# Report

| | final.contigs |
|---|---|
| # contigs (>= 0 bp) | 161952 |
| # contigs (>= 1000 bp) | 25167 |
| # contigs (>= 5000 bp) | 1190 |
| # contigs (>= 10000 bp) | 282 |
| # contigs (>= 25000 bp) | 35 |
| # contigs (>= 50000 bp) | 9 |
| Total length (>= 0 bp) | 123859441 |
| Total length (>= 1000 bp) | 51904151 |
| Total length (>= 5000 bp) | 11009046 |
| Total length (>= 10000 bp) | 4897402 |
| Total length (>= 25000 bp) | 1486506 |
| Total length (>= 50000 bp) | 650797 |
| # contigs | 89614 |
| Largest contig | 131335 |
| Total length | 95542768 |
| Reference length | 2224914 |
| N50 | 1095 |
| N75 | 703 |
| L50 | 21215 |
| L75 | 49092 |
| # misassemblies | 7 |
| # misassembled contigs | 7 |
| Misassembled contigs length | 7945 |
| # local misassemblies | 1 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 2 |
| # unaligned contigs | 88245 + 46 part |
| Unaligned length | 94245108 |
| Genome fraction (%) | 55.854 |
| Duplication ratio | 1.045 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1154.42 |
| # indels per 100 kbp | 7.73 |
| Largest alignment | 3896 |
| Total aligned length | 1280524 |

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).
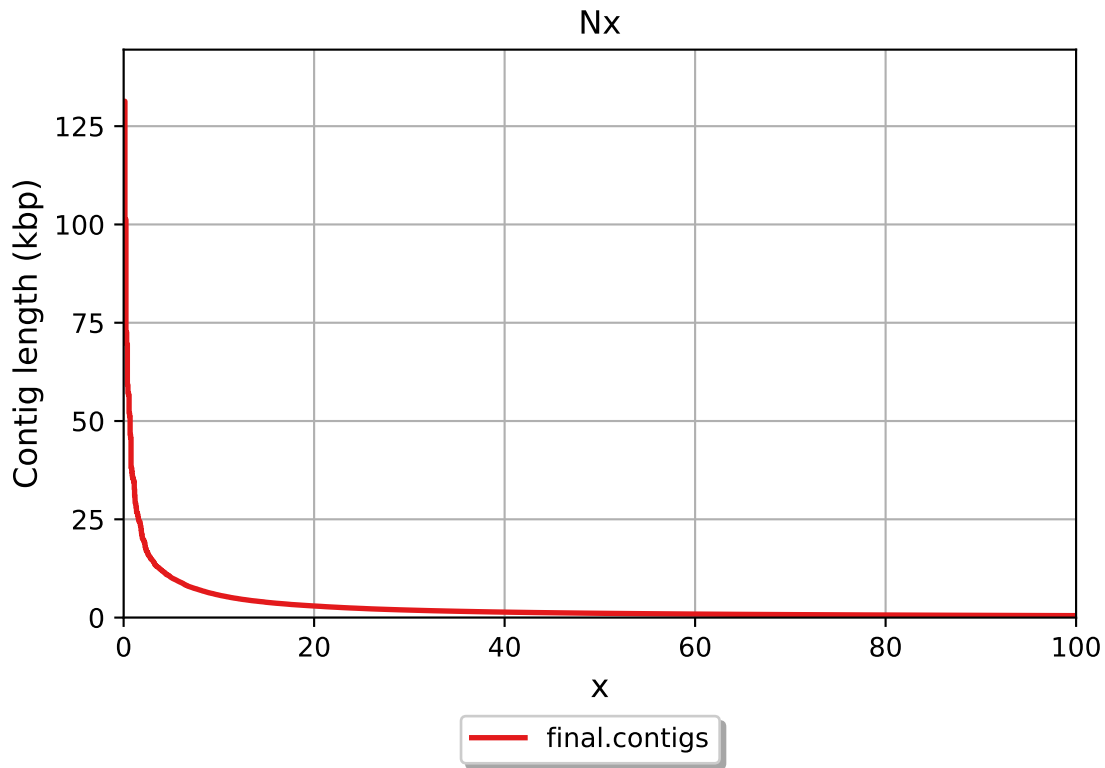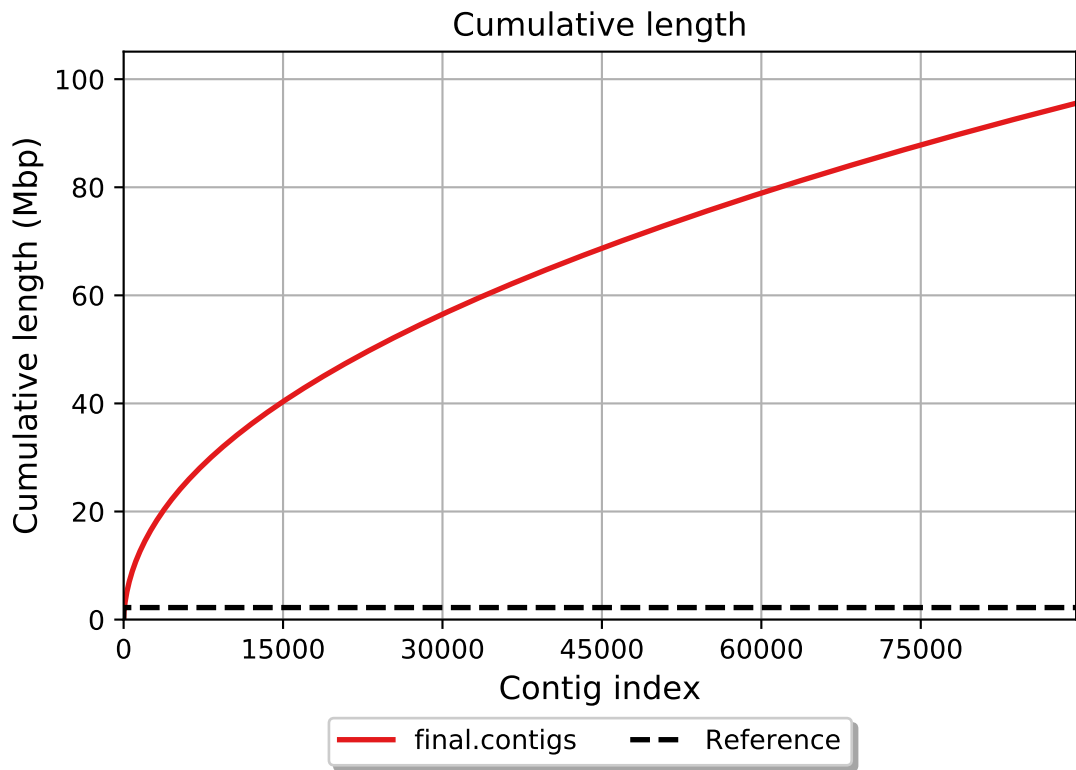
# Misassemblies report

|  | final.contigs |
|---|---|
| # misassemblies | 7 |
| # contig misassemblies | 7 |
| # c. relocations | 7 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # c. interspecies translocations | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # s. interspecies translocations | 0 |
| # misassembled contigs | 7 |
| Misassembled contigs length | 7945 |
| # possibly misassembled contigs | 46 |
| # possible misassemblies | 55 |
| # local misassemblies | 1 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 2 |
| # mismatches | 14346 |
| # indels | 96 |
| # indels (<= 5 bp) | 88 |
| # indels (> 5 bp) | 8 |
| Indels length | 334 |

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).
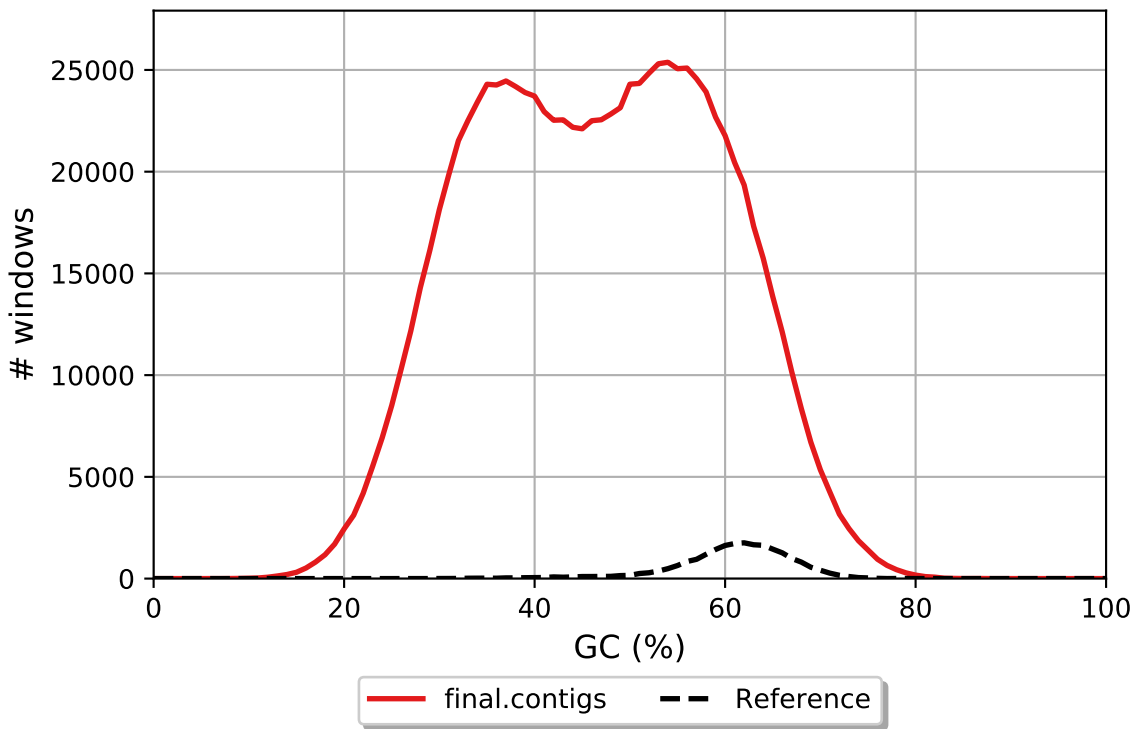
# Unaligned report

|  | final.contigs |
|---|---|
| # fully unaligned contigs | 88245 |
| Fully unaligned length | 94184447 |
| # partially unaligned contigs | 46 |
| Partially unaligned length | 60661 |
| # N's | 0 |

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).
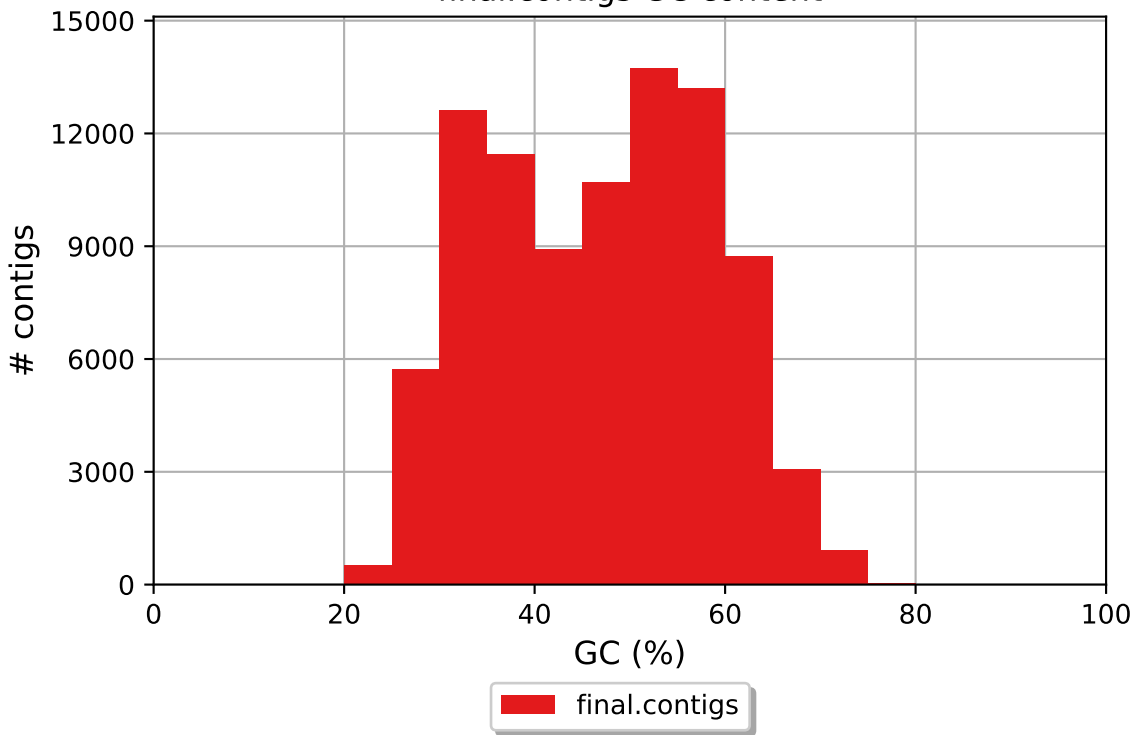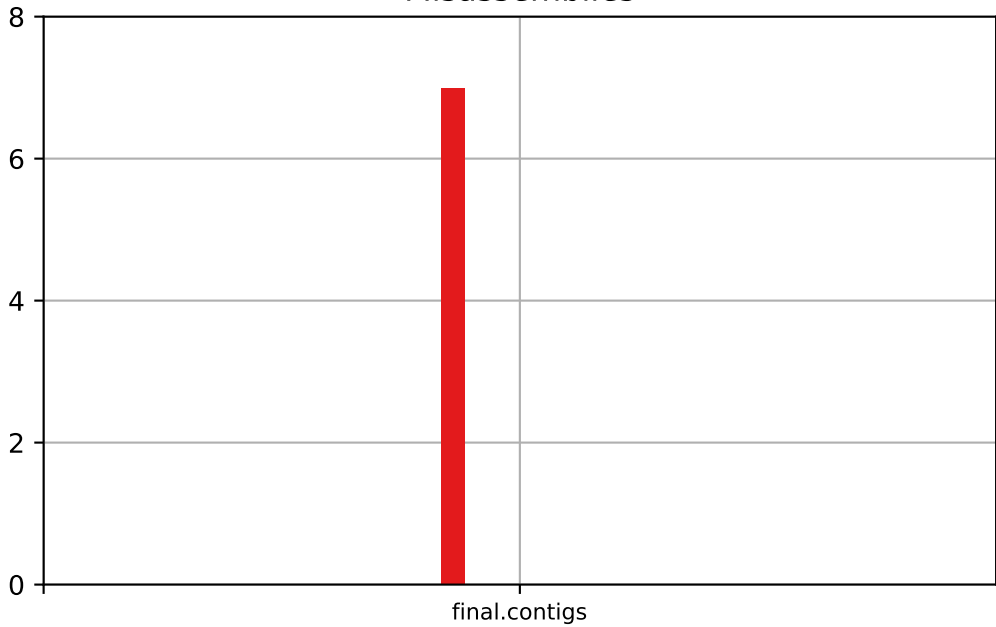
Nx

Cumulative length

GC content

final.contigs GC content

Misassemblies

final.contigs

# relocations
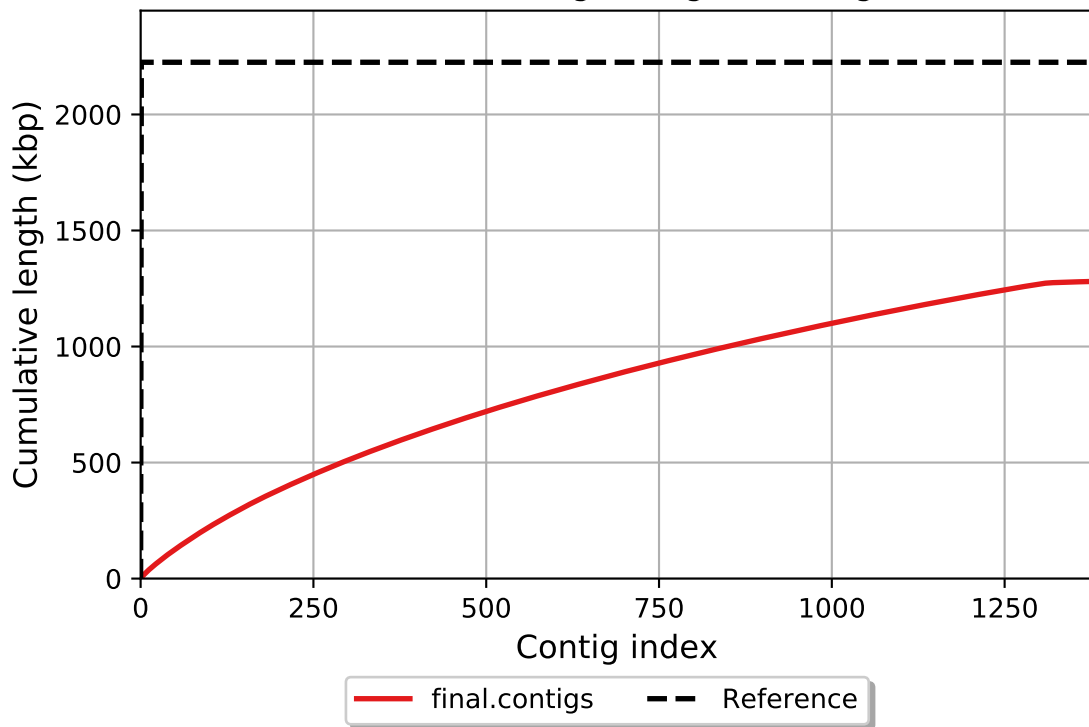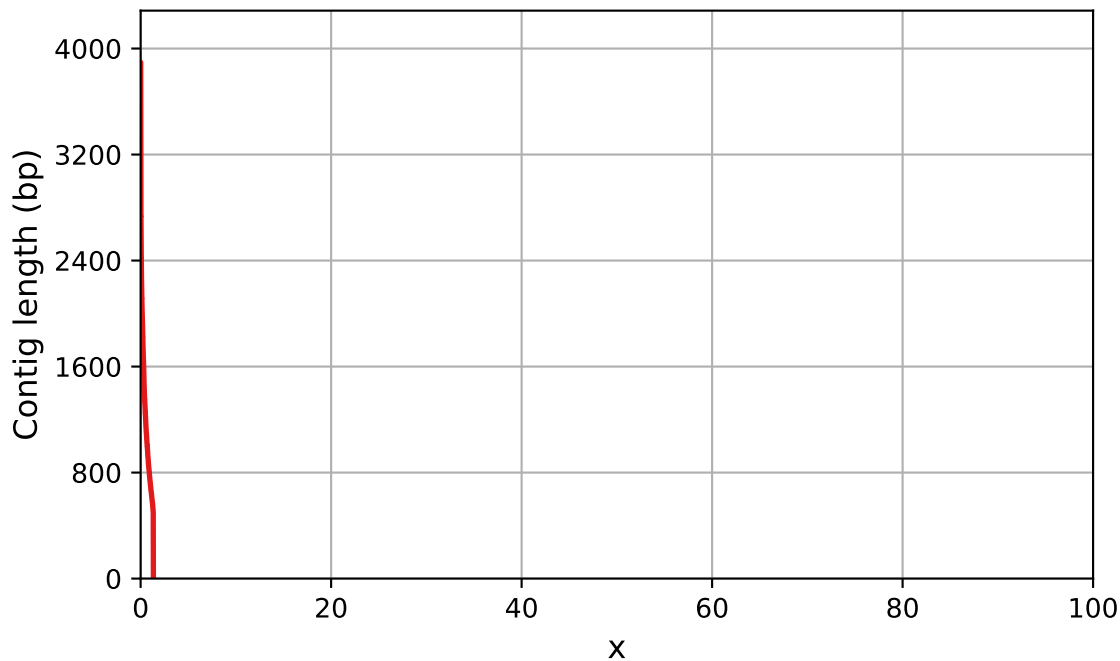
FRCurve (misassemblies)
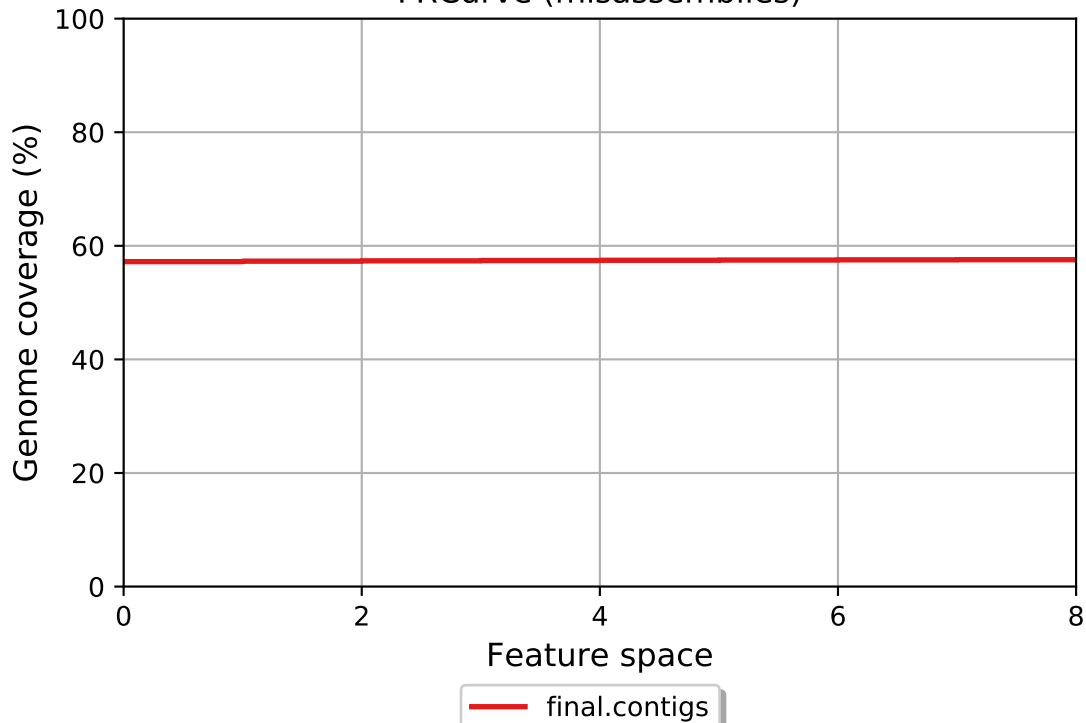
Cumulative length (aligned contigs)

NAx