

Report

	final.contigs
# contigs (≥ 0 bp)	1519
# contigs (≥ 1000 bp)	3
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	609335
Total length (≥ 1000 bp)	3352
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1519
Largest contig	1195
Total length	609335
Reference length	4641652
GC (%)	50.65
Reference GC (%)	50.79
N50	394
N75	346
L50	630
L75	1044
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	1515 + 2 part
Unaligned length	606741
Genome fraction (%)	0.056
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	810.50
# indels per 100 kbp	0.00
Largest alignment	1050
NGA50	-

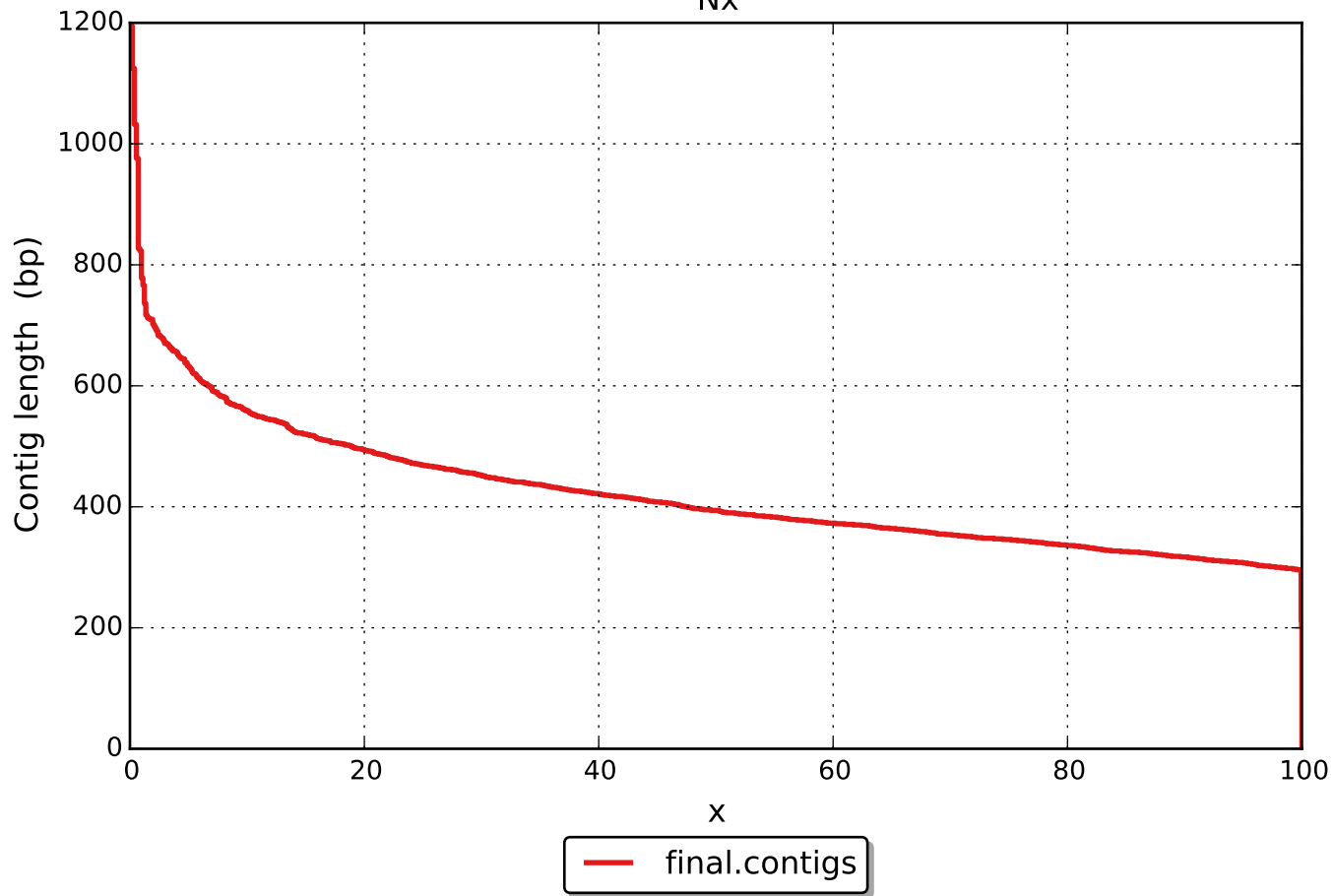
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	21
# indels	0
# short indels	0
# long indels	0
Indels length	0

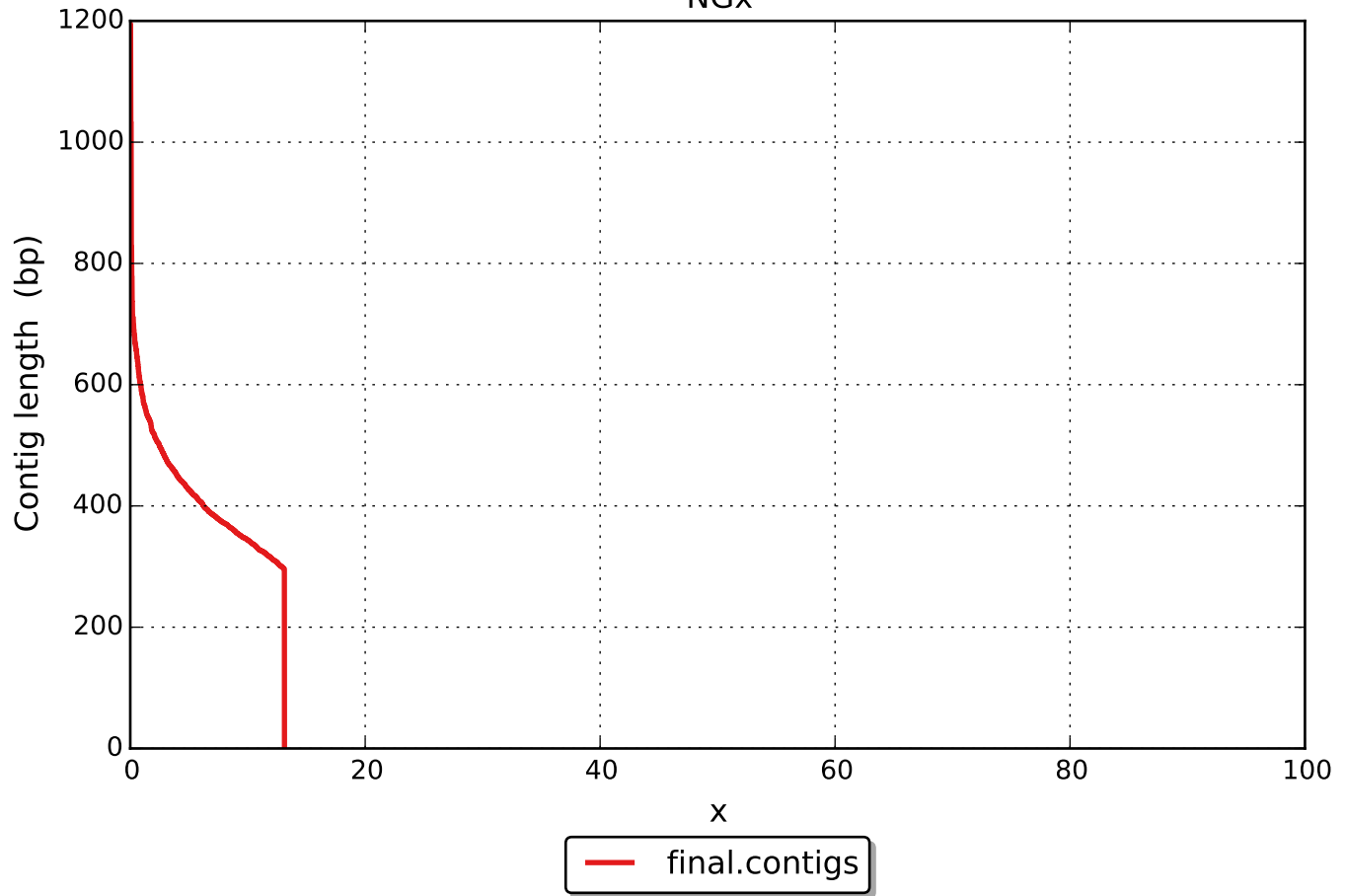
Unaligned report

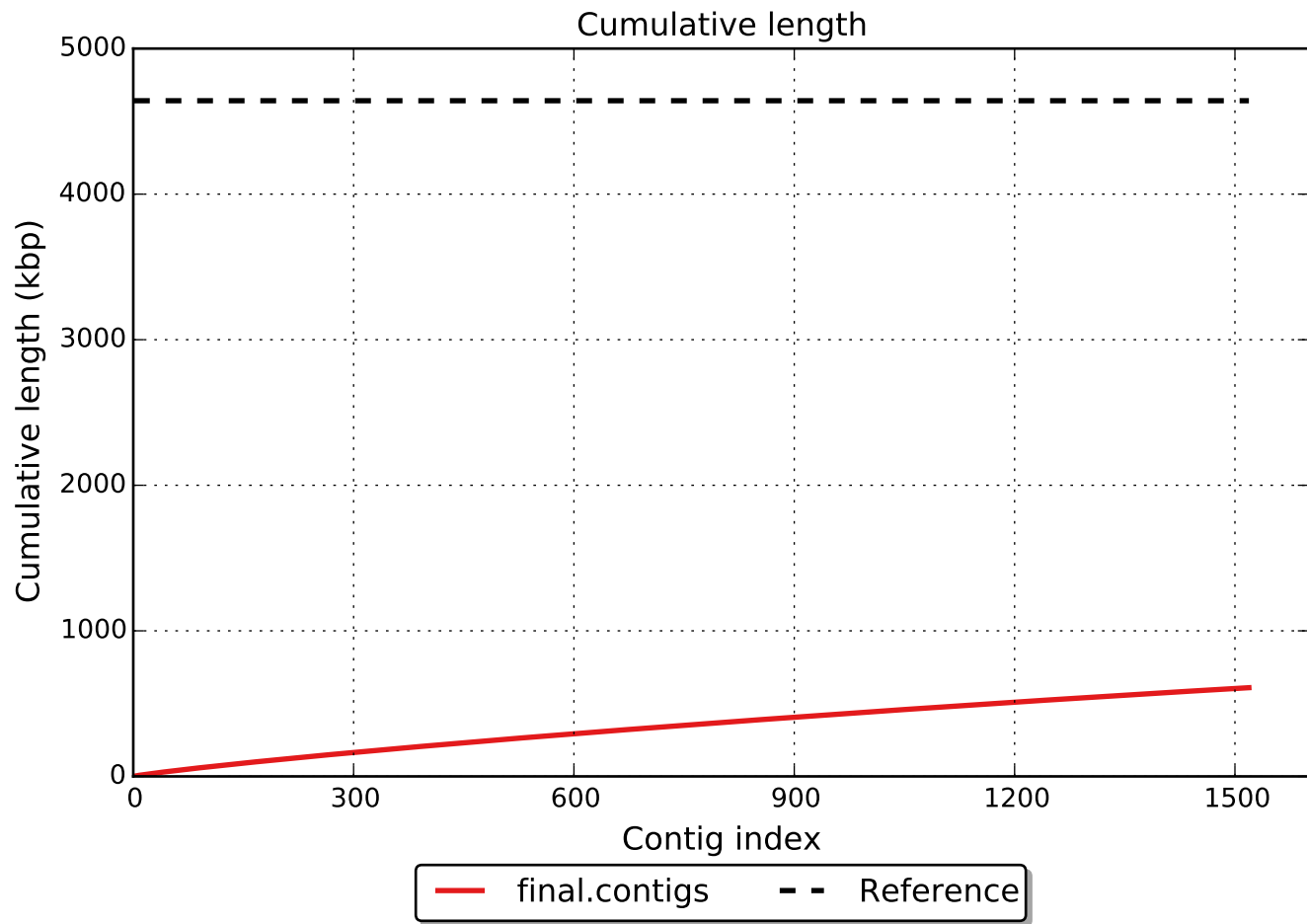
	final.contigs
# fully unaligned contigs	1515
Fully unaligned length	606542
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	199
# N's	0

Nx

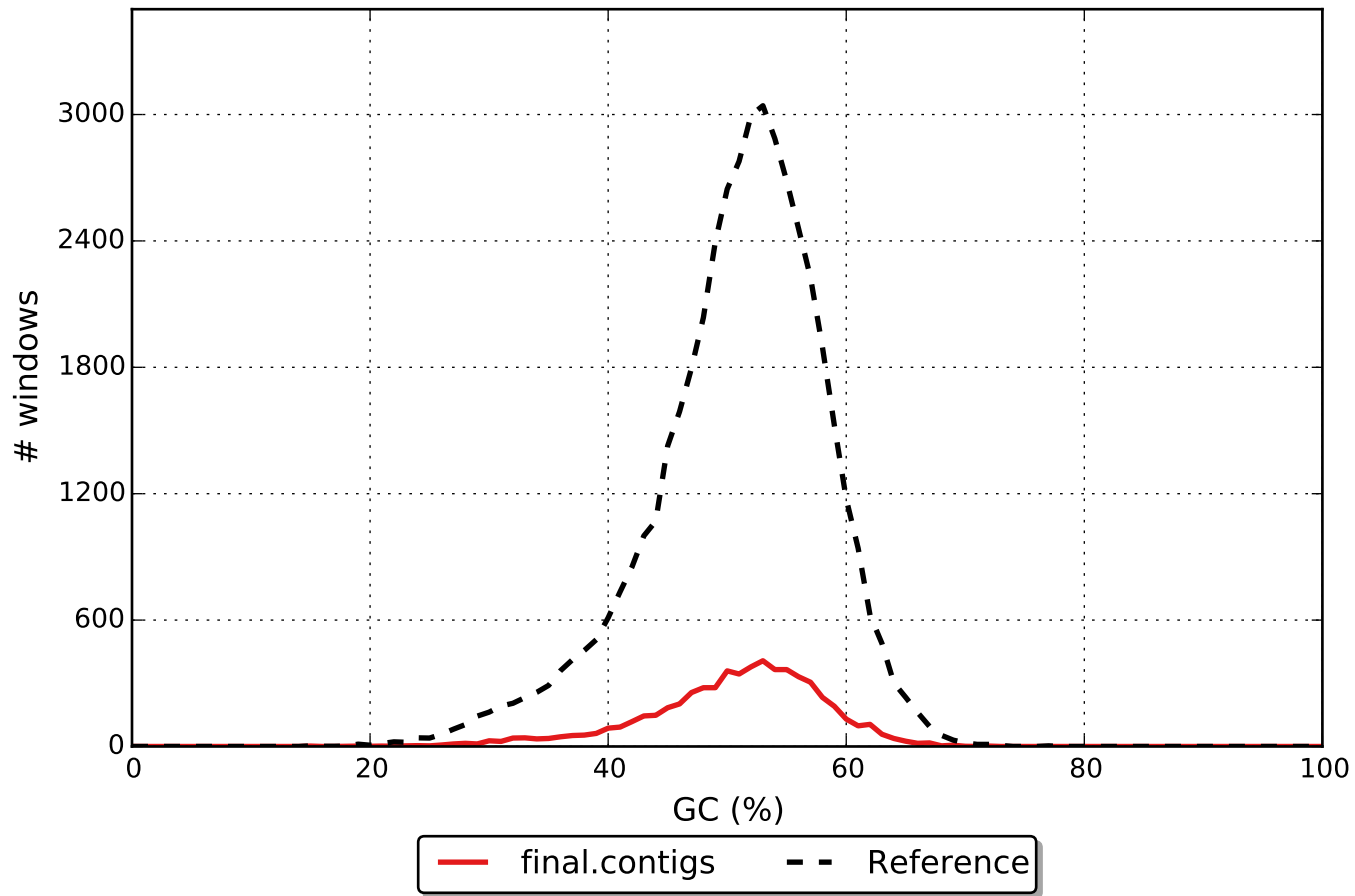


NGx





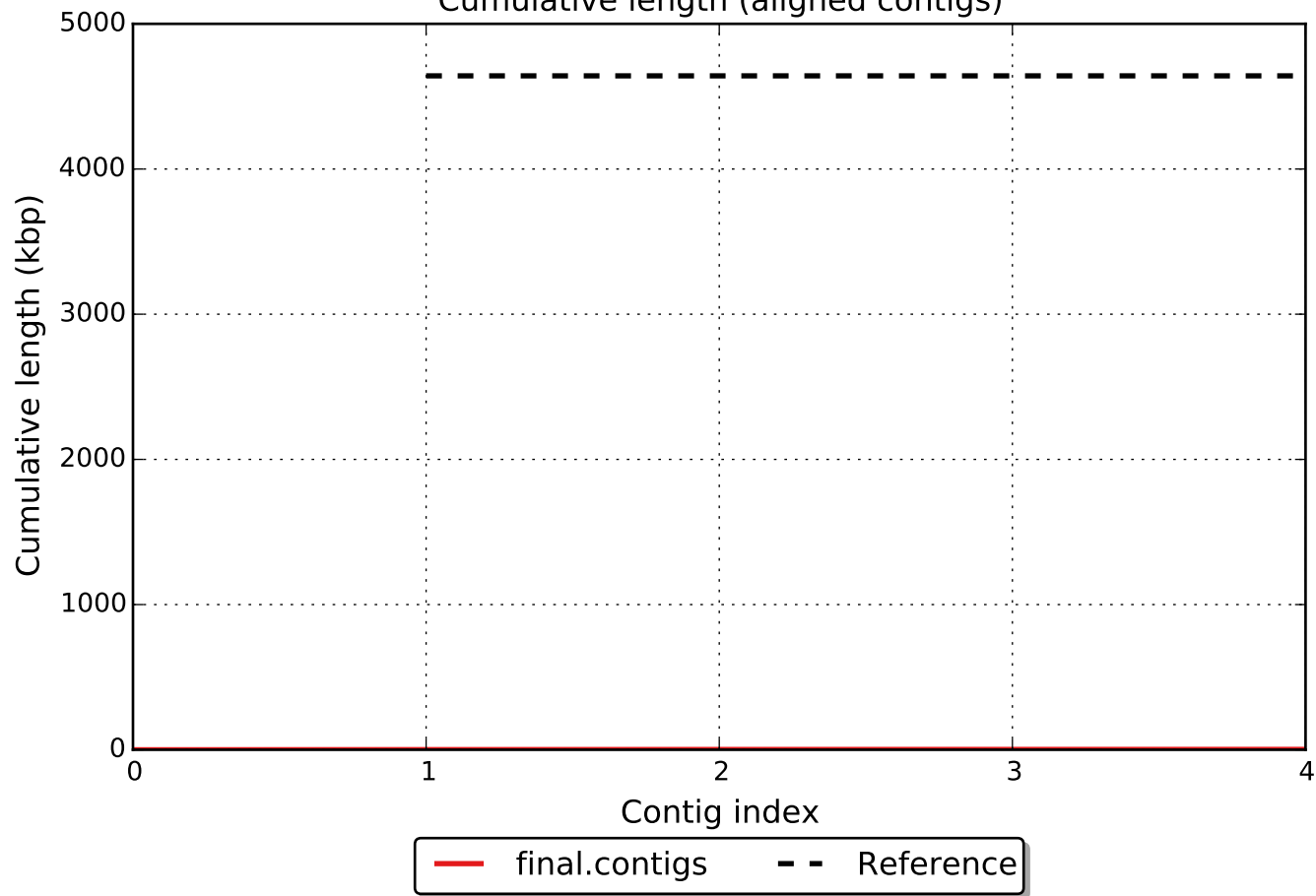
GC content



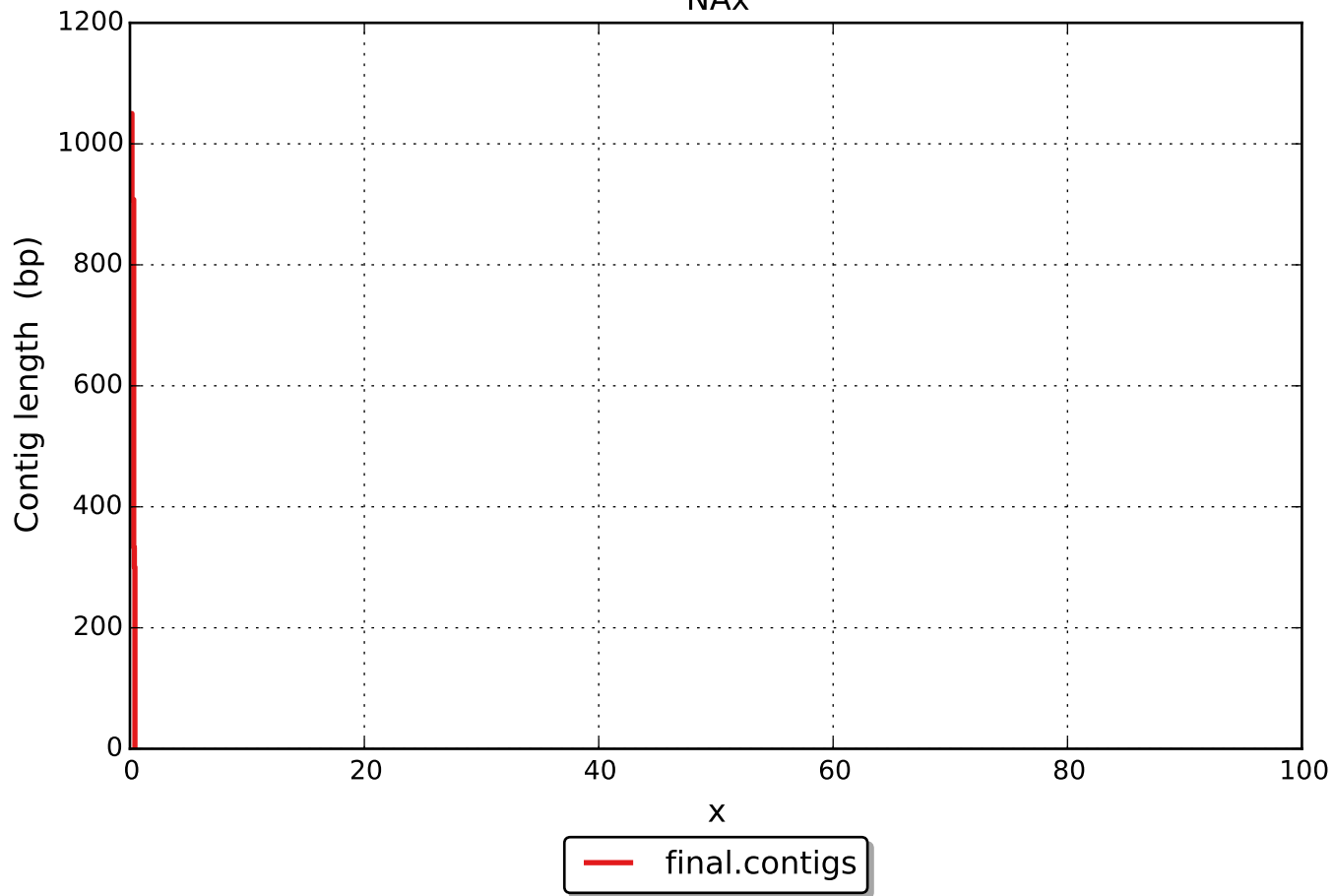
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

