Report

	final.contigs
# contigs (>= 1000 bp)	426
# contigs (>= 5000 bp)	280
# contigs (>= 10000 bp)	172
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	4
Total length (>= 1000 bp)	4796207
Total length (>= 5000 bp)	4398010
Total length (>= 10000 bp)	3594110
Total length (>= 25000 bp)	1602824
Total length (>= 50000 bp)	226490
# contigs	467
Largest contig	60780
Total length	4825499
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	18080
NG50	17795
N75	9824
NG75	9757
L50	82
LG50	83
L75	175
LG75	177
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.639
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.06
# indels per 100 kbp	0.00
Largest alignment	60780
NA50	18080
NGA50	17795
NA75	9824
NGA75	9757
LA50	82
LGA50	83
LA75	175
LGA75	177

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).
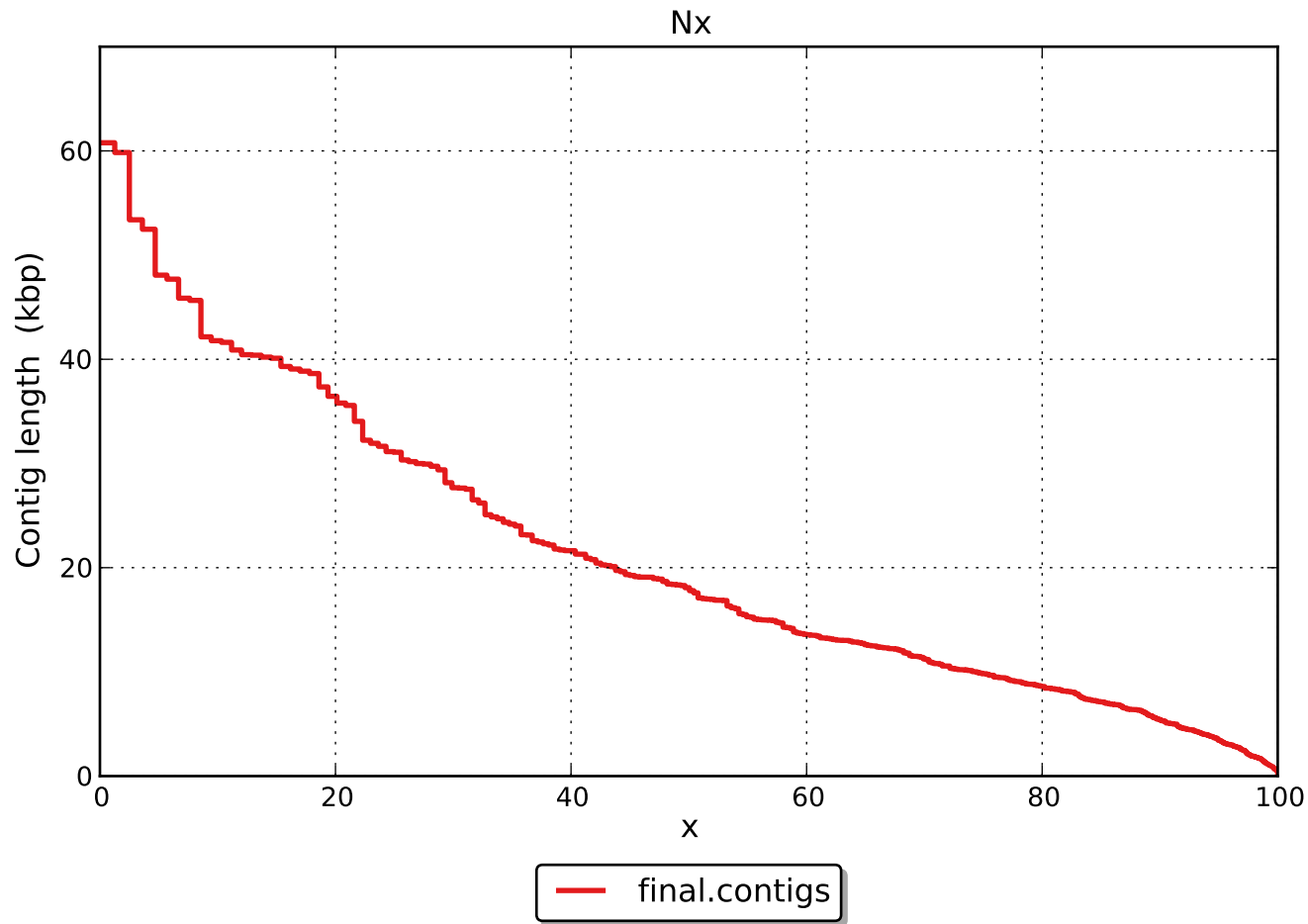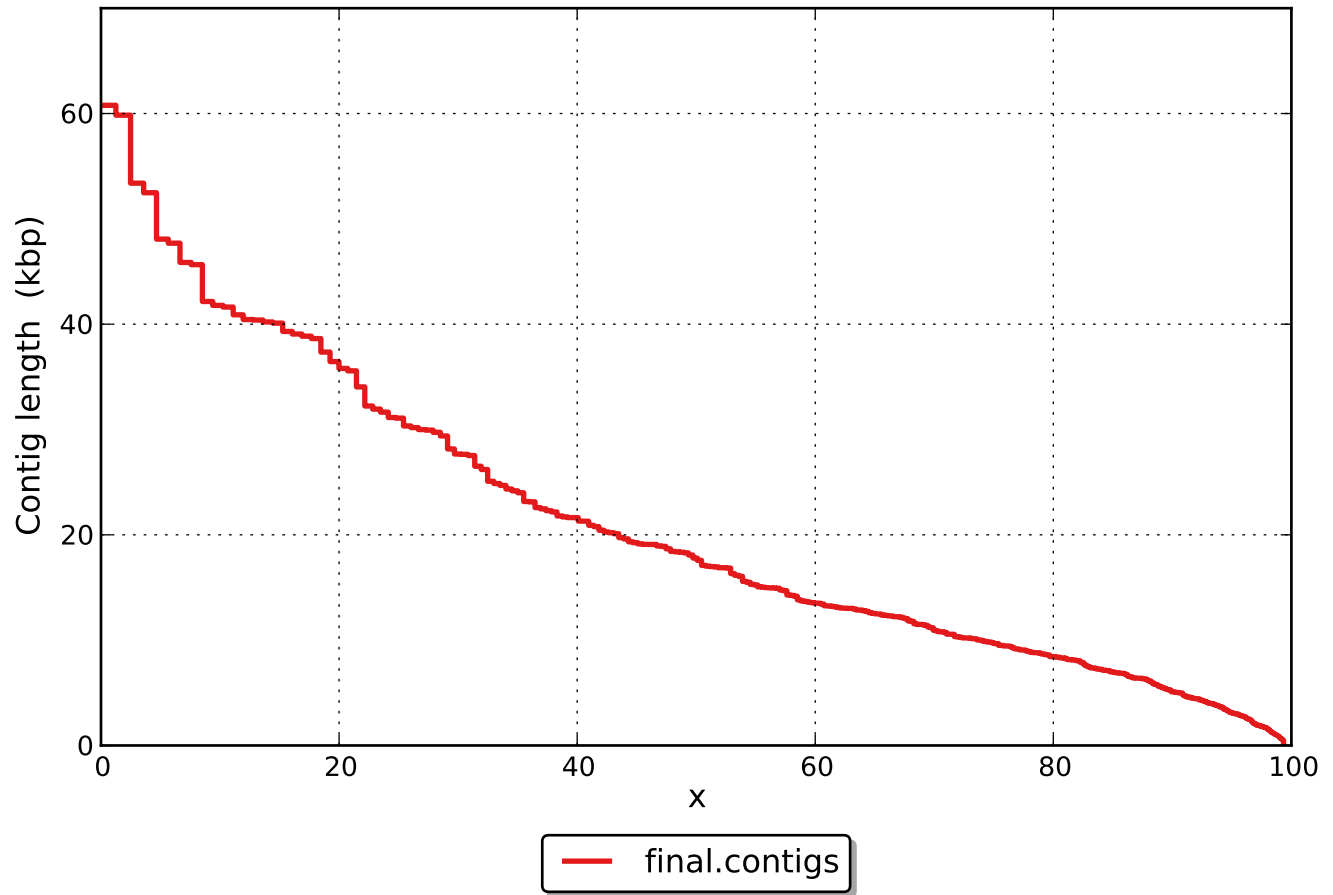
Misassemblies report

	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	51
# 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).
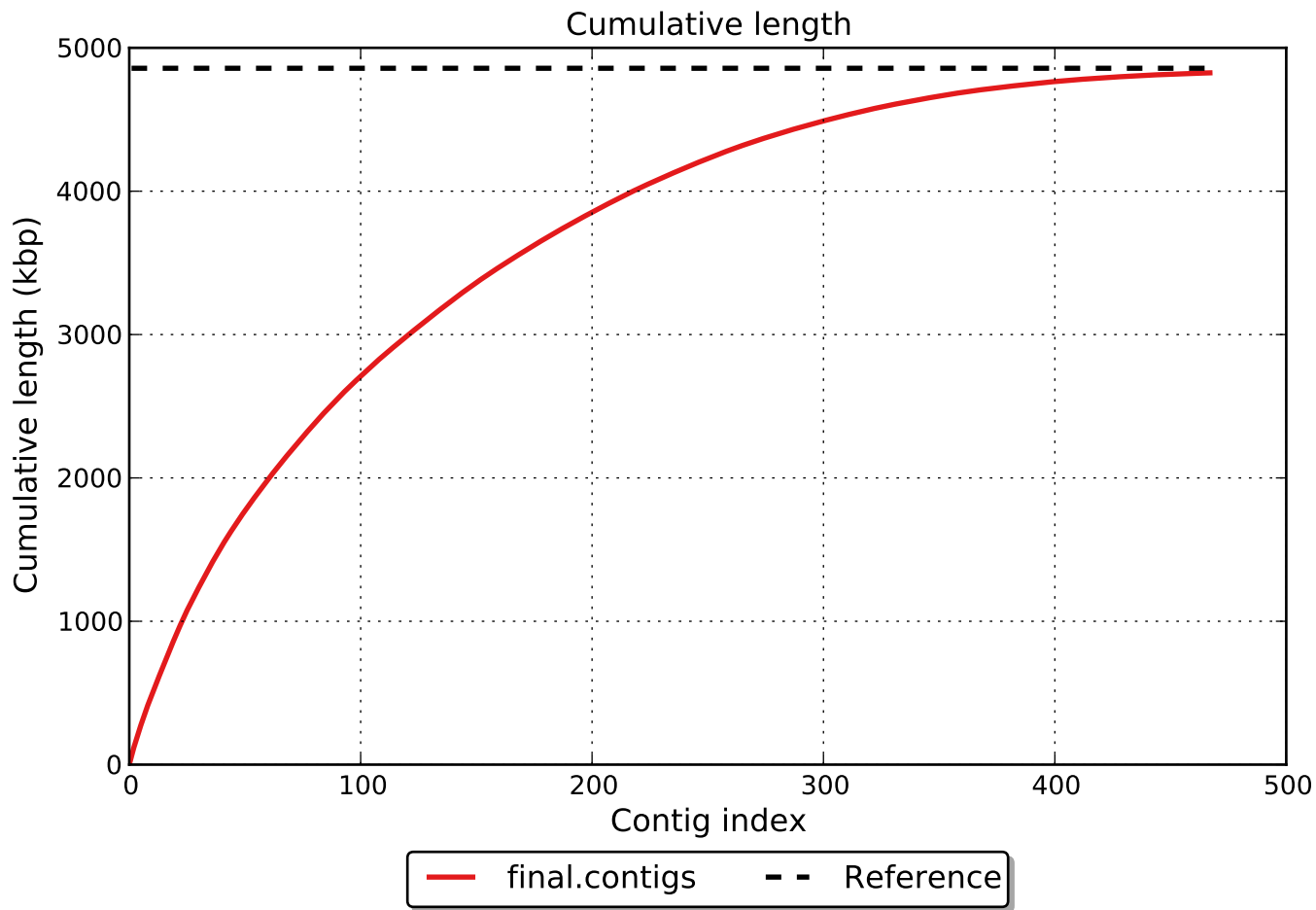
Unaligned report

	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).
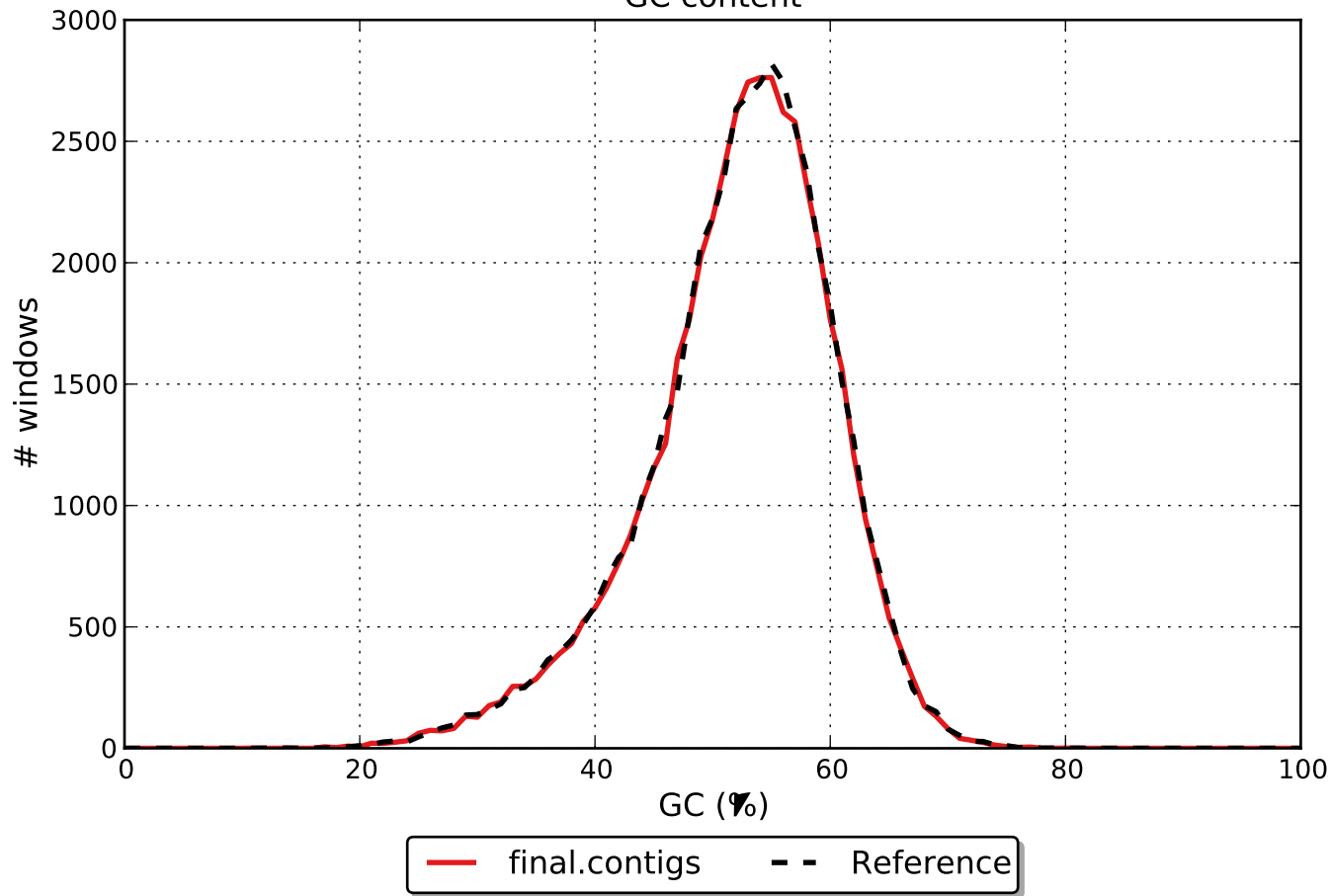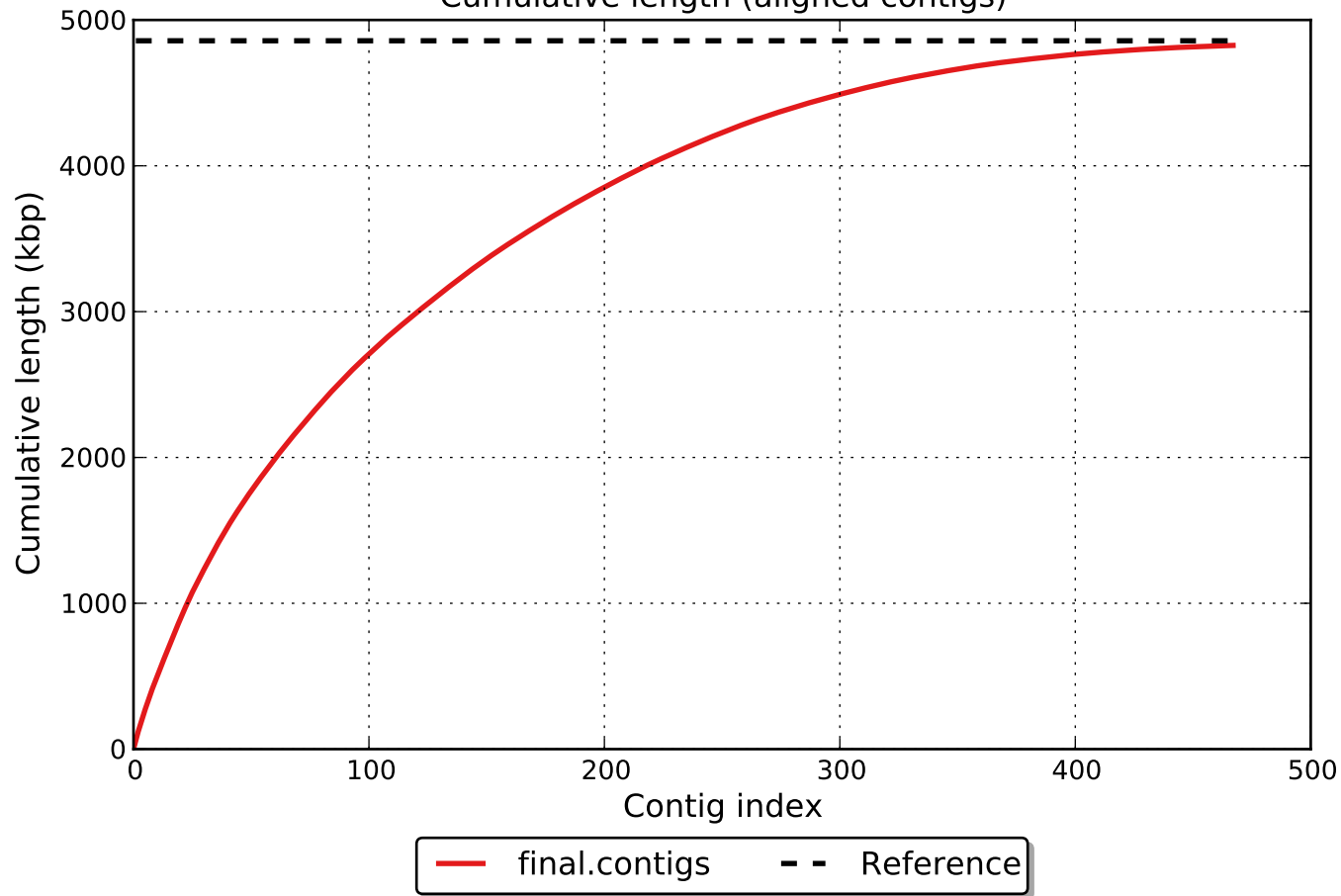
NGx

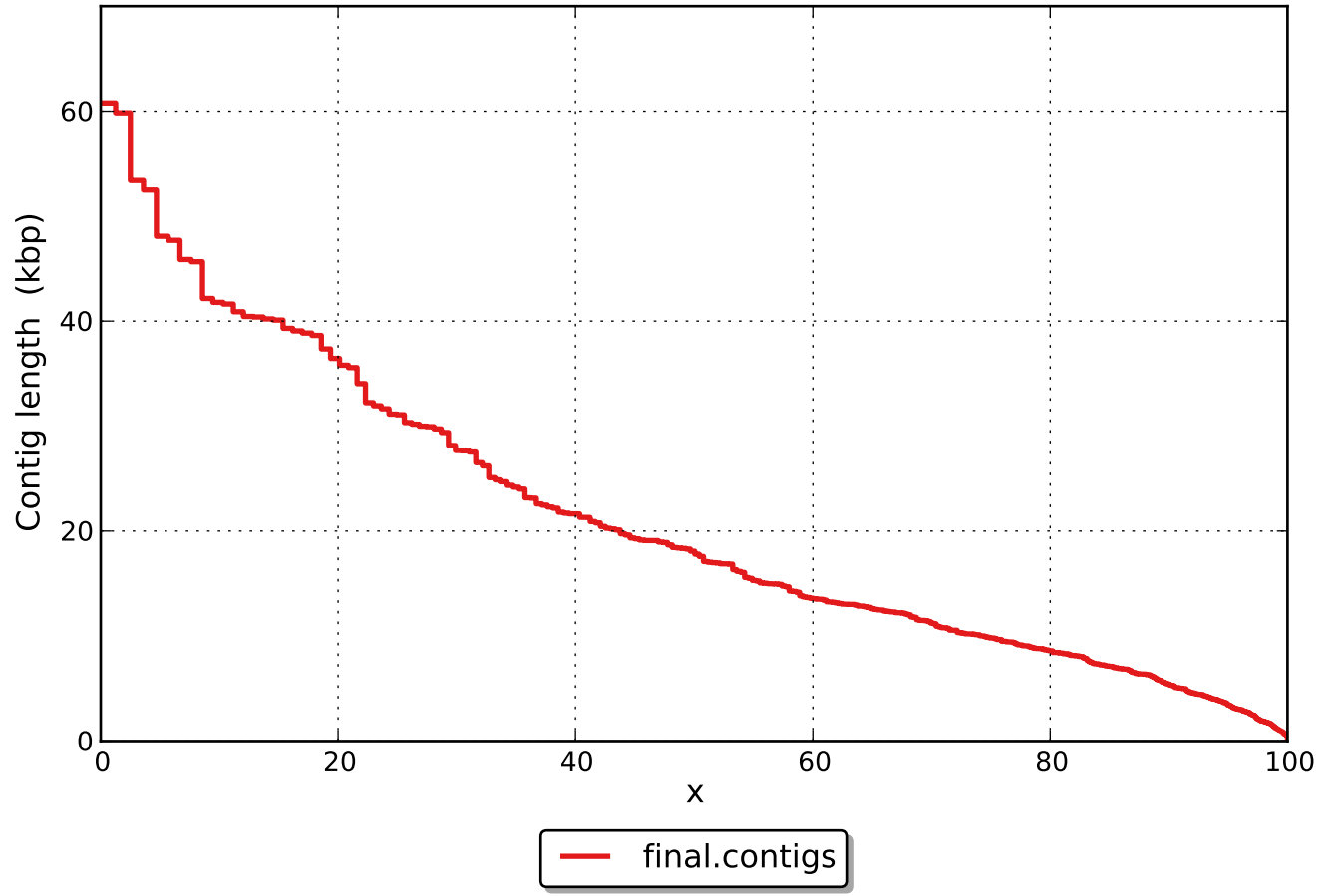Cumulative length

GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)