Report

	final.contigs
# contigs (>= 0 bp)	203
# contigs (>= 1000 bp)	199
Total length (>= 0 bp)	5561423
Total length (>= 1000 bp)	5559180
# contigs	203
Largest contig	168092
Total length	5561423
Reference length	5547323
GC (%)	50.49
Reference GC (%)	50.49
N50	43543
NG50	43543
N75	26367
NG75	26367
L50	37
LG50	37
L75	76
LG75	76
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.854
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.95
# indels per 100 kbp	0.00
Largest alignment	168092
NA50	43543
NGA50	43543
NA75	26367
NGA75	26367
LA50	37
LGA50	37
LA75	76
LGA75	76

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).
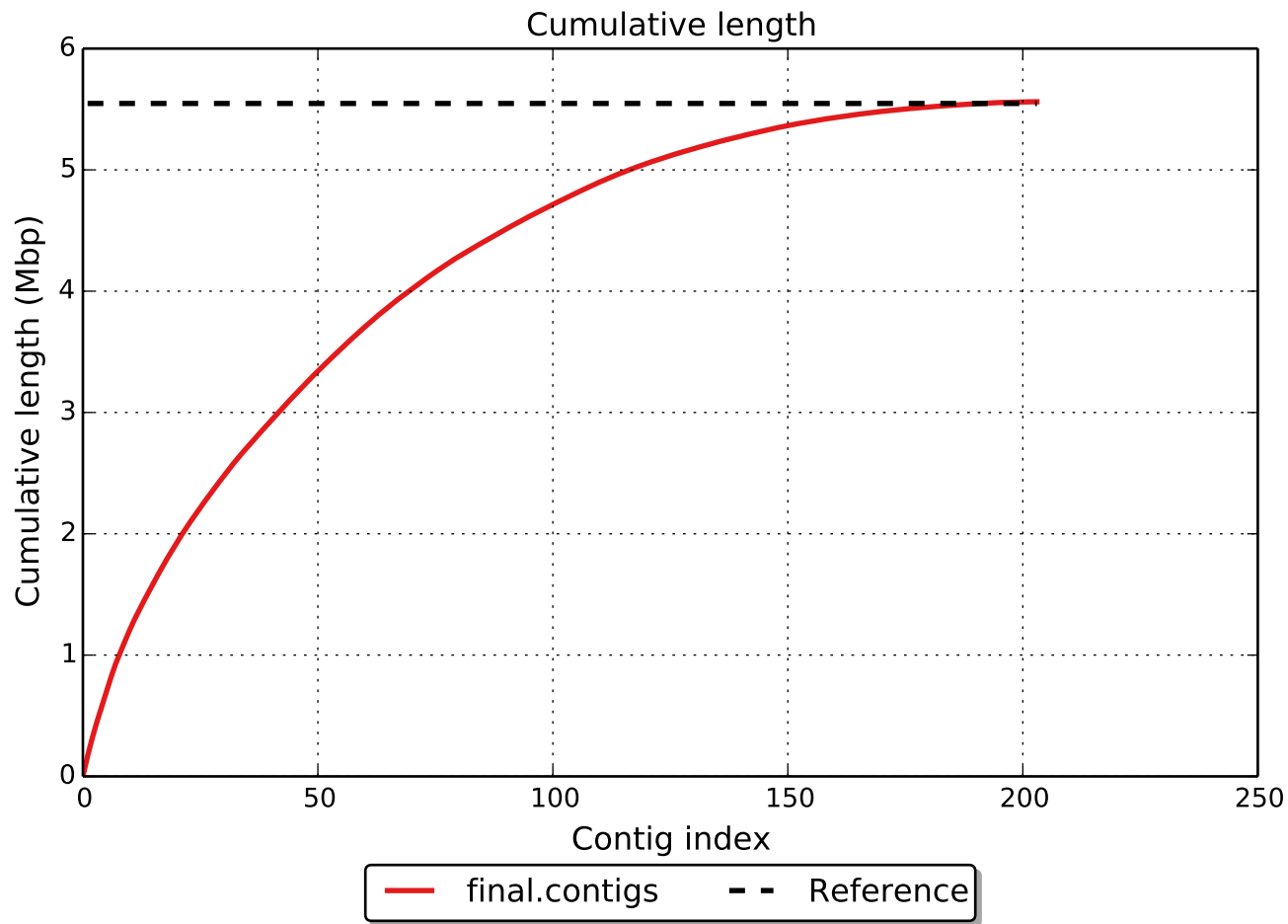
Misassemblies report

	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	385
# indels	0
# short indels	0
# long indels	0
Indels length	0

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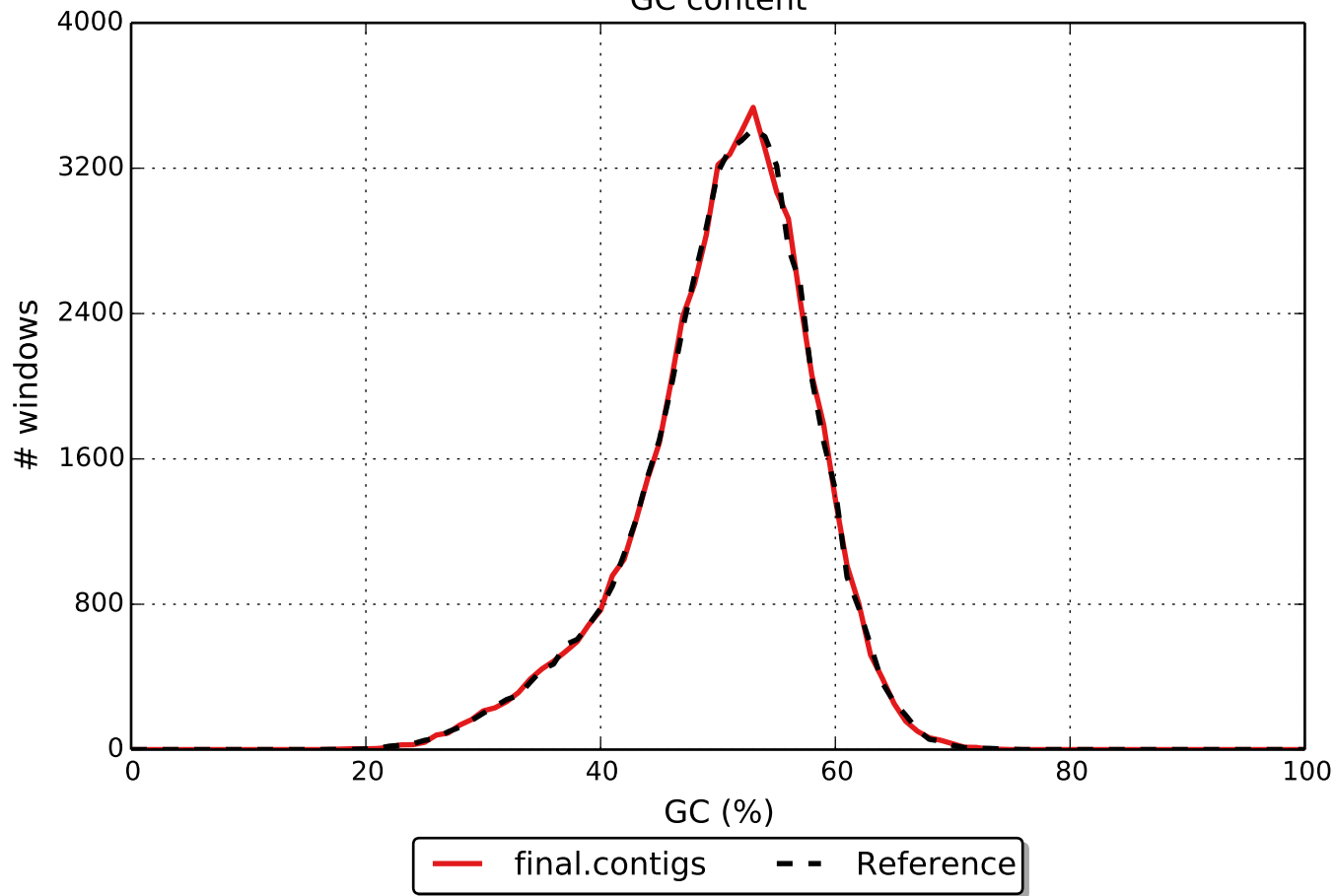(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
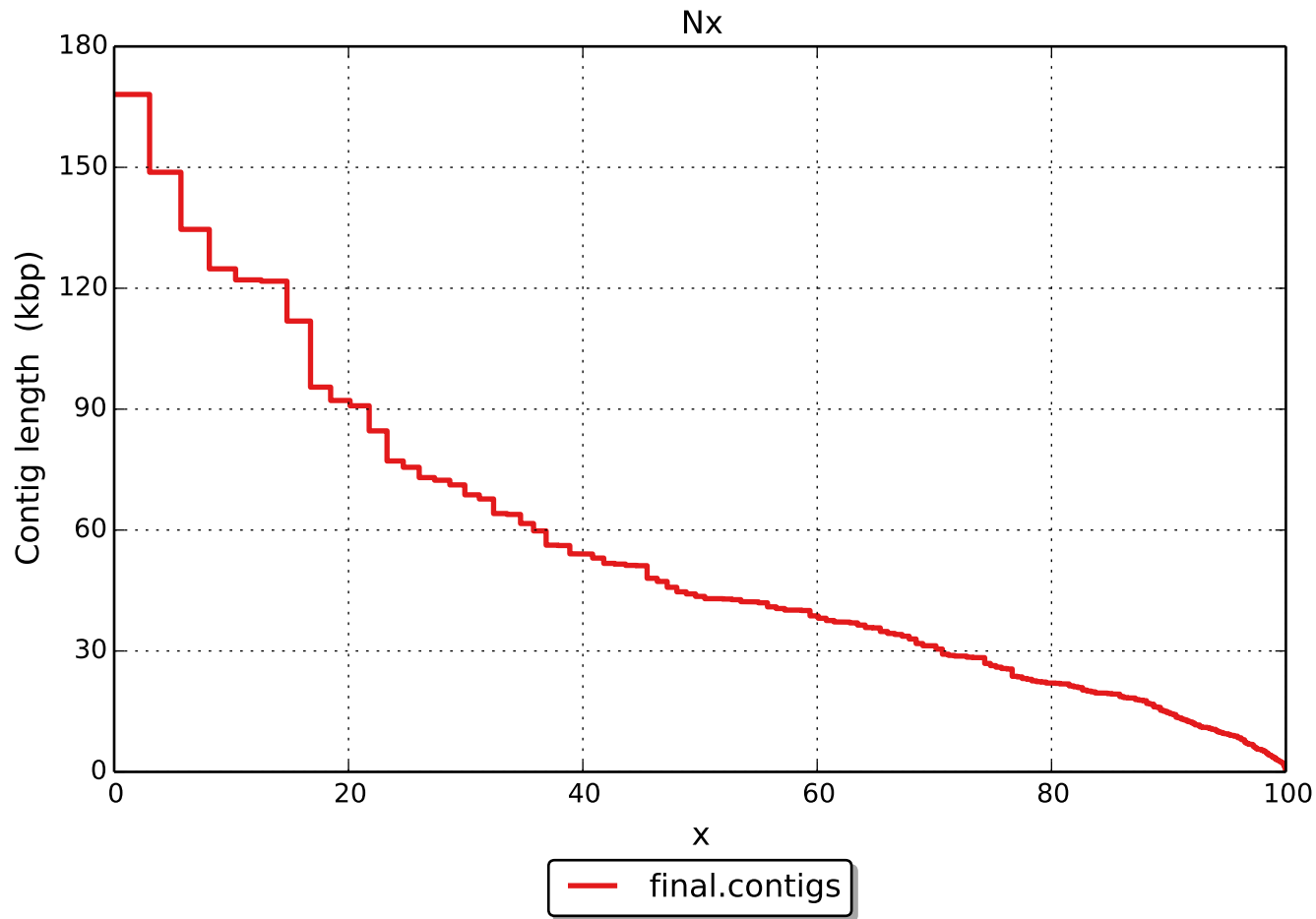
Unaligned report

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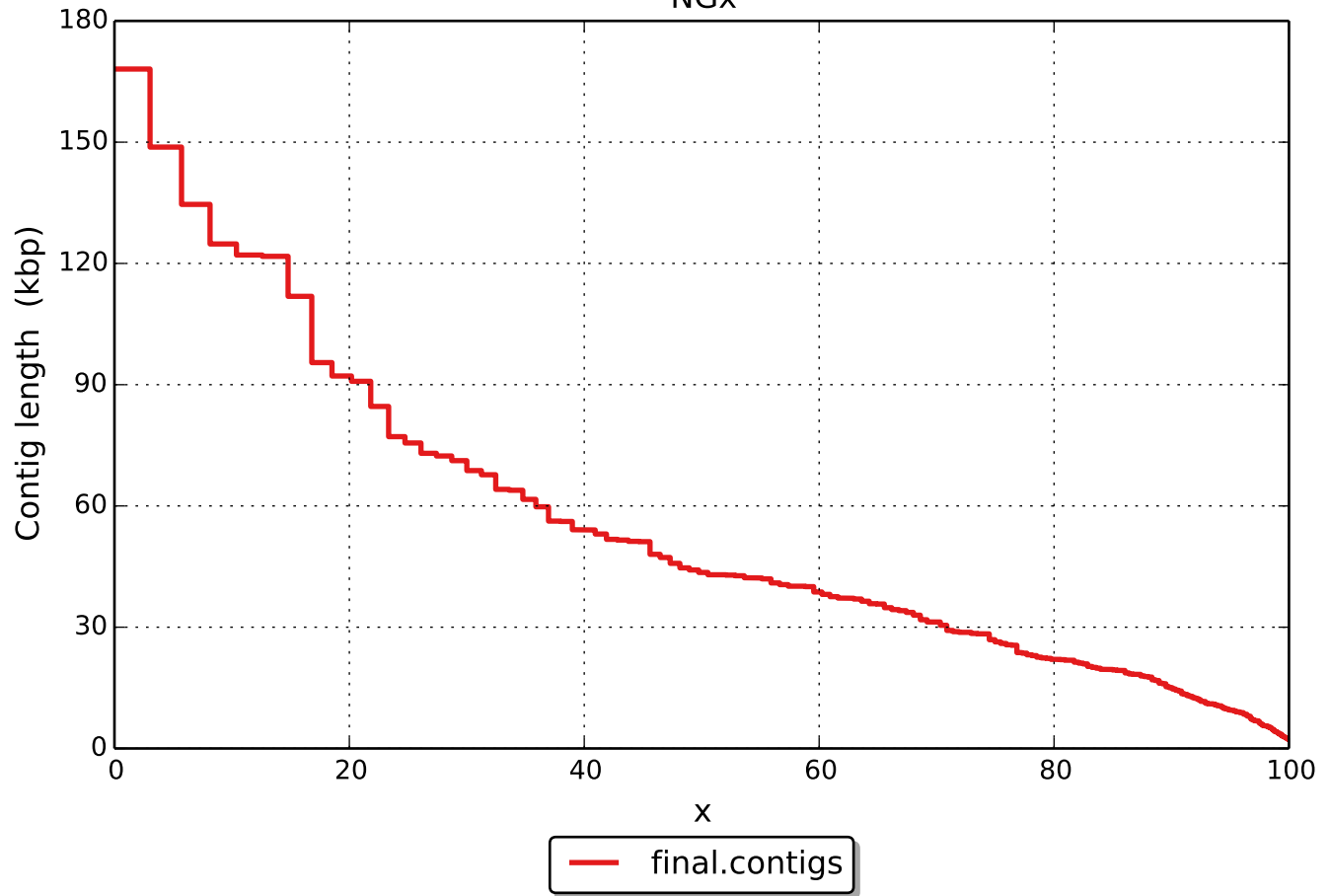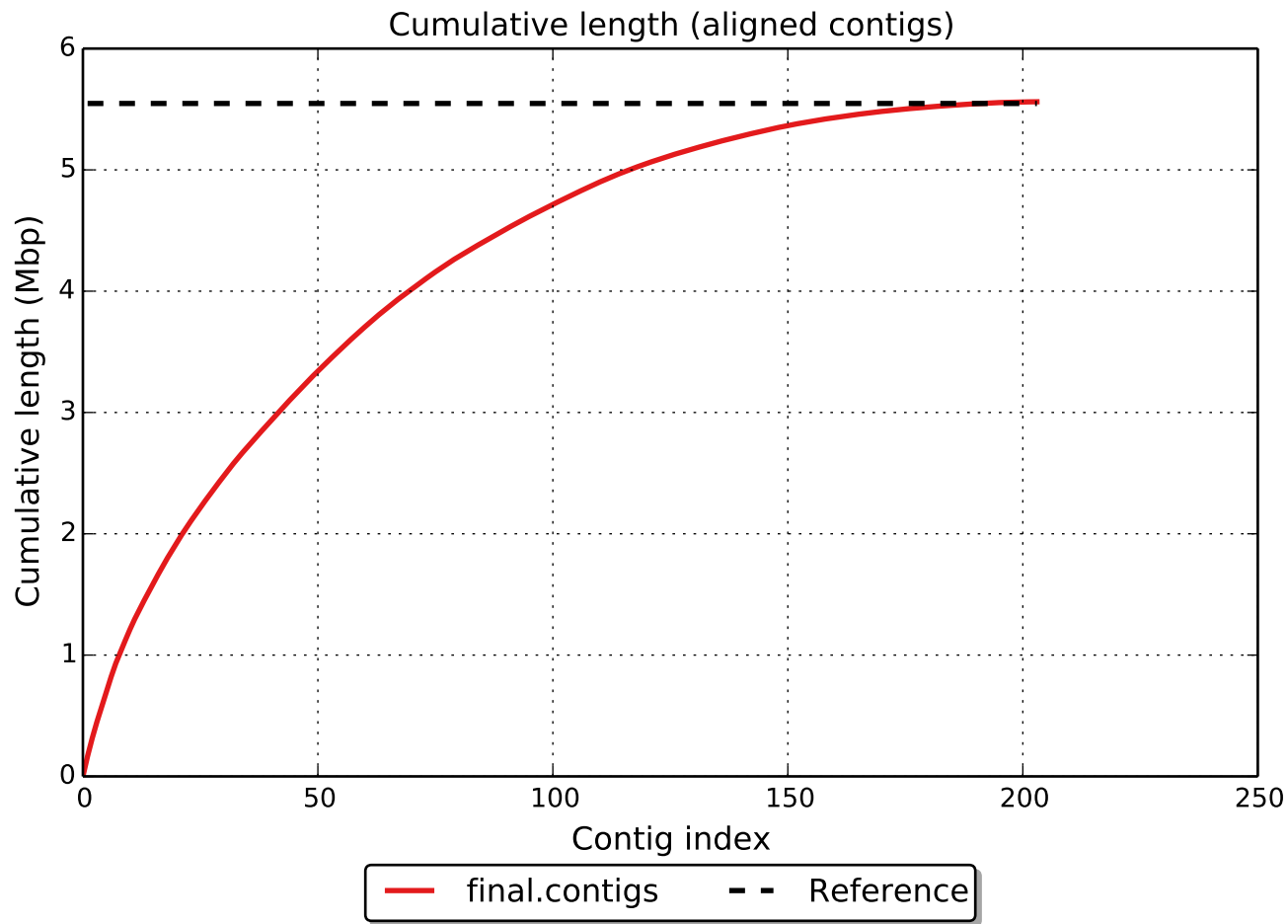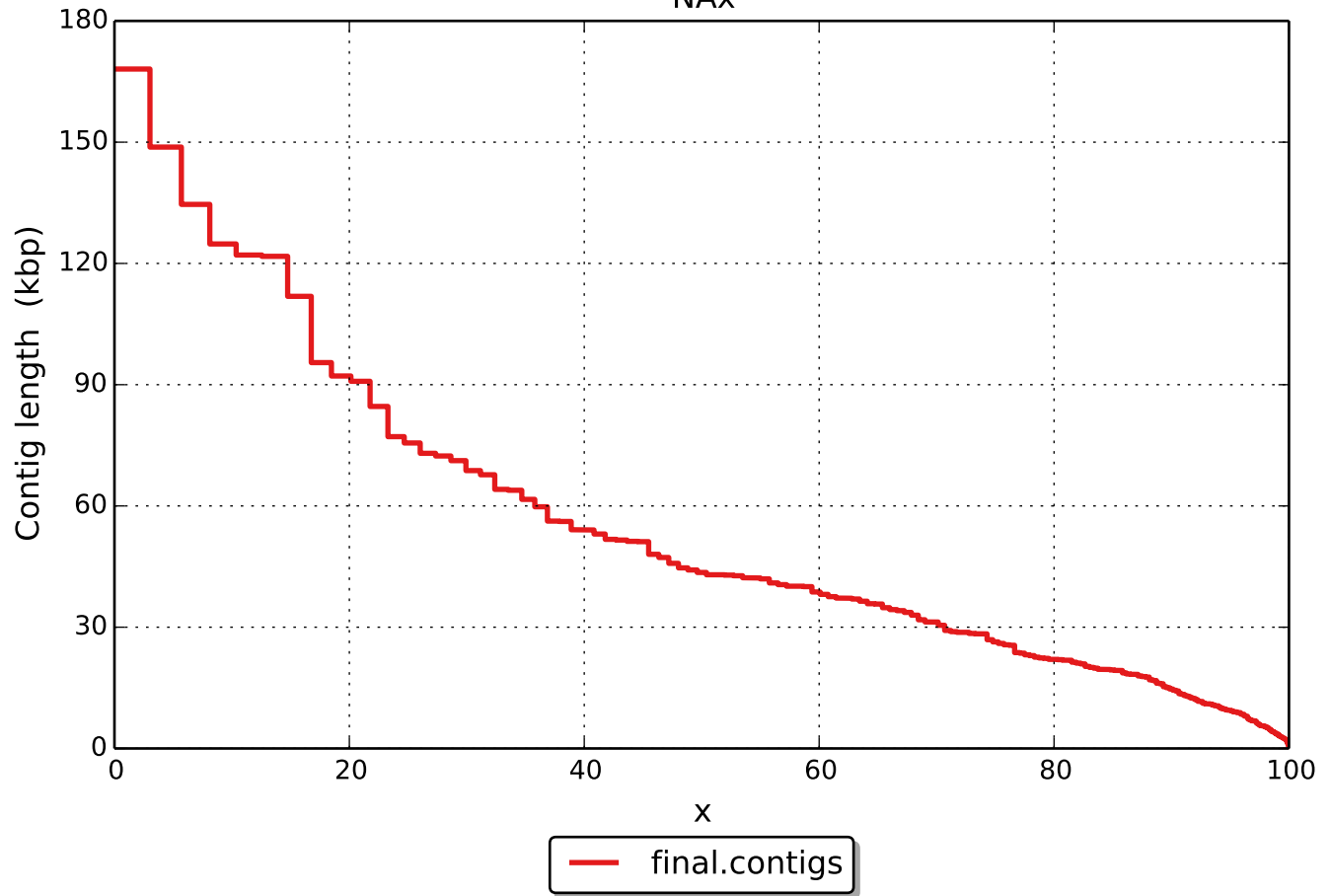(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

windows vs GC (%)

final.contigs
Reference

Nx

NGx

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NGAx