

# Report

|                             | smart_nanopore_50 |
|-----------------------------|-------------------|
| # contigs (>= 0 bp)         | 503               |
| # contigs (>= 1000 bp)      | 503               |
| # contigs (>= 5000 bp)      | 503               |
| # contigs (>= 10000 bp)     | 364               |
| # contigs (>= 25000 bp)     | 92                |
| # contigs (>= 50000 bp)     | 10                |
| Total length (>= 0 bp)      | 8884368           |
| Total length (>= 1000 bp)   | 8884368           |
| Total length (>= 5000 bp)   | 8884368           |
| Total length (>= 10000 bp)  | 7837288           |
| Total length (>= 25000 bp)  | 3462562           |
| Total length (>= 50000 bp)  | 636906            |
| # contigs                   | 503               |
| Largest contig              | 99953             |
| Total length                | 8884368           |
| Reference length            | 335799            |
| GC (%)                      | 33.97             |
| Reference GC (%)            | 35.65             |
| N50                         | 20880             |
| NG50                        | 81167             |
| N75                         | 14071             |
| NG75                        | 58310             |
| L50                         | 135               |
| LG50                        | 2                 |
| L75                         | 266               |
| LG75                        | 4                 |
| # misassemblies             | 353               |
| # misassembled contigs      | 161               |
| Misassembled contigs length | 3331351           |
| # local misassemblies       | 294               |
| # unaligned contigs         | 145 + 118 part    |
| Unaligned length            | 4013273           |
| Genome fraction (%)         | 67.690            |
| Duplication ratio           | 22.180            |
| # N's per 100 kbp           | 0.00              |
| # mismatches per 100 kbp    | 1061.14           |
| # indels per 100 kbp        | 2026.38           |
| Largest alignment           | 39702             |
| NGA50                       | 34078             |
| NGA75                       | 30436             |
| LGA50                       | 5                 |
| LGA75                       | 8                 |

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

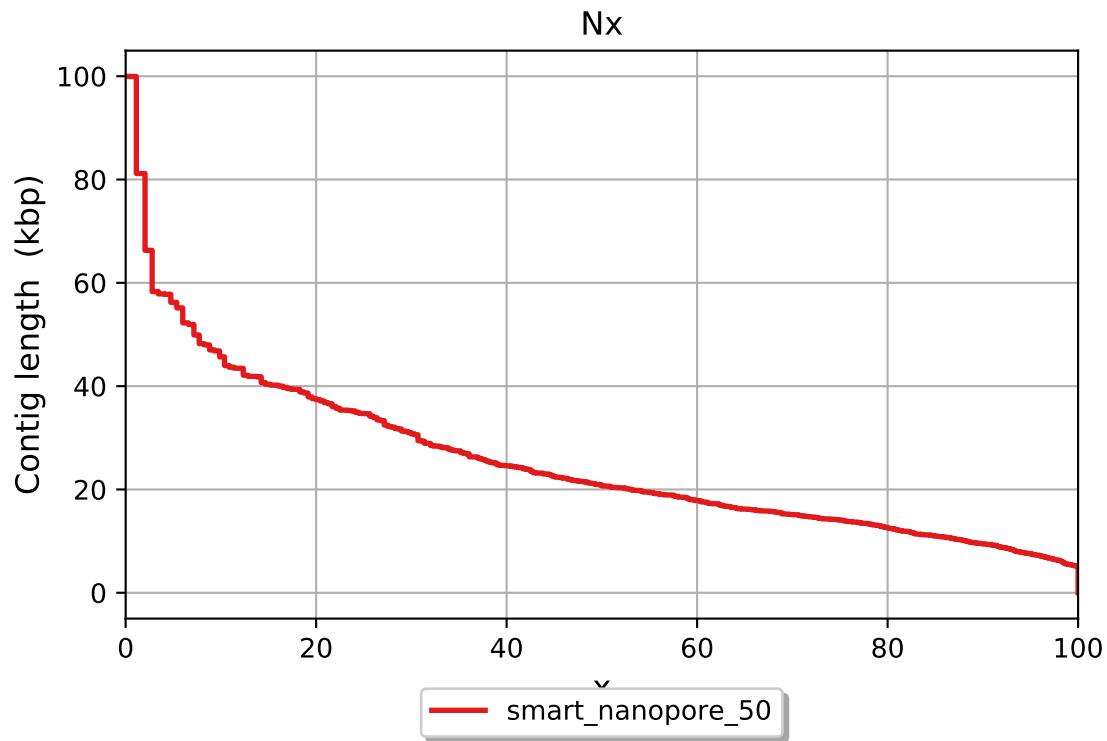
|                             | smart_nanopore_50 |
|-----------------------------|-------------------|
| # misassemblies             | 353               |
| # relocations               | 351               |
| # translocations            | 2                 |
| # inversions                | 0                 |
| # misassembled contigs      | 161               |
| Misassembled contigs length | 3331351           |
| # local misassemblies       | 294               |
| # mismatches                | 2412              |
| # indels                    | 4606              |
| # short indels              | 4533              |
| # long indels               | 73                |
| Indels length               | 6536              |

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

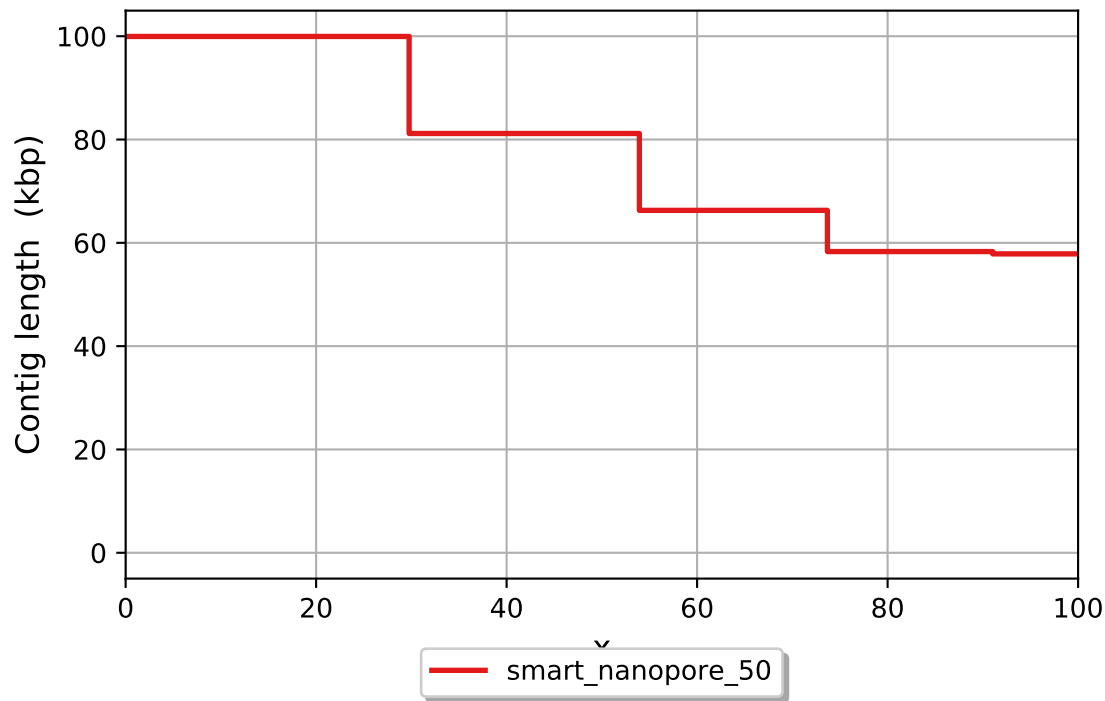
## Unaligned report

|                               | smart_nanopore_50 |
|-------------------------------|-------------------|
| # fully unaligned contigs     | 145               |
| Fully unaligned length        | 2277898           |
| # partially unaligned contigs | 118               |
| # with misassembly            | 49                |
| # both parts are significant  | 95                |
| Partially unaligned length    | 1735375           |
| # N's                         | 0                 |

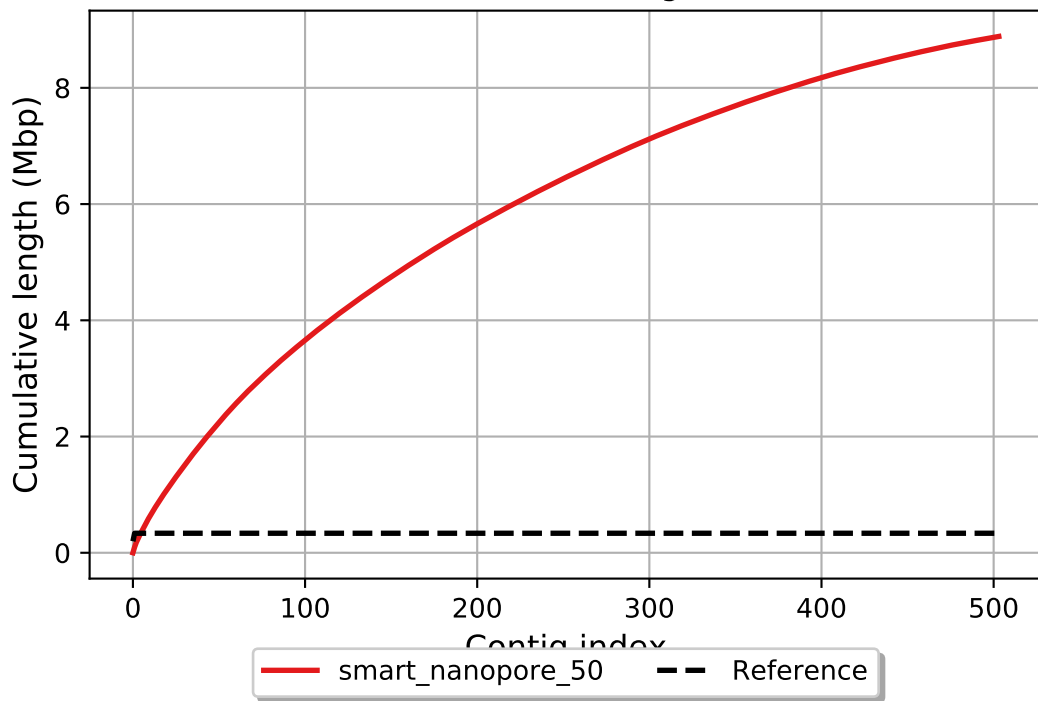
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



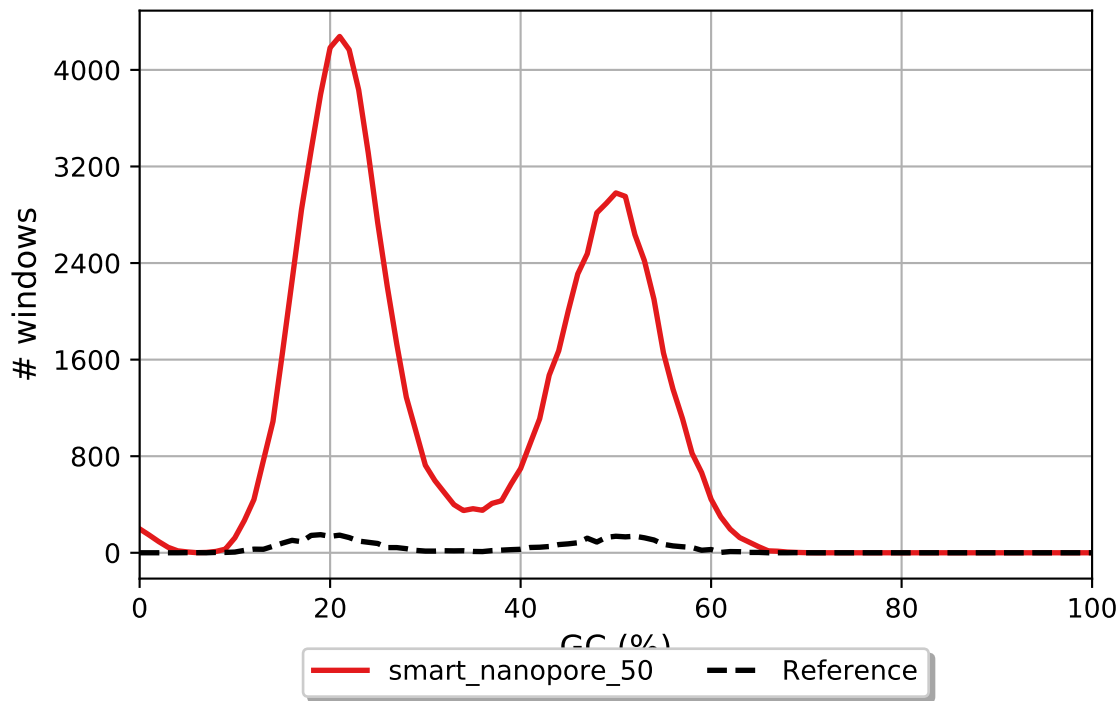
NGx



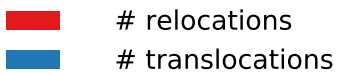
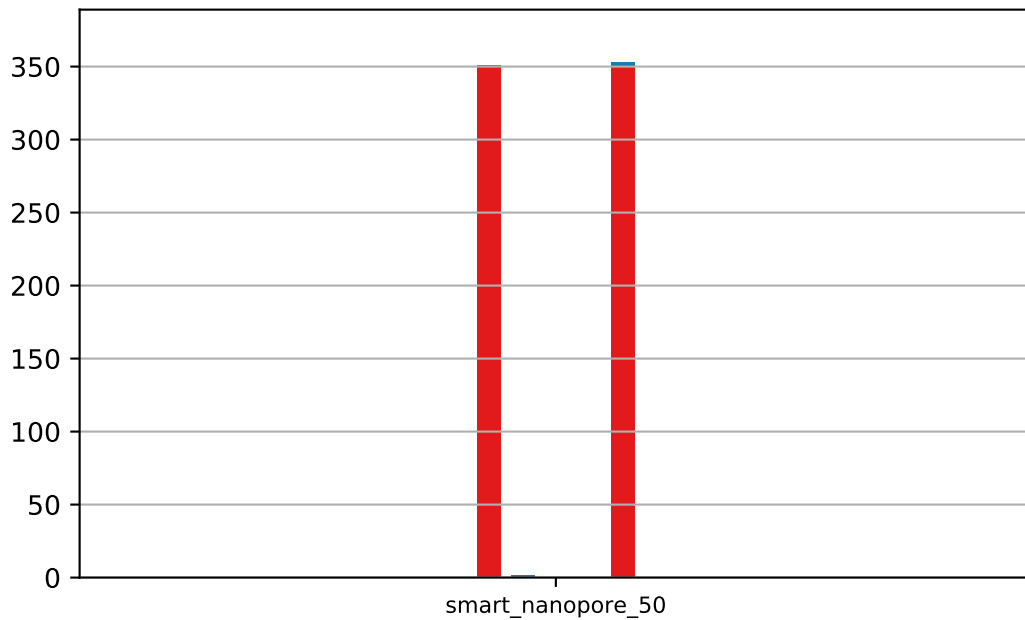
Cumulative length



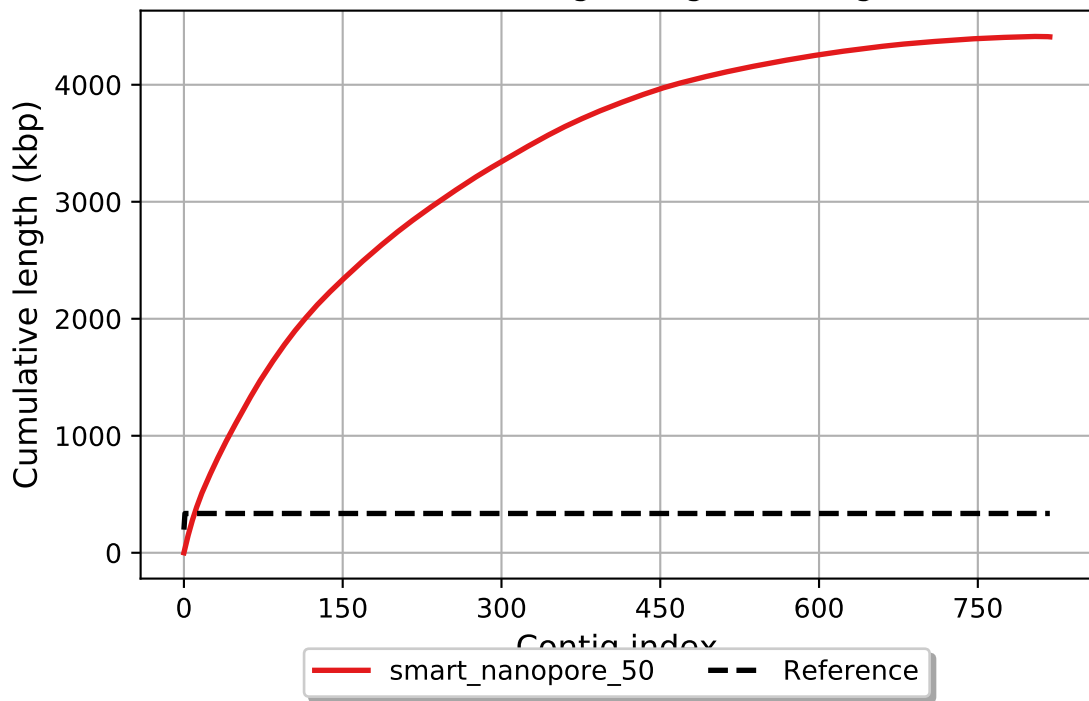
GC content



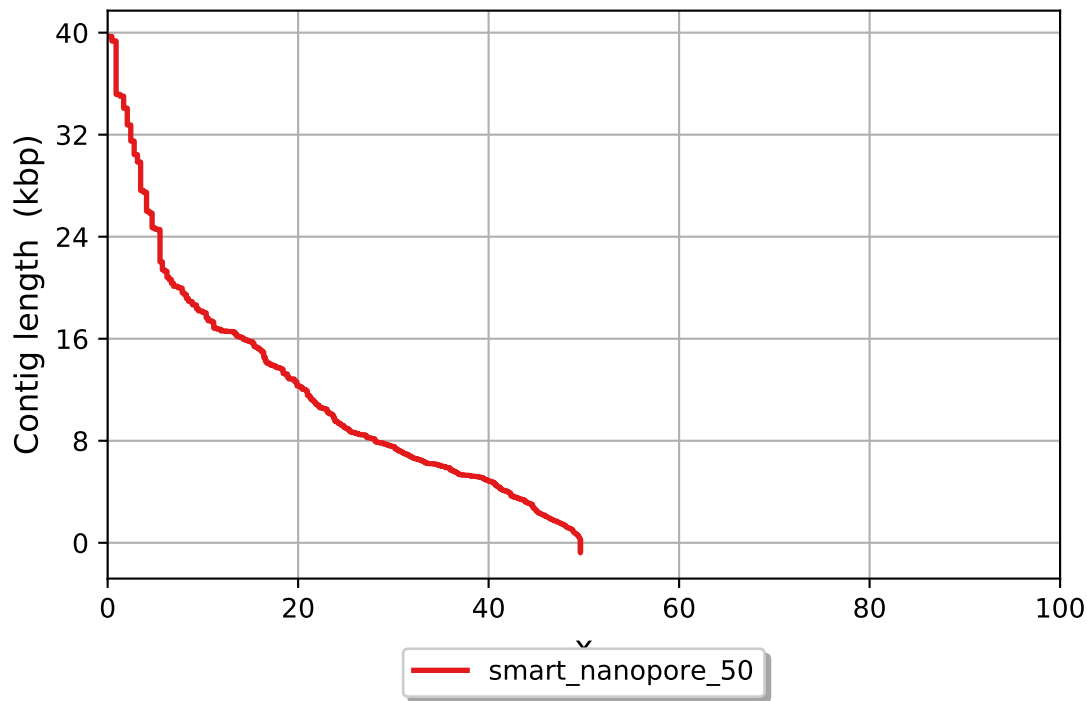
## Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

