

## Report

	scaffolds
# contigs ( $\geq 0$ bp)	101
# contigs ( $\geq 1000$ bp)	71
# contigs ( $\geq 5000$ bp)	50
# contigs ( $\geq 10000$ bp)	47
# contigs ( $\geq 25000$ bp)	41
# contigs ( $\geq 50000$ bp)	28
Total length ( $\geq 0$ bp)	4565542
Total length ( $\geq 1000$ bp)	4559535
Total length ( $\geq 5000$ bp)	4511316
Total length ( $\geq 10000$ bp)	4487368
Total length ( $\geq 25000$ bp)	4396206
Total length ( $\geq 50000$ bp)	3942251
# contigs	74
Largest contig	327060
Total length	4561751
Reference length	4641652
N50	173986
N75	78607
L50	10
L75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.226
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	59.90
# indels per 100 kbp	8.49
Largest alignment	327060
NA50	173986
NA75	78607
LA50	10
LA75	20

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  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	3
# mismatches	2731
# indels	387
# short indels	387
# long indels	0
Indels length	538

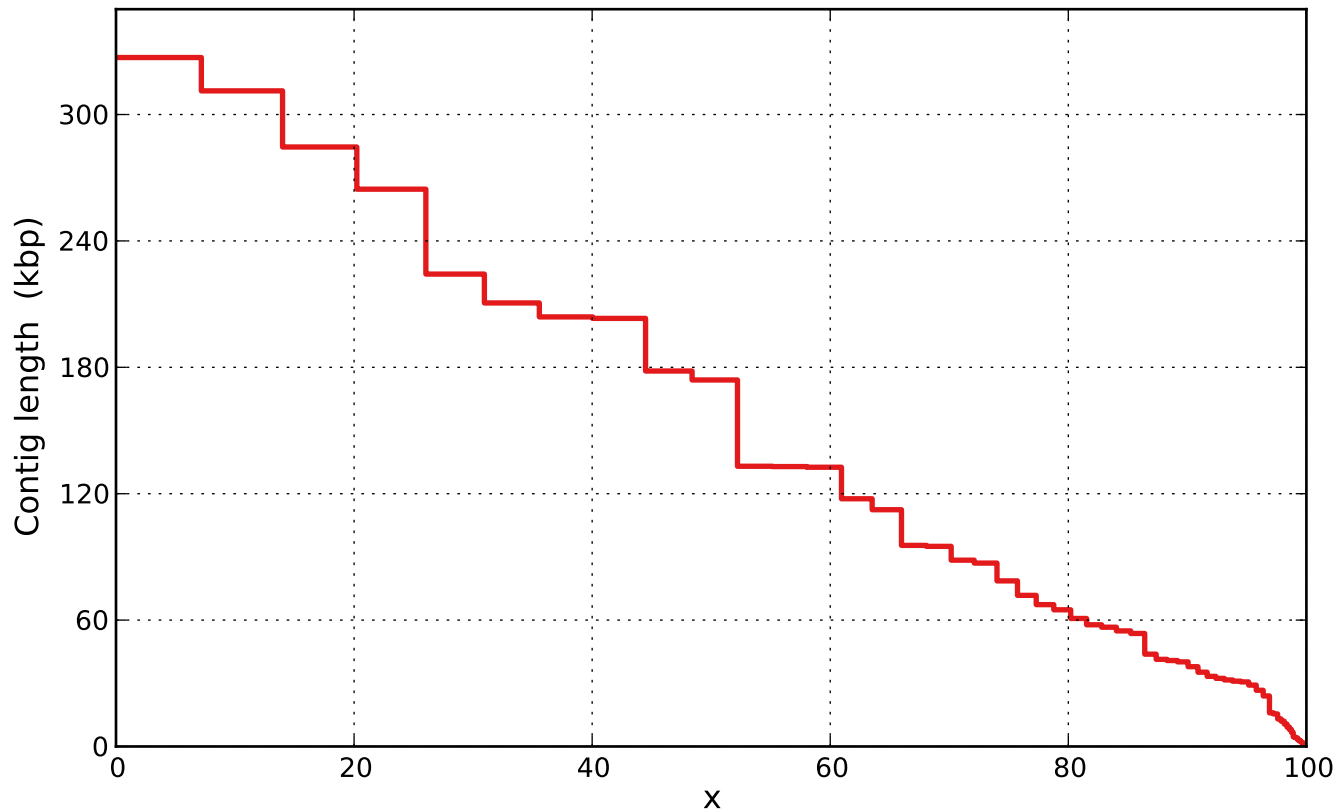
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

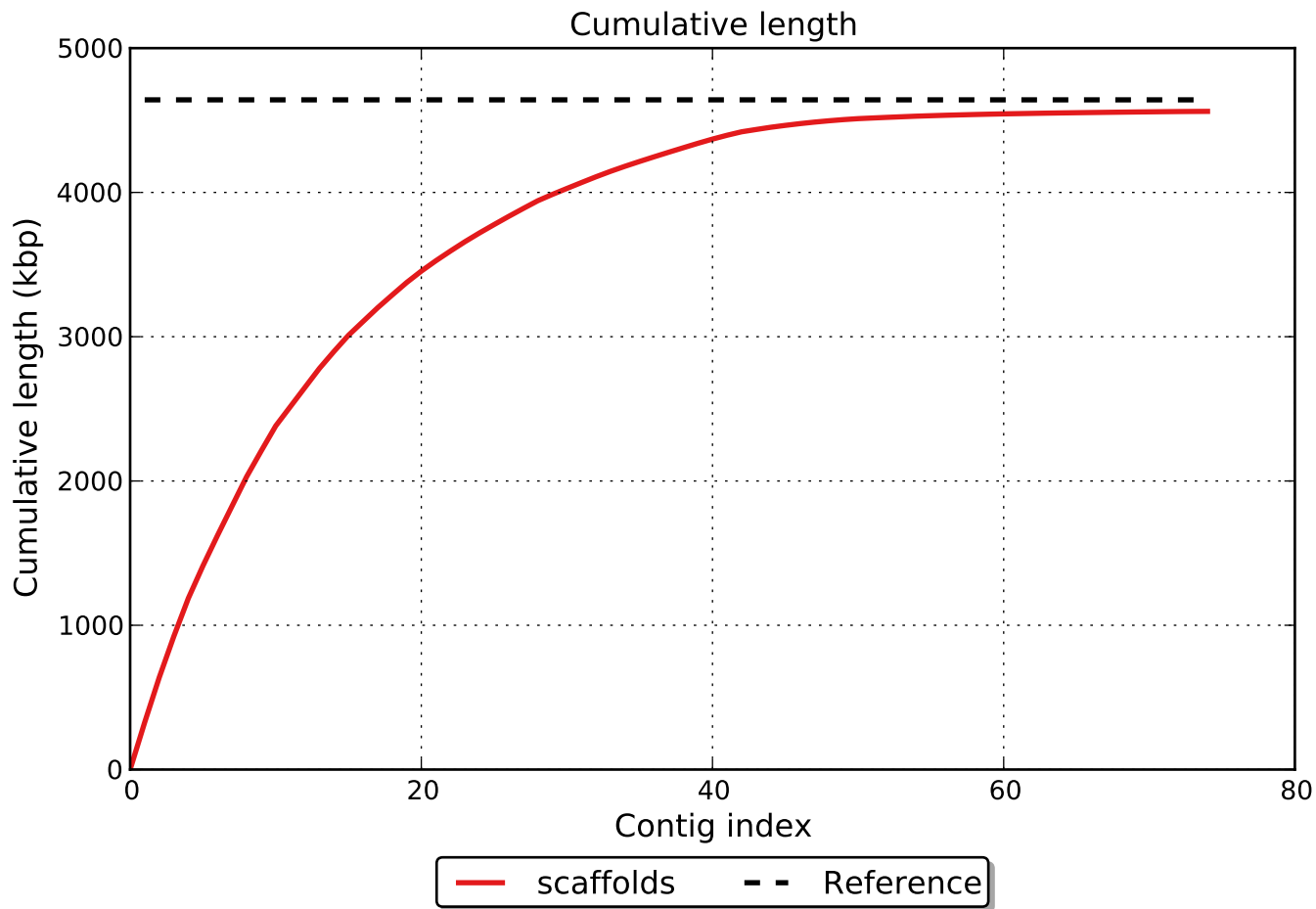
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

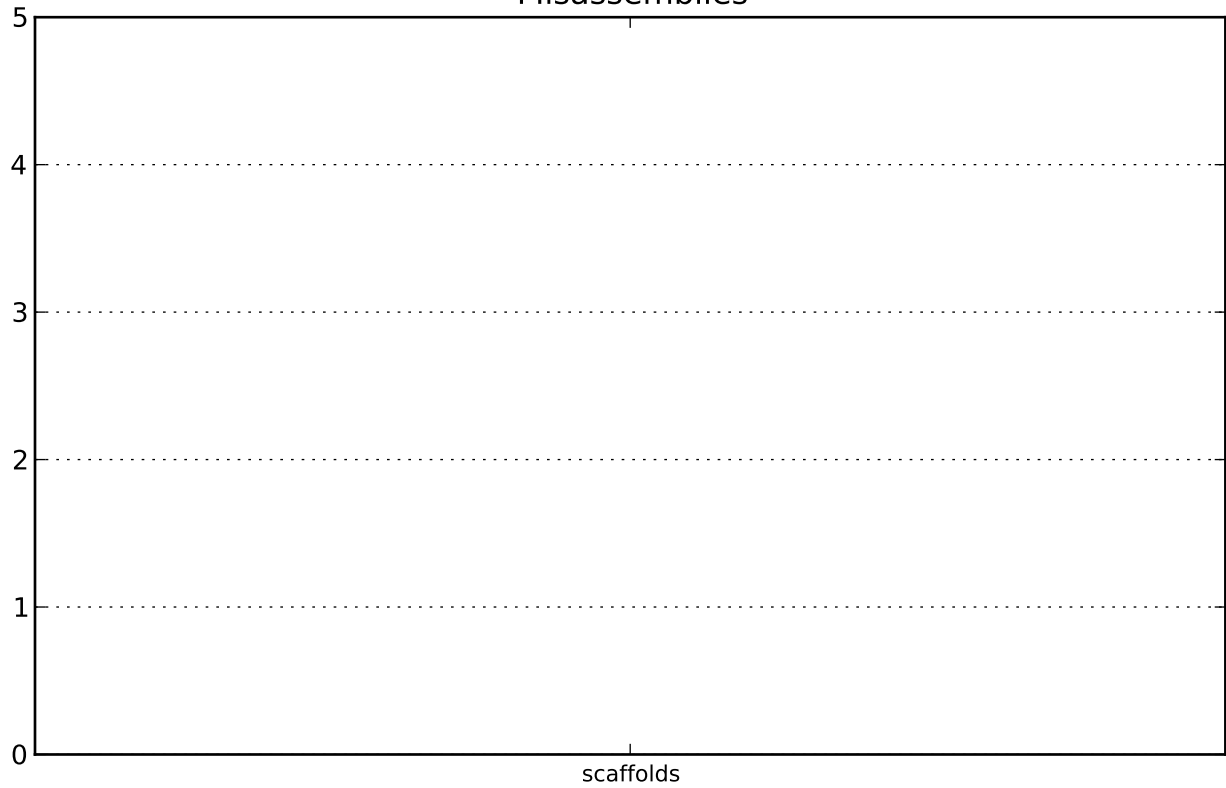
Nx



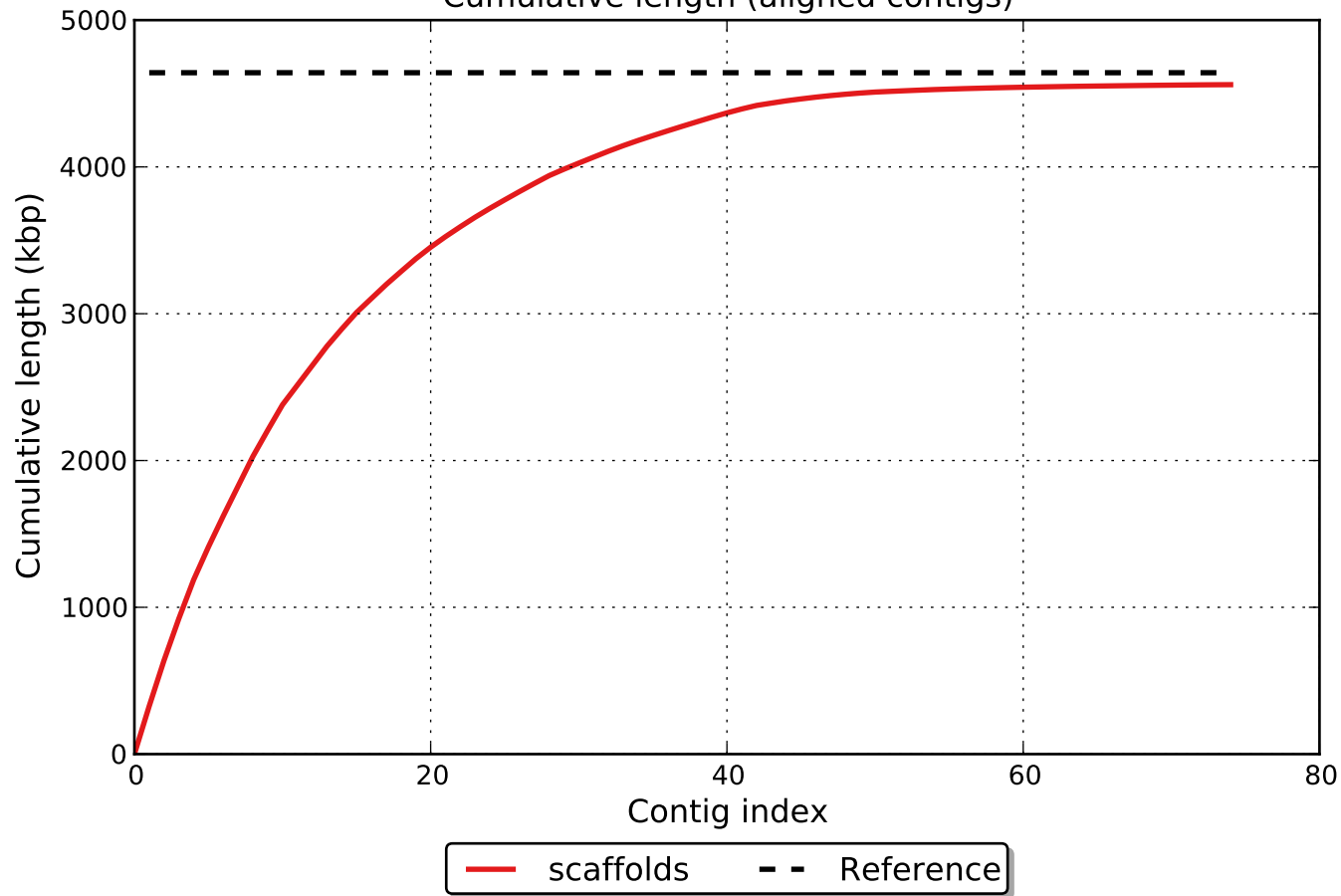
— scaffolds



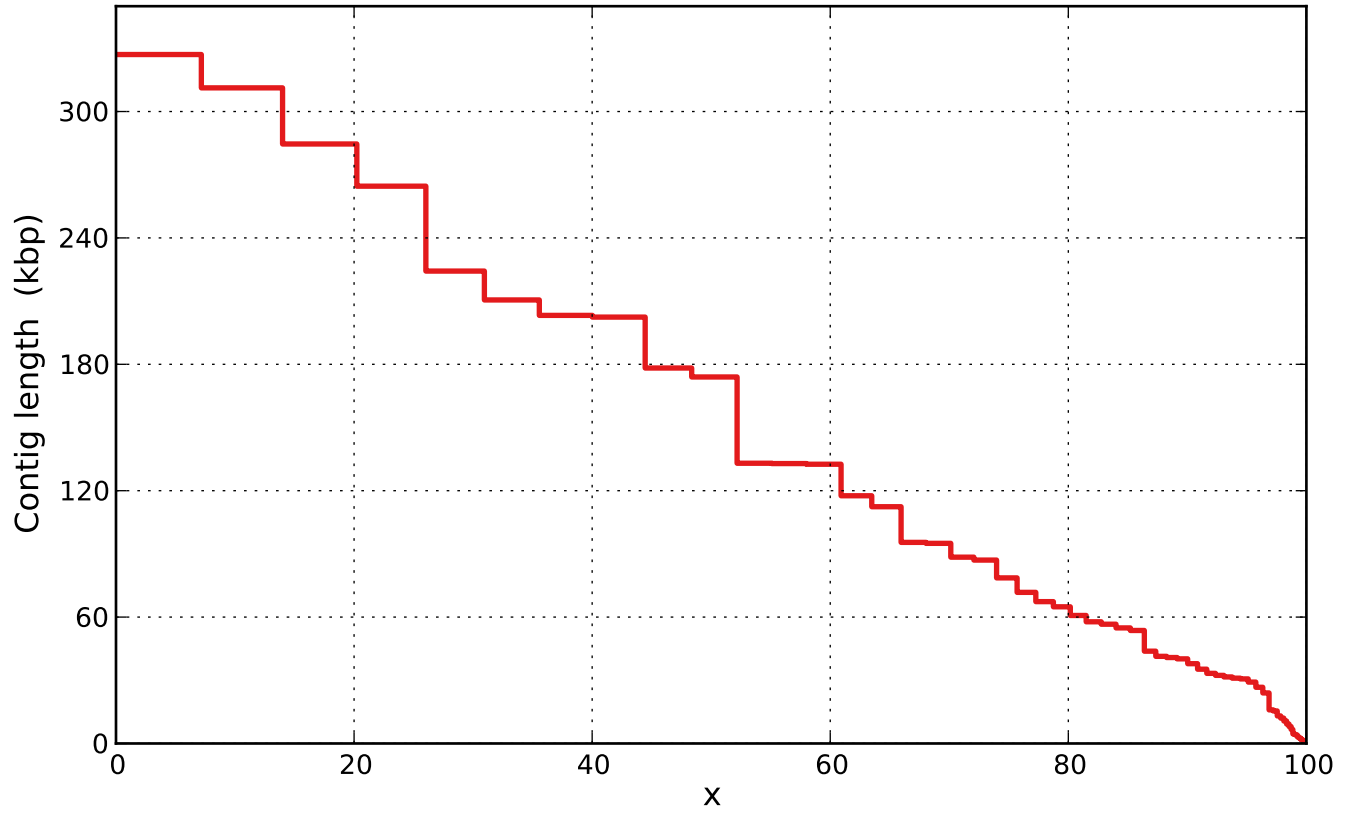
# Misassemblies



Cumulative length (aligned contigs)



NAx



— scaffolds