Report

	final.contigs
# contigs (>= 0 bp)	4934
# contigs (>= 1000 bp)	1033
Total length (>= 0 bp)	3654296
Total length (>= 1000 bp)	1517038
# contigs	3133
Largest contig	4208
Total length	3006464
Reference length	3785550
GC (%)	32.32
Reference GC (%)	32.26
N50	1007
NG50	855
N75	732
NG75	547
L50	1020
LG50	1440
L75	1895
LG75	2813
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	76.002
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	86.82
# indels per 100 kbp	0.00
Largest alignment	4208
NA50	1007
NGA50	855
NA75	732
NGA75	547
LA50	1020
LGA50	1440
LA75	1895
LGA75	2813

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).
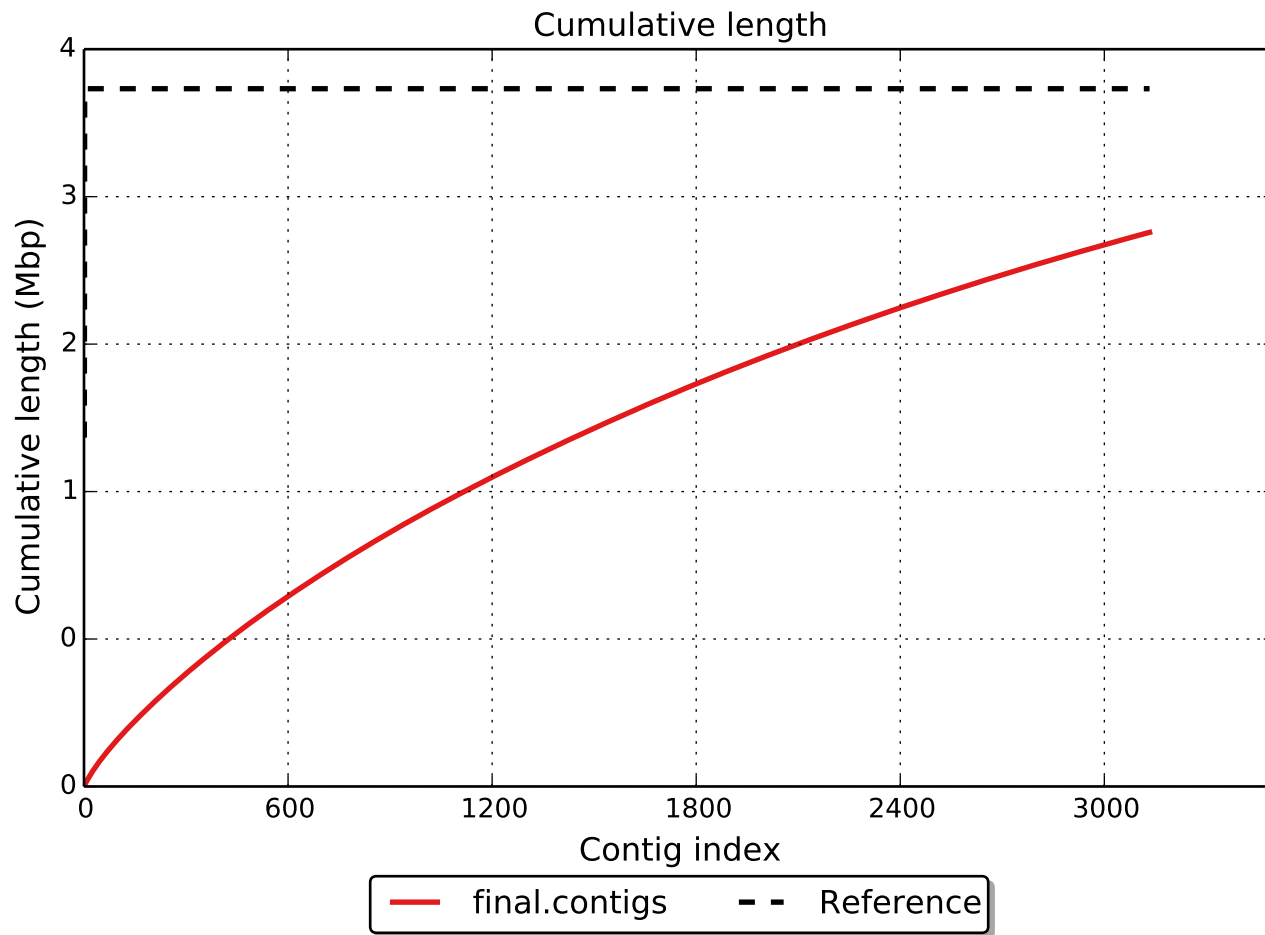
Misassemblies report

	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	2498
# indels	0
# short indels	0
# long indels	0
Indels length	0

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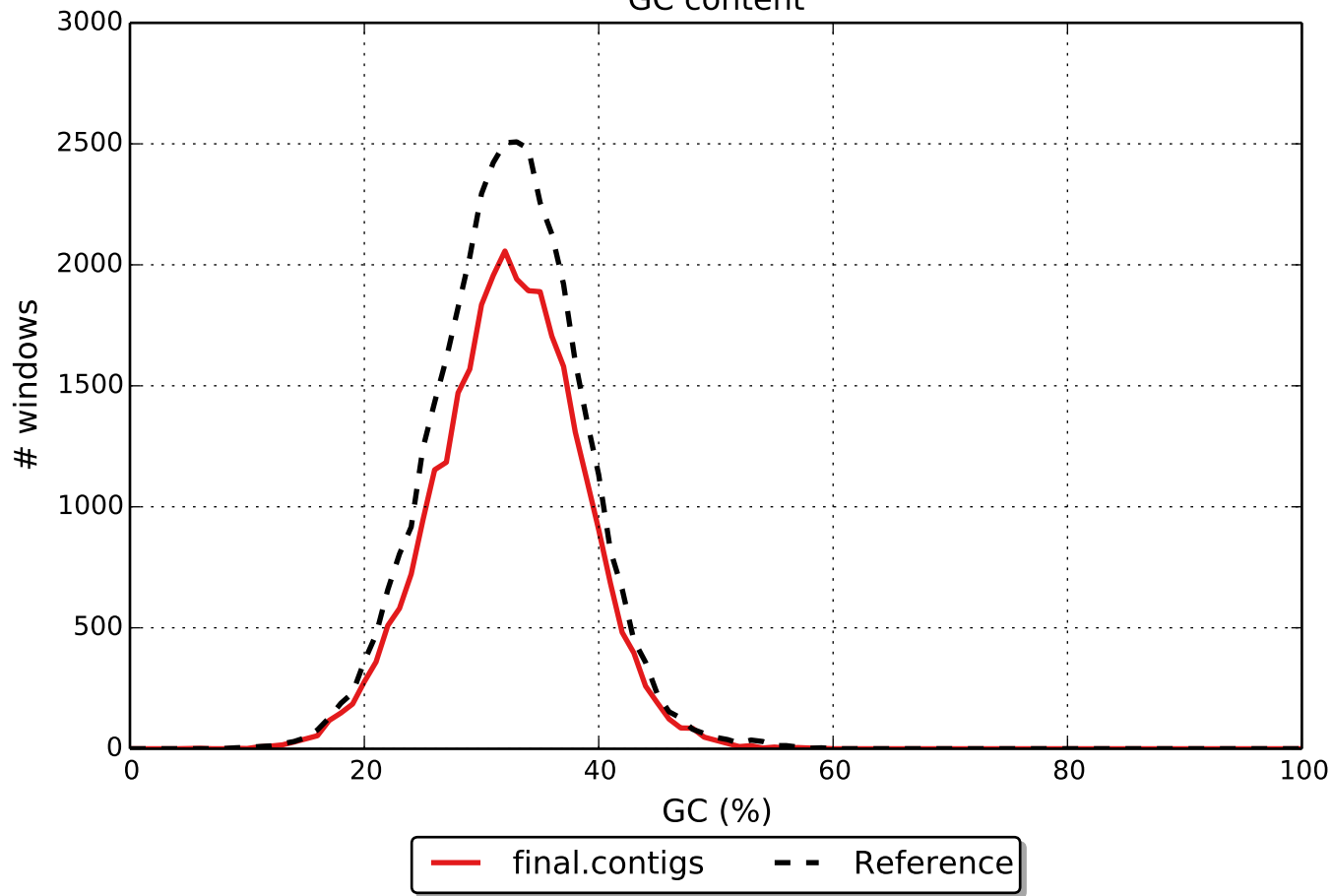(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
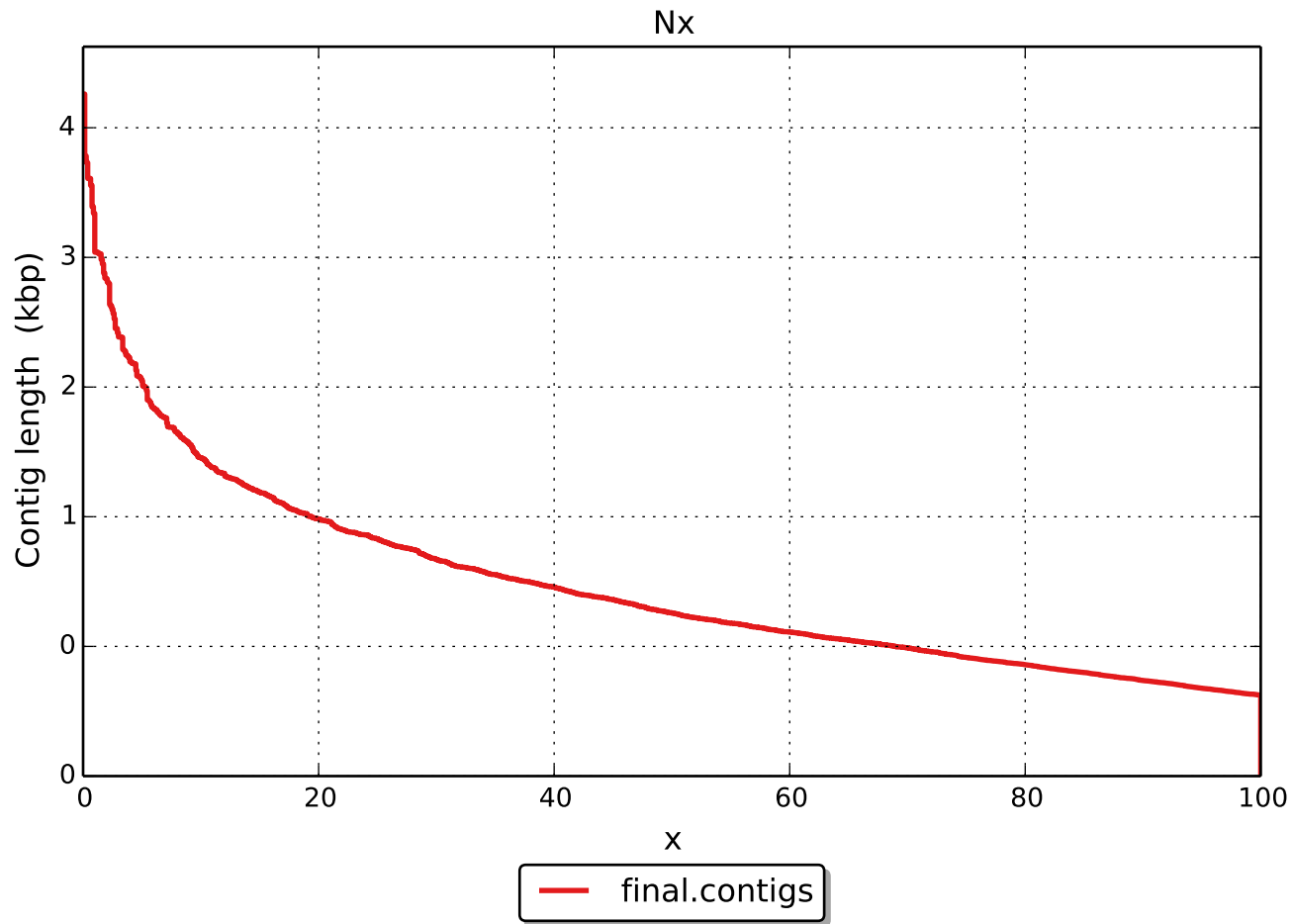
Unaligned report

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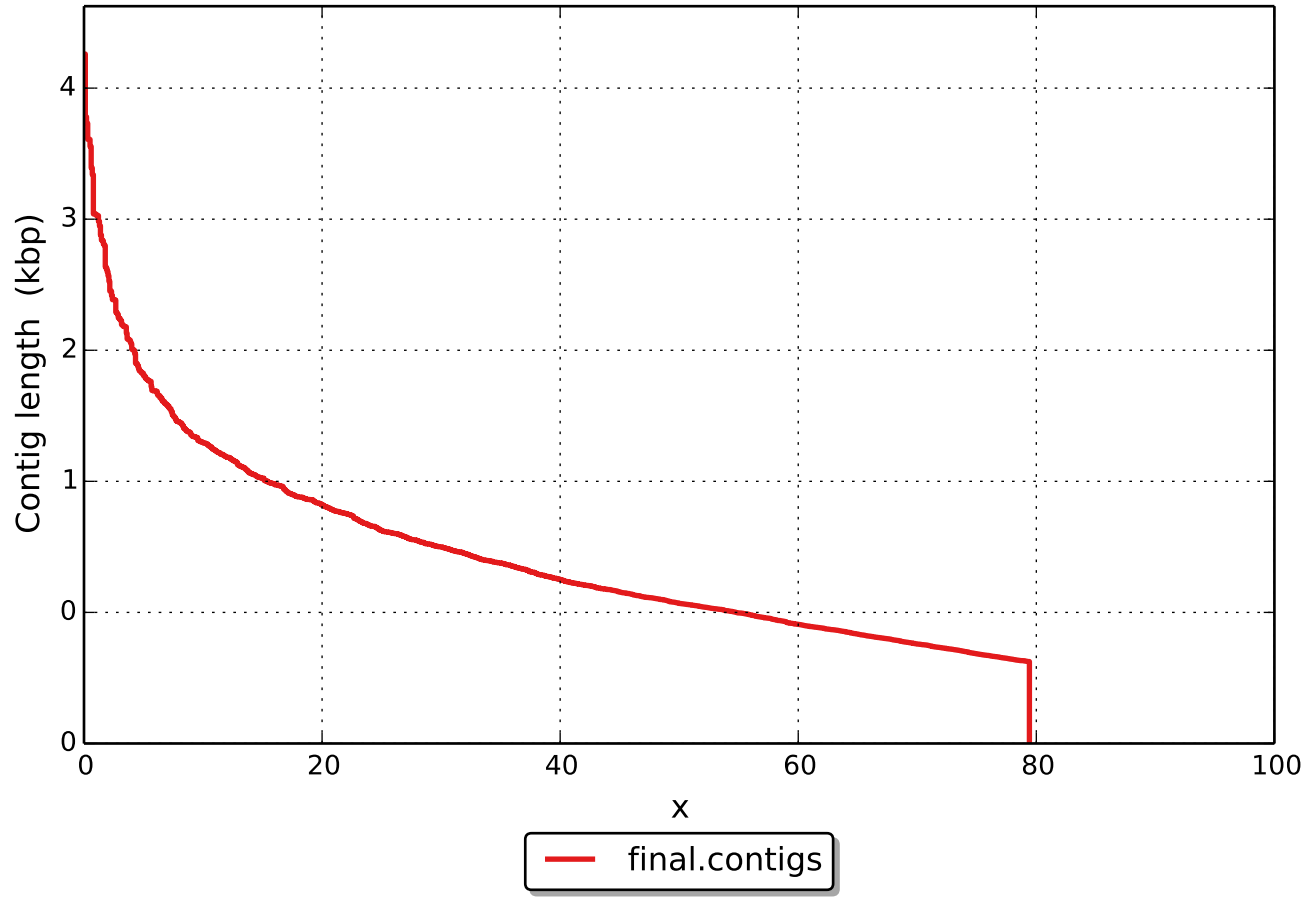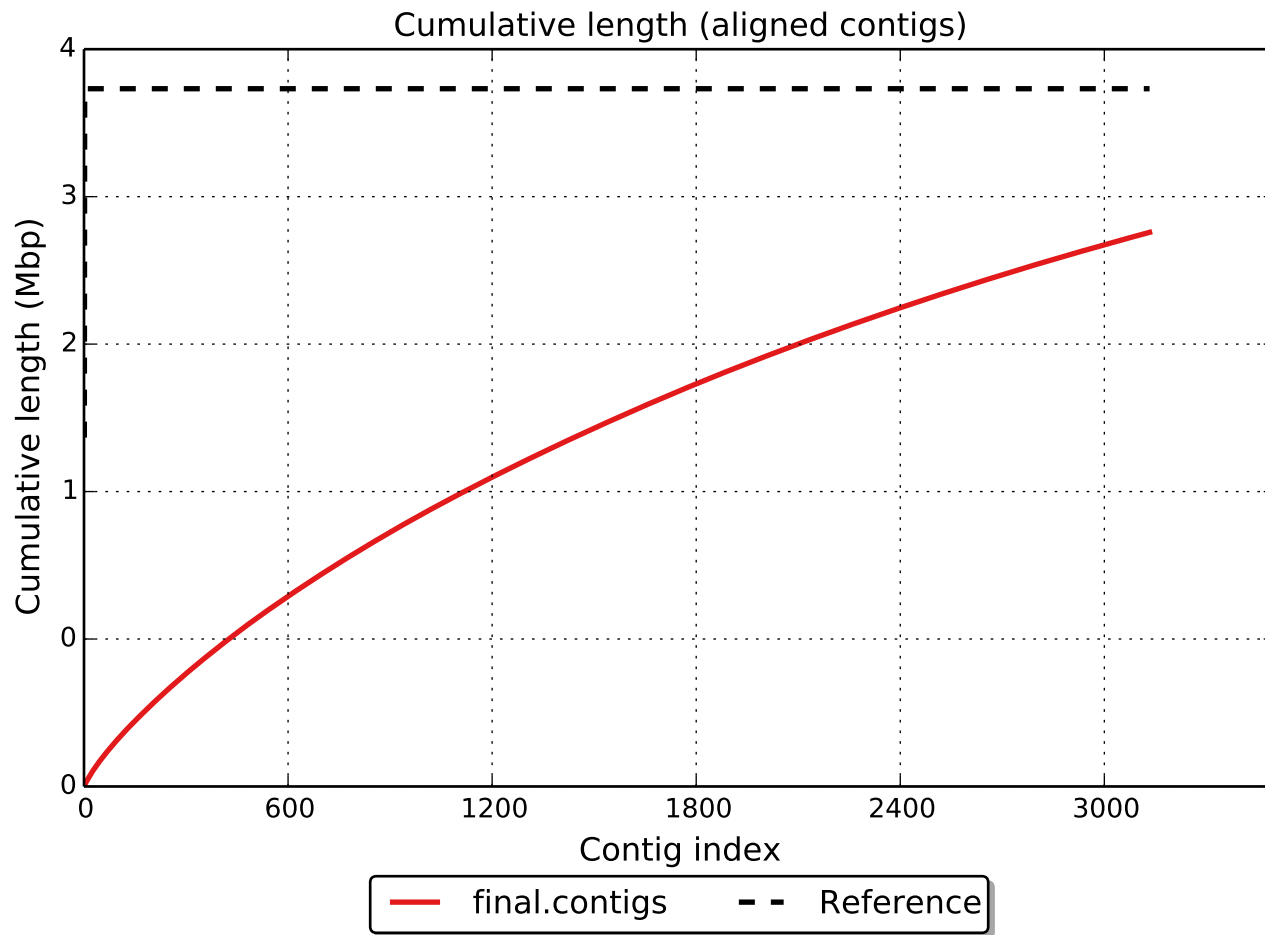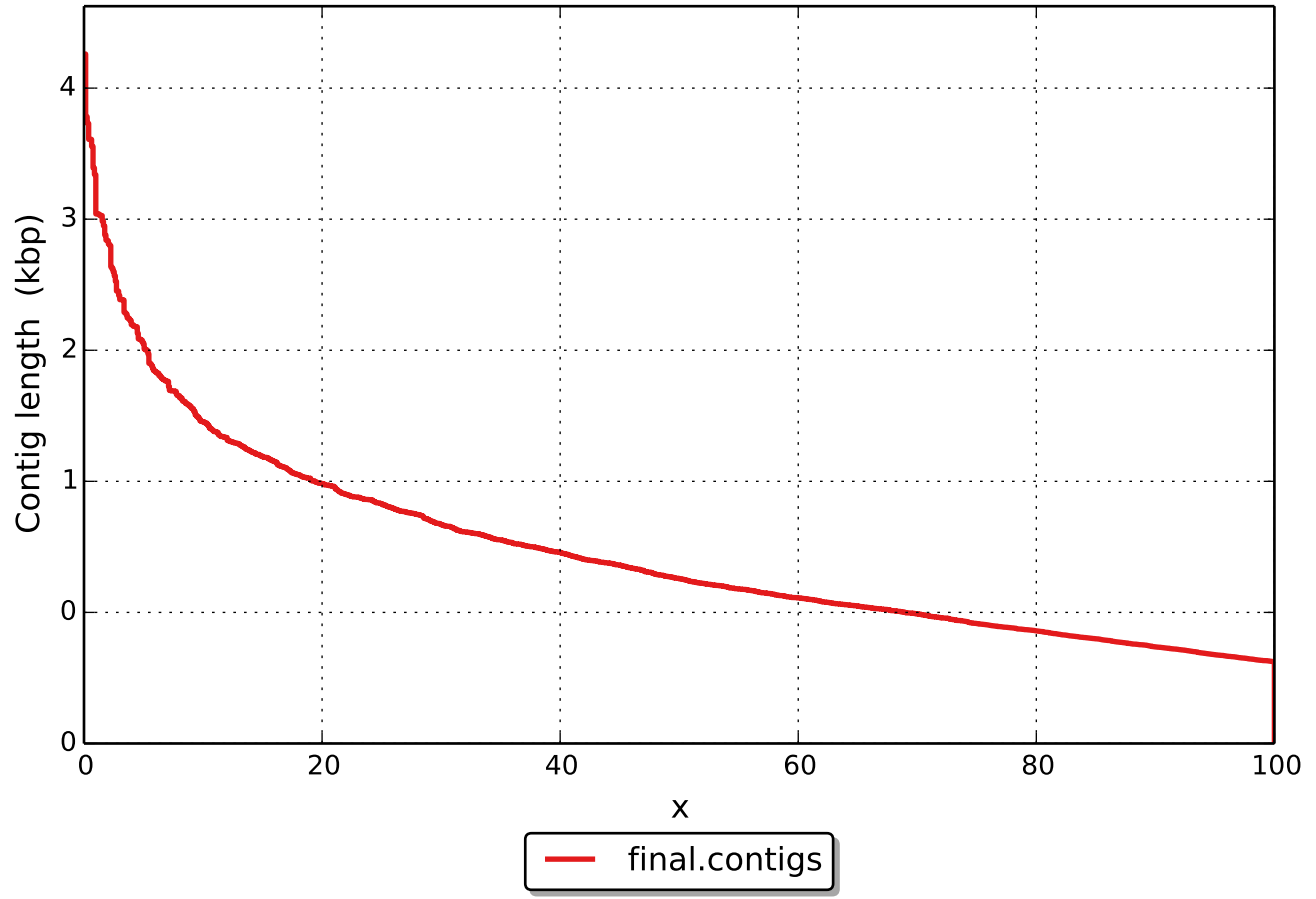(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

windows

GC (%)

final.contigs   Reference

NGx

Misassemblies

final.contigs

Cumulative length (aligned contigs)