

Report

| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|-----------------------------|--------------|------------|--------------|--------------|
| # contigs (>= 1000 bp) | 487 | 27 | 127 | 421 |
| # contigs (>= 5000 bp) | 55 | 6 | 5 | 66 |
| # contigs (>= 10000 bp) | 17 | 4 | 0 | 27 |
| # contigs (>= 25000 bp) | 2 | 1 | 0 | 5 |
| # contigs (>= 50000 bp) | 0 | 0 | 0 | 2 |
| Total length (>= 1000 bp) | 1309003 | 126629 | 226665 | 1542087 |
| Total length (>= 5000 bp) | 519063 | 88128 | 32434 | 754913 |
| Total length (>= 10000 bp) | 260365 | 76765 | 0 | 498705 |
| Total length (>= 25000 bp) | 52445 | 27531 | 0 | 223942 |
| Total length (>= 50000 bp) | 0 | 0 | 0 | 135104 |
| # contigs | 899 | 58 | 637 | 697 |
| Largest contig | 26521 | 27531 | 7676 | 81030 |
| Total length | 1610892 | 147380 | 569512 | 1737254 |
| Reference length | 7101224 | 7101224 | 7101224 | 7101224 |
| GC (%) | 42.72 | 42.82 | 42.11 | 42.72 |
| Reference GC (%) | 42.13 | 42.13 | 42.13 | 42.13 |
| N50 | 2354 | 13172 | 863 | 4148 |
| N75 | 1161 | 1684 | 639 | 1876 |
| L50 | 146 | 4 | 190 | 91 |
| L75 | 394 | 15 | 385 | 248 |
| # misassemblies | 9 | 0 | 3 | 16 |
| # misassembled contigs | 8 | 0 | 3 | 12 |
| Misassembled contigs length | 19610 | 0 | 2913 | 36406 |
| # local misassemblies | 7 | 4 | 473 | 15 |
| # structural variations | 1 | 0 | 0 | 2 |
| # unaligned contigs | 0 + 101 part | 0 + 8 part | 0 + 172 part | 0 + 181 part |
| Unaligned length | 208652 | 75871 | 97717 | 519399 |
| Genome fraction (%) | 19.561 | 0.969 | 6.032 | 16.585 |
| Duplication ratio | 1.009 | 1.039 | 1.101 | 1.034 |
| # N's per 100 kbp | 295.30 | 1206.41 | 7374.21 | 861.19 |
| # mismatches per 100 kbp | 1644.26 | 719.19 | 1253.60 | 1928.12 |
| # indels per 100 kbp | 44.49 | 17.44 | 18.44 | 53.32 |
| Largest alignment | 17129 | 5916 | 6308 | 36160 |
| NA50 | 1630 | - | 591 | 1306 |
| NGA50 | - | - | - | - |
| NA75 | 786 | - | 98 | - |
| LA50 | 228 | - | 258 | 281 |
| LA75 | 592 | - | 677 | - |

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

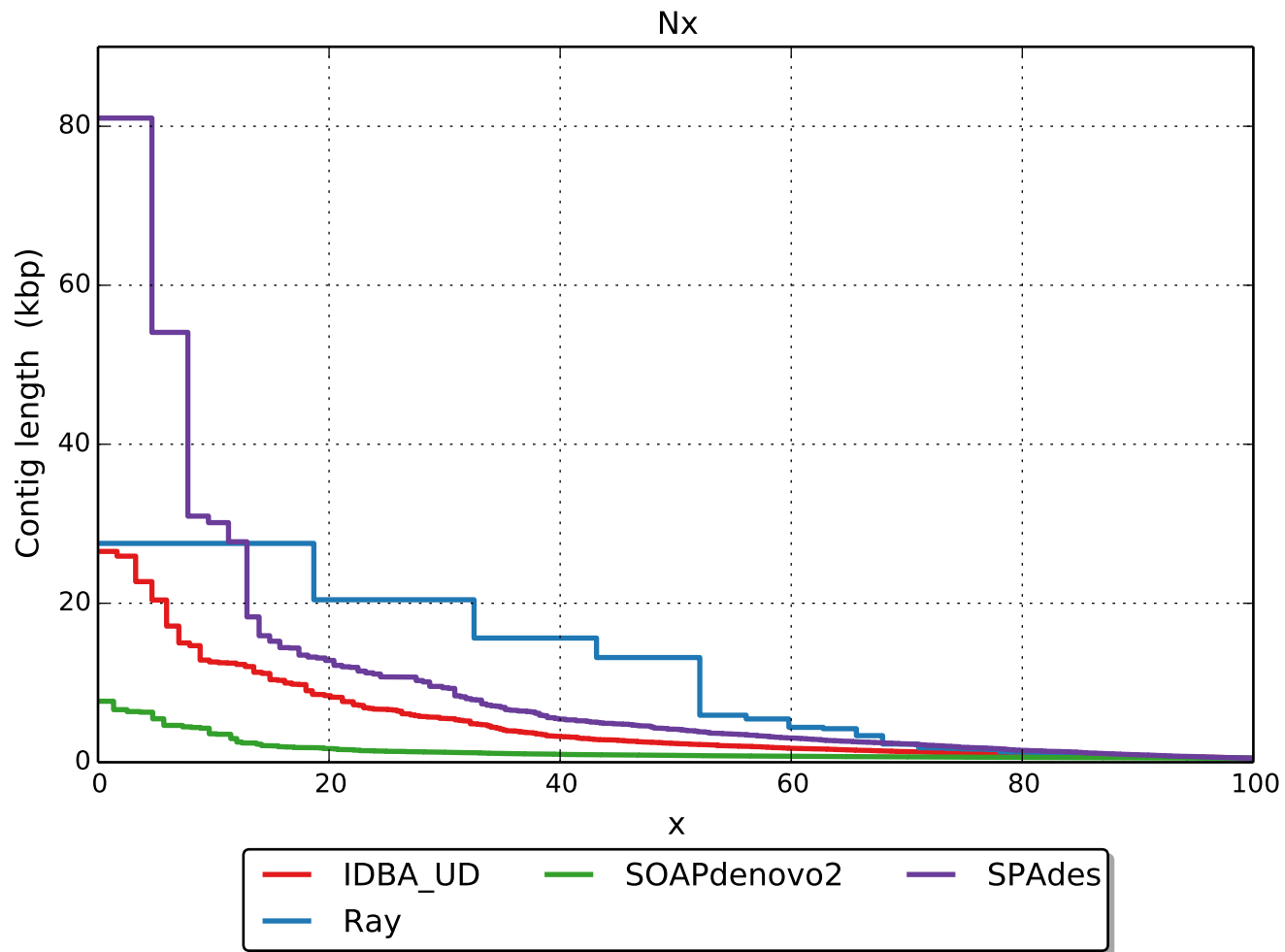
| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|---------------------------------|---------|-----|-------------|--------|
| # misassemblies | 9 | 0 | 3 | 16 |
| # relocations | 2 | 0 | 1 | 3 |
| # translocations | 5 | 0 | 2 | 13 |
| # inversions | 2 | 0 | 0 | 0 |
| # possibly misassembled contigs | 39 | 2 | 11 | 88 |
| # misassembled contigs | 8 | 0 | 3 | 12 |
| Misassembled contigs length | 19610 | 0 | 2913 | 36406 |
| # local misassemblies | 7 | 4 | 473 | 15 |
| # structural variations | 1 | 0 | 0 | 2 |
| # mismatches | 22840 | 495 | 5370 | 22708 |
| # indels | 618 | 12 | 79 | 628 |
| # short indels | 553 | 12 | 75 | 521 |
| # long indels | 65 | 0 | 4 | 107 |
| Indels length | 1616 | 19 | 135 | 2025 |

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).

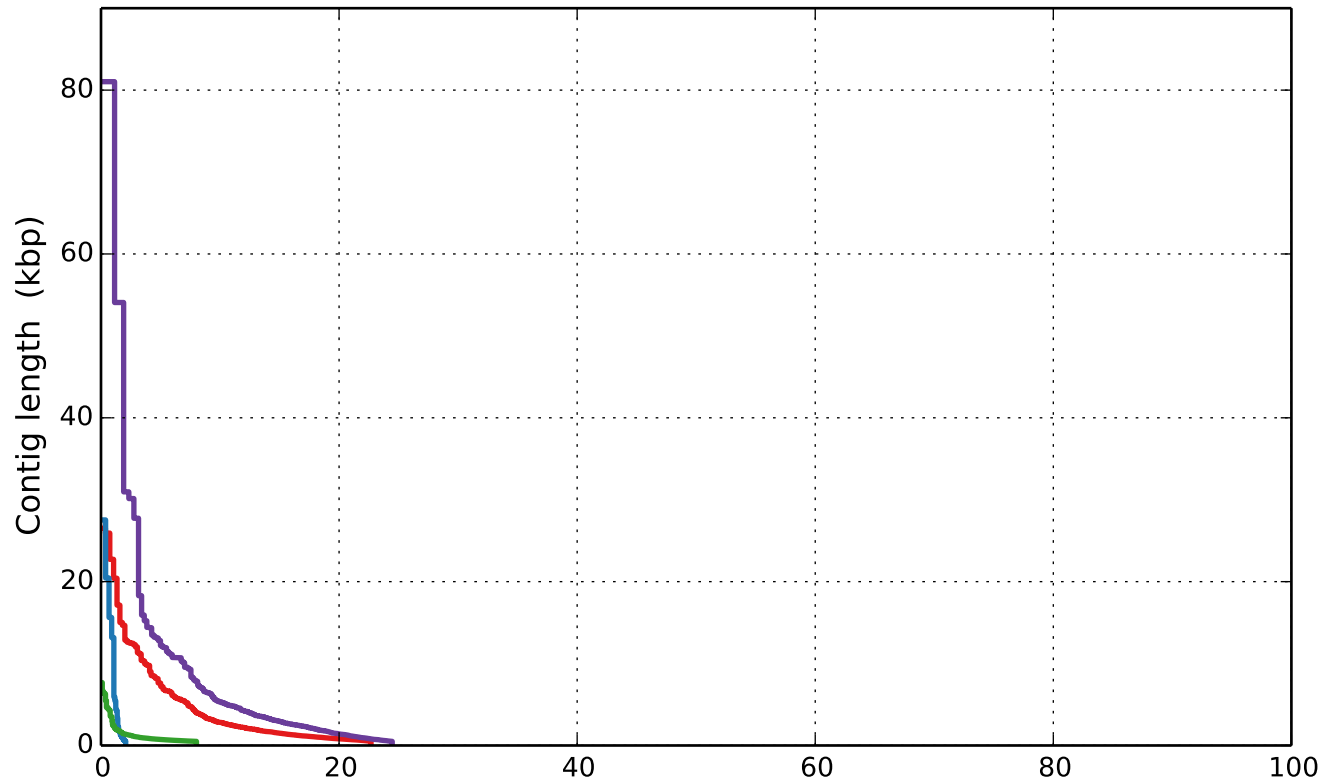
Unaligned report

| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|-------------------------------|---------|-------|-------------|--------|
| # fully unaligned contigs | 0 | 0 | 0 | 0 |
| Fully unaligned length | 0 | 0 | 0 | 0 |
| # partially unaligned contigs | 101 | 8 | 172 | 181 |
| # with misassembly | 5 | 1 | 55 | 5 |
| # both parts are significant | 35 | 2 | 4 | 80 |
| Partially unaligned length | 208652 | 75871 | 97717 | 519399 |
| # N's | 4757 | 1778 | 41997 | 14961 |

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).

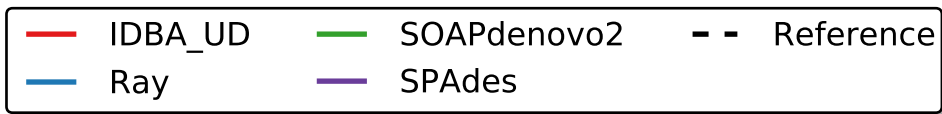
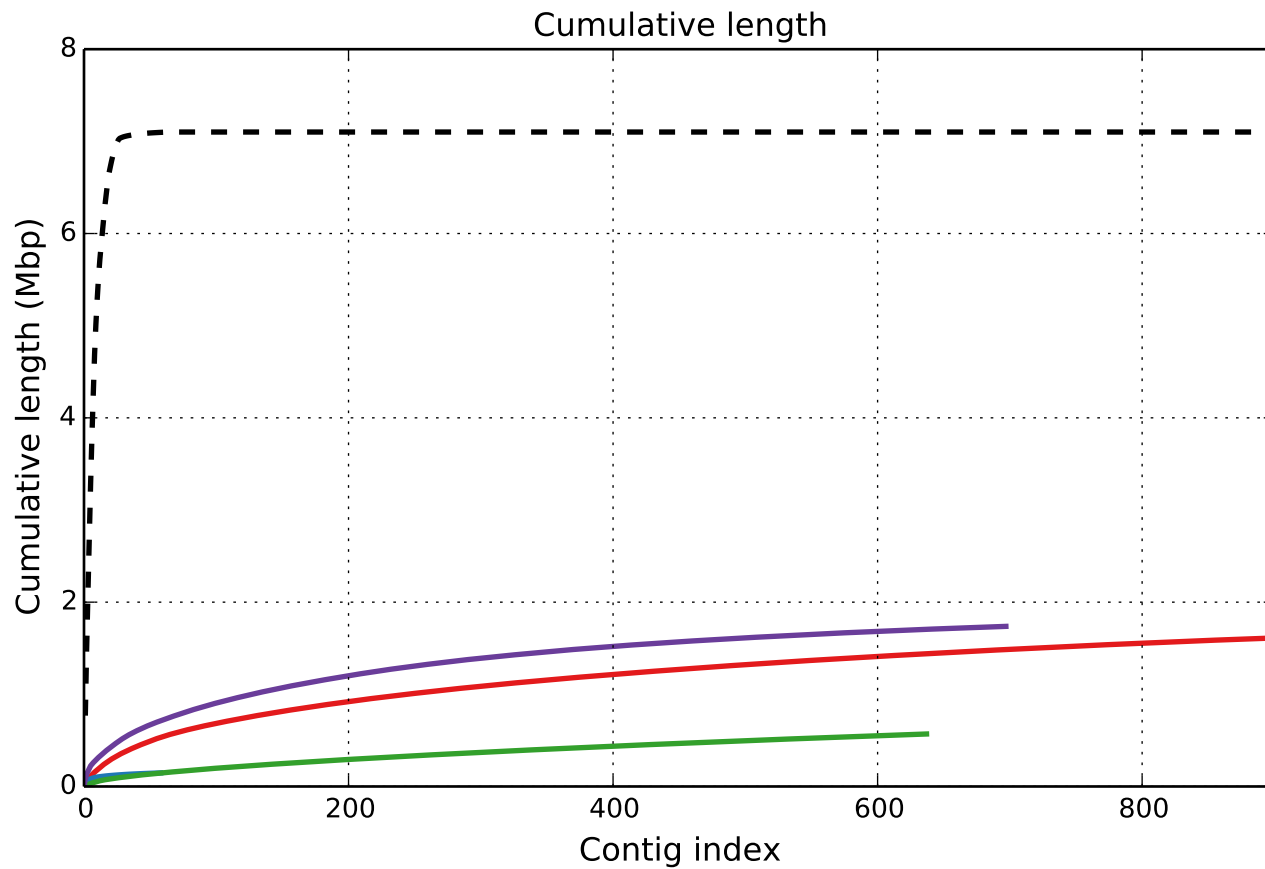


NGx

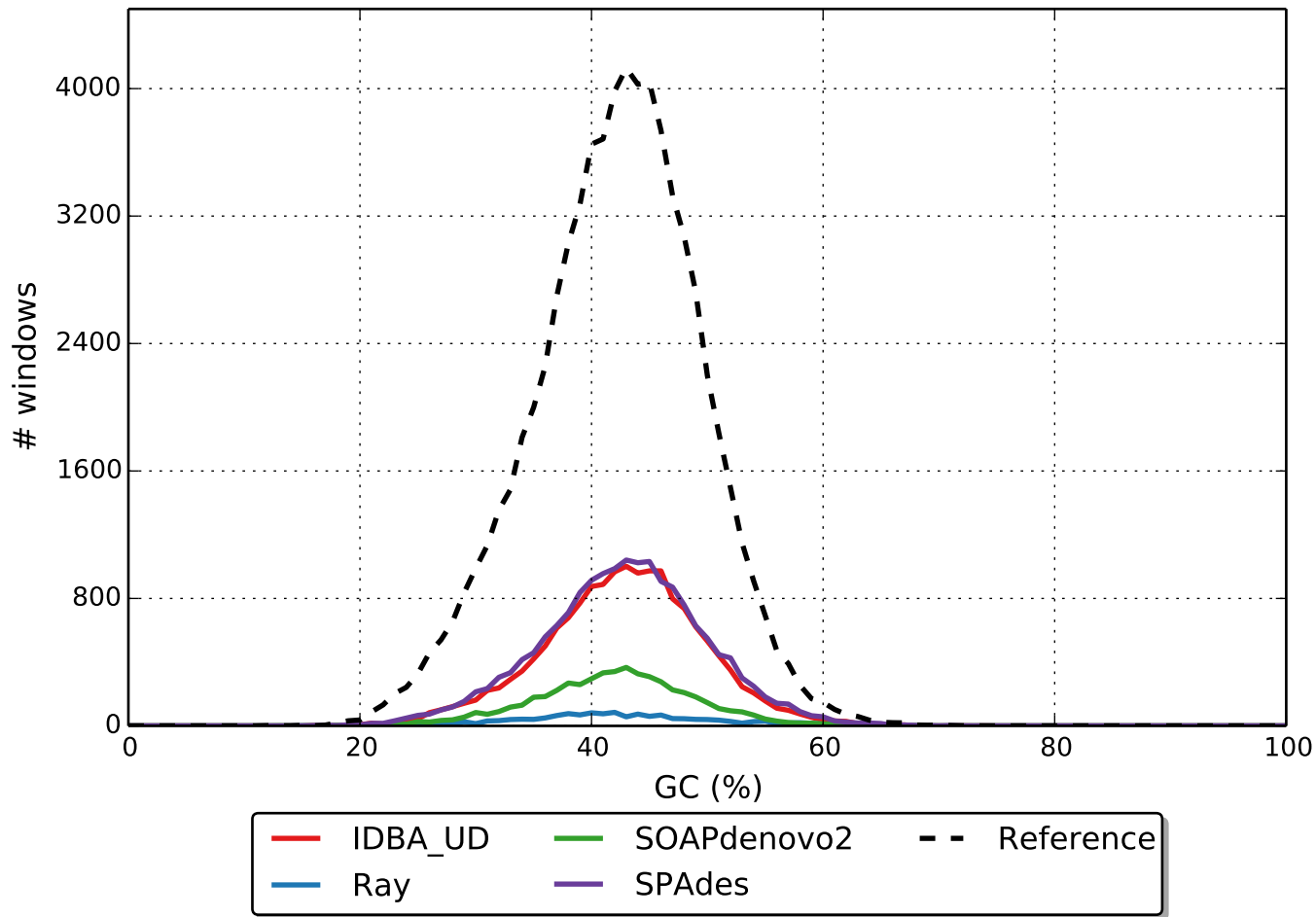


x





GC content



Misassemblies

