

Report

	scaffolds
# contigs (≥ 0 bp)	115
# contigs (≥ 1000 bp)	78
# contigs (≥ 5000 bp)	54
# contigs (≥ 10000 bp)	49
# contigs (≥ 25000 bp)	45
# contigs (≥ 50000 bp)	28
Total length (≥ 0 bp)	4565089
Total length (≥ 1000 bp)	4554363
Total length (≥ 5000 bp)	4495919
Total length (≥ 10000 bp)	4459233
Total length (≥ 25000 bp)	4401922
Total length (≥ 50000 bp)	3791601
# contigs	85
Largest contig	327052
Total length	4559054
Reference length	4641652
N50	132613
N75	72264
L50	11
L75	22
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	41750
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.159
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.61
# indels per 100 kbp	9.28
Largest alignment	327052
NA50	132613
NA75	72264
LA50	11
LA75	22

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	41750
# local misassemblies	4
# mismatches	2807
# indels	423
# short indels	422
# long indels	1
Indels length	640

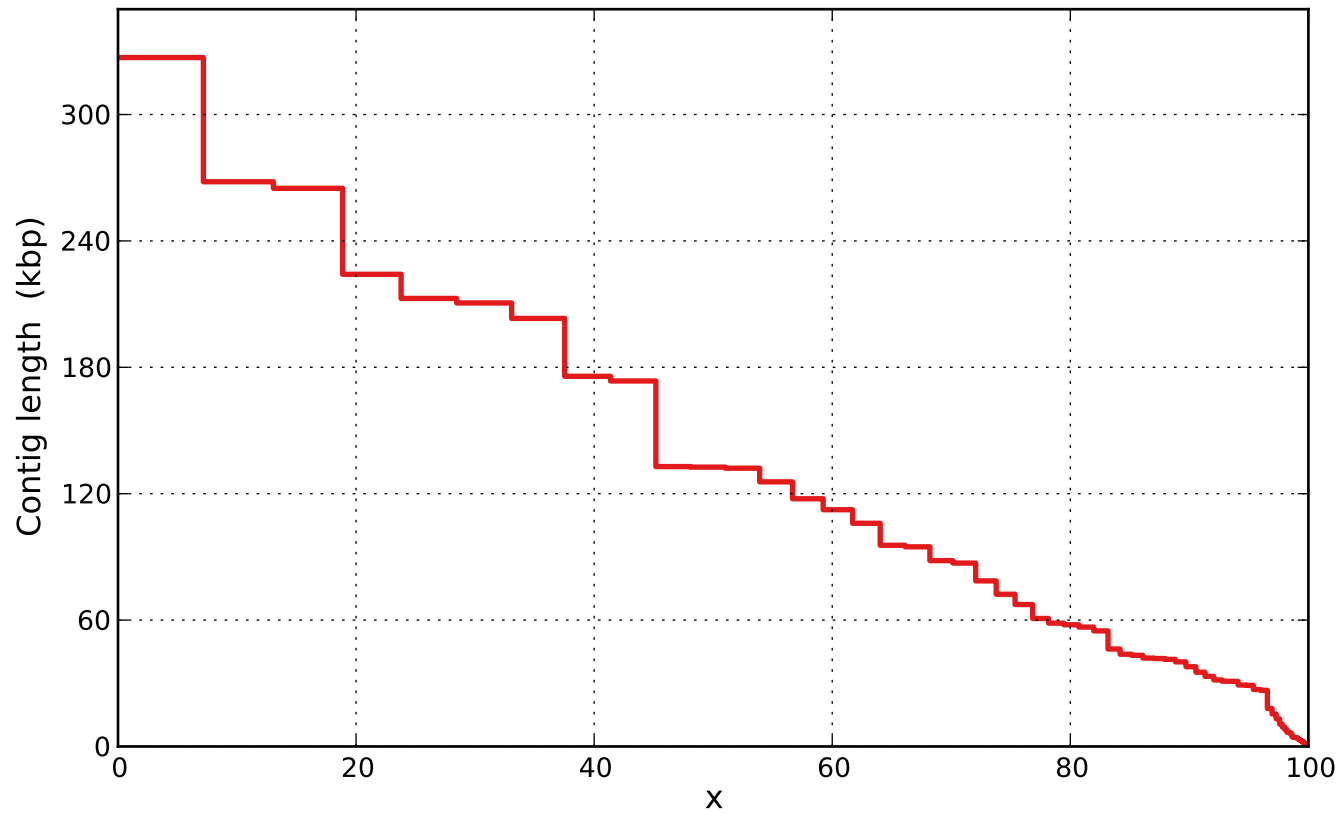
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

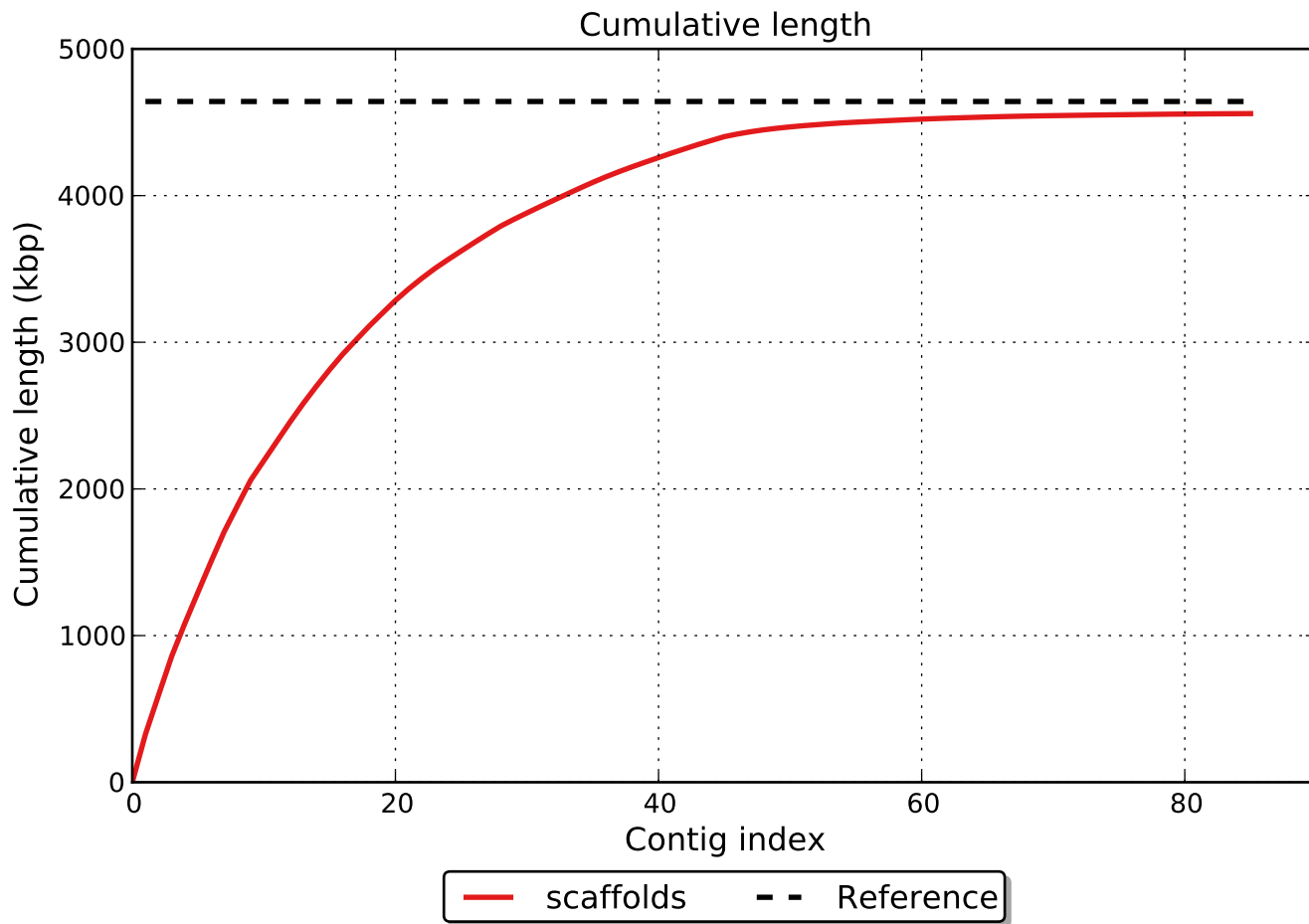
Unaligned report

	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).

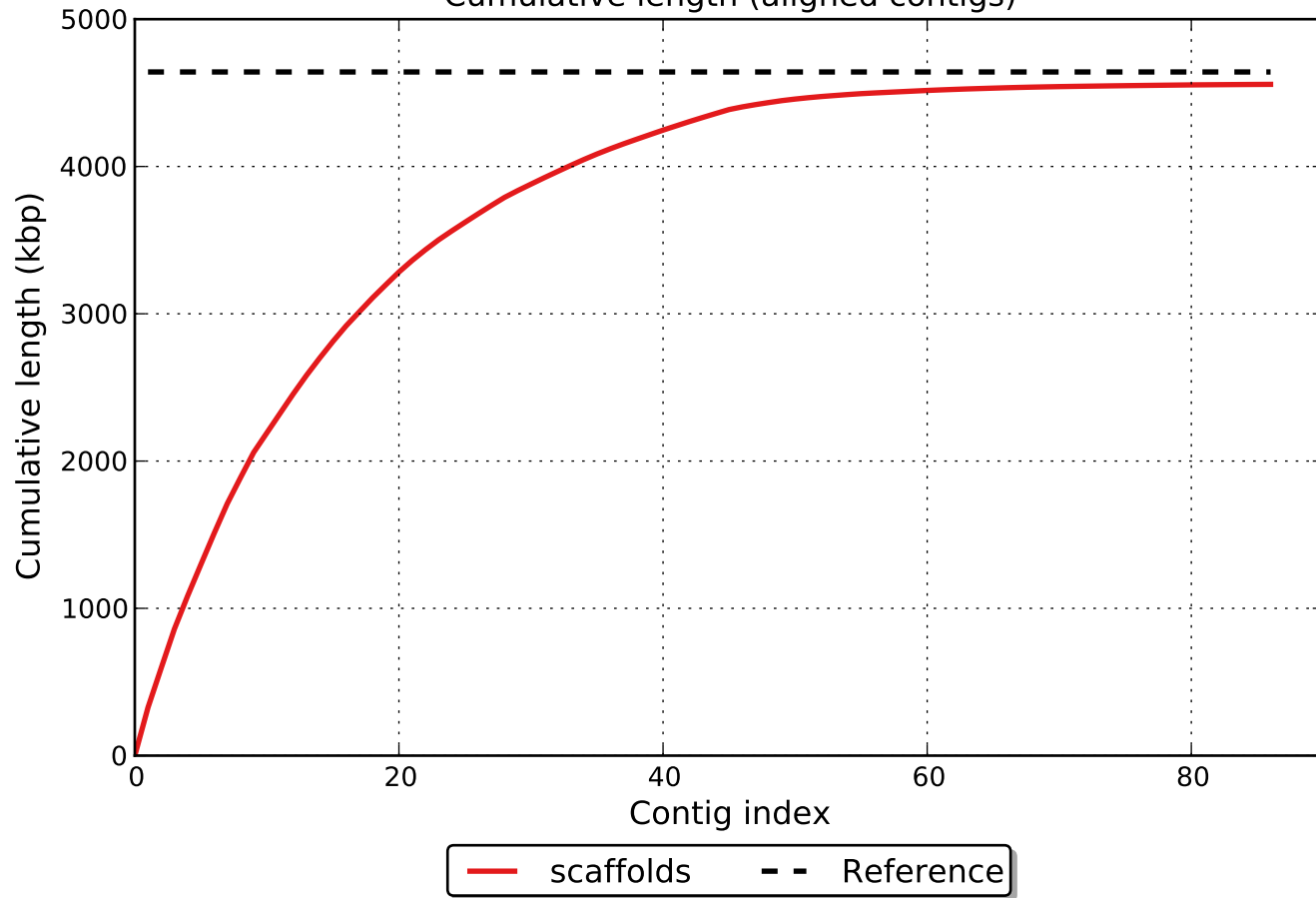
Nx







Cumulative length (aligned contigs)



NAx

