

Report

| | anonymous_gsa |
|-----------------------------|---------------|
| # contigs (>= 0 bp) | 1 |
| # contigs (>= 1000 bp) | 1 |
| # contigs (>= 5000 bp) | 1 |
| # contigs (>= 10000 bp) | 1 |
| # contigs (>= 25000 bp) | 1 |
| # contigs (>= 50000 bp) | 1 |
| Total length (>= 0 bp) | 4641795 |
| Total length (>= 1000 bp) | 4641795 |
| Total length (>= 5000 bp) | 4641795 |
| Total length (>= 10000 bp) | 4641795 |
| Total length (>= 25000 bp) | 4641795 |
| Total length (>= 50000 bp) | 4641795 |
| # contigs | 1 |
| Largest contig | 4641795 |
| Total length | 4641795 |
| Reference length | 4641652 |
| GC (%) | 50.79 |
| Reference GC (%) | 50.79 |
| N50 | 4641795 |
| NG50 | 4641795 |
| N75 | 4641795 |
| NG75 | 4641795 |
| L50 | 1 |
| LG50 | 1 |
| L75 | 1 |
| LG75 | 1 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 100.000 |
| Duplication ratio | 1.000 |
| # N's per 100 kbp | 3.15 |
| # mismatches per 100 kbp | 0.00 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 4641649 |
| NA50 | 4641649 |
| NGA50 | 4641649 |
| NA75 | 4641649 |
| NGA75 | 4641649 |
| 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

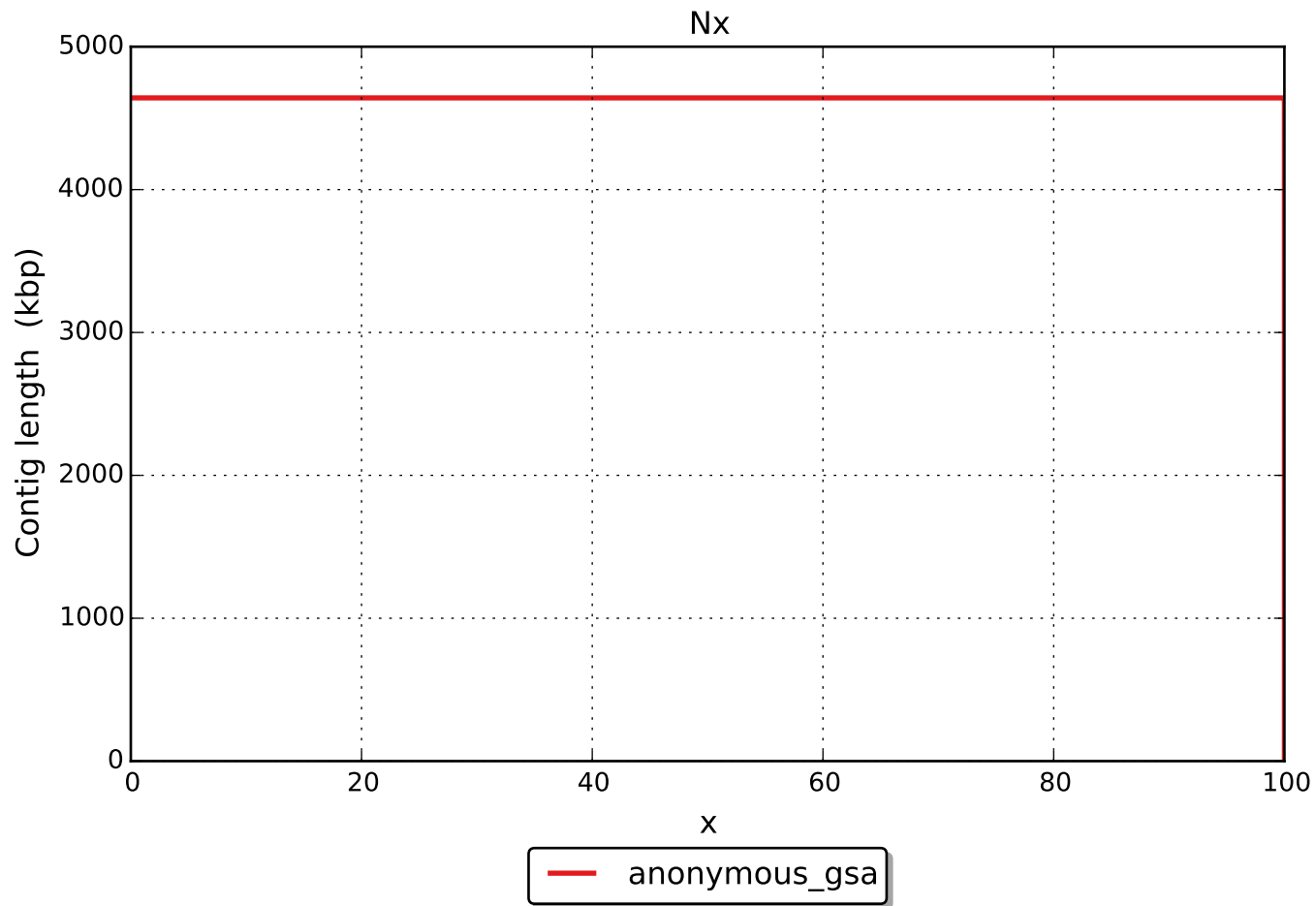
| | anonymous_gsa |
|-----------------------------|---------------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # mismatches | 0 |
| # indels | 0 |
| # short indels | 0 |
| # long indels | 0 |
| Indels length | 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).

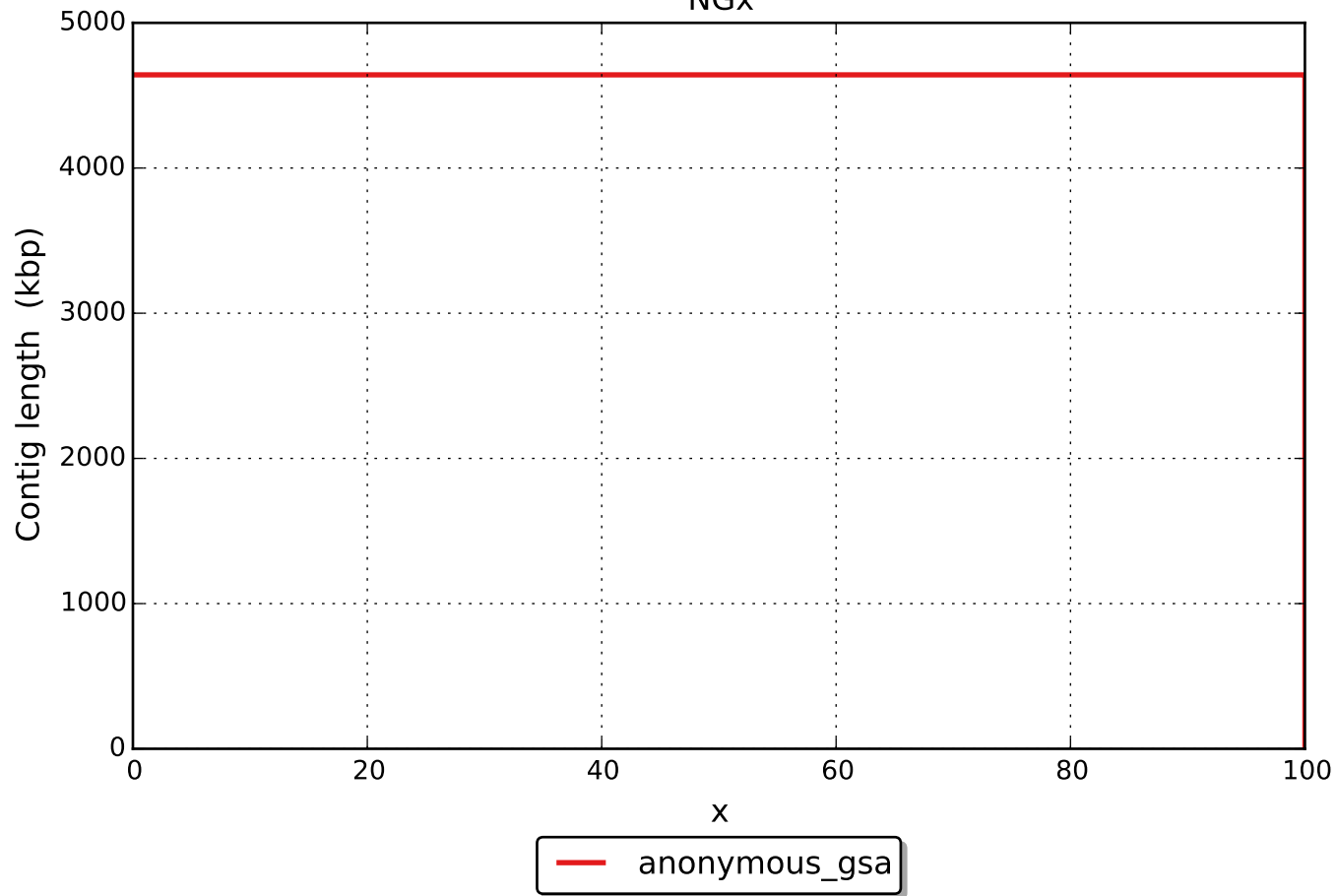
Unaligned report

| | anonymous_gsa |
|-------------------------------|---------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 146 |

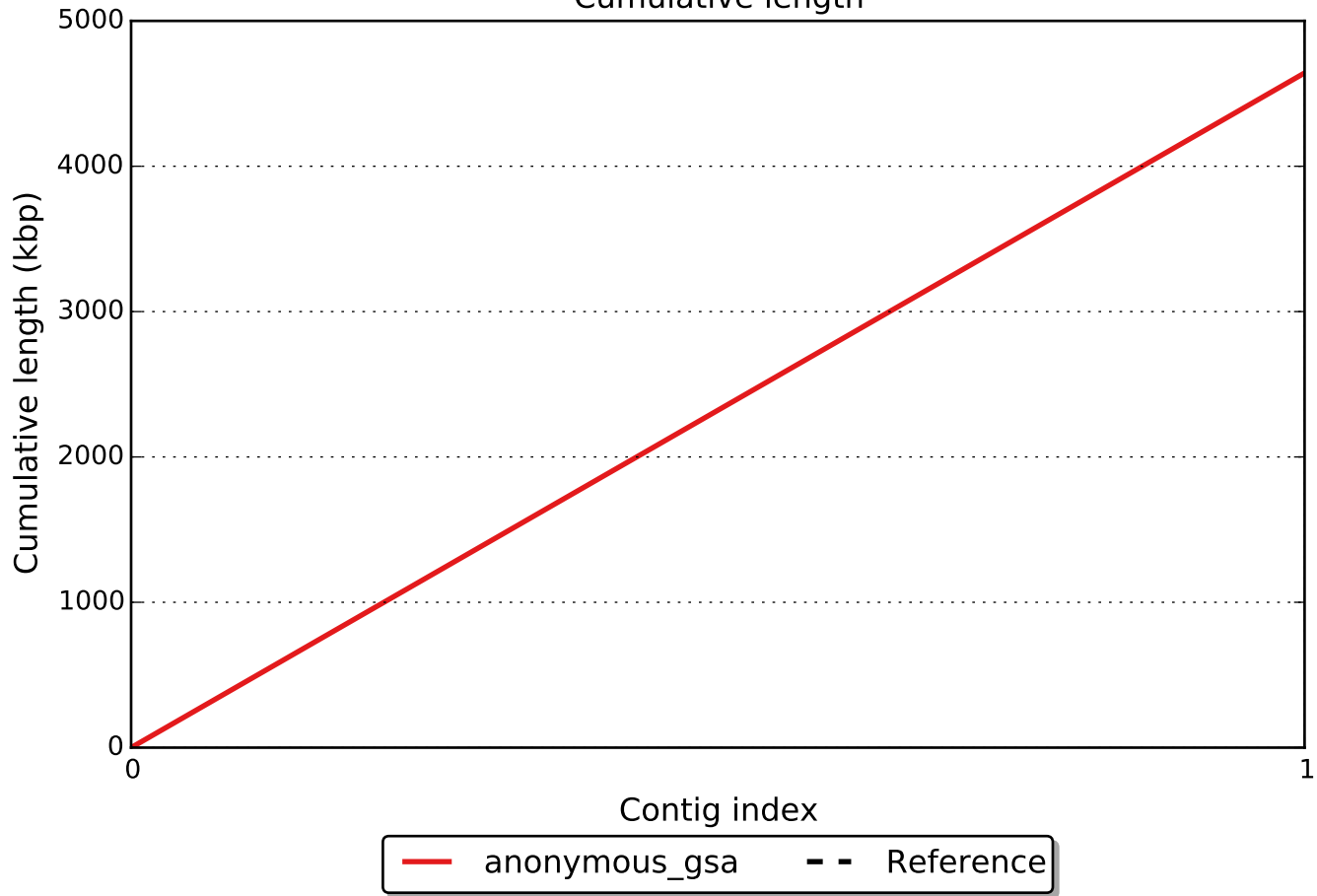
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



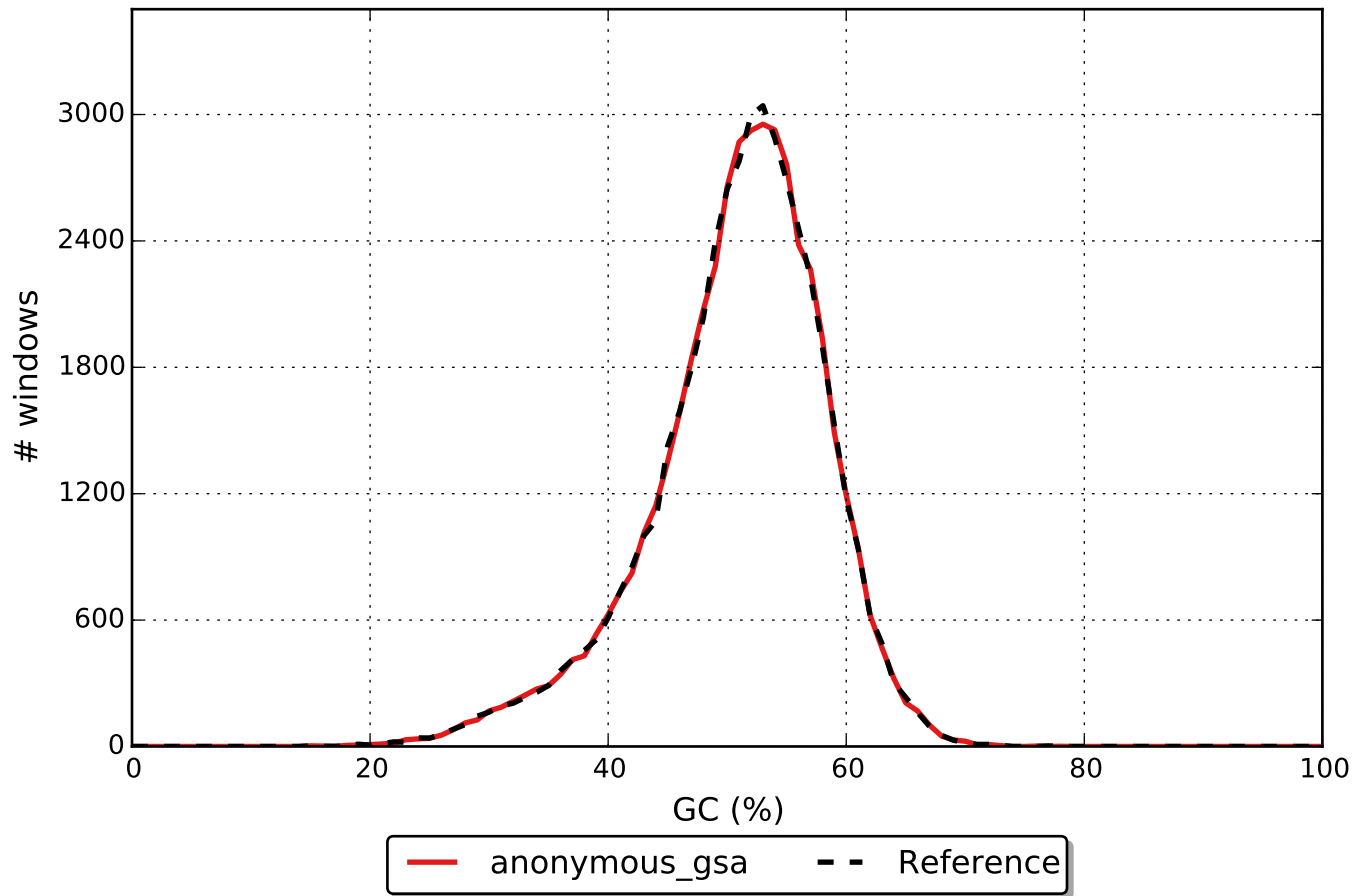
NGx



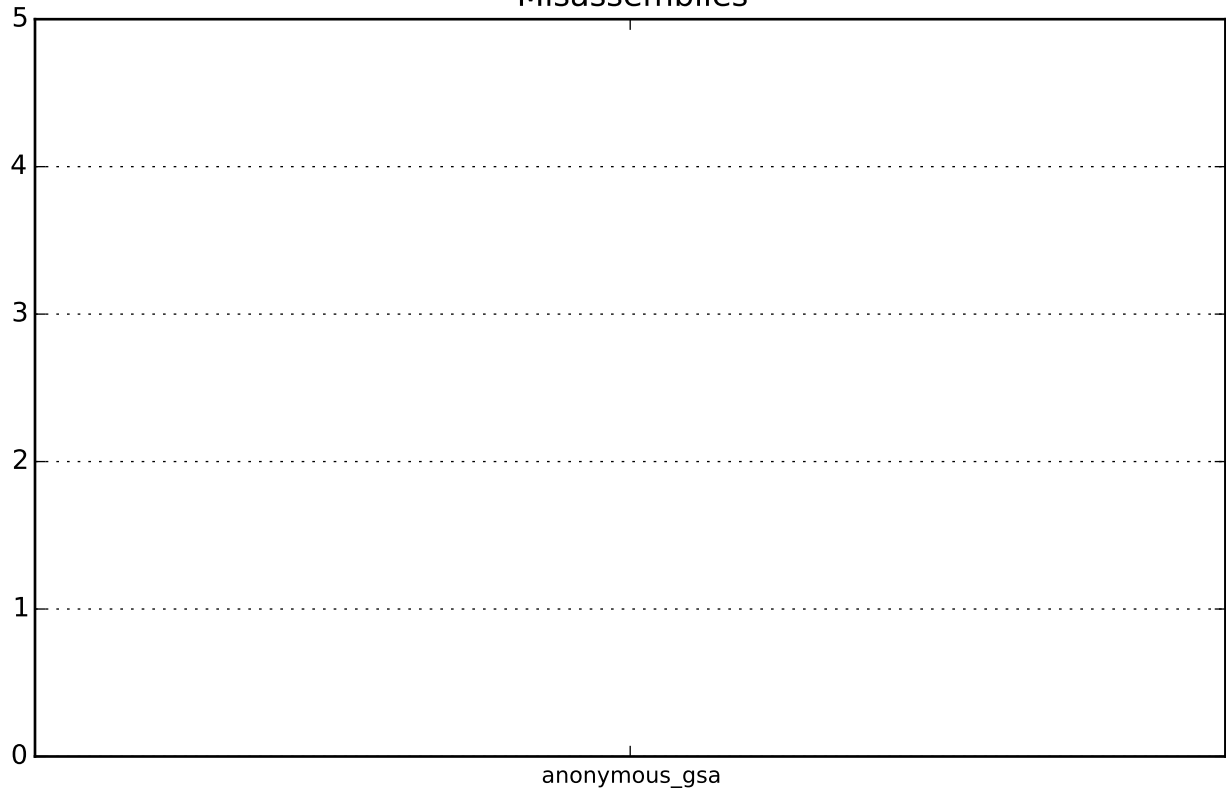
Cumulative length



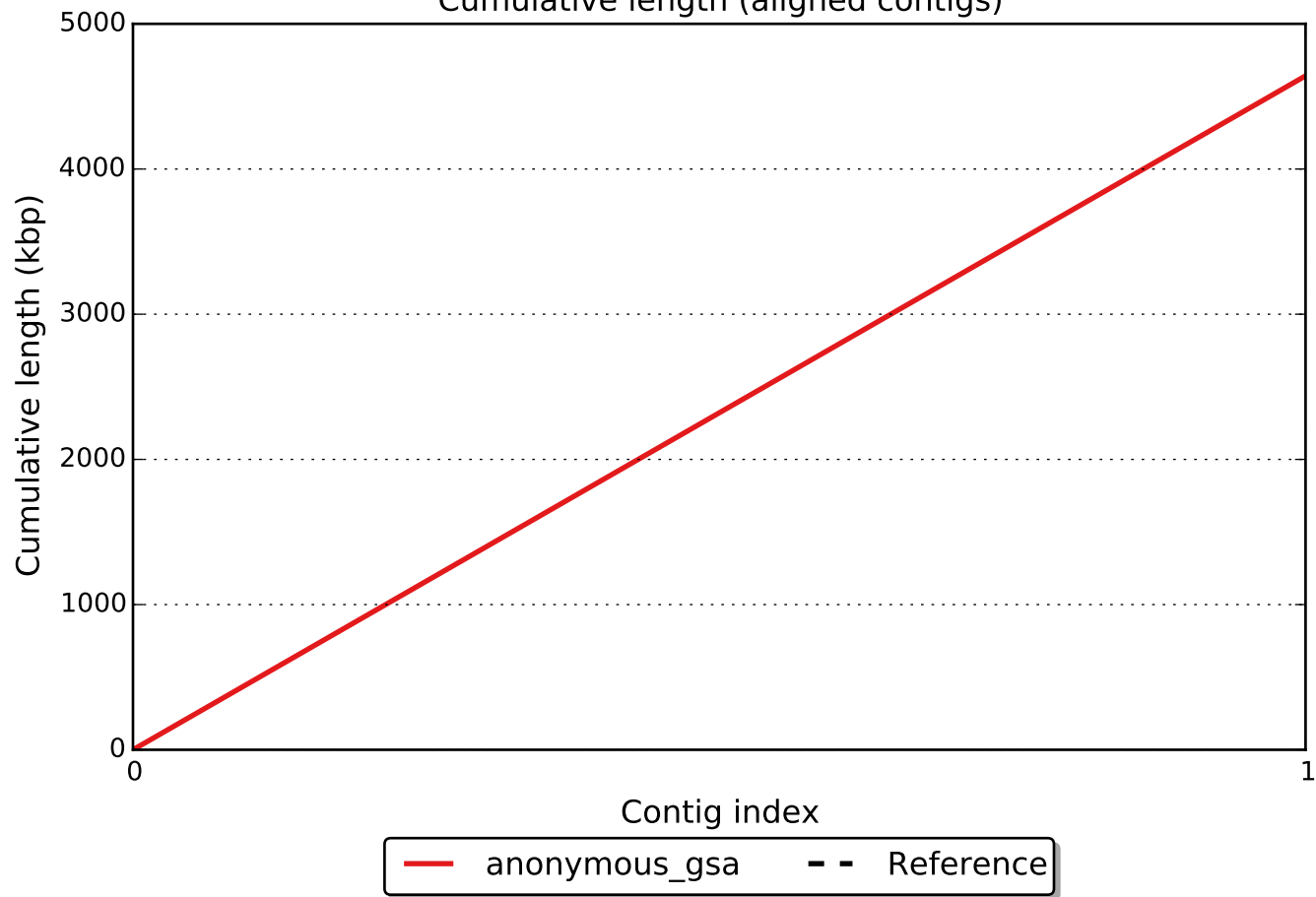
GC content



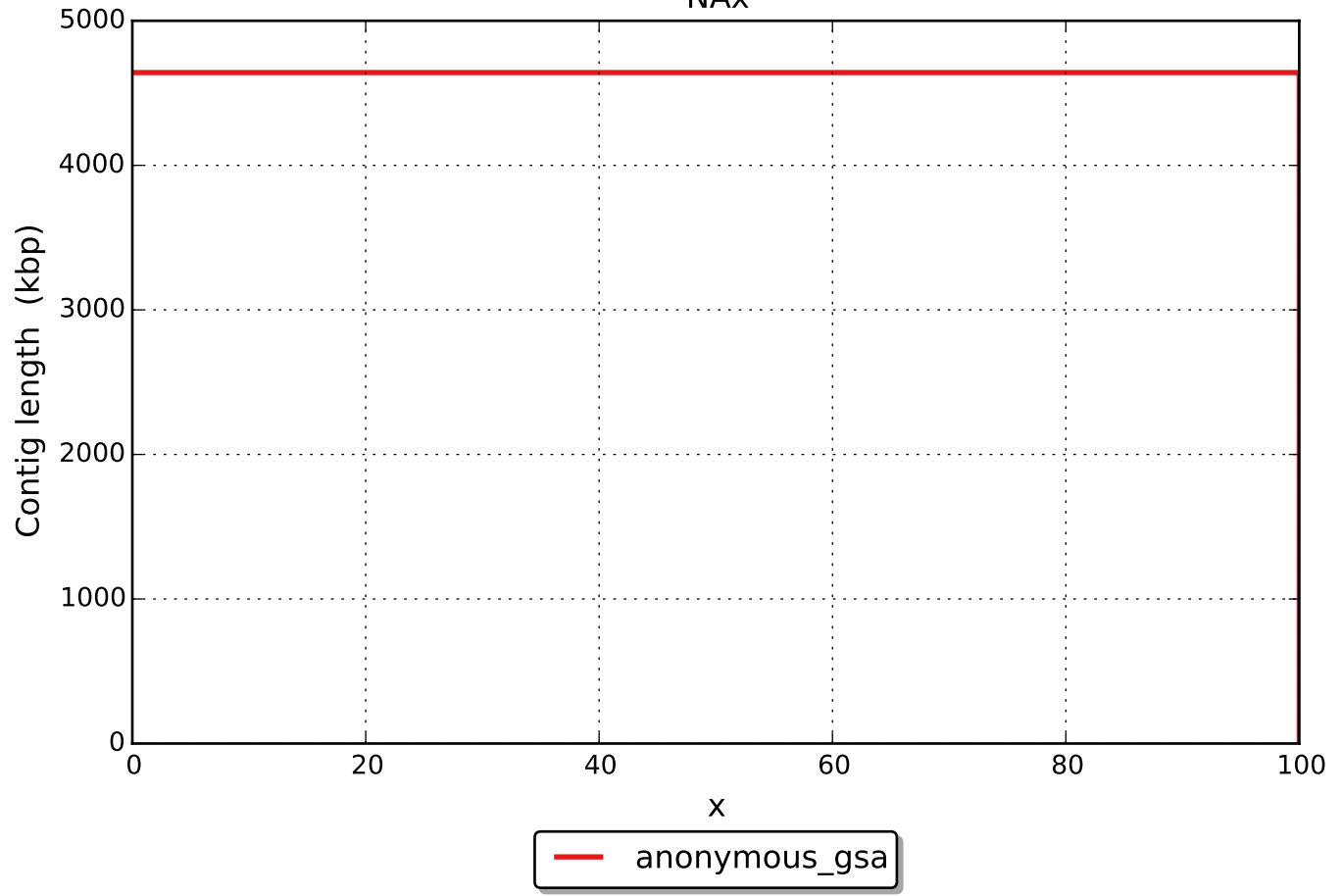
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

