

Report

| | spades se | spades pe | spades mp |
|-----------------------------|------------|------------|------------|
| # contigs (>= 0 bp) | 2 | 2 | 2 |
| # contigs (>= 1000 bp) | 2 | 2 | 2 |
| # contigs (>= 5000 bp) | 2 | 2 | 2 |
| # contigs (>= 10000 bp) | 2 | 2 | 2 |
| # contigs (>= 25000 bp) | 2 | 2 | 2 |
| # contigs (>= 50000 bp) | 2 | 2 | 2 |
| Total length (>= 0 bp) | 199972 | 199972 | 199972 |
| Total length (>= 1000 bp) | 199972 | 199972 | 199972 |
| Total length (>= 5000 bp) | 199972 | 199972 | 199972 |
| Total length (>= 10000 bp) | 199972 | 199972 | 199972 |
| Total length (>= 25000 bp) | 199972 | 199972 | 199972 |
| Total length (>= 50000 bp) | 199972 | 199972 | 199972 |
| # contigs | 2 | 2 | 2 |
| Largest contig | 99993 | 99993 | 99993 |
| Total length | 199972 | 199972 | 199972 |
| Reference length | 414184 | 414184 | 414184 |
| GC (%) | 36.95 | 36.95 | 36.95 |
| Reference GC (%) | 36.48 | 36.48 | 36.48 |
| N50 | 99993 | 99993 | 99993 |
| NG50 | - | - | - |
| N90 | 99979 | 99979 | 99979 |
| NG90 | - | - | - |
| auN | 99986.0 | 99986.0 | 99986.0 |
| aUNG | 48274.2 | 48274.2 | 48274.2 |
| L50 | 1 | 1 | 1 |
| LG50 | - | - | - |
| L90 | 2 | 2 | 2 |
| LG90 | - | - | - |
| # misassemblies | 33 | 33 | 33 |
| # misassembled contigs | 2 | 2 | 2 |
| Misassembled contigs length | 199972 | 199972 | 199972 |
| # local misassemblies | 10 | 10 | 10 |
| # scaffold gap ext. mis. | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 |
| # unaligned mis. contigs | 0 | 0 | 0 |
| # unaligned contigs | 0 + 0 part | 0 + 0 part | 0 + 0 part |
| Unaligned length | 0 | 0 | 0 |
| Genome fraction (%) | 48.103 | 48.103 | 48.103 |
| Duplication ratio | 0.972 | 0.972 | 0.970 |
| # N's per 100 kbp | 0.00 | 0.00 | 0.00 |
| # mismatches per 100 kbp | 300.41 | 300.41 | 301.01 |
| # indels per 100 kbp | 53.16 | 53.16 | 53.27 |
| Largest alignment | 20633 | 20633 | 20629 |
| Total aligned length | 193737 | 193737 | 193349 |
| NA50 | 7604 | 7604 | 7604 |
| NGA50 | - | - | - |
| NA90 | 2456 | 2456 | 2159 |
| NGA90 | - | - | - |
| auNA | 9685.1 | 9685.1 | 9686.2 |
| aUNGA | 4676.1 | 4676.1 | 4676.6 |
| LA50 | 8 | 8 | 8 |
| LGA50 | - | - | - |
| LA90 | 24 | 24 | 24 |
| 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

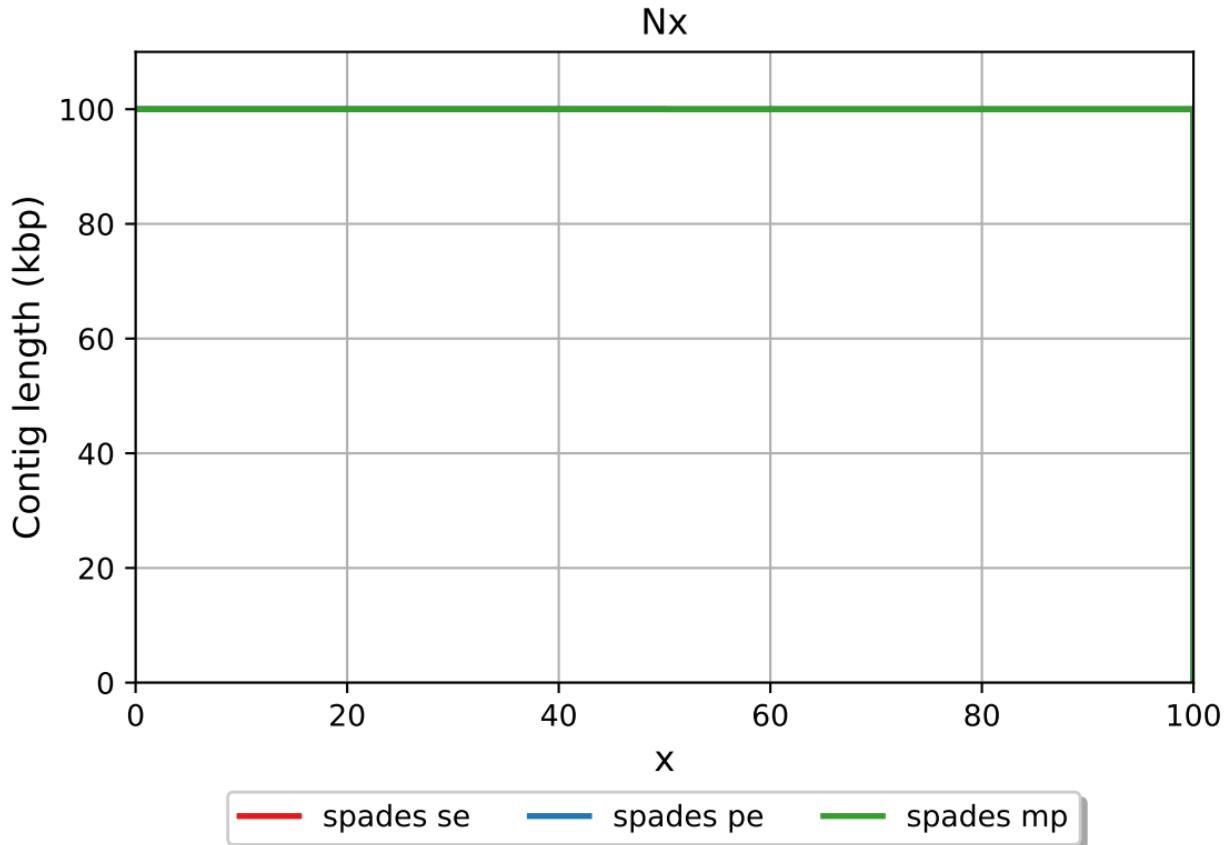
| | spades se | spades pe | spades mp |
|-----------------------------|-----------|-----------|-----------|
| # misassemblies | 33 | 33 | 33 |
| # contig misassemblies | 33 | 33 | 33 |
| # c. relocations | 33 | 33 | 33 |
| # c. translocations | 0 | 0 | 0 |
| # c. inversions | 0 | 0 | 0 |
| # scaffold misassemblies | 0 | 0 | 0 |
| # s. relocations | 0 | 0 | 0 |
| # s. translocations | 0 | 0 | 0 |
| # s. inversions | 0 | 0 | 0 |
| # misassembled contigs | 2 | 2 | 2 |
| Misassembled contigs length | 199972 | 199972 | 199972 |
| # local misassemblies | 10 | 10 | 10 |
| # scaffold gap ext. mis. | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 |
| # unaligned mis. contigs | 0 | 0 | 0 |
| # mismatches | 582 | 582 | 582 |
| # indels | 103 | 103 | 103 |
| # indels (<= 5 bp) | 34 | 34 | 34 |
| # indels (> 5 bp) | 69 | 69 | 69 |
| Indels length | 3418 | 3418 | 3418 |

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).

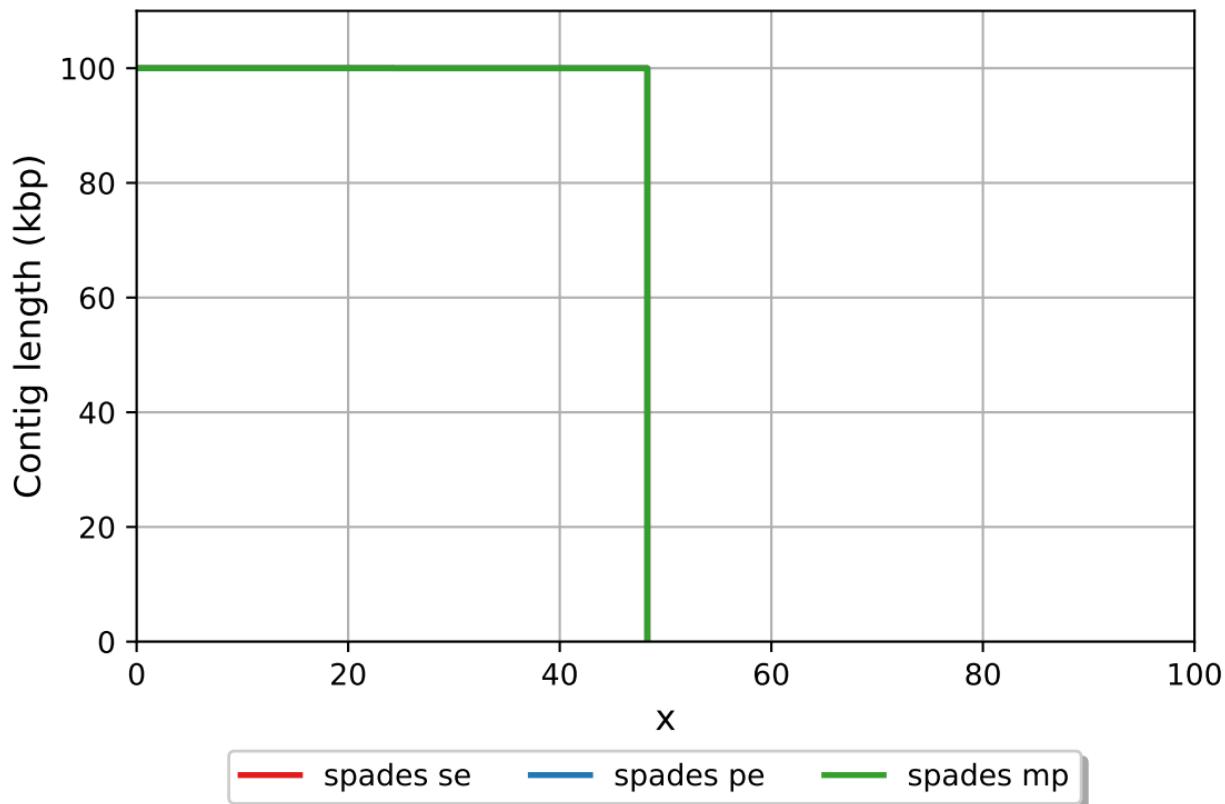
Unaligned report

| | spades se | spades pe | spades mp |
|-------------------------------|-----------|-----------|-----------|
| # fully unaligned contigs | 0 | 0 | 0 |
| Fully unaligned length | 0 | 0 | 0 |
| # partially unaligned contigs | 0 | 0 | 0 |
| Partially unaligned length | 0 | 0 | 0 |
| # N's | 0 | 0 | 0 |

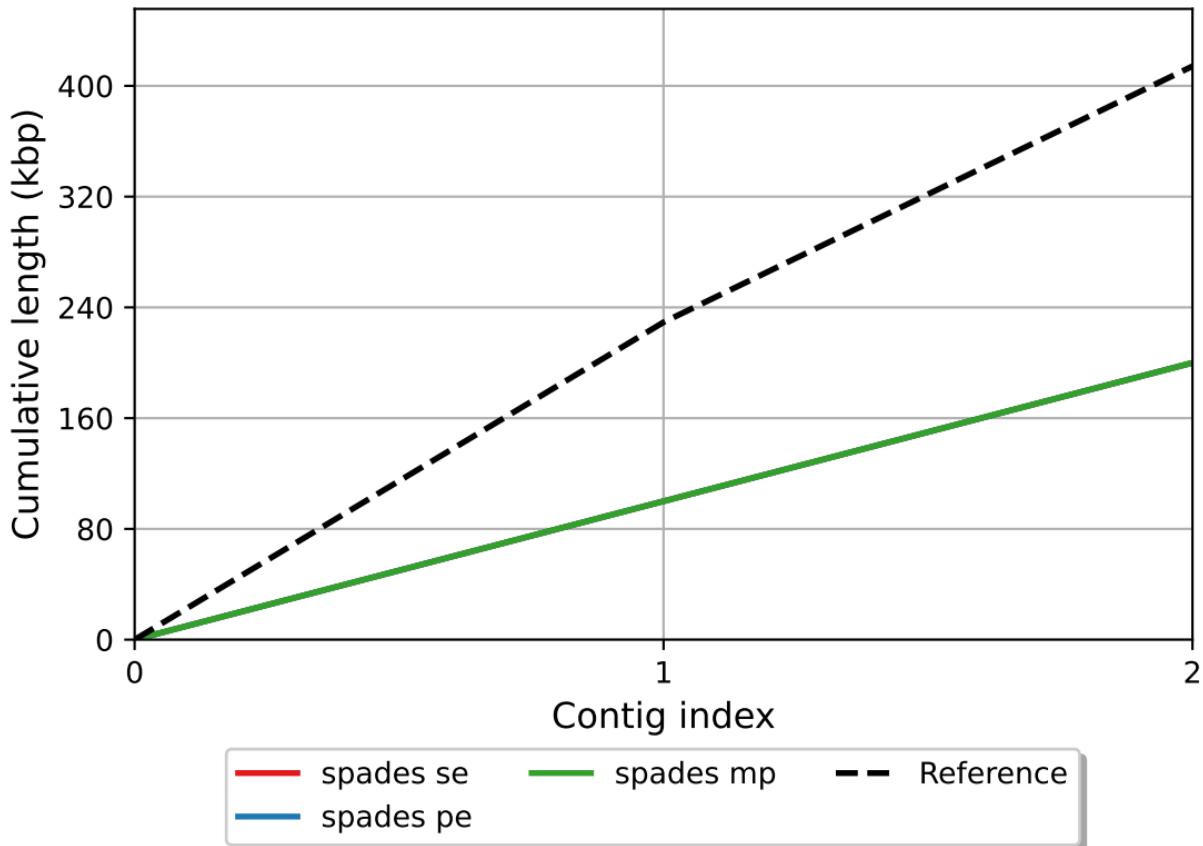
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



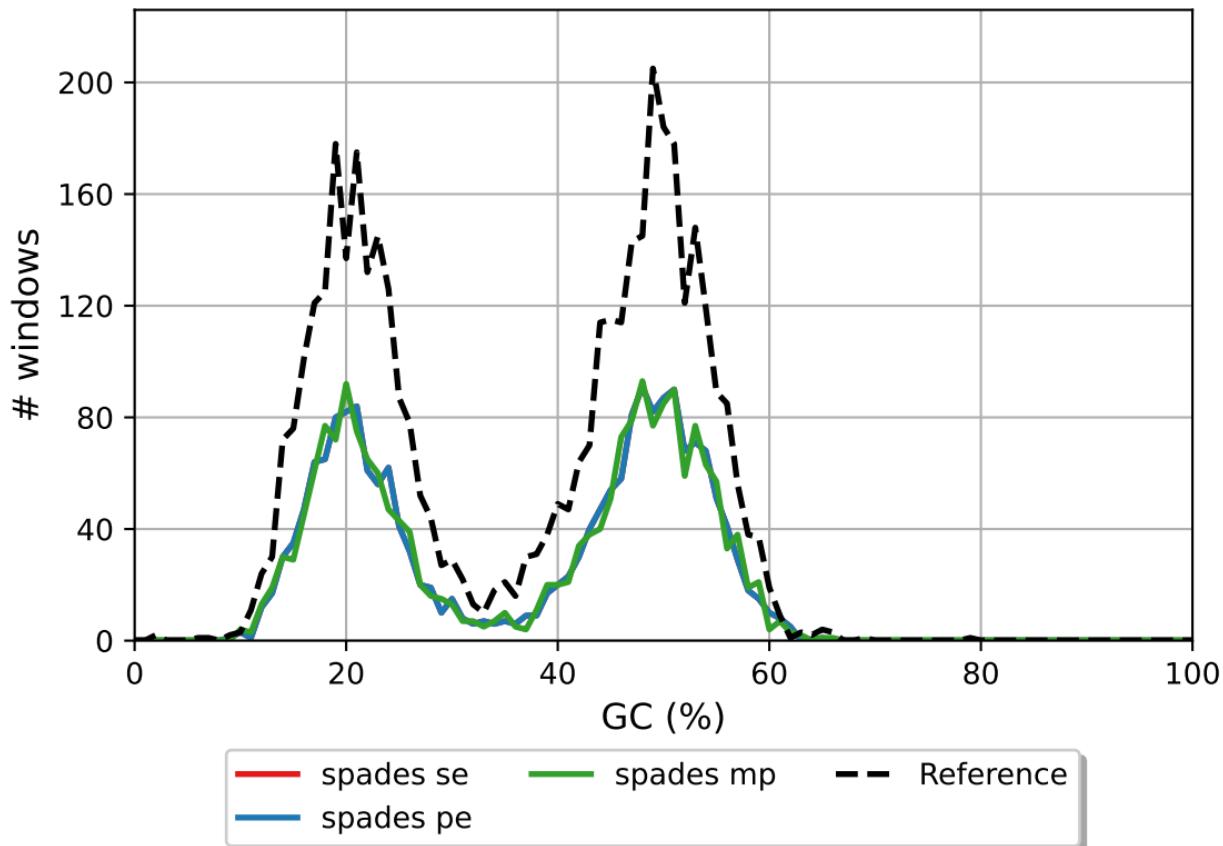
NGx



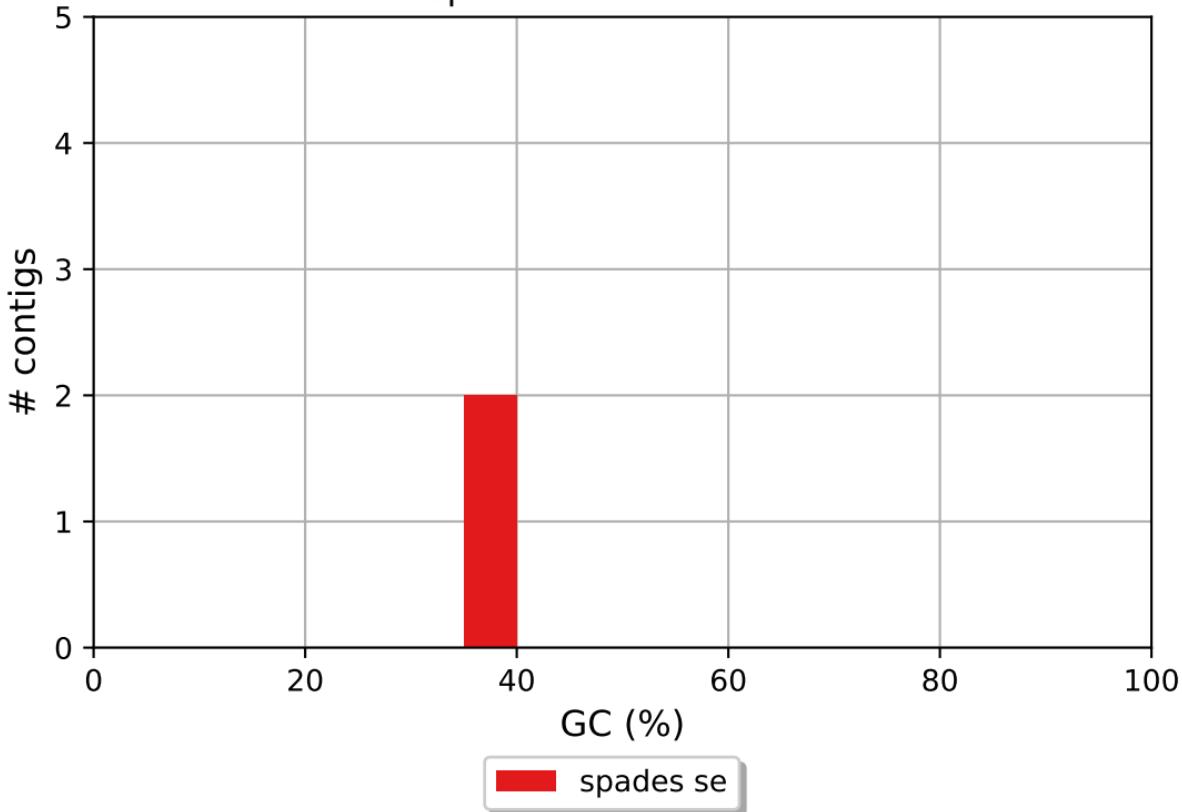
Cumulative length



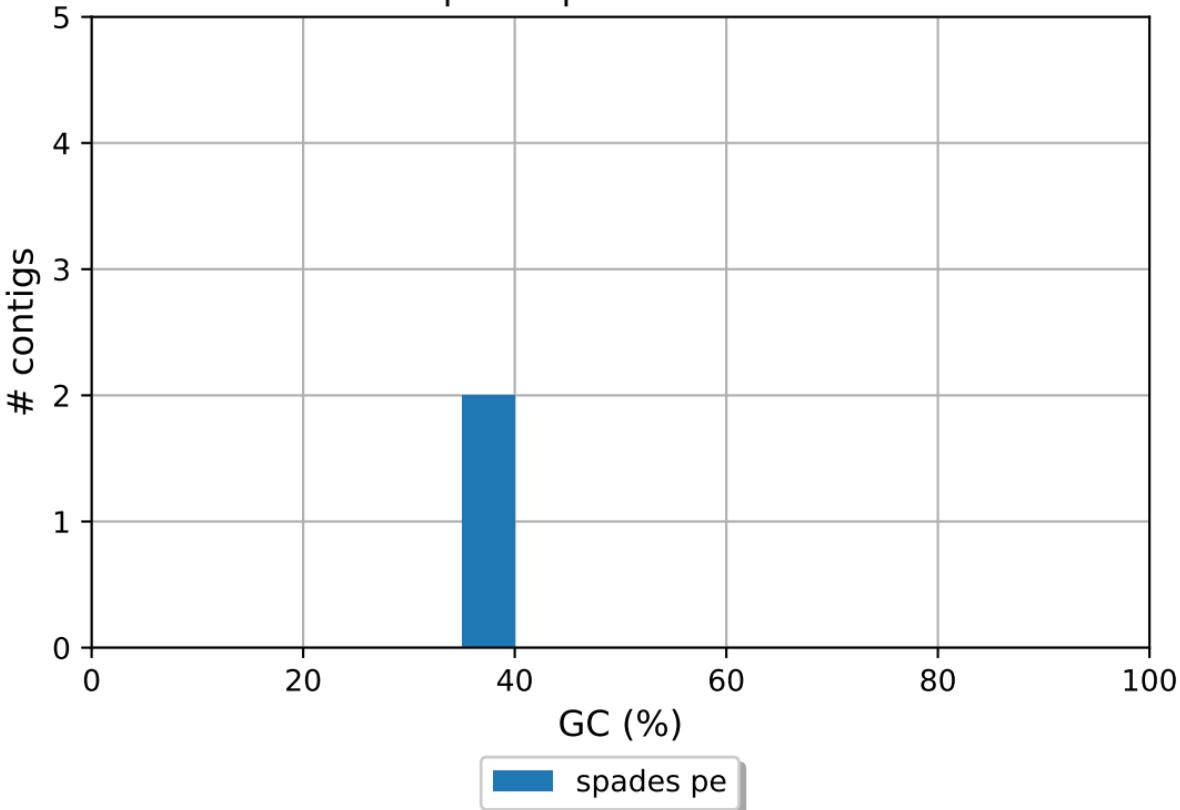
GC content



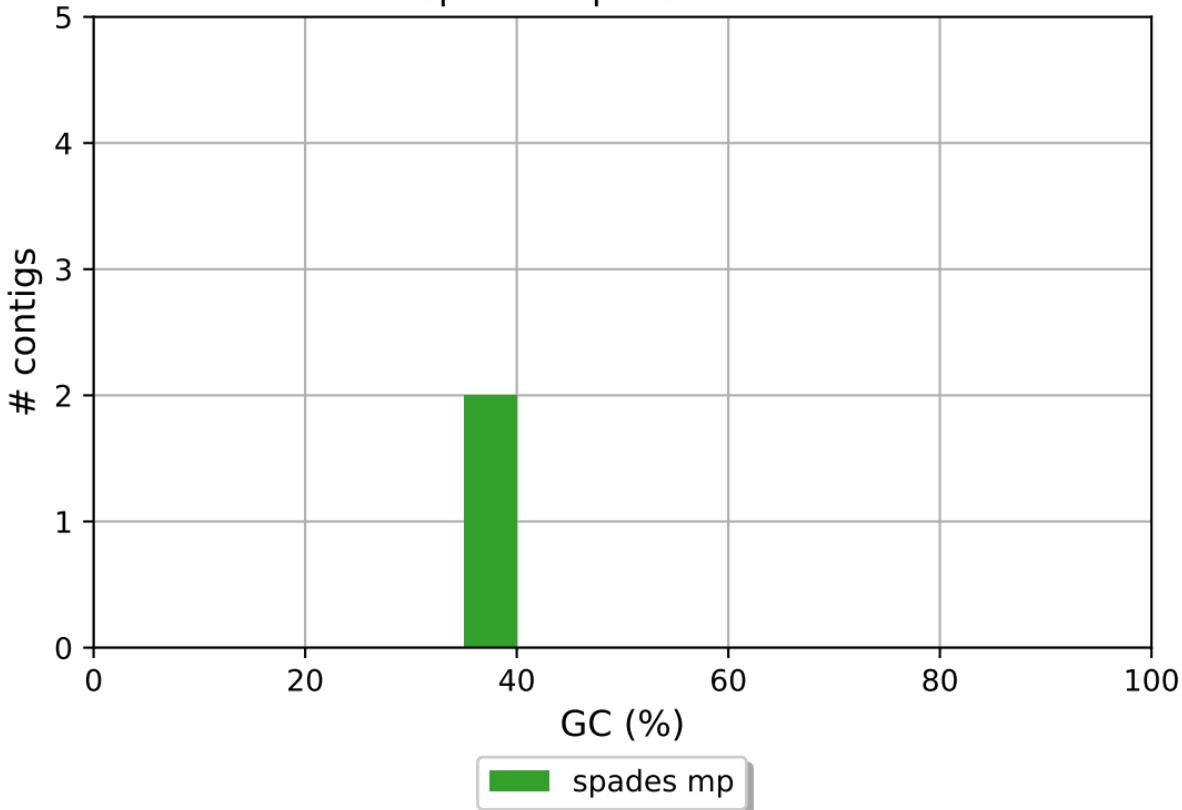
spades se GC content



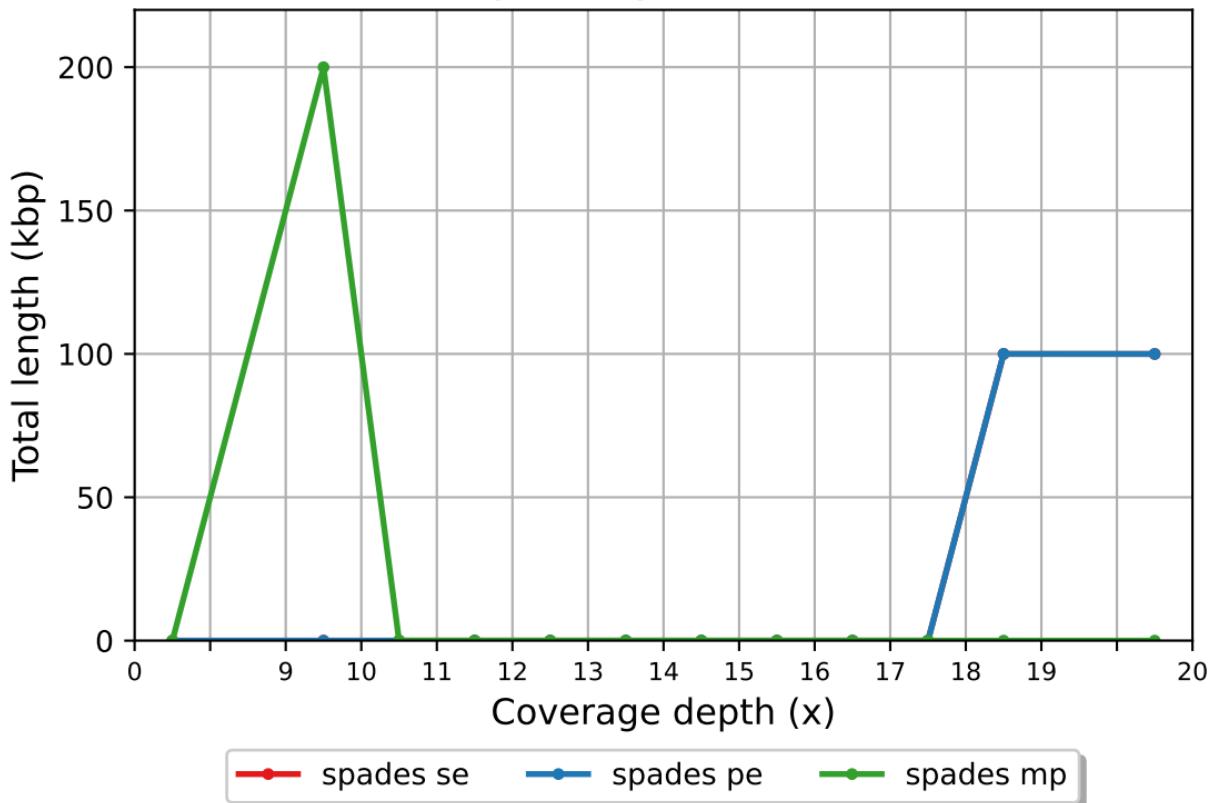
spades pe GC content



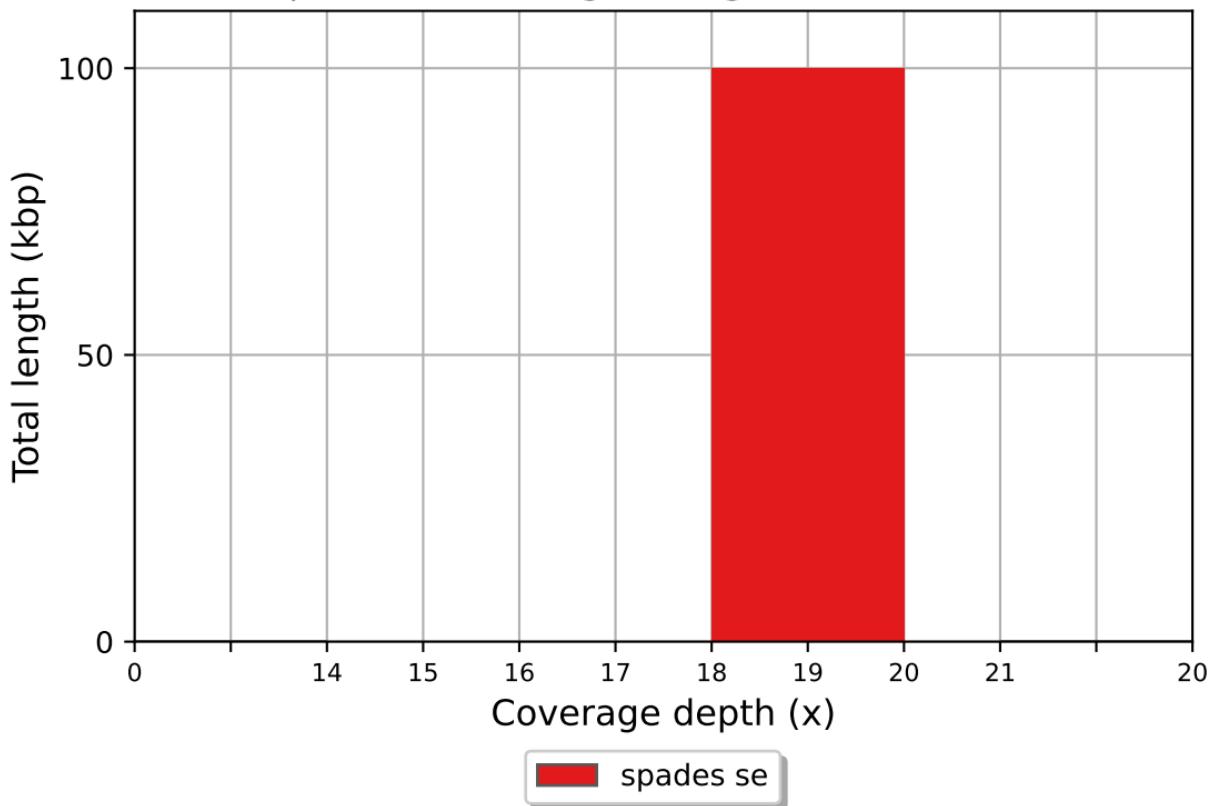
spades mp GC content



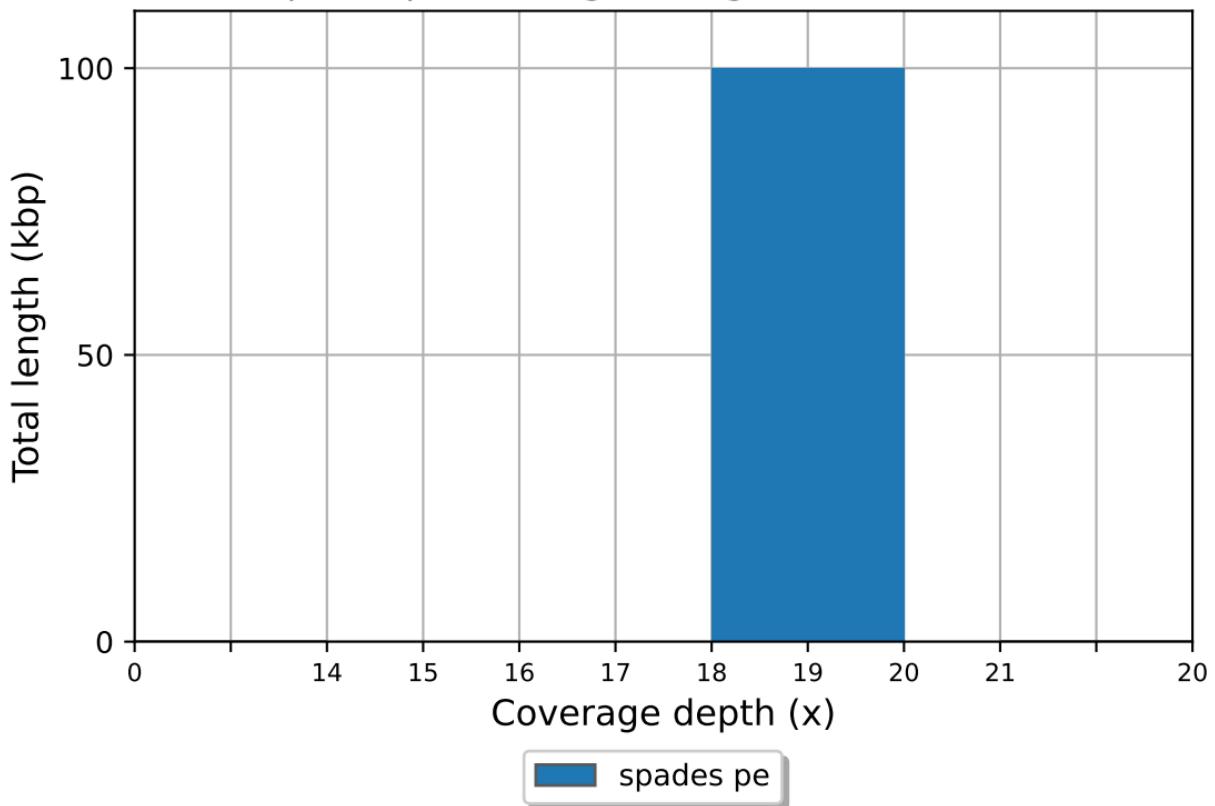
Coverage histogram (bin size: 1x)



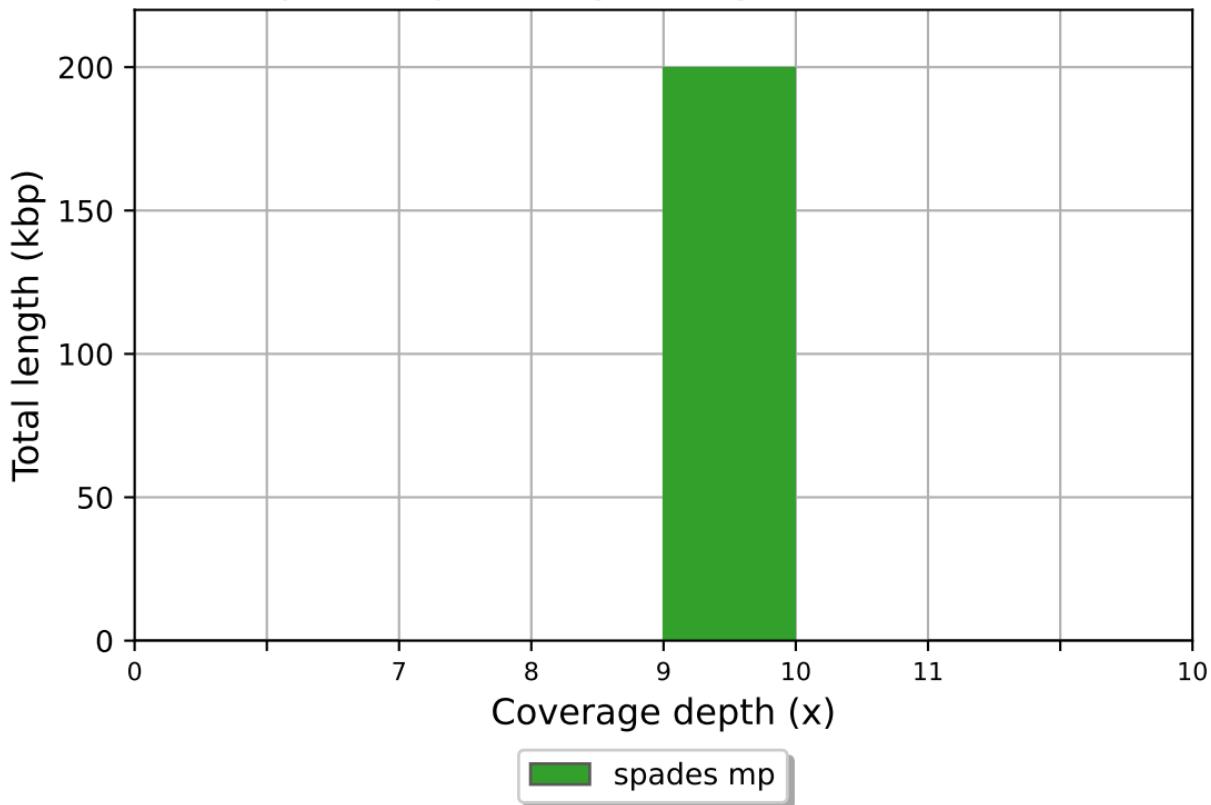
spades se coverage histogram (bin size: 1x)



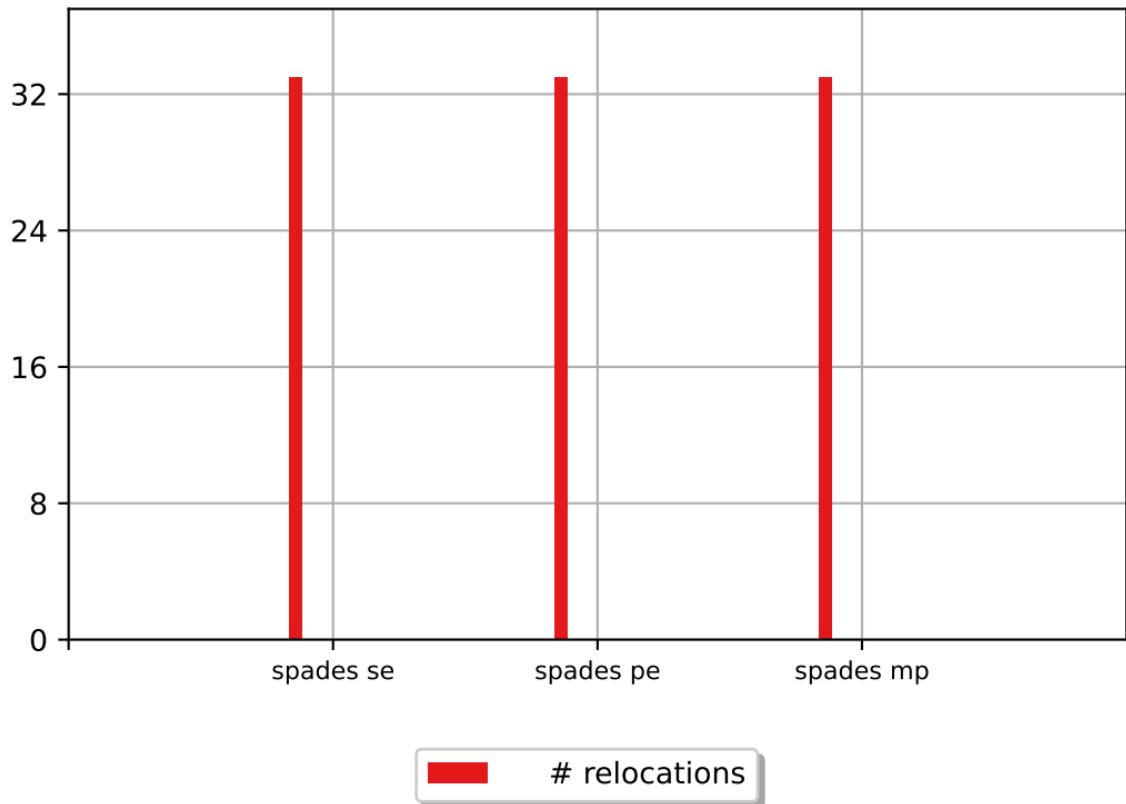
spades pe coverage histogram (bin size: 1x)



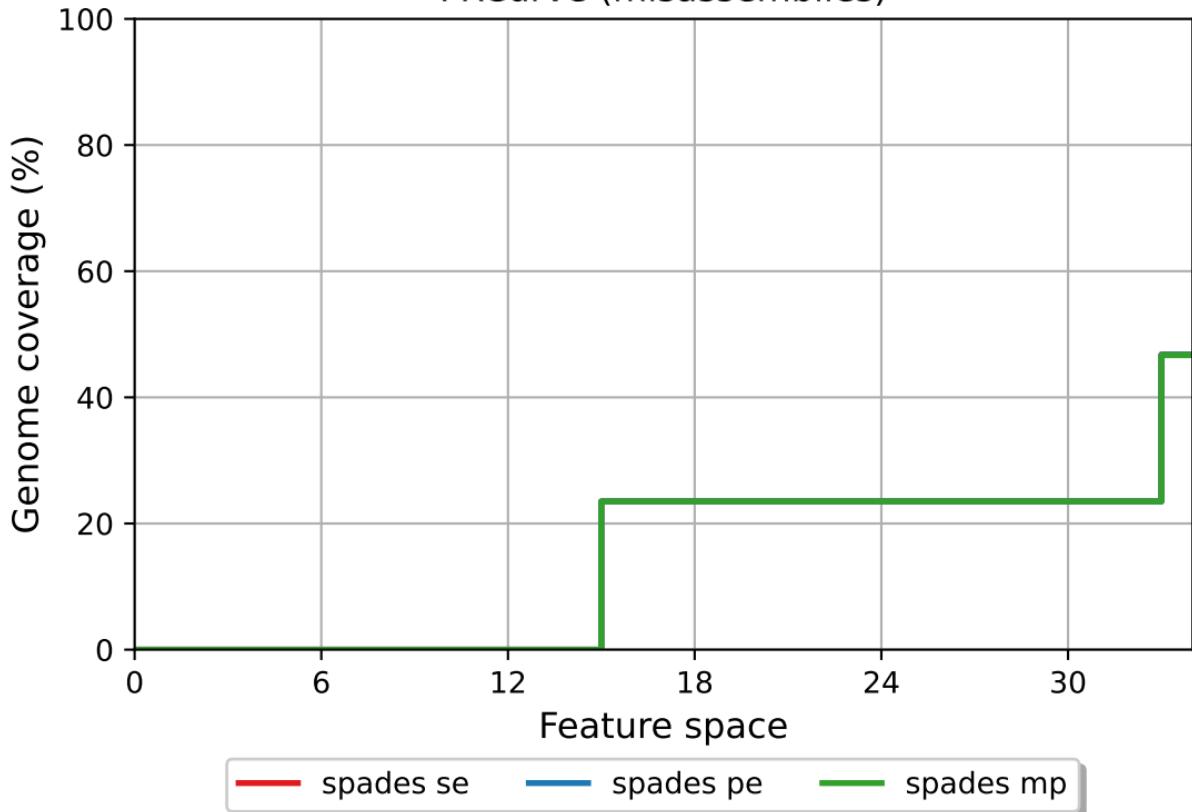
spades mp coverage histogram (bin size: 1x)



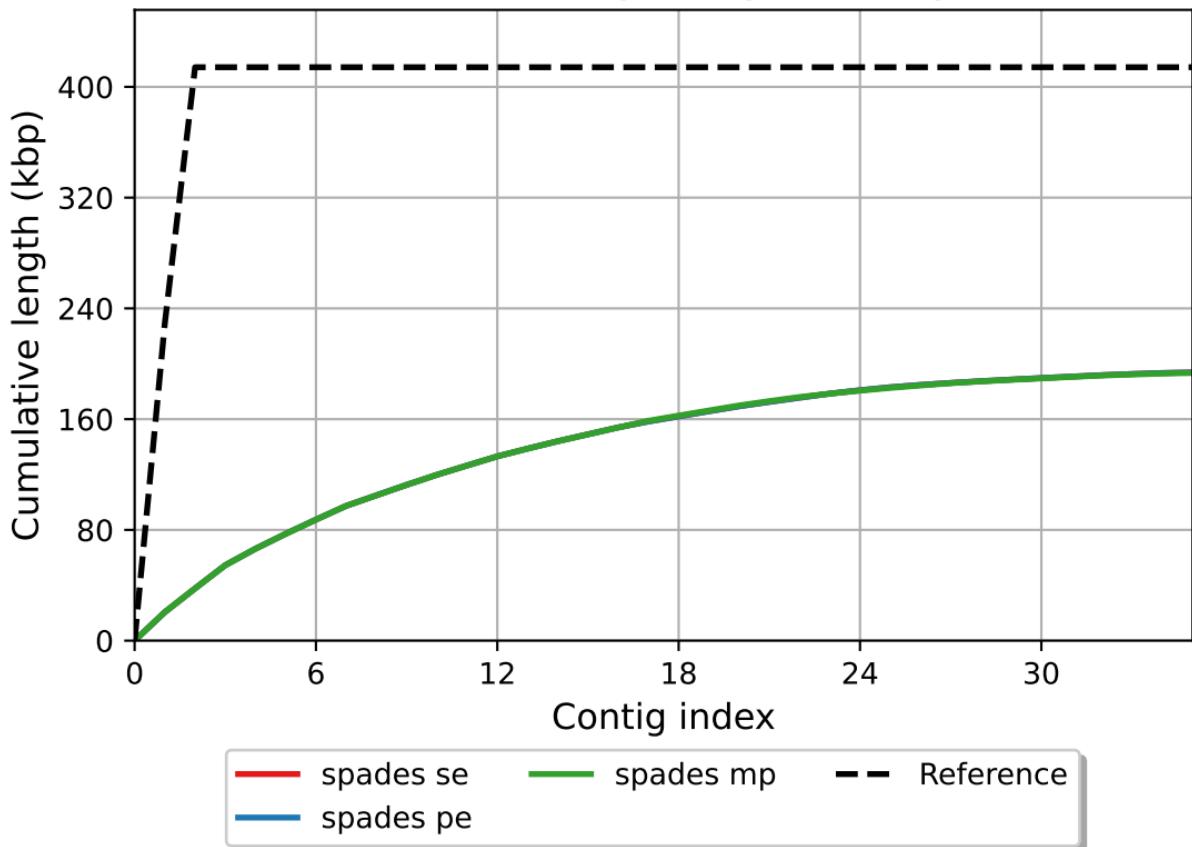
Misassemblies



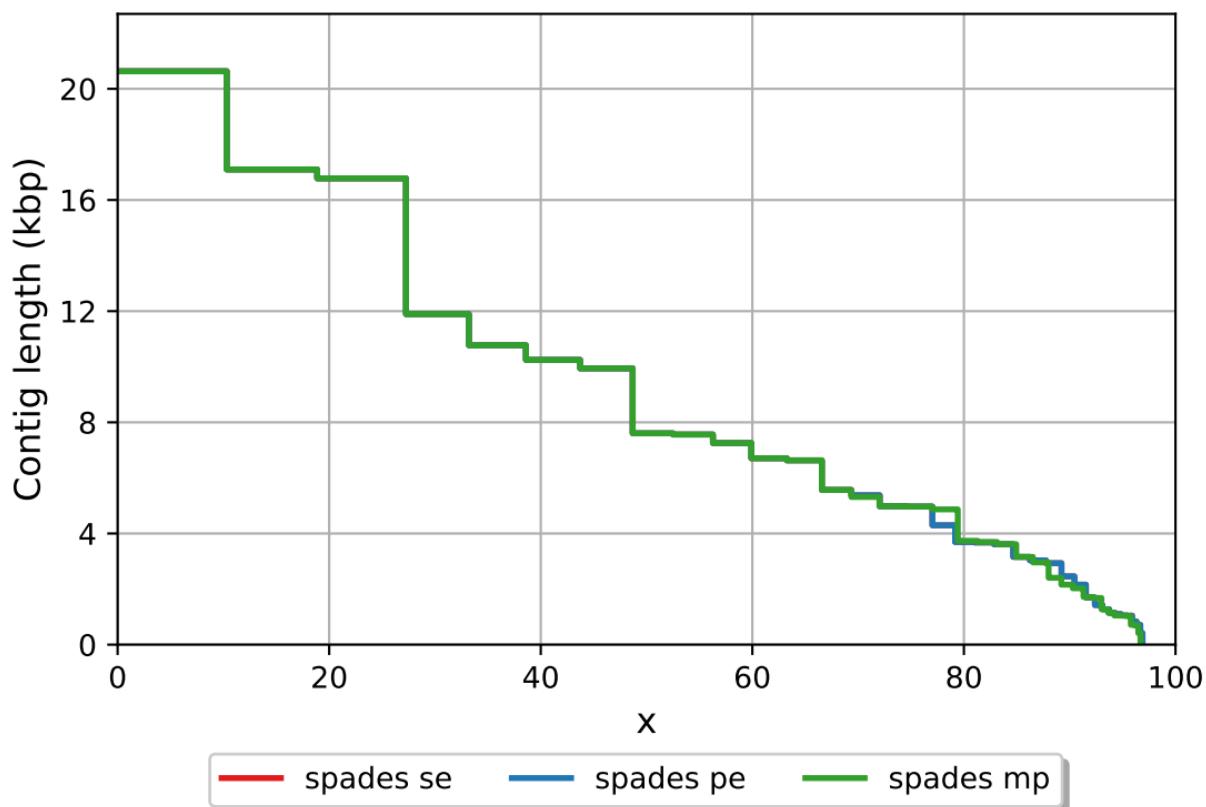
FRCurve (misassemblies)



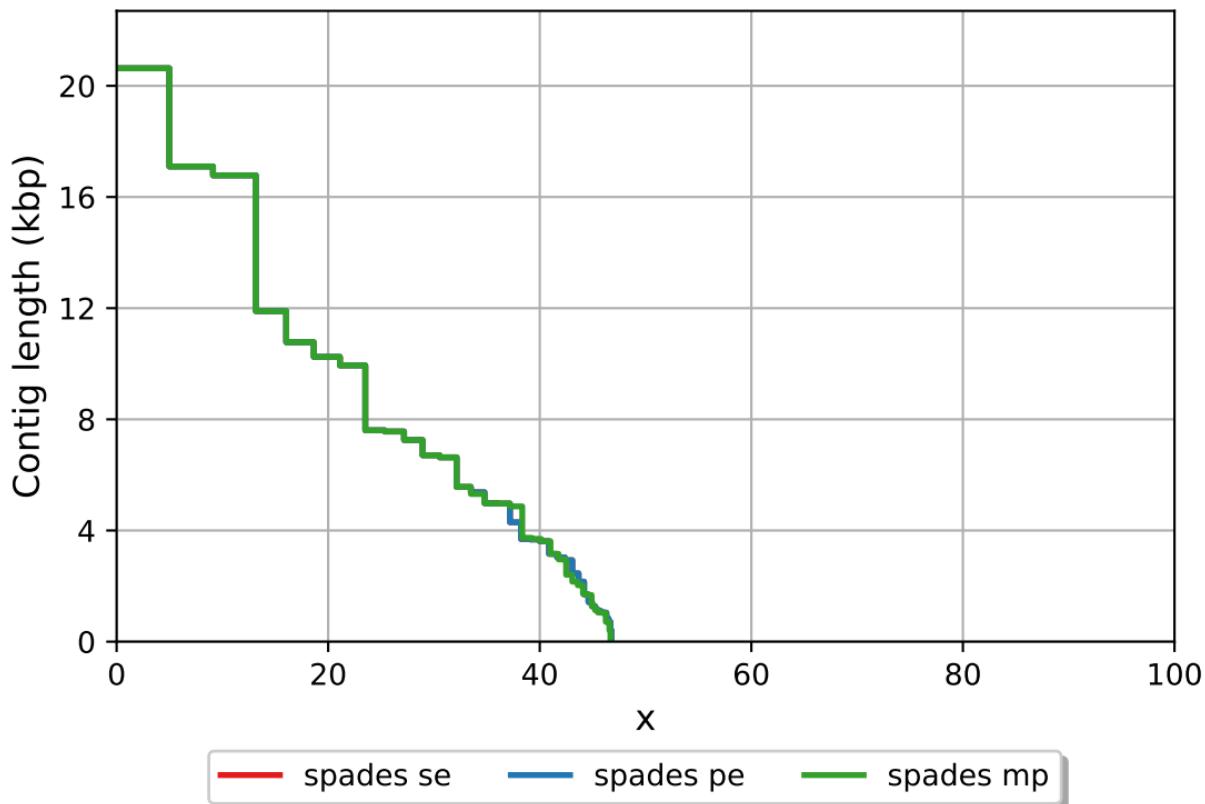
Cumulative length (aligned contigs)



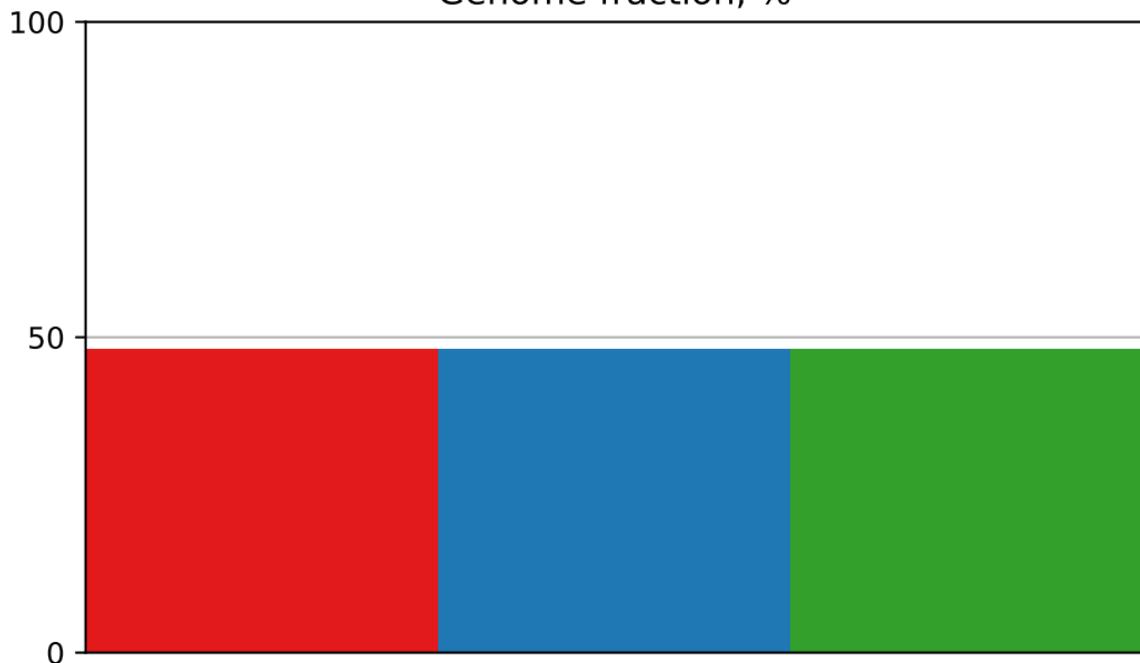
NAx



NGAx



Genome fraction, %



■ spades se ■ spades pe ■ spades mp