

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	132
# contigs ( $\geq 1000$ bp)	95
# contigs ( $\geq 5000$ bp)	70
# contigs ( $\geq 10000$ bp)	64
# contigs ( $\geq 25000$ bp)	51
# contigs ( $\geq 50000$ bp)	31
Total length ( $\geq 0$ bp)	4571426
Total length ( $\geq 1000$ bp)	4554255
Total length ( $\geq 5000$ bp)	4499164
Total length ( $\geq 10000$ bp)	4455529
Total length ( $\geq 25000$ bp)	4259867
Total length ( $\geq 50000$ bp)	3552688
# contigs	111
Largest contig	327151
Total length	4564918
Reference length	4641652
N50	111794
N75	54946
L50	14
L75	29
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	12
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.277
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.98
# indels per 100 kbp	0.09
Largest alignment	327151
NA50	111794
NA75	54946
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	12
# mismatches	136
# indels	4
# short indels	3
# long indels	1
Indels length	89

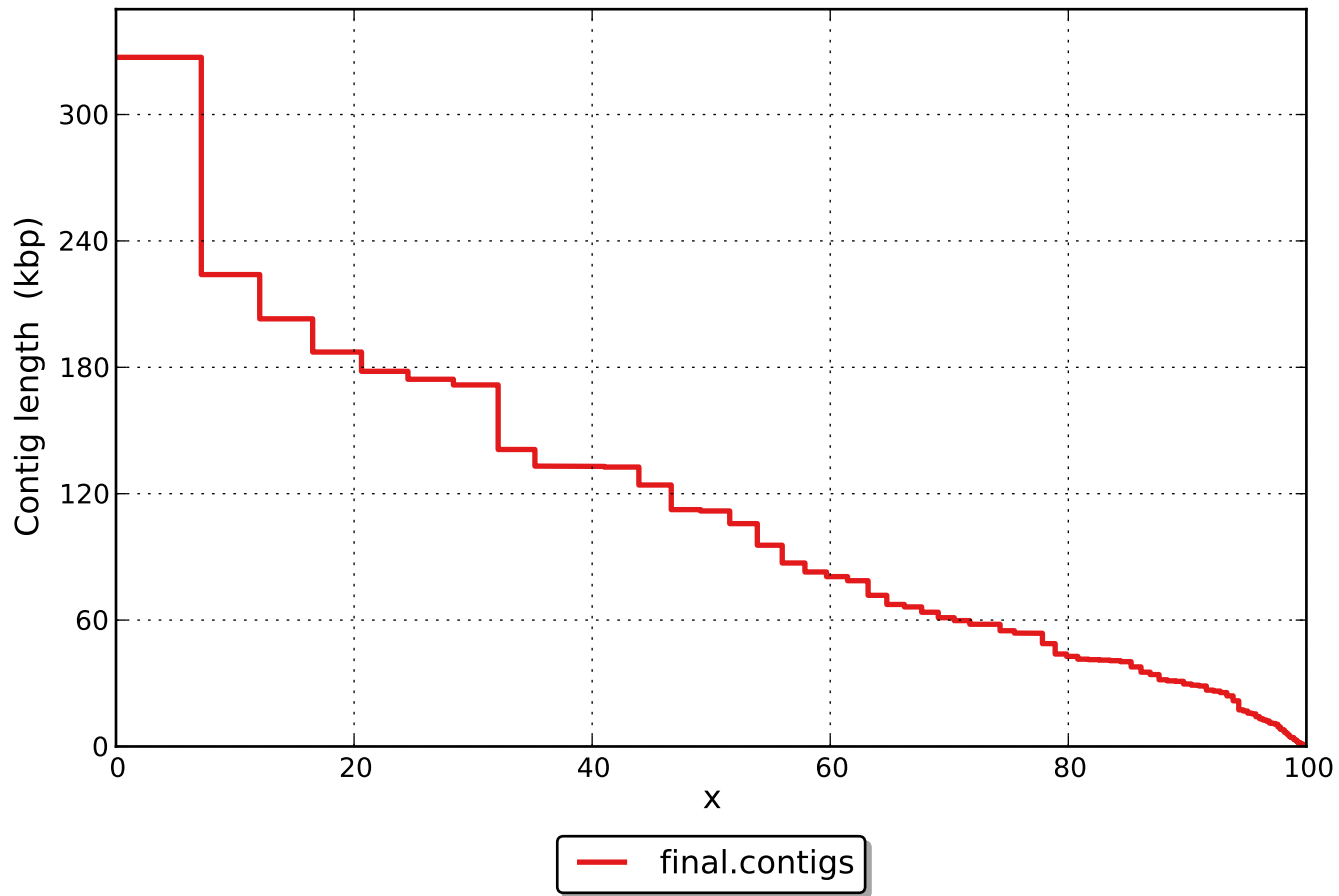
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

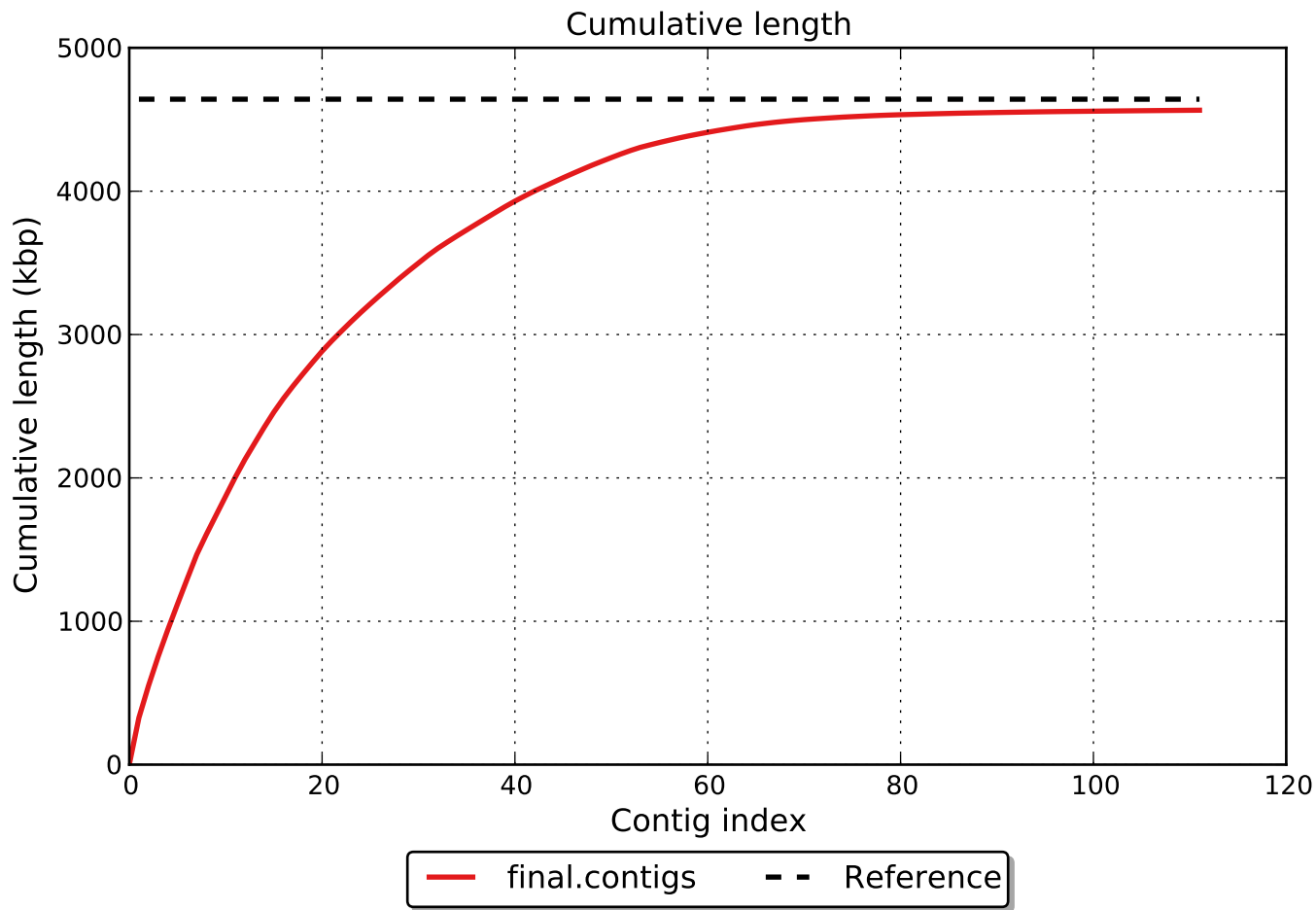
## Unaligned report

	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

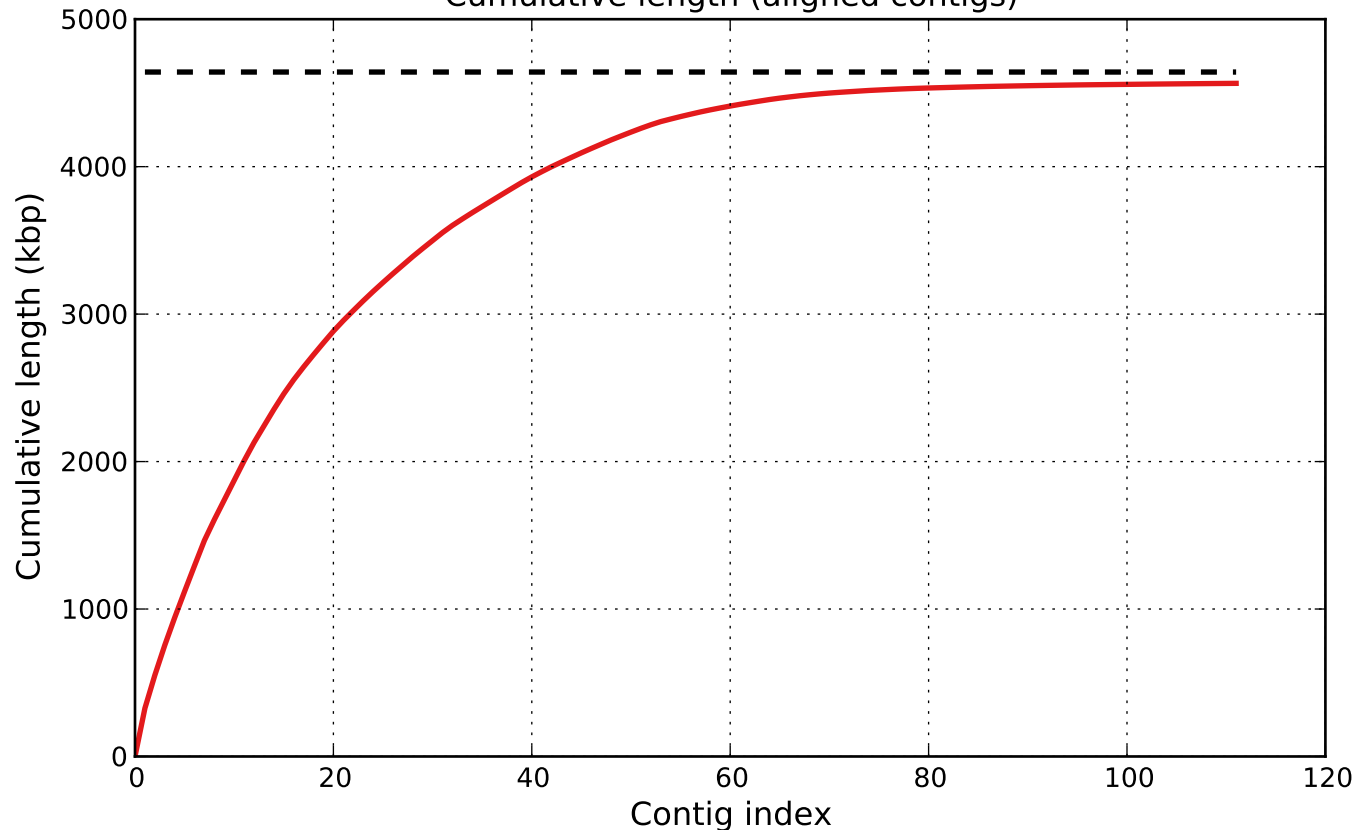




# Misassemblies



Cumulative length (aligned contigs)



NAx

