

Report

| | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 1000 bp) | 0 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 0 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 3 |
| Largest contig | 669 |
| Total length | 1793 |
| Reference length | 3442017 |
| GC (%) | 52.26 |
| Reference GC (%) | 58.88 |
| N50 | 622 |
| N75 | 502 |
| L50 | 2 |
| L75 | 3 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # structural variations | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 0.009 |
| Duplication ratio | 5.803 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 2589.00 |
| # indels per 100 kbp | 0.00 |
| Largest alignment | 215 |
| Total aligned length | 509 |
| NGA50 | - |

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 | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # interspecies translocations | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # possibly misassembled contigs | 0 |
| # possible misassemblies | 0 |
| # local misassemblies | 0 |
| # structural variations | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 8 |
| # indels | 0 |
| # indels (≤ 5 bp) | 0 |
| # indels (> 5 bp) | 0 |
| Indels length | 0 |

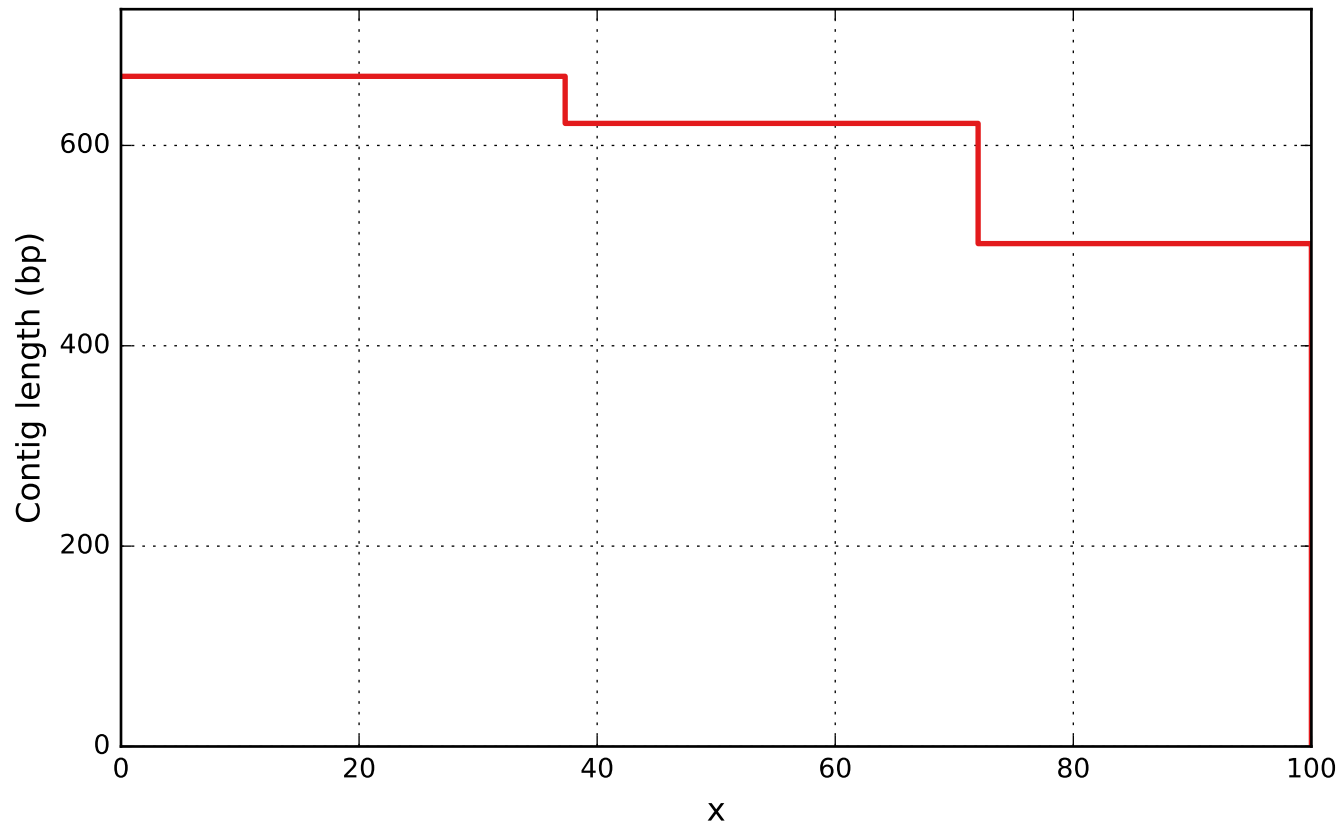
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

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

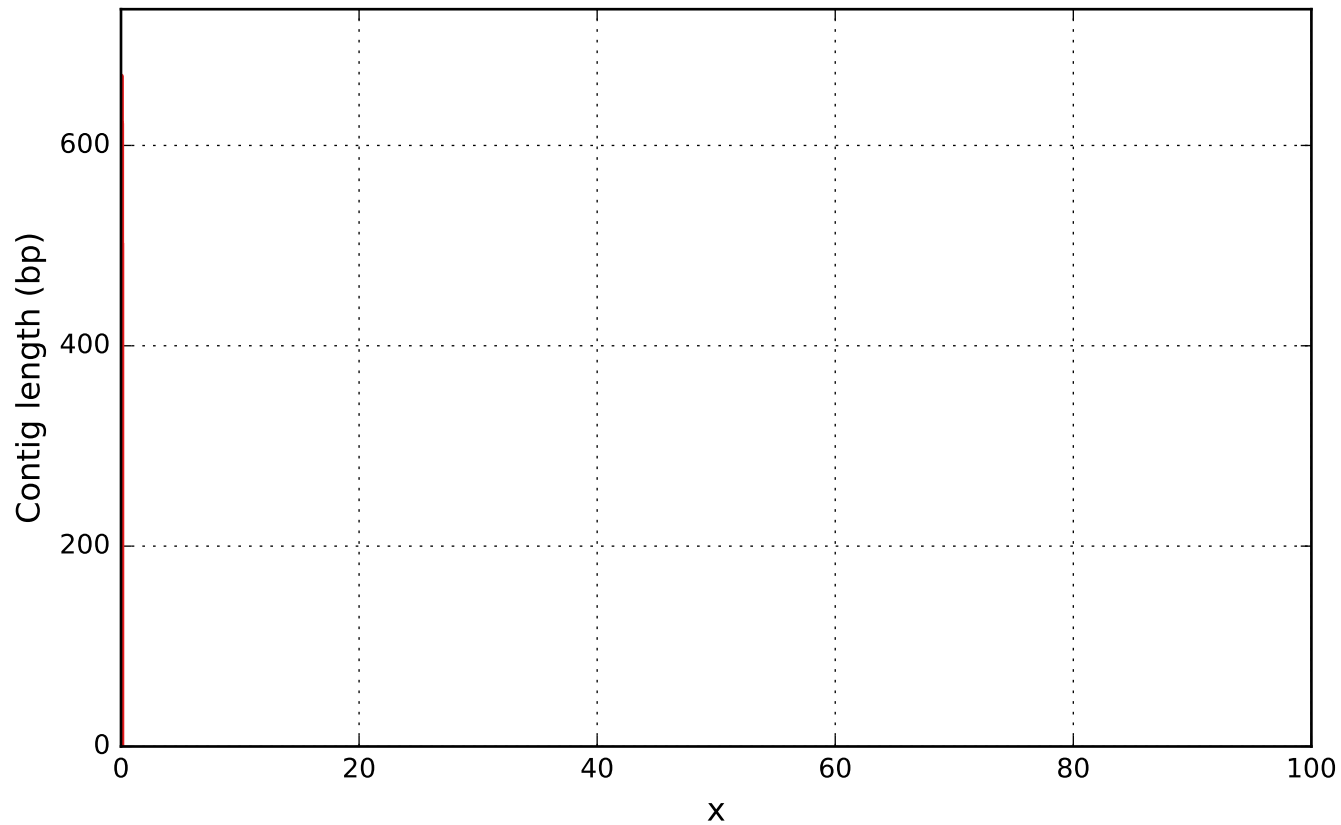
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

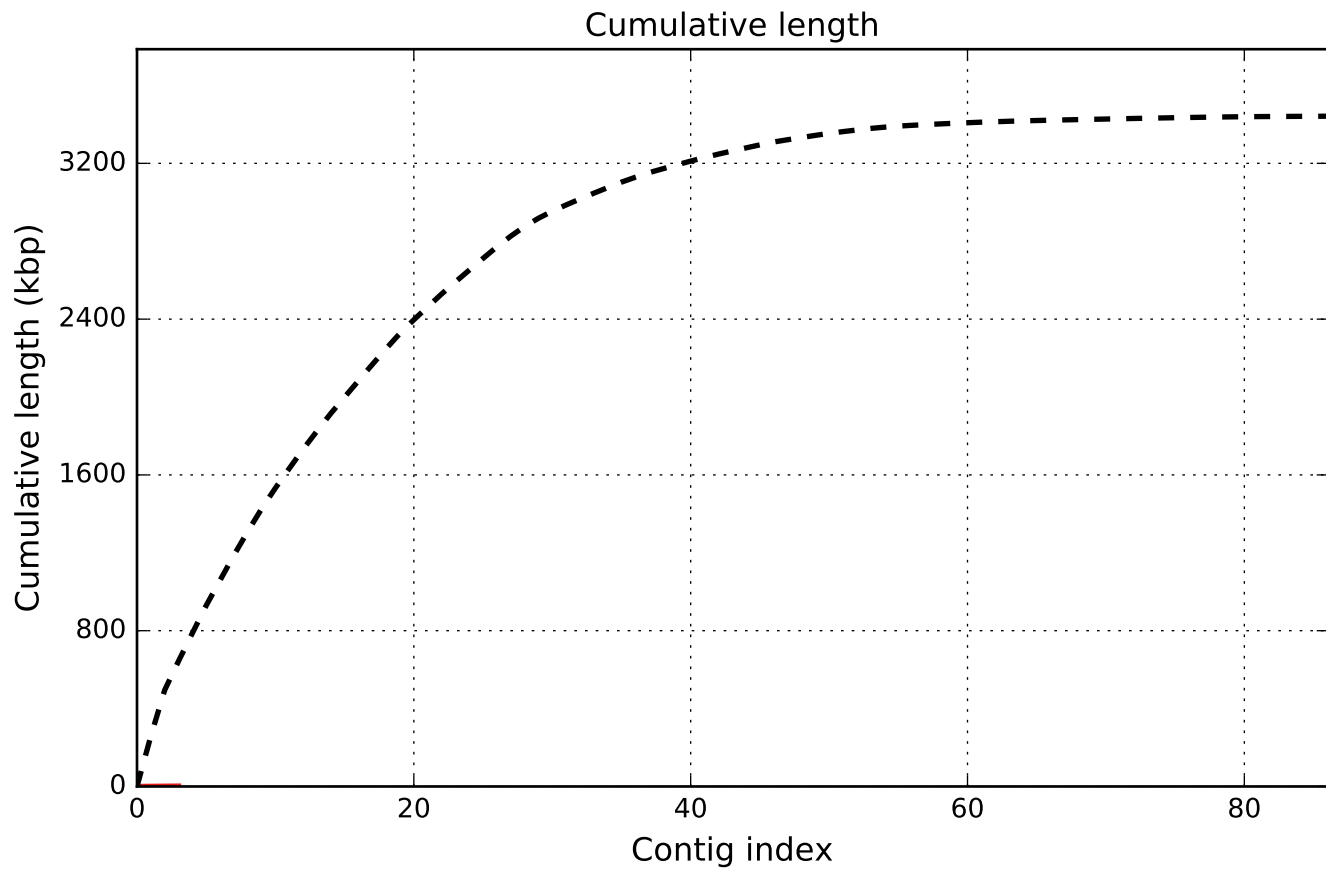


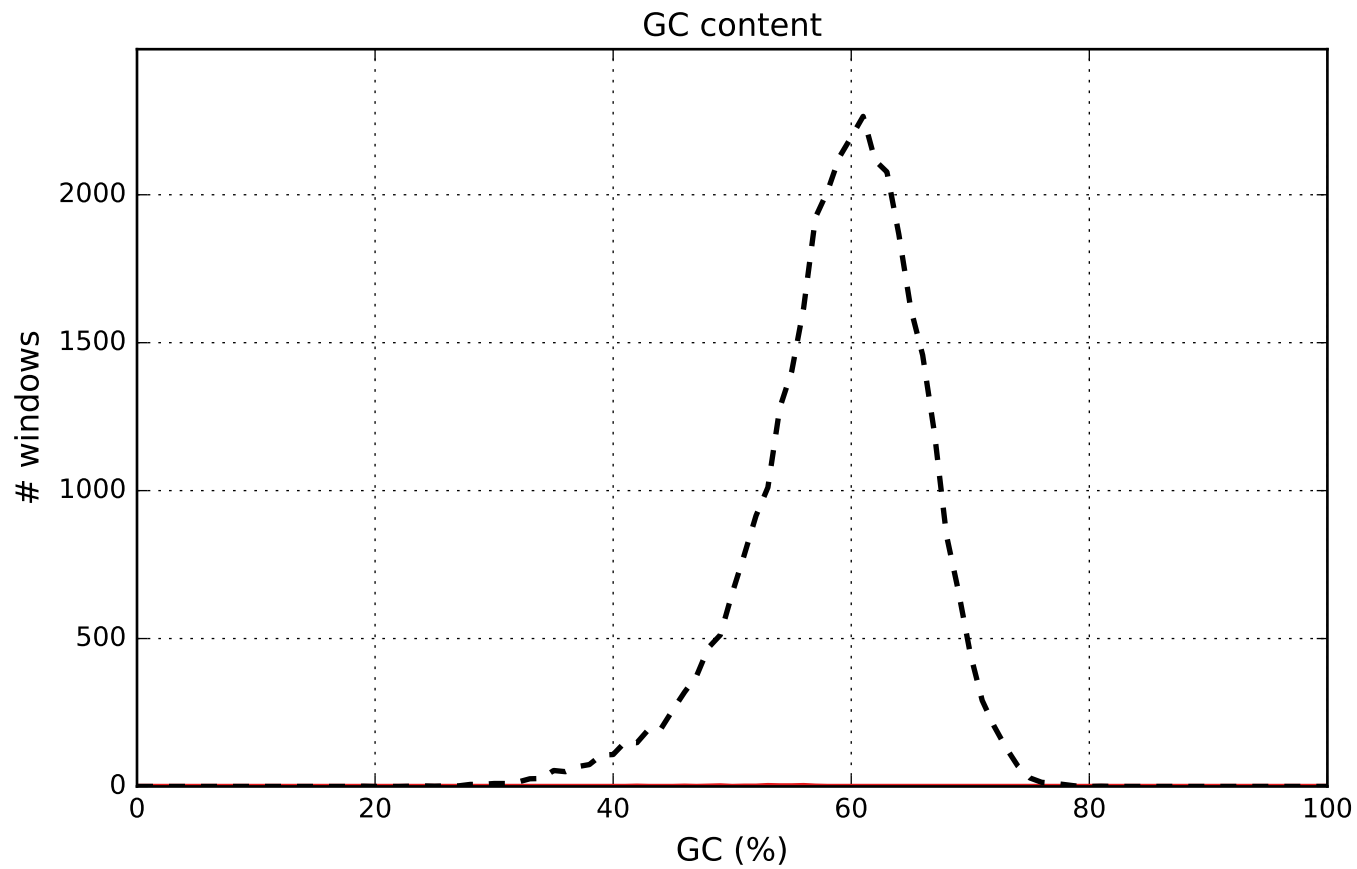
— final.contigs

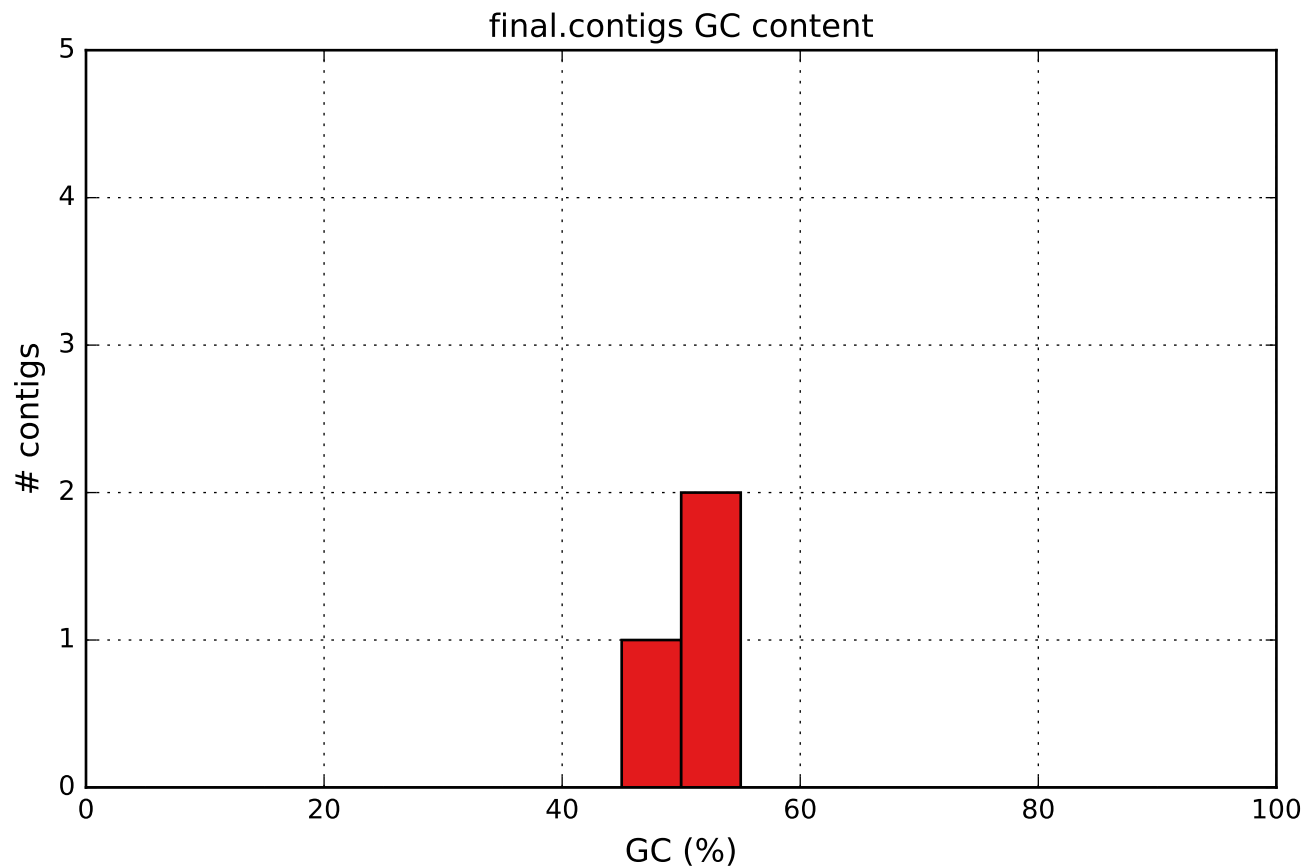
NGx



— final.contigs



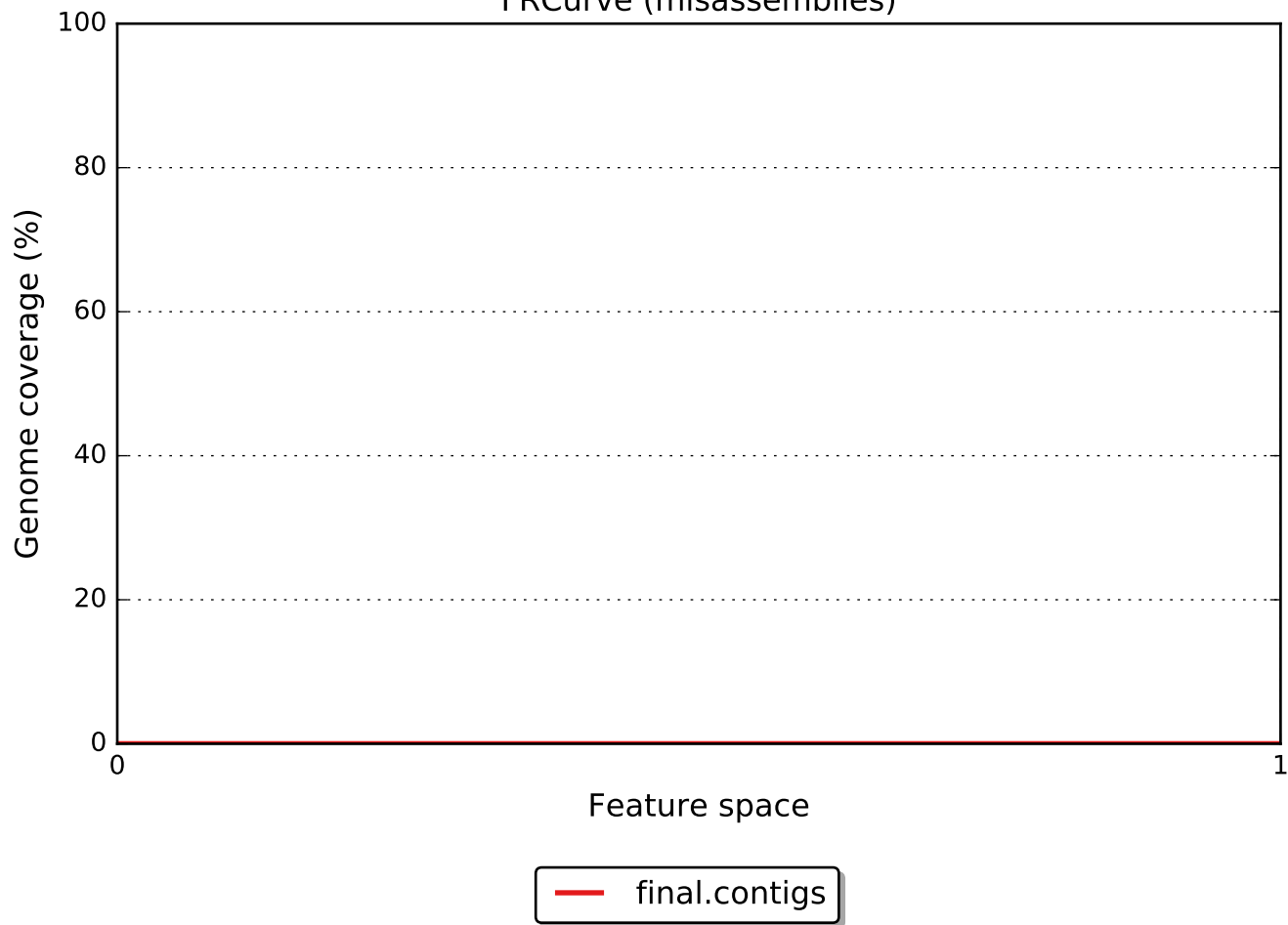




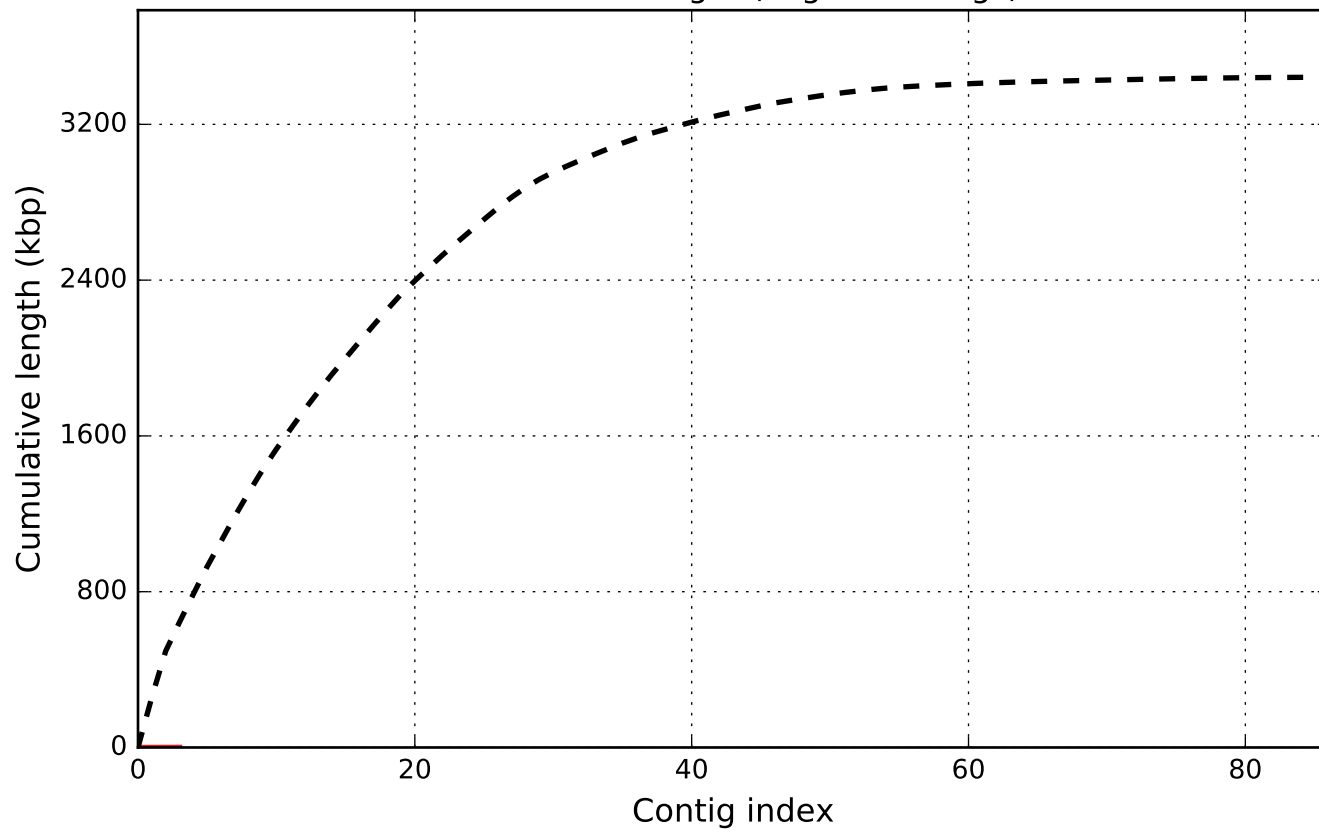
final.contigs



FRCurve (misassemblies)

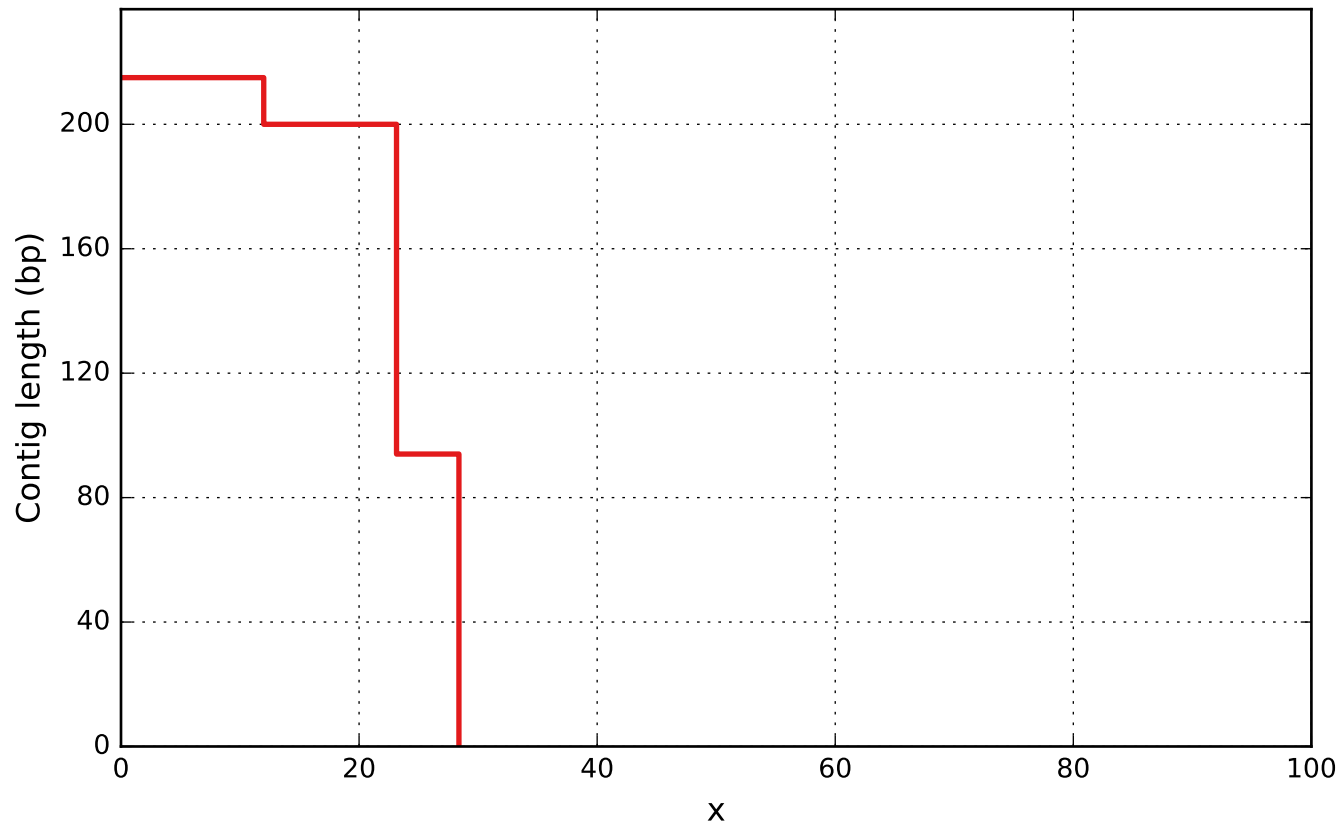


Cumulative length (aligned contigs)



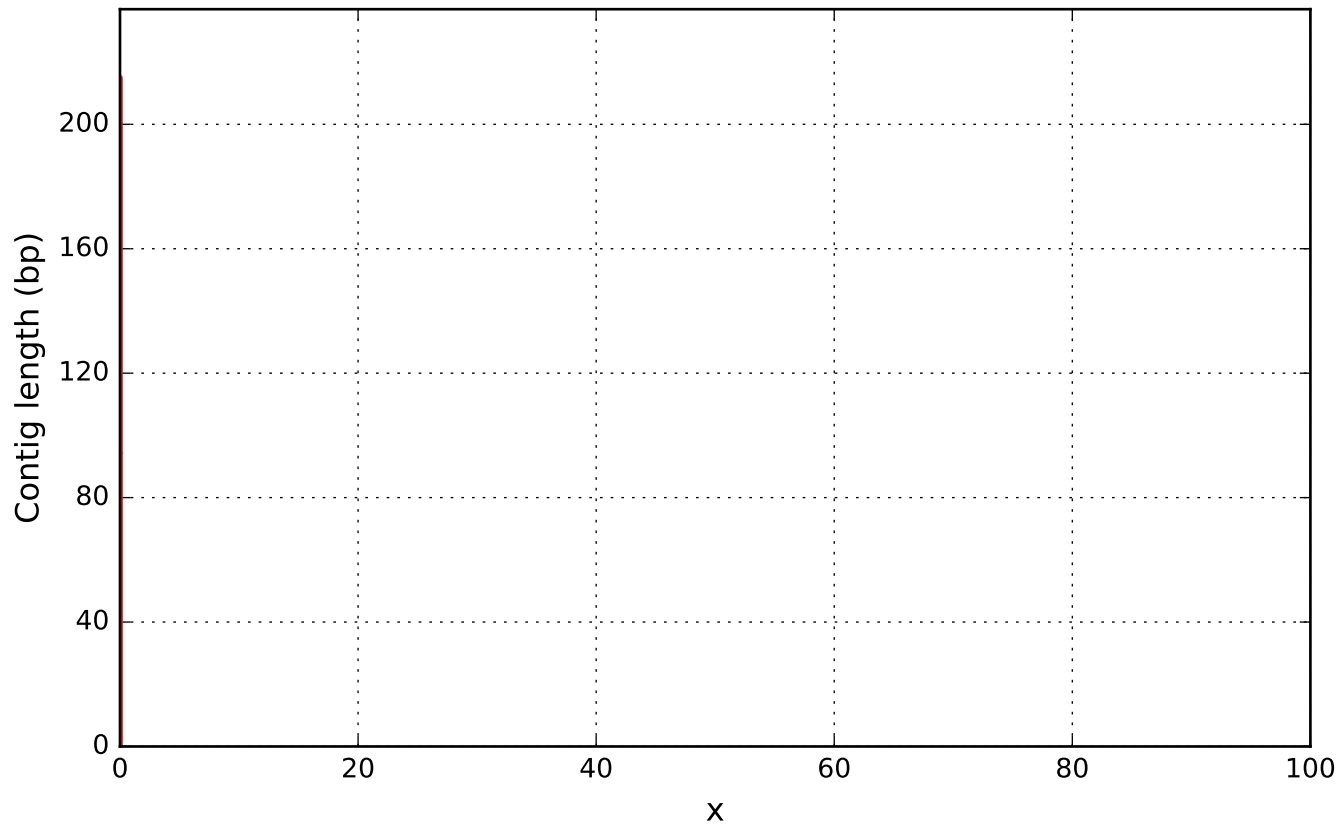
— final.contigs - - Reference

NAx



— final.contigs

NGAx



— final.contigs