

Report

	scaffolds
# contigs (≥ 0 bp)	86
# contigs (≥ 1000 bp)	67
# contigs (≥ 5000 bp)	50
# contigs (≥ 10000 bp)	47
# contigs (≥ 25000 bp)	41
# contigs (≥ 50000 bp)	27
Total length (≥ 0 bp)	4567559
Total length (≥ 1000 bp)	4562272
Total length (≥ 5000 bp)	4520571
Total length (≥ 10000 bp)	4496601
Total length (≥ 25000 bp)	4405357
Total length (≥ 50000 bp)	3920273
# contigs	72
Largest contig	327047
Total length	4565695
Reference length	4641652
N50	173978
N75	87062
L50	10
L75	20
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	45736
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.307
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	63.18
# indels per 100 kbp	8.81
Largest alignment	327047
NA50	173066
NA75	87062
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	45736
# local misassemblies	1
# mismatches	2883
# indels	402
# short indels	402
# long indels	0
Indels length	561

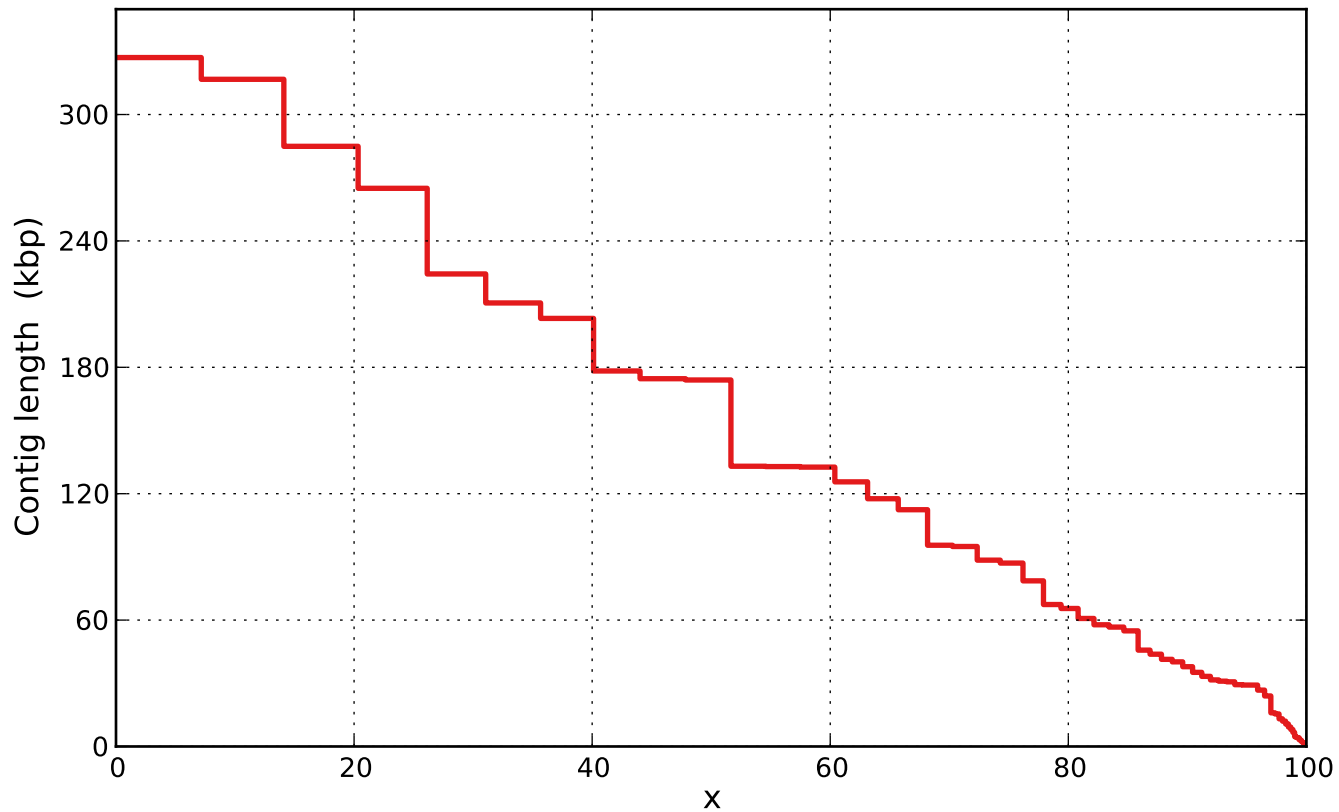
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

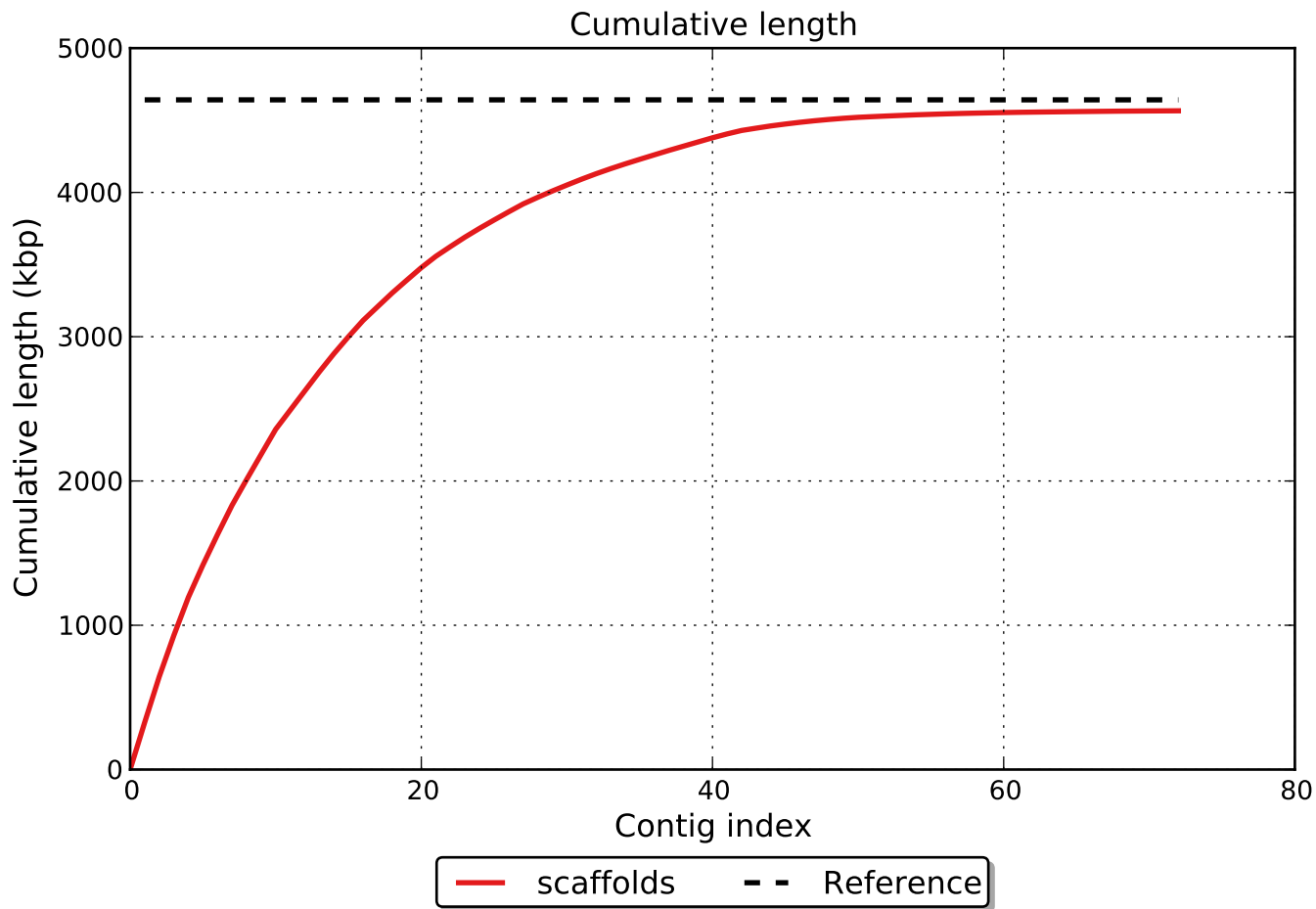
Unaligned report

	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).

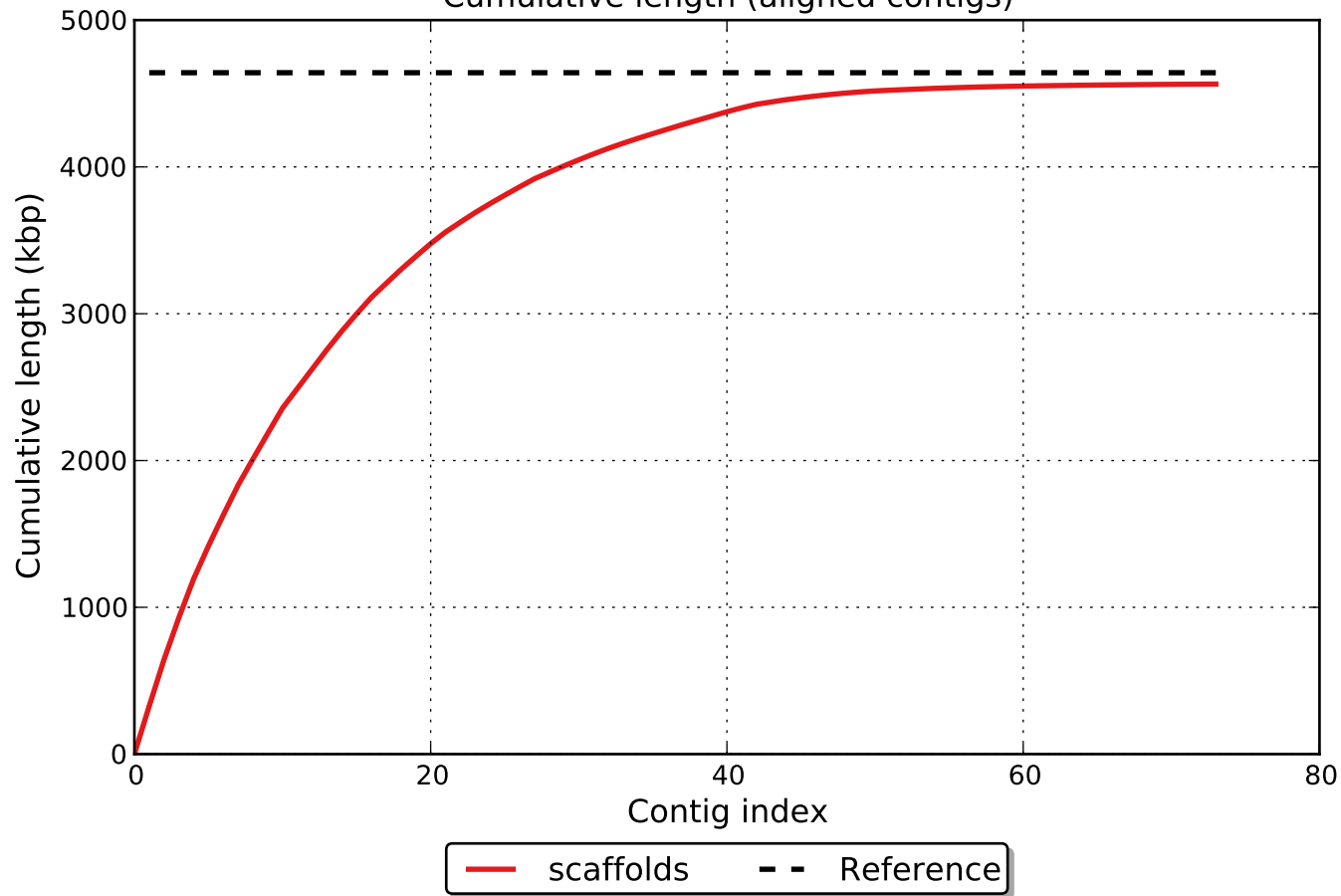
Nx



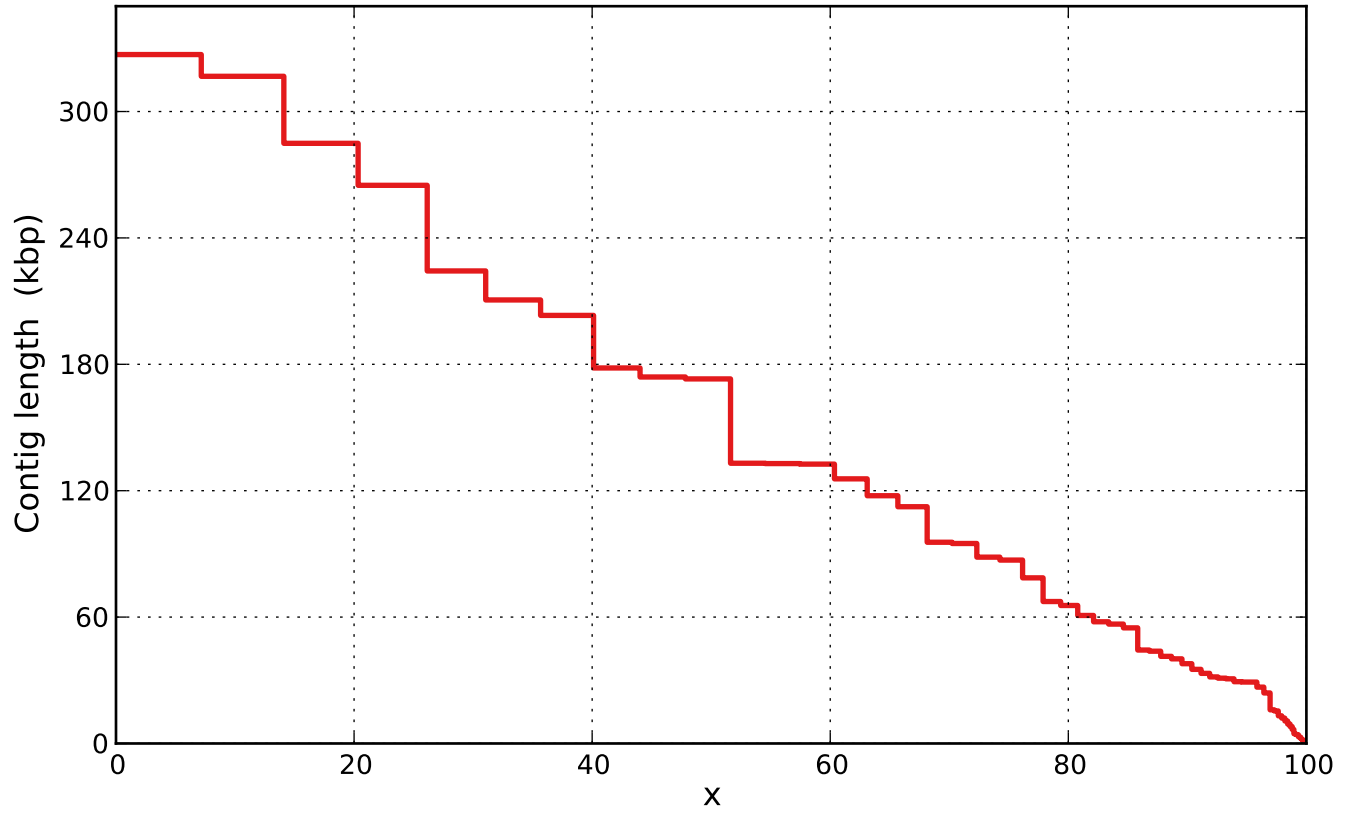




Cumulative length (aligned contigs)



NAx



— scaffolds