Report

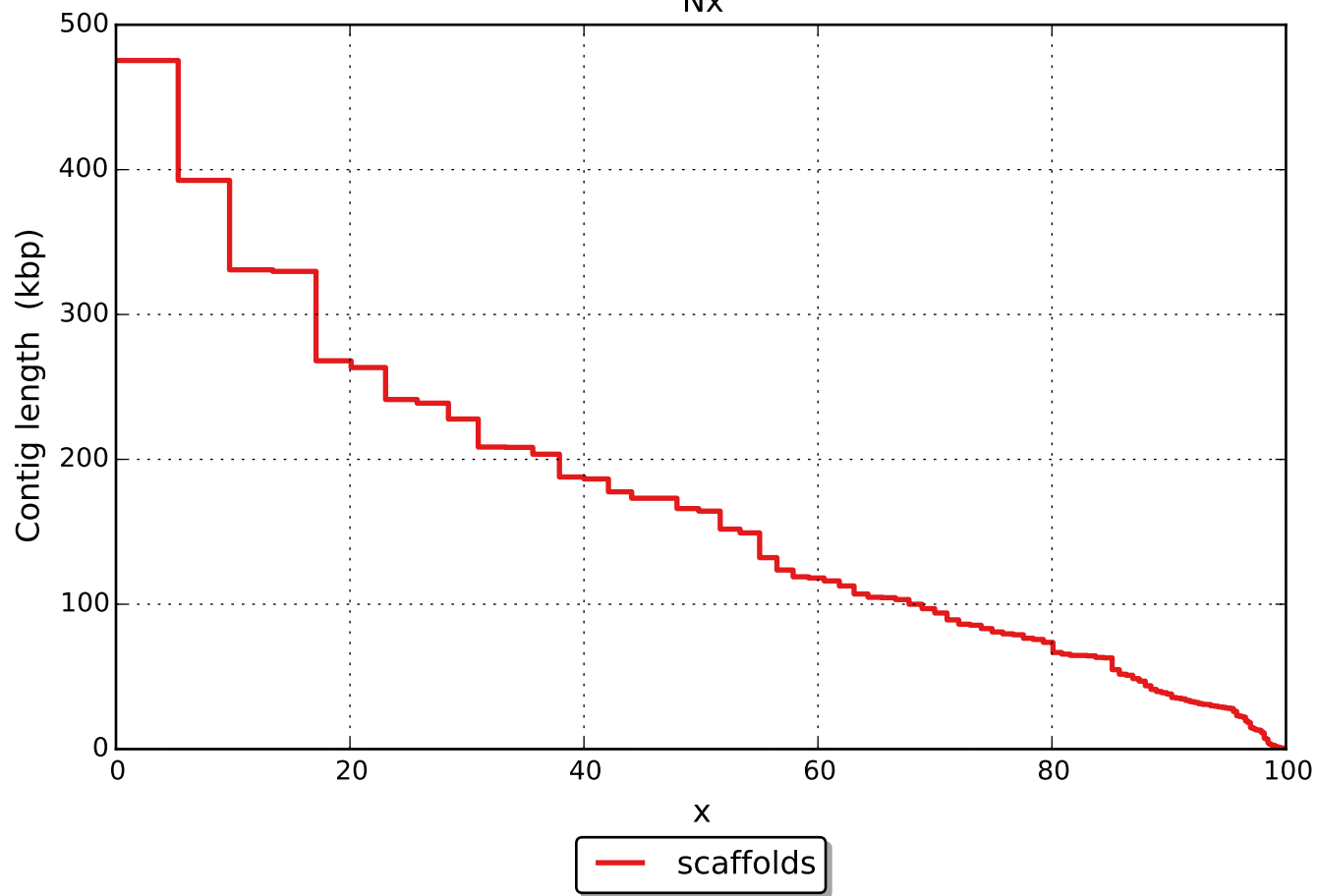|	scaffolds
# contigs (>= 0 bp)	408
# contigs (>= 1000 bp)	142
# contigs (>= 5000 bp)	94
# contigs (>= 10000 bp)	90
# contigs (>= 25000 bp)	77
# contigs (>= 50000 bp)	54
Total length (>= 0 bp)	9004717
Total length (>= 1000 bp)	8899397
Total length (>= 5000 bp)	8801812
Total length (>= 10000 bp)	8773143
Total length (>= 25000 bp)	8562938
Total length (>= 50000 bp)	7768873
# contigs	203
Largest contig	475325
Total length	8939282
Reference length	9283304
N50	164261
N75	80872
L50	19
L75	39
# misassemblies	229
# misassembled contigs	40
Misassembled contigs length	4147330
# local misassemblies	7
# unaligned contigs	32 + 1 part
Unaligned length	21165
Genome fraction (%)	49.301
Duplication ratio	1.949
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1155.02
# indels per 100 kbp	1.20
Largest alignment	475325
NA50	64354
NA75	23720
LA50	31
LA75	91

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	229
# relocations	203
# translocations	0
# inversions	22
# interspecies translocations	4
# possibly misassembled contigs	3
# misassembled contigs	40
Misassembled contigs length	4147330
# local misassemblies	7
# mismatches	52862
# indels	55
# short indels	53
# long indels	2
Indels length	68

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
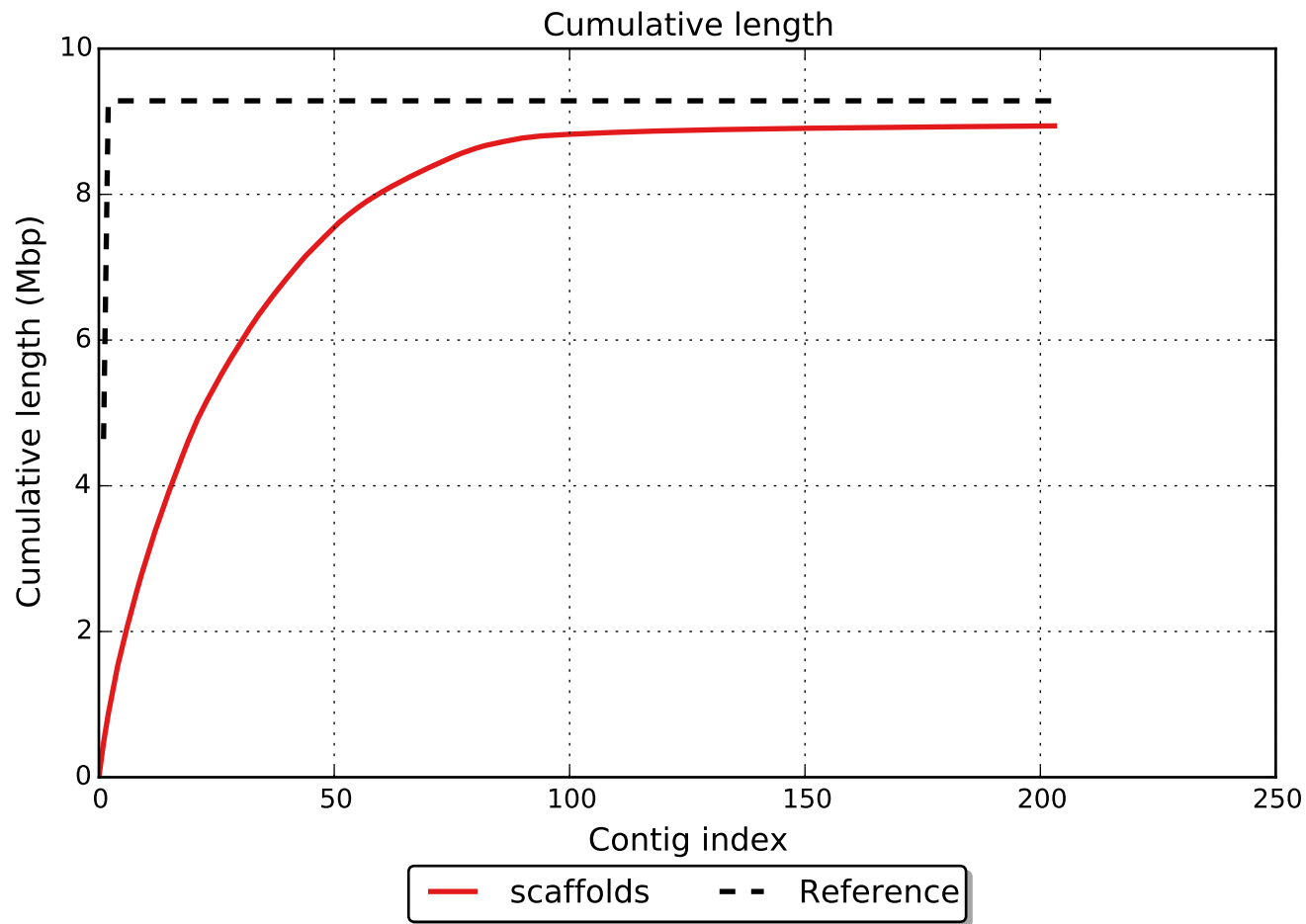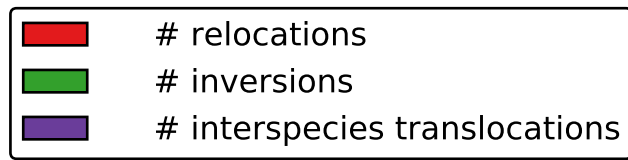
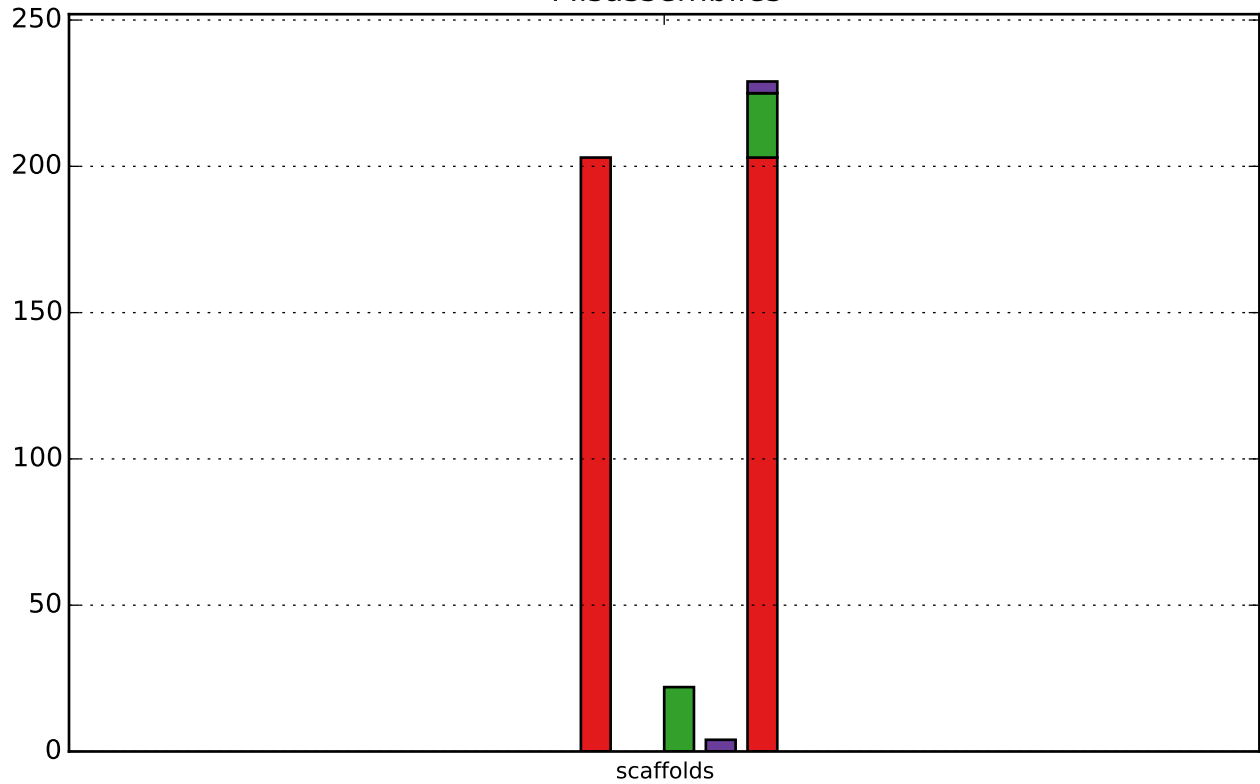|	scaffolds
# fully unaligned contigs	32
Fully unaligned length	20718
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	447
# N's	0

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

Cumulative length
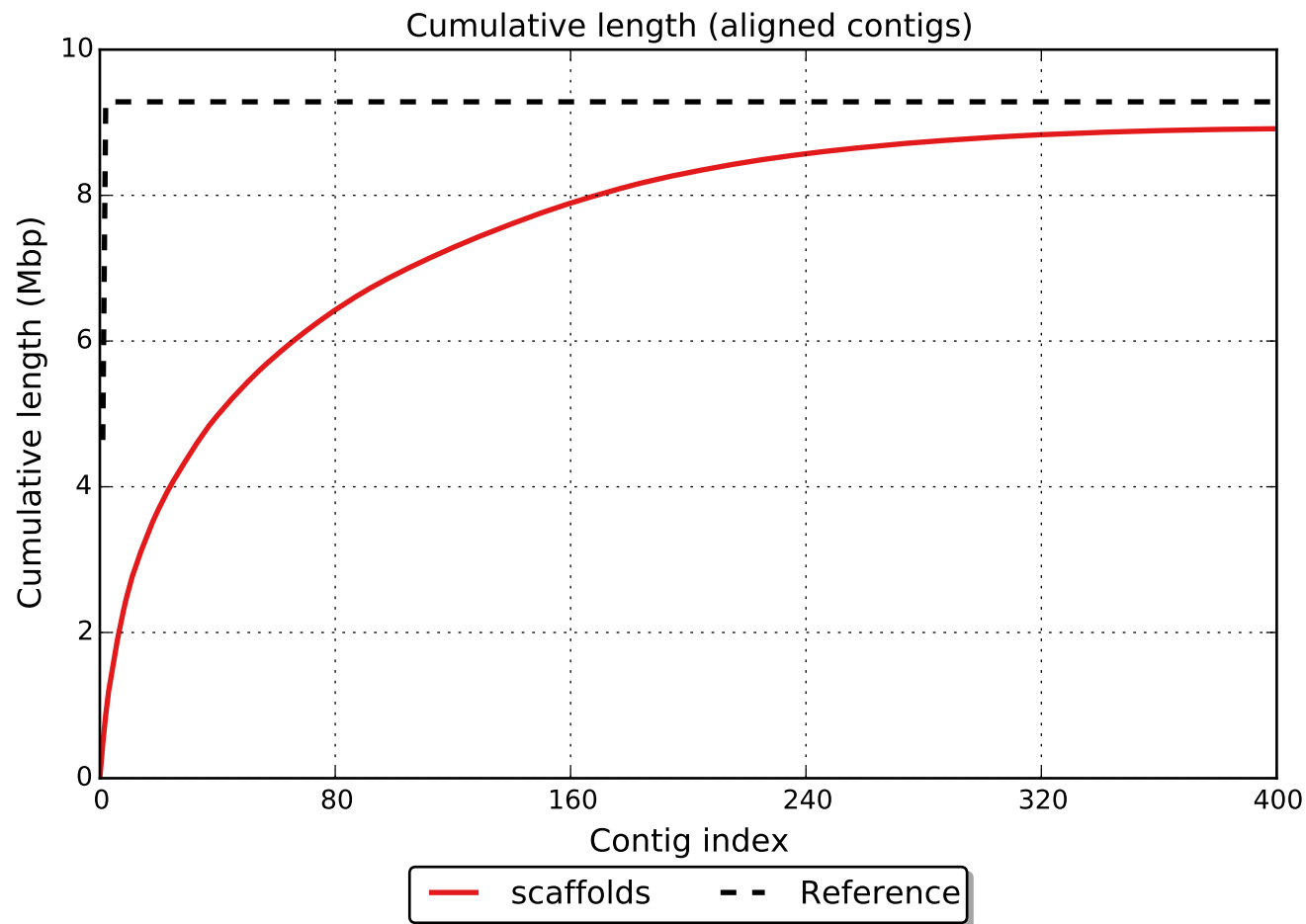
Misassemblies

scaffolds

- # relocations
- # inversions
- # interspecies translocations

Cumulative length (aligned contigs)