Report

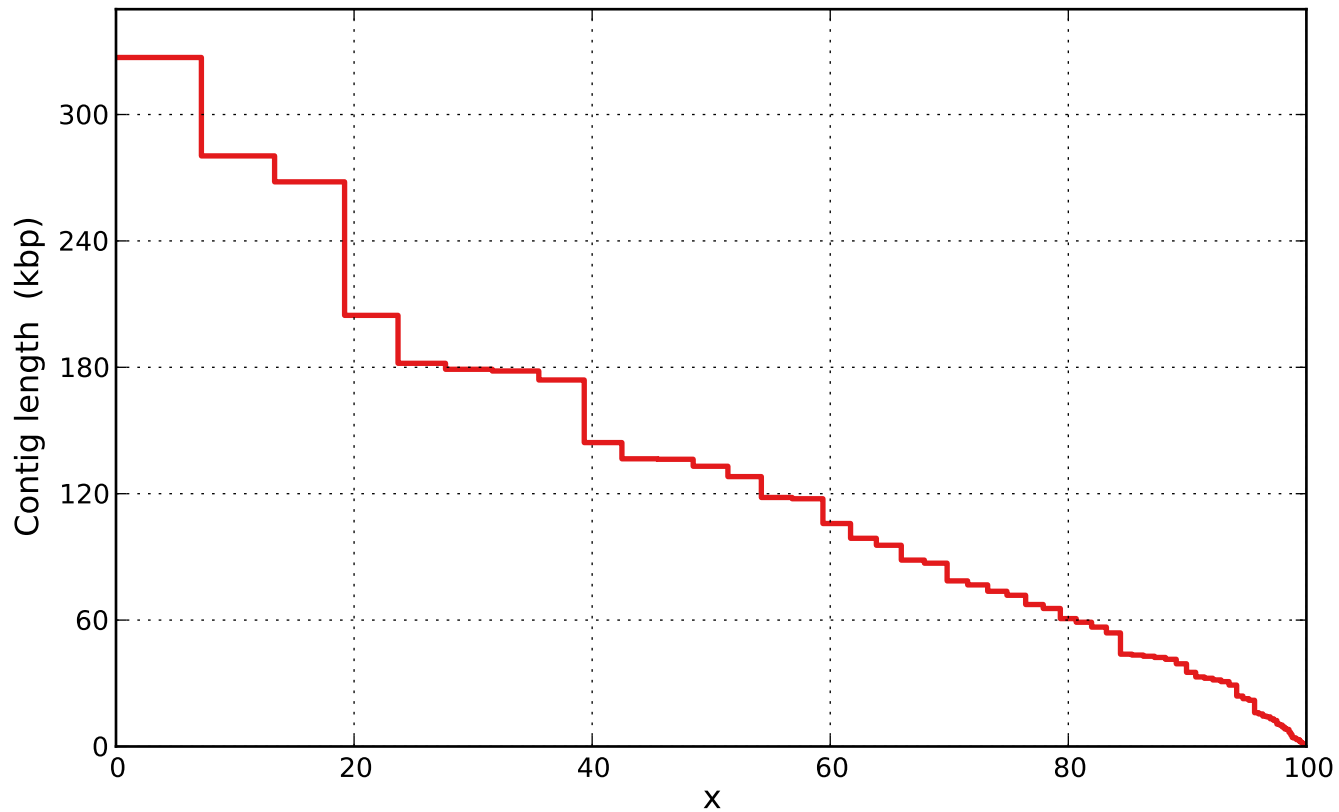|	scaffolds
# contigs (>= 0 bp)	120
# contigs (>= 1000 bp)	80
# contigs (>= 5000 bp)	58
# contigs (>= 10000 bp)	53
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4564447
Total length (>= 1000 bp)	4555230
Total length (>= 5000 bp)	4504638
Total length (>= 10000 bp)	4466805
Total length (>= 25000 bp)	4292037
Total length (>= 50000 bp)	3847017
# contigs	85
Largest contig	327076
Total length	4559095
Reference length	4641652
N50	133024
N75	71774
L50	12
L75	24
# misassemblies	7
# misassembled contigs	6
Misassembled contigs length	806527
# local misassemblies	7
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.174
Duplication ratio	1.000
# N's per 100 kbp	1.43
# mismatches per 100 kbp	67.44
# indels per 100 kbp	9.48
Largest alignment	327076
NA50	117600
NA75	62838
LA50	13
LA75	26

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	7
# relocations	7
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	6
Misassembled contigs length	806527
# local misassemblies	7
# mismatches	3073
# indels	432
# short indels	429
# long indels	3
Indels length	715

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).
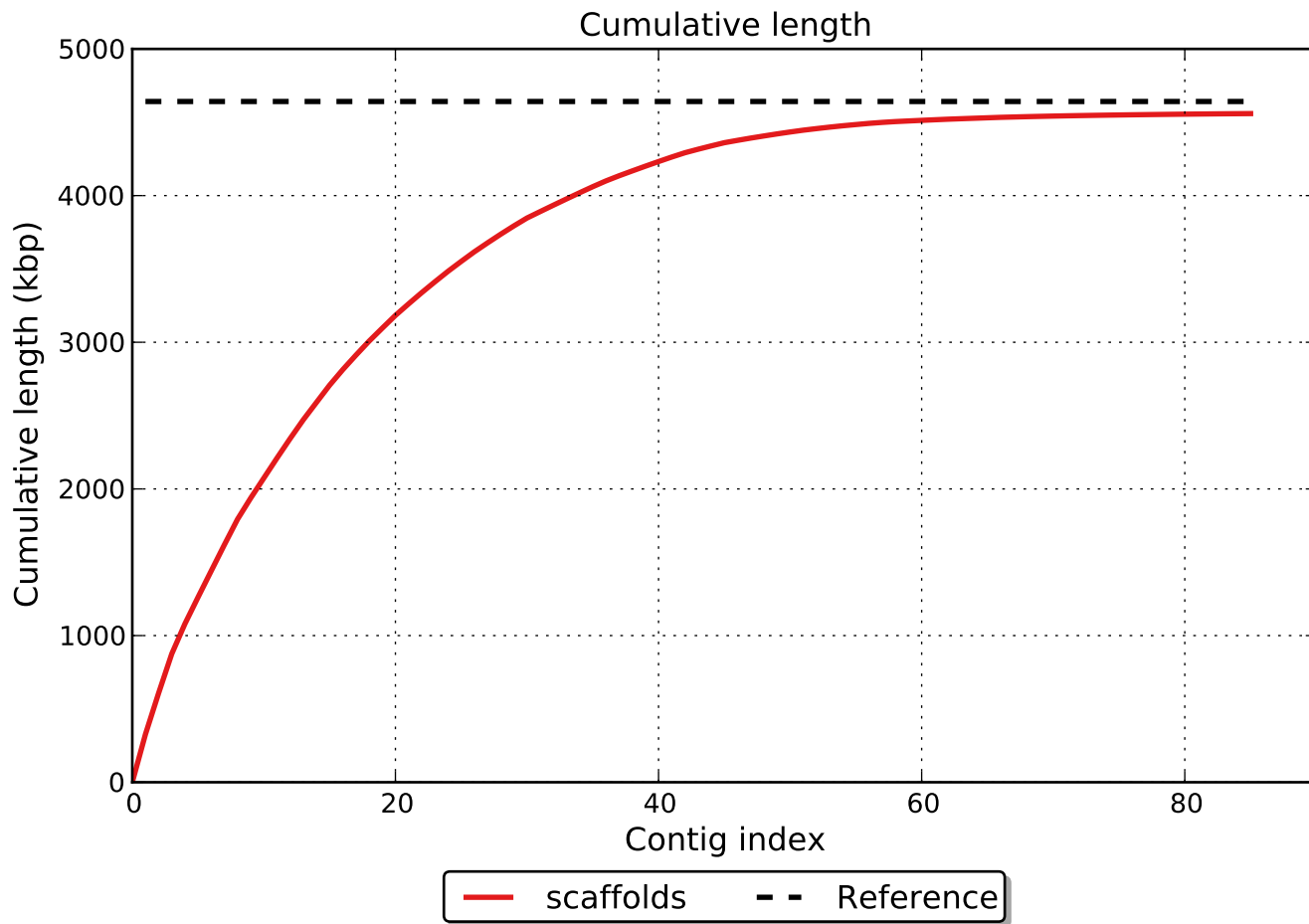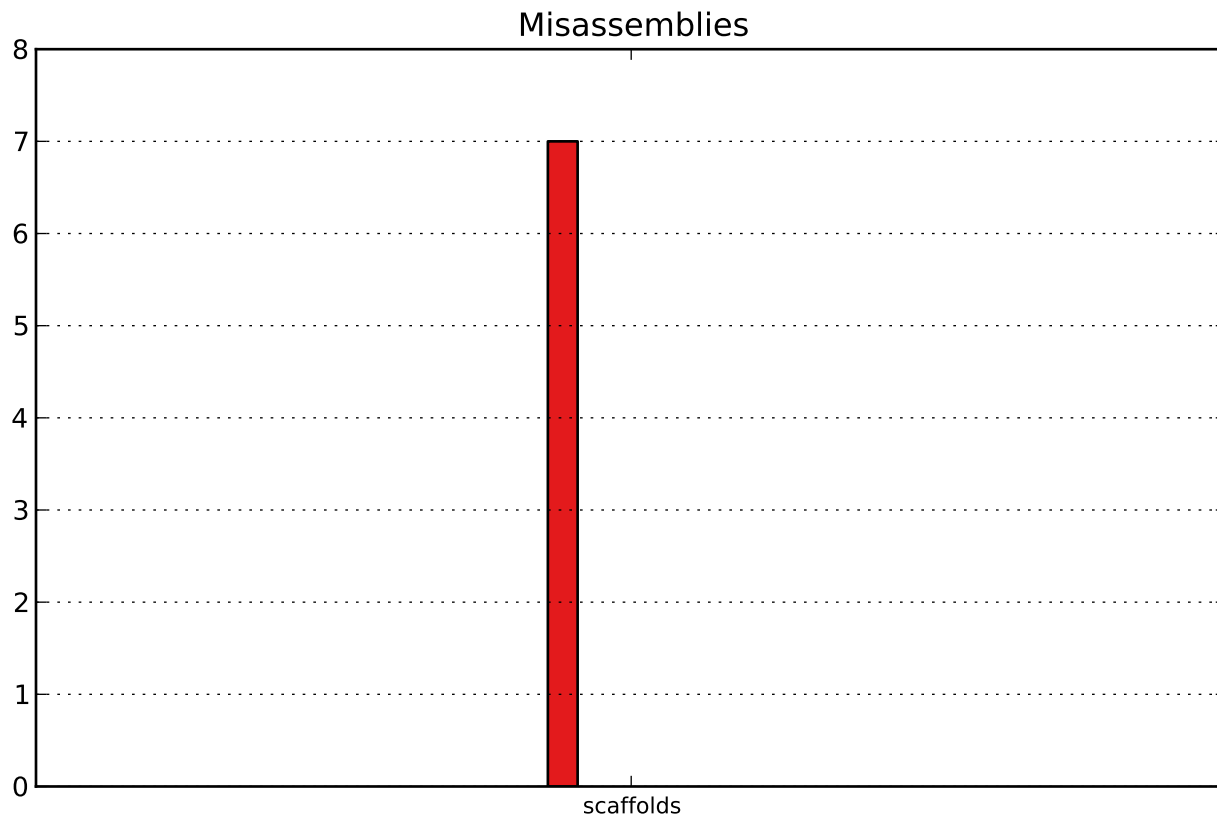
Unaligned report

	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	65

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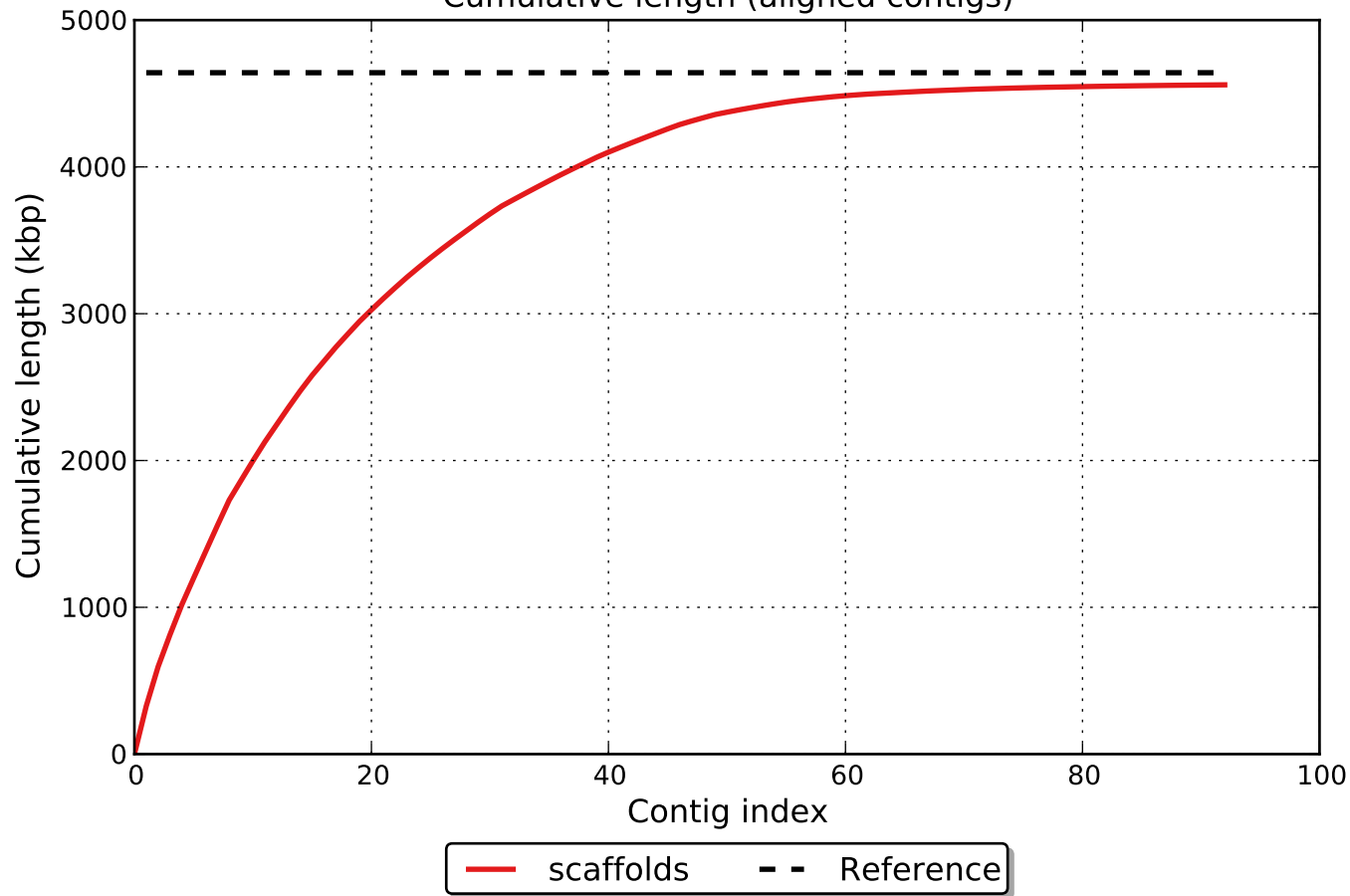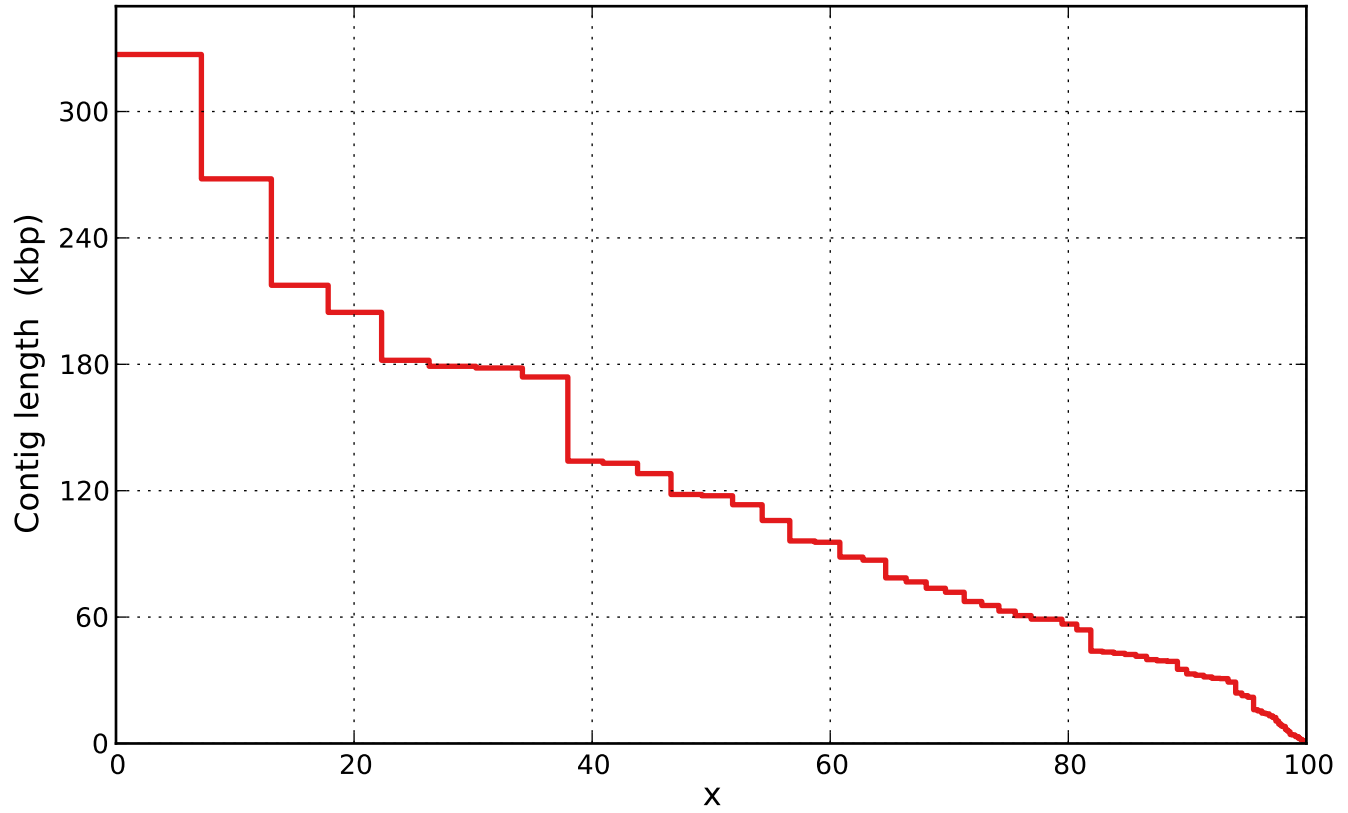(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

Cumulative length (aligned contigs)

NAx