Report

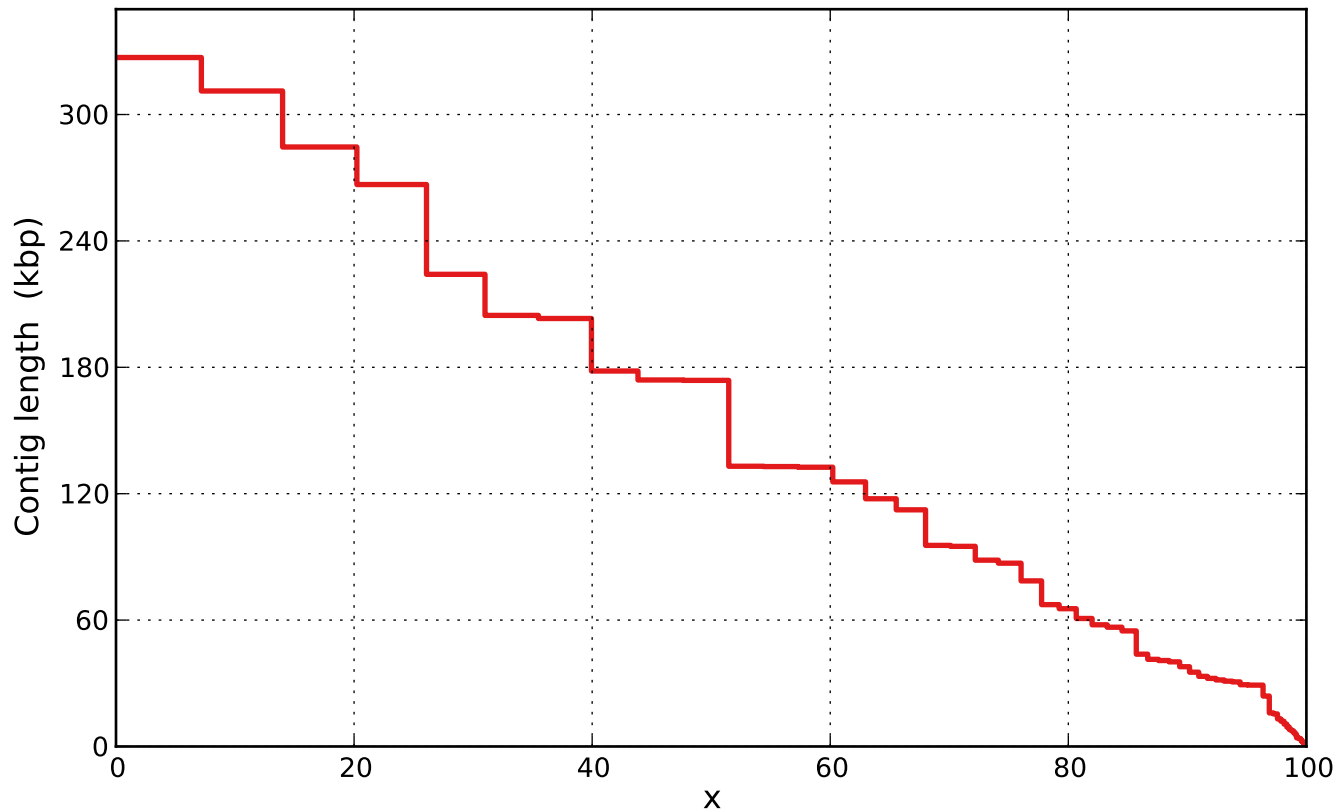|	scaffolds
# contigs (>= 0 bp)	100
# contigs (>= 1000 bp)	68
# contigs (>= 5000 bp)	52
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4564530
Total length (>= 1000 bp)	4559108
Total length (>= 5000 bp)	4522732
Total length (>= 10000 bp)	4485521
Total length (>= 25000 bp)	4394531
Total length (>= 50000 bp)	3908847
# contigs	70
Largest contig	327061
Total length	4560582
Reference length	4641652
N50	173797
N75	87010
L50	10
L75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.204
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	60.22
# indels per 100 kbp	8.88
Largest alignment	327061
NA50	172281
NA75	87010
LA50	10
LA75	20

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

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# mismatches	2745
# indels	405
# short indels	399
# long indels	6
Indels length	627

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

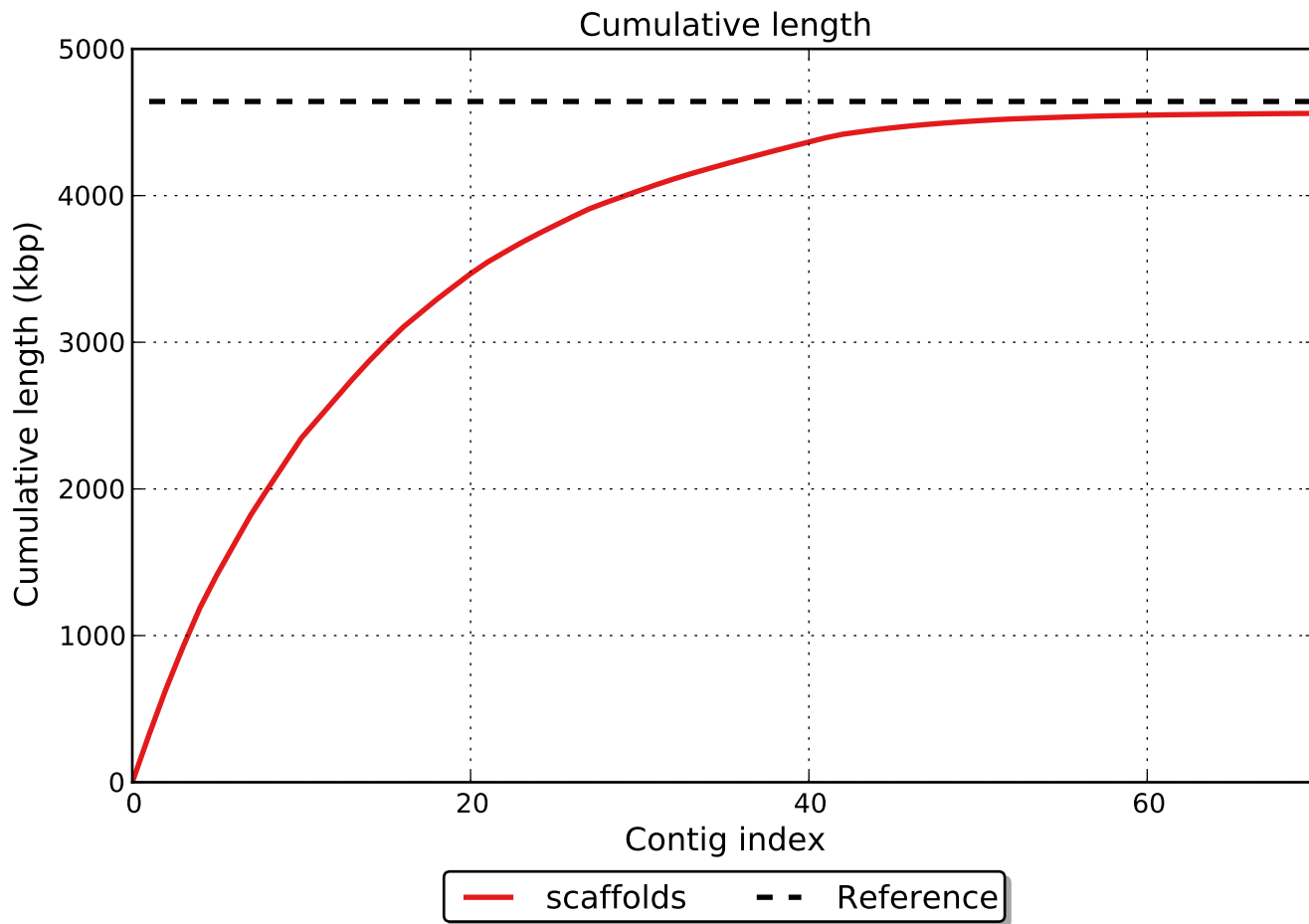|	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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
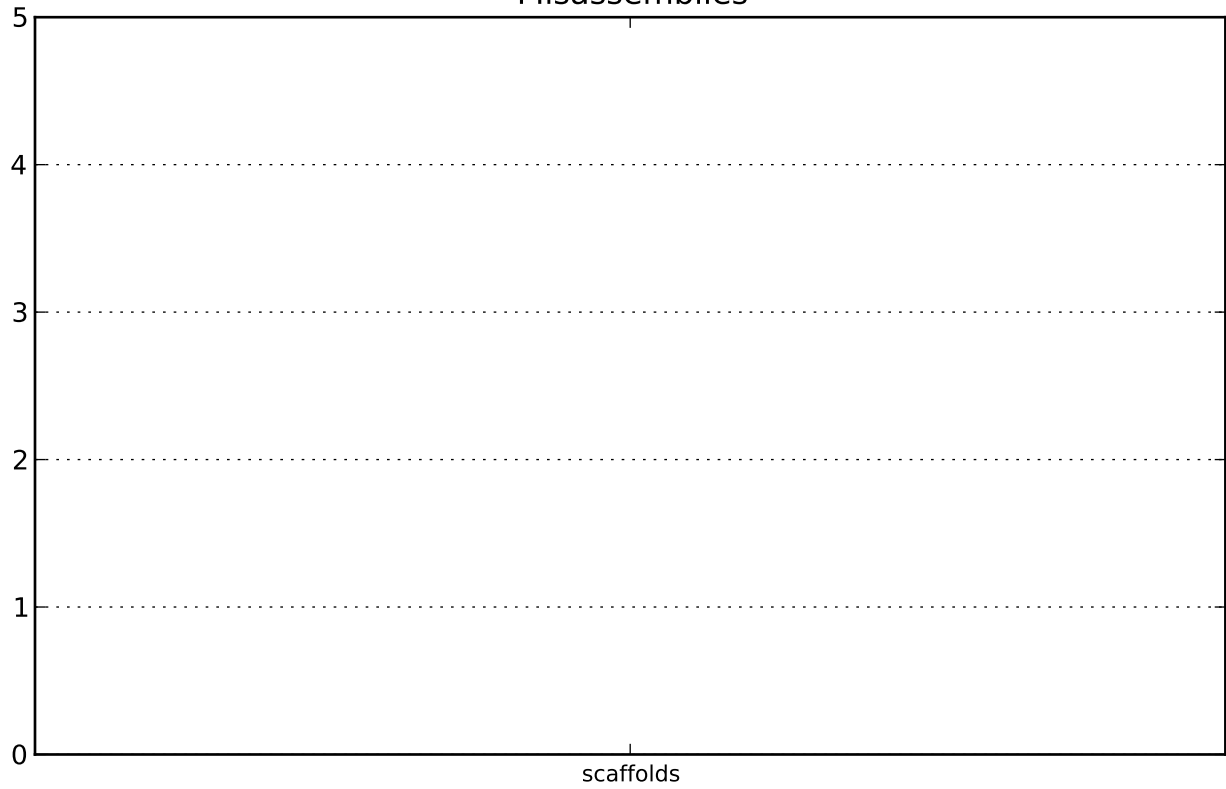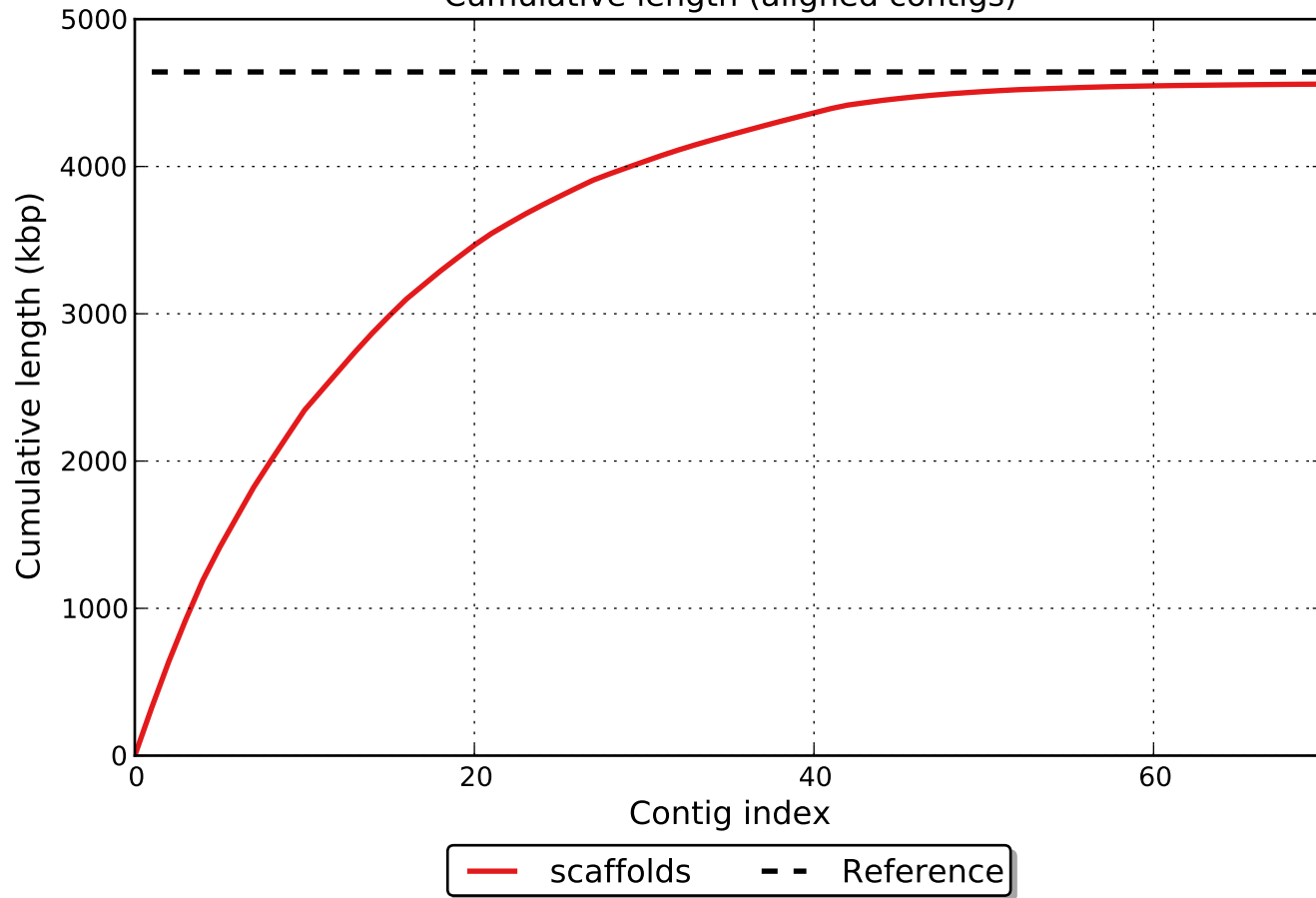
Misassemblies

scaffolds

Cumulative length (aligned contigs)