

Report

| | A_STAR | HipMer | marmgCAMI2 | Megahit | metaSPAdes | Miniasm | OPERA_MS_inhouse | SPAdes |
|-----------------------------|------------|------------|------------|------------|------------|------------|------------------|------------|
| # contigs (>= 1000 bp) | 2 | 2 | 1 | 3 | 3 | 1 | 1 | 1 |
| # contigs (>= 5000 bp) | 2 | 0 | 1 | 3 | 2 | 1 | 1 | 0 |
| # contigs (>= 10000 bp) | 2 | 0 | 1 | 2 | 2 | 1 | 1 | 0 |
| # contigs (>= 25000 bp) | 2 | 0 | 1 | 1 | 0 | 0 | 1 | 0 |
| # contigs (>= 50000 bp) | 2 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| Total length (>= 1000 bp) | 176172 | 9616 | 5396452 | 64369 | 24824 | 15161 | 64738 | 3821 |
| Total length (>= 5000 bp) | 176172 | 0 | 5396452 | 64369 | 21828 | 15161 | 64738 | 0 |
| Total length (>= 10000 bp) | 176172 | 0 | 5396452 | 58035 | 21828 | 15161 | 64738 | 0 |
| Total length (>= 25000 bp) | 176172 | 0 | 5396452 | 38660 | 0 | 0 | 64738 | 0 |
| Total length (>= 50000 bp) | 176172 | 0 | 5396452 | 0 | 0 | 0 | 64738 | 0 |
| # contigs | 2 | 2 | 1 | 3 | 3 | 1 | 1 | 1 |
| Largest contig | 88086 | 4808 | 5396452 | 38660 | 10914 | 15161 | 64738 | 3821 |
| Total length | 176172 | 9616 | 5396452 | 64369 | 24824 | 15161 | 64738 | 3821 |
| Reference length | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 |
| GC (%) | 41.71 | 42.28 | 43.29 | 41.11 | 40.11 | 40.68 | 42.23 | 41.74 |
| Reference GC (%) | 48.06 | 48.06 | 48.06 | 48.06 | 48.06 | 48.06 | 48.06 | 48.06 |
| N50 | 88086 | 4808 | 5396452 | 38660 | 10914 | 15161 | 64738 | 3821 |
| NG50 | 88086 | 4808 | 5396452 | 38660 | 10914 | 15161 | 64738 | 3821 |
| N75 | 88086 | 4808 | 5396452 | 19375 | 10914 | 15161 | 64738 | 3821 |
| NG75 | 88086 | 4808 | 5396452 | 38660 | 10914 | 15161 | 64738 | 3821 |
| L50 | 1 | 1 | 1 | 1 | 2 | 1 | 1 | 1 |
| LG50 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| L75 | 2 | 2 | 1 | 2 | 2 | 1 | 1 | 1 |
| LG75 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| # misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # misassembled contigs | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Misassembled contigs length | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # local misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold gap ext. mis. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # unaligned mis. contigs | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # unaligned contigs | 0 + 2 part | 0 + 2 part | 0 + 1 part | 0 + 3 part | 0 + 3 part | 0 + 1 part | 0 + 1 part | 0 + 1 part |
| Unaligned length | 175760 | 9204 | 5396246 | 63751 | 24206 | 14955 | 64532 | 3615 |
| Genome fraction (%) | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 |
| Duplication ratio | 2.000 | 2.000 | 1.000 | 3.000 | 3.000 | 1.000 | 1.000 | 1.000 |
| # N's per 100 kbp | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| # mismatches per 100 kbp | 0.00 | 0.00 | 0.00 | 1456.31 | 0.00 | 0.00 | 0.00 | 0.00 |
| # indels per 100 kbp | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Largest alignment | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 |
| Total aligned length | 412 | 412 | 206 | 618 | 618 | 206 | 206 | 206 |
| NGA50 | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 |
| NGA75 | 206 | 206 | 206 | 206 | 206 | 206 | 206 | 206 |
| LGA50 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| LGA75 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 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

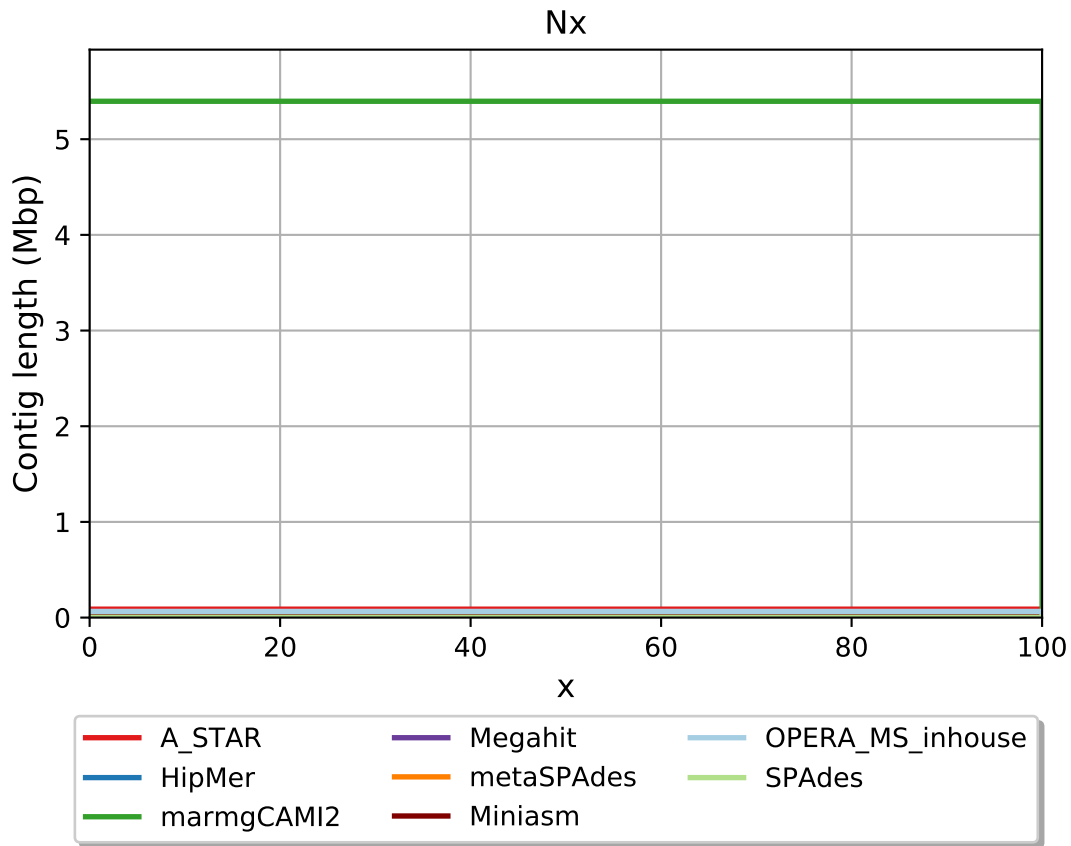
| | A_STAR | HipMer | marmgCAMI2 | Megahit | metaSPAdes | Miniasm | OPERA_MS_inhouse | SPAdes |
|---------------------------------|--------|--------|------------|---------|------------|---------|------------------|--------|
| # misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # contig misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # c. relocations | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # c. translocations | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # c. inversions | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # s. relocations | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # s. translocations | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # s. inversions | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # misassembled contigs | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Misassembled contigs length | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # possibly misassembled contigs | 2 | 2 | 1 | 3 | 3 | 1 | 1 | 1 |
| # possible misassemblies | 4 | 4 | 2 | 6 | 3 | 2 | 2 | 1 |
| # local misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold gap ext. mis. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # unaligned mis. contigs | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # mismatches | 0 | 0 | 0 | 3 | 0 | 0 | 0 | 0 |
| # indels | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # indels (<= 5 bp) | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # indels (> 5 bp) | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Indels length | 0 | 0 | 0 | 0 | 0 | 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).

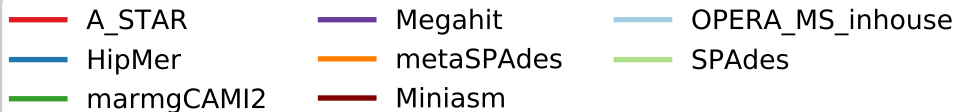
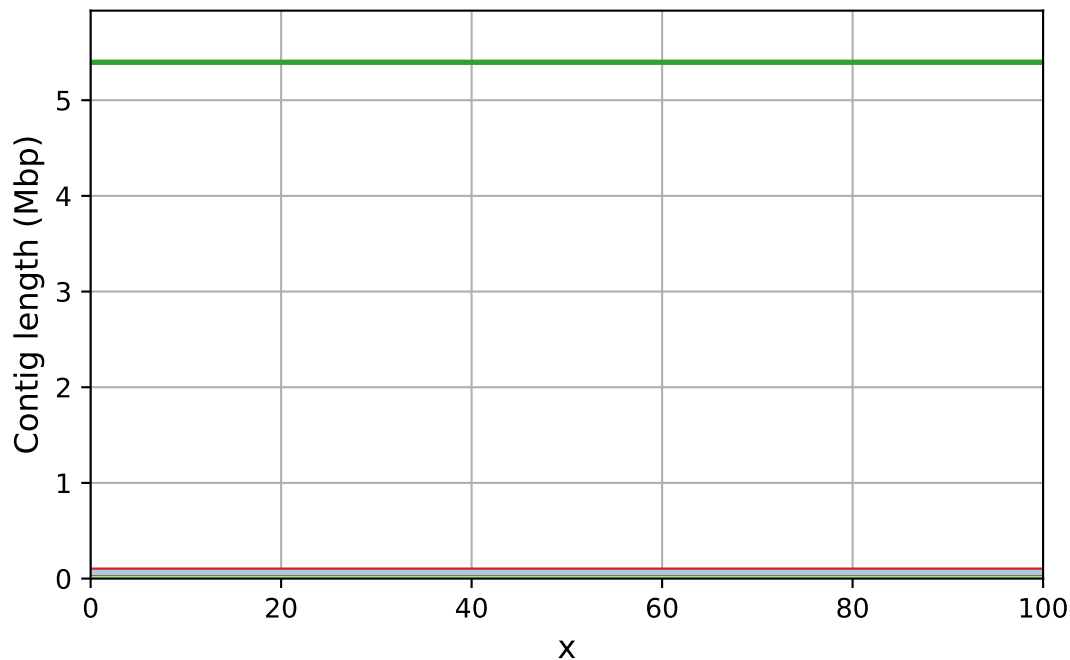
Unaligned report

| | A_STAR | HipMer | marmgCAMI2 | Megahit | metaSPAdes | Miniasm | OPERA_MS_inhouse | SPAdes |
|-------------------------------|--------|--------|------------|---------|------------|---------|------------------|--------|
| # fully unaligned contigs | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Fully unaligned length | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # partially unaligned contigs | 2 | 2 | 1 | 3 | 3 | 1 | 1 | 1 |
| Partially unaligned length | 175760 | 9204 | 5396246 | 63751 | 24206 | 14955 | 64532 | 3615 |
| # N's | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

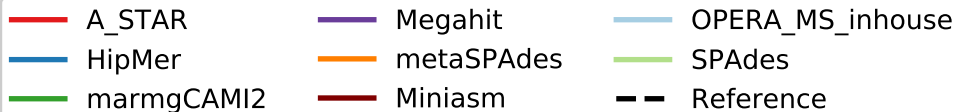
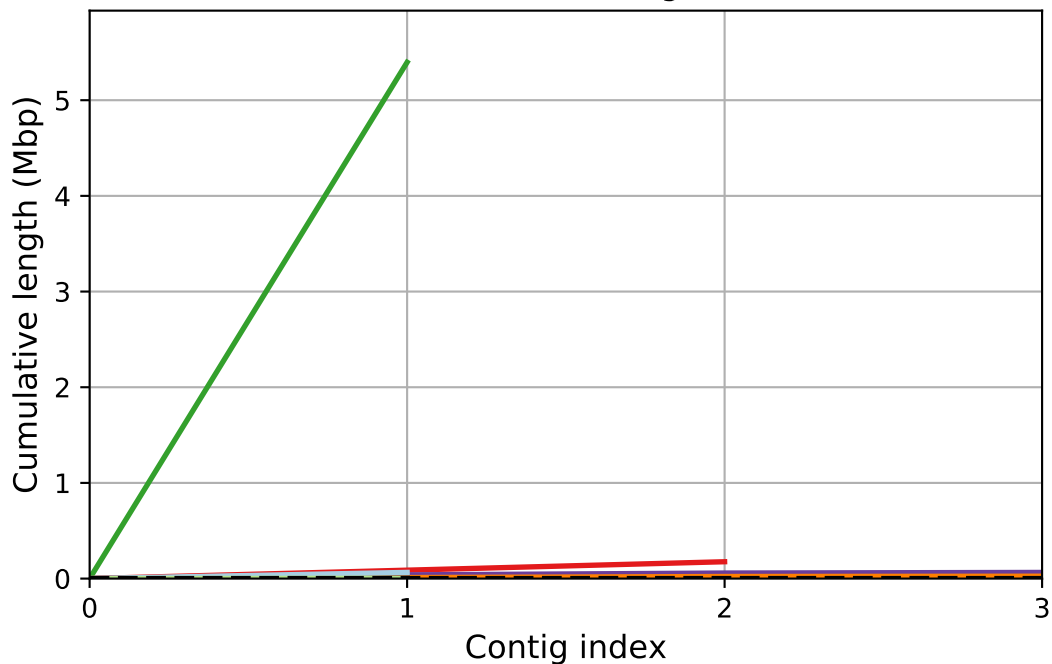
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



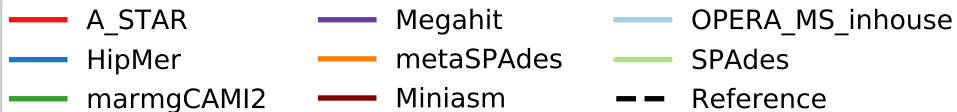
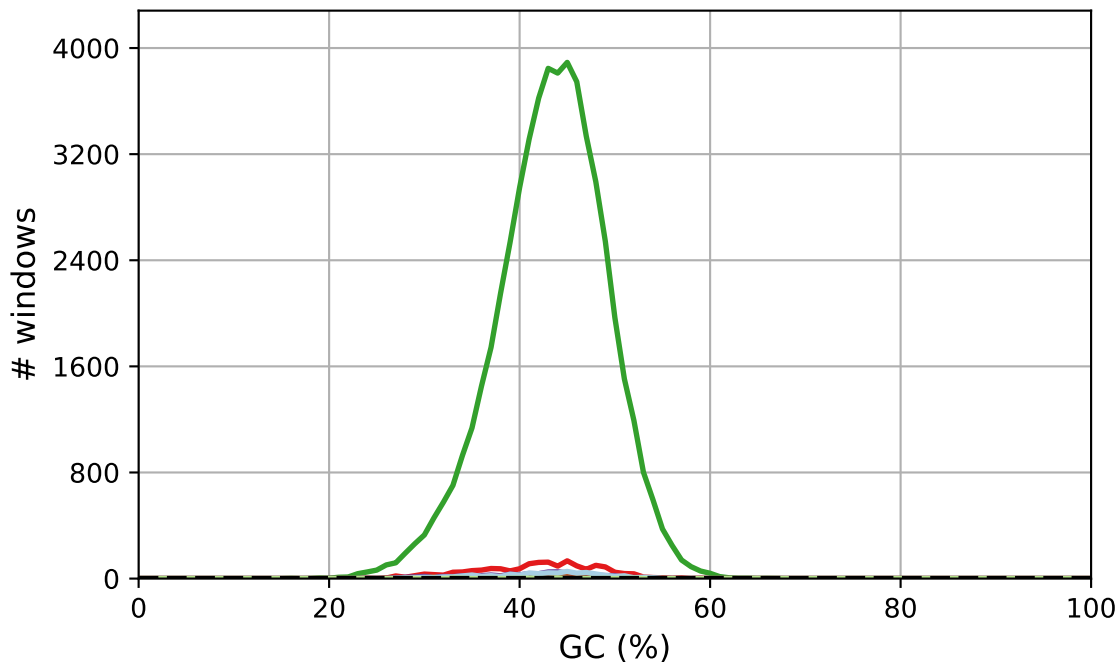
NGx



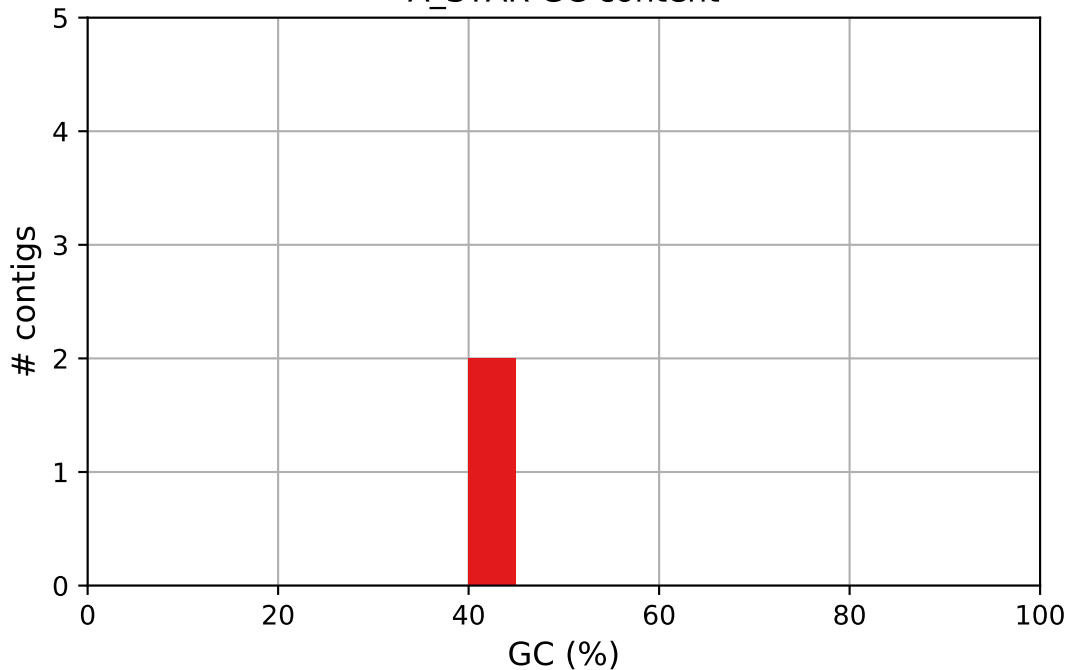
Cumulative length



GC content

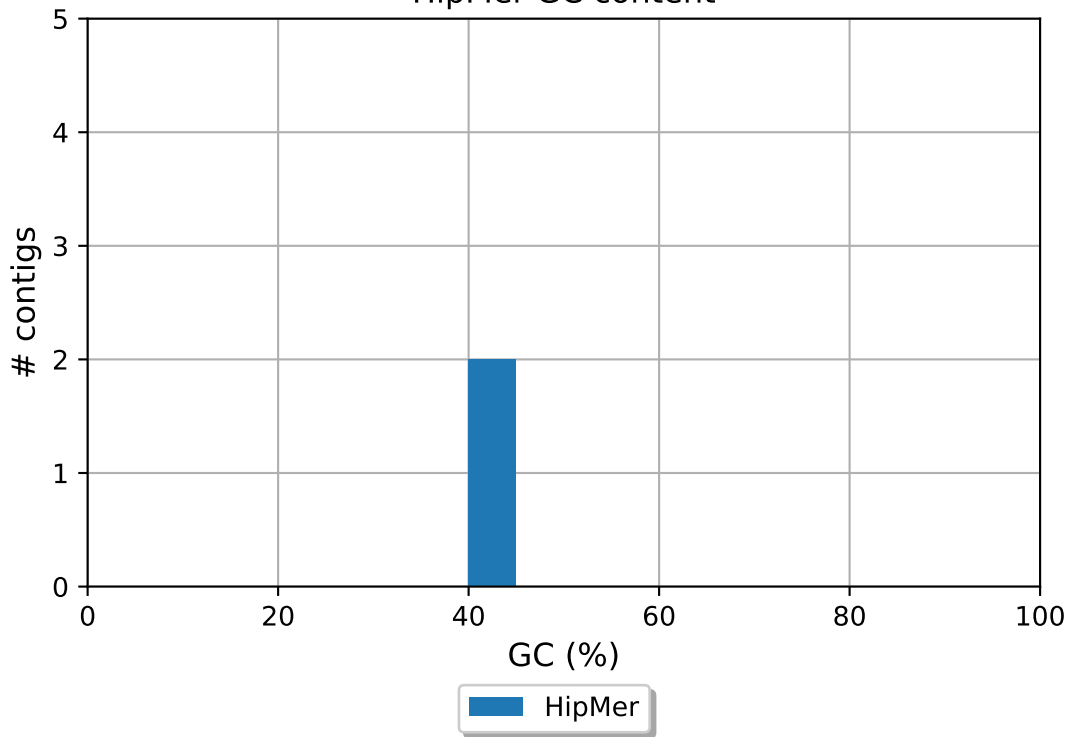


A_STAR GC content

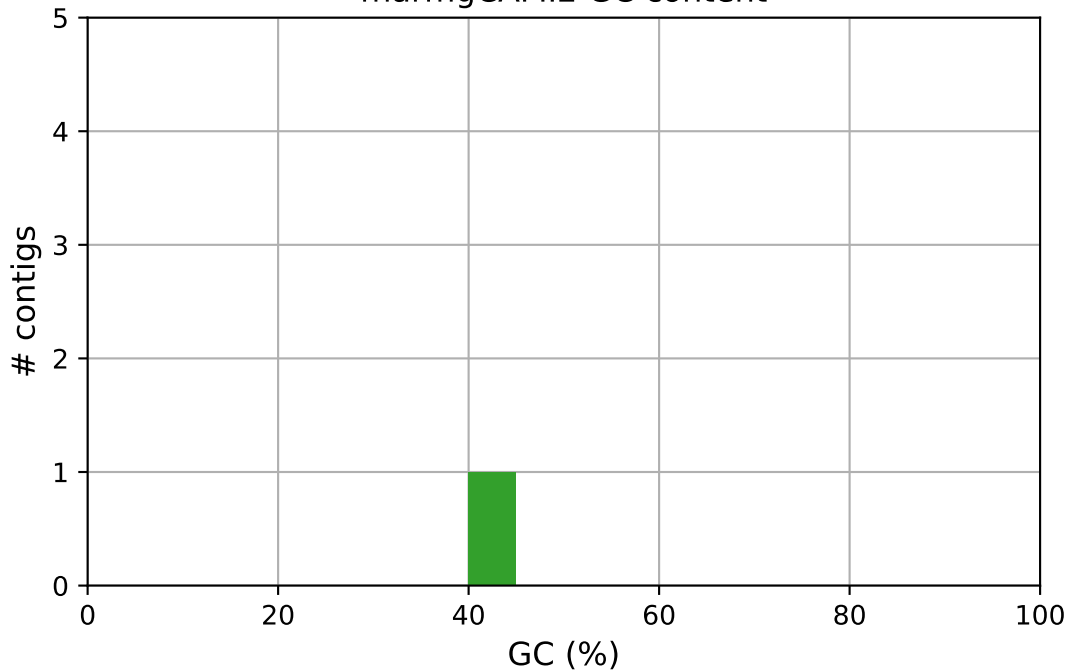


A_STAR

HipMer GC content

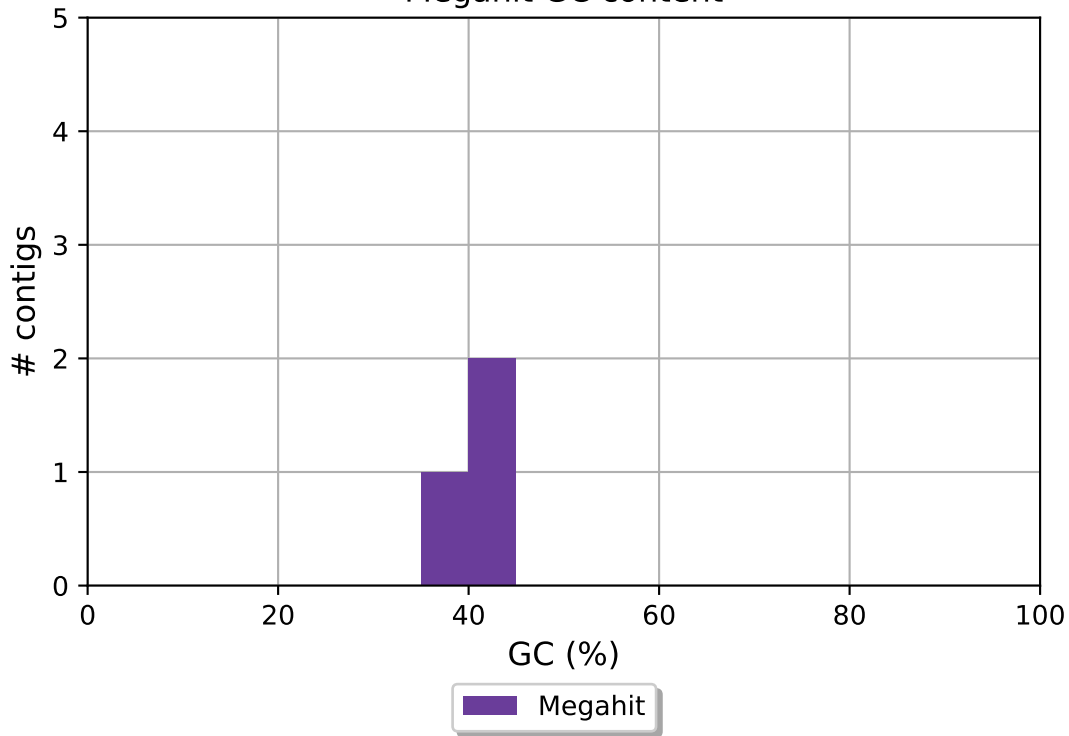


marmgCAMI2 GC content

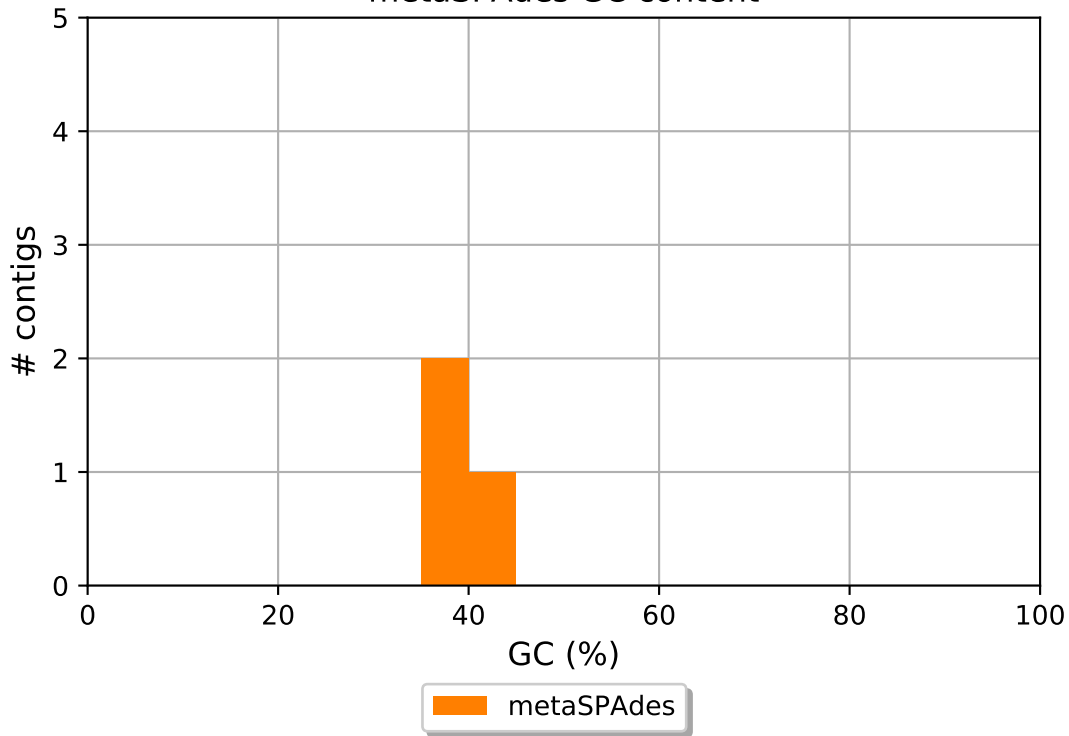


marmgCAMI2

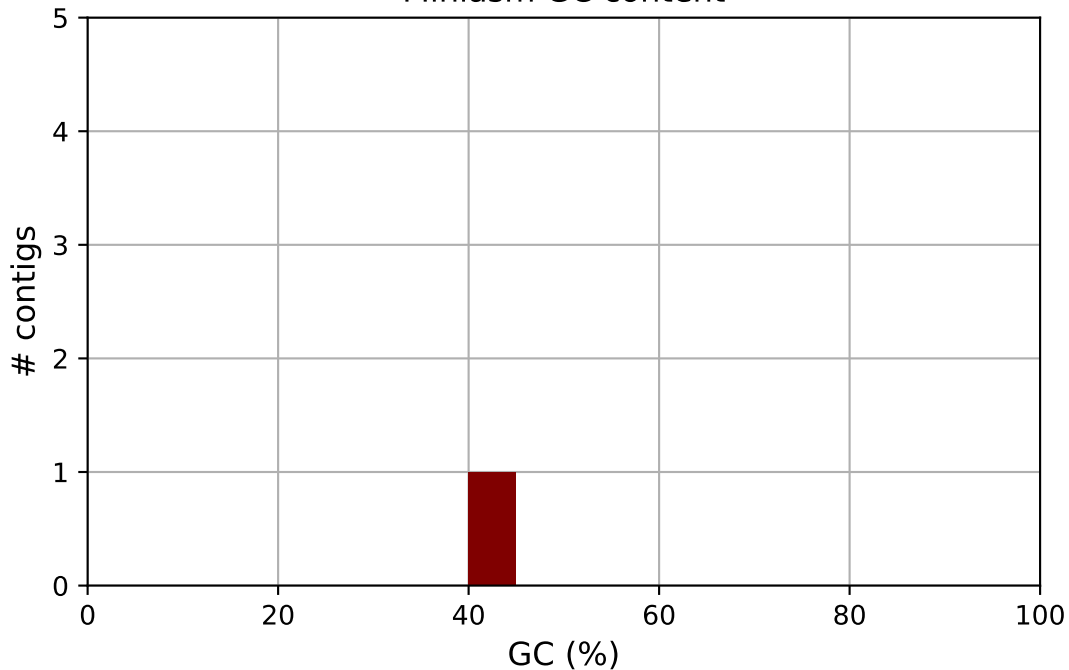
Megahit GC content



metaSPAdes GC content

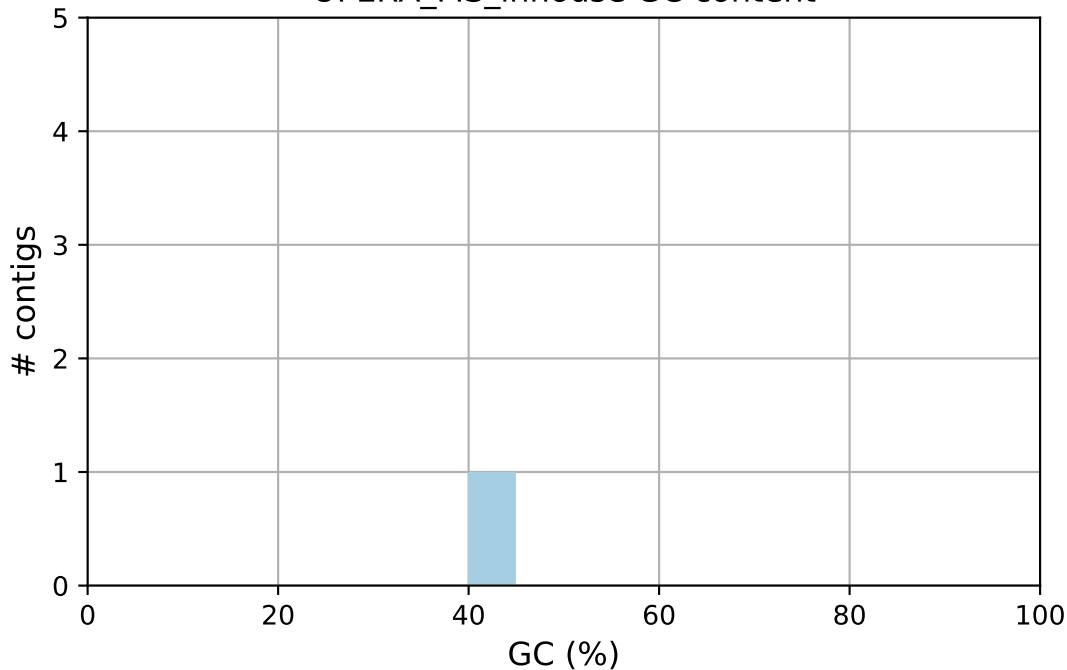


Miniasm GC content



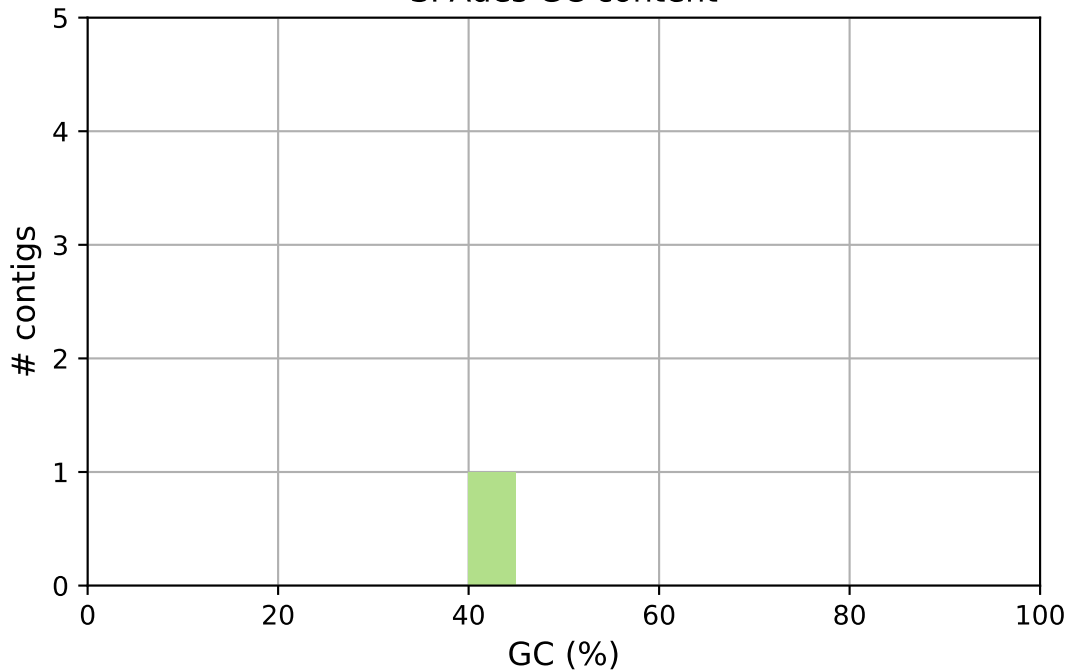
Miniasm

OPERA_MS_inhouse GC content



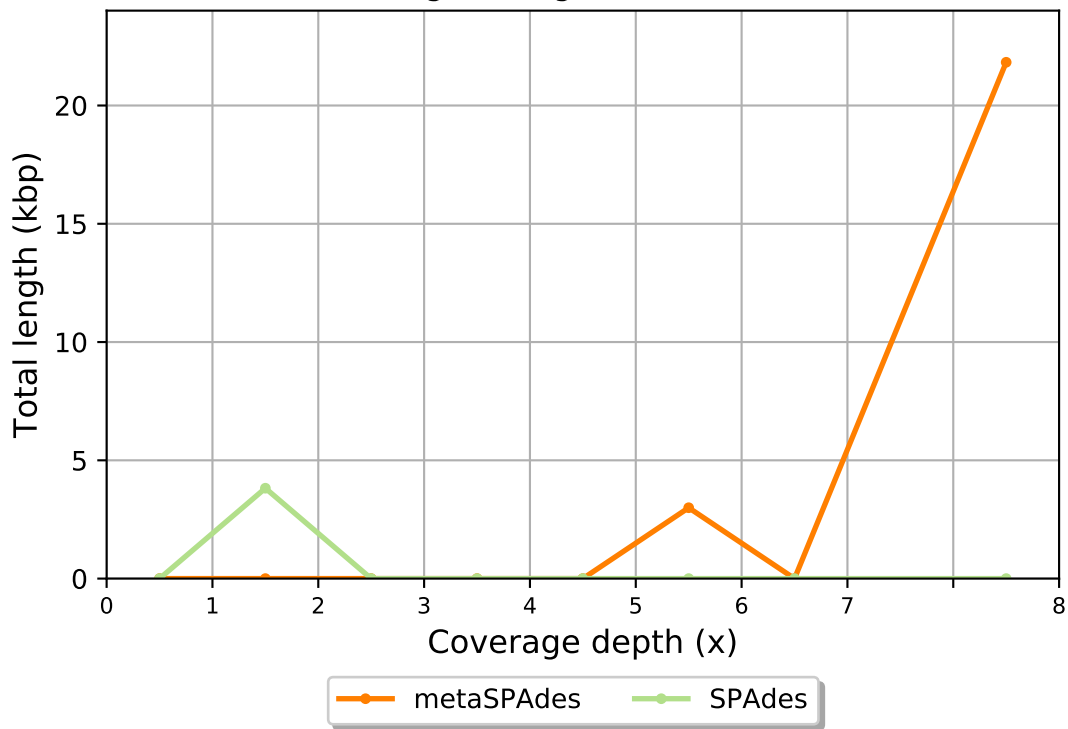
OPERA_MS_inhouse

SPAdes GC content

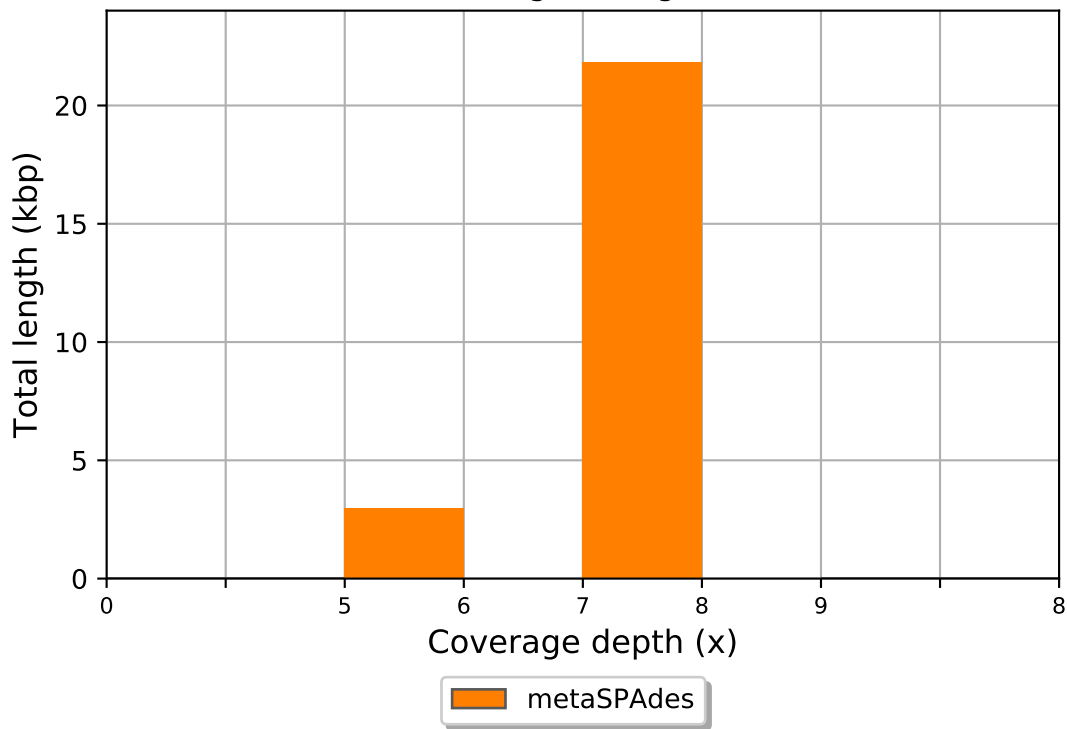


SPAdes

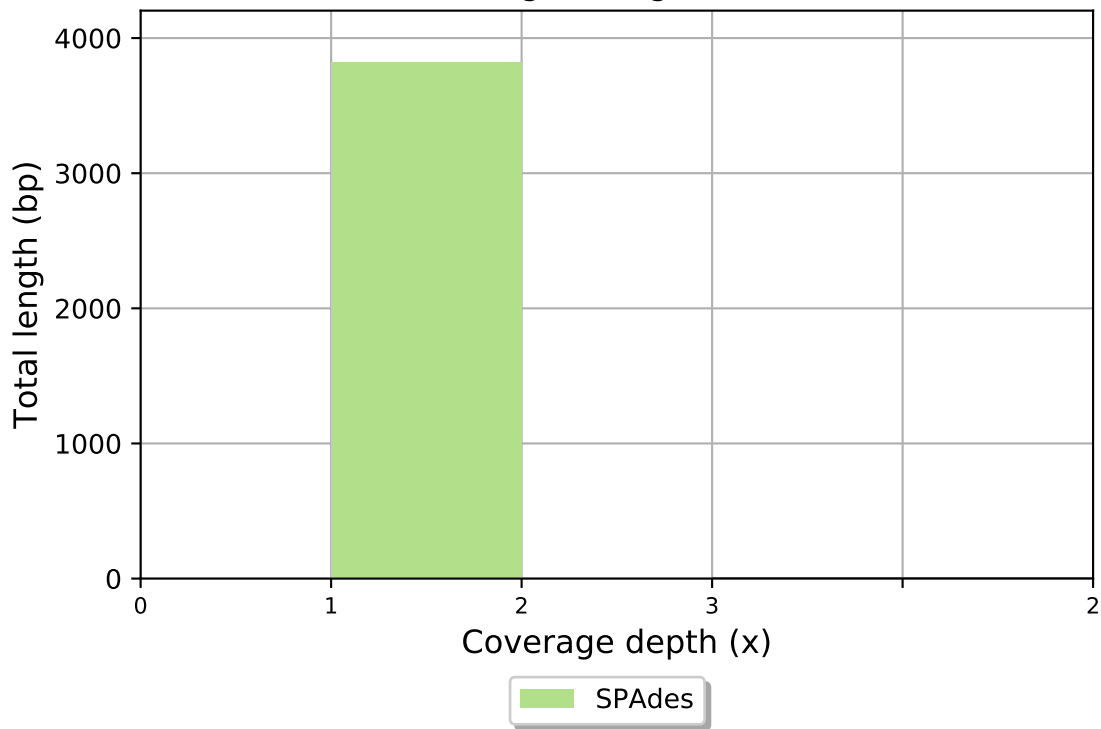
Coverage histogram (bin size: 1x)



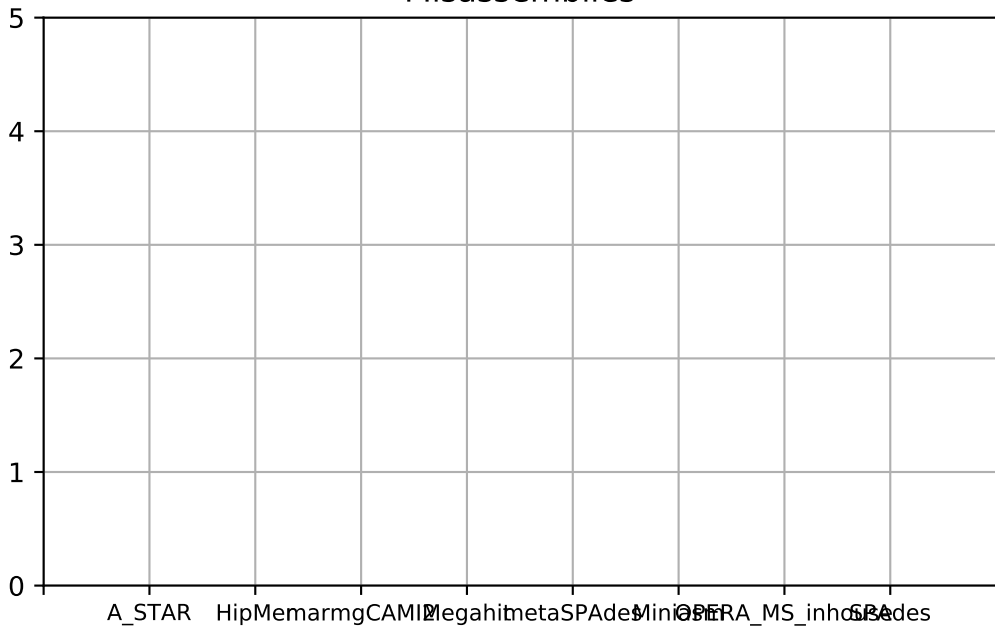
metaSPAdes coverage histogram (bin size: 1x)



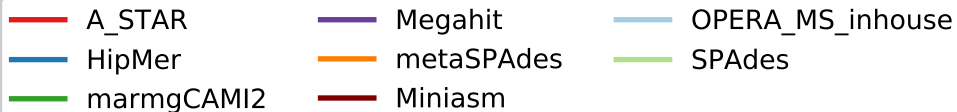
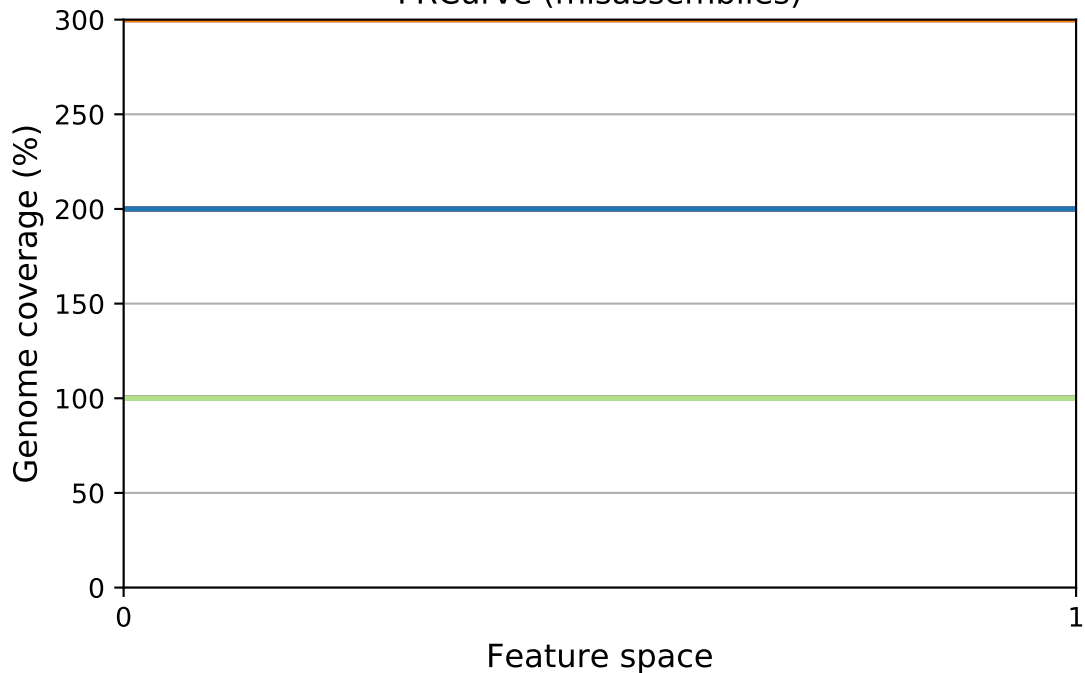
SPAdes coverage histogram (bin size: 1x)



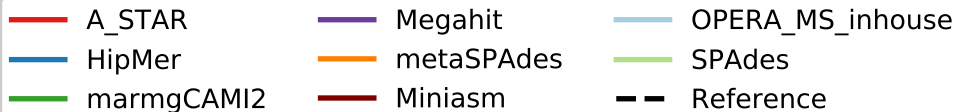
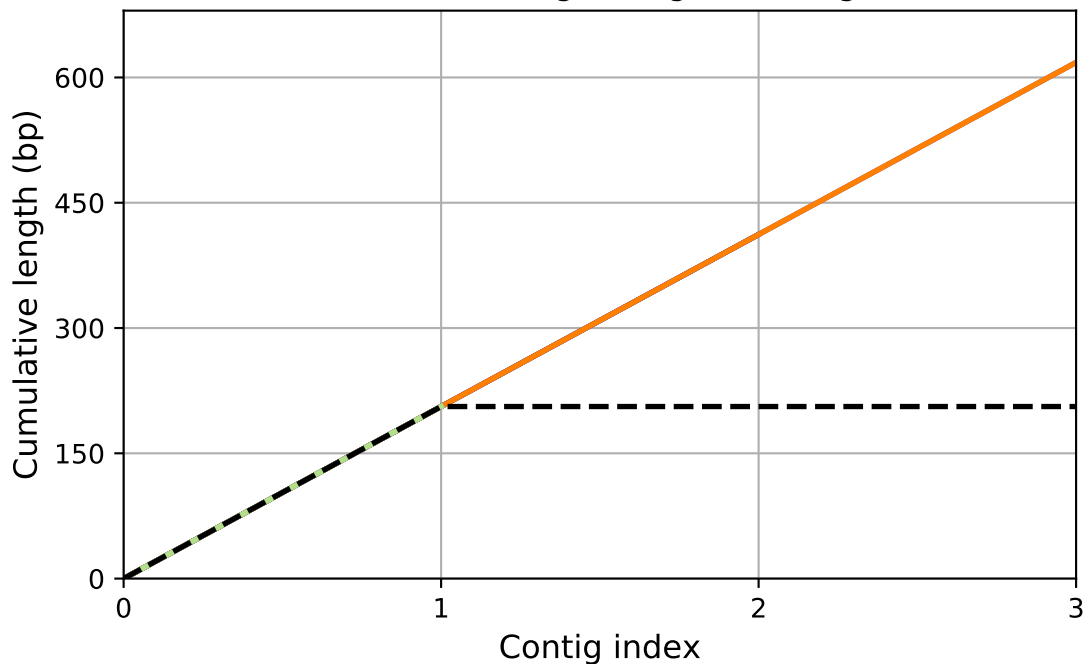
Misassemblies



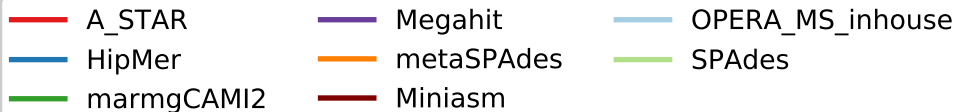
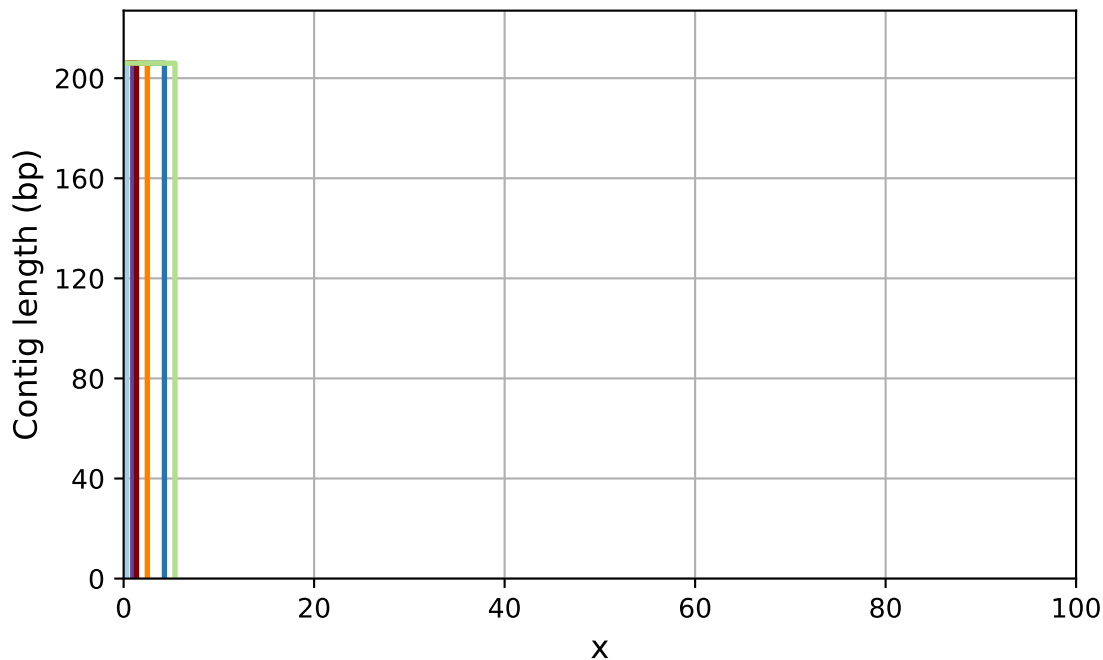
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAX



NGAx

