Report

	sim25M.Metasm
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	18879454
Total length (>= 1000 bp)	18879454
Total length (>= 5000 bp)	18879454
Total length (>= 10000 bp)	18879454
Total length (>= 25000 bp)	18879454
Total length (>= 50000 bp)	18879454
# contigs	1
Largest contig	18879454
Total length	18879454
Reference length	25000020
GC (%)	43.35
Reference GC (%)	43.69
N50	18879454
NG50	18879454
N75	18879454
NG75	18879454
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	20
# misassembled contigs	1
Misassembled contigs length	18879454
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	5.844
Duplication ratio	12.922
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.48
# indels per 100 kbp	1.98
Largest alignment	1459426
Total aligned length	18879454
NA50	1429087
NGA50	779223
NA75	646263
NGA75	402579
LA50	7
LGA50	10
LA75	12
LGA75	21

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

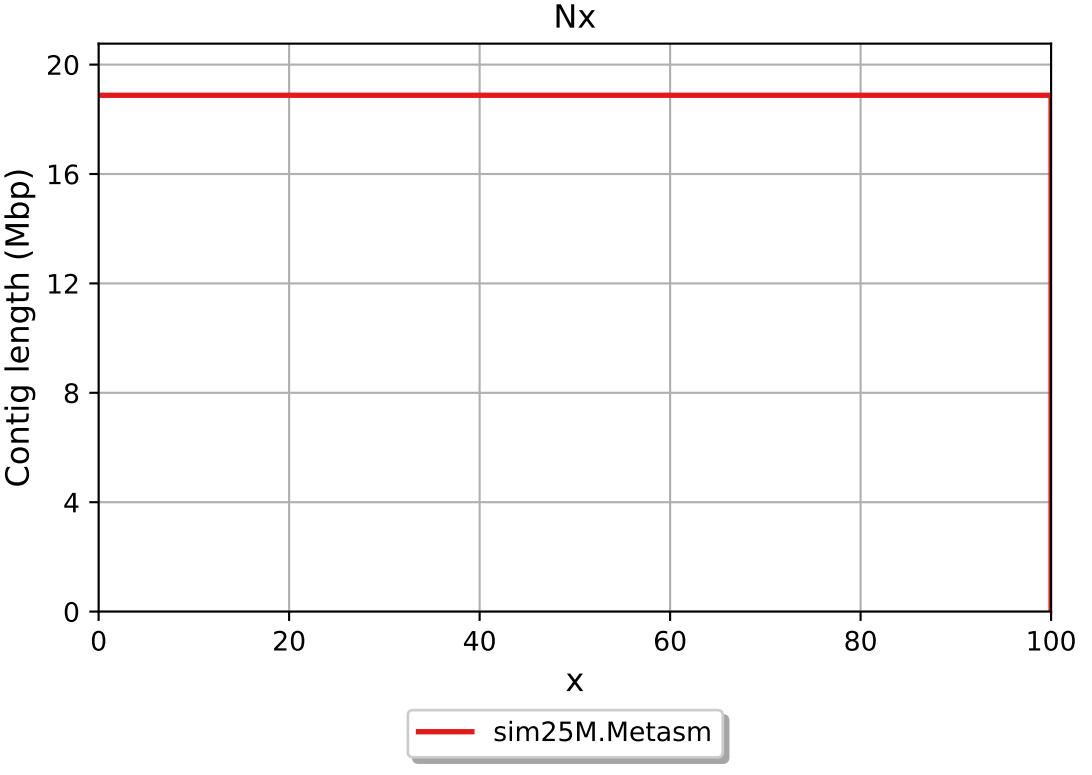
	sim25M.Metasm
# misassemblies	20
# relocations	20
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	18879454
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	7
# indels	29
# indels (<= 5 bp)	29
# indels (> 5 bp)	0
Indels length	31

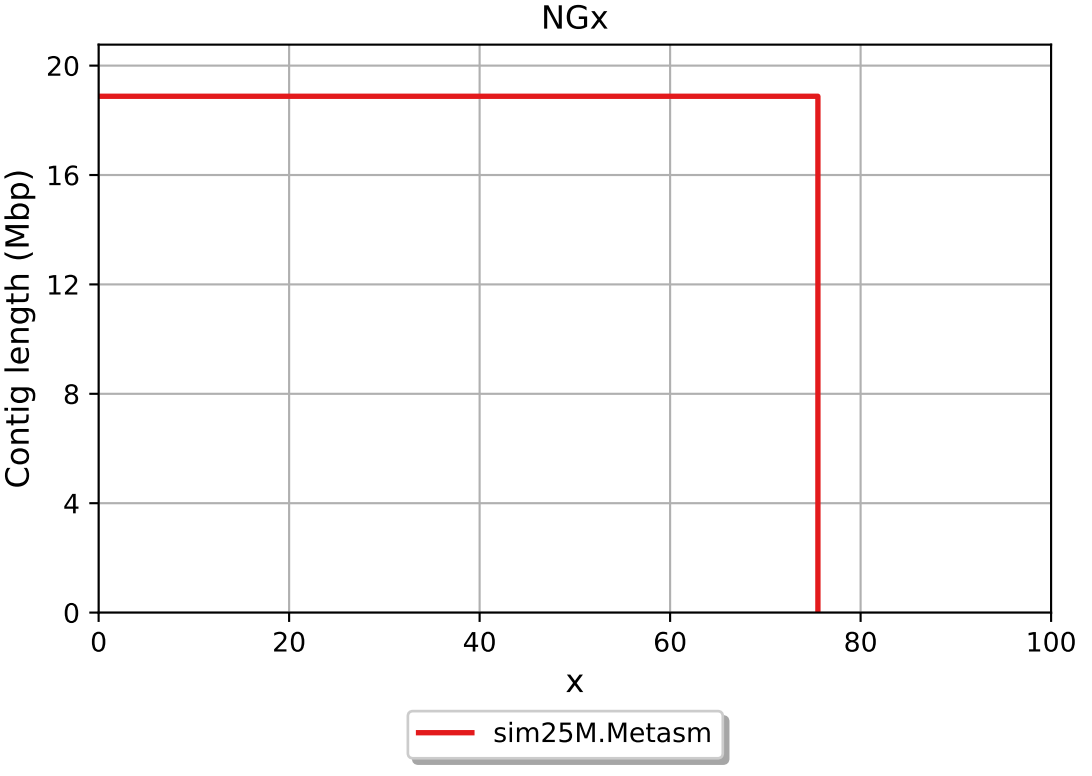
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

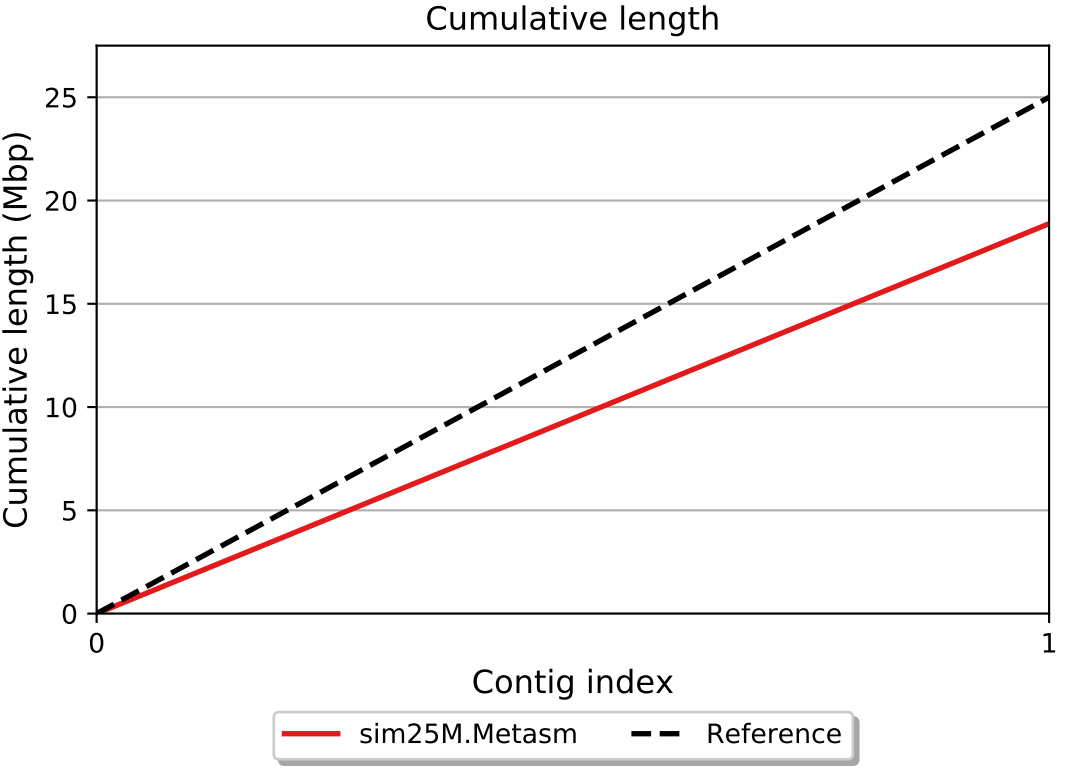
Unaligned report

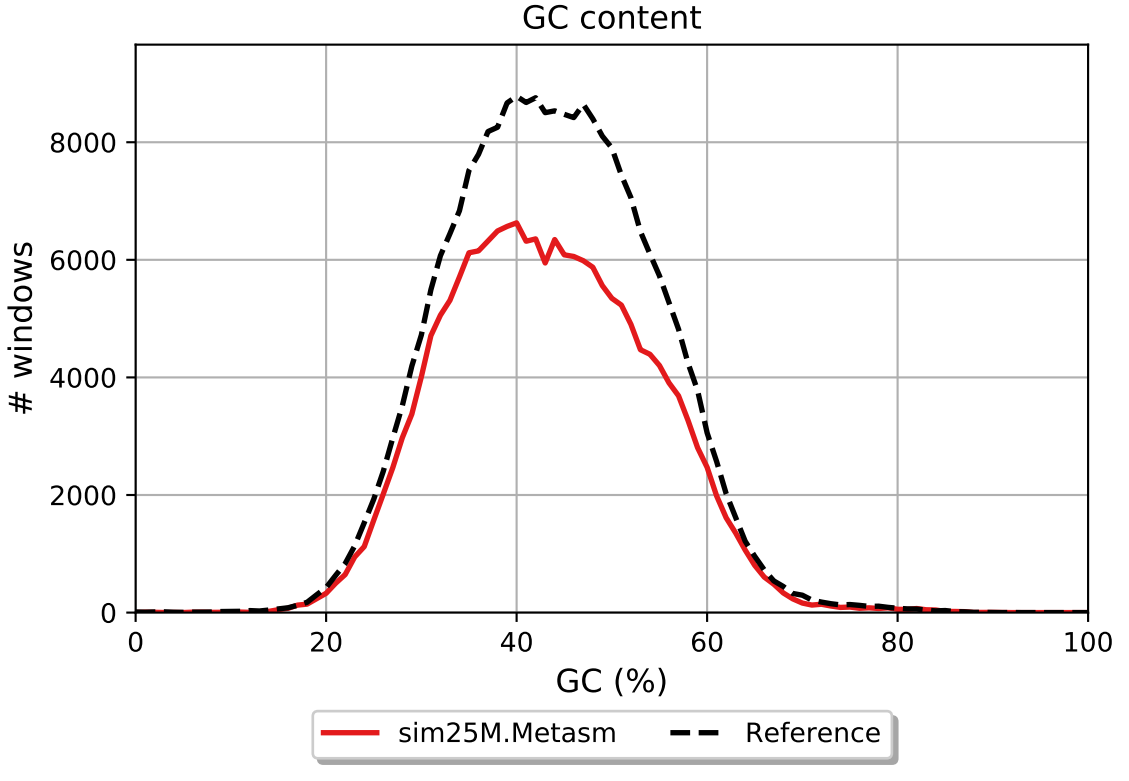
	sim25M.Metasm
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

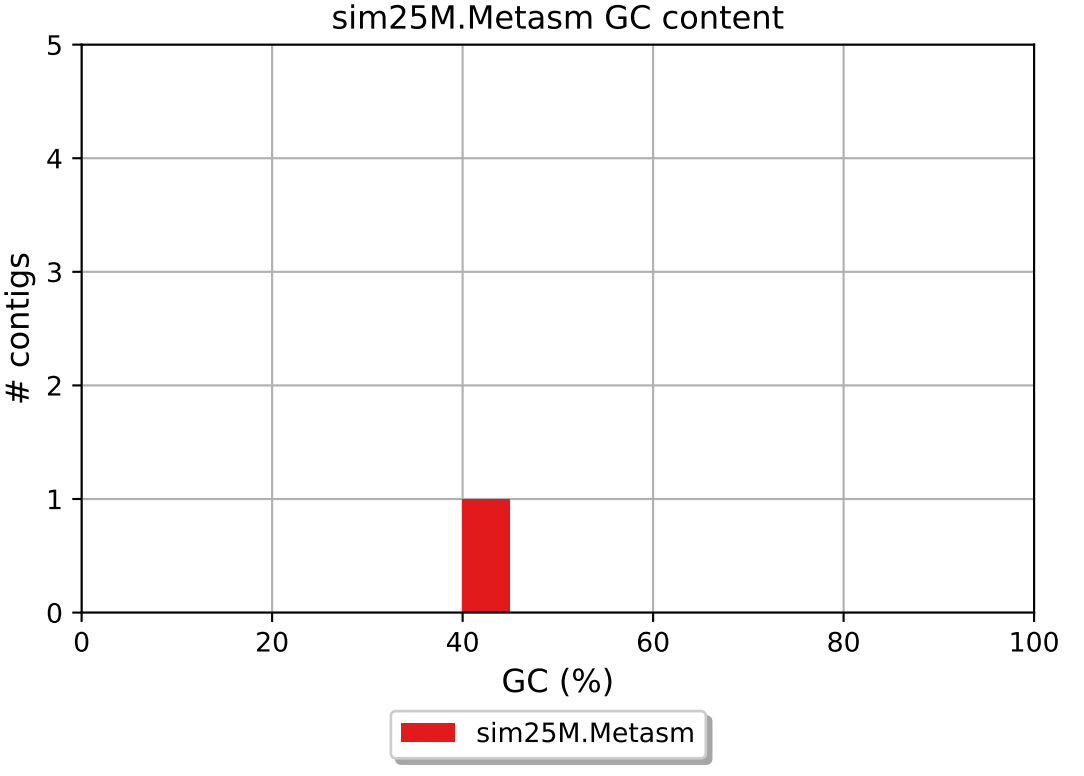
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

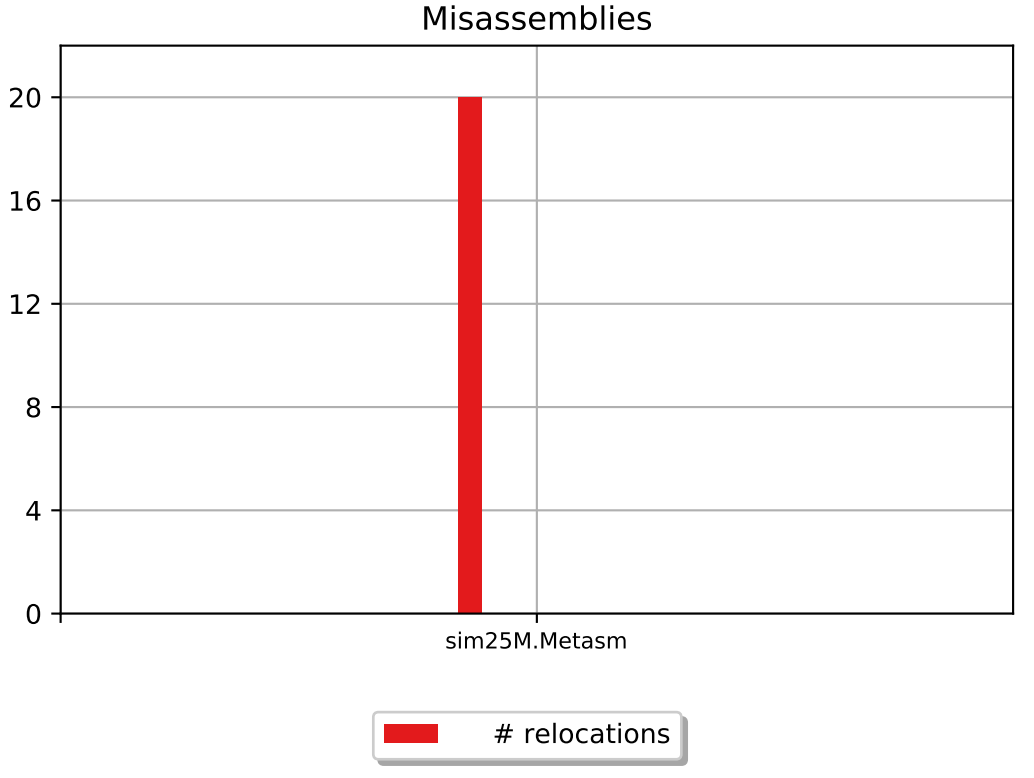

Nx
Contig length (Mbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
sim25M.Metasm

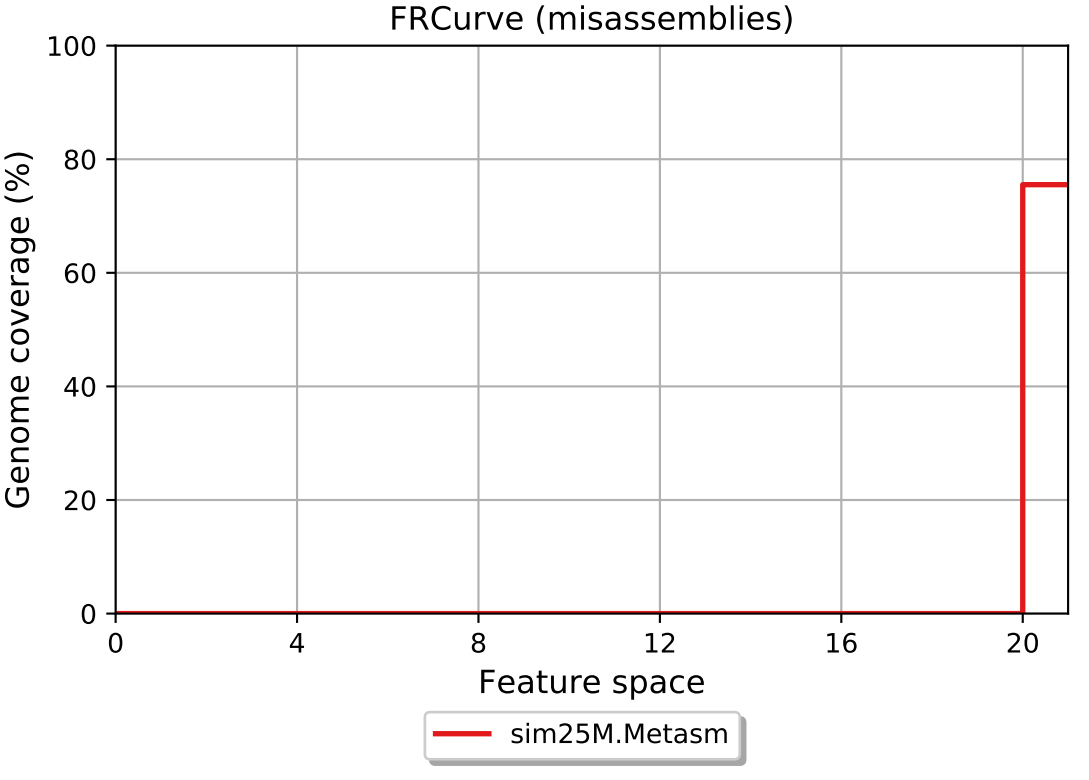

NGx
Contig length (Mbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
sim25M.Metasm

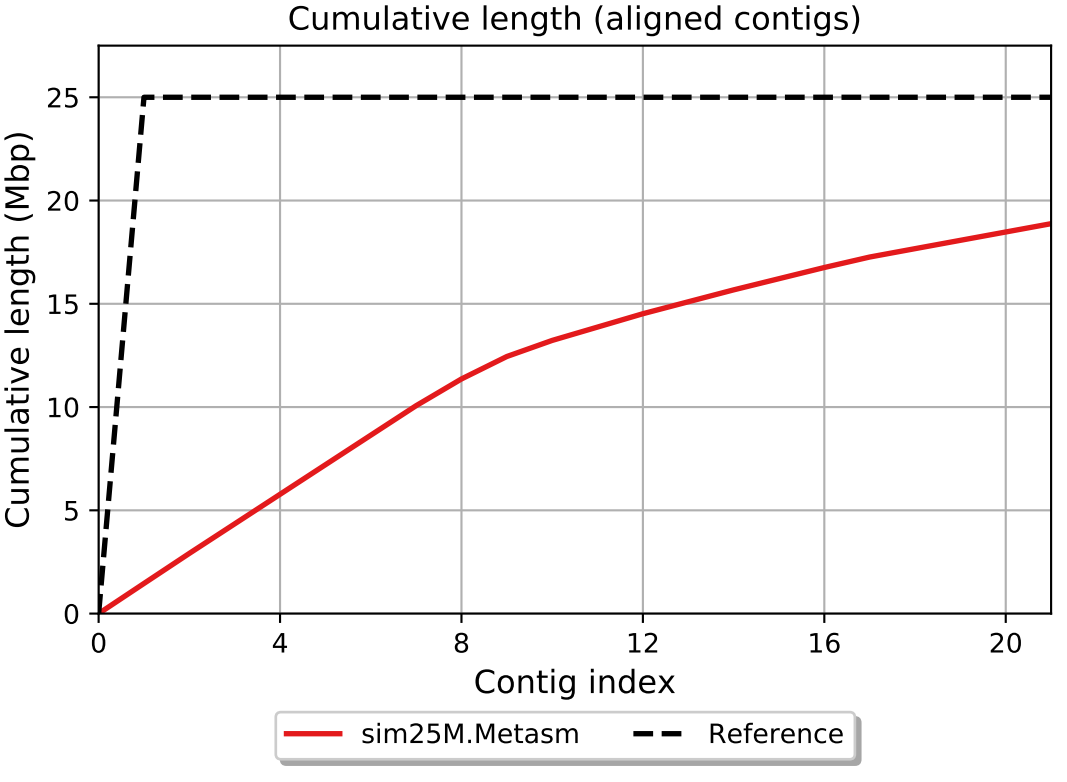

Cumulative length
Cumulative length (Mbp)
25
20
15
10
5
0
0
1
Contig index
sim25M.Metasm
Reference

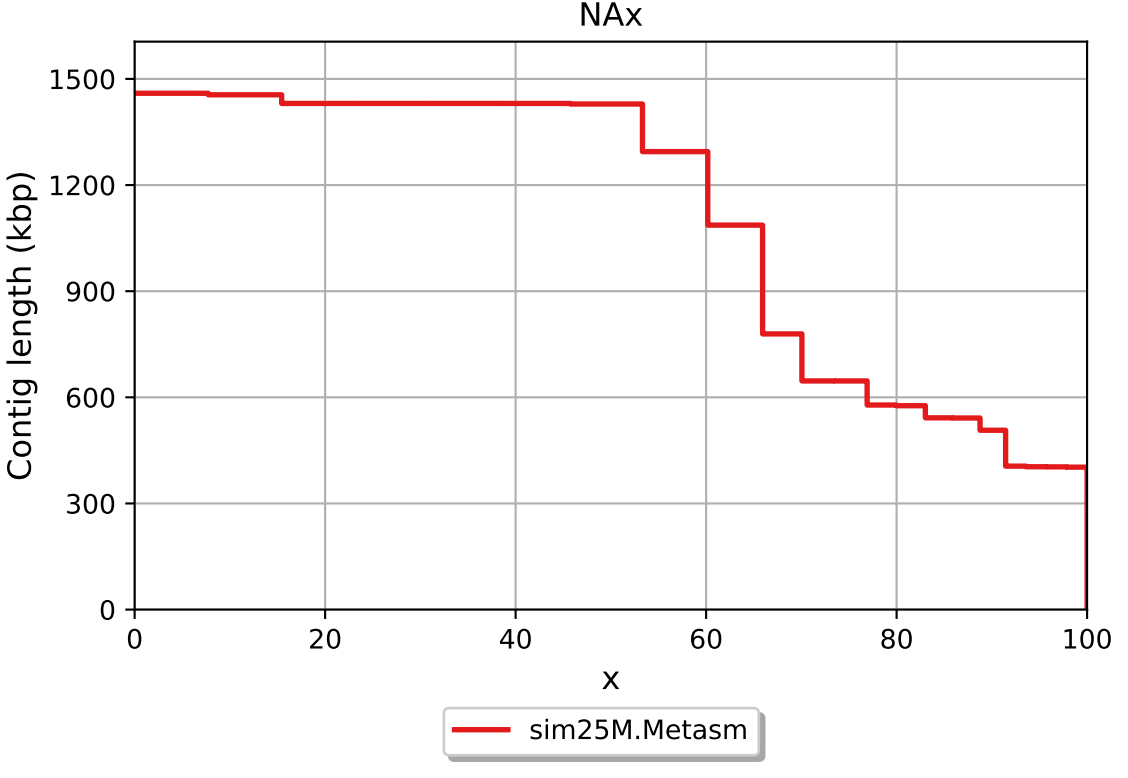

GC content
windows
8000
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
sim25M.Metasm
Reference

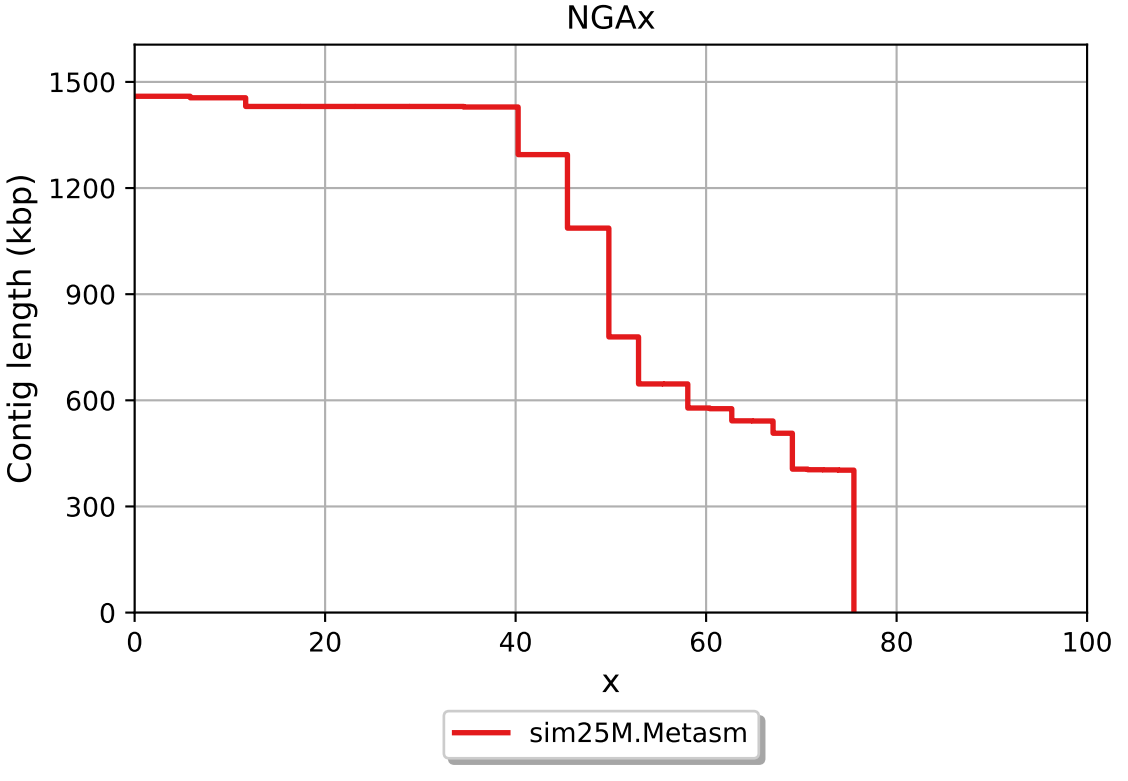

sim25M.Metasm GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
sim25M.Metasm


Misassemblies
20
16
12
8
4
0
sim25M.Metasm
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
4
8
12
16
20
Feature space
sim25M.Metasm


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
5
10
15
20
25
0
4
8
12
16
20
Contig index
sim25M.Metasm
Reference


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


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