Report

	scaffolds
# contigs (>= 0 bp)	125
# contigs (>= 1000 bp)	77
# contigs (>= 5000 bp)	64
# contigs (>= 10000 bp)	61
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	41
Total length (>= 0 bp)	9146130
Total length (>= 1000 bp)	9129851
Total length (>= 5000 bp)	9102772
Total length (>= 10000 bp)	9077538
Total length (>= 25000 bp)	8967925
Total length (>= 50000 bp)	8536857
# contigs	86
Largest contig	663492
Total length	9137424
Reference length	9283304
N50	263950
N75	151678
L50	12
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.459
Duplication ratio	1.000
# N's per 100 kbp	0.51
# mismatches per 100 kbp	166.05
# indels per 100 kbp	0.54
Largest alignment	663492
NA50	263950
NA75	151676
LA50	12
LA75	25

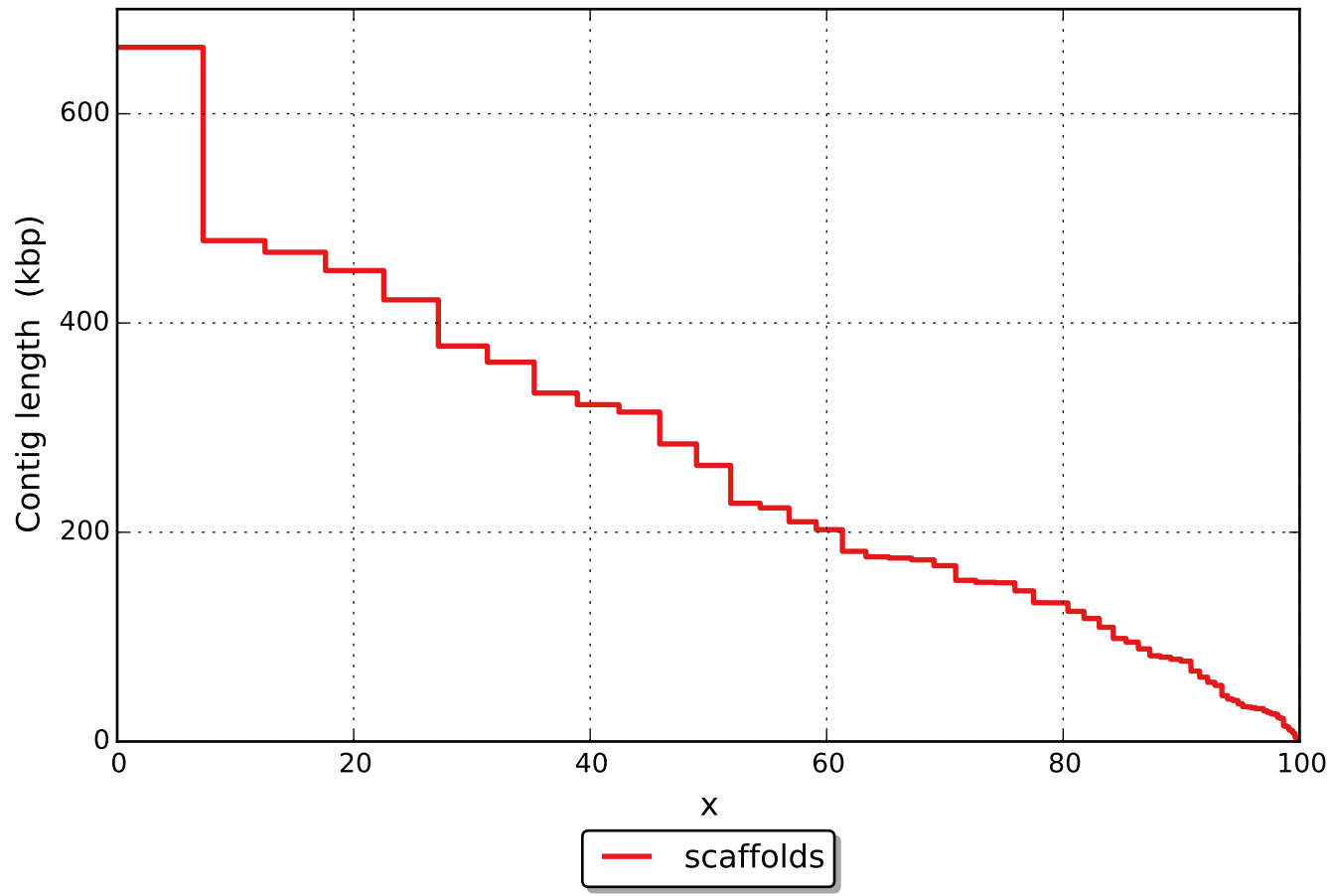All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	scaffolds
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	3
# mismatches	15177
# indels	49
# short indels	46
# long indels	3
Indels length	124

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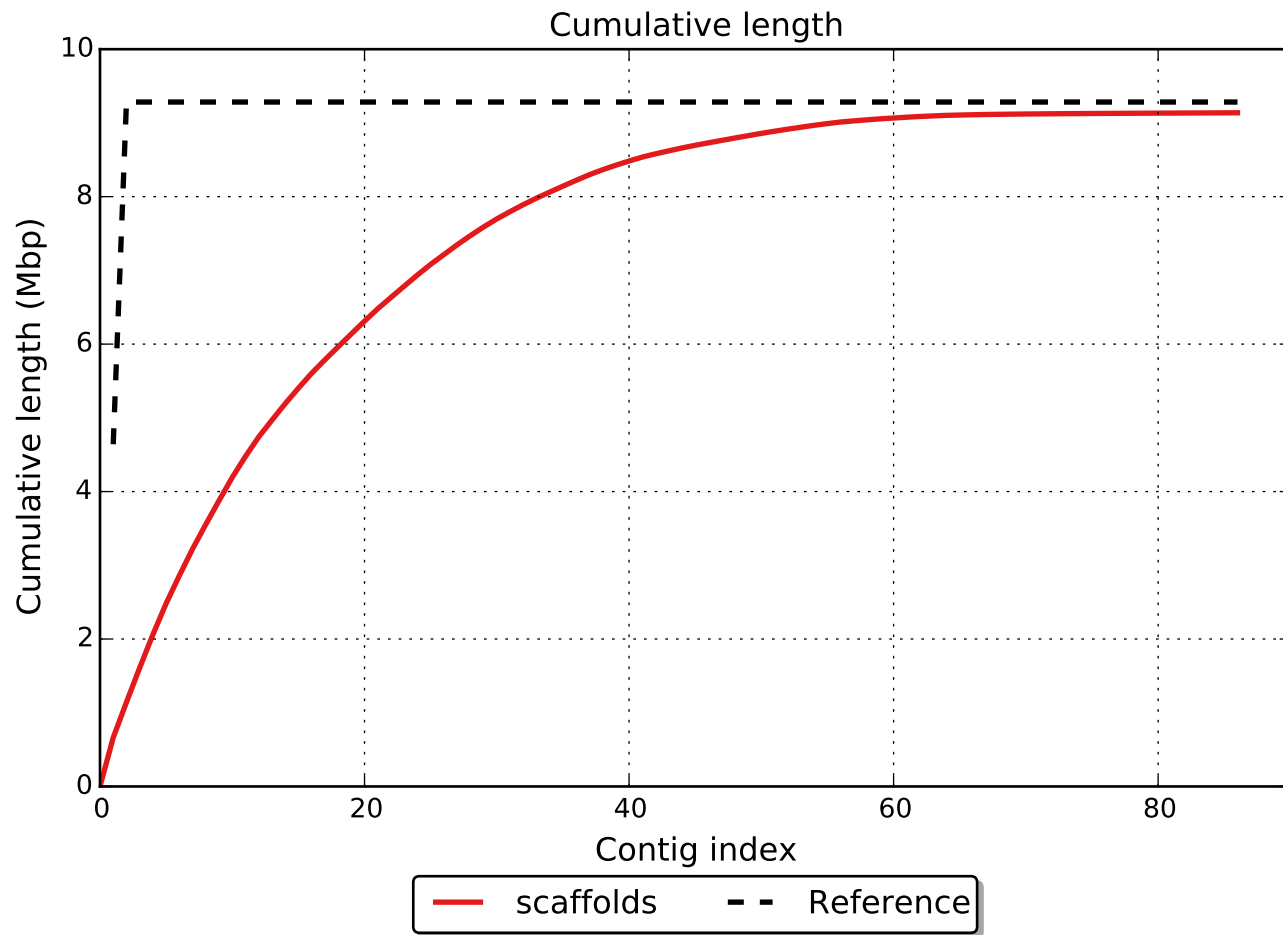(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
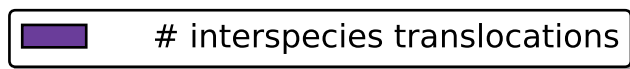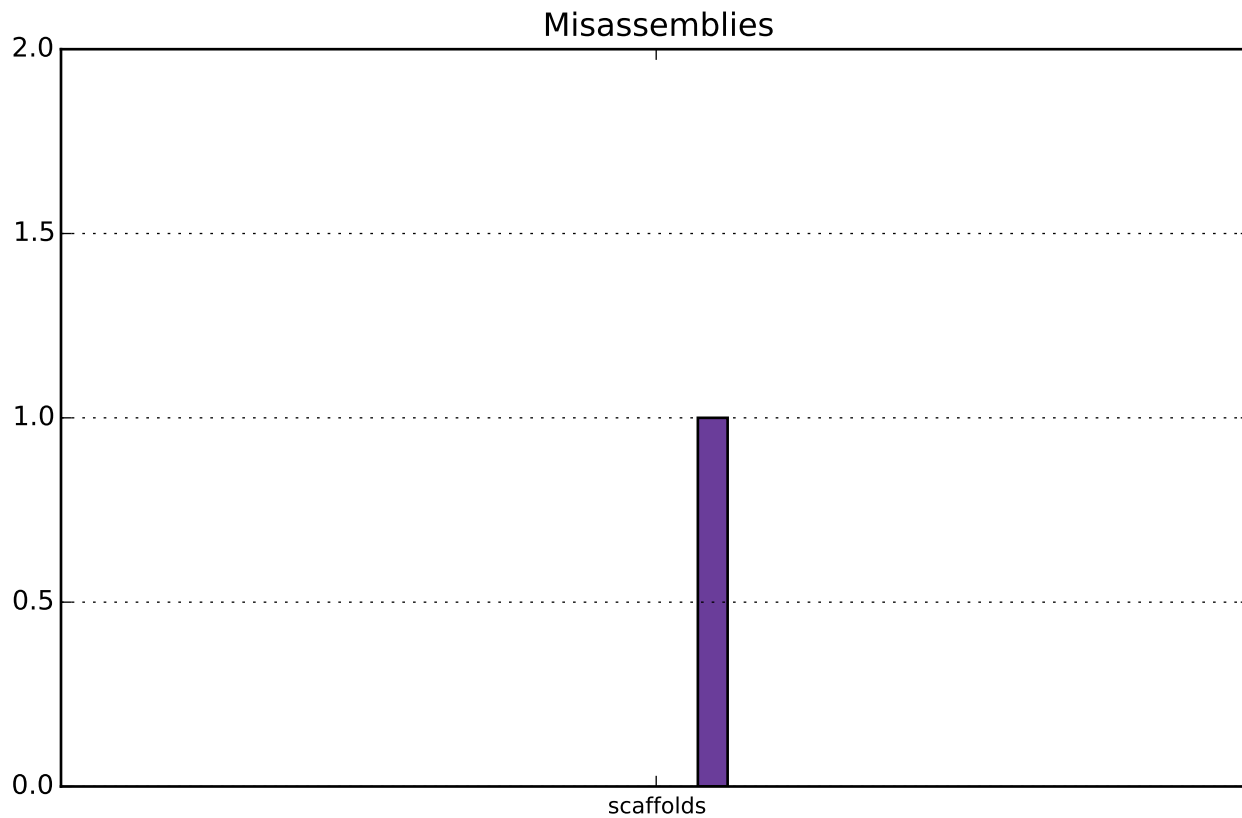
Unaligned report

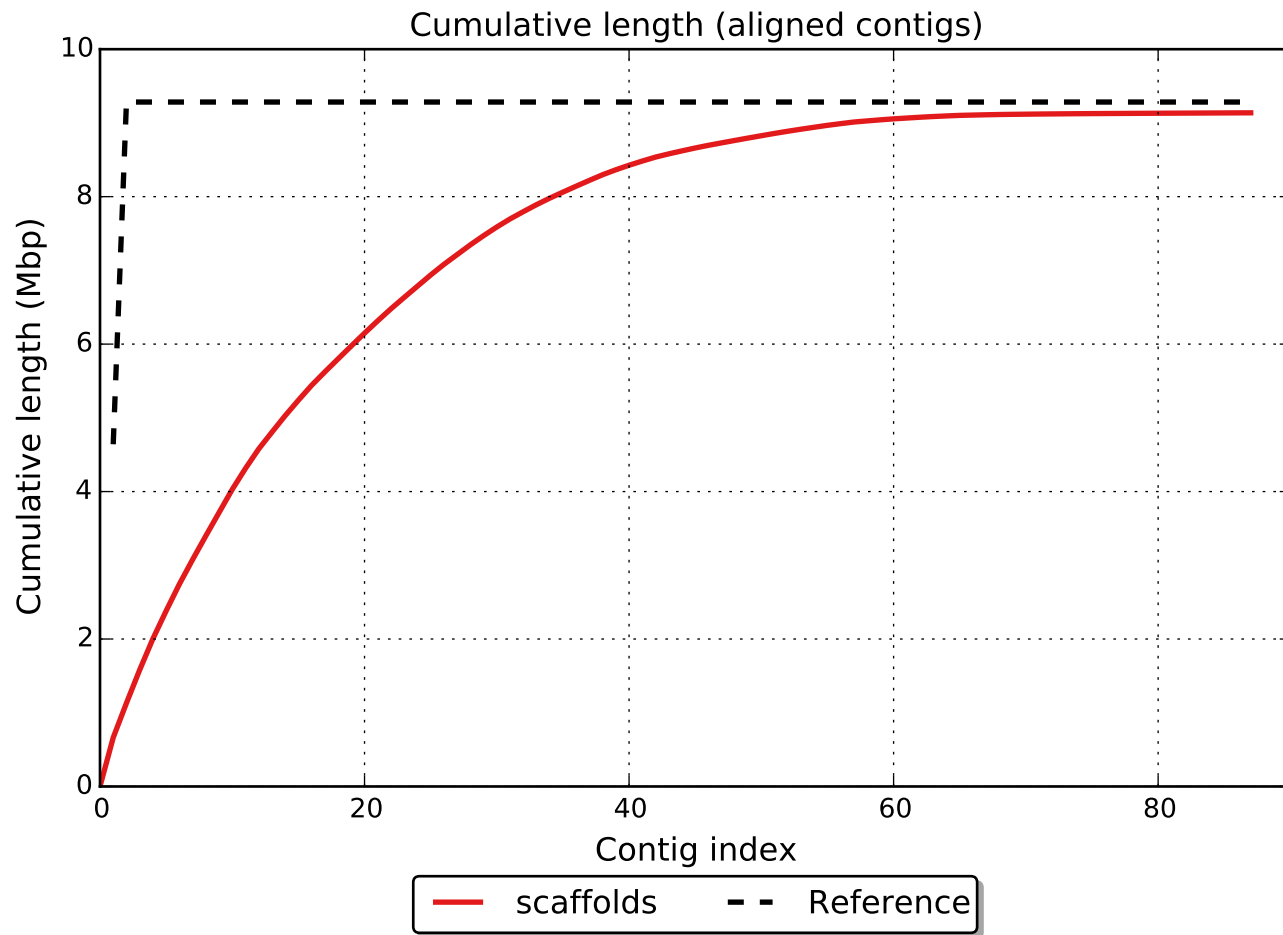|	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	47

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