

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1720
# contigs ( $\geq 1000$ bp)	1089
Total length ( $\geq 0$ bp)	10896284
Total length ( $\geq 1000$ bp)	10635632
# contigs	1259
Largest contig	67238
Total length	10754558
Reference length	10957366
GC (%)	50.39
Reference GC (%)	50.49
N50	17117
NG50	16605
N75	8418
NG75	8032
L50	197
LG50	203
L75	427
LG75	445
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	50
Genome fraction (%)	97.767
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.45
# indels per 100 kbp	0.05
Largest alignment	67238
NA50	17117
NGA50	16605
NA75	8418
NGA75	8032
LA50	197
LGA50	203
LA75	427
LGA75	445

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

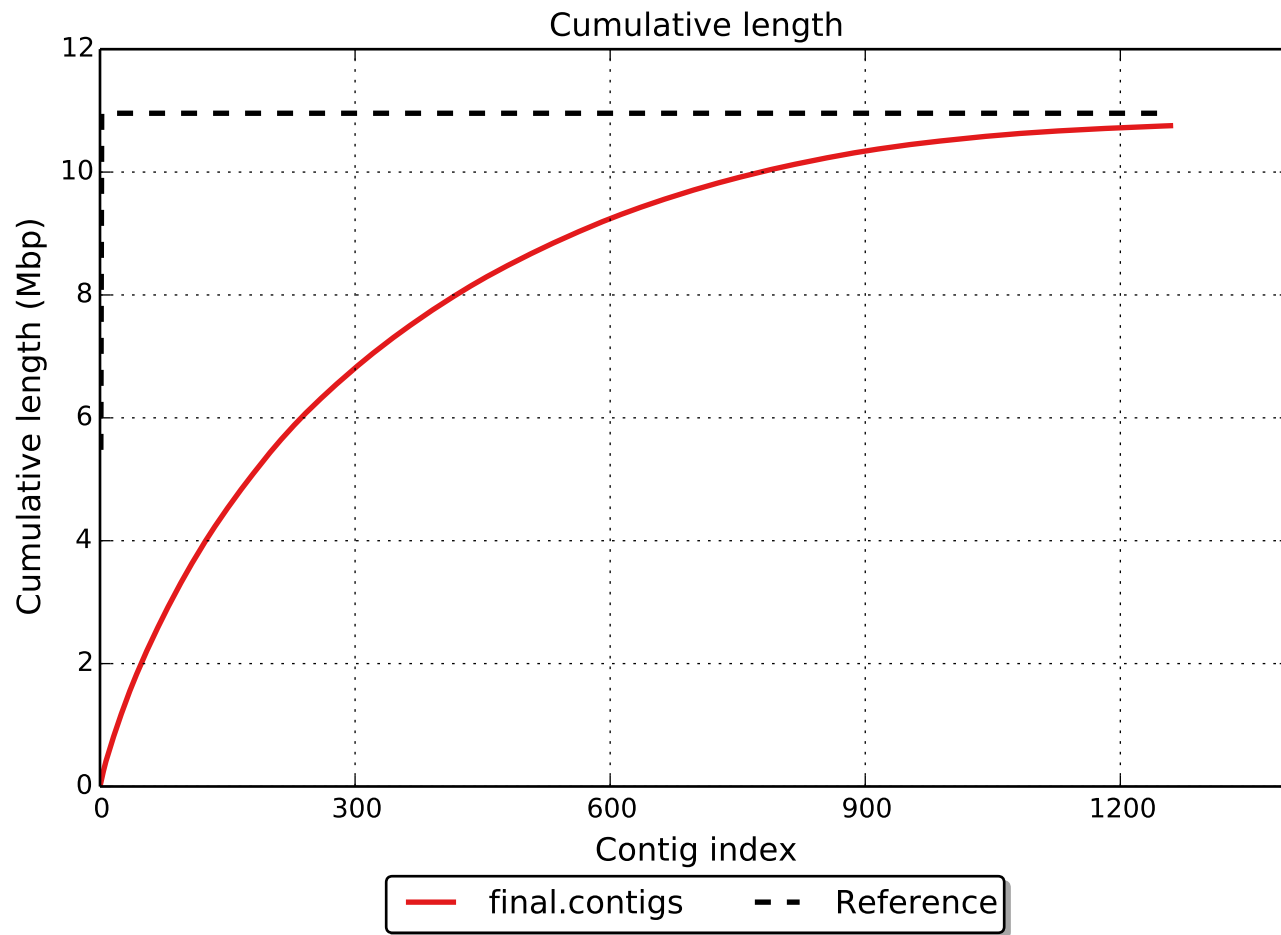
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	905
# indels	5
# short indels	3
# long indels	2
Indels length	28

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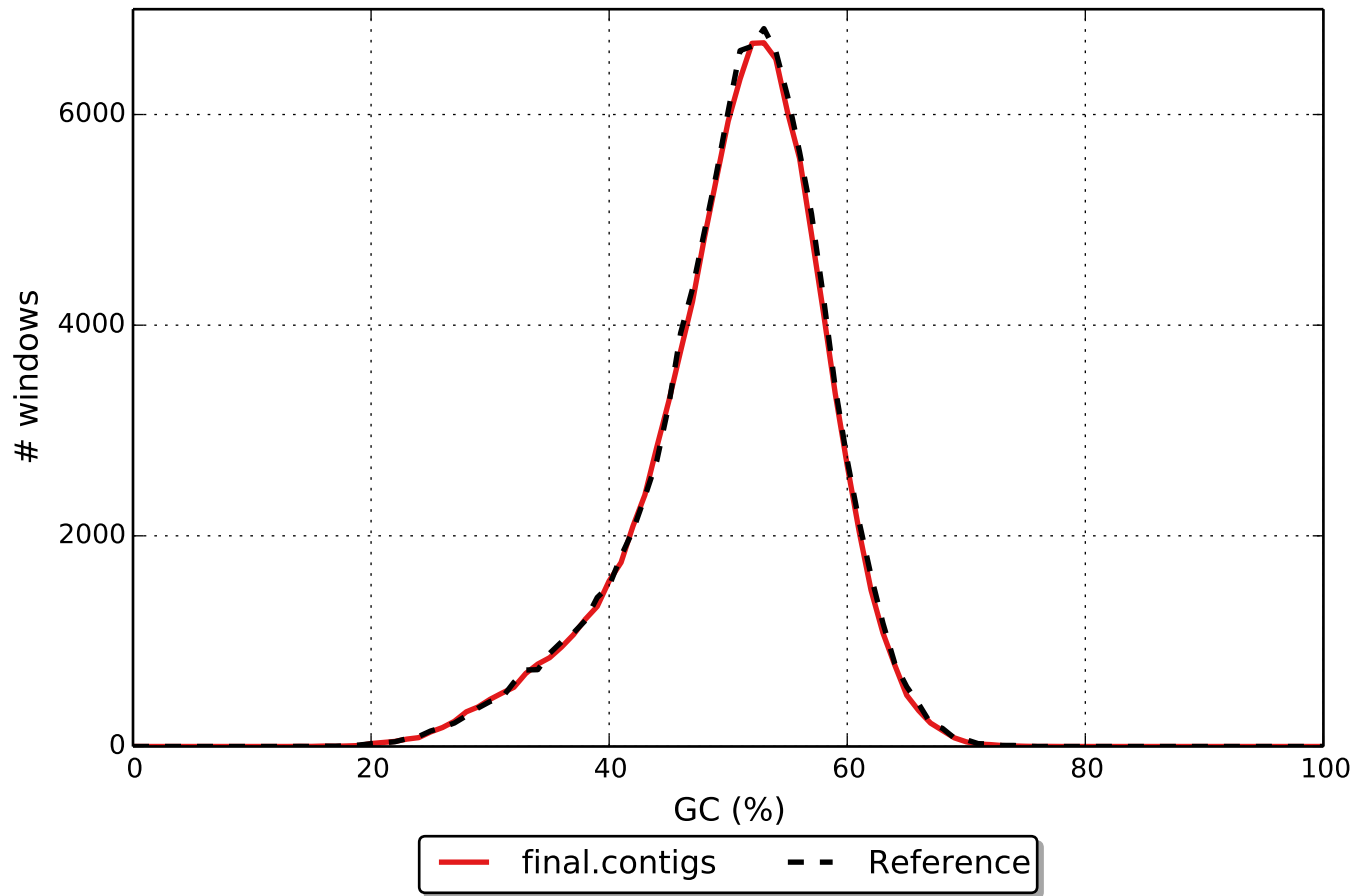
## Unaligned report

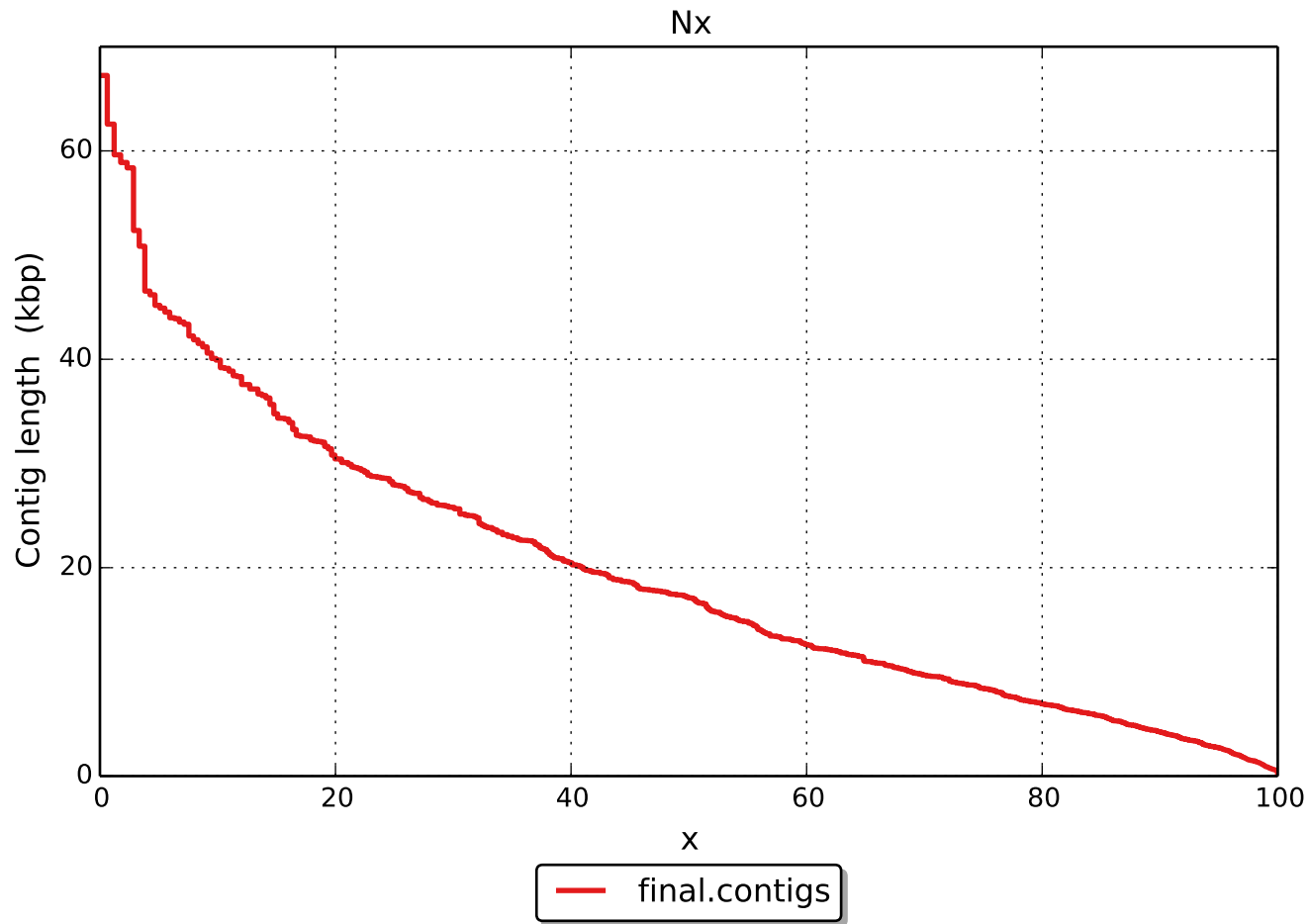
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	50
# N's	0

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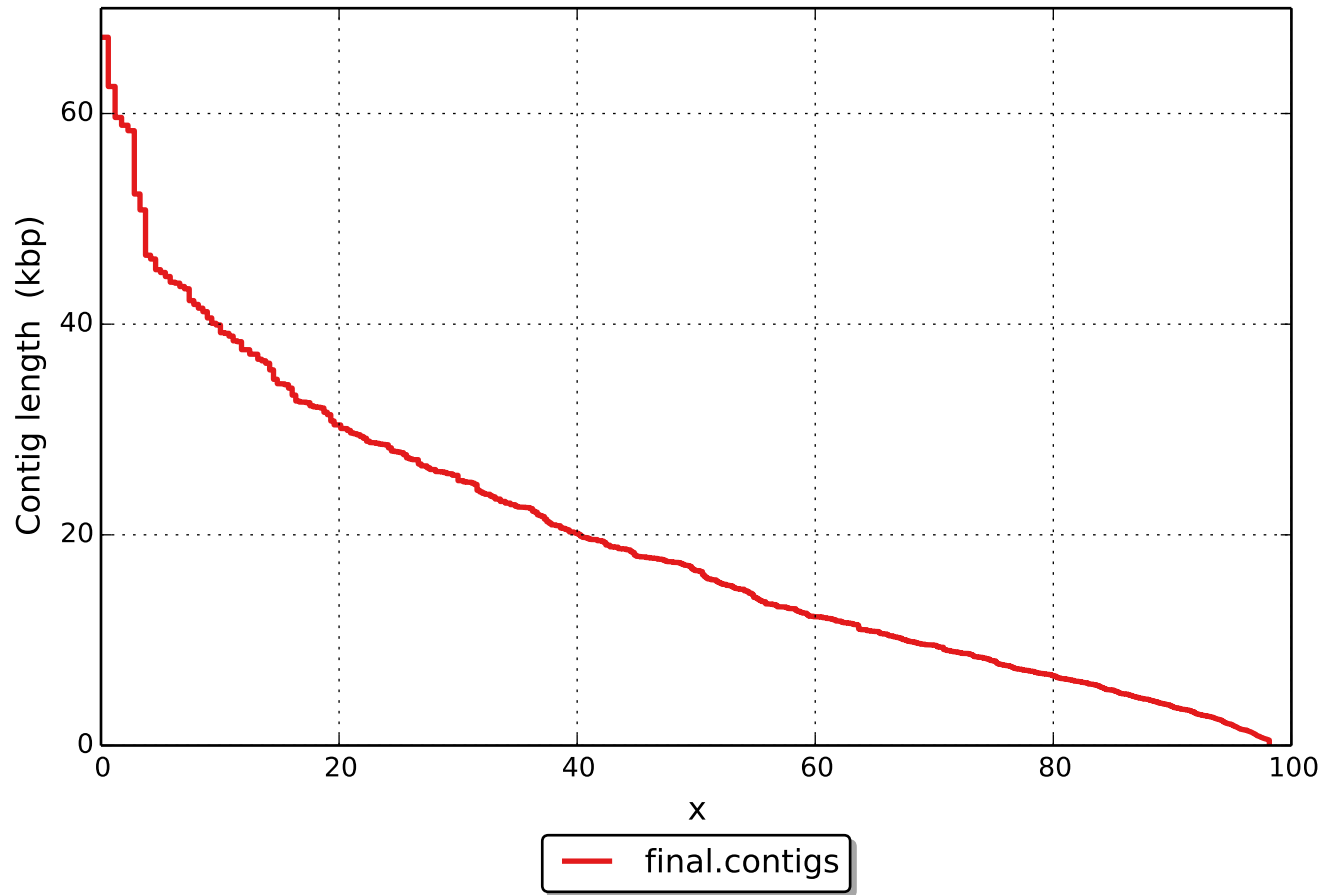


GC content





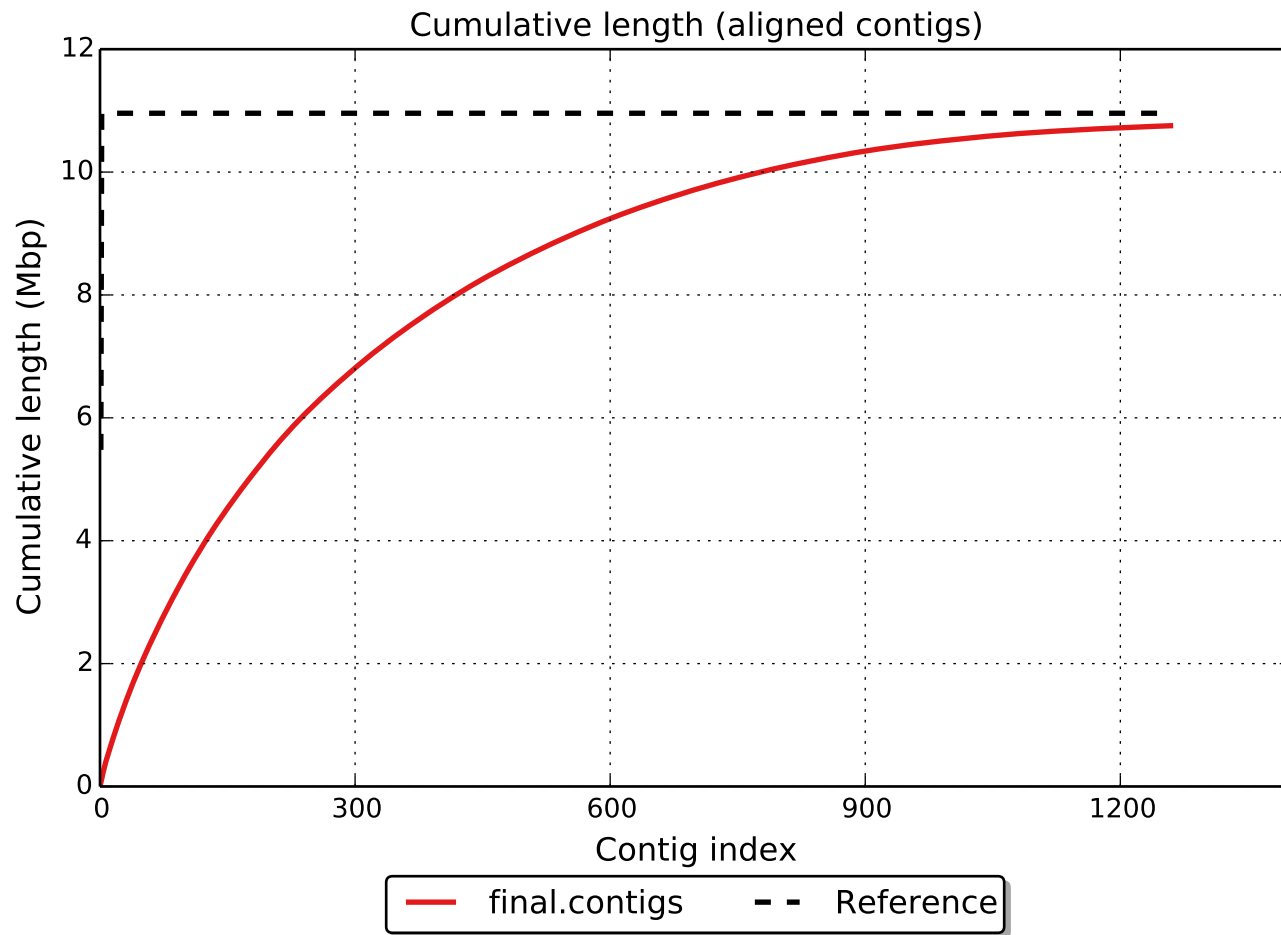
NGx



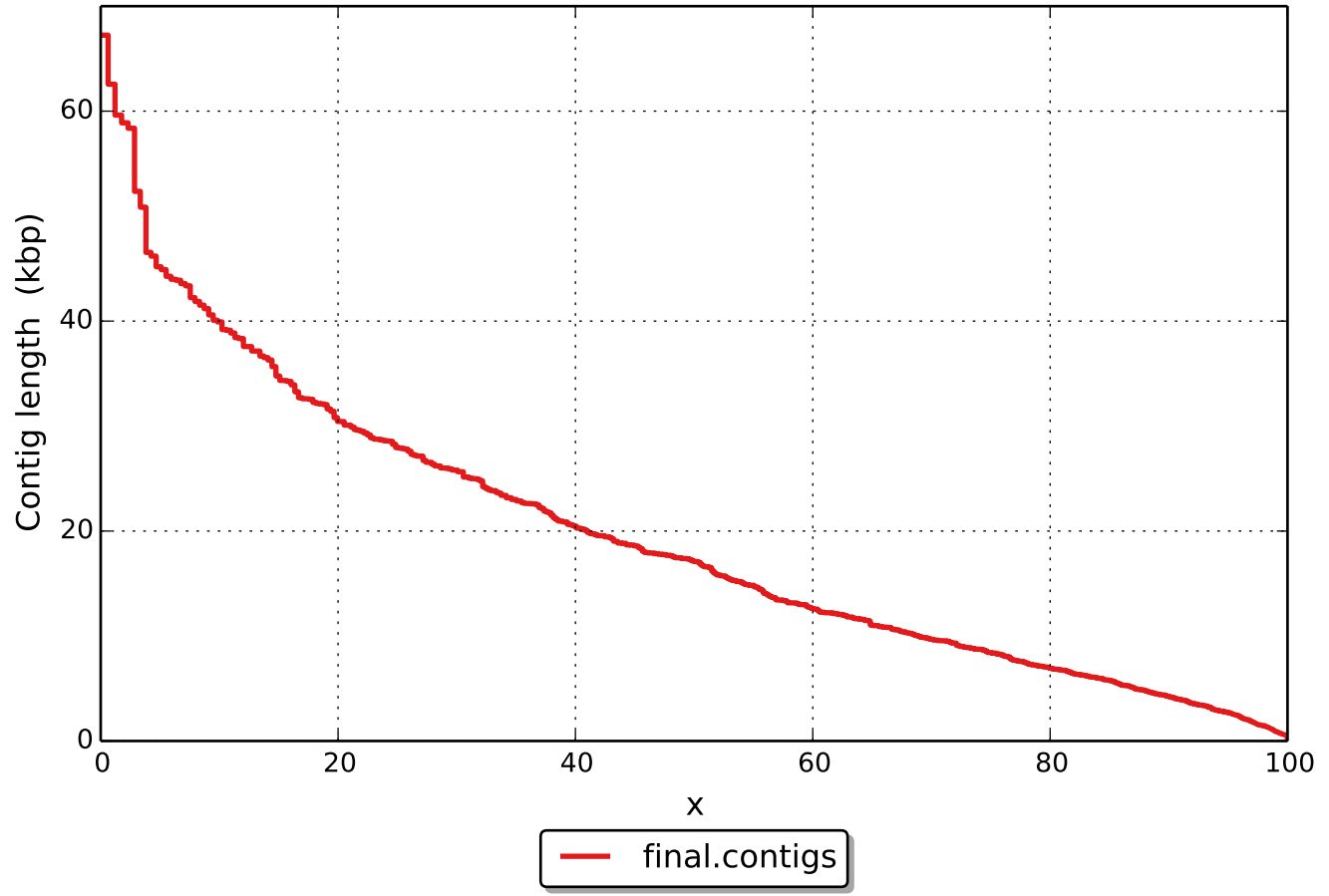
# Misassemblies







NAx



# NGAx

