Report

	final.contigs
# contigs (>= 0 bp)	619
# contigs (>= 1000 bp)	499
# contigs (>= 5000 bp)	397
# contigs (>= 10000 bp)	306
# contigs (>= 25000 bp)	132
# contigs (>= 50000 bp)	31
Total length (>= 0 bp)	9716506
Total length (>= 1000 bp)	9669402
Total length (>= 5000 bp)	9383424
Total length (>= 10000 bp)	8697964
Total length (>= 25000 bp)	5804716
Total length (>= 50000 bp)	2197625
# contigs	529
Largest contig	147879
Total length	9690961
Reference length	9714864
N50	31534
N75	18196
L50	98
L75	201
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.334
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.57
# indels per 100 kbp	0.00
Largest alignment	147879
NA50	31534
NA75	18196
LA50	98
LA75	201

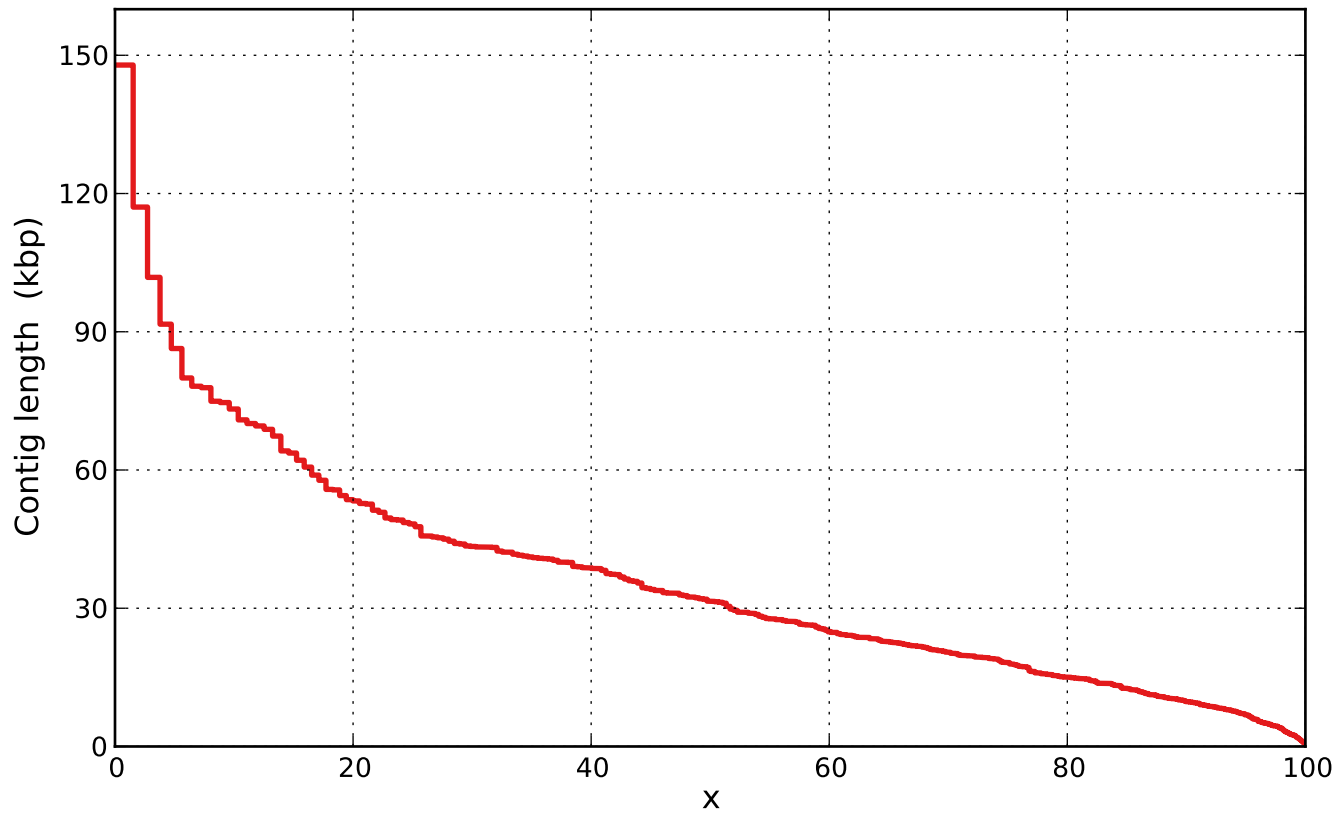All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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	55
# indels	0
# short indels	0
# long indels	0
Indels length	0

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

Unaligned report

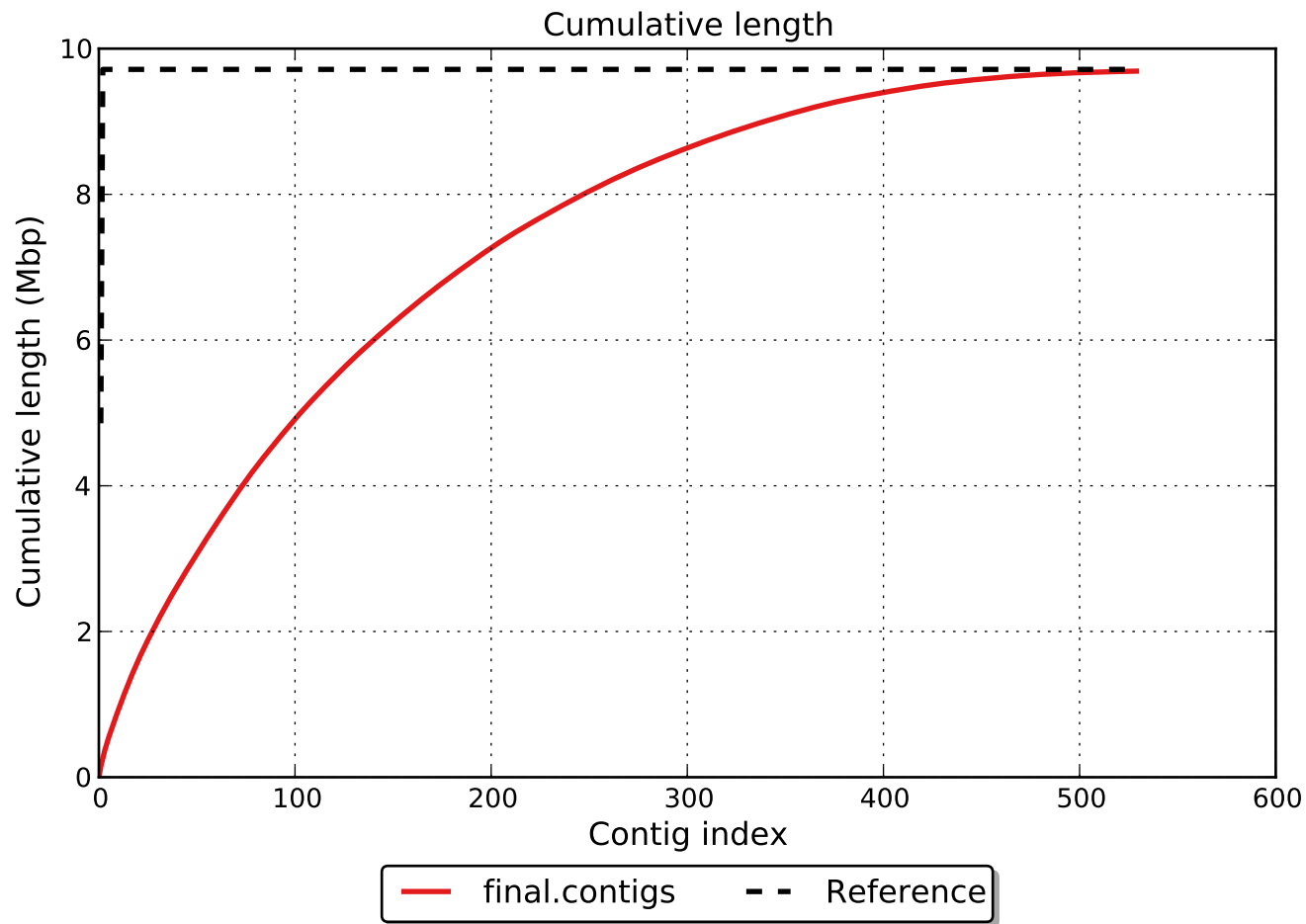|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

Cumulative length
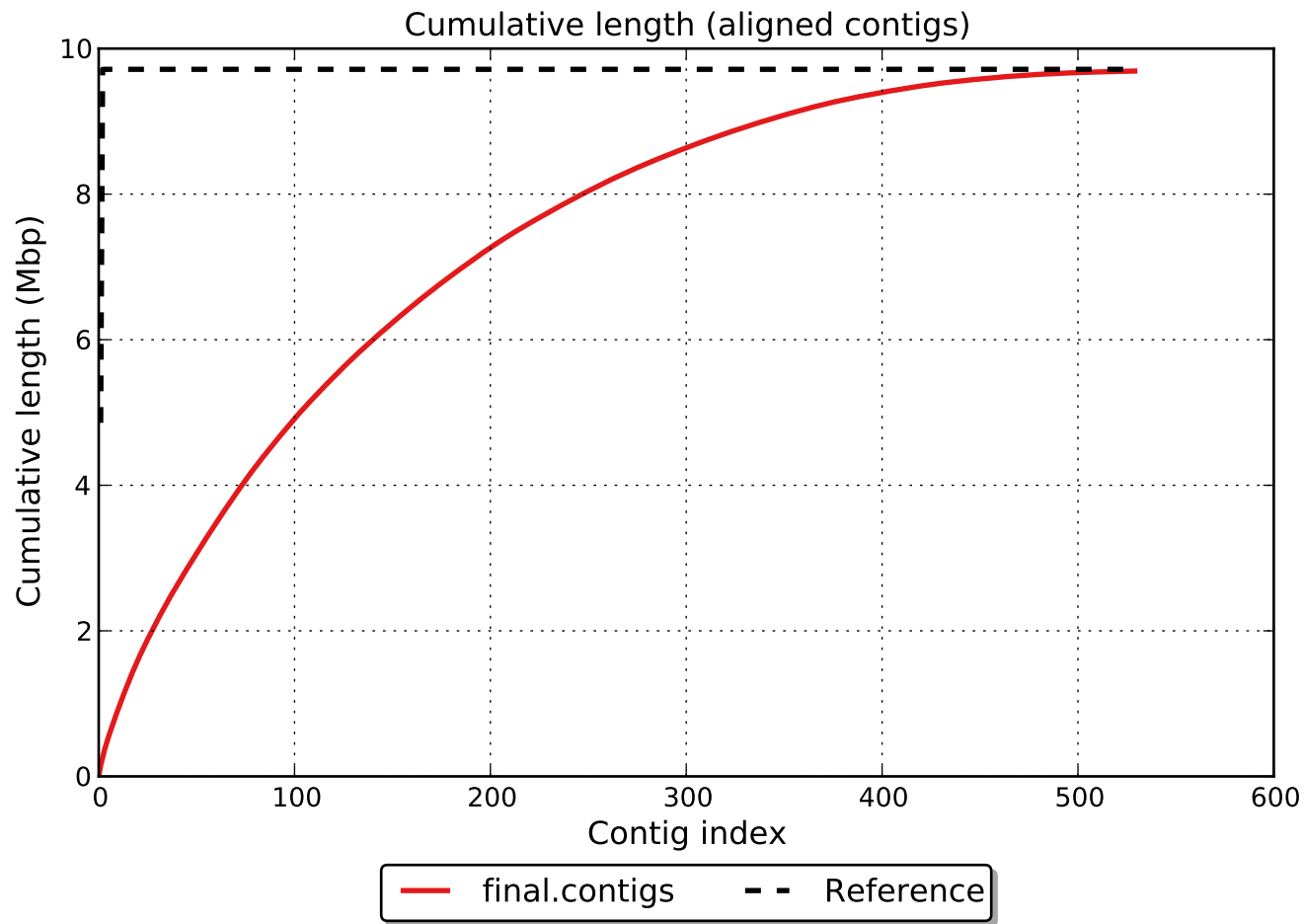
Misassemblies

final.contigs

Cumulative length (aligned contigs)