Report

	final.contigs
# contigs (>= 0 bp)	3912
# contigs (>= 1000 bp)	2149
Total length (>= 0 bp)	5274559
Total length (>= 1000 bp)	3989416
# contigs	3912
Largest contig	6941
Total length	5274559
Reference length	5478683
GC (%)	50.47
Reference GC (%)	50.49
N50	1590
NG50	1543
N75	1016
NG75	956
L50	1079
LG50	1144
L75	2116
LG75	2272
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.277
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	37.98
# indels per 100 kbp	0.00
Largest alignment	6941
NA50	1590
NGA50	1543
NA75	1016
NGA75	956
LA50	1079
LGA50	1144
LA75	2116
LGA75	2272

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).
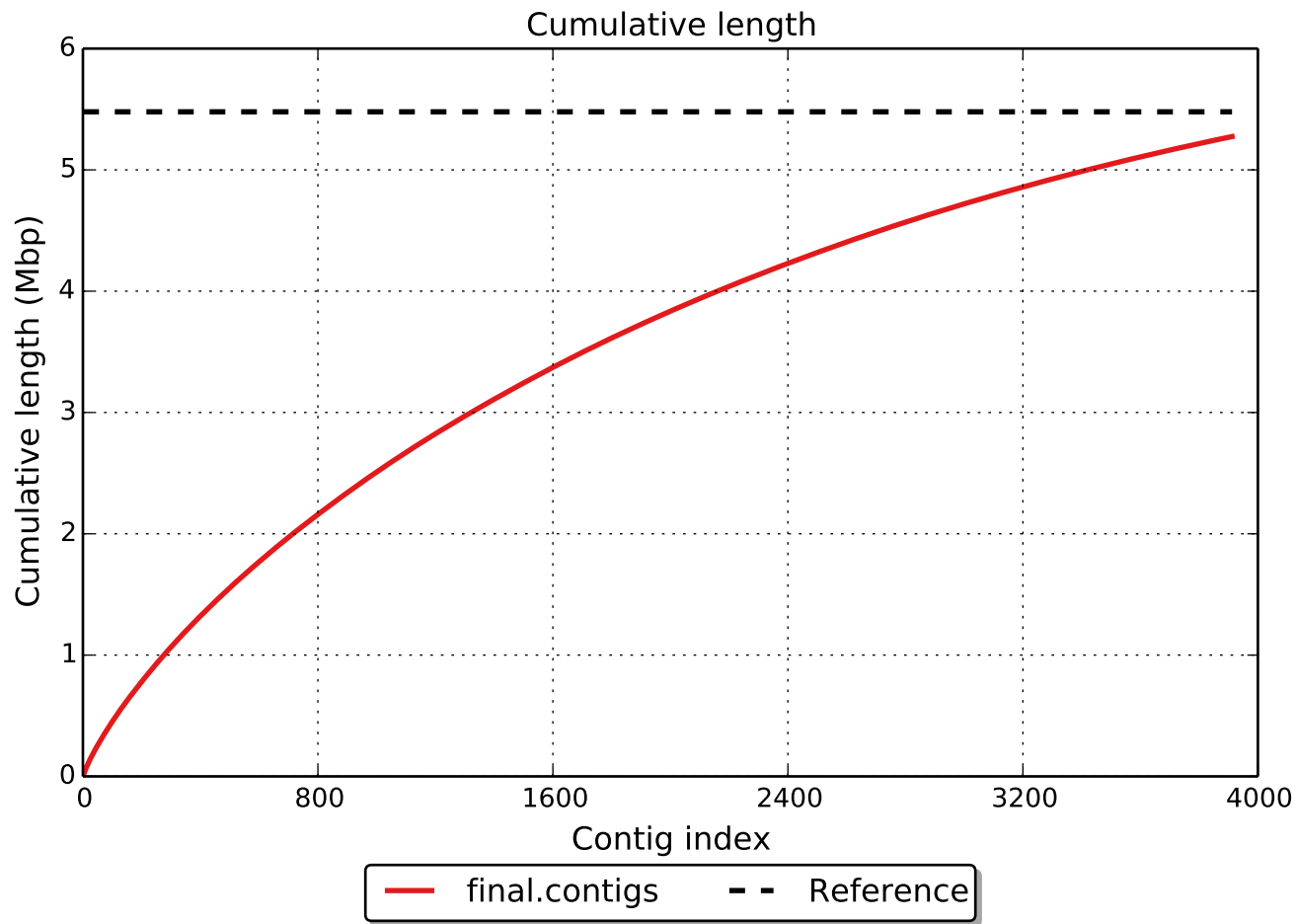
Misassemblies report

	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	1920
# indels	0
# short indels	0
# long indels	0
Indels length	0

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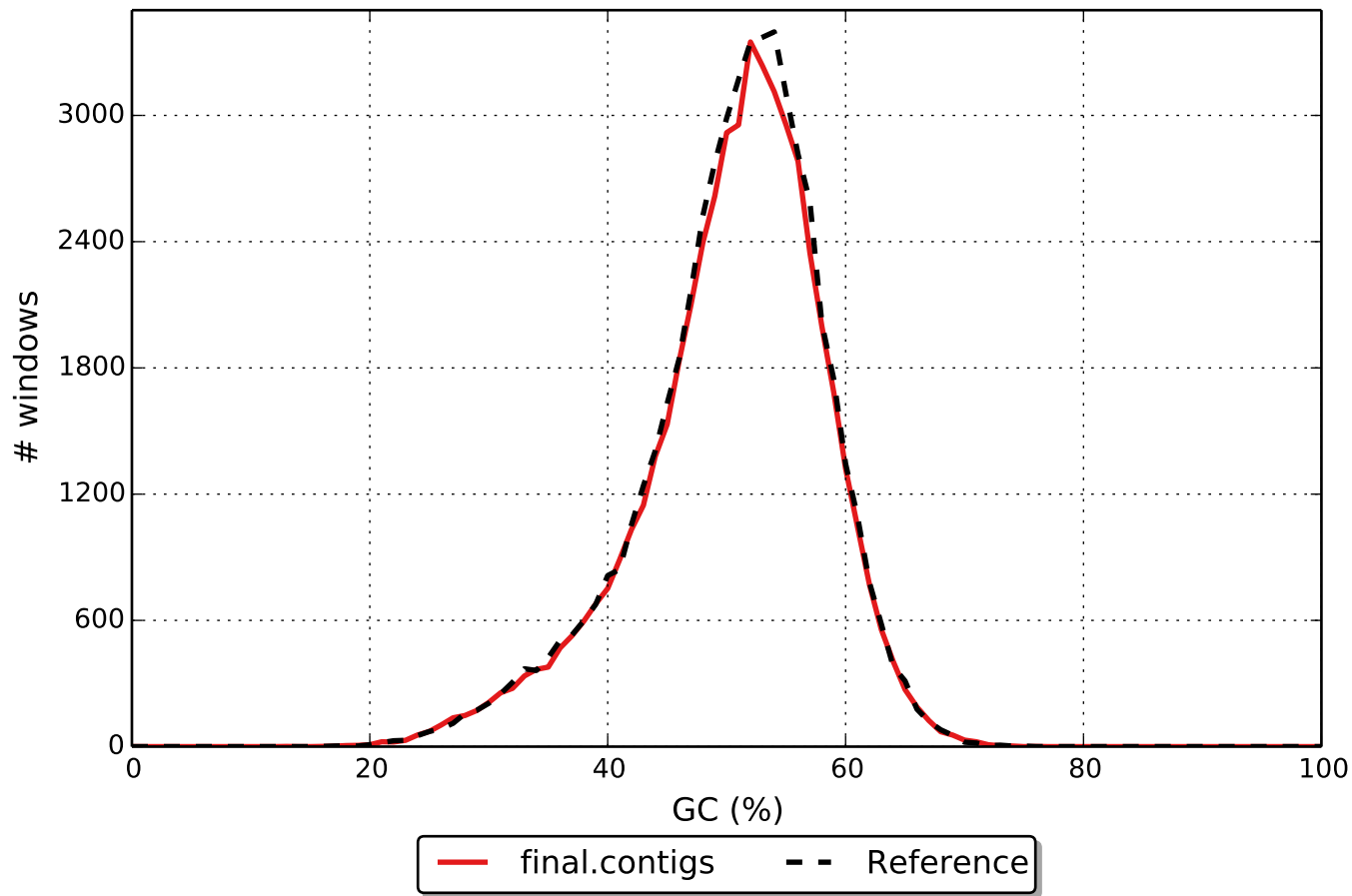(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
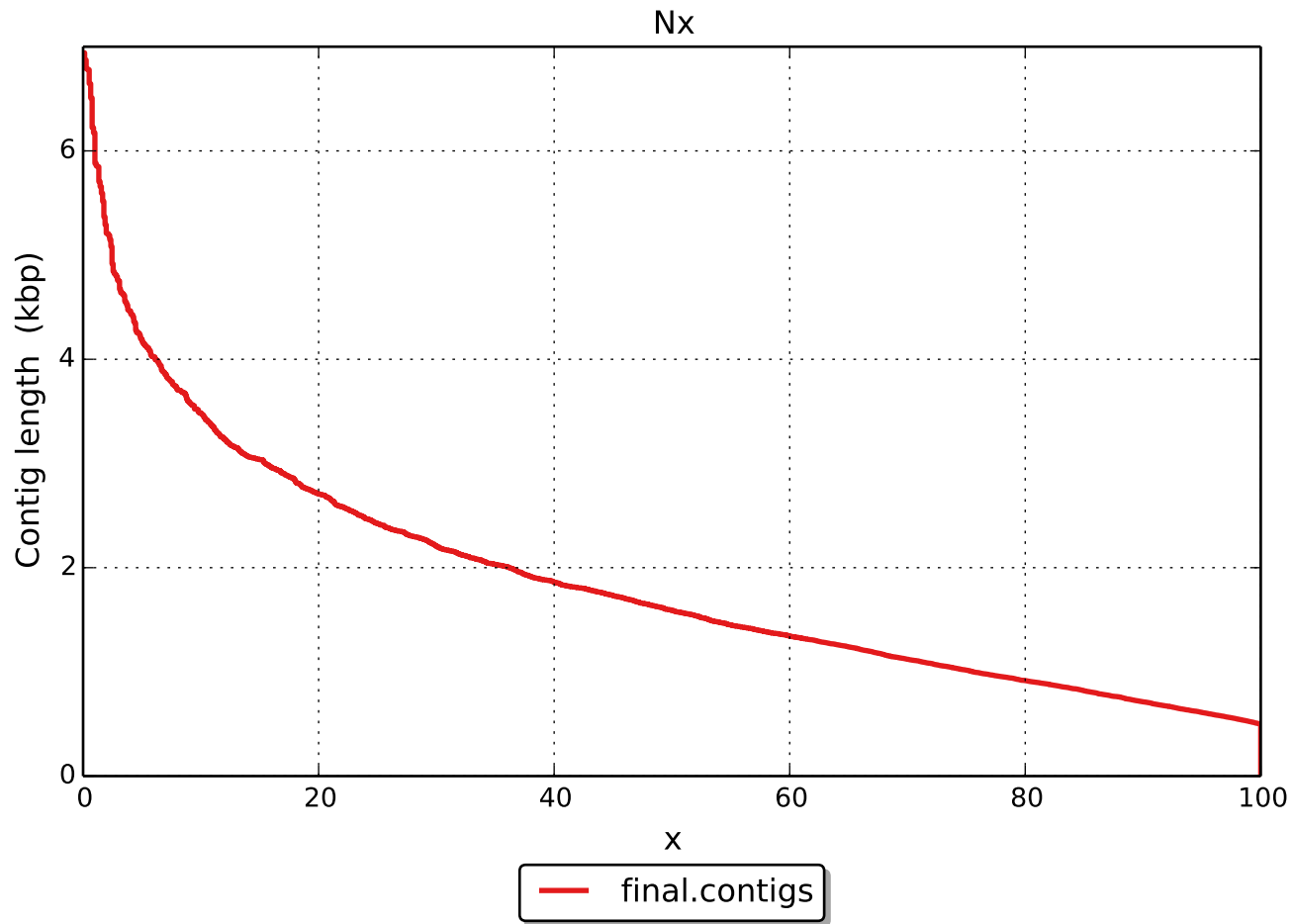
Unaligned report

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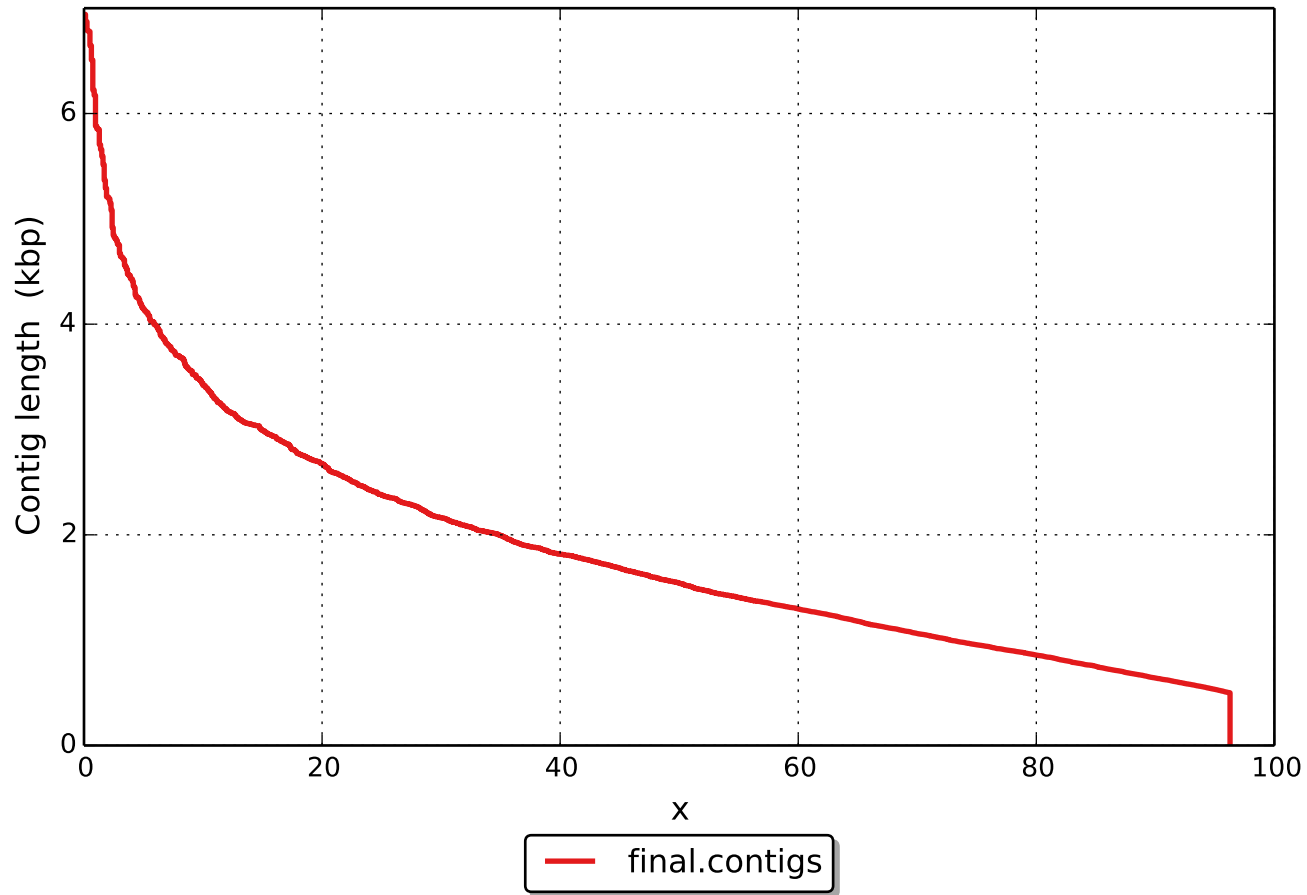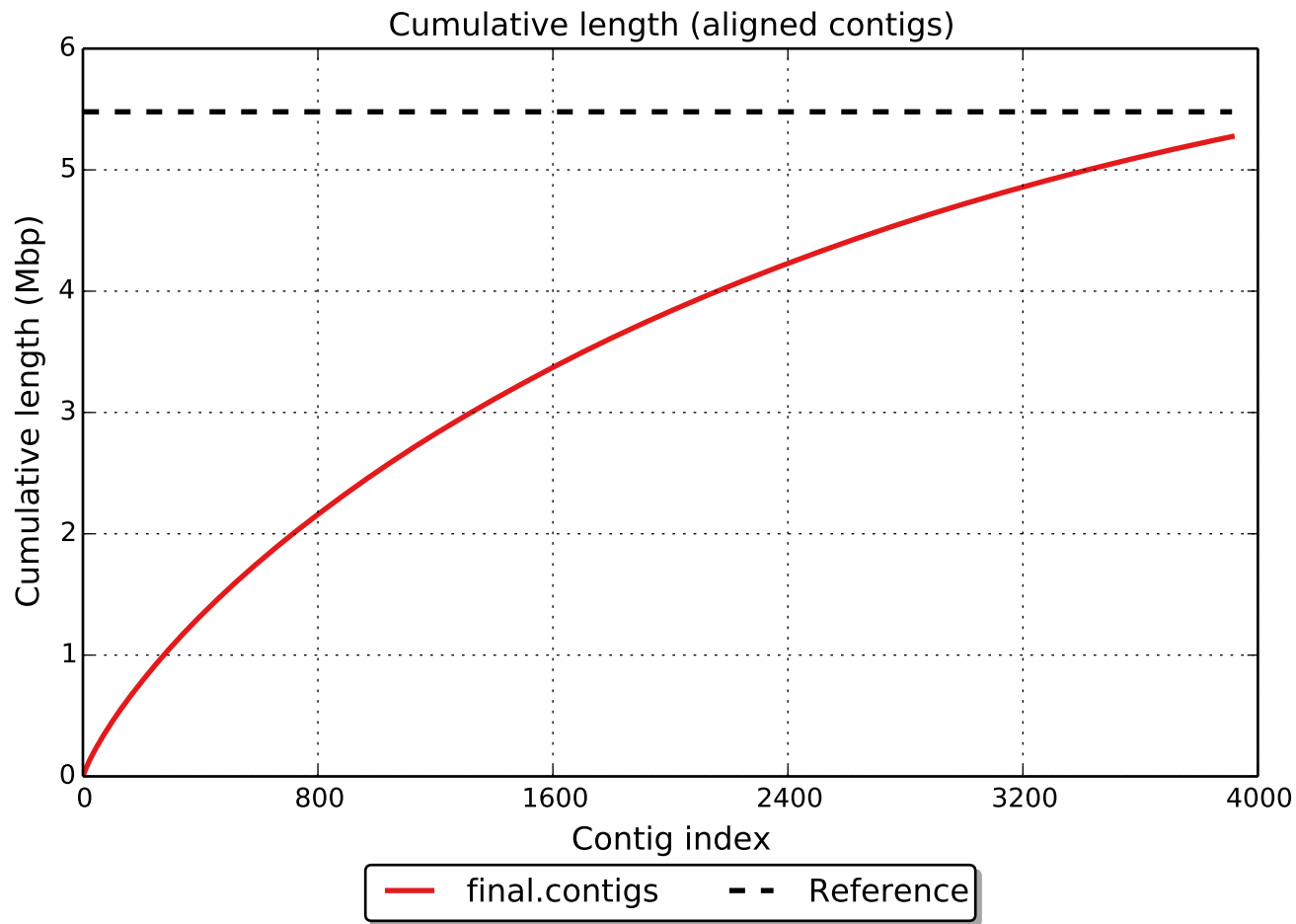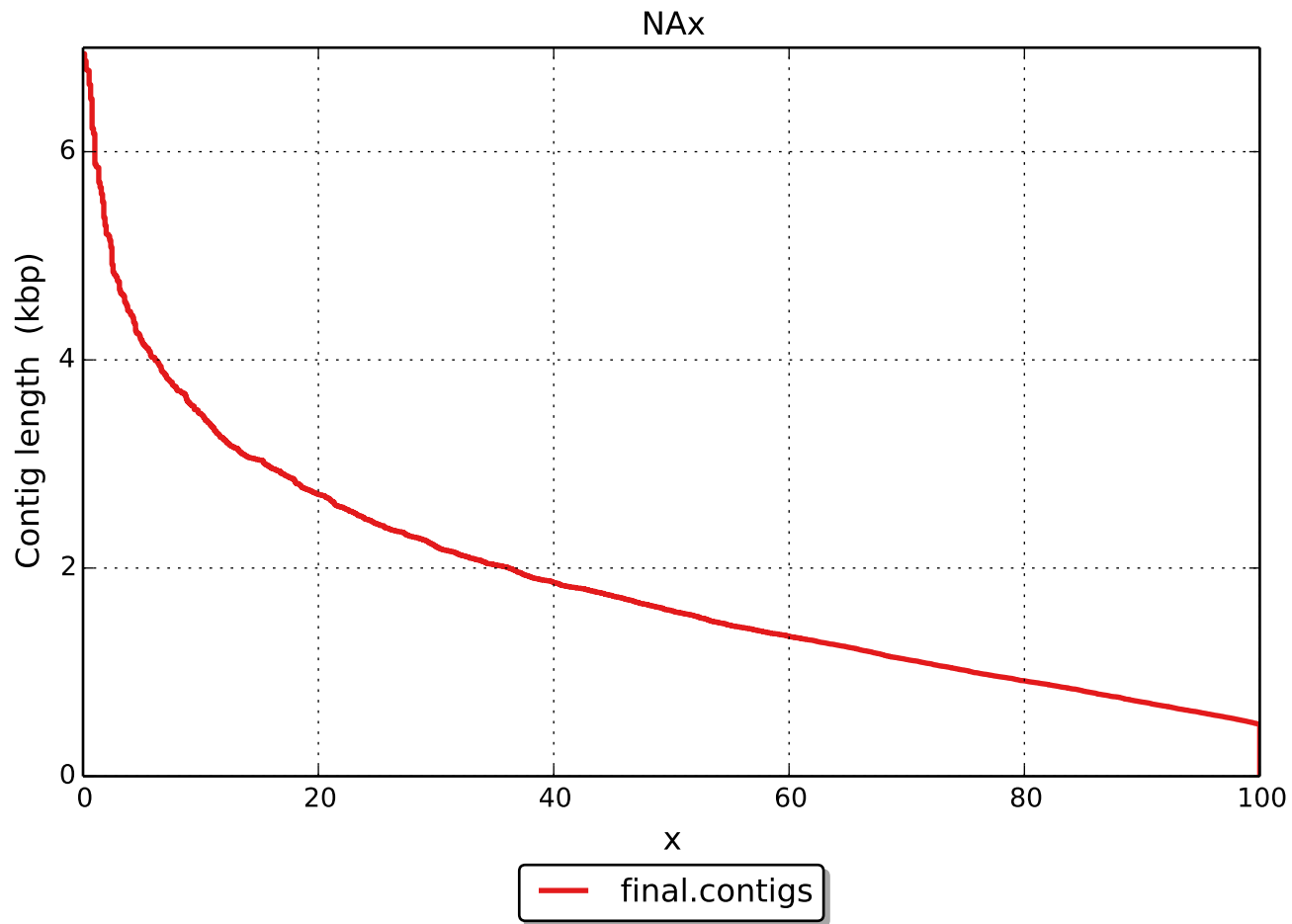(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

Nx

Contig length (kbp) vs x

final.contigs

NGx

Contig length (kbp)

x

final.contigs

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

final.contigs

NGAx