Report

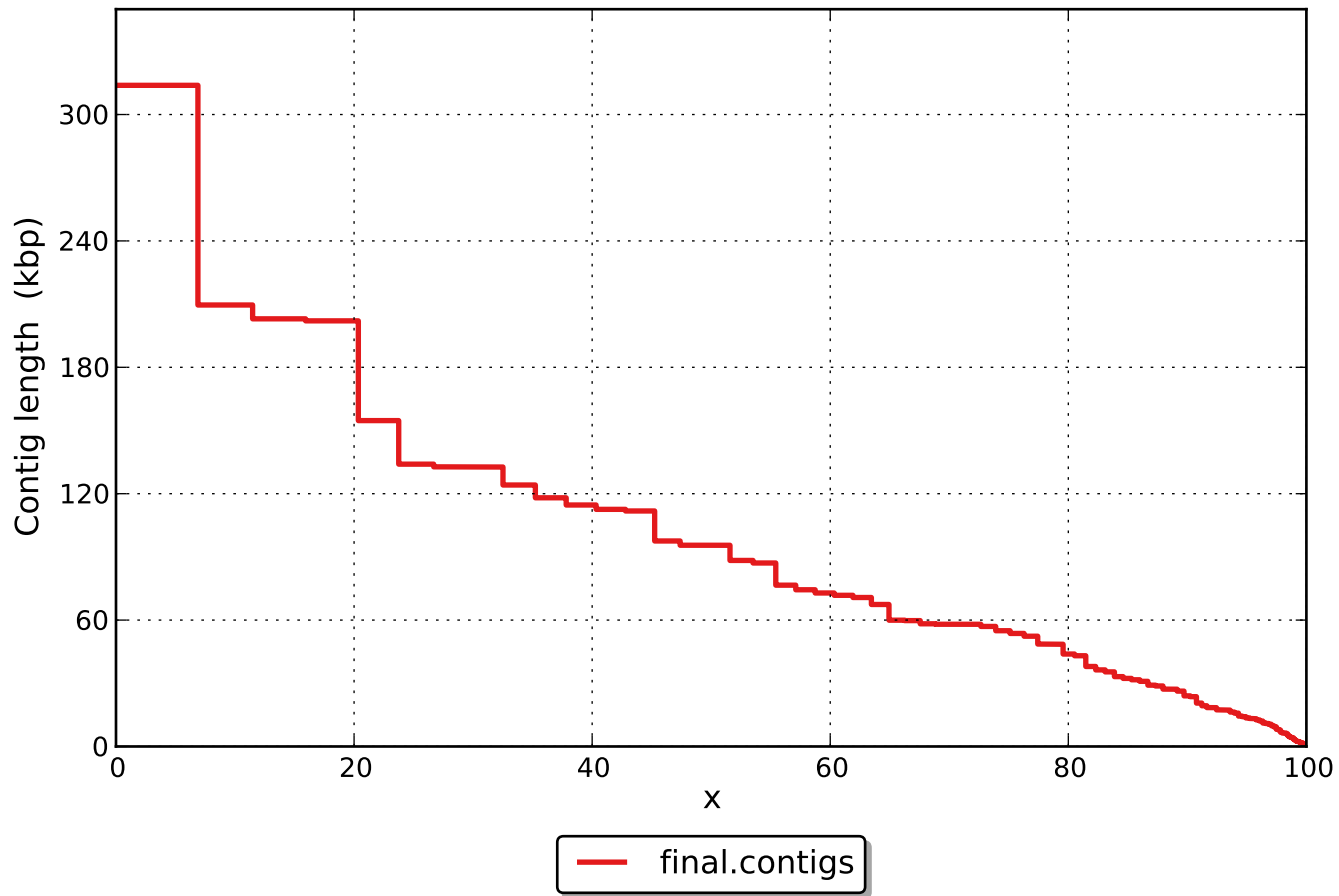|	final.contigs
# contigs (>= 0 bp)	134
# contigs (>= 1000 bp)	107
# contigs (>= 5000 bp)	80
# contigs (>= 10000 bp)	71
# contigs (>= 25000 bp)	50
# contigs (>= 50000 bp)	34
Total length (>= 0 bp)	4566717
Total length (>= 1000 bp)	4555575
Total length (>= 5000 bp)	4492569
Total length (>= 10000 bp)	4426372
Total length (>= 25000 bp)	4091857
Total length (>= 50000 bp)	3531445
# contigs	115
Largest contig	313863
Total length	4560765
Reference length	4641652
N50	95512
N75	54949
L50	16
L75	32
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	84874
# local misassemblies	12
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (%)	98.199
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.30
# indels per 100 kbp	10.16
Largest alignment	313863
NA50	95512
NA75	54949
LA50	16
LA75	32

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	3
# relocations	3
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	84874
# local misassemblies	12
# mismatches	2794
# indels	463
# short indels	462
# long indels	1
Indels length	740

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).
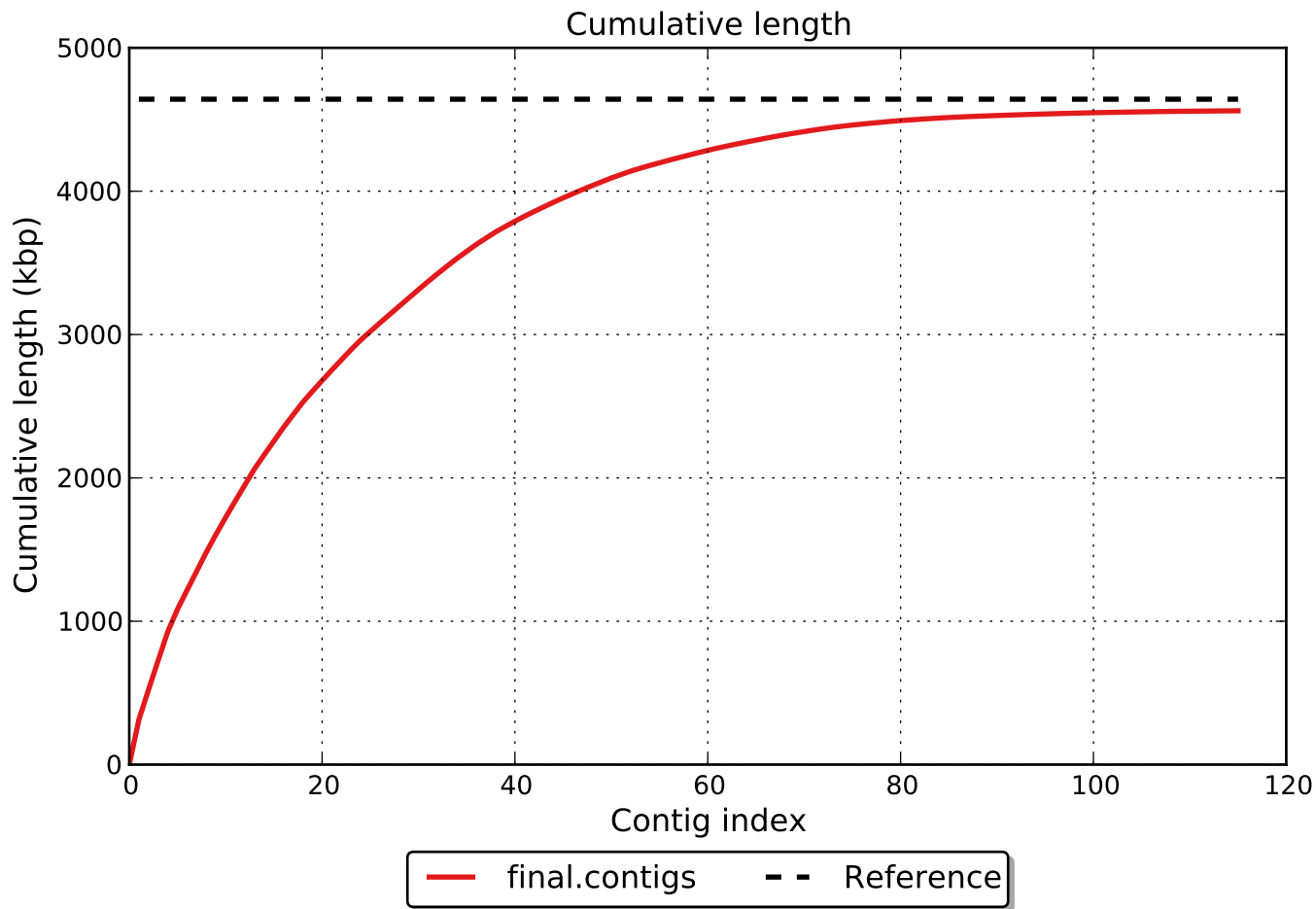
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

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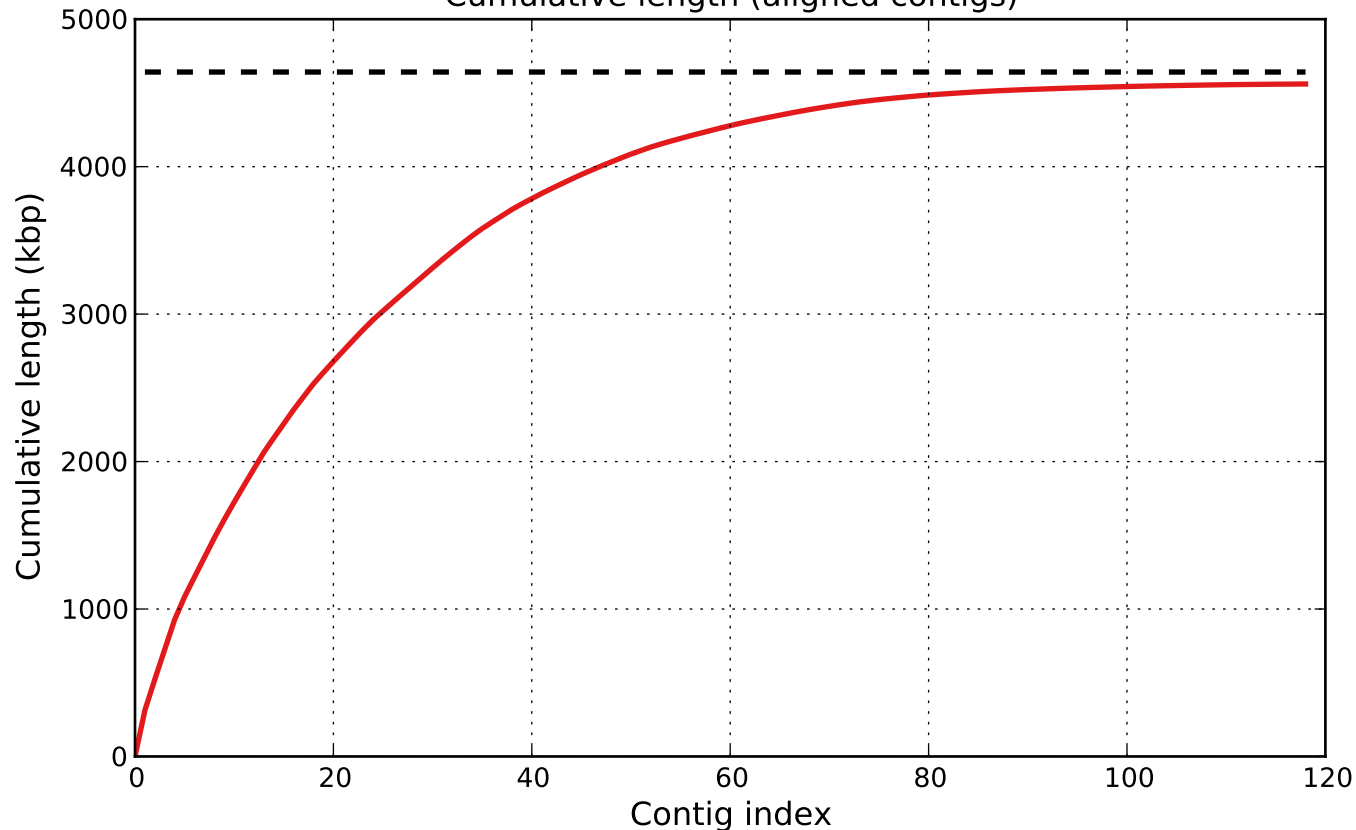(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies
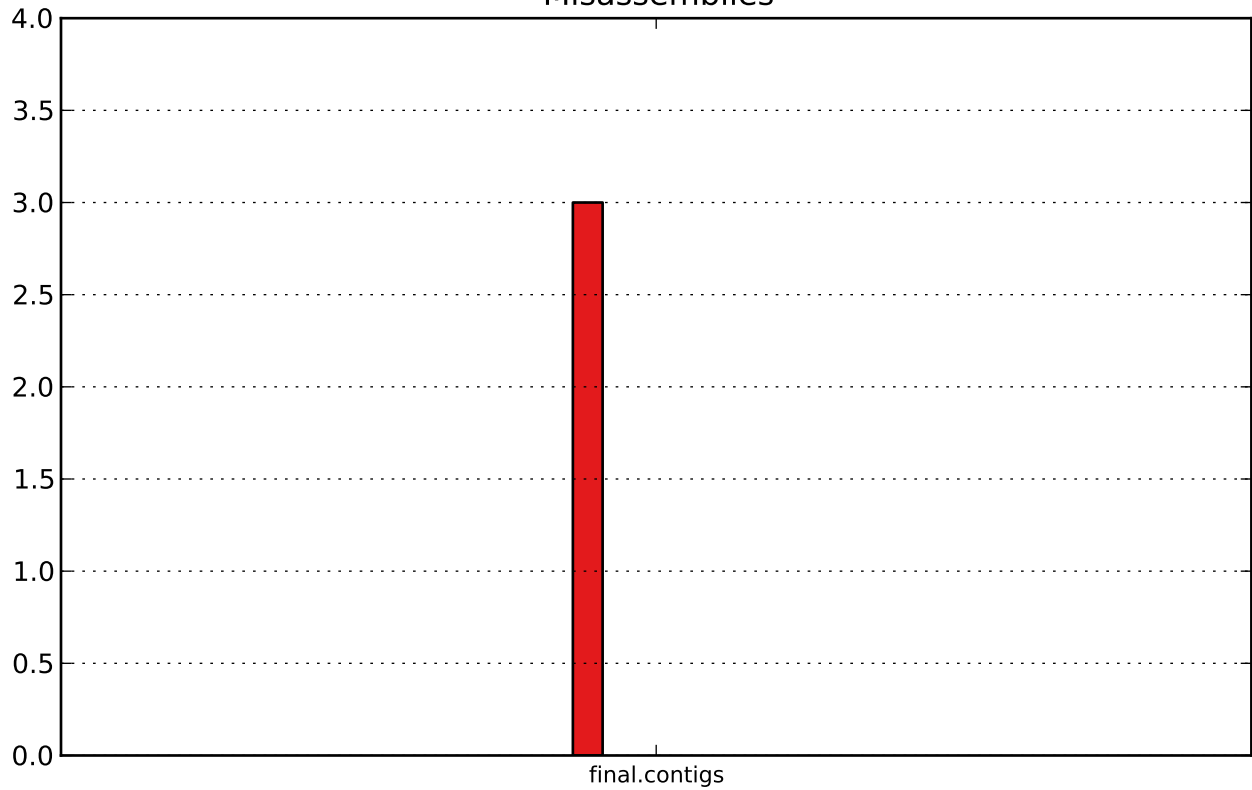
Cumulative length (aligned contigs)