Report

| | Flye_Polished | Canu_Polished |
|---|---|---|
| # contigs (>= 0 bp) | 11 | 29 |
| # contigs (>= 1000 bp) | 11 | 29 |
| # contigs (>= 5000 bp) | 10 | 29 |
| # contigs (>= 10000 bp) | 10 | 29 |
| # contigs (>= 25000 bp) | 10 | 28 |
| # contigs (>= 50000 bp) | 8 | 18 |
| Total length (>= 0 bp) | 34861082 | 35997303 |
| Total length (>= 1000 bp) | 34861082 | 35997303 |
| Total length (>= 5000 bp) | 34856925 | 35997303 |
| Total length (>= 10000 bp) | 34856925 | 35997303 |
| Total length (>= 25000 bp) | 34856925 | 35978808 |
| Total length (>= 50000 bp) | 34777534 | 35607977 |
| # contigs | 11 | 29 |
| Largest contig | 12197133 | 8143141 |
| Total length | 34861082 | 35997303 |
| Reference length | 34204973 | 34204973 |
| GC (%) | 22.74 | 22.76 |
| Reference GC (%) | 22.44 | 22.44 |
| N50 | 8060236 | 5606788 |
| NG50 | 8060236 | 5606788 |
| N90 | 4039478 | 3926766 |
| NG90 | 4039478 | 5028520 |
| auN | 8117212.2 | 5907817.2 |
| auNG | 8272914.0 | 6217385.0 |
| L50 | 2 | 3 |
| LG50 | 2 | 3 |
| L90 | 5 | 6 |
| LG90 | 5 | 5 |
| # misassemblies | 675 | 741 |
| # misassembled contigs | 9 | 26 |
| Misassembled contigs length | 34801372 | 35873046 |
| # local misassemblies | 161 | 163 |
| # scaffold gap ext. mis. | 1 | 2 |
| # scaffold gap loc. mis. | 0 | 0 |
| # unaligned mis. contigs | 0 | 0 |
| # unaligned contigs | 0 + 9 part | 0 + 14 part |
| Unaligned length | 426212 | 553592 |
| Genome fraction (%) | 97.172 | 97.059 |
| Duplication ratio | 1.035 | 1.066 |
| # N's per 100 kbp | 1.26 | 2.18 |
| # mismatches per 100 kbp | 139.15 | 142.25 |
| # indels per 100 kbp | 109.09 | 117.35 |
| Largest alignment | 1454451 | 1454400 |
| Total aligned length | 34374100 | 35379816 |
| NA50 | 404186 | 387049 |
| NGA50 | 404961 | 404880 |
| NA90 | 78783 | 34537 |
| NGA90 | 94427 | 90226 |
| auNA | 476499.9 | 460561.4 |
| auNGA | 485640.0 | 484694.7 |
| LA50 | 27 | 28 |
| LGA50 | 26 | 26 |
| LA90 | 94 | 117 |
| LGA90 | 87 | 89 |

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

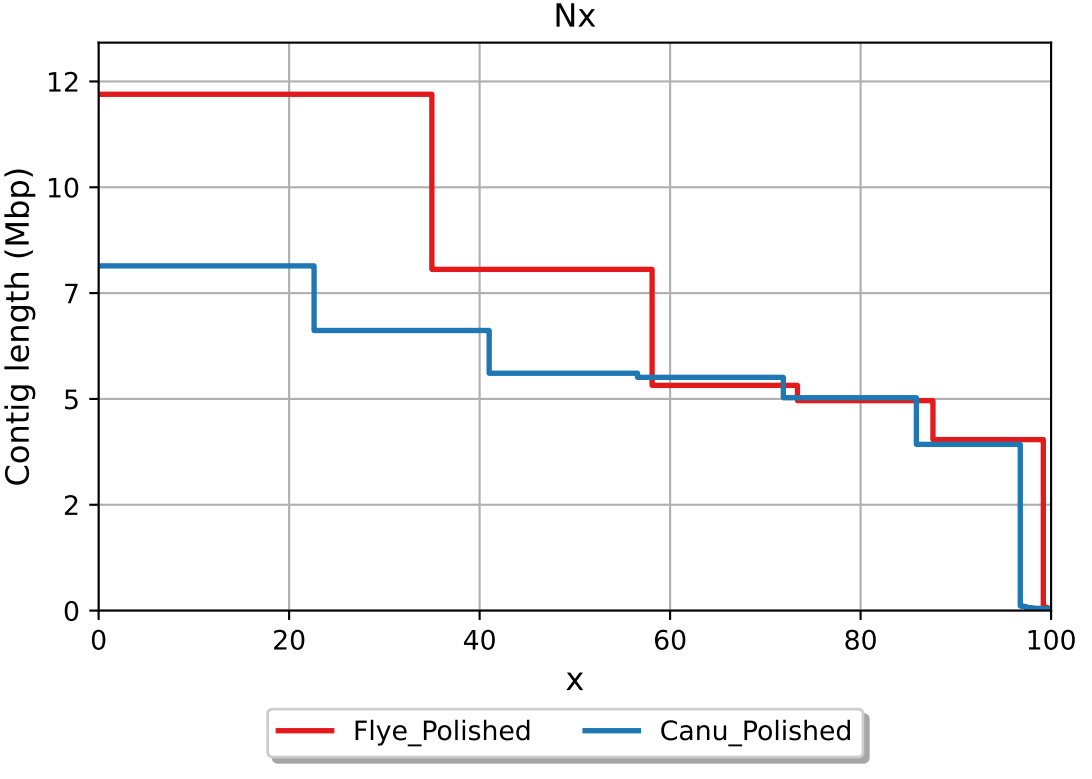
| | Flye_Polished | Canu_Polished |
|---|---|---|
| # misassemblies | 675 | 741 |
| # contig misassemblies | 671 | 731 |
| # c. relocations | 271 | 296 |
| # c. translocations | 388 | 424 |
| # c. inversions | 12 | 11 |
| # scaffold misassemblies | 4 | 10 |
| # s. relocations | 2 | 5 |
| # s. translocations | 2 | 5 |
| # s. inversions | 0 | 0 |
| # misassembled contigs | 9 | 26 |
| Misassembled contigs length | 34801372 | 35873046 |
| # local misassemblies | 161 | 163 |
| # scaffold gap ext. mis. | 1 | 2 |
| # scaffold gap loc. mis. | 0 | 0 |
| # unaligned mis. contigs | 0 | 0 |
| # mismatches | 47831 | 50328 |
| # indels | 37498 | 41517 |
| # indels (<= 5 bp) | 33409 | 36525 |
| # indels (> 5 bp) | 4089 | 4992 |
| Indels length | 123237 | 143403 |

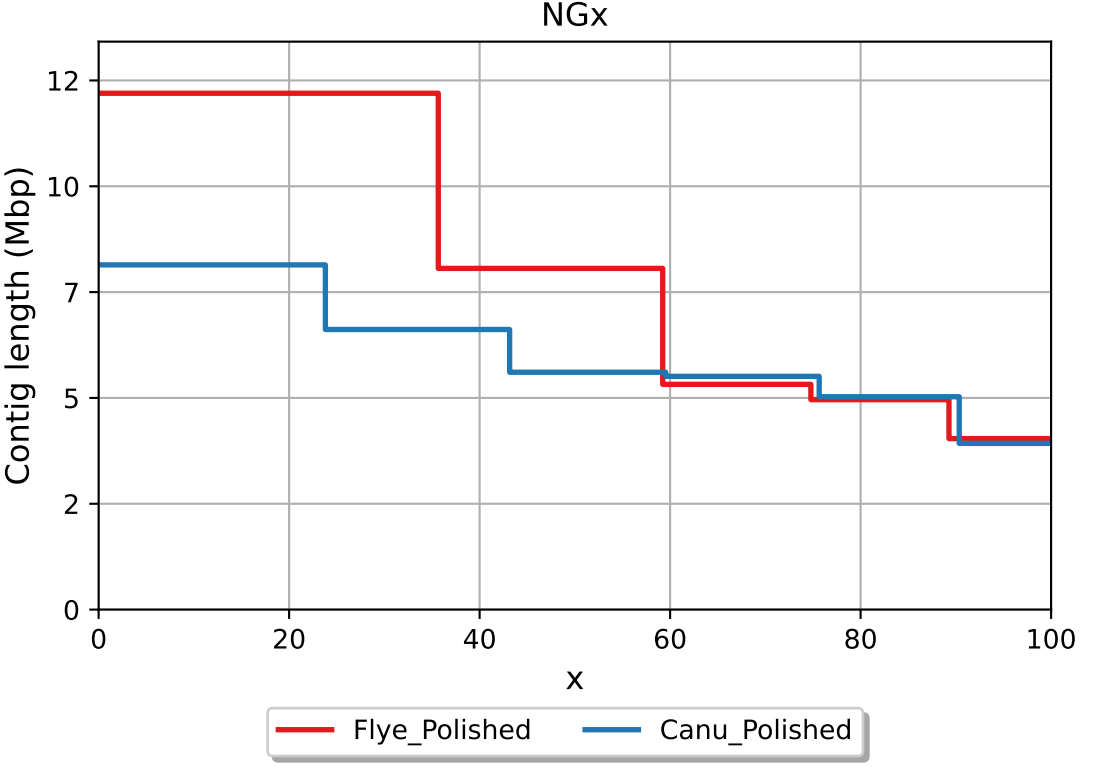
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

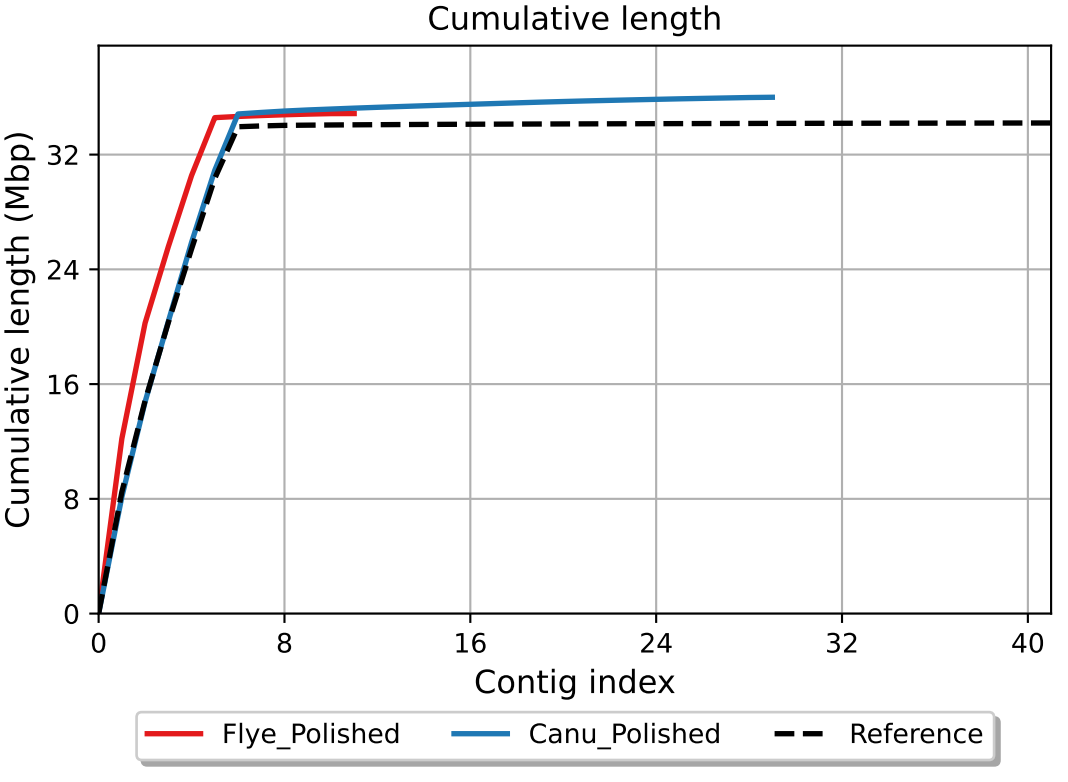
## Unaligned report

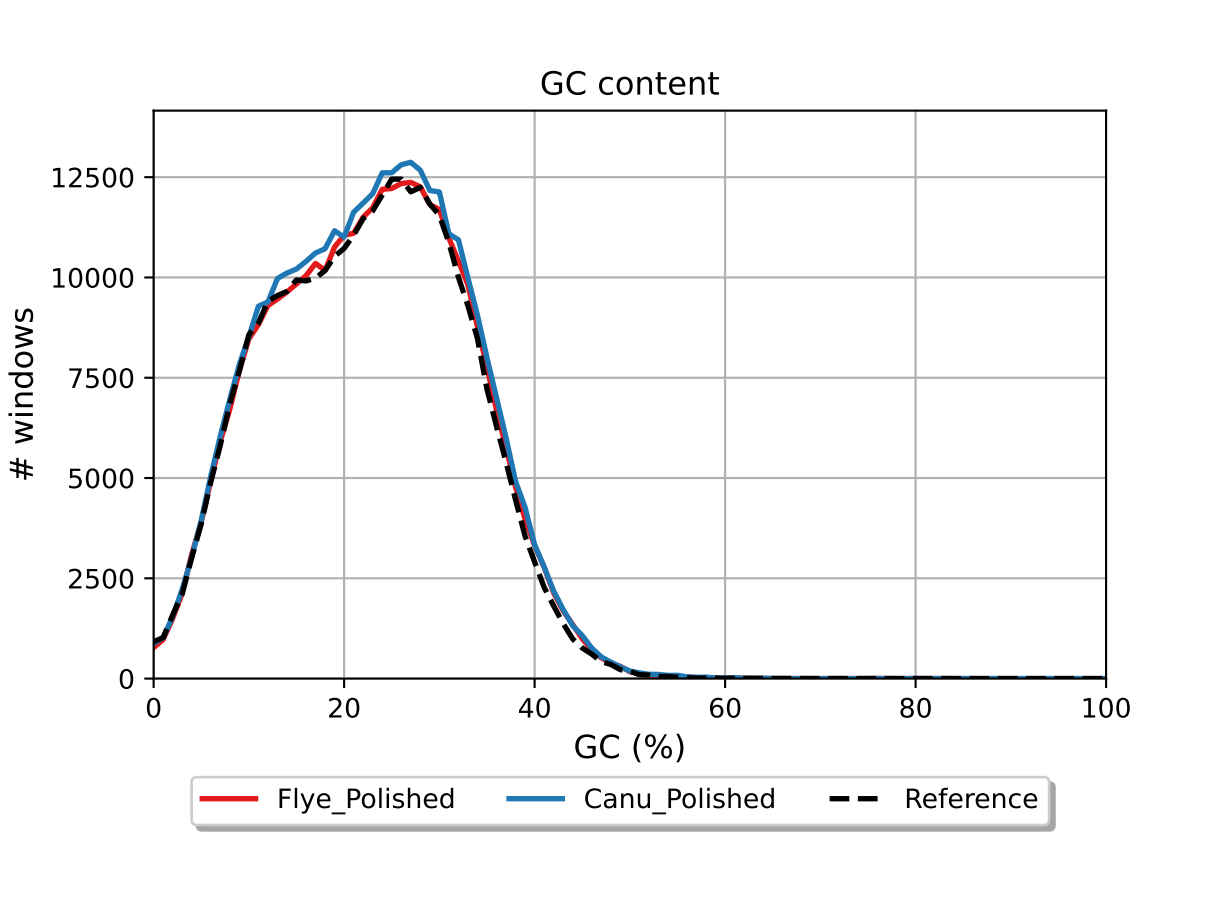
| | Flye_Polished | Canu_Polished |
|---|---|---|
| # fully unaligned contigs | 0 | 0 |
| Fully unaligned length | 0 | 0 |
| # partially unaligned contigs | 9 | 14 |
| Partially unaligned length | 426212 | 553592 |
| # N's | 438 | 786 |

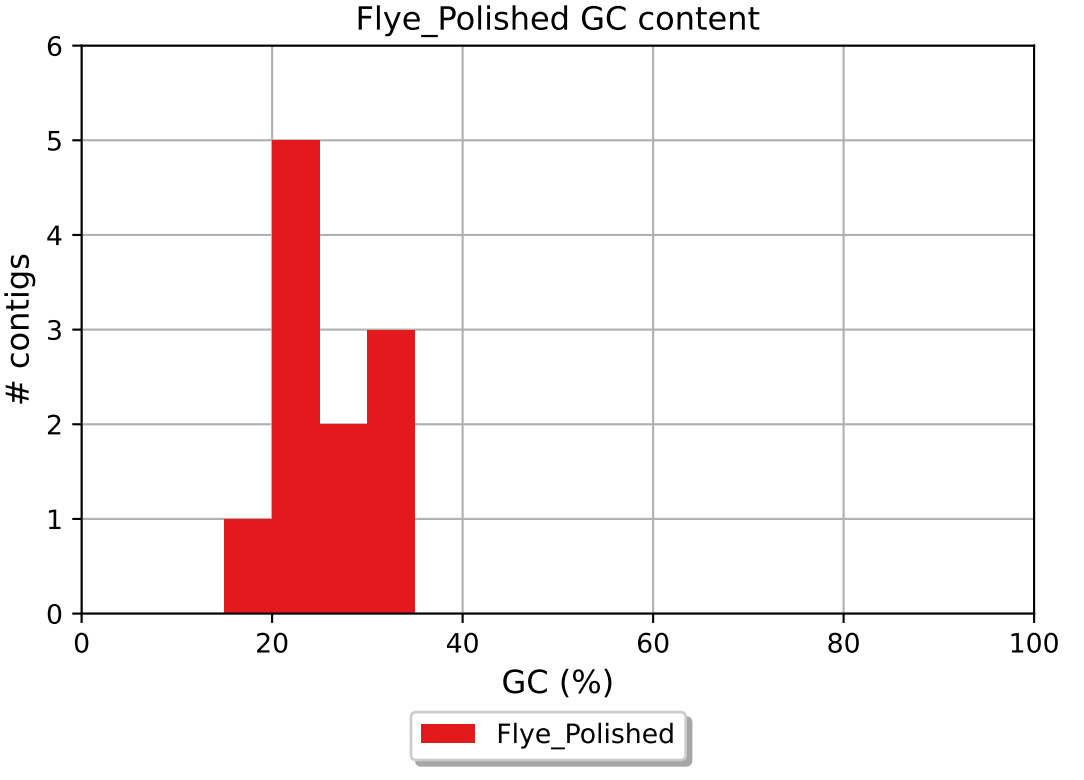
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

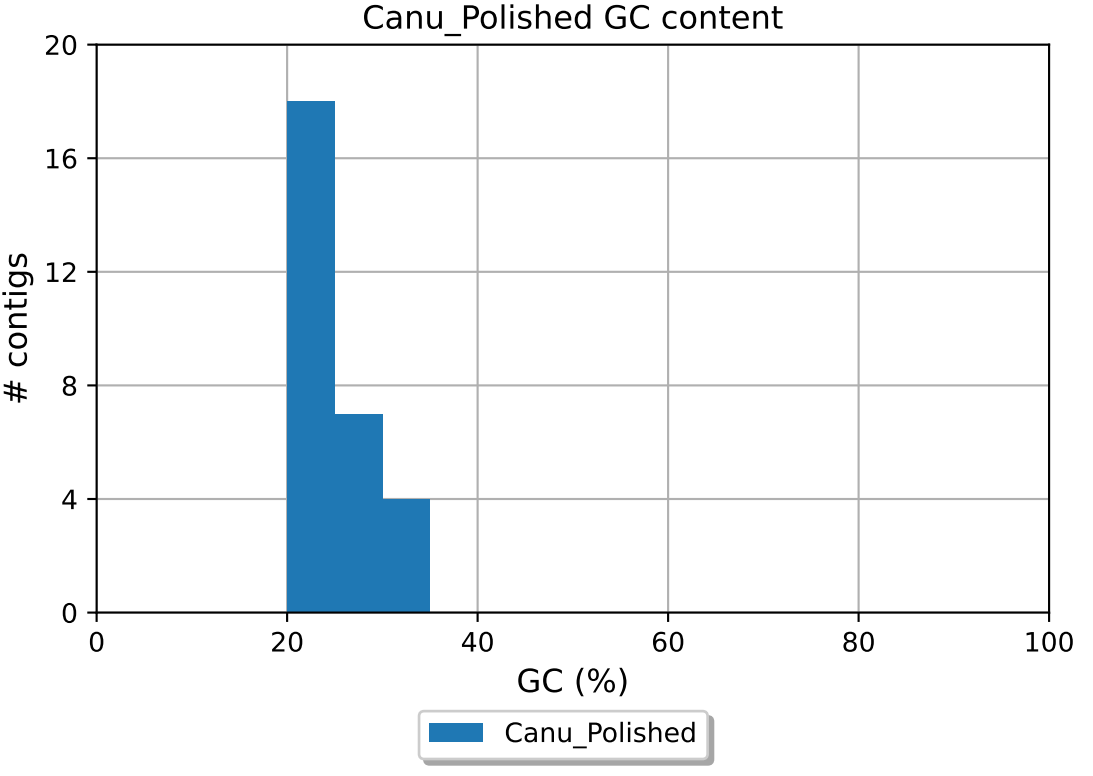

Nx
Contig length (Mbp)
12
10
7
5
2
0
0
20
40
60
80
100
x
Flye_Polished
Canu_Polished

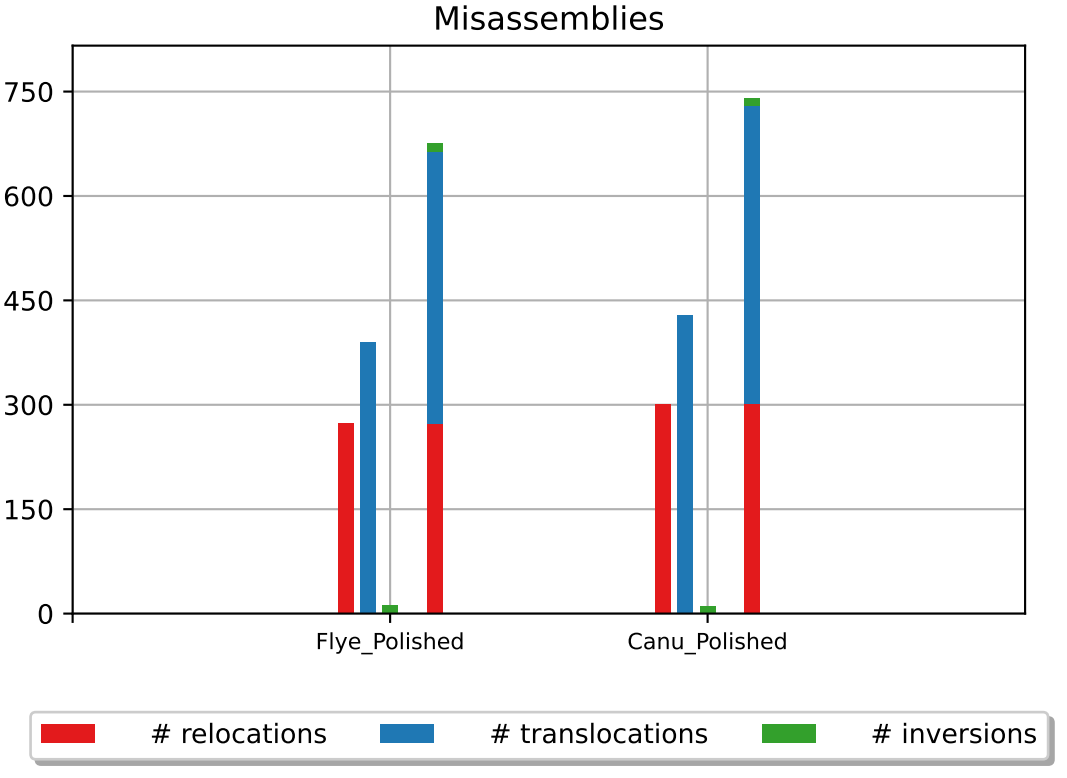

NGx
Contig length (Mbp)
0
2
5
7
10
12
0
20
40
60
80
100
x
Flye_Polished
Canu_Polished

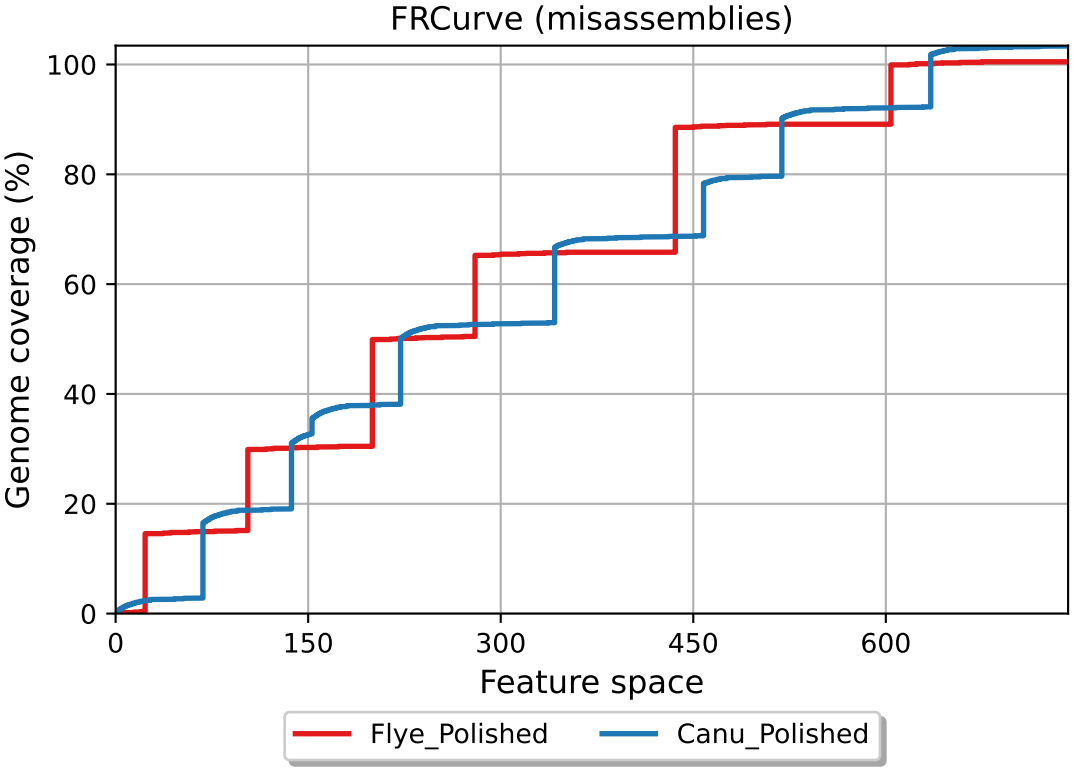

Cumulative length
Cumulative length (Mbp)
0
8
16
24
32
0
8
16
24
32
40
Contig index
Flye_Polished
Canu_Polished
Reference

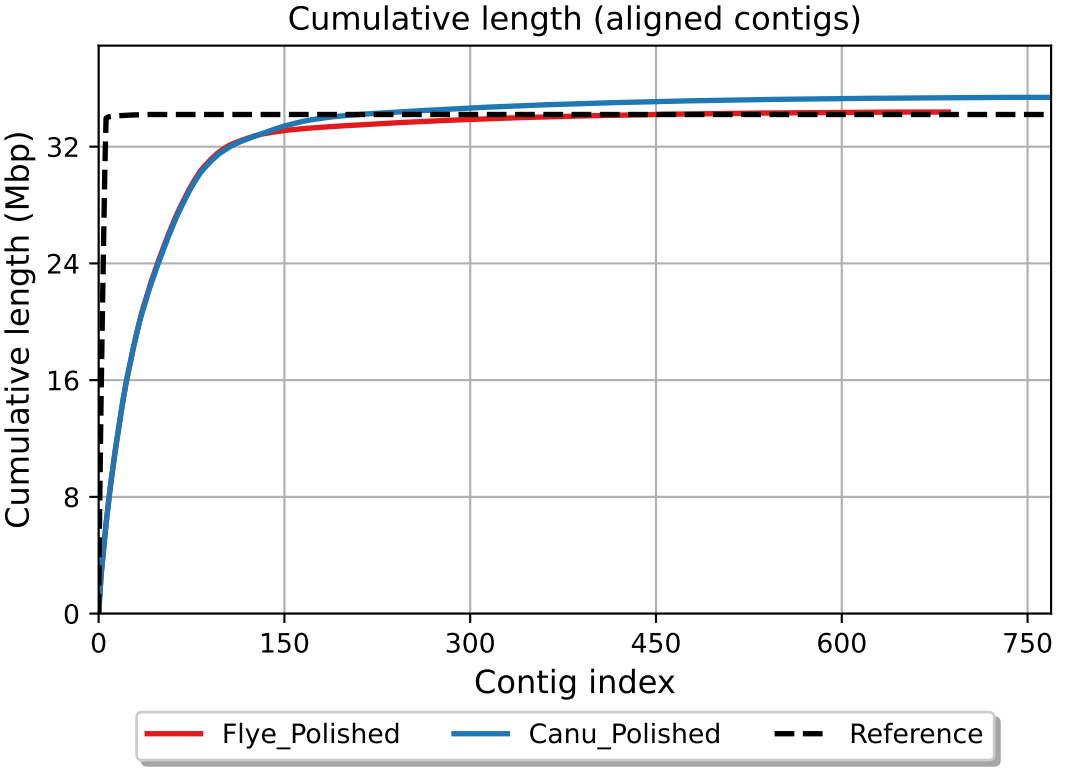

GC content
# windows
GC (%)
0
2500
5000
7500
10000
12500
0
20
40
60
80
100
Flye_Polished
Canu_Polished
Reference

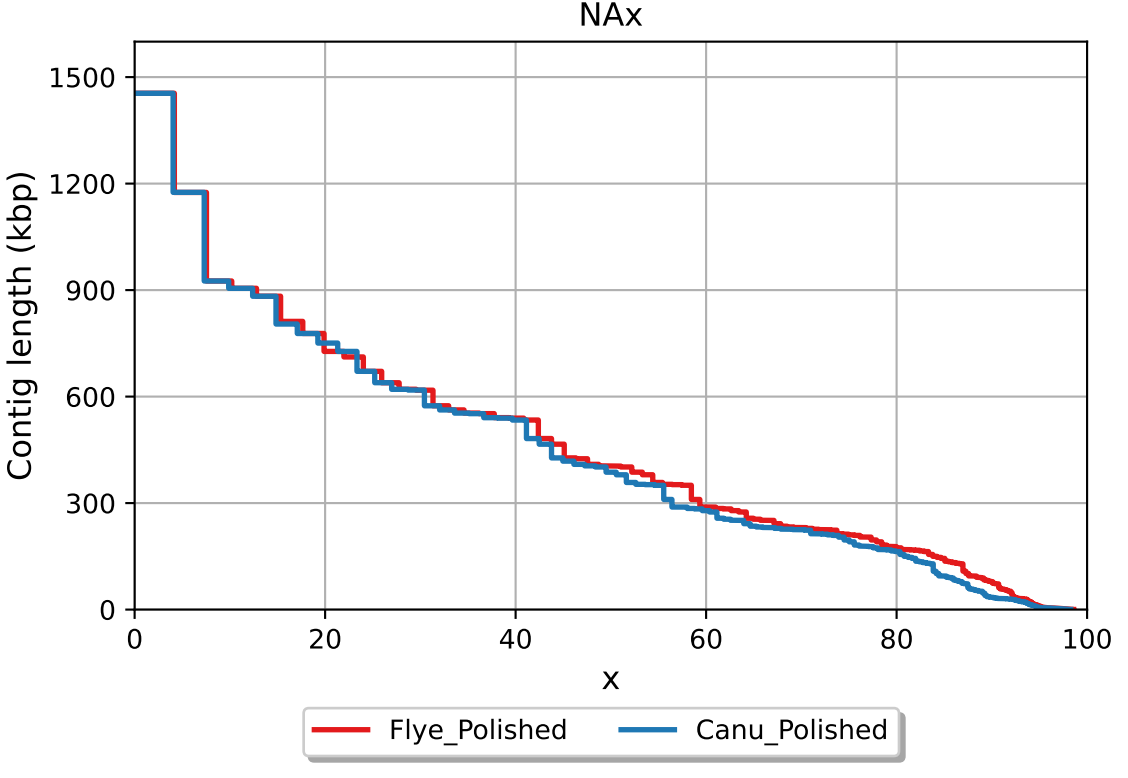

Flye_Polished GC content
# contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
Flye_Polished

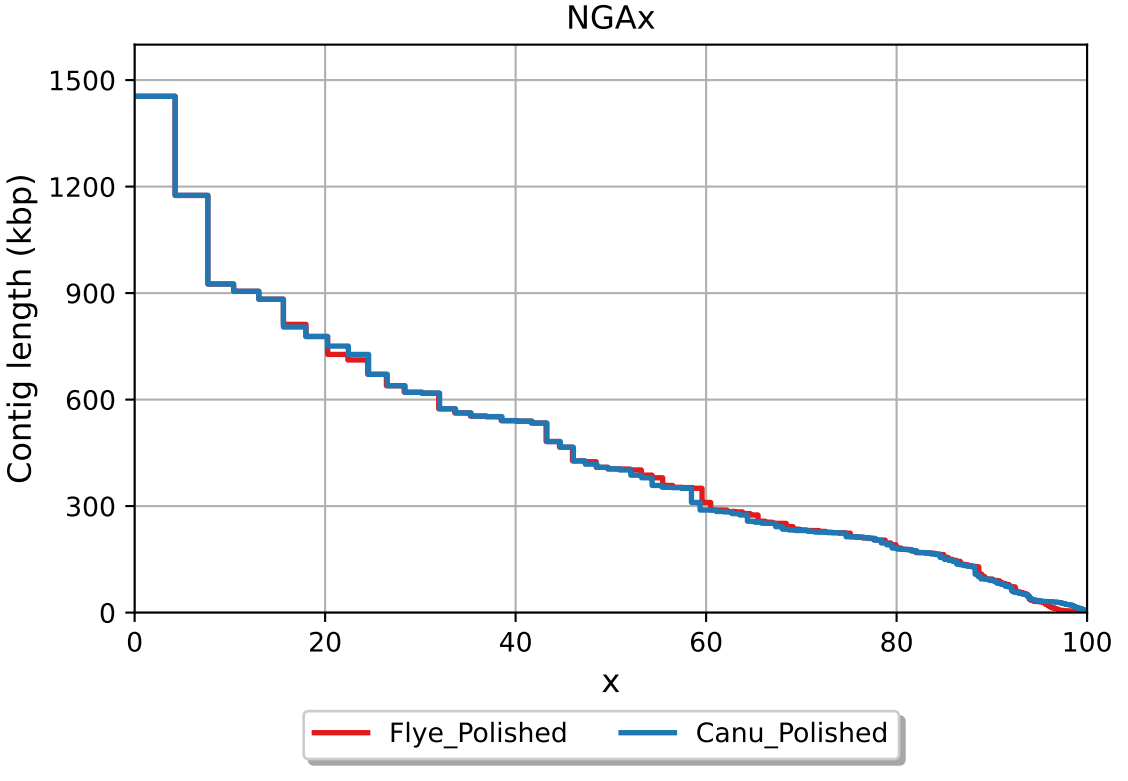

Canu_Polished GC content
# contigs
GC (%)
0
4
8
12
16
20
0
20
40
60
80
100
Canu_Polished

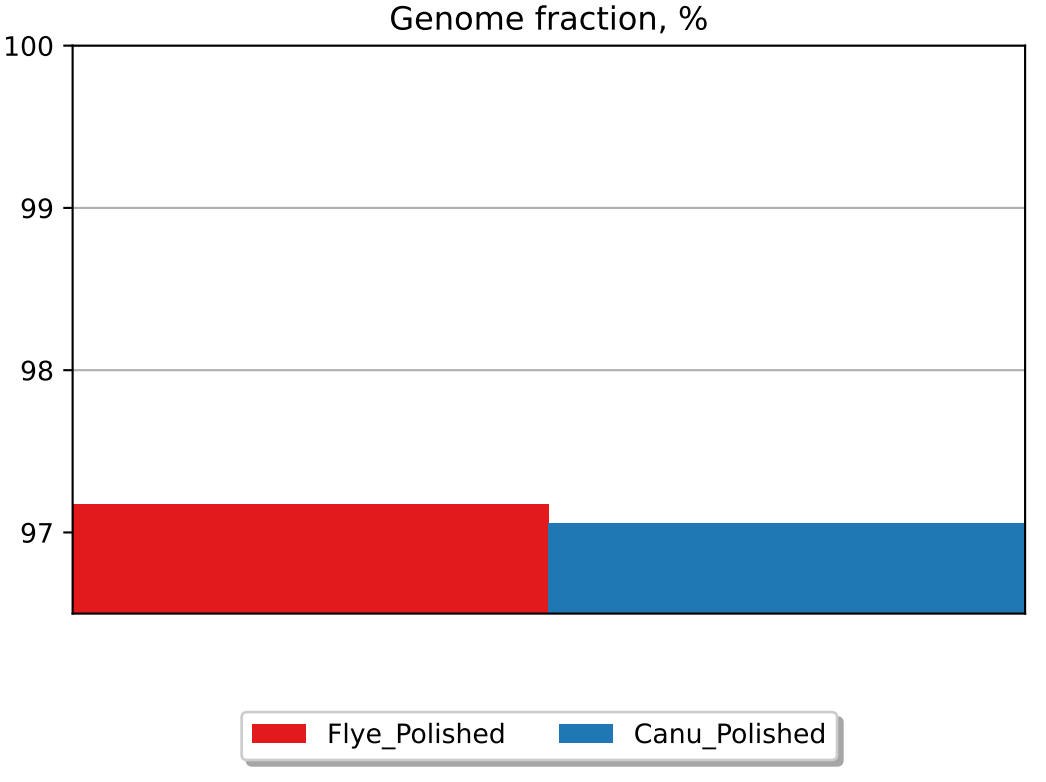

Misassemblies
750
600
450
300
150
0
Flye_Polished
Canu_Polished
# relocations
# translocations
# inversions


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
150
300
450
600
Feature space
Flye_Polished
Canu_Polished


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
8
16
24
32
0
150
300
450
600
750
Contig index
Flye_Polished
Canu_Polished
Reference


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
Flye_Polished
Canu_Polished


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
Flye_Polished
Canu_Polished


Genome fraction, %
100
99
98
97
Flye_Polished
Canu_Polished