

Report

	final.contigs
# contigs (>= 1000 bp)	719
# contigs (>= 5000 bp)	336
# contigs (>= 10000 bp)	137
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4531044
Total length (>= 5000 bp)	3480098
Total length (>= 10000 bp)	2070880
Total length (>= 25000 bp)	254116
Total length (>= 50000 bp)	0
# contigs	830
Largest contig	31539
Total length	4618323
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	8726
NG50	8708
N75	5076
NG75	4978
L50	163
LG50	164
L75	333
LG75	337
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3970
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	232
Genome fraction (%)	97.962
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	17.84
# indels per 100 kbp	0.13
Largest alignment	31539
NA50	8726
NGA50	8708
NA75	5076
NGA75	4978
LA50	163
LGA50	164
LA75	333
LGA75	337

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

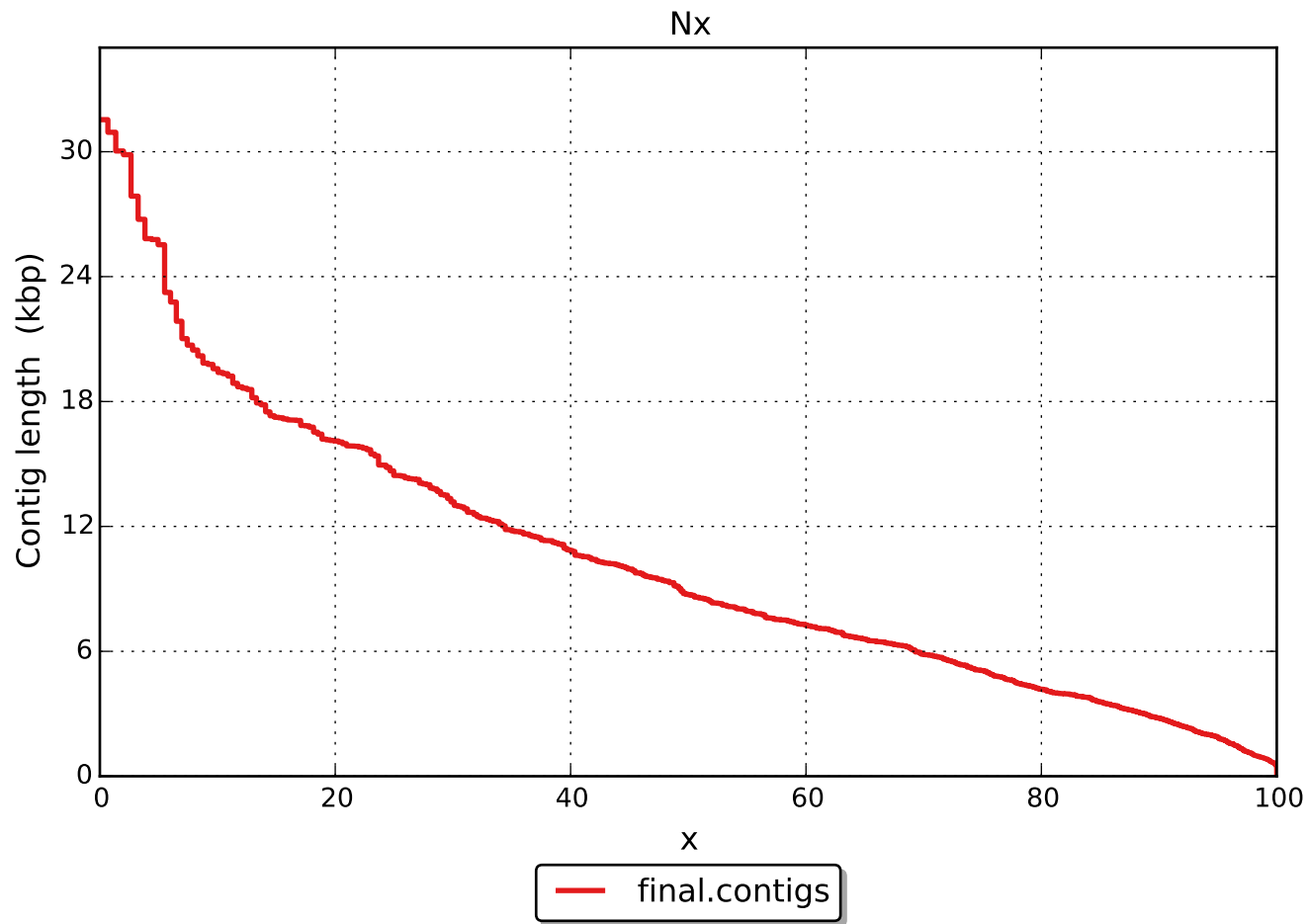
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	3970
# local misassemblies	2
# mismatches	811
# indels	6
# short indels	6
# long indels	0
Indels length	6

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).

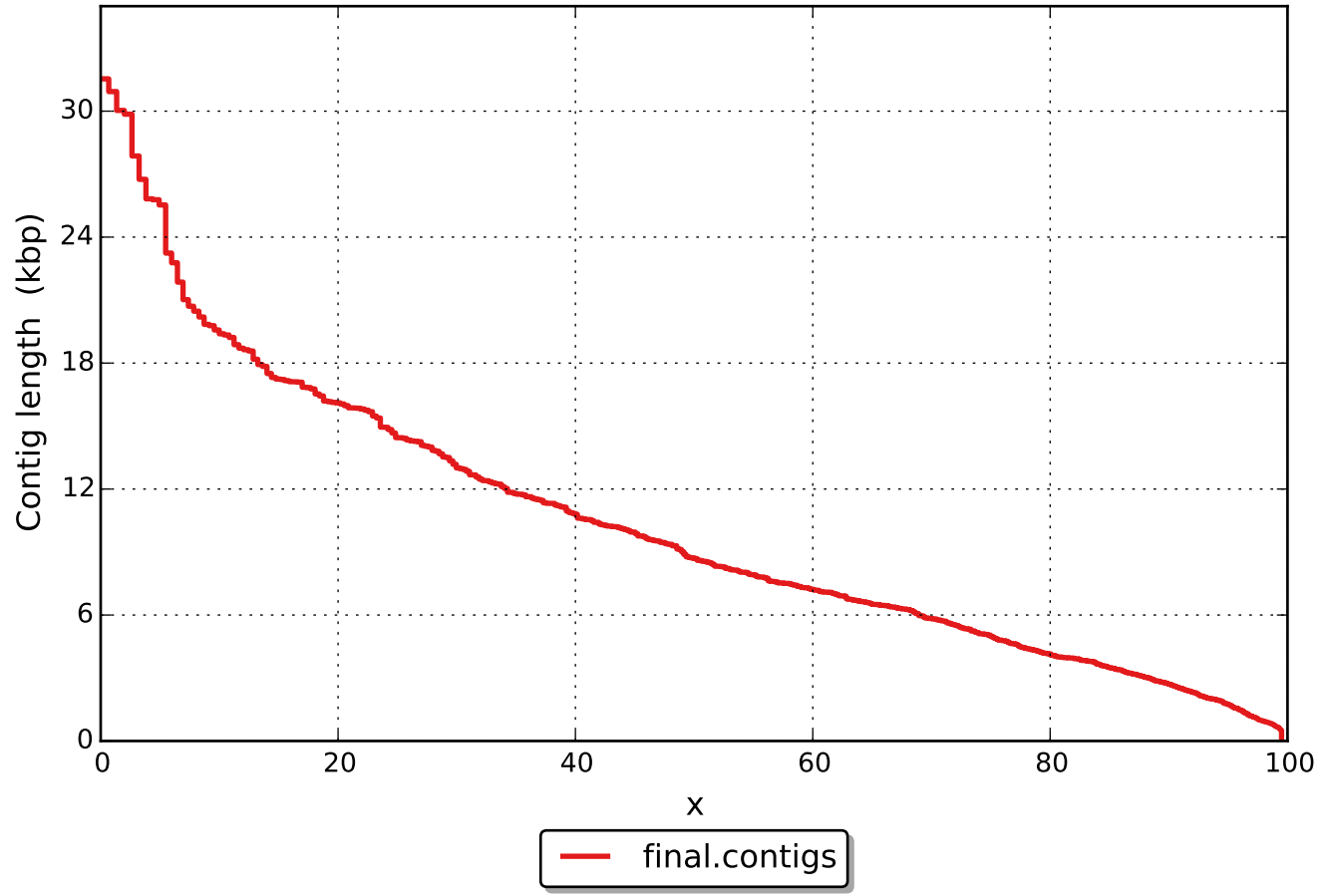
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	232
# N's	0

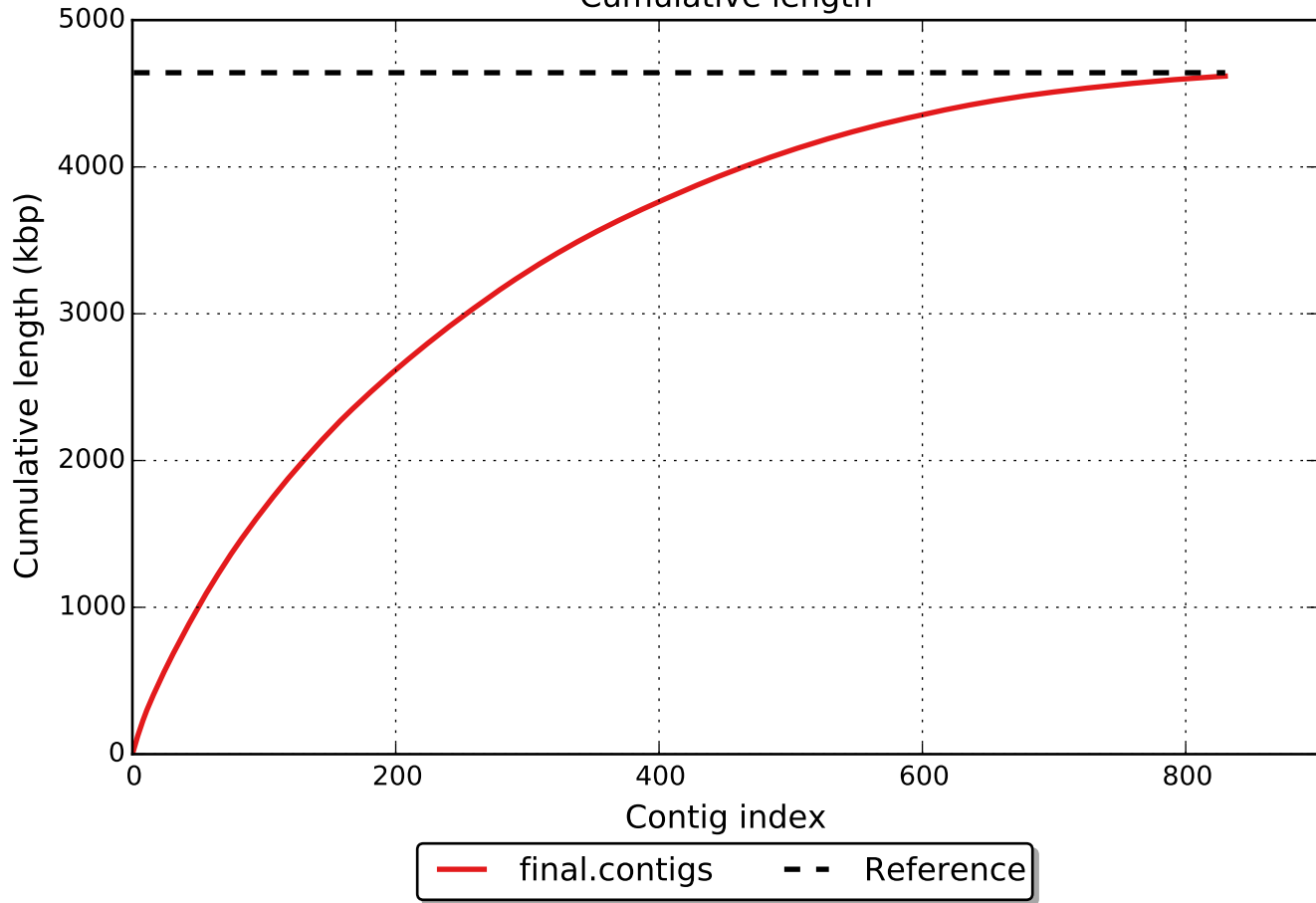
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



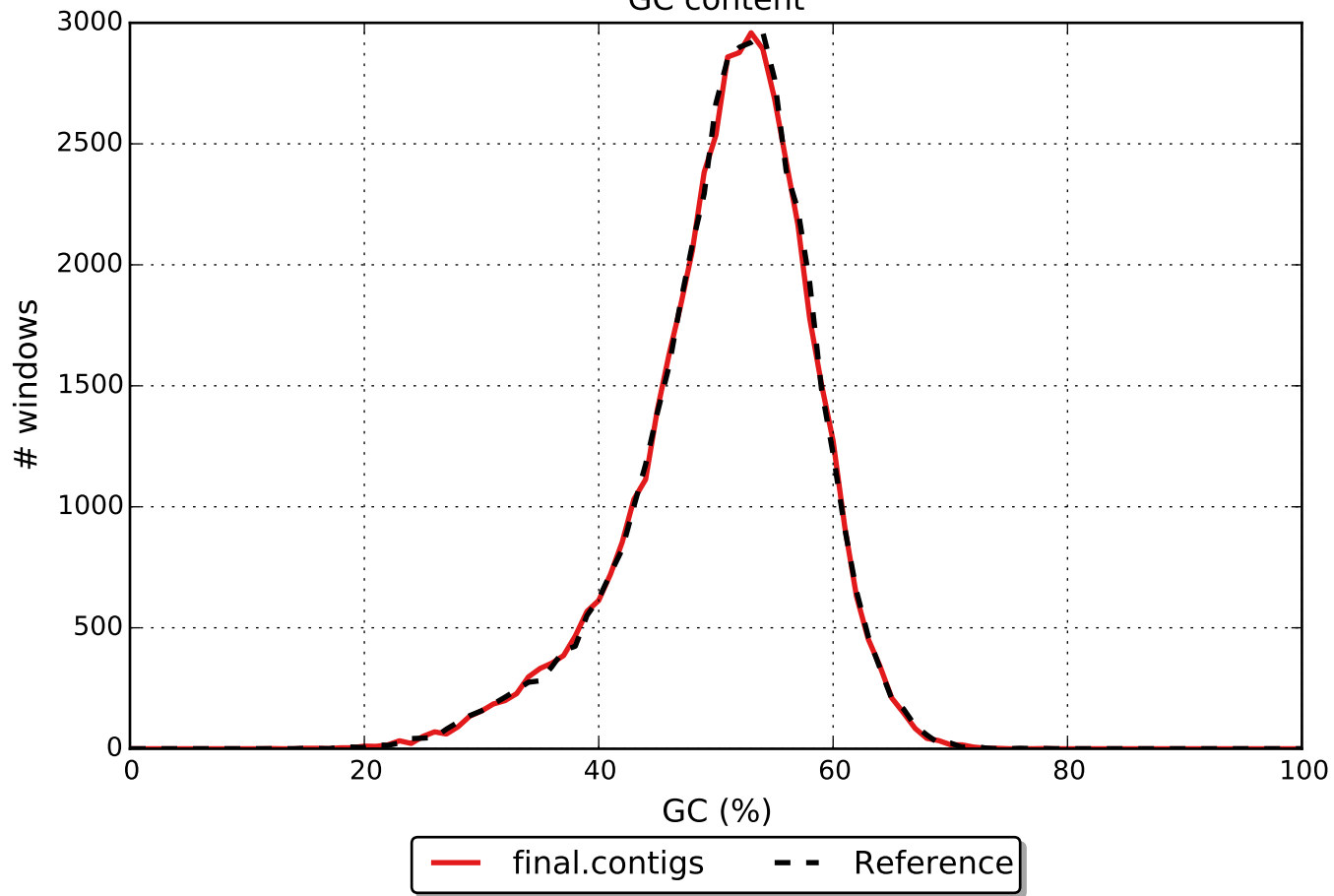
NGx

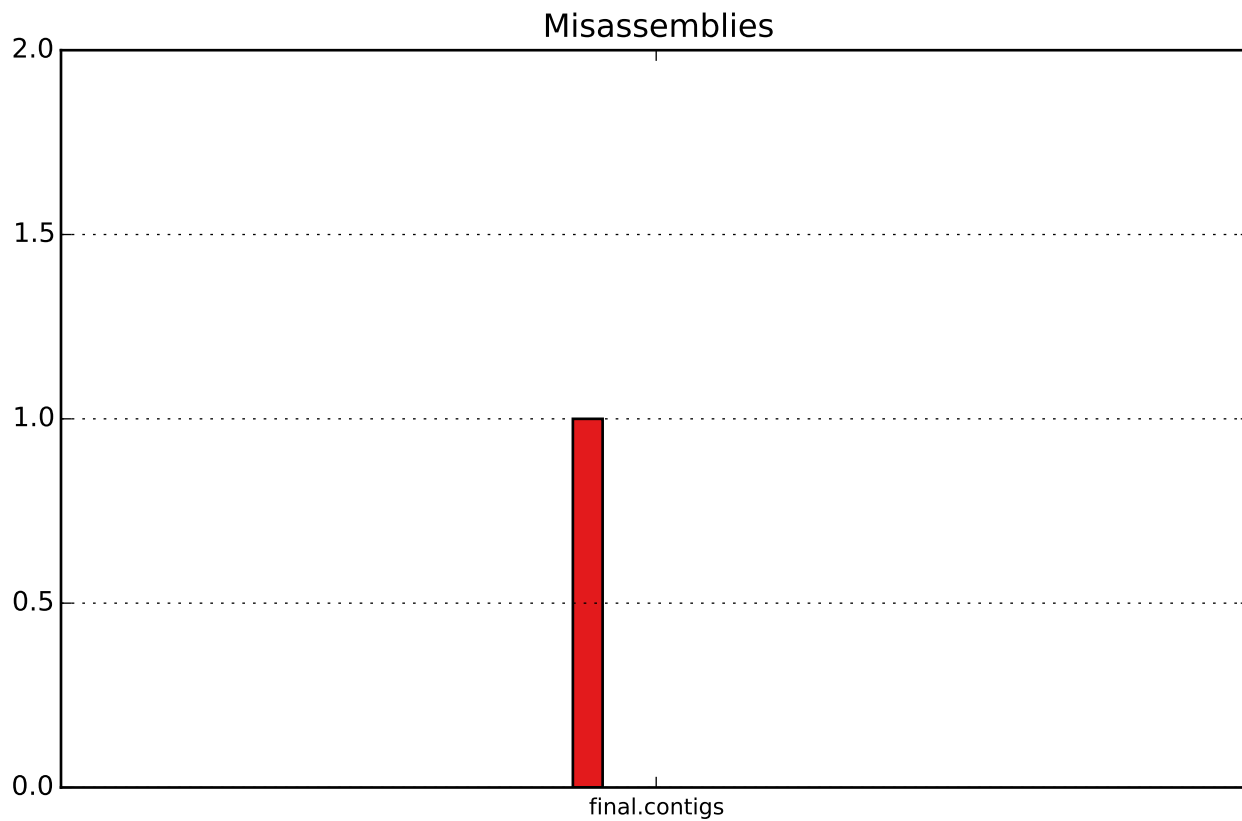


Cumulative length

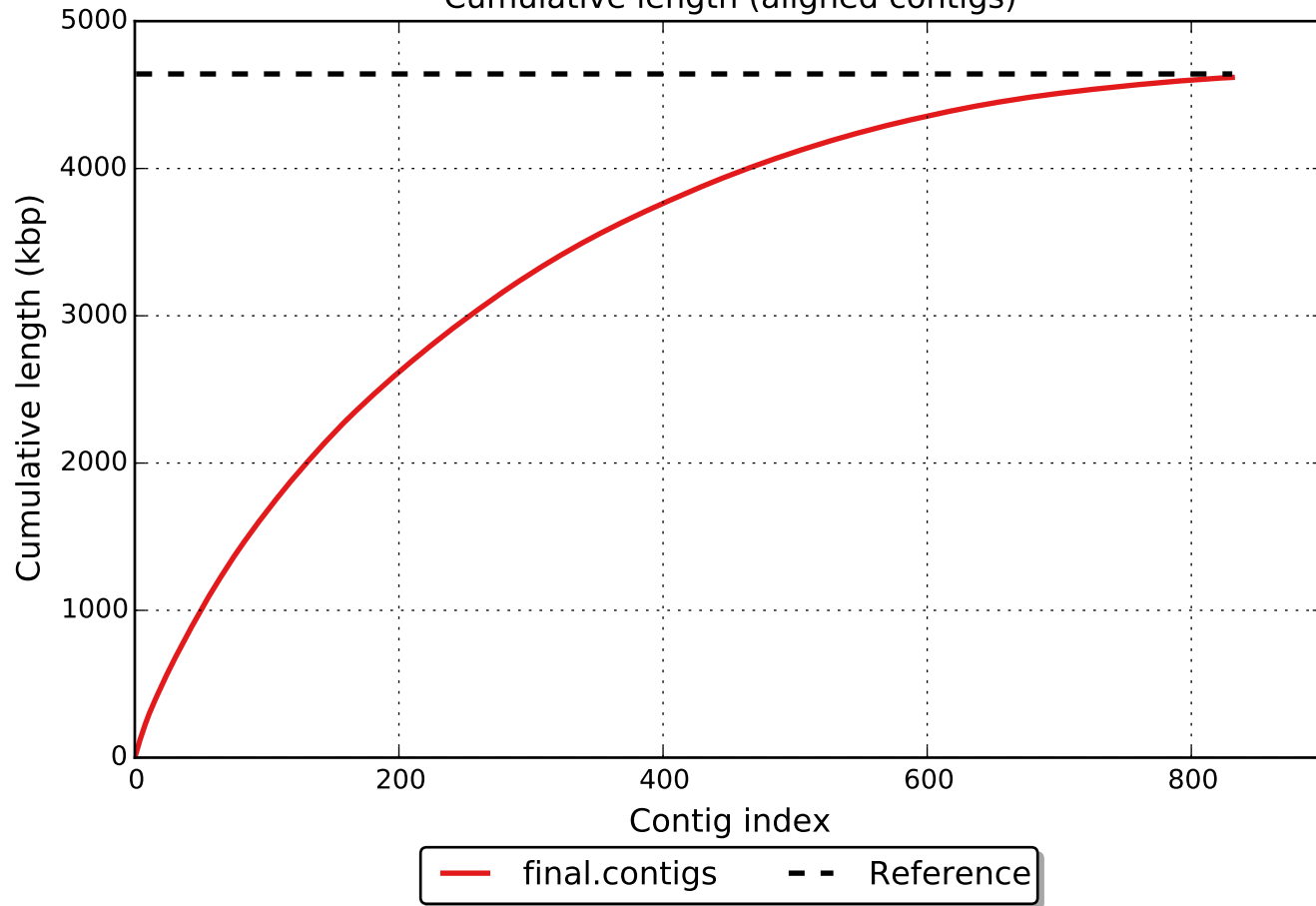


GC content

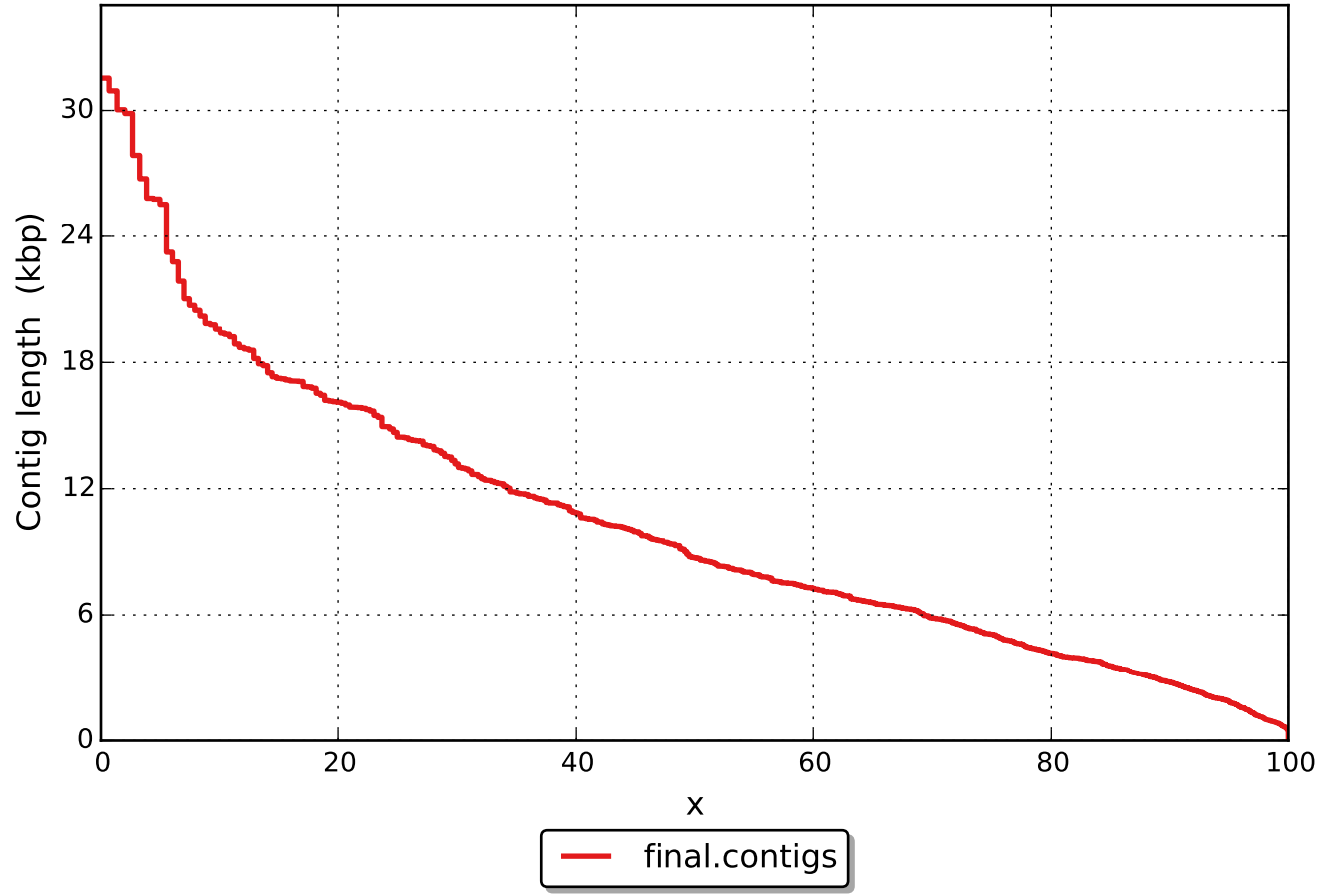




Cumulative length (aligned contigs)



NAx



NGAx

