

Report

	sim25M.CanuH
# contigs (>= 0 bp)	182
# contigs (>= 1000 bp)	182
# contigs (>= 5000 bp)	181
# contigs (>= 10000 bp)	157
# contigs (>= 25000 bp)	82
# contigs (>= 50000 bp)	58
Total length (>= 0 bp)	26035048
Total length (>= 1000 bp)	26035048
Total length (>= 5000 bp)	26030864
Total length (>= 10000 bp)	25835536
Total length (>= 25000 bp)	24819217
Total length (>= 50000 bp)	23943432
# contigs	182
Largest contig	1544089
Total length	26035048
Reference length	25000020
GC (%)	43.68
Reference GC (%)	43.69
N50	556356
NG50	644130
N75	303817
NG75	326121
L50	15
LG50	14
L75	30
LG75	27
# 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 (%)	99.266
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.05
# indels per 100 kbp	3.92
Largest alignment	1544089
Total aligned length	26035008
NA50	556355
NGA50	644130
NA75	303817
NGA75	326121
LA50	15
LGA50	14
LA75	30
LGA75	27

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

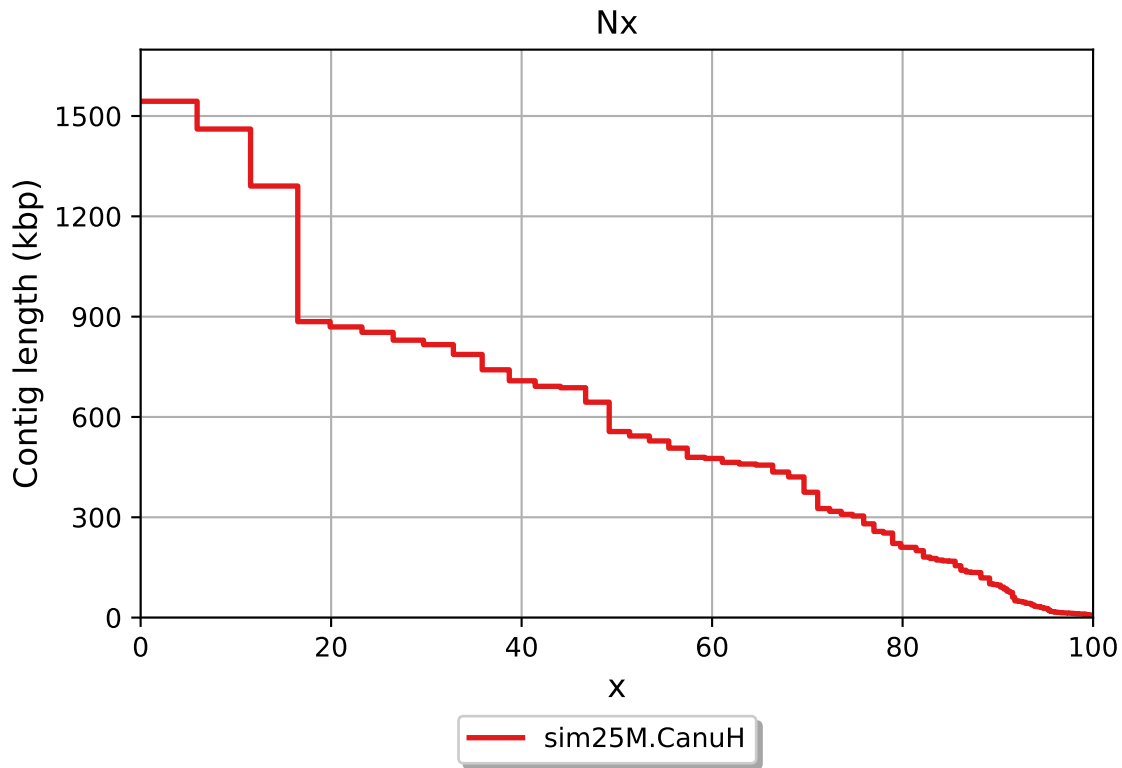
	sim25M.CanuH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	261
# indels	974
# indels (<= 5 bp)	974
# indels (> 5 bp)	0
Indels length	1059

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).

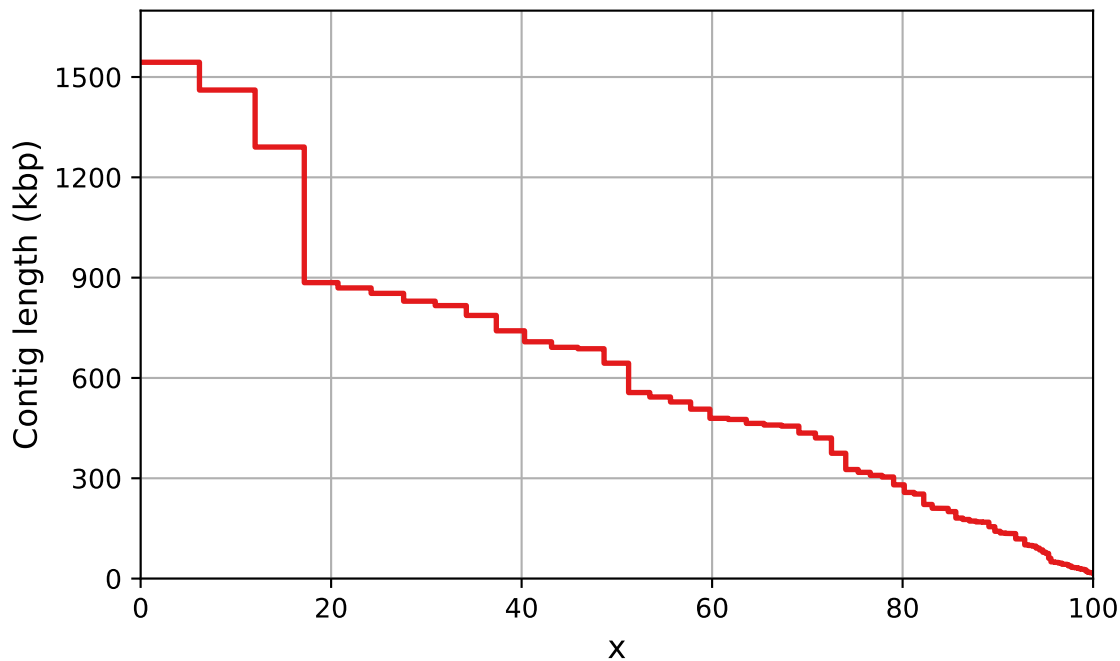
Unaligned report

	sim25M.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).

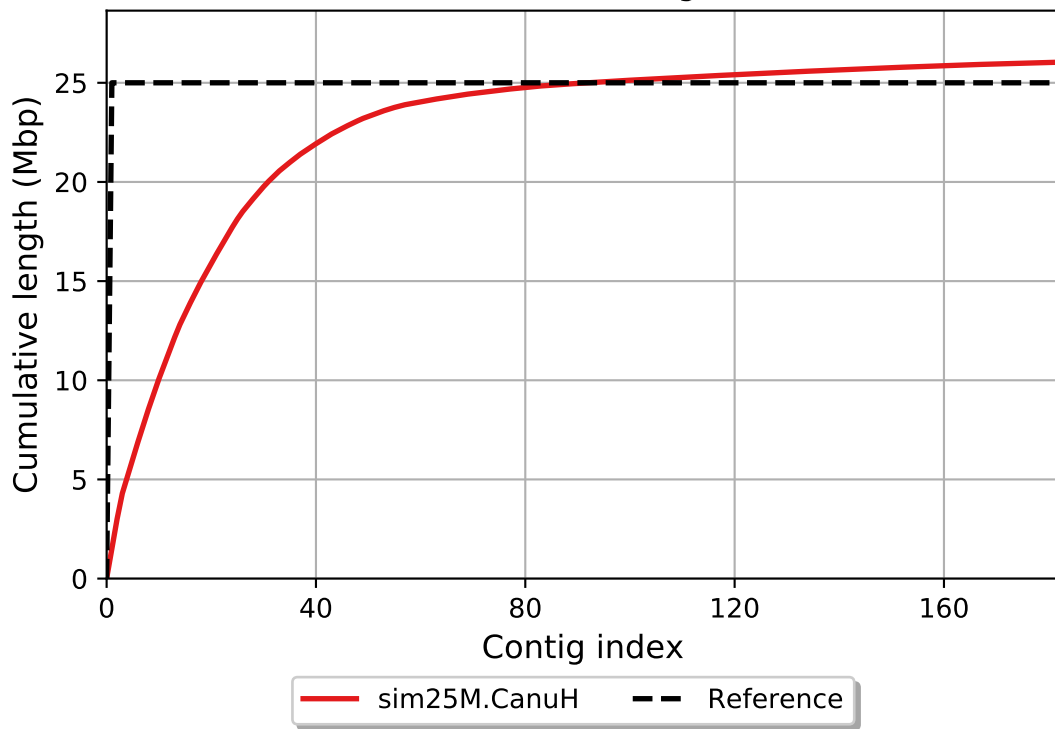


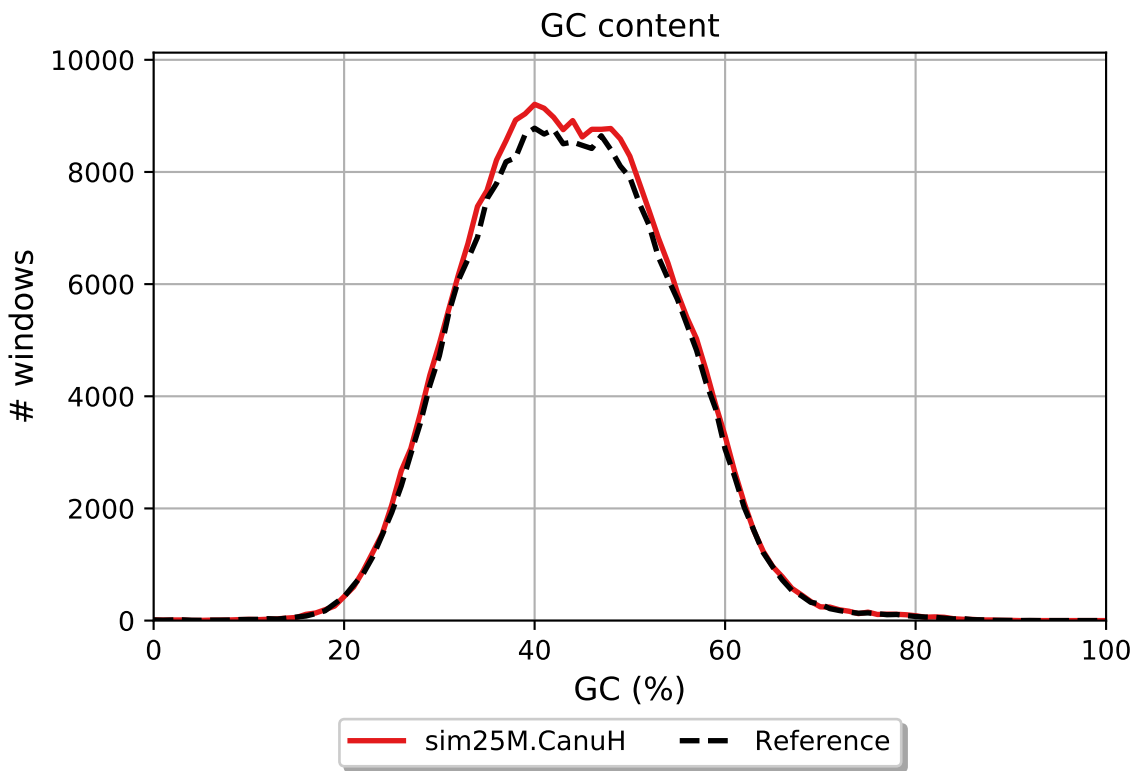
NGx



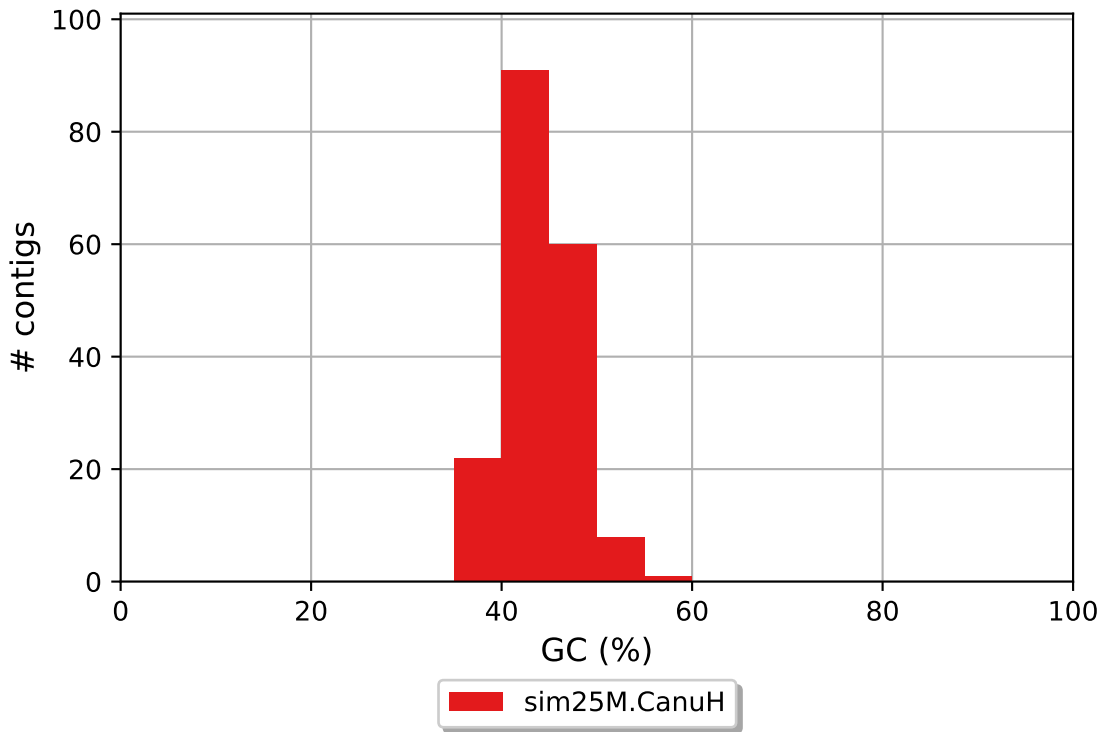
— sim25M.CanuH

Cumulative length





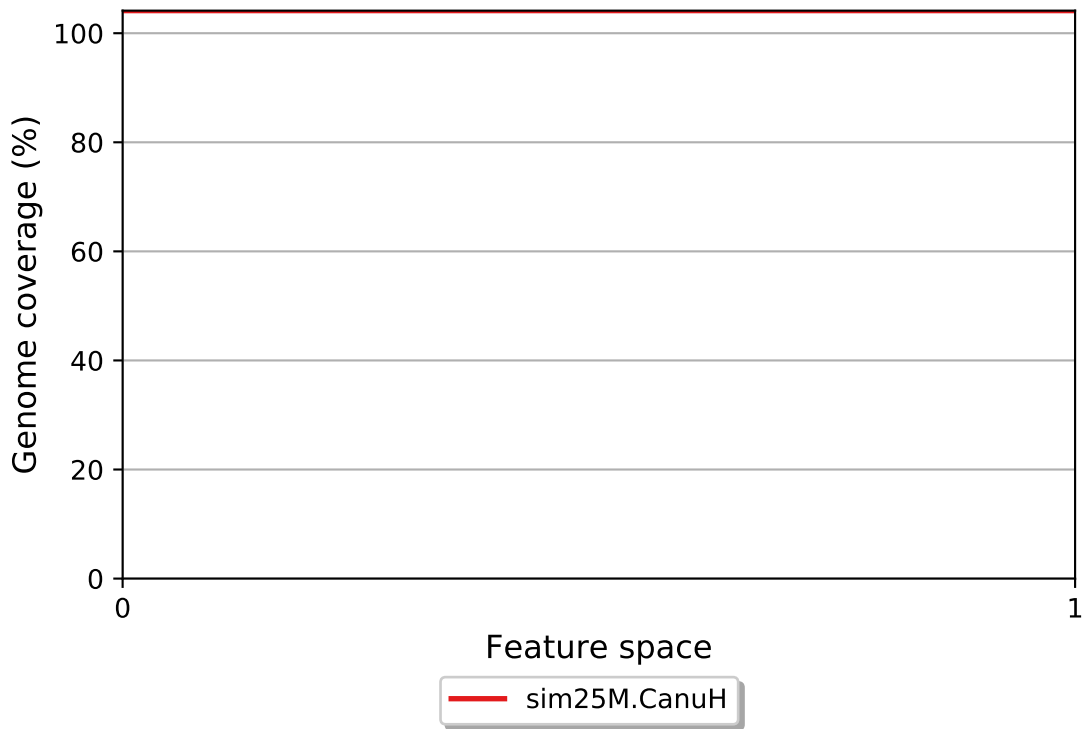
sim25M.CanuH GC content



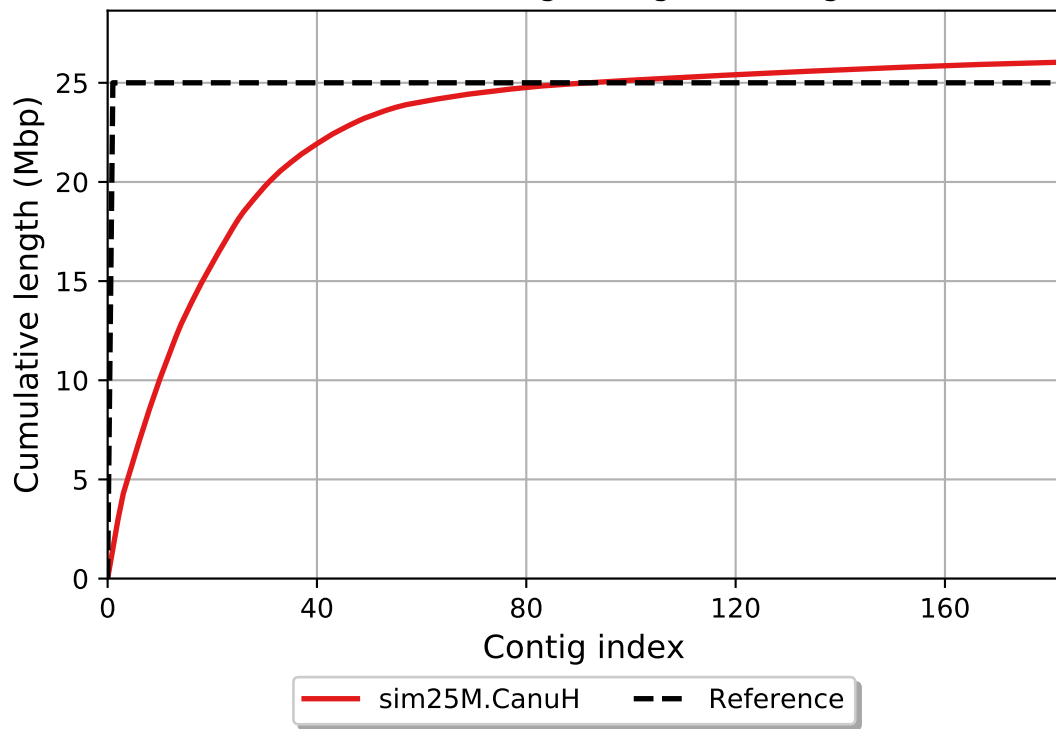
Misassemblies



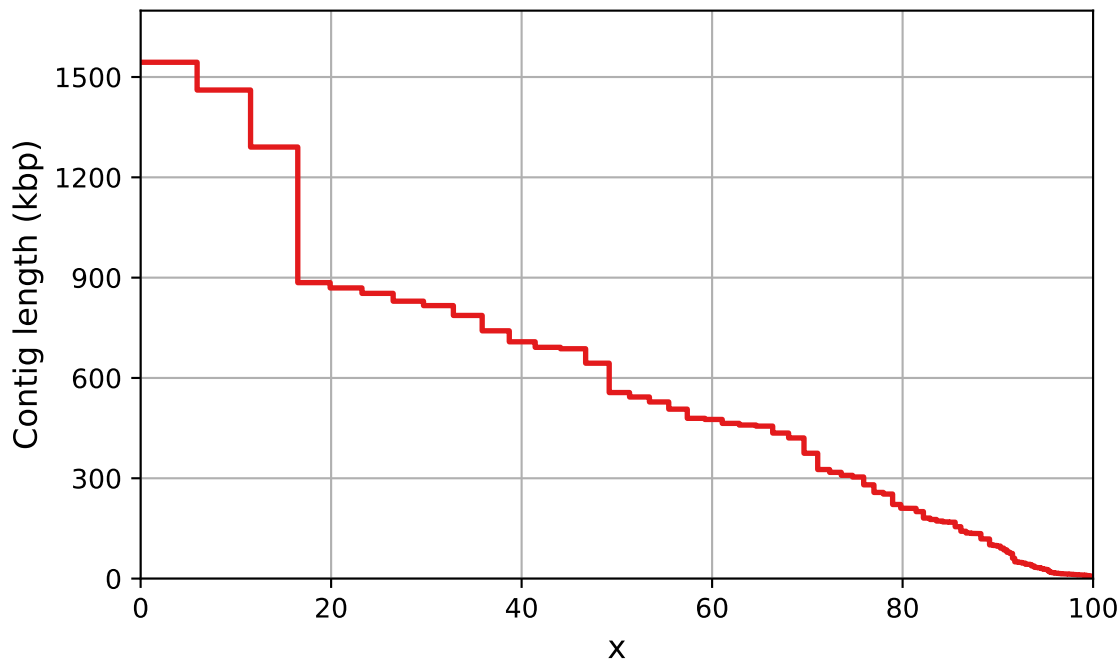
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— sim25M.CanuH

NGAx

