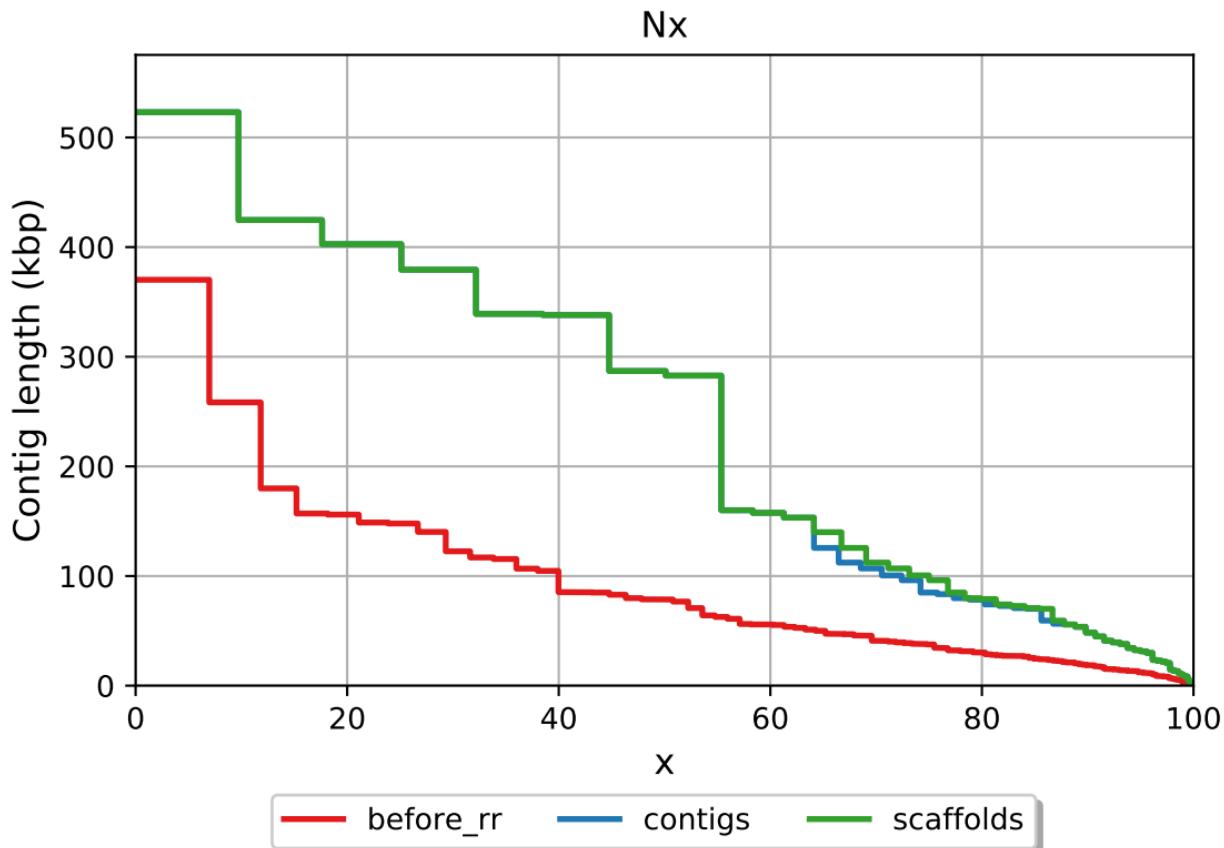


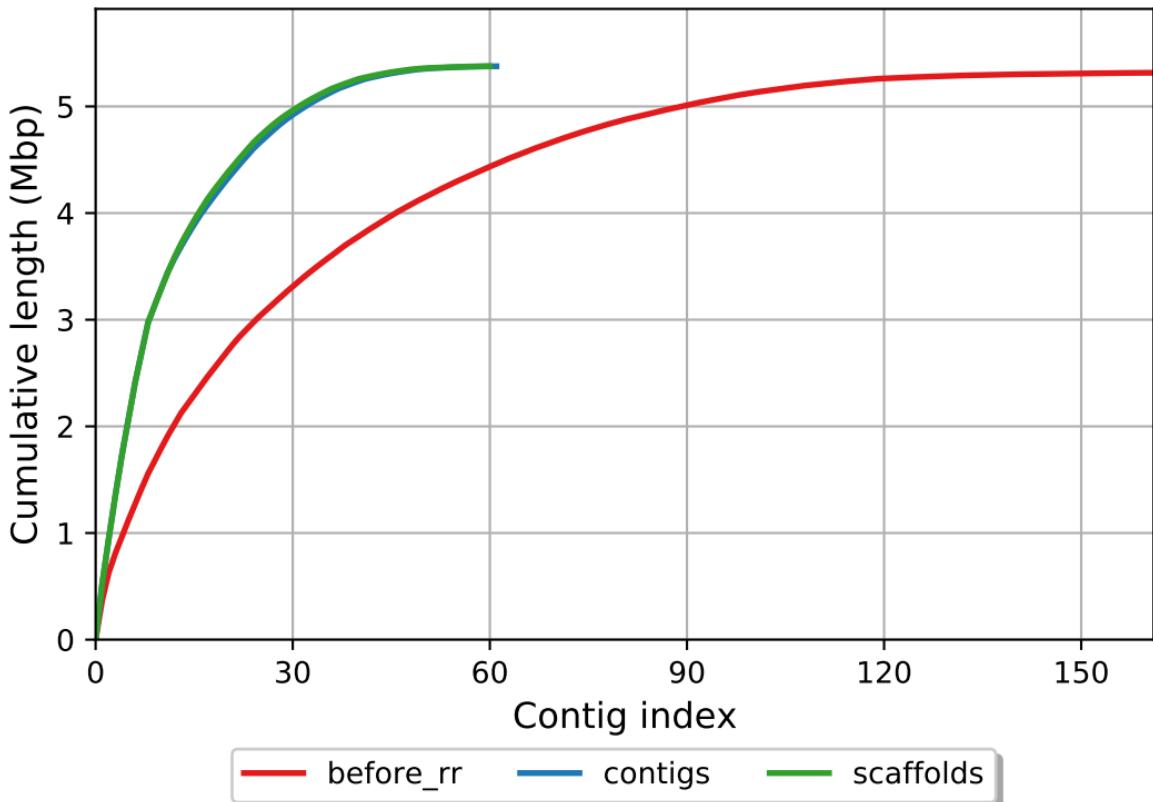
# Report

	before_rr	contigs	scaffolds
# contigs (>= 0 bp)	712	217	216
# contigs (>= 1000 bp)	140	60	59
# contigs (>= 5000 bp)	118	50	49
# contigs (>= 10000 bp)	99	46	45
# contigs (>= 25000 bp)	63	37	36
# contigs (>= 50000 bp)	33	28	27
Total length (>= 0 bp)	5414327	5410520	5411174
Total length (>= 1000 bp)	5301222	5375909	5376563
Total length (>= 5000 bp)	5254556	5352539	5353193
Total length (>= 10000 bp)	5118922	5320397	5321051
Total length (>= 25000 bp)	4514234	5168228	5168882
Total length (>= 50000 bp)	3466151	4828556	4829210
# contigs	161	61	60
Largest contig	370202	523019	523019
Total length	5315946	5376412	5377066
GC (%)	43.46	43.48	43.48
N50	78581	286996	286996
N75	37582	84920	100586
L50	20	7	7
L75	46	17	16
# N's per 100 kbp	0.00	0.00	5.43
# predicted genes (unique)	2835	2837	2837
# predicted genes (>= 0 bp)	2829 + 6 part	2850 + 3 part	2851 + 2 part
# predicted genes (>= 300 bp)	2737 + 6 part	2769 + 3 part	2770 + 2 part
# predicted genes (>= 1500 bp)	957 + 0 part	974 + 0 part	974 + 0 part
# predicted genes (>= 3000 bp)	237 + 0 part	243 + 0 part	243 + 0 part
# predicted rRNA genes	0 + 1 part	1 + 2 part	1 + 2 part

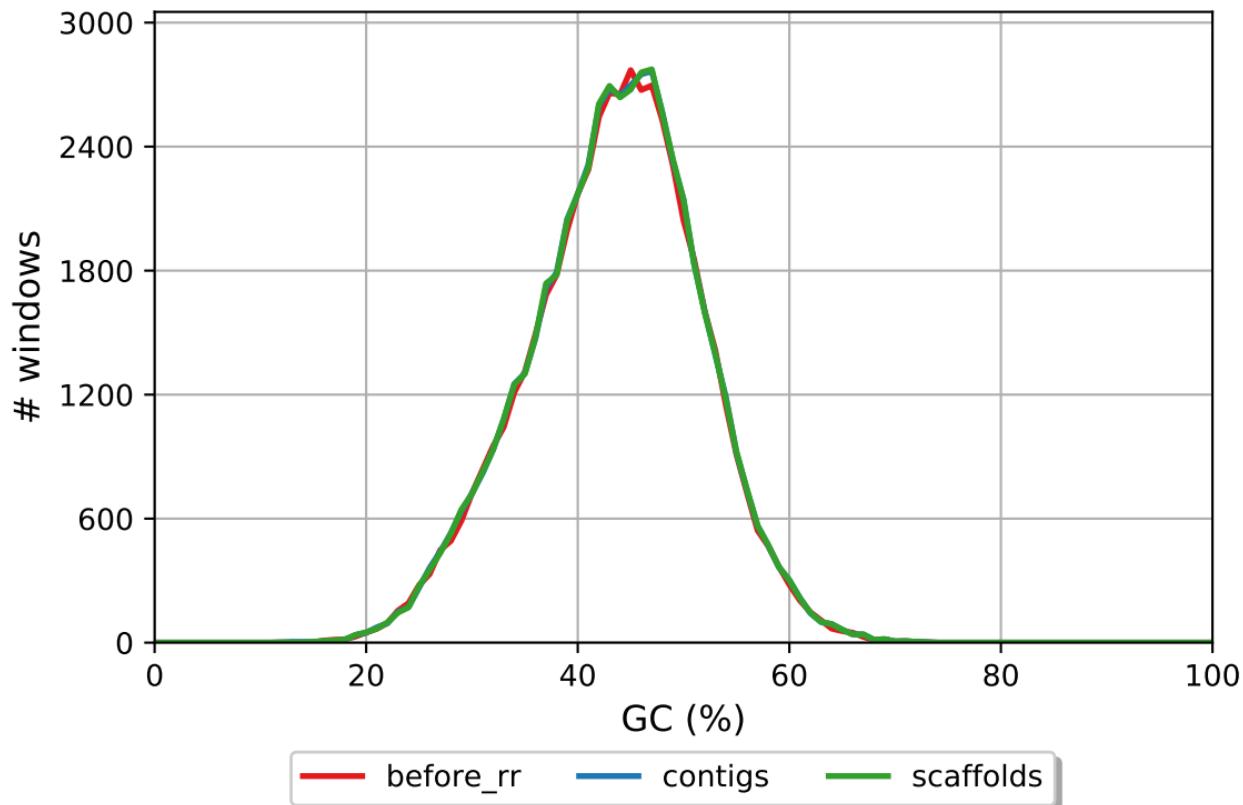
All statistics are based on contigs of size  $\geq$  500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



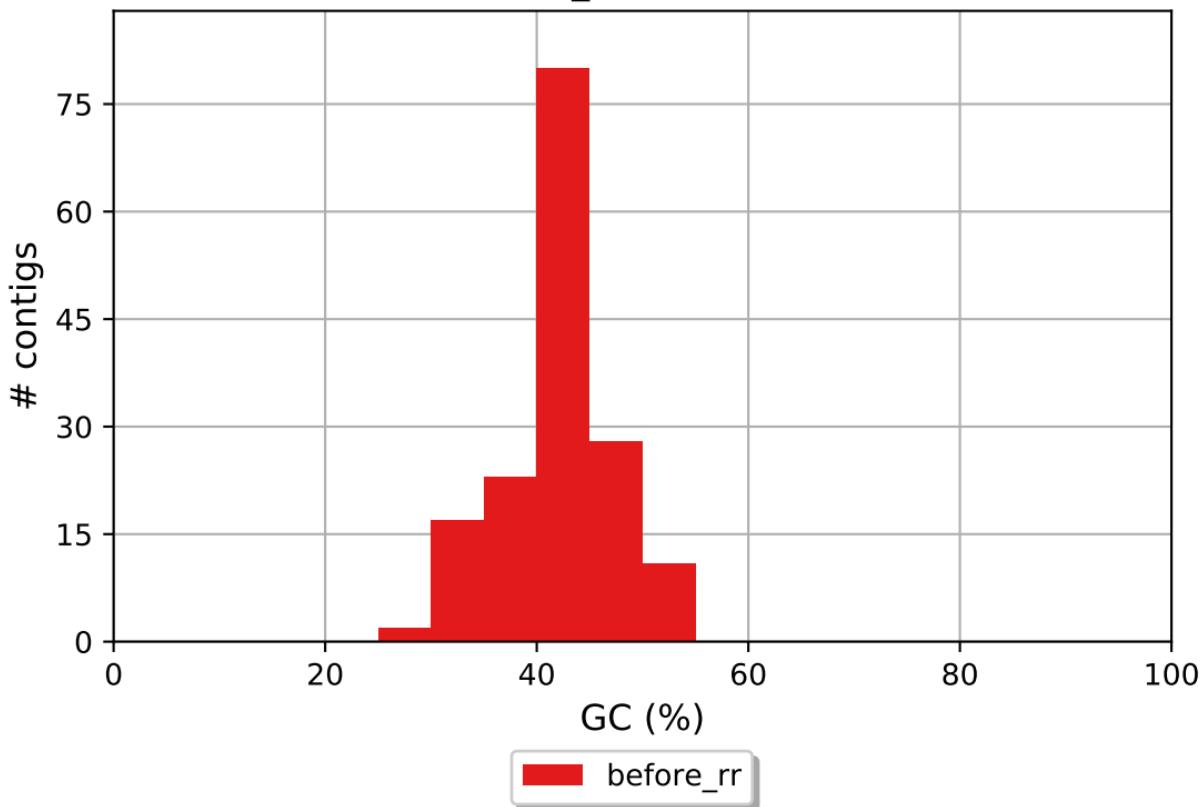
Cumulative length



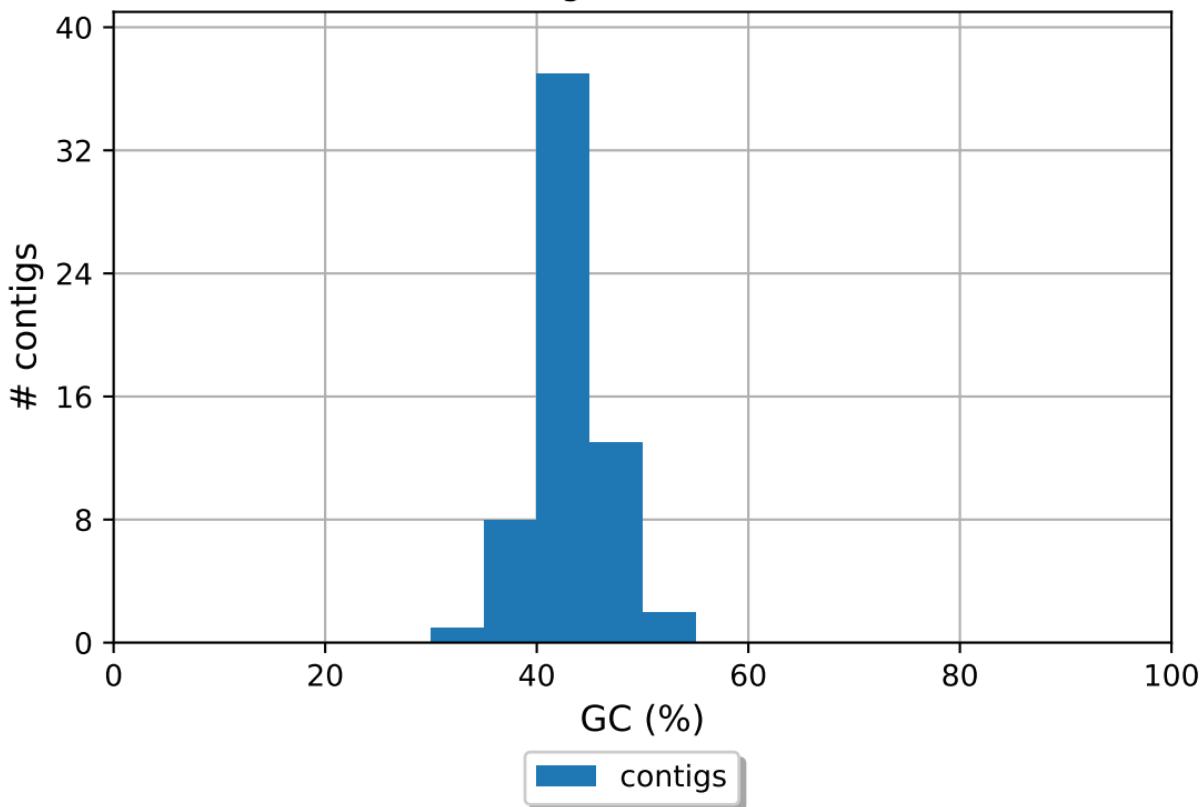
## GC content



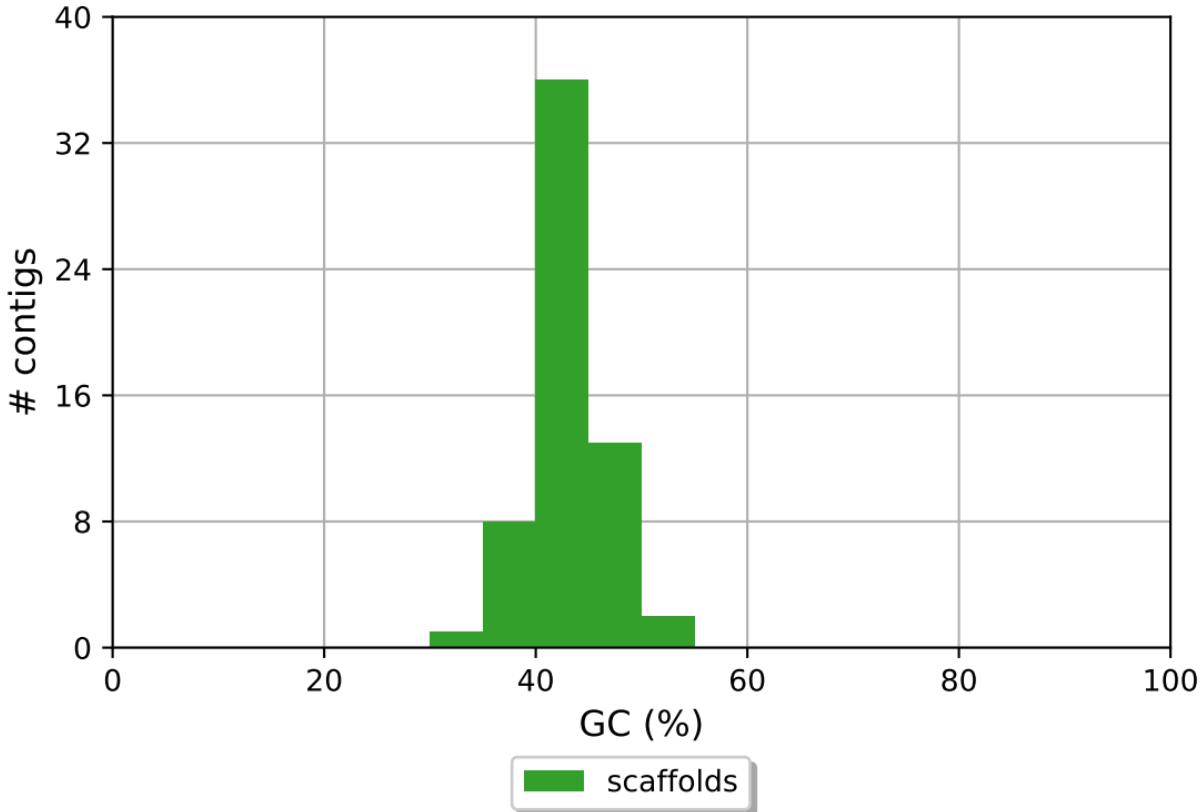
before\_rr GC content



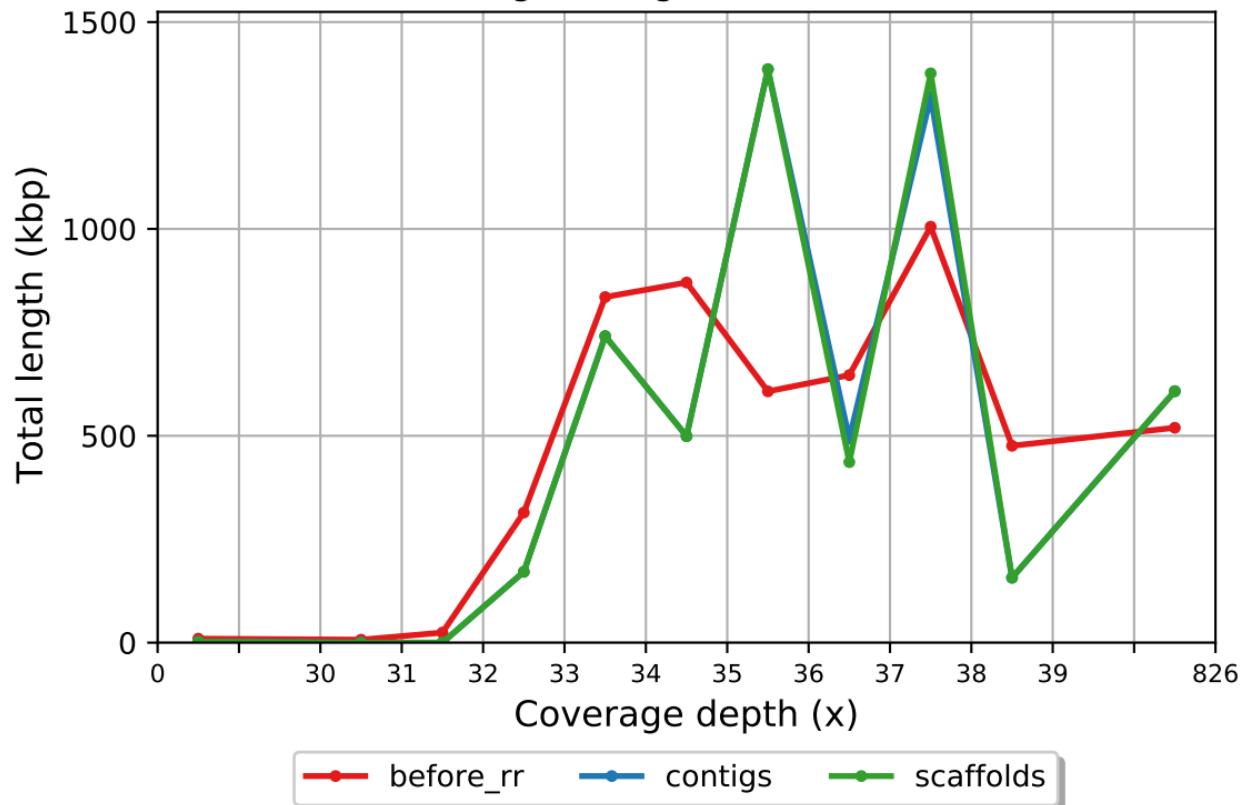
contigs GC content



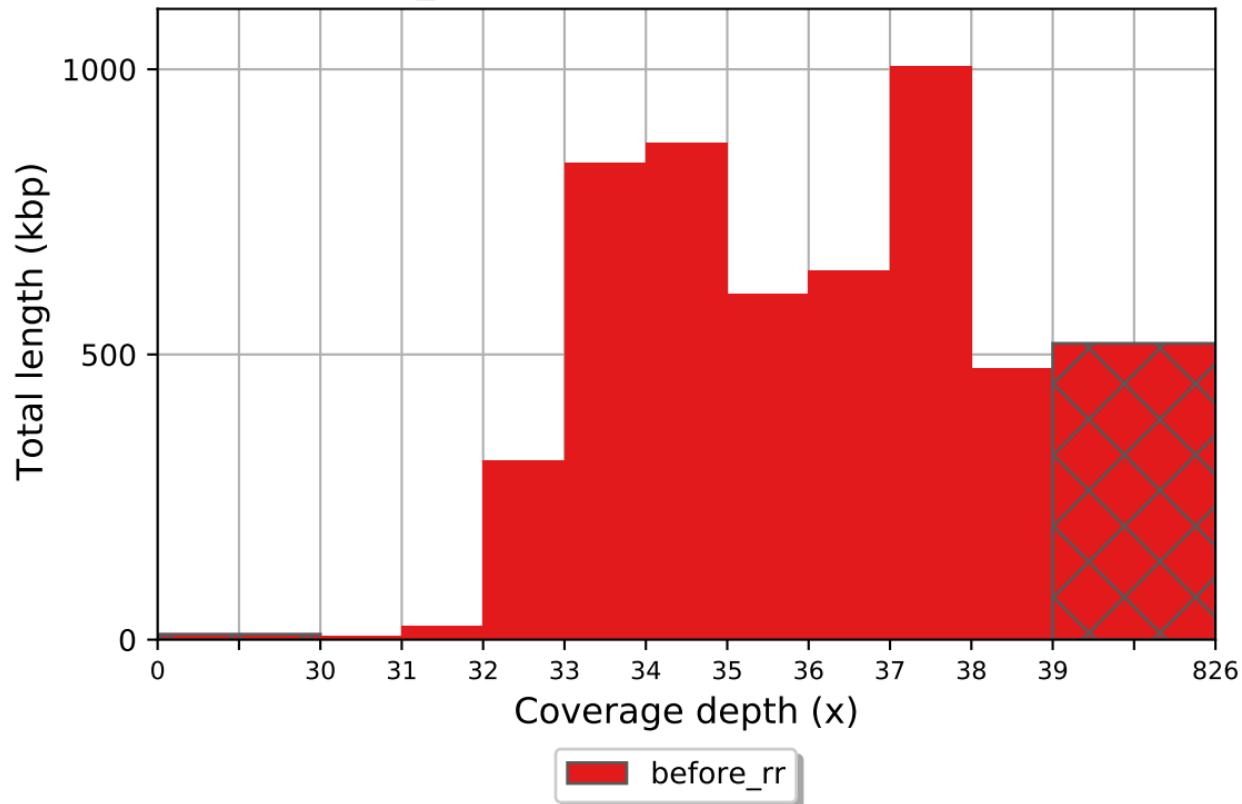
scaffolds GC content



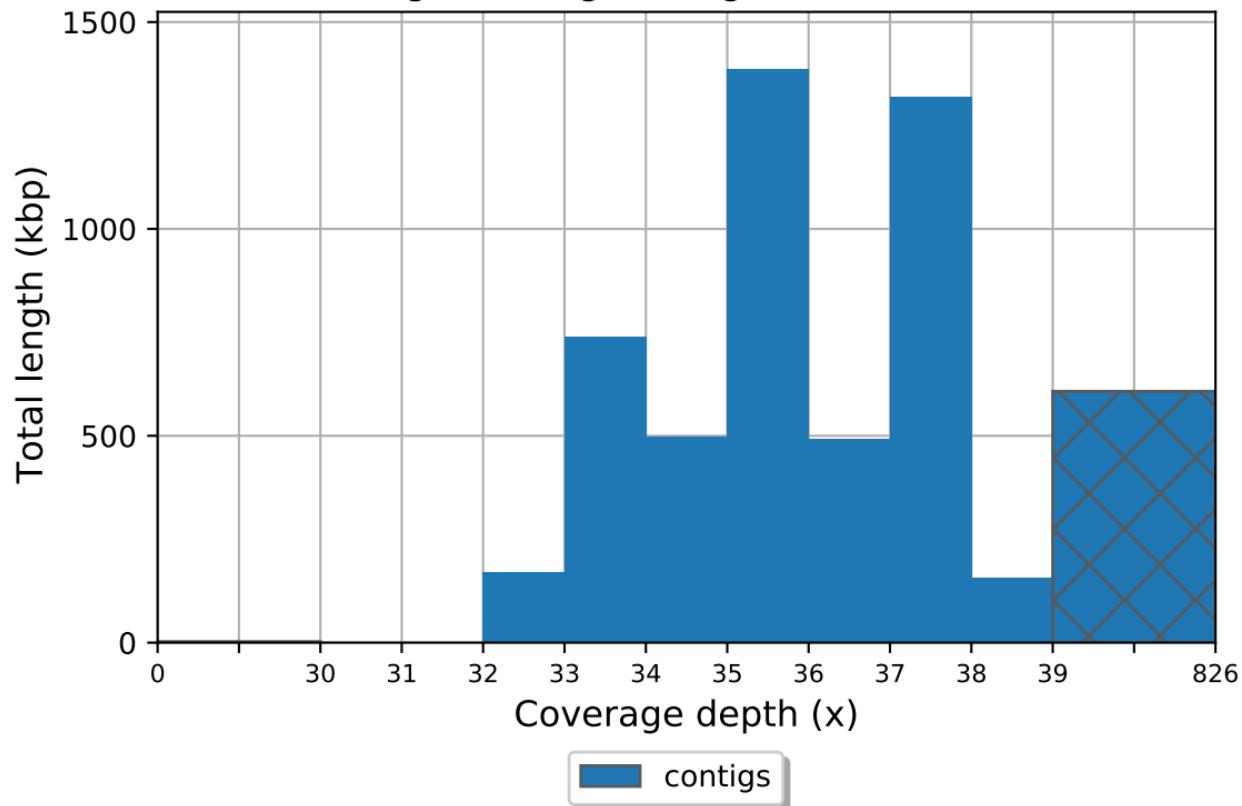
Coverage histogram (bin size: 1x)



before\_rr coverage histogram (bin size: 1x)



contigs coverage histogram (bin size: 1x)



scaffolds coverage histogram (bin size: 1x)

