Report

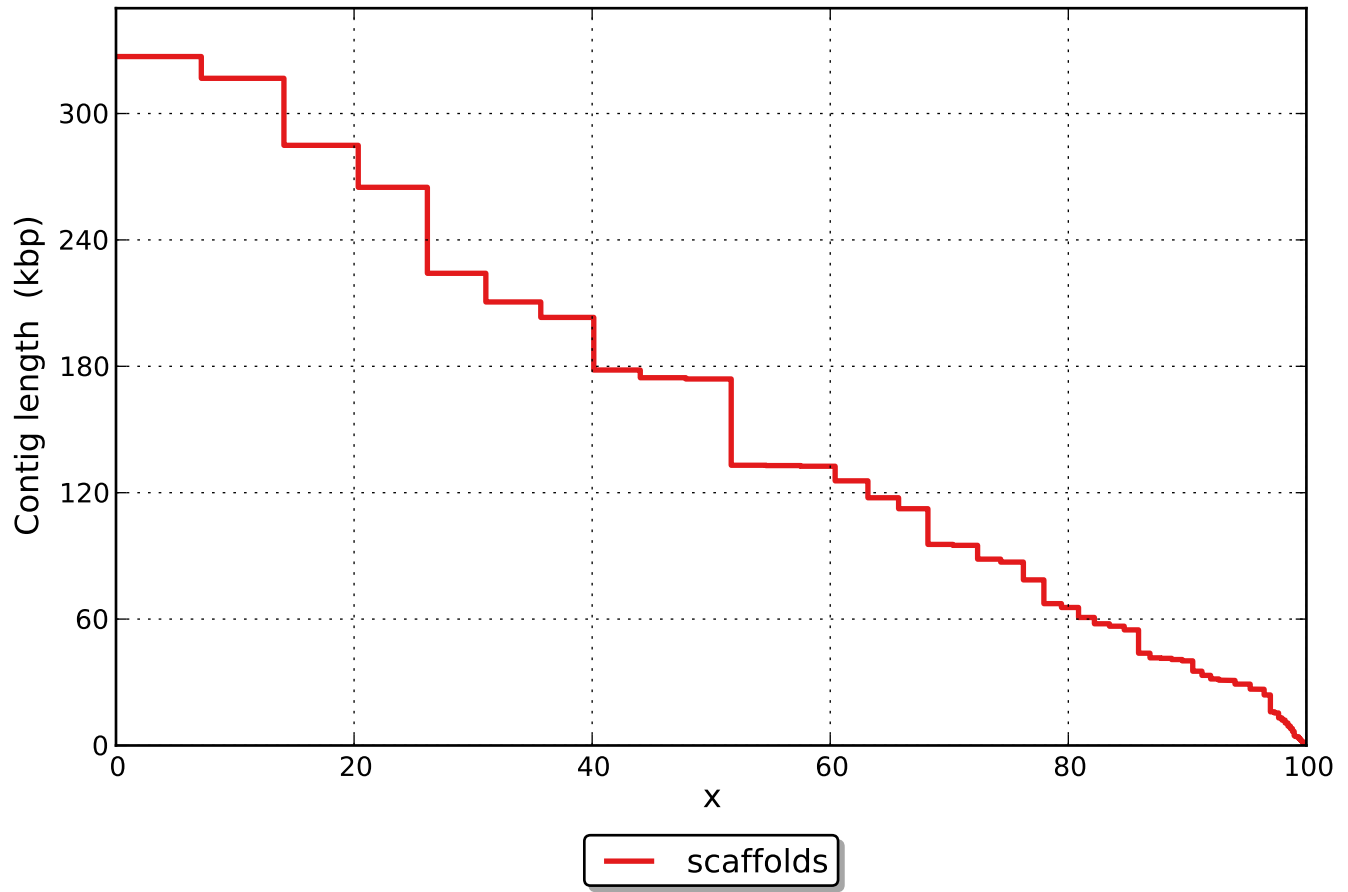|	scaffolds
# contigs (>= 0 bp)	91
# contigs (>= 1000 bp)	69
# contigs (>= 5000 bp)	50
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4566027
Total length (>= 1000 bp)	4560368
Total length (>= 5000 bp)	4516394
Total length (>= 10000 bp)	4492442
Total length (>= 25000 bp)	4401257
Total length (>= 50000 bp)	3919865
# contigs	73
Largest contig	327046
Total length	4563284
Reference length	4641652
N50	173984
N75	87058
L50	10
L75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.259
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.55
# indels per 100 kbp	8.75
Largest alignment	327046
NA50	173064
NA75	87058
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	2
# mismatches	2807
# indels	399
# short indels	399
# long indels	0
Indels length	568

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).
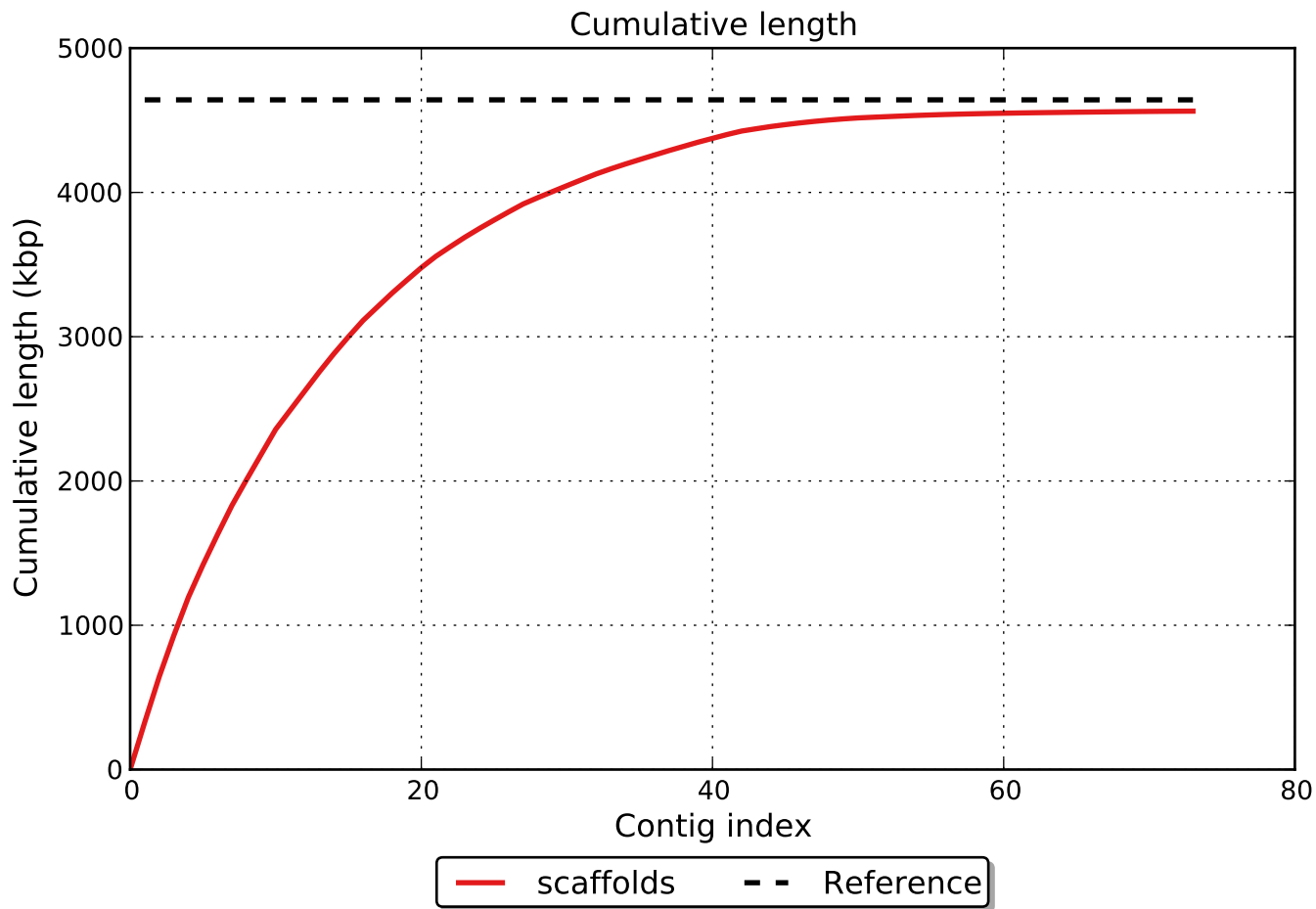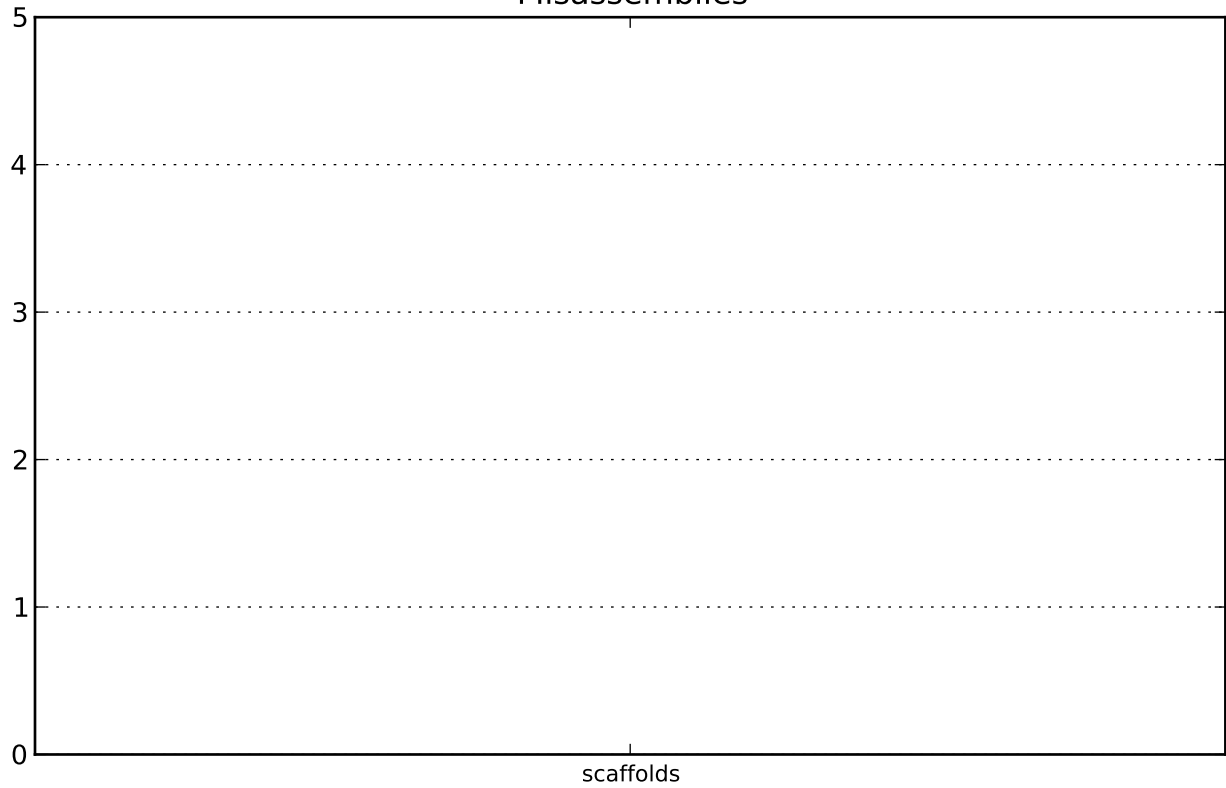
Unaligned report

	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
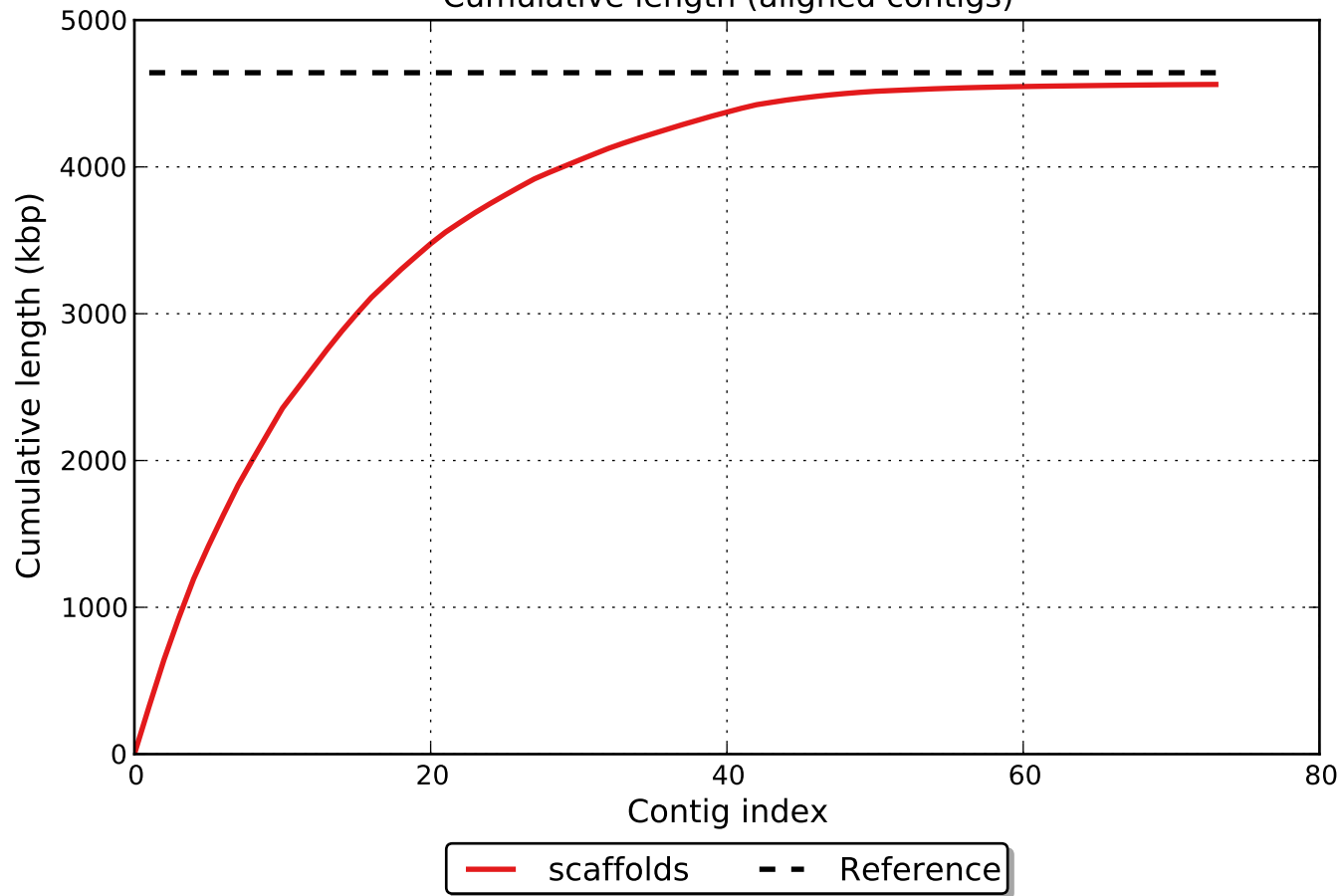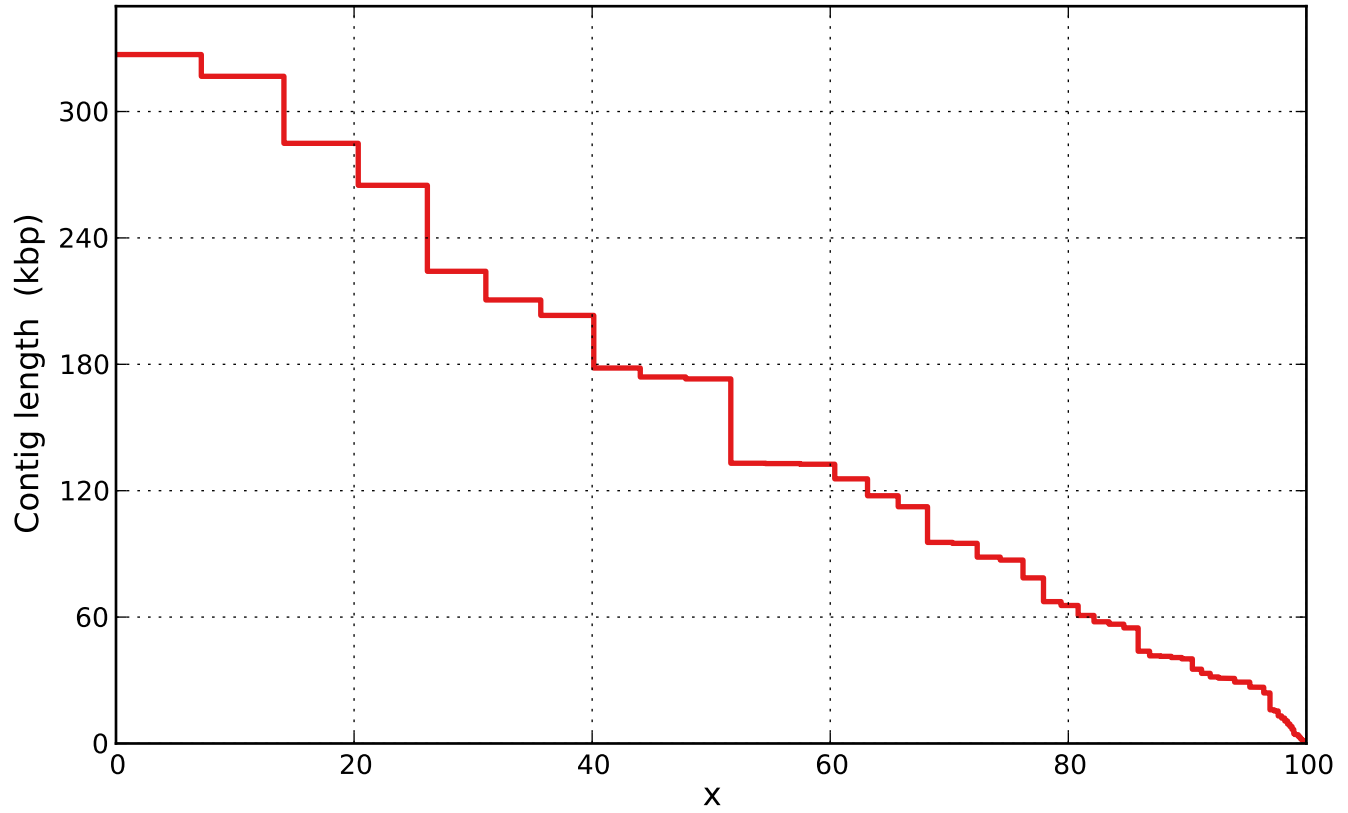(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

scaffolds

Cumulative length (aligned contigs)