# Report

| | sim25M.SoDe2H |
|---|---|
| # contigs (>= 0 bp) | 11831 |
| # contigs (>= 1000 bp) | 5652 |
| # contigs (>= 5000 bp) | 998 |
| # contigs (>= 10000 bp) | 225 |
| # contigs (>= 25000 bp) | 7 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 21604836 |
| Total length (>= 1000 bp) | 18699293 |
| Total length (>= 5000 bp) | 8461510 |
| Total length (>= 10000 bp) | 3215280 |
| Total length (>= 25000 bp) | 198900 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 8262 |
| Largest contig | 34118 |
| Total length | 20585734 |
| Reference length | 25000020 |
| GC (%) | 42.87 |
| Reference GC (%) | 43.69 |
| N50 | 3928 |
| NG50 | 2953 |
| N75 | 1899 |
| NG75 | 985 |
| L50 | 1412 |
| LG50 | 2060 |
| L75 | 3306 |
| LG75 | 5704 |
| # misassemblies | 1 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 16309 |
| # local misassemblies | 241 |
| # unaligned mis. contigs | 68 |
| # unaligned contigs | 1463 + 518 part |
| Unaligned length | 2757477 |
| Genome fraction (%) | 69.499 |
| Duplication ratio | 1.026 |
| # N's per 100 kbp | 4333.43 |
| # mismatches per 100 kbp | 153.15 |
| # indels per 100 kbp | 111.48 |
| Largest alignment | 33767 |
| Total aligned length | 17359847 |
| NA50 | 3467 |
| NGA50 | 2369 |
| NA75 | 1175 |
| LA50 | 1515 |
| LGA50 | 2283 |
| LA75 | 4022 |

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

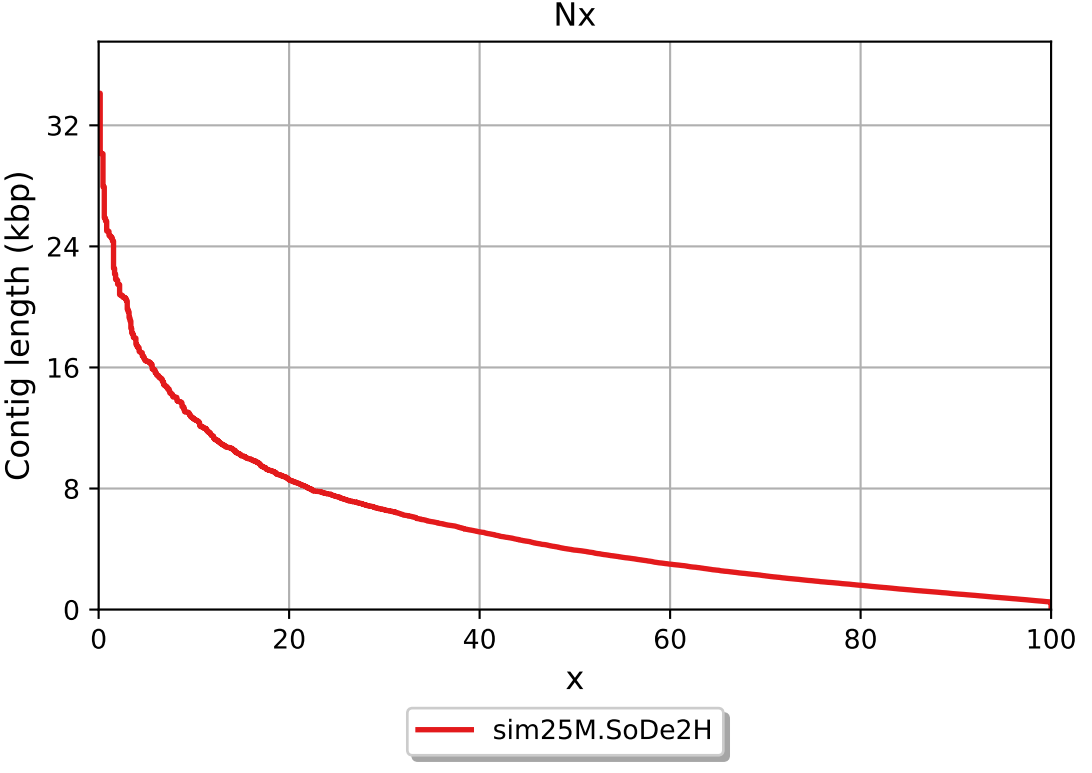
| | sim25M.SoDe2H |
|---|---|
| # misassemblies | 1 |
| # relocations | 1 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 1 |
| Misassembled contigs length | 16309 |
| # local misassemblies | 241 |
| # unaligned mis. contigs | 68 |
| # mismatches | 26610 |
| # indels | 19369 |
| # indels (<= 5 bp) | 15043 |
| # indels (> 5 bp) | 4326 |
| Indels length | 71065 |

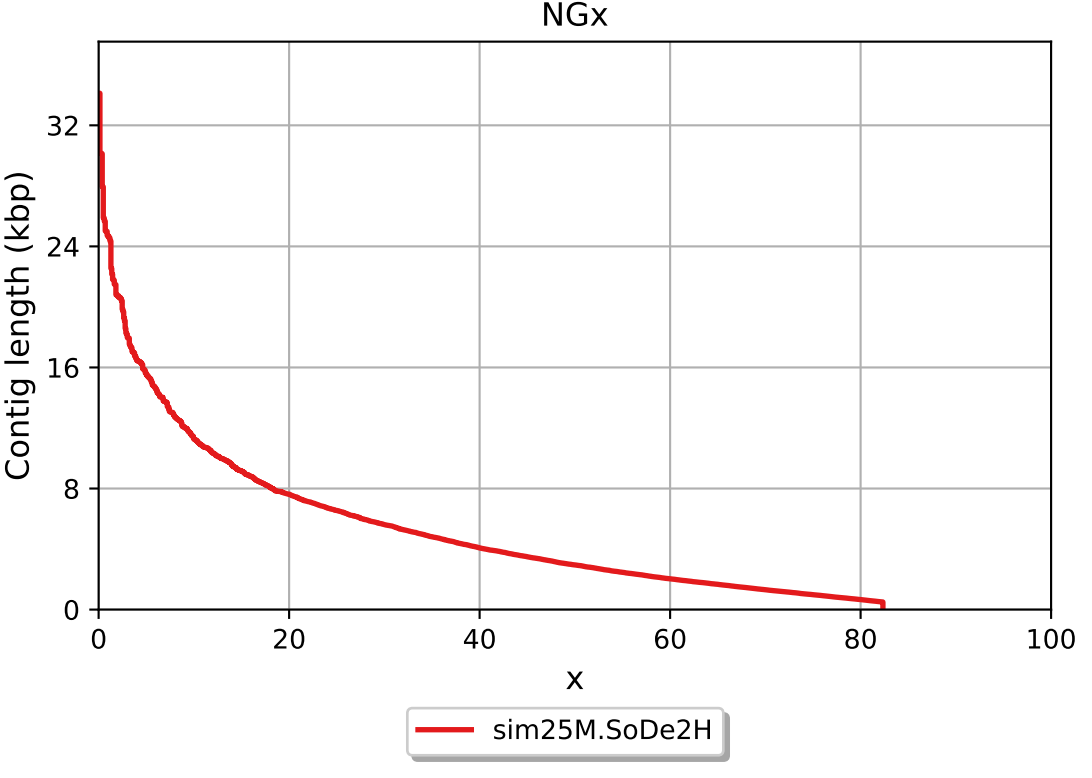
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

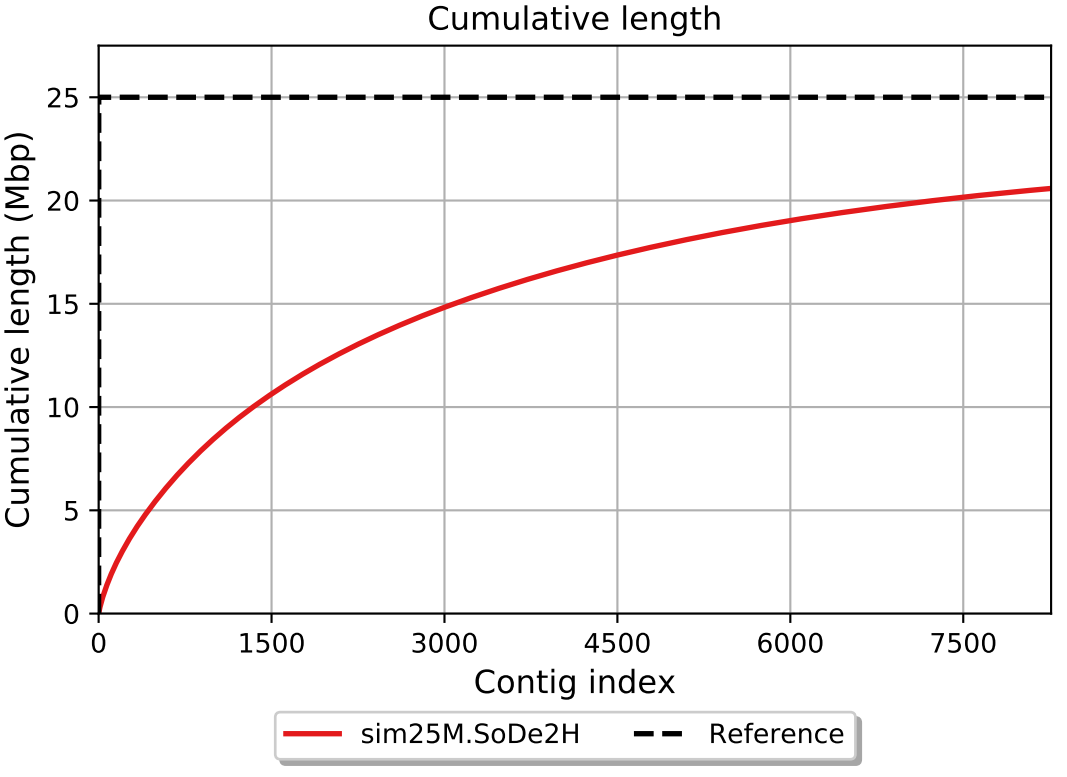
# Unaligned report

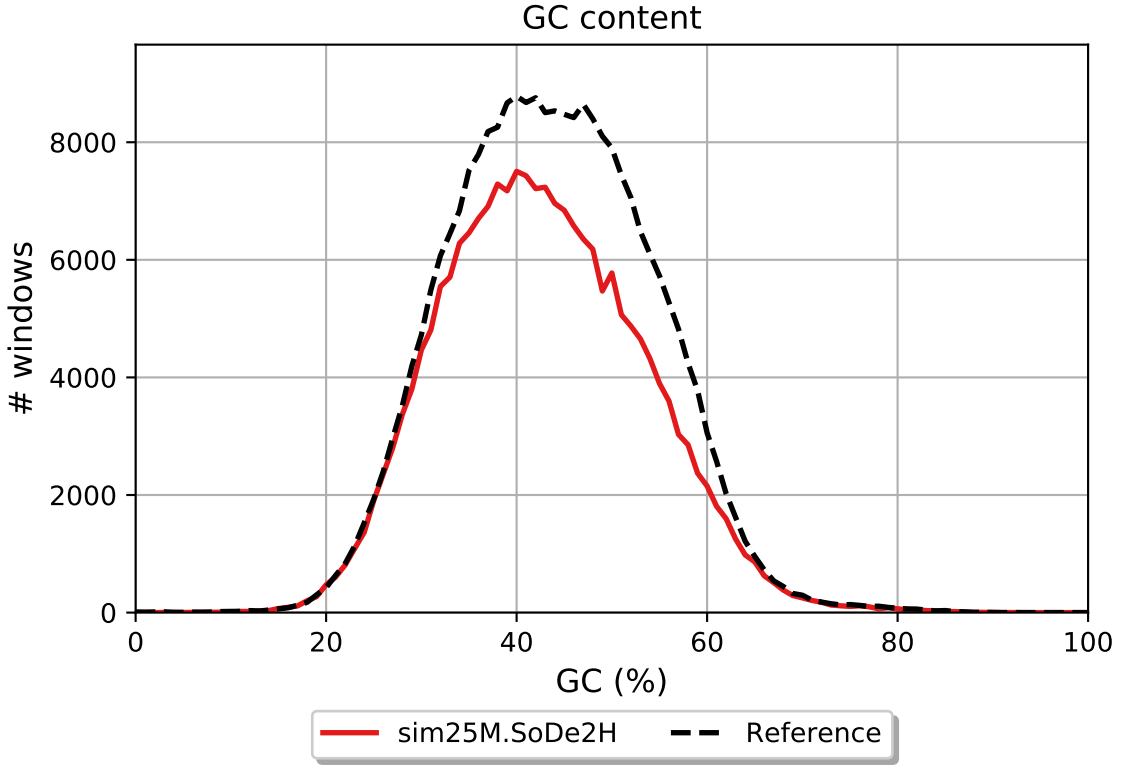
| | sim25M.SoDe2H |
|---|---|
| # fully unaligned contigs | 1463 |
| Fully unaligned length | 2031023 |
| # partially unaligned contigs | 518 |
| Partially unaligned length | 726454 |
| # N's | 892068 |

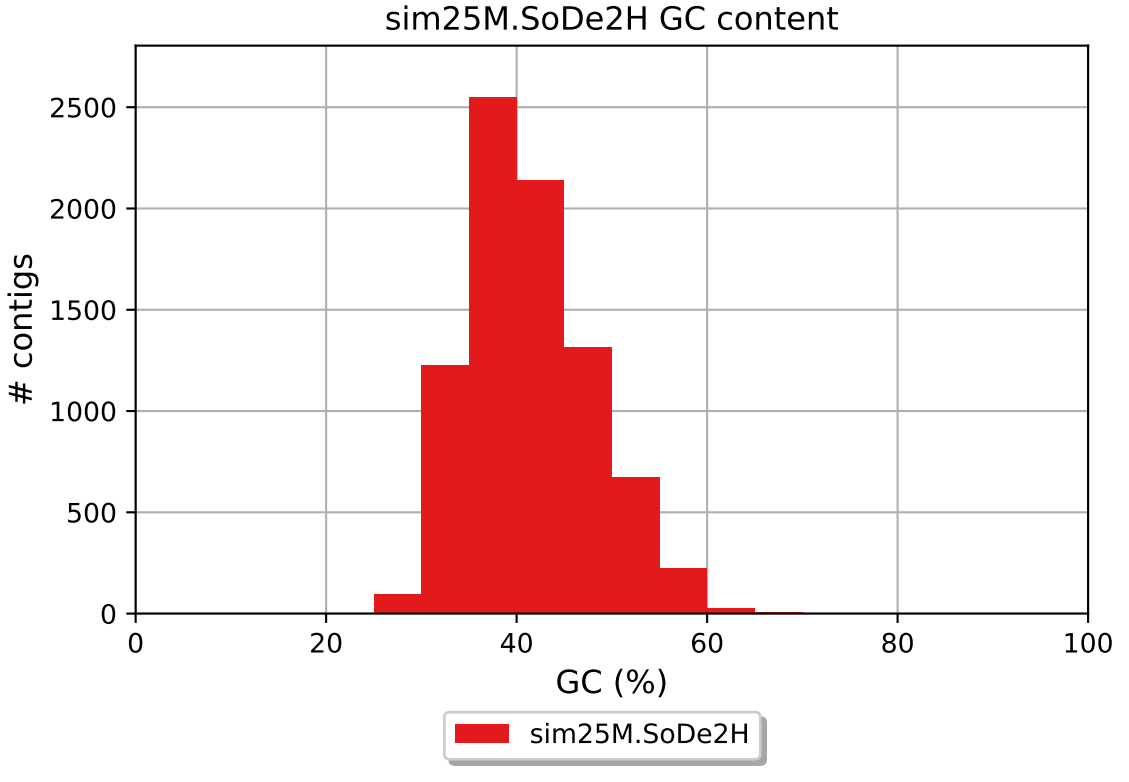
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
32
24
16
8
0
0
20
40
60
80
100
x
sim25M.SoDe2H

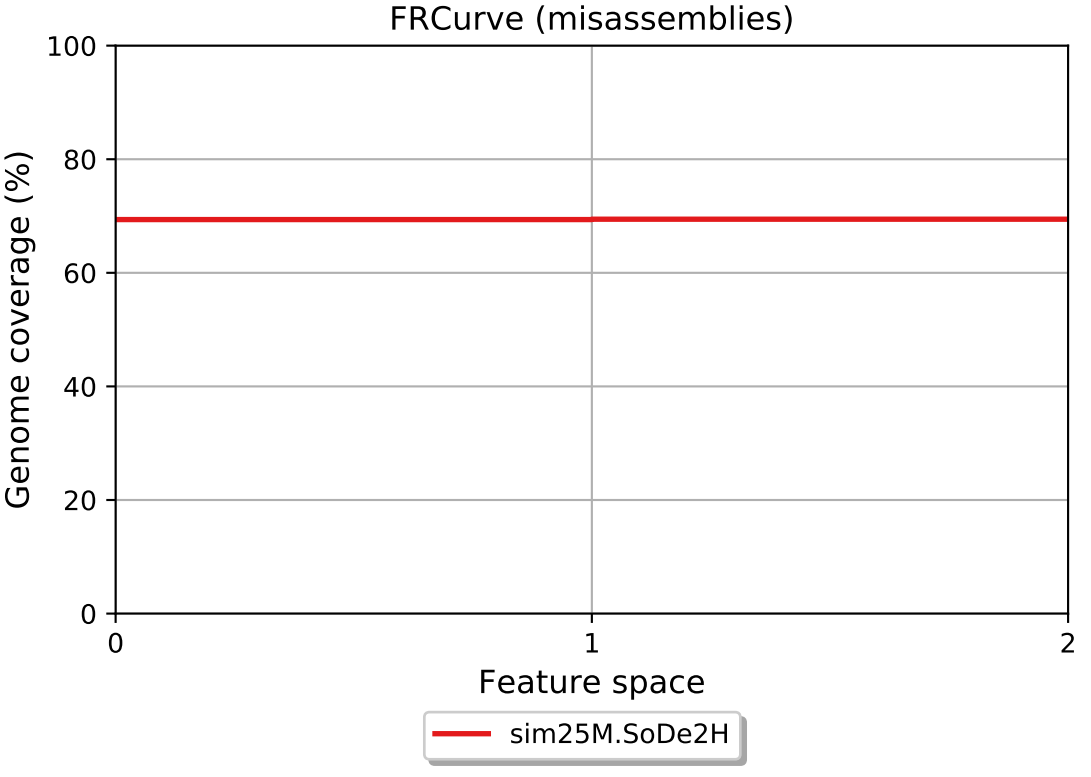

NGx
Contig length (kbp)
32
24
16
8
0
0
20
40
60
80
100
x
sim25M.SoDe2H

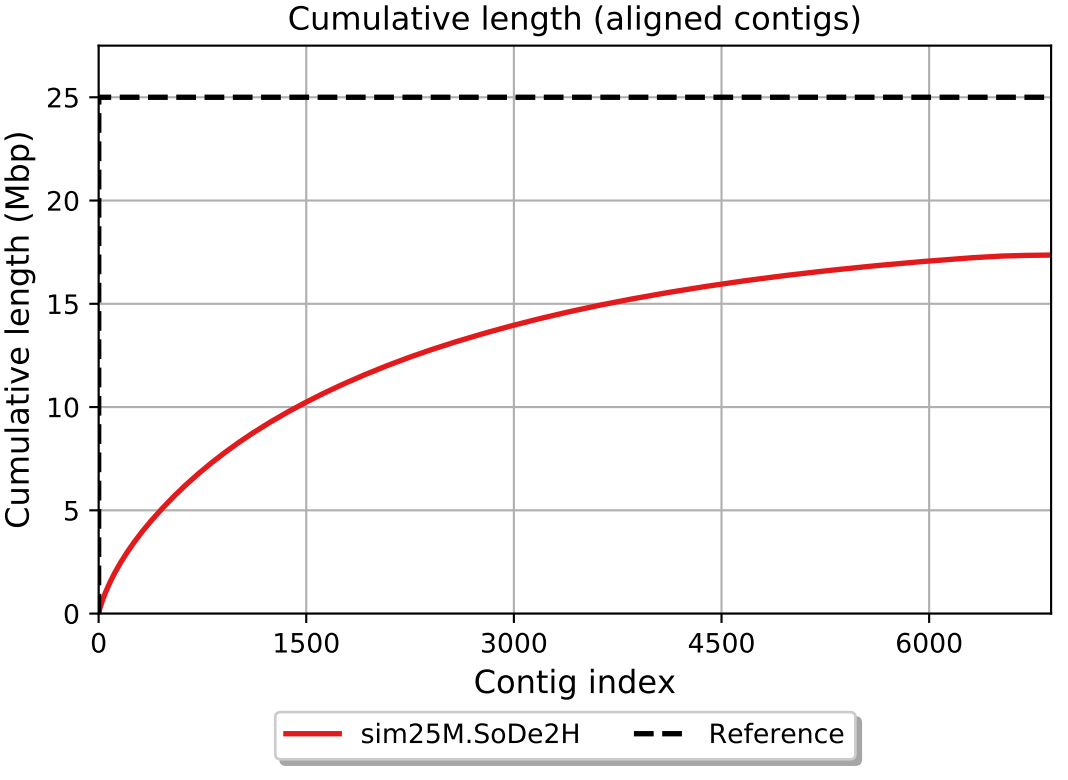

Cumulative length
Cumulative length (Mbp)
25
20
15
10
5
0
0
1500
3000
4500
6000
7500
Contig index
sim25M.SoDe2H
Reference

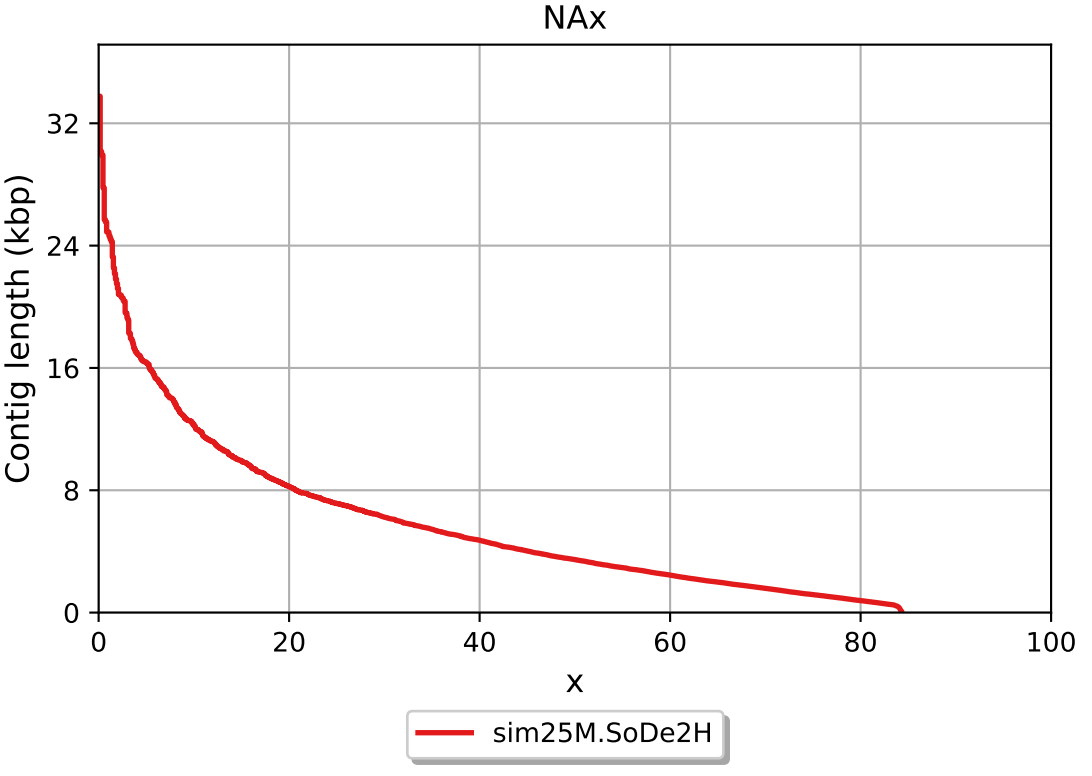

GC content
8000
6000
4000
2000
0
# windows
0
20
40
60
80
100
GC (%)
sim25M.SoDe2H
Reference

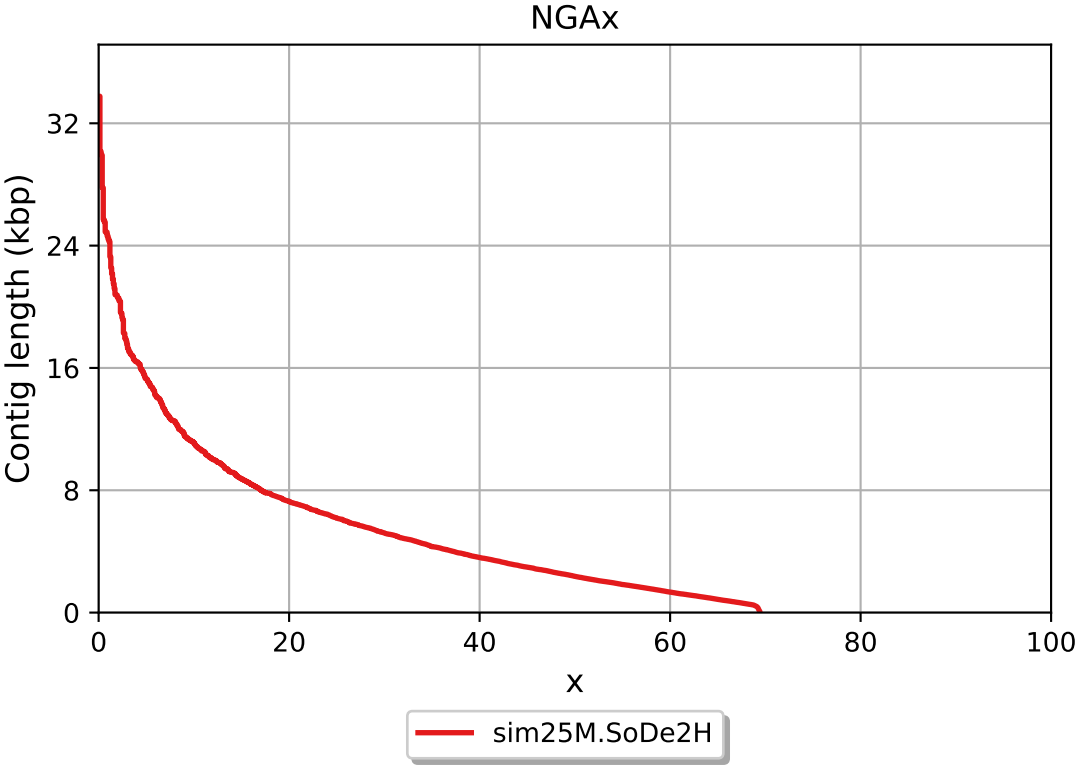

sim25M.SoDe2H GC content
# contigs
2500
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
sim25M.SoDe2H

Misassemblies
5
4
3
2
1
0
sim25M.SoDe2H
# relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
sim25M.SoDe2H


Cumulative length (aligned contigs)
Cumulative length (Mbp)
25
20
15
10
5
0
0
1500
3000
4500
6000
Contig index
sim25M.SoDe2H
Reference


NAx
Contig length (kbp)
32
24
16
8
0
0
20
40
60
80
100
x
sim25M.SoDe2H


NGAx
Contig length (kbp)
32
24
16
8
0
0
20
40
60
80
100
x
sim25M.SoDe2H