

## Report

	sim5M.SGAL
# contigs (>= 0 bp)	1817
# contigs (>= 1000 bp)	667
# contigs (>= 5000 bp)	334
# contigs (>= 10000 bp)	156
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5121547
Total length (>= 1000 bp)	4776595
Total length (>= 5000 bp)	3894551
Total length (>= 10000 bp)	2631081
Total length (>= 25000 bp)	510612
Total length (>= 50000 bp)	0
# contigs	800
Largest contig	46979
Total length	4868971
Reference length	5000040
GC (%)	35.74
Reference GC (%)	35.84
N50	10870
NG50	10435
N75	5920
NG75	5659
L50	138
LG50	144
L75	290
LG75	307
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.530
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.10
Largest alignment	46979
Total aligned length	4868971
NA50	10870
NGA50	10435
NA75	5920
NGA75	5659
LA50	138
LGA50	144
LA75	290
LGA75	307

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.SGAL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	5
# indels ( $\leq 5$ bp)	1
# indels ( $> 5$ bp)	4
Indels length	132

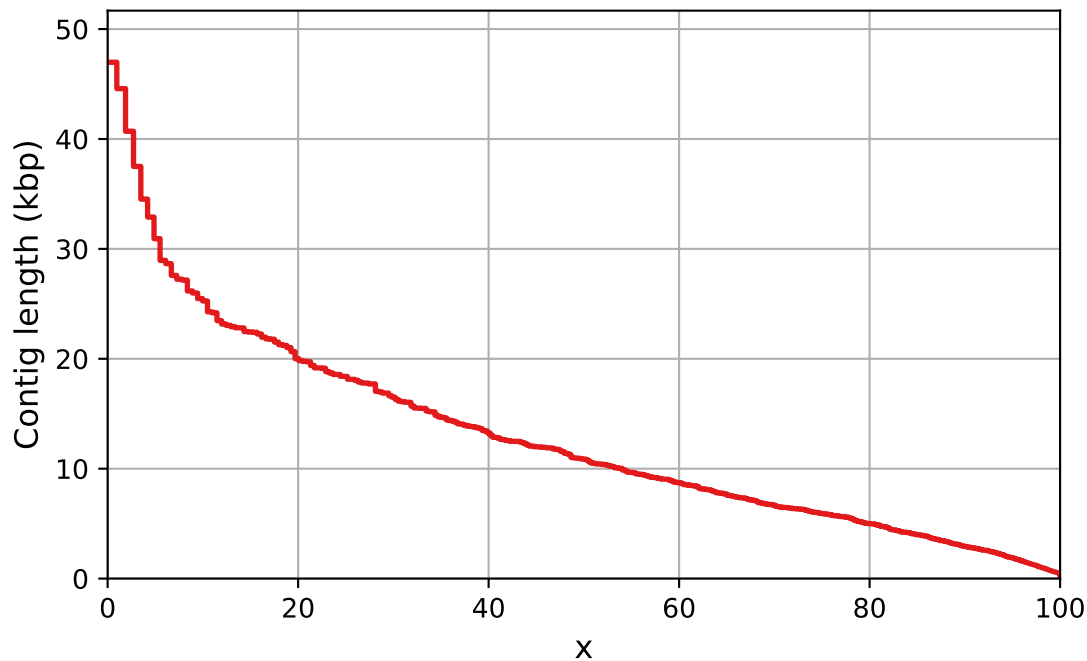
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	sim5M.SGAL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

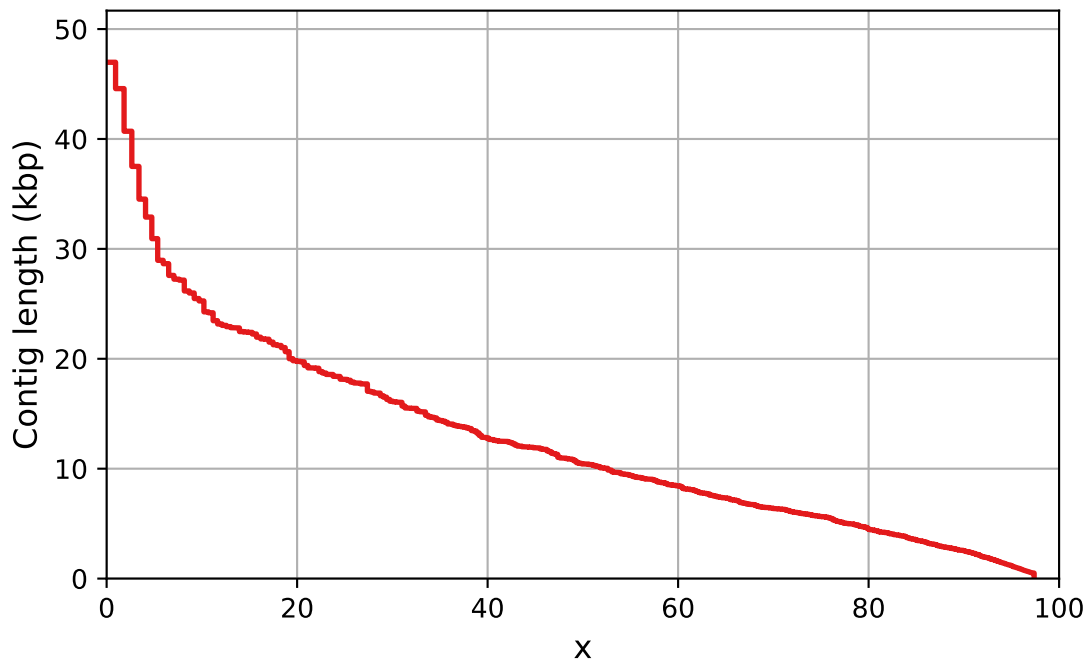
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



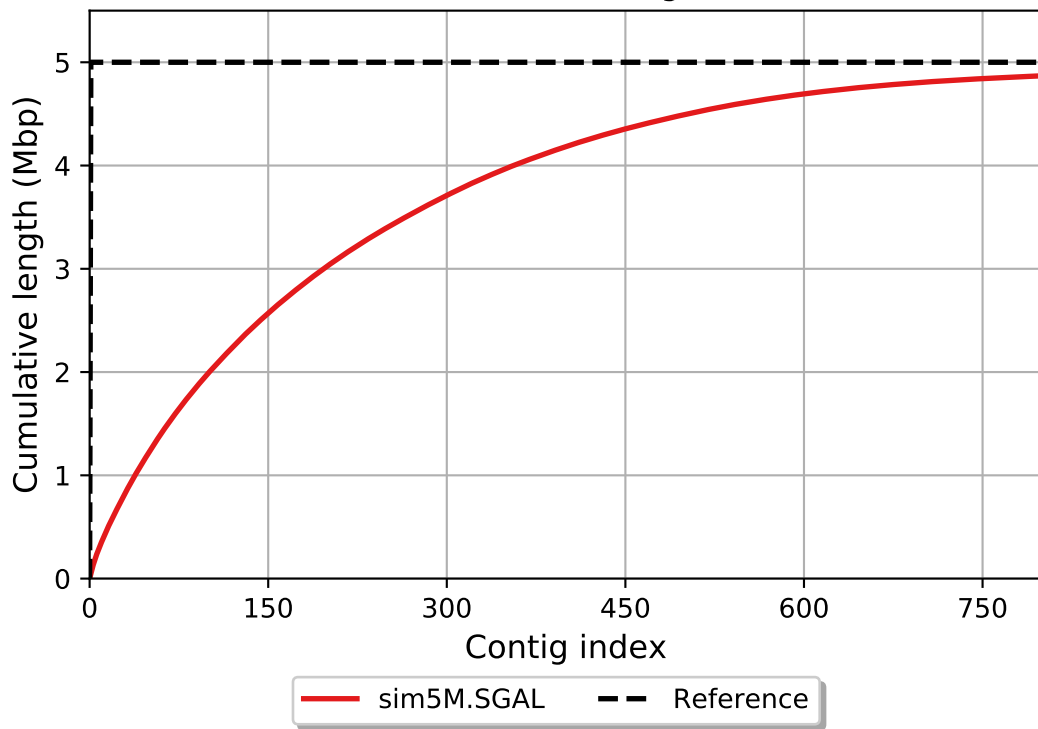
— sim5M.SGAL

NGx

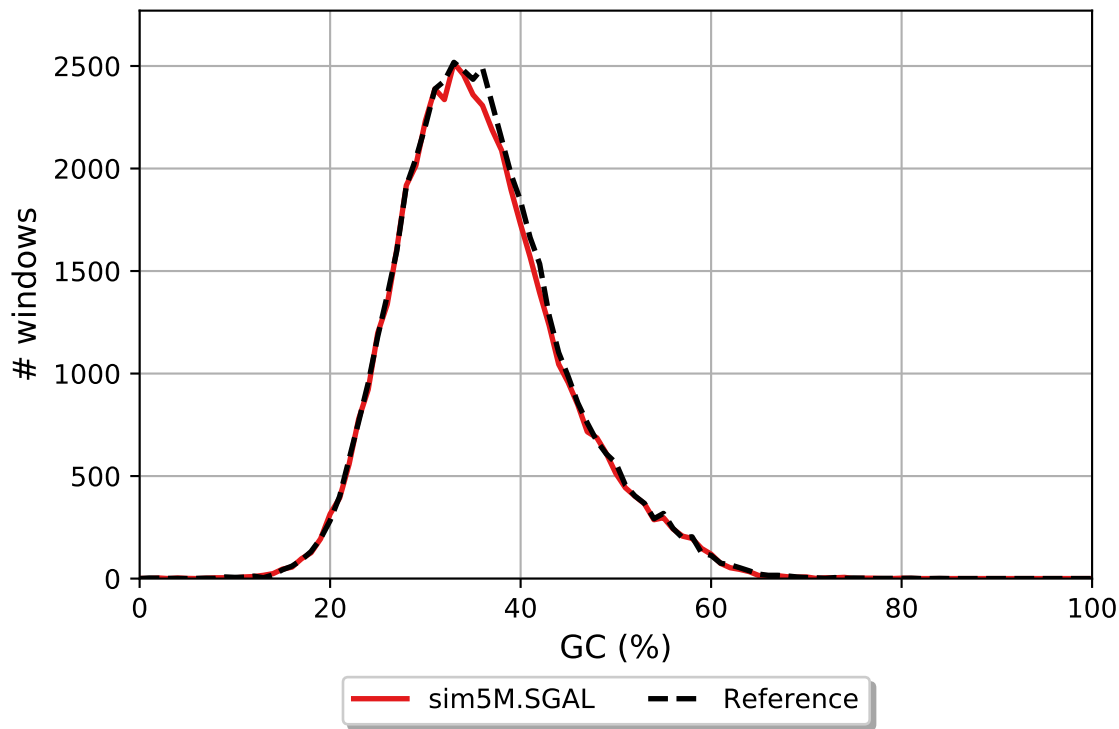


— sim5M.SGAL

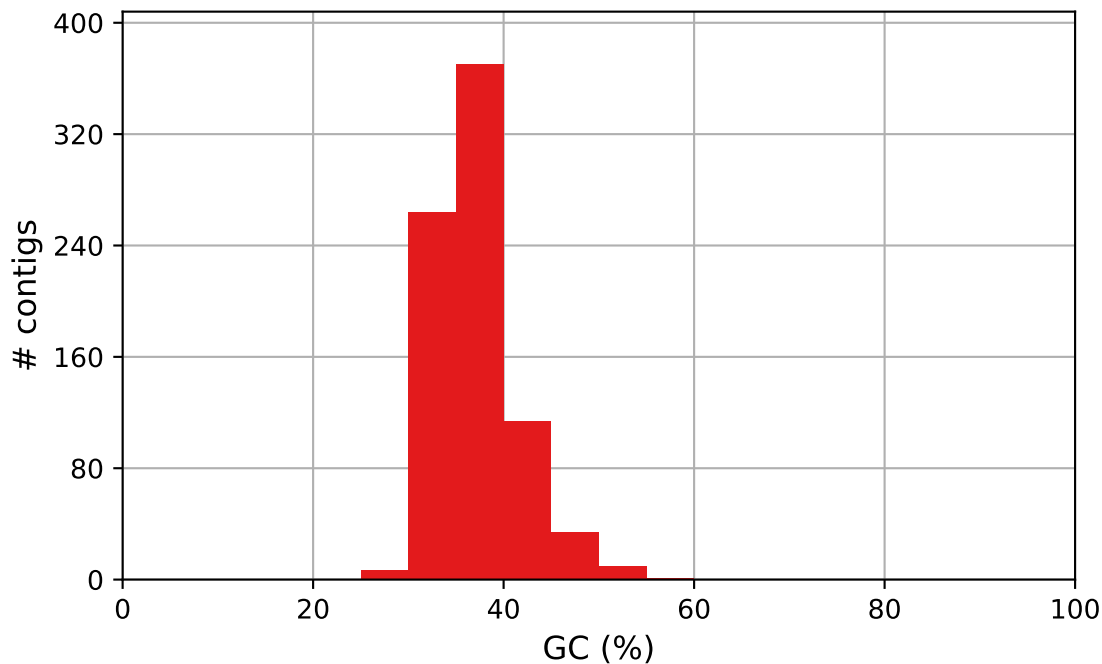
Cumulative length



## GC content



sim5M.SGAL GC content



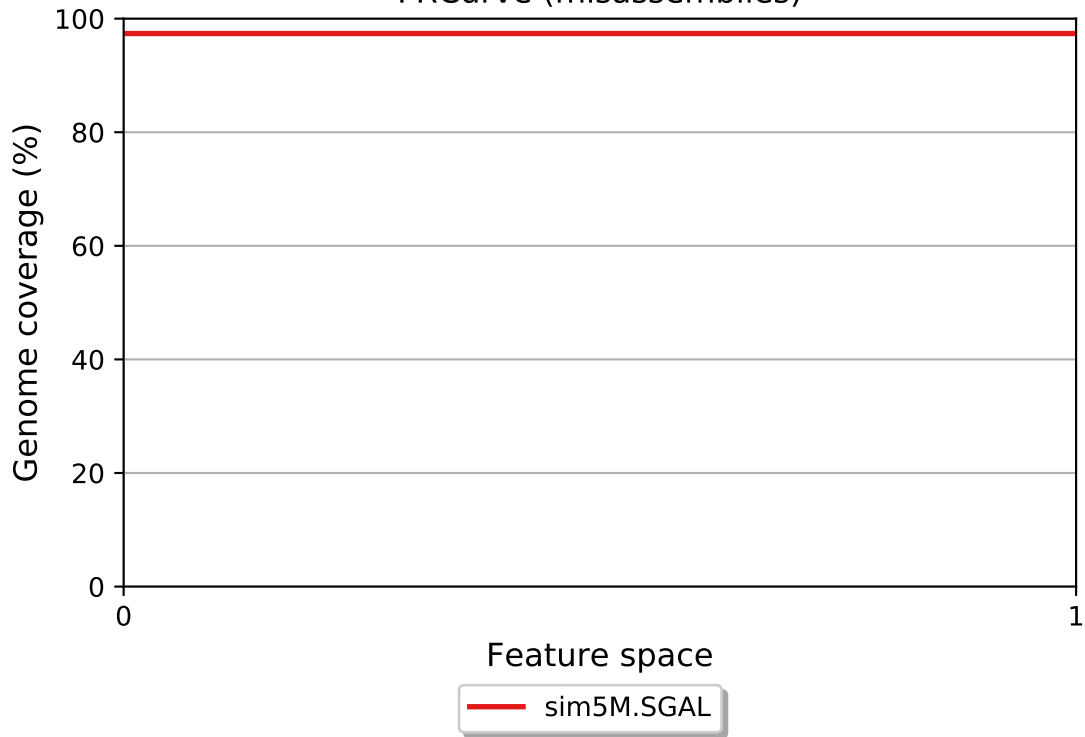
sim5M.SGAL



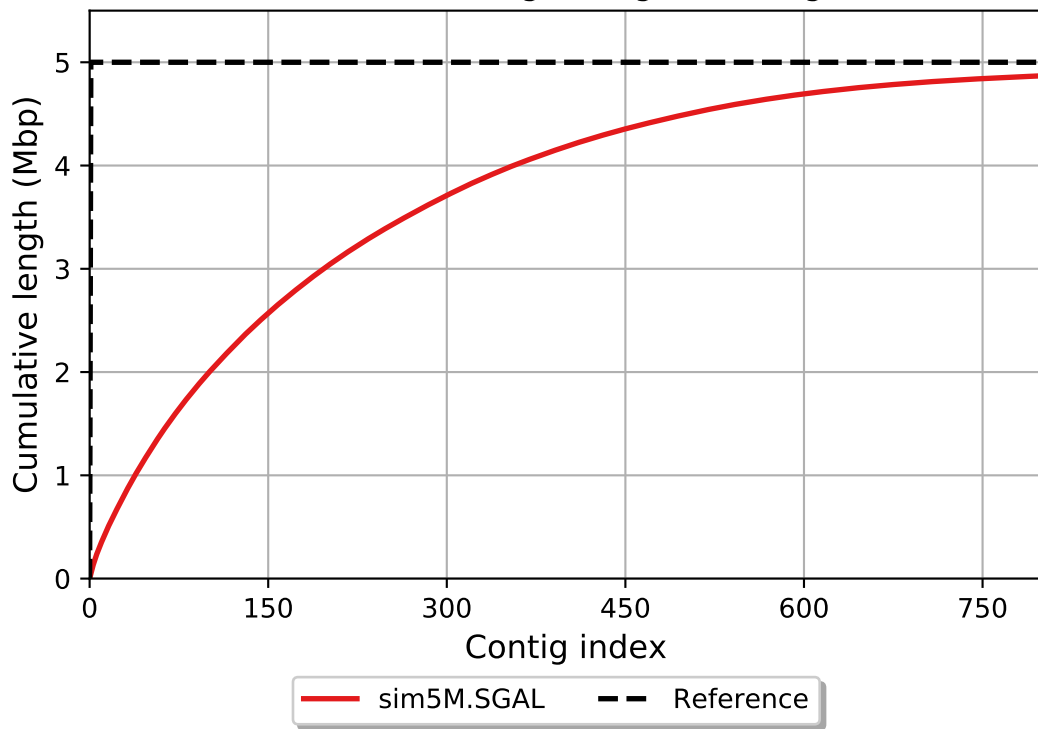
## Misassemblies



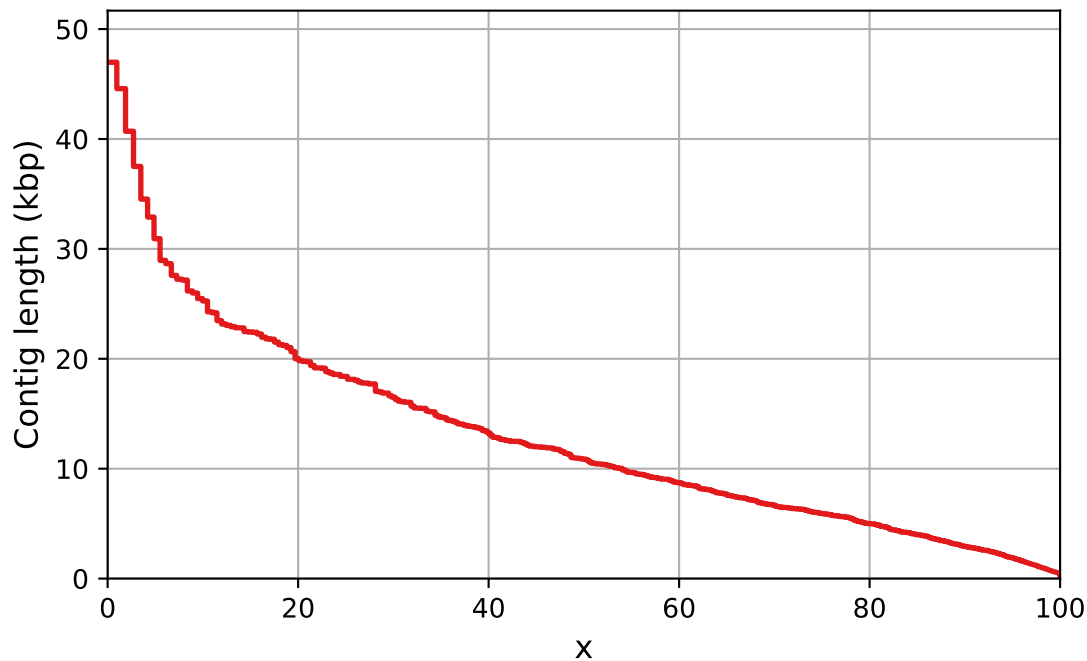
FRCurve (misassemblies)



Cumulative length (aligned contigs)

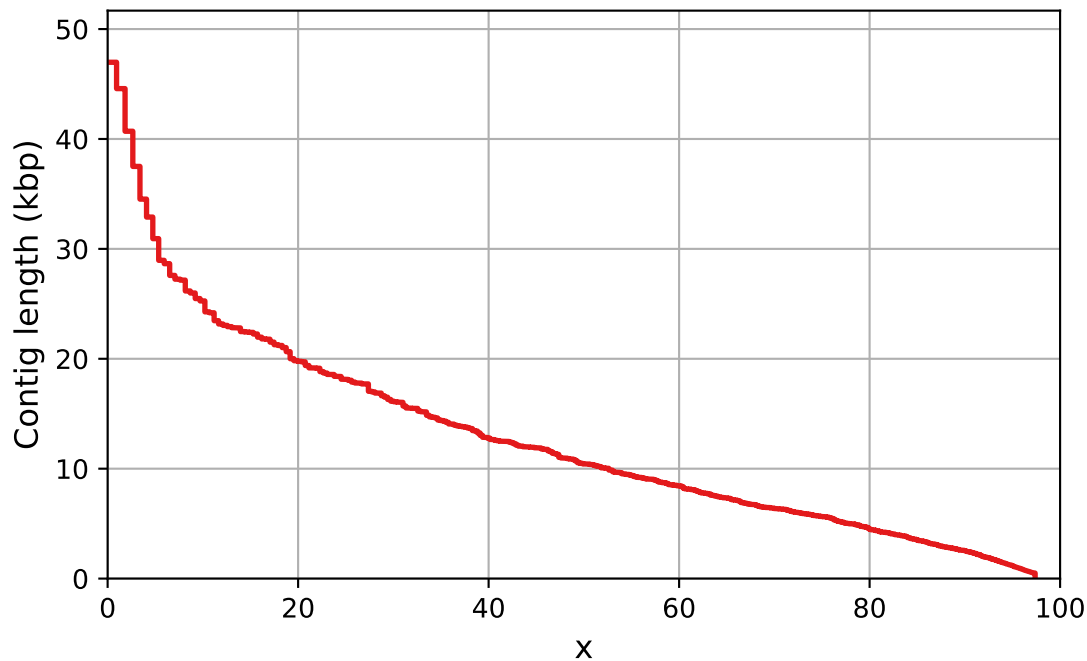


NAx



— sim5M.SGAL

# NGAx



— sim5M.SGAL