Report

	final.contigs
# contigs (>= 0 bp)	945
# contigs (>= 1000 bp)	706
Total length (>= 0 bp)	3771960
Total length (>= 1000 bp)	3642377
# contigs	818
Largest contig	29446
Total length	3729908
Reference length	3785550
GC (%)	32.25
Reference GC (%)	32.25
N50	7320
NG50	7208
N75	4004
NG75	3895
L50	162
LG50	166
L75	332
LG75	342
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.733
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	19.95
# indels per 100 kbp	0.00
Largest alignment	29446
NA50	7320
NGA50	7208
NA75	4004
NGA75	3895
LA50	162
LGA50	166
LA75	332
LGA75	342

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).
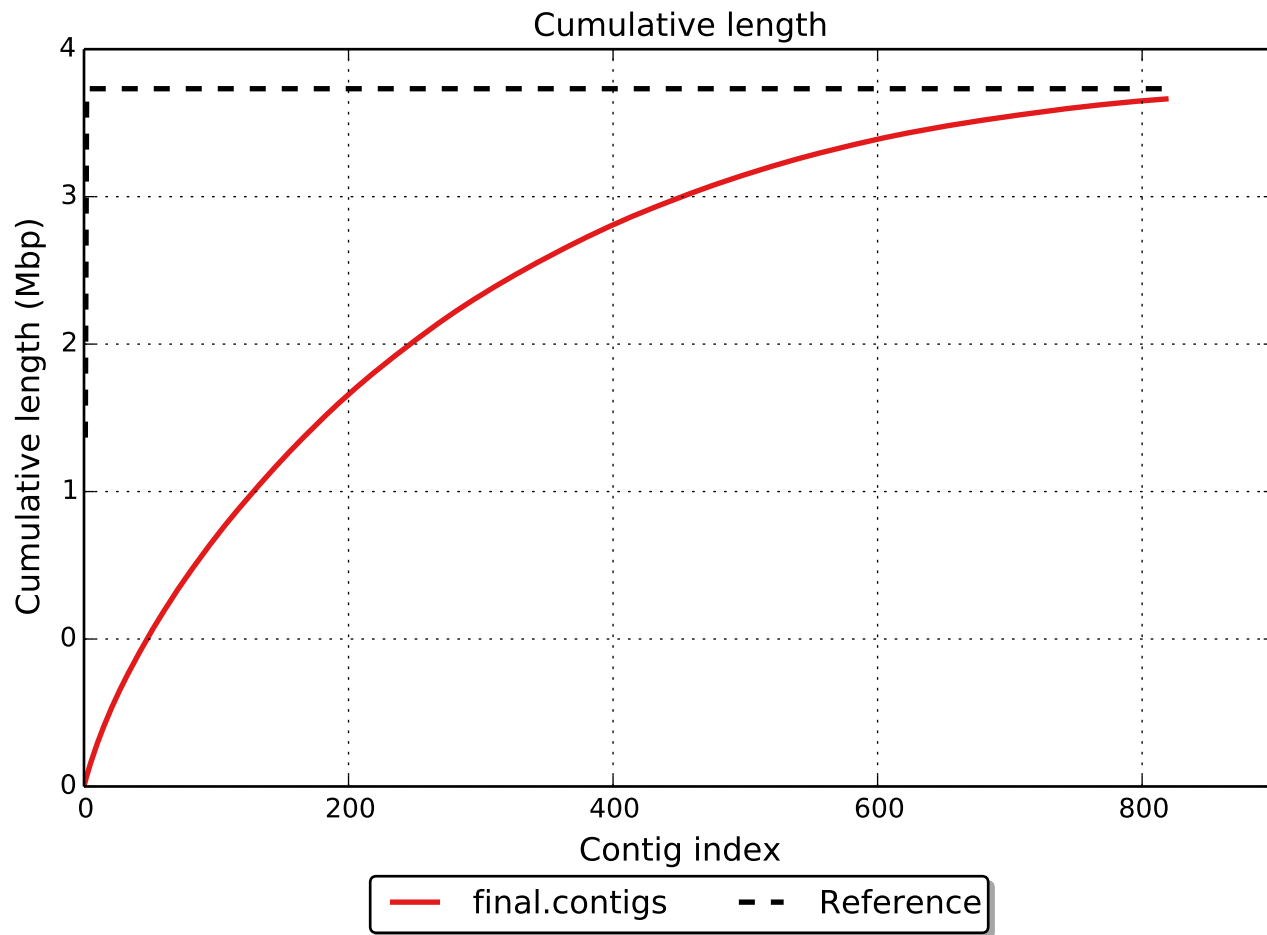
Misassemblies report

	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	738
# indels	0
# short indels	0
# long indels	0
Indels length	0

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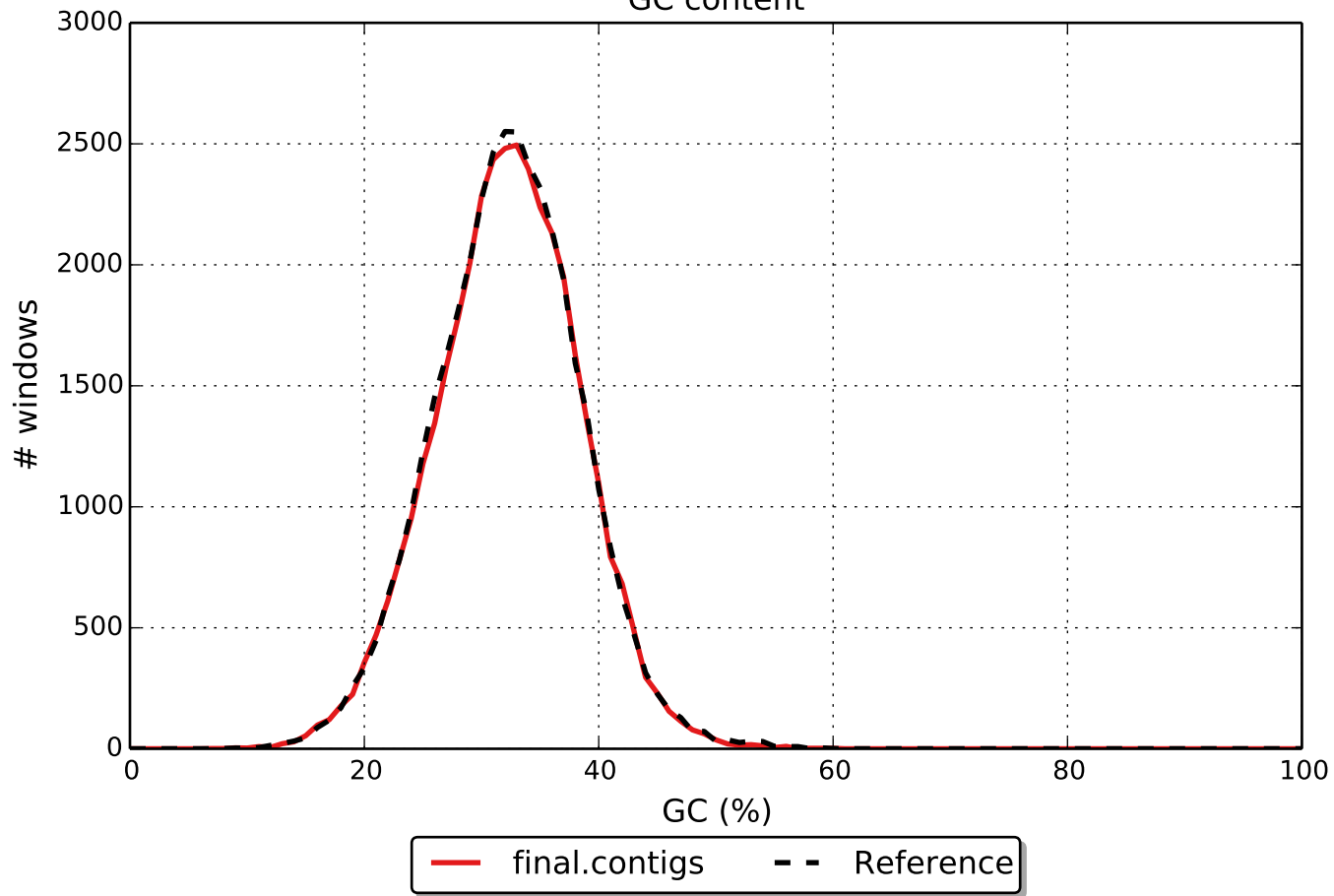(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
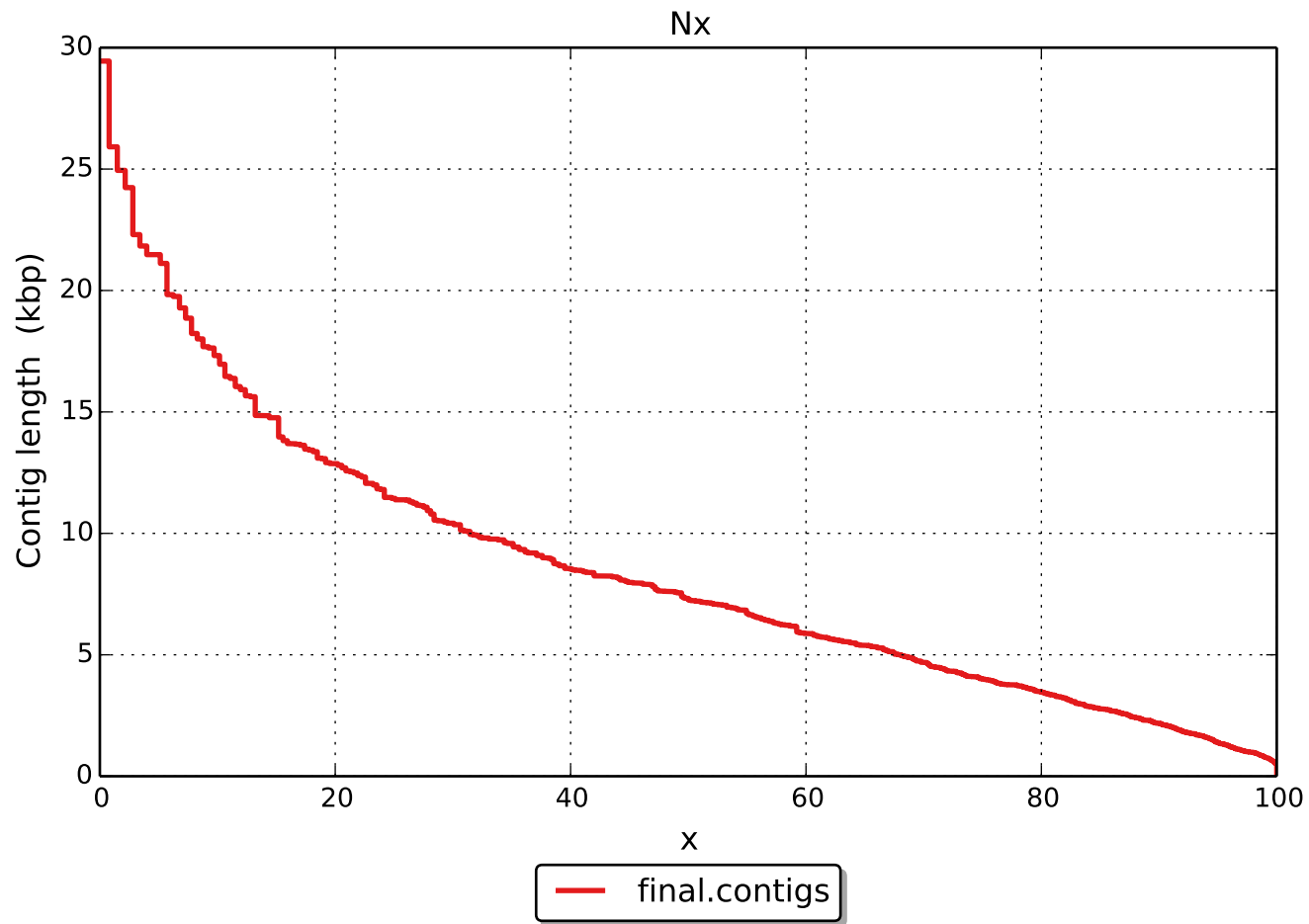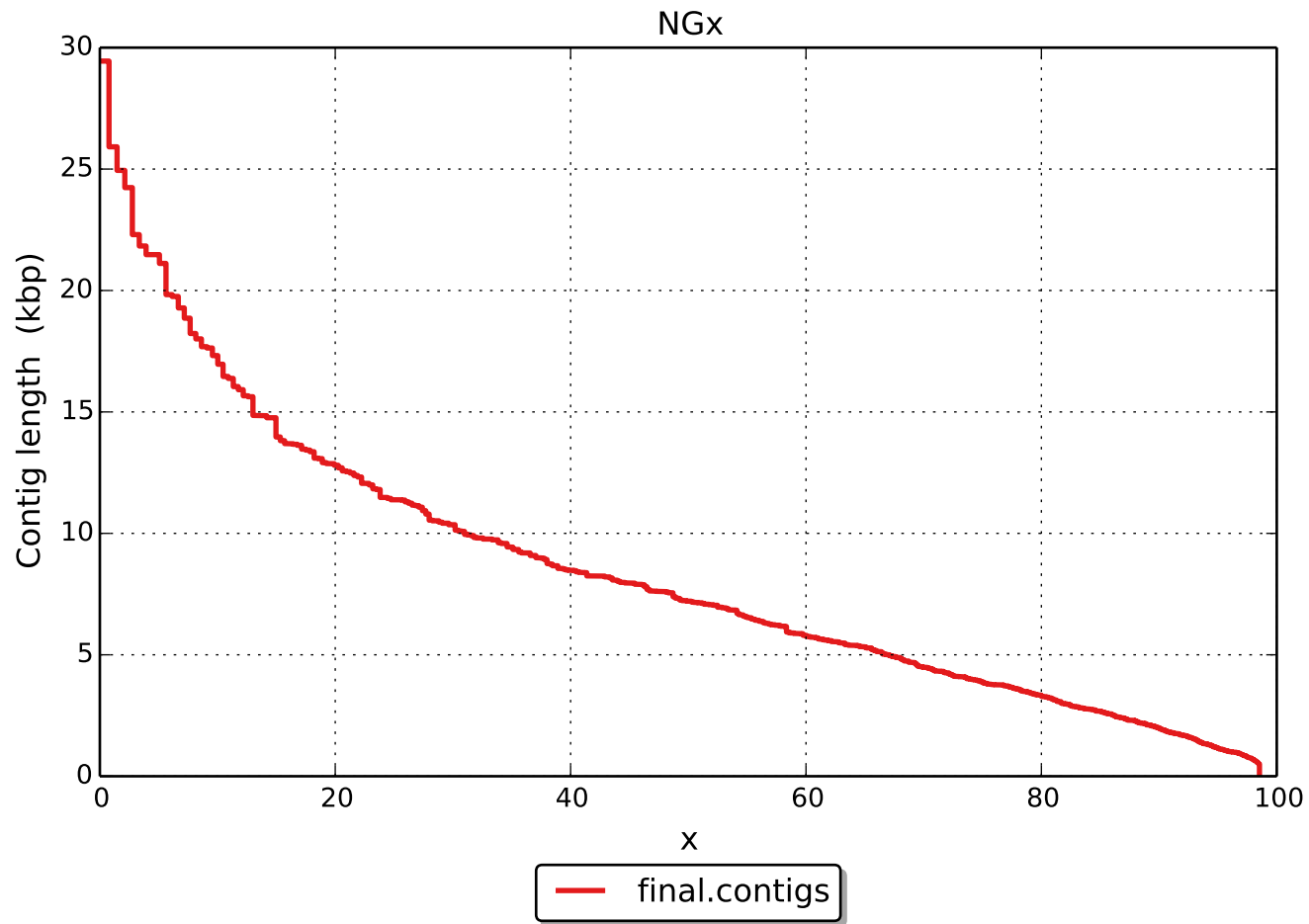
Unaligned report

	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).
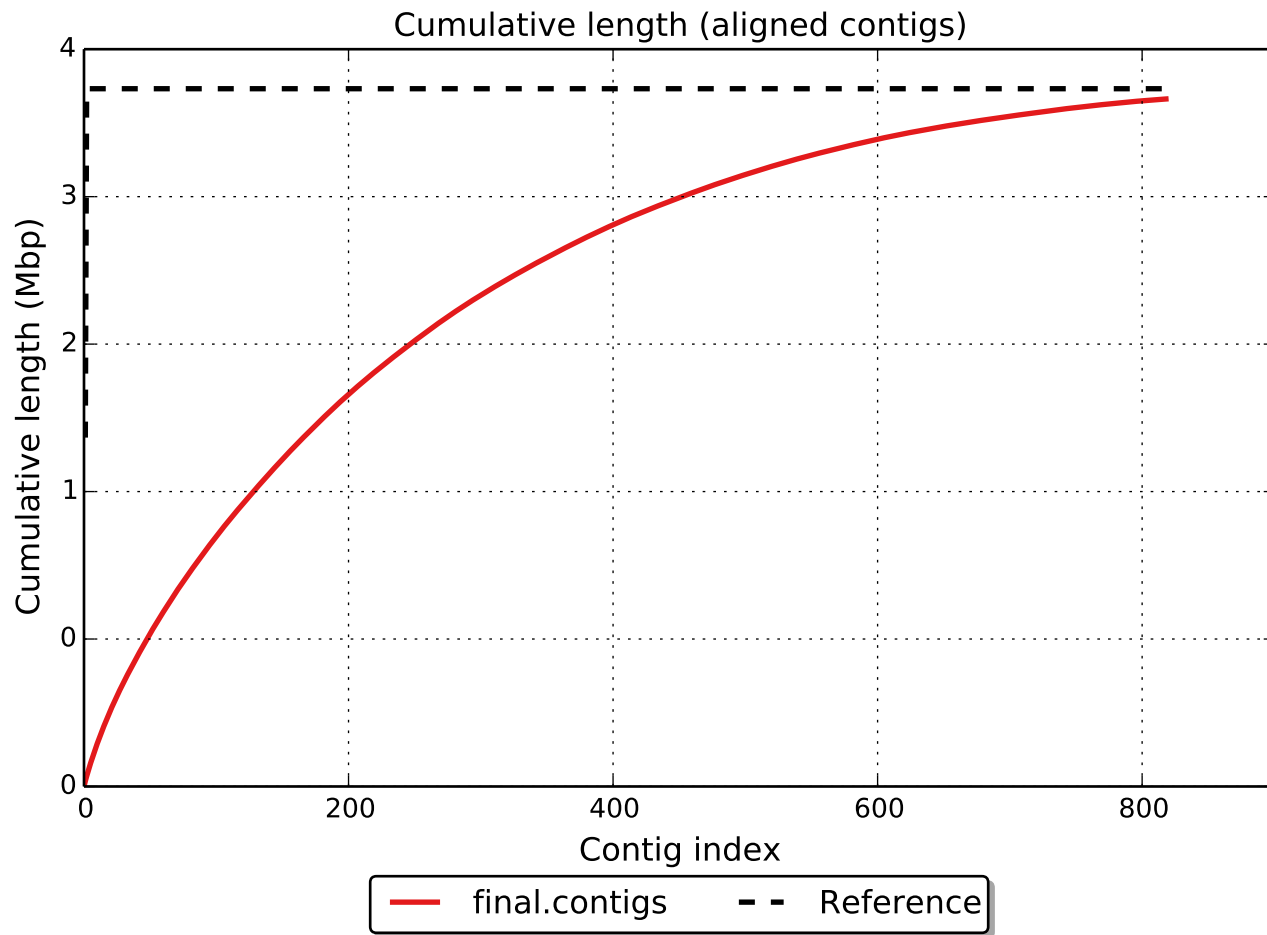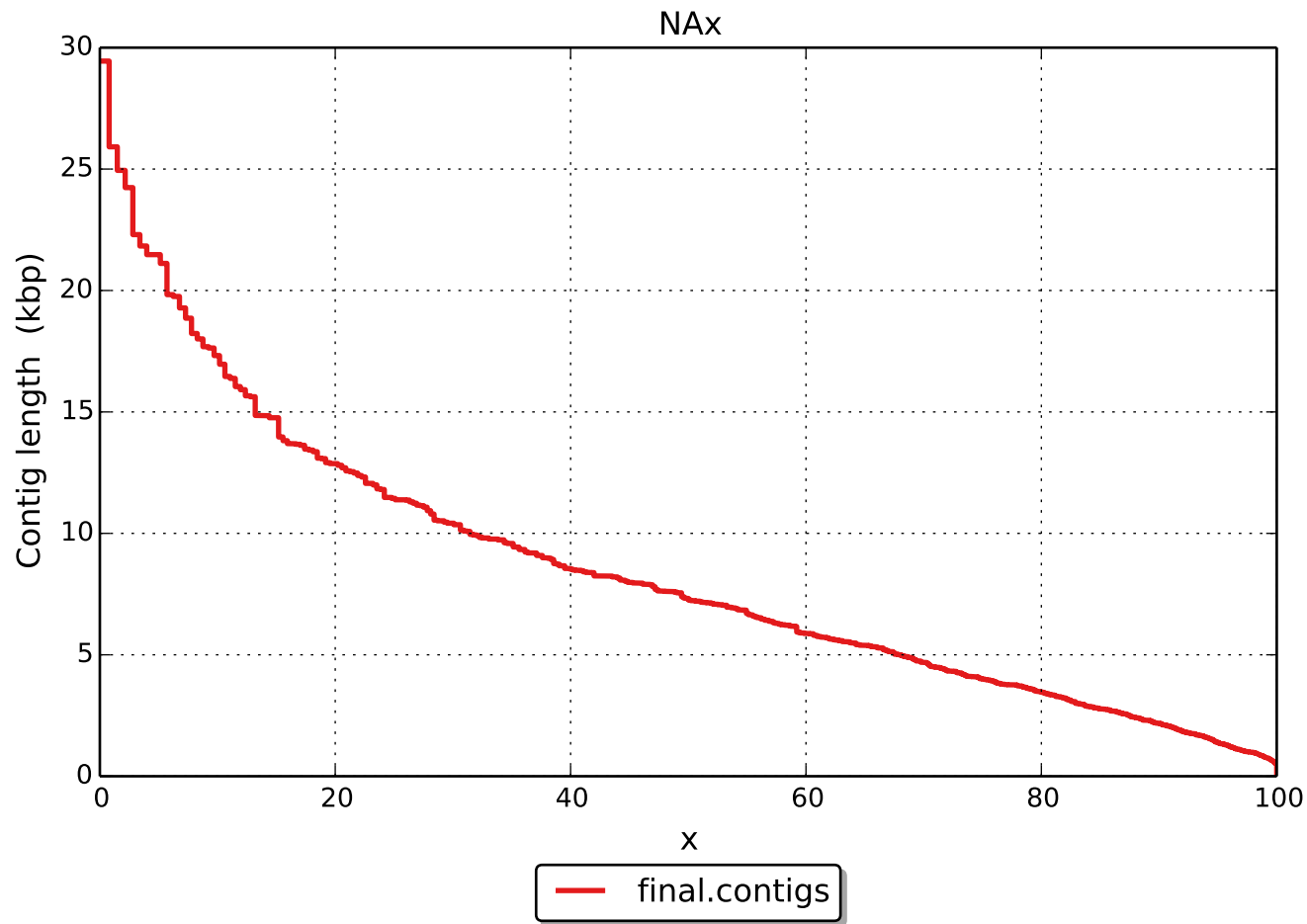
Cumulative length

Nx

NGx

Contig length (kbp)

x

final.contigs

Misassemblies

final.contigs

Cumulative length (aligned contigs)