

Report

| | finalprojectSalinibacter-8_fa | finalprojectSalinibacter-8_fa_broken |
|-----------------------------|-------------------------------|--------------------------------------|
| # contigs (>= 0 bp) | 433 | - |
| # contigs (>= 1000 bp) | 39 | 41 |
| Total length (>= 0 bp) | 3850338 | - |
| Total length (>= 1000 bp) | 3791162 | 3791062 |
| # contigs | 42 | 44 |
| Largest contig | 437425 | 437425 |
| Total length | 3793344 | 3793244 |
| Reference length | 3901694 | 3901694 |
| GC (%) | 66.00 | 66.00 |
| Reference GC (%) | 65.70 | 65.70 |
| N50 | 361772 | 198258 |
| NG50 | 361772 | 198258 |
| N90 | 46336 | 46336 |
| NG90 | 42616 | 42616 |
| auN | 261889.5 | 241977.1 |
| auNG | 254616.9 | 235251.2 |
| L50 | 5 | 6 |
| LG50 | 5 | 6 |
| L90 | 19 | 20 |
| LG90 | 21 | 22 |
| # misassemblies | 58 | 58 |
| # misassembled contigs | 19 | 21 |
| Misassembled contigs length | 2841678 | 2841578 |
| # local misassemblies | 39 | 39 |
| # scaffold gap ext. mis. | 0 | - |
| # scaffold gap loc. mis. | 1 | - |
| # unaligned mis. contigs | 4 | 4 |
| # unaligned contigs | 2 + 29 part | 2 + 30 part |
| Unaligned length | 443854 | 443854 |
| Genome fraction (%) | 85.404 | 85.404 |
| Duplication ratio | 1.007 | 1.007 |
| # N's per 100 kbp | 3.30 | 0.66 |
| # mismatches per 100 kbp | 858.44 | 858.57 |
| # indels per 100 kbp | 40.58 | 40.52 |
| # genomic features | 3106 + 112 part | 3105 + 113 part |
| # predicted rRNA genes | 3 + 0 part | 3 + 0 part |
| Largest alignment | 349783 | 349783 |
| Total aligned length | 3346192 | 3346142 |
| NA50 | 78772 | 78772 |
| NGA50 | 78772 | 71514 |
| NA90 | - | - |
| NGA90 | - | - |
| auNA | 107912.5 | 107769.7 |
| auNGA | 104915.8 | 104774.1 |
| LA50 | 13 | 13 |
| LGA50 | 13 | 14 |
| 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

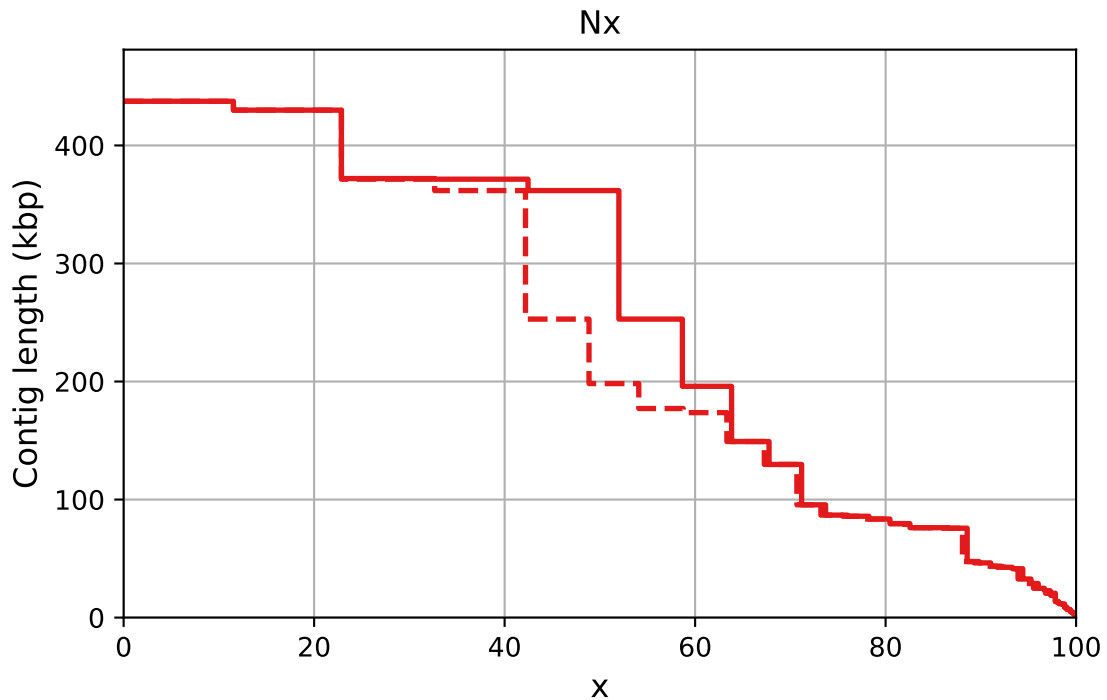
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|-----------------------------|-------------------------------|--------------------------------------|
| # misassemblies | 58 | 58 |
| # contig misassemblies | 58 | 58 |
| # c. relocations | 57 | 57 |
| # c. translocations | 1 | 1 |
| # c. inversions | 0 | 0 |
| # scaffold misassemblies | 0 | 0 |
| # s. relocations | 0 | 0 |
| # s. translocations | 0 | 0 |
| # s. inversions | 0 | 0 |
| # misassembled contigs | 19 | 21 |
| Misassembled contigs length | 2841678 | 2841578 |
| # local misassemblies | 39 | 39 |
| # scaffold gap ext. mis. | 0 | - |
| # scaffold gap loc. mis. | 1 | - |
| # unaligned mis. contigs | 4 | 4 |
| # mismatches | 28725 | 28729 |
| # indels | 1358 | 1356 |
| # indels (<= 5 bp) | 1126 | 1125 |
| # indels (> 5 bp) | 232 | 231 |
| Indels length | 8459 | 8362 |

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

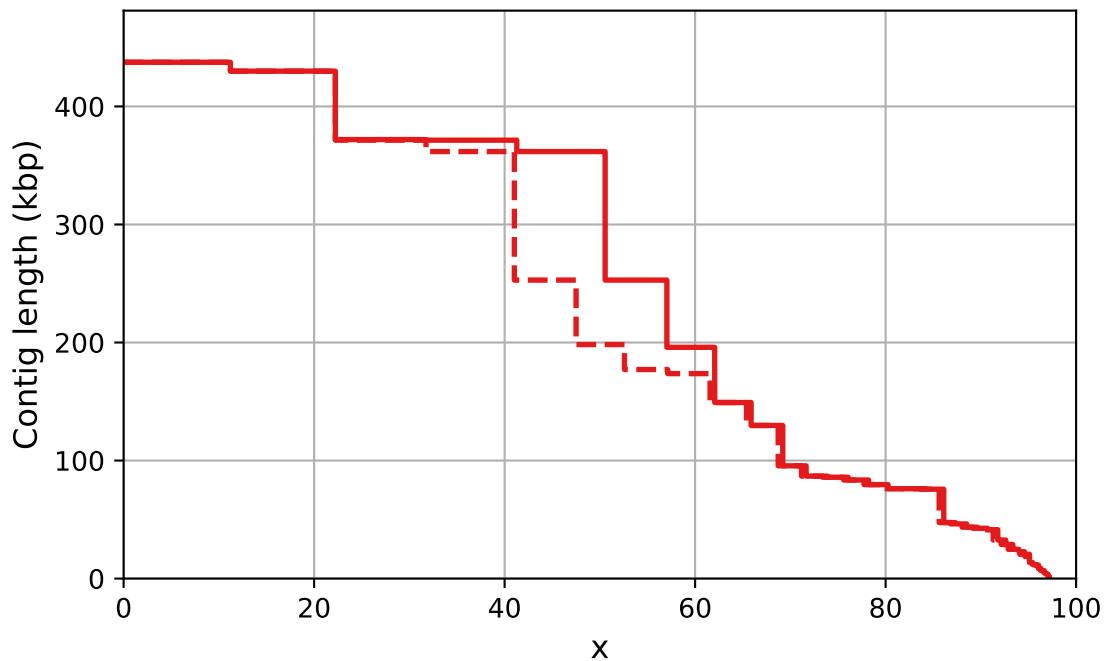
| | finalprojectSalinibacter-8_fa | finalprojectSalinibacter-8_fa_broken |
|-------------------------------|-------------------------------|--------------------------------------|
| # fully unaligned contigs | 2 | 2 |
| Fully unaligned length | 8768 | 8768 |
| # partially unaligned contigs | 29 | 30 |
| Partially unaligned length | 435086 | 435086 |
| # N's | 125 | 25 |

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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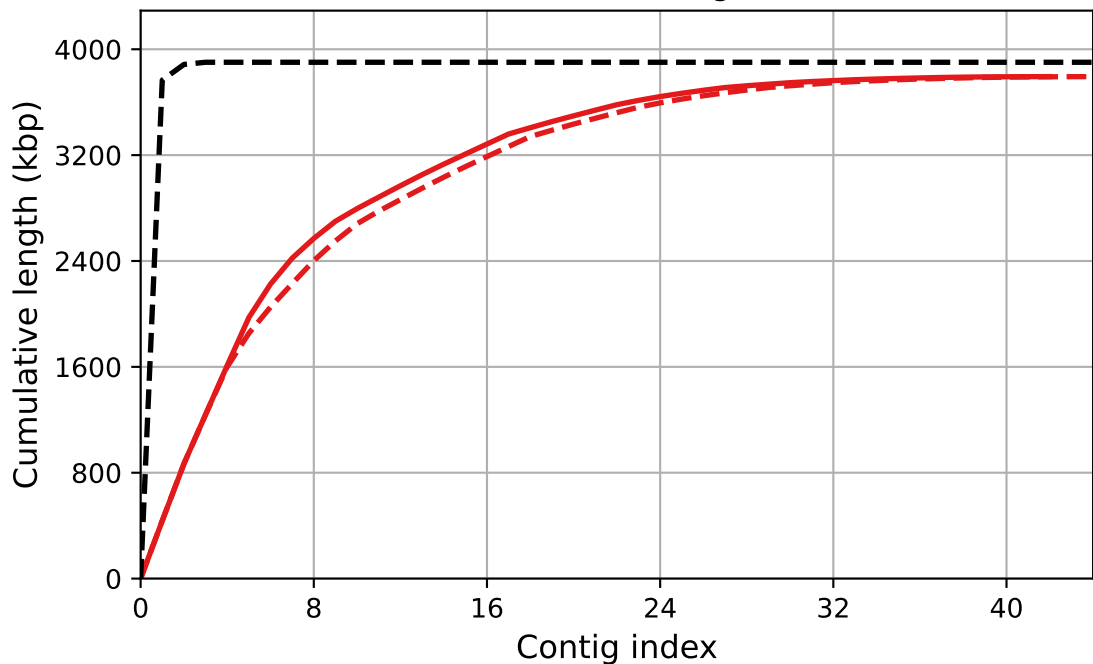
NGx



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Cumulative length

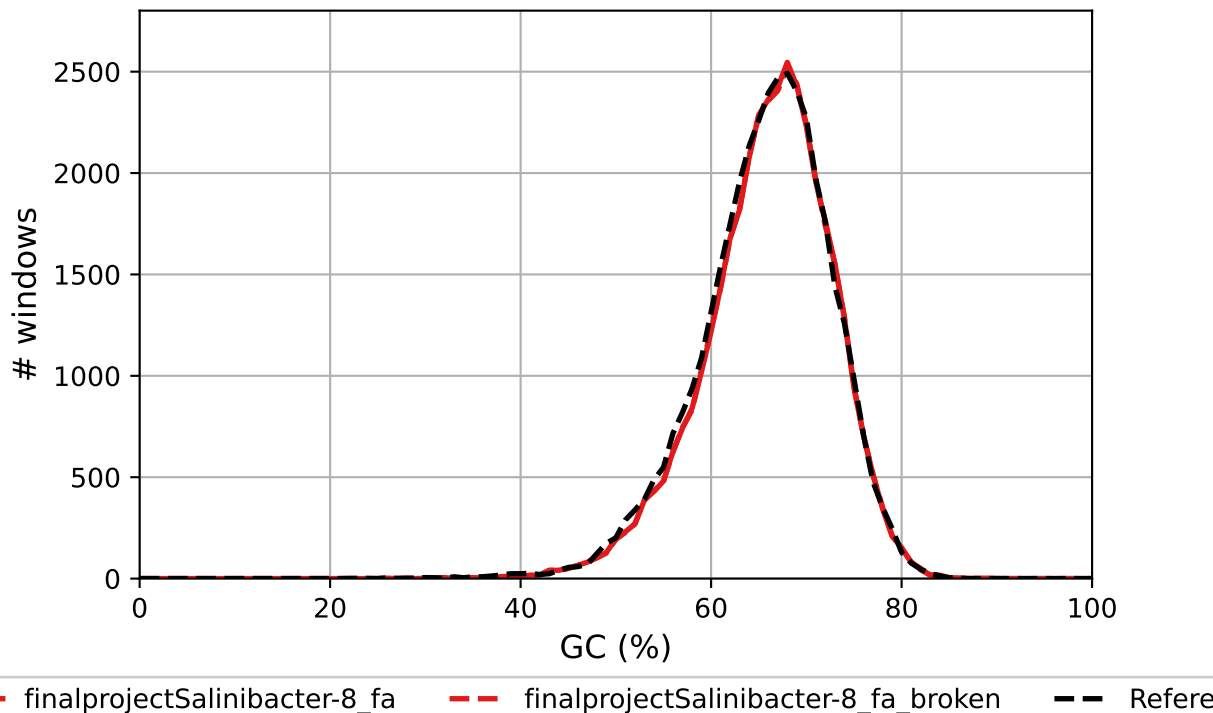


finalprojectSalinibacter-8_fa

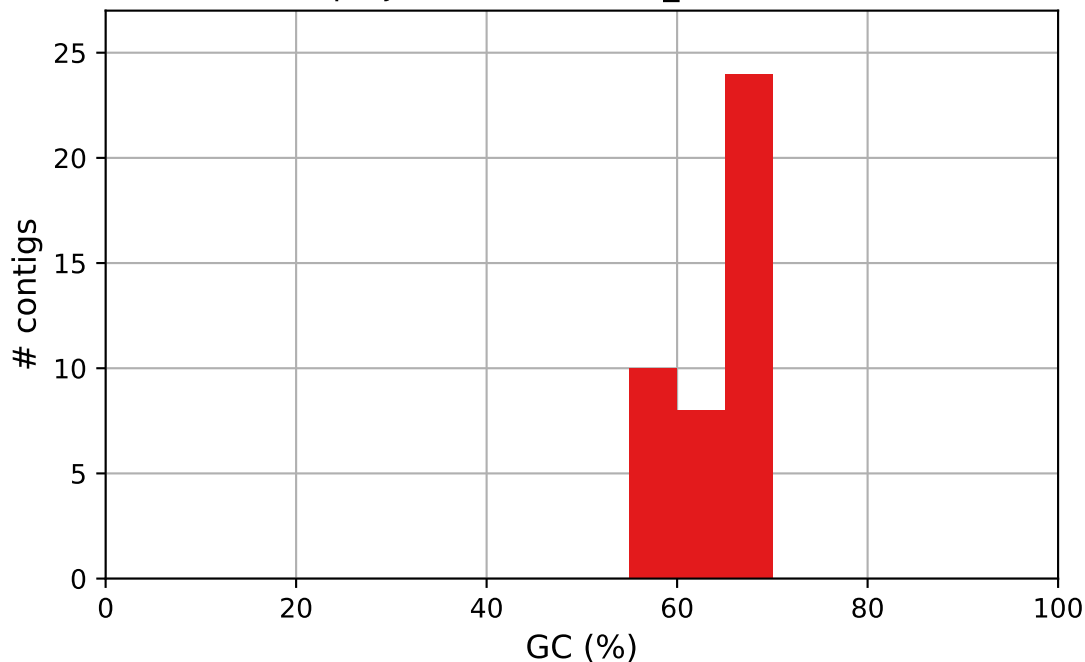
finalprojectSalinibacter-8_fa_broken

Refere

GC content

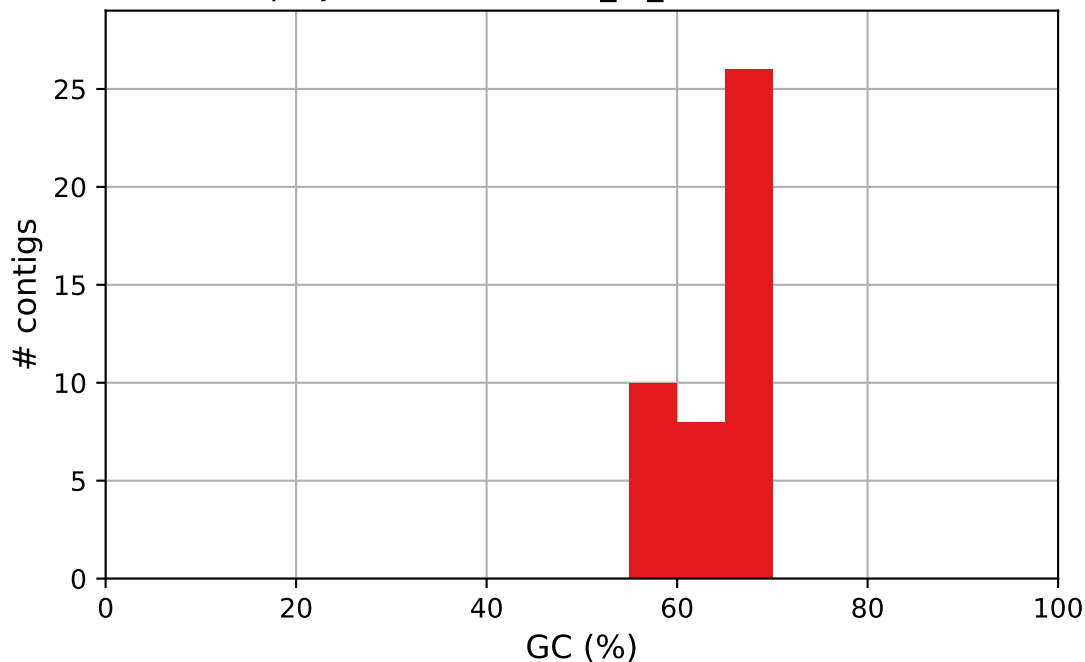


finalprojectSalinibacter-8_fa GC content



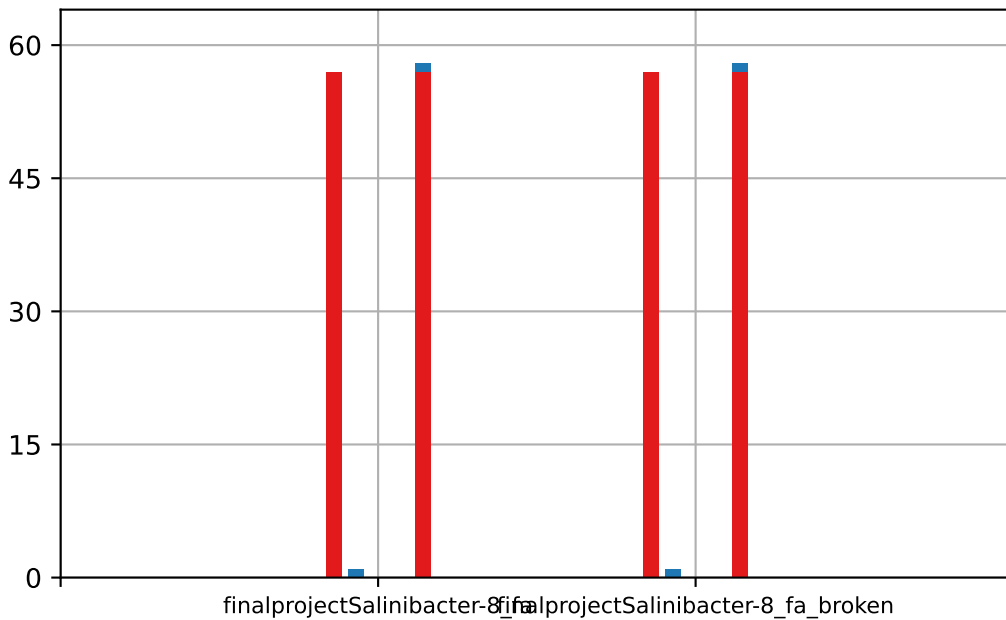
finalprojectSalinibacter-8_fa

finalprojectSalinibacter-8_fa_broken GC content



finalprojectSalinibacter-8_fa_broken

Misassemblies

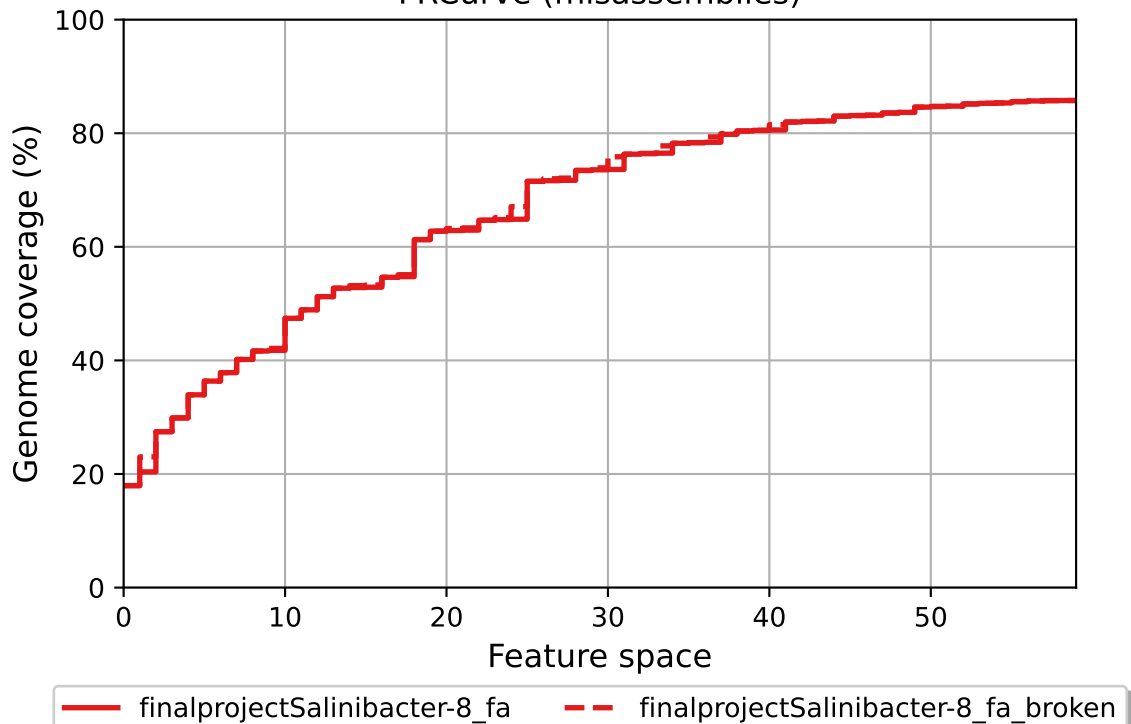


relocations

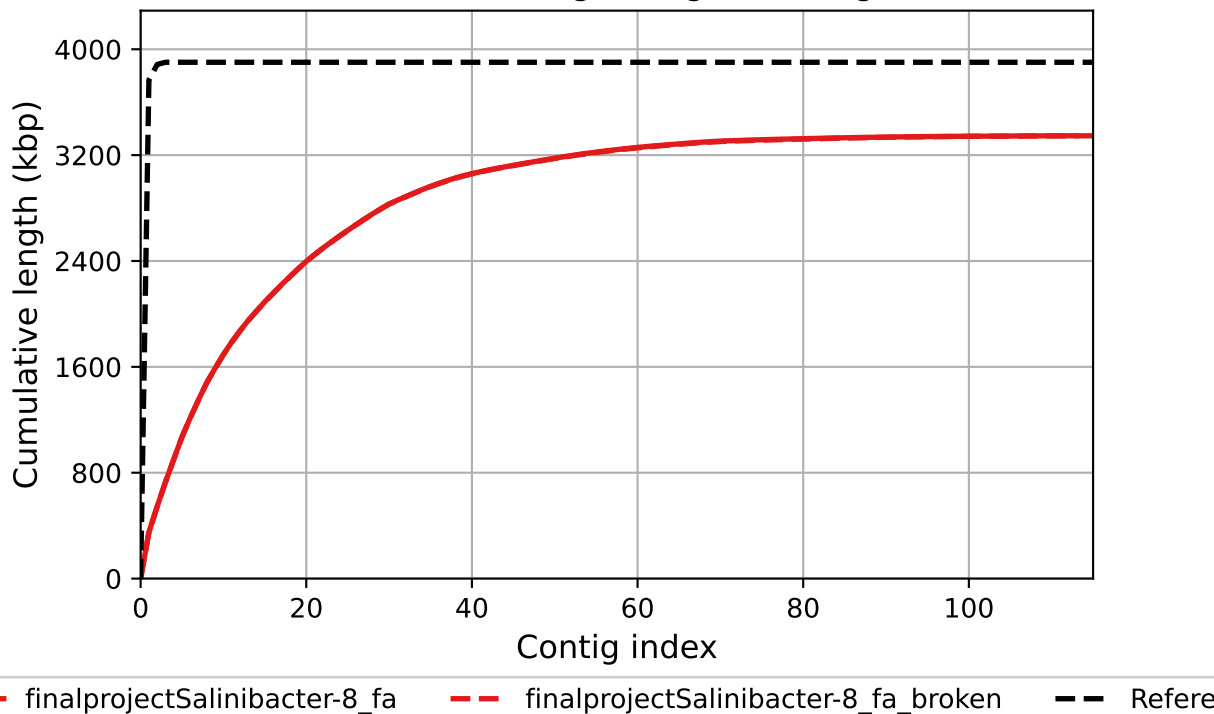


translocations

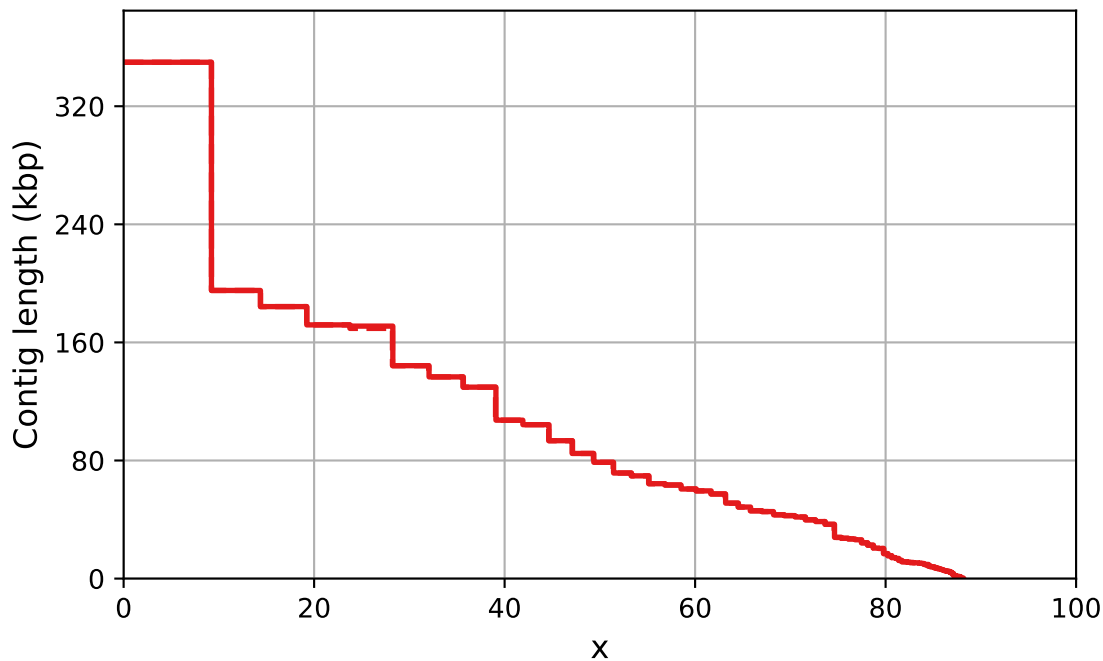
FRCurve (misassemblies)



Cumulative length (aligned contigs)

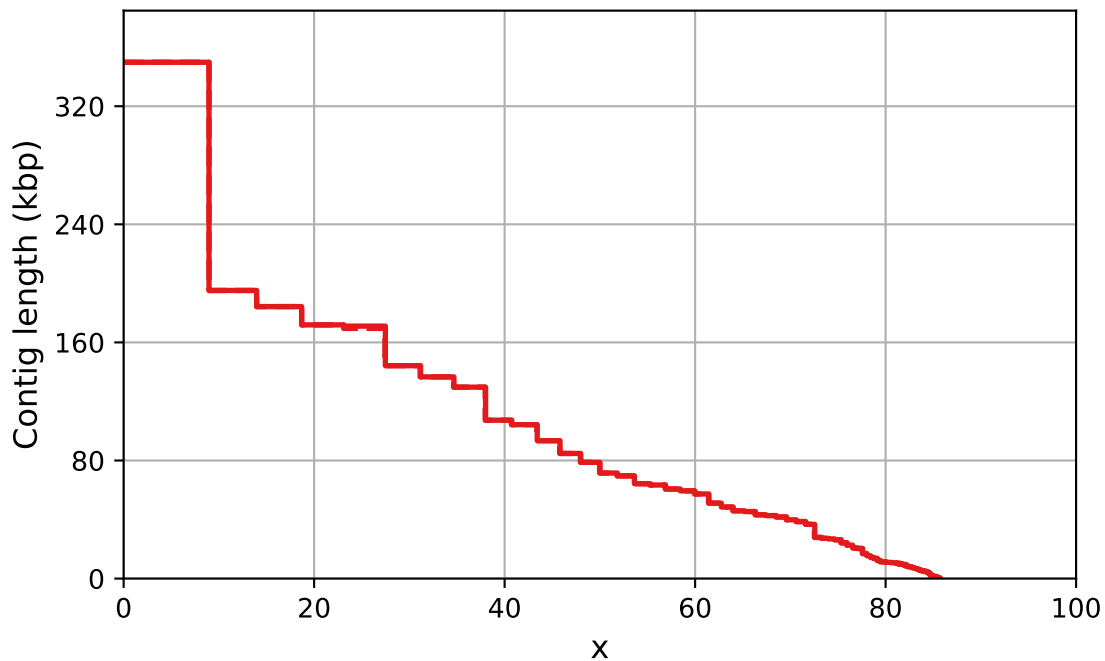


NAx

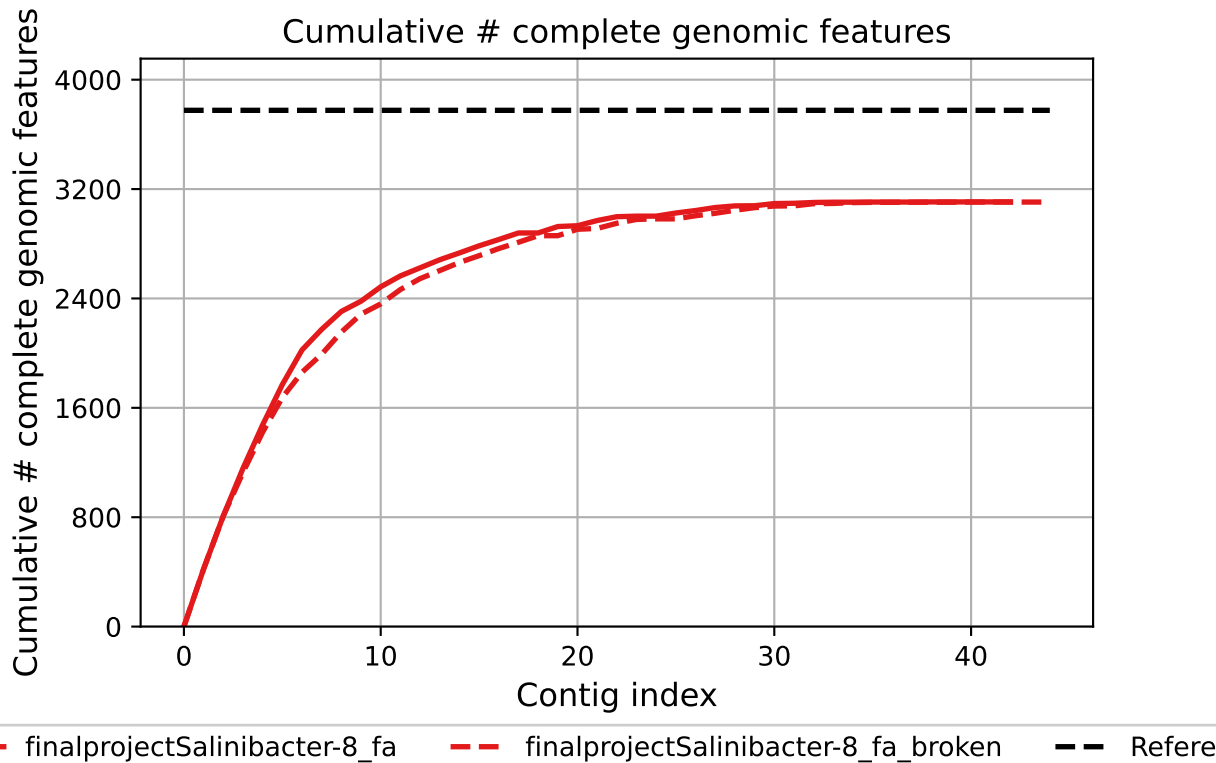


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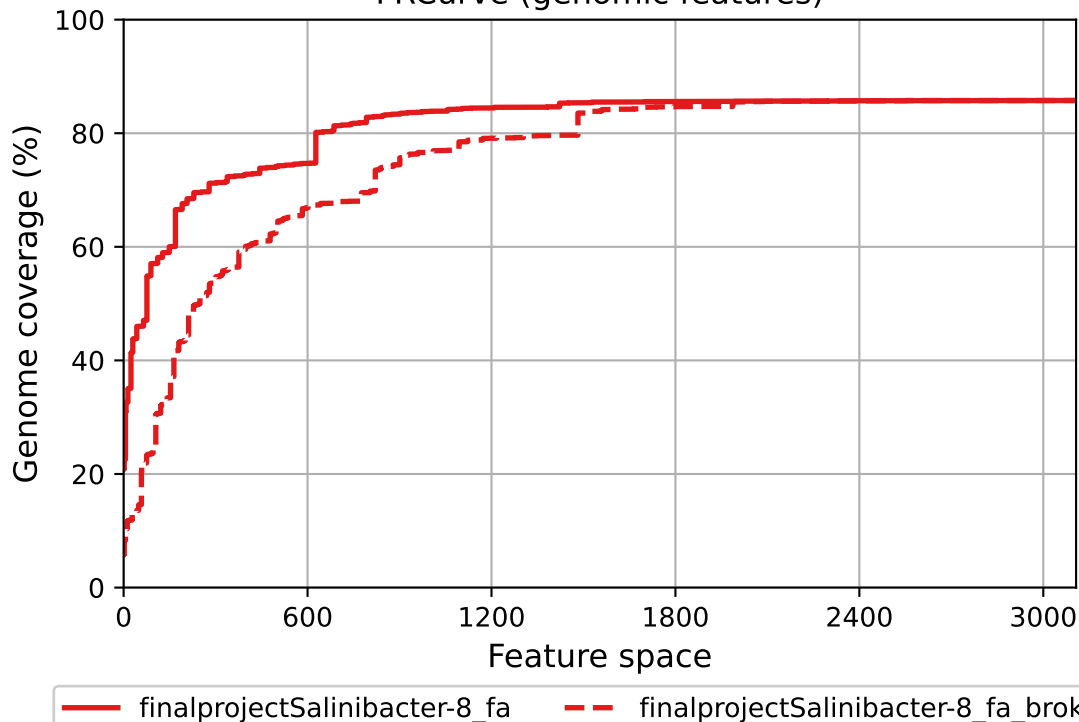
NGAx



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FRCurve (genomic features)



complete genomic features



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Genome fraction, %

100

50



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