

## Report

	scaffolds
# contigs ( $\geq 0$ bp)	94
# contigs ( $\geq 1000$ bp)	67
# contigs ( $\geq 5000$ bp)	49
# contigs ( $\geq 10000$ bp)	46
# contigs ( $\geq 25000$ bp)	40
# contigs ( $\geq 50000$ bp)	27
Total length ( $\geq 0$ bp)	4567633
Total length ( $\geq 1000$ bp)	4559920
Total length ( $\geq 5000$ bp)	4520879
Total length ( $\geq 10000$ bp)	4496826
Total length ( $\geq 25000$ bp)	4407539
Total length ( $\geq 50000$ bp)	3946955
# contigs	73
Largest contig	327051
Total length	4564385
Reference length	4641652
N50	173974
N75	87051
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 (▼)	98.283
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.22
# indels per 100 kbp	8.46
Largest alignment	327051
NA50	173974
NA75	87051
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	2793
# indels	386
# short indels	386
# long indels	0
Indels length	555

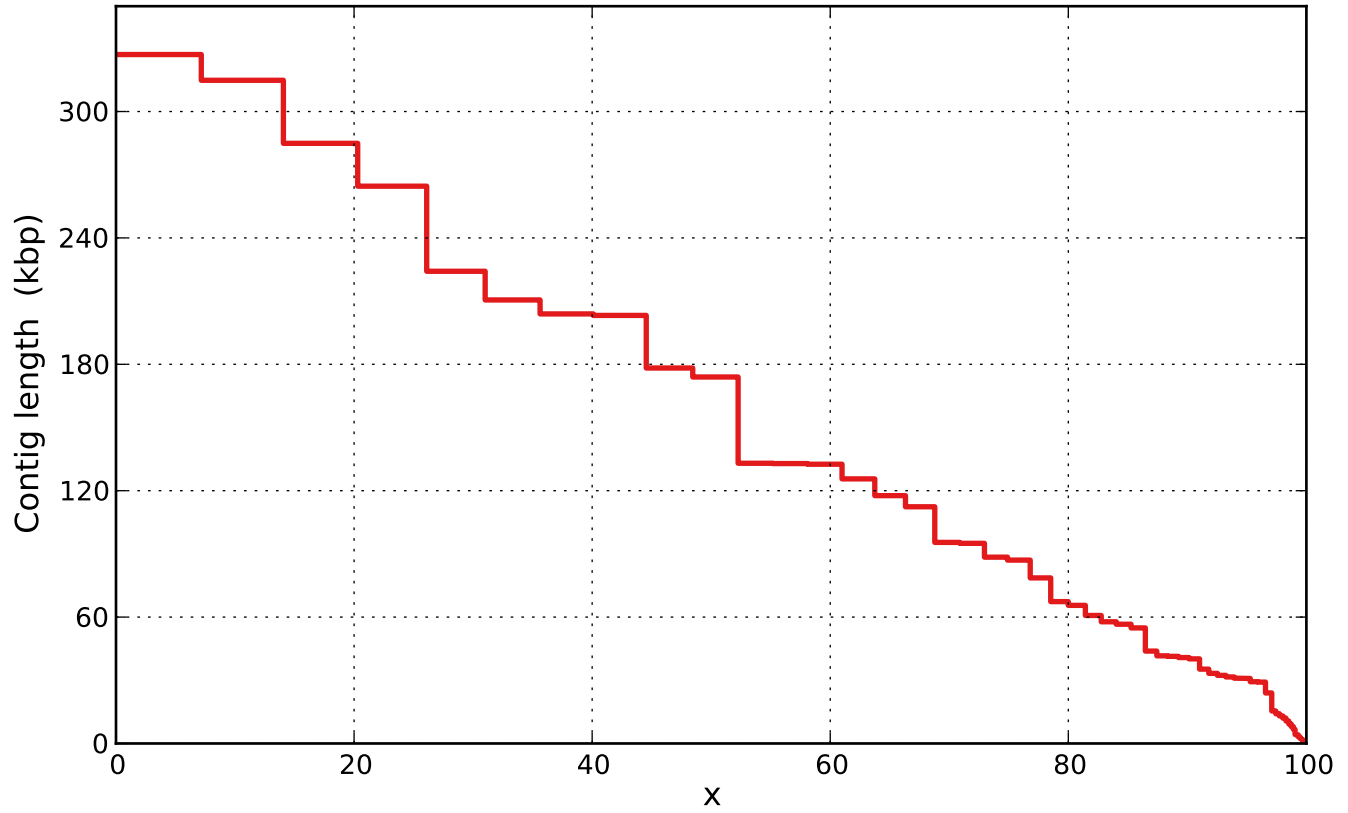
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

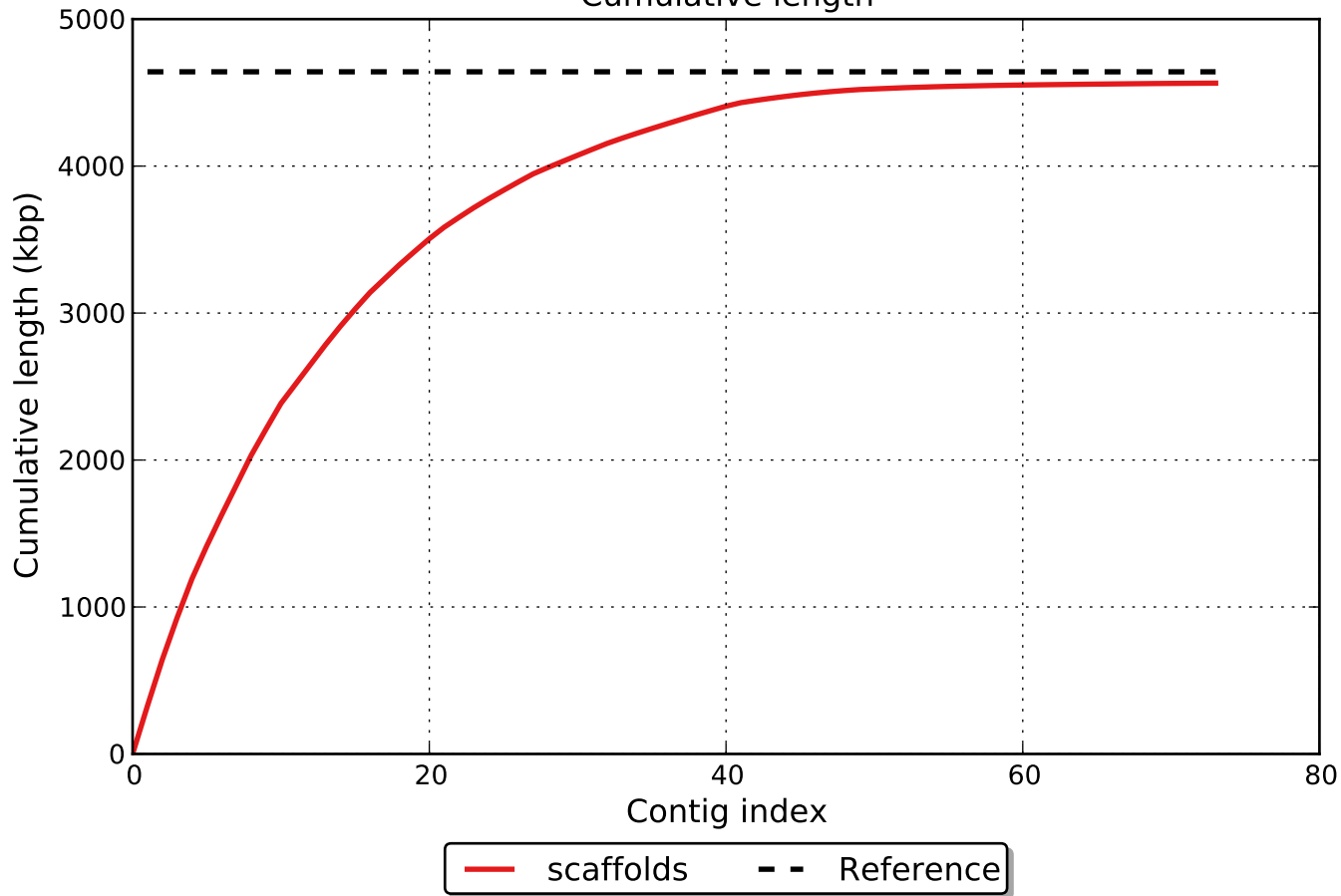
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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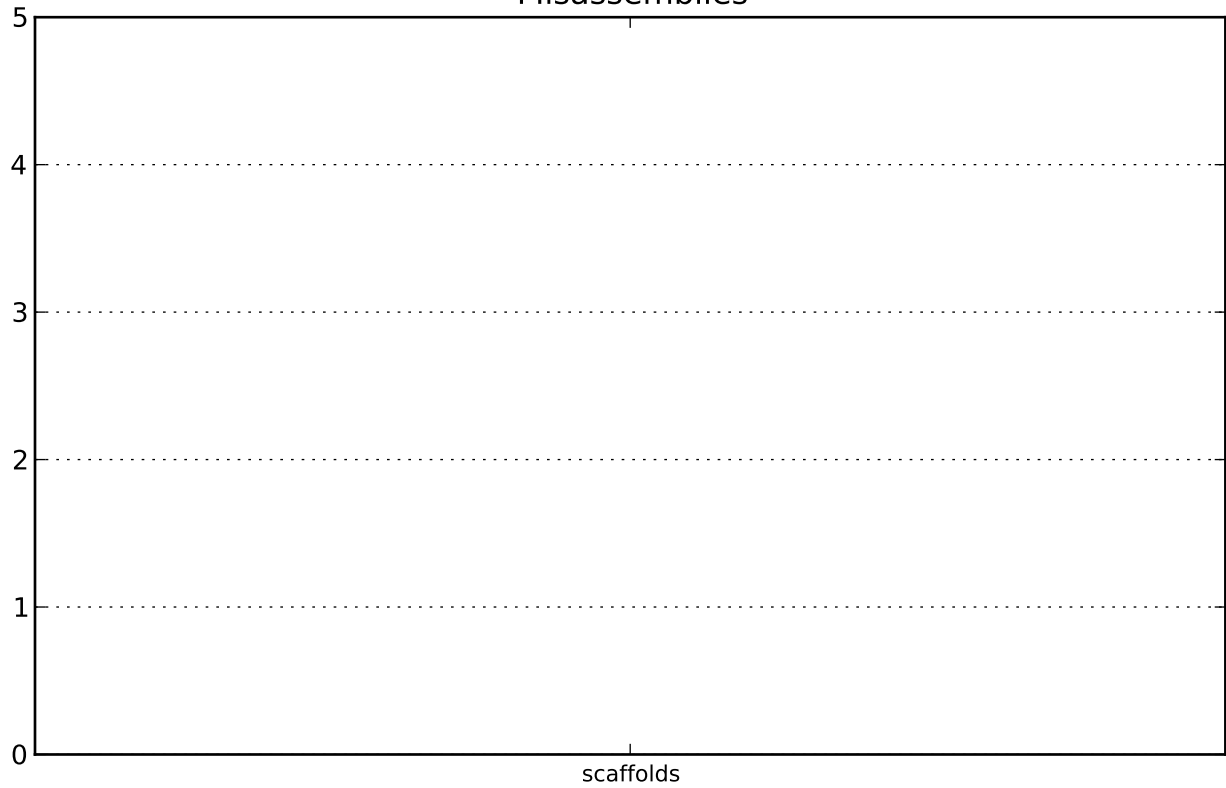
Nx



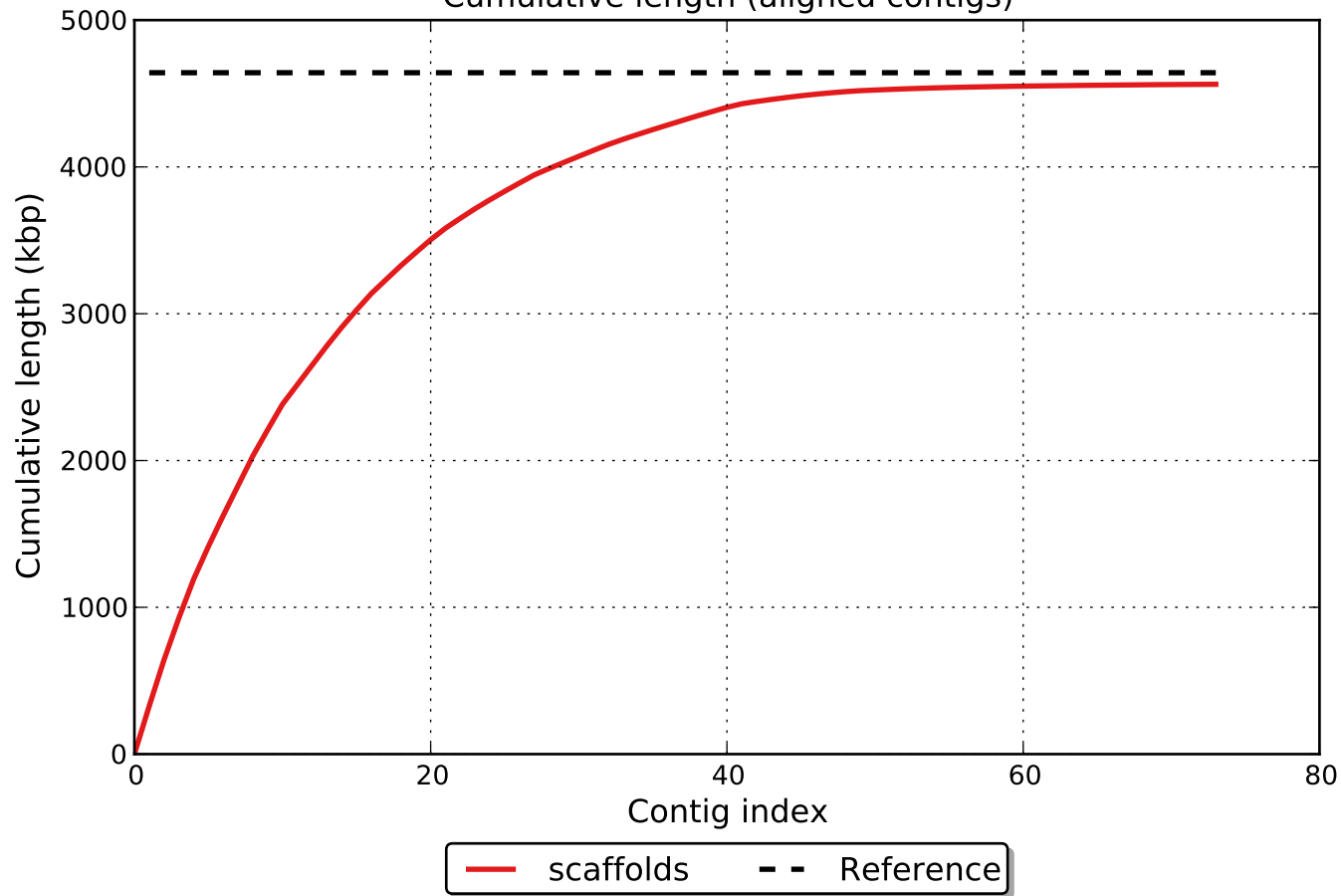
Cumulative length



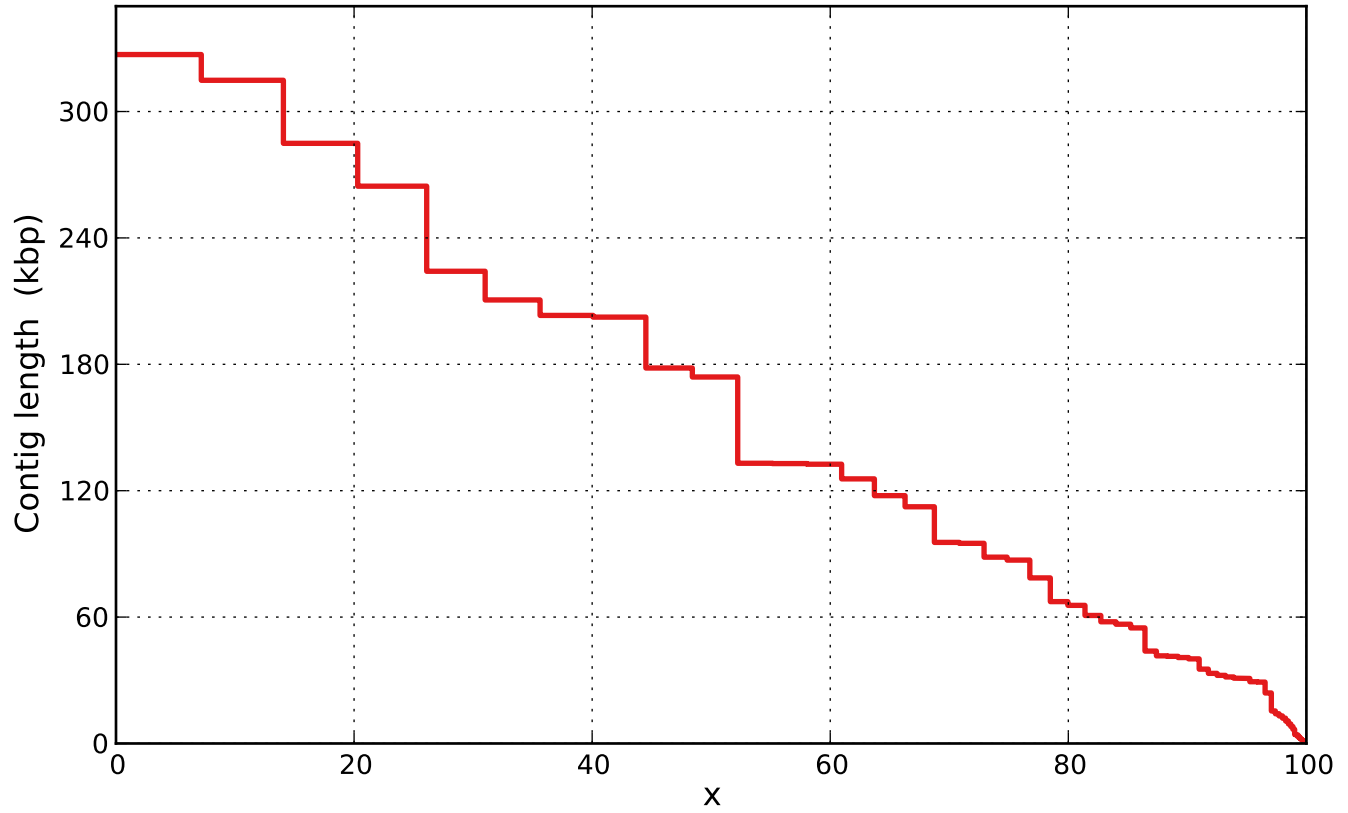
# Misassemblies



Cumulative length (aligned contigs)



NAx



— scaffolds