

Report

| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|-----------------------------|-------------|-------------|-------------|-------------|
| # contigs (>= 1000 bp) | 66 | 32 | 28 | 52 |
| # contigs (>= 5000 bp) | 20 | 4 | 2 | 17 |
| # contigs (>= 10000 bp) | 13 | 1 | 1 | 7 |
| # contigs (>= 25000 bp) | 8 | 0 | 0 | 4 |
| # contigs (>= 50000 bp) | 3 | 0 | 0 | 0 |
| Total length (>= 1000 bp) | 649035 | 100558 | 65975 | 347006 |
| Total length (>= 5000 bp) | 543217 | 33988 | 18302 | 265693 |
| Total length (>= 10000 bp) | 490807 | 10965 | 12707 | 185446 |
| Total length (>= 25000 bp) | 428709 | 0 | 0 | 139187 |
| Total length (>= 50000 bp) | 265753 | 0 | 0 | 0 |
| # contigs | 107 | 48 | 74 | 78 |
| Largest contig | 135115 | 10965 | 12707 | 45766 |
| Total length | 677980 | 111955 | 96090 | 365516 |
| Reference length | 3995628 | 3995628 | 3995628 | 3995628 |
| GC (%) | 41.58 | 41.88 | 39.73 | 39.86 |
| Reference GC (%) | 40.09 | 40.09 | 40.09 | 40.09 |
| N50 | 41370 | 3541 | 1603 | 12830 |
| N75 | 9101 | 1895 | 797 | 4802 |
| L50 | 5 | 10 | 15 | 7 |
| L75 | 15 | 21 | 35 | 19 |
| # misassemblies | 2 | 2 | 2 | 5 |
| # misassembled contigs | 2 | 2 | 2 | 4 |
| Misassembled contigs length | 1949 | 5041 | 1474 | 22213 |
| # local misassemblies | 1 | 8 | 20 | 1 |
| # structural variations | 1 | 0 | 0 | 0 |
| # unaligned contigs | 0 + 62 part | 0 + 18 part | 0 + 27 part | 0 + 51 part |
| Unaligned length | 555102 | 41568 | 22222 | 251133 |
| Genome fraction (%) | 2.964 | 1.585 | 1.742 | 2.612 |
| Duplication ratio | 1.038 | 1.111 | 1.061 | 1.096 |
| # N's per 100 kbp | 99.56 | 2026.71 | 1996.05 | 468.65 |
| # mismatches per 100 kbp | 2104.50 | 1848.58 | 1685.49 | 2210.85 |
| # indels per 100 kbp | 93.74 | 34.73 | 18.68 | 58.46 |
| Largest alignment | 5378 | 8592 | 11065 | 6828 |
| NA50 | - | 706 | 731 | - |
| NGA50 | - | - | - | - |
| LA50 | - | 31 | 28 | - |

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 | 2 | 2 | 5 |
| # relocations | 1 | 2 | 2 | 5 |
| # translocations | 0 | 0 | 0 | 0 |
| # inversions | 1 | 0 | 0 | 0 |
| # possibly misassembled contigs | 23 | 9 | 5 | 27 |
| # misassembled contigs | 2 | 2 | 2 | 4 |
| Misassembled contigs length | 1949 | 5041 | 1474 | 22213 |
| # local misassemblies | 1 | 8 | 20 | 1 |
| # structural variations | 1 | 0 | 0 | 0 |
| # mismatches | 2492 | 1171 | 1173 | 2307 |
| # indels | 111 | 22 | 13 | 61 |
| # short indels | 101 | 22 | 13 | 58 |
| # long indels | 10 | 0 | 0 | 3 |
| Indels length | 243 | 23 | 13 | 97 |

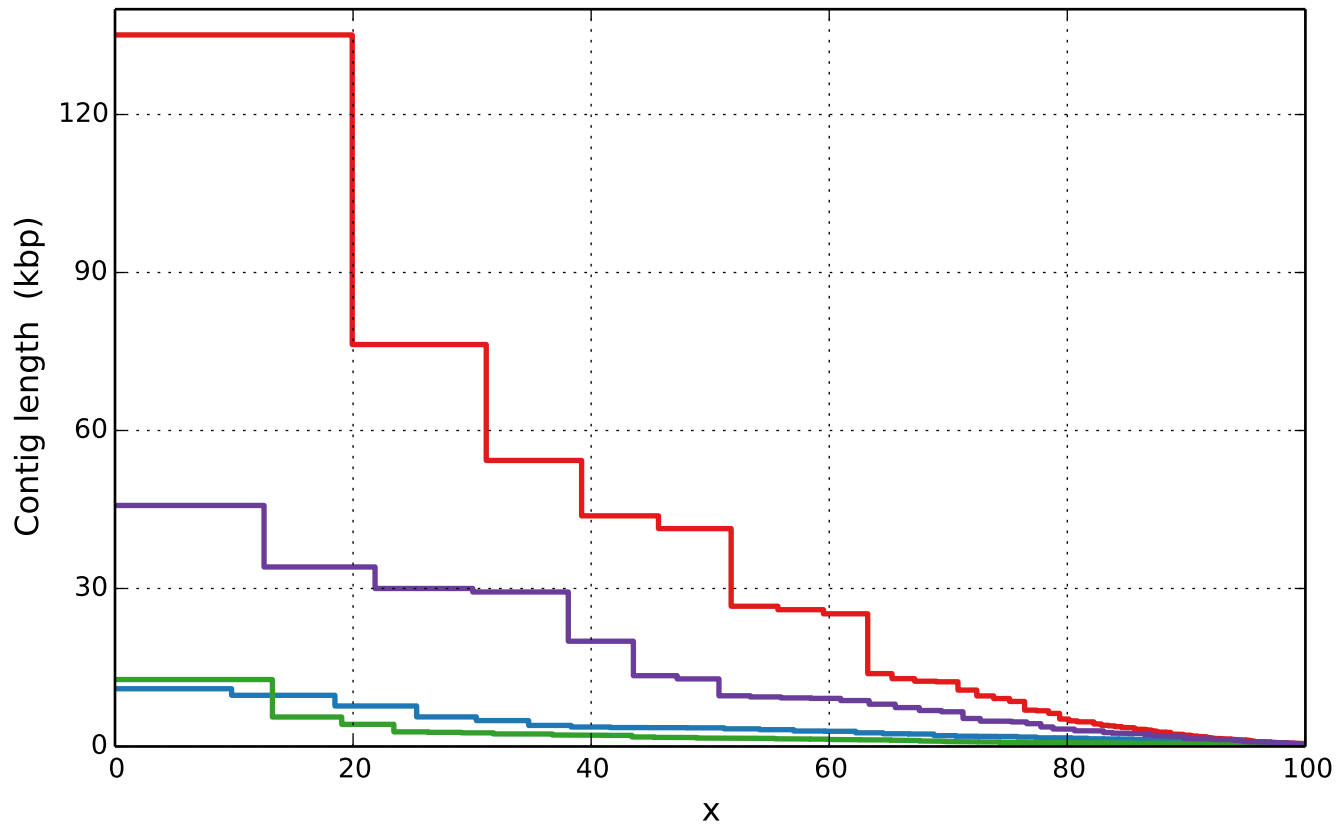
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |
|-------------------------------|---------|-------|-------------|--------|
| # fully unaligned contigs | 0 | 0 | 0 | 0 |
| Fully unaligned length | 0 | 0 | 0 | 0 |
| # partially unaligned contigs | 62 | 18 | 27 | 51 |
| # with misassembly | 6 | 3 | 4 | 8 |
| # both parts are significant | 22 | 5 | 3 | 24 |
| Partially unaligned length | 555102 | 41568 | 22222 | 251133 |
| # N's | 675 | 2269 | 1918 | 1713 |

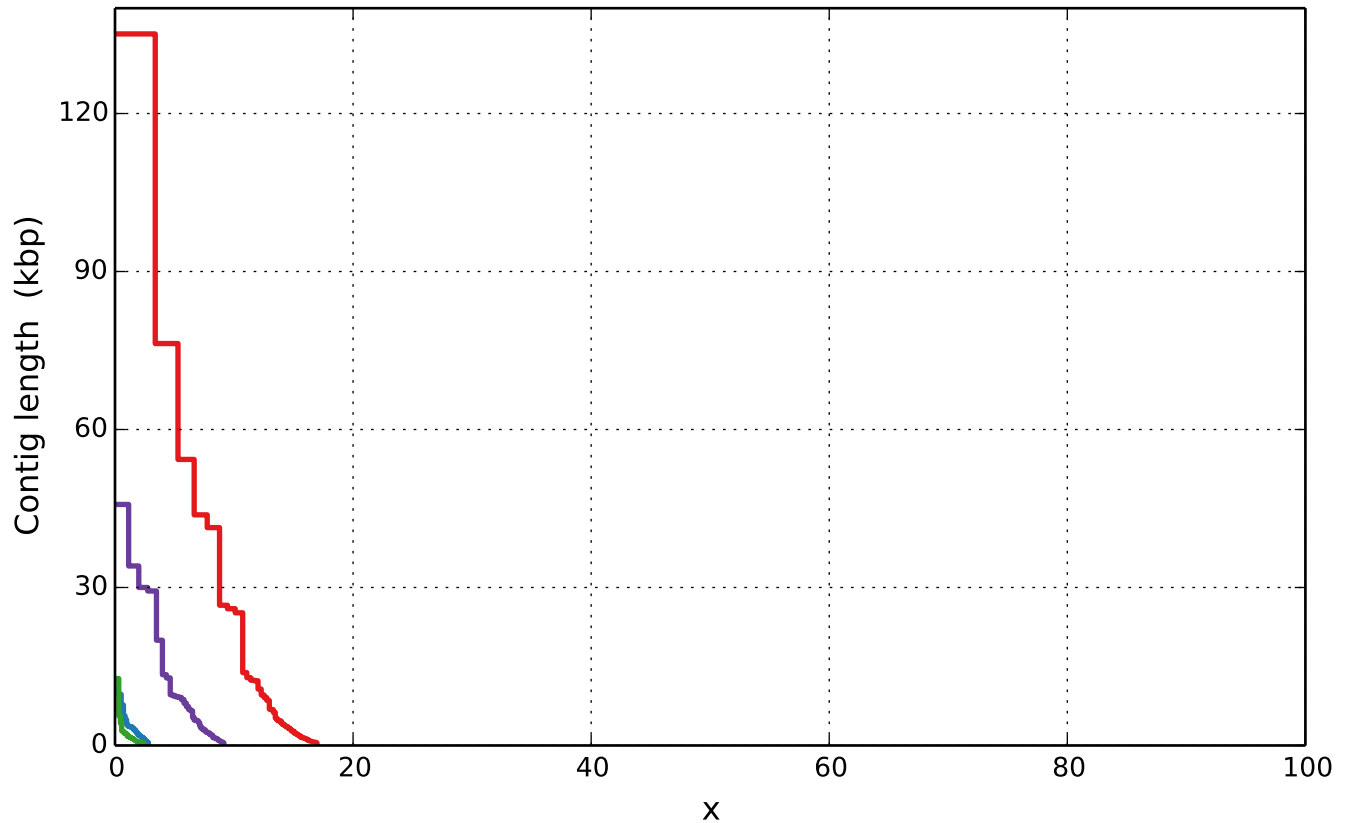
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

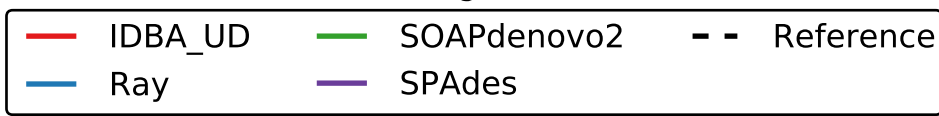
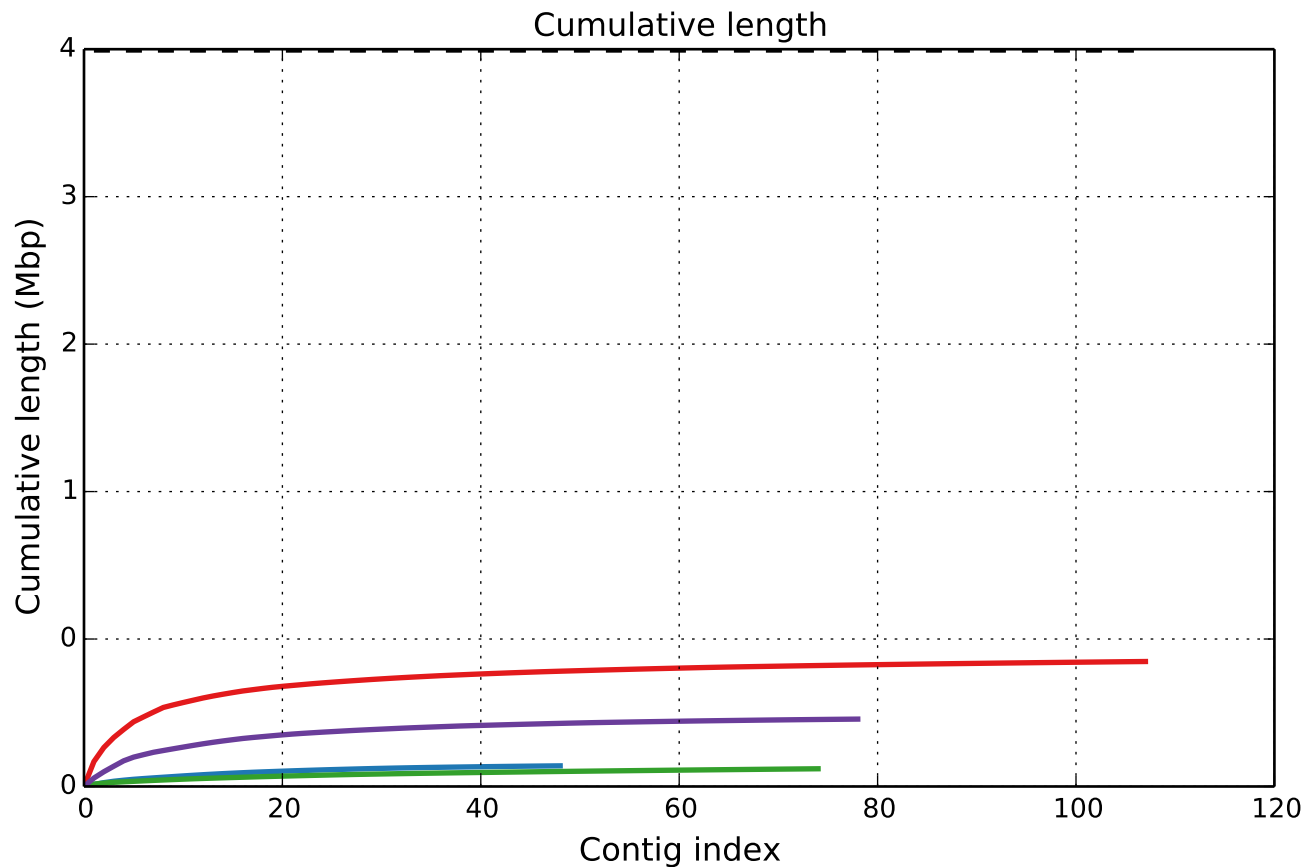
Nx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

NGx





GC content

