

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	801
# contigs ( $\geq 1000$ bp)	647
# contigs ( $\geq 5000$ bp)	464
# contigs ( $\geq 10000$ bp)	320
# contigs ( $\geq 25000$ bp)	110
# contigs ( $\geq 50000$ bp)	15
Total length ( $\geq 0$ bp)	9281077
Total length ( $\geq 1000$ bp)	9217309
Total length ( $\geq 5000$ bp)	8680679
Total length ( $\geq 10000$ bp)	7648265
Total length ( $\geq 25000$ bp)	4157605
Total length ( $\geq 50000$ bp)	966351
# contigs	684
Largest contig	95788
Total length	9245899
Reference length	9283304
N50	23232
N75	13502
L50	130
L75	259
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	15109
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	99.148
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.09
# indels per 100 kbp	0.00
Largest alignment	95788
NA50	23232
NA75	13501
LA50	130
LA75	259

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

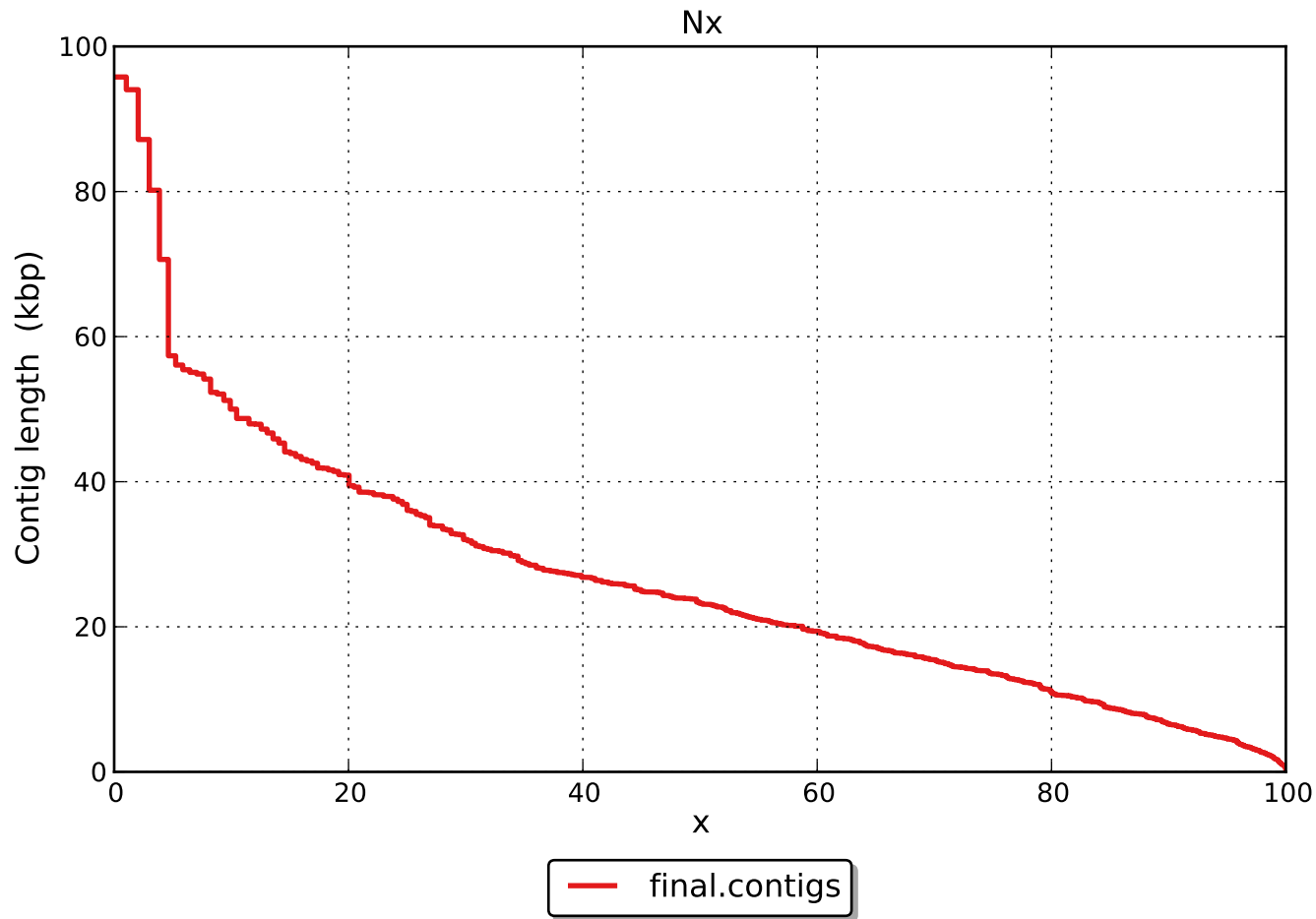
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	15109
# local misassemblies	0
# mismatches	100
# indels	0
# short indels	0
# long indels	0
Indels length	0

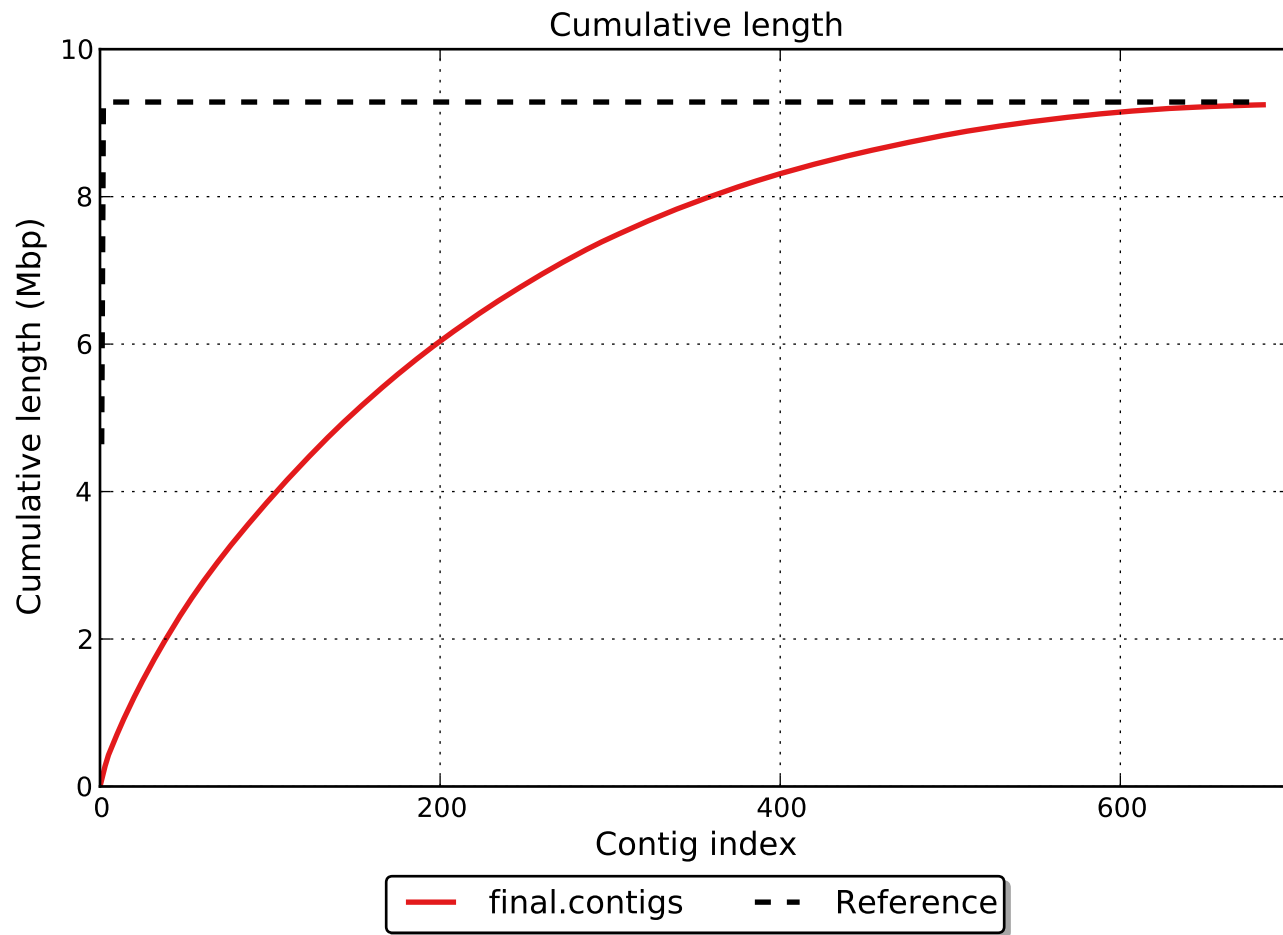
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

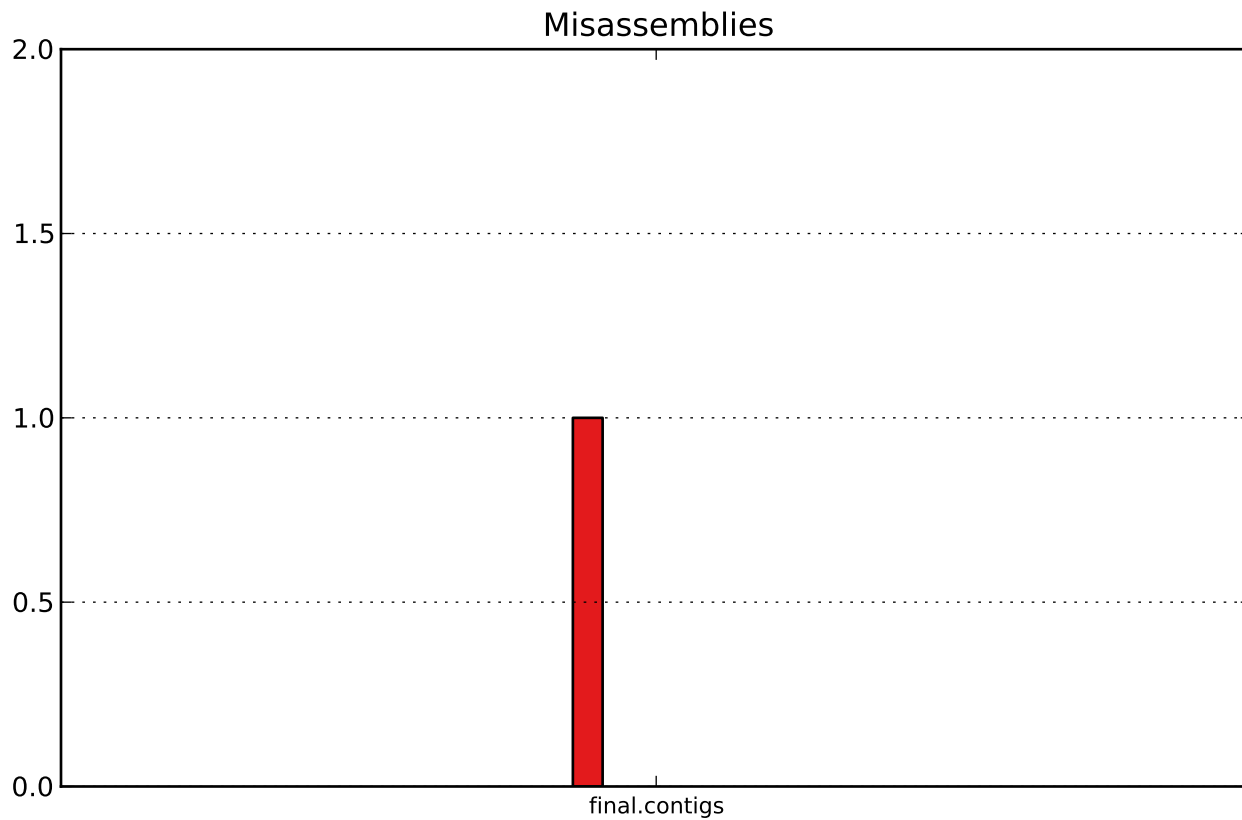
## Unaligned report

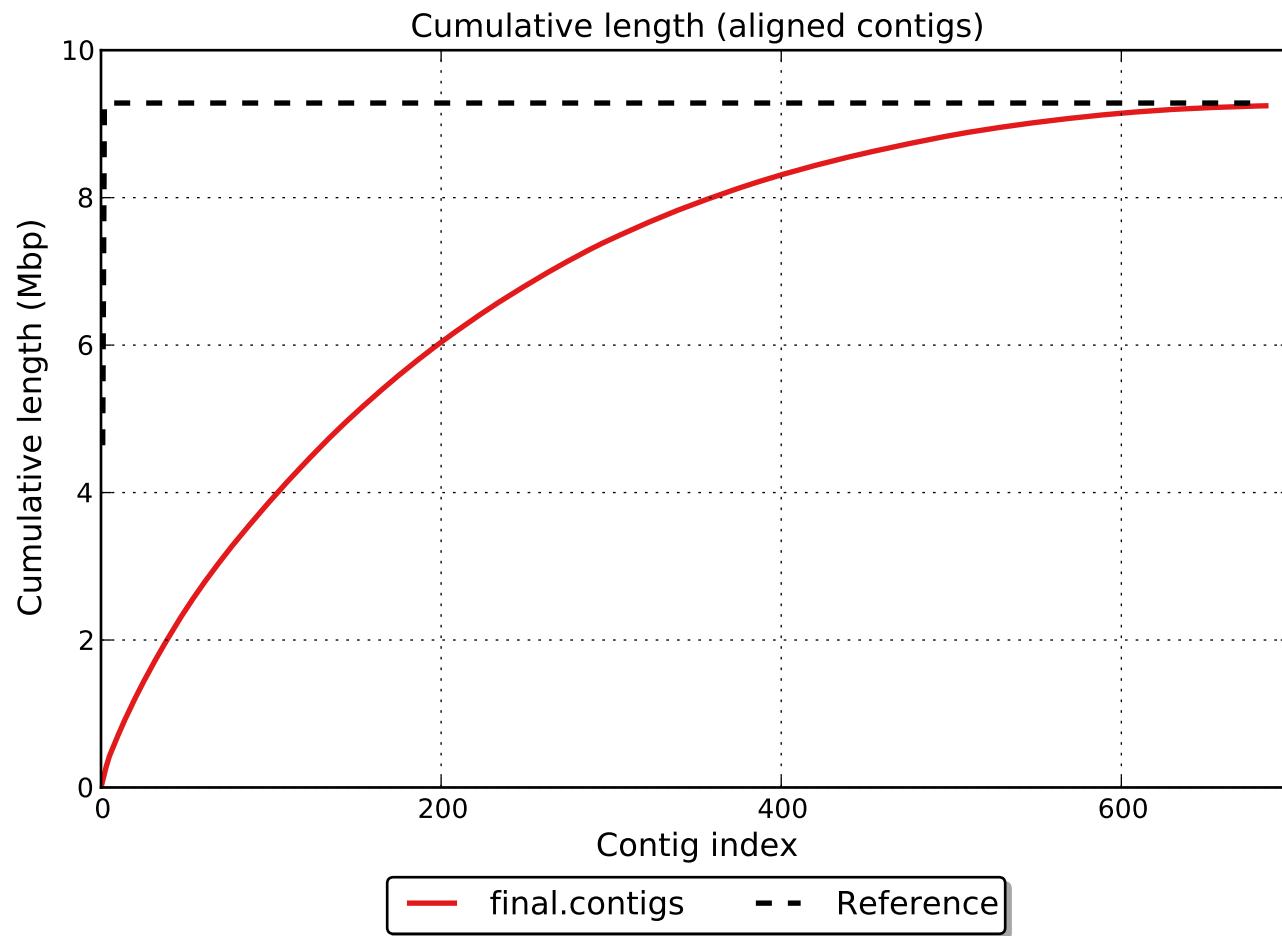
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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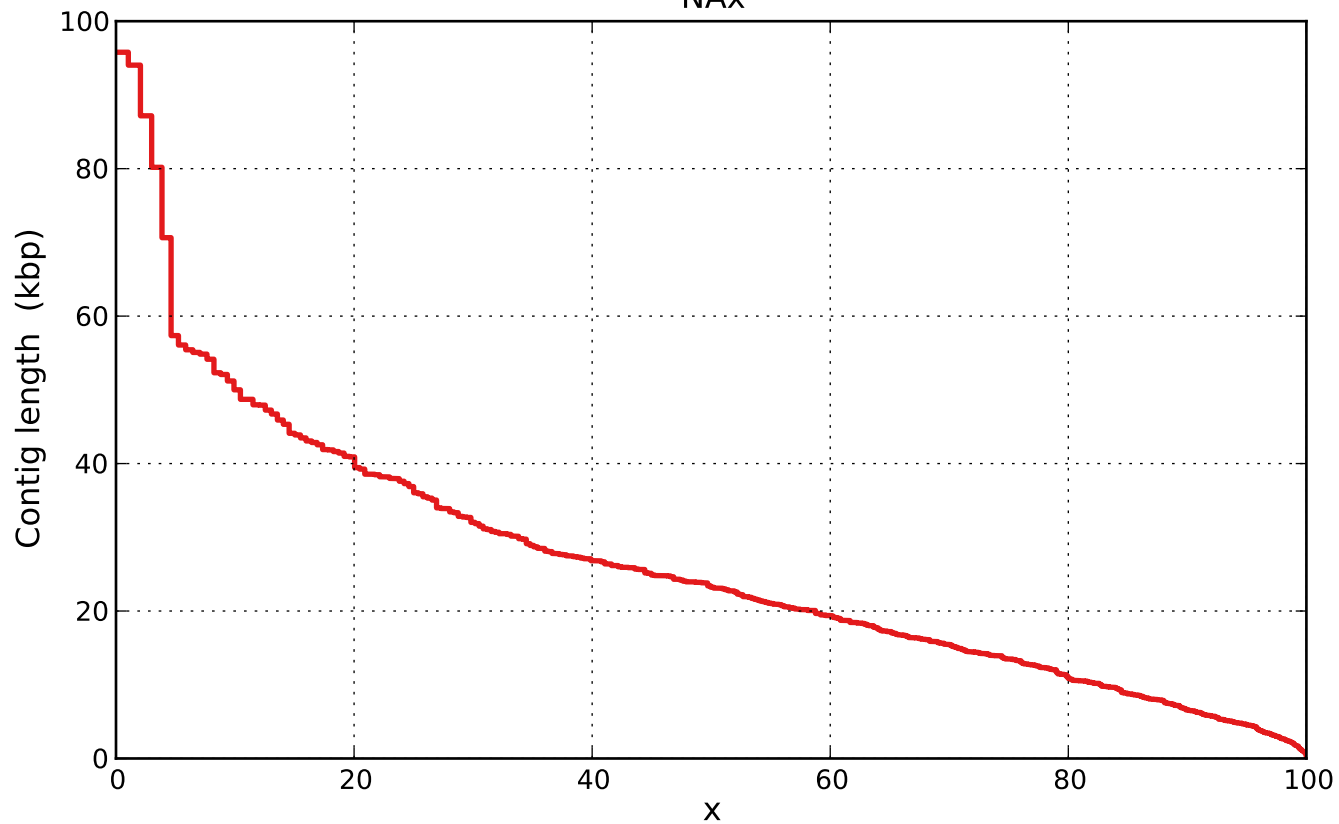








NAx



— final.contigs