Report

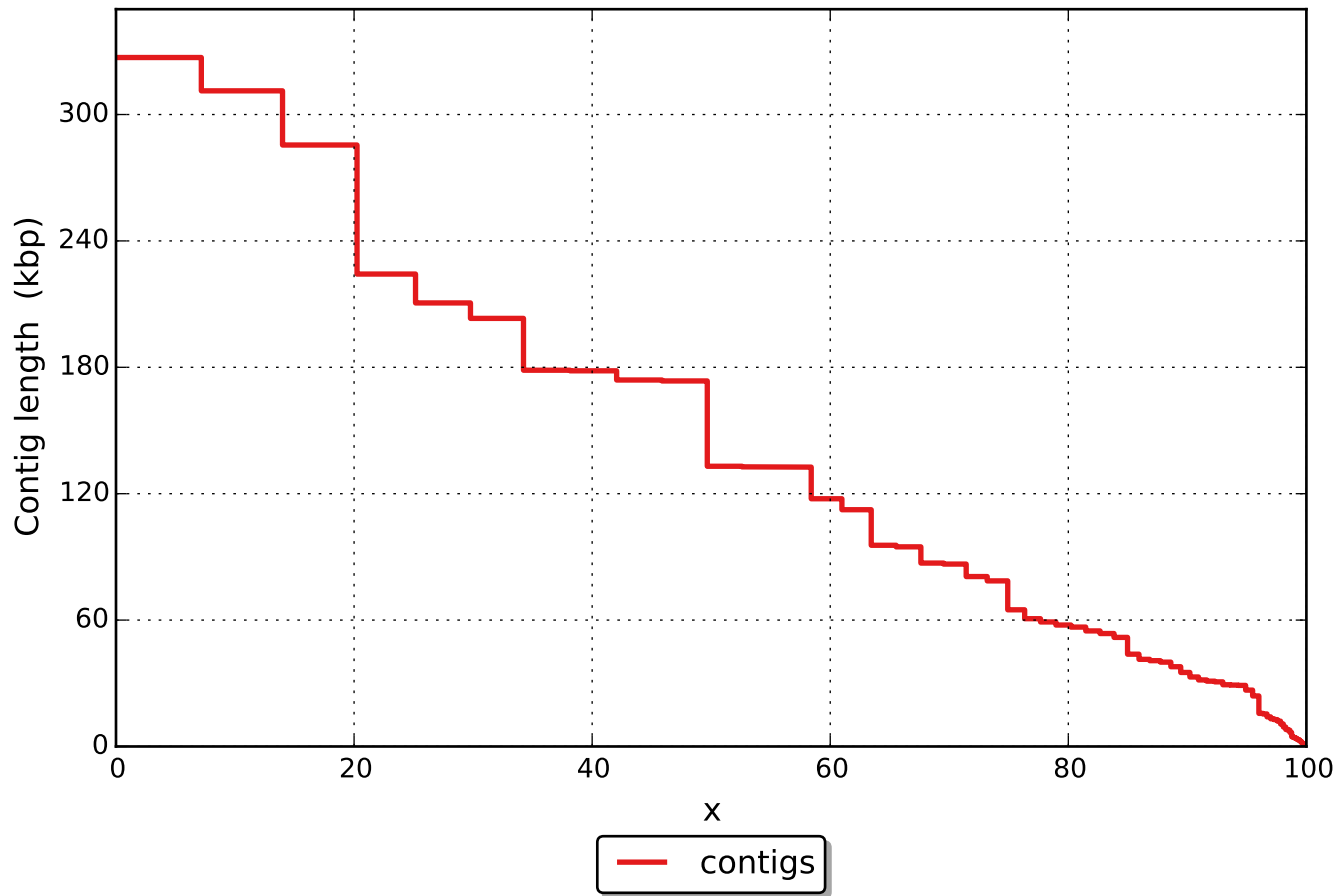|	contigs
# contigs (>= 0 bp)	159
# contigs (>= 1000 bp)	78
# contigs (>= 5000 bp)	55
# contigs (>= 10000 bp)	51
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4572064
Total length (>= 1000 bp)	4560063
Total length (>= 5000 bp)	4505992
Total length (>= 10000 bp)	4474300
Total length (>= 25000 bp)	4356528
Total length (>= 50000 bp)	3877152
# contigs	82
Largest contig	327064
Total length	4562656
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133023
NG50	133023
N75	64884
NG75	64884
L50	11
LG50	11
L75	22
LG75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.159
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.38
# indels per 100 kbp	0.66
Largest alignment	327064
NA50	133023
NGA50	133023
NA75	64884
NGA75	64884
LA50	11
LGA50	11
LA75	22
LGA75	22

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

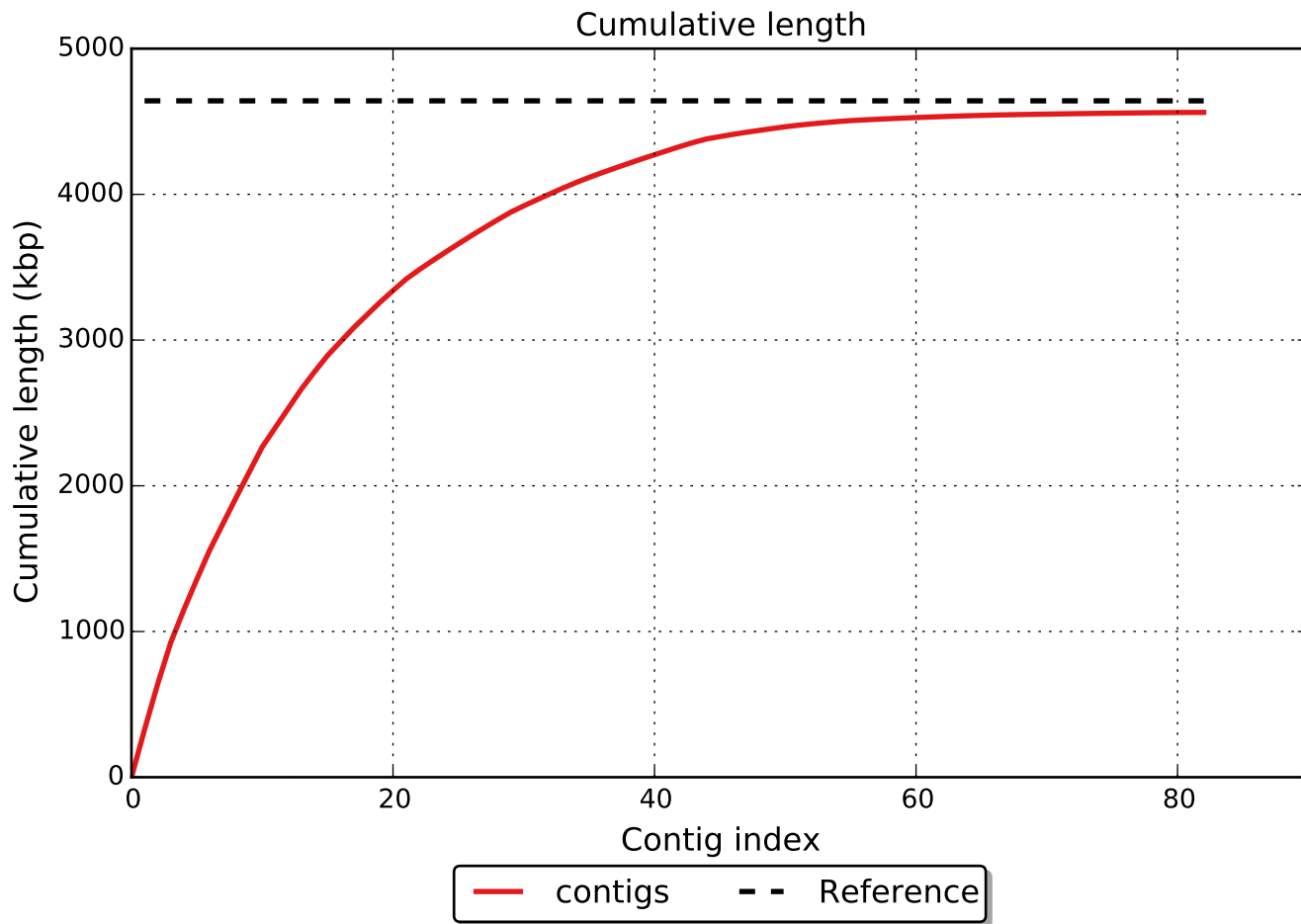|	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	382
# indels	30
# short indels	30
# long indels	0
Indels length	38

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

	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).
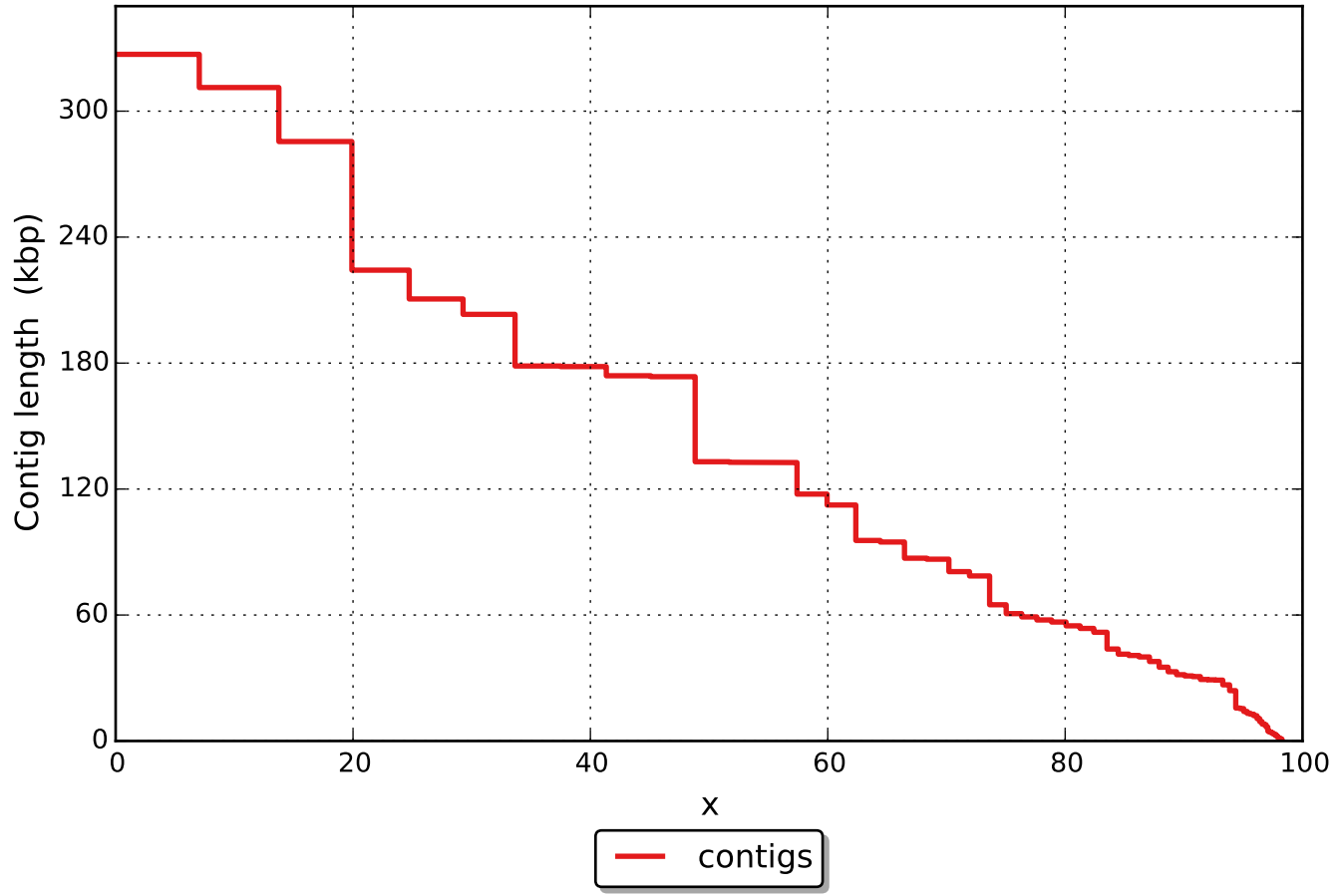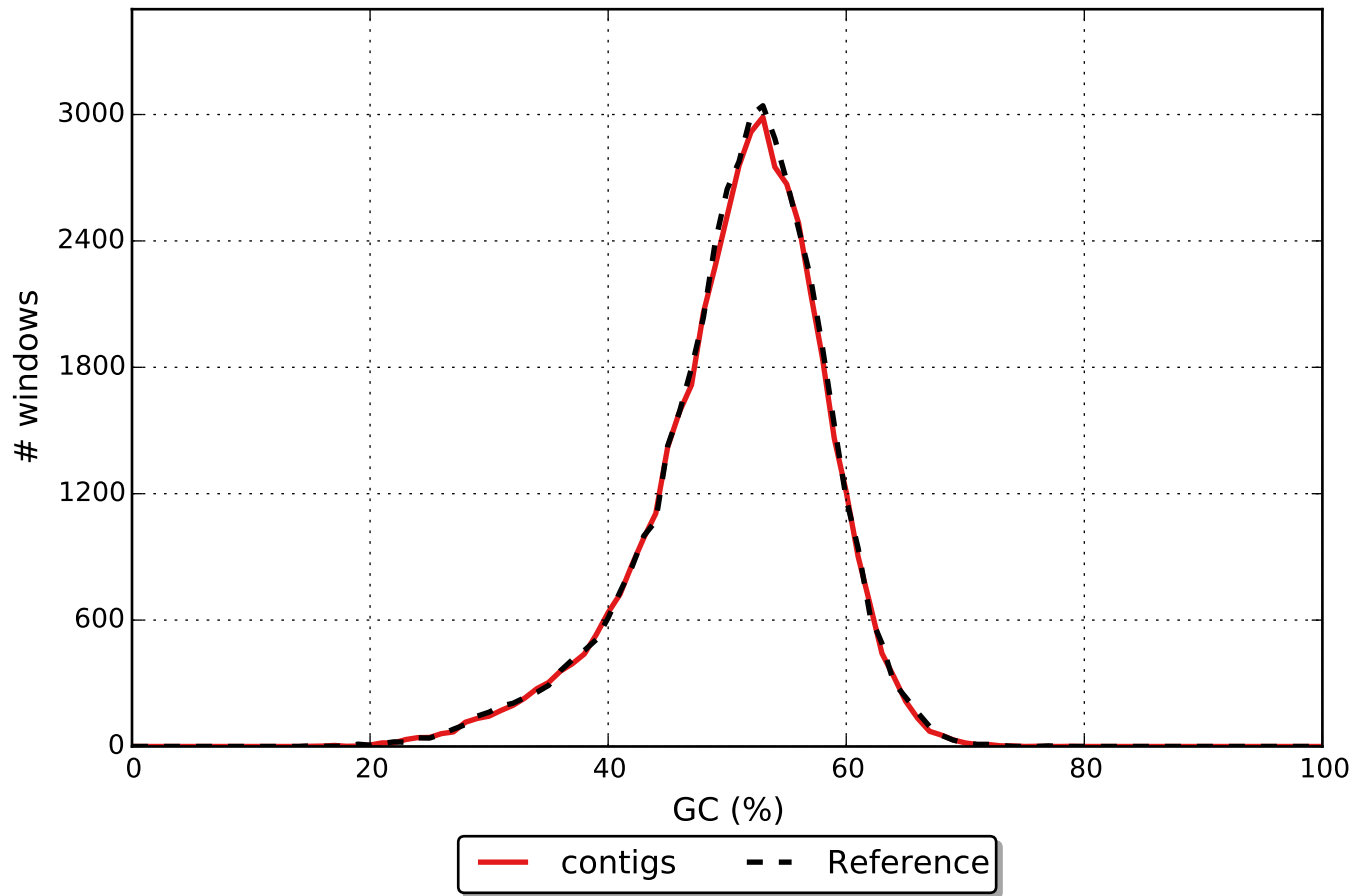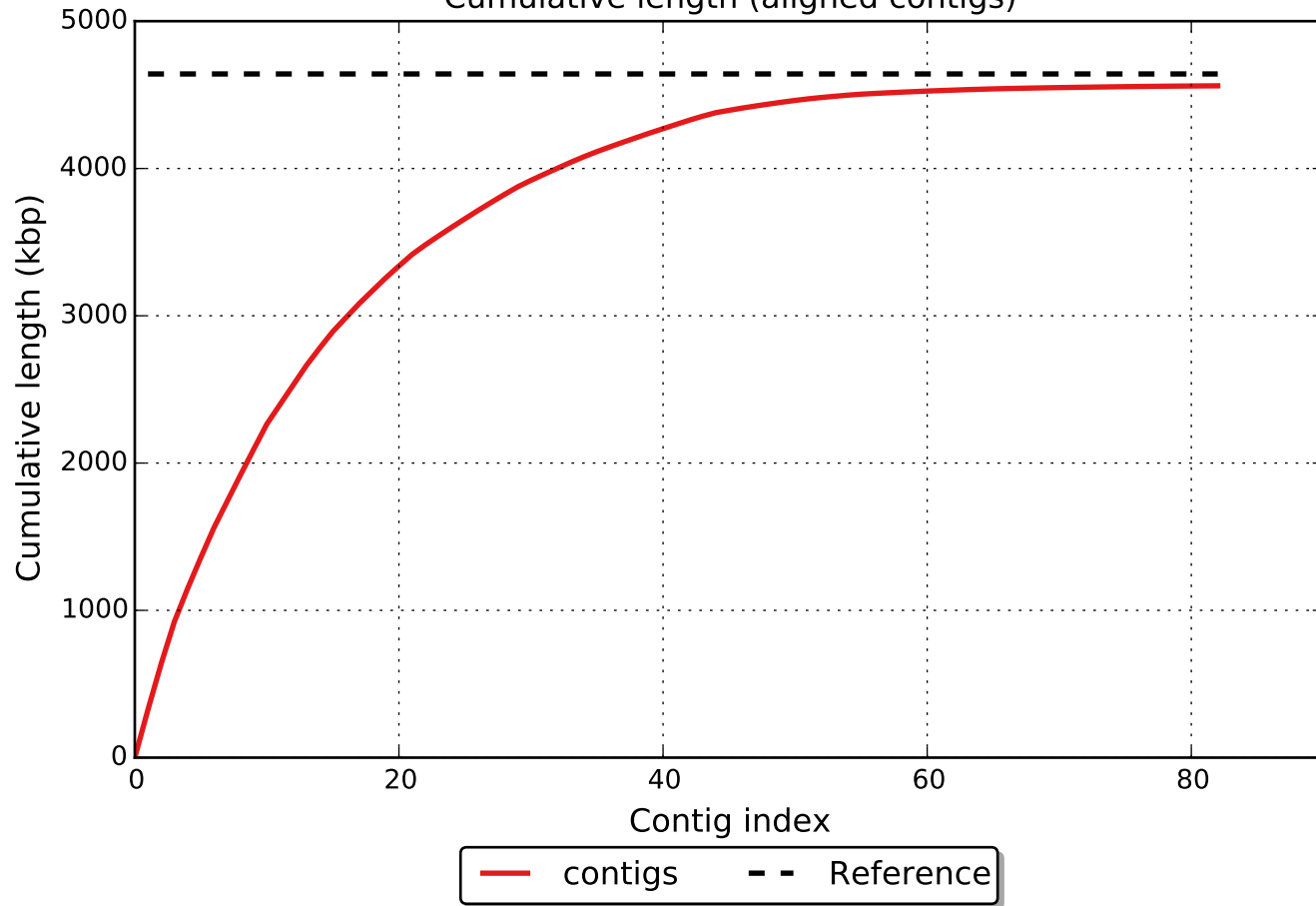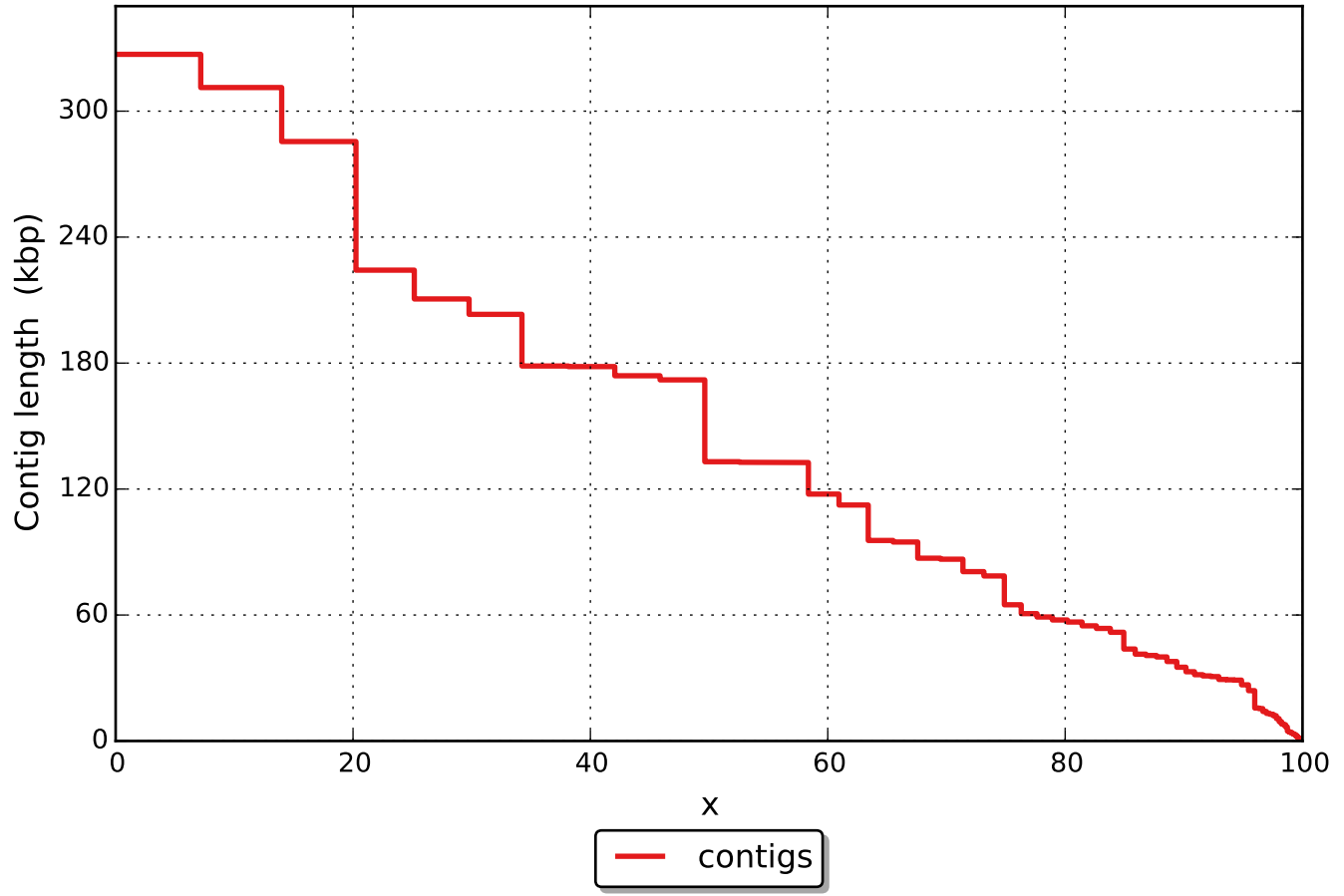
Cumulative length

GC content

Misassemblies

contigs

Cumulative length (aligned contigs)