Report

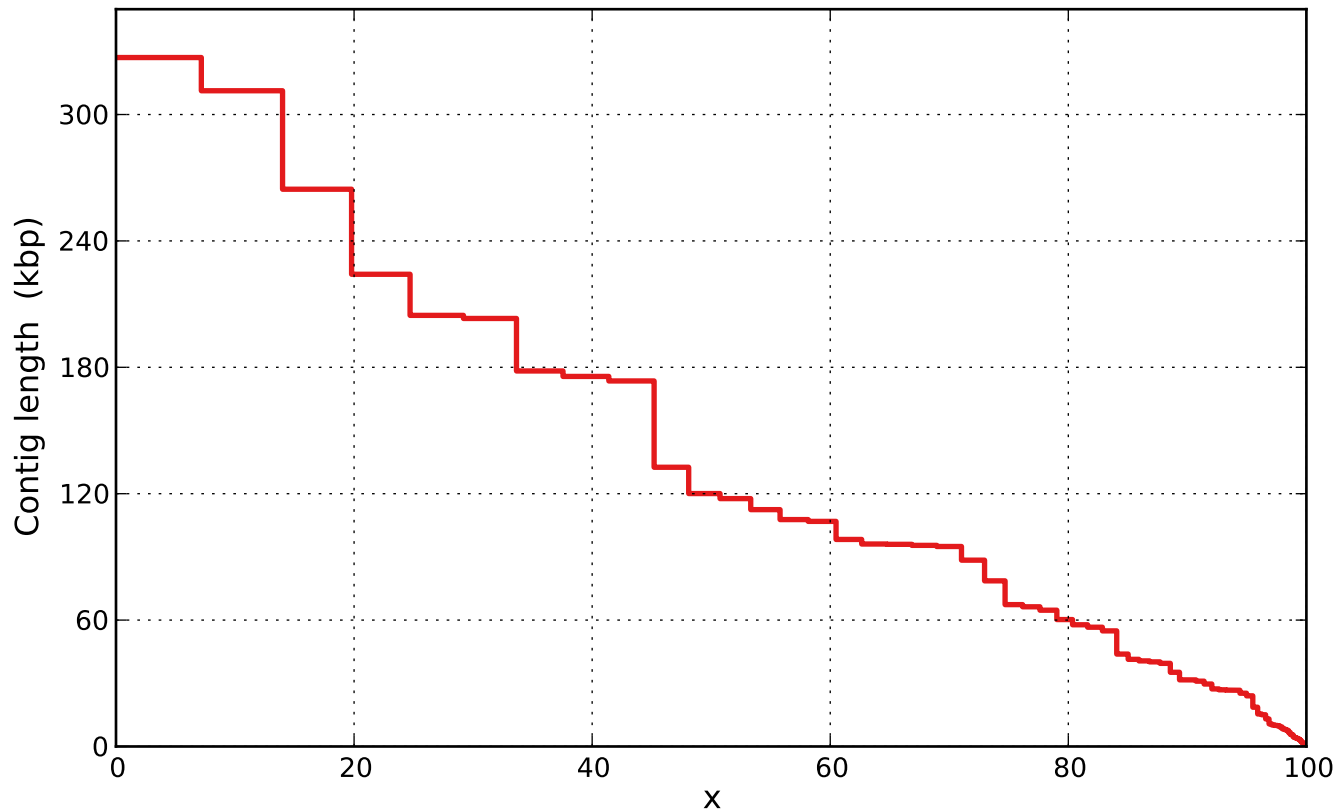|	scaffolds
# contigs (>= 0 bp)	108
# contigs (>= 1000 bp)	79
# contigs (>= 5000 bp)	60
# contigs (>= 10000 bp)	52
# contigs (>= 25000 bp)	44
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4566025
Total length (>= 1000 bp)	4558446
Total length (>= 5000 bp)	4511261
Total length (>= 10000 bp)	4449976
Total length (>= 25000 bp)	4332798
Total length (>= 50000 bp)	3835290
# contigs	84
Largest contig	327053
Total length	4562233
Reference length	4641652
N50	120066
N75	67343
L50	11
L75	23
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	140539
# local misassemblies	7
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.210
Duplication ratio	1.001
# N's per 100 kbp	2.37
# mismatches per 100 kbp	63.37
# indels per 100 kbp	8.75
Largest alignment	327053
NA50	120066
NA75	66312
LA50	11
LA75	23

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	3
# relocations	3
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	140539
# local misassemblies	7
# mismatches	2889
# indels	399
# short indels	397
# long indels	2
Indels length	670

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).
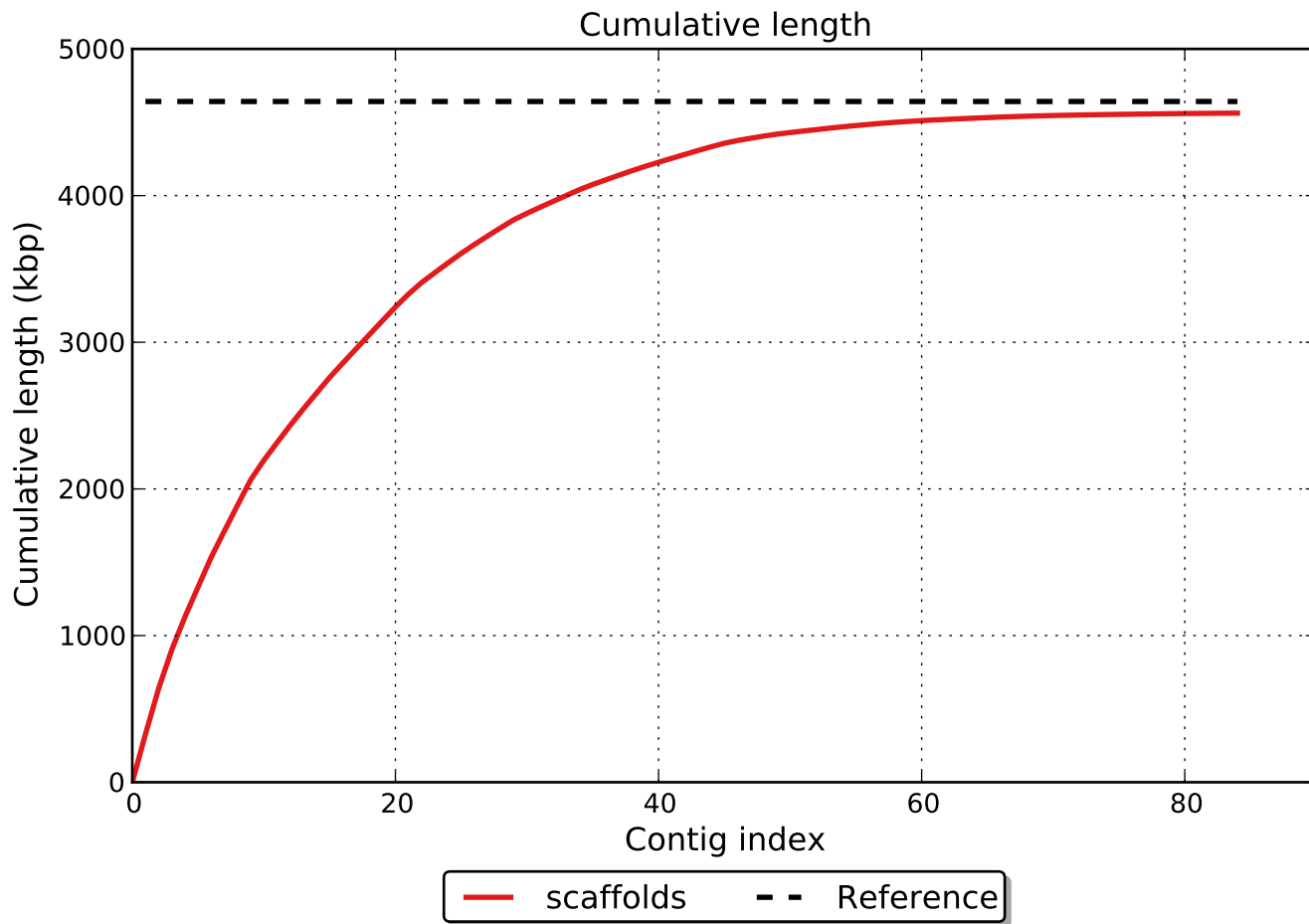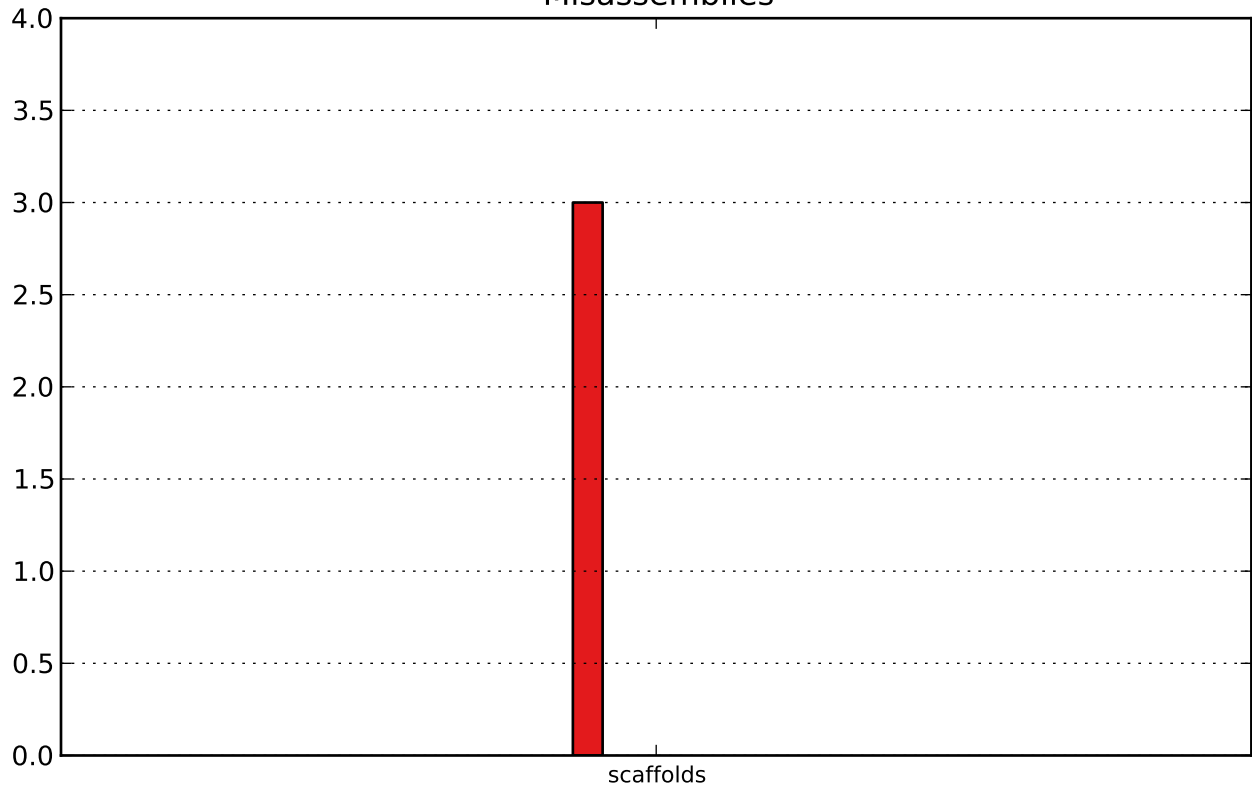
Unaligned report

	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	108

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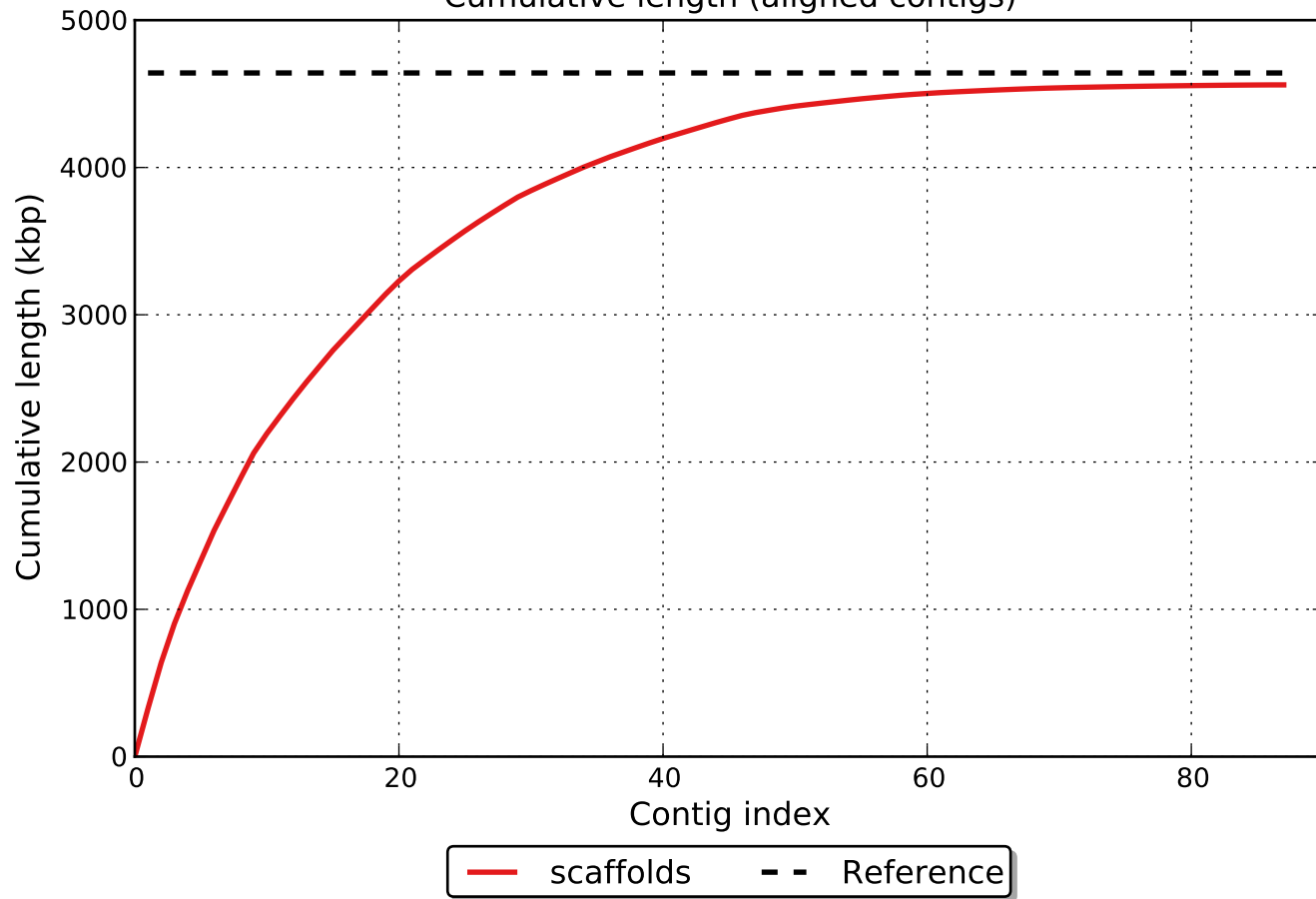(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Cumulative length (aligned contigs)

NAx