

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	4597
# contigs ( $\geq 1000$ bp)	1269
Total length ( $\geq 0$ bp)	3802915
Total length ( $\geq 1000$ bp)	1974481
# contigs	3045
Largest contig	5155
Total length	3249332
Reference length	3785550
GC (%)	32.28
Reference GC (%)	32.26
N50	1173
NG50	1050
N75	816
NG75	651
L50	948
LG50	1190
L75	1780
LG75	2329
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	82.107
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	59.33
# indels per 100 kbp	0.00
Largest alignment	5155
NA50	1173
NGA50	1050
NA75	816
NGA75	651
LA50	948
LGA50	1190
LA75	1780
LGA75	2329

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

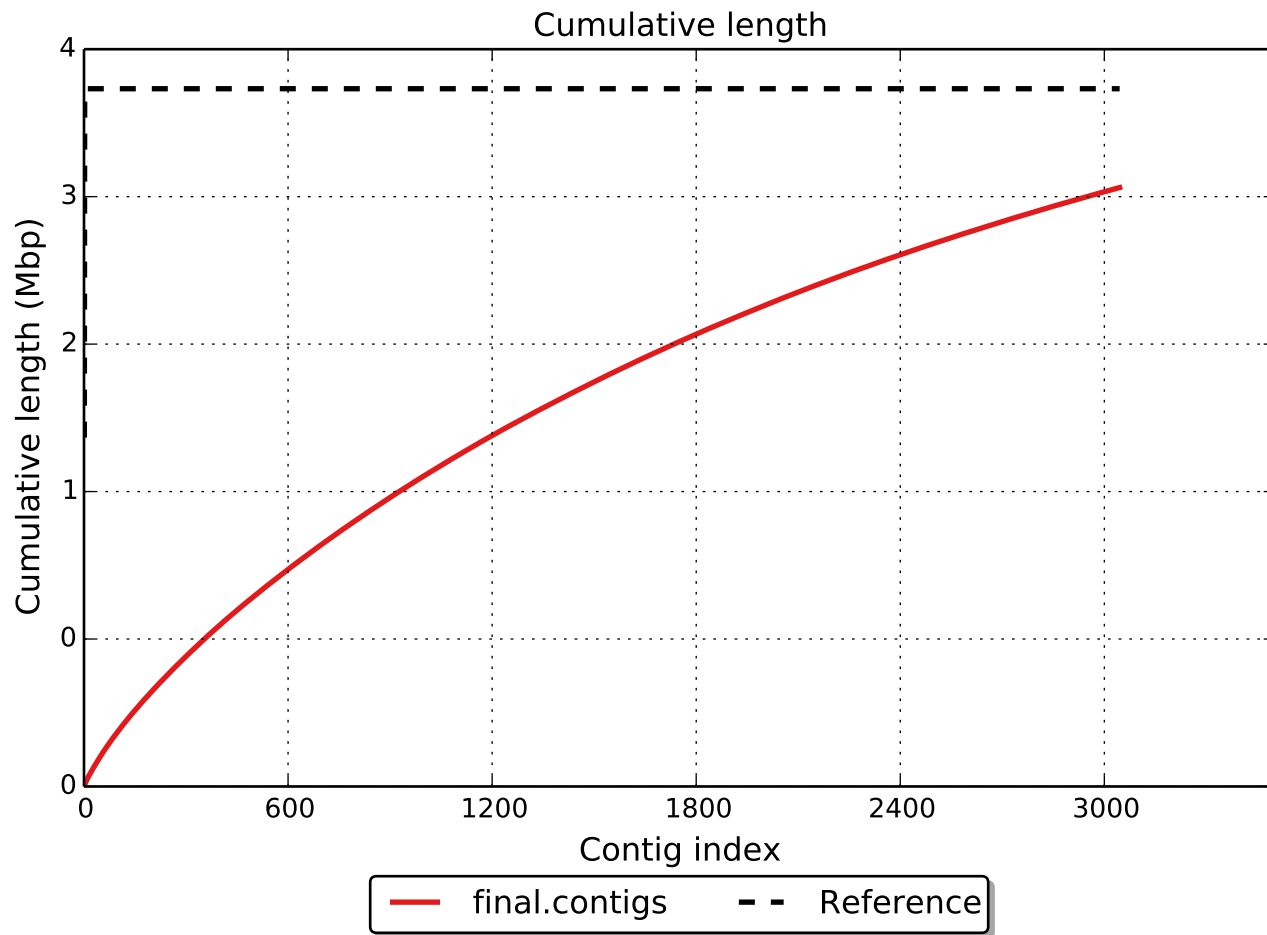
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1844
# indels	0
# short indels	0
# long indels	0
Indels length	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).

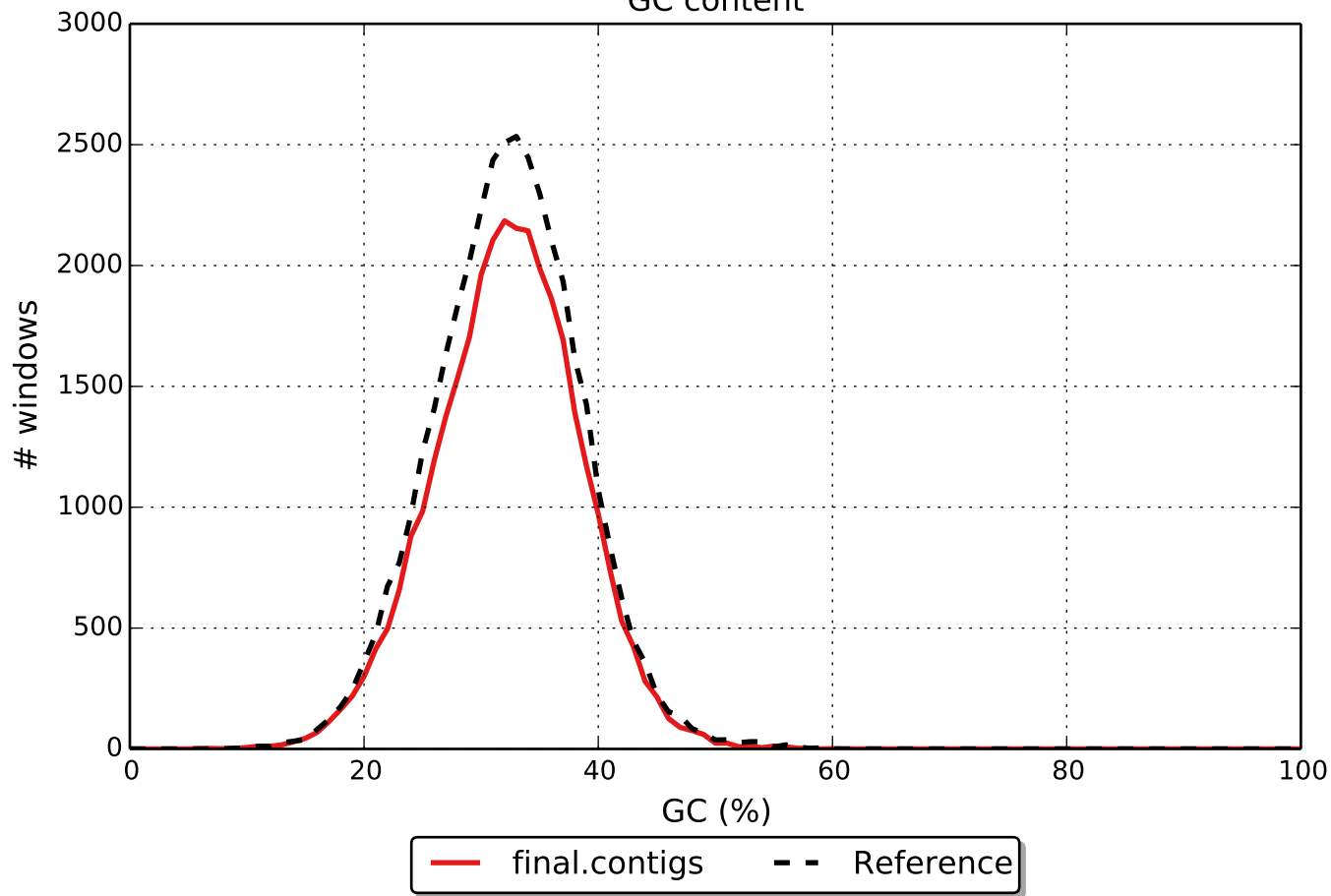
## Unaligned report

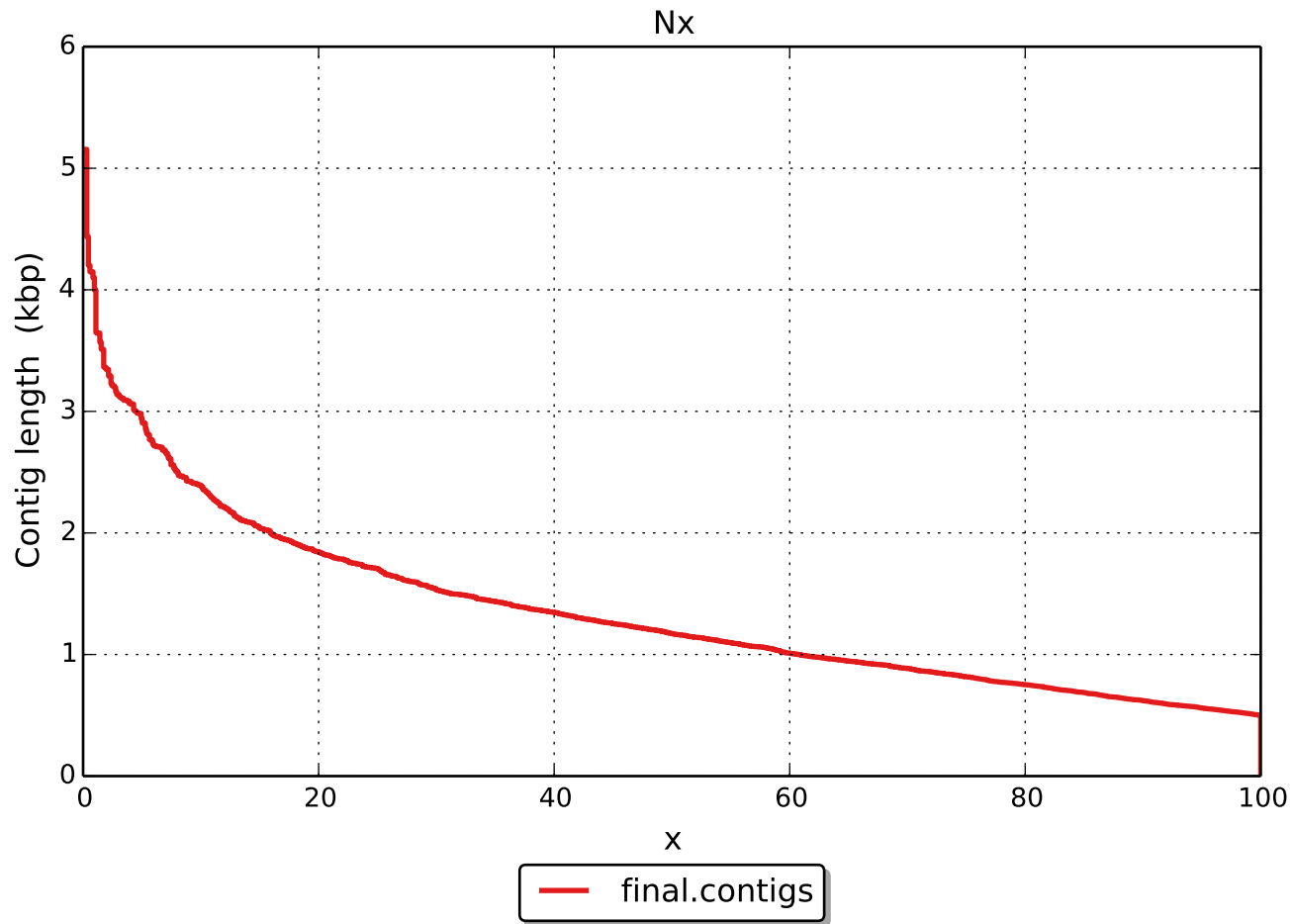
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

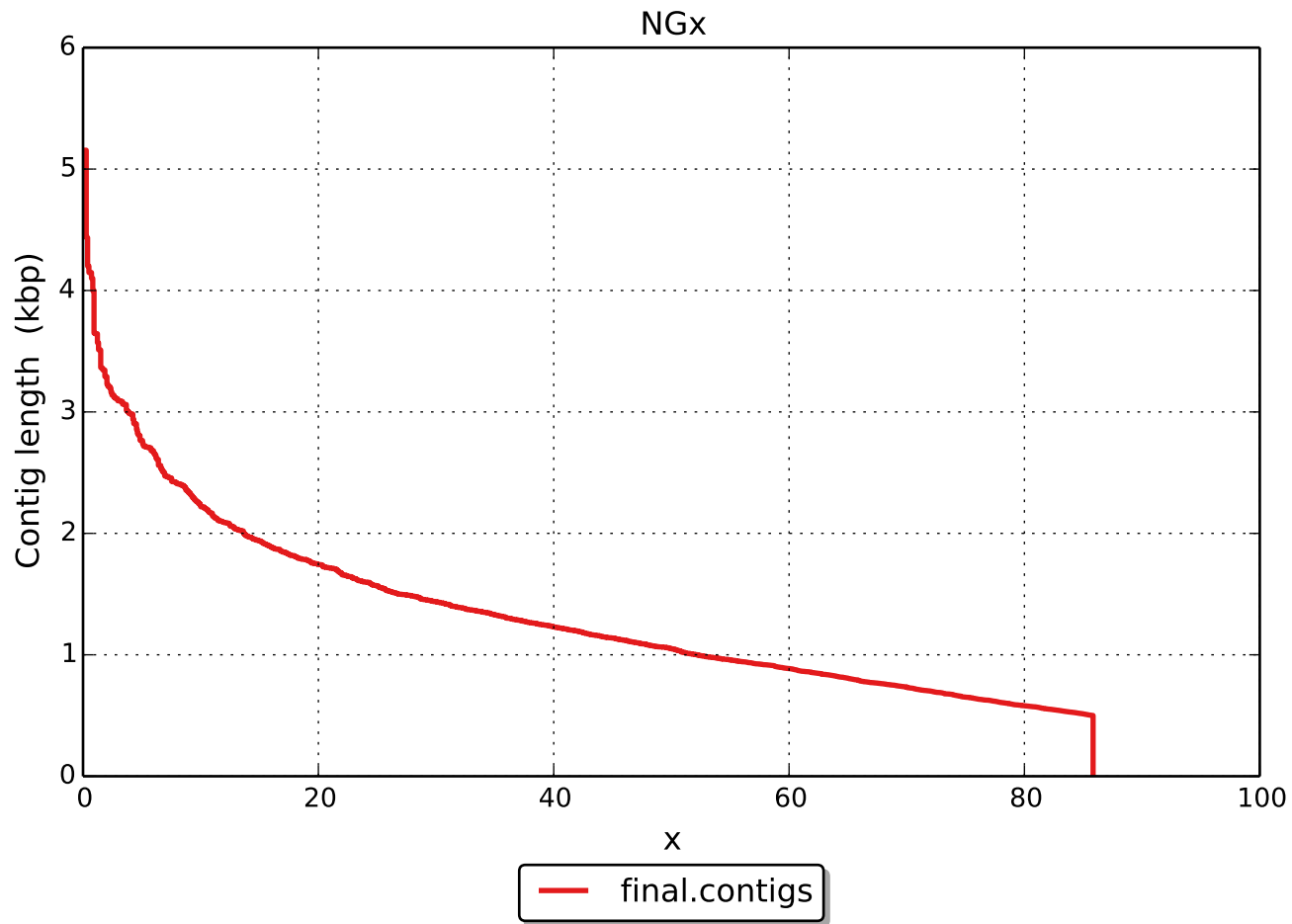
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content



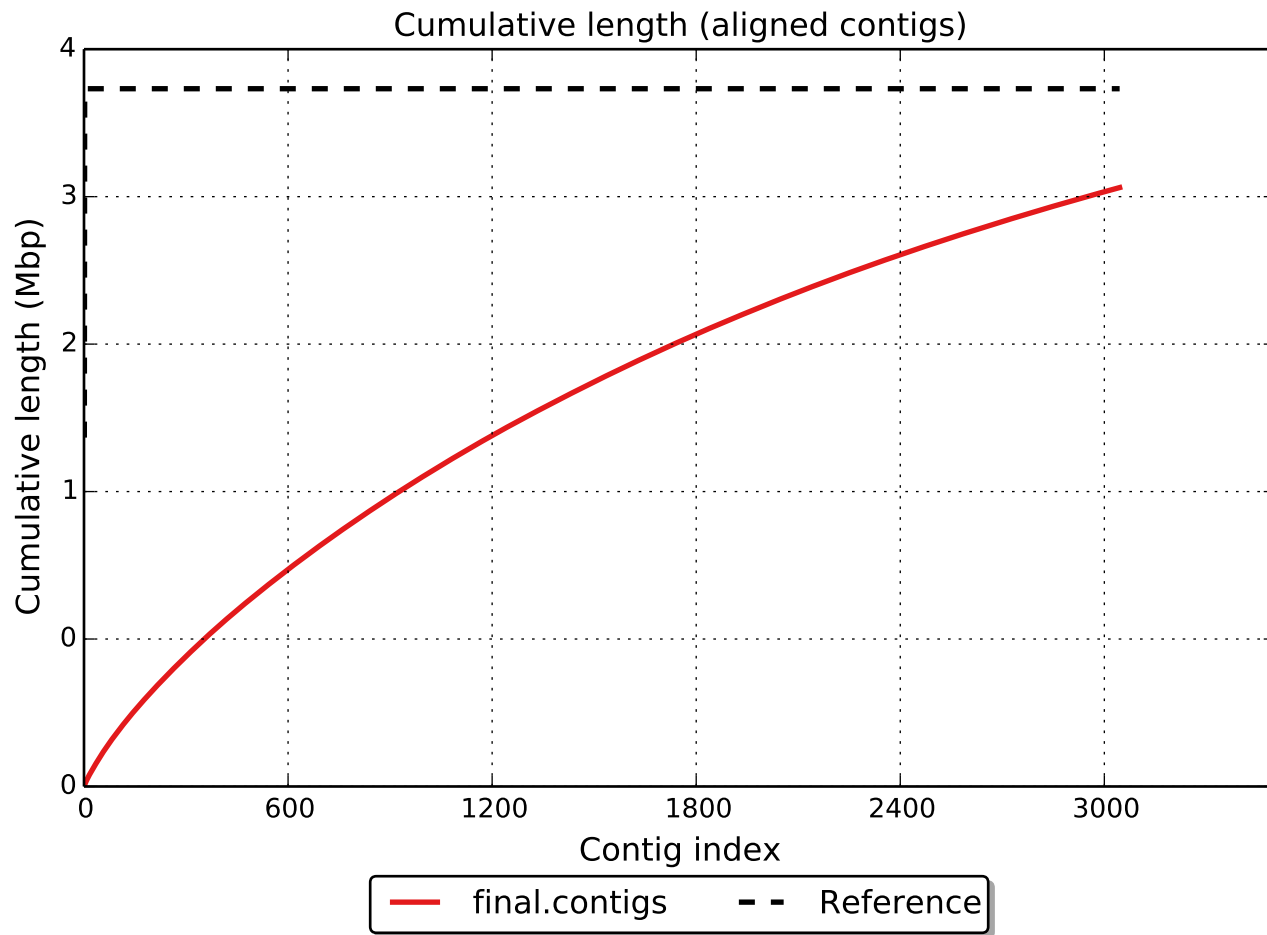


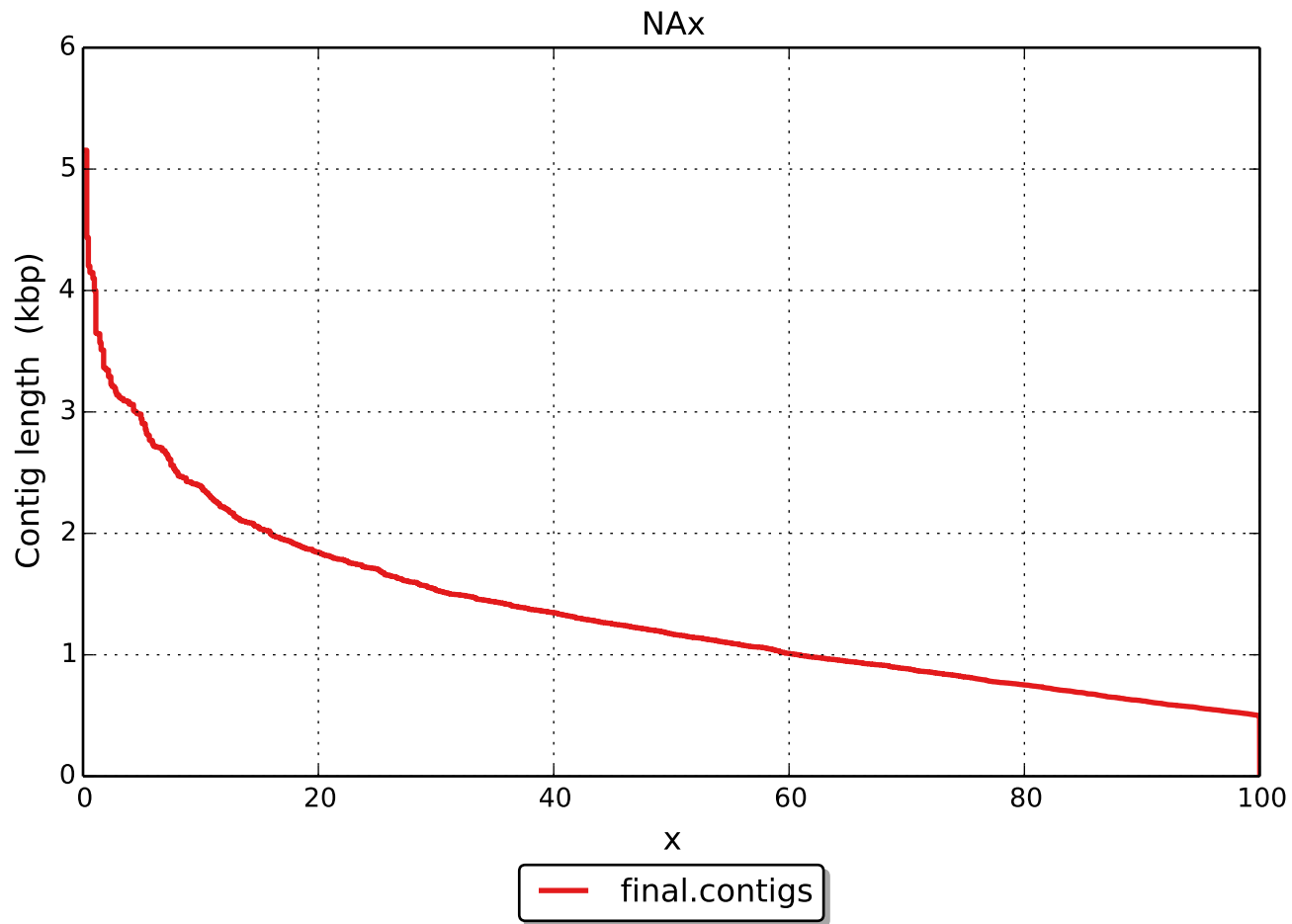


# Misassemblies









NGAx

