

Report

	final.contigs
# contigs (>= 1000 bp)	879
# contigs (>= 5000 bp)	371
# contigs (>= 10000 bp)	106
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4617128
Total length (>= 5000 bp)	3257240
Total length (>= 10000 bp)	1466905
Total length (>= 25000 bp)	56305
Total length (>= 50000 bp)	0
# contigs	989
Largest contig	30268
Total length	4697694
Reference length	4641652
GC (℥)	50.78
Reference GC (℥)	50.78
N50	6828
NG50	6869
N75	4287
NG75	4442
L50	215
LG50	211
L75	429
LG75	419
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.629
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.09
# indels per 100 kbp	0.00
Largest alignment	30268
NA50	6828
NGA50	6869
NA75	4287
NGA75	4442
LA50	215
LGA50	211
LA75	429
LGA75	419

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

## Misassemblies report

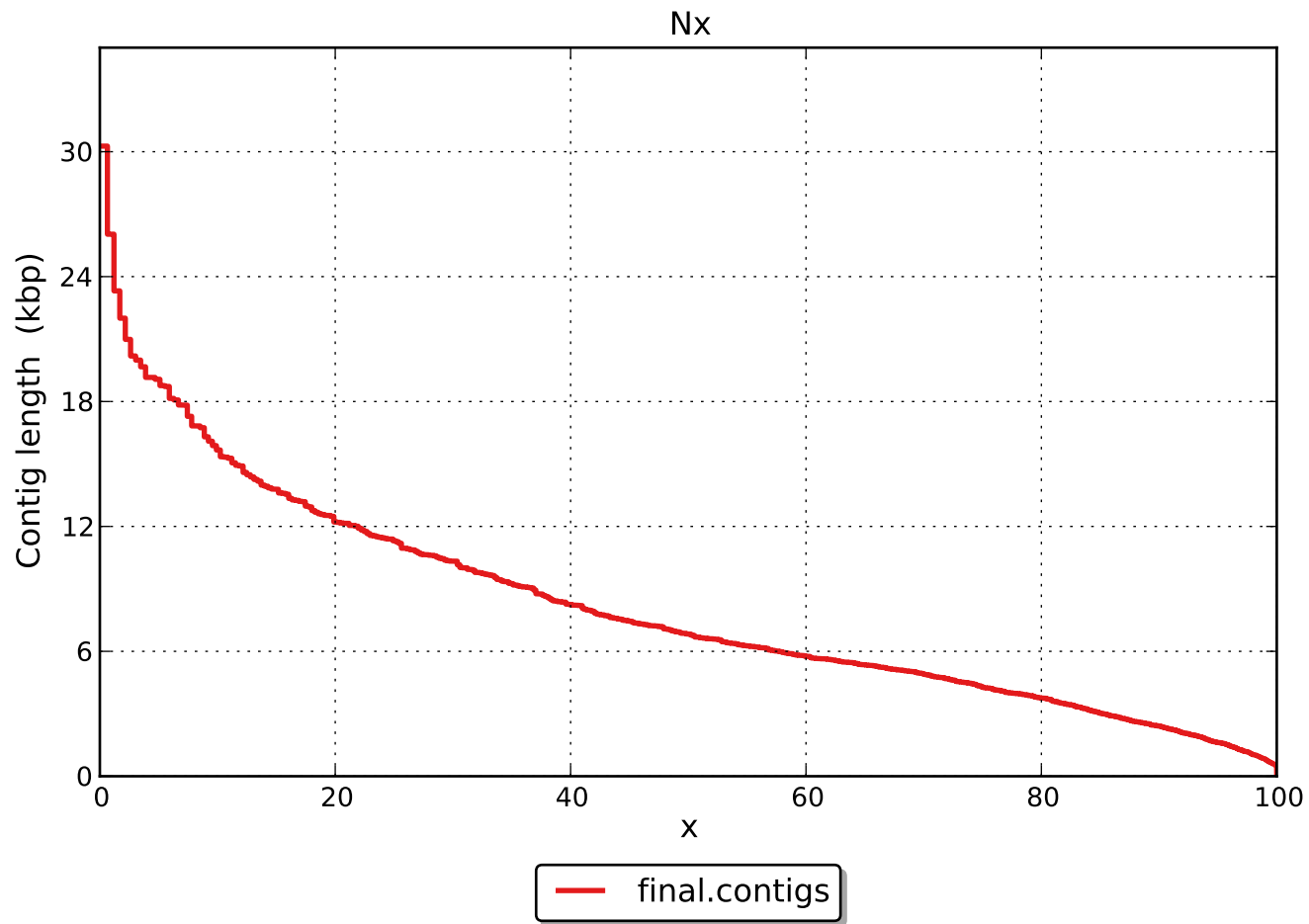
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	4
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

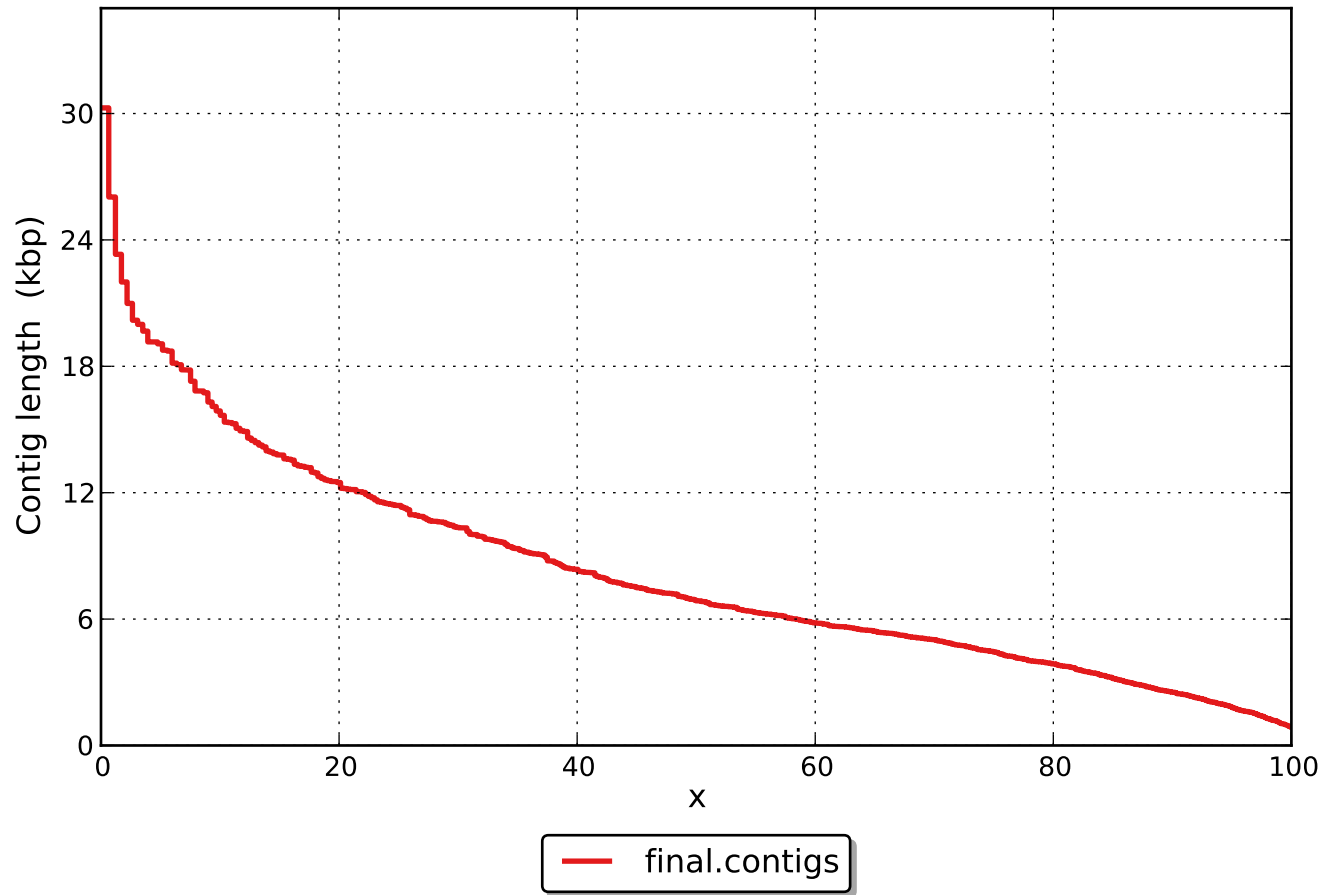
## Unaligned report

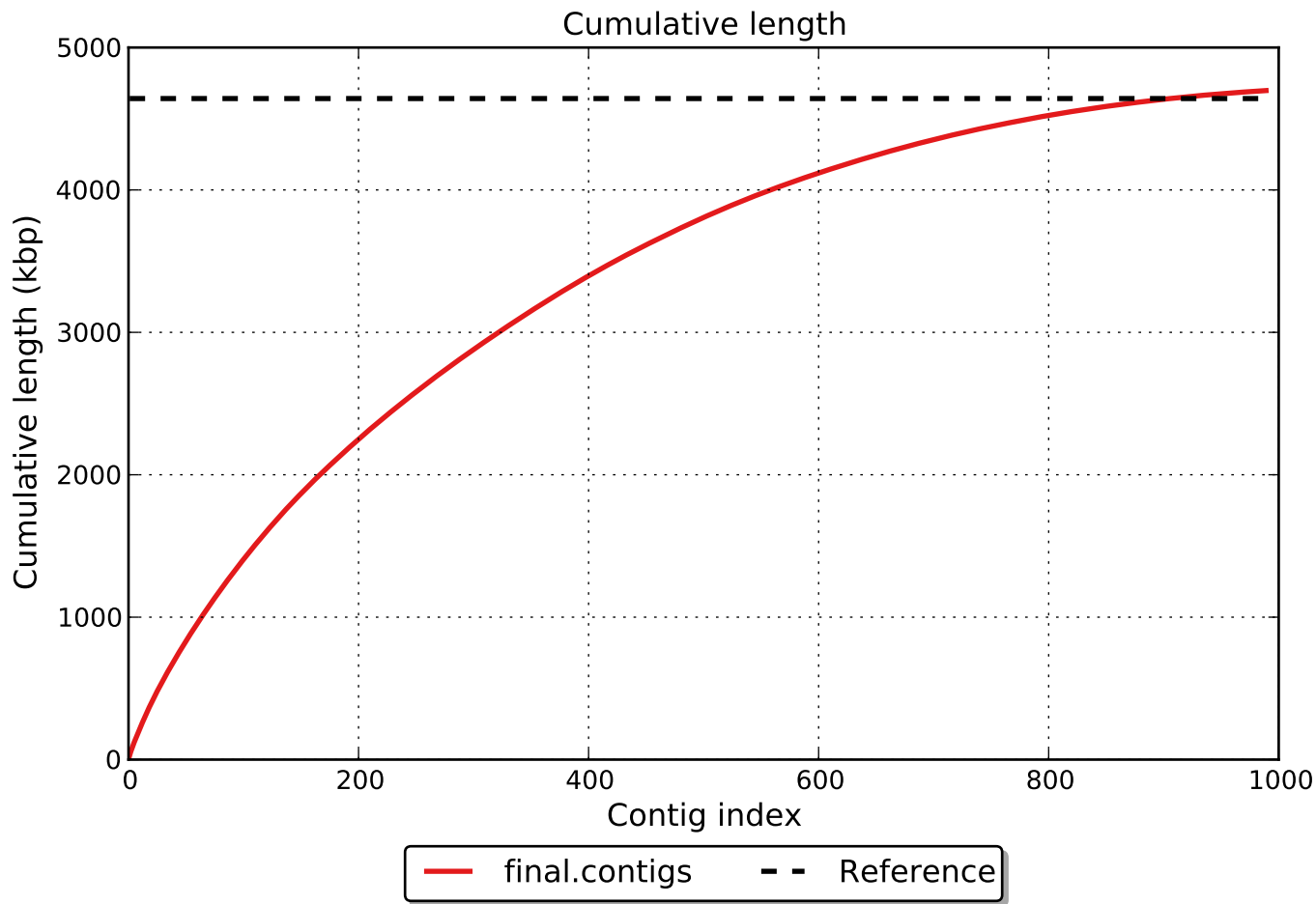
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

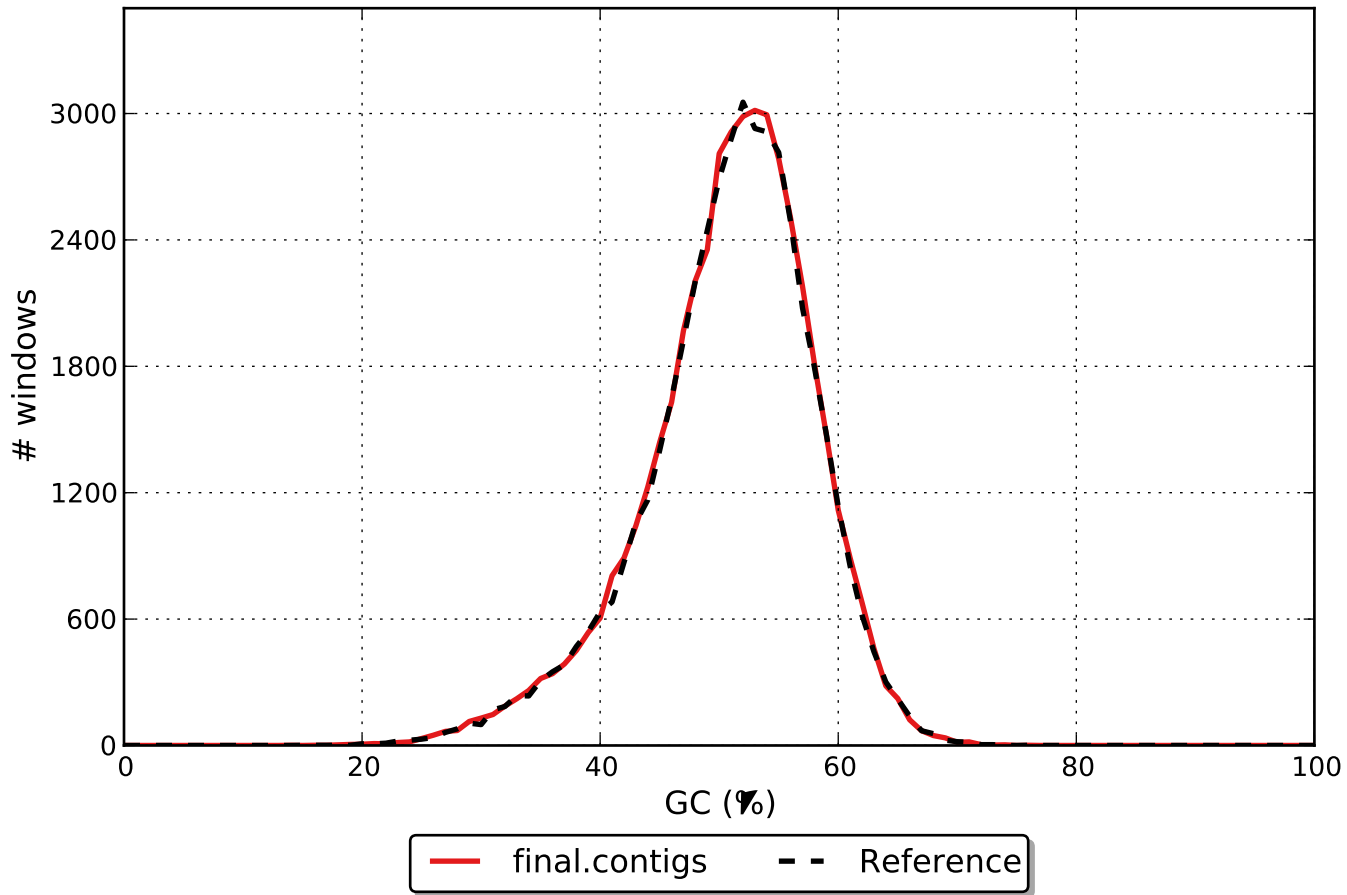


NGx

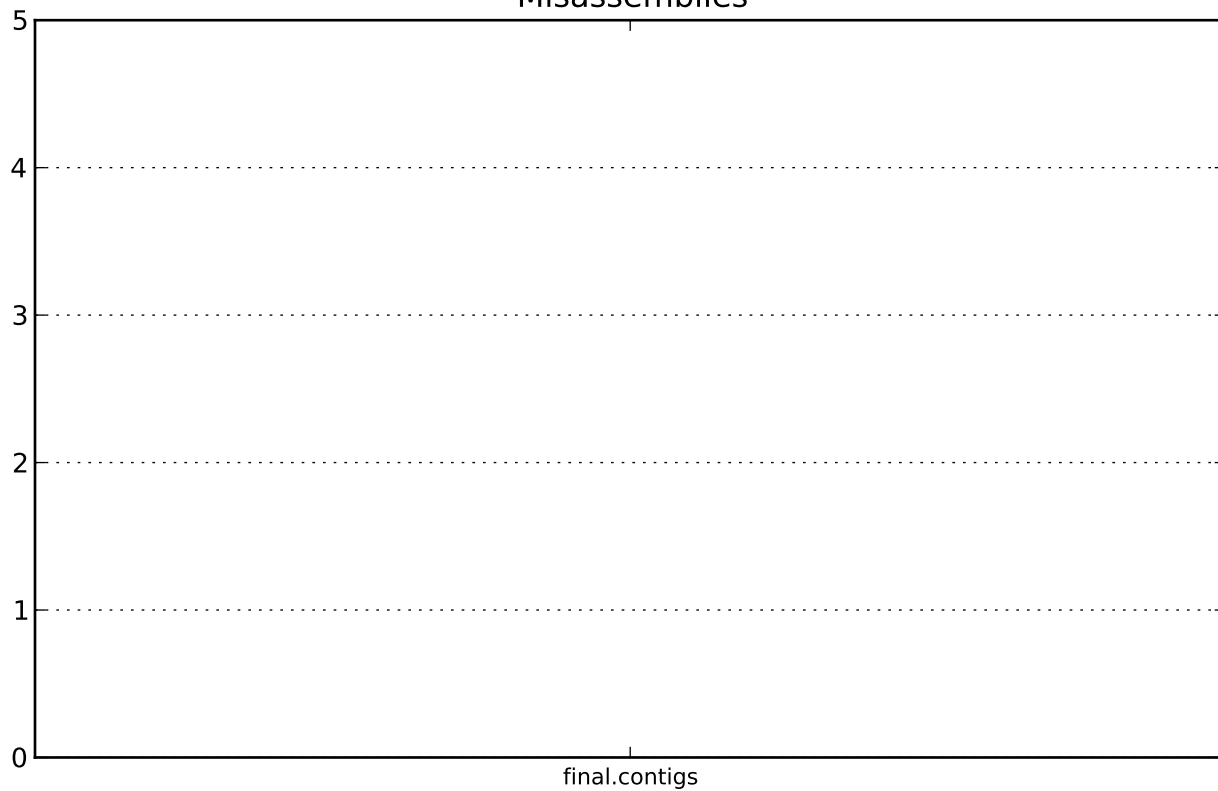




GC content

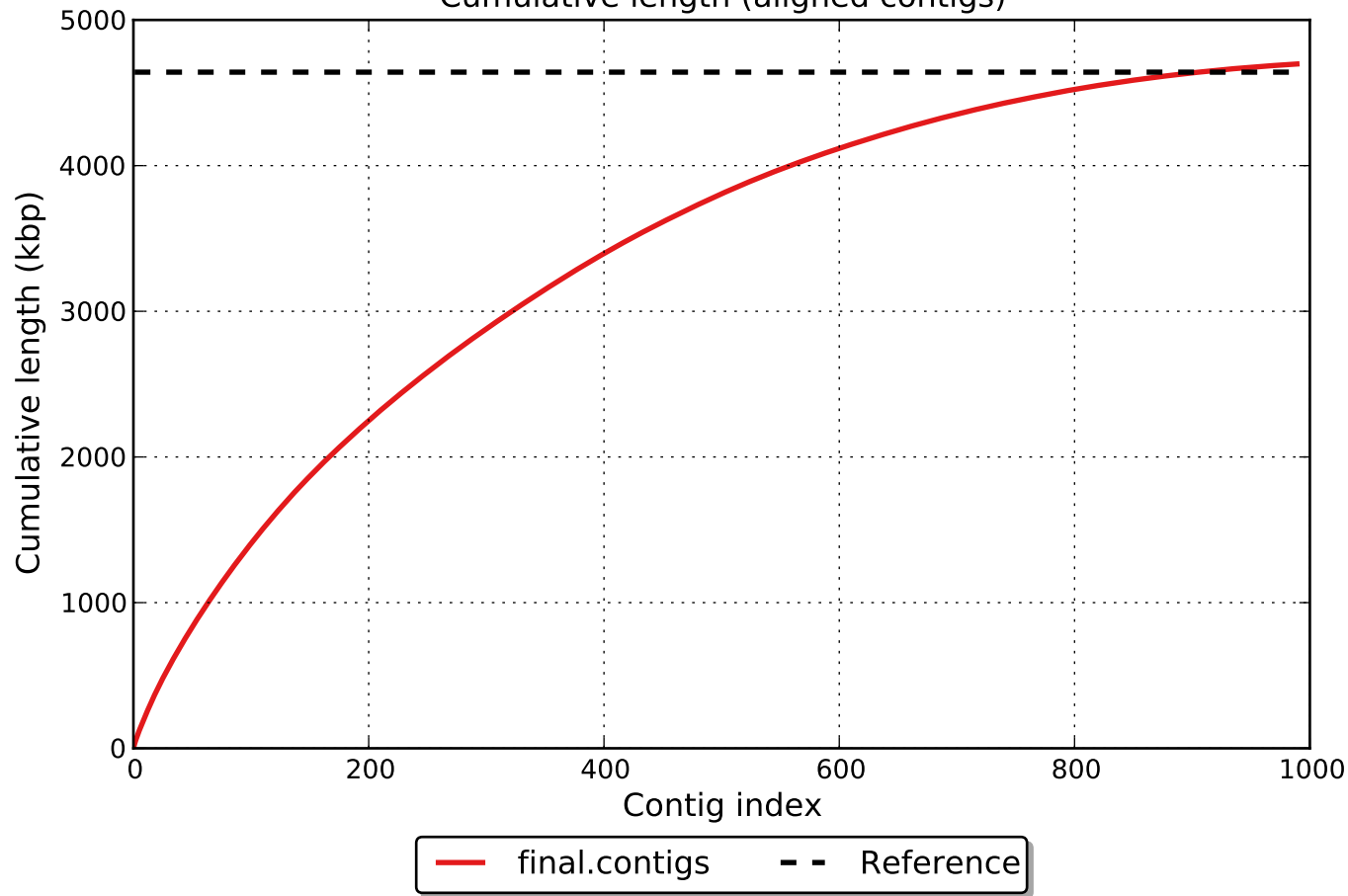


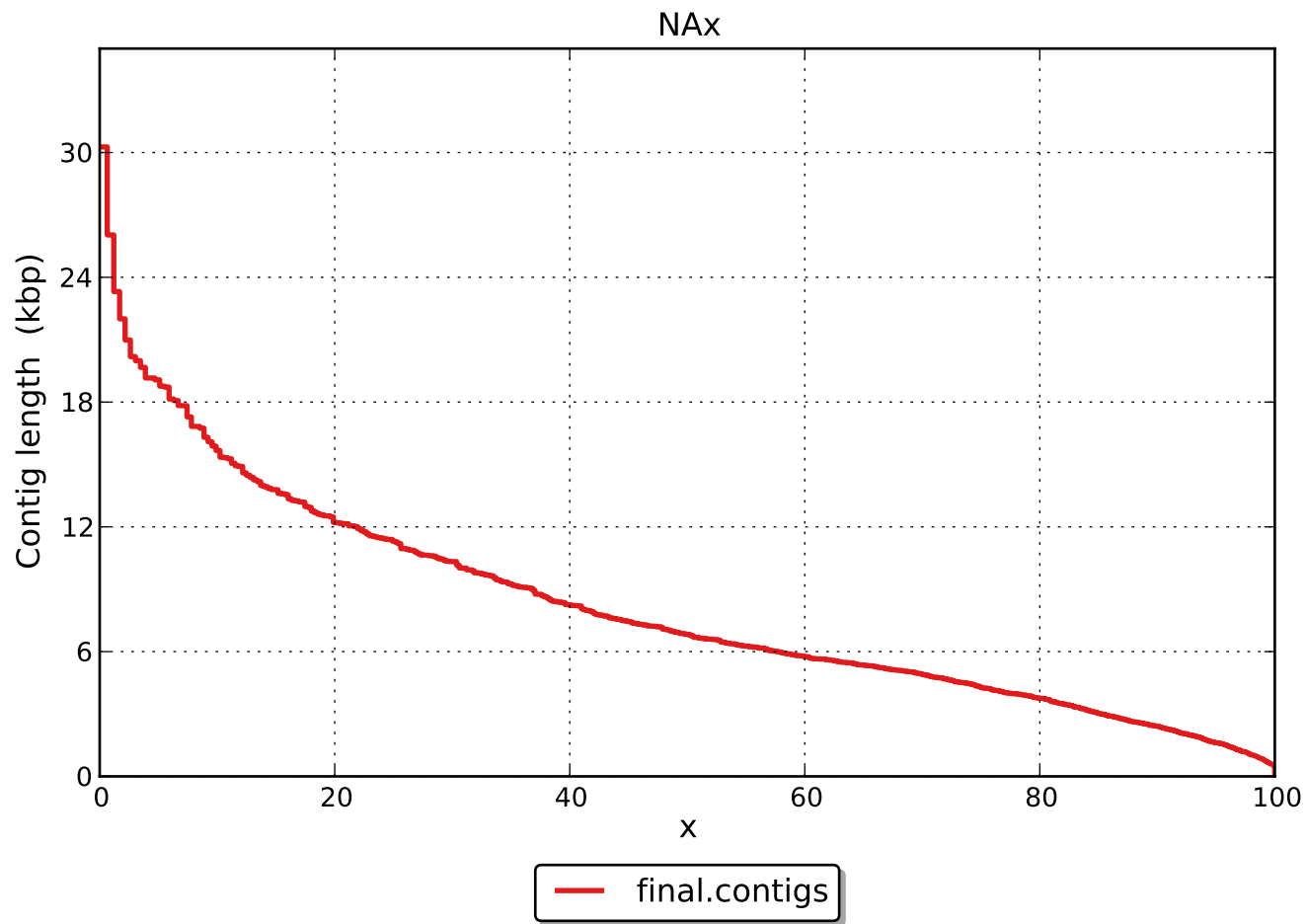
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

