

# Report

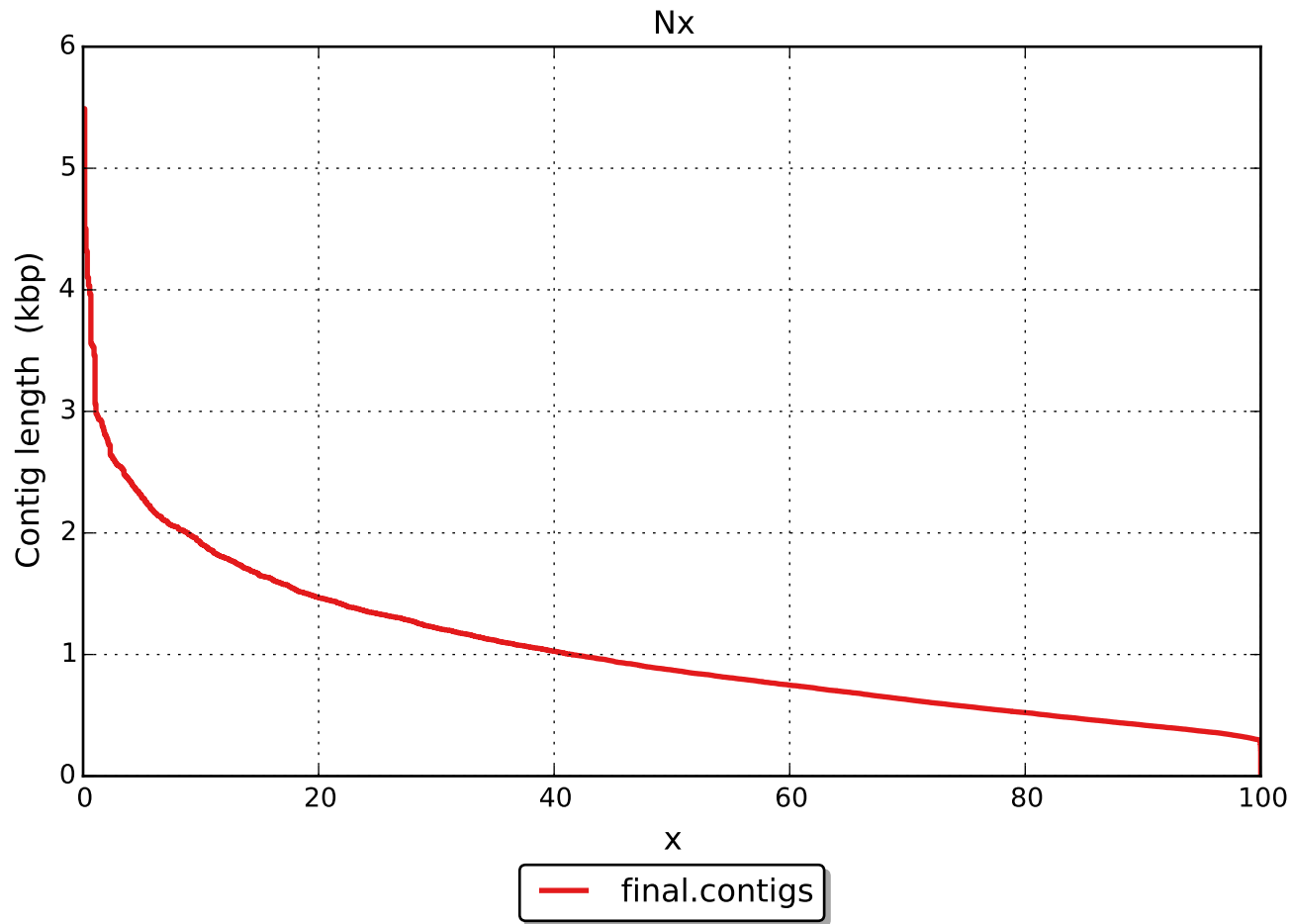
	final.contigs
# contigs ( $\geq 0$ bp)	5222
# contigs ( $\geq 1000$ bp)	1126
# contigs ( $\geq 5000$ bp)	1
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	3995685
Total length ( $\geq 1000$ bp)	1659247
Total length ( $\geq 5000$ bp)	5490
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	5222
Largest contig	5490
Total length	3995685
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	873
NG50	770
N75	573
NG75	448
L50	1490
LG50	1884
L75	2899
LG75	3854
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	9227
# local misassemblies	1
# unaligned contigs	2103 + 18 part
Unaligned length	1322399
Genome fraction (%)	56.808
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	562.34
# indels per 100 kbp	0.11
Largest alignment	5093
NA50	672
NGA50	506
LA50	1696
LGA50	2248

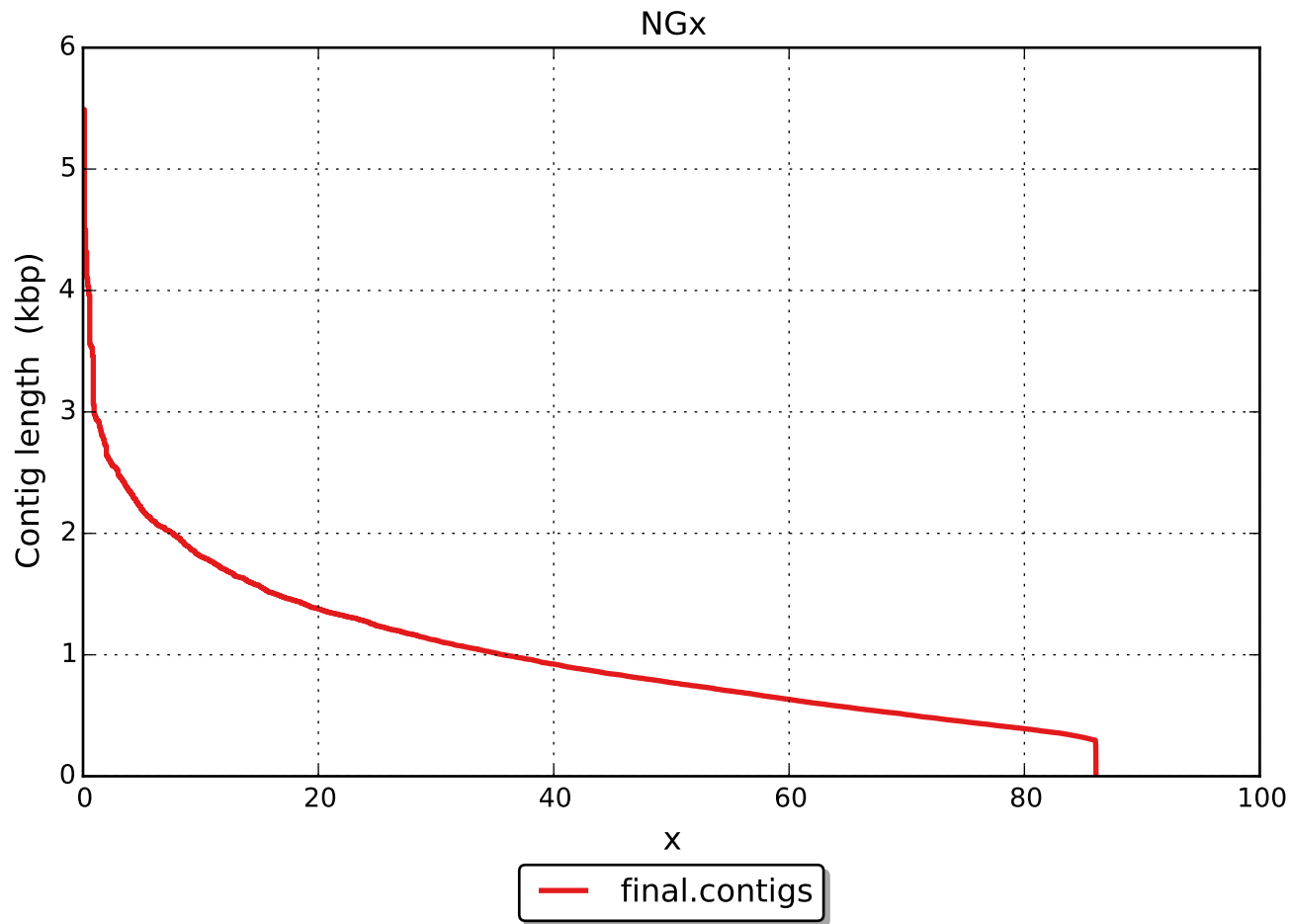
## Misassemblies report

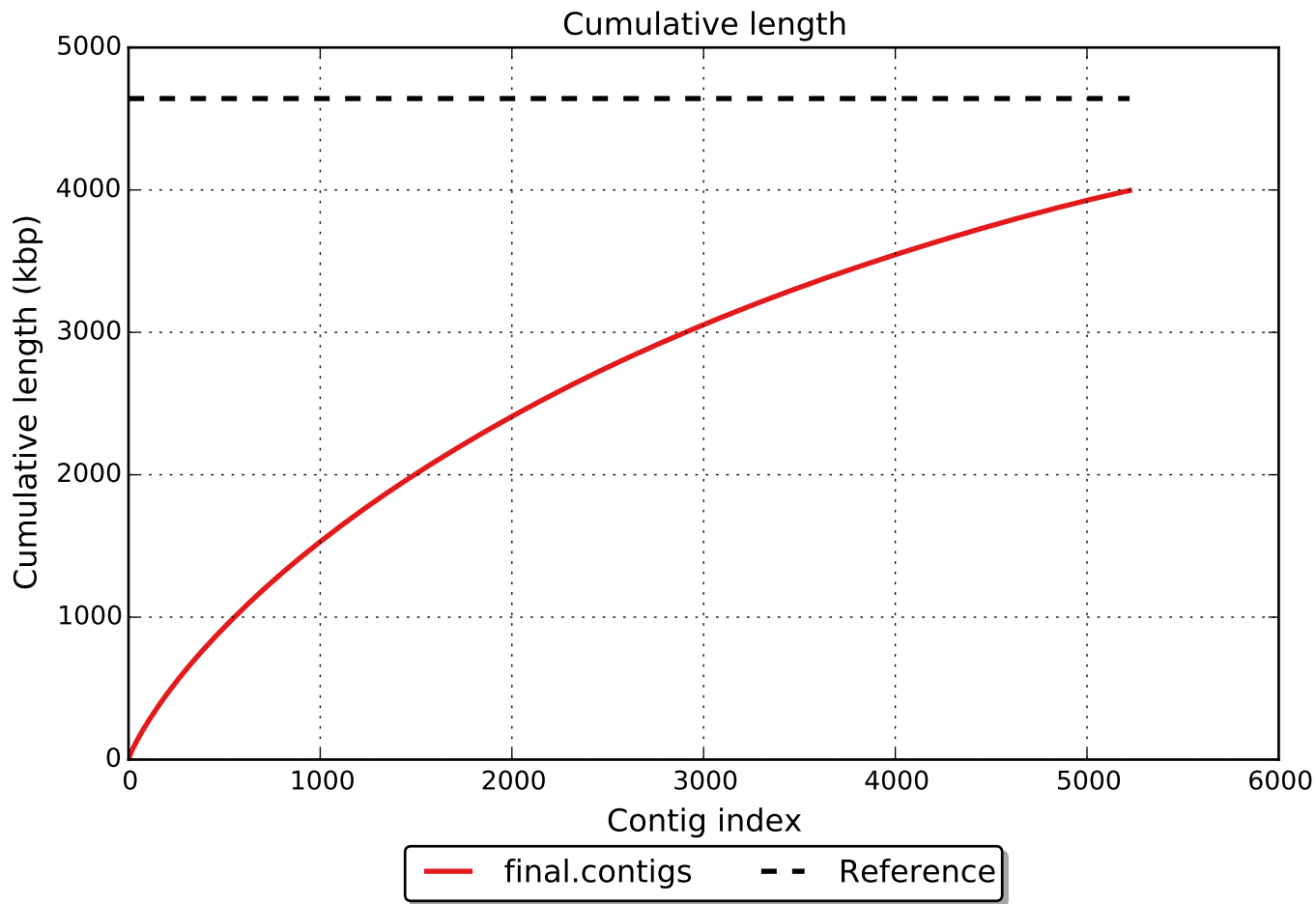
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	9227
# local misassemblies	1
# mismatches	14828
# indels	3
# short indels	3
# long indels	0
Indels length	3

## Unaligned report

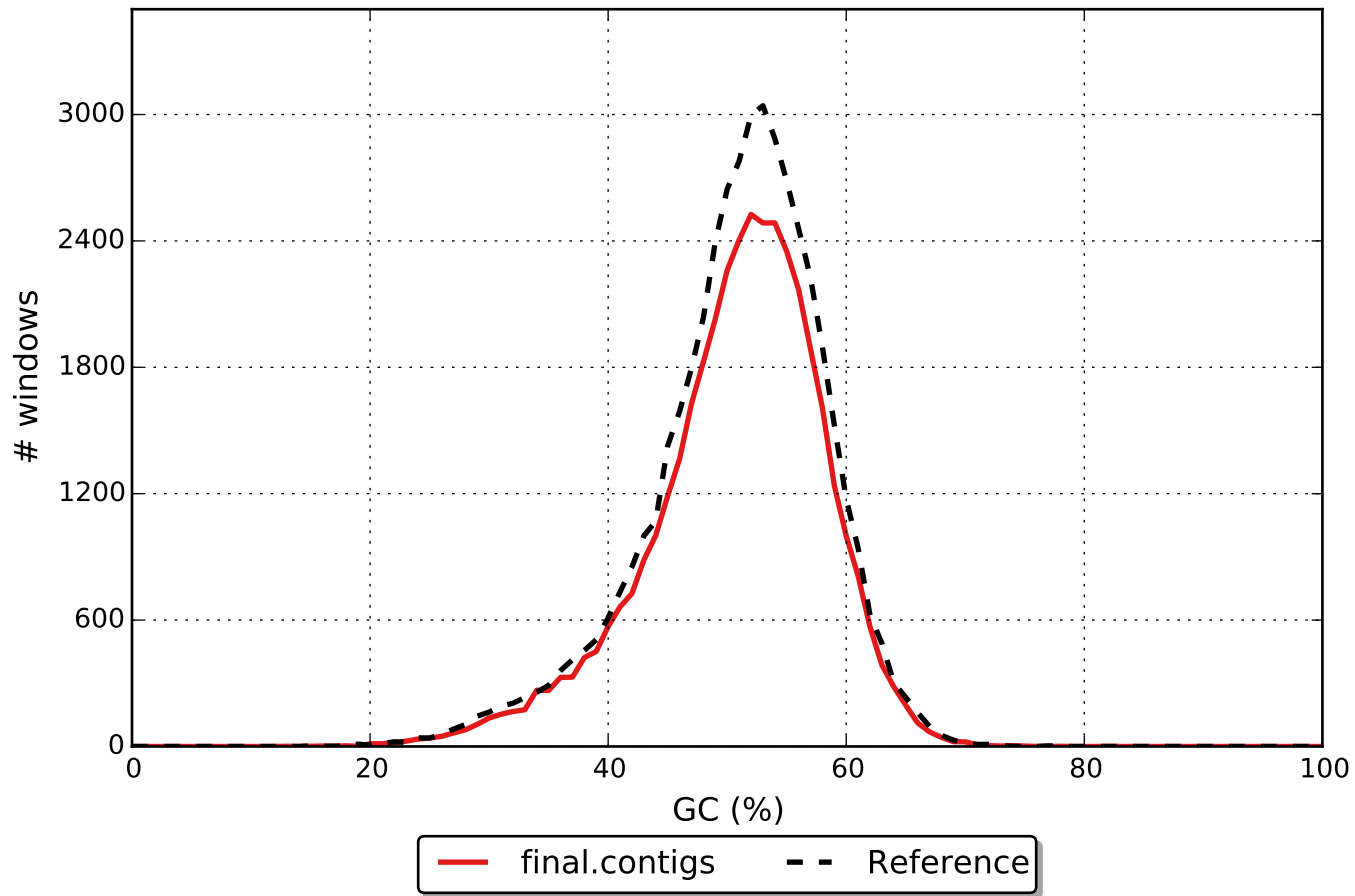
	final.contigs
# fully unaligned contigs	2103
Fully unaligned length	1315603
# partially unaligned contigs	18
# with misassembly	0
# both parts are significant	18
Partially unaligned length	6796
# N's	0



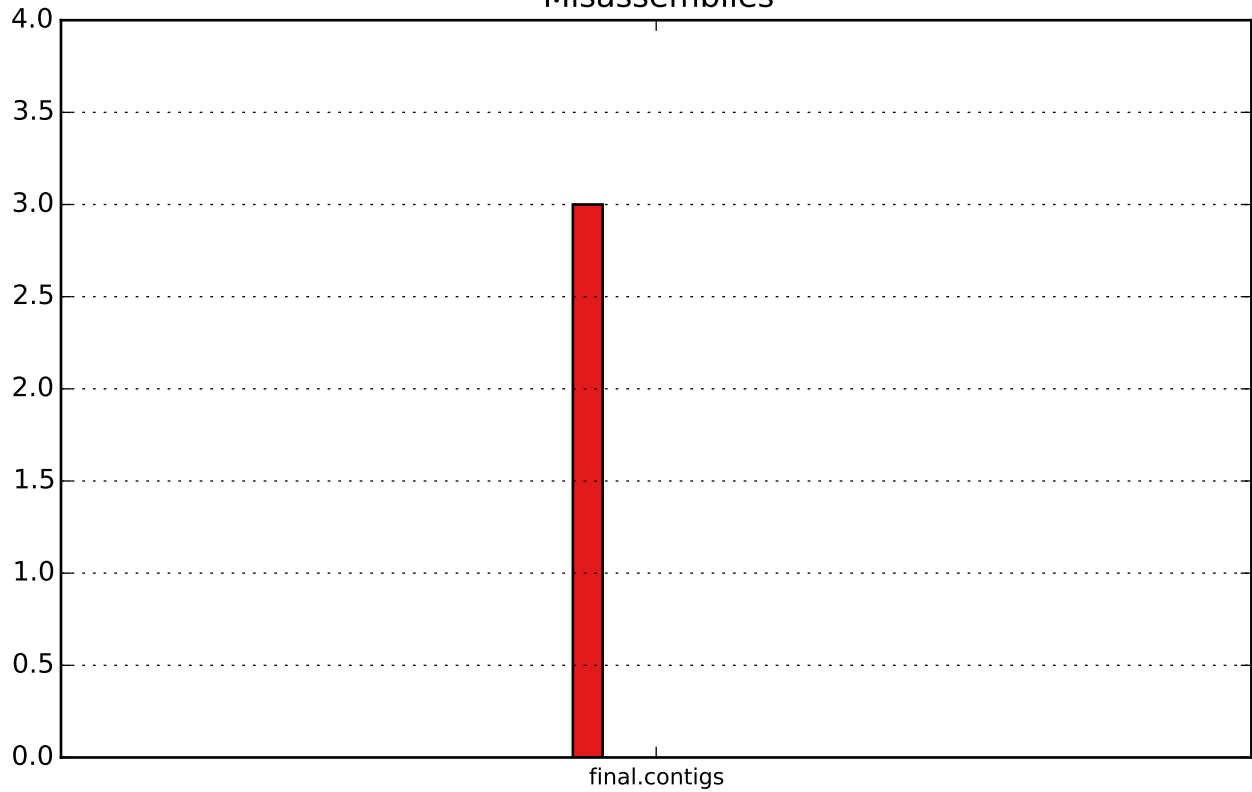




# GC content

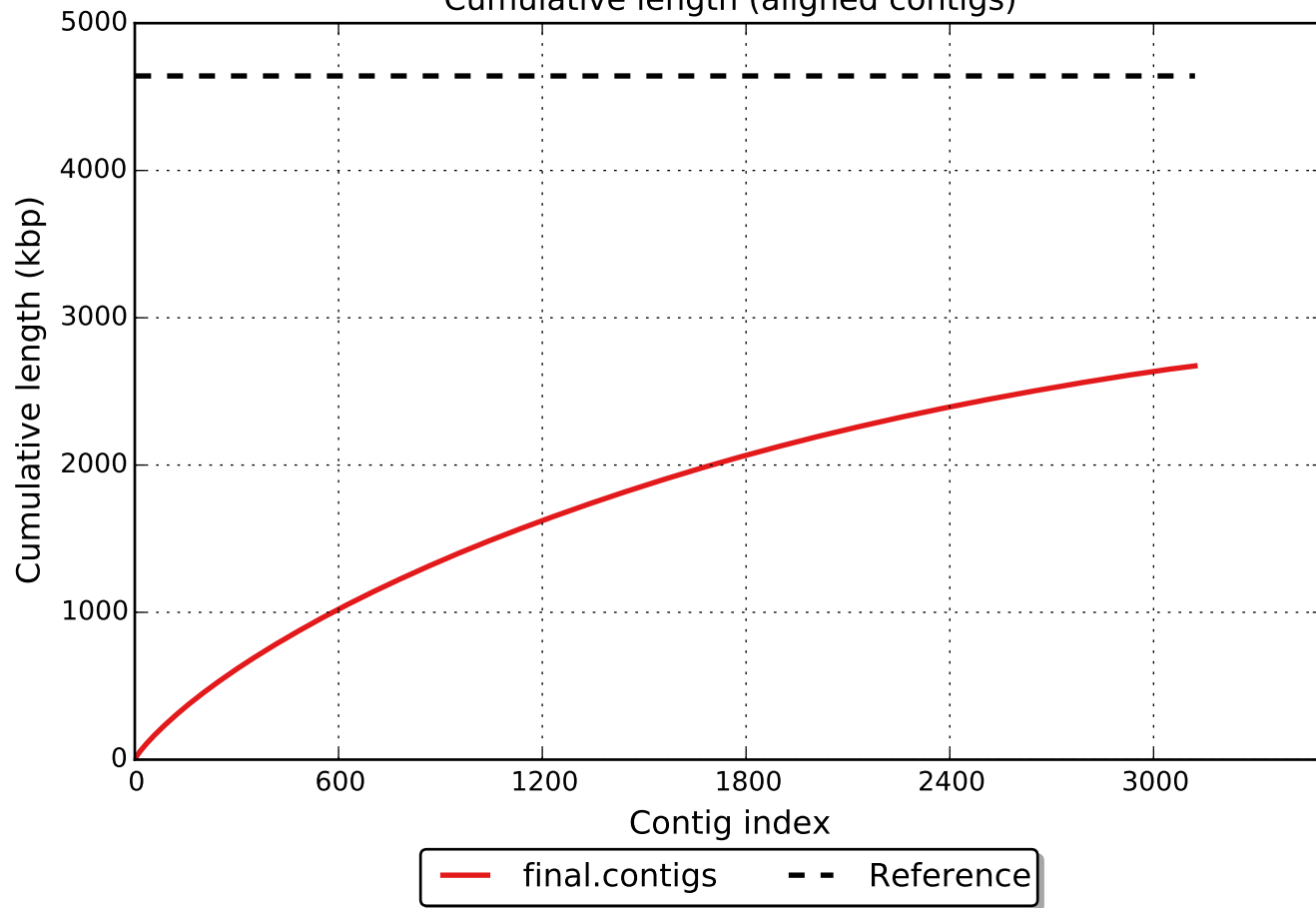


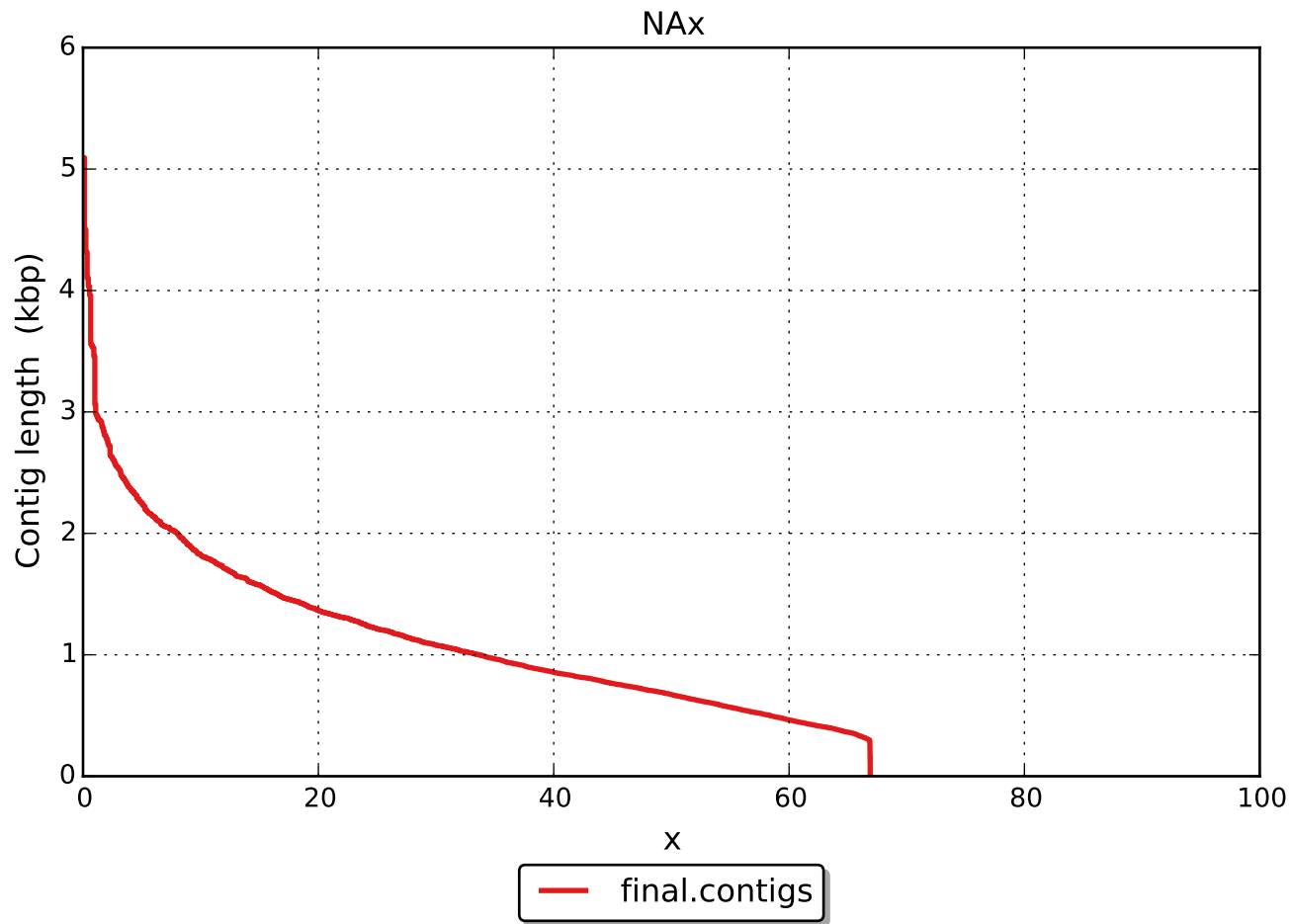
# Misassemblies





Cumulative length (aligned contigs)





NGAx

