Report

	sim25M.CanuH.p1
# 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)	26034850
Total length (>= 1000 bp)	26034850
Total length (>= 5000 bp)	26030666
Total length (>= 10000 bp)	25835341
Total length (>= 25000 bp)	24819078
Total length (>= 50000 bp)	23943364
# contigs	182
Largest contig	1544088
Total length	26034850
Reference length	25000020
GC (%)	43.68
Reference GC (%)	43.69
N50	556355
NG50	644129
N75	303814
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	0.94
# indels per 100 kbp	1.78
Largest alignment	1544088
Total aligned length	26034810
NA50	556354
NGA50	644129
NA75	303814
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

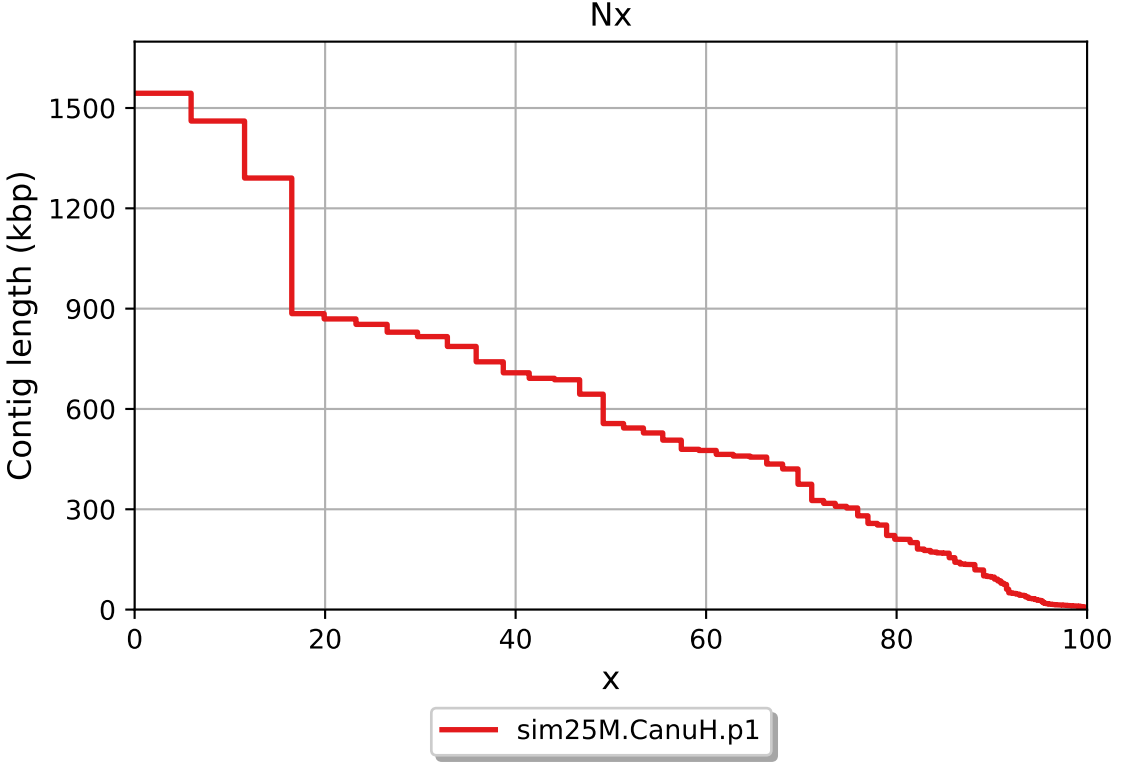
	sim25M.CanuH.p1
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	233
# indels	442
# indels (<= 5 bp)	440
# indels (> 5 bp)	2
Indels length	514

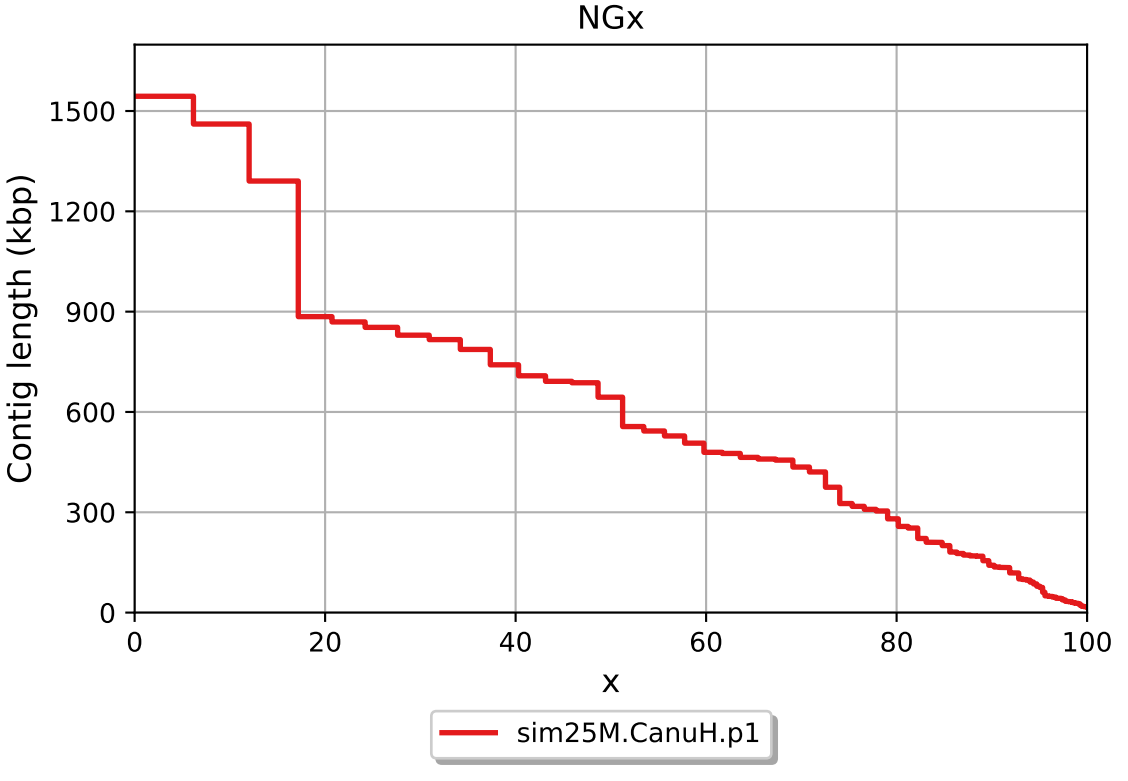
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

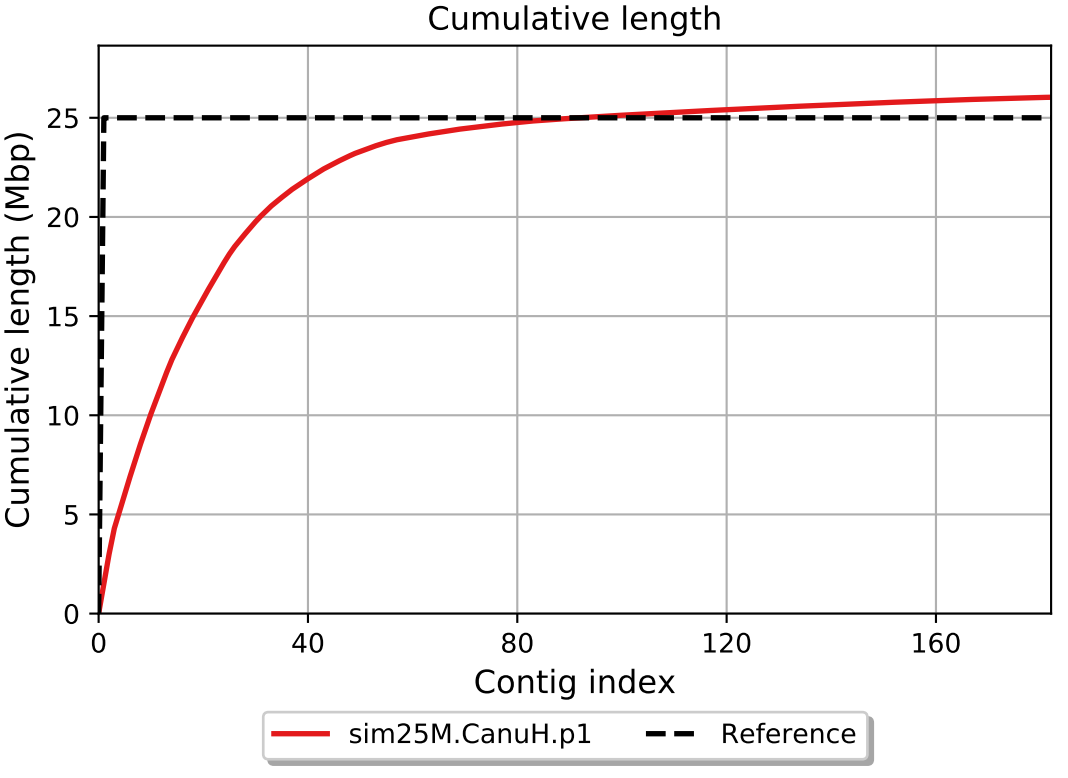
Unaligned report

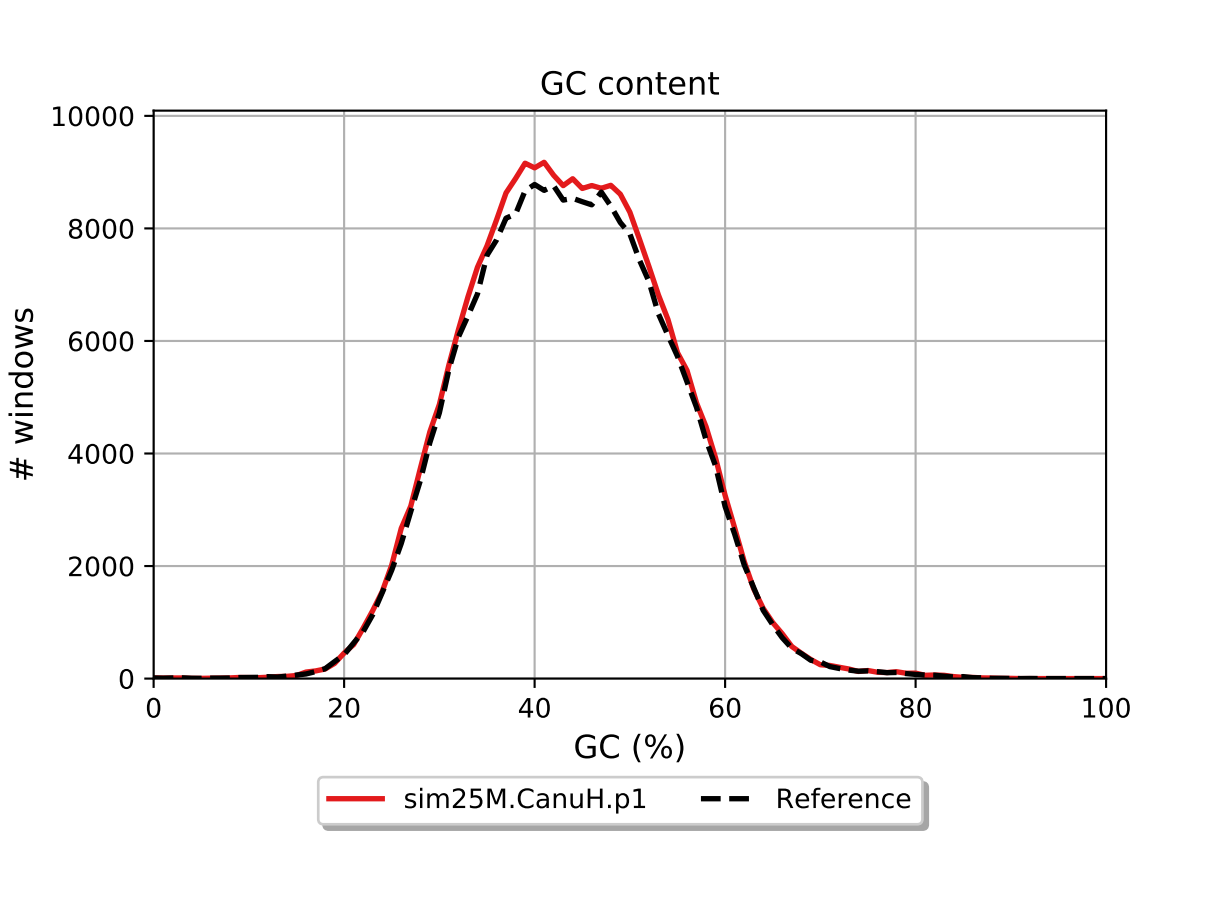
	sim25M.CanuH.p1
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

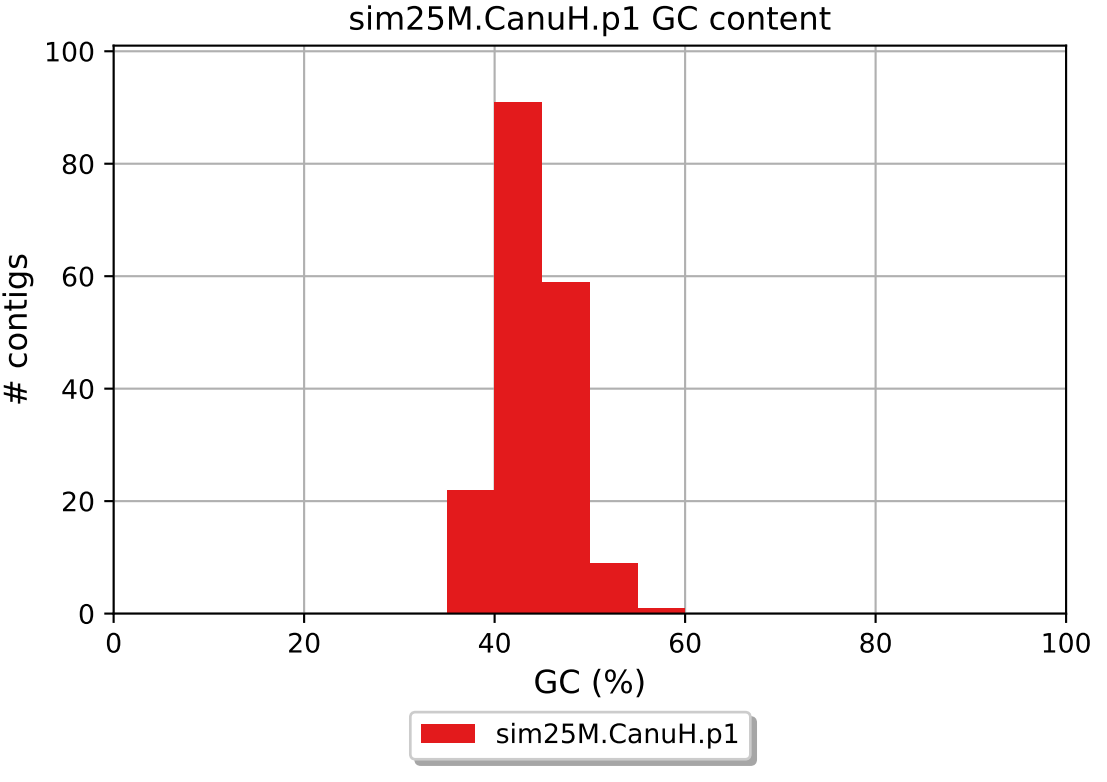
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
sim25M.CanuH.p1

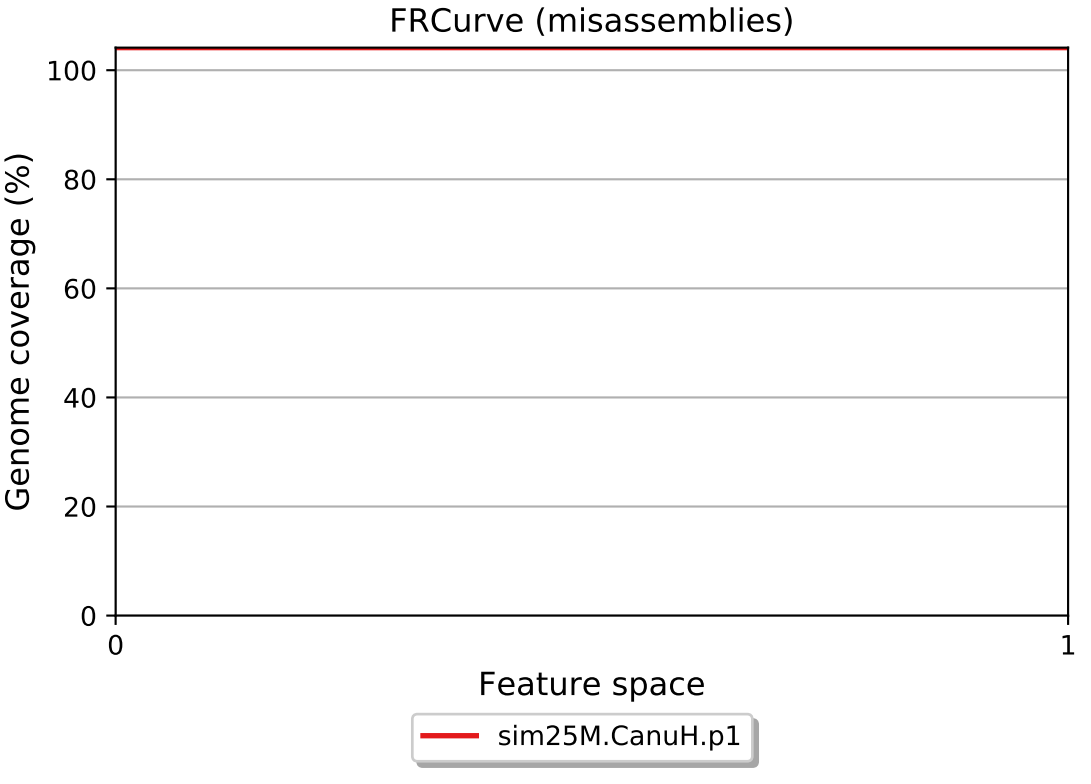

NGx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
sim25M.CanuH.p1

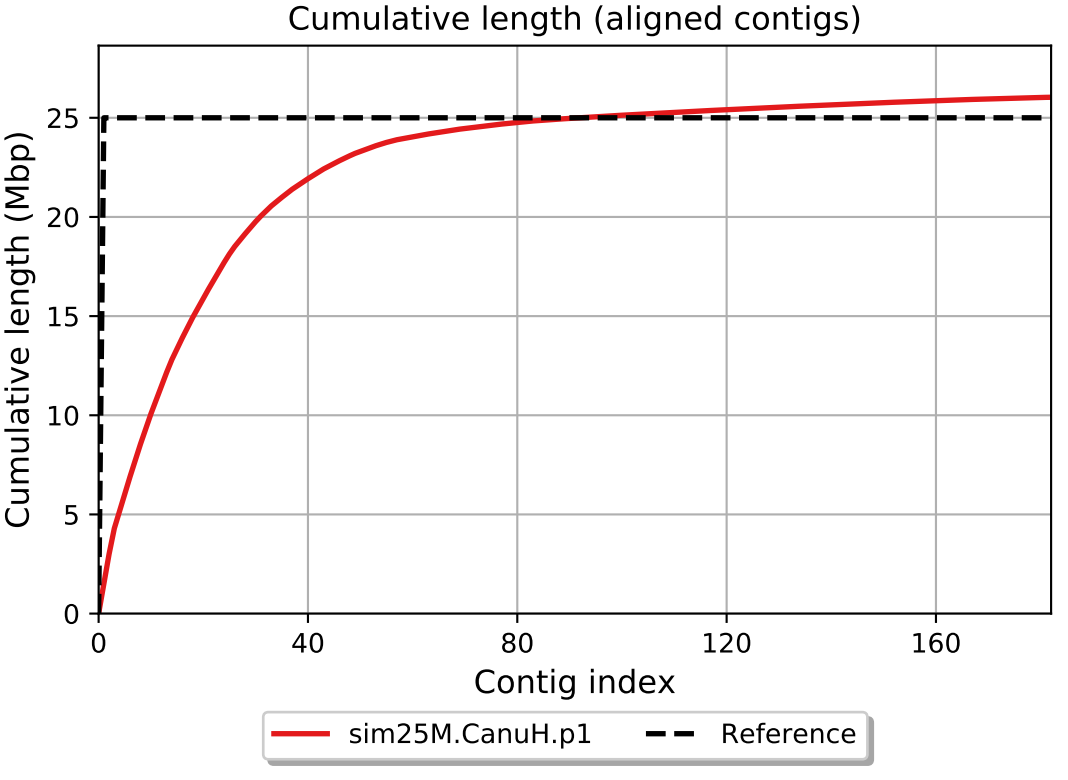

Cumulative length
Cumulative length (Mbp)
0
5
10
15
20
25
0
40
80
120
160
Contig index
sim25M.CanuH.p1
Reference

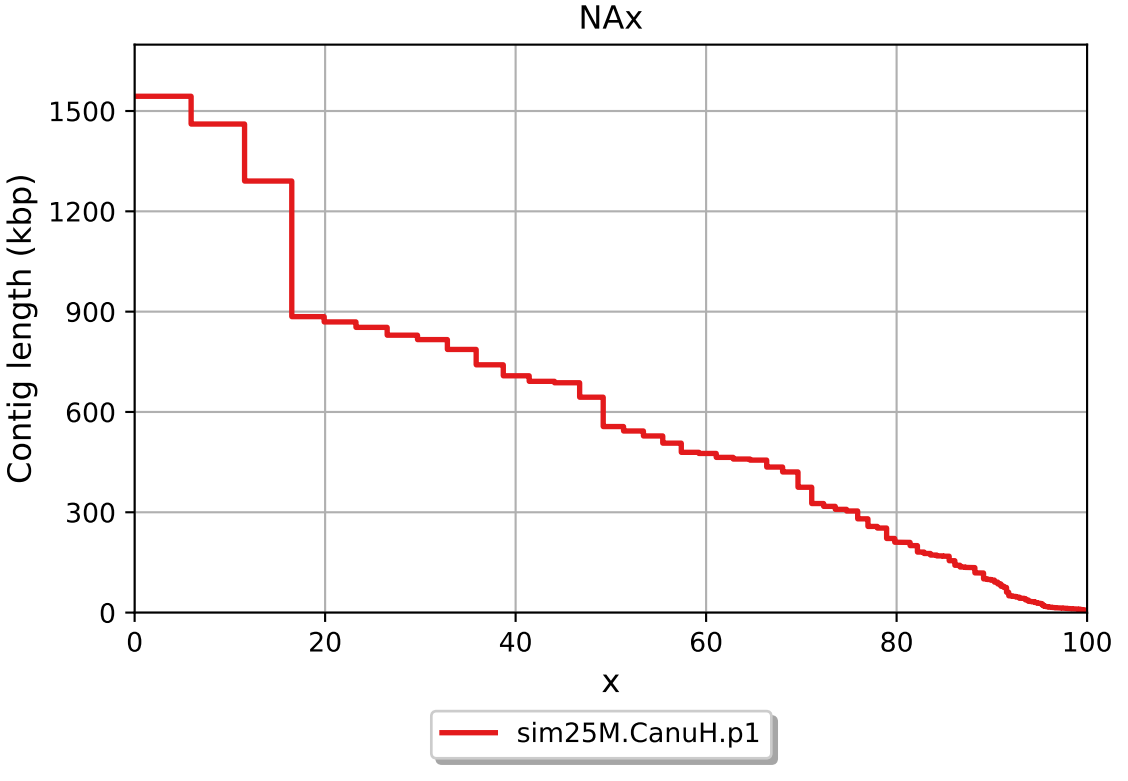

GC content
10000
8000
6000
4000
2000
0
windows
0
20
40
60
80
100
GC (%)
sim25M.CanuH.p1
Reference

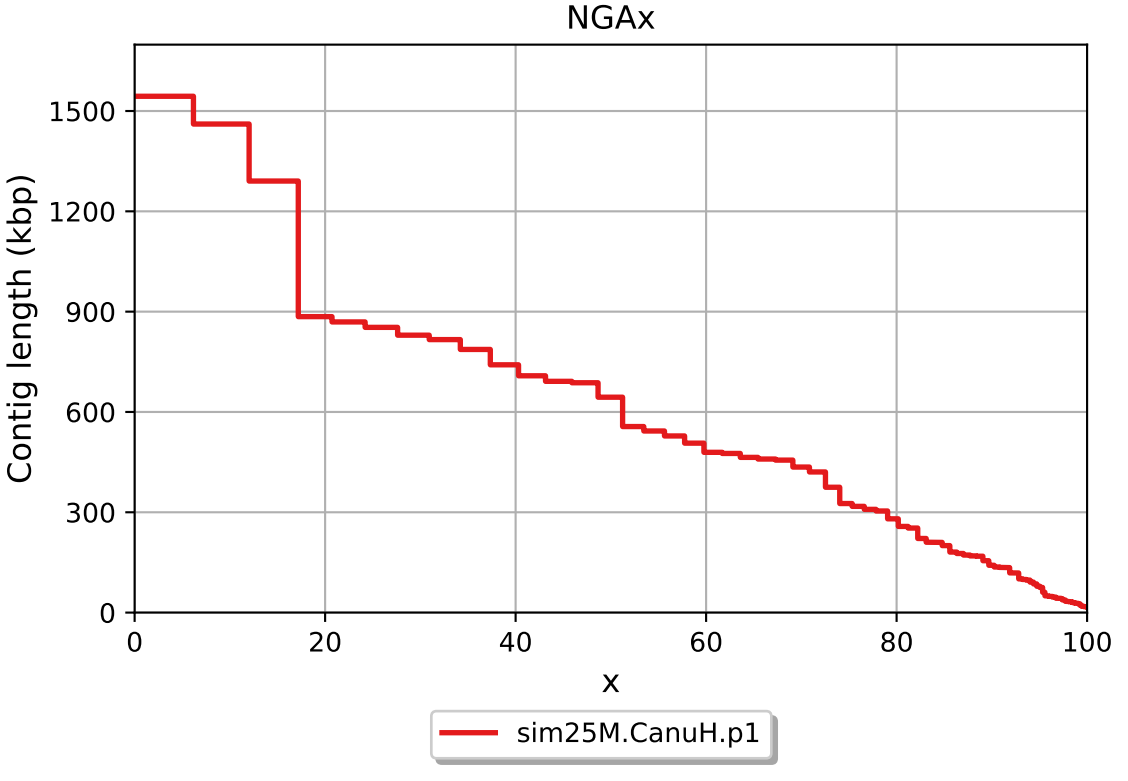

sim25M.CanuH.p1 GC content
contigs
GC (%)
0
20
40
60
80
100
sim25M.CanuH.p1

Misassemblies
5
4
3
2
1
0
sim25M.CanuH.p1


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
sim25M.CanuH.p1


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
5
10
15
20
25
0
40
80
120
160
Contig index
sim25M.CanuH.p1
Reference


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
sim25M.CanuH.p1


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
sim25M.CanuH.p1