

# Report

	final.contigs
# contigs ( $\geq 0$ bp)	3817
# contigs ( $\geq 1000$ bp)	119
# 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)	1910447
Total length ( $\geq 1000$ bp)	147351
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	3817
Largest contig	2634
Total length	1910447
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	503
N75	397
L50	1368
L75	2439
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	7880
# local misassemblies	0
# unaligned contigs	2297 + 8 part
Unaligned length	1138866
Genome fraction (%)	16.557
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	610.01
# indels per 100 kbp	0.91
Largest alignment	2463
NGA50	-

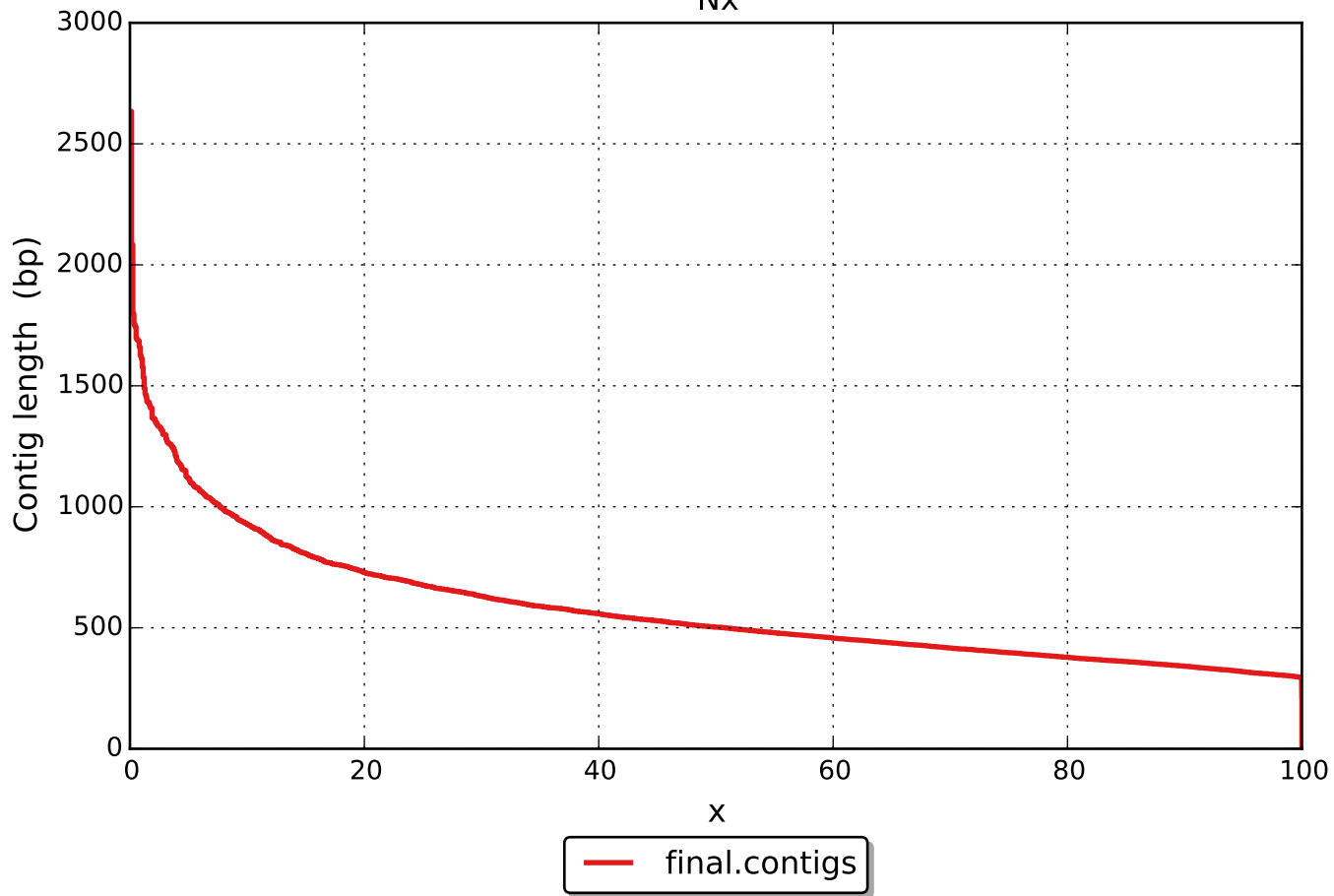
## Misassemblies report

	final.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	4
Misassembled contigs length	7880
# local misassemblies	0
# mismatches	4688
# indels	7
# short indels	7
# long indels	0
Indels length	7

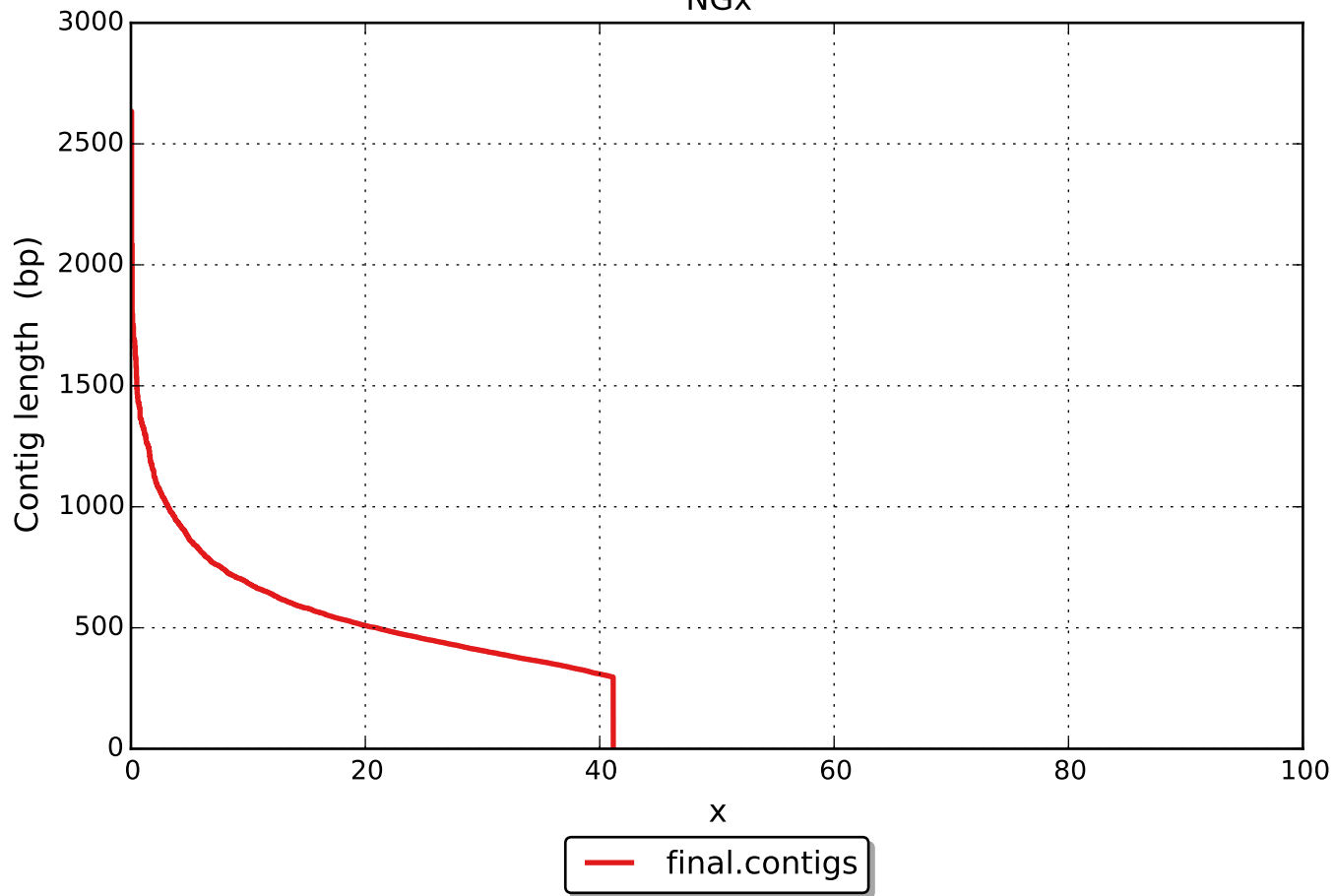
## Unaligned report

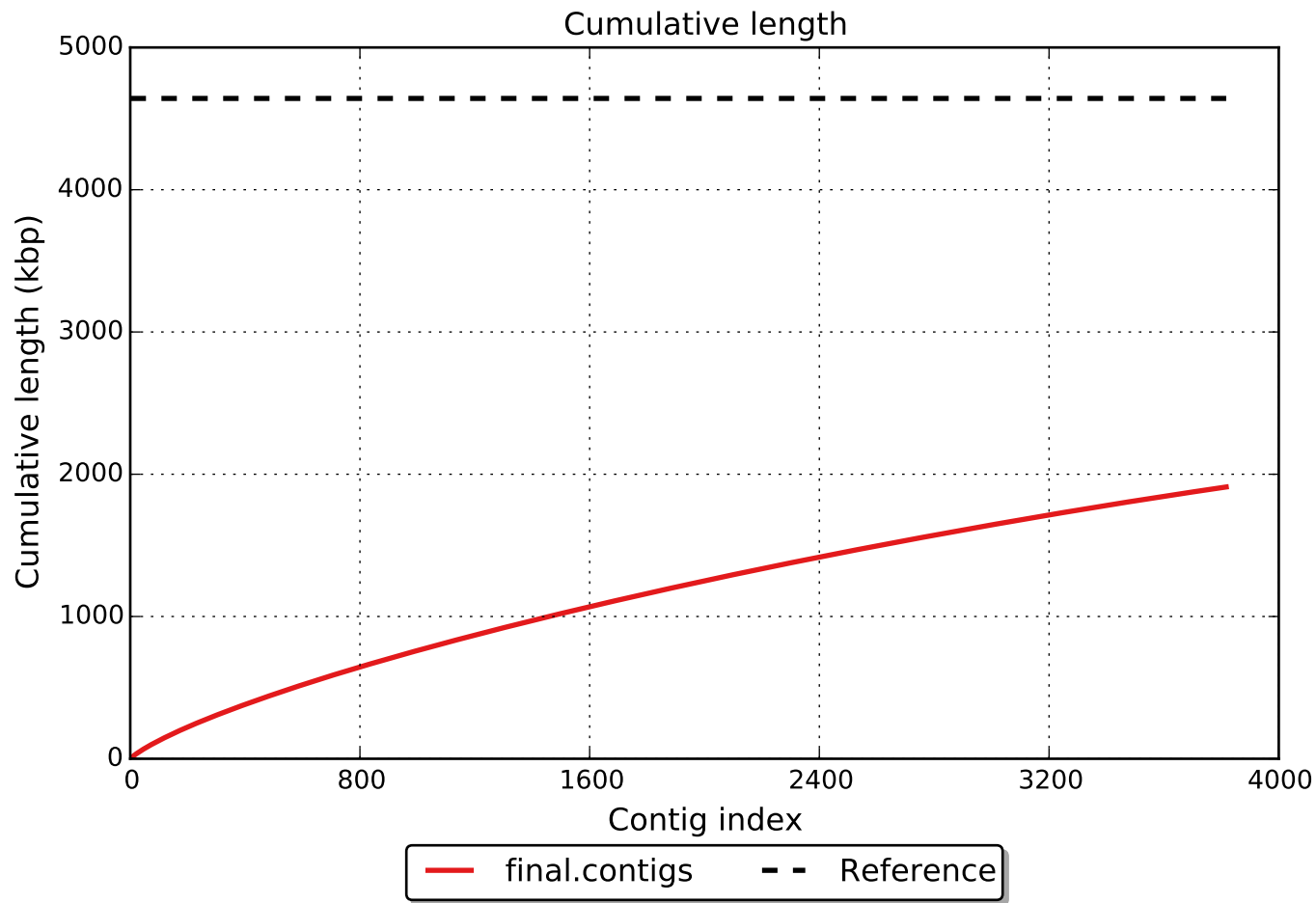
	final.contigs
# fully unaligned contigs	2297
Fully unaligned length	1136254
# partially unaligned contigs	8
# with misassembly	0
# both parts are significant	8
Partially unaligned length	2612
# N's	0

Nx

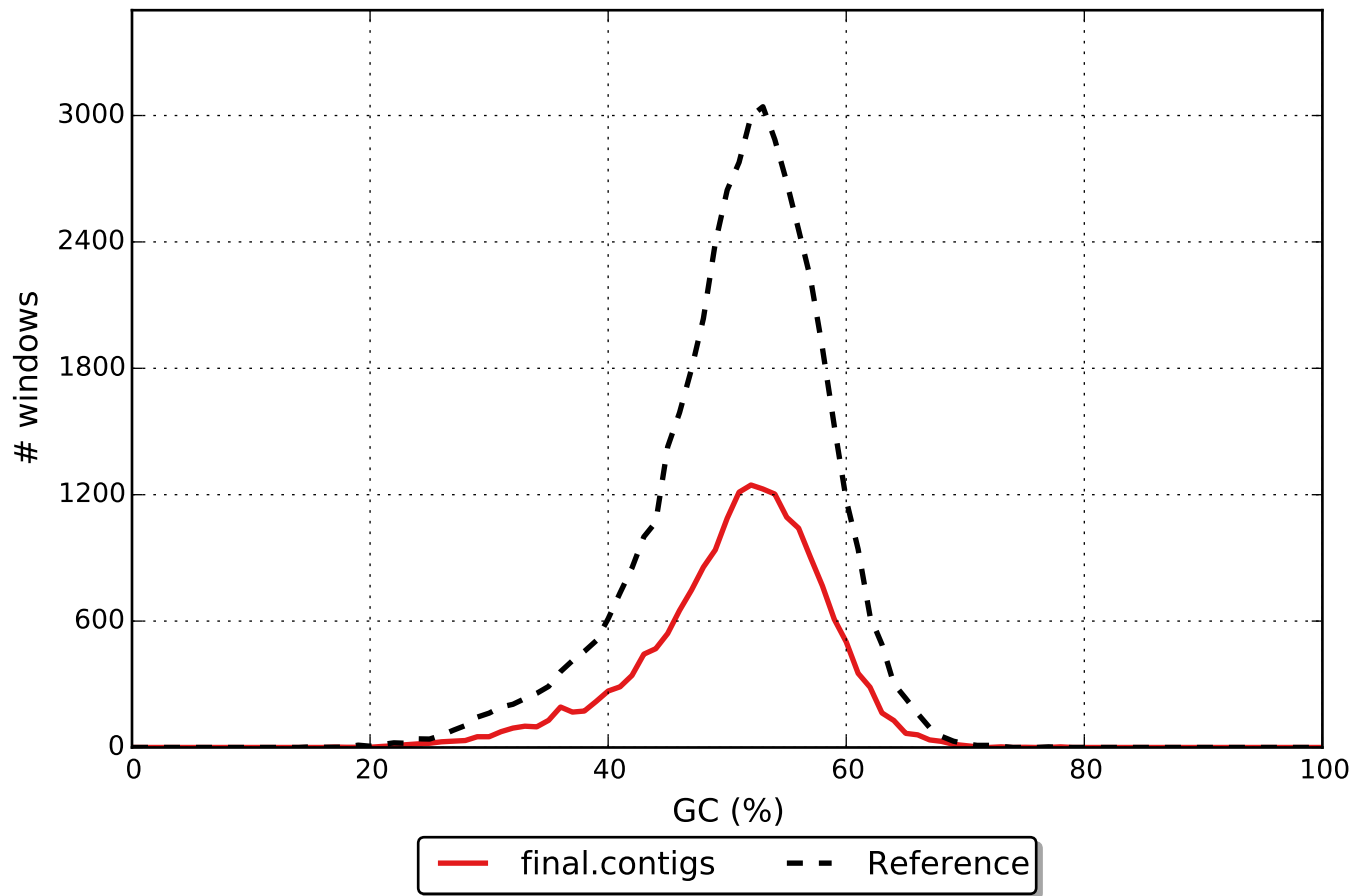


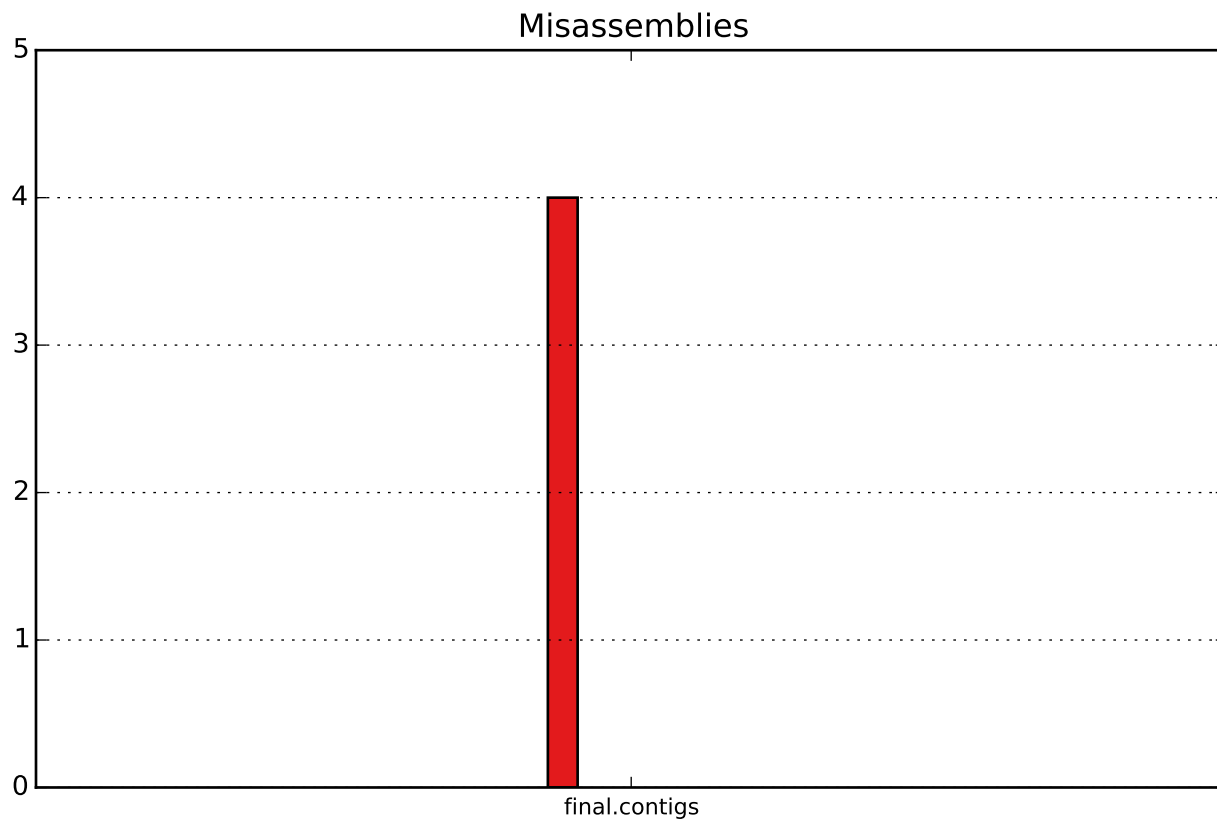
NGx





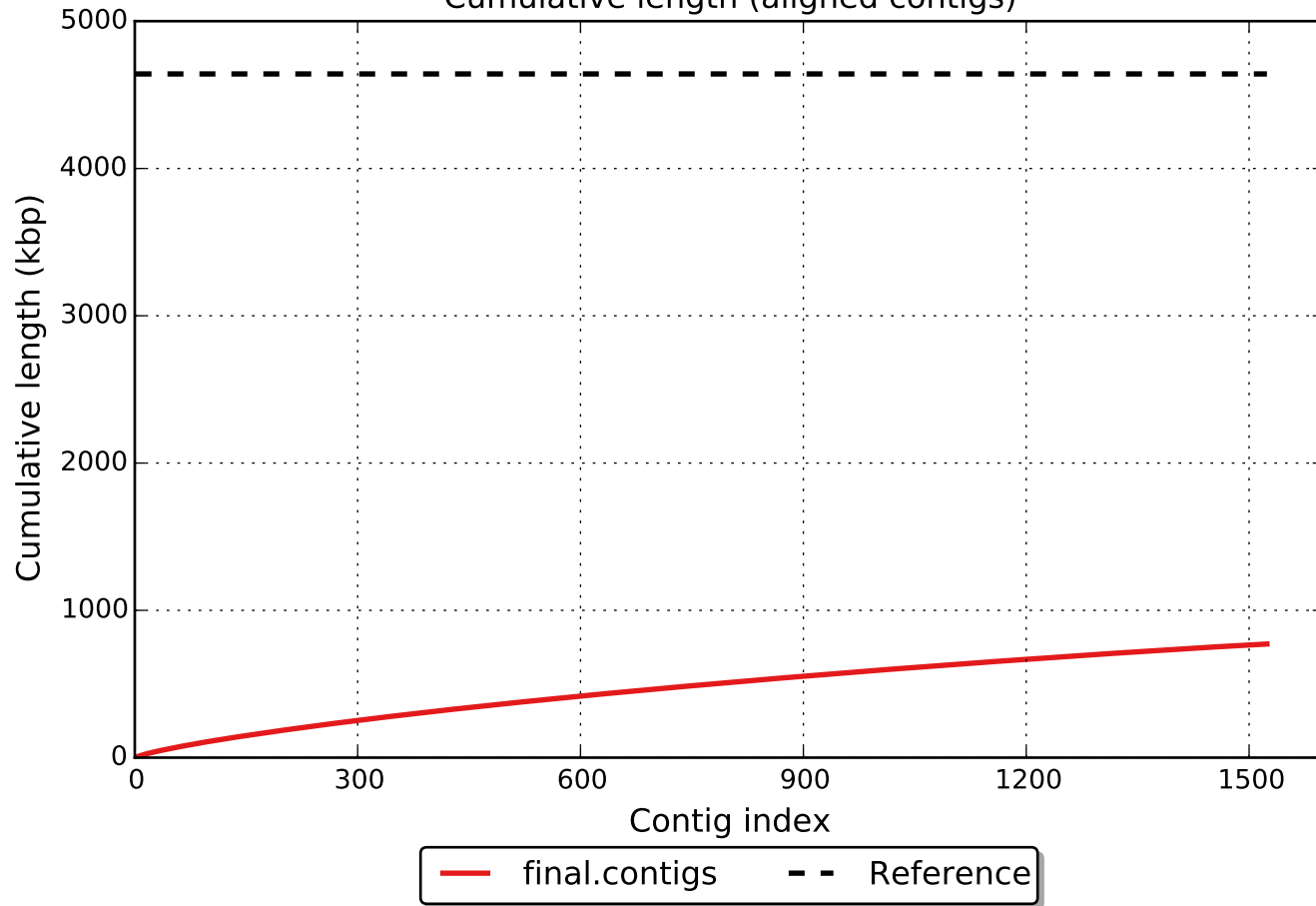
GC content



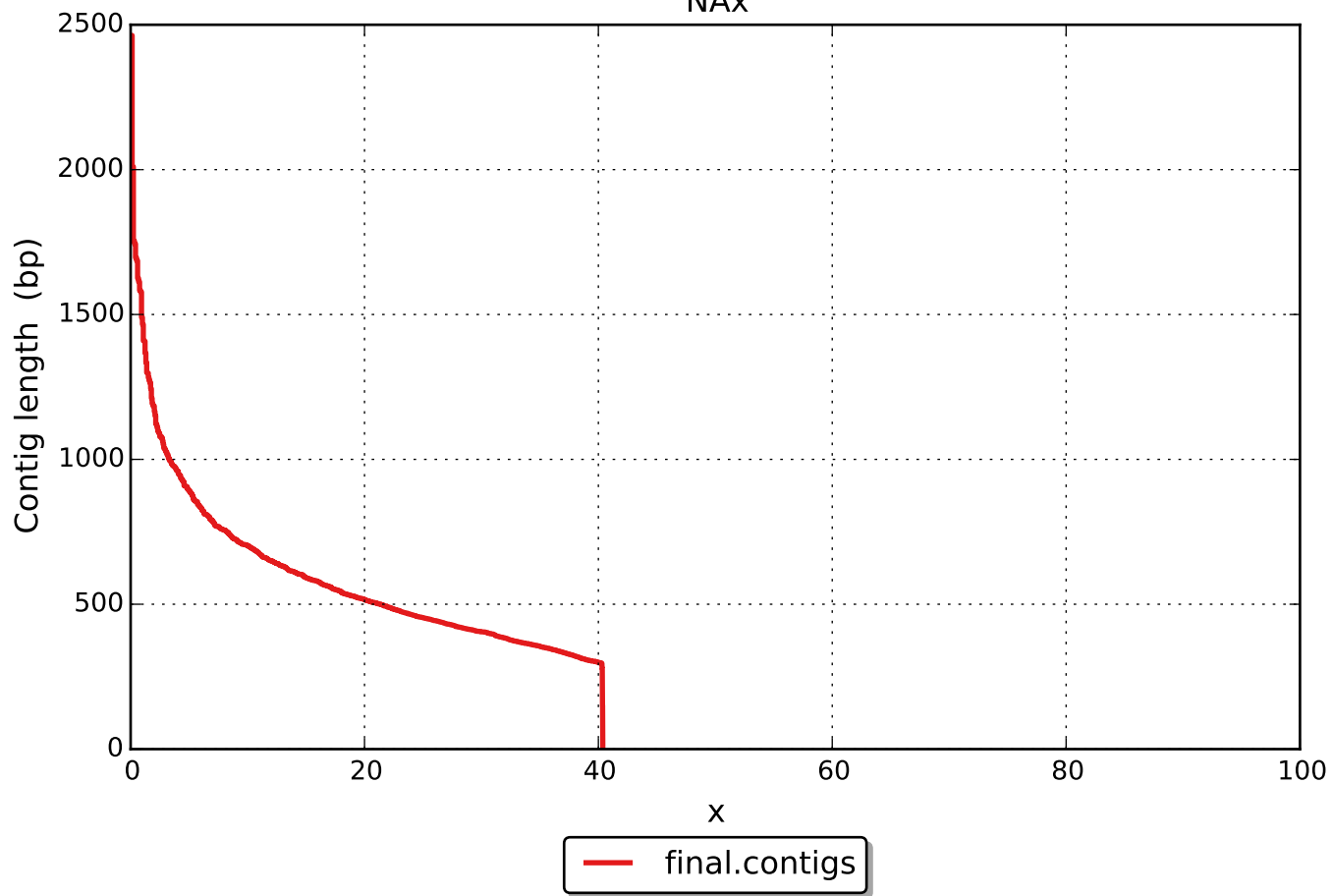




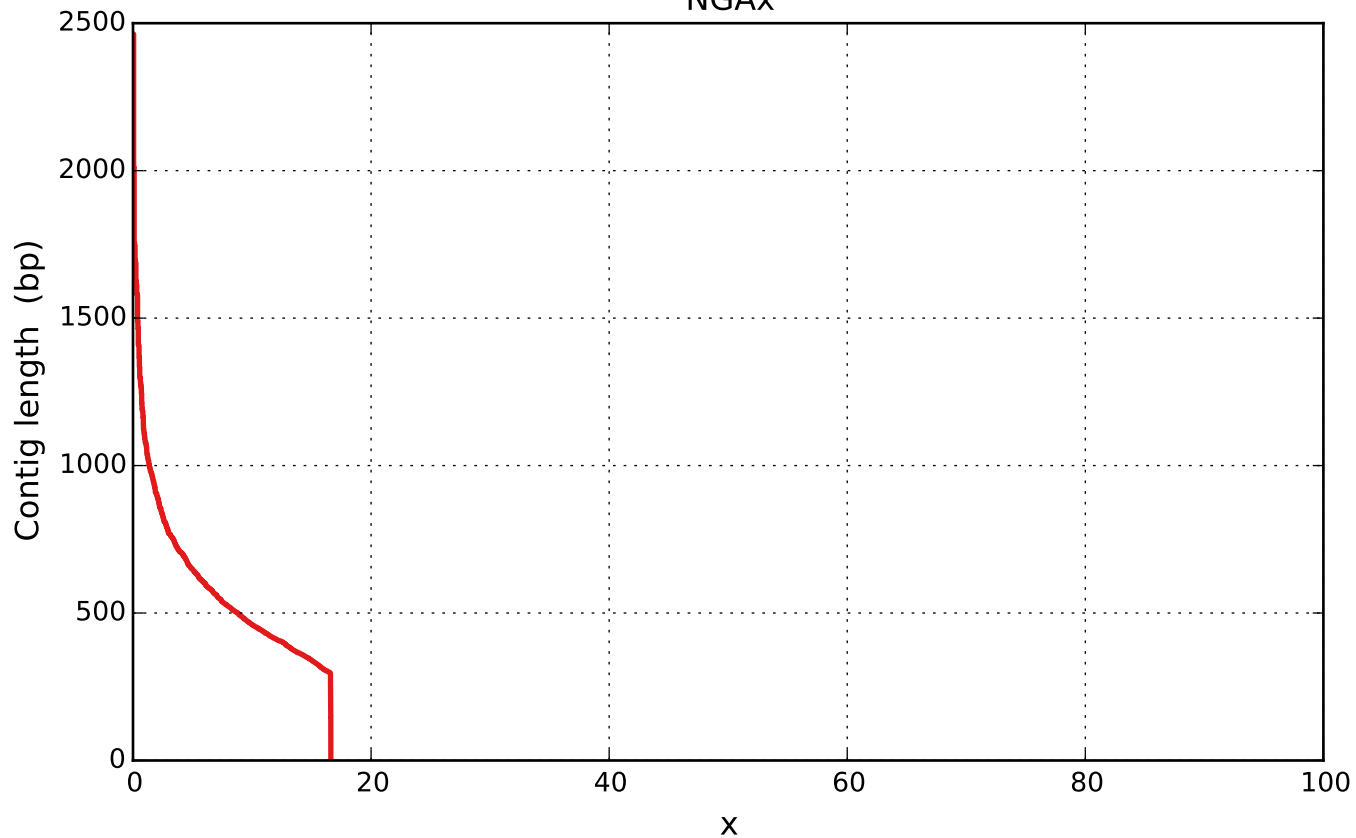
Cumulative length (aligned contigs)



NAx



NGAx



— final.contigs