

# Report

	final.contigs
# contigs ( $\geq 0$ bp)	8138
# contigs ( $\geq 1000$ bp)	3546
# contigs ( $\geq 5000$ bp)	59
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	9660778
Total length ( $\geq 1000$ bp)	7023557
Total length ( $\geq 5000$ bp)	365760
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	6259
Largest contig	9656
Total length	8985422
Reference length	9283304
N50	1744
N75	1077
L50	1649
L75	3272
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	93.155
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.33
# indels per 100 kbp	0.00
Largest alignment	9656
NA50	1744
NA75	1077
LA50	1649
LA75	3272

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

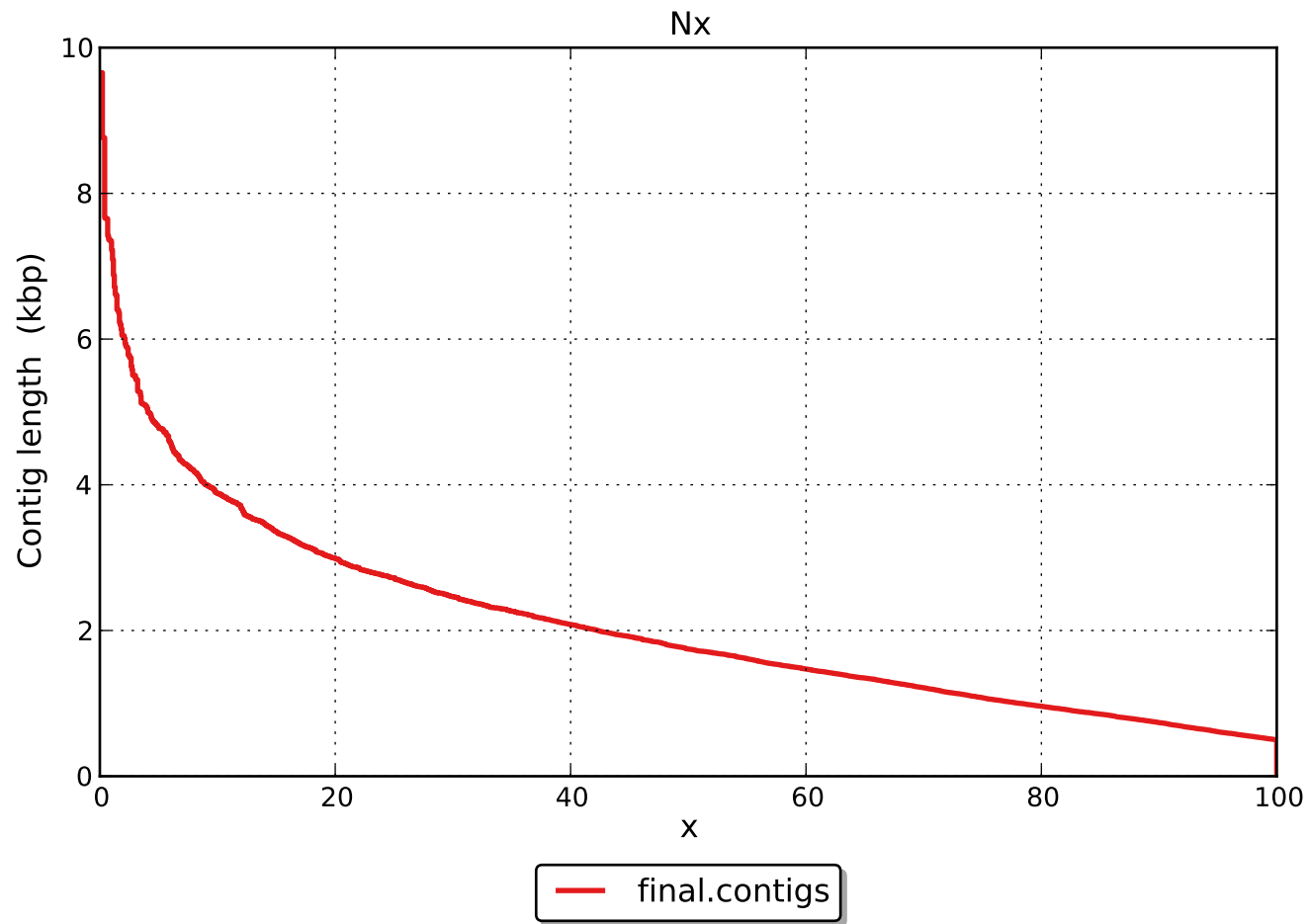
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	807
# indels	0
# short indels	0
# long indels	0
Indels length	0

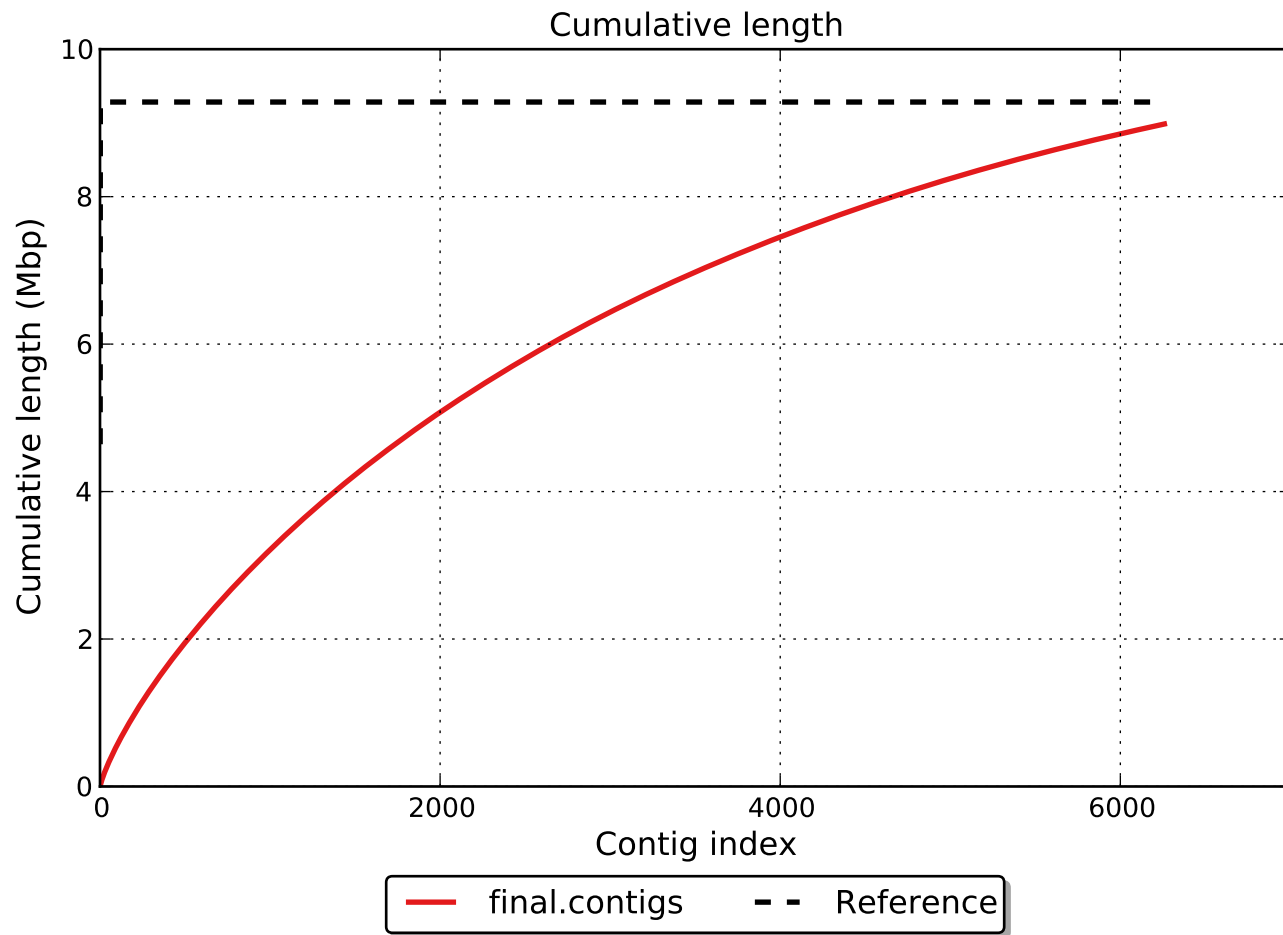
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## Unaligned report

	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



