

Report

	final.contigs
# contigs (≥ 0 bp)	20580
# contigs (≥ 1000 bp)	799
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	7832962
Total length (≥ 1000 bp)	1091104
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	20580
Largest contig	3029
Total length	7832962
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	350
NG50	547
N75	285
NG75	377
L50	6316
LG50	2492
L75	12532
LG75	5115
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	309
# local misassemblies	2
# unaligned contigs	8038 + 44 part
Unaligned length	2644420
Genome fraction (%)	90.198
Duplication ratio	1.239
# N's per 100 kbp	0.00
# mismatches per 100 kbp	153.58
# indels per 100 kbp	0.00
Largest alignment	3029
NA50	260
NGA50	544
NGA75	299
LA50	7063
LGA50	2494
LGA75	5481

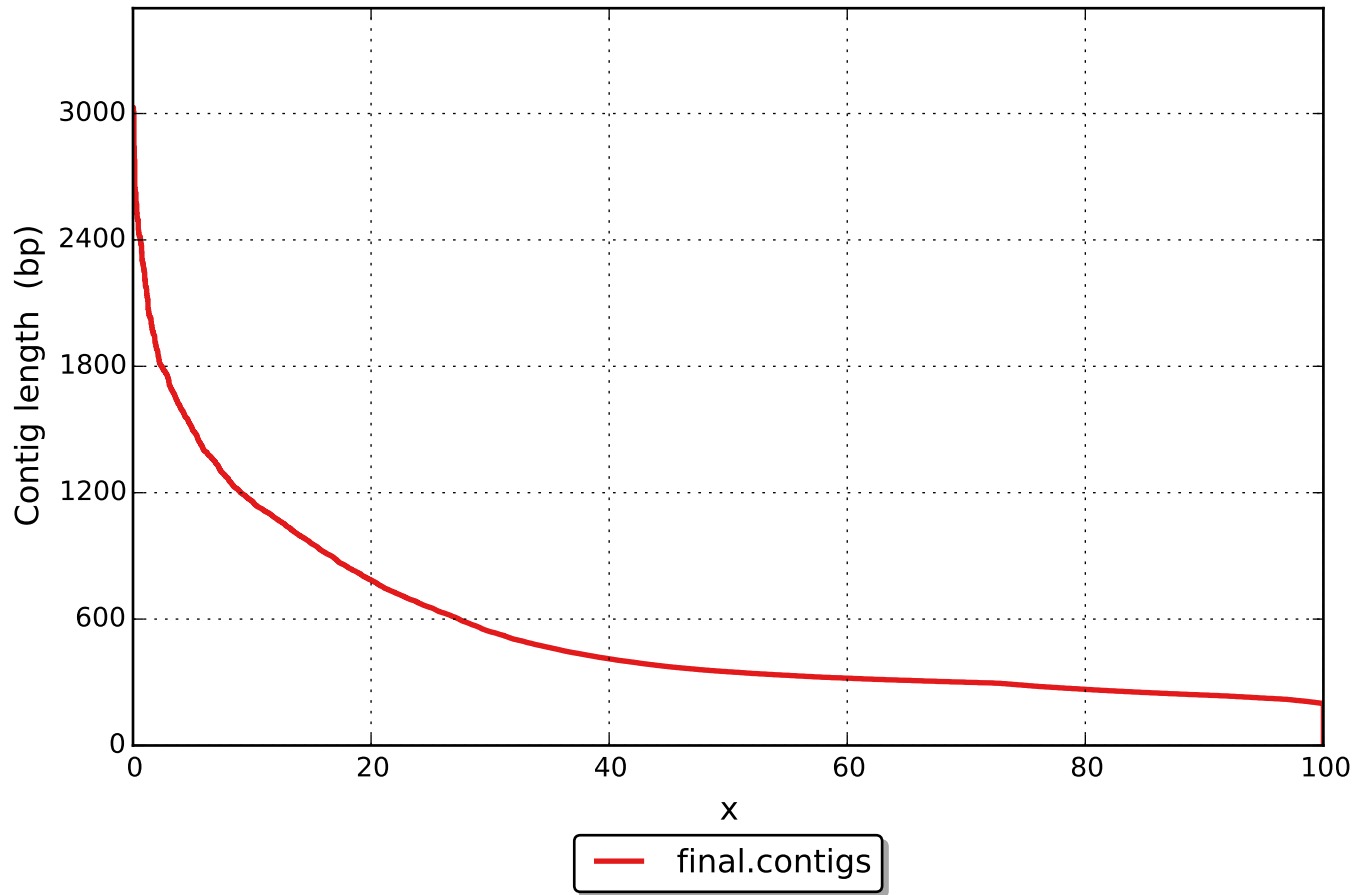
Misassemblies report

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	309
# local misassemblies	2
# mismatches	6430
# indels	0
# short indels	0
# long indels	0
Indels length	0

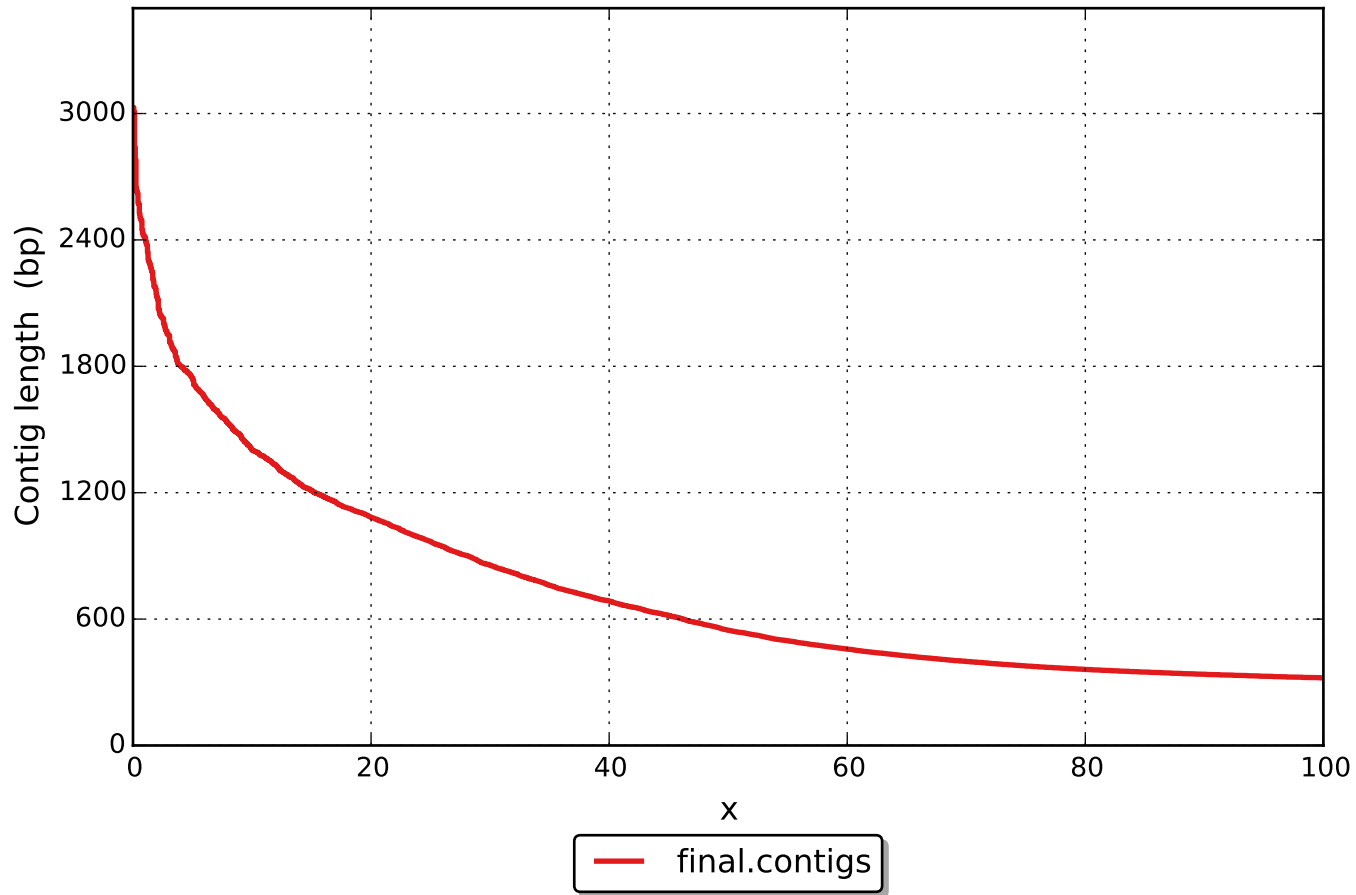
Unaligned report

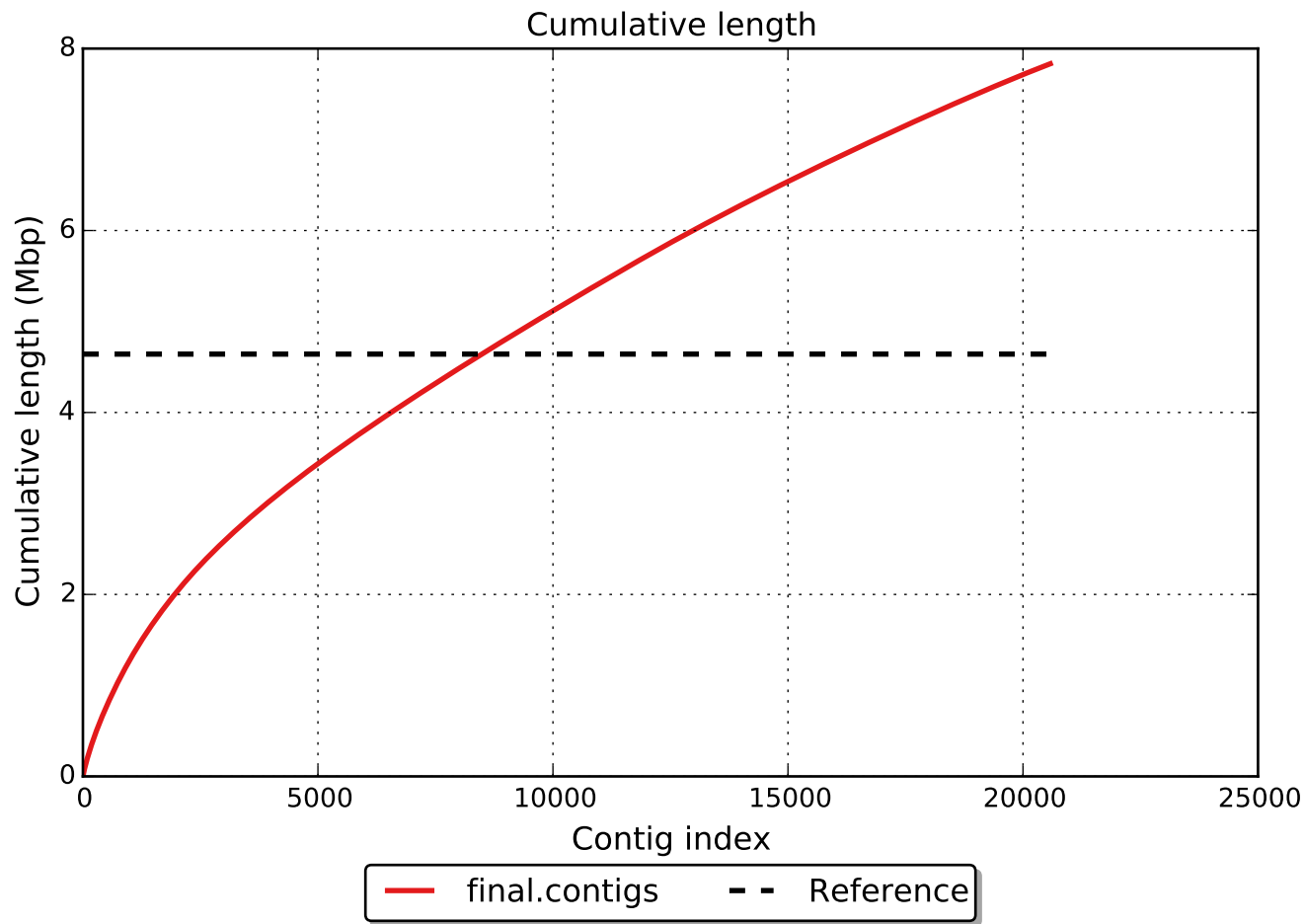
	final.contigs
# fully unaligned contigs	8038
Fully unaligned length	2636193
# partially unaligned contigs	44
# with misassembly	0
# both parts are significant	44
Partially unaligned length	8227
# N's	0

Nx

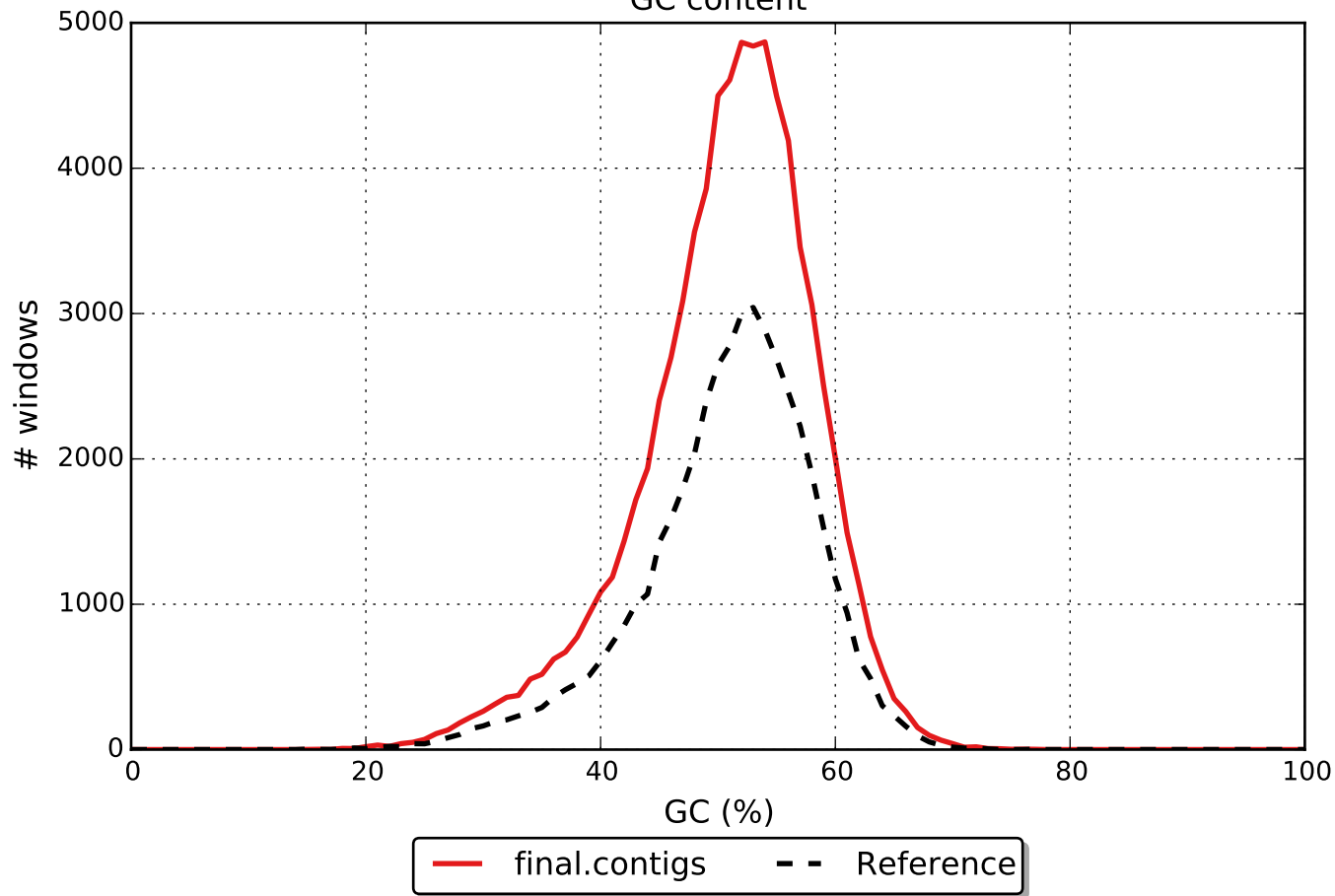


NGx

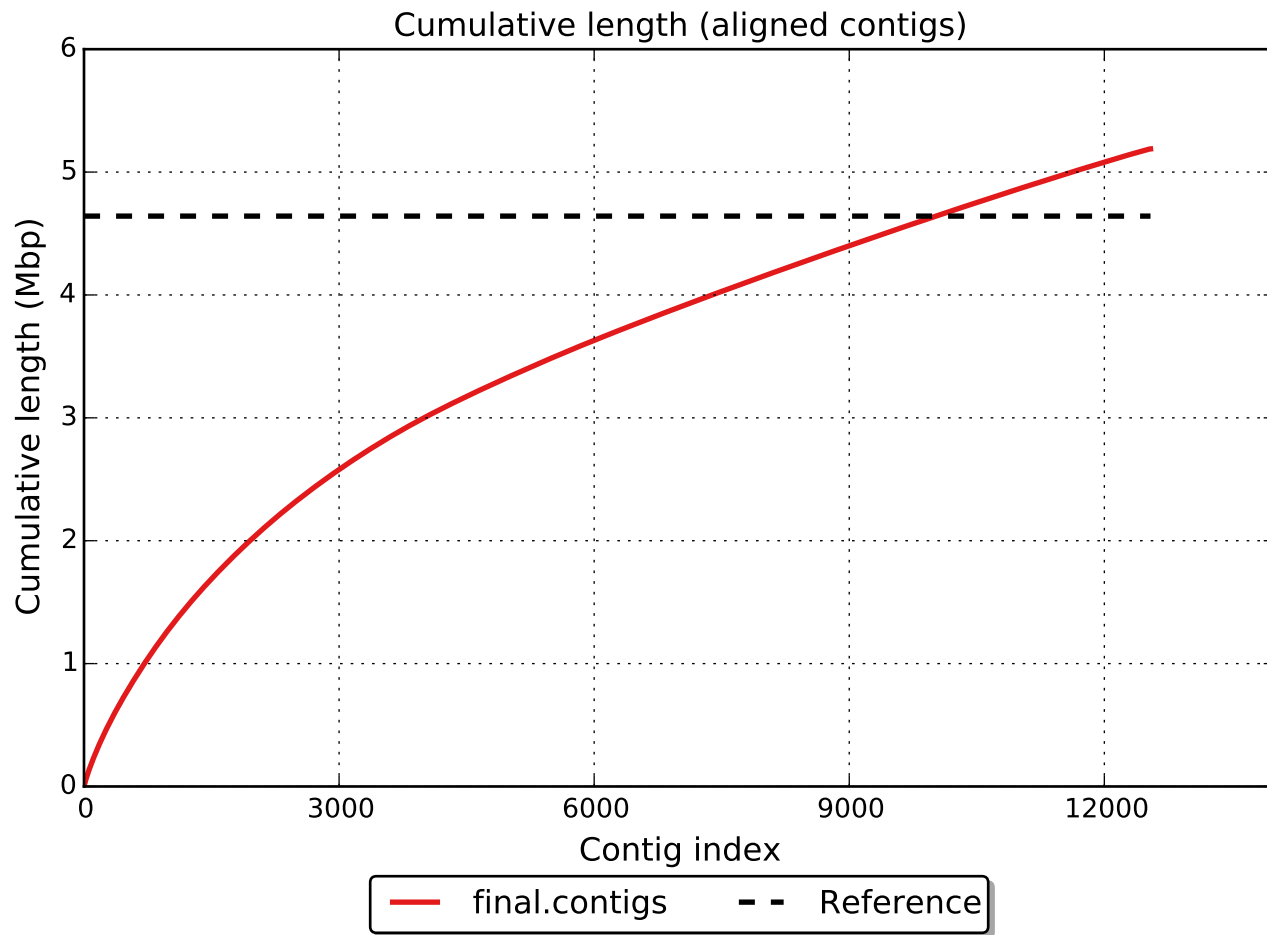




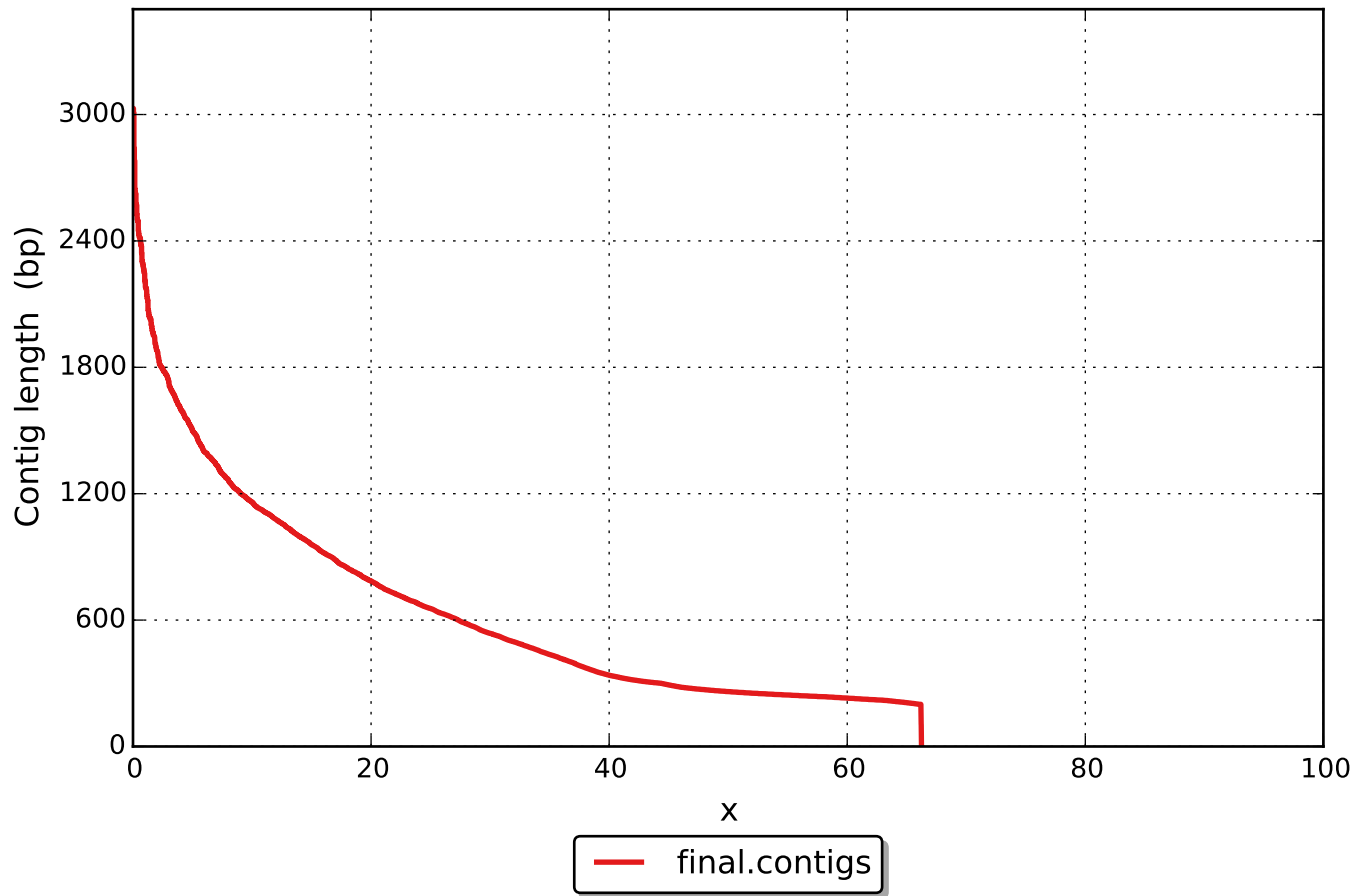
GC content







NAx



NGAx

