

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	720
# contigs ( $\geq 1000$ bp)	574
Total length ( $\geq 0$ bp)	3550224
Total length ( $\geq 1000$ bp)	3451156
# contigs	720
Largest contig	25589
Total length	3550224
Reference length	1892775
GC (%)	32.29
Reference GC (%)	32.26
N50	8280
NG50	15075
N75	4612
NG75	10815
L50	126
LG50	50
L75	265
LG75	88
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	4797
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.202
Duplication ratio	2.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	529.11
# indels per 100 kbp	0.17
Largest alignment	25589
NA50	581
NGA50	8004
NGA75	4033
LA50	347
LGA50	70
LGA75	153

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

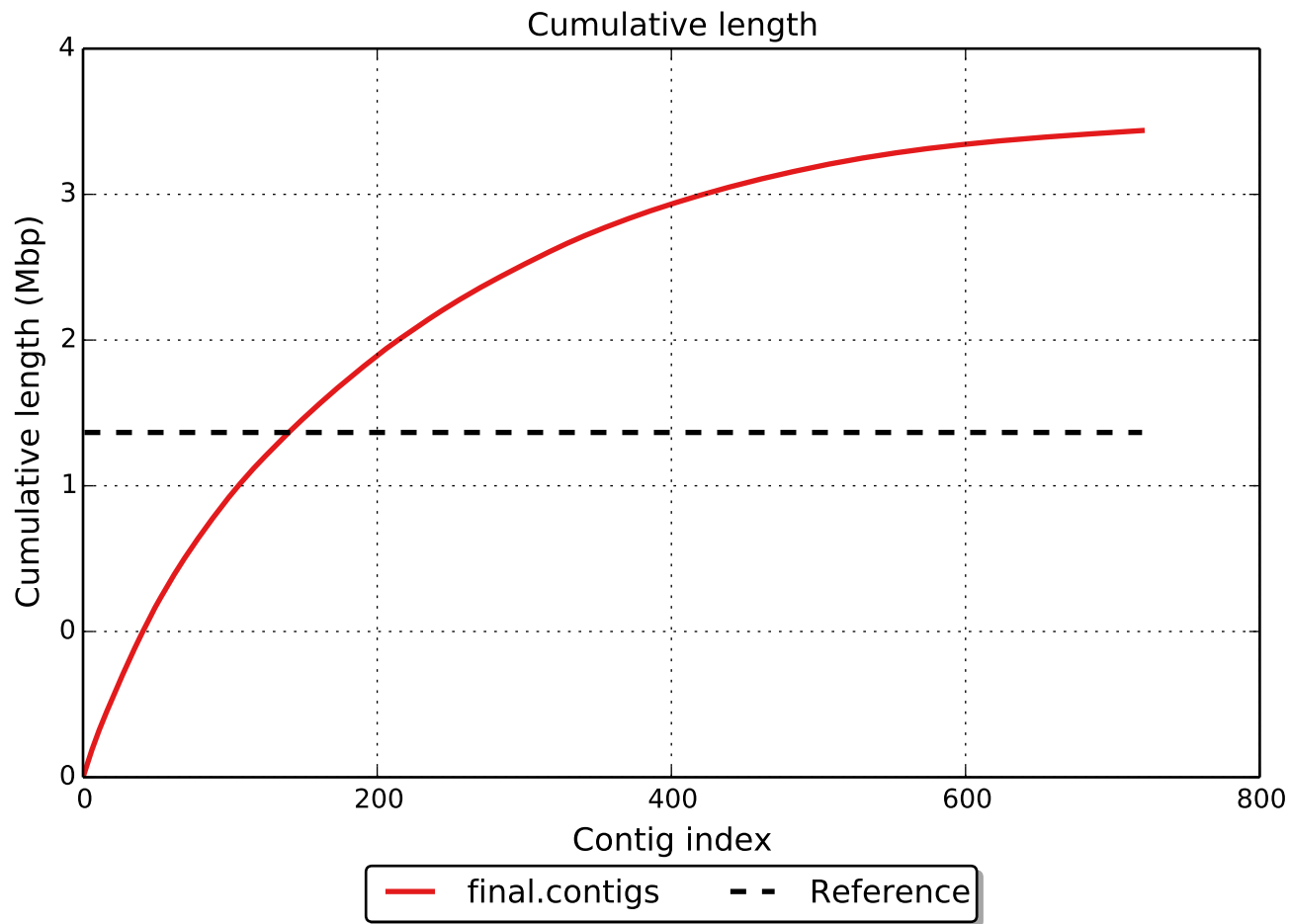
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	4797
# local misassemblies	0
# mismatches	9334
# indels	3
# short indels	2
# long indels	1
Indels length	82

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).

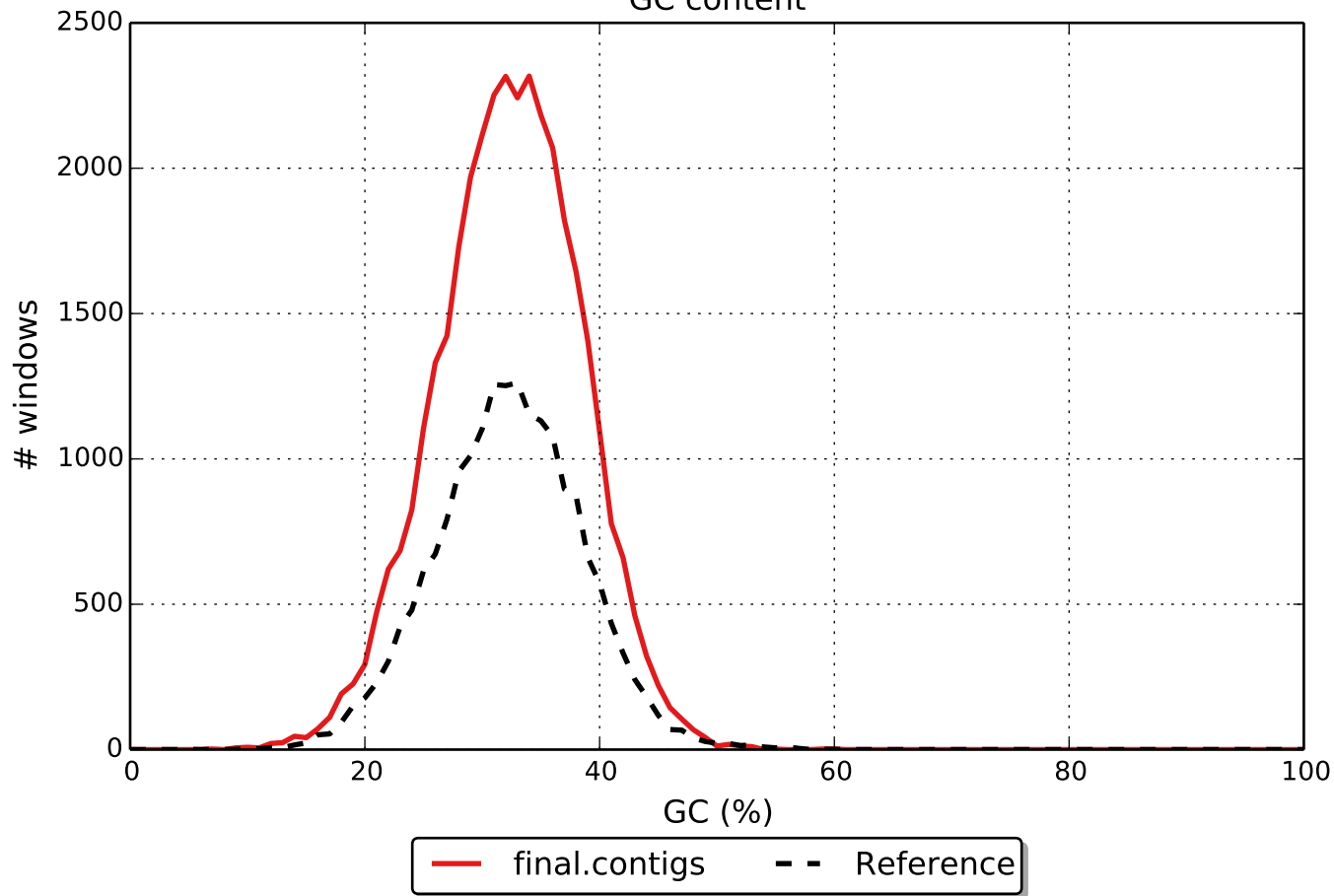
## Unaligned report

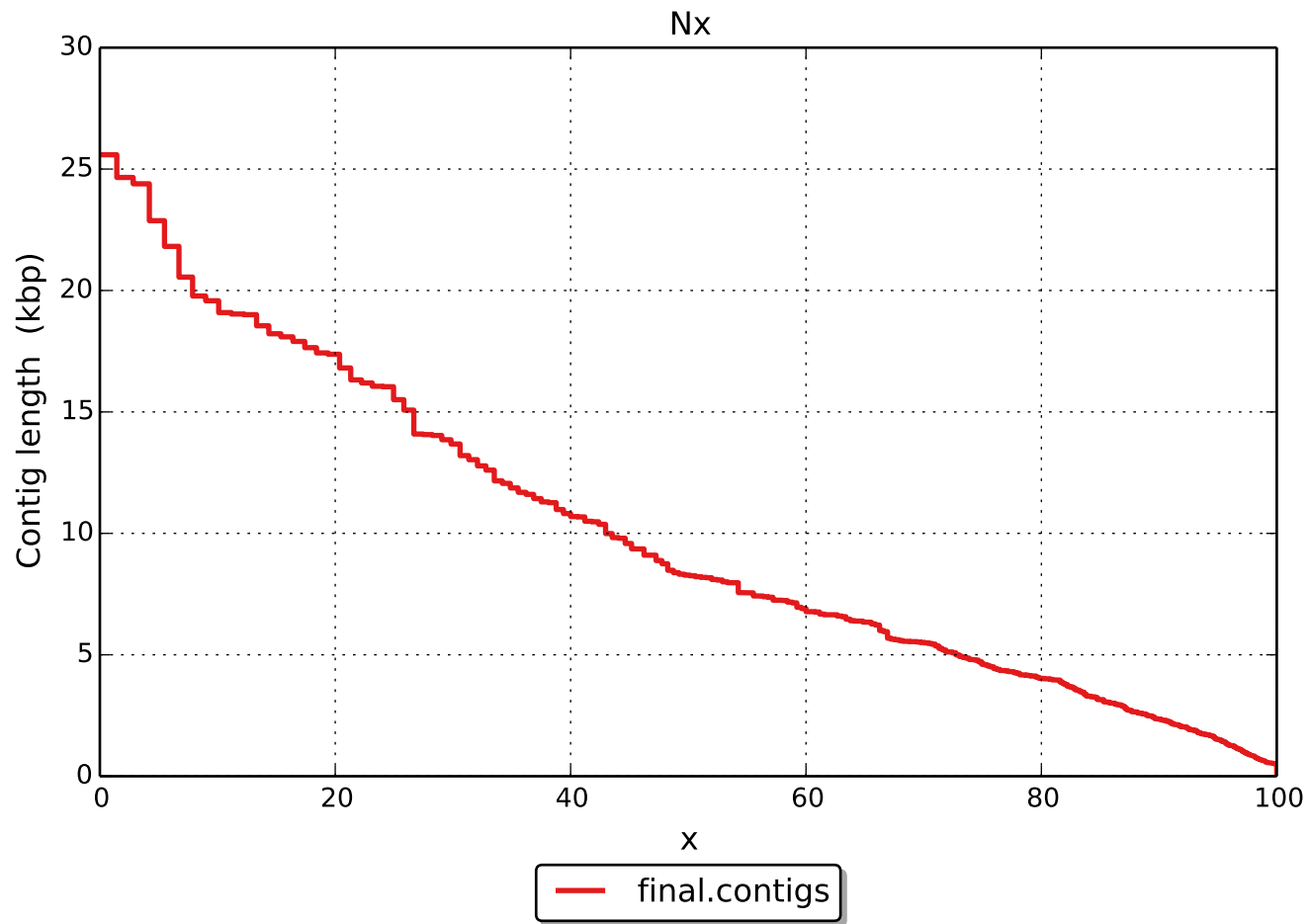
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

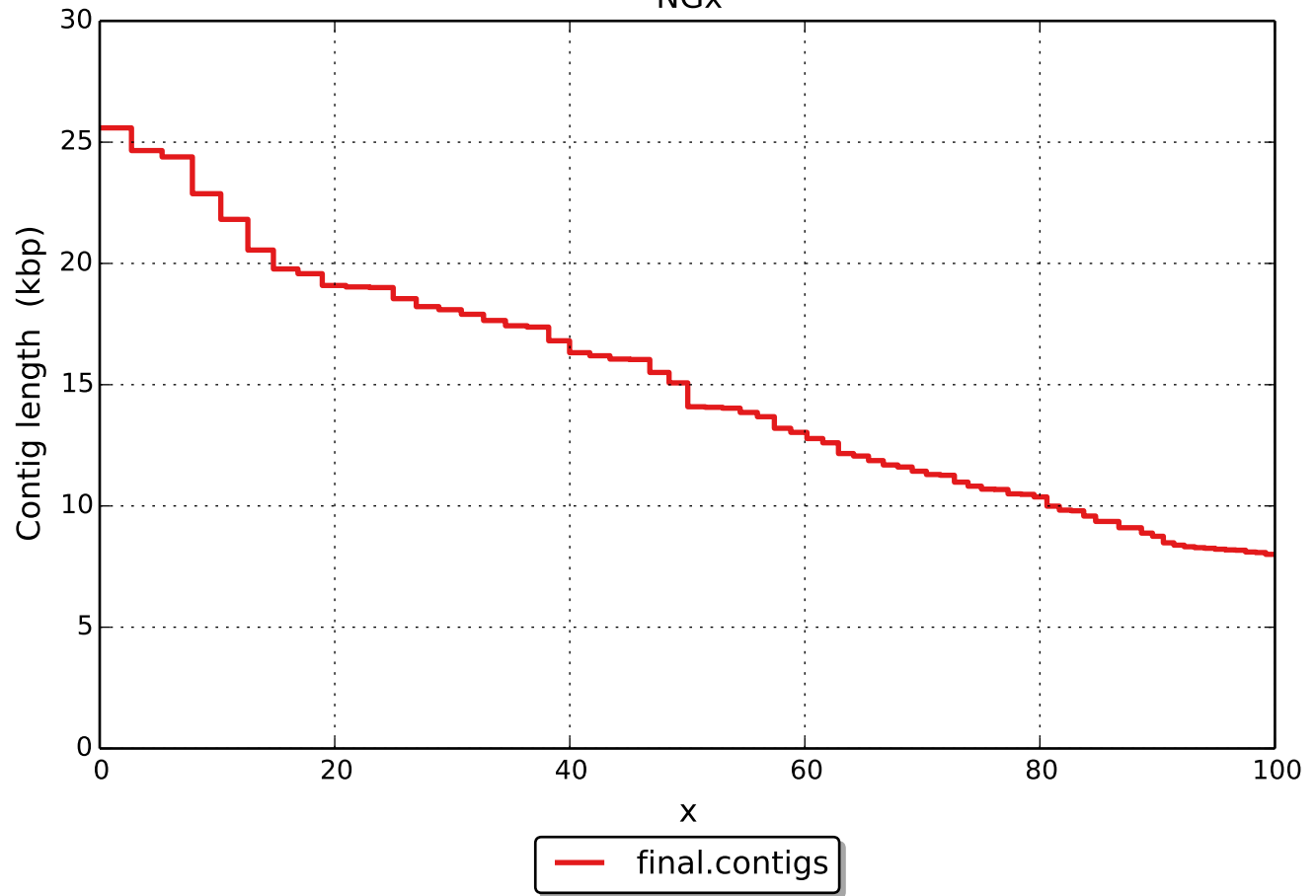


GC content

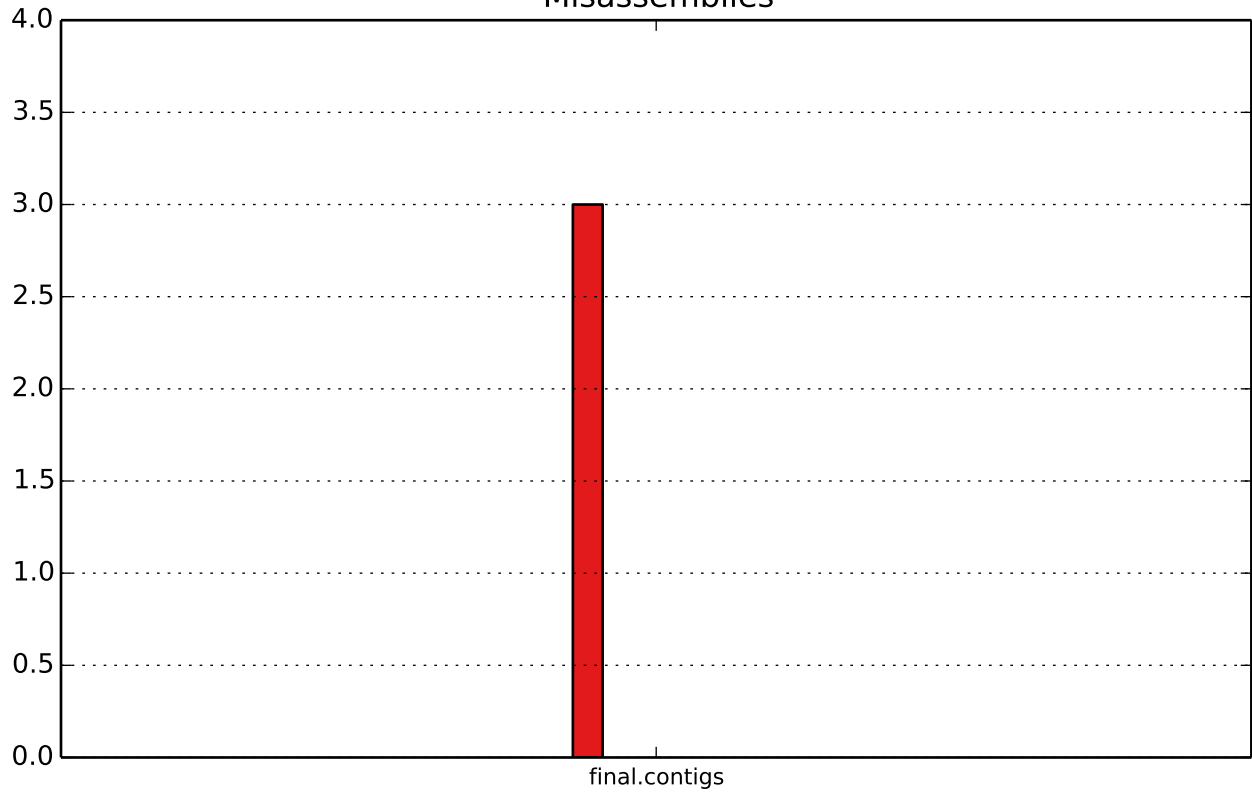




NGx

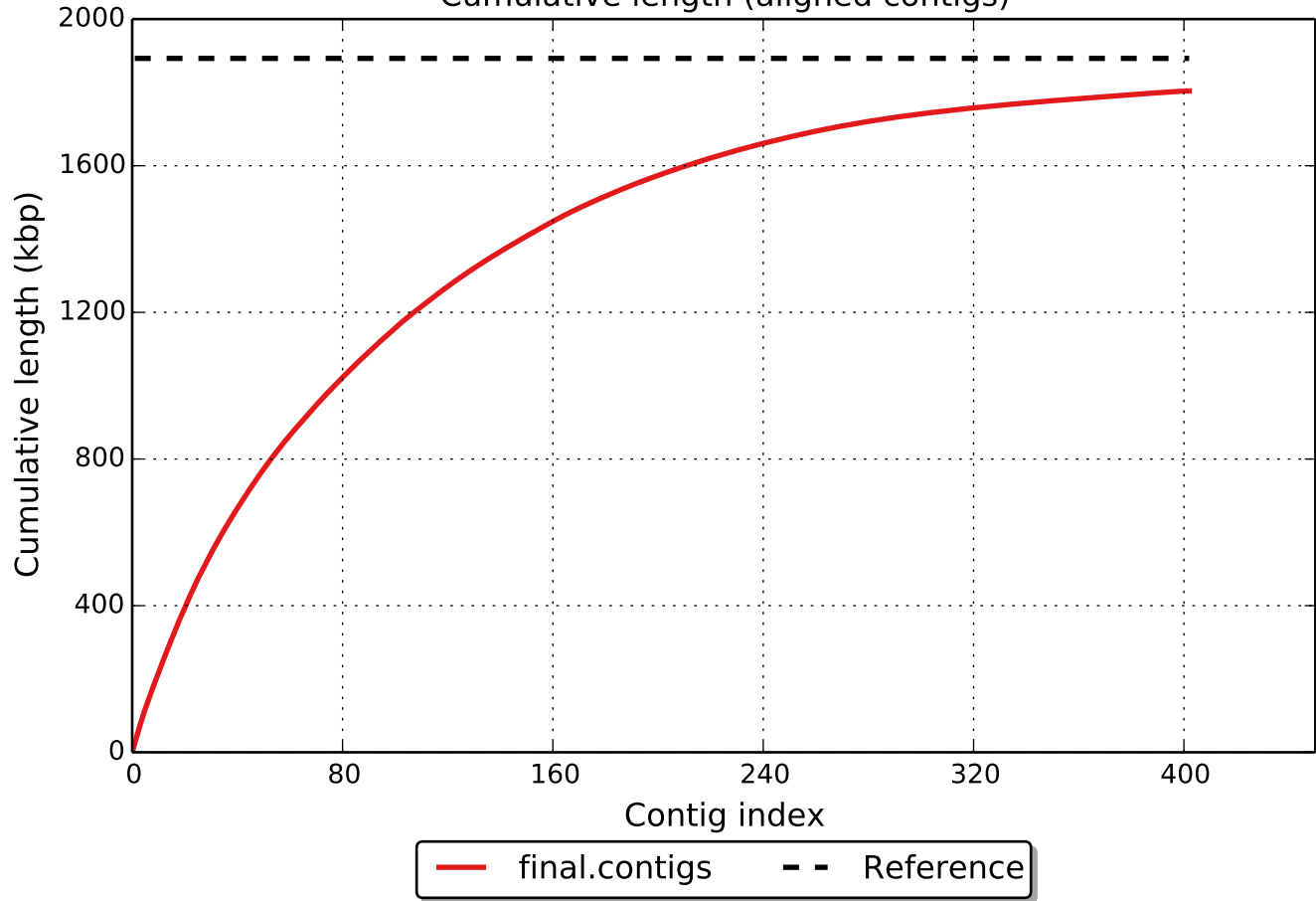


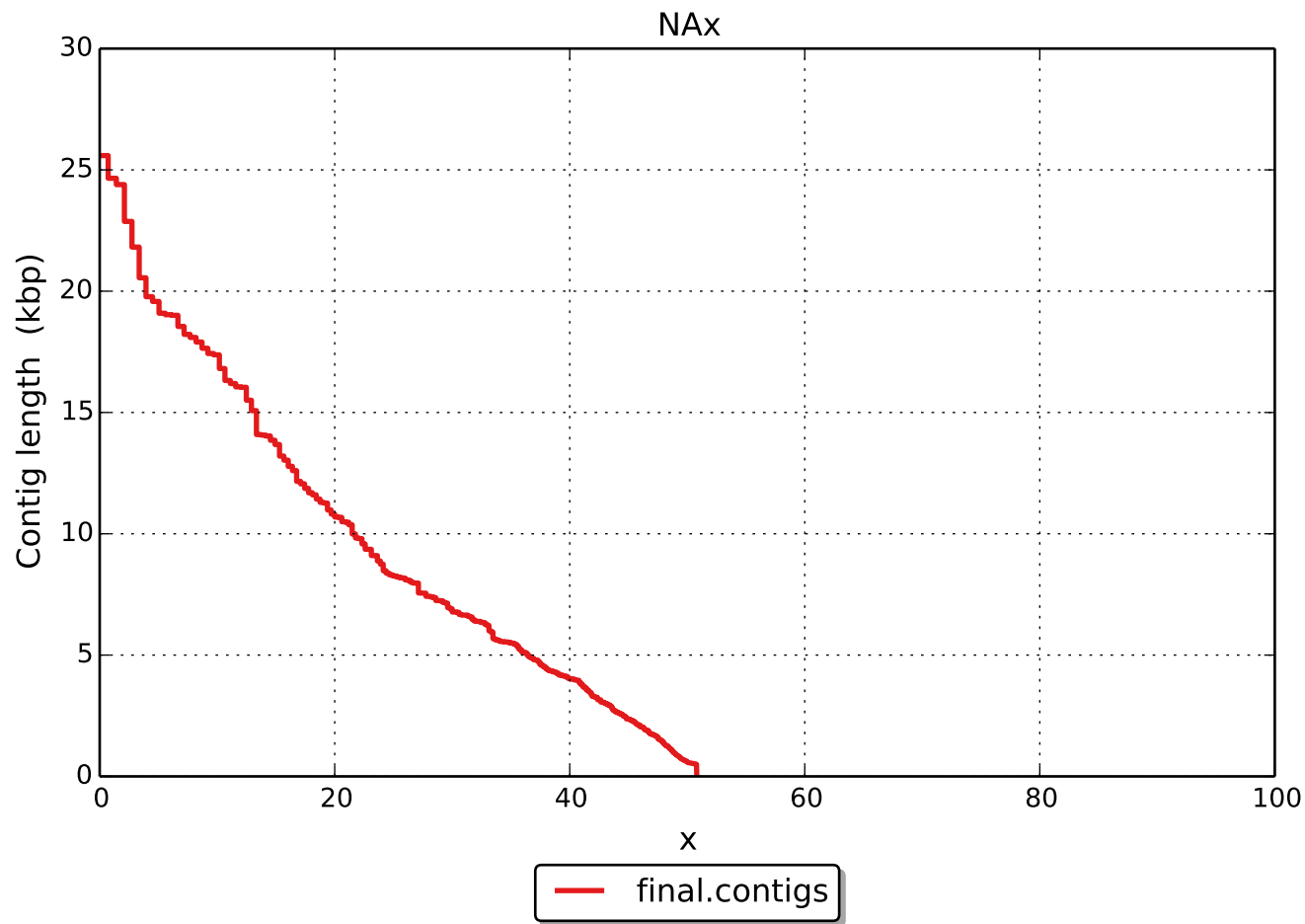
# Misassemblies





Cumulative length (aligned contigs)





NGAx

