

Report

	scaffolds
# contigs (≥ 0 bp)	131
# contigs (≥ 1000 bp)	84
# contigs (≥ 5000 bp)	66
# contigs (≥ 10000 bp)	58
# contigs (≥ 25000 bp)	49
# contigs (≥ 50000 bp)	29
Total length (≥ 0 bp)	4566986
Total length (≥ 1000 bp)	4552327
Total length (≥ 5000 bp)	4510469
Total length (≥ 10000 bp)	4453156
Total length (≥ 25000 bp)	4312237
Total length (≥ 50000 bp)	3602344
# contigs	92
Largest contig	327069
Total length	4558430
Reference length	4641652
N50	115758
N75	57779
L50	13
L75	26
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	202679
# local misassemblies	9
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.169
Duplication ratio	1.000
# N's per 100 kbp	8.23
# mismatches per 100 kbp	60.64
# indels per 100 kbp	8.25
Largest alignment	327069
NA50	115758
NA75	56686
LA50	13
LA75	27

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	202679
# local misassemblies	9
# mismatches	2763
# indels	376
# short indels	373
# long indels	3
Indels length	650

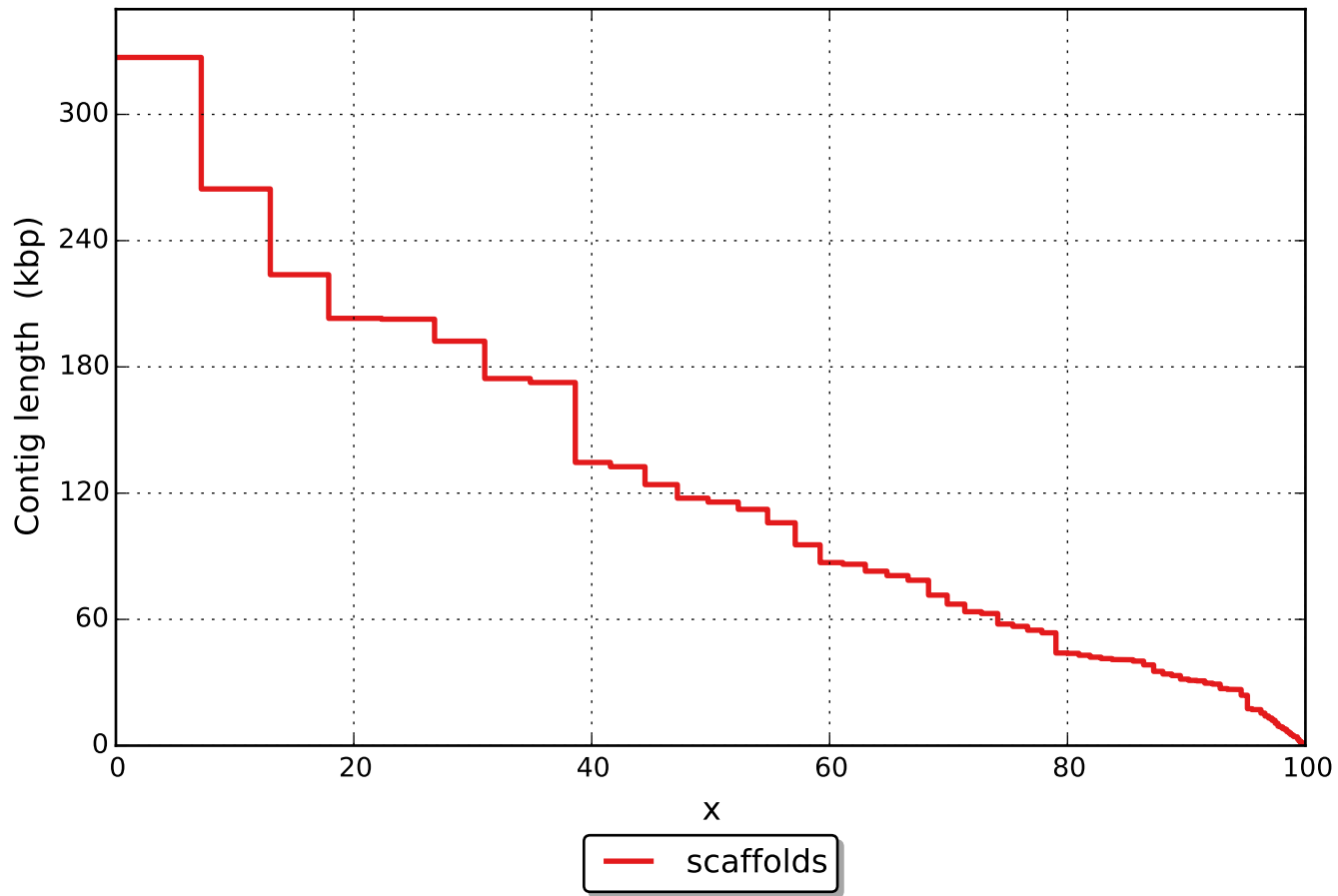
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

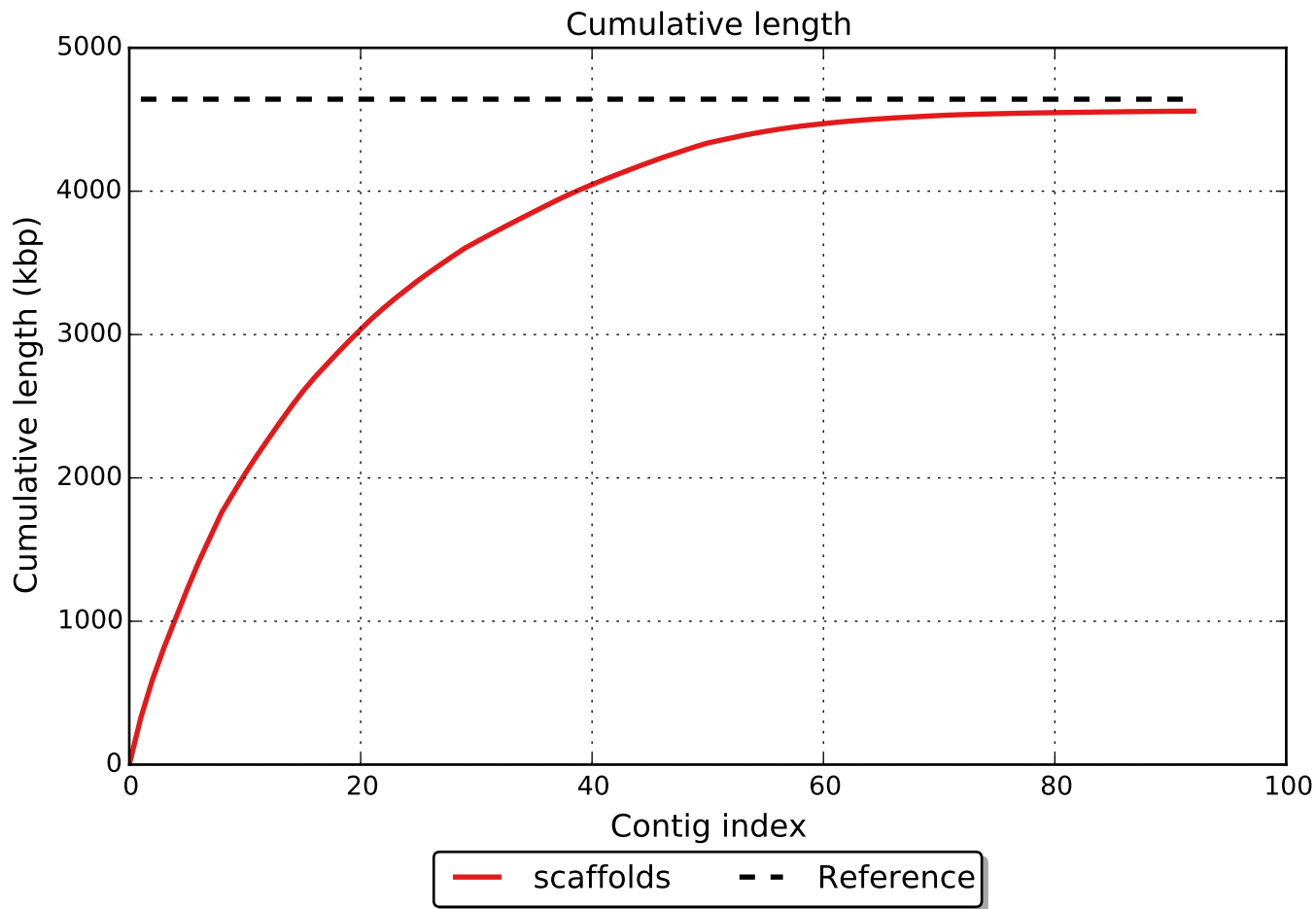
Unaligned report

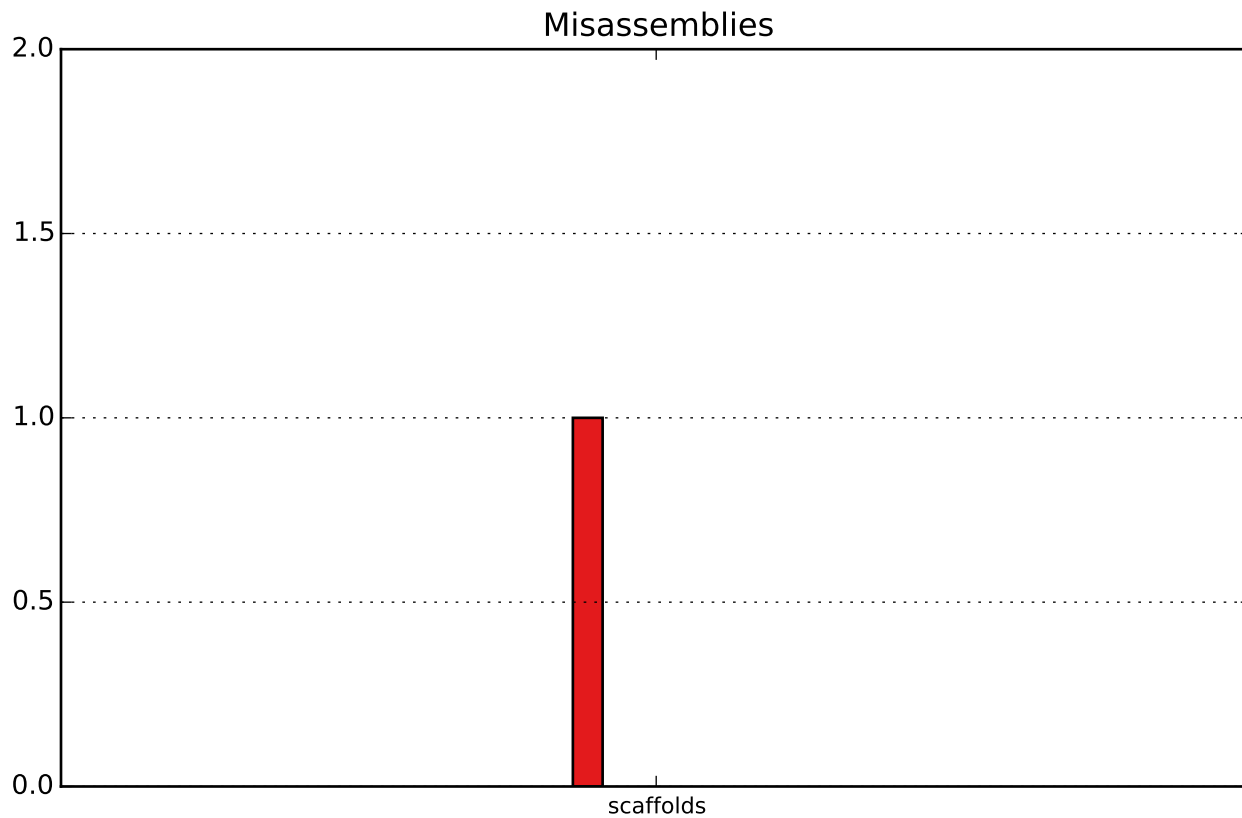
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	375

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).

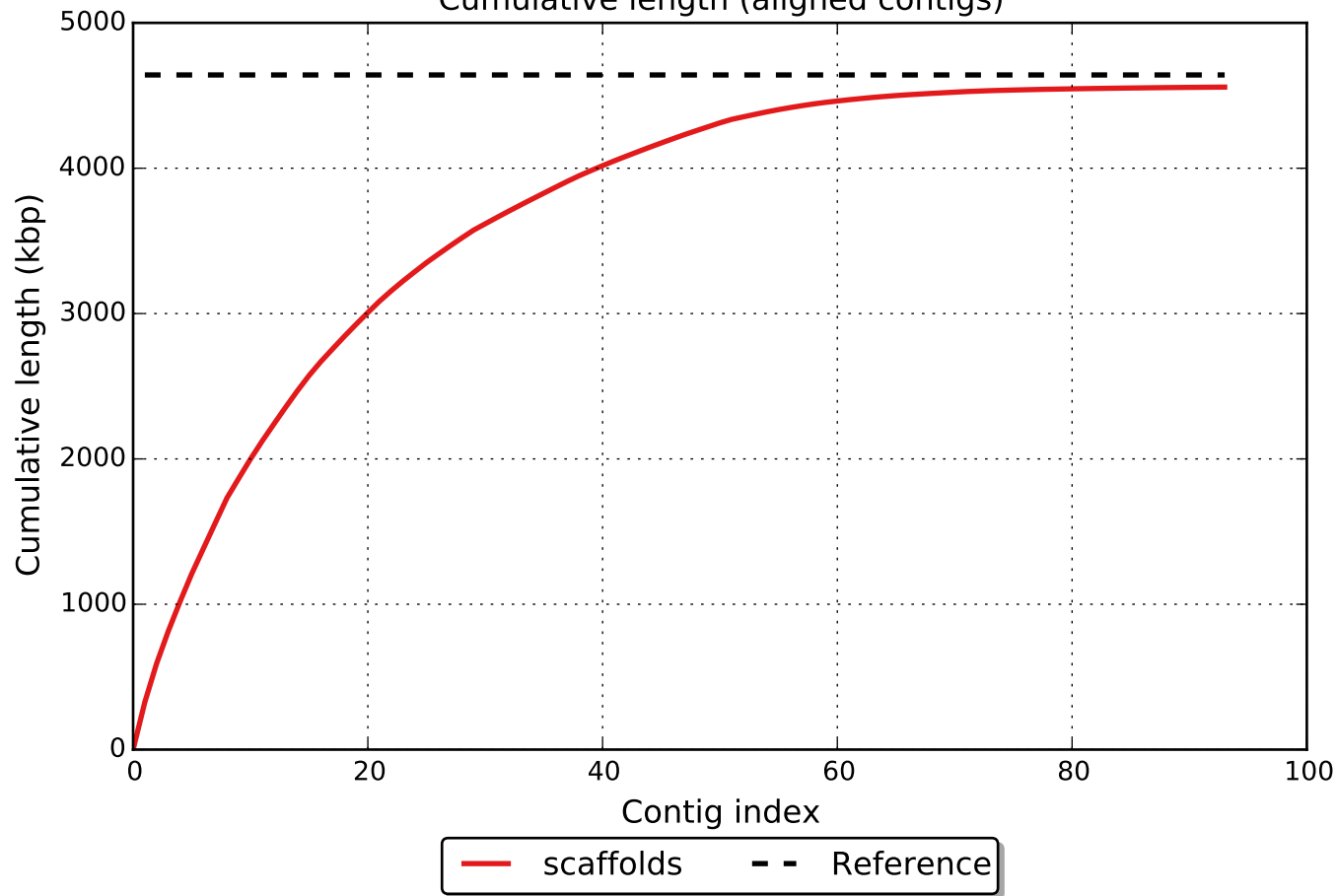
Nx







Cumulative length (aligned contigs)



NAx

