Report

	final.contigs
# contigs (>= 0 bp)	1232
# contigs (>= 1000 bp)	1082
Total length (>= 0 bp)	5628931
Total length (>= 1000 bp)	5515993
# contigs	1232
Largest contig	30455
Total length	5628931
Reference length	5547323
GC (%)	50.49
Reference GC (%)	50.49
N50	6926
NG50	7028
N75	3914
NG75	4042
L50	257
LG50	251
L75	527
LG75	511
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	17136
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	6052
Genome fraction (%)	99.385
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.57
# indels per 100 kbp	0.02
Largest alignment	30455
NA50	6926
NGA50	7018
NA75	3897
NGA75	4034
LA50	257
LGA50	252
LA75	528
LGA75	513

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).
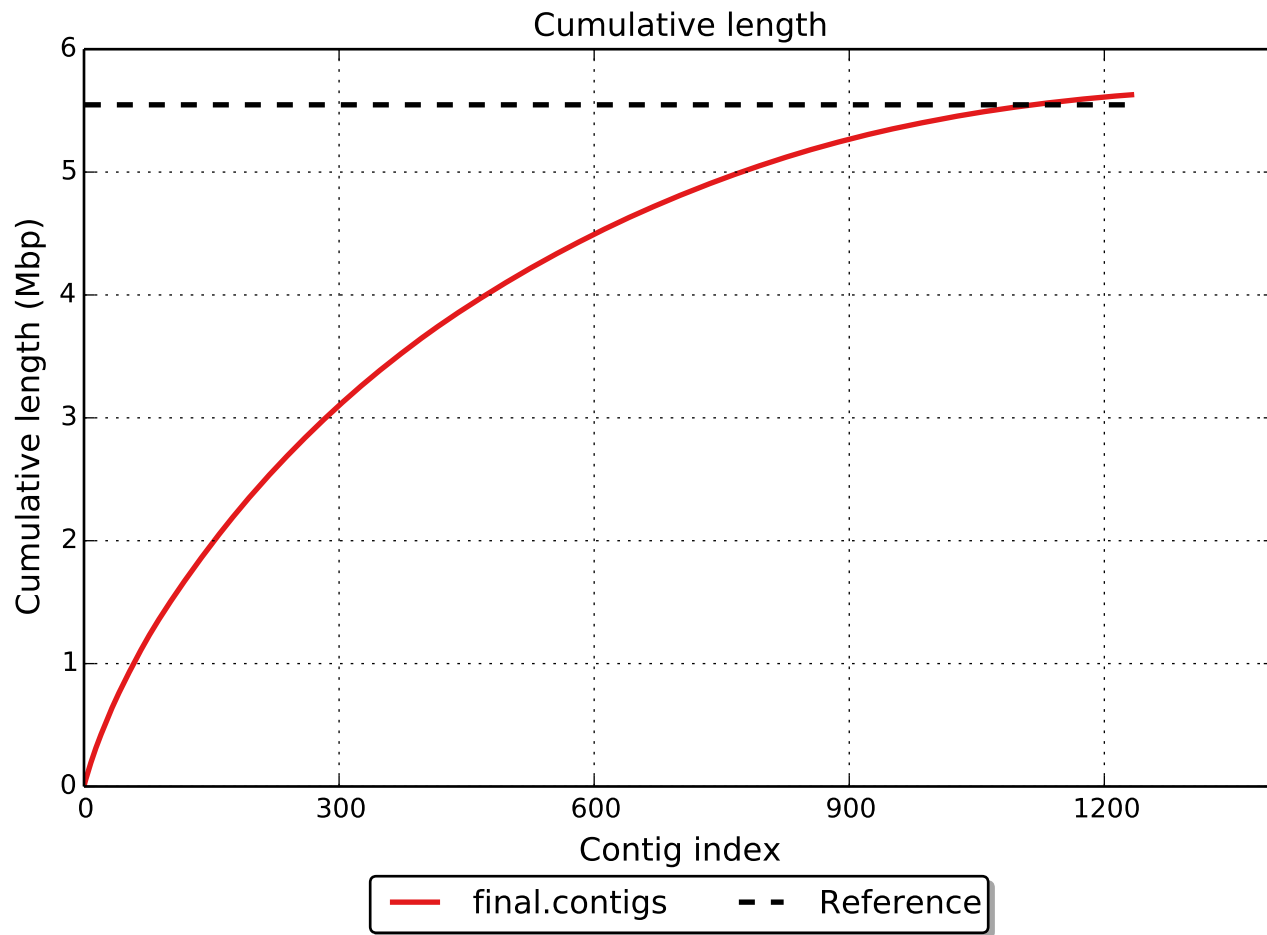
Misassemblies report

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	1
Misassembled contigs length	17136
# local misassemblies	0
# mismatches	583
# indels	1
# short indels	1
# long indels	0
Indels length	1

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).
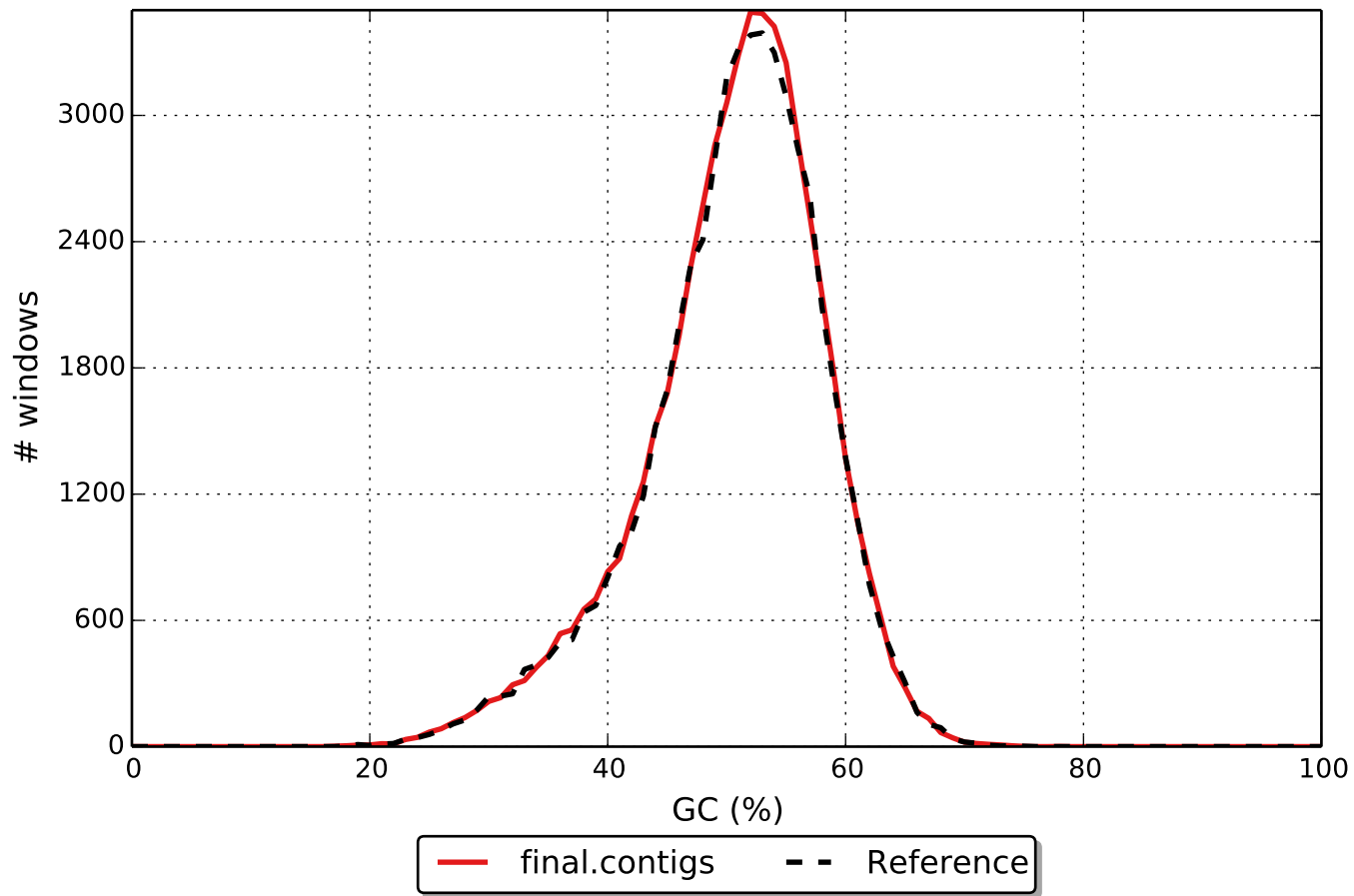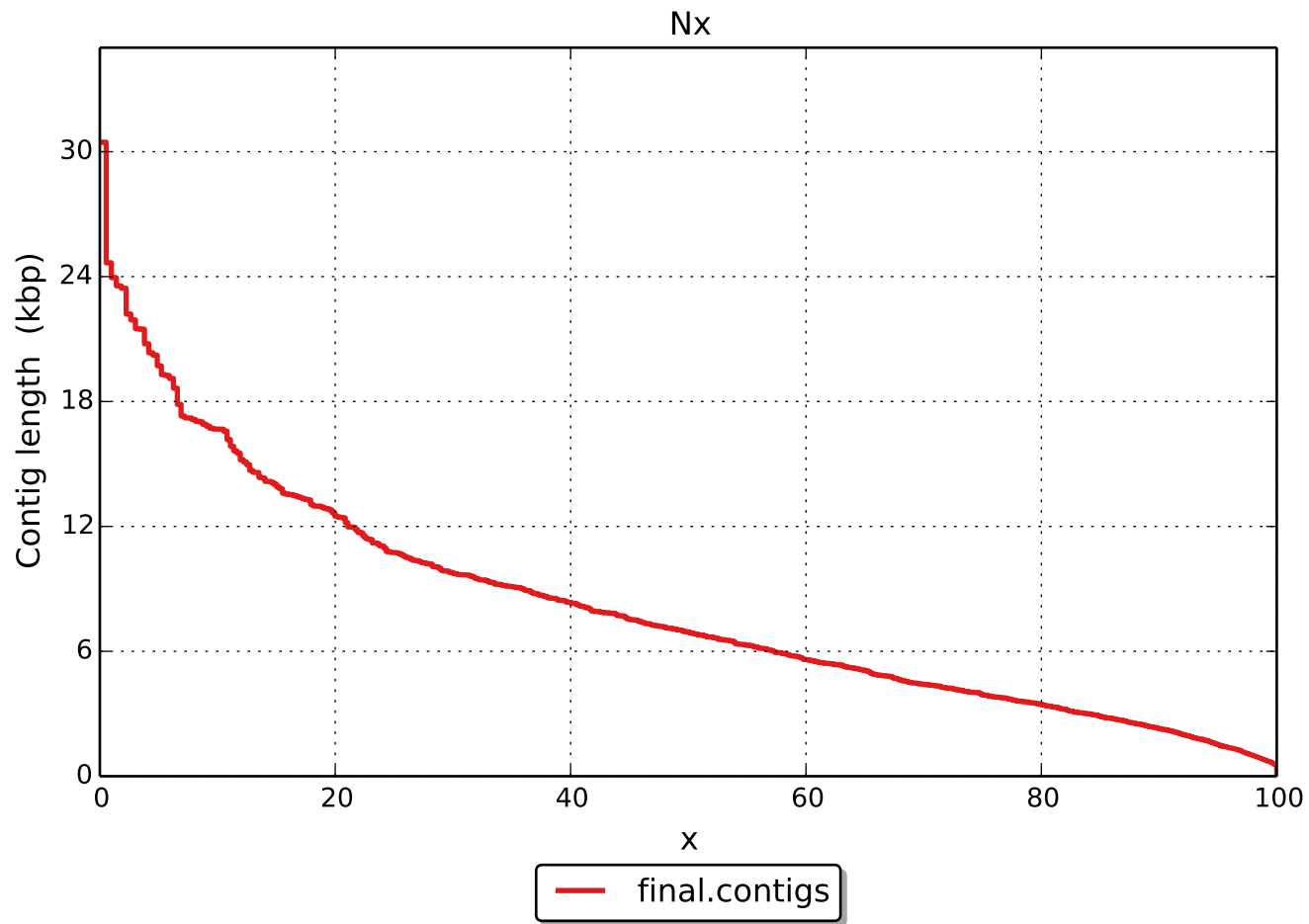
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	1
# both parts are significant	2
Partially unaligned length	6052
# N's	0

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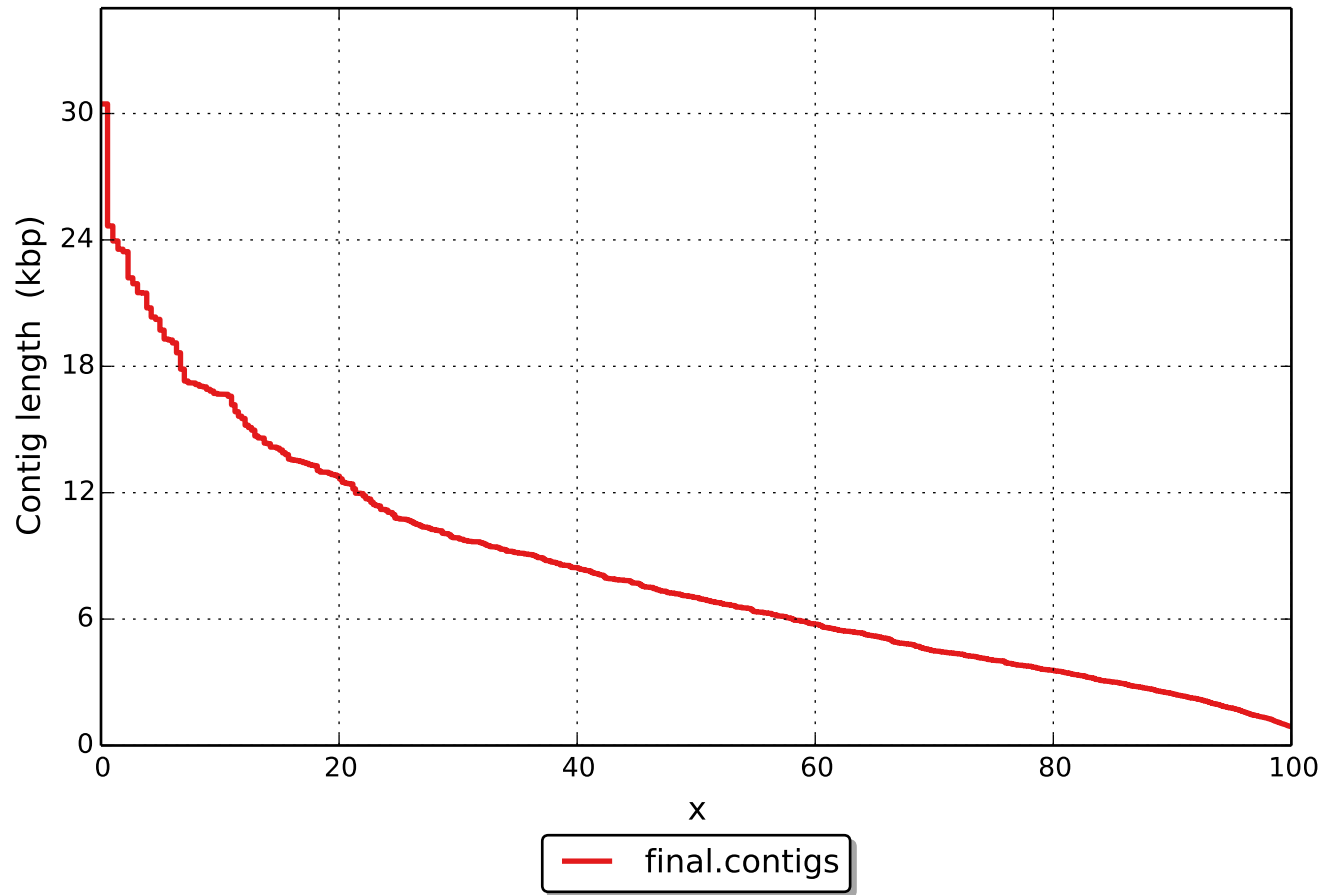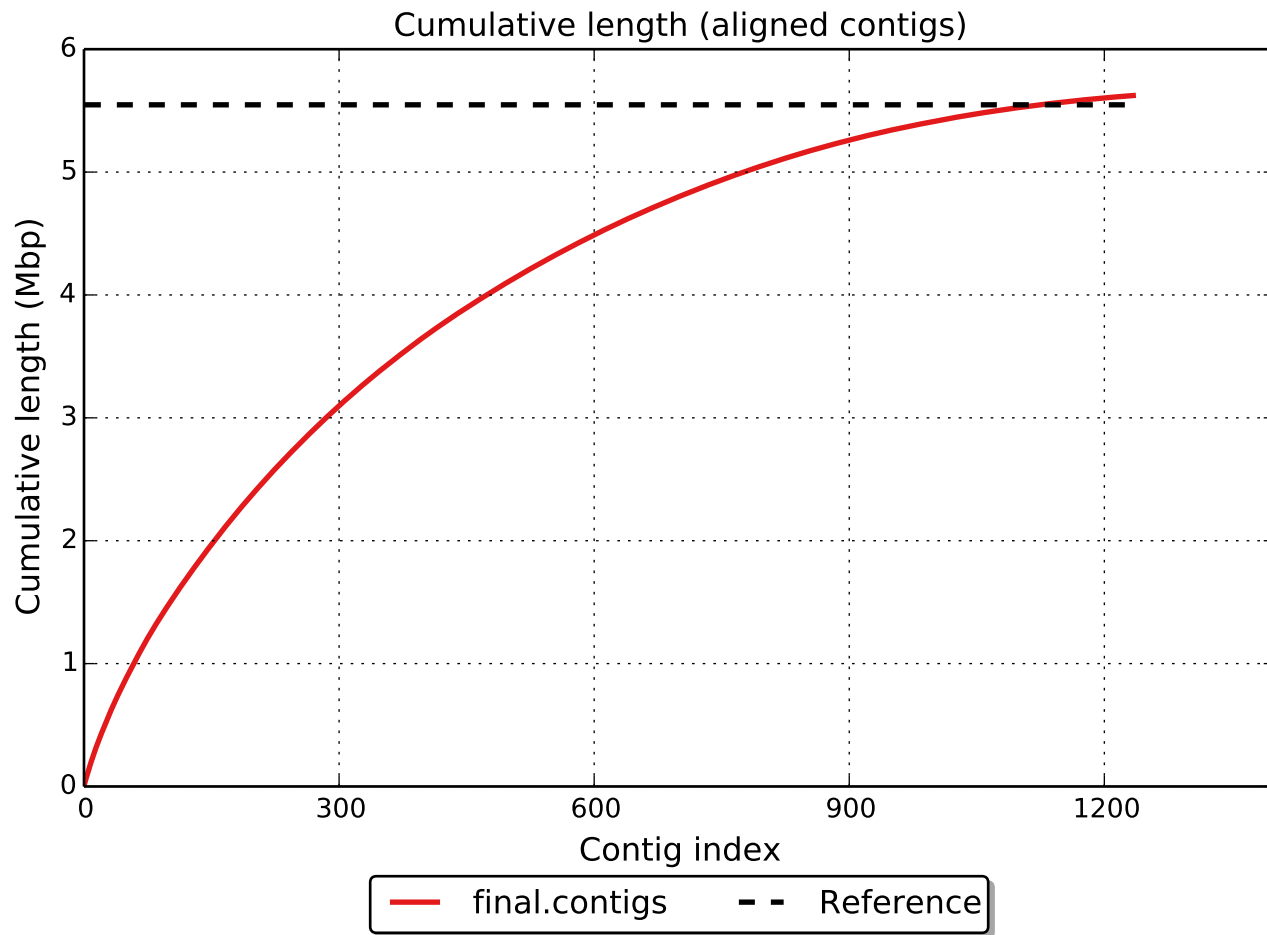(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length
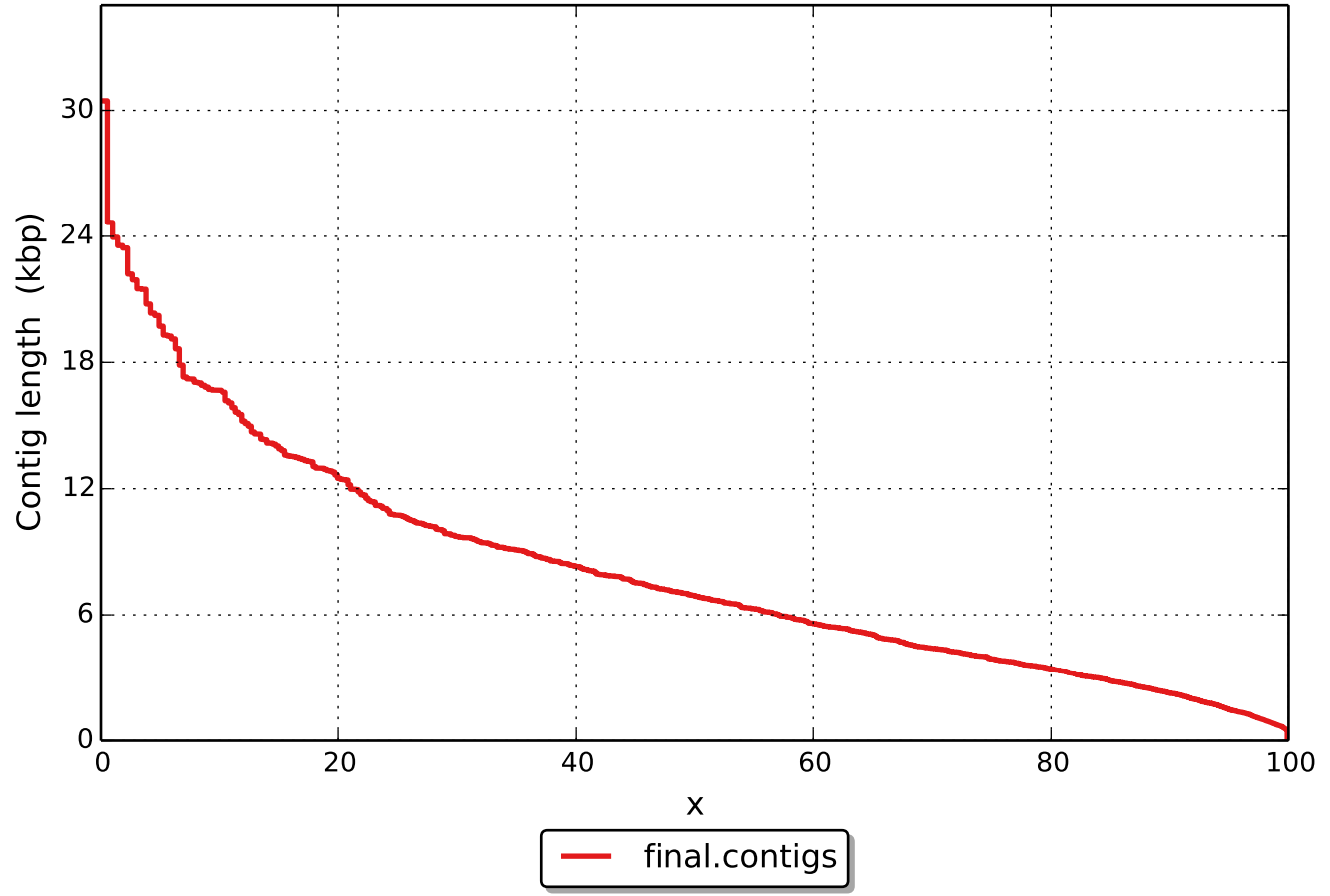
GC content

windows

GC (%)

final.contigs — — Reference

NGx

Misassemblies

final.contigs

relocations

Cumulative length (aligned contigs)