

Report

	contigs
# contigs (≥ 0 bp)	168
# contigs (≥ 1000 bp)	87
# contigs (≥ 5000 bp)	62
# contigs (≥ 10000 bp)	57
# contigs (≥ 25000 bp)	47
# contigs (≥ 50000 bp)	31
Total length (≥ 0 bp)	4567292
Total length (≥ 1000 bp)	4548539
Total length (≥ 5000 bp)	4493976
Total length (≥ 10000 bp)	4458325
Total length (≥ 25000 bp)	4312386
Total length (≥ 50000 bp)	3762852
# contigs	97
Largest contig	221601
Total length	4555330
Reference length	4639675
GC (%)	50.74
Reference GC (%)	50.79
N50	129054
NG50	129054
N75	60768
NG75	59669
L50	14
LG50	14
L75	26
LG75	27
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	542
Genome fraction (%)	98.142
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.03
# indels per 100 kbp	0.33
Largest alignment	221546
Total aligned length	4554465
NA50	129054
NGA50	129054
NA75	60768
NGA75	59669
LA50	14
LGA50	14
LA75	26
LGA75	27

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

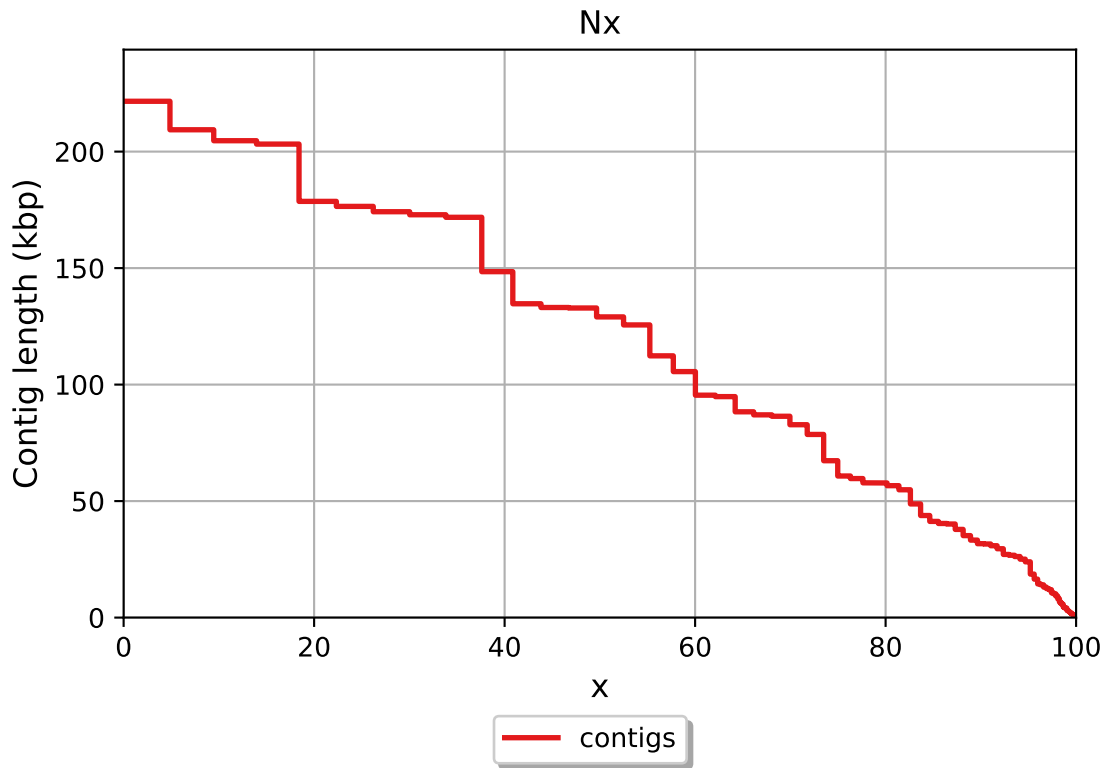
	contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	47
# indels	15
# indels (<= 5 bp)	12
# indels (> 5 bp)	3
Indels length	77

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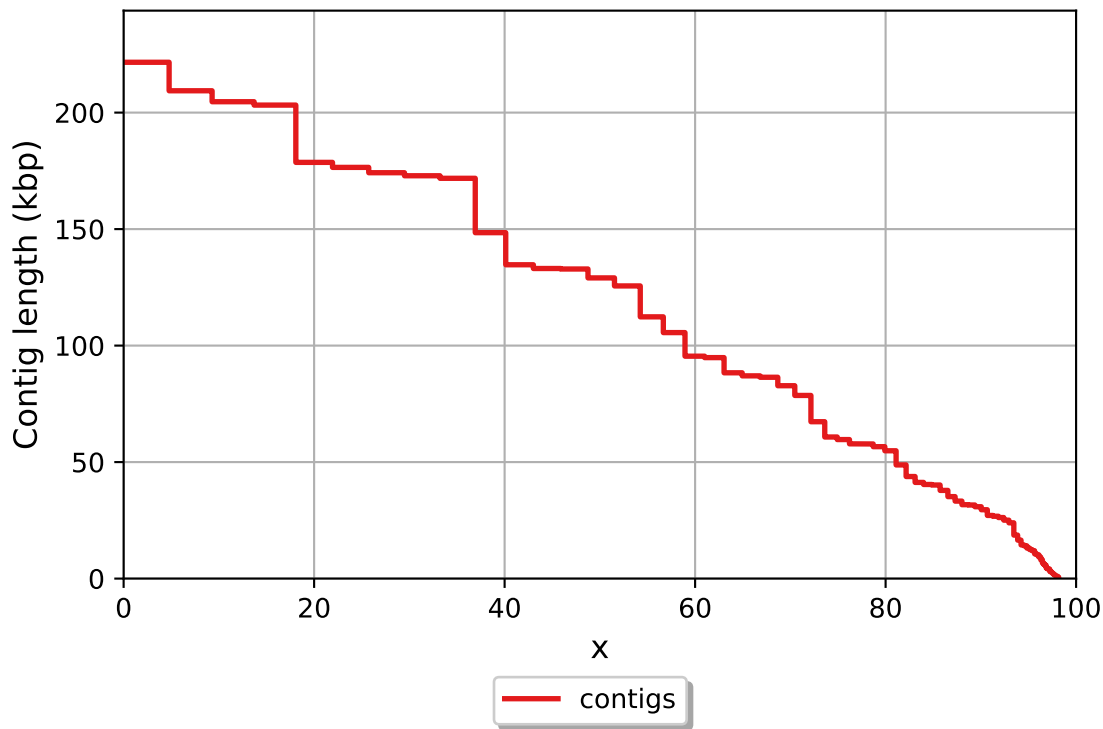
Unaligned report

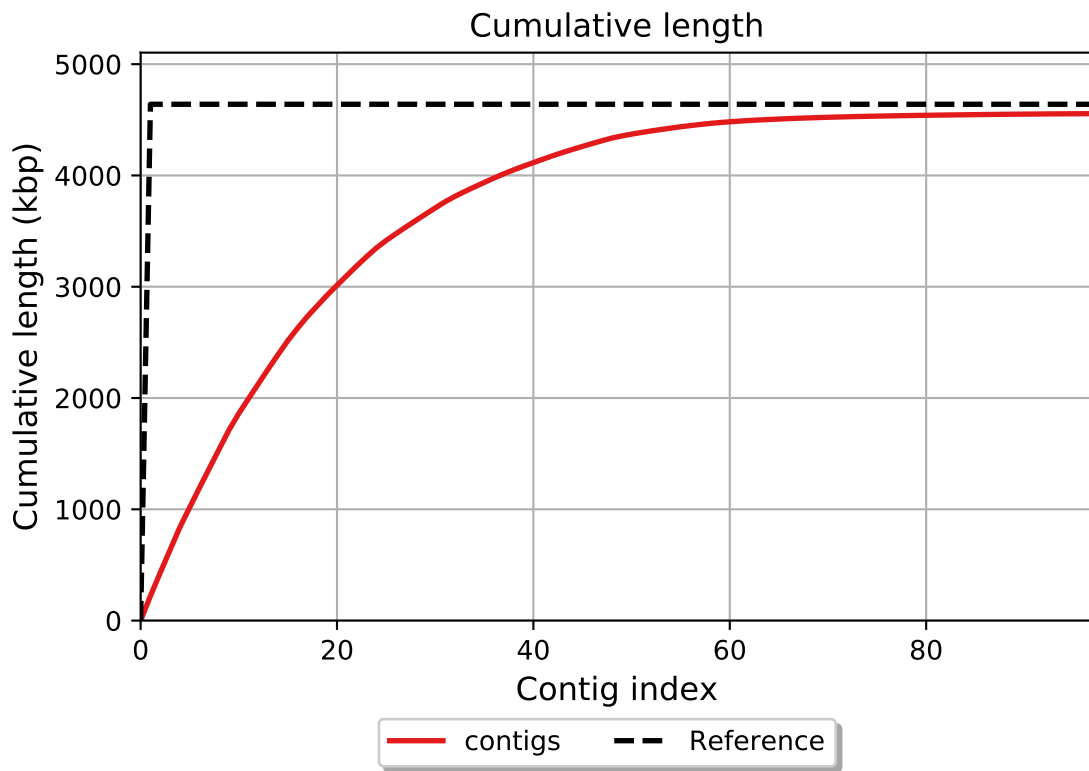
	contigs
# fully unaligned contigs	1
Fully unaligned length	542
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

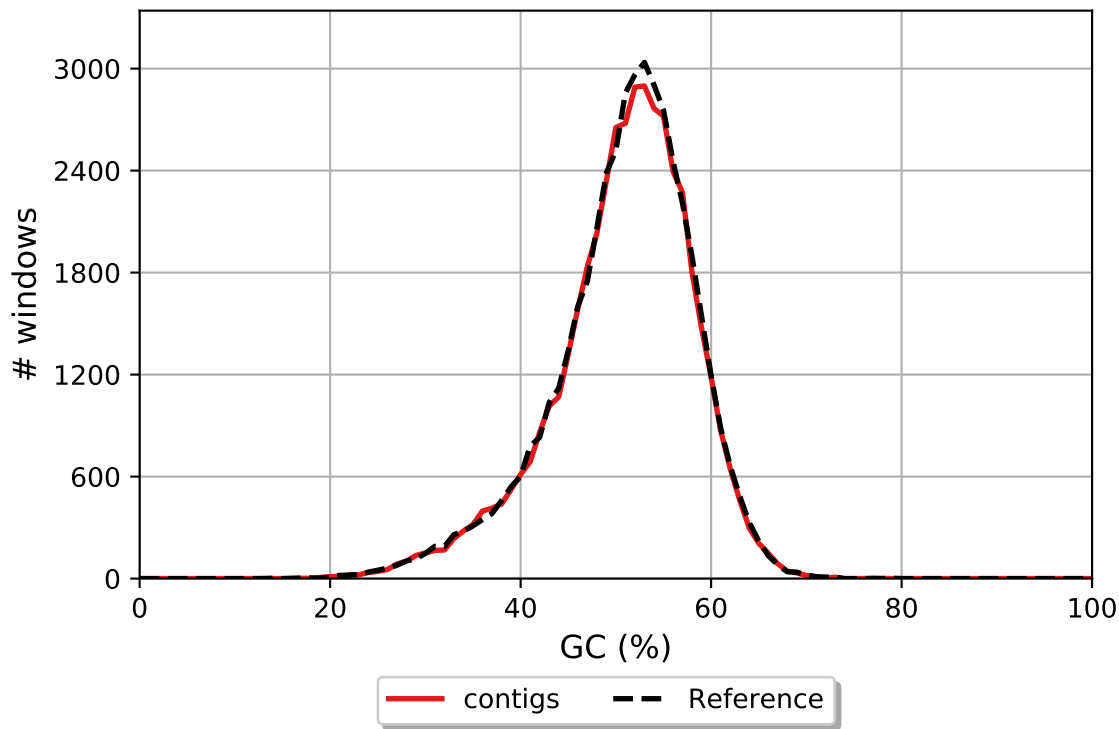


NGx

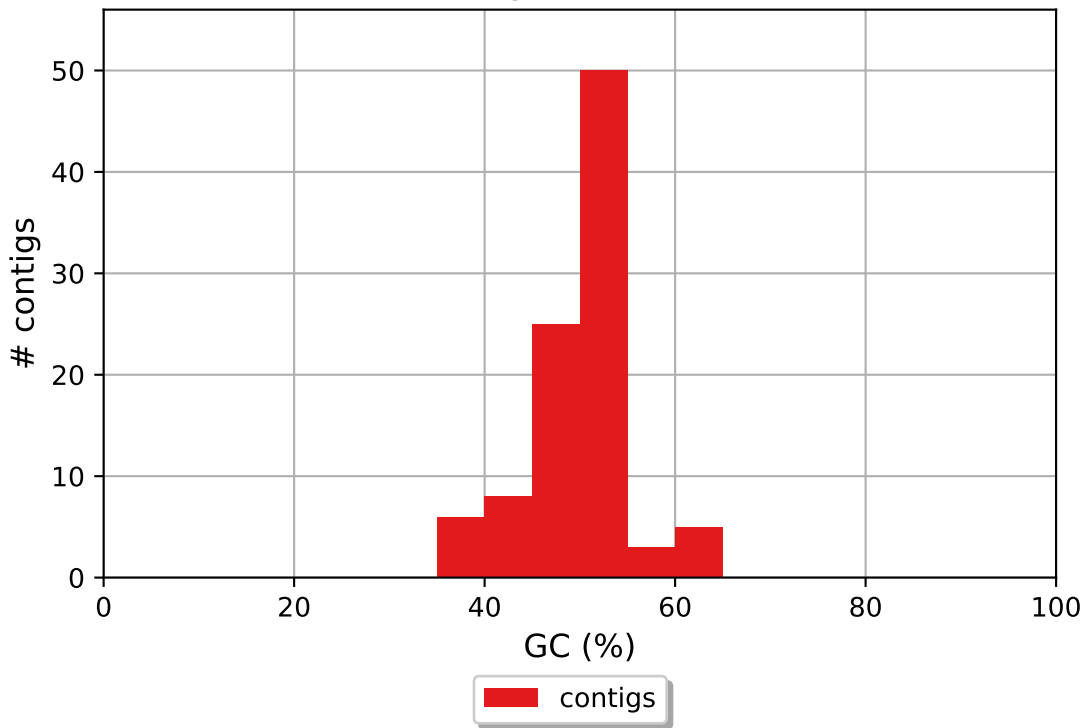




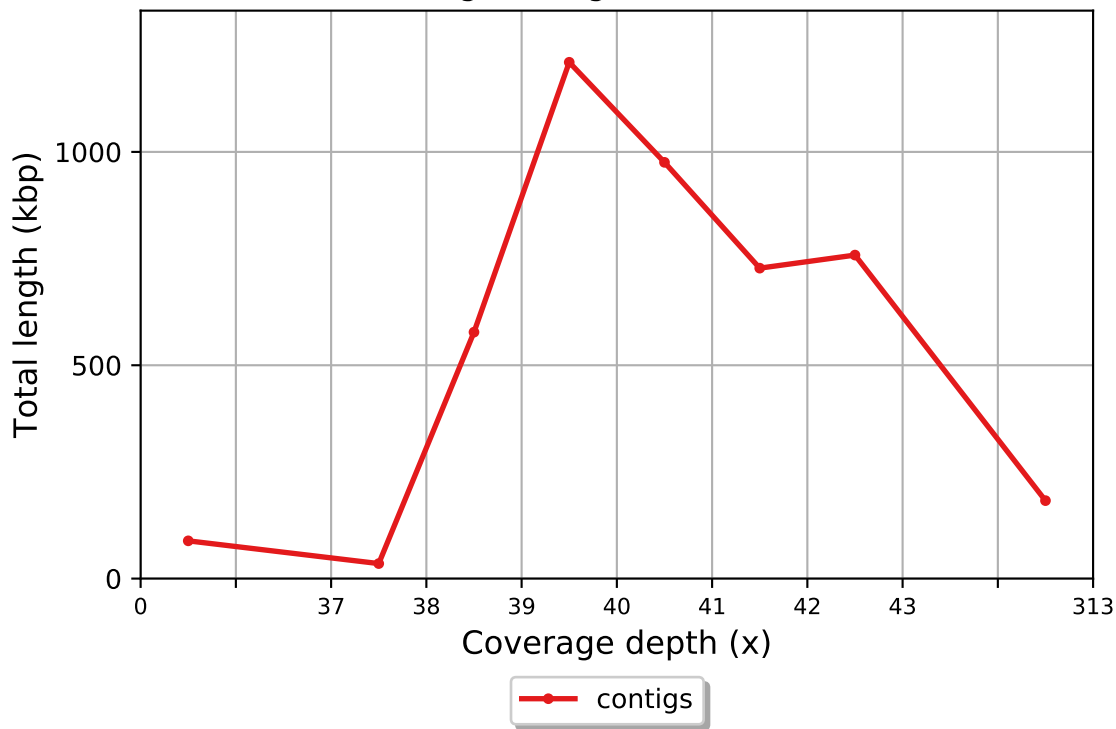
GC content



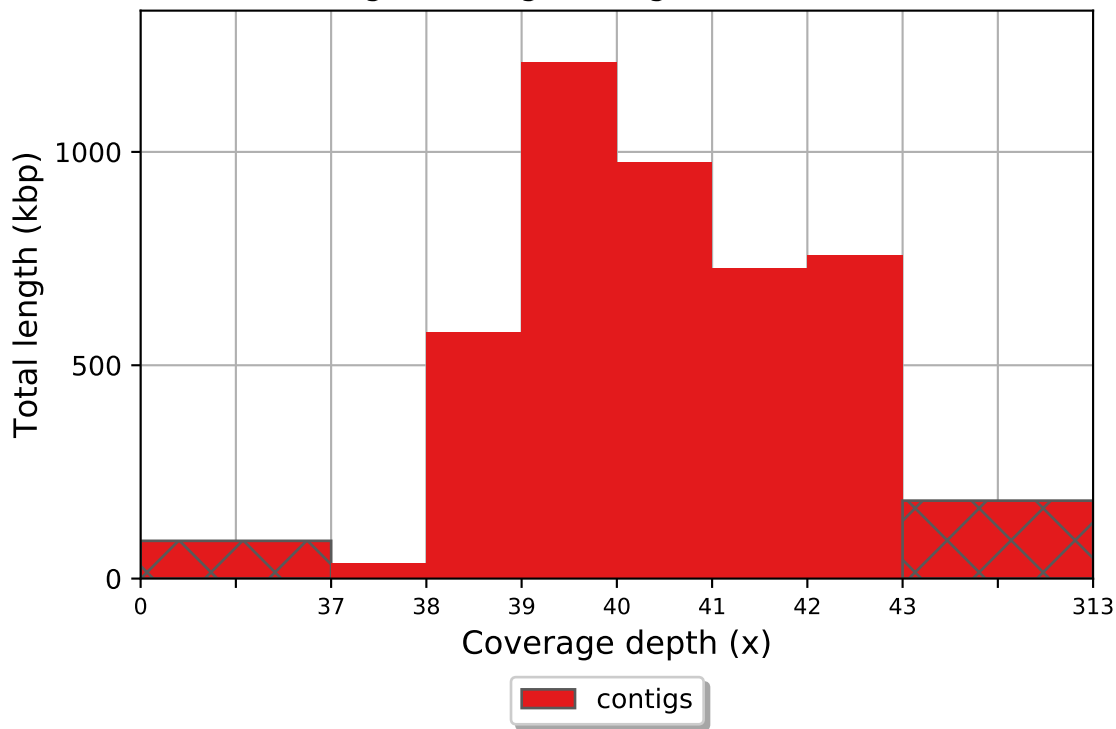
contigs GC content



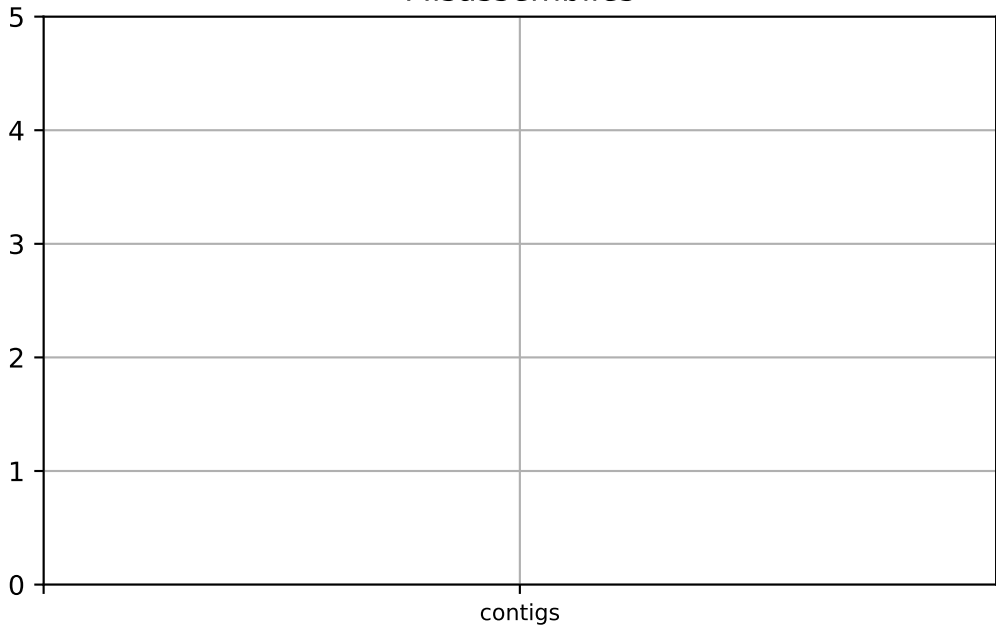
Coverage histogram (bin size: 1x)



contigs coverage histogram (bin size: 1x)



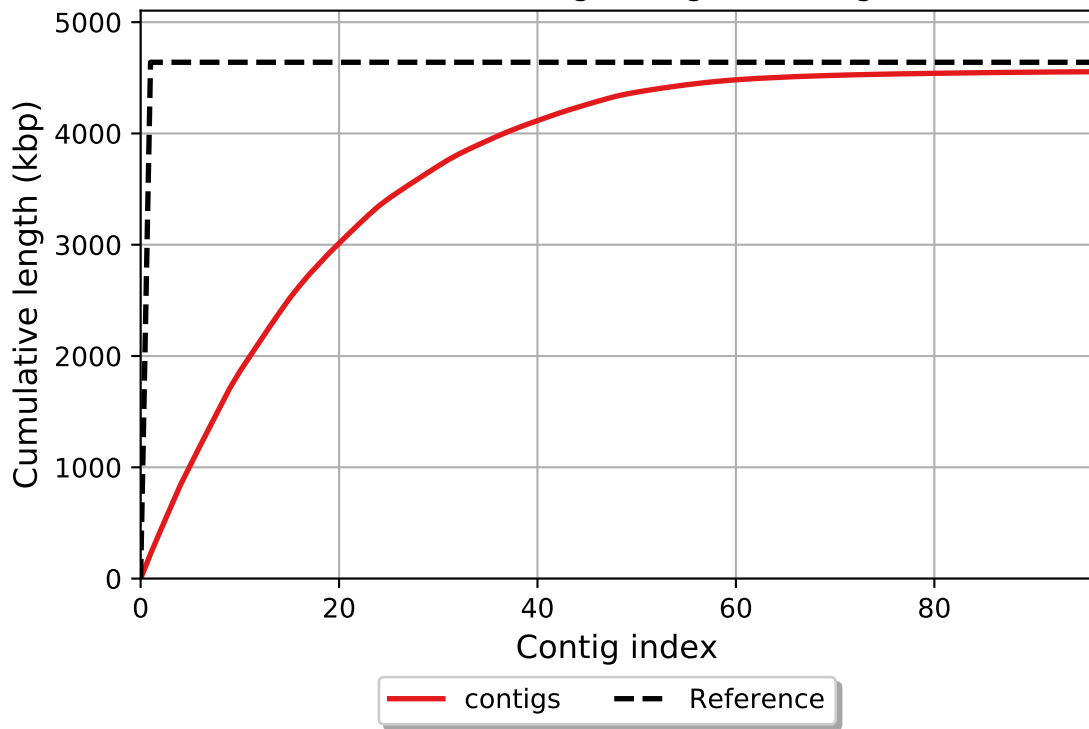
Misassemblies



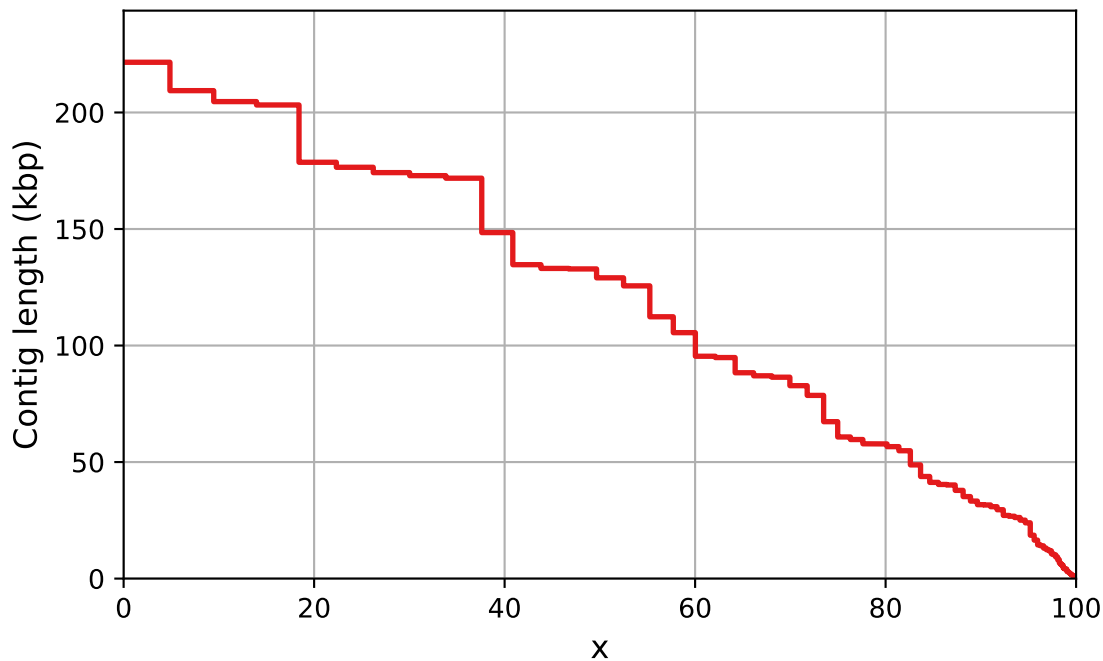
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



contigs

NGAx

