Report

	final.contigs
# contigs (>= 0 bp)	4741
# contigs (>= 1000 bp)	1555
Total length (>= 0 bp)	4639742
Total length (>= 1000 bp)	2419677
# contigs	4741
Largest contig	7611
Total length	4639742
Reference length	5478683
GC (%)	50.37
Reference GC (%)	50.50
N50	1033
NG50	900
N75	721
NG75	598
L50	1457
LG50	1893
L75	2816
LG75	3774
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	79.466
Duplication ratio	1.066
# N's per 100 kbp	0.00
# mismatches per 100 kbp	385.65
# indels per 100 kbp	0.16
Largest alignment	7611
NA50	1033
NGA50	900
NA75	721
NGA75	598
LA50	1457
LGA50	1893
LA75	2816
LGA75	3774

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).
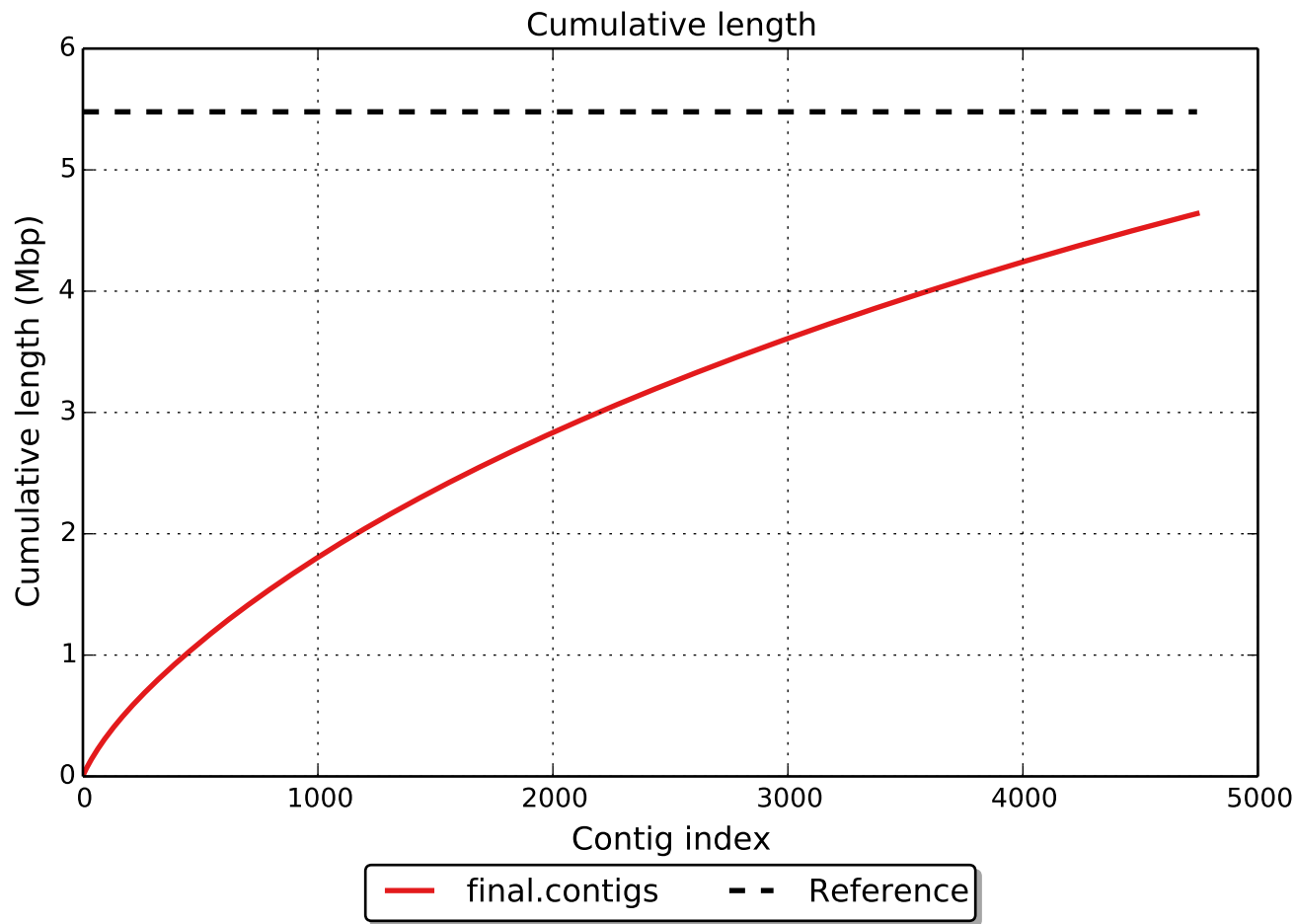
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	16790
# indels	7
# short indels	6
# long indels	1
Indels length	12

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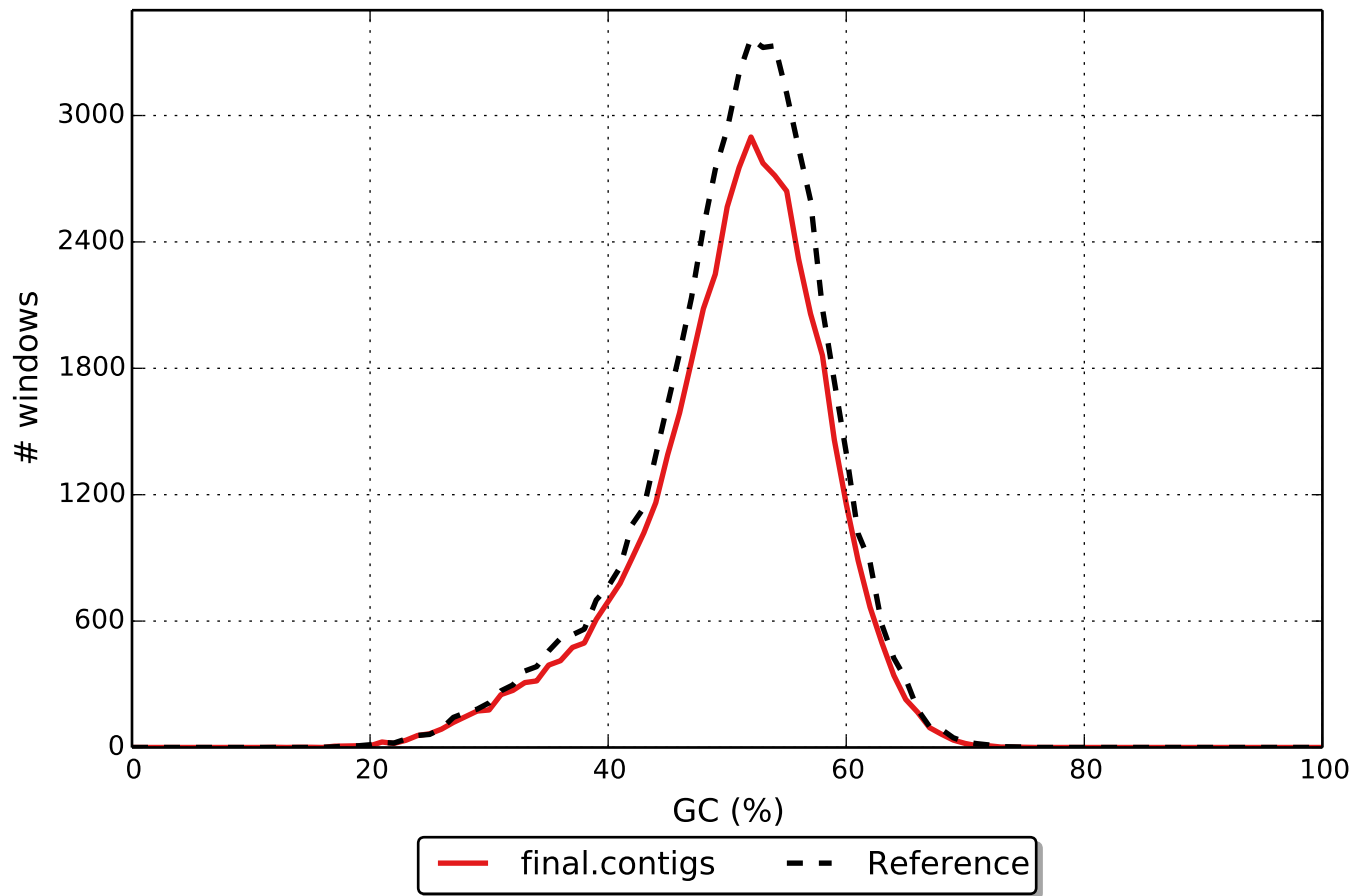(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
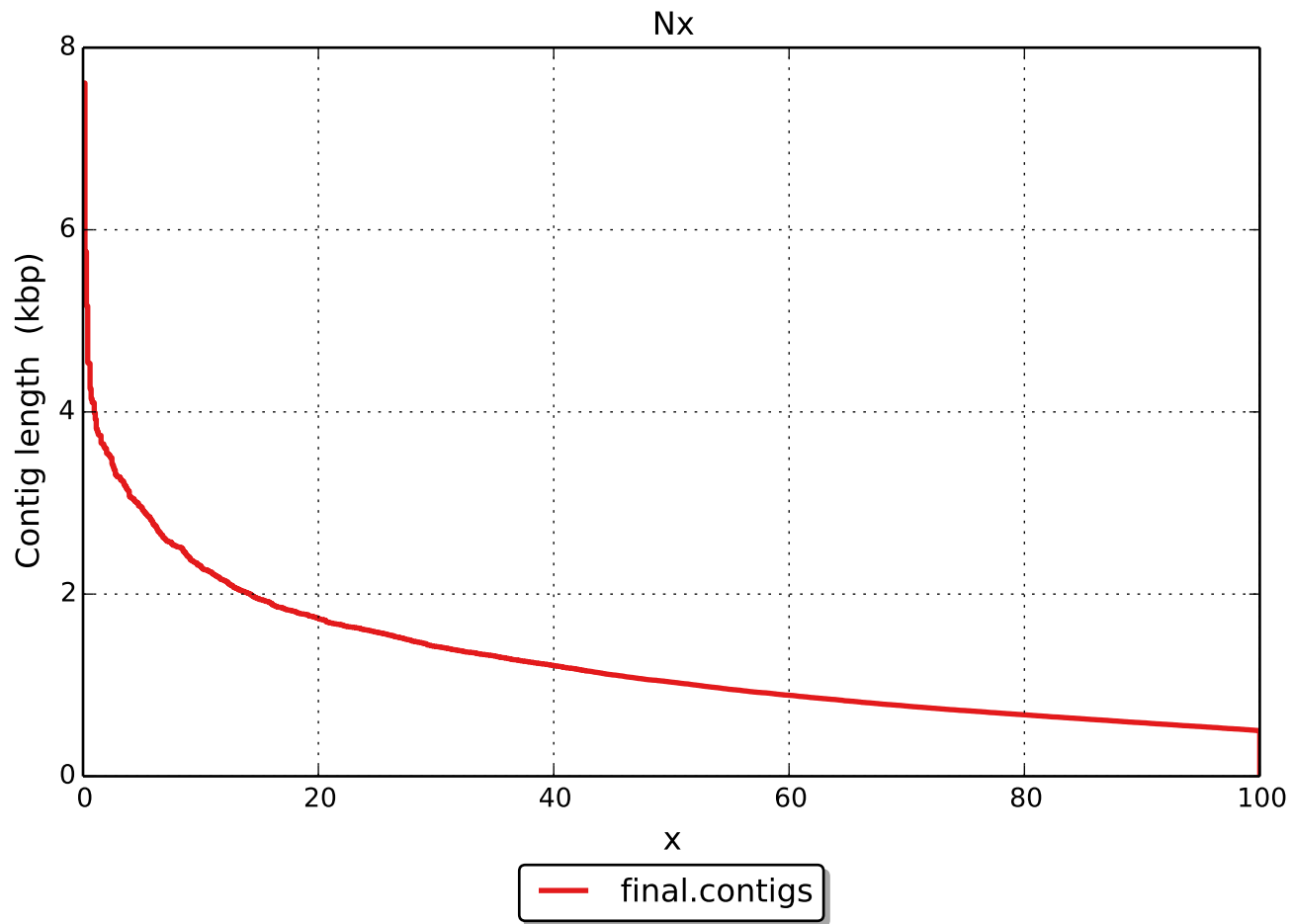
Unaligned report

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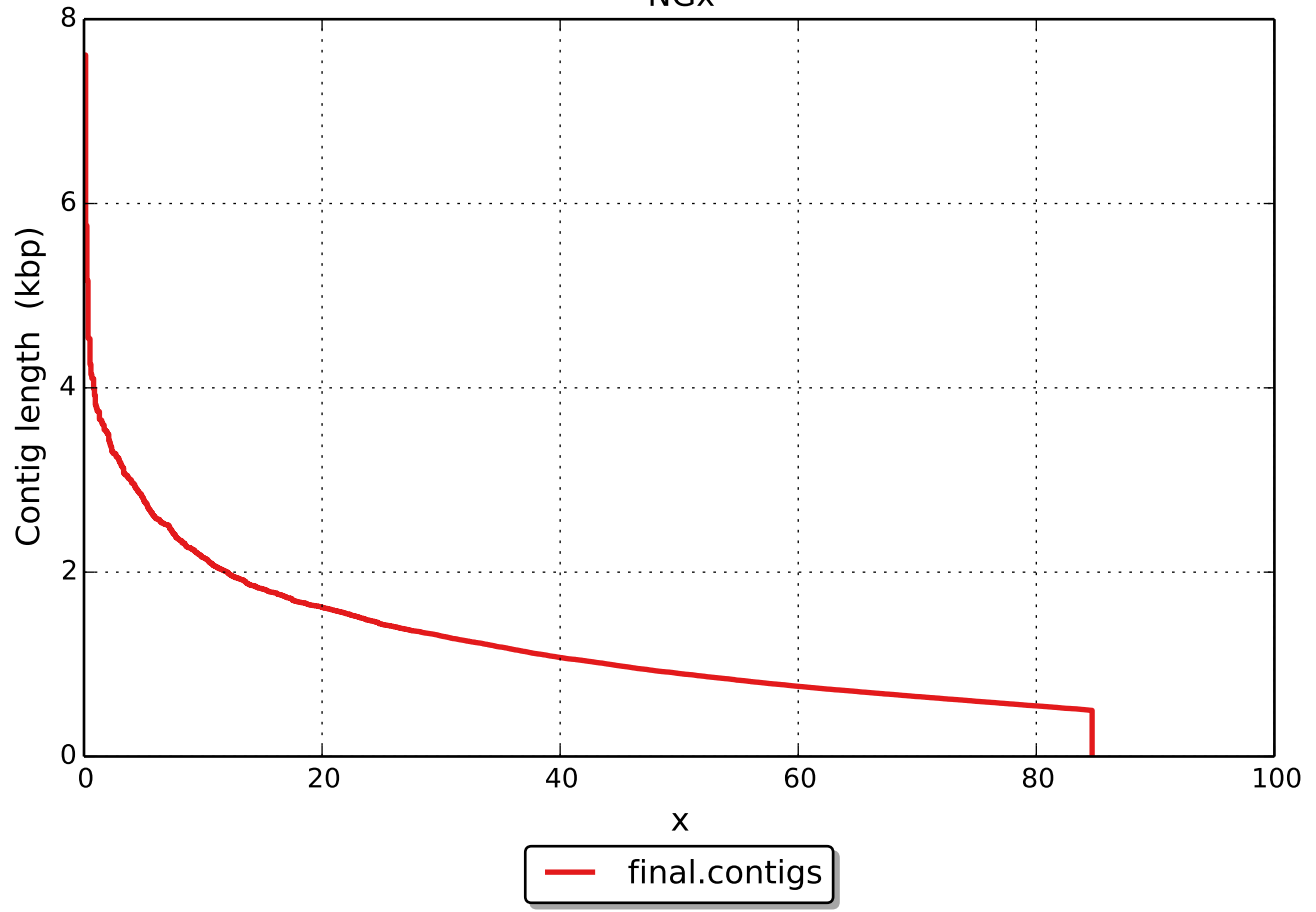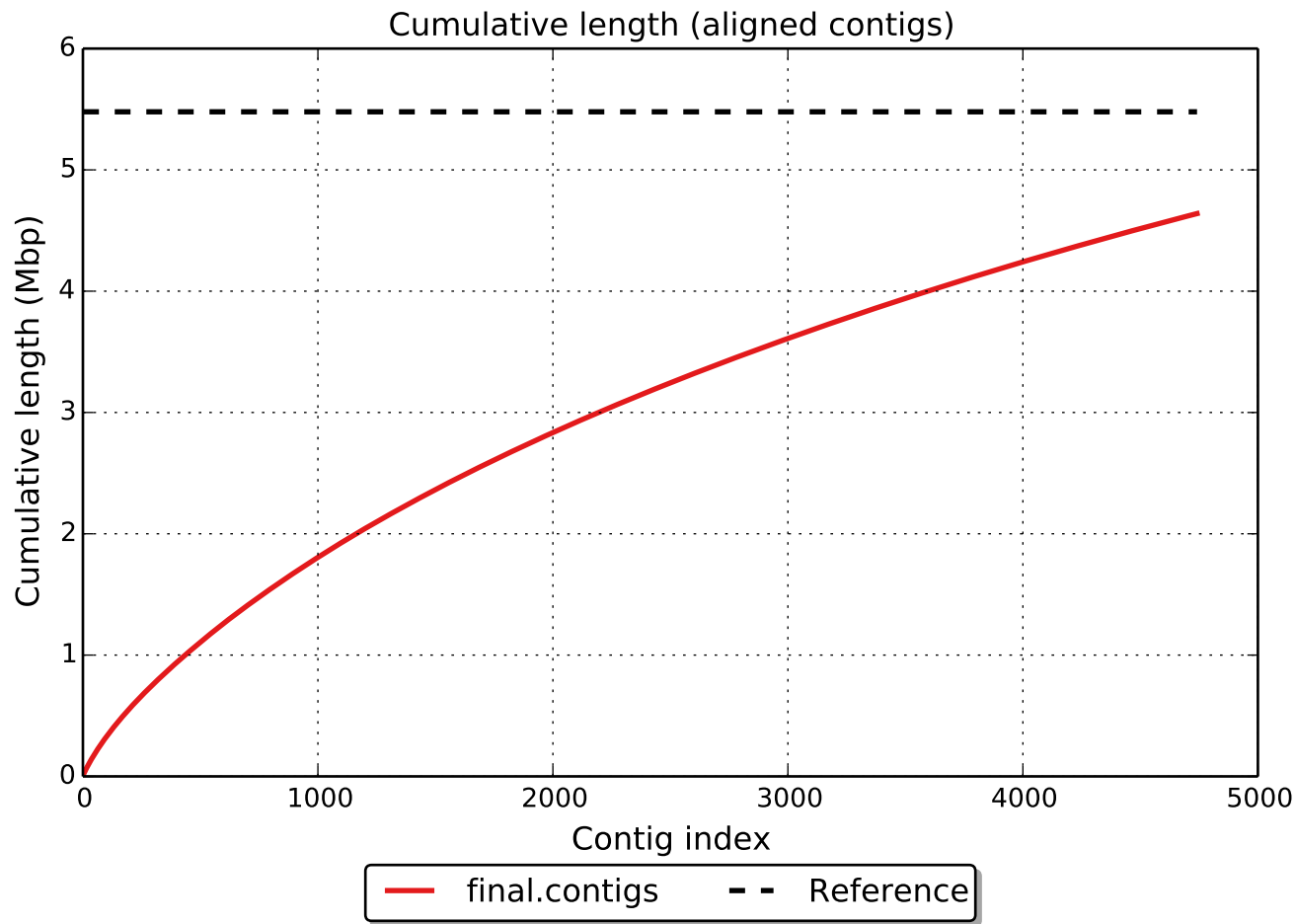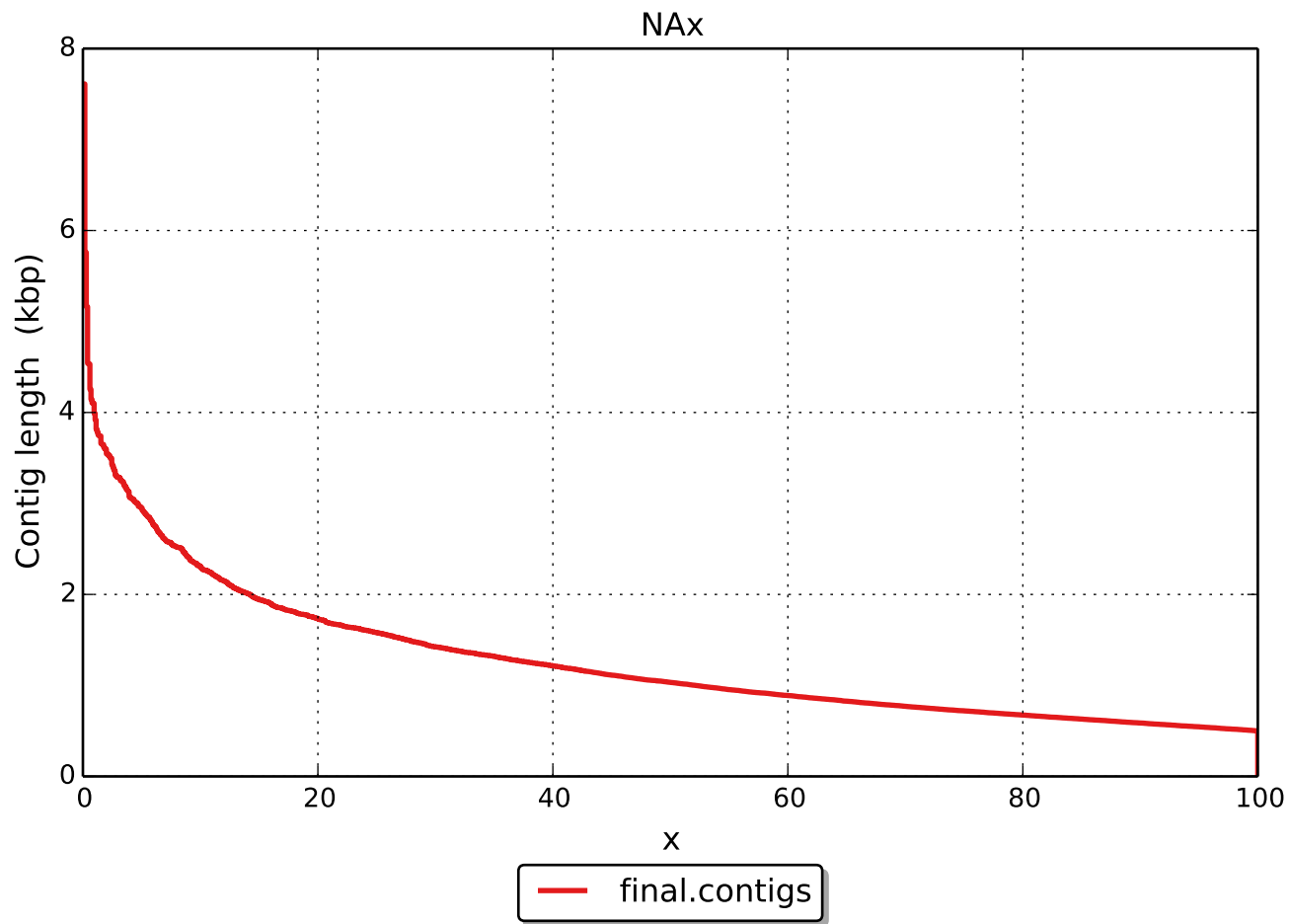(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

NGx

Contig length (kbp)

x

final.contigs

Misassemblies

final.contigs

Cumulative length (aligned contigs)