

## Report

	scaffolds
# contigs ( $\geq 0$ bp)	27
# contigs ( $\geq 1000$ bp)	3
# contigs ( $\geq 5000$ bp)	1
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	15868
Total length ( $\geq 1000$ bp)	8216
Total length ( $\geq 5000$ bp)	5574
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	6
Largest contig	5574
Total length	10576
Reference length	4641652
N50	5574
N75	1240
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	62
Genome fraction (▼)	0.224
Duplication ratio	1.009
# N's per 100 kbp	538.96
# mismatches per 100 kbp	662.25
# indels per 100 kbp	163.16
Largest alignment	5542
NA50	5542
NA75	1228
LA50	1
LA75	3

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

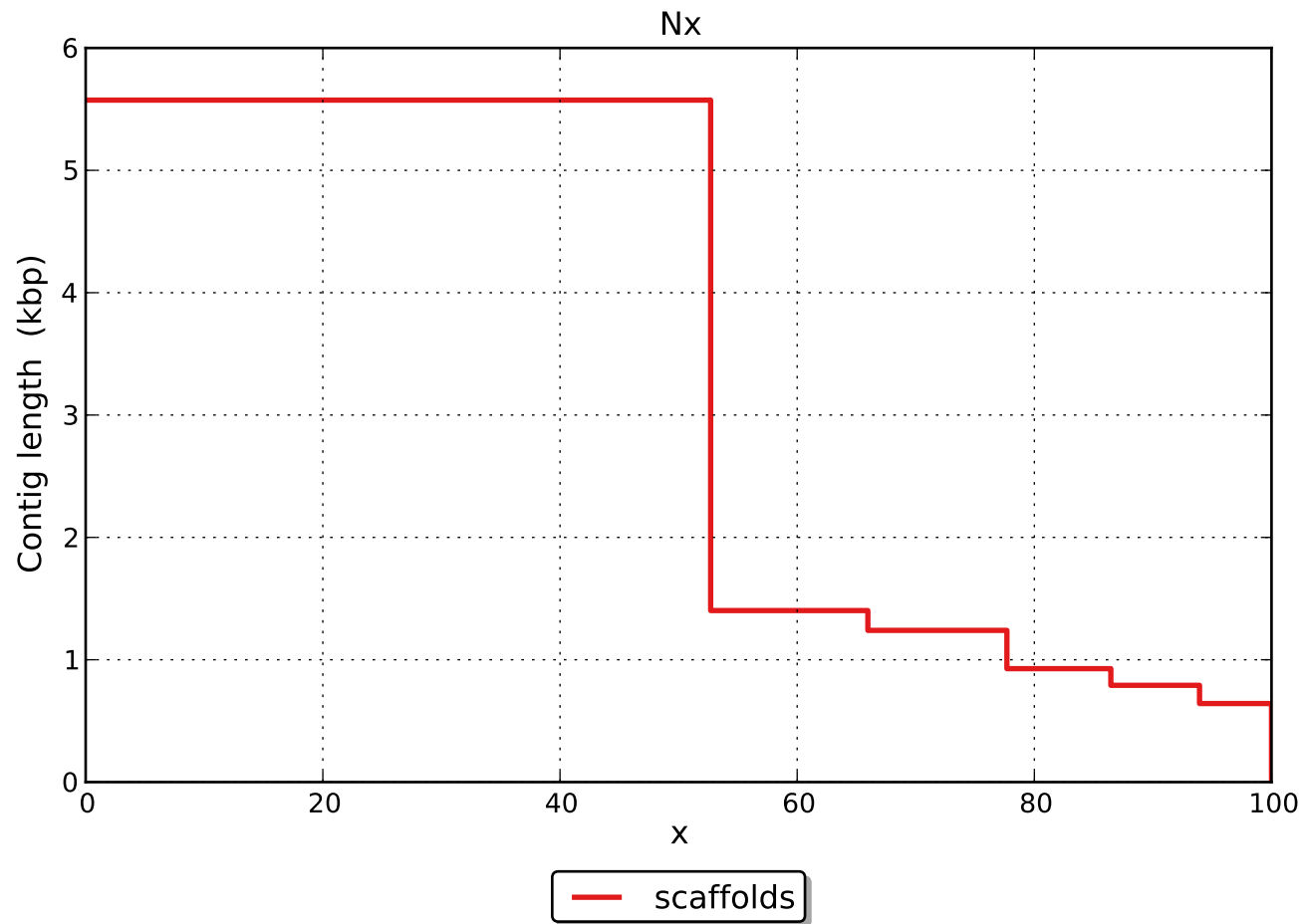
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	69
# indels	17
# short indels	13
# long indels	4
Indels length	93

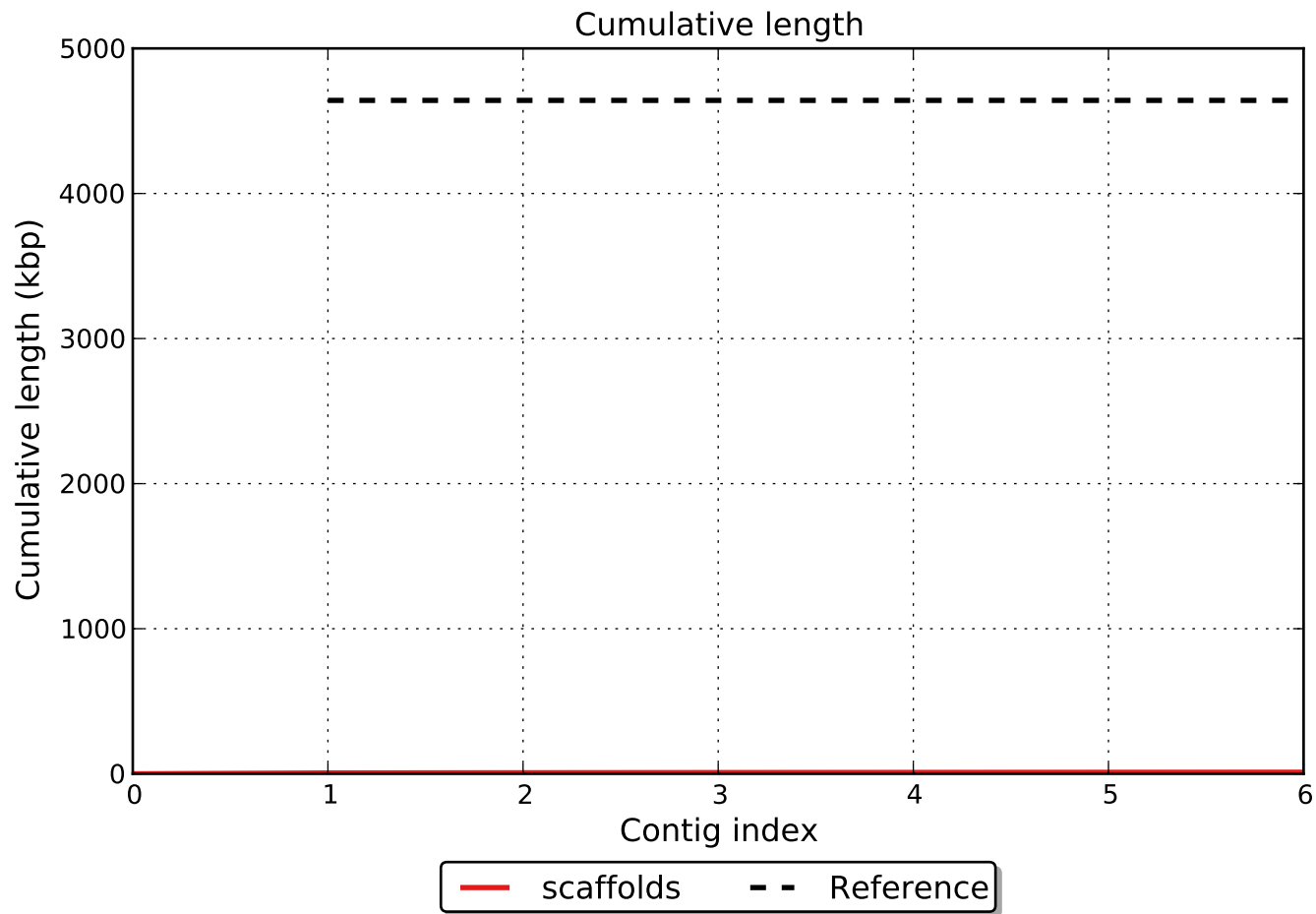
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

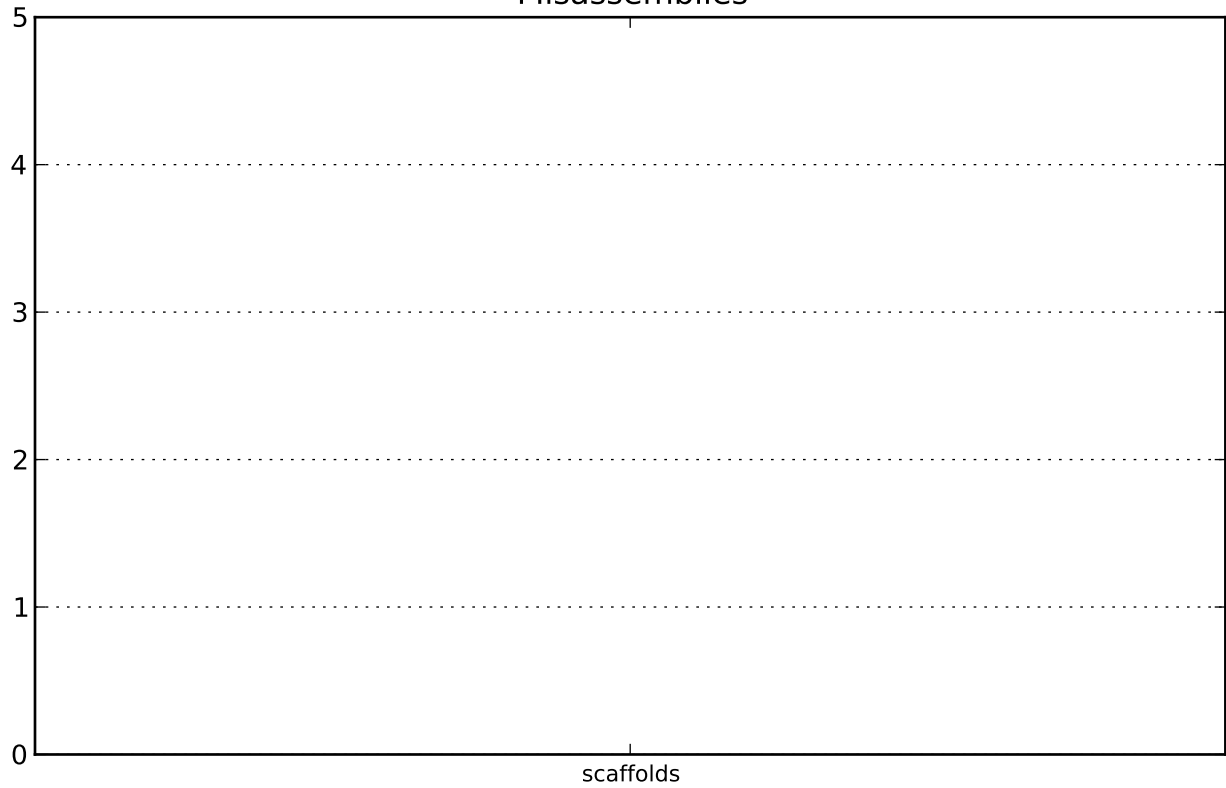
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	62
# N's	57

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# Misassemblies



Cumulative length (aligned contigs)

