

Report

| | ABYSS | A_STAR | HipMer | marmgCAMI2 | Megahit | metaSPAdes | Miniasm | OPERA_MS_inhouse | SPAdes |
|-----------------------------|------------|-------------|------------|------------|-------------|------------|------------|------------------|------------|
| # contigs (>= 1000 bp) | 6 | 18 | 5 | 1 | 11 | 9 | 4 | 2 | 2 |
| # contigs (>= 5000 bp) | 6 | 13 | 5 | 1 | 11 | 9 | 4 | 2 | 2 |
| # contigs (>= 10000 bp) | 6 | 13 | 5 | 1 | 11 | 9 | 4 | 2 | 2 |
| # contigs (>= 25000 bp) | 6 | 9 | 4 | 1 | 10 | 9 | 4 | 2 | 2 |
| # contigs (>= 50000 bp) | 4 | 6 | 4 | 1 | 8 | 9 | 4 | 2 | 2 |
| Total length (>= 1000 bp) | 500944 | 2178583 | 2731938 | 1859369 | 1991448 | 4558984 | 8381890 | 1513471 | 1854709 |
| Total length (>= 5000 bp) | 500944 | 2164197 | 2731938 | 1859369 | 1991448 | 4558984 | 8381890 | 1513471 | 1854709 |
| Total length (>= 10000 bp) | 500944 | 2164197 | 2731938 | 1859369 | 1991448 | 4558984 | 8381890 | 1513471 | 1854709 |
| Total length (>= 25000 bp) | 500944 | 2115033 | 2707560 | 1859369 | 1966961 | 4558984 | 8381890 | 1513471 | 1854709 |
| Total length (>= 50000 bp) | 424122 | 2022878 | 2707560 | 1859369 | 1912003 | 4558984 | 8381890 | 1513471 | 1854709 |
| # contigs | 6 | 18 | 5 | 1 | 12 | 9 | 4 | 2 | 2 |
| Largest contig | 148370 | 421667 | 1524395 | 1859369 | 541757 | 762996 | 2428999 | 763998 | 1091680 |
| Total length | 500944 | 2178583 | 2731938 | 1859369 | 1992135 | 4558984 | 8381890 | 1513471 | 1854709 |
| Reference length | 7308 | 7308 | 7308 | 7308 | 7308 | 7308 | 7308 | 7308 | 7308 |
| GC (%) | 43.32 | 42.70 | 43.04 | 43.04 | 42.67 | 42.95 | 49.45 | 42.97 | 42.99 |
| Reference GC (%) | 36.21 | 36.21 | 36.21 | 36.21 | 36.21 | 36.21 | 36.21 | 36.21 | 36.21 |
| N50 | 148370 | 327935 | 1524395 | 1859369 | 541642 | 762974 | 2428999 | 763998 | 1091680 |
| NG50 | 148370 | 421667 | 1524395 | 1859369 | 541757 | 762996 | 2428999 | 763998 | 1091680 |
| N75 | 63691 | 261837 | 642266 | 1859369 | 194498 | 504133 | 2428999 | 749473 | 763029 |
| NG75 | 148370 | 421667 | 1524395 | 1859369 | 541757 | 762996 | 2428999 | 763998 | 1091680 |
| L50 | 2 | 3 | 1 | 1 | 2 | 3 | 2 | 1 | 1 |
| LG50 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| L75 | 4 | 5 | 2 | 1 | 5 | 6 | 3 | 2 | 2 |
| LG75 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| # misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # misassembled contigs | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Misassembled contigs length | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # local misassemblies | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| # scaffold gap ext. mis. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # unaligned mis. contigs | 0 | 2 | 1 | 1 | 0 | 0 | 4 | 1 | 1 |
| # unaligned contigs | 0 + 6 part | 0 + 18 part | 0 + 5 part | 0 + 1 part | 0 + 11 part | 0 + 9 part | 0 + 4 part | 0 + 2 part | 0 + 2 part |
| Unaligned length | 486120 | 2151938 | 2716626 | 1852061 | 1971784 | 4537060 | 8369894 | 1506634 | 1847368 |
| Genome fraction (%) | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 89.997 | 95.265 | 100.000 |
| Duplication ratio | 2.028 | 3.646 | 2.095 | 1.000 | 2.785 | 3.000 | 1.824 | 0.982 | 1.005 |
| # N's per 100 kbp | 41.52 | 122.88 | 32.10 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 5.39 |
| # mismatches per 100 kbp | 0.00 | 574.71 | 0.00 | 0.00 | 766.28 | 0.00 | 471.34 | 215.46 | 0.00 |
| # indels per 100 kbp | 0.00 | 82.10 | 54.73 | 0.00 | 41.05 | 0.00 | 805.84 | 114.91 | 13.68 |
| Largest alignment | 3437 | 3303 | 3370 | 3437 | 3504 | 3437 | 2105 | 3303 | 3470 |
| Total aligned length | 14616 | 23968 | 14512 | 7308 | 20296 | 21924 | 11996 | 6837 | 7341 |
| NGA50 | 3437 | 3303 | 2617 | 2095 | 3303 | 3437 | 1933 | 2104 | 2095 |
| NGA75 | 3437 | 3303 | 2617 | 2095 | 3303 | 3437 | 1933 | 667 | 2095 |
| LGA50 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 | 2 |
| LGA75 | 2 | 2 | 2 | 2 | 2 | 2 | 3 | 3 | 2 |

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

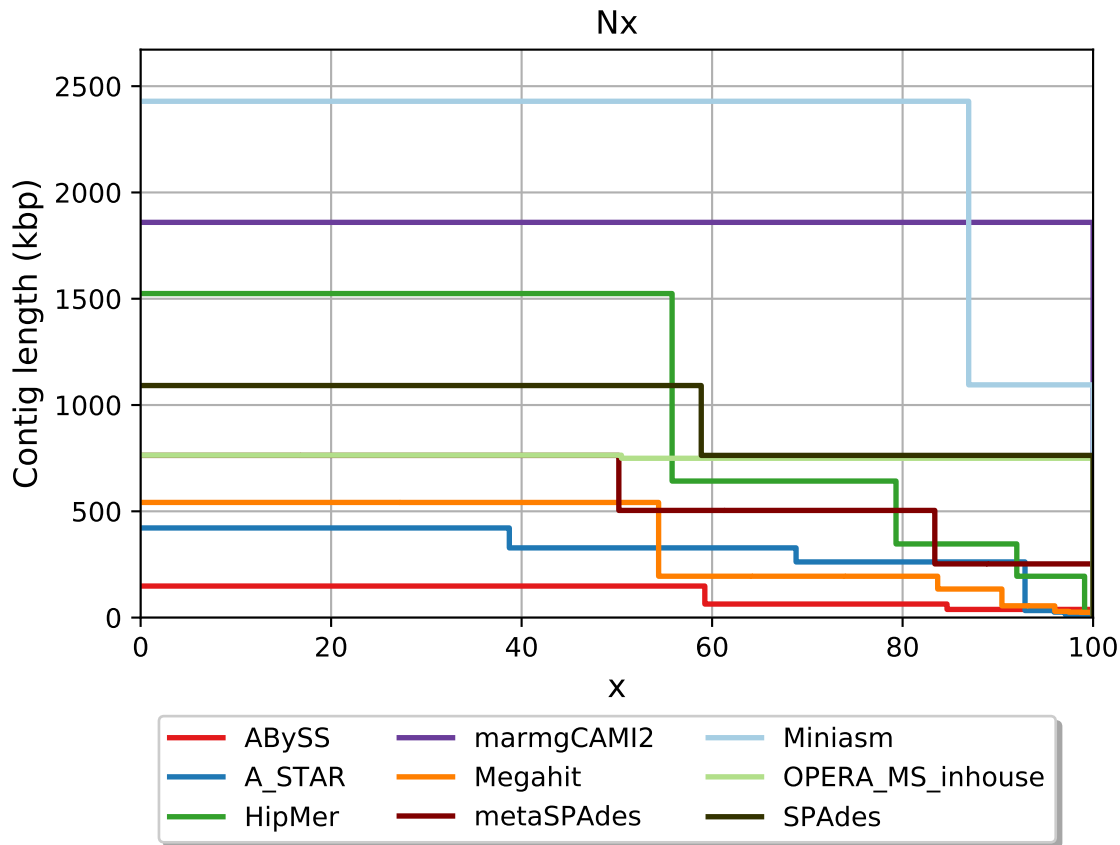
| | ABySS | A_STAR | HipMer | marmgCAMI2 | Megahit | metaSPAdes | Miniasm | OPERA_MS_inhouse | SPAdes |
|---------------------------------|-------|--------|--------|------------|---------|------------|---------|------------------|--------|
| # misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # contig misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # c. relocations | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # c. translocations | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # c. inversions | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold misassemblies | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # s. relocations | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # s. translocations | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # s. inversions | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # misassembled contigs | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Misassembled contigs length | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # possibly misassembled contigs | 6 | 14 | 4 | 0 | 11 | 9 | 0 | 1 | 1 |
| # possible misassemblies | 12 | 21 | 6 | 0 | 18 | 18 | 0 | 2 | 2 |
| # local misassemblies | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| # scaffold gap ext. mis. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # unaligned mis. contigs | 0 | 2 | 1 | 1 | 0 | 0 | 4 | 1 | 1 |
| # mismatches | 0 | 42 | 0 | 0 | 56 | 0 | 31 | 15 | 0 |
| # indels | 0 | 6 | 4 | 0 | 3 | 0 | 53 | 8 | 1 |
| # indels (<= 5 bp) | 0 | 2 | 0 | 0 | 0 | 0 | 52 | 7 | 0 |
| # indels (> 5 bp) | 0 | 4 | 4 | 0 | 3 | 0 | 1 | 1 | 1 |
| Indels length | 0 | 406 | 138 | 0 | 268 | 0 | 71 | 145 | 33 |

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).

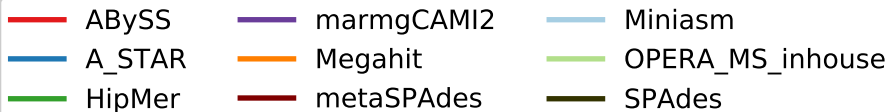
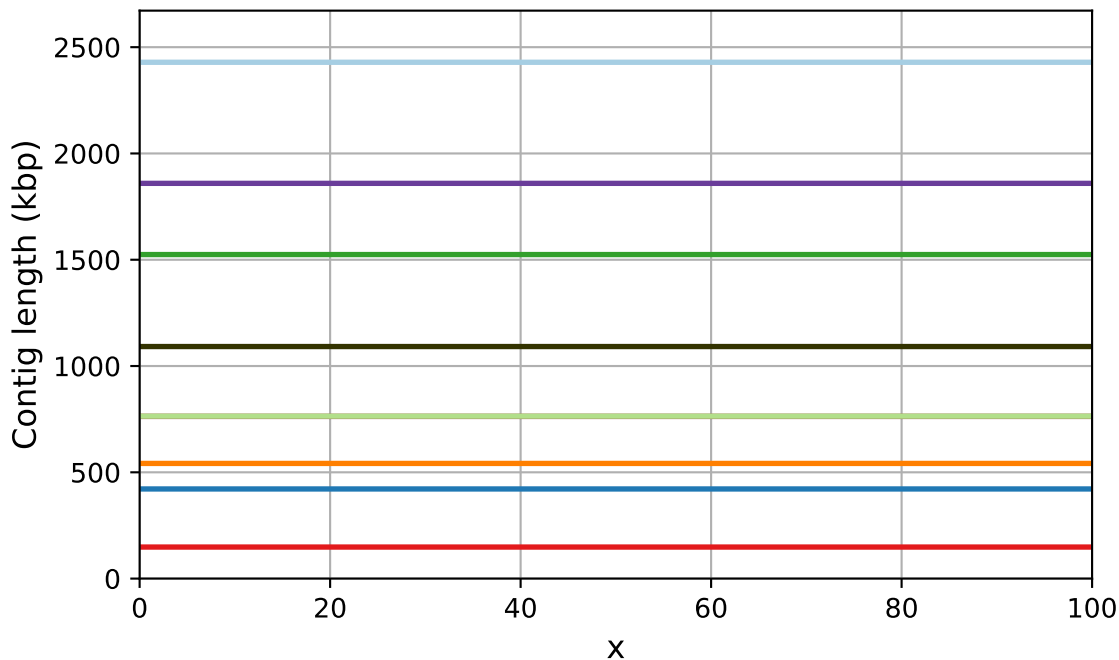
Unaligned report

| | ABYSS | A_STAR | HipMer | marmgCAMI2 | Megahit | metaSPAdes | Miniasm | OPERA_MS_inhouse | SPAdes |
|-------------------------------|--------|---------|---------|------------|---------|------------|---------|------------------|---------|
| # fully unaligned contigs | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Fully unaligned length | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| # partially unaligned contigs | 6 | 18 | 5 | 1 | 11 | 9 | 4 | 2 | 2 |
| Partially unaligned length | 486120 | 2151938 | 2716626 | 1852061 | 1971784 | 4537060 | 8369894 | 1506634 | 1847368 |
| # N's | 208 | 2677 | 877 | 0 | 0 | 0 | 0 | 0 | 100 |

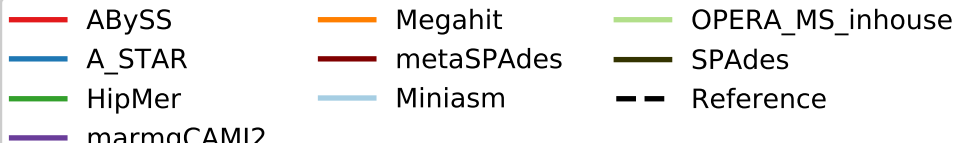
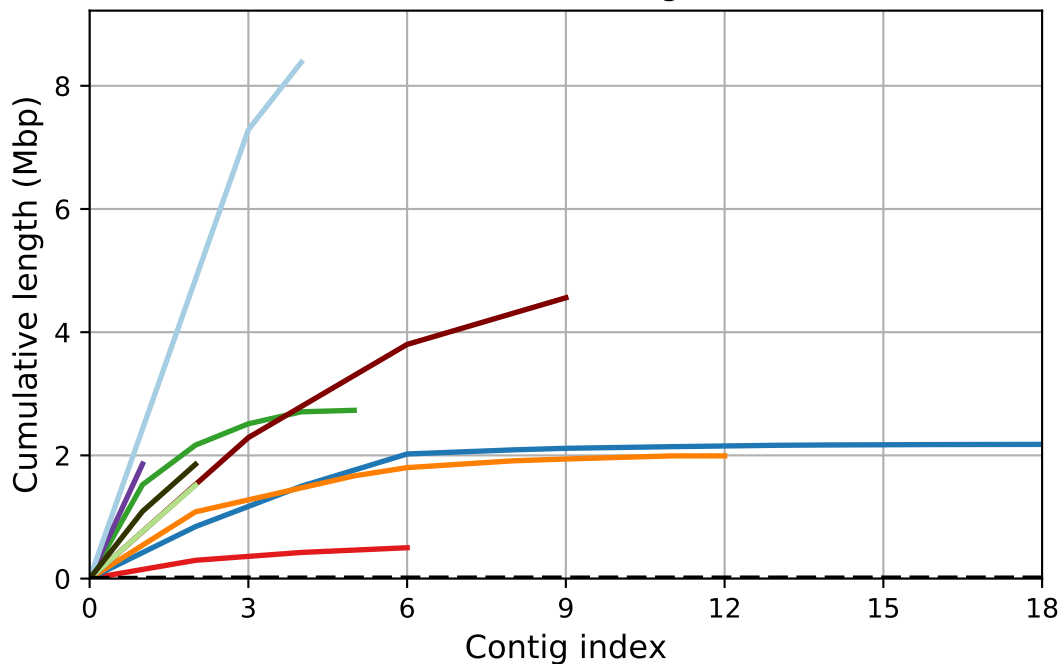
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



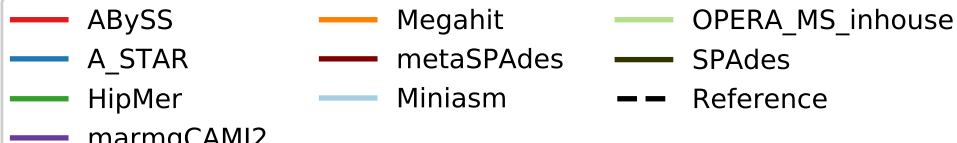
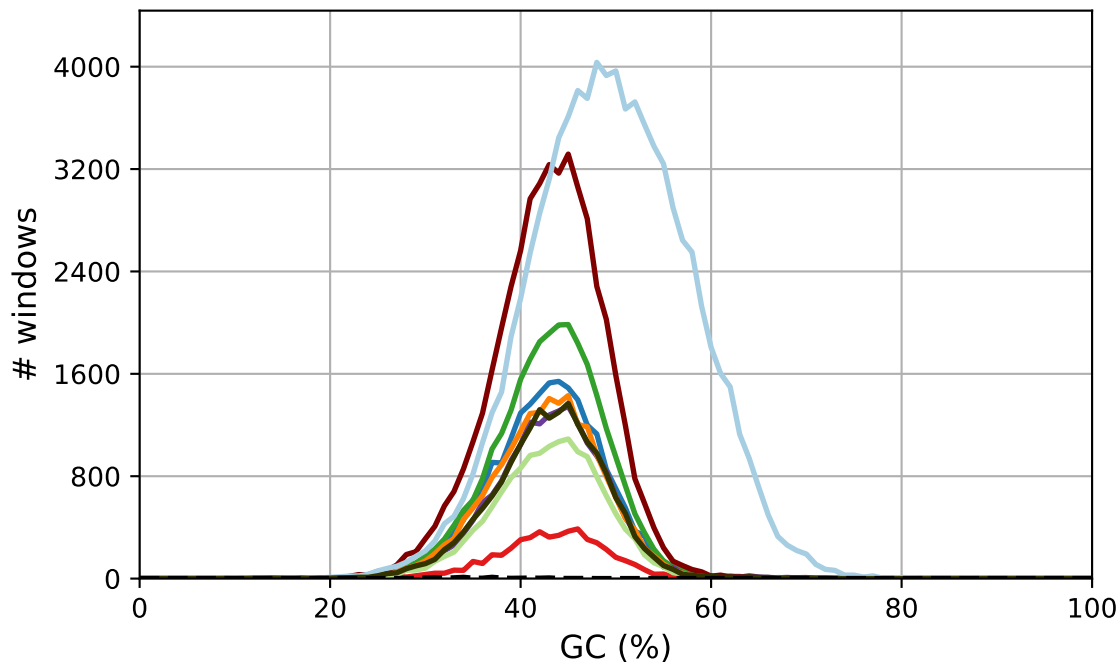
NGx



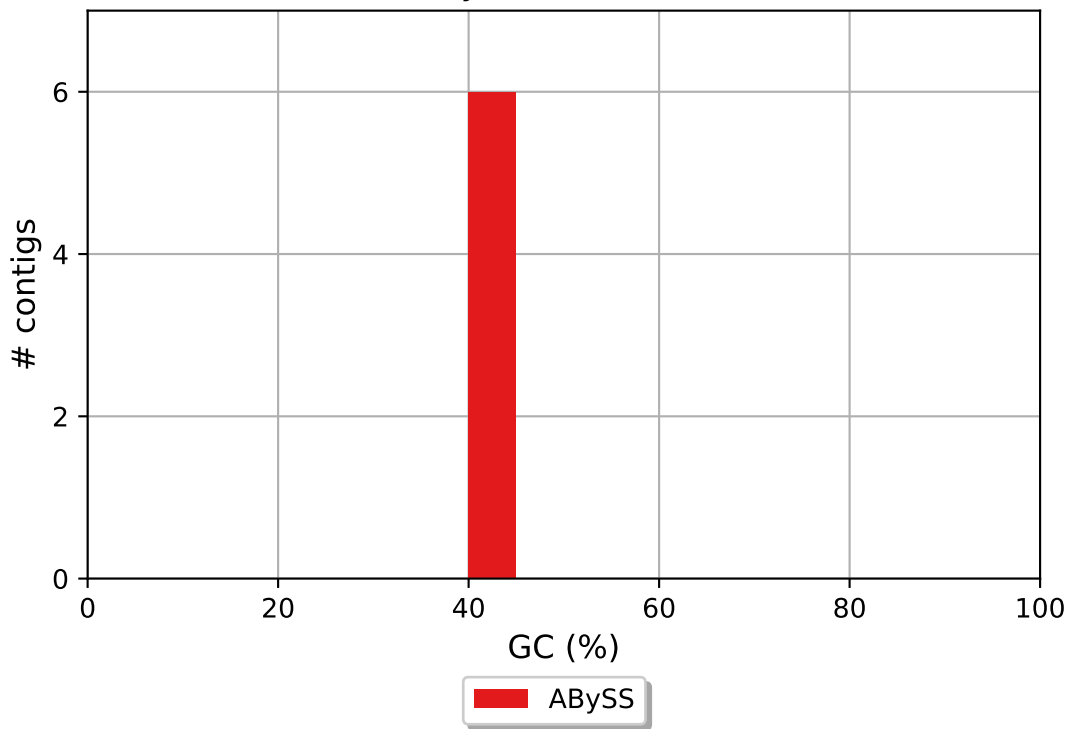
Cumulative length



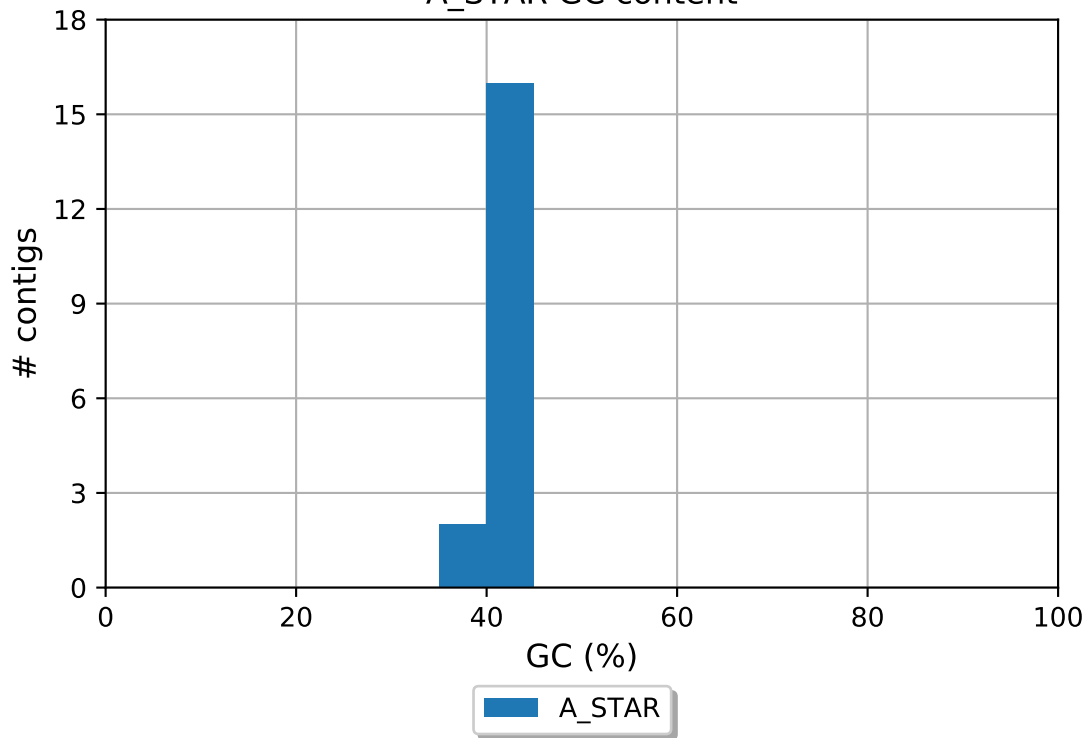
GC content



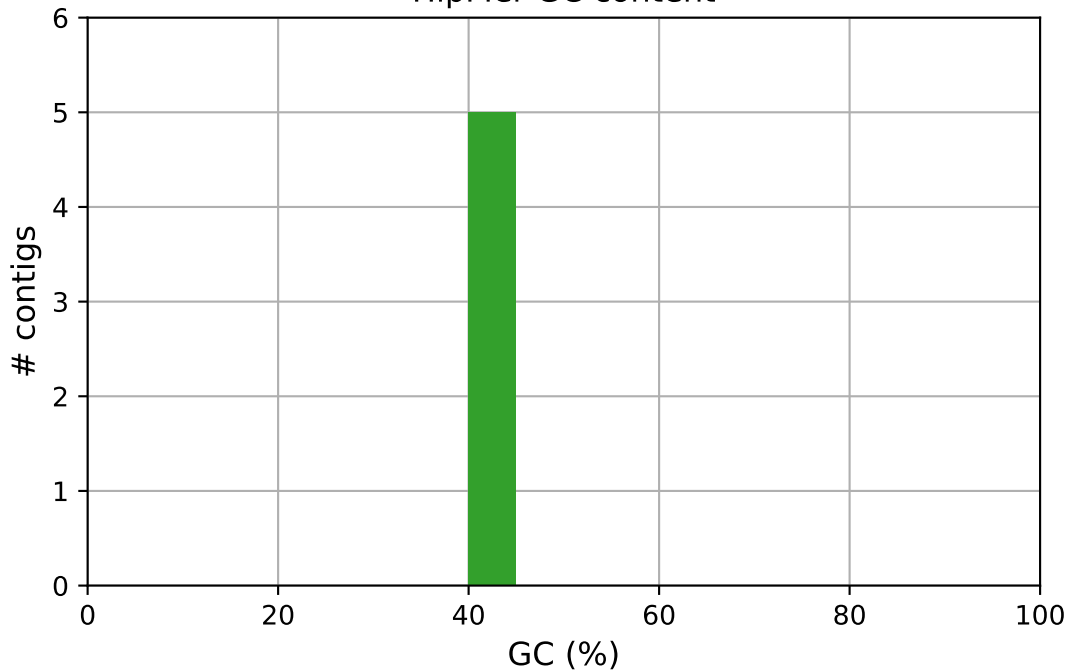
ABySS GC content



A_STAR GC content

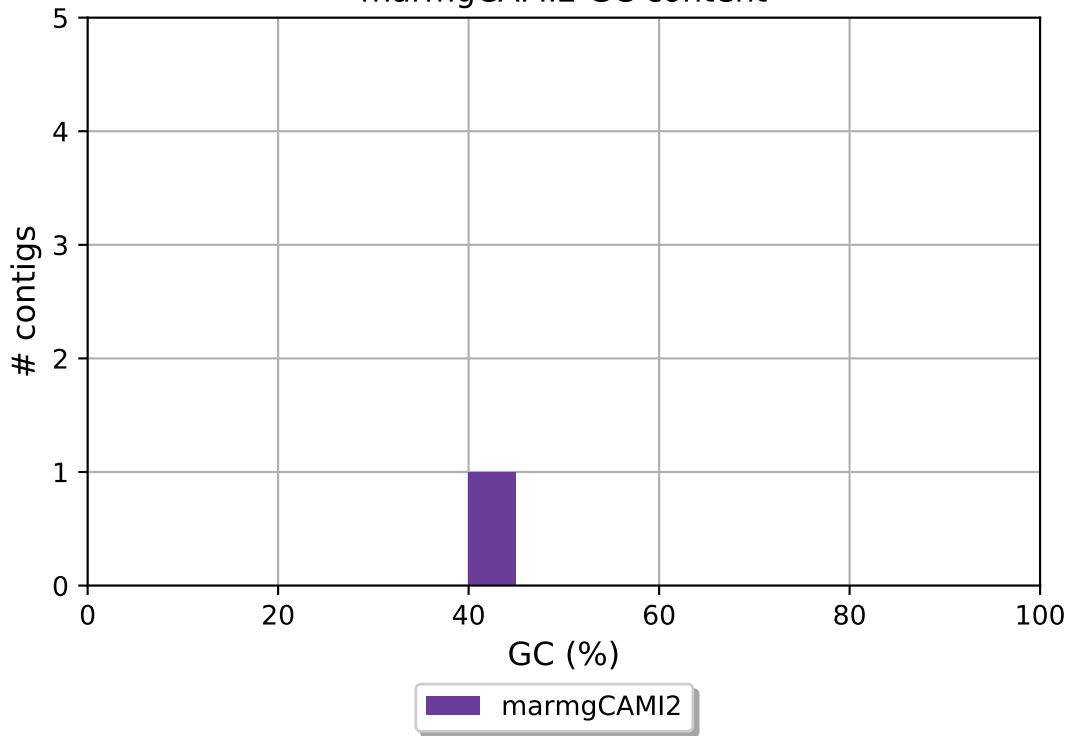


HipMer GC content

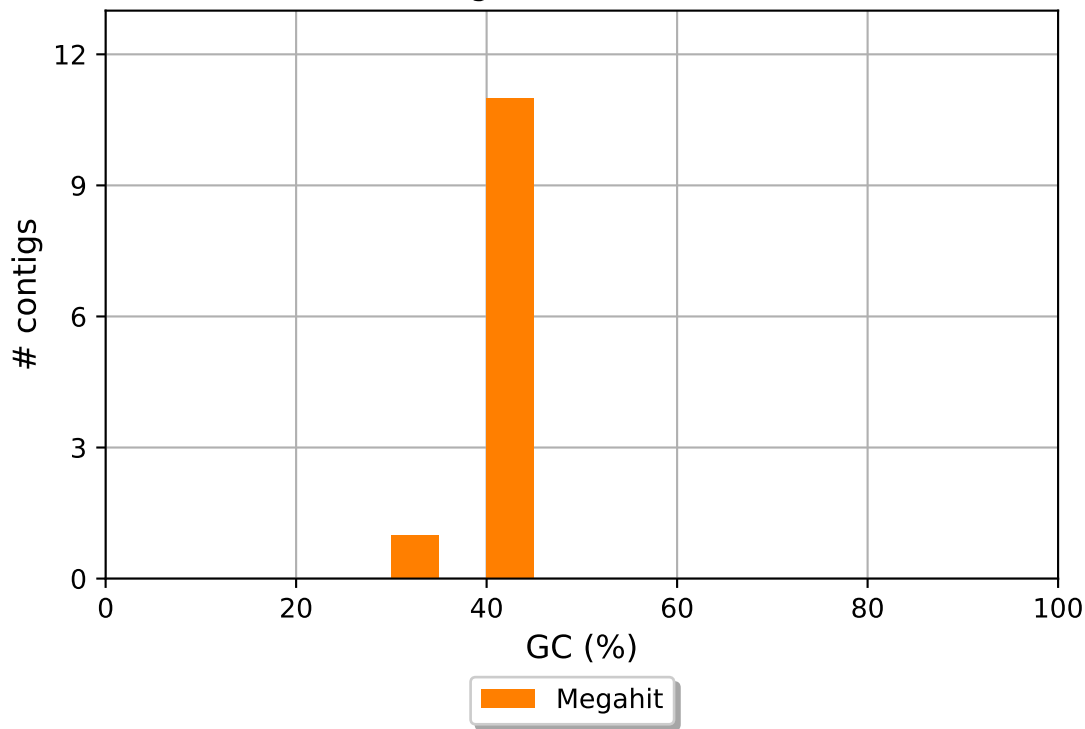


 HipMer

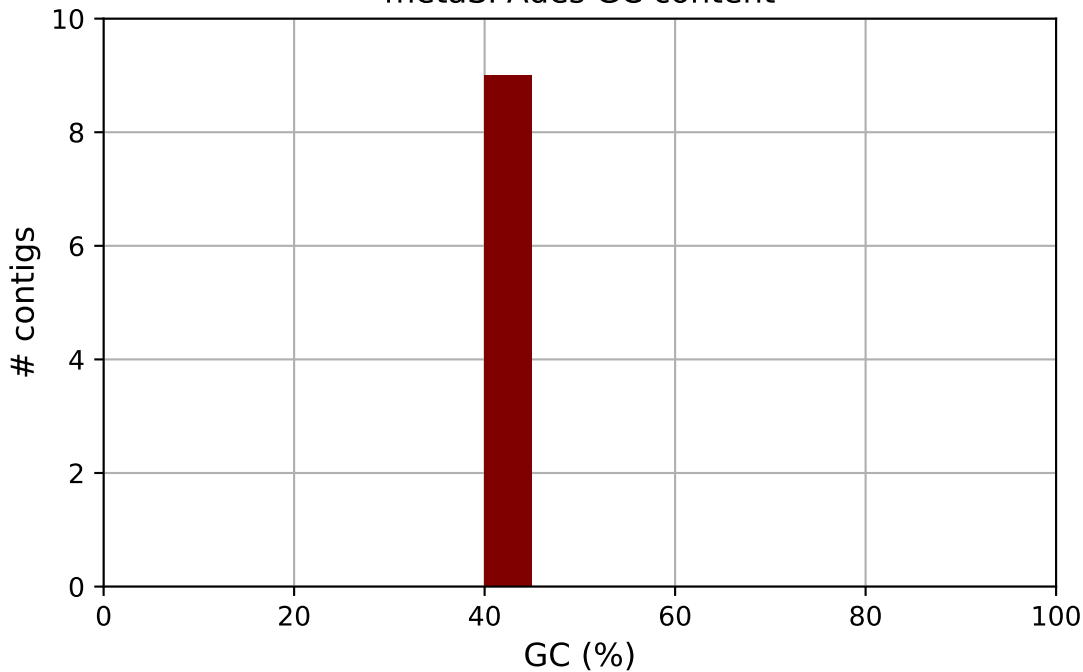
marmgCAMI2 GC content



Megahit GC content

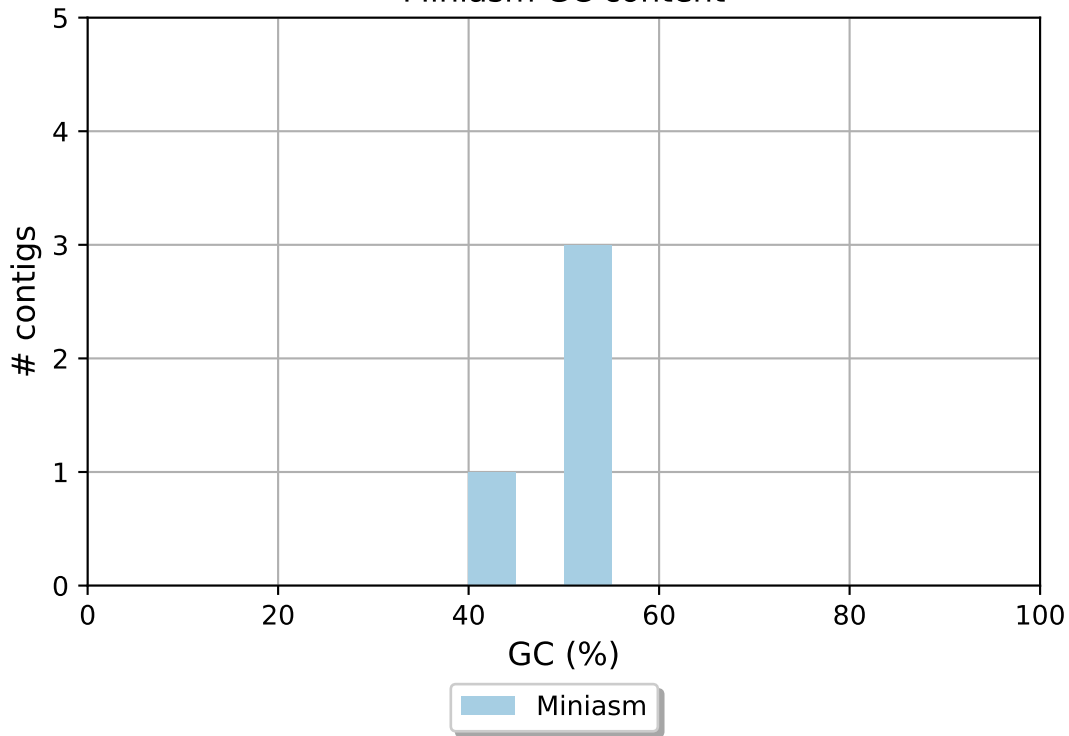


metaSPAdes GC content

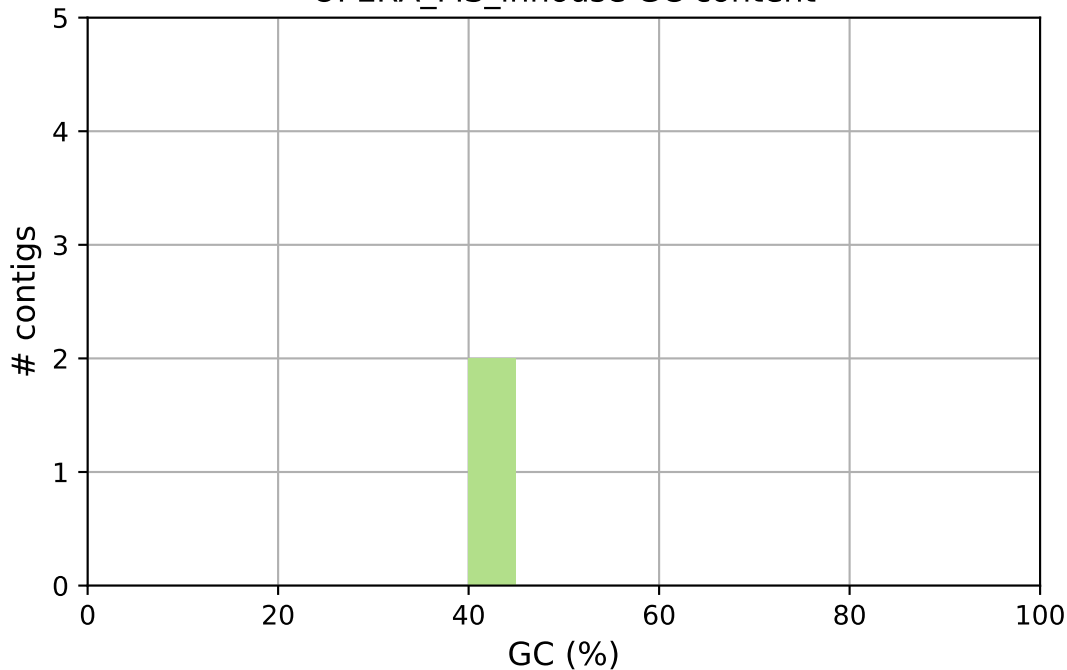


metaSPAdes

Miniasm GC content

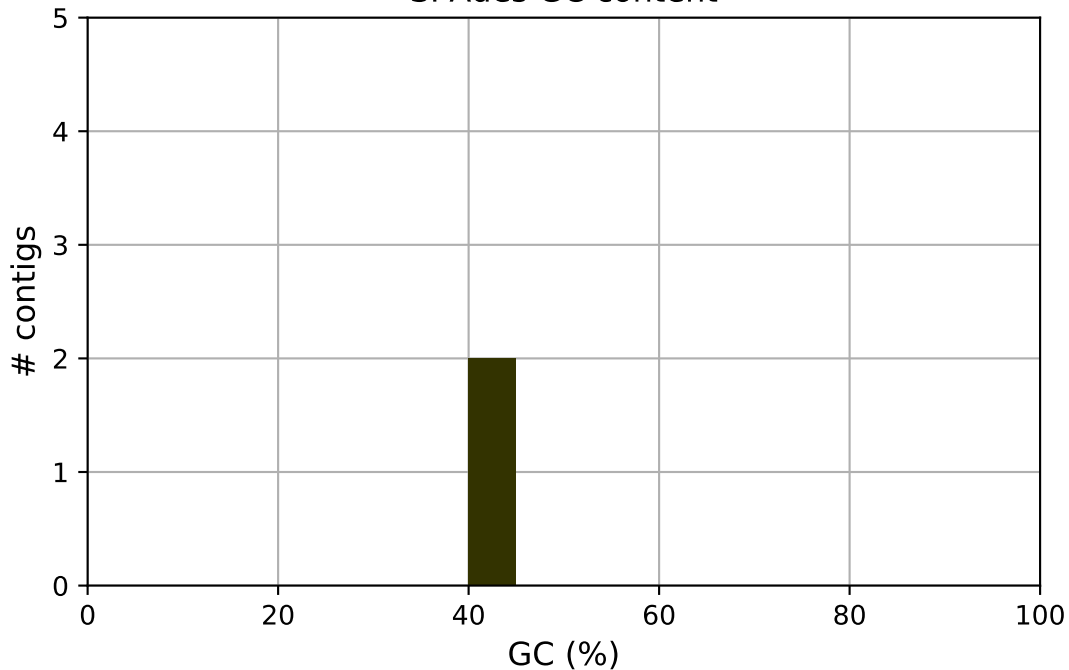


OPERA_MS_inhouse GC content



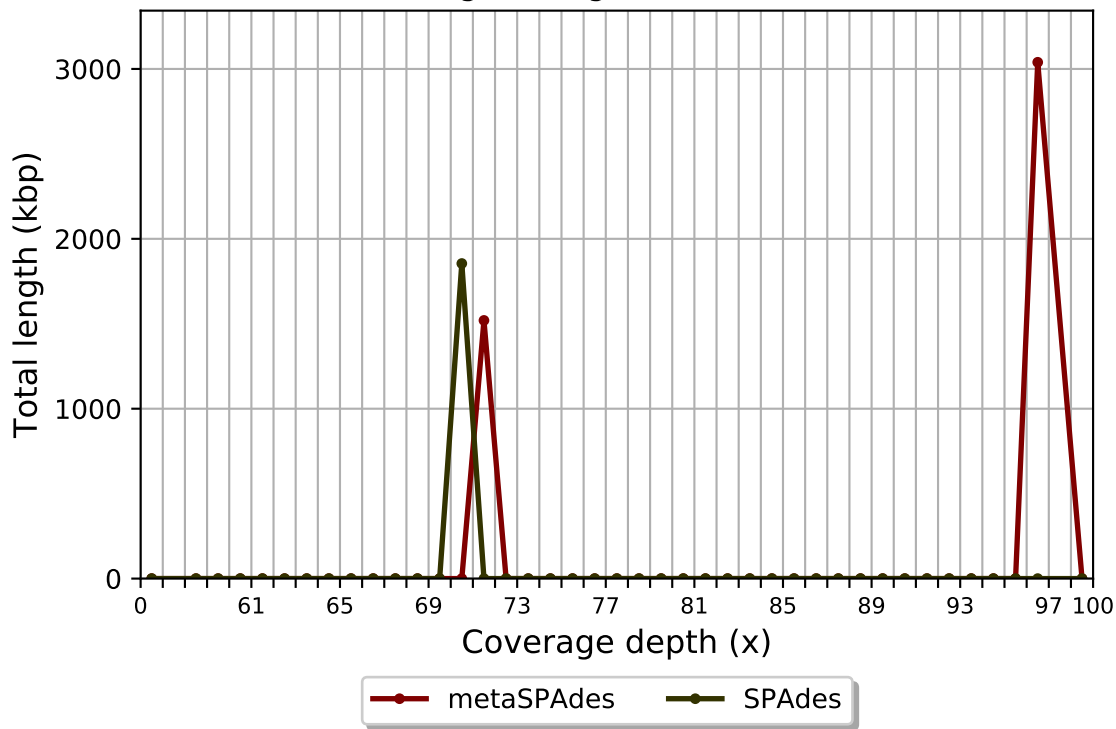
OPERA_MS_inhouse

SPAdes GC content

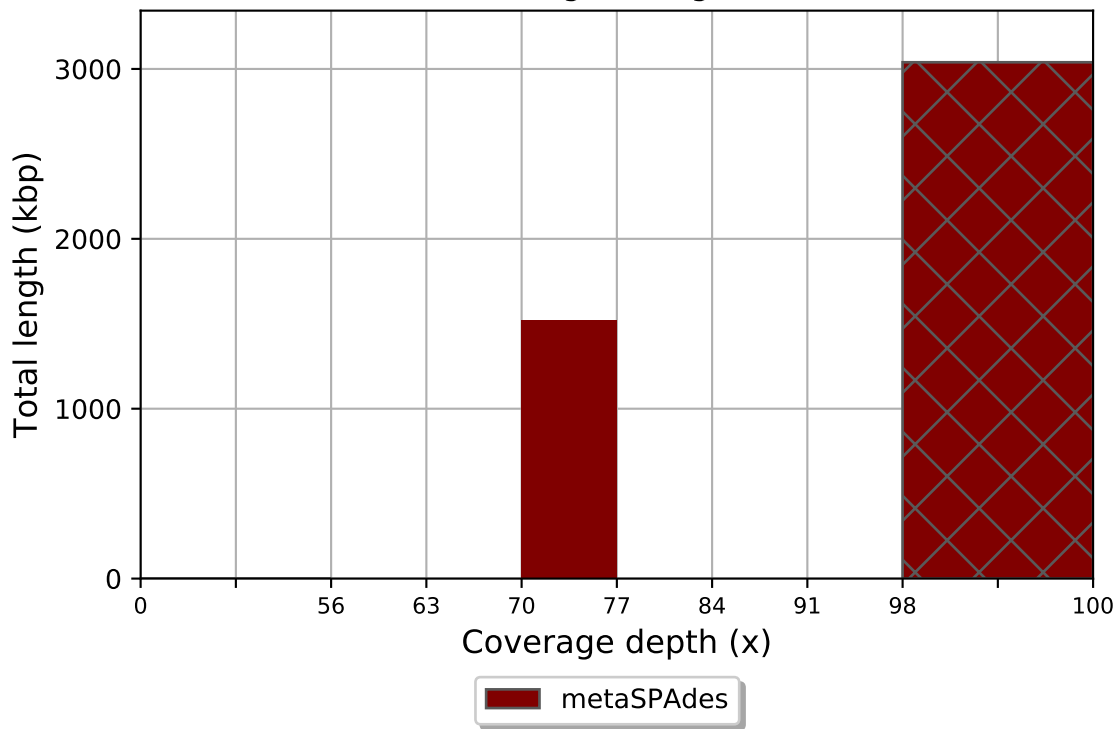


SPAdes

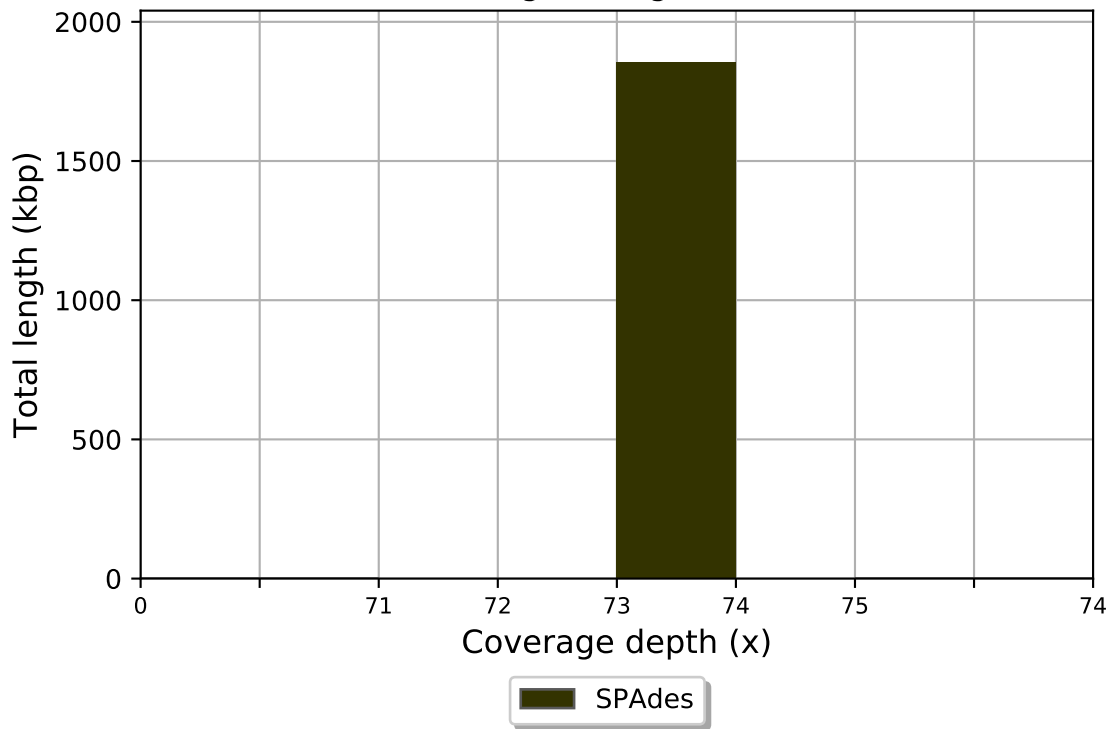
Coverage histogram (bin size: 1x)



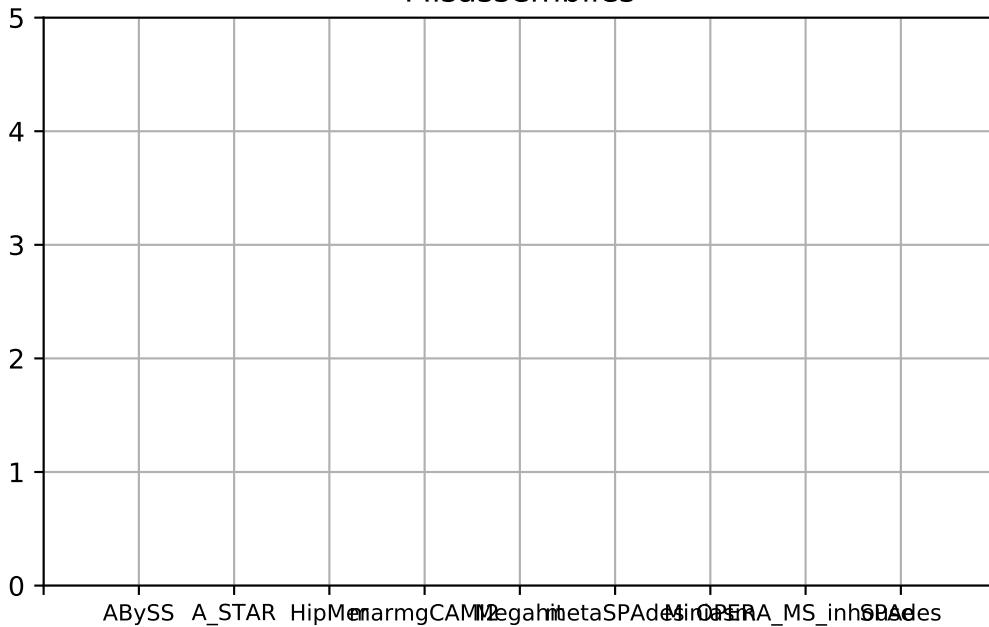
metaSPAdes coverage histogram (bin size: 7x)



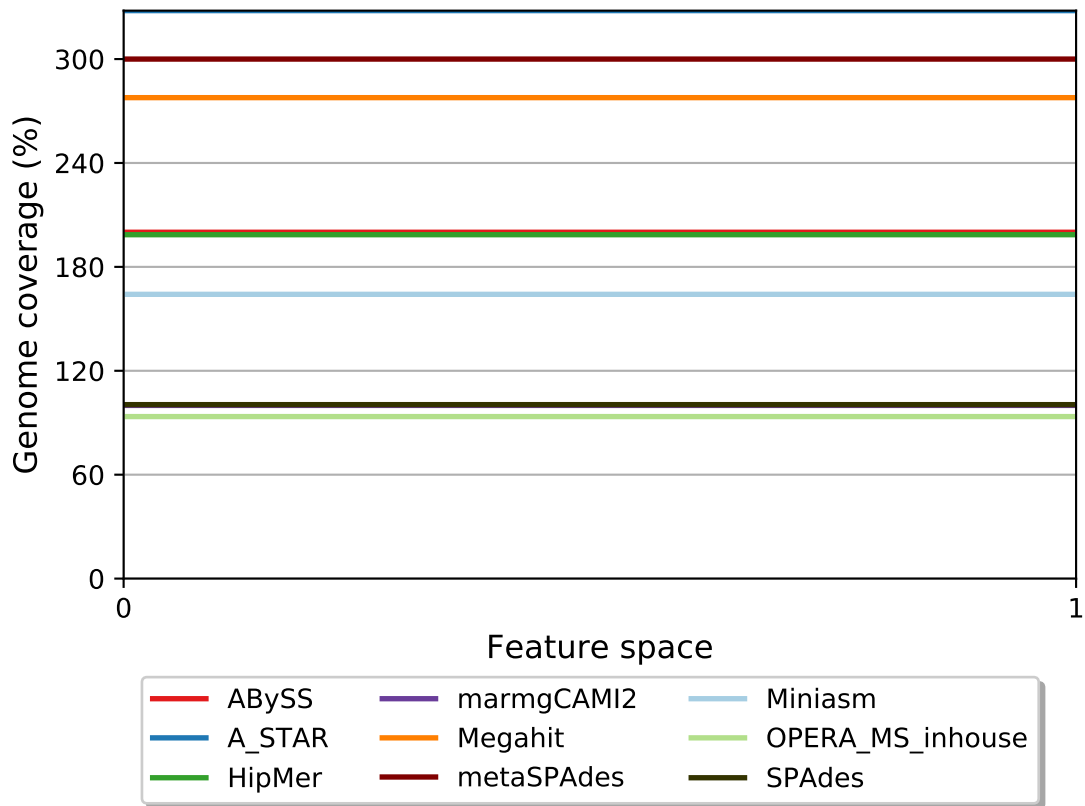
SPAdes coverage histogram (bin size: 1x)



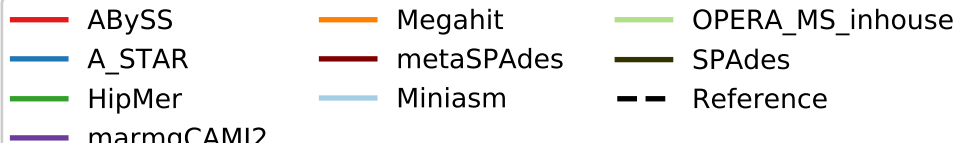
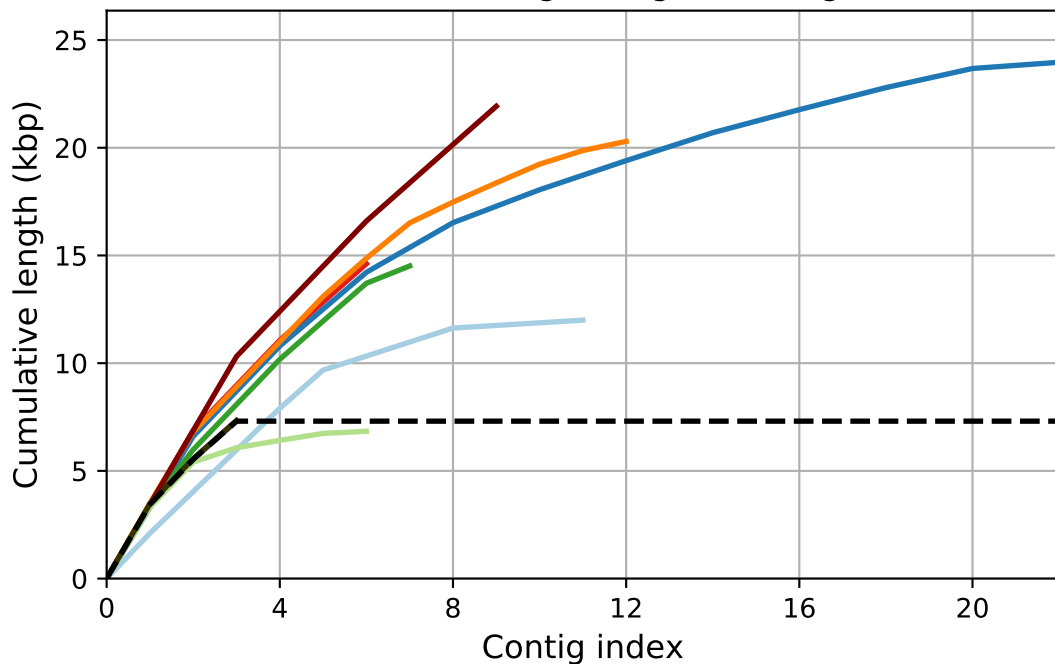
Misassemblies



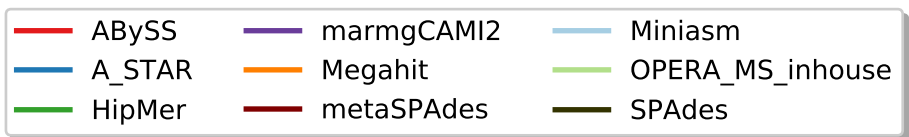
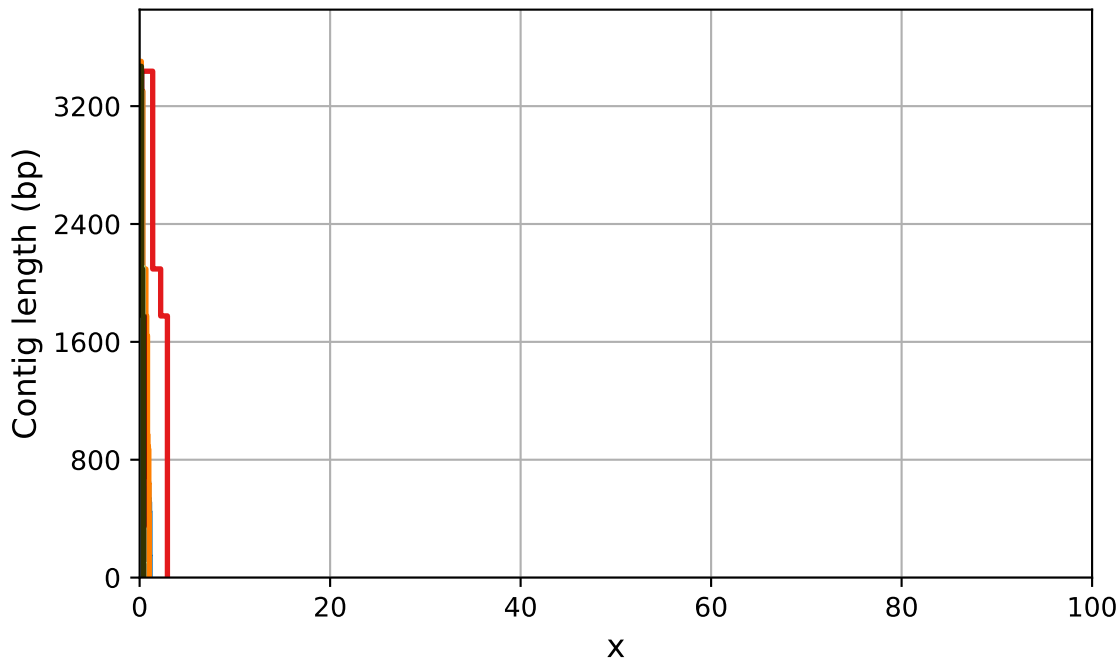
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



NGAx

