Report

	final.contigs
# contigs (>= 0 bp)	1397
# contigs (>= 1000 bp)	1129
Total length (>= 0 bp)	5270039
Total length (>= 1000 bp)	5078297
# contigs	1397
Largest contig	29757
Total length	5270039
Reference length	5478683
GC (%)	50.25
Reference GC (%)	50.49
N50	5916
NG50	5609
N75	3268
NG75	2992
L50	262
LG50	280
L75	562
LG75	612
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	6073
Genome fraction (%)	94.116
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	24.44
# indels per 100 kbp	0.06
Largest alignment	27862
NA50	5911
NGA50	5601
NA75	3266
NGA75	2986
LA50	263
LGA50	281
LA75	564
LGA75	614

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).
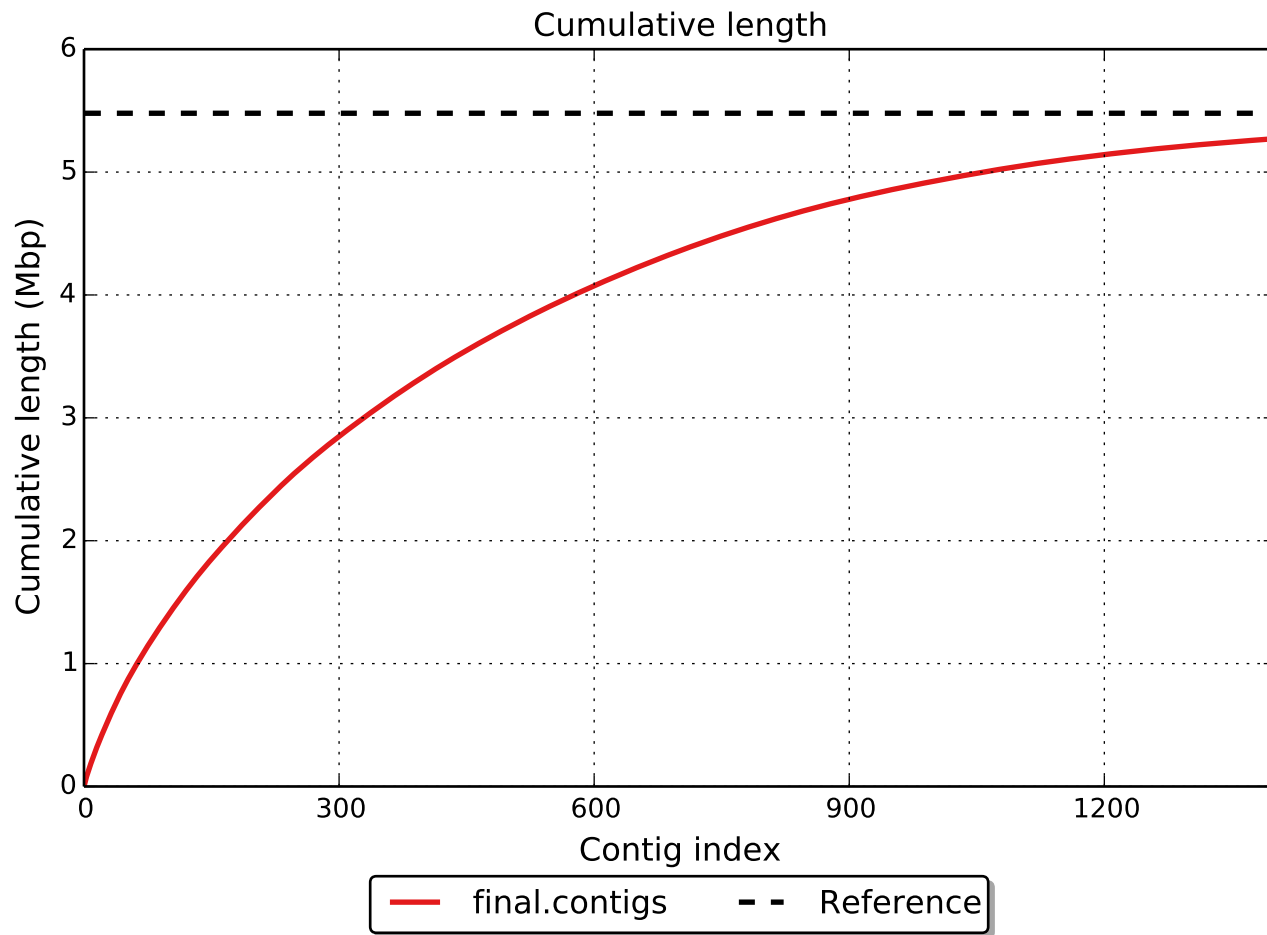
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	1260
# indels	3
# short indels	1
# long indels	2
Indels length	31

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).
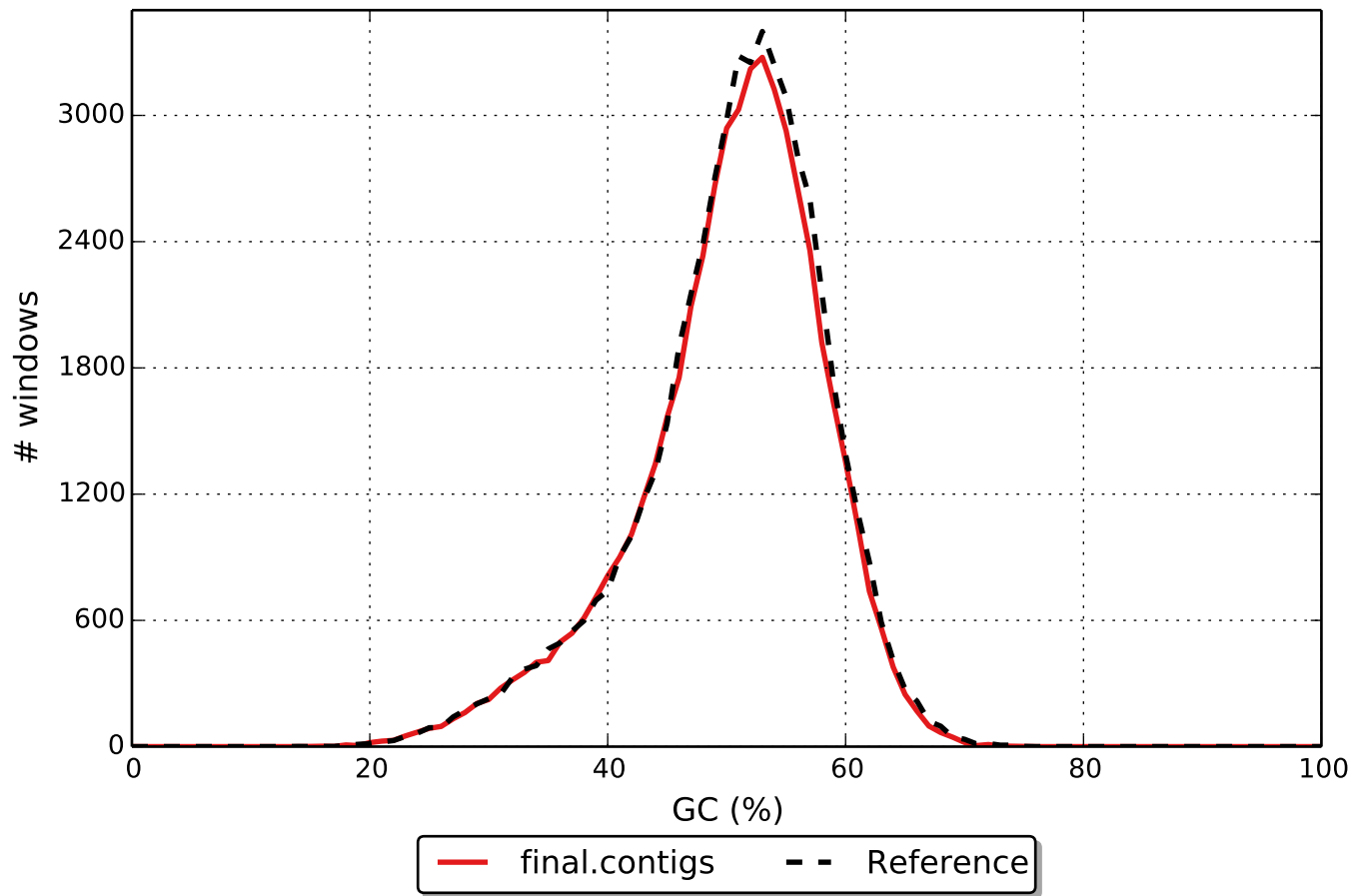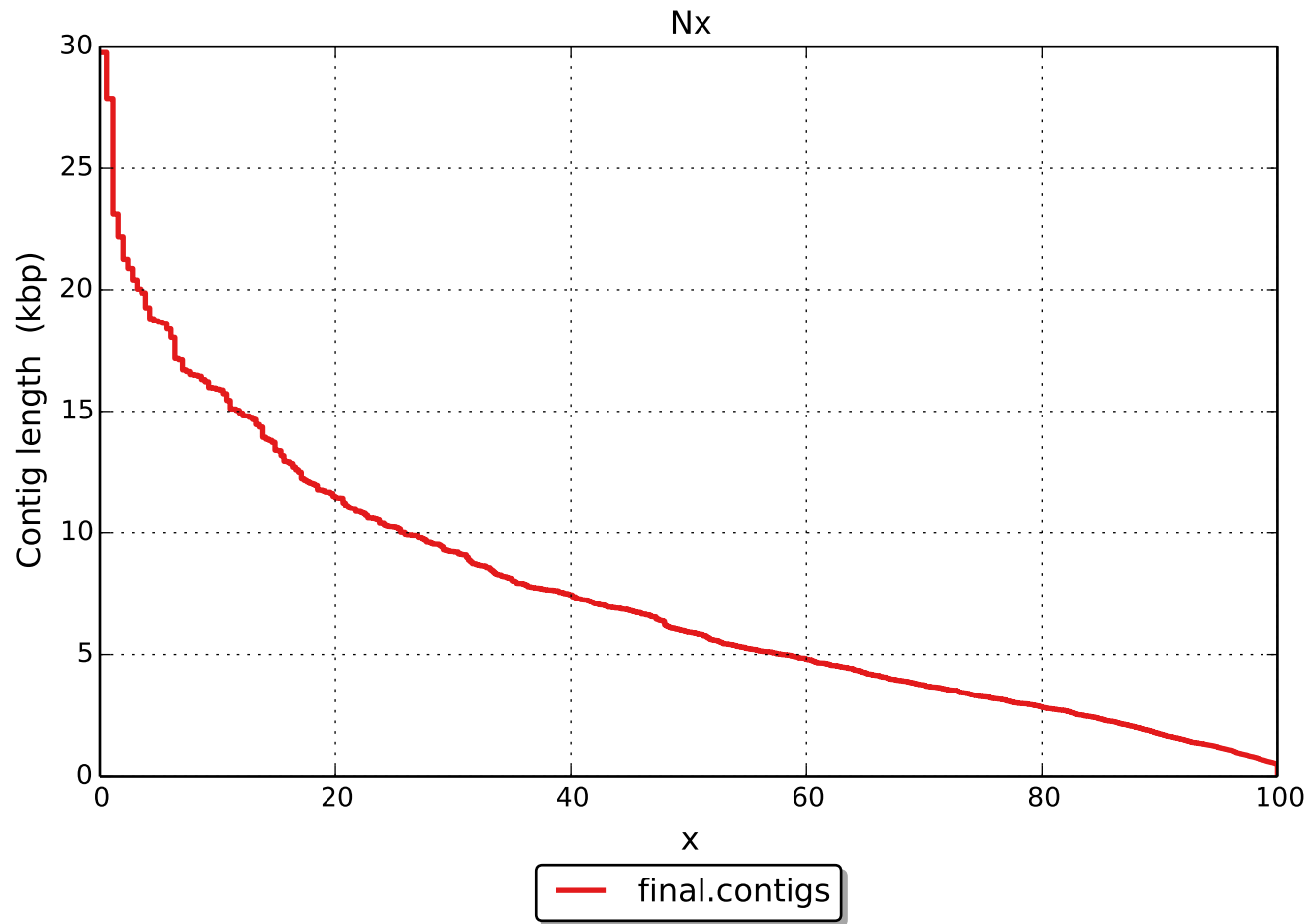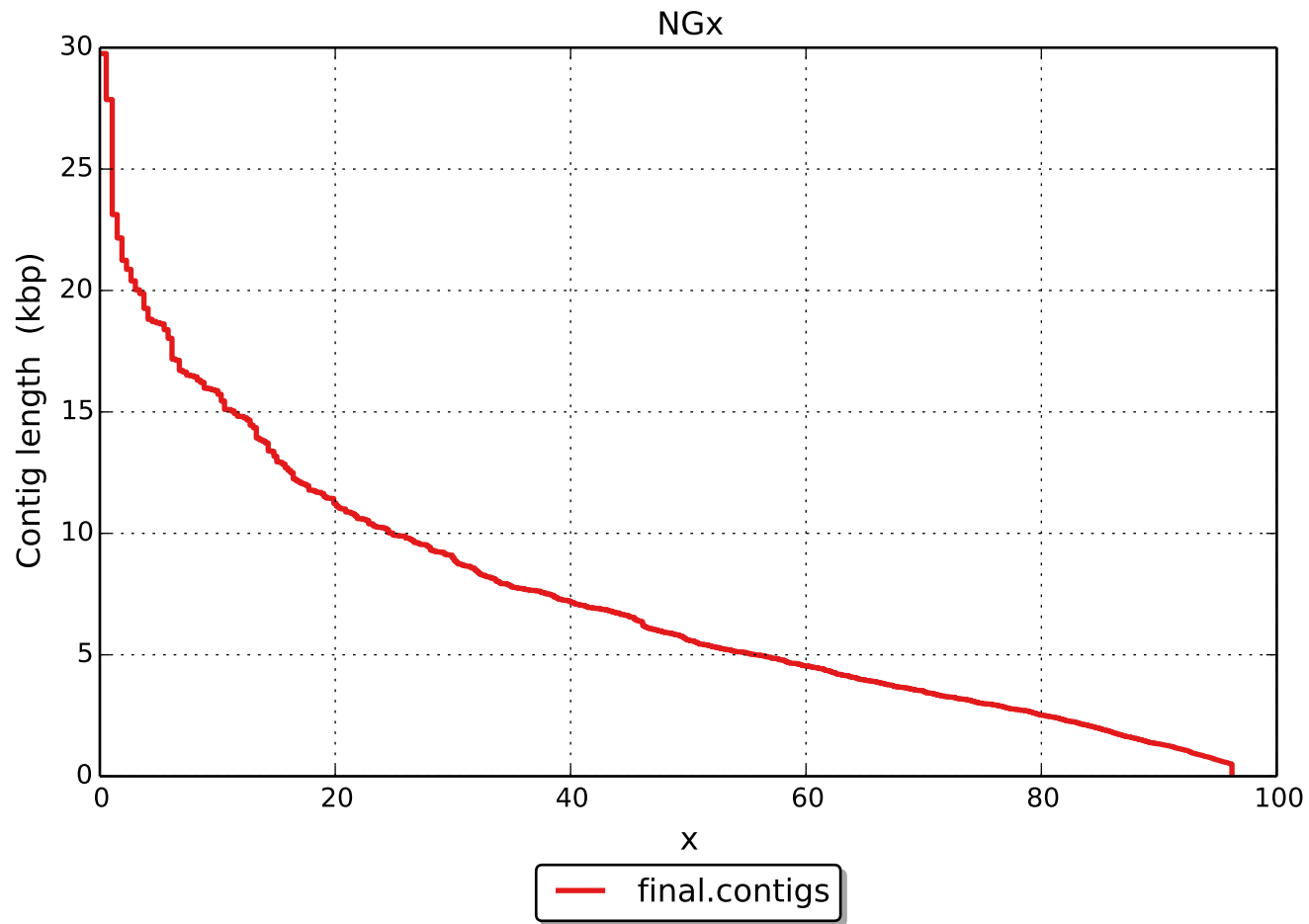
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	6073
# 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).
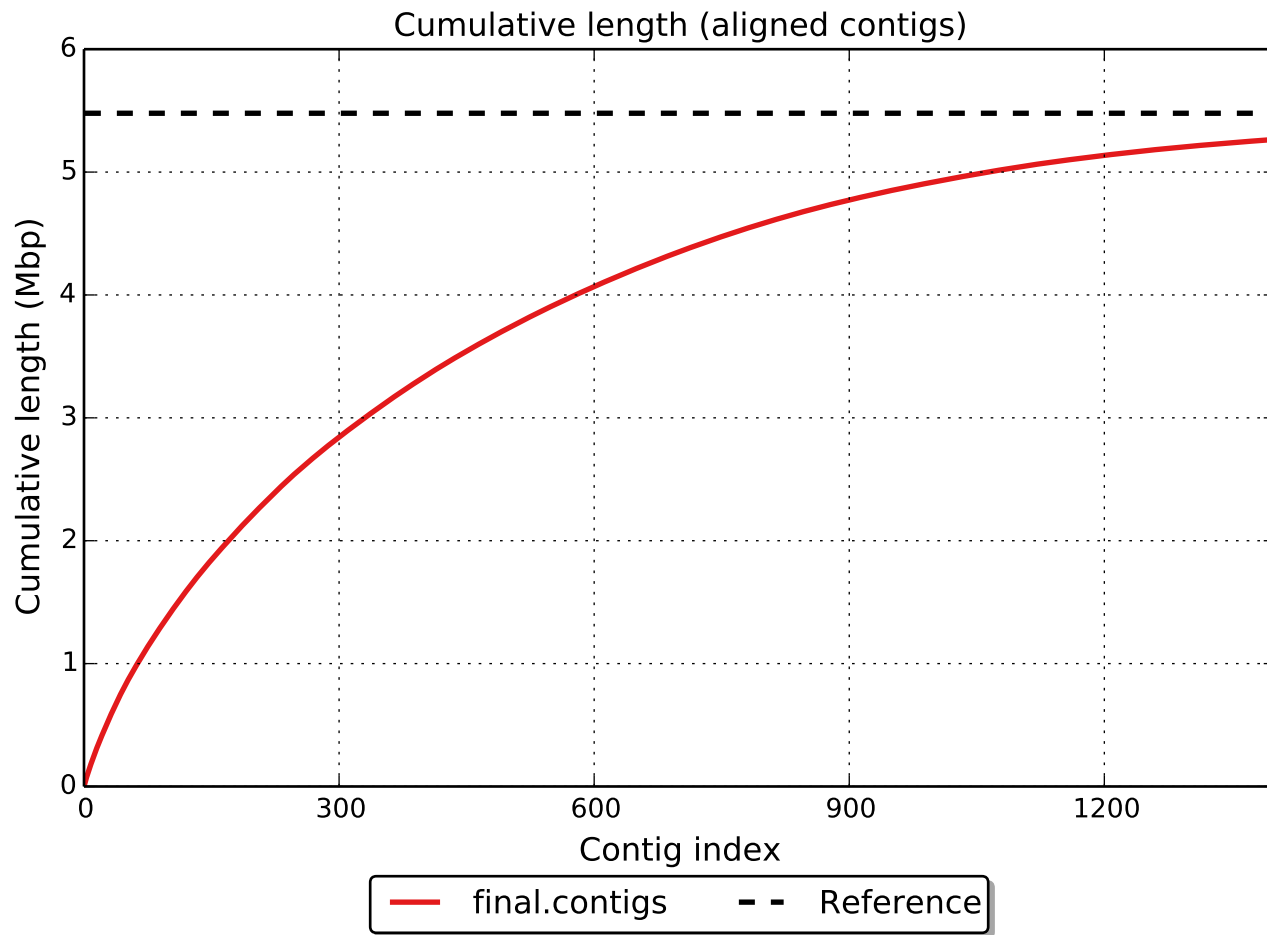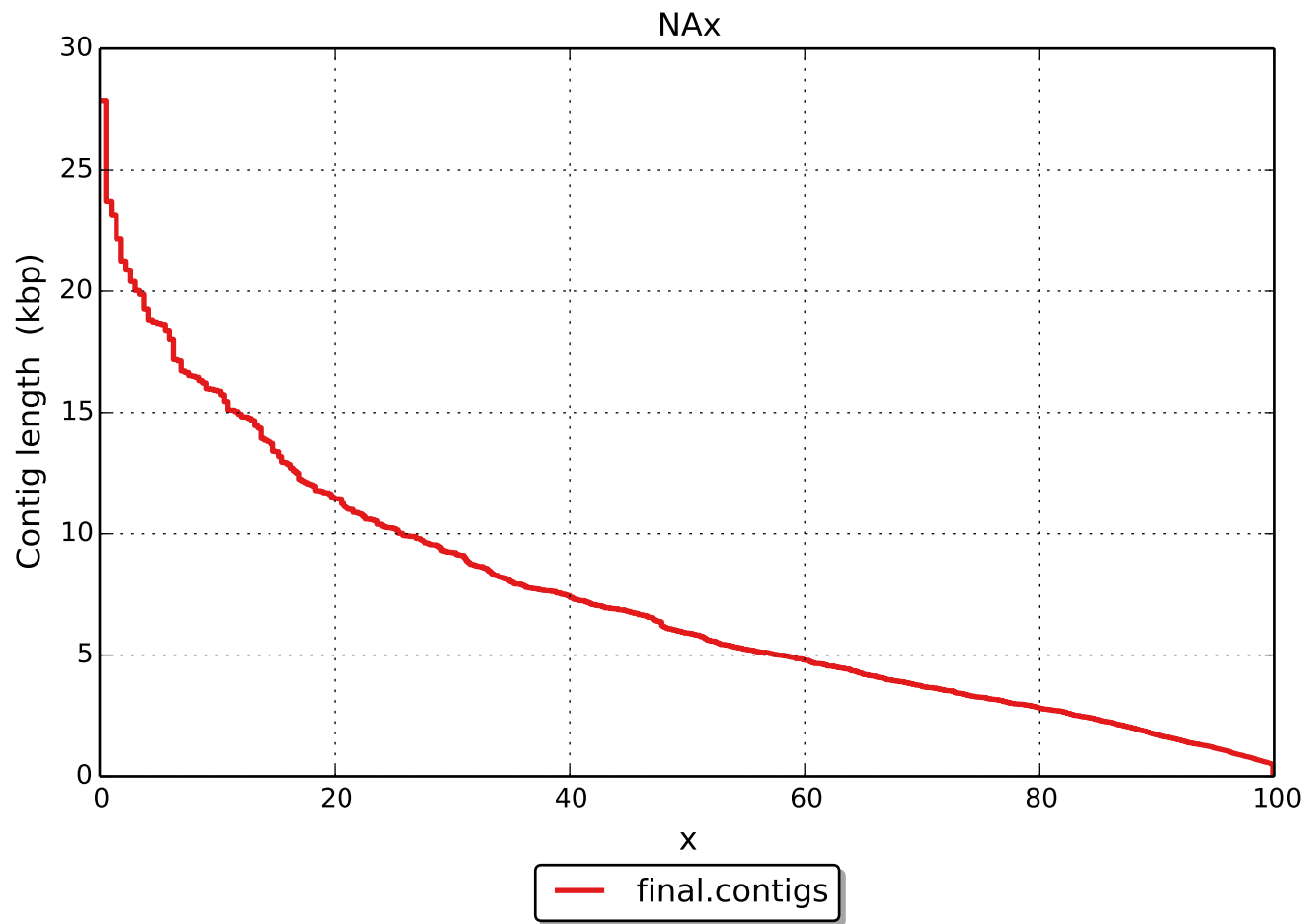
Cumulative length

GC content

windows

GC (%)

final.contigs — — Reference

NGx

Misassemblies

final.contigs

Cumulative length (aligned contigs)