

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	128
# contigs ( $\geq 1000$ bp)	95
# contigs ( $\geq 5000$ bp)	70
# contigs ( $\geq 10000$ bp)	64
# contigs ( $\geq 25000$ bp)	52
# contigs ( $\geq 50000$ bp)	33
Total length ( $\geq 0$ bp)	4567938
Total length ( $\geq 1000$ bp)	4554504
Total length ( $\geq 5000$ bp)	4497649
Total length ( $\geq 10000$ bp)	4453778
Total length ( $\geq 25000$ bp)	4280978
Total length ( $\geq 50000$ bp)	3616607
# contigs	105
Largest contig	327049
Total length	4561016
Reference length	4641652
N50	97563
N75	56868
L50	14
L75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	13
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.209
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	59.23
# indels per 100 kbp	9.10
Largest alignment	327049
NA50	97563
NA75	56868
LA50	14
LA75	30

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	13
# mismatches	2700
# indels	415
# short indels	414
# long indels	1
Indels length	689

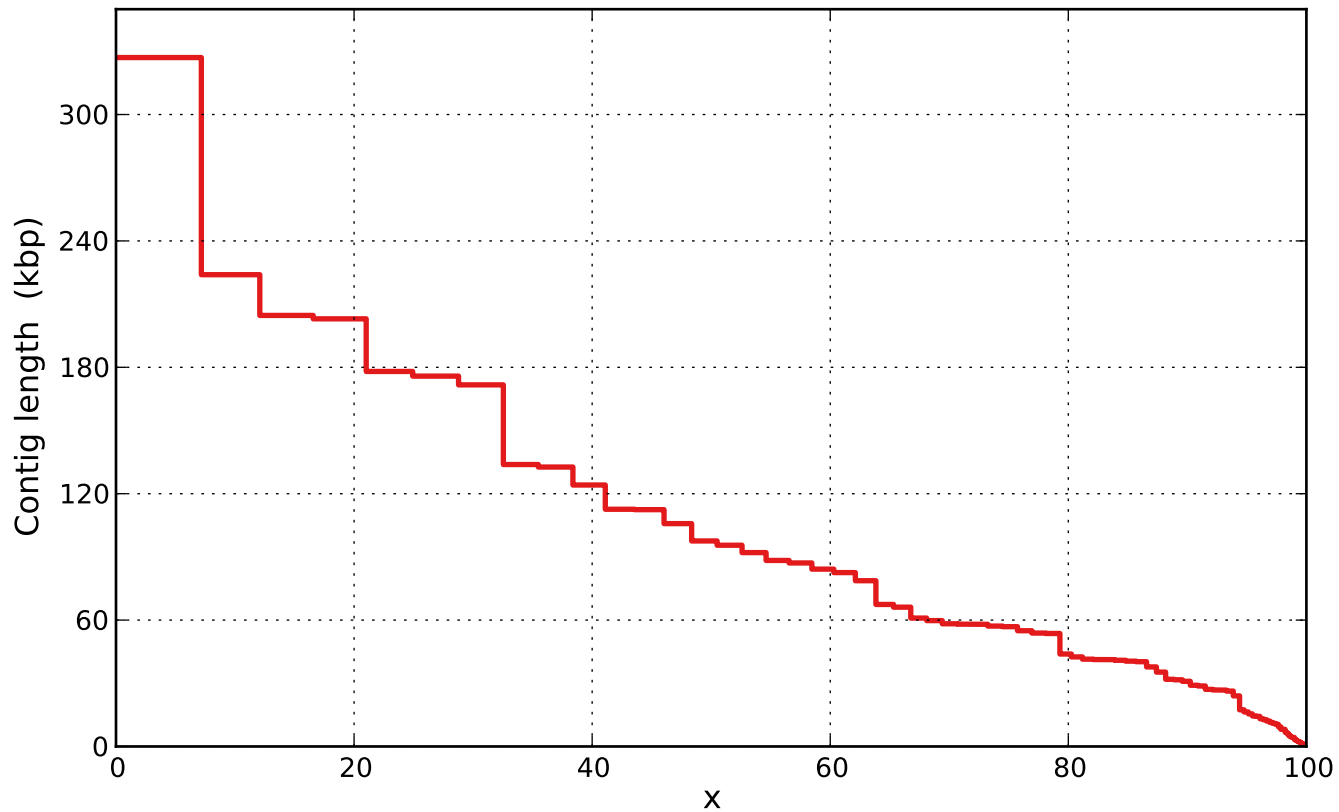
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

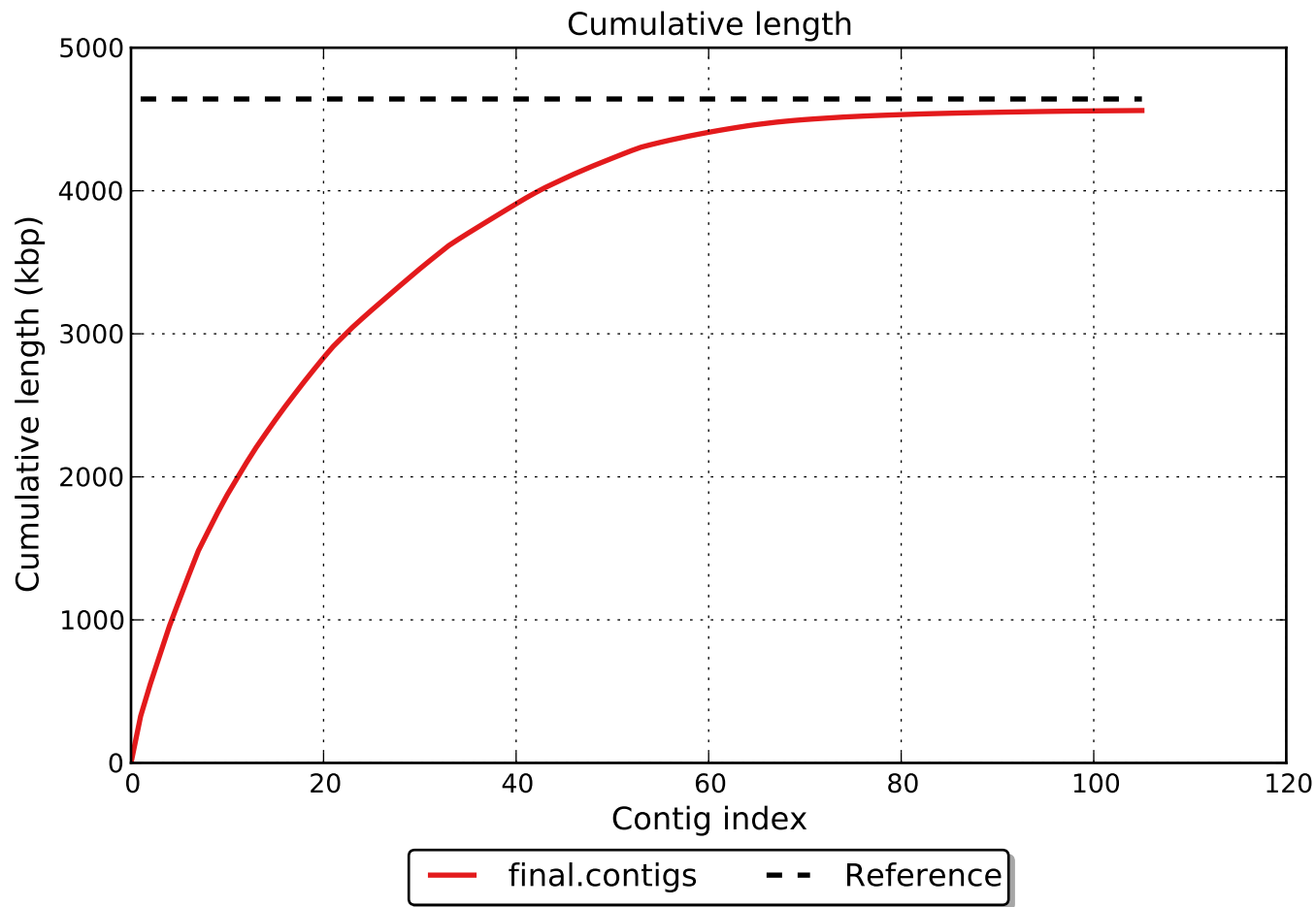
## Unaligned report

	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

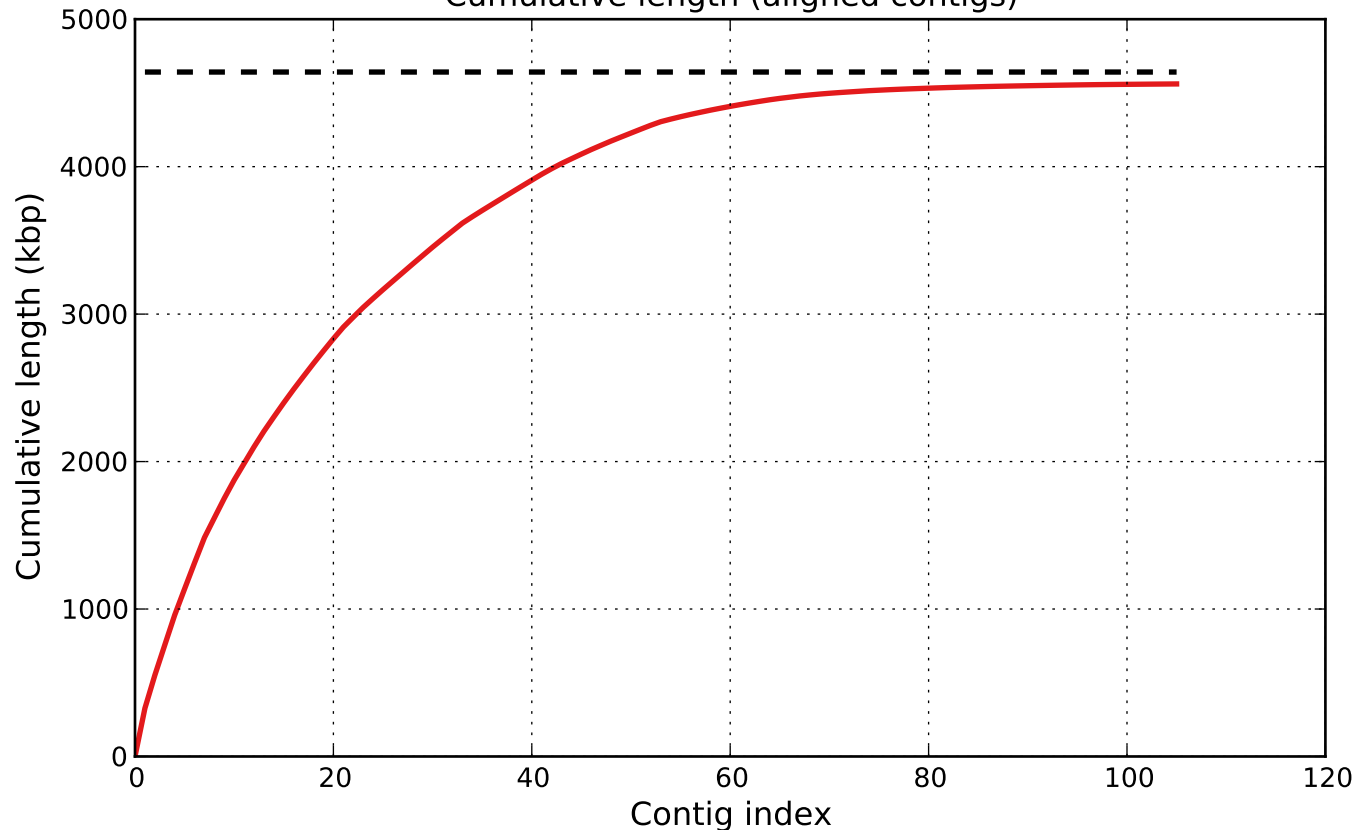




# Misassemblies



Cumulative length (aligned contigs)



NAx

