

Report

| GCA_024662175.1_ASM2466217v1_genomic | |
|--------------------------------------|----------------|
| # contigs (>= 0 bp) | 18 |
| # contigs (>= 1000 bp) | 18 |
| # contigs (>= 5000 bp) | 18 |
| # contigs (>= 10000 bp) | 18 |
| # contigs (>= 25000 bp) | 15 |
| # contigs (>= 50000 bp) | 2 |
| Total length (>= 0 bp) | 1417706 |
| Total length (>= 1000 bp) | 1417706 |
| Total length (>= 5000 bp) | 1417706 |
| Total length (>= 10000 bp) | 1417706 |
| Total length (>= 25000 bp) | 1357402 |
| Total length (>= 50000 bp) | 974305 |
| # contigs | 18 |
| Largest contig | 920773 |
| Total length | 1417706 |
| Reference length | 1521208 |
| GC (%) | 28.16 |
| Reference GC (%) | 28.18 |
| N50 | 920773 |
| NG50 | 920773 |
| N90 | 28768 |
| NG90 | 21173 |
| auN | 608890.7 |
| auNG | 567462.2 |
| L50 | 1 |
| LG50 | 1 |
| L90 | 12 |
| LG90 | 16 |
| # misassemblies | 18 |
| # misassembled contigs | 10 |
| Misassembled contigs length | 1203046 |
| # local misassemblies | 14 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 3 |
| # unaligned contigs | 0 + 15 part |
| Unaligned length | 177750 |
| Genome fraction (%) | 78.659 |
| Duplication ratio | 1.036 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 844.86 |
| # indels per 100 kbp | 51.95 |
| # genomic features | 1255 + 46 part |
| Largest alignment | 905132 |
| Total aligned length | 1239616 |
| NA50 | 905132 |
| NGA50 | 905132 |
| NA90 | - |
| NGA90 | - |
| auNA | 582296.2 |
| auNGA | 542677.2 |
| LA50 | 1 |
| LGA50 | 1 |
| LA90 | - |
| LGA90 | - |

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

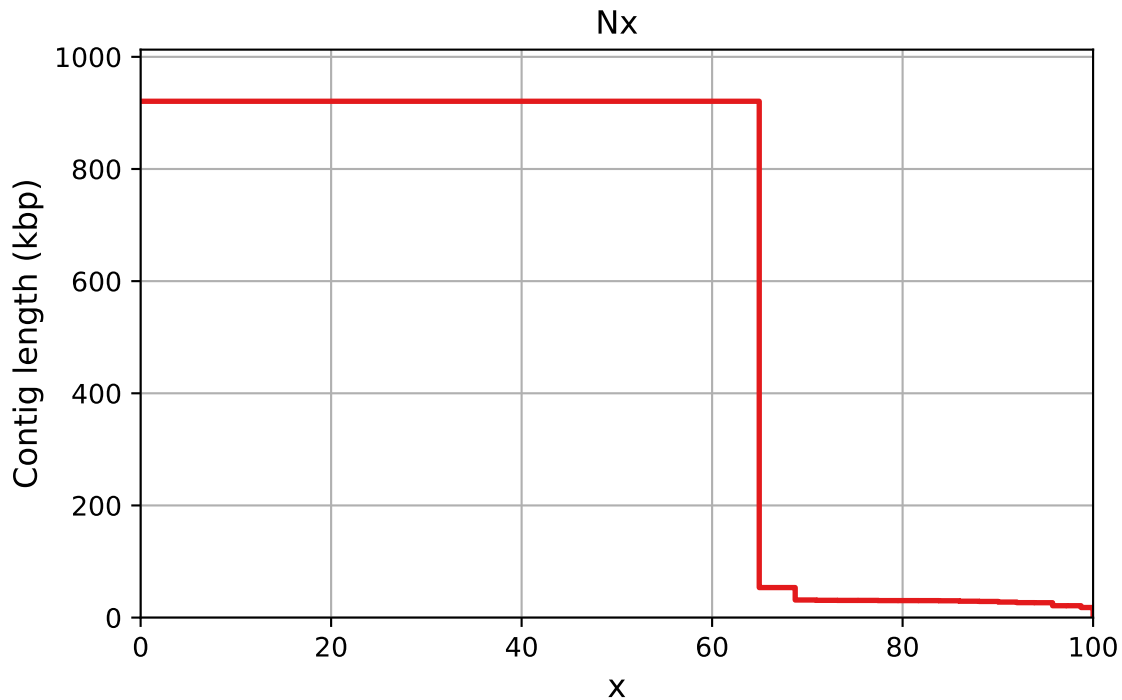
| | GCA_024662175.1_ASM2466217v1_genomic |
|-----------------------------|--------------------------------------|
| # misassemblies | 18 |
| # contig misassemblies | 18 |
| # c. relocations | 5 |
| # c. translocations | 13 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 10 |
| Misassembled contigs length | 1203046 |
| # local misassemblies | 14 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 3 |
| # mismatches | 10473 |
| # indels | 644 |
| # indels (<= 5 bp) | 577 |
| # indels (> 5 bp) | 67 |
| Indels length | 4262 |

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

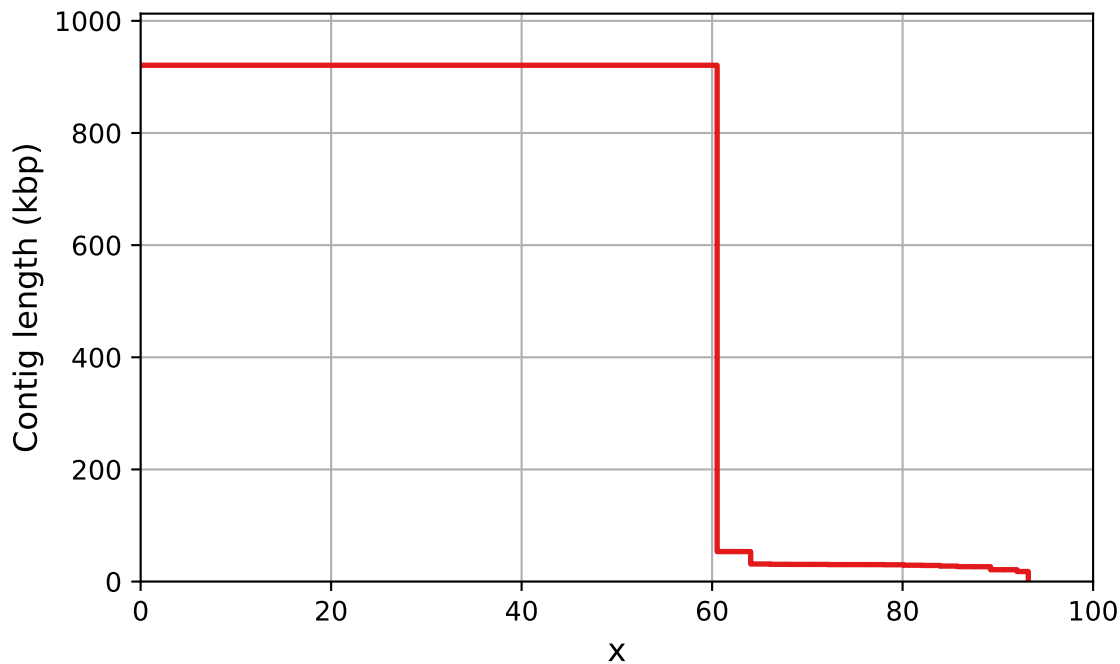
| | GCA_024662175.1_ASM2466217v1_genomic |
|-------------------------------|--------------------------------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 15 |
| Partially unaligned length | 177750 |
| # N's | 0 |

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).

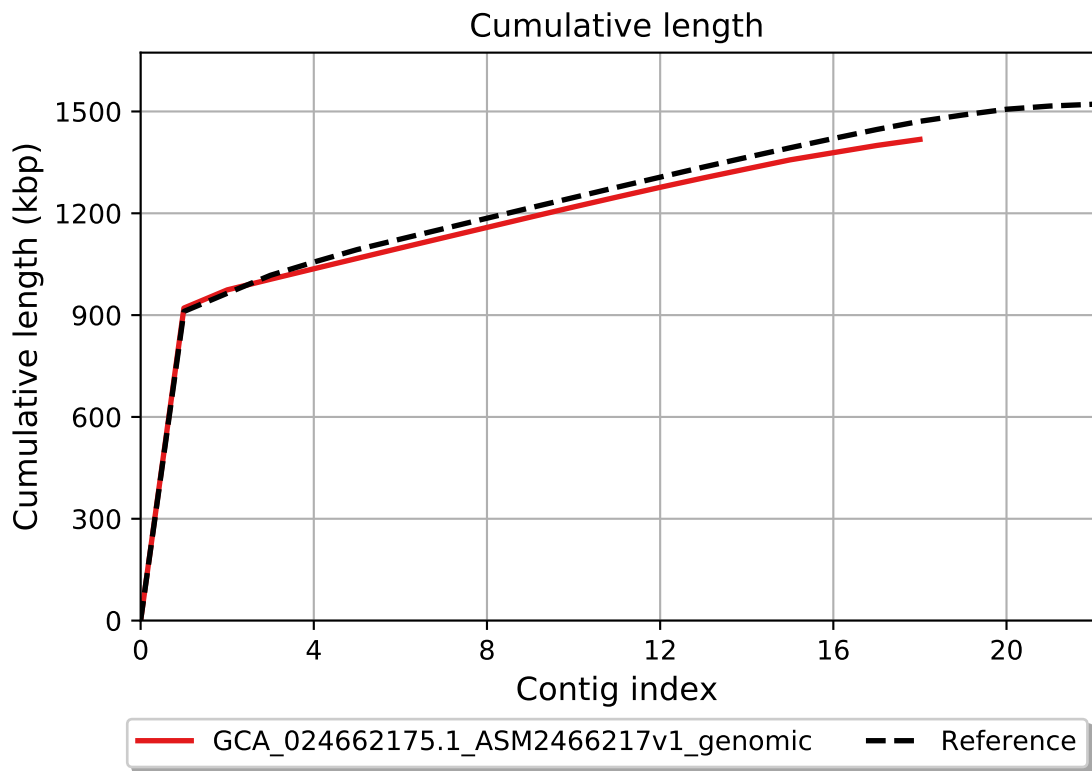


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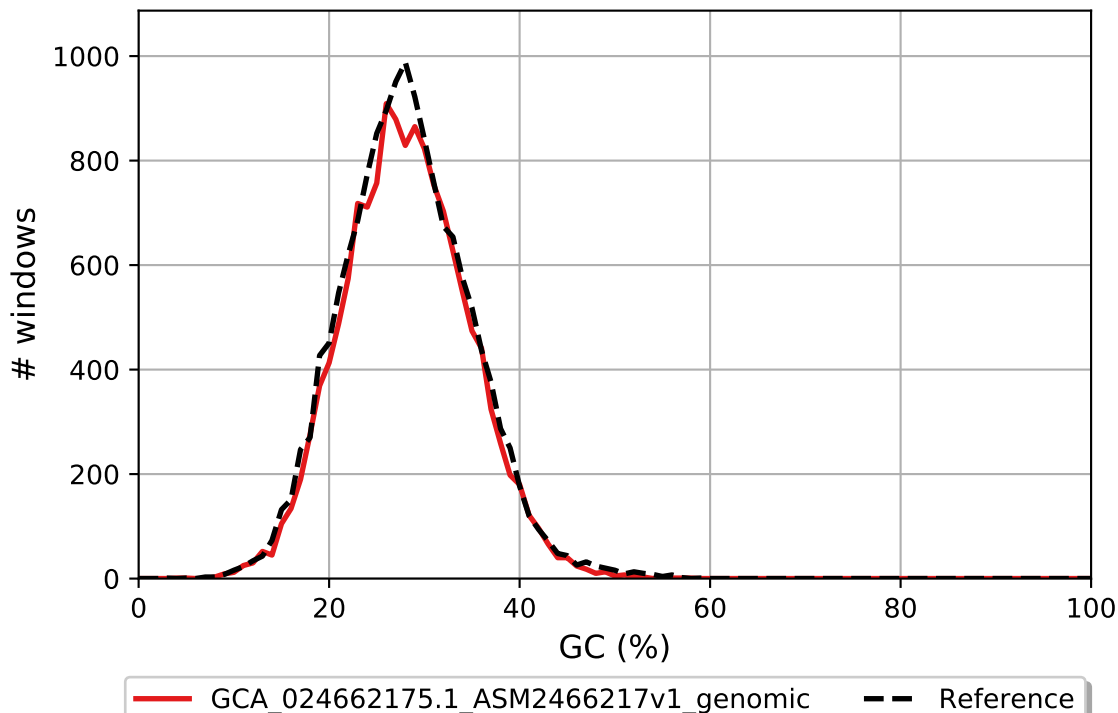
NGx



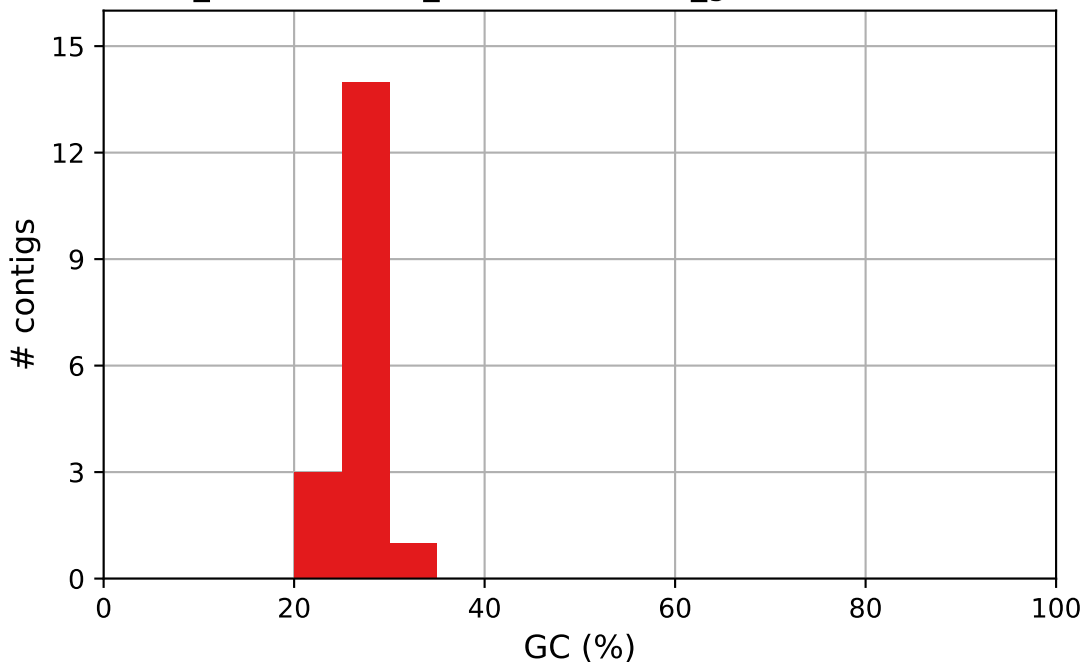
— GCA_024662175.1_ASM2466217v1_genomic



GC content

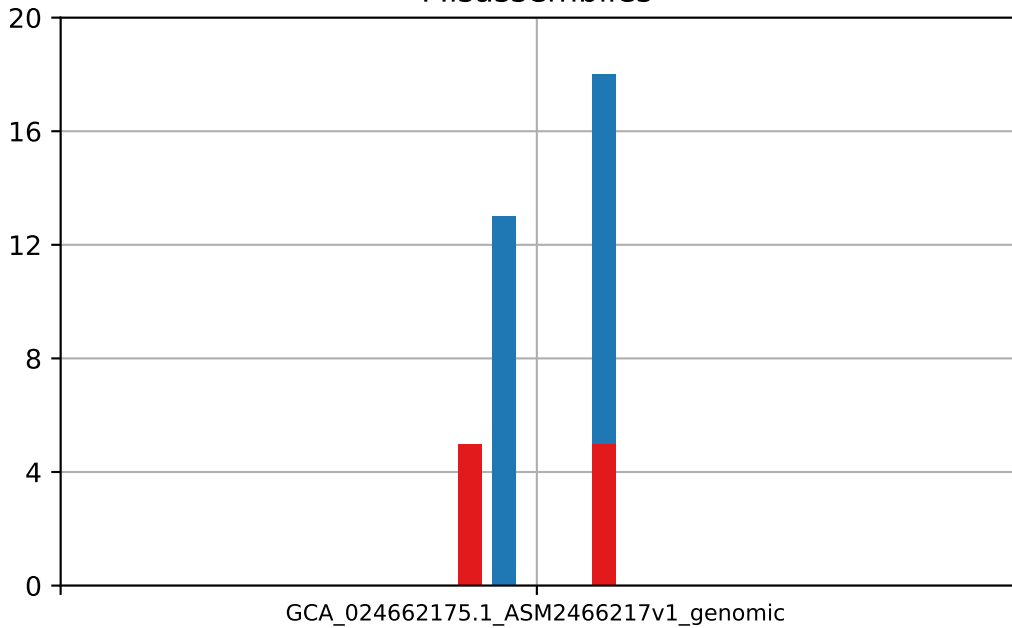


GCA_024662175.1_ASM2466217v1_genomic GC content



GCA_024662175.1_ASM2466217v1_genomic

Misassemblies

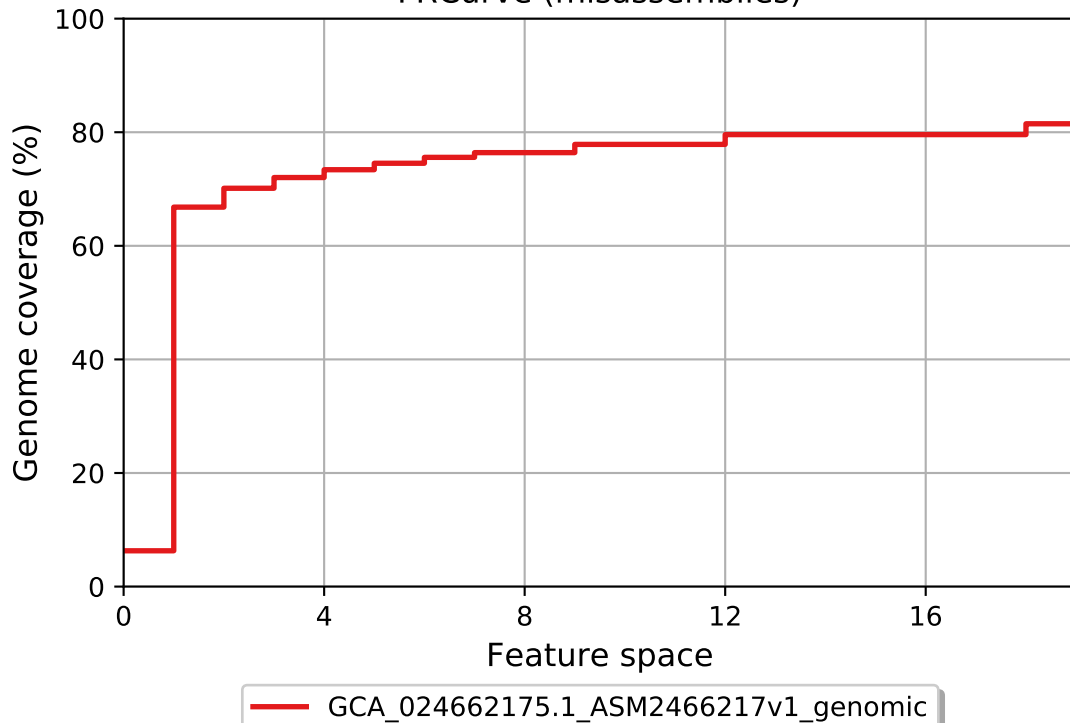


relocations

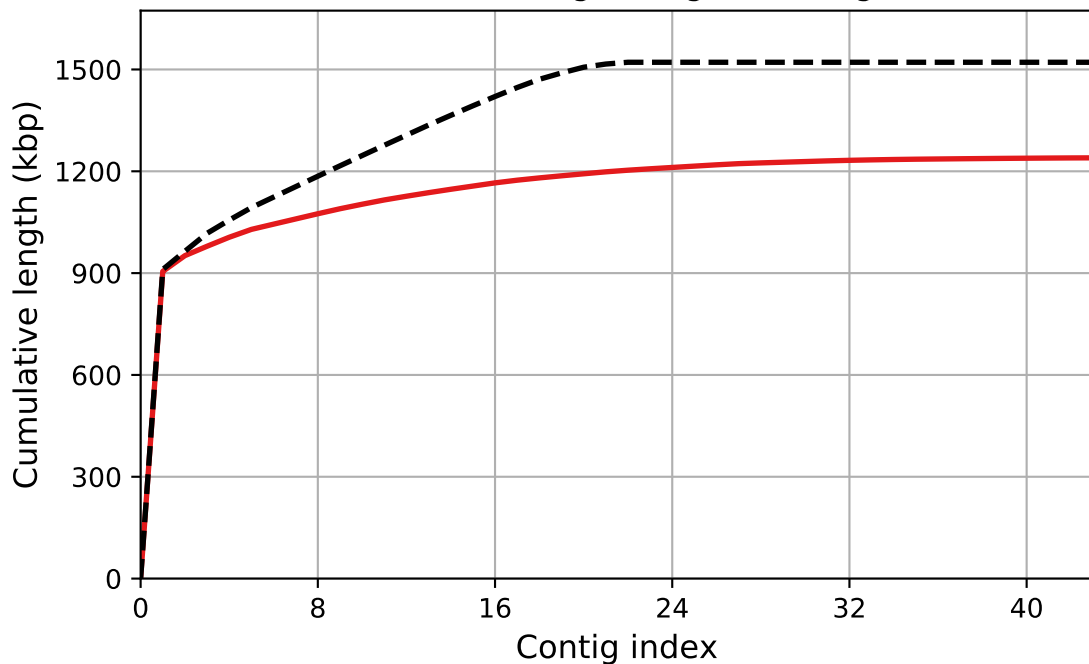


translocations

FRCurve (misassemblies)



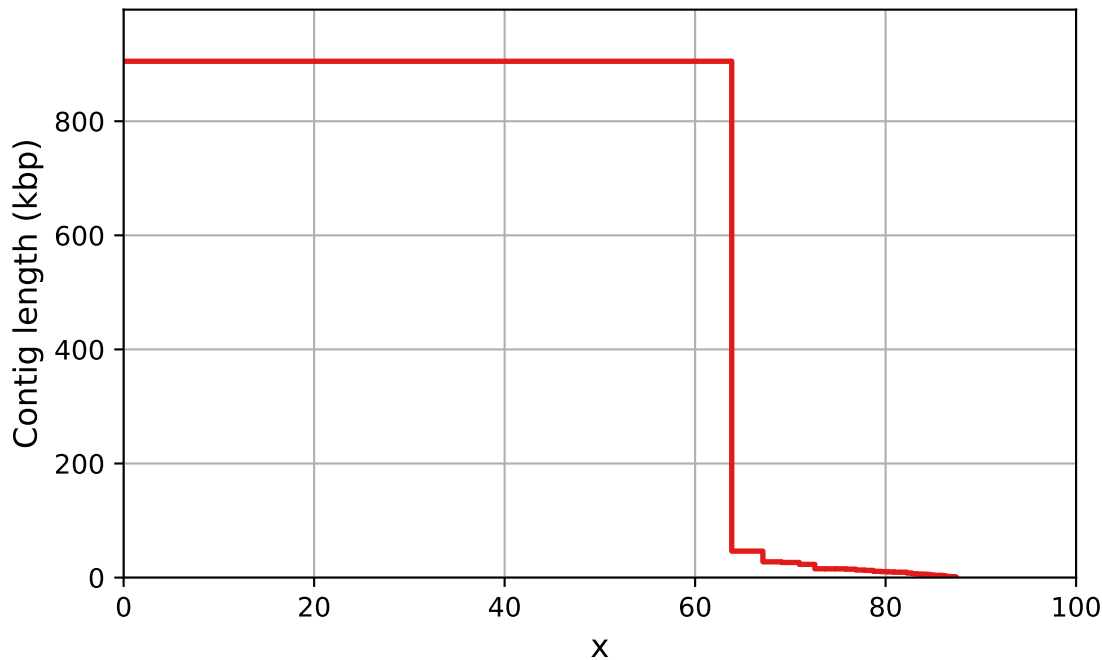
Cumulative length (aligned contigs)



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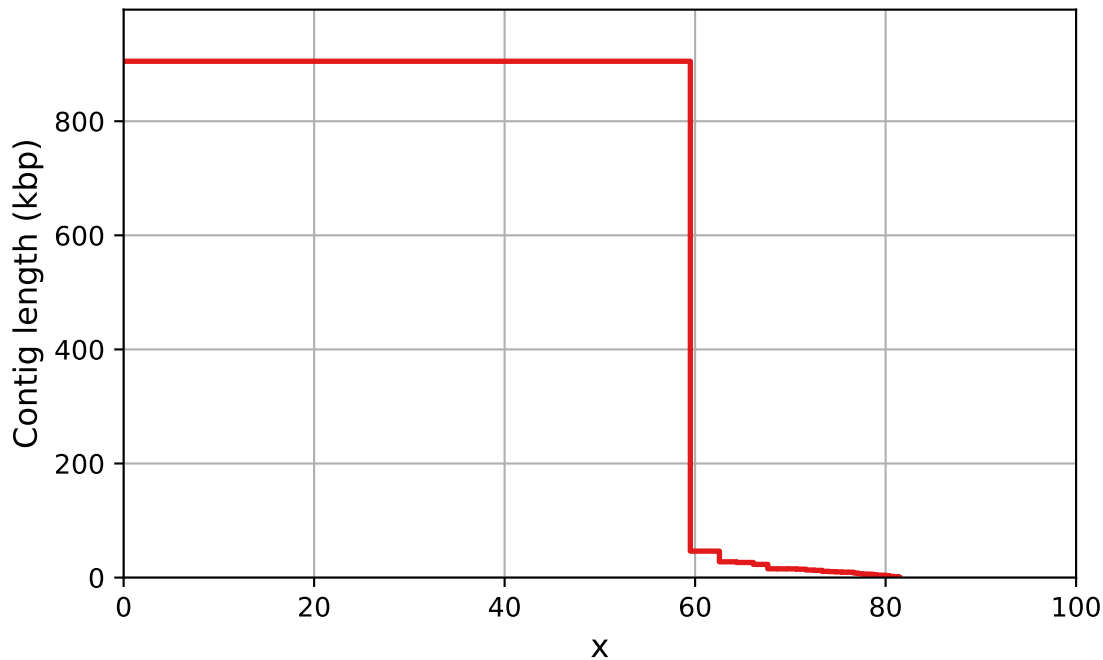
Reference

NAx

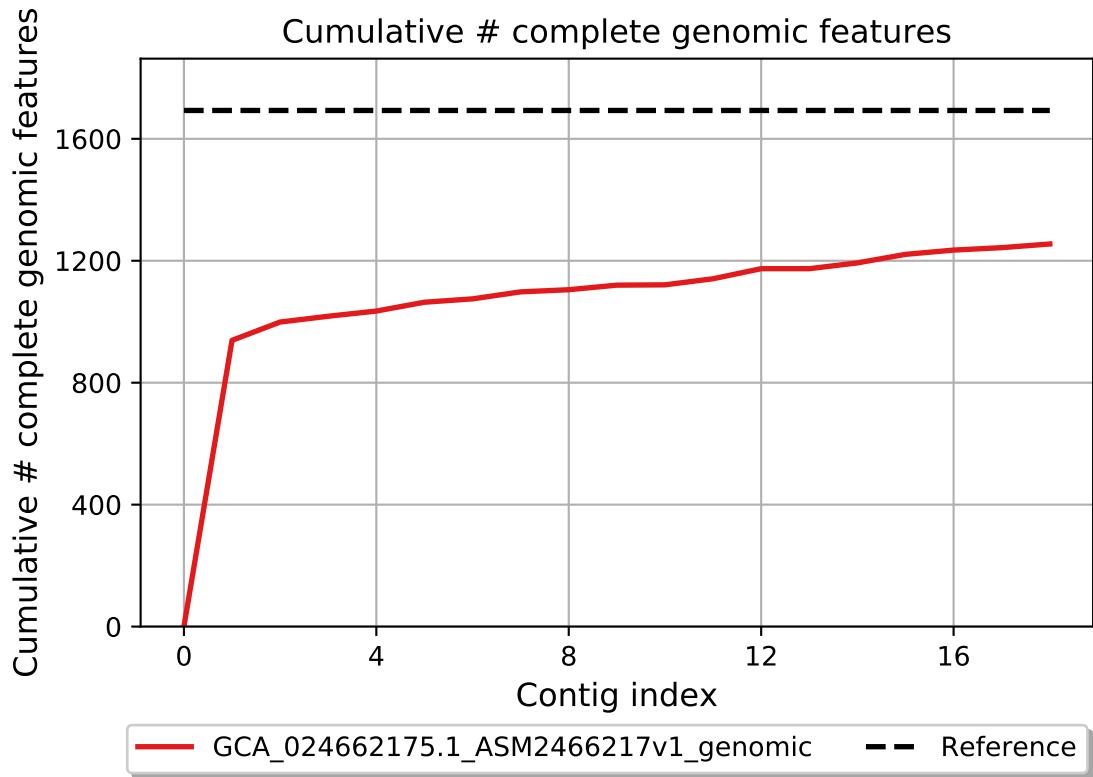


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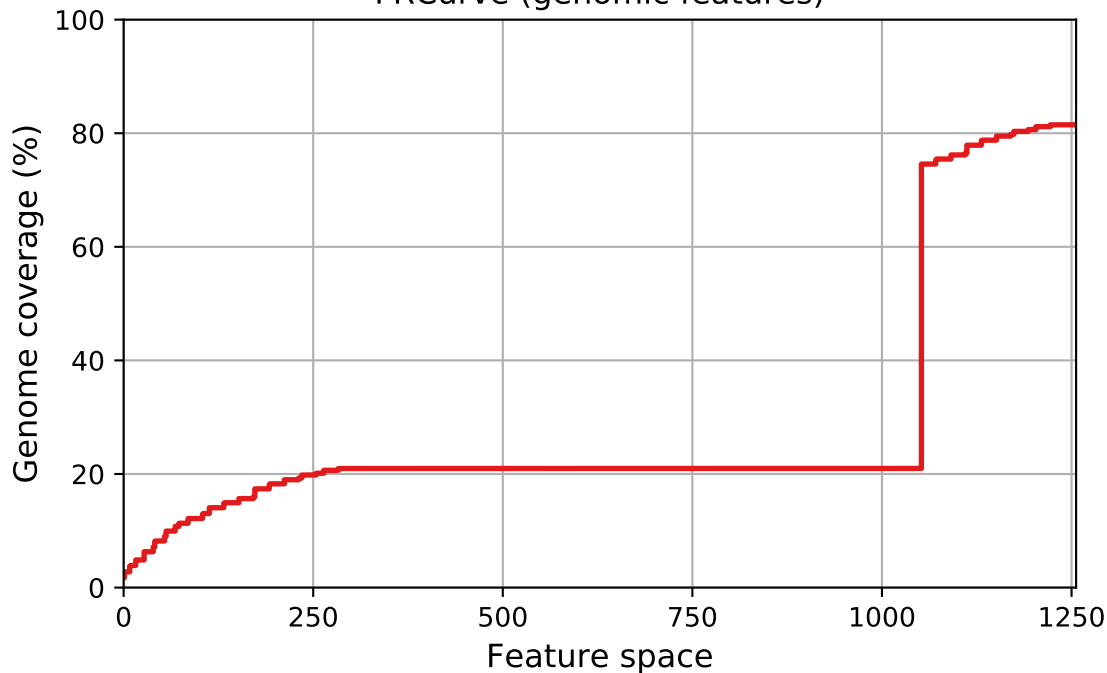
NGAx



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FRCurve (genomic features)



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