

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	6466
# contigs ( $\geq 1000$ bp)	3363
# contigs ( $\geq 5000$ bp)	222
# contigs ( $\geq 10000$ bp)	6
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	9882619
Total length ( $\geq 1000$ bp)	8267530
Total length ( $\geq 5000$ bp)	1401787
Total length ( $\geq 10000$ bp)	65584
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	4740
Largest contig	13353
Total length	9288600
Reference length	9283304
N50	2555
N75	1543
L50	1169
L75	2324
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	2
# unaligned contigs	1 + 2 part
Unaligned length	852
Genome fraction (%)	96.288
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	48.58
# indels per 100 kbp	0.04
Largest alignment	13353
NA50	2554
NA75	1542
LA50	1169
LA75	2325

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

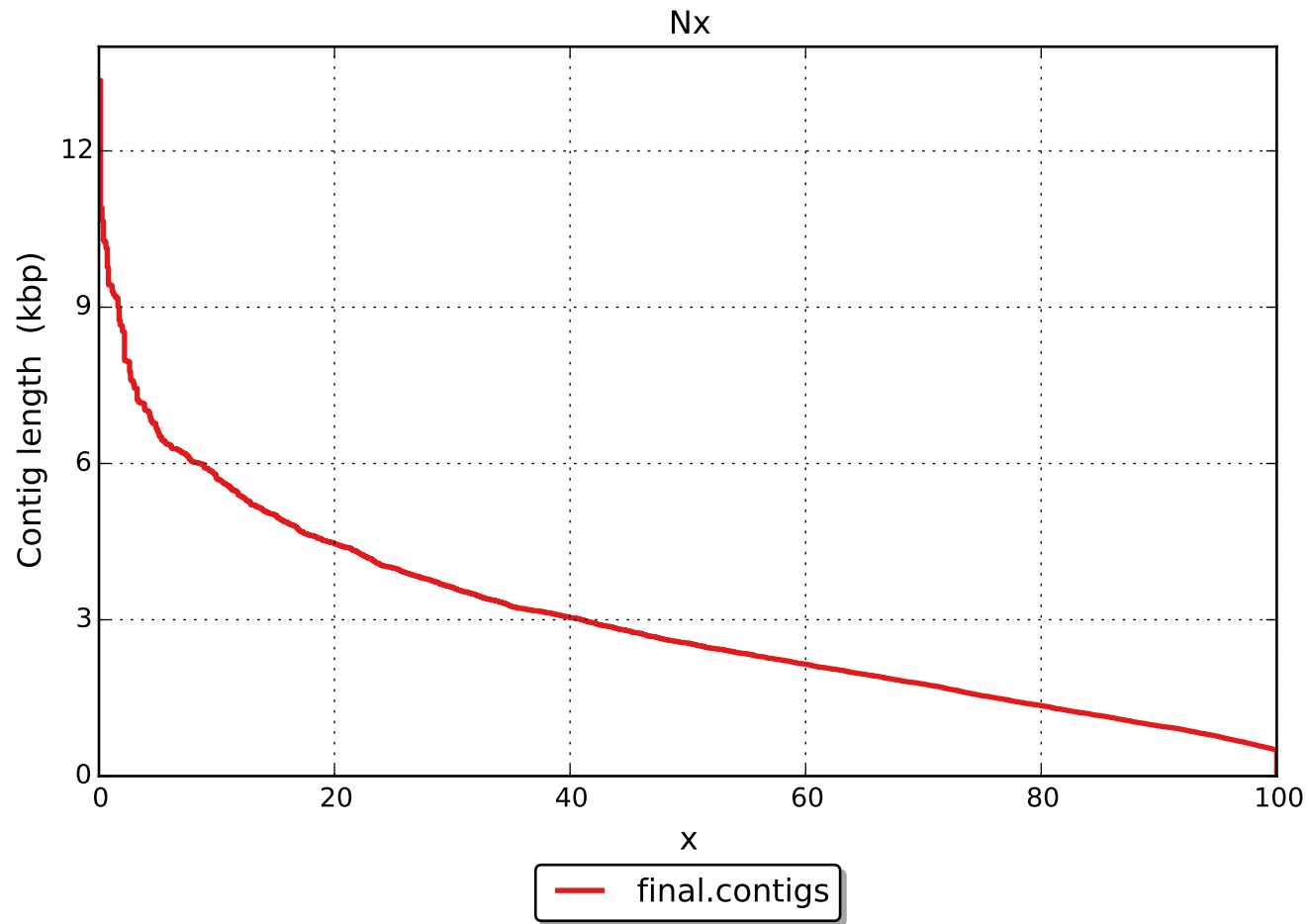
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	2
# mismatches	4342
# indels	4
# short indels	4
# long indels	0
Indels length	4

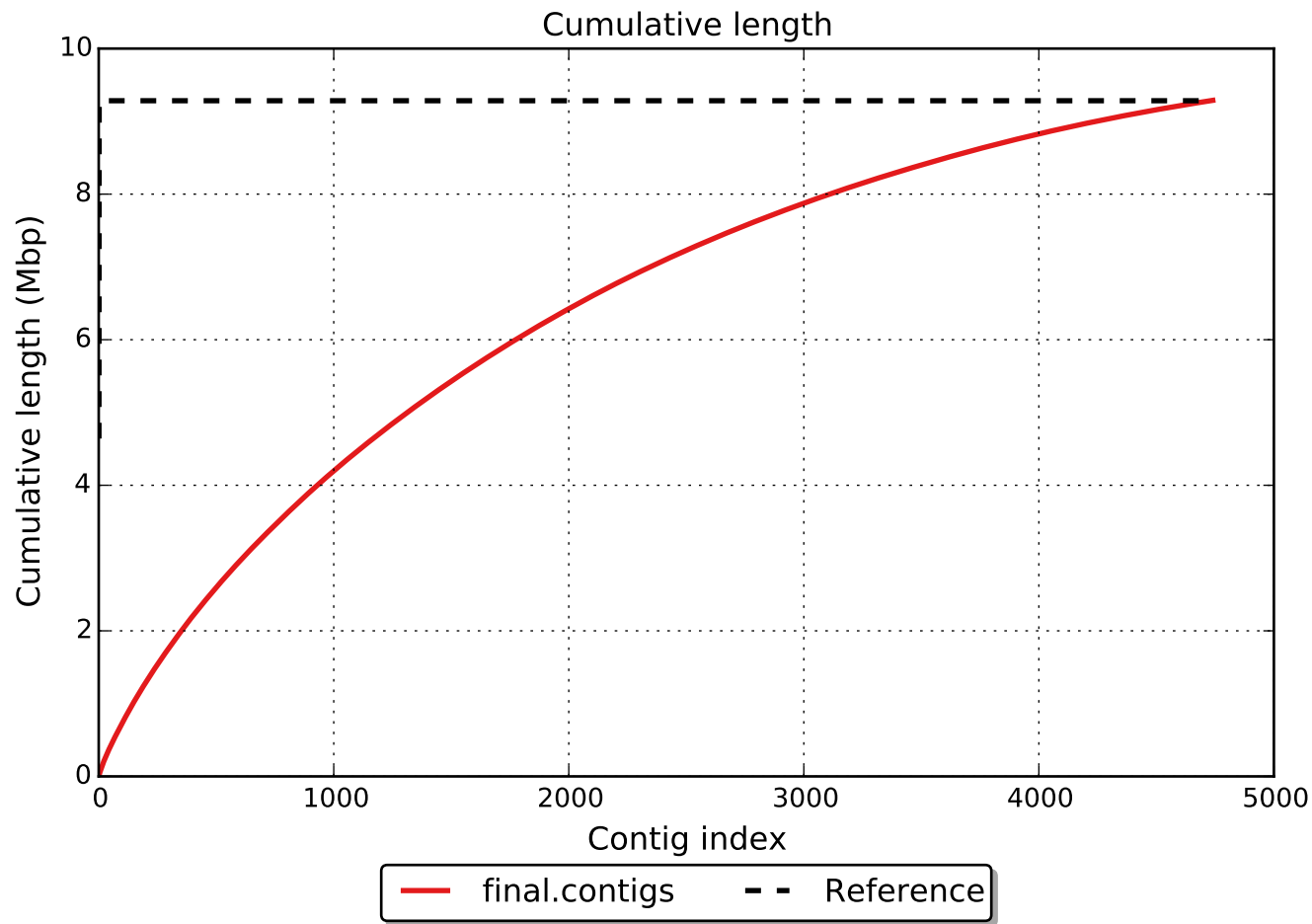
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

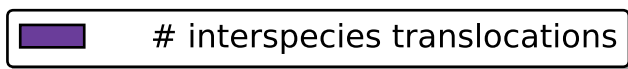
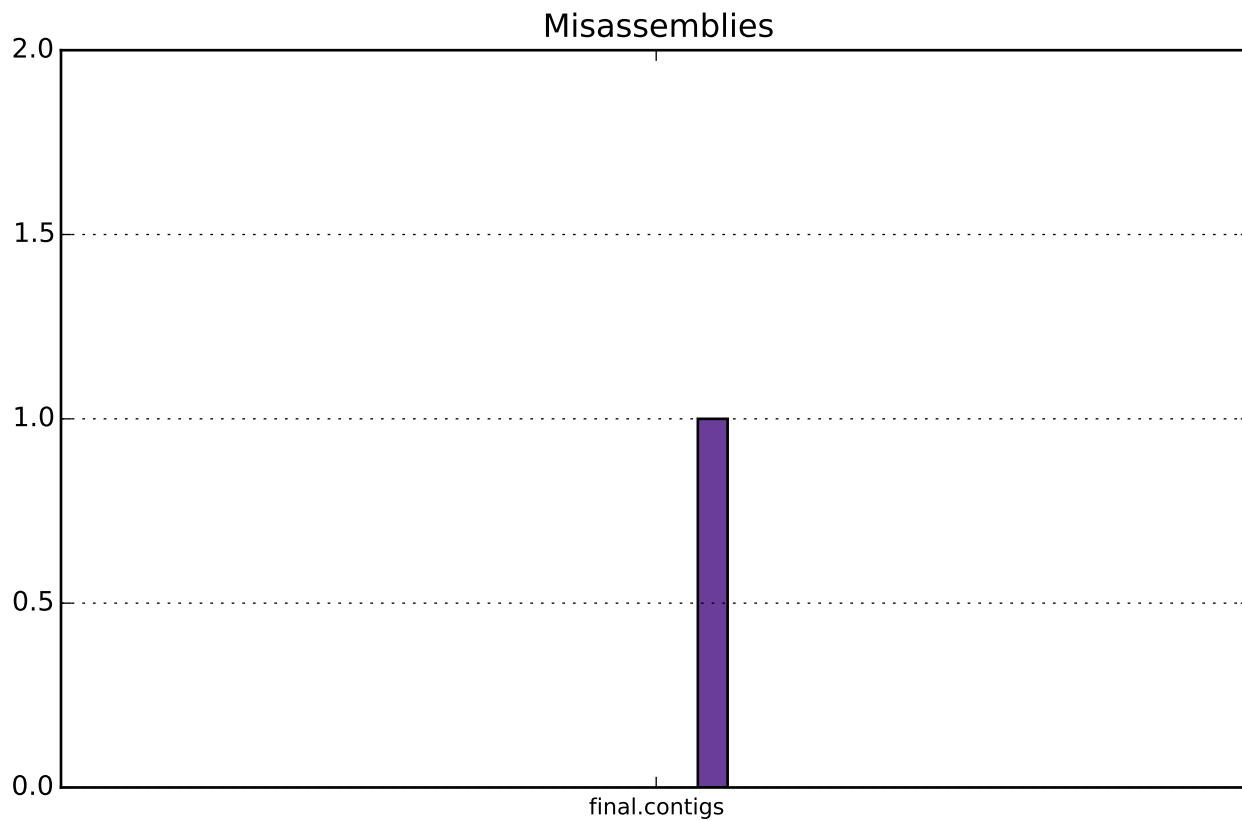
## Unaligned report

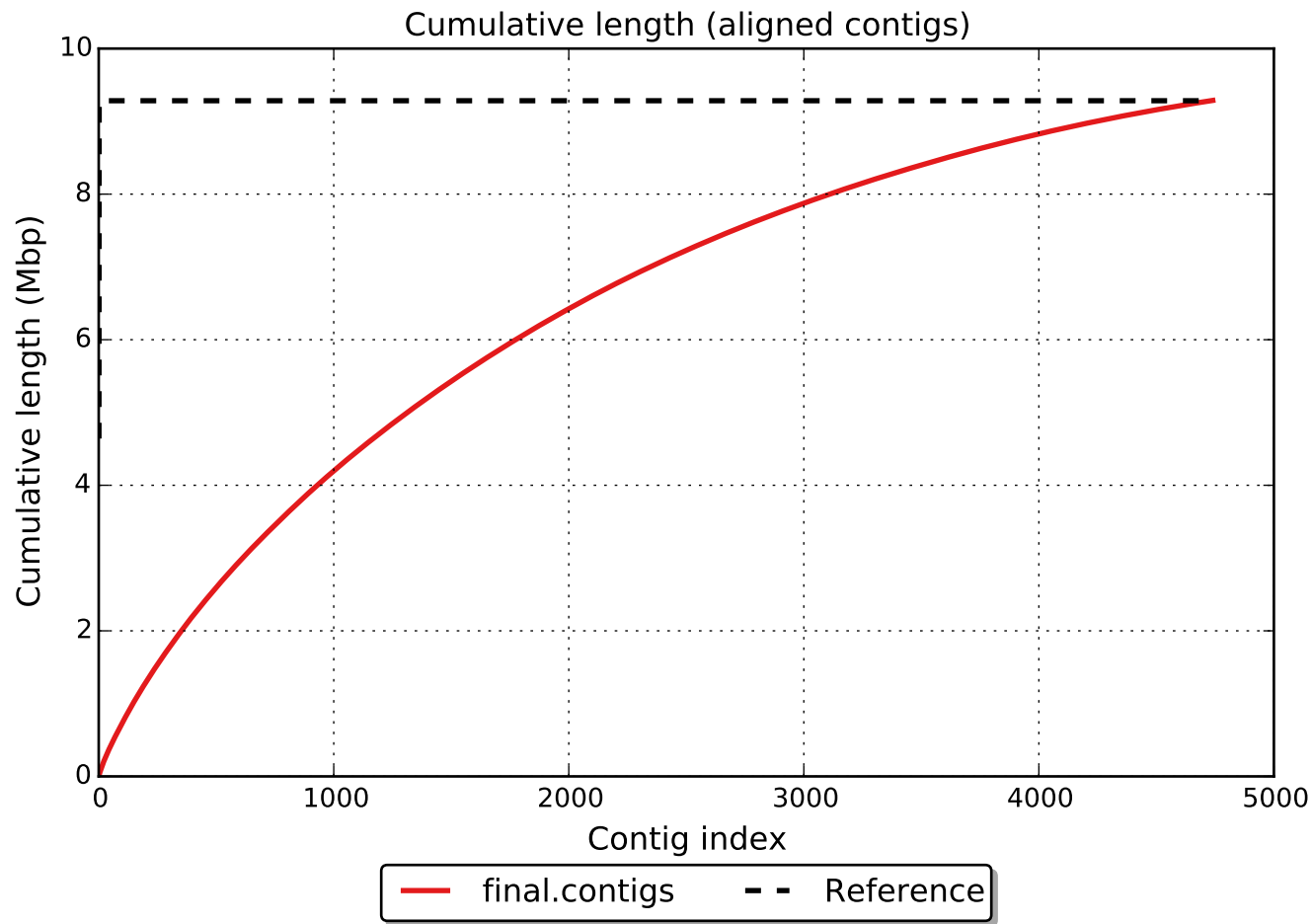
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	555
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	297
# N's	0

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NAx

