

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	5179
# contigs ( $\geq 1000$ bp)	1106
# contigs ( $\geq 5000$ bp)	2
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	3977249
Total length ( $\geq 1000$ bp)	1642138
Total length ( $\geq 5000$ bp)	10187
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	3451
Largest contig	5185
Total length	3288682
Reference length	4641652
N50	999
N75	719
L50	1109
L75	2080
# misassemblies	11
# misassembled contigs	11
Misassembled contigs length	18308
# local misassemblies	3
# unaligned contigs	1 + 5 part
Unaligned length	1278
Genome fraction (▼)	68.984
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	968.05
# indels per 100 kbp	1.06
Largest alignment	5185
NA50	998
NA75	718
LA50	1112
LA75	2086

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

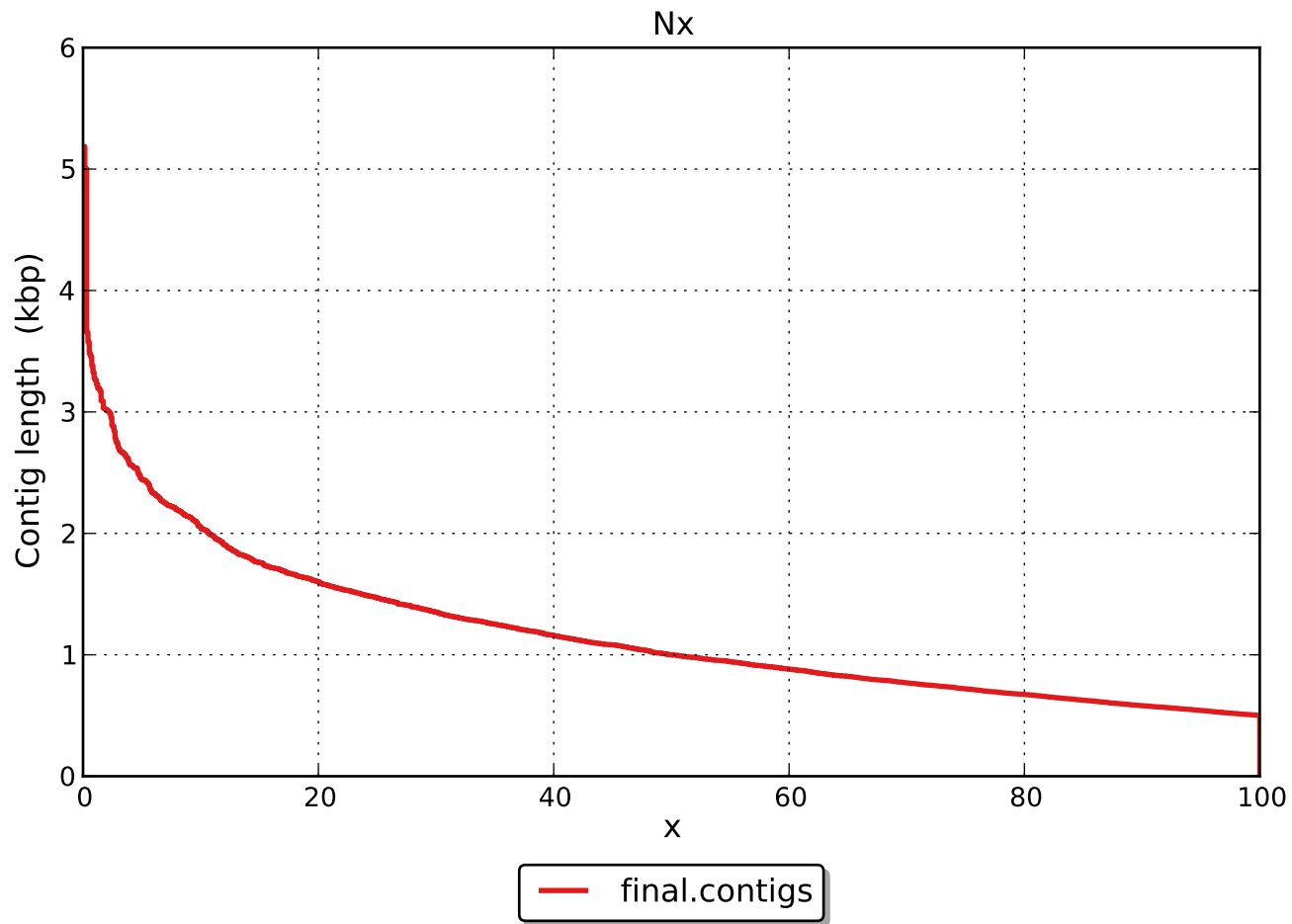
	final.contigs
# misassemblies	11
# relocations	11
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	11
Misassembled contigs length	18308
# local misassemblies	3
# mismatches	30997
# indels	34
# short indels	34
# long indels	0
Indels length	45

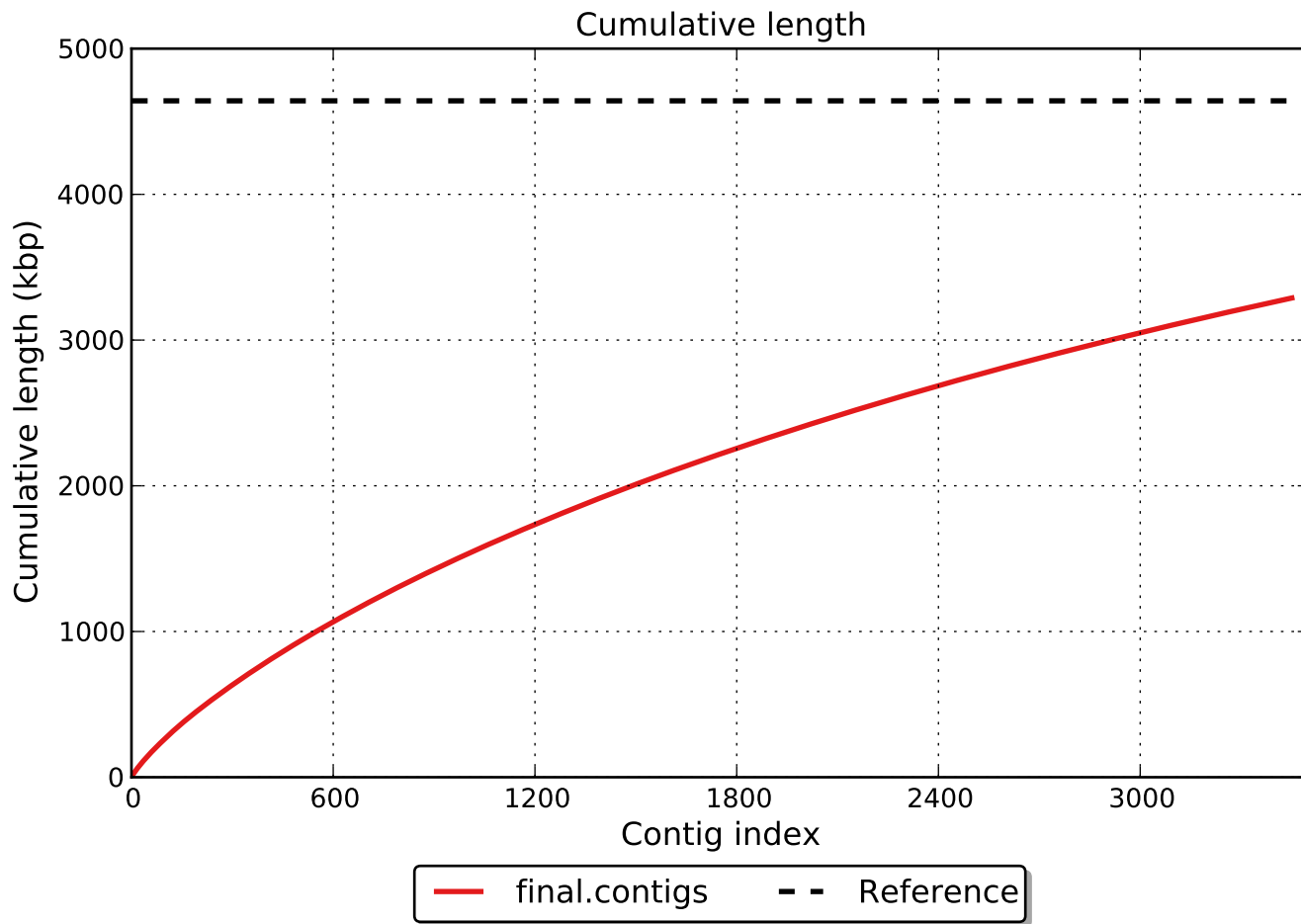
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

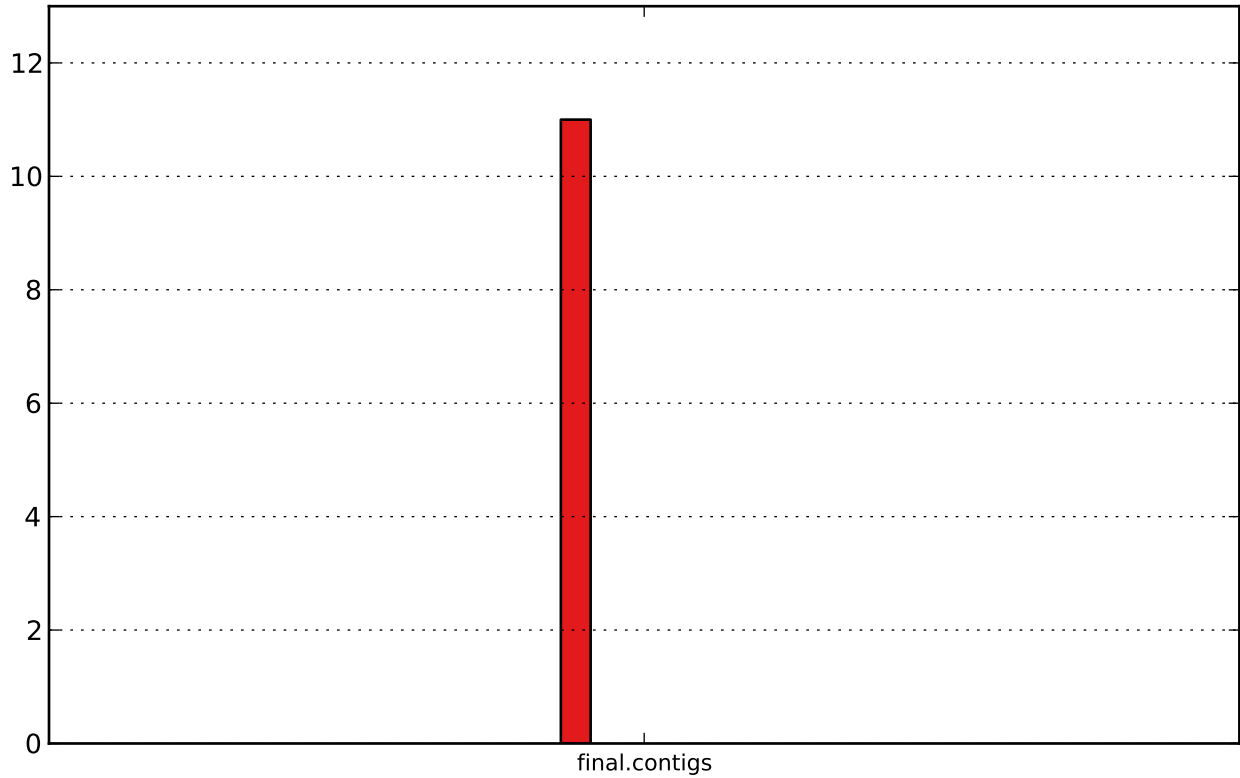
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	963
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	315
# N's	0

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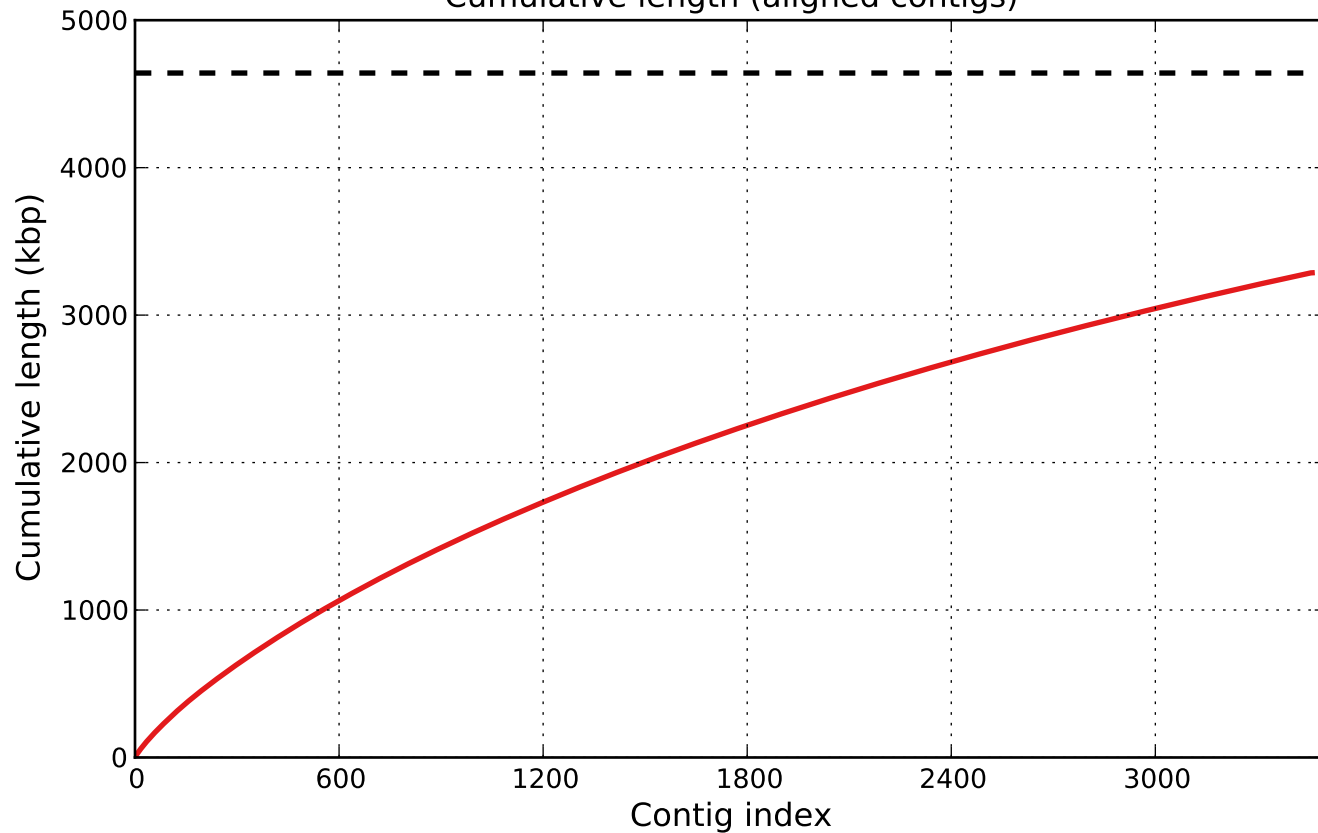


# Misassemblies



 # relocations

Cumulative length (aligned contigs)



— final.contigs      - - Reference

