

Report

| | sim25M.SpadesL |
|-----------------------------|----------------|
| # contigs (>= 0 bp) | 2498 |
| # contigs (>= 1000 bp) | 654 |
| # contigs (>= 5000 bp) | 504 |
| # contigs (>= 10000 bp) | 427 |
| # contigs (>= 25000 bp) | 269 |
| # contigs (>= 50000 bp) | 147 |
| Total length (>= 0 bp) | 25013233 |
| Total length (>= 1000 bp) | 24519054 |
| Total length (>= 5000 bp) | 24196984 |
| Total length (>= 10000 bp) | 23642716 |
| Total length (>= 25000 bp) | 20980046 |
| Total length (>= 50000 bp) | 16678707 |
| # contigs | 891 |
| Largest contig | 413672 |
| Total length | 24677390 |
| Reference length | 25000020 |
| GC (%) | 43.72 |
| Reference GC (%) | 43.69 |
| N50 | 90427 |
| NG50 | 87387 |
| N75 | 37984 |
| NG75 | 36639 |
| L50 | 83 |
| LG50 | 85 |
| L75 | 189 |
| LG75 | 196 |
| # misassemblies | 35 |
| # misassembled contigs | 32 |
| Misassembled contigs length | 3165778 |
| # local misassemblies | 13 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 2 part |
| Unaligned length | 1680 |
| Genome fraction (%) | 98.437 |
| Duplication ratio | 1.003 |
| # N's per 100 kbp | 1.22 |
| # mismatches per 100 kbp | 28.89 |
| # indels per 100 kbp | 0.99 |
| Largest alignment | 413564 |
| Total aligned length | 24673647 |
| NA50 | 84415 |
| NGA50 | 83370 |
| NA75 | 36548 |
| NGA75 | 34884 |
| LA50 | 89 |
| LGA50 | 91 |
| LA75 | 202 |
| LGA75 | 209 |

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

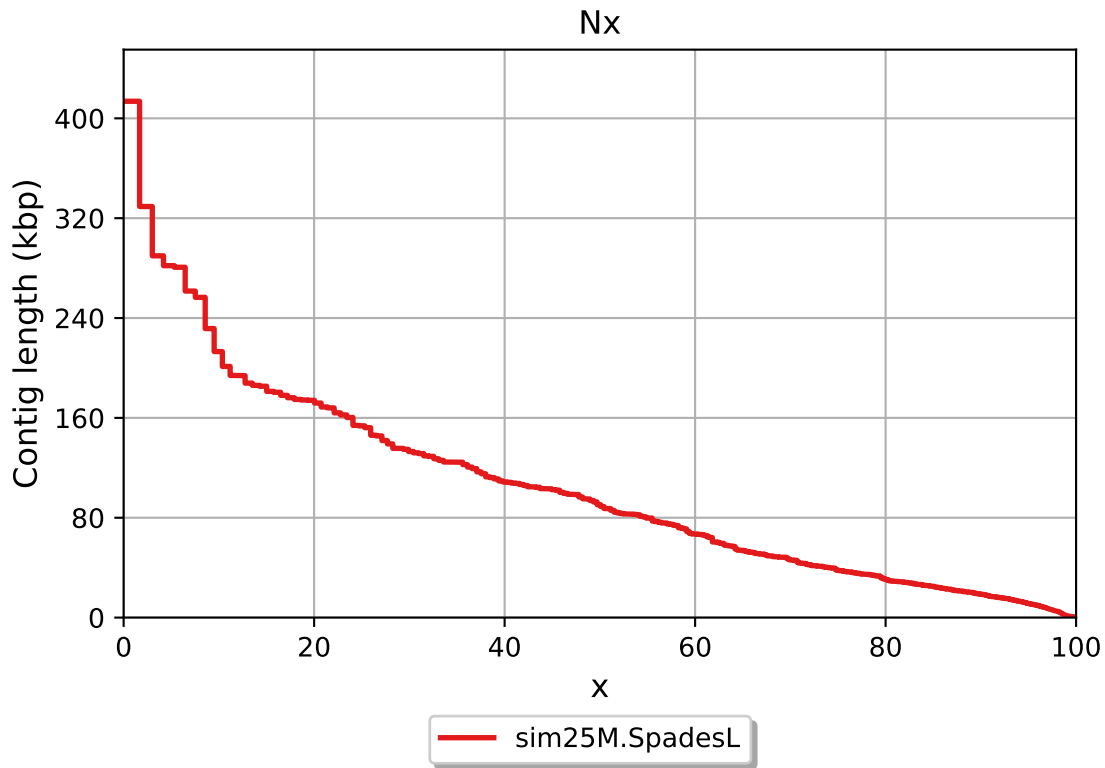
| | sim25M.SpadesL |
|-----------------------------|----------------|
| # misassemblies | 35 |
| # relocations | 35 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 32 |
| Misassembled contigs length | 3165778 |
| # local misassemblies | 13 |
| # unaligned mis. contigs | 0 |
| # mismatches | 7110 |
| # indels | 244 |
| # indels (≤ 5 bp) | 217 |
| # indels (> 5 bp) | 27 |
| Indels length | 1016 |

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).

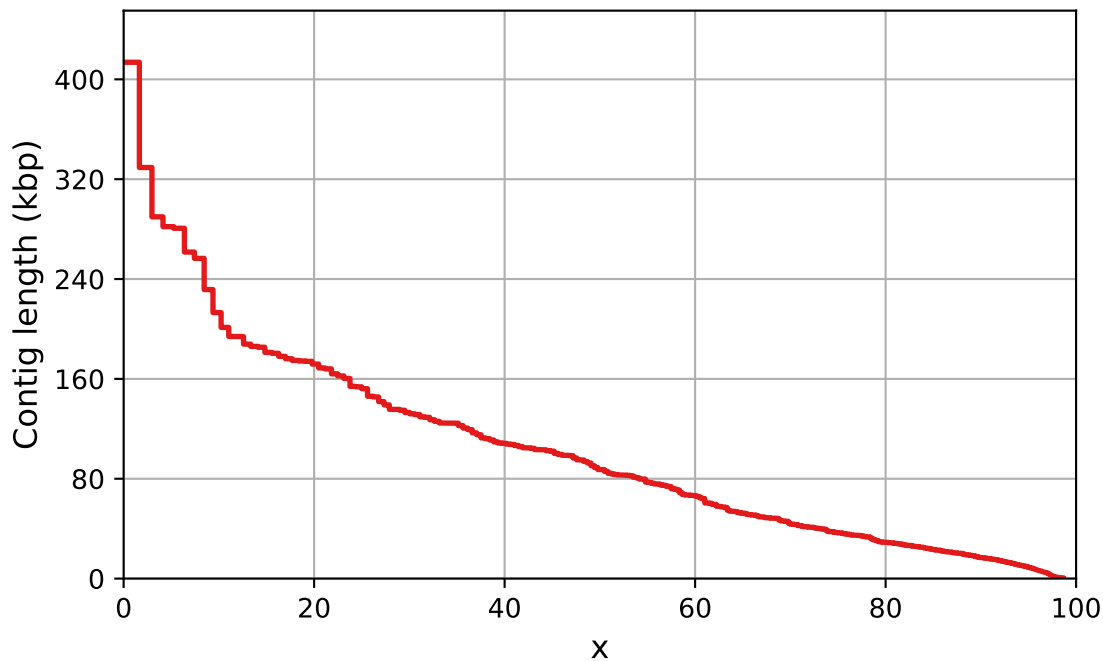
Unaligned report

| | sim25M.SpadesL |
|-------------------------------|----------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 2 |
| Partially unaligned length | 1680 |
| # N's | 300 |

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).

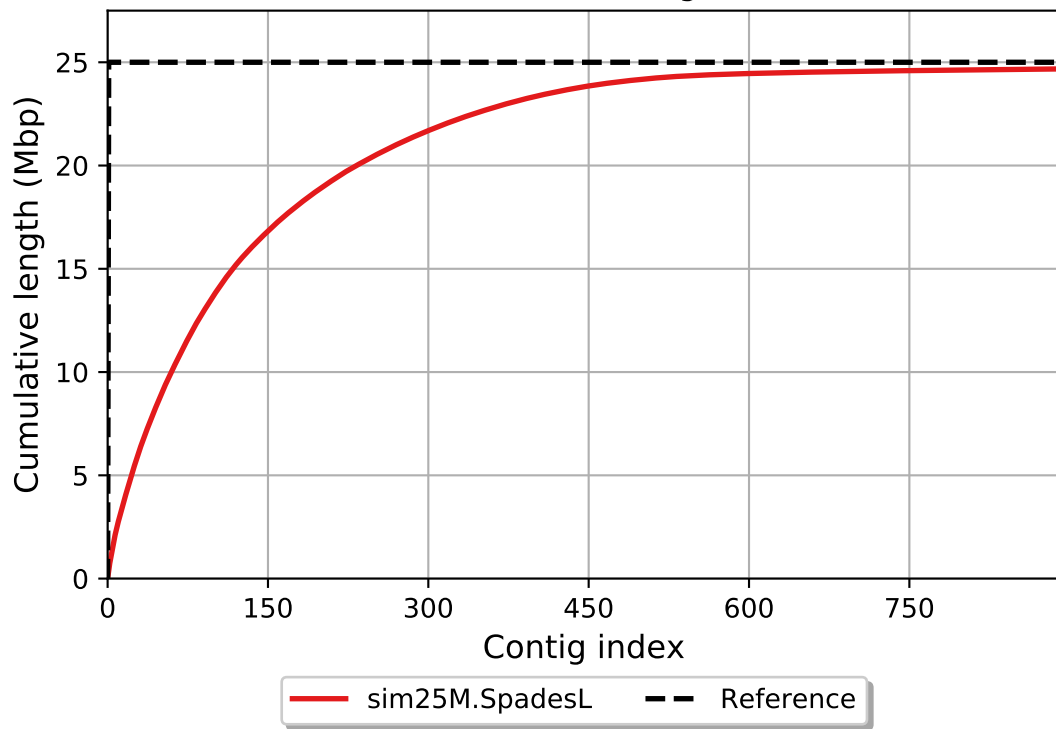


NGx

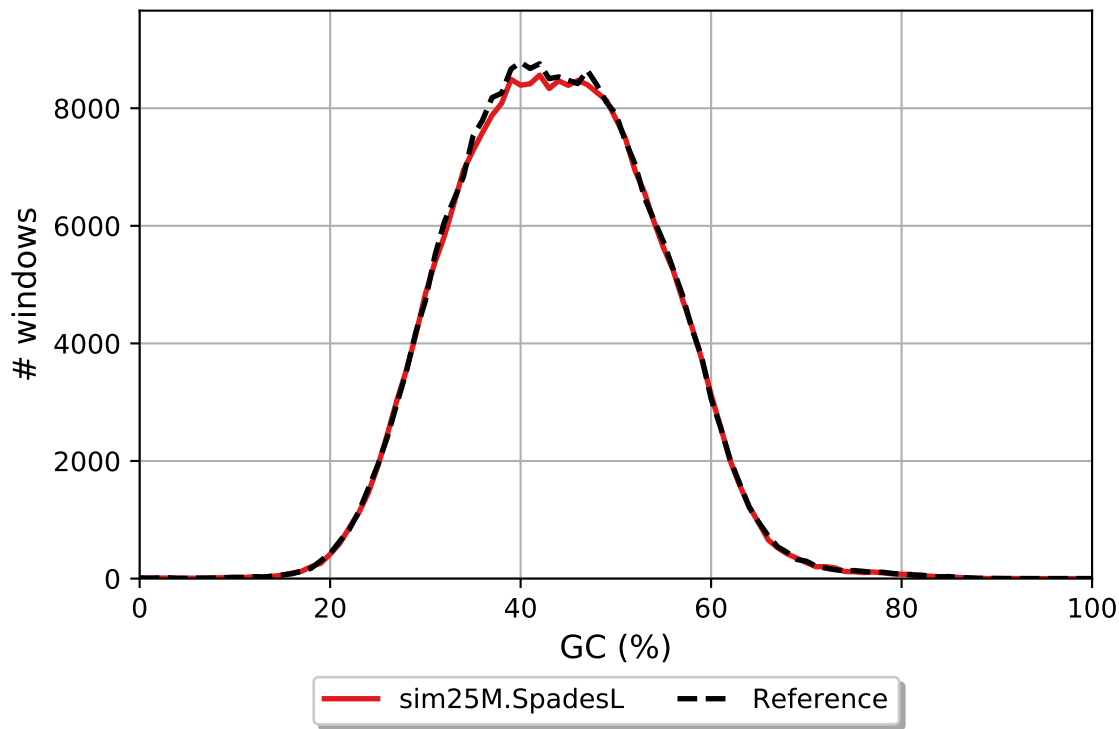


— sim25M.SpadesL

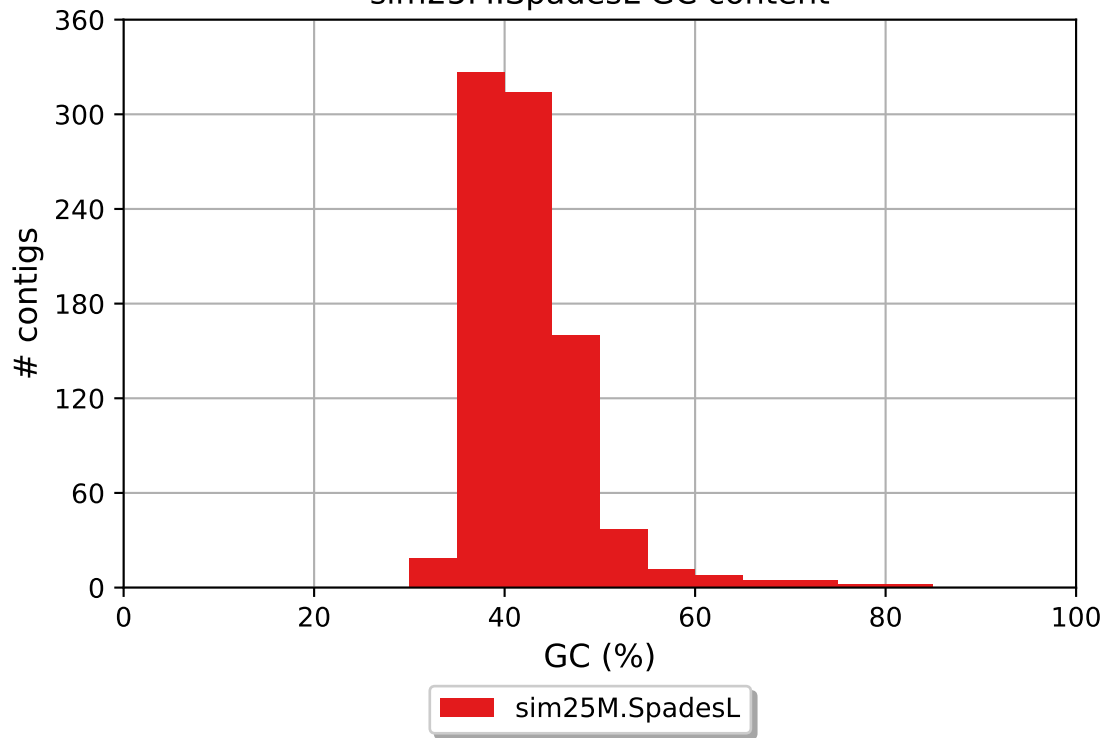
Cumulative length



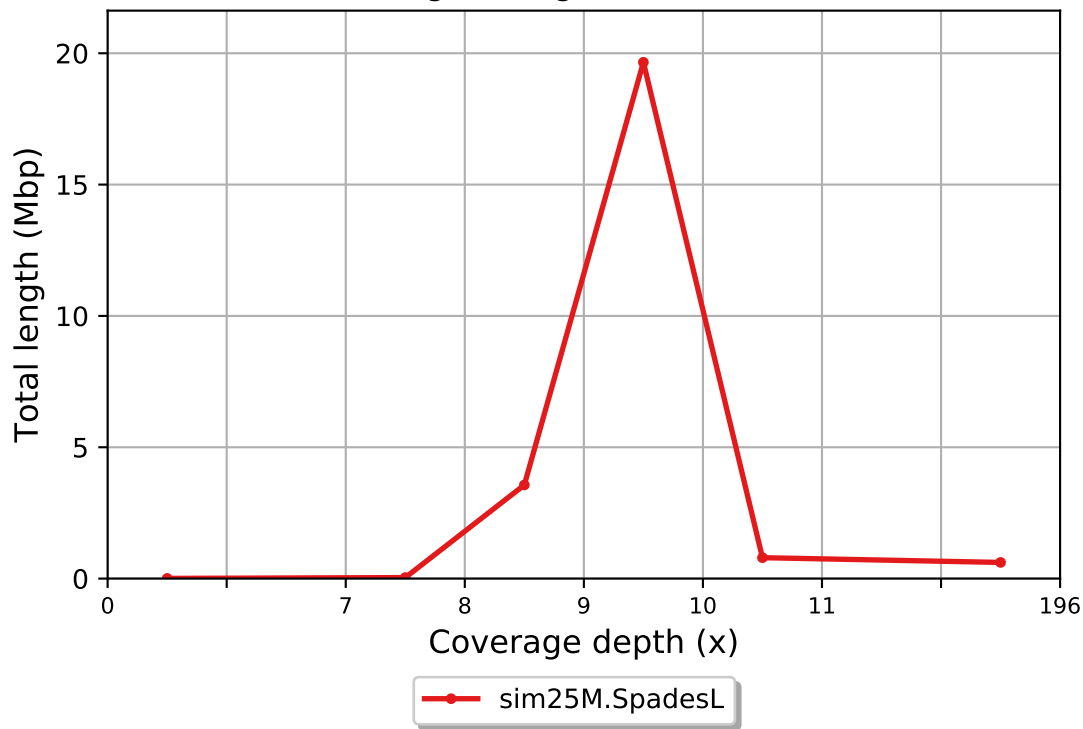
GC content



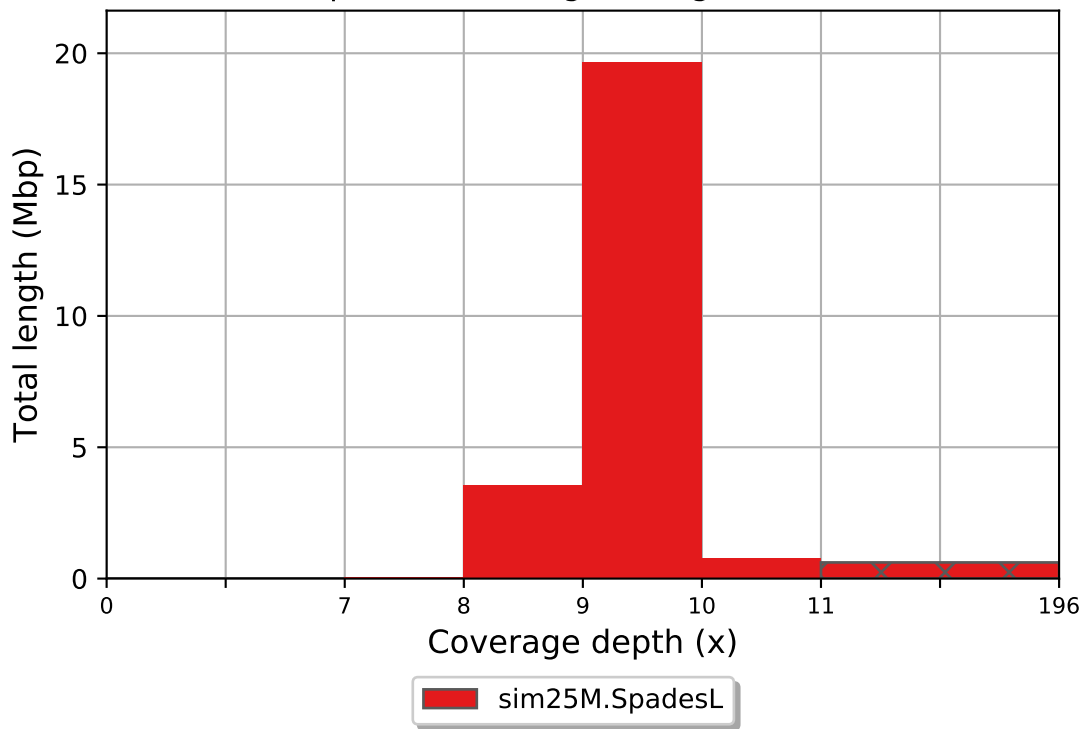
sim25M.SpadesL GC content



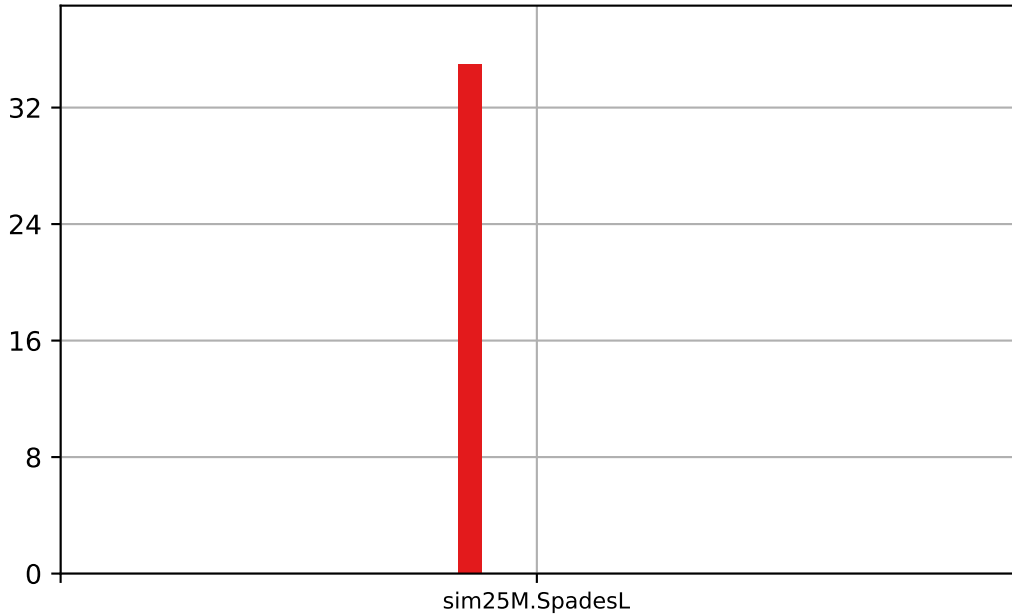
Coverage histogram (bin size: 1x)



sim25M.SpadesL coverage histogram (bin size: 1x)

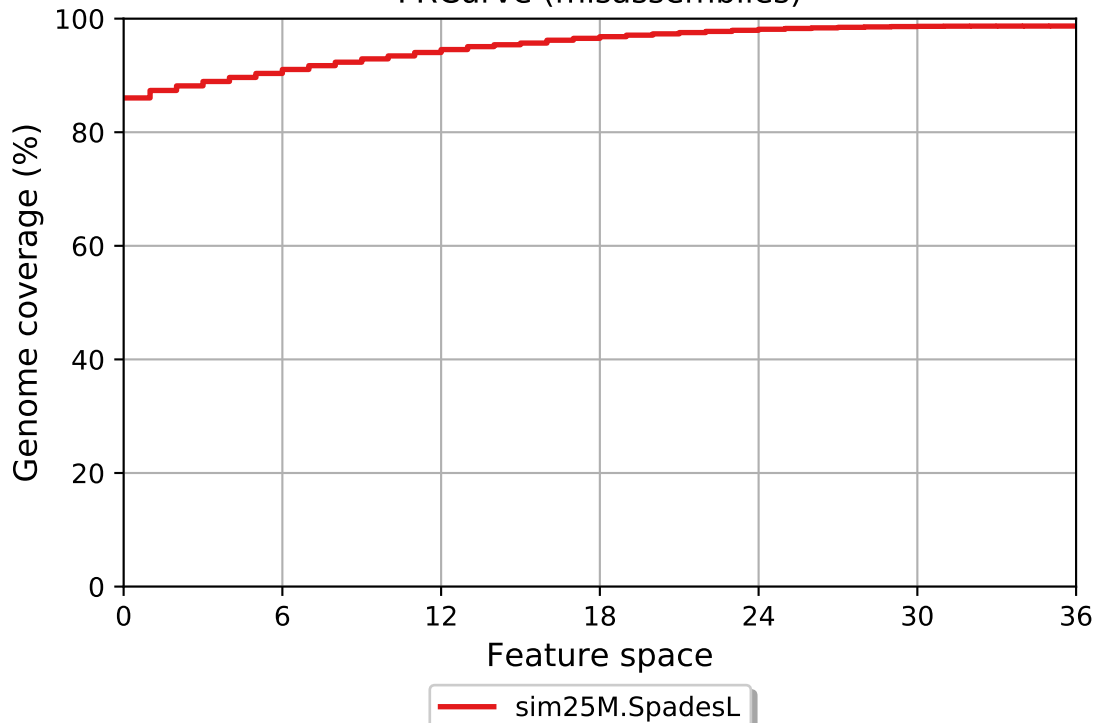


Misassemblies

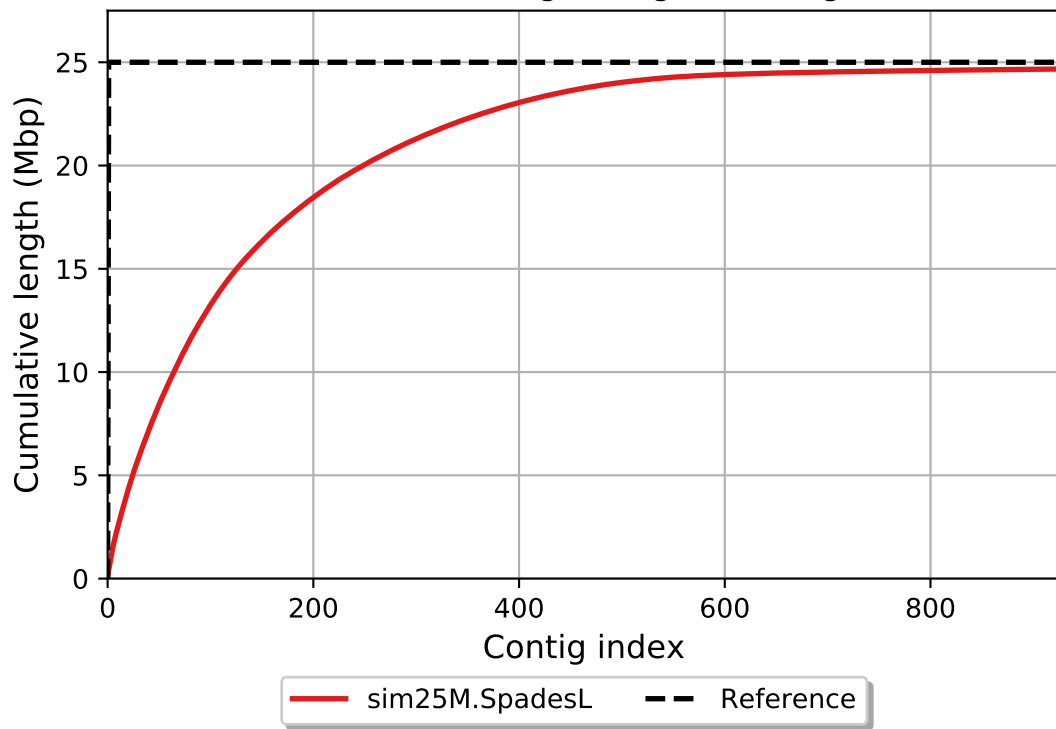


 # relocations

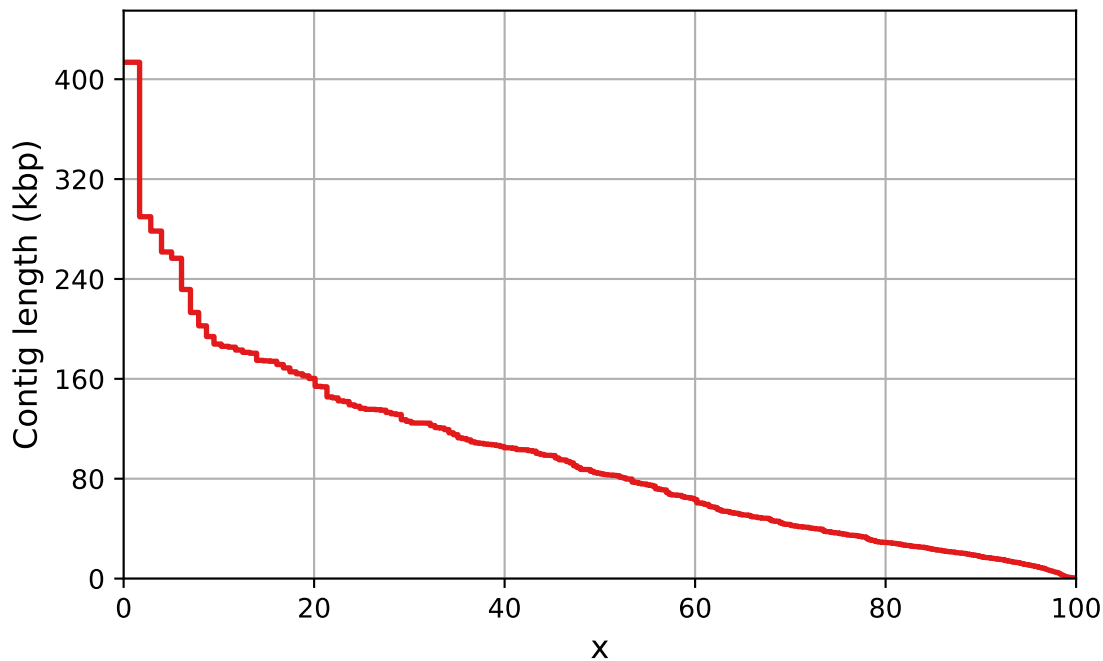
FRCurve (misassemblies)



Cumulative length (aligned contigs)

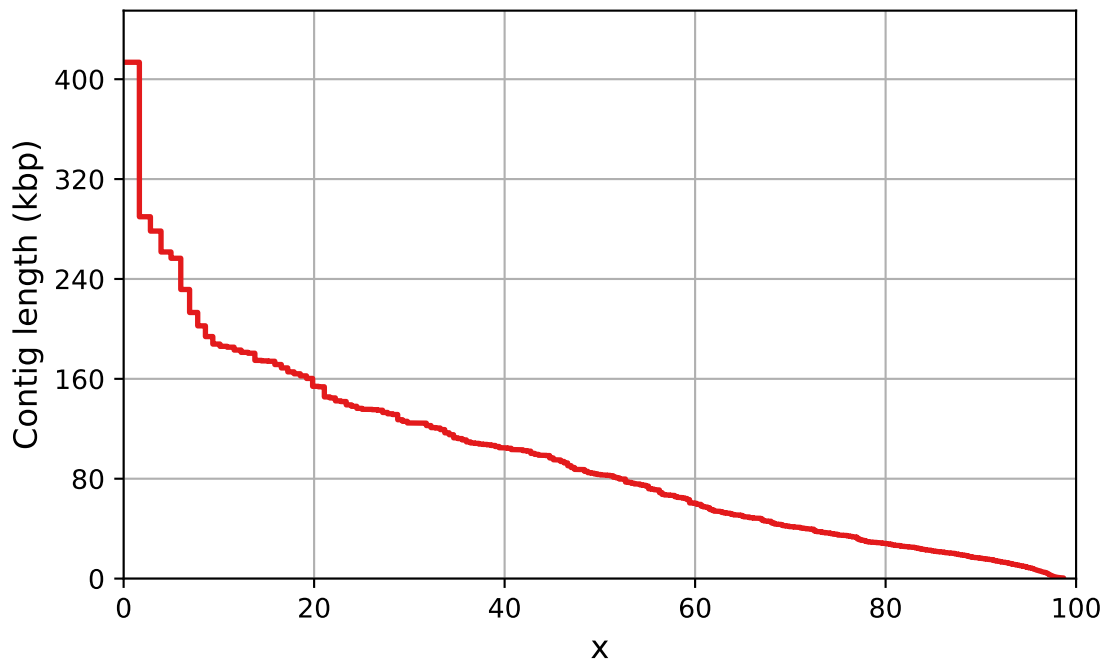


NAx



— sim25M.SpadesL

NGAx



— sim25M.SpadesL