# Report

| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|---|---|---|---|---|
| # contigs (>= 1000 bp) | 421 | 191 | 226 | 376 |
| # contigs (>= 5000 bp) | 79 | 31 | 11 | 70 |
| # contigs (>= 10000 bp) | 20 | 17 | 3 | 24 |
| # contigs (>= 25000 bp) | 2 | 9 | 1 | 3 |
| # contigs (>= 50000 bp) | 0 | 3 | 0 | 0 |
| Total length (>= 1000 bp) | 1471294 | 1035305 | 490615 | 1353228 |
| Total length (>= 5000 bp) | 742973 | 706868 | 113159 | 732346 |
| Total length (>= 10000 bp) | 338971 | 610533 | 64160 | 404450 |
| Total length (>= 25000 bp) | 79470 | 481455 | 38203 | 115705 |
| Total length (>= 50000 bp) | 0 | 259615 | 0 | 0 |
| # contigs | 828 | 389 | 564 | 772 |
| Largest contig | 39739 | 104842 | 38203 | 44309 |
| Total length | 1752526 | 1177177 | 719761 | 1631348 |
| Reference length | 2131358 | 2131358 | 2131358 | 2131358 |
| GC (%) | 41.13 | 40.55 | 40.80 | 41.10 |
| Reference GC (%) | 41.97 | 41.97 | 41.97 | 41.97 |
| N50 | 3910 | 12145 | 1462 | 3714 |
| NG50 | 2464 | 862 | - | 2129 |
| N75 | 1538 | 2278 | 869 | 1483 |
| NG75 | 737 | - | - | 541 |
| L50 | 109 | 16 | 117 | 90 |
| LG50 | 169 | 225 | - | 179 |
| L75 | 296 | 87 | 280 | 268 |
| LG75 | 571 | - | - | 709 |
| # misassemblies | 20 | 11 | 4 | 16 |
| # misassembled contigs | 15 | 8 | 4 | 12 |
| Misassembled contigs length | 63429 | 127568 | 4175 | 126920 |
| # local misassemblies | 60 | 20 | 14 | 18 |
| # structural variations | 0 | 0 | 1 | 0 |
| # unaligned contigs | 0 + 442 part | 0 + 163 part | 0 + 249 part | 0 + 356 part |
| Unaligned length | 975912 | 693548 | 343953 | 706466 |
| Genome fraction (%) | 31.089 | 18.491 | 17.156 | 34.599 |
| Duplication ratio | 1.172 | 1.227 | 1.028 | 1.254 |
| # N's per 100 kbp | 0.17 | 743.73 | 4285.31 | 78.83 |
| # mismatches per 100 kbp | 2910.90 | 3050.35 | 2589.03 | 3229.09 |
| # indels per 100 kbp | 64.44 | 71.81 | 51.69 | 69.57 |
| Largest alignment | 11901 | 21104 | 5910 | 20167 |
| NA50 | - | - | 174 | 528 |
| NGA50 | - | - | - | - |
| LA50 | - | - | 494 | 507 |

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).
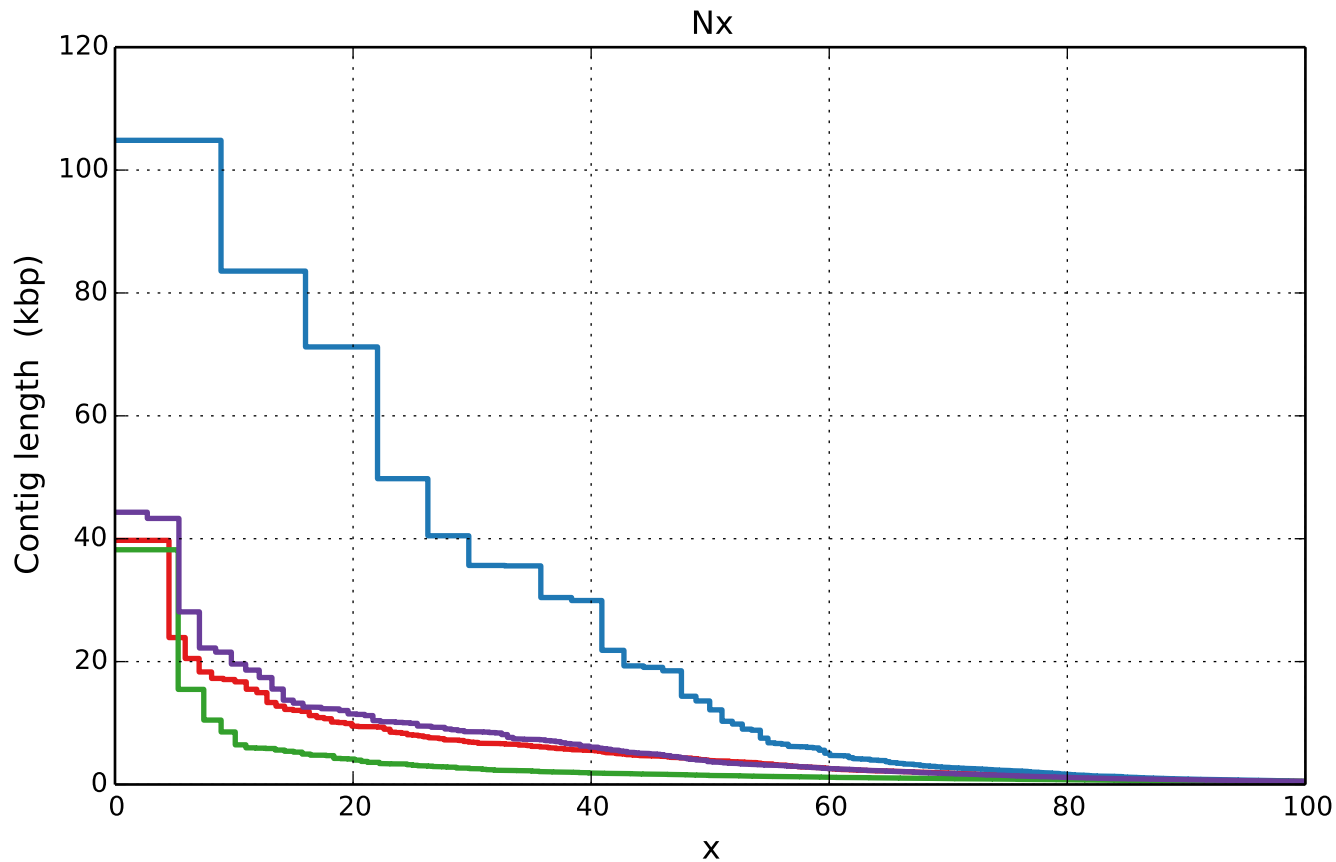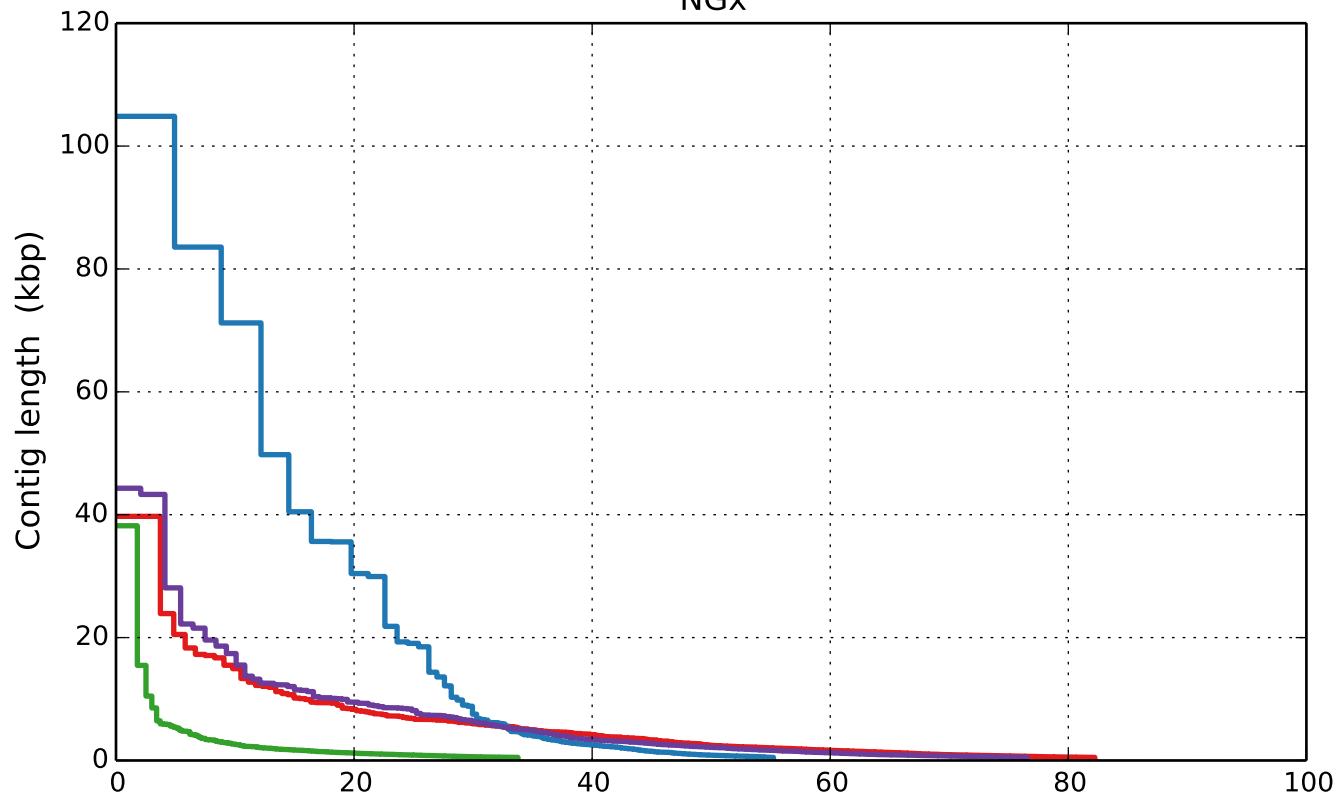
# Misassemblies report

| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|---|---|---|---|---|
| # misassemblies | 20 | 11 | 4 | 16 |
| # relocations | 1 | 3 | 0 | 4 |
| # translocations | 19 | 8 | 4 | 12 |
| # inversions | 0 | 0 | 0 | 0 |
| # possibly misassembled contigs | 102 | 38 | 25 | 76 |
| # misassembled contigs | 15 | 8 | 4 | 12 |
| Misassembled contigs length | 63429 | 127568 | 4175 | 126920 |
| # local misassemblies | 60 | 20 | 14 | 18 |
| # structural variations | 0 | 0 | 1 | 0 |
| # mismatches | 19288 | 12022 | 9467 | 23812 |
| # indels | 427 | 283 | 189 | 513 |
| # short indels | 357 | 276 | 164 | 502 |
| # long indels | 70 | 7 | 25 | 11 |
| Indels length | 2554 | 441 | 706 | 848 |

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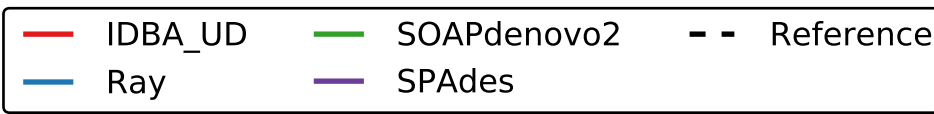(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
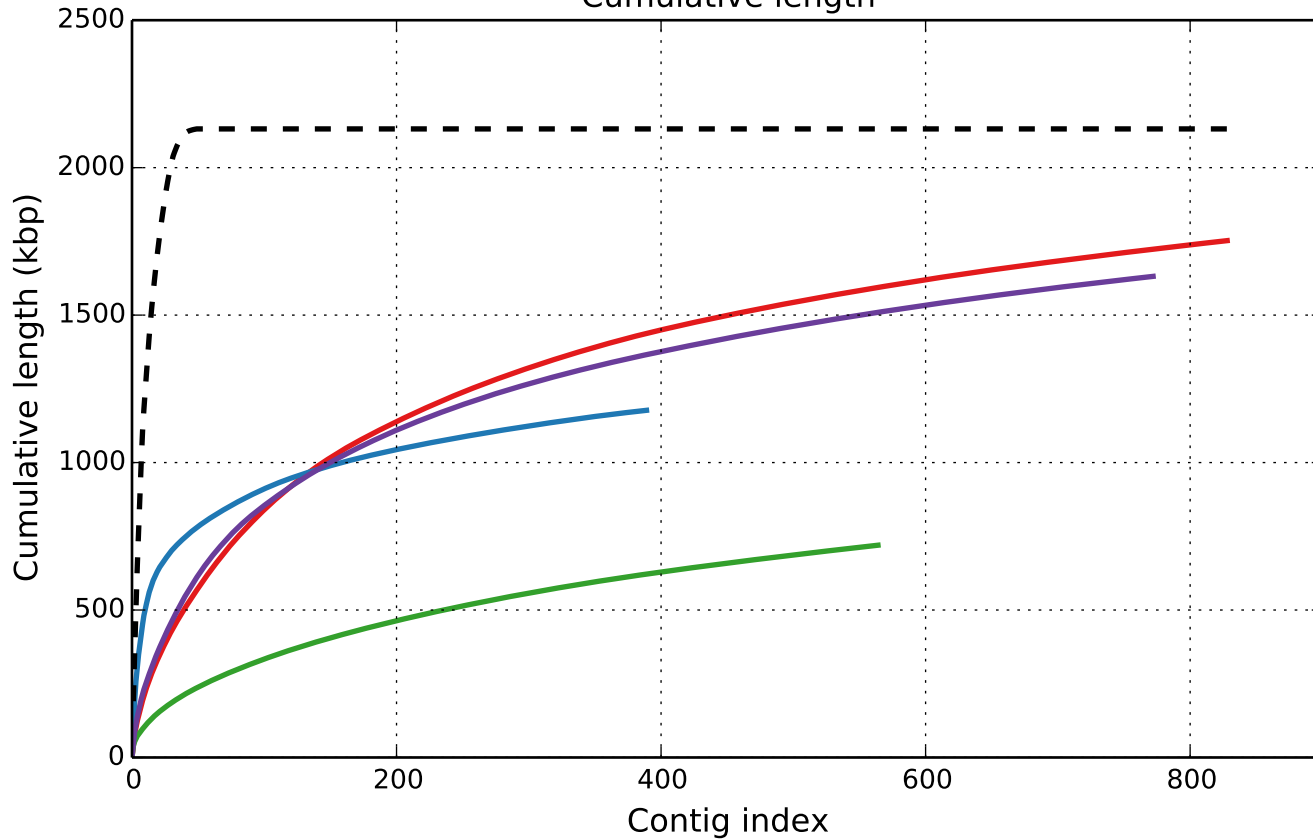
# Unaligned report

| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|---|---|---|---|---|
| # fully unaligned contigs | 0 | 0 | 0 | 0 |
| Fully unaligned length | 0 | 0 | 0 | 0 |
| # partially unaligned contigs | 442 | 163 | 249 | 356 |
| # with misassembly | 32 | 9 | 18 | 12 |
| # both parts are significant | 87 | 34 | 25 | 66 |
| Partially unaligned length | 975912 | 693548 | 343953 | 706466 |
| # N's | 3 | 8755 | 30844 | 1286 |

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).
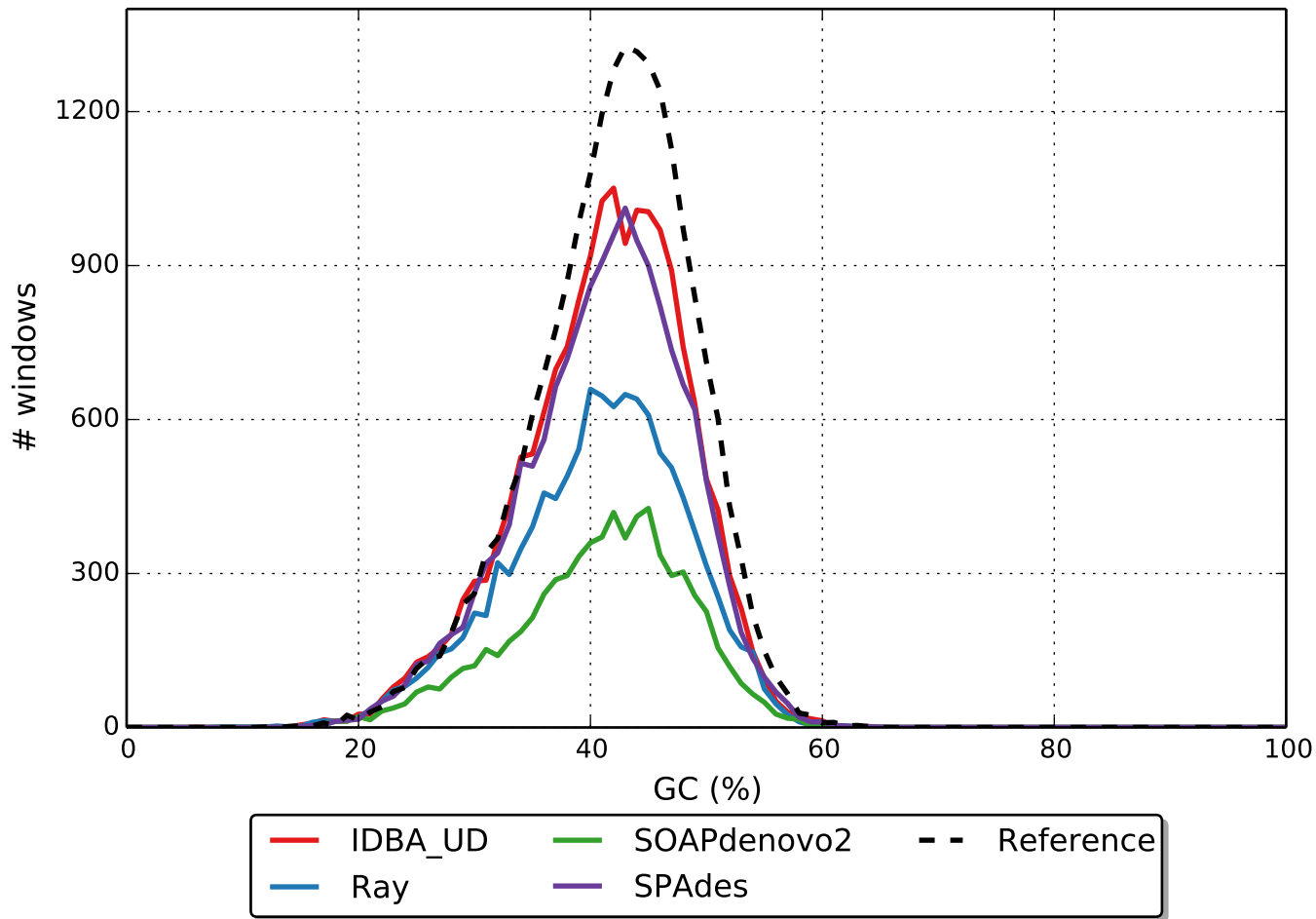
Cumulative length

GC content

# windows

GC (%)

IDBA_UD — SOAPdenovo2 — Reference
Ray — SPAdes

Misassemblies
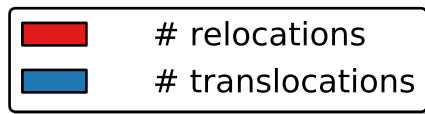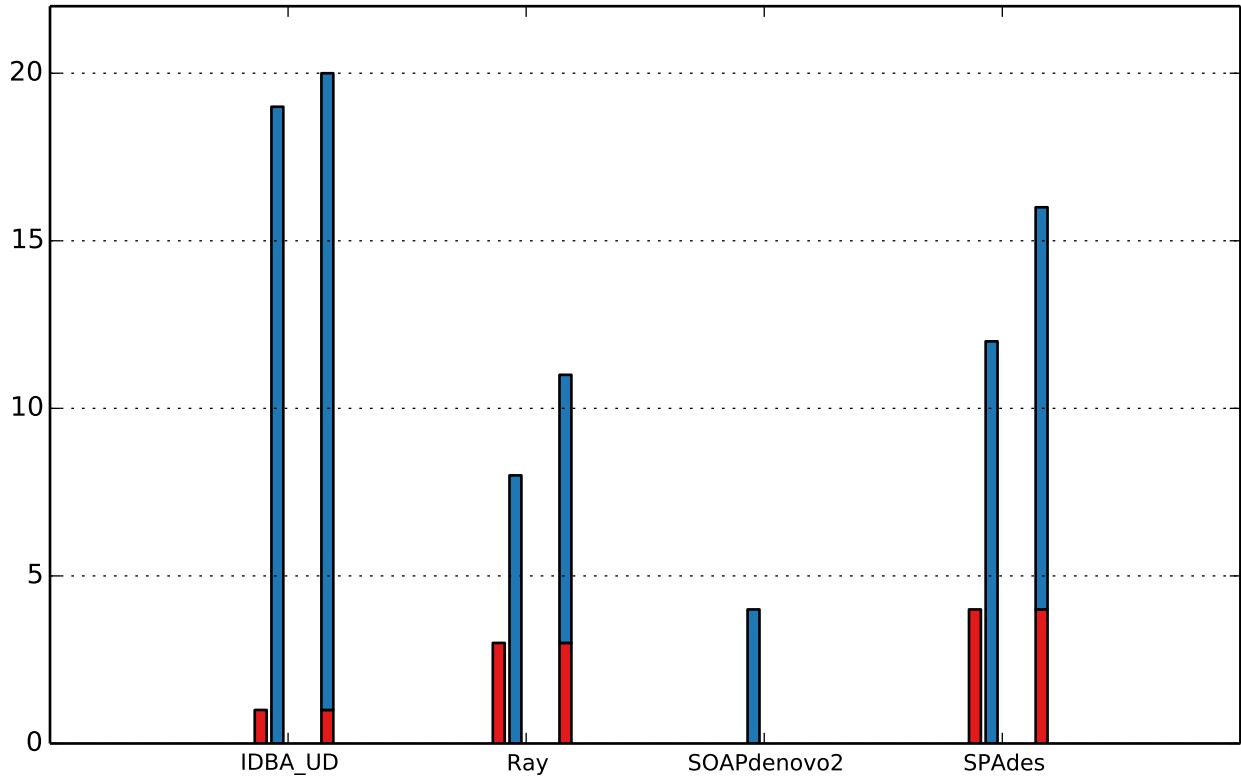
Cumulative length (aligned contigs)

Genome fraction, %

Legend: IDBA_UD, Ray, SOAPdenovo2, SPAdes