

Report

| | uniq_contigs_contigs_contigs_contigs_contigs |
|-----------------------------|--|
| # contigs (>= 0 bp) | 872 |
| # contigs (>= 1000 bp) | 131 |
| # contigs (>= 5000 bp) | 40 |
| # contigs (>= 10000 bp) | 38 |
| # contigs (>= 25000 bp) | 30 |
| # contigs (>= 50000 bp) | 28 |
| Total length (>= 0 bp) | 56022645 |
| Total length (>= 1000 bp) | 55596894 |
| Total length (>= 5000 bp) | 55456151 |
| Total length (>= 10000 bp) | 55445440 |
| Total length (>= 25000 bp) | 55330556 |
| Total length (>= 50000 bp) | 55272859 |
| # contigs | 872 |
| Largest contig | 11609236 |
| Total length | 56022645 |
| Reference length | 59128983 |
| GC (%) | 48.37 |
| Reference GC (%) | 48.36 |
| N50 | 4792422 |
| NG50 | 4009636 |
| N75 | 2133444 |
| NG75 | 2068710 |
| L50 | 4 |
| LG50 | 5 |
| L75 | 9 |
| LG75 | 10 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # possible TEs | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 374 + 0 part |
| Unaligned length | 162432 |
| Genome fraction (%) | 99.878 |
| Duplication ratio | 1.002 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 0.03 |
| # indels per 100 kbp | 0.03 |
| Largest alignment | 11609236 |
| Total aligned length | 55860204 |
| NA50 | 4792422 |
| NGA50 | 4009636 |
| NA75 | 2133444 |
| NGA75 | 2068710 |
| LA50 | 4 |
| LGA50 | 5 |
| LA75 | 9 |
| LGA75 | 10 |

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

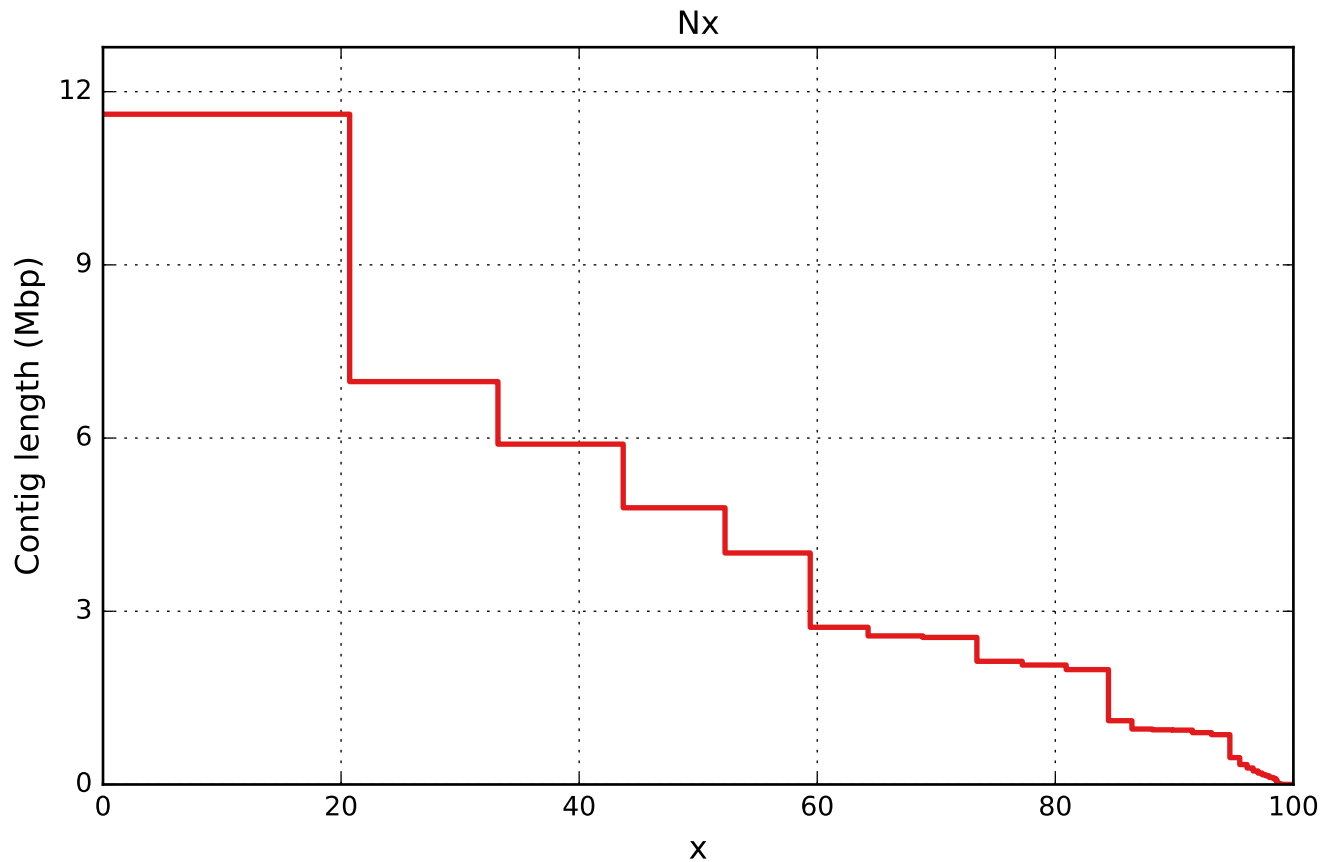
| | uniq_contigs_contigs_contigs_contigs_contigs |
|--|--|
| # misassemblies | 0 |
| # contig misassemblies | 0 |
| # c. relocations | 0 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # misassemblies caused by fragmented reference | 0 |
| # possible TEs | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 16 |
| # indels | 16 |
| # indels (<= 5 bp) | 8 |
| # indels (> 5 bp) | 8 |
| Indels length | 1129 |

All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

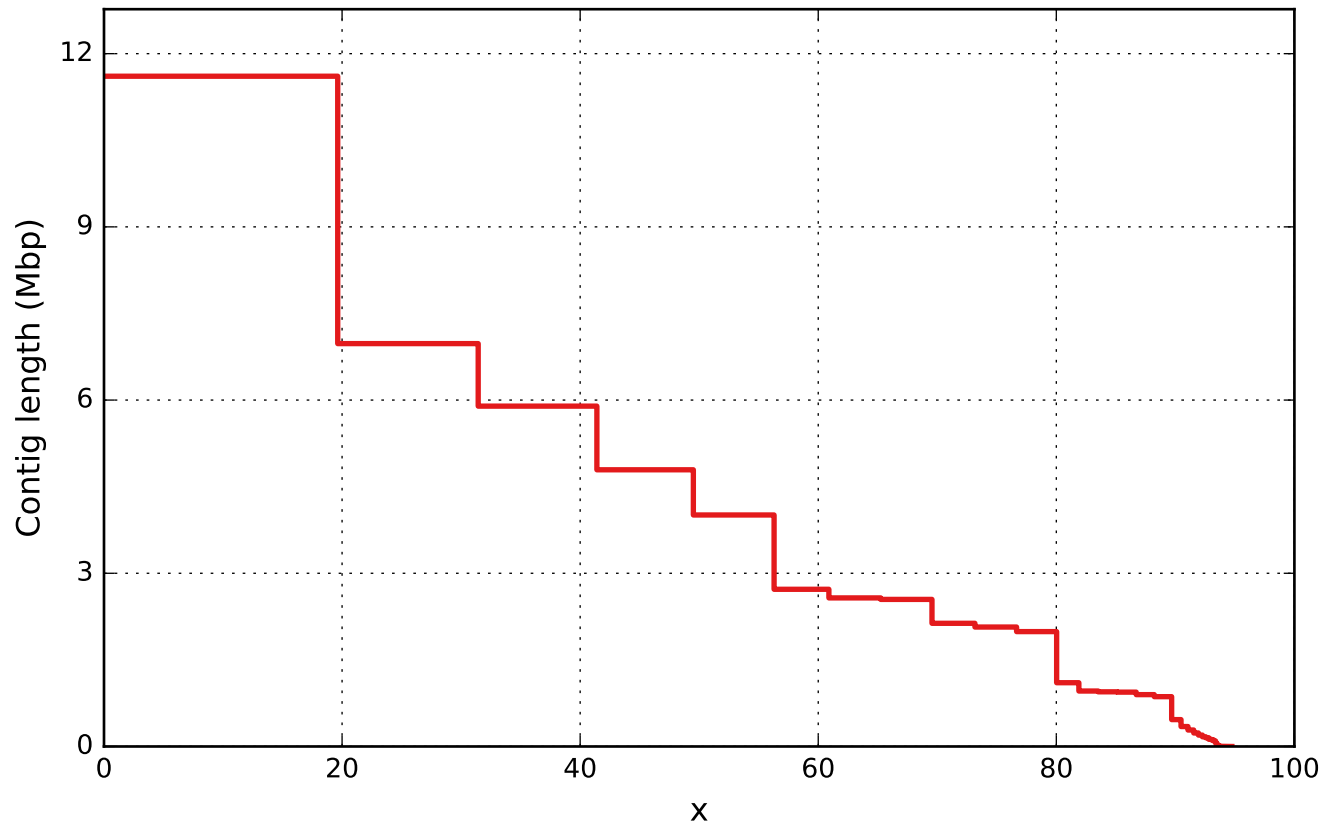
| | uniq_contigs_contigs_contigs_contigs |
|-------------------------------|--------------------------------------|
| # fully unaligned contigs | 374 |
| Fully unaligned length | 162432 |
| # partially unaligned contigs | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

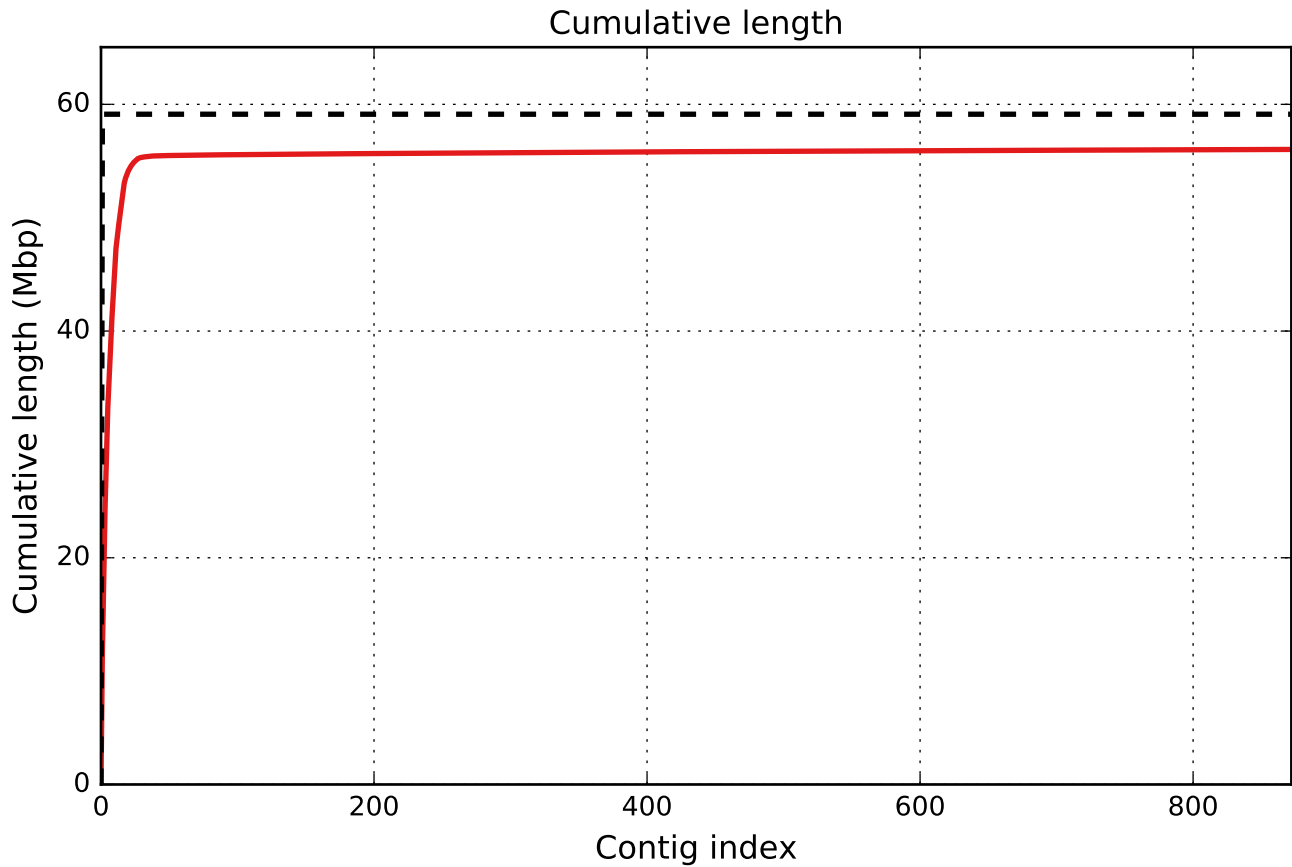


— uniq_contigs_contigs_contigs_contigs

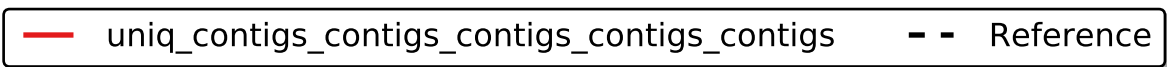
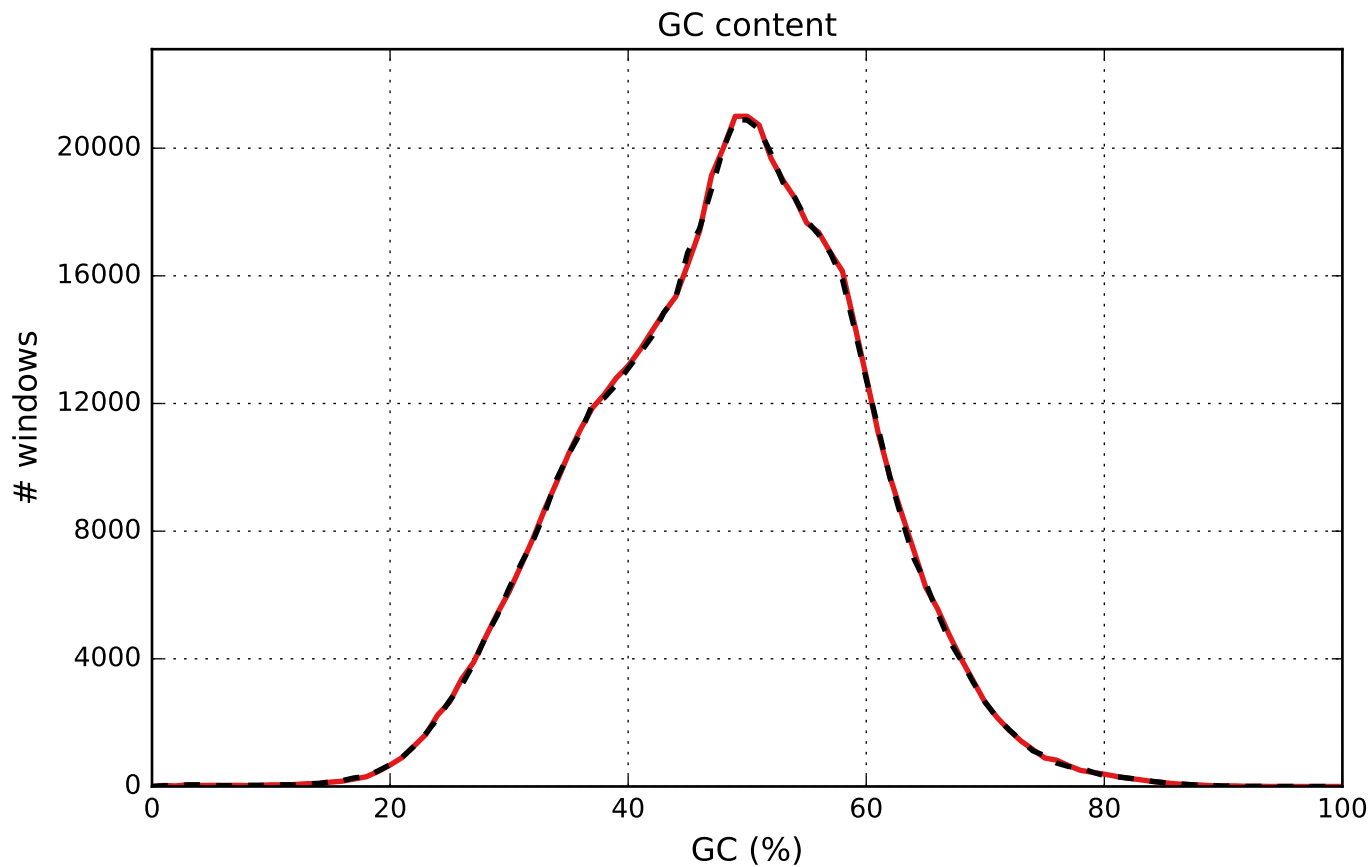
NGx

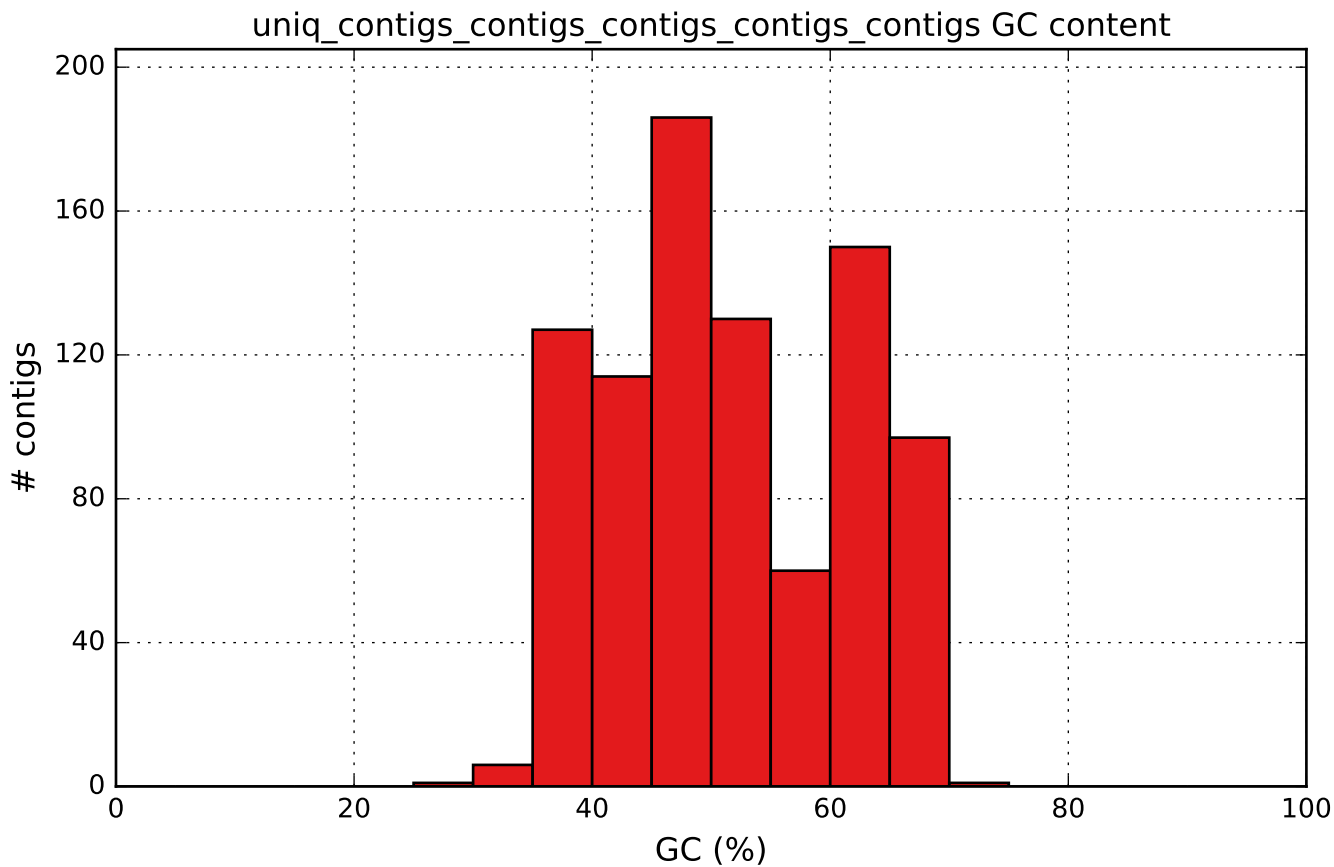


— uniq_contigs_contigs_contigs_contigs

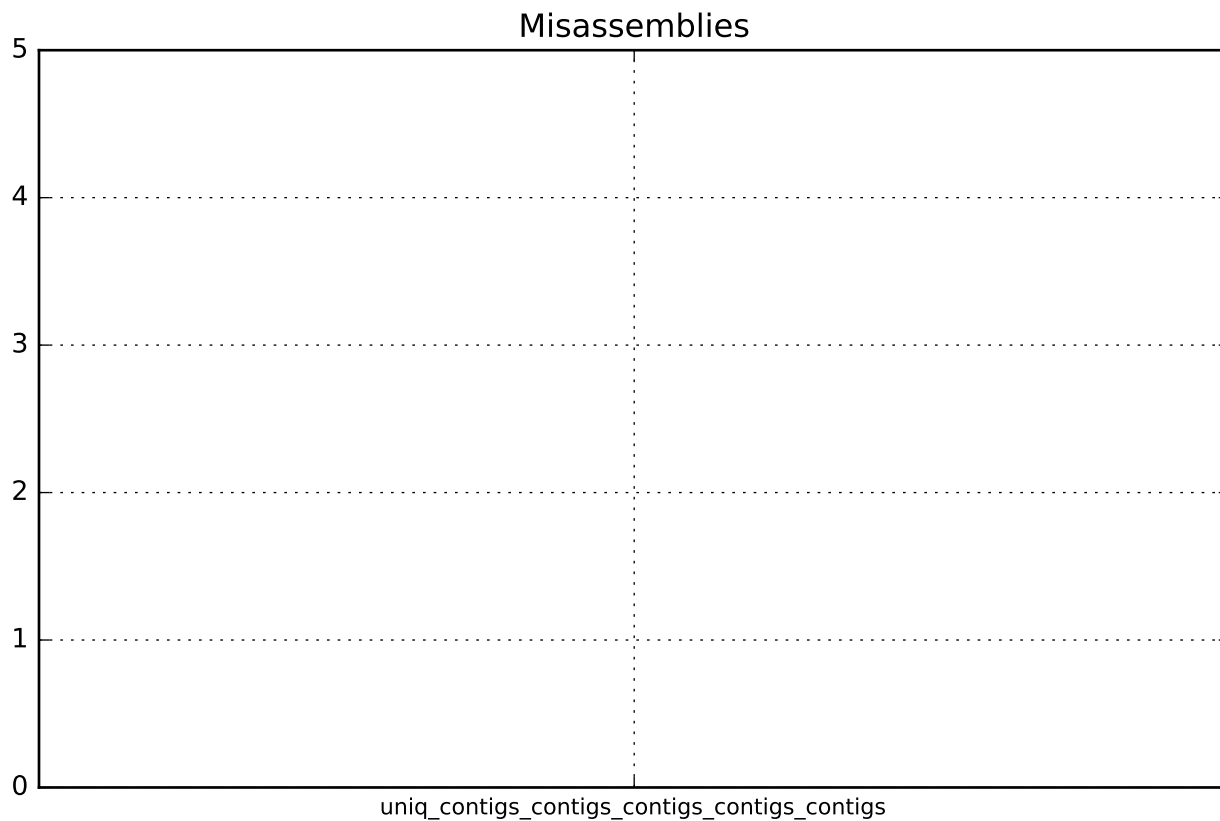


— uniq_contigs_contigs_contigs_contigs - - Reference





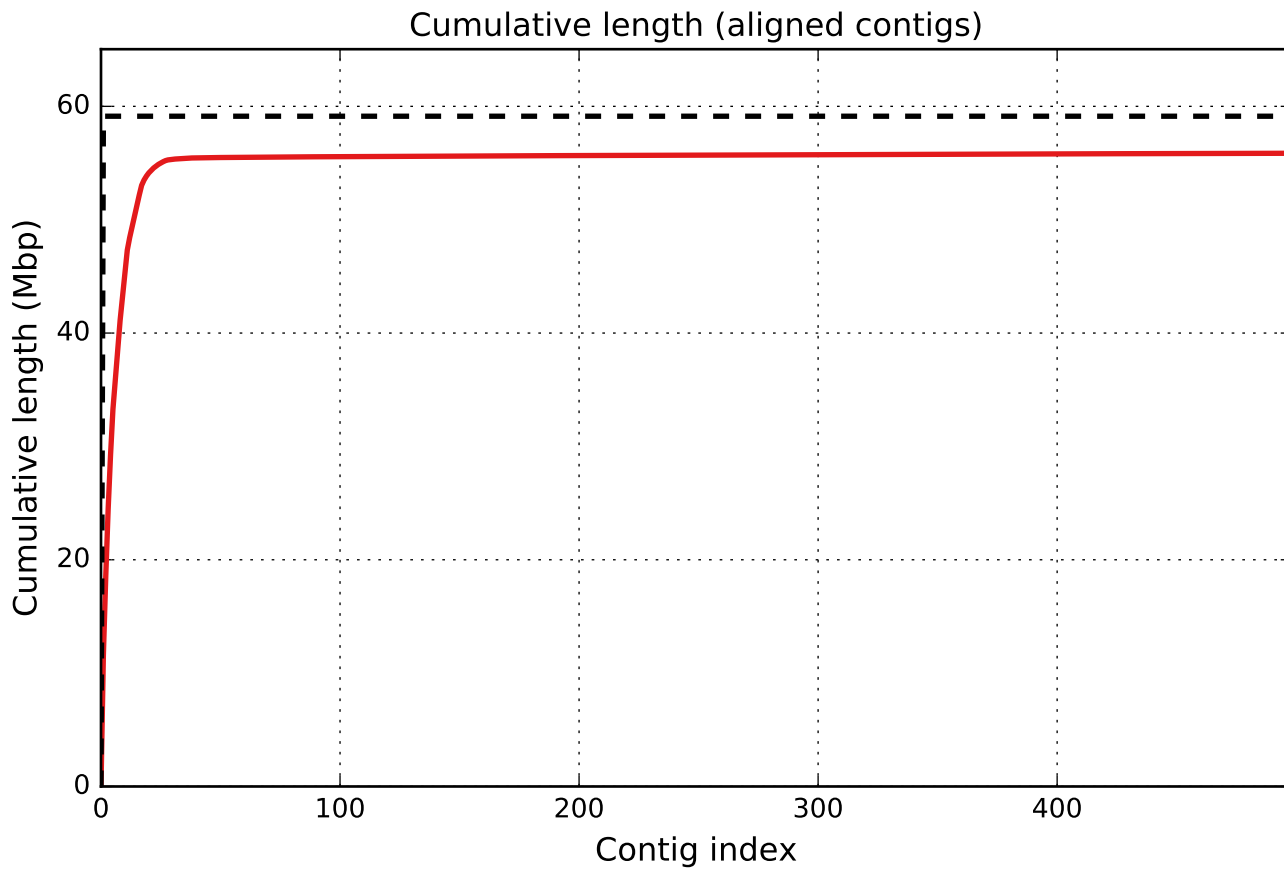
uniq_contigs_contigs_contigs_contigs_contigs



FRCurve (misassemblies)

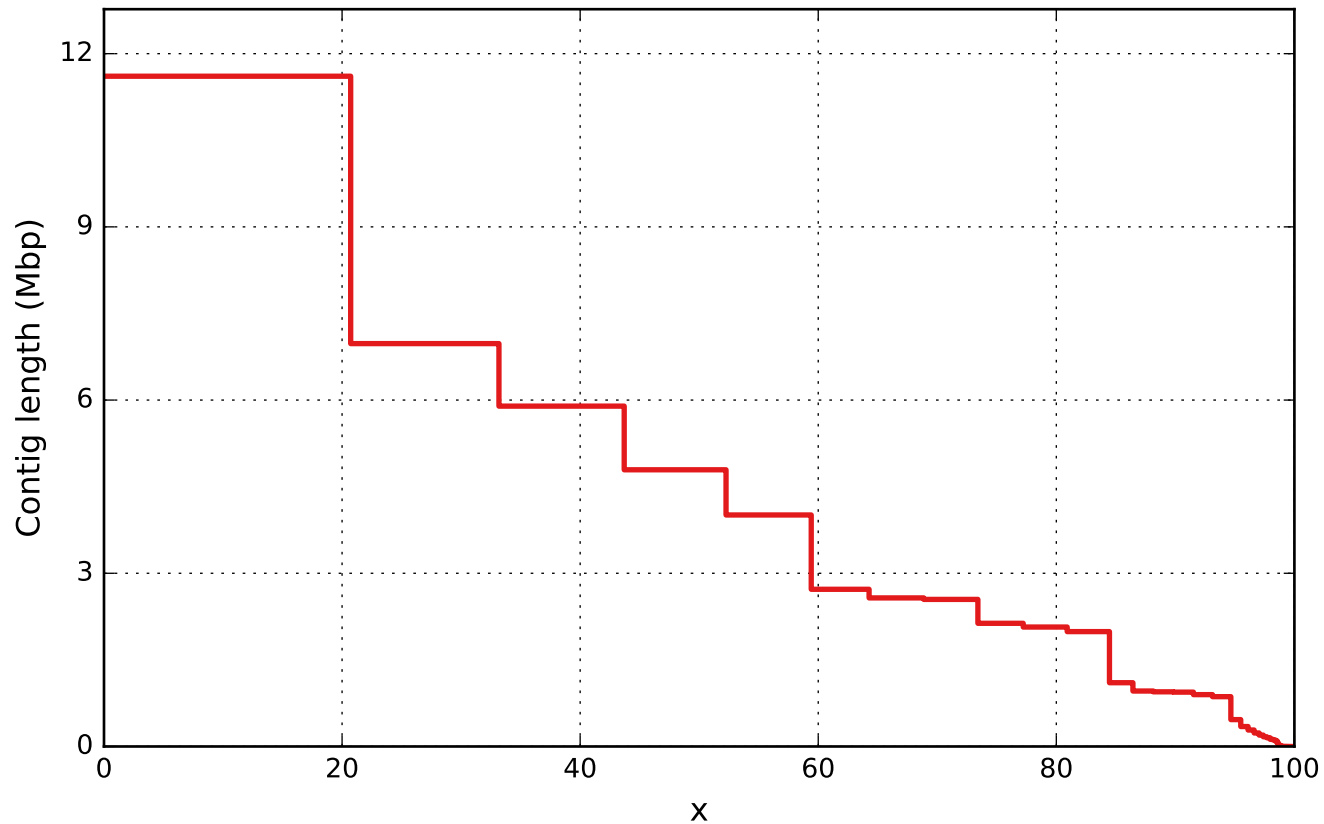


— uniq_contigs_contigs_contigs_contigs_contigs



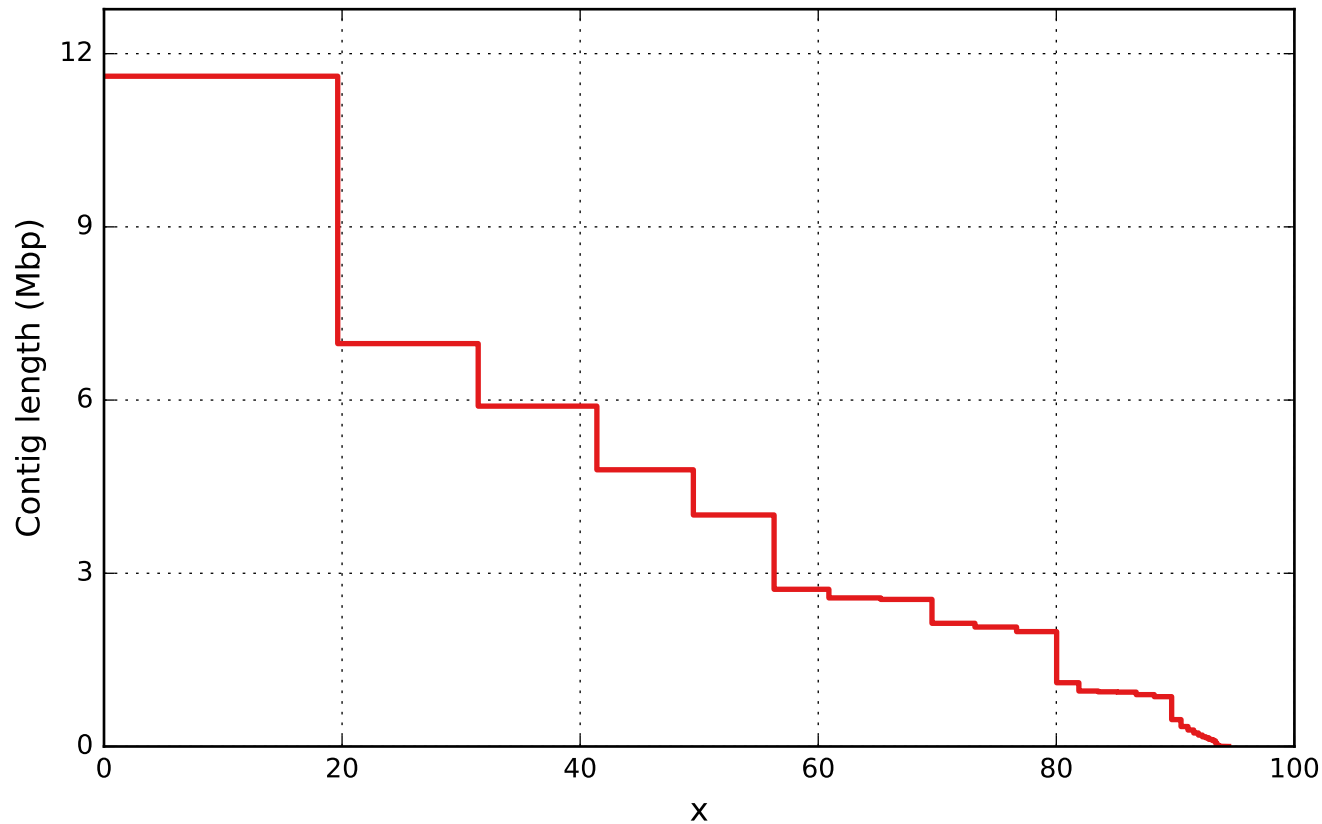
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NAx



— uniq_contigs_contigs_contigs_contigs

NGAx



— uniq_contigs_contigs_contigs_contigs