

Report

	final.contigs
# contigs (≥ 0 bp)	6148
# contigs (≥ 1000 bp)	2069
# contigs (≥ 5000 bp)	7
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	5749970
Total length (≥ 1000 bp)	3424770
Total length (≥ 5000 bp)	38826
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	4306
Largest contig	6290
Total length	5037635
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	1307
NG50	1391
N75	885
NG75	982
L50	1273
LG50	1127
L75	2444
LG75	2127
# misassemblies	14
# misassembled contigs	14
Misassembled contigs length	31146
# local misassemblies	0
# unaligned contigs	27 + 27 part
Unaligned length	19422
Genome fraction (%)	94.547
Duplication ratio	1.143
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1174.65
# indels per 100 kbp	1.48
Largest alignment	6290
NA50	1300
NGA50	1388
NA75	880
NGA75	976
LA50	1278
LGA50	1130
LA75	2454
LGA75	2134

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Misassemblies report

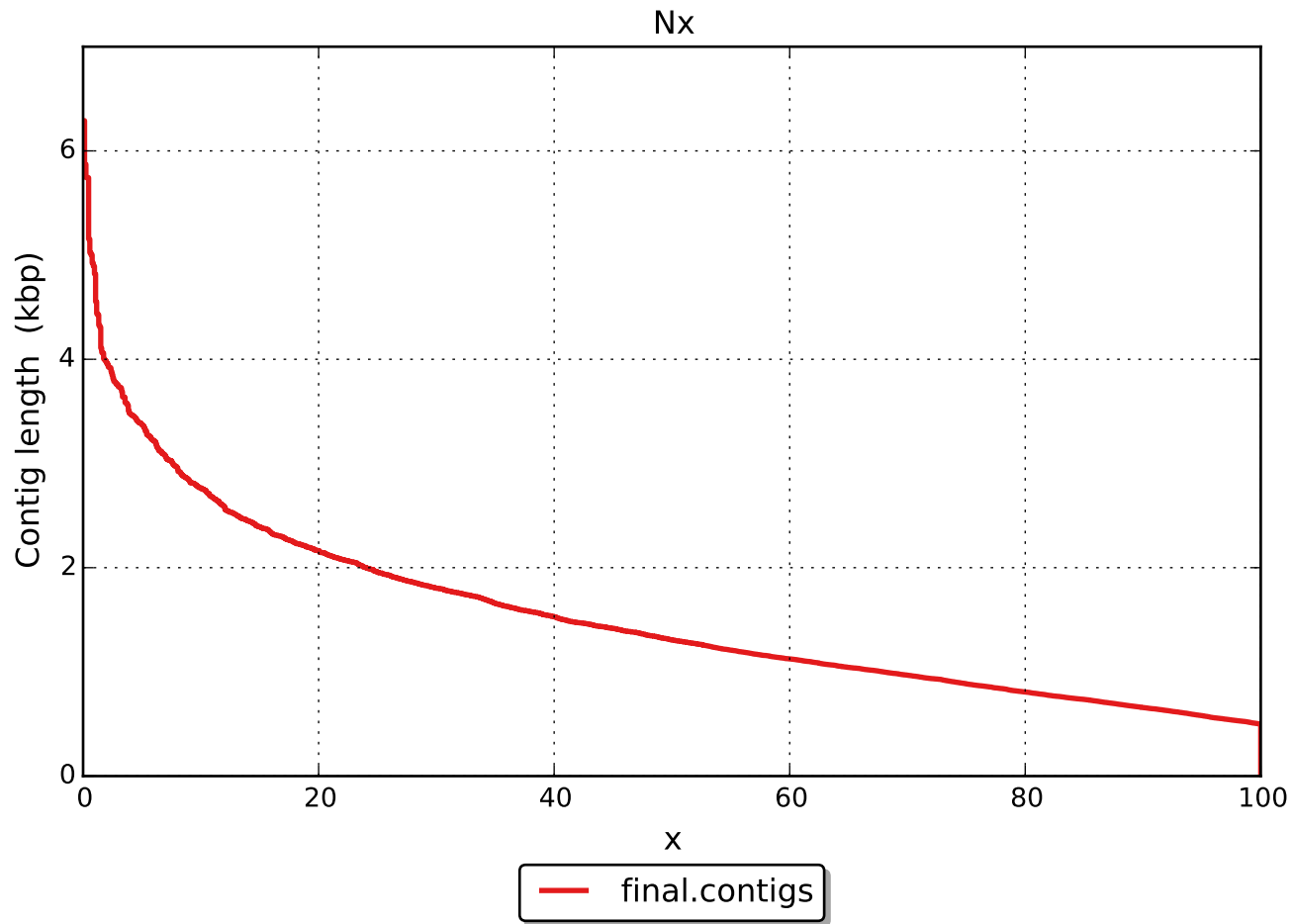
	final.contigs
# misassemblies	14
# relocations	14
# translocations	0
# inversions	0
# misassembled contigs	14
Misassembled contigs length	31146
# local misassemblies	0
# mismatches	51550
# indels	65
# short indels	65
# long indels	0
Indels length	69

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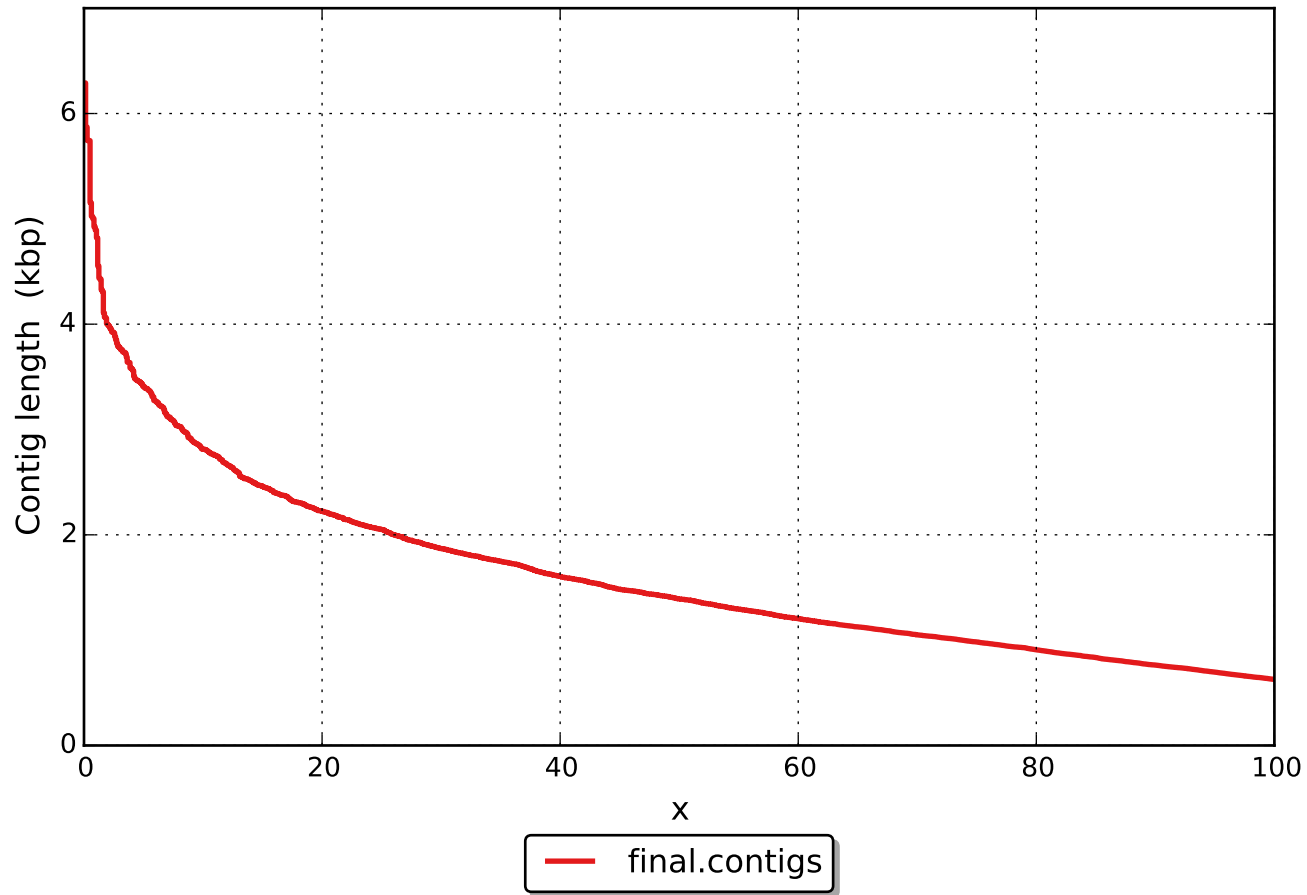
Unaligned report

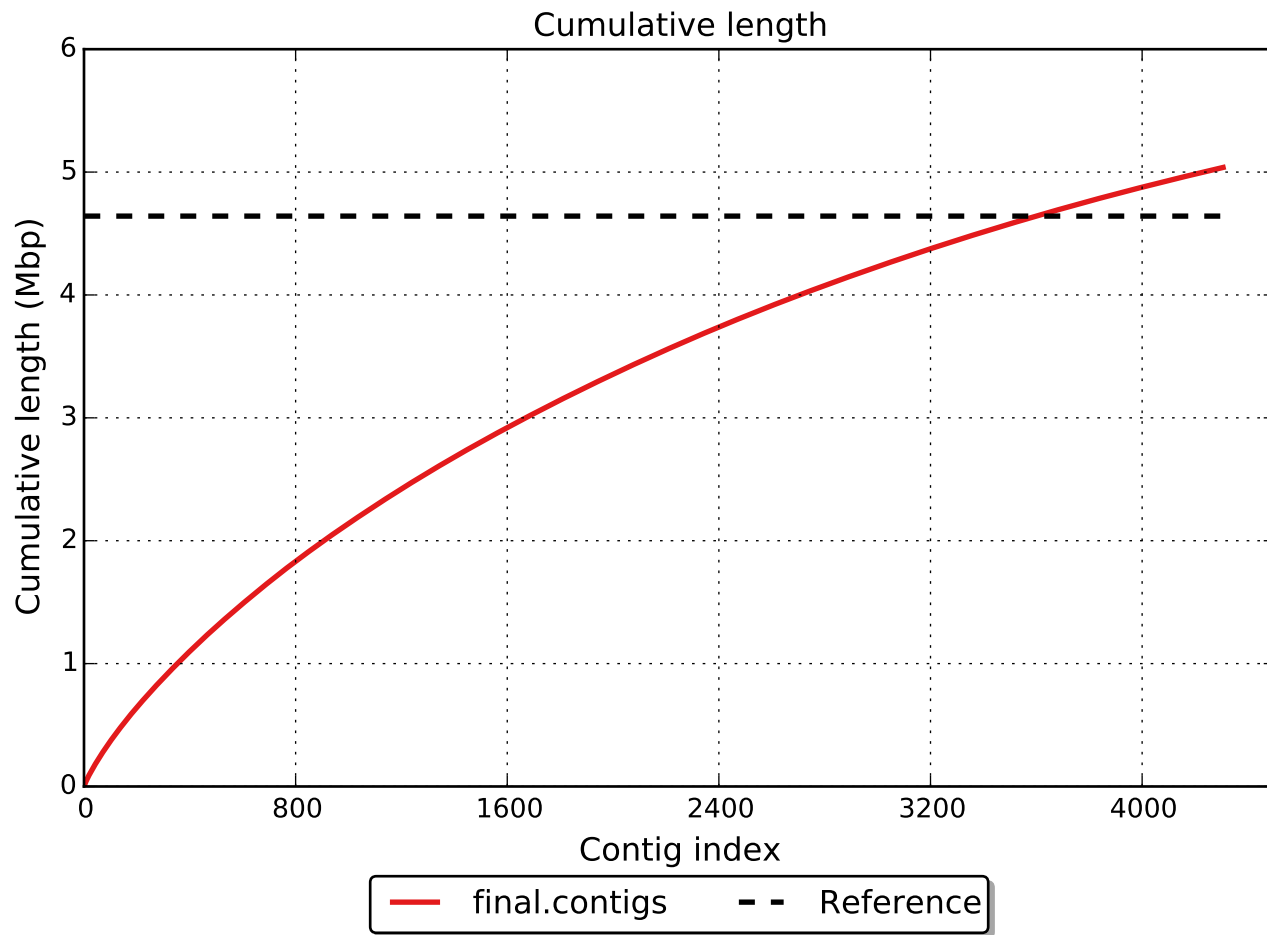
	final.contigs
# fully unaligned contigs	27
Fully unaligned length	16988
# partially unaligned contigs	27
# with misassembly	0
# both parts are significant	0
Partially unaligned length	2434
# N's	0

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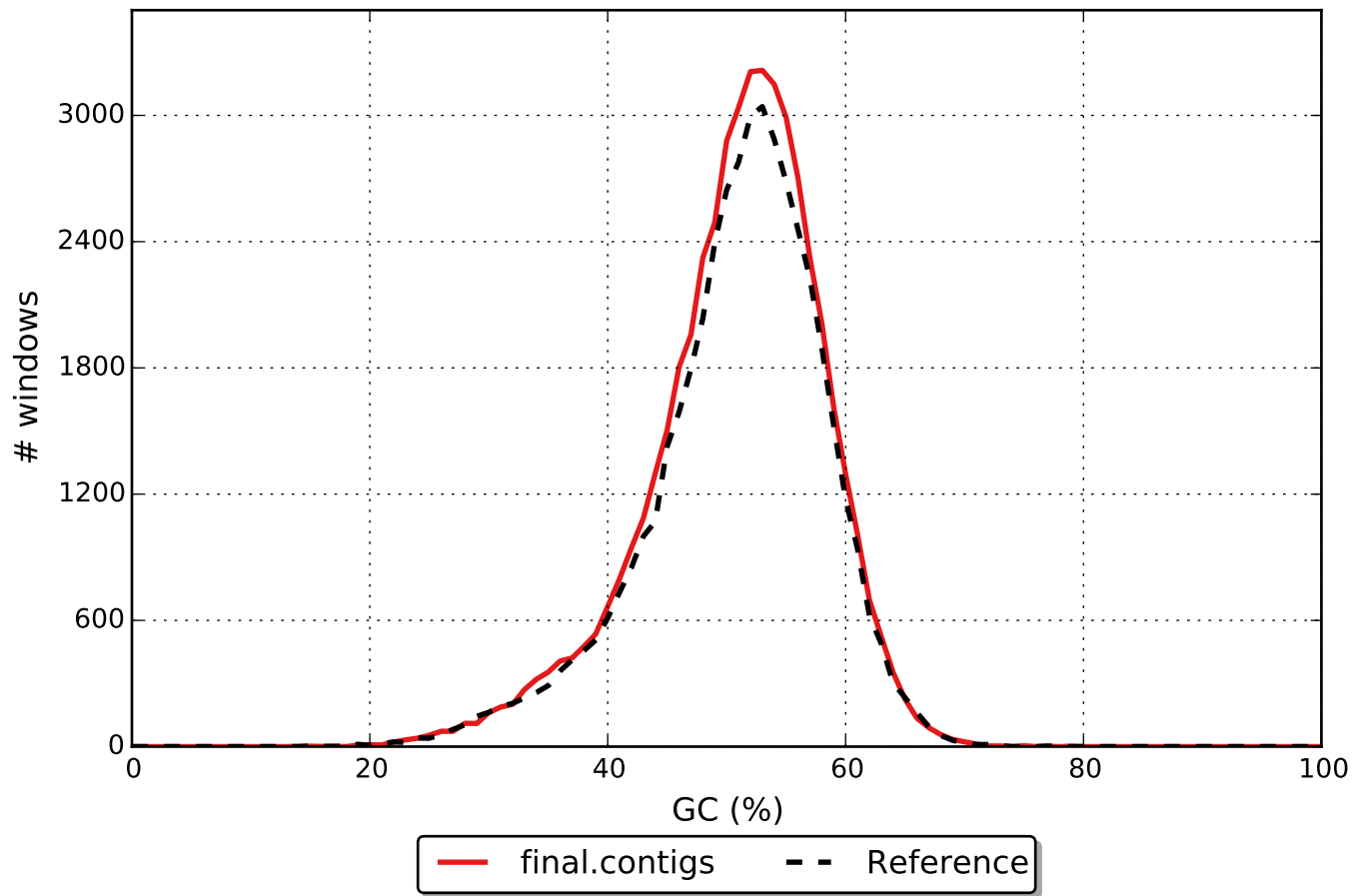


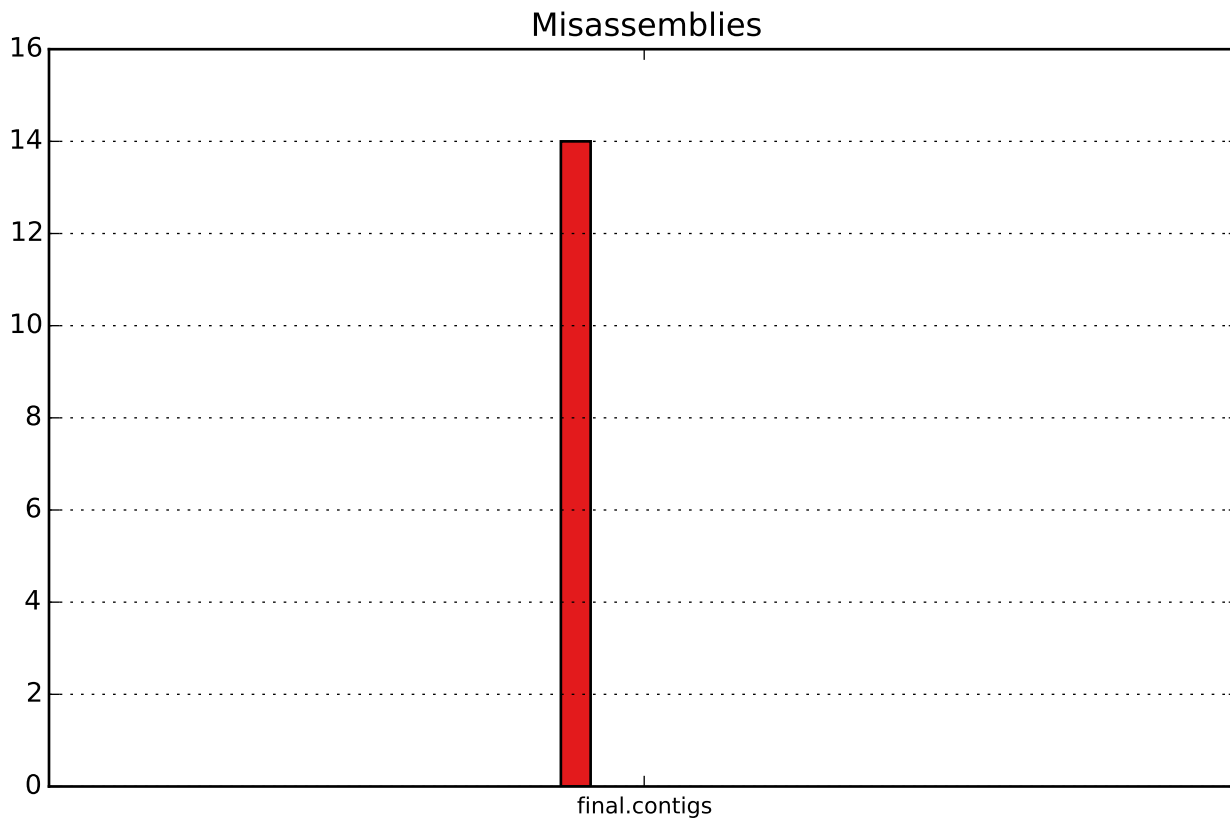
NGx

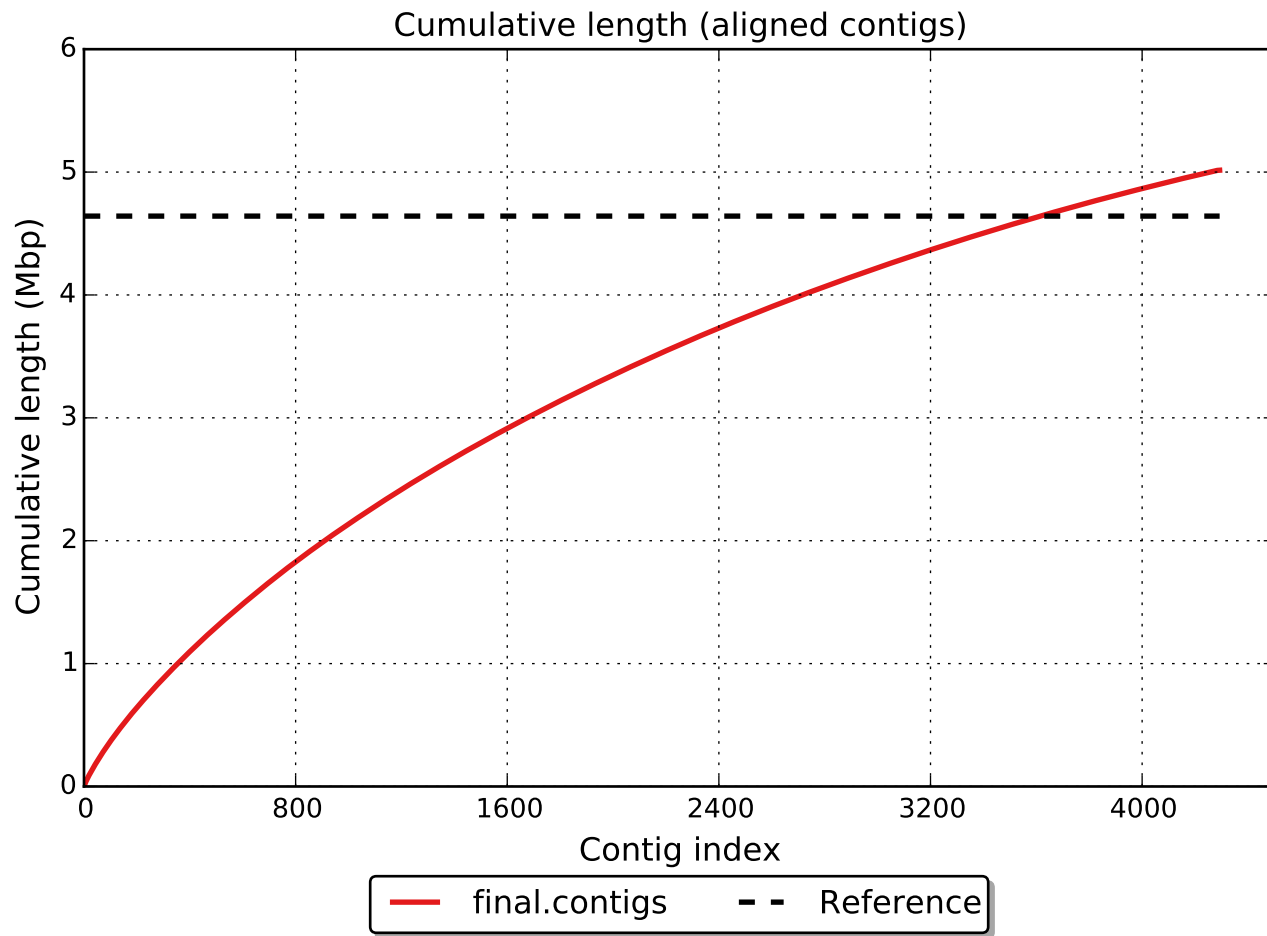




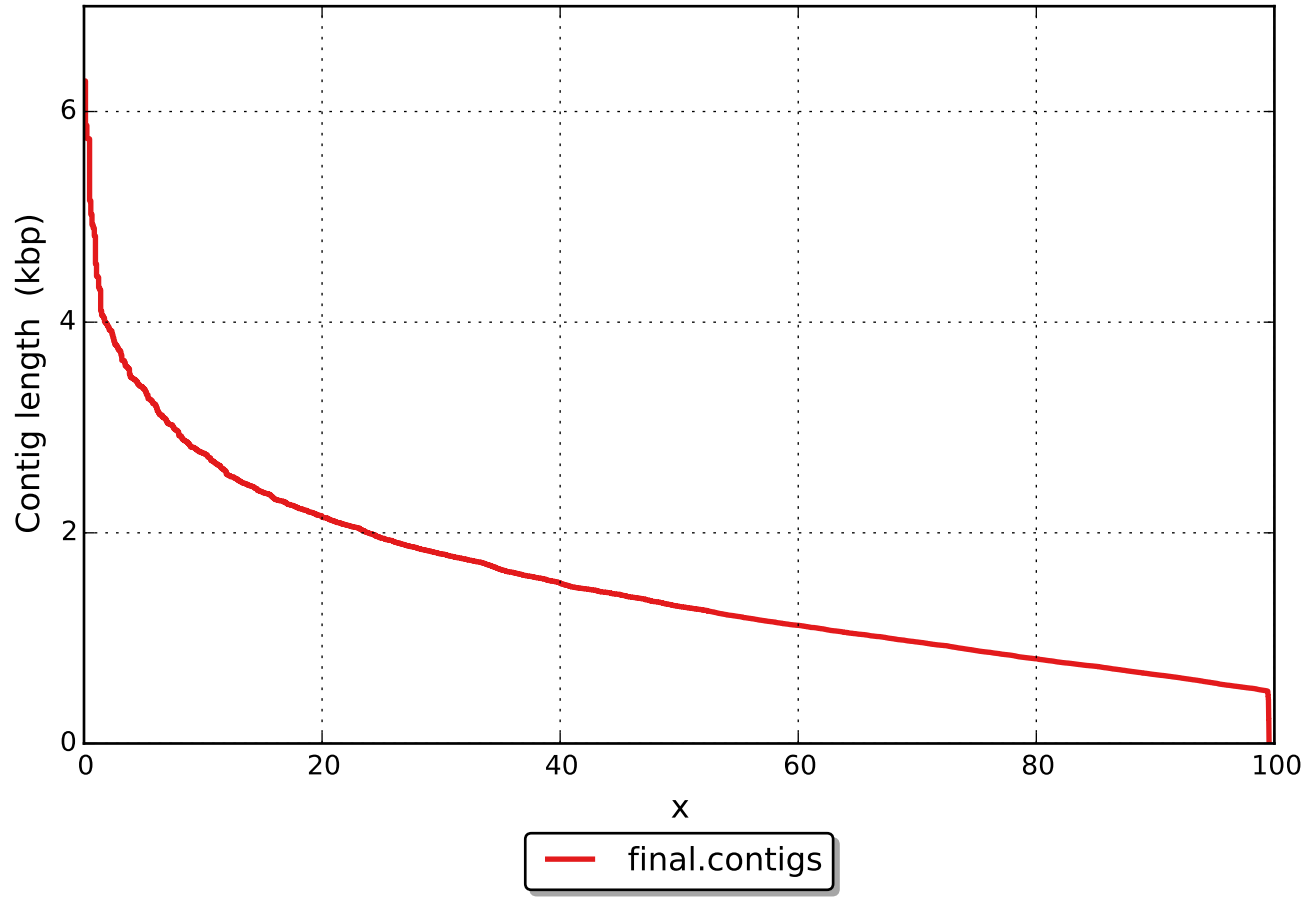
GC content







NAx



NGAx

