

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	863
# contigs ( $\geq 1000$ bp)	725
Total length ( $\geq 0$ bp)	5280257
Total length ( $\geq 1000$ bp)	5184932
# contigs	863
Largest contig	62726
Total length	5280257
Reference length	5478683
GC (%)	50.28
Reference GC (%)	50.49
N50	11538
NG50	10766
N75	6041
NG75	5217
L50	137
LG50	146
L75	298
LG75	325
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2838
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	16702
Genome fraction (%)	94.690
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.00
# indels per 100 kbp	0.12
Largest alignment	62726
NA50	11433
NGA50	10605
NA75	5951
NGA75	5173
LA50	138
LGA50	147
LA75	301
LGA75	328

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

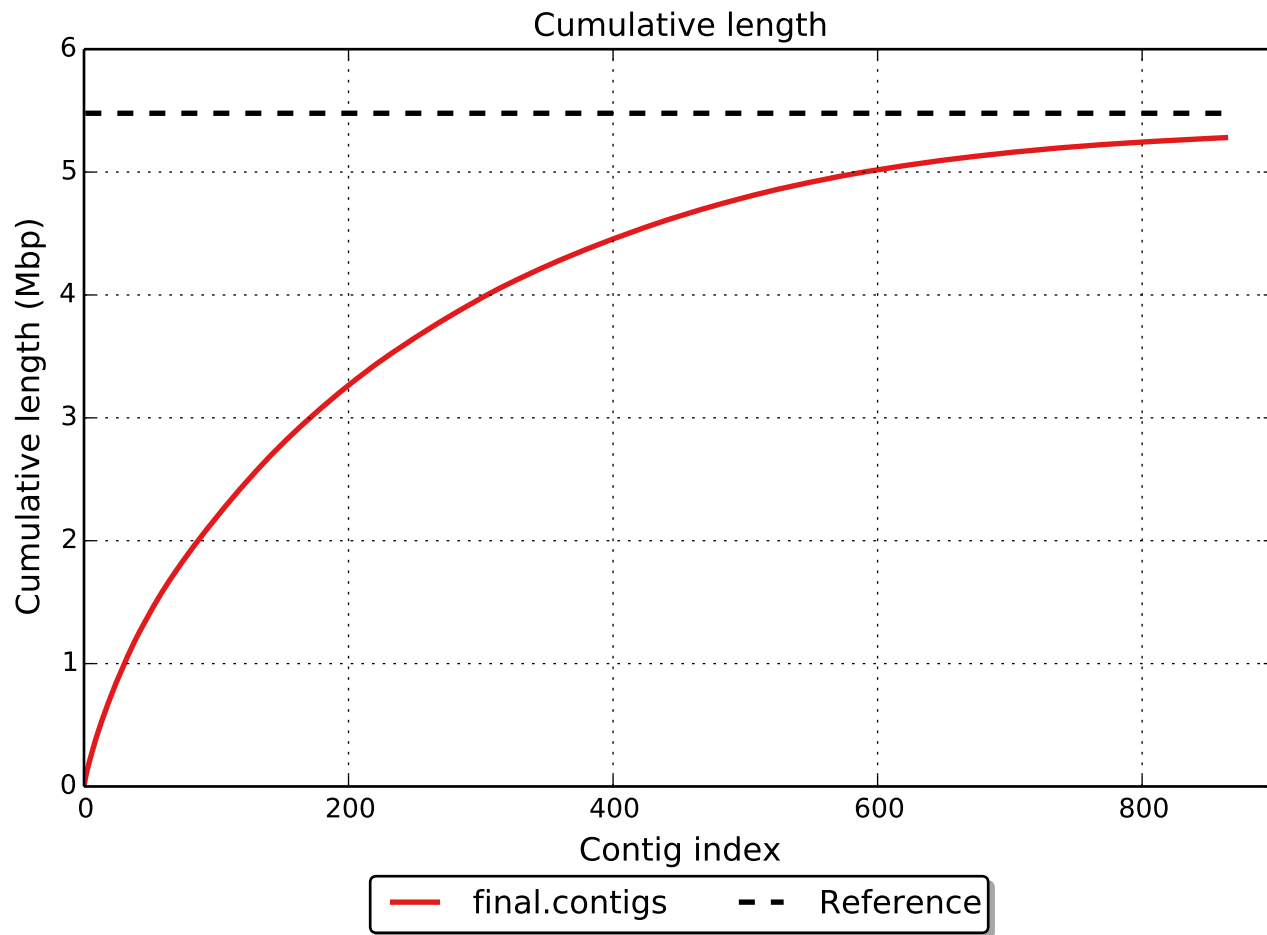
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	1
Misassembled contigs length	2838
# local misassemblies	0
# mismatches	1193
# indels	6
# short indels	3
# long indels	3
Indels length	36

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).

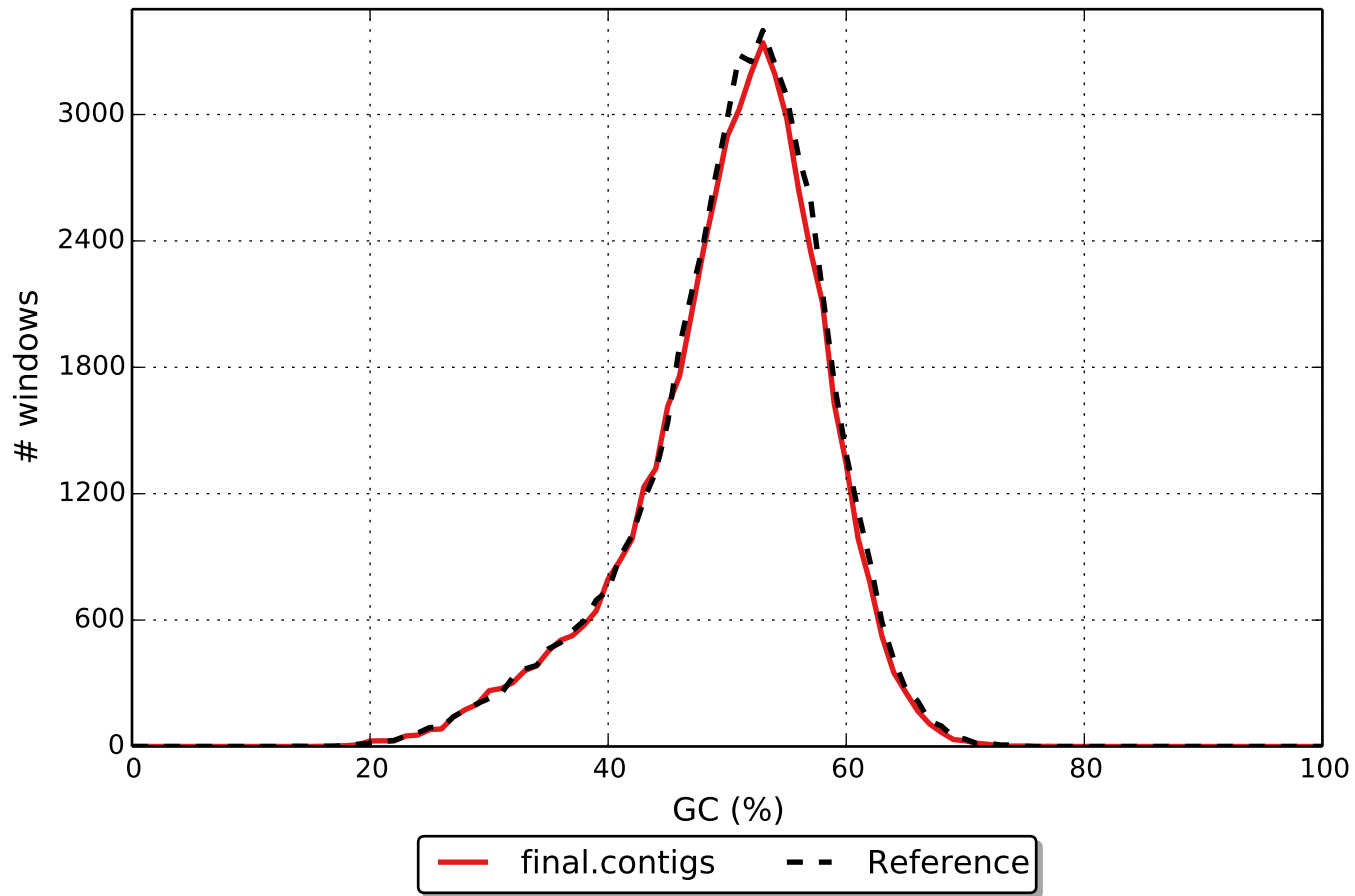
## Unaligned report

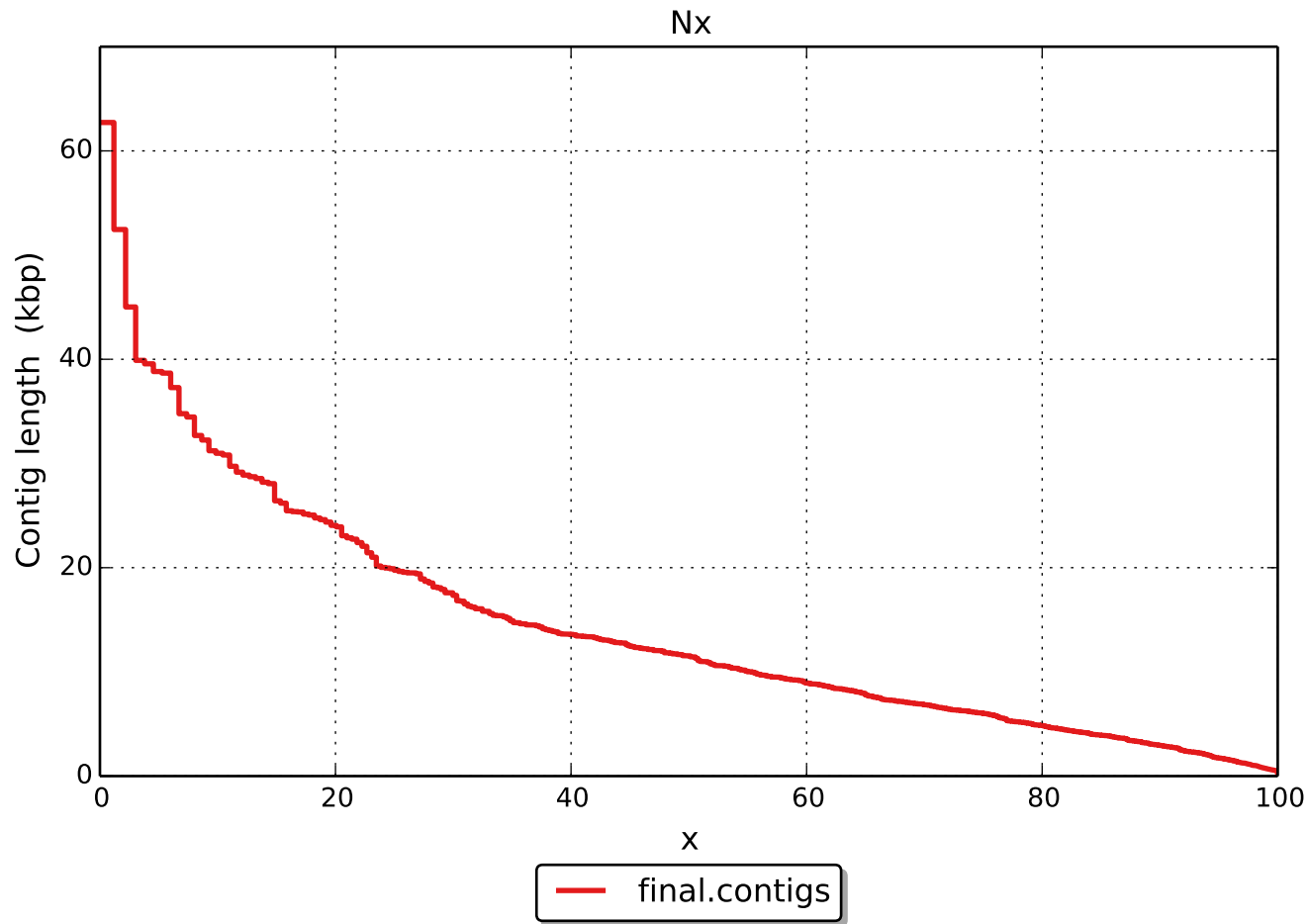
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	16702
# N's	0

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).

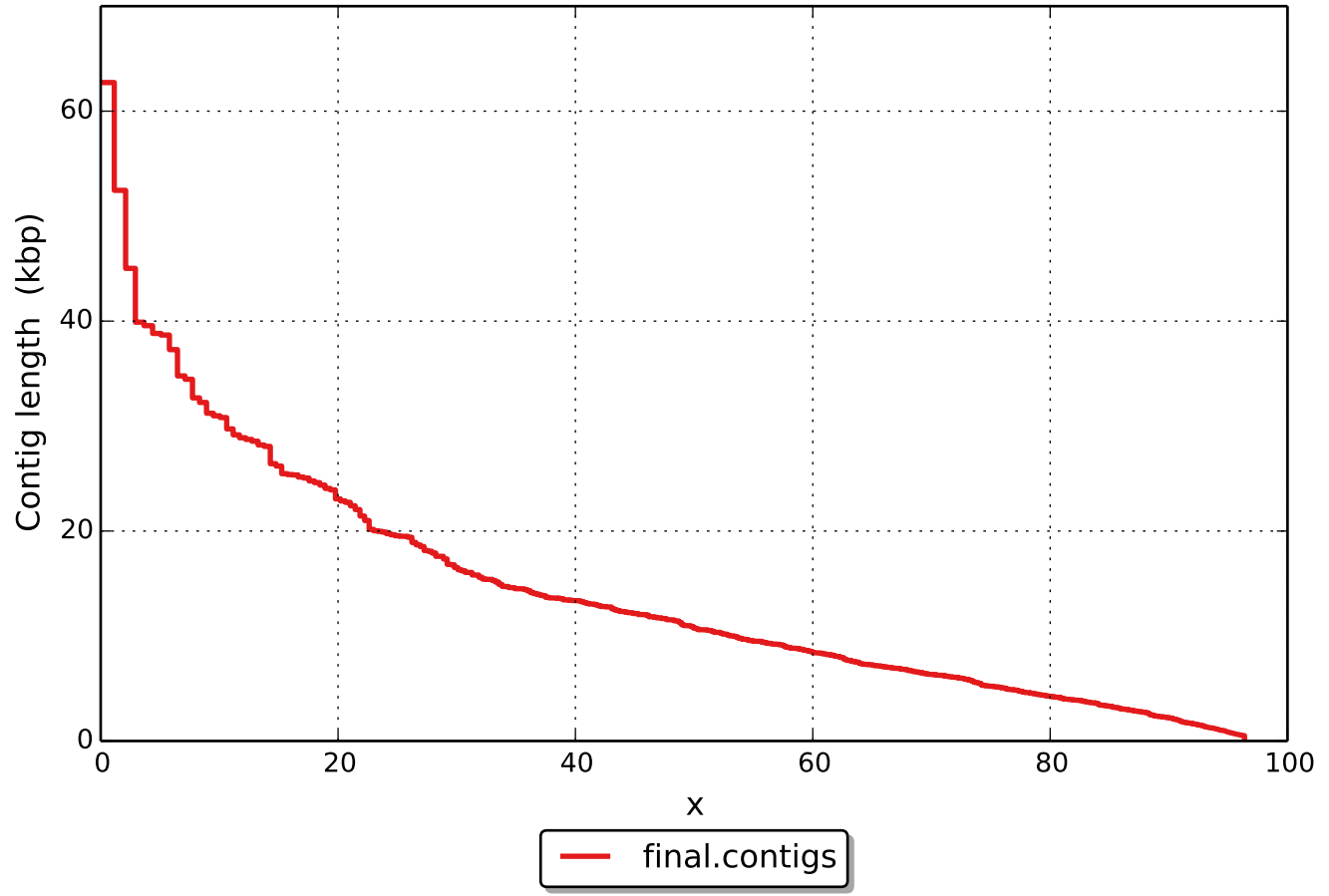


GC content





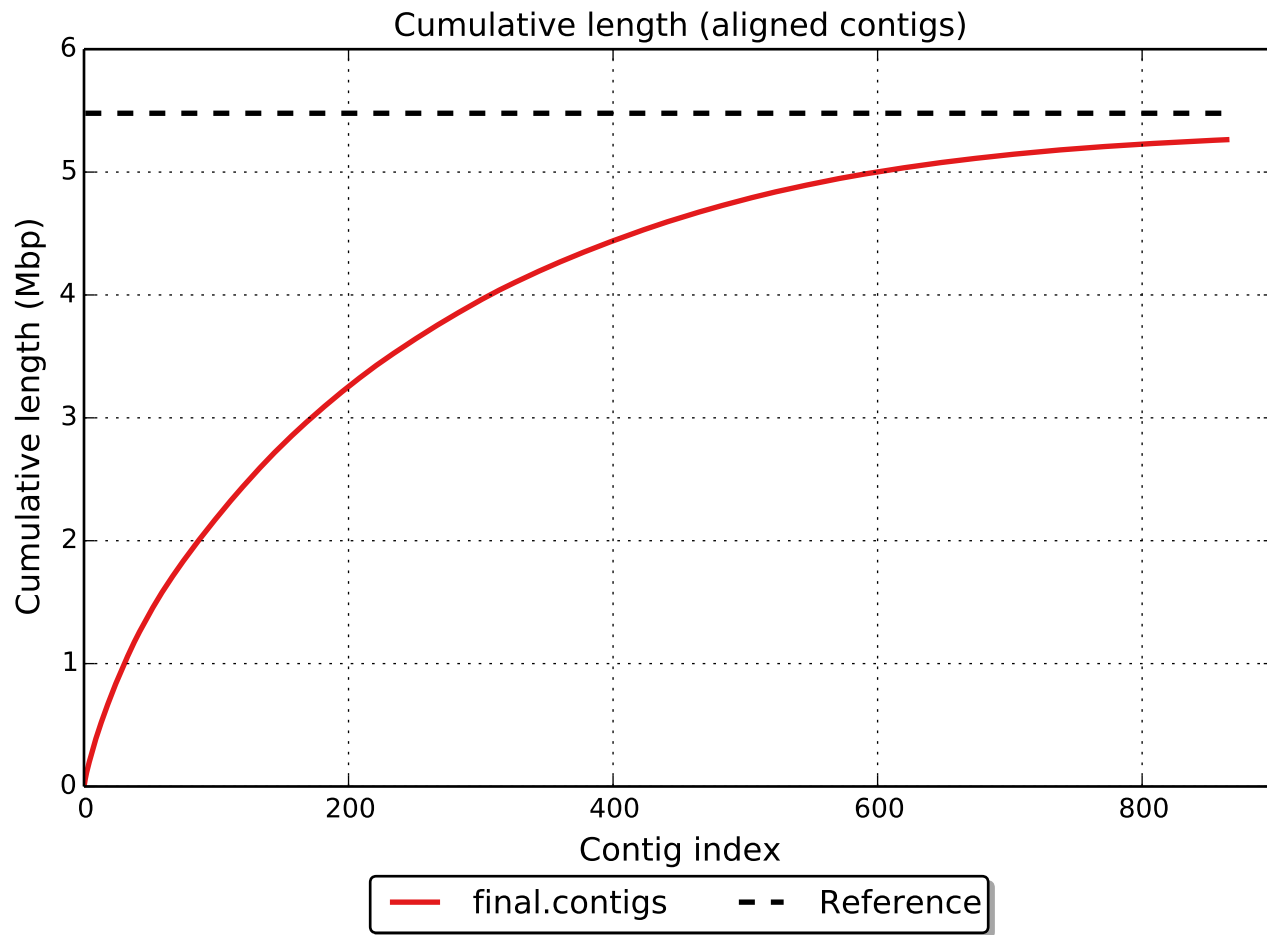
NGx



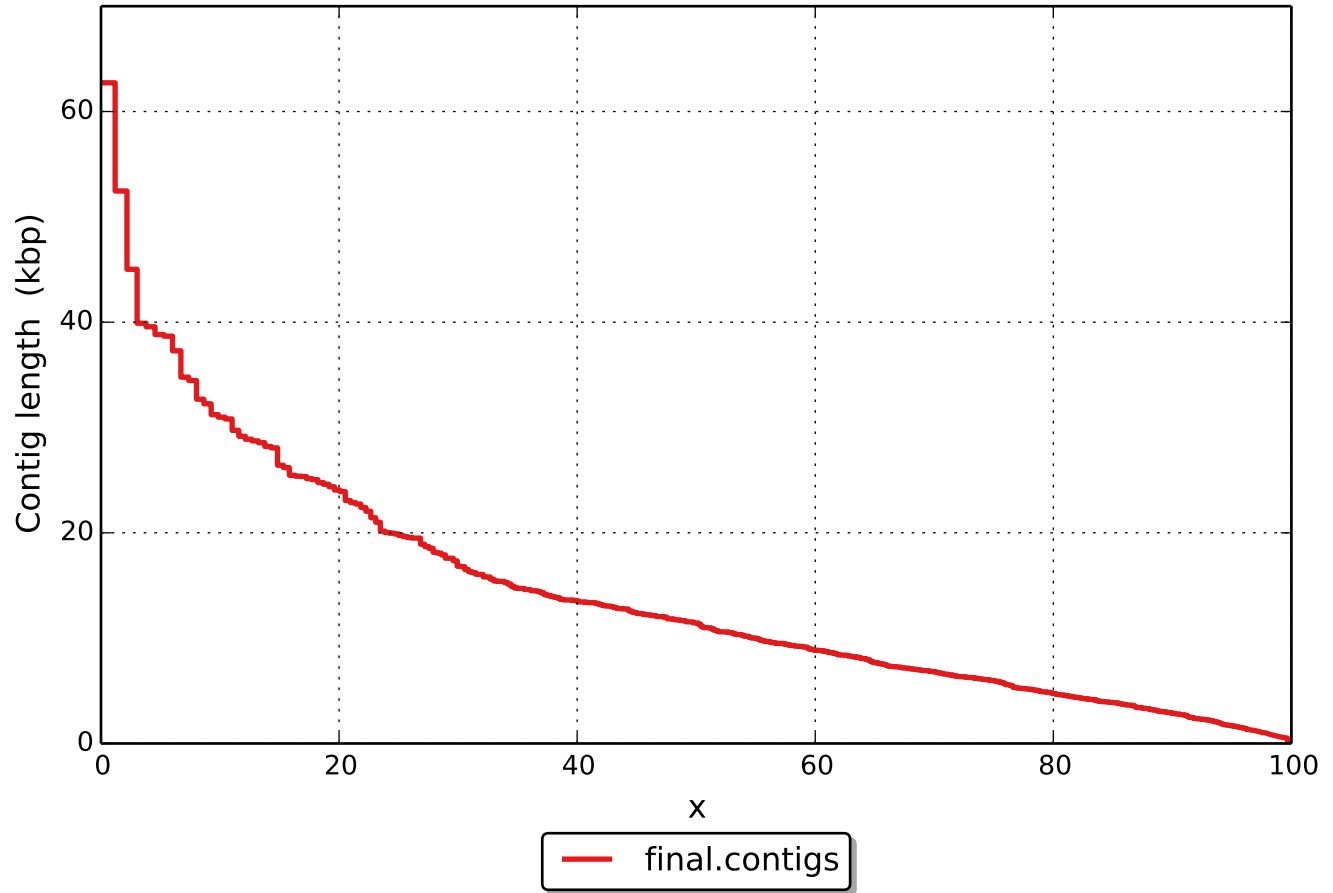
# Misassemblies







NAx



# NGAx

