

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	2269
# contigs ( $\geq 1000$ bp)	1511
# contigs ( $\geq 5000$ bp)	108
# contigs ( $\geq 10000$ bp)	4
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	4392029
Total length ( $\geq 1000$ bp)	3903367
Total length ( $\geq 5000$ bp)	709559
Total length ( $\geq 10000$ bp)	48458
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	2044
Largest contig	14149
Total length	4302638
Reference length	4641652
N50	2830
N75	1666
L50	500
L75	997
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	30951
# local misassemblies	10
# unaligned contigs	0 + 4 part
Unaligned length	169
Genome fraction (▼)	91.983
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	207.35
# indels per 100 kbp	9.84
Largest alignment	14149
NA50	2825
NA75	1662
LA50	502
LA75	1000

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

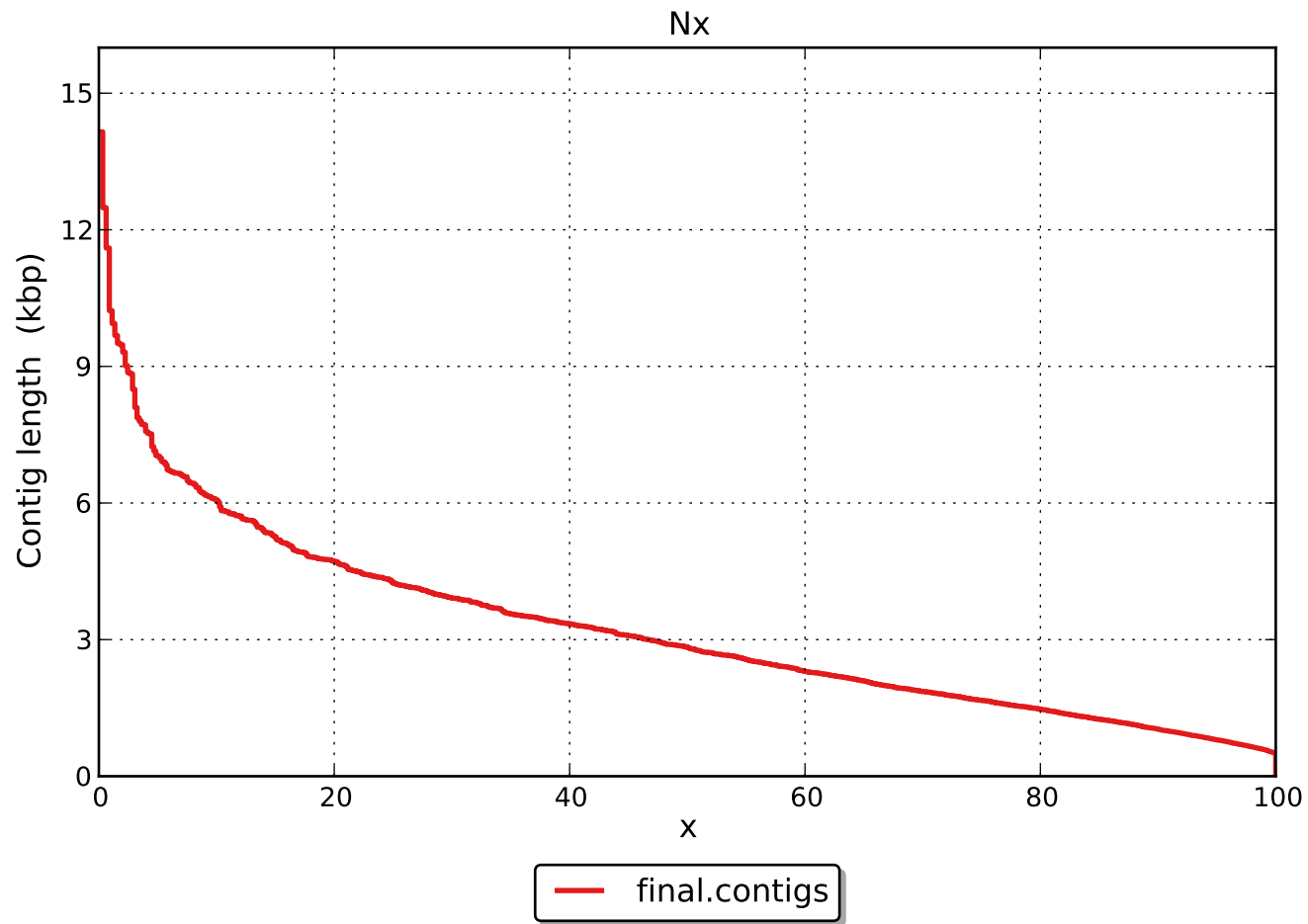
	final.contigs
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	7
Misassembled contigs length	30951
# local misassemblies	10
# mismatches	8853
# indels	420
# short indels	416
# long indels	4
Indels length	714

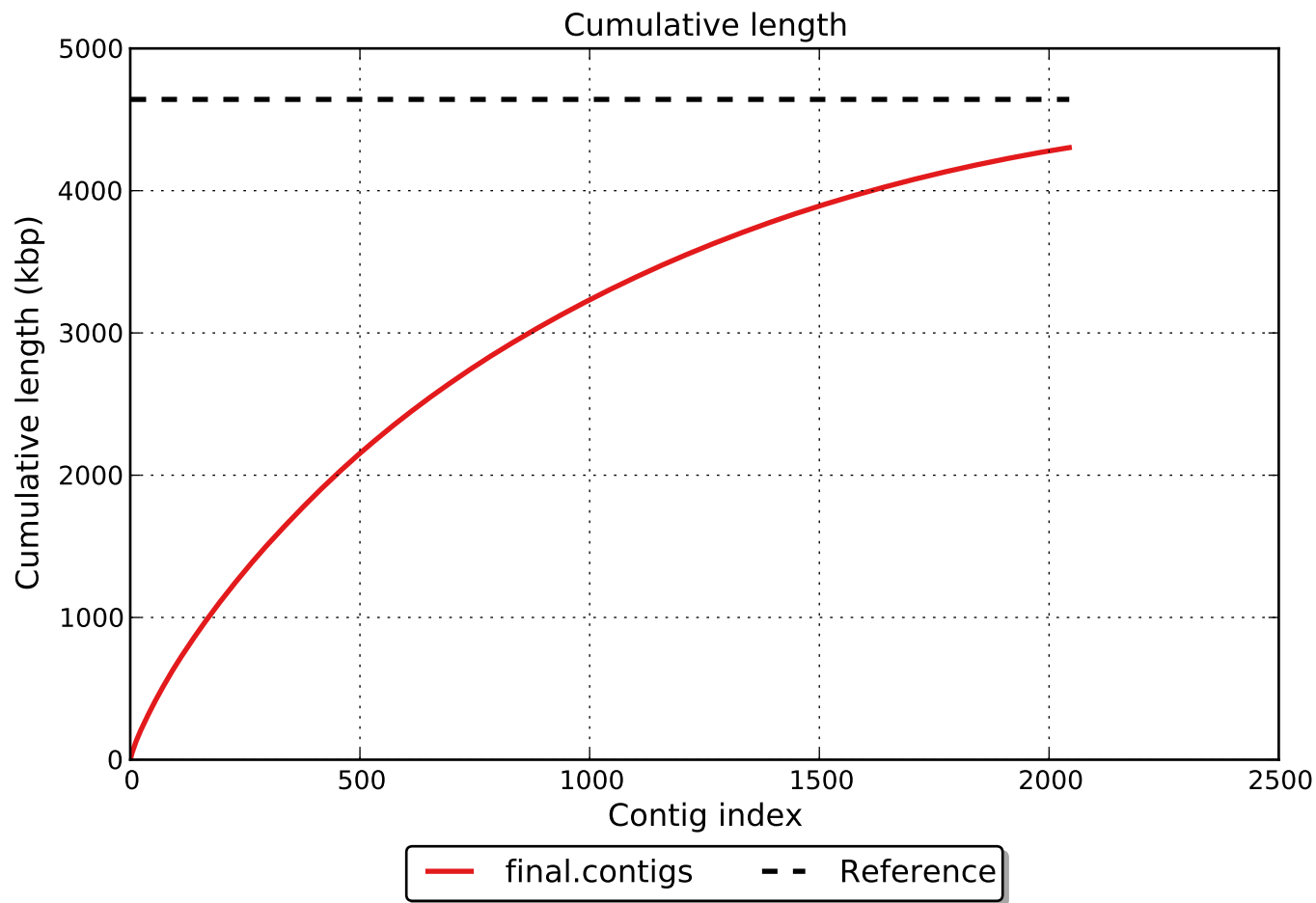
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

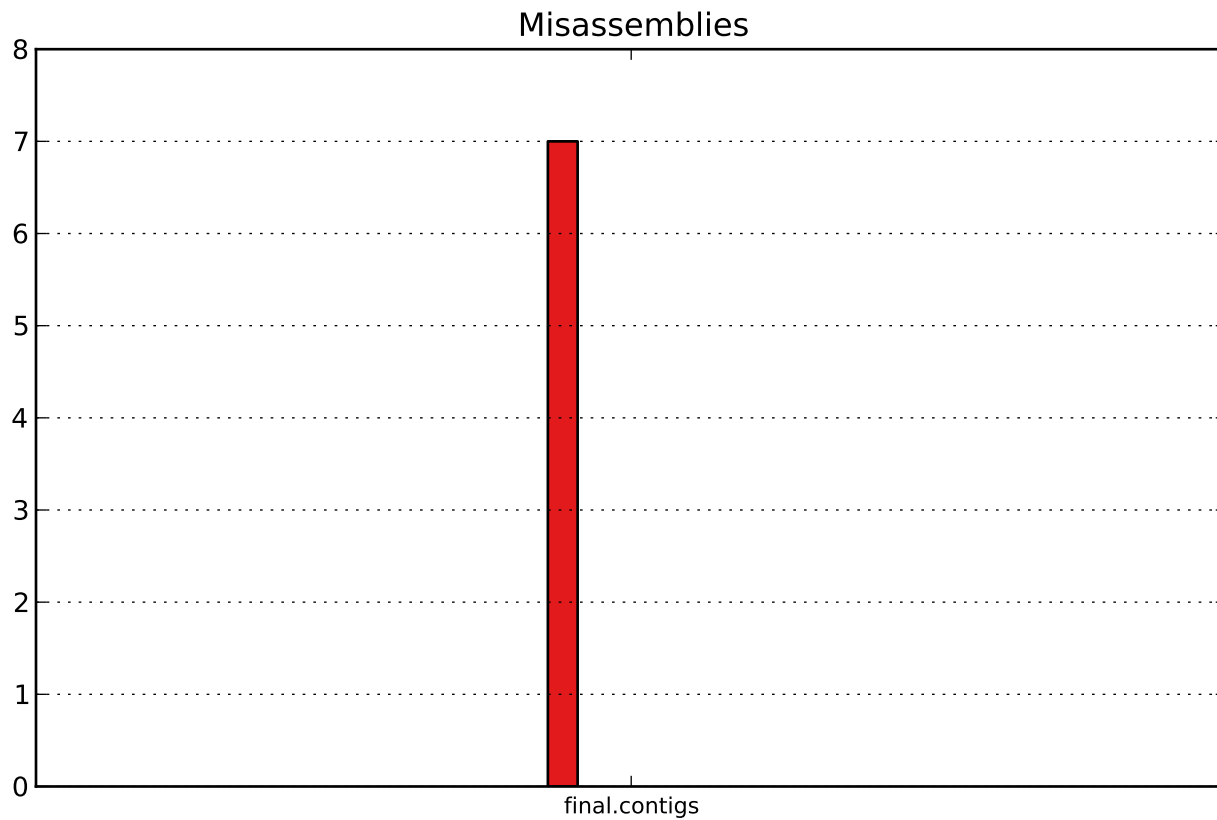
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	169
# N's	0

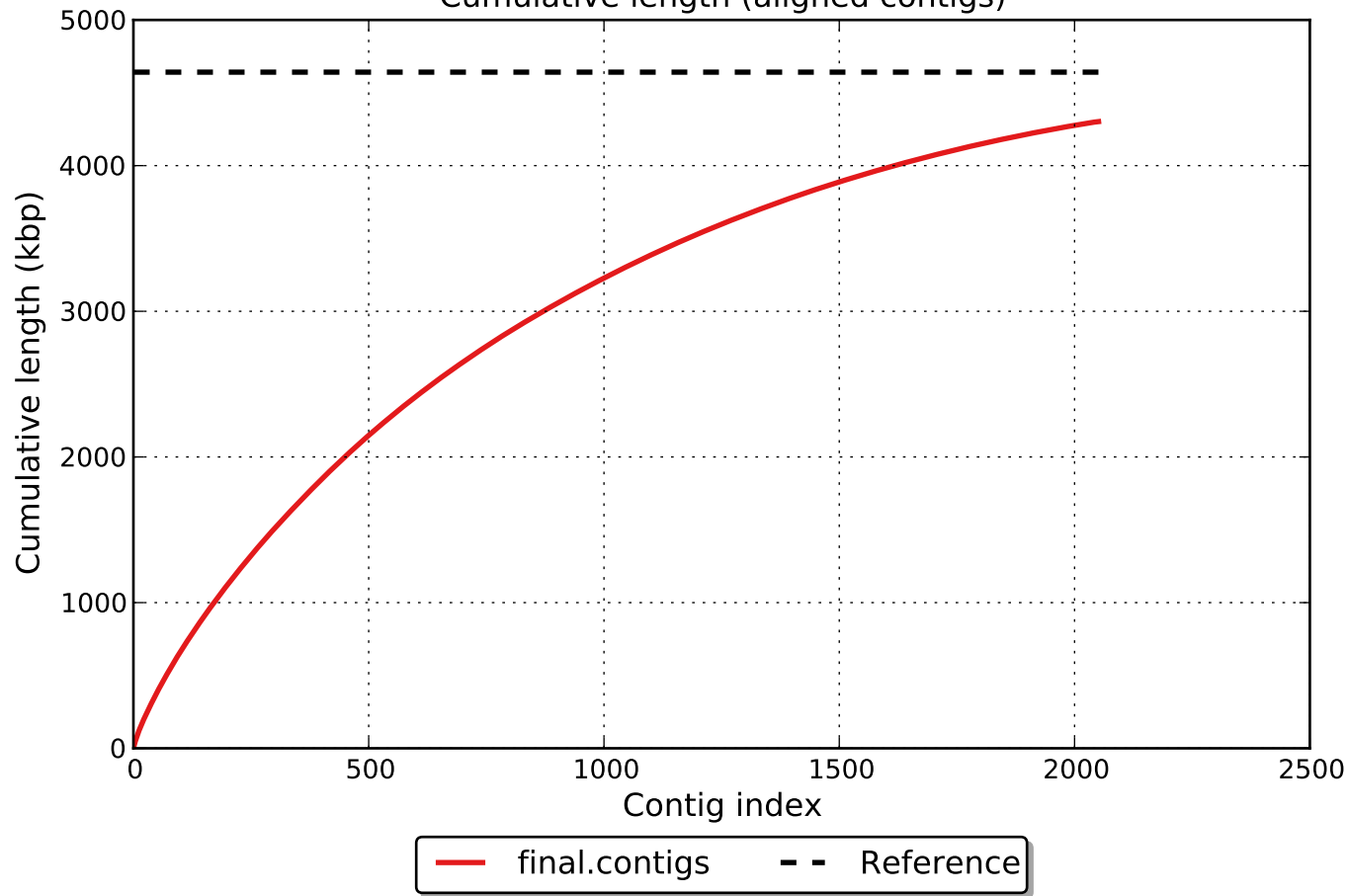
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







Cumulative length (aligned contigs)



NAx

