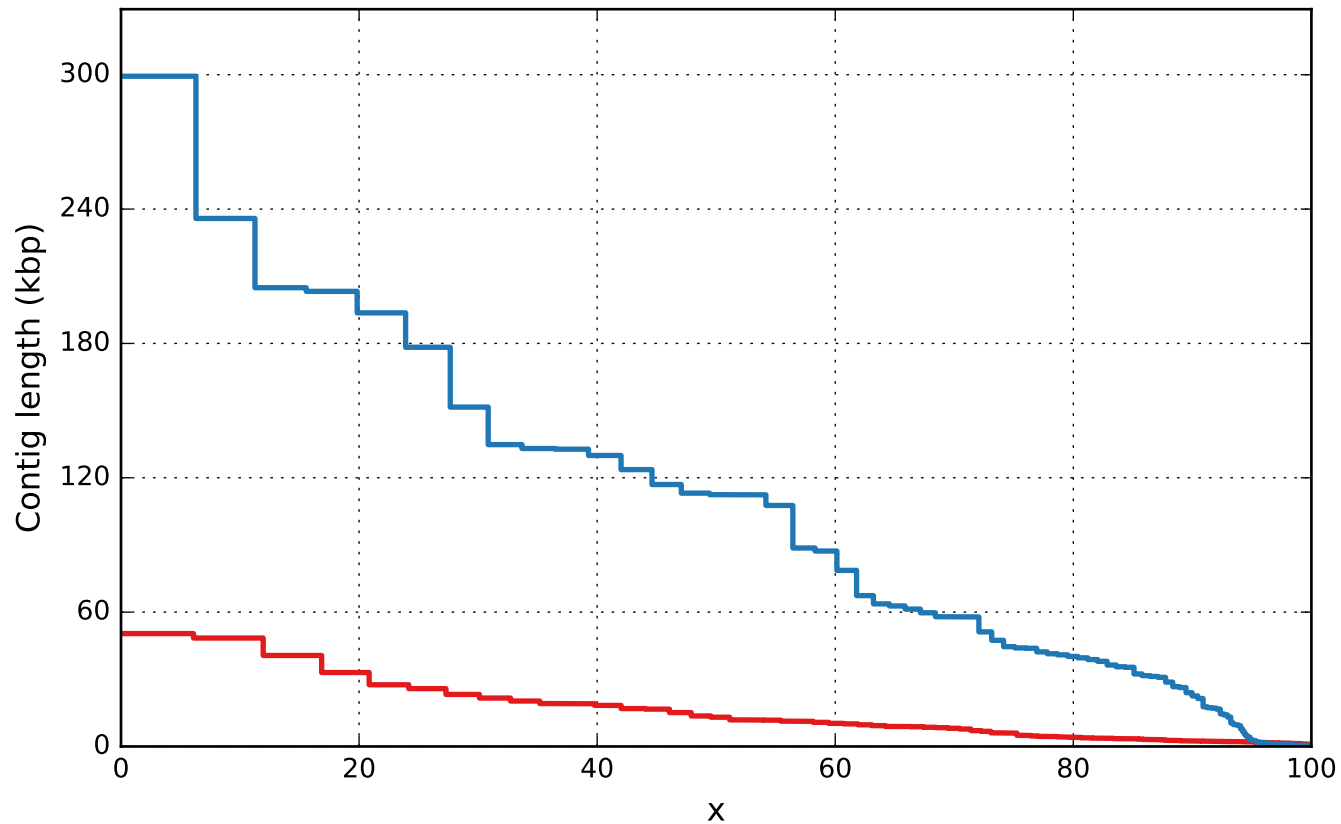


## Report

	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	499397863	499397863
GC (%)	69.95	50.77
Reference GC (%)	34.09	34.09
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

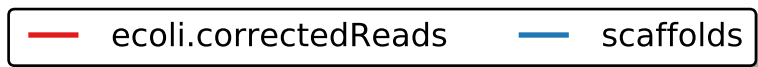
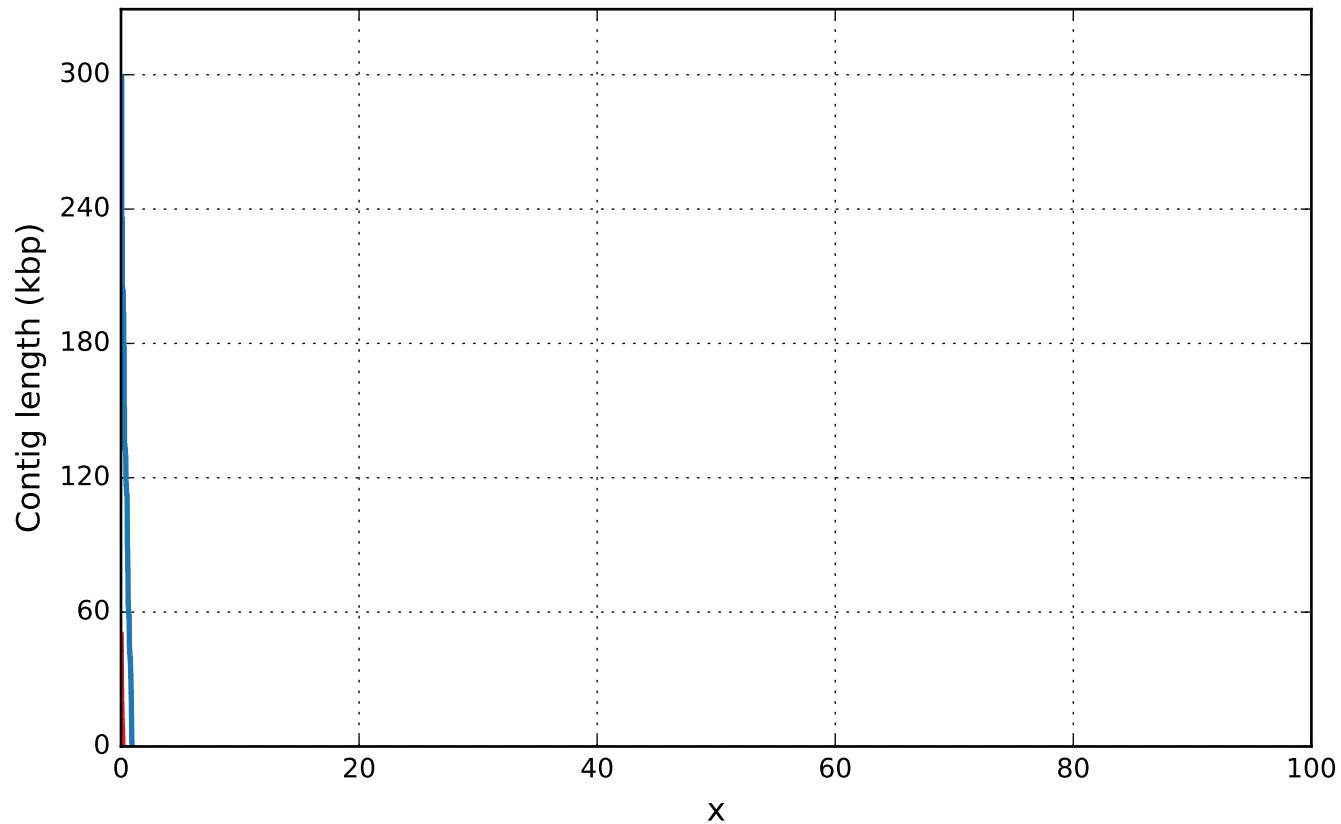


ecoli.correctedReads

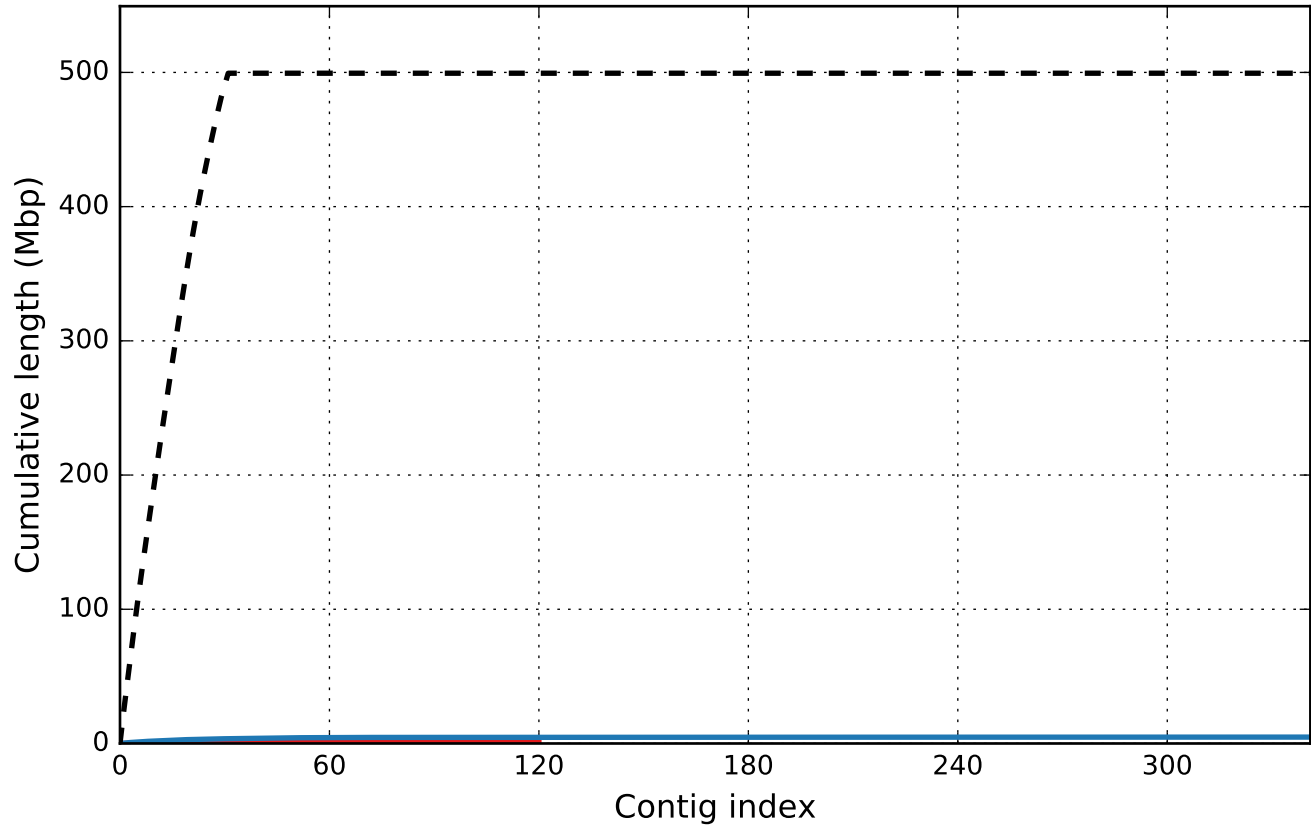


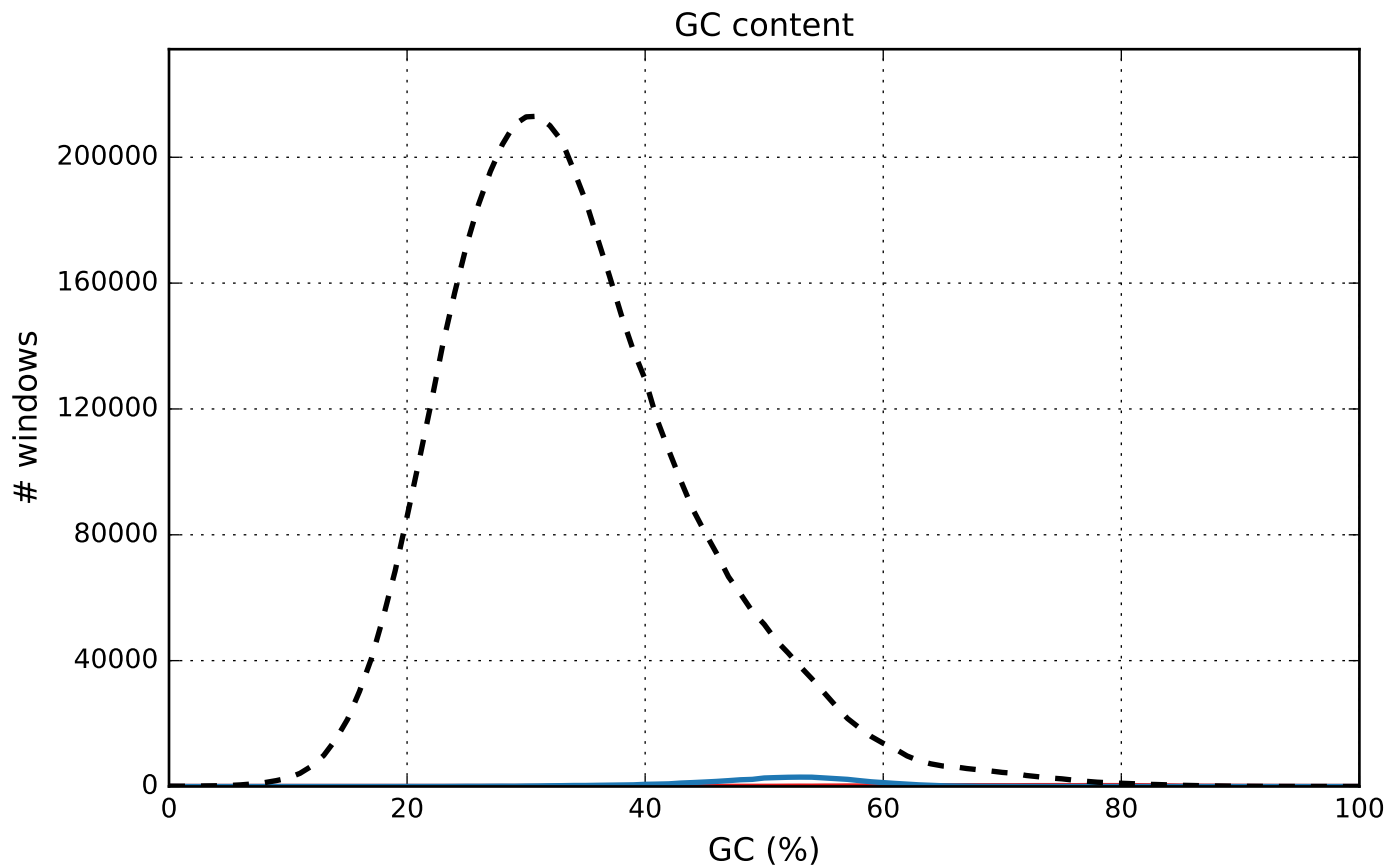
scaffolds

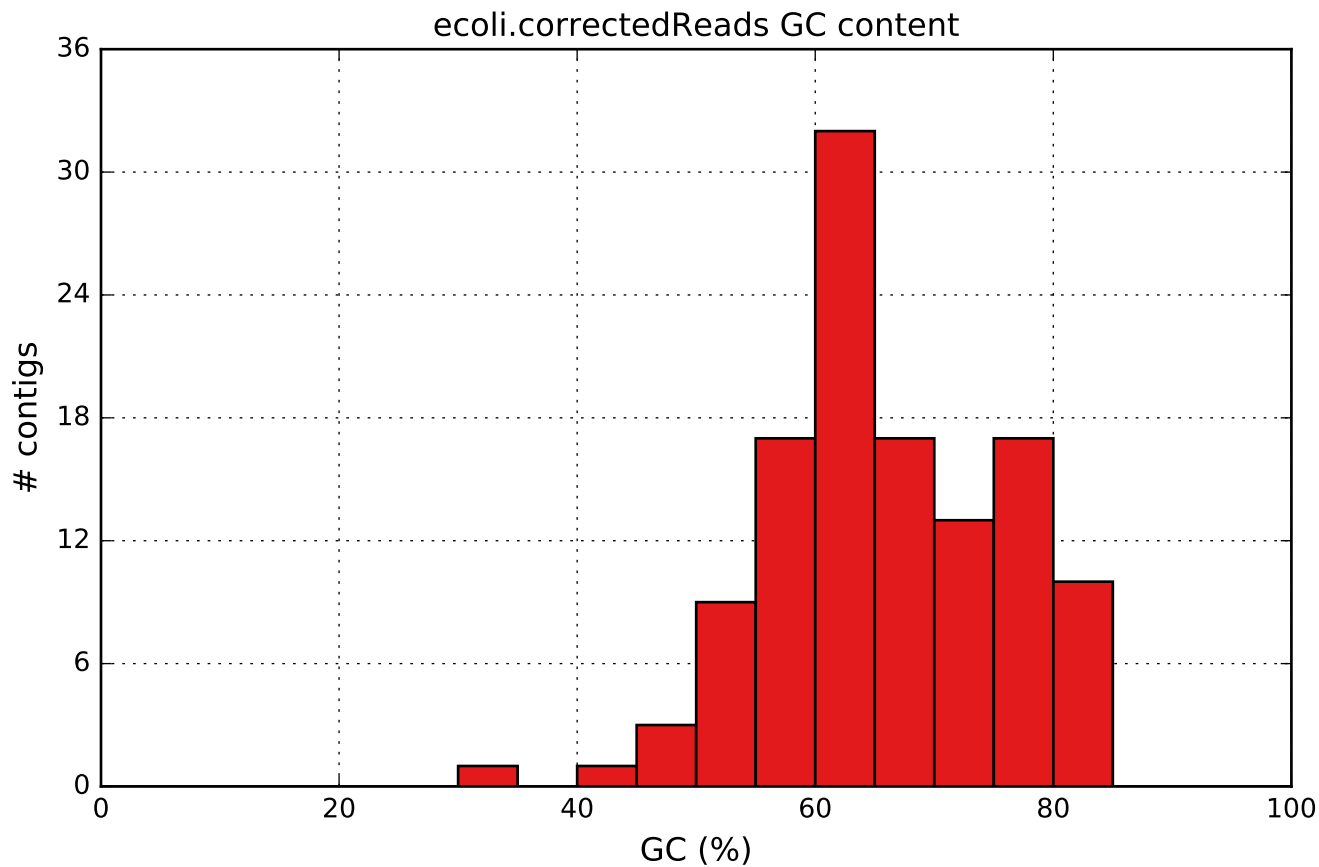
NGx



Cumulative length

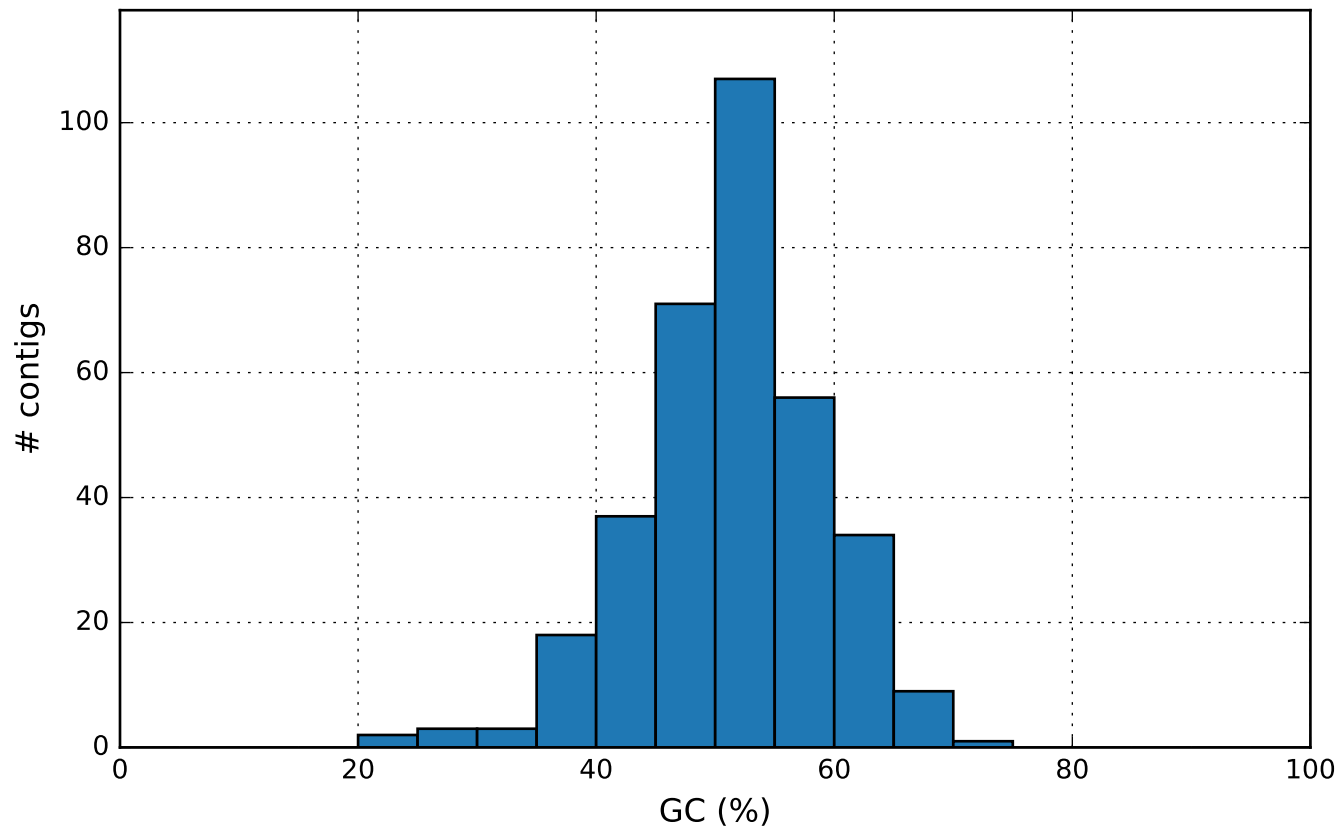






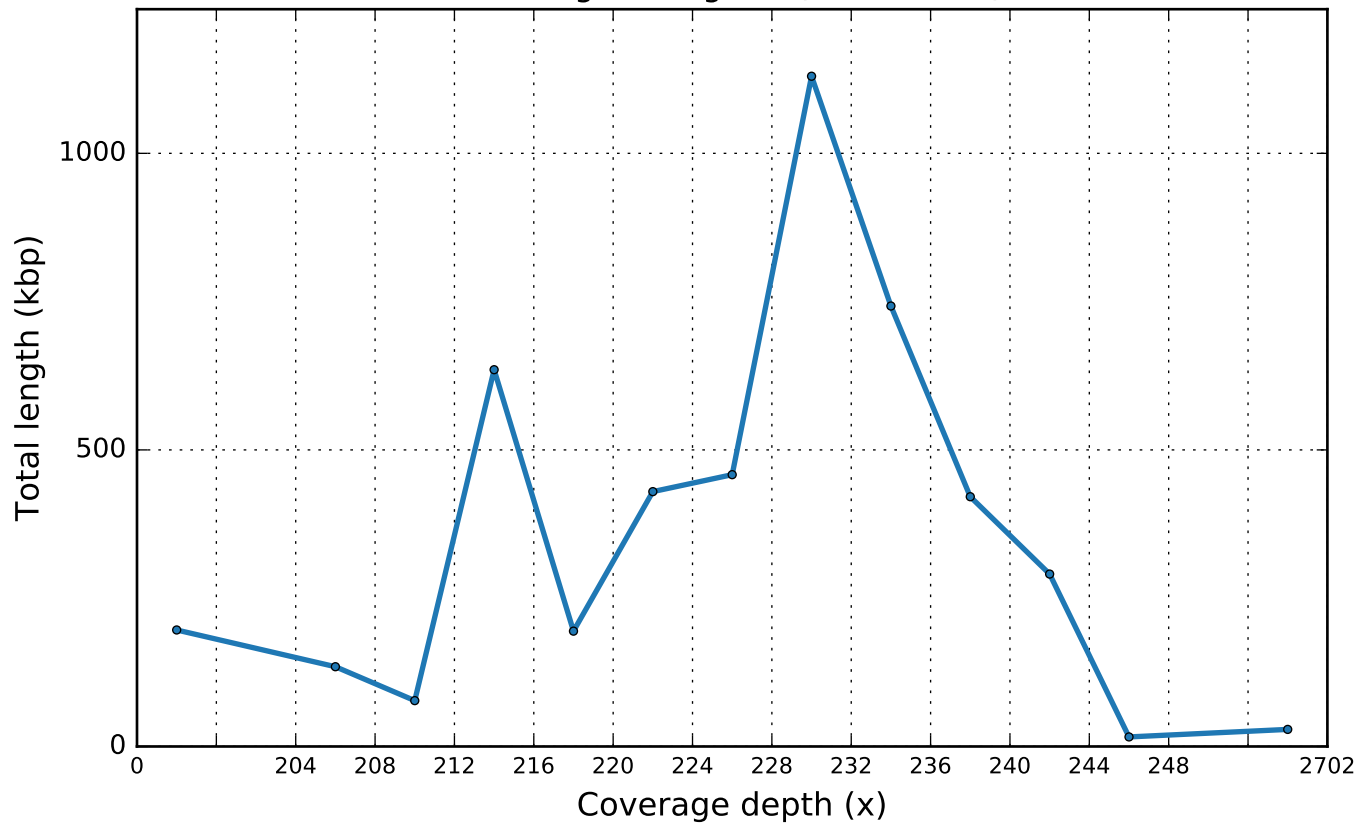
ecoli.correctedReads

scaffolds GC content



scaffolds

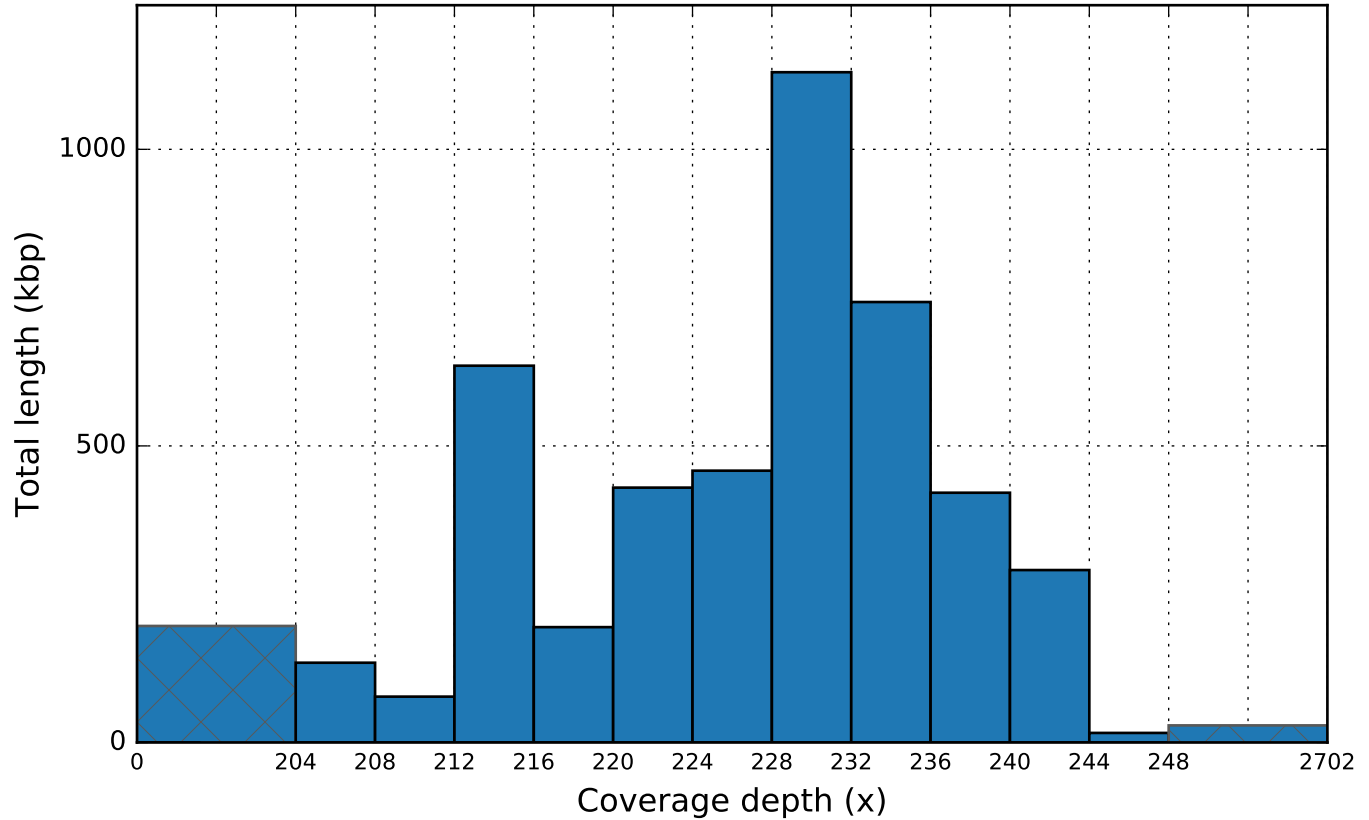
Coverage histogram (bin size: 4x)



—●— scaffolds



scaffolds coverage histogram (bin size: 4x)



scaffolds