Report

	final.contigs
# contigs (>= 0 bp)	1123
# contigs (>= 1000 bp)	831
Total length (>= 0 bp)	5056487
Total length (>= 1000 bp)	4860265
# contigs	1123
Largest contig	39846
Total length	5056487
Reference length	5547323
GC (%)	50.27
Reference GC (%)	50.48
N50	8603
NG50	7975
N75	4507
NG75	3245
L50	177
LG50	206
L75	378
LG75	474
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.125
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	521.69
# indels per 100 kbp	0.04
Largest alignment	39846
NA50	8603
NGA50	7975
NA75	4507
NGA75	3245
LA50	177
LGA50	206
LA75	378
LGA75	474

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).
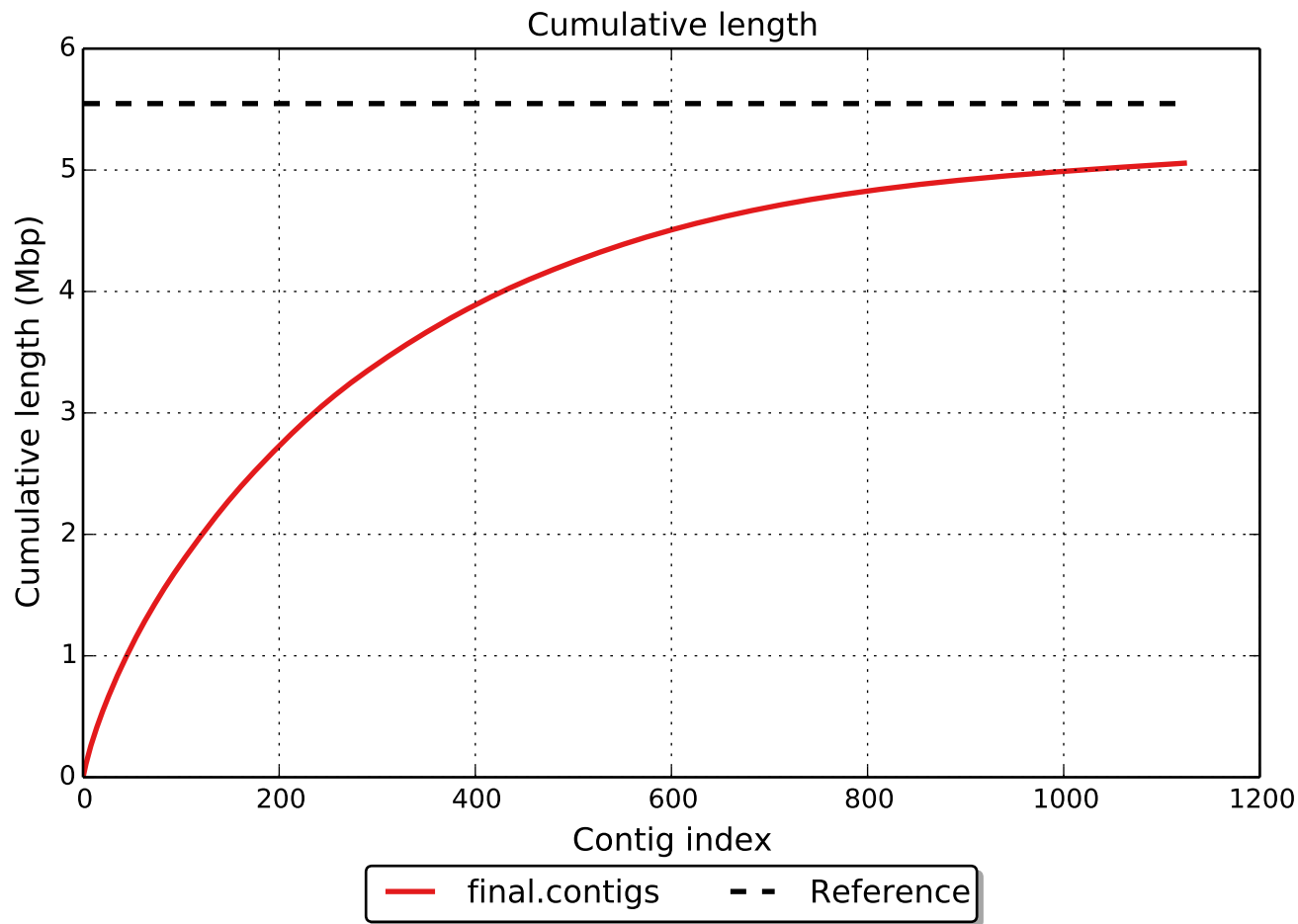
Misassemblies report

	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	26082
# indels	2
# short indels	2
# long indels	0
Indels length	4

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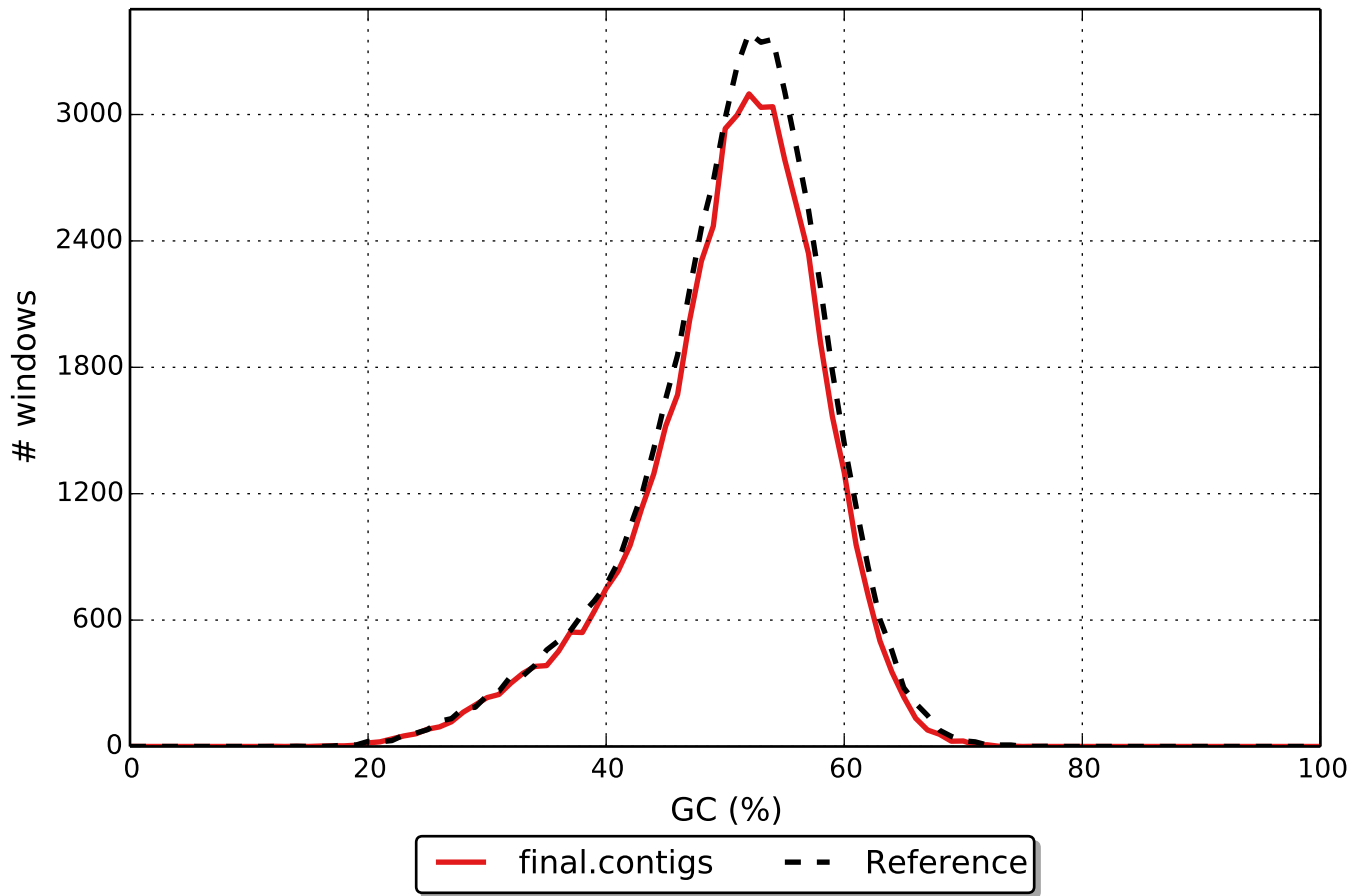(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
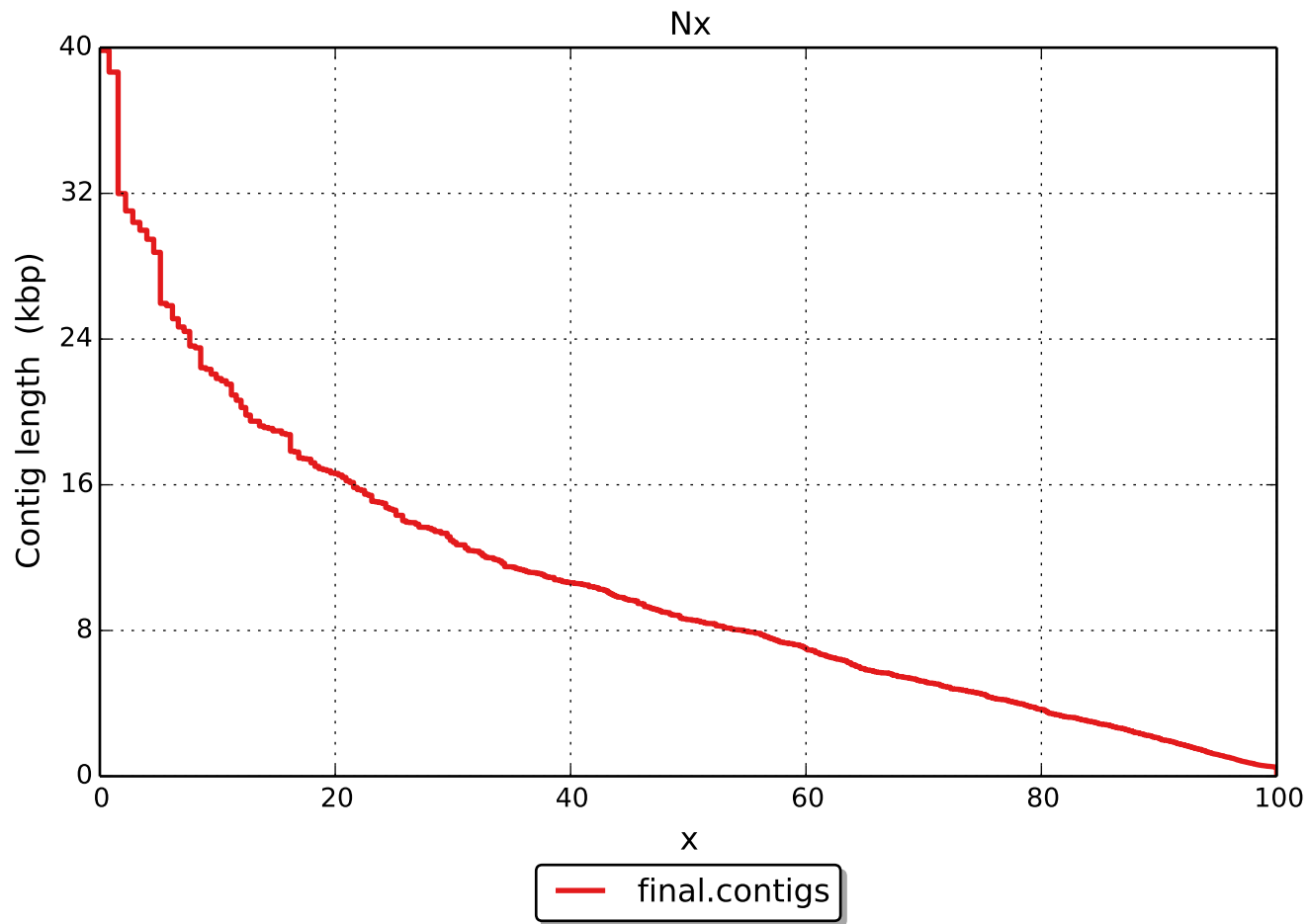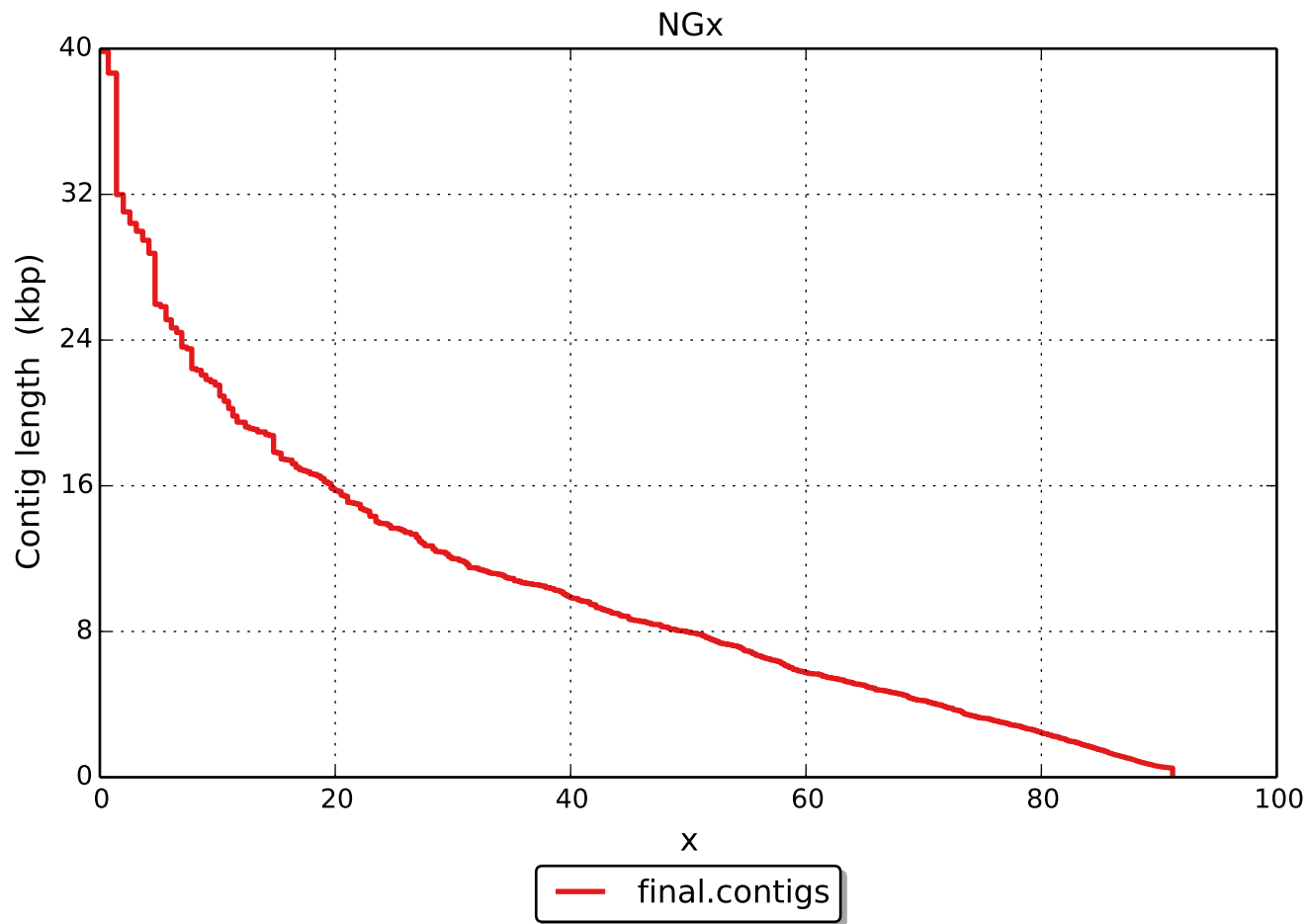
Unaligned report

	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).
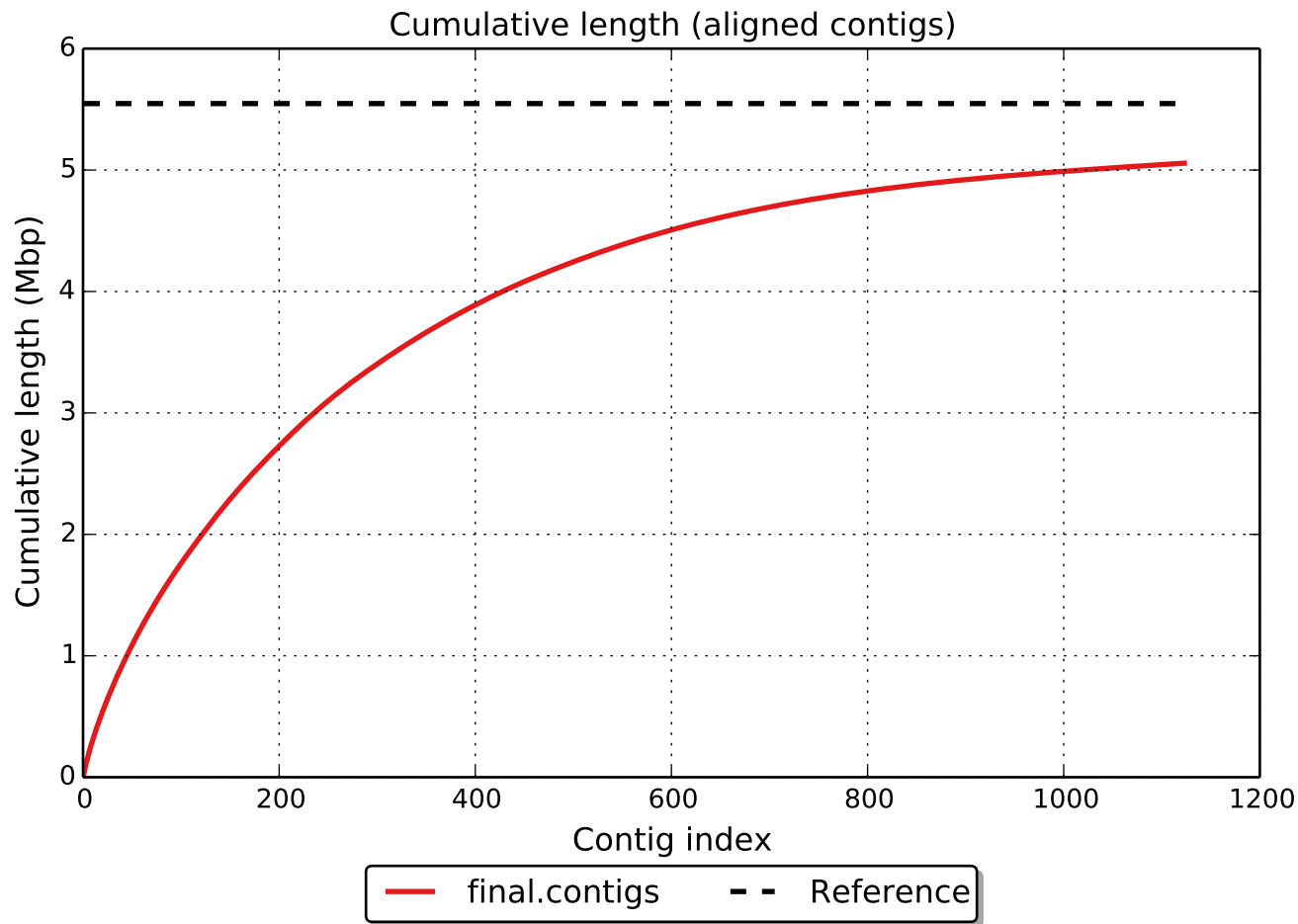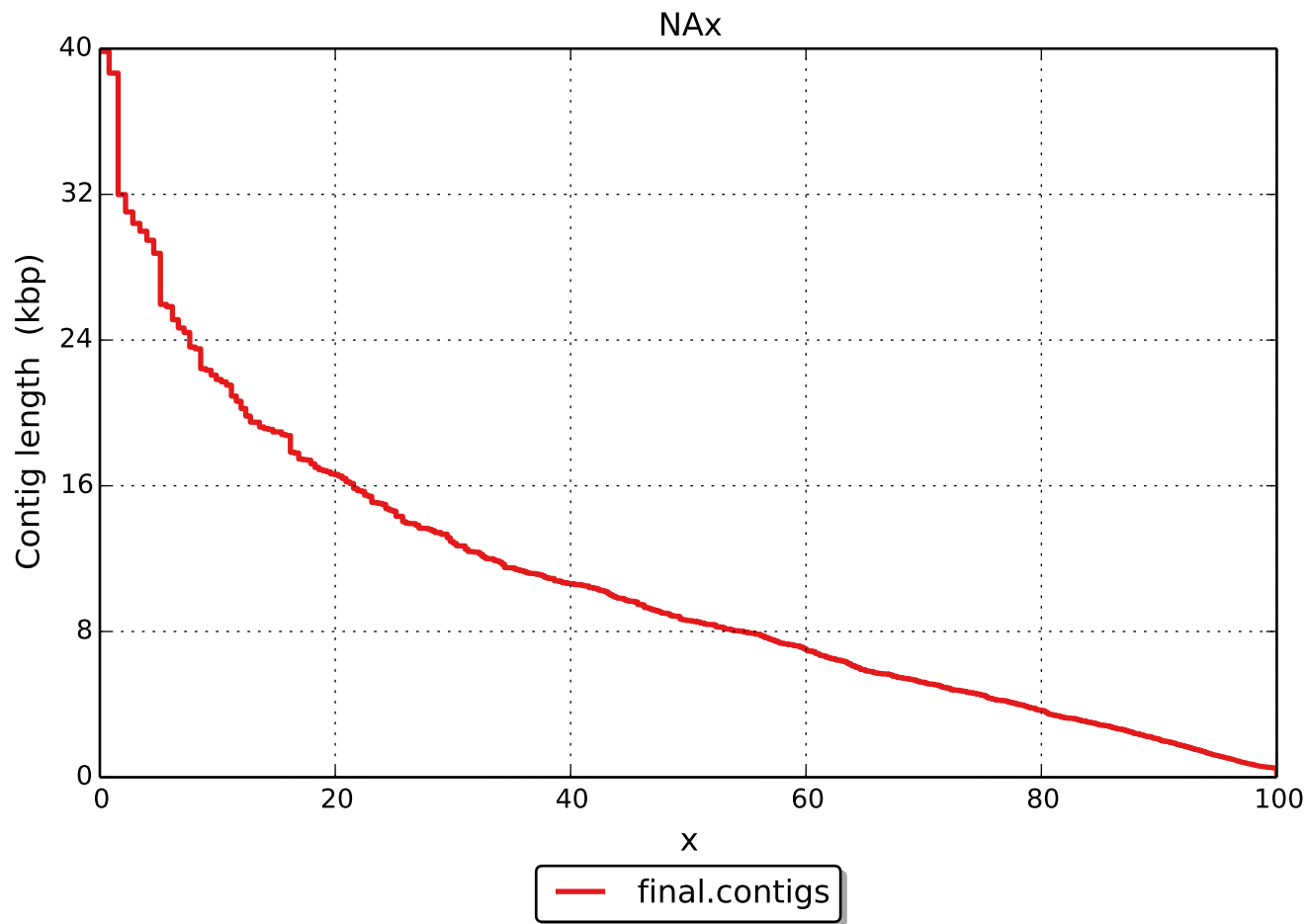
Cumulative length

GC content

windows vs GC (%)

Nx

NGx

Misassemblies

final.contigs

Cumulative length (aligned contigs)