Report

	final.contigs
# contigs (>= 1000 bp)	1584
# contigs (>= 5000 bp)	200
# contigs (>= 10000 bp)	15
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4584630
Total length (>= 5000 bp)	1387218
Total length (>= 10000 bp)	192434
Total length (>= 25000 bp)	31374
Total length (>= 50000 bp)	0
# contigs	2074
Largest contig	31374
Total length	4944876
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.23
N50	3259
NG50	3311
N75	1931
NG75	1993
L50	477
LG50	463
L75	968
LG75	935
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	56
Genome fraction (%)	98.269
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	40.56
# indels per 100 kbp	0.04
Largest alignment	31374
NA50	3259
NGA50	3311
NA75	1931
NGA75	1993
LA50	477
LGA50	463
LA75	968
LGA75	935

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).
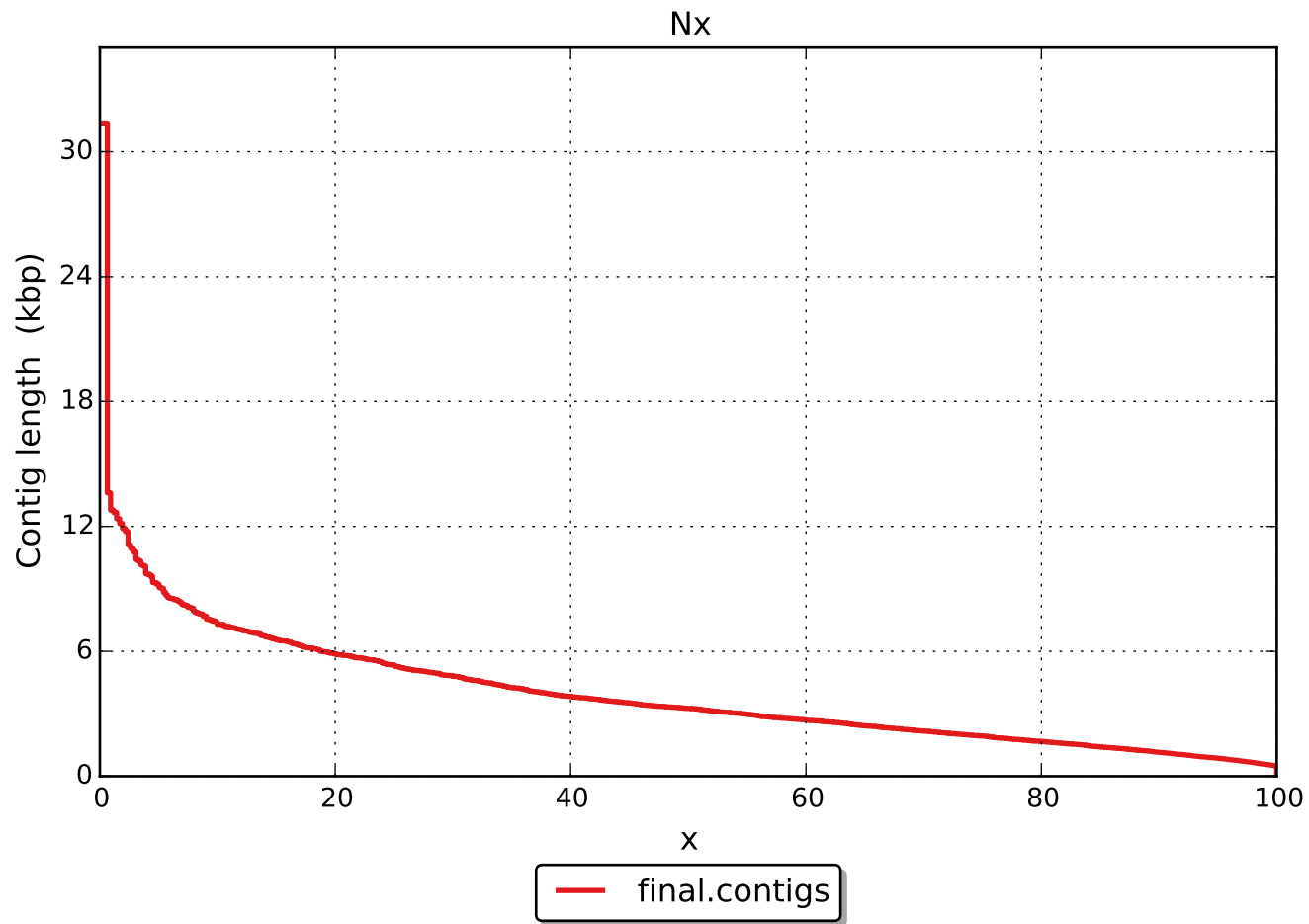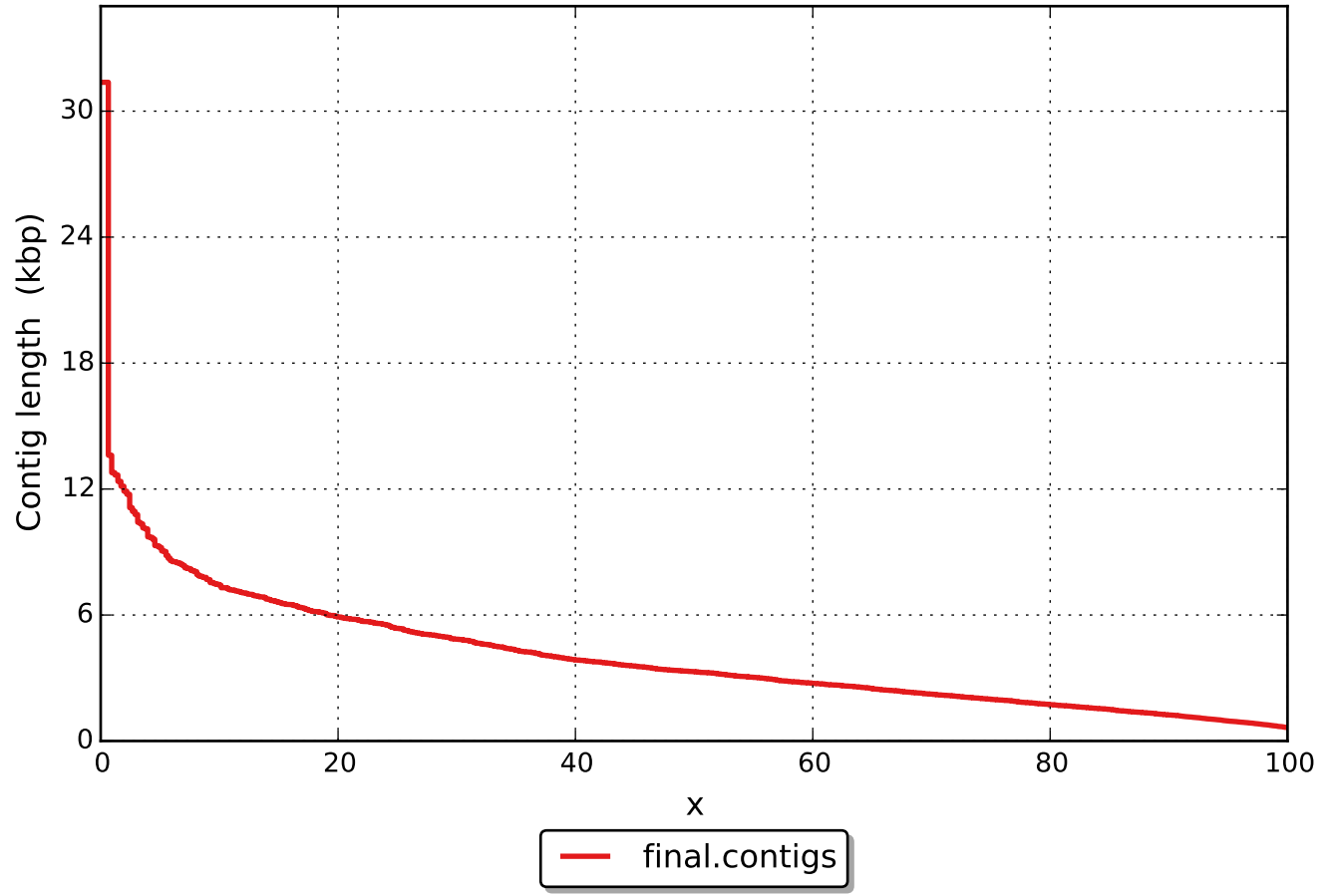
Misassemblies report

	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	1936
# indels	2
# short indels	2
# long indels	0
Indels length	2

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

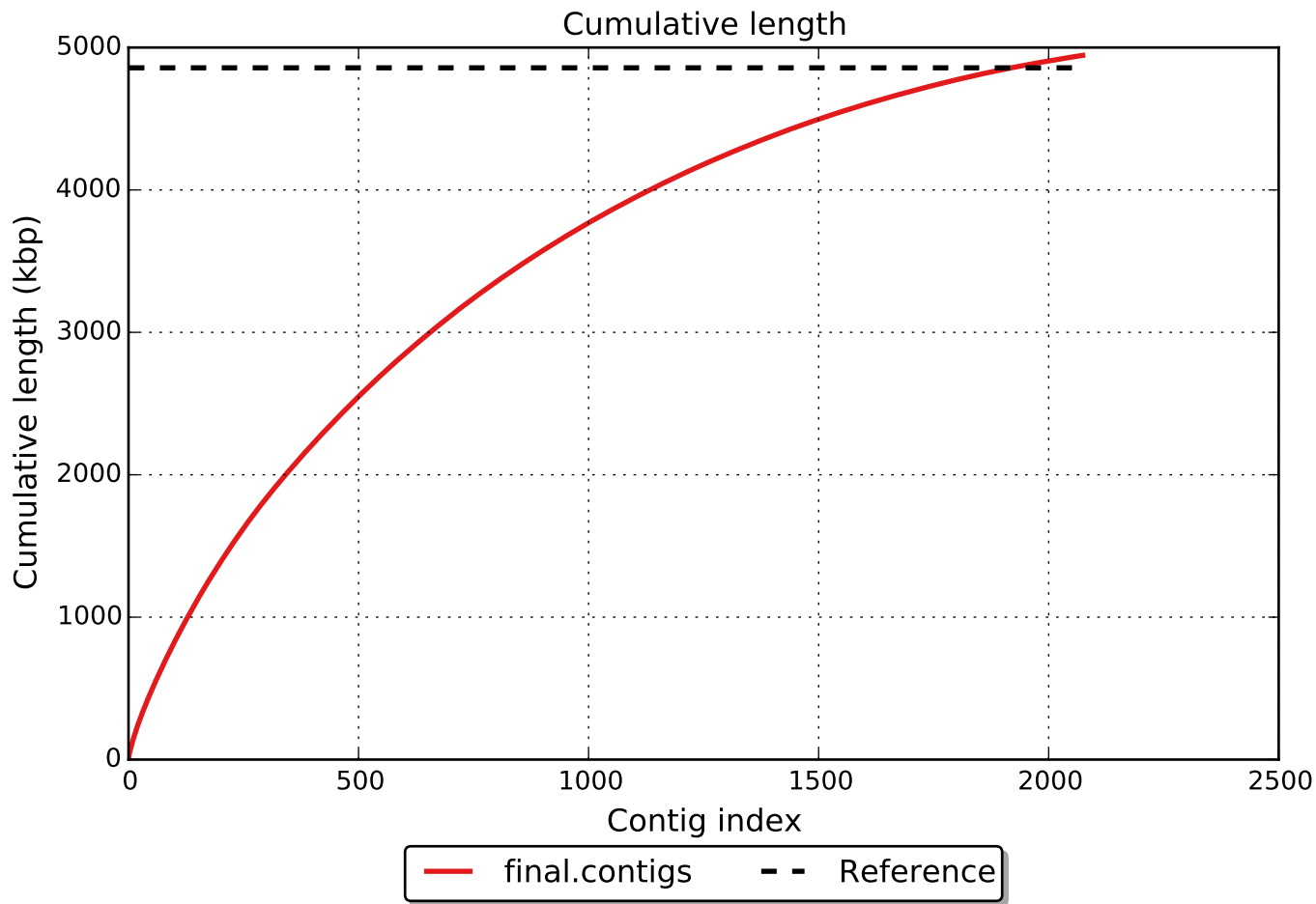|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	56
# N's	0

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
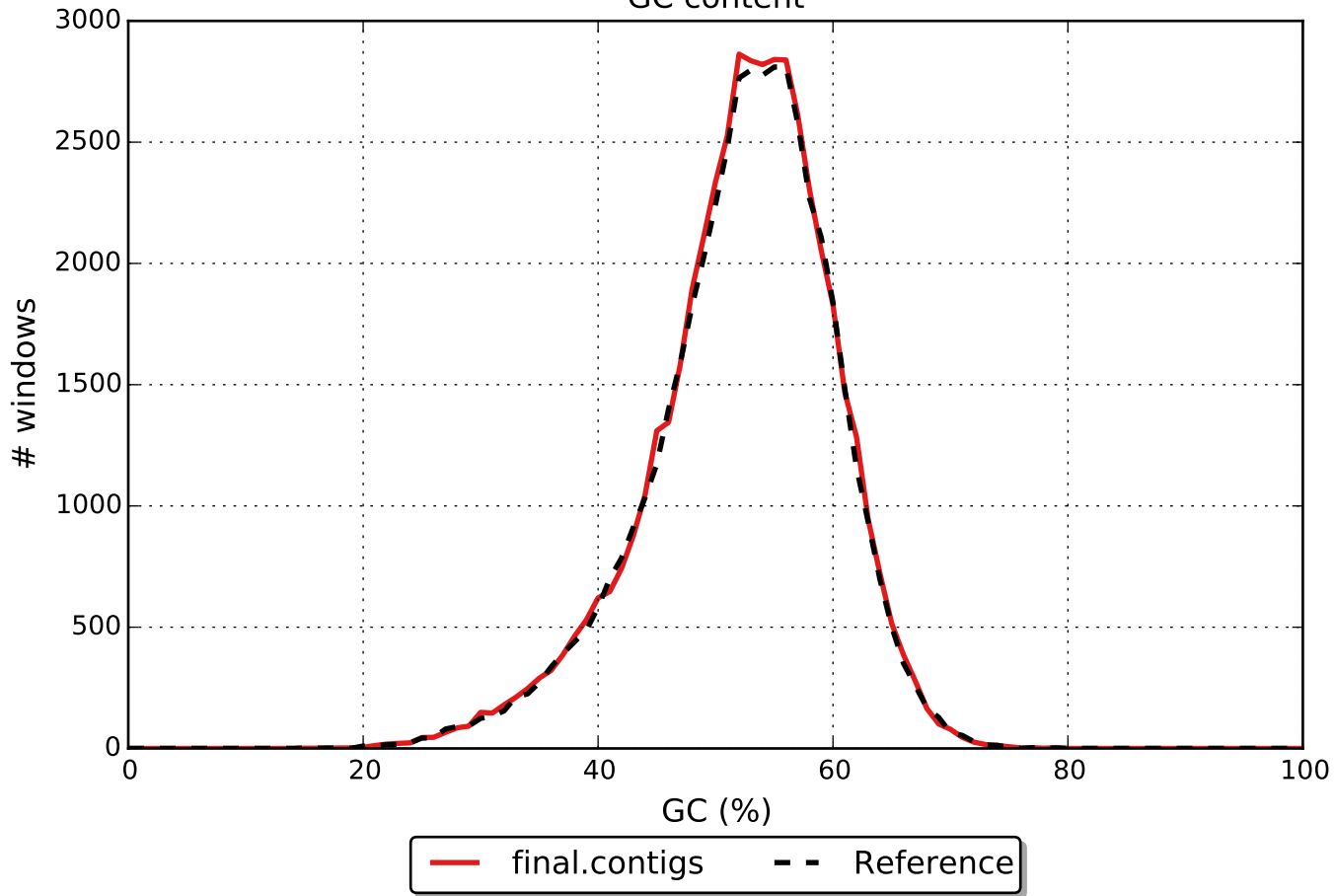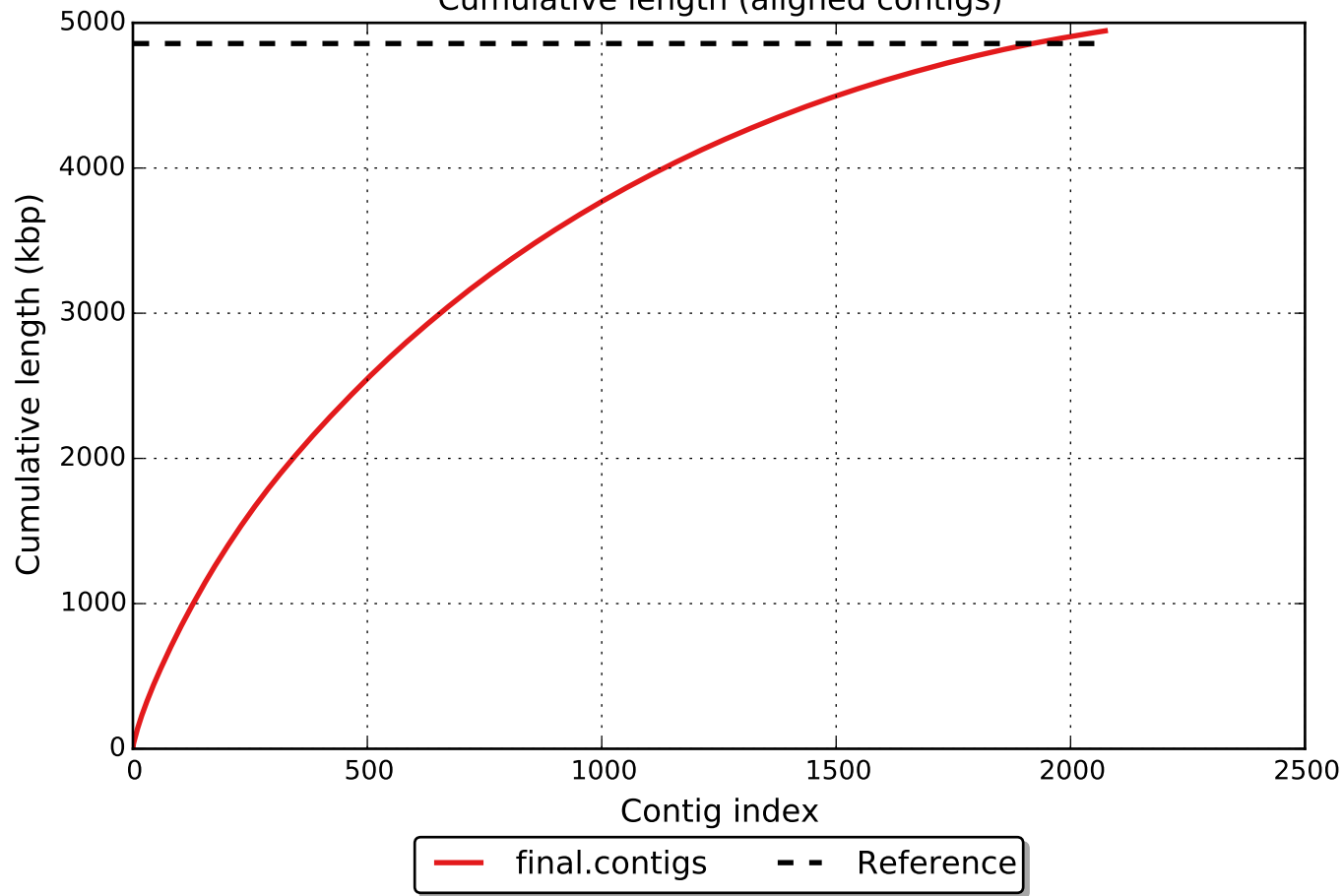
GC content

windows

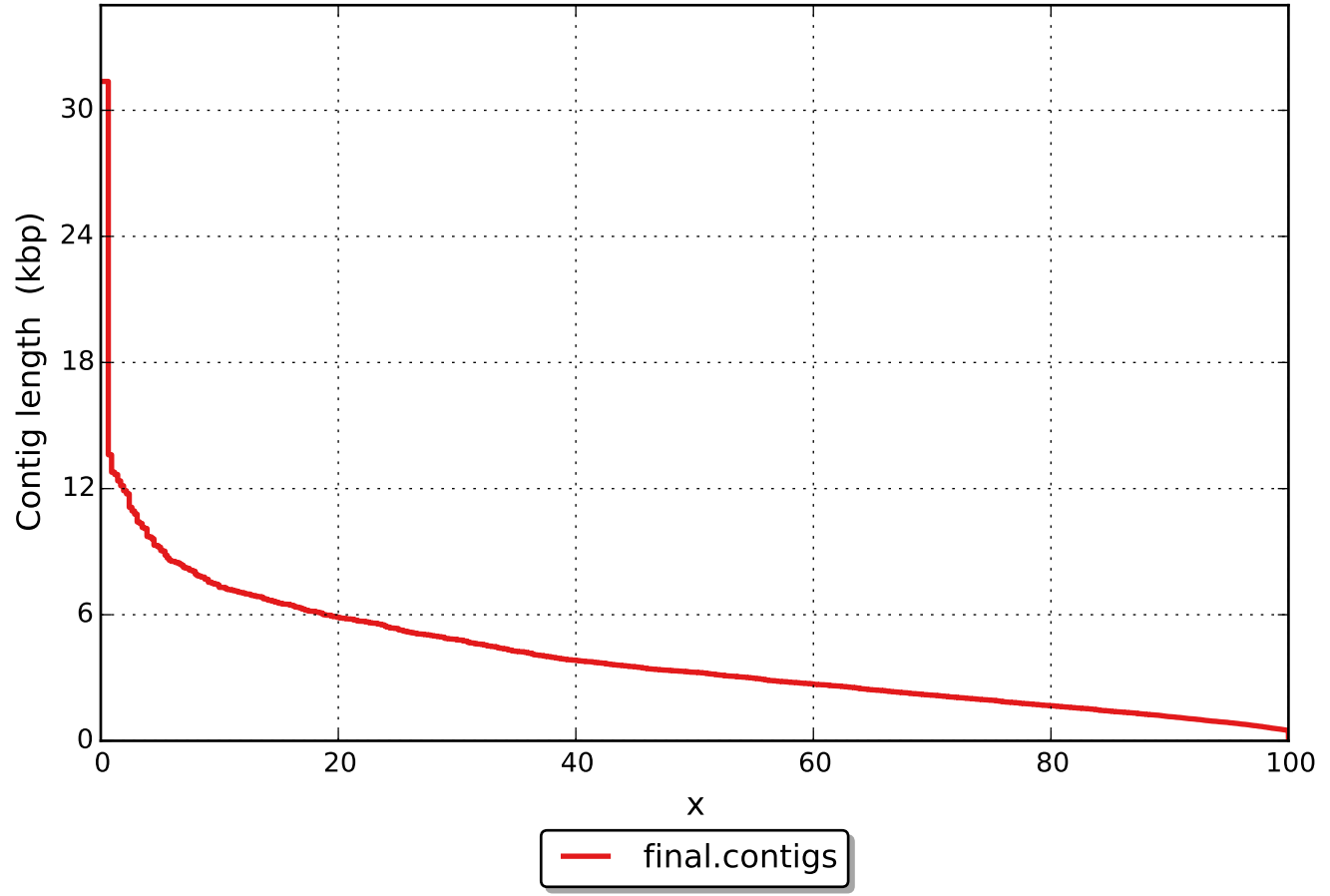GC (%)

final.contigs — — — Reference

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NGAx