

Report

	scaffolds
# contigs (≥ 0 bp)	84
# contigs (≥ 1000 bp)	65
# contigs (≥ 5000 bp)	50
# contigs (≥ 10000 bp)	47
# contigs (≥ 25000 bp)	41
# contigs (≥ 50000 bp)	27
Total length (≥ 0 bp)	4568117
Total length (≥ 1000 bp)	4562692
Total length (≥ 5000 bp)	4528217
Total length (≥ 10000 bp)	4504264
Total length (≥ 25000 bp)	4413070
Total length (≥ 50000 bp)	3919931
# contigs	70
Largest contig	327050
Total length	4566115
Reference length	4641652
N50	173984
N75	87061
L50	10
L75	20
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	45684
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.313
Duplication ratio	1.001
# N's per 100 kbp	2.96
# mismatches per 100 kbp	62.83
# indels per 100 kbp	8.88
Largest alignment	327050
NA50	173069
NA75	87061
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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	45684
# local misassemblies	1
# mismatches	2867
# indels	405
# short indels	404
# long indels	1
Indels length	595

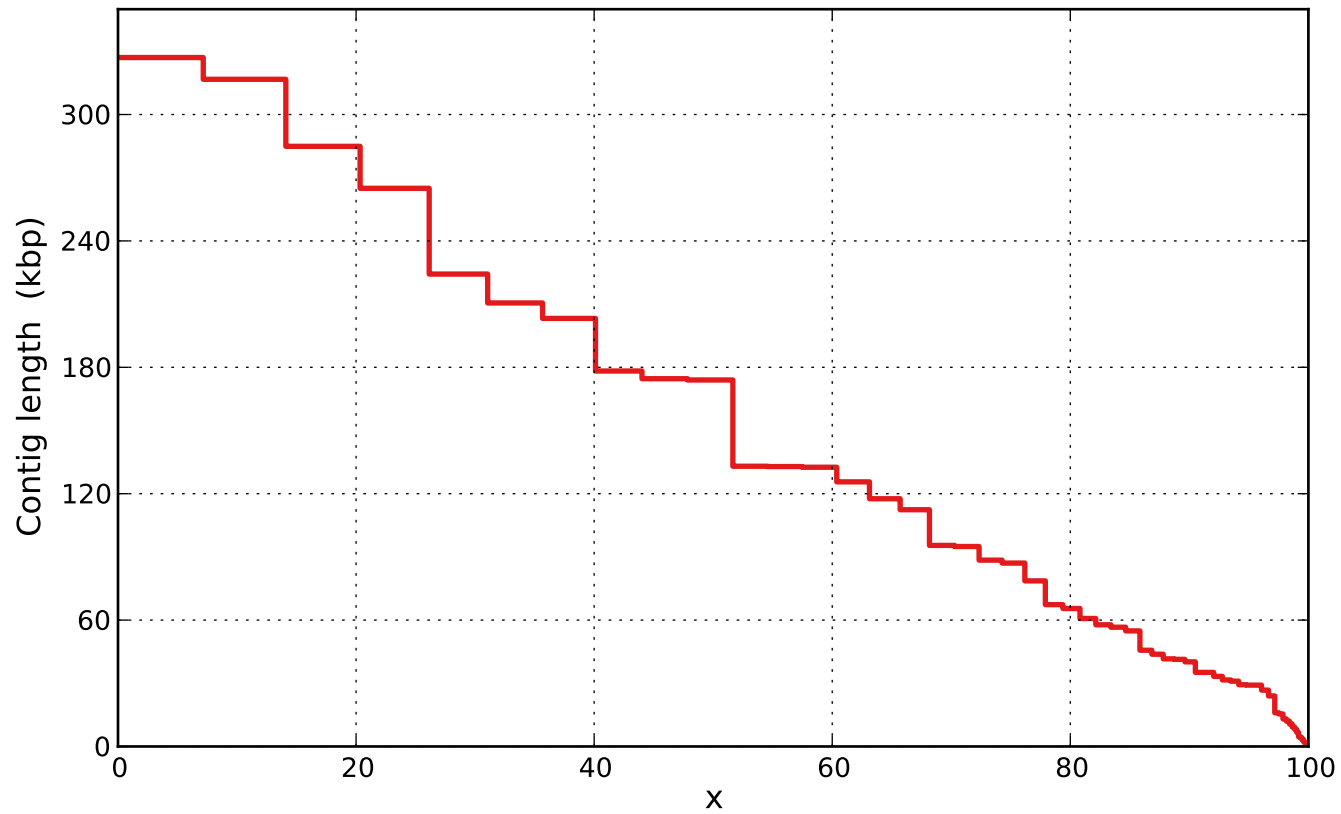
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

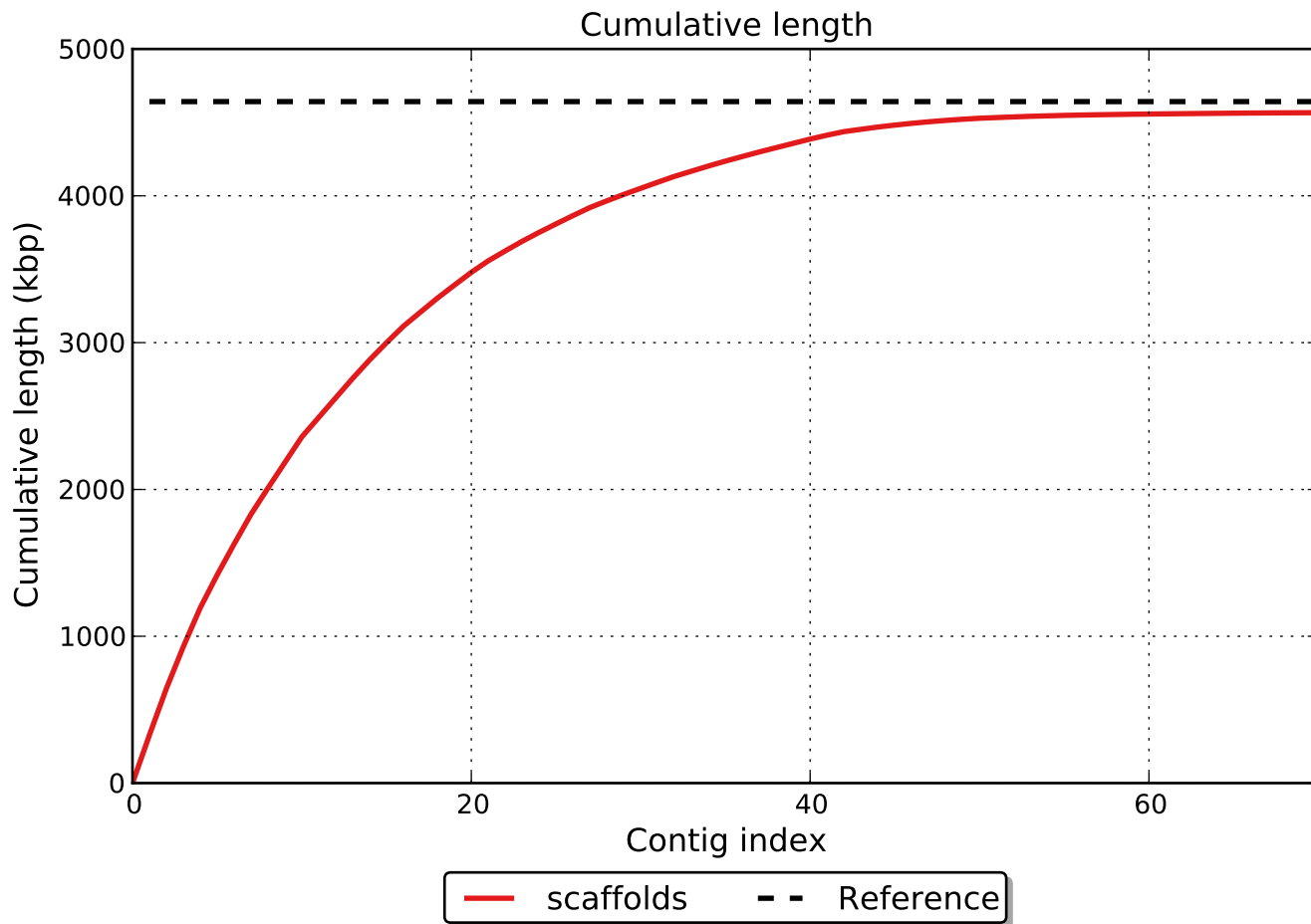
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	135

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).

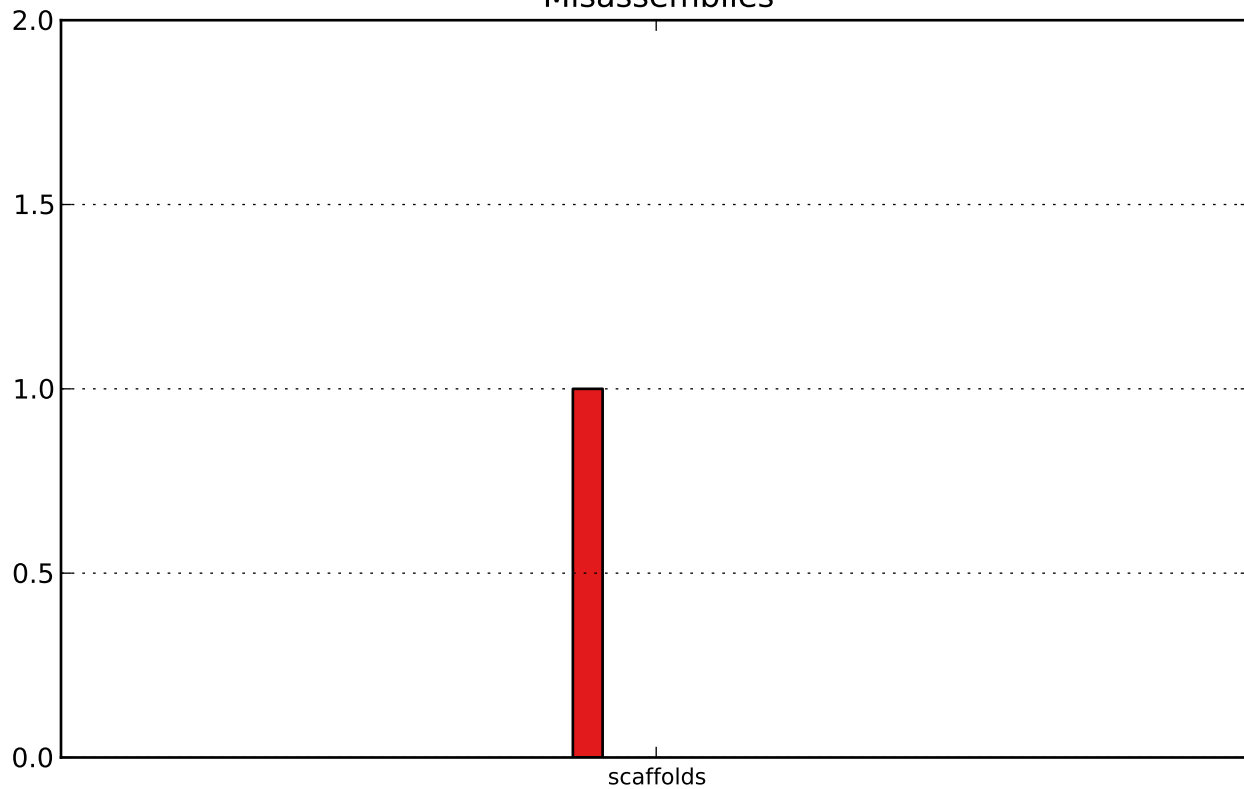
Nx



— scaffolds

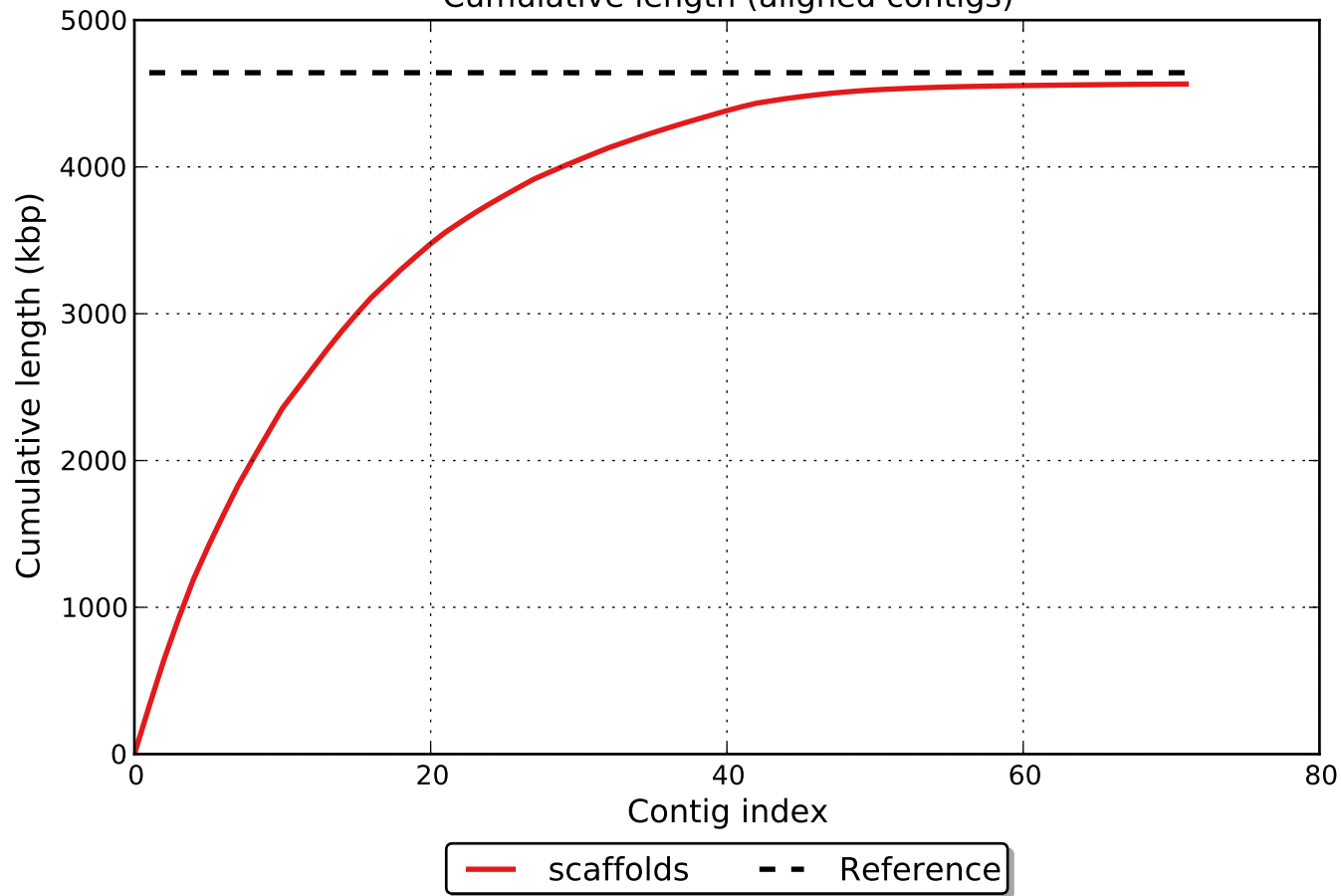


Misassemblies



 # relocations

Cumulative length (aligned contigs)



NAx

