Report

	sim5M.CanuH
# contigs (>= 0 bp)	17
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	6
Total length (>= 0 bp)	5135279
Total length (>= 1000 bp)	5135279
Total length (>= 5000 bp)	5135279
Total length (>= 10000 bp)	5110300
Total length (>= 25000 bp)	4998119
Total length (>= 50000 bp)	4998119
# contigs	17
Largest contig	1474850
Total length	5135279
Reference length	5000040
GC (%)	35.86
Reference GC (%)	35.84
N50	1313778
NG50	1313778
N75	623531
NG75	623531
L50	2
LG50	2
L75	4
LG75	4
# 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 (%)	99.910
Duplication ratio	1.028
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.48
# indels per 100 kbp	0.42
Largest alignment	1474850
Total aligned length	5135271
NA50	1313776
NGA50	1313776
NA75	623528
NGA75	623528
LA50	2
LGA50	2
LA75	4
LGA75	4

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

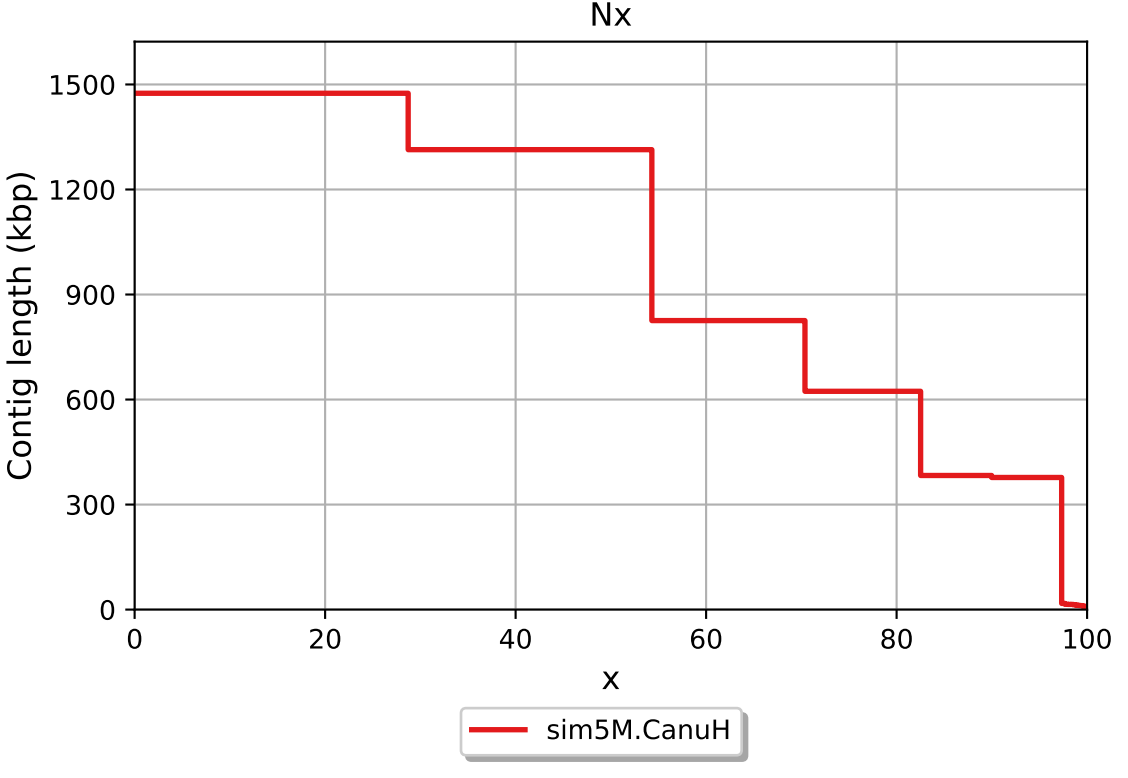
	sim5M.CanuH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	24
# indels	21
# indels (<= 5 bp)	21
# indels (> 5 bp)	0
Indels length	24

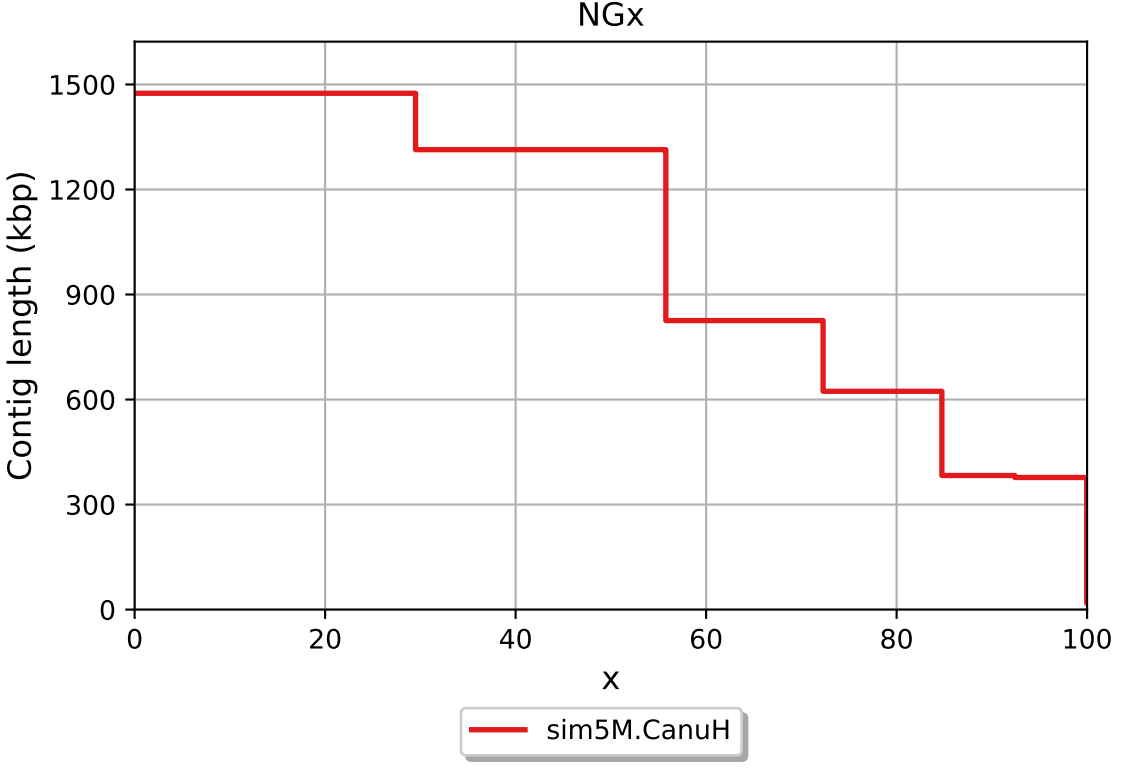
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

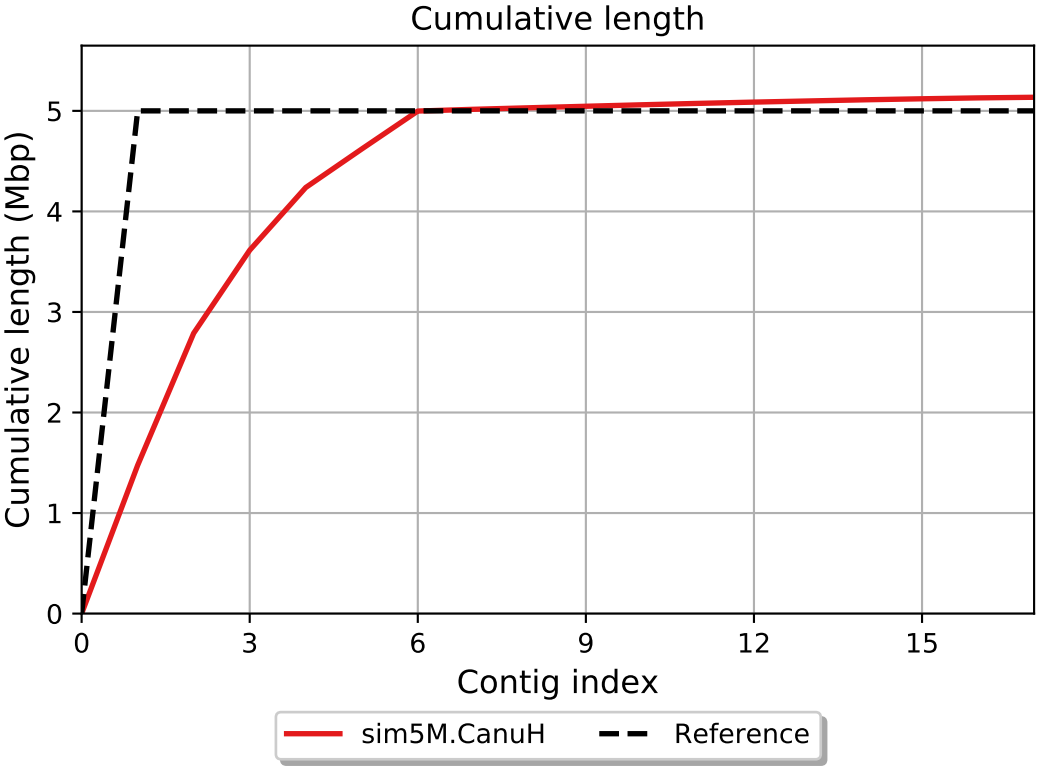
Unaligned report

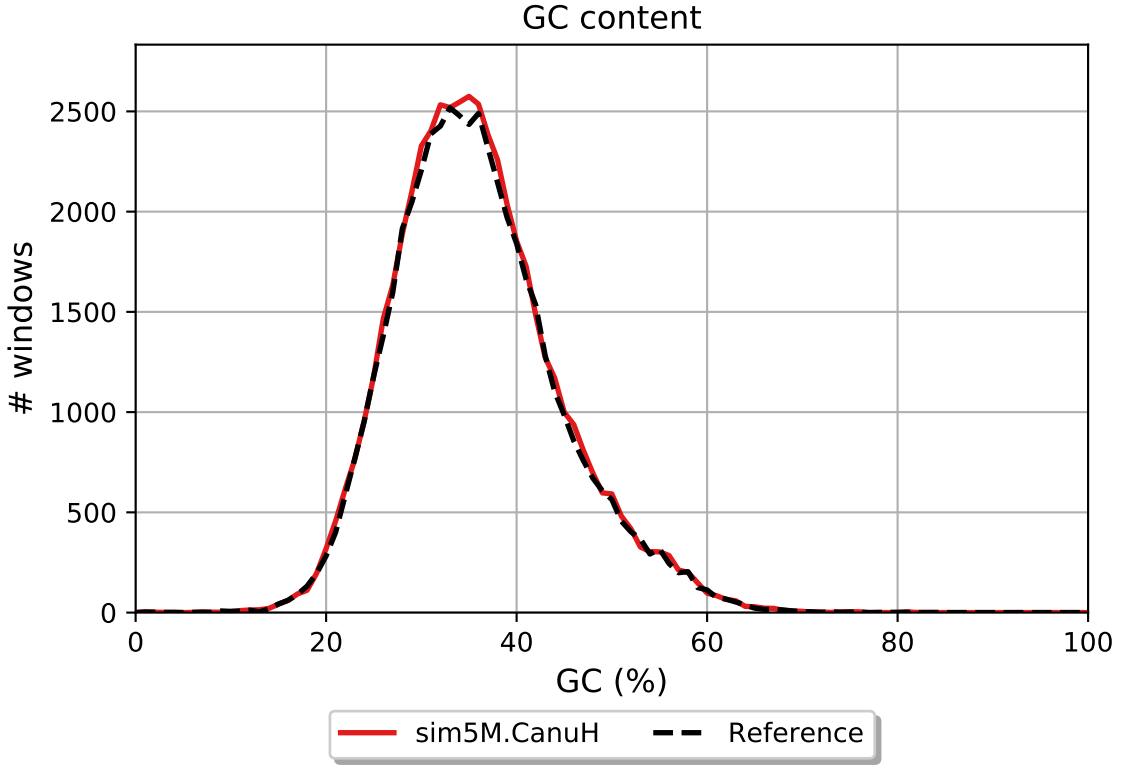
	sim5M.CanuH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

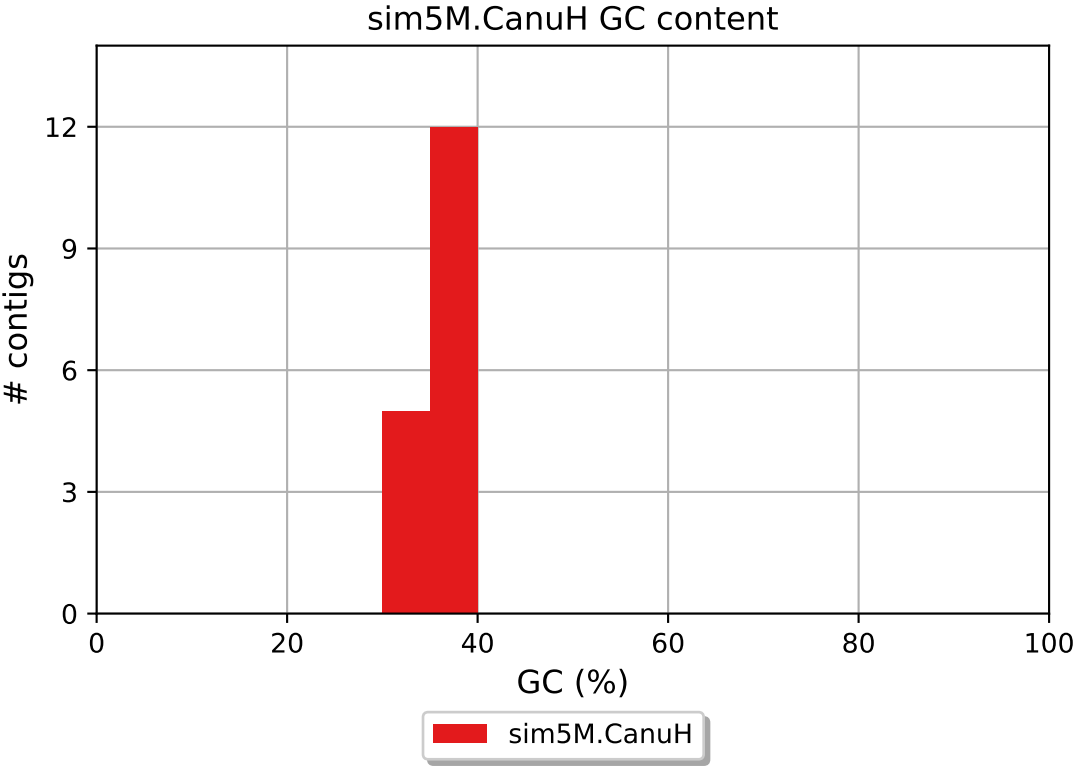
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

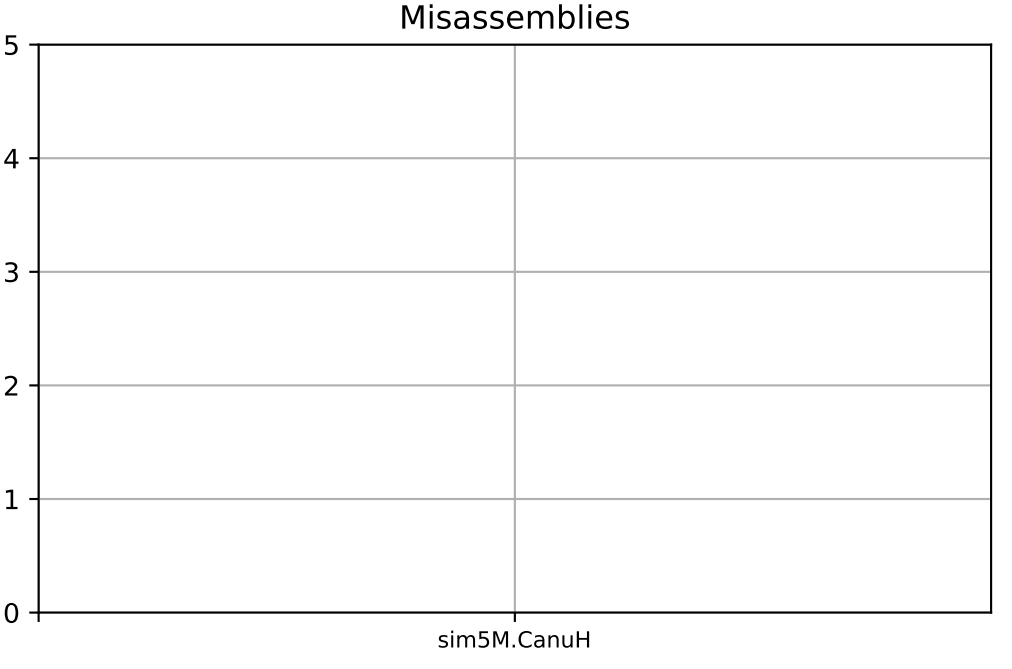

Nx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
sim5M.CanuH

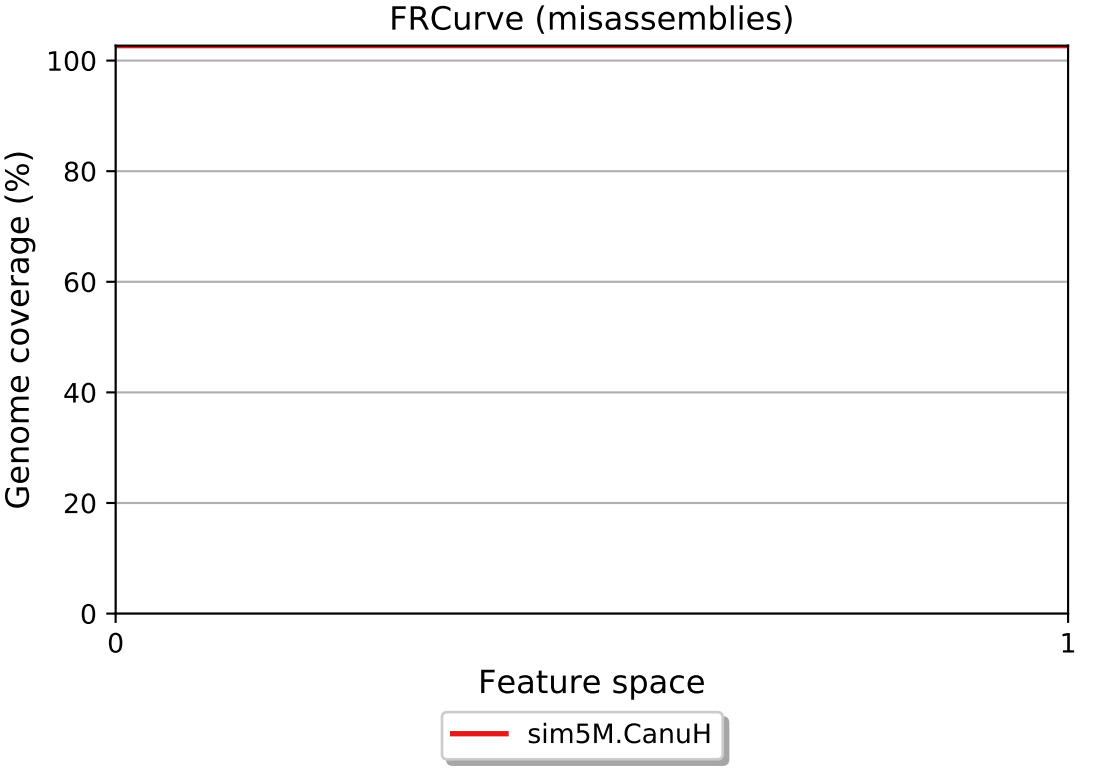

NGx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
sim5M.CanuH

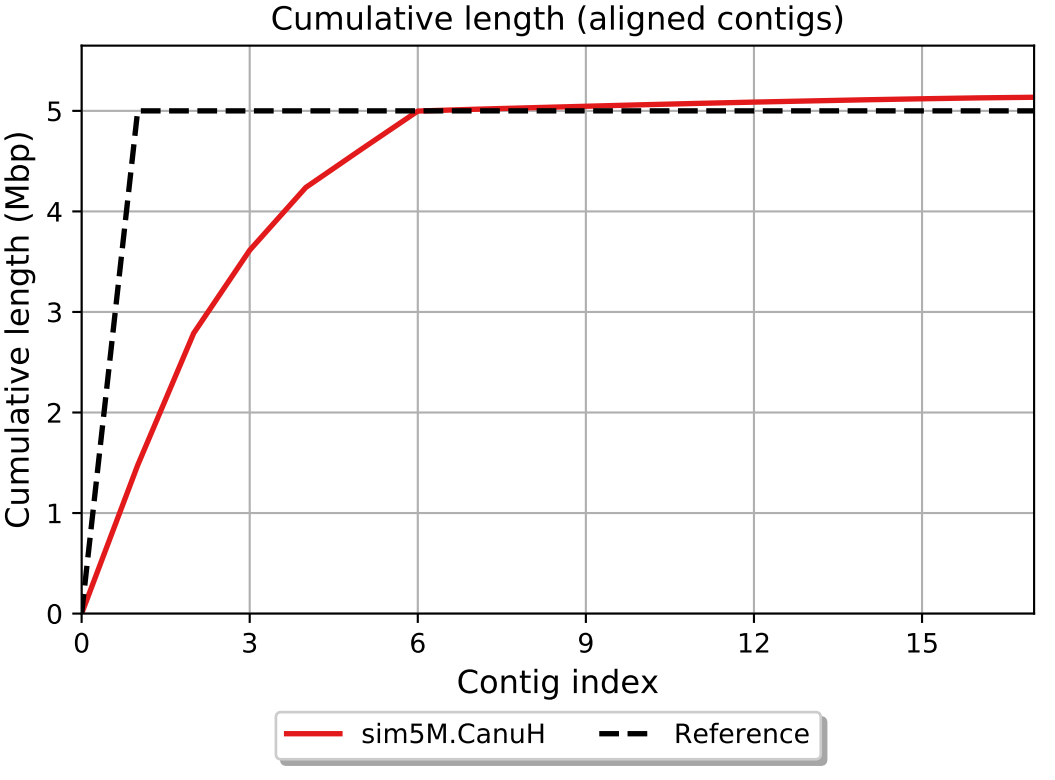

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
3
6
9
12
15
Contig index
sim5M.CanuH
Reference

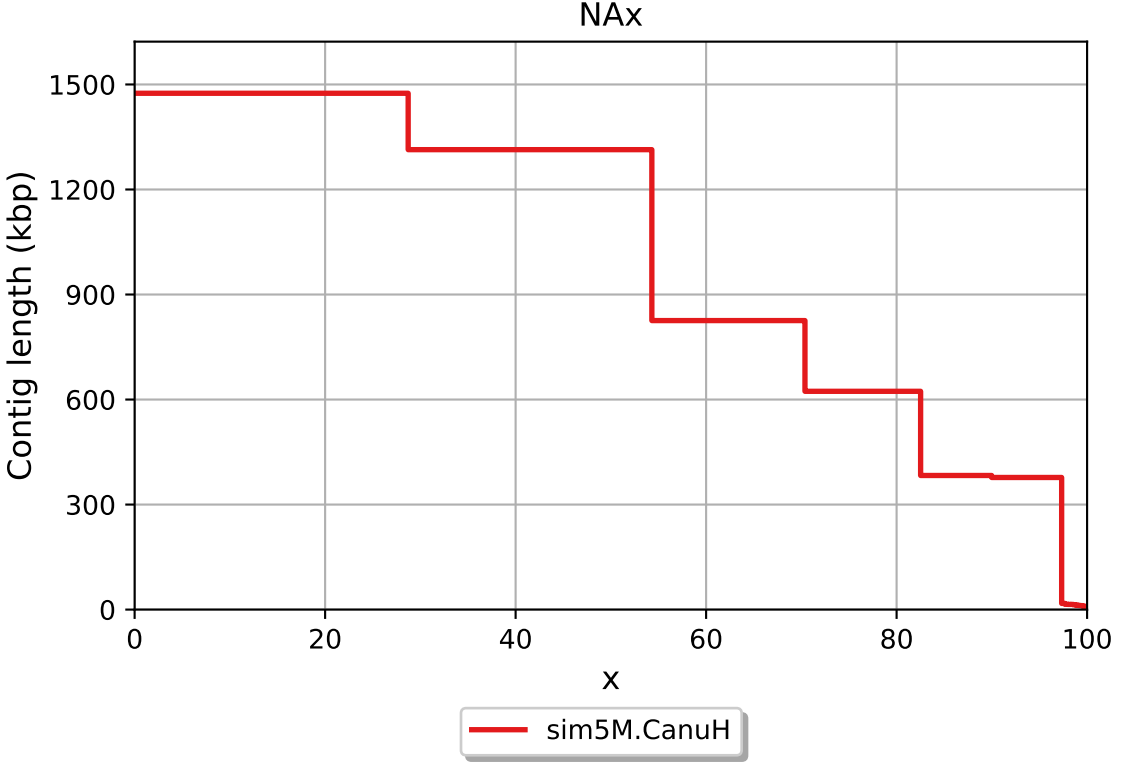

GC content
windows
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
sim5M.CanuH
Reference

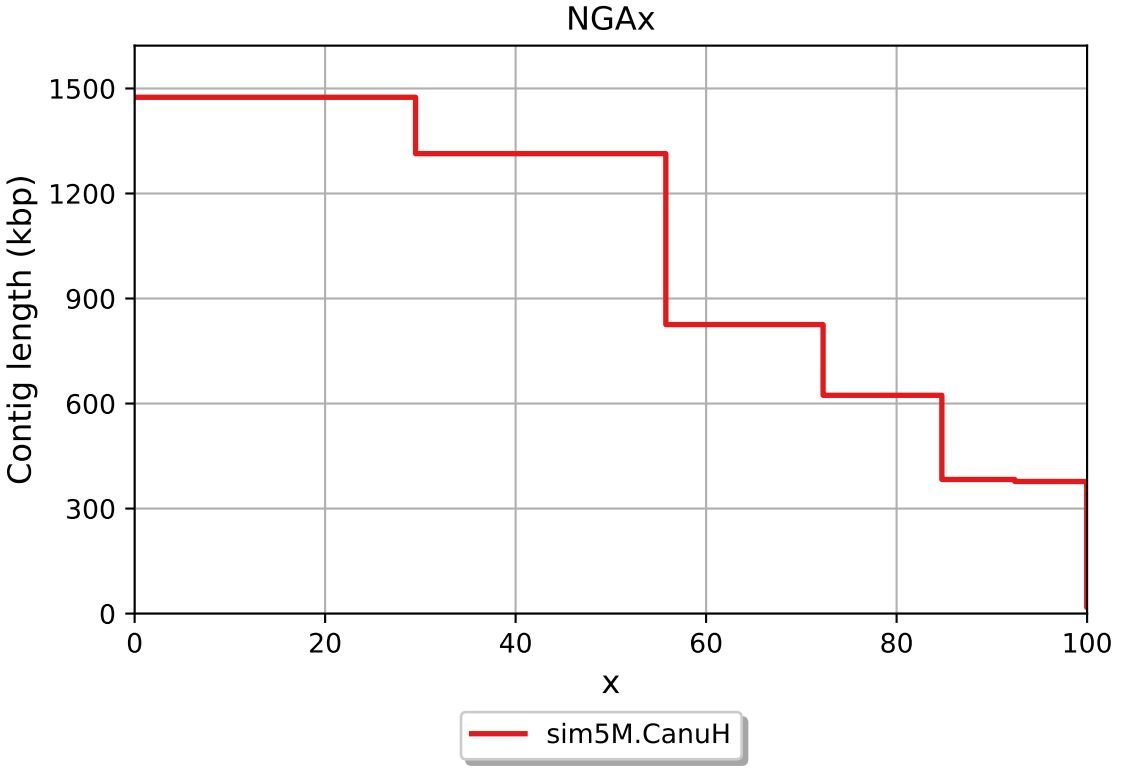

sim5M.CanuH GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
sim5M.CanuH


Misassemblies
5
4
3
2
1
0
sim5M.CanuH


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
sim5M.CanuH


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
3
6
9
12
15
Contig index
sim5M.CanuH
Reference


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
sim5M.CanuH


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
sim5M.CanuH