

# Report

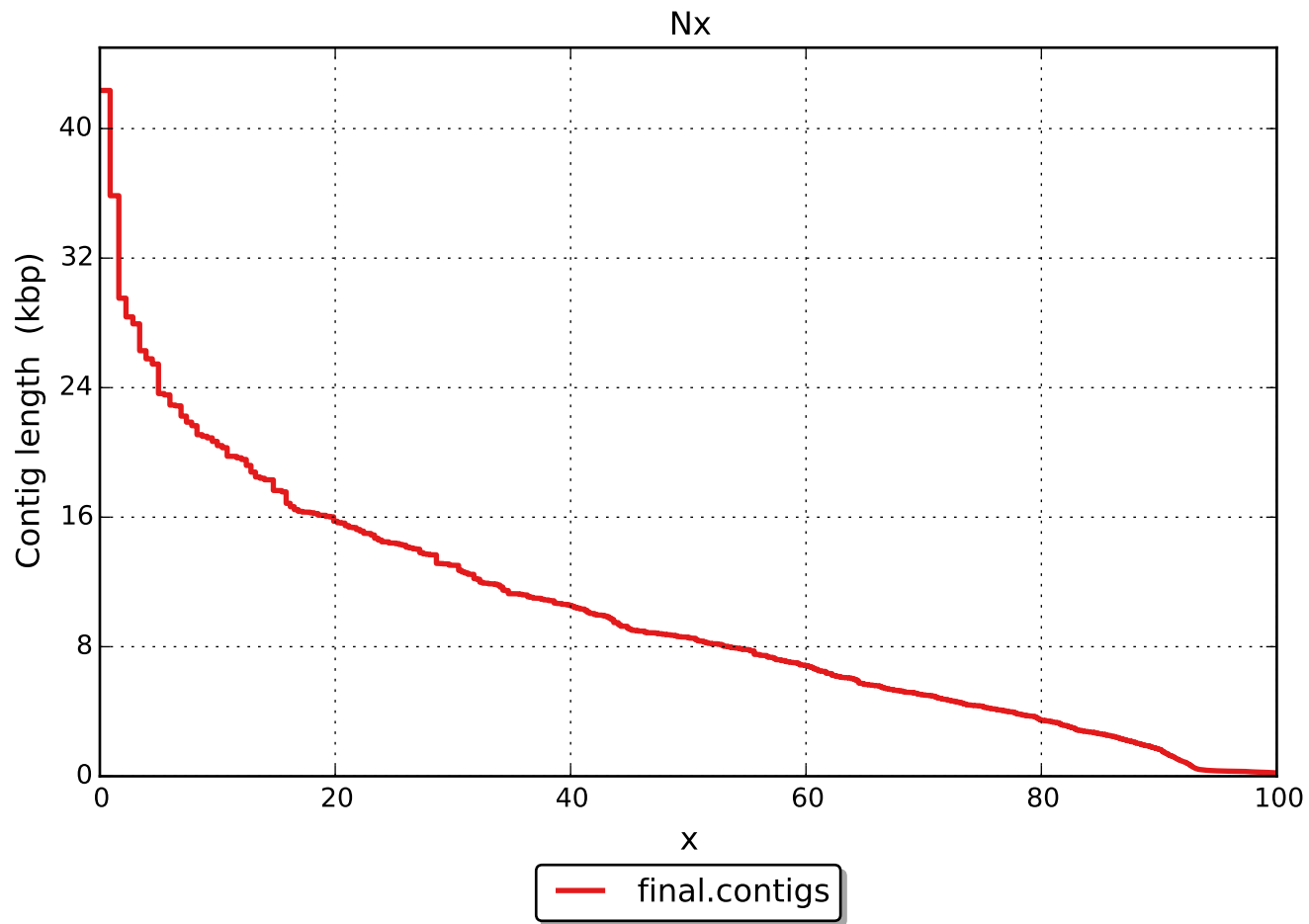
	final.contigs
# contigs (>= 0 bp)	1919
# contigs (>= 1000 bp)	694
# contigs (>= 5000 bp)	325
# contigs (>= 10000 bp)	132
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4850290
Total length (>= 1000 bp)	4448339
Total length (>= 5000 bp)	3410710
Total length (>= 10000 bp)	2038742
Total length (>= 25000 bp)	241570
Total length (>= 50000 bp)	0
# contigs	1919
Largest contig	42357
Total length	4850290
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	8578
NG50	8768
N75	4311
NG75	4753
L50	175
LG50	163
L75	375
LG75	340
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	640 + 9 part
Unaligned length	208506
Genome fraction (%)	98.056
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.66
# indels per 100 kbp	0.00
Largest alignment	42357
NA50	8578
NGA50	8768
NA75	4311
NGA75	4753
LA50	175
LGA50	163
LA75	375
LGA75	340

## Misassemblies report

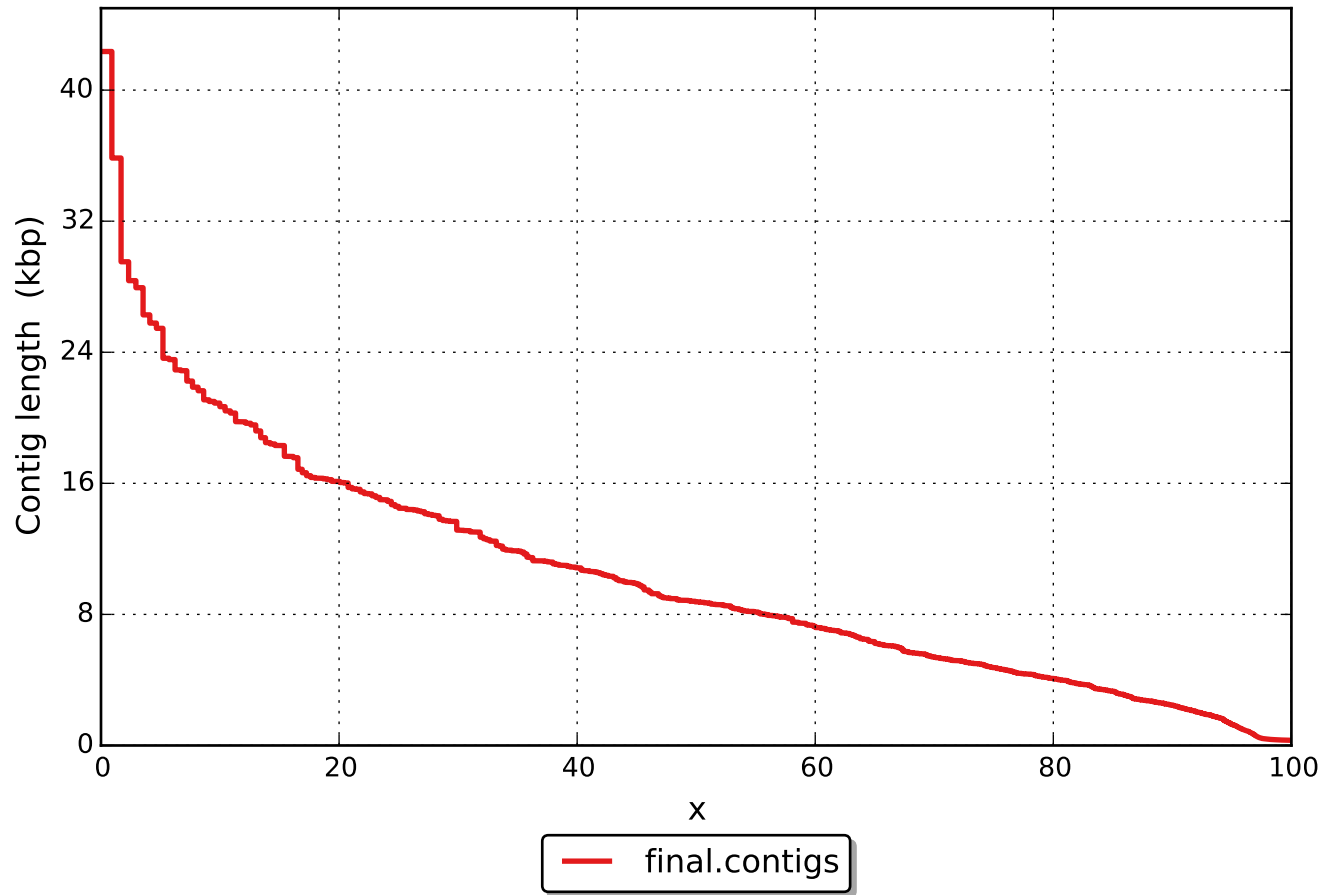
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	394
# indels	0
# short indels	0
# long indels	0
Indels length	0

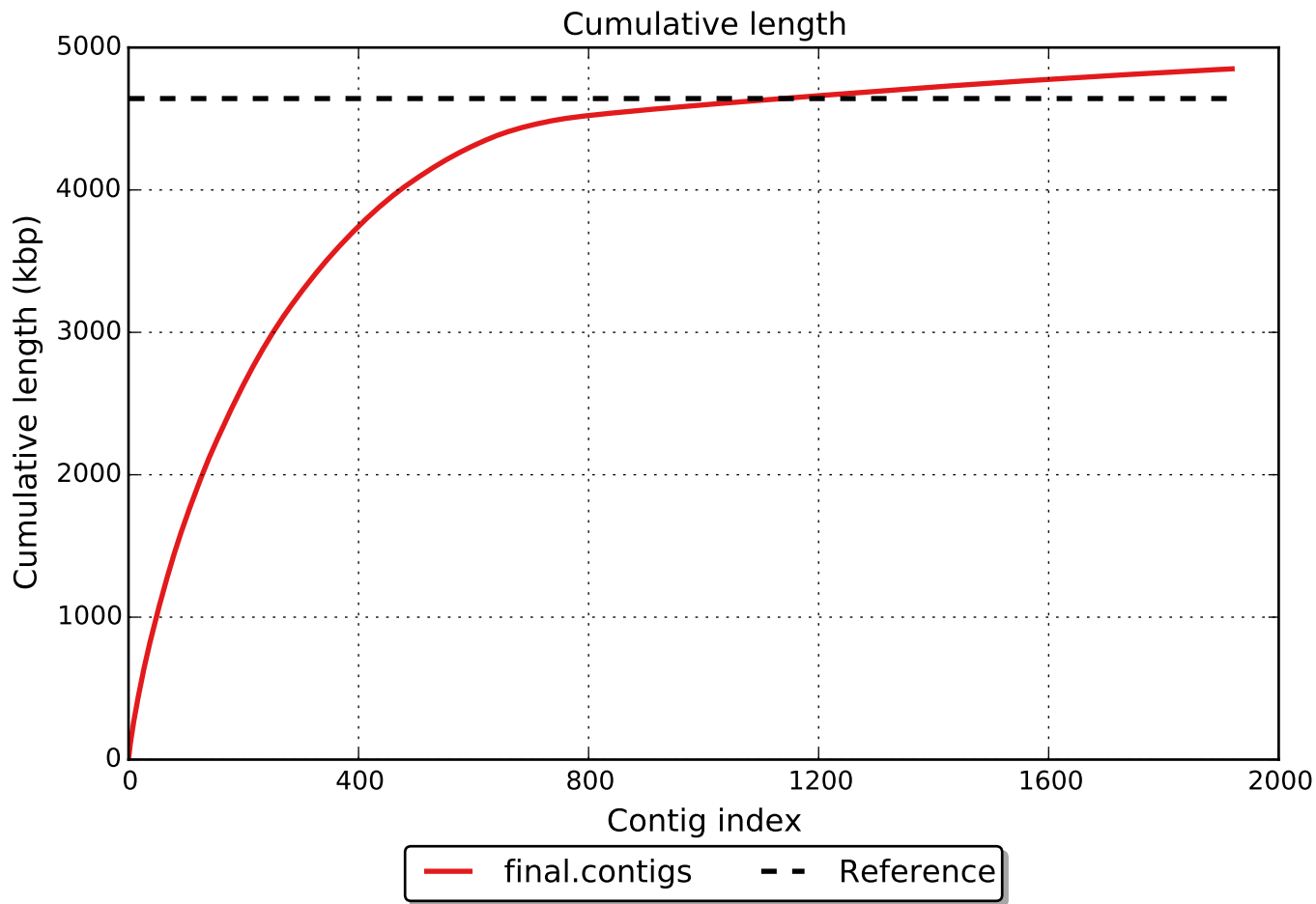
## Unaligned report

	final.contigs
# fully unaligned contigs	640
Fully unaligned length	206625
# partially unaligned contigs	9
# with misassembly	0
# both parts are significant	9
Partially unaligned length	1881
# N's	0

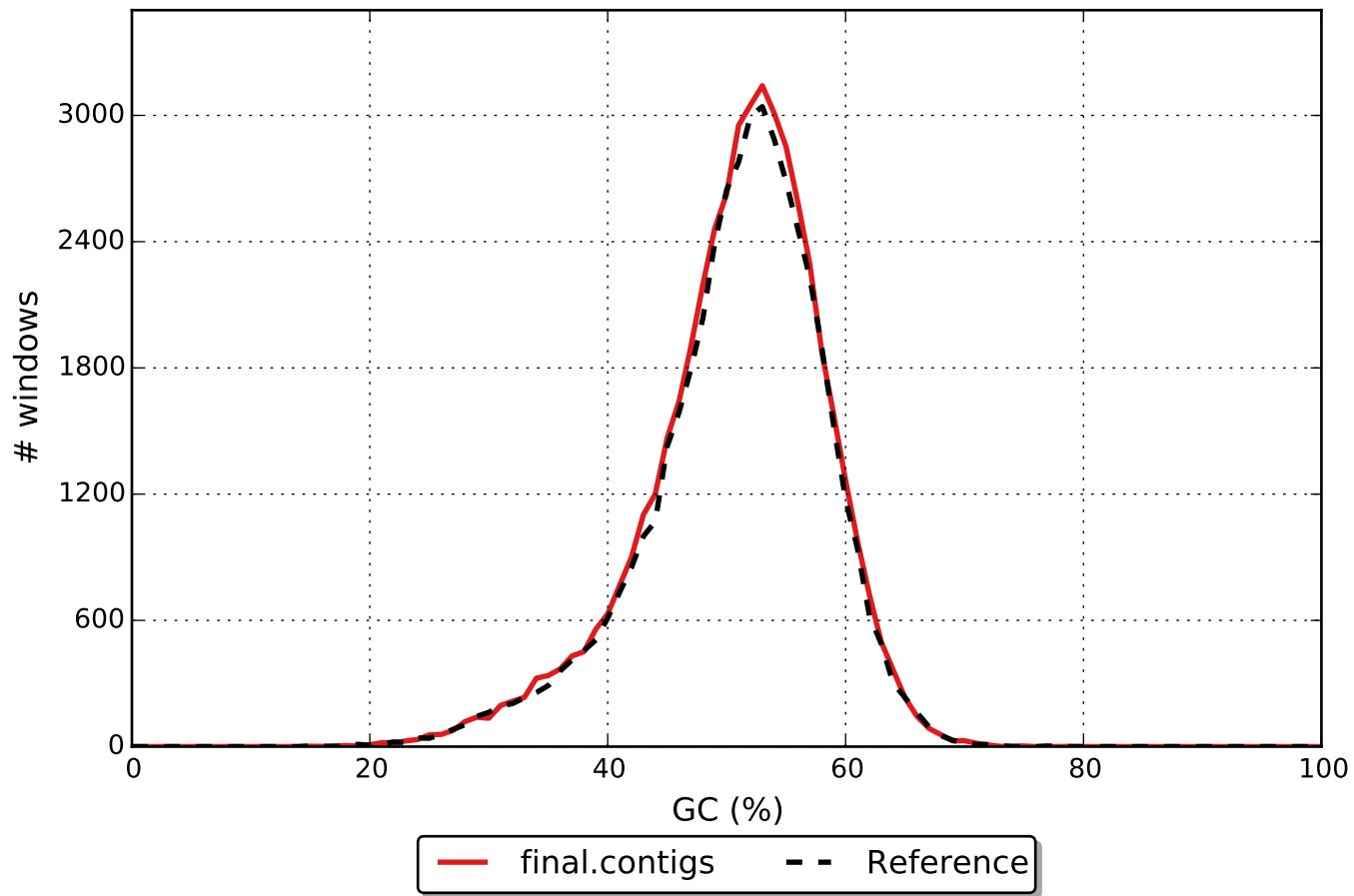


NGx





GC content

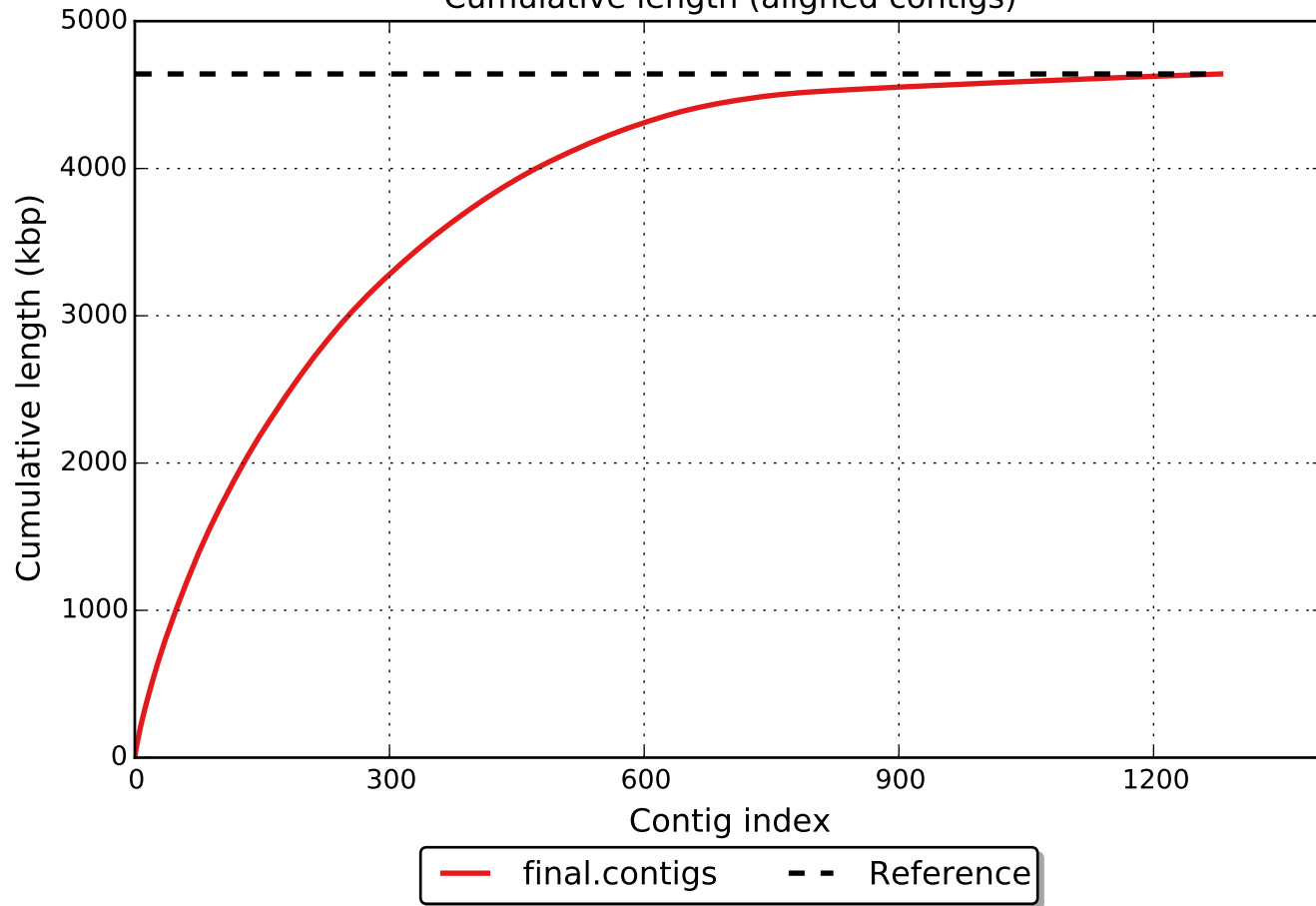


# Misassemblies

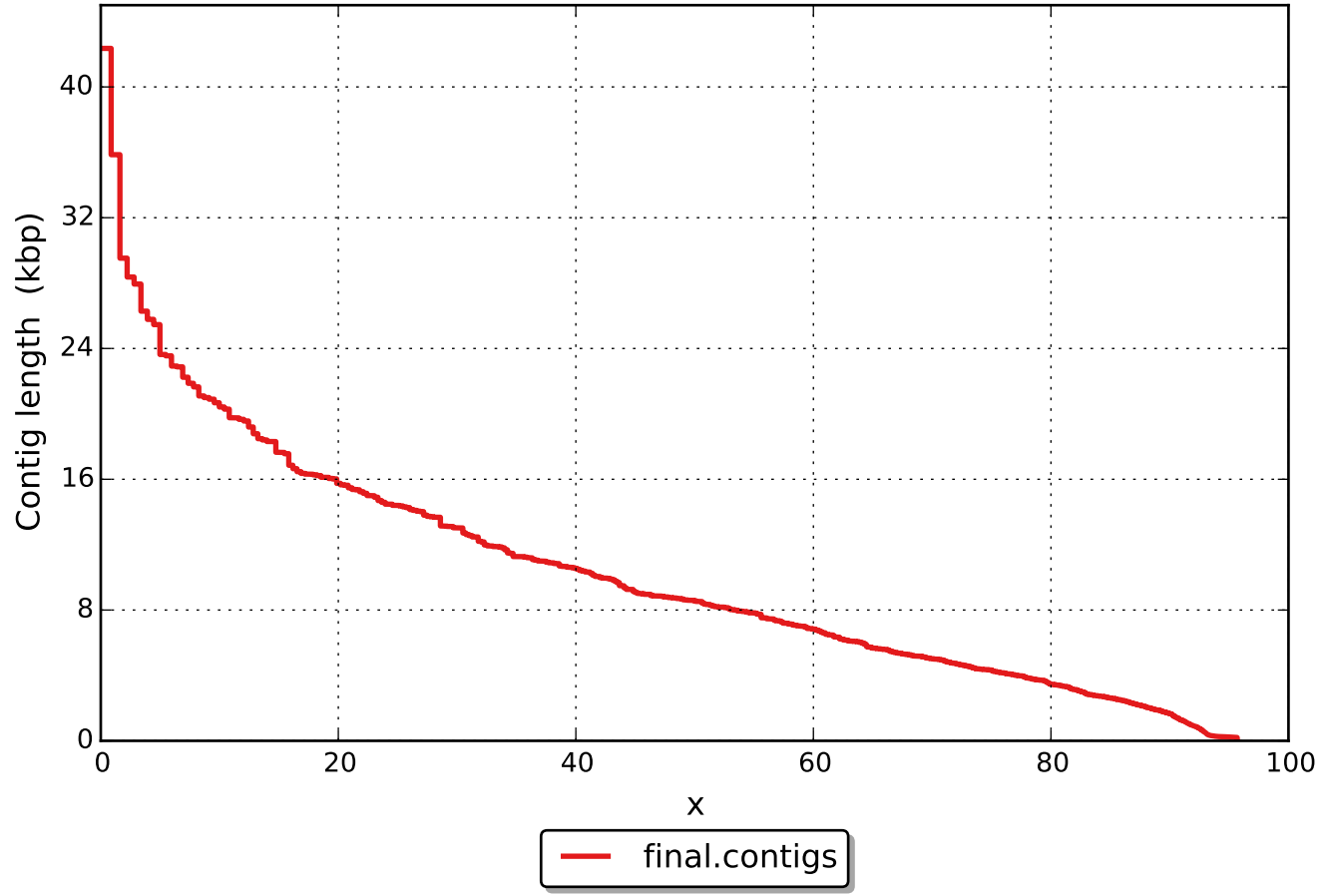




Cumulative length (aligned contigs)



NAx



# NGAx

