

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	145
# contigs ( $\geq 1000$ bp)	95
# contigs ( $\geq 5000$ bp)	71
# contigs ( $\geq 10000$ bp)	66
# contigs ( $\geq 25000$ bp)	49
# contigs ( $\geq 50000$ bp)	32
Total length ( $\geq 0$ bp)	4574208
Total length ( $\geq 1000$ bp)	4553116
Total length ( $\geq 5000$ bp)	4499119
Total length ( $\geq 10000$ bp)	4463368
Total length ( $\geq 25000$ bp)	4193515
Total length ( $\geq 50000$ bp)	3603122
# contigs	110
Largest contig	327143
Total length	4562904
Reference length	4641652
N50	110840
N75	56864
L50	14
L75	29
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.246
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.26
# indels per 100 kbp	8.79
Largest alignment	327143
NA50	110840
NA75	56864
LA50	14
LA75	29

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	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# mismatches	2611
# indels	401
# short indels	400
# long indels	1
Indels length	667

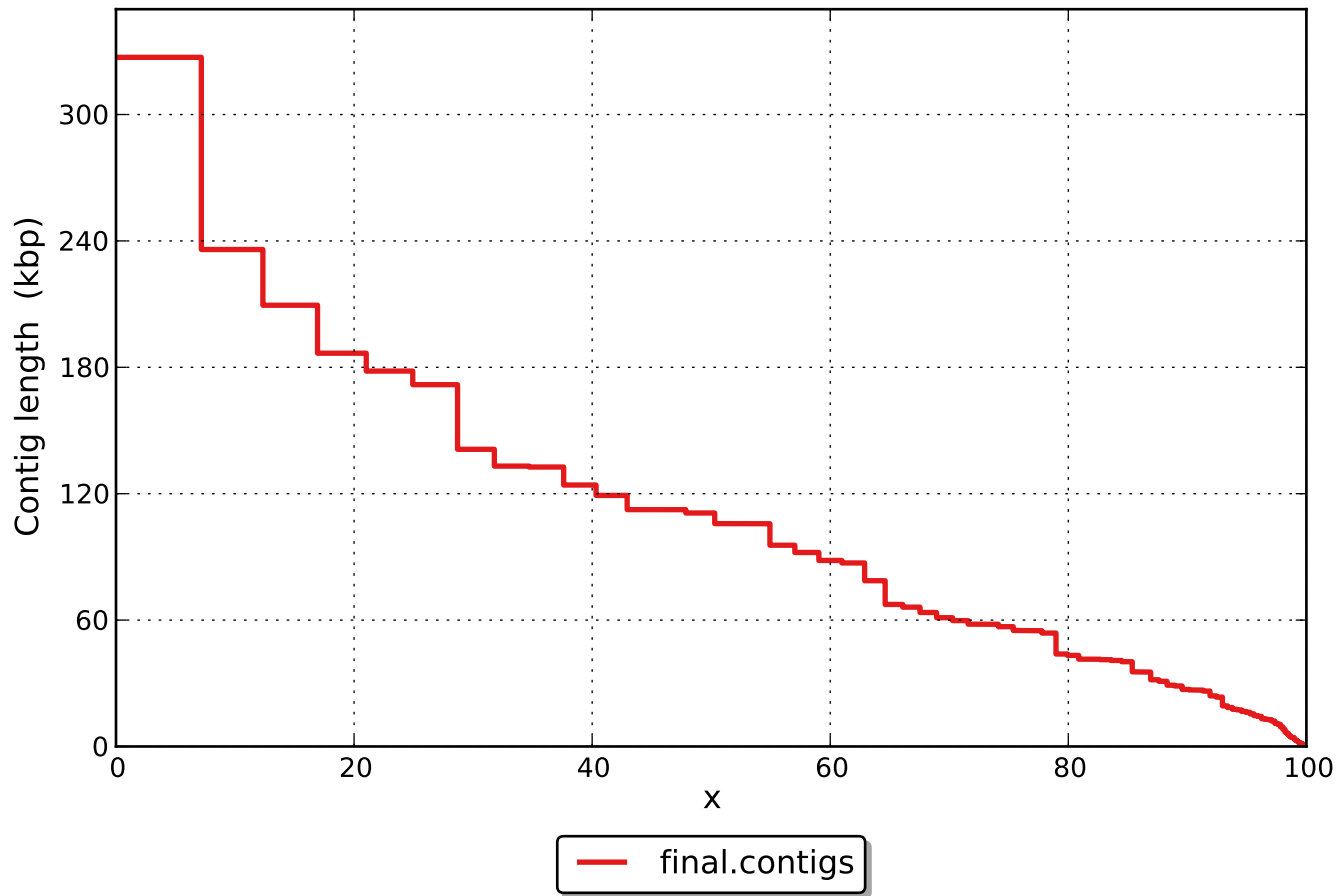
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

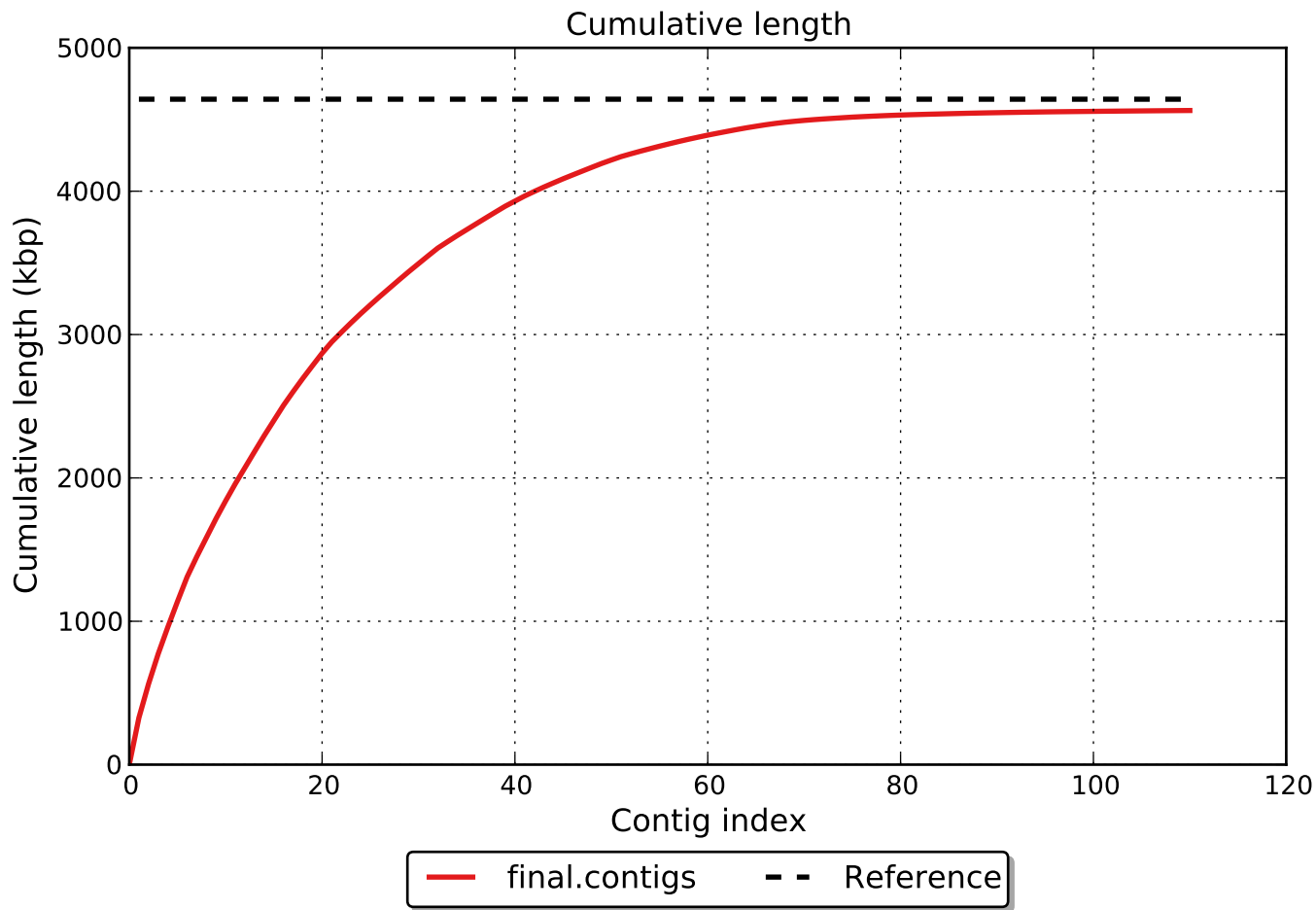
## Unaligned report

	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).

Nx

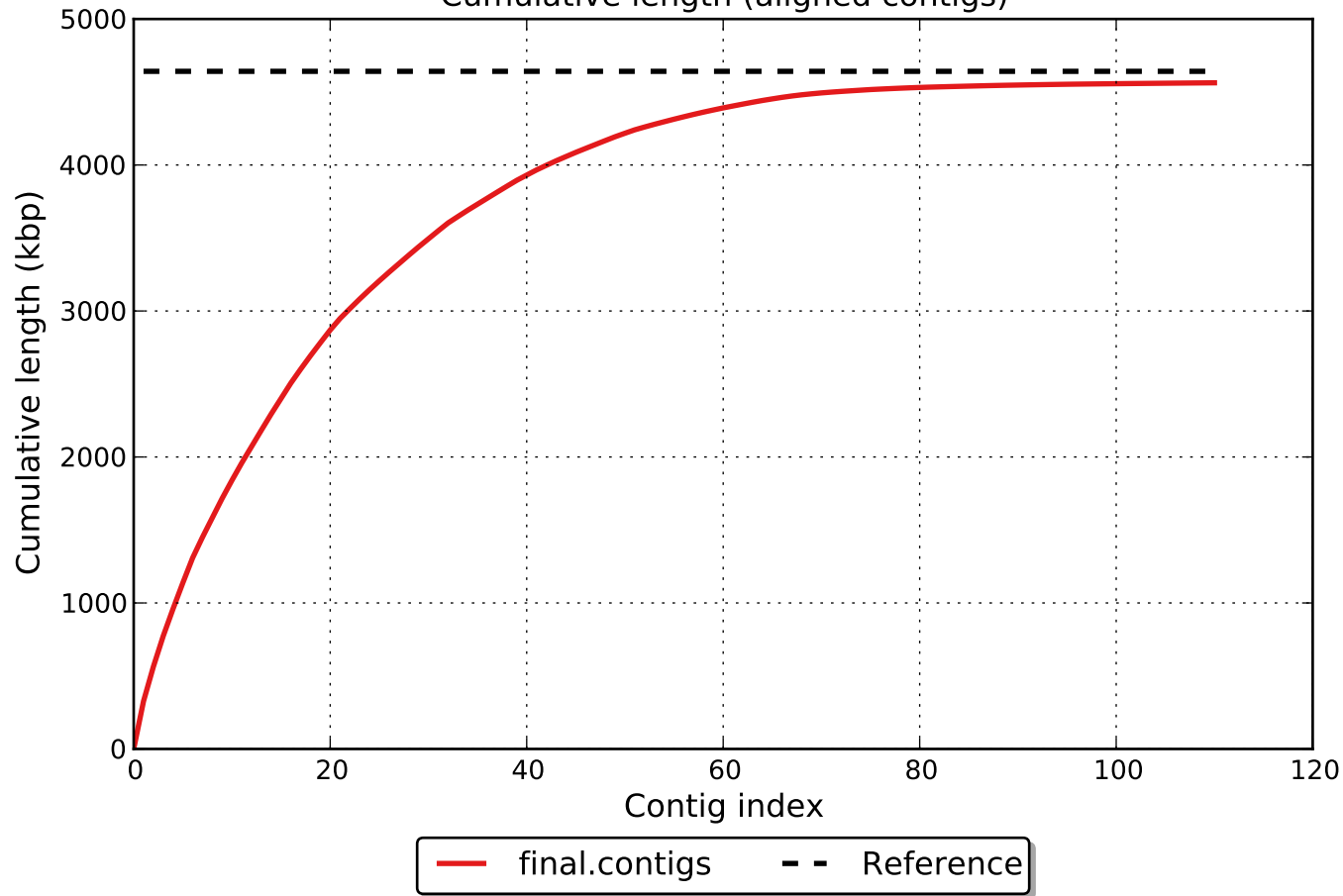




# Misassemblies



Cumulative length (aligned contigs)



NAx

