Report

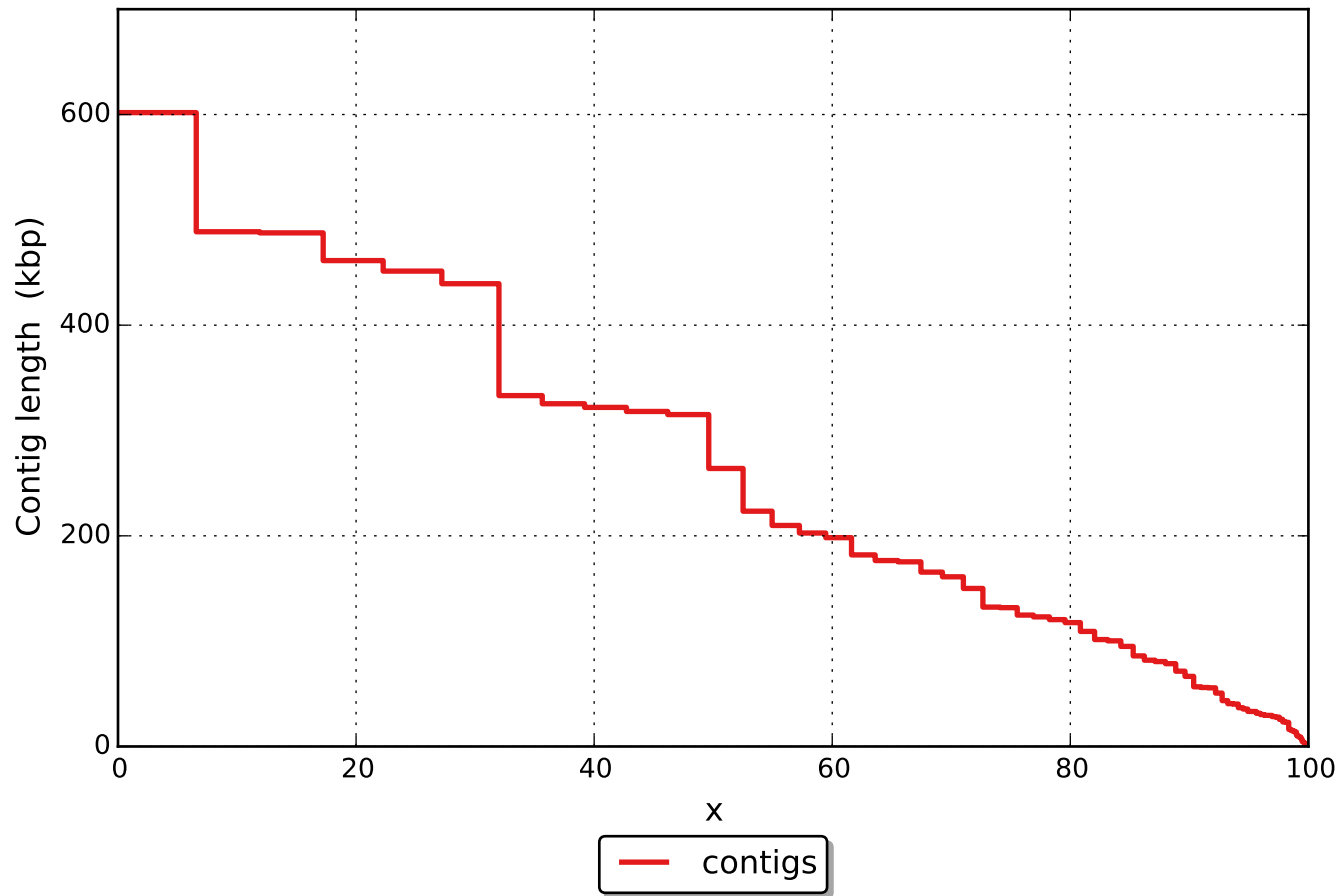|	contigs
# contigs (>= 0 bp)	147
# contigs (>= 1000 bp)	84
# contigs (>= 5000 bp)	67
# contigs (>= 10000 bp)	63
# contigs (>= 25000 bp)	56
# contigs (>= 50000 bp)	42
Total length (>= 0 bp)	9168920
Total length (>= 1000 bp)	9144650
Total length (>= 5000 bp)	9108381
Total length (>= 10000 bp)	9074911
Total length (>= 25000 bp)	8958447
Total length (>= 50000 bp)	8492499
# contigs	99
Largest contig	601815
Total length	9155947
Reference length	9283304
N50	263950
N75	131793
L50	12
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36823
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.144
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	194.98
# indels per 100 kbp	0.84
Largest alignment	601815
NA50	263950
NA75	131793
LA50	12
LA75	24

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

	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36823
# local misassemblies	1
# mismatches	17946
# indels	77
# short indels	77
# long indels	0
Indels length	81

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).
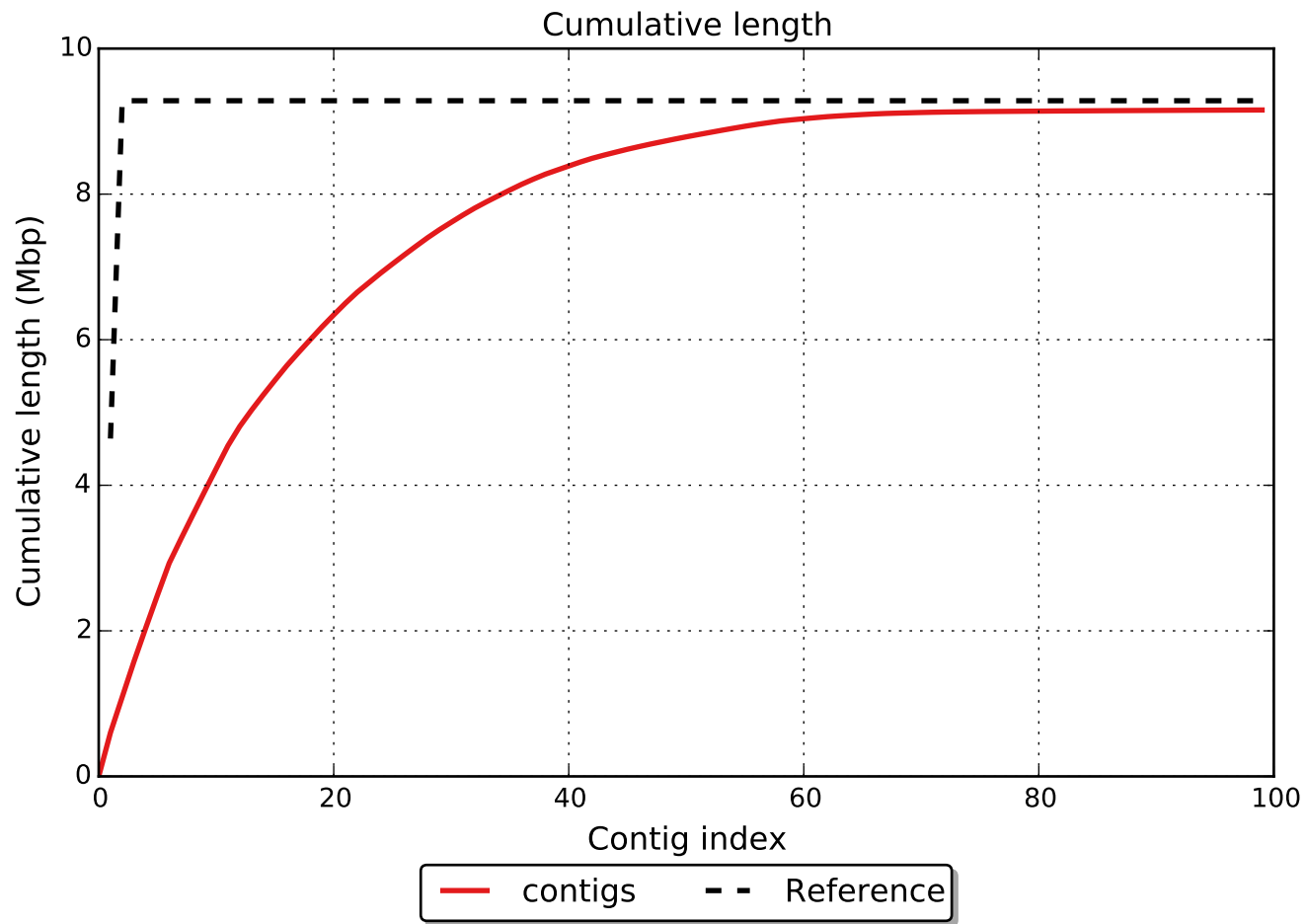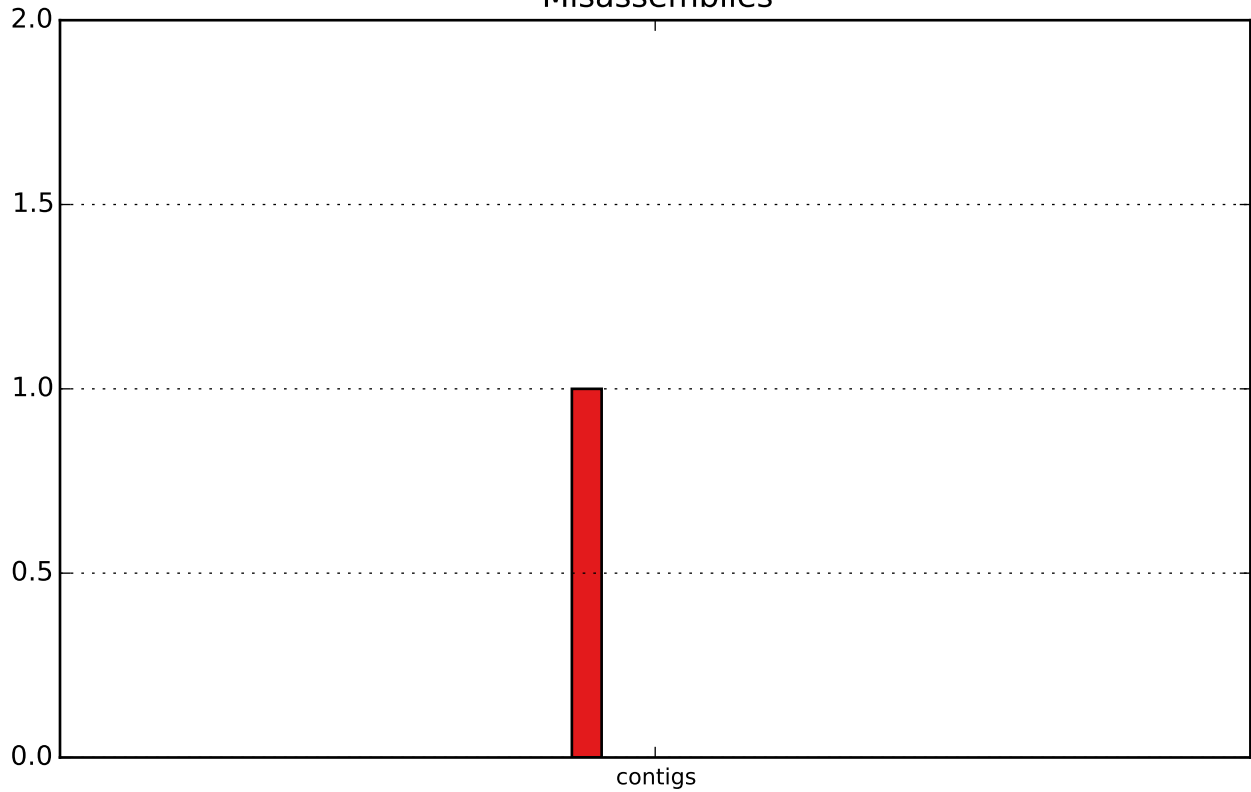
Unaligned report

	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).
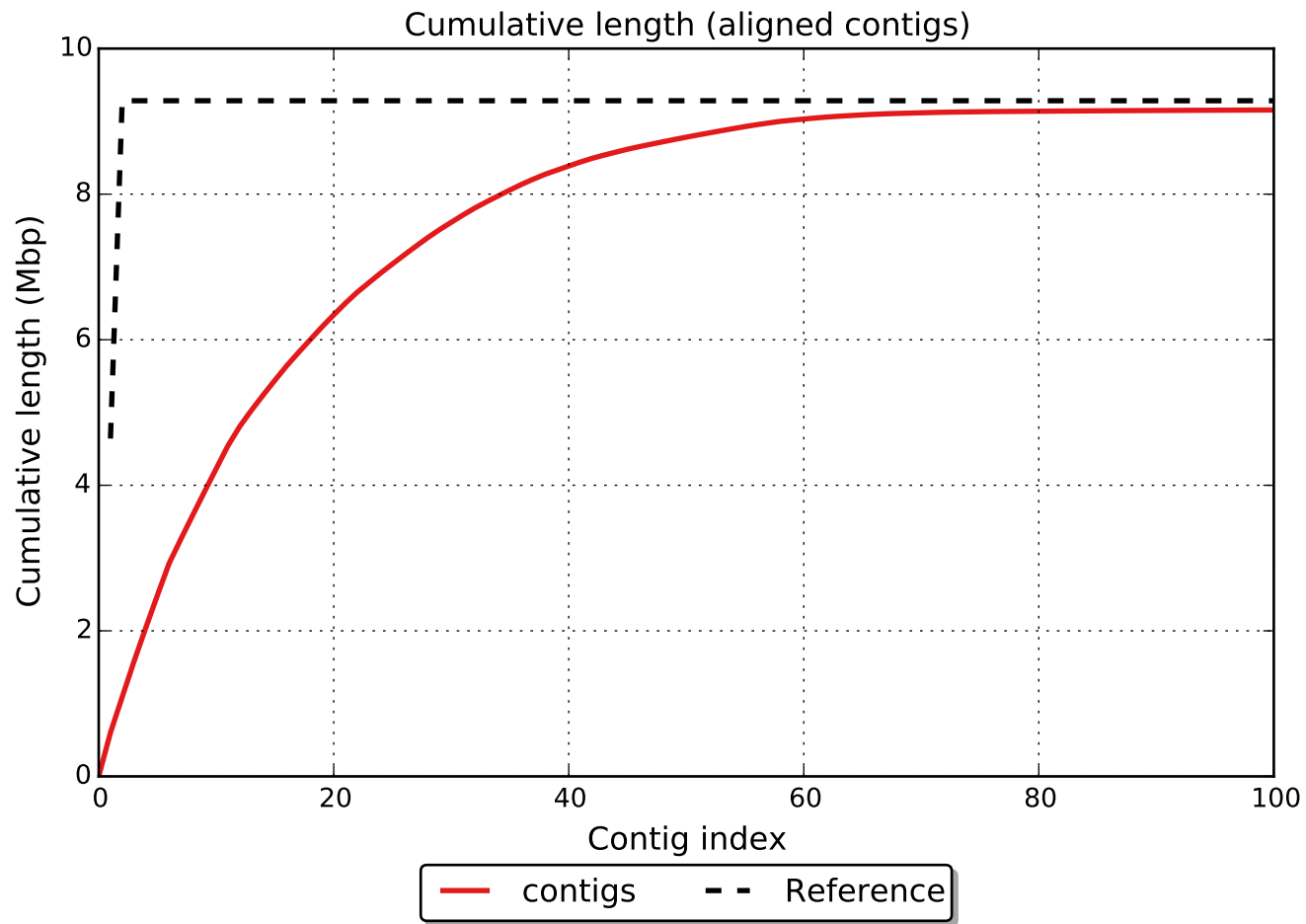
Cumulative length

Misassemblies

Cumulative length (aligned contigs)