Report

	final.contigs
# contigs (>= 1000 bp)	1084
# contigs (>= 5000 bp)	313
# contigs (>= 10000 bp)	53
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4488810
Total length (>= 5000 bp)	2481760
Total length (>= 10000 bp)	713597
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1283
Largest contig	20716
Total length	4634842
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	5312
NG50	5312
N75	3161
NG75	3136
L50	282
LG50	282
L75	564
LG75	566
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.439
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.88
# indels per 100 kbp	0.11
Largest alignment	20716
NA50	5312
NGA50	5312
NA75	3161
NGA75	3136
LA50	282
LGA50	282
LA75	564
LGA75	566

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).
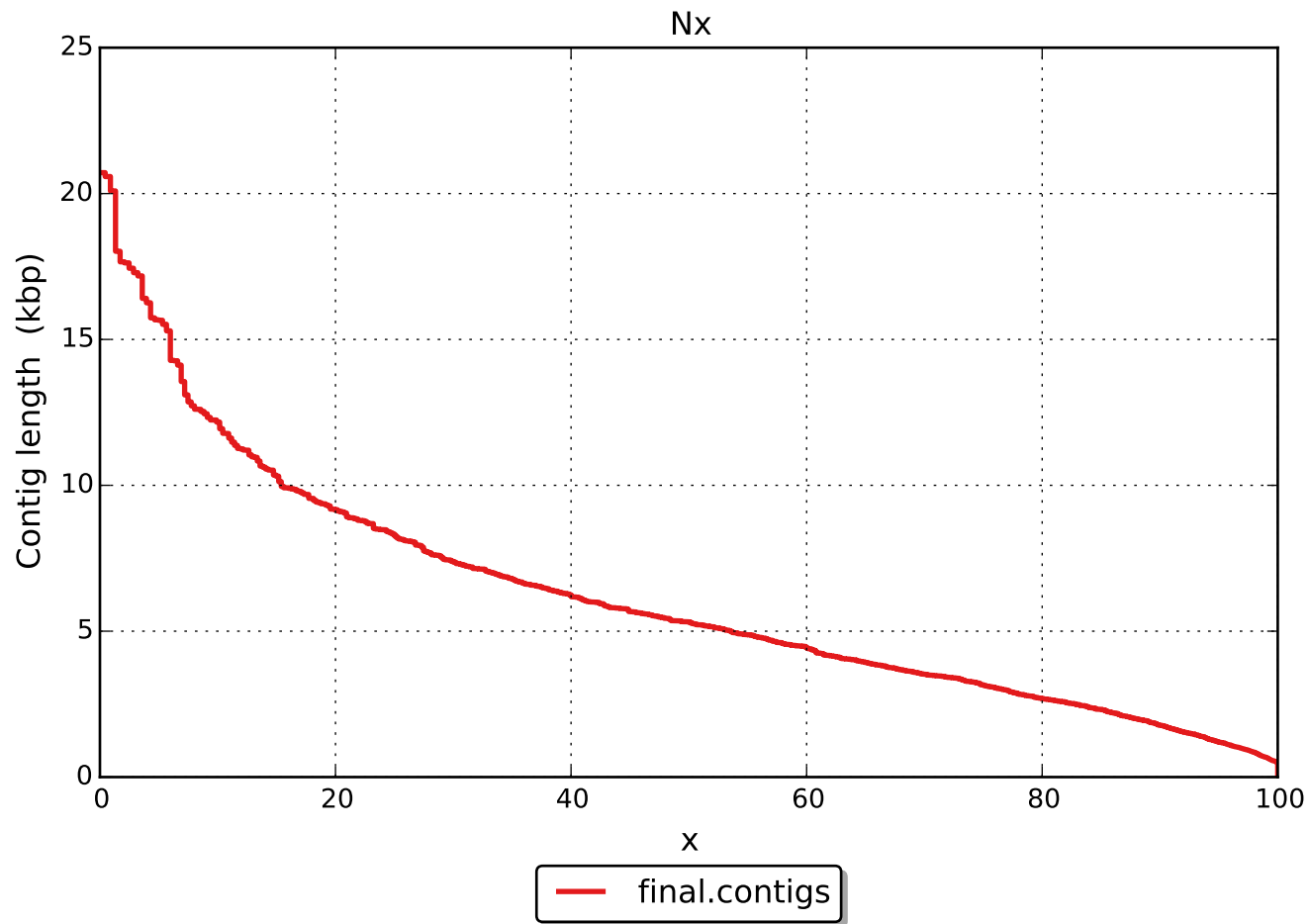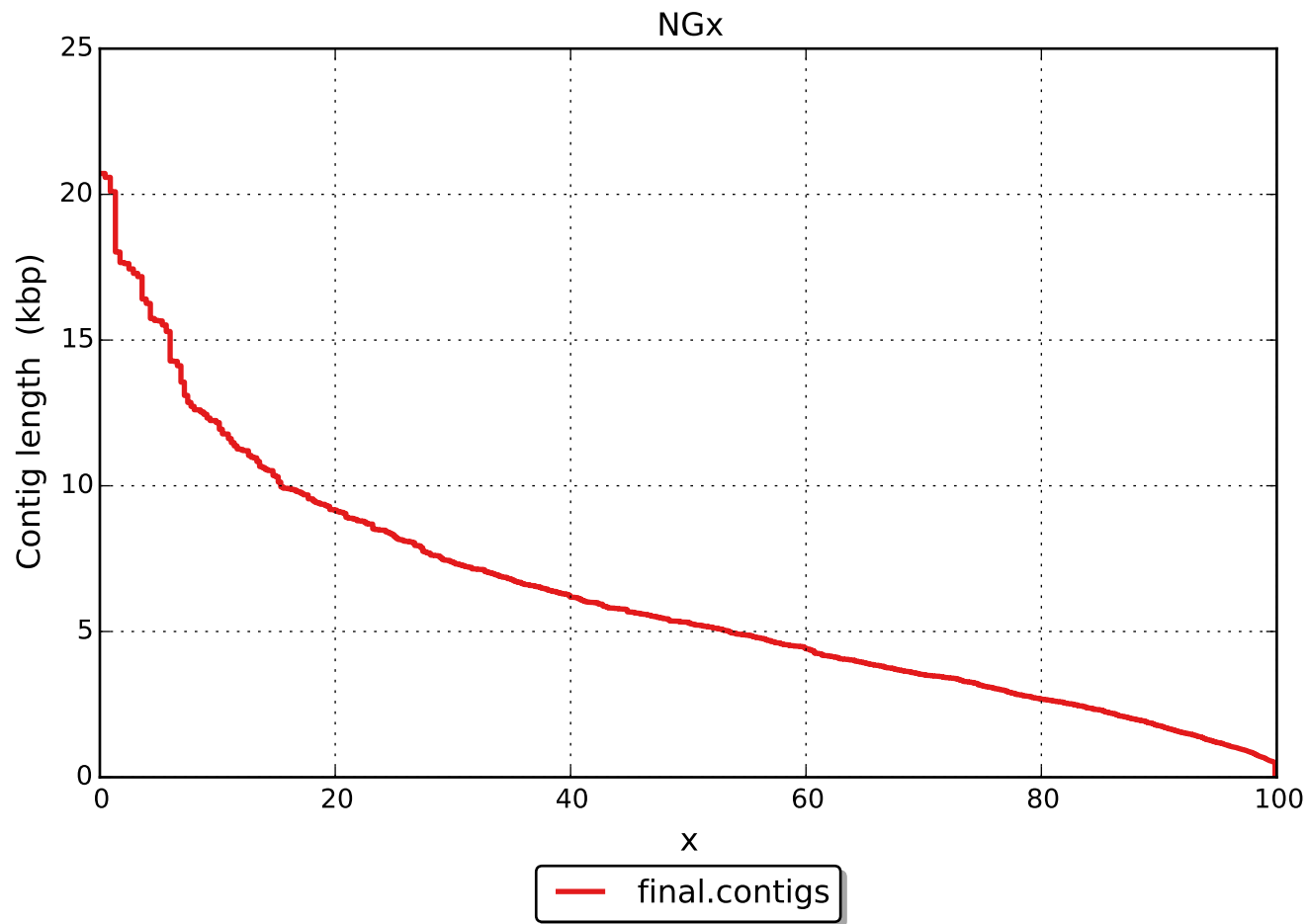
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	1080
# indels	5
# short indels	5
# long indels	0
Indels length	5

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).
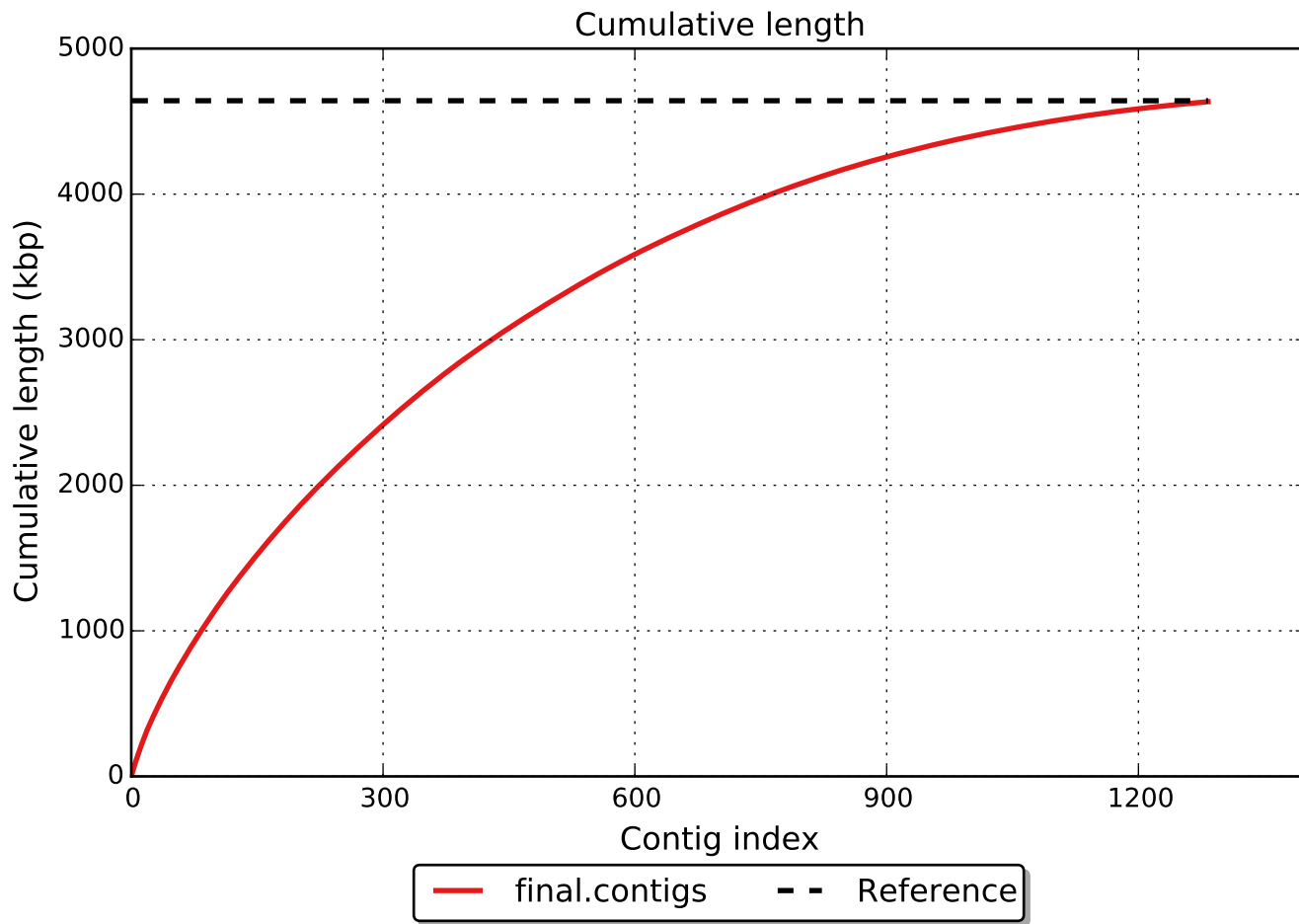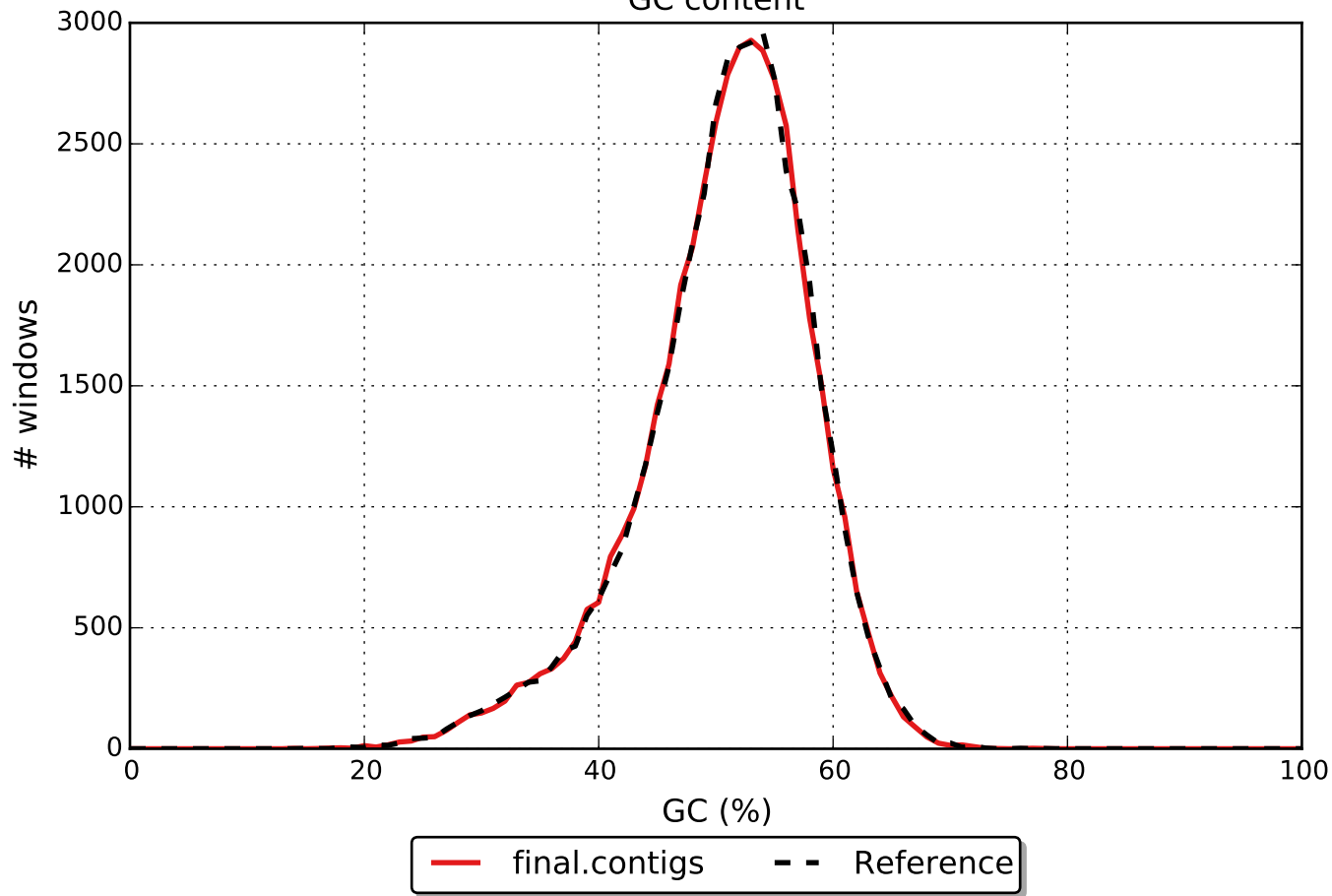
Unaligned report

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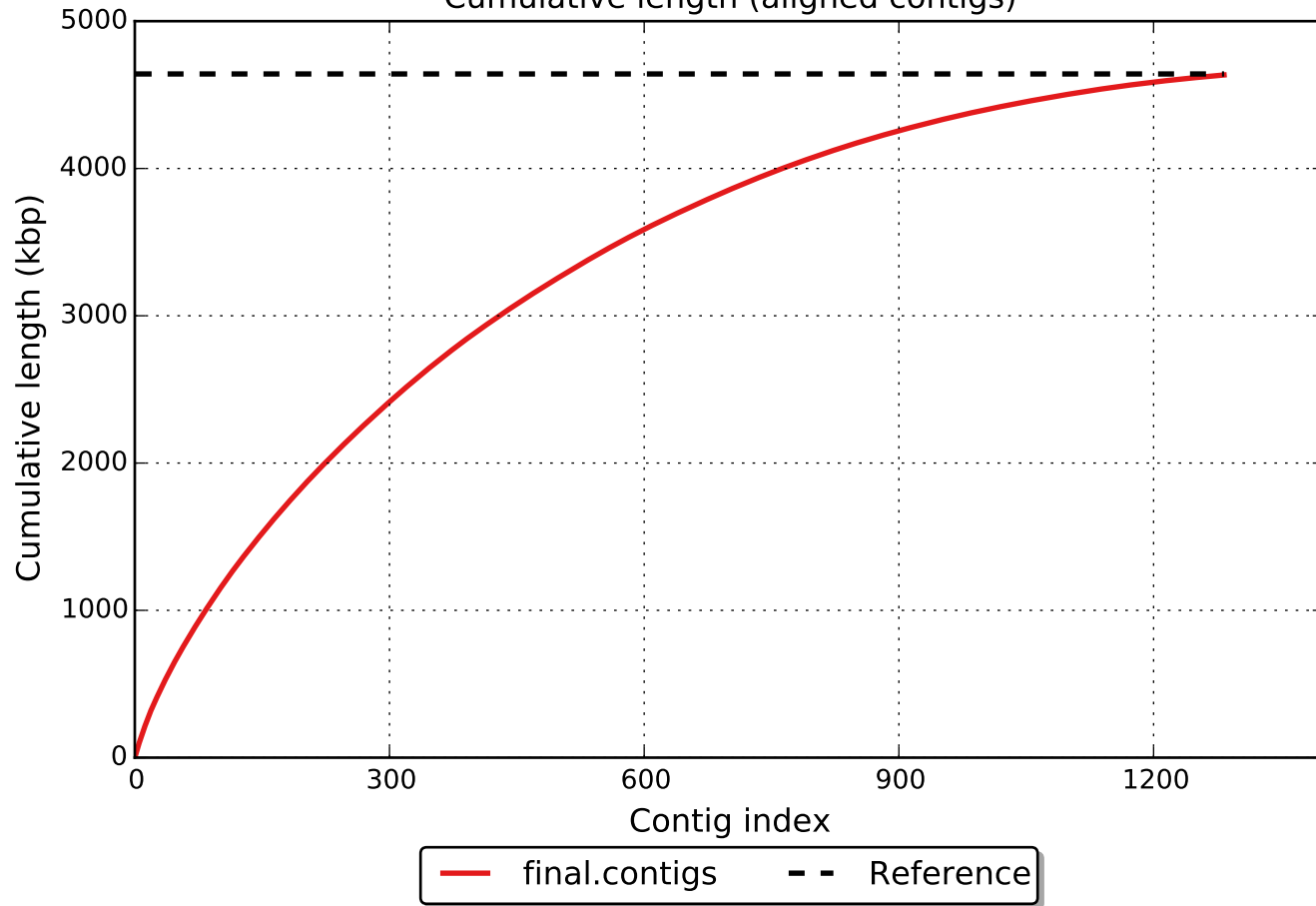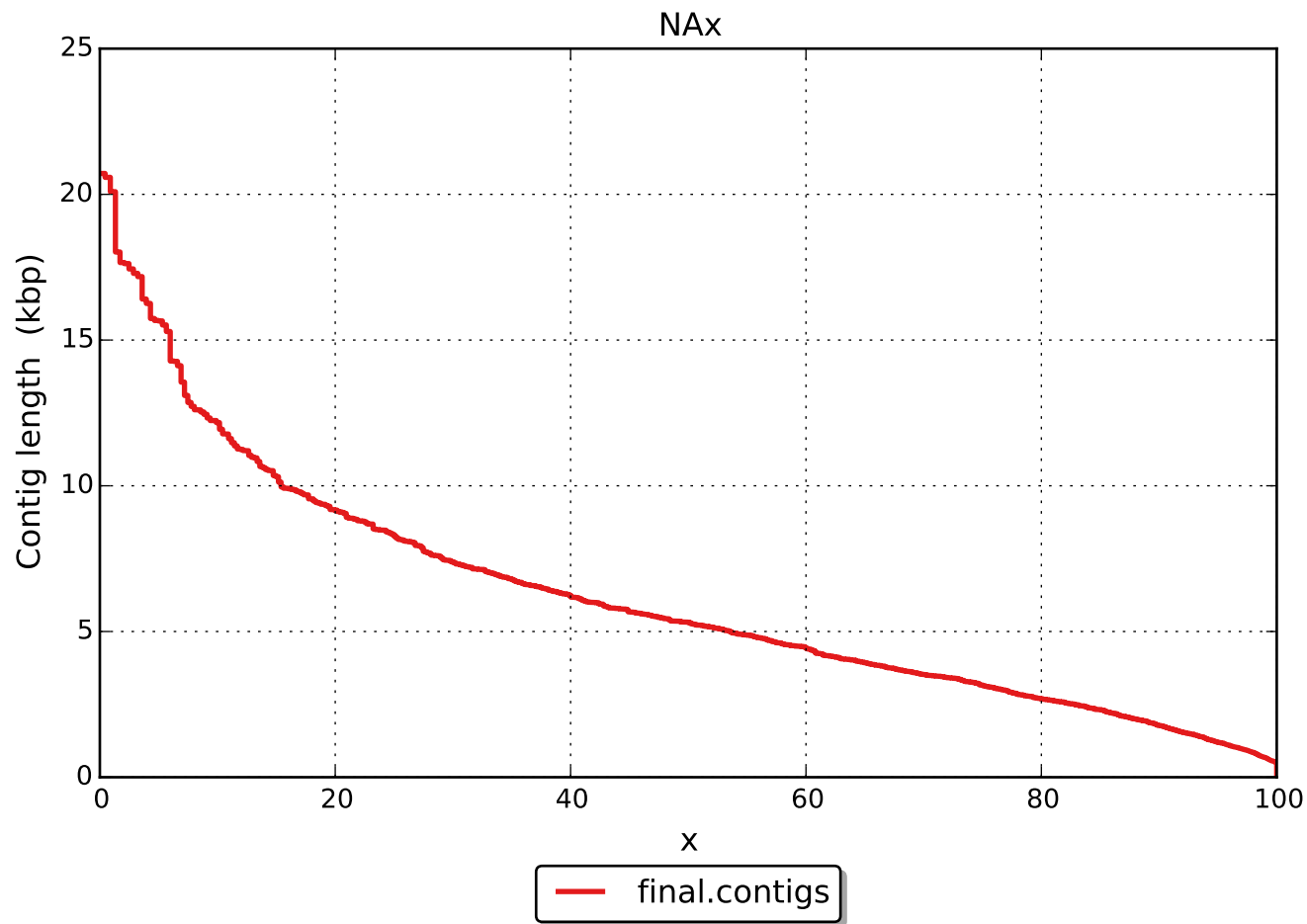(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)