# Report

| | Gold_Assembly | IDBA_UD | SOAPdenovo2 | SPAdes |
|---|---|---|---|---|
| # contigs (>= 1000 bp) | 428 | 62 | 1 | 70 |
| # contigs (>= 5000 bp) | 0 | 5 | 0 | 13 |
| # contigs (>= 10000 bp) | 0 | 1 | 0 | 6 |
| # contigs (>= 25000 bp) | 0 | 0 | 0 | 1 |
| # contigs (>= 50000 bp) | 0 | 0 | 0 | 0 |
| Total length (>= 1000 bp) | 582539 | 129353 | 1067 | 265613 |
| Total length (>= 5000 bp) | 0 | 43314 | 0 | 167272 |
| Total length (>= 10000 bp) | 0 | 17646 | 0 | 119842 |
| Total length (>= 25000 bp) | 0 | 0 | 0 | 30167 |
| Total length (>= 50000 bp) | 0 | 0 | 0 | 0 |
| # contigs | 1769 | 481 | 26 | 619 |
| Largest contig | 3535 | 17646 | 1067 | 30167 |
| Total length | 1516561 | 403578 | 15719 | 615390 |
| Reference length | 4675770 | 4675770 | 4675770 | 4675770 |
| GC (%) | 69.37 | 67.81 | 66.83 | 68.76 |
| Reference GC (%) | 68.94 | 68.94 | 68.94 | 68.94 |
| N50 | 870 | 773 | 579 | 833 |
| N75 | 669 | 603 | 527 | 610 |
| L50 | 616 | 146 | 12 | 117 |
| L75 | 1114 | 297 | 19 | 339 |
| # misassemblies | 0 | 22 | 1 | 17 |
| # misassembled contigs | 0 | 21 | 1 | 17 |
| Misassembled contigs length | 0 | 16565 | 814 | 12126 |
| # local misassemblies | 1 | 0 | 0 | 0 |
| # structural variations | 0 | 0 | 0 | 0 |
| # unaligned contigs | 0 + 40 part | 0 + 177 part | 0 + 0 part | 0 + 214 part |
| Unaligned length | 16388 | 131193 | 0 | 264155 |
| Genome fraction (%) | 31.993 | 5.812 | 0.334 | 7.484 |
| Duplication ratio | 1.003 | 1.002 | 1.008 | 1.004 |
| # N's per 100 kbp | 0.00 | 0.00 | 38.17 | 0.00 |
| # mismatches per 100 kbp | 1771.03 | 2034.81 | 1922.95 | 2696.49 |
| # indels per 100 kbp | 23.13 | 27.96 | 44.87 | 32.01 |
| Largest alignment | 3535 | 1275 | 1067 | 1594 |
| NA50 | 859 | 525 | 576 | 472 |
| NGA50 | - | - | - | - |
| NA75 | 661 | - | 527 | - |
| LA50 | 625 | 301 | 12 | 484 |
| LA75 | 1128 | - | 19 | - |

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).
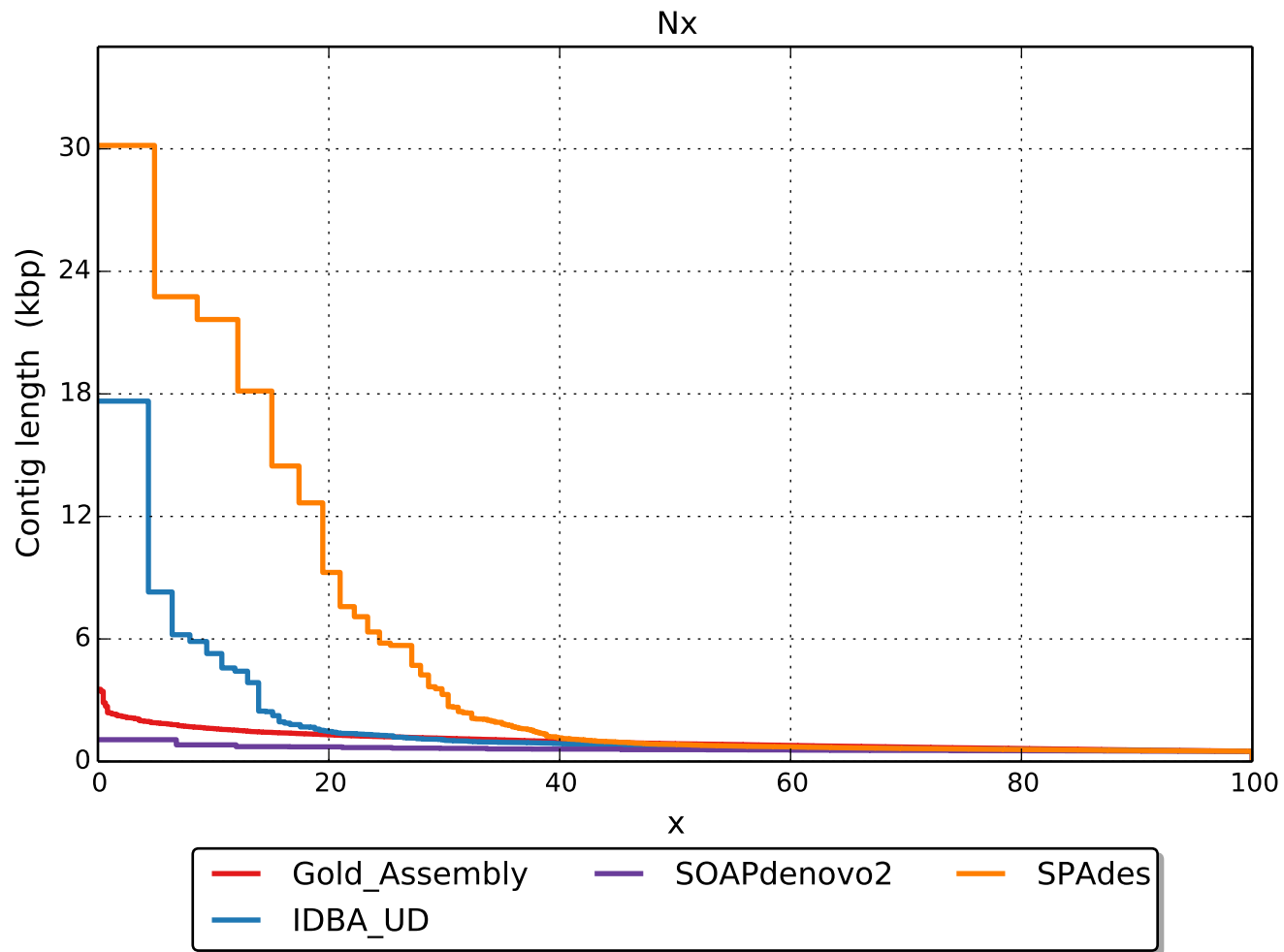
# Misassemblies report

| | Gold_Assembly | IDBA_UD | SOAPdenovo2 | SPAdes |
|---|---|---|---|---|
| # misassemblies | 0 | 22 | 1 | 17 |
| # relocations | 0 | 4 | 0 | 1 |
| # translocations | 0 | 18 | 1 | 16 |
| # inversions | 0 | 0 | 0 | 0 |
| # possibly misassembled contigs | 4 | 8 | 0 | 8 |
| # misassembled contigs | 0 | 21 | 1 | 17 |
| Misassembled contigs length | 0 | 16565 | 814 | 12126 |
| # local misassemblies | 1 | 0 | 0 | 0 |
| # structural variations | 0 | 0 | 0 | 0 |
| # mismatches | 26493 | 5530 | 300 | 9436 |
| # indels | 346 | 76 | 7 | 112 |
| # short indels | 319 | 74 | 6 | 108 |
| # long indels | 27 | 2 | 1 | 4 |
| Indels length | 661 | 99 | 23 | 161 |

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).
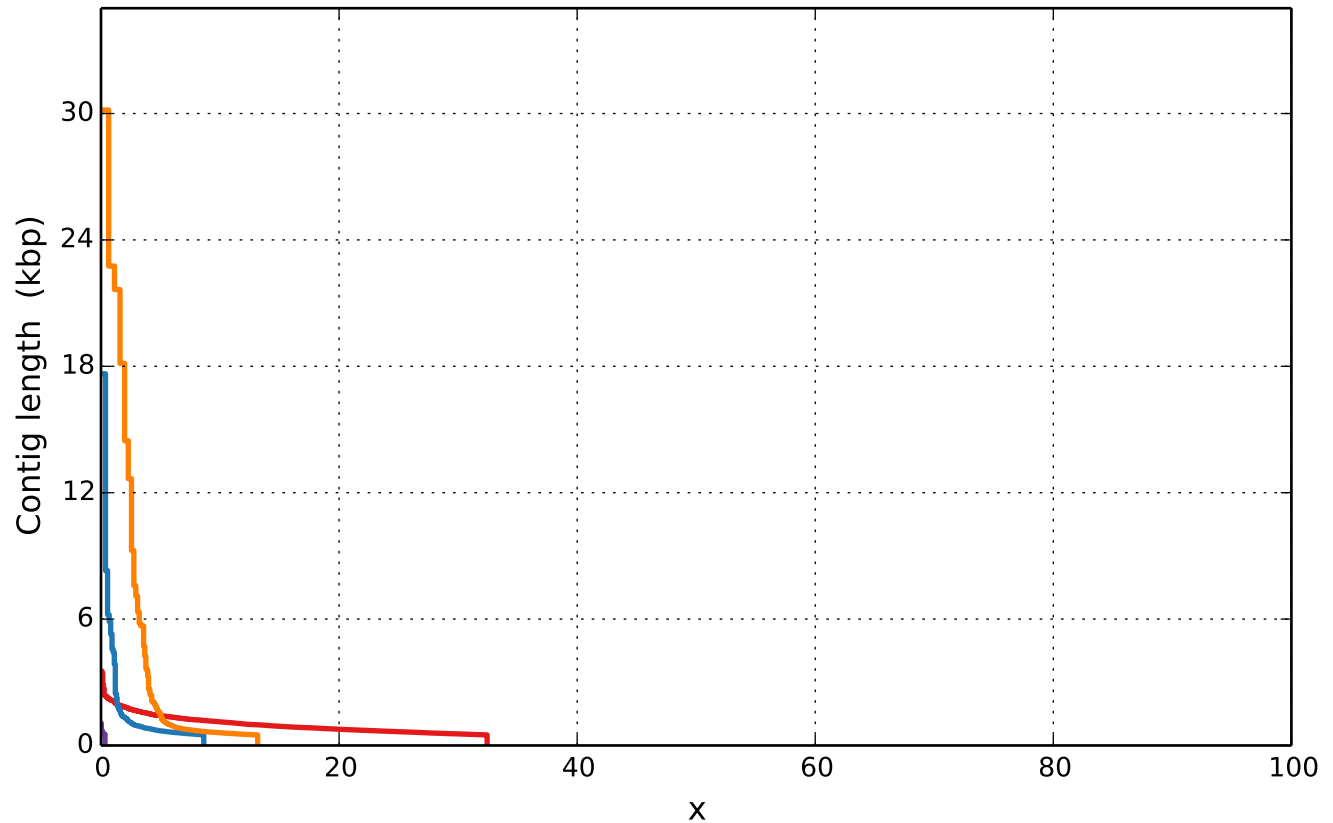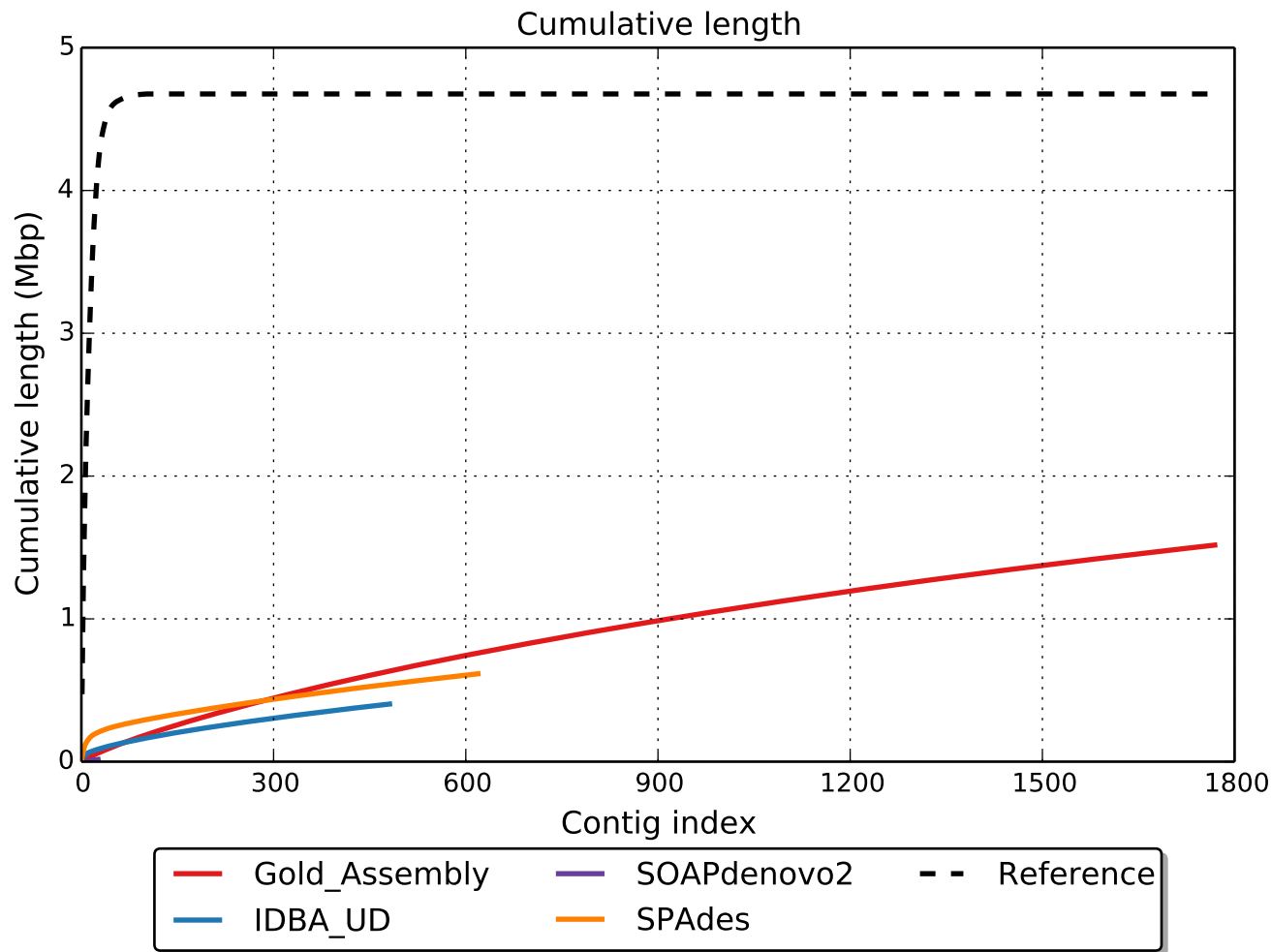
# Unaligned report

|  | Gold_Assembly | IDBA_UD | SOAPdenovo2 | SPAdes |
|---|---|---|---|---|
| # fully unaligned contigs | 0 | 0 | 0 | 0 |
| Fully unaligned length | 0 | 0 | 0 | 0 |
| # partially unaligned contigs | 40 | 177 | 0 | 214 |
| # with misassembly | 1 | 0 | 0 | 0 |
| # both parts are significant | 4 | 8 | 0 | 8 |
| Partially unaligned length | 16388 | 131193 | 0 | 264155 |
| # N's | 0 | 0 | 6 | 0 |

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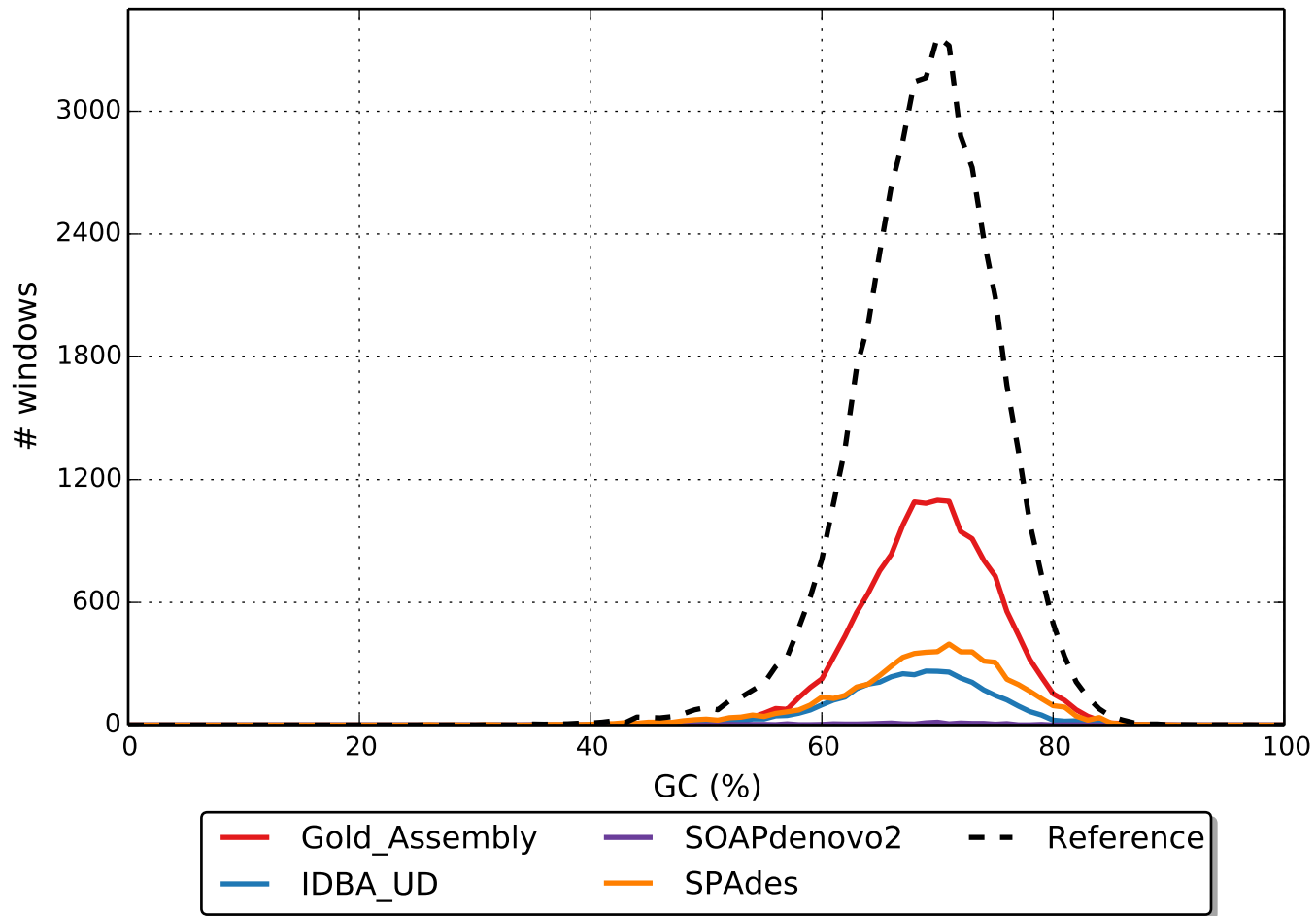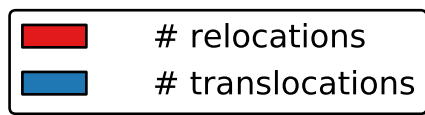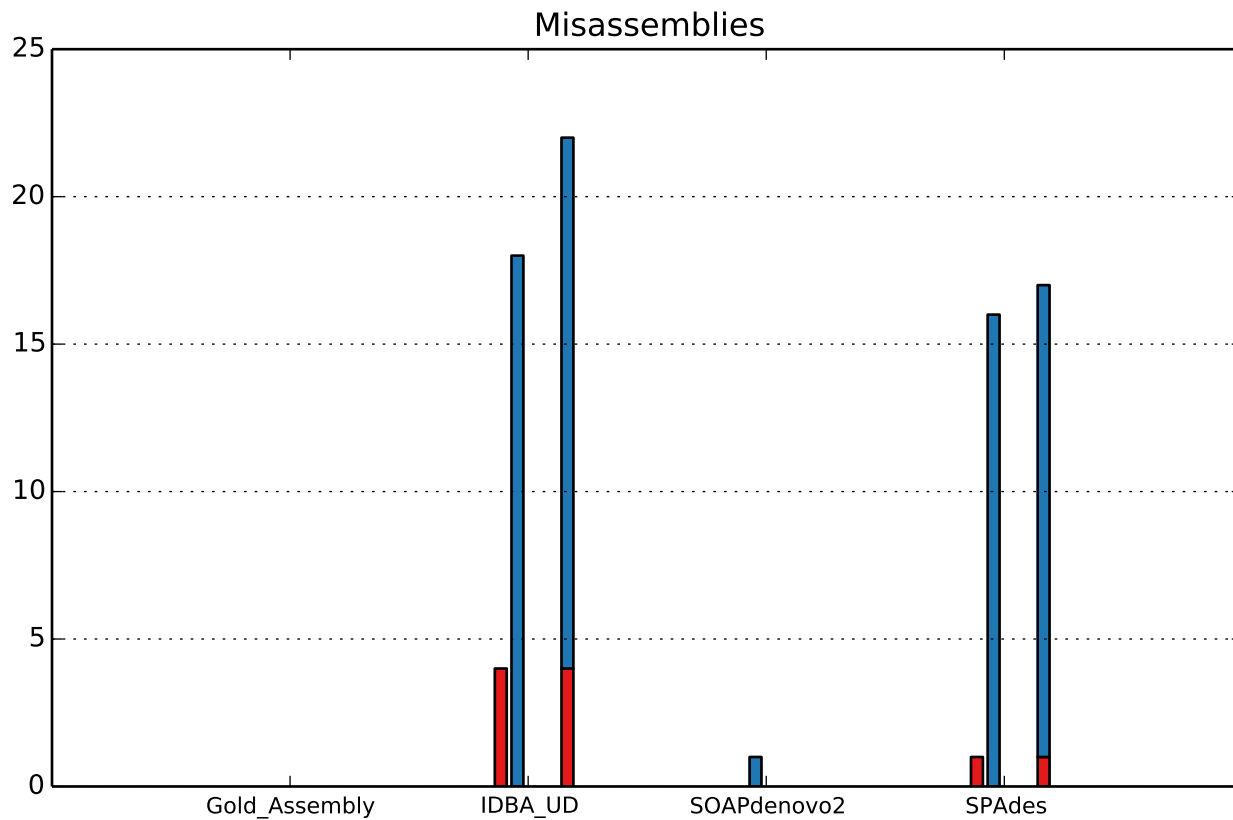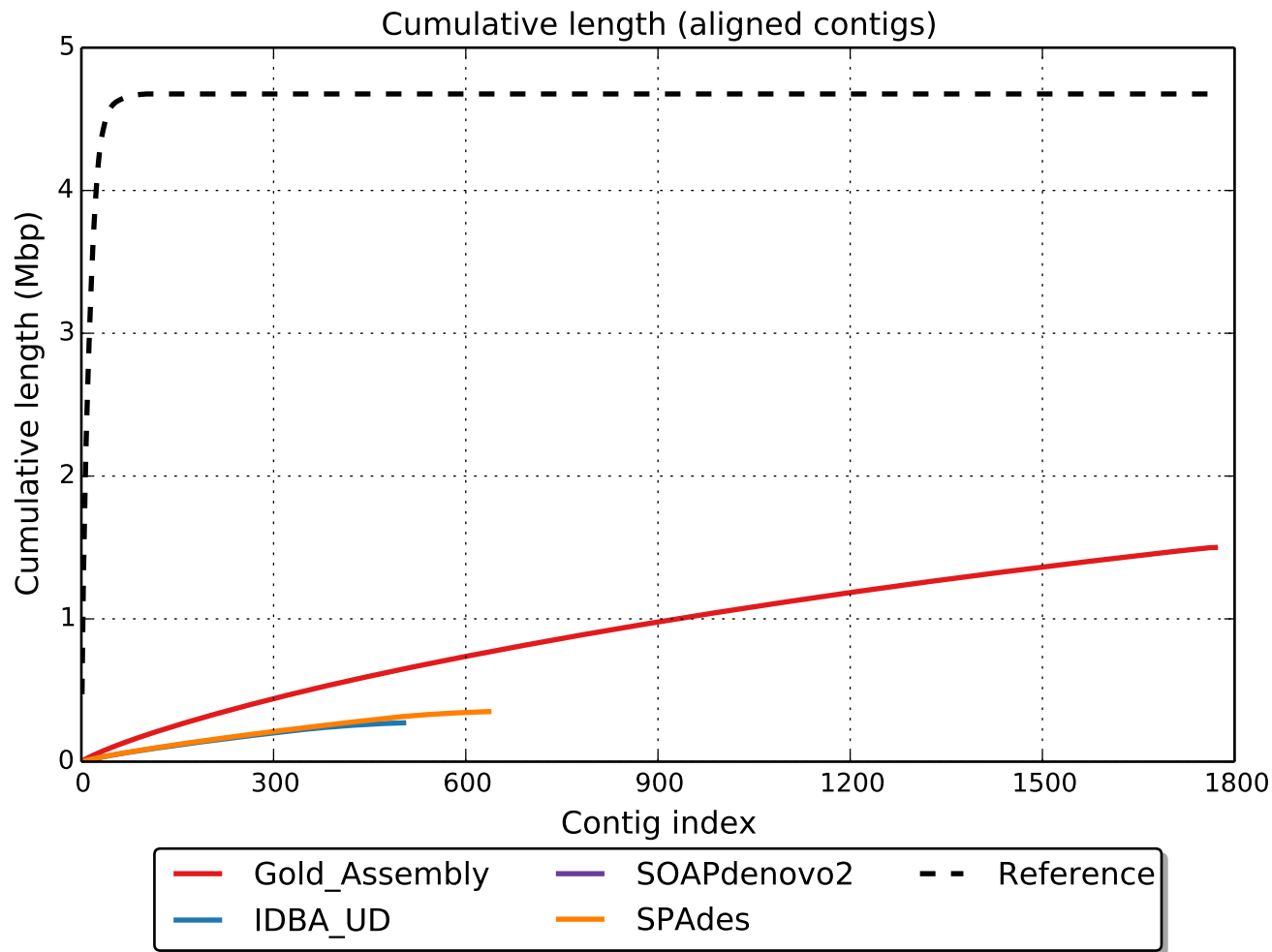(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Contig length (kbp)

x

Gold_Assembly    SOAPdenovo2    SPAdes
IDBA_UD

NGx

**Cumulative length**

Cumulative length (Mbp) vs Contig index

Legend:
- Gold_Assembly
- IDBA_UD
- SOAPdenovo2
- SPAdes
- Reference

GC content

Misassemblies

Cumulative length (aligned contigs)

NAx

Contig length  (kbp)

x

Gold_Assembly    SOAPdenovo2    SPAdes

IDBA_UD

NGAx

Genome fraction, %