

Report

	scaffolds
# contigs (≥ 0 bp)	990
# contigs (≥ 1000 bp)	220
# contigs (≥ 5000 bp)	156
# contigs (≥ 10000 bp)	127
# contigs (≥ 25000 bp)	84
# contigs (≥ 50000 bp)	52
Total length (≥ 0 bp)	8105679
Total length (≥ 1000 bp)	7814423
Total length (≥ 5000 bp)	7652012
Total length (≥ 10000 bp)	7445873
Total length (≥ 25000 bp)	6706003
Total length (≥ 50000 bp)	5605771
# contigs	279
Largest contig	347033
Total length	7851669
Reference length	9283304
N50	85464
N75	42511
L50	25
L75	59
# misassemblies	156
# misassembled contigs	39
Misassembled contigs length	3025443
# local misassemblies	4
# unaligned contigs	26 + 1 part
Unaligned length	15985
Genome fraction (%)	49.464
Duplication ratio	1.712
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1312.44
# indels per 100 kbp	1.24
Largest alignment	347033
NA50	50928
NA75	21304
LA50	43
LA75	107

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	156
# relocations	133
# translocations	0
# inversions	21
# interspecies translocations	2
# possibly misassembled contigs	1
# misassembled contigs	39
Misassembled contigs length	3025443
# local misassemblies	4
# mismatches	60266
# indels	57
# short indels	57
# long indels	0
Indels length	71

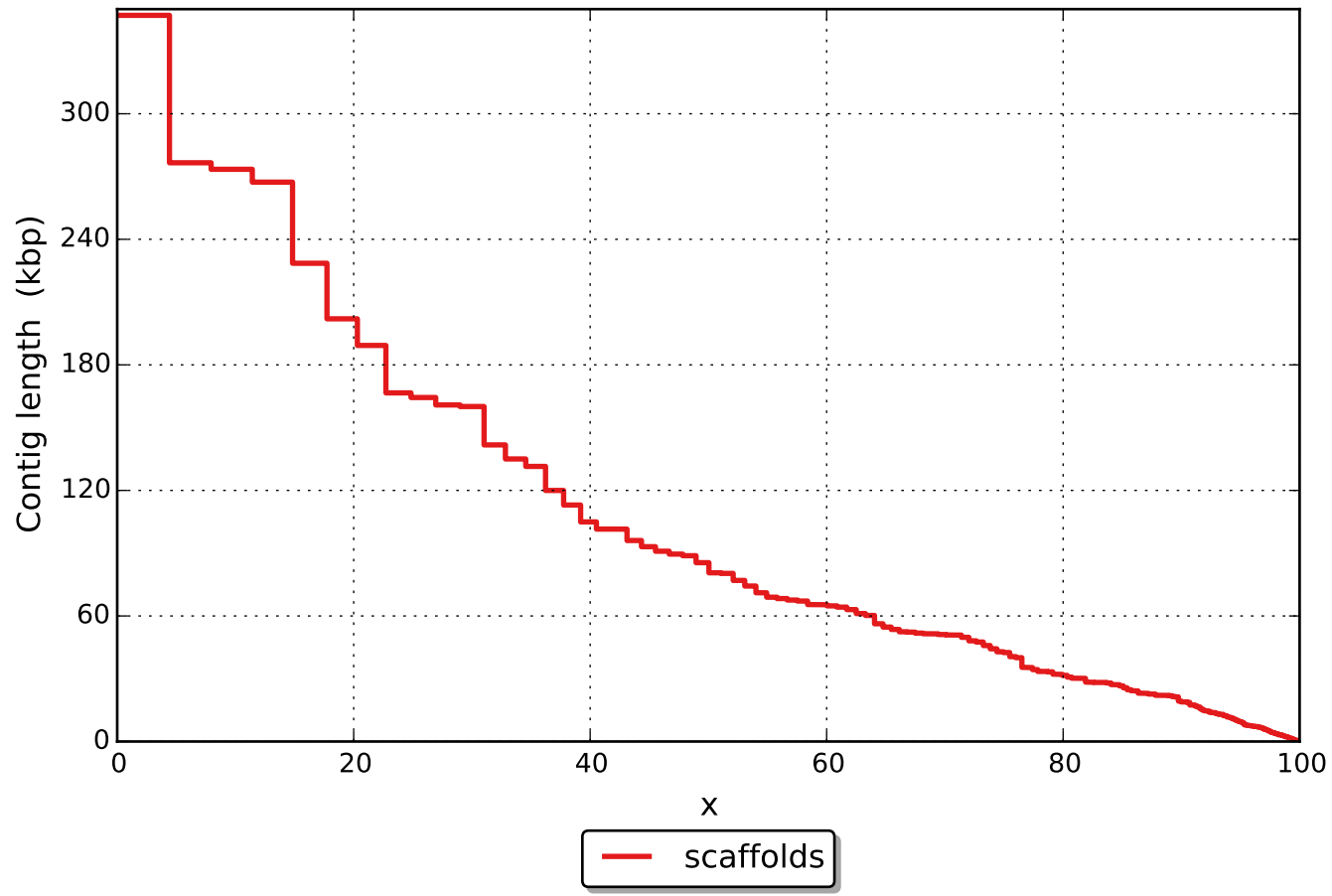
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

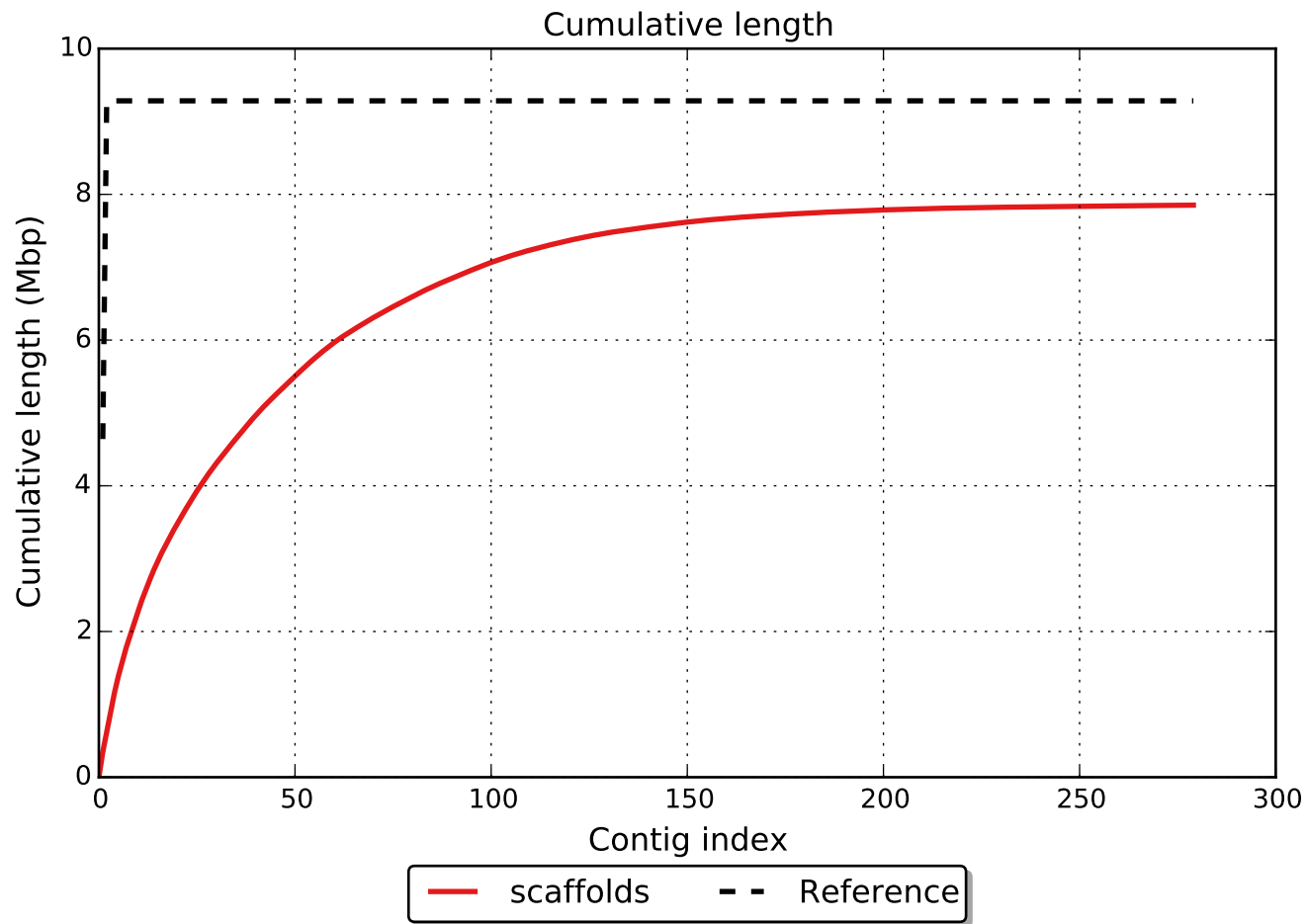
Unaligned report

	scaffolds
# fully unaligned contigs	26
Fully unaligned length	15909
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	76
# N's	0

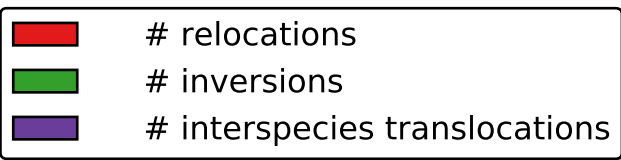
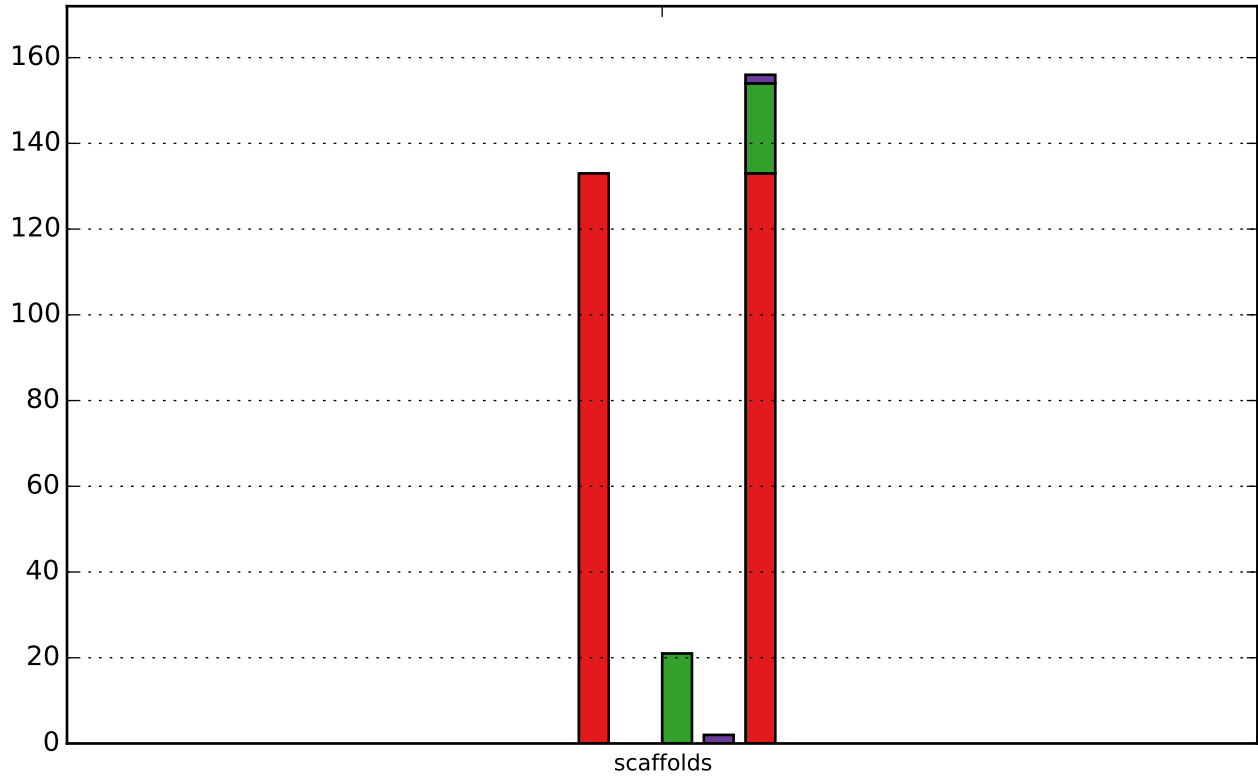
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

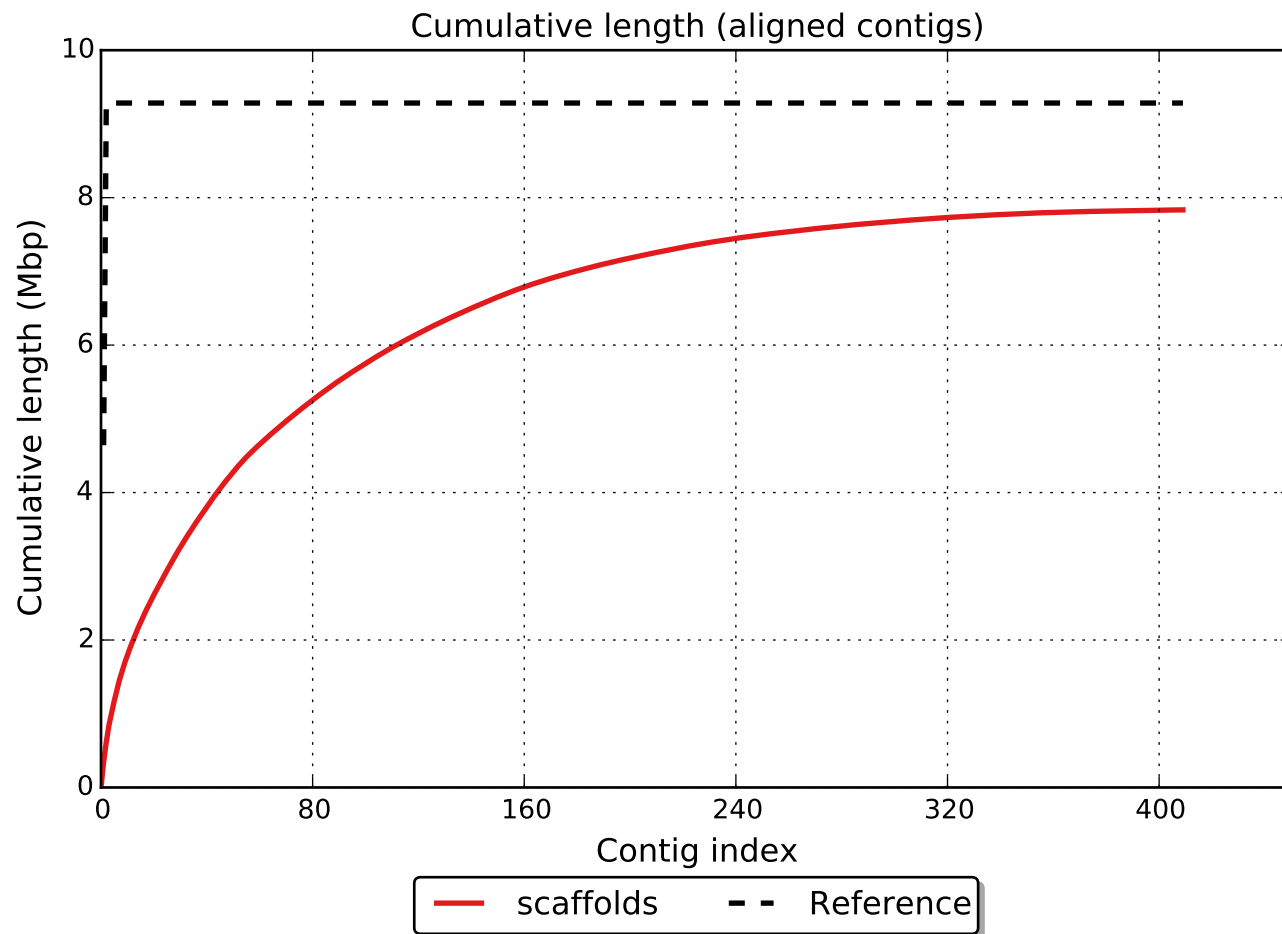
Nx





Misassemblies





NAx

