

Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 1000 bp)	2	1
# contigs (>= 5000 bp)	1	1
# contigs (>= 10000 bp)	1	1
# contigs (>= 25000 bp)	1	1
# contigs (>= 50000 bp)	0	0
Total length (>= 1000 bp)	49590	49658
Total length (>= 5000 bp)	48458	49658
Total length (>= 10000 bp)	48458	49658
Total length (>= 25000 bp)	48458	49658
Total length (>= 50000 bp)	0	0
# contigs	3	3
Largest contig	48458	49658
Total length	50304	51135
Reference length	54999	54999
GC (%)	45.77	45.73
Reference GC (%)	45.96	45.96
N50	48458	49658
NG50	48458	49658
N75	48458	49658
NG75	48458	49658
L50	1	1
LG50	1	1
L75	1	1
LG75	1	1
# misassemblies	1	0
# misassembled contigs	1	0
Misassembled contigs length	48458	0
# local misassemblies	0	0
# scaffold gap size misassemblies	0	0
# unaligned mis. contigs	1	0
# unaligned contigs	0 + 1 part	0 + 0 part
Unaligned length	665	0
Genome fraction (%)	90.254	91.920
Duplication ratio	1.000	1.011
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	26.19	25.71
# indels per 100 kbp	0.00	0.00
Largest alignment	37178	49658
Total aligned length	49639	50555
NA50	37178	49658
NGA50	37178	49658
NA75	11280	49658
NGA75	11280	49658
LA50	1	1
LGA50	1	1
LA75	2	1
LGA75	2	1

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	1	0
# relocations	1	0
# translocations	0	0
# inversions	0	0
# interspecies translocations	2	1
# misassembled contigs	1	0
Misassembled contigs length	48458	0
# possibly misassembled contigs	0	0
# possible misassemblies	0	0
# local misassemblies	0	0
# scaffold gap size misassemblies	0	0
# unaligned mis. contigs	1	0
# mismatches	13	13
# indels	0	0
# indels (<= 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	0	0

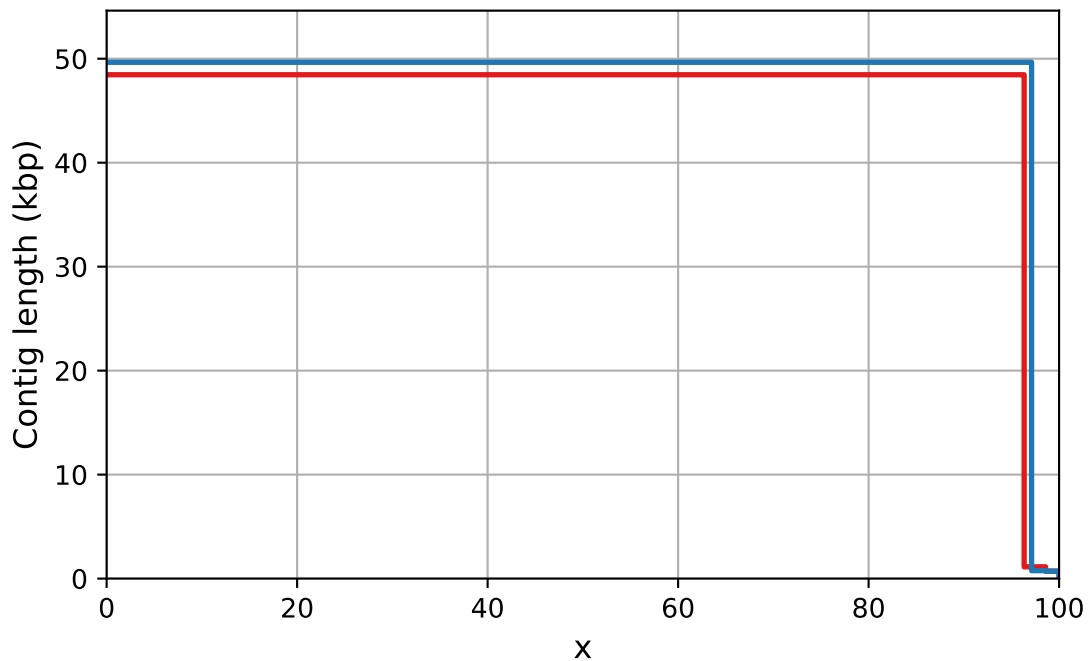
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	1	0
Partially unaligned length	665	0
# N's	0	0

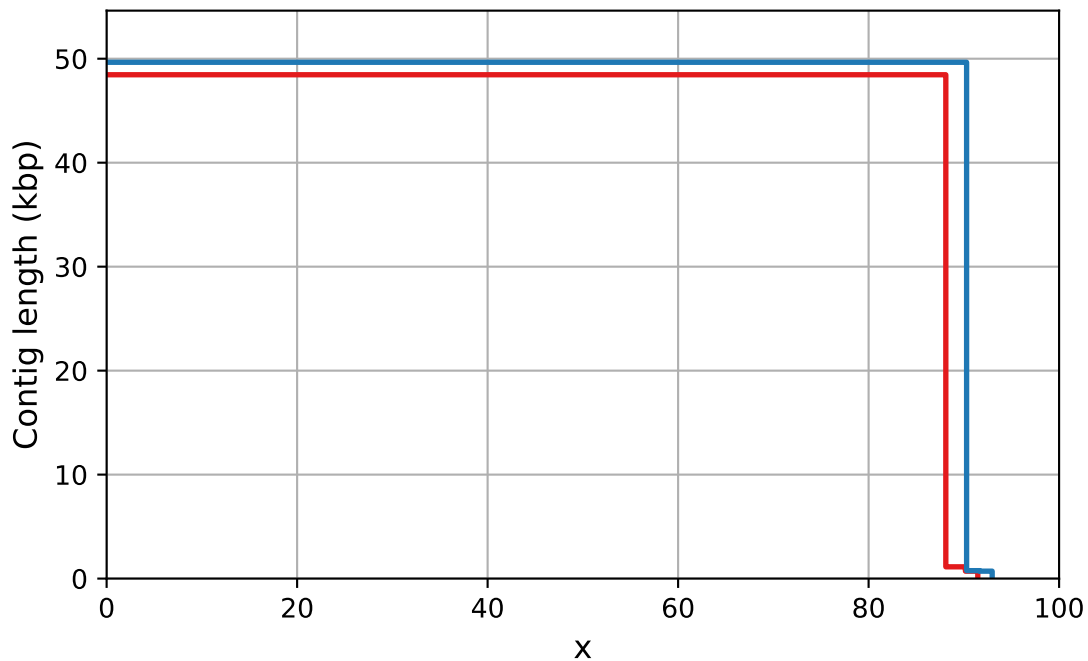
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



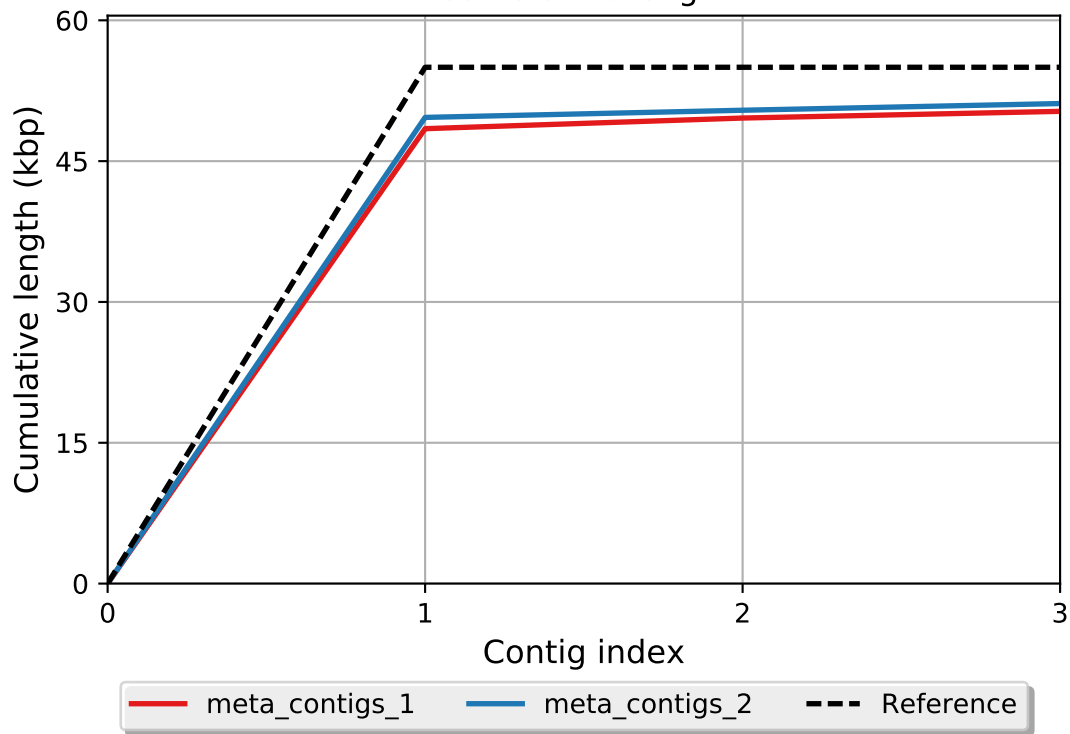
— meta_contigs_1 — meta_contigs_2

NGx

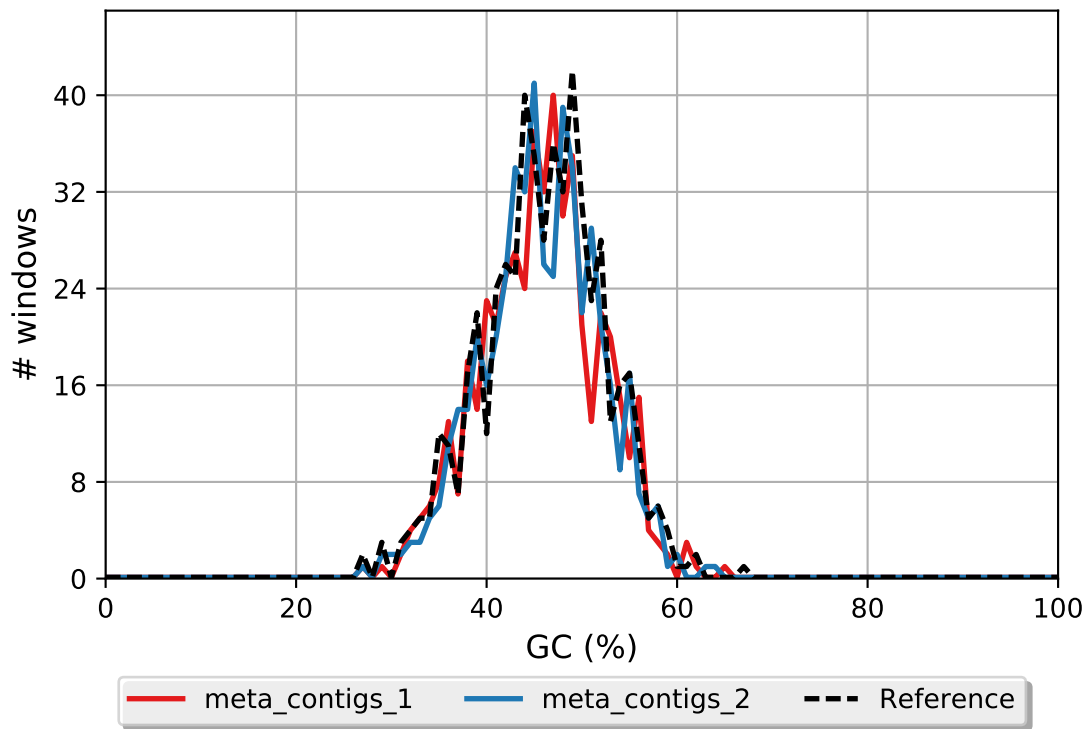


— meta_contigs_1 — meta_contigs_2

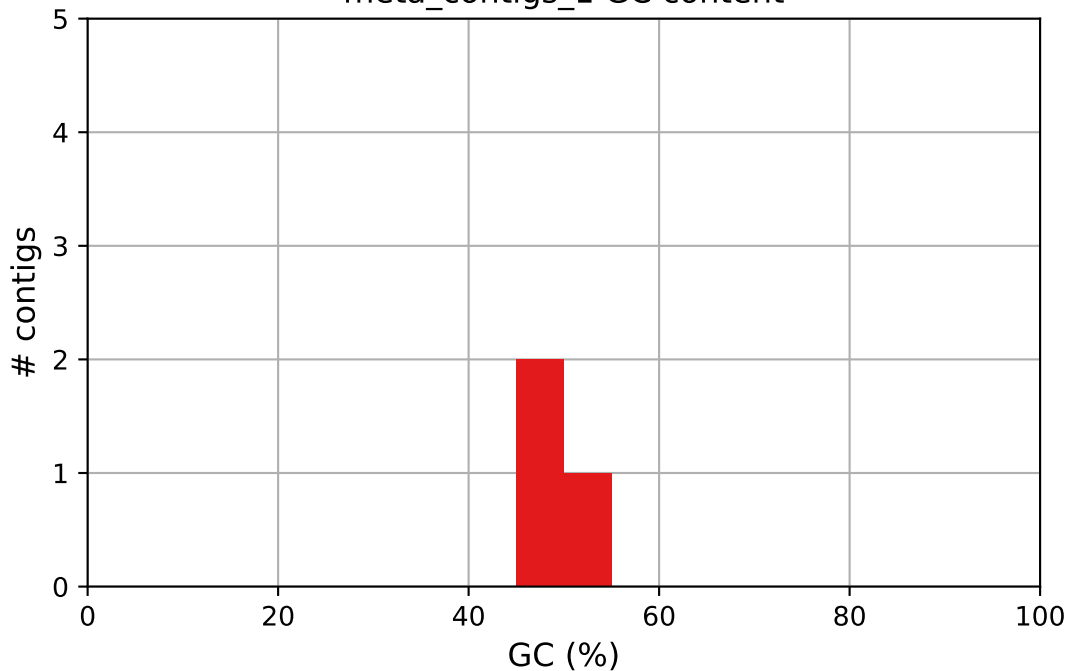
Cumulative length



GC content

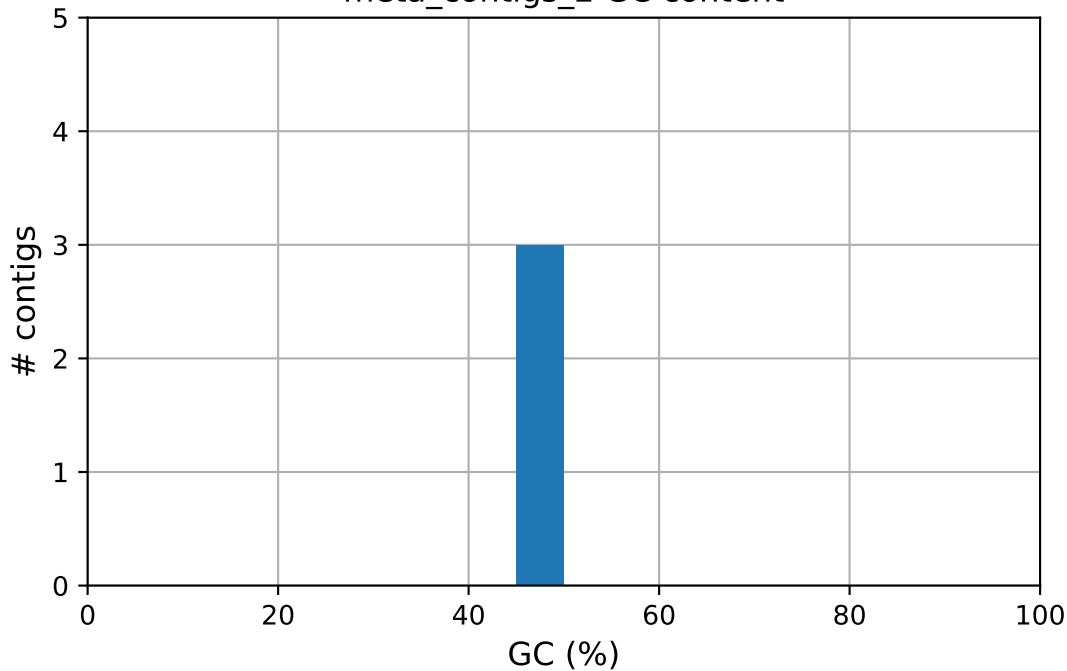


meta_contigs_1 GC content



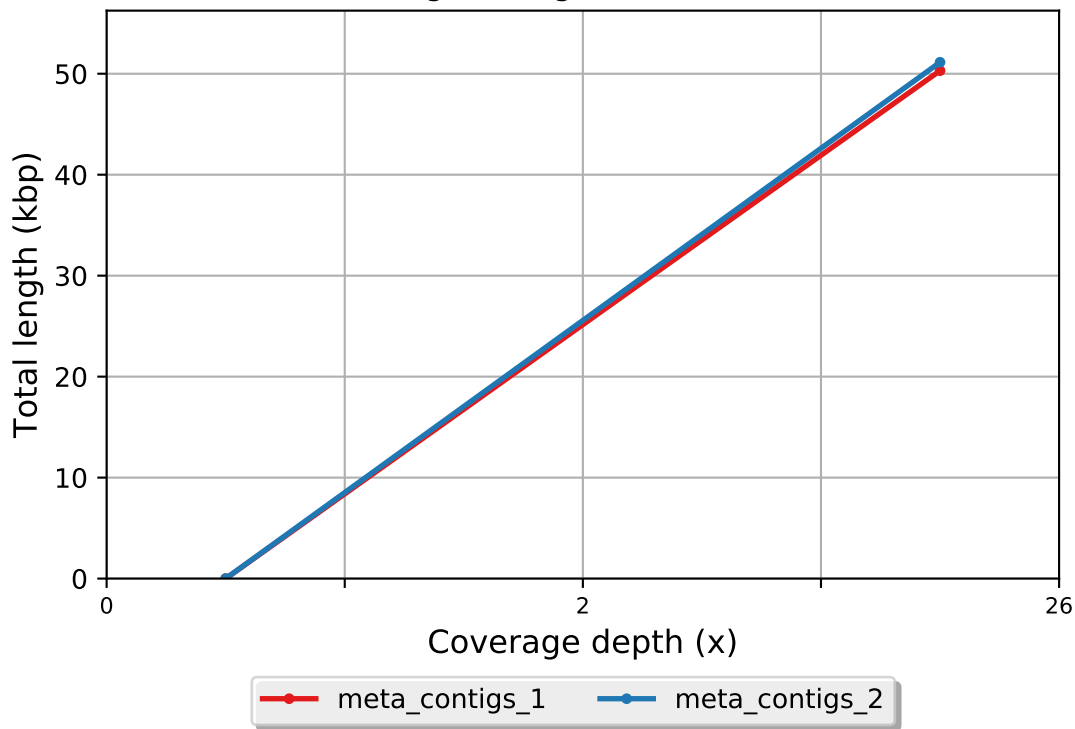
meta_contigs_1

meta_contigs_2 GC content

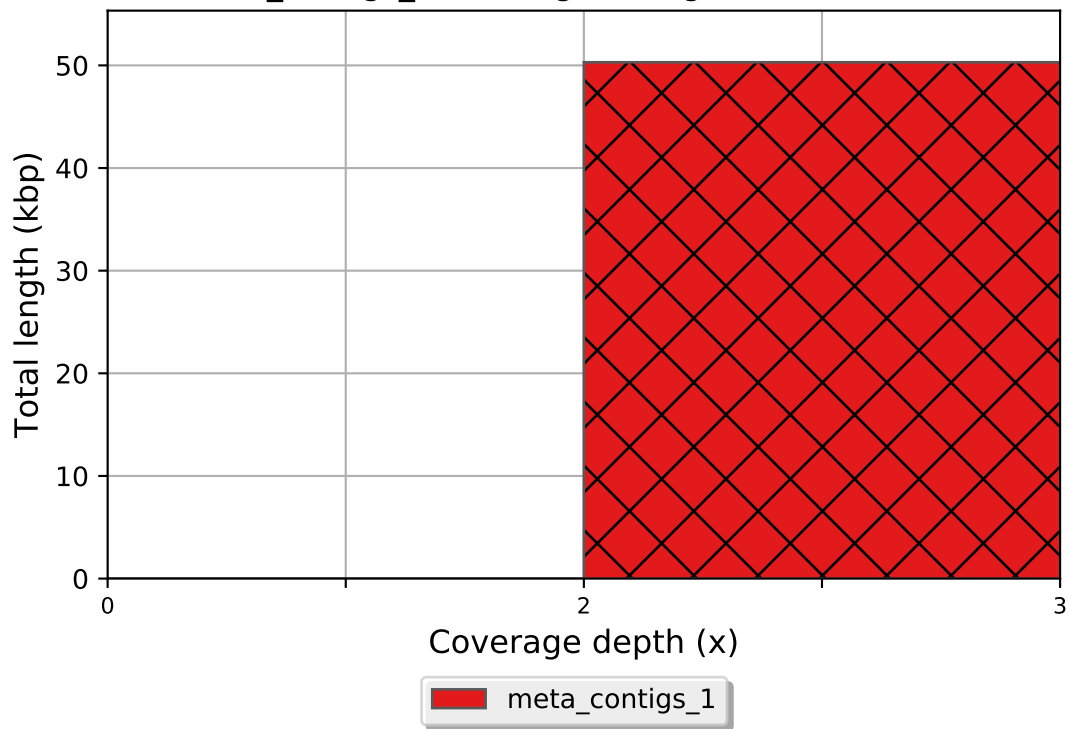


meta_contigs_2

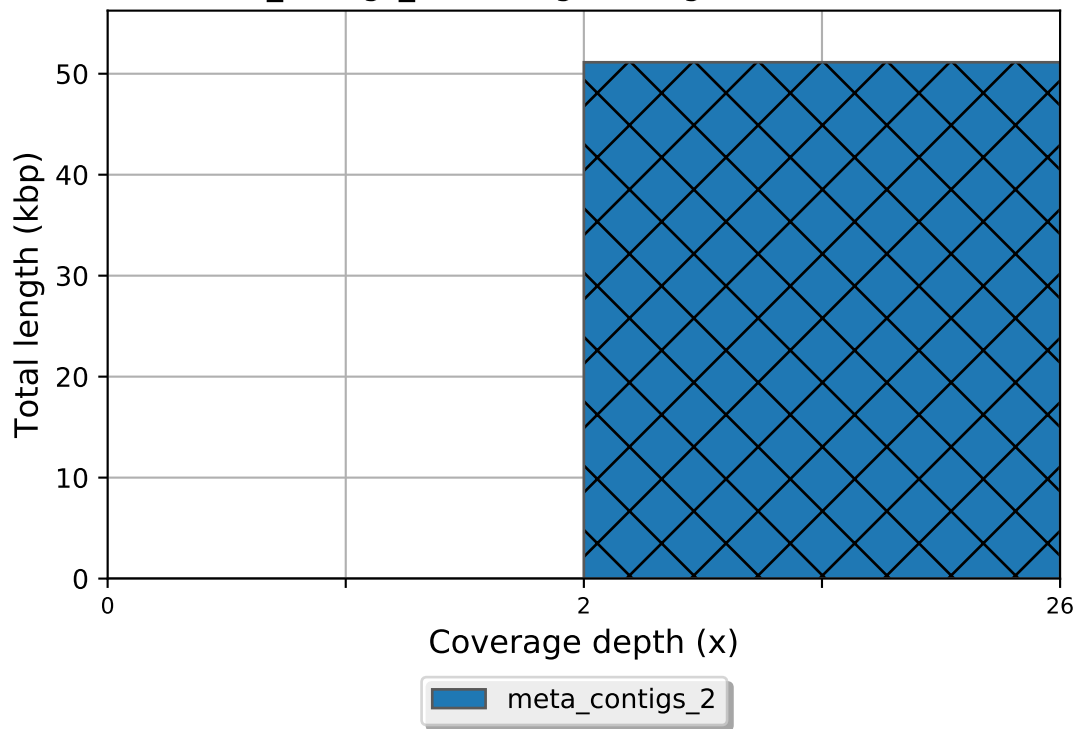
Coverage histogram (bin size: 1x)



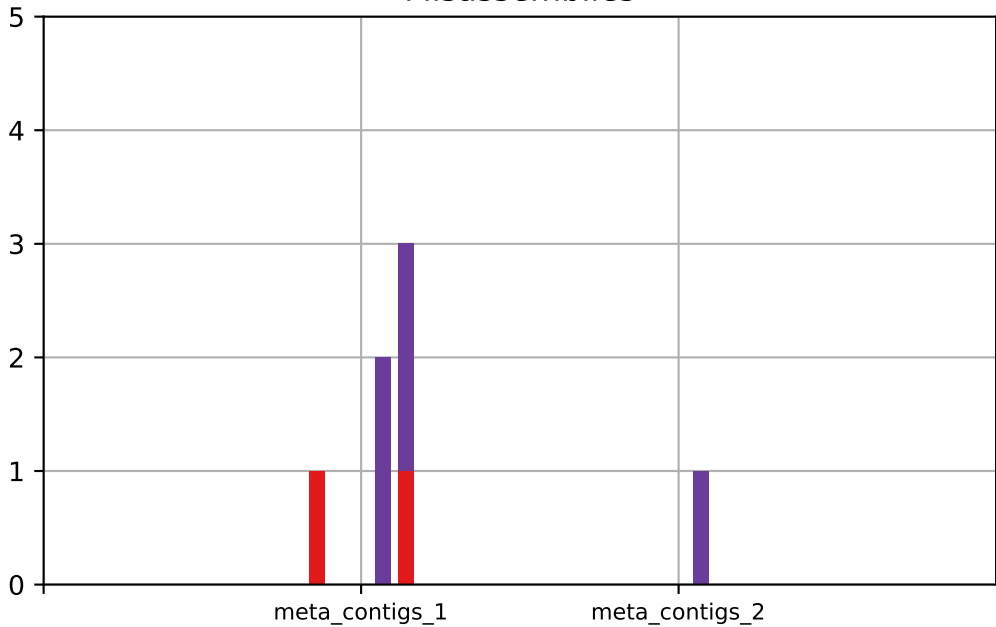
meta_contigs_1 coverage histogram (bin size: 1x)



meta_contigs_2 coverage histogram (bin size: 1x)



Misassemblies

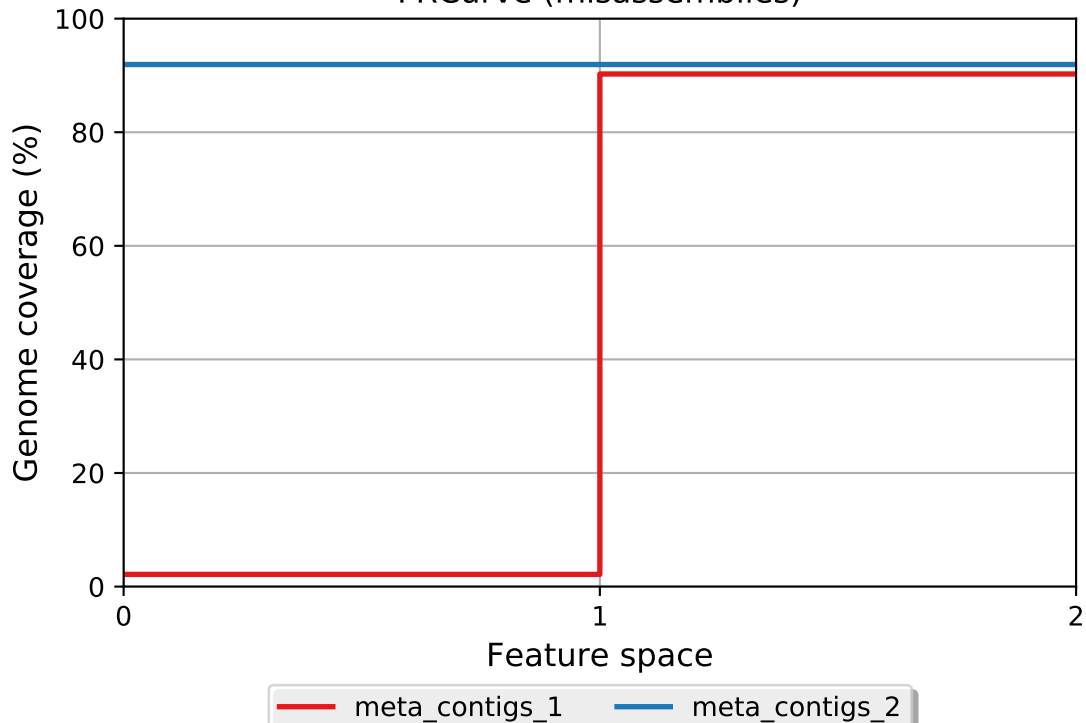


relocations

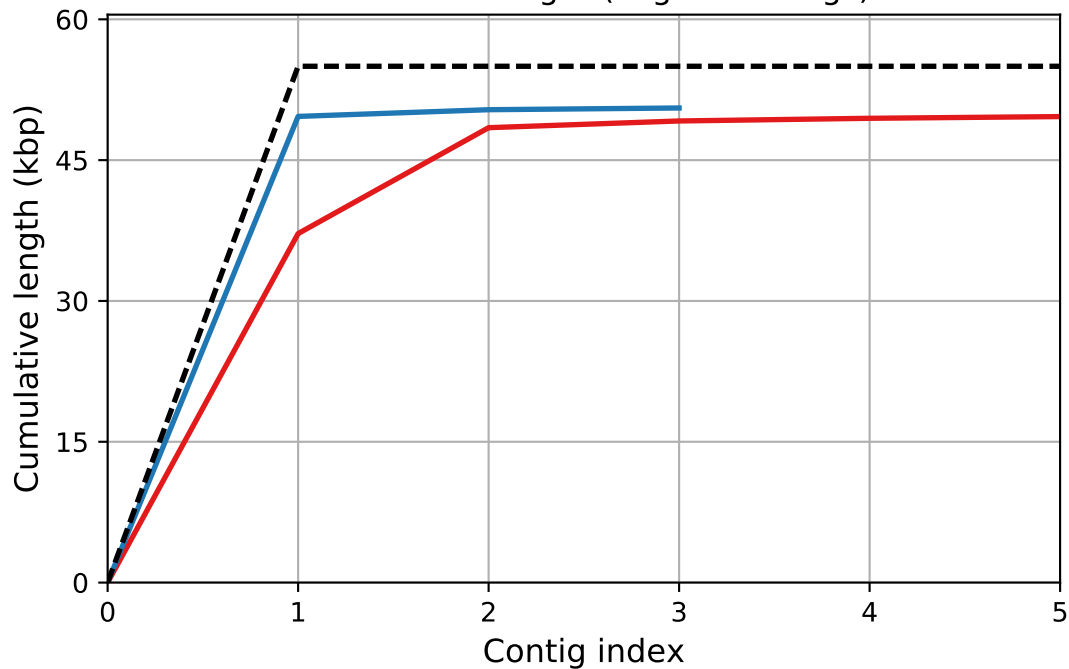


interspecies translocations

FRCurve (misassemblies)

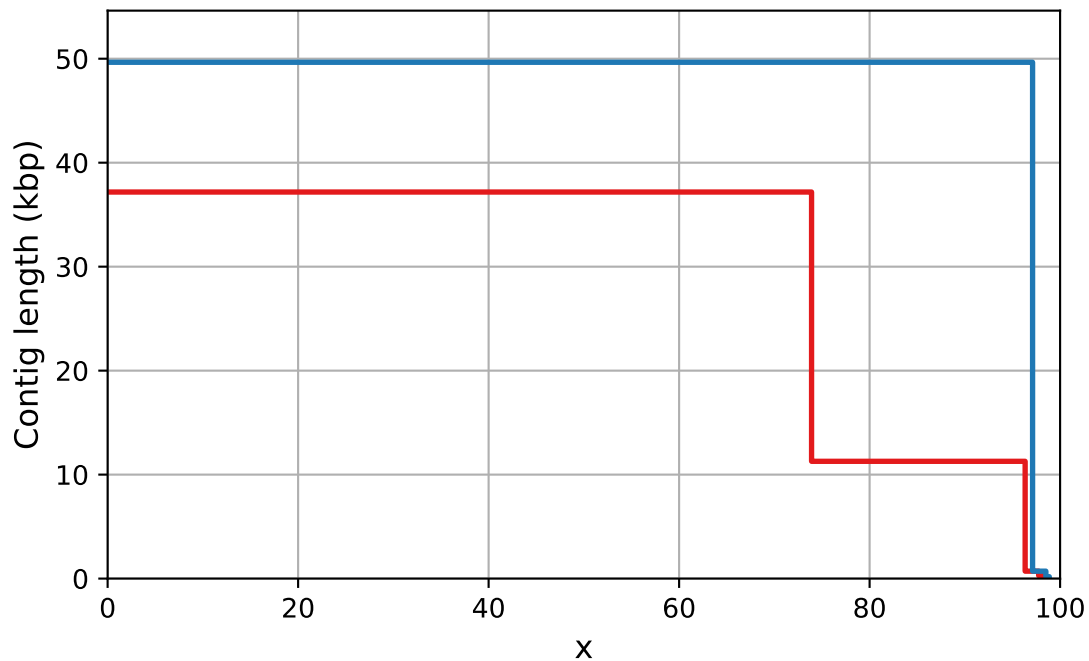


Cumulative length (aligned contigs)



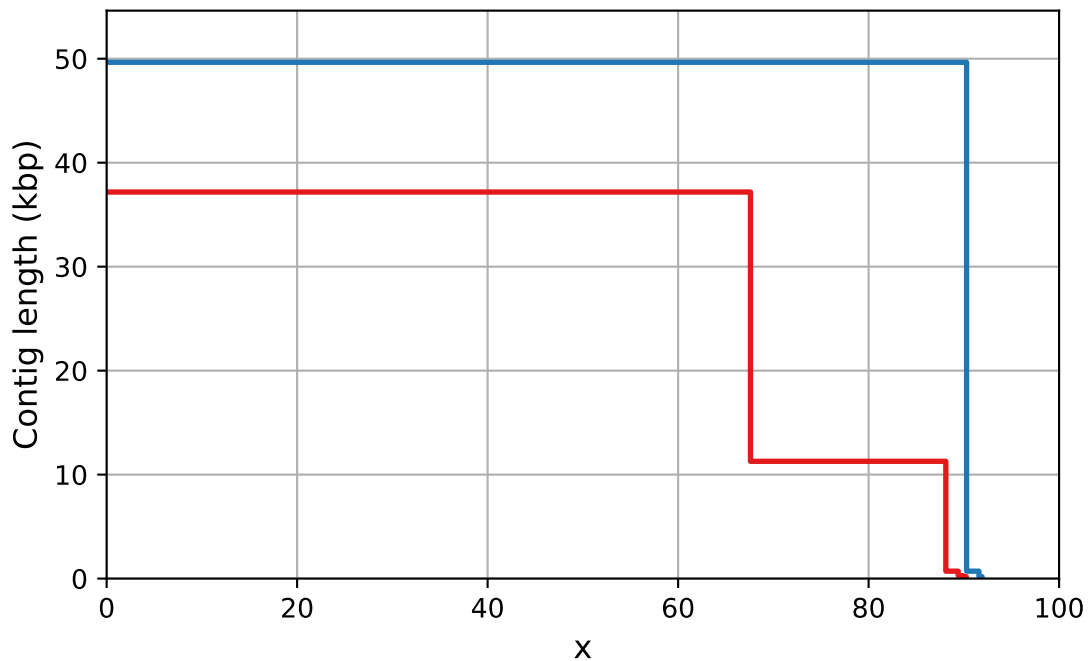
— meta_contigs_1 — meta_contigs_2 - - - Reference

NAx



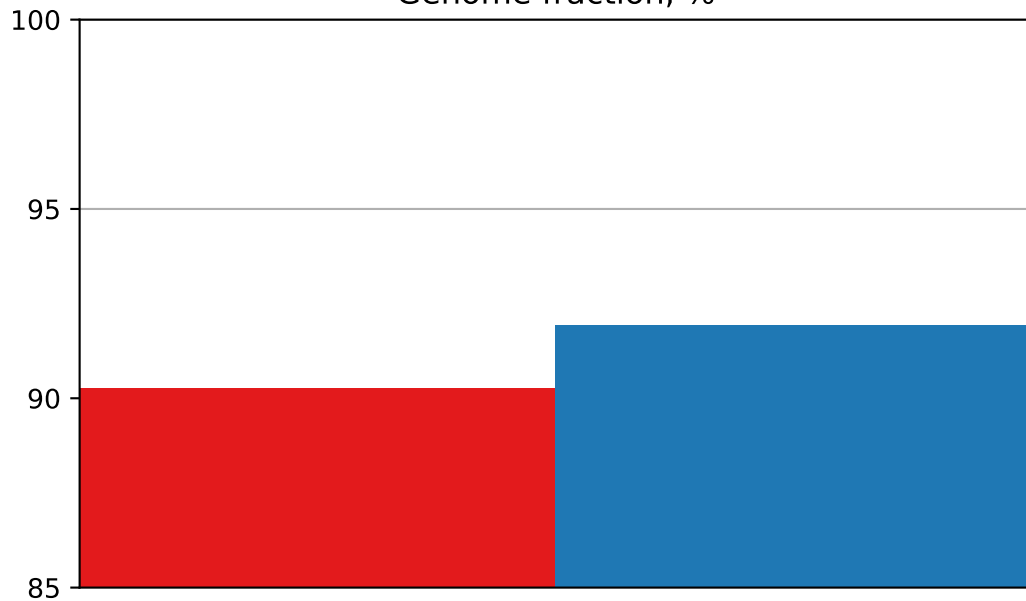
— meta_contigs_1 — meta_contigs_2

NGAx



— meta_contigs_1 — meta_contigs_2

Genome fraction, %



meta_contigs_1



meta_contigs_2