Report

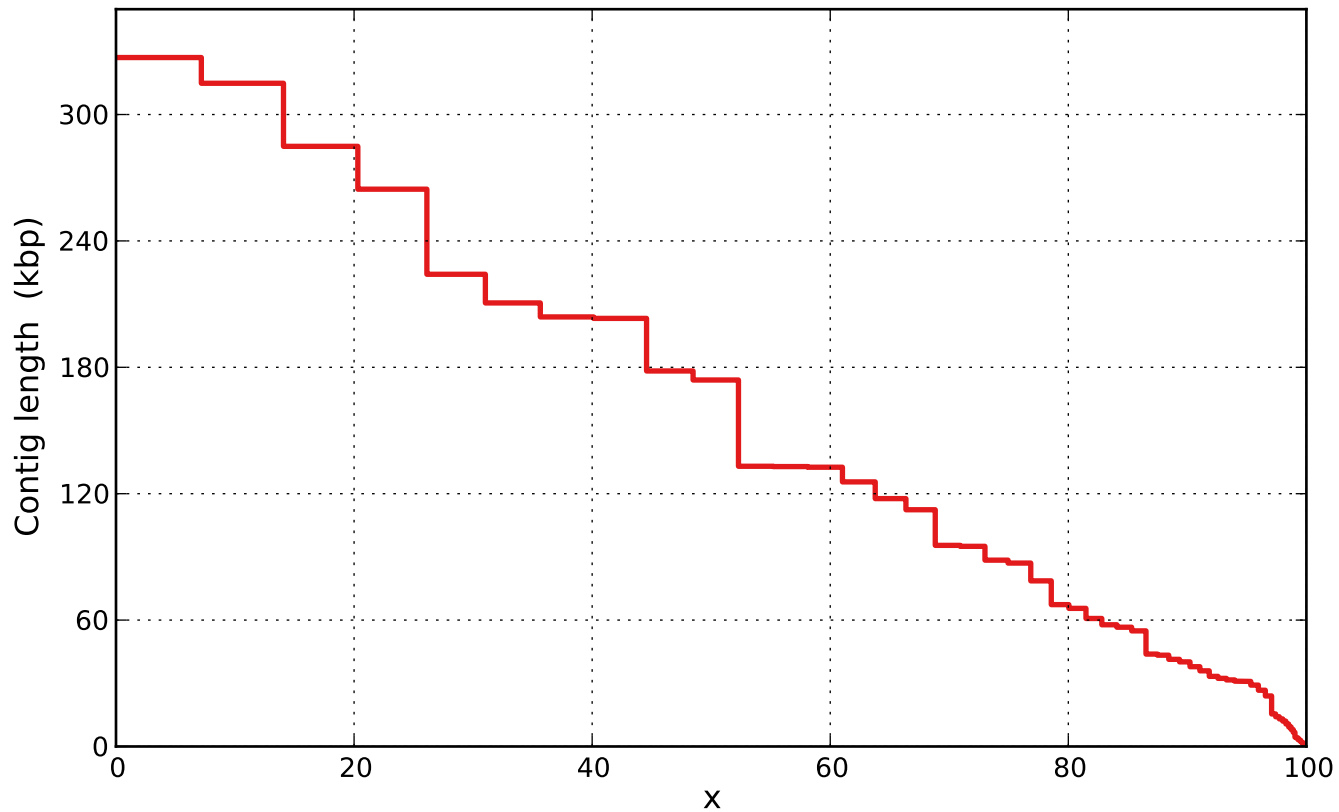|	scaffolds
# contigs (>= 0 bp)	95
# contigs (>= 1000 bp)	67
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	46
# contigs (>= 25000 bp)	40
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4565404
Total length (>= 1000 bp)	4557596
Total length (>= 5000 bp)	4517905
Total length (>= 10000 bp)	4493834
Total length (>= 25000 bp)	4404514
Total length (>= 50000 bp)	3947084
# contigs	73
Largest contig	327052
Total length	4561806
Reference length	4641652
N50	173973
N75	87064
L50	10
L75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.228
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.19
# indels per 100 kbp	8.31
Largest alignment	327052
NA50	173973
NA75	87064
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	3
# mismatches	2790
# indels	379
# short indels	379
# long indels	0
Indels length	543

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).
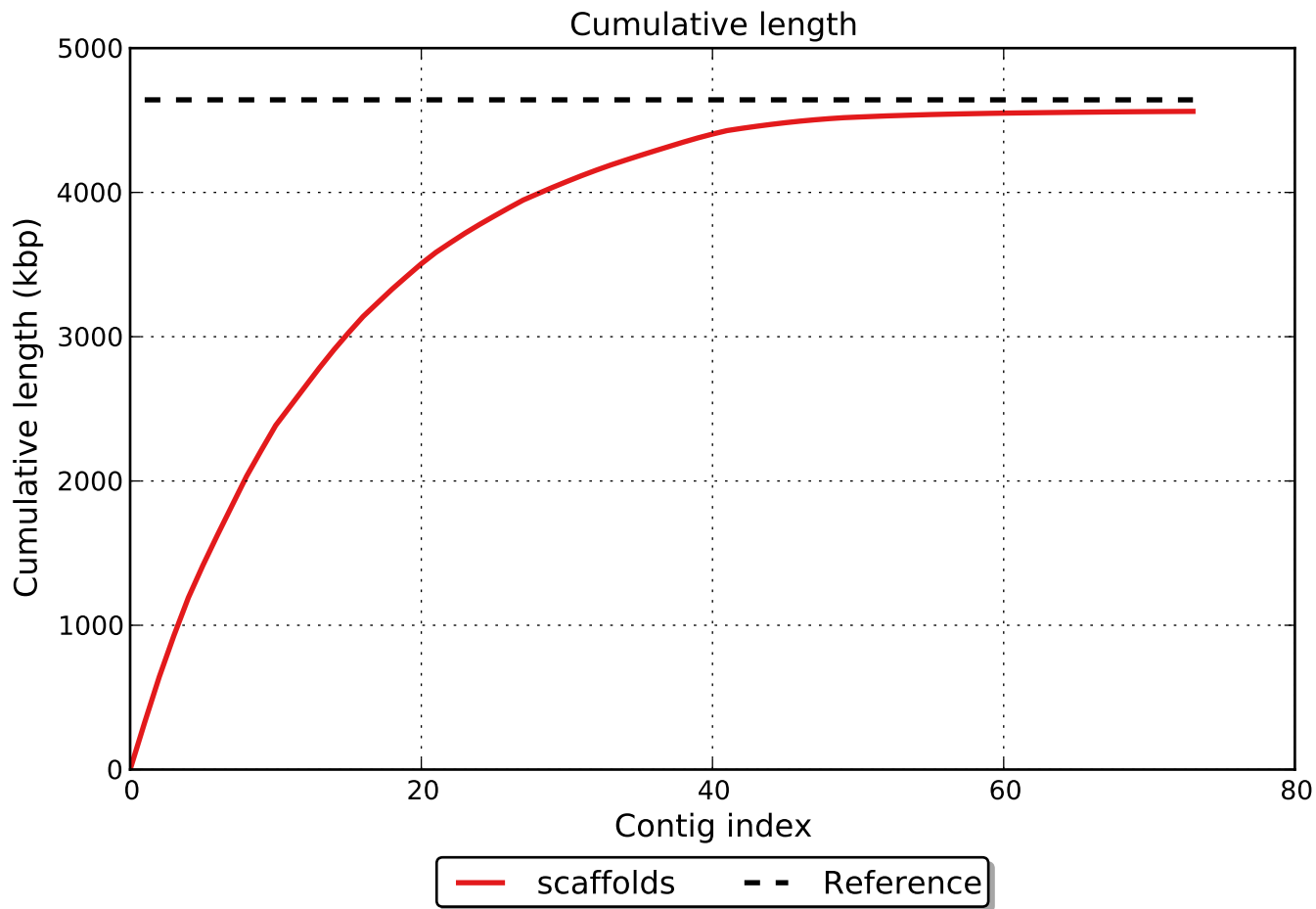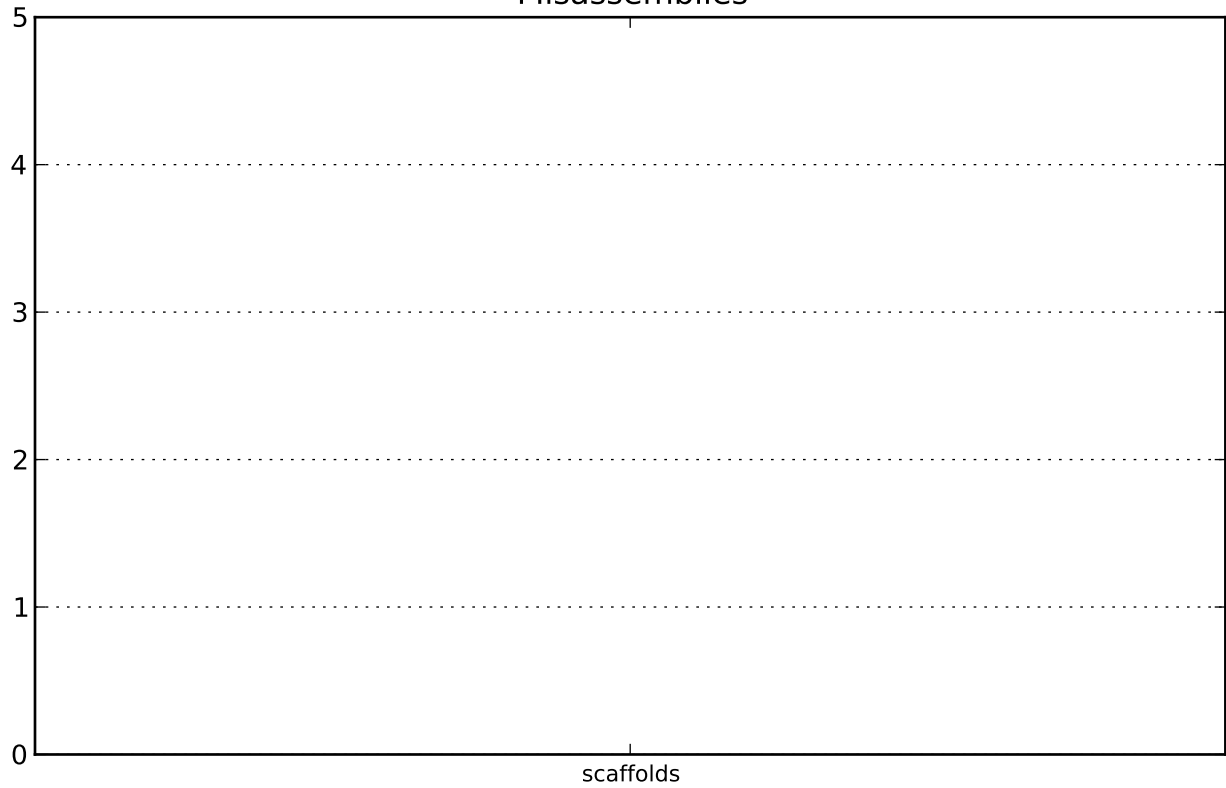
Unaligned report

	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).
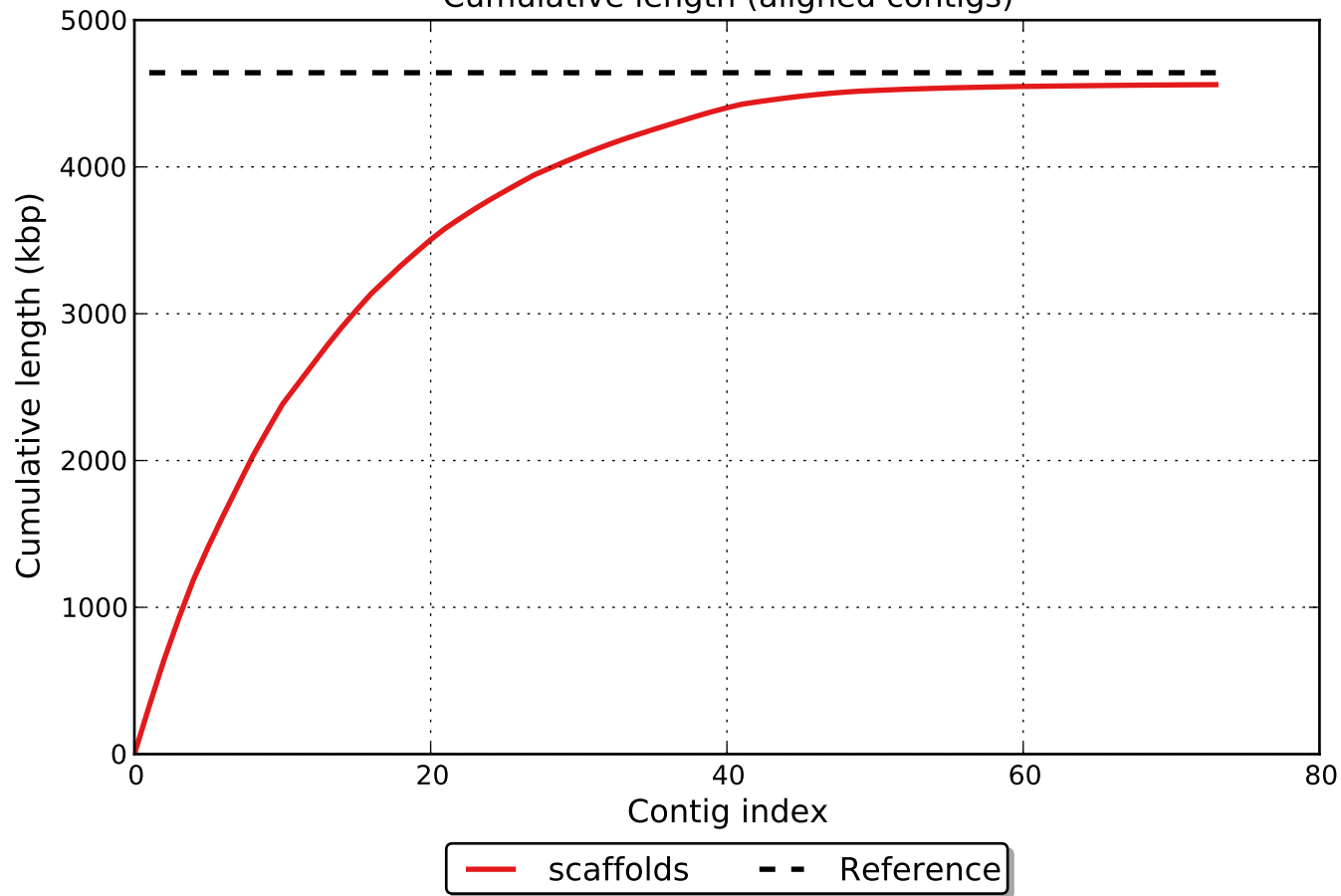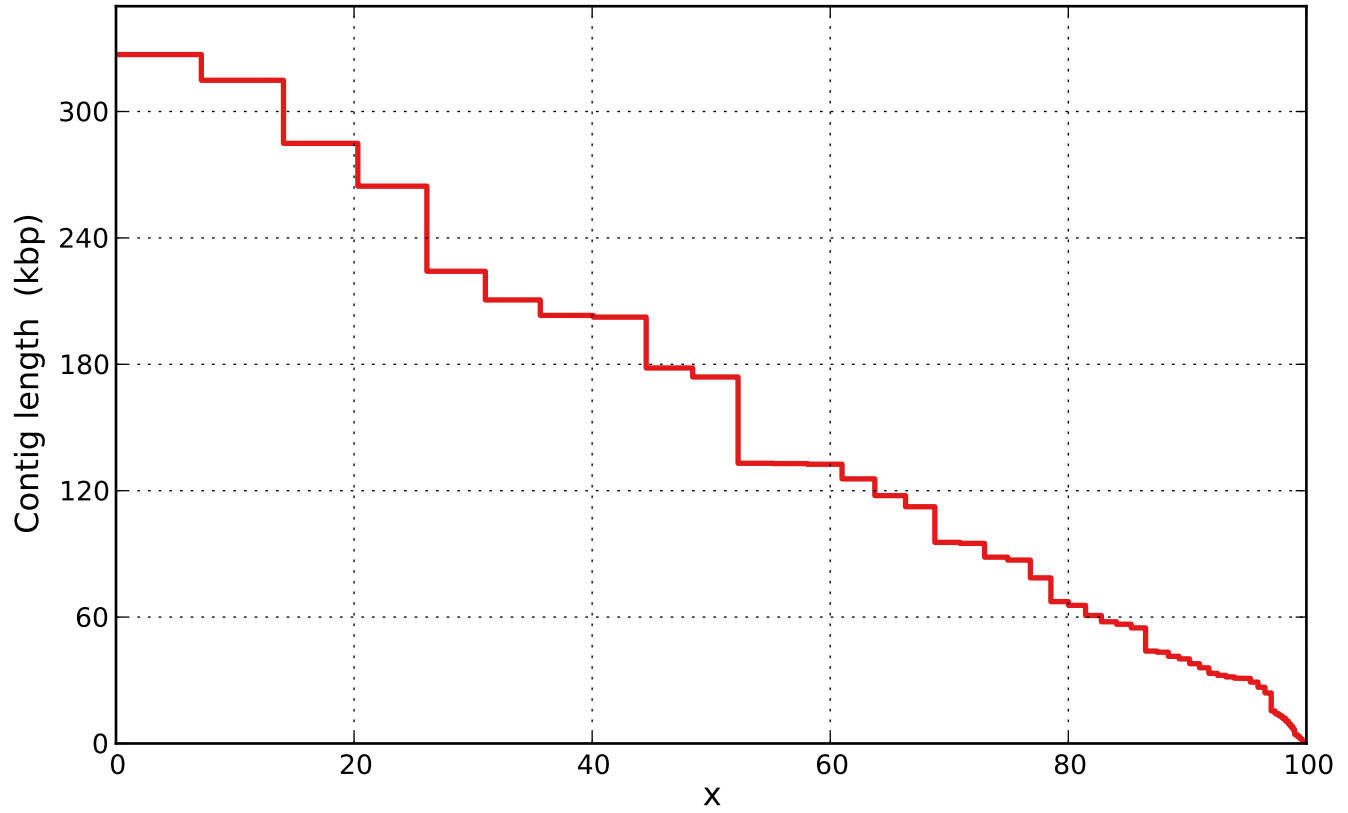
Cumulative length

Cumulative length (kbp) vs. Contig index

Legend: scaffolds, Reference

Misassemblies

scaffolds

Cumulative length (aligned contigs)