

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	10401
# contigs ( $\geq 1000$ bp)	3681
# contigs ( $\geq 5000$ bp)	9
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	10055662
Total length ( $\geq 1000$ bp)	6187570
Total length ( $\geq 5000$ bp)	48199
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	7660
Largest contig	5692
Total length	9058013
Reference length	9714864
N50	1329
N75	887
L50	2235
L75	4326
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	89.397
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	22.30
# indels per 100 kbp	0.03
Largest alignment	5692
NA50	1329
NA75	886
LA50	2235
LA75	4326

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

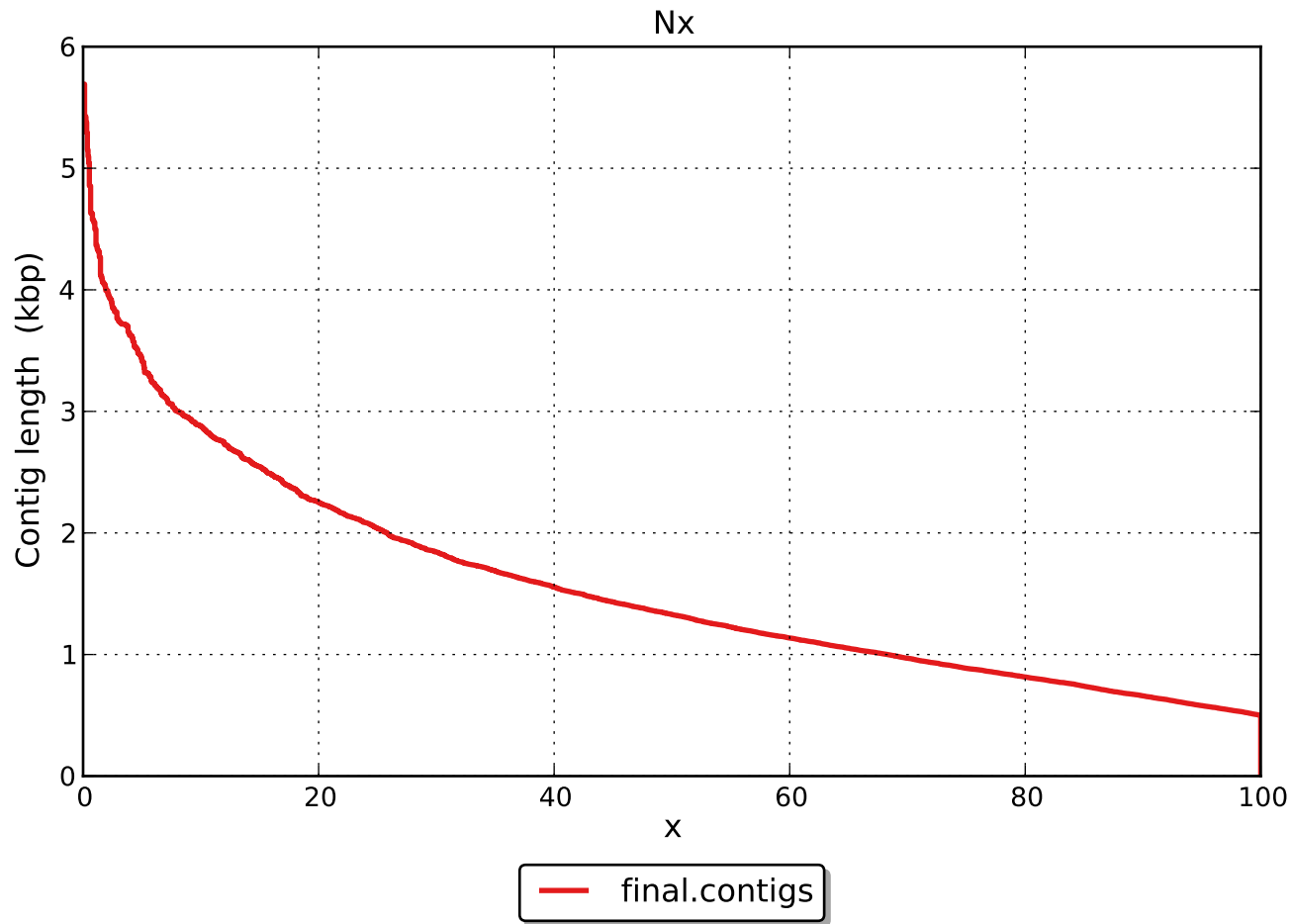
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1937
# indels	3
# short indels	3
# long indels	0
Indels length	3

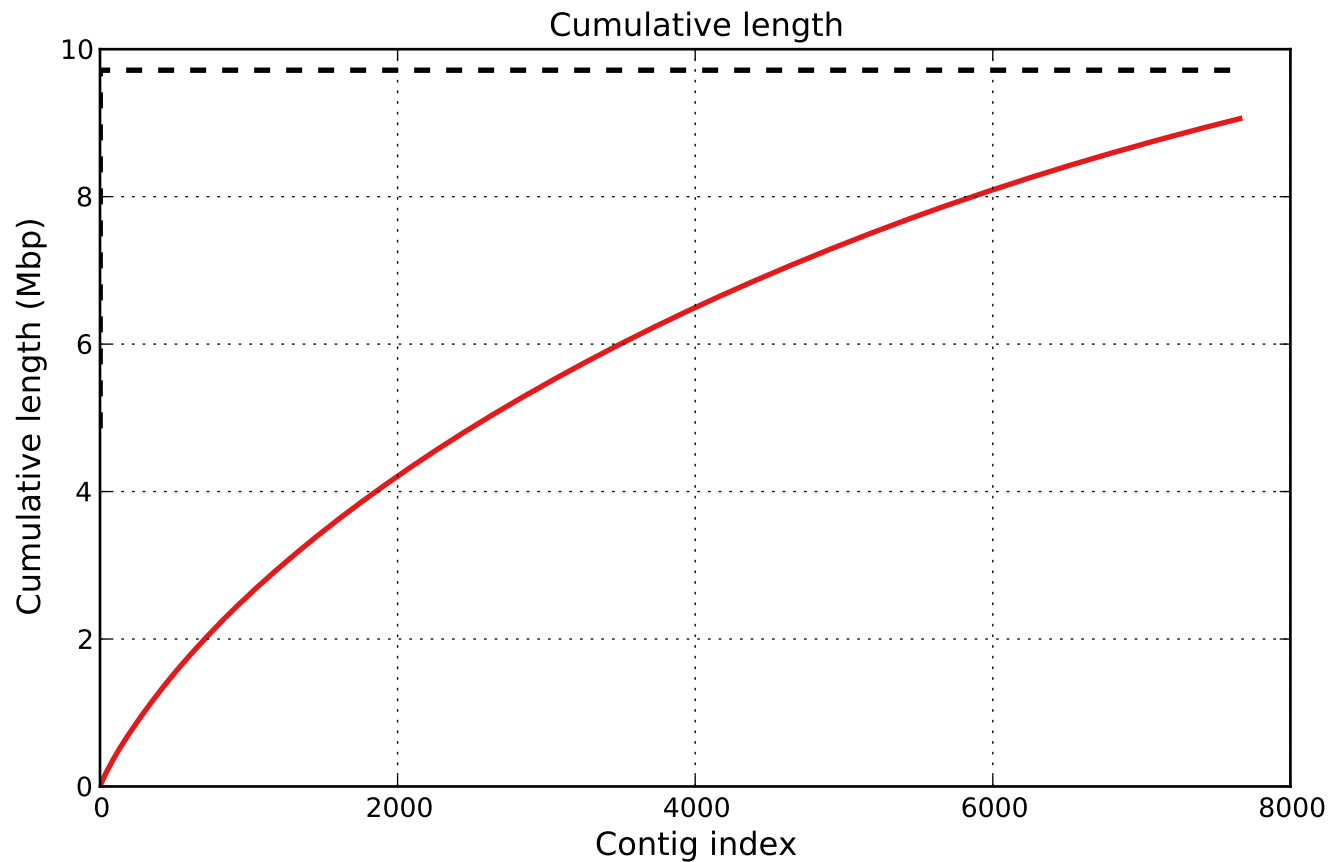
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## Unaligned report

	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).





# Misassemblies



