Report

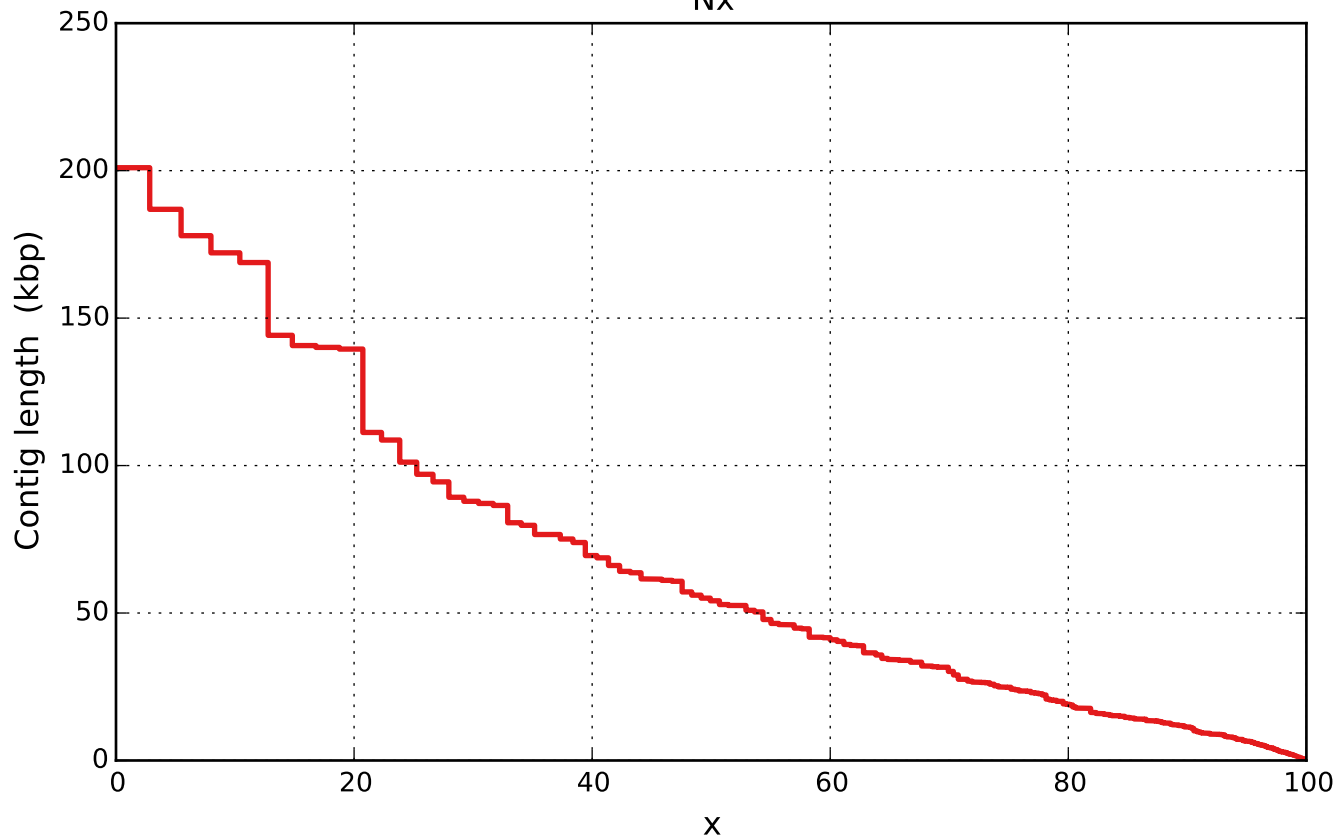|	scaffolds
# contigs (>= 0 bp)	1110
# contigs (>= 1000 bp)	297
# contigs (>= 5000 bp)	209
# contigs (>= 10000 bp)	155
# contigs (>= 25000 bp)	82
# contigs (>= 50000 bp)	42
Total length (>= 0 bp)	7356224
Total length (>= 1000 bp)	7060857
Total length (>= 5000 bp)	6844889
Total length (>= 10000 bp)	6443865
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	115
# misassembled contigs	42
Misassembled contigs length	2166860
# local misassemblies	4
# unaligned contigs	21 + 4 part
Unaligned length	12653
Genome fraction (%)	49.320
Duplication ratio	1.550
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1205.08
# indels per 100 kbp	0.96
Largest alignment	200996
NA50	34007
NA75	15950
LA50	53
LA75	128

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	115
# relocations	97
# translocations	0
# inversions	17
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	42
Misassembled contigs length	2166860
# local misassemblies	4
# mismatches	55175
# indels	44
# short indels	44
# long indels	0
Indels length	50

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).
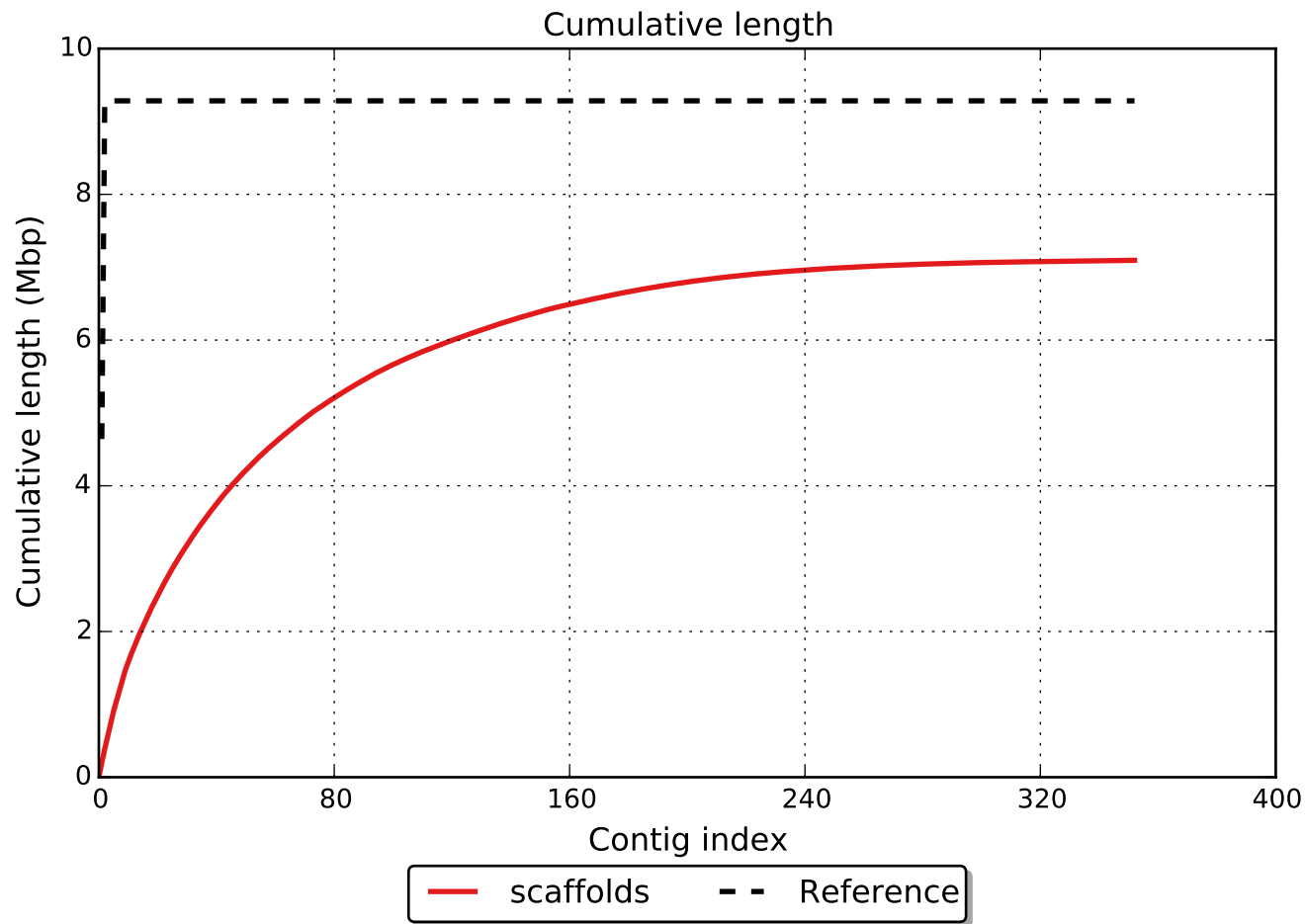
Unaligned report

	scaffolds
# fully unaligned contigs	21
Fully unaligned length	11824
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	829
# 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).
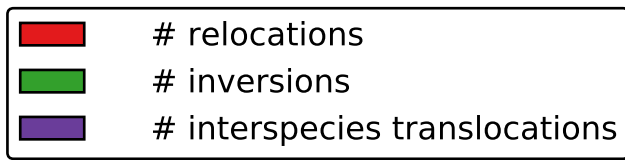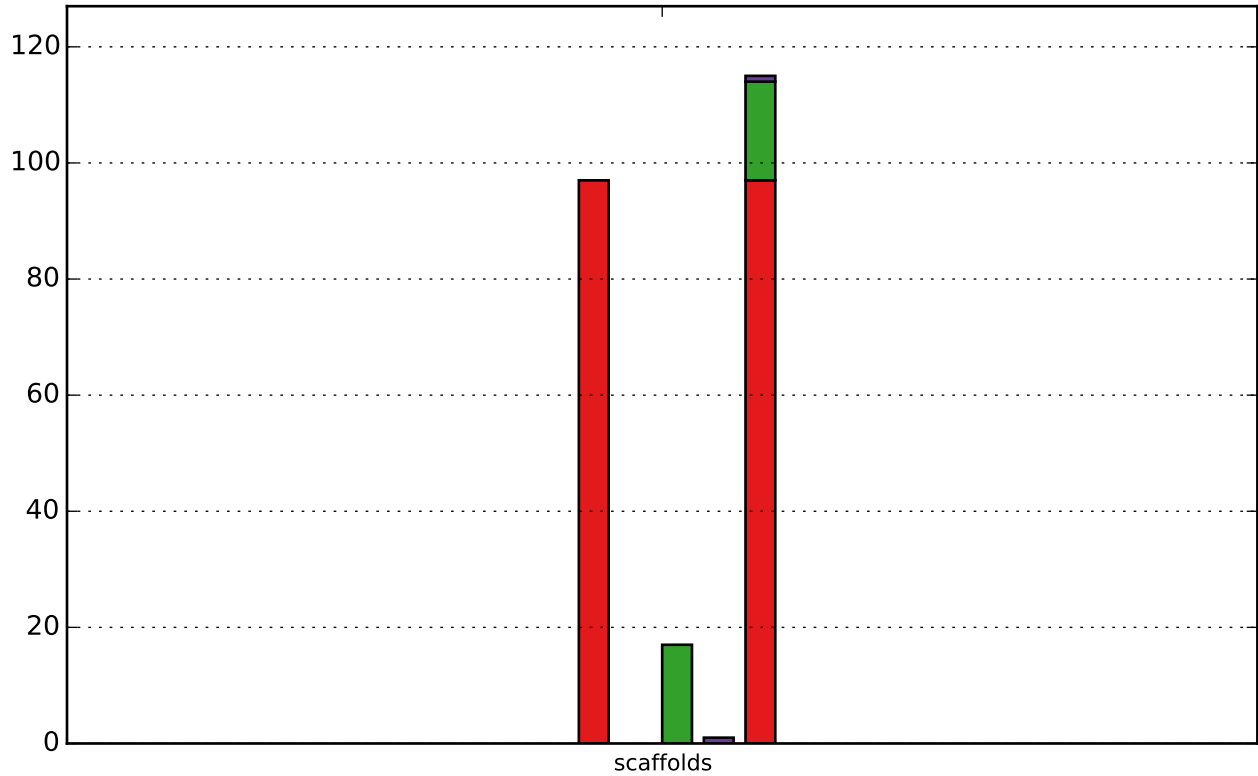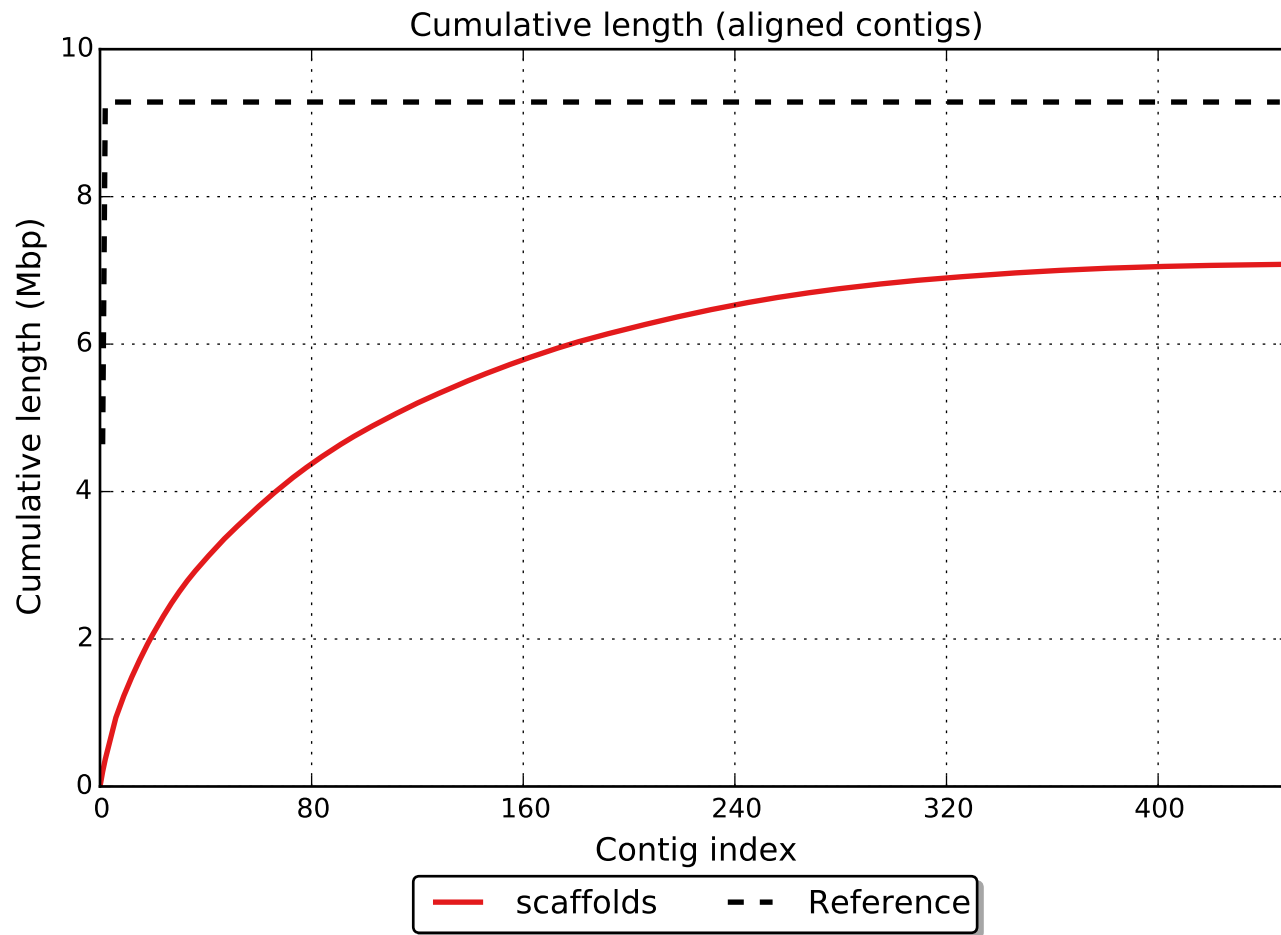
Cumulative length

Misassemblies

Legend:
- # relocations
- # inversions
- # interspecies translocations

Cumulative length (aligned contigs)