

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	4296
# contigs ( $\geq 1000$ bp)	2644
# contigs ( $\geq 5000$ bp)	481
# contigs ( $\geq 10000$ bp)	70
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	9714758
Total length ( $\geq 1000$ bp)	8902352
Total length ( $\geq 5000$ bp)	3568772
Total length ( $\geq 10000$ bp)	853604
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	3283
Largest contig	24045
Total length	9370529
Reference length	9283304
N50	4051
N75	2381
L50	731
L75	1481
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	2 + 1 part
Unaligned length	1091
Genome fraction (%)	98.078
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	31.85
# indels per 100 kbp	0.03
Largest alignment	24045
NA50	4051
NA75	2381
LA50	731
LA75	1481

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

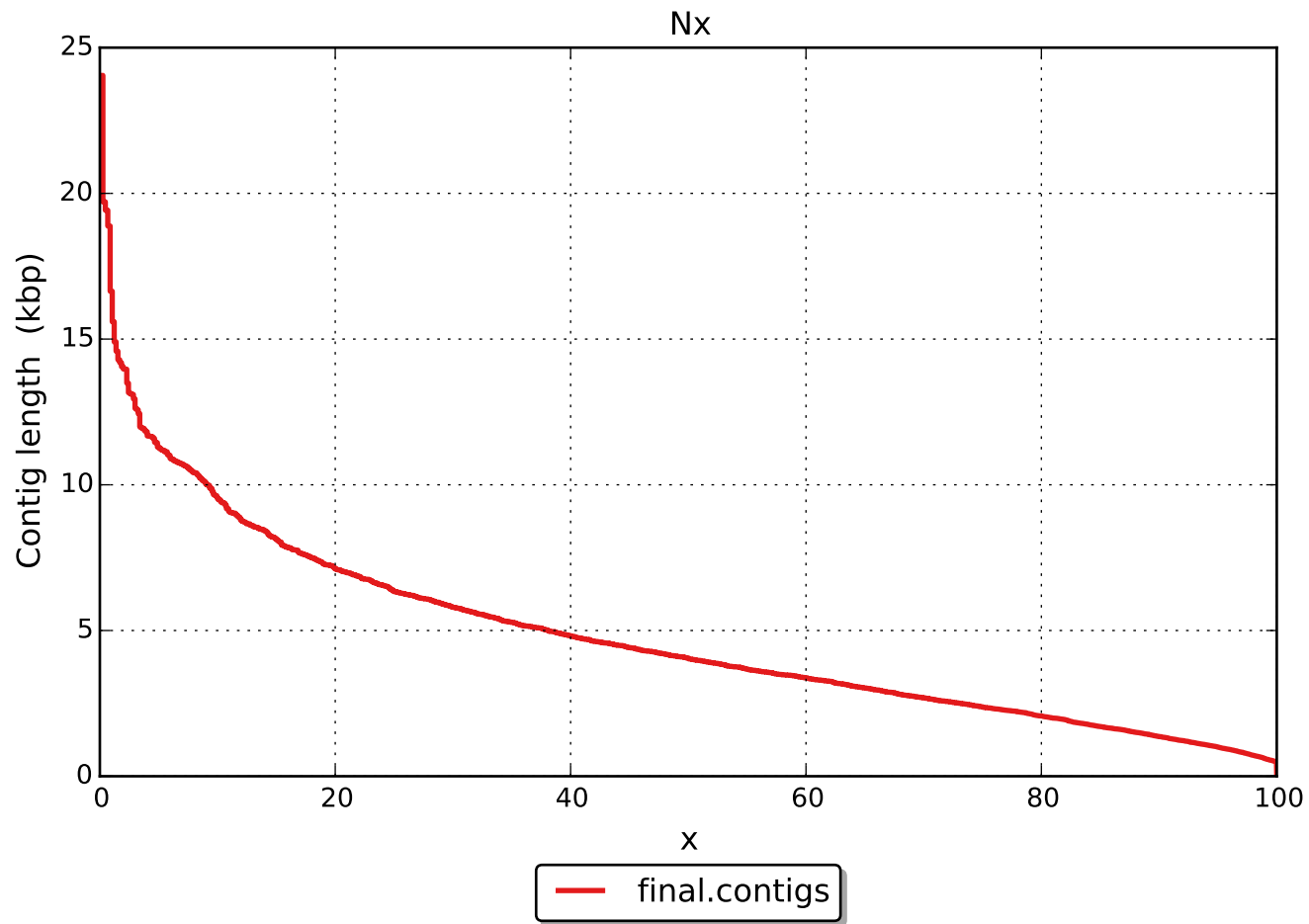
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	2900
# indels	3
# short indels	3
# long indels	0
Indels length	3

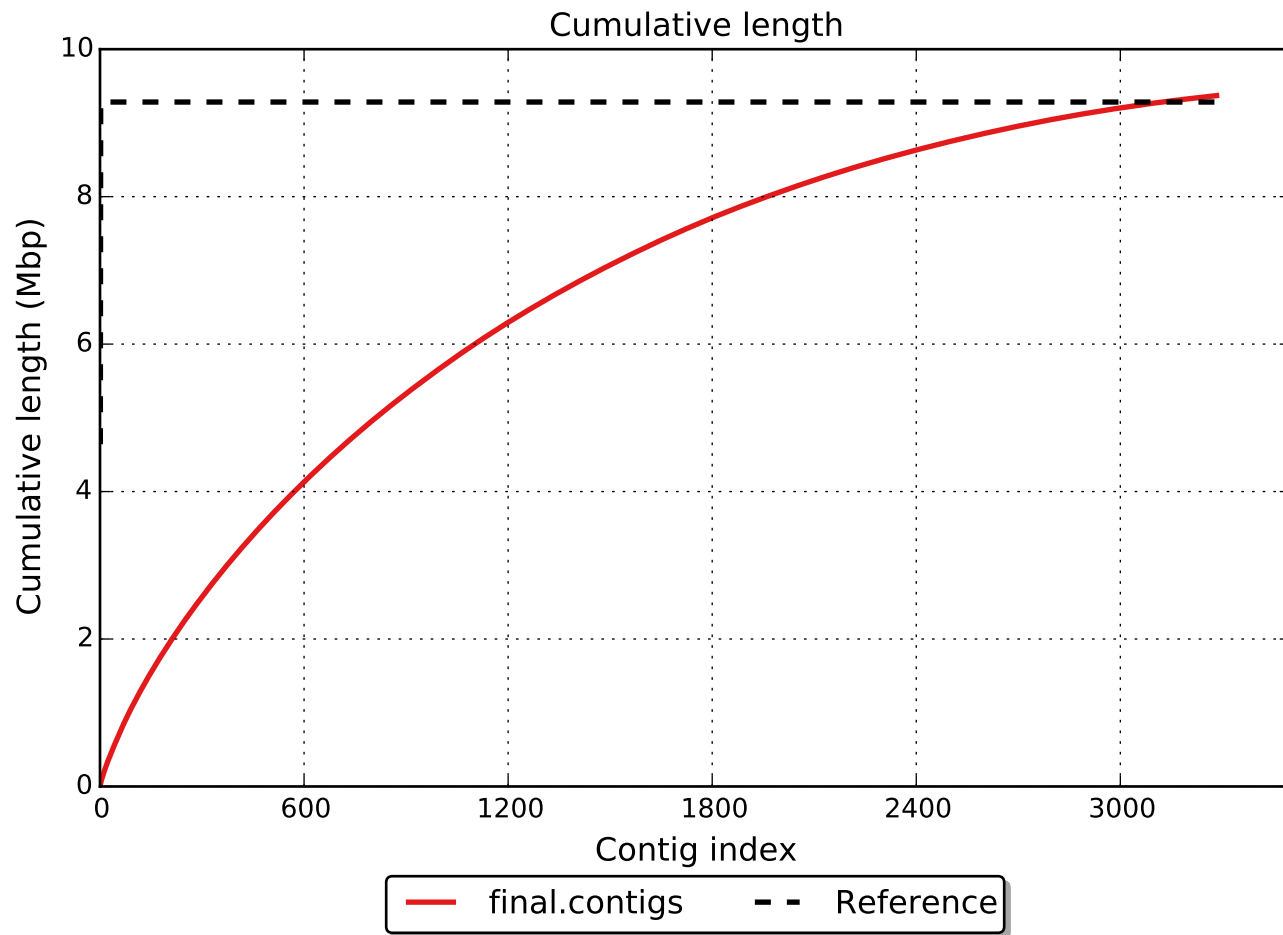
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## Unaligned report

	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1033
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	58
# 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

