Report

	final.contigs
# contigs (>= 1000 bp)	883
# contigs (>= 5000 bp)	376
# contigs (>= 10000 bp)	117
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4843091
Total length (>= 5000 bp)	3478882
Total length (>= 10000 bp)	1678363
Total length (>= 25000 bp)	82693
Total length (>= 50000 bp)	0
# contigs	982
Largest contig	31188
Total length	4916559
Reference length	4857432
GC (%)	52.24
Reference GC (%)	52.23
N50	7489
NG50	7541
N75	4434
NG75	4565
L50	209
LG50	205
L75	421
LG75	411
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.709
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	31188
NA50	7489
NGA50	7541
NA75	4434
NGA75	4565
LA50	209
LGA50	205
LA75	421
LGA75	411

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).
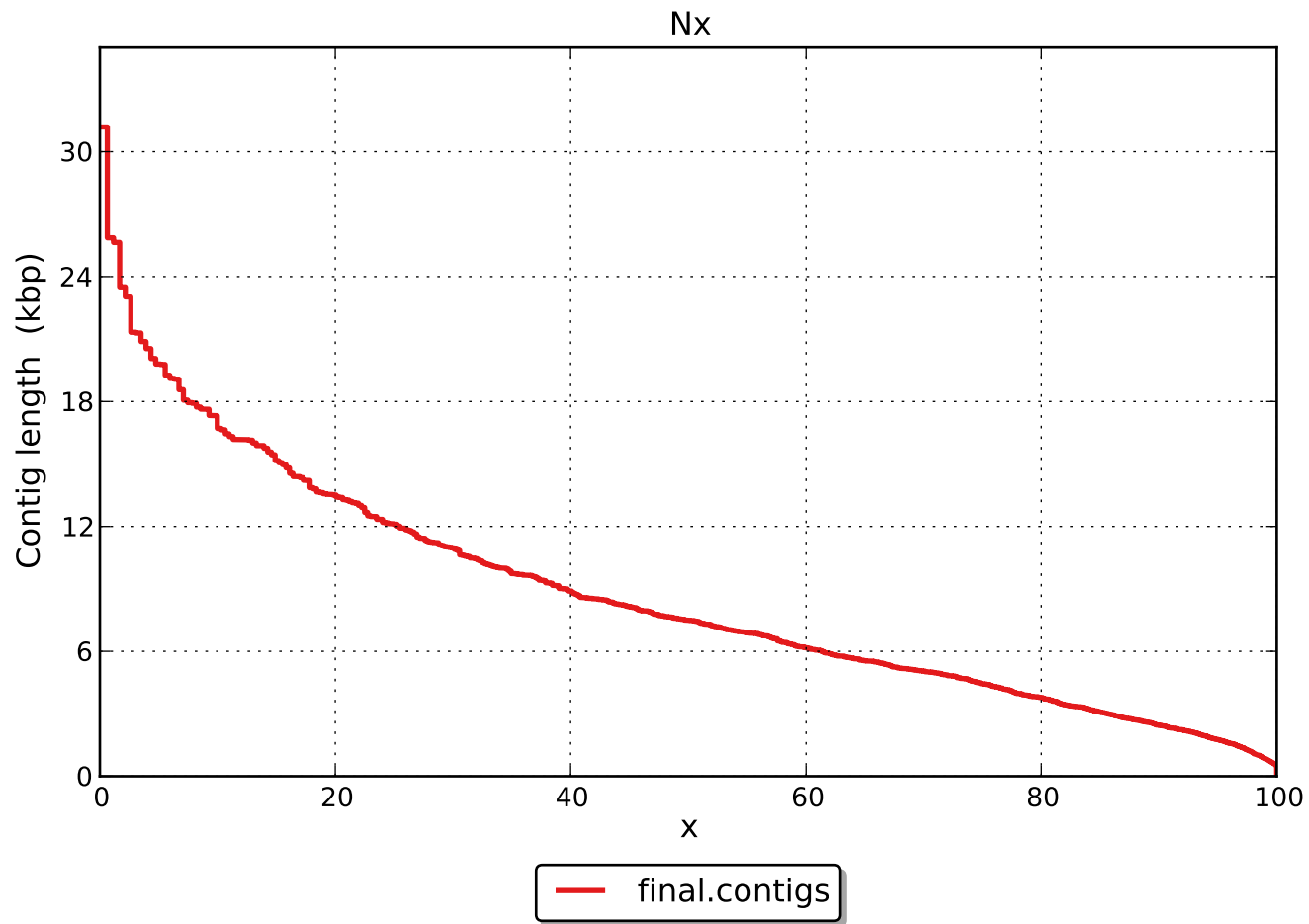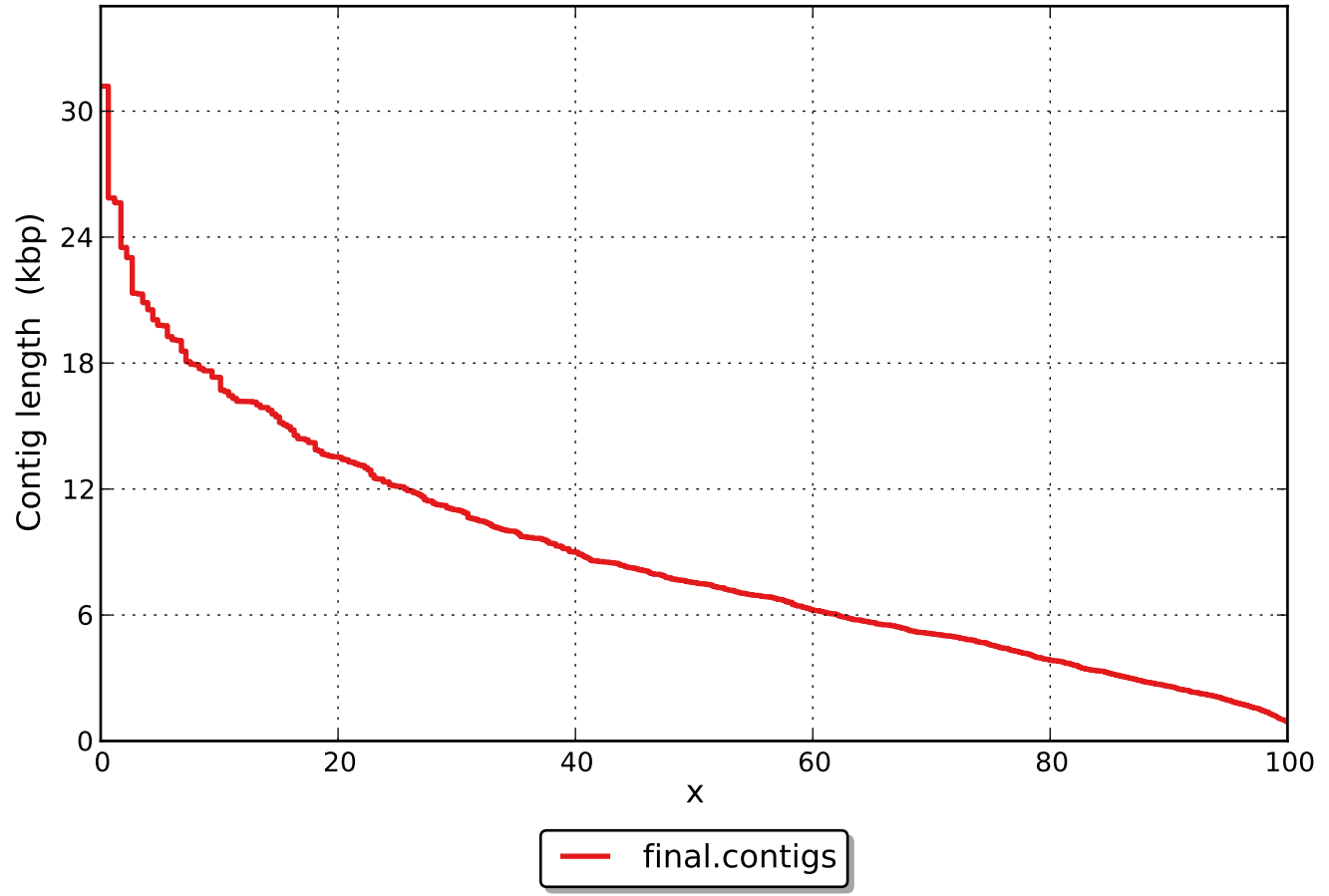
Misassemblies report

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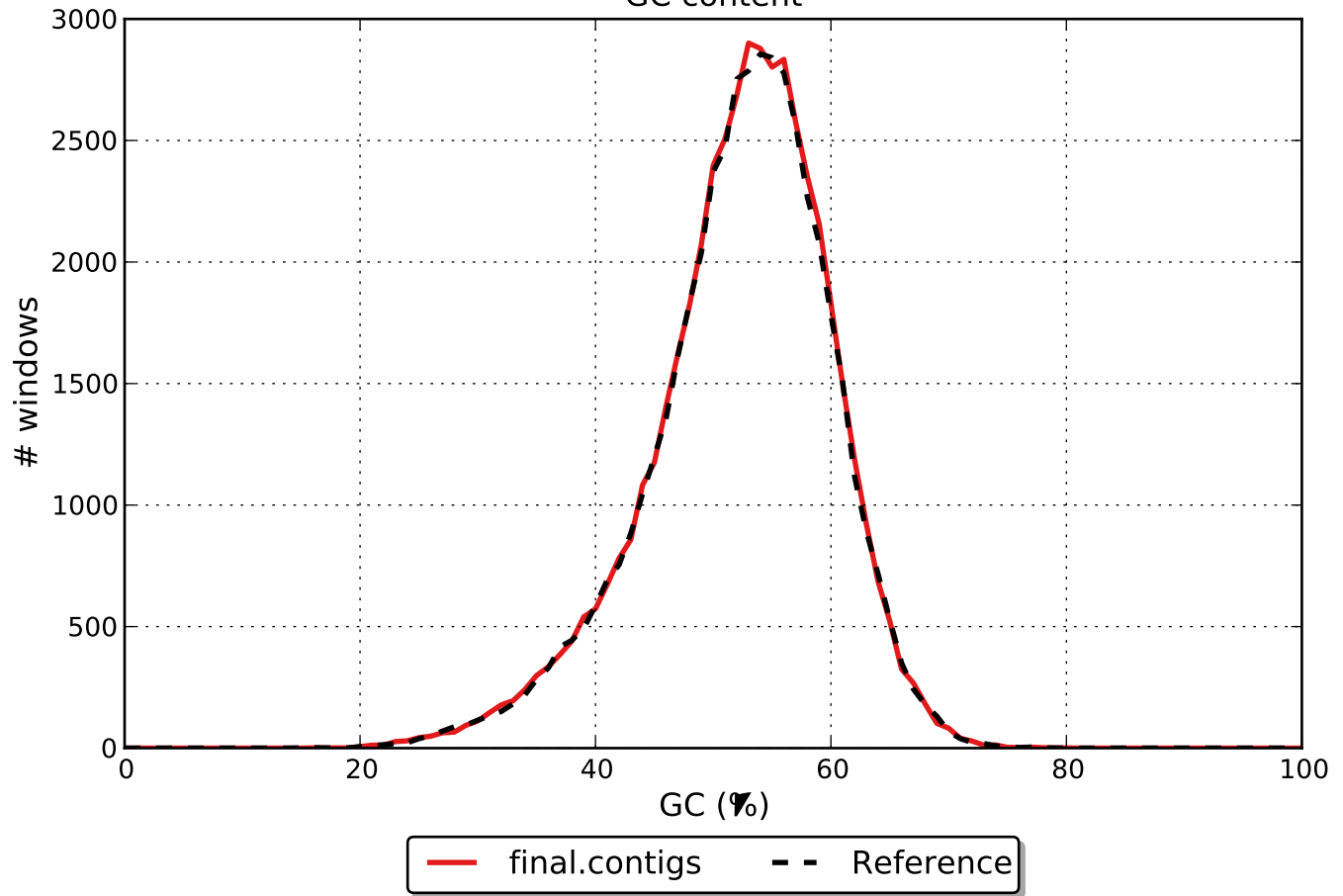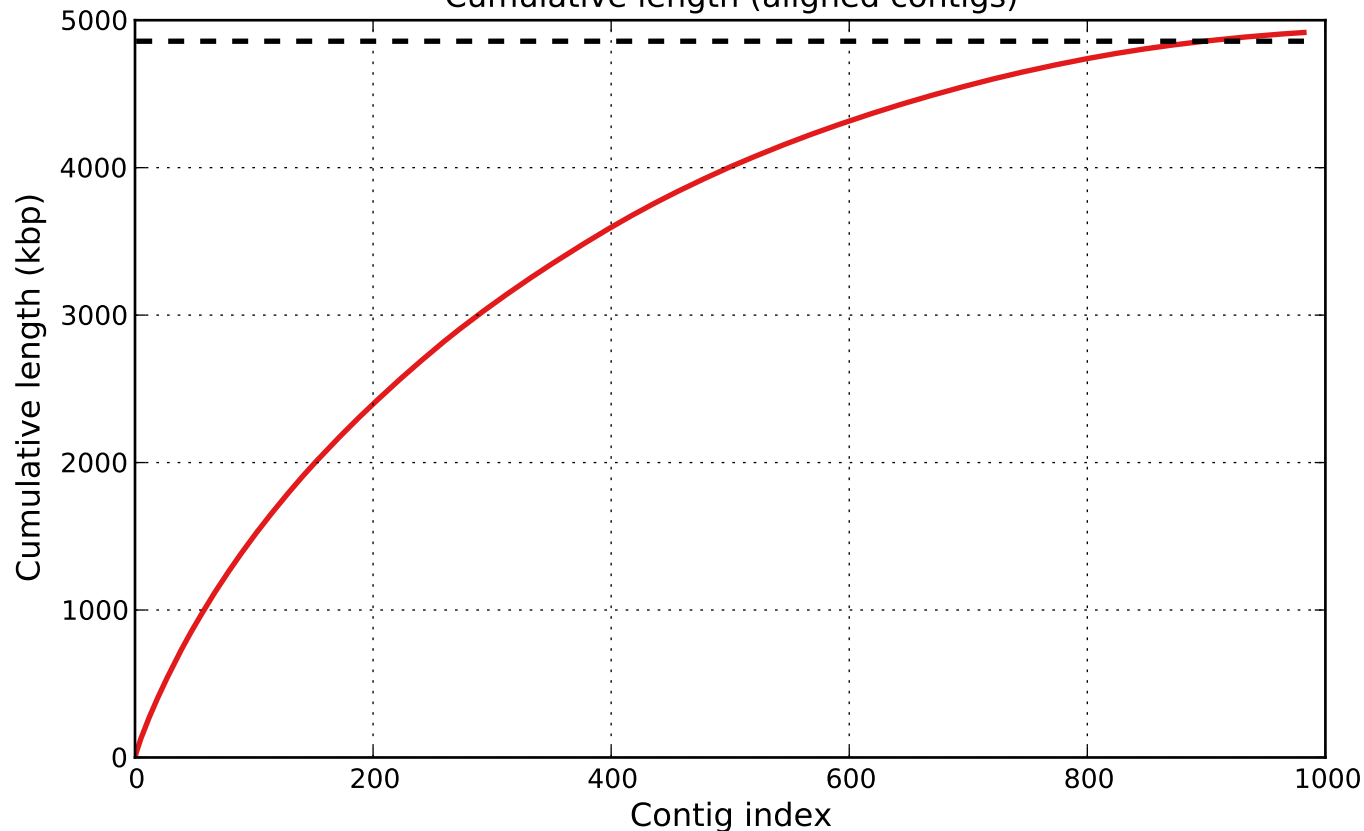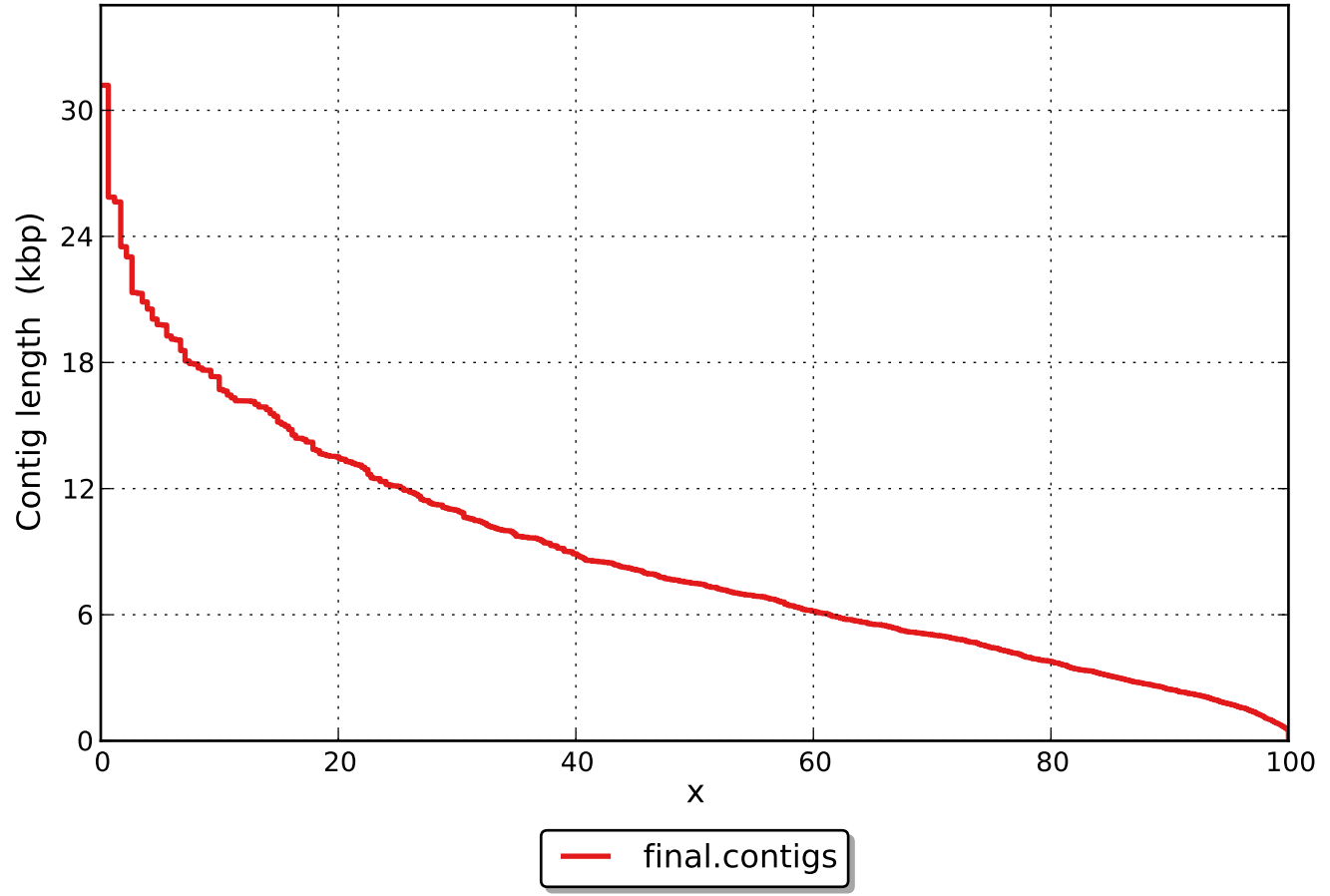(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

windows

GC (%)

final.contigs
Reference
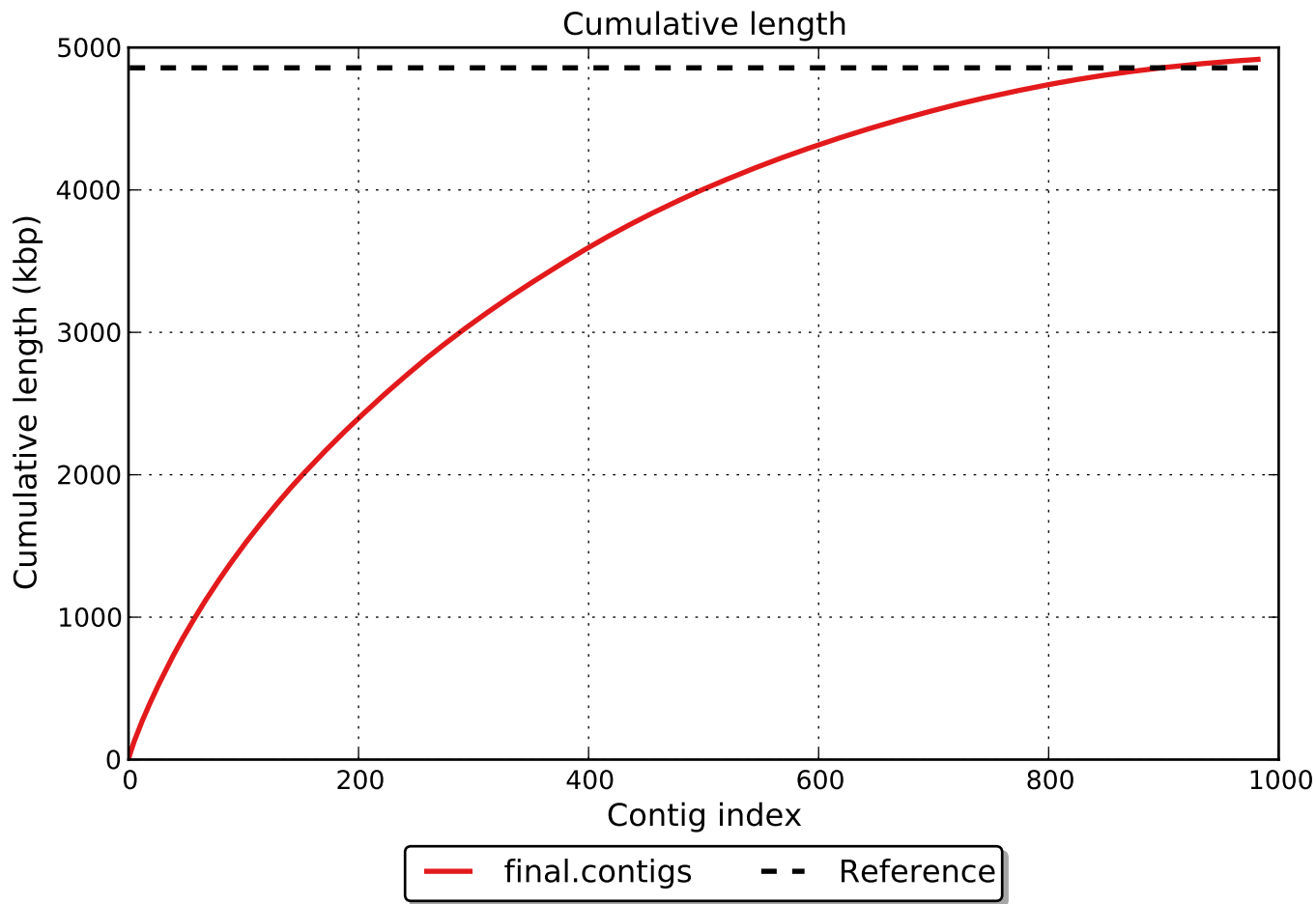
Misassemblies

final.contigs

Cumulative length (aligned contigs)