Report

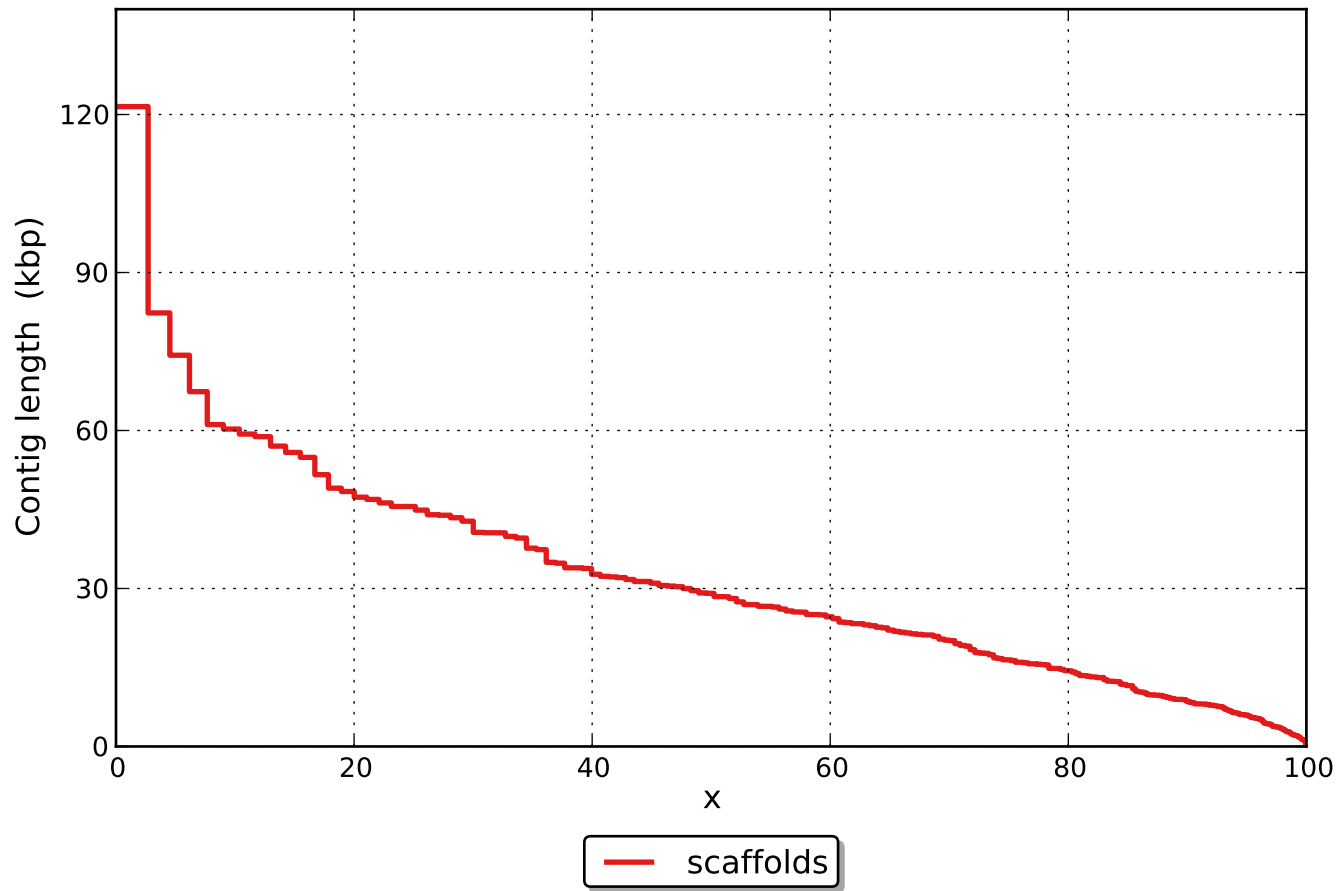|	scaffolds
# contigs (>= 0 bp)	285
# contigs (>= 1000 bp)	258
# contigs (>= 5000 bp)	197
# contigs (>= 10000 bp)	139
# contigs (>= 25000 bp)	66
# contigs (>= 50000 bp)	12
Total length (>= 0 bp)	4512756
Total length (>= 1000 bp)	4501264
Total length (>= 5000 bp)	4338910
Total length (>= 10000 bp)	3900987
Total length (>= 25000 bp)	2663145
Total length (>= 50000 bp)	804429
# contigs	266
Largest contig	121503
Total length	4506802
Reference length	4641652
N50	29078
N75	16437
L50	51
L75	101
# misassemblies	14
# misassembled contigs	12
Misassembled contigs length	343554
# local misassemblies	11
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.953
Duplication ratio	1.001
# N's per 100 kbp	149.77
# mismatches per 100 kbp	9.40
# indels per 100 kbp	8.93
Largest alignment	82326
NA50	28464
NA75	15692
LA50	52
LA75	104

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	14
# relocations	13
# translocations	0
# inversions	1
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	12
Misassembled contigs length	343554
# local misassemblies	11
# mismatches	423
# indels	402
# short indels	173
# long indels	229
Indels length	3821

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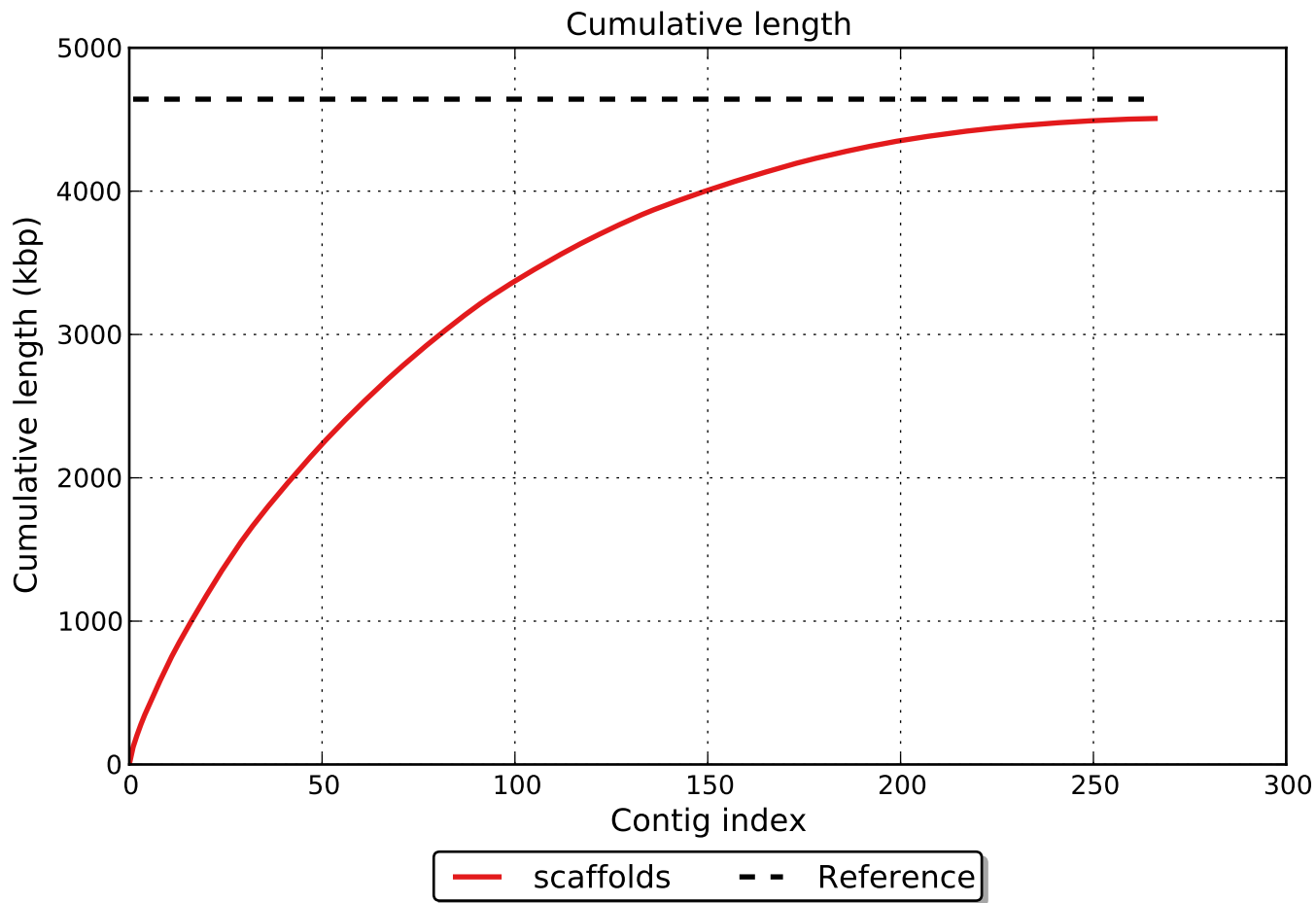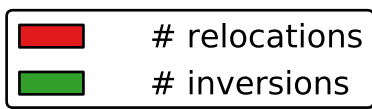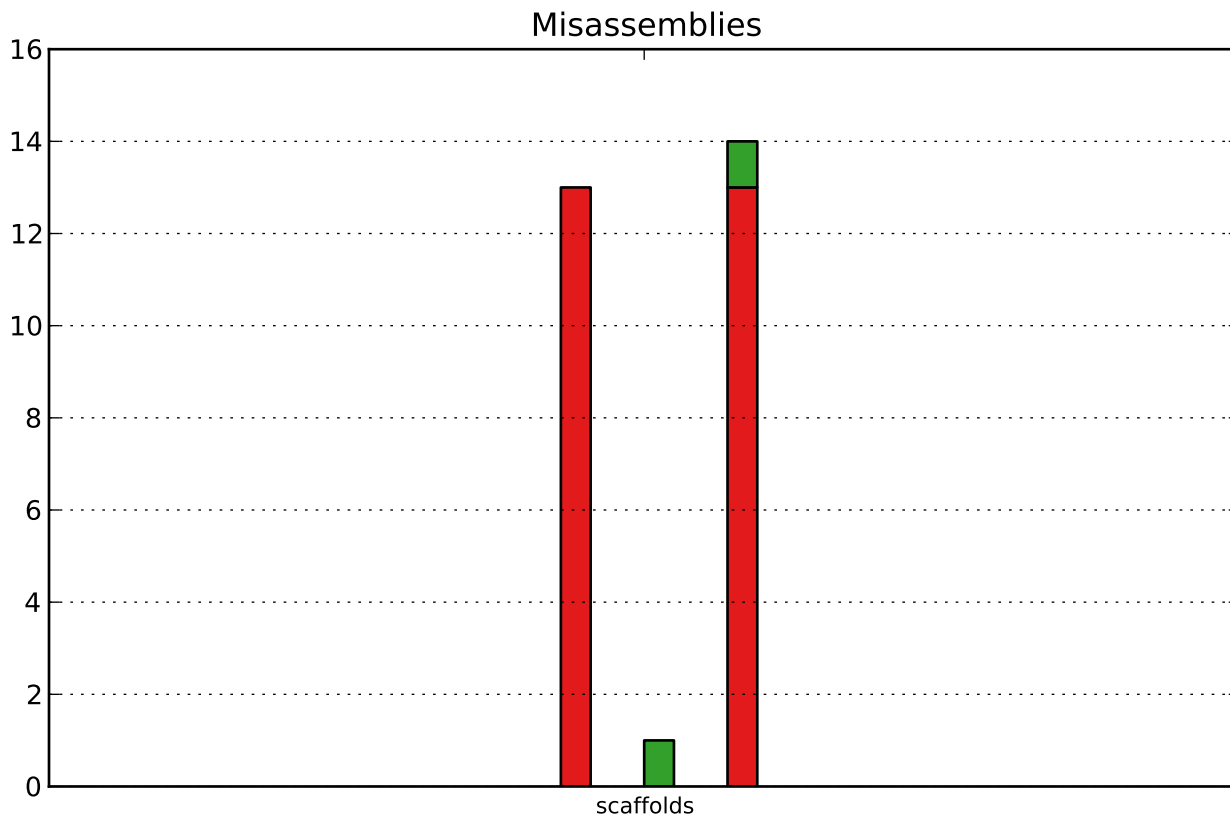(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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	6750

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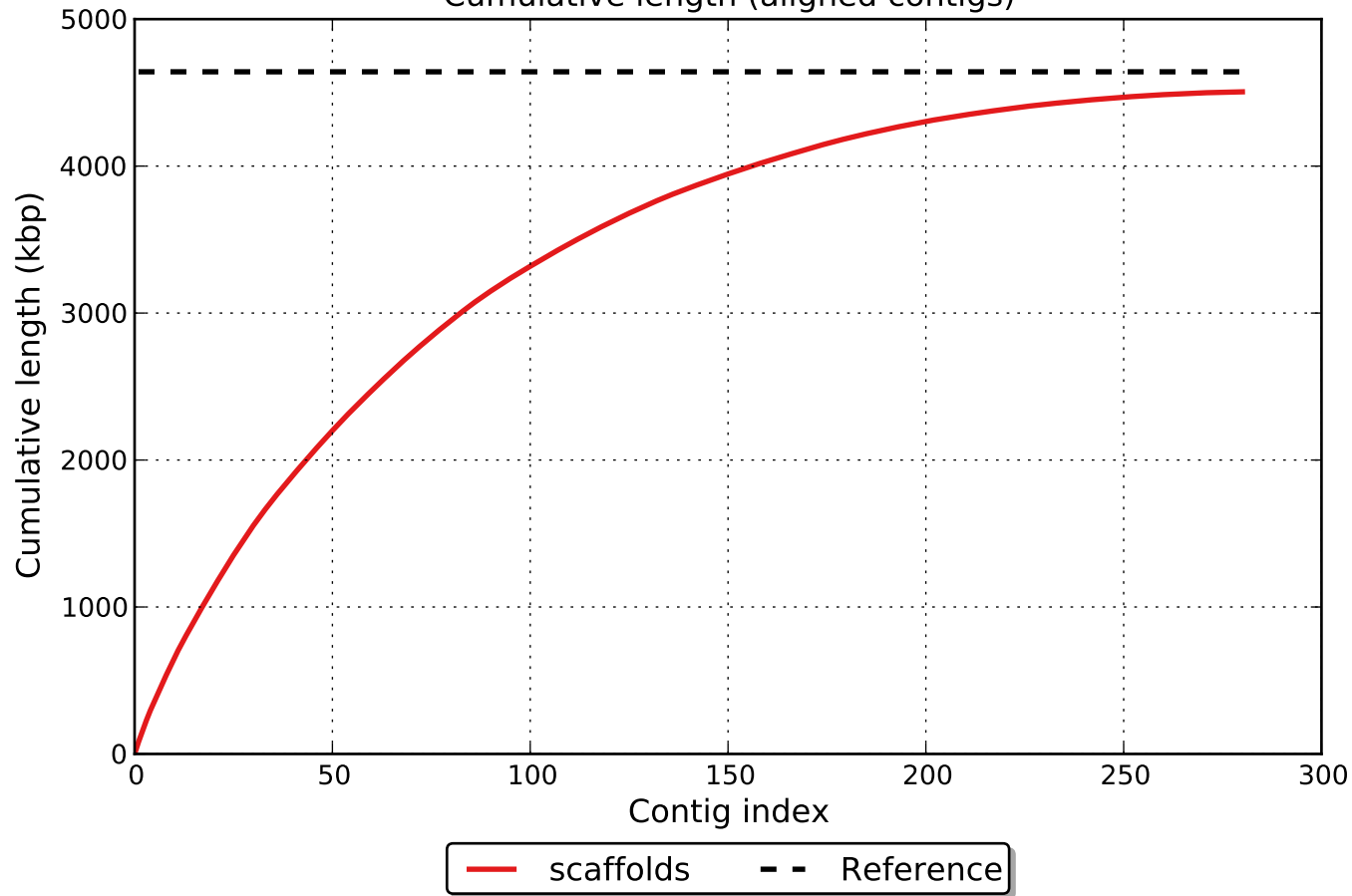(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies