

## Report

	scaffolds
# contigs ( $\geq 0$ bp)	226
# contigs ( $\geq 1000$ bp)	191
# contigs ( $\geq 5000$ bp)	139
# contigs ( $\geq 10000$ bp)	117
# contigs ( $\geq 25000$ bp)	71
# contigs ( $\geq 50000$ bp)	27
Total length ( $\geq 0$ bp)	4532279
Total length ( $\geq 1000$ bp)	4517569
Total length ( $\geq 5000$ bp)	4374580
Total length ( $\geq 10000$ bp)	4219421
Total length ( $\geq 25000$ bp)	3512915
Total length ( $\geq 50000$ bp)	2084849
# contigs	204
Largest contig	138275
Total length	4527463
Reference length	4641652
N50	44576
N75	26493
L50	31
L75	67
# misassemblies	15
# misassembled contigs	14
Misassembled contigs length	568607
# local misassemblies	10
# unaligned contigs	0 + 2 part
Unaligned length	3972
Genome fraction (▼)	97.366
Duplication ratio	1.001
# N's per 100 kbp	147.79
# mismatches per 100 kbp	105.35
# indels per 100 kbp	18.30
Largest alignment	138275
NA50	39635
NA75	23916
LA50	33
LA75	70

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	15
# relocations	15
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	1
# misassembled contigs	14
Misassembled contigs length	568607
# local misassemblies	10
# mismatches	4761
# indels	827
# short indels	604
# long indels	223
Indels length	4119

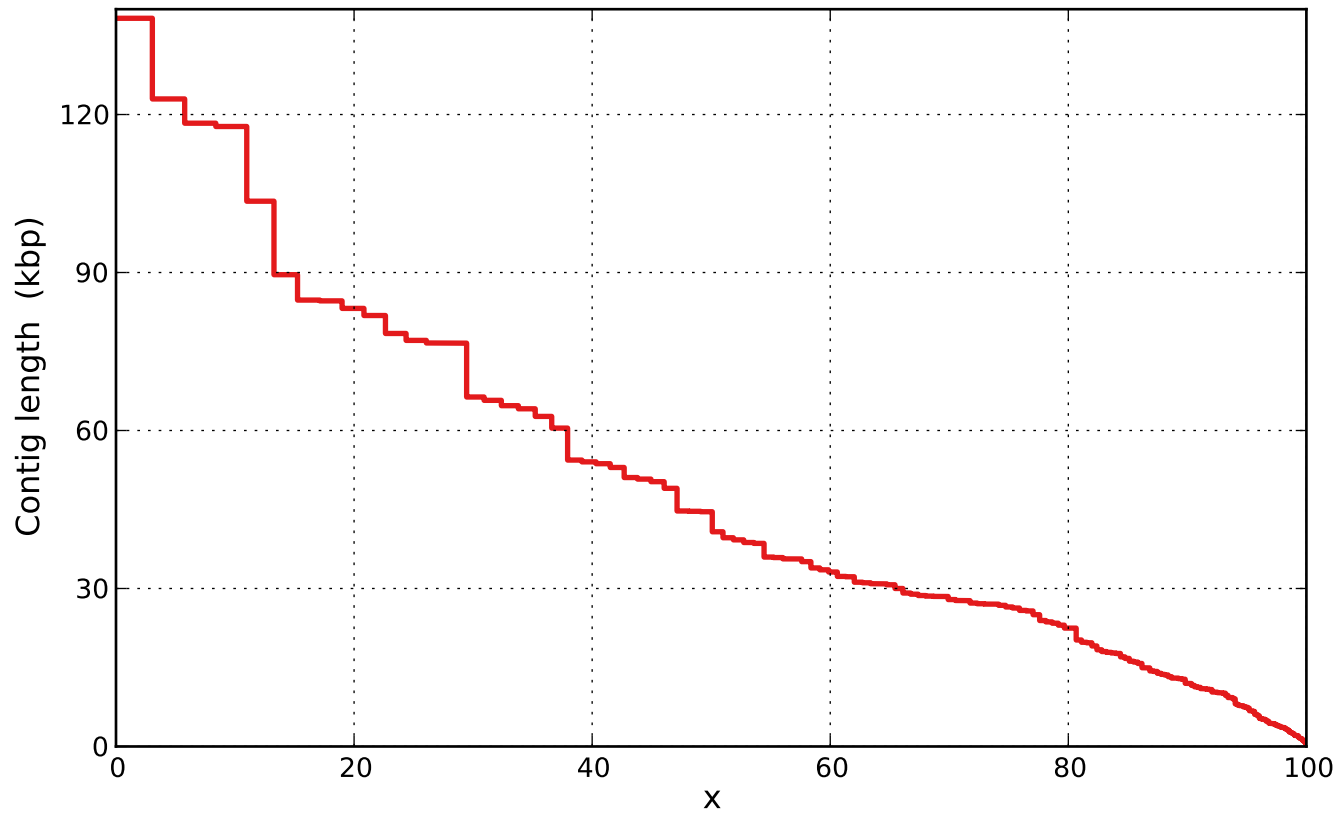
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

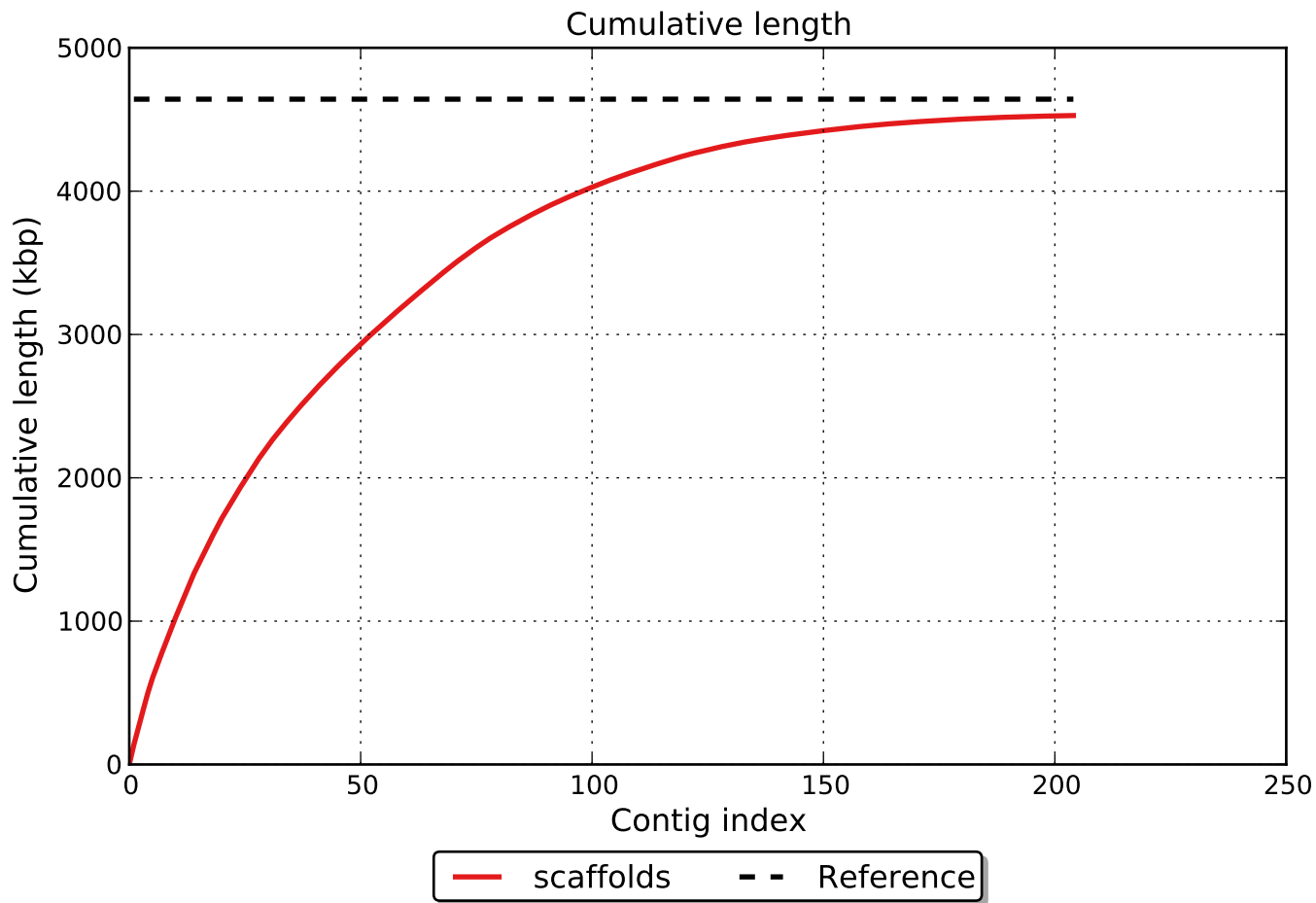
## Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	3972
# N's	6691

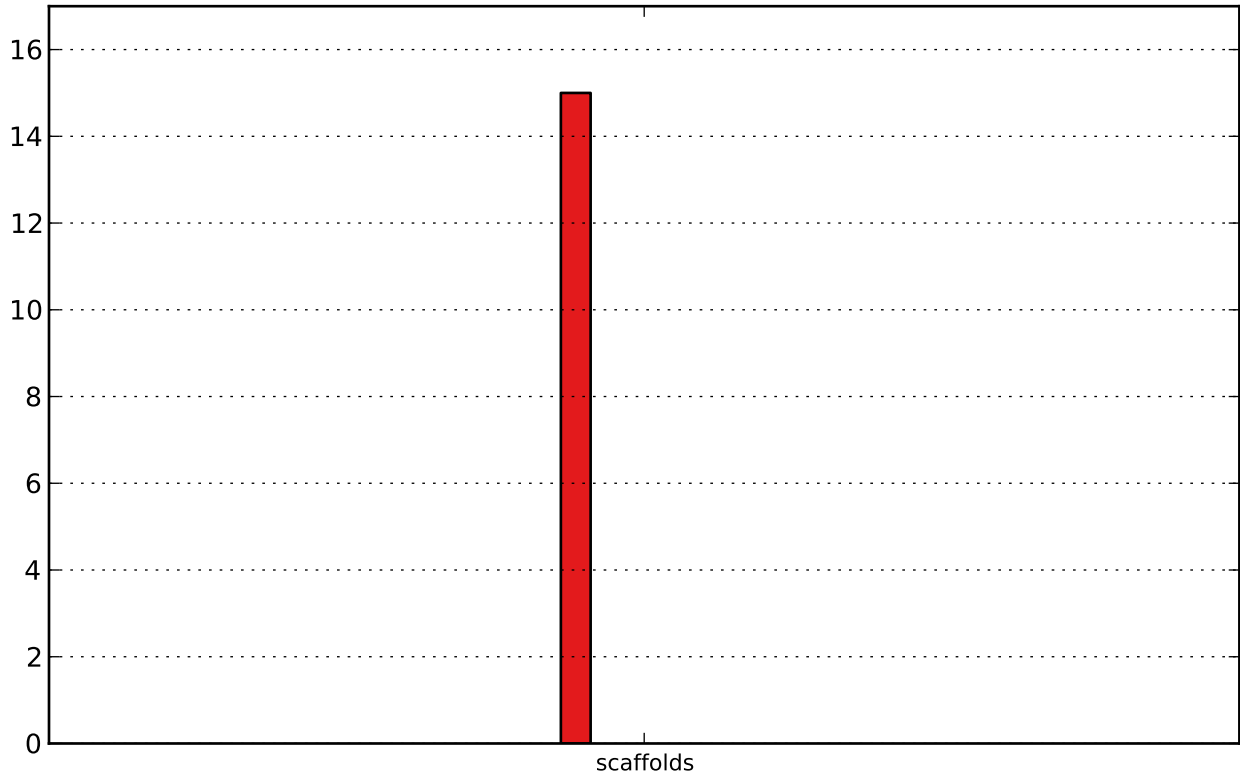
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



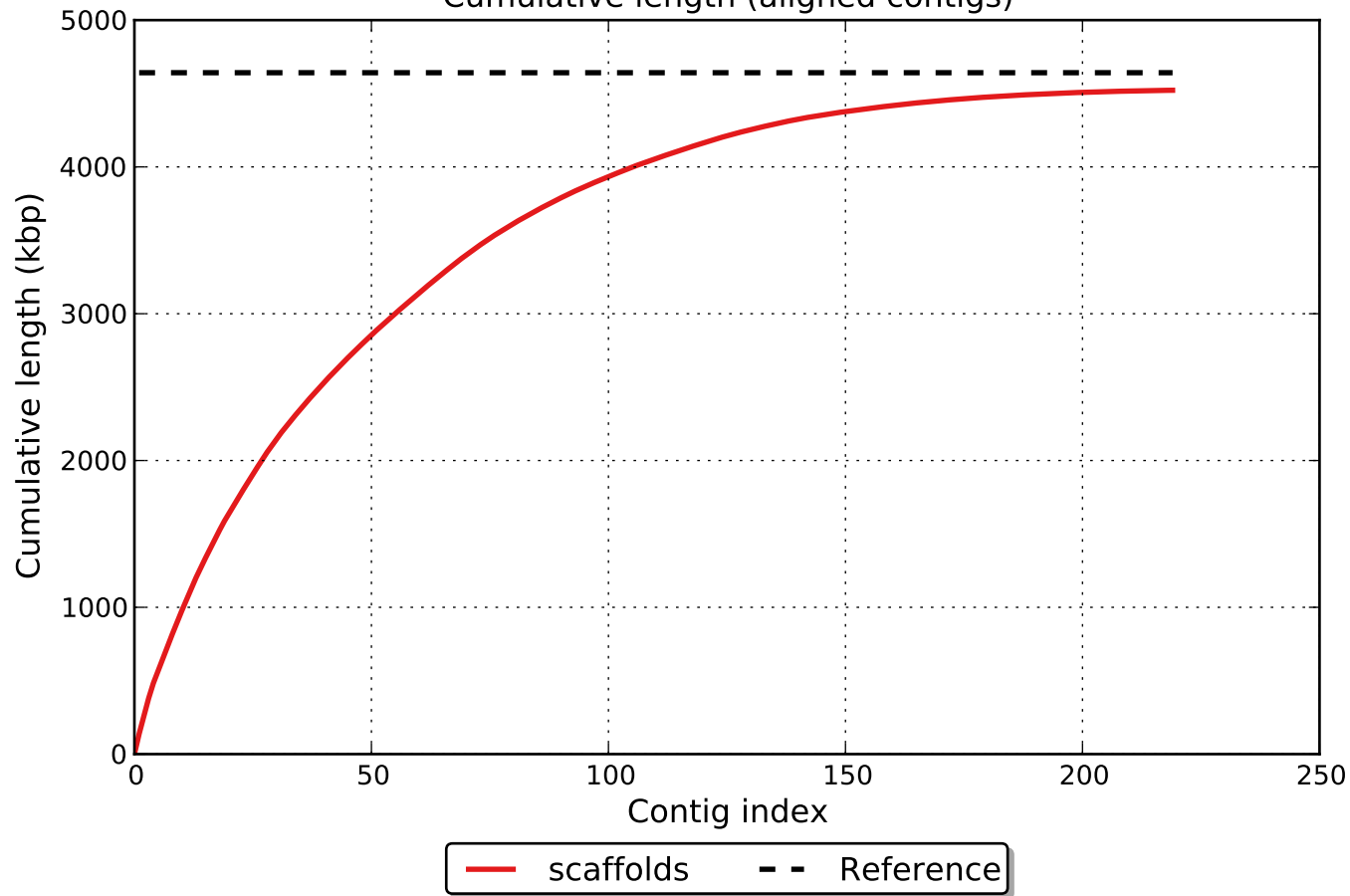


# Misassemblies



 # relocations

Cumulative length (aligned contigs)



NAx

