

# Report

|                             | Gold_Assembly | IDBA_UD     | Ray        | SOAPdenovo2 | SPAdes       |
|-----------------------------|---------------|-------------|------------|-------------|--------------|
| # contigs (>= 1000 bp)      | 522           | 52          | 0          | 2           | 79           |
| # contigs (>= 5000 bp)      | 0             | 6           | 0          | 0           | 15           |
| # contigs (>= 10000 bp)     | 0             | 2           | 0          | 0           | 7            |
| # contigs (>= 25000 bp)     | 0             | 0           | 0          | 0           | 1            |
| # contigs (>= 50000 bp)     | 0             | 0           | 0          | 0           | 0            |
| Total length (>= 1000 bp)   | 712757        | 135801      | 0          | 2400        | 302281       |
| Total length (>= 5000 bp)   | 0             | 54264       | 0          | 0           | 174956       |
| Total length (>= 10000 bp)  | 0             | 28393       | 0          | 0           | 120547       |
| Total length (>= 25000 bp)  | 0             | 0           | 0          | 0           | 34515        |
| Total length (>= 50000 bp)  | 0             | 0           | 0          | 0           | 0            |
| # contigs                   | 2251          | 479         | 1          | 29          | 658          |
| Largest contig              | 3535          | 17153       | 564        | 1333        | 34515        |
| Total length                | 1913455       | 408856      | 564        | 18341       | 667514       |
| Reference length            | 4628173       | 4628173     | 4628173    | 4628173     | 4628173      |
| GC (%)                      | 69.31         | 68.11       | 64.54      | 66.69       | 68.22        |
| Reference GC (%)            | 68.77         | 68.77       | 68.77      | 68.77       | 68.77        |
| N50                         | 861           | 753         | 564        | 570         | 850          |
| N75                         | 661           | 586         | 564        | 527         | 606          |
| L50                         | 785           | 133         | 1          | 12          | 114          |
| L75                         | 1420          | 291         | 1          | 21          | 354          |
| # misassemblies             | 7             | 8           | 0          | 1           | 4            |
| # misassembled contigs      | 6             | 8           | 0          | 1           | 4            |
| Misassembled contigs length | 8046          | 7457        | 0          | 1333        | 4024         |
| # local misassemblies       | 4             | 1           | 0          | 0           | 0            |
| # structural variations     | 0             | 0           | 0          | 0           | 0            |
| # unaligned contigs         | 0 + 35 part   | 0 + 87 part | 0 + 0 part | 0 + 1 part  | 0 + 142 part |
| Unaligned length            | 8385          | 118167      | 0          | 723         | 284666       |
| Genome fraction (%)         | 40.755        | 6.269       | 0.012      | 0.376       | 8.240        |
| Duplication ratio           | 1.010         | 1.002       | 1.000      | 1.012       | 1.004        |
| # N's per 100 kbp           | 0.00          | 0.00        | 0.00       | 81.78       | 0.00         |
| # mismatches per 100 kbp    | 1553.97       | 1868.66     | 0.00       | 1499.57     | 2533.85      |
| # indels per 100 kbp        | 28.42         | 42.39       | 0.00       | 34.47       | 32.52        |
| Largest alignment           | 3535          | 2198        | 564        | 1067        | 1594         |
| NA50                        | 856           | 560         | 564        | 545         | 506          |
| NGA50                       | -             | -           | -          | -           | -            |
| NA75                        | 657           | -           | 564        | 526         | -            |
| LA50                        | 791           | 287         | 1          | 14          | 515          |
| LA75                        | 1431          | -           | 1          | 22          | -            |

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

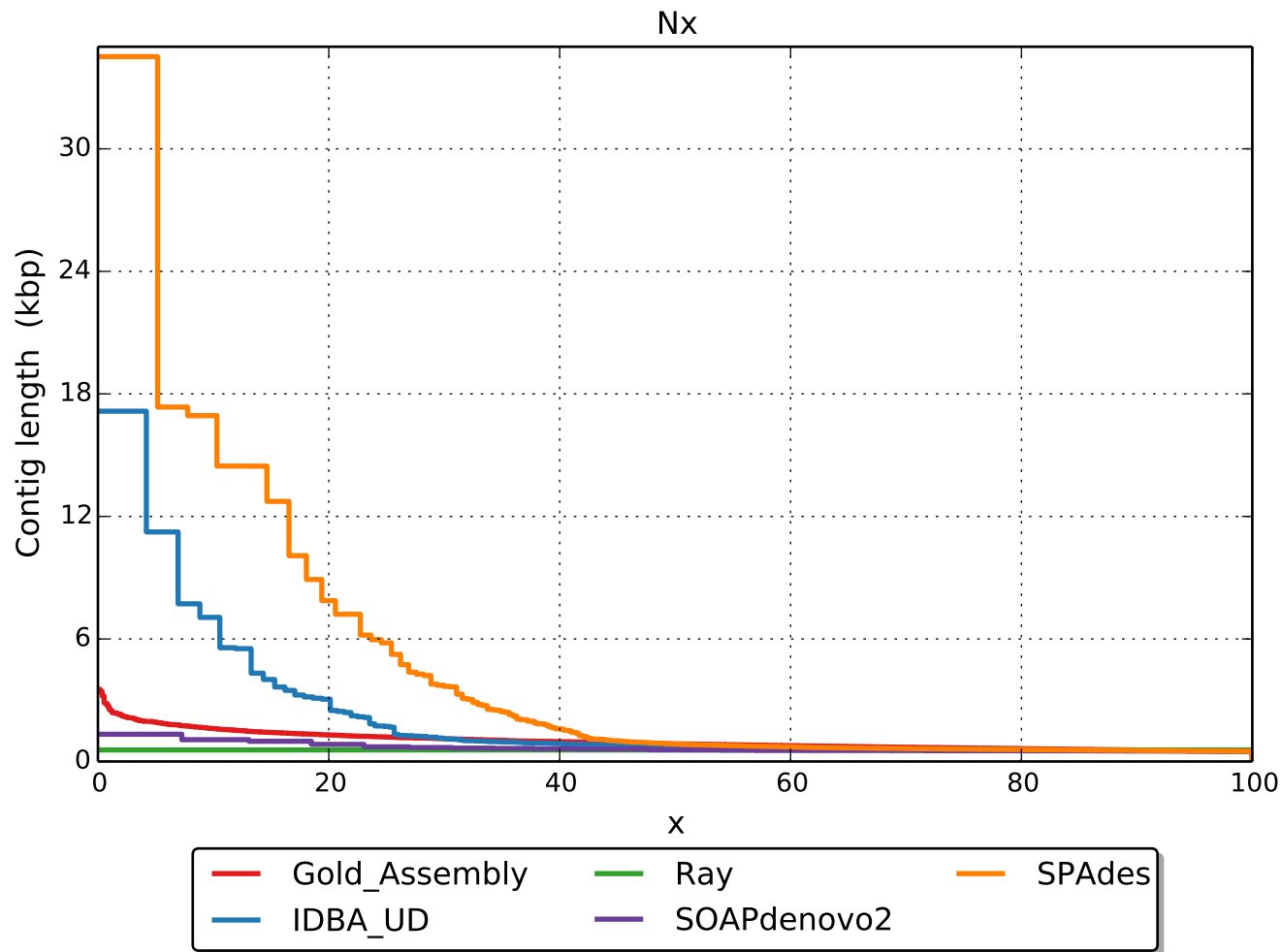
|                                 | Gold_Assembly | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|---------------------------------|---------------|---------|-----|-------------|--------|
| # misassemblies                 | 7             | 8       | 0   | 1           | 4      |
| # relocations                   | 2             | 4       | 0   | 0           | 1      |
| # translocations                | 5             | 3       | 0   | 1           | 3      |
| # inversions                    | 0             | 1       | 0   | 0           | 0      |
| # possibly misassembled contigs | 2             | 6       | 0   | 0           | 6      |
| # misassembled contigs          | 6             | 8       | 0   | 1           | 4      |
| Misassembled contigs length     | 8046          | 7457    | 0   | 1333        | 4024   |
| # local misassemblies           | 4             | 1       | 0   | 0           | 0      |
| # structural variations         | 0             | 0       | 0   | 0           | 0      |
| # mismatches                    | 29311         | 5422    | 0   | 261         | 9663   |
| # indels                        | 536           | 123     | 0   | 6           | 124    |
| # short indels                  | 488           | 115     | 0   | 4           | 118    |
| # long indels                   | 48            | 8       | 0   | 2           | 6      |
| Indels length                   | 1246          | 240     | 0   | 28          | 220    |

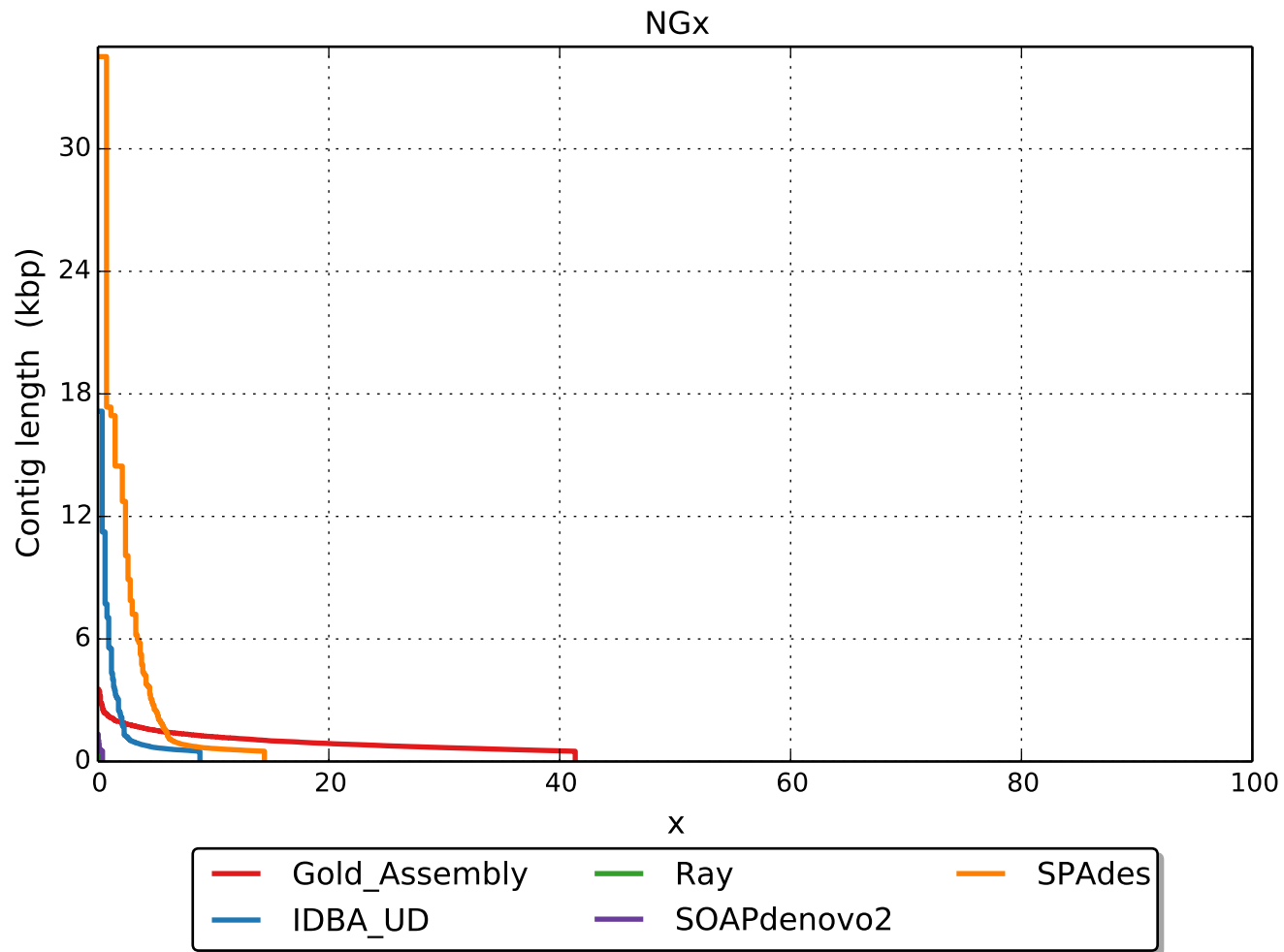
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

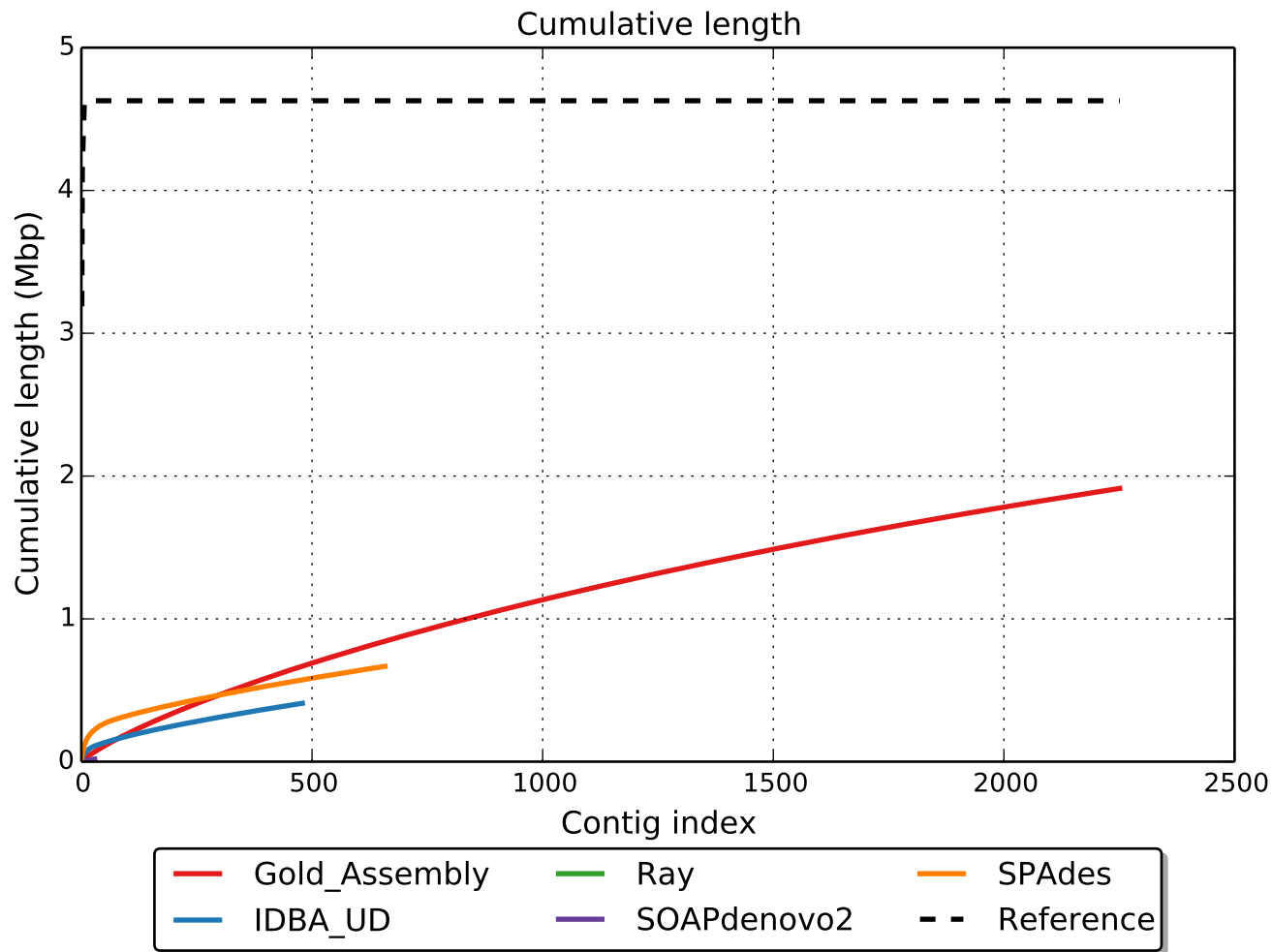
## Unaligned report

|                               | Gold_Assembly | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|-------------------------------|---------------|---------|-----|-------------|--------|
| # fully unaligned contigs     | 0             | 0       | 0   | 0           | 0      |
| Fully unaligned length        | 0             | 0       | 0   | 0           | 0      |
| # partially unaligned contigs | 35            | 87      | 0   | 1           | 142    |
| # with misassembly            | 0             | 1       | 0   | 0           | 1      |
| # both parts are significant  | 0             | 6       | 0   | 0           | 5      |
| Partially unaligned length    | 8385          | 118167  | 0   | 723         | 284666 |
| # N's                         | 0             | 0       | 0   | 15          | 0      |

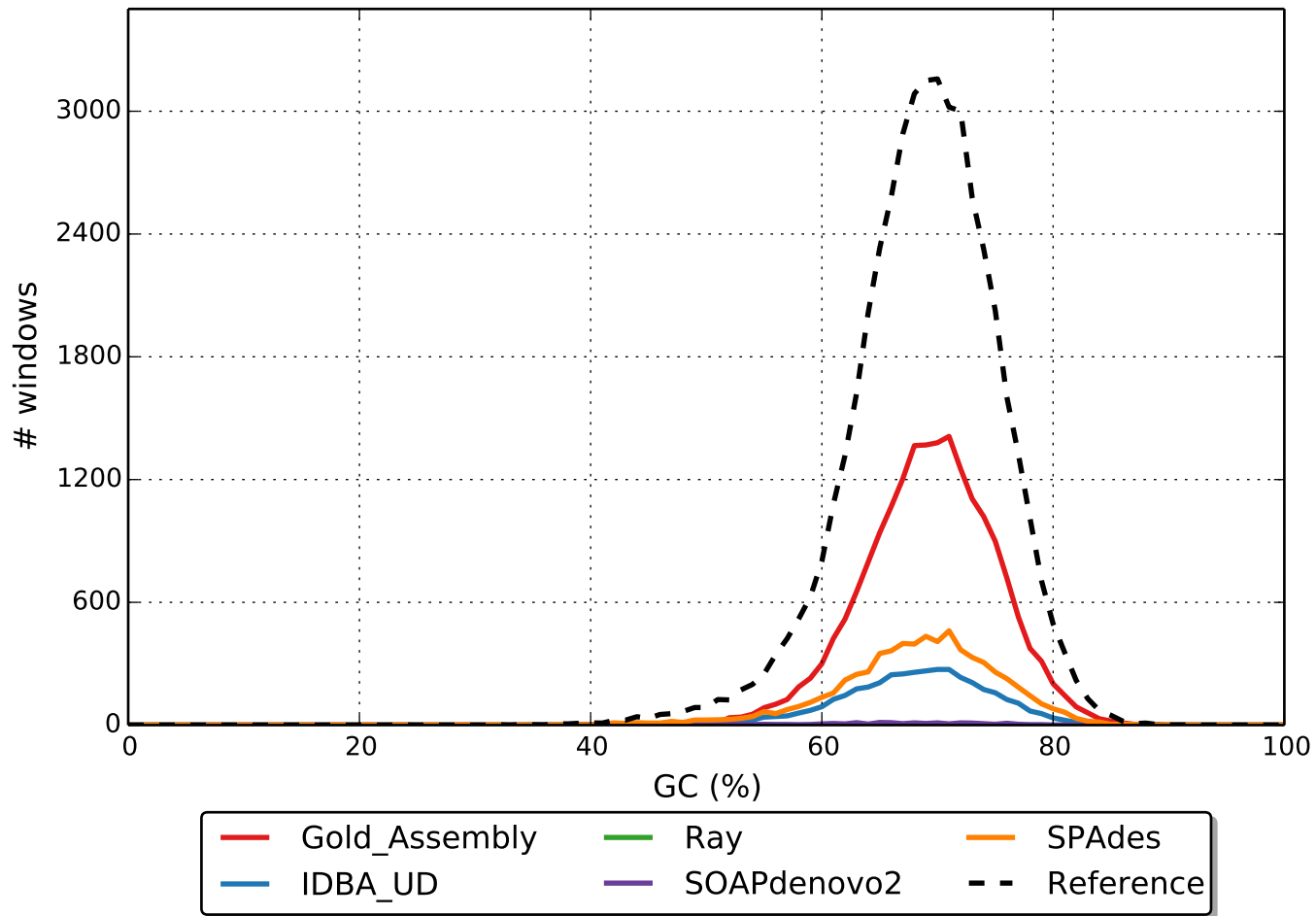
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



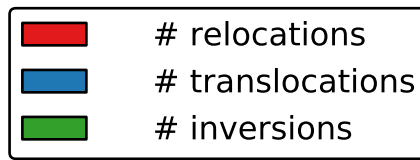
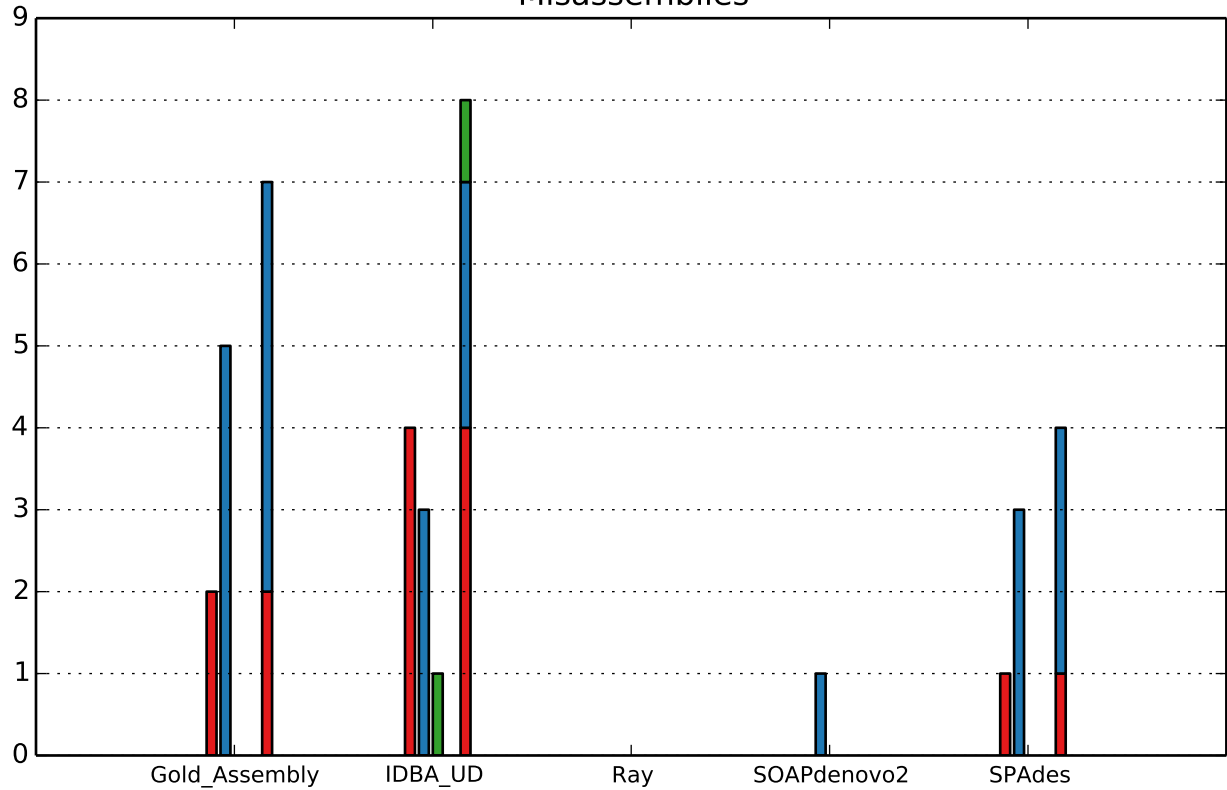




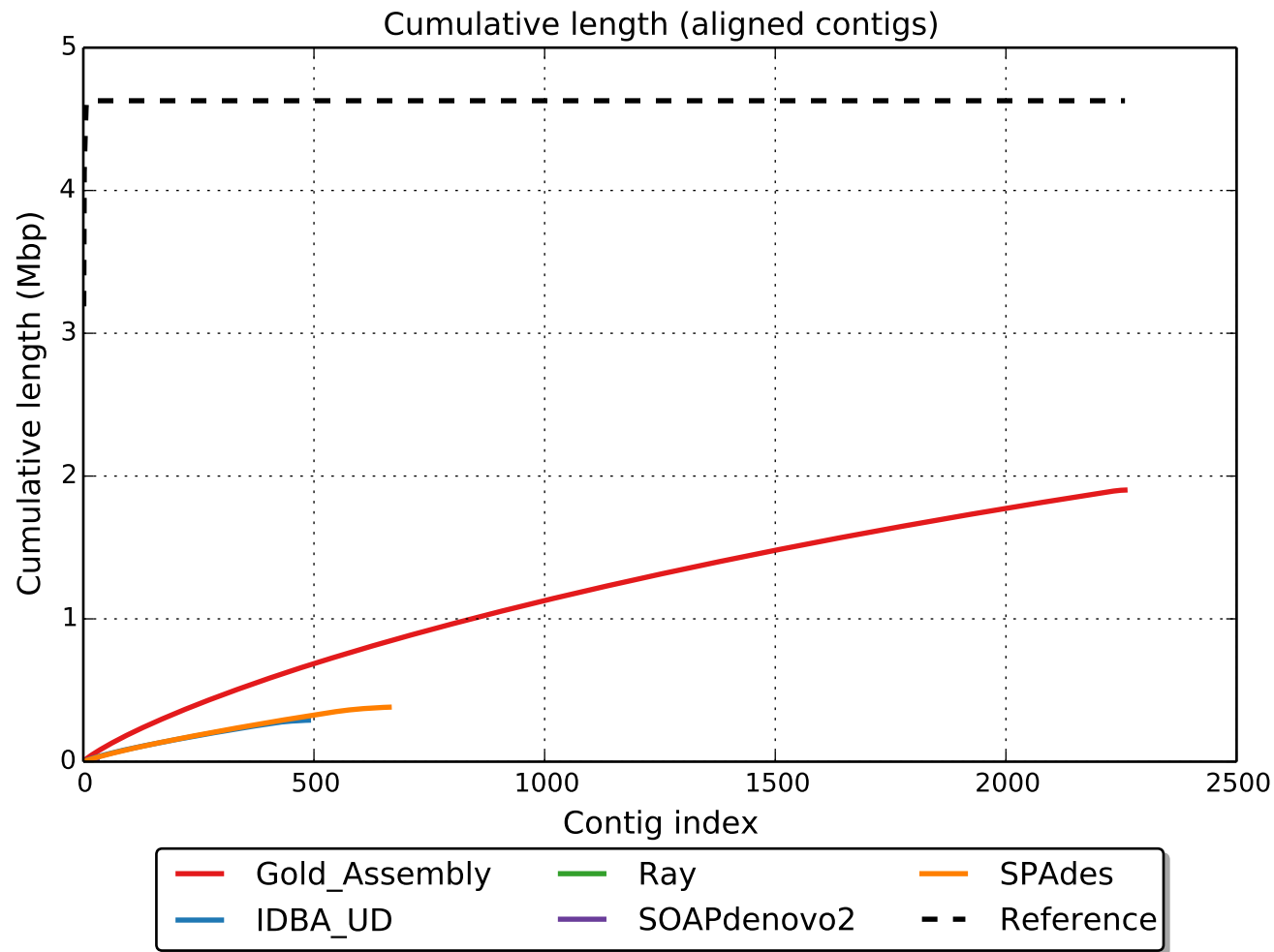
GC content



# Misassemblies







NAx

