

# Report

	final.contigs
# contigs (>= 0 bp)	37328
# contigs (>= 1000 bp)	1913
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	16928197
Total length (>= 1000 bp)	2916630
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	37328
Largest contig	4310
Total length	16928197
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	407
NG50	1175
N75	335
NG75	863
L50	12250
LG50	1363
L75	23806
LG75	2522
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	35031 + 59 part
Unaligned length	14320355
Genome fraction (%)	53.890
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	508.52
# indels per 100 kbp	0.44
Largest alignment	4310
NGA50	663
LGA50	1642

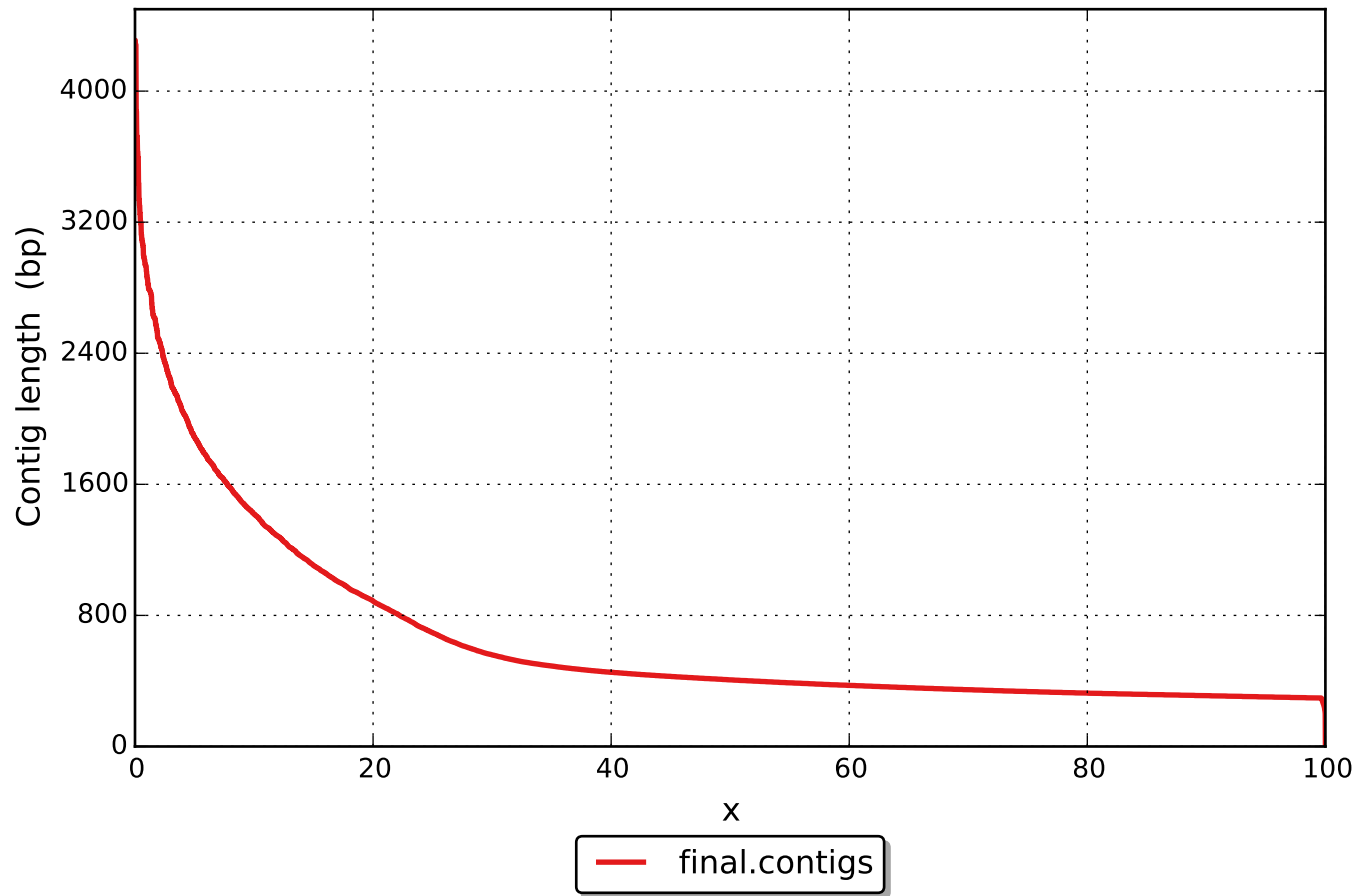
## Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	12720
# indels	11
# short indels	11
# long indels	0
Indels length	11

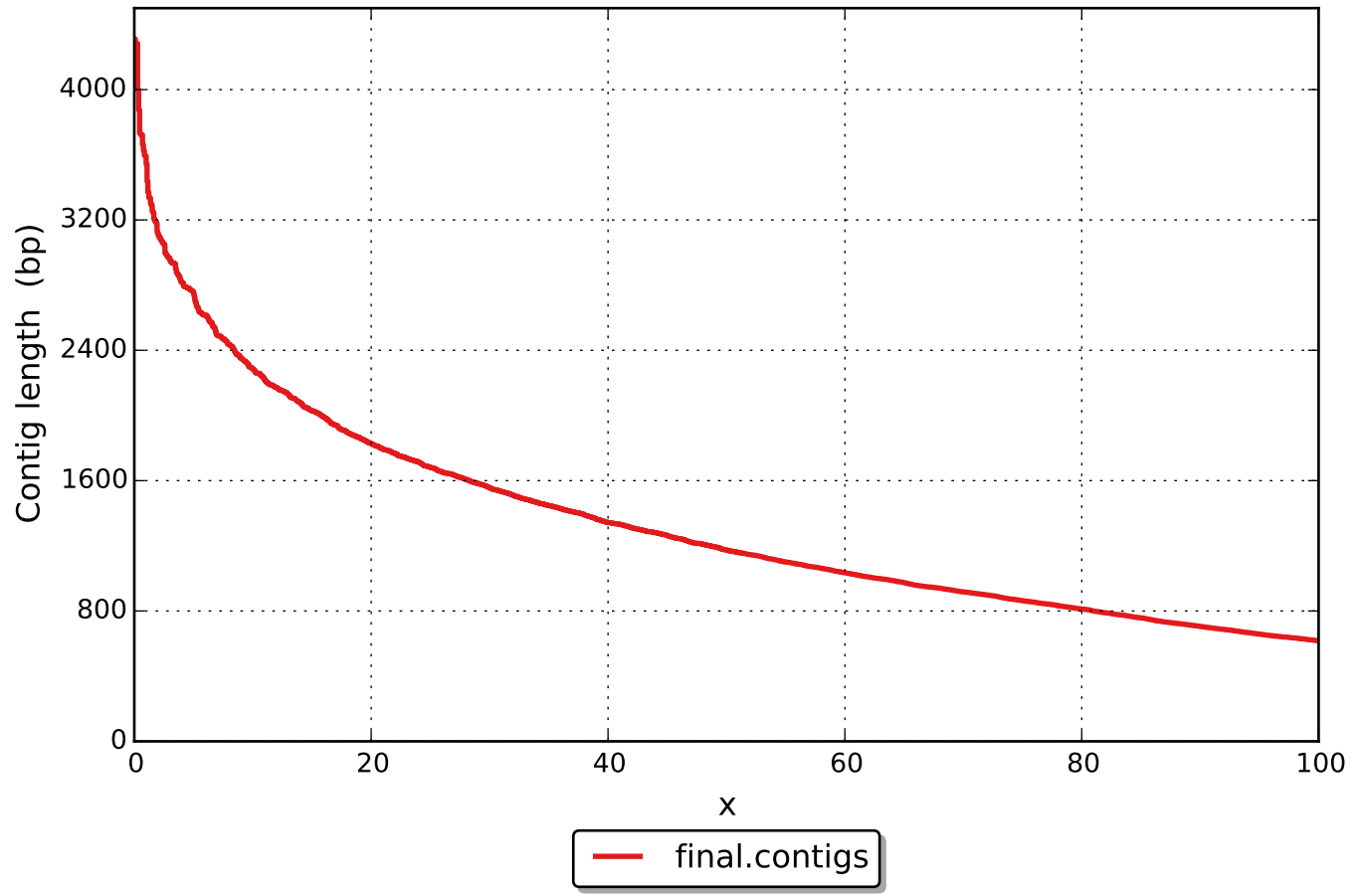
## Unaligned report

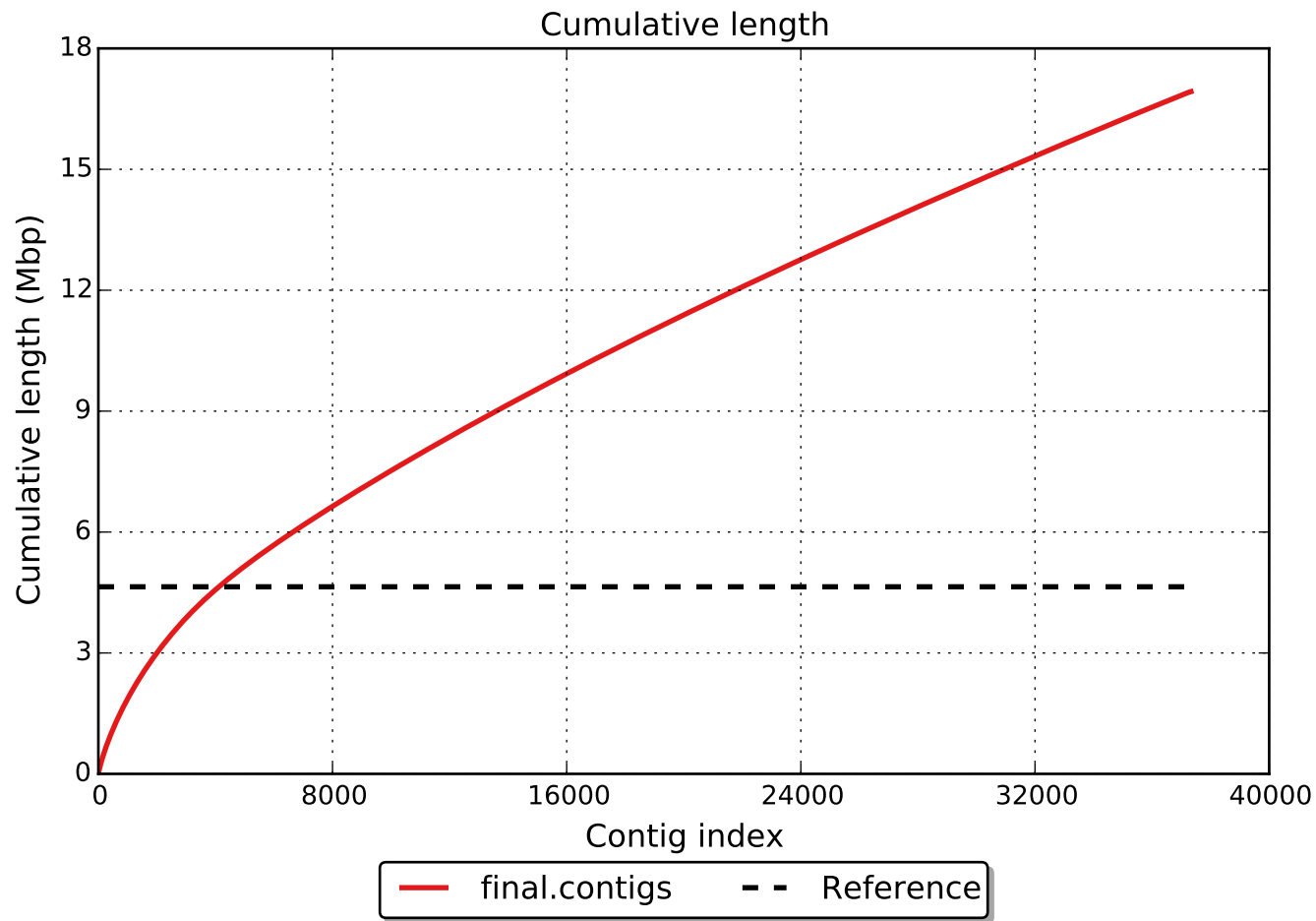
	final.contigs
# fully unaligned contigs	35031
Fully unaligned length	14303115
# partially unaligned contigs	59
# with misassembly	0
# both parts are significant	59
Partially unaligned length	17240
# N's	0

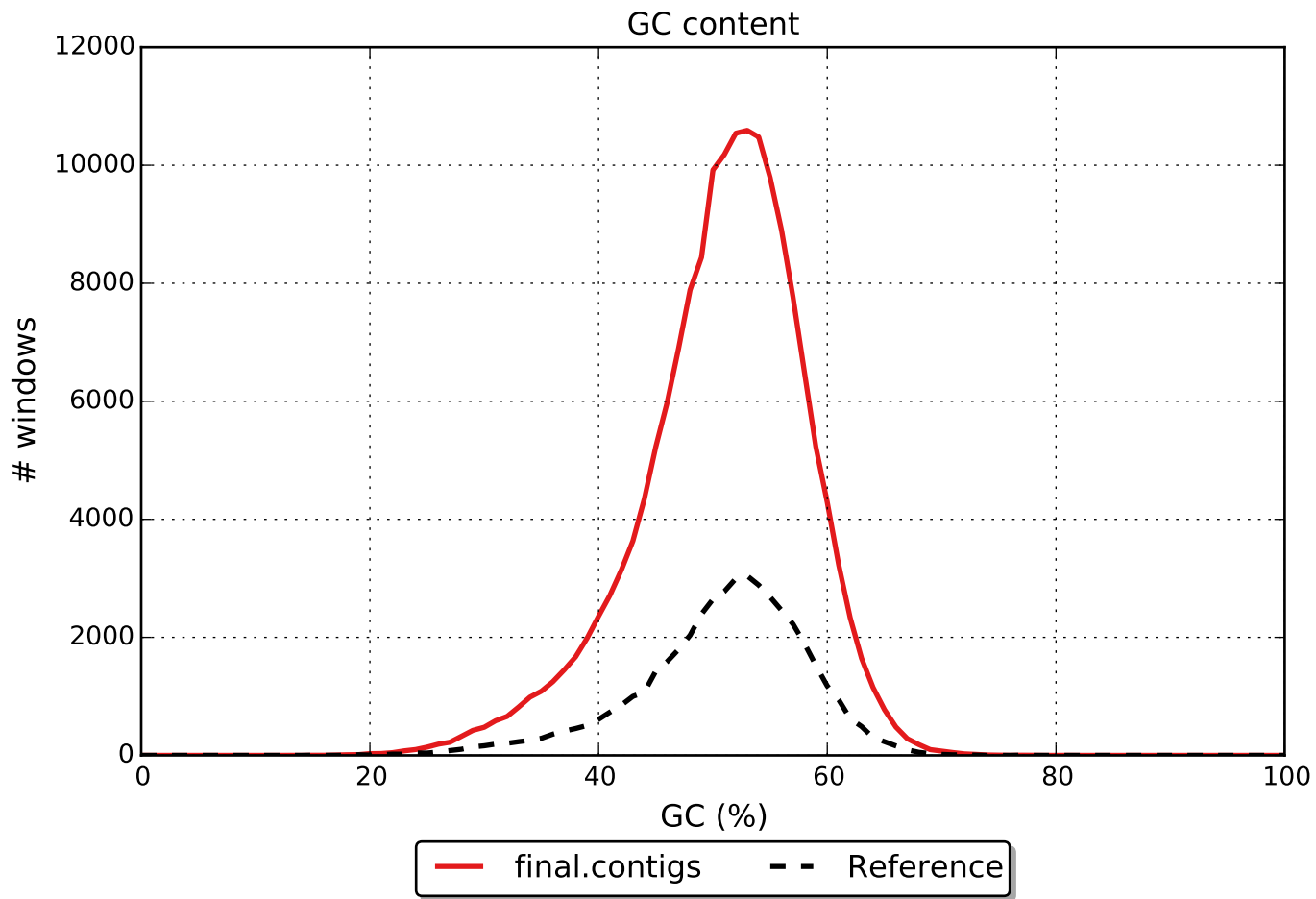
Nx



NGx





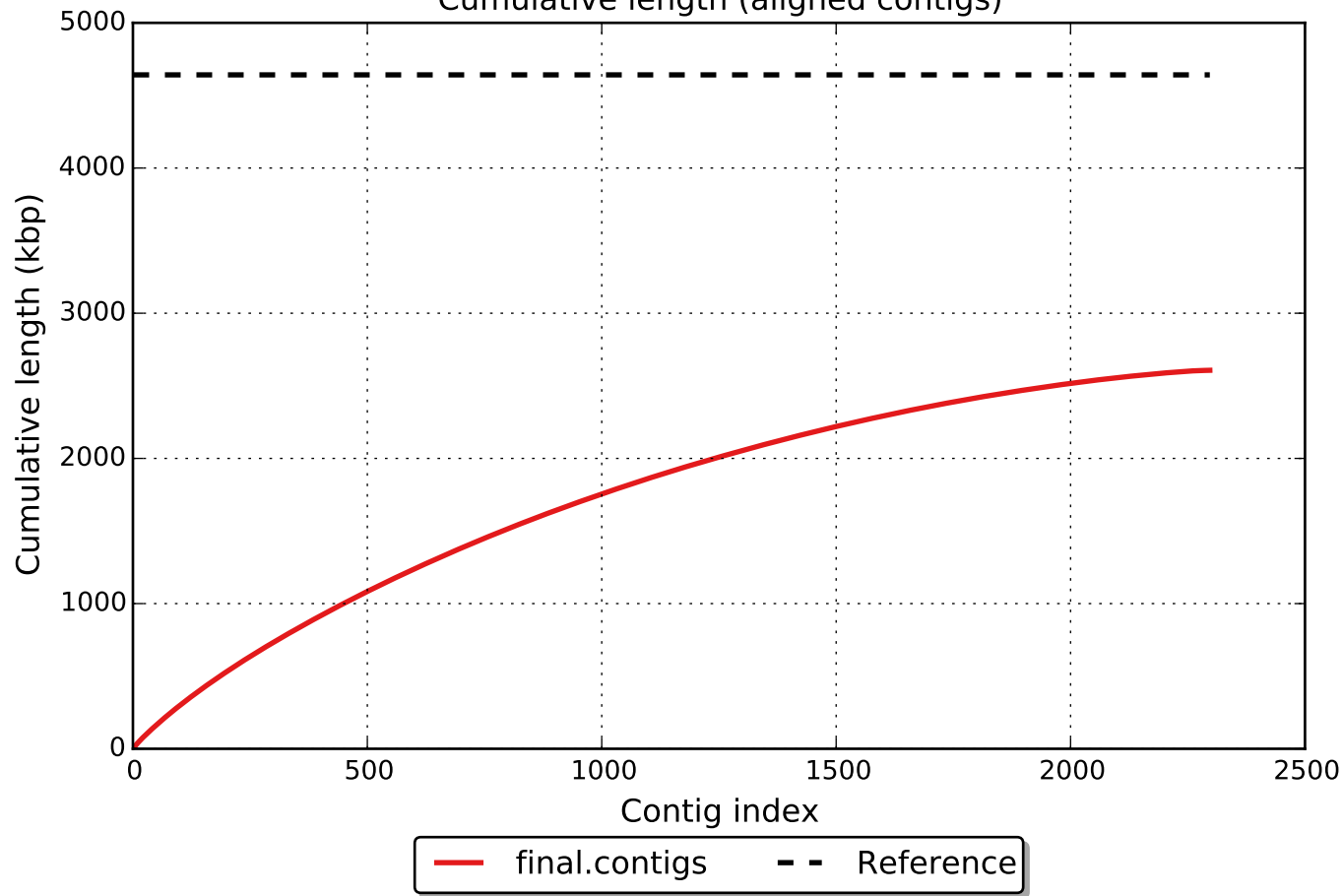


# Misassemblies

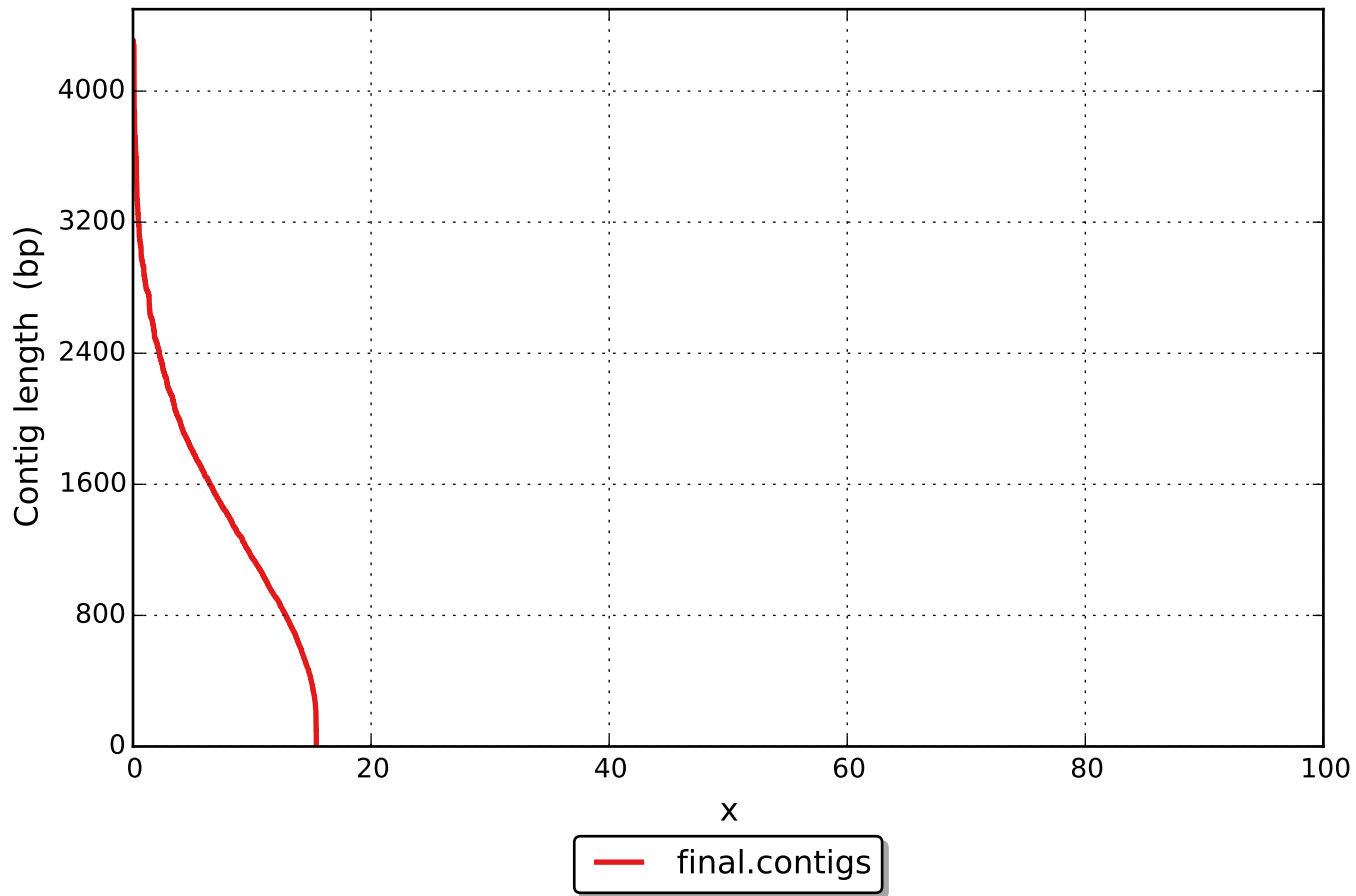




Cumulative length (aligned contigs)



NAx



NGAx

