

Report

	scaffolds
# contigs (≥ 0 bp)	229
# contigs (≥ 1000 bp)	99
# contigs (≥ 5000 bp)	77
# contigs (≥ 10000 bp)	74
# contigs (≥ 25000 bp)	66
# contigs (≥ 50000 bp)	48
Total length (≥ 0 bp)	9110170
Total length (≥ 1000 bp)	9058514
Total length (≥ 5000 bp)	9020683
Total length (≥ 10000 bp)	8998158
Total length (≥ 25000 bp)	8853949
Total length (≥ 50000 bp)	8231677
# contigs	132
Largest contig	600951
Total length	9079929
Reference length	9283304
N50	200817
N75	110783
L50	16
L75	31
# misassemblies	261
# misassembled contigs	37
Misassembled contigs length	4271262
# local misassemblies	10
# unaligned contigs	22 + 5 part
Unaligned length	81336
Genome fraction (%)	49.477
Duplication ratio	1.959
# N's per 100 kbp	0.00
# mismatches per 100 kbp	752.94
# indels per 100 kbp	1.22
Largest alignment	600951
NA50	65859
NA75	19000
LA50	26
LA75	95

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	261
# relocations	236
# translocations	0
# inversions	22
# interspecies translocations	3
# possibly misassembled contigs	27
# misassembled contigs	37
Misassembled contigs length	4271262
# local misassemblies	10
# mismatches	34583
# indels	56
# short indels	56
# long indels	0
Indels length	57

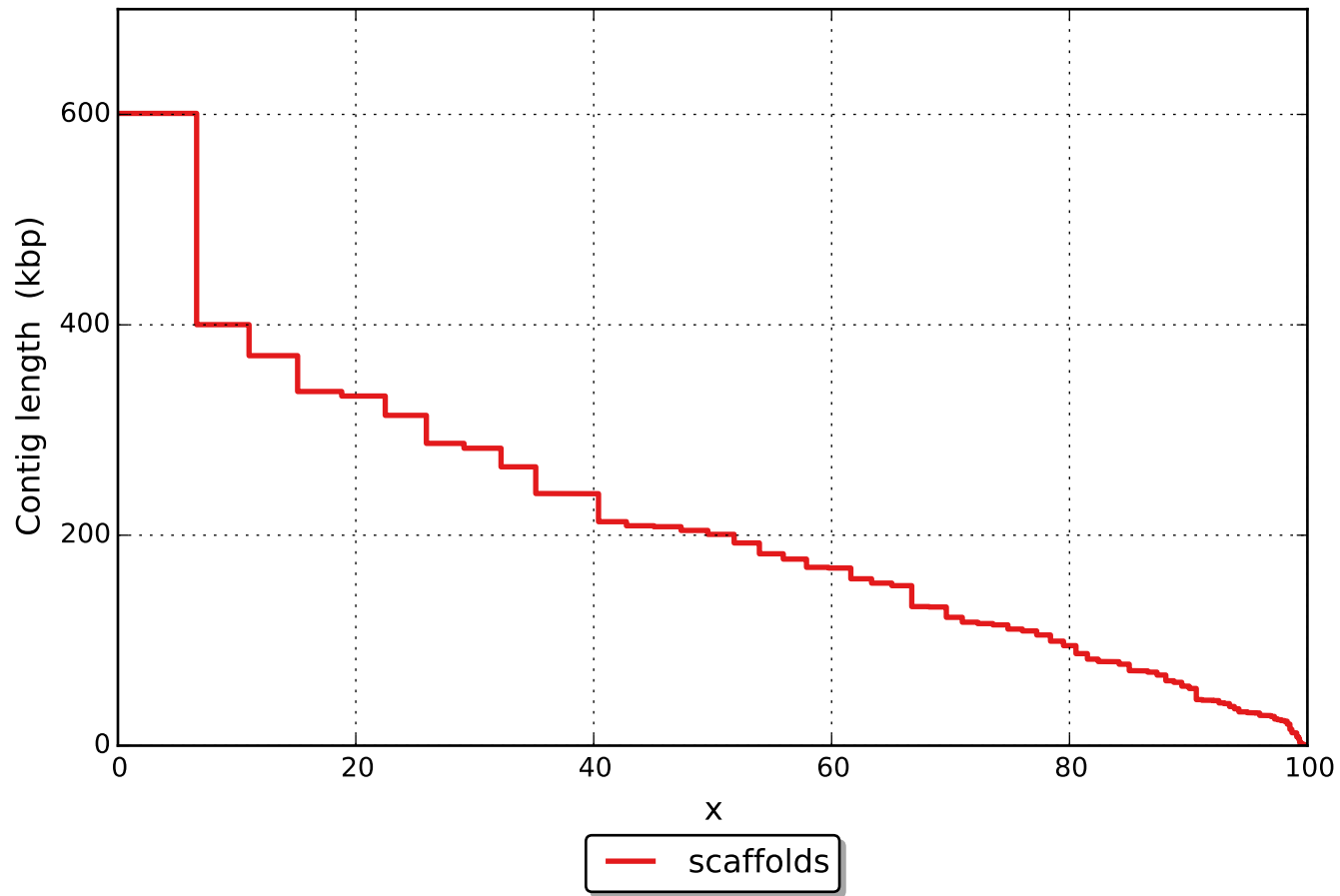
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

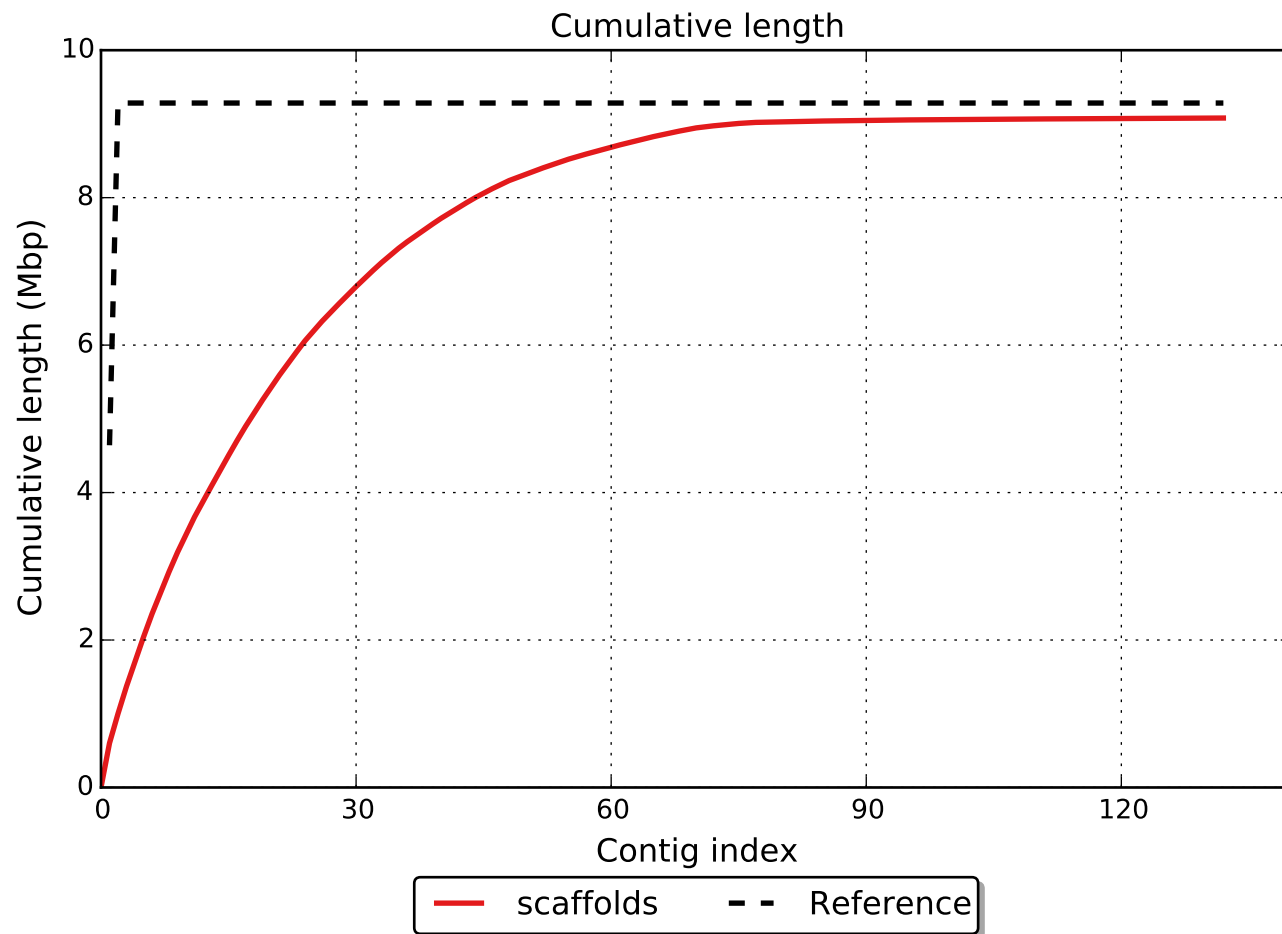
Unaligned report

	scaffolds
# fully unaligned contigs	22
Fully unaligned length	20880
# partially unaligned contigs	5
# with misassembly	1
# both parts are significant	3
Partially unaligned length	60456
# N's	0

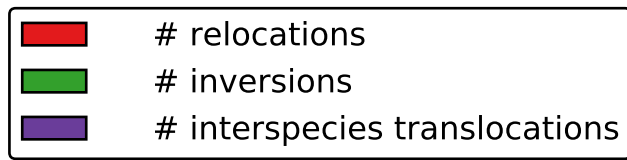
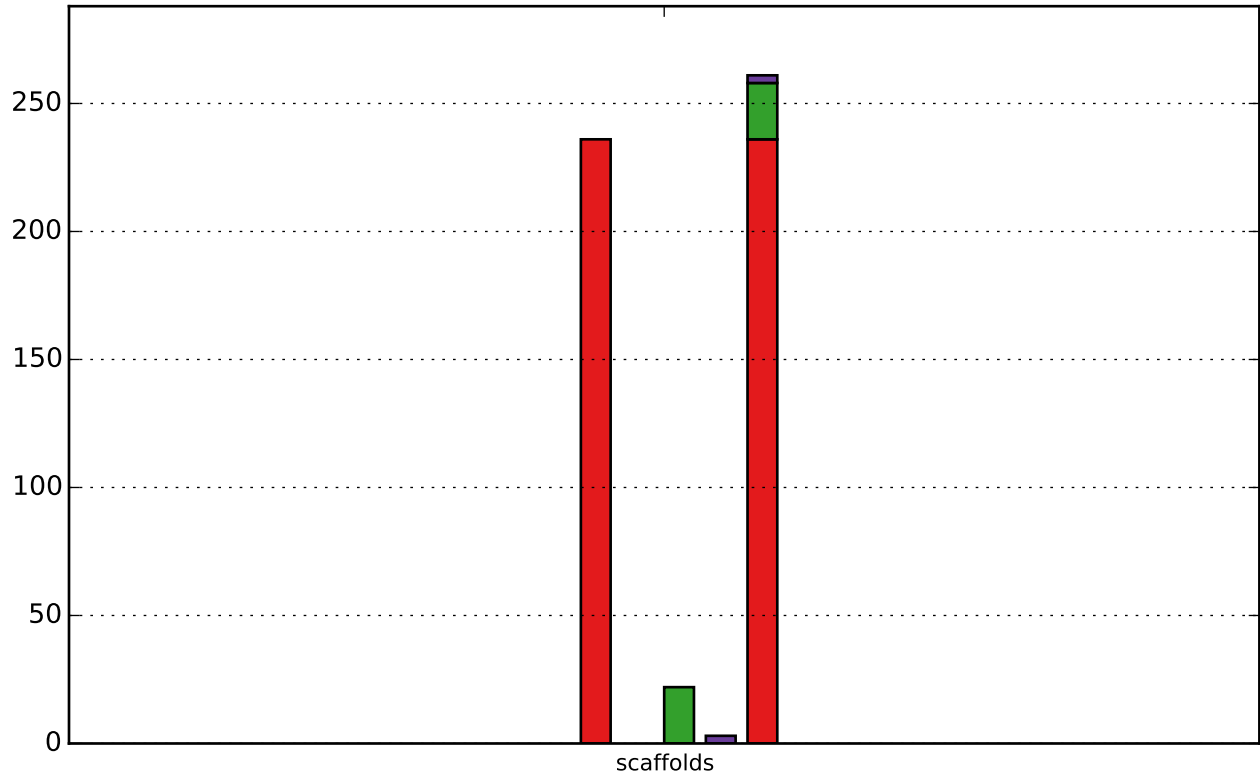
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

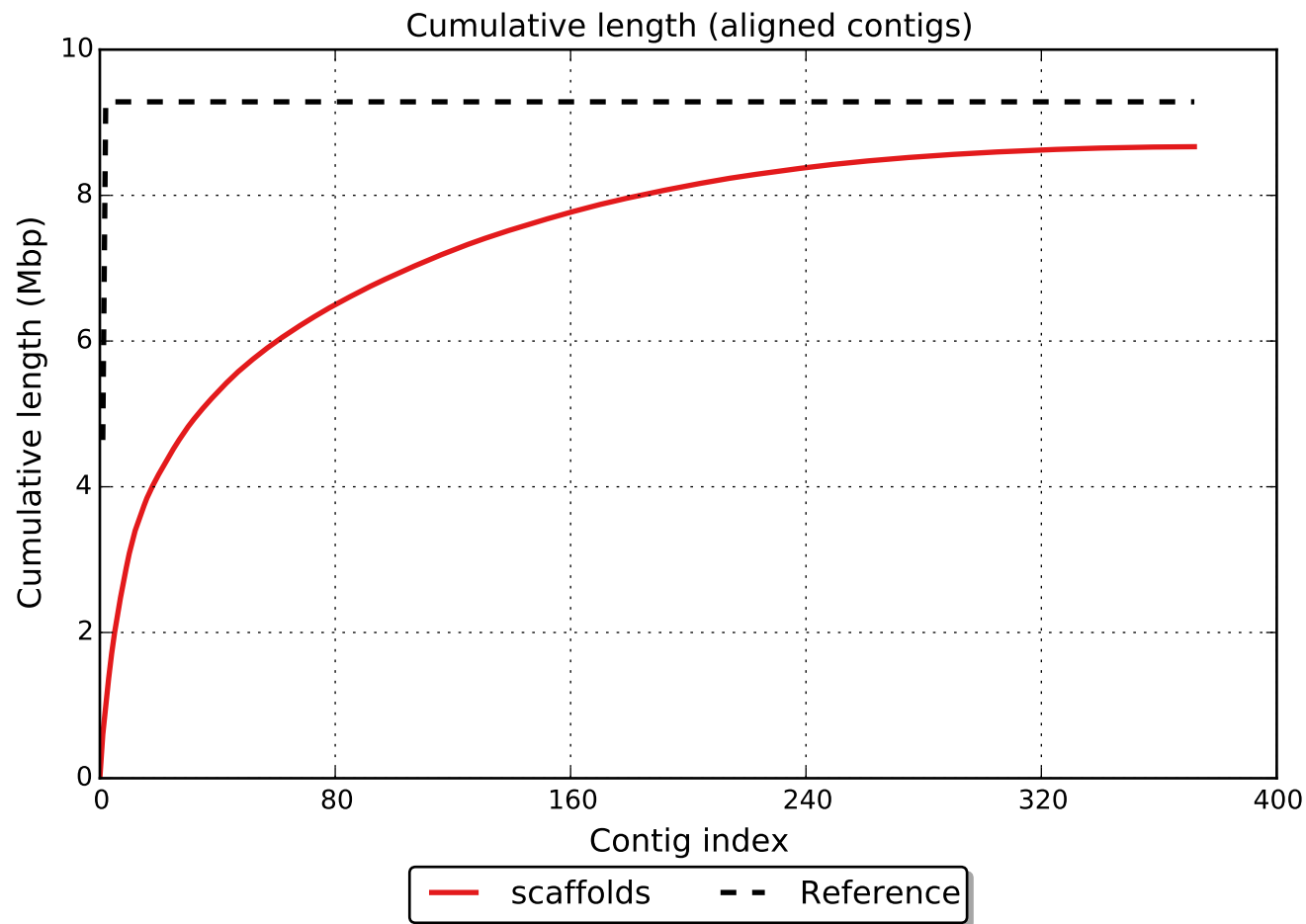
Nx





Misassemblies





NAx

