

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)	186573	177895
Total length (>= 1000 bp)	173555	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	180170	172703
Reference length	179997	179997
N50	48458	49658
N75	17535	27260
L50	2	2
L75	4	3
# misassemblies	3	2
# misassembled contigs	2	2
Misassembled contigs length	49590	54984
# local misassemblies	0	0
# scaffold gap size misassemblies	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	2 + 0 part	1 + 0 part
Unaligned length	2730	885
Genome fraction (%)	95.635	95.537
Duplication ratio	1.031	1.004
# N's per 100 kbp	7.77	0.00
# mismatches per 100 kbp	33.11	27.33
# indels per 100 kbp	1.16	0.00
Largest alignment	55106	49658
Total aligned length	177411	171457
NA50	37178	27260
NA75	17534	18119
LA50	2	3
LA75	4	4

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	3	2
# relocations	1	1
# translocations	0	0
# inversions	0	0
# interspecies translocations	2	1
# misassembled contigs	2	2
Misassembled contigs length	49590	54984
# possibly misassembled contigs	0	0
# possible misassemblies	0	0
# local misassemblies	0	0
# scaffold gap size misassemblies	0	0
# unaligned mis. contigs	0	0
# mismatches	57	47
# indels	2	0
# indels (<= 5 bp)	2	0
# indels (> 5 bp)	0	0
Indels length	2	0

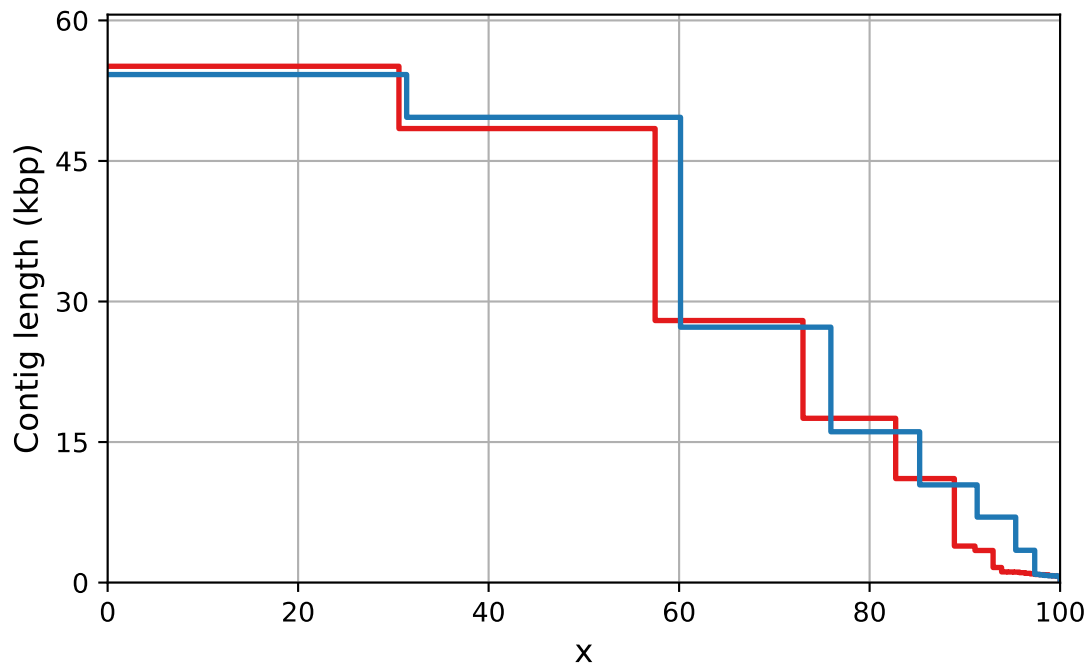
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	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	14	0

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).

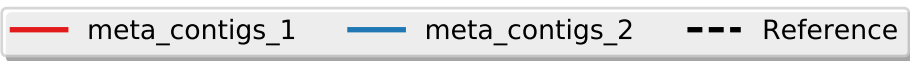
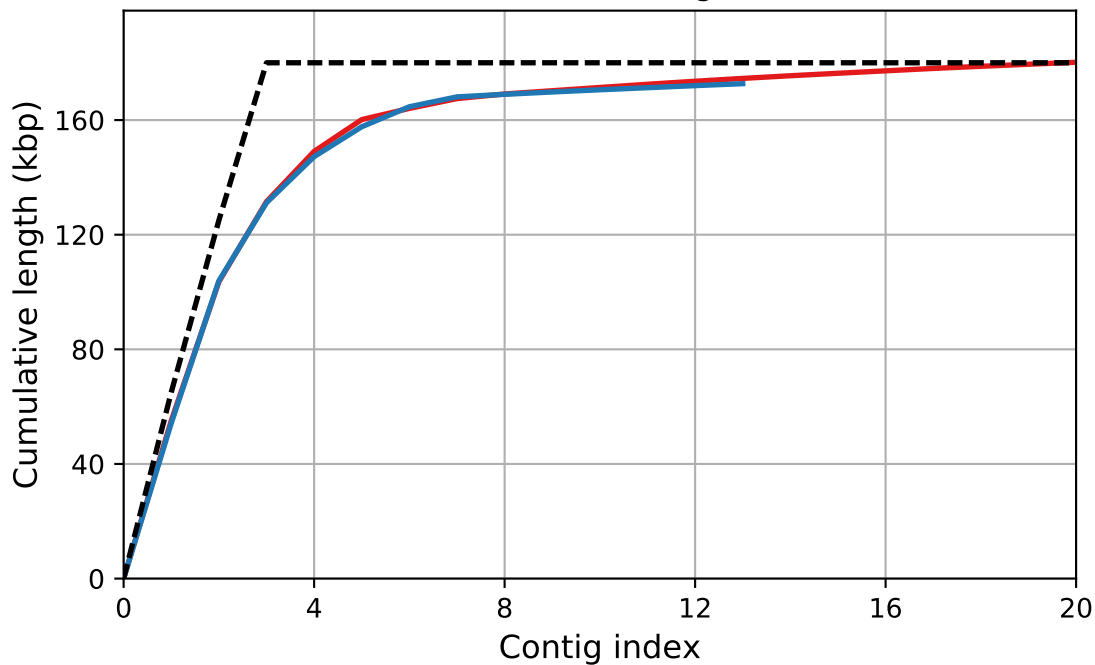
Nx

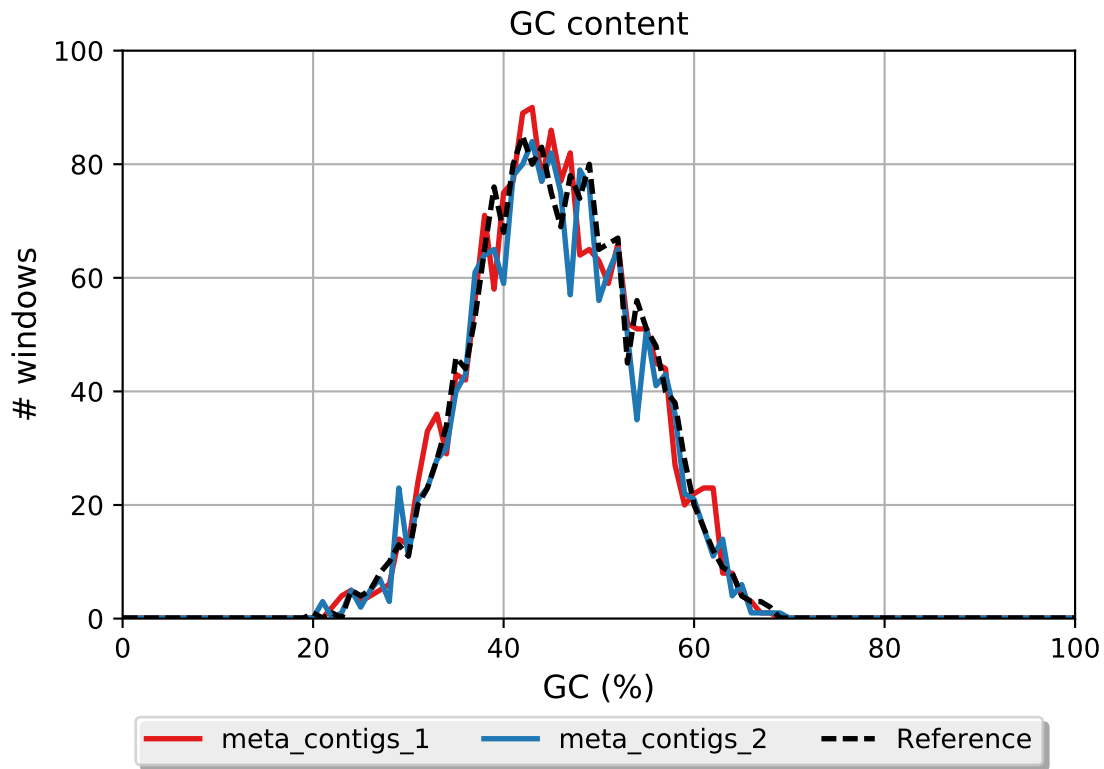


— meta_contigs_1

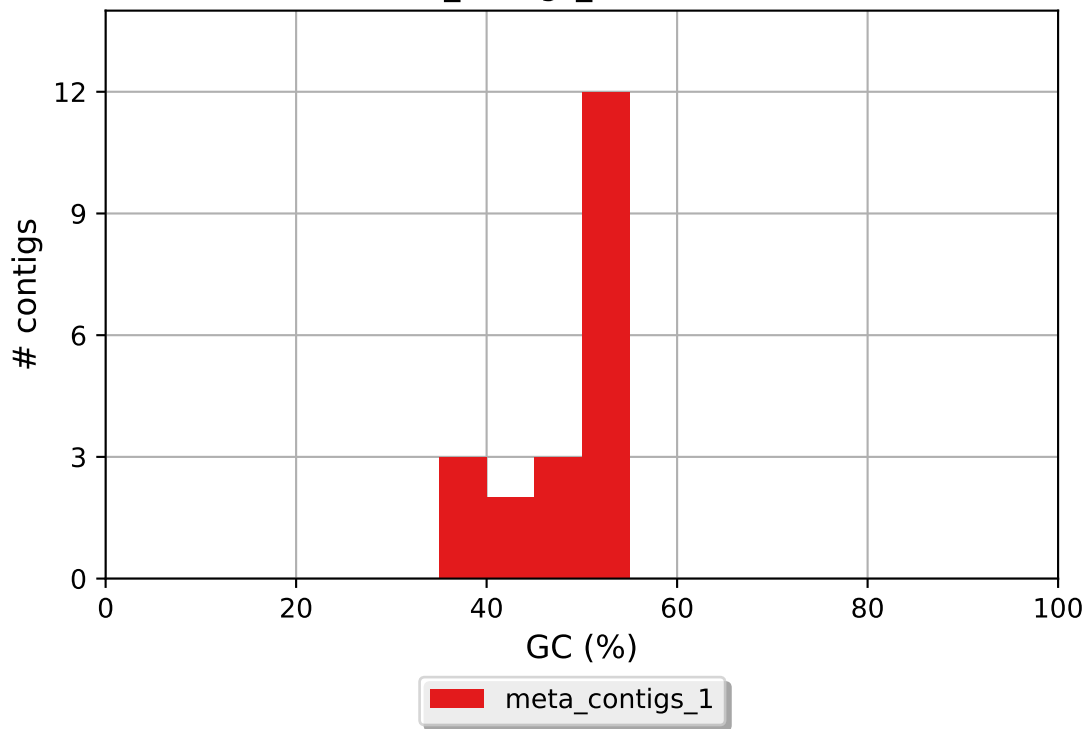
— meta_contigs_2

Cumulative length

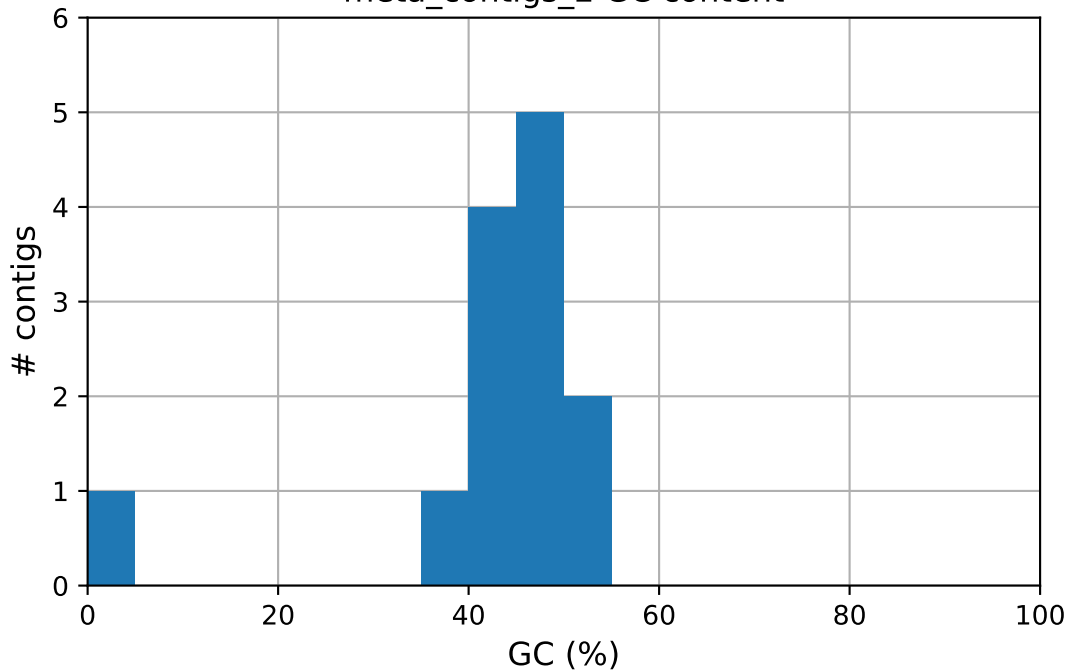




meta_contigs_1 GC content

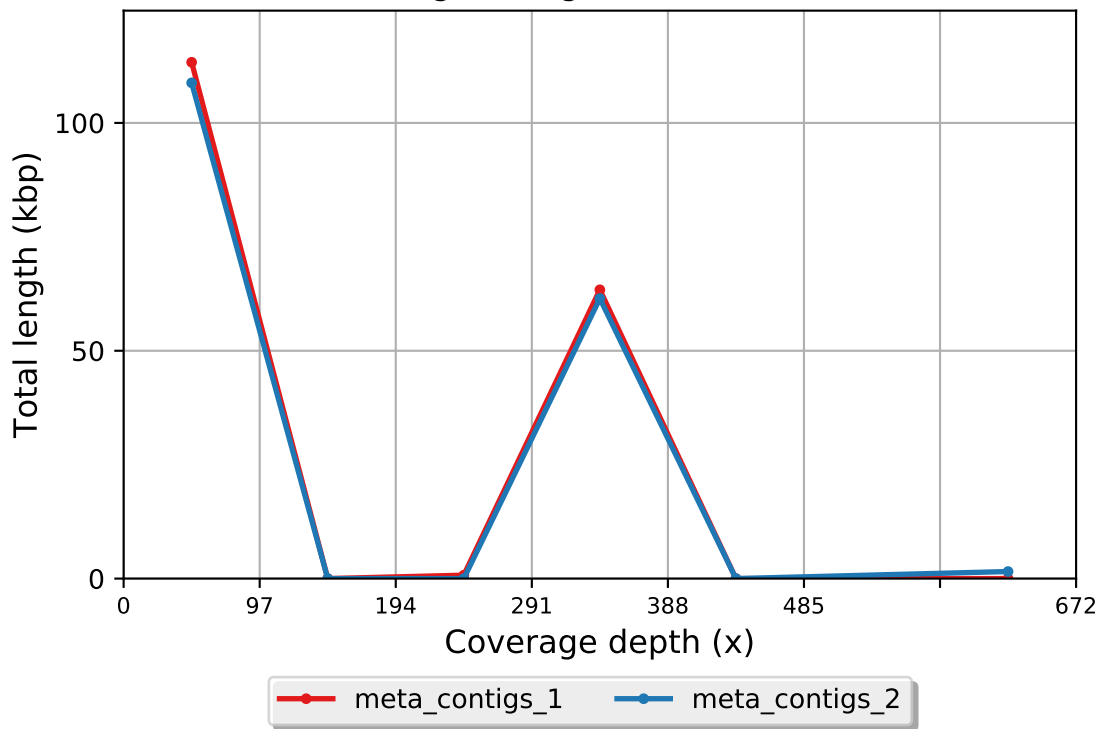


meta_contigs_2 GC content

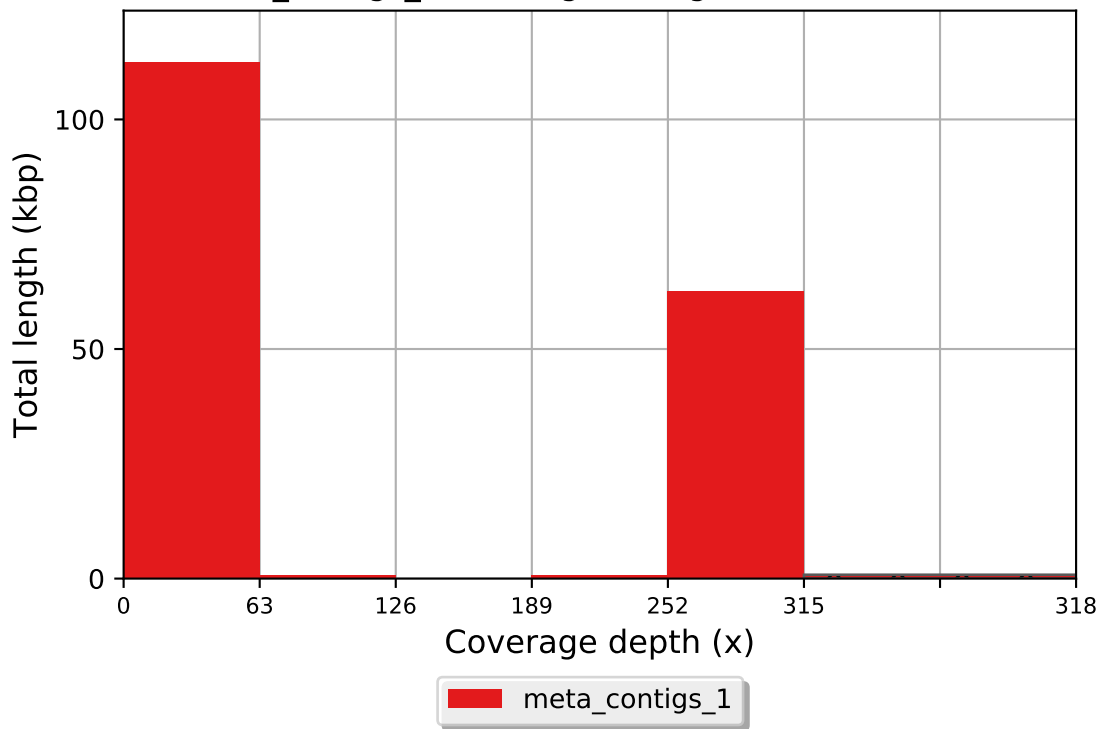


meta_contigs_2

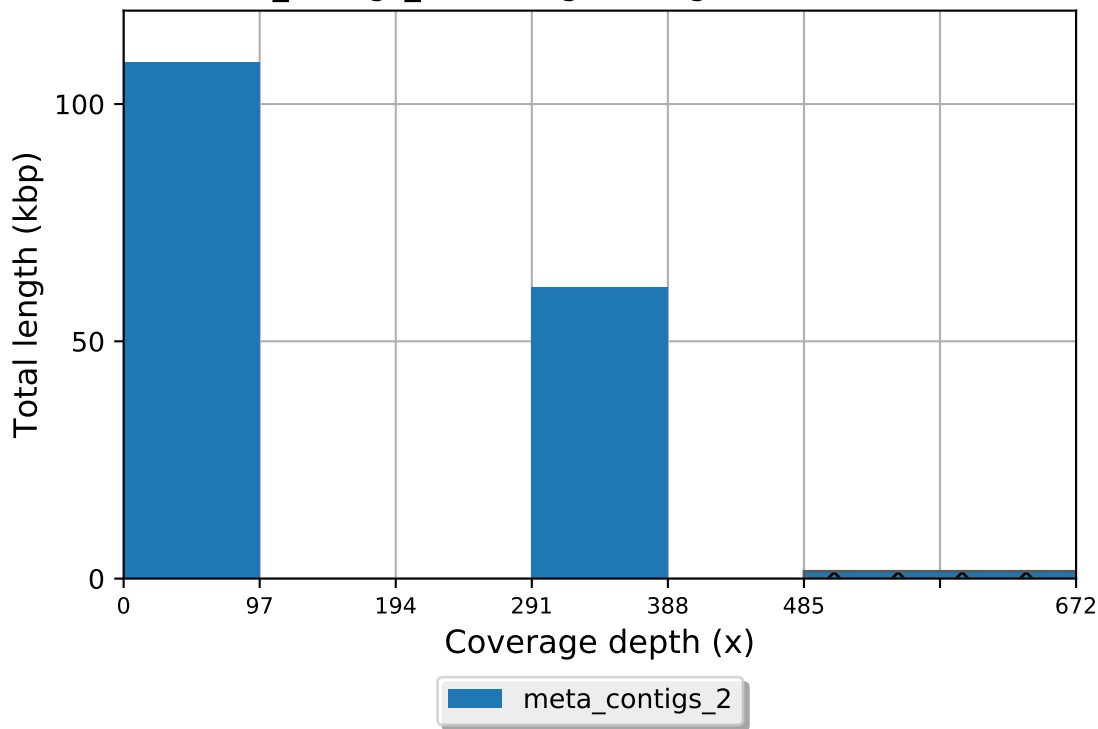
Coverage histogram (bin size: 97x)



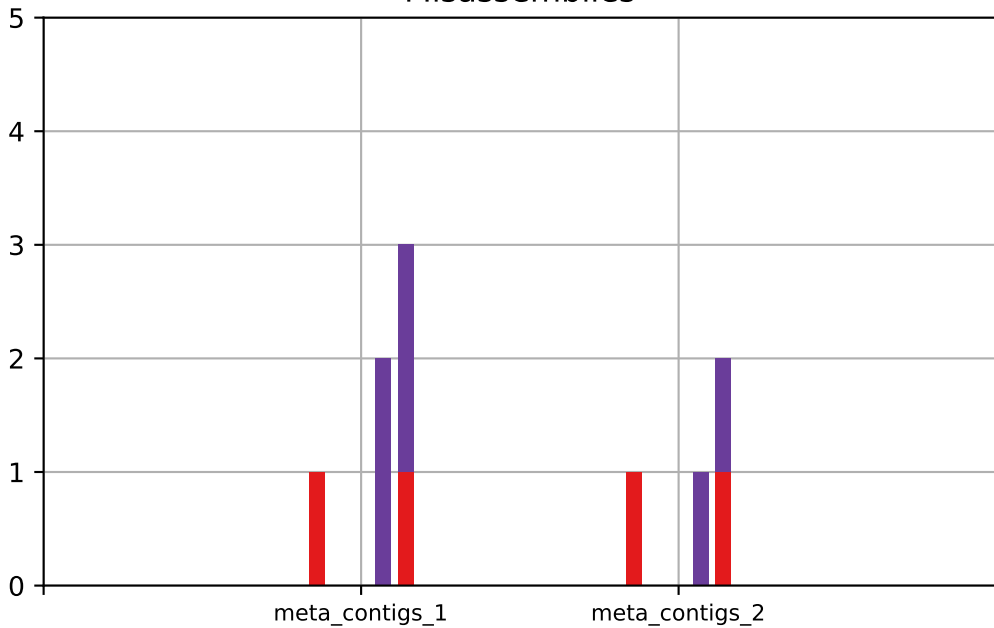
meta_contigs_1 coverage histogram (bin size: 63x)



meta_contigs_2 coverage histogram (bin size: 97x)



Misassemblies

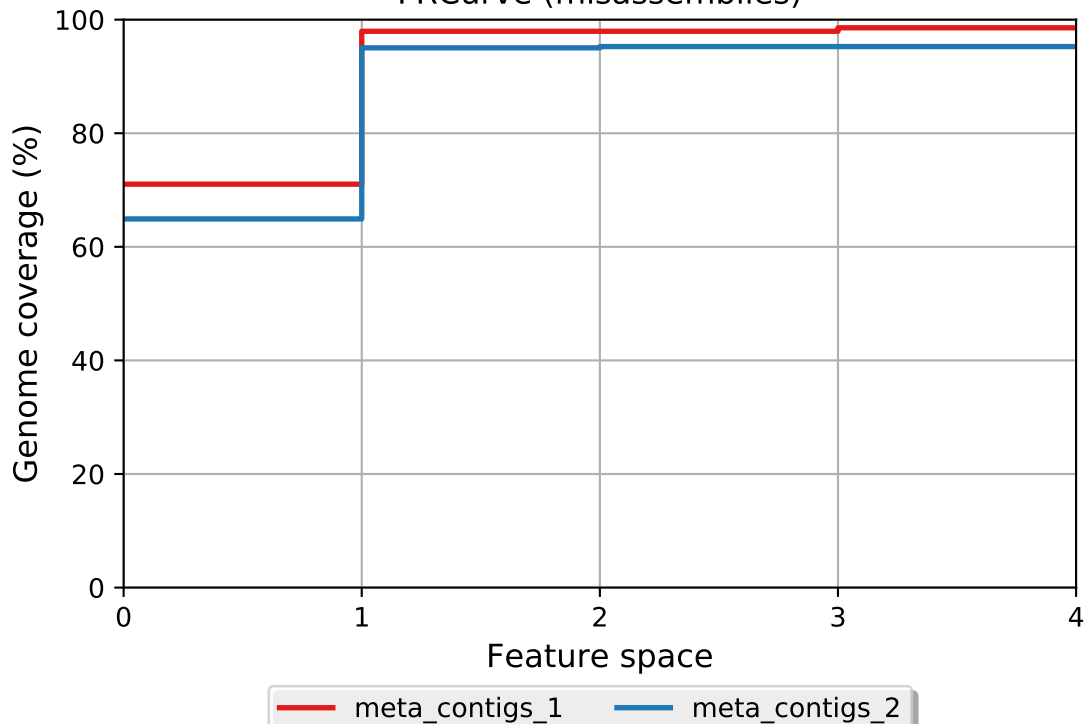


relocations

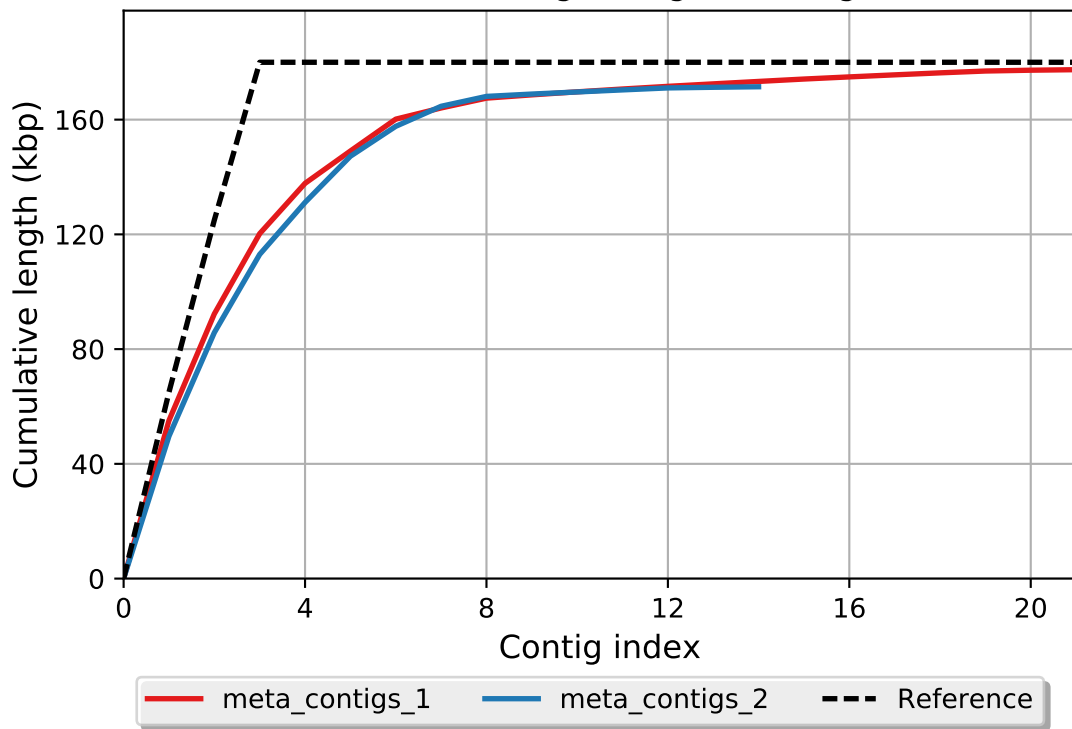


interspecies translocations

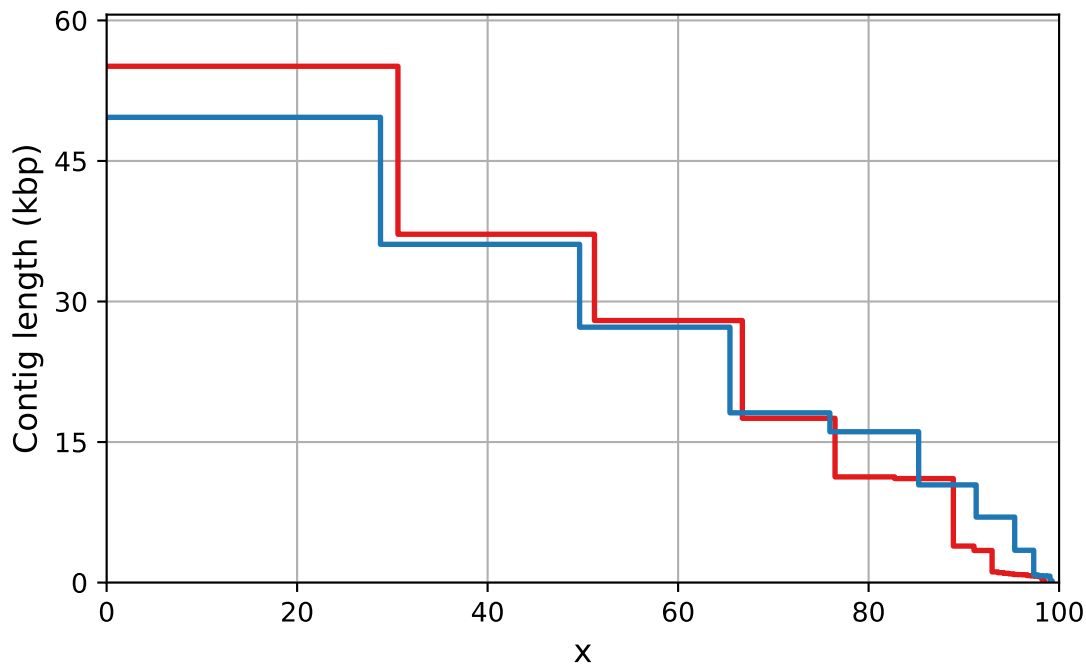
FRCurve (misassemblies)



Cumulative length (aligned contigs)



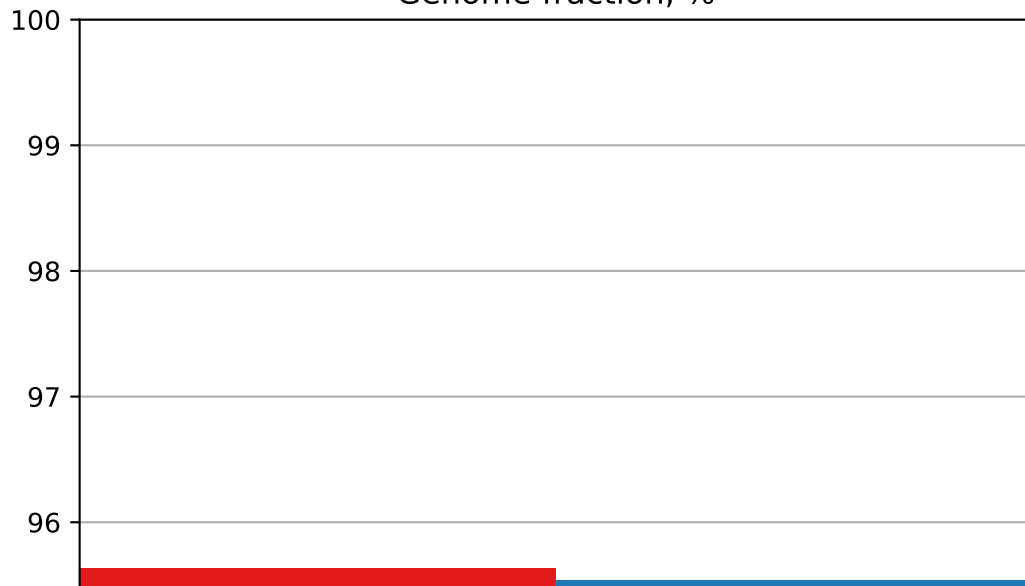
NAx



meta_contigs_1

meta_contigs_2

Genome fraction, %



meta_contigs_1



meta_contigs_2