Report

	sim25M.SpadesH
# contigs (>= 0 bp)	1978
# contigs (>= 1000 bp)	457
# contigs (>= 5000 bp)	334
# contigs (>= 10000 bp)	286
# contigs (>= 25000 bp)	204
# contigs (>= 50000 bp)	134
Total length (>= 0 bp)	24987397
Total length (>= 1000 bp)	24571185
Total length (>= 5000 bp)	24327298
Total length (>= 10000 bp)	23961066
Total length (>= 25000 bp)	22548009
Total length (>= 50000 bp)	20107292
# contigs	669
Largest contig	494497
Total length	24713527
Reference length	25000020
GC (%)	43.72
Reference GC (%)	43.69
N50	159119
NG50	152292
N75	67532
NG75	65000
L50	49
LG50	50
L75	107
LG75	111
# misassemblies	16
# misassembled contigs	16
Misassembled contigs length	2215287
# local misassemblies	11
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.686
Duplication ratio	1.002
# N's per 100 kbp	2.02
# mismatches per 100 kbp	24.39
# indels per 100 kbp	0.92
Largest alignment	494497
Total aligned length	24711599
NA50	140014
NGA50	139195
NA75	66116
NGA75	64502
LA50	52
LGA50	53
LA75	113
LGA75	116

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

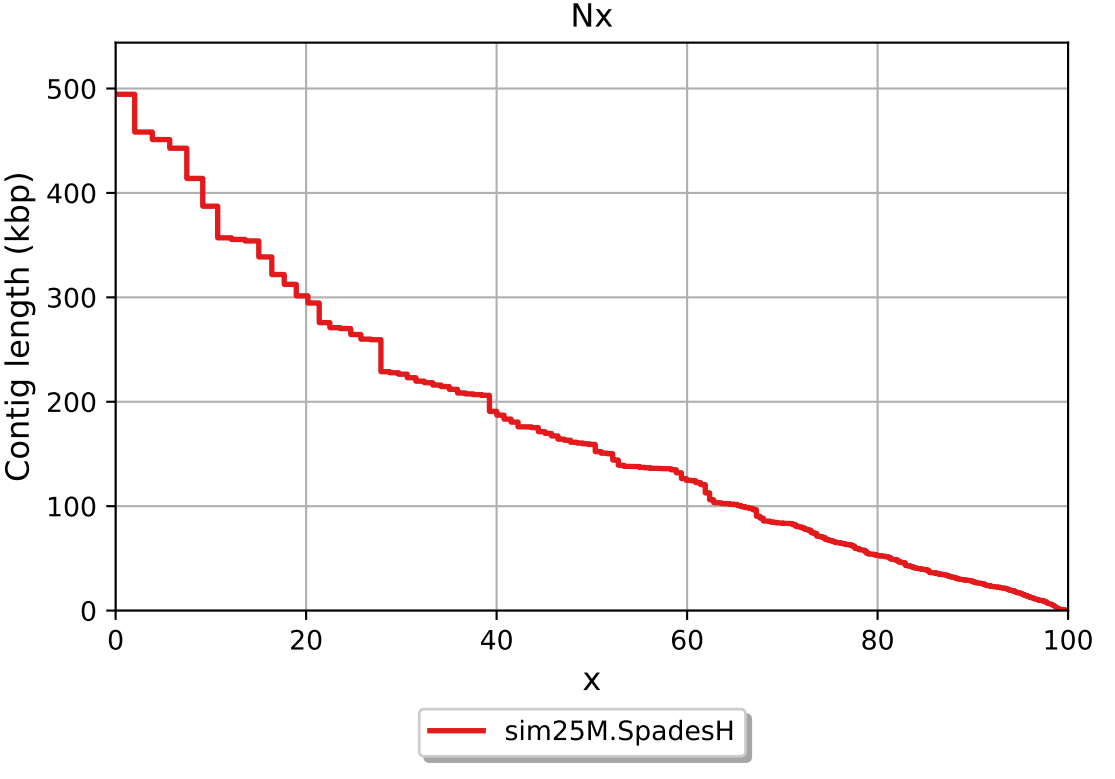
	sim25M.SpadesH
# misassemblies	16
# relocations	16
# translocations	0
# inversions	0
# misassembled contigs	16
Misassembled contigs length	2215287
# local misassemblies	11
# unaligned mis. contigs	0
# mismatches	6018
# indels	227
# indels (<= 5 bp)	202
# indels (> 5 bp)	25
Indels length	985

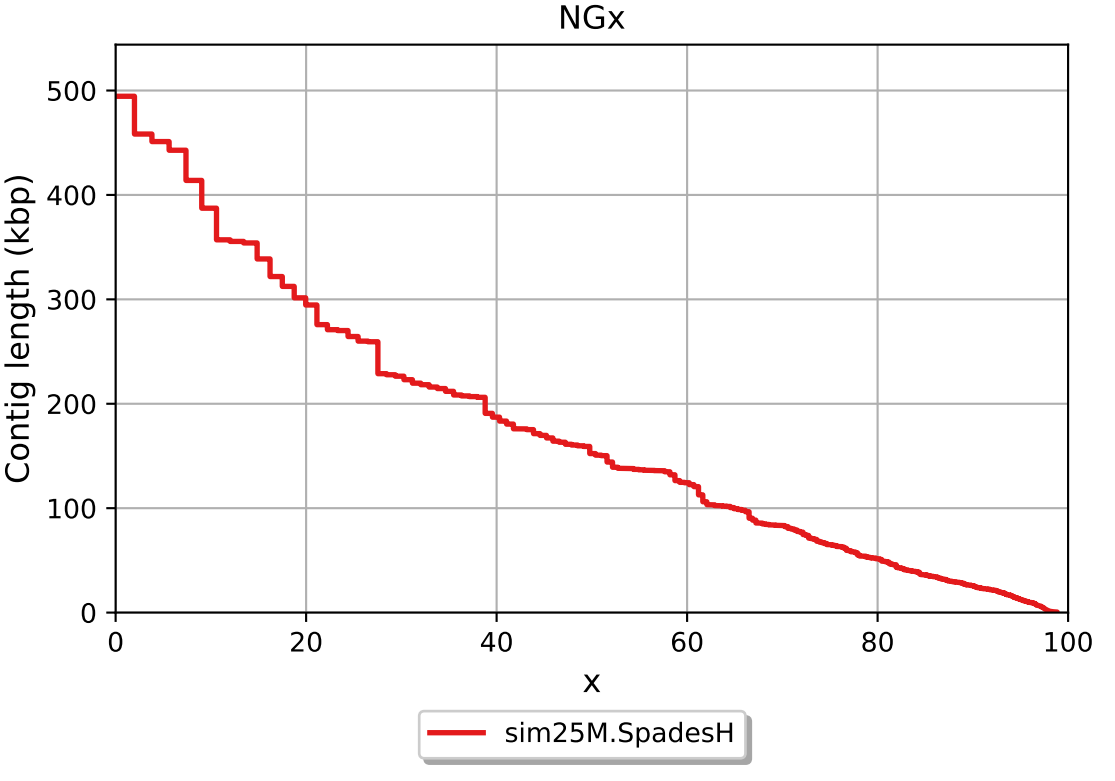
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

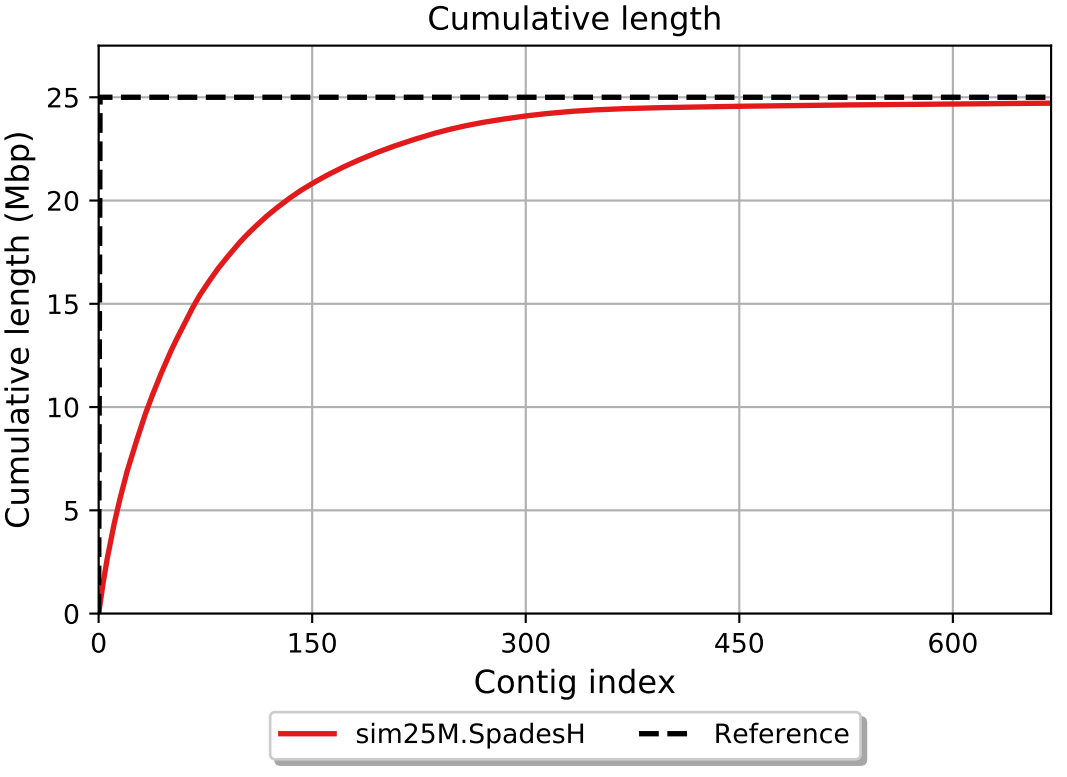
Unaligned report

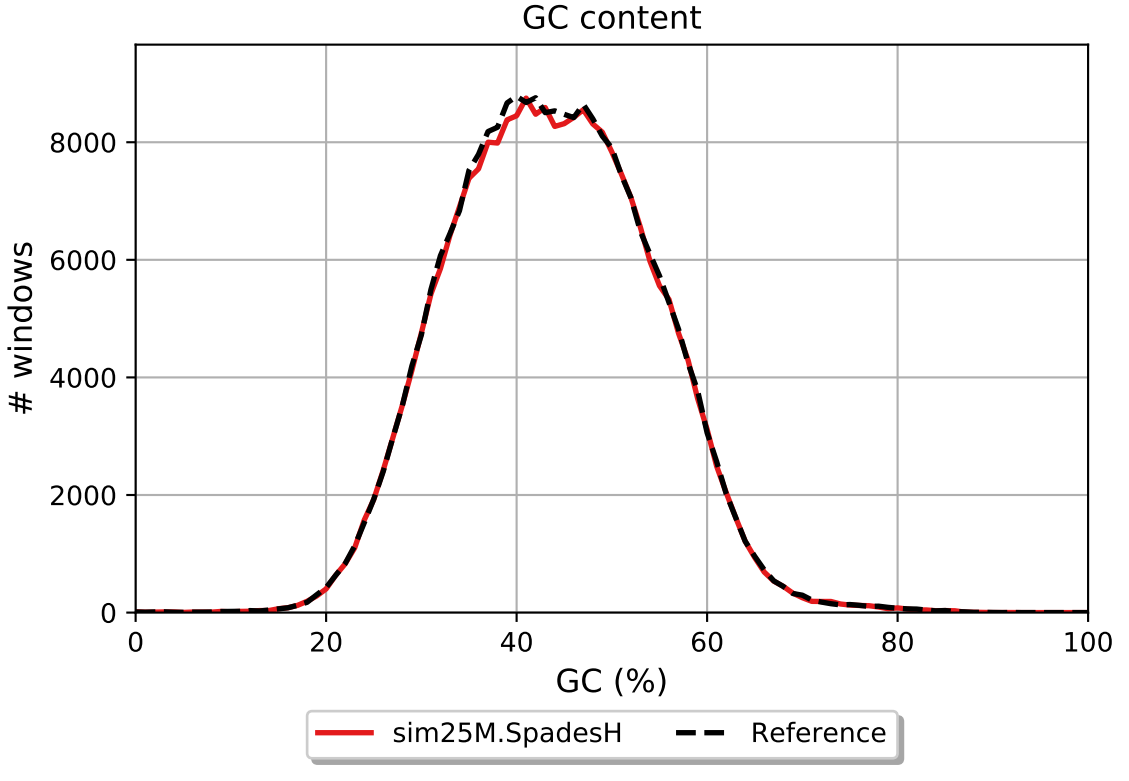
	sim25M.SpadesH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	499

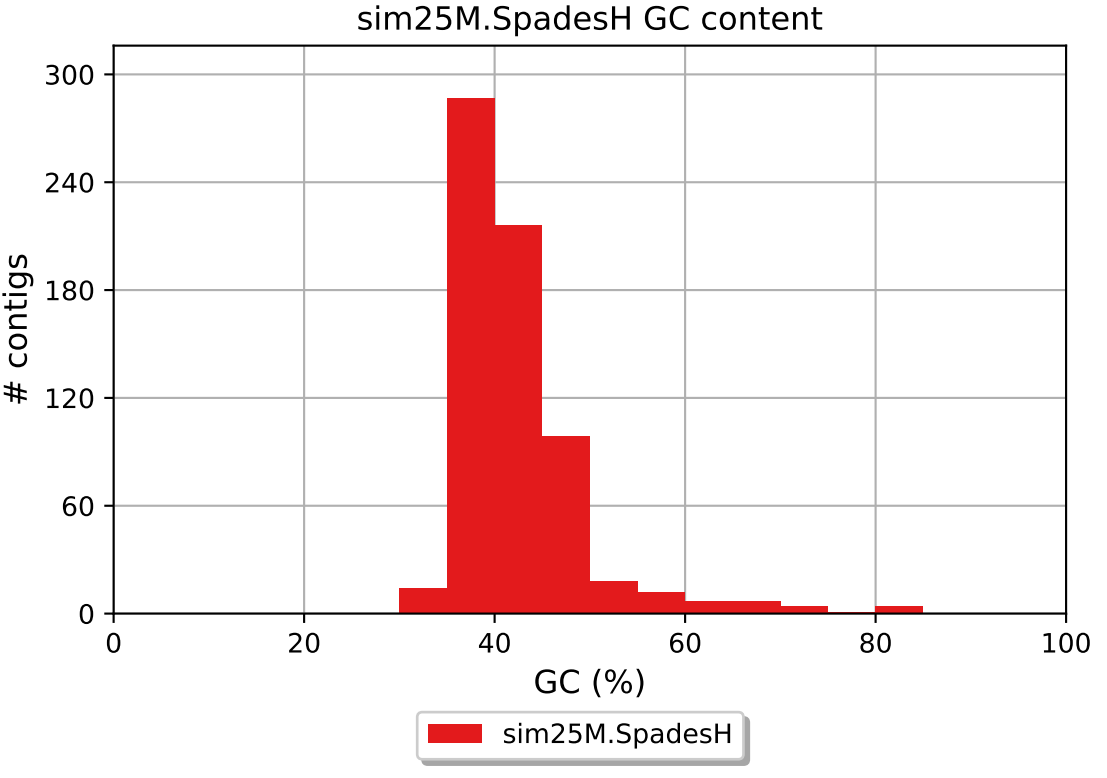
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

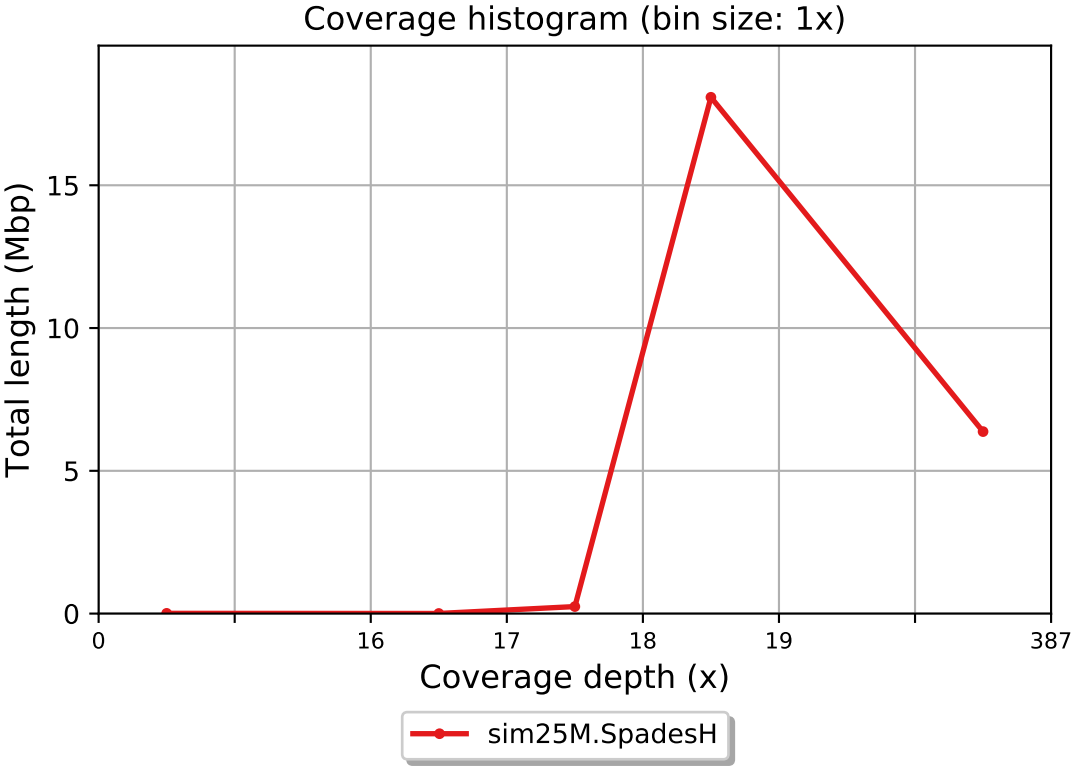

Nx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
sim25M.SpadesH

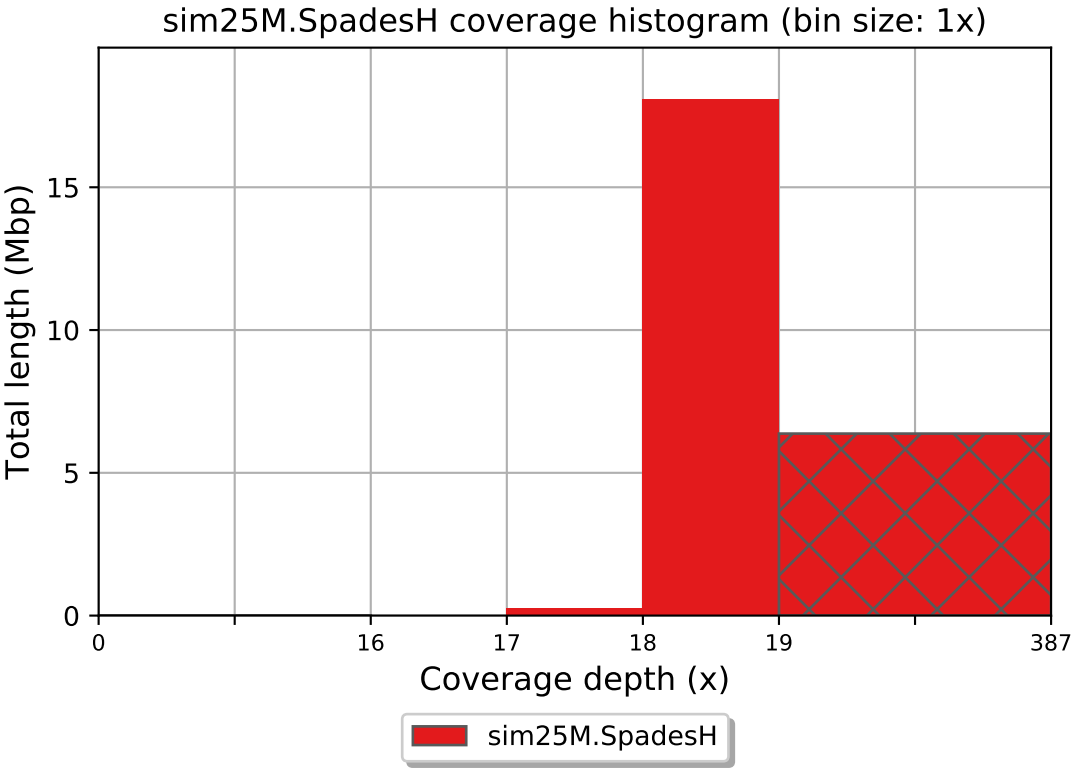

NGx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
sim25M.SpadesH

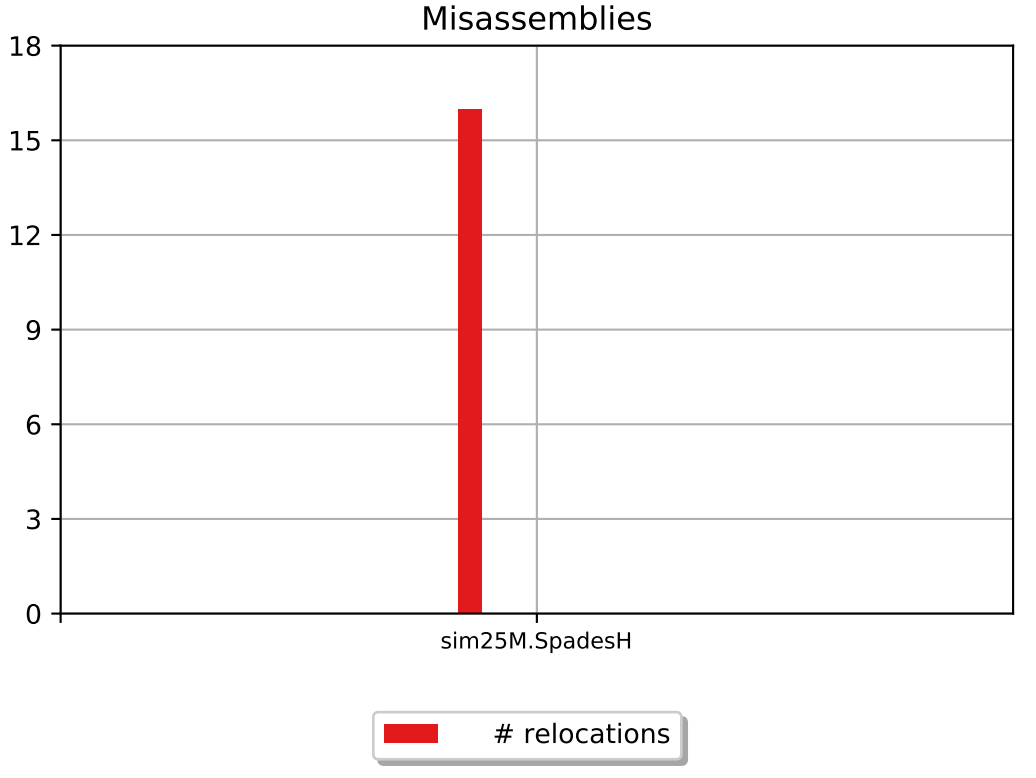

Cumulative length
Cumulative length (Mbp)
25
20
15
10
5
0
0
150
300
450
600
Contig index
sim25M.SpadesH
Reference

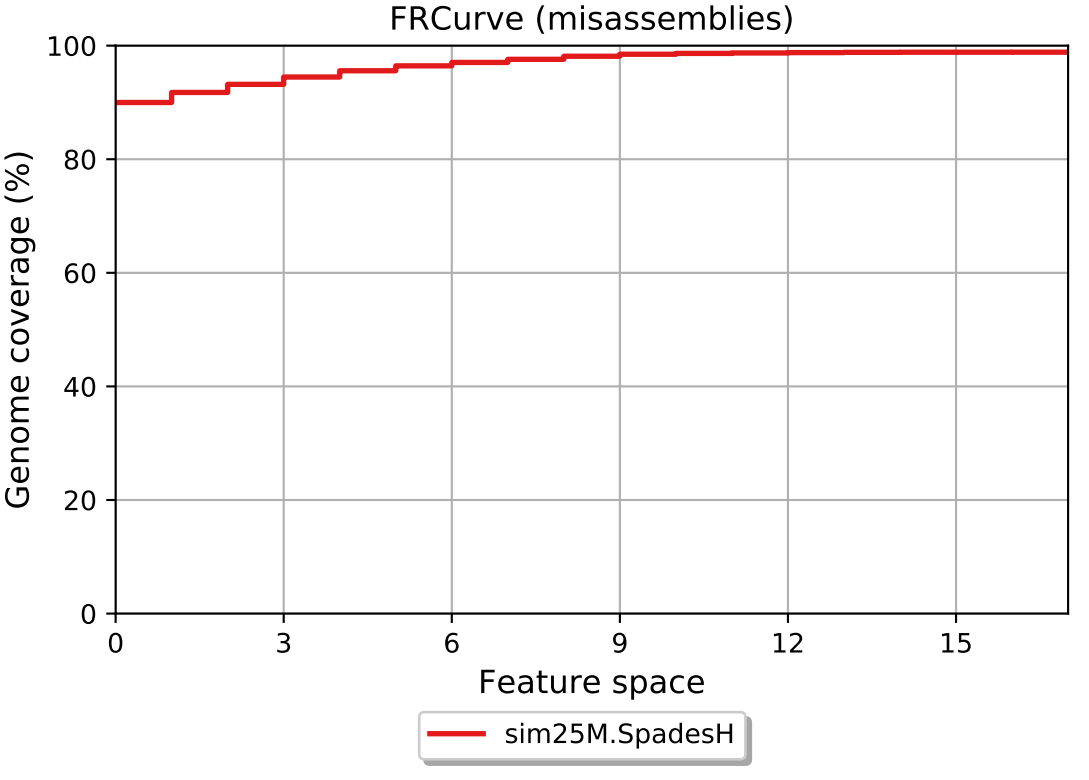

GC content
windows
GC (%)
0
2000
4000
6000
8000
0
20
40
60
80
100
sim25M.SpadesH
Reference

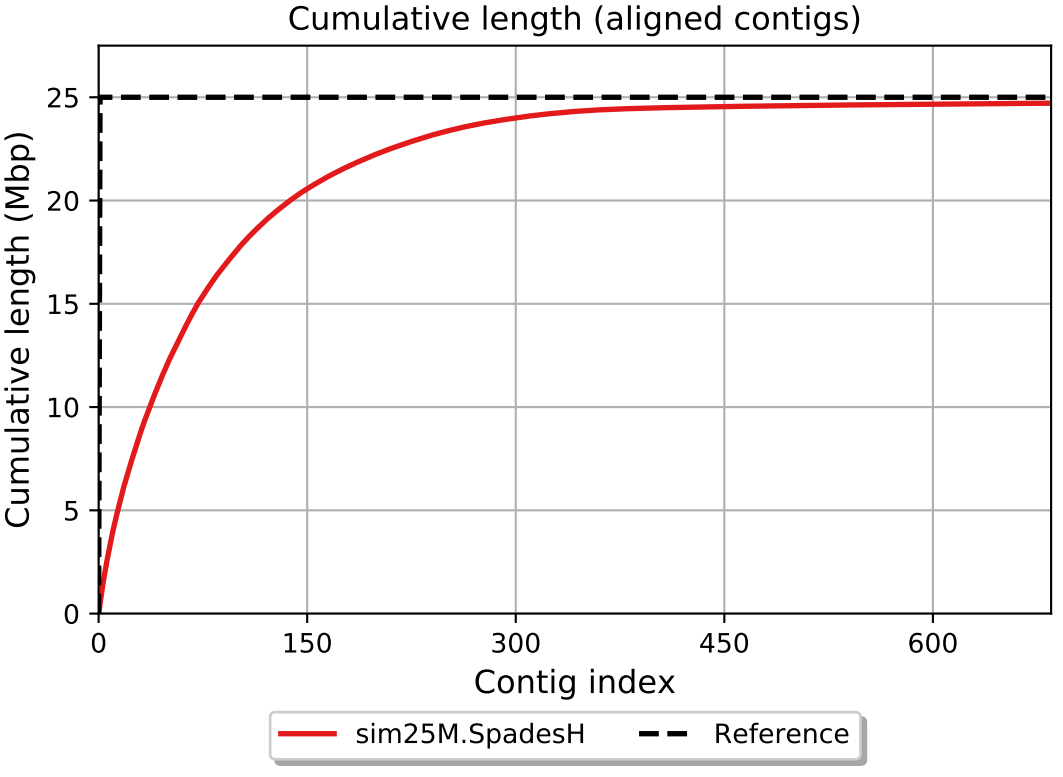

sim25M.SpadesH GC content
contigs
300
240
180
120
60
0
0
20
40
60
80
100
GC (%)
sim25M.SpadesH

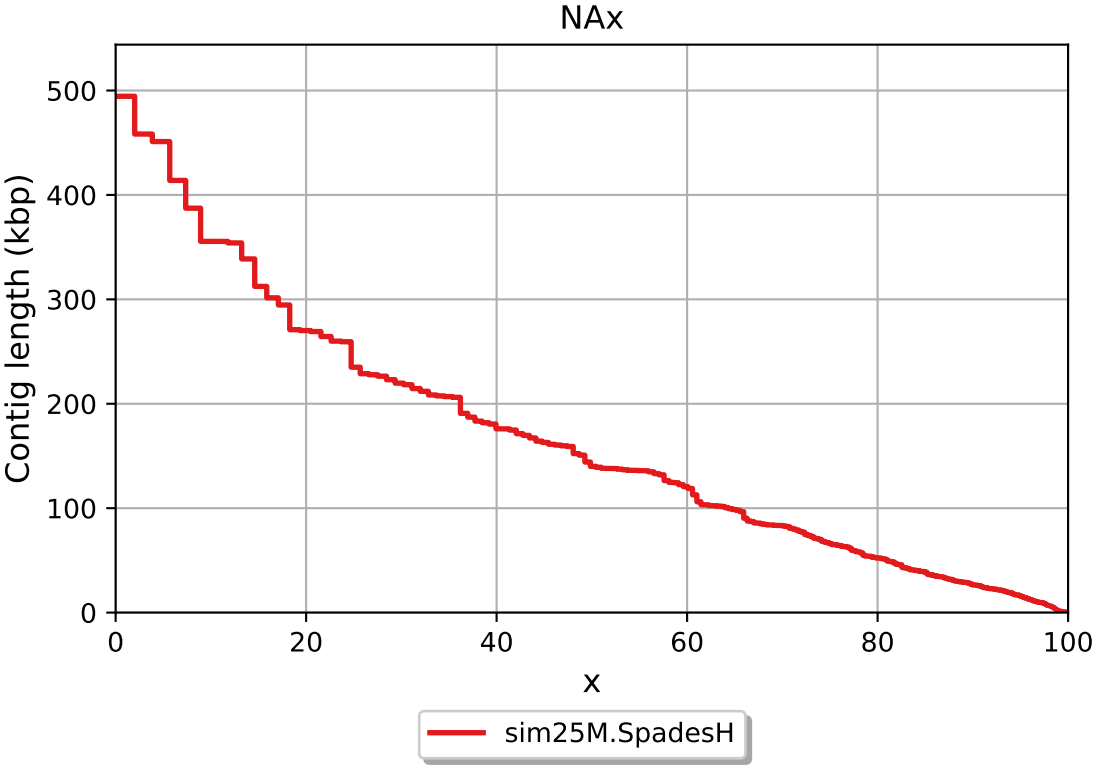

Coverage histogram (bin size: 1x)
Total length (Mbp)
0
5
10
15
0
16
17
18
19
387
Coverage depth (x)
sim25M.SpadesH

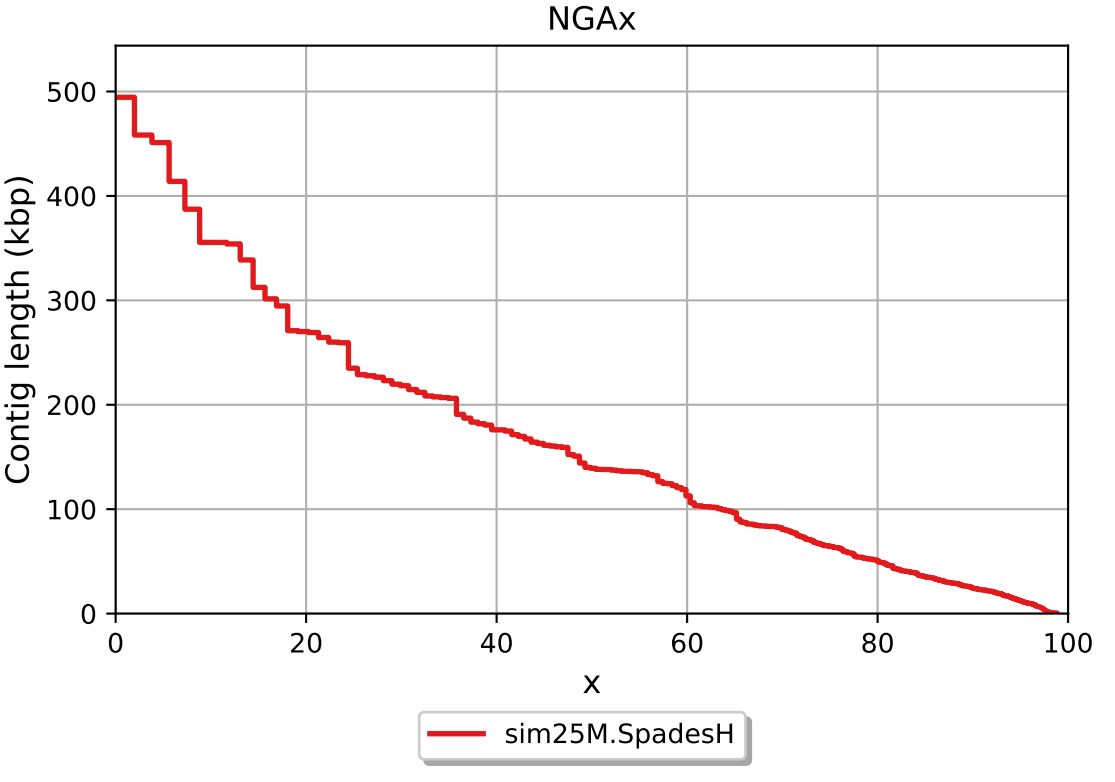

sim25M.SpadesH coverage histogram (bin size: 1x)
Total length (Mbp)
0
5
10
15
0
16
17
18
19
387
Coverage depth (x)
sim25M.SpadesH


Misassemblies
18
15
12
9
6
3
0
sim25M.SpadesH
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
3
6
9
12
15
Feature space
sim25M.SpadesH


Cumulative length (aligned contigs)
Cumulative length (Mbp)
25
20
15
10
5
0
0
150
300
450
600
Contig index
sim25M.SpadesH
Reference


NAx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
sim25M.SpadesH


NGAx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
sim25M.SpadesH