Report

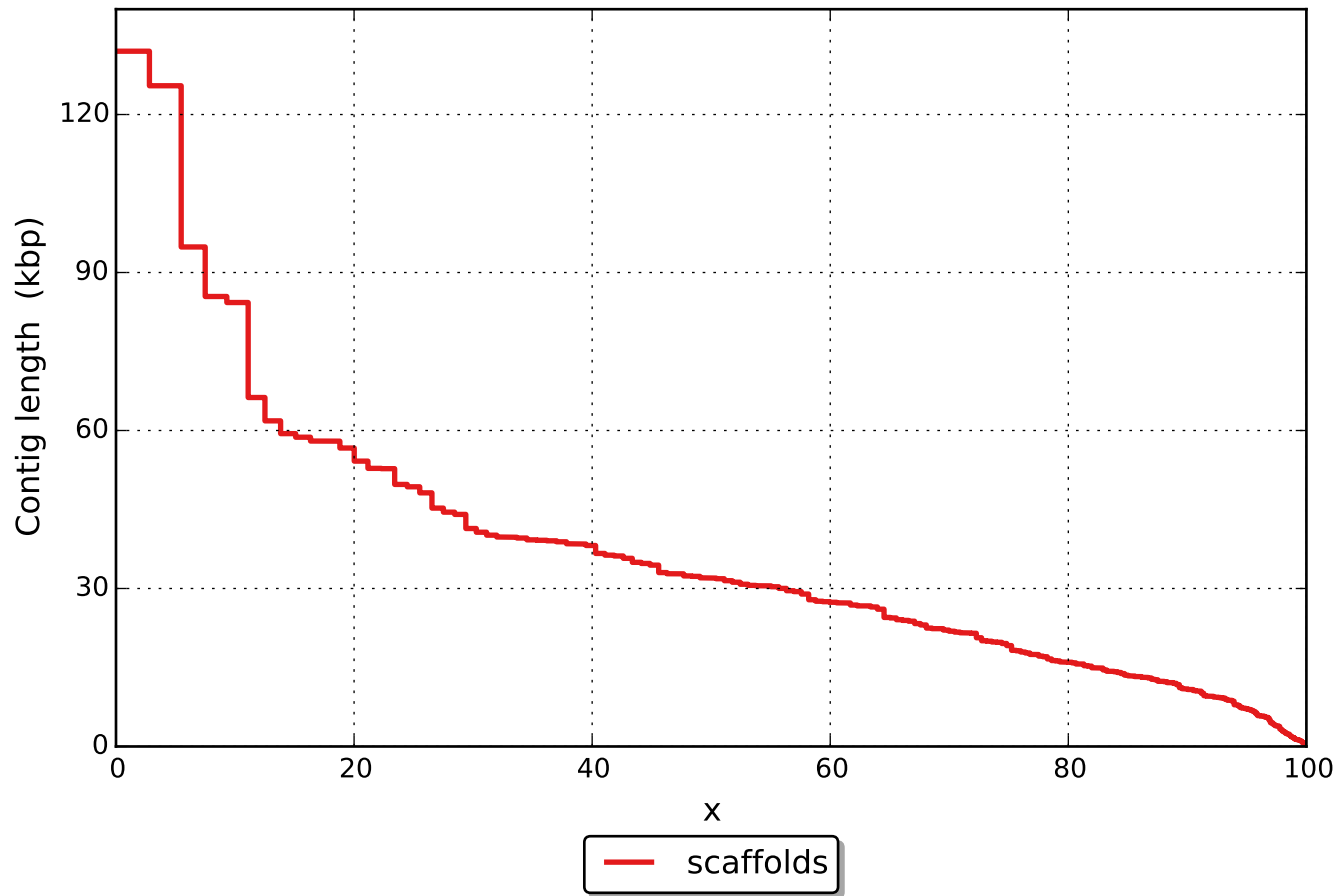|	scaffolds
# contigs (>= 0 bp)	920
# contigs (>= 1000 bp)	238
# contigs (>= 5000 bp)	182
# contigs (>= 10000 bp)	148
# contigs (>= 25000 bp)	71
# contigs (>= 50000 bp)	15
Total length (>= 0 bp)	4912814
Total length (>= 1000 bp)	4681396
Total length (>= 5000 bp)	4554718
Total length (>= 10000 bp)	4296558
Total length (>= 25000 bp)	3033633
Total length (>= 50000 bp)	1100704
# contigs	271
Largest contig	132022
Total length	4701919
Reference length	9283304
N50	31972
N75	19156
L50	48
L75	94
# misassemblies	25
# misassembled contigs	19
Misassembled contigs length	706576
# local misassemblies	4
# unaligned contigs	9 + 9 part
Unaligned length	6763
Genome fraction (%)	49.644
Duplication ratio	1.031
# N's per 100 kbp	25.88
# mismatches per 100 kbp	933.98
# indels per 100 kbp	0.91
Largest alignment	125463
NA50	29578
NA75	17458
LA50	53
LA75	103

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	25
# relocations	18
# translocations	0
# inversions	6
# interspecies translocations	1
# possibly misassembled contigs	1
# misassembled contigs	19
Misassembled contigs length	706576
# local misassemblies	4
# mismatches	43043
# indels	42
# short indels	38
# long indels	4
Indels length	265

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).
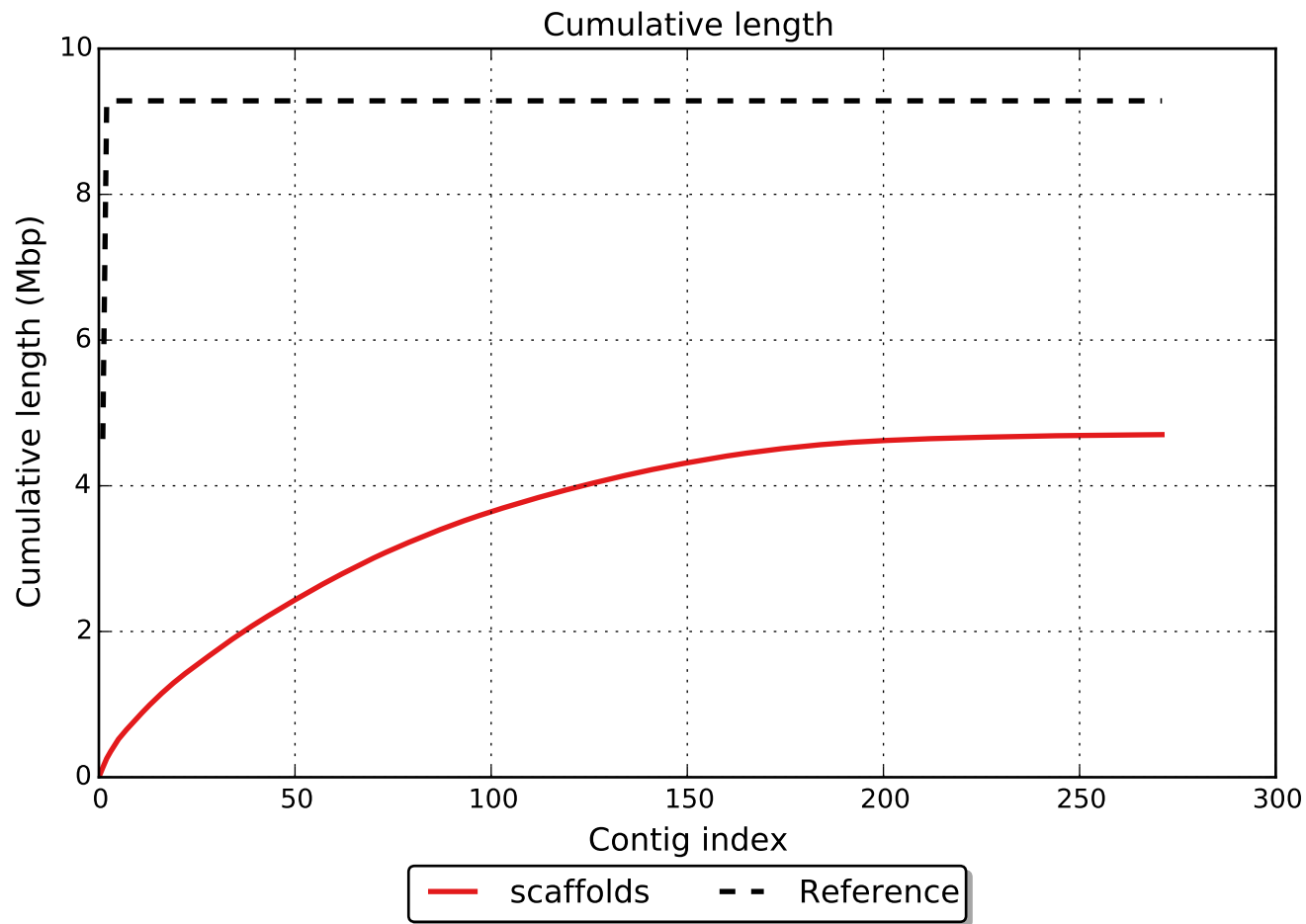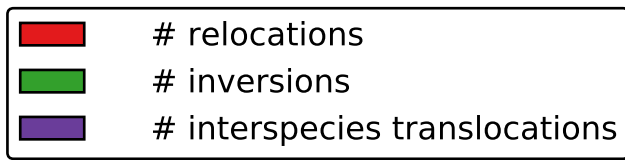
Unaligned report

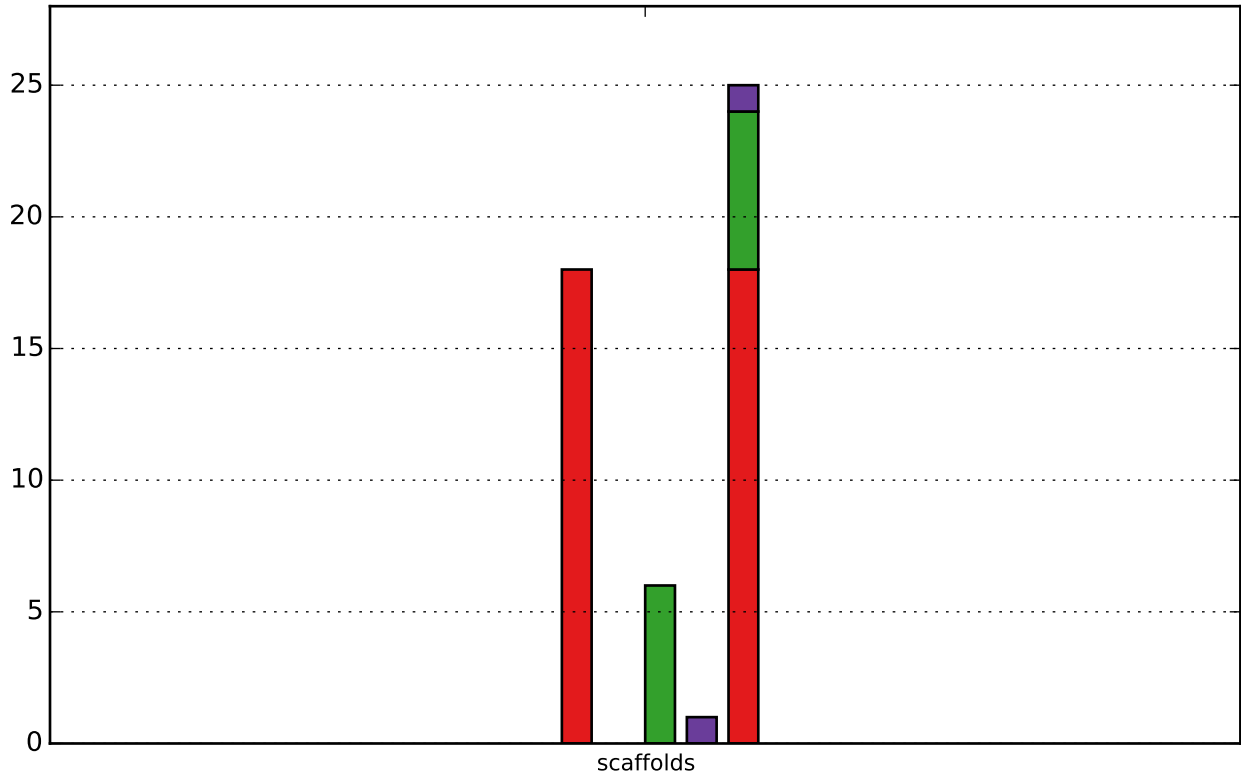|	scaffolds
# fully unaligned contigs	9
Fully unaligned length	5129
# partially unaligned contigs	9
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1634
# N's	1217

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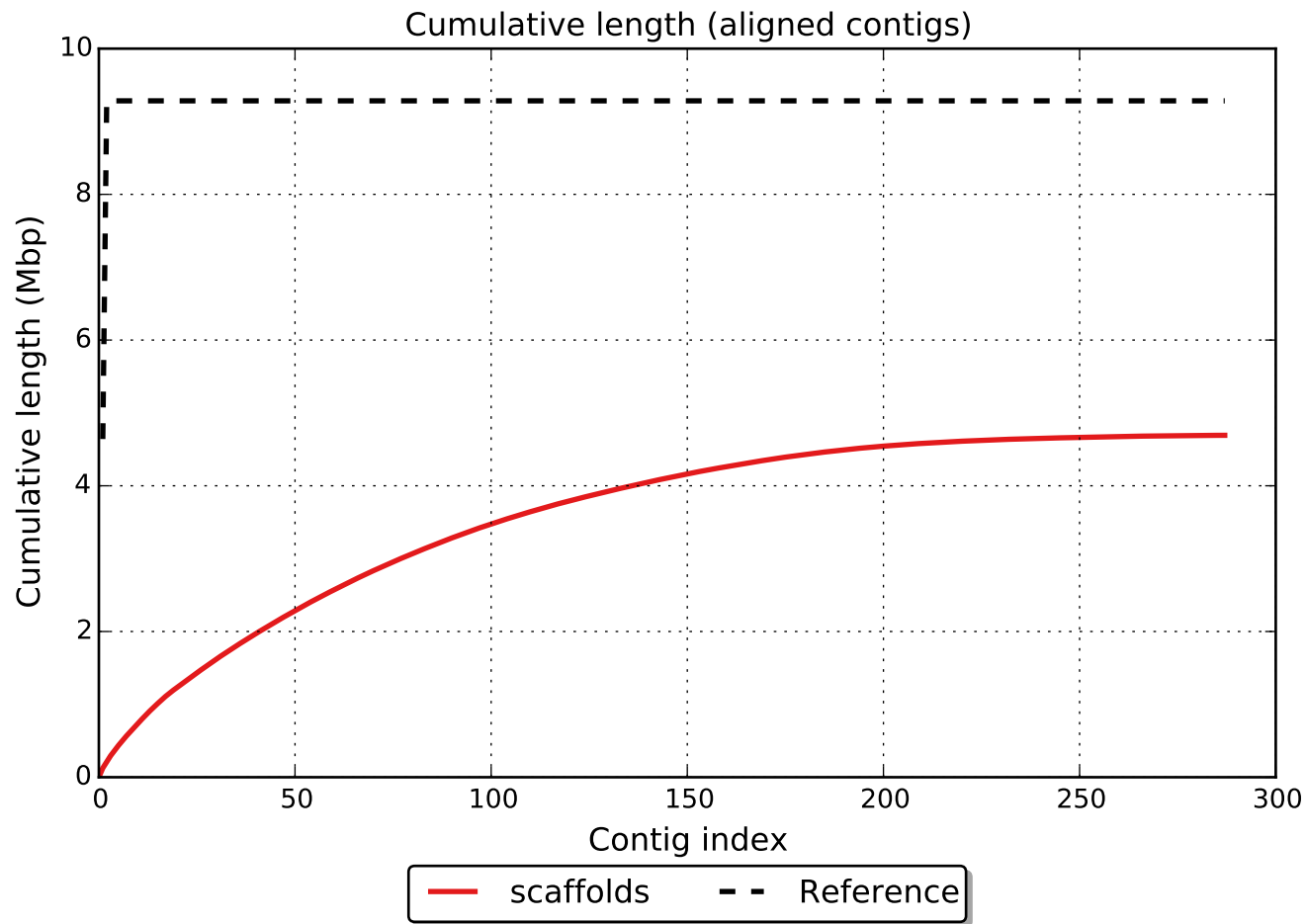(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

Cumulative length (aligned contigs)