

## Report

	scaffolds
# contigs ( $\geq 0$ bp)	90
# contigs ( $\geq 1000$ bp)	69
# contigs ( $\geq 5000$ bp)	51
# contigs ( $\geq 10000$ bp)	48
# contigs ( $\geq 25000$ bp)	42
# contigs ( $\geq 50000$ bp)	27
Total length ( $\geq 0$ bp)	4567074
Total length ( $\geq 1000$ bp)	4560692
Total length ( $\geq 5000$ bp)	4519718
Total length ( $\geq 10000$ bp)	4495765
Total length ( $\geq 25000$ bp)	4404583
Total length ( $\geq 50000$ bp)	3878746
# contigs	75
Largest contig	327049
Total length	4564761
Reference length	4641652
N50	171225
N75	87058
L50	10
L75	20
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	171225
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.287
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	62.87
# indels per 100 kbp	8.83
Largest alignment	327049
NA50	133027
NA75	84850
LA50	10
LA75	21

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	171225
# local misassemblies	2
# mismatches	2868
# indels	403
# short indels	403
# long indels	0
Indels length	569

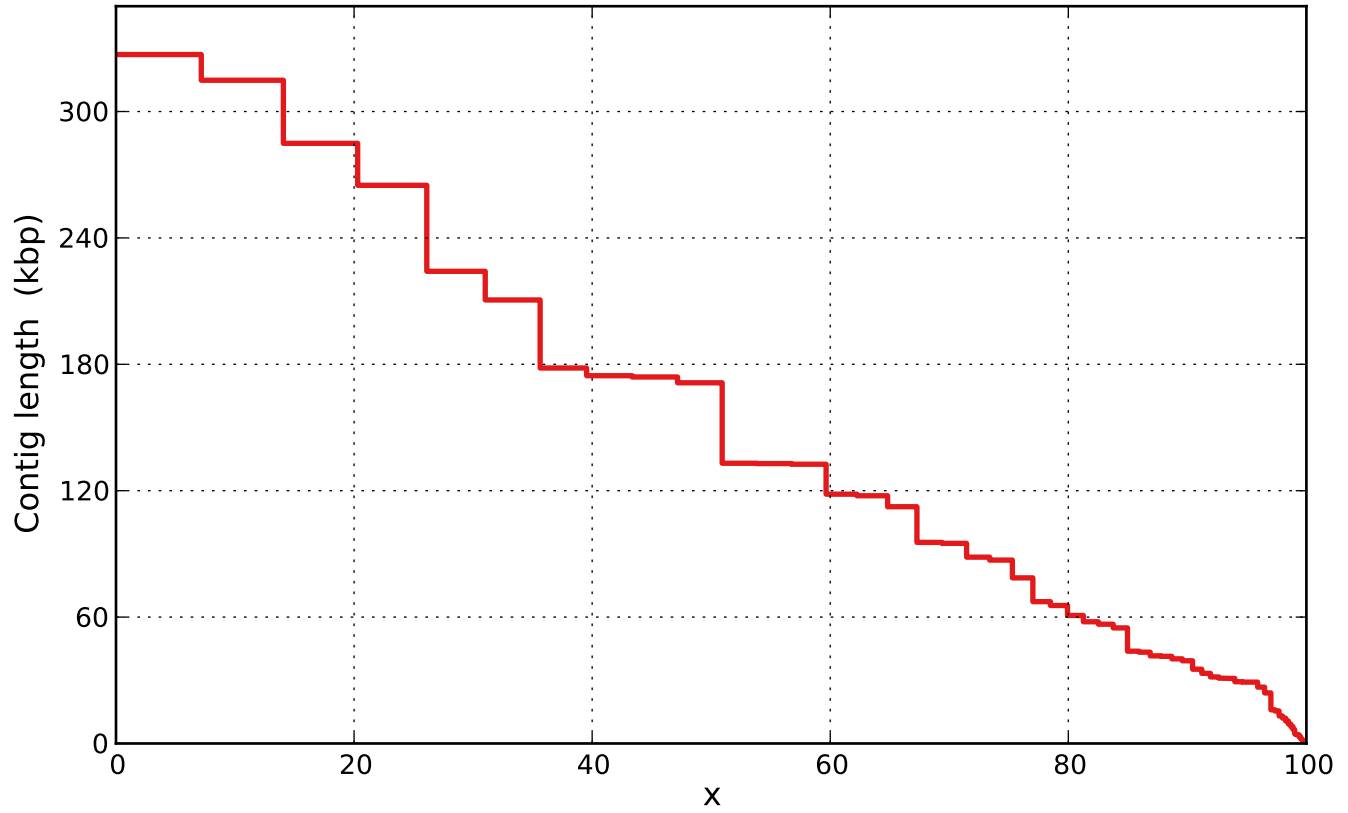
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

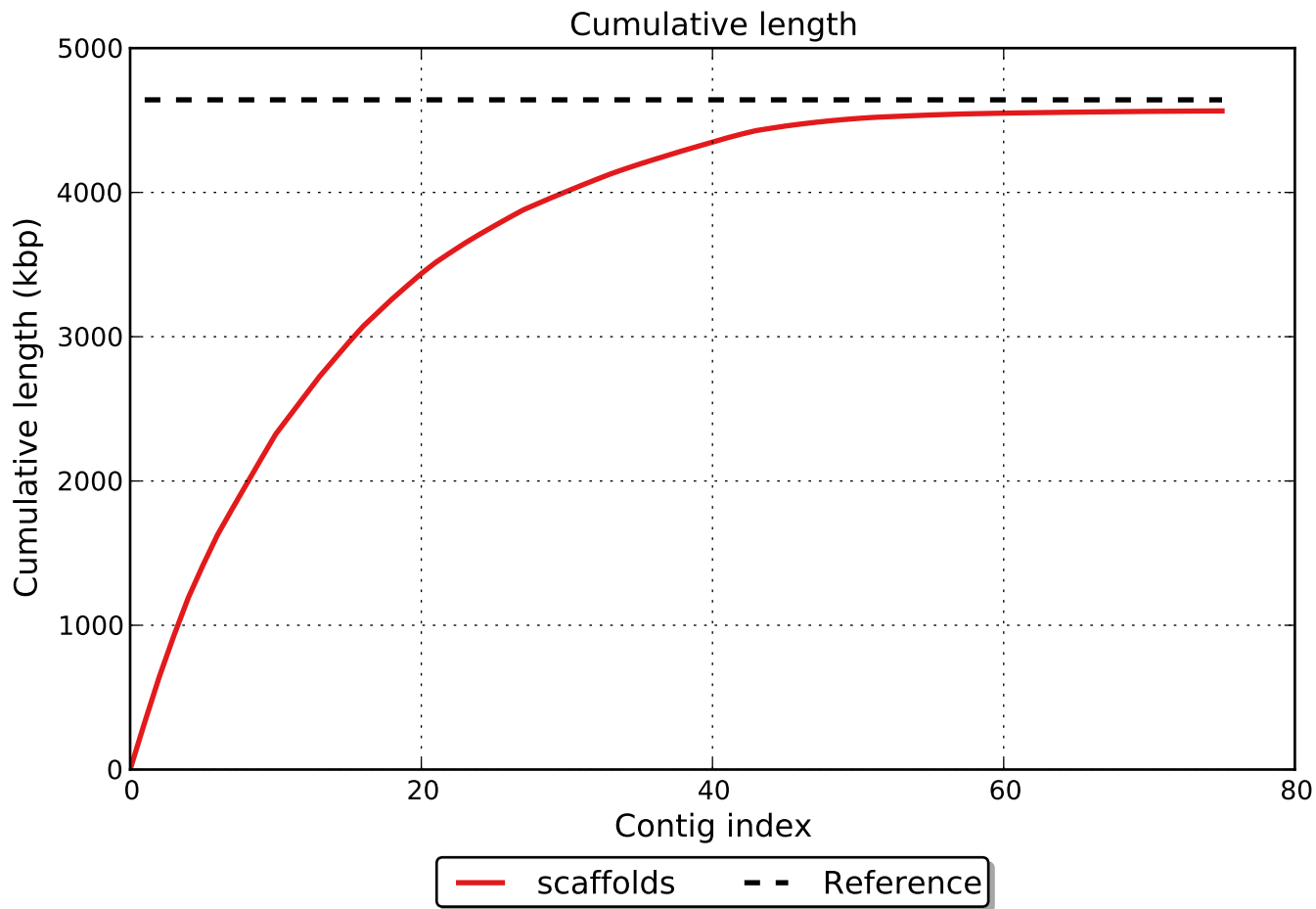
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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Nx

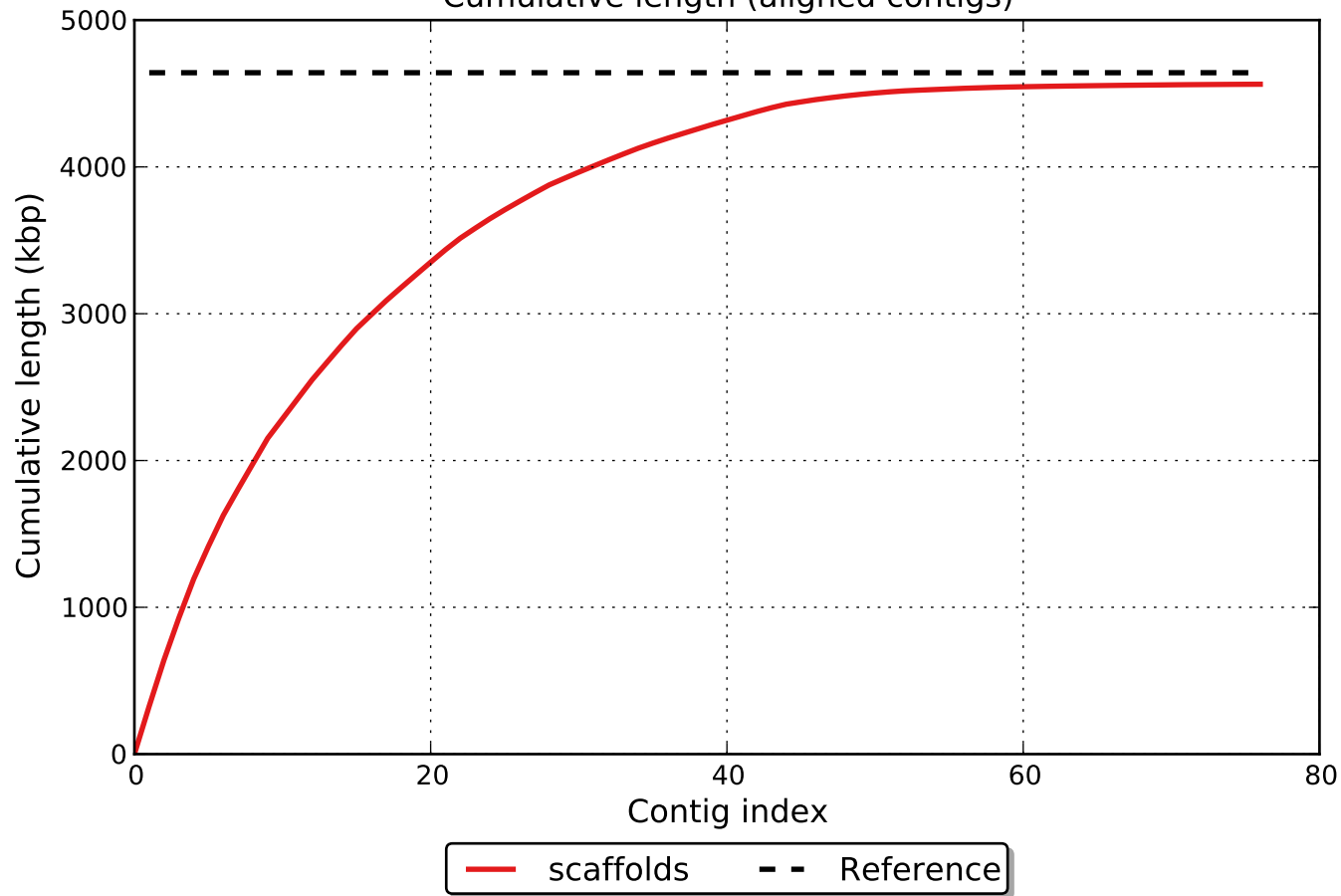


scaffolds

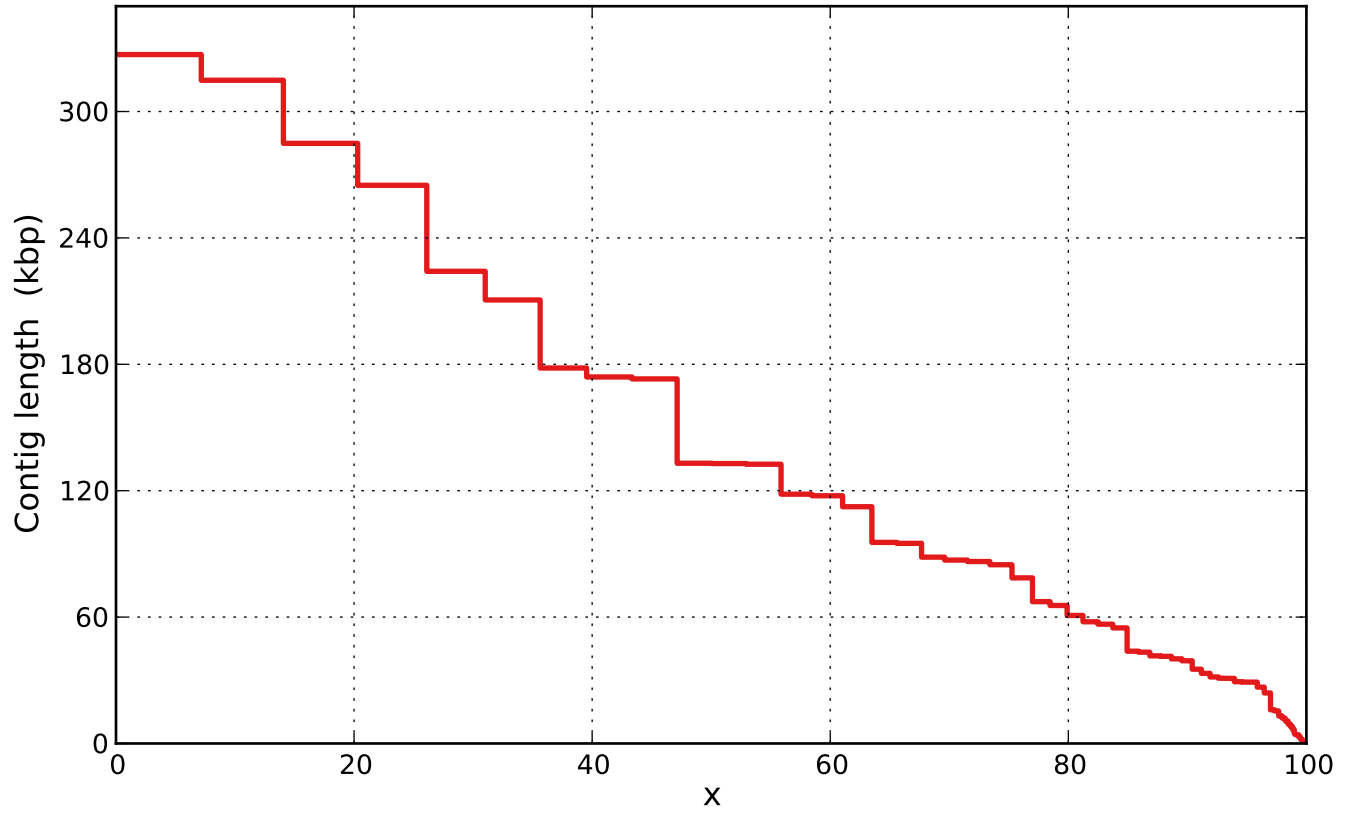




Cumulative length (aligned contigs)



NAx



— scaffolds