Report

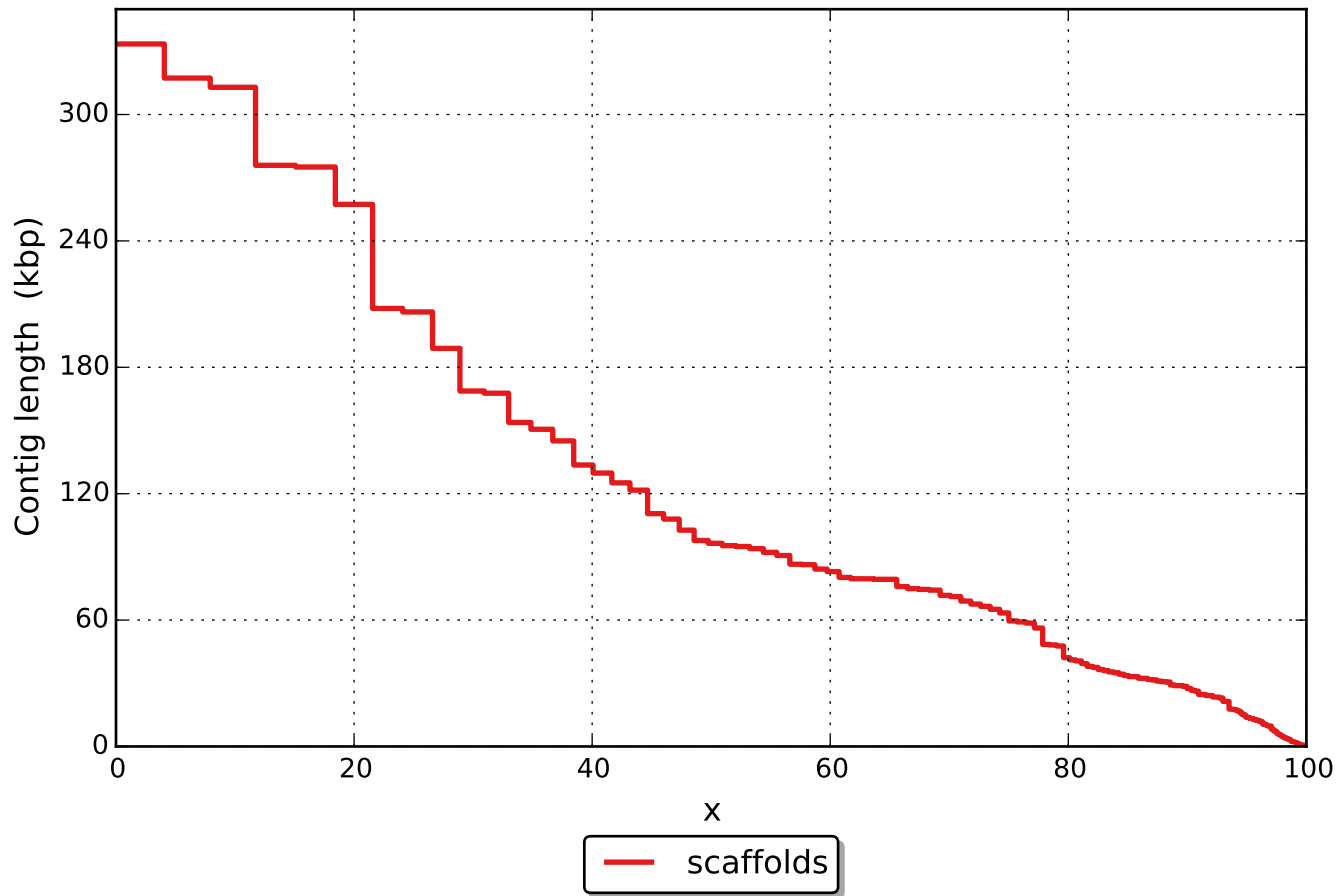|	scaffolds
# contigs (>= 0 bp)	880
# contigs (>= 1000 bp)	180
# contigs (>= 5000 bp)	124
# contigs (>= 10000 bp)	111
# contigs (>= 25000 bp)	83
# contigs (>= 50000 bp)	52
Total length (>= 0 bp)	8453644
Total length (>= 1000 bp)	8181545
Total length (>= 5000 bp)	8046360
Total length (>= 10000 bp)	7950075
Total length (>= 25000 bp)	7476560
Total length (>= 50000 bp)	6399646
# contigs	242
Largest contig	333495
Total length	8221188
Reference length	9283304
N50	96440
N75	63382
L50	23
L75	48
# misassemblies	178
# misassembled contigs	38
Misassembled contigs length	3564233
# local misassemblies	7
# unaligned contigs	19 + 2 part
Unaligned length	12677
Genome fraction (%)	50.306
Duplication ratio	1.758
# N's per 100 kbp	0.63
# mismatches per 100 kbp	1416.19
# indels per 100 kbp	1.22
Largest alignment	317313
NA50	54877
NA75	24175
LA50	40
LA75	100

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	178
# relocations	148
# translocations	0
# inversions	25
# interspecies translocations	5
# possibly misassembled contigs	3
# misassembled contigs	38
Misassembled contigs length	3564233
# local misassemblies	7
# mismatches	66137
# indels	57
# short indels	57
# long indels	0
Indels length	65

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Unaligned report
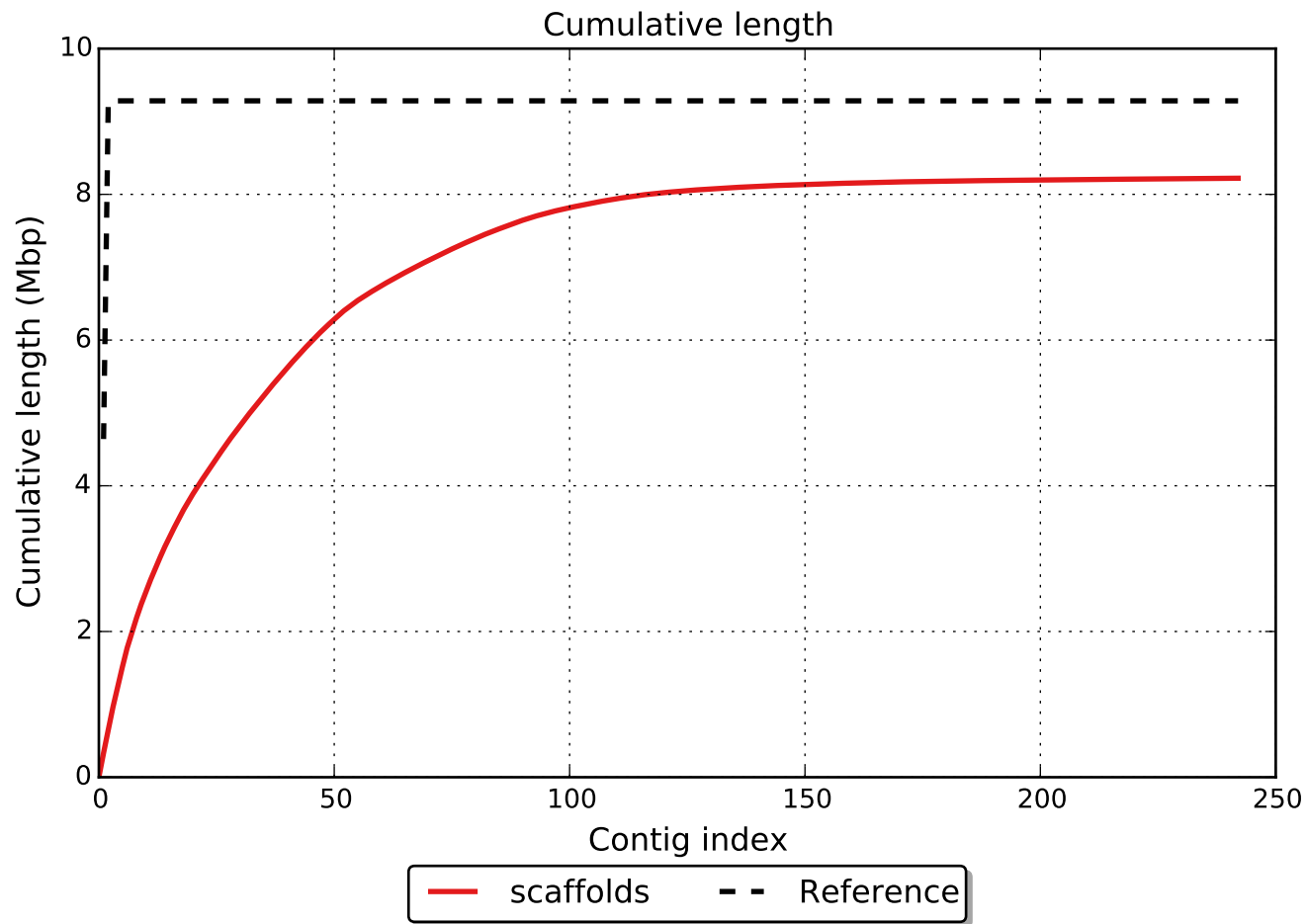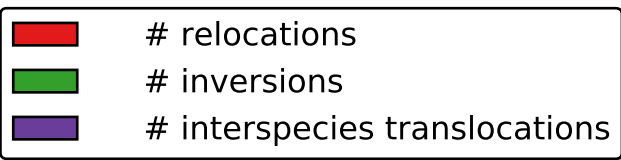
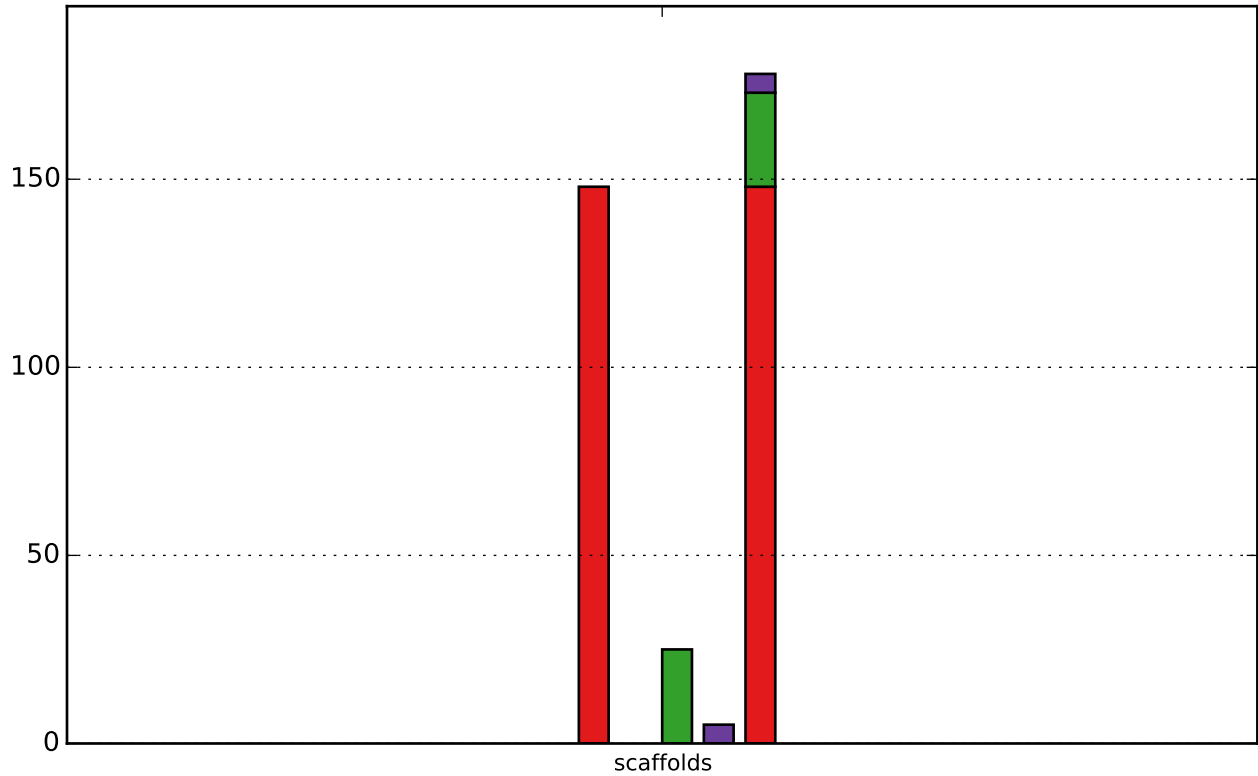|	scaffolds
# fully unaligned contigs	19
Fully unaligned length	11444
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	1233
# N's	52

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
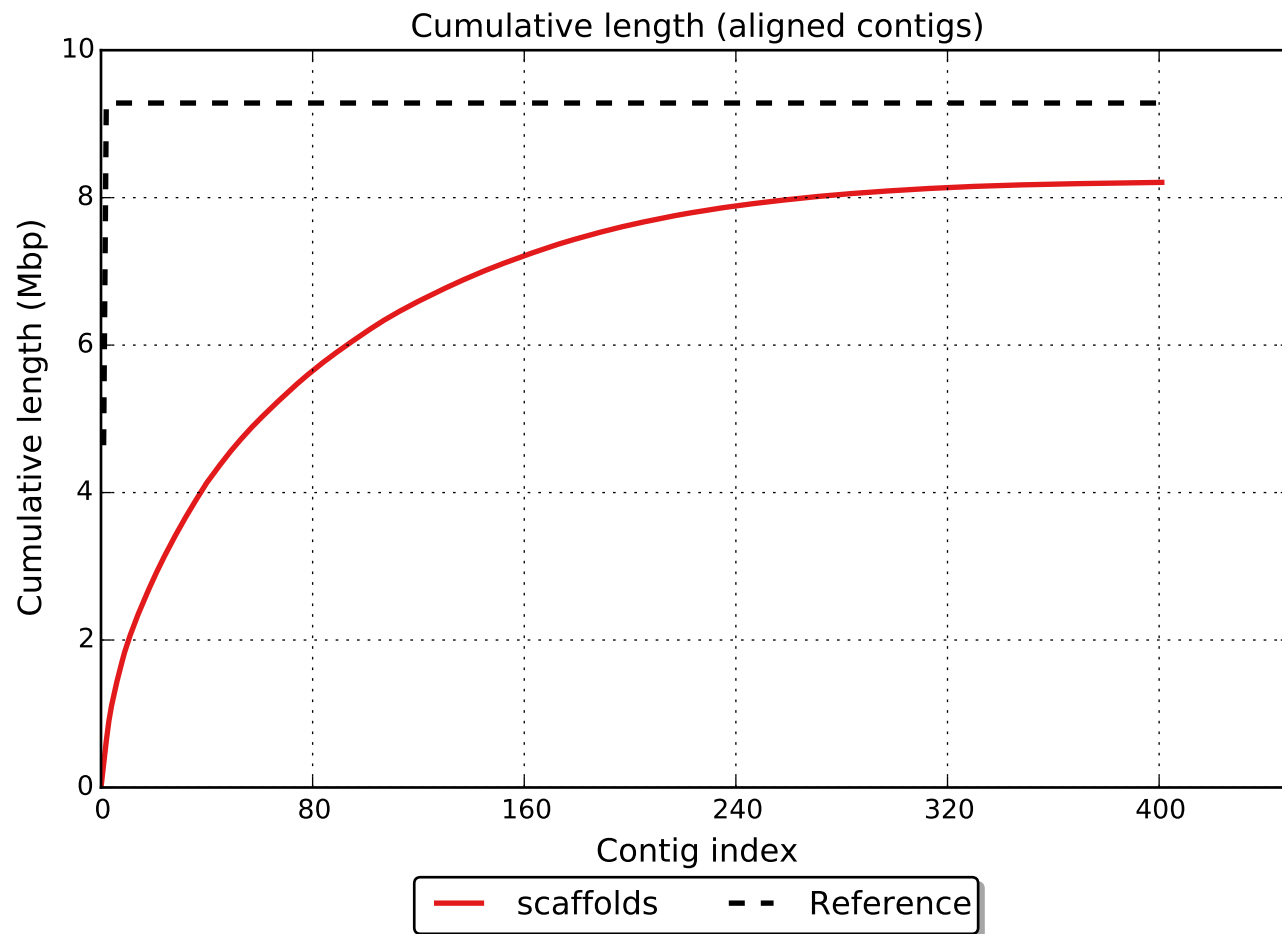
Misassemblies

Cumulative length (aligned contigs)

NAx