

## Report

|                             | spades_ctg   | mulksq_ctg   |
|-----------------------------|--------------|--------------|
| # contigs (>= 0 bp)         | 181          | 176          |
| # contigs (>= 1000 bp)      | 109          | 101          |
| # contigs (>= 5000 bp)      | 77           | 69           |
| # contigs (>= 10000 bp)     | 70           | 64           |
| # contigs (>= 25000 bp)     | 50           | 44           |
| # contigs (>= 50000 bp)     | 34           | 27           |
| Total length (>= 0 bp)      | 4580979      | 4578907      |
| Total length (>= 1000 bp)   | 4555691      | 4551511      |
| Total length (>= 5000 bp)   | 4475742      | 4471944      |
| Total length (>= 10000 bp)  | 4414933      | 4431621      |
| Total length (>= 25000 bp)  | 4050646      | 4072537      |
| Total length (>= 50000 bp)  | 3493993      | 3459938      |
| # contigs                   | 120          | 117          |
| Largest contig              | 292708       | 292708       |
| Total length                | 4563290      | 4562515      |
| Reference length            | 114179       | 114179       |
| GC (%)                      | 68.82        | 68.82        |
| Reference GC (%)            | 70.07        | 70.07        |
| N50                         | 84722        | 111873       |
| NG50                        | 292708       | 292708       |
| N75                         | 51238        | 55037        |
| NG75                        | 292708       | 292708       |
| L50                         | 16           | 13           |
| LG50                        | 1            | 1            |
| L75                         | 33           | 27           |
| LG75                        | 1            | 1            |
| # misassemblies             | 0            | 0            |
| # misassembled contigs      | 0            | 0            |
| Misassembled contigs length | 0            | 0            |
| # local misassemblies       | 0            | 0            |
| # scaffold gap ext. mis.    | 0            | 0            |
| # scaffold gap loc. mis.    | 0            | 0            |
| # unaligned mis. contigs    | 0            | 0            |
| # unaligned contigs         | 112 + 4 part | 111 + 4 part |
| Unaligned length            | 4448536      | 4447781      |
| Genome fraction (%)         | 100.000      | 100.000      |
| Duplication ratio           | 1.005        | 1.005        |
| # N's per 100 kbp           | 0.00         | 0.00         |
| # mismatches per 100 kbp    | 7.01         | 7.01         |
| # indels per 100 kbp        | 2.63         | 2.63         |
| Largest alignment           | 58318        | 112704       |
| Total aligned length        | 114662       | 114642       |
| NGA50                       | 58318        | 112704       |
| NGA75                       | 36015        | 112704       |
| LGA50                       | 1            | 1            |
| LGA75                       | 2            | 1            |

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

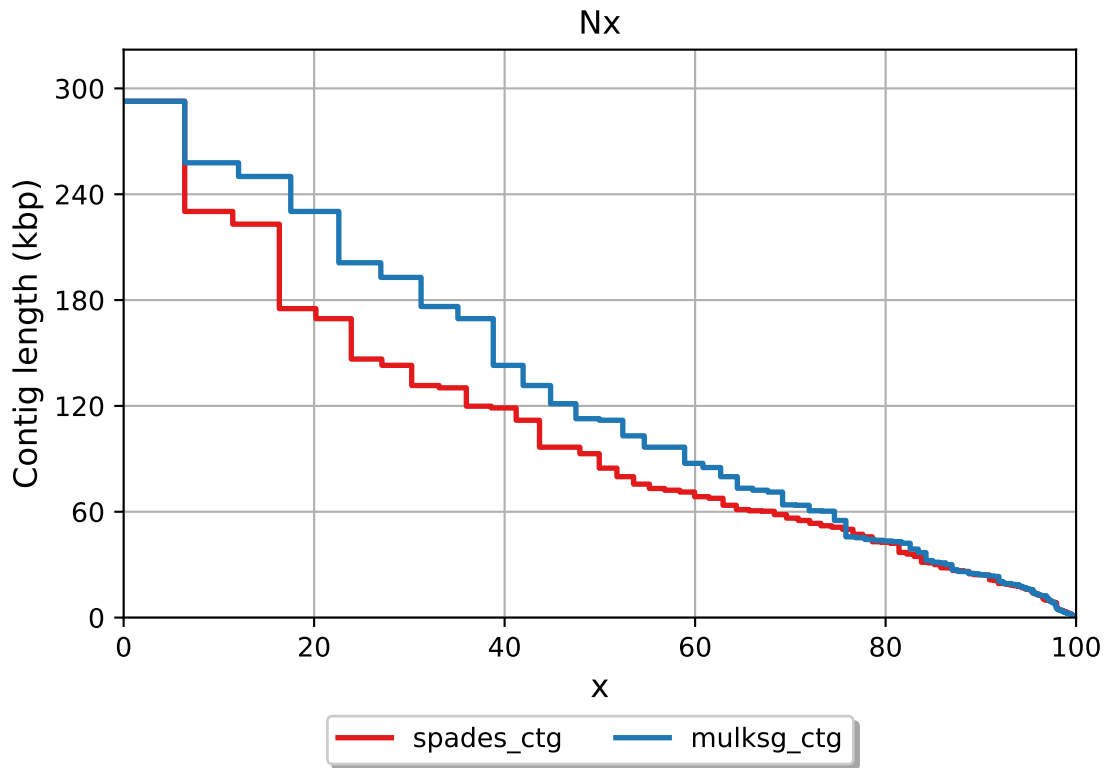
|                             | spades_ctg | mulksq_ctg |
|-----------------------------|------------|------------|
| # misassemblies             | 0          | 0          |
| # contig misassemblies      | 0          | 0          |
| # c. relocations            | 0          | 0          |
| # c. translocations         | 0          | 0          |
| # c. inversions             | 0          | 0          |
| # scaffold misassemblies    | 0          | 0          |
| # s. relocations            | 0          | 0          |
| # s. translocations         | 0          | 0          |
| # s. inversions             | 0          | 0          |
| # misassembled contigs      | 0          | 0          |
| Misassembled contigs length | 0          | 0          |
| # local misassemblies       | 0          | 0          |
| # scaffold gap ext. mis.    | 0          | 0          |
| # scaffold gap loc. mis.    | 0          | 0          |
| # unaligned mis. contigs    | 0          | 0          |
| # mismatches                | 8          | 8          |
| # indels                    | 3          | 3          |
| # indels (<= 5 bp)          | 3          | 3          |
| # indels (> 5 bp)           | 0          | 0          |
| Indels length               | 3          | 3          |

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).

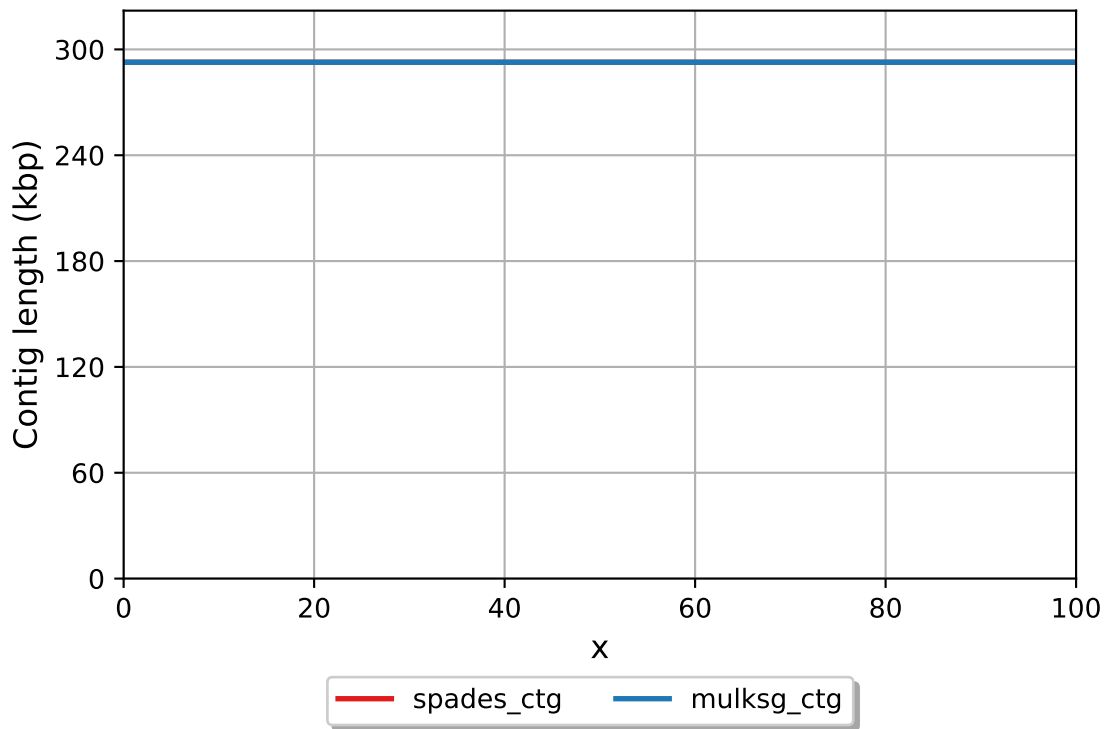
## Unaligned report

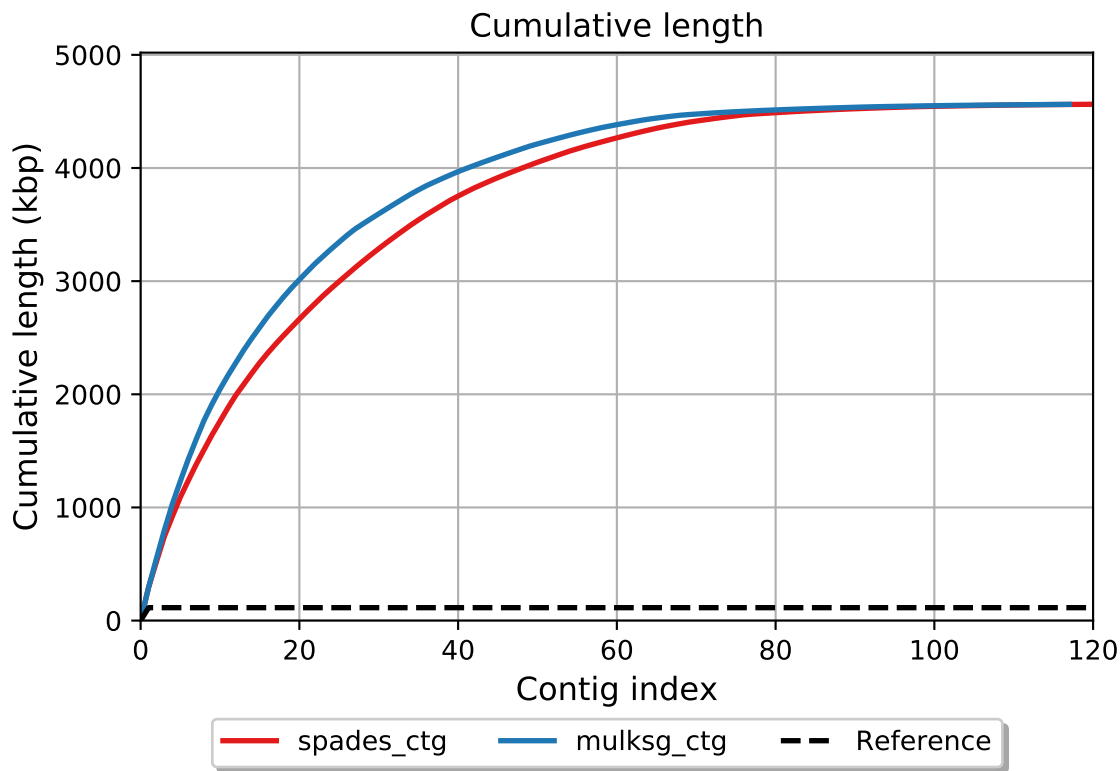
|                               | spades_ctg | mulks_g_ctg |
|-------------------------------|------------|-------------|
| # fully unaligned contigs     | 112        | 111         |
| Fully unaligned length        | 4261003    | 4260303     |
| # partially unaligned contigs | 4          | 4           |
| Partially unaligned length    | 187533     | 187478      |
| # N's                         | 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).

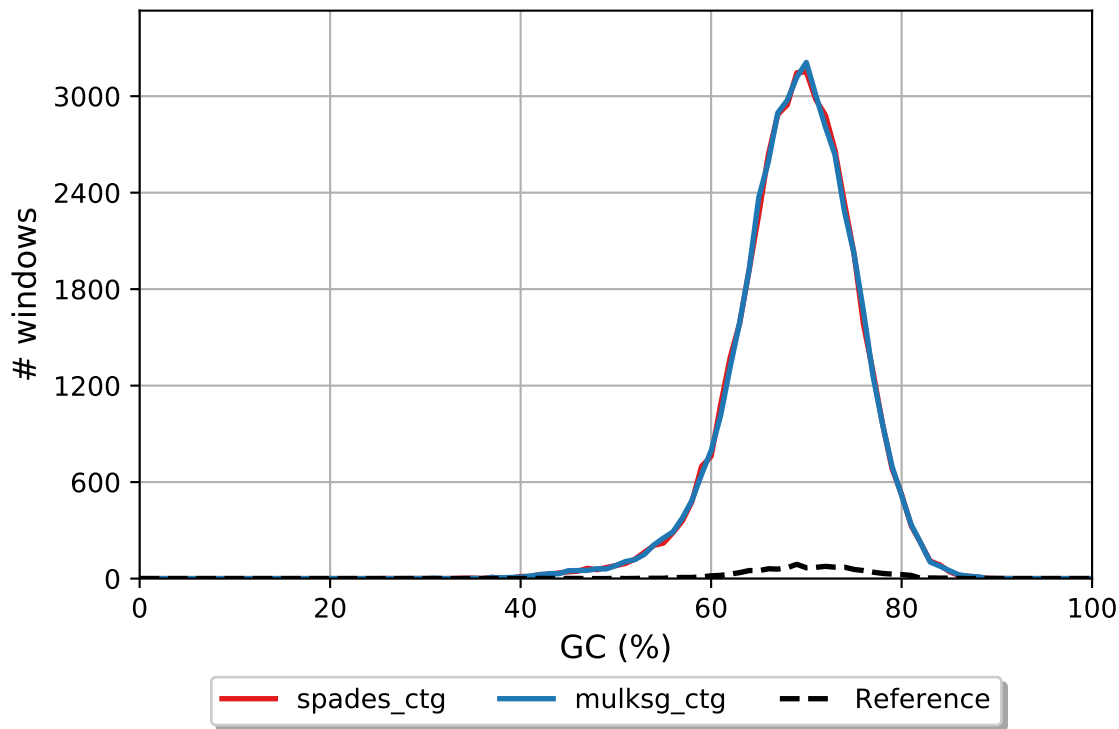


# NGx

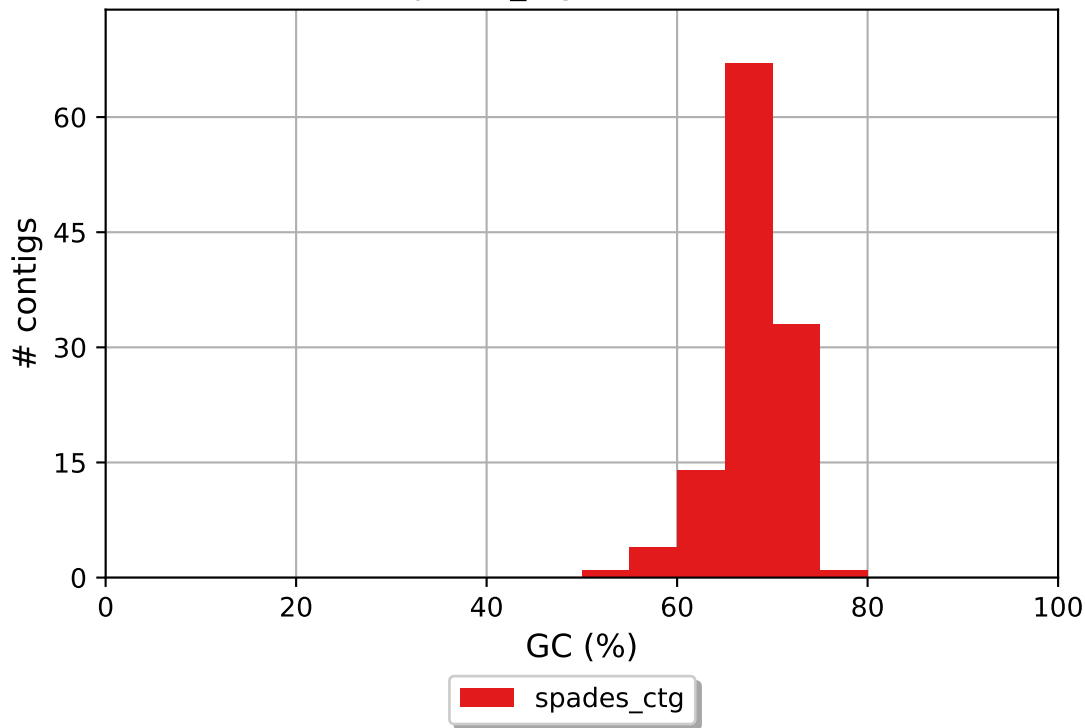




GC content

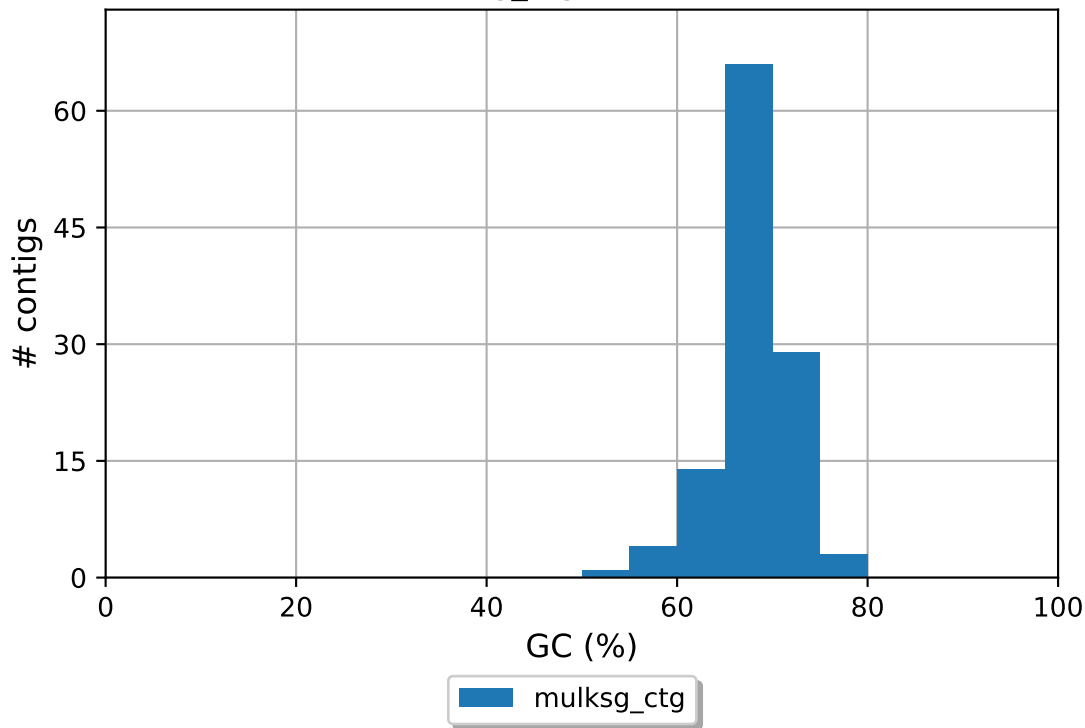


spades\_ctg GC content

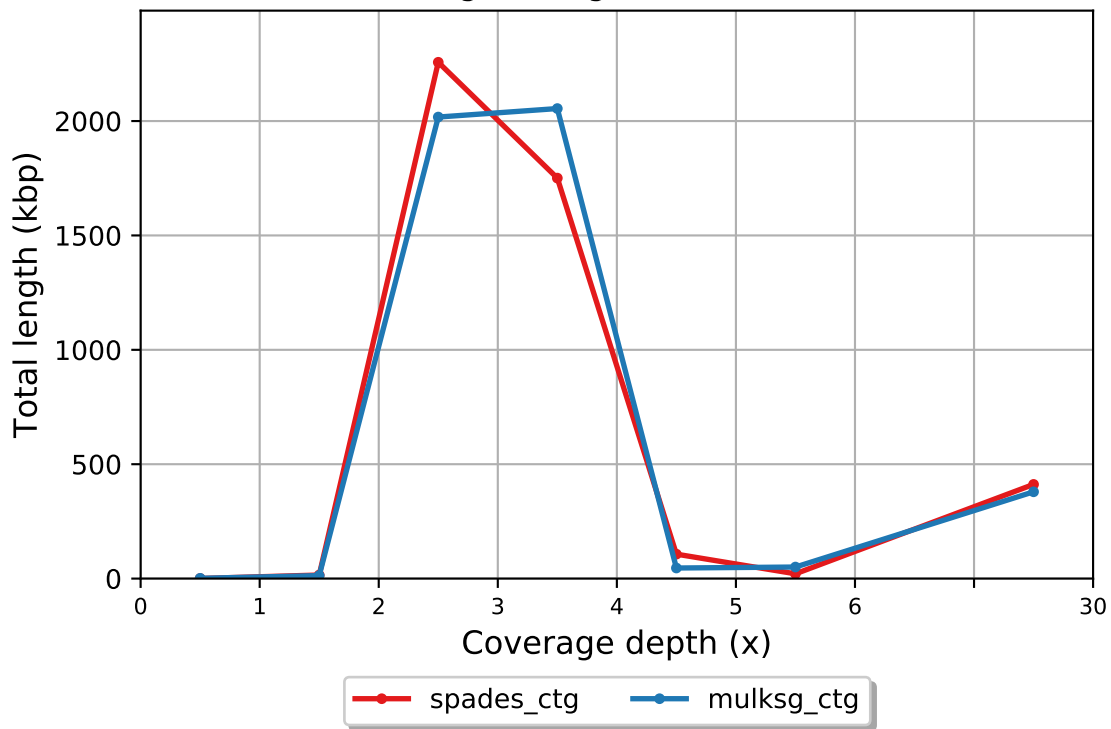




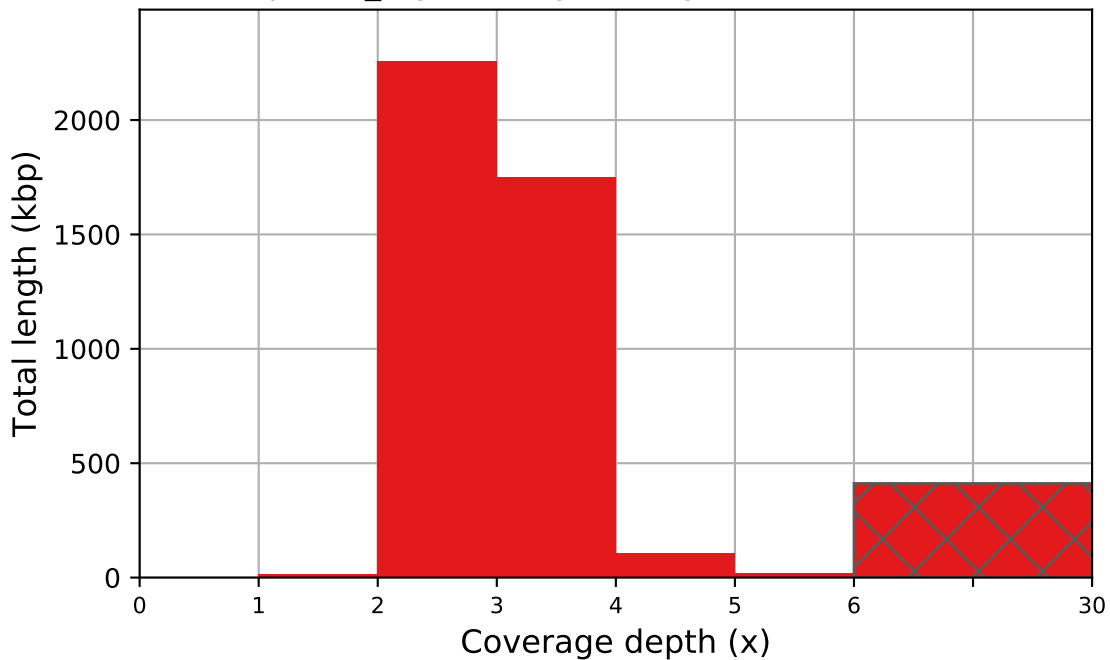
mulksg\_ctg GC content



Coverage histogram (bin size: 1x)

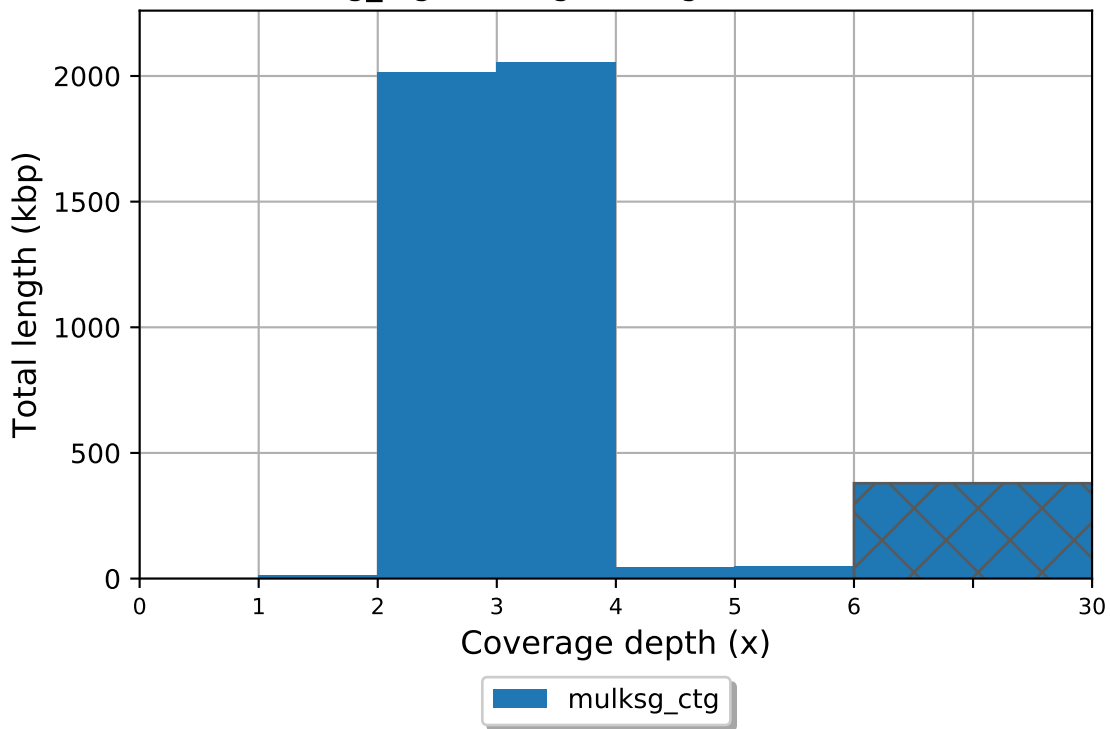


spades\_ctg coverage histogram (bin size: 1x)



spades\_ctg

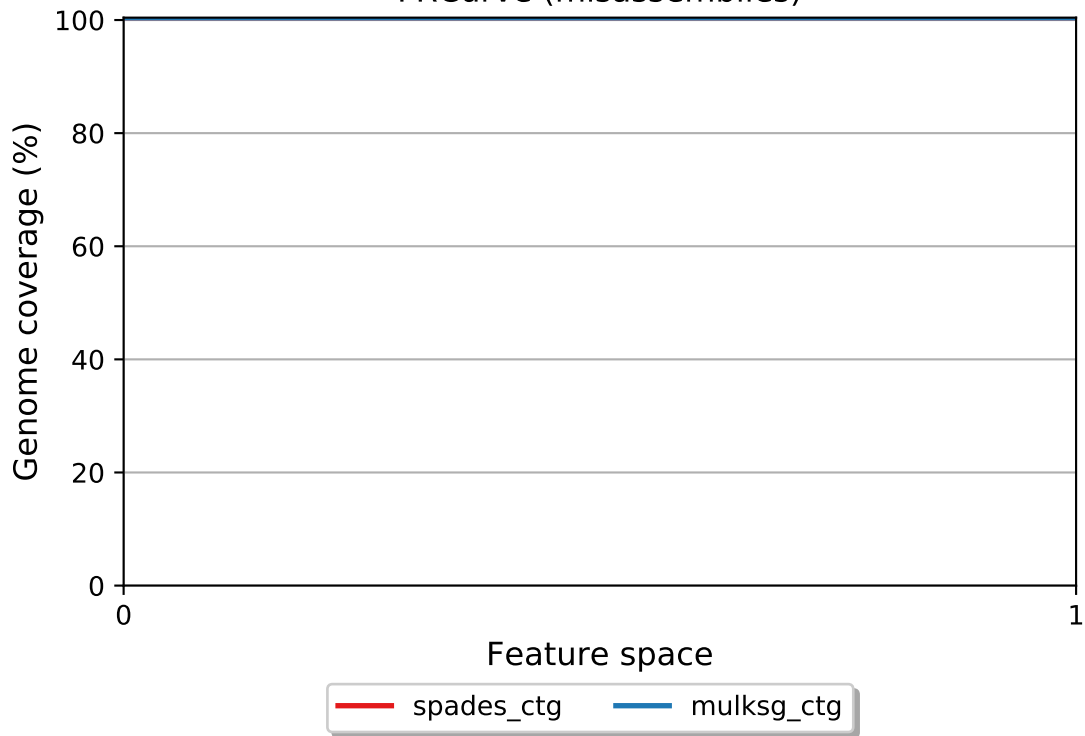
mulksg\_ctg coverage histogram (bin size: 1x)



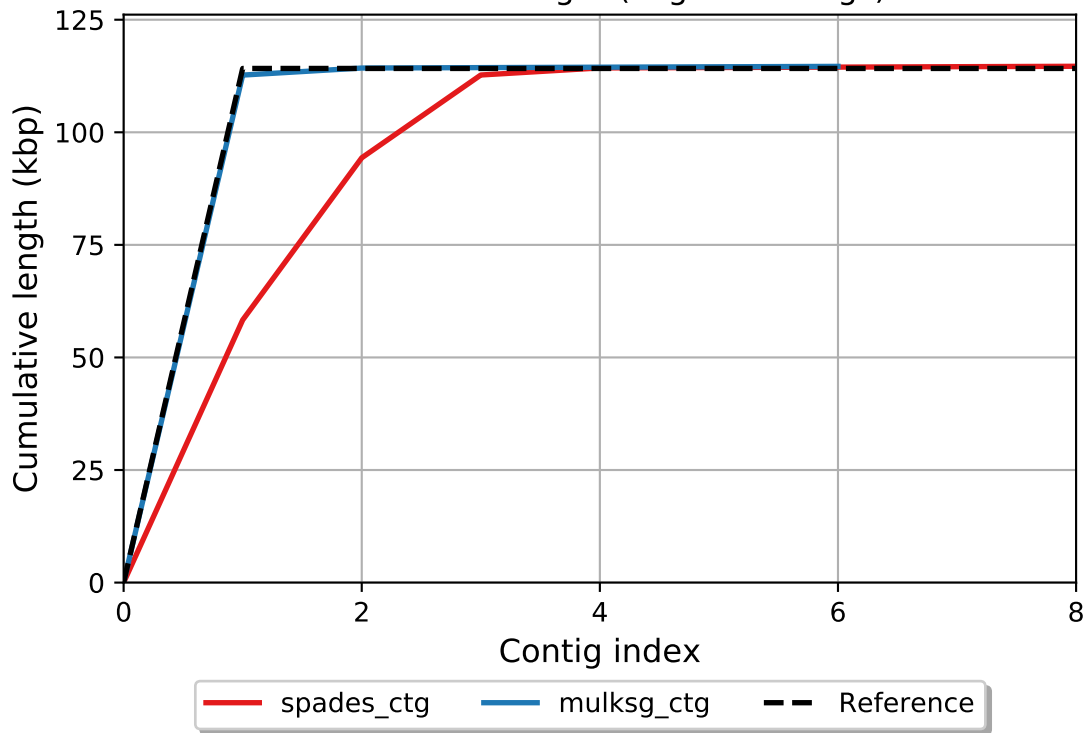
## Misassemblies



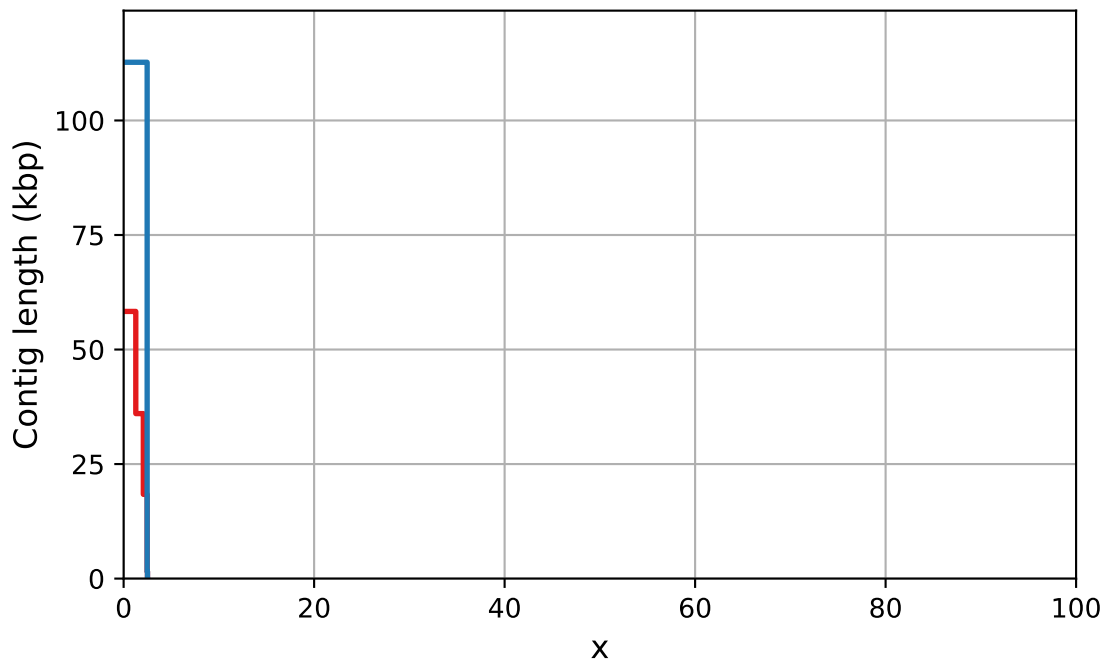
FRCurve (misassemblies)



Cumulative length (aligned contigs)



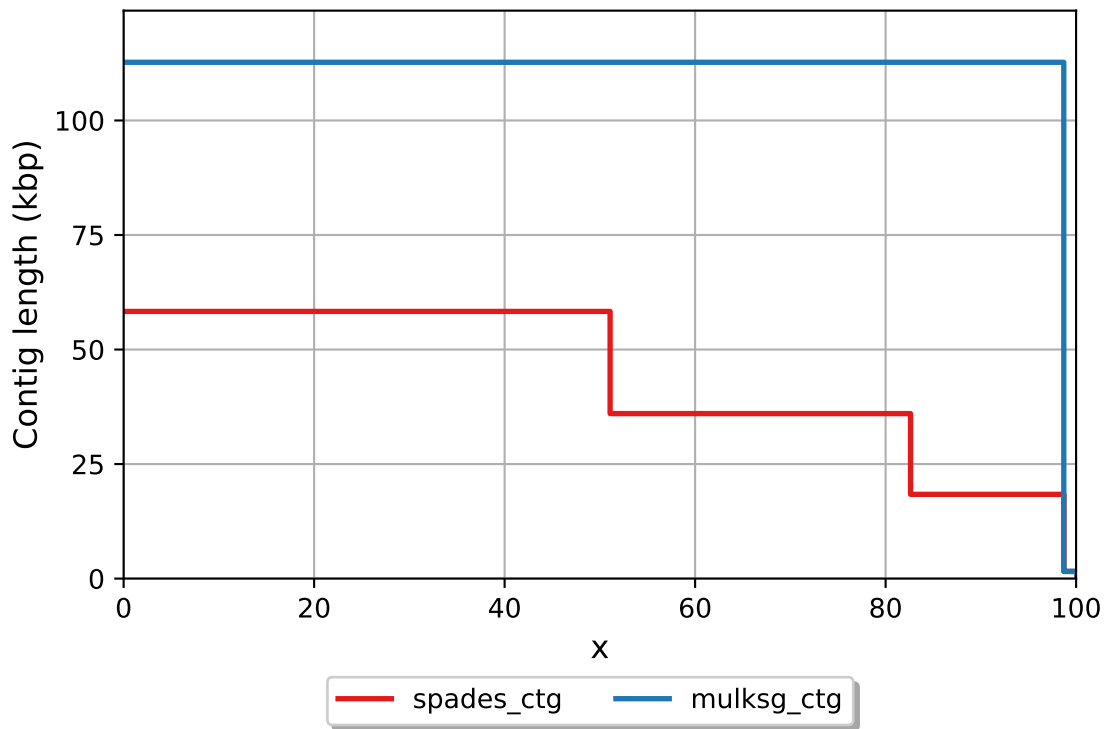
NAx



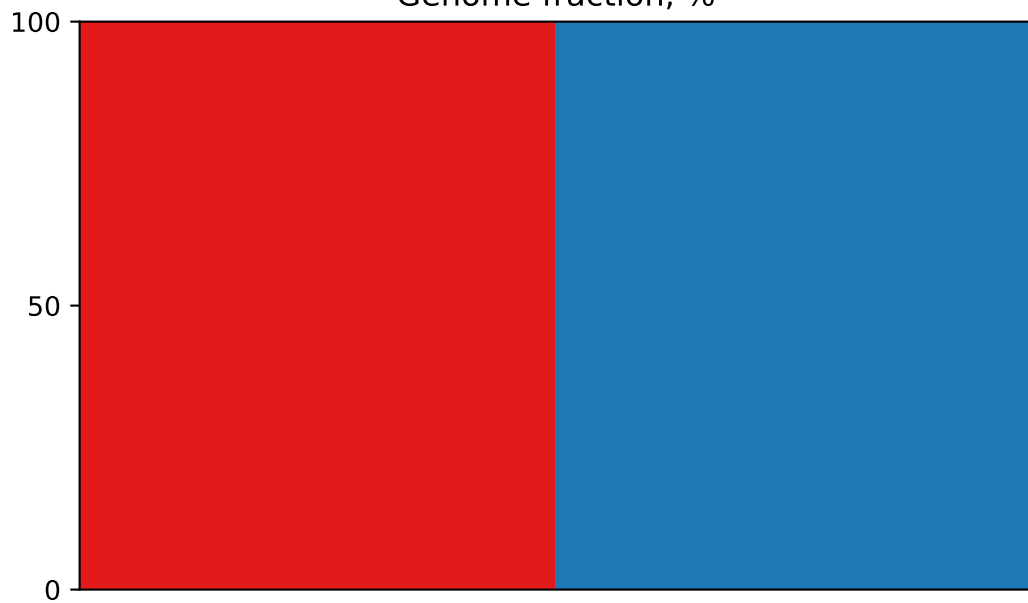
spades\_ctg mulksg\_ctg



# NGAx



Genome fraction, %



spades\_ctg



mulksg\_ctg