Report

	final.contigs
# contigs (>= 0 bp)	2600
# contigs (>= 1000 bp)	1773
Total length (>= 0 bp)	11009440
Total length (>= 1000 bp)	10638239
# contigs	2046
Largest contig	41898
Total length	10836142
Reference length	11094646
GC (%)	50.39
Reference GC (%)	50.48
N50	8692
NG50	8452
N75	4699
NG75	4451
L50	388
LG50	404
L75	808
LG75	850
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2233
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.164
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	36.95
# indels per 100 kbp	0.32
Largest alignment	41898
NA50	8692
NGA50	8452
NA75	4699
NGA75	4451
LA50	388
LGA50	404
LA75	808
LGA75	850

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).
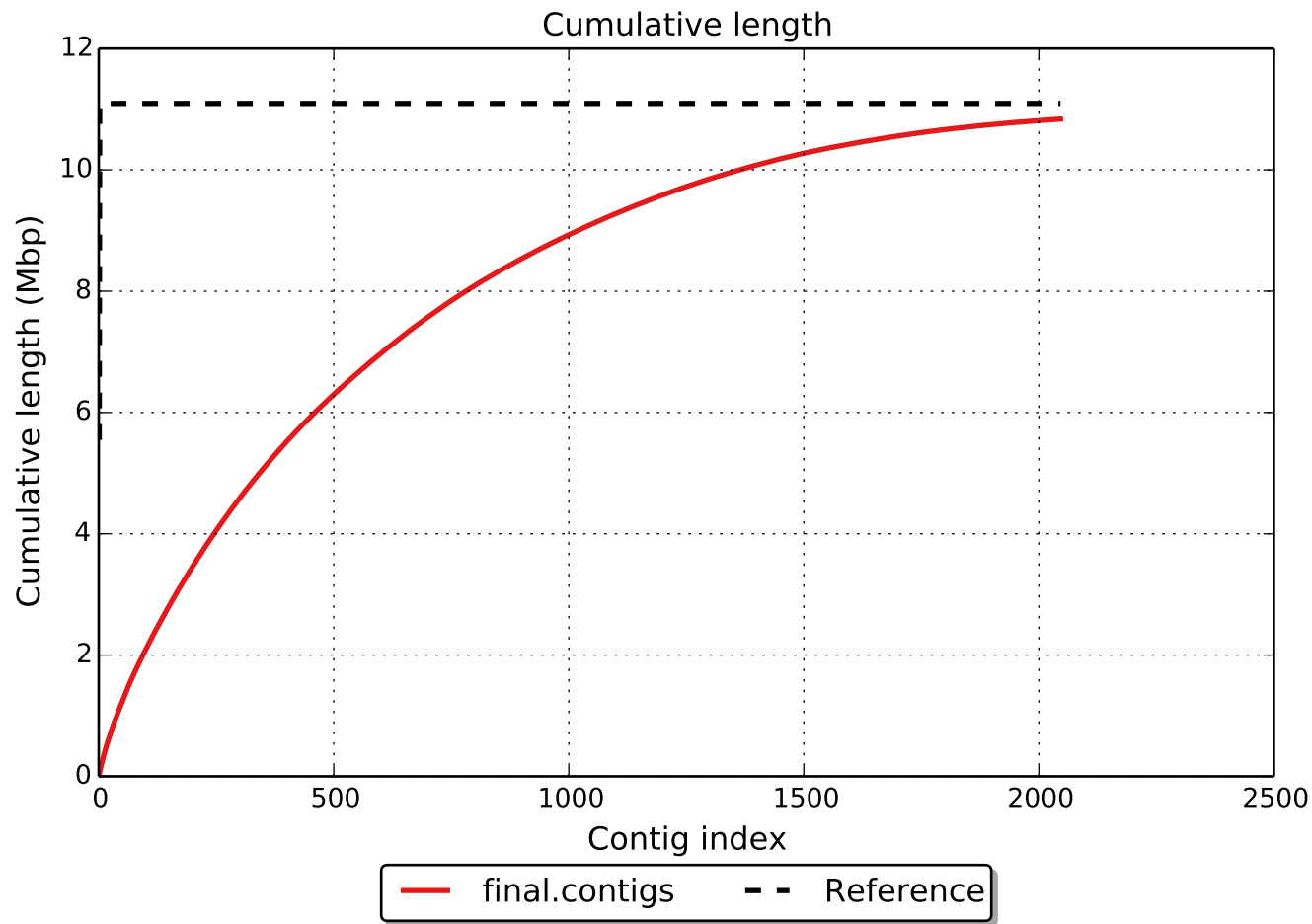
Misassemblies report

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2233
# local misassemblies	3
# mismatches	3983
# indels	35
# short indels	34
# long indels	1
Indels length	40

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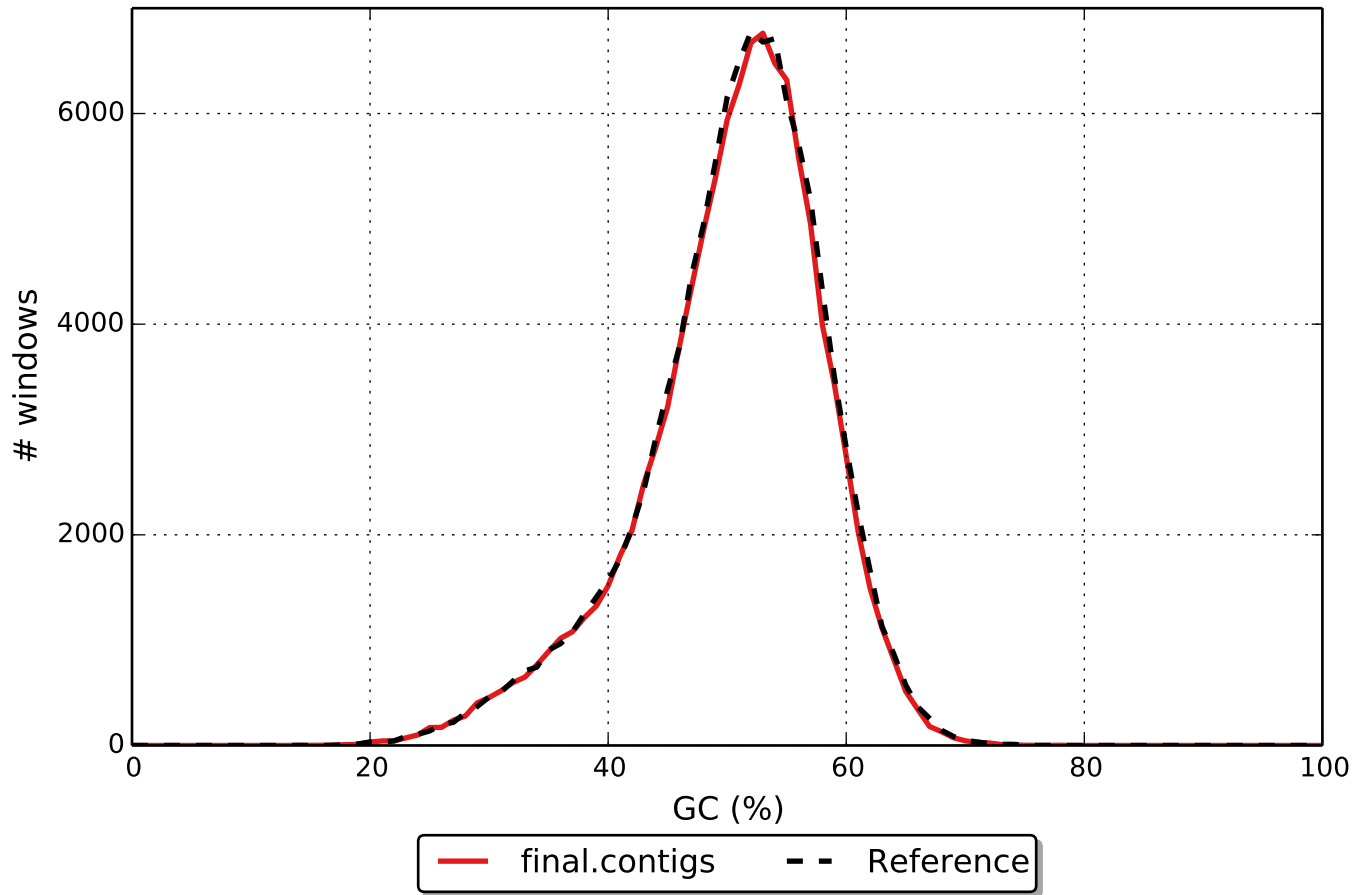(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
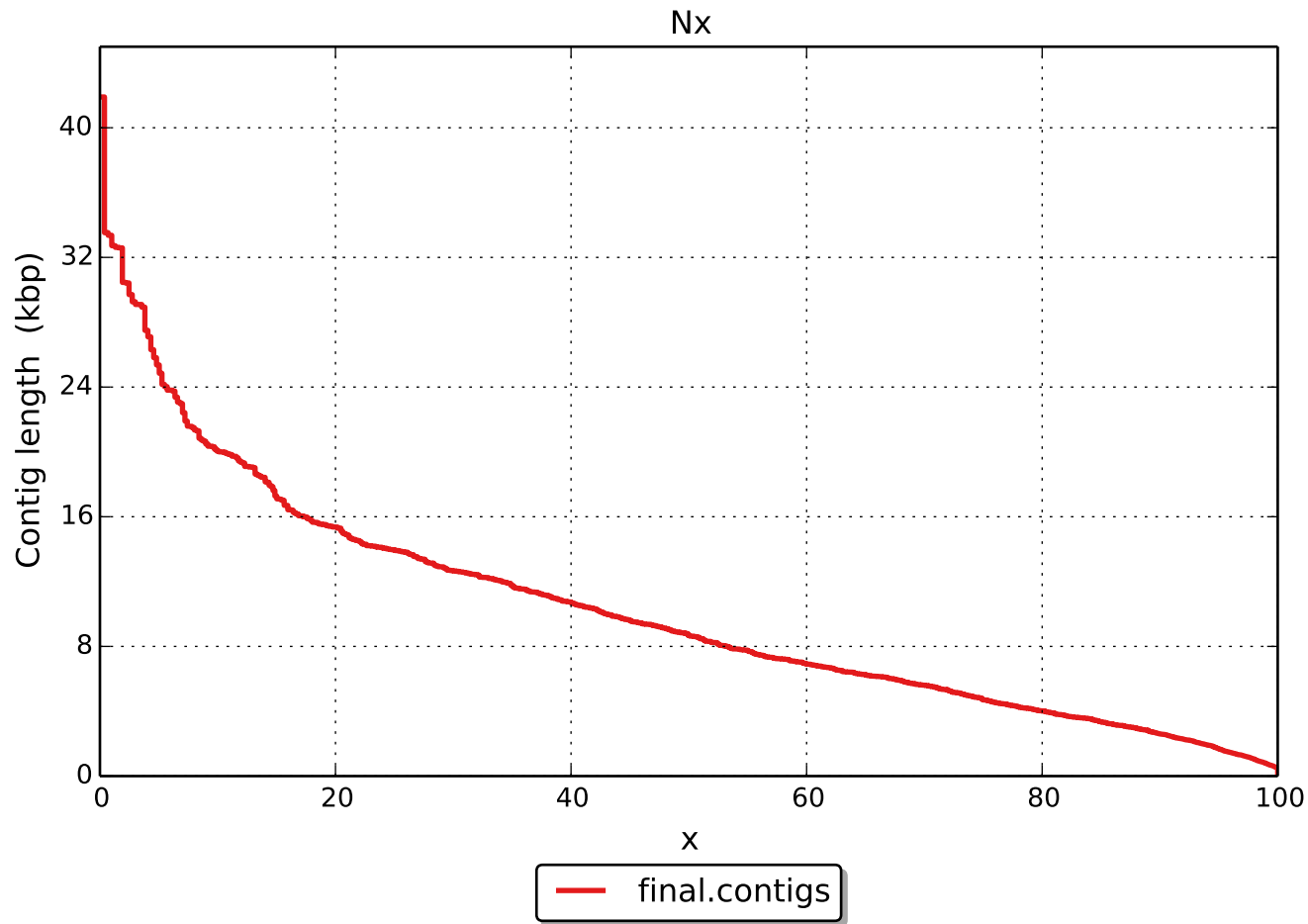
Unaligned report

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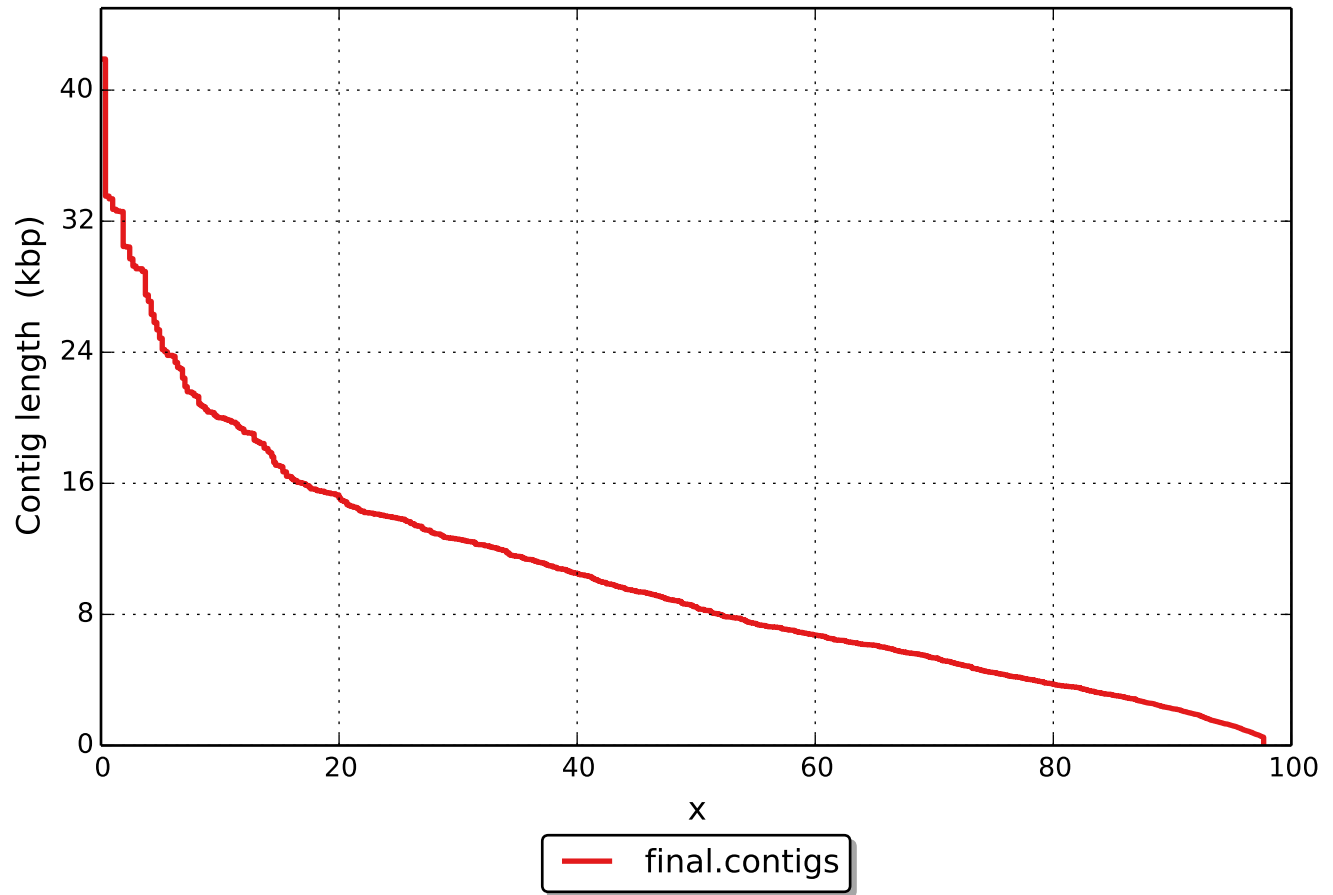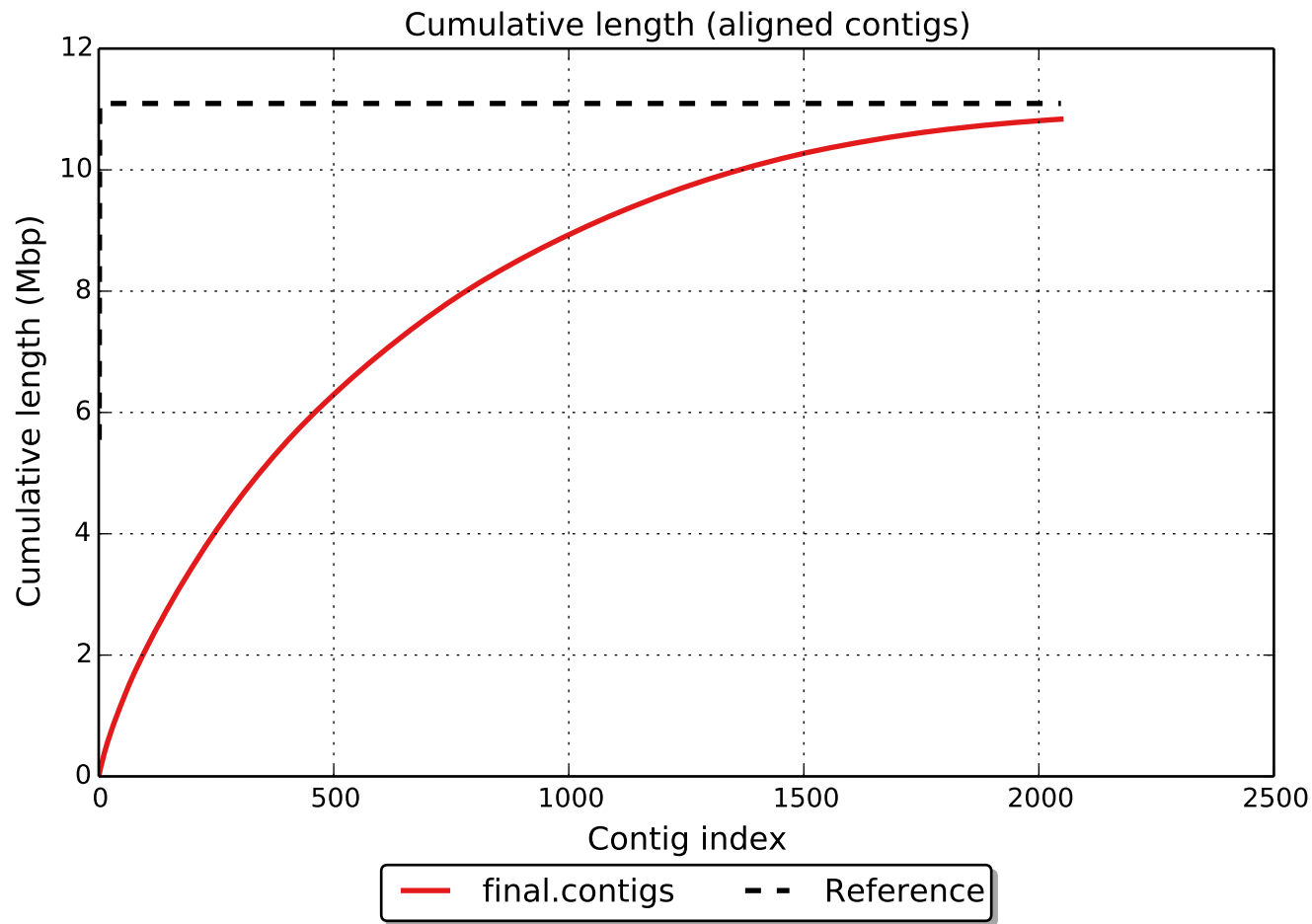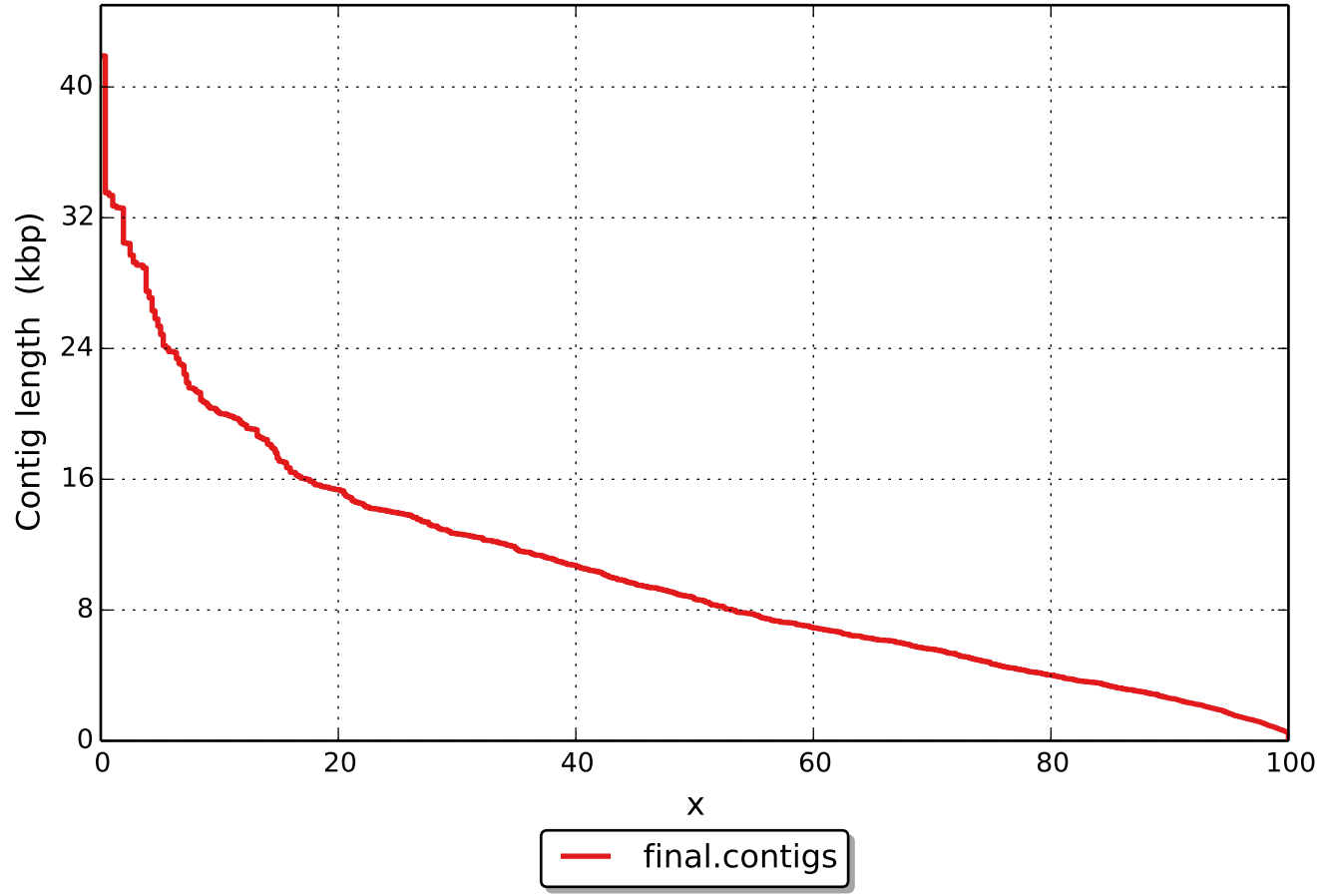(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

Nx

NGx

Contig length (kbp)

x

final.contigs

Misassemblies

Cumulative length (aligned contigs)