Report

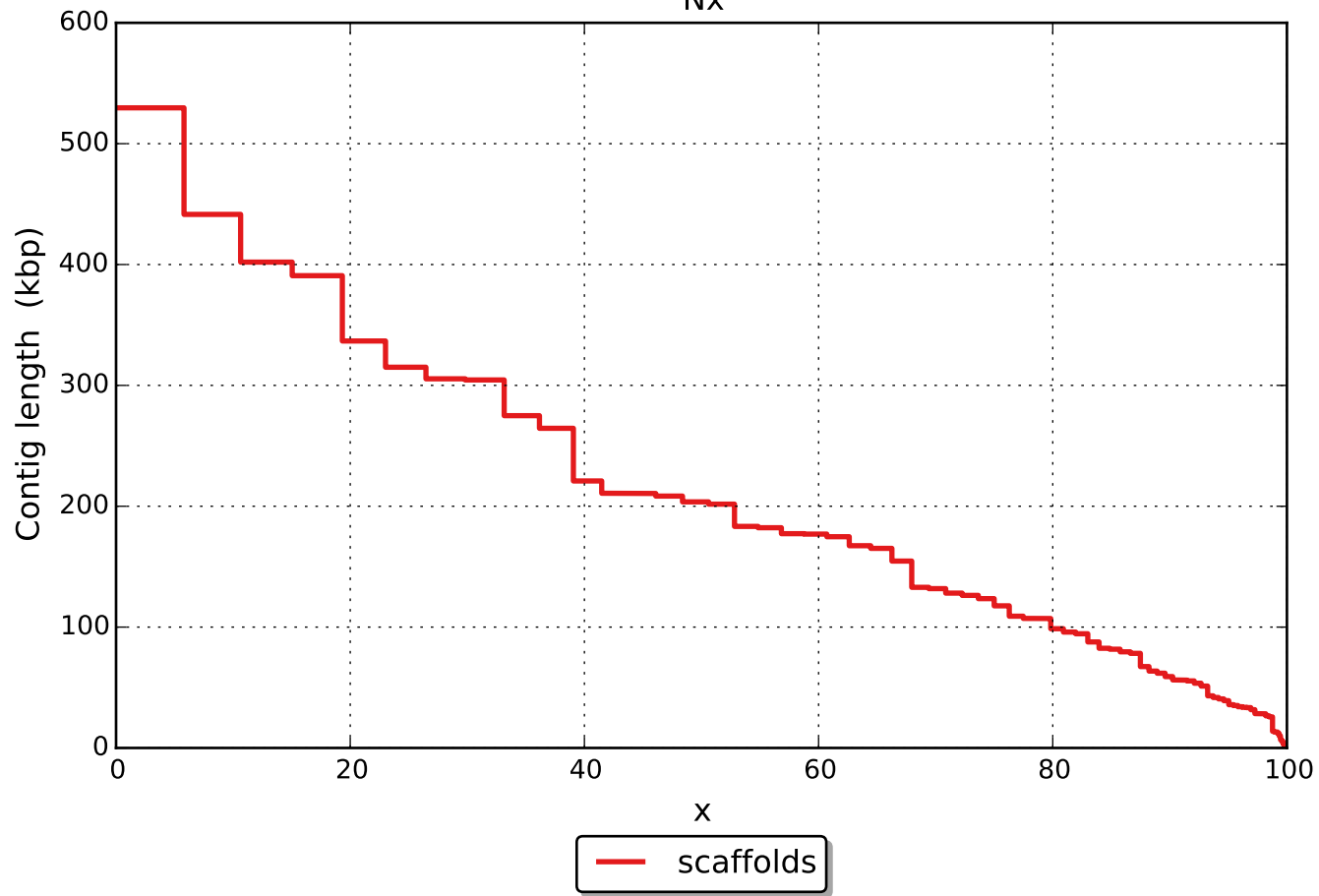|	scaffolds
# contigs (>= 0 bp)	159
# contigs (>= 1000 bp)	86
# contigs (>= 5000 bp)	73
# contigs (>= 10000 bp)	69
# contigs (>= 25000 bp)	65
# contigs (>= 50000 bp)	50
Total length (>= 0 bp)	9142640
Total length (>= 1000 bp)	9118271
Total length (>= 5000 bp)	9095669
Total length (>= 10000 bp)	9067176
Total length (>= 25000 bp)	9015059
Total length (>= 50000 bp)	8509469
# contigs	99
Largest contig	529644
Total length	9127470
Reference length	9283304
N50	203618
N75	117603
L50	15
L75	30
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	648881
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.378
Duplication ratio	1.000
# N's per 100 kbp	0.24
# mismatches per 100 kbp	342.45
# indels per 100 kbp	0.81
Largest alignment	529644
NA50	201734
NA75	109022
LA50	16
LA75	31

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	4
# relocations	3
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	648881
# local misassemblies	3
# mismatches	31275
# indels	74
# short indels	73
# long indels	1
Indels length	101

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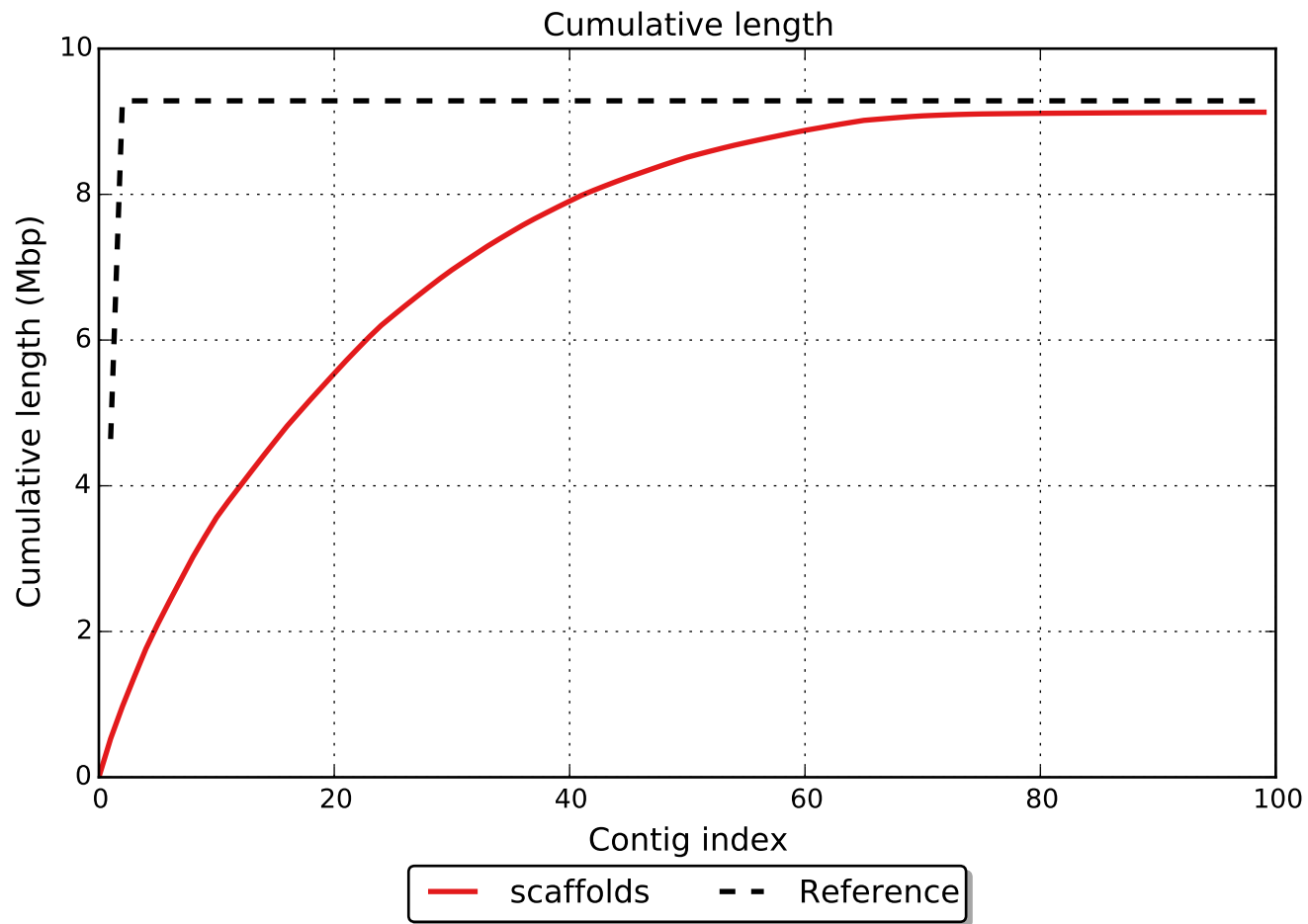(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
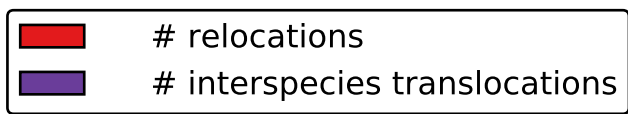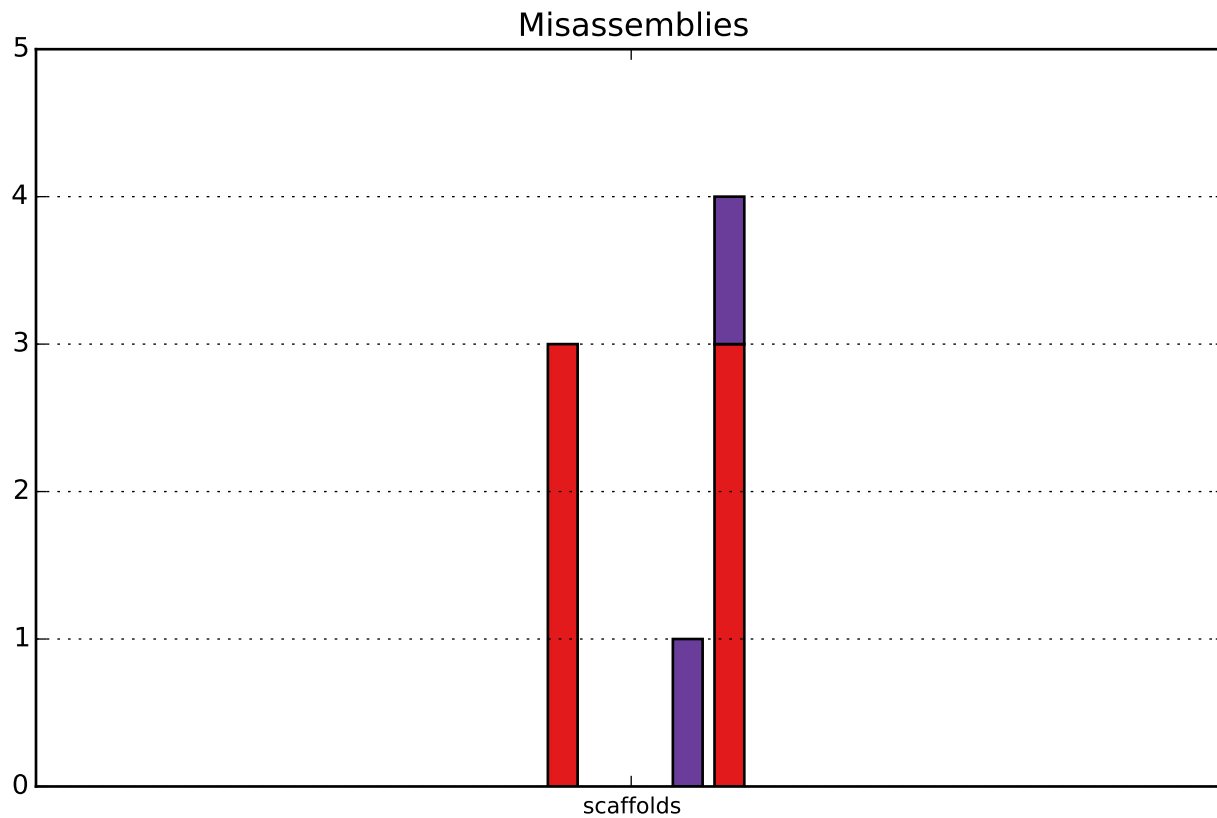
Unaligned report

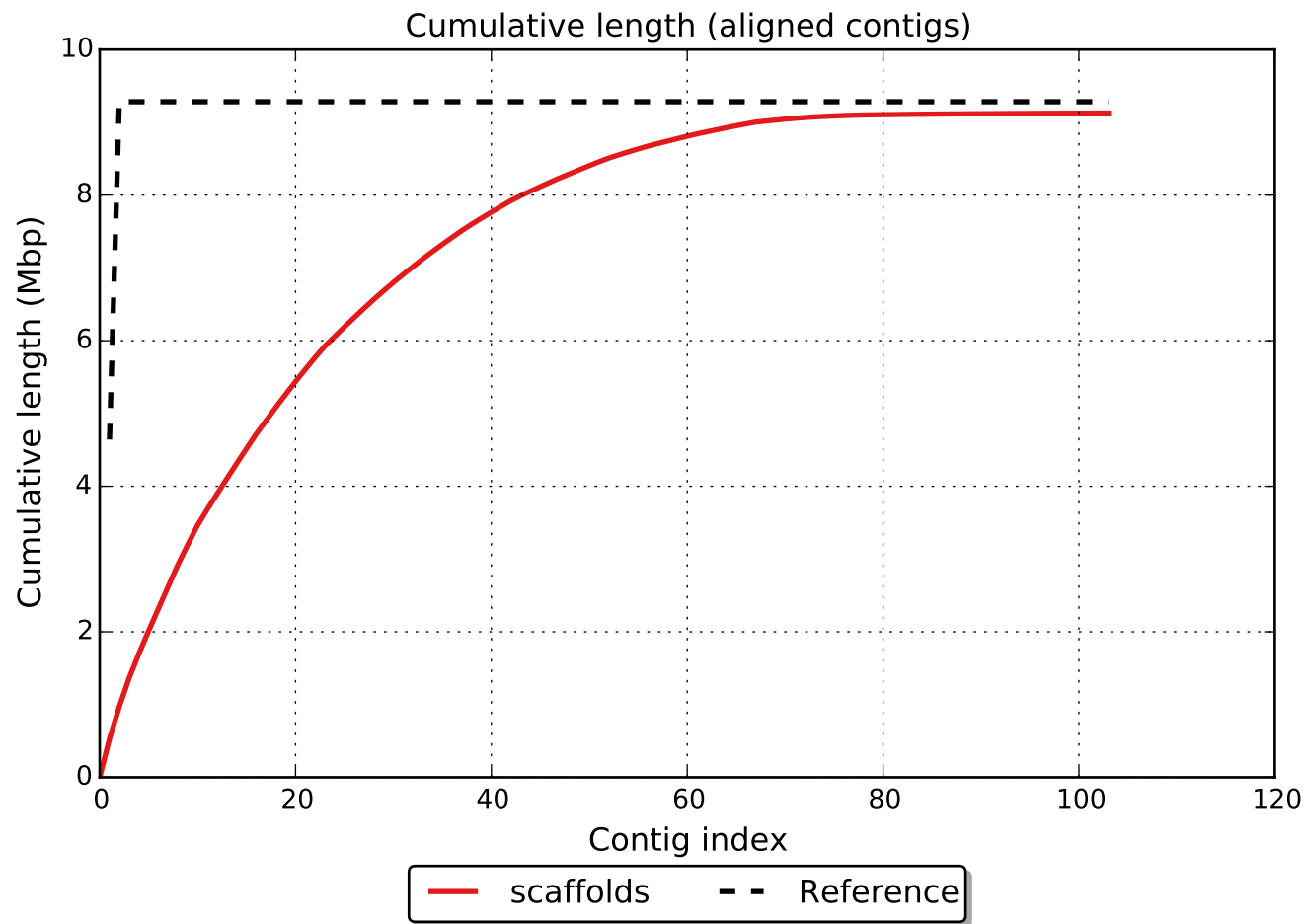|	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	22

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

Cumulative length (aligned contigs)