

Report

| | UpperBound | canu_assembly | canu_assembly_polished | flye_assembly | flye_assembly_polished | trinity_assembly |
|-----------------------------|------------|---------------|------------------------|---------------|------------------------|------------------|
| # contigs (>= 0 bp) | 2860 | 192 | 192 | 164 | 164 | 52054 |
| # contigs (>= 1000 bp) | 1353 | 192 | 192 | 103 | 103 | 28175 |
| # contigs (>= 5000 bp) | 569 | 185 | 185 | 59 | 59 | 339 |
| # contigs (>= 10000 bp) | 401 | 183 | 183 | 49 | 49 | 4 |
| # contigs (>= 25000 bp) | 293 | 162 | 162 | 37 | 37 | 0 |
| # contigs (>= 50000 bp) | 237 | 112 | 112 | 31 | 31 | 0 |
| Total length (>= 0 bp) | 116955384 | 122977739 | 123001103 | 119963782 | 119950311 | 68125446 |
| Total length (>= 1000 bp) | 116367221 | 122977739 | 123001103 | 119925361 | 119911914 | 55897272 |
| Total length (>= 5000 bp) | 114532013 | 122951239 | 122974598 | 119824915 | 119811844 | 1956651 |
| Total length (>= 10000 bp) | 113379028 | 122937652 | 122960987 | 119752542 | 119739466 | 44274 |
| Total length (>= 25000 bp) | 111728696 | 122573799 | 122598770 | 119566446 | 119553357 | 0 |
| Total length (>= 50000 bp) | 109768690 | 120695097 | 120723224 | 119355633 | 119342541 | 0 |
| # contigs | 780 | 190 | 190 | 70 | 70 | 3377 |
| Largest contig | 5908332 | 11567090 | 11570839 | 15013467 | 15013354 | 12038 |
| Total length | 115355266 | 122973098 | 122996456 | 119869541 | 119856063 | 13022569 |
| Reference length | 119667750 | 119667750 | 119667750 | 119667750 | 119667750 | 119667750 |
| GC (%) | 36.03 | 36.27 | 36.26 | 36.05 | 36.05 | 42.44 |
| Reference GC (%) | 36.06 | 36.06 | 36.06 | 36.06 | 36.06 | 36.06 |
| N50 | 1267987 | 3435125 | 3436535 | 14082887 | 14082808 | 3742 |
| NG50 | 1192679 | 3435988 | 3437141 | 14082887 | 14082808 | - |
| N90 | 111615 | 426854 | 427111 | 3443320 | 3443144 | 3117 |
| NG90 | 81614 | 566322 | 566539 | 3443320 | 3443144 | - |
| auN | 1925616.6 | 4810862.4 | 4813051.9 | 12051185.8 | 12051151.6 | 4042.8 |
| auNG | 1856222.8 | 4943743.4 | 4946932.9 | 12071507.2 | 12070115.7 | 439.9 |
| L50 | 22 | 10 | 10 | 5 | 5 | 1418 |
| LG50 | 23 | 9 | 9 | 5 | 5 | - |
| L90 | 164 | 45 | 45 | 9 | 9 | 2952 |
| LG90 | 205 | 39 | 39 | 9 | 9 | - |
| # misassemblies | 0 | 757 | 754 | 563 | 567 | 101 |
| # misassembled contigs | 0 | 119 | 122 | 28 | 28 | 101 |
| Misassembled contigs length | 0 | 110796582 | 111026108 | 116362090 | 116354205 | 432513 |
| # local misassemblies | 0 | 3552 | 3585 | 3413 | 3372 | 1032 |
| # scaffold gap ext. mis. | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 | 4 | 4 | 0 |
| # possible TEs | 0 | 66 | 66 | 34 | 34 | 0 |
| # unaligned mis. contigs | 0 | 38 | 33 | 11 | 10 | 646 |
| # unaligned contigs | 0 + 0 part | 6 + 154 part | 7 + 152 part | 4 + 43 part | 4 + 42 part | 338 + 2564 part |
| Unaligned length | 0 | 13537717 | 13496215 | 13427090 | 13385889 | 6542141 |
| Genome fraction (%) | 96.192 | 88.649 | 88.680 | 88.536 | 88.561 | 2.507 |
| Duplication ratio | 1.004 | 1.032 | 1.032 | 1.006 | 1.006 | 2.113 |
| # N's per 100 kbp | 2.30 | 0.00 | 0.00 | 1.00 | 0.71 | 0.00 |
| # mismatches per 100 kbp | 0.04 | 808.35 | 810.05 | 777.67 | 779.47 | 526.32 |
| # indels per 100 kbp | 0.00 | 176.23 | 137.92 | 148.94 | 130.95 | 41.63 |
| # genomic features | 0 + 0 part | 0 + 0 part | 0 + 0 part | 0 + 0 part | 0 + 0 part | 0 + 0 part |
| Largest alignment | 5908332 | 4489636 | 4683090 | 5385170 | 6764147 | 12035 |
| Total aligned length | 115354915 | 109333158 | 109380563 | 106439499 | 106466102 | 6331294 |
| NA50 | 1267987 | 525319 | 525522 | 633886 | 633901 | - |
| NGA50 | 1192679 | 589651 | 589824 | 633886 | 633901 | - |
| NA90 | 111615 | - | - | - | - | - |
| NGA90 | 81614 | 7219 | 7392 | - | - | - |
| auNA | 1925616.5 | 1011382.9 | 1100022.6 | 1418374.9 | 1580511.8 | 1205.0 |
| auNGA | 1856222.8 | 1039318.4 | 1130621.1 | 1420766.6 | 1582998.9 | 131.1 |
| LA50 | 22 | 46 | 45 | 36 | 35 | - |
| LGA50 | 23 | 43 | 42 | 36 | 35 | - |
| LA90 | 164 | - | - | - | - | - |
| LGA90 | 205 | 695 | 678 | - | - | - |

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

| | UpperBound | canu_assembly | canu_assembly_polished | flye_assembly | flye_assembly_polished | trinity_assembly |
|-----------------------------|------------|---------------|------------------------|---------------|------------------------|------------------|
| # misassemblies | 0 | 757 | 754 | 563 | 567 | 101 |
| # contig misassemblies | 0 | 757 | 754 | 559 | 564 | 101 |
| # c. relocations | 0 | 571 | 568 | 458 | 464 | 37 |
| # c. translocations | 0 | 174 | 173 | 92 | 91 | 58 |
| # c. inversions | 0 | 12 | 13 | 9 | 9 | 6 |
| # scaffold misassemblies | 0 | 0 | 0 | 4 | 3 | 0 |
| # s. relocations | 0 | 0 | 0 | 4 | 3 | 0 |
| # s. translocations | 0 | 0 | 0 | 0 | 0 | 0 |
| # s. inversions | 0 | 0 | 0 | 0 | 0 | 0 |
| # misassembled contigs | 0 | 119 | 122 | 28 | 28 | 101 |
| Misassembled contigs length | 0 | 110796582 | 111026108 | 116362090 | 116354205 | 432513 |
| # local misassemblies | 0 | 3552 | 3585 | 3413 | 3372 | 1032 |
| # scaffold gap ext. mis. | 0 | 0 | 0 | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 | 4 | 4 | 0 |
| # possible TEs | 0 | 66 | 66 | 34 | 34 | 0 |
| # unaligned mis. contigs | 0 | 38 | 33 | 11 | 10 | 646 |
| # mismatches | 48 | 883797 | 886034 | 827753 | 829872 | 33323 |
| # indels | 2 | 192674 | 150856 | 158529 | 139415 | 2636 |
| # indels (<= 5 bp) | 1 | 160425 | 118571 | 126909 | 107775 | 1472 |
| # indels (> 5 bp) | 1 | 32249 | 32285 | 31620 | 31640 | 1164 |
| Indels length | 490 | 1885177 | 1878720 | 1809918 | 1832836 | 96488 |

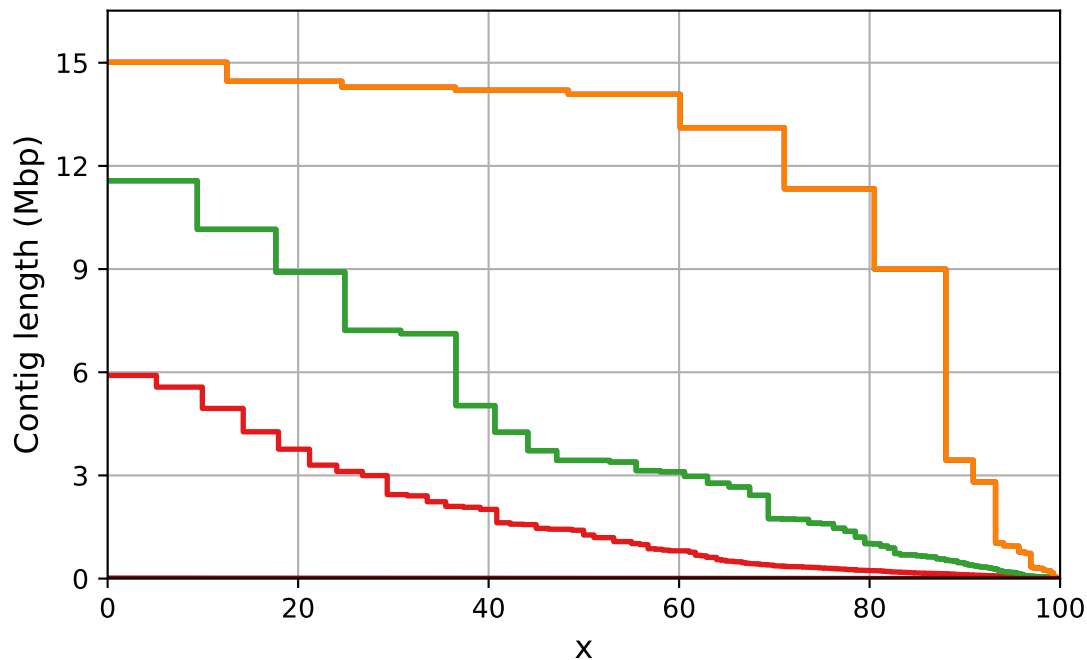
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | UpperBound | canu_assembly | canu_assembly_polished | flye_assembly | flye_assembly_polished | trinity_assembly |
|-------------------------------|------------|---------------|------------------------|---------------|------------------------|------------------|
| # fully unaligned contigs | 0 | 6 | 7 | 4 | 4 | 338 |
| Fully unaligned length | 0 | 65902 | 80409 | 20876 | 20476 | 1212466 |
| # partially unaligned contigs | 0 | 154 | 152 | 43 | 42 | 2564 |
| Partially unaligned length | 0 | 13471815 | 13415806 | 13406214 | 13365413 | 5329675 |
| # N's | 2658 | 0 | 0 | 1200 | 855 | 0 |

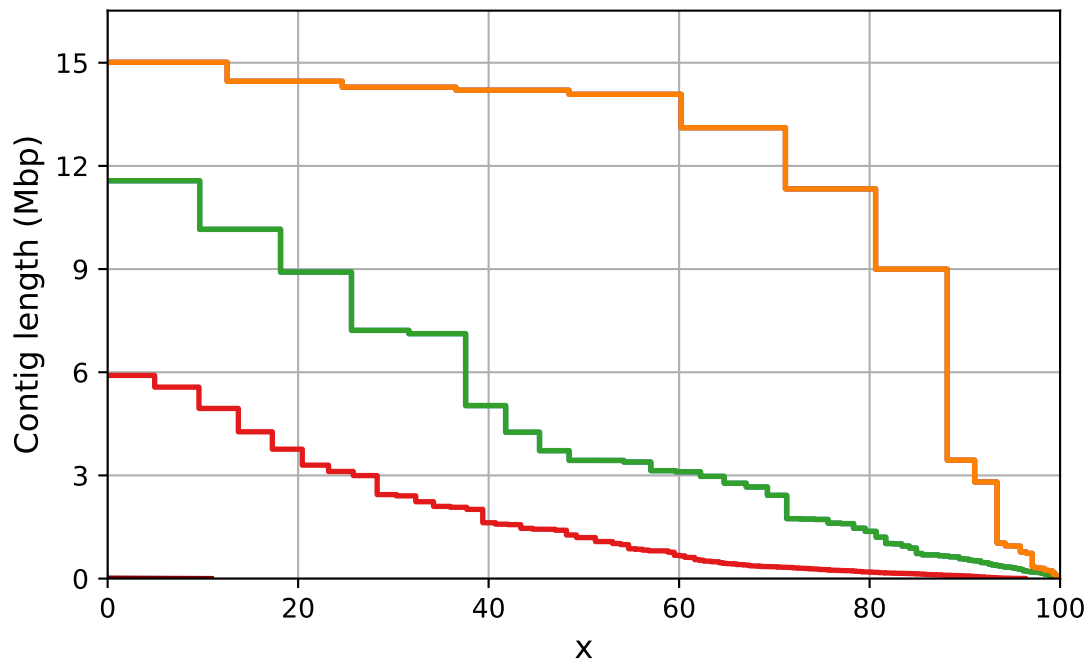
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



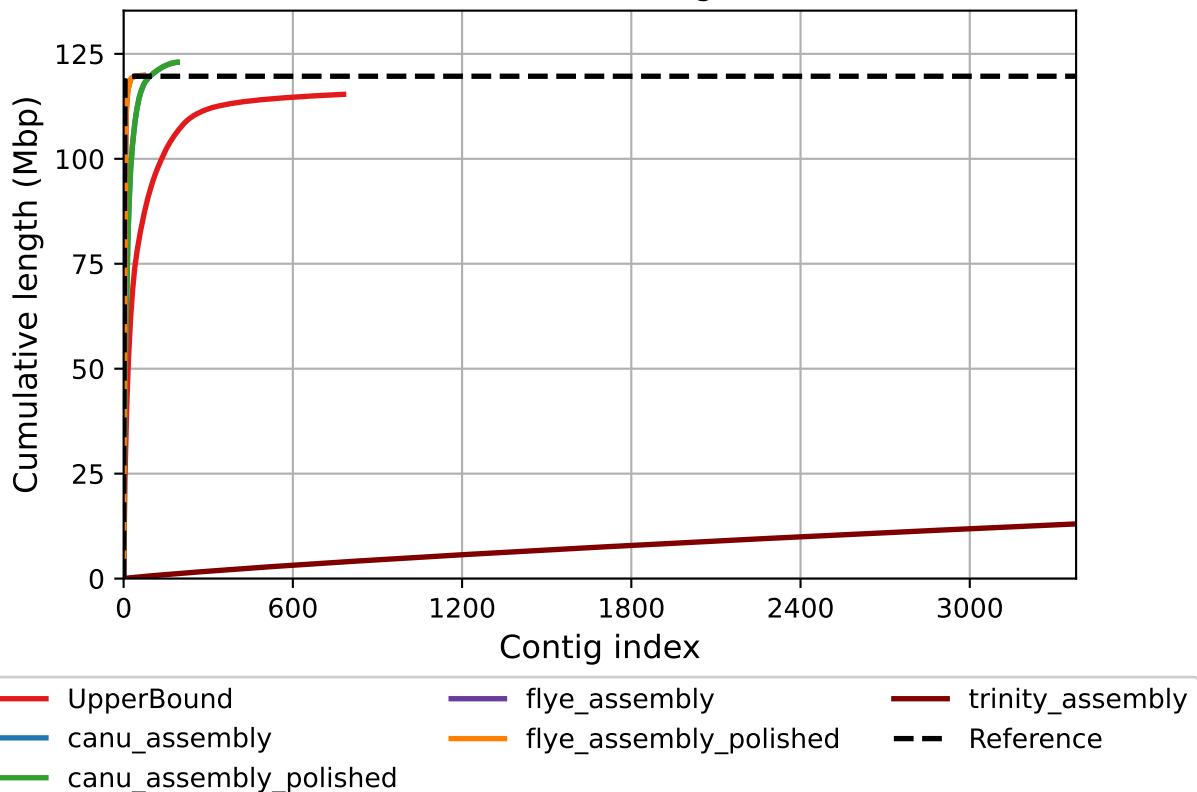
UpperBound canu_assembly_polished flye_assembly_polished
canu_assembly flye_assembly trinity_assembly

NGx

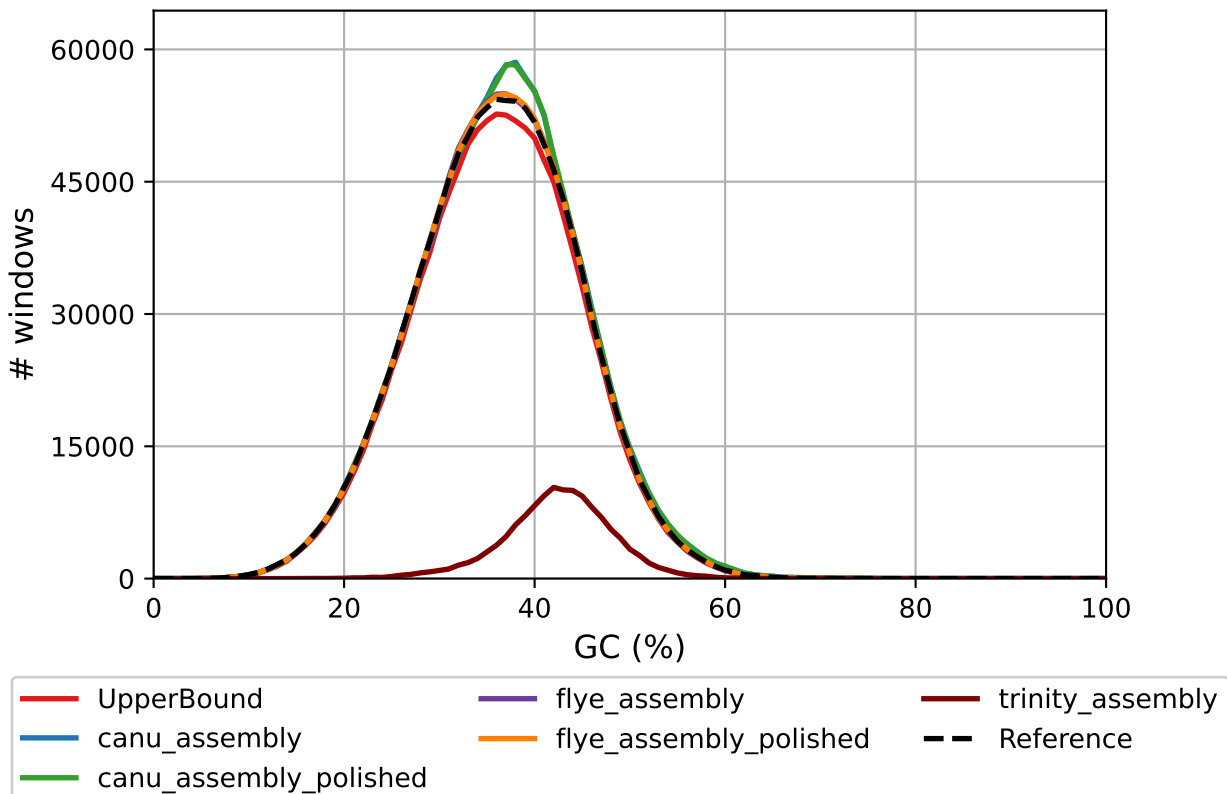


- UpperBound
- canu_assembly_polished
- flye_assembly_polished
- canu_assembly
- flye_assembly
- trinity_assembly

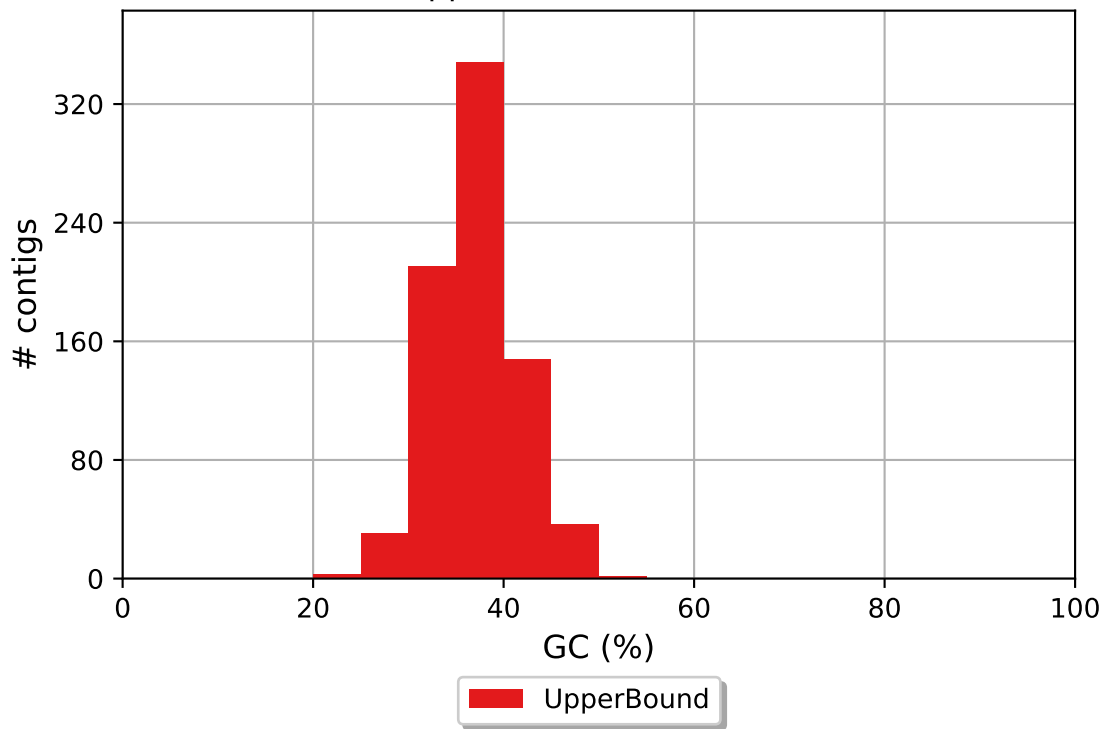
Cumulative length



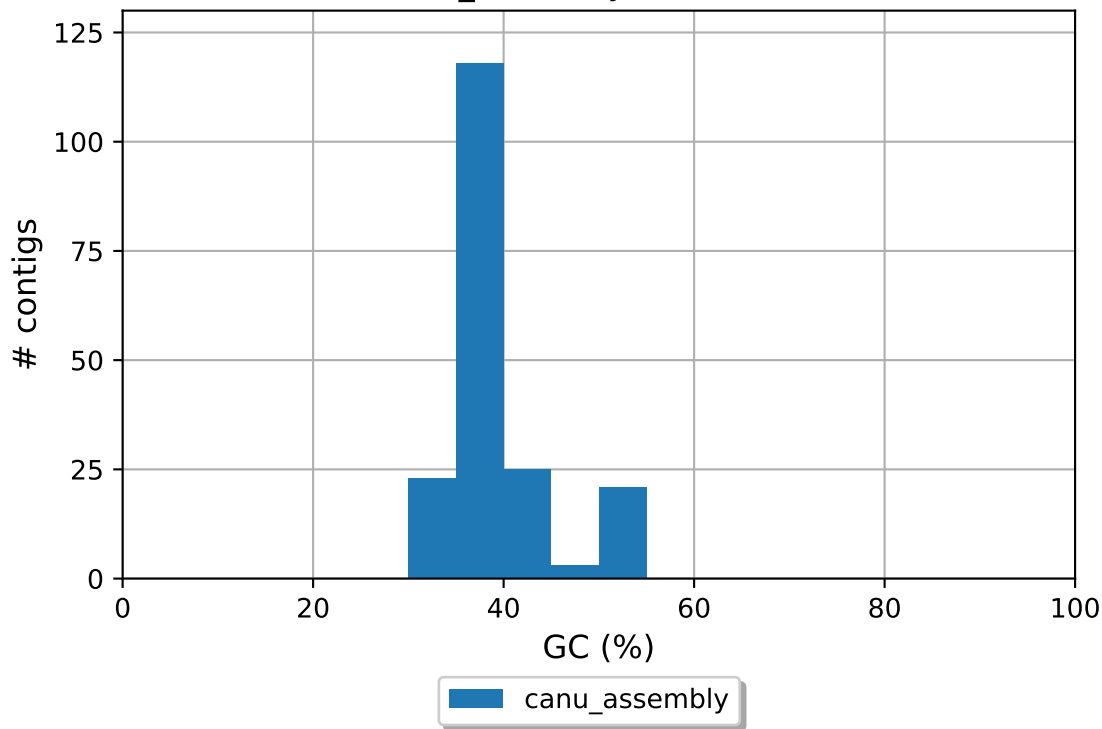
GC content



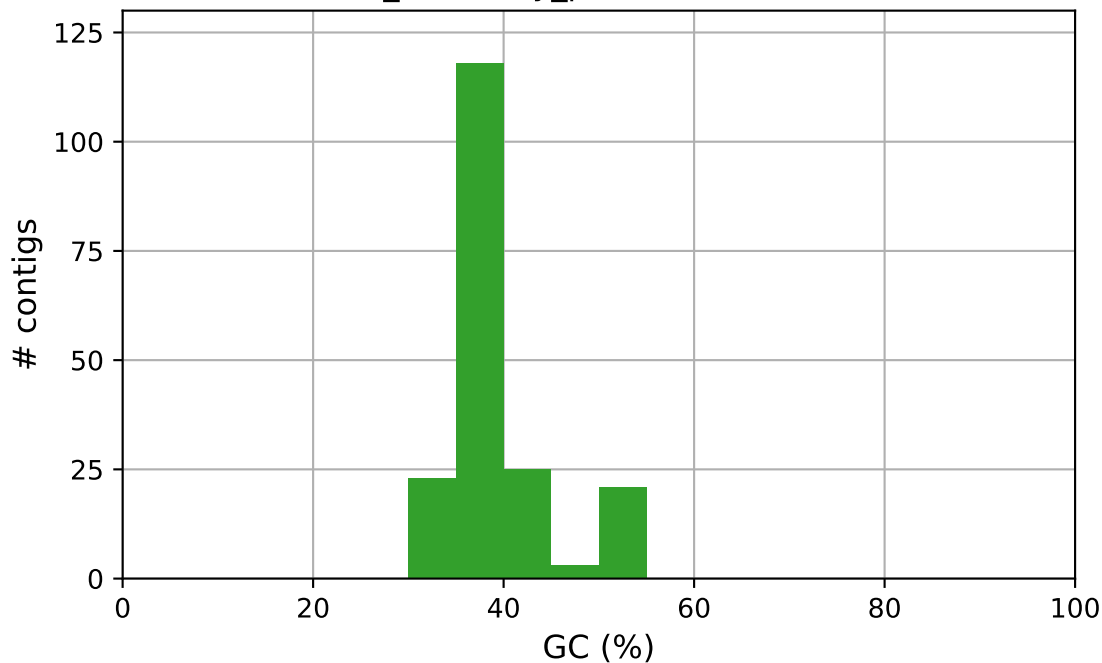
UpperBound GC content



canu_assembly GC content

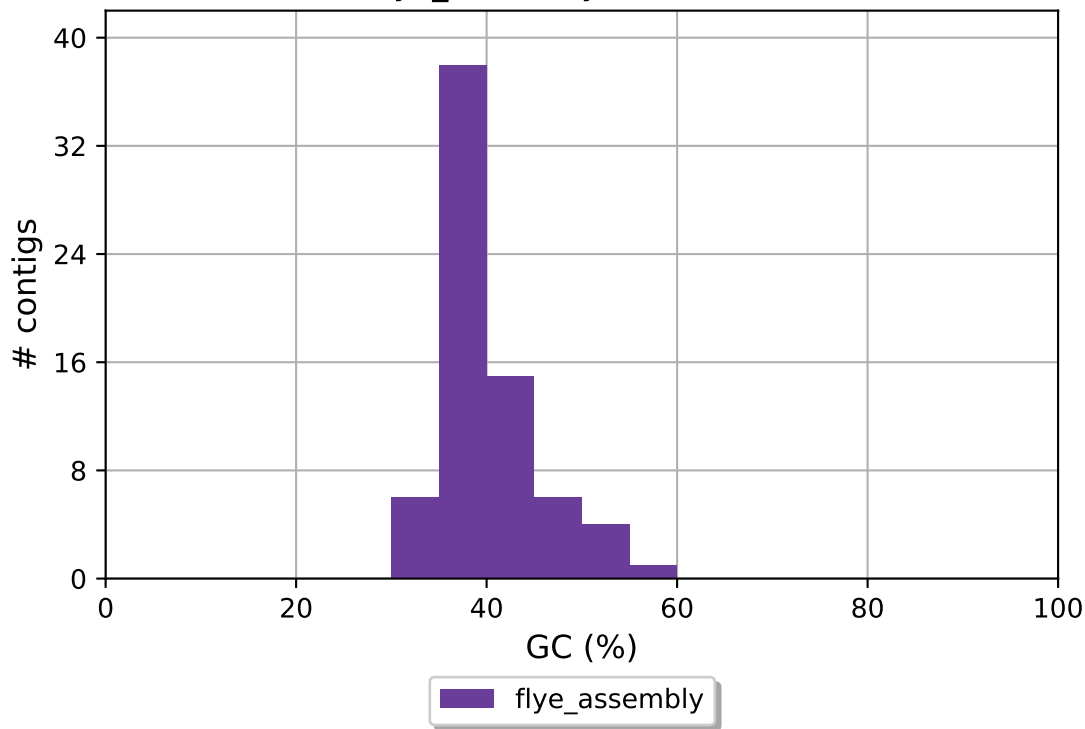


canu_assembly_polished GC content

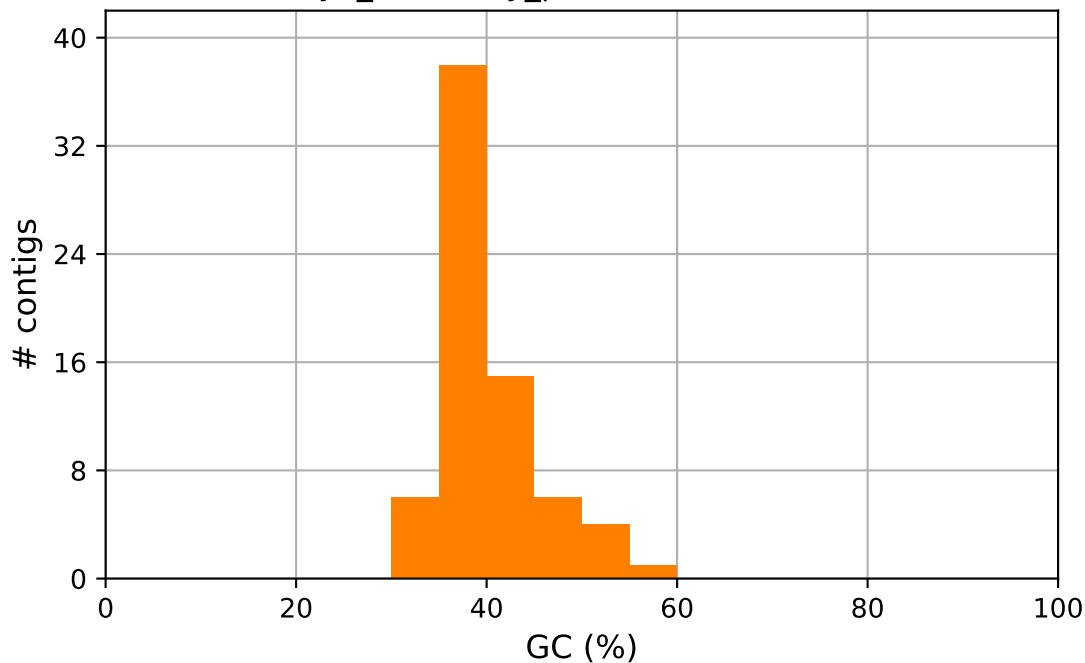


canu_assembly_polished

flye_assembly GC content

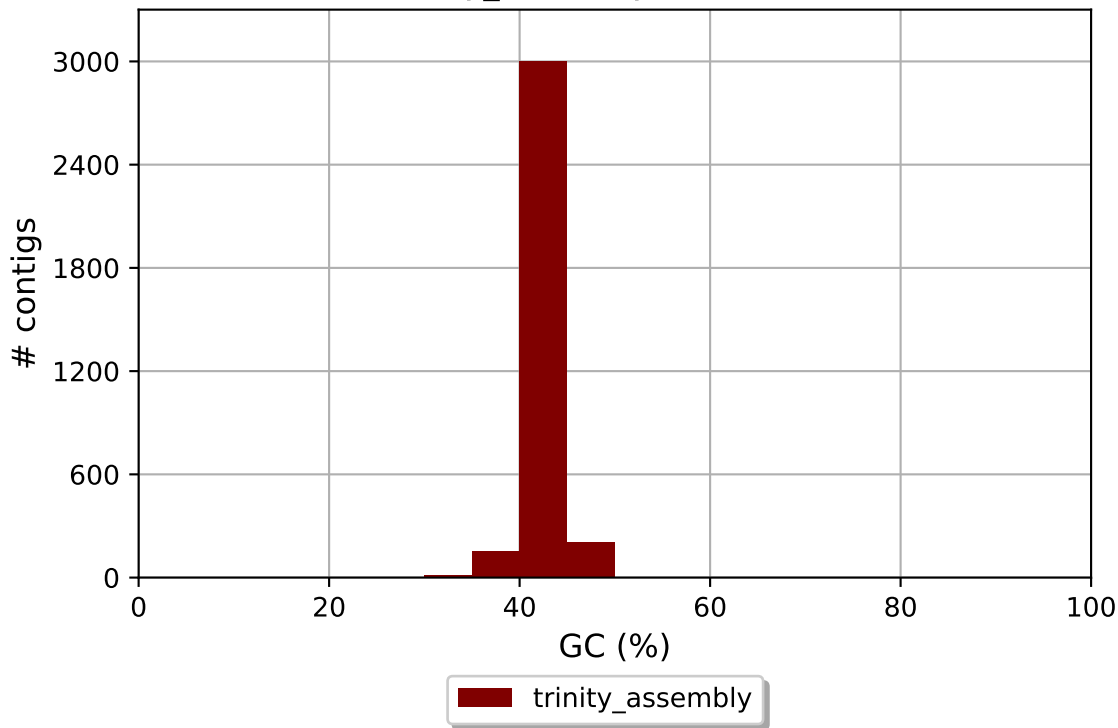


flye_assembly_polished GC content

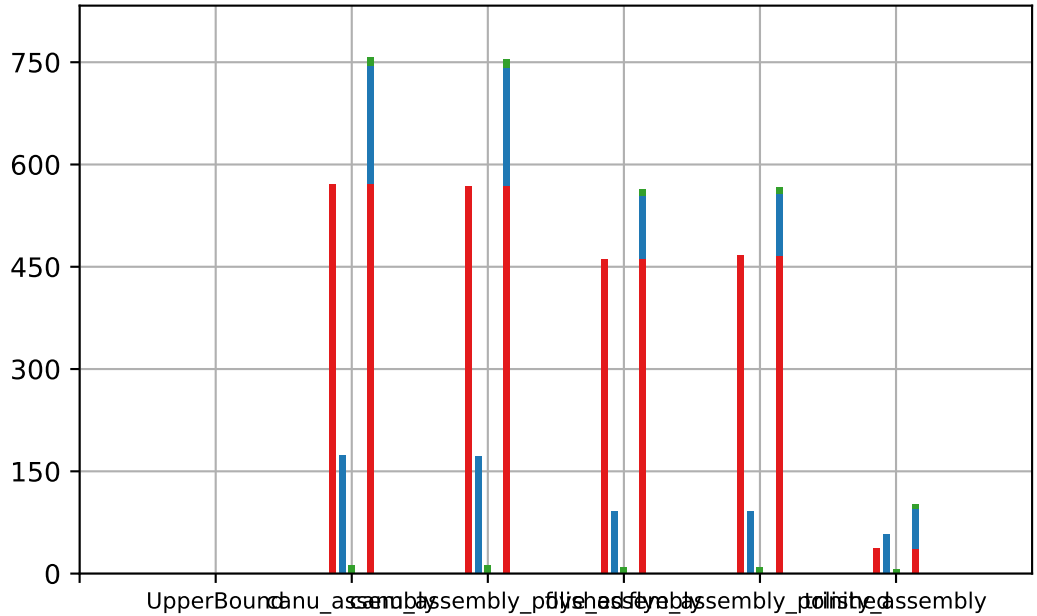


flye_assembly_polished

trinity_assembly GC content

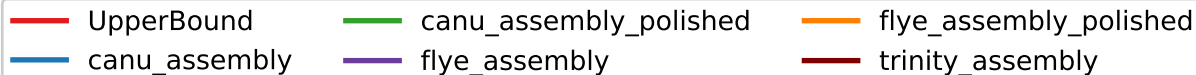
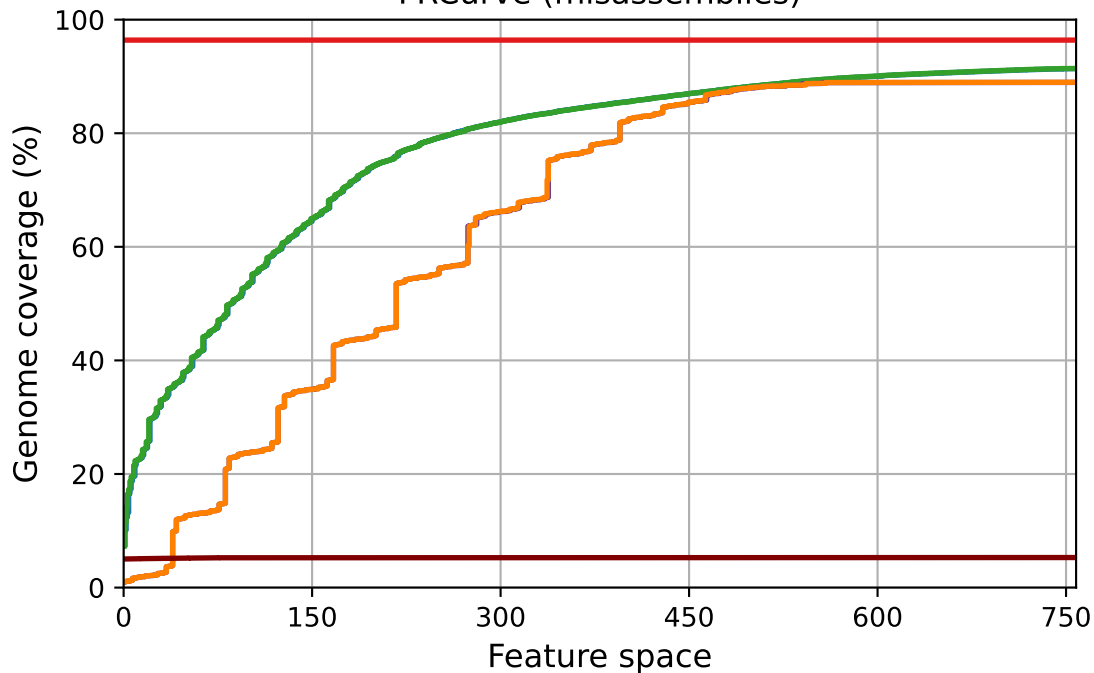


Misassemblies

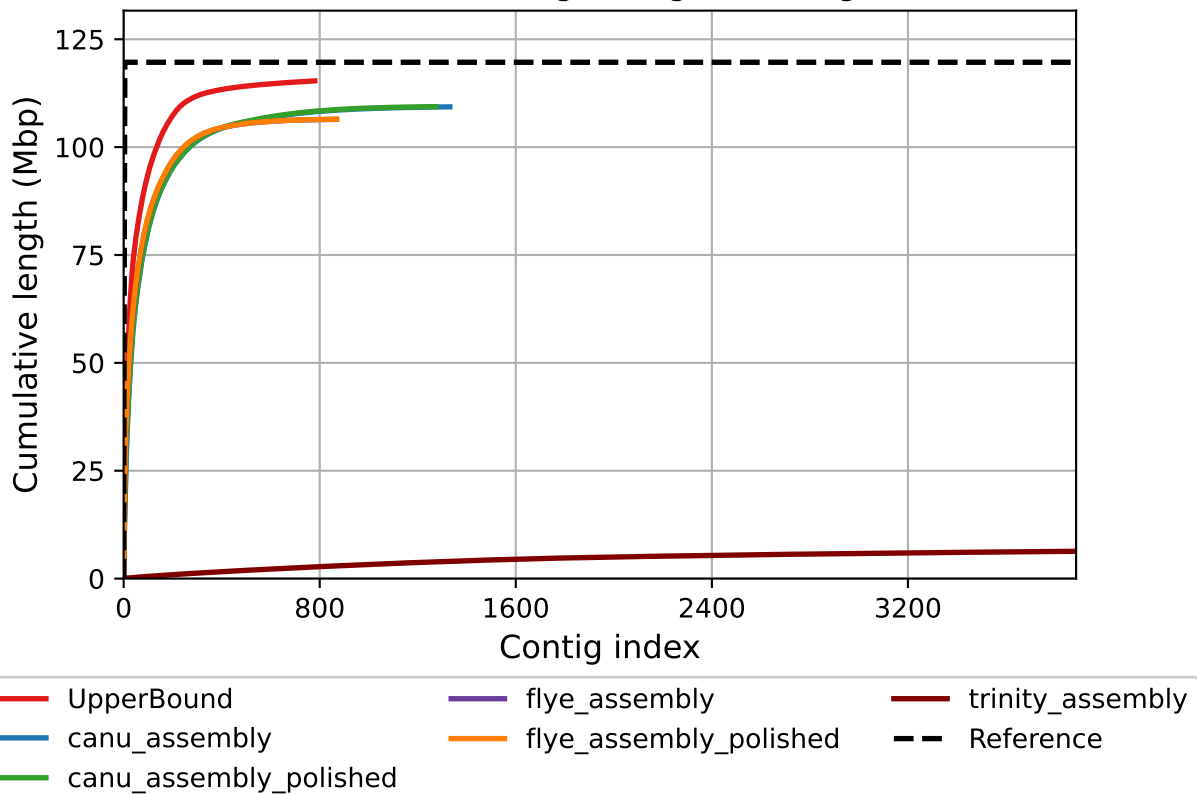


■ # relocations ■ # translocations ■ # inversions

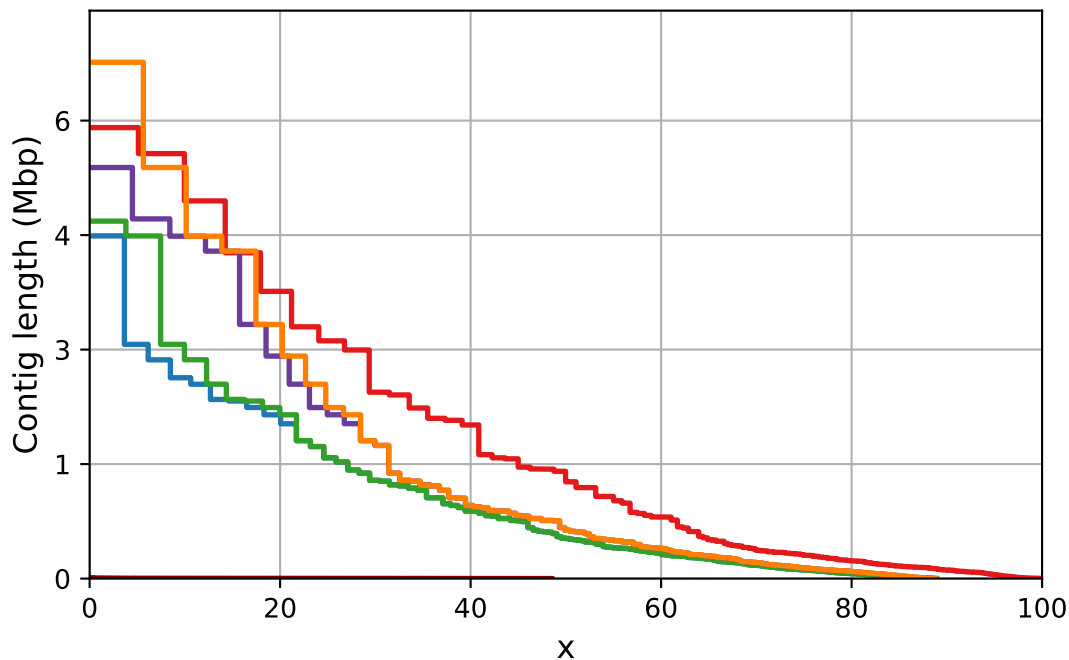
FRCurve (misassemblies)



Cumulative length (aligned contigs)

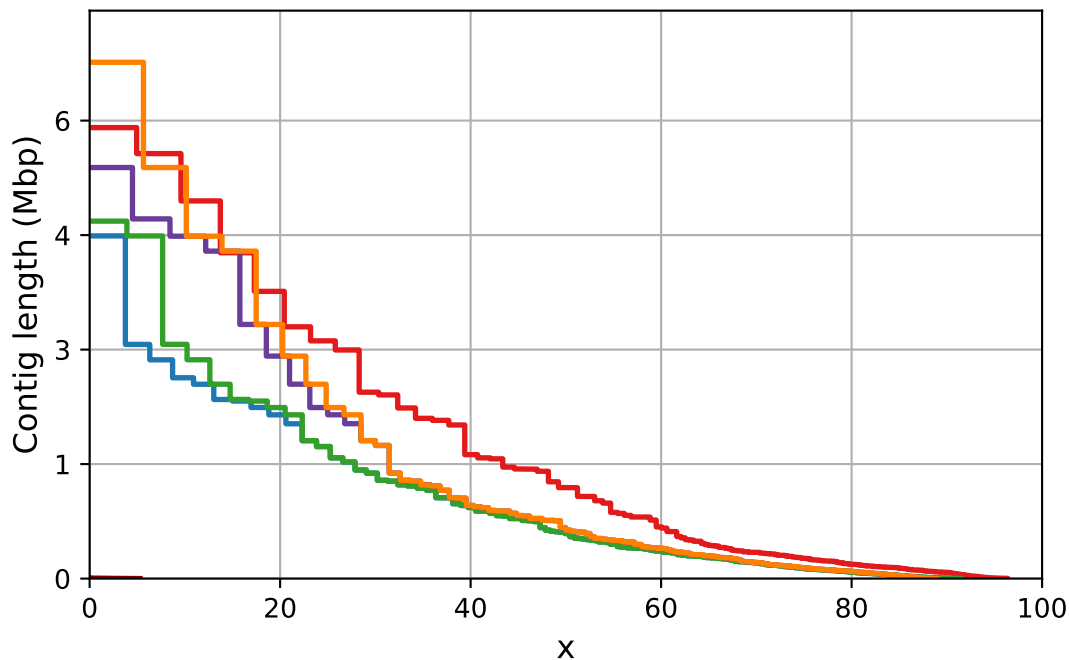


NAx



- UpperBound
- canu_assembly_polished
- flye_assembly_polished
- canu_assembly
- flye_assembly
- trinity_assembly

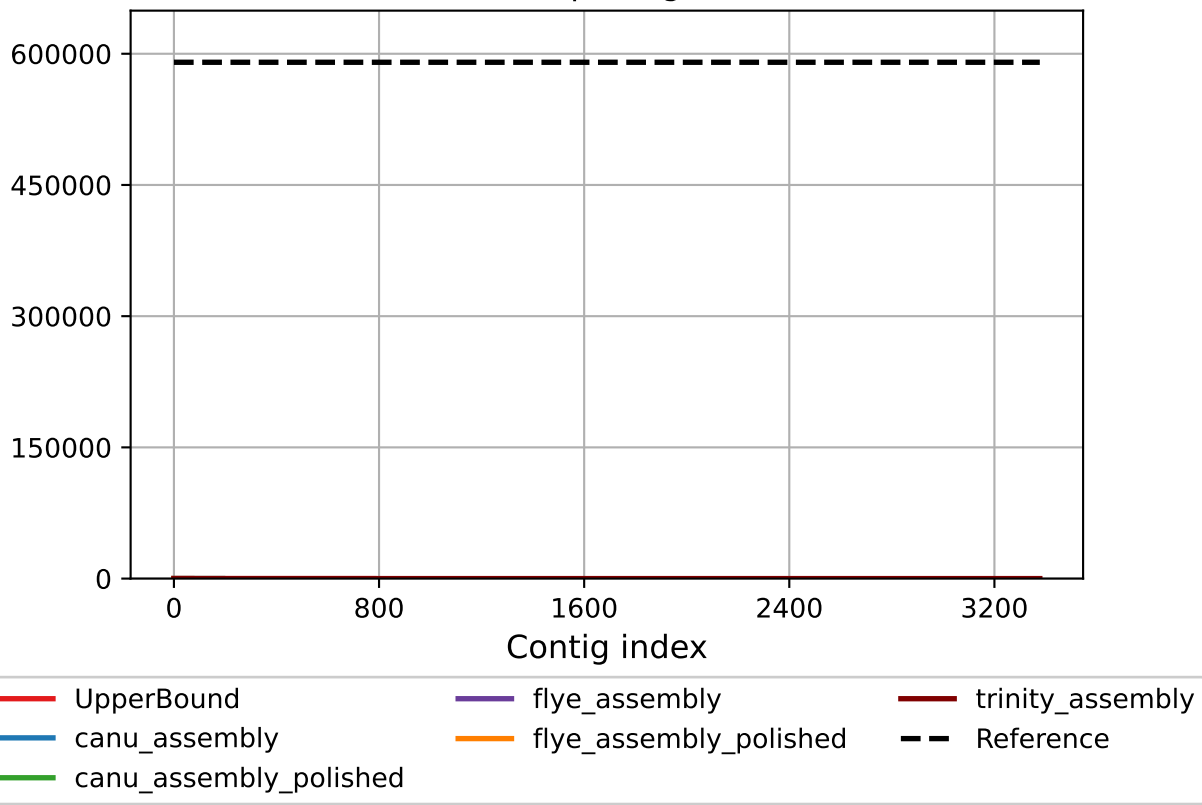
NGAx



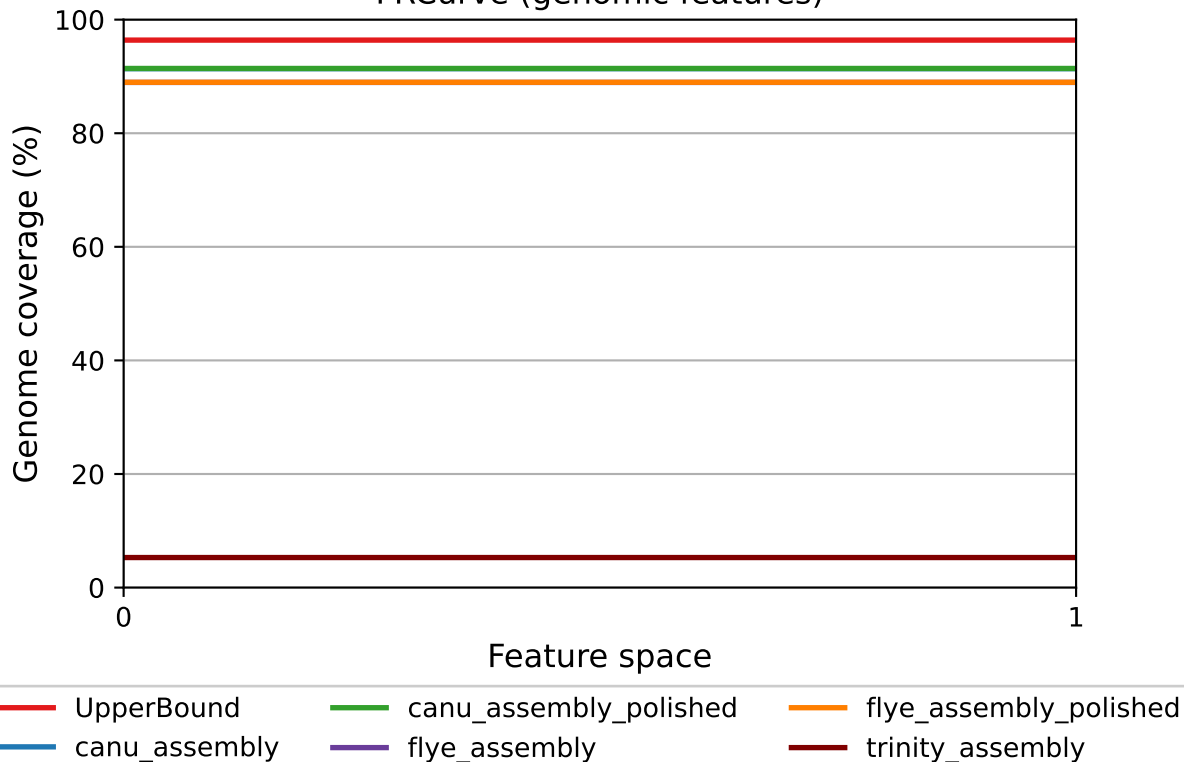
- | | | |
|---|---|--|
| — UpperBound | — canu_assembly_polished | — flye_assembly_polished |
| — canu_assembly | — flye_assembly | — trinity_assembly |

Cumulative # complete genomic features

Cumulative # complete genomic features



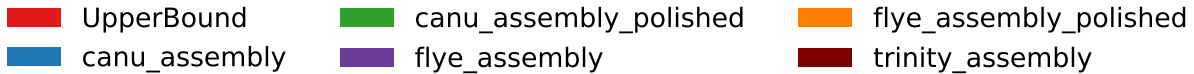
FRCurve (genomic features)



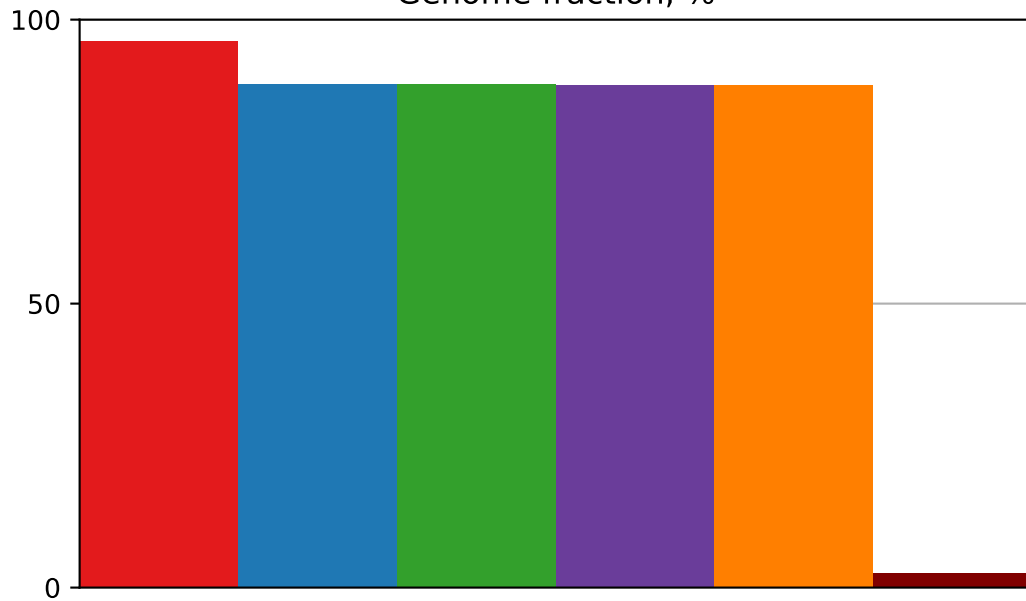
complete genomic features

1

0



Genome fraction, %



| | | |
|---------------|------------------------|------------------------|
| UpperBound | canu_assembly_polished | flye_assembly_polished |
| canu_assembly | flye_assembly | trinity_assembly |