

Report

	final.contigs
# contigs (≥ 0 bp)	9788
# contigs (≥ 1000 bp)	1316
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	6323622
Total length (≥ 1000 bp)	1750397
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	9788
Largest contig	3484
Total length	6323622
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	721
NG50	870
N75	493
NG75	670
L50	2994
LG50	1929
L75	5651
LG75	3455
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	9267 + 13 part
Unaligned length	5772197
Genome fraction (%)	11.783
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	754.41
# indels per 100 kbp	0.55
Largest alignment	3481
NGA50	-

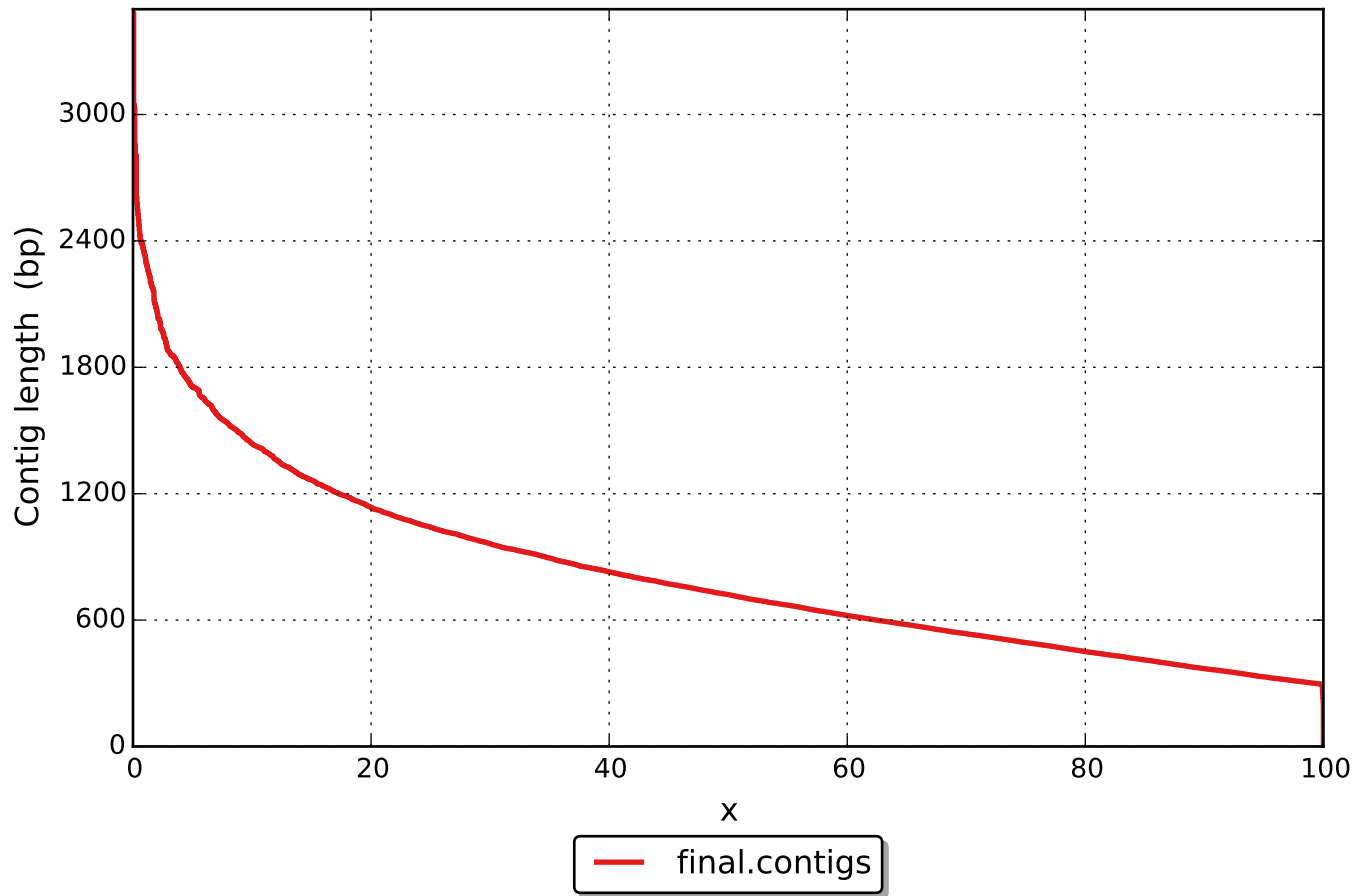
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	4126
# indels	3
# short indels	3
# long indels	0
Indels length	3

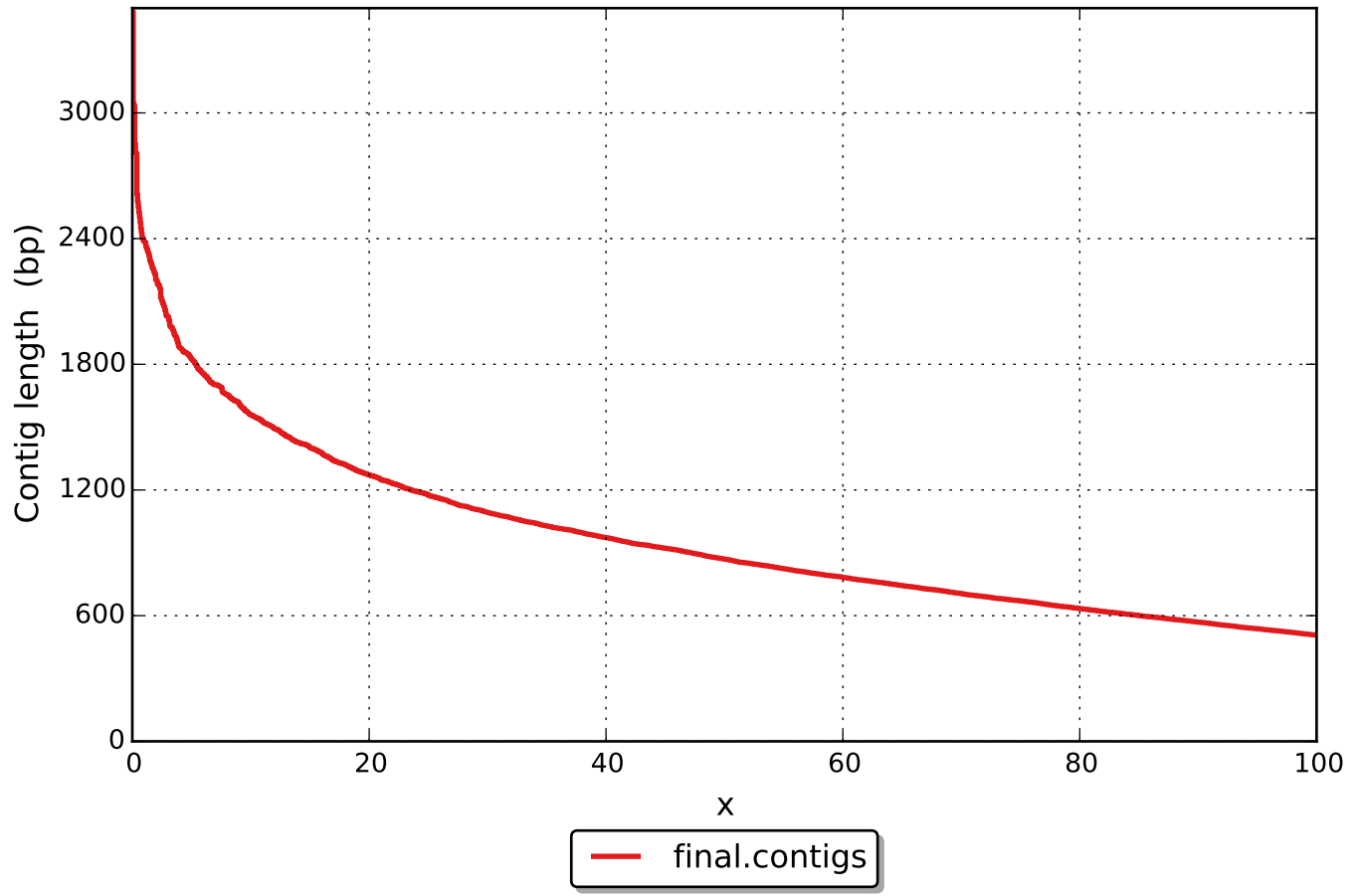
Unaligned report

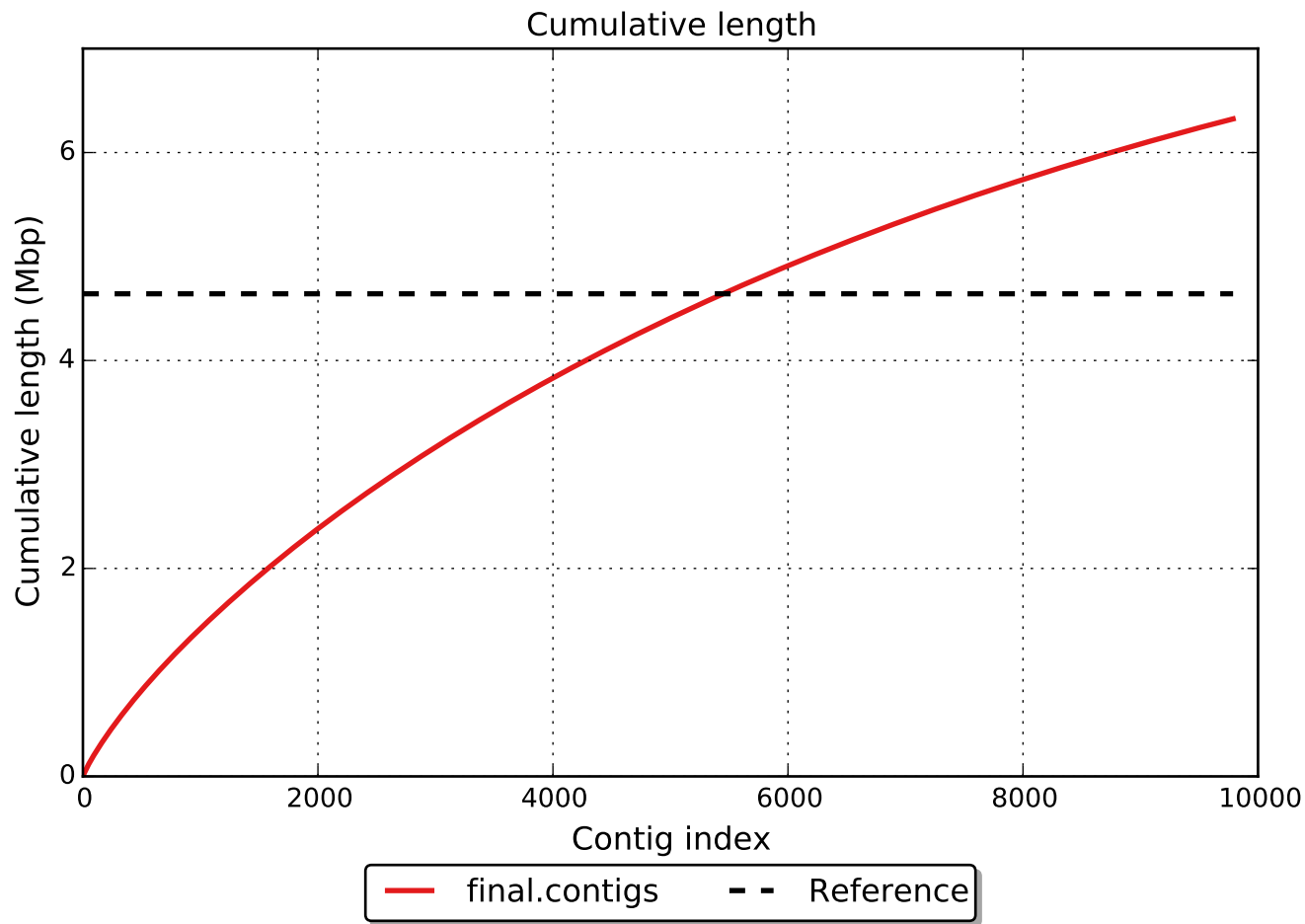
	final.contigs
# fully unaligned contigs	9267
Fully unaligned length	5767237
# partially unaligned contigs	13
# with misassembly	0
# both parts are significant	13
Partially unaligned length	4960
# N's	0

Nx

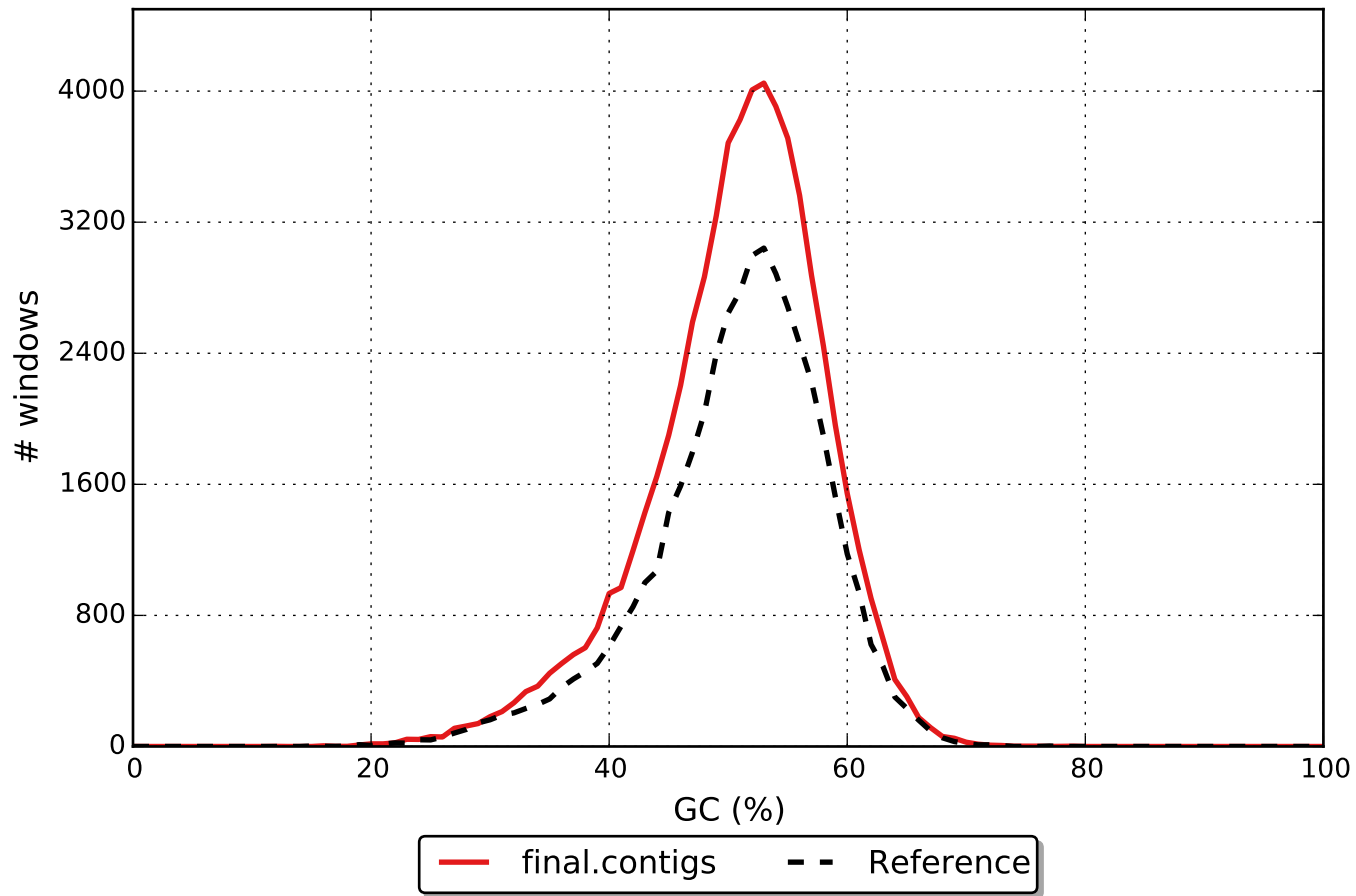


NGx





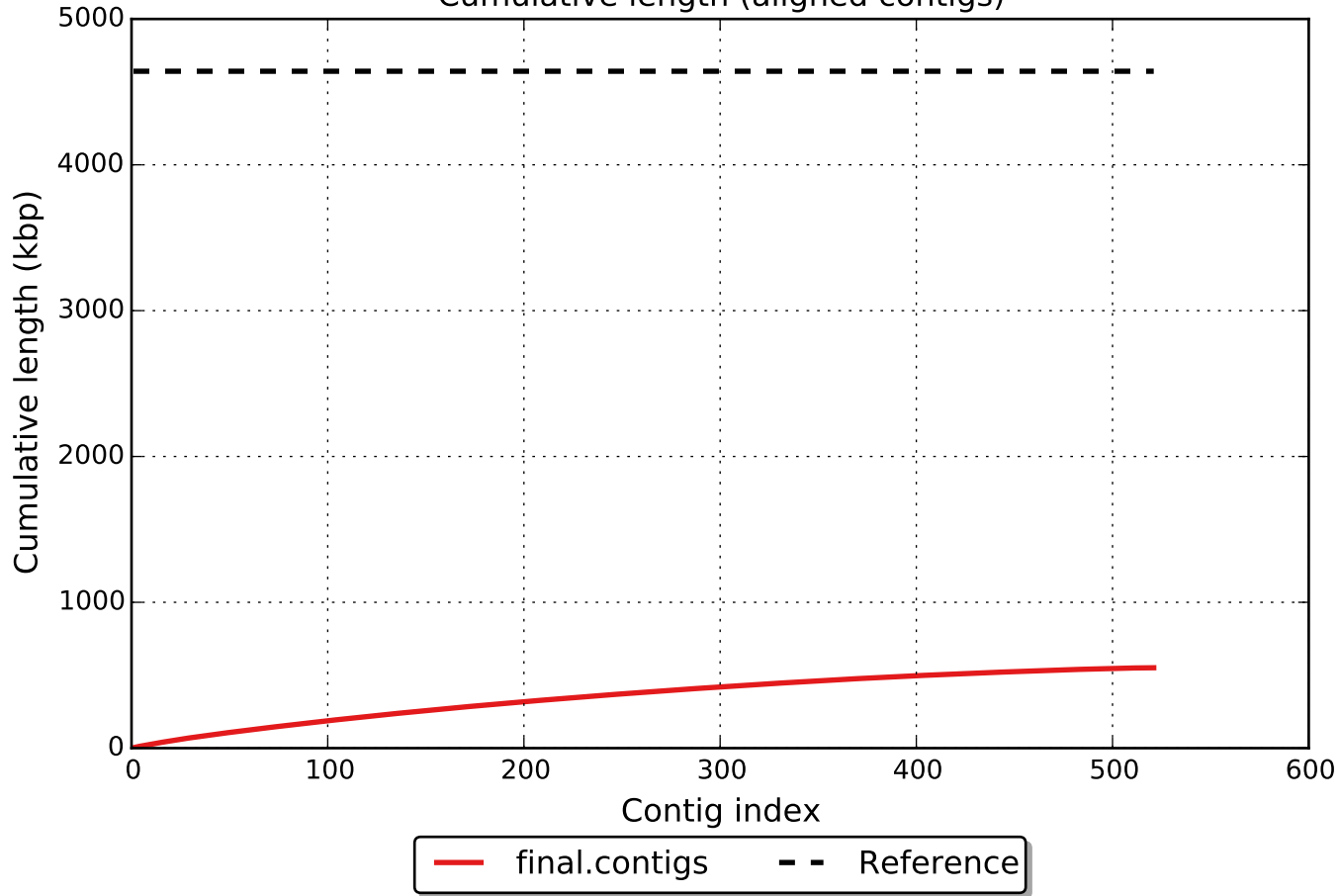
GC content



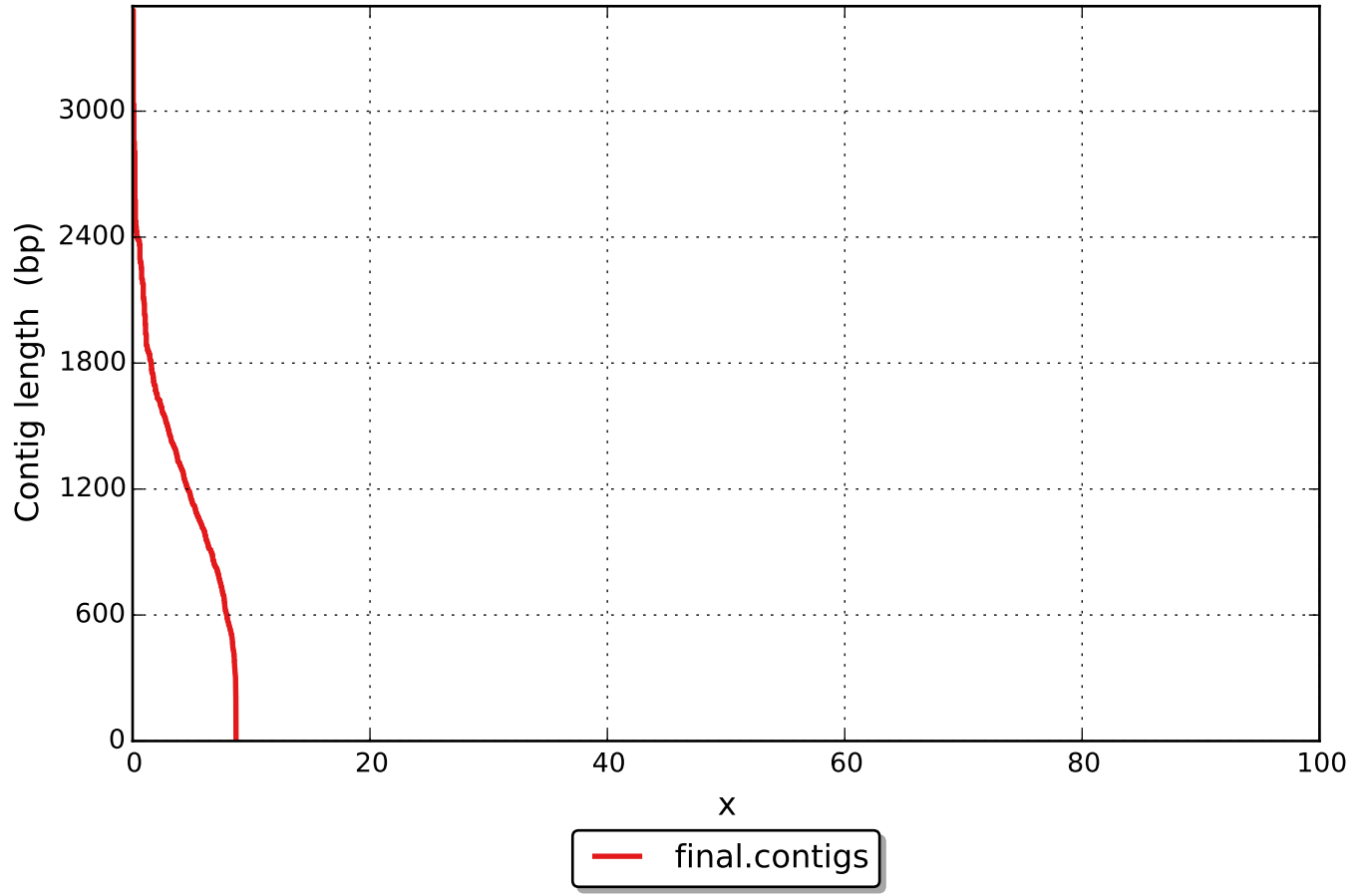
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

