

# Report

	scaffolds
# contigs ( $\geq 0$ bp)	135
# contigs ( $\geq 1000$ bp)	90
# contigs ( $\geq 5000$ bp)	67
# contigs ( $\geq 10000$ bp)	58
# contigs ( $\geq 25000$ bp)	47
# contigs ( $\geq 50000$ bp)	29
Total length ( $\geq 0$ bp)	4564173
Total length ( $\geq 1000$ bp)	4552031
Total length ( $\geq 5000$ bp)	4502499
Total length ( $\geq 10000$ bp)	4436896
Total length ( $\geq 25000$ bp)	4255107
Total length ( $\geq 50000$ bp)	3632805
# contigs	97
Largest contig	327072
Total length	4556946
Reference length	4641652
N50	132558
N75	57779
L50	12
L75	26
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	127522
# local misassemblies	7
# unaligned contigs	0 + 1 part
Unaligned length	189
Genome fraction (%)	98.105
Duplication ratio	1.001
# N's per 100 kbp	6.14
# mismatches per 100 kbp	62.32
# indels per 100 kbp	8.78
Largest alignment	327072
NA50	132558
NA75	56344
LA50	12
LA75	26

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	2
# relocations	2
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	127522
# local misassemblies	7
# mismatches	2838
# indels	400
# short indels	385
# long indels	15
Indels length	831

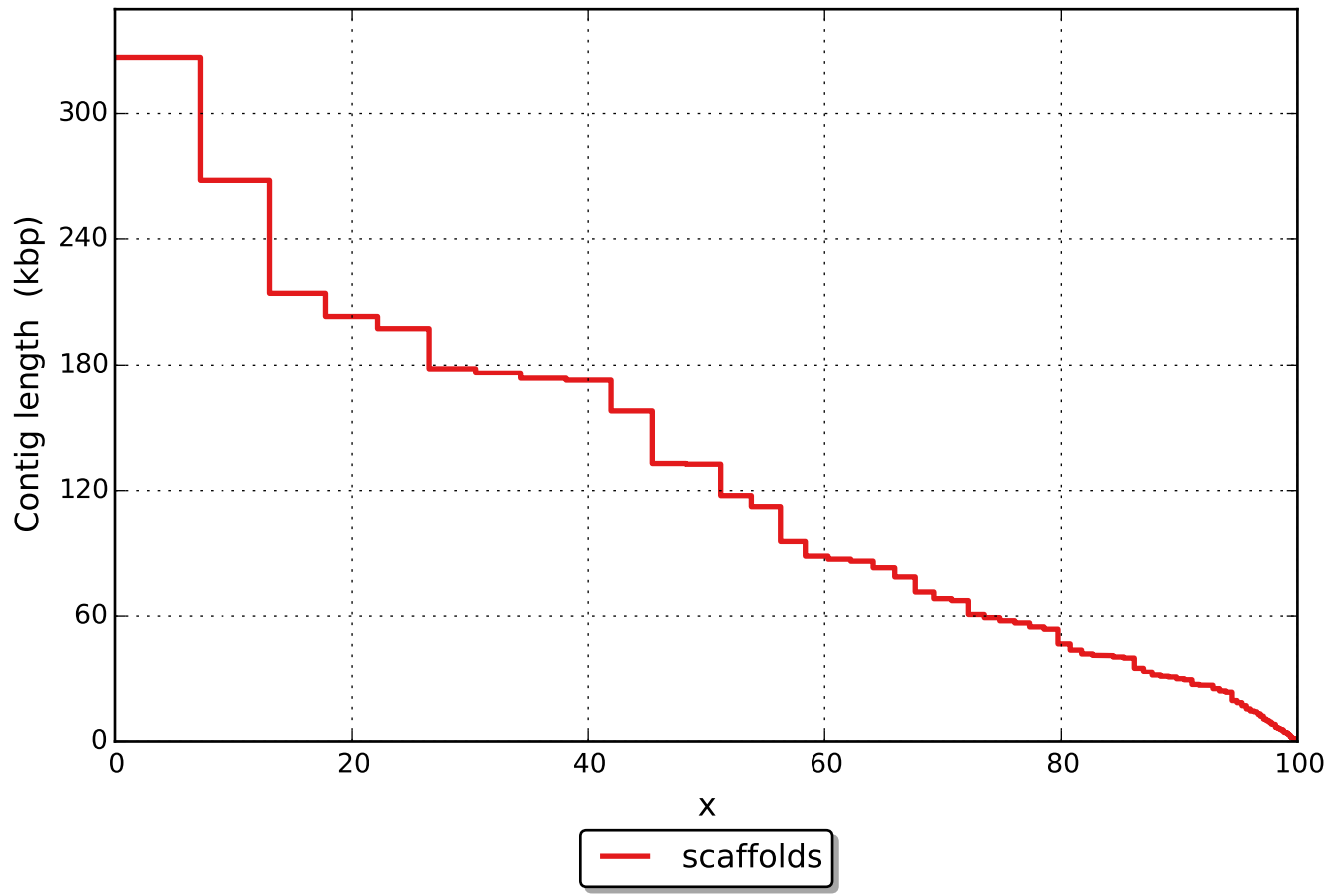
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

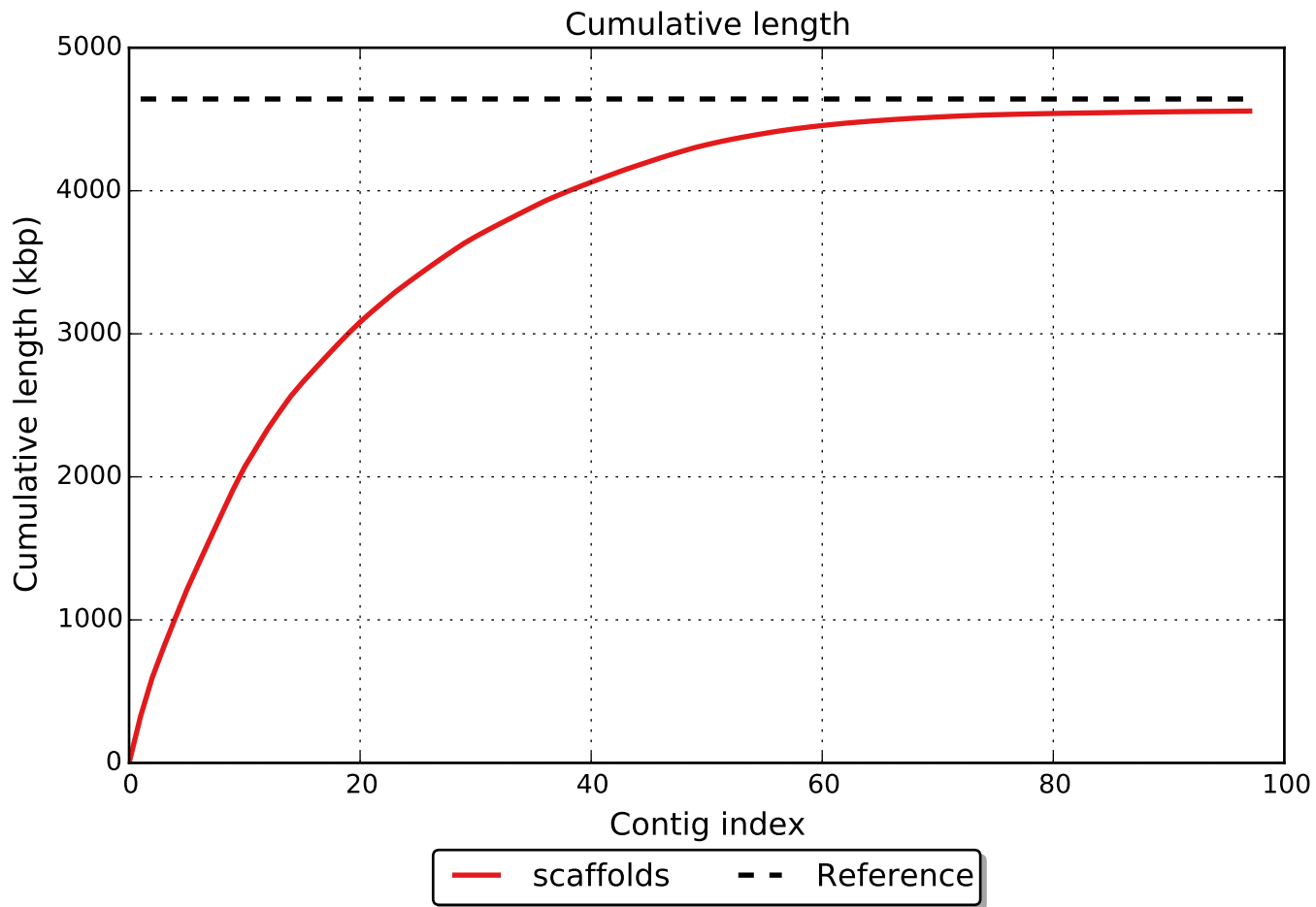
## Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	189
# N's	280

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).

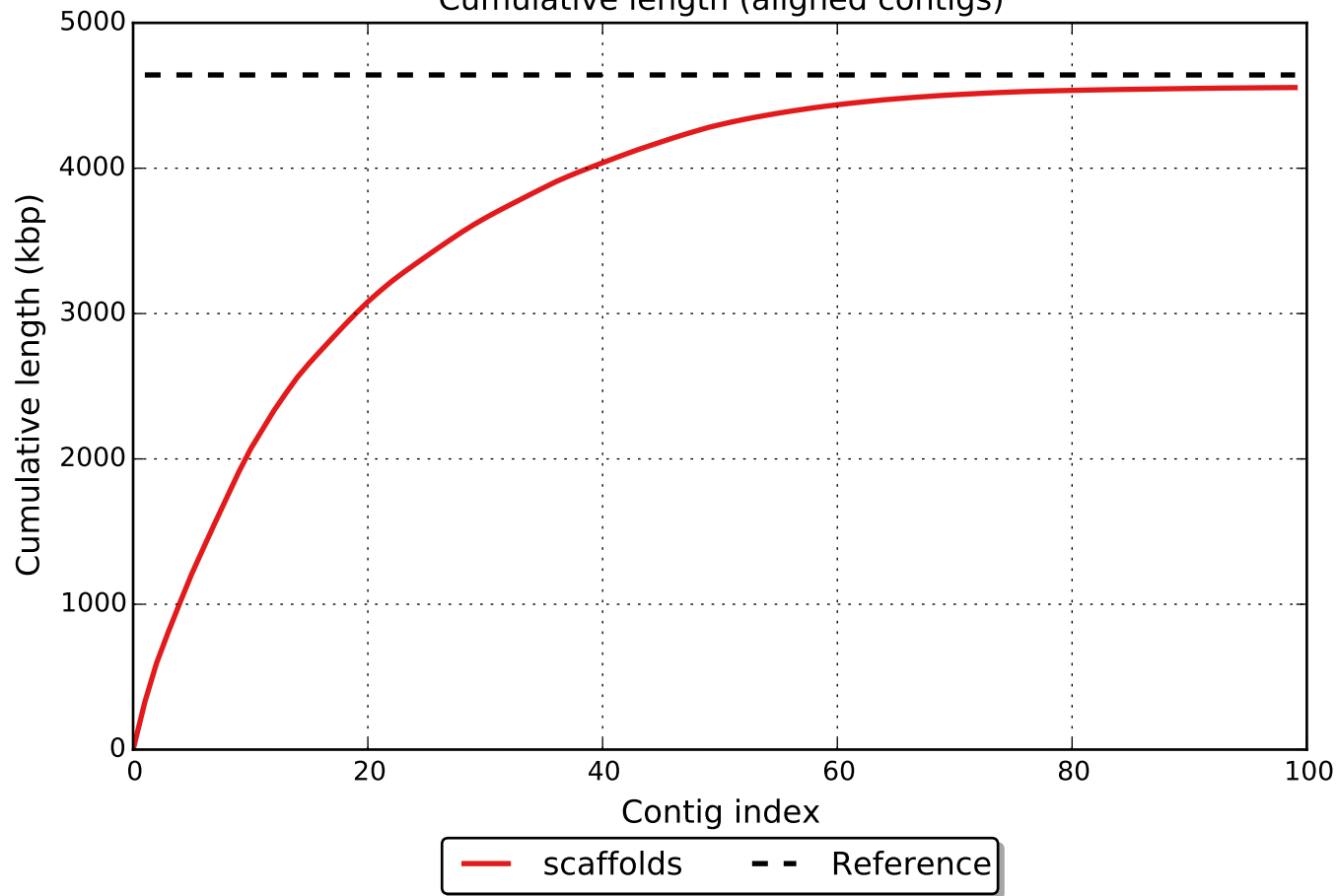
Nx







Cumulative length (aligned contigs)



NAx

