

## Report

	final.contigs
# contigs ( $\geq$ 1000 bp)	864
# contigs ( $\geq$ 5000 bp)	29
# contigs ( $\geq$ 10000 bp)	0
# contigs ( $\geq$ 25000 bp)	0
# contigs ( $\geq$ 50000 bp)	0
Total length ( $\geq$ 1000 bp)	1888990
Total length ( $\geq$ 5000 bp)	168714
Total length ( $\geq$ 10000 bp)	0
Total length ( $\geq$ 25000 bp)	0
Total length ( $\geq$ 50000 bp)	0
# contigs	1793
Largest contig	7626
Total length	2509857
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.78
N50	1883
NG50	589
N75	1008
L50	403
LG50	1442
L75	858
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	3619
# local misassemblies	2
# unaligned contigs	0 + 6 part
Unaligned length	783
Genome fraction (%)	52.273
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	406.38
# indels per 100 kbp	0.16
Largest alignment	7626
NA50	1883
NGA50	589
NA75	1008
LA50	403
LGA50	1442
LA75	858

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

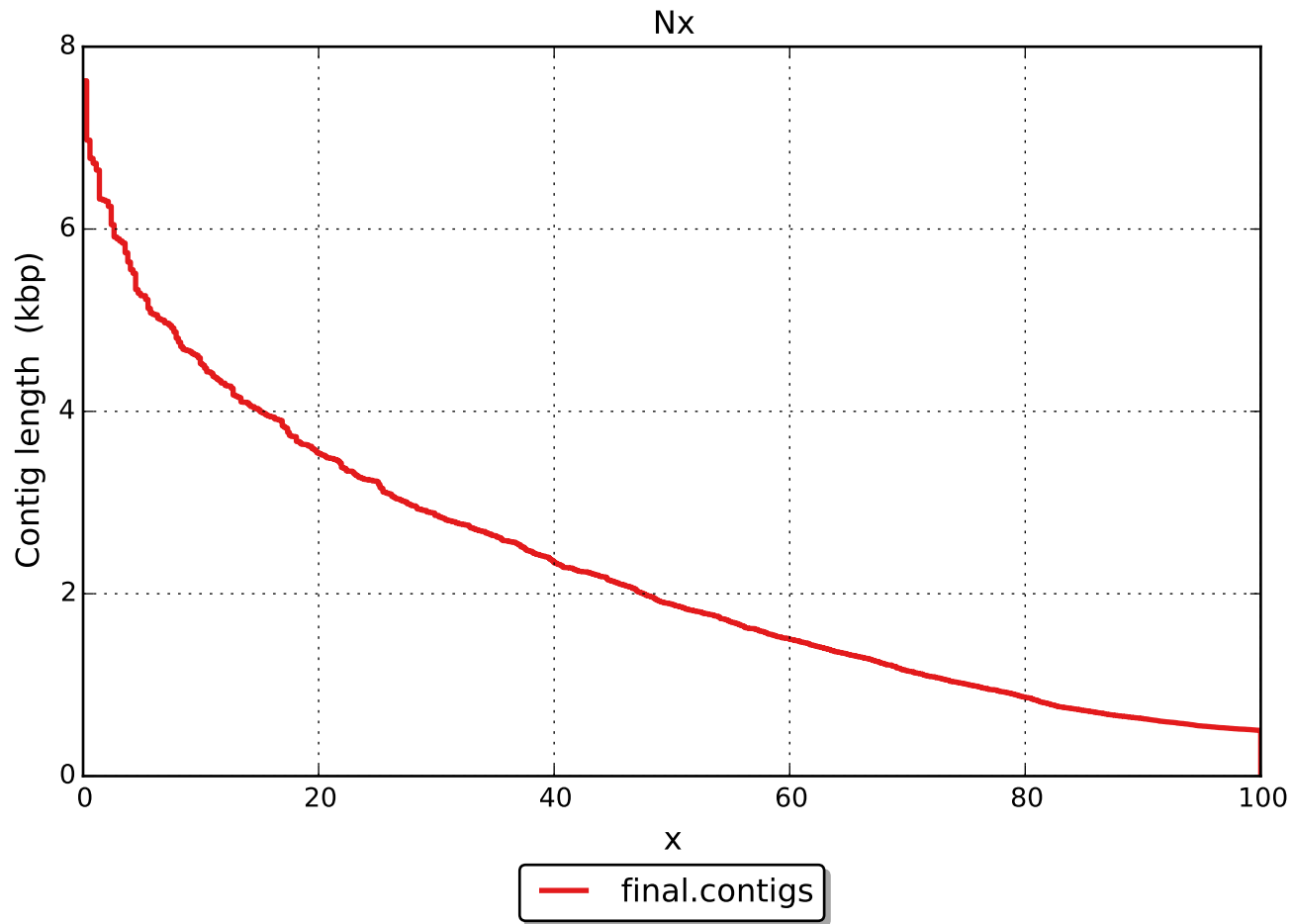
	final.contigs
# misassemblies	3
# relocations	2
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	3619
# local misassemblies	2
# mismatches	9860
# indels	4
# short indels	4
# long indels	0
Indels length	4

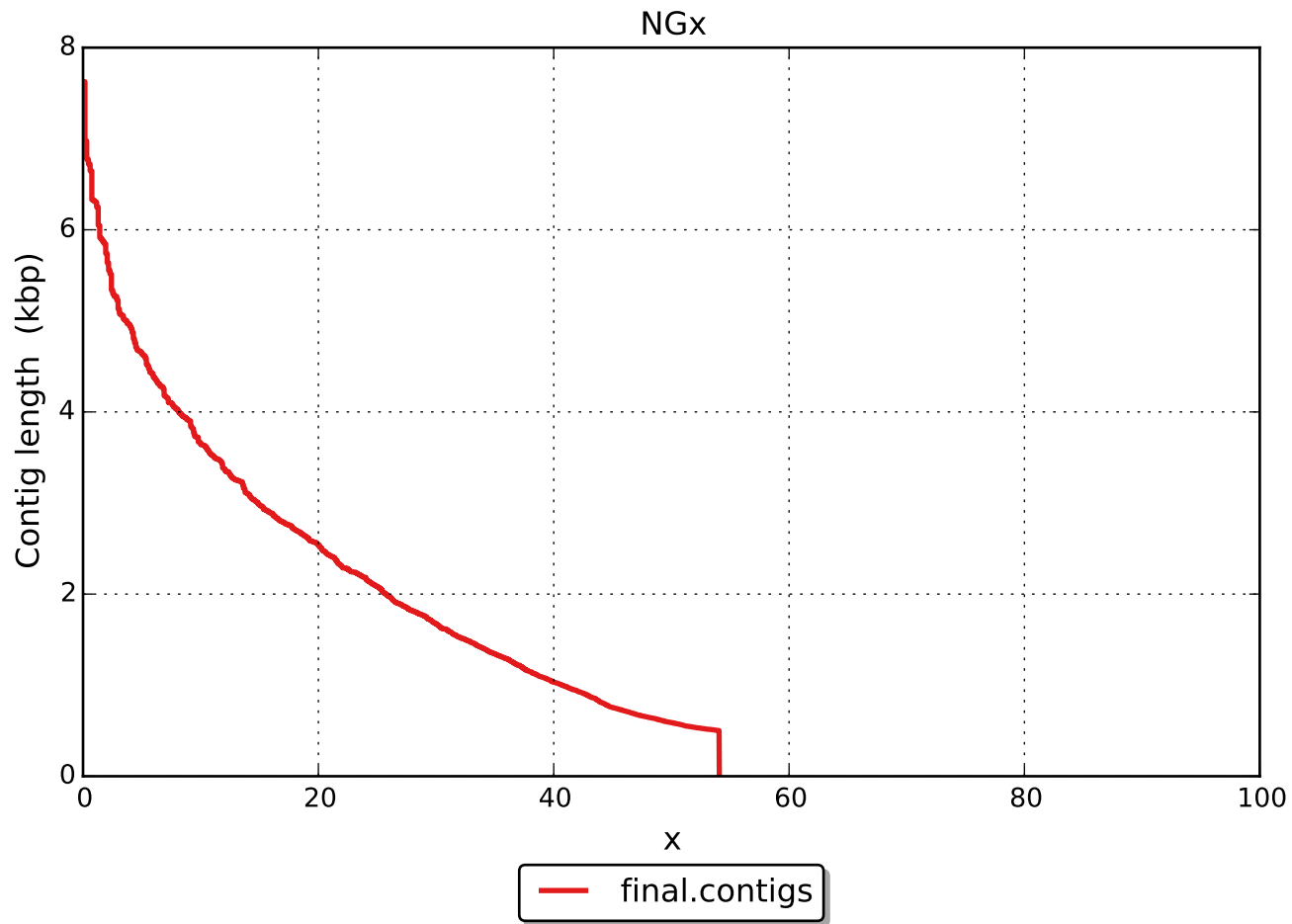
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

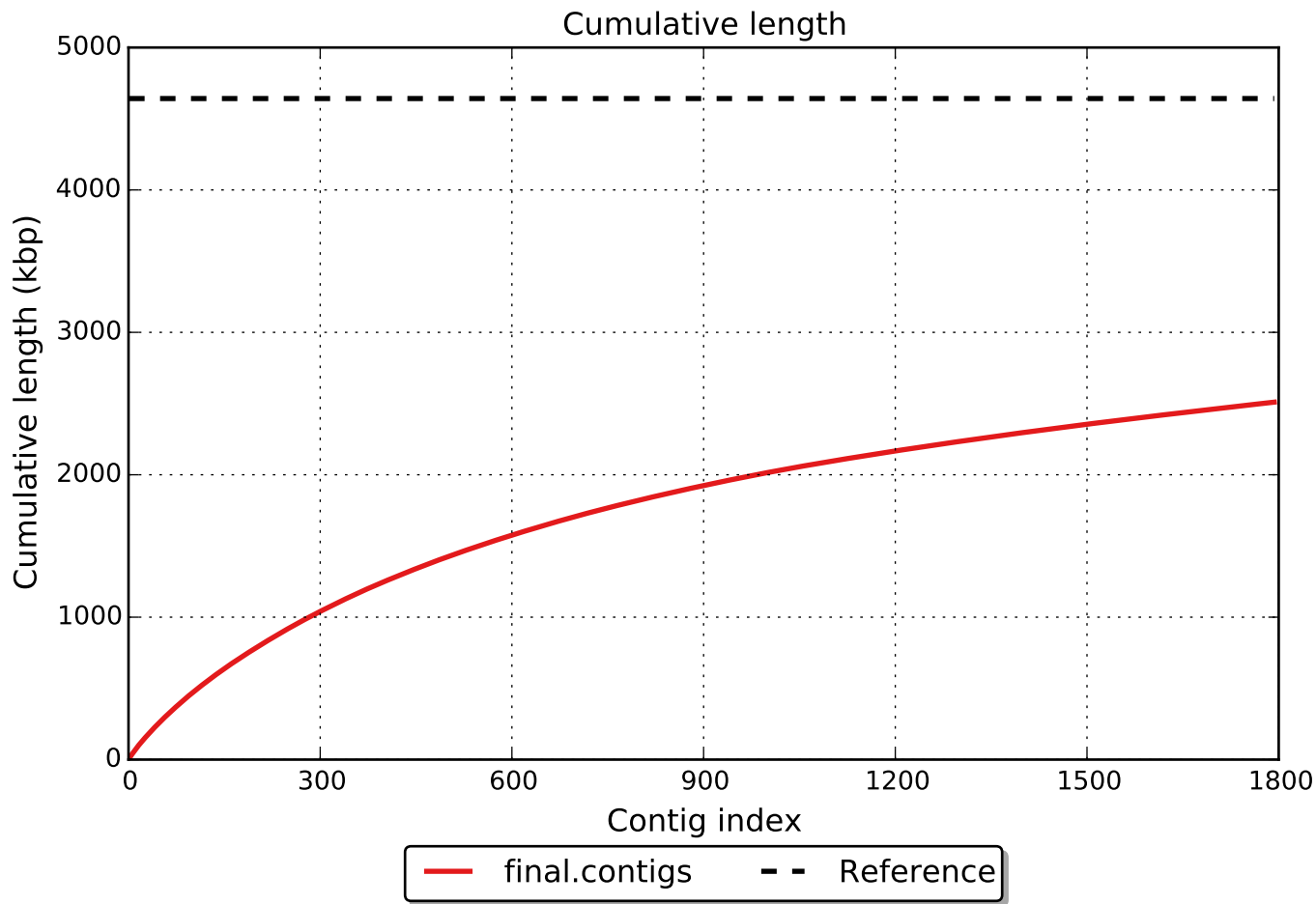
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	0
Partially unaligned length	783
# N's	0

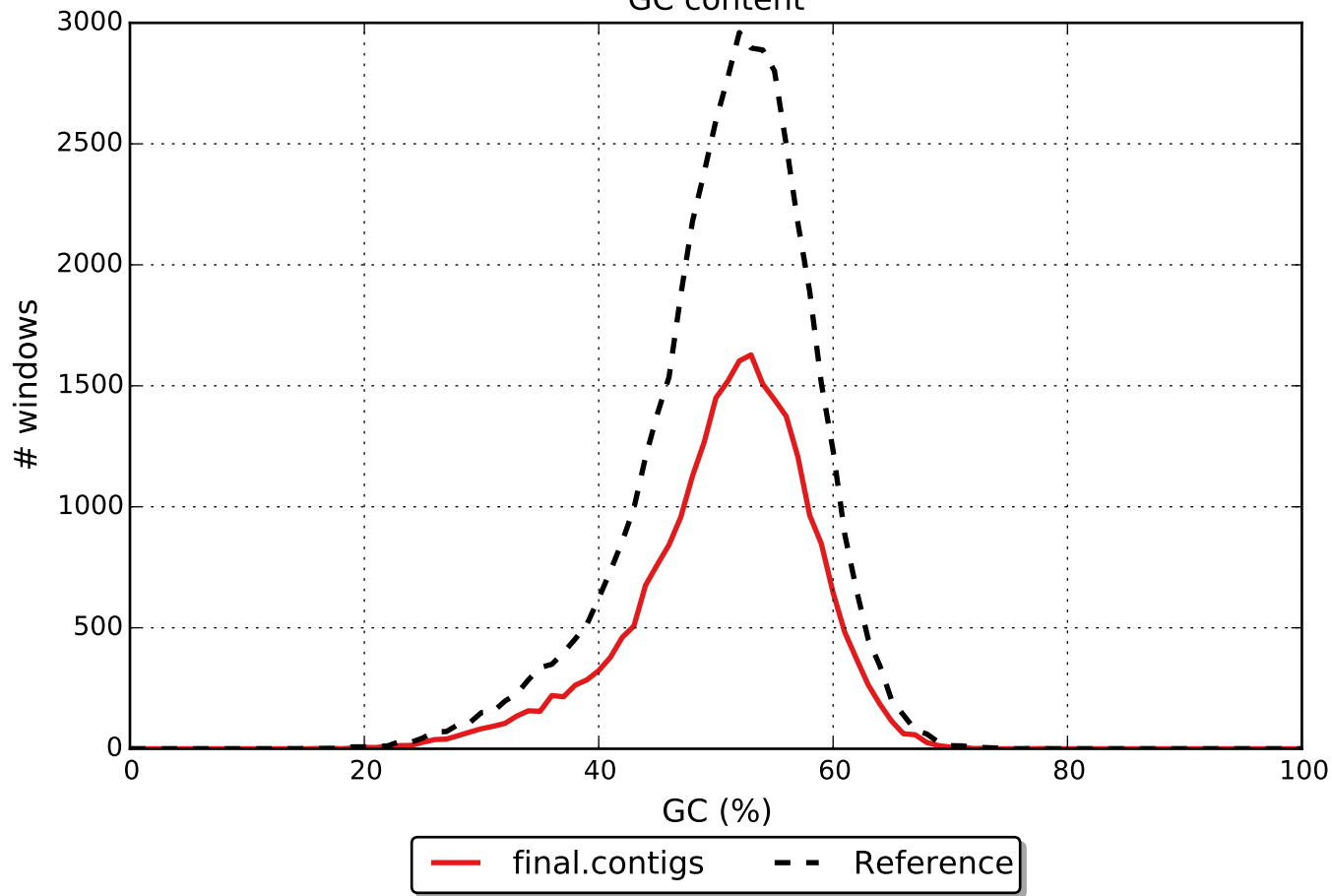
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



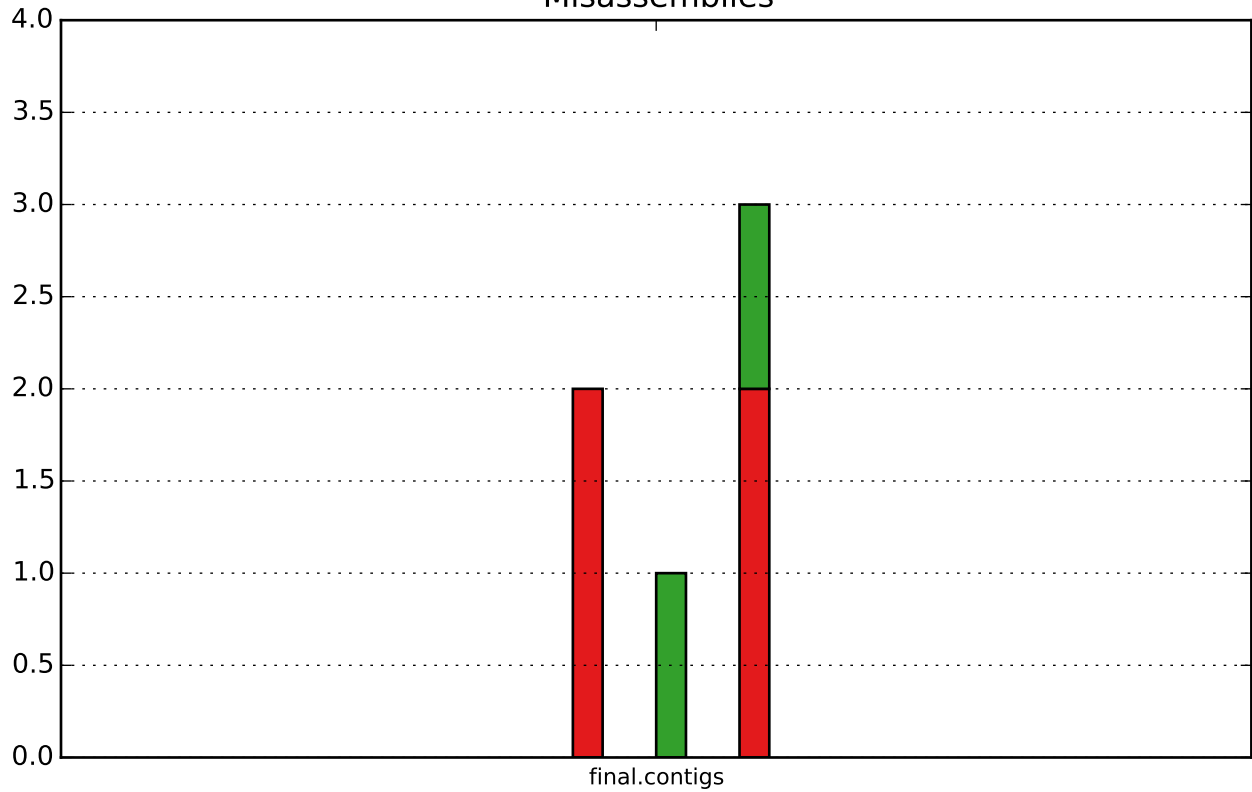




# GC content

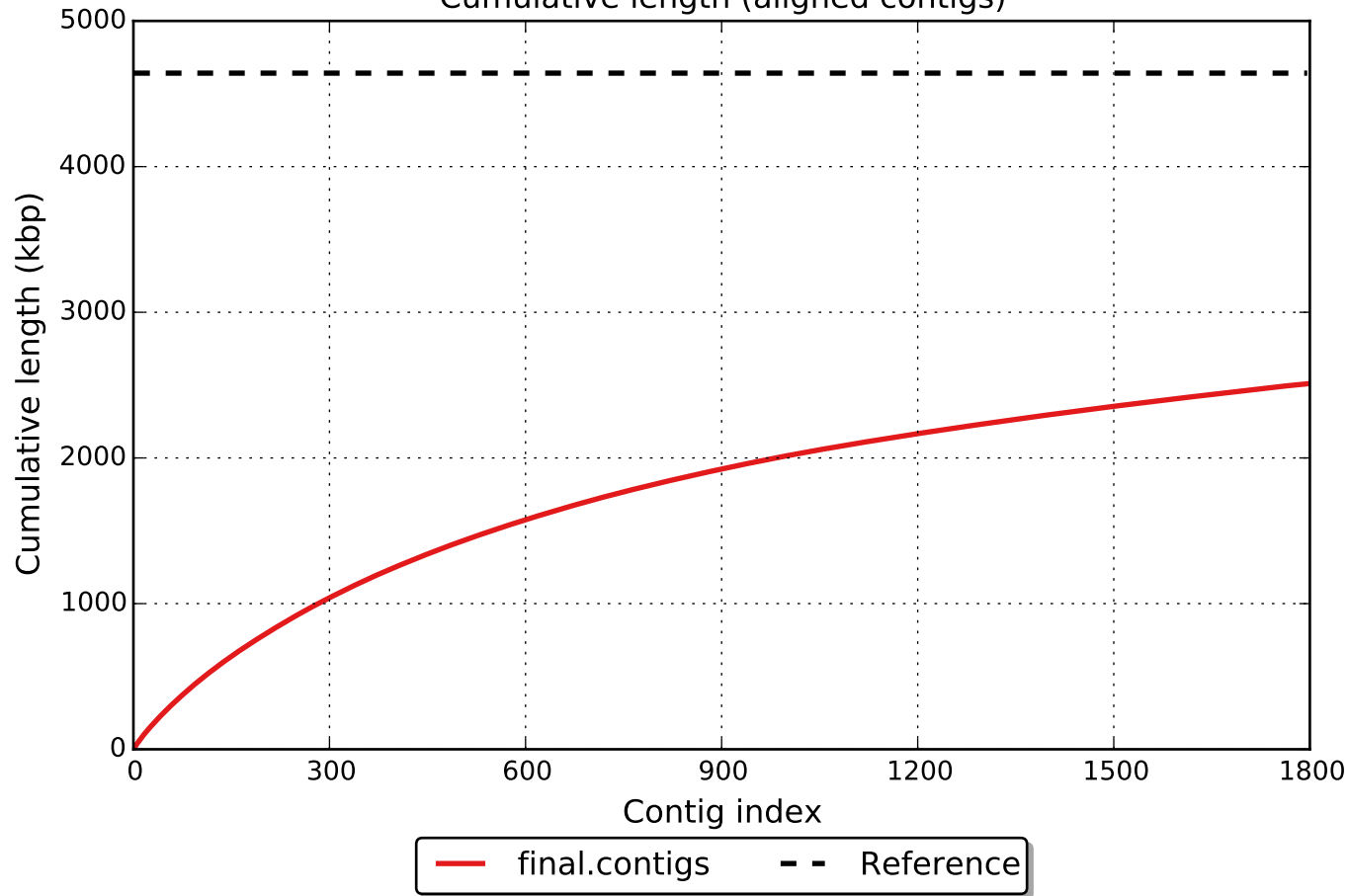


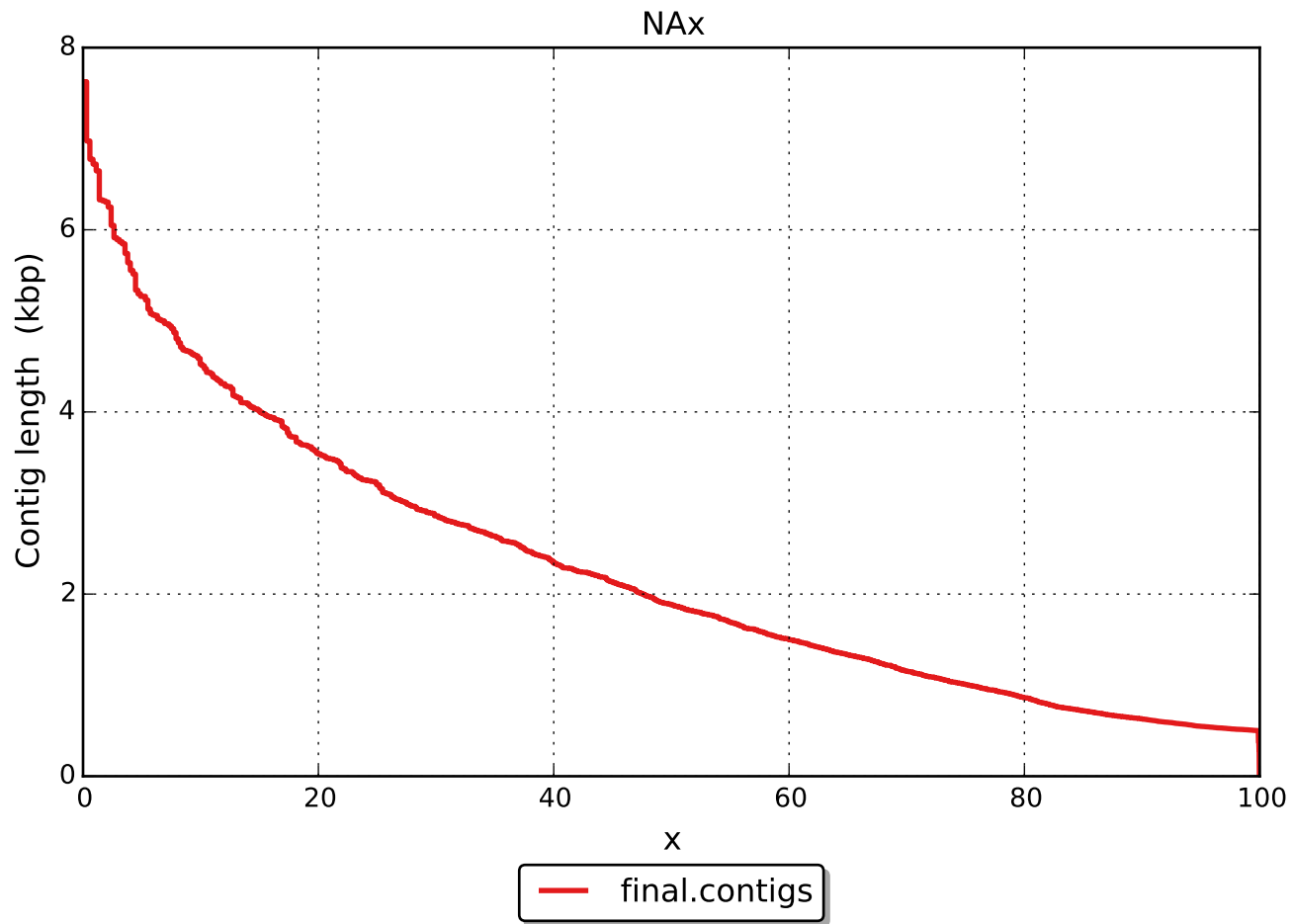
# Misassemblies





Cumulative length (aligned contigs)





NGAx

