

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	2457
# contigs ( $\geq 1000$ bp)	710
Total length ( $\geq 0$ bp)	2345482
Total length ( $\geq 1000$ bp)	1130041
# contigs	2457
Largest contig	5291
Total length	2345482
Reference length	1892775
GC (%)	32.30
Reference GC (%)	32.26
N50	984
NG50	1129
N75	701
NG75	853
L50	754
LG50	538
L75	1462
LG75	1022
# misassemblies	30
# misassembled contigs	30
Misassembled contigs length	30021
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	246
Genome fraction (%)	86.611
Duplication ratio	1.431
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1006.50
# indels per 100 kbp	0.18
Largest alignment	5291
NA50	982
NGA50	1125
NA75	698
NGA75	851
LA50	757
LGA50	540
LA75	1468
LGA75	1026

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

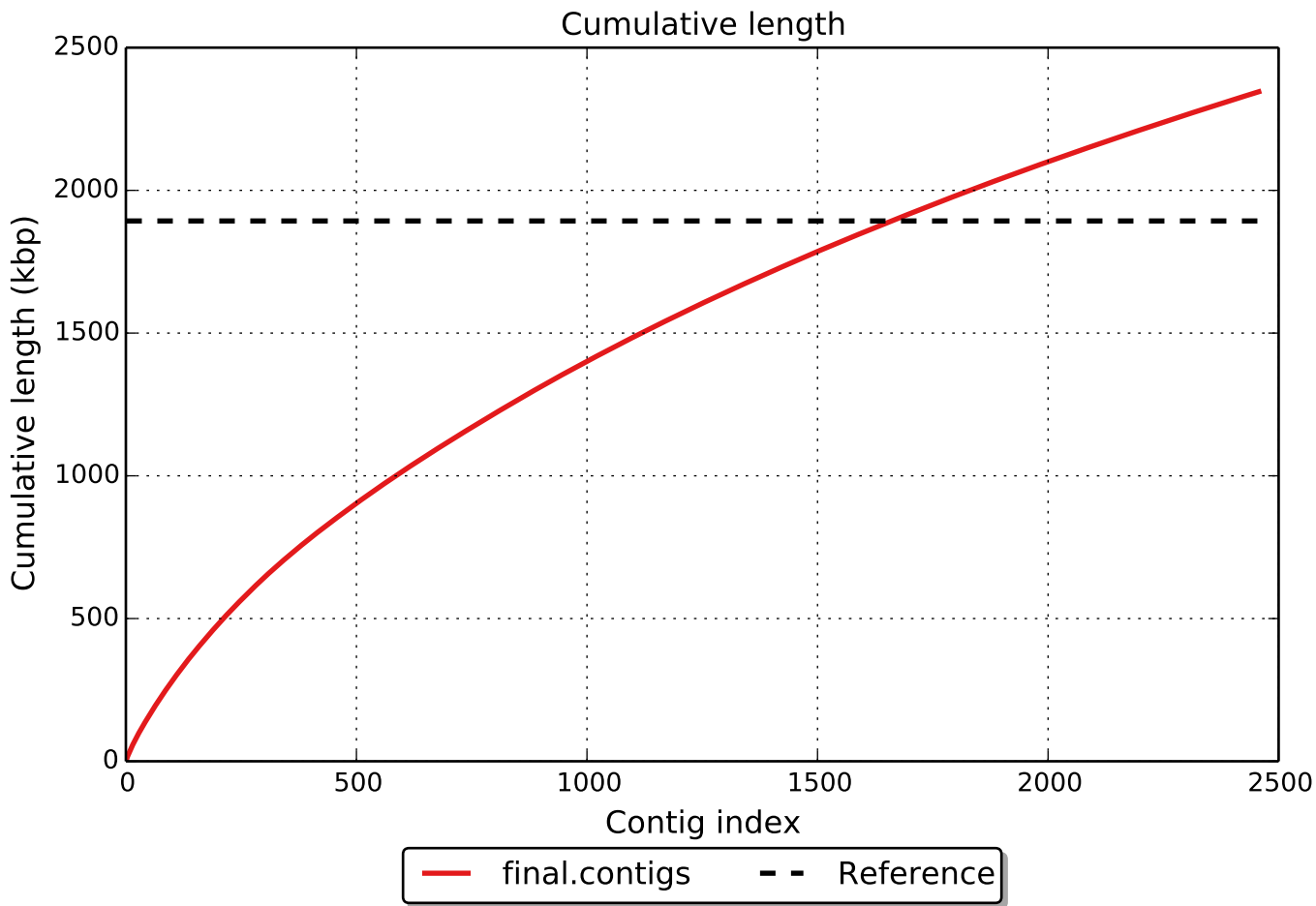
	final.contigs
# misassemblies	30
# relocations	28
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	30
Misassembled contigs length	30021
# local misassemblies	0
# mismatches	16500
# indels	3
# short indels	2
# long indels	1
Indels length	20

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).

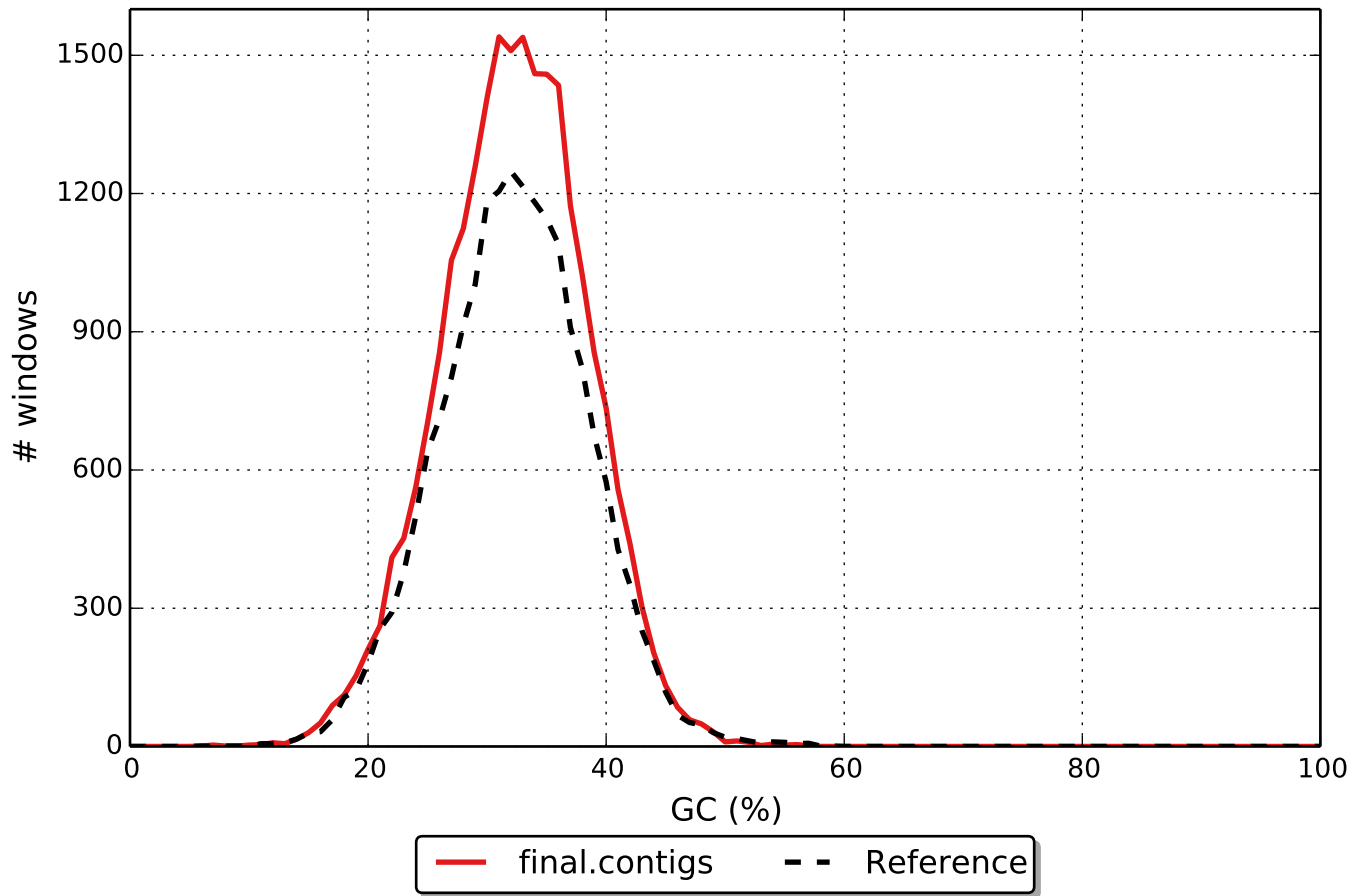
## Unaligned report

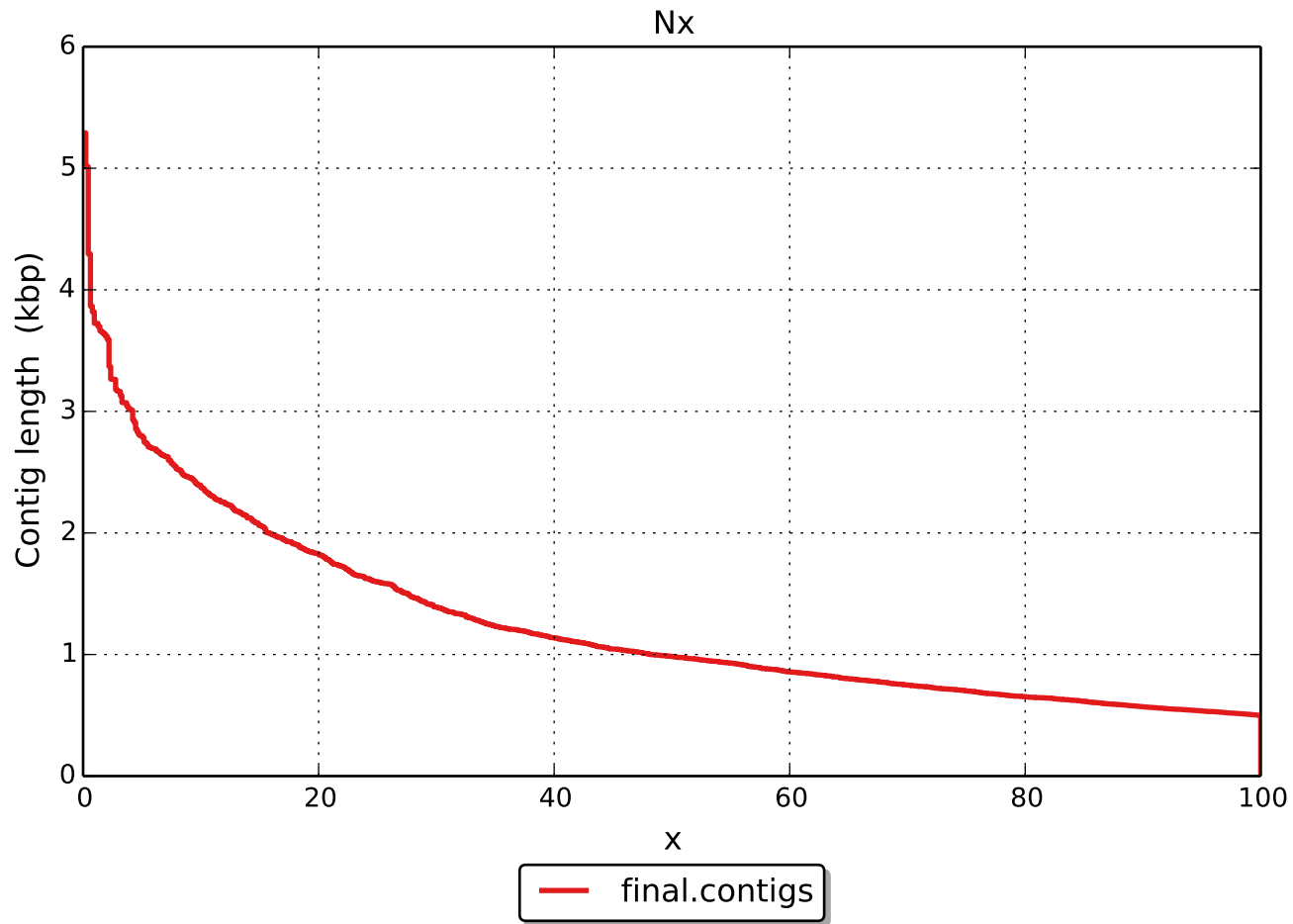
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	246
# N's	0

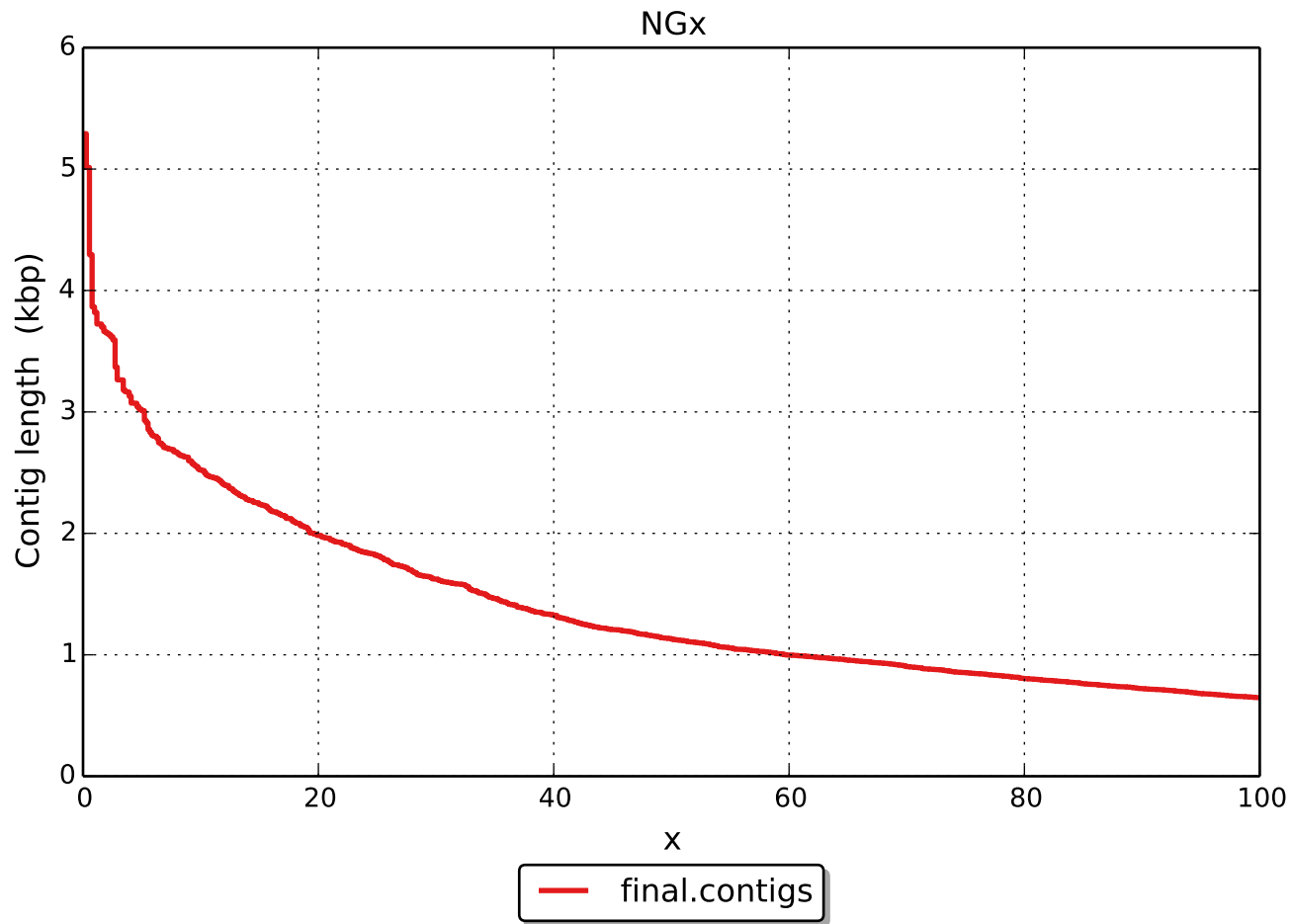
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



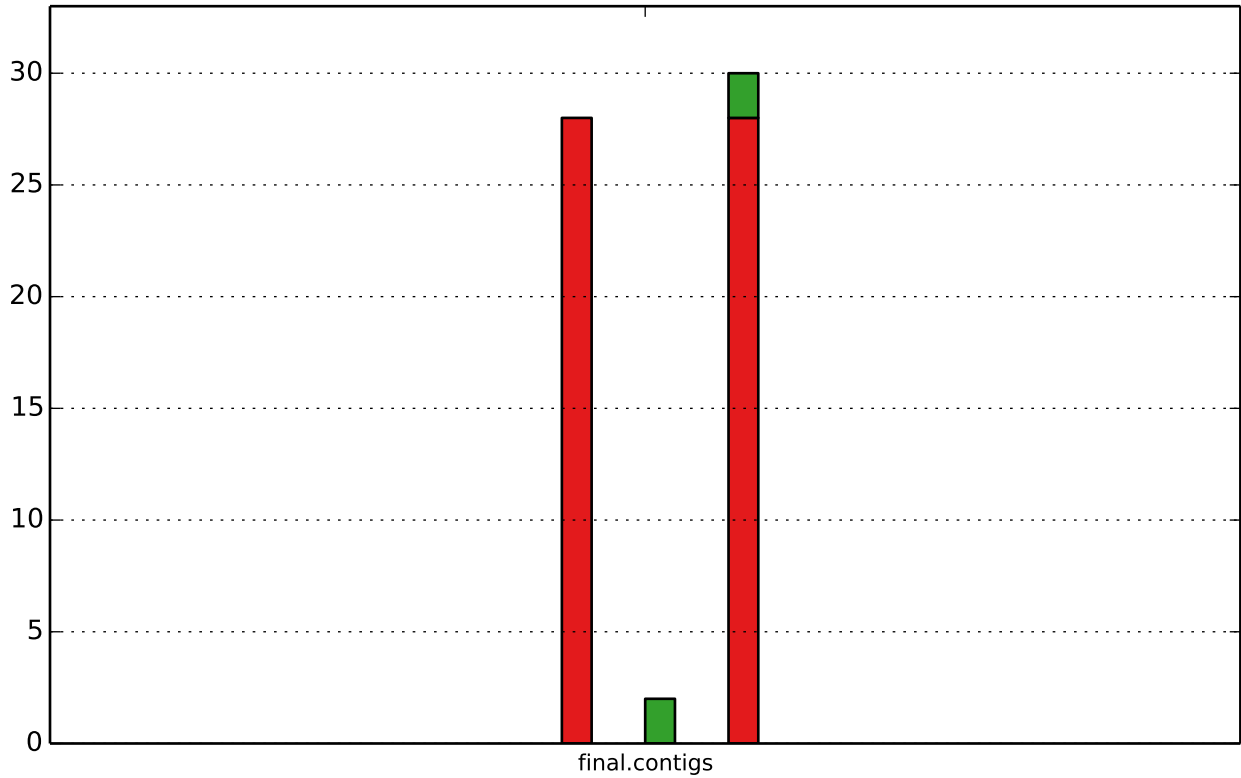
GC content





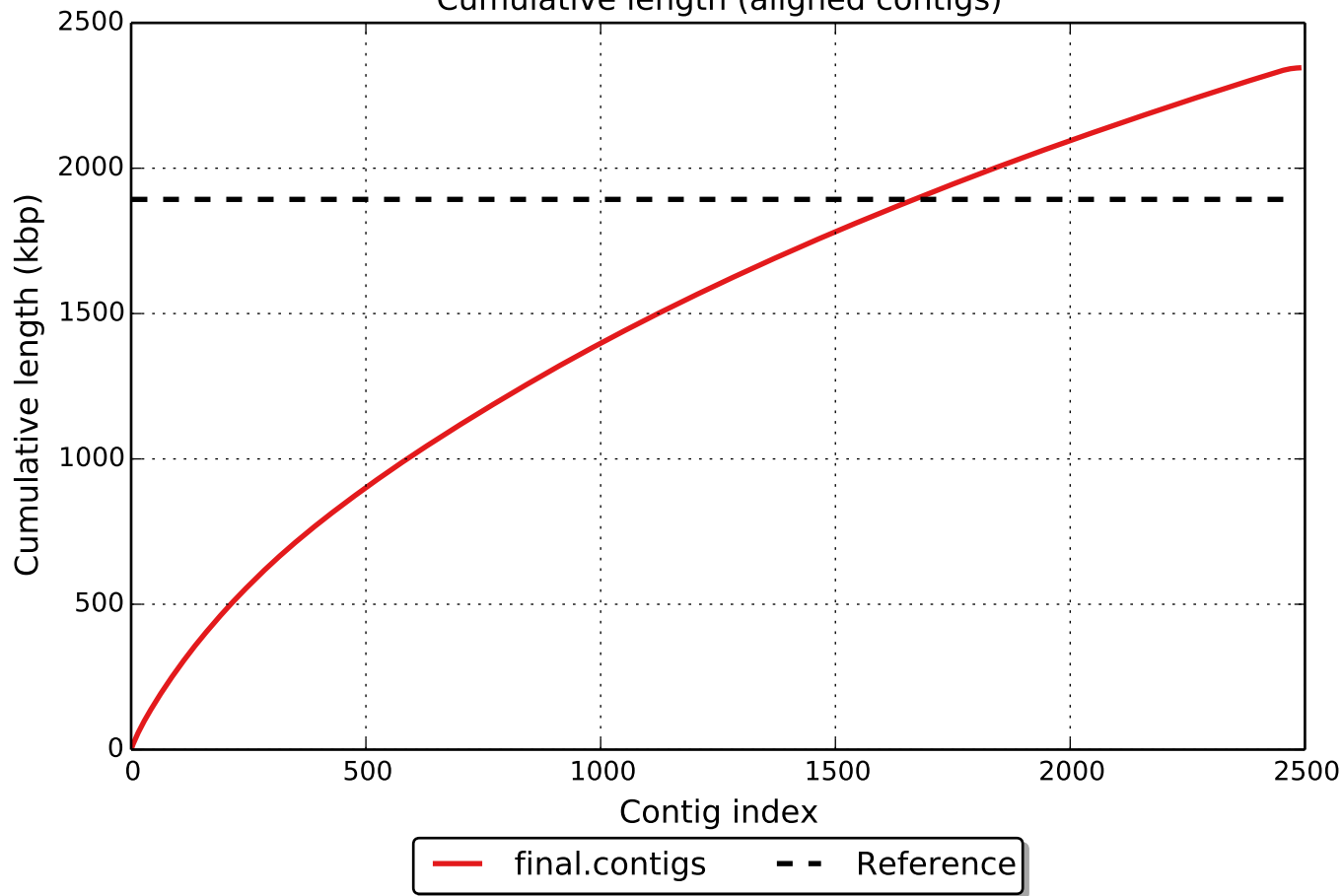


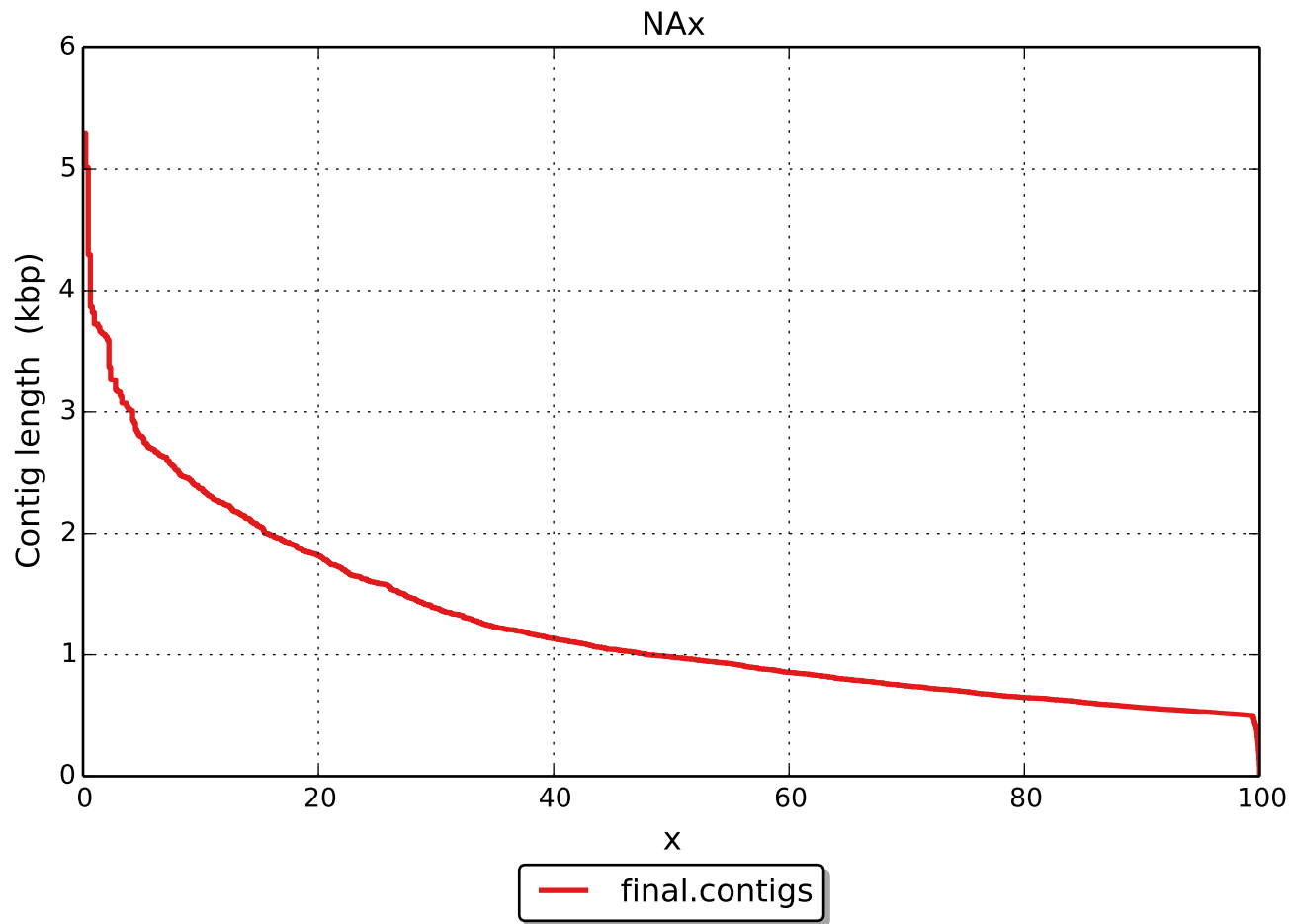
# Misassemblies





Cumulative length (aligned contigs)





NGAx

