# Report

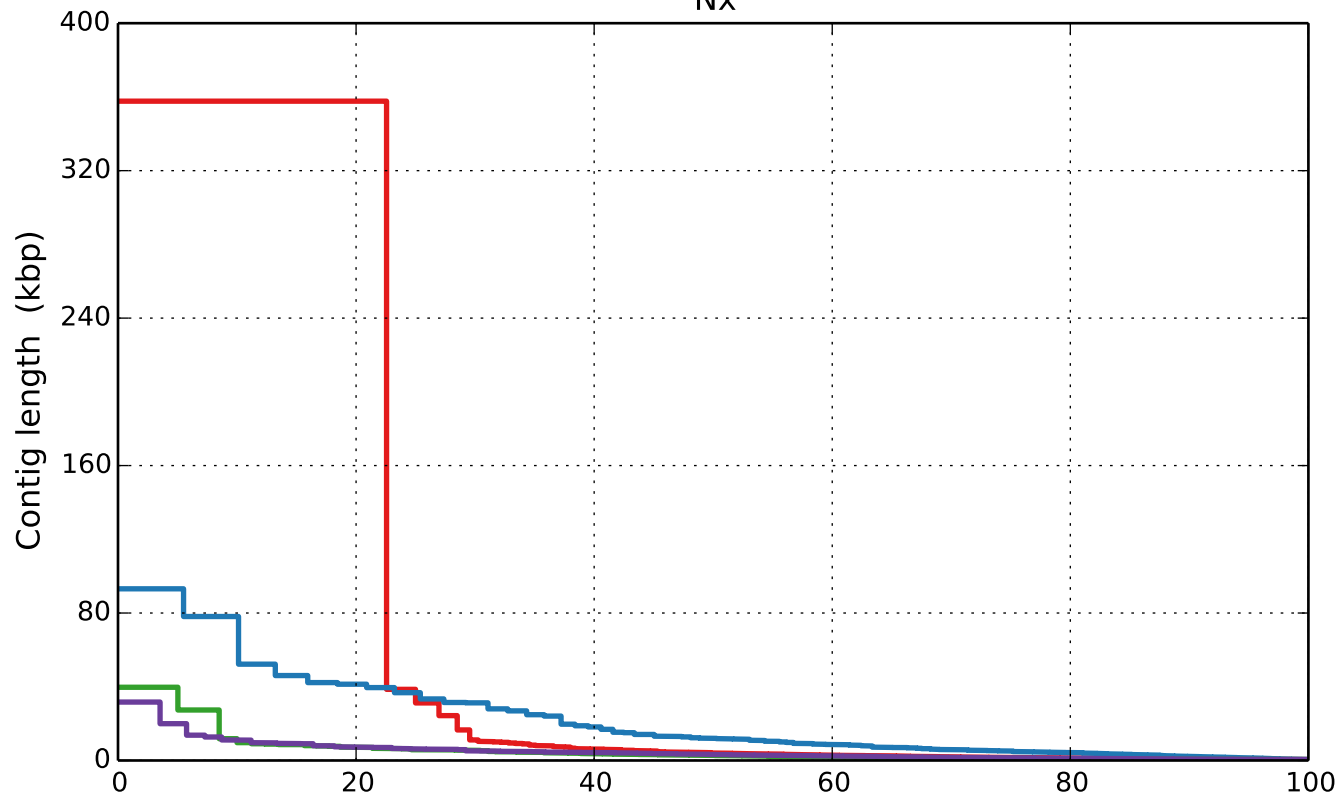| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|---|---|---|---|---|
| # contigs (>= 1000 bp) | 365 | 234 | 210 | 247 |
| # contigs (>= 5000 bp) | 40 | 86 | 27 | 33 |
| # contigs (>= 10000 bp) | 9 | 39 | 3 | 6 |
| # contigs (>= 25000 bp) | 3 | 13 | 2 | 1 |
| # contigs (>= 50000 bp) | 1 | 3 | 0 | 0 |
| Total length (>= 1000 bp) | 1381962 | 1640676 | 615724 | 755834 |
| Total length (>= 5000 bp) | 718350 | 1271452 | 245594 | 287626 |
| Total length (>= 10000 bp) | 510194 | 949577 | 78922 | 100276 |
| Total length (>= 25000 bp) | 427504 | 580548 | 67107 | 31690 |
| Total length (>= 50000 bp) | 357694 | 223488 | 0 | 0 |
| # contigs | 661 | 306 | 460 | 444 |
| Largest contig | 357694 | 93136 | 39722 | 31690 |
| Total length | 1585481 | 1691178 | 789550 | 896703 |
| Reference length | 2118767 | 2118767 | 2118767 | 2118767 |
| GC (%) | 37.89 | 38.35 | 38.08 | 38.03 |
| Reference GC (%) | 38.86 | 38.86 | 38.86 | 38.86 |
| N50 | 4054 | 11998 | 2743 | 3256 |
| NG50 | 2239 | 7989 | - | - |
| N75 | 1621 | 5111 | 1088 | 1434 |
| NG75 | - | 1563 | - | - |
| L50 | 57 | 30 | 69 | 73 |
| LG50 | 146 | 52 | - | - |
| L75 | 215 | 86 | 188 | 177 |
| LG75 | - | 194 | - | - |
| # misassemblies | 12 | 17 | 3 | 7 |
| # misassembled contigs | 7 | 13 | 2 | 7 |
| Misassembled contigs length | 13622 | 132113 | 5007 | 23398 |
| # local misassemblies | 20 | 44 | 16 | 7 |
| # structural variations | 0 | 1 | 0 | 0 |
| # unaligned contigs | 0 + 238 part | 0 + 128 part | 0 + 262 part | 0 + 144 part |
| Unaligned length | 842364 | 984116 | 503622 | 283596 |
| Genome fraction (%) | 31.768 | 27.465 | 12.637 | 27.233 |
| Duplication ratio | 1.104 | 1.215 | 1.068 | 1.063 |
| # N's per 100 kbp | 0.00 | 849.70 | 6388.58 | 267.87 |
| # mismatches per 100 kbp | 2669.36 | 2858.34 | 1914.09 | 2747.13 |
| # indels per 100 kbp | 48.14 | 81.97 | 56.40 | 57.89 |
| Largest alignment | 10215 | 23548 | 5552 | 9151 |
| NA50 | - | - | - | 987 |
| NGA50 | - | - | - | - |
| LA50 | - | - | - | 195 |

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 | 12 | 17 | 3 | 7 |
| # relocations | 4 | 12 | 2 | 4 |
| # translocations | 8 | 5 | 1 | 3 |
| # inversions | 0 | 0 | 0 | 0 |
| # possibly misassembled contigs | 65 | 92 | 55 | 57 |
| # misassembled contigs | 7 | 13 | 2 | 7 |
| Misassembled contigs length | 13622 | 132113 | 5007 | 23398 |
| # local misassemblies | 20 | 44 | 16 | 7 |
| # structural variations | 0 | 1 | 0 | 0 |
| # mismatches | 17967 | 16633 | 5125 | 15851 |
| # indels | 324 | 477 | 151 | 334 |
| # short indels | 276 | 440 | 89 | 307 |
| # long indels | 48 | 37 | 62 | 27 |
| Indels length | 1562 | 1175 | 1604 | 996 |

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

| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|---|---|---|---|---|
| # fully unaligned contigs | 0 | 0 | 0 | 0 |
| Fully unaligned length | 0 | 0 | 0 | 0 |
| # partially unaligned contigs | 238 | 128 | 262 | 144 |
| # with misassembly | 17 | 23 | 39 | 8 |
| # both parts are significant | 59 | 74 | 48 | 49 |
| Partially unaligned length | 842364 | 984116 | 503622 | 283596 |
| # N's | 0 | 14370 | 50441 | 2402 |

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).
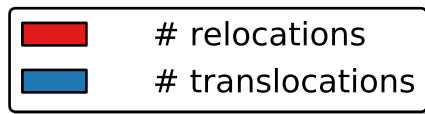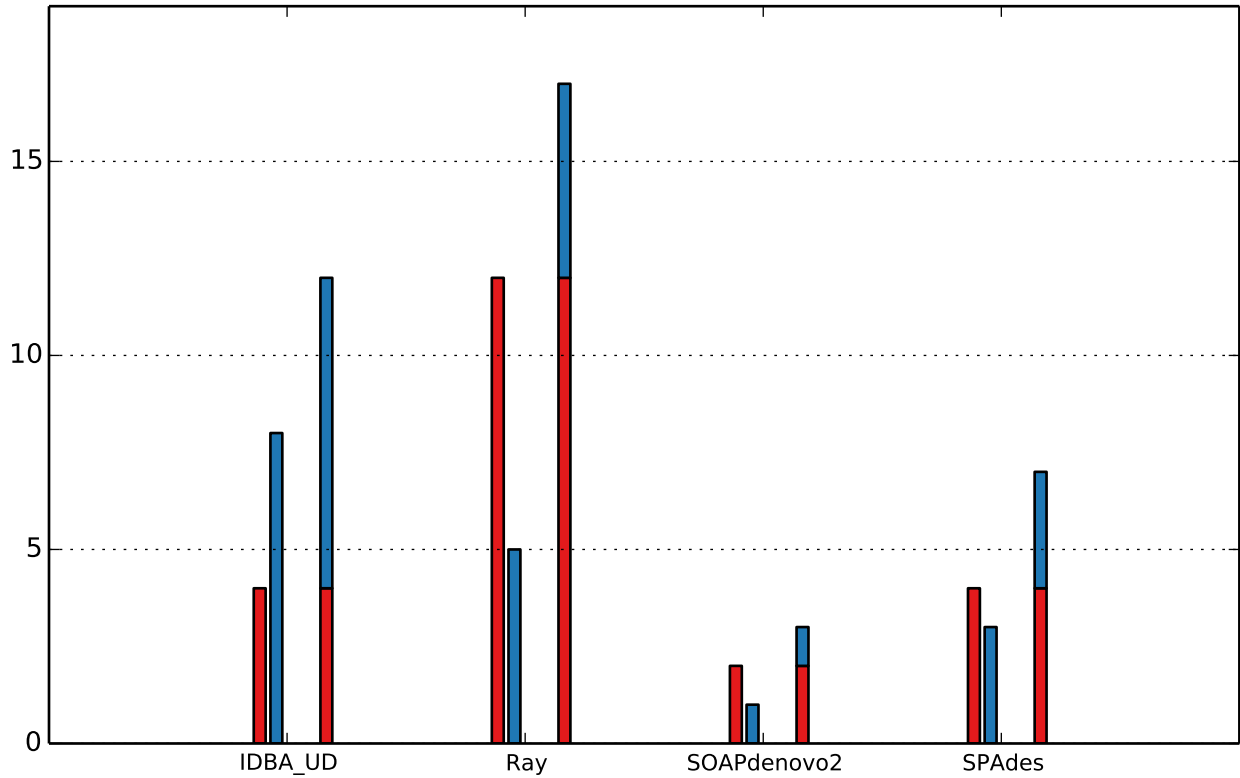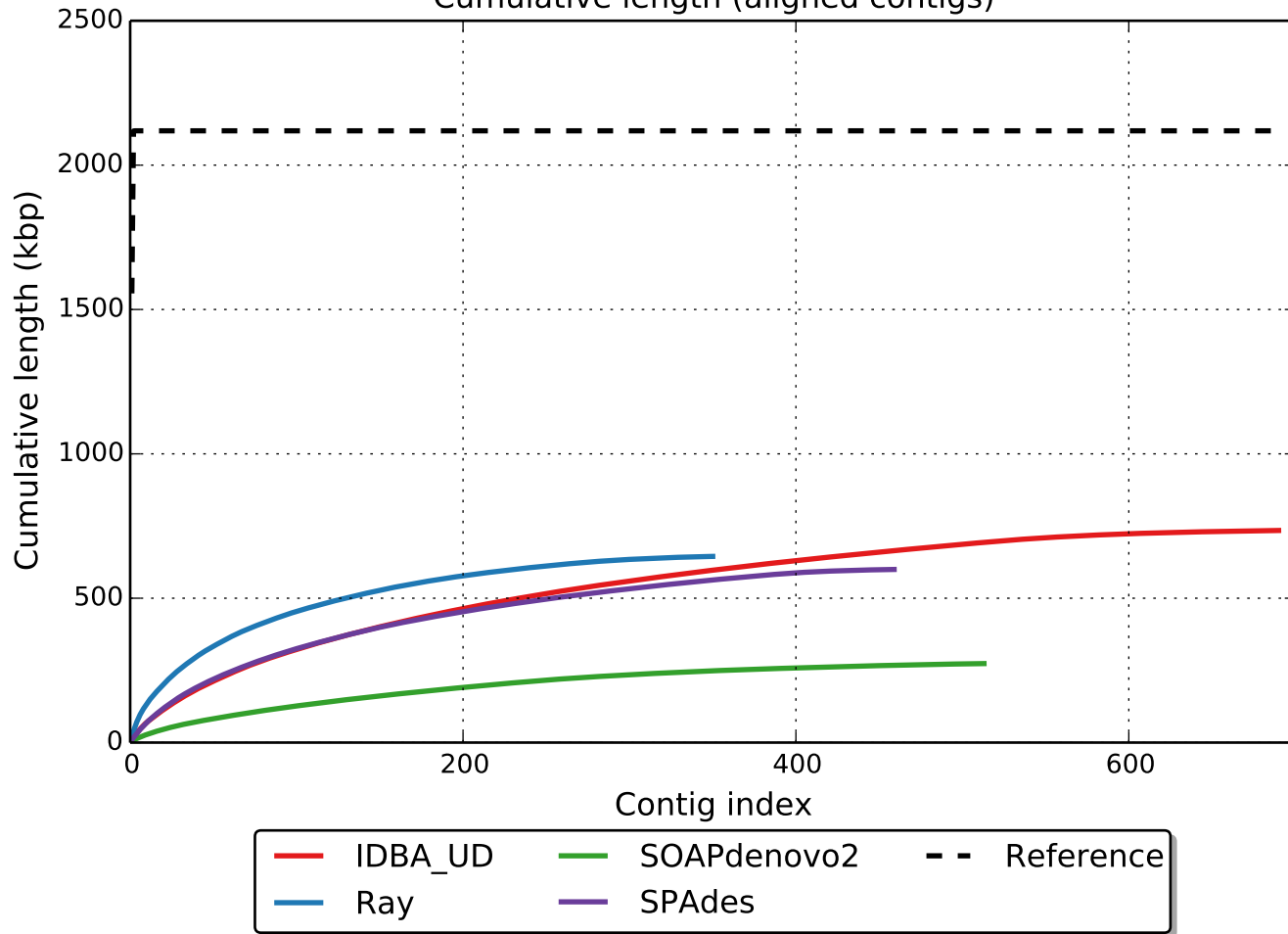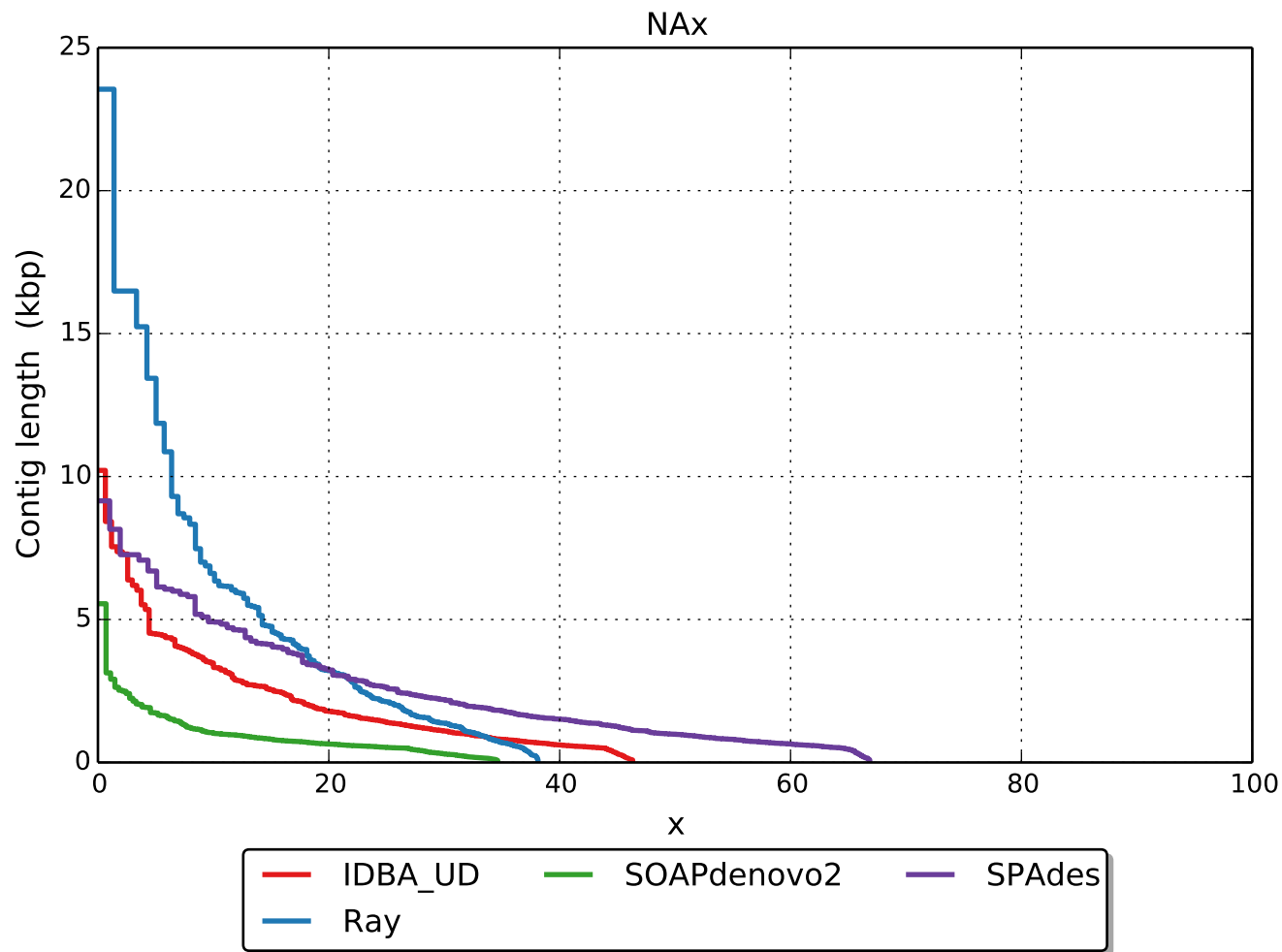
Nx
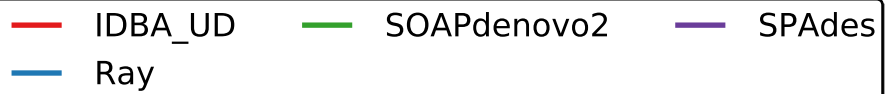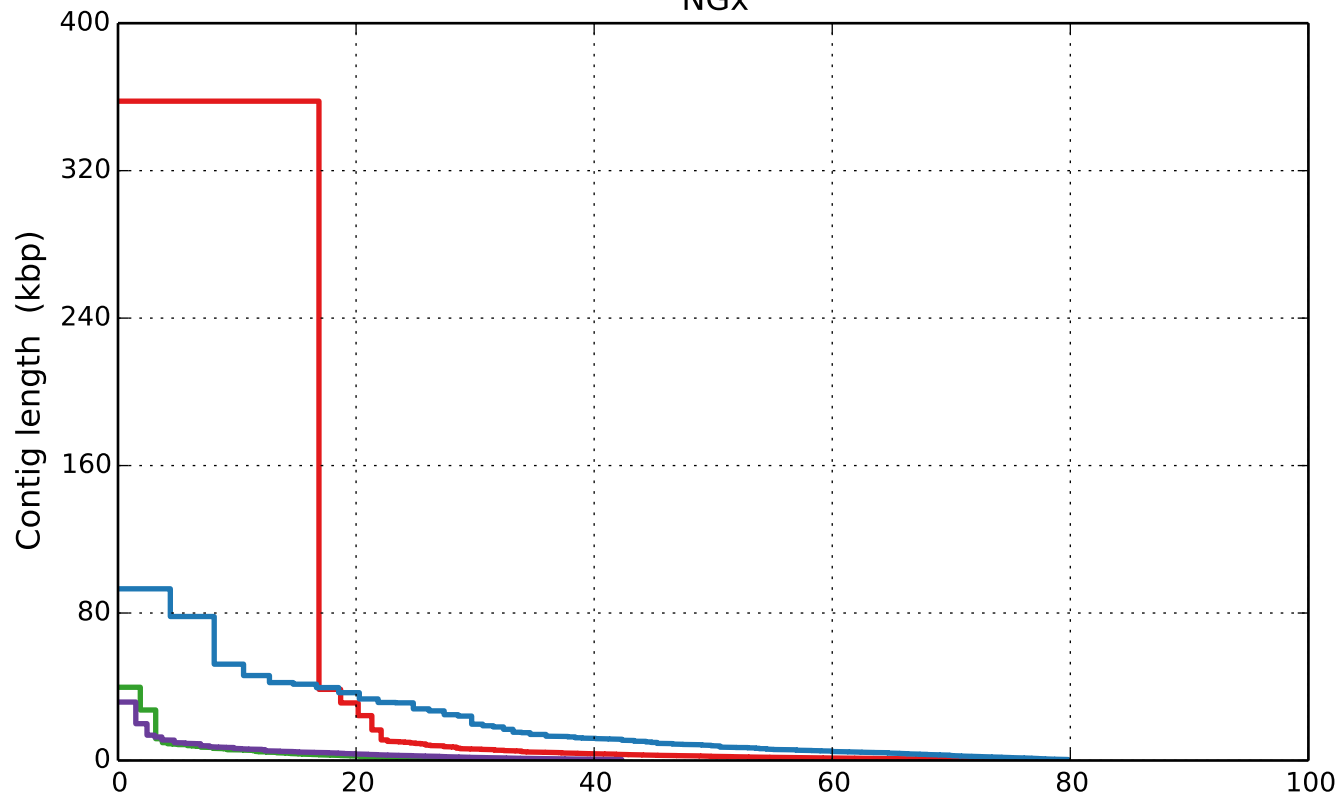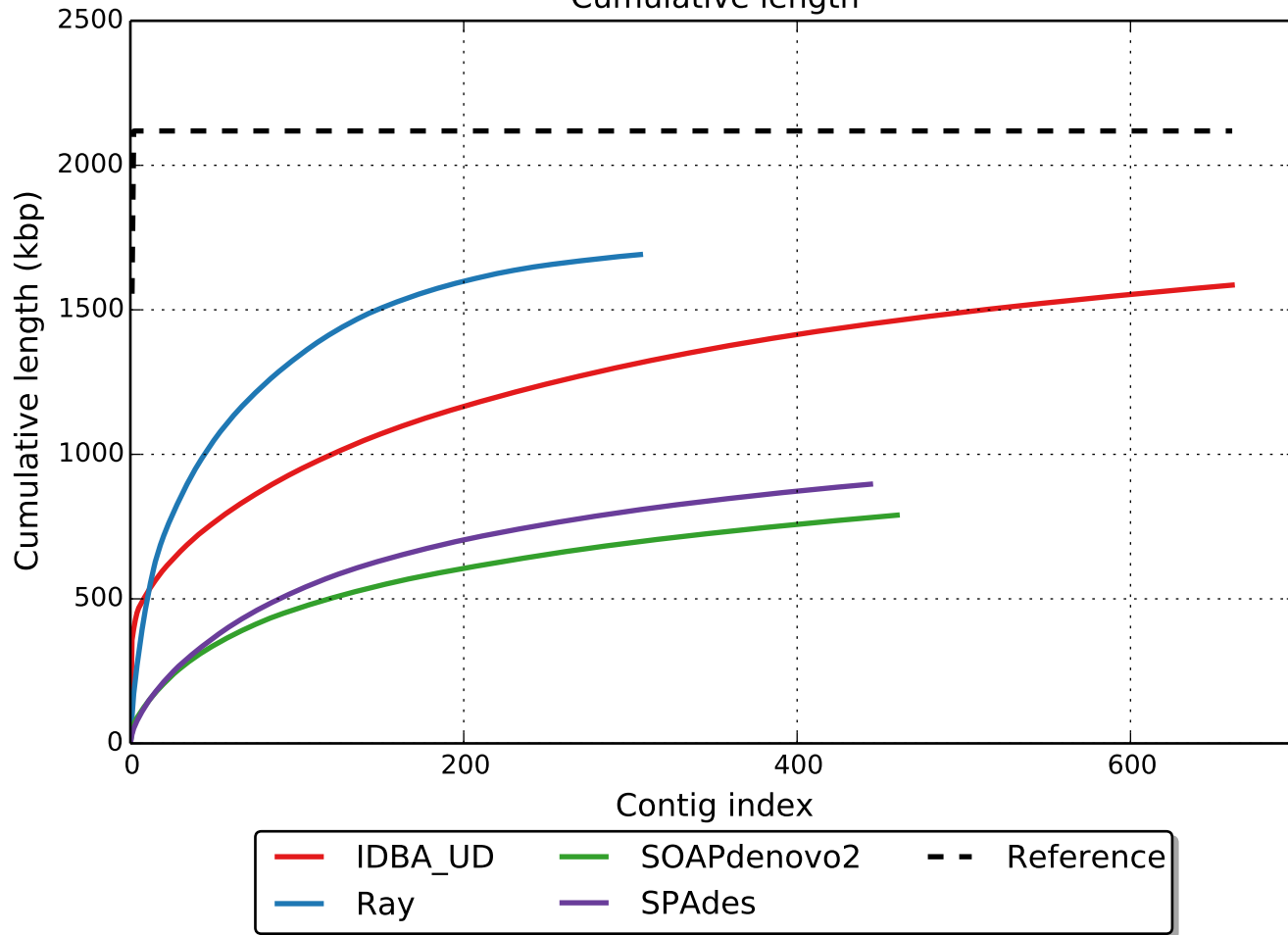
Cumulative length

GC content
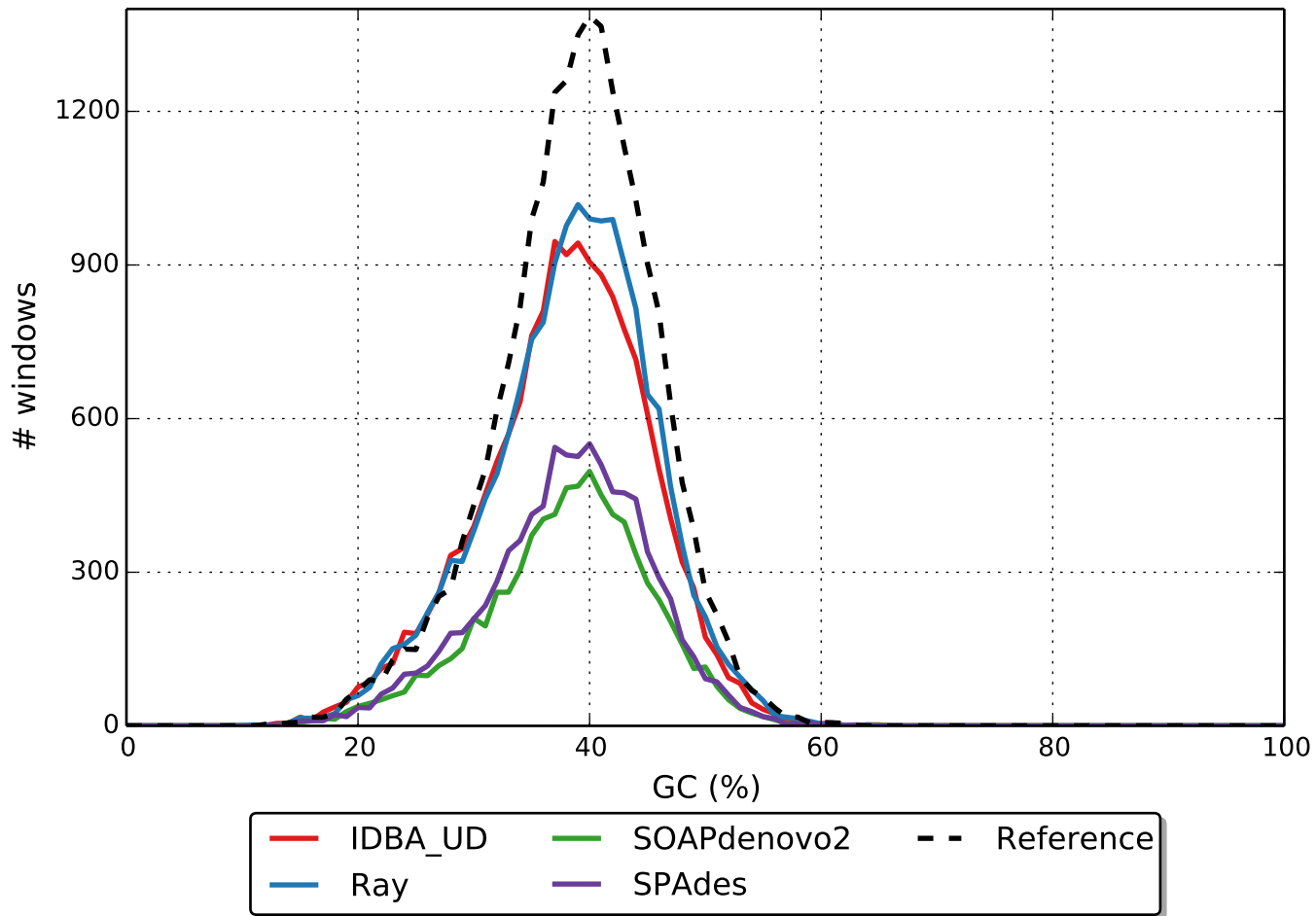
Misassemblies

Cumulative length (aligned contigs)

Genome fraction, %

Legend: IDBA_UD, Ray, SOAPdenovo2, SPAdes