

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	147
# contigs ( $\geq 1000$ bp)	99
# contigs ( $\geq 5000$ bp)	74
# contigs ( $\geq 10000$ bp)	68
# contigs ( $\geq 25000$ bp)	50
# contigs ( $\geq 50000$ bp)	34
Total length ( $\geq 0$ bp)	4575297
Total length ( $\geq 1000$ bp)	4554027
Total length ( $\geq 5000$ bp)	4498418
Total length ( $\geq 10000$ bp)	4454662
Total length ( $\geq 25000$ bp)	4168582
Total length ( $\geq 50000$ bp)	3606295
# contigs	113
Largest contig	246979
Total length	4563917
Reference length	4641652
N50	95645
N75	56778
L50	15
L75	31
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	9
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (▼)	98.269
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.89
# indels per 100 kbp	9.56
Largest alignment	246979
NA50	95645
NA75	56778
LA50	15
LA75	31

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	9
# mismatches	2686
# indels	436
# short indels	430
# long indels	6
Indels length	786

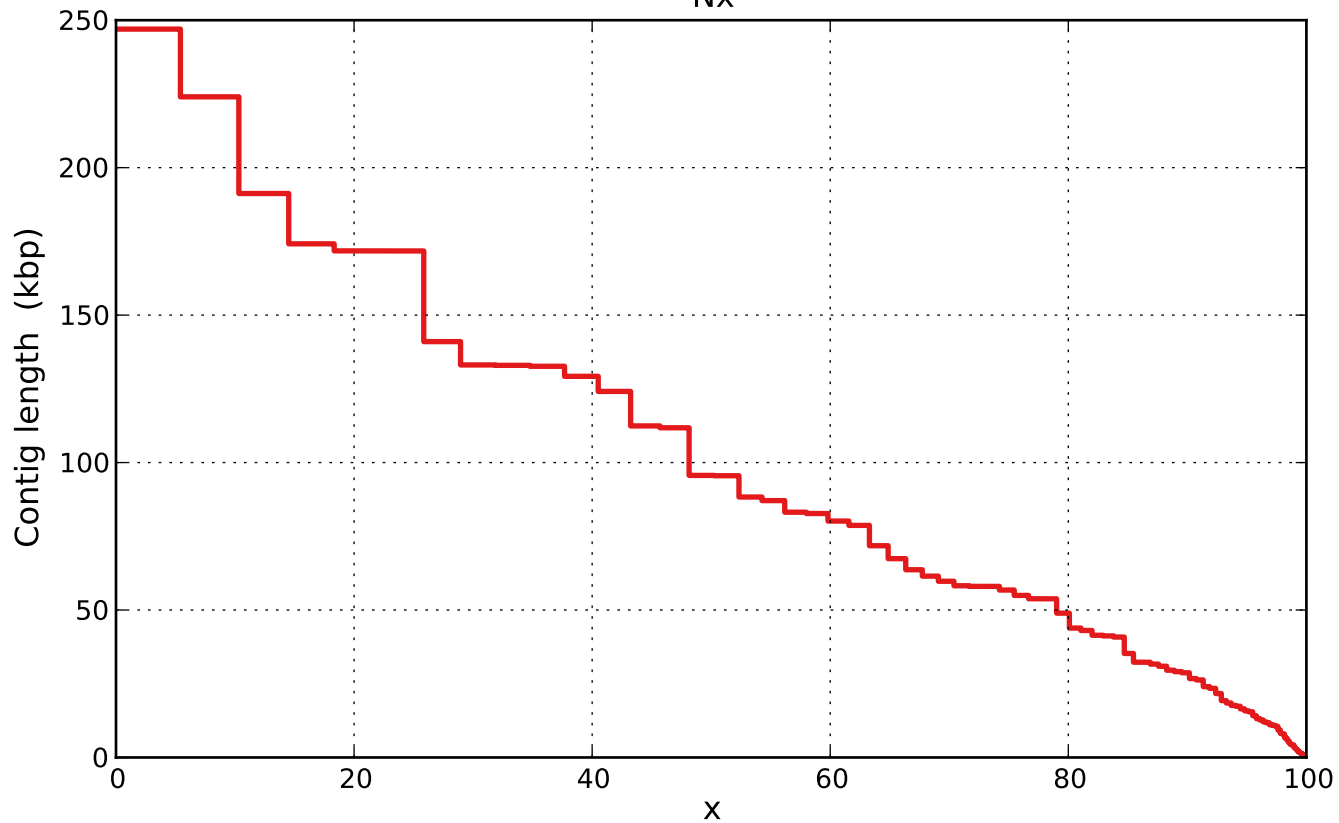
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

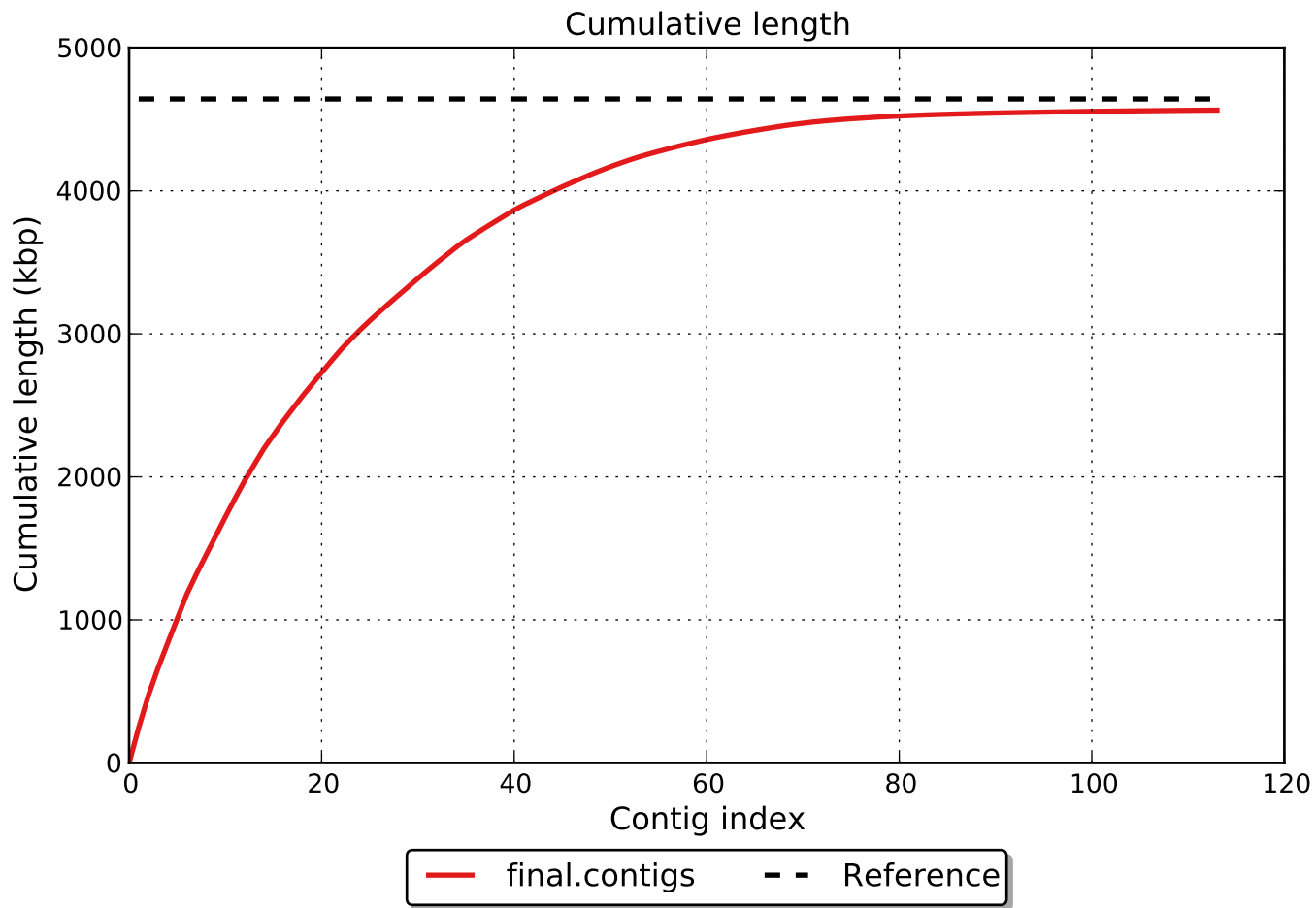
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

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



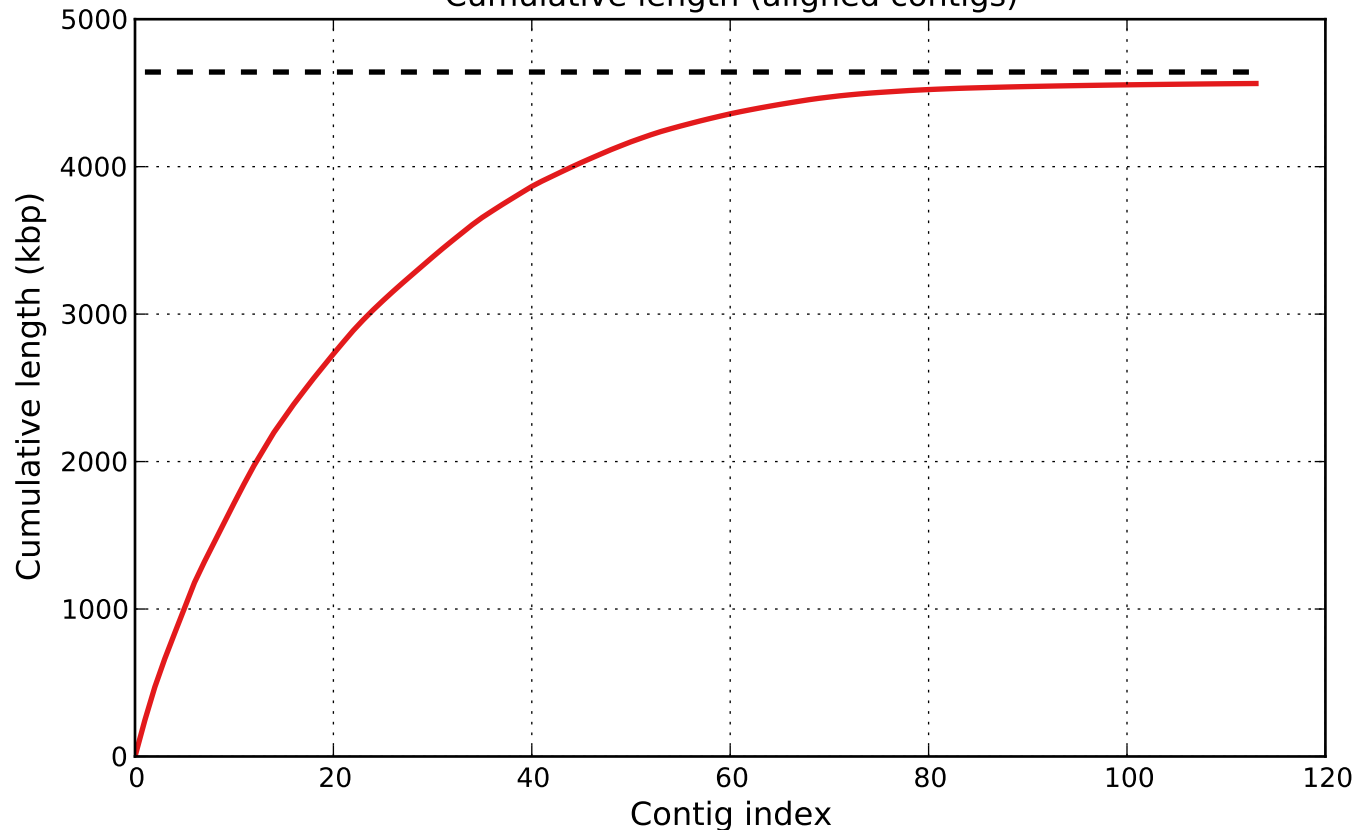
— final.contigs



# Misassemblies

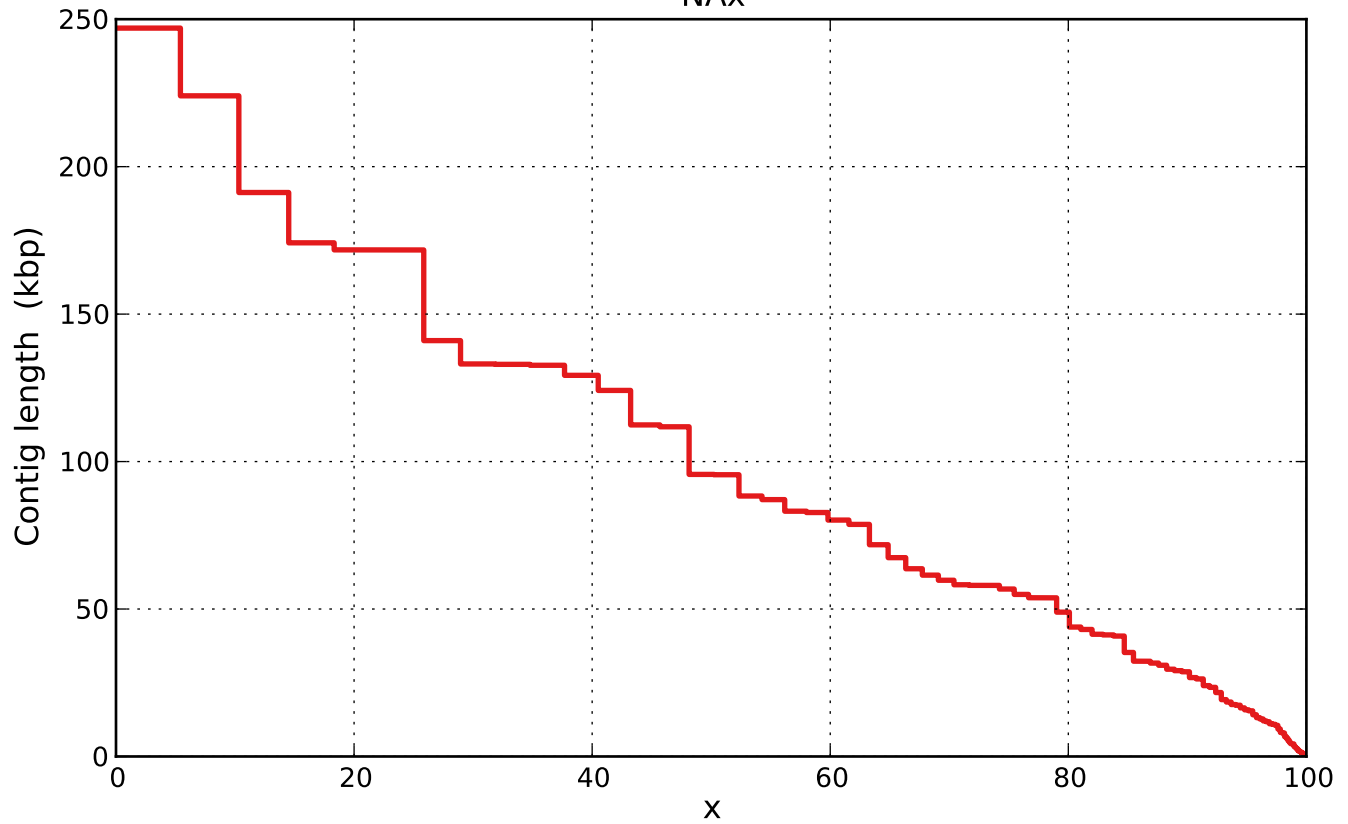


Cumulative length (aligned contigs)



— final.contigs      - - Reference

NAx



— final.contigs