

Report

| | AJ218.MiniH.p1 |
|-----------------------------|----------------|
| # contigs (>= 0 bp) | 2 |
| # contigs (>= 1000 bp) | 2 |
| # contigs (>= 5000 bp) | 2 |
| # contigs (>= 10000 bp) | 2 |
| # contigs (>= 25000 bp) | 2 |
| # contigs (>= 50000 bp) | 2 |
| Total length (>= 0 bp) | 5667286 |
| Total length (>= 1000 bp) | 5667286 |
| Total length (>= 5000 bp) | 5667286 |
| Total length (>= 10000 bp) | 5667286 |
| Total length (>= 25000 bp) | 5667286 |
| Total length (>= 50000 bp) | 5667286 |
| # contigs | 2 |
| Largest contig | 5464938 |
| Total length | 5667286 |
| Reference length | 5465981 |
| GC (%) | 57.15 |
| Reference GC (%) | 57.29 |
| N50 | 5464938 |
| NG50 | 5464938 |
| N75 | 5464938 |
| NG75 | 5464938 |
| L50 | 1 |
| LG50 | 1 |
| L75 | 1 |
| LG75 | 1 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 1 |
| # unaligned mis. contigs | 1 |
| # unaligned contigs | 0 + 1 part |
| Unaligned length | 190132 |
| Genome fraction (%) | 99.994 |
| Duplication ratio | 1.002 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 0.48 |
| # indels per 100 kbp | 30.55 |
| Largest alignment | 5464934 |
| Total aligned length | 5477150 |
| NA50 | 5464934 |
| NGA50 | 5464934 |
| NA75 | 5464934 |
| NGA75 | 5464934 |
| LA50 | 1 |
| LGA50 | 1 |
| LA75 | 1 |
| LGA75 | 1 |

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

| | AJ218.MiniH.p1 |
|-----------------------------|----------------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 1 |
| # unaligned mis. contigs | 1 |
| # mismatches | 26 |
| # indels | 1670 |
| # indels (≤ 5 bp) | 1665 |
| # indels (> 5 bp) | 5 |
| Indels length | 2383 |

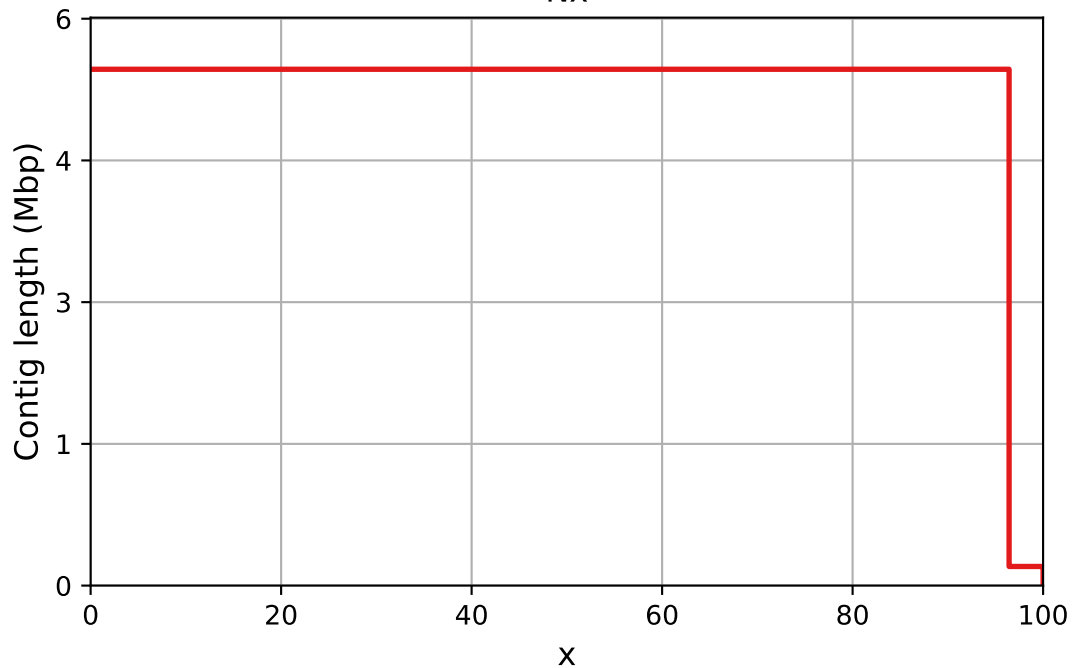
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | AJ218.MiniH.p1 |
|-------------------------------|----------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 1 |
| Partially unaligned length | 190132 |
| # N's | 0 |

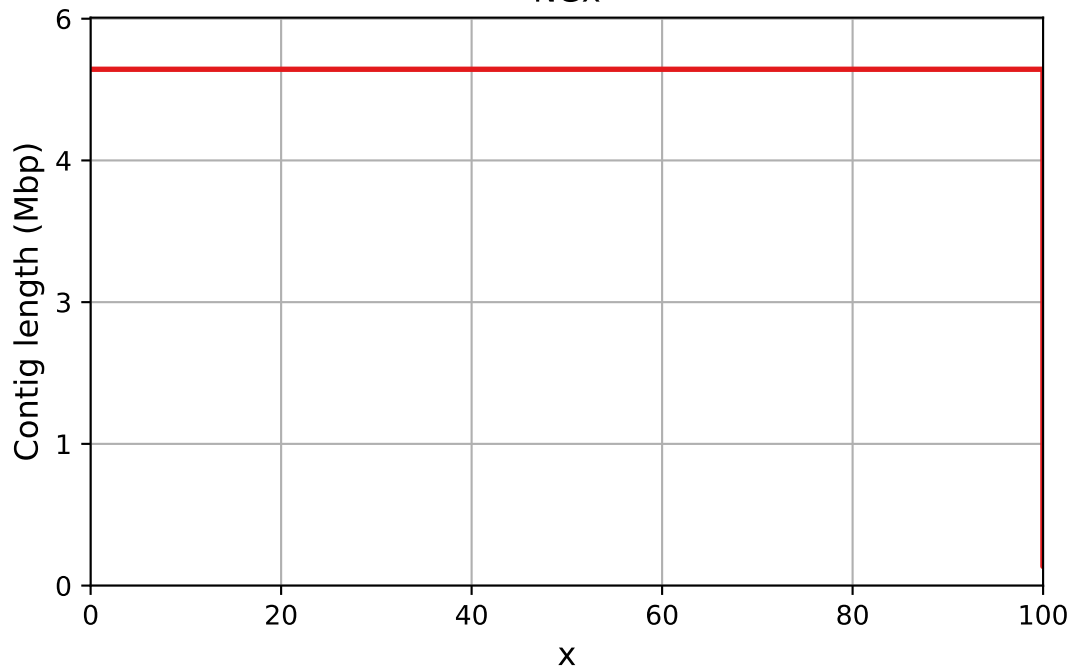
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

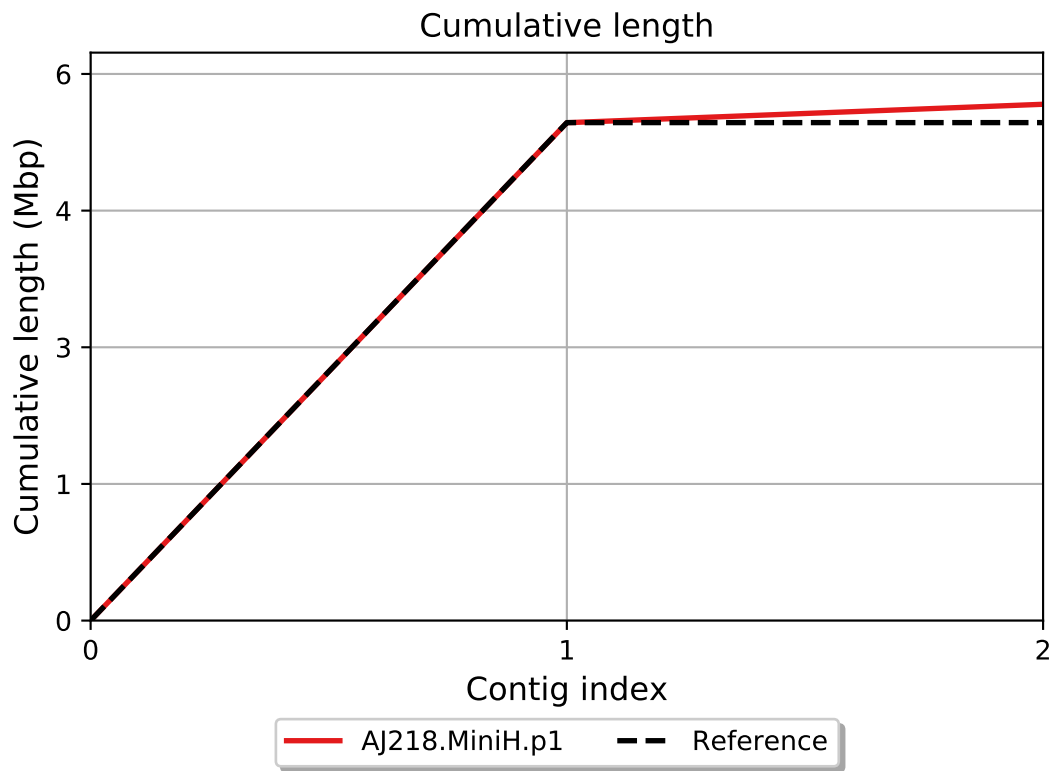


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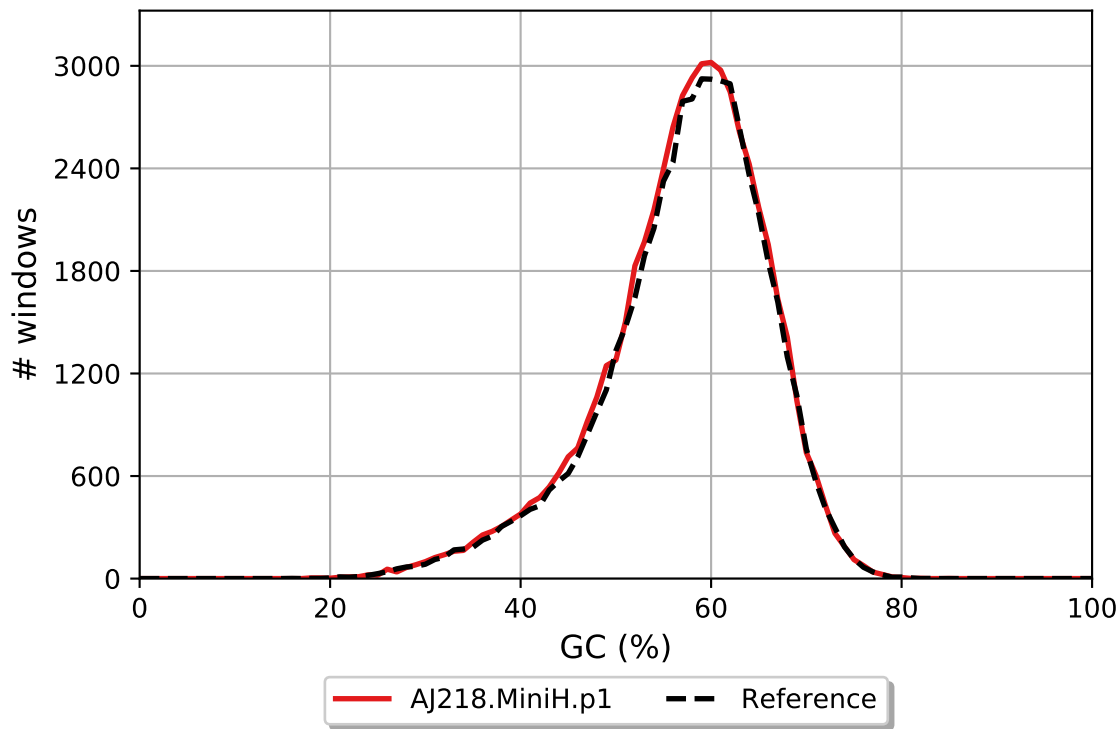
NGx



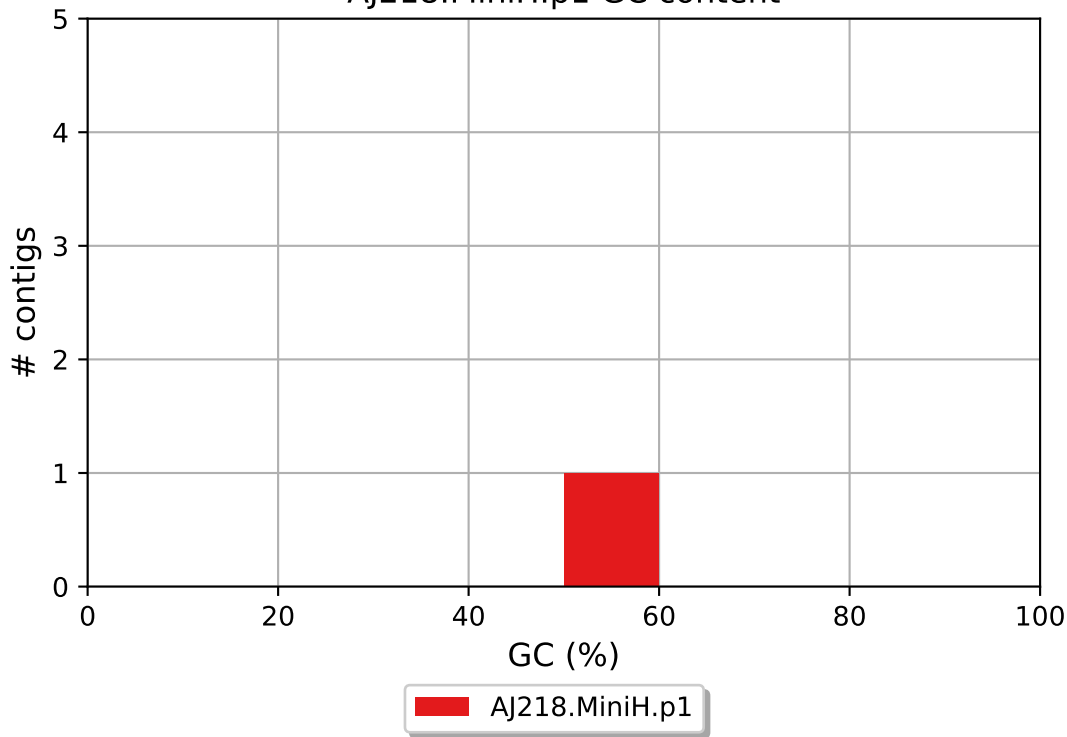
AJ218.MiniH.p1



GC content



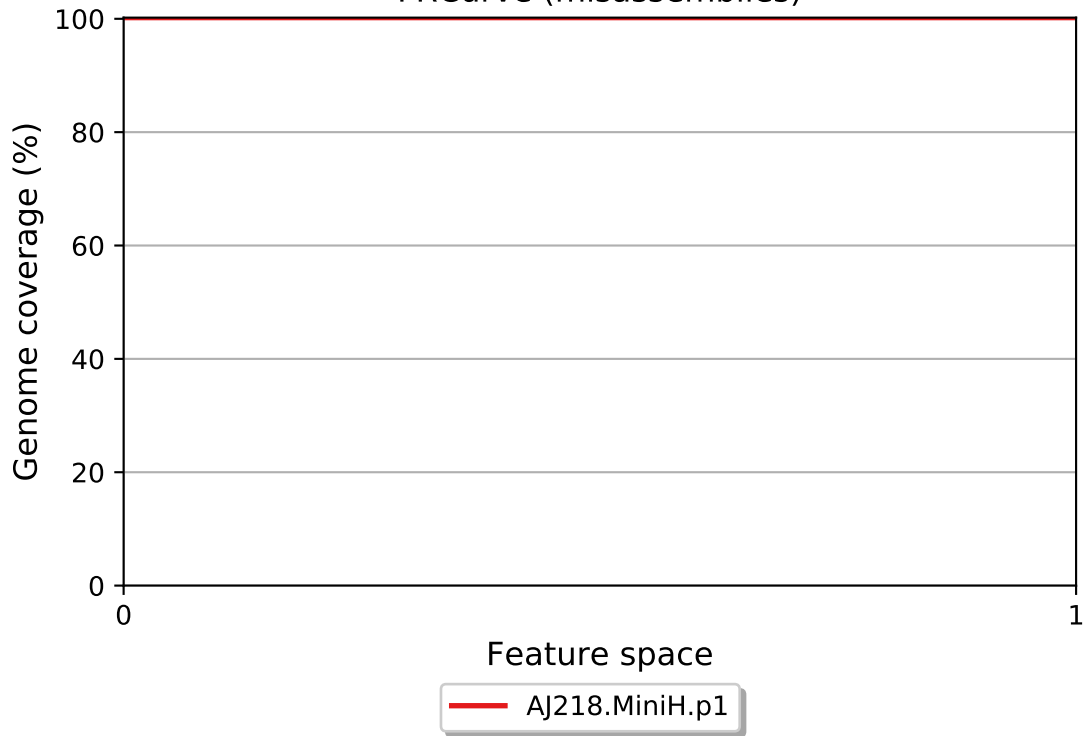
AJ218.MiniH.p1 GC content

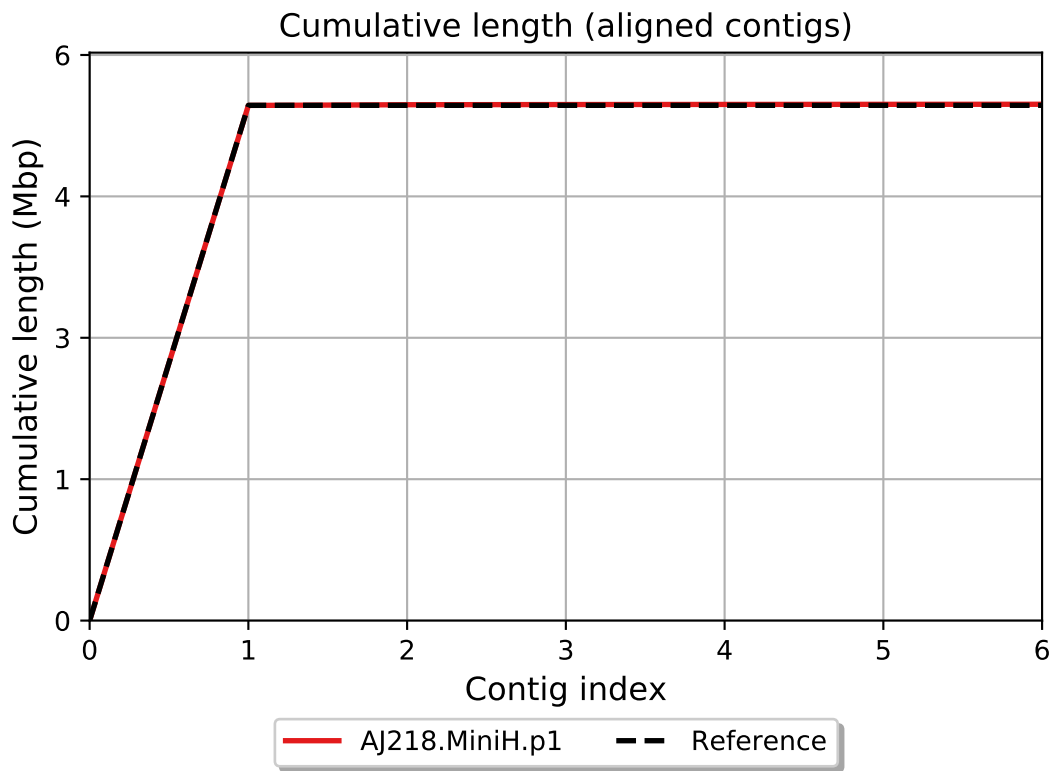


Misassemblies

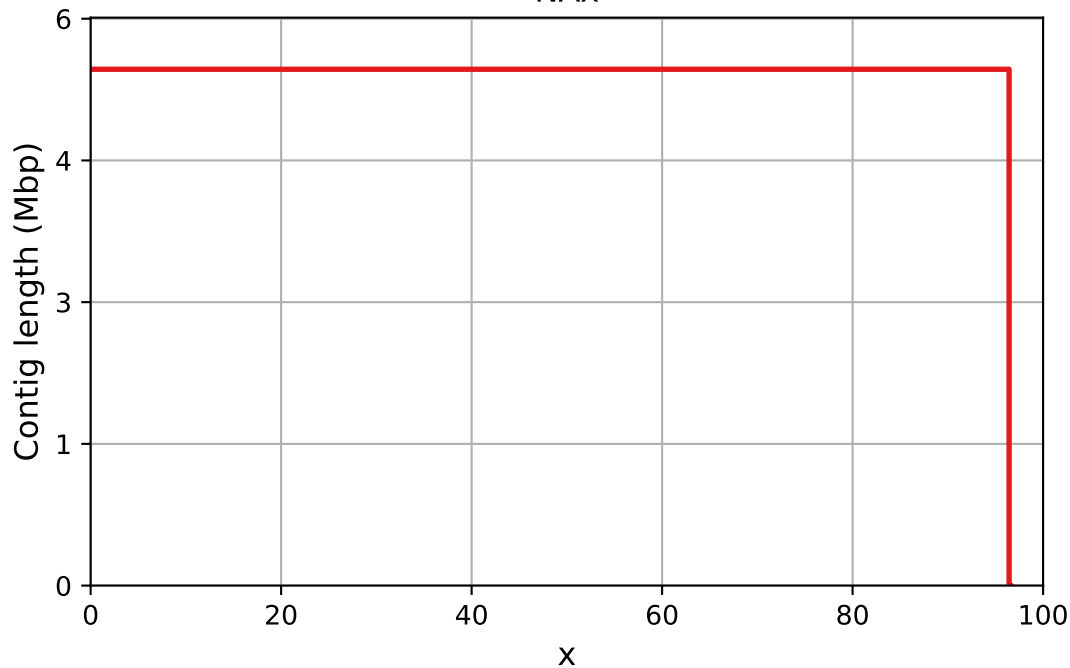


FRCurve (misassemblies)



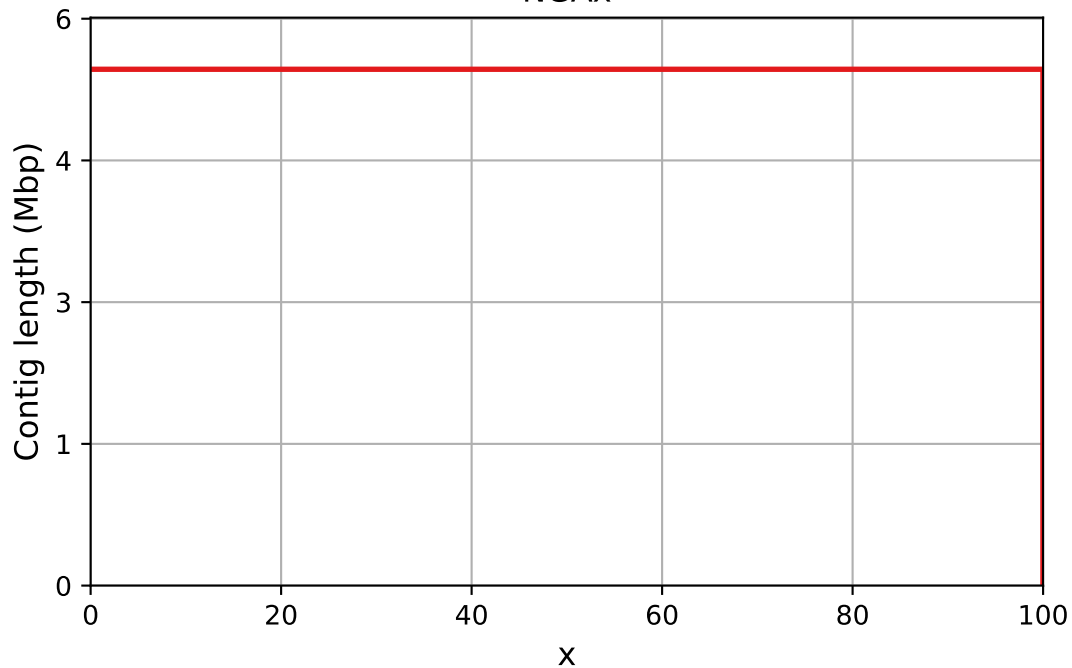


NAx



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NGAx



AJ218.MiniH.p1