Report

	final.contigs
# contigs (>= 0 bp)	19079
# contigs (>= 1000 bp)	1825
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	10223444
Total length (>= 1000 bp)	2641490
Total length (>= 5000 bp)	11201
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5856
Largest contig	6045
Total length	5441810
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	981
NG50	1074
N75	702
NG75	817
L50	1906
LG50	1516
L75	3547
LG75	2756
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	4558 + 31 part
Unaligned length	3763126
Genome fraction (%)	35.419
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	638.92
# indels per 100 kbp	0.18
Largest alignment	6045
NGA50	-

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).
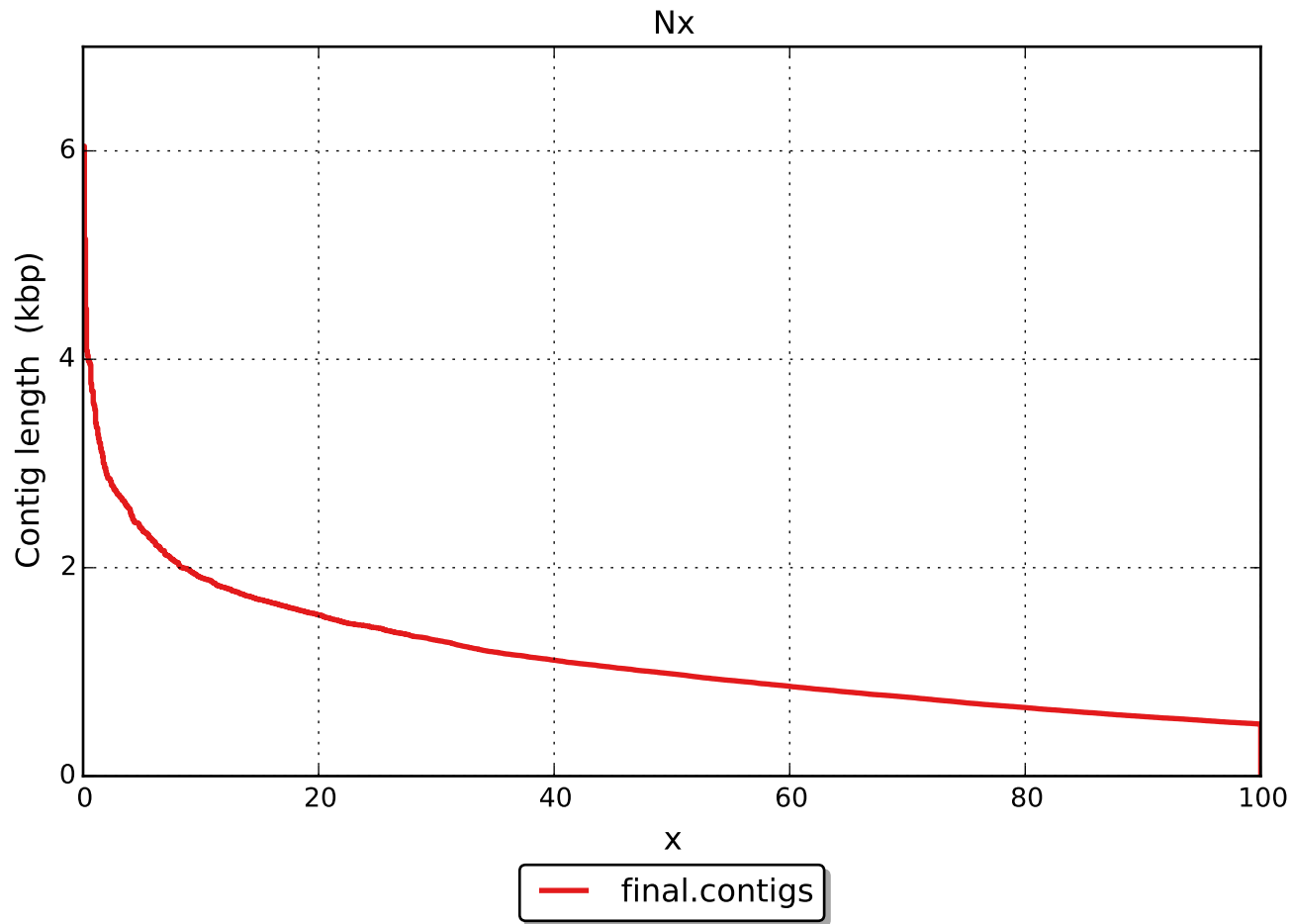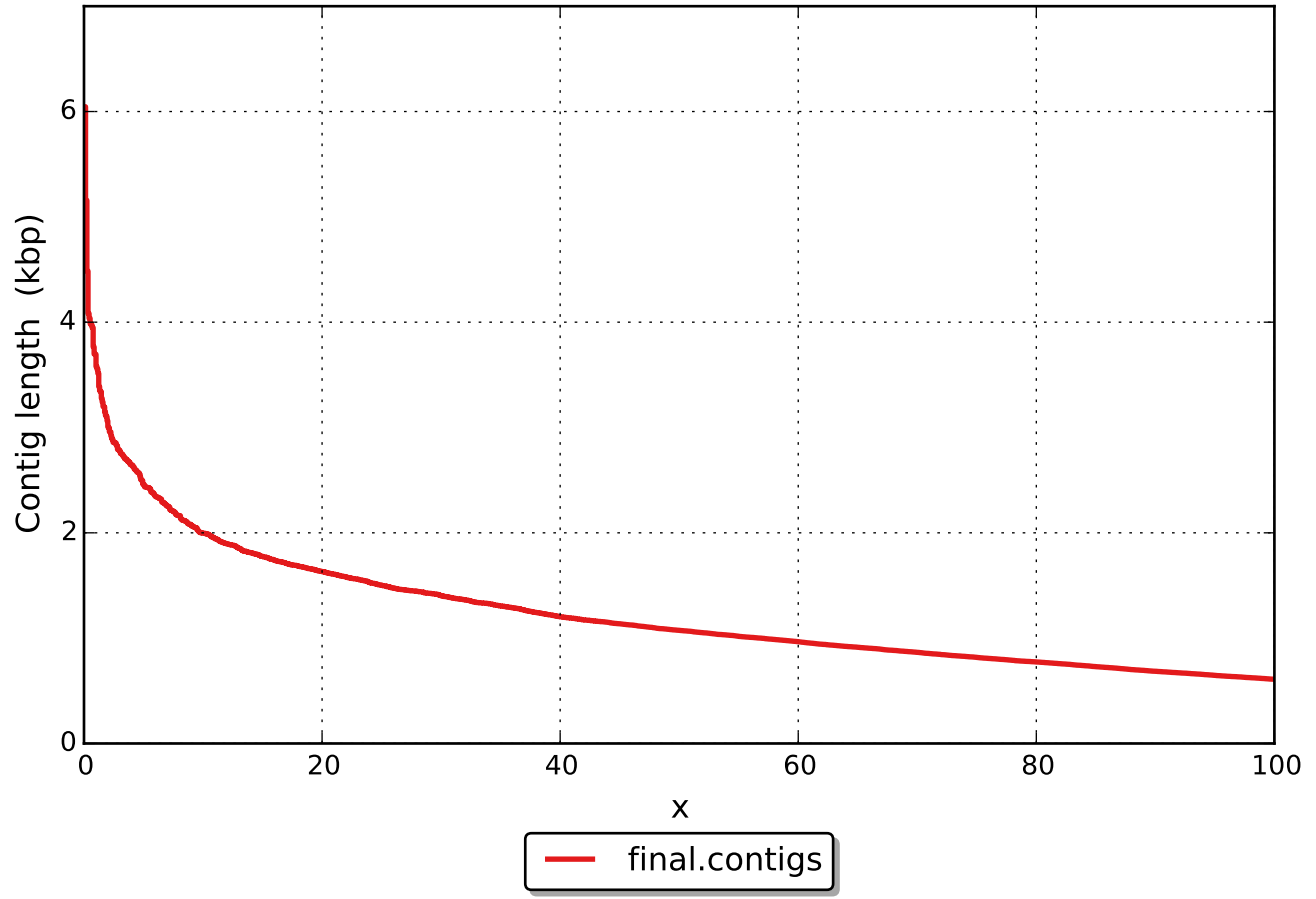
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10504
# indels	3
# short indels	3
# long indels	0
Indels length	3

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).
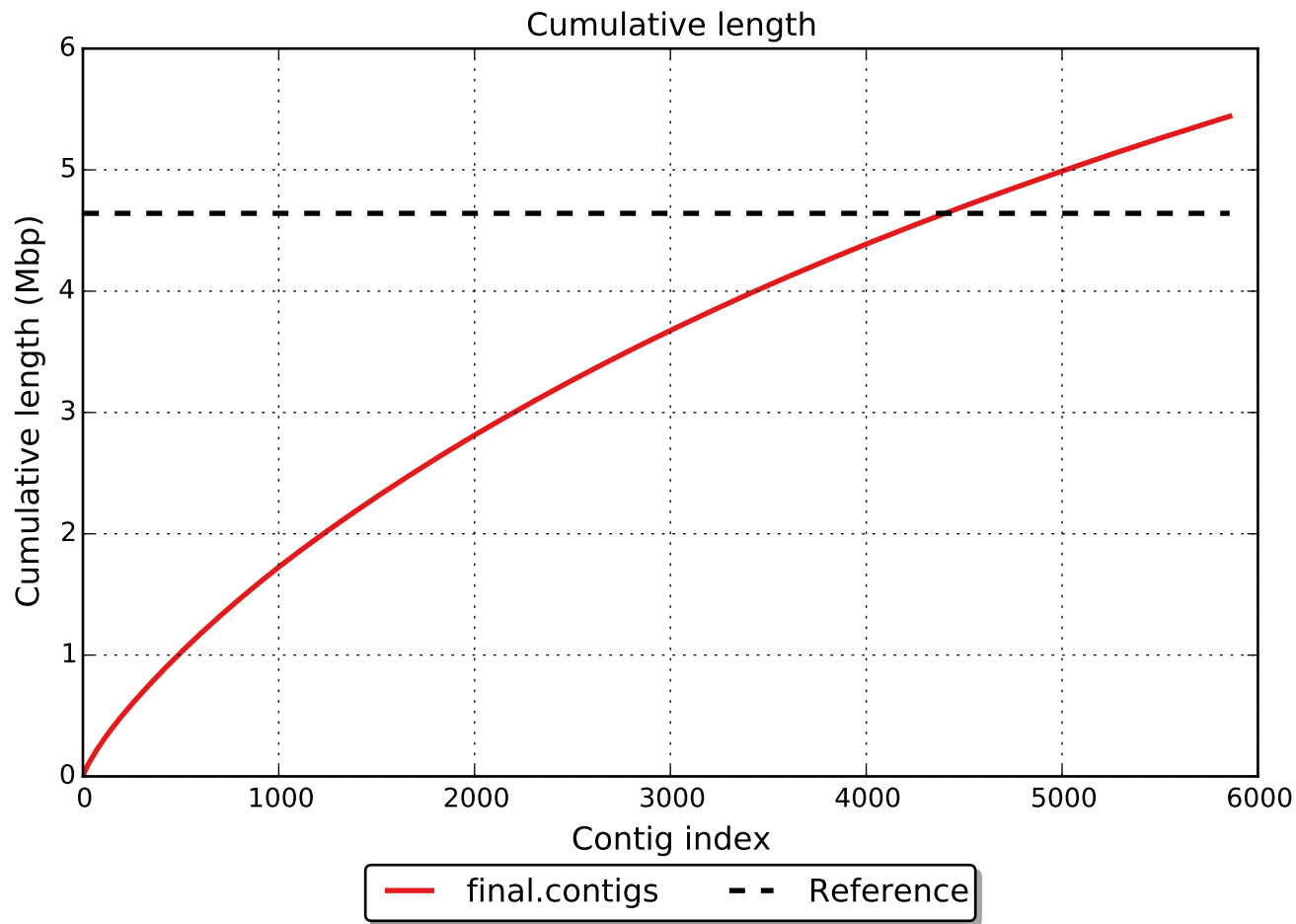
Unaligned report

	final.contigs
# fully unaligned contigs	4558
Fully unaligned length	3747577
# partially unaligned contigs	31
# with misassembly	1
# both parts are significant	0
Partially unaligned length	15549
# N's	0

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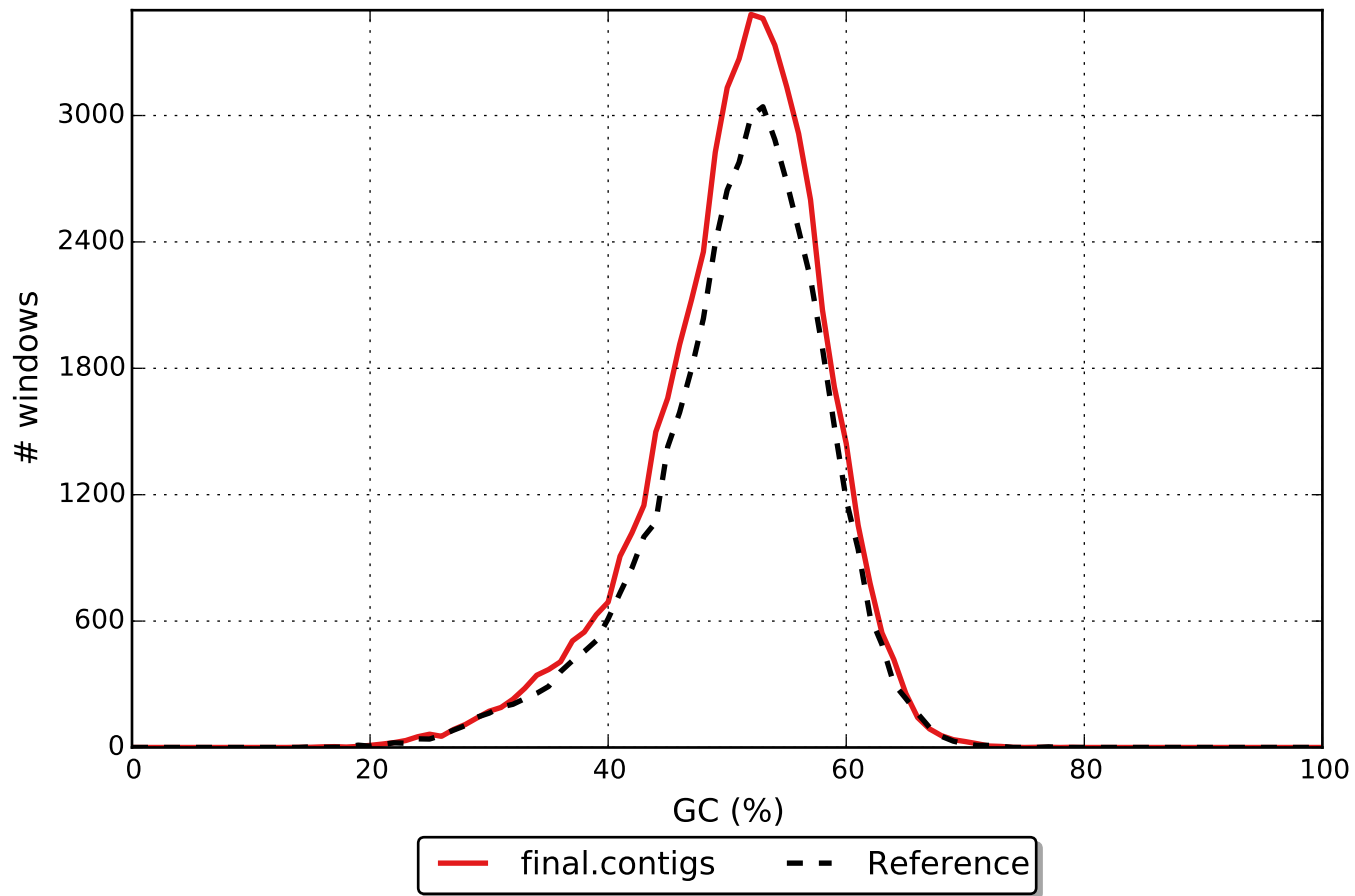(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

NGx

Contig length (kbp) vs x
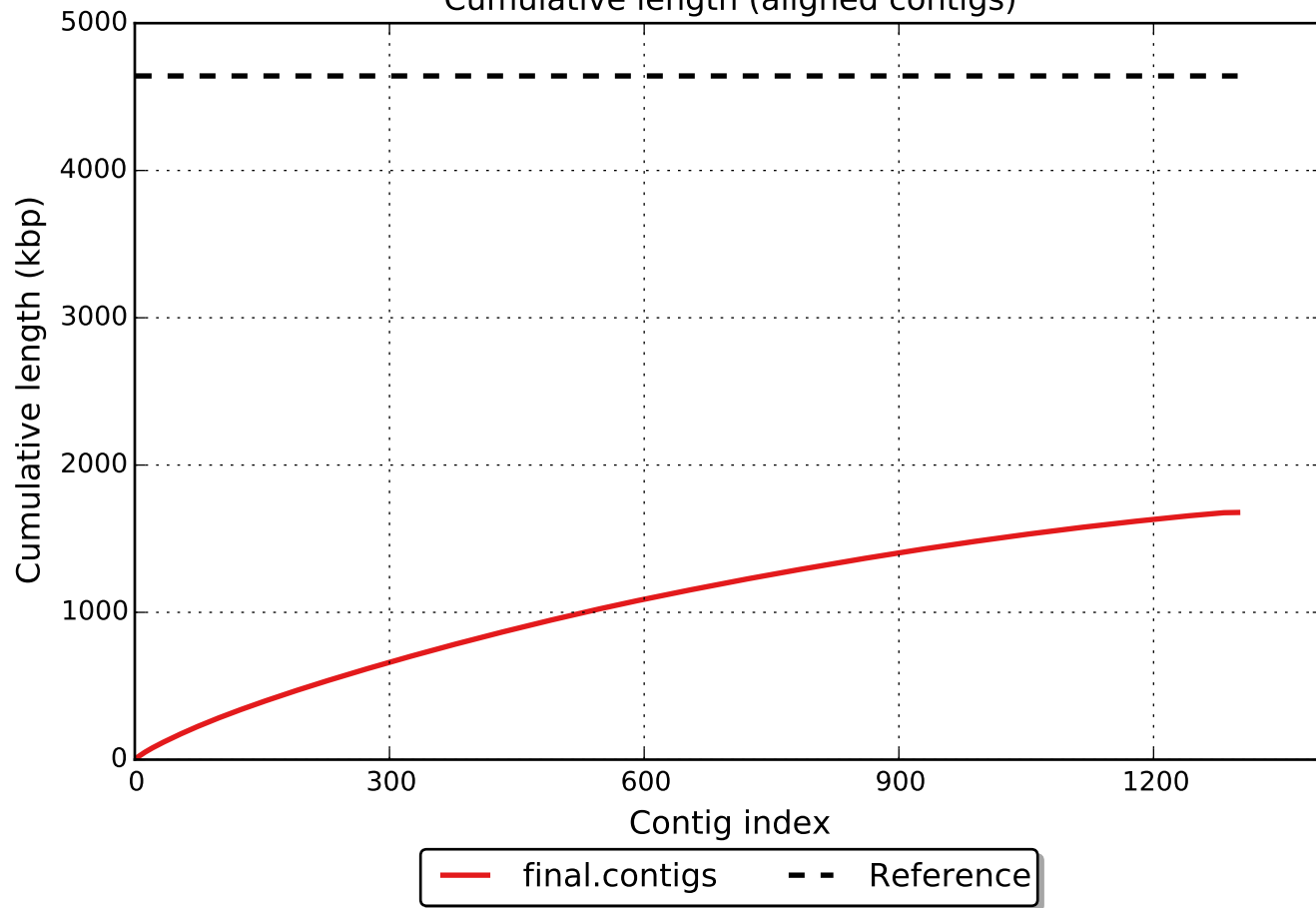
final.contigs

Cumulative length

GC content

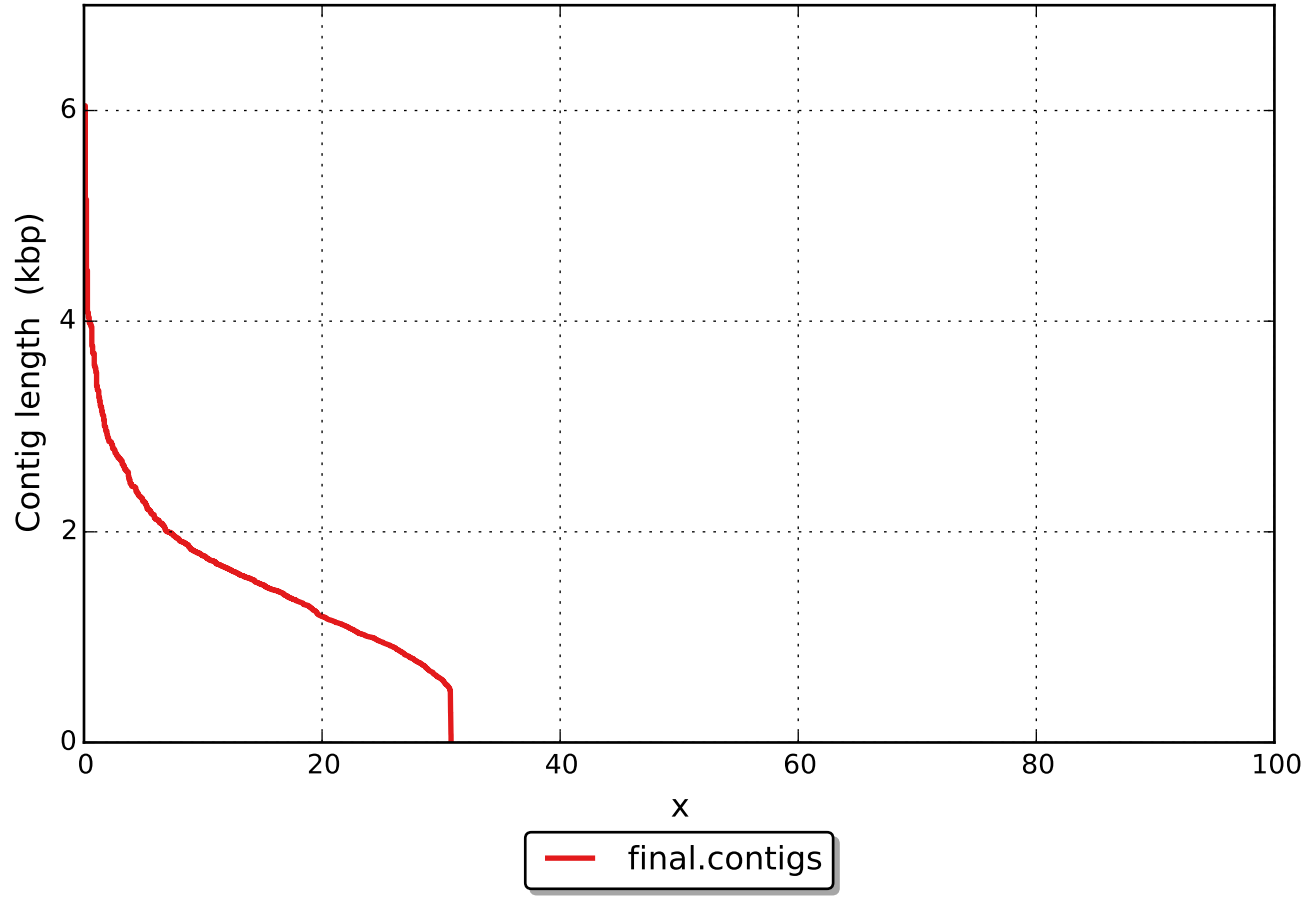# windows

GC (%)

final.contigs   Reference

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx