

Report

	final.contigs
# contigs (>= 0 bp)	1069
# contigs (>= 1000 bp)	508
Total length (>= 0 bp)	10898729
Total length (>= 1000 bp)	10690343
# contigs	612
Largest contig	134607
Total length	10762487
Reference length	11094646
GC (%)	50.40
Reference GC (%)	50.49
N50	38882
NG50	36429
N75	22936
NG75	21908
L50	86
LG50	90
L75	177
LG75	188
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	785
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.680
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.79
# indels per 100 kbp	0.13
Largest alignment	134607
NA50	38882
NGA50	36429
NA75	22936
NGA75	21908
LA50	86
LGA50	90
LA75	177
LGA75	188

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

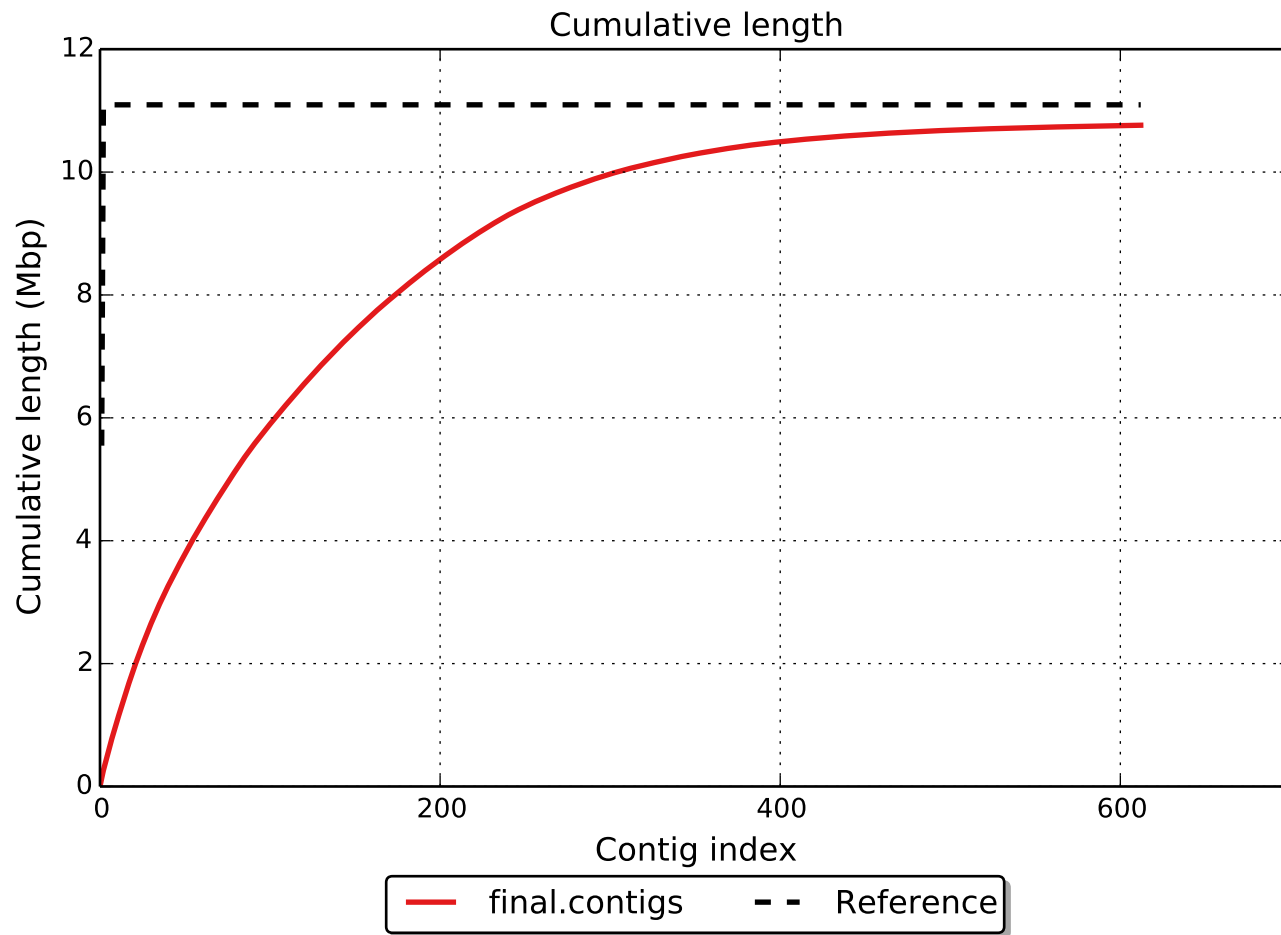
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	785
# local misassemblies	2
# mismatches	407
# indels	14
# short indels	12
# long indels	2
Indels length	33

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).

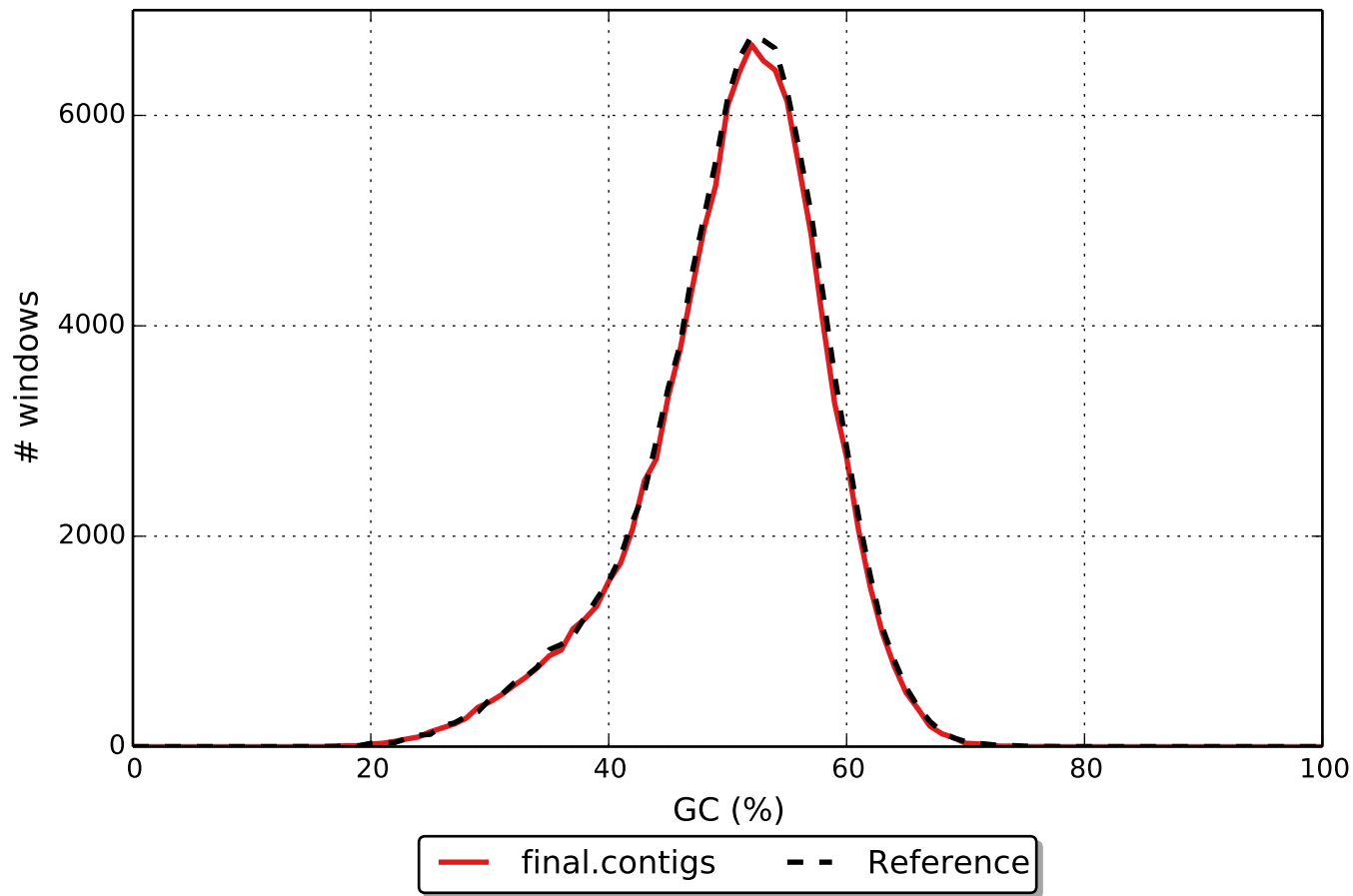
Unaligned report

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

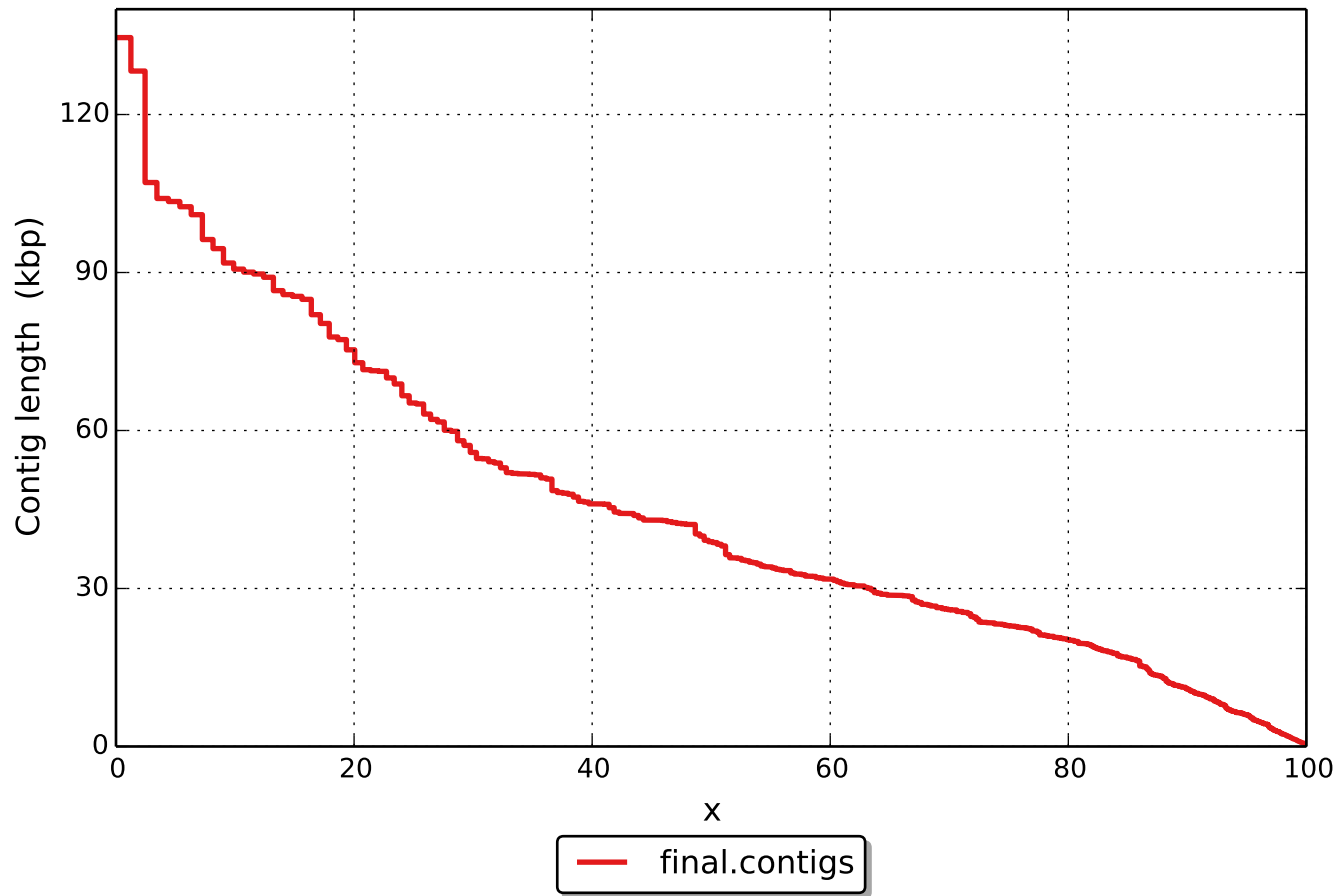
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



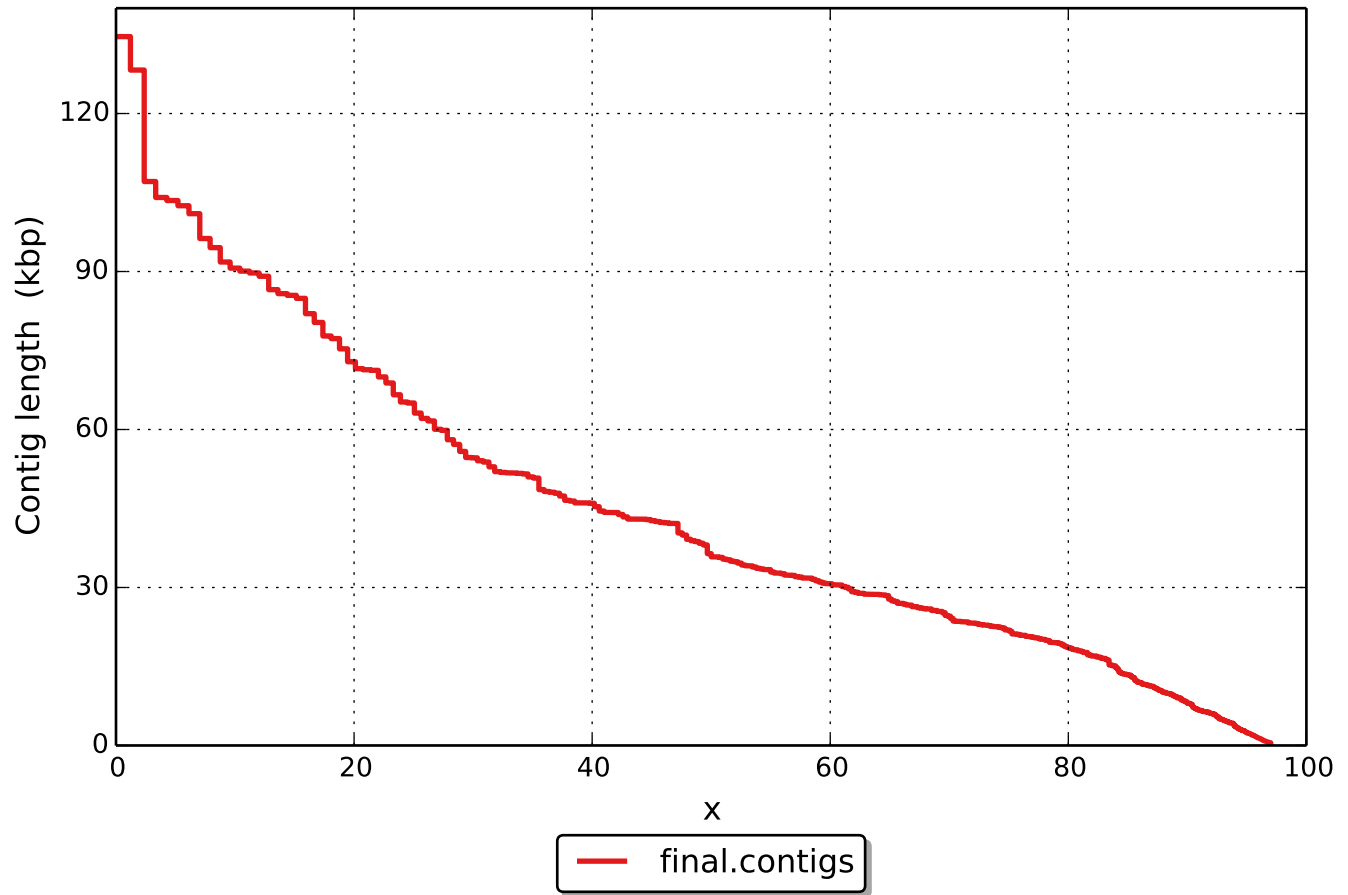
GC content



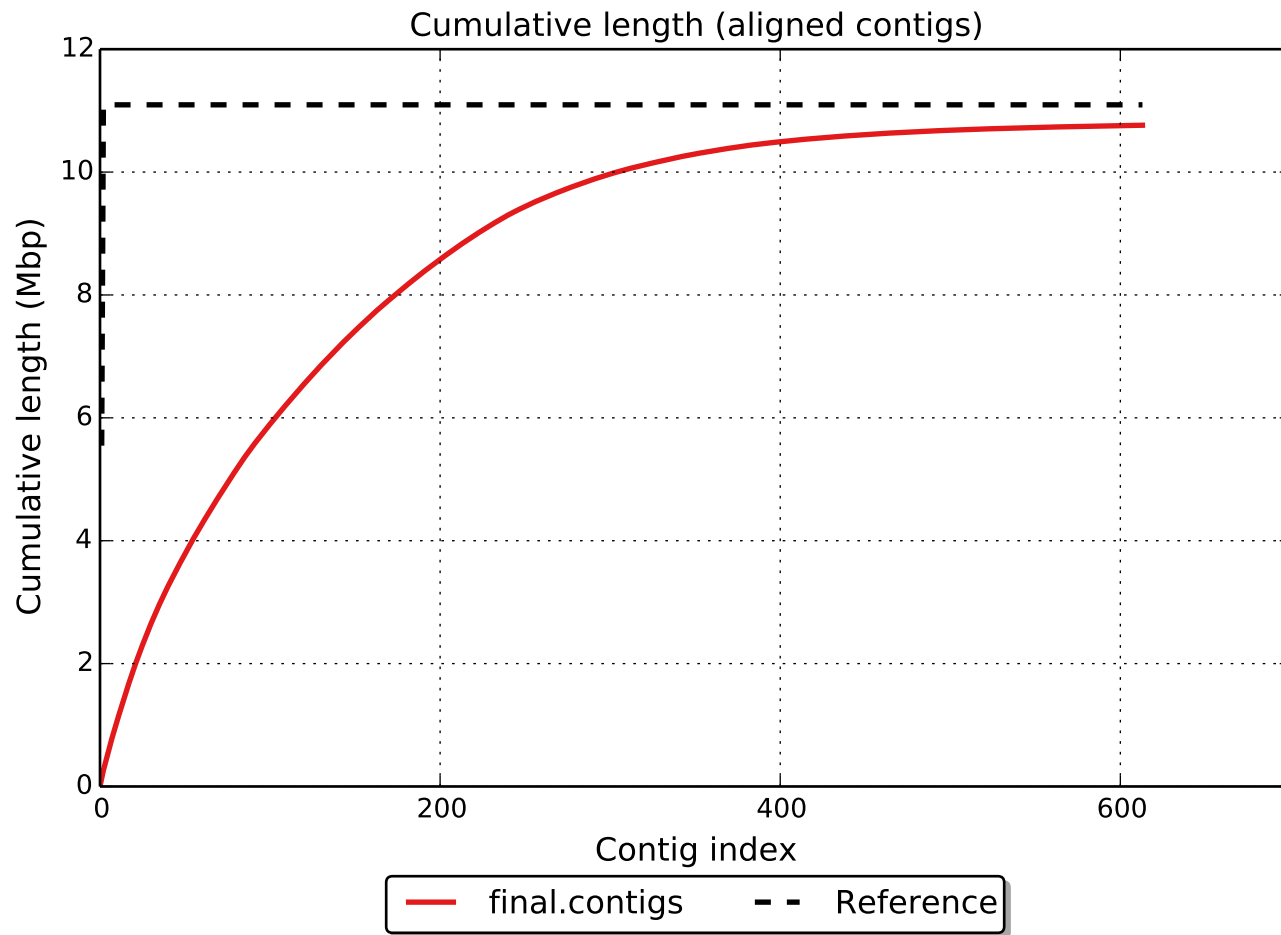
Nx



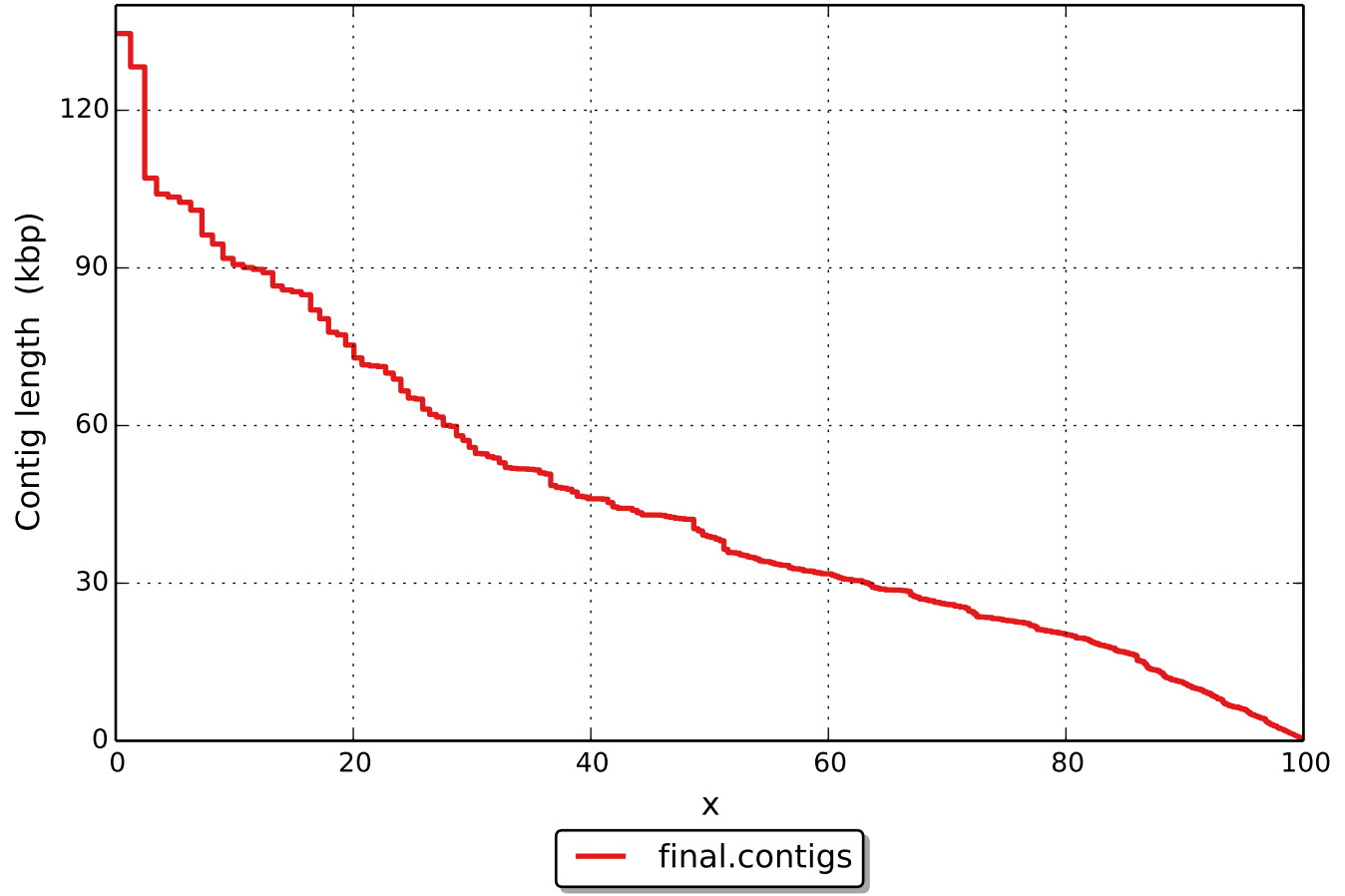
NGx







NAx



NGAx

