Report

	scaffolds
# contigs (>= 0 bp)	302
# contigs (>= 1000 bp)	121
# contigs (>= 5000 bp)	92
# contigs (>= 10000 bp)	87
# contigs (>= 25000 bp)	75
# contigs (>= 50000 bp)	58
Total length (>= 0 bp)	9077926
Total length (>= 1000 bp)	9011157
Total length (>= 5000 bp)	8960493
Total length (>= 10000 bp)	8921146
Total length (>= 25000 bp)	8704633
Total length (>= 50000 bp)	8130674
# contigs	154
Largest contig	527156
Total length	9033467
Reference length	9283304
N50	132337
N75	86976
L50	19
L75	39
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.190
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	641.60
# indels per 100 kbp	0.85
Largest alignment	527156
NA50	132337
NA75	86976
LA50	19
LA75	39

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

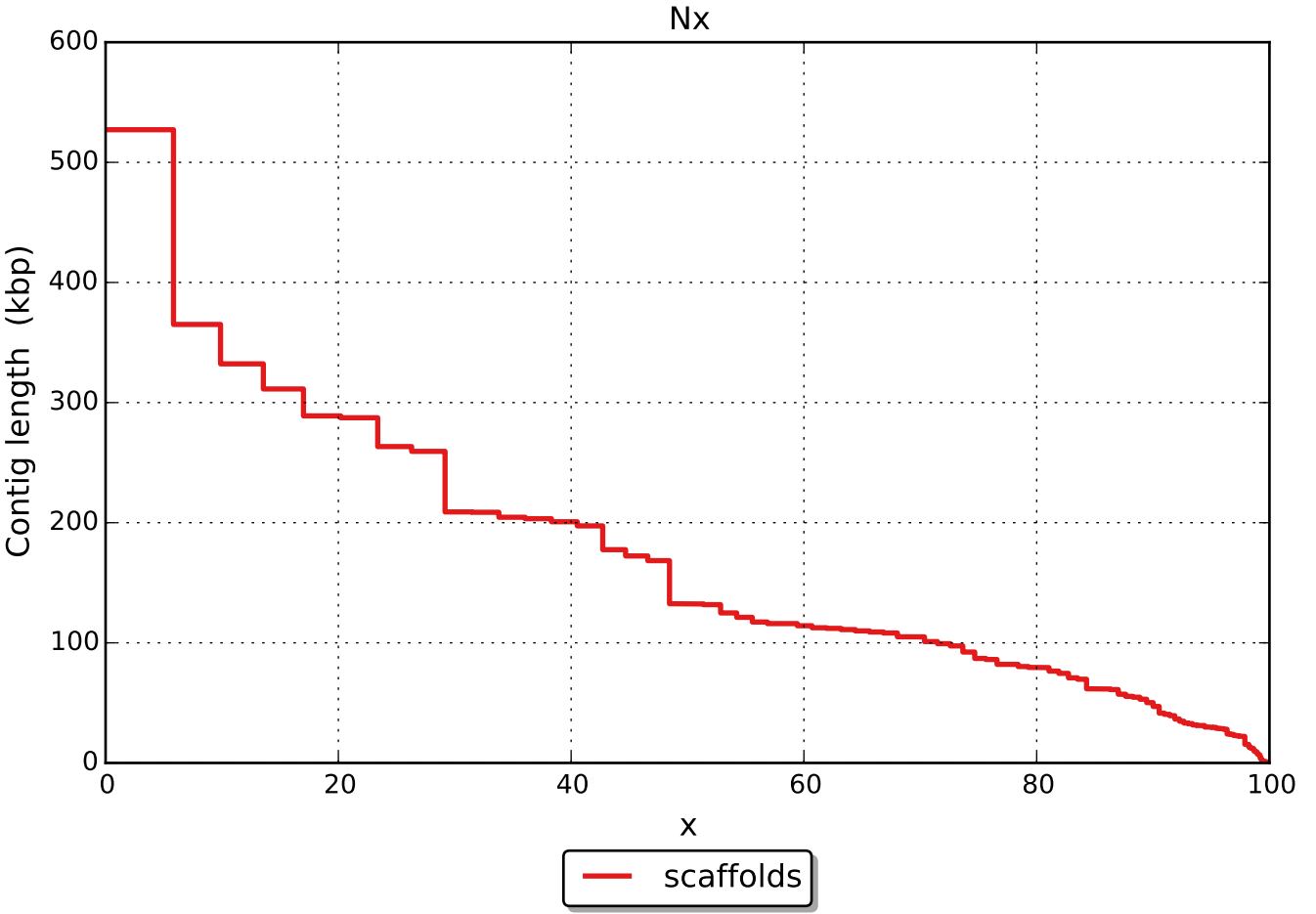
	scaffolds
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# mismatches	57888
# indels	77
# short indels	77
# long indels	0
Indels length	84

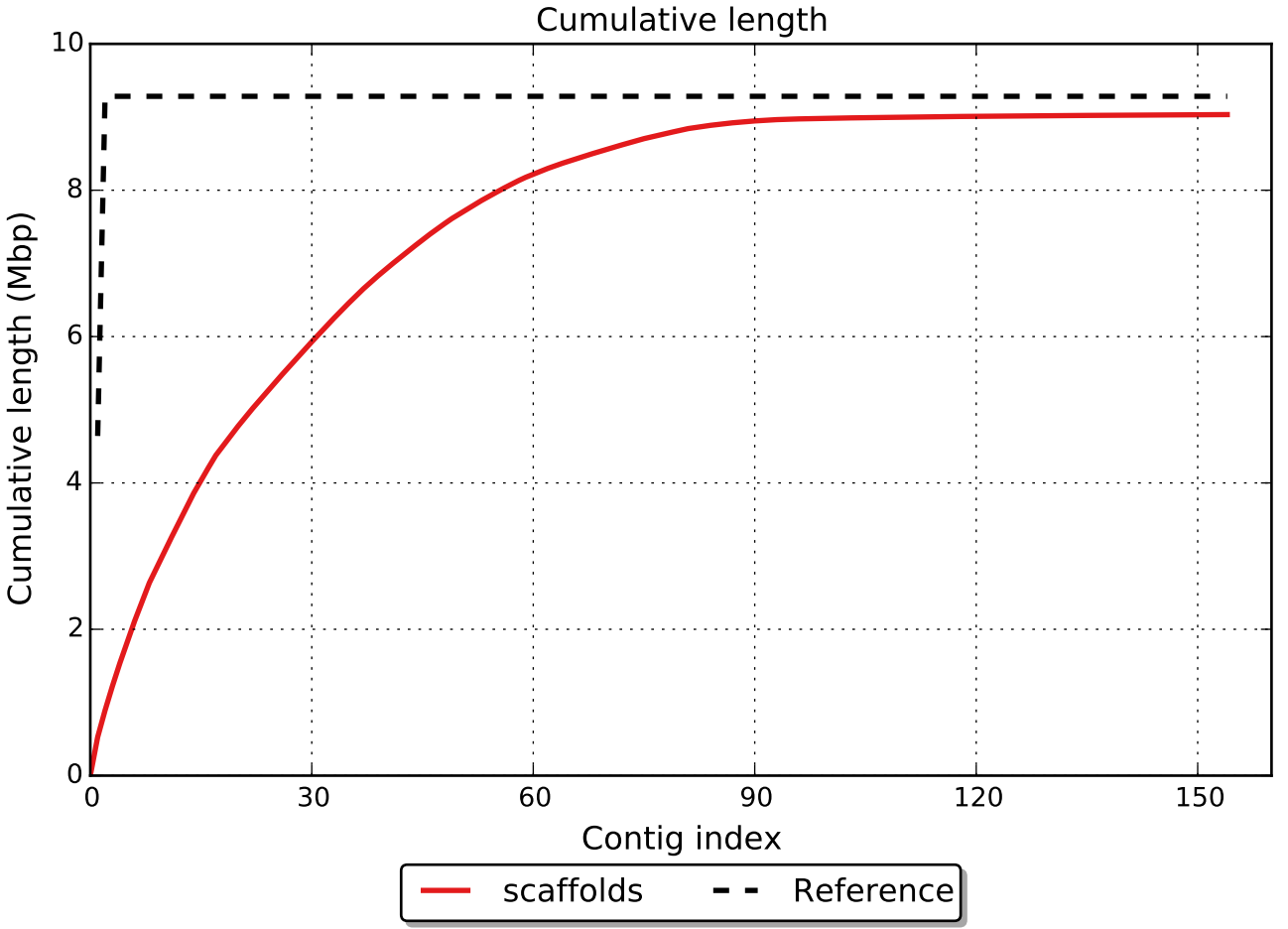
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

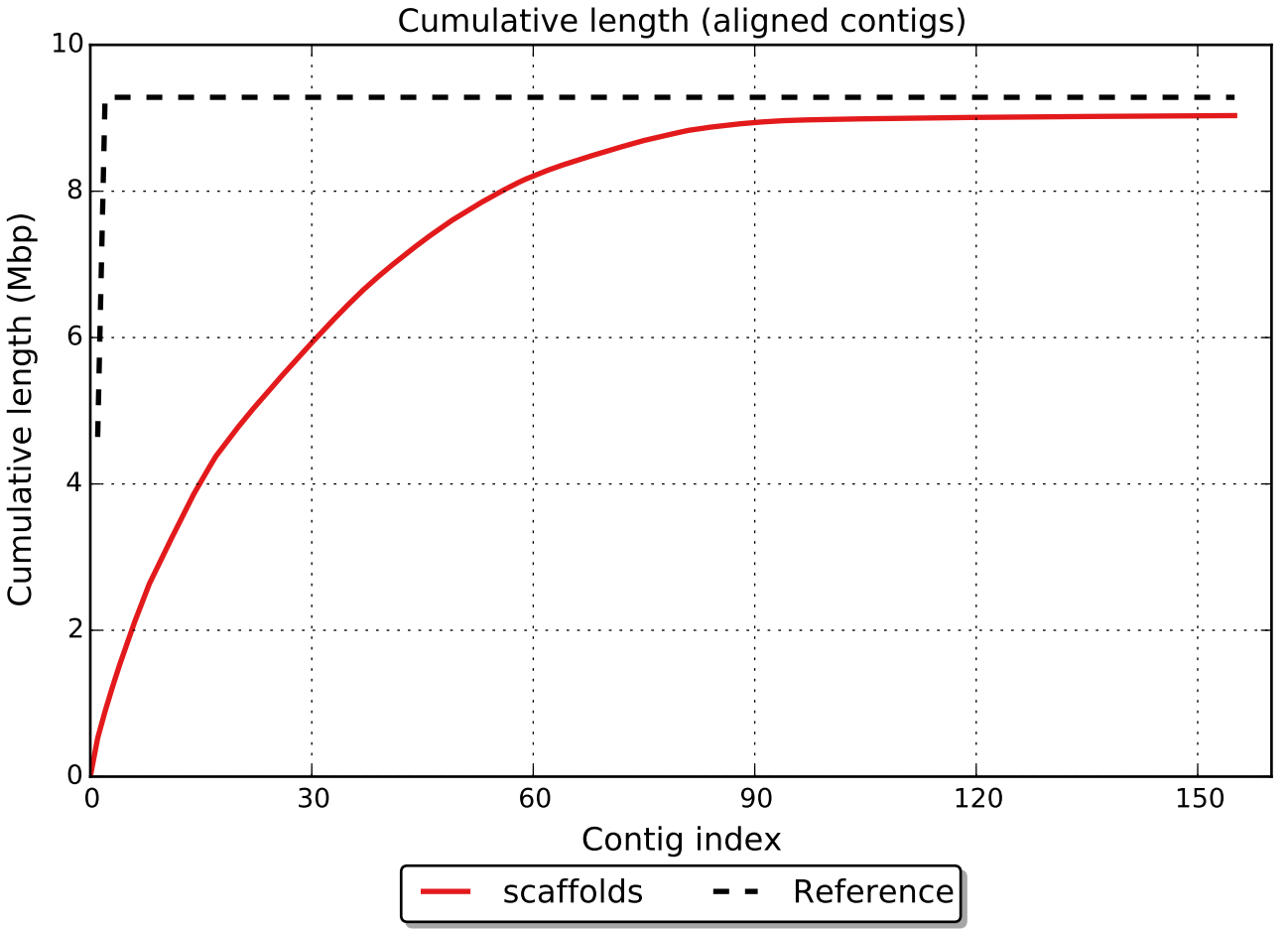
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

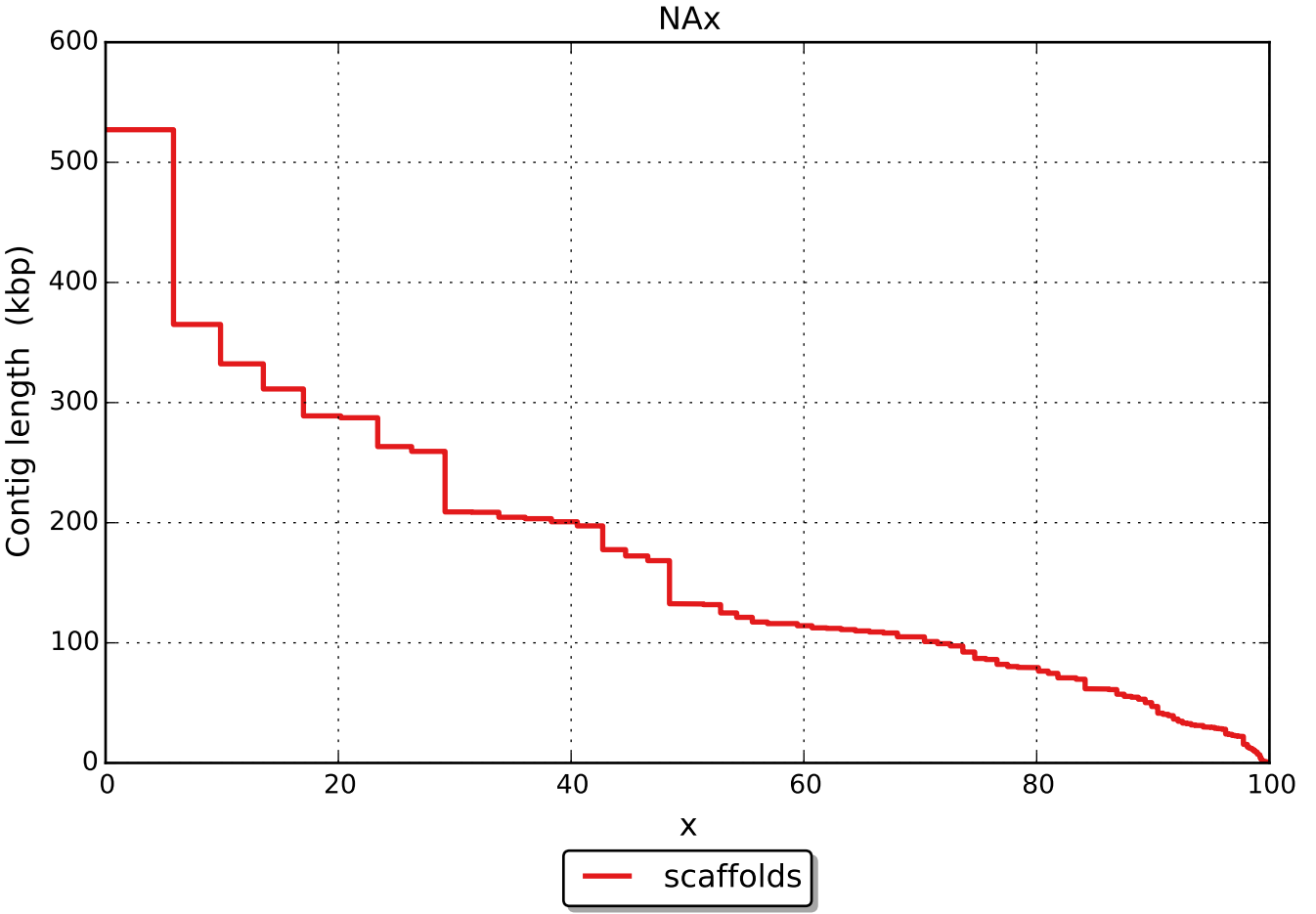
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
scaffolds


Cumulative length
Cumulative length (Mbp)
10
8
6
4
2
0
0
30
60
90
120
150
Contig index
scaffolds
Reference


Misassemblies
2.0
1.5
1.0
0.5
0.0
scaffolds
interspecies translocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
2
4
6
8
10
0
30
60
90
120
150
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
scaffolds