Report

	scaffolds
# contigs (>= 0 bp)	990
# contigs (>= 1000 bp)	220
# contigs (>= 5000 bp)	156
# contigs (>= 10000 bp)	127
# contigs (>= 25000 bp)	84
# contigs (>= 50000 bp)	52
Total length (>= 0 bp)	8105679
Total length (>= 1000 bp)	7814423
Total length (>= 5000 bp)	7652012
Total length (>= 10000 bp)	7445873
Total length (>= 25000 bp)	6706003
Total length (>= 50000 bp)	5605771
# contigs	279
Largest contig	347033
Total length	7851669
Reference length	9283304
N50	85464
N75	42511
L50	25
L75	59
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	156398
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.069
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1009.96
# indels per 100 kbp	0.68
Largest alignment	347033
NA50	80338
NA75	40561
LA50	26
LA75	60

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

Misassemblies report

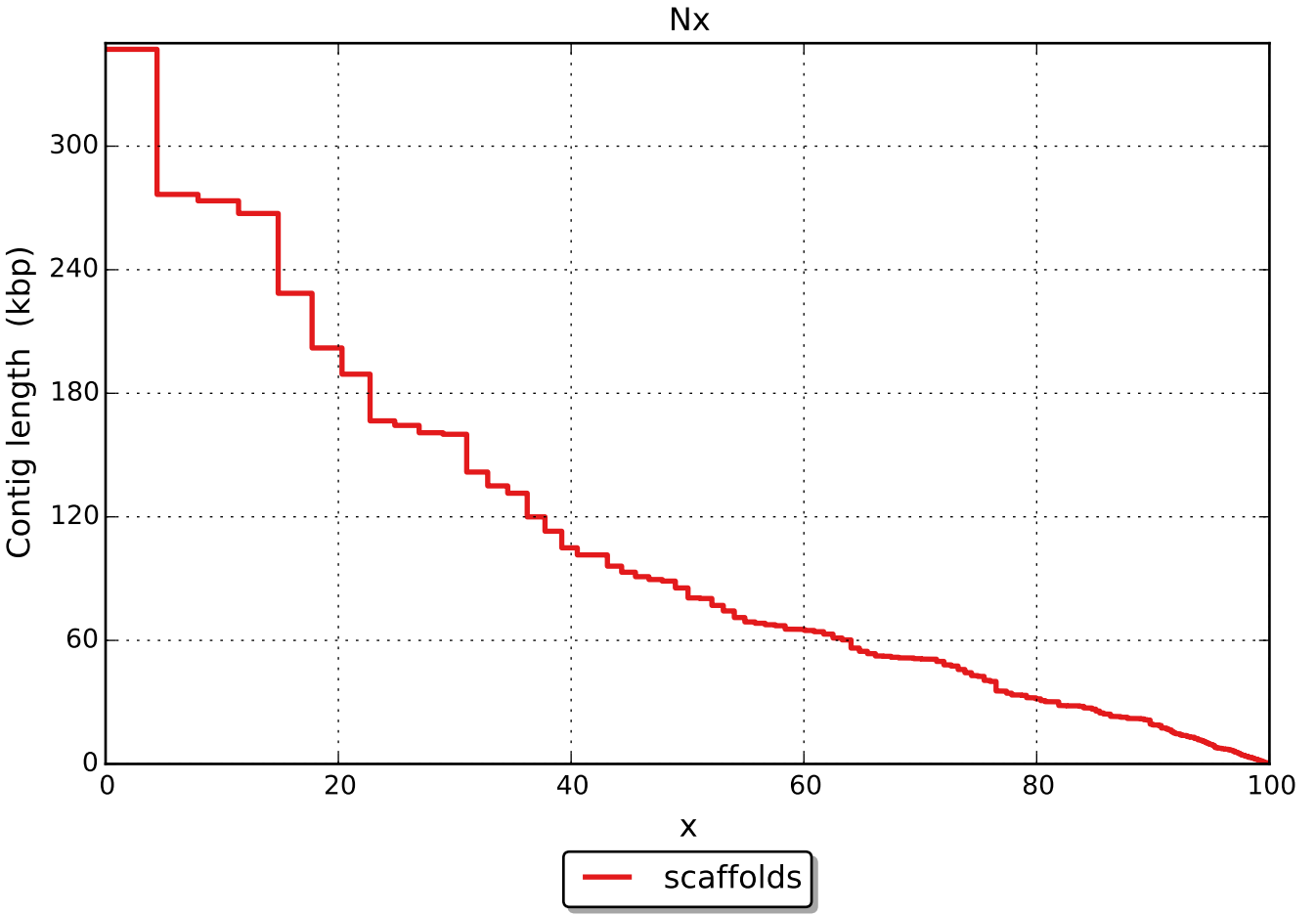
	scaffolds
# misassemblies	2
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	156398
# local misassemblies	3
# mismatches	78821
# indels	53
# short indels	53
# long indels	0
Indels length	63

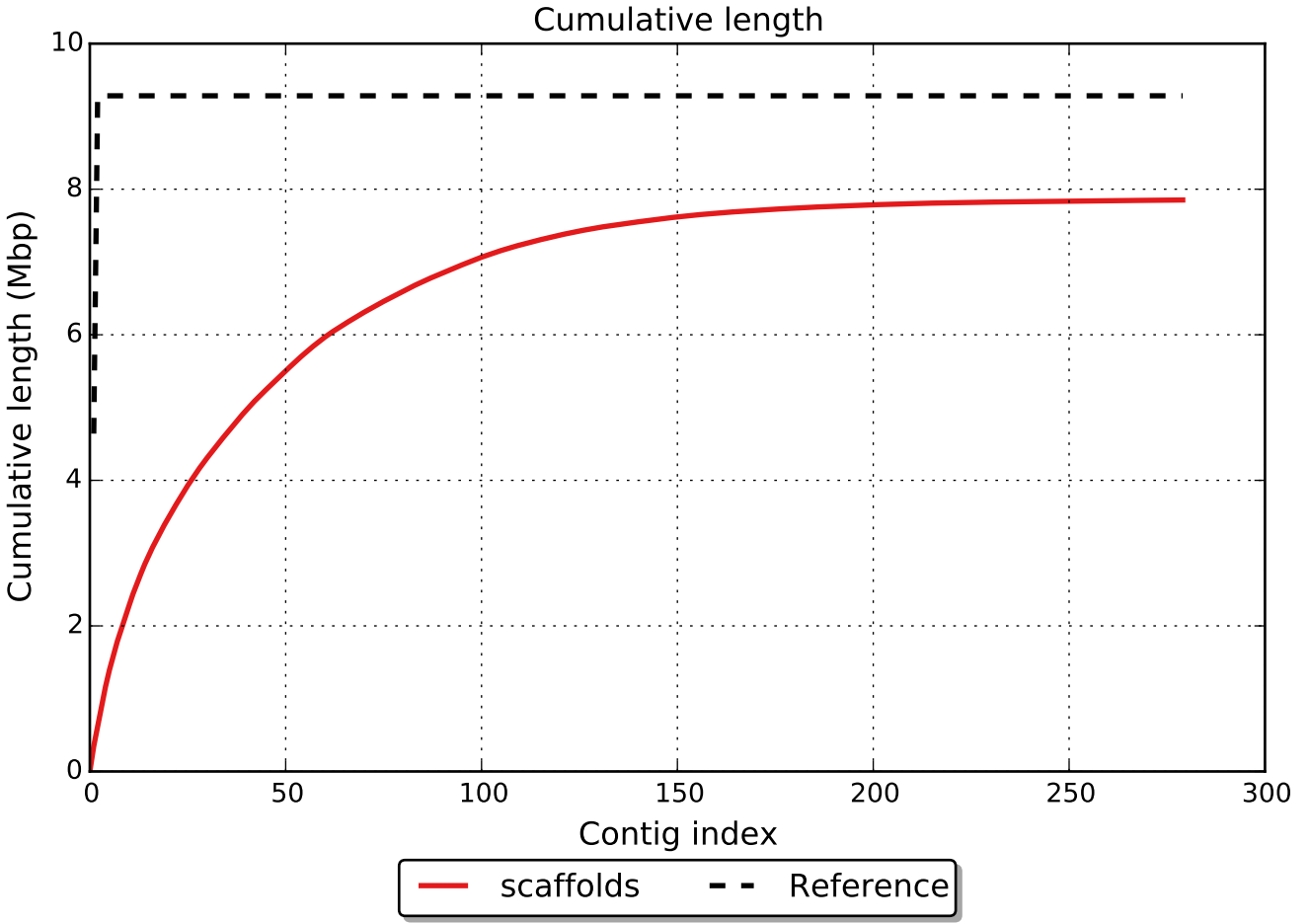
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

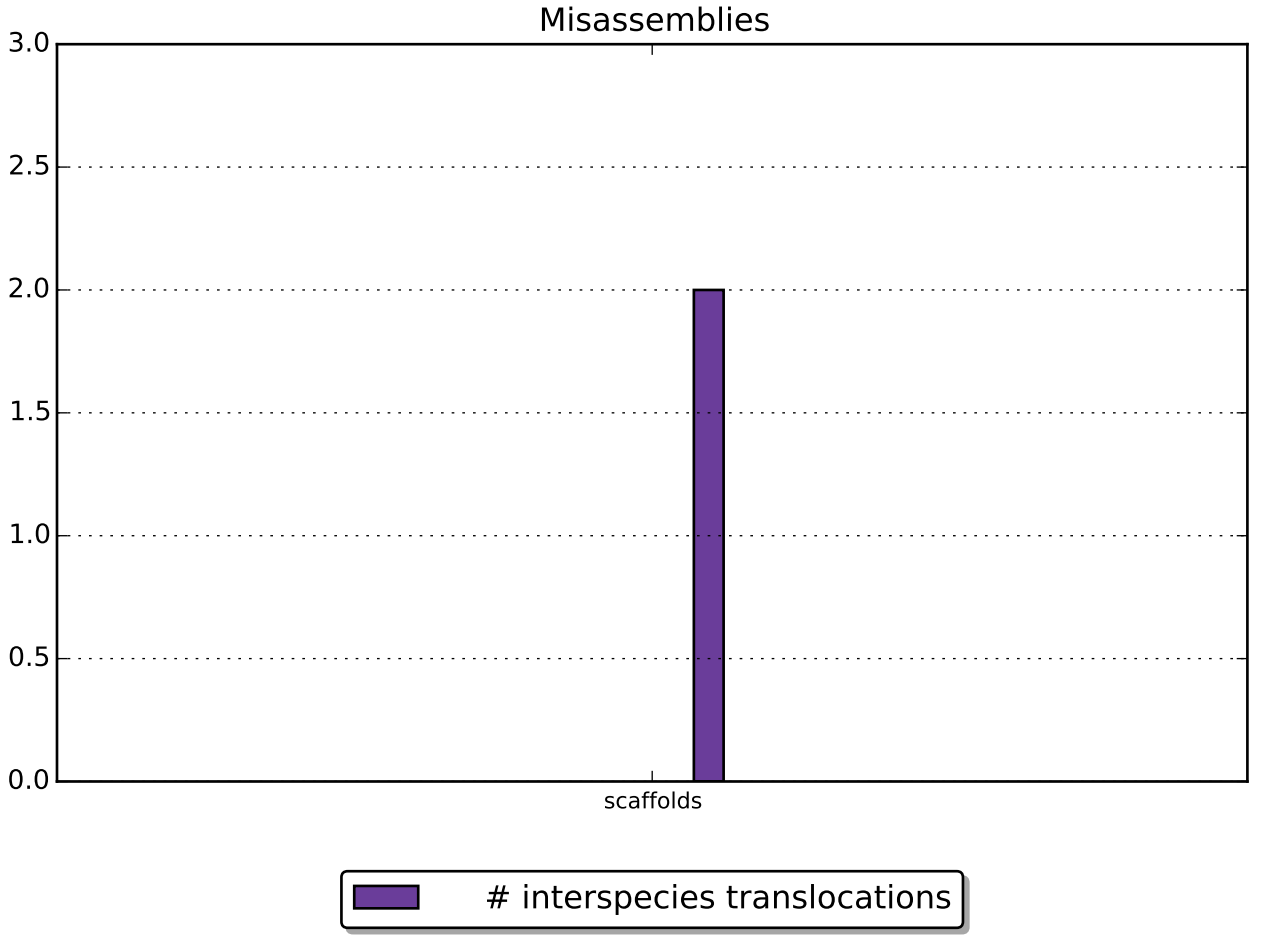
Unaligned report

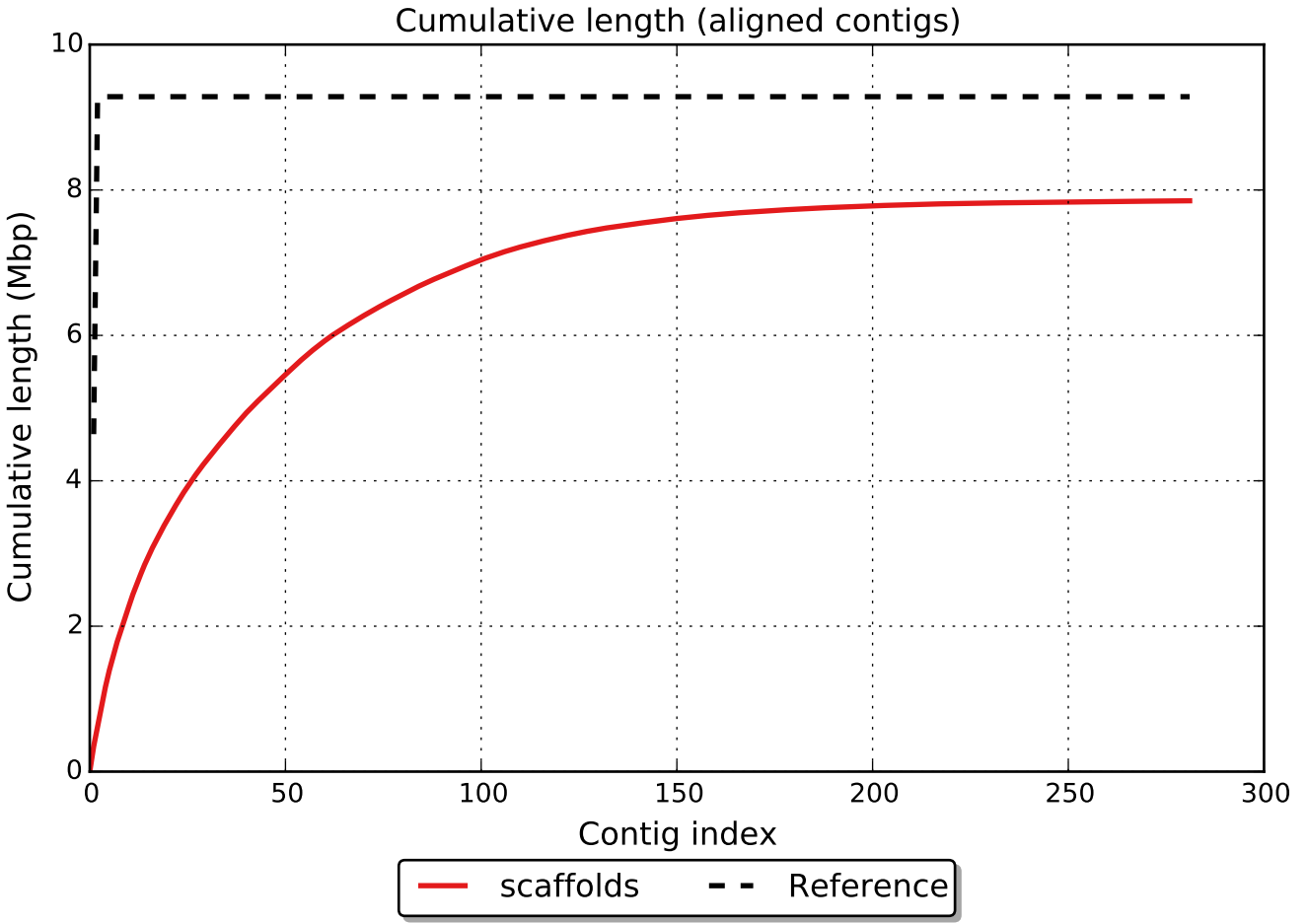
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

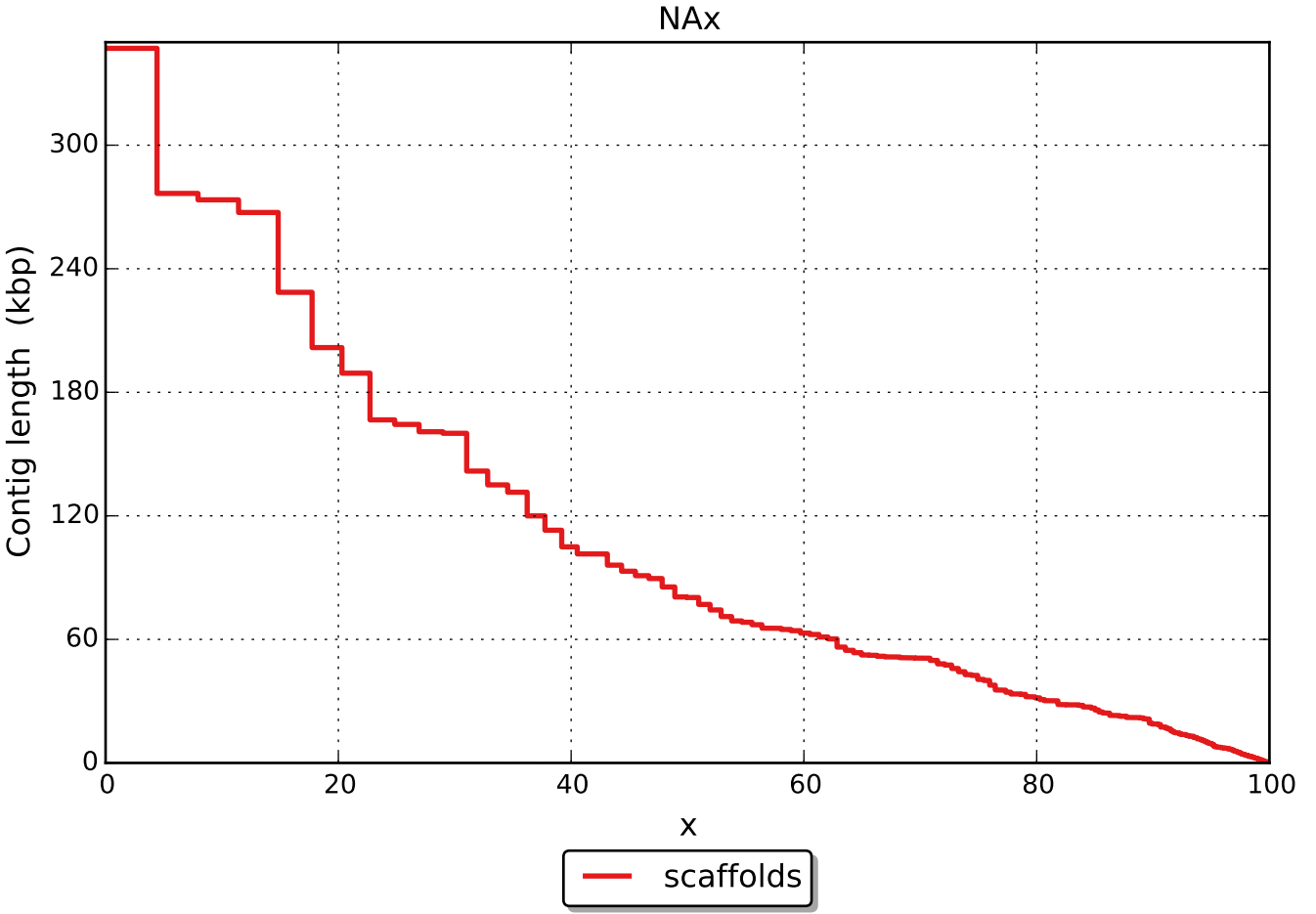
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds


Cumulative length
Cumulative length (Mbp)
Contig index
0
2
4
6
8
10
0
50
100
150
200
250
300
scaffolds
Reference


Misassemblies
3.0
2.5
2.0
1.5
1.0
0.5
0.0
scaffolds
interspecies translocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
2
4
6
8
10
0
50
100
150
200
250
300
scaffolds
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds