Report

	sim25M.CanuL.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1800
# contigs (>= 5000 bp)	1384
# contigs (>= 10000 bp)	423
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	13804774
Total length (>= 1000 bp)	13751456
Total length (>= 5000 bp)	12332410
Total length (>= 10000 bp)	5220112
Total length (>= 25000 bp)	27290
Total length (>= 50000 bp)	0
# contigs	1827
Largest contig	27290
Total length	13771338
Reference length	25000020
GC (%)	43.80
Reference GC (%)	43.69
N50	8908
NG50	4760
N75	6712
L50	600
LG50	1419
L75	1043
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	36 + 2 part
Unaligned length	137327
Genome fraction (%)	41.056
Duplication ratio	1.328
# N's per 100 kbp	0.00
# mismatches per 100 kbp	89.88
# indels per 100 kbp	314.12
Largest alignment	27290
Total aligned length	13626586
NA50	8884
NGA50	4658
NA75	6678
LA50	601
LGA50	1426
LA75	1046

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

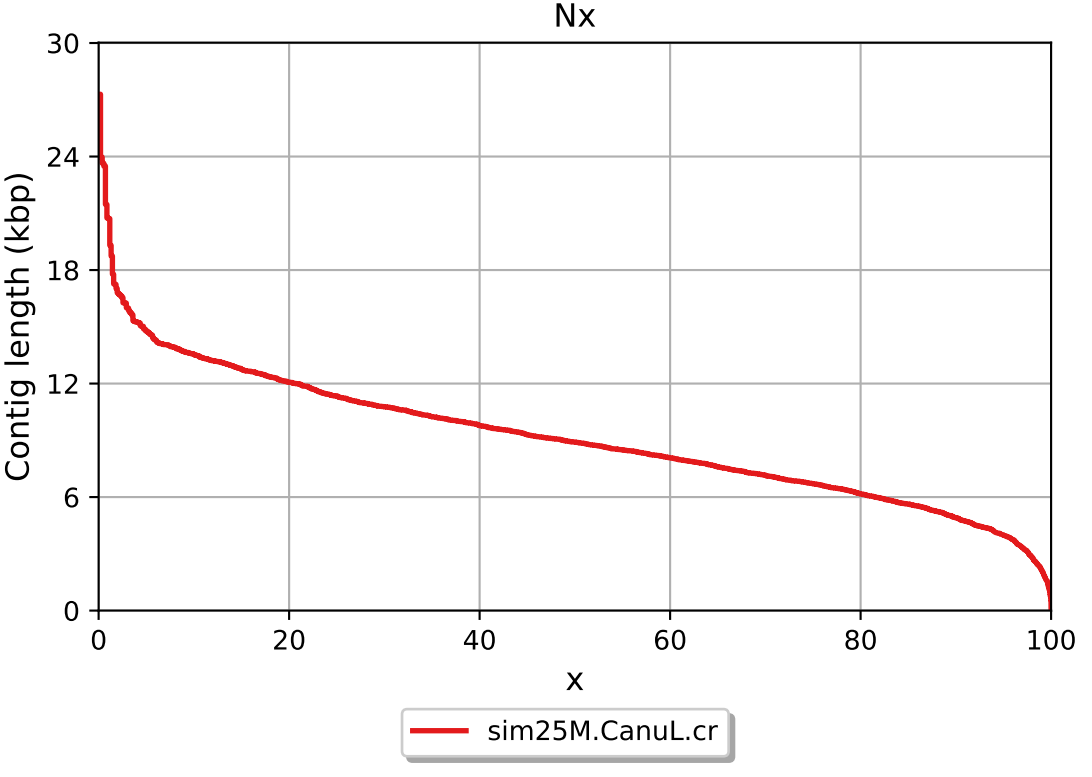
	sim25M.CanuL.cr
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	9225
# indels	32242
# indels (<= 5 bp)	32232
# indels (> 5 bp)	10
Indels length	35250

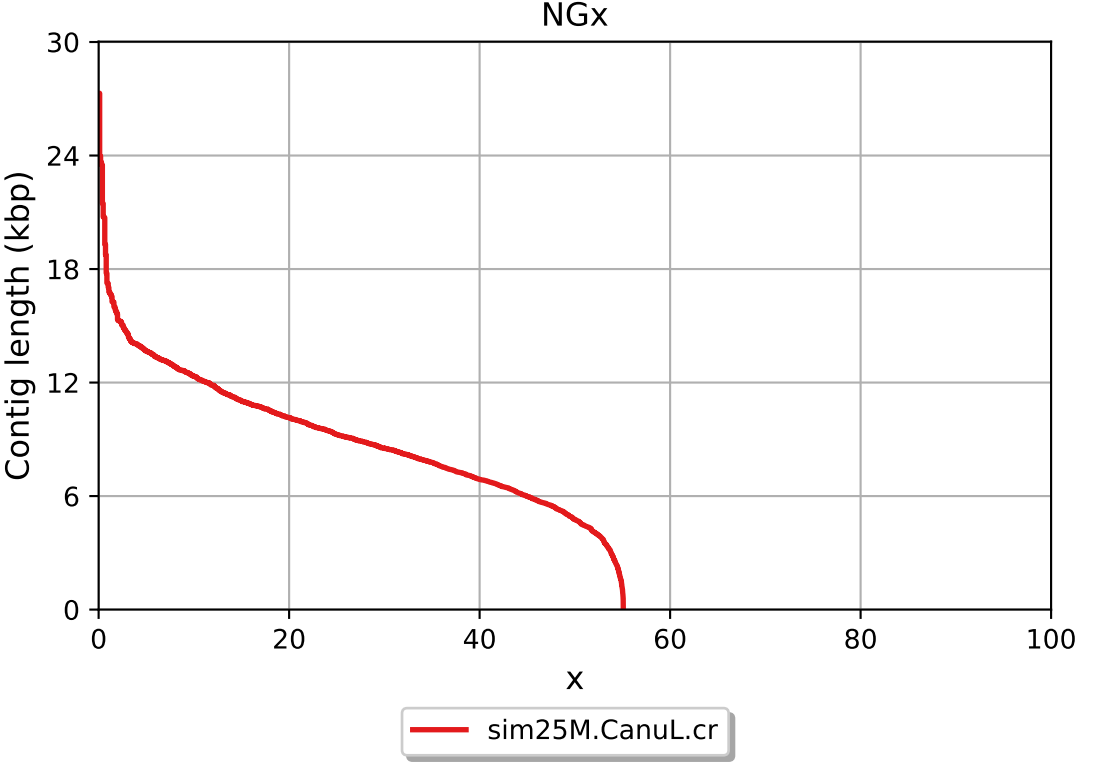
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

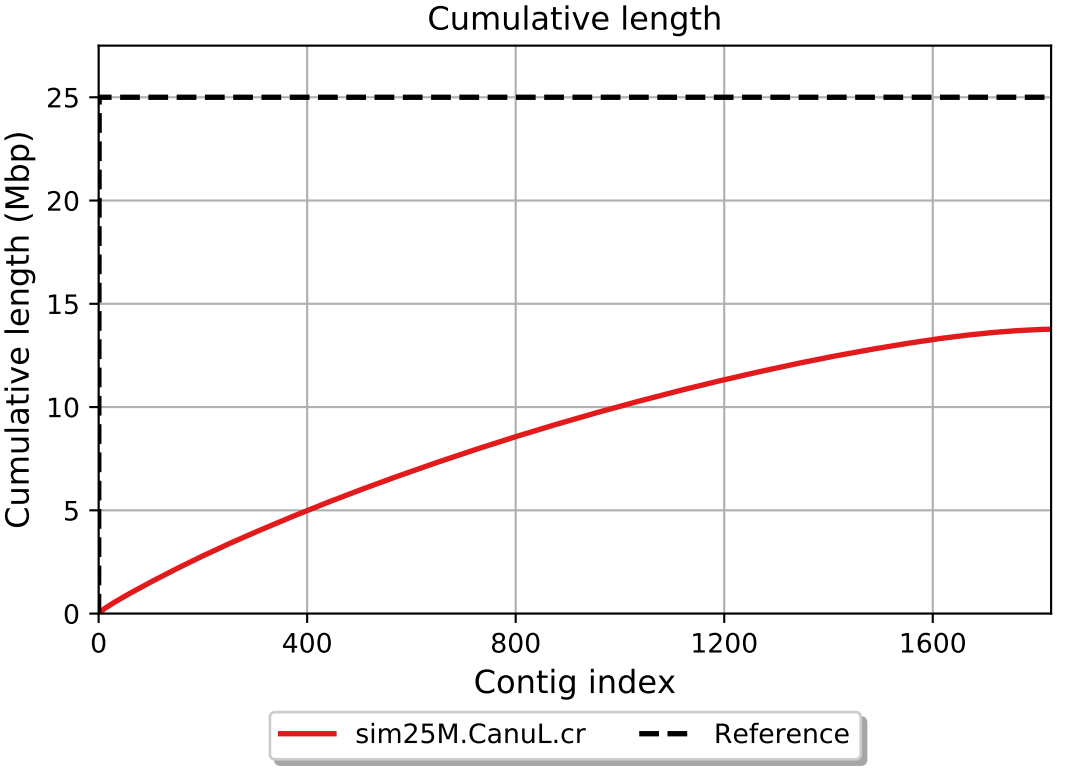
Unaligned report

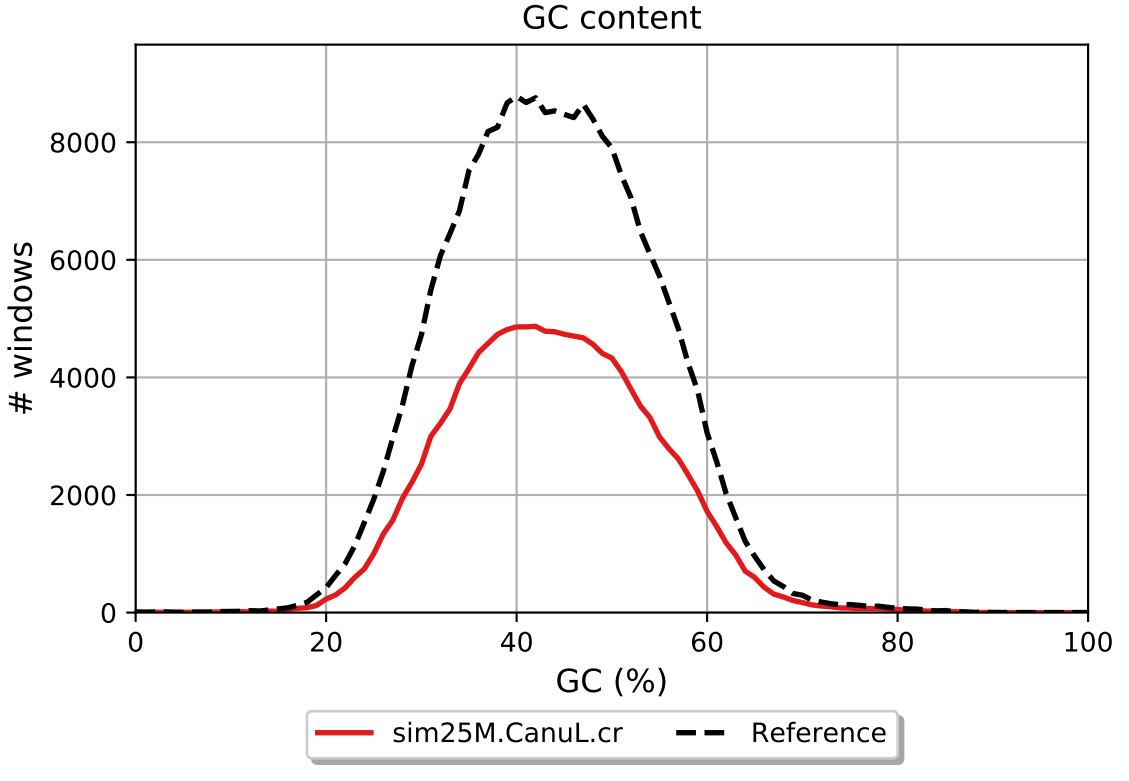
	sim25M.CanuL.cr
# fully unaligned contigs	36
Fully unaligned length	126010
# partially unaligned contigs	2
Partially unaligned length	11317
# N's	0

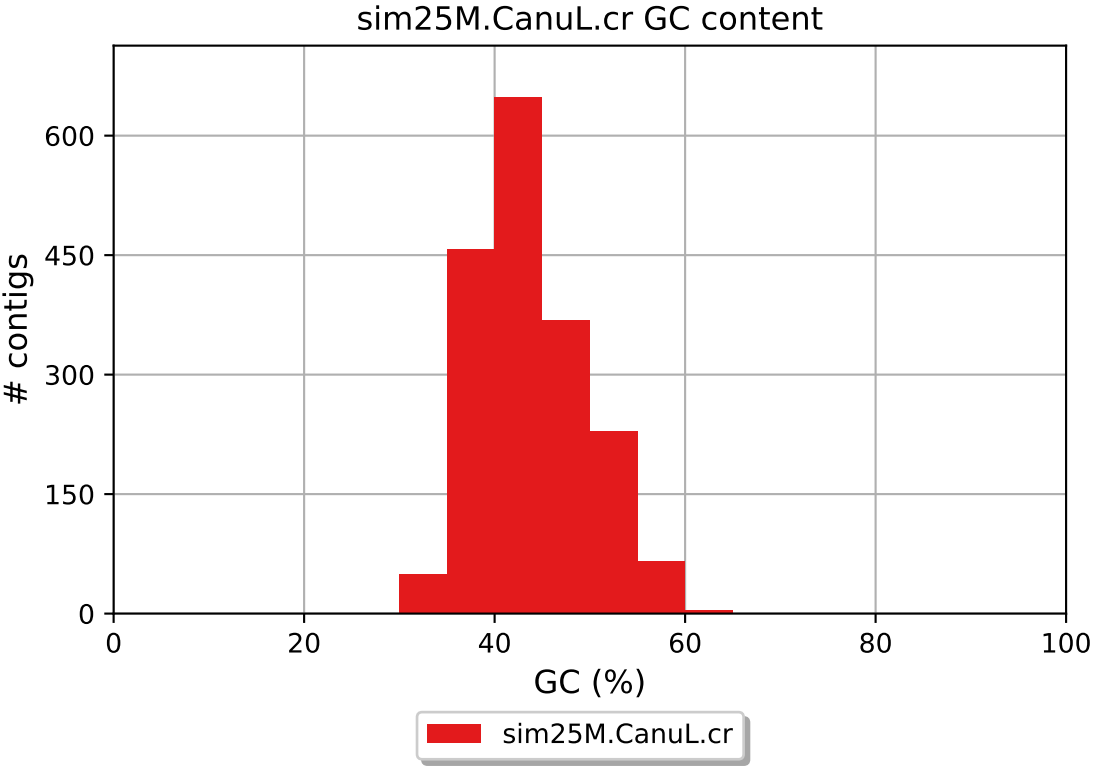
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
sim25M.CanuL.cr

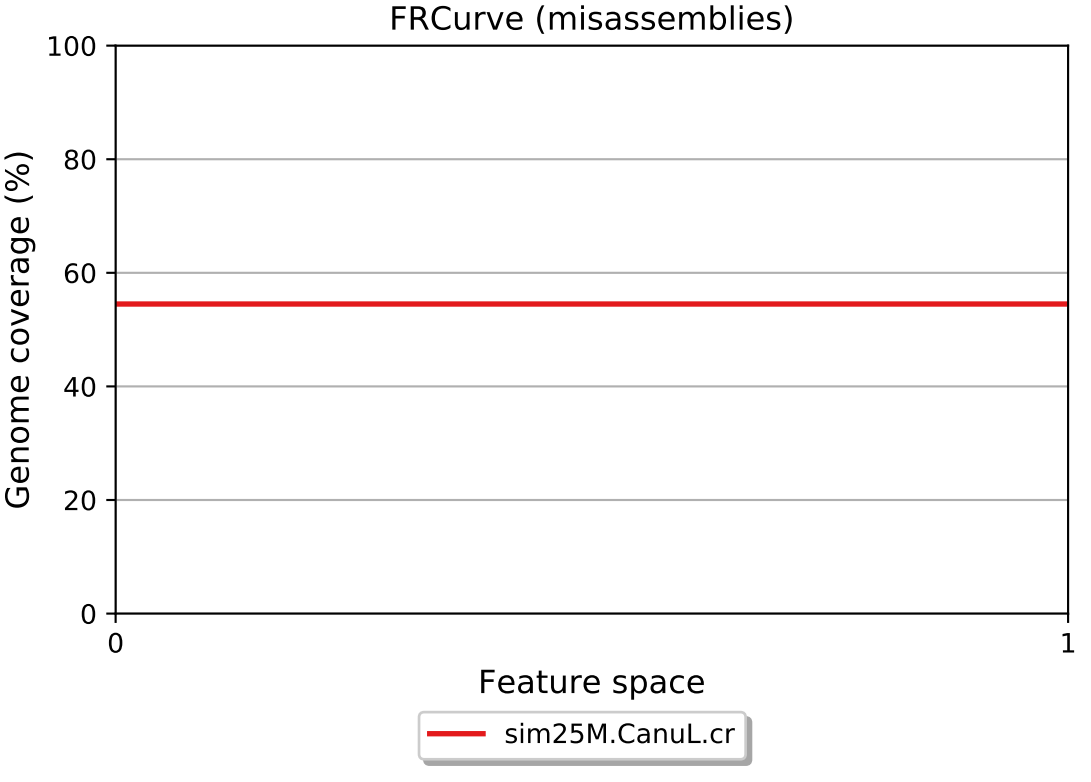

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
sim25M.CanuL.cr

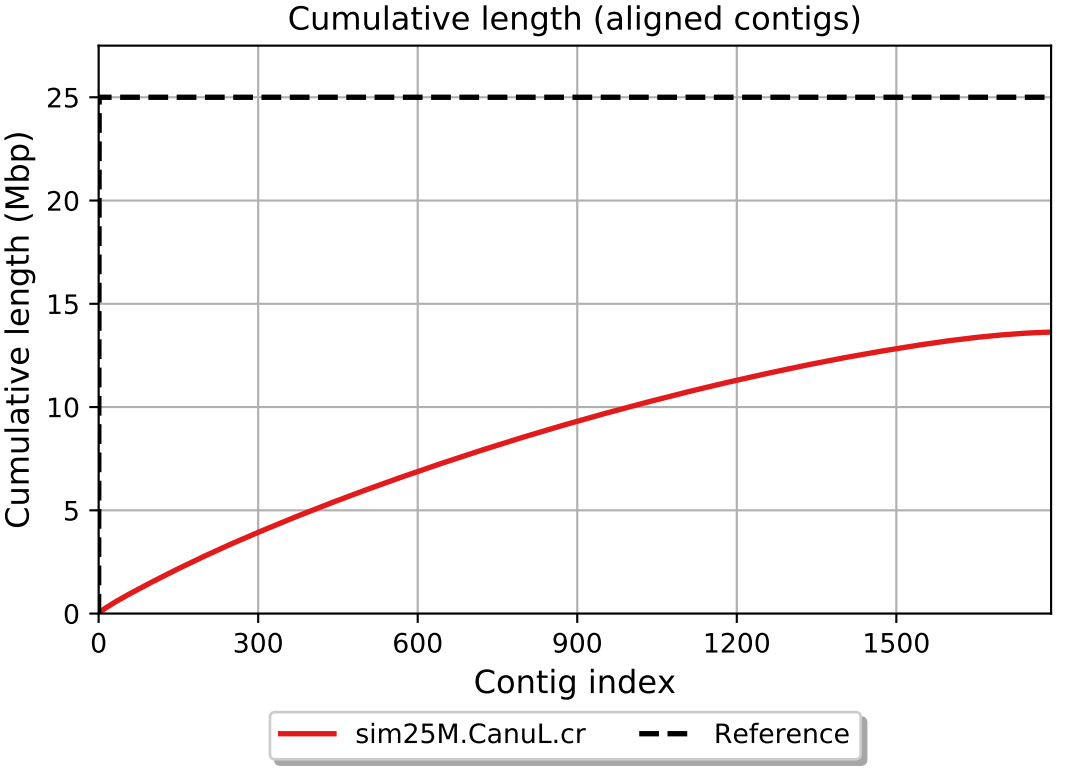

Cumulative length
Cumulative length (Mbp)
25
20
15
10
5
0
0
400
800
1200
1600
Contig index
sim25M.CanuL.cr
Reference

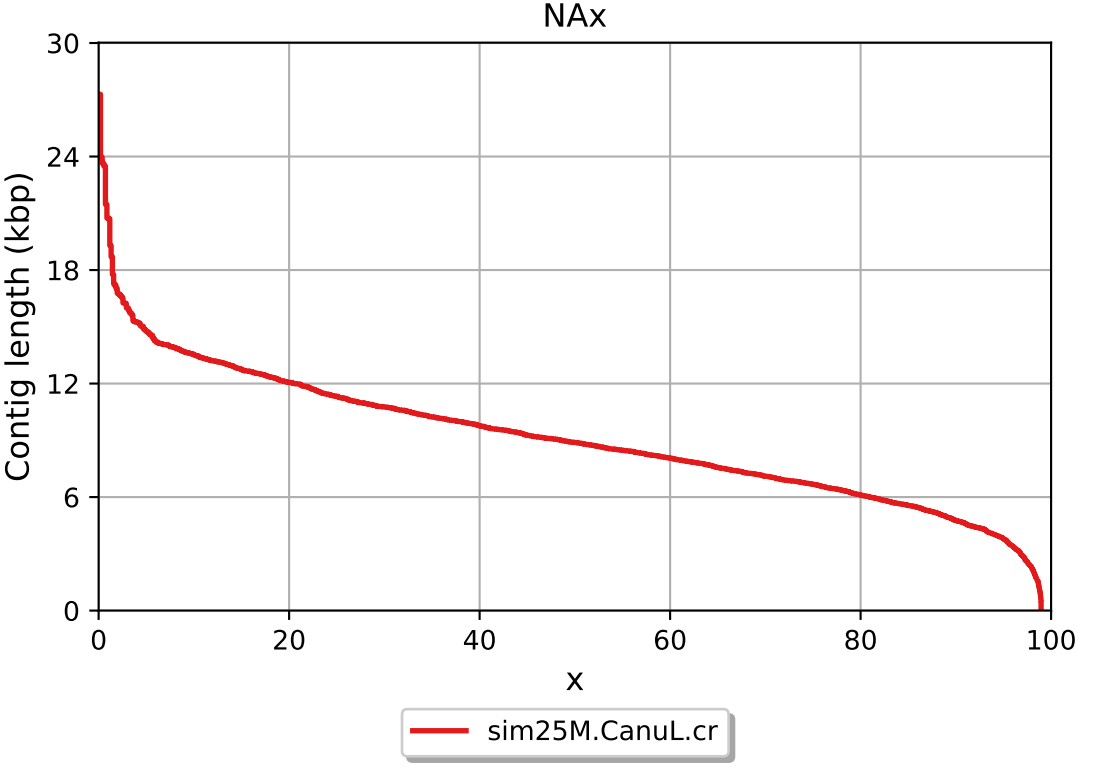

GC content
windows
8000
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
sim25M.CanuL.cr
Reference

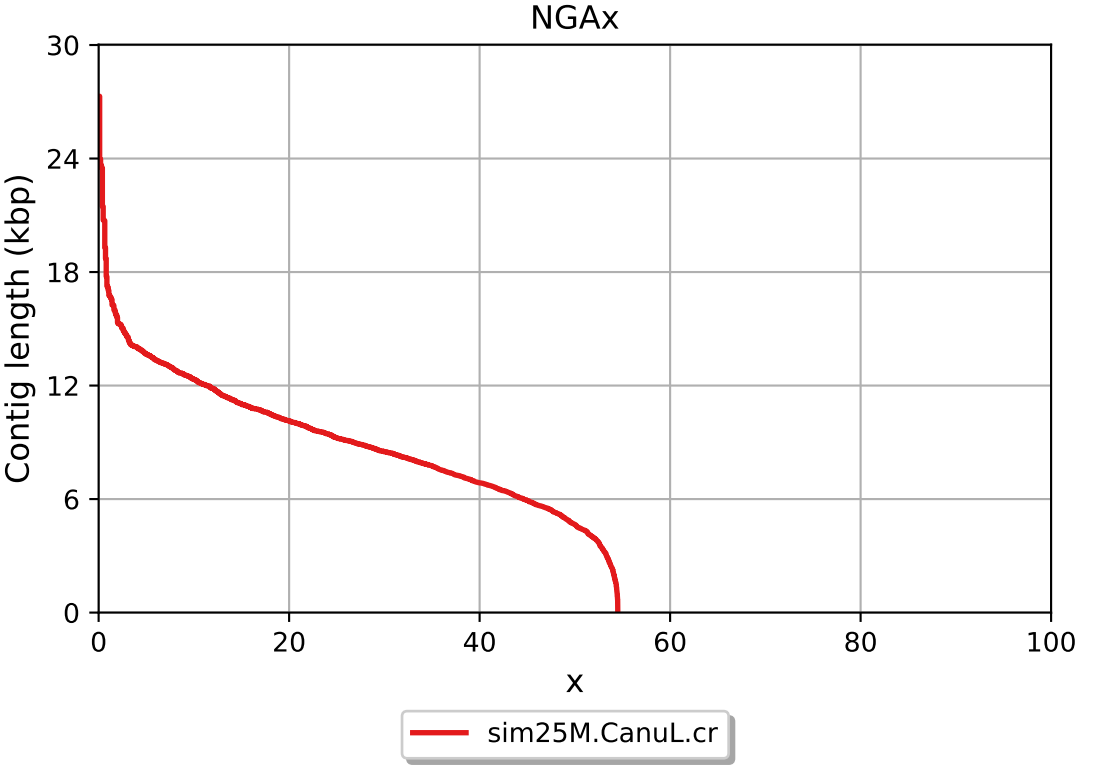

sim25M.CanuL.cr GC content
contigs
0
150
300
450
600
0
20
40
60
80
100
GC (%)
sim25M.CanuL.cr

Misassemblies
5
4
3
2
1
0
sim25M.CanuL.cr


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
25
20
15
10
5
0
0
300
600
900
1200
1500
Contig index
sim25M.CanuL.cr
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
sim25M.CanuL.cr


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
sim25M.CanuL.cr