Report

	scaffolds
# contigs (>= 0 bp)	1110
# contigs (>= 1000 bp)	297
# contigs (>= 5000 bp)	209
# contigs (>= 10000 bp)	155
# contigs (>= 25000 bp)	82
# contigs (>= 50000 bp)	42
Total length (>= 0 bp)	7356224
Total length (>= 1000 bp)	7060857
Total length (>= 5000 bp)	6844889
Total length (>= 10000 bp)	6443865
Total length (>= 25000 bp)	5259063
Total length (>= 50000 bp)	3855778
# contigs	352
Largest contig	200996
Total length	7094731
Reference length	9283304
N50	54145
N75	24817
L50	37
L75	85
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	127194
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.594
Duplication ratio	1.167
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1109.80
# indels per 100 kbp	0.68
Largest alignment	200996
NA50	52872
NA75	24195
LA50	37
LA75	86

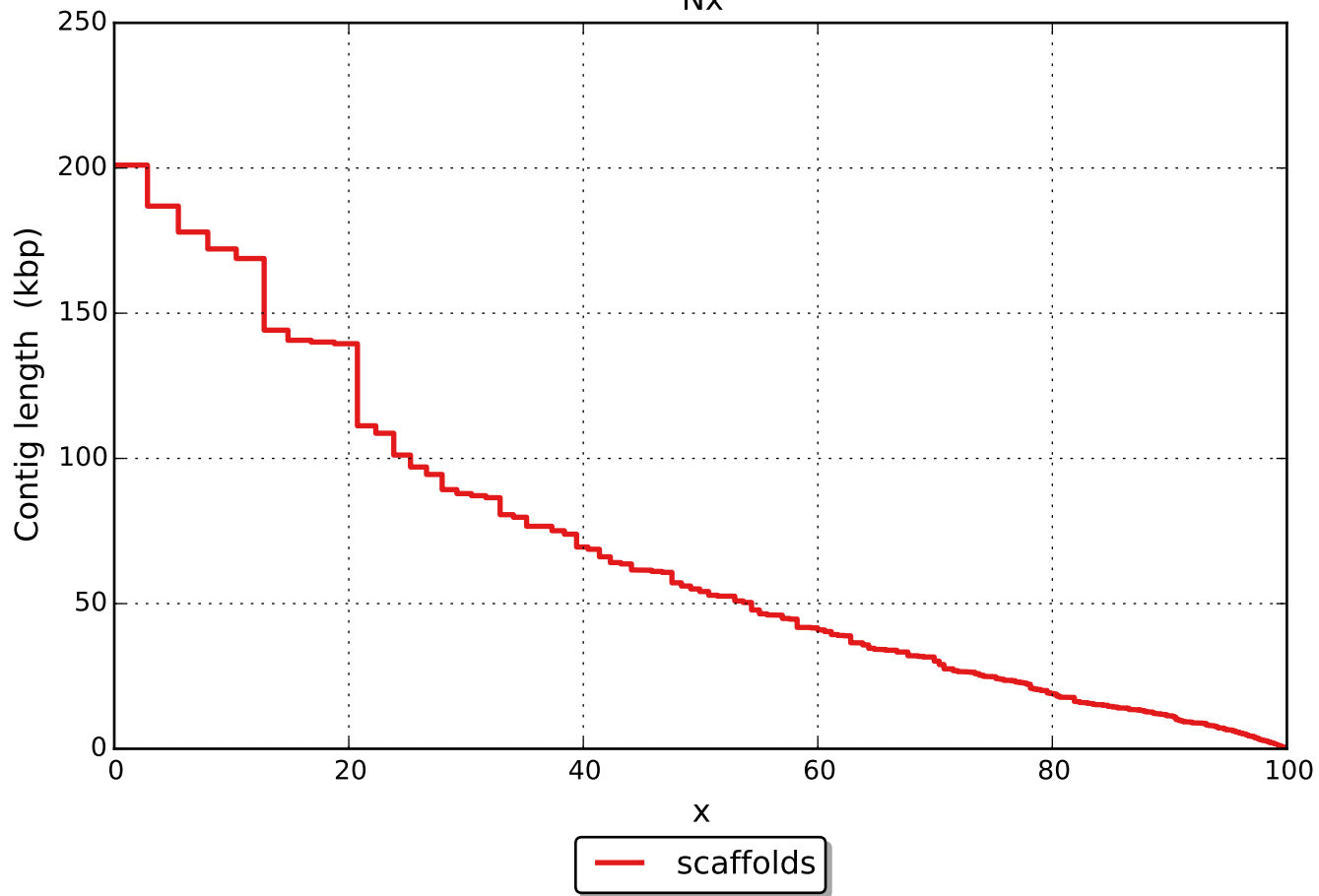All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	scaffolds
# misassemblies	2
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	127194
# local misassemblies	4
# mismatches	90244
# indels	55
# short indels	55
# long indels	0
Indels length	61

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).
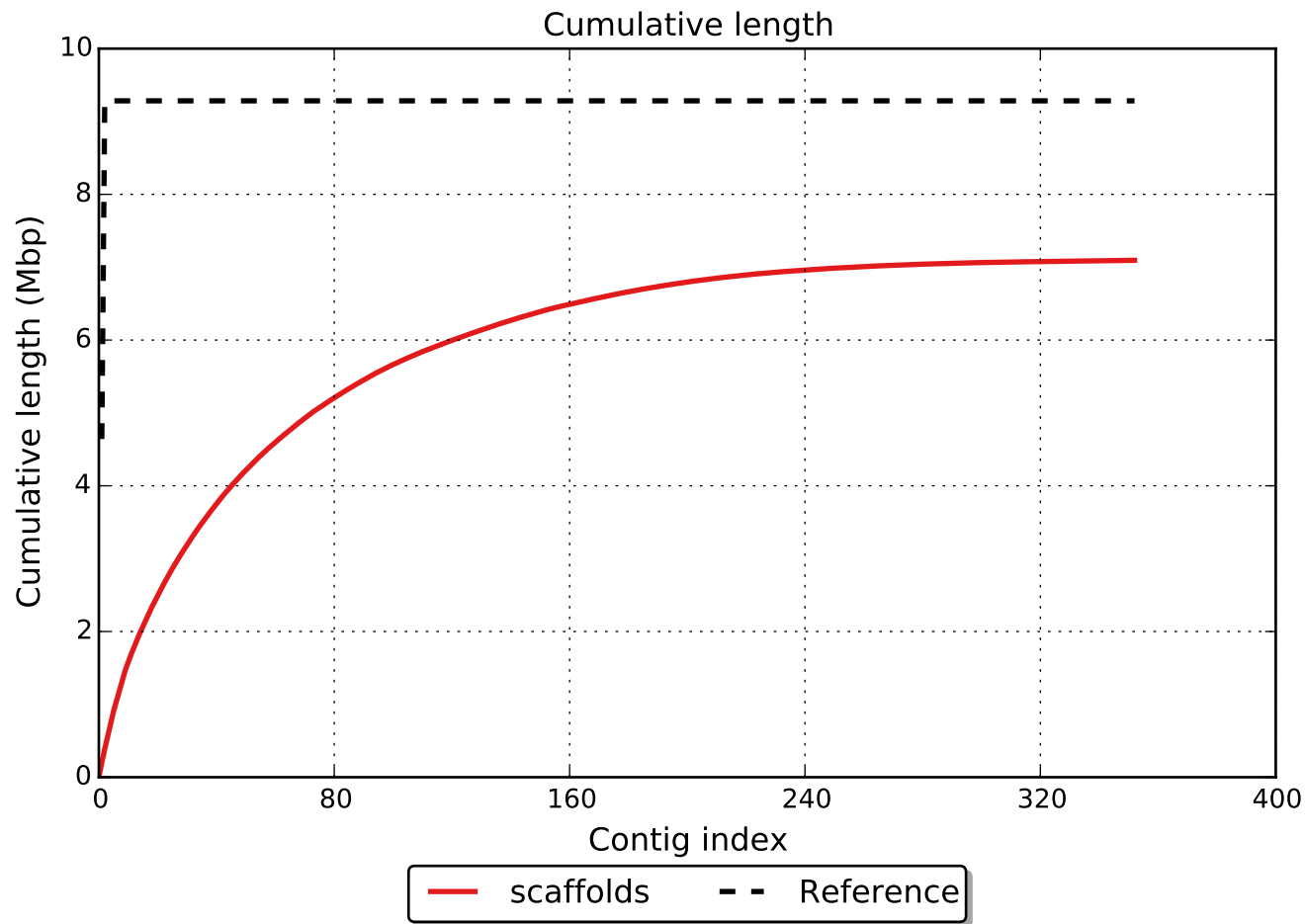
Unaligned report

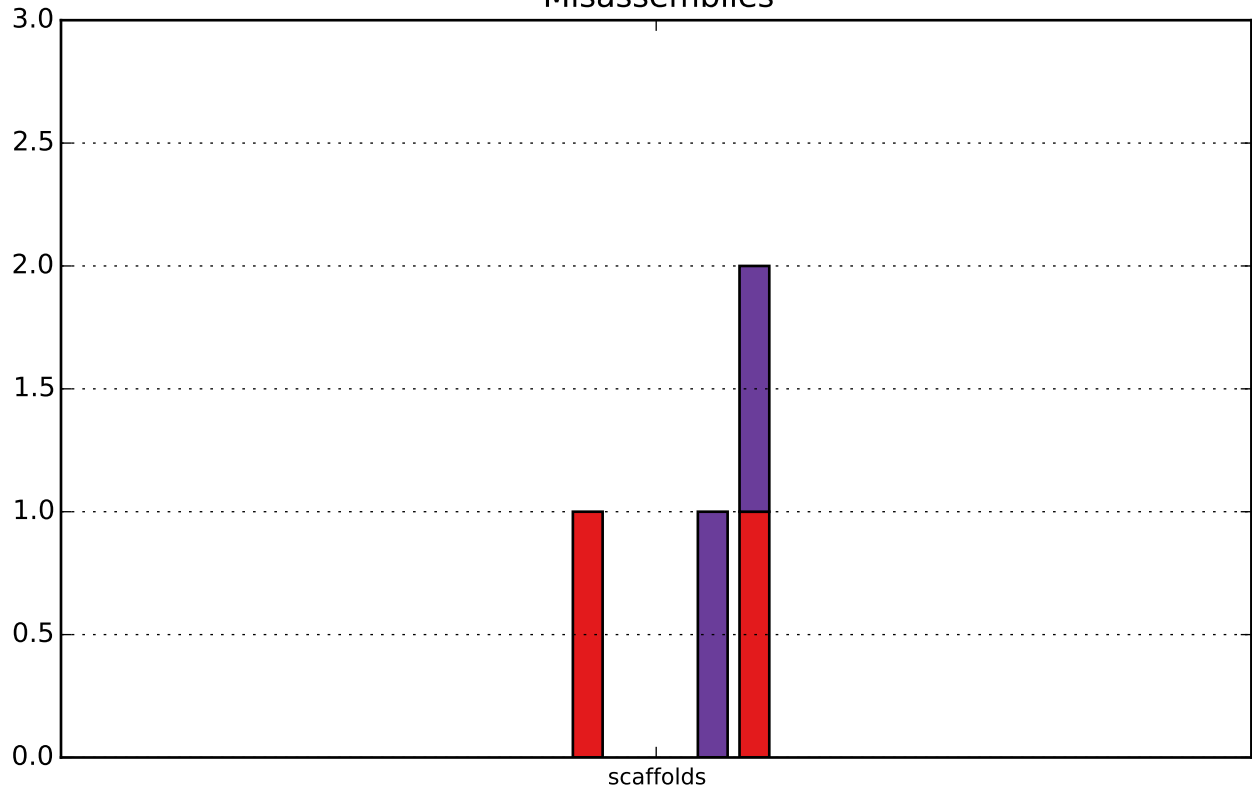|	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

Cumulative length
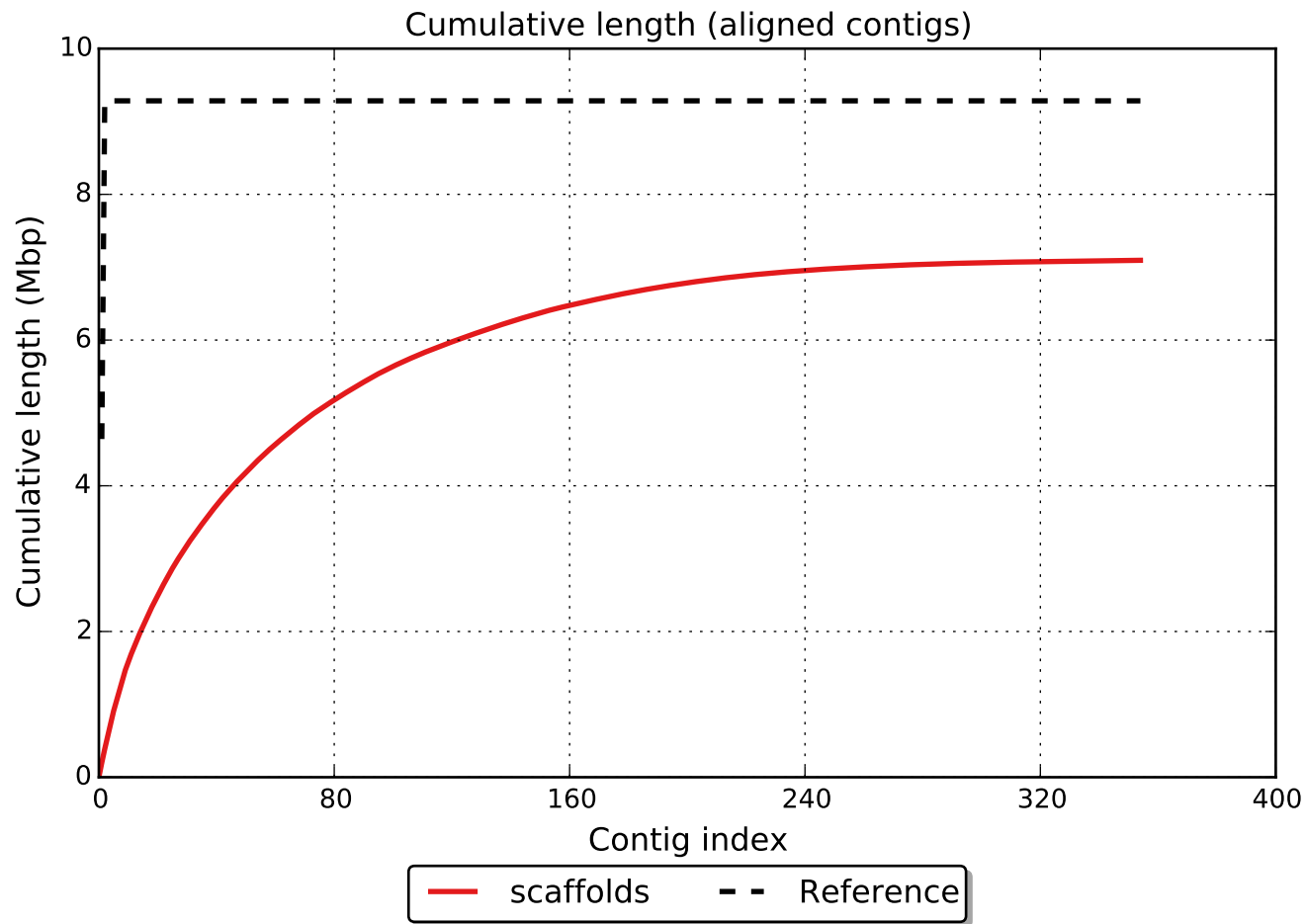
Misassemblies

scaffolds

■ # relocations
■ # interspecies translocations

Cumulative length (aligned contigs)

NAx