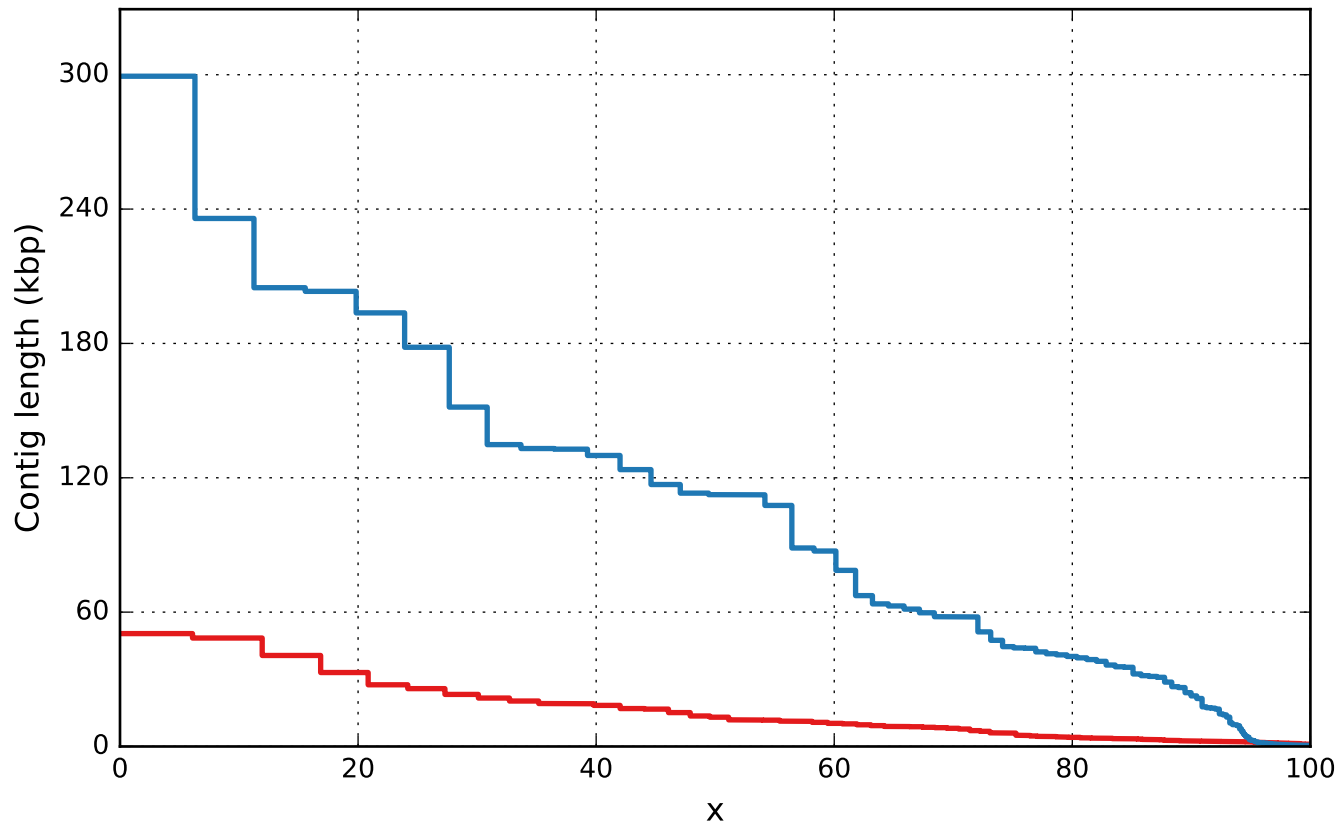


## Report

|                                | ecoli.correctedReads | scaffolds    |
|--------------------------------|----------------------|--------------|
| # contigs (>= 0 bp)            | 120                  | 3136         |
| # contigs (>= 1000 bp)         | 120                  | 142          |
| # contigs (>= 5000 bp)         | 40                   | 67           |
| # contigs (>= 10000 bp)        | 25                   | 61           |
| # contigs (>= 25000 bp)        | 6                    | 50           |
| # contigs (>= 50000 bp)        | 1                    | 29           |
| Total length (>= 0 bp)         | 827543               | 5543314      |
| Total length (>= 1000 bp)      | 827543               | 4623355      |
| Total length (>= 5000 bp)      | 627803               | 4492303      |
| Total length (>= 10000 bp)     | 512308               | 4443471      |
| Total length (>= 25000 bp)     | 225892               | 4254326      |
| Total length (>= 50000 bp)     | 50413                | 3477992      |
| # contigs                      | 120                  | 341          |
| Largest contig                 | 50413                | 299336       |
| Total length                   | 827543               | 4755000      |
| Reference length               | 435265205            | 435265205    |
| GC (%)                         | 69.95                | 50.77        |
| Reference GC (%)               | 36.86                | 36.86        |
| N50                            | 13074                | 112463       |
| N75                            | 5968                 | 44584        |
| L50                            | 17                   | 15           |
| L75                            | 39                   | 31           |
| # unaligned contigs            | 120 + 0 part         | 341 + 0 part |
| Unaligned length               | 827543               | 4755000      |
| # N's per 100 kbp              | 0.00                 | 25.24        |
| # predicted genes (unique)     | 847                  | 3804         |
| # predicted genes (>= 0 bp)    | 847                  | 3804         |
| # predicted genes (>= 300 bp)  | 616                  | 3541         |
| # predicted genes (>= 1500 bp) | 80                   | 657          |
| # predicted genes (>= 3000 bp) | 16                   | 80           |
| 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).

Nx

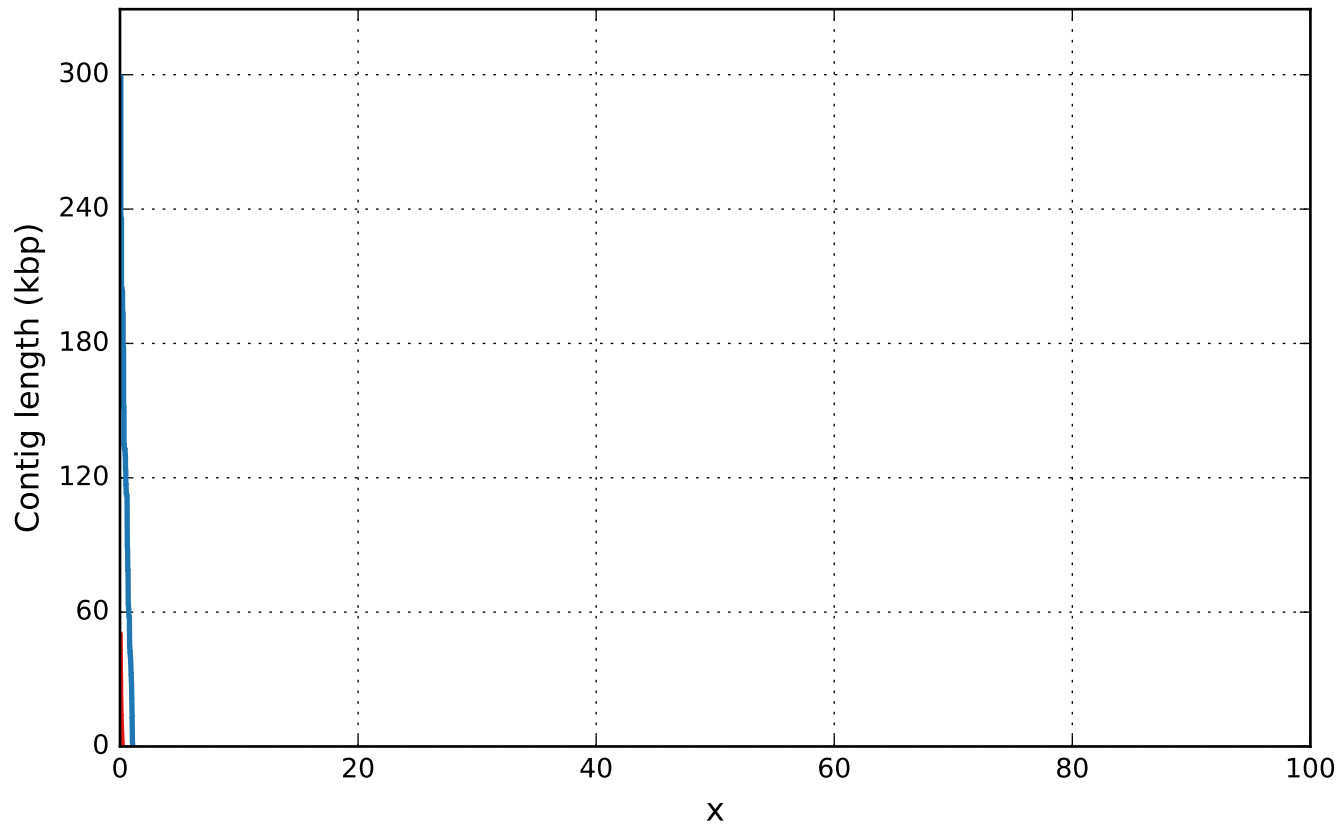


ecoli.correctedReads

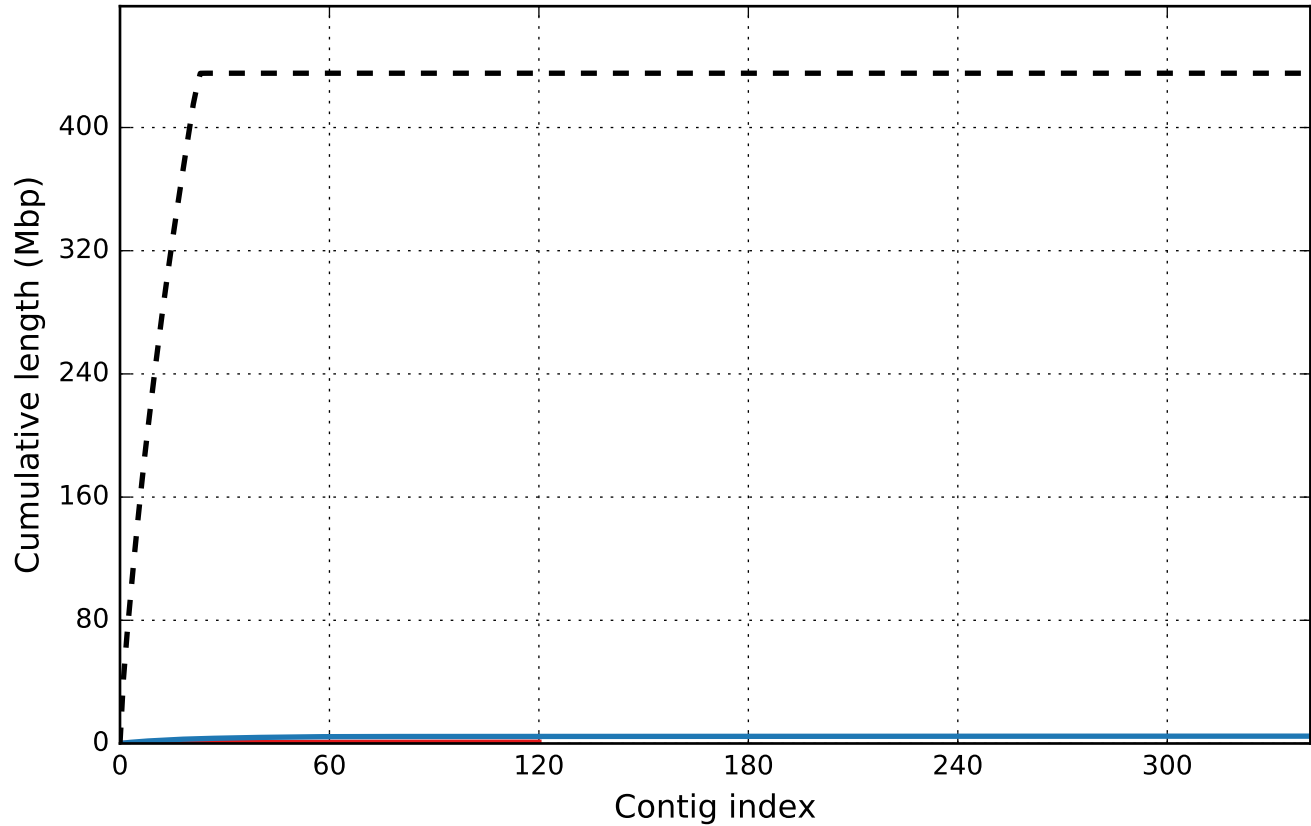


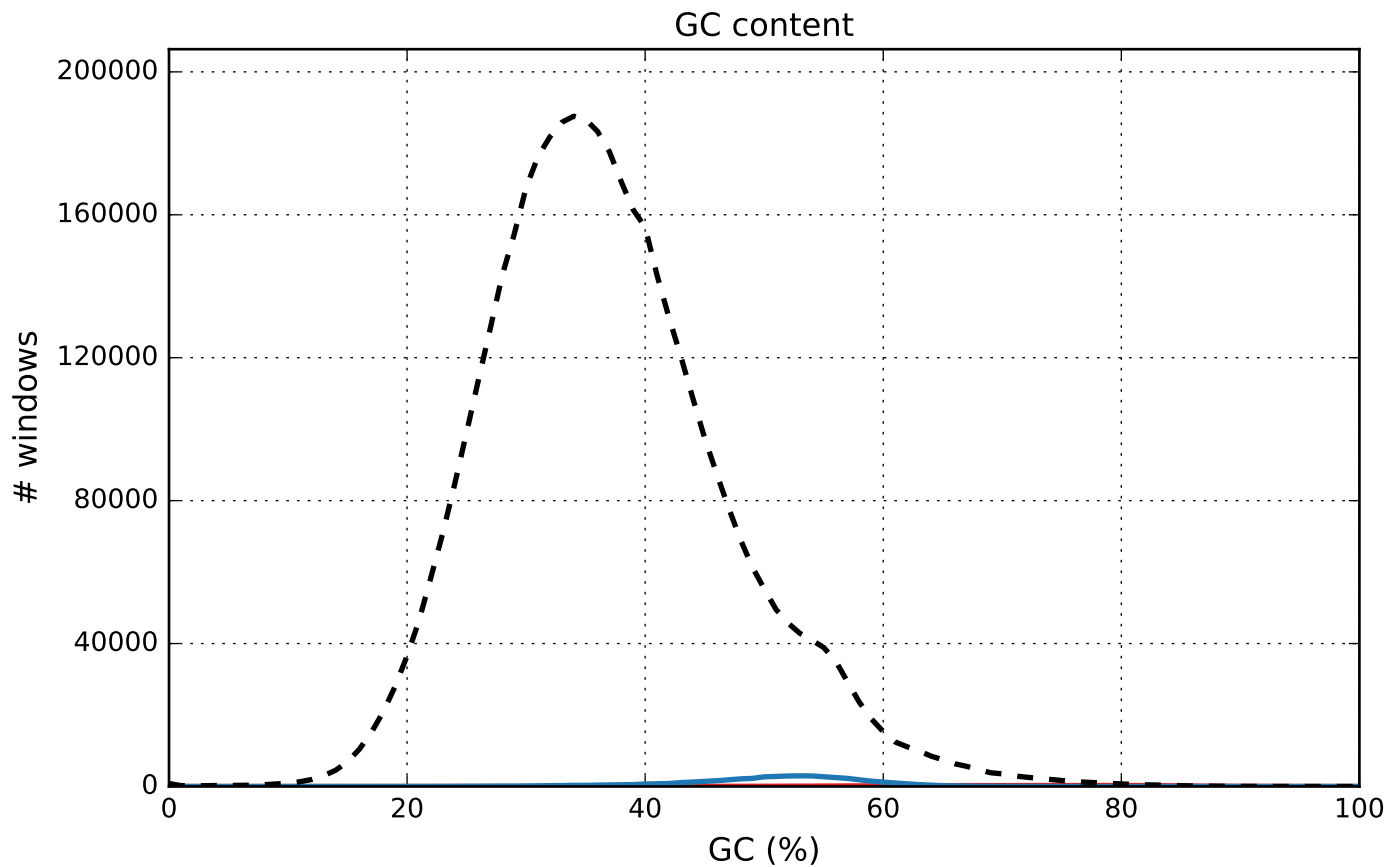
scaffolds

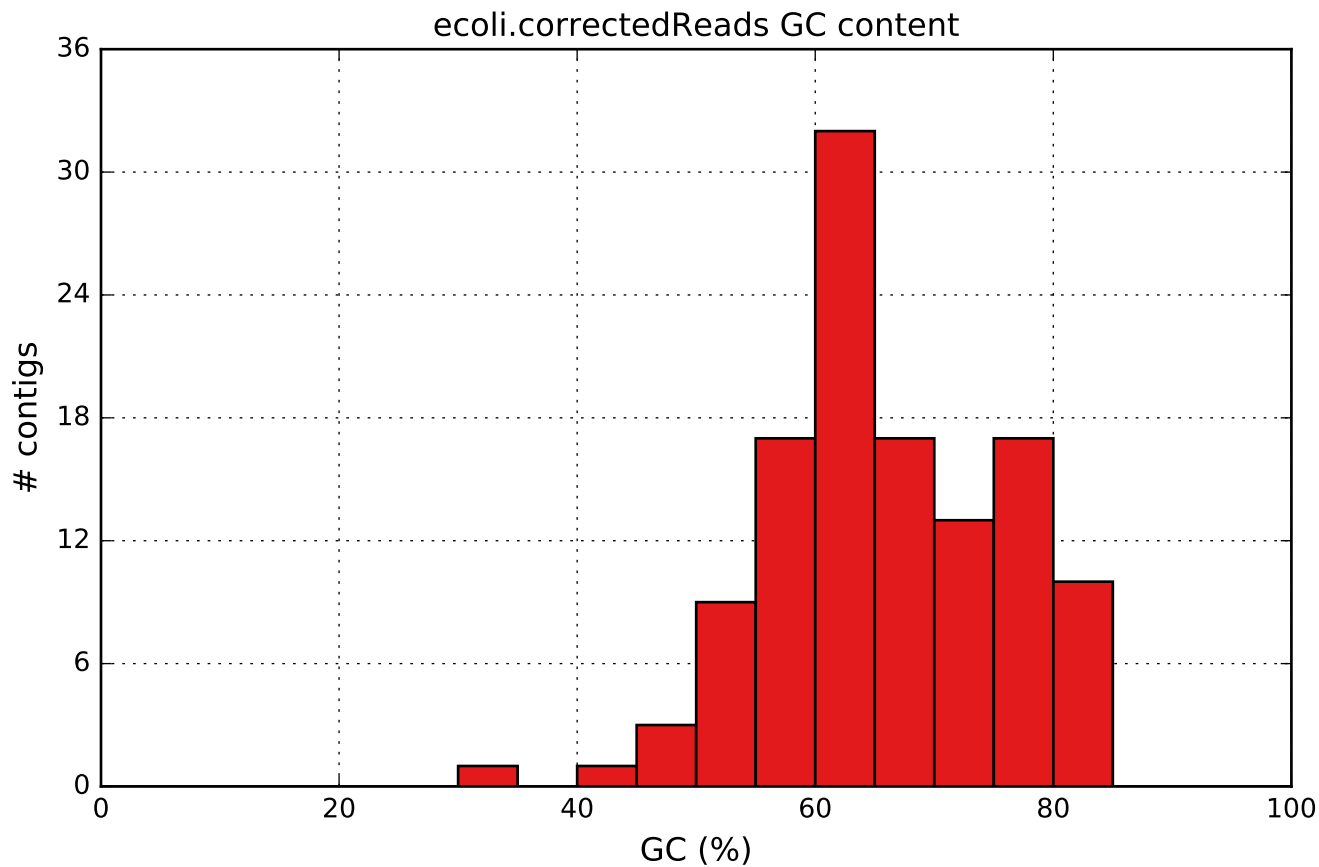
NGx



Cumulative length

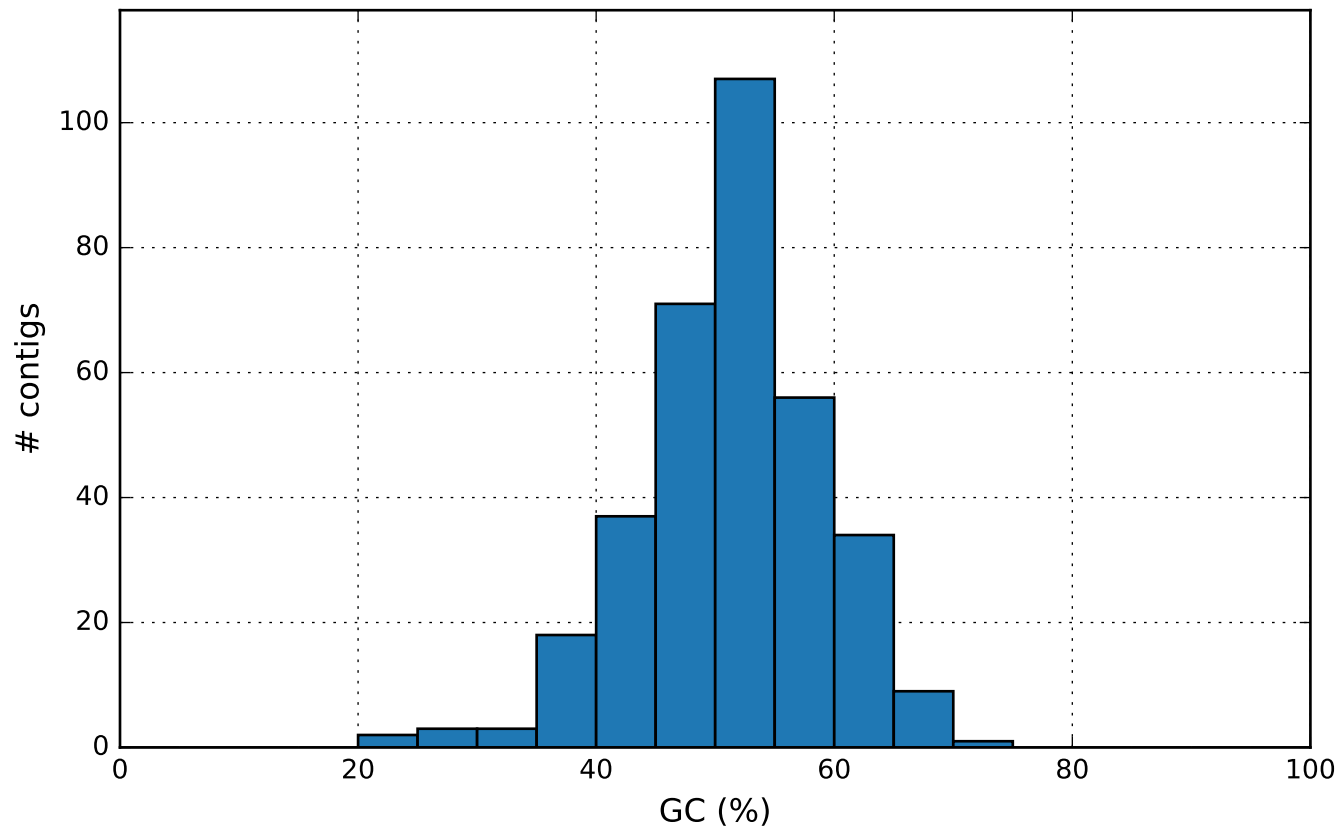






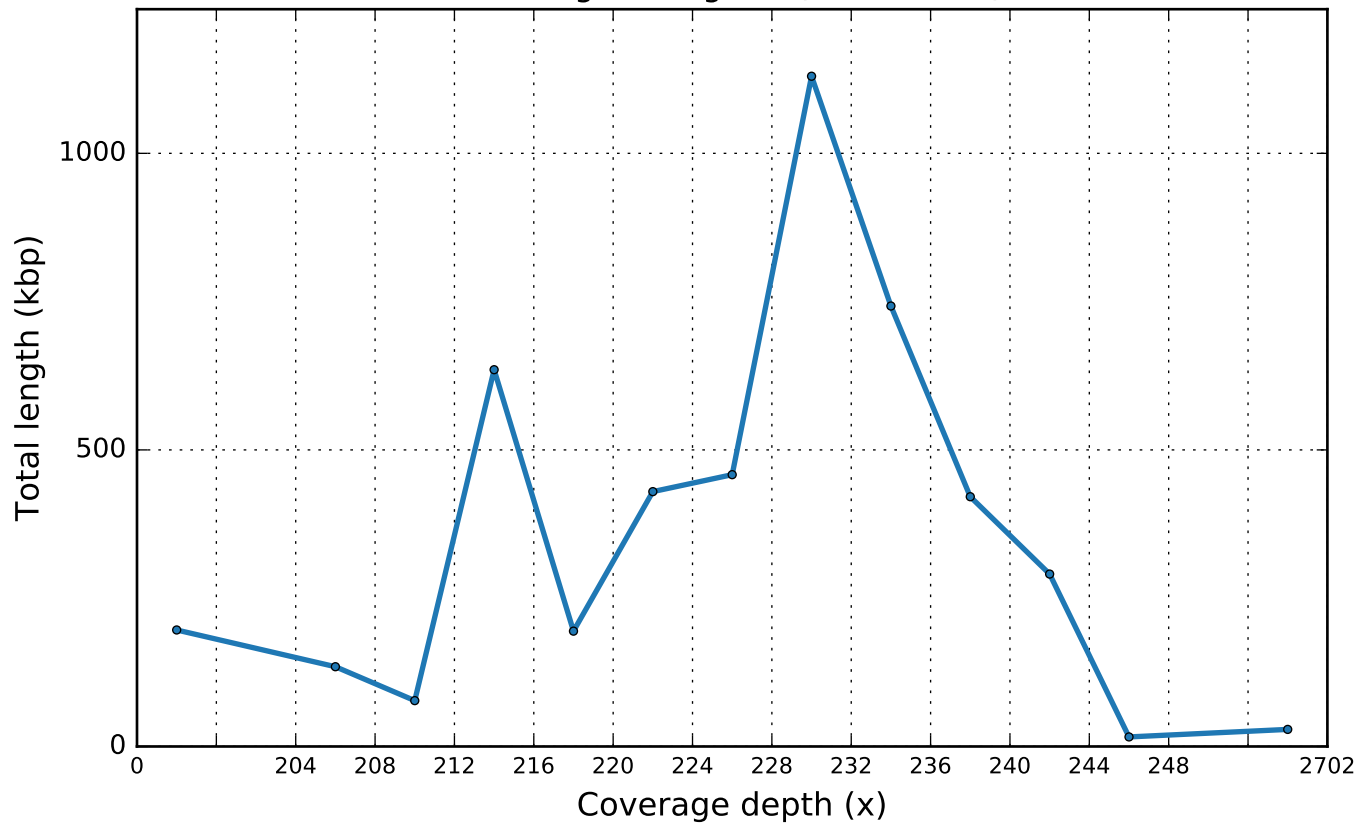
ecoli.correctedReads

scaffolds GC content



scaffolds

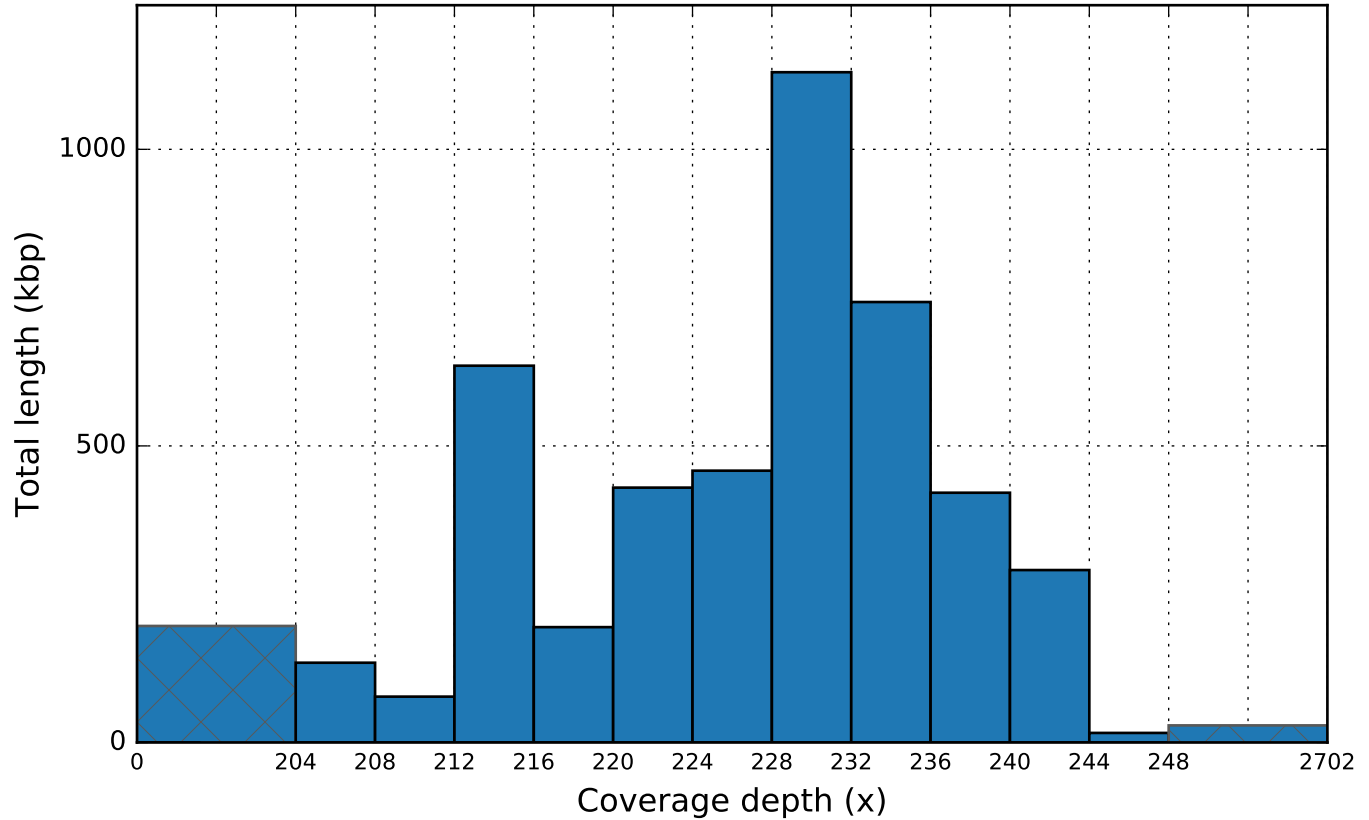
Coverage histogram (bin size: 4x)



—●— scaffolds



scaffolds coverage histogram (bin size: 4x)



scaffolds