

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1711
# contigs ( $\geq 1000$ bp)	1387
# contigs ( $\geq 5000$ bp)	721
# contigs ( $\geq 10000$ bp)	304
# contigs ( $\geq 25000$ bp)	28
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	9802167
Total length ( $\geq 1000$ bp)	9637650
Total length ( $\geq 5000$ bp)	7853375
Total length ( $\geq 10000$ bp)	4850485
Total length ( $\geq 25000$ bp)	800053
Total length ( $\geq 50000$ bp)	0
# contigs	1539
Largest contig	38916
Total length	9747184
Reference length	9714864
N50	9942
N75	5870
L50	307
L75	621
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	99.324
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.53
# indels per 100 kbp	0.00
Largest alignment	38916
NA50	9942
NA75	5870
LA50	307
LA75	621

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

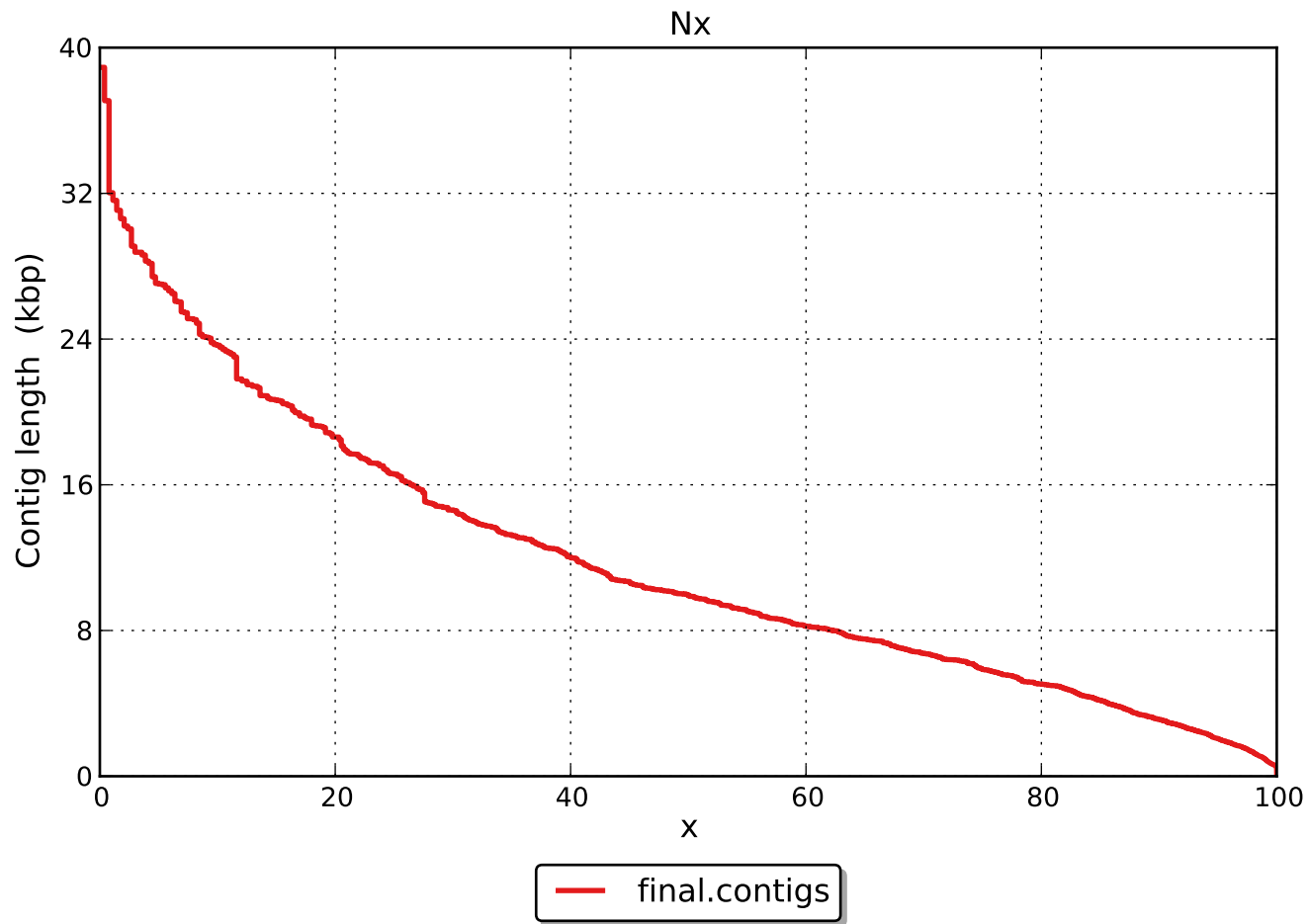
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	148
# indels	0
# short indels	0
# long indels	0
Indels length	0

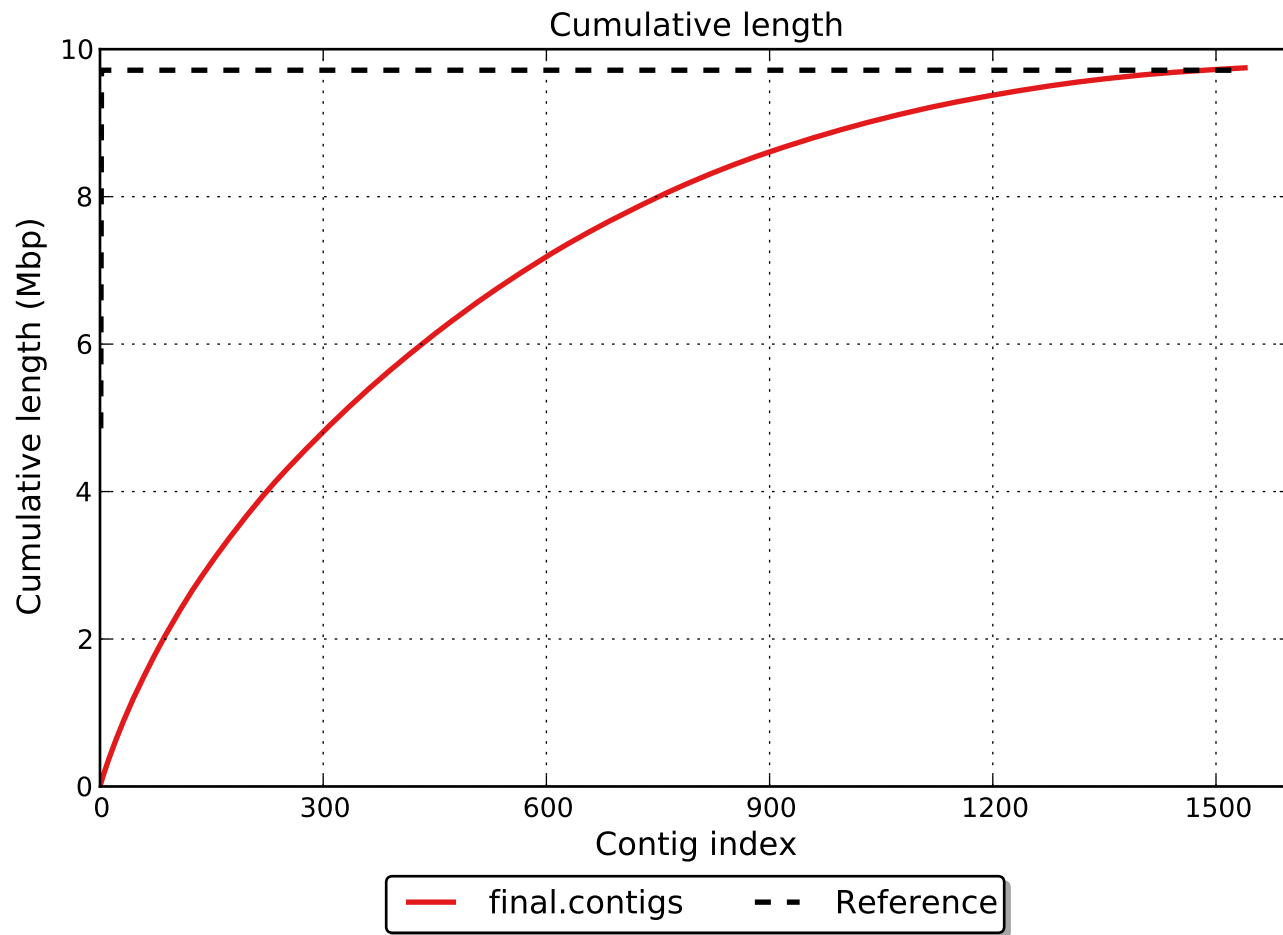
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## Unaligned report

	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



