

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	4753
# contigs ( $\geq 1000$ bp)	1689
Total length ( $\geq 0$ bp)	4646767
Total length ( $\geq 1000$ bp)	2482846
# contigs	4753
Largest contig	4277
Total length	4646767
Reference length	5478683
GC (%)	50.50
Reference GC (%)	50.50
N50	1042
NG50	927
N75	743
NG75	612
L50	1533
LG50	1956
L75	2857
LG75	3781
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1784
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	80.971
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	71.93
# indels per 100 kbp	0.07
Largest alignment	4277
NA50	1042
NGA50	927
NA75	743
NGA75	612
LA50	1534
LGA50	1956
LA75	2858
LGA75	3782

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

## Misassemblies report

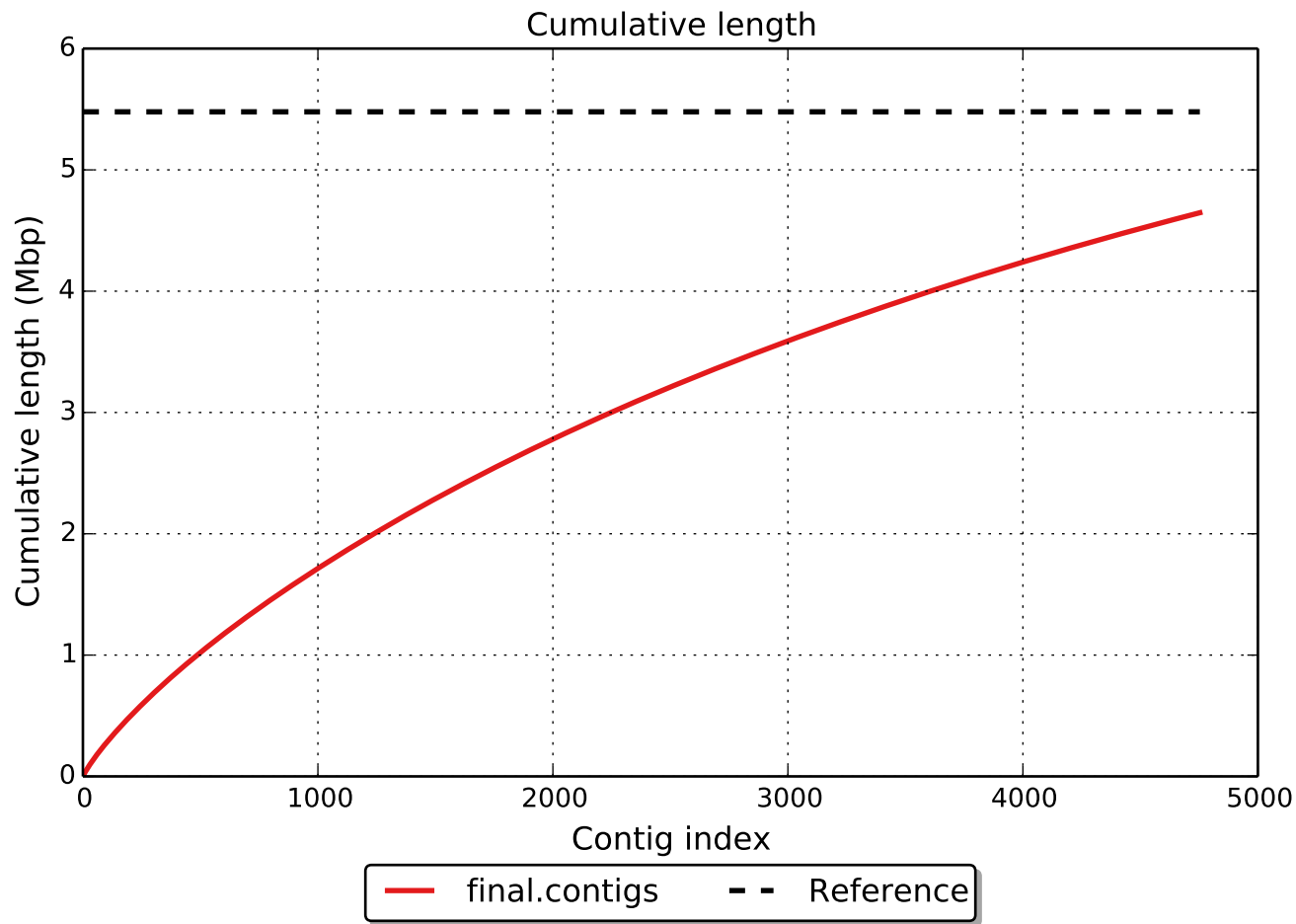
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1784
# local misassemblies	0
# mismatches	3191
# indels	3
# short indels	0
# long indels	3
Indels length	45

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

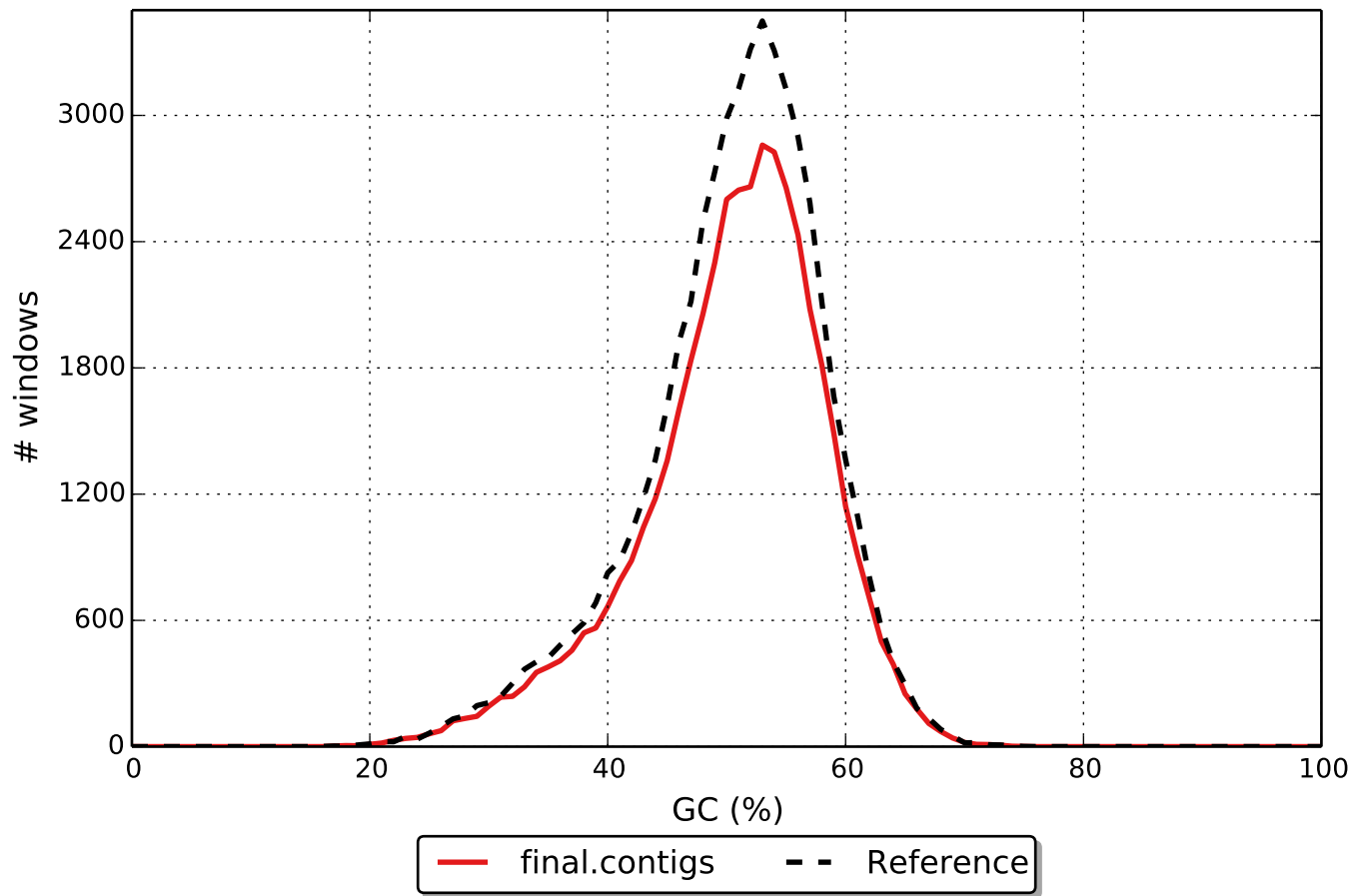
## Unaligned report

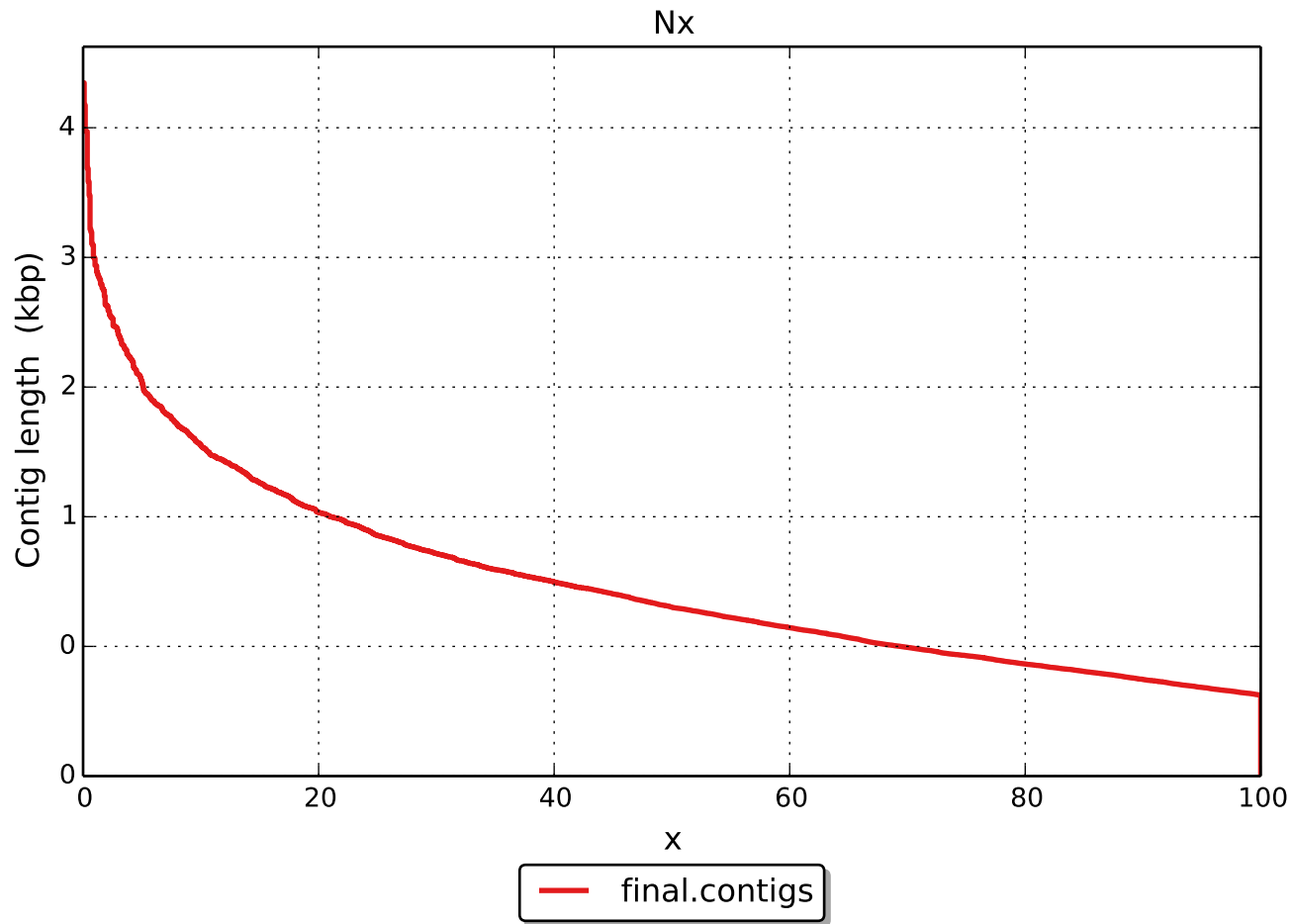
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

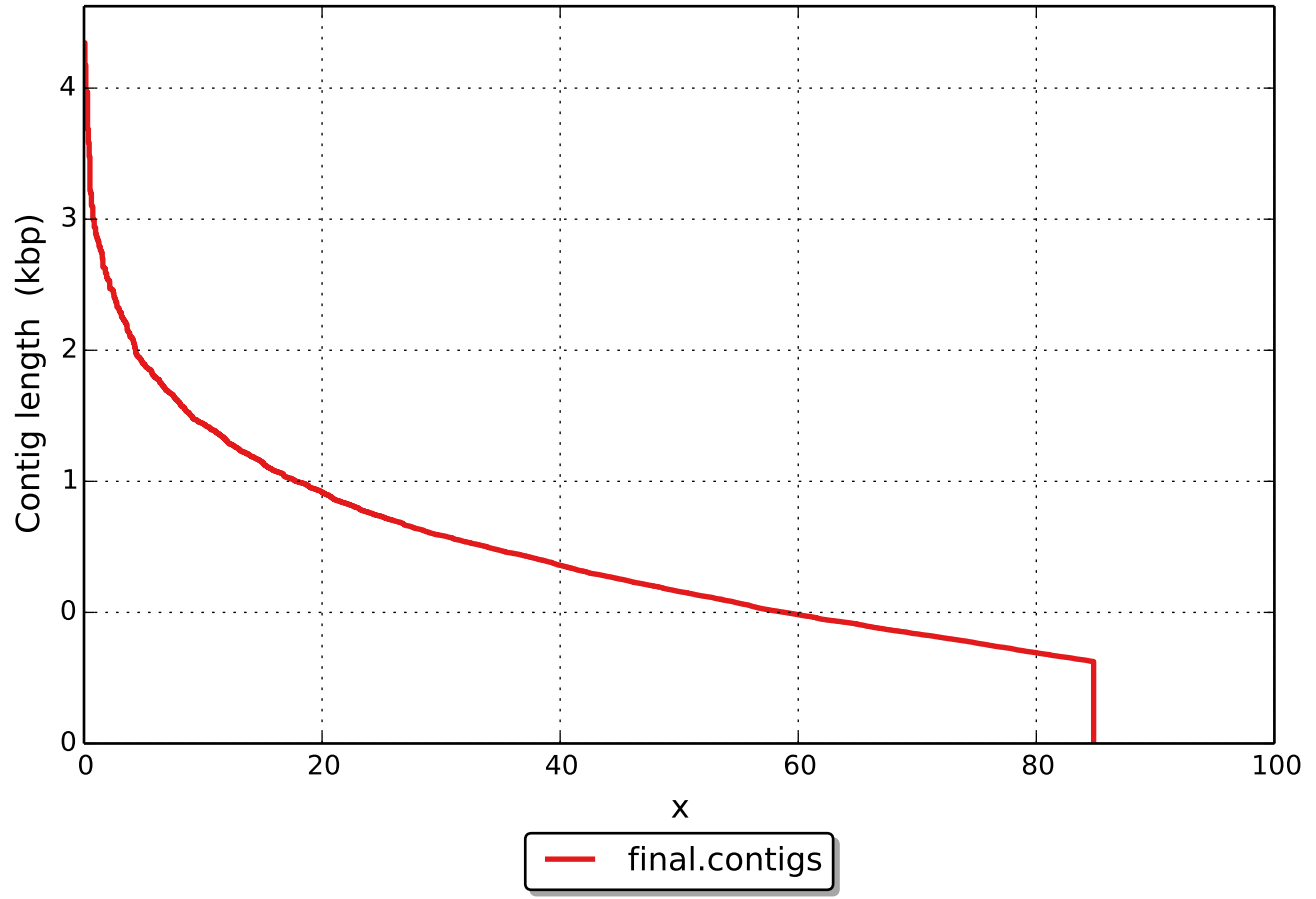


GC content



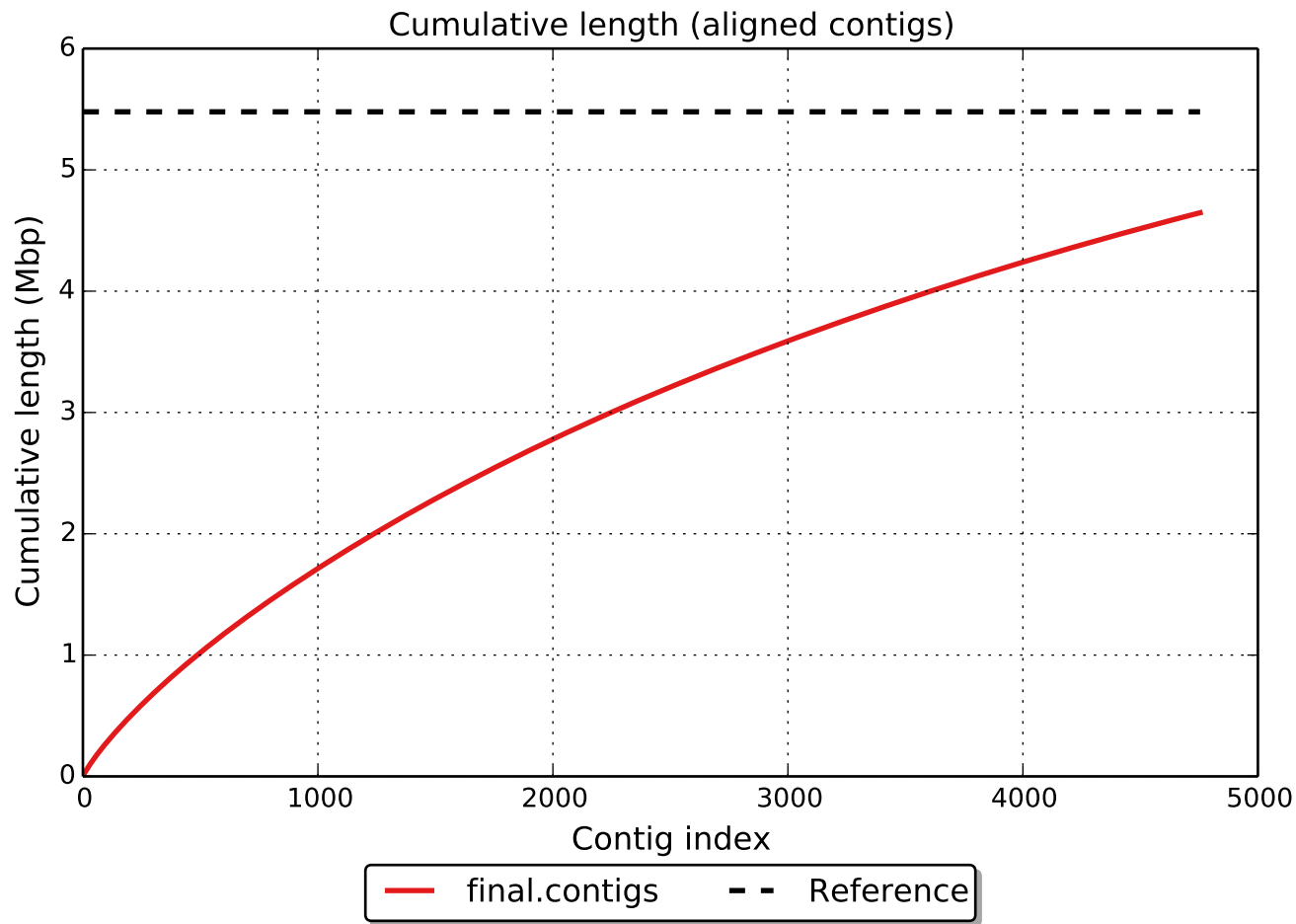


NGx

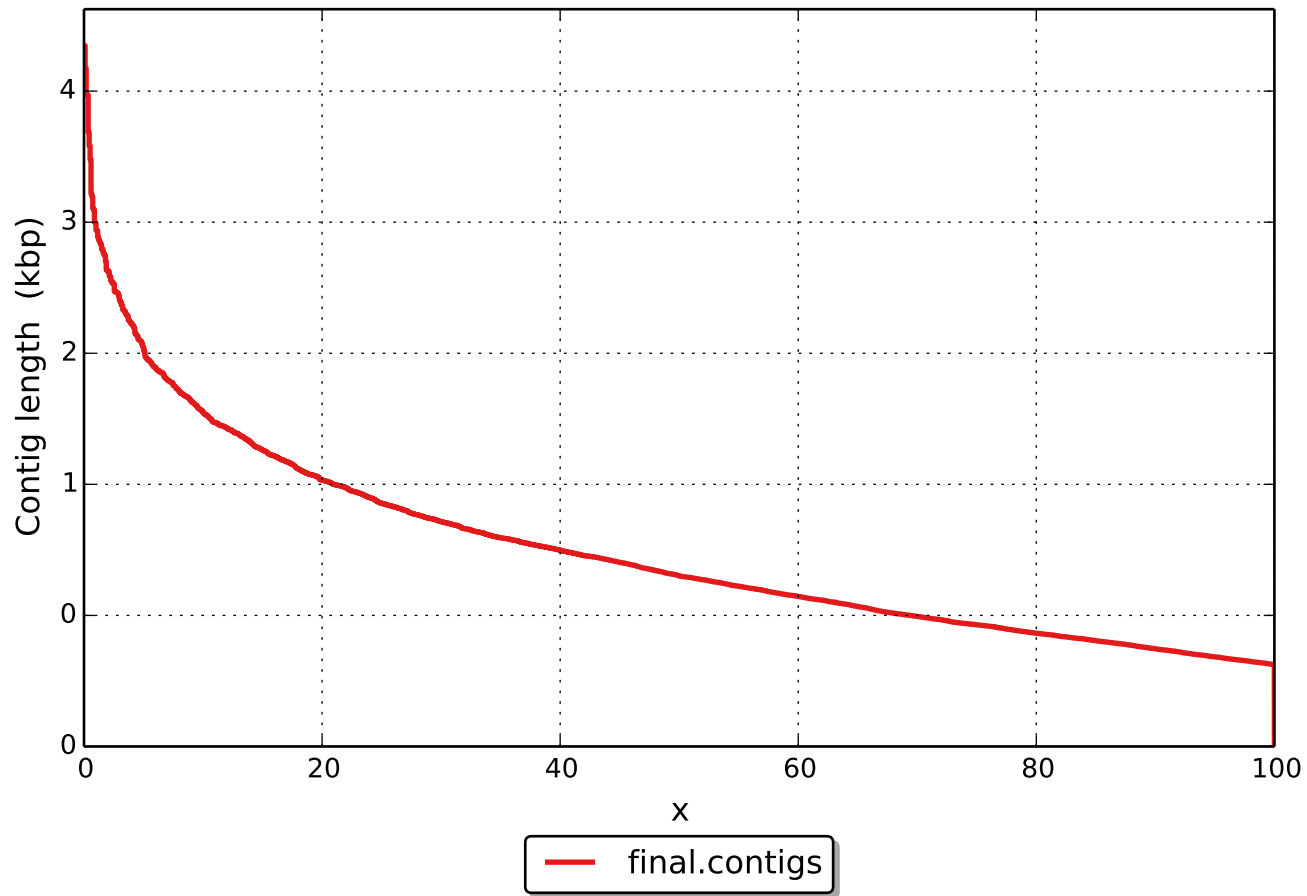








NAx



NGAx

