

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	4279
# contigs ( $\geq 1000$ bp)	1368
# contigs ( $\geq 5000$ bp)	1
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	3891727
Total length ( $\geq 1000$ bp)	2118029
Total length ( $\geq 5000$ bp)	5220
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	3311
Largest contig	5220
Total length	3503625
Reference length	4641652
N50	1159
N75	803
L50	1028
L75	1941
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	7102
# local misassemblies	6
# unaligned contigs	1 + 11 part
Unaligned length	1662
Genome fraction (▼)	73.853
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	584.60
# indels per 100 kbp	9.77
Largest alignment	5220
NA50	1157
NA75	802
LA50	1029
LA75	1944

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

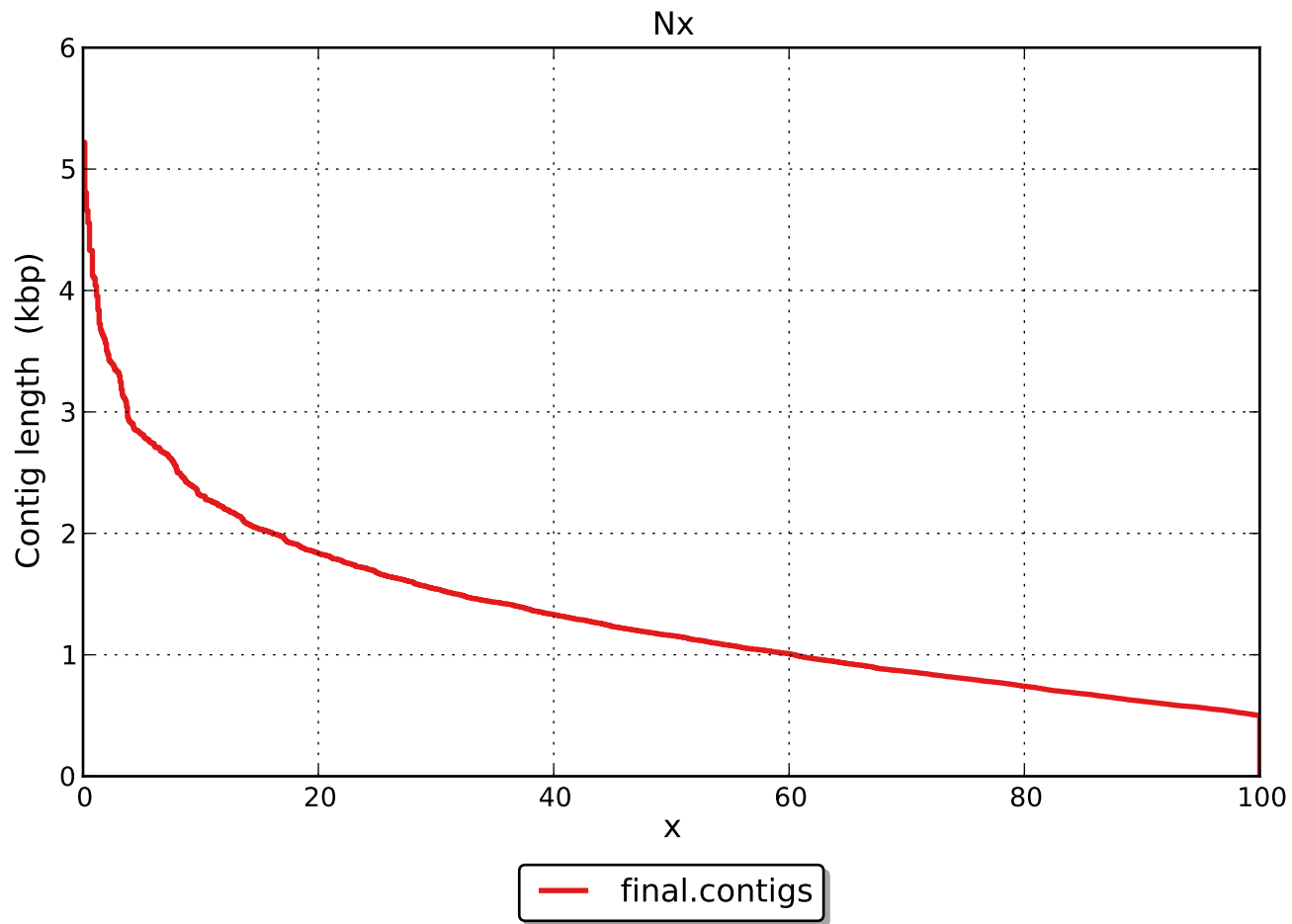
	final.contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	7102
# local misassemblies	6
# mismatches	20040
# indels	335
# short indels	332
# long indels	3
Indels length	518

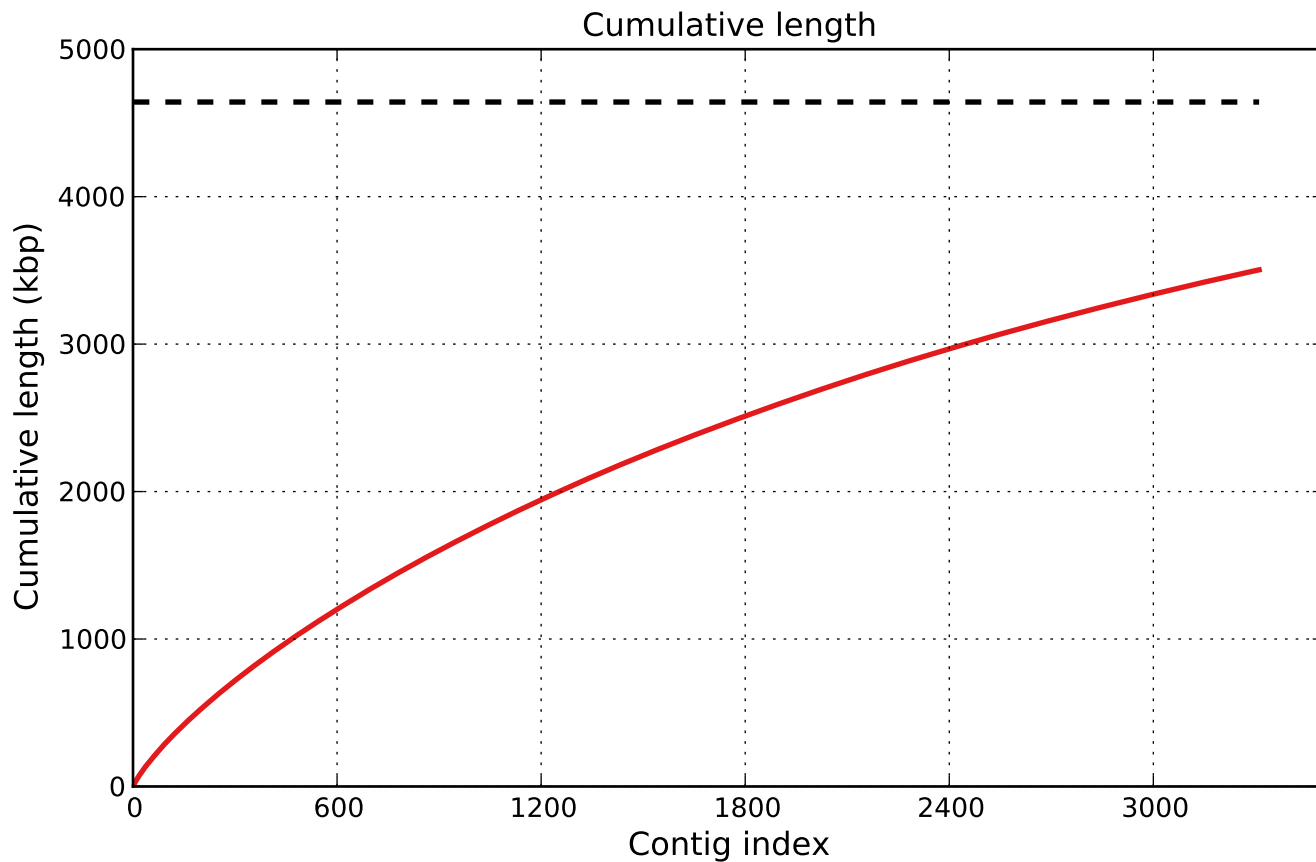
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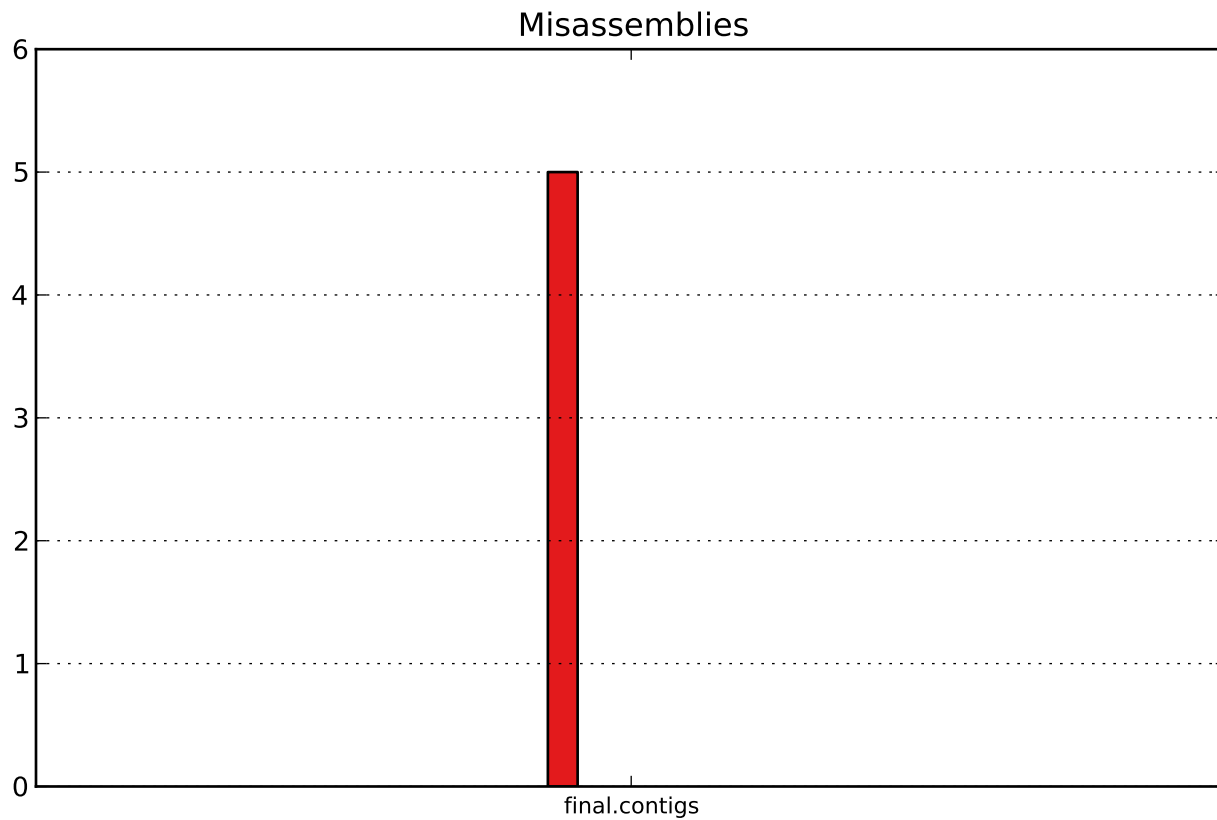
## Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	928
# partially unaligned contigs	11
# with misassembly	0
# both parts are significant	0
Partially unaligned length	734
# N's	0

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Cumulative length (aligned contigs)

