

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	8506
# contigs ( $\geq 1000$ bp)	3841
# contigs ( $\geq 5000$ bp)	86
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	10466654
Total length ( $\geq 1000$ bp)	7975783
Total length ( $\geq 5000$ bp)	507399
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	6060
Largest contig	9054
Total length	9612070
Reference length	9714864
N50	1958
N75	1218
L50	1599
L75	3146
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	1545
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	377
Genome fraction (%)	94.710
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.87
# indels per 100 kbp	0.02
Largest alignment	9054
NA50	1958
NA75	1218
LA50	1599
LA75	3146

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

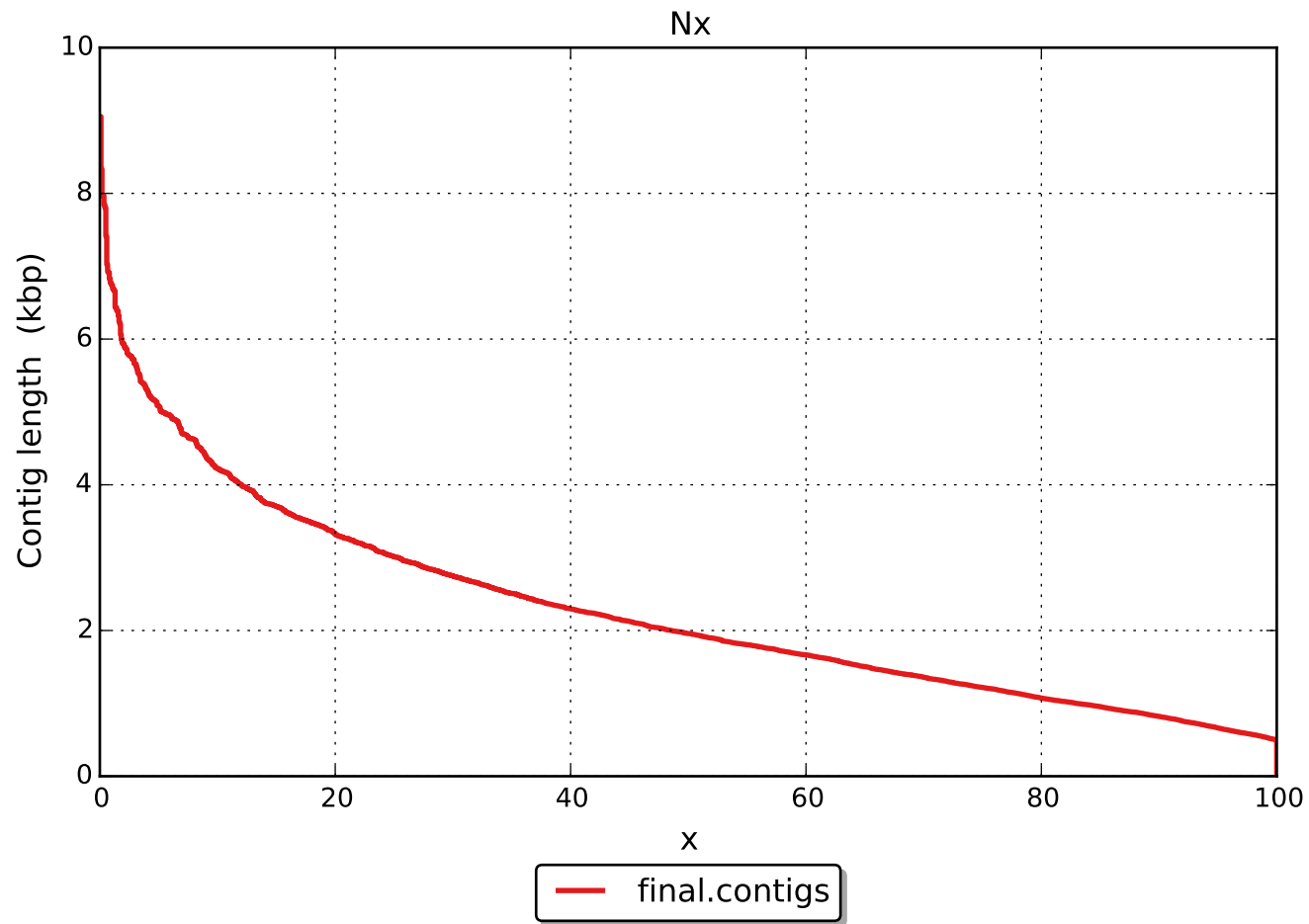
	final.contigs
# misassemblies	2
# relocations	0
# translocations	0
# inversions	2
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	1545
# local misassemblies	0
# mismatches	5325
# indels	2
# short indels	2
# long indels	0
Indels length	2

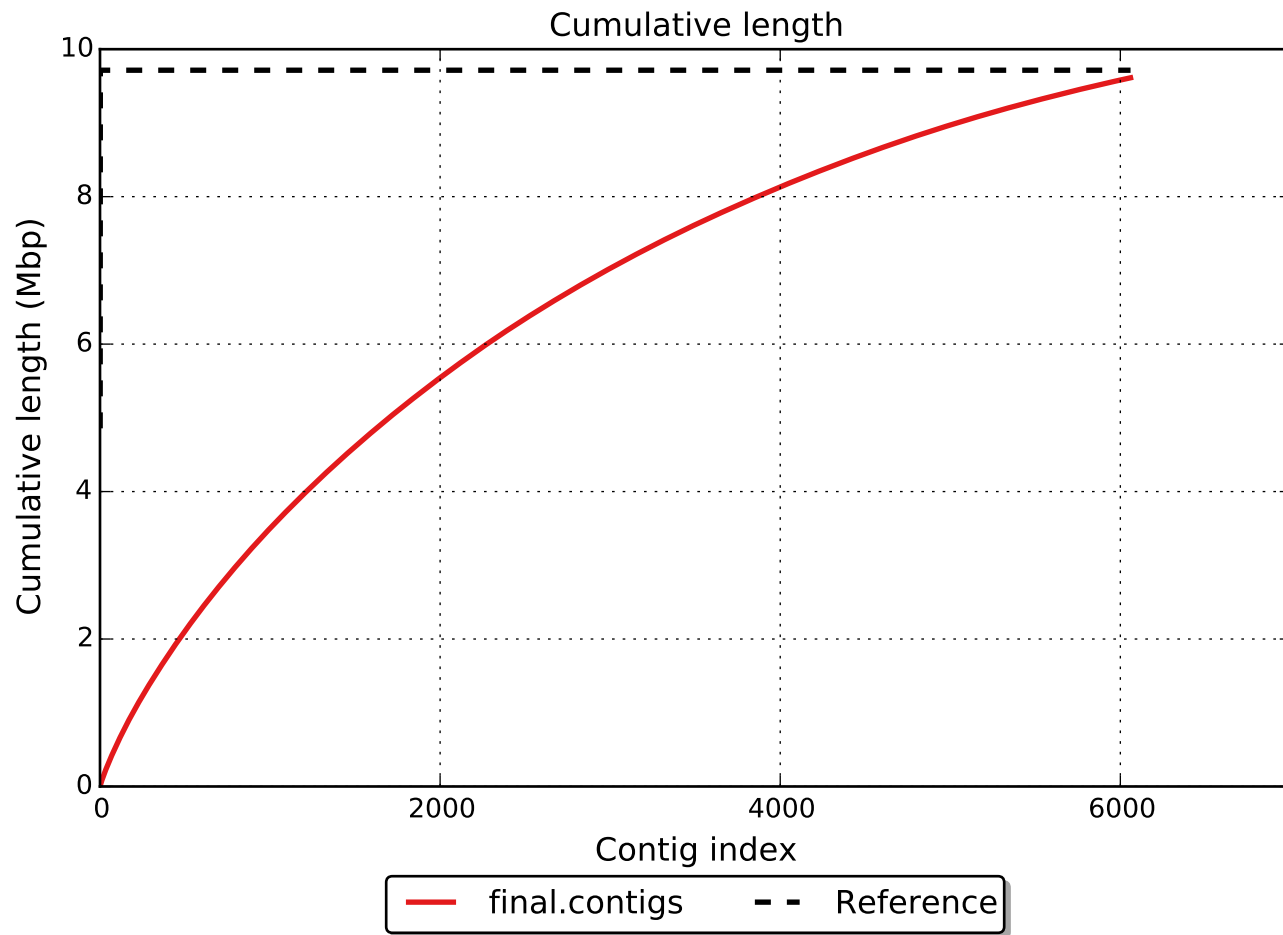
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## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	377
# 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

