Report

	scaffolds
# contigs (>= 0 bp)	137
# contigs (>= 1000 bp)	78
# contigs (>= 5000 bp)	66
# contigs (>= 10000 bp)	62
# contigs (>= 25000 bp)	55
# contigs (>= 50000 bp)	41
Total length (>= 0 bp)	9157004
Total length (>= 1000 bp)	9135989
Total length (>= 5000 bp)	9112641
Total length (>= 10000 bp)	9079171
Total length (>= 25000 bp)	8963305
Total length (>= 50000 bp)	8497357
# contigs	89
Largest contig	657825
Total length	9144127
Reference length	9283304
N50	315111
N75	131793
L50	11
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36823
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.555
Duplication ratio	1.000
# N's per 100 kbp	0.84
# mismatches per 100 kbp	192.12
# indels per 100 kbp	0.68
Largest alignment	657825
NA50	315111
NA75	131793
LA50	11
LA75	24

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

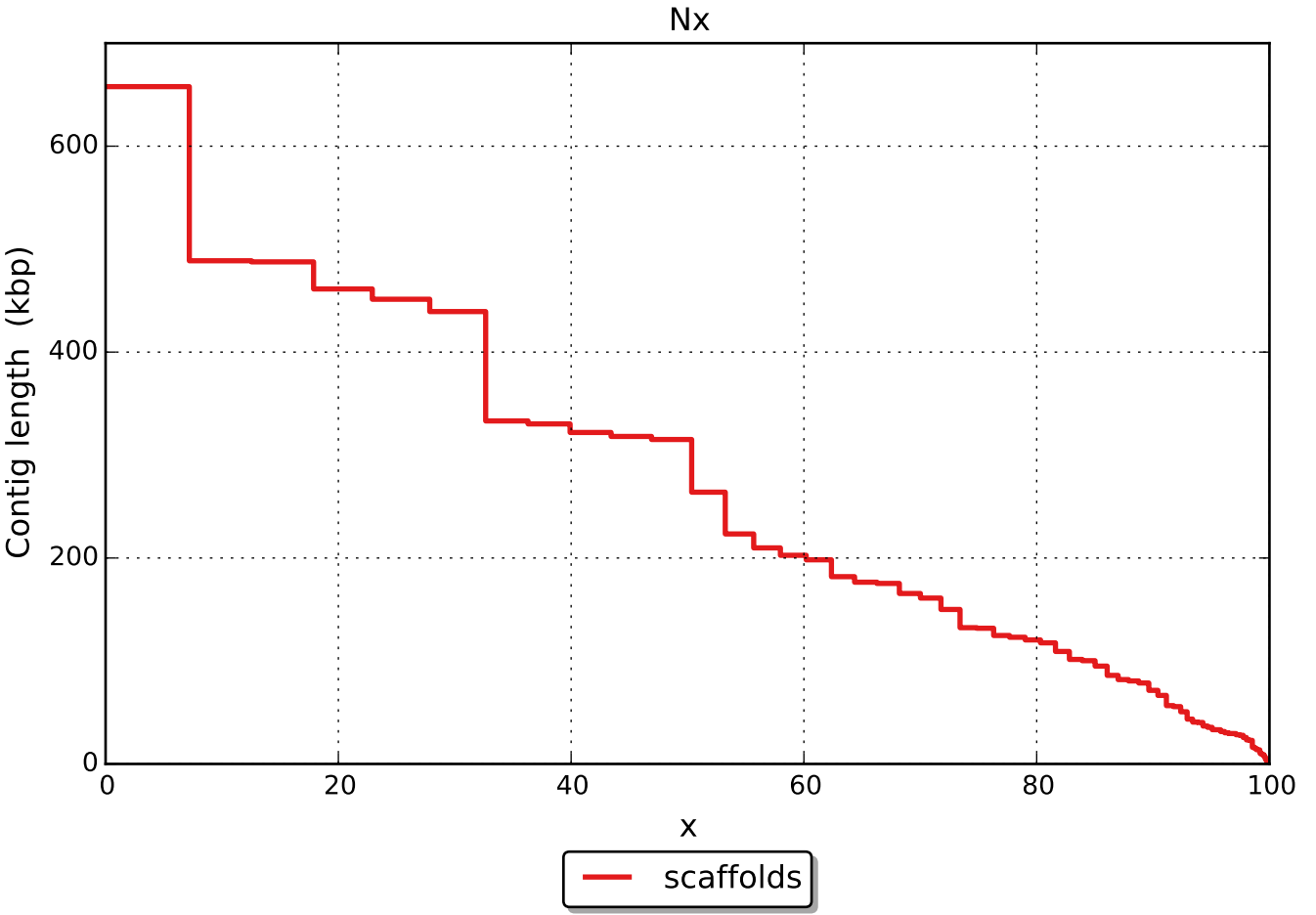
	scaffolds
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36823
# local misassemblies	1
# mismatches	17577
# indels	62
# short indels	61
# long indels	1
Indels length	131

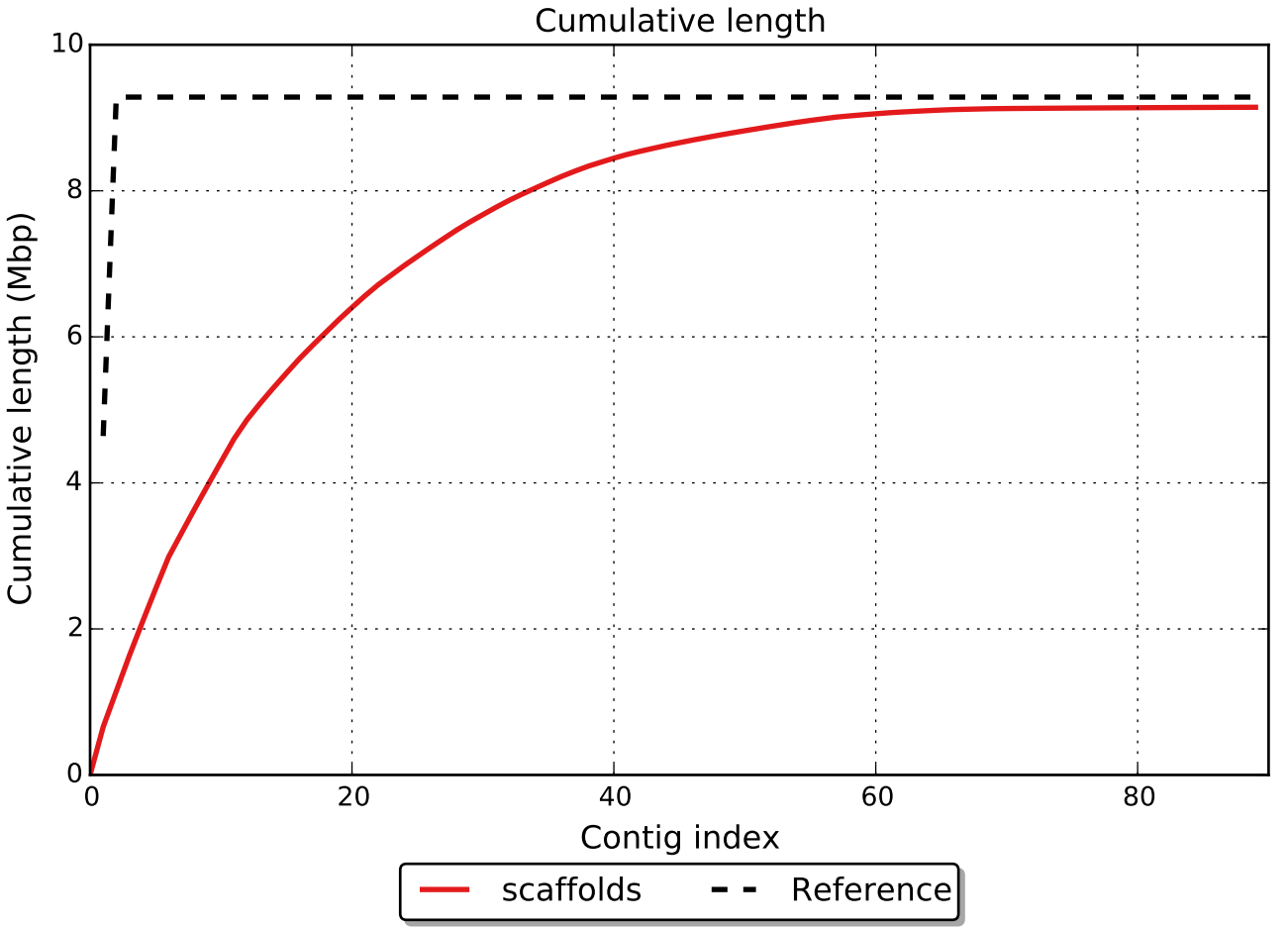
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

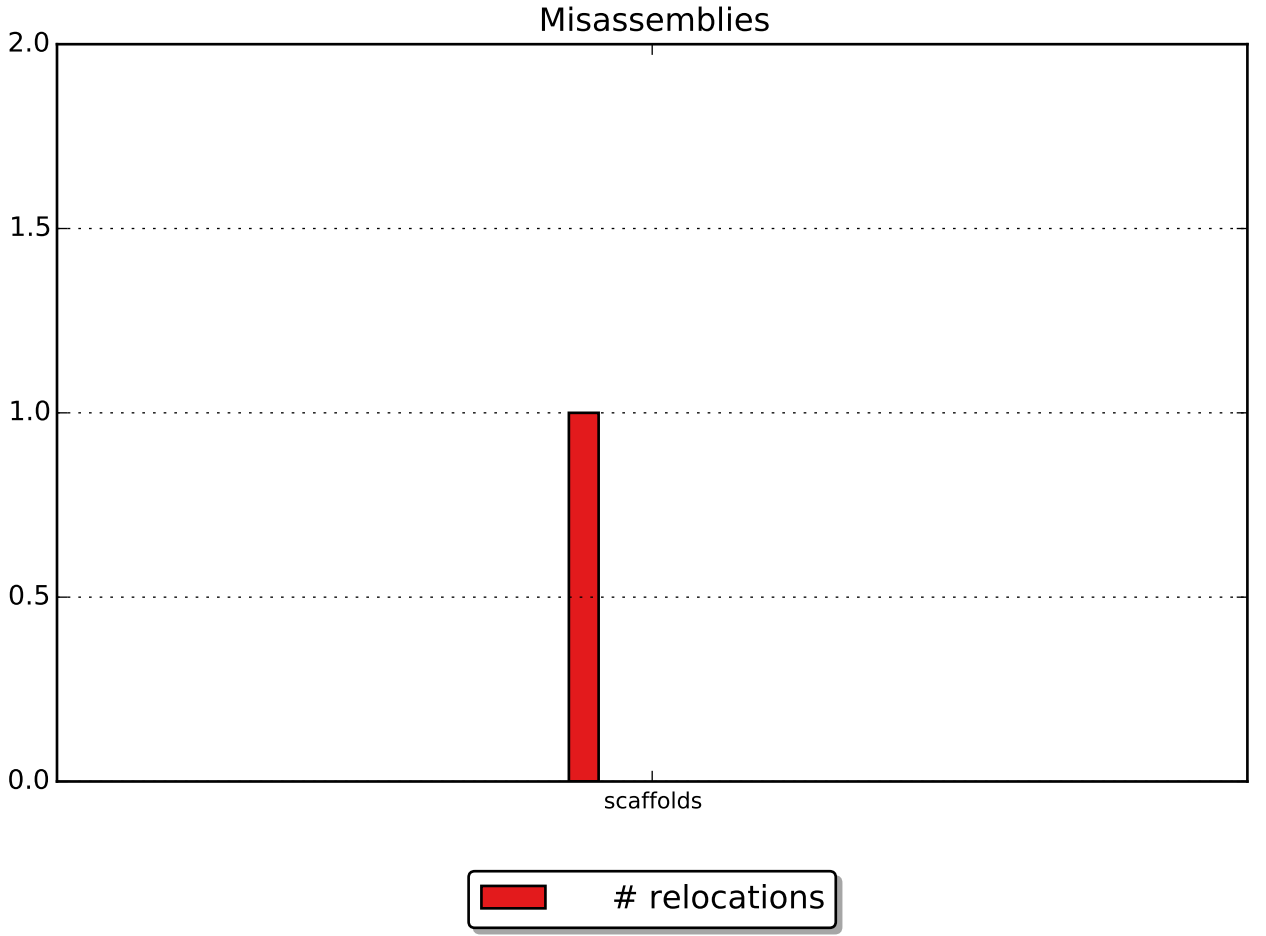
Unaligned report

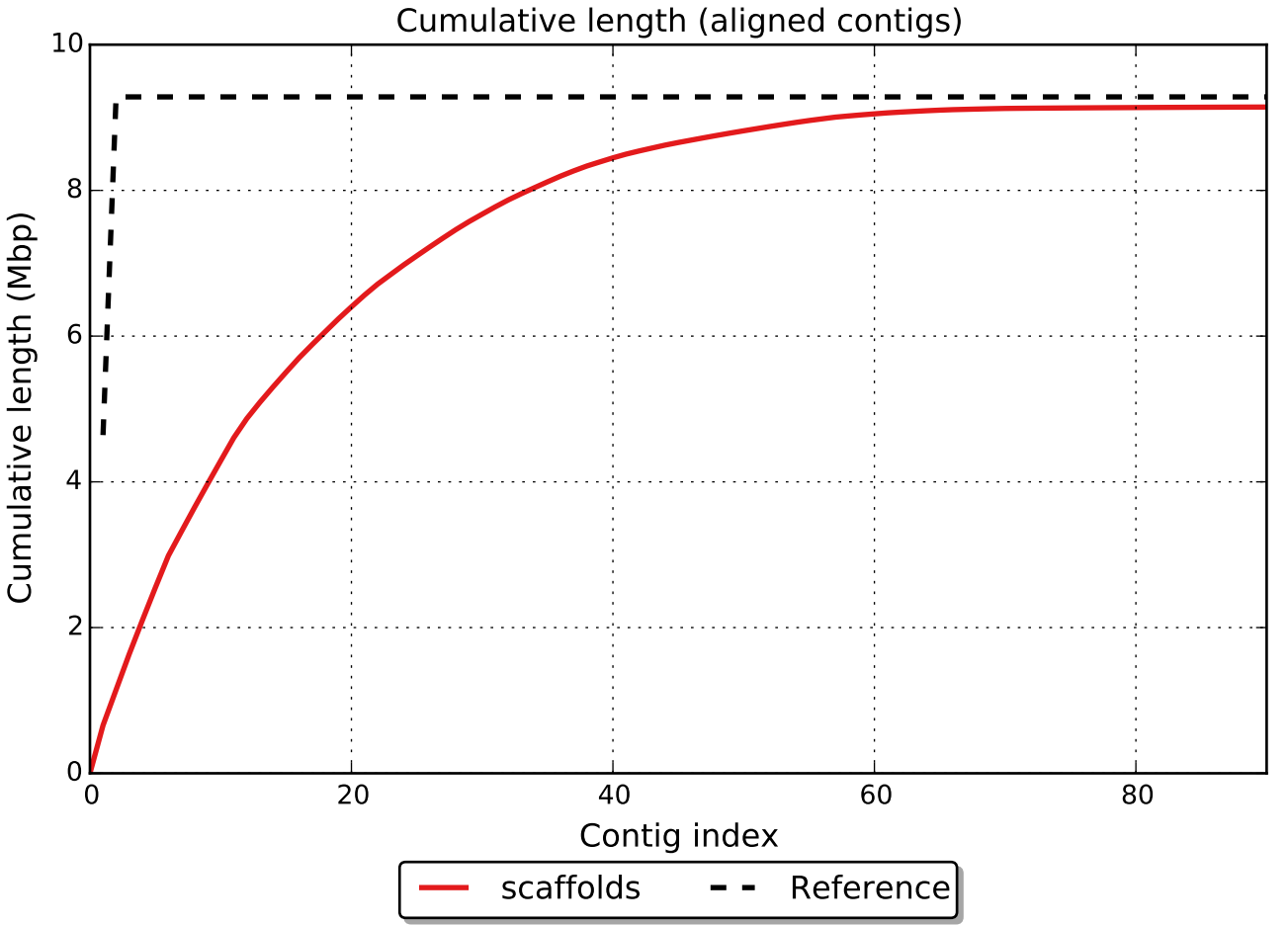
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	77

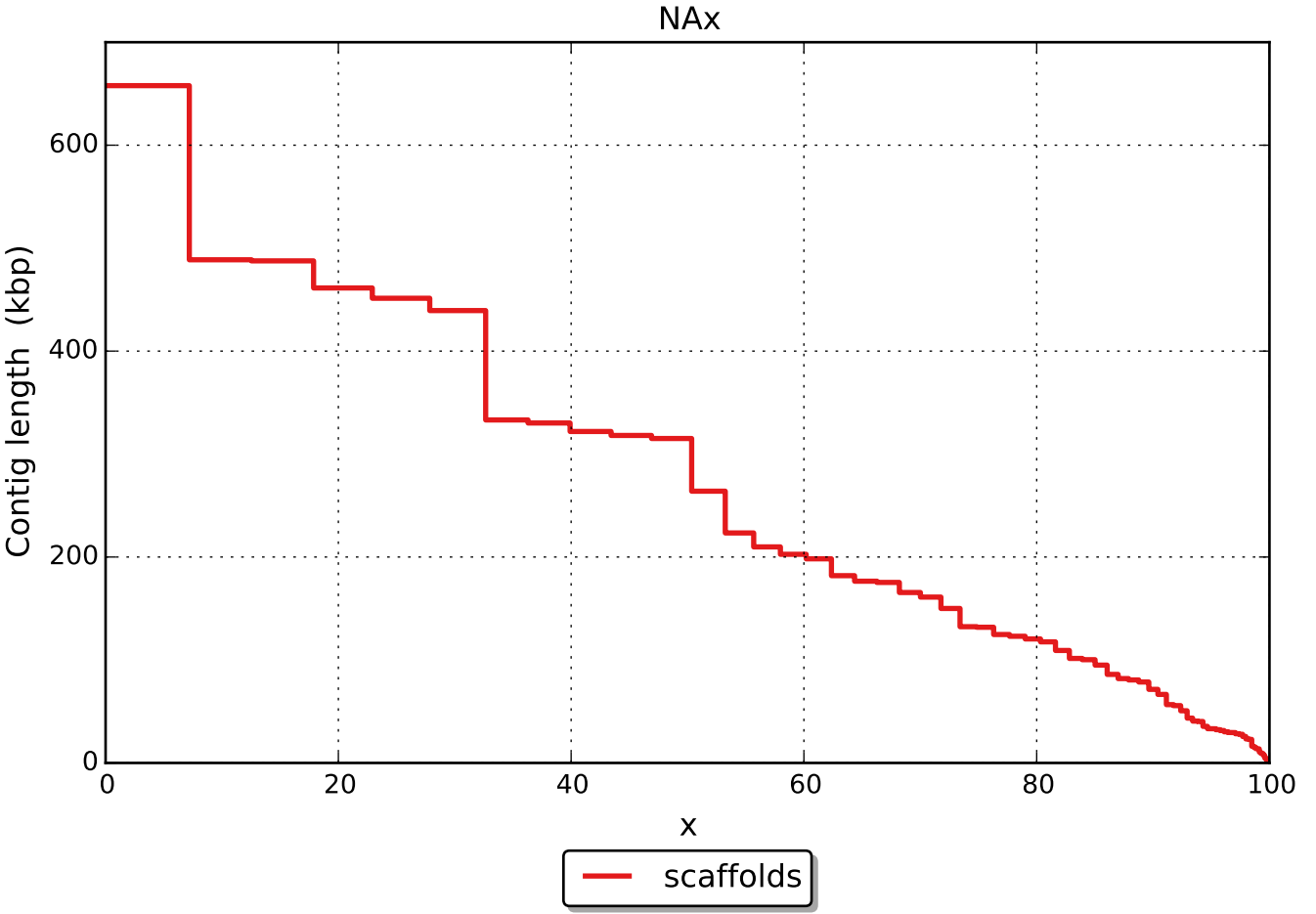
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


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


Cumulative length
Cumulative length (Mbp)
10
8
6
4
2
0
0
20
40
60
80
Contig index
scaffolds
Reference


Misassemblies
2.0
1.5
1.0
0.5
0.0
scaffolds
relocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
2
4
6
8
10
0
20
40
60
80
Contig index
scaffolds
Reference


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