

## Report

	final.contigs
# contigs (>= 0 bp)	10511
# contigs (>= 1000 bp)	4157
Total length (>= 0 bp)	11202559
Total length (>= 1000 bp)	7652287
# contigs	7654
Largest contig	6941
Total length	10201188
Reference length	10957366
GC (%)	50.37
Reference GC (%)	50.49
N50	1567
NG50	1467
N75	1000
NG75	897
L50	2120
LG50	2370
L75	4156
LG75	4756
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.203
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.42
# indels per 100 kbp	0.08
Largest alignment	6941
NA50	1567
NGA50	1467
NA75	1000
NGA75	897
LA50	2120
LGA50	2370
LA75	4156
LGA75	4756

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

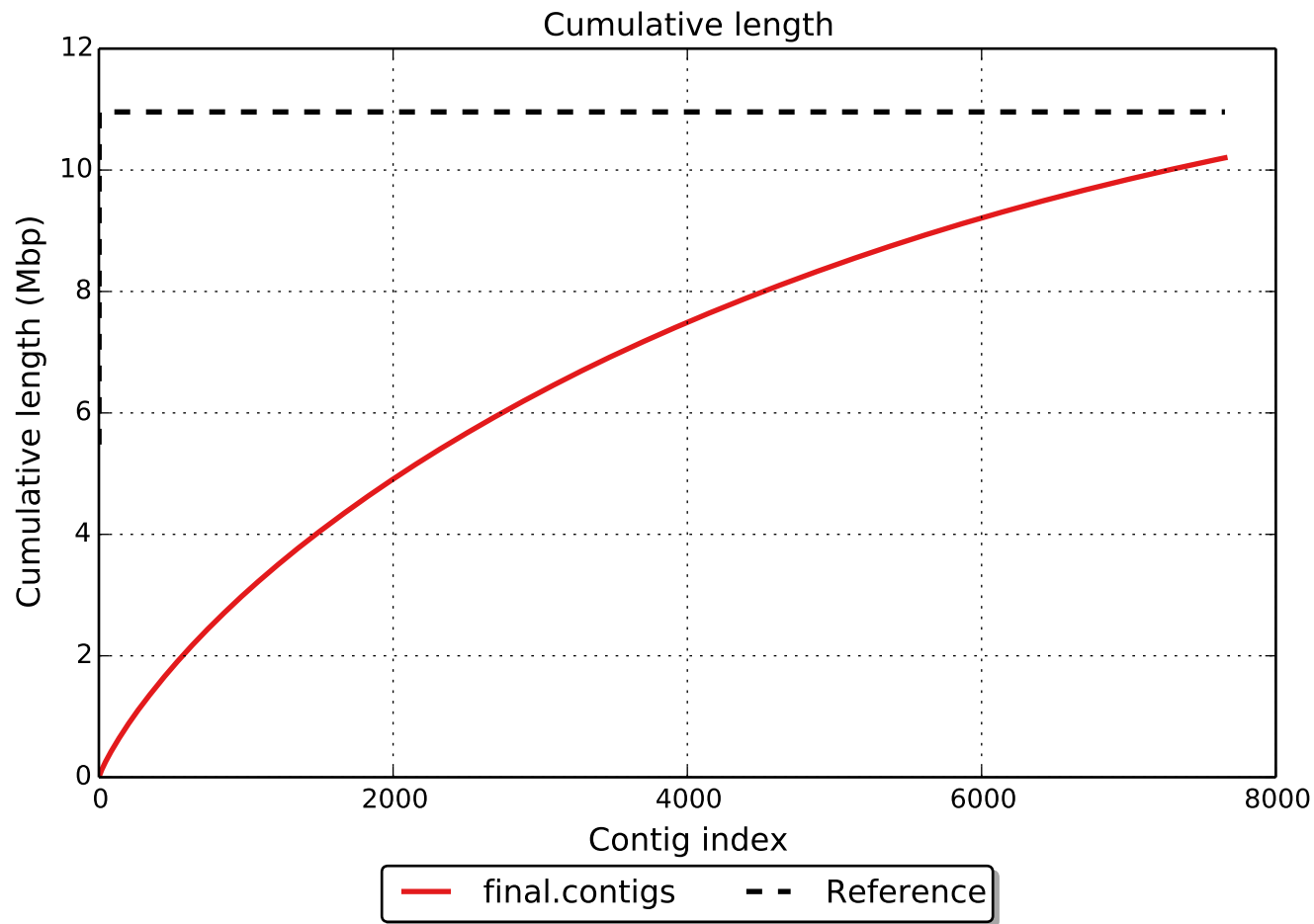
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	5675
# indels	8
# short indels	7
# long indels	1
Indels length	15

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).

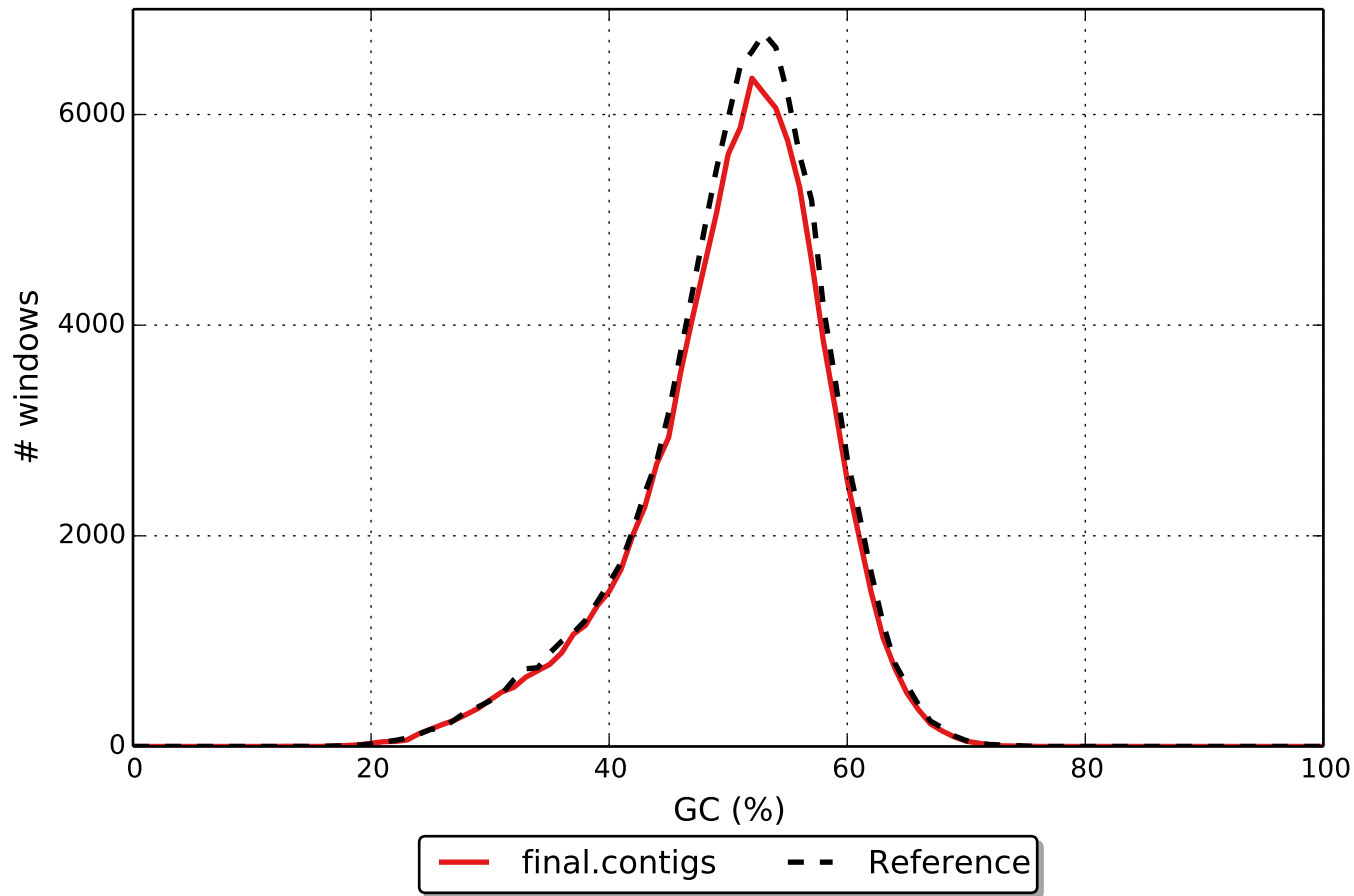
## Unaligned report

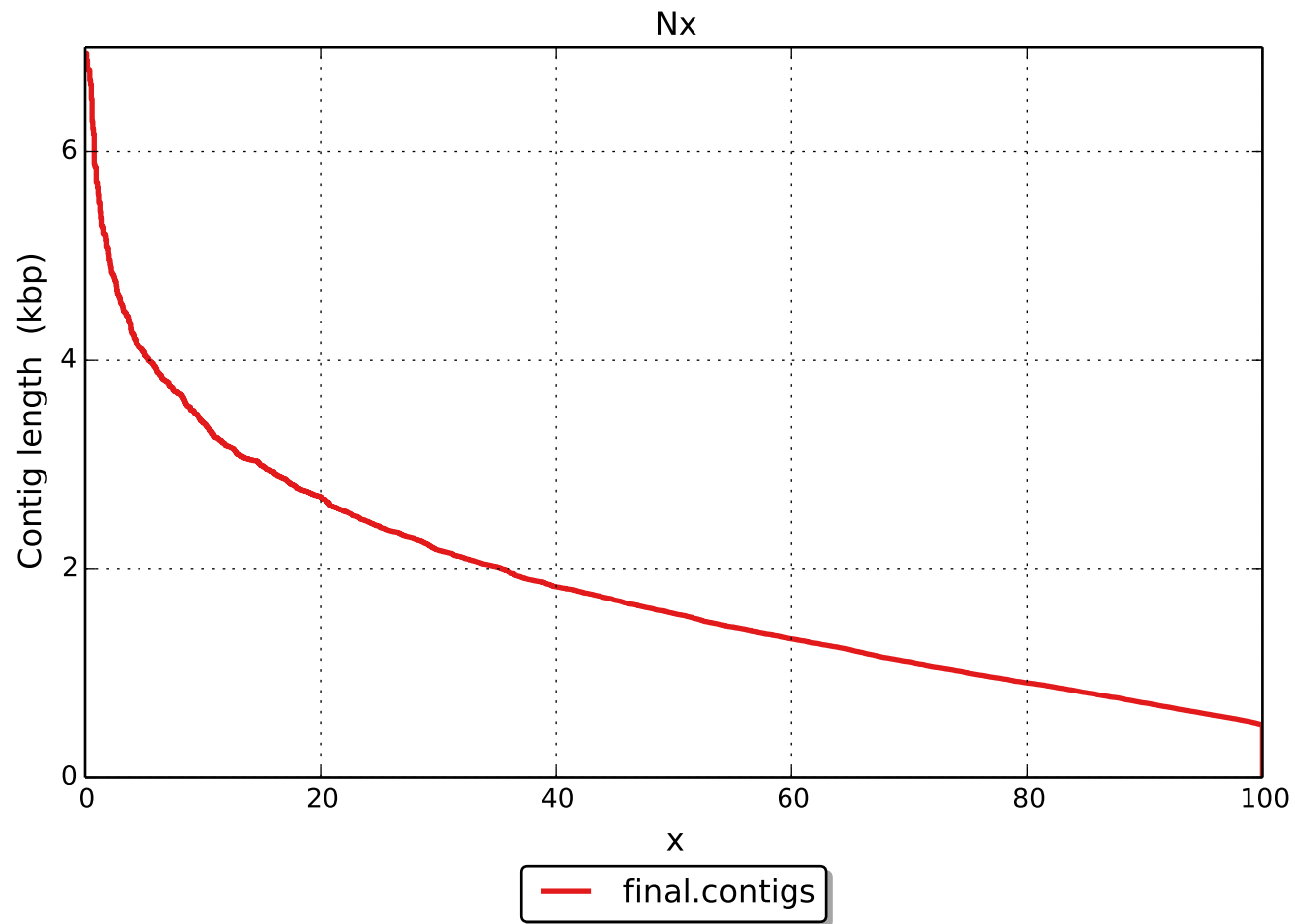
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

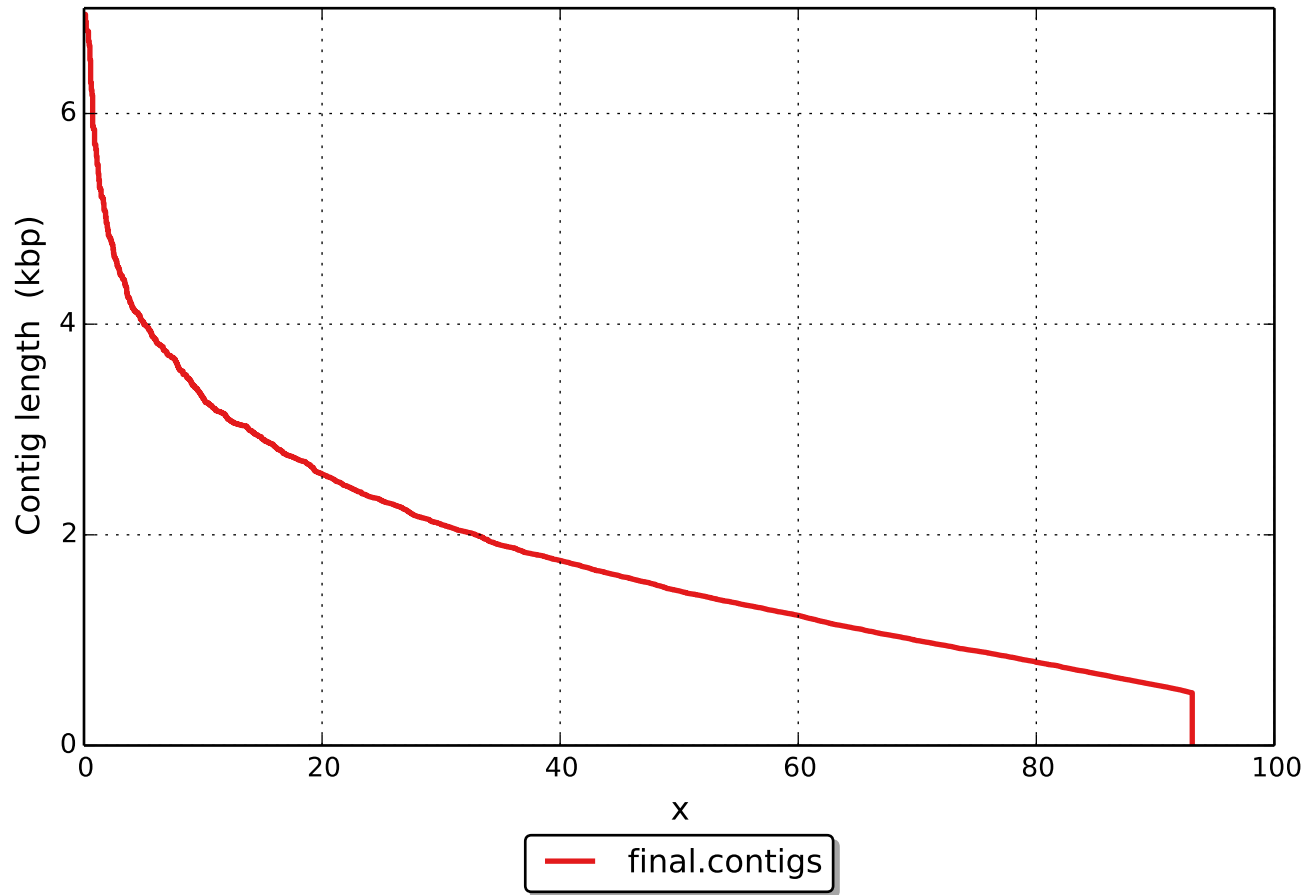


GC content





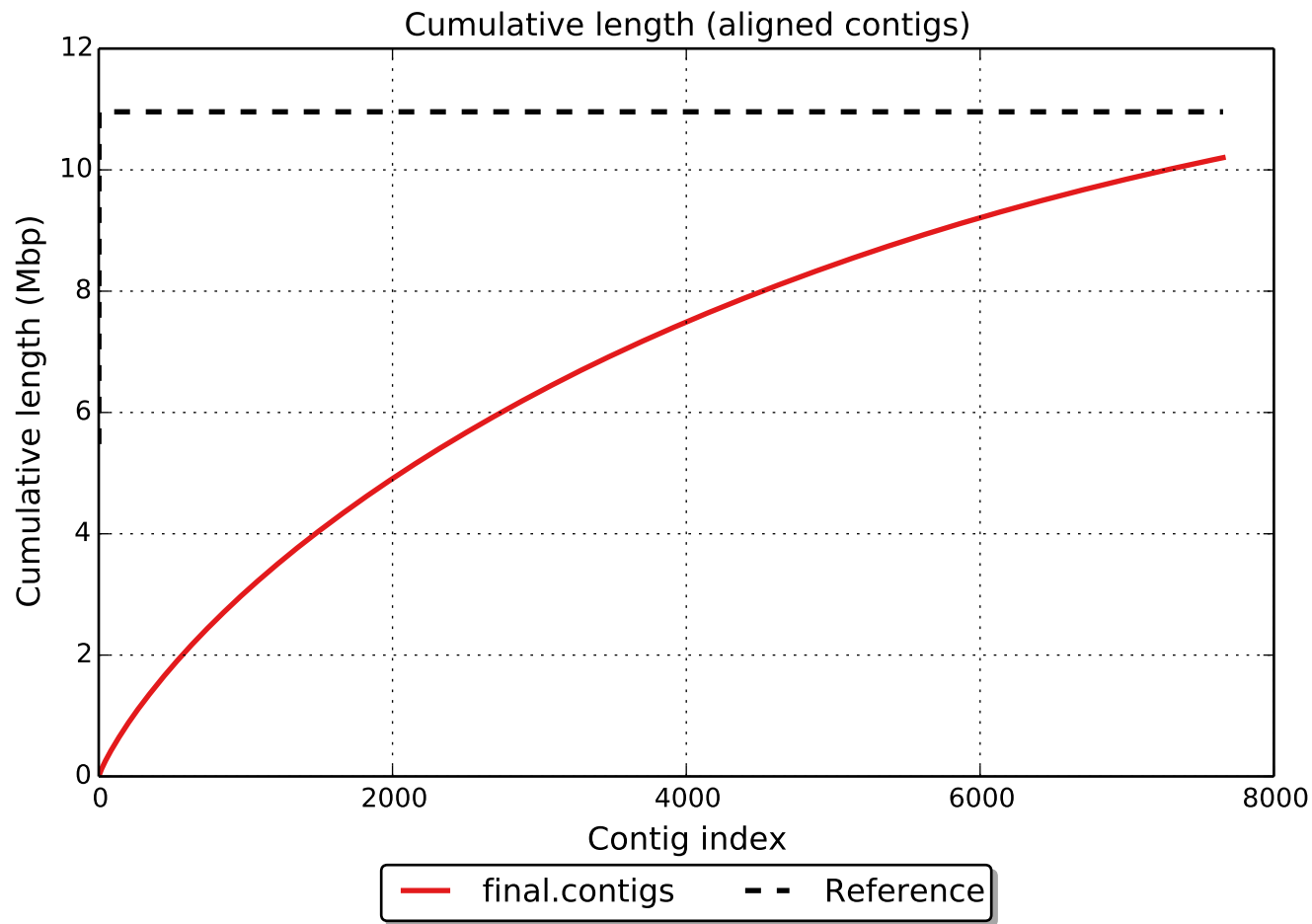
NGx



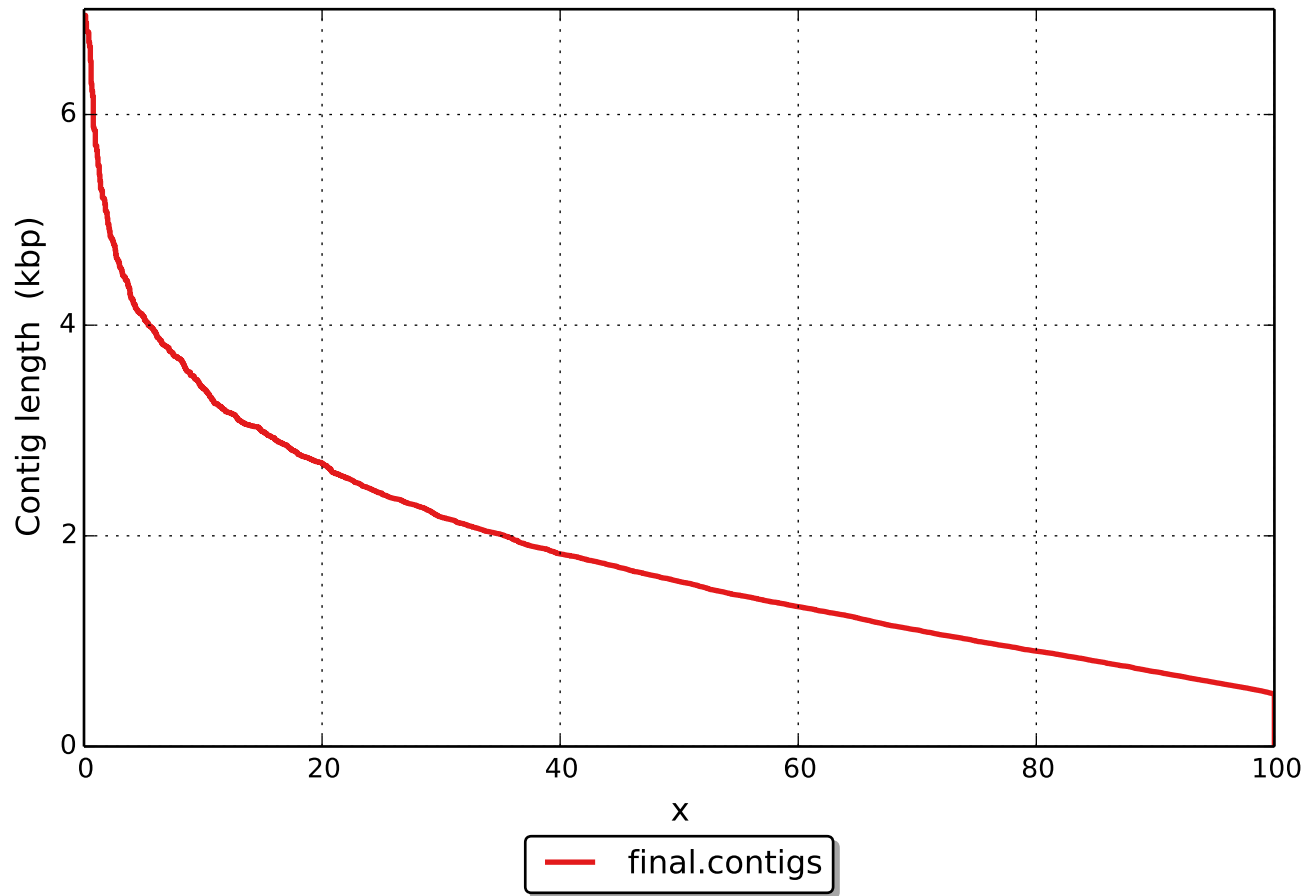
# Misassemblies







NAx



NGAx

