Report

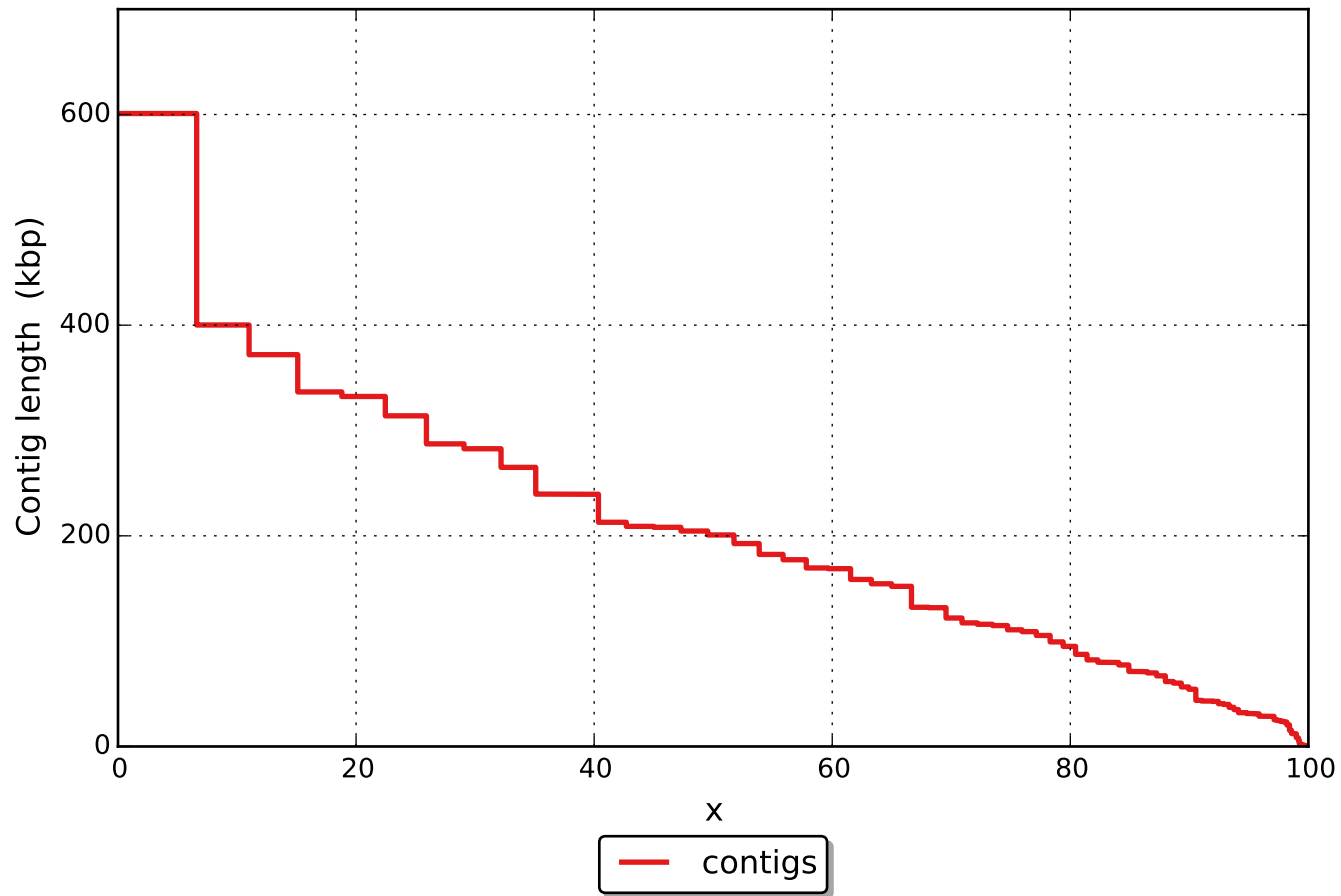|	contigs
# contigs (>= 0 bp)	240
# contigs (>= 1000 bp)	105
# contigs (>= 5000 bp)	77
# contigs (>= 10000 bp)	74
# contigs (>= 25000 bp)	66
# contigs (>= 50000 bp)	48
Total length (>= 0 bp)	9123427
Total length (>= 1000 bp)	9068952
Total length (>= 5000 bp)	9023066
Total length (>= 10000 bp)	9000541
Total length (>= 25000 bp)	8856332
Total length (>= 50000 bp)	8233238
# contigs	142
Largest contig	600951
Total length	9093038
Reference length	9283304
N50	200817
N75	110783
L50	16
L75	31
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.924
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	548.66
# indels per 100 kbp	0.81
Largest alignment	600951
NA50	200817
NA75	110783
LA50	16
LA75	31

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	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	49877
# indels	74
# short indels	74
# long indels	0
Indels length	74

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).
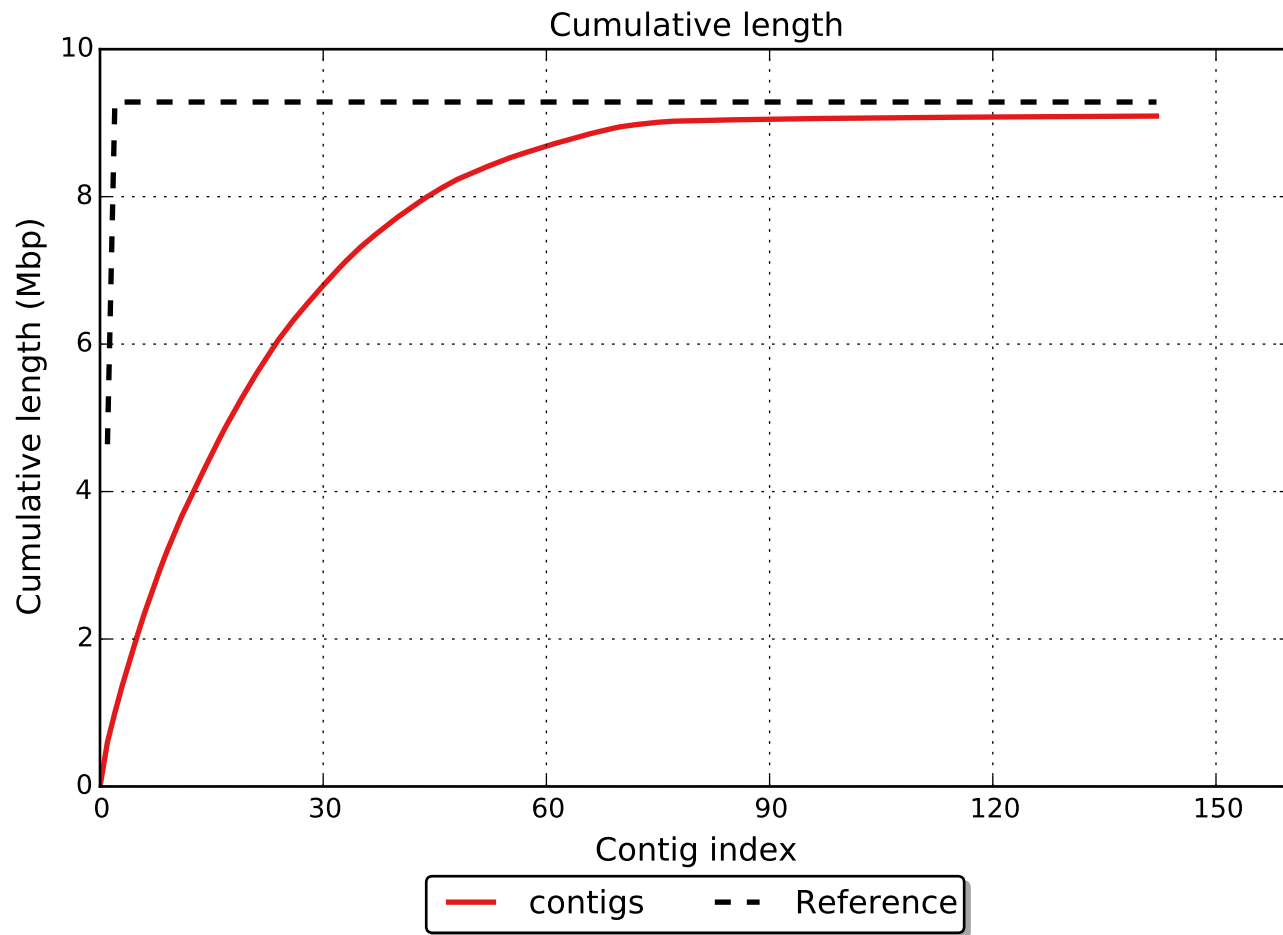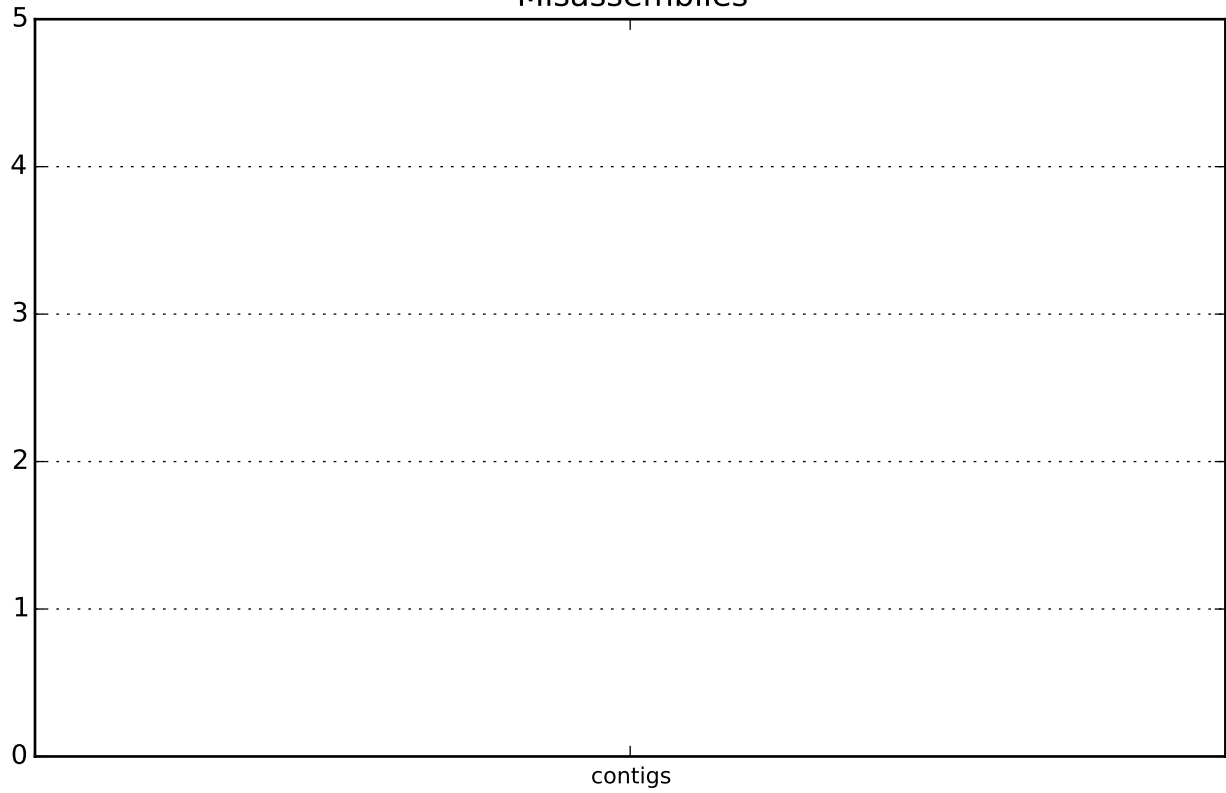
Unaligned report

	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
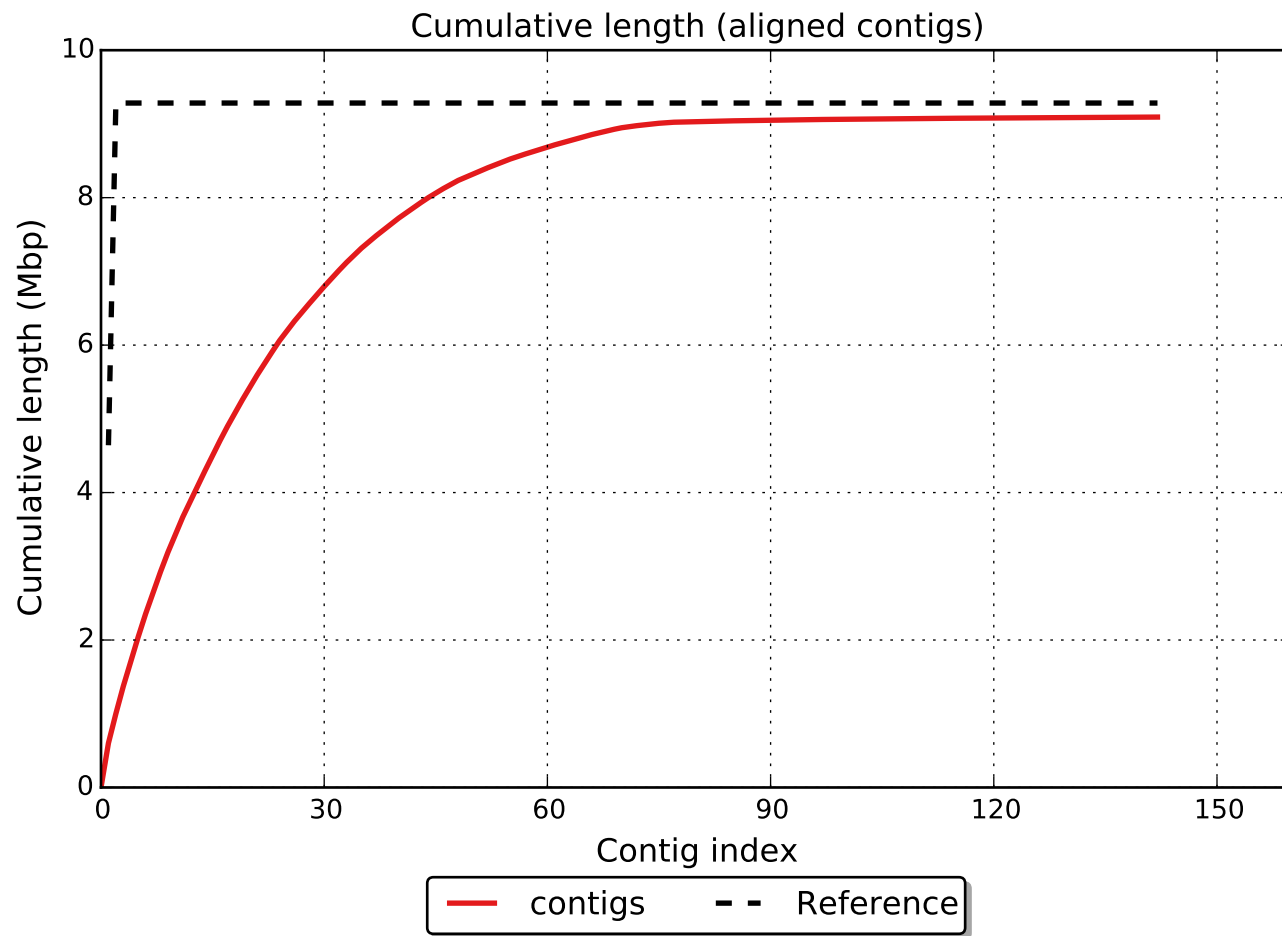
Misassemblies

contigs

Cumulative length (aligned contigs)