

Report

| | pilon | efaecium.contigs |
|-----------------------------|------------|------------------|
| # contigs (>= 0 bp) | 8 | 8 |
| # contigs (>= 1000 bp) | 8 | 8 |
| # contigs (>= 5000 bp) | 8 | 8 |
| # contigs (>= 10000 bp) | 7 | 7 |
| # contigs (>= 25000 bp) | 5 | 5 |
| # contigs (>= 50000 bp) | 2 | 2 |
| Total length (>= 0 bp) | 3141050 | 3142355 |
| Total length (>= 1000 bp) | 3141050 | 3142355 |
| Total length (>= 5000 bp) | 3141050 | 3142355 |
| Total length (>= 10000 bp) | 3132750 | 3132621 |
| Total length (>= 25000 bp) | 3103593 | 3103475 |
| Total length (>= 50000 bp) | 2992680 | 2992580 |
| # contigs | 8 | 8 |
| Largest contig | 2773703 | 2773588 |
| Total length | 3141050 | 3142355 |
| Reference length | 2765010 | 2765010 |
| GC (%) | 37.78 | 37.78 |
| Reference GC (%) | 38.11 | 38.11 |
| N50 | 2773703 | 2773588 |
| NG50 | 2773703 | 2773588 |
| N75 | 2773703 | 2773588 |
| NG75 | 2773703 | 2773588 |
| L50 | 1 | 1 |
| LG50 | 1 | 1 |
| L75 | 1 | 1 |
| LG75 | 1 | 1 |
| # misassemblies | 3 | 4 |
| # misassembled contigs | 2 | 2 |
| Misassembled contigs length | 2782003 | 2783322 |
| # local misassemblies | 0 | 0 |
| # unaligned mis. contigs | 1 | 1 |
| # unaligned contigs | 4 + 3 part | 4 + 3 part |
| Unaligned length | 322065 | 322051 |
| Genome fraction (%) | 100.000 | 100.000 |
| Duplication ratio | 1.020 | 1.020 |
| # N's per 100 kbp | 0.00 | 0.00 |
| # mismatches per 100 kbp | 0.00 | 0.04 |
| # indels per 100 kbp | 0.22 | 4.38 |
| Largest alignment | 2195417 | 2195330 |
| Total aligned length | 2818986 | 2820305 |
| NA50 | 2195417 | 2195330 |
| NGA50 | 2195417 | 2195330 |
| NA75 | 578286 | 578258 |
| NGA75 | 2195417 | 2195330 |
| LA50 | 1 | 1 |
| LGA50 | 1 | 1 |
| LA75 | 2 | 2 |
| LGA75 | 1 | 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

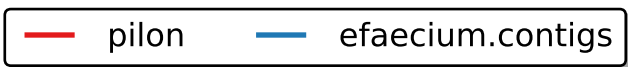
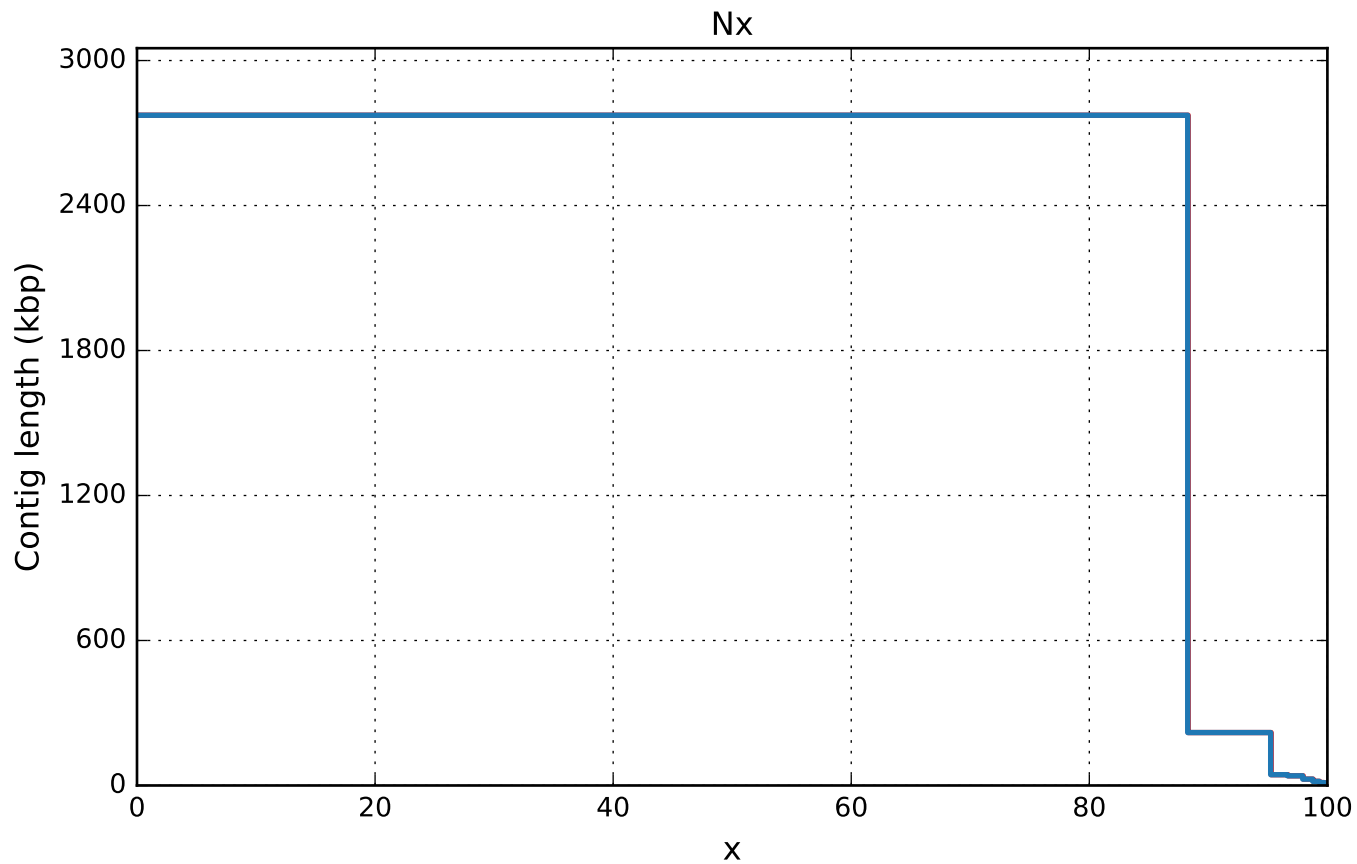
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|-----------------------------|---------|------------------|
| # misassemblies | 3 | 4 |
| # relocations | 3 | 4 |
| # translocations | 0 | 0 |
| # inversions | 0 | 0 |
| # misassembled contigs | 2 | 2 |
| Misassembled contigs length | 2782003 | 2783322 |
| # local misassemblies | 0 | 0 |
| # unaligned mis. contigs | 1 | 1 |
| # mismatches | 0 | 1 |
| # indels | 6 | 121 |
| # indels (<= 5 bp) | 6 | 121 |
| # indels (> 5 bp) | 0 | 0 |
| Indels length | 6 | 123 |

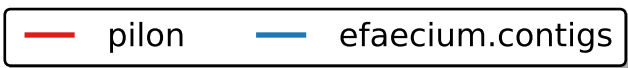
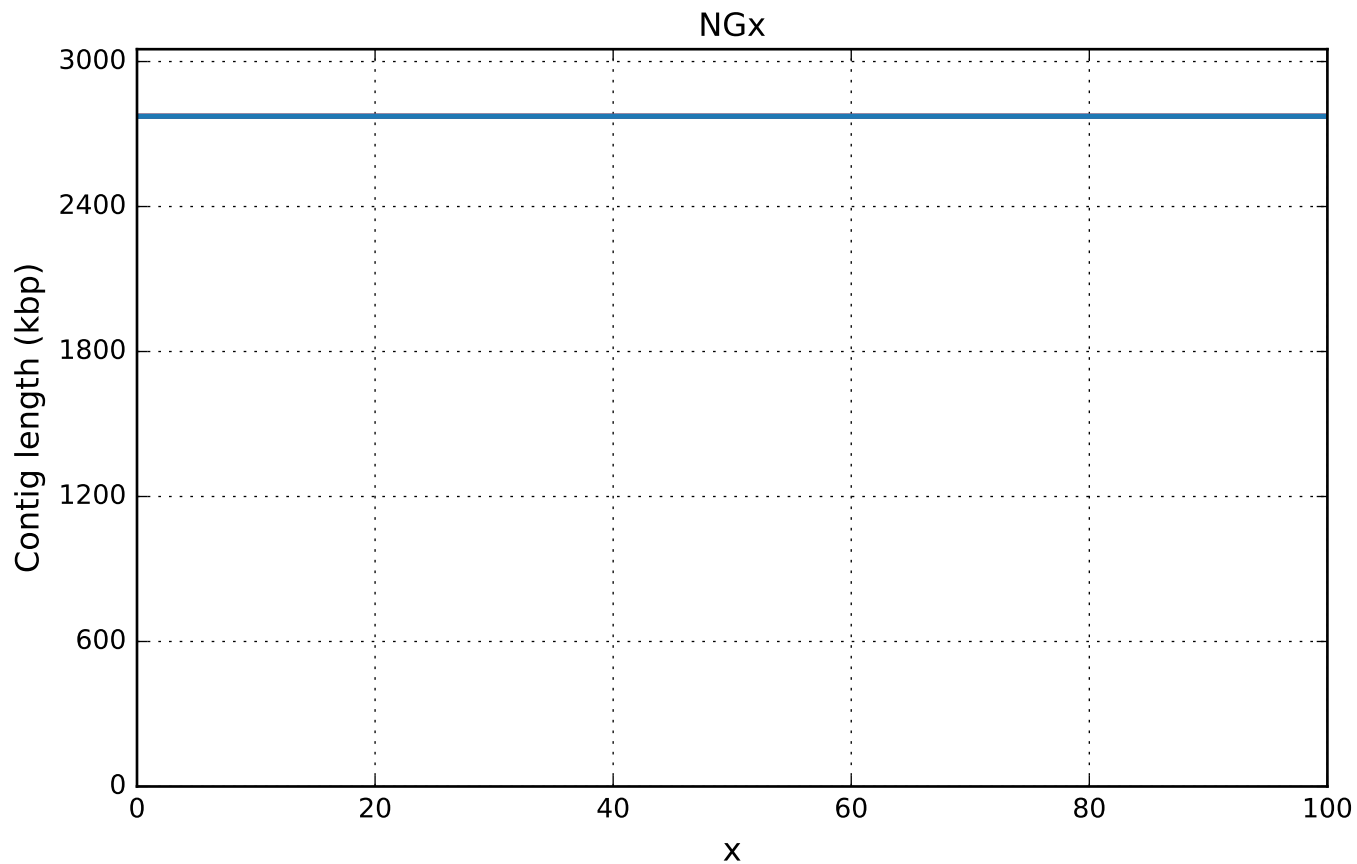
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

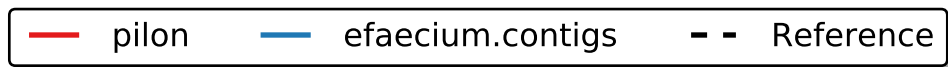
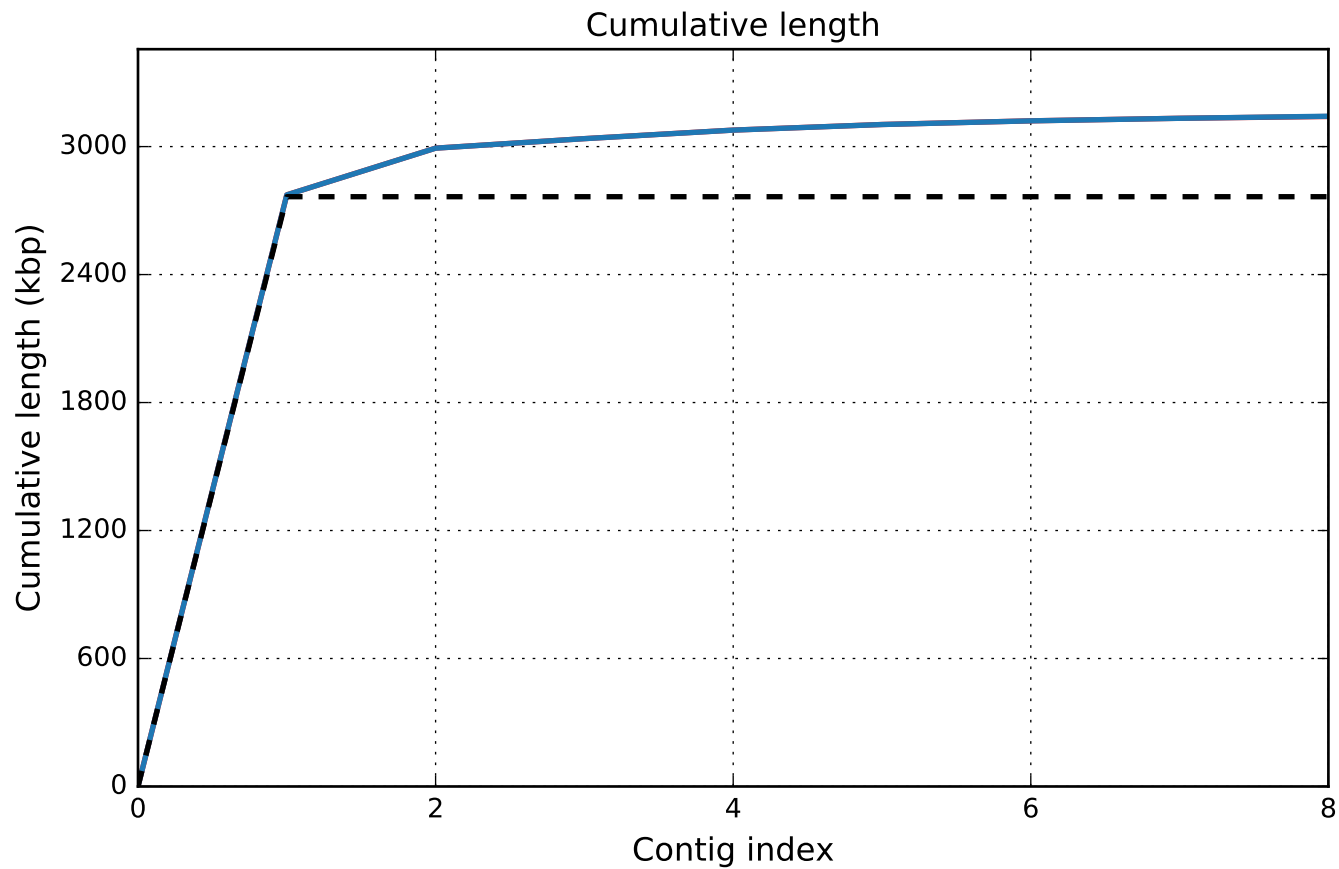
Unaligned report

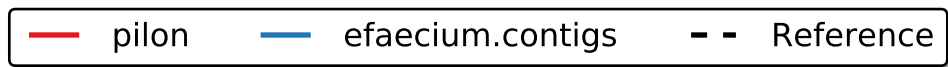
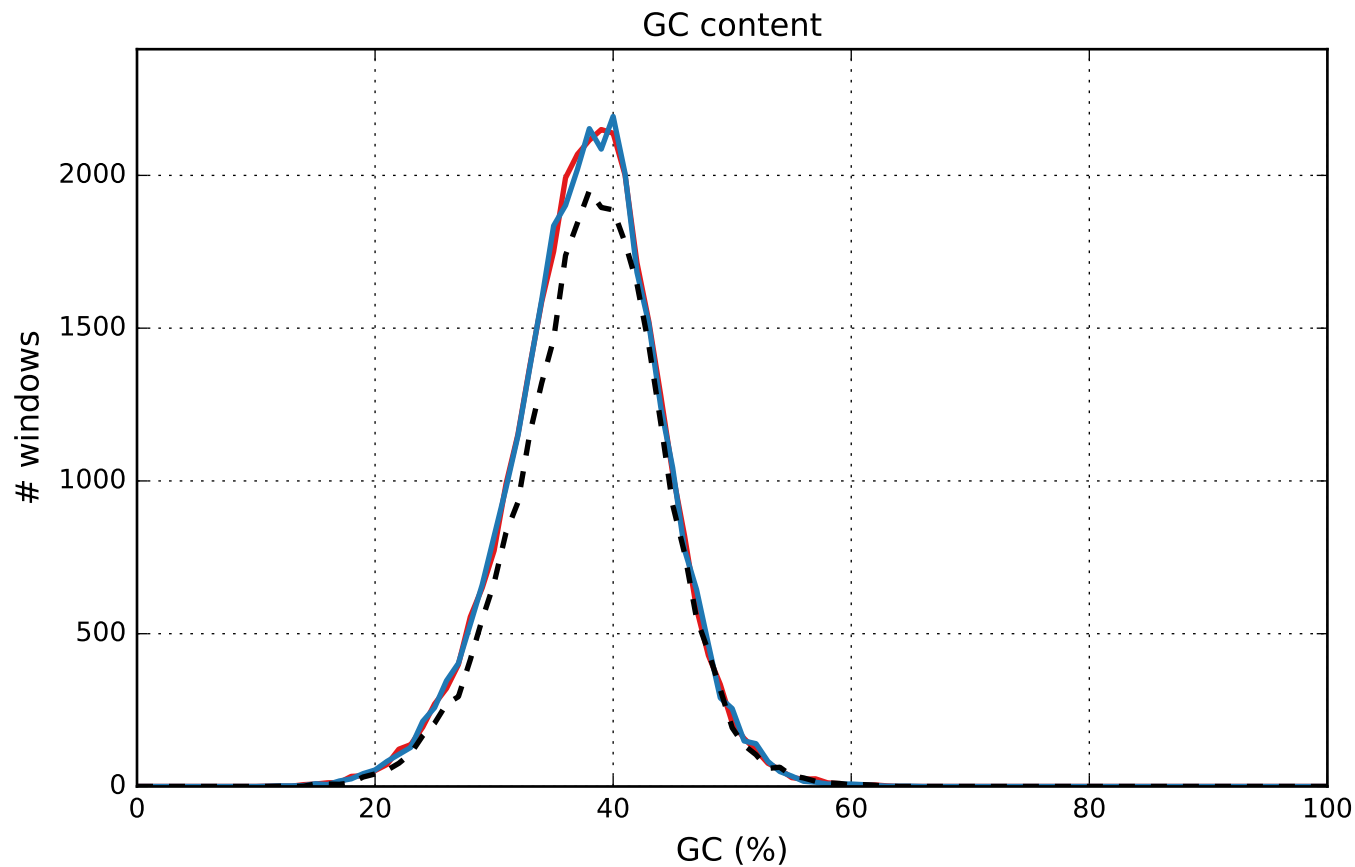
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|-------------------------------|--------|------------------|
| # fully unaligned contigs | 4 | 4 |
| Fully unaligned length | 100053 | 100025 |
| # partially unaligned contigs | 3 | 3 |
| Partially unaligned length | 222012 | 222026 |
| # N's | 0 | 0 |

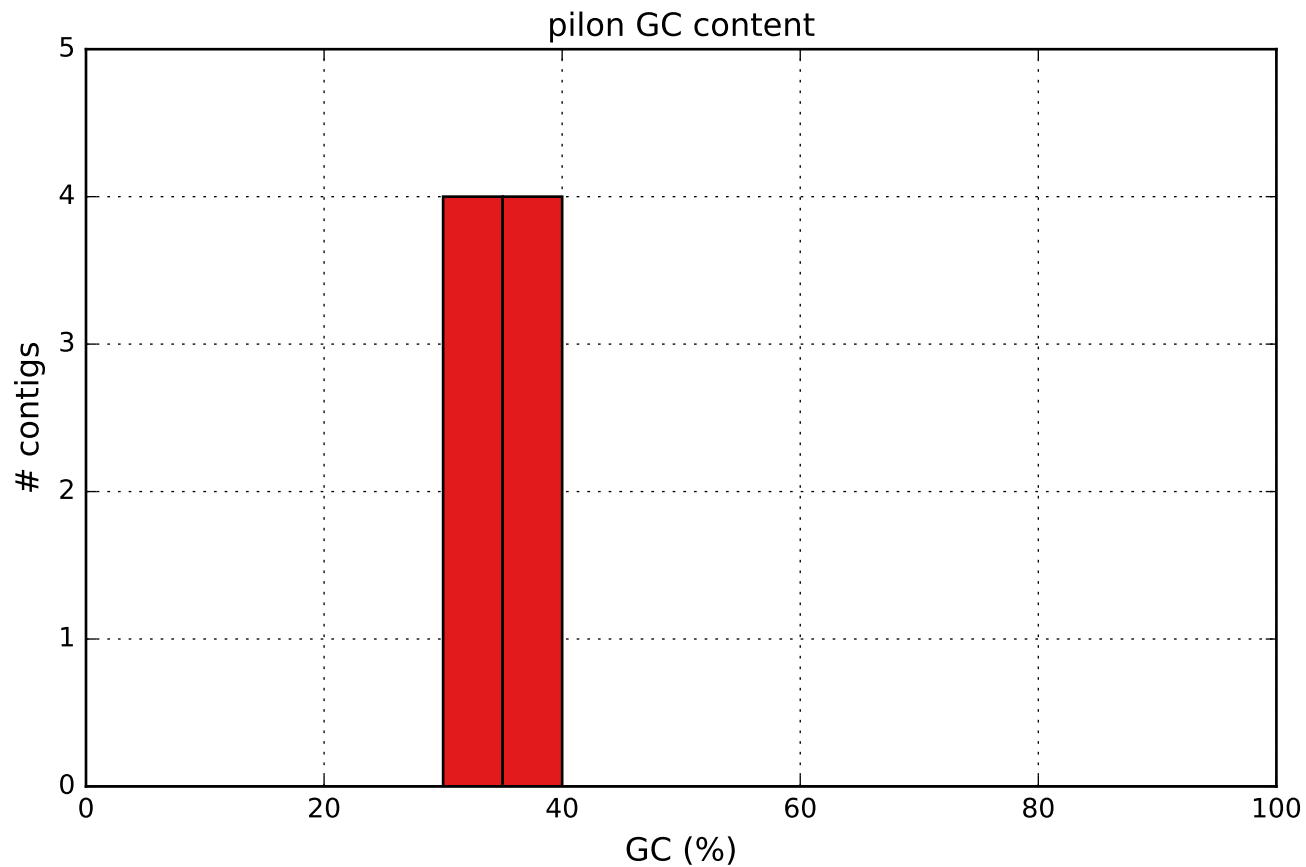
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

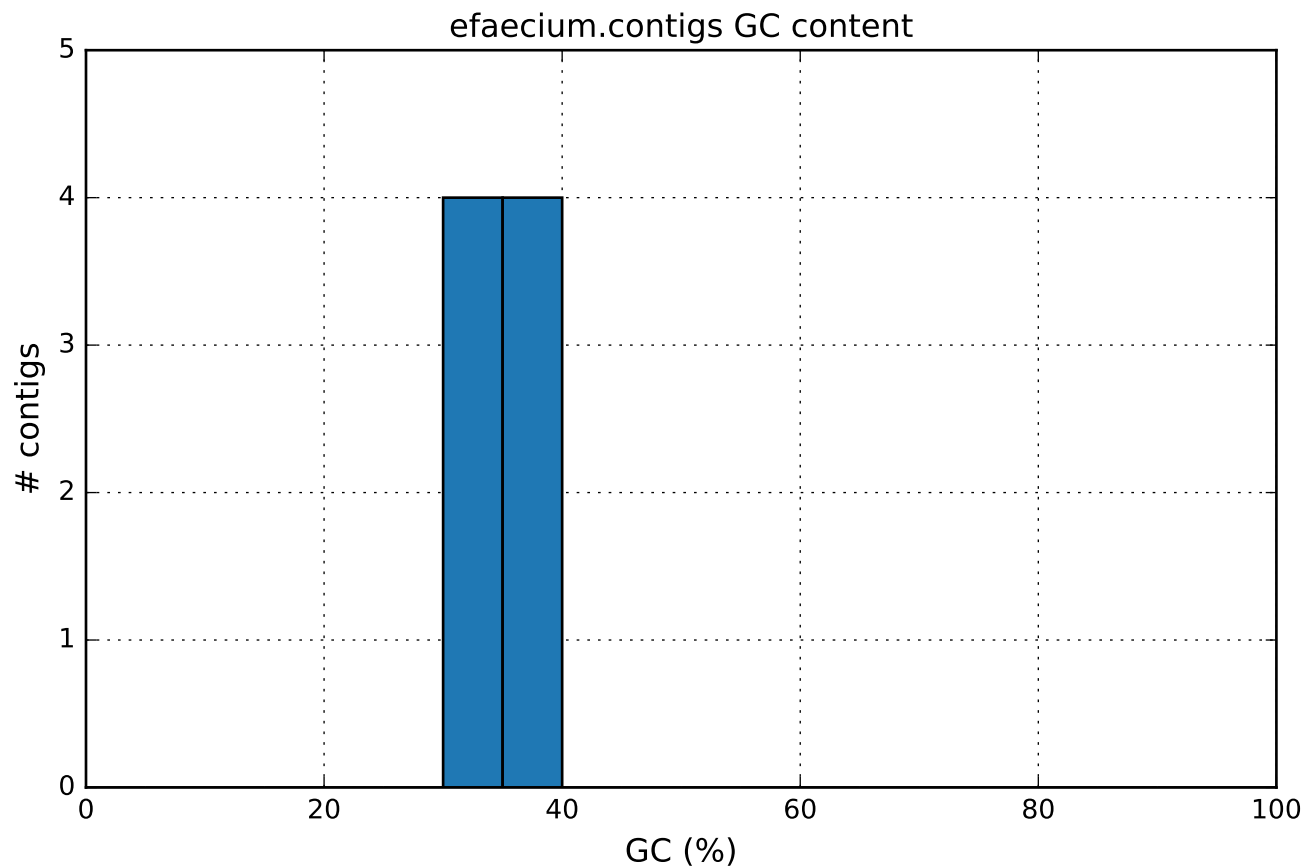




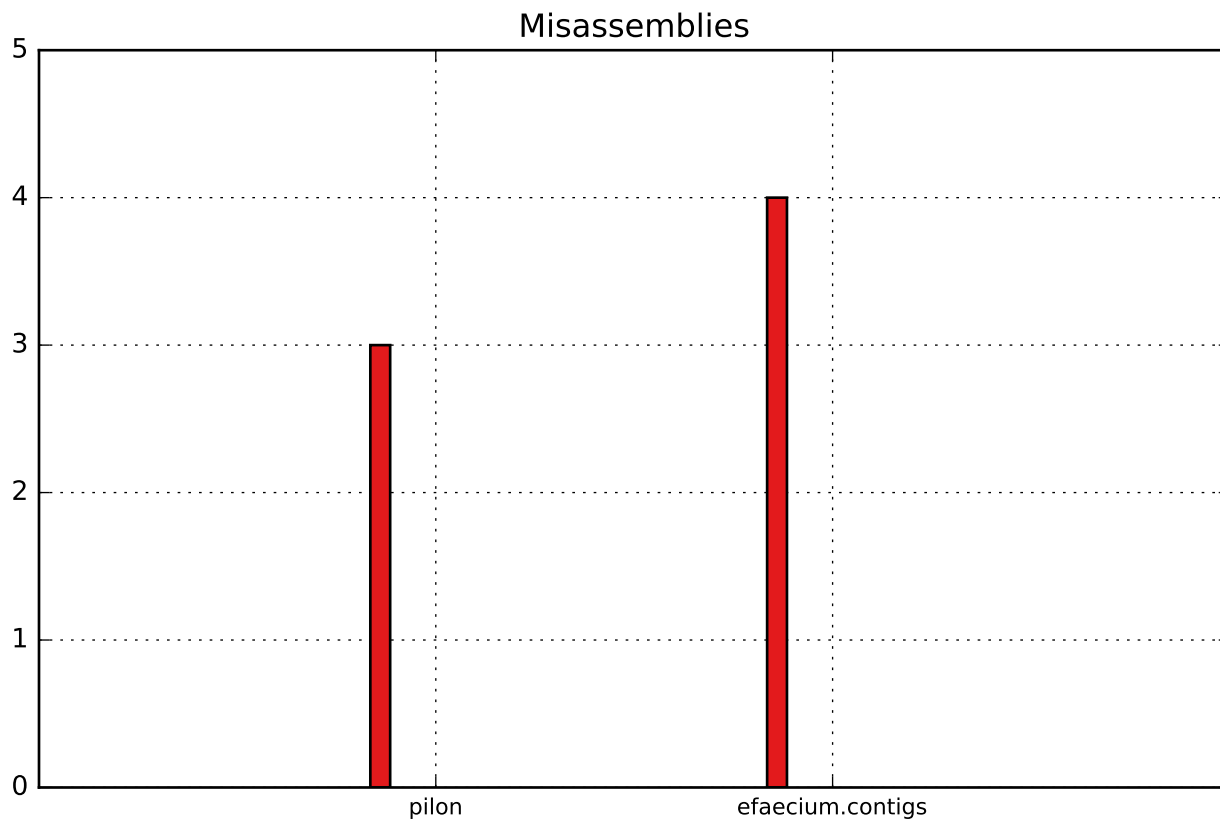




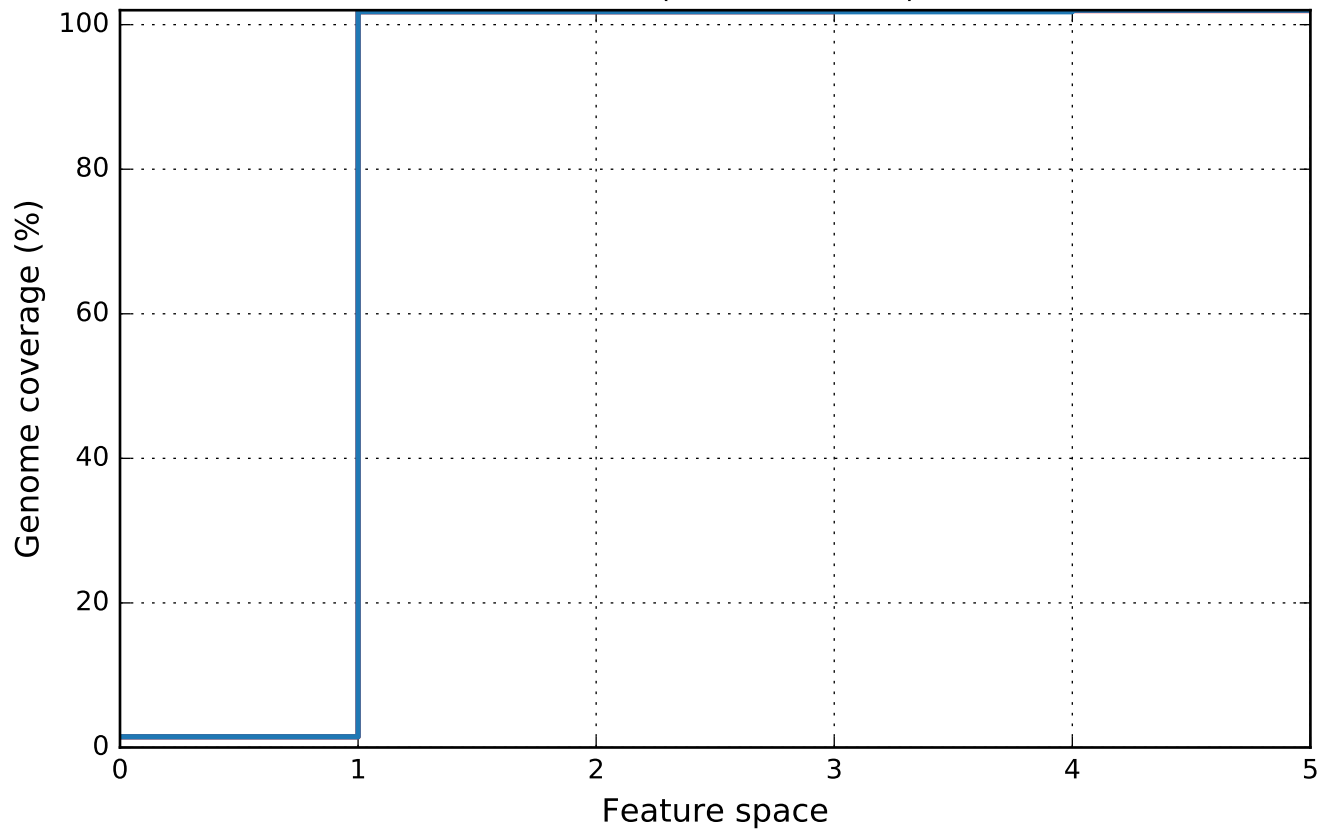




efaecium.contigs

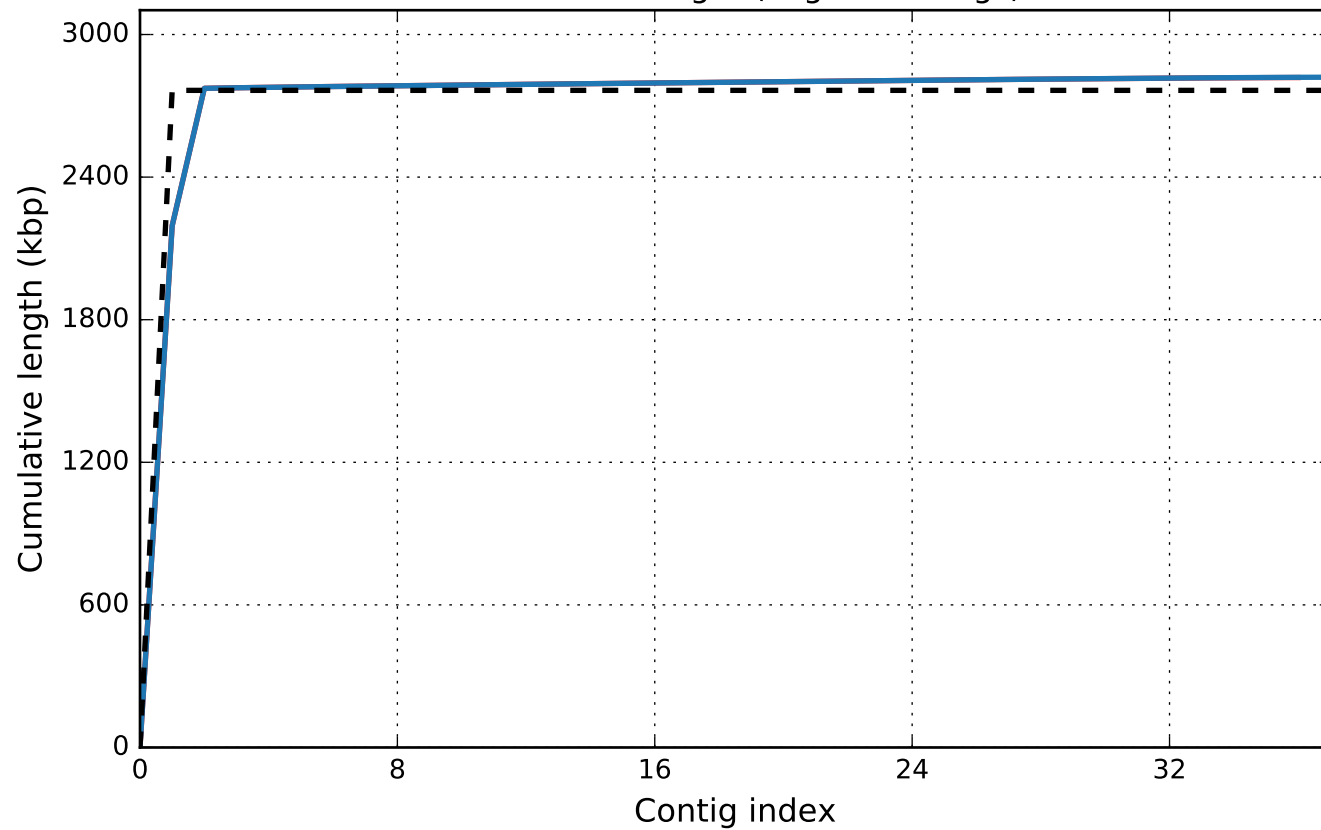


FRCurve (misassemblies)

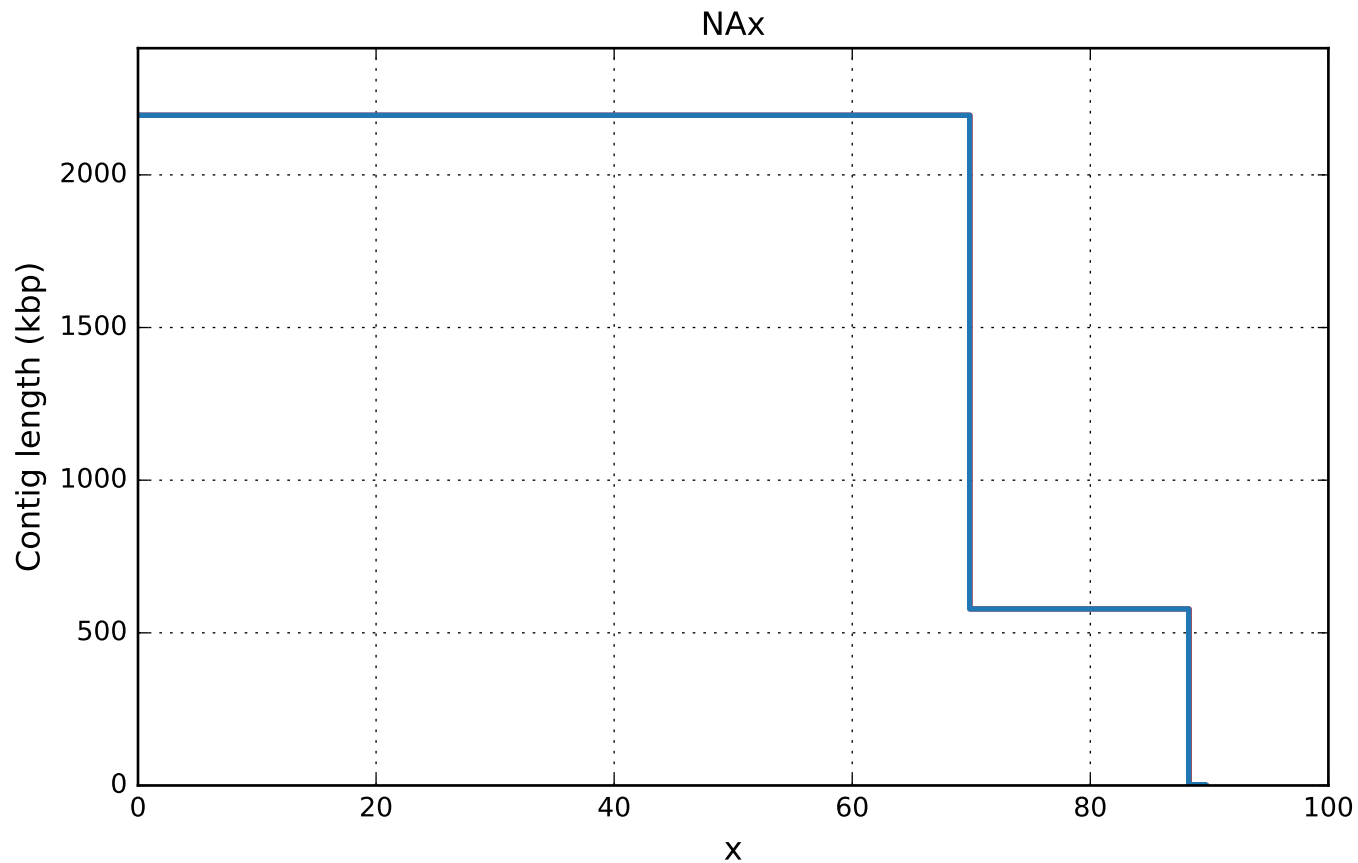


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Cumulative length (aligned contigs)

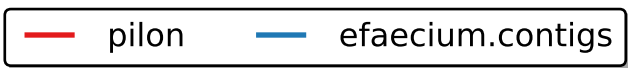
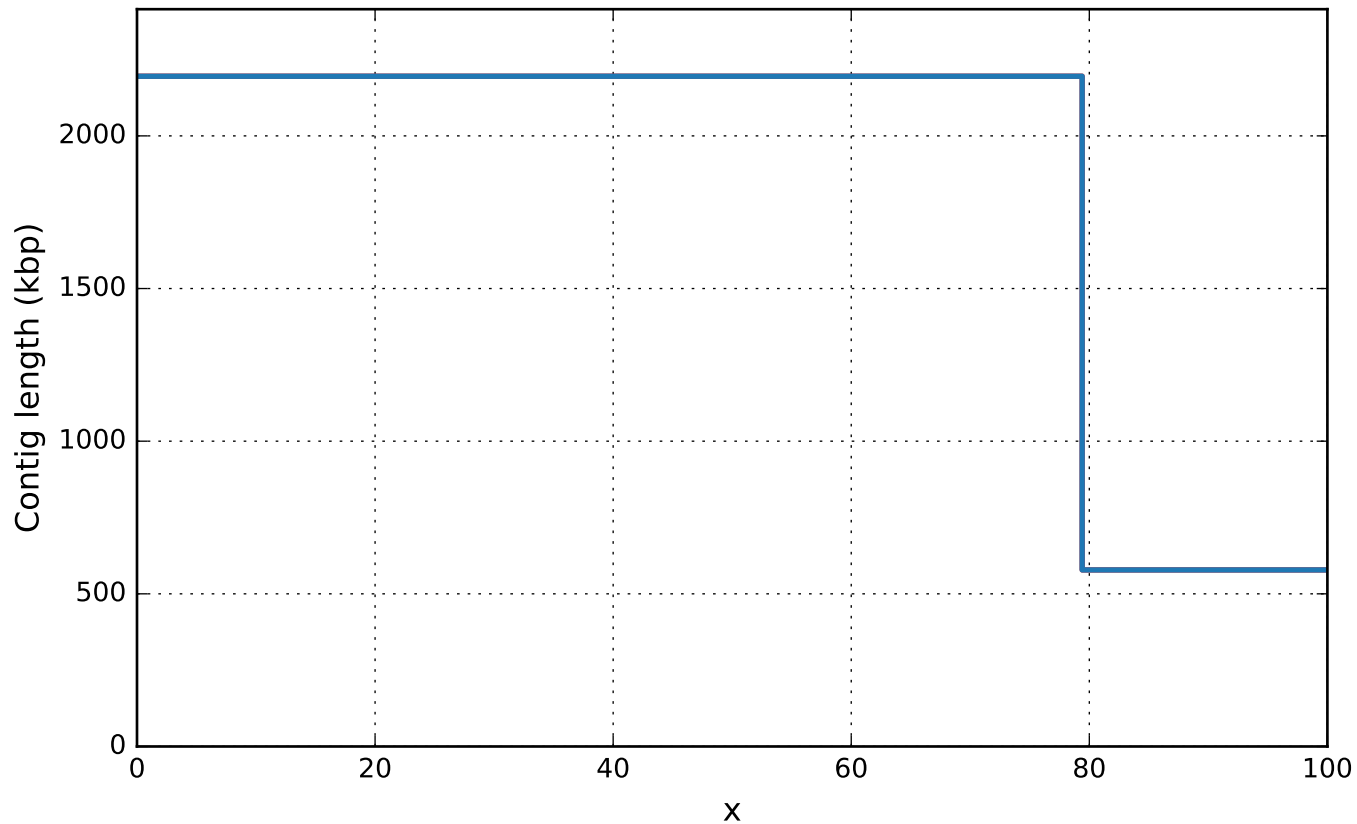


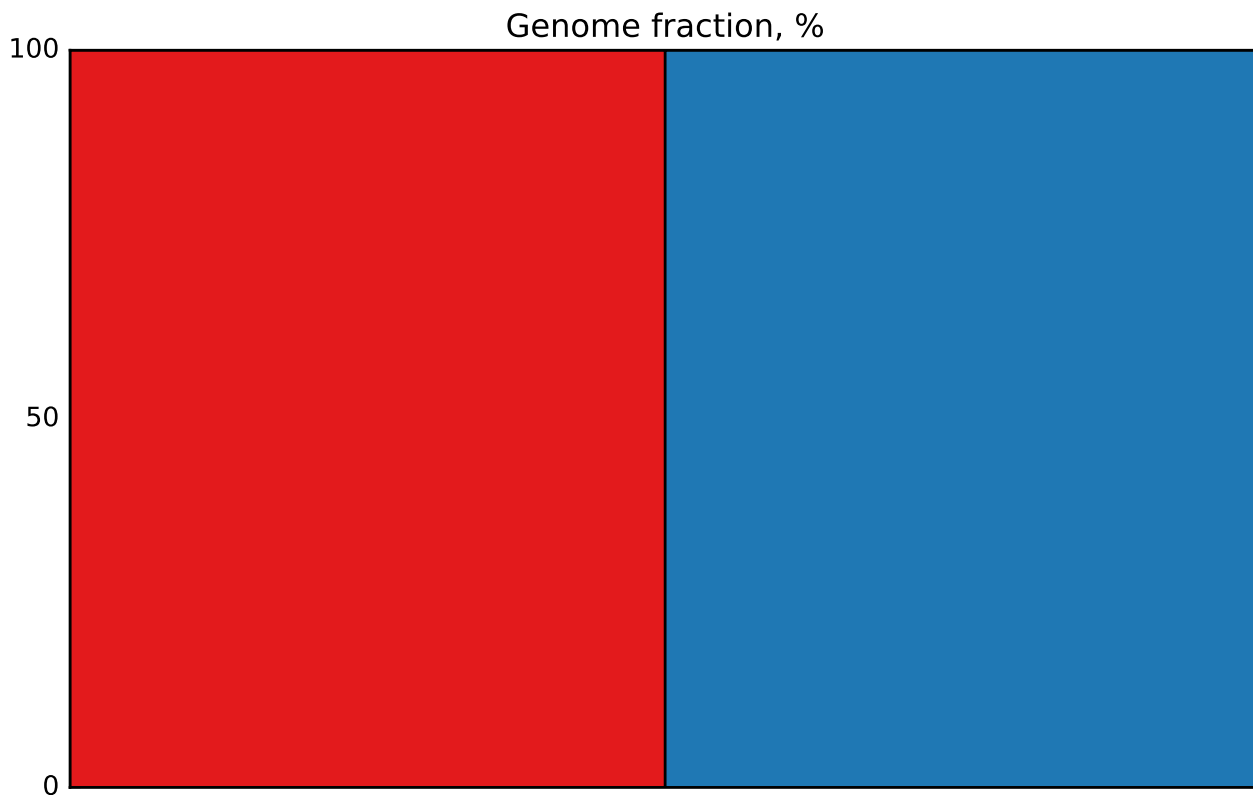
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NGAx





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