

Report

	meta_contigs_1	meta_contigs_2
# contigs (>= 1000 bp)	6	4
# contigs (>= 5000 bp)	3	4
# contigs (>= 10000 bp)	3	3
# contigs (>= 25000 bp)	1	1
# contigs (>= 50000 bp)	0	0
Total length (>= 1000 bp)	64988	60775
Total length (>= 5000 bp)	56606	60775
Total length (>= 10000 bp)	56606	53787
Total length (>= 25000 bp)	27969	27260
Total length (>= 50000 bp)	0	0
# contigs	11	8
Largest contig	27969	27260
Total length	69110	63778
Reference length	64999	64999
GC (%)	40.75	40.78
Reference GC (%)	40.73	40.73
N50	17535	16099
NG50	17535	16099
N75	11102	10428
NG75	11102	10428
L50	2	2
LG50	2	2
L75	3	3
LG75	3	3
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	1
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	98.397	96.609
Duplication ratio	1.081	1.016
# N's per 100 kbp	18.81	0.00
# mismatches per 100 kbp	65.67	27.07
# indels per 100 kbp	3.13	0.00
Largest alignment	27969	27260
Total aligned length	69108	63351
NA50	17534	16099
NGA50	17534	16099
NA75	11101	10428
NGA75	11101	10428
LA50	2	2
LGA50	2	2
LA75	3	3
LGA75	3	3

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

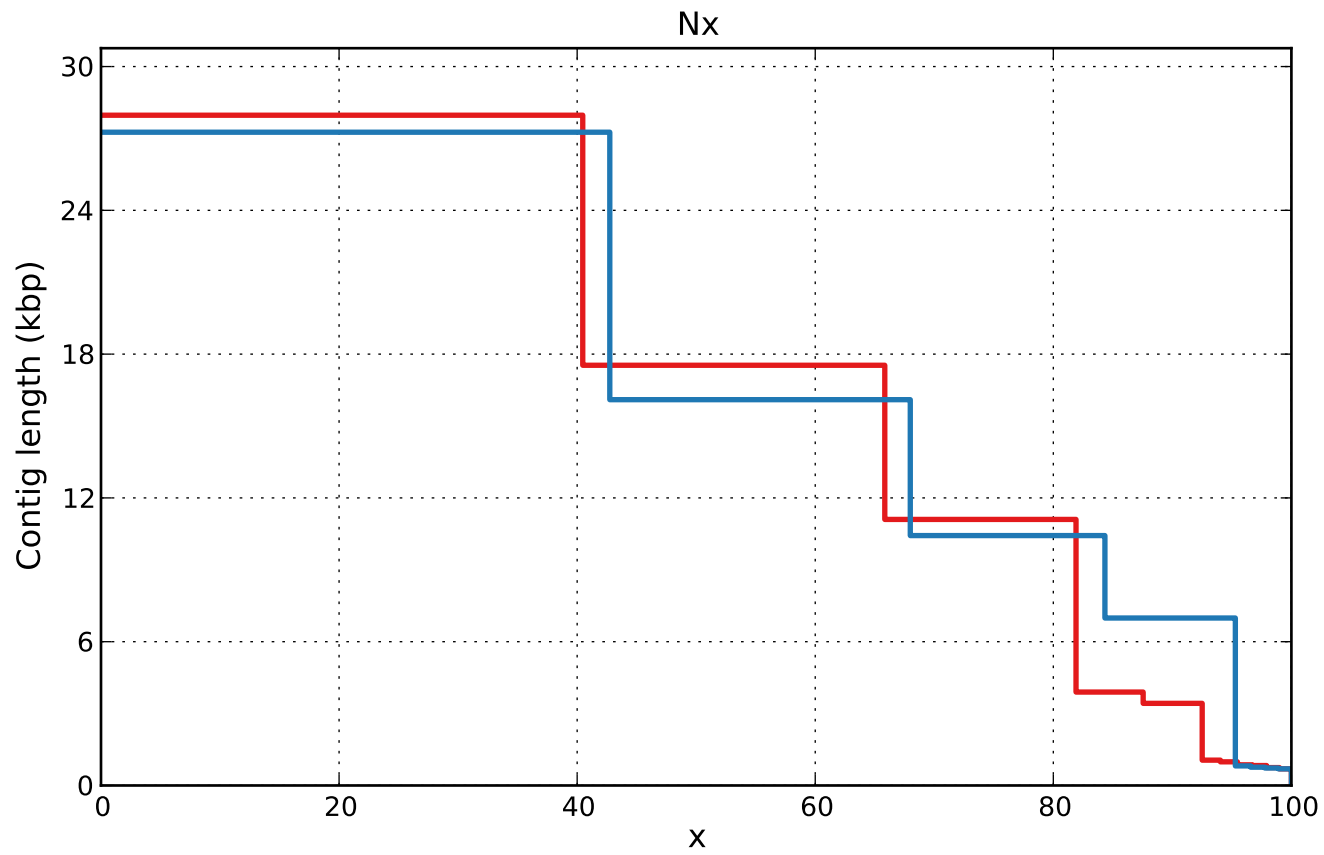
	meta_contigs_1	meta_contigs_2
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# possibly misassembled contigs	0	0
# possible misassemblies	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	1
# mismatches	42	17
# 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  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

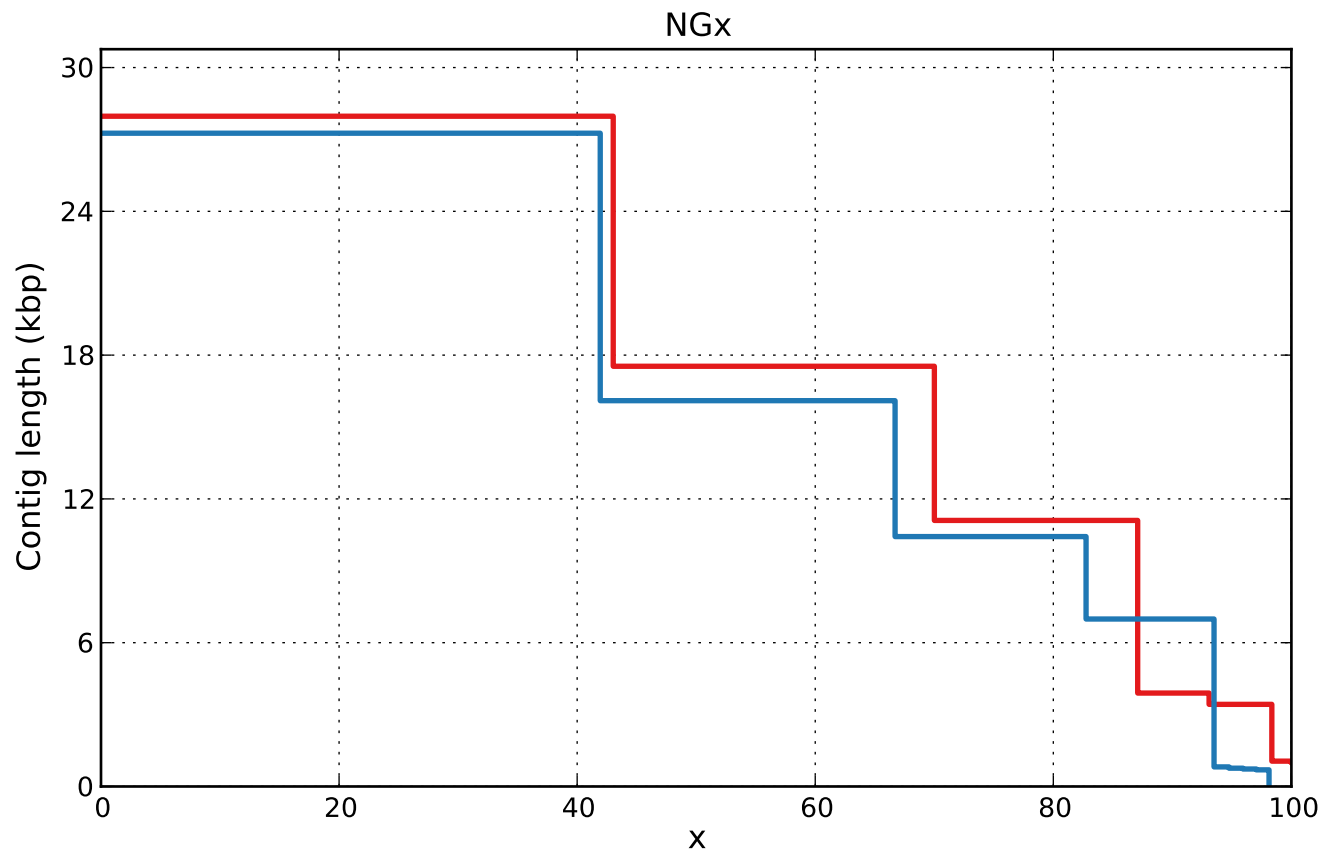
## Unaligned report

	meta_contigs_1	meta_contigs_2
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	13	0

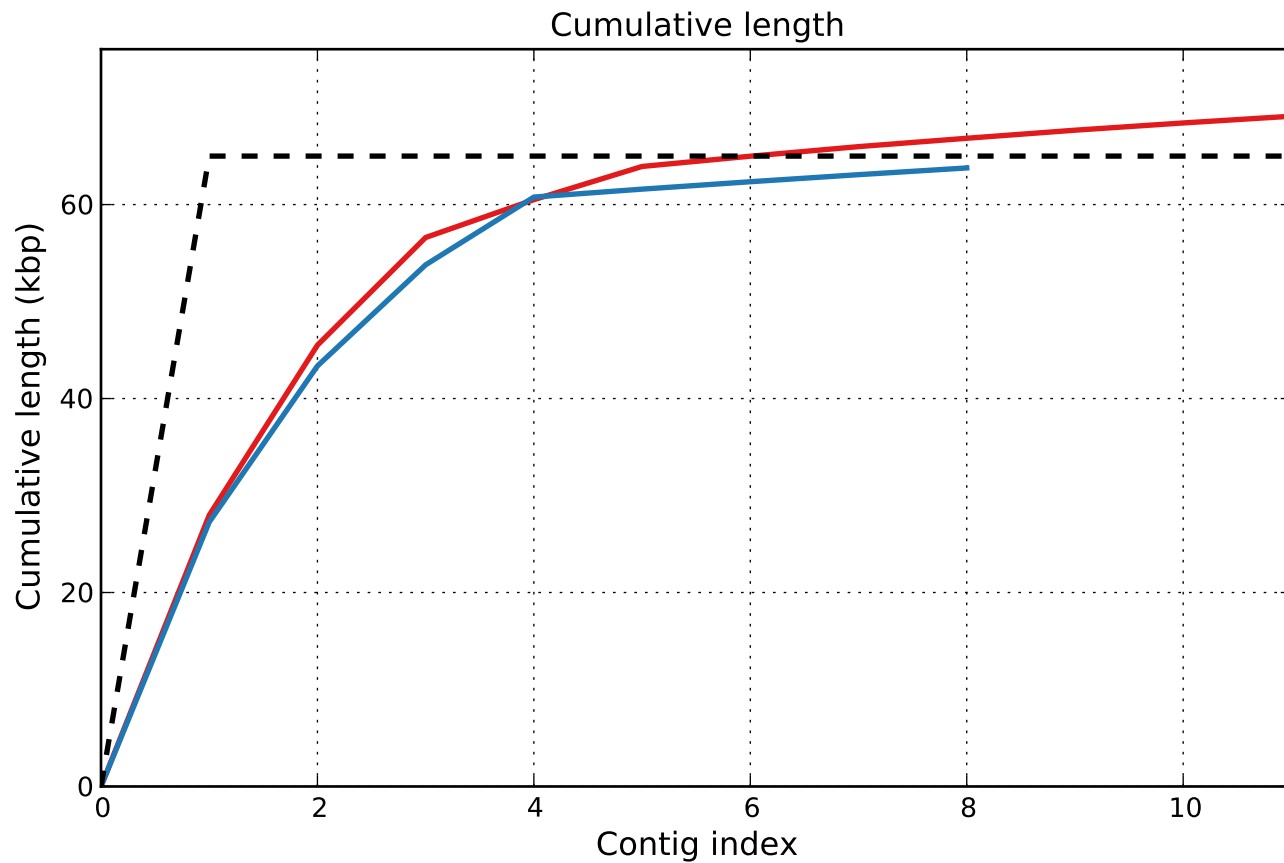
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



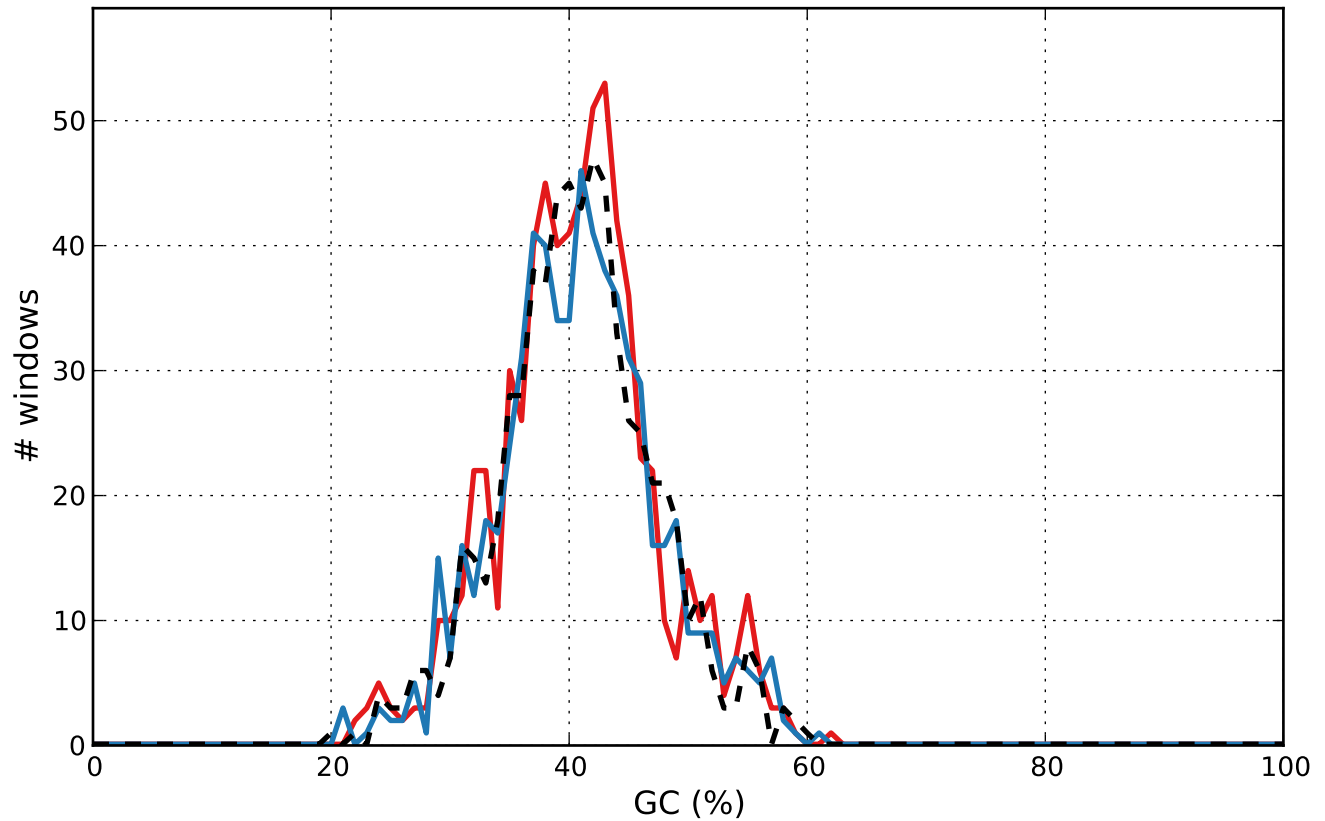
— meta\_contigs\_1 — meta\_contigs\_2



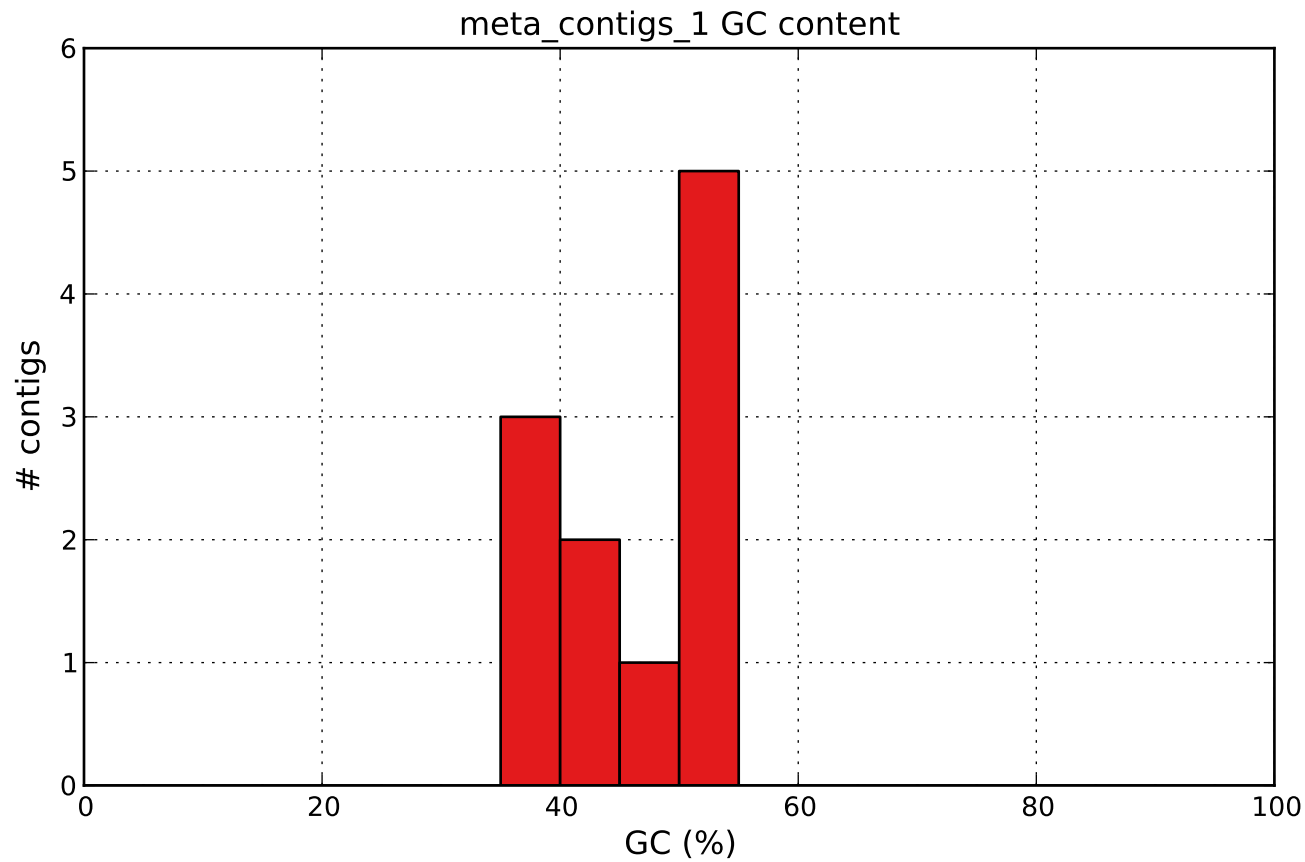
— meta\_contigs\_1 — meta\_contigs\_2



GC content

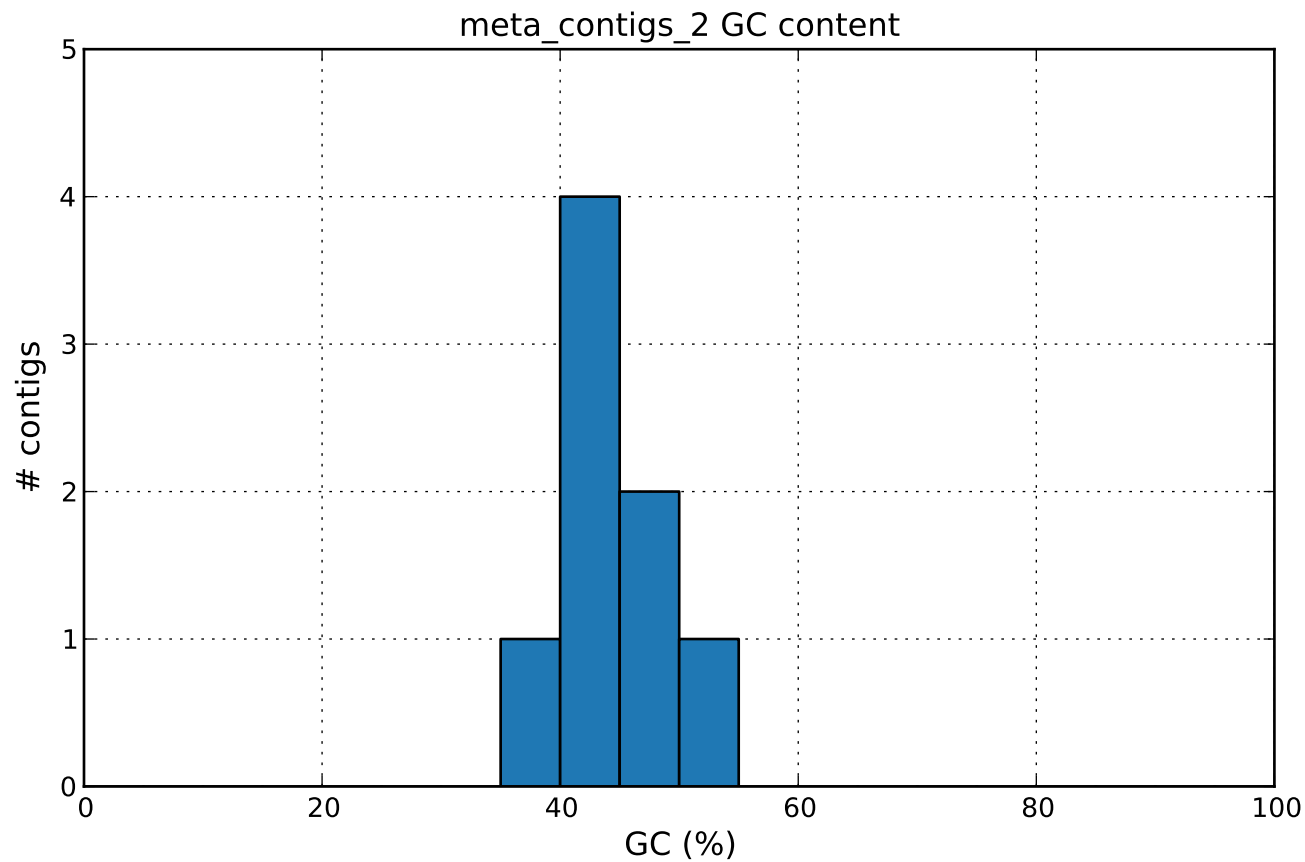


— meta\_contigs\_1    — meta\_contigs\_2    - - Reference



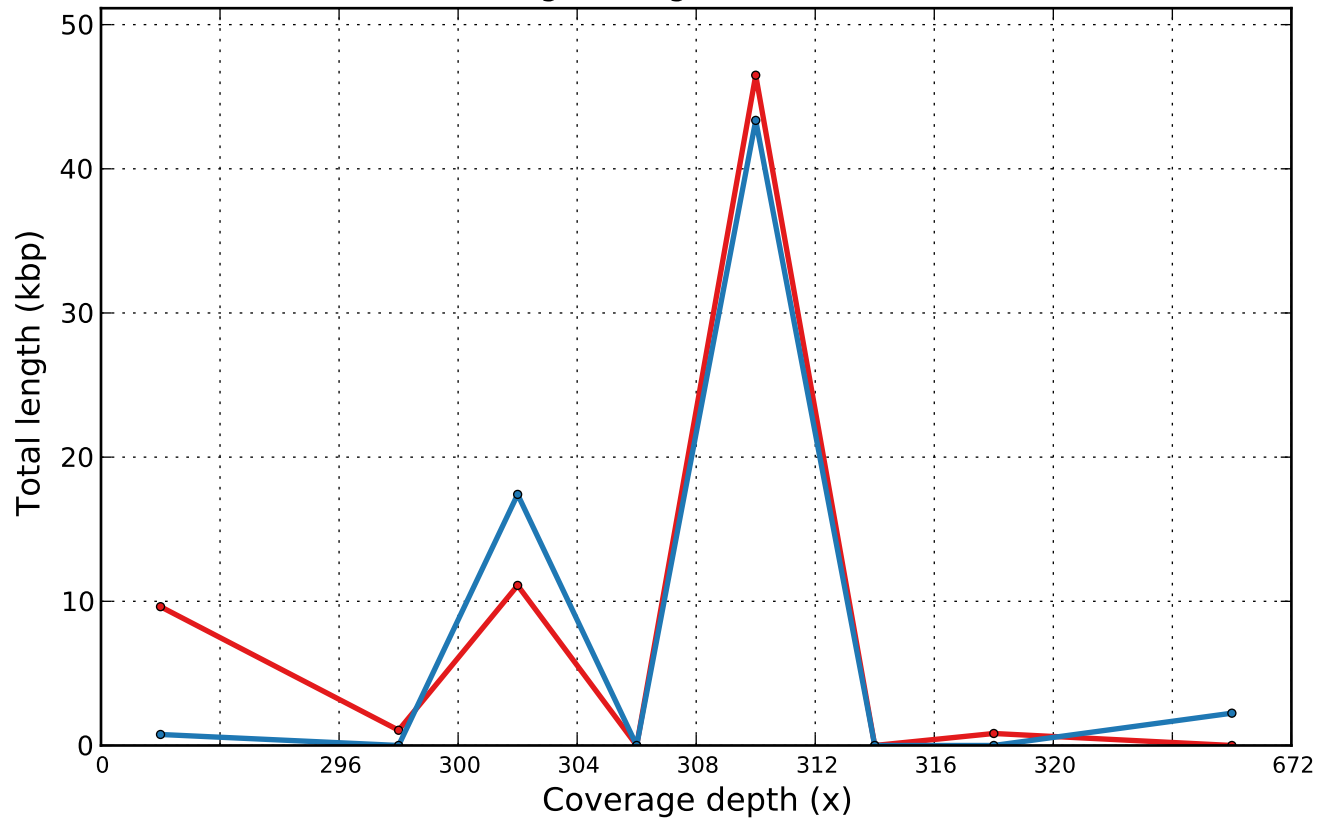
meta\_contigs\_1





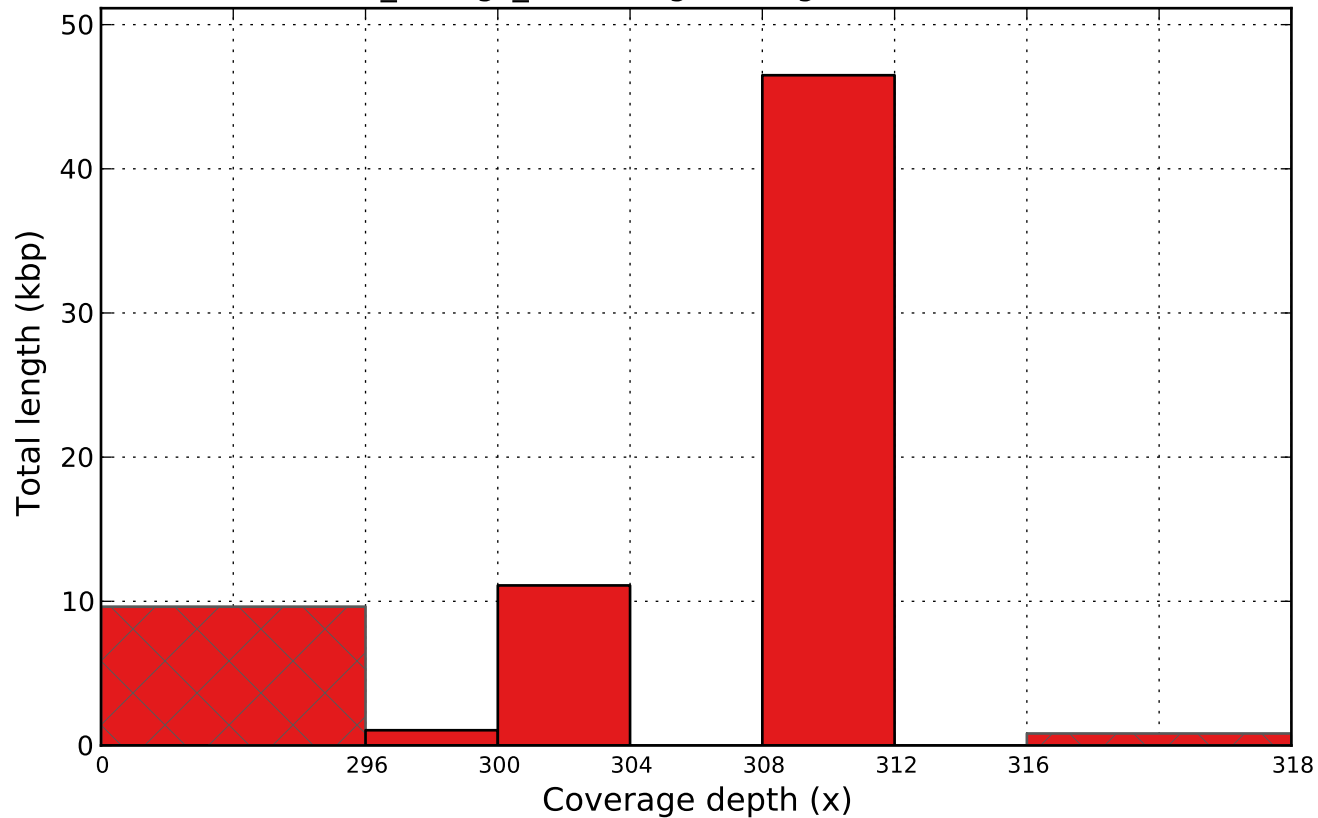
meta\_contigs\_2

Coverage histogram (bin size: 4x)



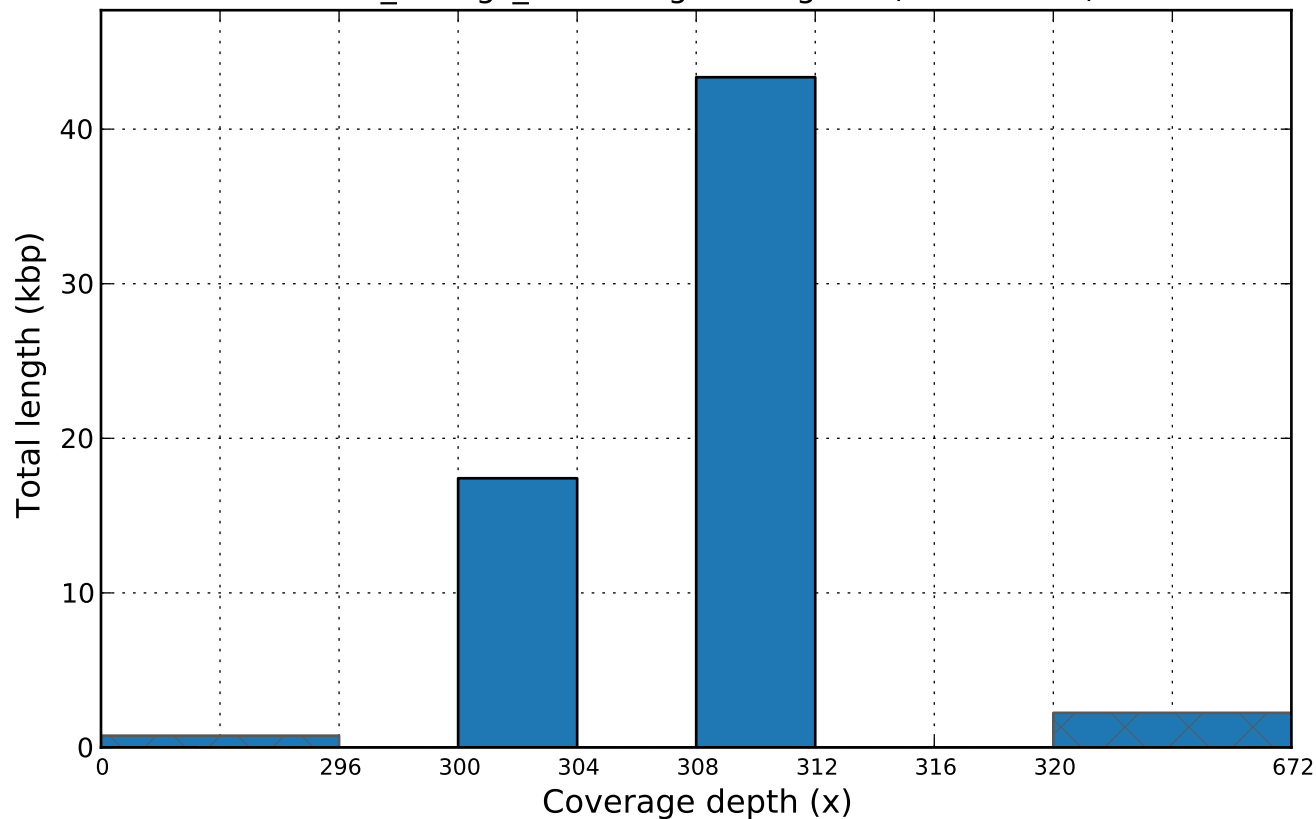
meta\_contigs\_1   meta\_contigs\_2

meta\_contigs\_1 coverage histogram (bin size: 4x)



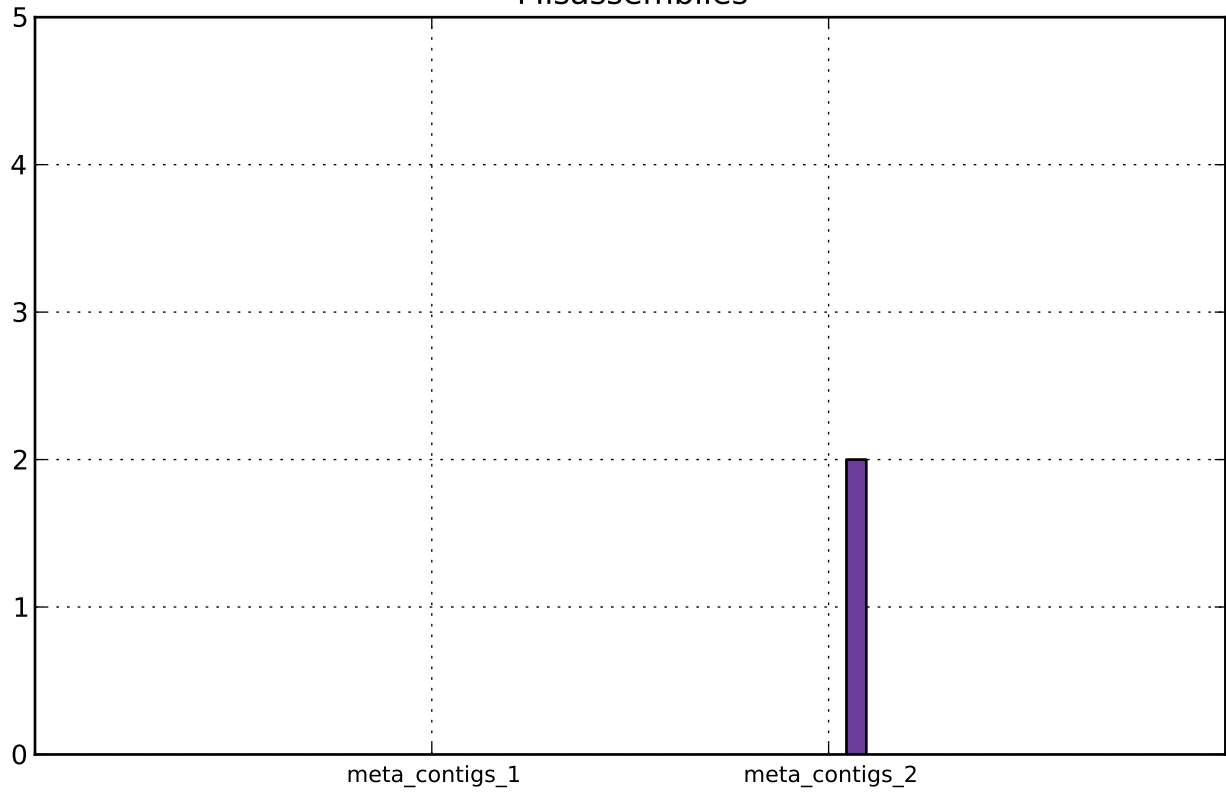
meta\_contigs\_1

meta\_contigs\_2 coverage histogram (bin size: 4x)



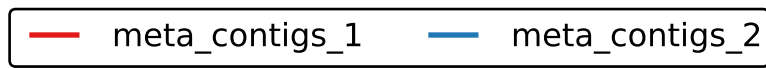
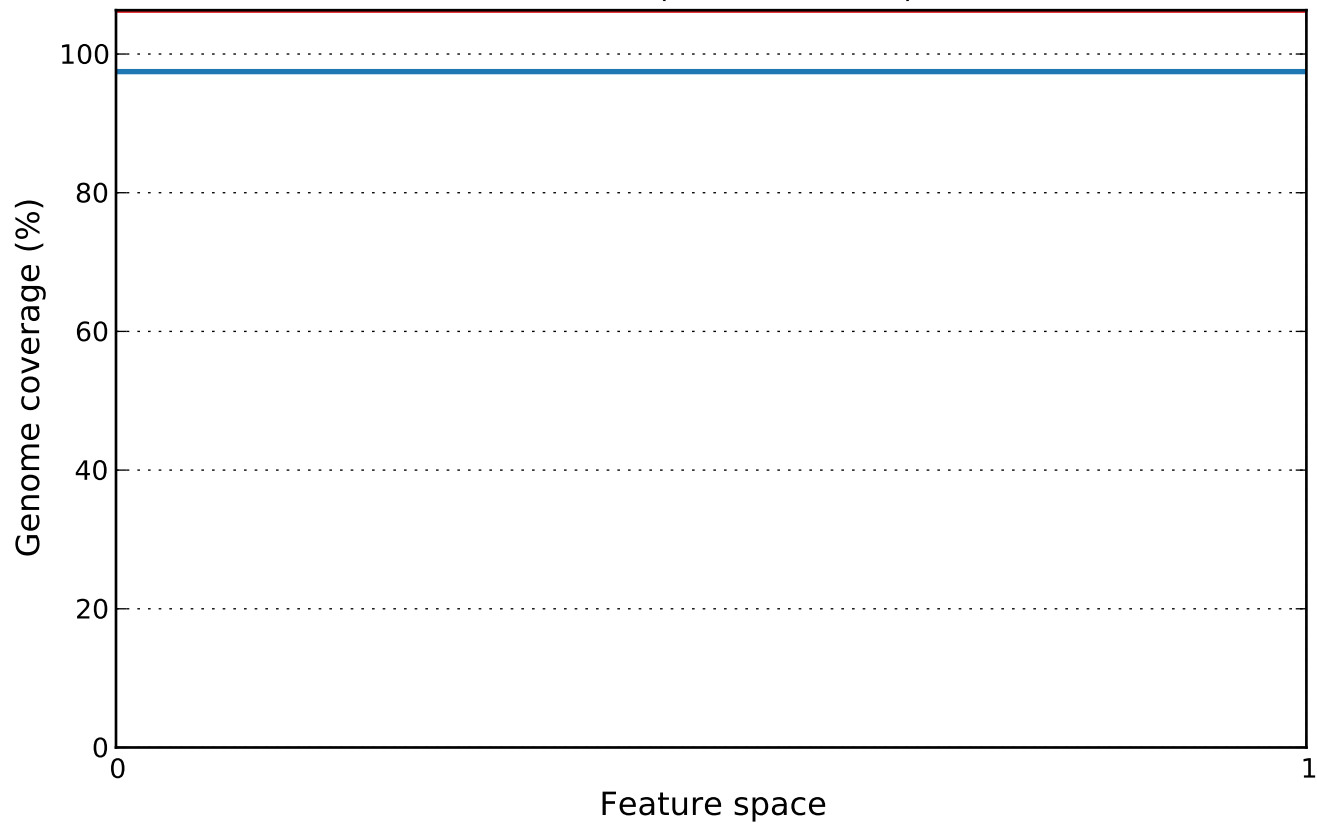
meta\_contigs\_2

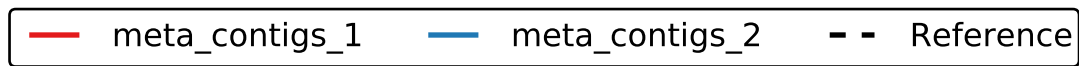
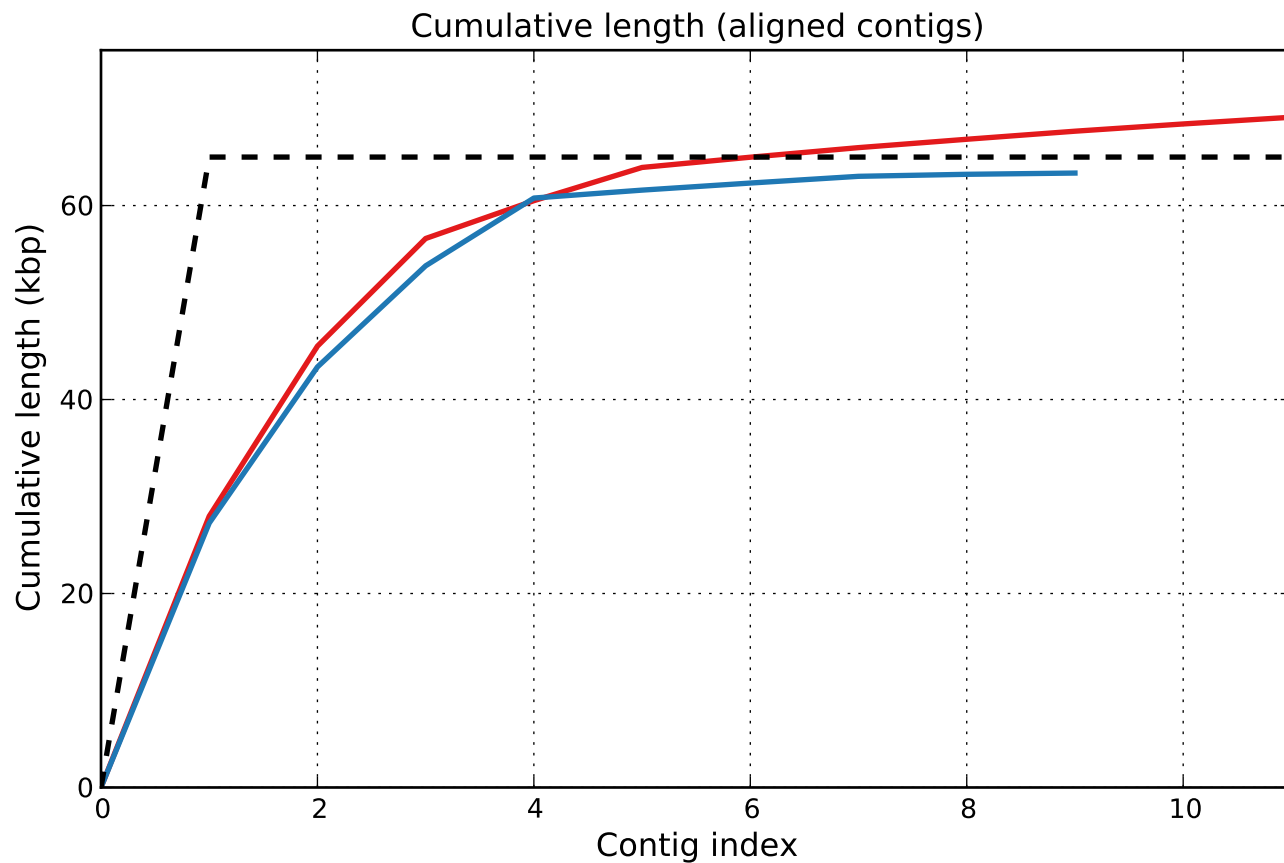
# Misassemblies

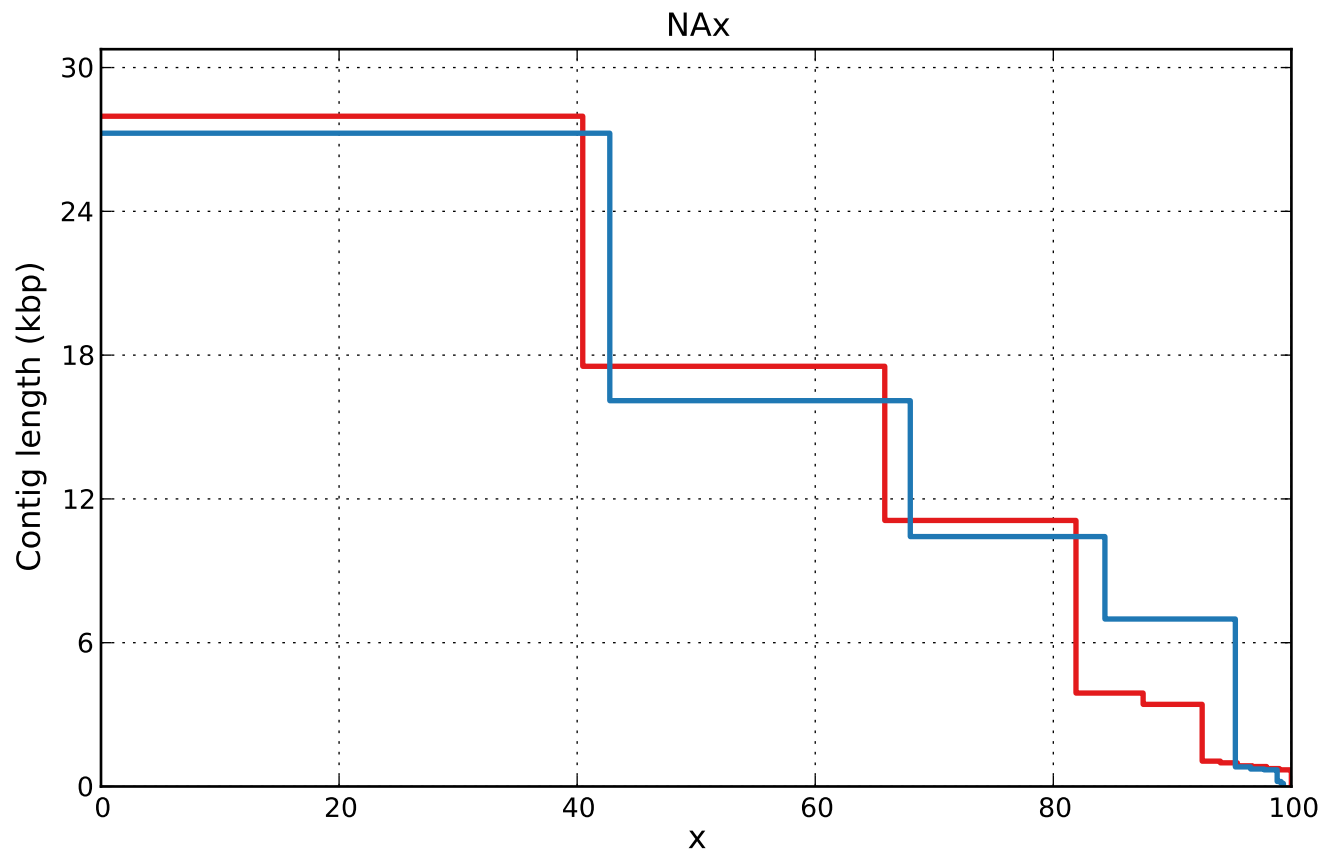


 # interspecies translocations

FRCurve (misassemblies)



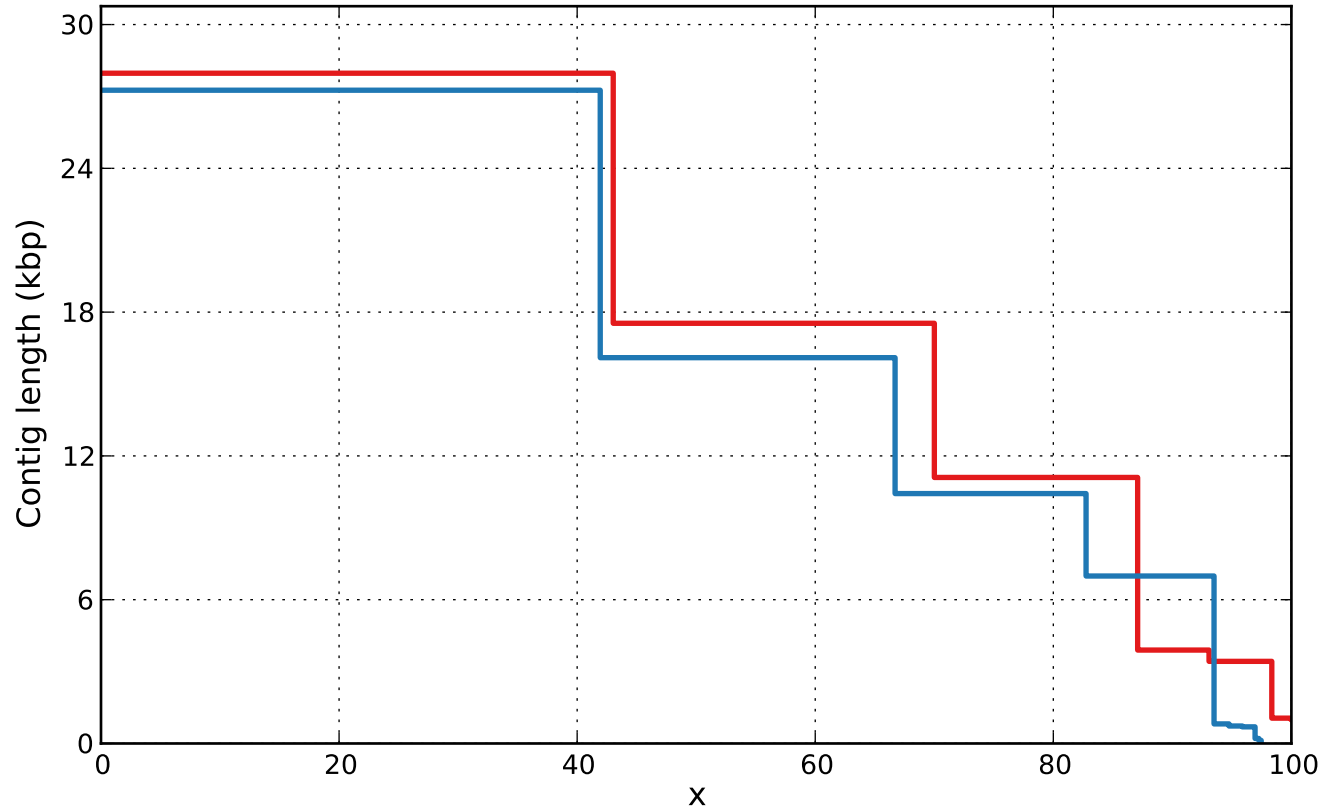




— meta\_contigs\_1 — meta\_contigs\_2



# NGAx



— meta\_contigs\_1 — meta\_contigs\_2

