

# Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 0 bp)	45	32
# contigs (>= 1000 bp)	12	7
# contigs (>= 5000 bp)	5	6
# contigs (>= 10000 bp)	5	5
# contigs (>= 25000 bp)	3	3
# contigs (>= 50000 bp)	1	1
Total length (>= 0 bp)	186593	177895
Total length (>= 1000 bp)	173575	168101
Total length (>= 5000 bp)	160170	164654
Total length (>= 10000 bp)	160170	157666
Total length (>= 25000 bp)	131533	131139
Total length (>= 50000 bp)	55106	54221
# contigs	20	13
Largest contig	55106	54221
Total length	180190	172703
Reference length	179997	179997
N50	48458	49658
N90	3898	10428
auN	36838.5	38106.6
L50	2	2
L90	6	5
# misassemblies	2	4
# misassembled contigs	2	2
Misassembled contigs length	49610	54984
# local misassemblies	0	0
# scaffold gap ext. mis.	1	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	2 + 0 part	1 + 0 part
Unaligned length	2730	885
Genome fraction (%)	95.608	95.537
Duplication ratio	1.031	1.004
# N's per 100 kbp	18.87	0.00
# mismatches per 100 kbp	44.53	33.17
# indels per 100 kbp	3.38	0.00
Largest alignment	55106	49658
Total aligned length	177407	171818
NA50	37178	27260
NA90	3898	10428
auNA	32158.8	30524.4
LA50	2	3
LA90	7	6

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

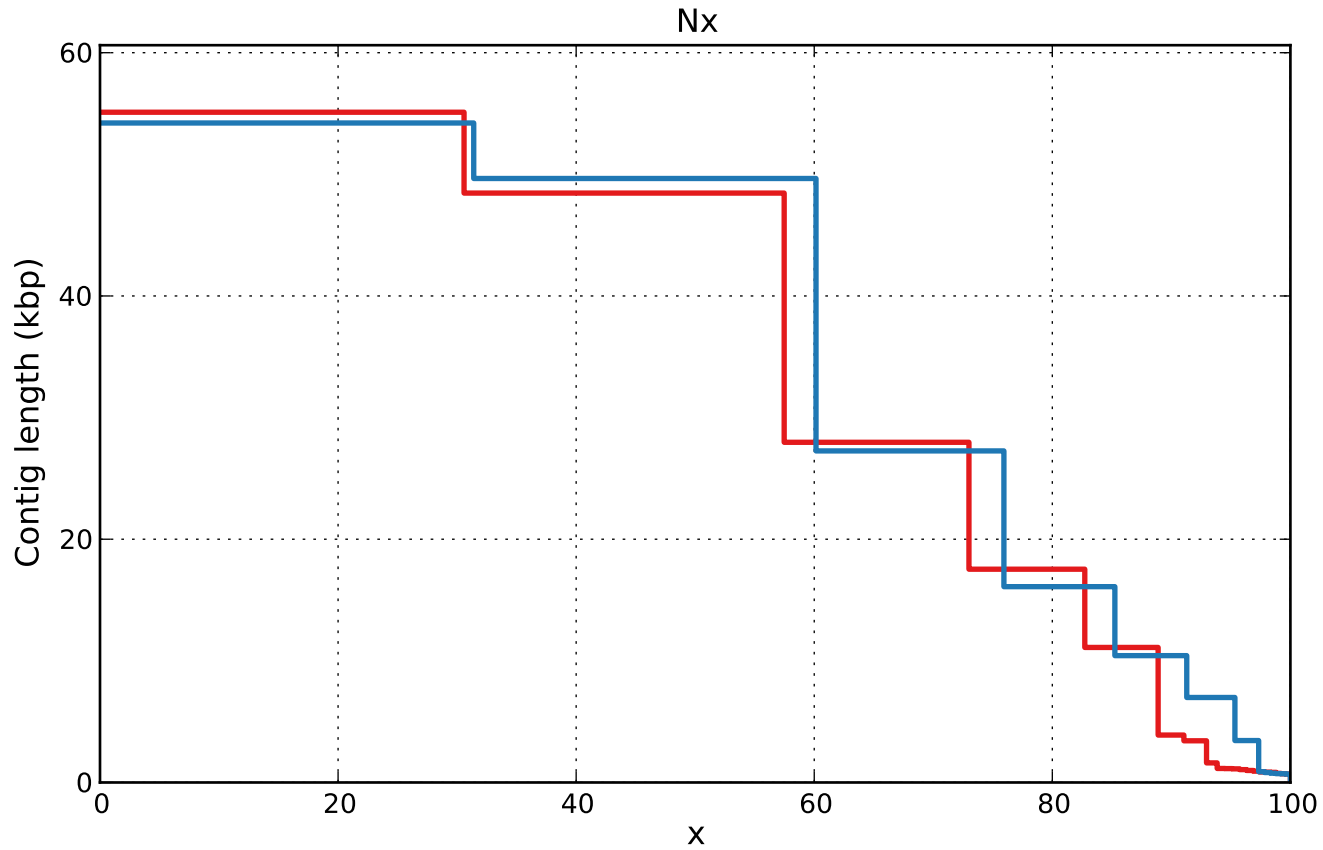
	meta_contigs_1	meta_contigs_2
# misassemblies	2	4
# contig misassemblies	2	4
# c. relocations	1	1
# c. translocations	0	0
# c. inversions	0	0
# c. interspecies translocations	1	3
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# s. interspecies translocations	0	0
# misassembled contigs	2	2
Misassembled contigs length	49610	54984
# possibly misassembled contigs	0	0
# possible misassemblies	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	1	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	79	57
# indels	6	0
# indels (<= 5 bp)	6	0
# indels (> 5 bp)	0	0
Indels length	7	0

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

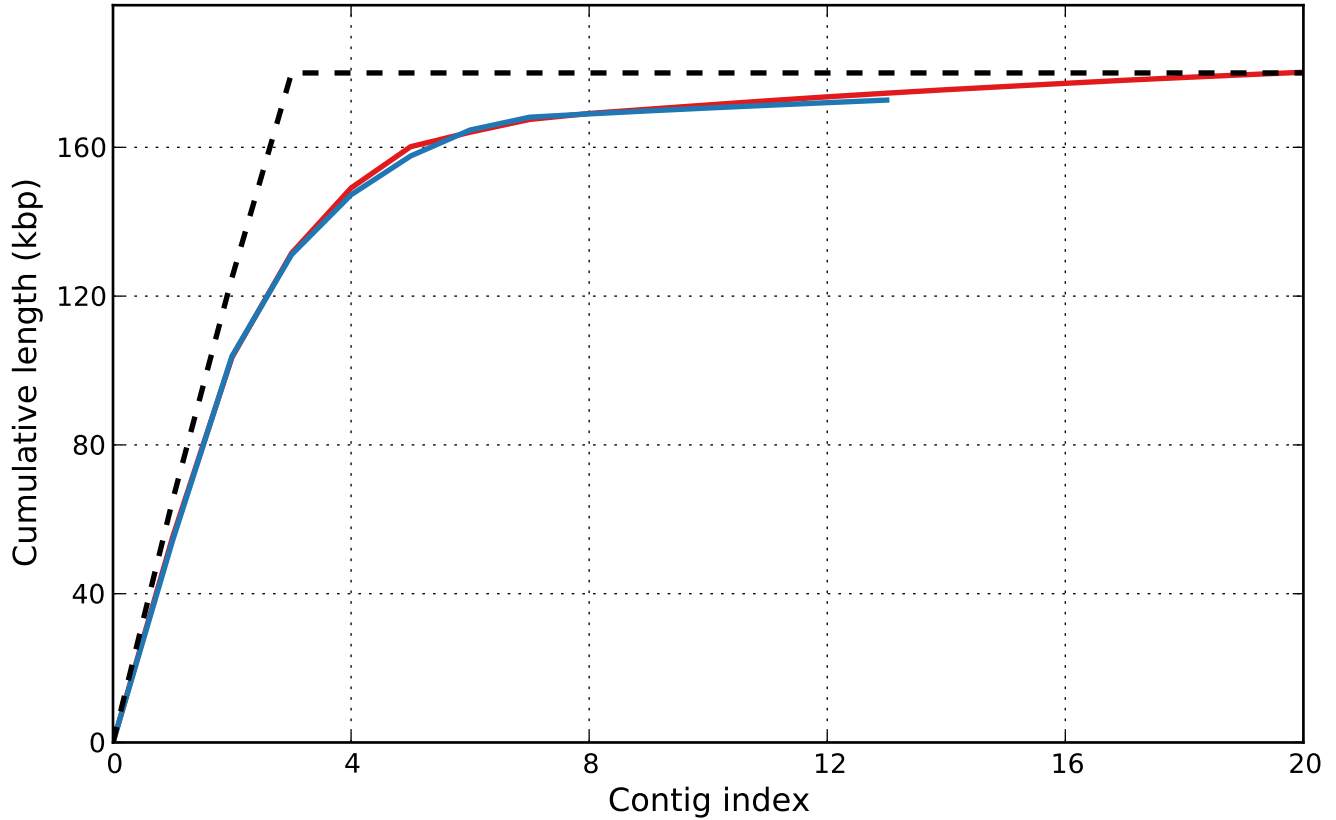
## Unaligned report

	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	2	1
Fully unaligned length	2730	885
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	34	0

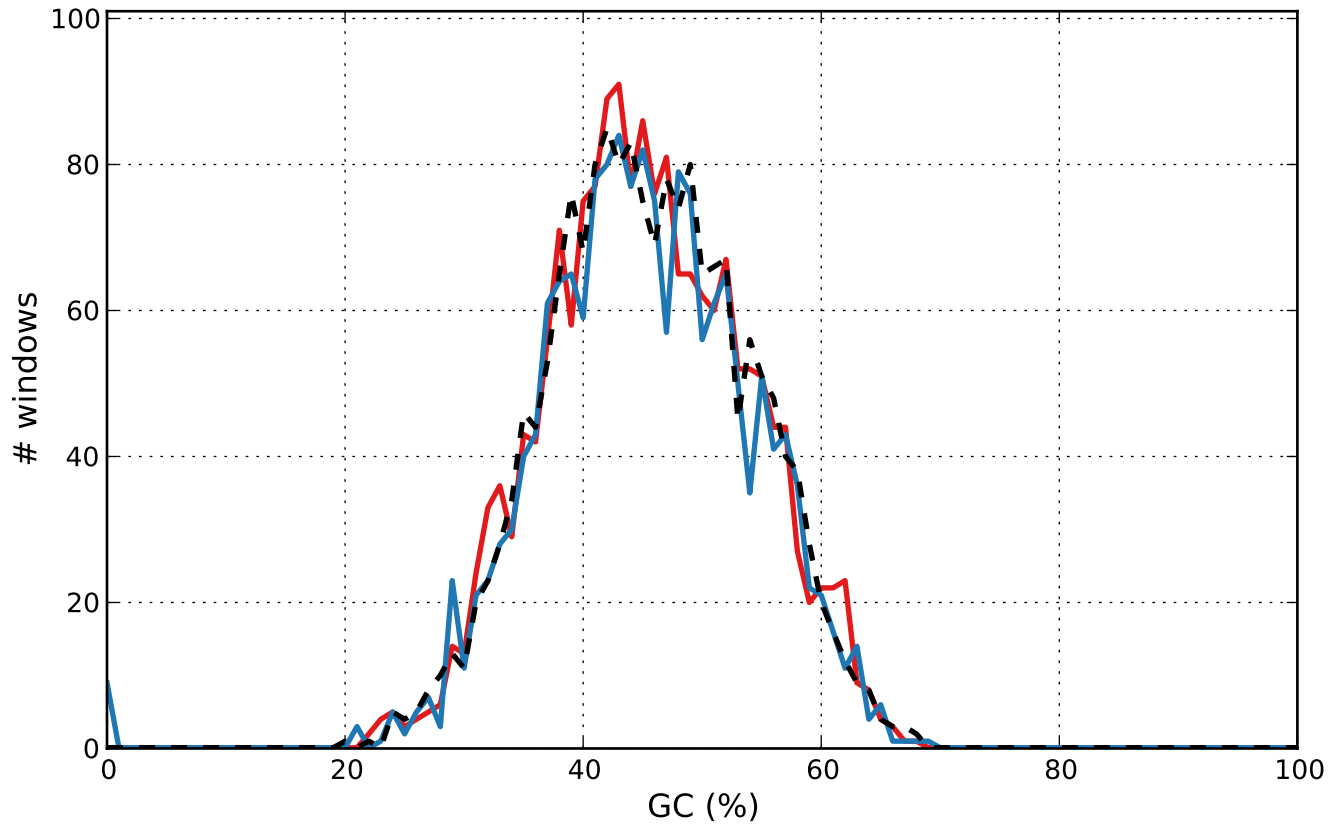
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



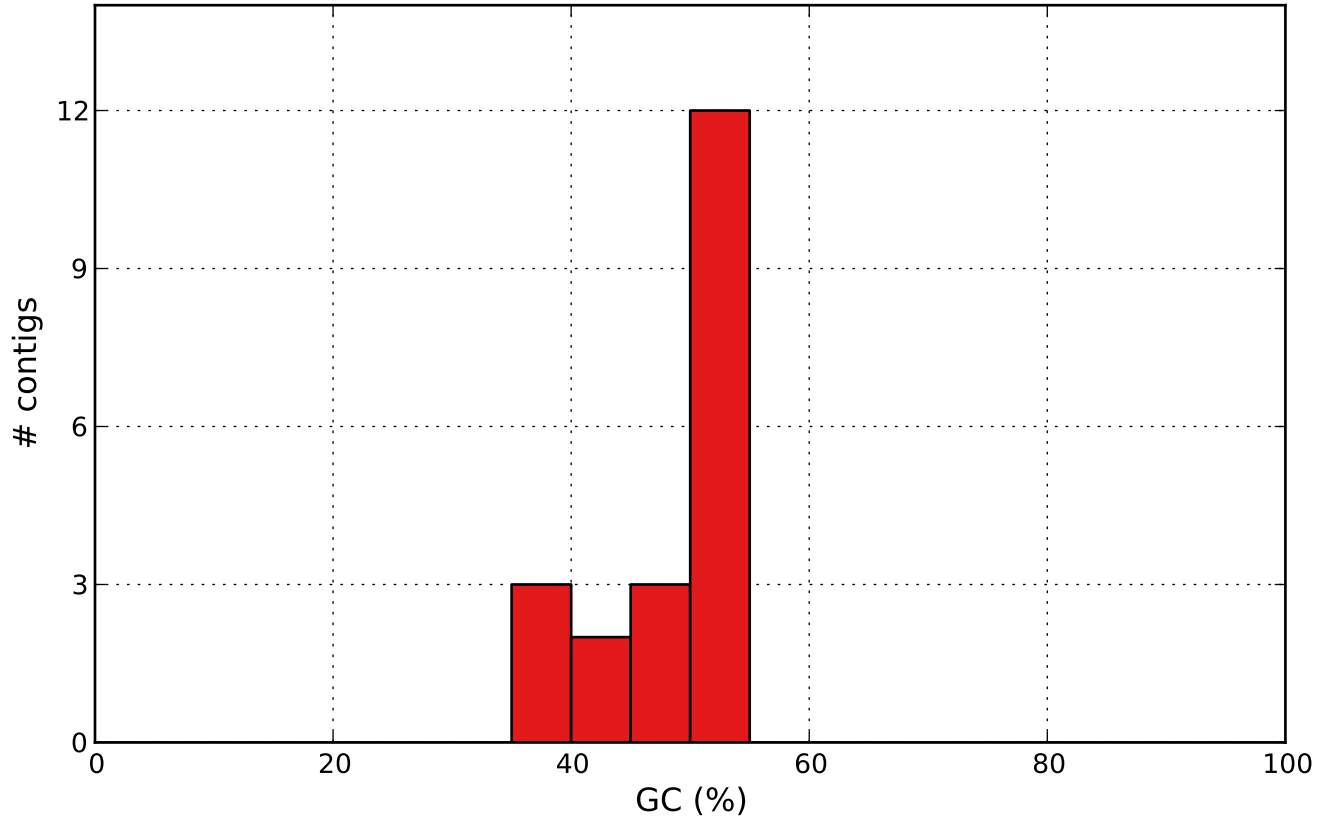
Cumulative length



GC content

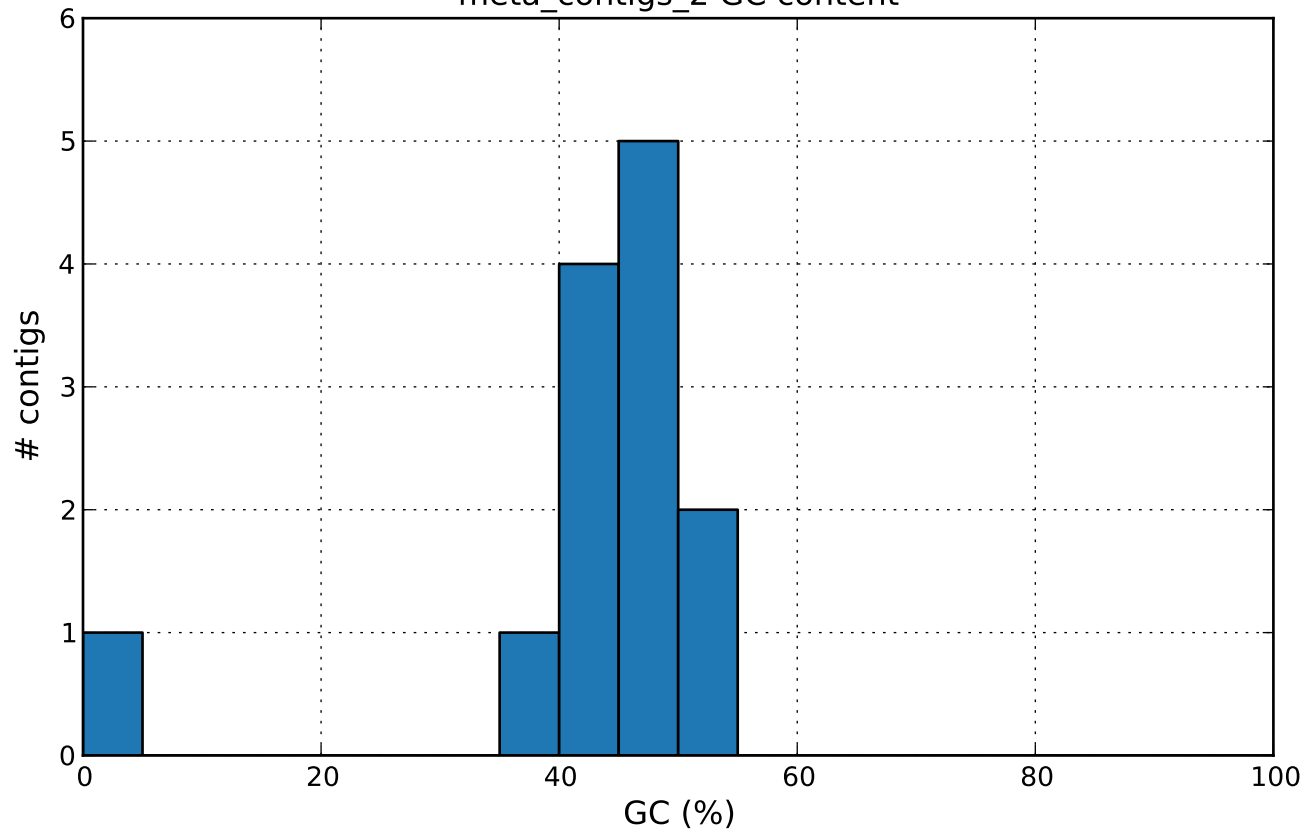


meta\_contigs\_1 GC content



meta\_contigs\_1

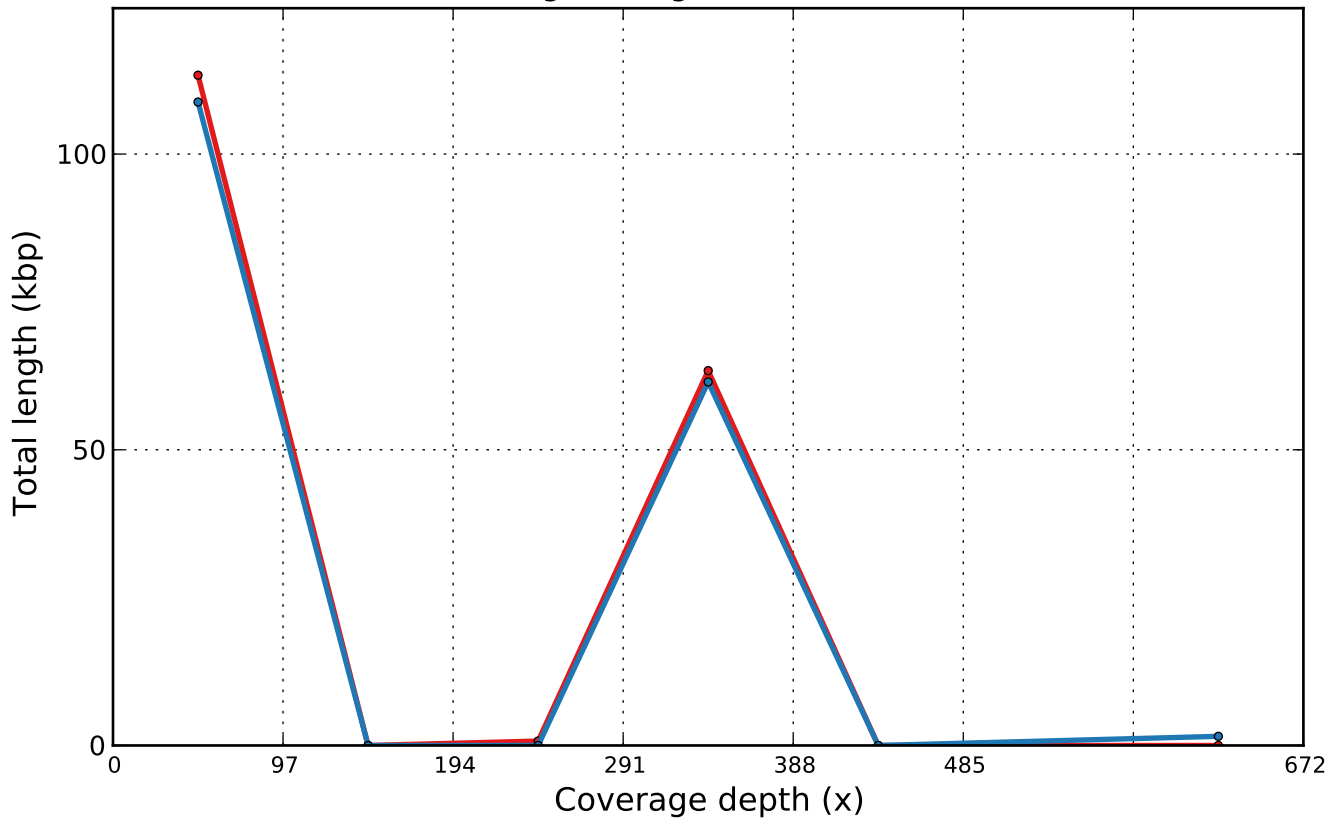
meta\_contigs\_2 GC content



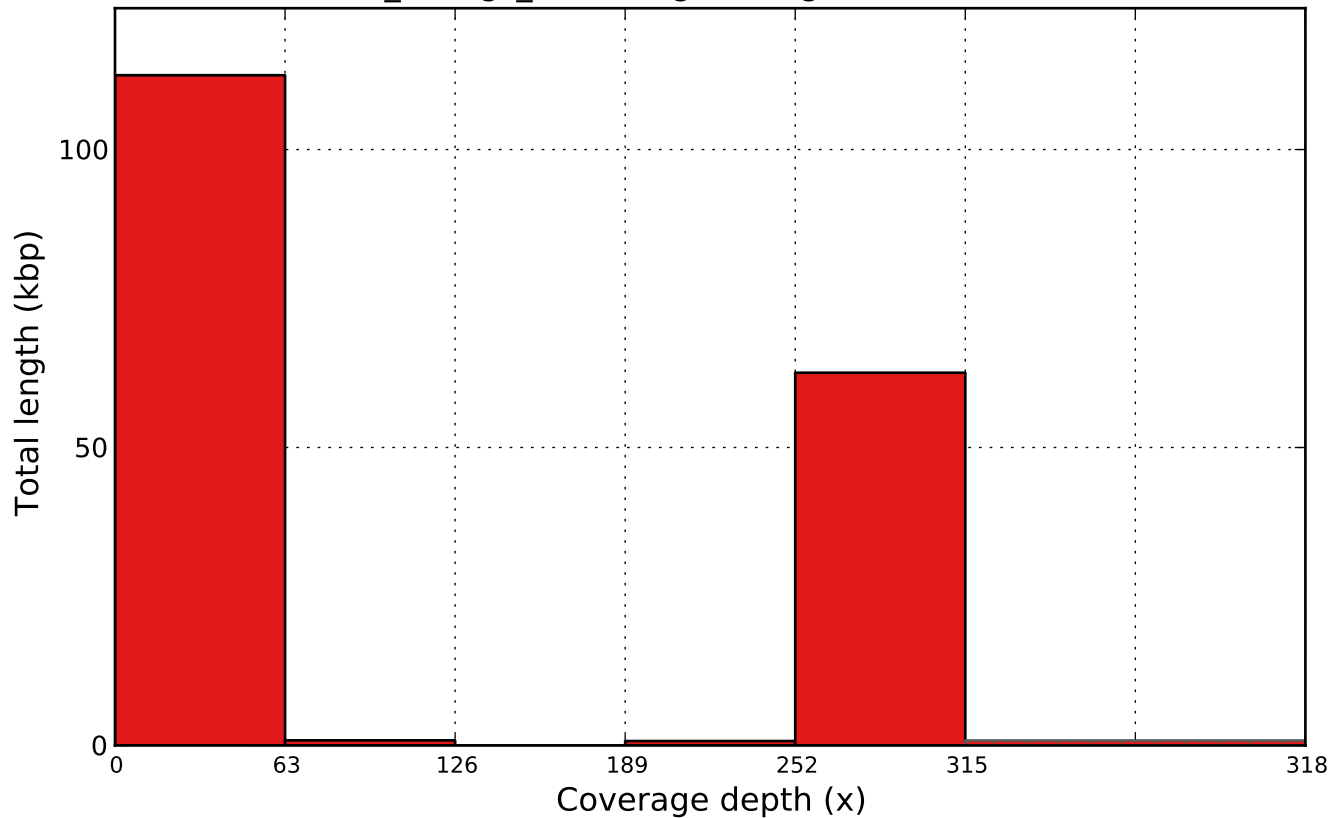
meta\_contigs\_2



Coverage histogram (bin size: 97x)

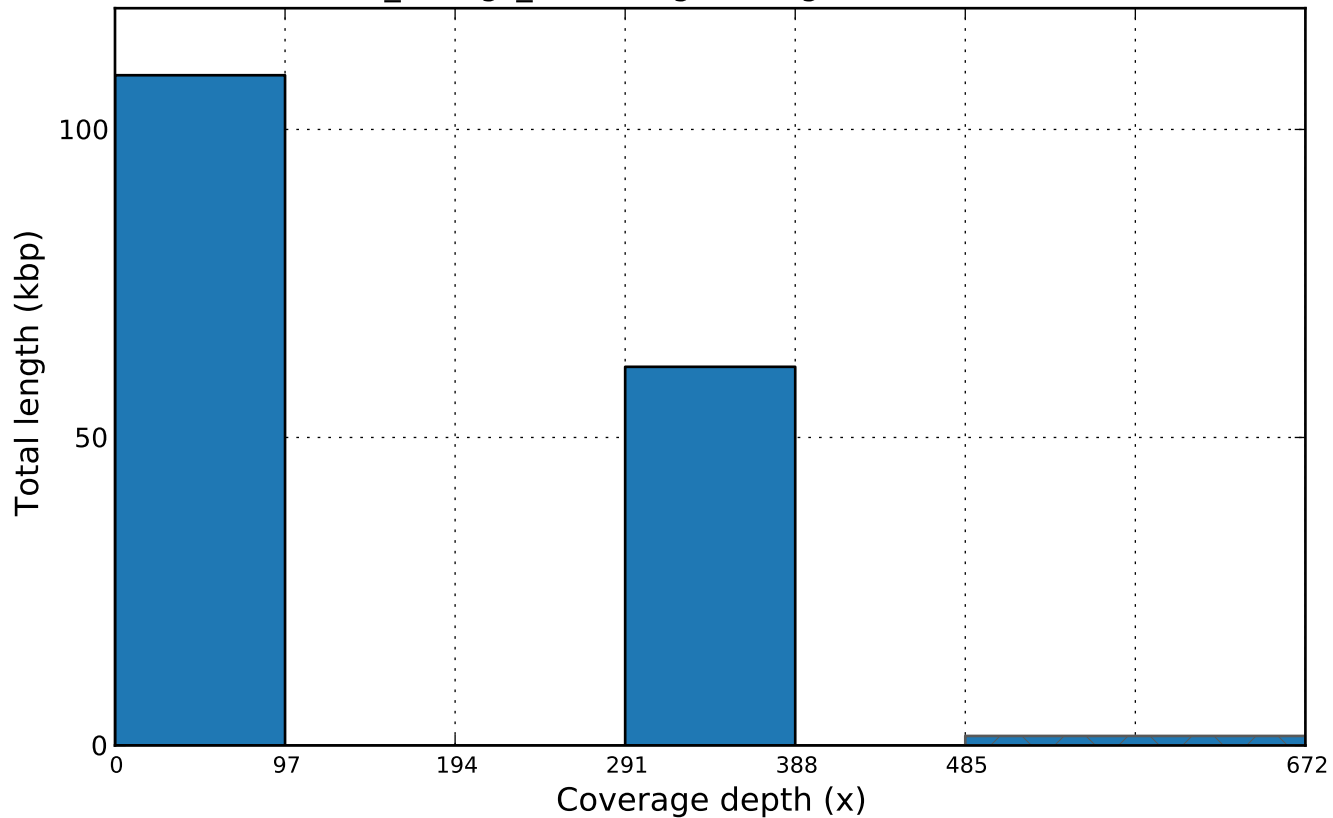


meta\_contigs\_1 coverage histogram (bin size: 63x)



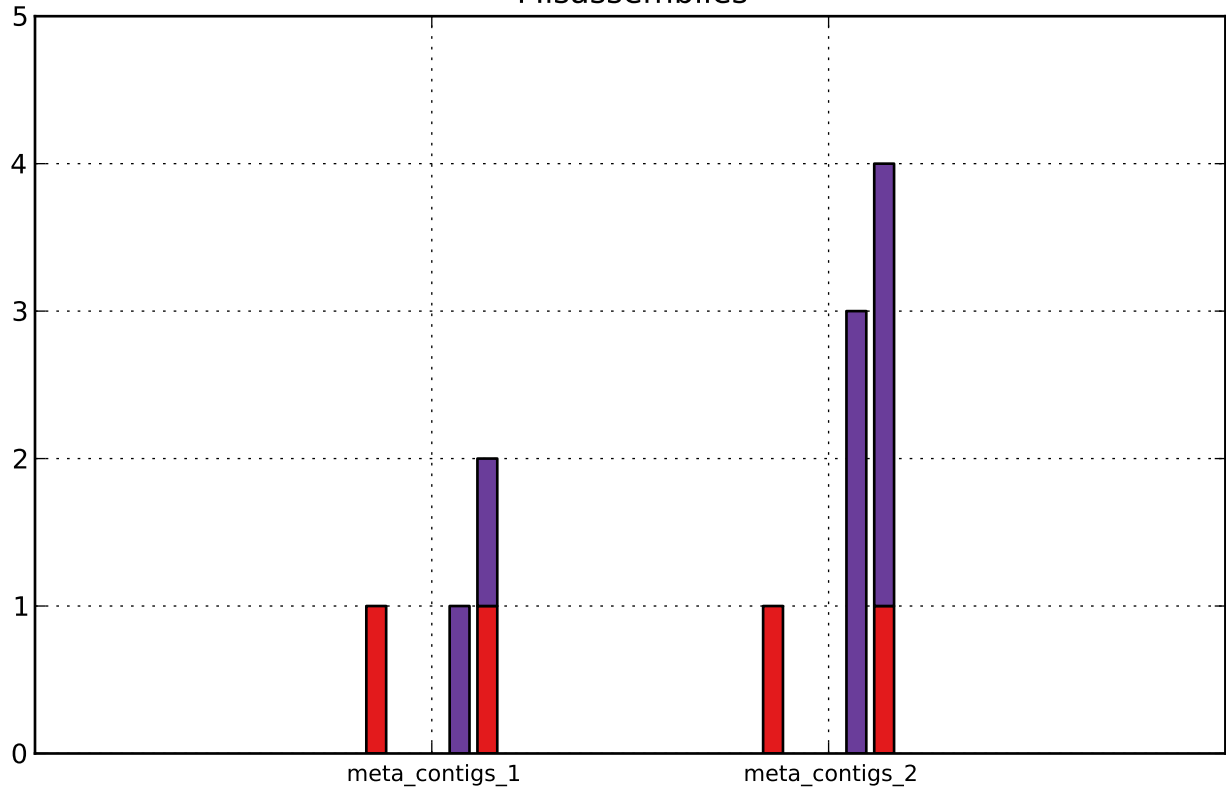
meta\_contigs\_1

meta\_contigs\_2 coverage histogram (bin size: 97x)

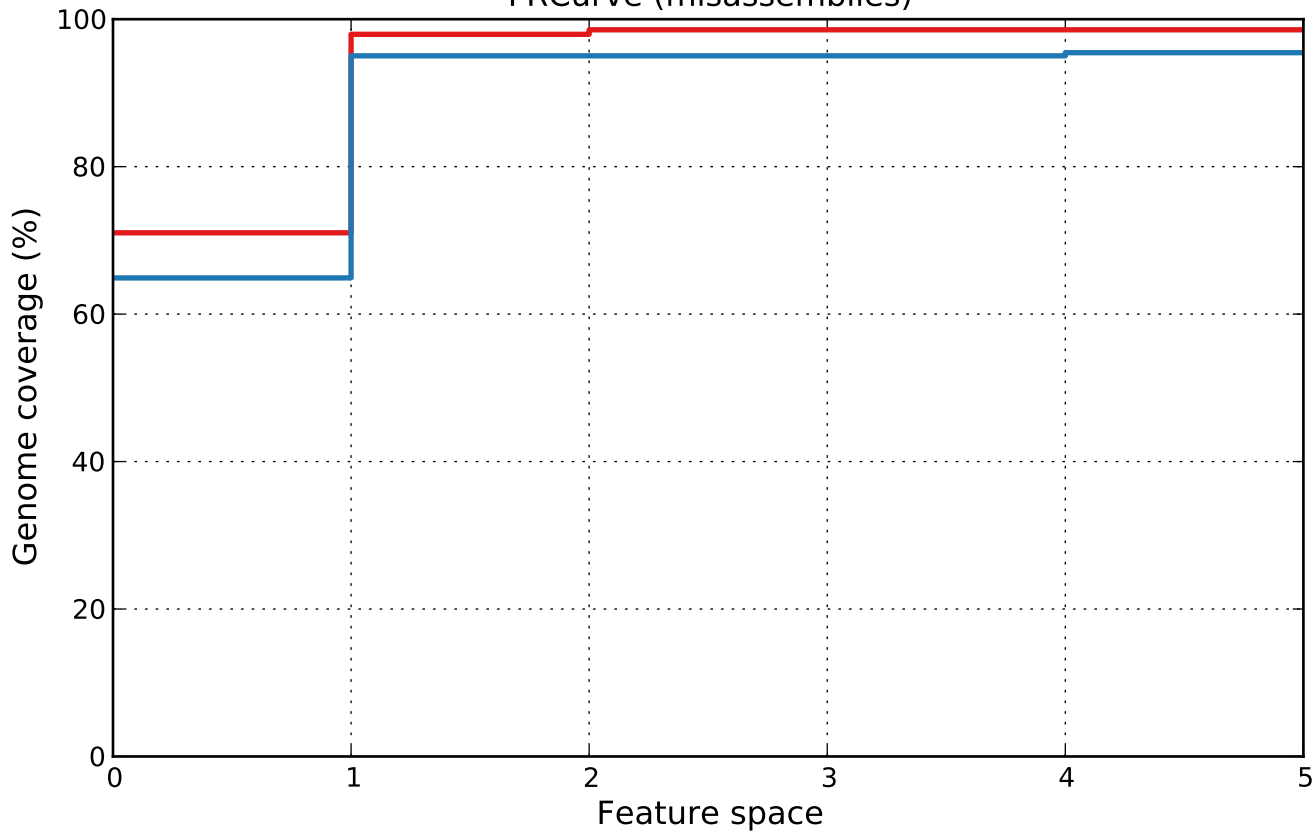


meta\_contigs\_2

# Misassemblies

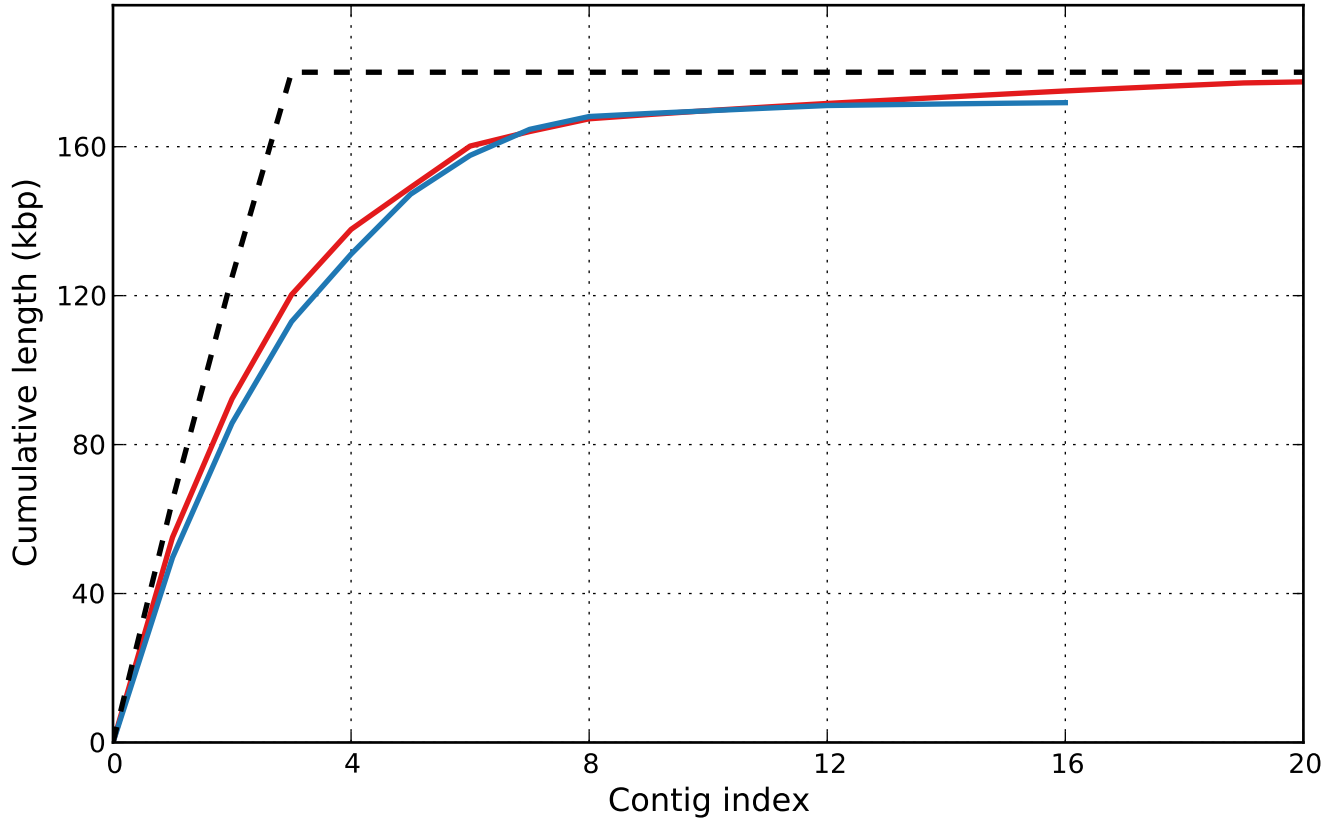


FRCurve (misassemblies)

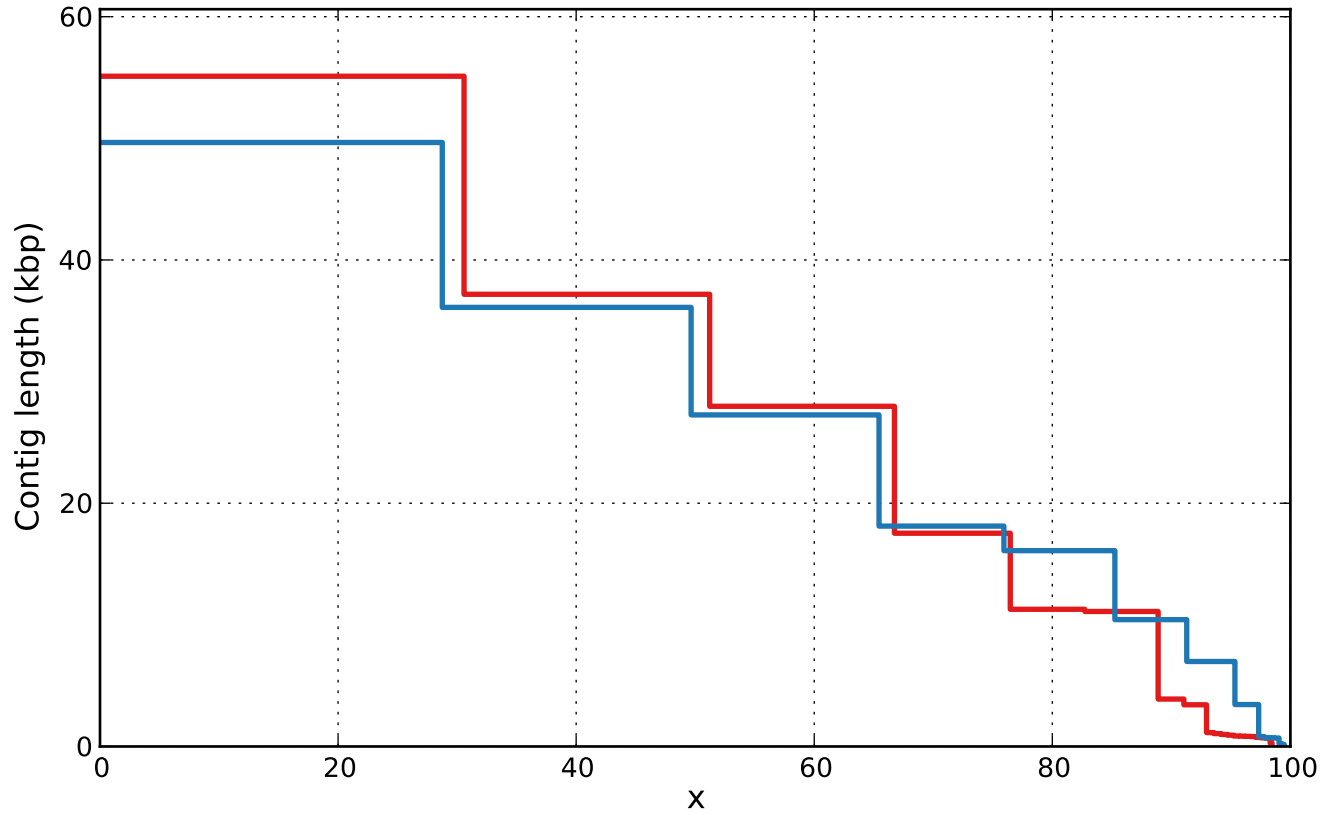


— meta\_contigs\_1    — meta\_contigs\_2

Cumulative length (aligned contigs)



NAx



Genome fraction, %

