

# Report

	scaffolds
# contigs ( $\geq 0$ bp)	2040
# contigs ( $\geq 1000$ bp)	11
# 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)	682956
Total length ( $\geq 1000$ bp)	18193
Total length ( $\geq 5000$ bp)	5473
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	233
Largest contig	5473
Total length	157650
Reference length	4641652
N50	632
N75	548
L50	90
L75	158
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	8125
# local misassemblies	0
# unaligned contigs	28 + 5 part
Unaligned length	18347
Genome fraction (▼)	2.995
Duplication ratio	1.002
# N's per 100 kbp	1410.72
# mismatches per 100 kbp	353.14
# indels per 100 kbp	51.06
Largest alignment	5390
NA50	600
NA75	527
LA50	94
LA75	165

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

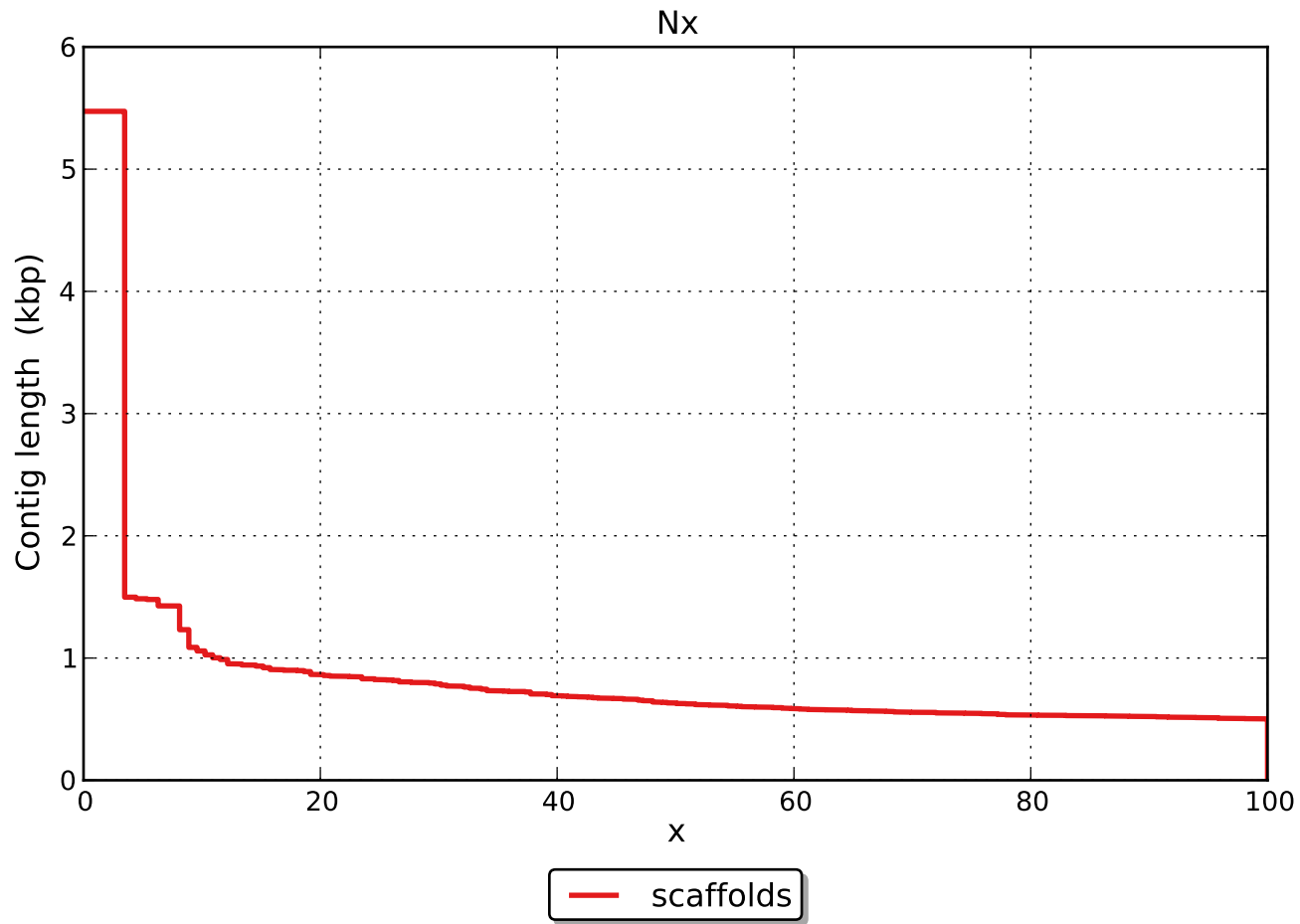
	scaffolds
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	8125
# local misassemblies	0
# mismatches	491
# indels	71
# short indels	42
# long indels	29
Indels length	537

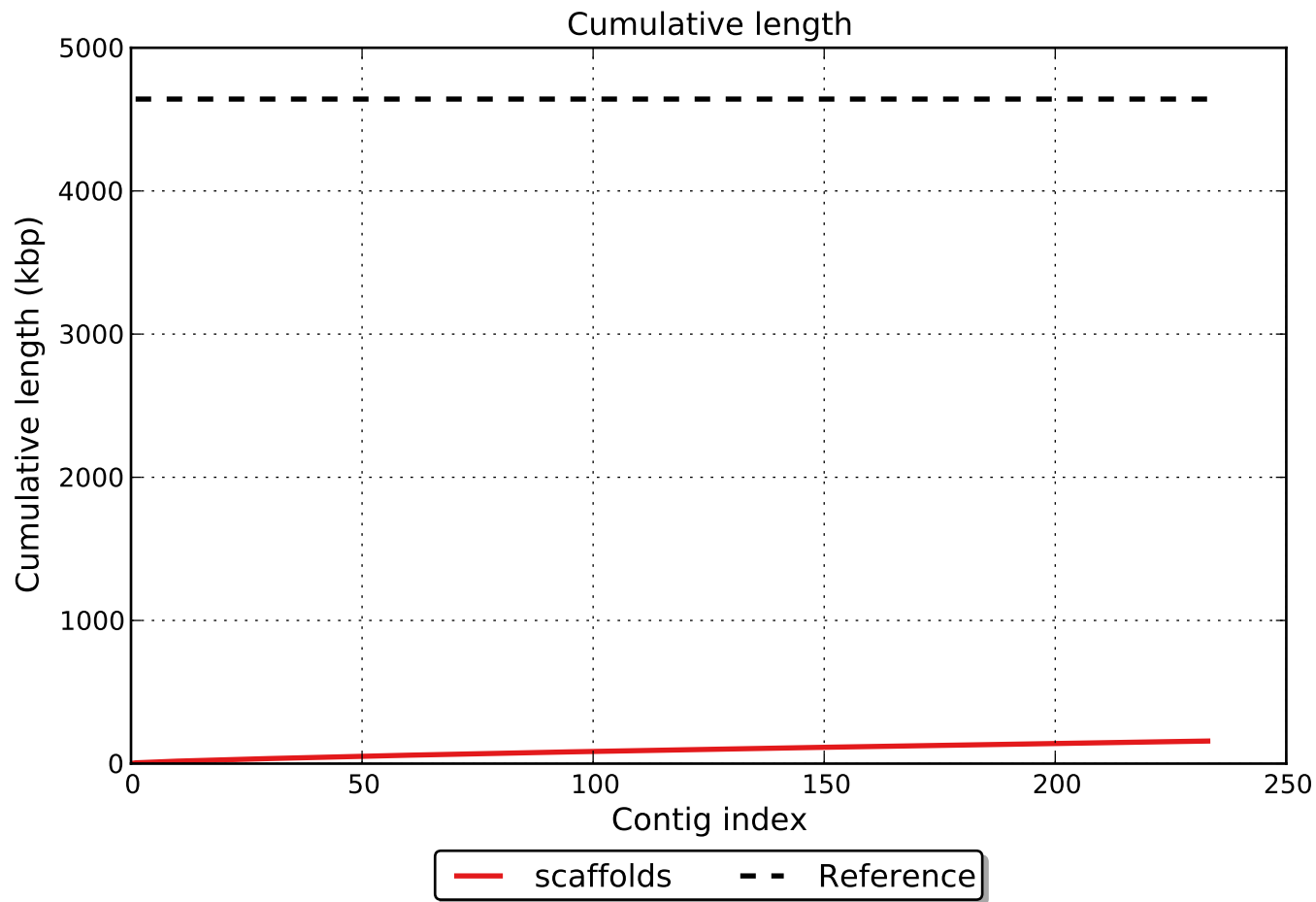
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

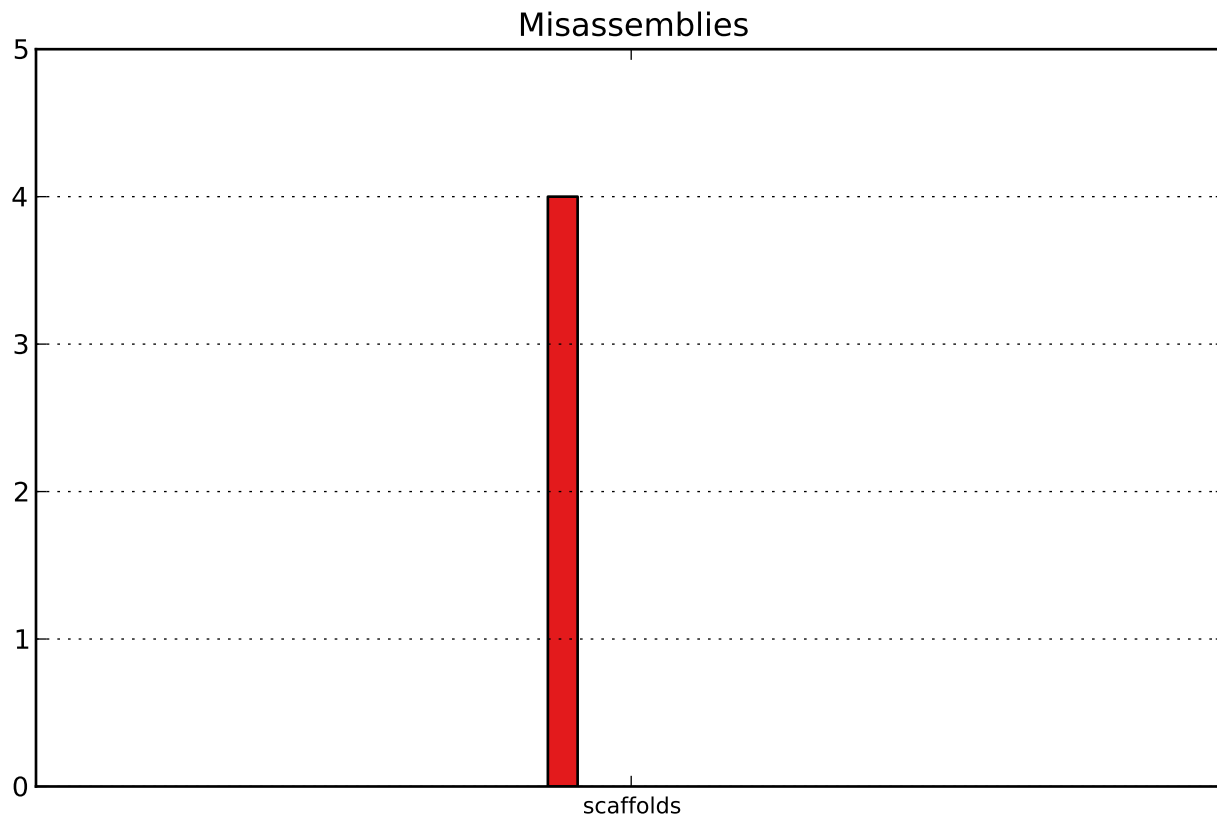
## Unaligned report

	scaffolds
# fully unaligned contigs	28
Fully unaligned length	17463
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	884
# N's	2224

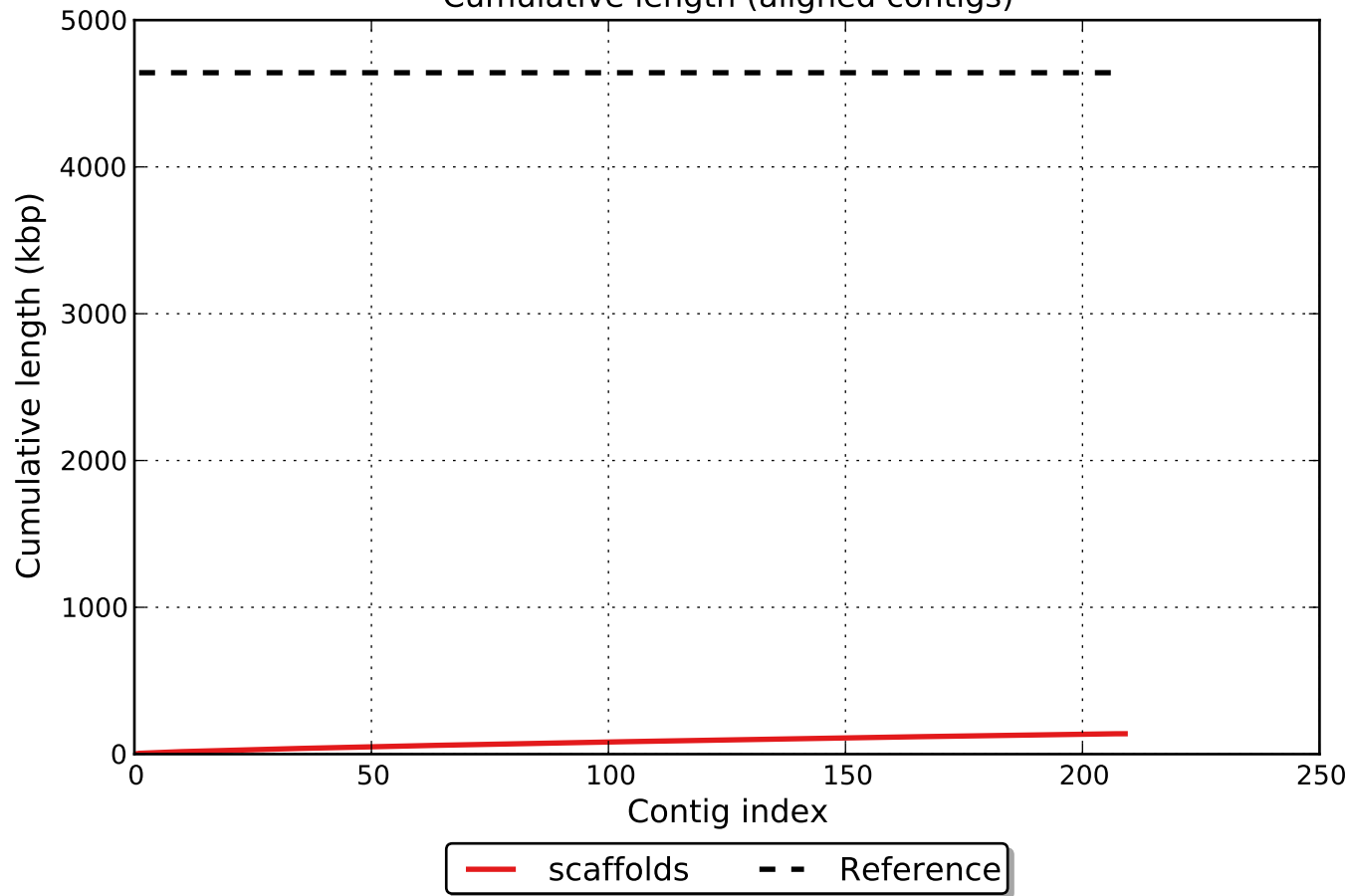
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



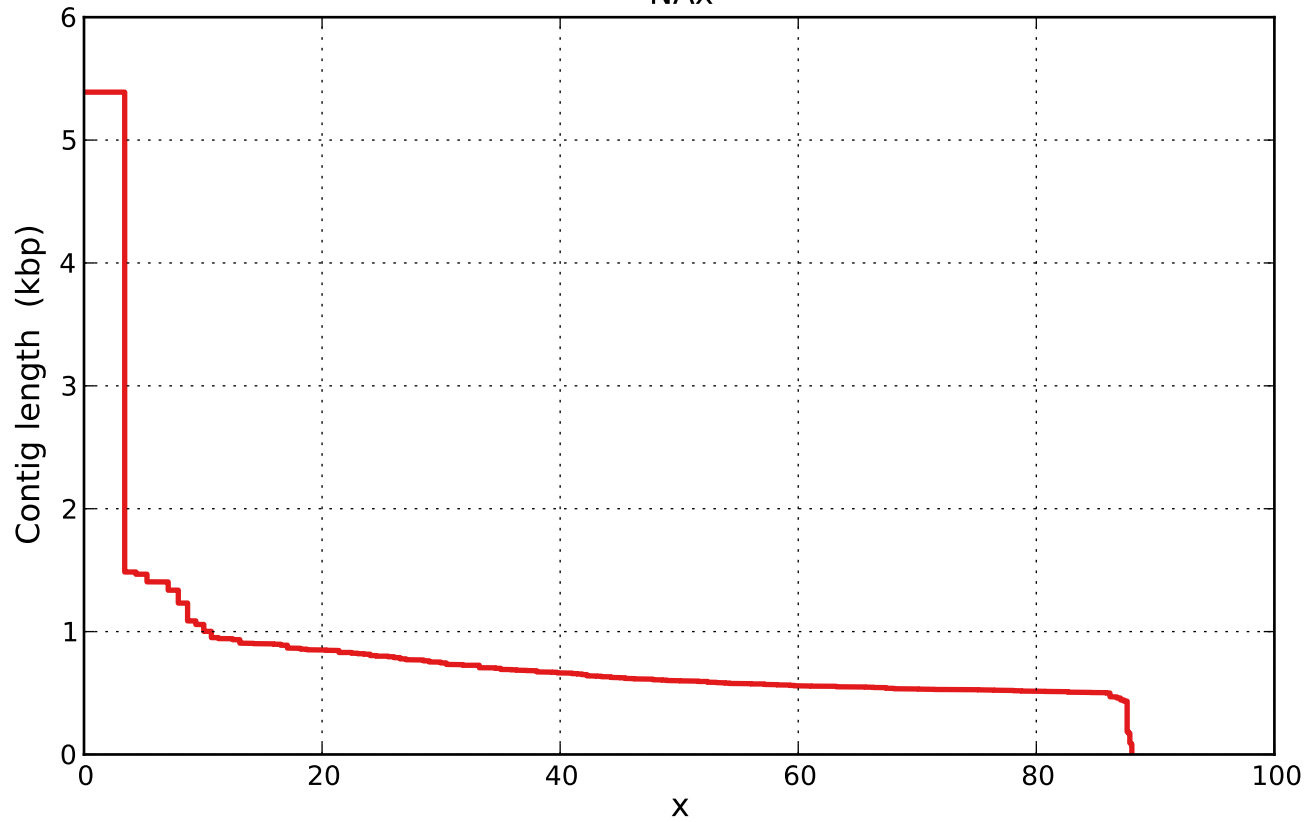




Cumulative length (aligned contigs)



NAx



— scaffolds