

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	592
# contigs ( $\geq 1000$ bp)	475
Total length ( $\geq 0$ bp)	5234778
Total length ( $\geq 1000$ bp)	5152716
# contigs	592
Largest contig	98802
Total length	5234778
Reference length	5478683
GC (%)	50.28
Reference GC (%)	50.49
N50	19751
NG50	19362
N75	10400
NG75	8678
L50	77
LG50	83
L75	167
LG75	187
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	25881
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.940
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.77
# indels per 100 kbp	0.10
Largest alignment	98802
NA50	19751
NGA50	18971
NA75	10329
NGA75	8678
LA50	77
LGA50	84
LA75	168
LGA75	187

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

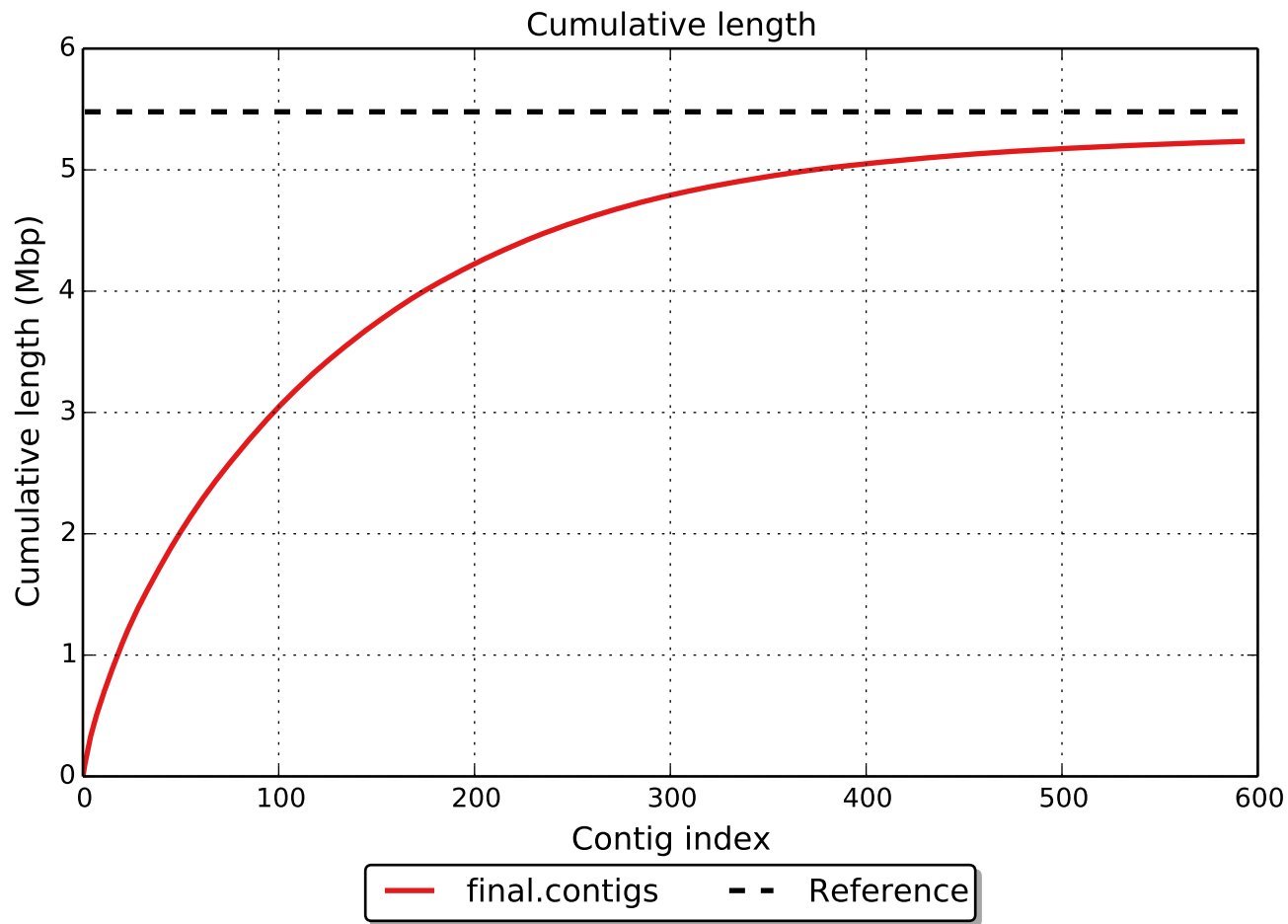
	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	25881
# local misassemblies	2
# mismatches	196
# indels	5
# short indels	3
# long indels	2
Indels length	27

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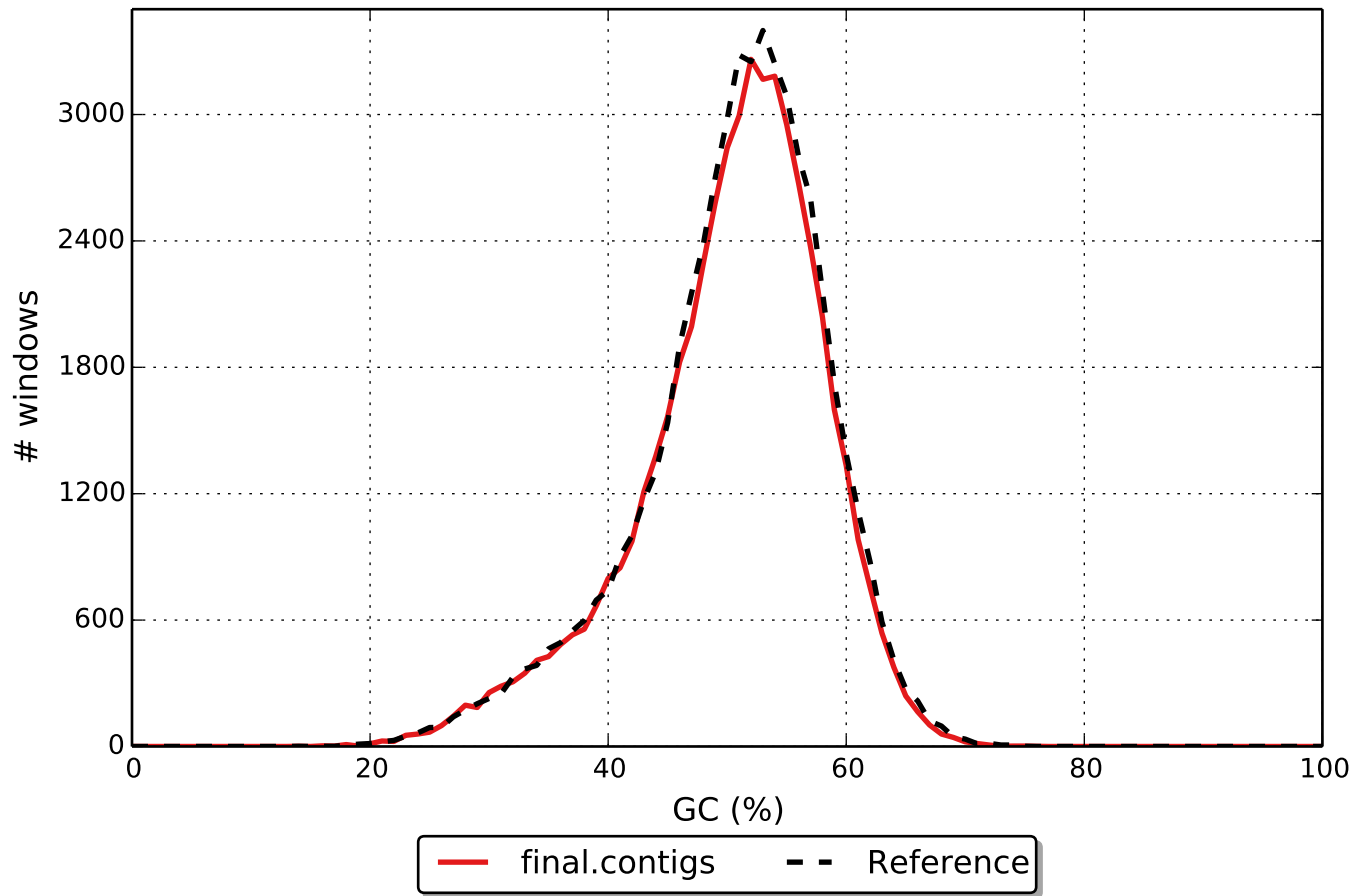
## Unaligned report

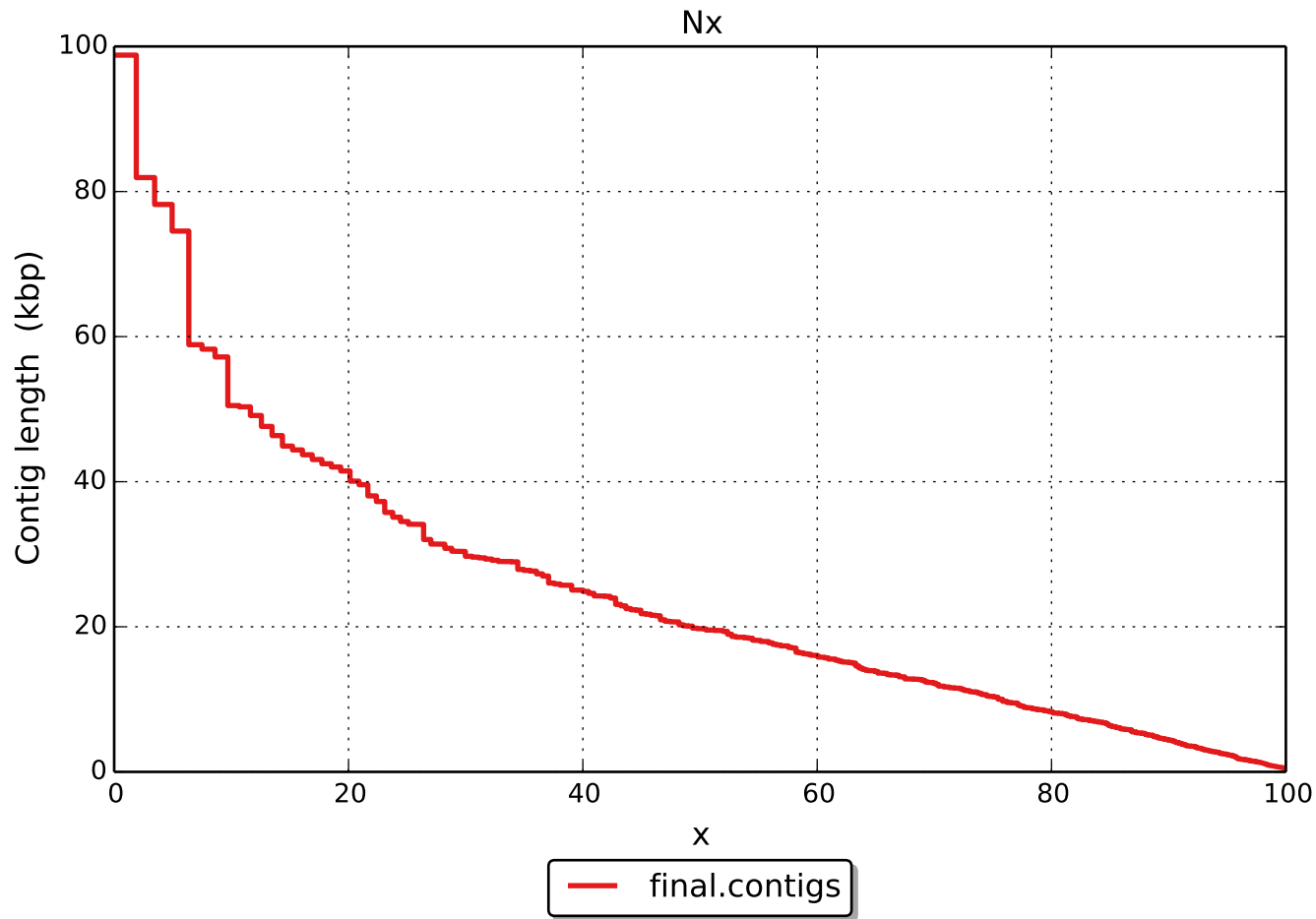
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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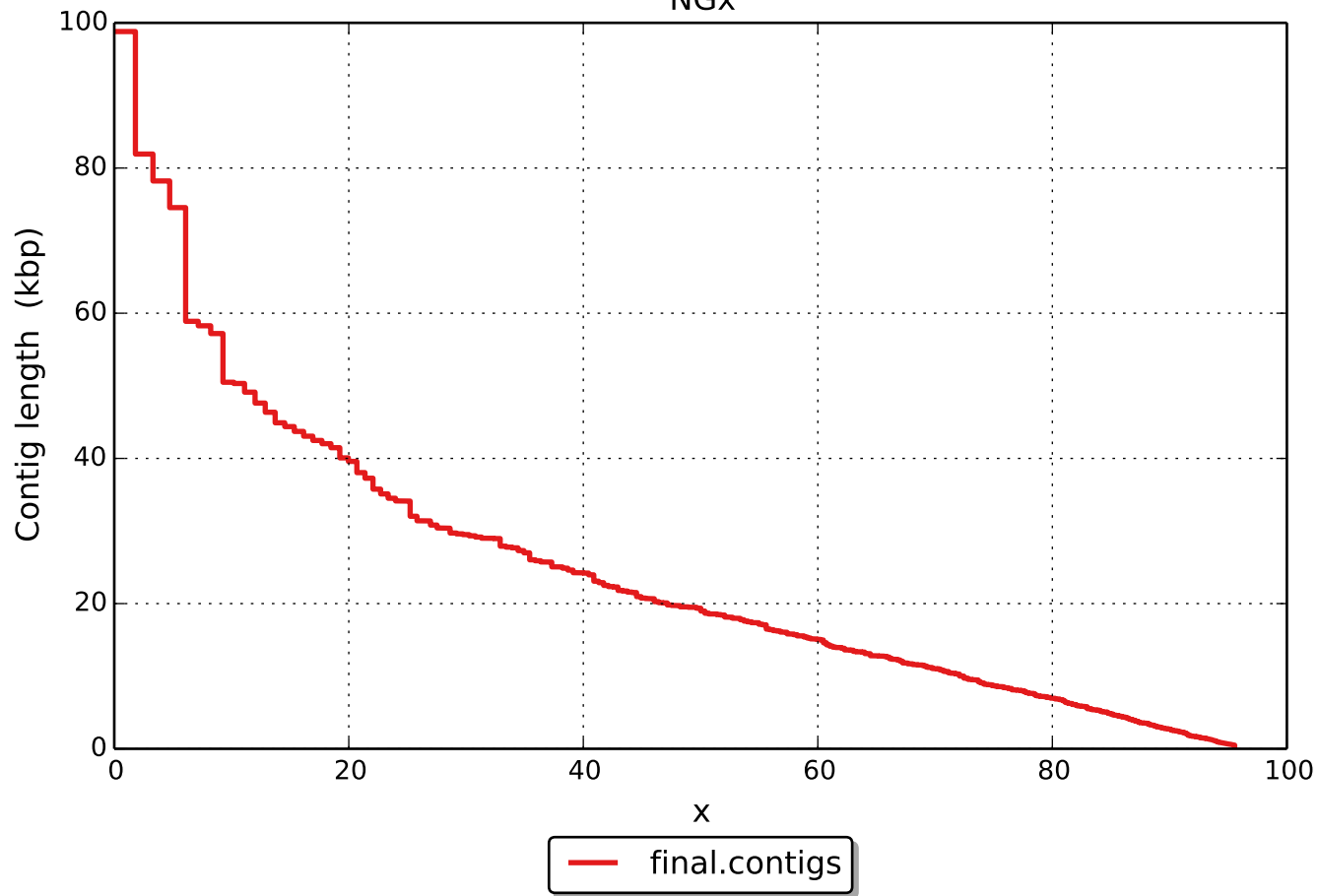


GC content

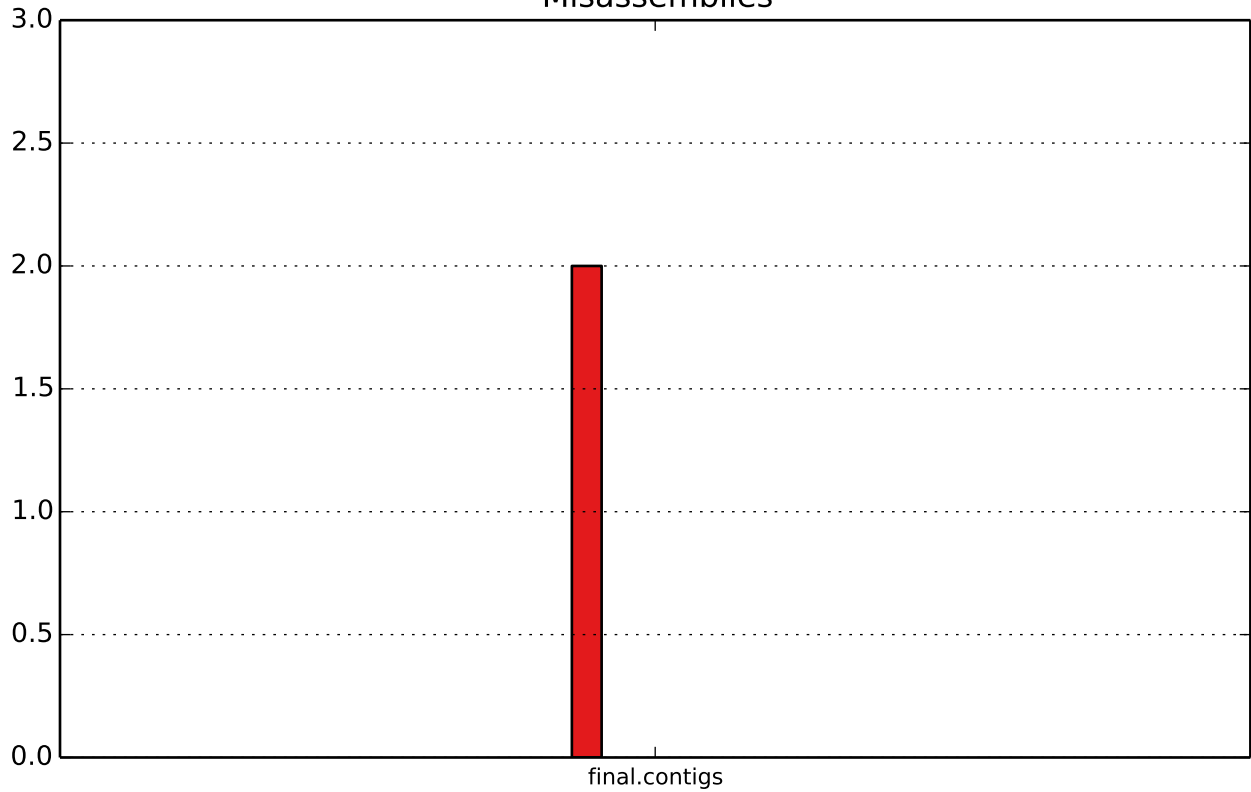




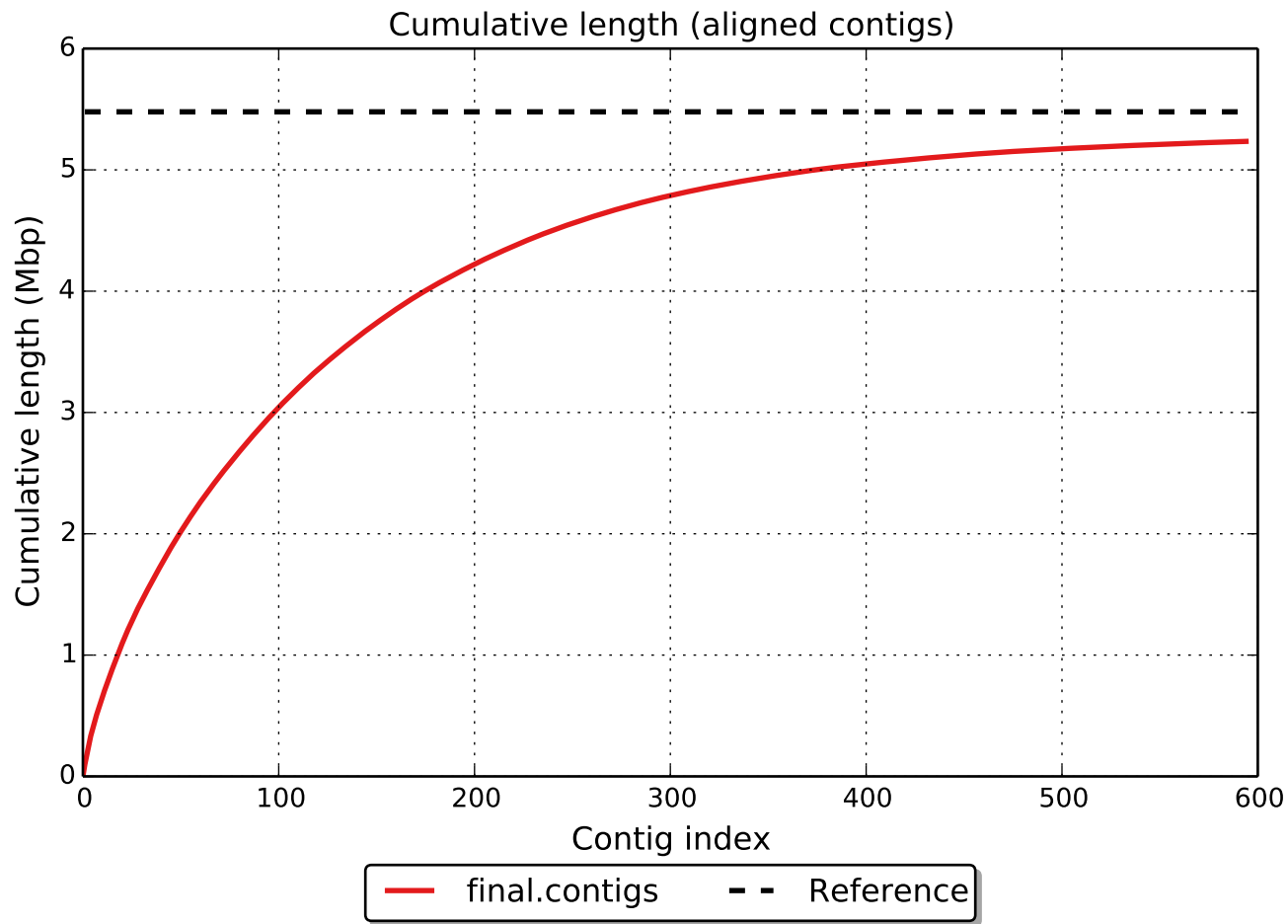
NGx



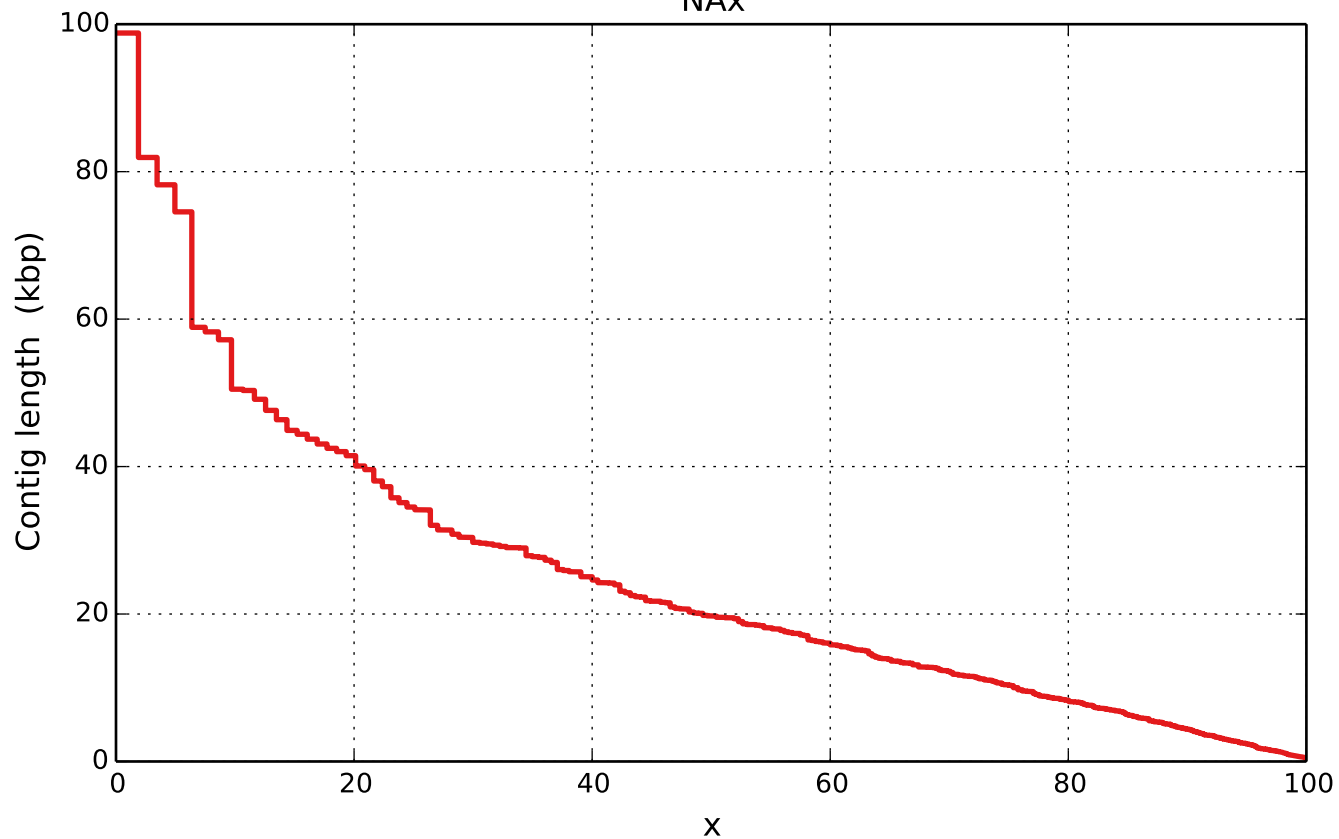
# Misassemblies







NAx



— final.contigs

# NGAx

