

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	4641652	4641652
GC (%)	69.95	50.77
Reference GC (%)	50.79	50.79
N50	13074	112463
NG50	-	113140
N75	5968	44584
NG75	-	47412
L50	17	15
LG50	-	14
L75	39	31
LG75	-	30
# misassemblies	-	10
# misassembled contigs	-	7
Misassembled contigs length	-	557810
# local misassemblies	-	16
# unaligned mis. contigs	-	0
# unaligned contigs	120 + 0 part	235 + 9 part
Unaligned length	827543	258701
Genome fraction (%)	-	96.736
Duplication ratio	-	1.001
# N's per 100 kbp	0.00	25.24
# mismatches per 100 kbp	-	2.56
# indels per 100 kbp	-	0.29
# 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
Largest alignment	-	299242
Total aligned length	-	4492997
NA50	-	102431
NGA50	-	107574
NA75	-	42240
NGA75	-	43852
LA50	-	16
LGA50	-	15
LA75	-	34
LGA75	-	32

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

	ecoli.correctedReads	scaffolds
# misassemblies	-	10
# relocations	-	8
# translocations	-	0
# inversions	-	2
# misassembled contigs	-	7
Misassembled contigs length	-	557810
# local misassemblies	-	16
# unaligned mis. contigs	-	0
# mismatches	-	115
# indels	-	13
# indels (<= 5 bp)	-	8
# indels (> 5 bp)	-	5
Indels length	-	233

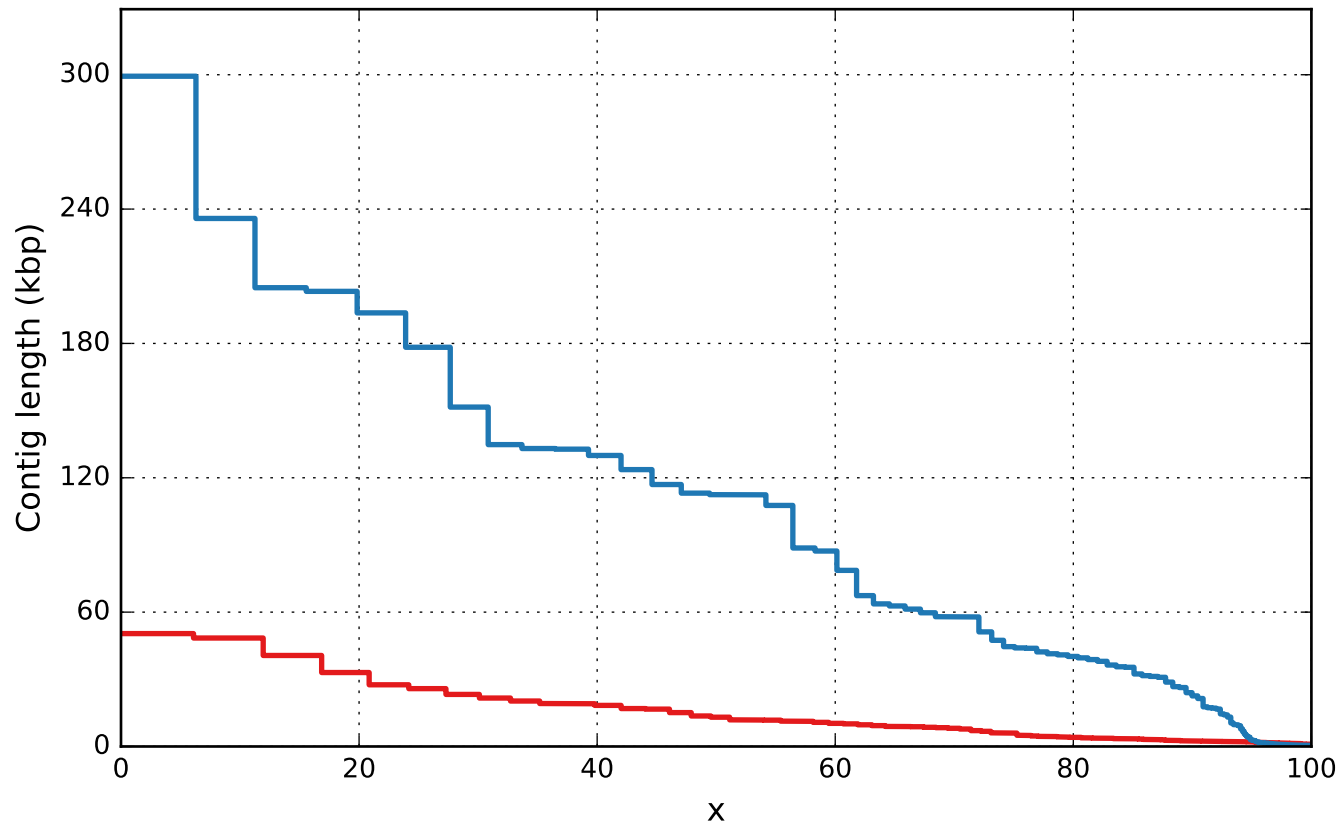
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	ecoli.correctedReads	scaffolds
# fully unaligned contigs	120	235
Fully unaligned length	827543	197630
# partially unaligned contigs	-	9
Partially unaligned length	-	61071
# N's	0	1200

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

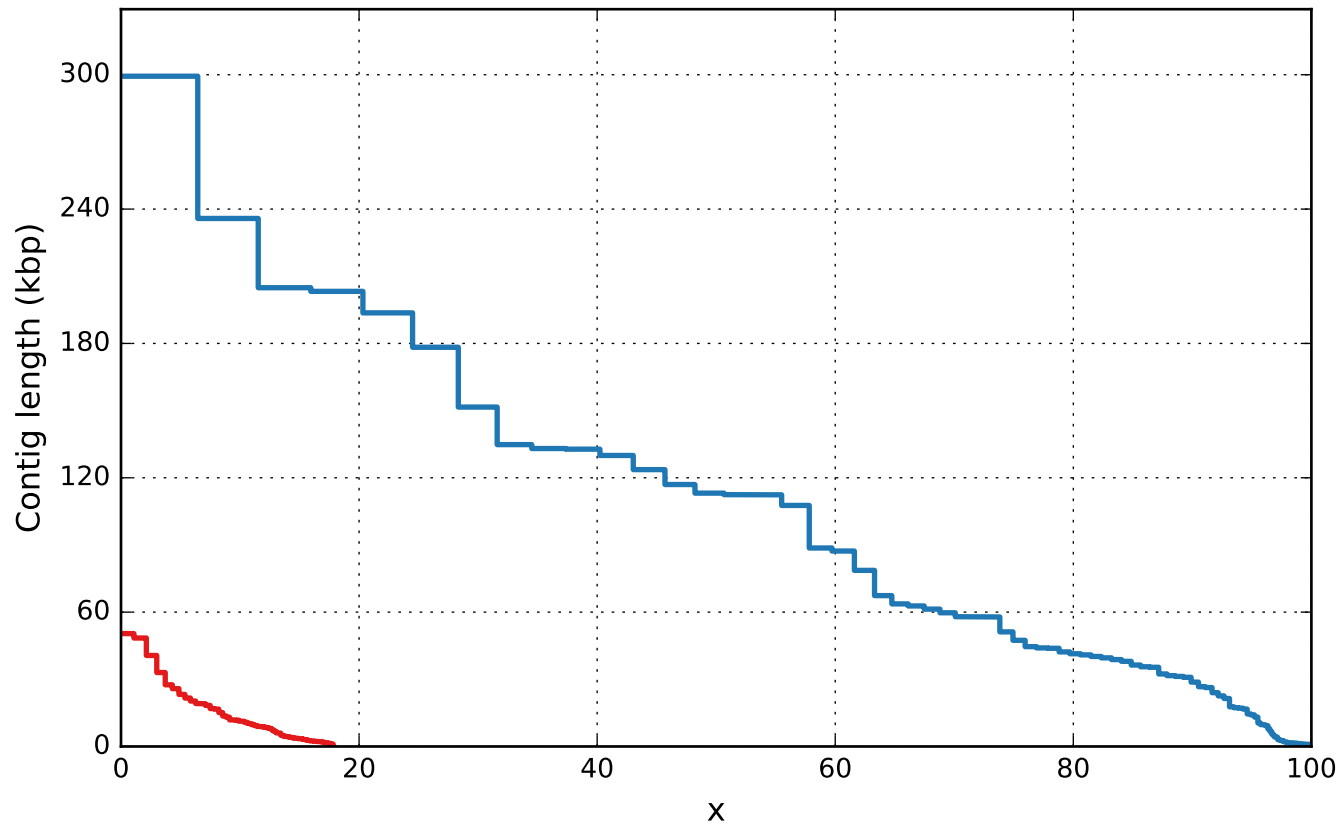


ecoli.correctedReads



scaffolds

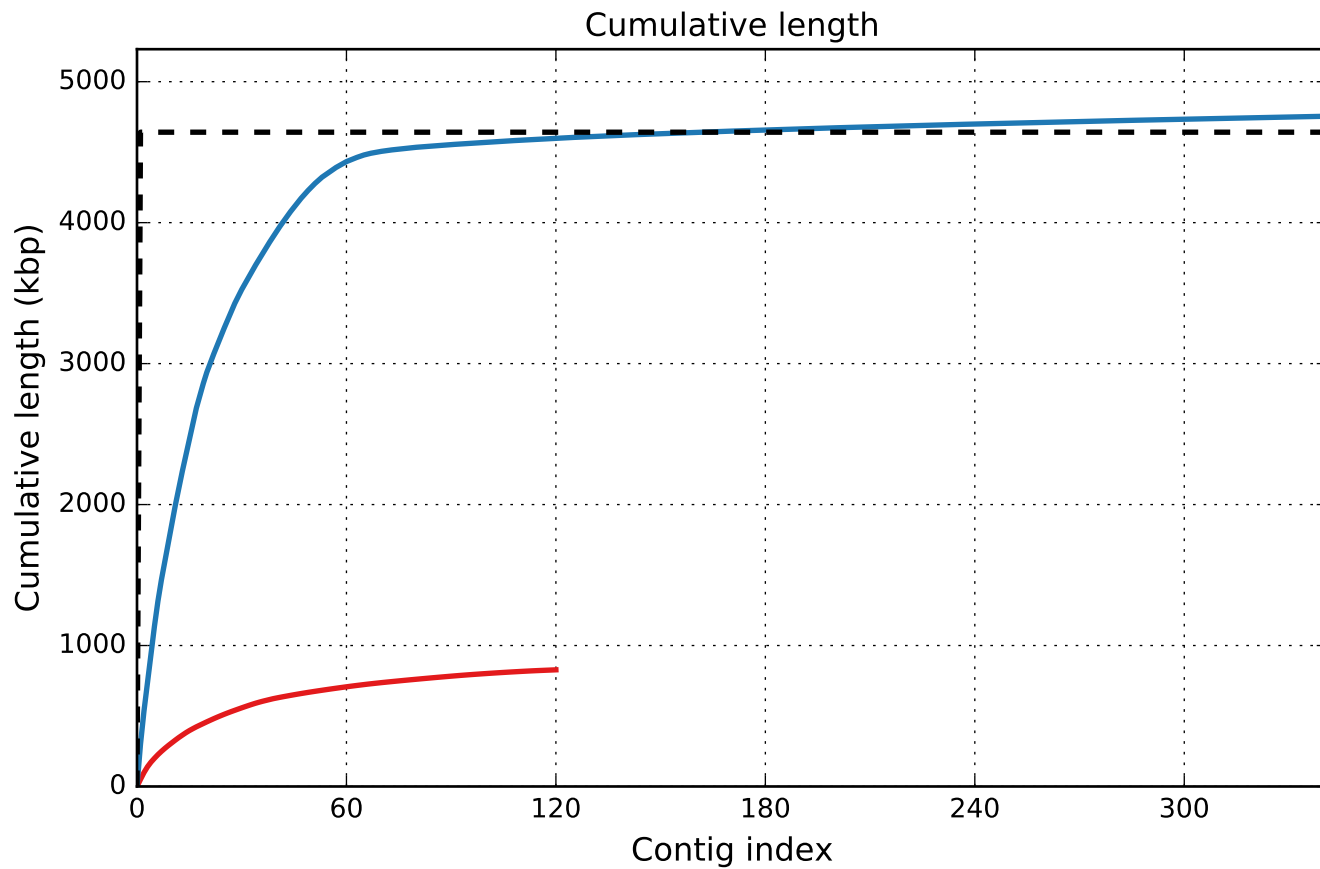
NGx



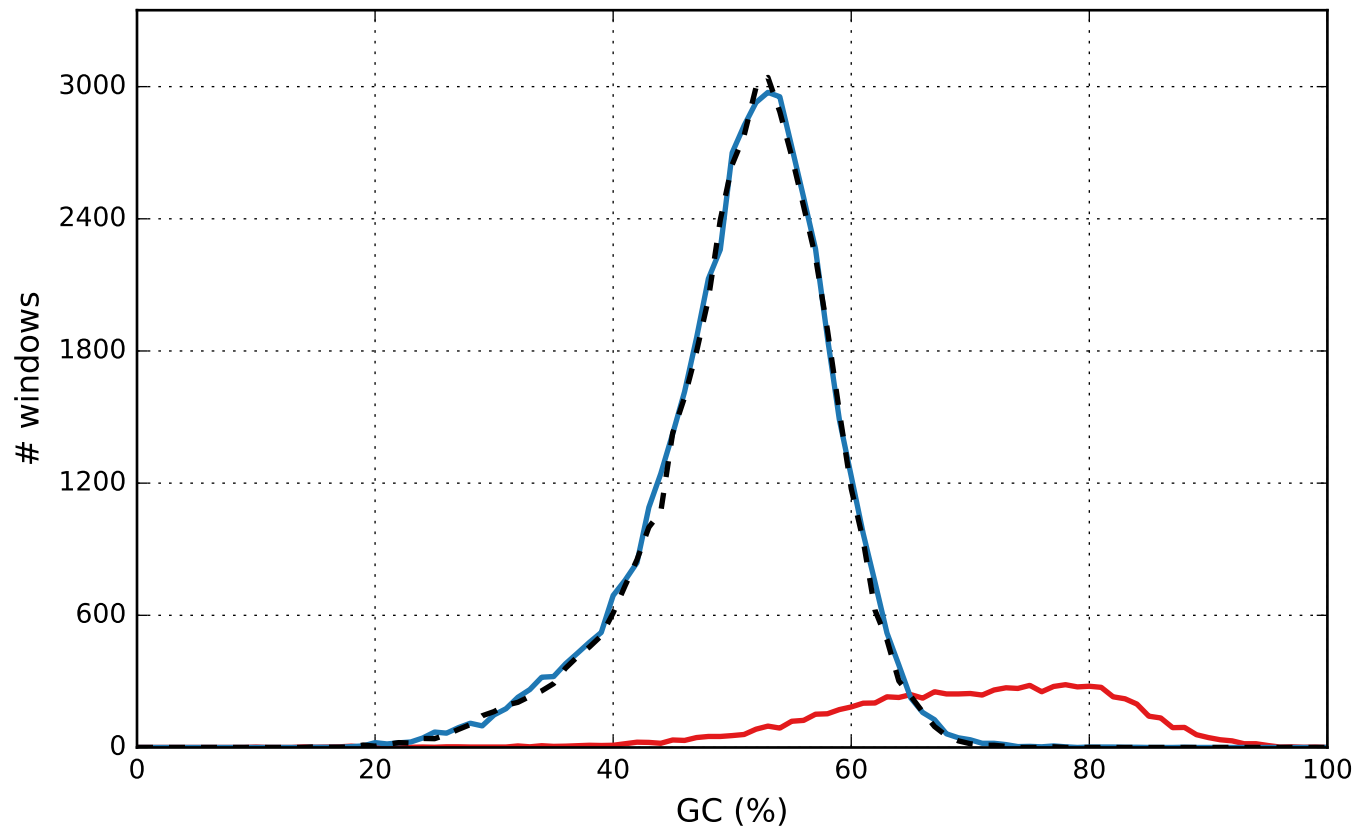
ecoli.correctedReads

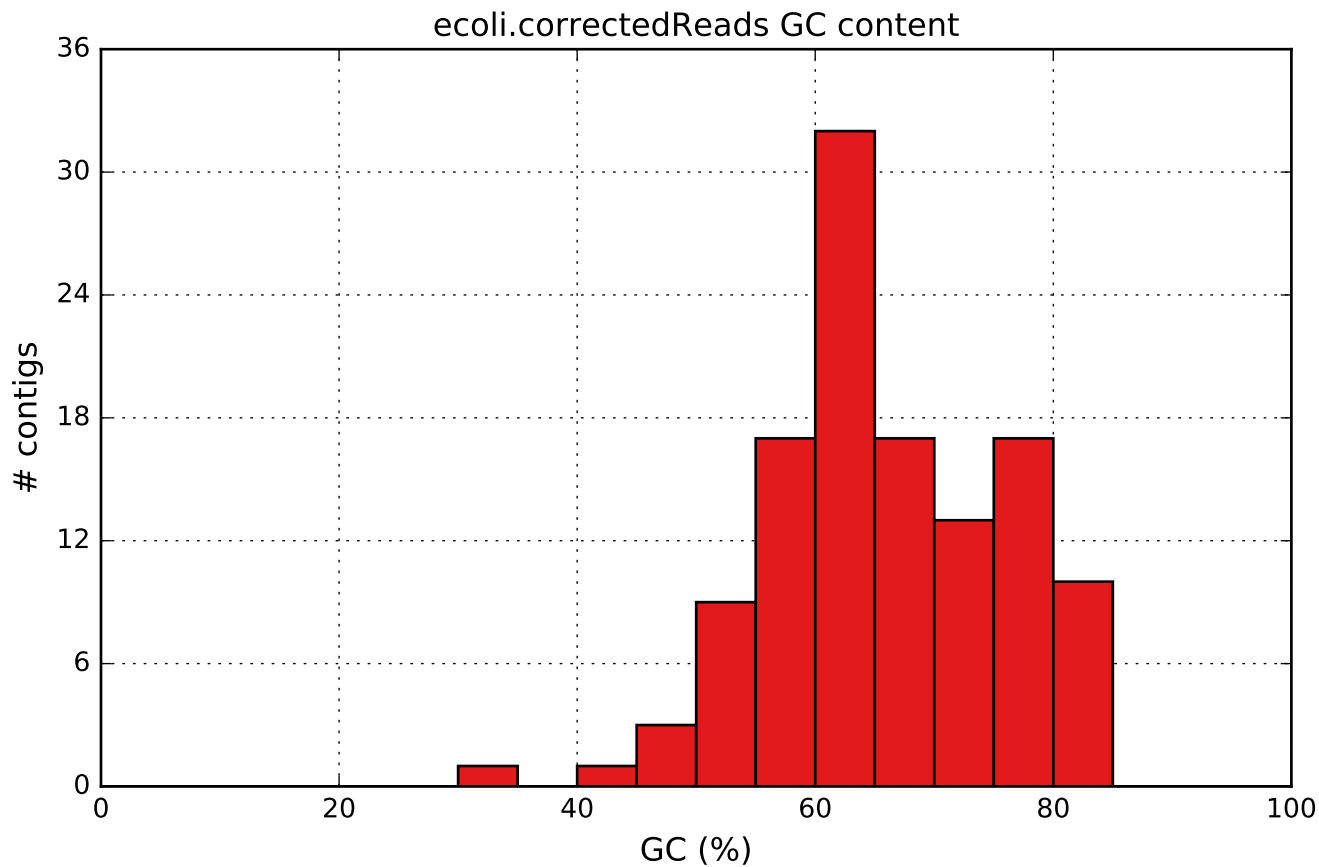


scaffolds



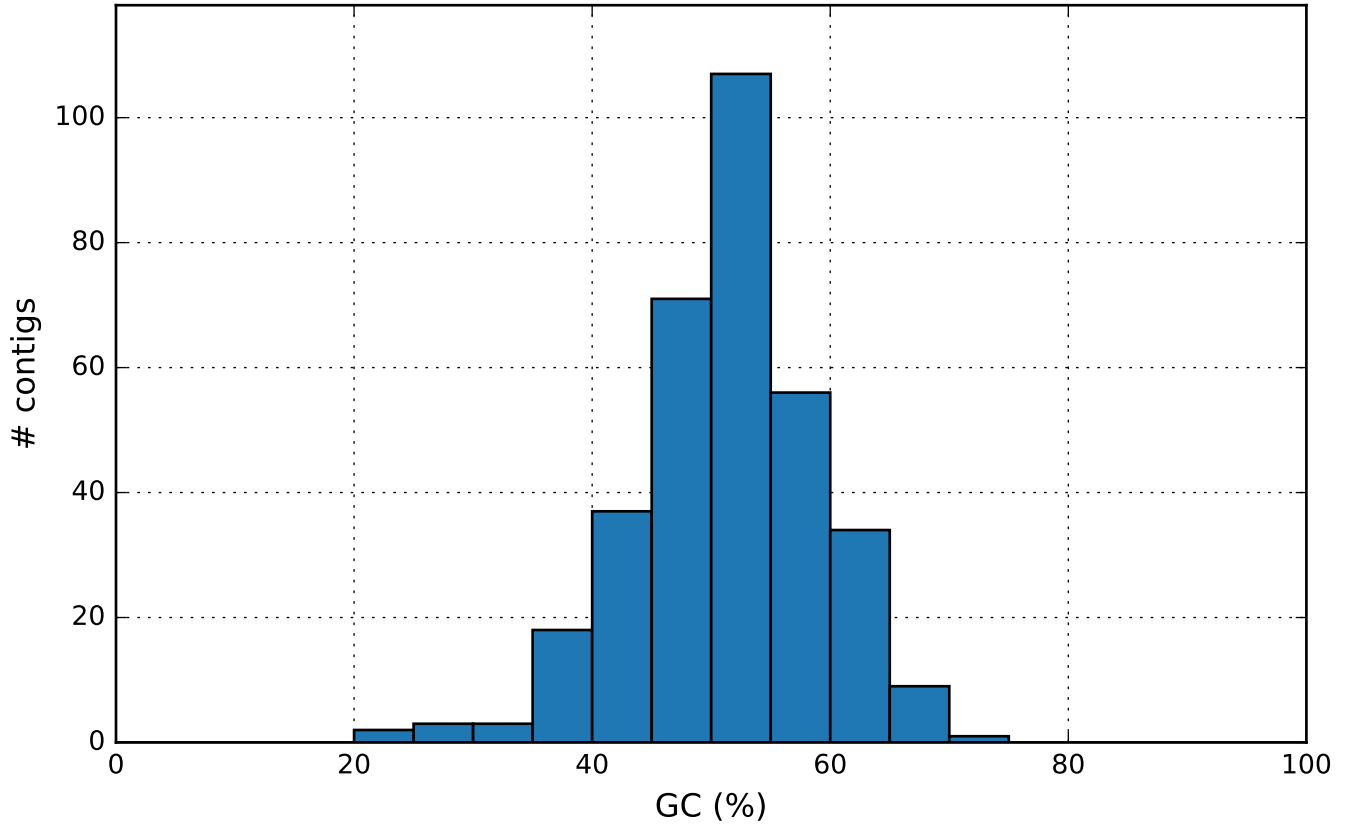
GC content





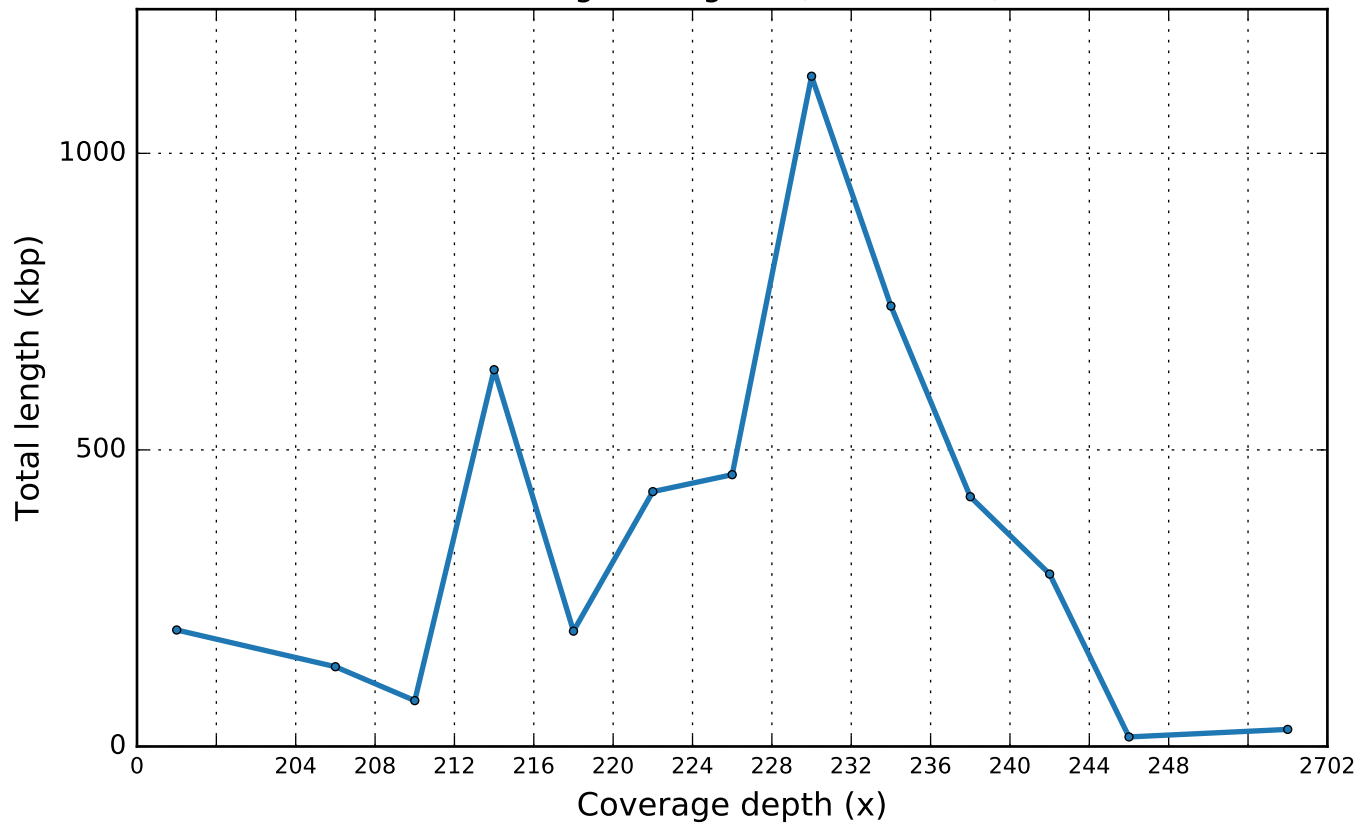
ecoli.correctedReads

scaffolds GC content



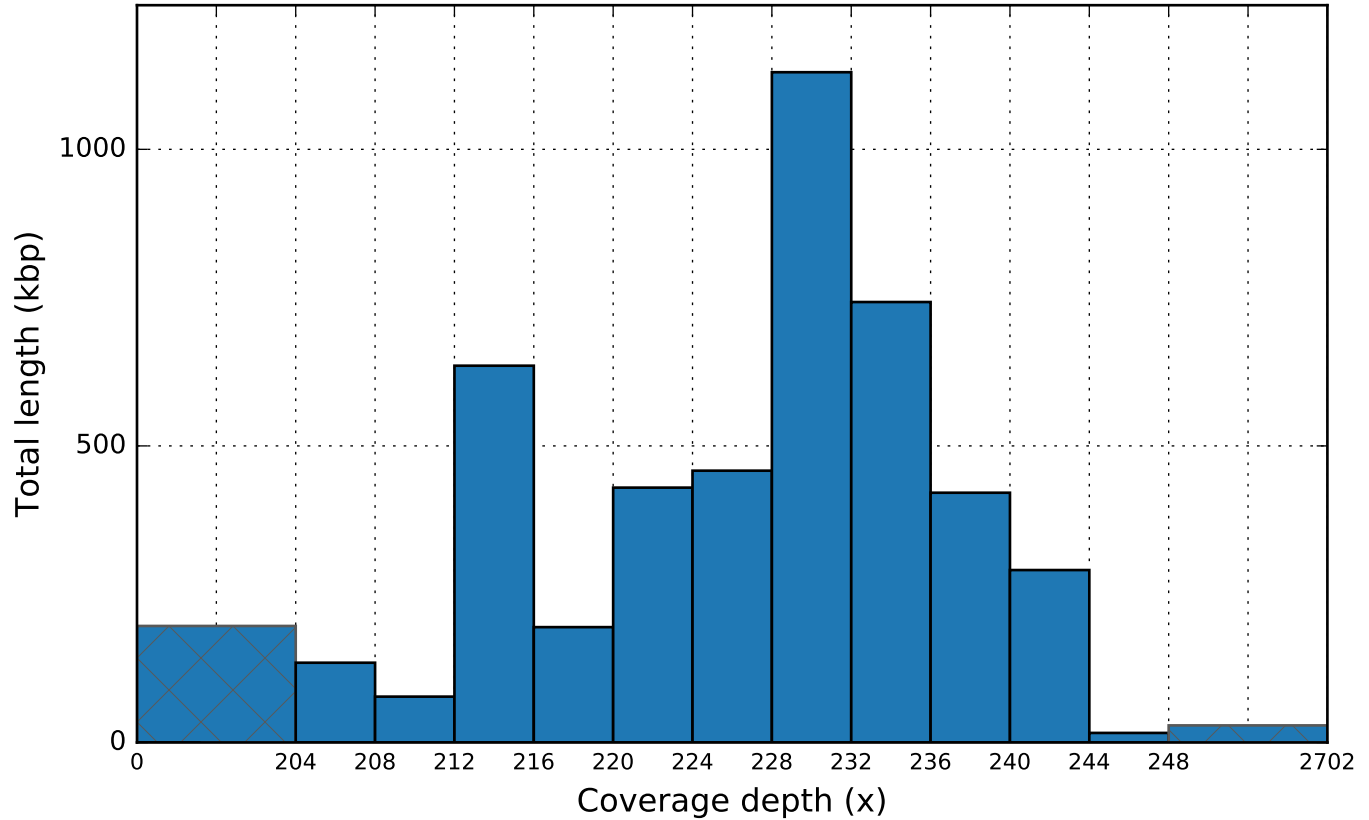
scaffolds

Coverage histogram (bin size: 4x)



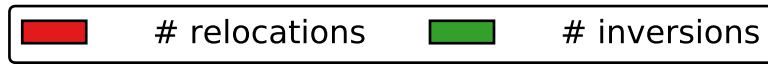
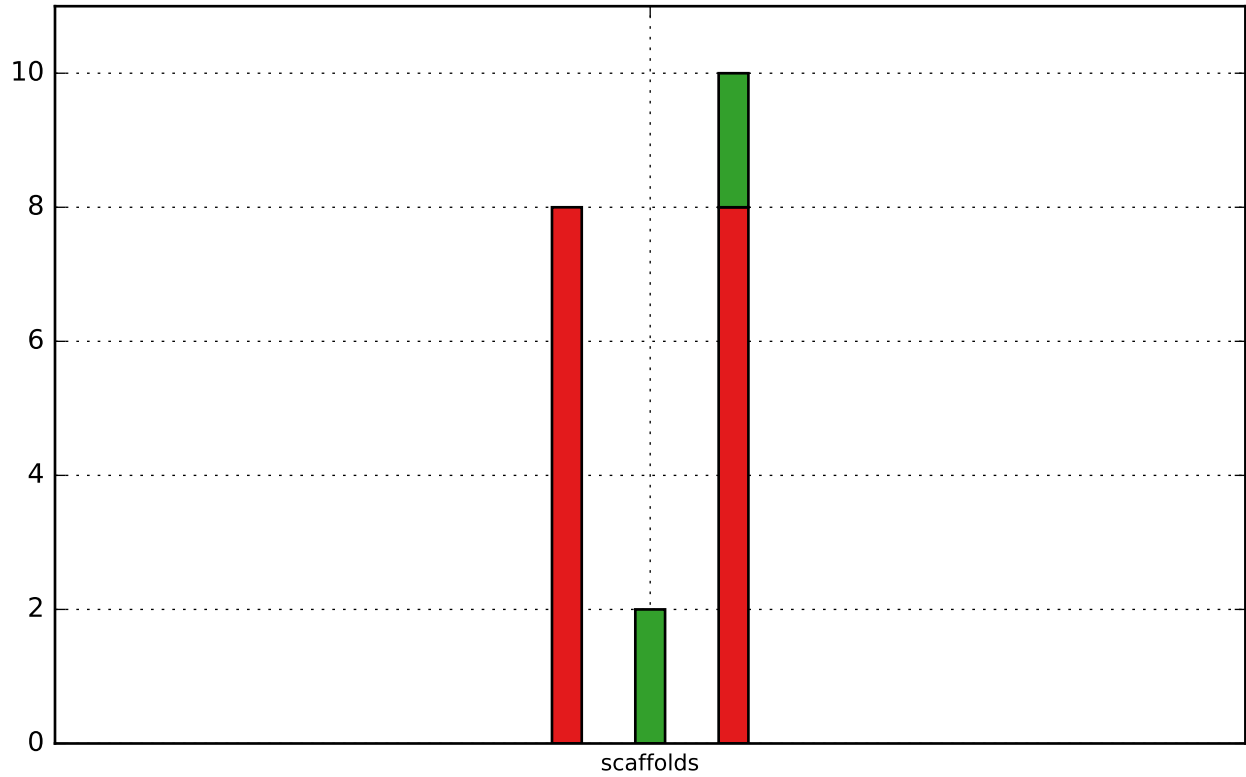
—●— scaffolds

scaffolds coverage histogram (bin size: 4x)

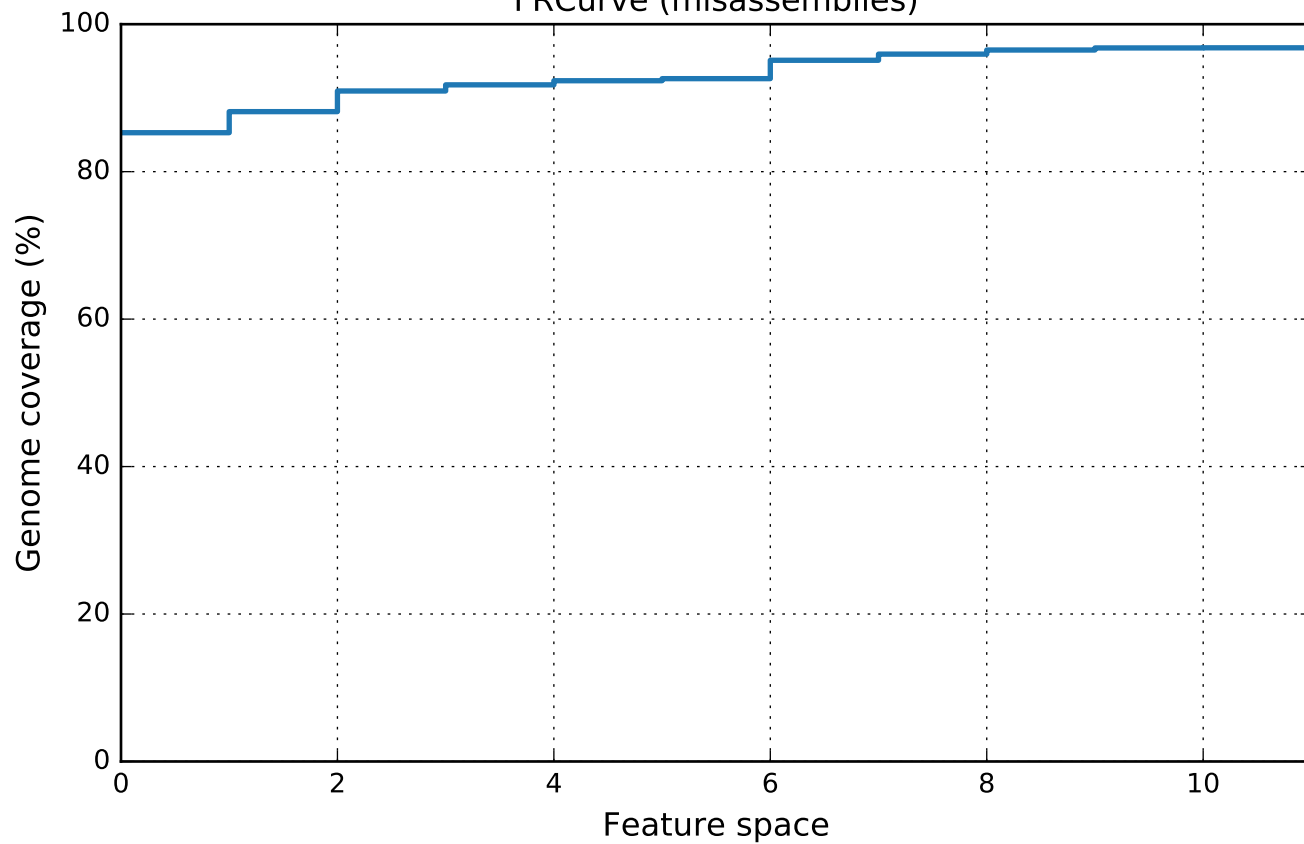


scaffolds

Misassemblies

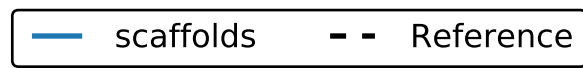
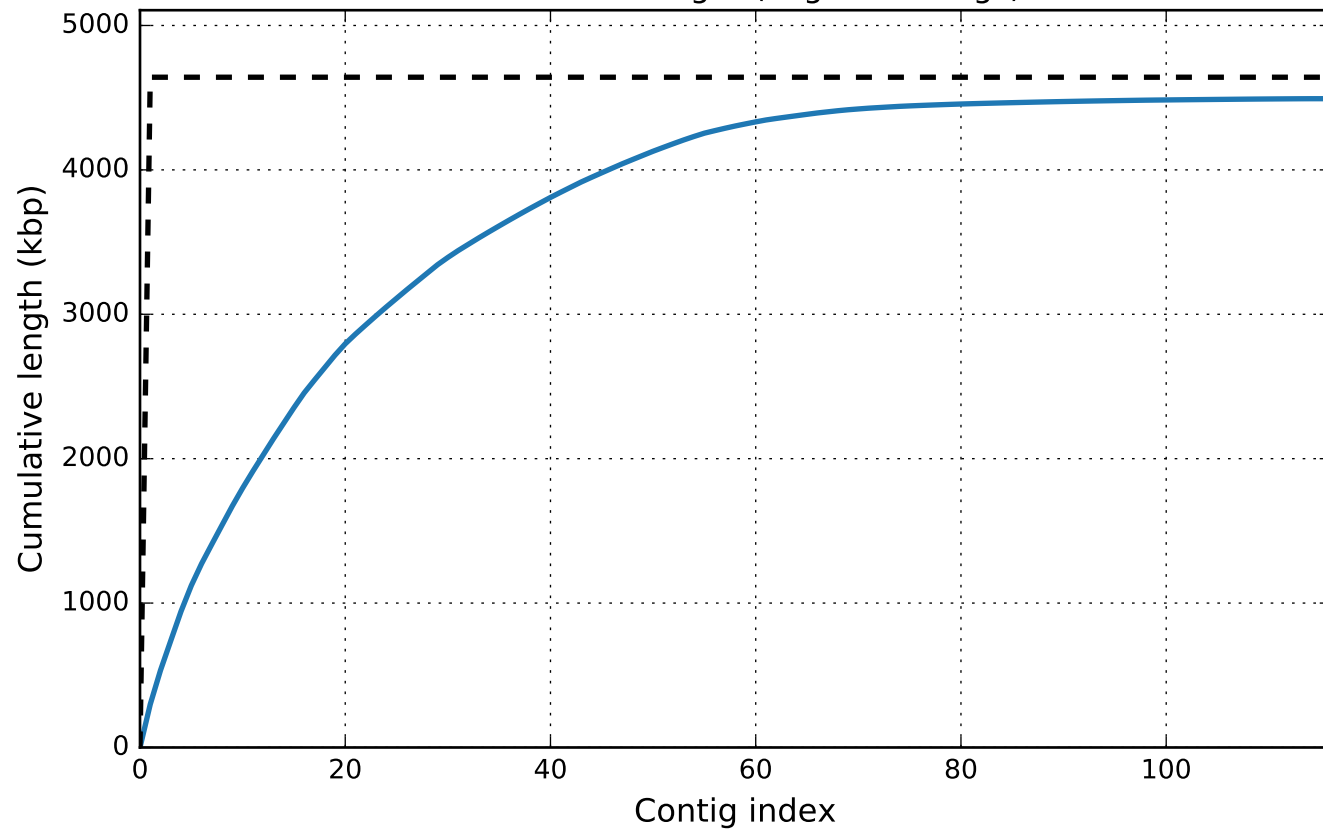


FRCurve (misassemblies)

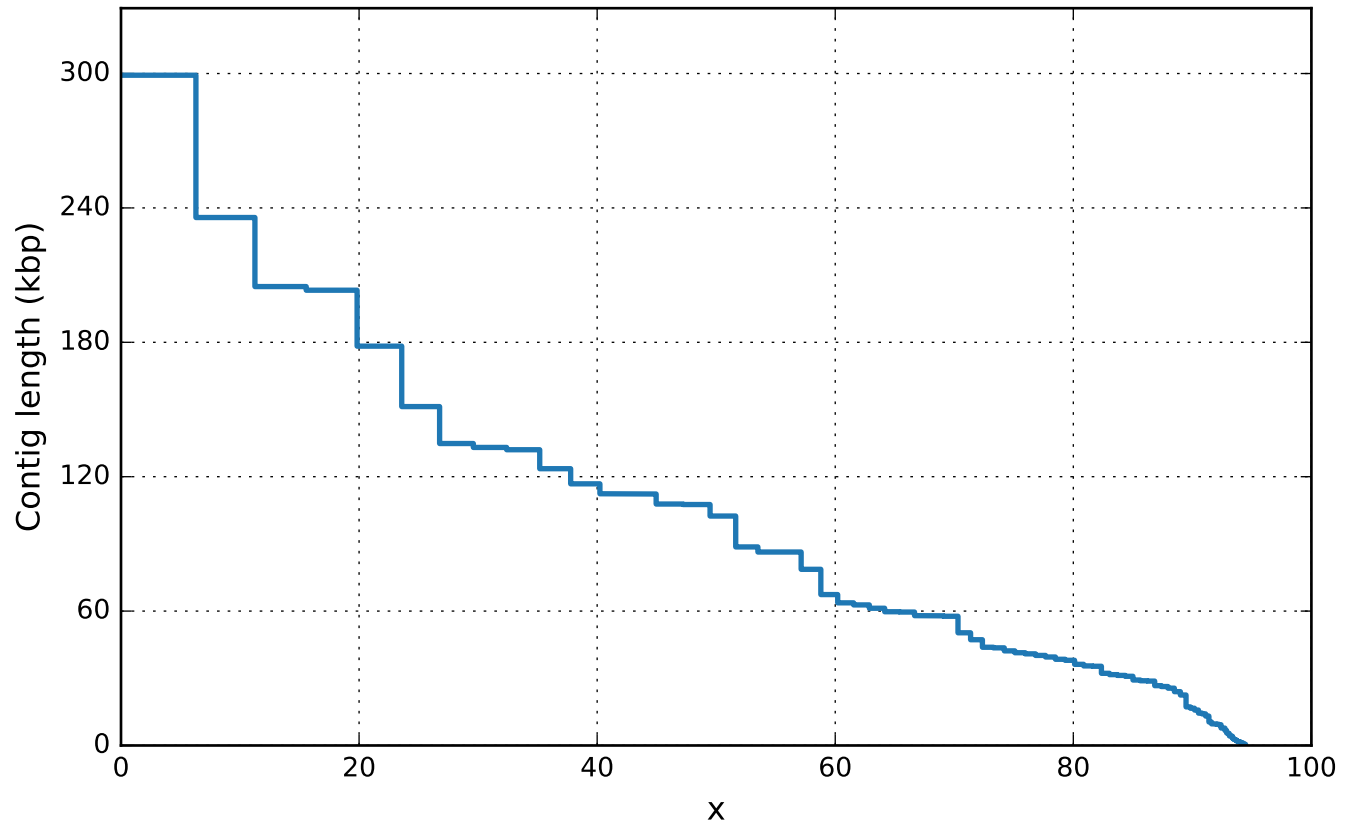


scaffolds

Cumulative length (aligned contigs)

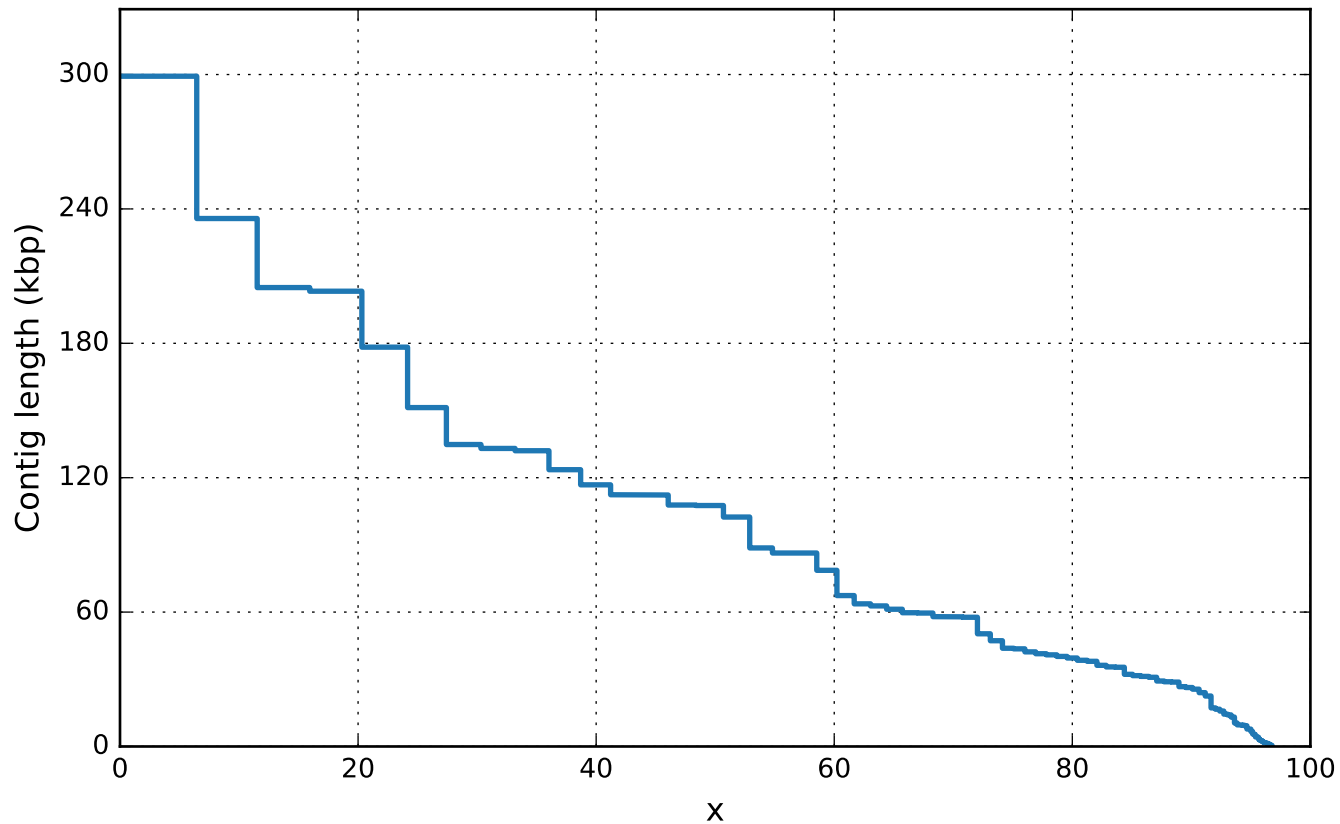


NAx



scaffolds

NGAx



— scaffolds