

## Report

	scaffolds
# contigs ( $\geq 0$ bp)	3416
# contigs ( $\geq 1000$ bp)	1204
# contigs ( $\geq 5000$ bp)	7
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	3310104
Total length ( $\geq 1000$ bp)	2119803
Total length ( $\geq 5000$ bp)	39798
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	2337
Largest contig	6658
Total length	2945903
Reference length	4641652
N50	1451
N75	941
L50	668
L75	1297
# misassemblies	19
# misassembled contigs	19
Misassembled contigs length	53549
# local misassemblies	5
# unaligned contigs	98 + 25 part
Unaligned length	131032
Genome fraction (▼)	60.455
Duplication ratio	1.003
# N's per 100 kbp	1157.85
# mismatches per 100 kbp	16.21
# indels per 100 kbp	39.56
Largest alignment	6658
NA50	1368
NA75	868
LA50	693
LA75	1366

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

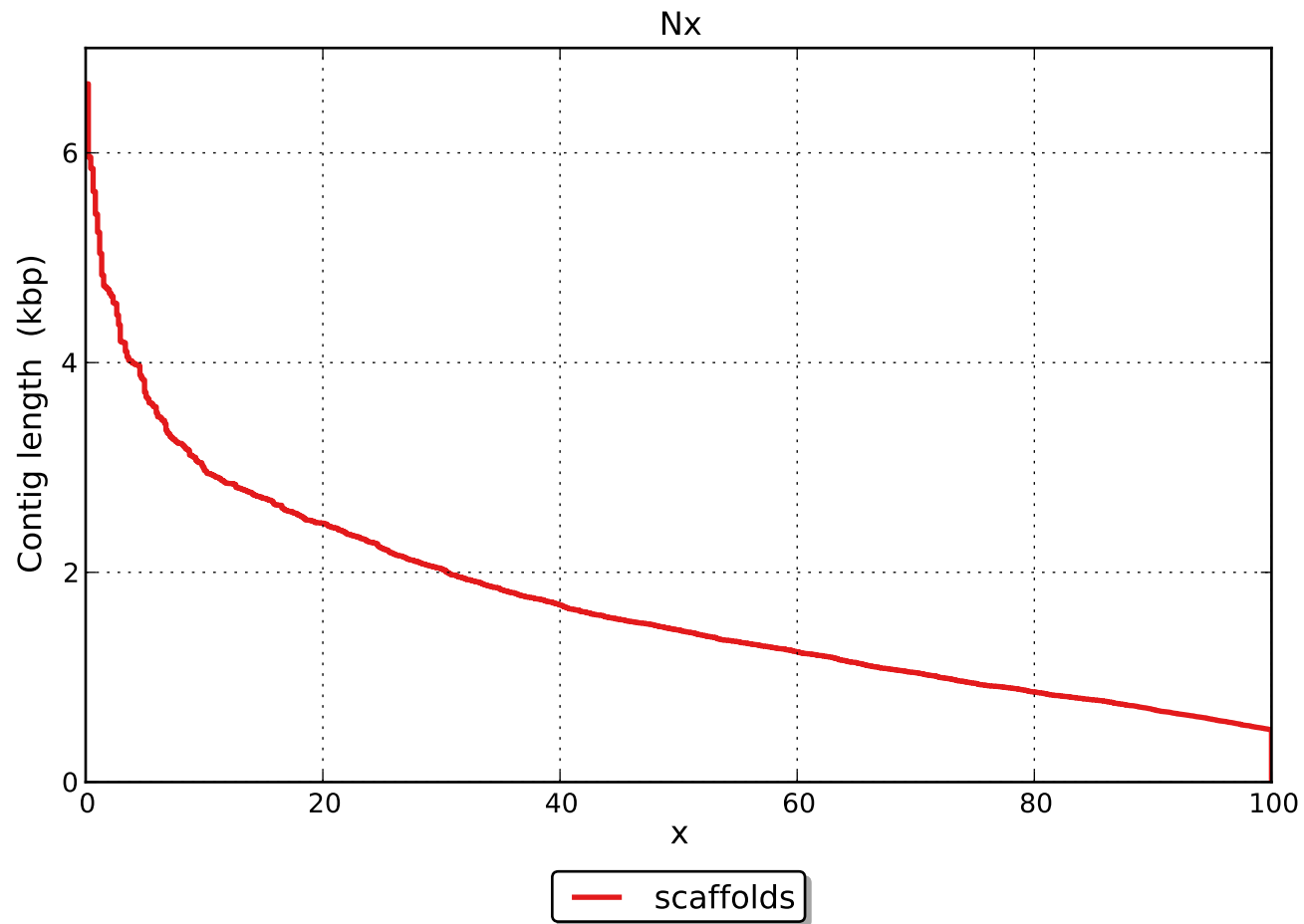
	scaffolds
# misassemblies	19
# relocations	19
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	11
# misassembled contigs	19
Misassembled contigs length	53549
# local misassemblies	5
# mismatches	455
# indels	1110
# short indels	390
# long indels	720
Indels length	11631

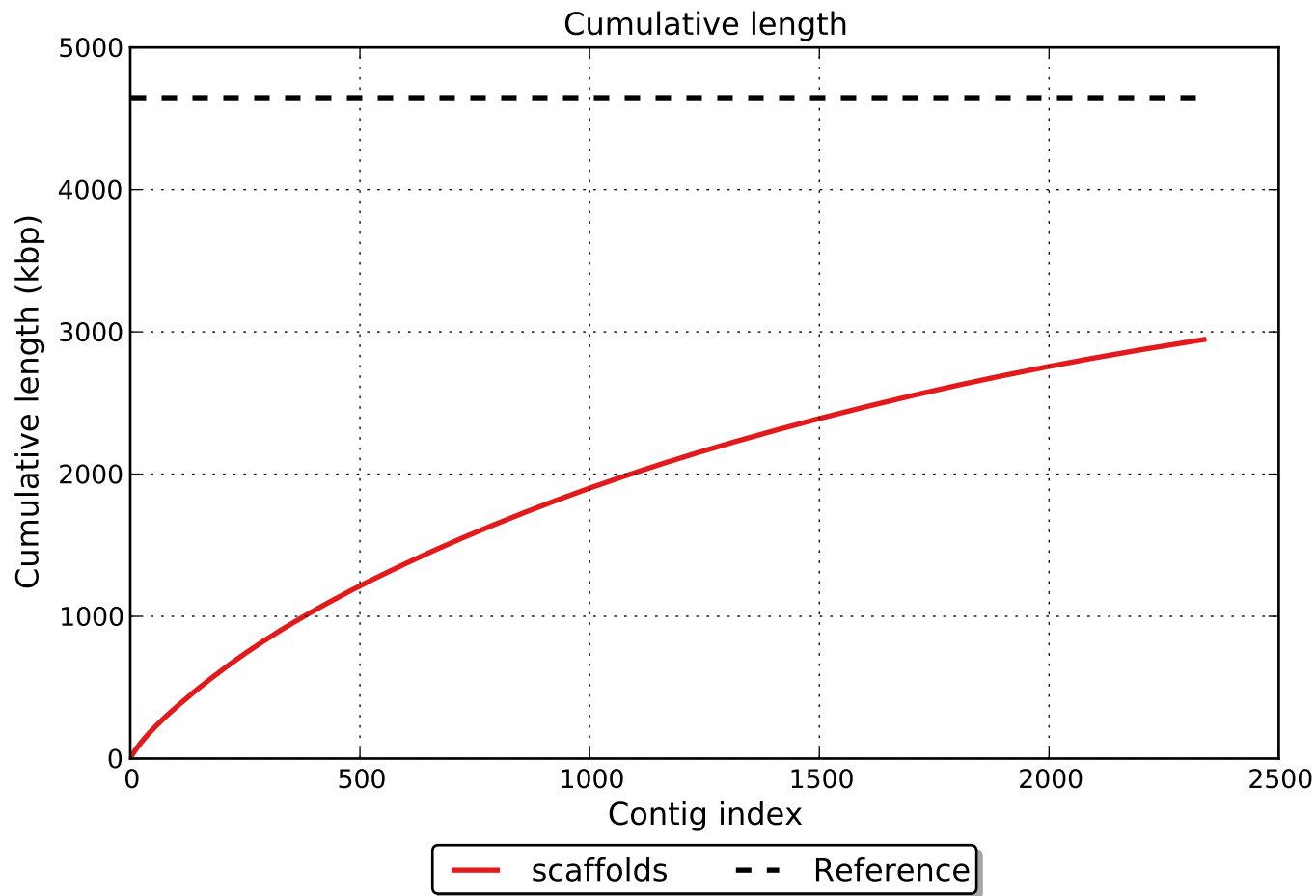
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

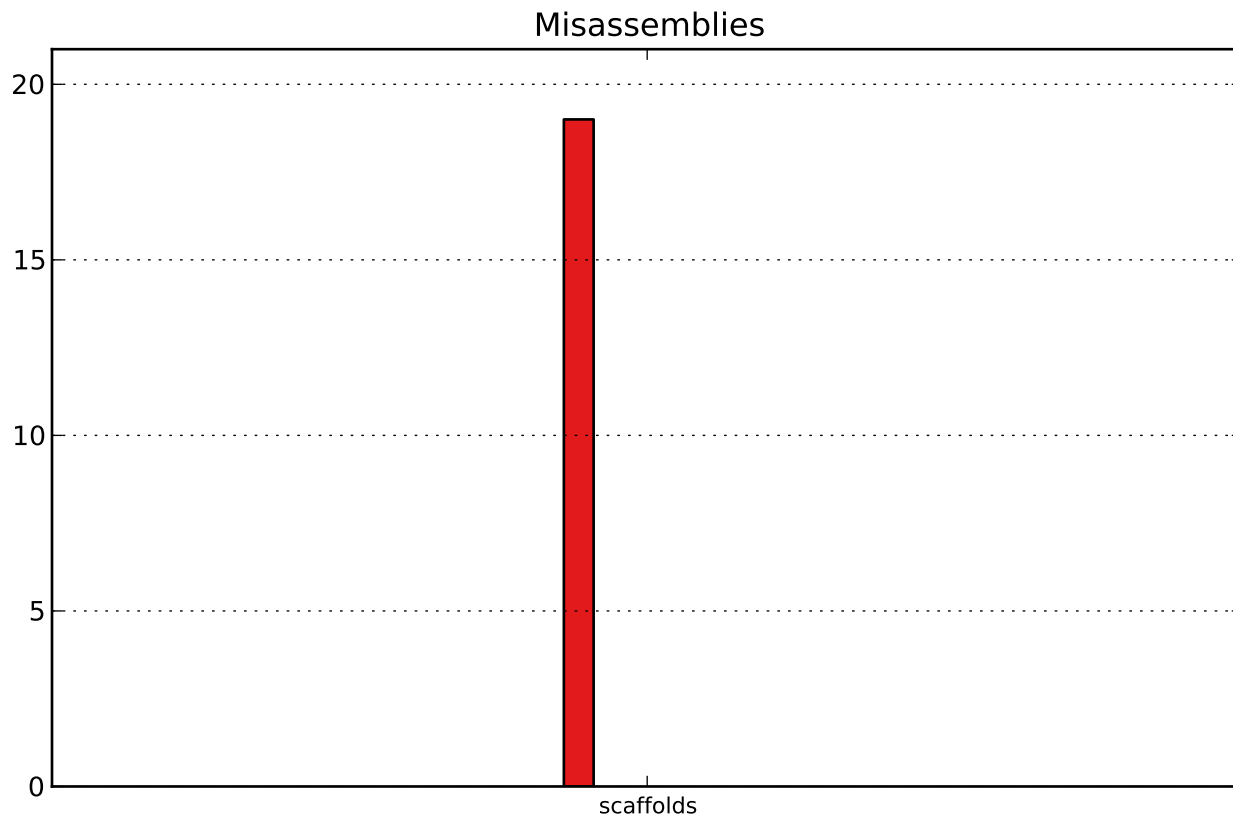
## Unaligned report

	scaffolds
# fully unaligned contigs	98
Fully unaligned length	111397
# partially unaligned contigs	25
# with misassembly	1
# both parts are significant	10
Partially unaligned length	19635
# N's	34109

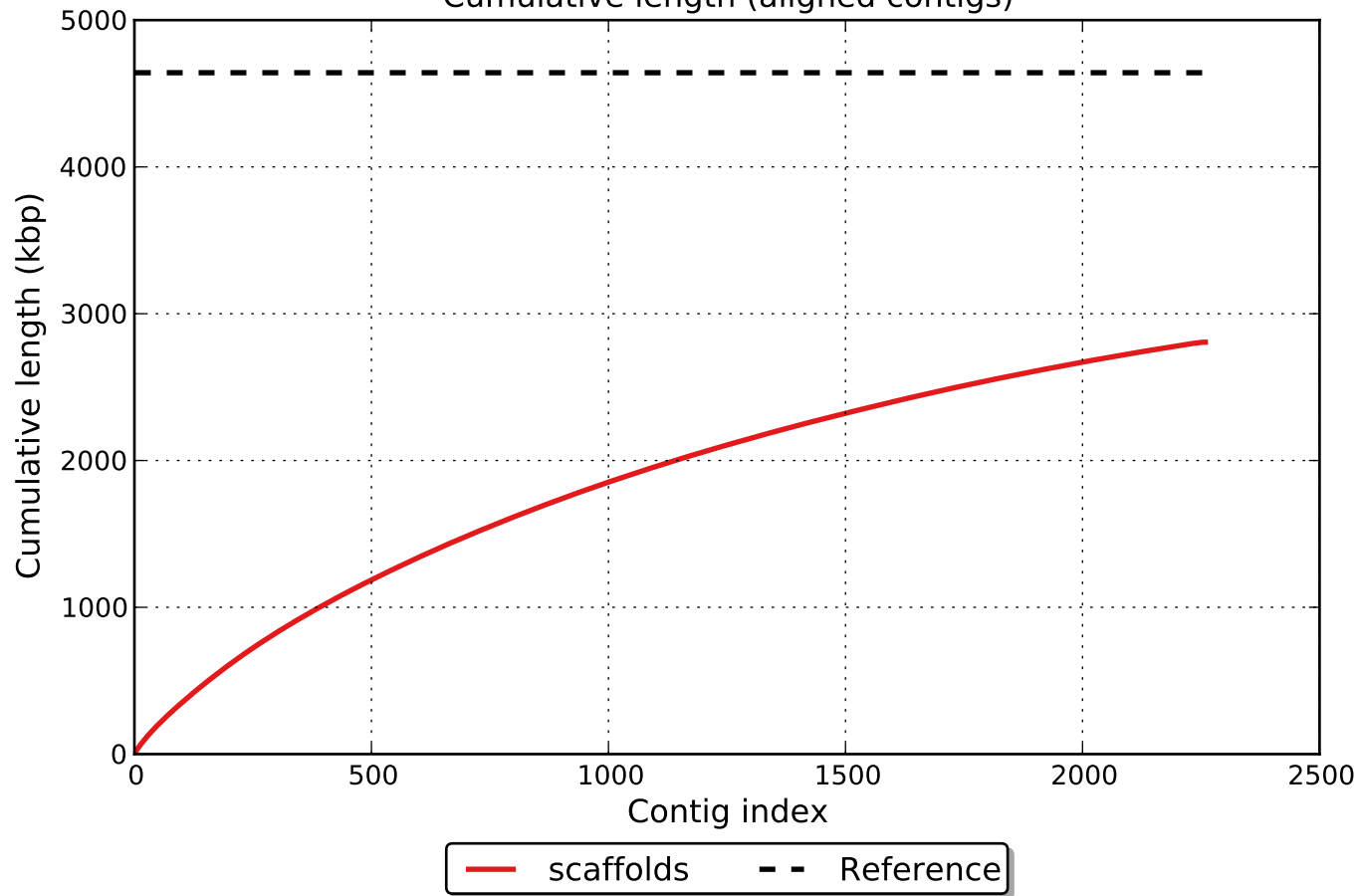
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







Cumulative length (aligned contigs)



NAx

