

## Report

	final.contigs
# contigs (>= 0 bp)	3742
# contigs (>= 1000 bp)	2008
Total length (>= 0 bp)	4926629
Total length (>= 1000 bp)	3662871
# contigs	3742
Largest contig	6941
Total length	4926629
Reference length	5478683
GC (%)	50.27
Reference GC (%)	50.49
N50	1547
NG50	1408
N75	988
NG75	833
L50	1042
LG50	1230
L75	2041
LG75	2497
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	86.419
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	39.88
# indels per 100 kbp	0.08
Largest alignment	6941
NA50	1547
NGA50	1408
NA75	988
NGA75	833
LA50	1042
LGA50	1230
LA75	2041
LGA75	2497

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

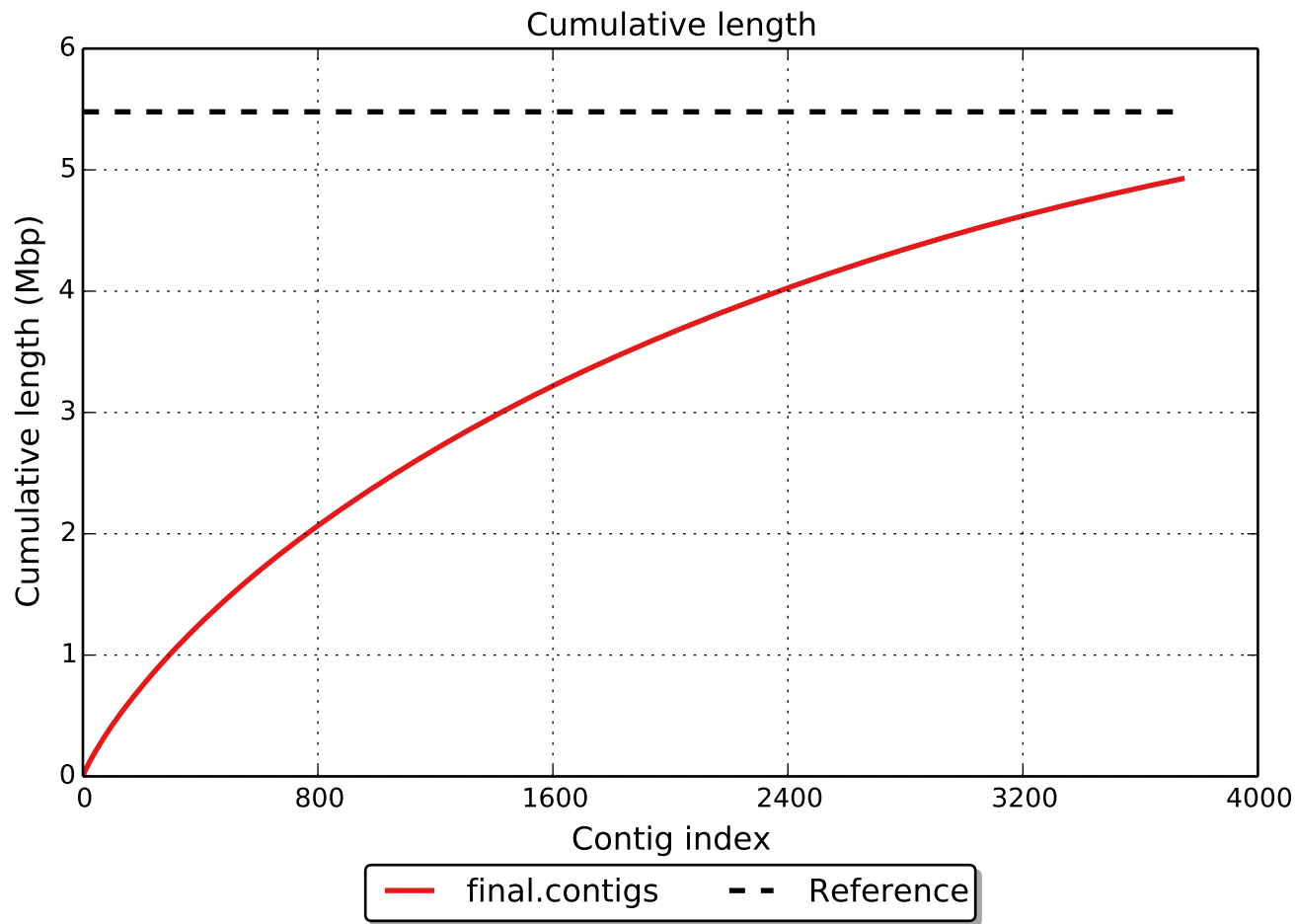
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1888
# indels	4
# short indels	3
# long indels	1
Indels length	11

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).

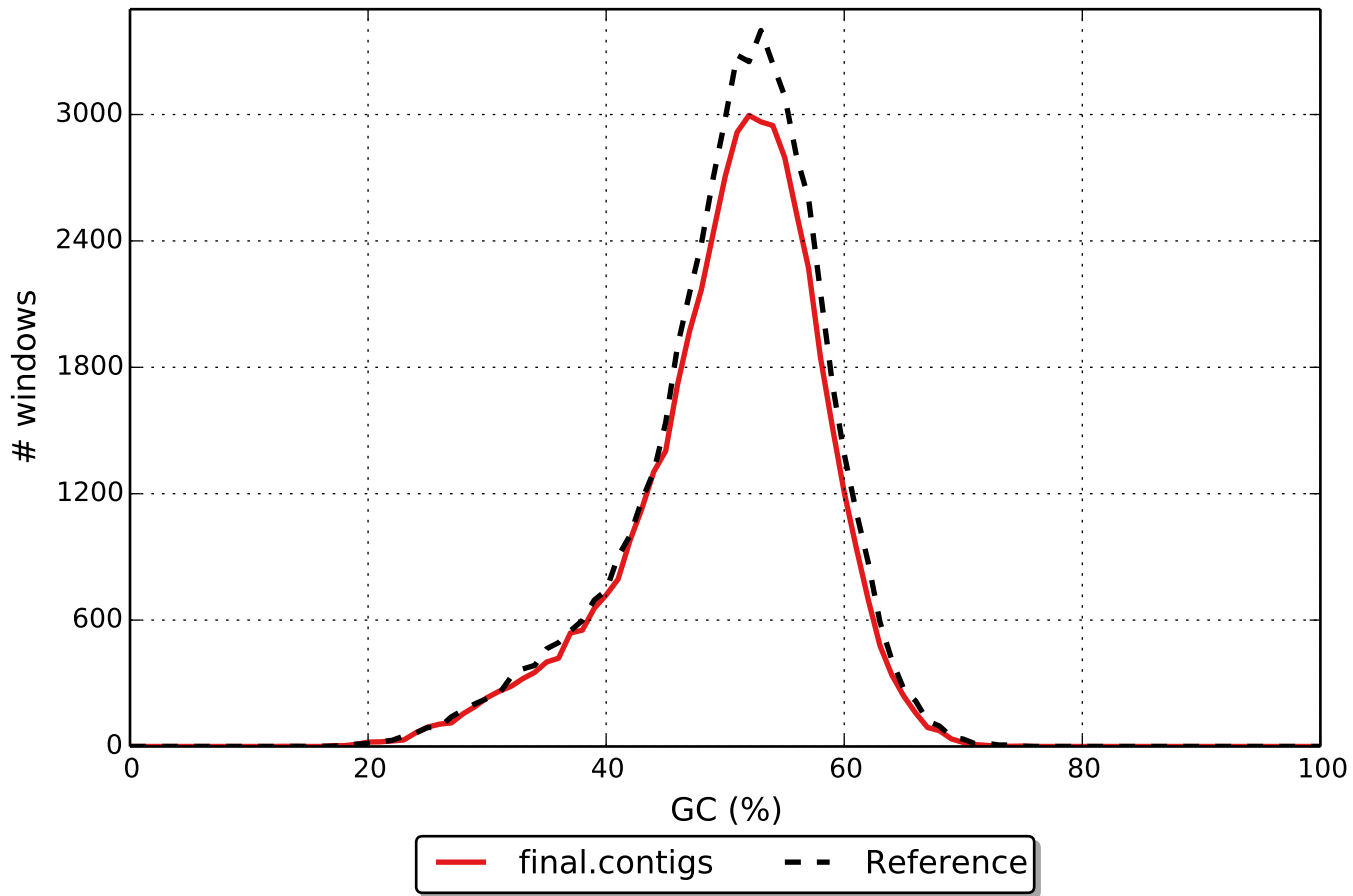
## Unaligned report

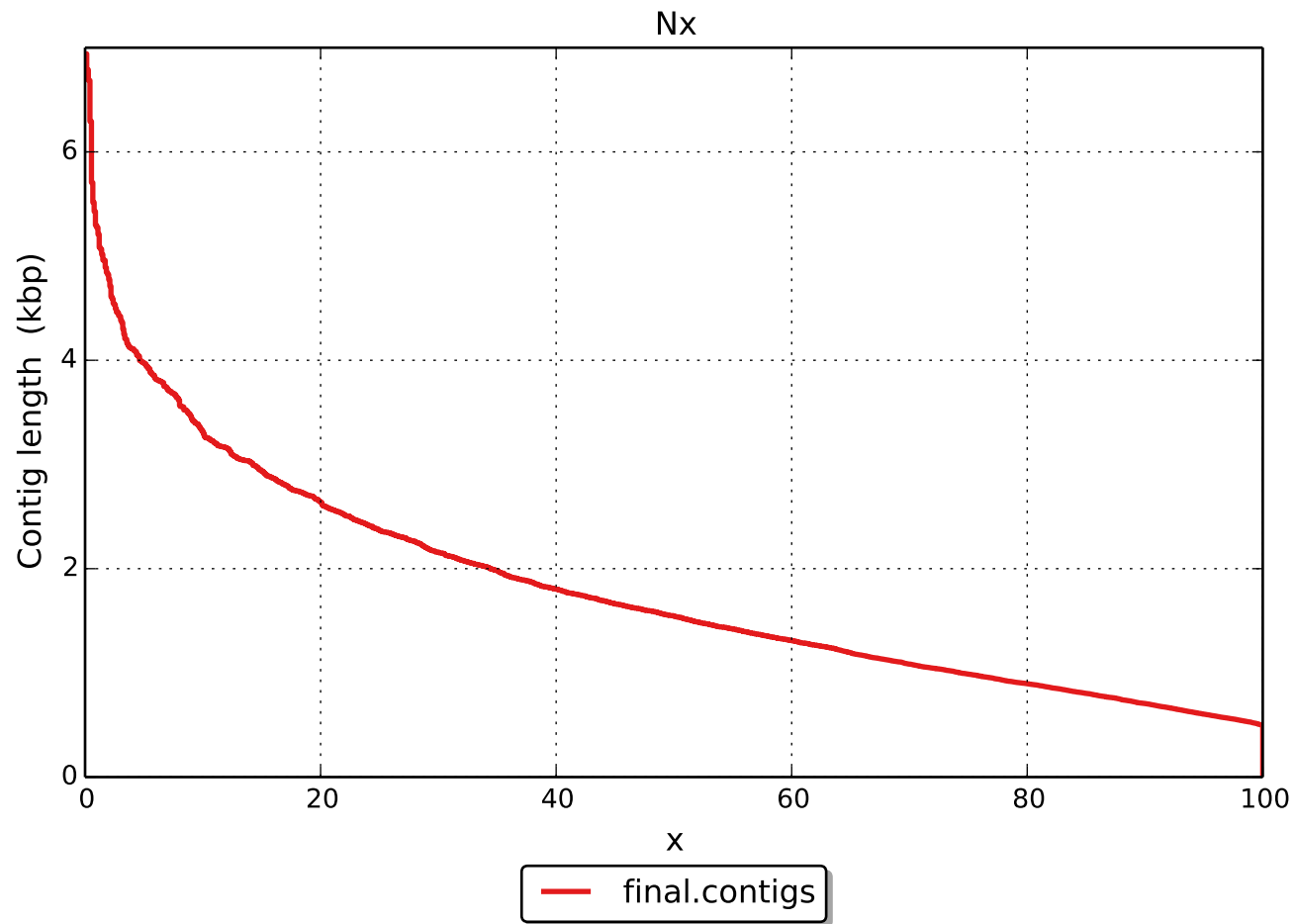
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

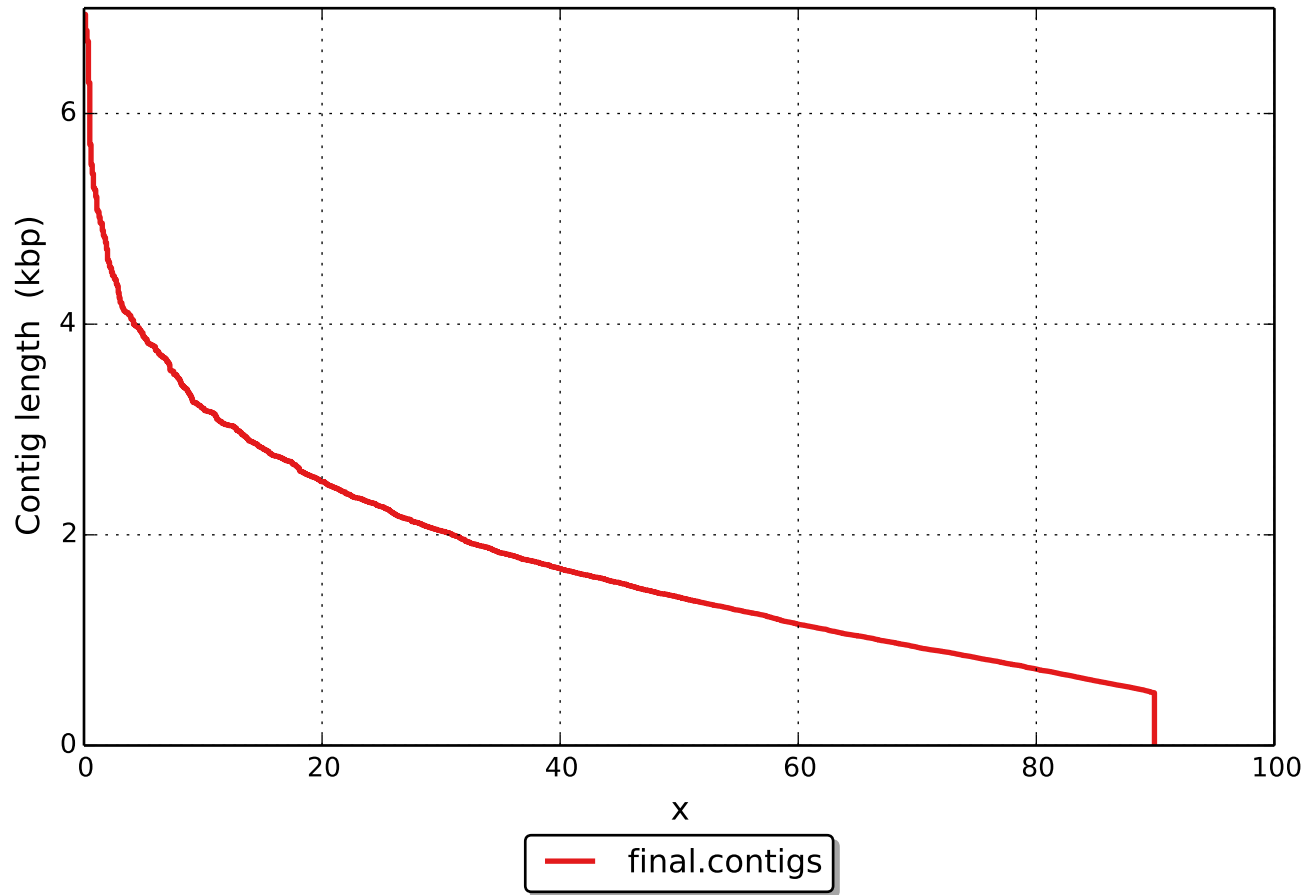


GC content





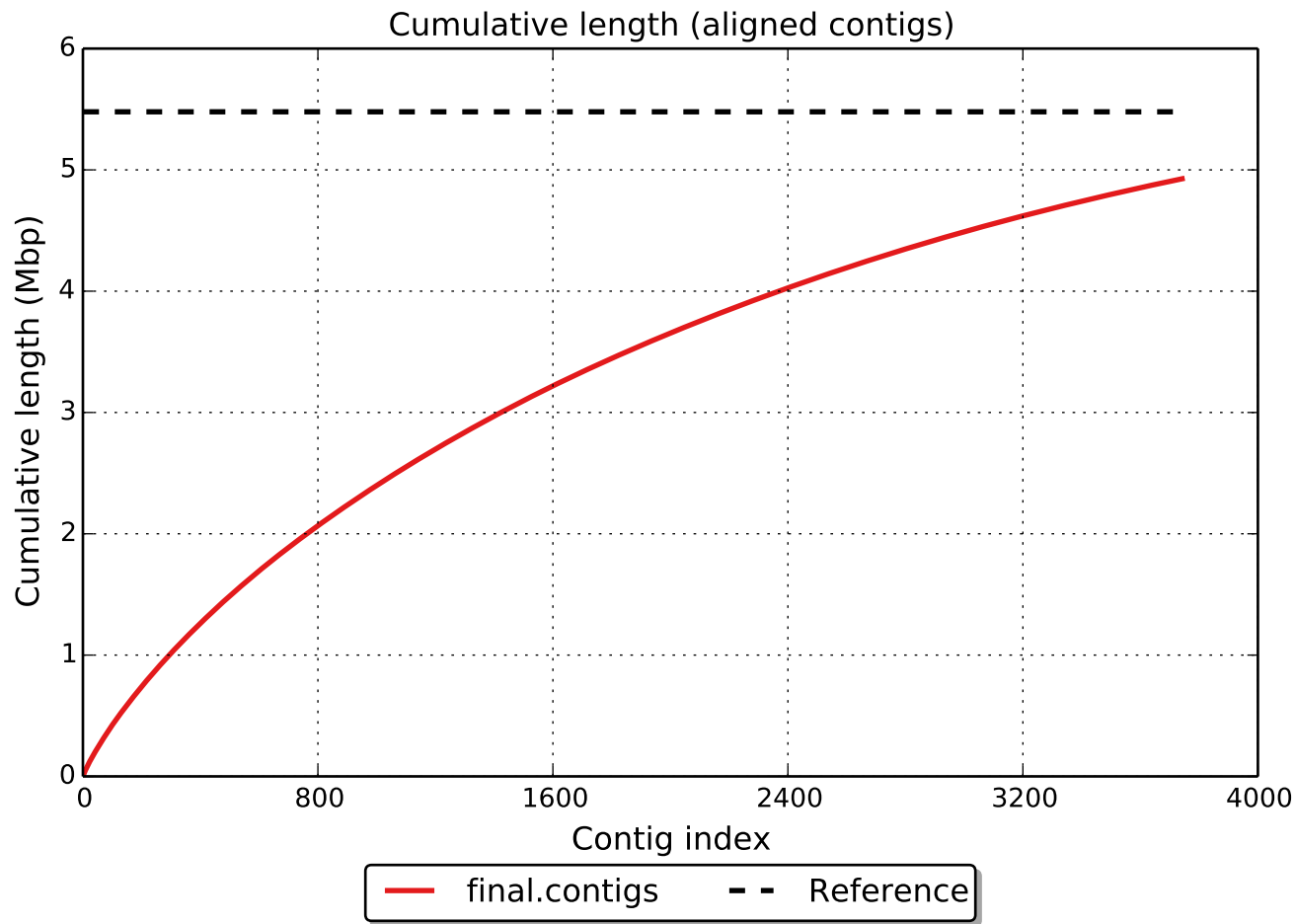
NGx



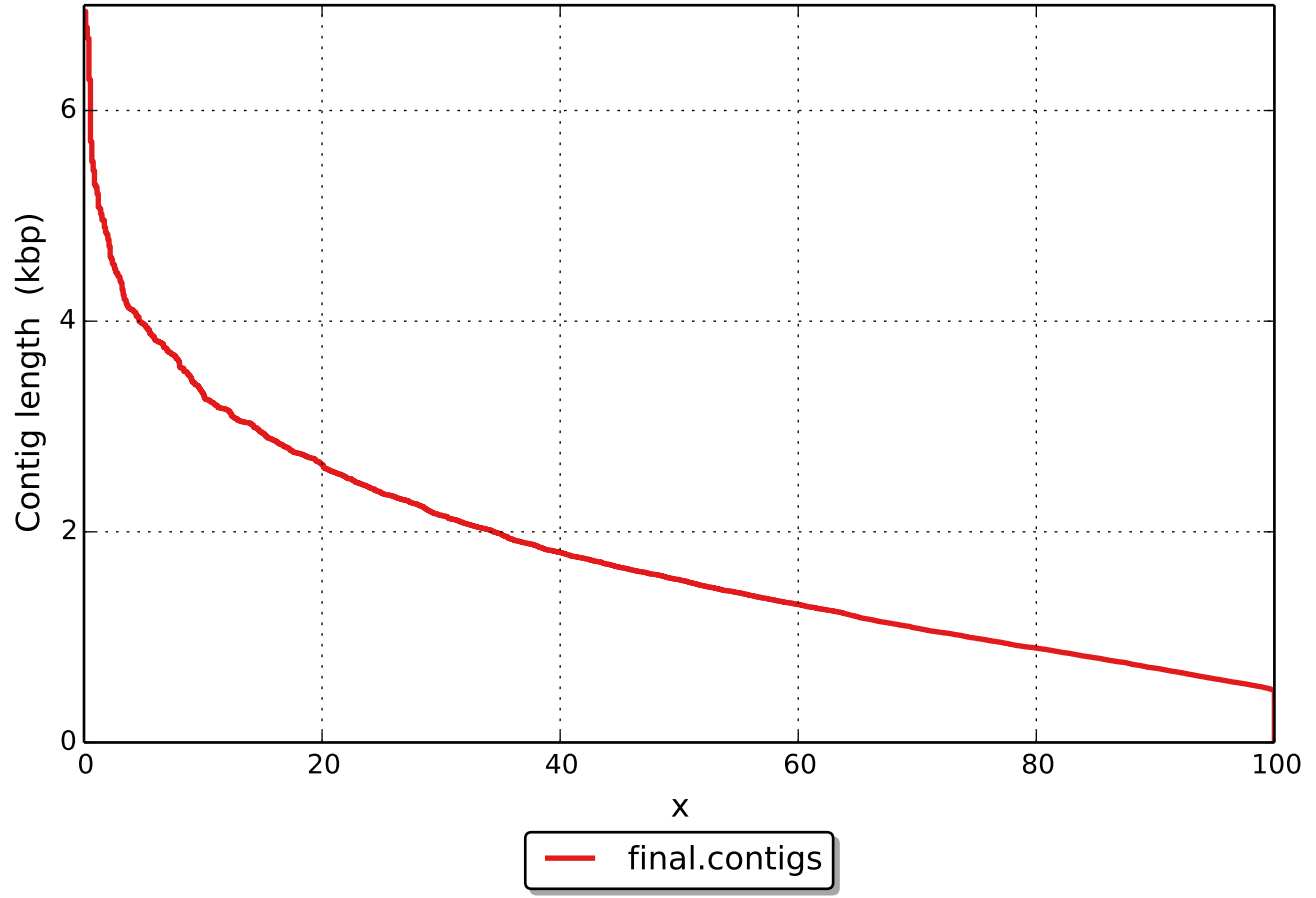
# Misassemblies







NAx



NGAx

