

# Report

	sim5M.CanuH.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1993
# contigs (>= 5000 bp)	1644
# contigs (>= 10000 bp)	482
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	15876604
Total length (>= 1000 bp)	15871428
Total length (>= 5000 bp)	14562802
Total length (>= 10000 bp)	5957960
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1999
Largest contig	23216
Total length	15876382
Reference length	5000040
GC (%)	35.77
Reference GC (%)	35.84
N50	8886
NG50	12548
N75	6848
NG75	11504
L50	693
LG50	172
L75	1201
LG75	276
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	1794
Genome fraction (%)	96.034
Duplication ratio	3.306
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.50
# indels per 100 kbp	13.14
Largest alignment	23216
Total aligned length	15871038
NA50	8881
NGA50	12548
NA75	6847
NGA75	11499
LA50	693
LGA50	172
LA75	1201
LGA75	276

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

	sim5M.CanuH.cr
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	216
# indels	631
# indels ( $\leq 5$ bp)	630
# indels ( $> 5$ bp)	1
Indels length	719

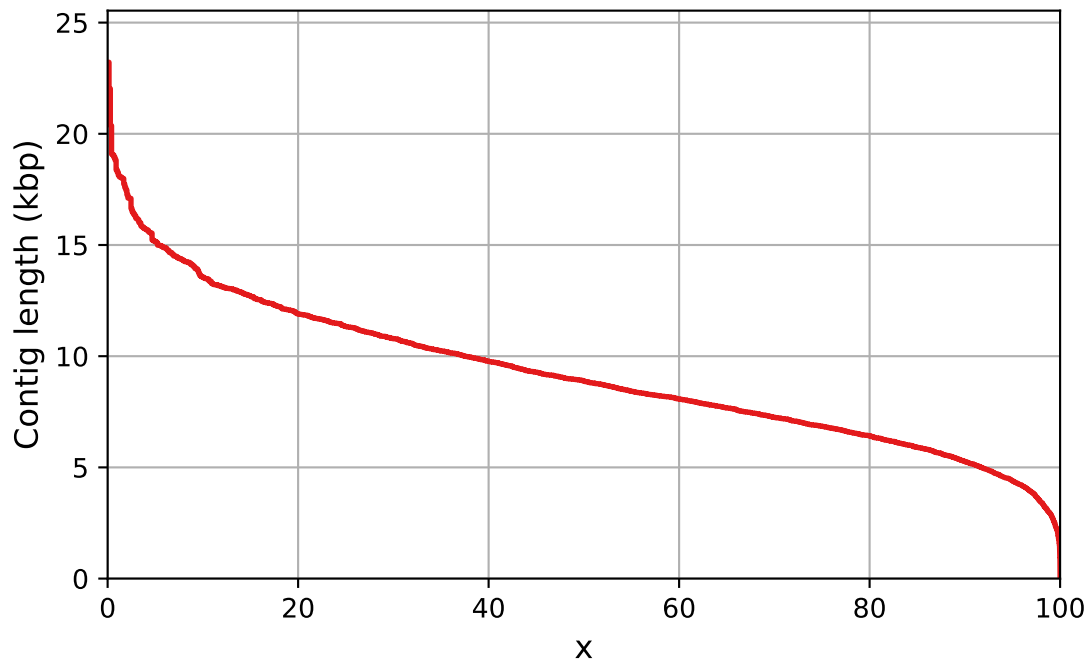
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	sim5M.CanuH.cr
# fully unaligned contigs	1
Fully unaligned length	1794
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

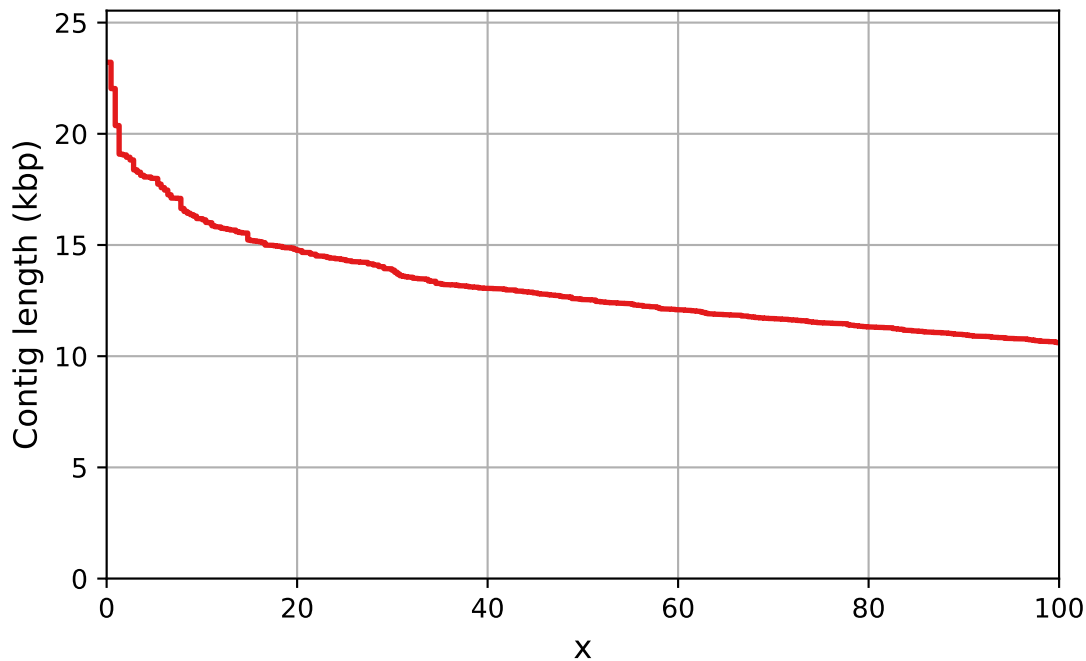
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



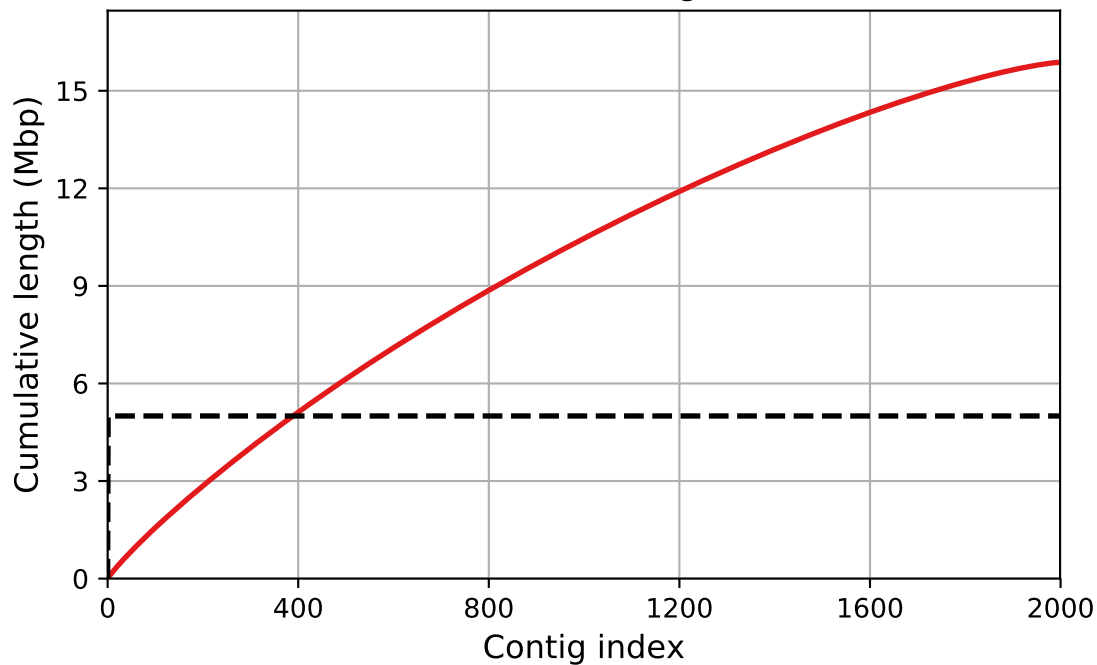
— sim5M.CanuH.cr

## NGx



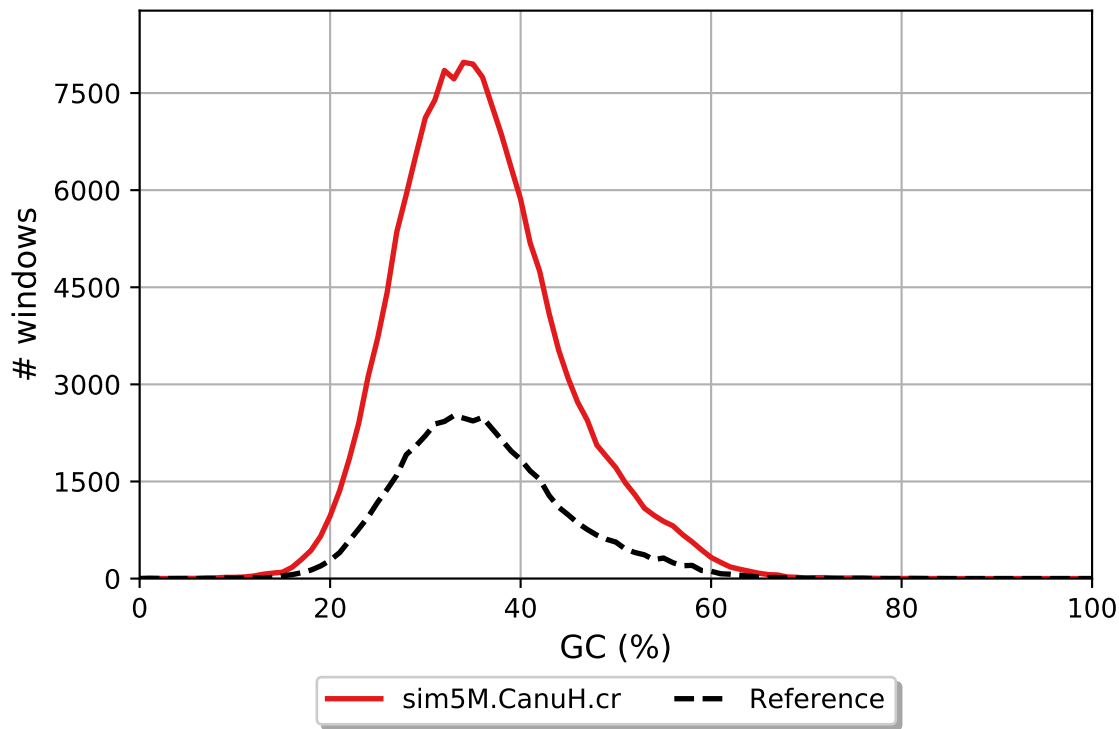
— sim5M.CanuH.cr

Cumulative length

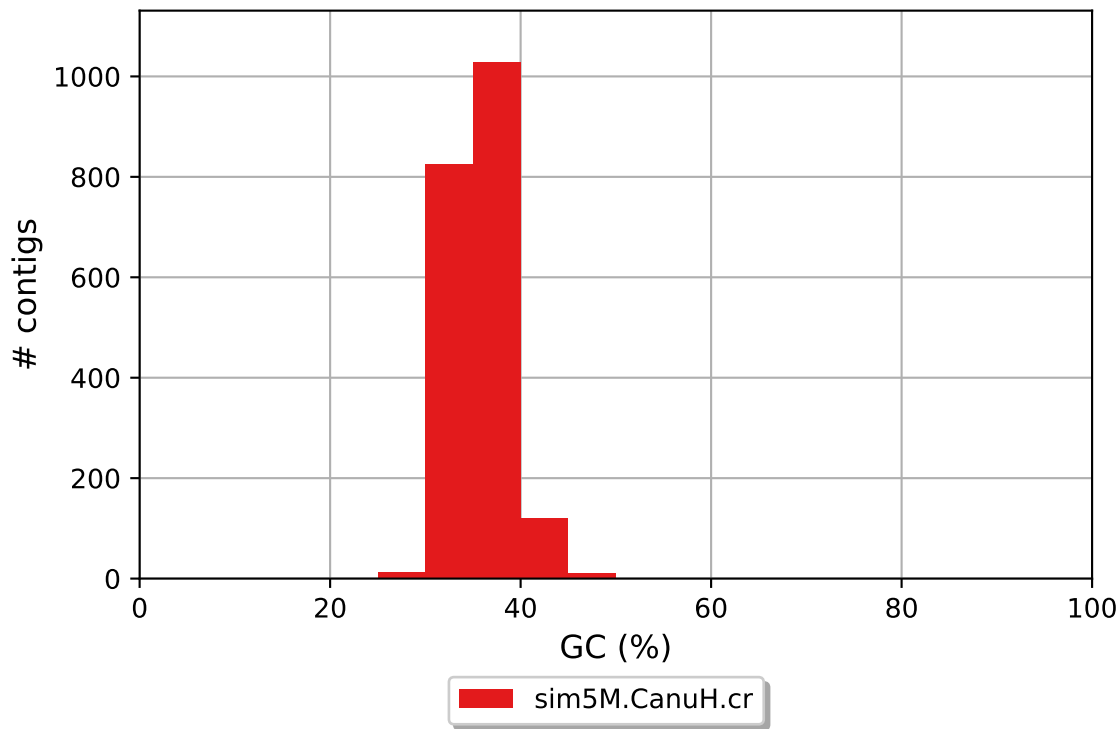


— sim5M.CanuH.cr    - - Reference

## GC content



sim5M.CanuH.cr GC content

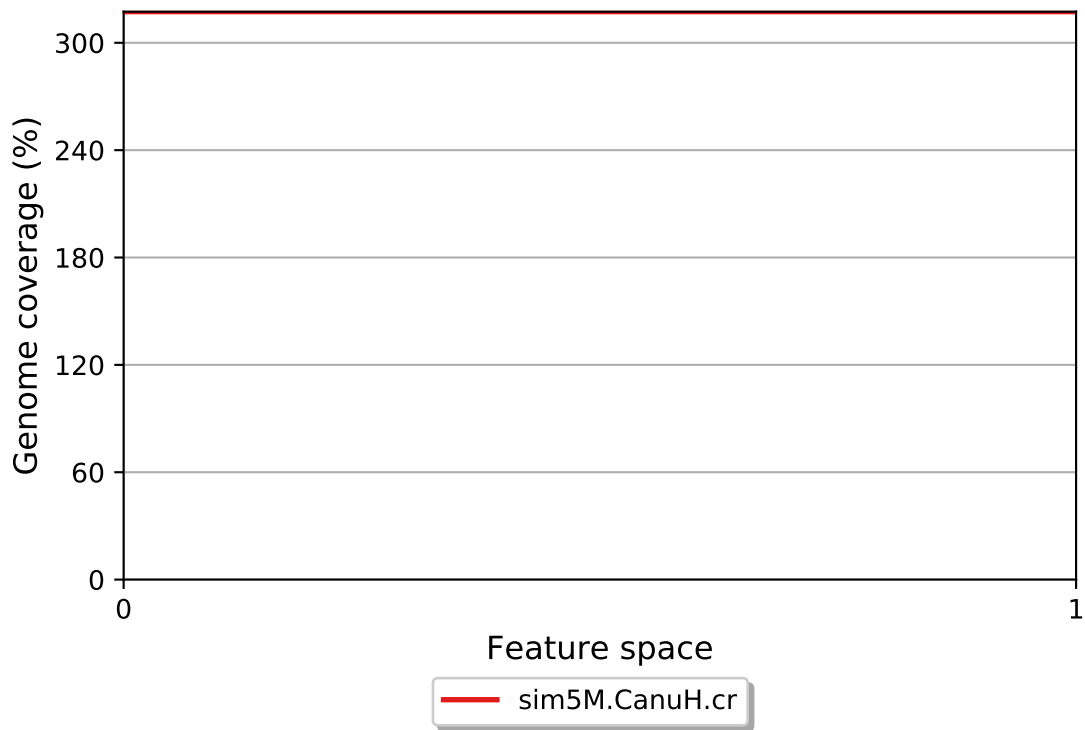




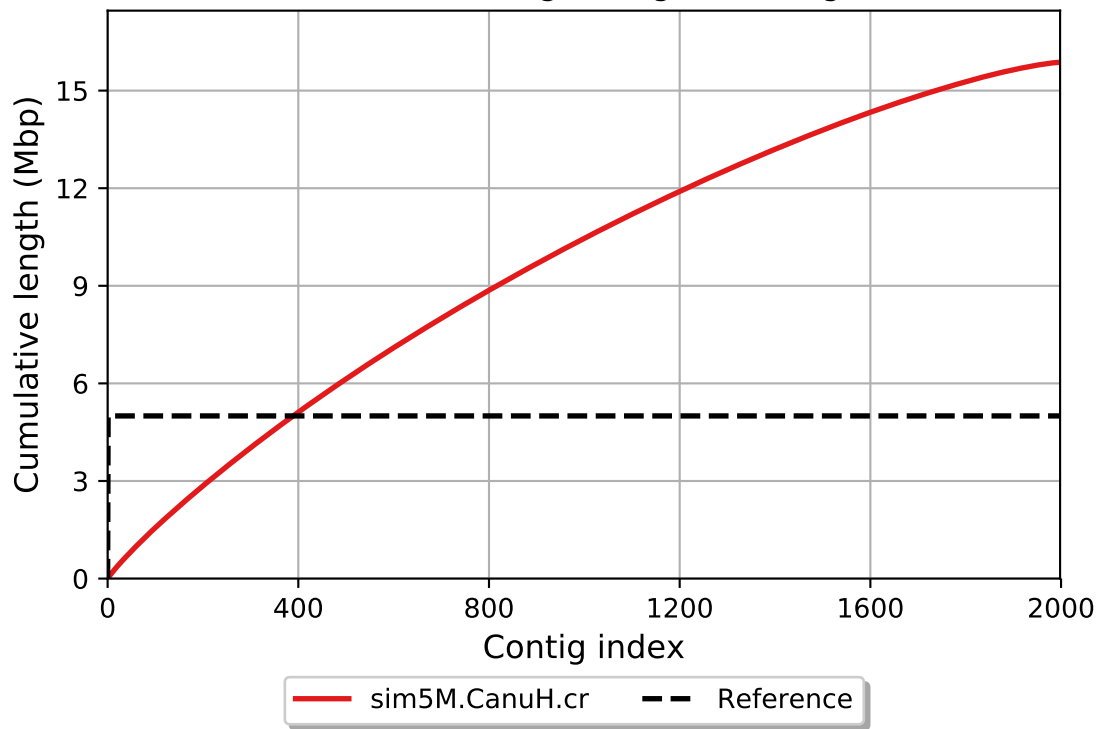
## Misassemblies



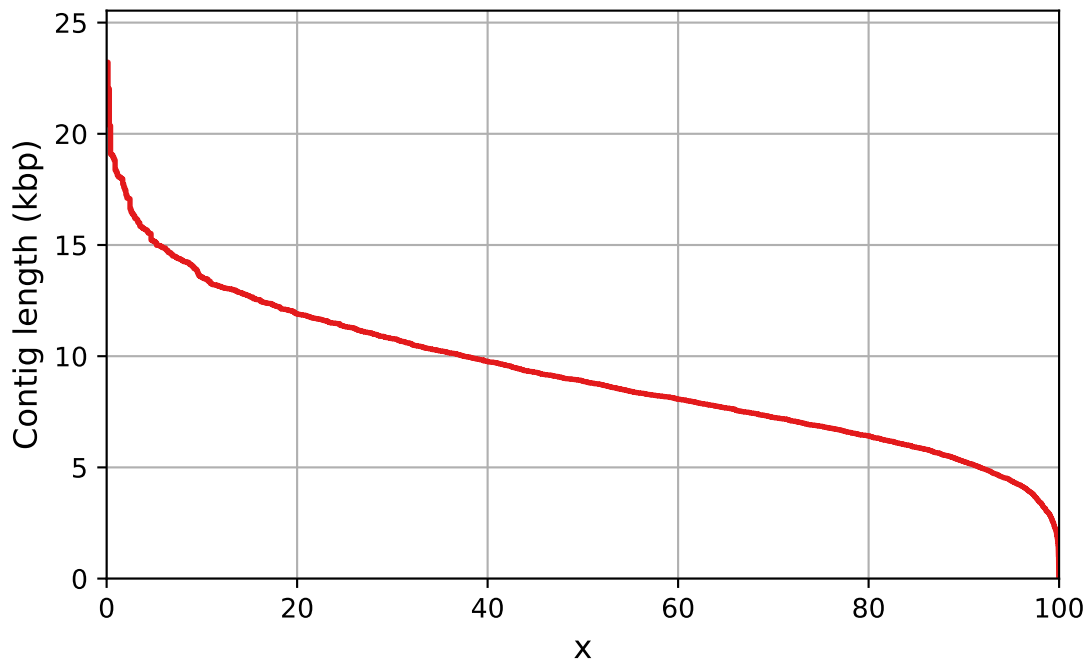
FRCurve (misassemblies)



Cumulative length (aligned contigs)

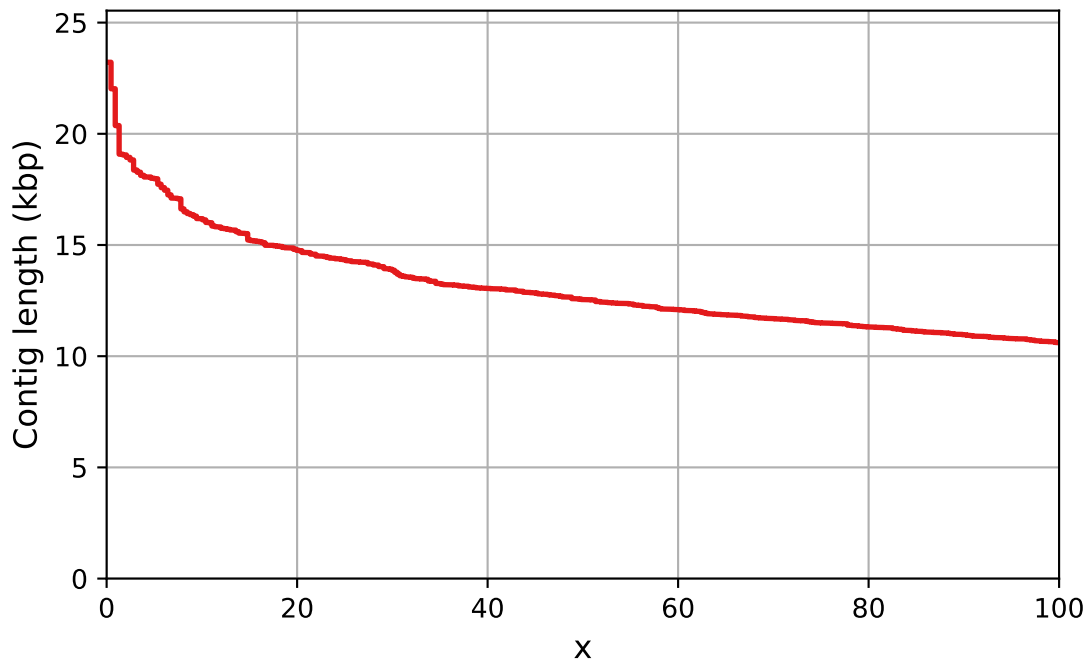


NAx



— sim5M.CanuH.cr

## NGAx



— sim5M.CanuH.cr