

Report

| | CV29_velvet_contigs |
|-----------------------------|---------------------|
| # contigs (>= 0 bp) | 541 |
| # contigs (>= 1000 bp) | 16 |
| # contigs (>= 5000 bp) | 0 |
| # contigs (>= 10000 bp) | 0 |
| # contigs (>= 25000 bp) | 0 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 163765 |
| Total length (>= 1000 bp) | 24443 |
| Total length (>= 5000 bp) | 0 |
| Total length (>= 10000 bp) | 0 |
| Total length (>= 25000 bp) | 0 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 66 |
| Largest contig | 2877 |
| Total length | 59242 |
| Reference length | 29903 |
| GC (%) | 46.83 |
| Reference GC (%) | 37.97 |
| N50 | 942 |
| NG50 | 1380 |
| N75 | 680 |
| NG75 | 1093 |
| L50 | 22 |
| LG50 | 9 |
| L75 | 41 |
| LG75 | 15 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 65 + 0 part |
| Unaligned length | 58650 |
| Genome fraction (%) | 1.729 |
| Duplication ratio | 1.145 |
| # N's per 100 kbp | 126.60 |
| # mismatches per 100 kbp | 0.00 |
| # indels per 100 kbp | 0.00 |
| # genomic features | 0 + 6 part |
| Largest alignment | 517 |
| Total aligned length | 517 |
| 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

| | CV29_velvet_contigs |
|-----------------------------|---------------------|
| # misassemblies | 0 |
| # contig misassemblies | 0 |
| # c. relocations | 0 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 0 |
| # indels | 0 |
| # indels (<= 5 bp) | 0 |
| # indels (> 5 bp) | 0 |
| Indels length | 0 |

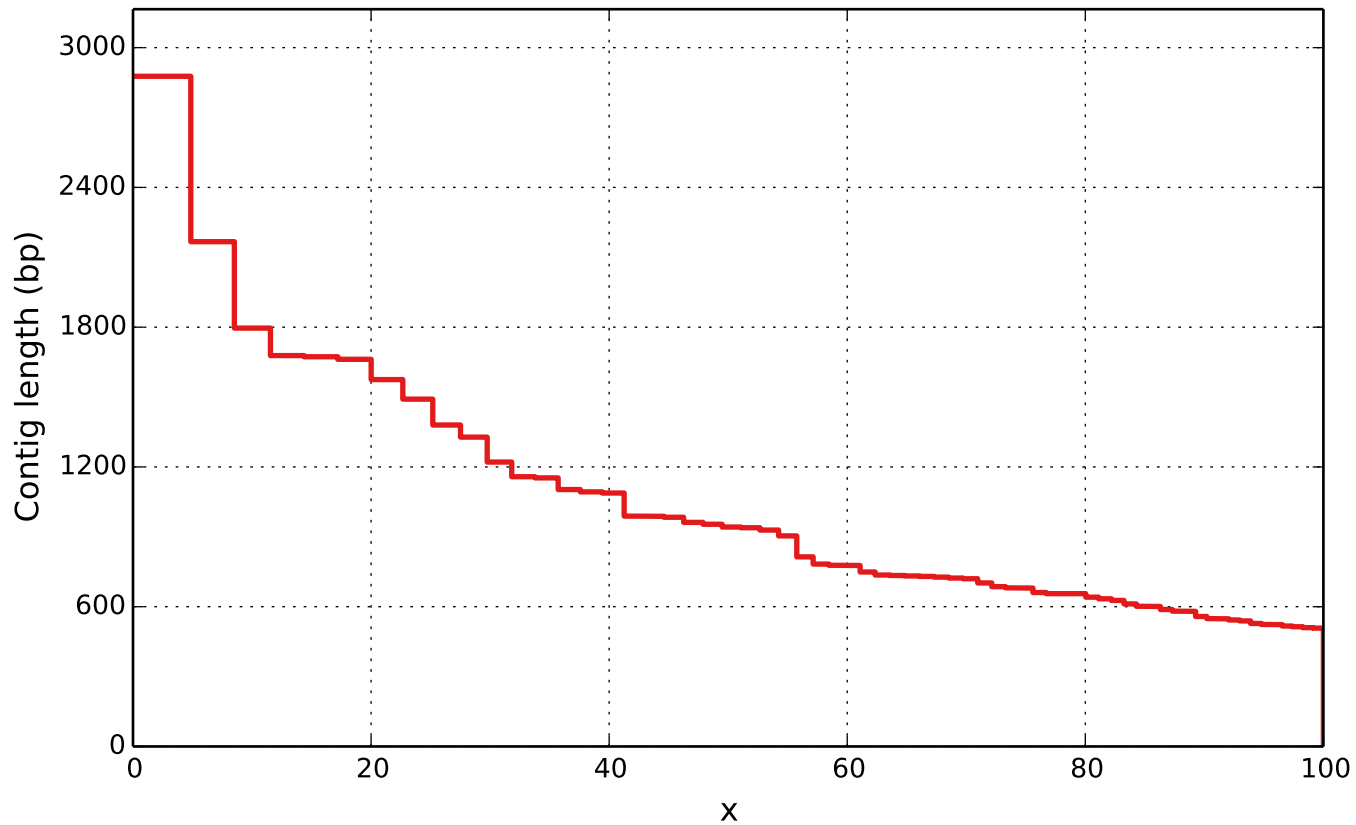
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | CV29_velvet_contigs |
|-------------------------------|---------------------|
| # fully unaligned contigs | 65 |
| Fully unaligned length | 58650 |
| # partially unaligned contigs | 0 |
| Partially unaligned length | 0 |
| # N's | 75 |

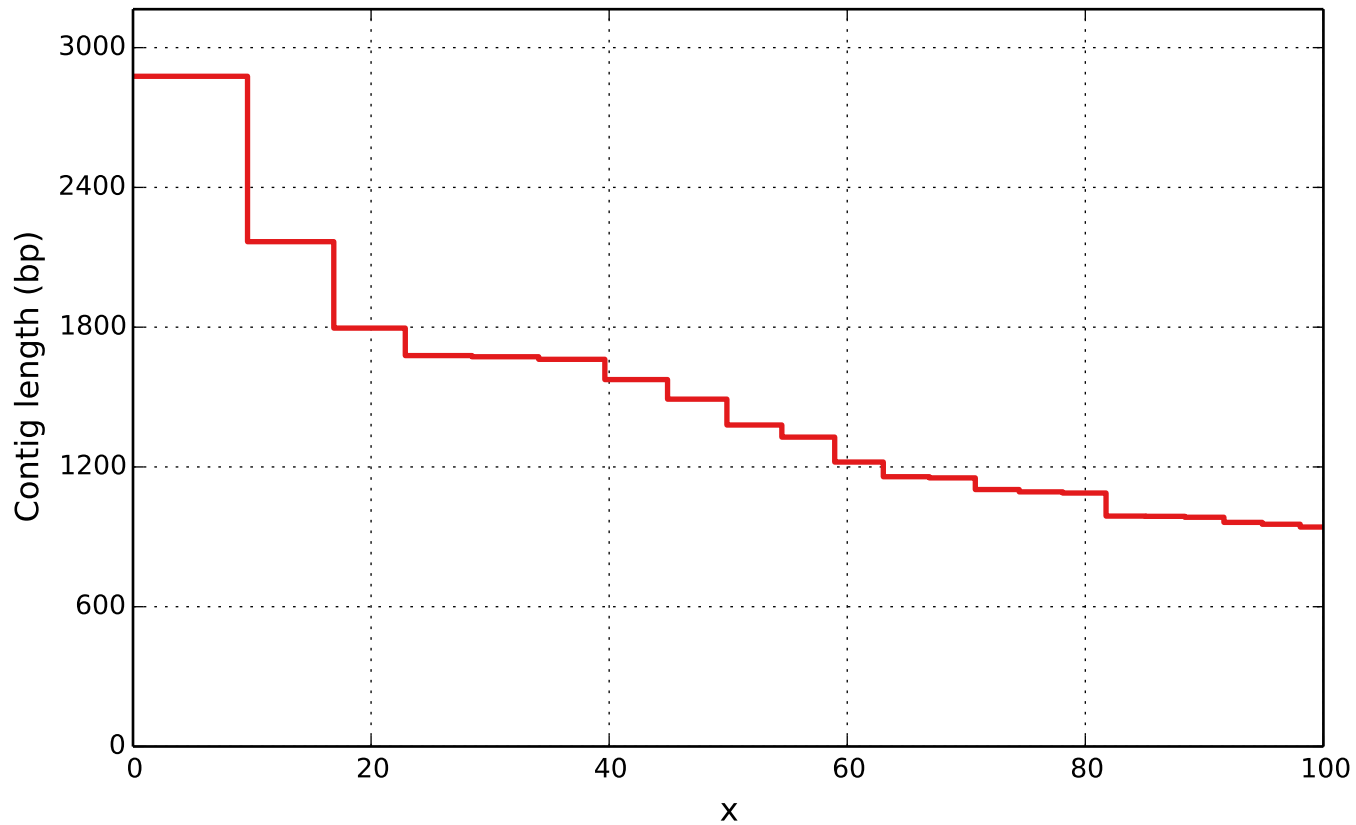
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

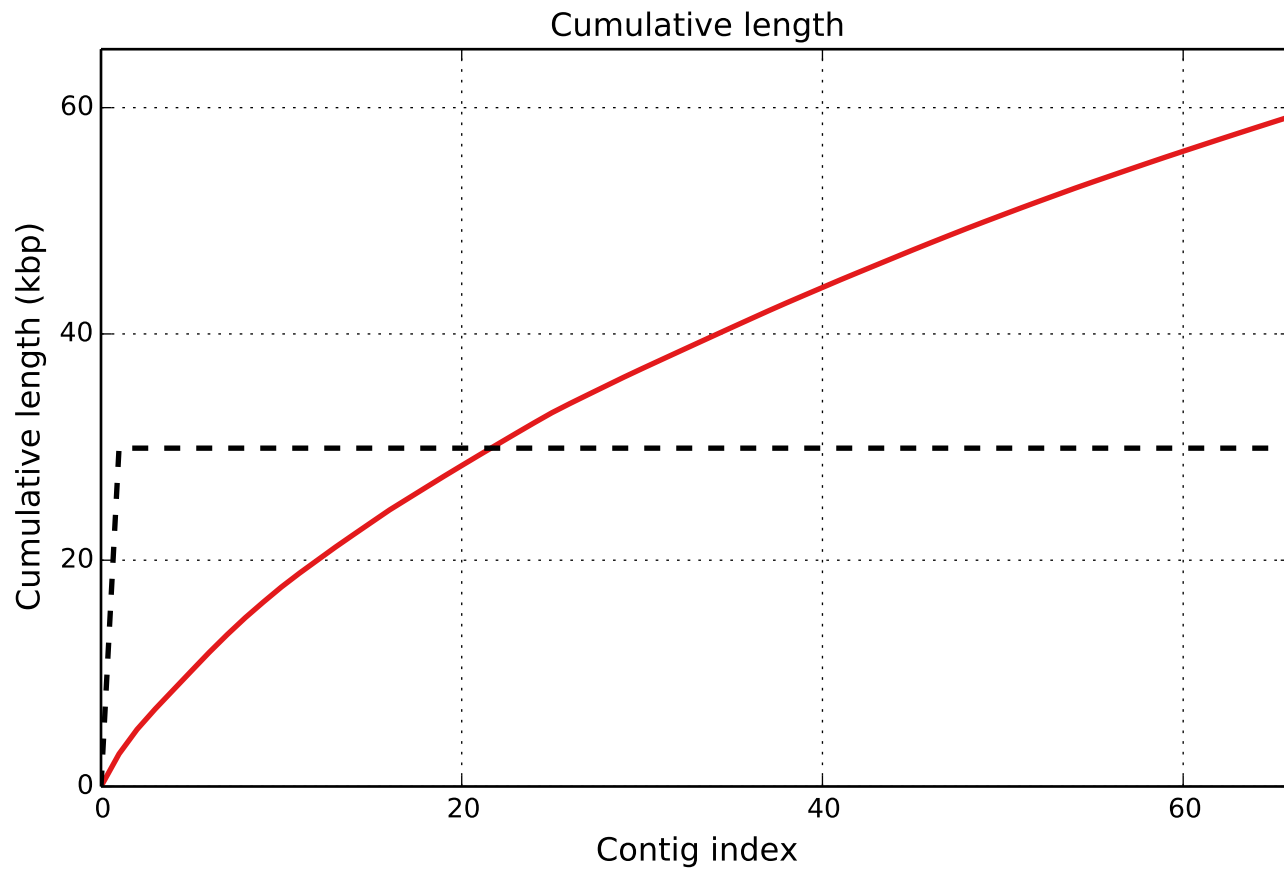


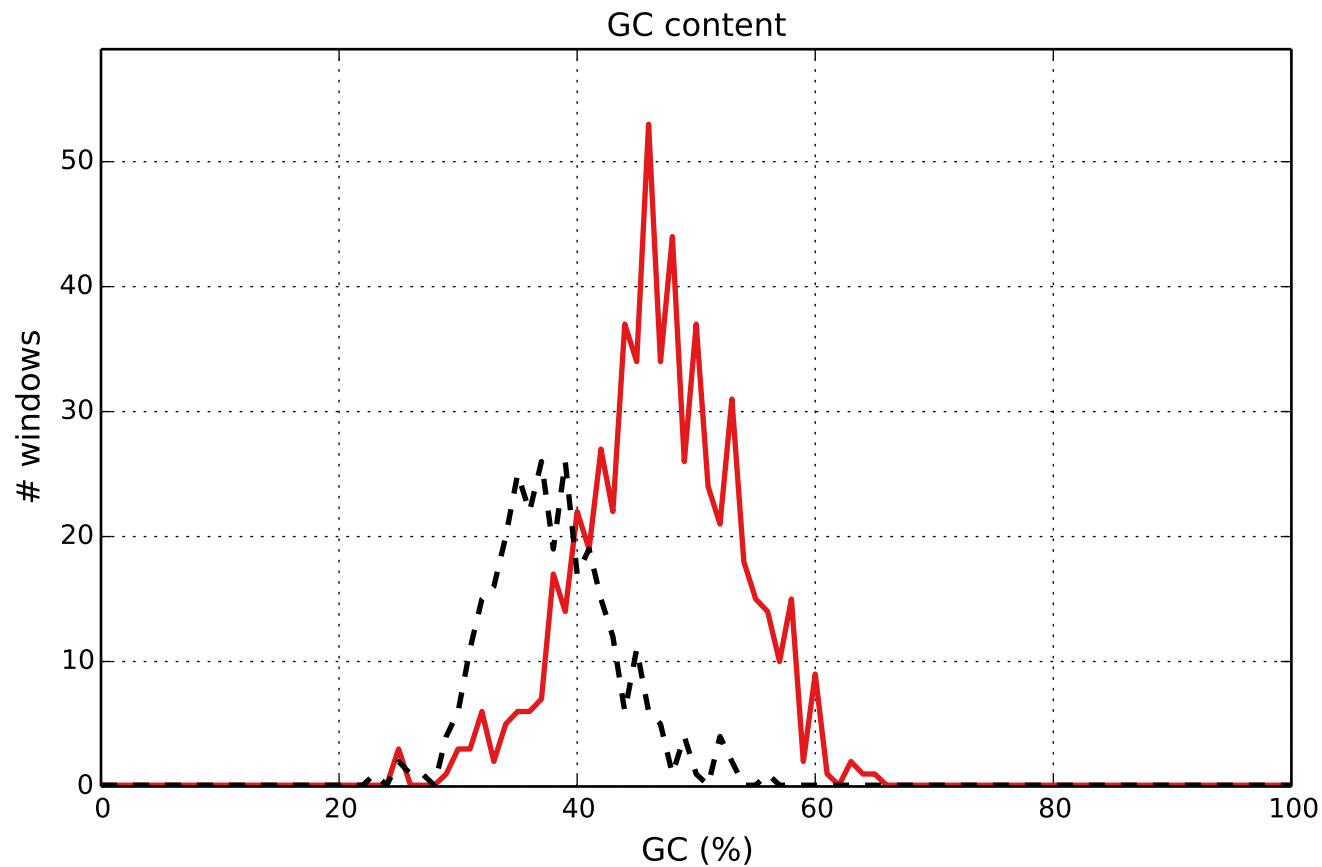
CV29_velvet_contigs

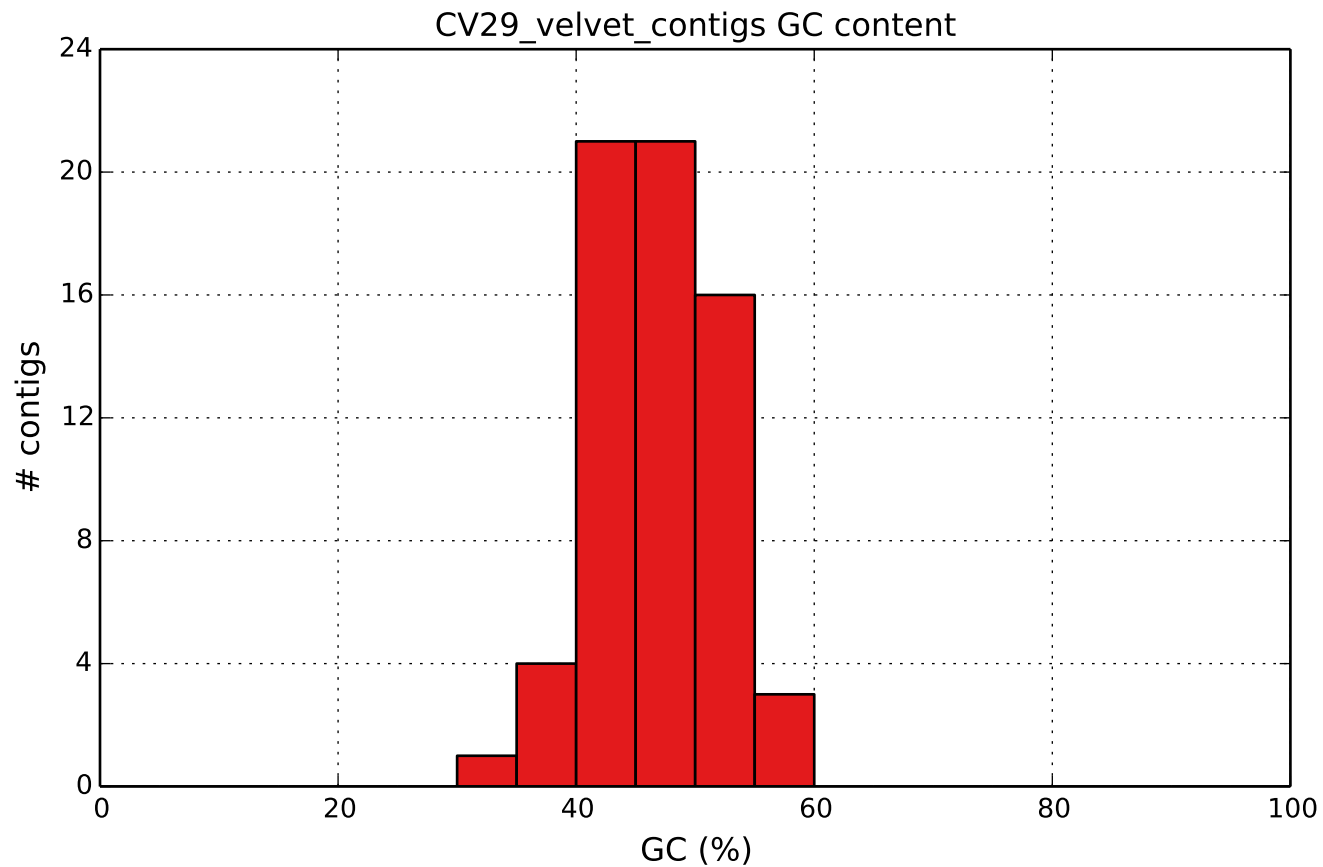
NGx



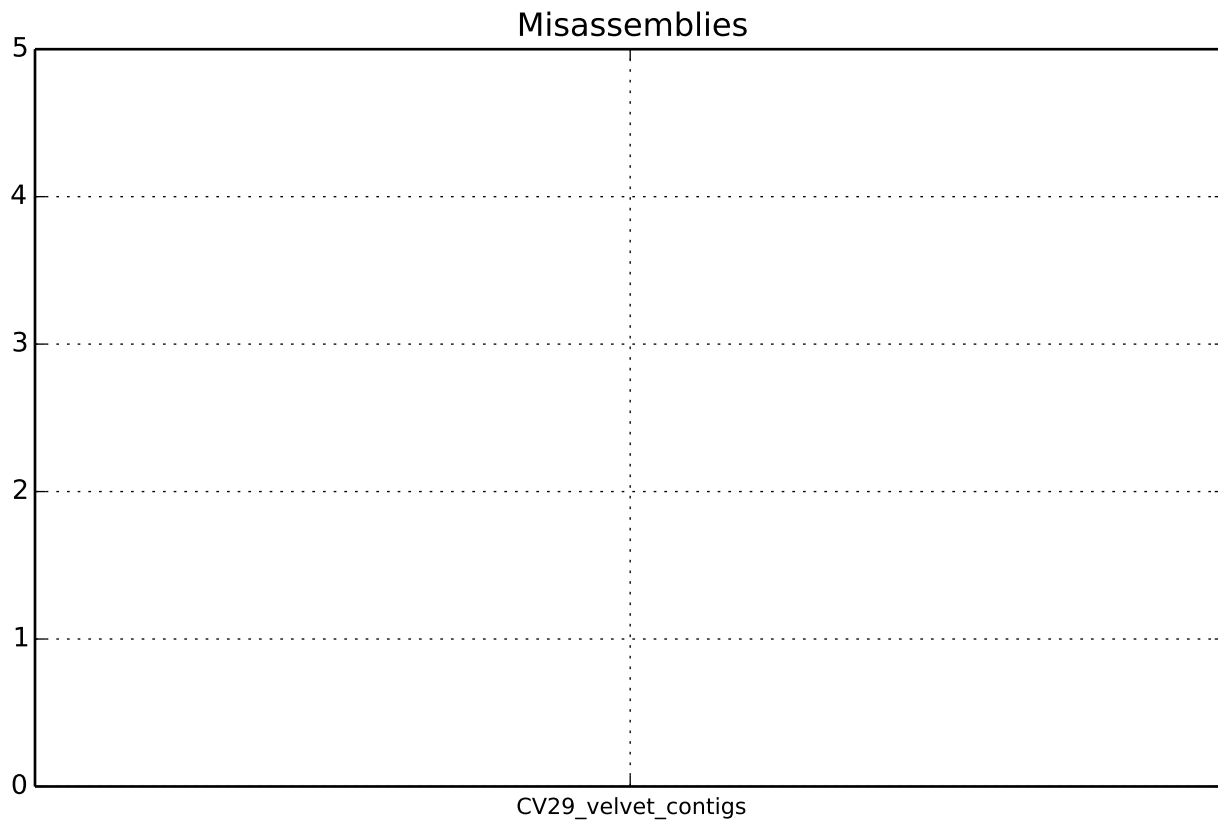
CV29_velvet_contigs



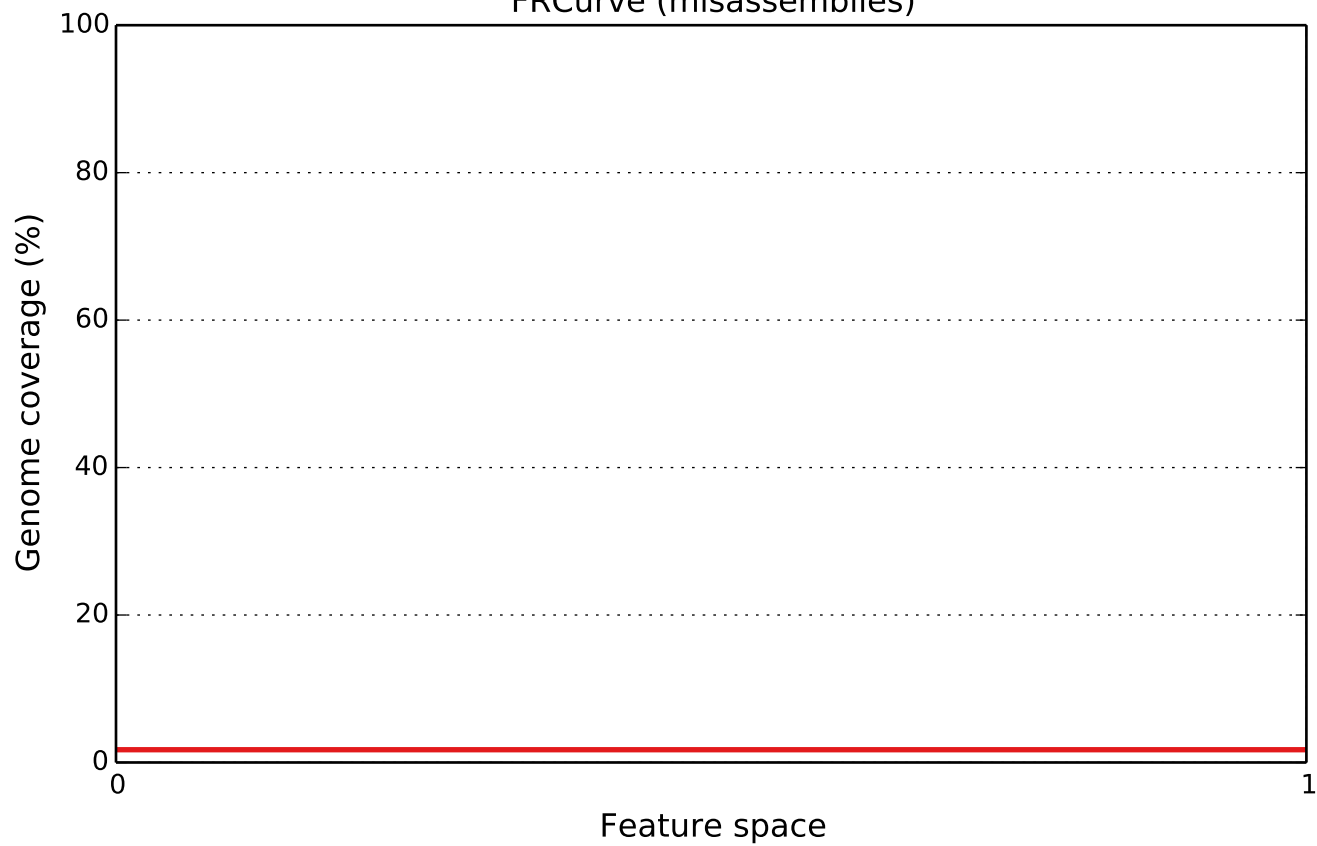




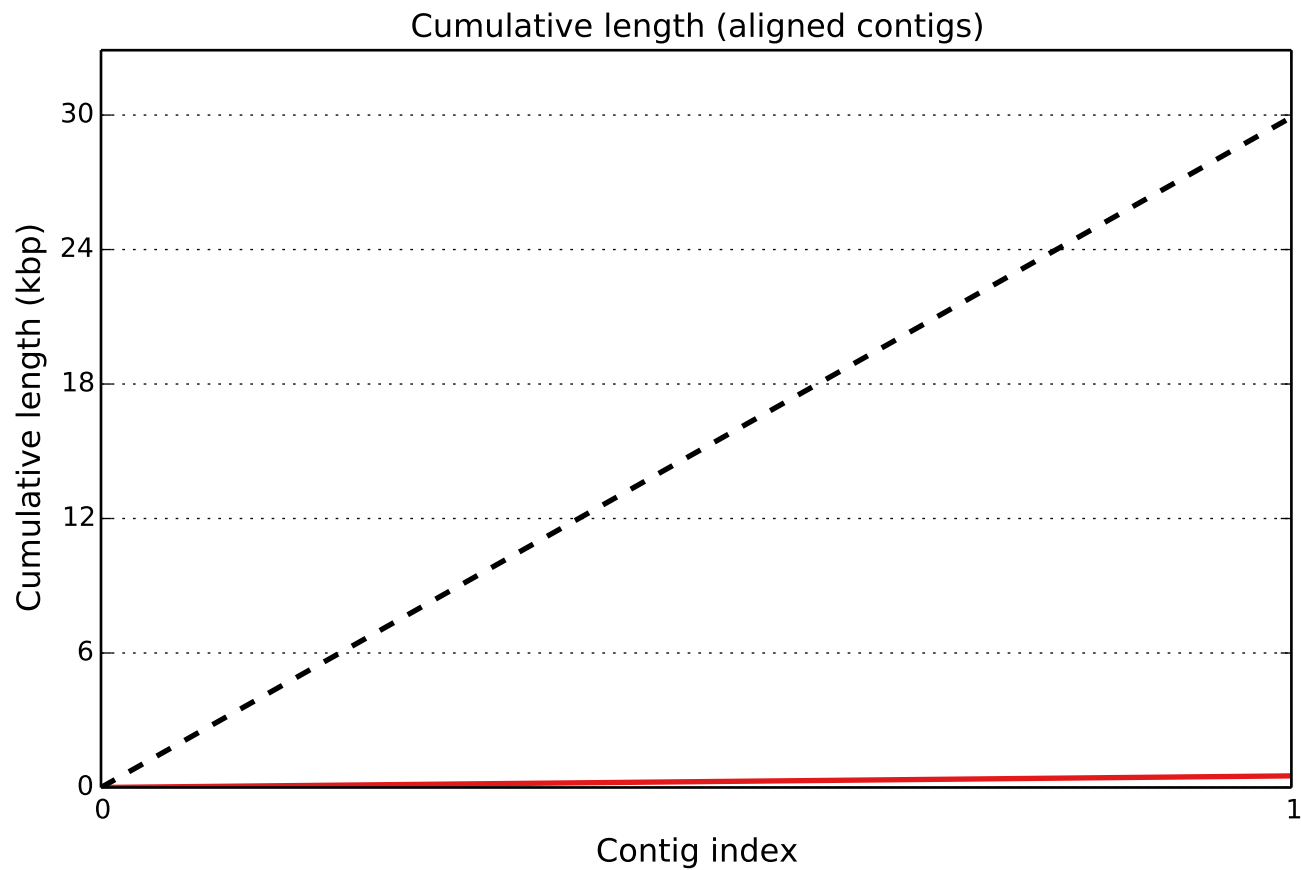
CV29_velvet_contigs



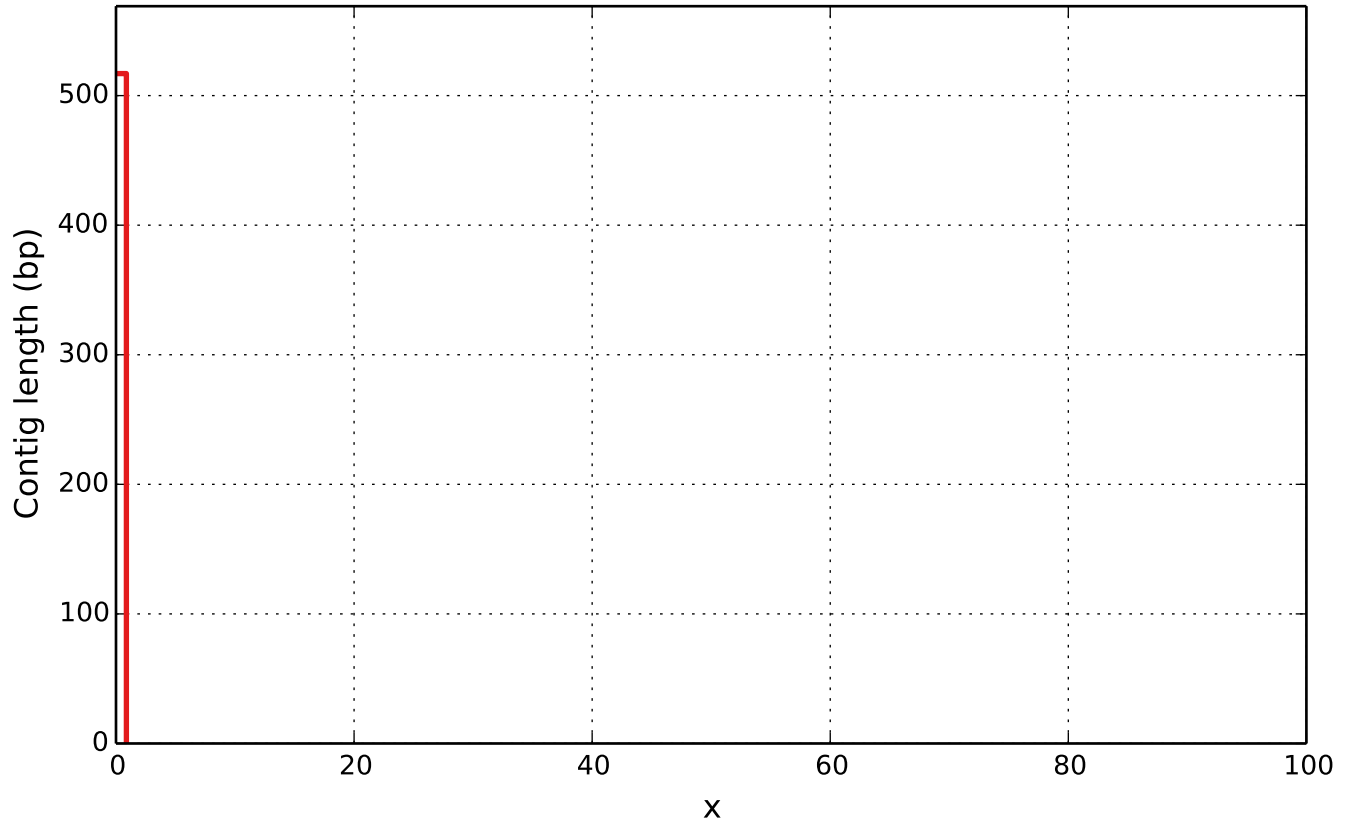
FRCurve (misassemblies)



CV29_velvet_contigs

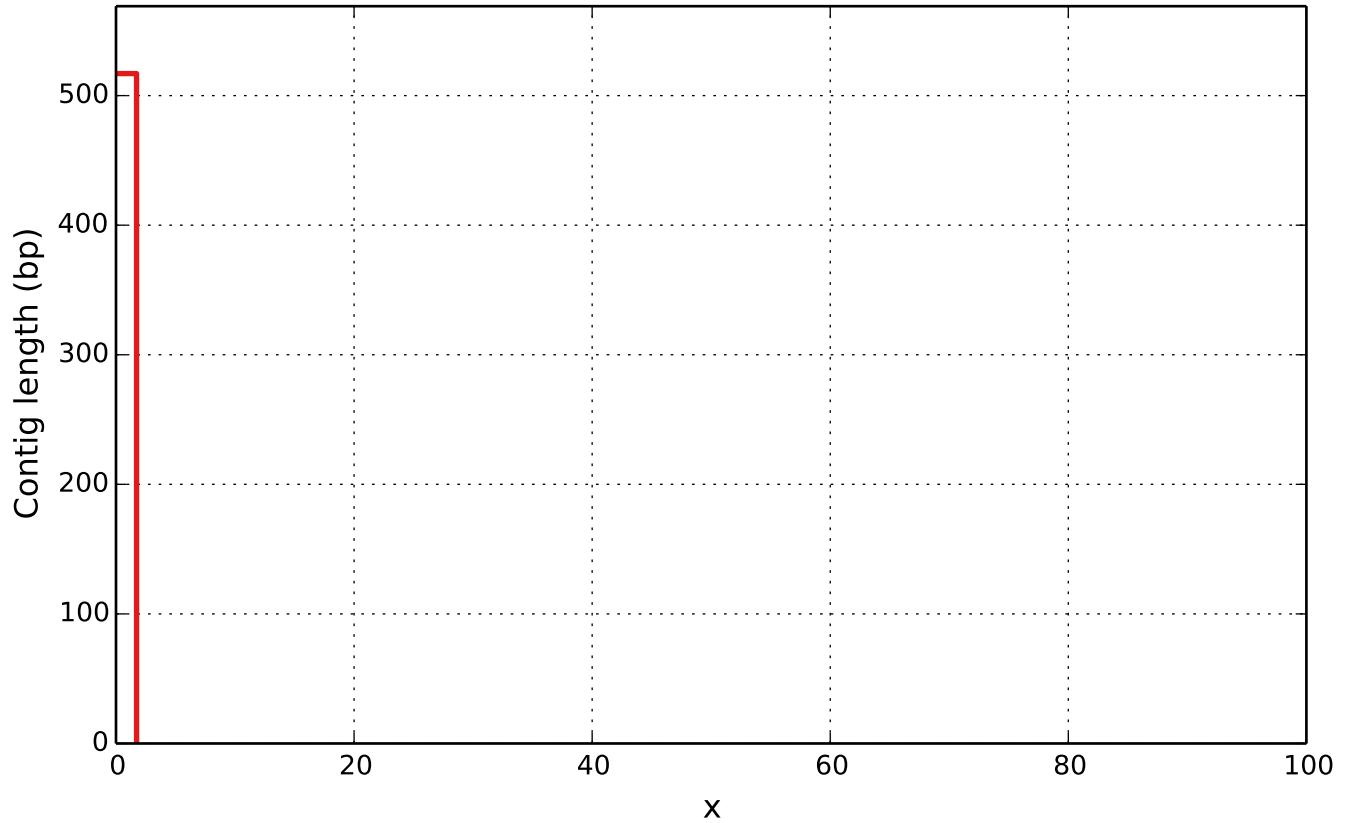


NAx

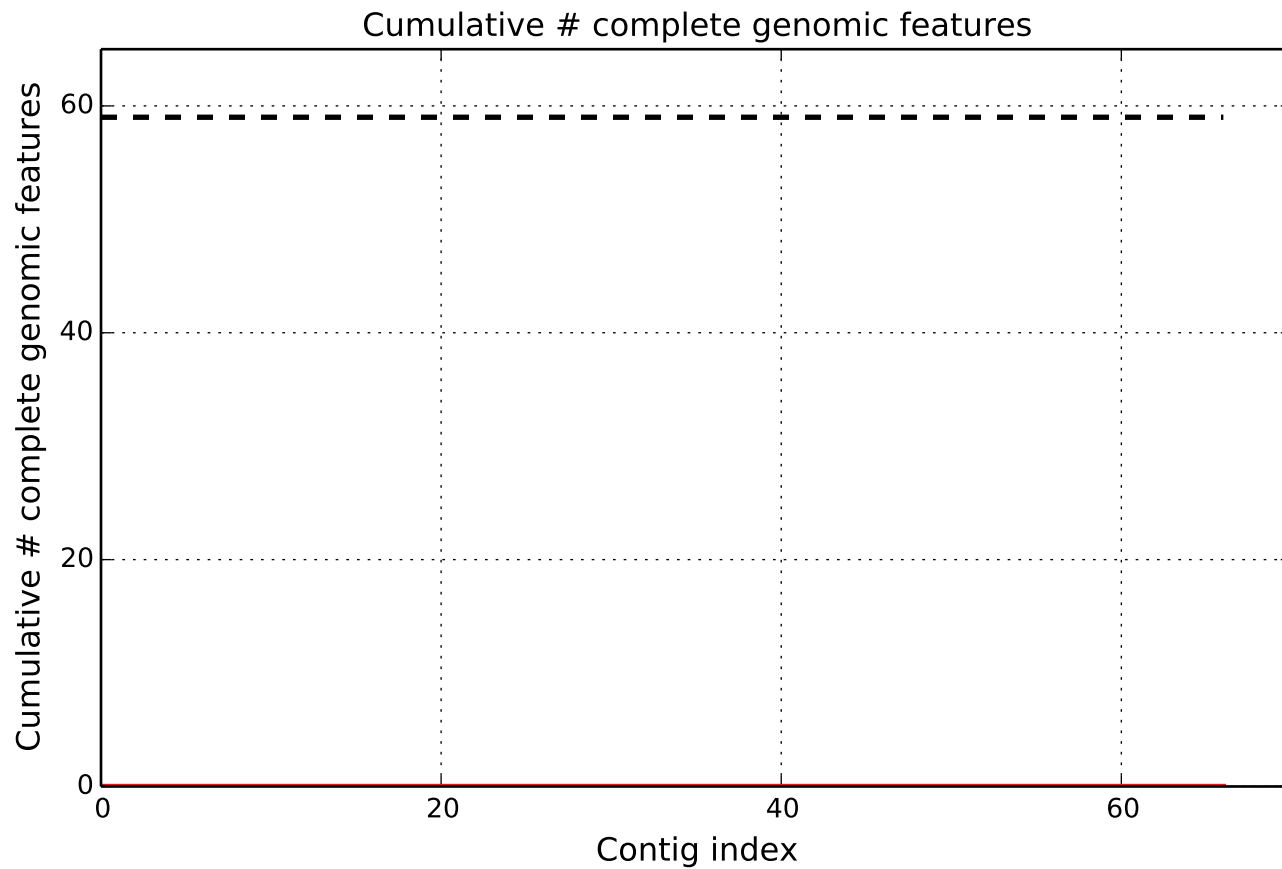


CV29_velvet_contigs

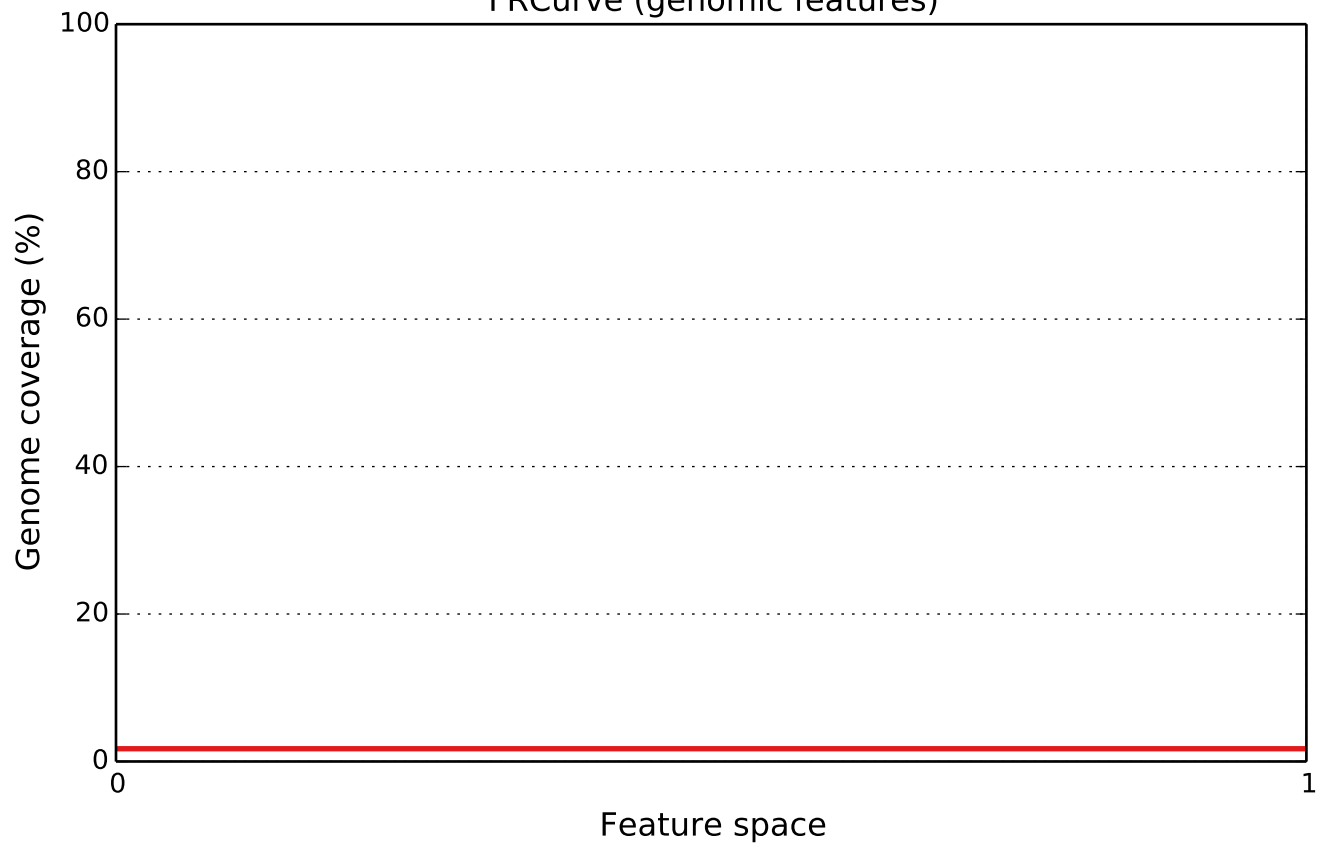
NGAx



— CV29_velvet_contigs



FRCurve (genomic features)



CV29_velvet_contigs