

Report

| | spades_scf | mulksq_scf |
|-----------------------------|--------------|--------------|
| # contigs (>= 0 bp) | 66 | 64 |
| # contigs (>= 1000 bp) | 49 | 49 |
| # contigs (>= 5000 bp) | 30 | 31 |
| # contigs (>= 10000 bp) | 26 | 26 |
| # contigs (>= 25000 bp) | 22 | 22 |
| # contigs (>= 50000 bp) | 22 | 22 |
| Total length (>= 0 bp) | 3944158 | 3944228 |
| Total length (>= 1000 bp) | 3935896 | 3937116 |
| Total length (>= 5000 bp) | 3892275 | 3896046 |
| Total length (>= 10000 bp) | 3864094 | 3861317 |
| Total length (>= 25000 bp) | 3795728 | 3799144 |
| Total length (>= 50000 bp) | 3795728 | 3799144 |
| # contigs | 56 | 55 |
| Largest contig | 382053 | 382053 |
| Total length | 3941139 | 3941568 |
| Reference length | 2961149 | 2961149 |
| GC (%) | 47.50 | 47.50 |
| Reference GC (%) | 47.70 | 47.70 |
| N50 | 199447 | 199447 |
| NG50 | 260649 | 260649 |
| N75 | 141668 | 141668 |
| NG75 | 192074 | 192074 |
| L50 | 7 | 7 |
| LG50 | 5 | 5 |
| L75 | 13 | 13 |
| LG75 | 8 | 8 |
| # misassemblies | 3 | 2 |
| # misassembled contigs | 2 | 2 |
| Misassembled contigs length | 523776 | 516808 |
| # local misassemblies | 3 | 3 |
| # scaffold gap ext. mis. | 1 | 1 |
| # scaffold gap loc. mis. | 0 | 0 |
| # unaligned mis. contigs | 3 | 3 |
| # unaligned contigs | 24 + 11 part | 23 + 10 part |
| Unaligned length | 1026247 | 1026471 |
| Genome fraction (%) | 98.286 | 98.292 |
| Duplication ratio | 1.002 | 1.002 |
| # N's per 100 kbp | 2.46 | 2.46 |
| # mismatches per 100 kbp | 9.31 | 8.66 |
| # indels per 100 kbp | 2.37 | 2.37 |
| Largest alignment | 382053 | 382053 |
| Total aligned length | 2914802 | 2914602 |
| NA50 | 152282 | 152375 |
| NGA50 | 192074 | 192074 |
| NGA75 | 110108 | 126528 |
| LA50 | 9 | 9 |
| LGA50 | 6 | 6 |
| LGA75 | 11 | 11 |

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

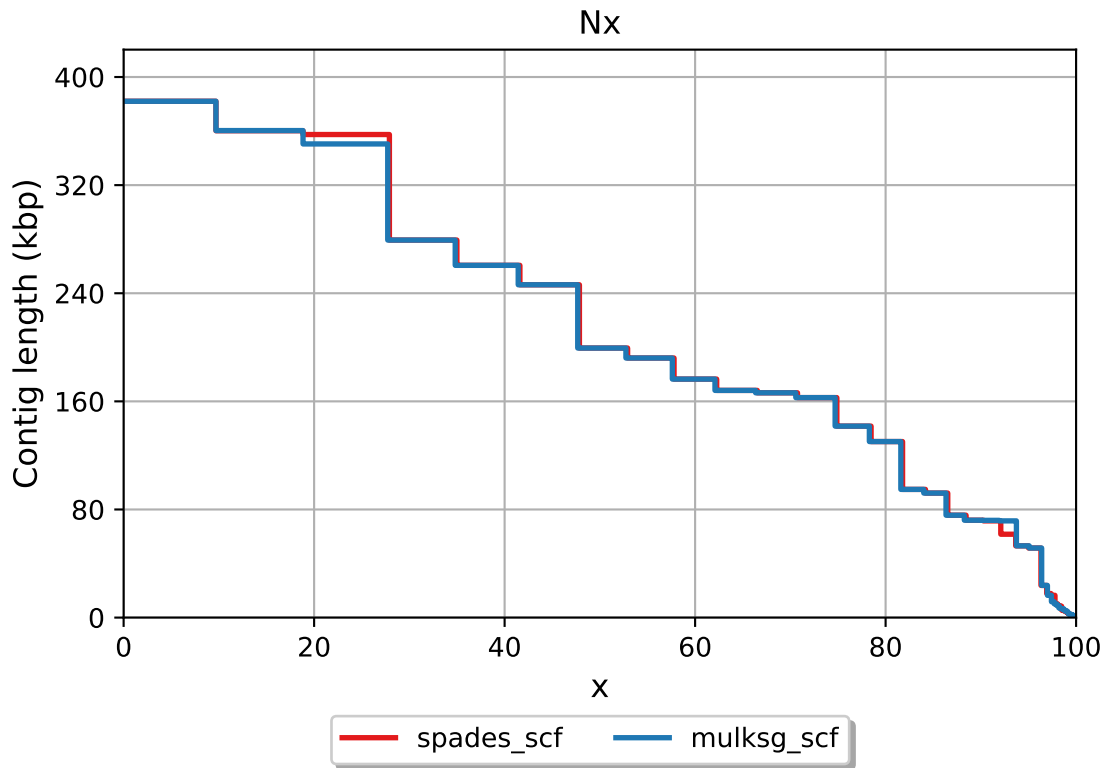
| | spades_scf | mulksf_scf |
|-----------------------------|------------|------------|
| # misassemblies | 3 | 2 |
| # contig misassemblies | 3 | 2 |
| # c. relocations | 3 | 2 |
| # c. translocations | 0 | 0 |
| # c. inversions | 0 | 0 |
| # scaffold misassemblies | 0 | 0 |
| # s. relocations | 0 | 0 |
| # s. translocations | 0 | 0 |
| # s. inversions | 0 | 0 |
| # misassembled contigs | 2 | 2 |
| Misassembled contigs length | 523776 | 516808 |
| # local misassemblies | 3 | 3 |
| # scaffold gap ext. mis. | 1 | 1 |
| # scaffold gap loc. mis. | 0 | 0 |
| # unaligned mis. contigs | 3 | 3 |
| # mismatches | 271 | 252 |
| # indels | 69 | 69 |
| # indels (<= 5 bp) | 65 | 65 |
| # indels (> 5 bp) | 4 | 4 |
| Indels length | 110 | 110 |

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).

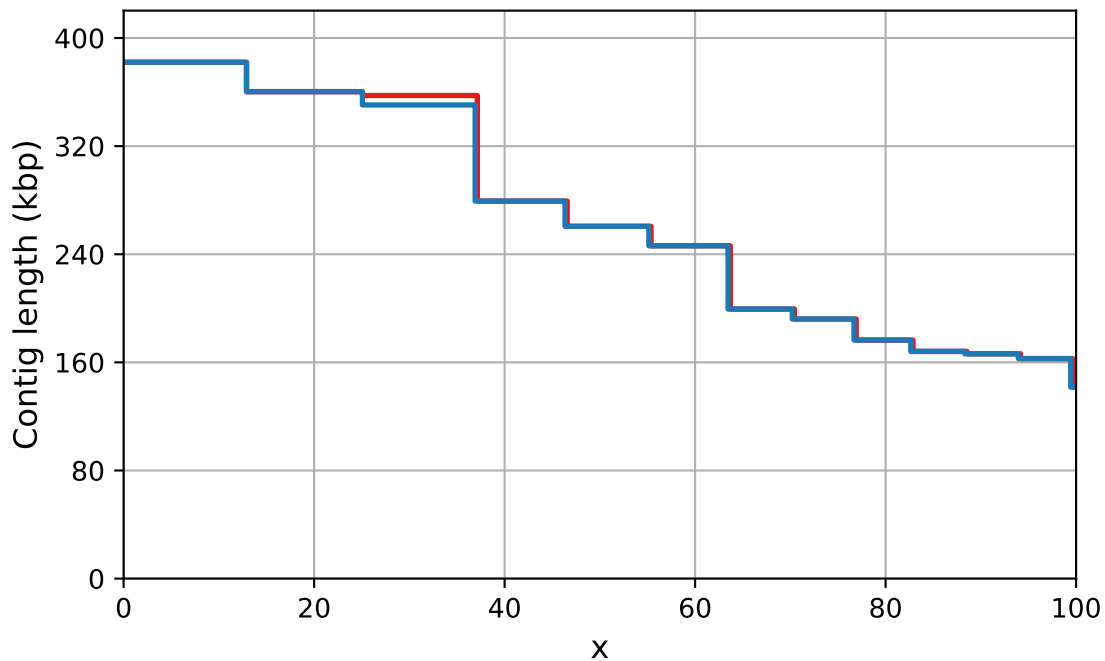
Unaligned report

| | spades_scf | mulksg_scf |
|-------------------------------|------------|------------|
| # fully unaligned contigs | 24 | 23 |
| Fully unaligned length | 54997 | 66415 |
| # partially unaligned contigs | 11 | 10 |
| Partially unaligned length | 971250 | 960056 |
| # N's | 97 | 97 |

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).

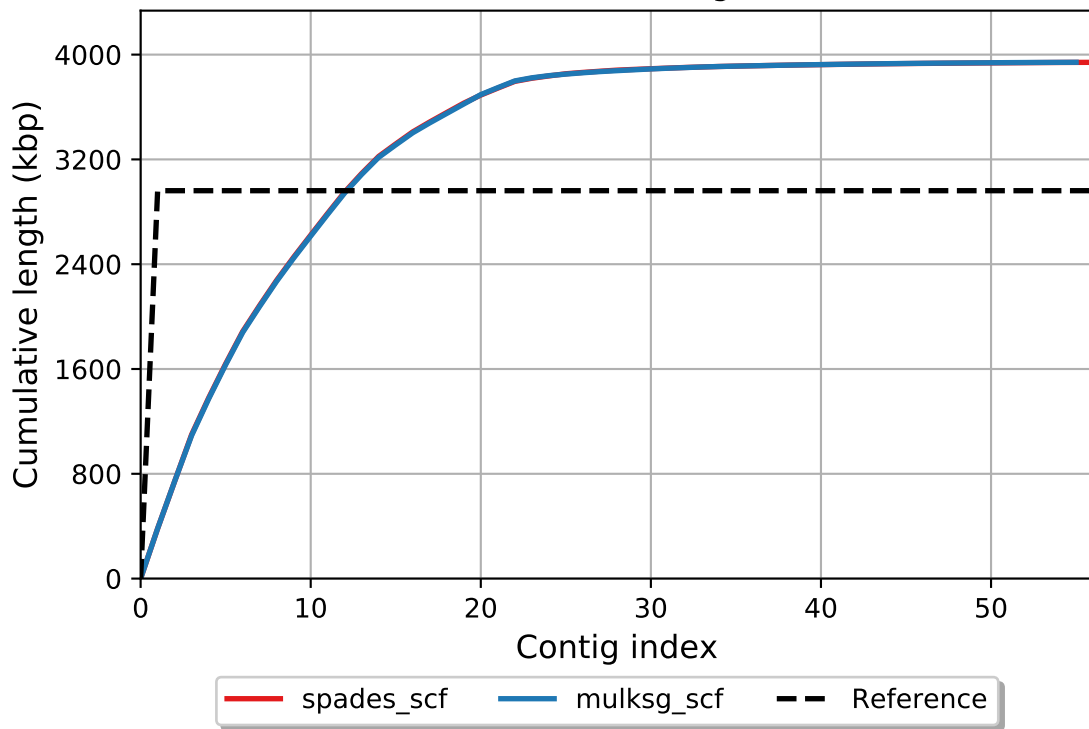


NGx

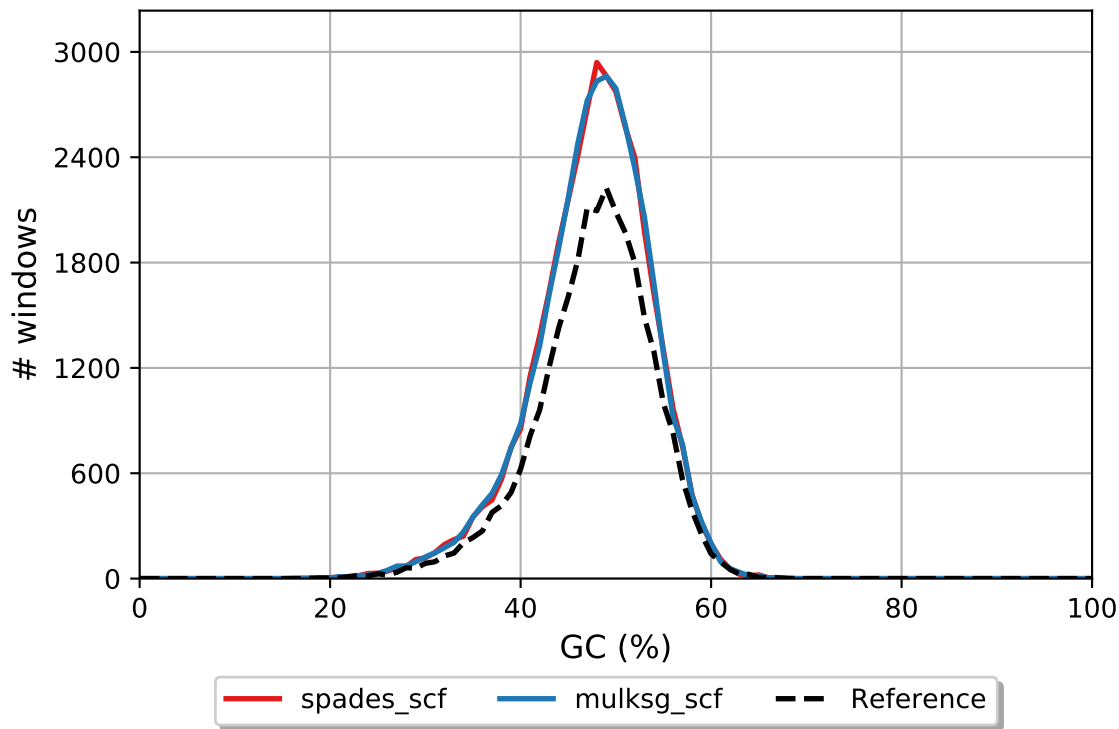


— spades_scf — mulksg_scf

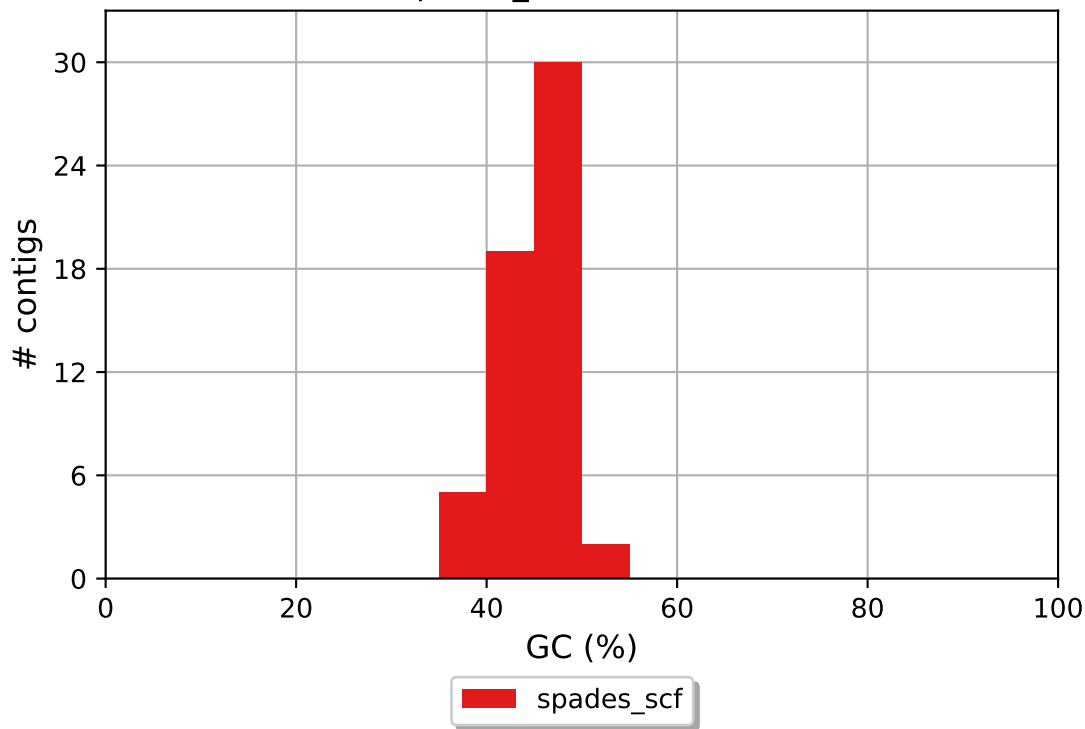
Cumulative length



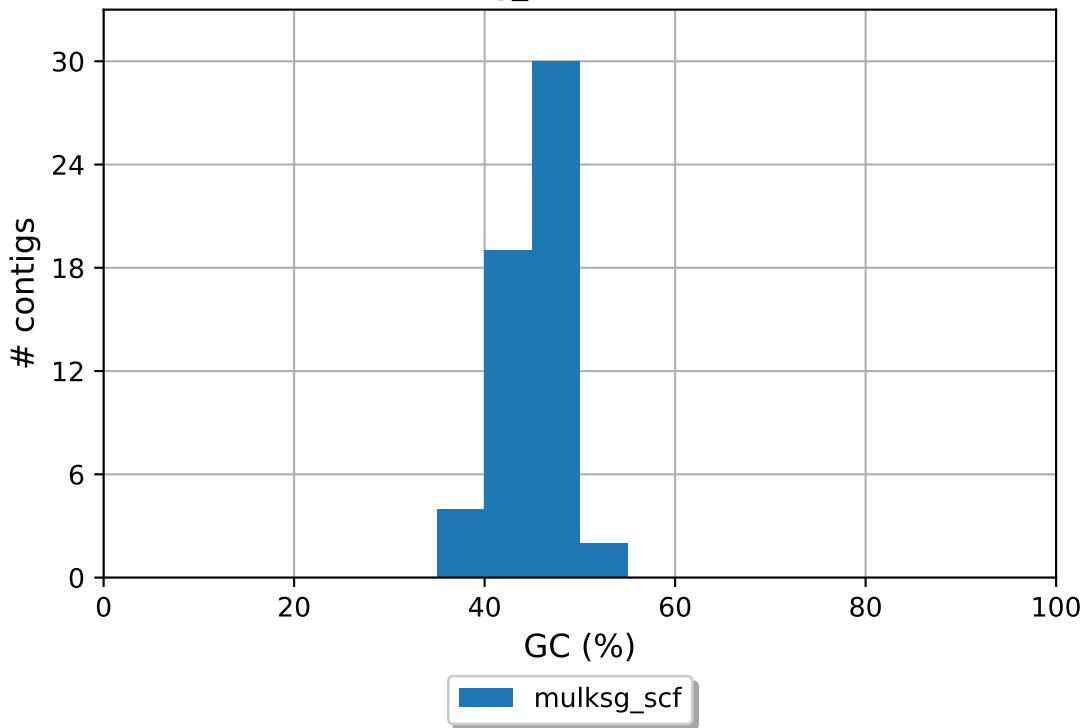
GC content



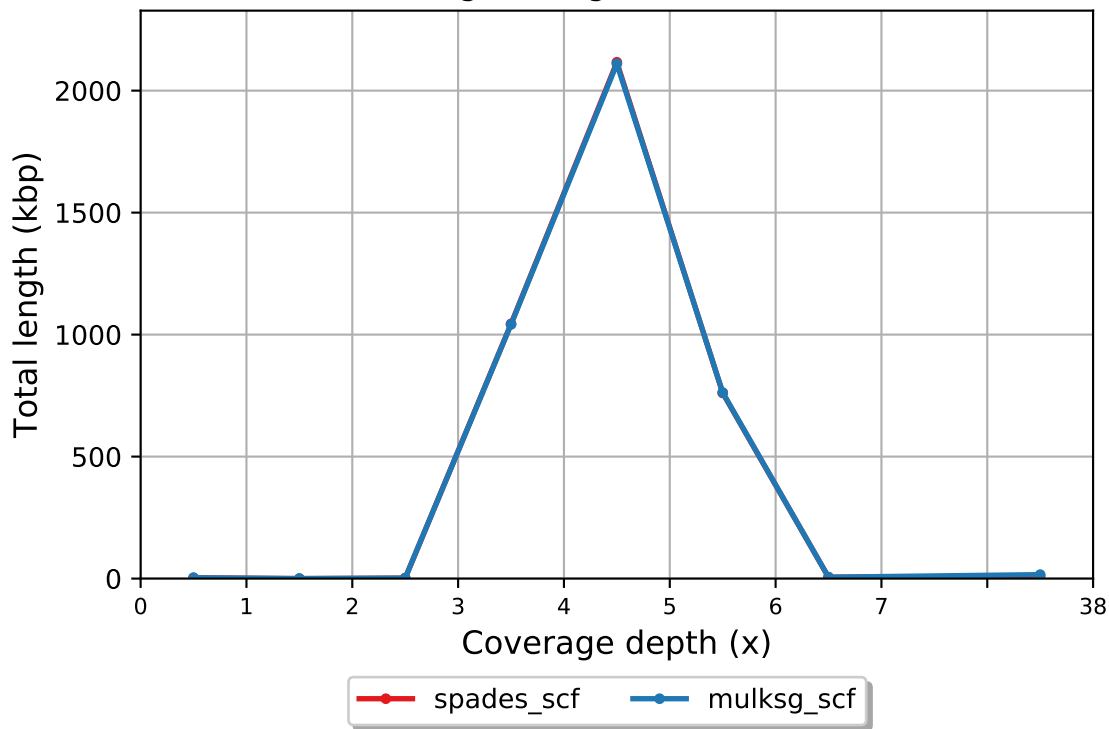
spades_scf GC content



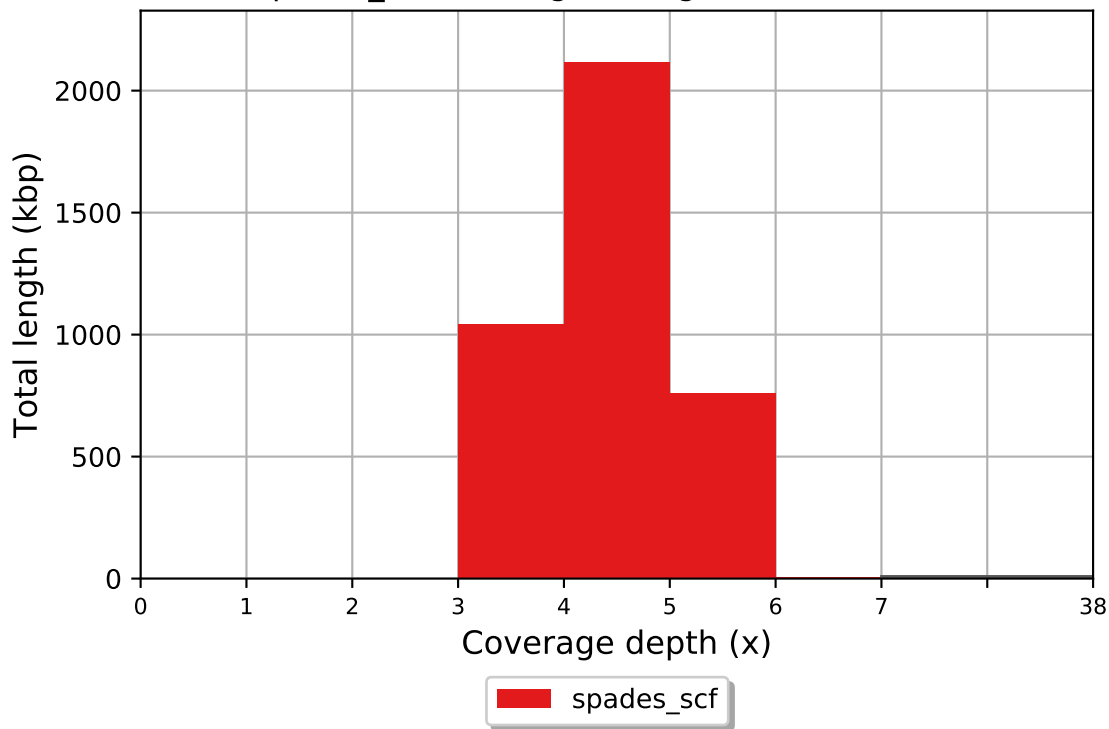
mulksg_scf GC content



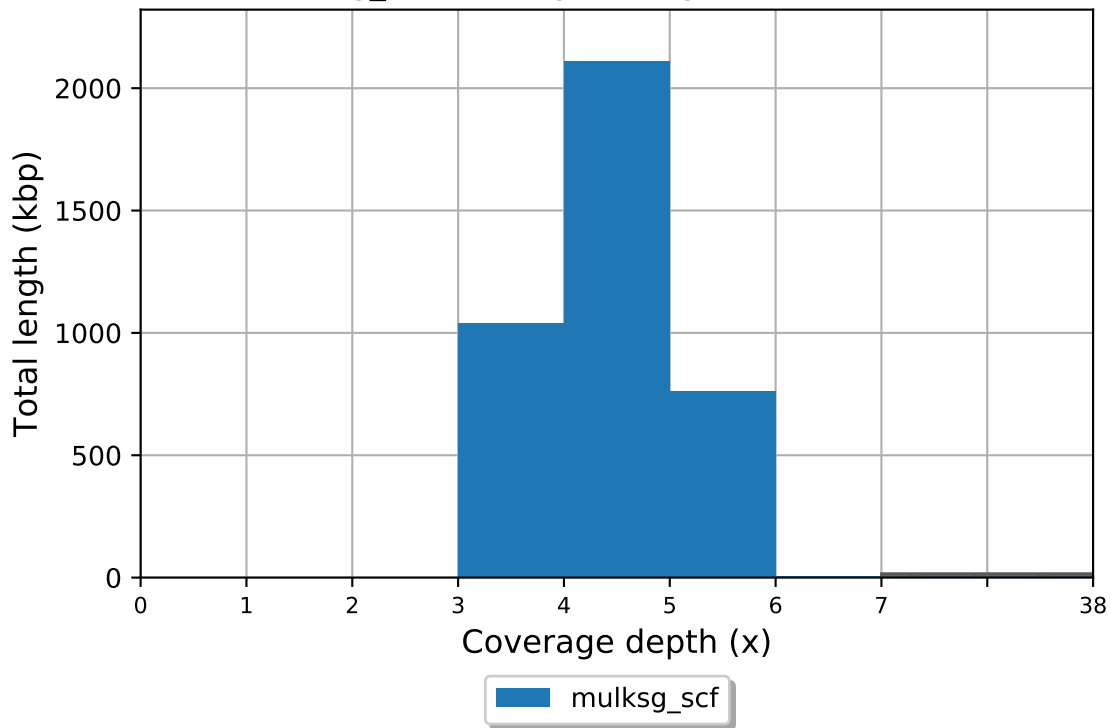
Coverage histogram (bin size: 1x)



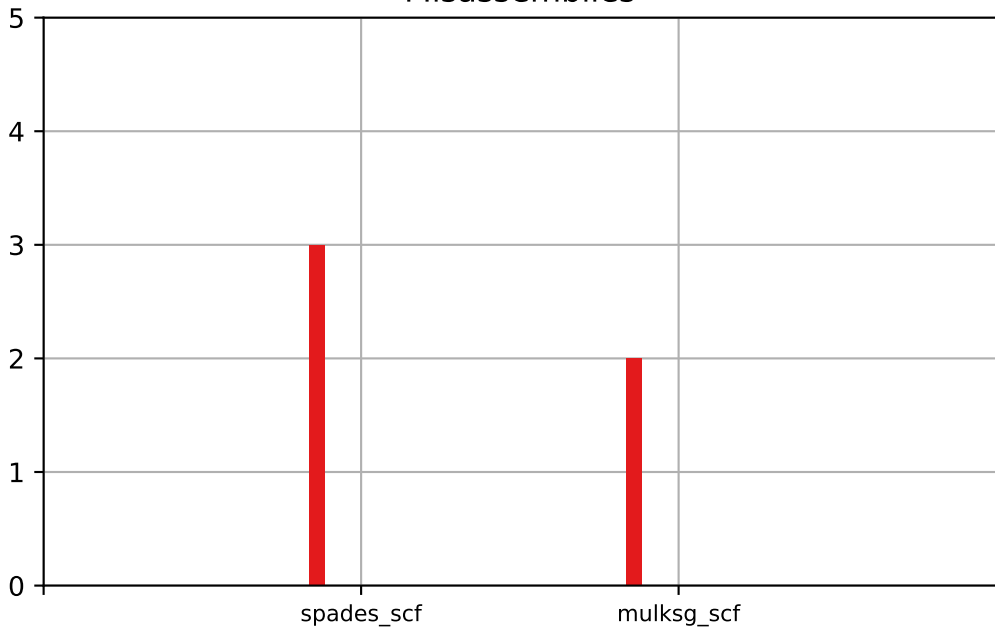
spades_scf coverage histogram (bin size: 1x)



mulksg_scf coverage histogram (bin size: 1x)

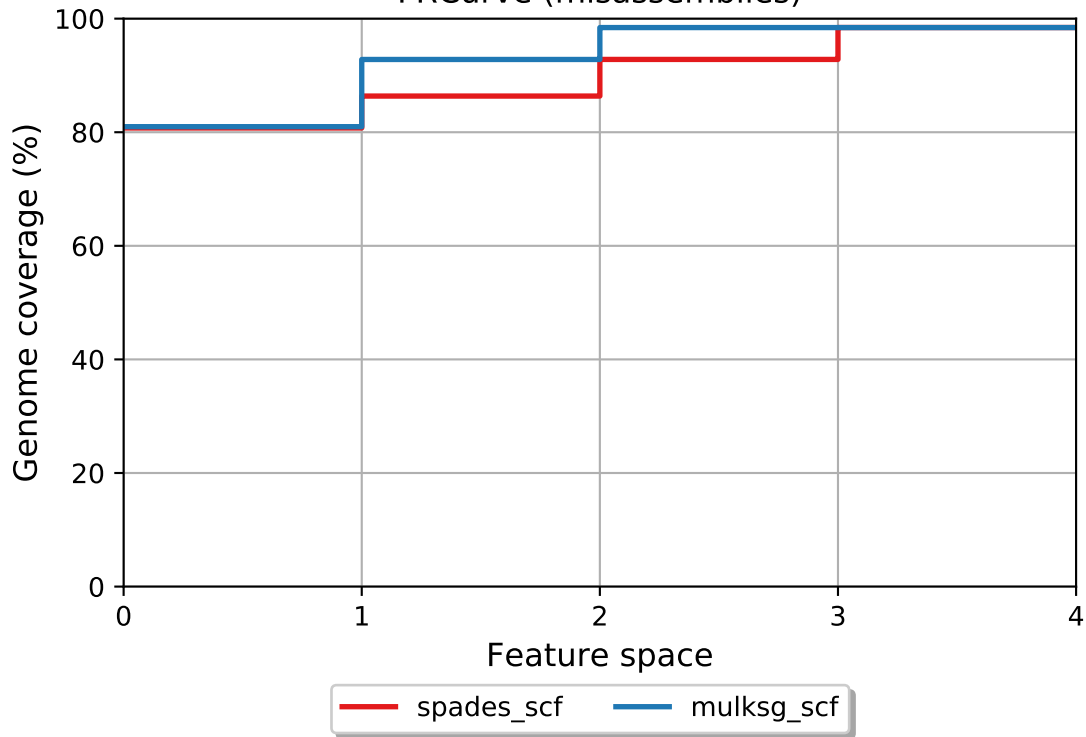


Misassemblies

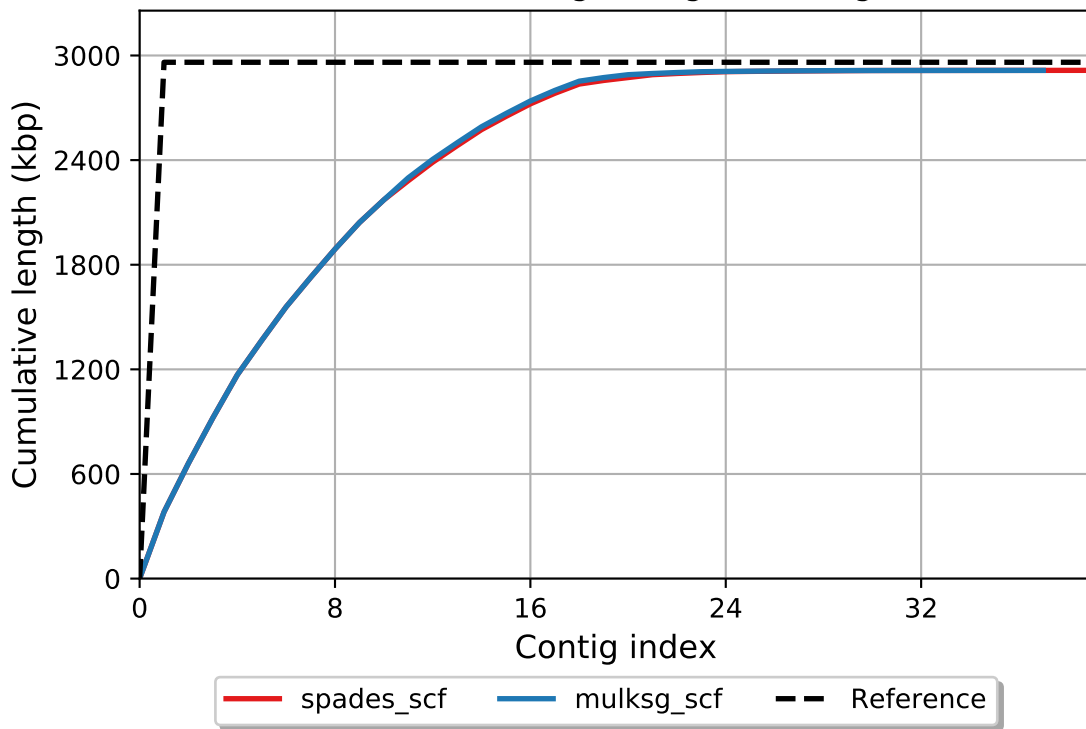


 # relocations

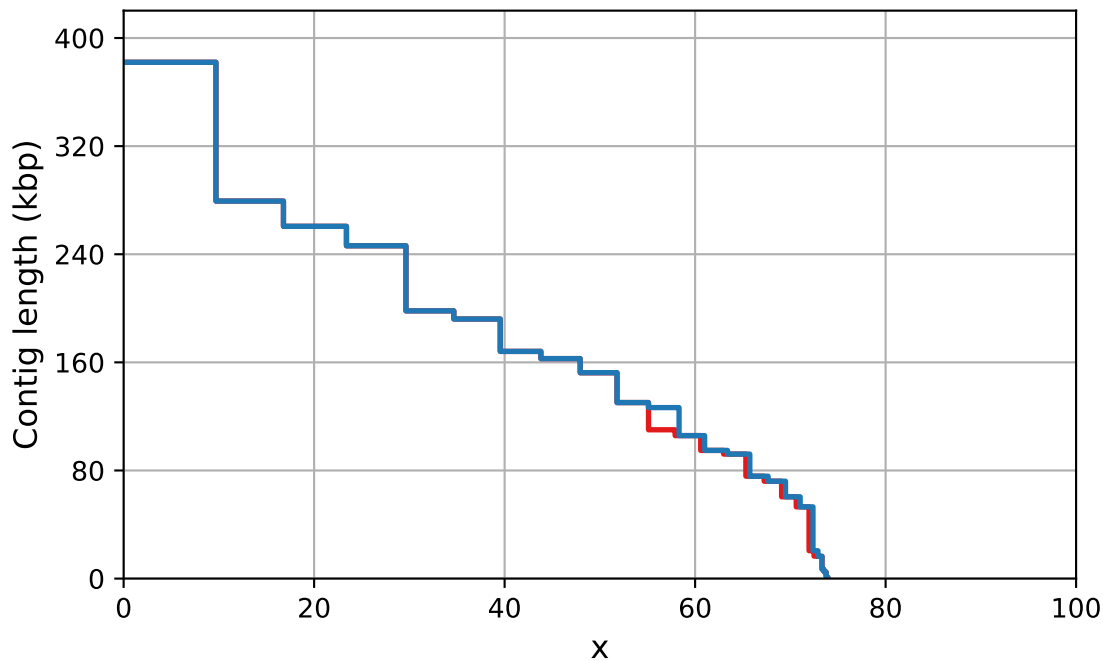
FRCurve (misassemblies)



Cumulative length (aligned contigs)

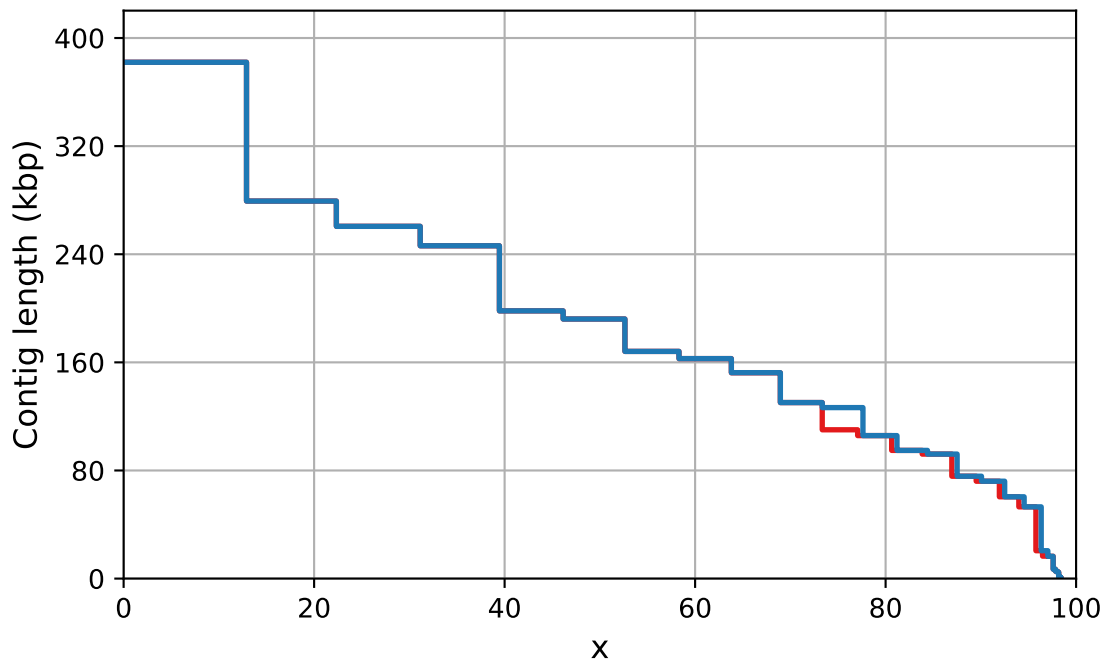


NAx



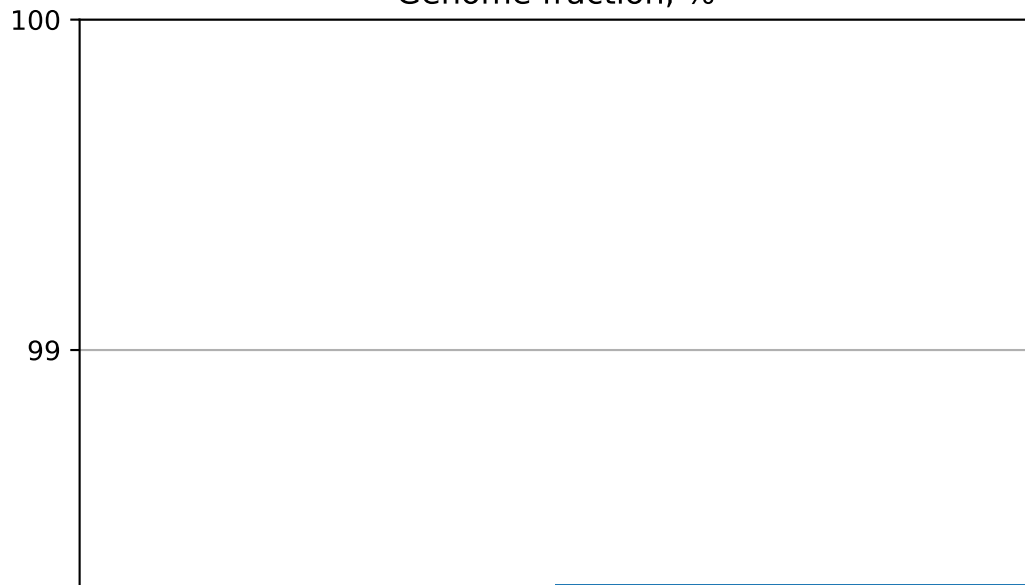
— spades_scf — mulksg_scf

NGAx



spades_scf mulksg_scf

Genome fraction, %



spades_scf mulksg_scf