

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	462
# contigs ( $\geq 1000$ bp)	359
Total length ( $\geq 0$ bp)	3737538
Total length ( $\geq 1000$ bp)	3697428
# contigs	379
Largest contig	61161
Total length	3713459
Reference length	3785550
GC (%)	32.26
Reference GC (%)	32.26
N50	15222
NG50	14650
N75	8940
NG75	8617
L50	78
LG50	80
L75	155
LG75	161
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.338
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16.28
# indels per 100 kbp	0.00
Largest alignment	61161
NA50	15222
NGA50	14650
NA75	8940
NGA75	8617
LA50	78
LGA50	80
LA75	155
LGA75	161

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

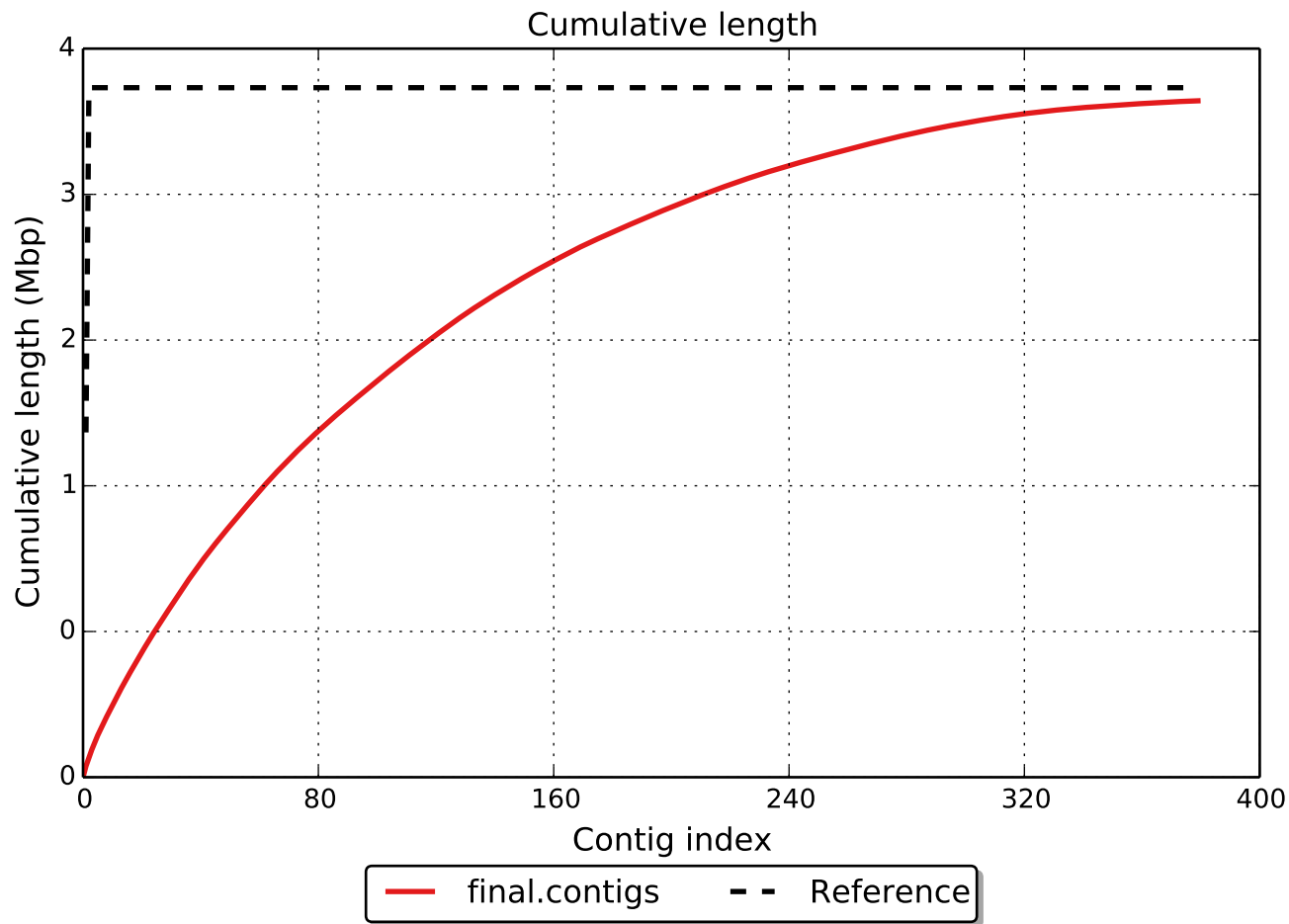
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	606
# indels	0
# short indels	0
# long indels	0
Indels length	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).

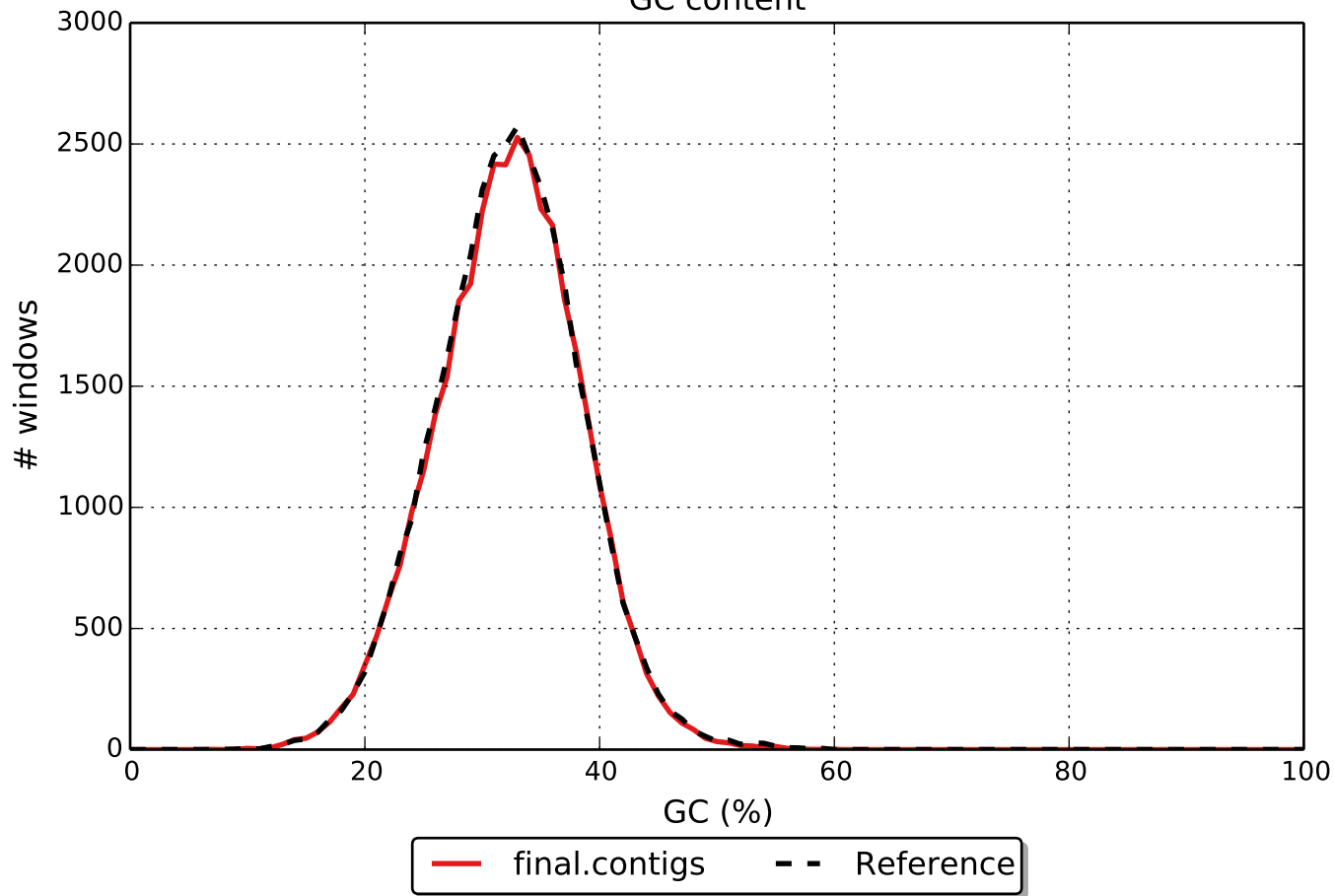
## Unaligned report

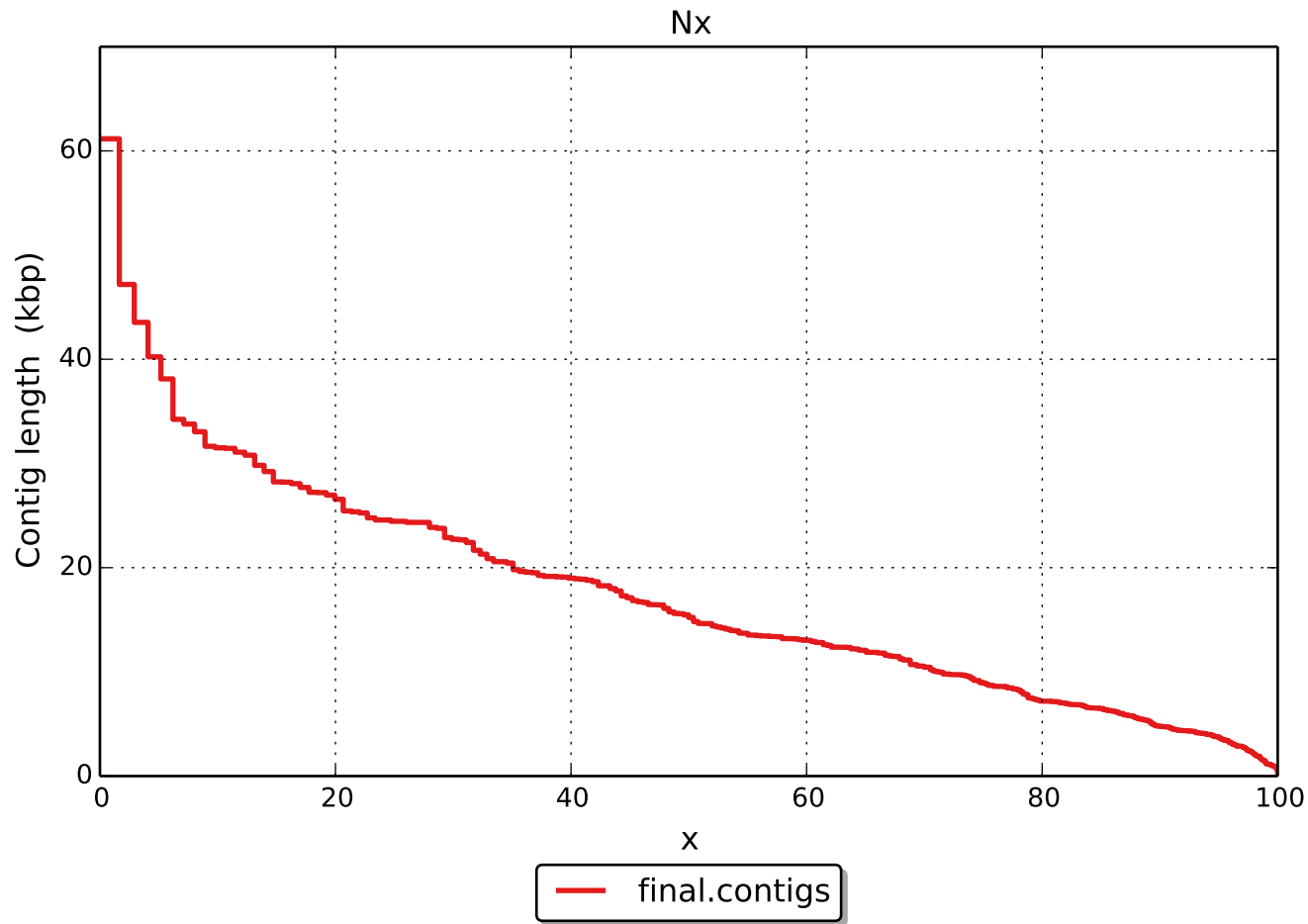
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

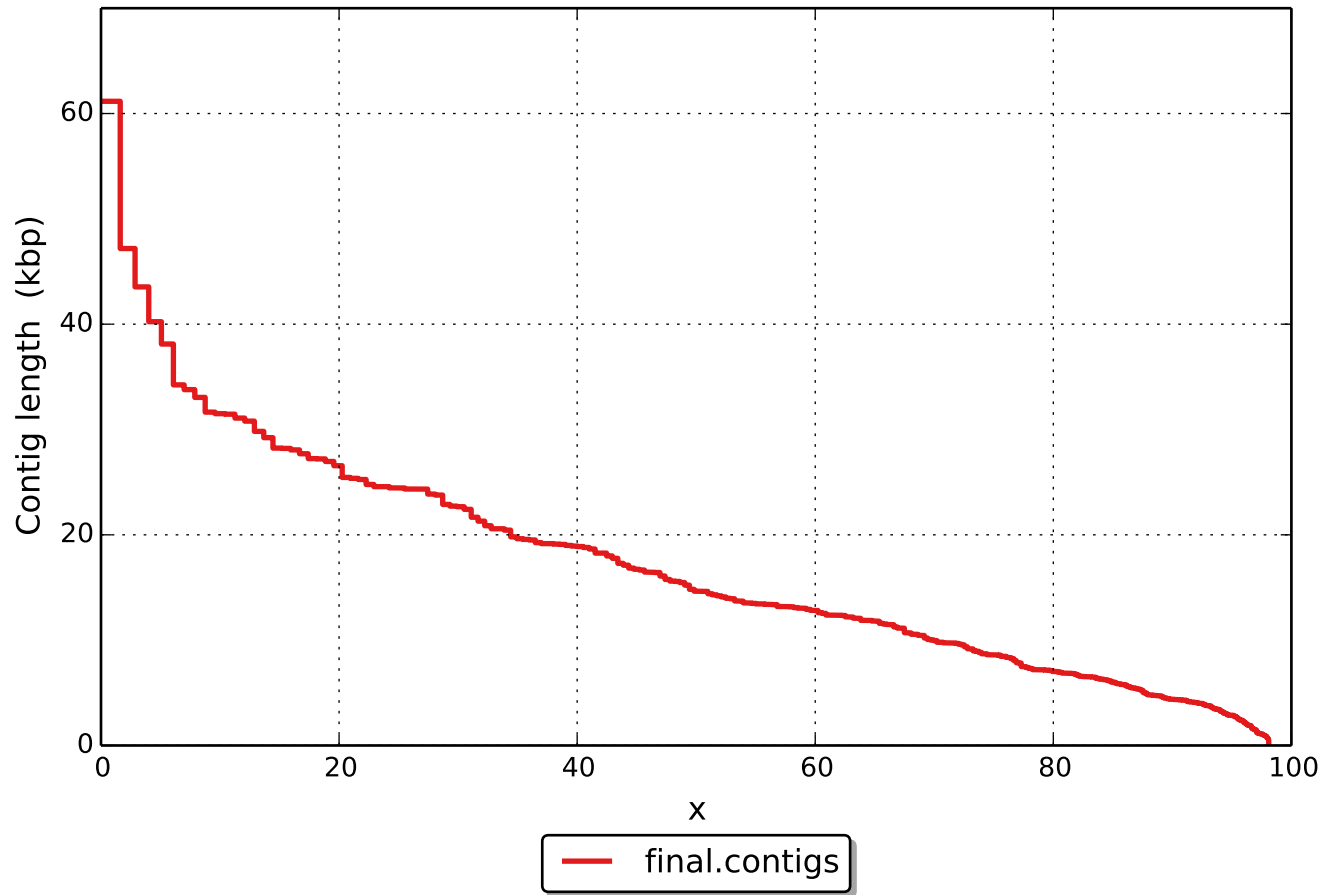


GC content

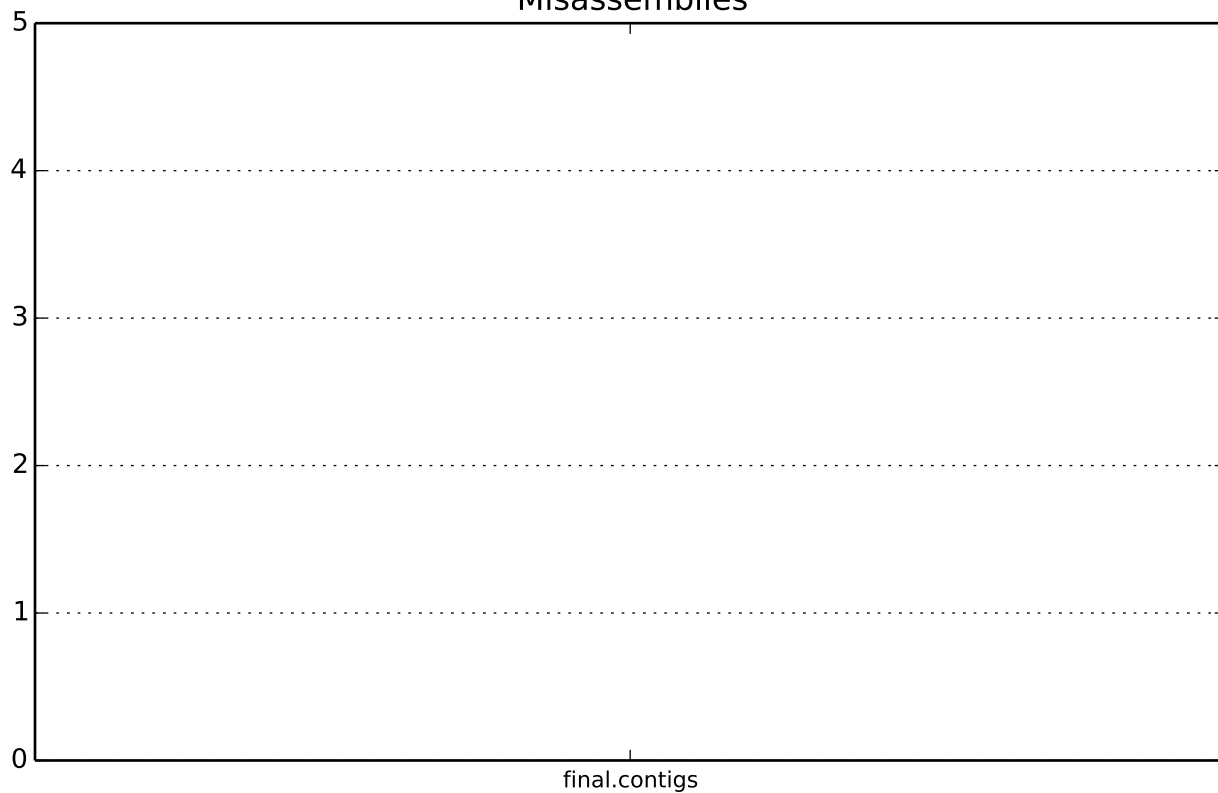




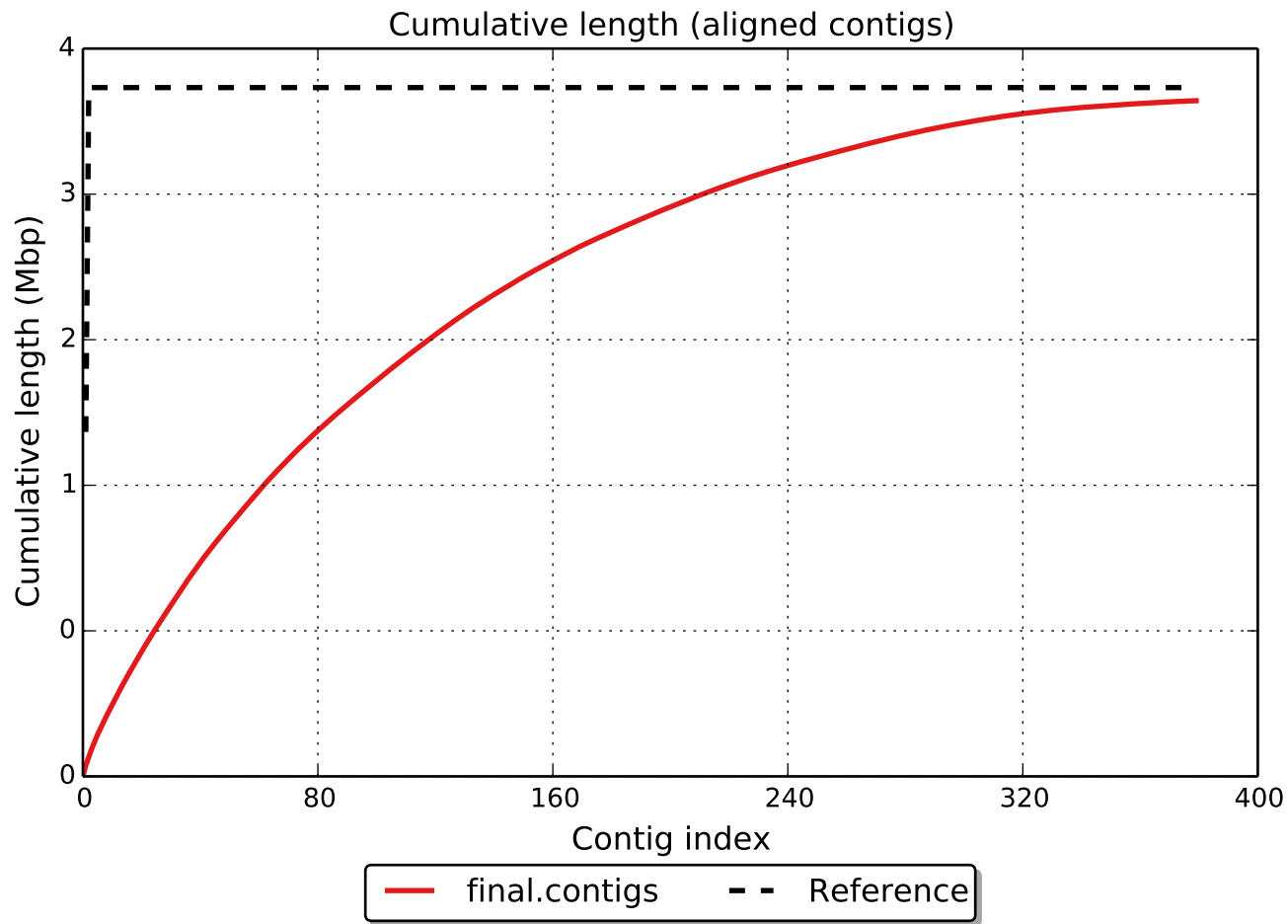
NGx



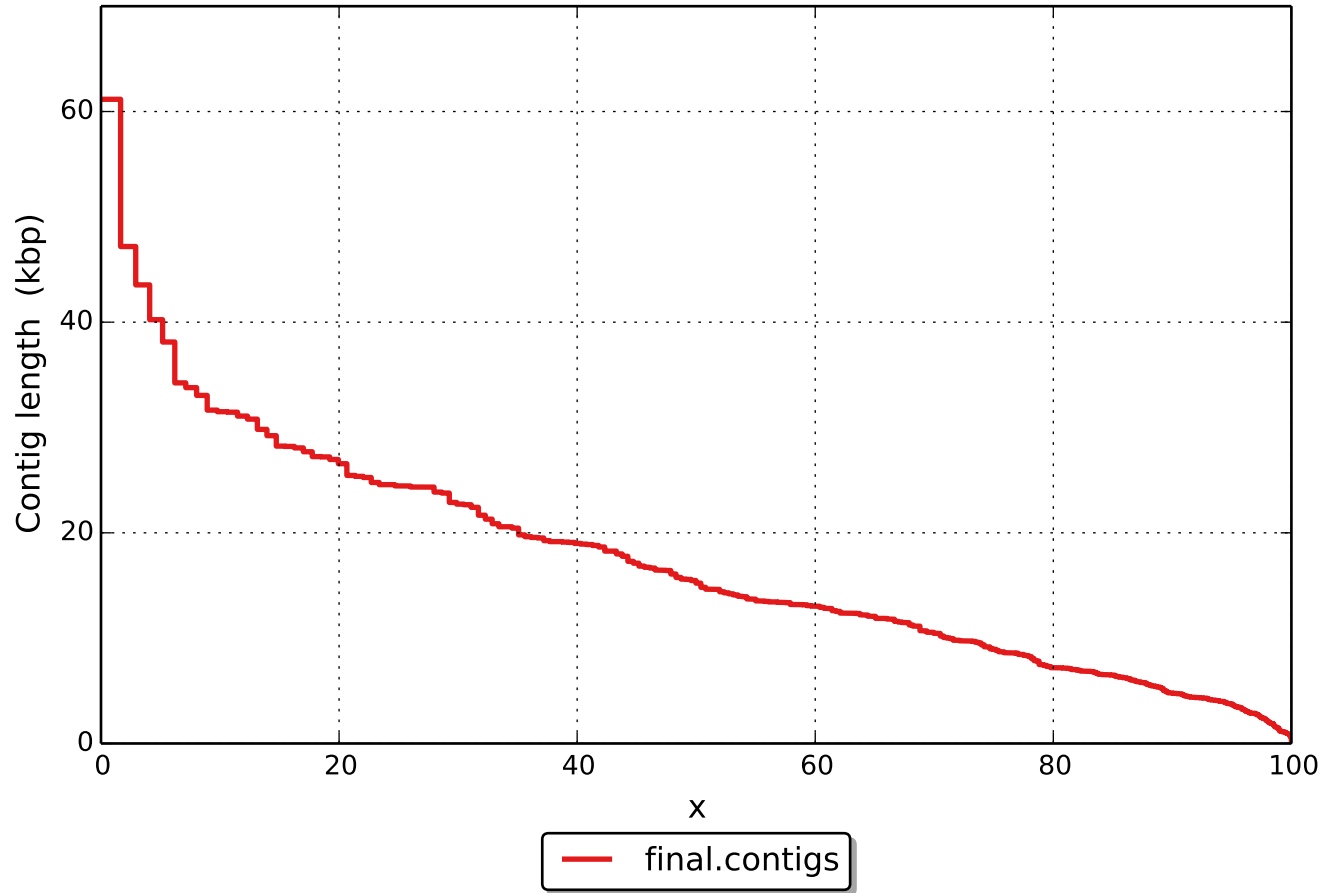
# Misassemblies







NAx



# NGAx

