

Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 1000 bp)	3	2
# contigs (>= 5000 bp)	1	1
# contigs (>= 10000 bp)	1	1
# contigs (>= 25000 bp)	1	1
# contigs (>= 50000 bp)	1	1
Total length (>= 1000 bp)	57379	57668
Total length (>= 5000 bp)	55106	54221
Total length (>= 10000 bp)	55106	54221
Total length (>= 25000 bp)	55106	54221
Total length (>= 50000 bp)	55106	54221
# contigs	5	3
Largest contig	55106	54221
Total length	59158	58431
Reference length	59999	59999
GC (%)	50.17	50.11
Reference GC (%)	50.25	50.25
N50	55106	54221
NG50	55106	54221
N75	55106	54221
NG75	55106	54221
L50	1	1
LG50	1	1
L75	1	1
LG75	1	1
# misassemblies	0	1
# misassembled contigs	0	1
Misassembled contigs length	0	54221
# local misassemblies	0	0
# scaffold gap size misassemblies	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 1 part
Unaligned length	0	544
Genome fraction (%)	97.575	96.422
Duplication ratio	1.010	1.001
# N's per 100 kbp	1.69	0.00
# mismatches per 100 kbp	23.91	25.93
# indels per 100 kbp	0.00	0.00
Largest alignment	55106	36102
Total aligned length	58664	57887
NA50	55106	36102
NGA50	55106	36102
NA75	55106	18119
NGA75	55106	18119
LA50	1	1
LGA50	1	1
LA75	1	2
LGA75	1	2

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	0	1
# relocations	0	1
# translocations	0	0
# inversions	0	0
# interspecies translocations	2	1
# misassembled contigs	0	1
Misassembled contigs length	0	54221
# 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	14	15
# indels	0	0
# indels (<= 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	0	0

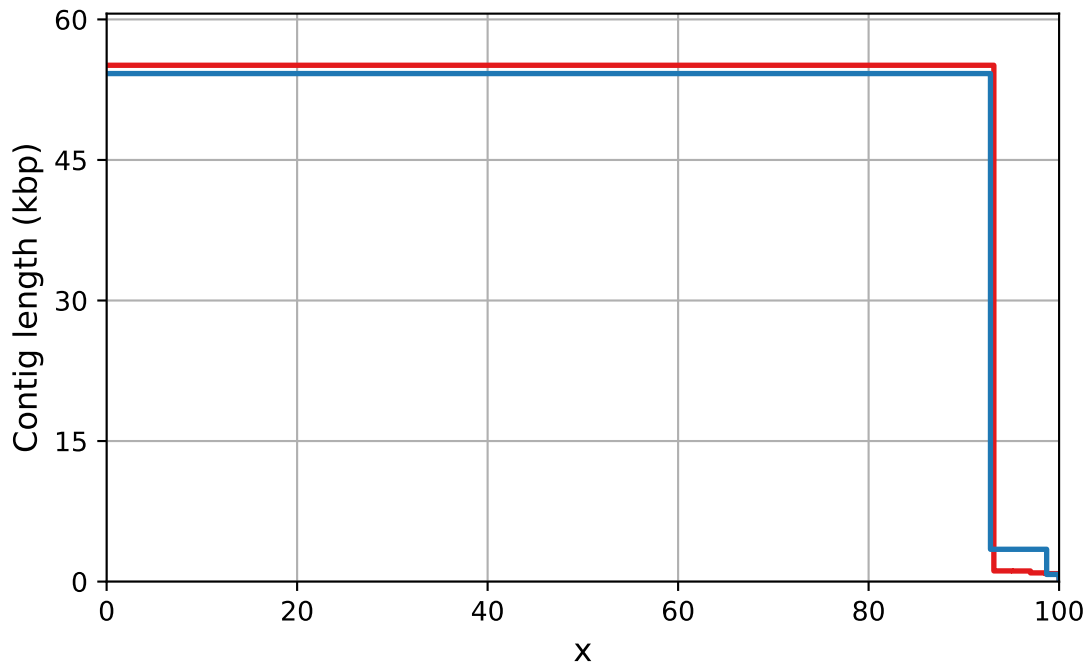
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	1
Partially unaligned length	0	544
# N's	1	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).

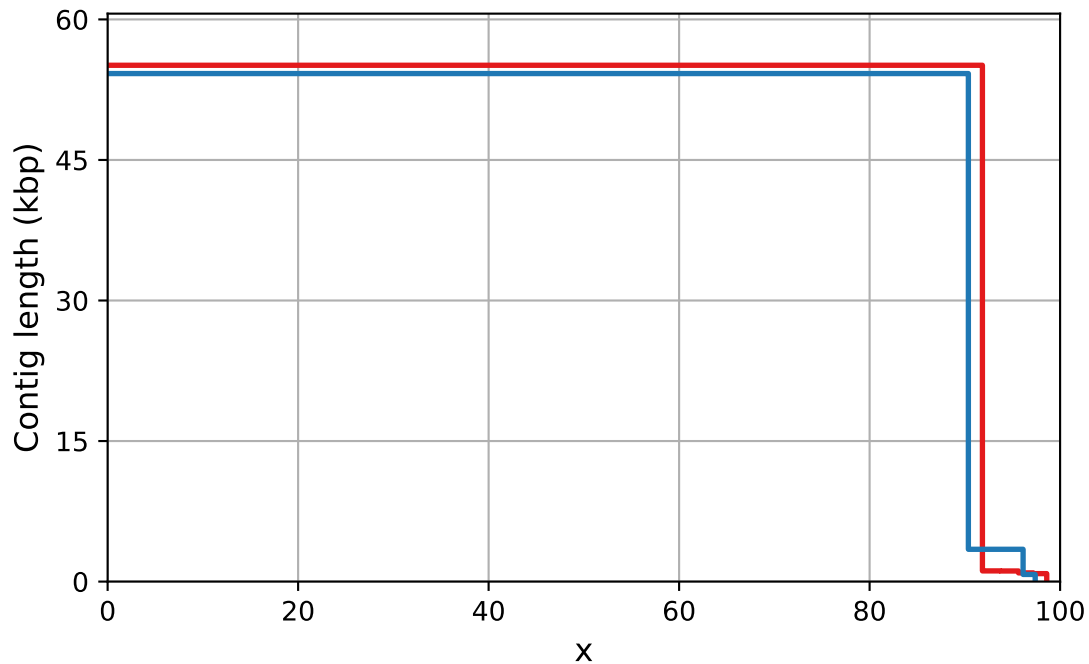
Nx



— meta_contigs_1

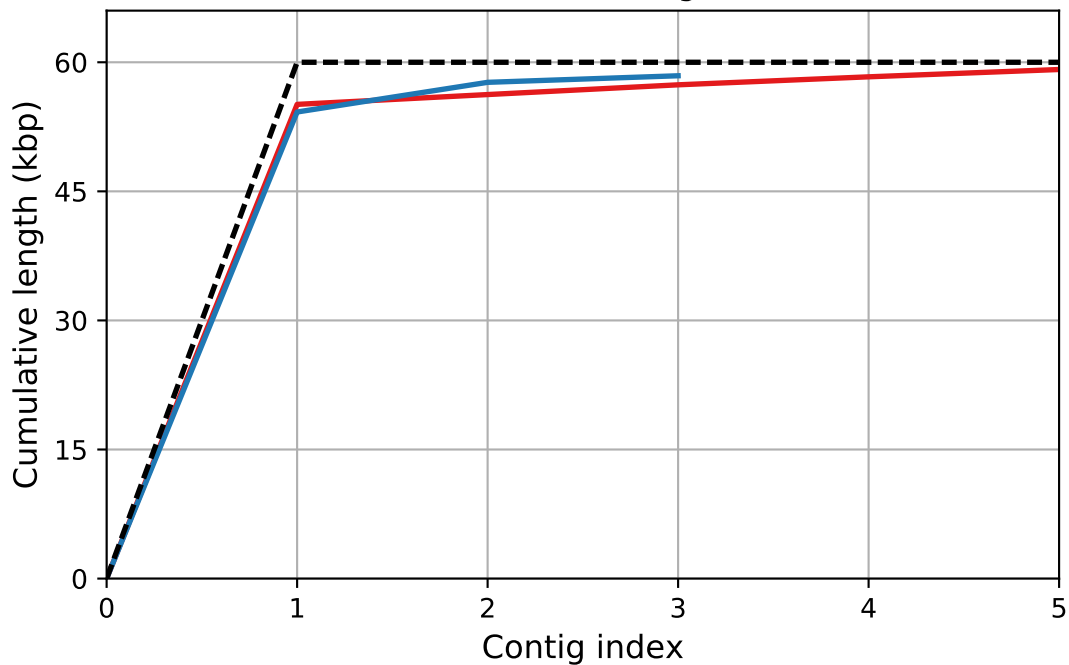
— meta_contigs_2

NGx



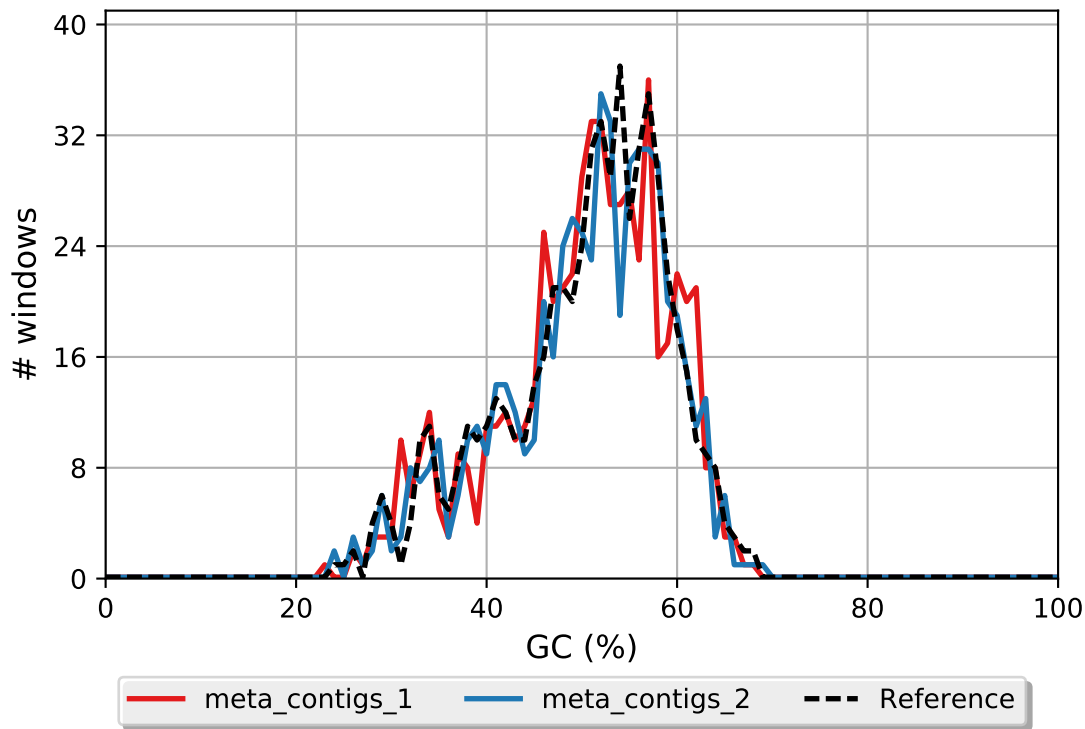
— meta_contigs_1 — meta_contigs_2

Cumulative length

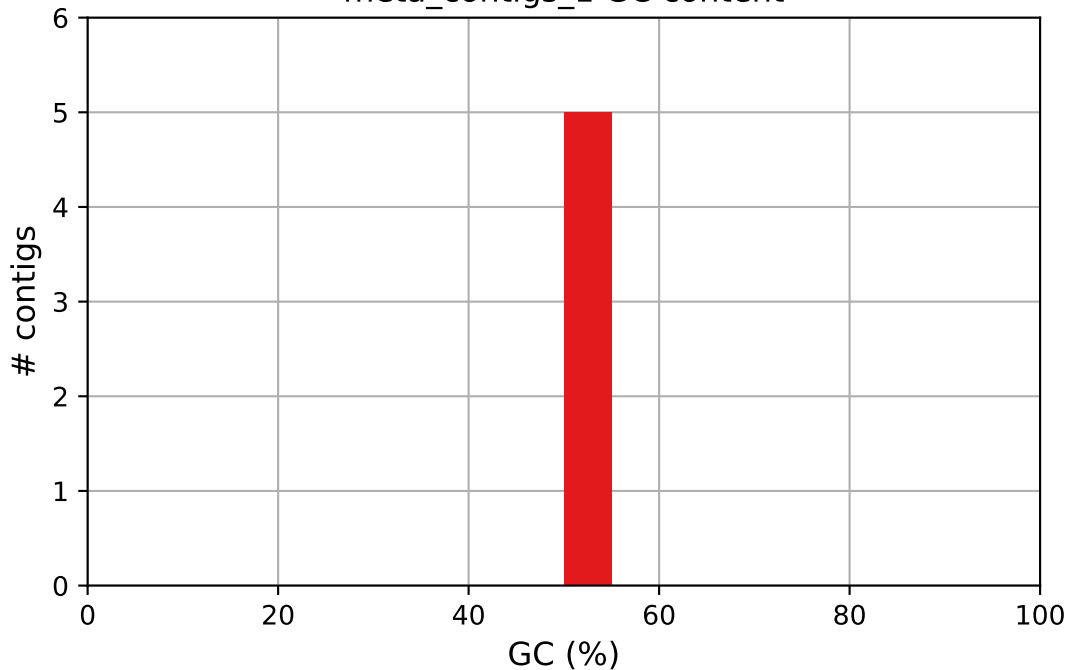


— meta_contigs_1 — meta_contigs_2 - - - Reference

GC content

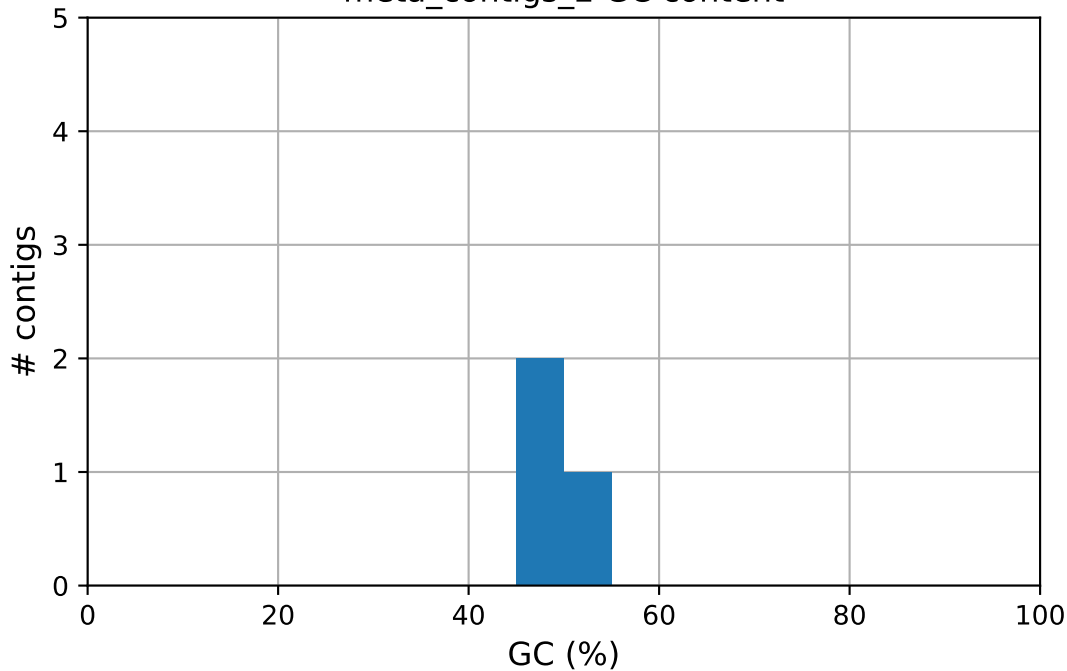


meta_contigs_1 GC content



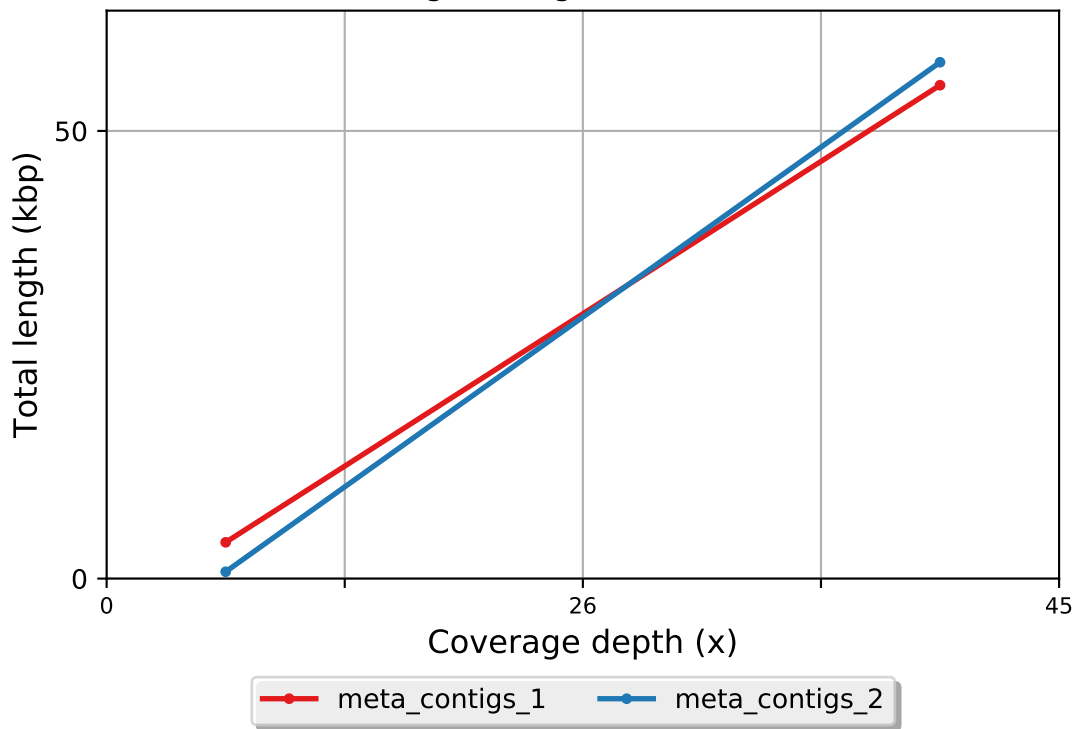
meta_contigs_1

meta_contigs_2 GC content

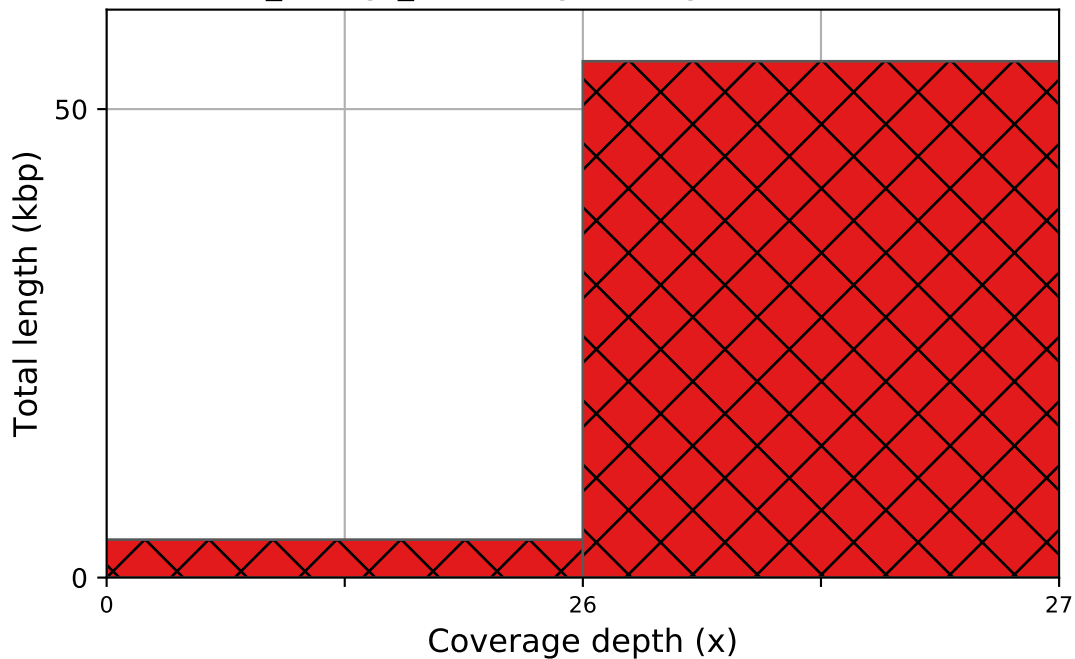


meta_contigs_2

Coverage histogram (bin size: 1x)

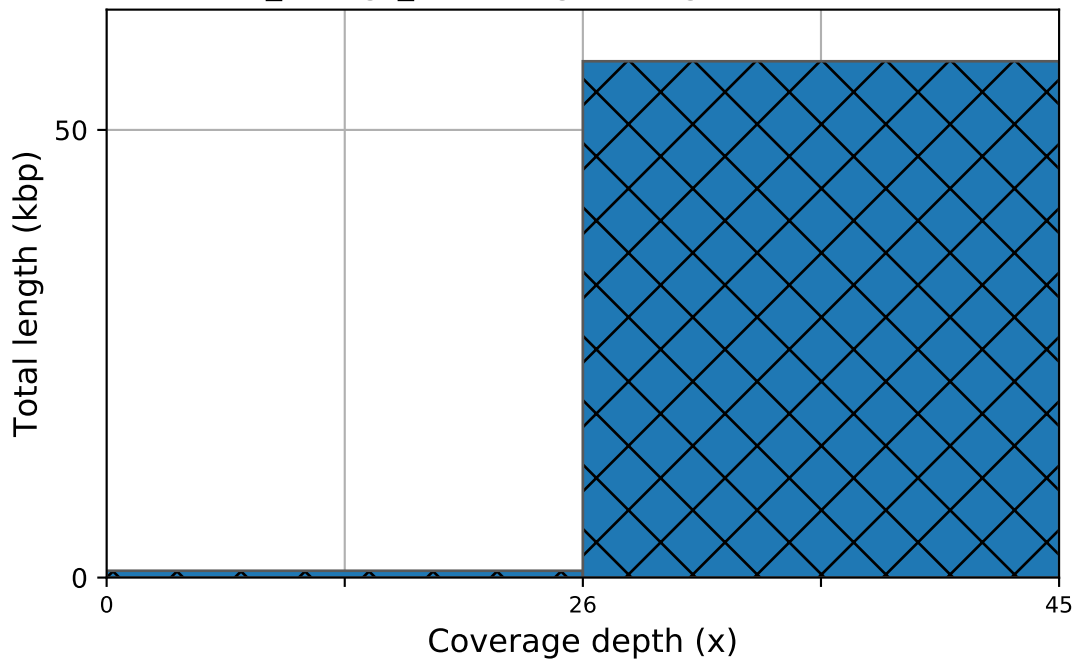


meta_contigs_1 coverage histogram (bin size: 1x)



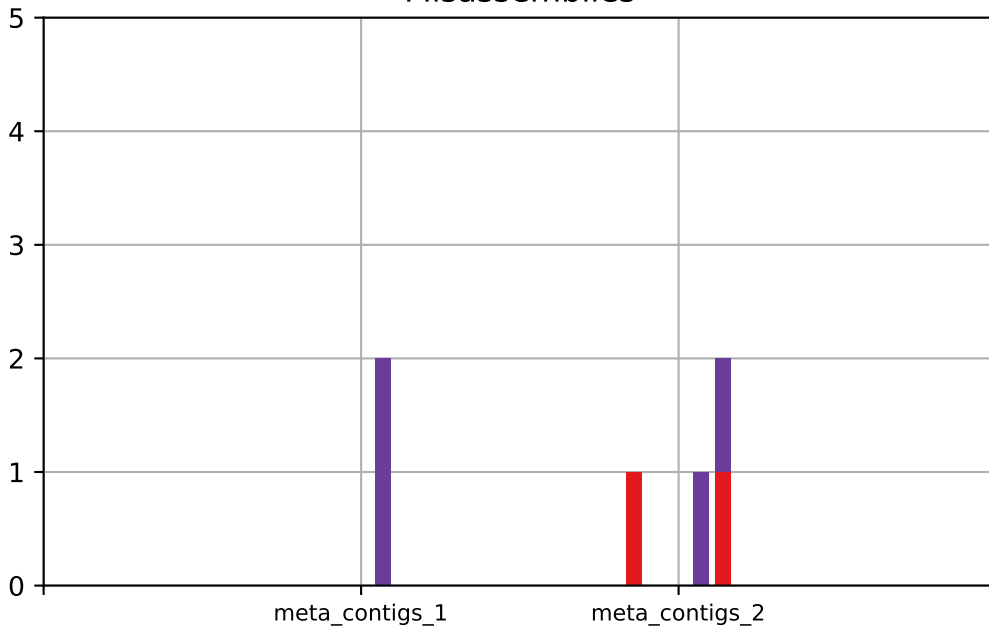
meta_contigs_1

meta_contigs_2 coverage histogram (bin size: 1x)



meta_contigs_2

Misassemblies

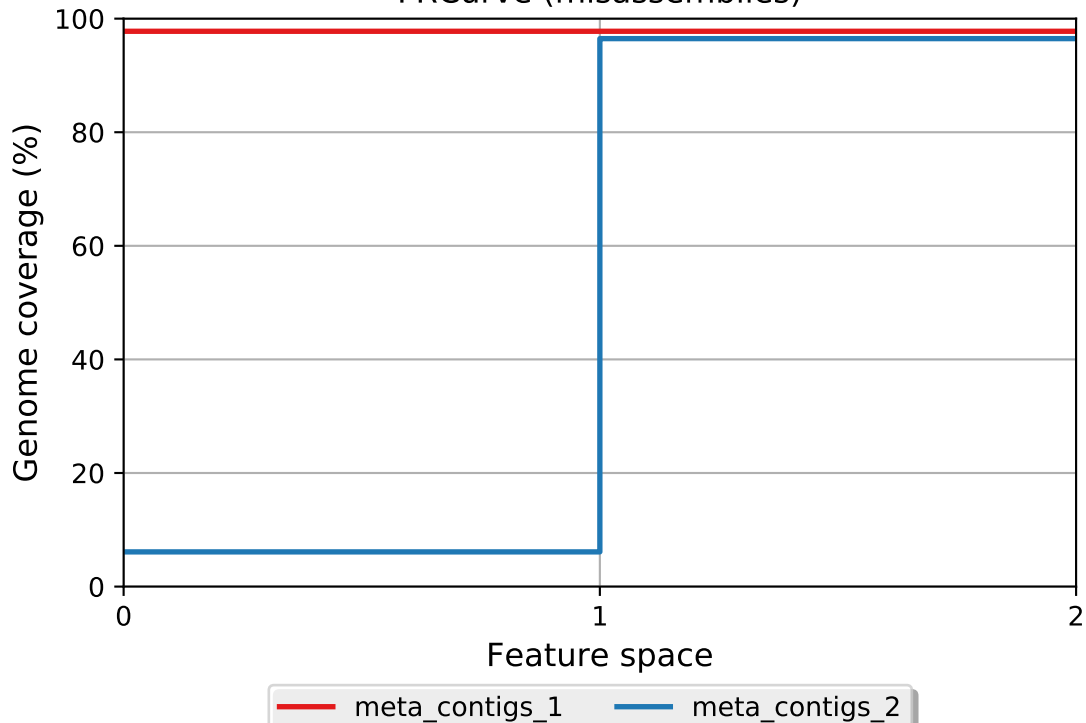


relocations

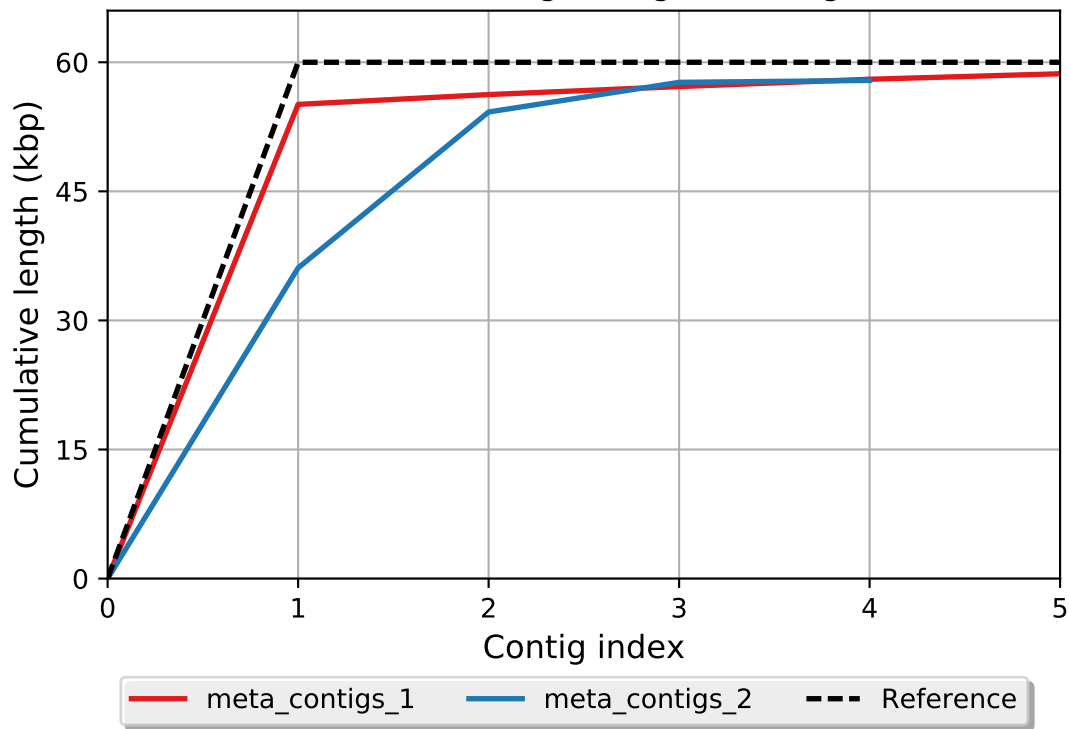


interspecies translocations

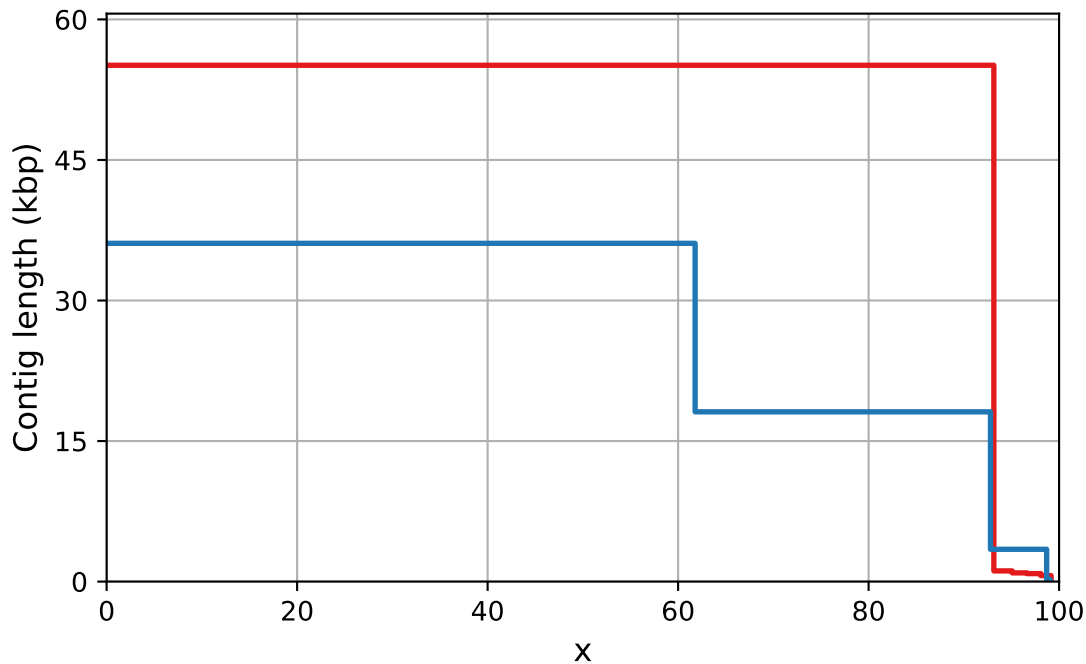
FRCurve (misassemblies)



Cumulative length (aligned contigs)

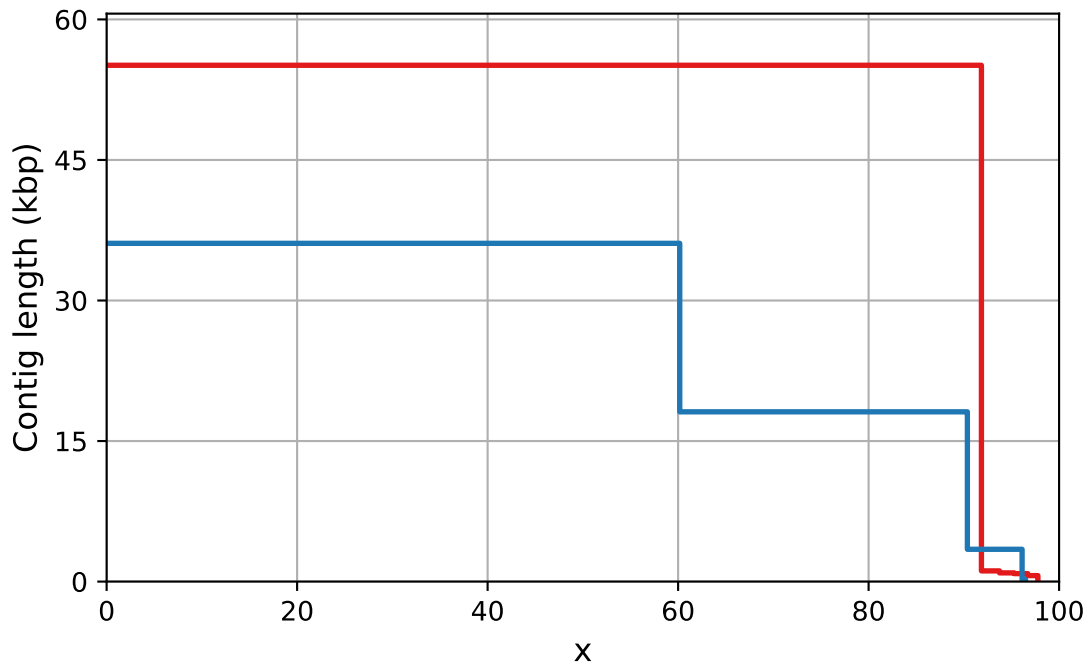


NAx



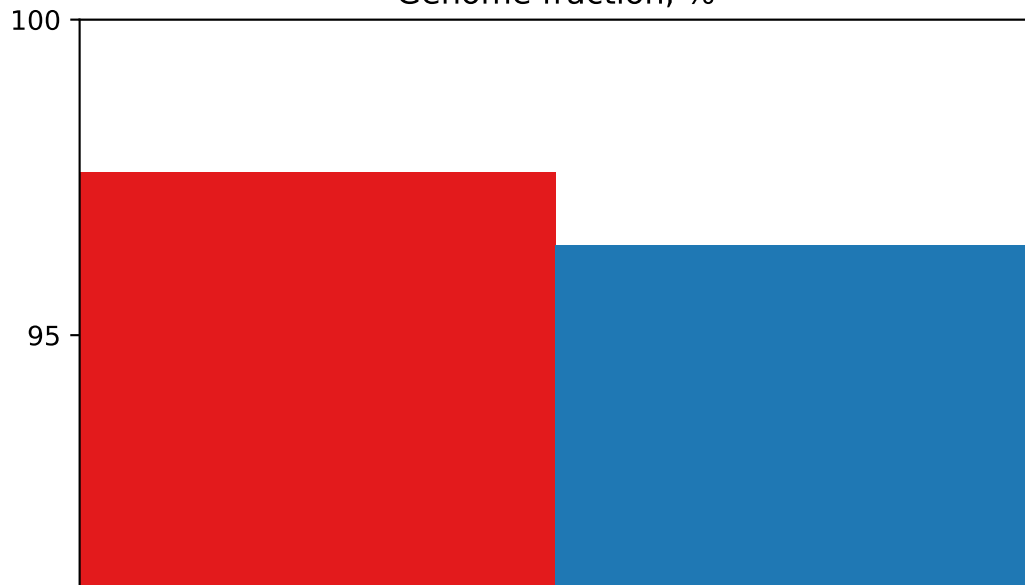
— meta_contigs_1 — meta_contigs_2

NGAx



— meta_contigs_1 — meta_contigs_2

Genome fraction, %



meta_contigs_1



meta_contigs_2