

# Report

|                             | IDBA_UD    | Ray        | SOAPdenovo2 | SPAdes     |
|-----------------------------|------------|------------|-------------|------------|
| # contigs (>= 1000 bp)      | 8          | 3          | 4           | 7          |
| # contigs (>= 5000 bp)      | 2          | 0          | 0           | 2          |
| # contigs (>= 10000 bp)     | 1          | 0          | 0           | 2          |
| # contigs (>= 25000 bp)     | 0          | 0          | 0           | 0          |
| # contigs (>= 50000 bp)     | 0          | 0          | 0           | 0          |
| Total length (>= 1000 bp)   | 29076      | 5654       | 5882        | 43606      |
| Total length (>= 5000 bp)   | 16522      | 0          | 0           | 25038      |
| Total length (>= 10000 bp)  | 10239      | 0          | 0           | 25038      |
| Total length (>= 25000 bp)  | 0          | 0          | 0           | 0          |
| Total length (>= 50000 bp)  | 0          | 0          | 0           | 0          |
| # contigs                   | 8          | 6          | 10          | 8          |
| Largest contig              | 10239      | 2666       | 1936        | 12822      |
| Total length                | 29076      | 7473       | 9931        | 44365      |
| Reference length            | 2972256    | 2972256    | 2972256     | 2972256    |
| GC (%)                      | 39.92      | 39.72      | 38.49       | 41.23      |
| Reference GC (%)            | 28.84      | 28.84      | 28.84       | 28.84      |
| N50                         | 6283       | 1560       | 1224        | 12216      |
| N75                         | 2168       | 1428       | 684         | 4461       |
| L50                         | 2          | 2          | 4           | 2          |
| L75                         | 4          | 3          | 7           | 4          |
| # misassemblies             | 1          | 0          | 0           | 1          |
| # misassembled contigs      | 1          | 0          | 0           | 1          |
| Misassembled contigs length | 2168       | 0          | 0           | 1018       |
| # local misassemblies       | 0          | 0          | 3           | 0          |
| # structural variations     | 0          | 0          | 0           | 0          |
| # unaligned contigs         | 0 + 4 part | 0 + 1 part | 0 + 5 part  | 0 + 7 part |
| Unaligned length            | 12135      | 205        | 2565        | 25171      |
| Genome fraction (%)         | 0.551      | 0.232      | 0.242       | 0.642      |
| Duplication ratio           | 1.034      | 1.055      | 1.023       | 1.006      |
| # N's per 100 kbp           | 24.07      | 0.00       | 10623.30    | 139.75     |
| # mismatches per 100 kbp    | 3472.90    | 2337.06    | 2820.23     | 3914.27    |
| # indels per 100 kbp        | 158.69     | 0.00       | 55.57       | 188.64     |
| Largest alignment           | 6238       | 2666       | 1878        | 11683      |
| NA50                        | 1169       | 1560       | 668         | -          |
| NGA50                       | -          | -          | -           | -          |
| NA75                        | -          | 1427       | -           | -          |
| LA50                        | 6          | 2          | 5           | -          |
| LA75                        | -          | 3          | -           | -          |

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

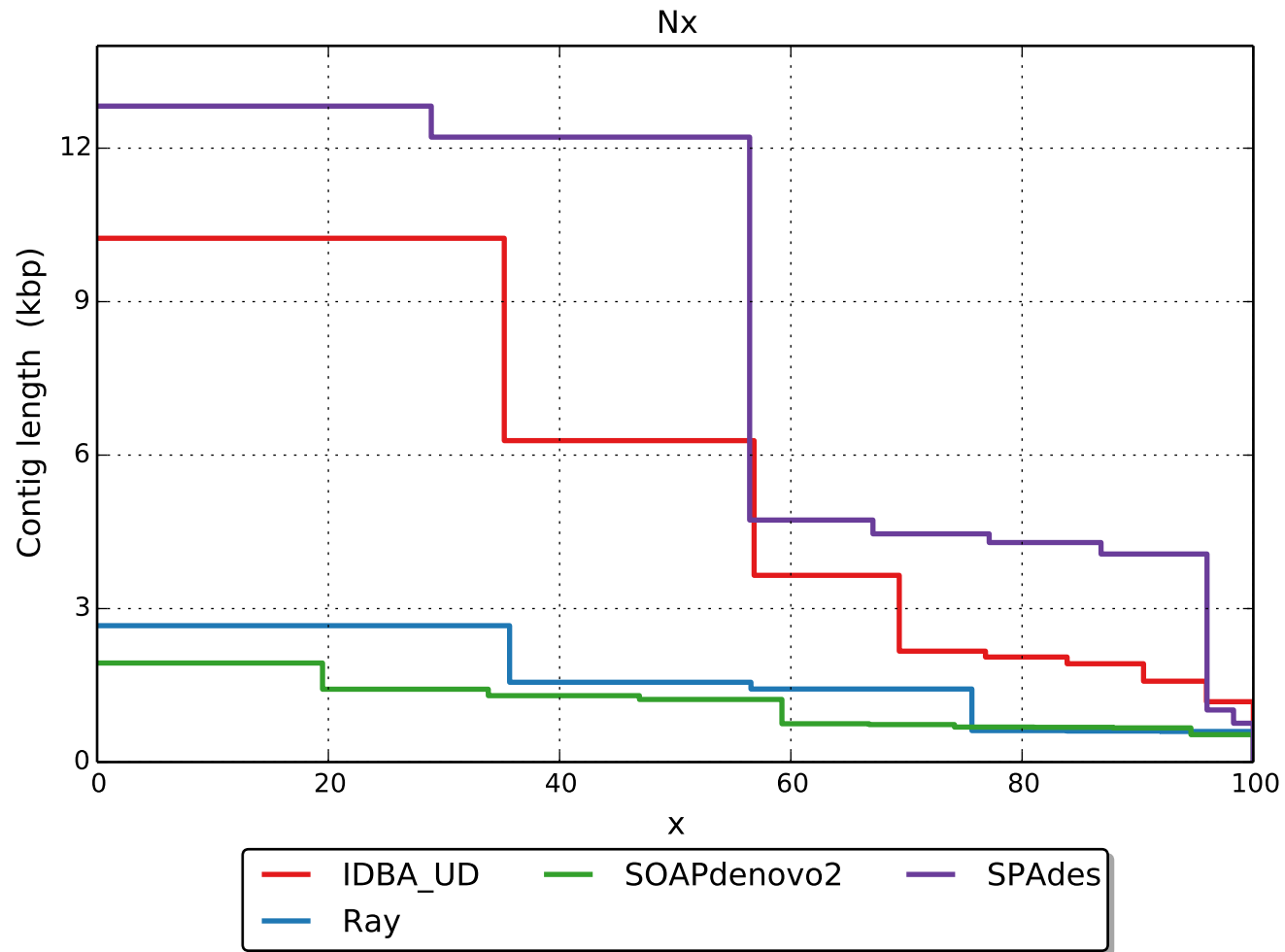
|                                 | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|---------------------------------|---------|-----|-------------|--------|
| # misassemblies                 | 1       | 0   | 0           | 1      |
| # relocations                   | 1       | 0   | 0           | 1      |
| # translocations                | 0       | 0   | 0           | 0      |
| # inversions                    | 0       | 0   | 0           | 0      |
| # possibly misassembled contigs | 2       | 0   | 0           | 4      |
| # misassembled contigs          | 1       | 0   | 0           | 1      |
| Misassembled contigs length     | 2168    | 0   | 0           | 1018   |
| # local misassemblies           | 0       | 0   | 3           | 0      |
| # structural variations         | 0       | 0   | 0           | 0      |
| # mismatches                    | 569     | 161 | 203         | 747    |
| # indels                        | 26      | 0   | 4           | 36     |
| # short indels                  | 24      | 0   | 4           | 35     |
| # long indels                   | 2       | 0   | 0           | 1      |
| Indels length                   | 50      | 0   | 4           | 51     |

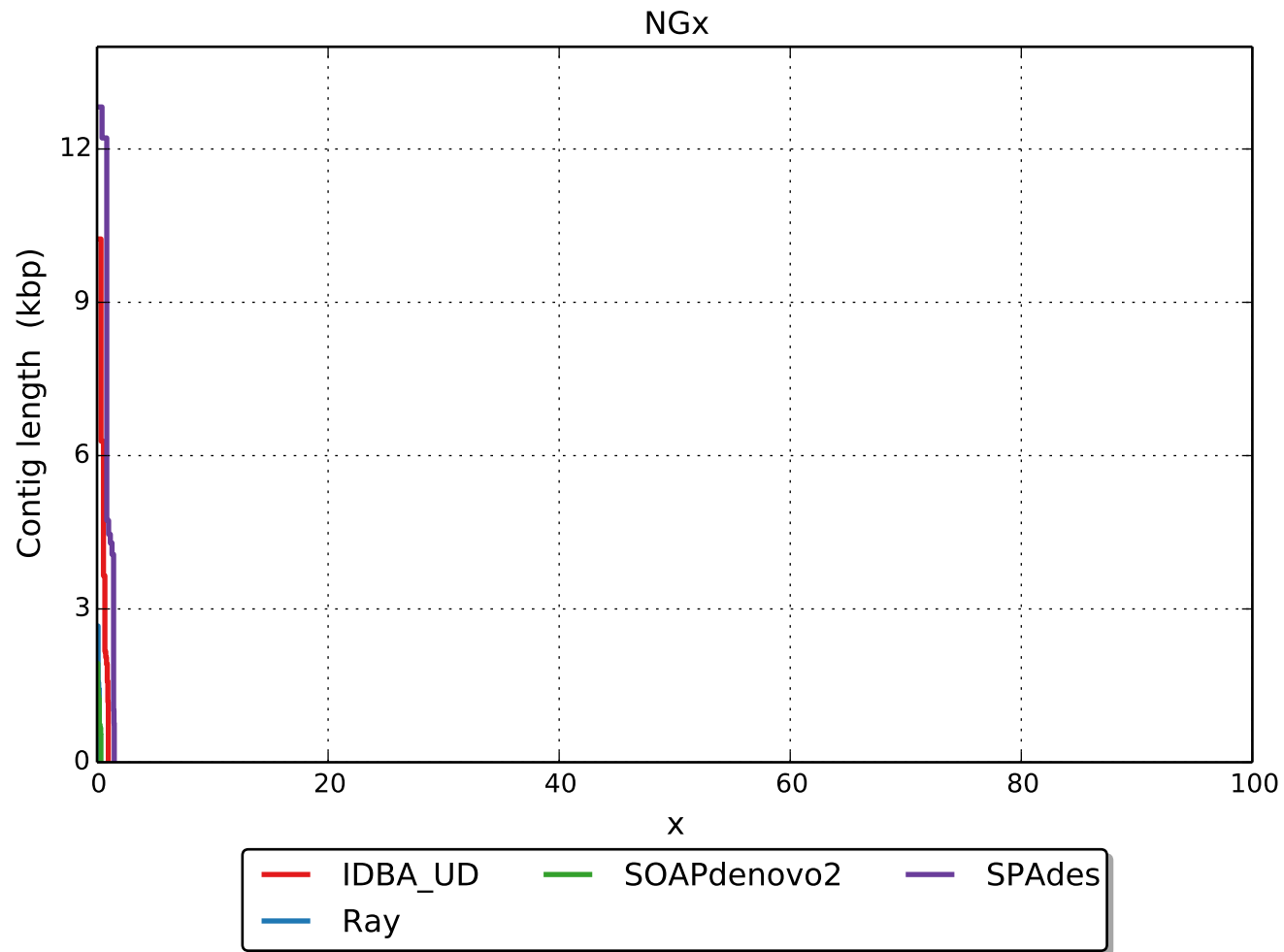
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

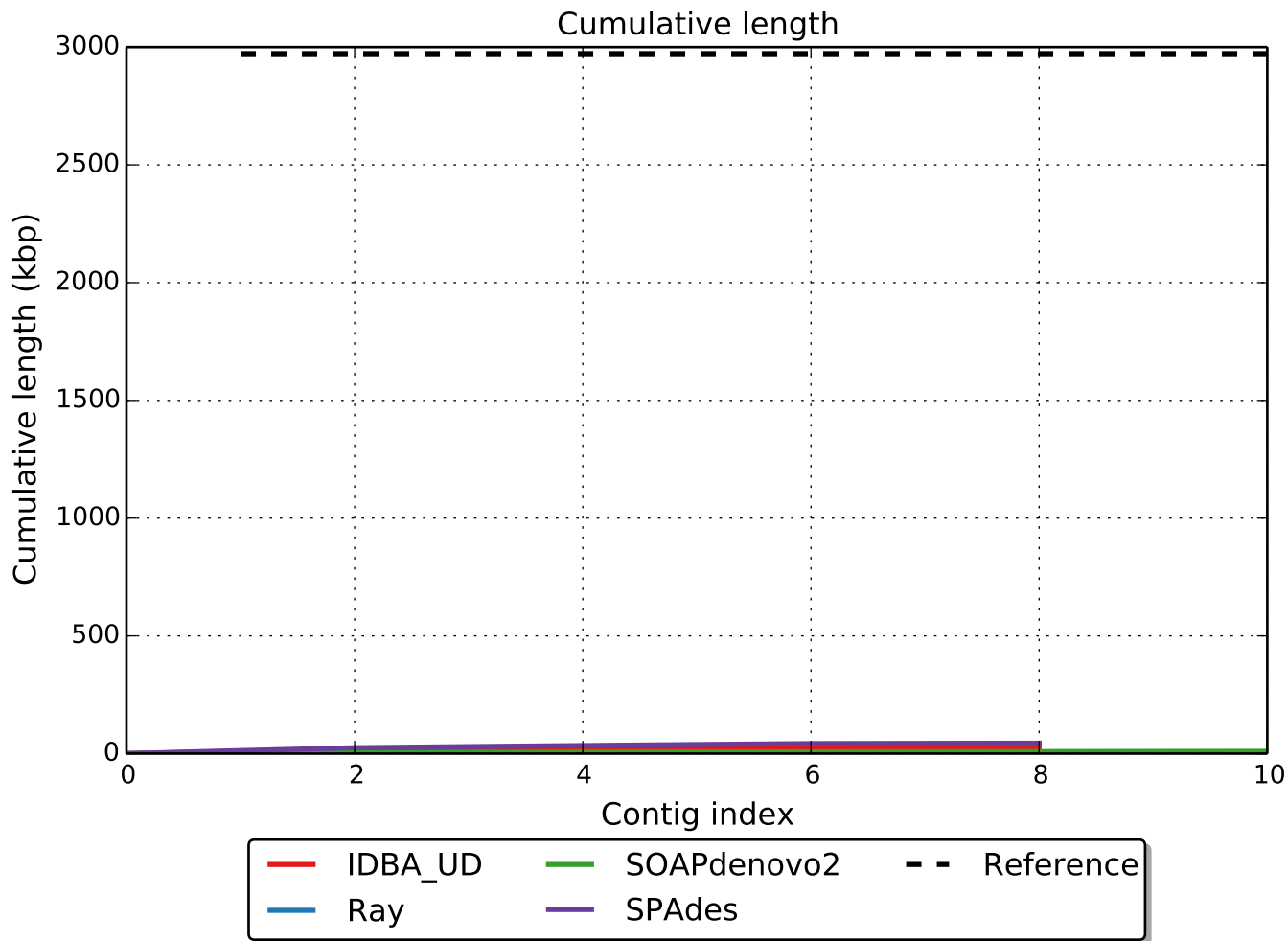
## Unaligned report

|                               | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|-------------------------------|---------|-----|-------------|--------|
| # fully unaligned contigs     | 0       | 0   | 0           | 0      |
| Fully unaligned length        | 0       | 0   | 0           | 0      |
| # partially unaligned contigs | 4       | 1   | 5           | 7      |
| # with misassembly            | 1       | 0   | 0           | 0      |
| # both parts are significant  | 2       | 0   | 0           | 4      |
| Partially unaligned length    | 12135   | 205 | 2565        | 25171  |
| # N's                         | 7       | 0   | 1055        | 62     |

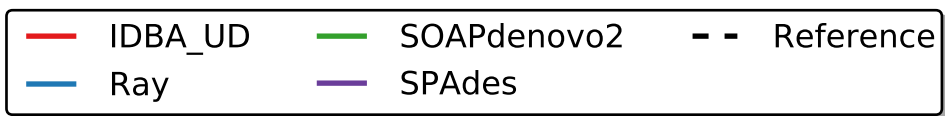
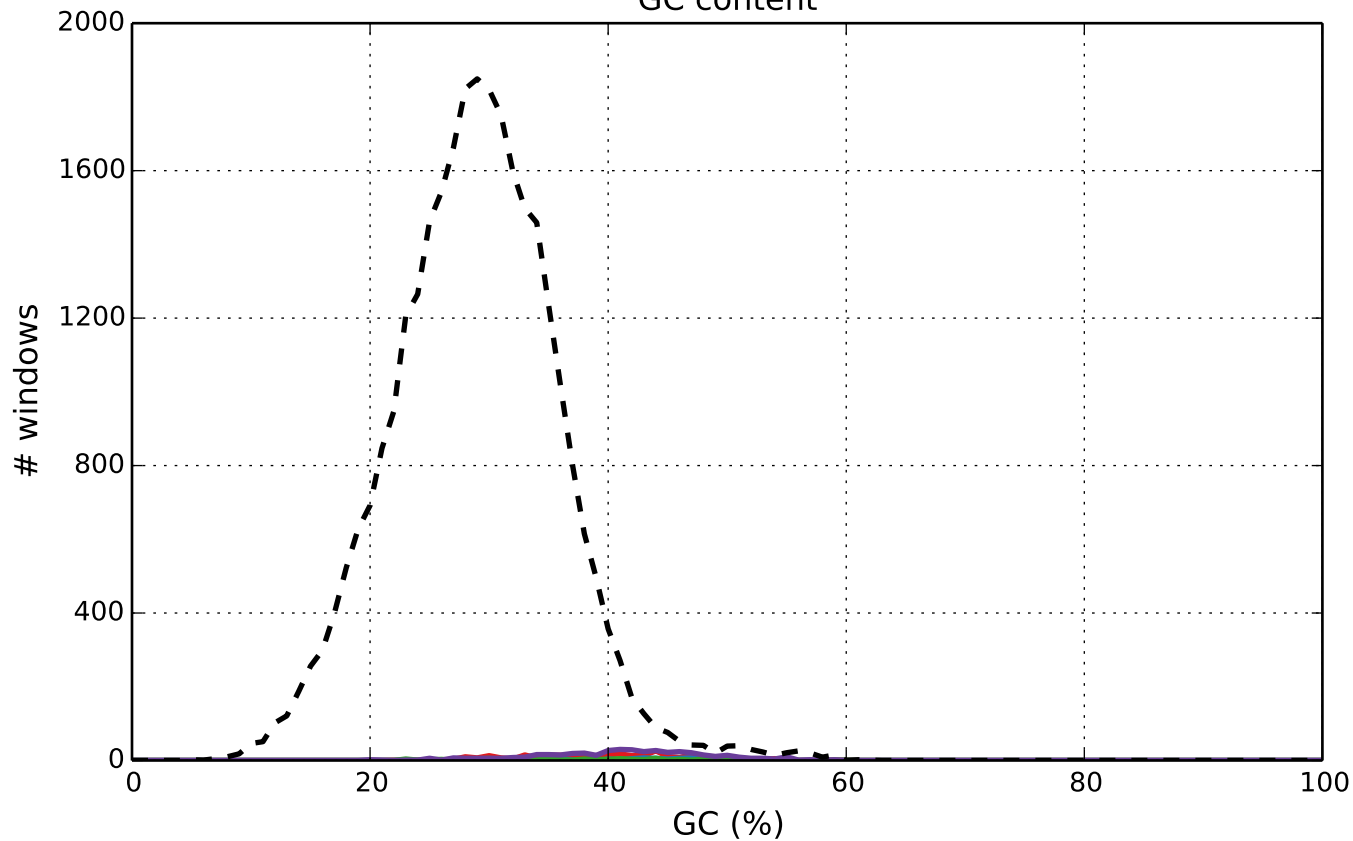
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

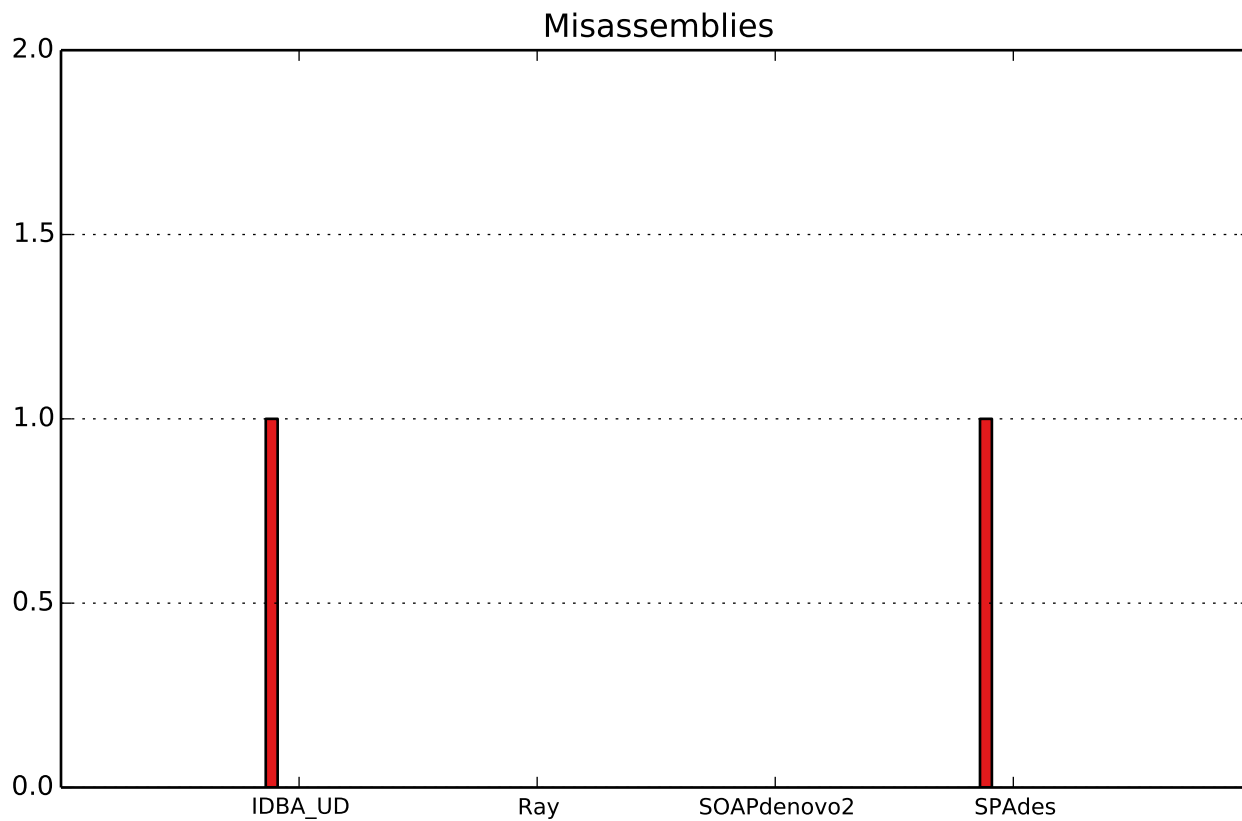






GC content

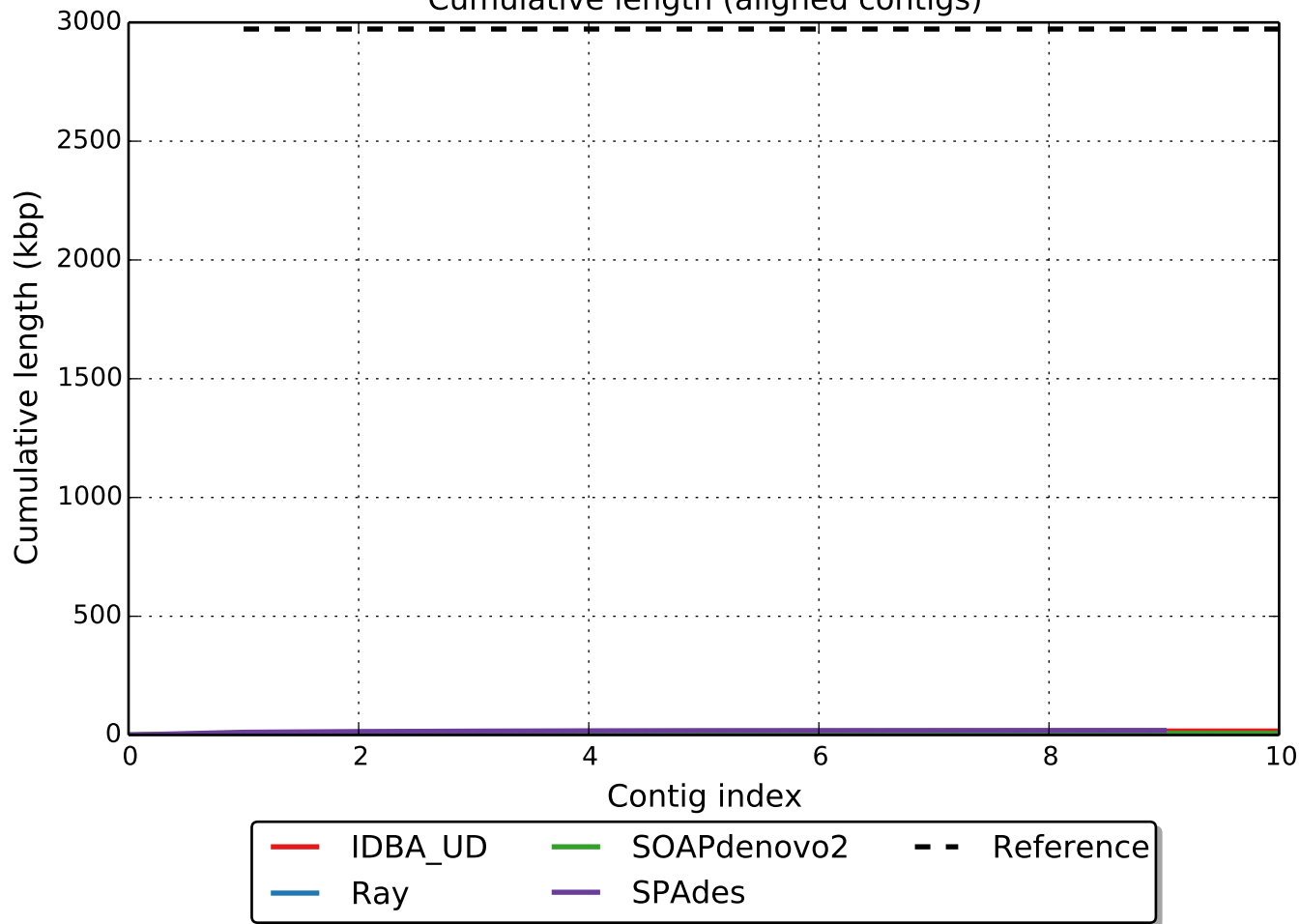


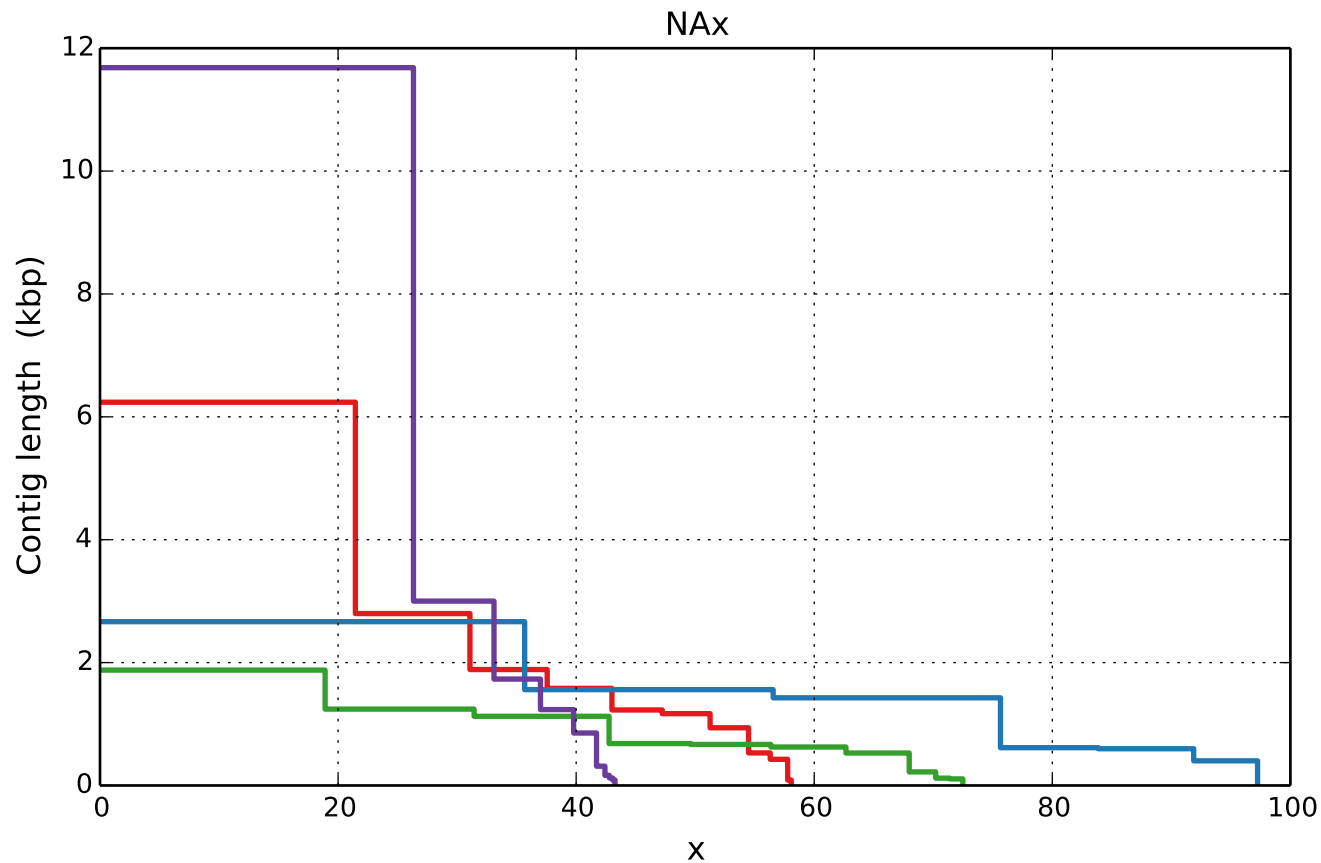


 # relocations



Cumulative length (aligned contigs)





IDBA\_UD    SOAPdenovo2    SPAdes  
Ray

