

# Report

|                             | IDBA_UD     | Ray        | SOAPdenovo2 | SPAdes      |
|-----------------------------|-------------|------------|-------------|-------------|
| # contigs (>= 1000 bp)      | 296         | 11         | 8           | 273         |
| # contigs (>= 5000 bp)      | 10          | 0          | 0           | 17          |
| # contigs (>= 10000 bp)     | 4           | 0          | 0           | 6           |
| # contigs (>= 25000 bp)     | 2           | 0          | 0           | 3           |
| # contigs (>= 50000 bp)     | 2           | 0          | 0           | 0           |
| Total length (>= 1000 bp)   | 745928      | 21053      | 15507       | 667301      |
| Total length (>= 5000 bp)   | 258717      | 0          | 0           | 206614      |
| Total length (>= 10000 bp)  | 219953      | 0          | 0           | 136311      |
| Total length (>= 25000 bp)  | 189402      | 0          | 0           | 87373       |
| Total length (>= 50000 bp)  | 189402      | 0          | 0           | 0           |
| # contigs                   | 715         | 23         | 77          | 545         |
| Largest contig              | 132307      | 3350       | 4208        | 32408       |
| Total length                | 1052207     | 28762      | 60047       | 862767      |
| Reference length            | 3142181     | 3142181    | 3142181     | 3142181     |
| GC (%)                      | 39.37       | 39.19      | 38.99       | 38.76       |
| Reference GC (%)            | 37.20       | 37.20      | 37.20       | 37.20       |
| N50                         | 1662        | 1560       | 704         | 1855        |
| N75                         | 923         | 754        | 594         | 1063        |
| L50                         | 123         | 7          | 27          | 96          |
| L75                         | 341         | 12         | 50          | 254         |
| # misassemblies             | 2           | 0          | 1           | 2           |
| # misassembled contigs      | 2           | 0          | 1           | 2           |
| Misassembled contigs length | 2975        | 0          | 981         | 6496        |
| # local misassemblies       | 2           | 2          | 3           | 4           |
| # structural variations     | 0           | 0          | 0           | 0           |
| # unaligned contigs         | 0 + 36 part | 0 + 3 part | 0 + 3 part  | 0 + 61 part |
| Unaligned length            | 237225      | 2250       | 1458        | 195454      |
| Genome fraction (%)         | 25.775      | 0.800      | 1.855       | 20.921      |
| Duplication ratio           | 1.006       | 1.055      | 1.005       | 1.015       |
| # N's per 100 kbp           | 108.53      | 876.16     | 343.06      | 613.72      |
| # mismatches per 100 kbp    | 999.90      | 1535.46    | 1305.88     | 1076.41     |
| # indels per 100 kbp        | 40.62       | 23.87      | 6.86        | 70.58       |
| Largest alignment           | 8418        | 3348       | 4205        | 6902        |
| NA50                        | 954         | 1358       | 699         | 1055        |
| NGA50                       | -           | -          | -           | -           |
| NA75                        | 539         | 604        | 573         | 508         |
| LA50                        | 310         | 8          | 27          | 226         |
| LA75                        | 669         | 16         | 51          | 516         |

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

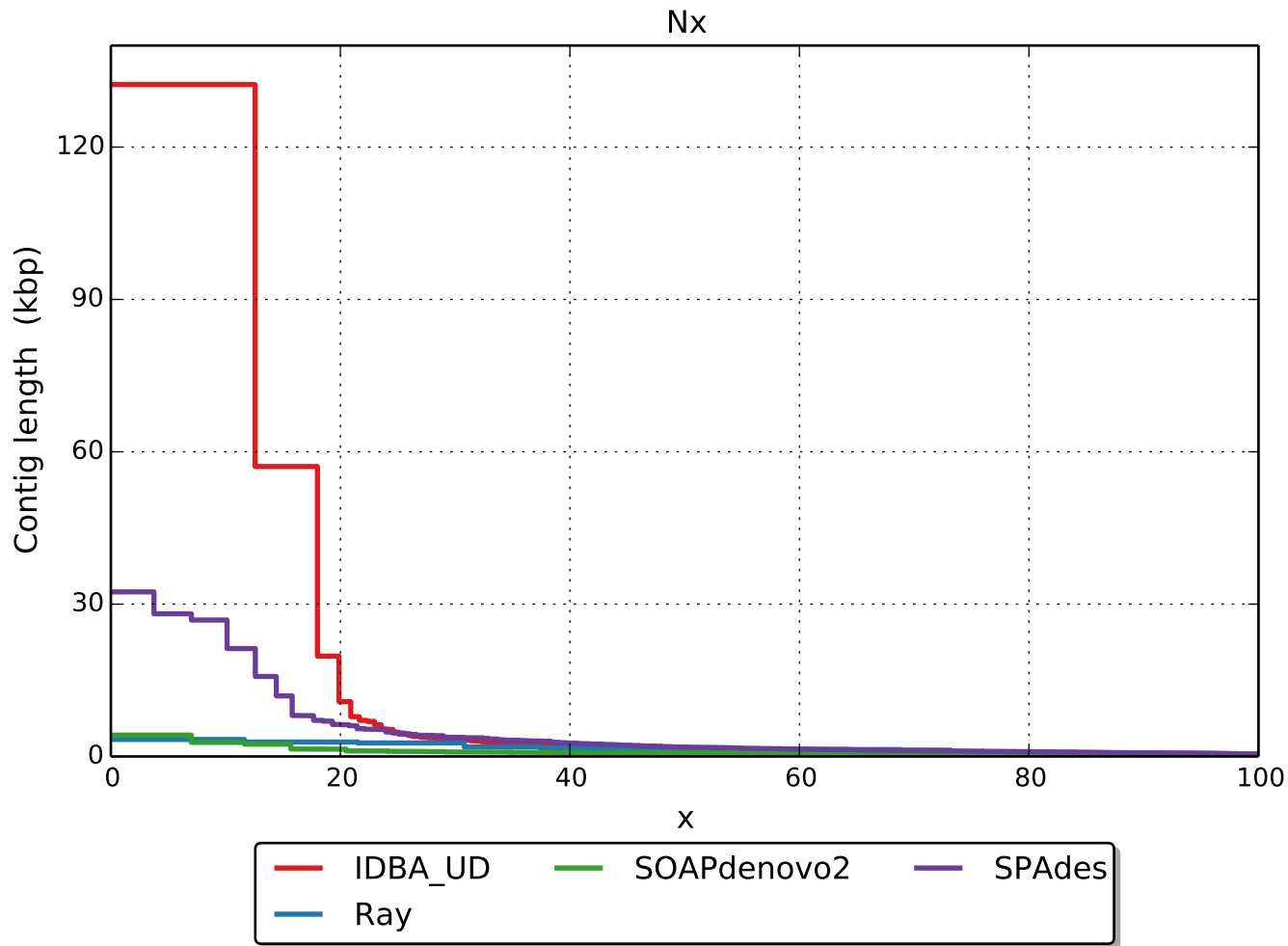
|                                 | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|---------------------------------|---------|-----|-------------|--------|
| # misassemblies                 | 2       | 0   | 1           | 2      |
| # relocations                   | 2       | 0   | 1           | 2      |
| # translocations                | 0       | 0   | 0           | 0      |
| # inversions                    | 0       | 0   | 0           | 0      |
| # possibly misassembled contigs | 11      | 1   | 0           | 29     |
| # misassembled contigs          | 2       | 0   | 1           | 2      |
| Misassembled contigs length     | 2975    | 0   | 981         | 6496   |
| # local misassemblies           | 2       | 2   | 3           | 4      |
| # structural variations         | 0       | 0   | 0           | 0      |
| # mismatches                    | 8098    | 386 | 761         | 7076   |
| # indels                        | 329     | 6   | 4           | 464    |
| # short indels                  | 272     | 6   | 4           | 340    |
| # long indels                   | 57      | 0   | 0           | 124    |
| Indels length                   | 1132    | 7   | 4           | 2046   |

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).

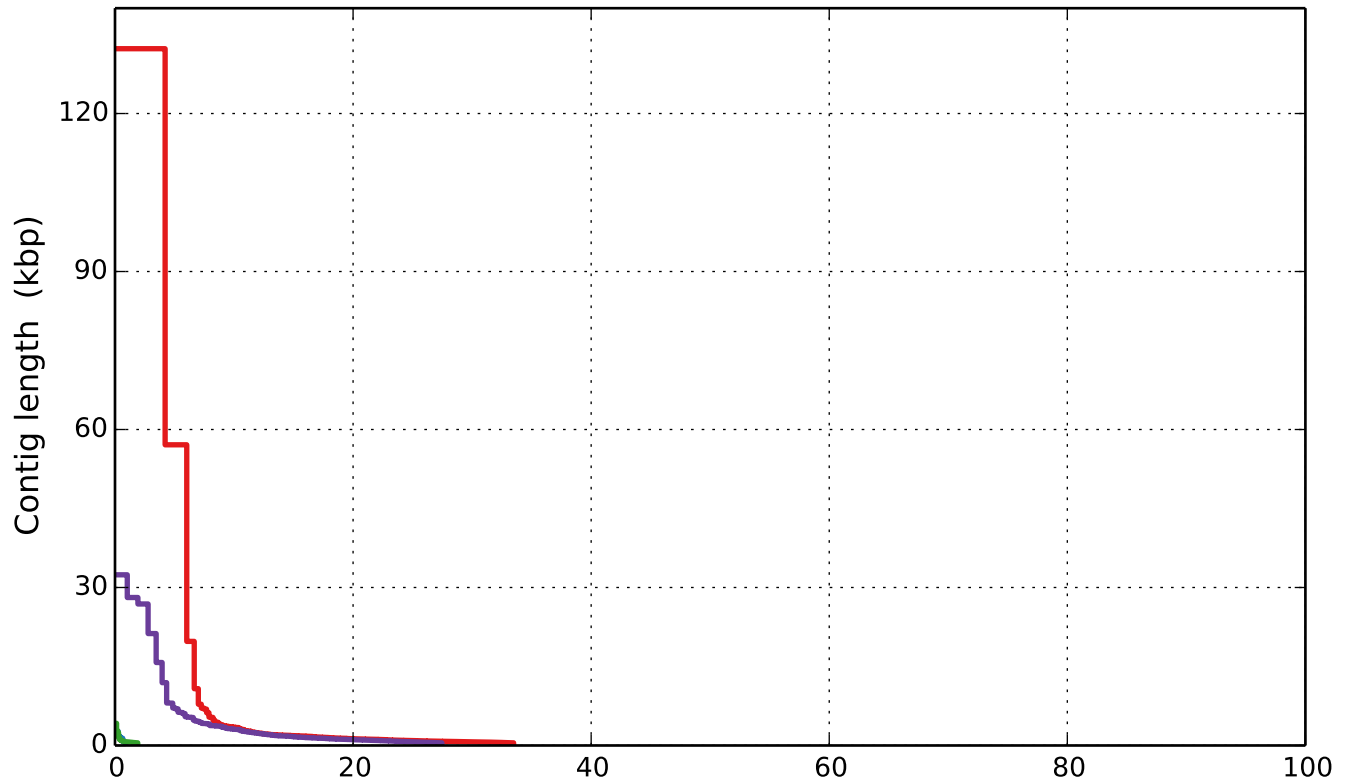
## Unaligned report

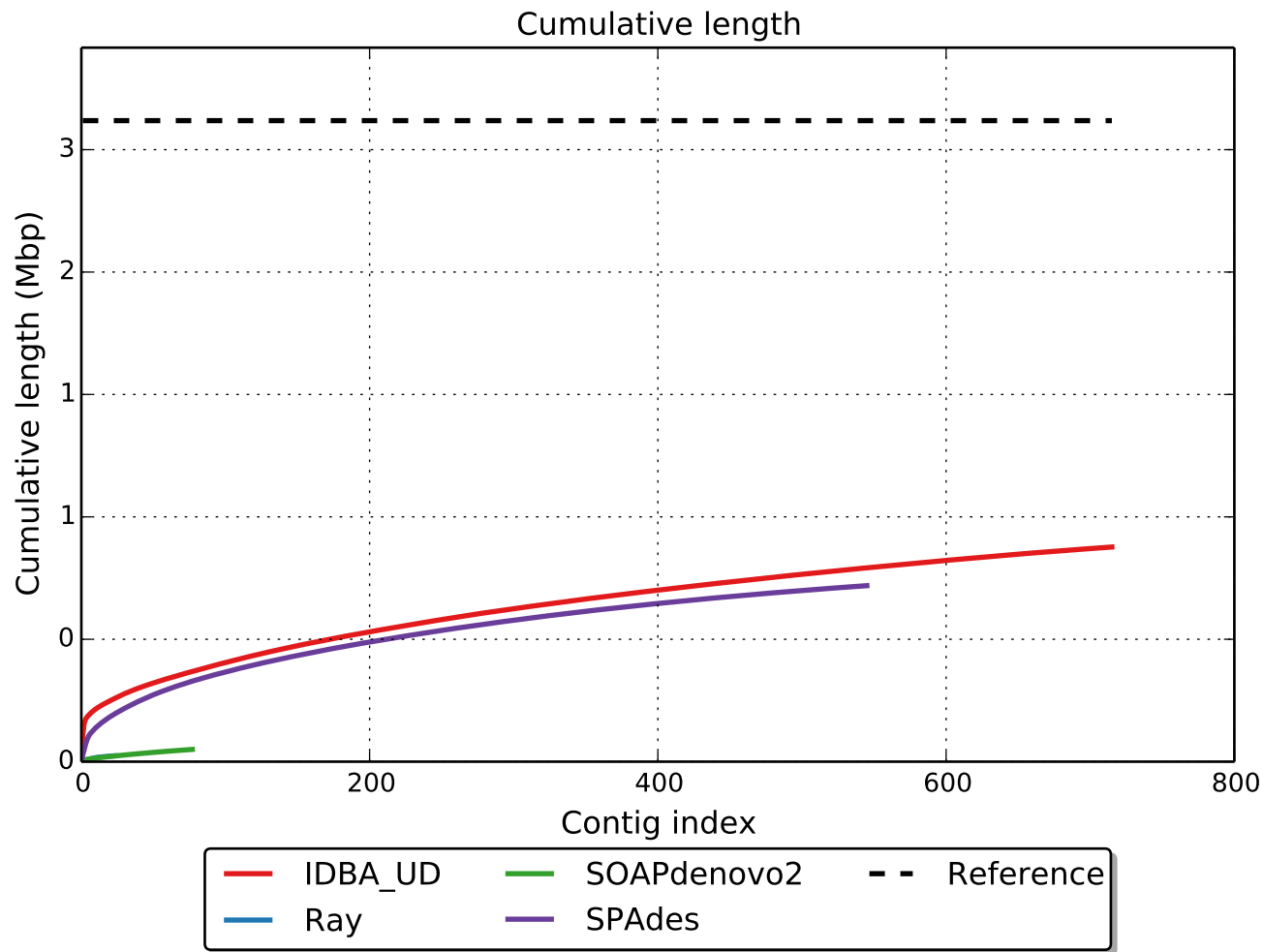
|                               | IDBA_UD | Ray  | SOAPdenovo2 | SPAdes |
|-------------------------------|---------|------|-------------|--------|
| # fully unaligned contigs     | 0       | 0    | 0           | 0      |
| Fully unaligned length        | 0       | 0    | 0           | 0      |
| # partially unaligned contigs | 36      | 3    | 3           | 61     |
| # with misassembly            | 1       | 1    | 0           | 5      |
| # both parts are significant  | 10      | 0    | 0           | 23     |
| Partially unaligned length    | 237225  | 2250 | 1458        | 195454 |
| # N's                         | 1142    | 252  | 206         | 5295   |

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).

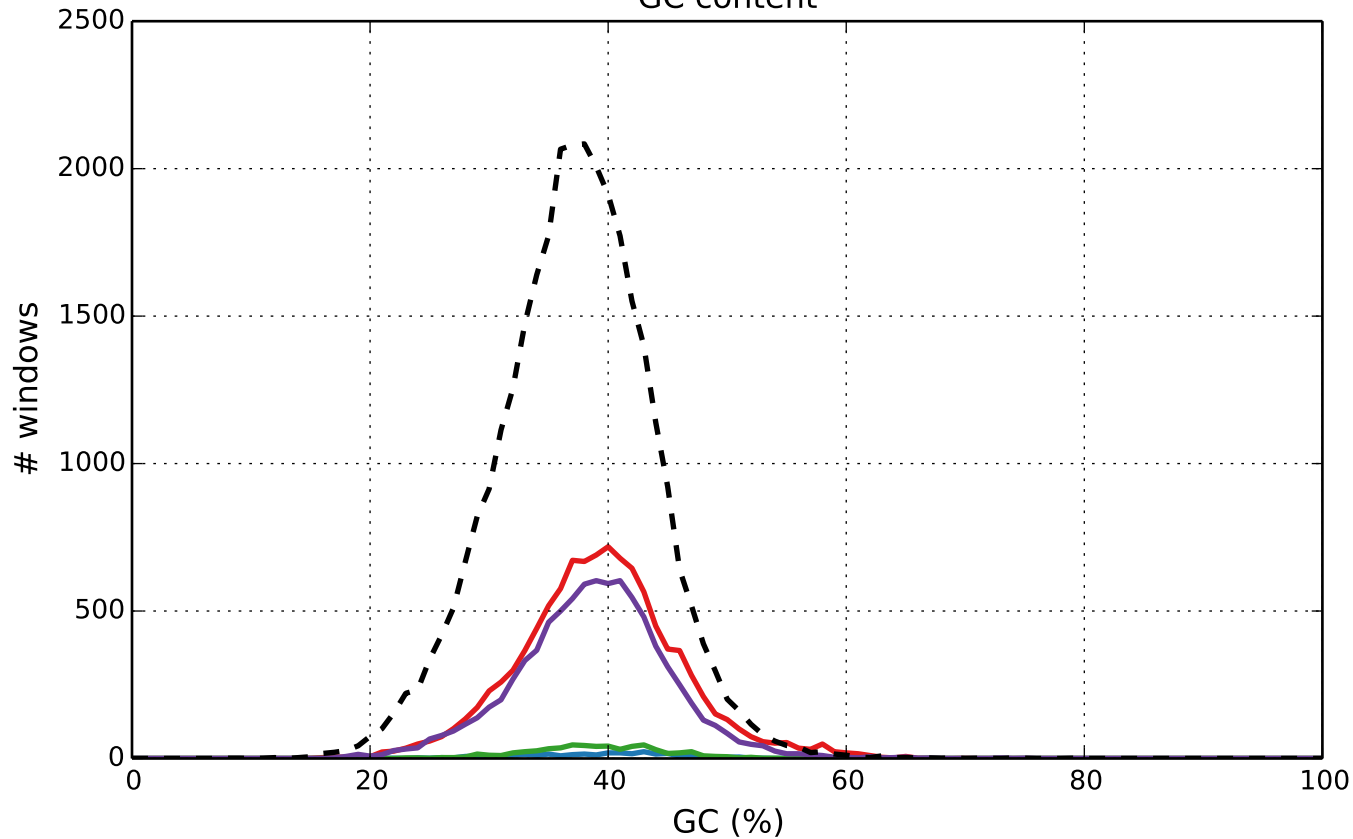


NGx

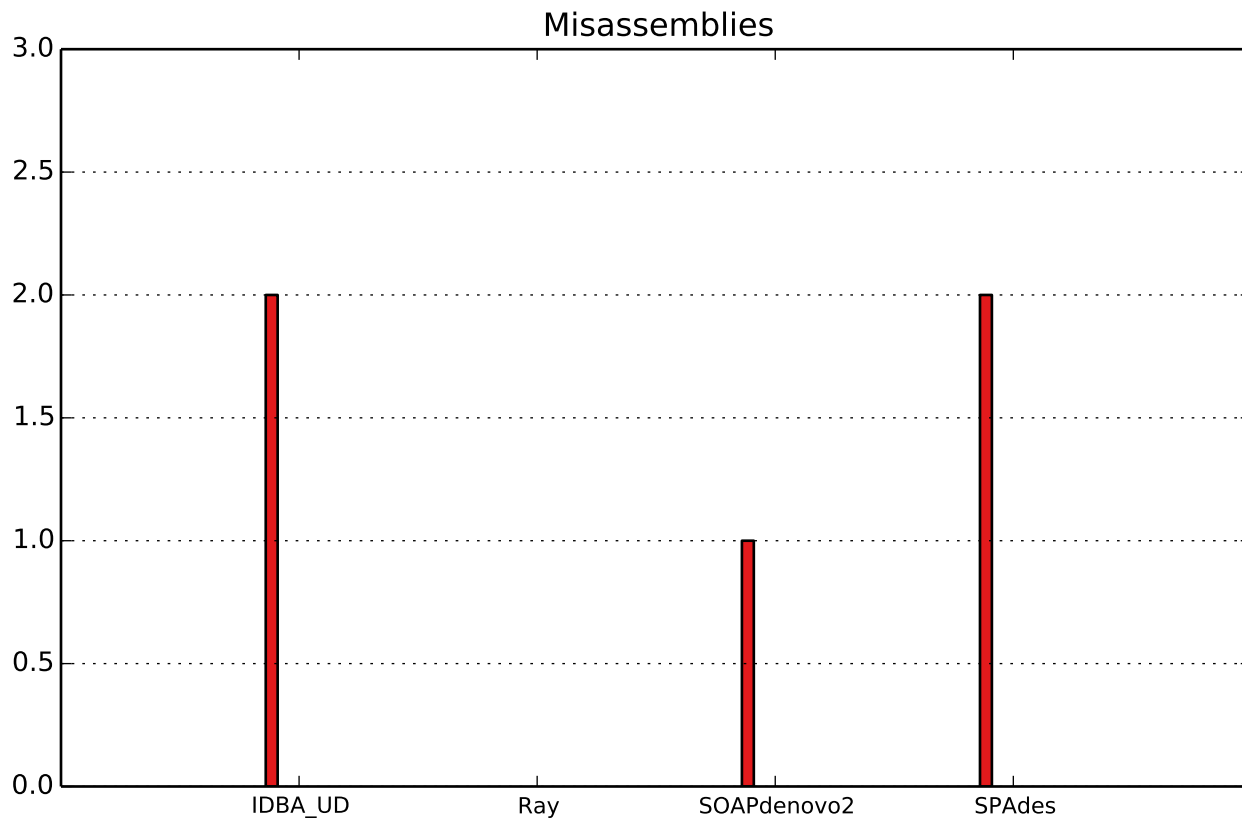




GC content

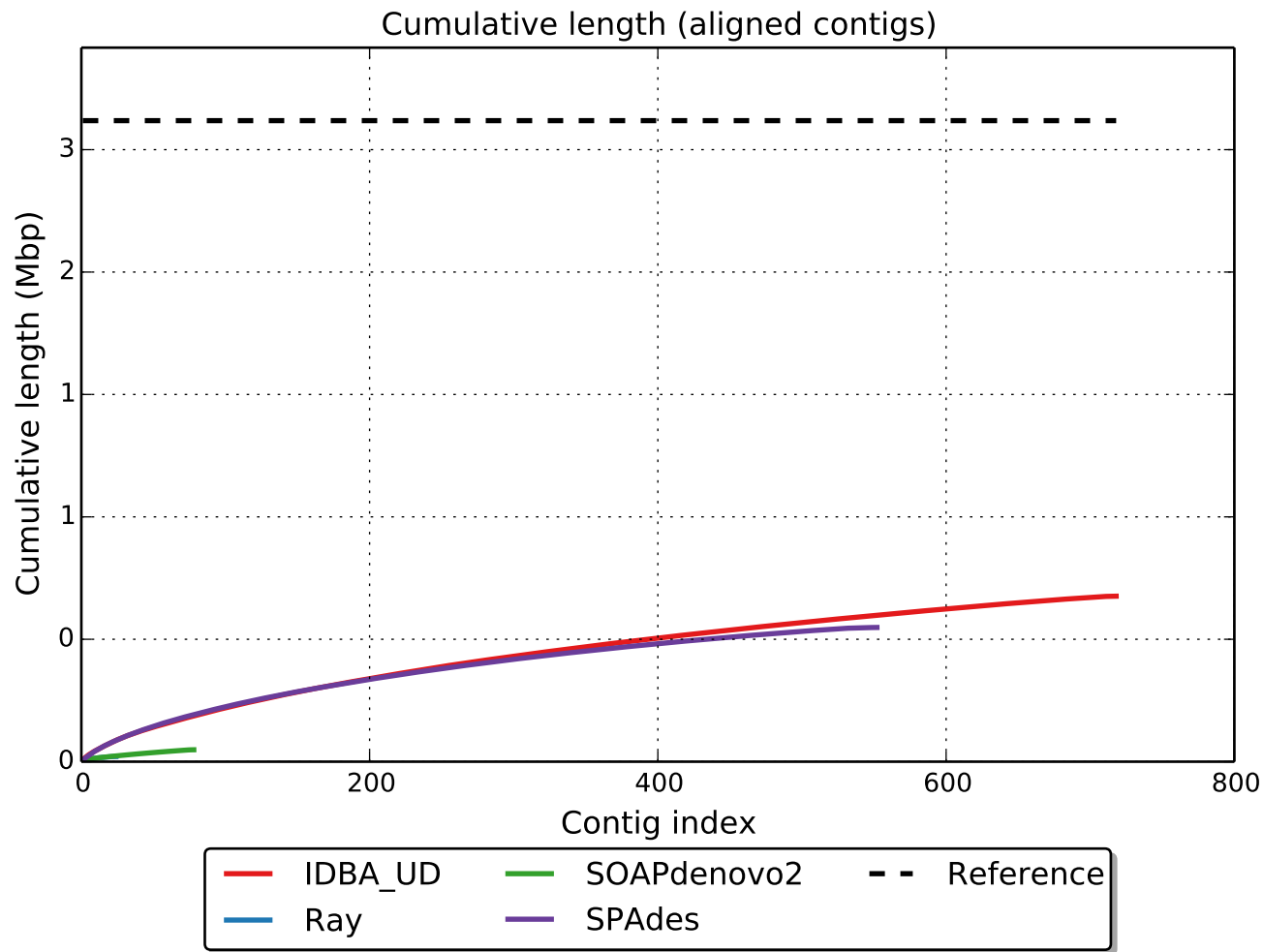


|         |             |           |
|---------|-------------|-----------|
| IDBA_UD | SOAPdenovo2 | Reference |
| Ray     | SPAdes      |           |

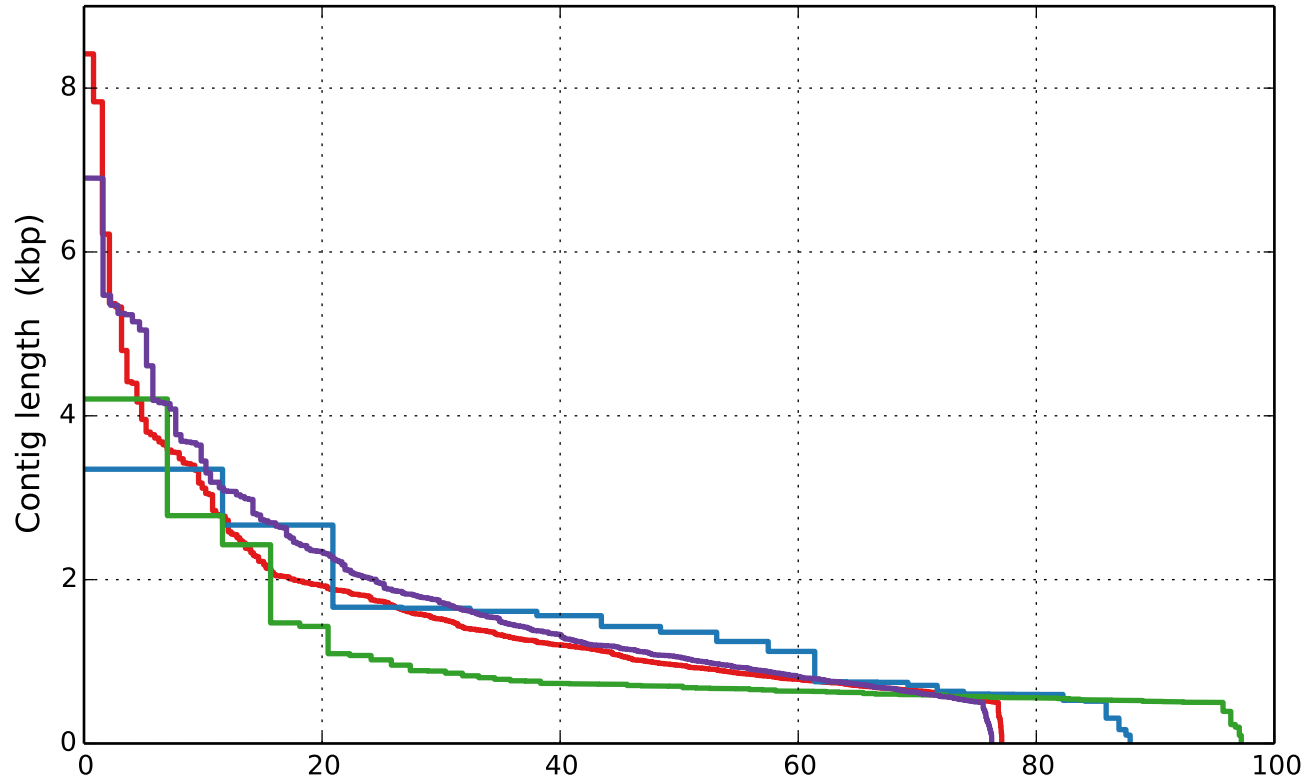


 # relocations





NAx



# NGAx

