

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1262
# contigs ( $\geq 1000$ bp)	768
# contigs ( $\geq 5000$ bp)	533
# contigs ( $\geq 10000$ bp)	360
# contigs ( $\geq 25000$ bp)	91
# contigs ( $\geq 50000$ bp)	12
Total length ( $\geq 0$ bp)	9869769
Total length ( $\geq 1000$ bp)	9683180
Total length ( $\geq 5000$ bp)	9020135
Total length ( $\geq 10000$ bp)	7759725
Total length ( $\geq 25000$ bp)	3378668
Total length ( $\geq 50000$ bp)	767458
# contigs	828
Largest contig	78175
Total length	9727167
Reference length	9714864
N50	19710
N75	11615
L50	159
L75	318
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.378
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	24.48
# indels per 100 kbp	0.01
Largest alignment	78175
NA50	19710
NA75	11615
LA50	159
LA75	318

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

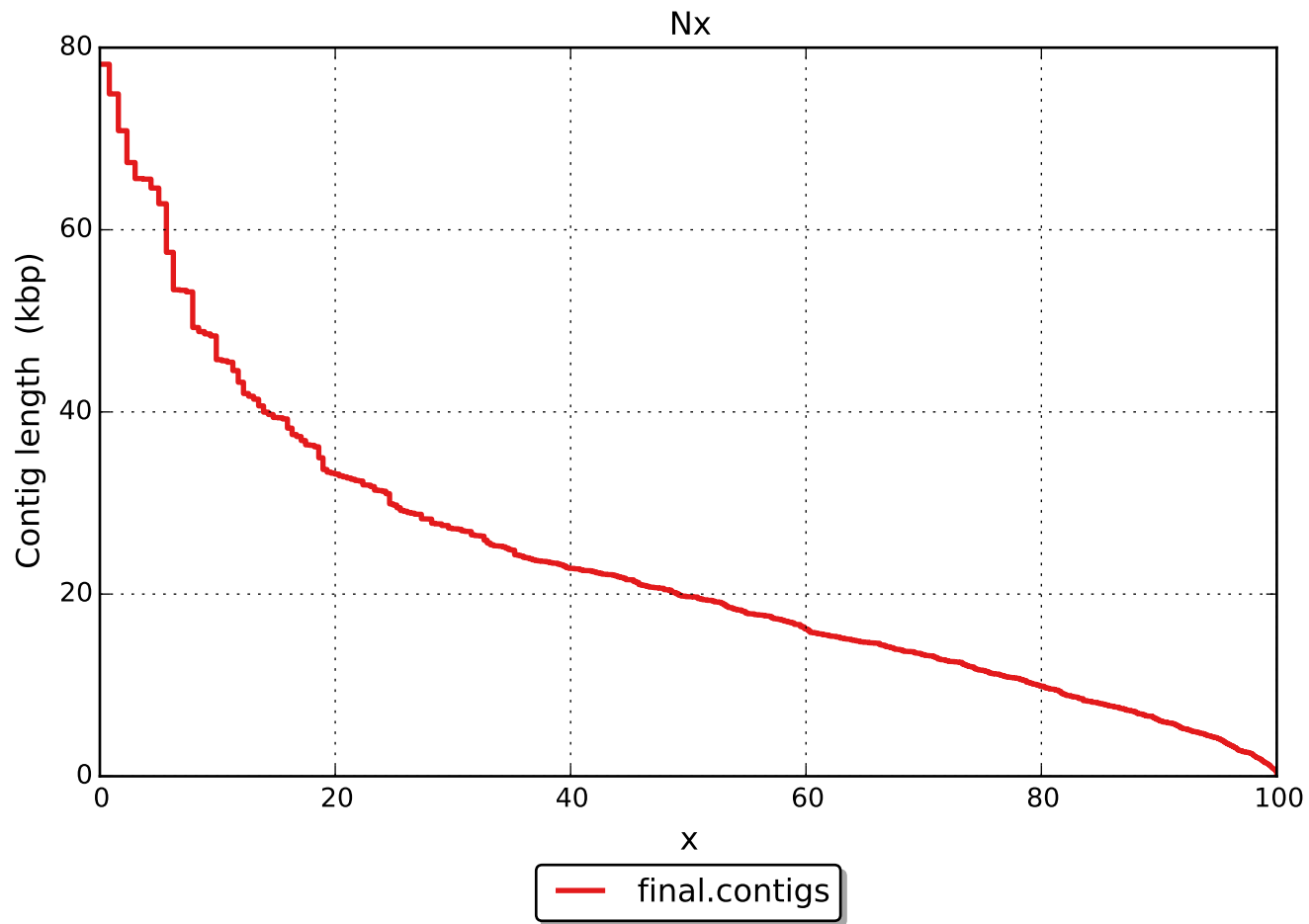
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	2363
# indels	1
# short indels	1
# long indels	0
Indels length	1

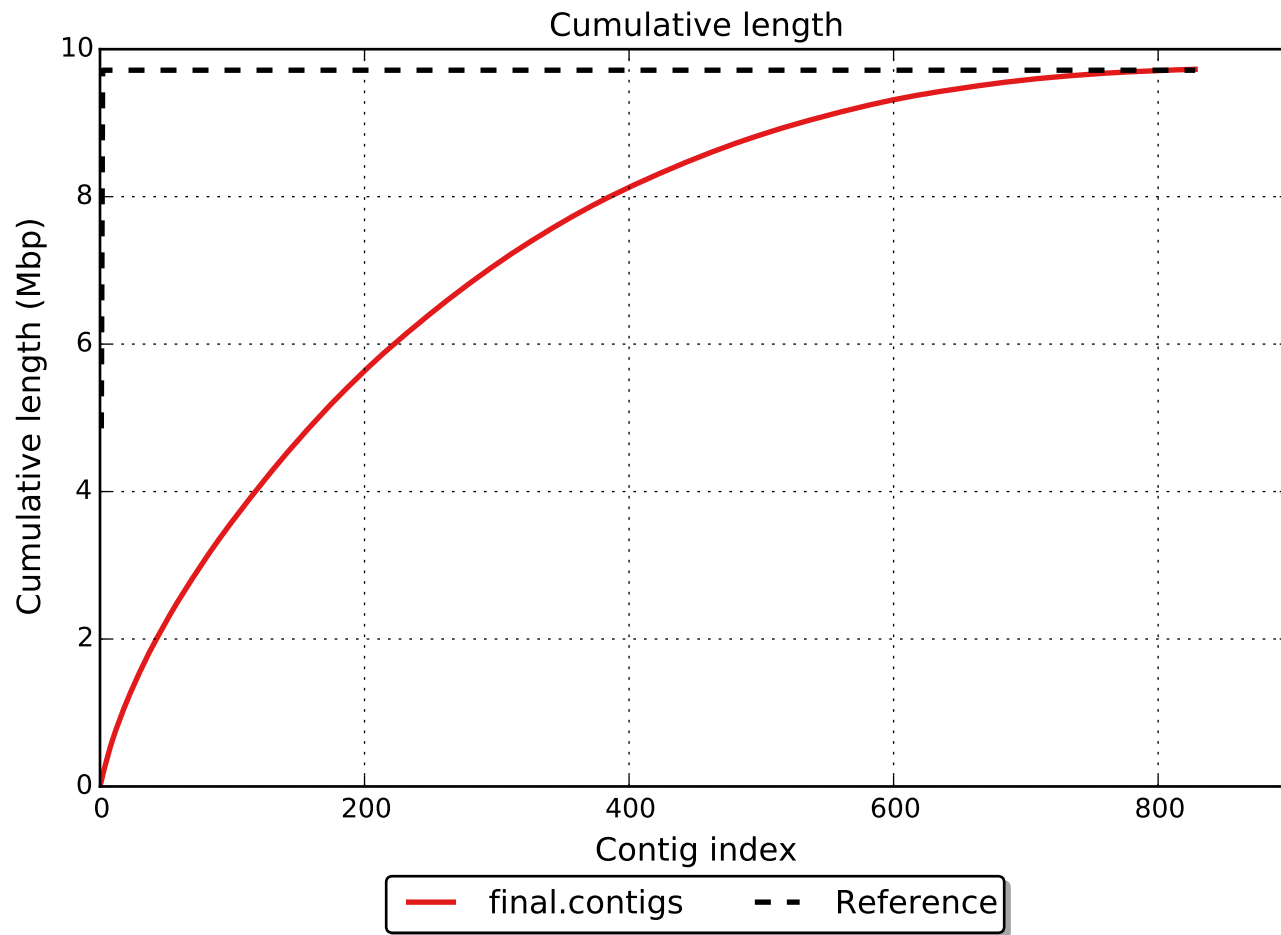
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## Unaligned report

	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

