Report

	scaffolds
# contigs (>= 0 bp)	156
# contigs (>= 1000 bp)	117
# contigs (>= 5000 bp)	90
# contigs (>= 10000 bp)	75
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4554872
Total length (>= 1000 bp)	4542294
Total length (>= 5000 bp)	4470400
Total length (>= 10000 bp)	4359028
Total length (>= 25000 bp)	4040495
Total length (>= 50000 bp)	3287630
# contigs	124
Largest contig	233189
Total length	4547231
Reference length	4641652
N50	95475
N75	42936
L50	17
L75	35
# misassemblies	11
# misassembled contigs	7
Misassembled contigs length	569905
# local misassemblies	16
# unaligned contigs	0 + 1 part
Unaligned length	3863
Genome fraction (%)	97.805
Duplication ratio	1.001
# N's per 100 kbp	11.92
# mismatches per 100 kbp	69.94
# indels per 100 kbp	10.00
Largest alignment	202546
NA50	82910
NA75	40166
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

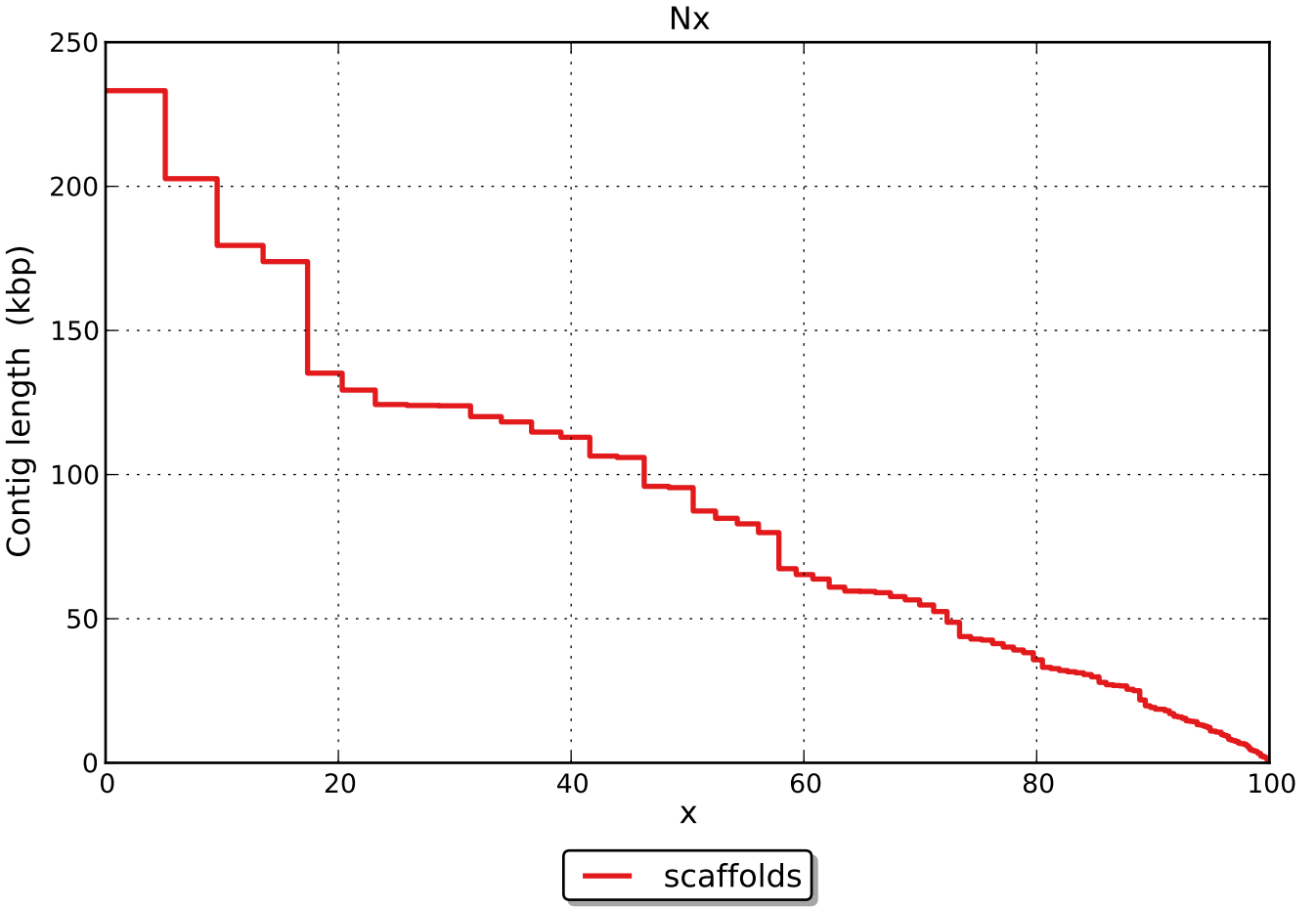
	scaffolds
# misassemblies	11
# relocations	11
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	1
# misassembled contigs	7
Misassembled contigs length	569905
# local misassemblies	16
# mismatches	3175
# indels	454
# short indels	440
# long indels	14
Indels length	878

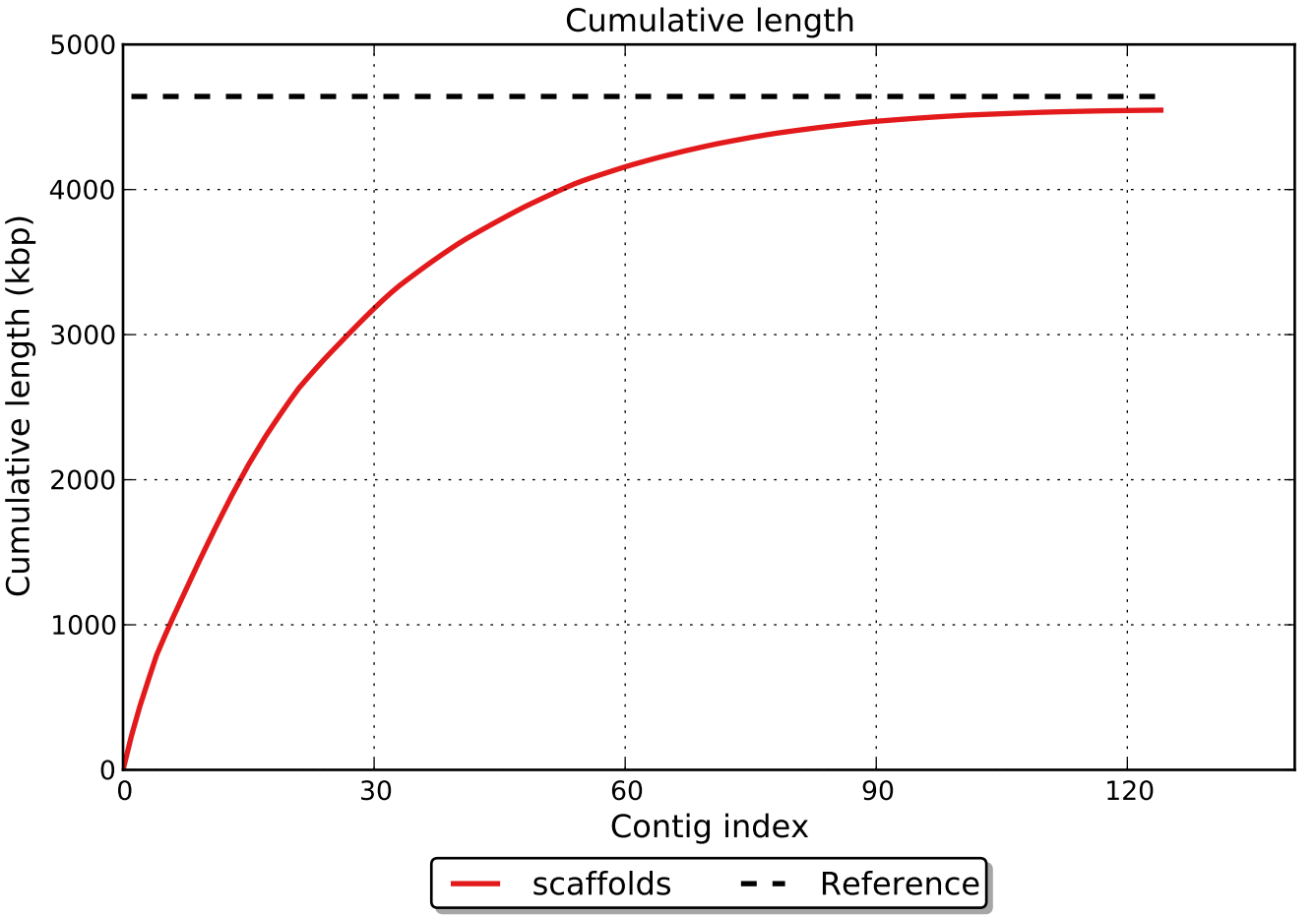
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

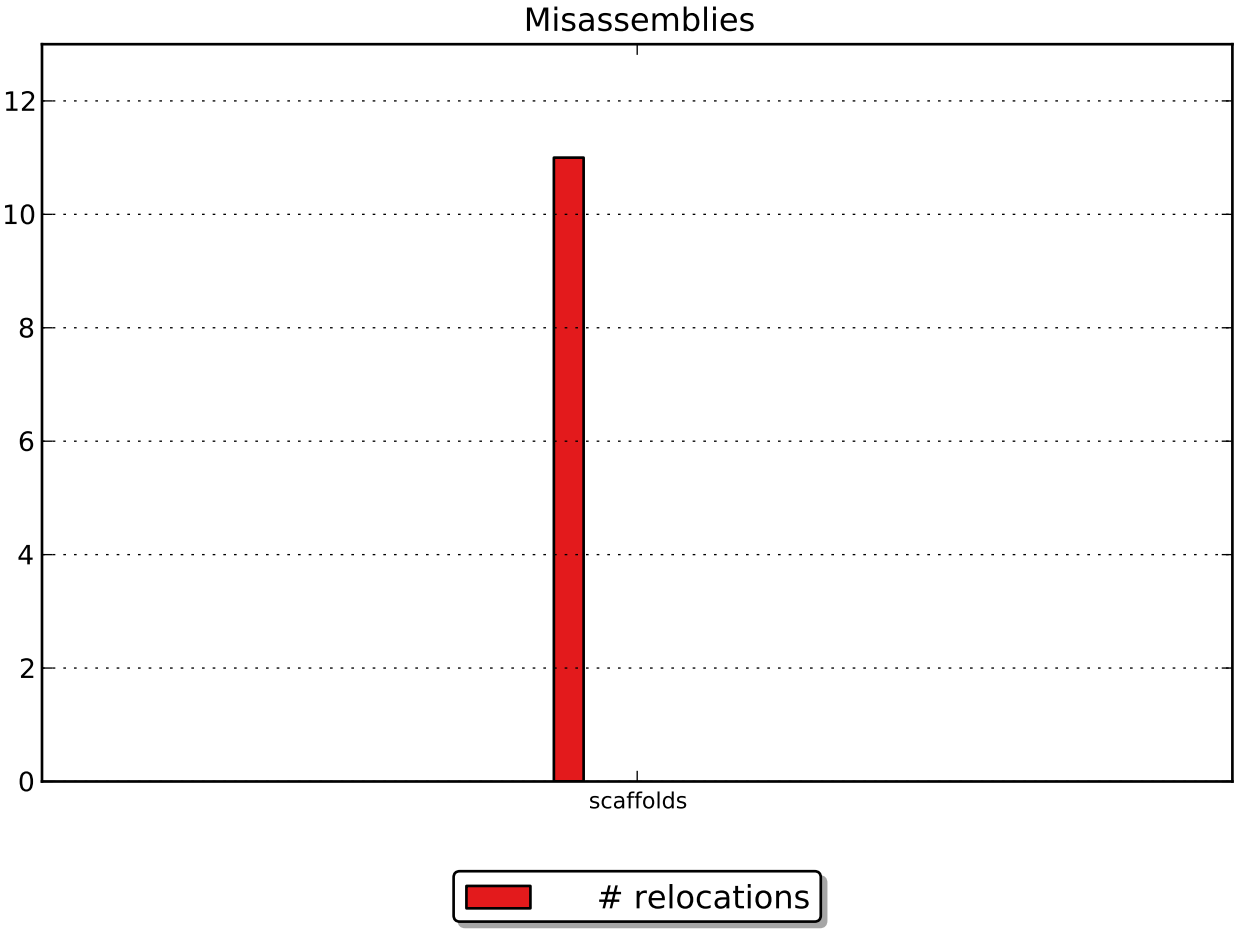
Unaligned report

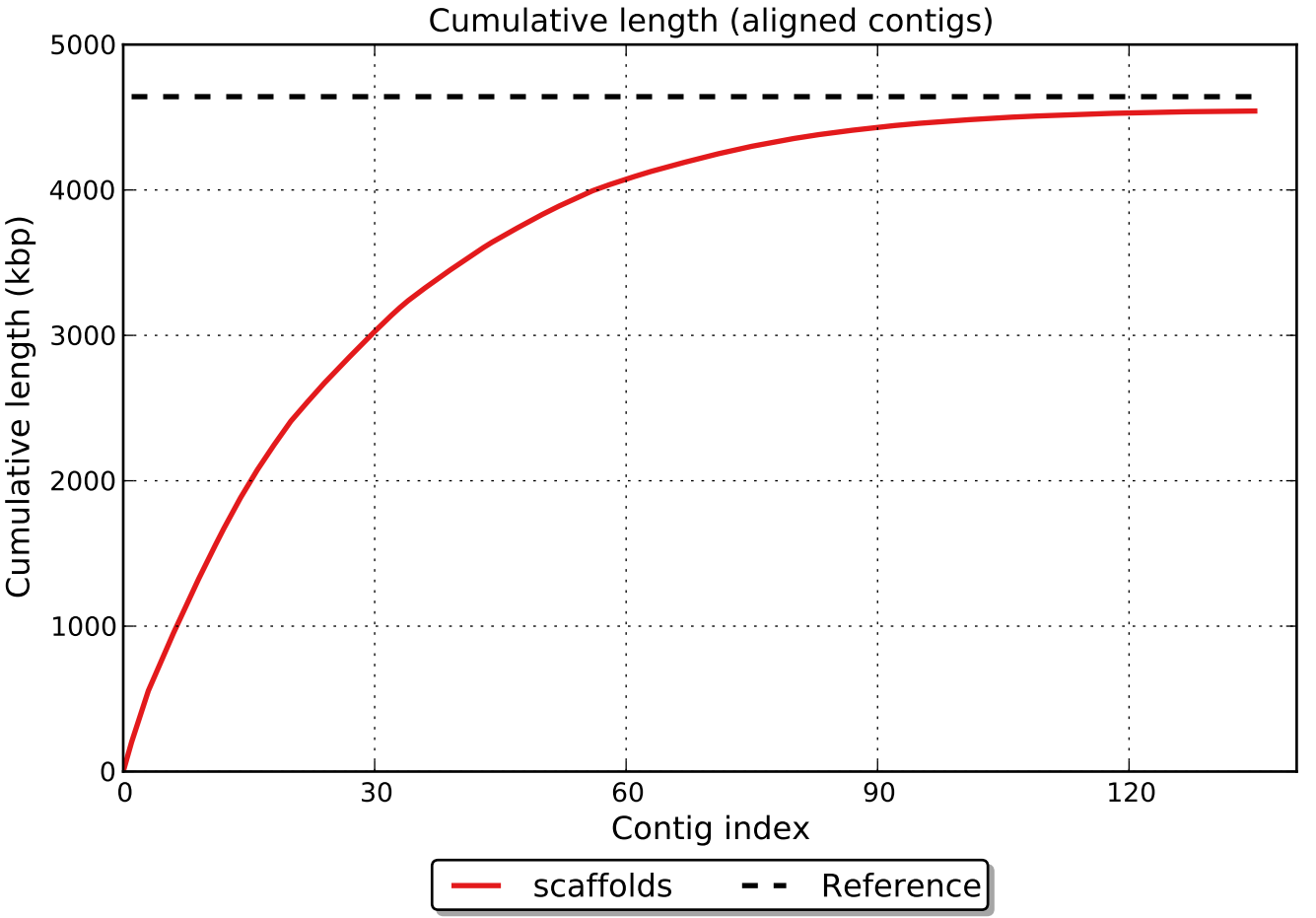
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	3863
# N's	542

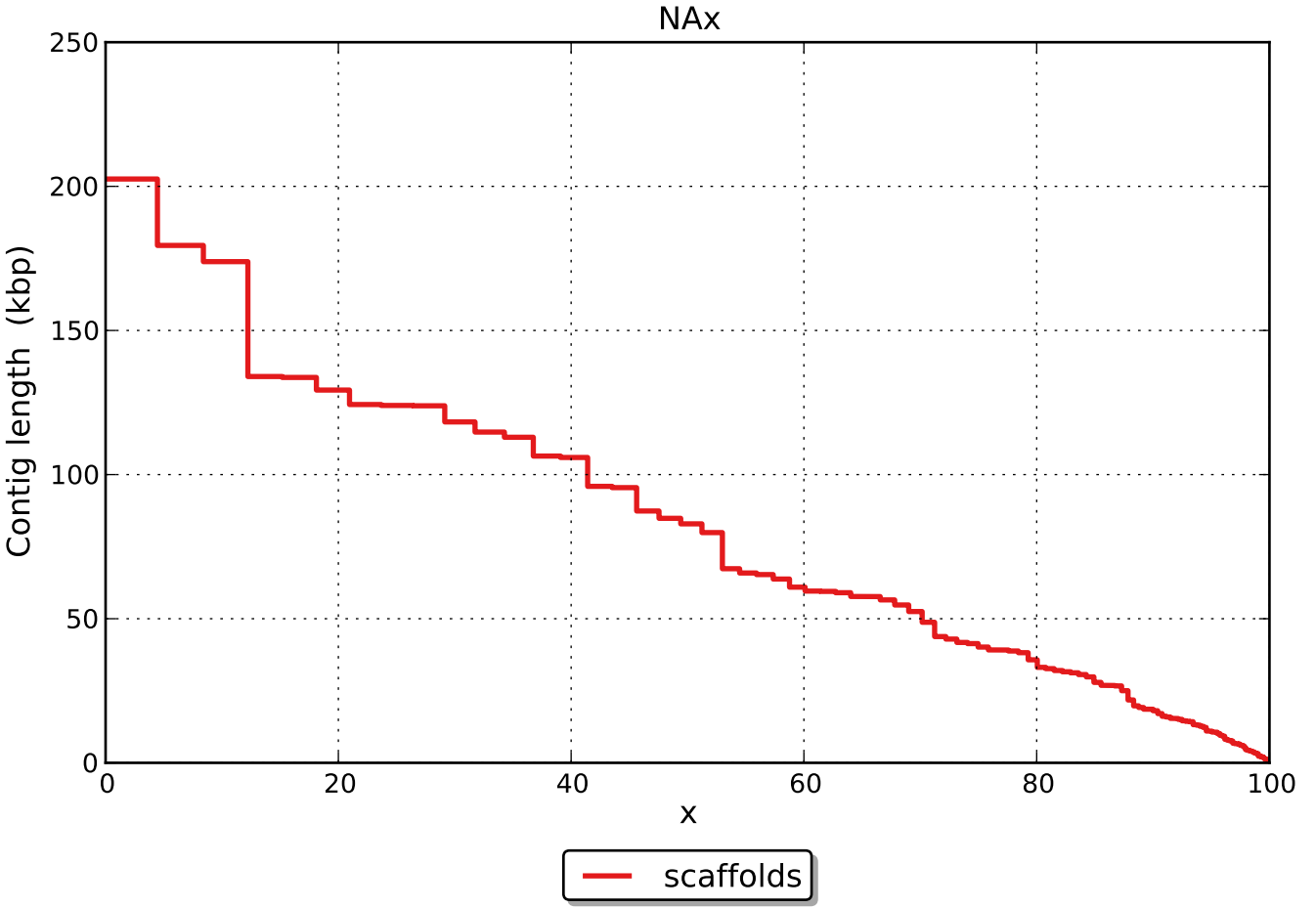
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
scaffolds


Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
Contig index
scaffolds
Reference


Misassemblies
12
10
8
6
4
2
0
scaffolds
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
scaffolds