Report

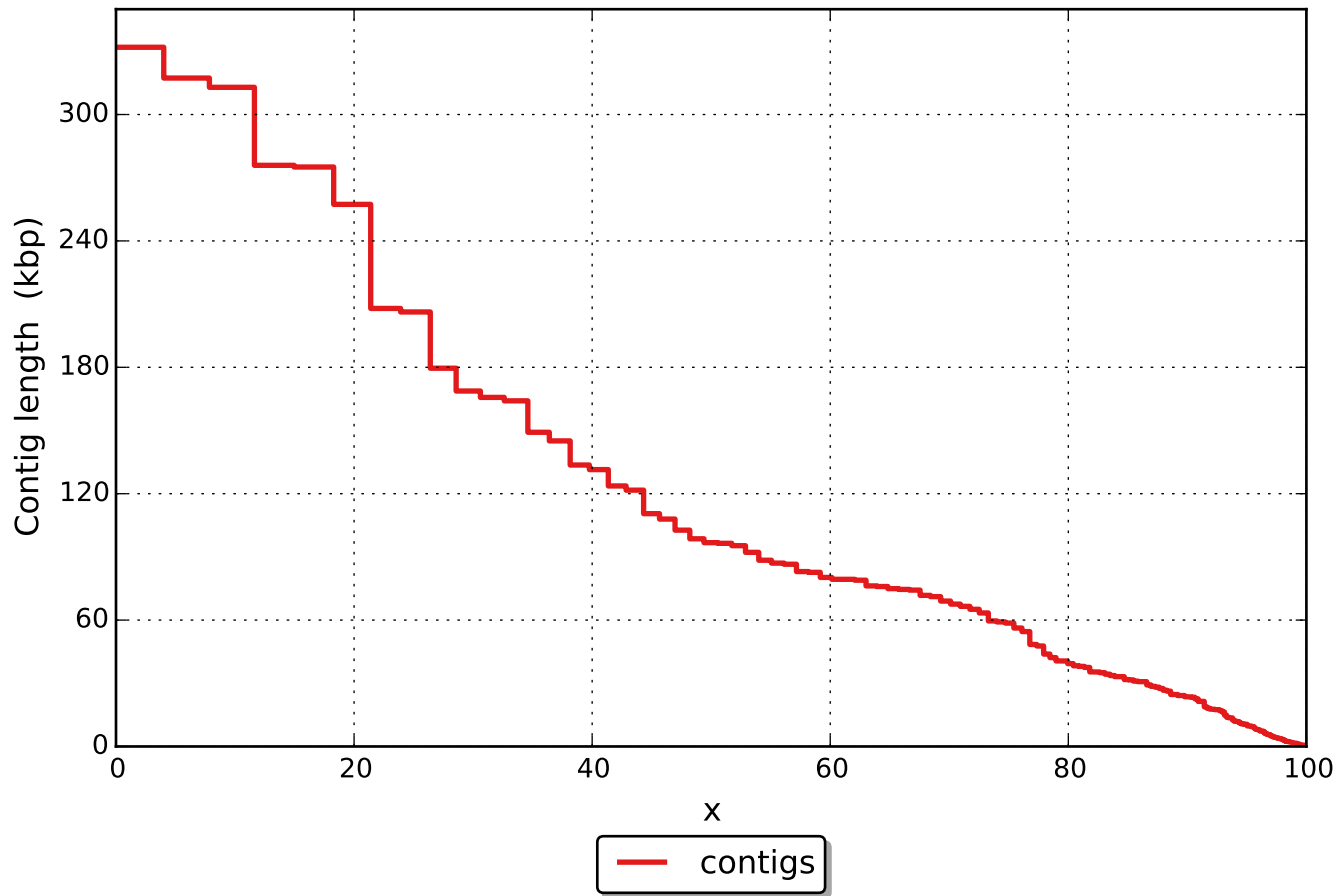|	contigs
# contigs (>= 0 bp)	917
# contigs (>= 1000 bp)	220
# contigs (>= 5000 bp)	133
# contigs (>= 10000 bp)	111
# contigs (>= 25000 bp)	80
# contigs (>= 50000 bp)	52
Total length (>= 0 bp)	8504957
Total length (>= 1000 bp)	8232005
Total length (>= 5000 bp)	8027570
Total length (>= 10000 bp)	7862901
Total length (>= 25000 bp)	7330881
Total length (>= 50000 bp)	6351879
# contigs	287
Largest contig	331931
Total length	8274540
Reference length	9283304
N50	96756
N75	58576
L50	23
L75	50
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	294991
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.921
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	991.56
# indels per 100 kbp	0.83
Largest alignment	331931
NA50	96756
NA75	54537
LA50	23
LA75	51

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	3
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	294991
# local misassemblies	5
# mismatches	80931
# indels	68
# short indels	68
# long indels	0
Indels length	82

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).
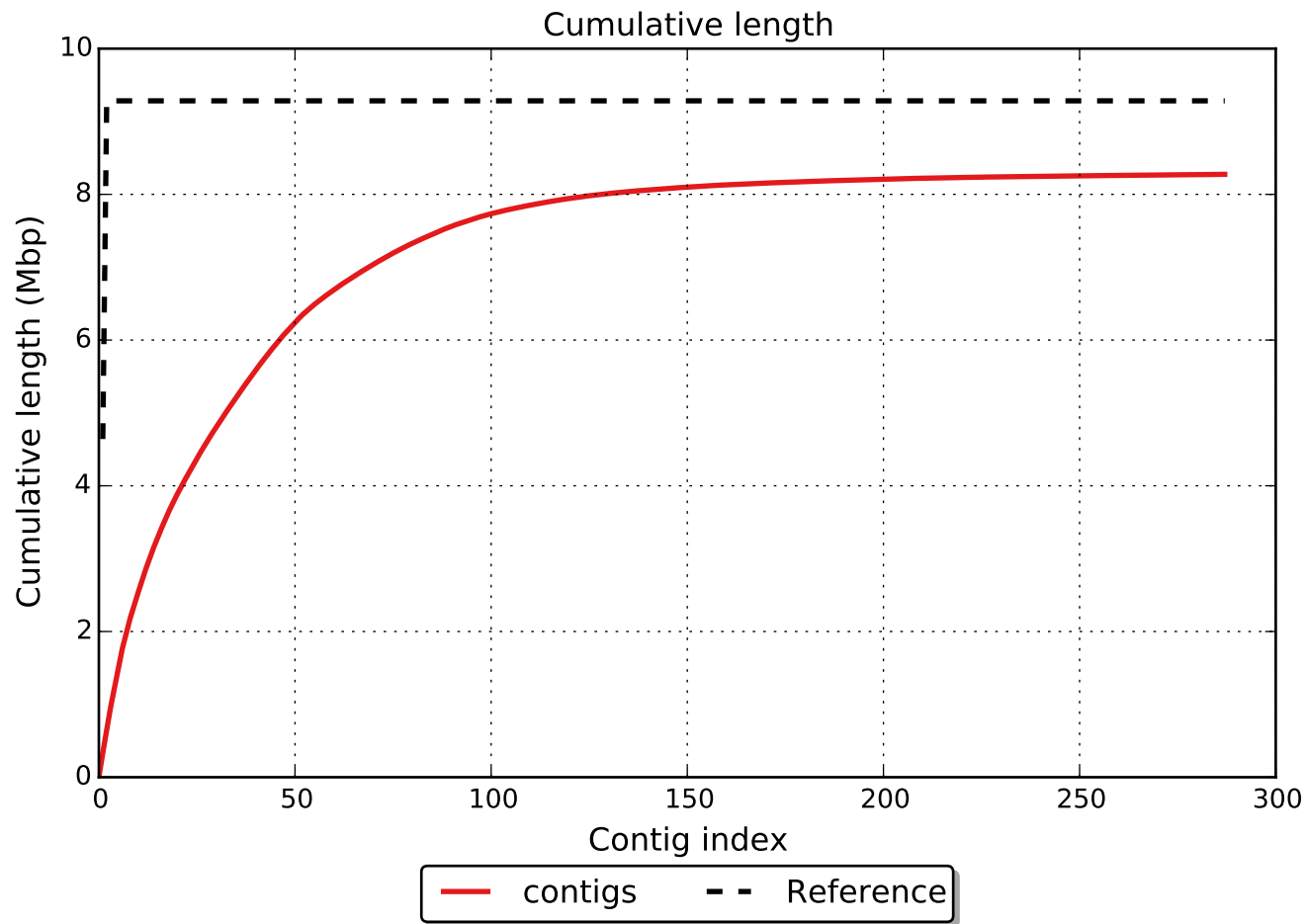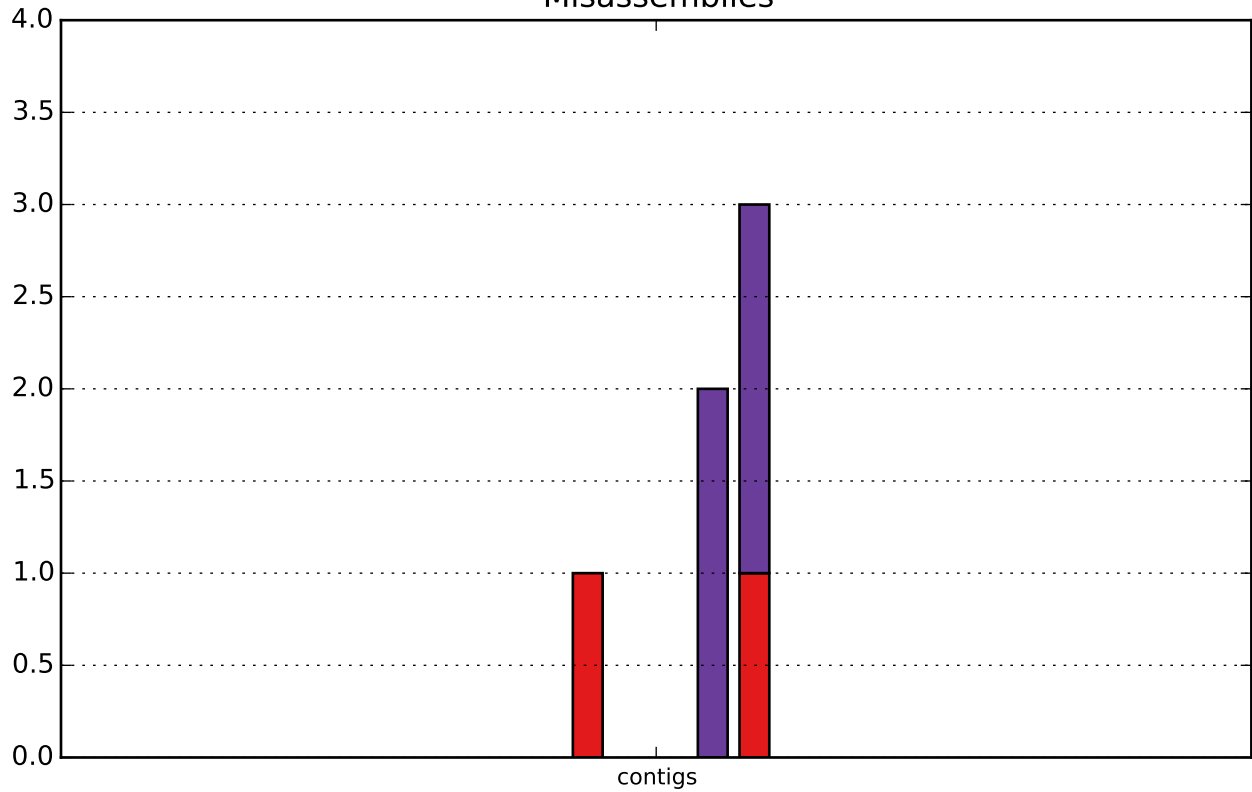
Unaligned report

	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).
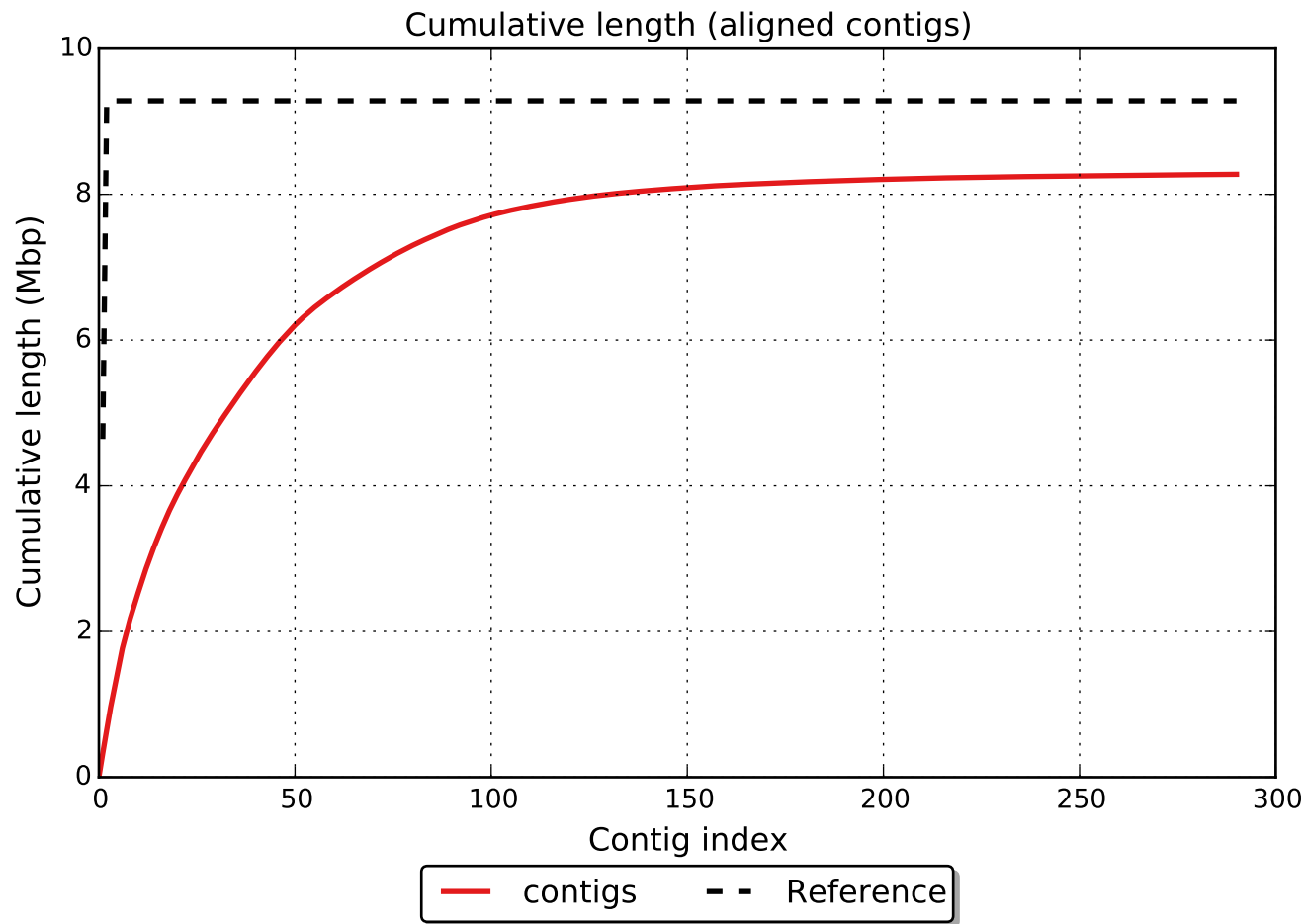
Cumulative length

Misassemblies

Cumulative length (aligned contigs)