

# Report

	scaffolds
# contigs ( $\geq 0$ bp)	2184
# contigs ( $\geq 1000$ bp)	24
# 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)	815157
Total length ( $\geq 1000$ bp)	35865
Total length ( $\geq 5000$ bp)	5456
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	399
Largest contig	5456
Total length	276411
Reference length	4641652
N50	667
N75	557
L50	155
L75	269
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	5973
# local misassemblies	0
# unaligned contigs	48 + 5 part
Unaligned length	33042
Genome fraction (▼)	5.215
Duplication ratio	1.005
# N's per 100 kbp	1613.18
# mismatches per 100 kbp	53.70
# indels per 100 kbp	47.09
Largest alignment	5416
NA50	633
NA75	529
LA50	163
LA75	285

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

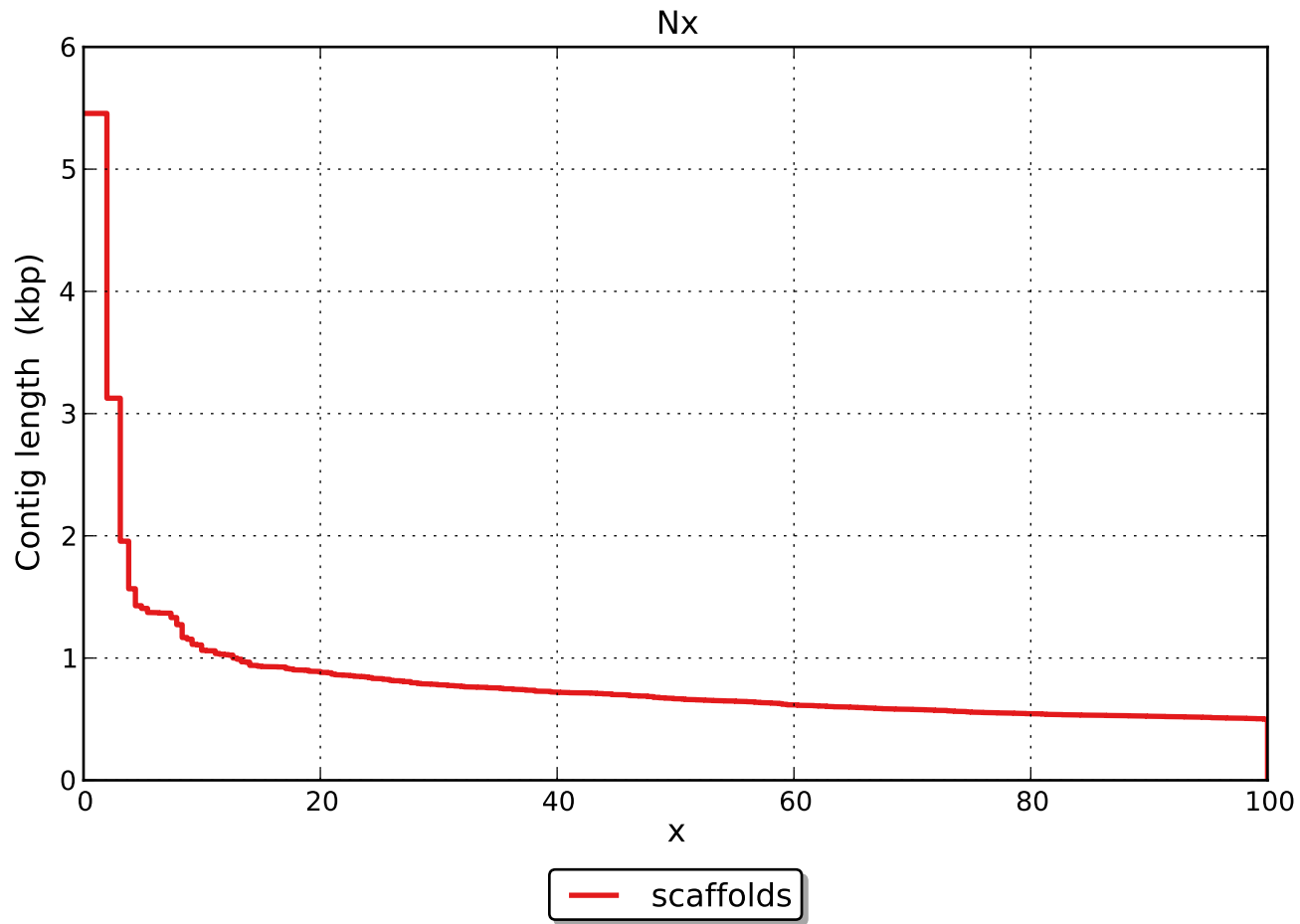
	scaffolds
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	5973
# local misassemblies	0
# mismatches	130
# indels	114
# short indels	37
# long indels	77
Indels length	1223

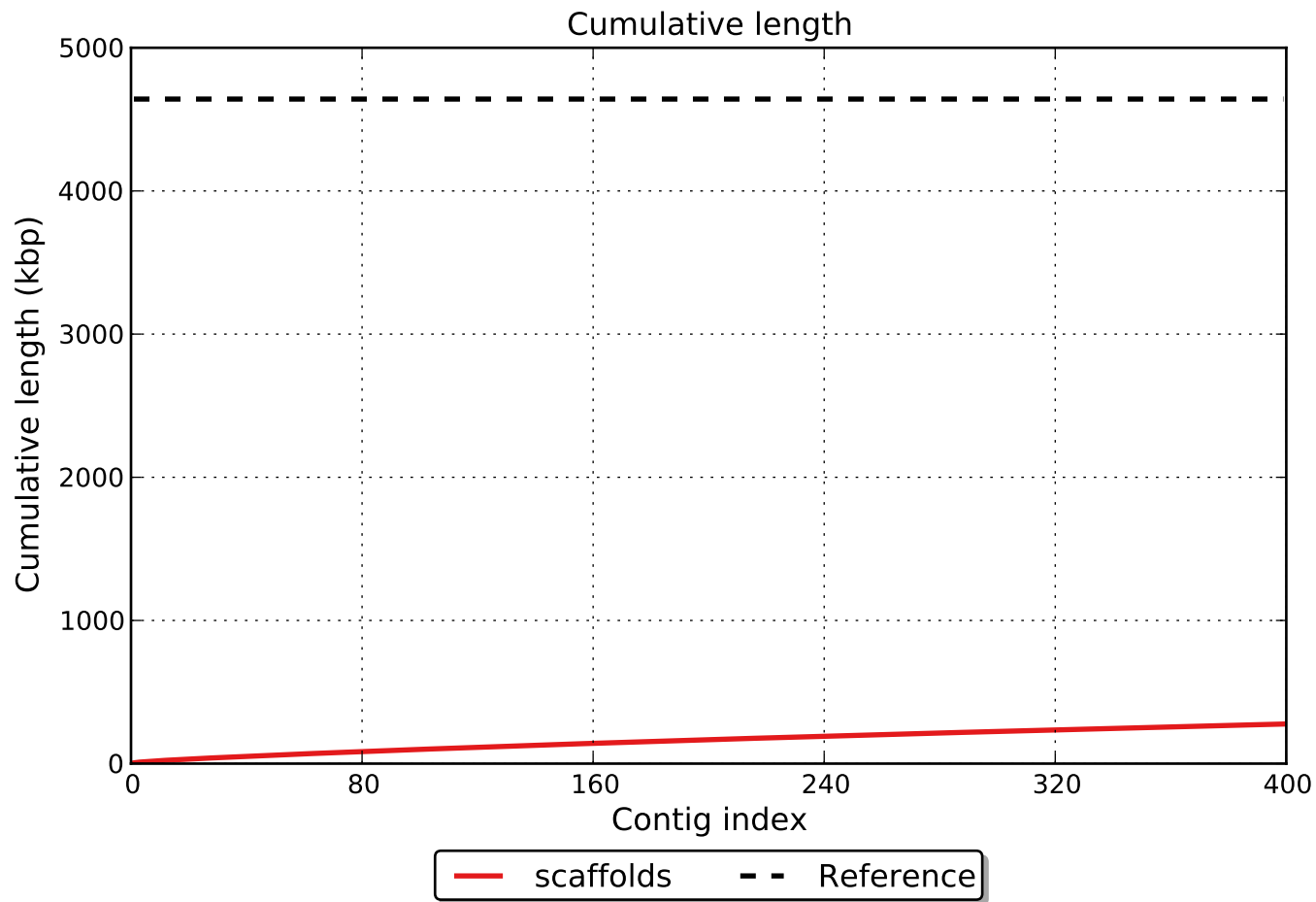
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

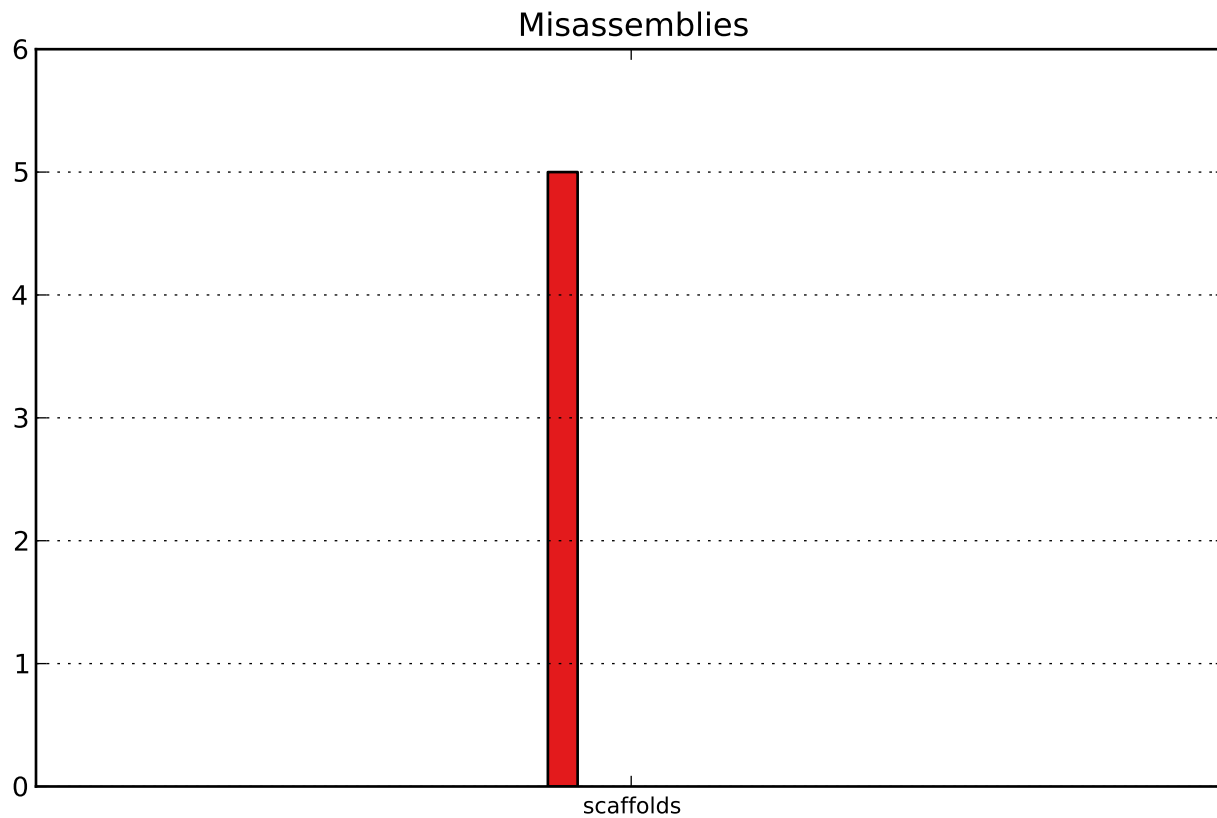
## Unaligned report

	scaffolds
# fully unaligned contigs	48
Fully unaligned length	32883
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	159
# N's	4459

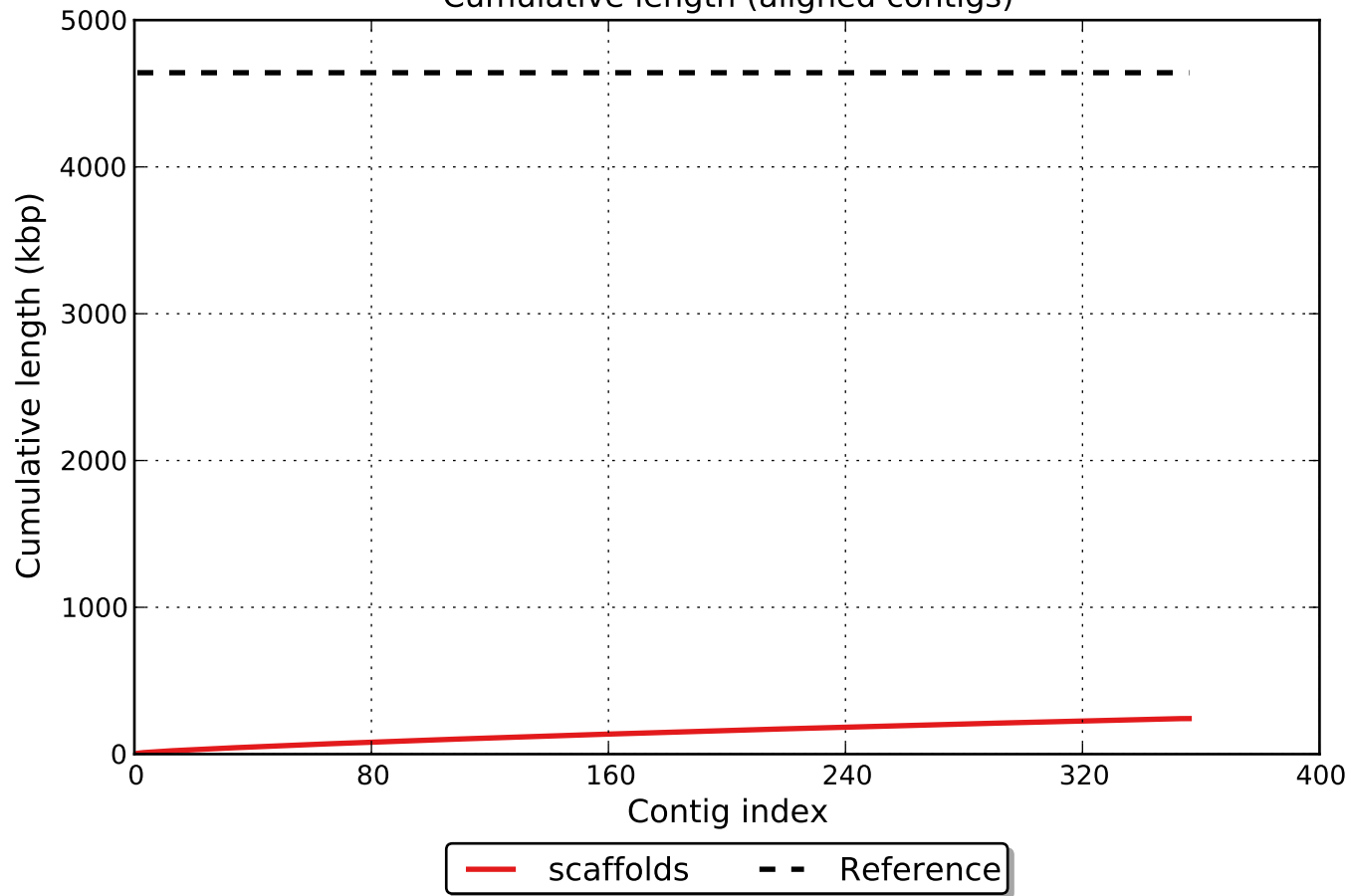
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



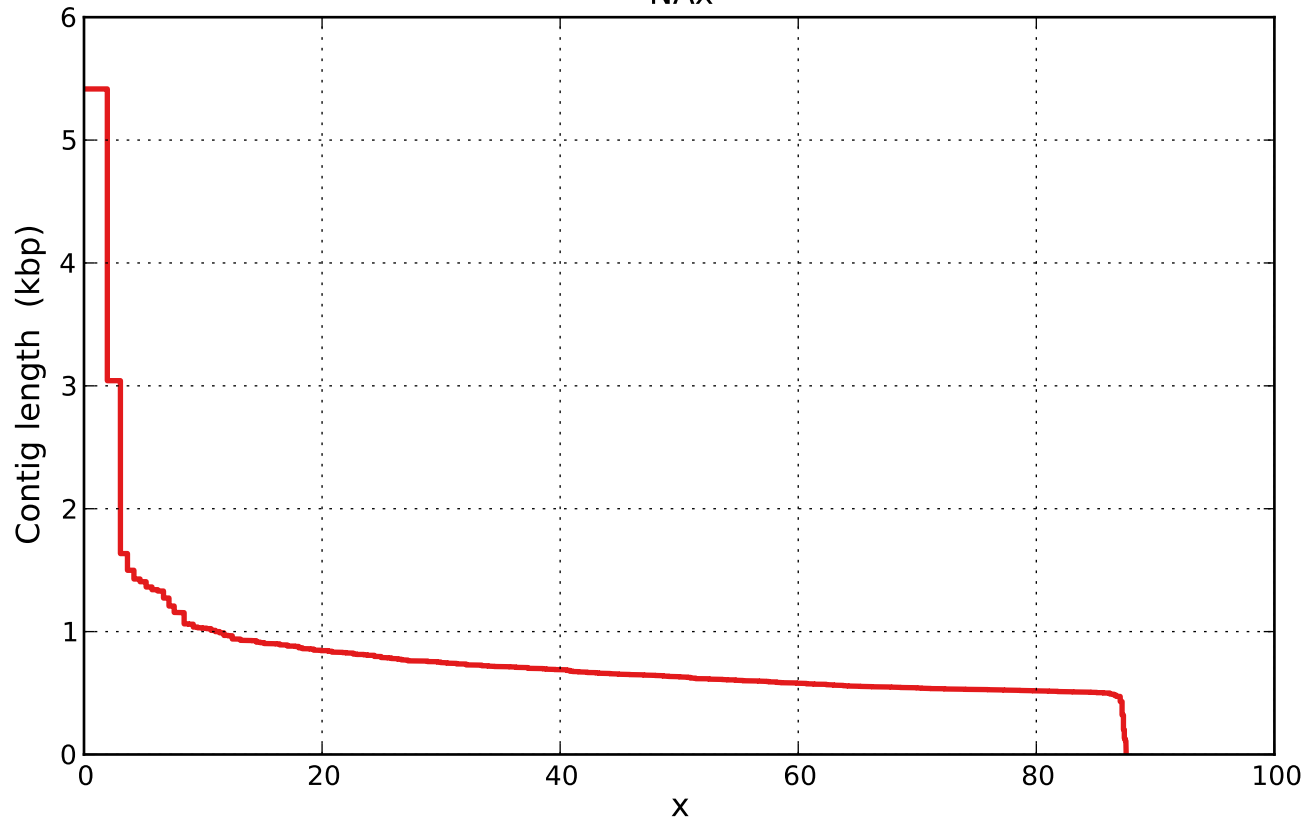




Cumulative length (aligned contigs)



NAx



— scaffolds