

|                             | Report          |                 |                 |
|-----------------------------|-----------------|-----------------|-----------------|
|                             | 22-324_filtered | 22-335_filtered | 22-311_filtered |
| # contigs (>= 0 bp)         | 274             | 241             | 242             |
| # contigs (>= 1000 bp)      | 6               | 4               | 5               |
| # contigs (>= 5000 bp)      | 0               | 0               | 0               |
| # contigs (>= 10000 bp)     | 0               | 0               | 0               |
| # contigs (>= 25000 bp)     | 0               | 0               | 0               |
| # contigs (>= 50000 bp)     | 0               | 0               | 0               |
| Total length (>= 0 bp)      | 97127           | 85480           | 86933           |
| Total length (>= 1000 bp)   | 8553            | 5290            | 6748            |
| Total length (>= 5000 bp)   | 0               | 0               | 0               |
| Total length (>= 10000 bp)  | 0               | 0               | 0               |
| Total length (>= 25000 bp)  | 0               | 0               | 0               |
| Total length (>= 50000 bp)  | 0               | 0               | 0               |
| # contigs                   | 22              | 16              | 24              |
| Largest contig              | 1780            | 1762            | 1605            |
| Total length                | 17540           | 12509           | 17611           |
| Reference length            | 5230549         | 5230549         | 5230549         |
| GC (%)                      | 59.53           | 62.32           | 60.58           |
| Reference GC (%)            | 63.78           | 63.78           | 63.78           |
| N50                         | 718             | 678             | 619             |
| NG50                        | -               | -               | -               |
| N90                         | 506             | 522             | 518             |
| NG90                        | -               | -               | -               |
| auN                         | 1006.6          | 943.0           | 879.2           |
| auNG                        | 3.4             | 2.3             | 3.0             |
| L50                         | 7               | 6               | 9               |
| LG50                        | -               | -               | -               |
| L90                         | 19              | 14              | 21              |
| LG90                        | -               | -               | -               |
| # misassemblies             | 5               | 5               | 5               |
| # misassembled contigs      | 4               | 3               | 3               |
| Misassembled contigs length | 5781            | 4023            | 3686            |
| # local misassemblies       | 0               | 0               | 0               |
| # scaffold gap ext. mis.    | 0               | 0               | 0               |
| # scaffold gap loc. mis.    | 0               | 0               | 0               |
| # unaligned mis. contigs    | 0               | 0               | 2               |
| # unaligned contigs         | 2 + 2 part      | 0 + 2 part      | 0 + 2 part      |
| Unaligned length            | 3515            | 1423            | 1374            |
| Genome fraction (%)         | 0.257           | 0.205           | 0.303           |
| Duplication ratio           | 0.997           | 0.994           | 1.006           |
| # N's per 100 kbp           | 57.01           | 0.00            | 0.00            |
| # mismatches per 100 kbp    | 754.46          | 629.82          | 463.95          |
| # indels per 100 kbp        | 14.94           | 9.40            | 0.00            |
| Largest alignment           | 1192            | 1192            | 1192            |
| Total aligned length        | 13387           | 10638           | 15950           |
| NA50                        | 507             | 532             | 562             |
| NGA50                       | -               | -               | -               |
| NA90                        | -               | -               | 125             |
| NGA90                       | -               | -               | -               |
| auNA                        | 493.9           | 521.8           | 559.9           |
| auNGA                       | 1.7             | 1.2             | 1.9             |
| LA50                        | 13              | 10              | 13              |
| LGA50                       | -               | -               | -               |
| LA90                        | -               | -               | 31              |
| LGA90                       | -               | -               | -               |

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

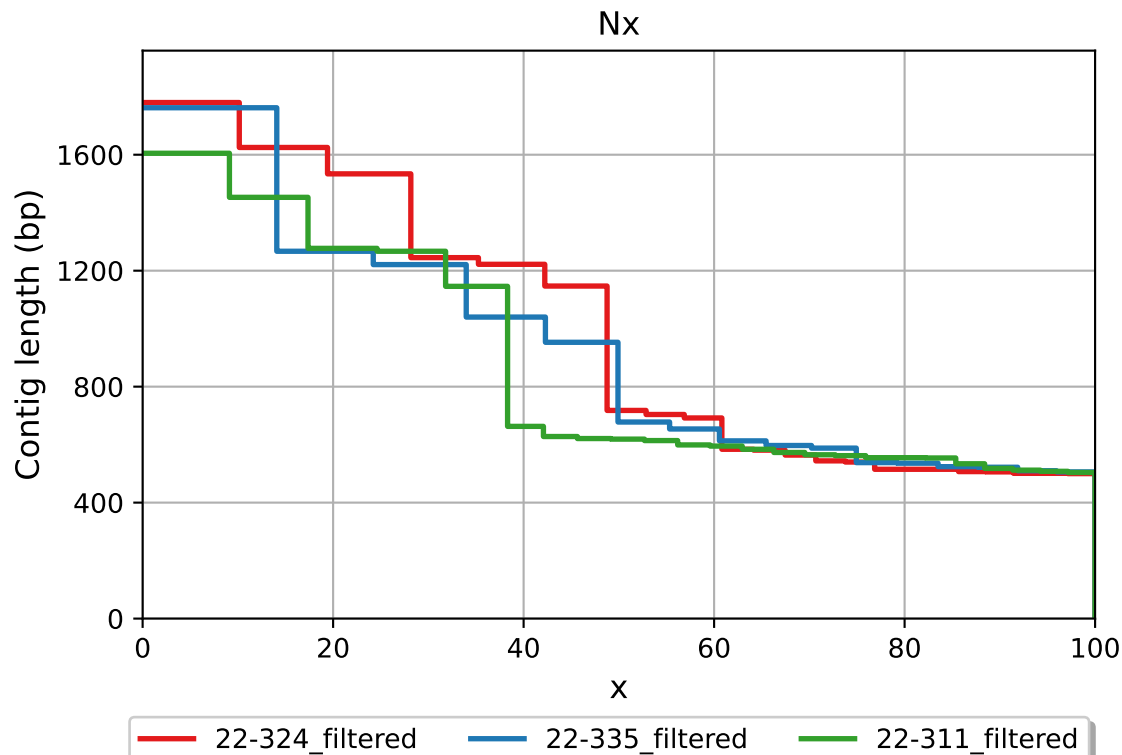
|                             | 22-324_filtered | 22-335_filtered | 22-311_filtered |
|-----------------------------|-----------------|-----------------|-----------------|
| # misassemblies             | 5               | 5               | 5               |
| # contig misassemblies      | 5               | 5               | 5               |
| # c. relocations            | 0               | 0               | 0               |
| # c. translocations         | 5               | 5               | 5               |
| # c. inversions             | 0               | 0               | 0               |
| # scaffold misassemblies    | 0               | 0               | 0               |
| # s. relocations            | 0               | 0               | 0               |
| # s. translocations         | 0               | 0               | 0               |
| # s. inversions             | 0               | 0               | 0               |
| # misassembled contigs      | 4               | 3               | 3               |
| Misassembled contigs length | 5781            | 4023            | 3686            |
| # local misassemblies       | 0               | 0               | 0               |
| # scaffold gap ext. mis.    | 0               | 0               | 0               |
| # scaffold gap loc. mis.    | 0               | 0               | 0               |
| # unaligned mis. contigs    | 0               | 0               | 2               |
| # mismatches                | 101             | 67              | 74              |
| # indels                    | 2               | 1               | 0               |
| # indels (<= 5 bp)          | 1               | 1               | 0               |
| # indels (> 5 bp)           | 1               | 0               | 0               |
| Indels length               | 38              | 1               | 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).

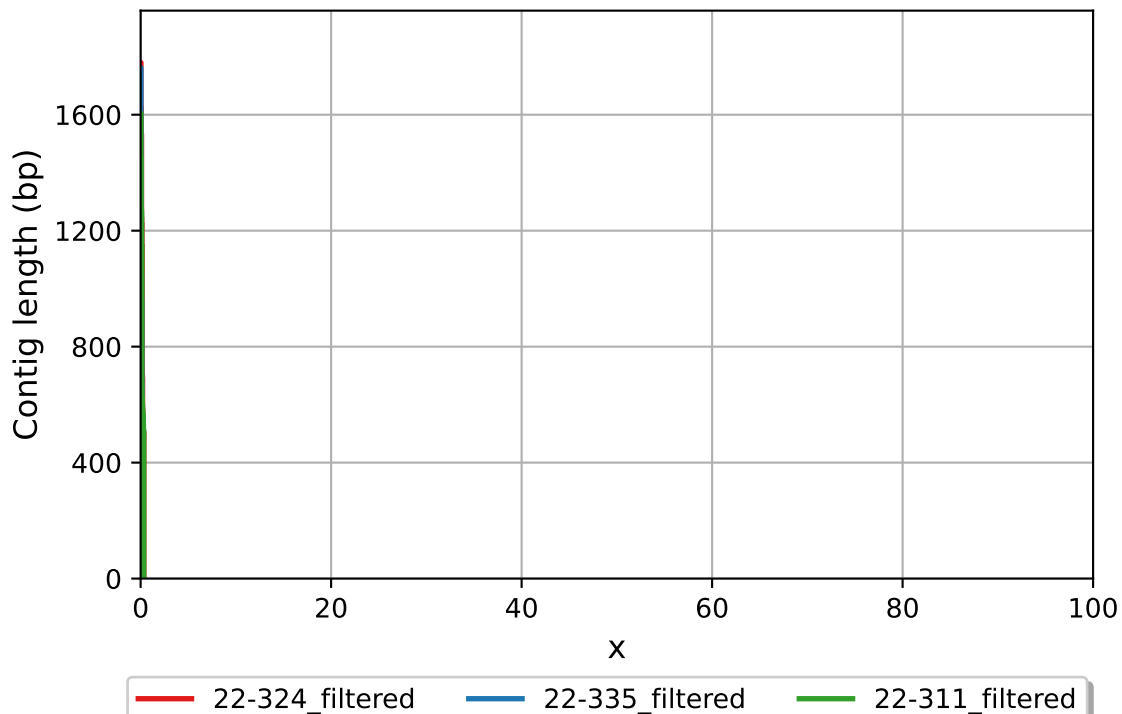
## Unaligned report

|                               | 22-324_filtered | 22-335_filtered | 22-311_filtered |
|-------------------------------|-----------------|-----------------|-----------------|
| # fully unaligned contigs     | 2               | 0               | 0               |
| Fully unaligned length        | 2329            | 0               | 0               |
| # partially unaligned contigs | 2               | 2               | 2               |
| Partially unaligned length    | 1186            | 1423            | 1374            |
| # N's                         | 10              | 0               | 0               |

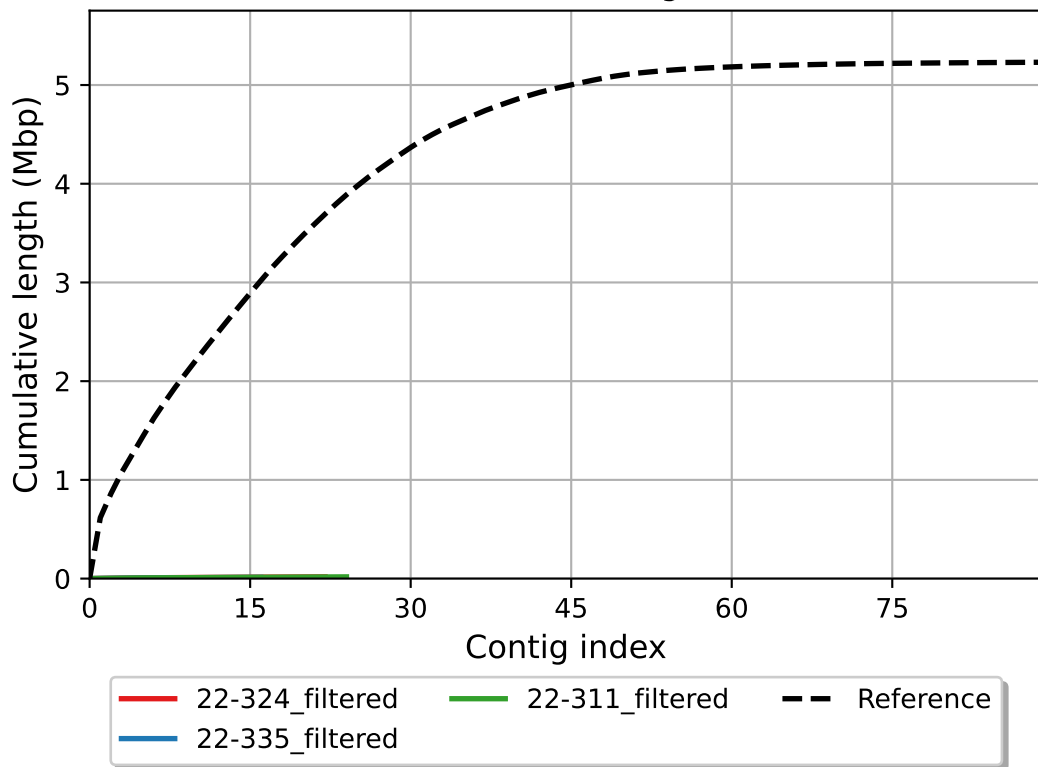
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



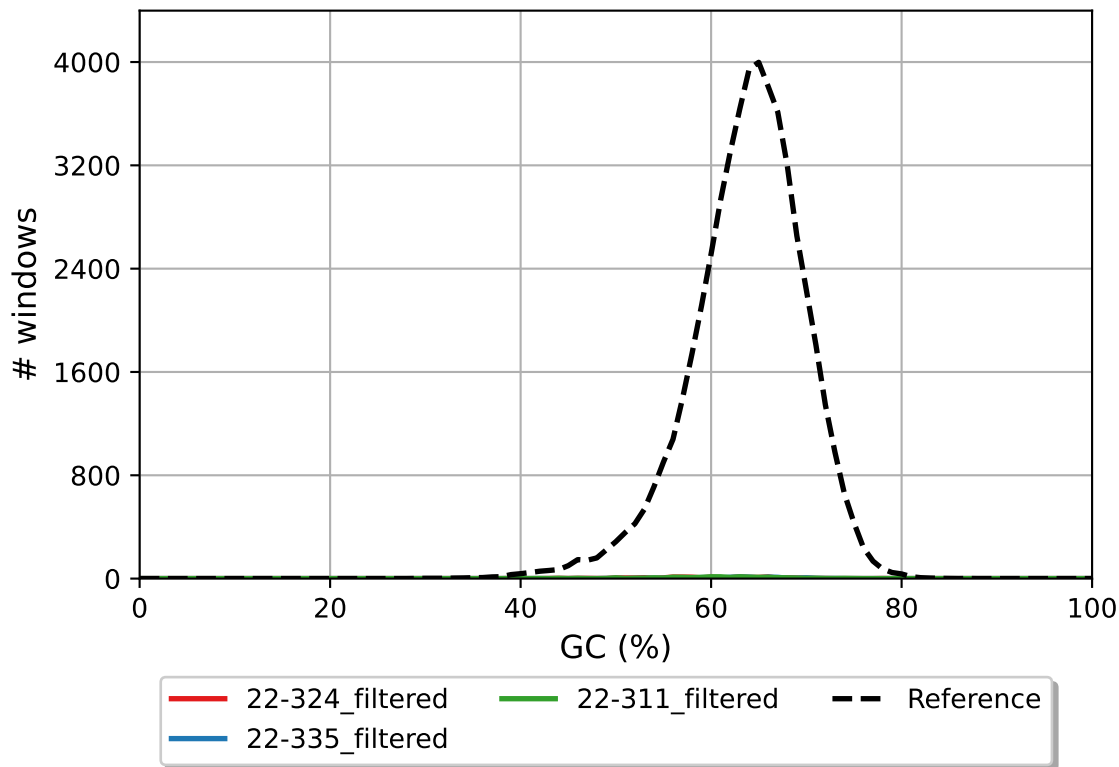
# NGx



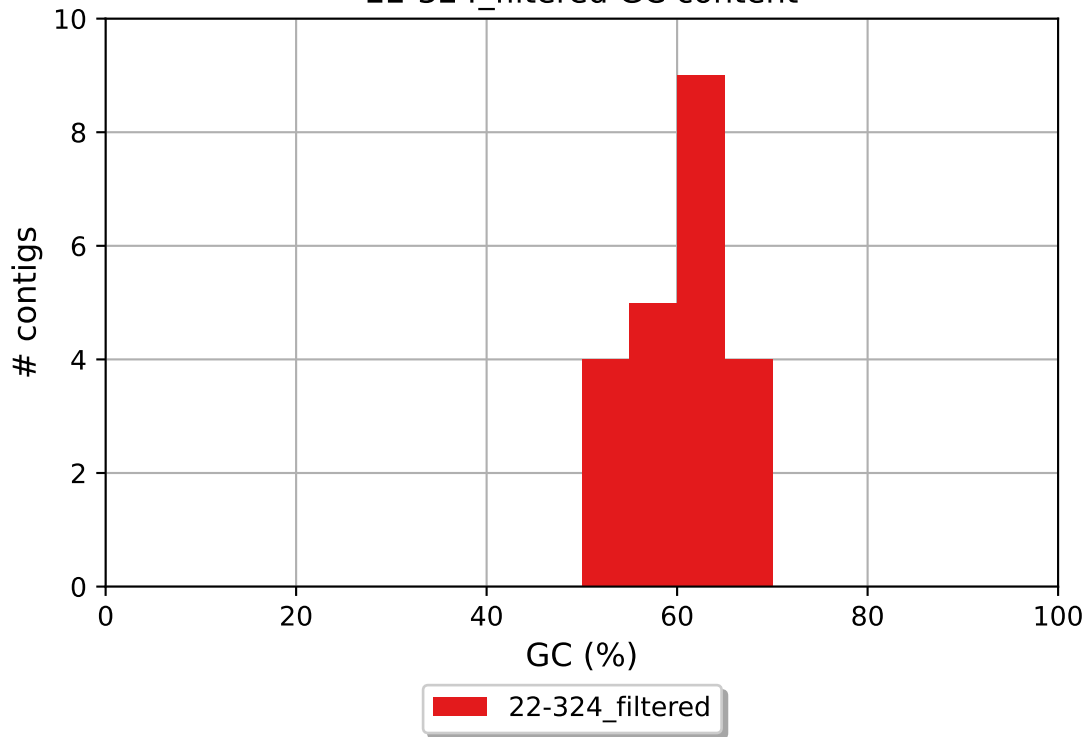
Cumulative length



GC content

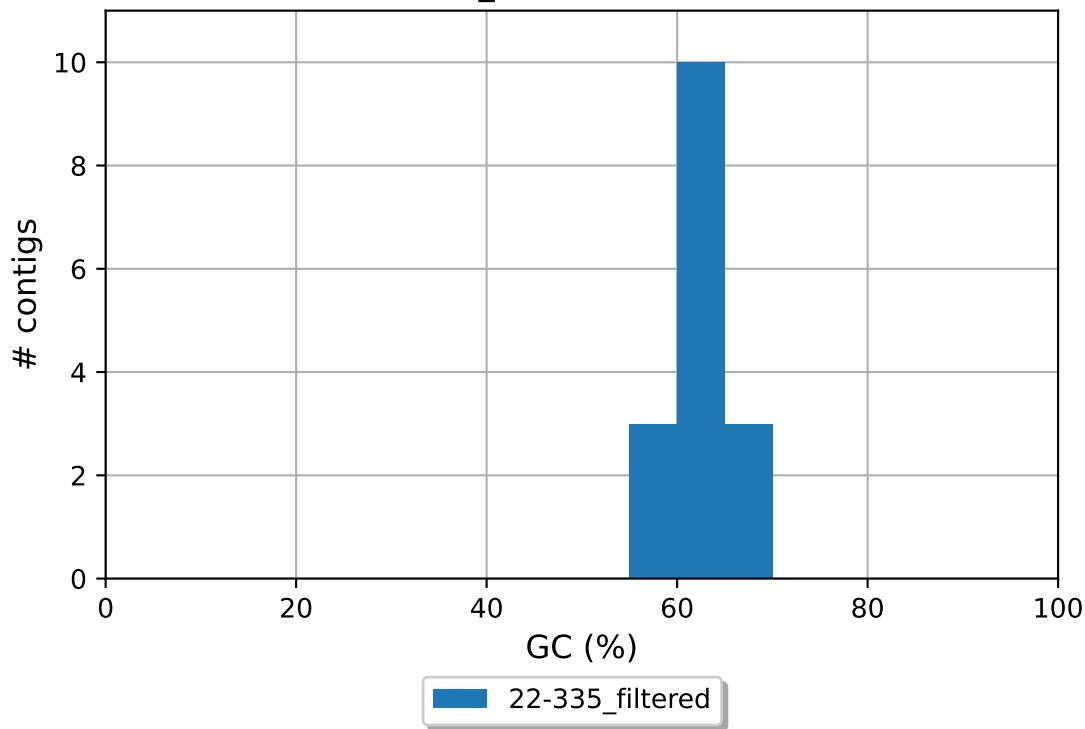


22-324\_filtered GC content

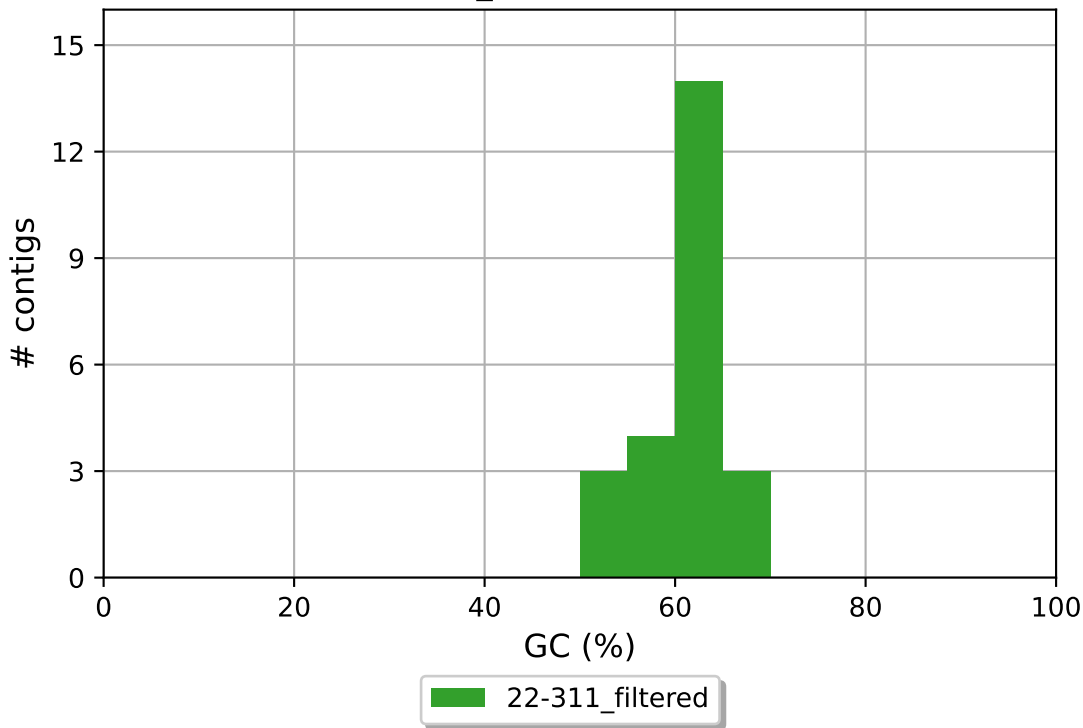




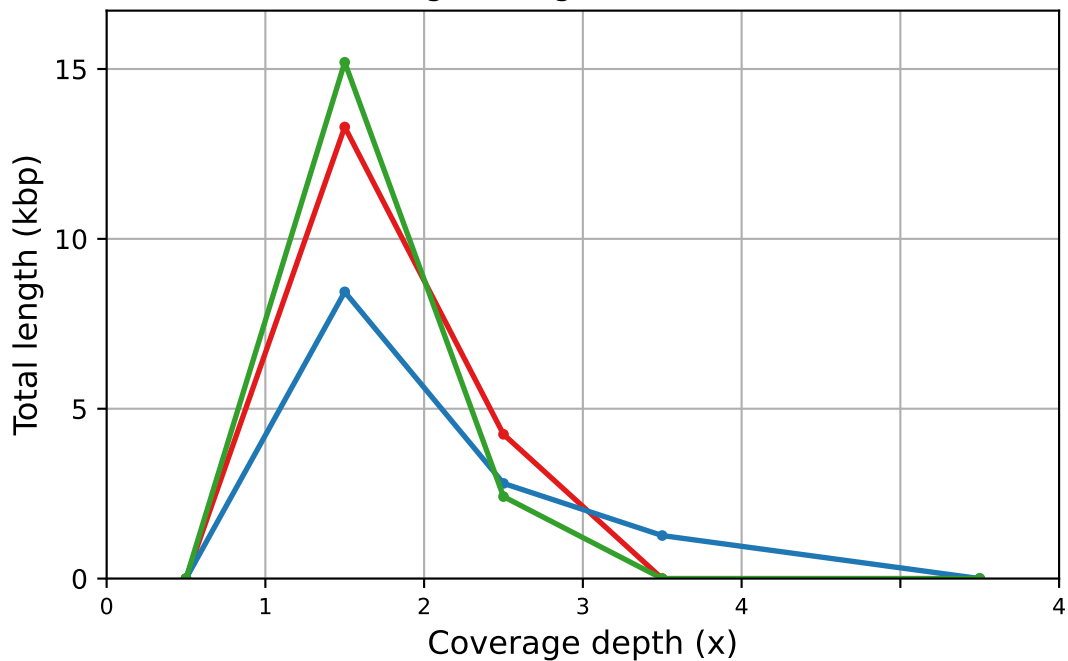
22-335\_filtered GC content



22-311\_filtered GC content

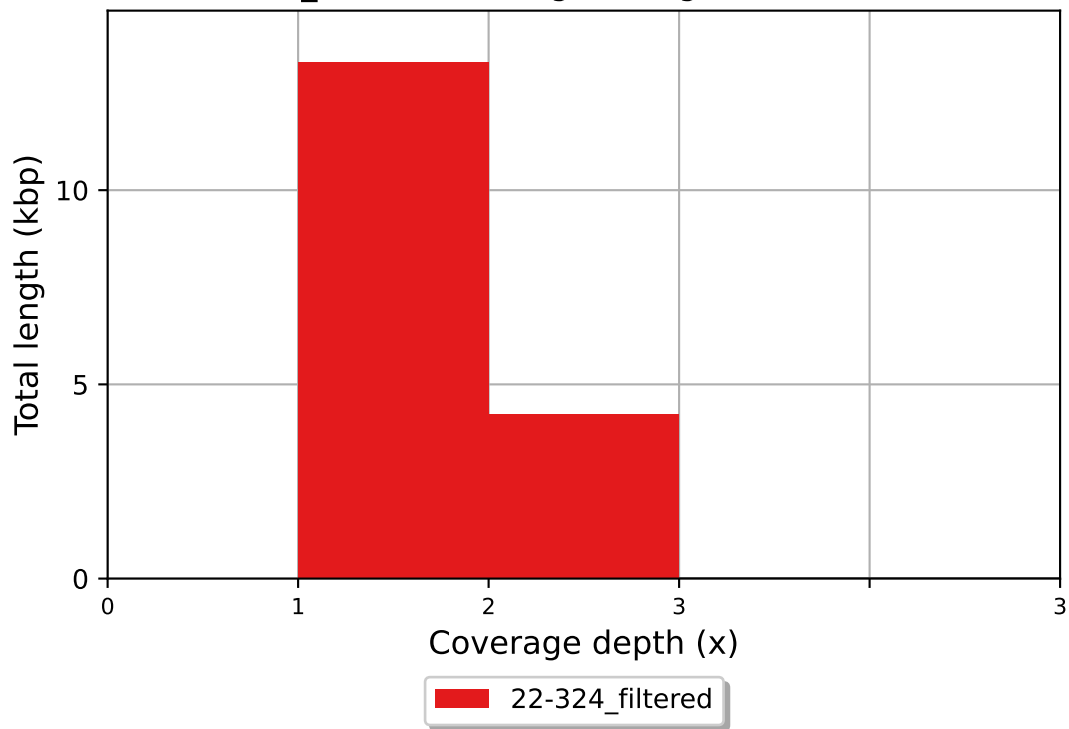


Coverage histogram (bin size: 1x)

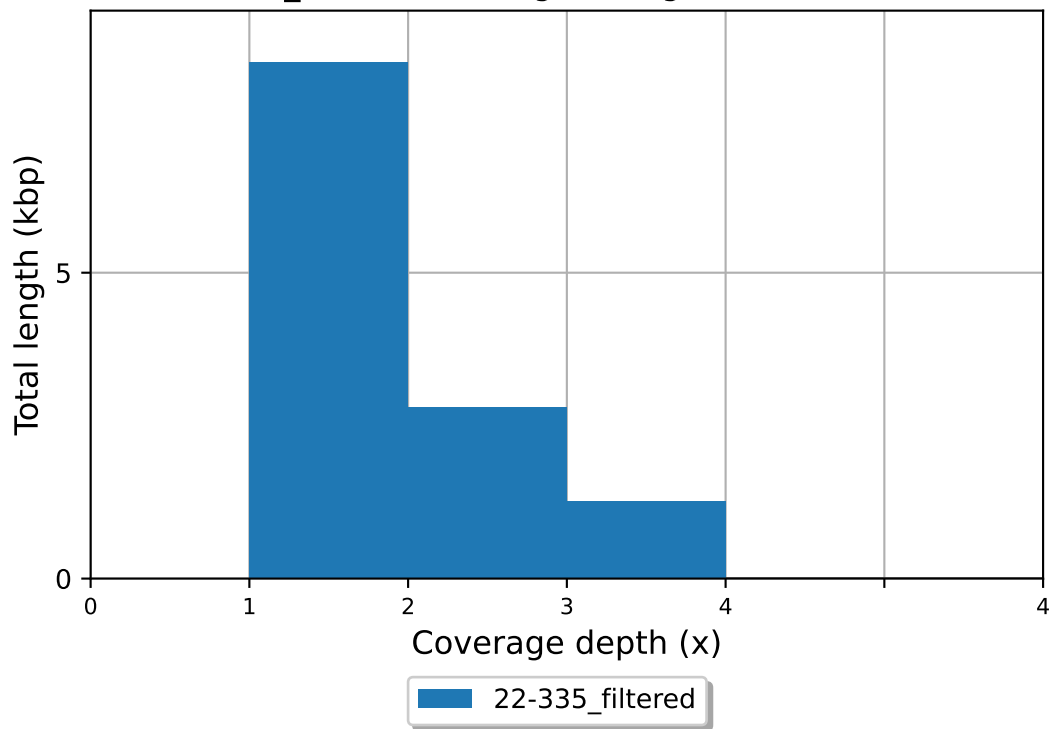


—●— 22-324\_filtered    —●— 22-335\_filtered    —●— 22-311\_filtered

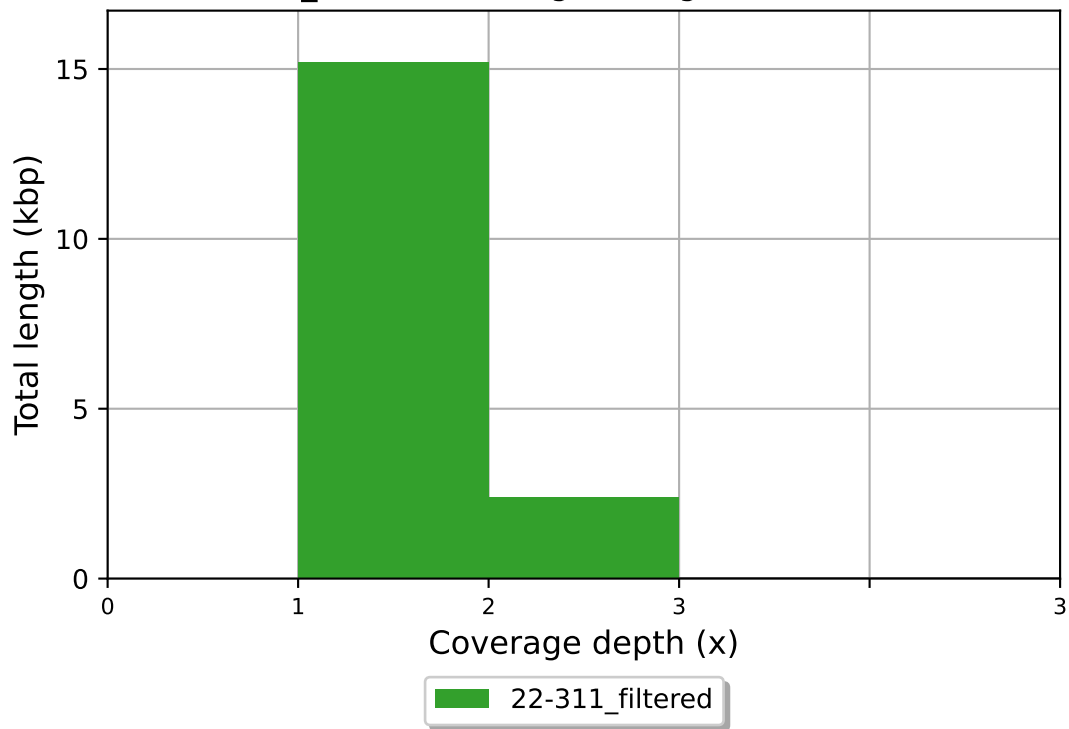
22-324\_filtered coverage histogram (bin size: 1x)



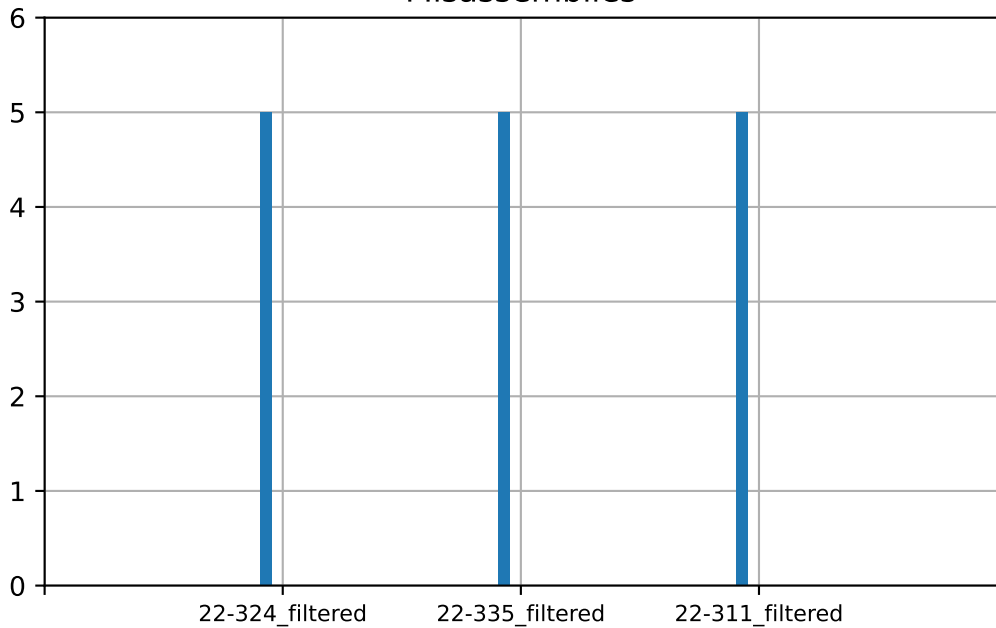
22-335\_filtered coverage histogram (bin size: 1x)



22-311\_filtered coverage histogram (bin size: 1x)

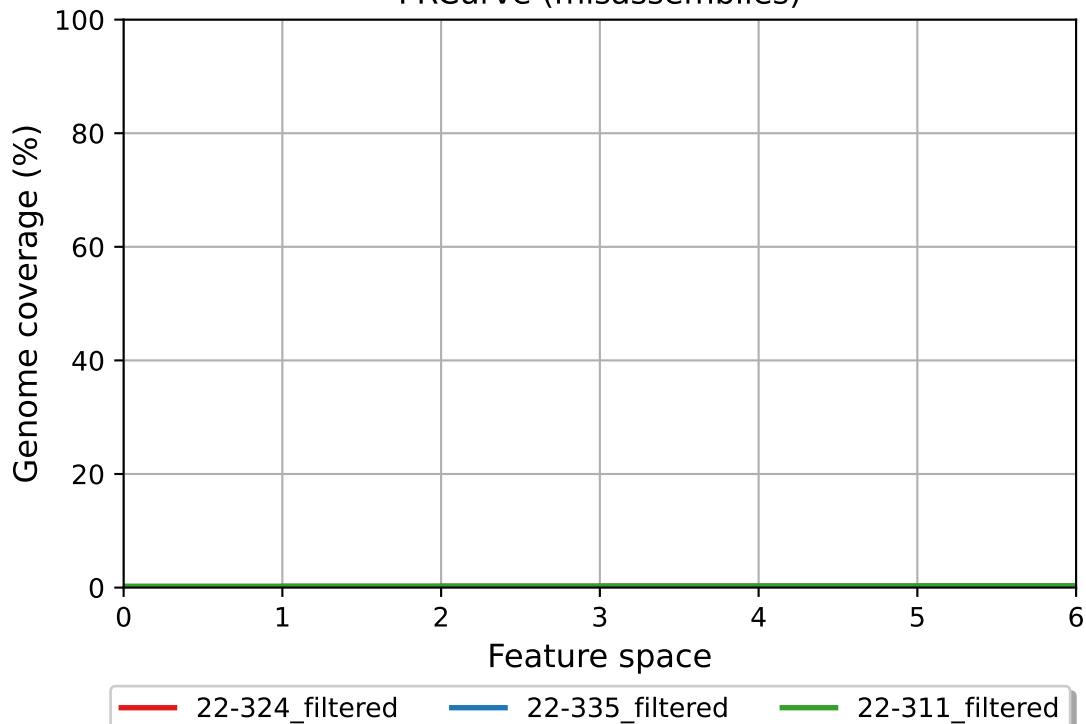


## Misassemblies



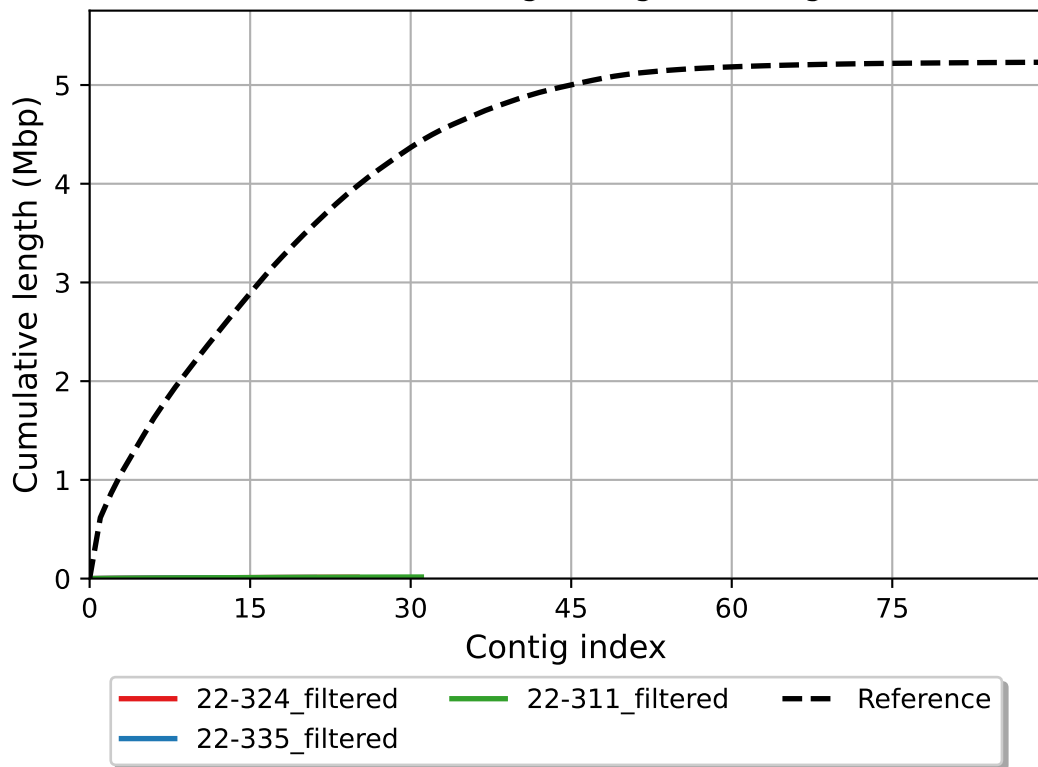
# translocations

FRCurve (misassemblies)

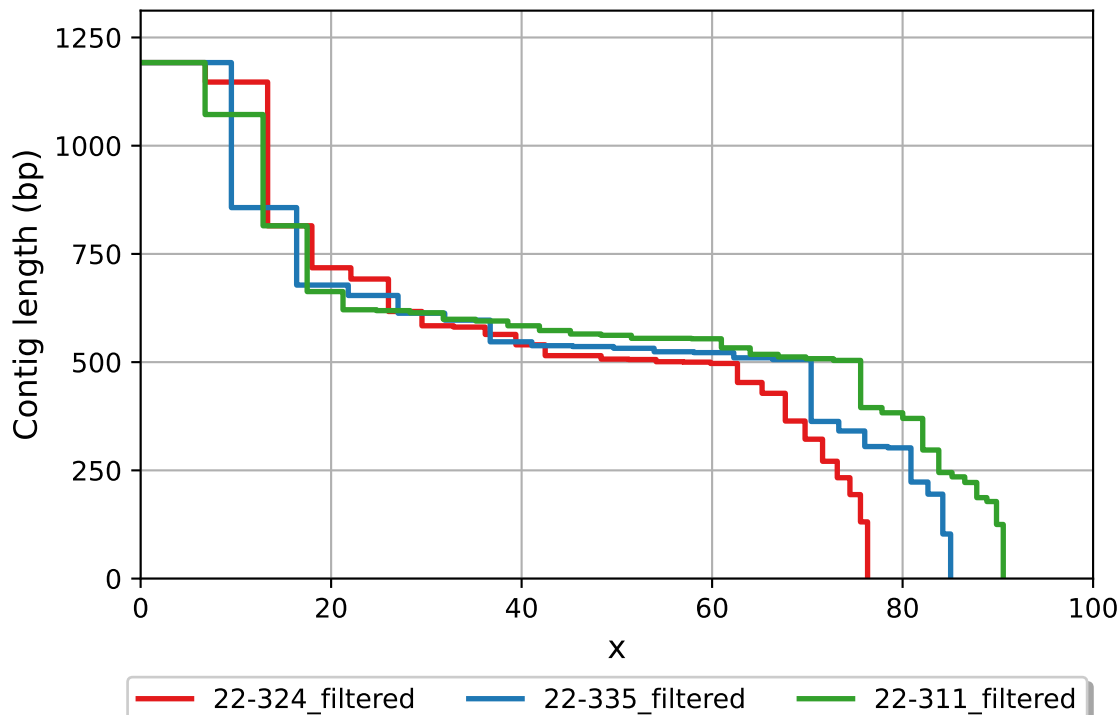




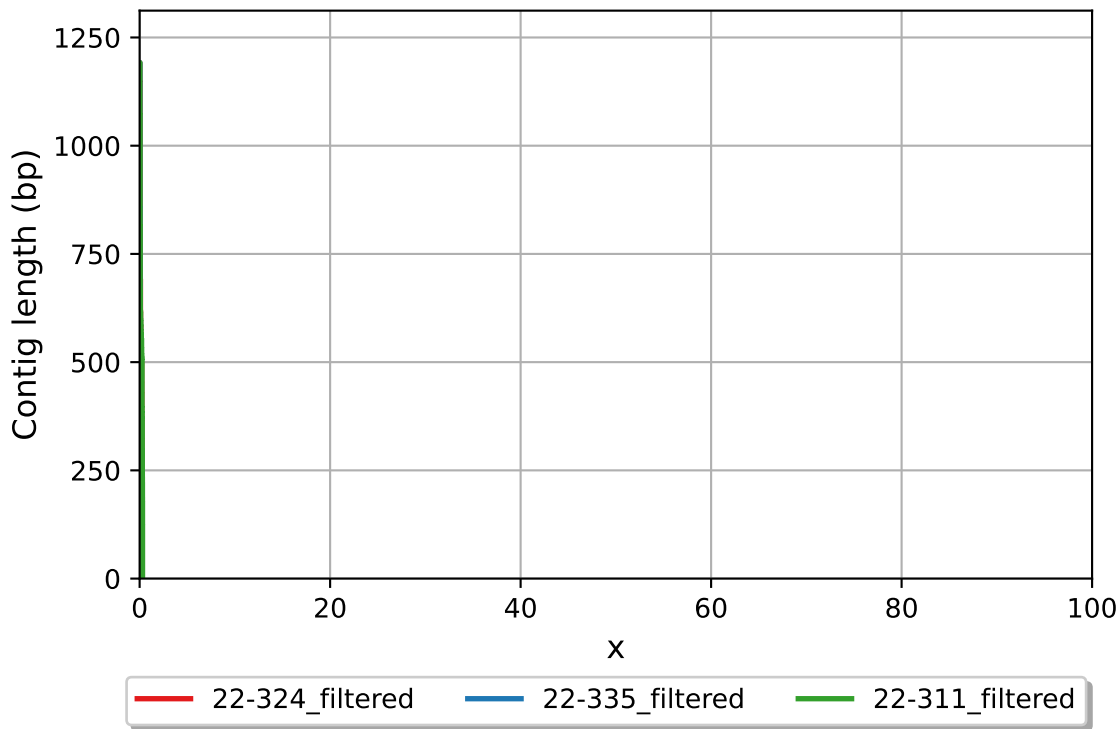
Cumulative length (aligned contigs)



NAx



# NGAx



# Genome fraction, %

100

50



22-324\_filtered



22-335\_filtered



22-311\_filtered