Report

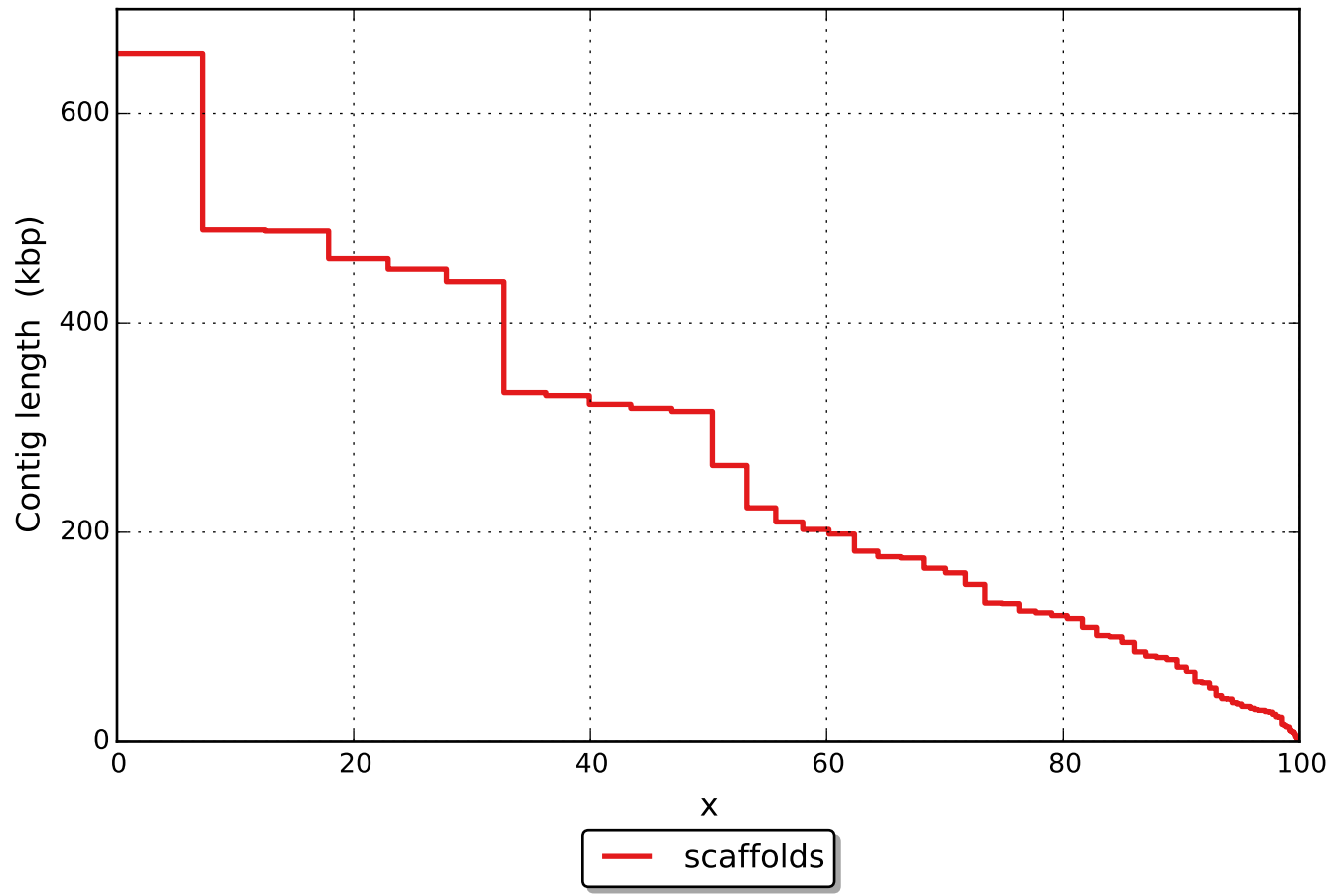|	scaffolds
# contigs (>= 0 bp)	137
# contigs (>= 1000 bp)	78
# contigs (>= 5000 bp)	66
# contigs (>= 10000 bp)	62
# contigs (>= 25000 bp)	55
# contigs (>= 50000 bp)	41
Total length (>= 0 bp)	9157004
Total length (>= 1000 bp)	9135989
Total length (>= 5000 bp)	9112641
Total length (>= 10000 bp)	9079171
Total length (>= 25000 bp)	8963305
Total length (>= 50000 bp)	8497357
# contigs	89
Largest contig	657825
Total length	9144127
Reference length	9283304
N50	315111
N75	131793
L50	11
L75	24
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	48 + 18 part
Unaligned length	4507980
Genome fraction (%)	49.893
Duplication ratio	1.001
# N's per 100 kbp	0.84
# mismatches per 100 kbp	248.07
# indels per 100 kbp	1.01
Largest alignment	657825
NA50	27820
LA50	16

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	8
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	11490
# indels	47
# short indels	46
# long indels	1
Indels length	116

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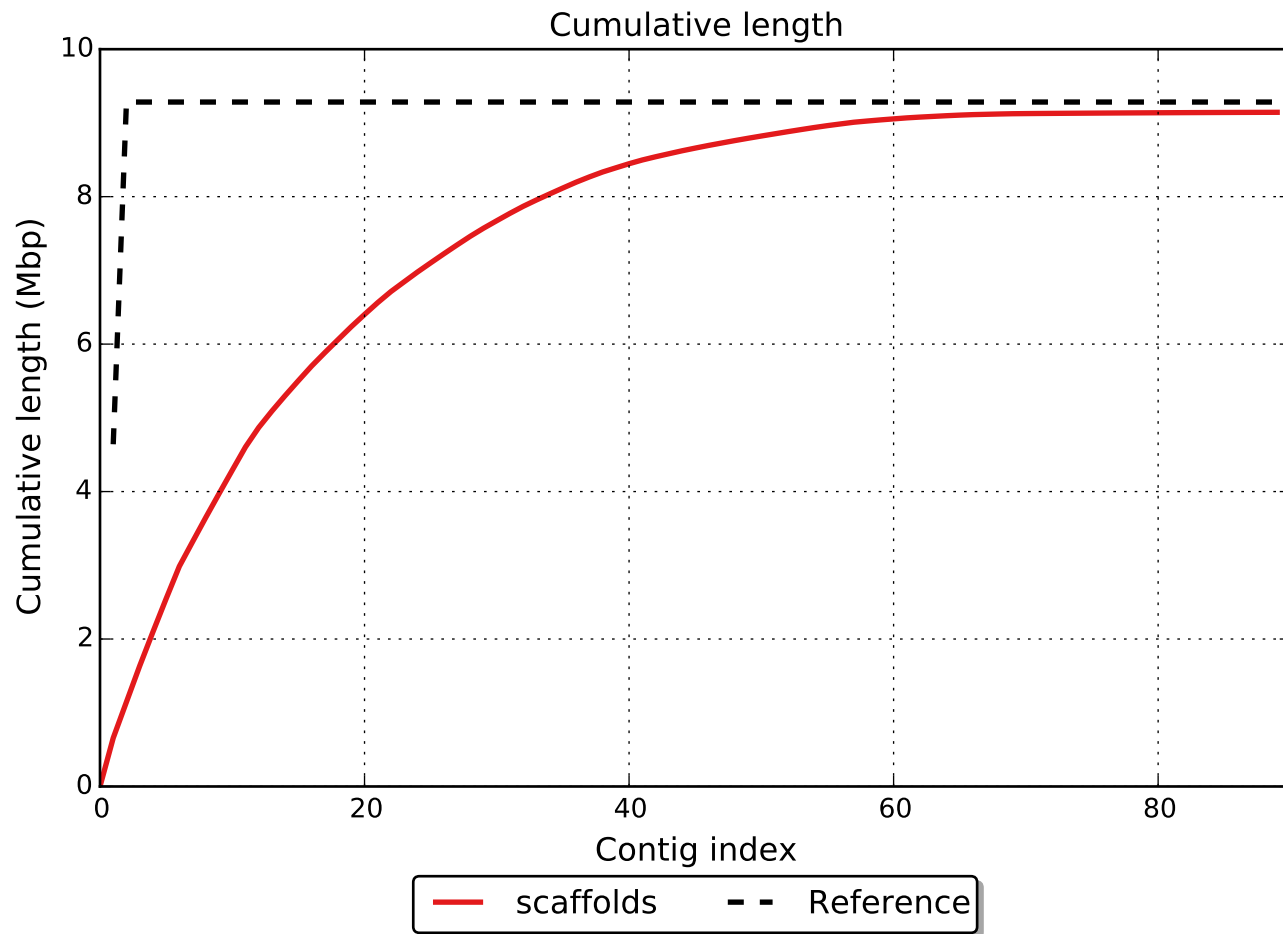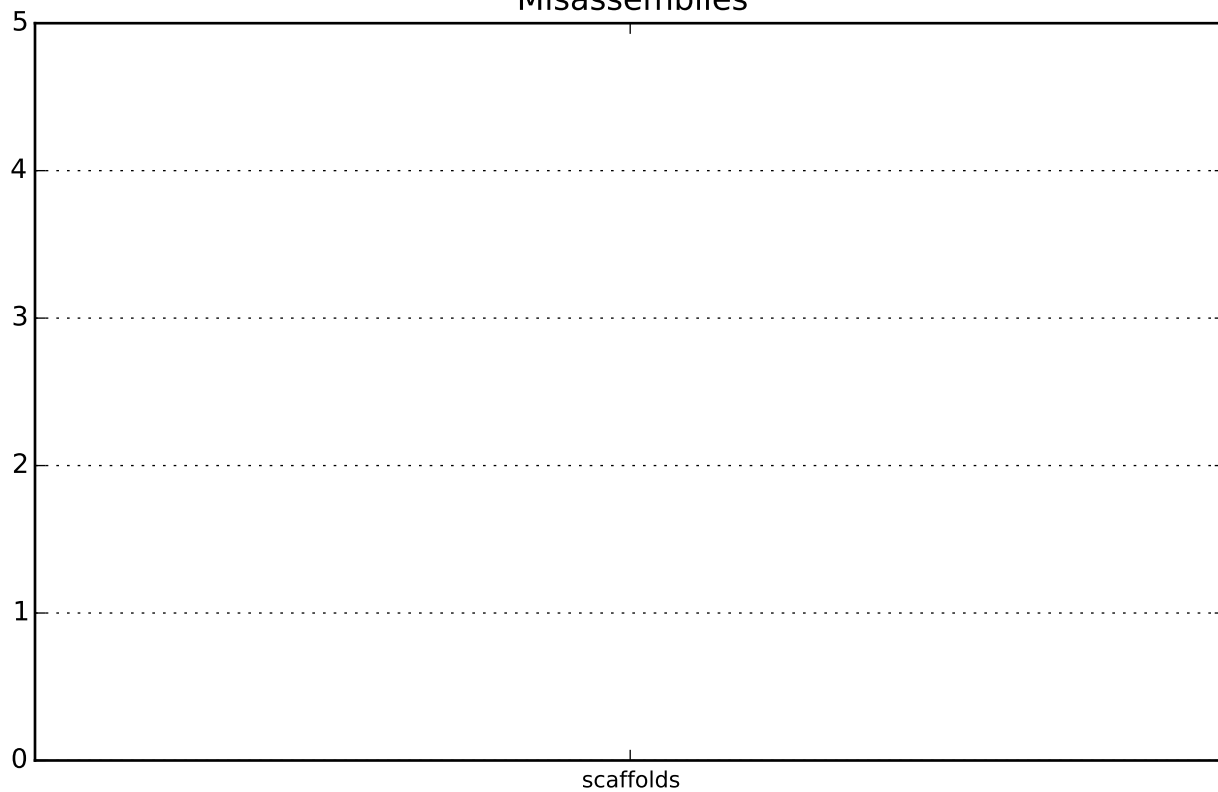(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	48
Fully unaligned length	2812320
# partially unaligned contigs	18
# with misassembly	4
# both parts are significant	8
Partially unaligned length	1695660
# N's	77

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).
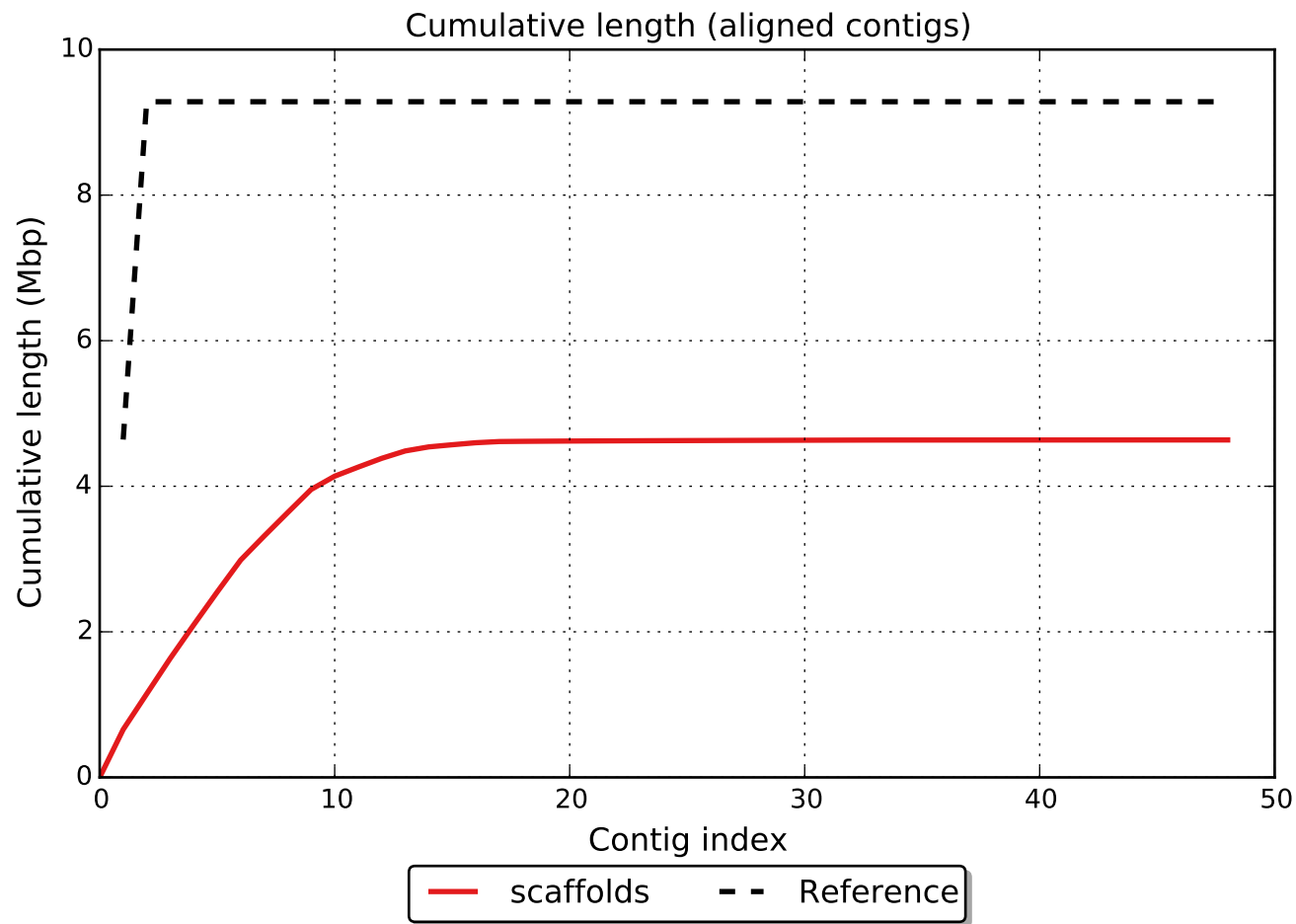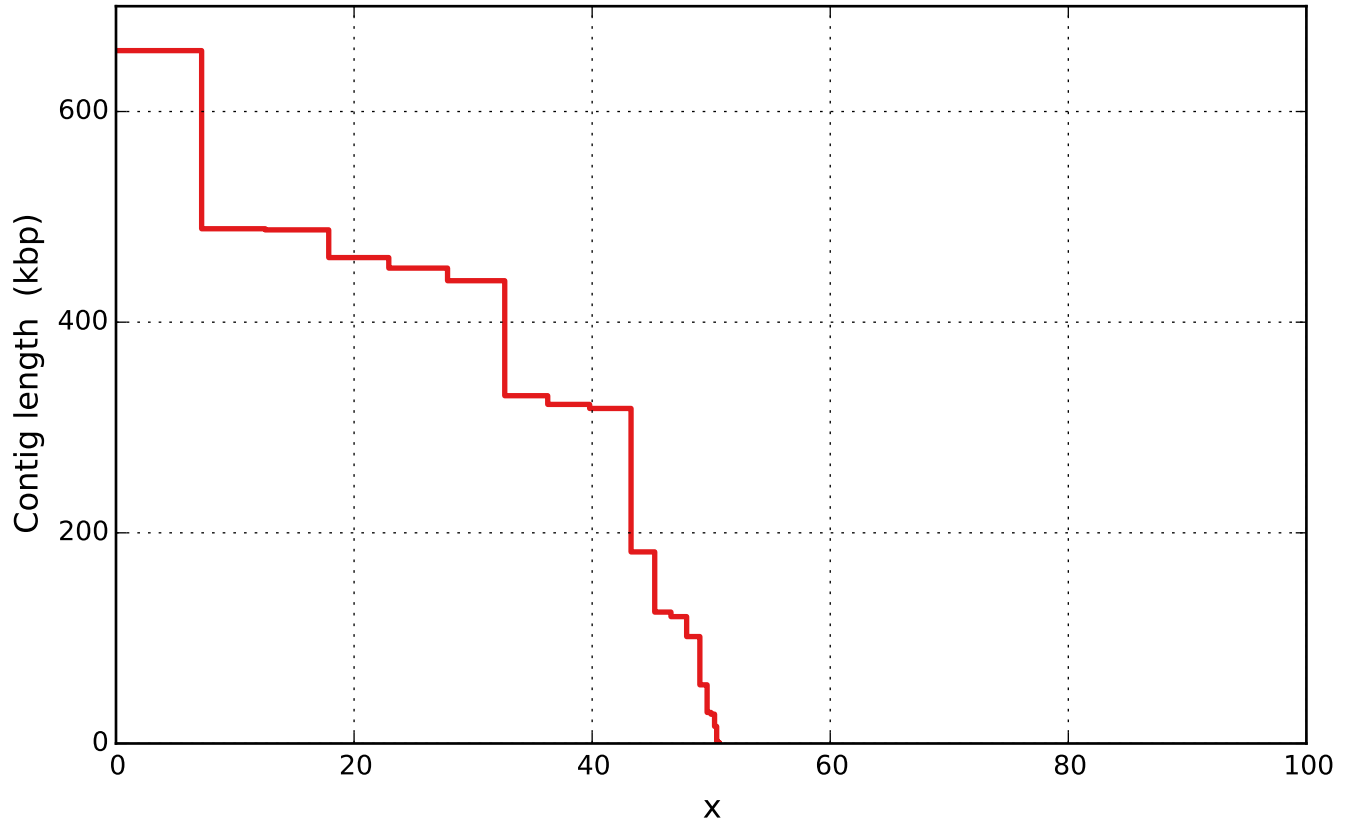
Cumulative length

Misassemblies

scaffolds

NAx

Contig length (kbp) vs x — scaffolds