

# Report

	scaffolds
# contigs ( $\geq 0$ bp)	1110
# contigs ( $\geq 1000$ bp)	297
# contigs ( $\geq 5000$ bp)	209
# contigs ( $\geq 10000$ bp)	155
# contigs ( $\geq 25000$ bp)	82
# contigs ( $\geq 50000$ bp)	42
Total length ( $\geq 0$ bp)	7356224
Total length ( $\geq 1000$ bp)	7060857
Total length ( $\geq 5000$ bp)	6844889
Total length ( $\geq 10000$ bp)	6443865
Total length ( $\geq 25000$ bp)	5259063
Total length ( $\geq 50000$ bp)	3855778
# contigs	352
Largest contig	200996
Total length	7094731
Reference length	9283304
N50	54145
N75	24817
L50	37
L75	85
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	127194
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	75.346
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1004.13
# indels per 100 kbp	0.66
Largest alignment	200996
NA50	52872
NA75	24175
LA50	37
LA75	86

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	1
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	127194
# local misassemblies	4
# mismatches	70235
# indels	46
# short indels	46
# long indels	0
Indels length	52

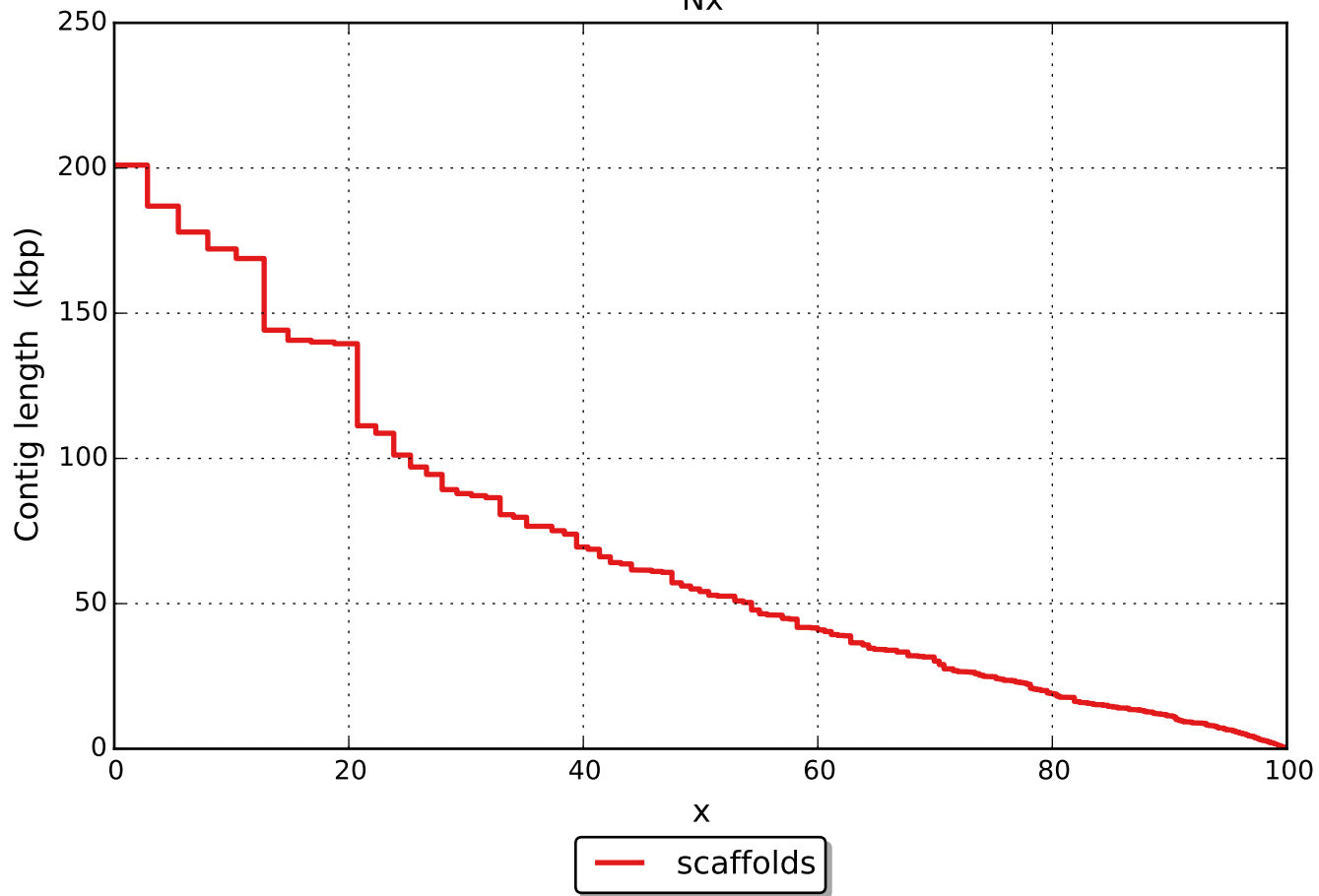
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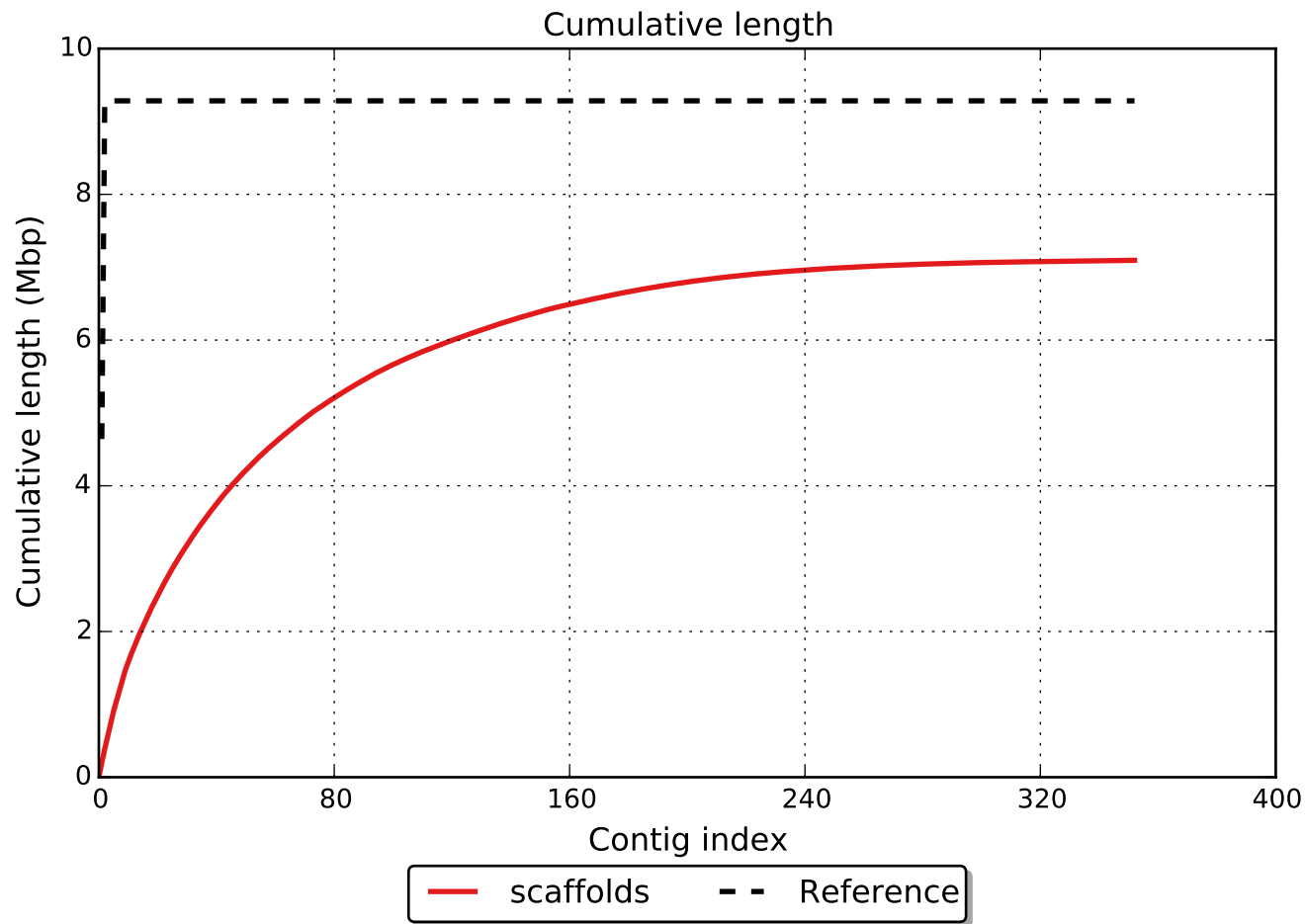
## Unaligned report

	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	0

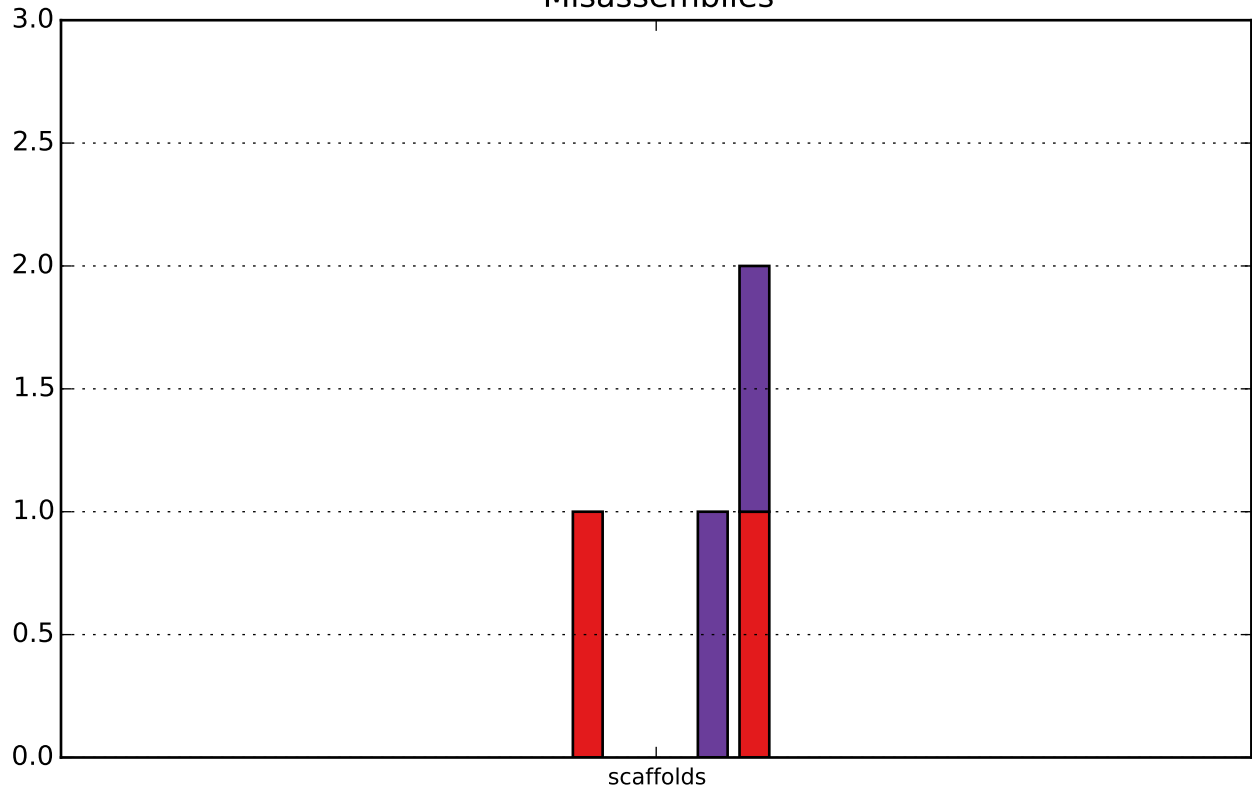
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

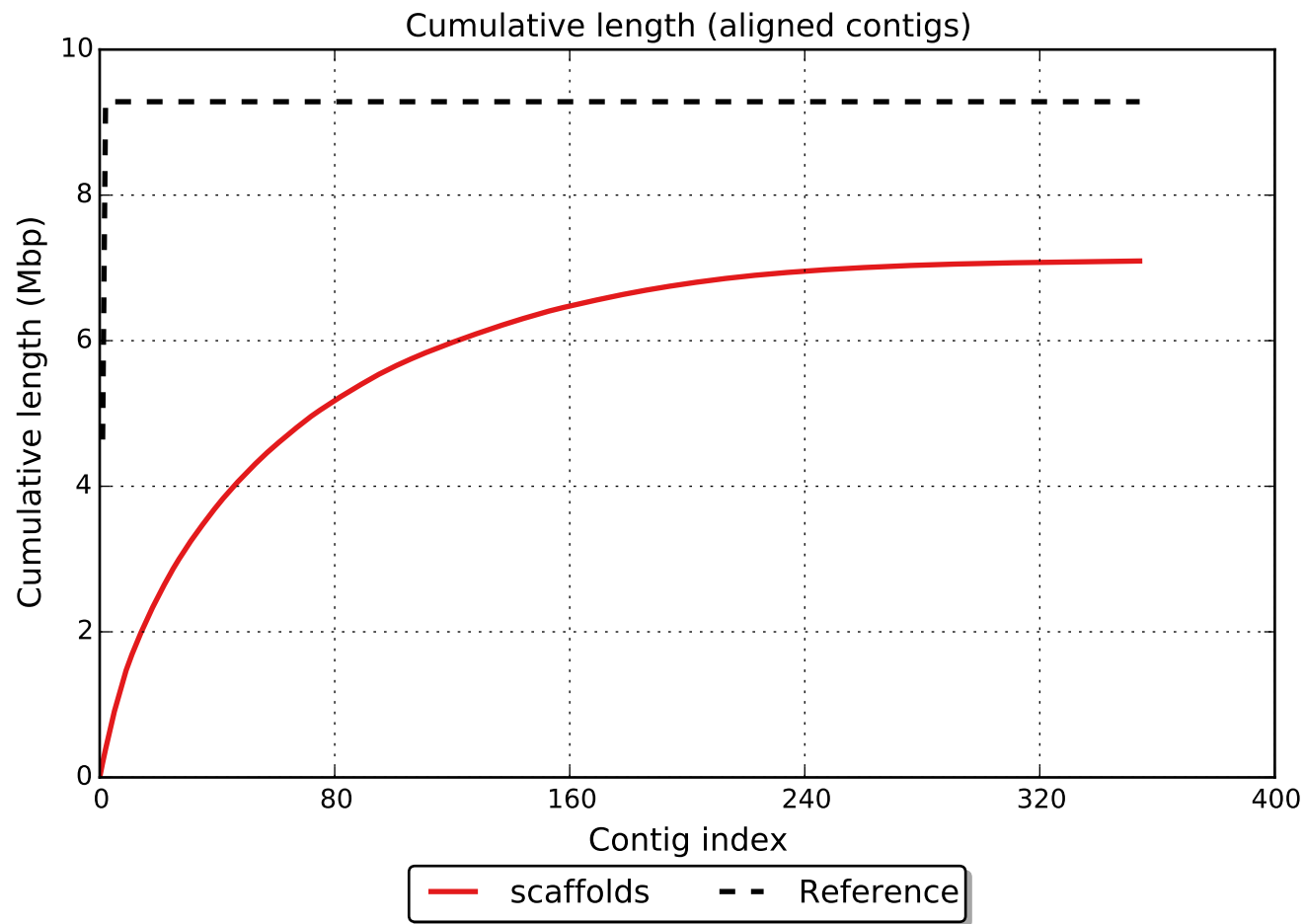
Nx



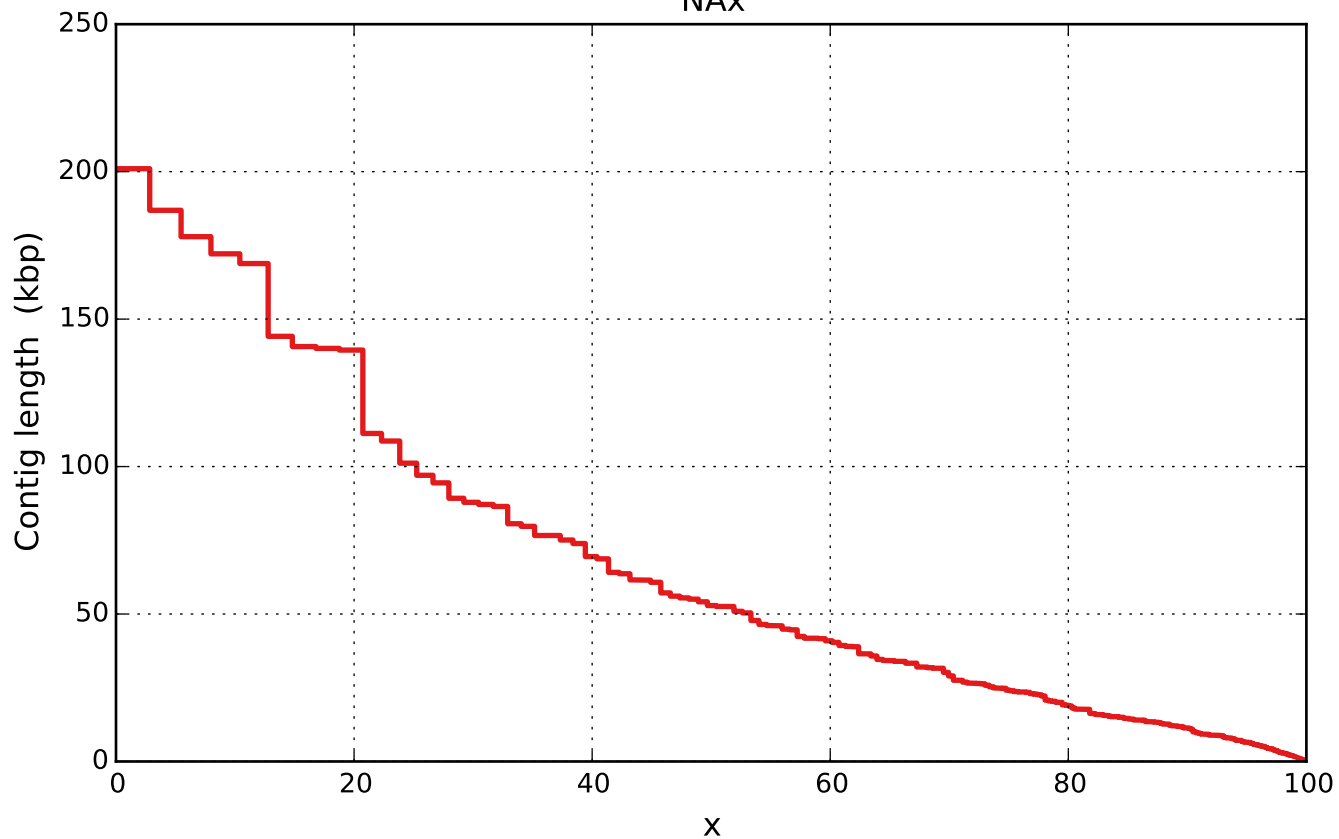


# Misassemblies





NAx



— scaffolds