

Report

	final.contigs
# contigs (≥ 0 bp)	15392
# contigs (≥ 1000 bp)	2448
Total length (≥ 0 bp)	10336527
Total length (≥ 1000 bp)	3427742
# contigs	9120
Largest contig	4257
Total length	8100357
Reference length	11094646
GC (%)	50.36
Reference GC (%)	50.48
N50	912
NG50	735
N75	683
L50	3099
LG50	4930
L75	5676
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	788
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	122
Genome fraction (%)	77.422
Duplication ratio	1.067
# N's per 100 kbp	0.00
# mismatches per 100 kbp	242.67
# indels per 100 kbp	0.14
Largest alignment	4257
NA50	912
NGA50	735
NA75	683
LA50	3099
LGA50	4931
LA75	5676

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

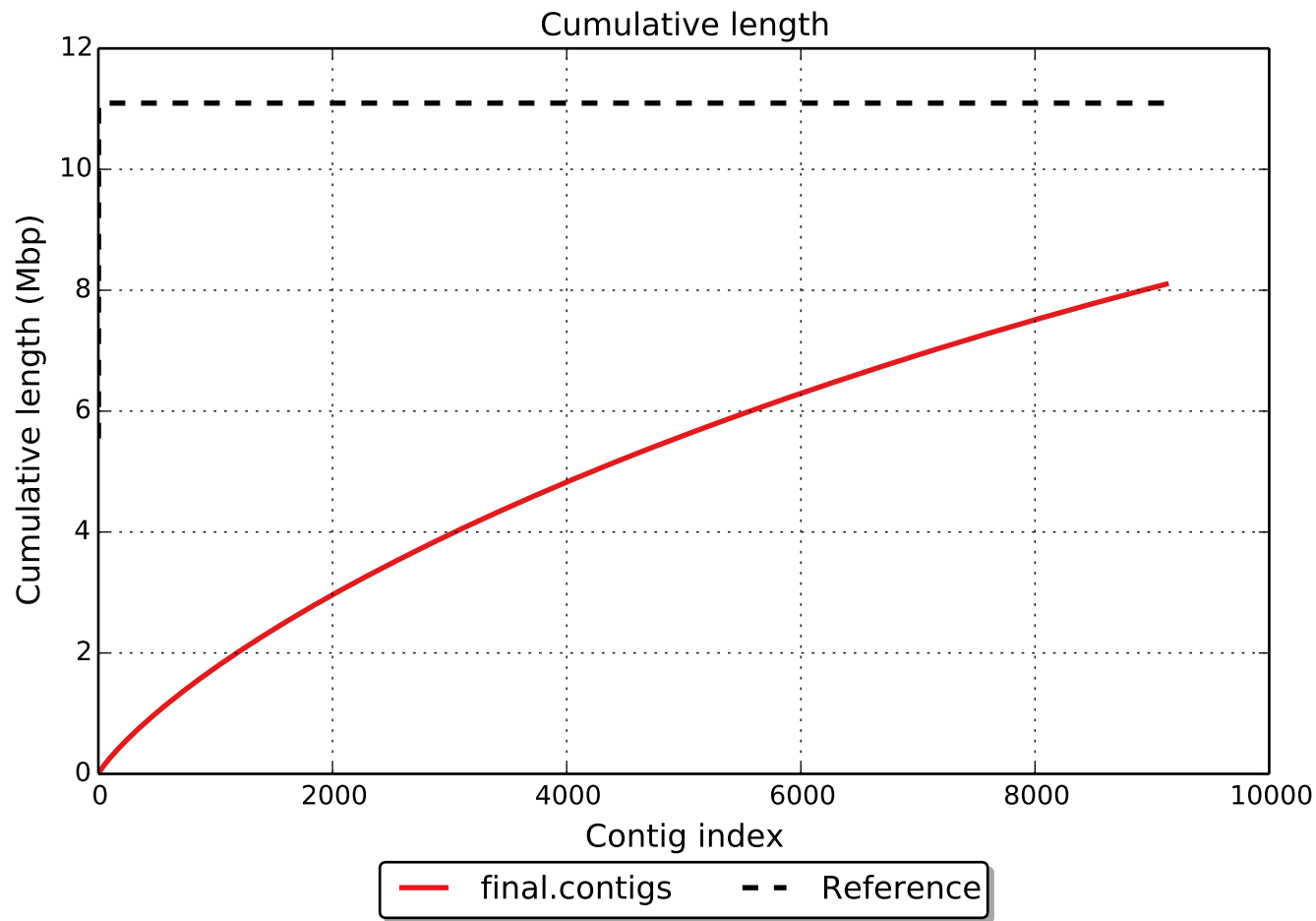
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	788
# local misassemblies	0
# mismatches	20845
# indels	12
# short indels	10
# long indels	2
Indels length	40

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).

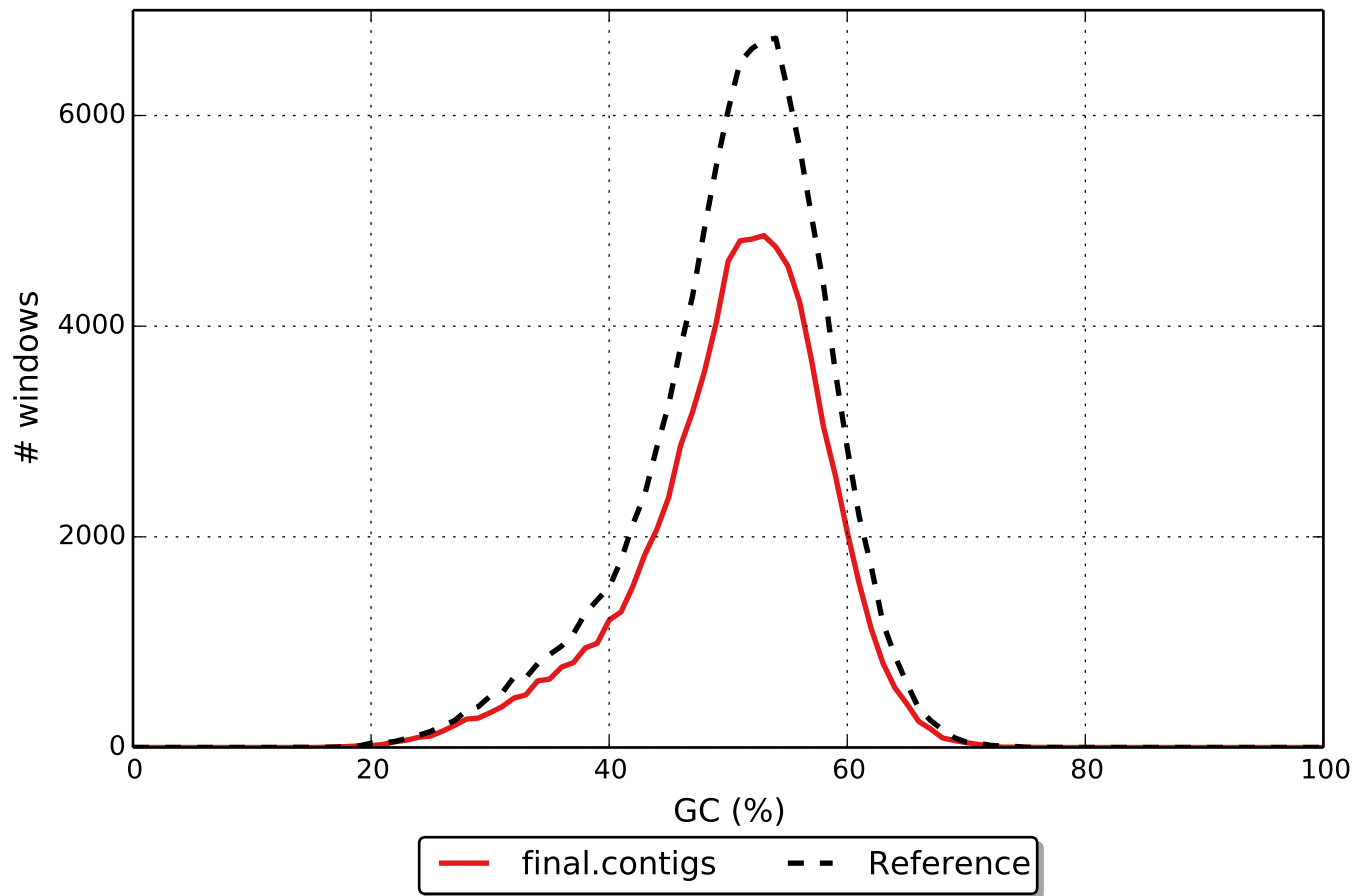
Unaligned report

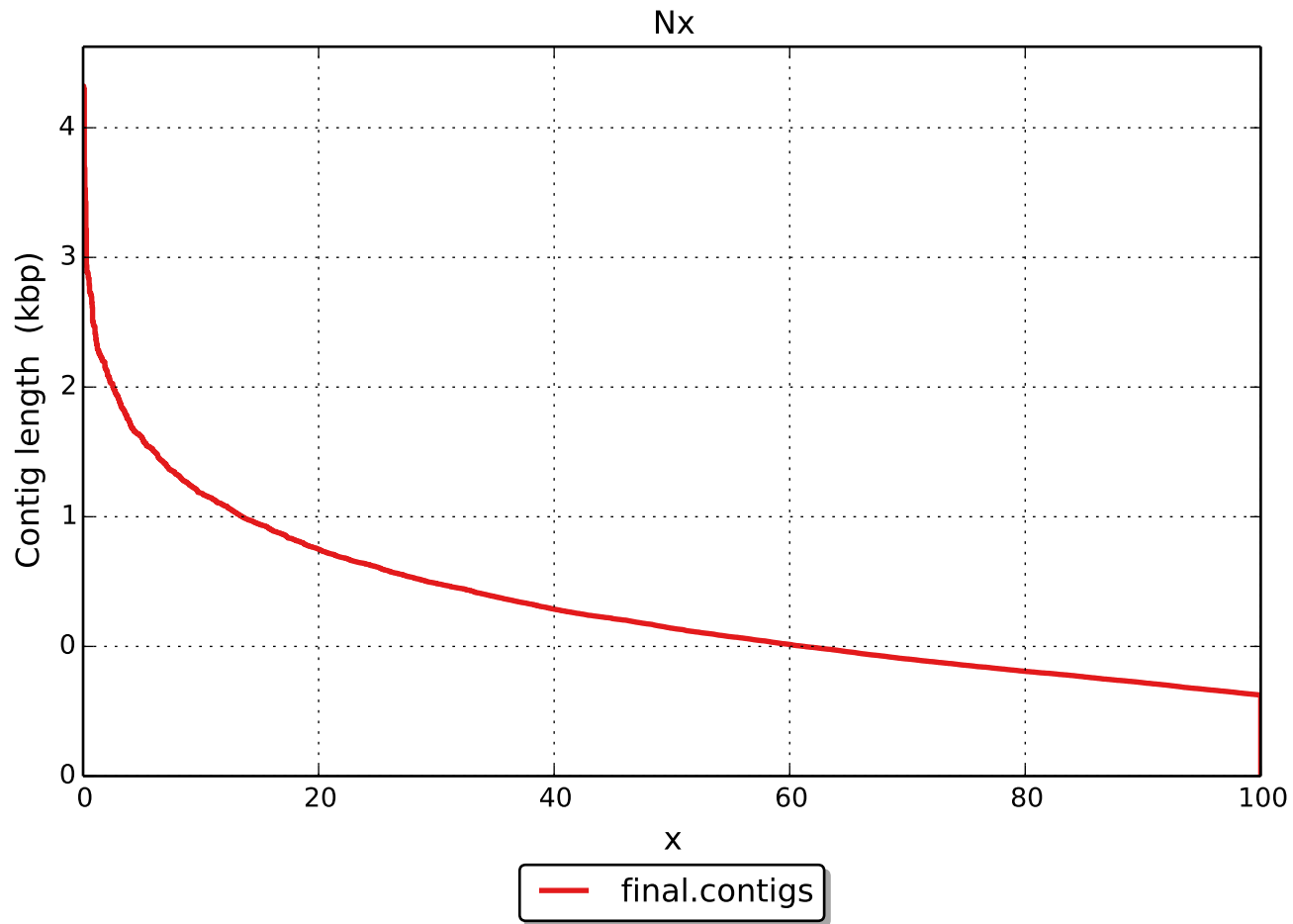
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	122
# N's	0

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).

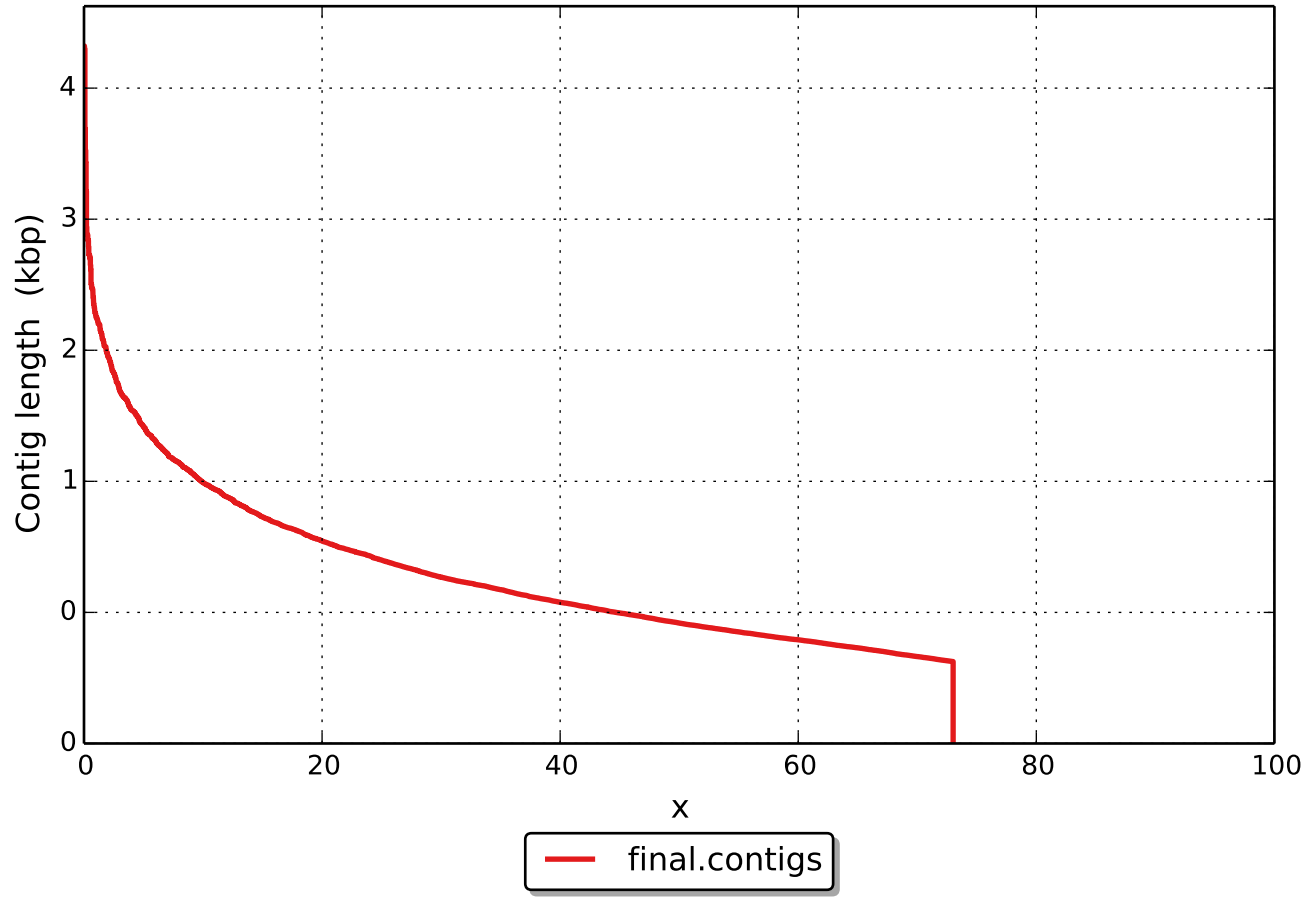


GC content

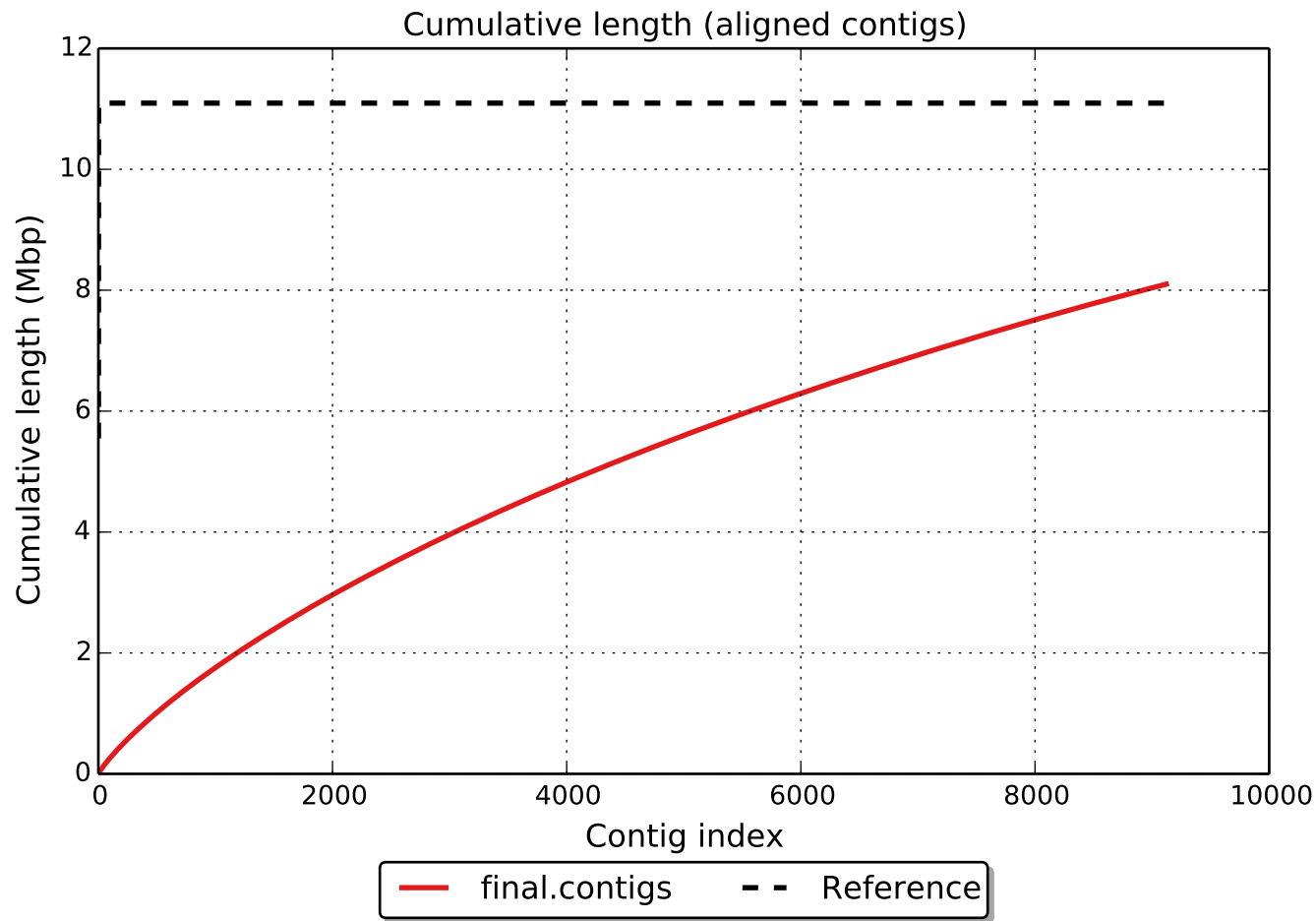




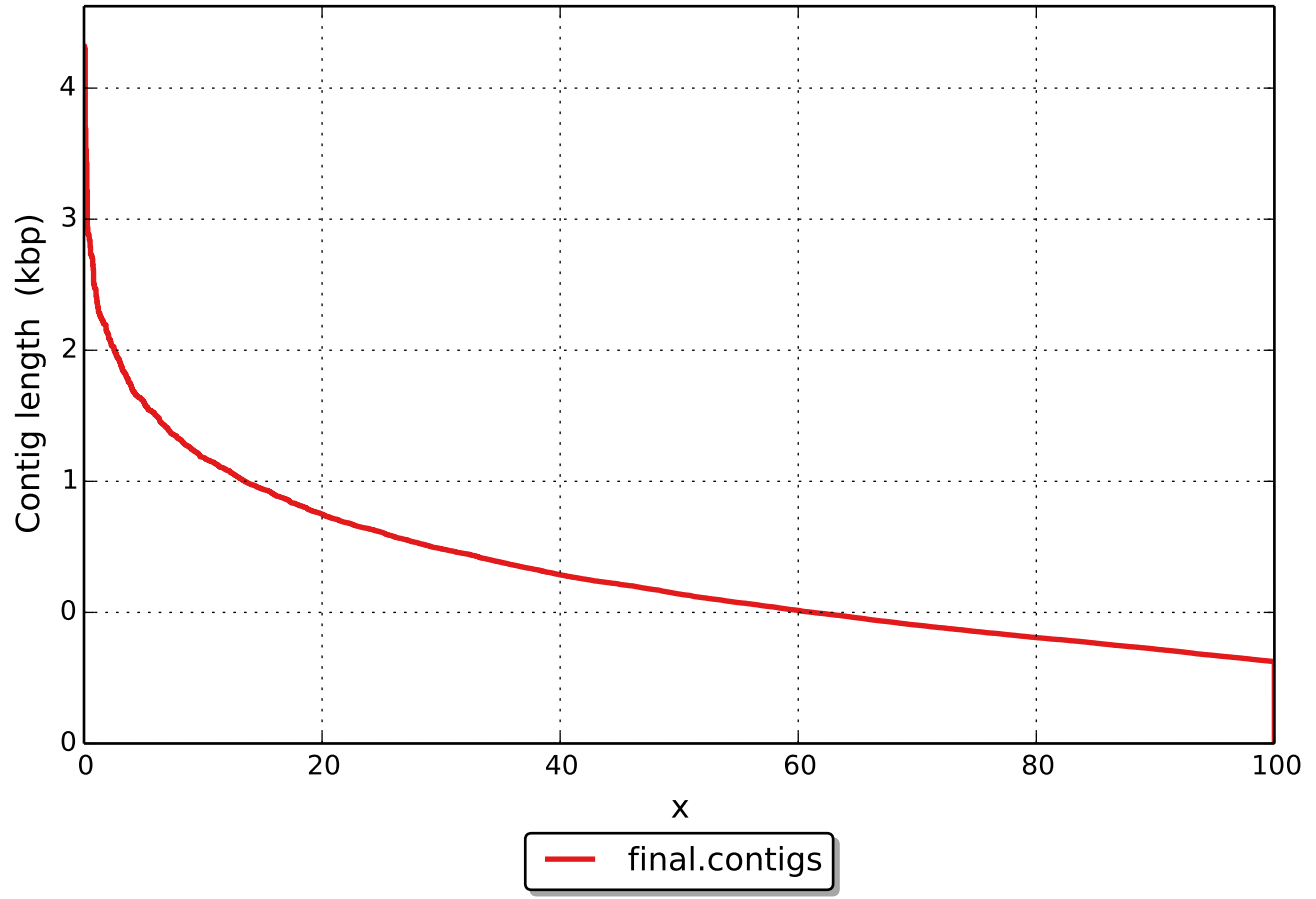
NGx







NAx



NGAx

