

## Report

	scaffolds
# contigs ( $\geq 0$ bp)	131
# contigs ( $\geq 1000$ bp)	96
# contigs ( $\geq 5000$ bp)	71
# contigs ( $\geq 10000$ bp)	61
# contigs ( $\geq 25000$ bp)	48
# contigs ( $\geq 50000$ bp)	28
Total length ( $\geq 0$ bp)	4557478
Total length ( $\geq 1000$ bp)	4547722
Total length ( $\geq 5000$ bp)	4483250
Total length ( $\geq 10000$ bp)	4405320
Total length ( $\geq 25000$ bp)	4186378
Total length ( $\geq 50000$ bp)	3493098
# contigs	100
Largest contig	327041
Total length	4551090
Reference length	4641652
N50	111983
N75	54869
L50	13
L75	27
# misassemblies	7
# misassembled contigs	5
Misassembled contigs length	472041
# local misassemblies	12
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	97.938
Duplication ratio	1.001
# N's per 100 kbp	13.54
# mismatches per 100 kbp	69.29
# indels per 100 kbp	10.62
Largest alignment	327041
NA50	97502
NA75	46259
LA50	14
LA75	30

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	7
# relocations	7
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	472041
# local misassemblies	12
# mismatches	3150
# indels	483
# short indels	474
# long indels	9
Indels length	898

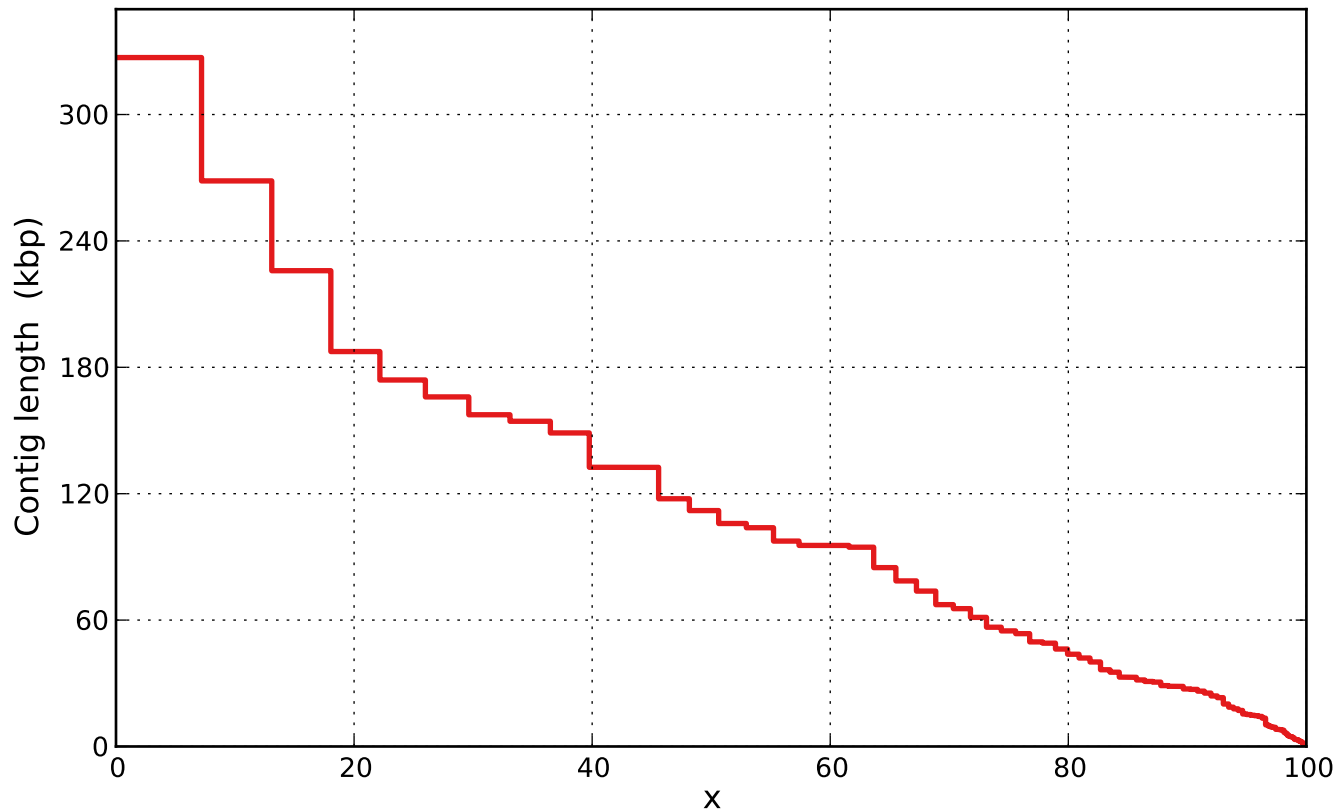
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

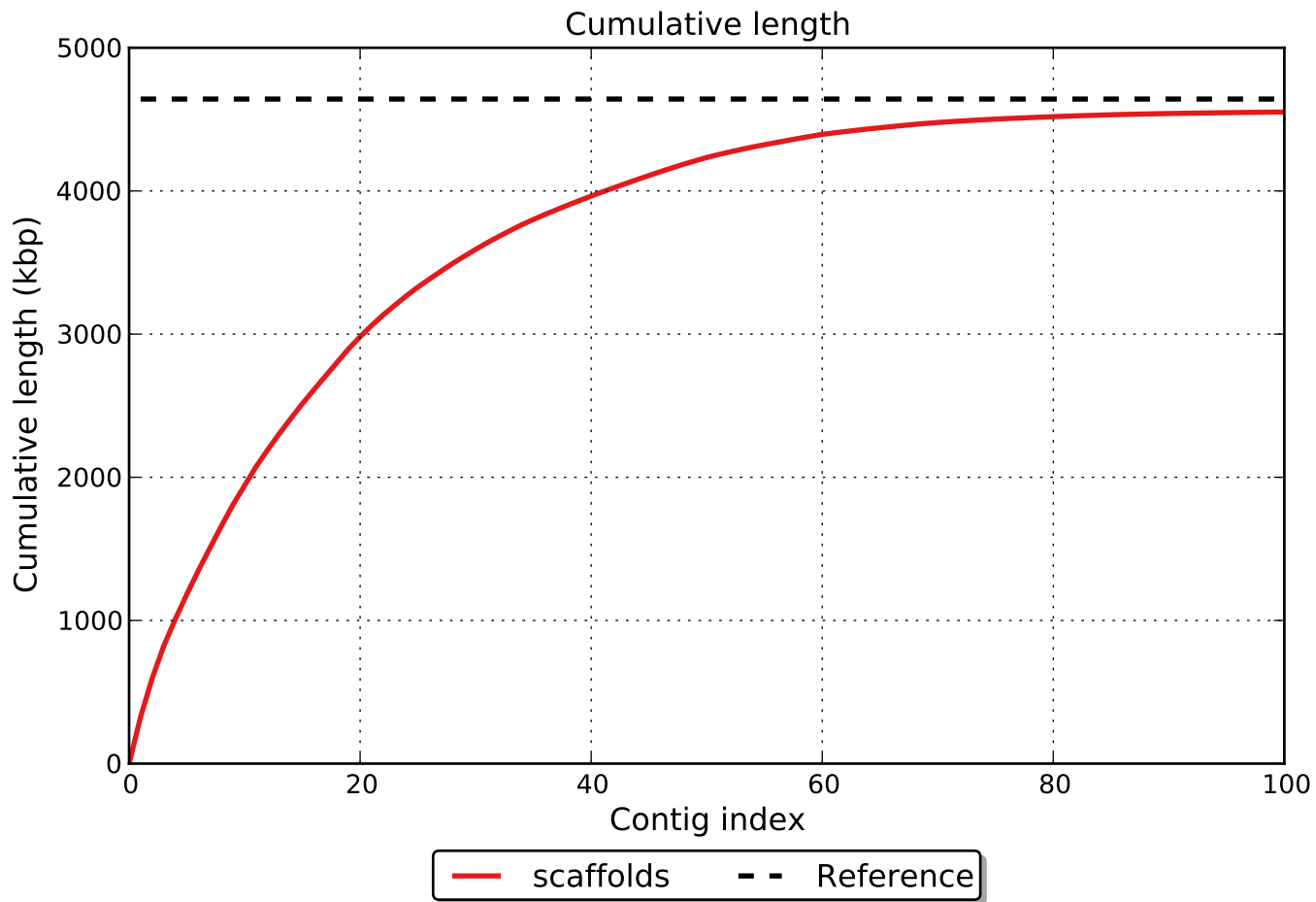
## Unaligned report

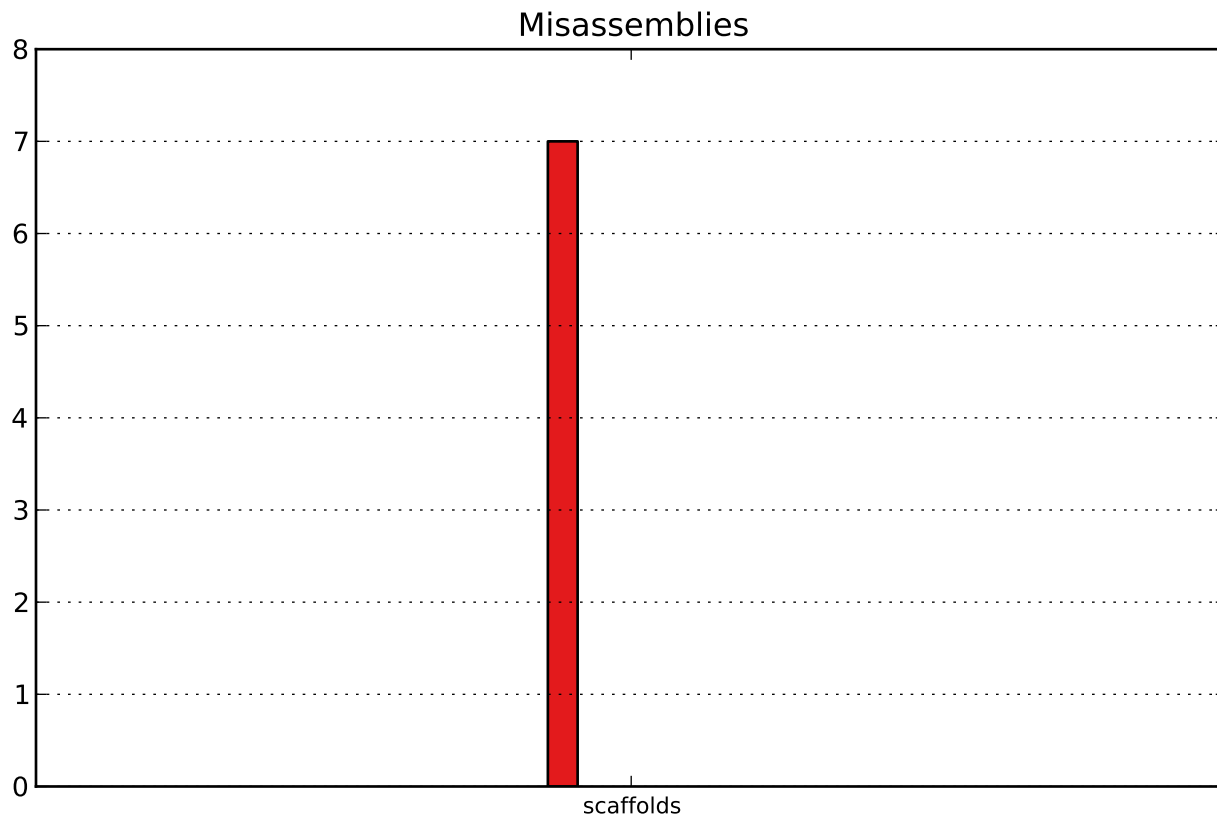
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	616

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).

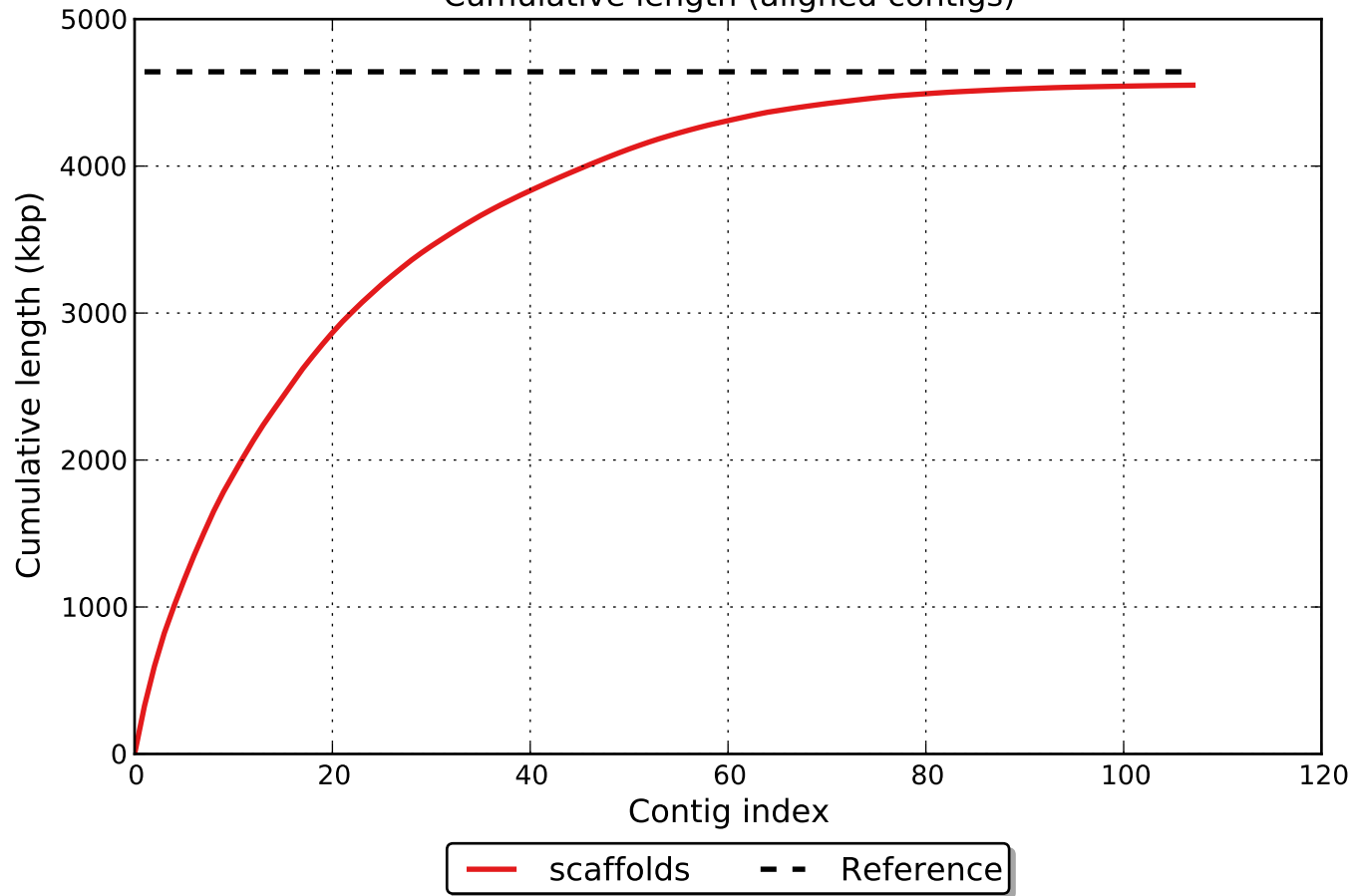
Nx



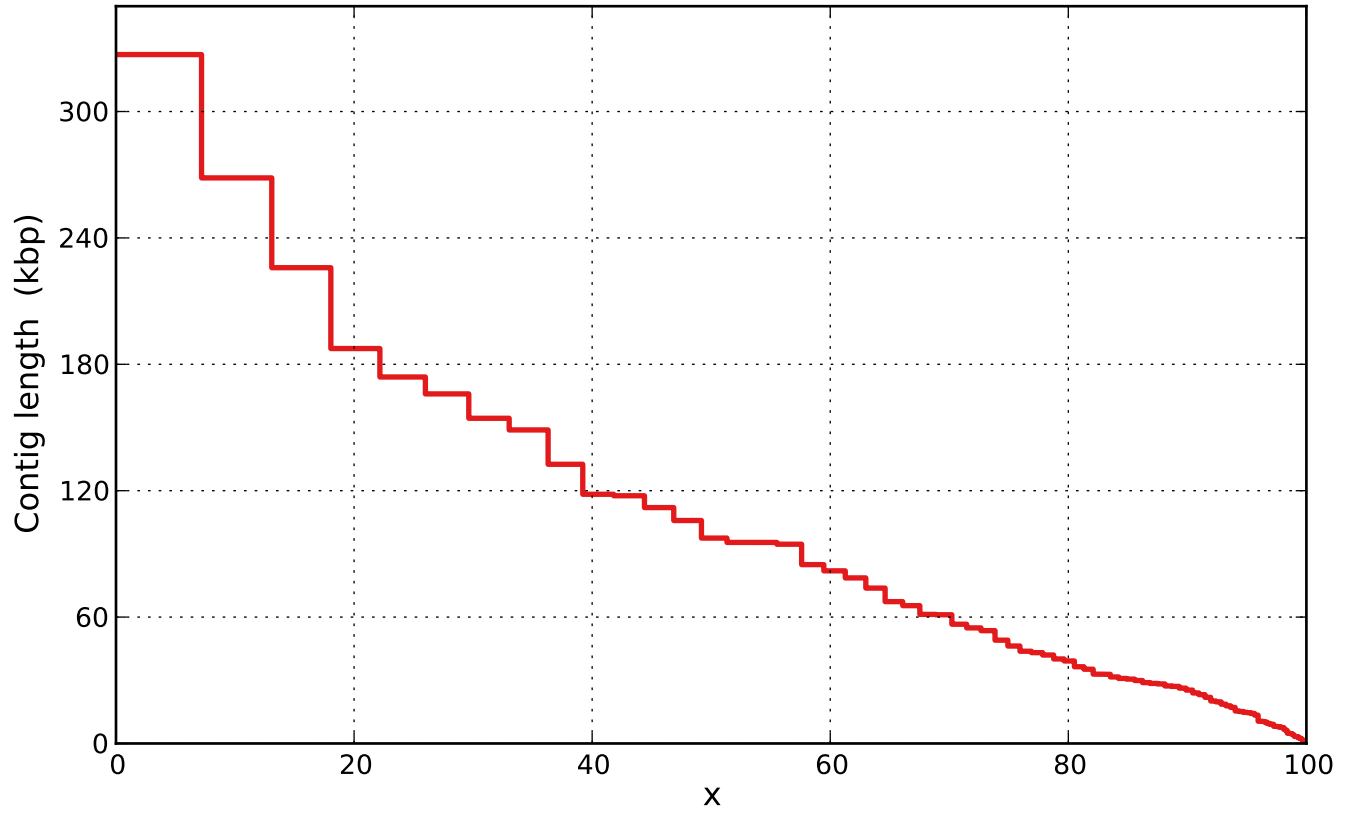




Cumulative length (aligned contigs)



NAx



— scaffolds