

Report

	scaffolds
# contigs (≥ 0 bp)	86
# contigs (≥ 1000 bp)	66
# contigs (≥ 5000 bp)	49
# contigs (≥ 10000 bp)	46
# contigs (≥ 25000 bp)	40
# contigs (≥ 50000 bp)	27
Total length (≥ 0 bp)	4568596
Total length (≥ 1000 bp)	4563383
Total length (≥ 5000 bp)	4525467
Total length (≥ 10000 bp)	4501501
Total length (≥ 25000 bp)	4410285
Total length (≥ 50000 bp)	3949594
# contigs	70
Largest contig	327056
Total length	4566281
Reference length	4641652
N50	173981
N75	87060
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 (▼)	98.324
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.29
# indels per 100 kbp	8.50
Largest alignment	327056
NA50	173981
NA75	87060
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	2797
# indels	388
# short indels	388
# long indels	0
Indels length	533

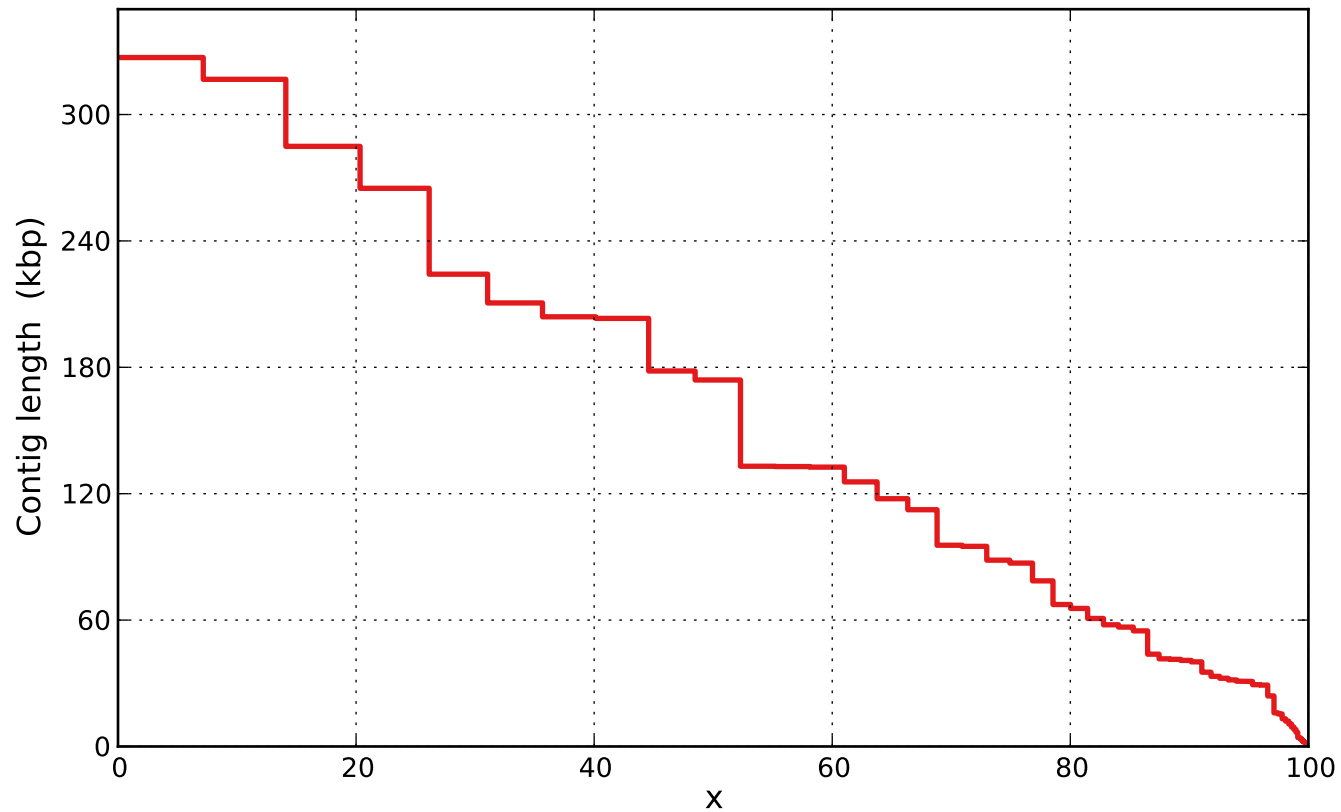
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

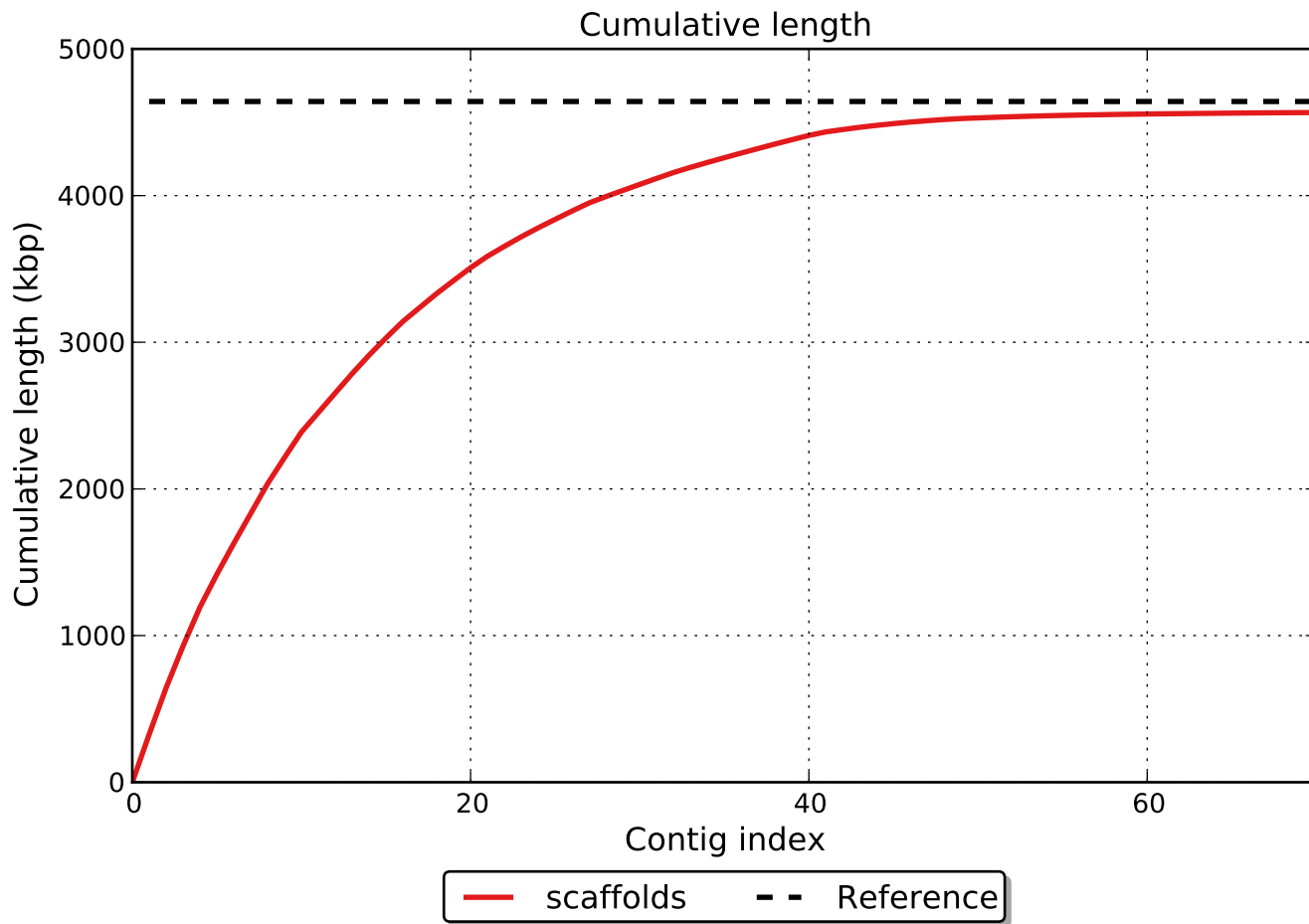
Unaligned report

	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

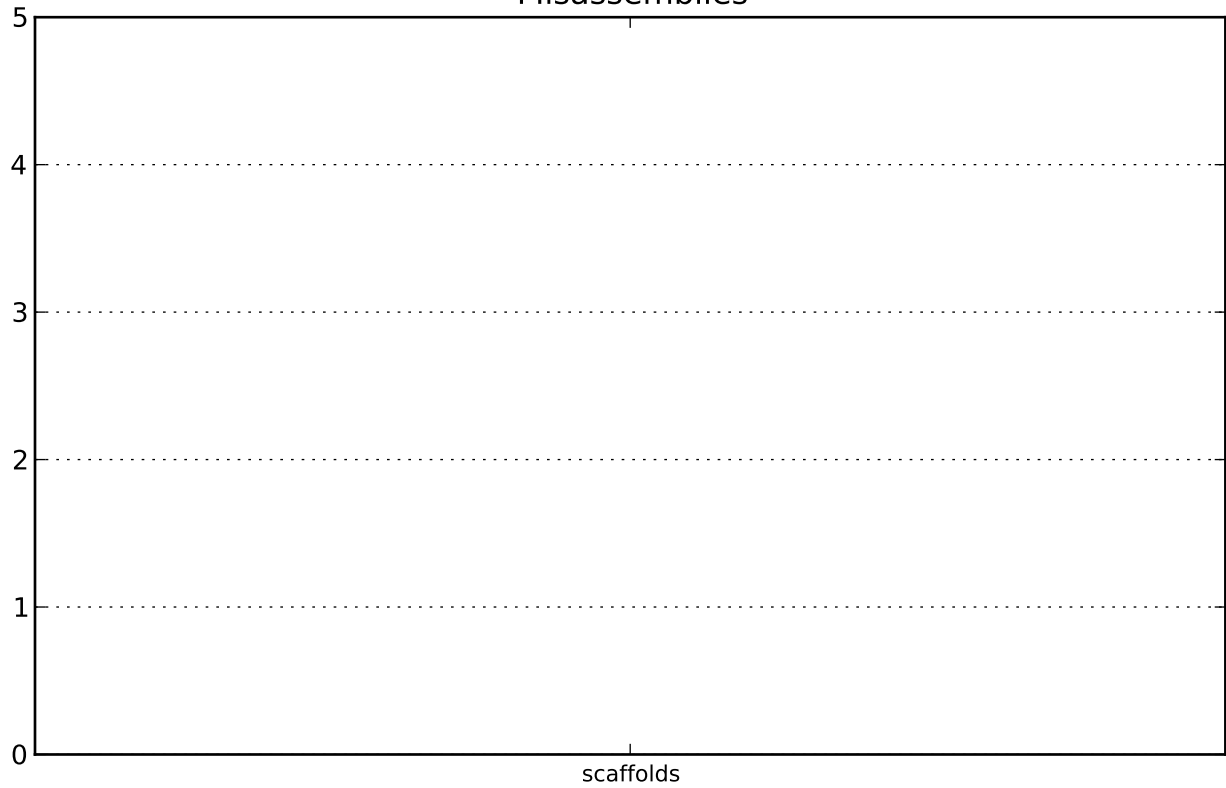
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

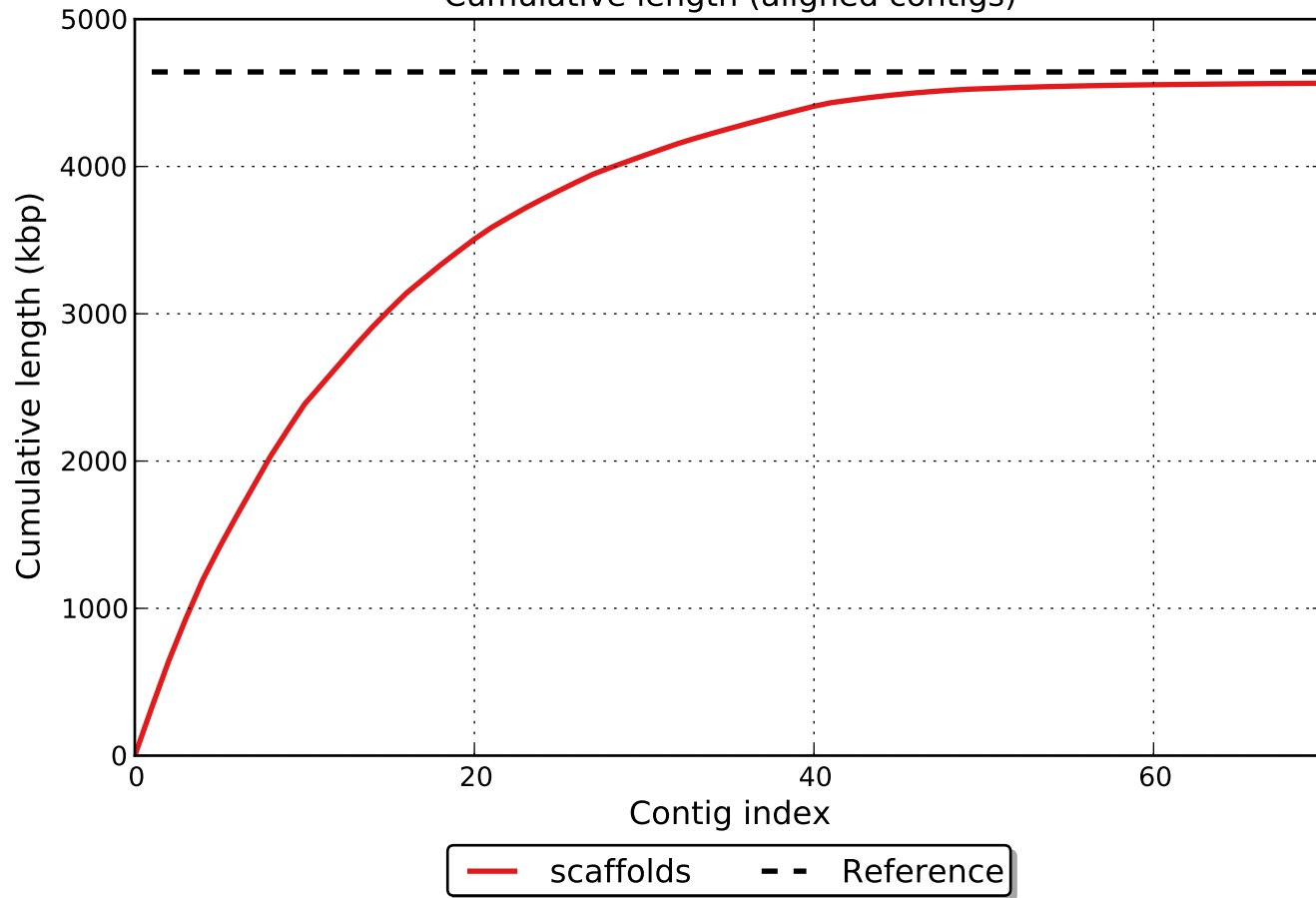




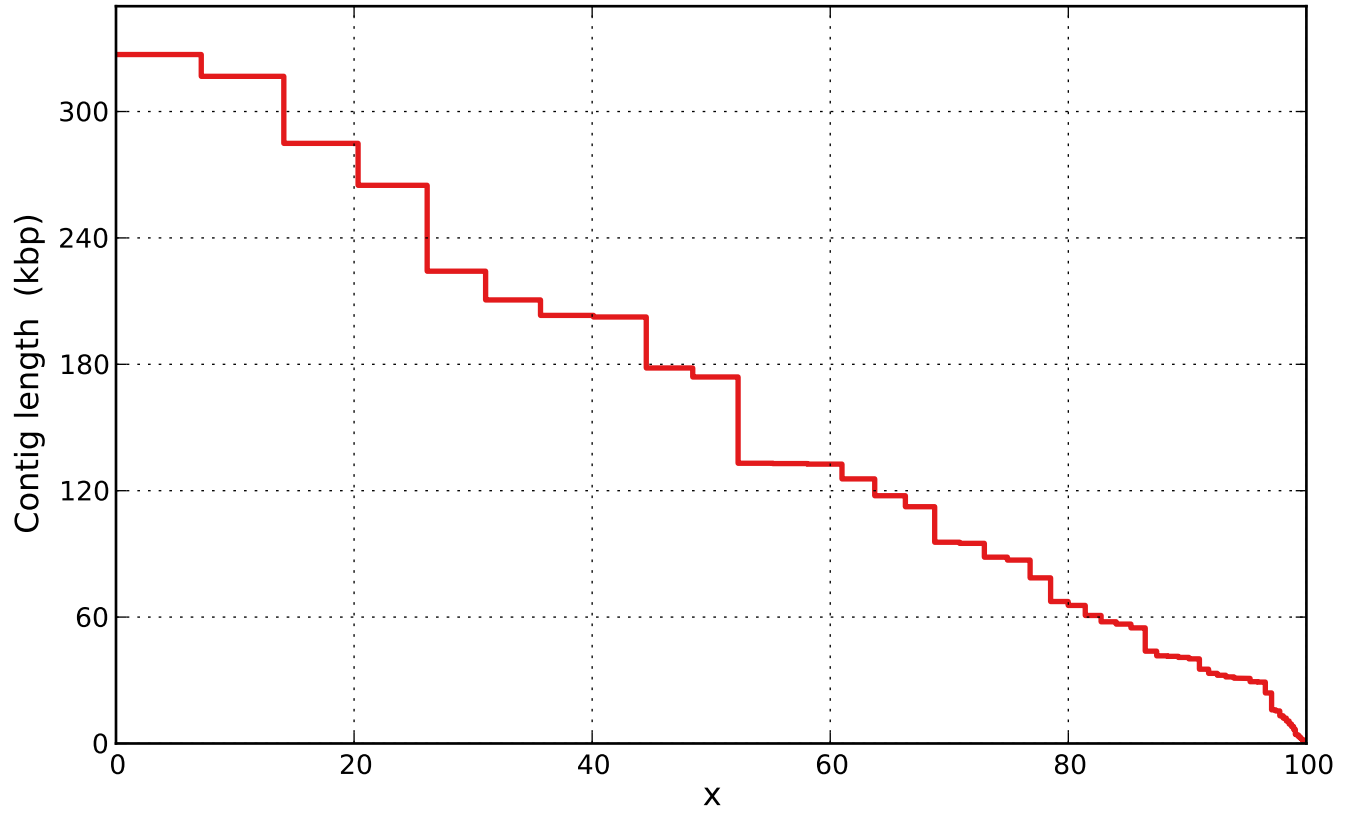
Misassemblies



Cumulative length (aligned contigs)



NAx



— scaffolds