

Report

	scaffolds
# contigs (≥ 0 bp)	90
# contigs (≥ 1000 bp)	67
# contigs (≥ 5000 bp)	49
# contigs (≥ 10000 bp)	46
# contigs (≥ 25000 bp)	40
# contigs (≥ 50000 bp)	27
Total length (≥ 0 bp)	4568102
Total length (≥ 1000 bp)	4561512
Total length (≥ 5000 bp)	4522537
Total length (≥ 10000 bp)	4498467
Total length (≥ 25000 bp)	4409098
Total length (≥ 50000 bp)	3947942
# contigs	72
Largest contig	327055
Total length	4565287
Reference length	4641652
N50	173973
N75	87062
L50	10
L75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.302
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.50
# indels per 100 kbp	8.20
Largest alignment	327055
NA50	173973
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	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	2806
# indels	374
# short indels	374
# long indels	0
Indels length	538

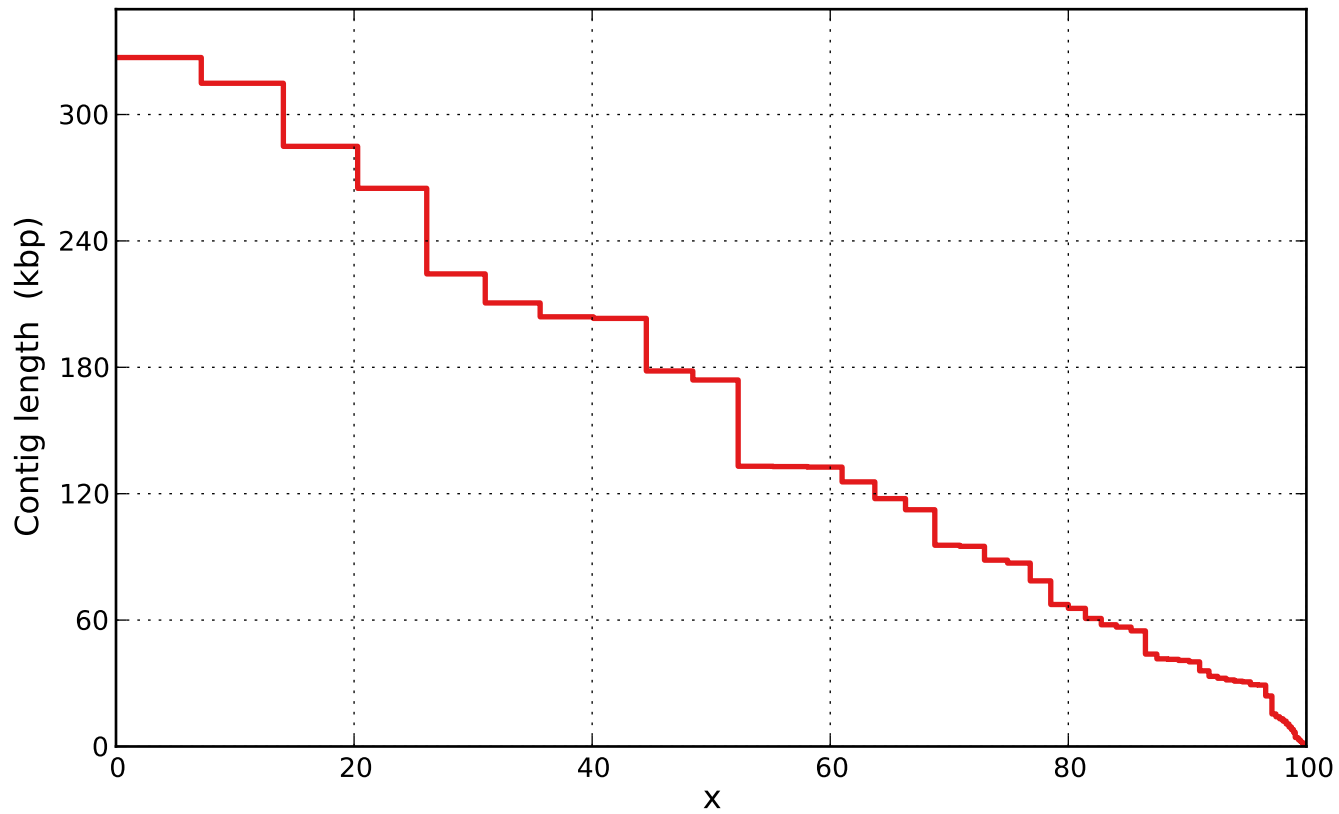
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

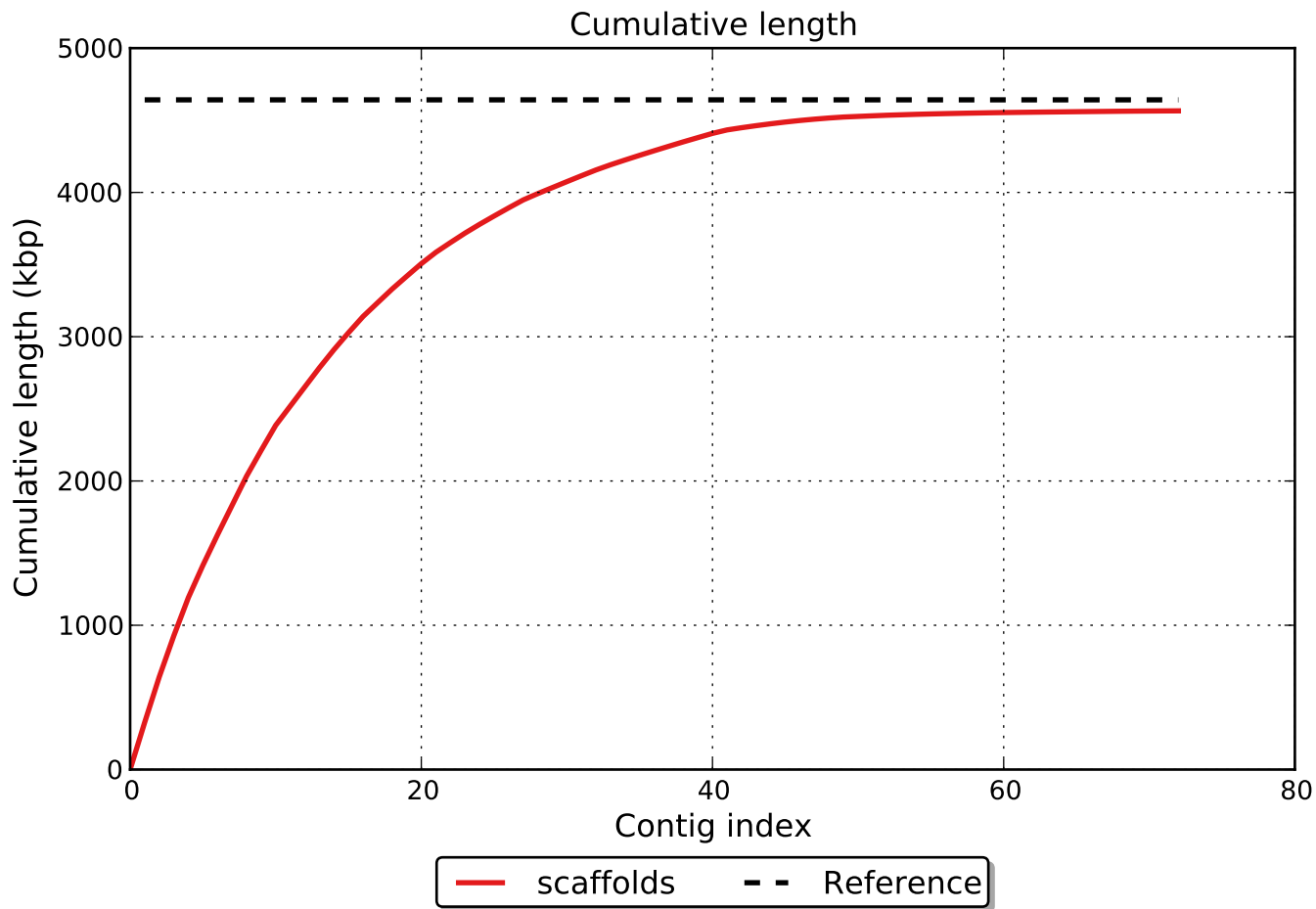
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

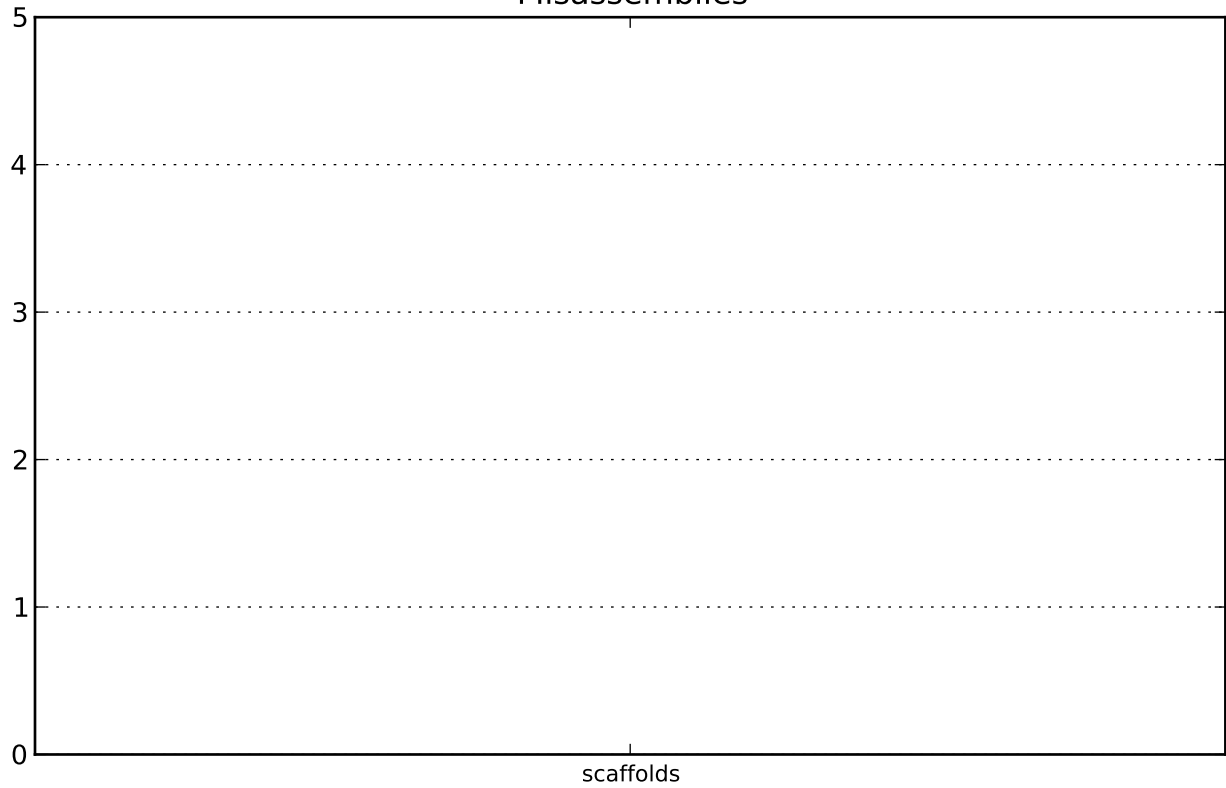
Nx



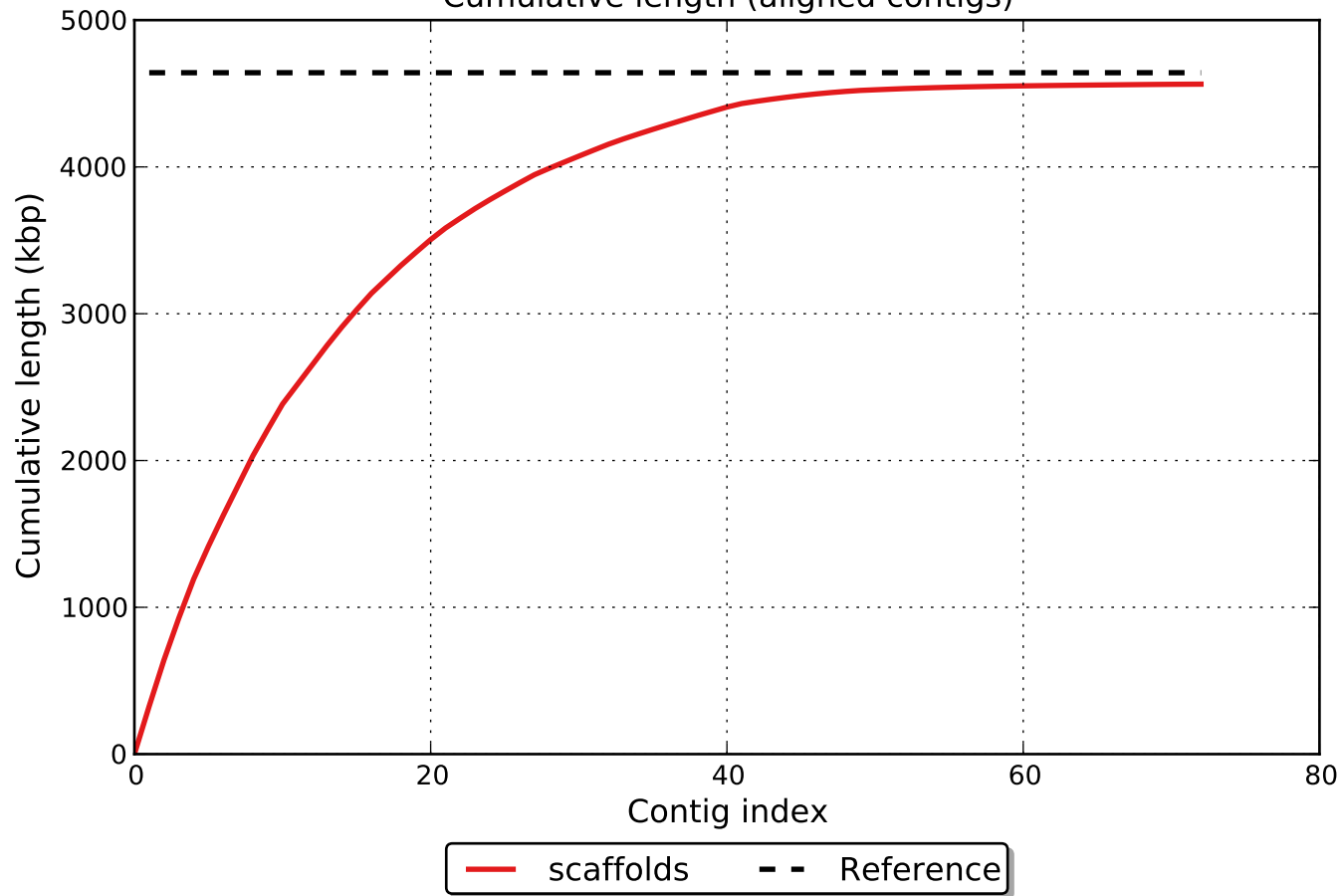
scaffolds



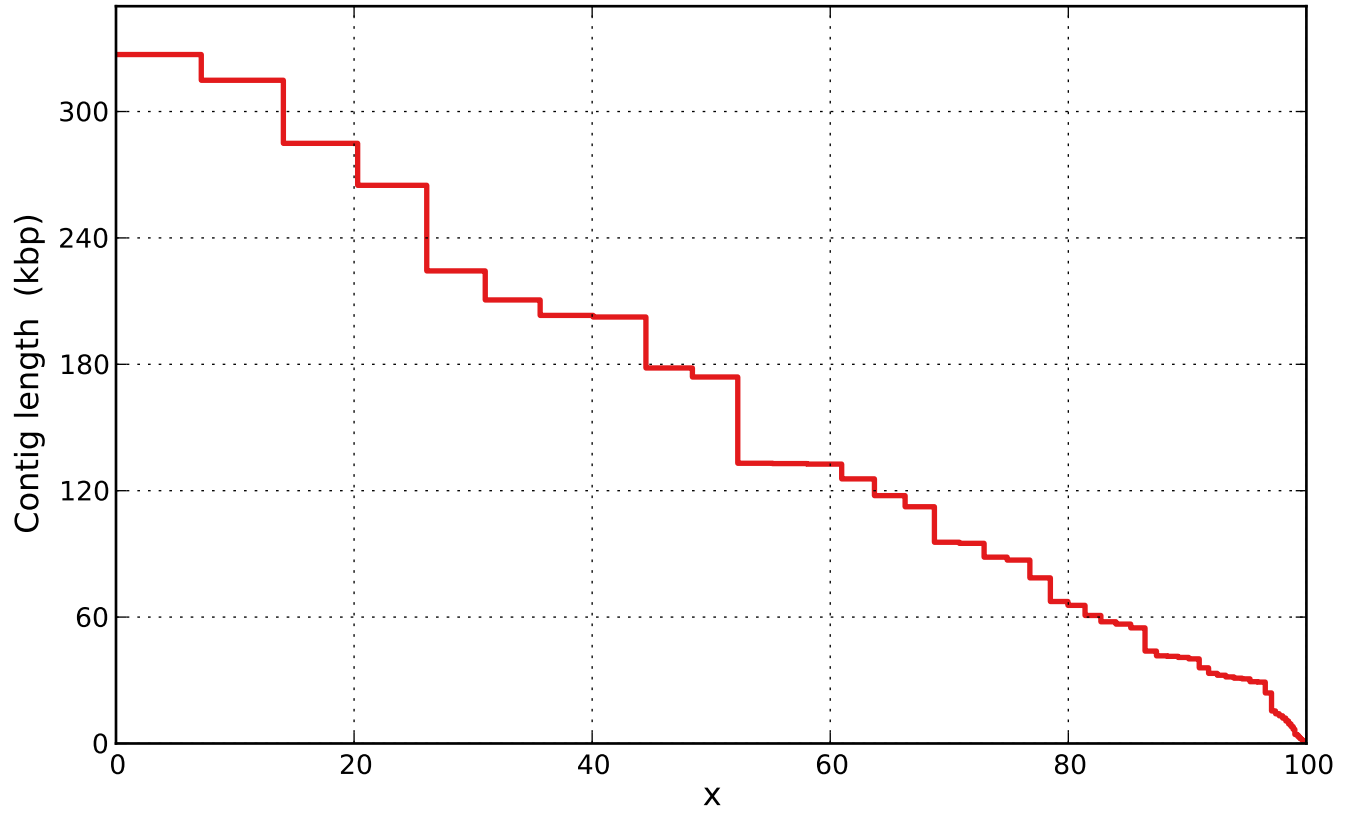
Misassemblies



Cumulative length (aligned contigs)



NAx



— scaffolds