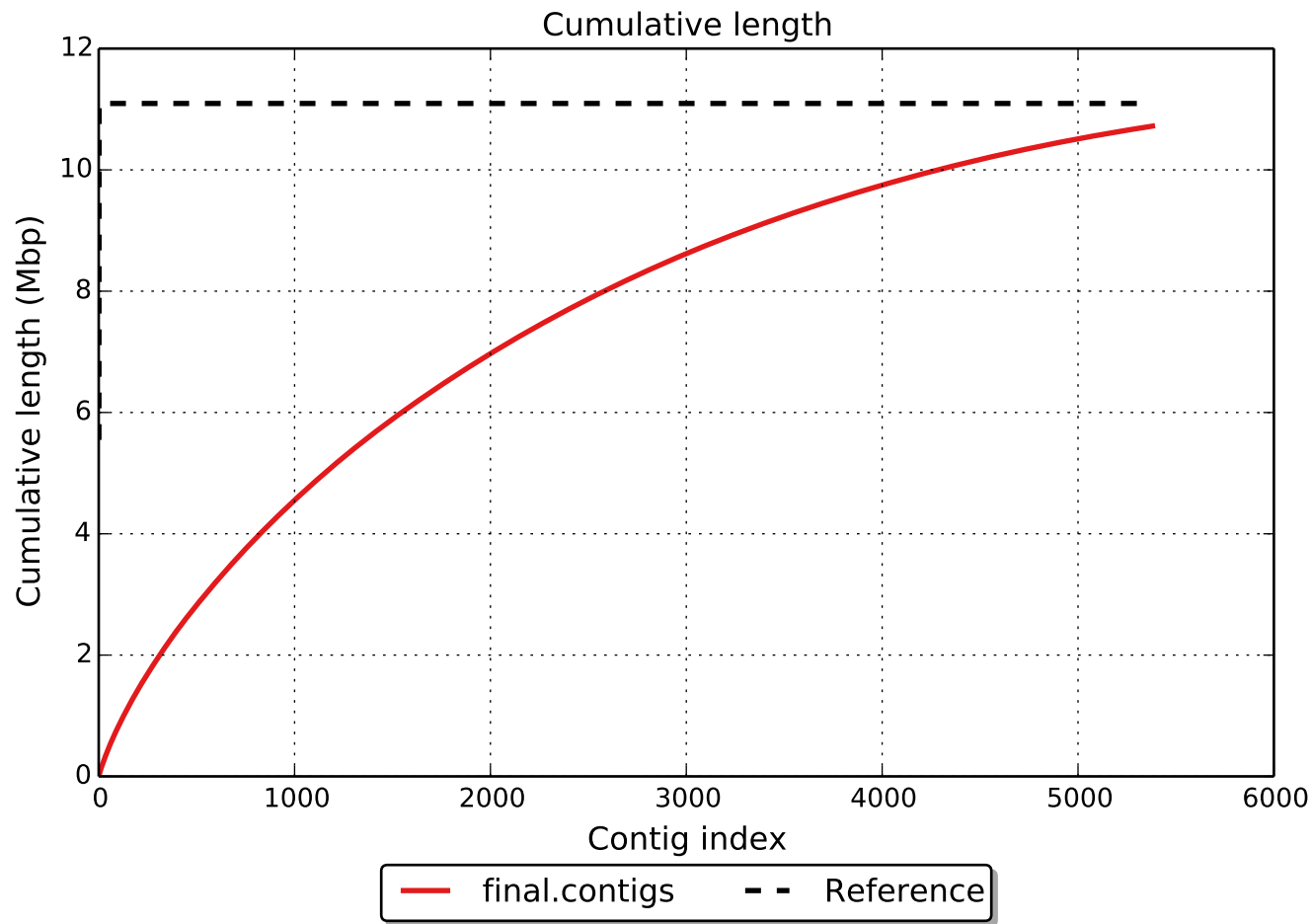
Misassemblies report

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1135
# local misassemblies	0
# mismatches	4579
# indels	17
# short indels	15
# long indels	2
Indels length	42

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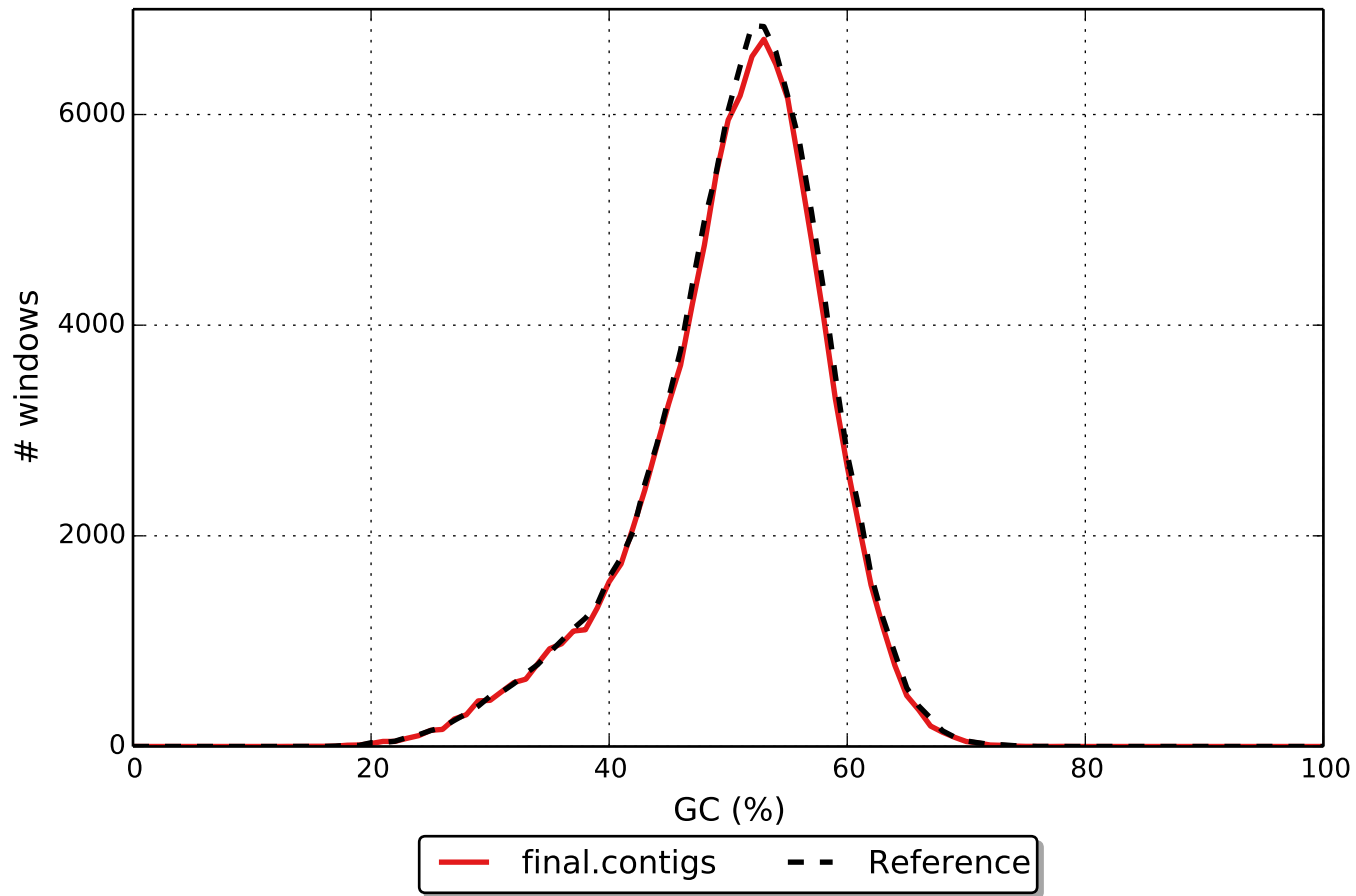(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
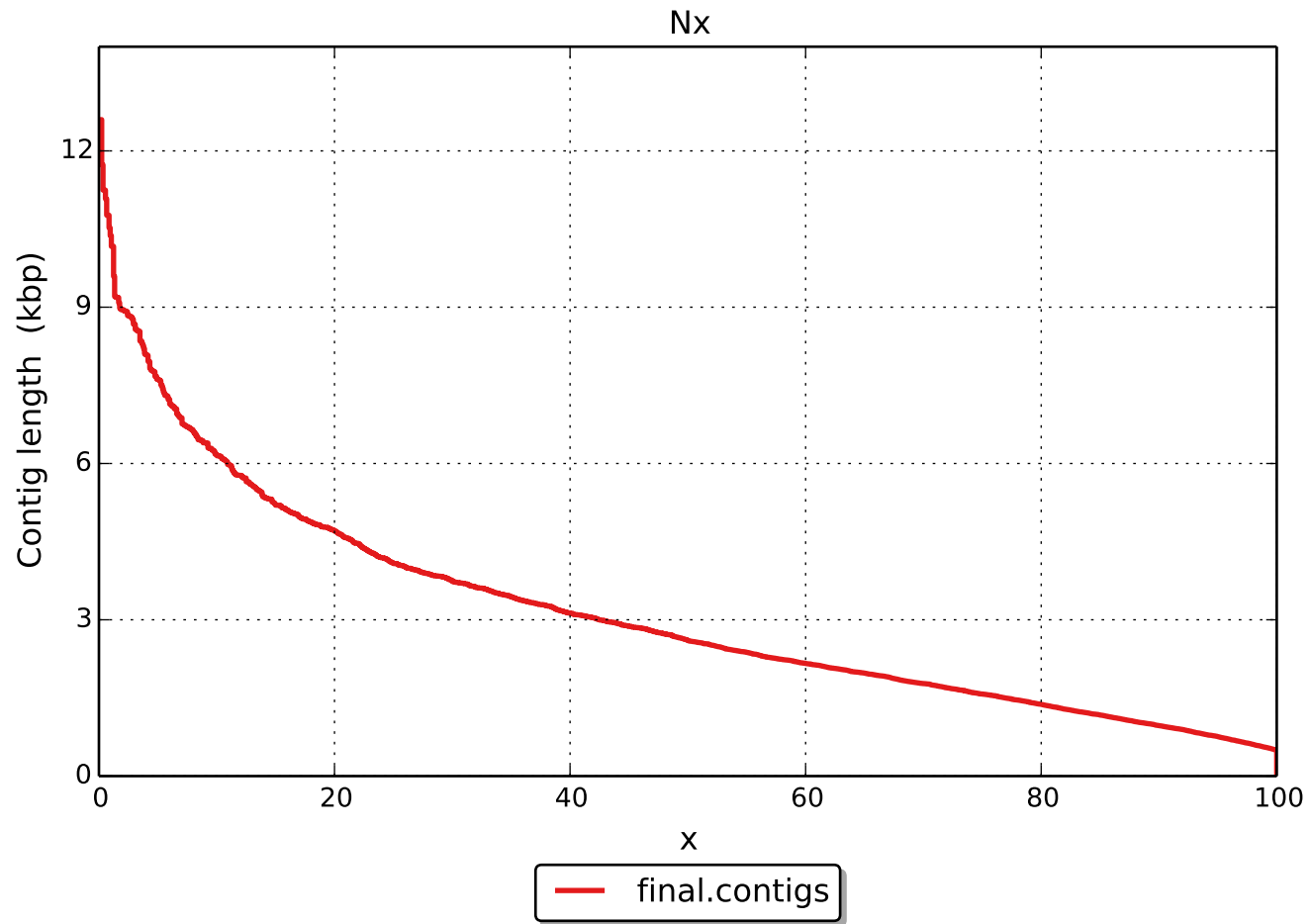
Unaligned report

	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
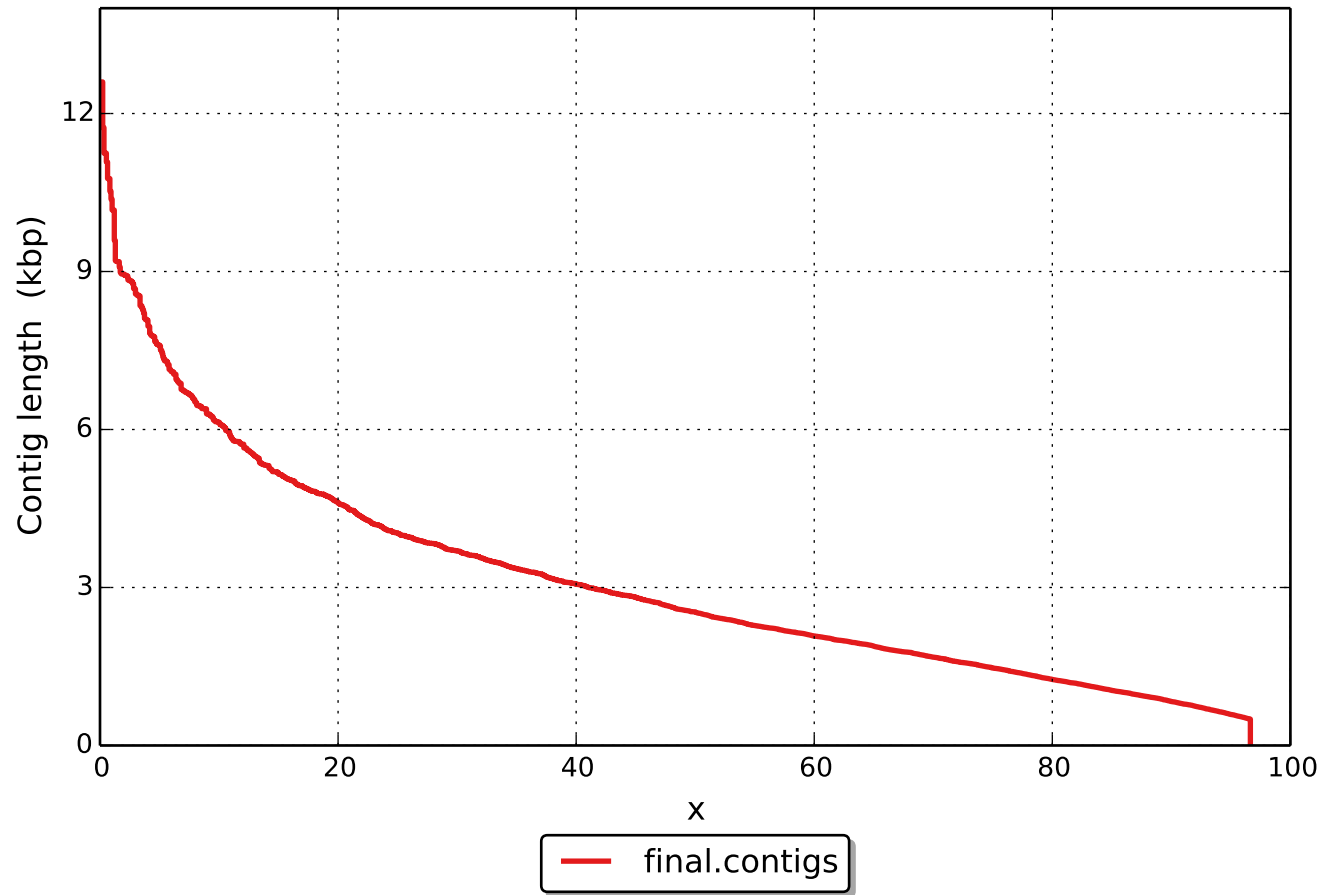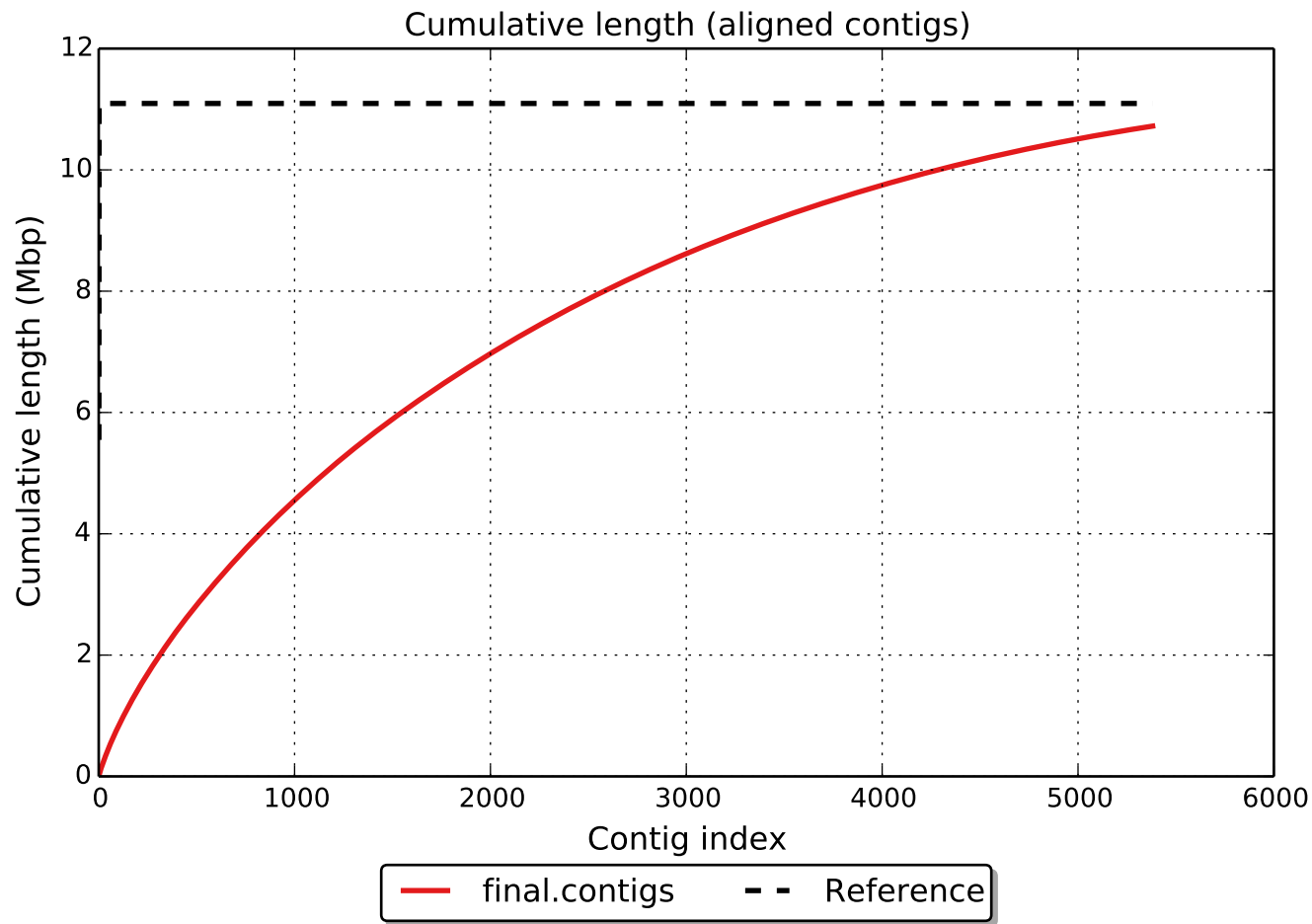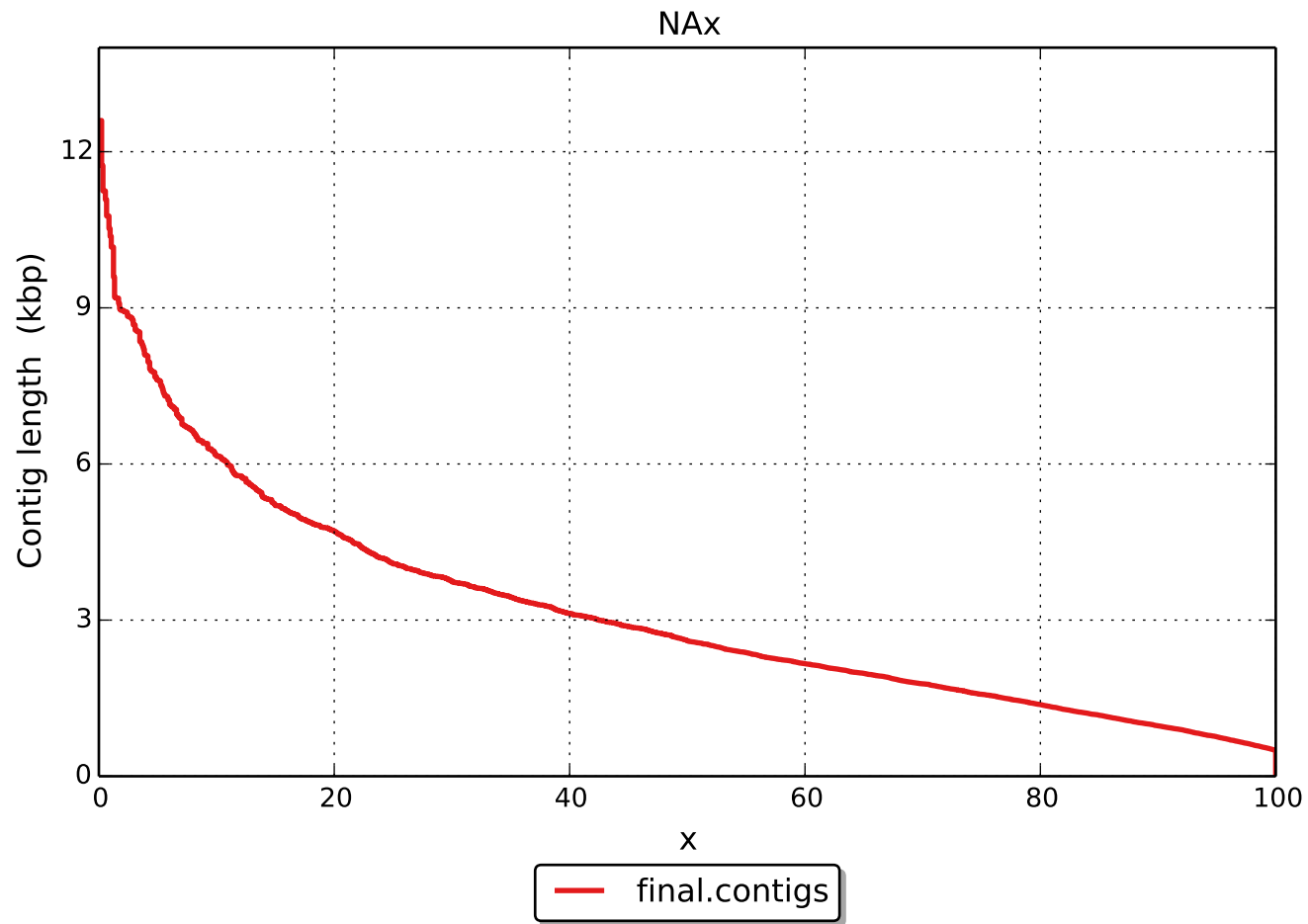(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

NGx

Misassemblies

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

final.contigs