

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	5236
# contigs ( $\geq 1000$ bp)	3300
Total length ( $\geq 0$ bp)	11099999
Total length ( $\geq 1000$ bp)	10082801
# contigs	4235
Largest contig	19900
Total length	10767902
Reference length	10957366
GC (%)	50.39
Reference GC (%)	50.49
N50	3544
NG50	3502
N75	2050
NG75	1976
L50	946
LG50	973
L75	1933
LG75	2003
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	13586
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	116
Genome fraction (%)	95.314
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	26.98
# indels per 100 kbp	0.05
Largest alignment	19900
NA50	3544
NGA50	3502
NA75	2050
NGA75	1976
LA50	946
LGA50	973
LA75	1934
LGA75	2005

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

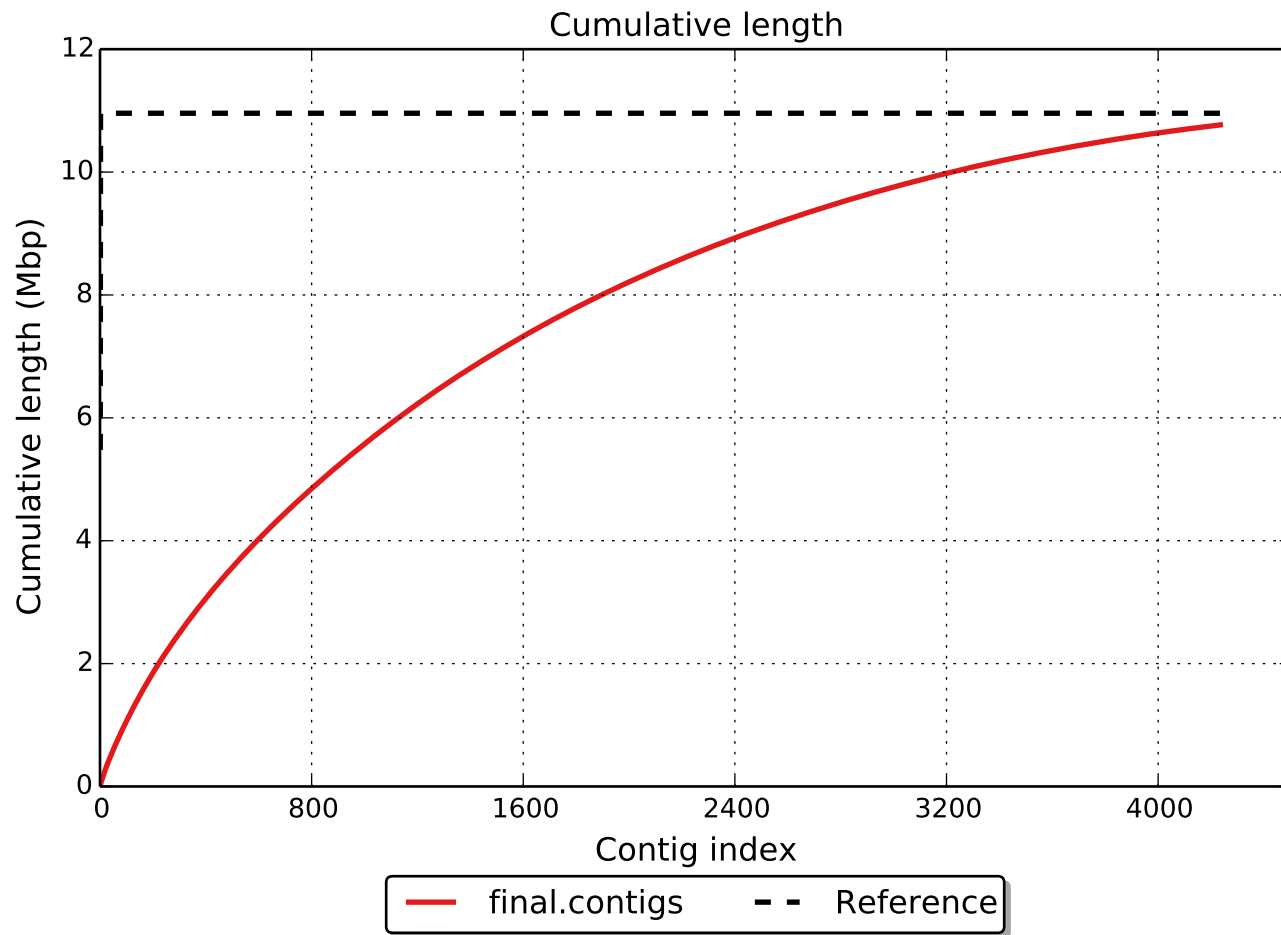
	final.contigs
# misassemblies	2
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	13586
# local misassemblies	0
# mismatches	2818
# indels	5
# short indels	3
# long indels	2
Indels length	28

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).

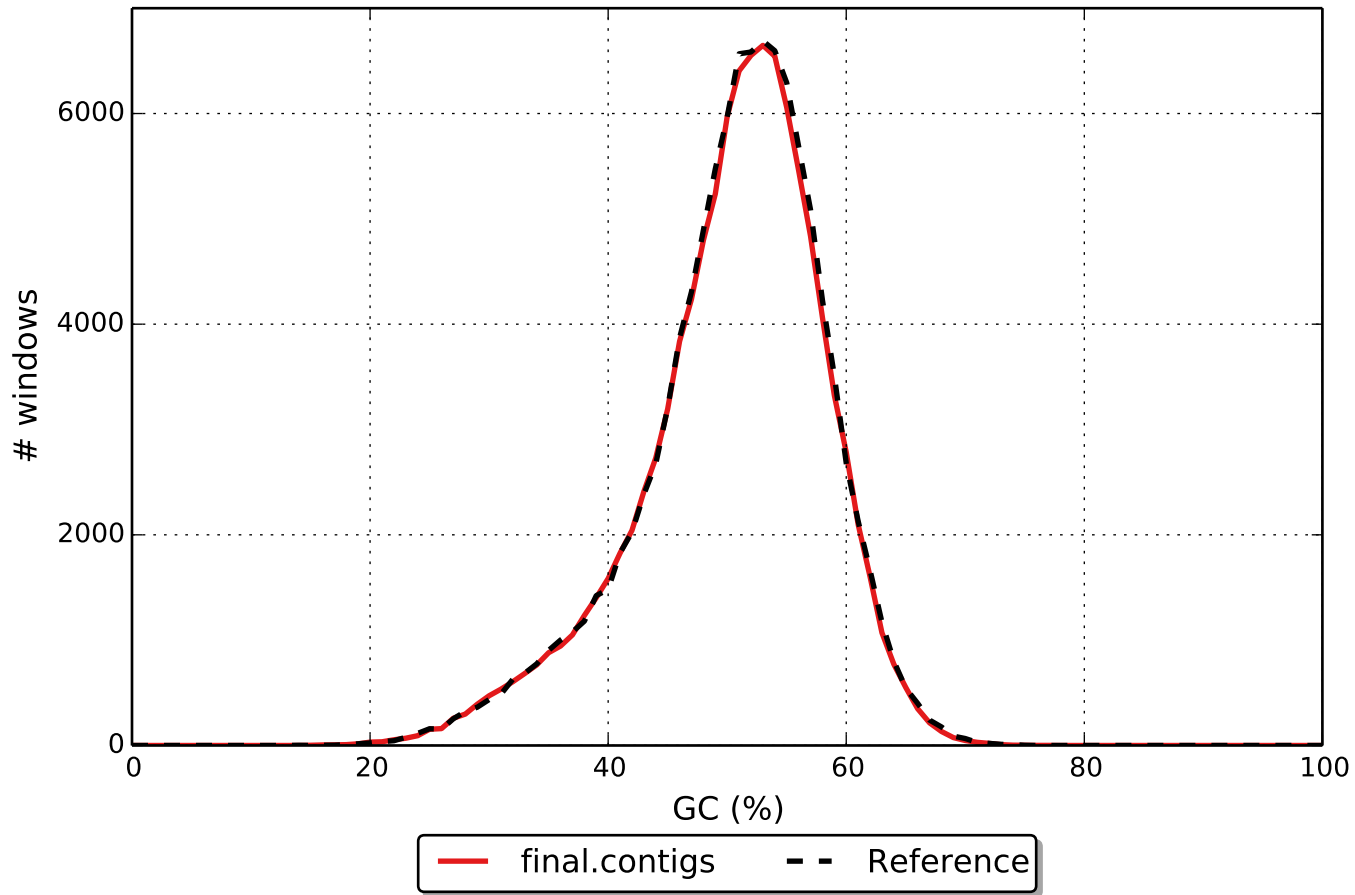
## Unaligned report

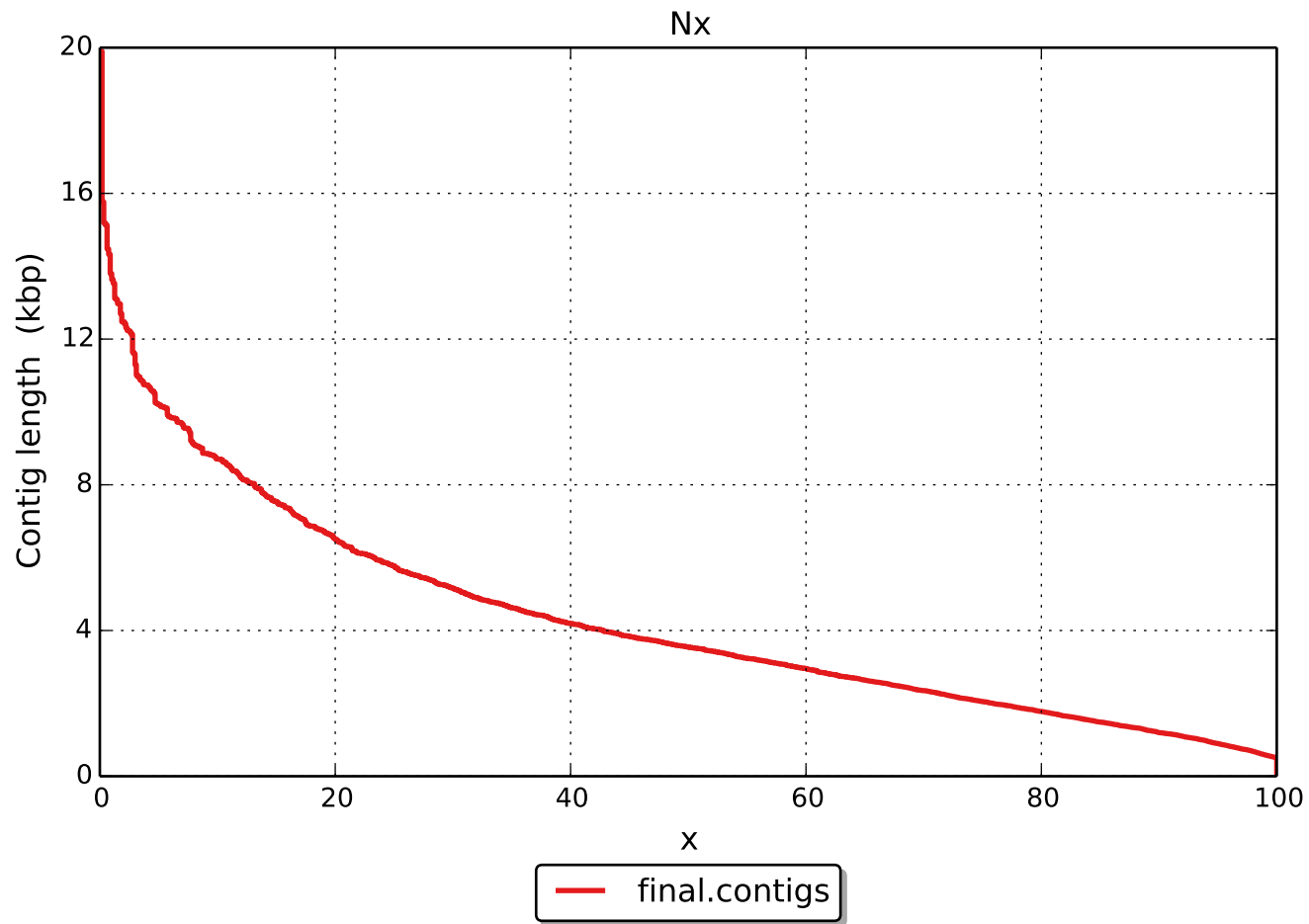
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	116
# N's	0

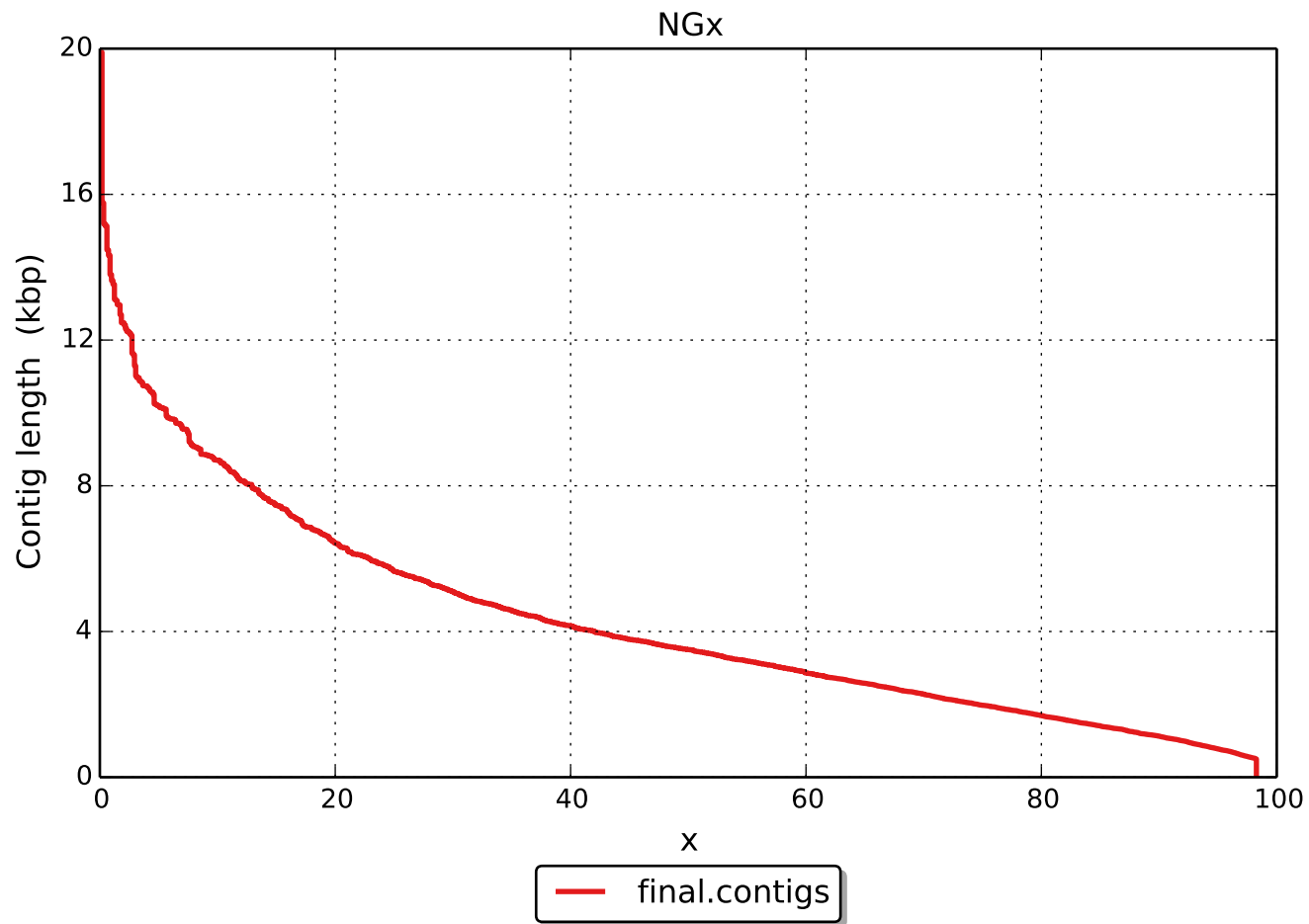
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



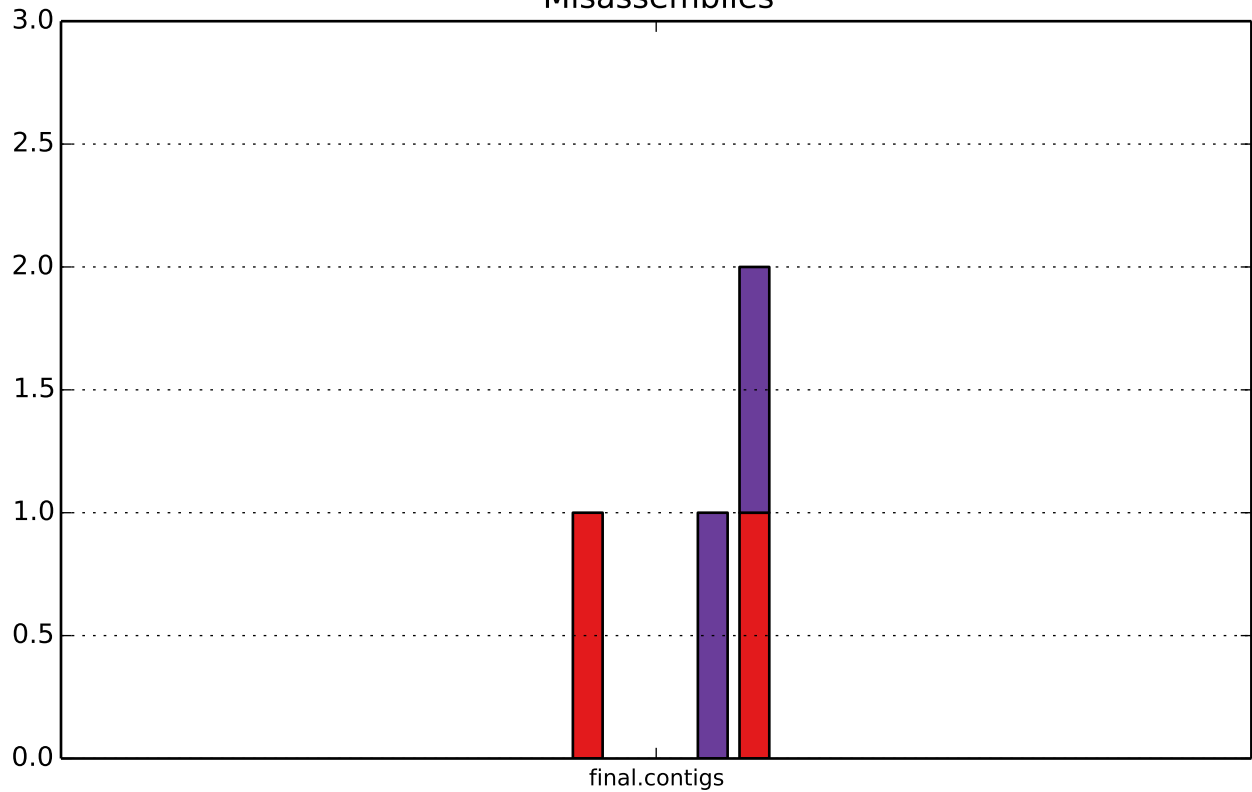
GC content



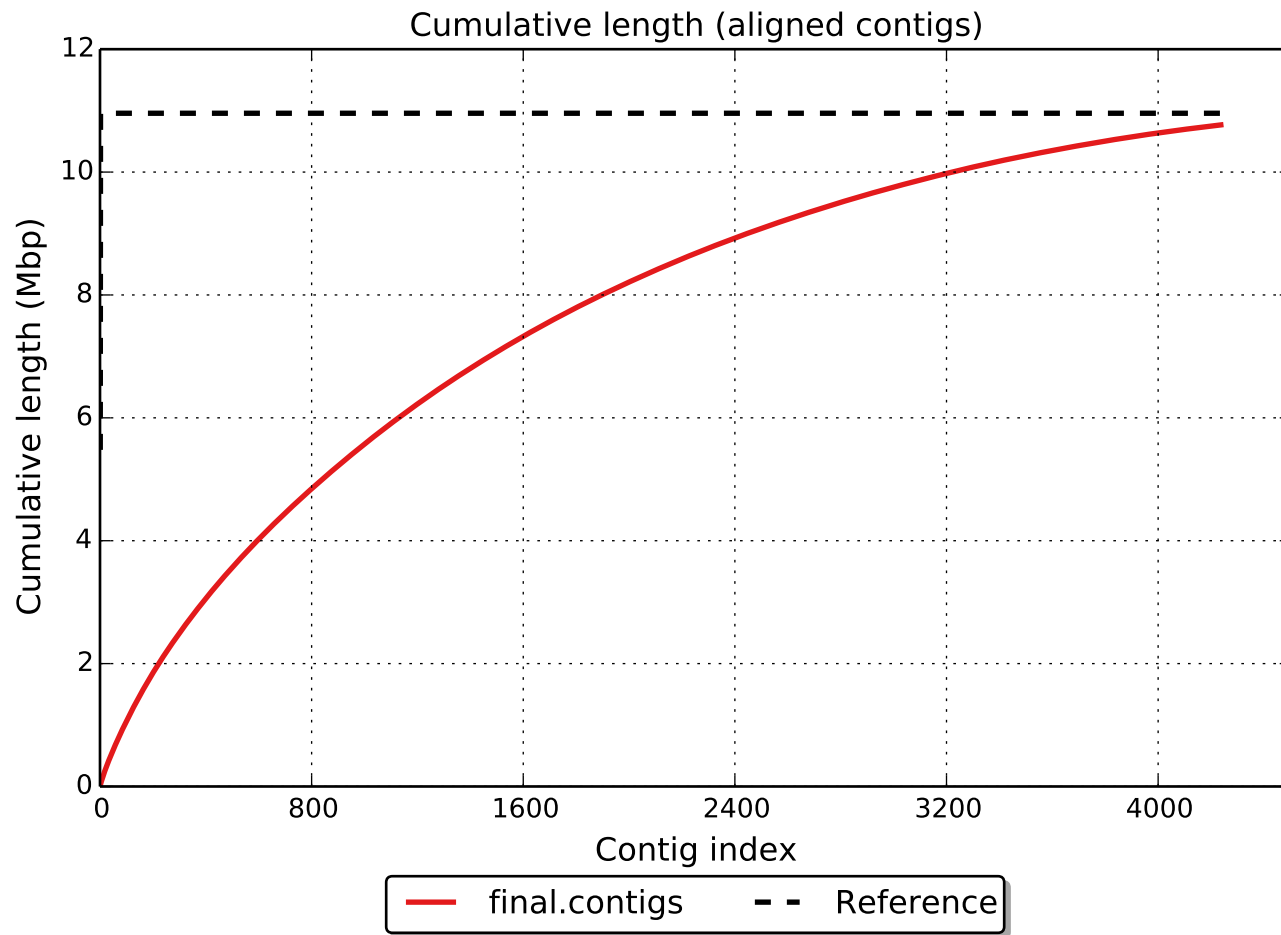


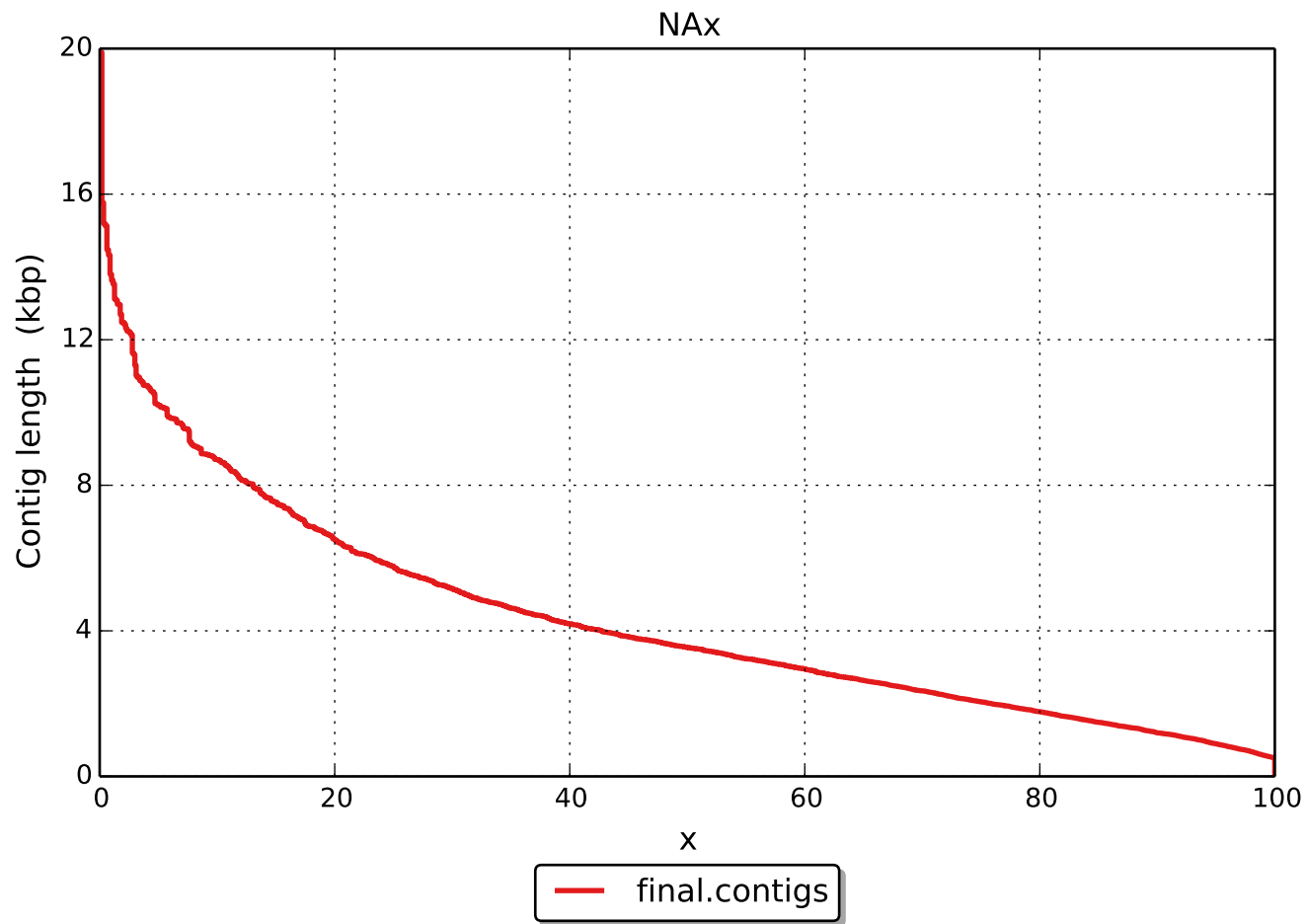


# Misassemblies









NGAx

