

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
N90	3427	6988
NG90	3898	6988
auN	18007.5	18221.4
auNG	19146.5	17879.1
L50	2	2
LG50	2	2
L90	5	4
LG90	4	4
# misassemblies	0	3
# misassembled contigs	0	1
Misassembled contigs length	0	763
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	98.397	96.609
Duplication ratio	1.081	1.015
# N's per 100 kbp	18.81	0.00
# mismatches per 100 kbp	54.99	65.89
# indels per 100 kbp	7.24	9.41
Largest alignment	27969	27260
Total aligned length	69108	63741
NA50	17534	16099
NGA50	17534	16099
NA90	3427	6988
NGA90	3898	6988
auNA	18006.7	18214.4
auNGA	19145.6	17872.2
LA50	2	2
LGA50	2	2
LA90	5	4
LGA90	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

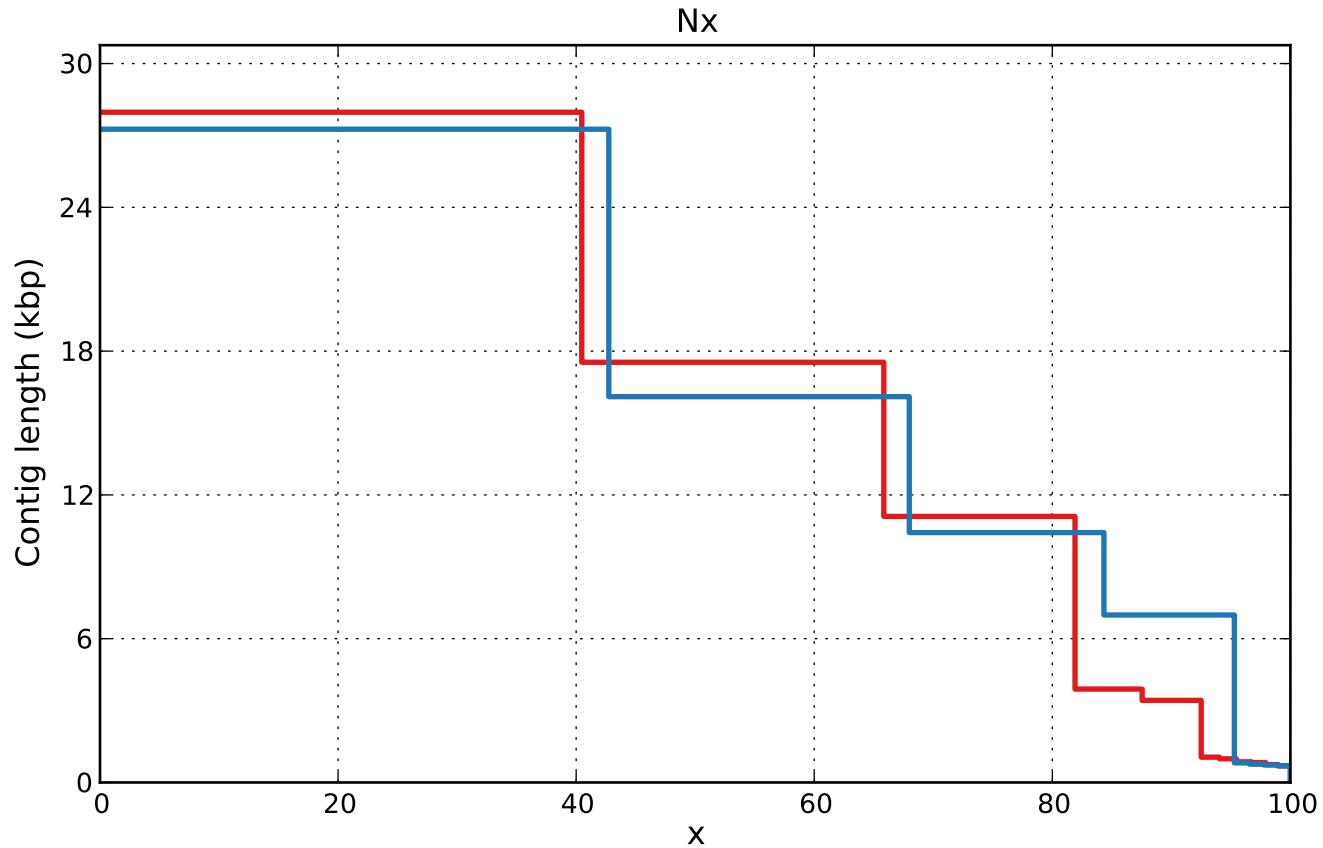
	meta_contigs_1	meta_contigs_2
# misassemblies	0	3
# contig misassemblies	0	3
# c. relocations	0	3
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	1
Misassembled contigs length	0	763
# possibly 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	0
# mismatches	38	42
# indels	5	6
# indels (<= 5 bp)	5	6
# indels (> 5 bp)	0	0
Indels length	6	16

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).

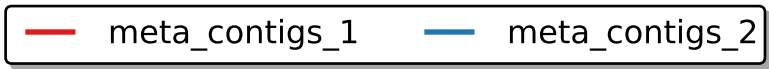
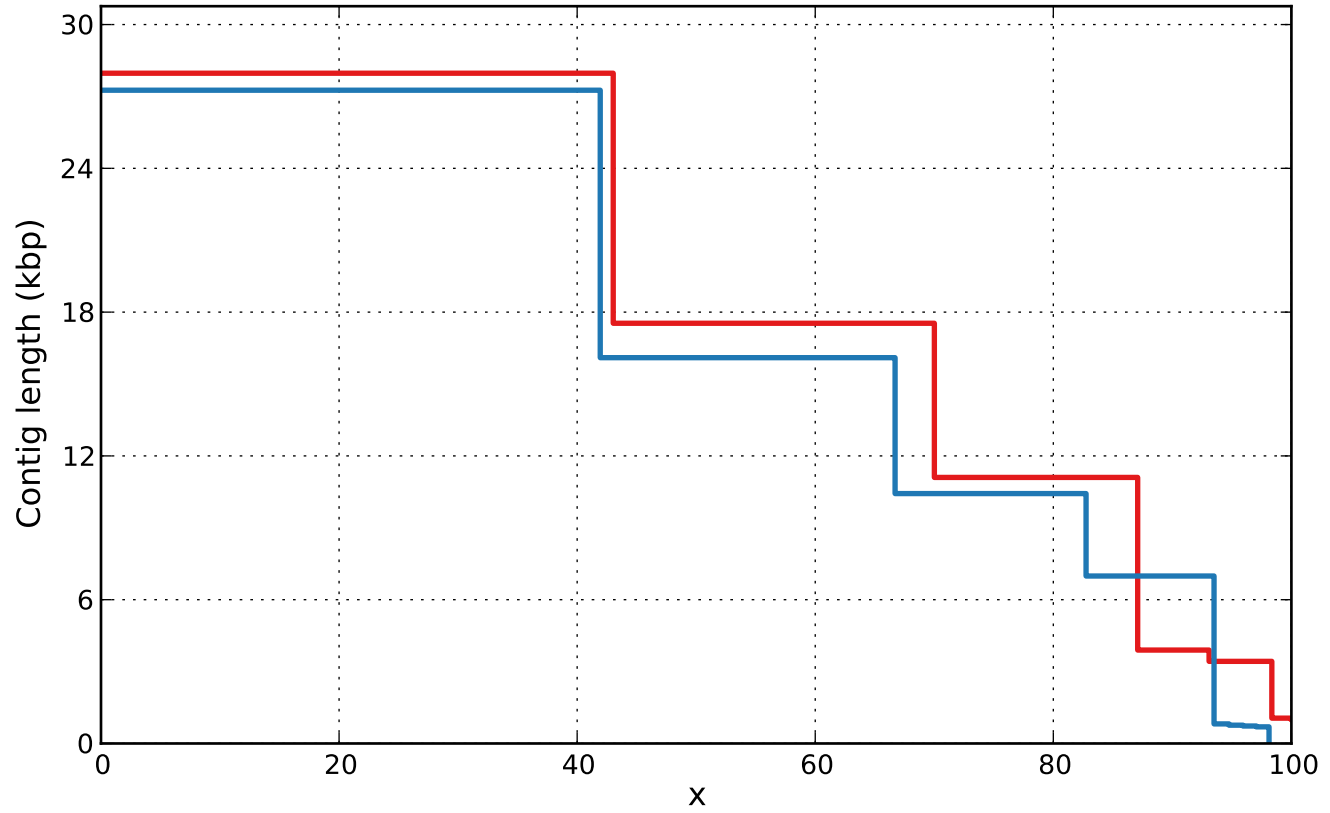
Unaligned report

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

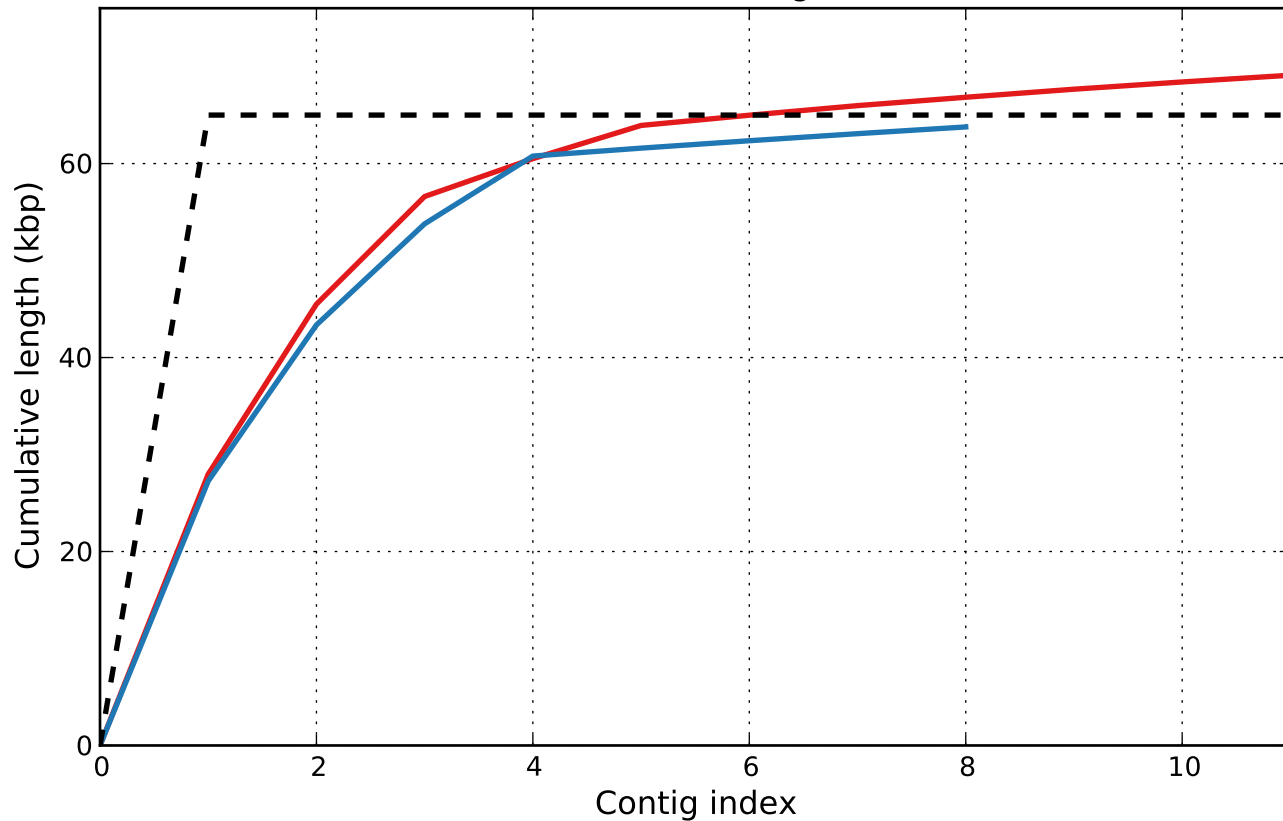
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



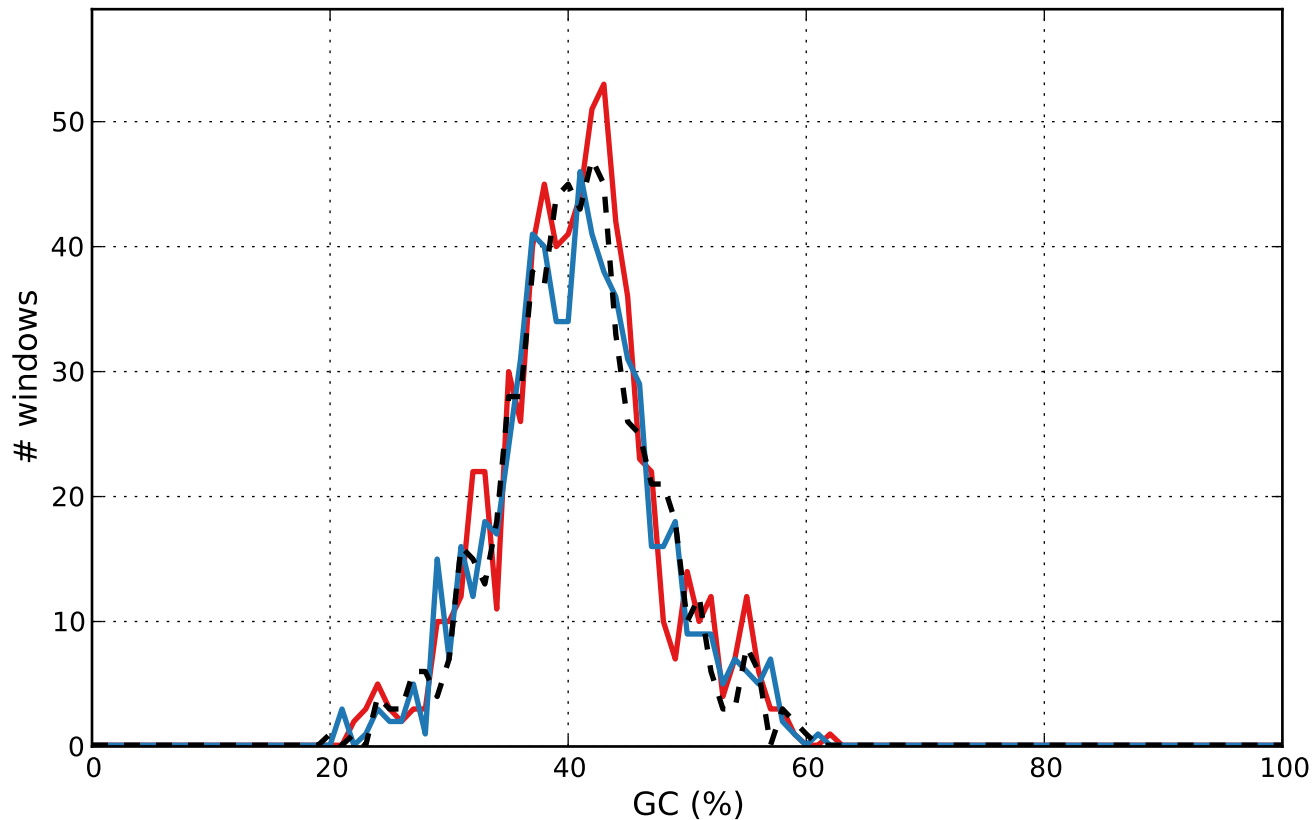
NGx



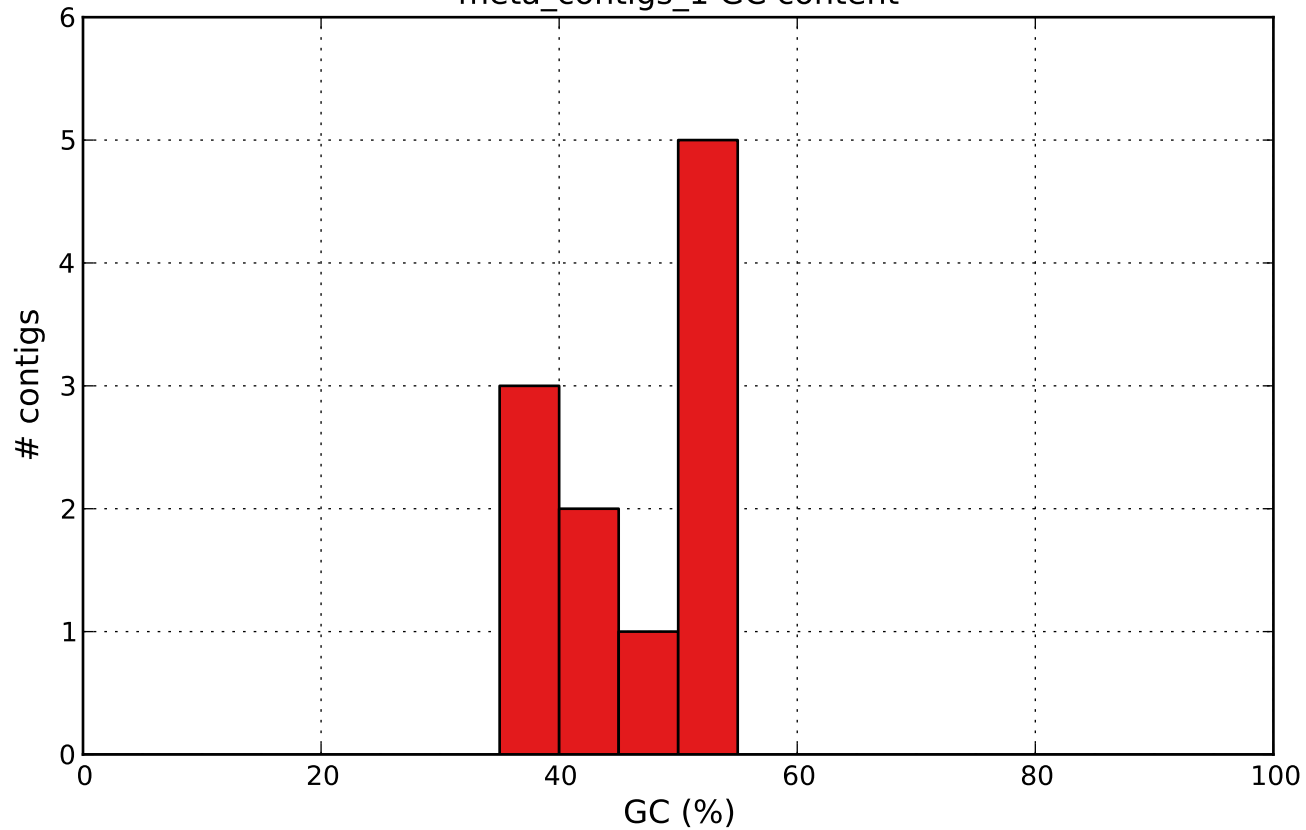
Cumulative length



GC content

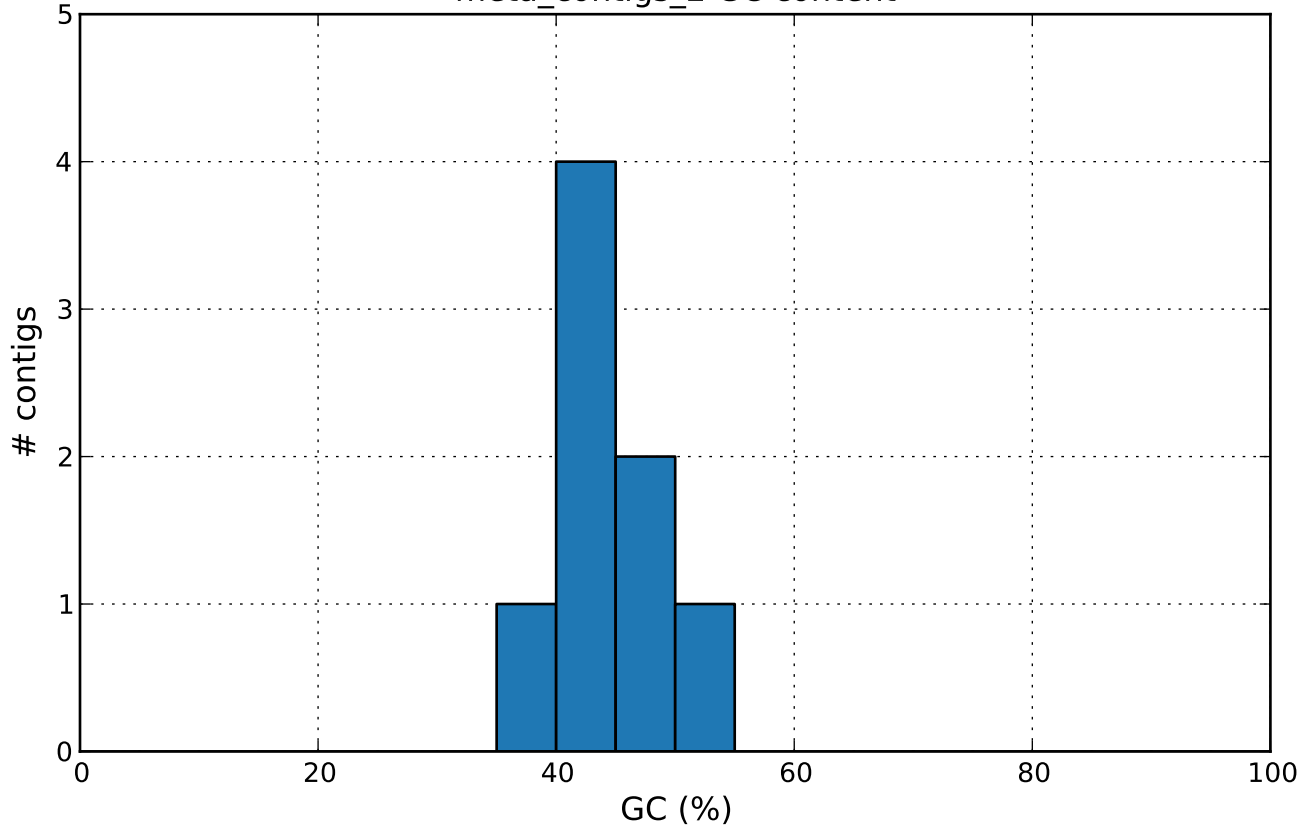


meta_contigs_1 GC content



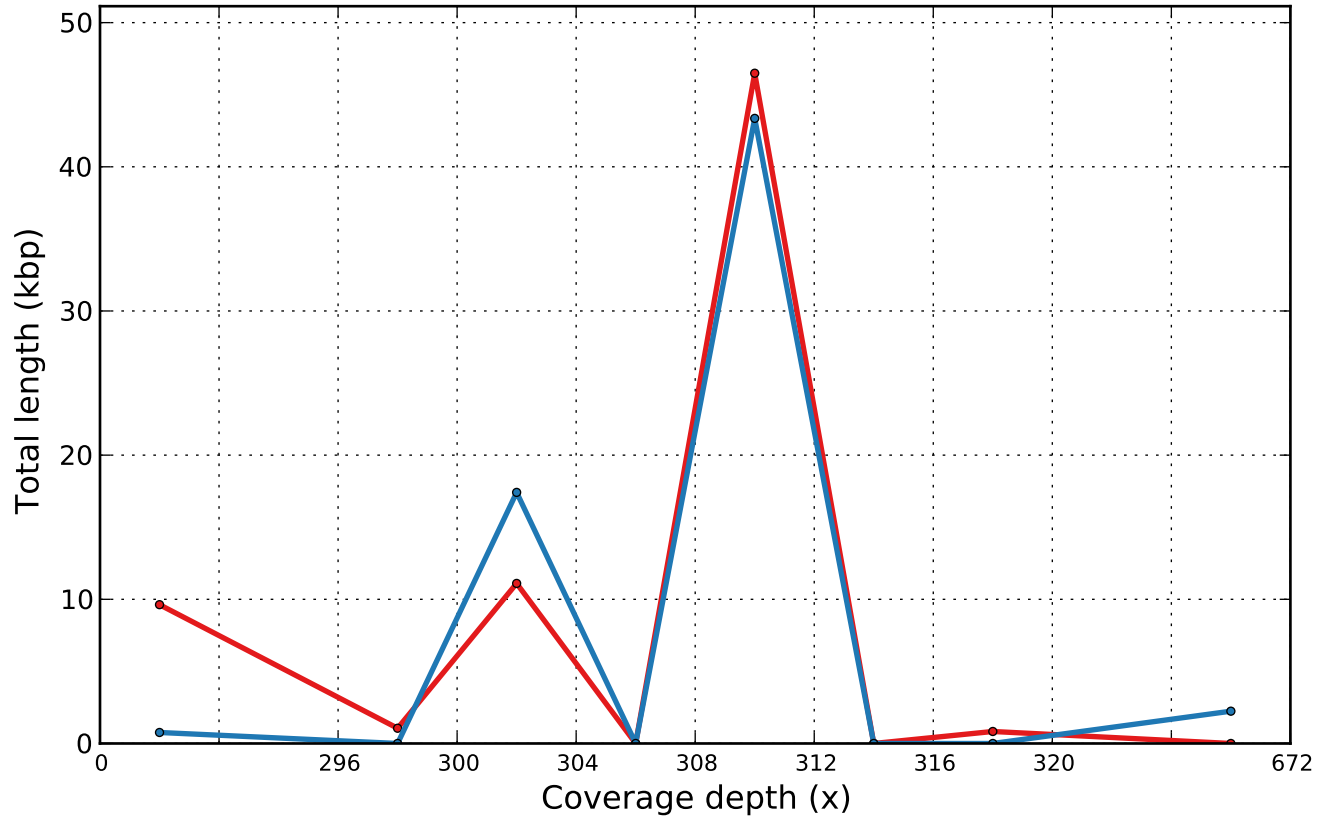
meta_contigs_1

meta_contigs_2 GC content



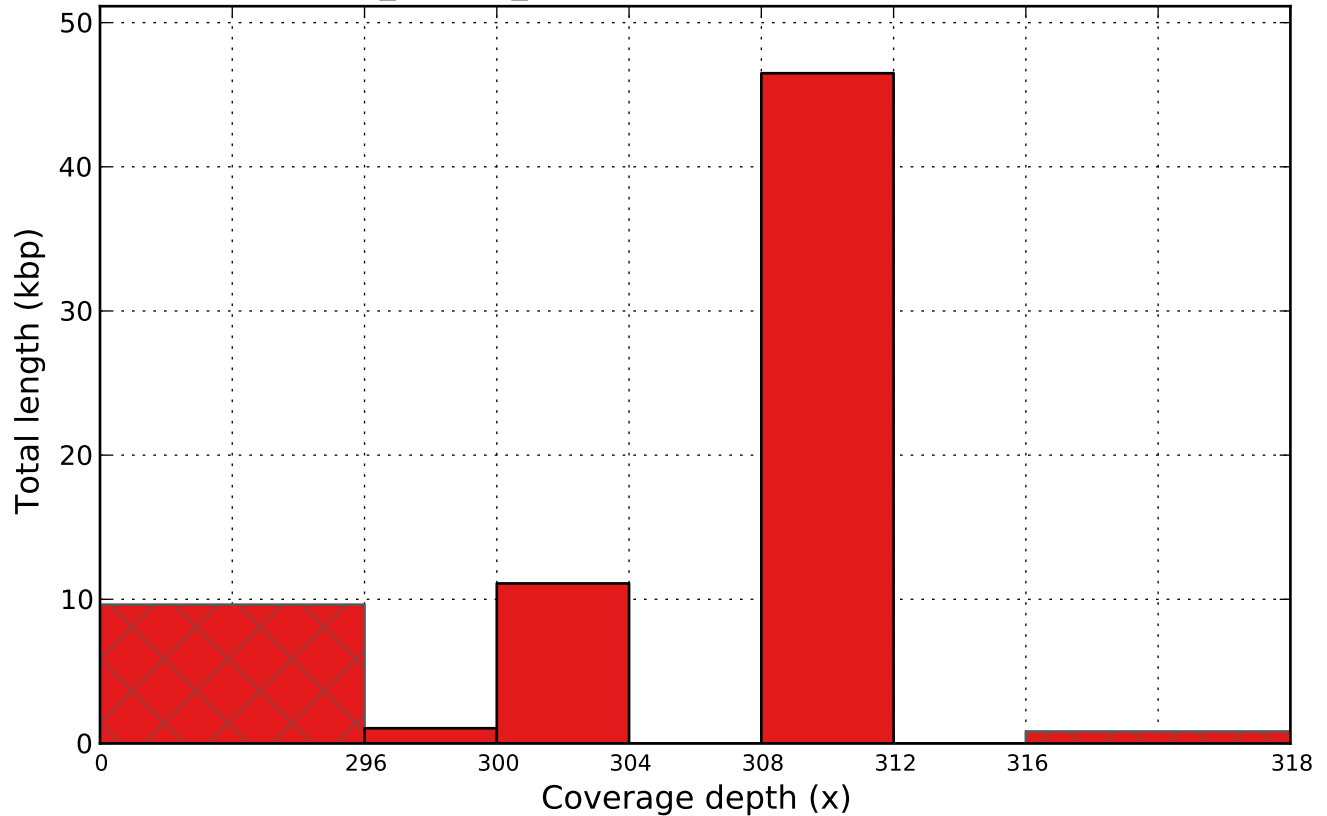
meta_contigs_2

Coverage histogram (bin size: 4x)



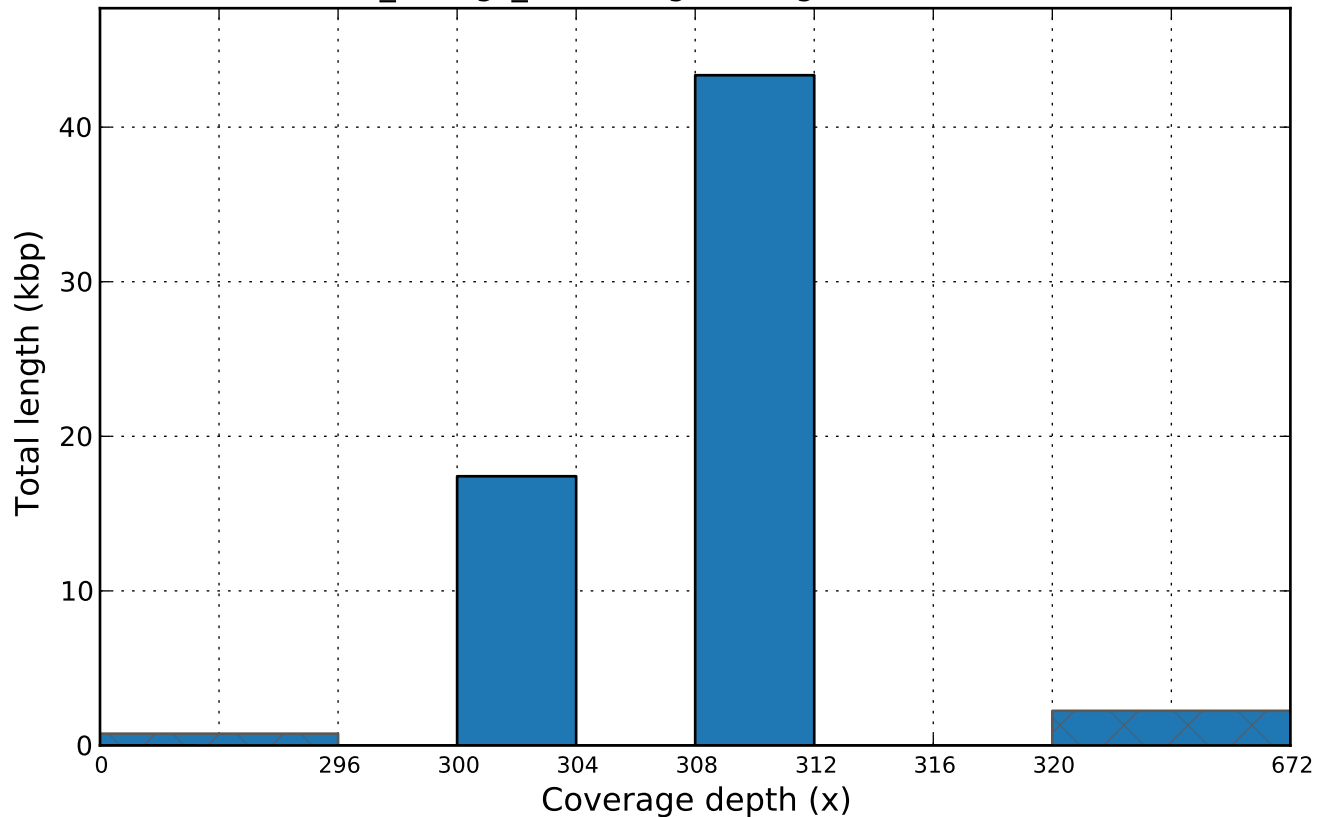
meta_contigs_1 meta_contigs_2

meta_contigs_1 coverage histogram (bin size: 4x)



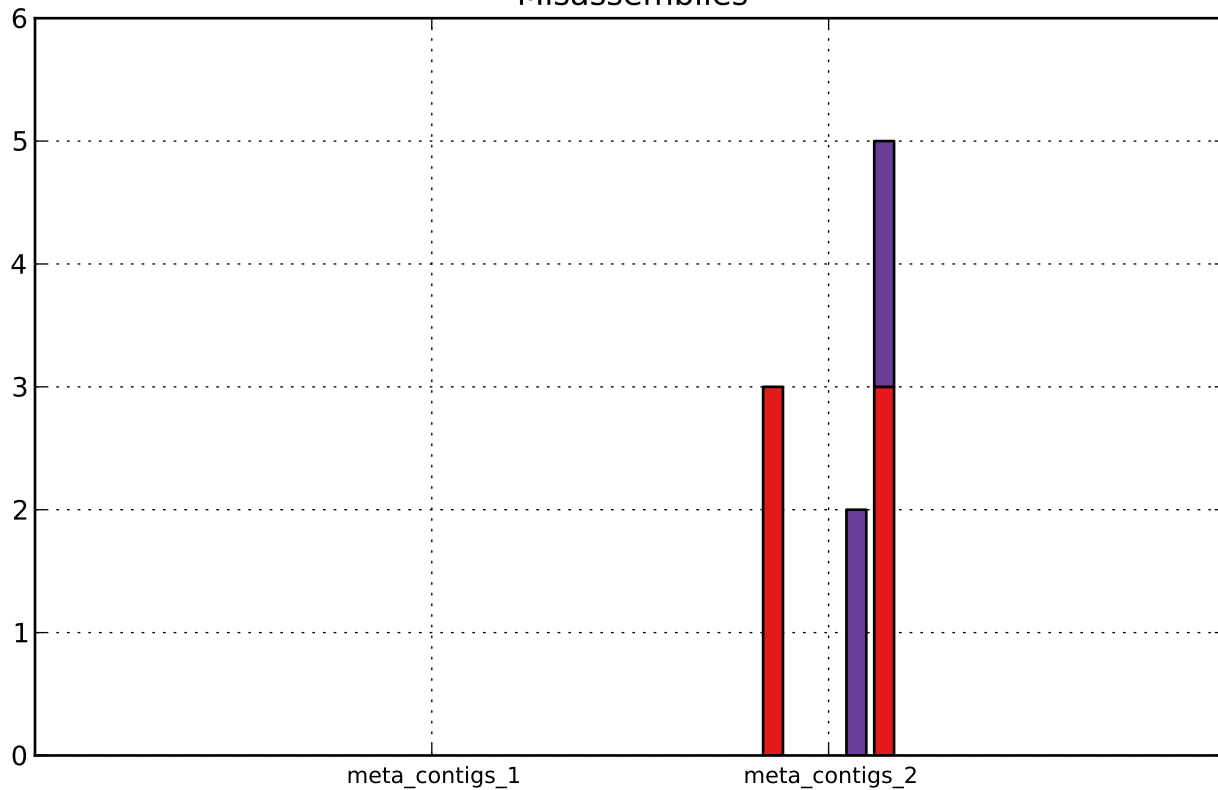
meta_contigs_1

meta_contigs_2 coverage histogram (bin size: 4x)

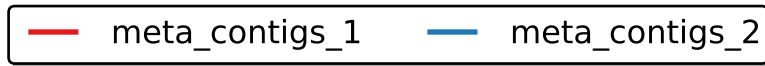
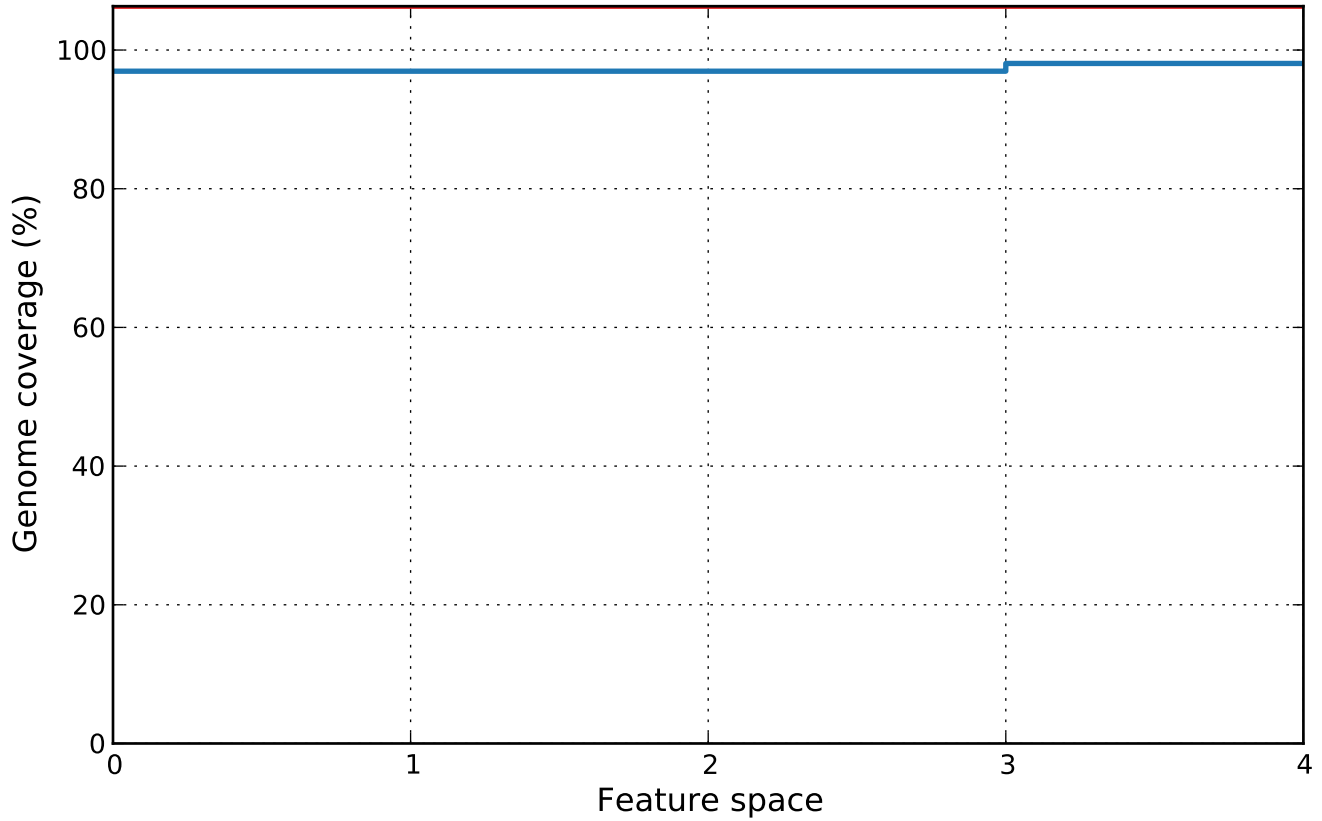


meta_contigs_2

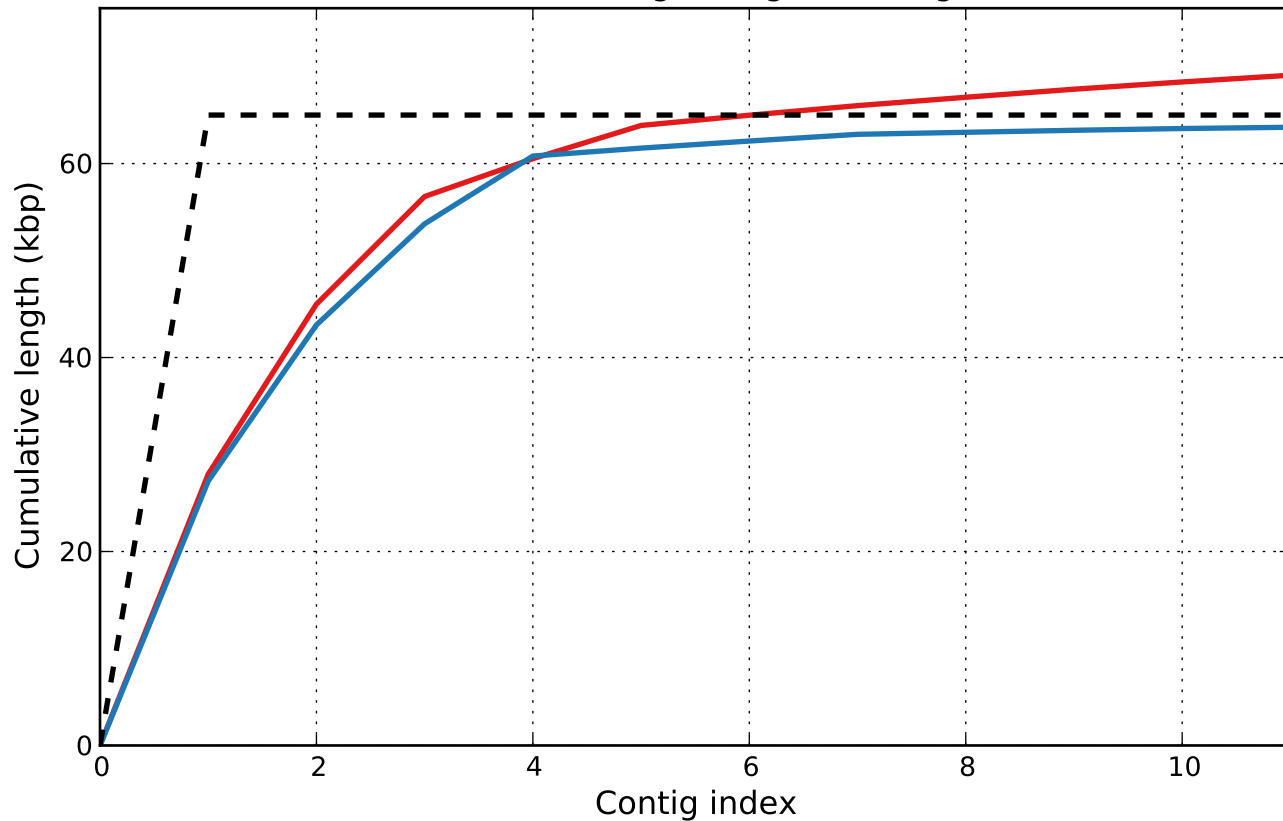
Misassemblies



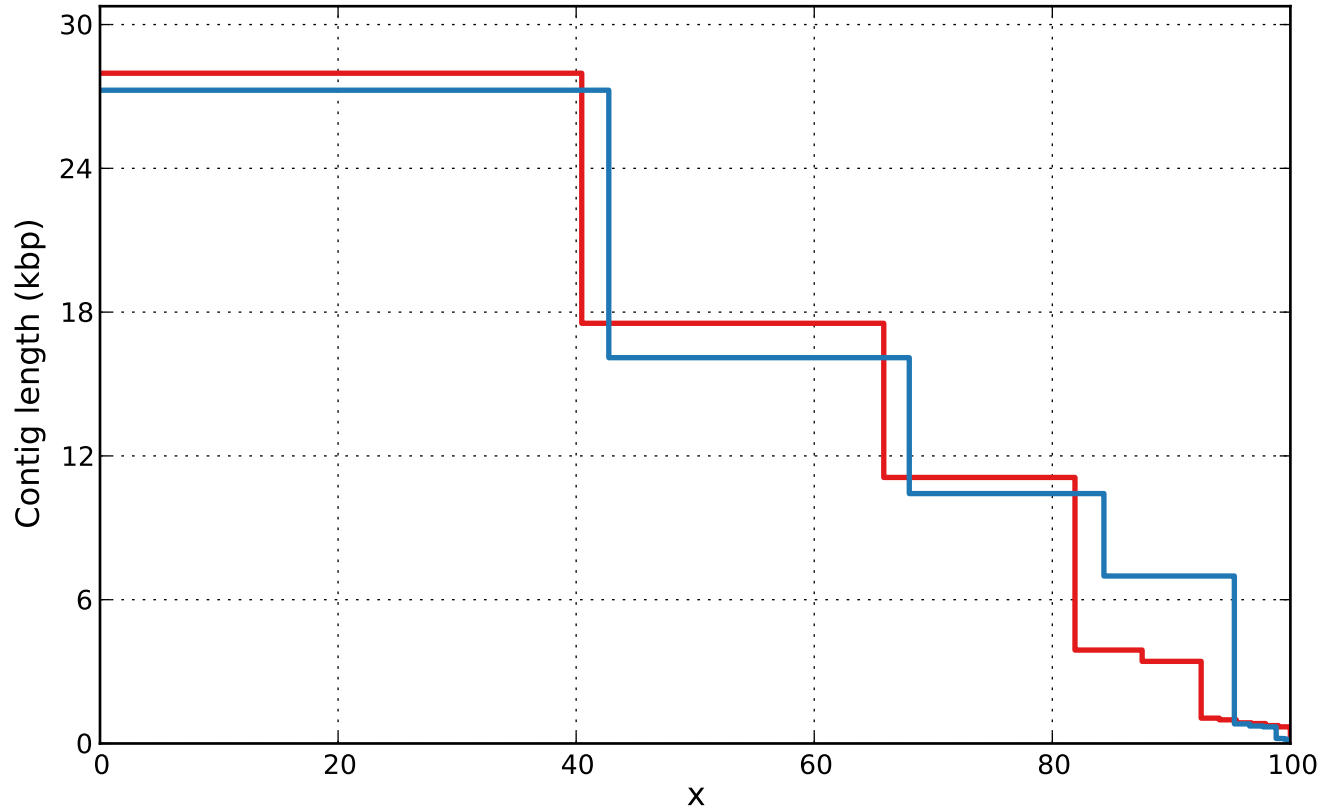
FRCurve (misassemblies)



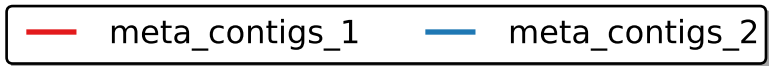
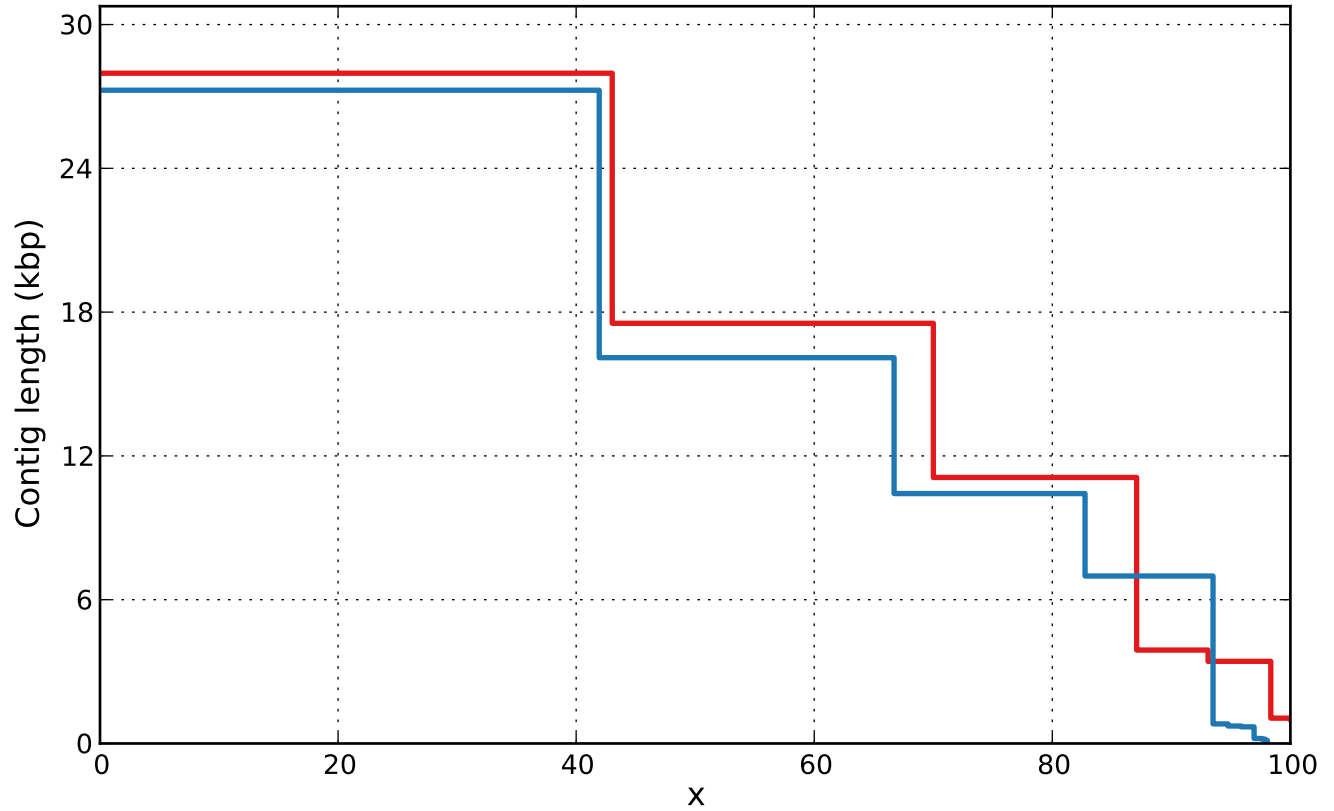
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

