

# Report

	final.contigs
# contigs ( $\geq 0$ bp)	3657
# contigs ( $\geq 1000$ bp)	575
# contigs ( $\geq 5000$ bp)	0
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	2482272
Total length ( $\geq 1000$ bp)	804538
Total length ( $\geq 5000$ bp)	0
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	3657
Largest contig	3631
Total length	2482272
Reference length	4641652
GC (%)	50.82
Reference GC (%)	50.79
N50	764
NG50	350
N75	514
L50	1078
LG50	3150
L75	2074
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	5007
# local misassemblies	1
# unaligned contigs	11 + 15 part
Unaligned length	10568
Genome fraction (%)	53.208
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.75
# indels per 100 kbp	0.20
Largest alignment	3631
NA50	760
NGA50	345
NA75	510
LA50	1083
LGA50	3172
LA75	2086

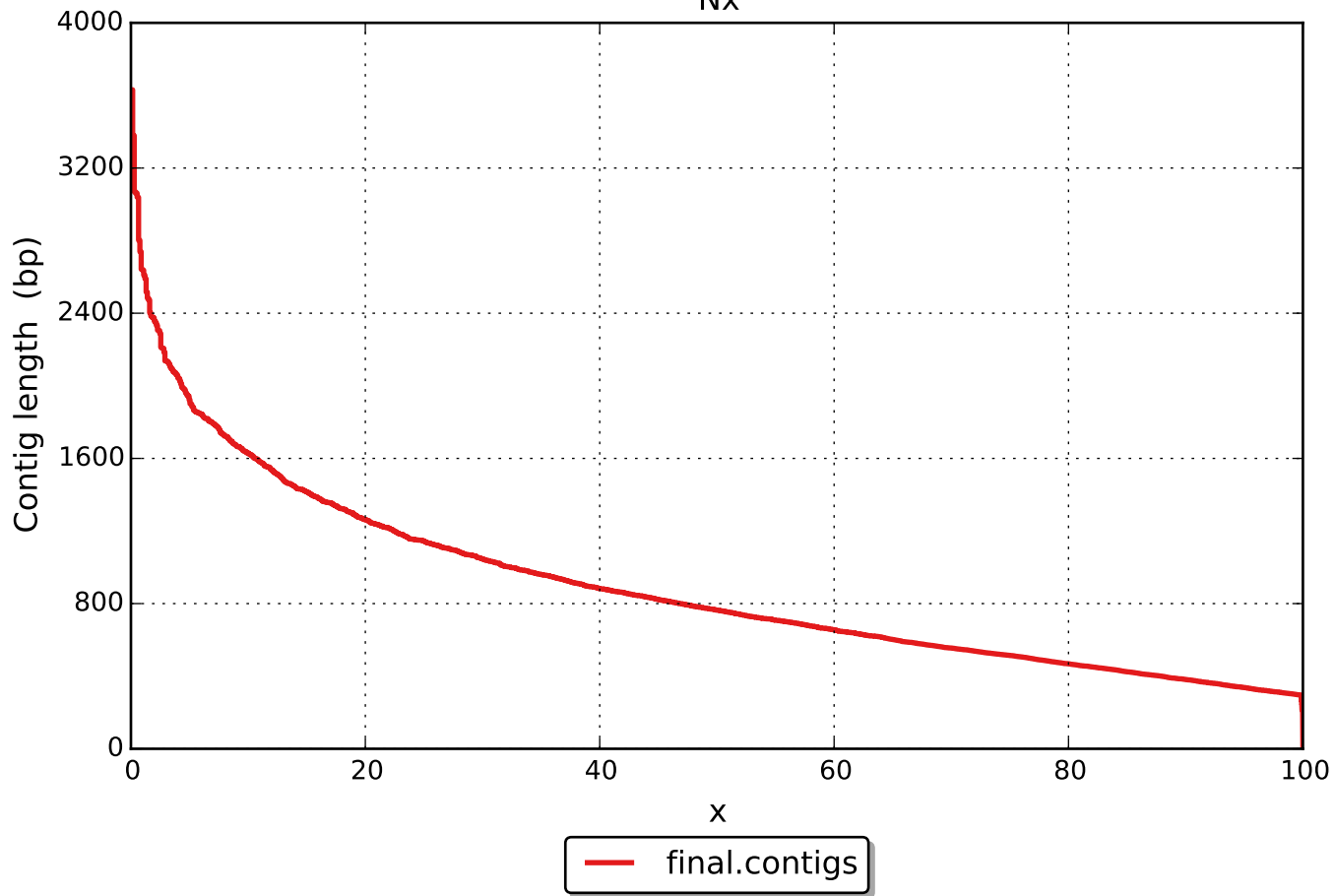
## Misassemblies report

	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	5007
# local misassemblies	1
# mismatches	68
# indels	5
# short indels	5
# long indels	0
Indels length	5

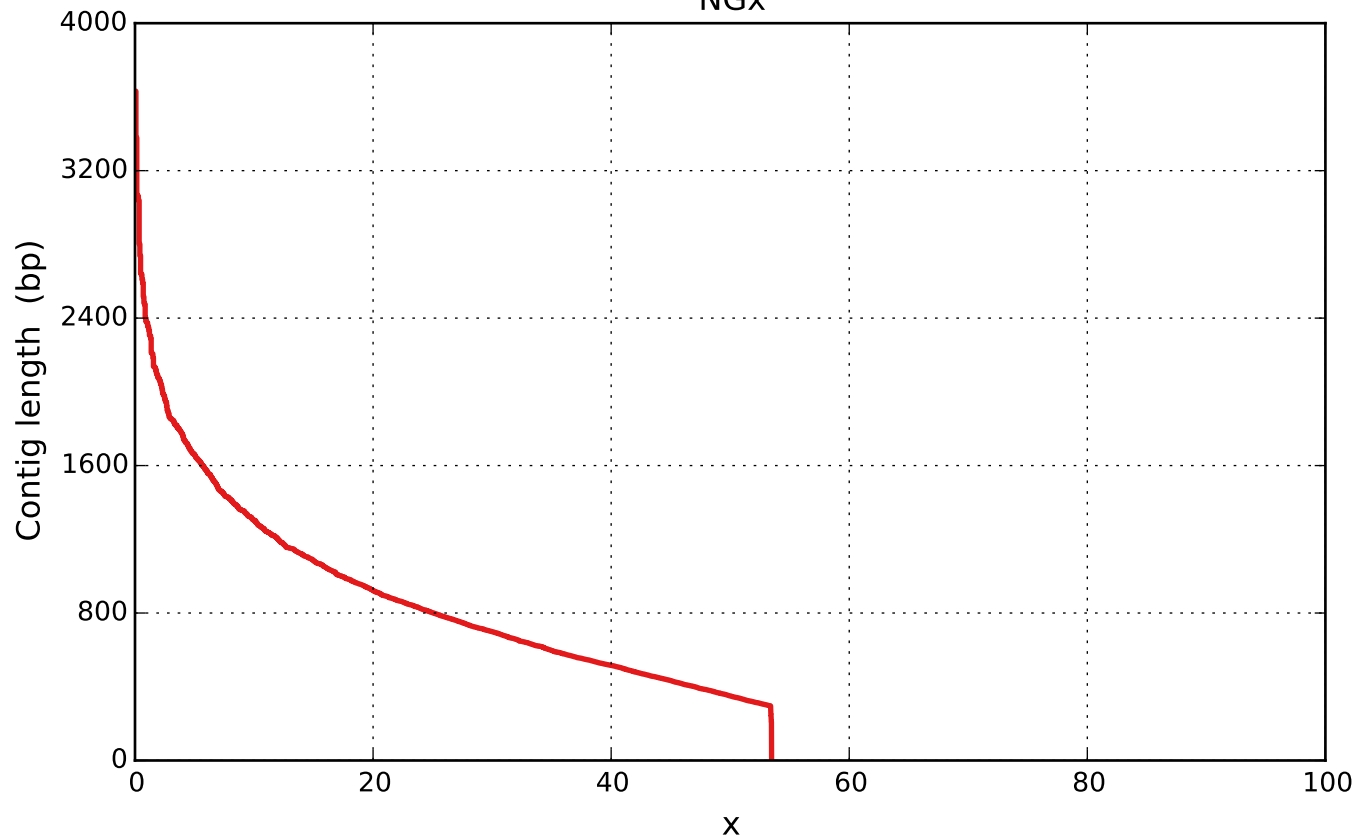
## Unaligned report

	final.contigs
# fully unaligned contigs	11
Fully unaligned length	7390
# partially unaligned contigs	15
# with misassembly	0
# both parts are significant	15
Partially unaligned length	3178
# N's	0

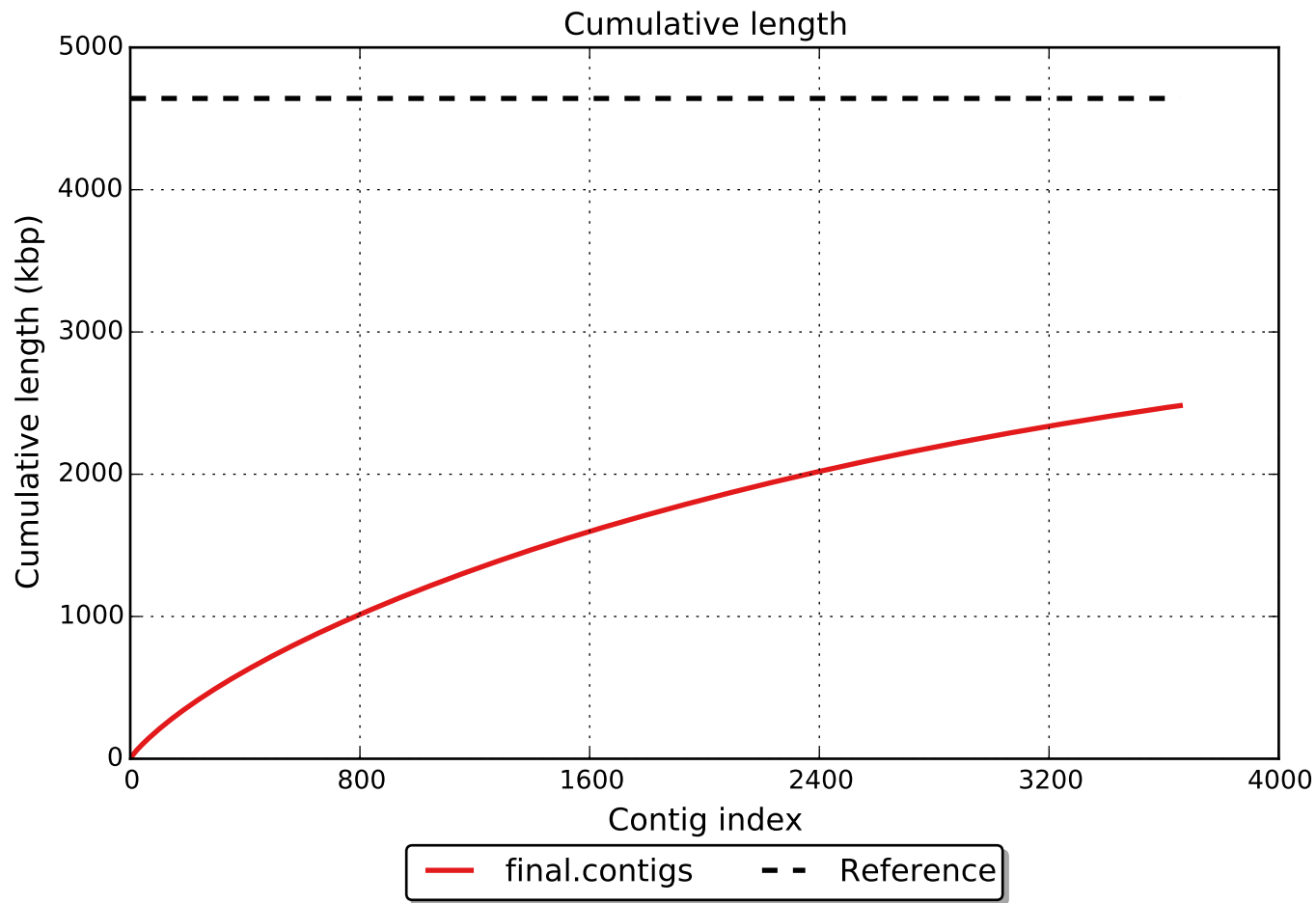
Nx



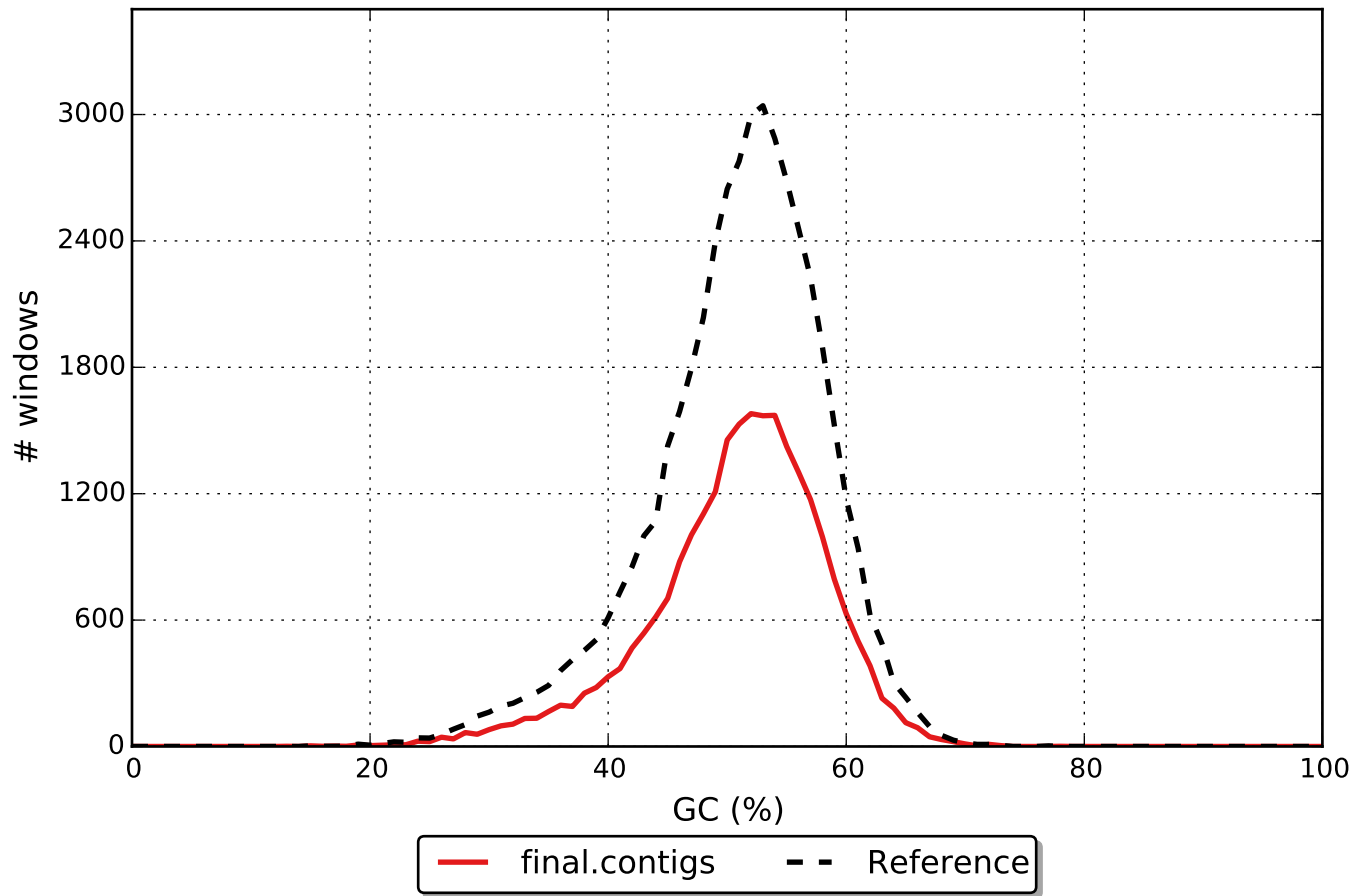
NGx



— final.contigs



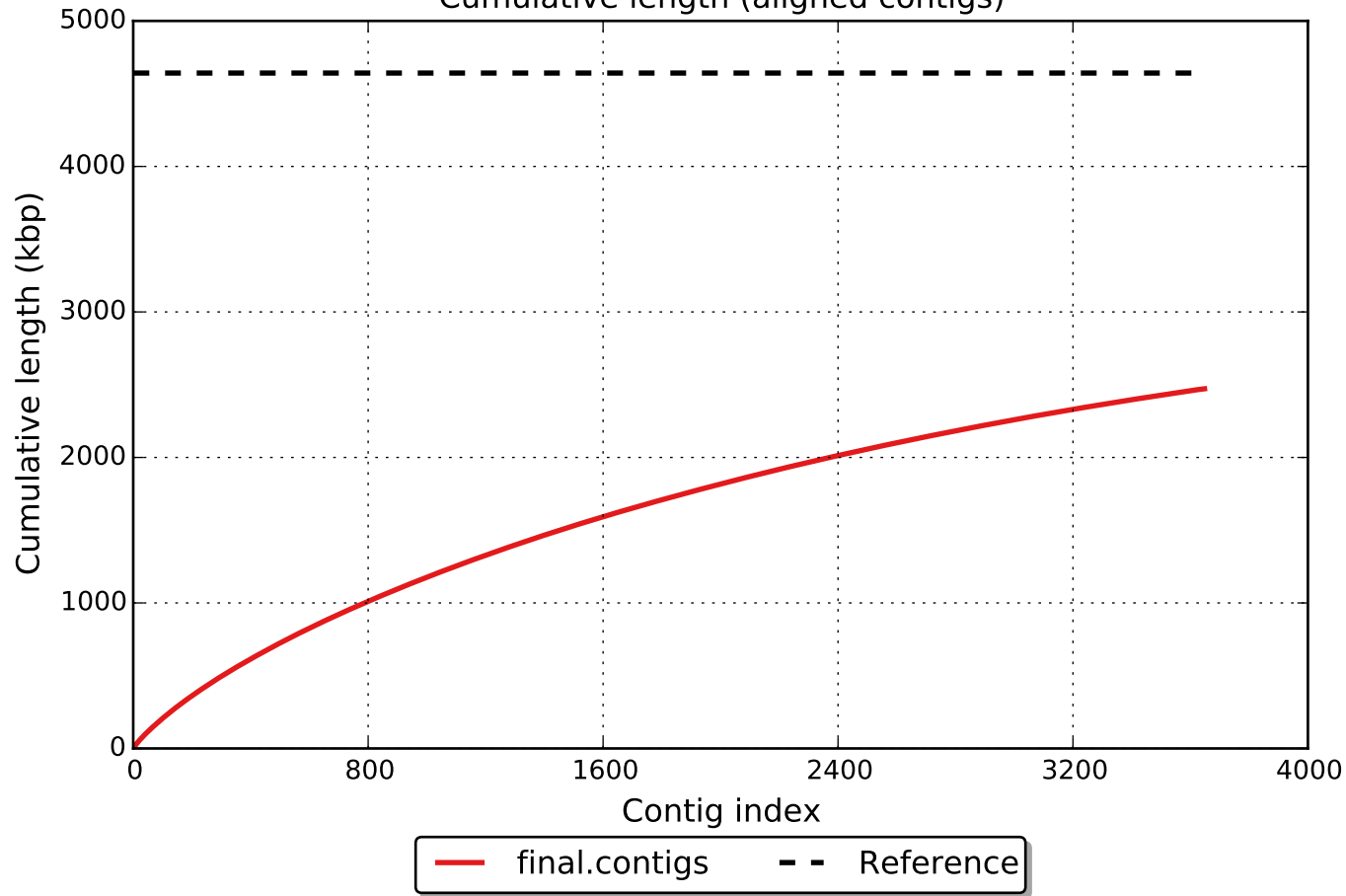
GC content



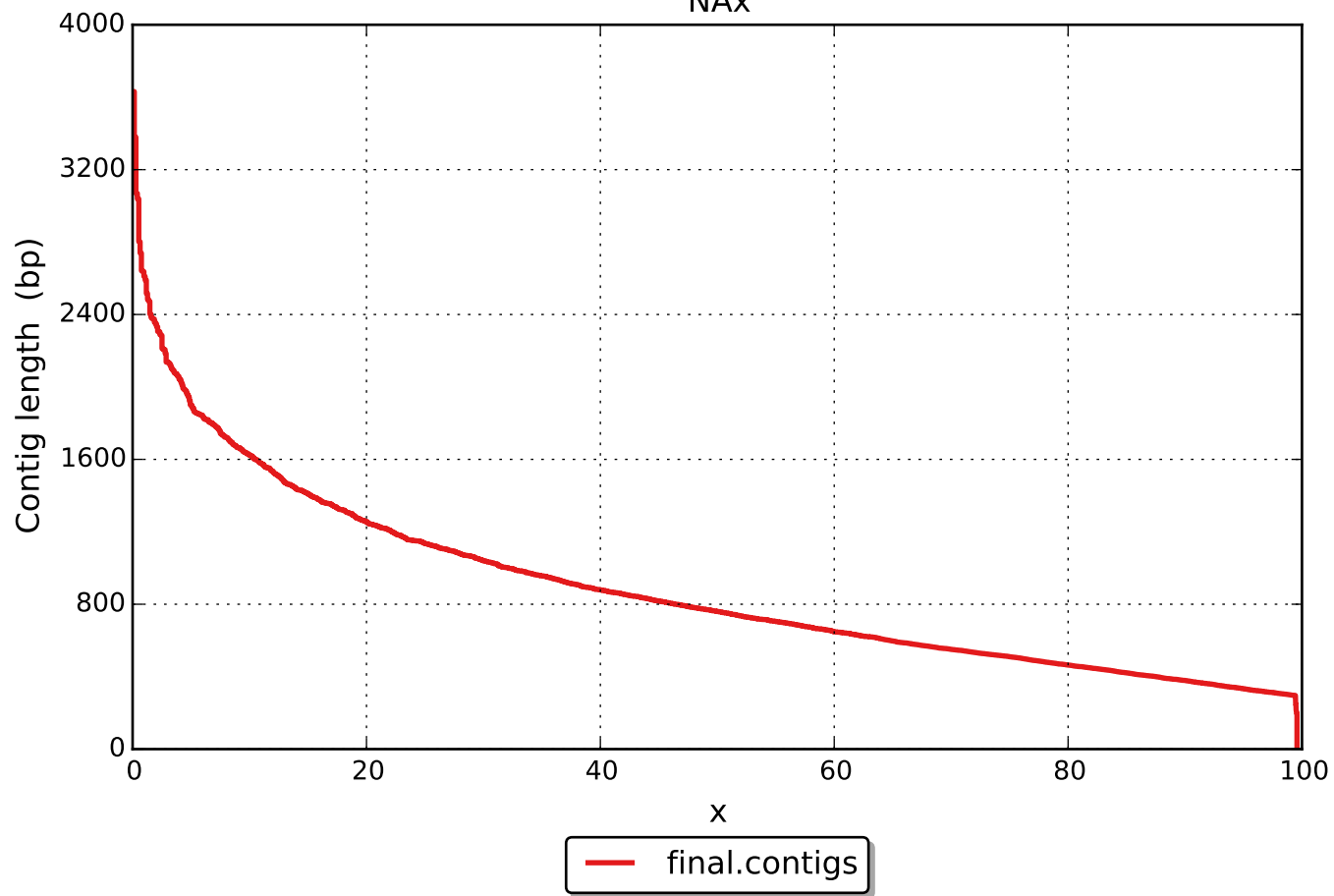




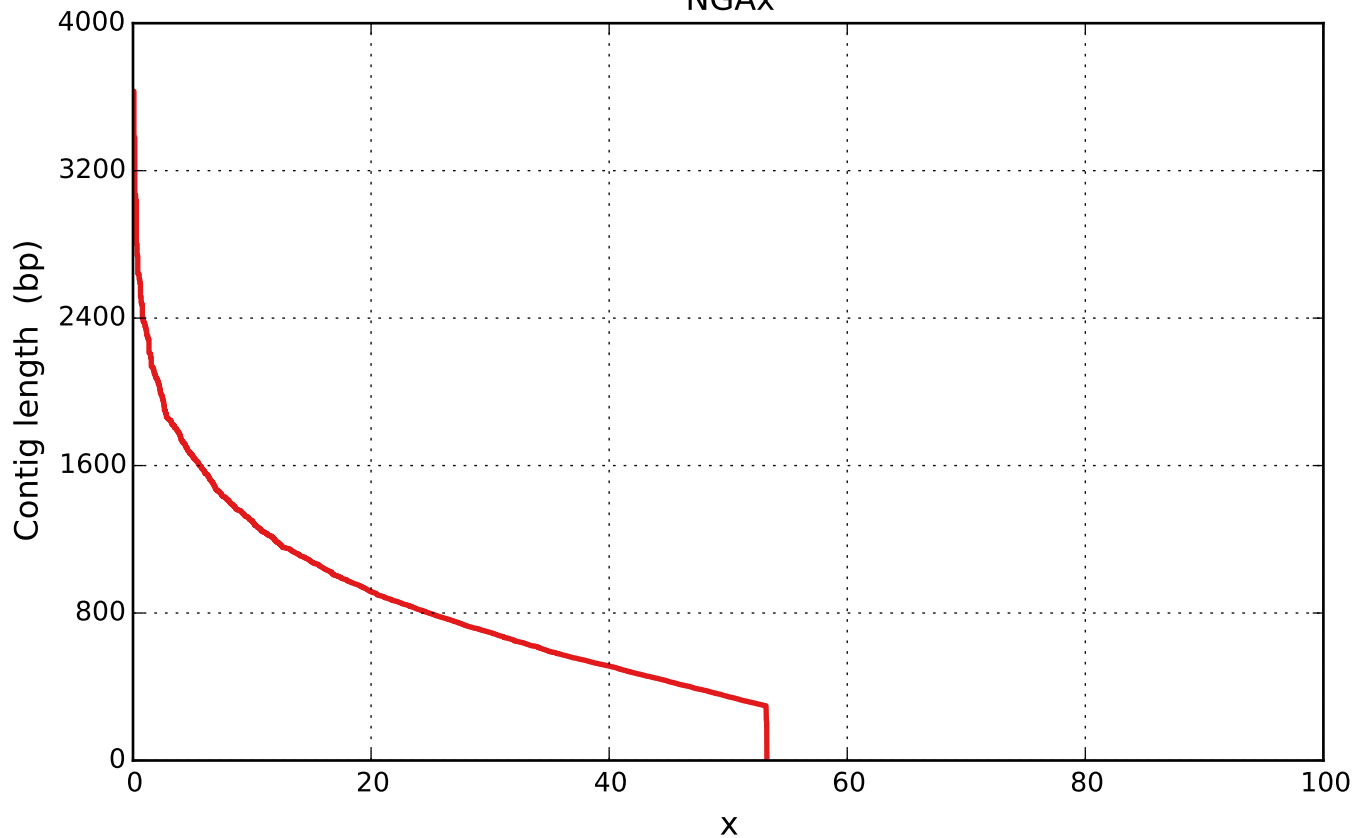
Cumulative length (aligned contigs)



NAx



NGAx



— final.contigs