

Report

	scaffolds
# contigs (≥ 0 bp)	281
# contigs (≥ 1000 bp)	114
# contigs (≥ 5000 bp)	90
# contigs (≥ 10000 bp)	86
# contigs (≥ 25000 bp)	76
# contigs (≥ 50000 bp)	60
Total length (≥ 0 bp)	9061206
Total length (≥ 1000 bp)	8997240
Total length (≥ 5000 bp)	8949107
Total length (≥ 10000 bp)	8917074
Total length (≥ 25000 bp)	8752641
Total length (≥ 50000 bp)	8226933
# contigs	153
Largest contig	332068
Total length	9023049
Reference length	9283304
N50	164195
N75	91954
L50	21
L75	39
# misassemblies	268
# misassembled contigs	38
Misassembled contigs length	4252810
# local misassemblies	6
# unaligned contigs	16 + 1 part
Unaligned length	12948
Genome fraction (%)	49.411
Duplication ratio	1.966
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1051.80
# indels per 100 kbp	1.46
Largest alignment	300358
NA50	62146
NA75	22499
LA50	34
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	268
# relocations	236
# translocations	0
# inversions	32
# interspecies translocations	0
# possibly misassembled contigs	4
# misassembled contigs	38
Misassembled contigs length	4252810
# local misassemblies	6
# mismatches	48246
# indels	67
# short indels	66
# long indels	1
Indels length	77

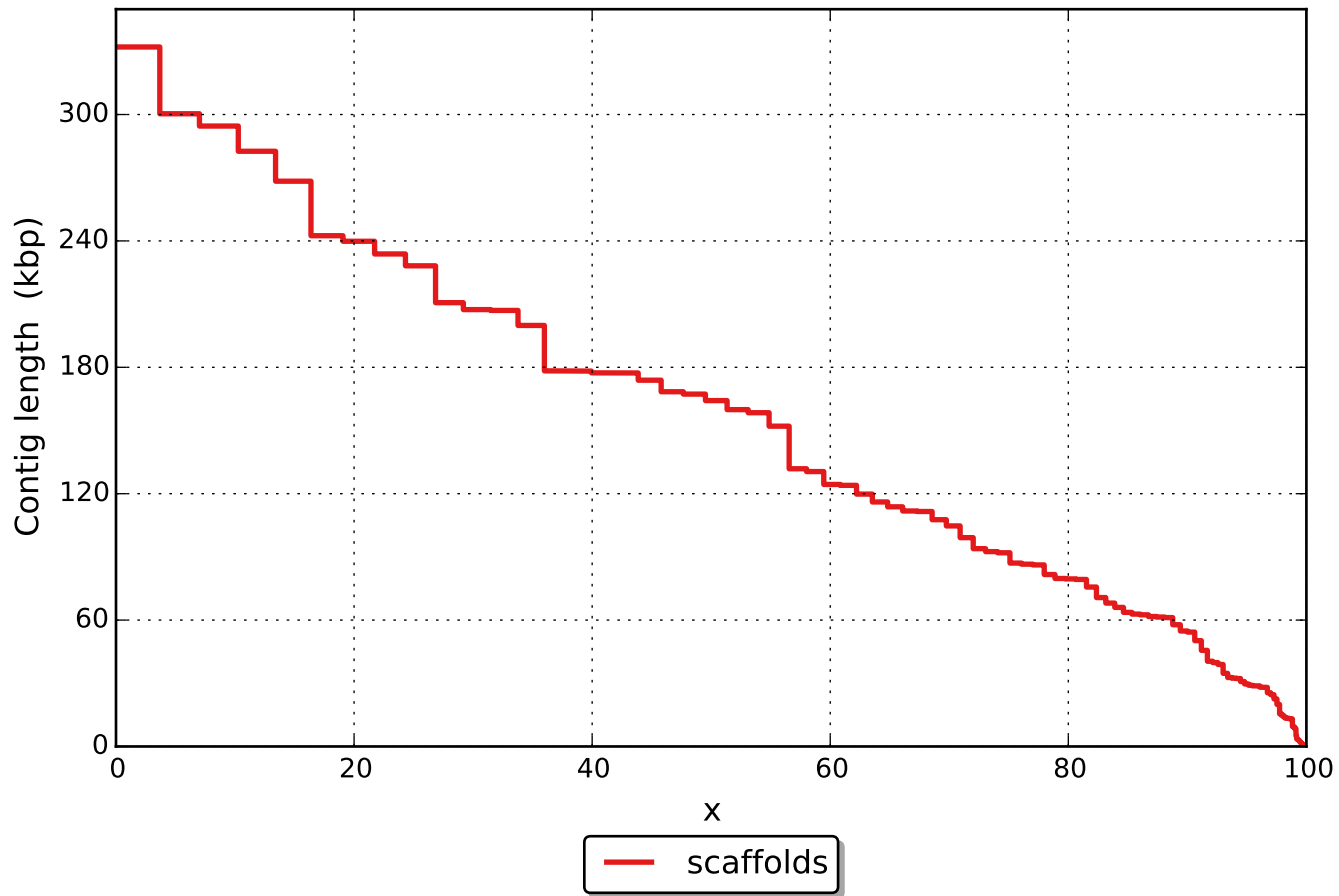
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

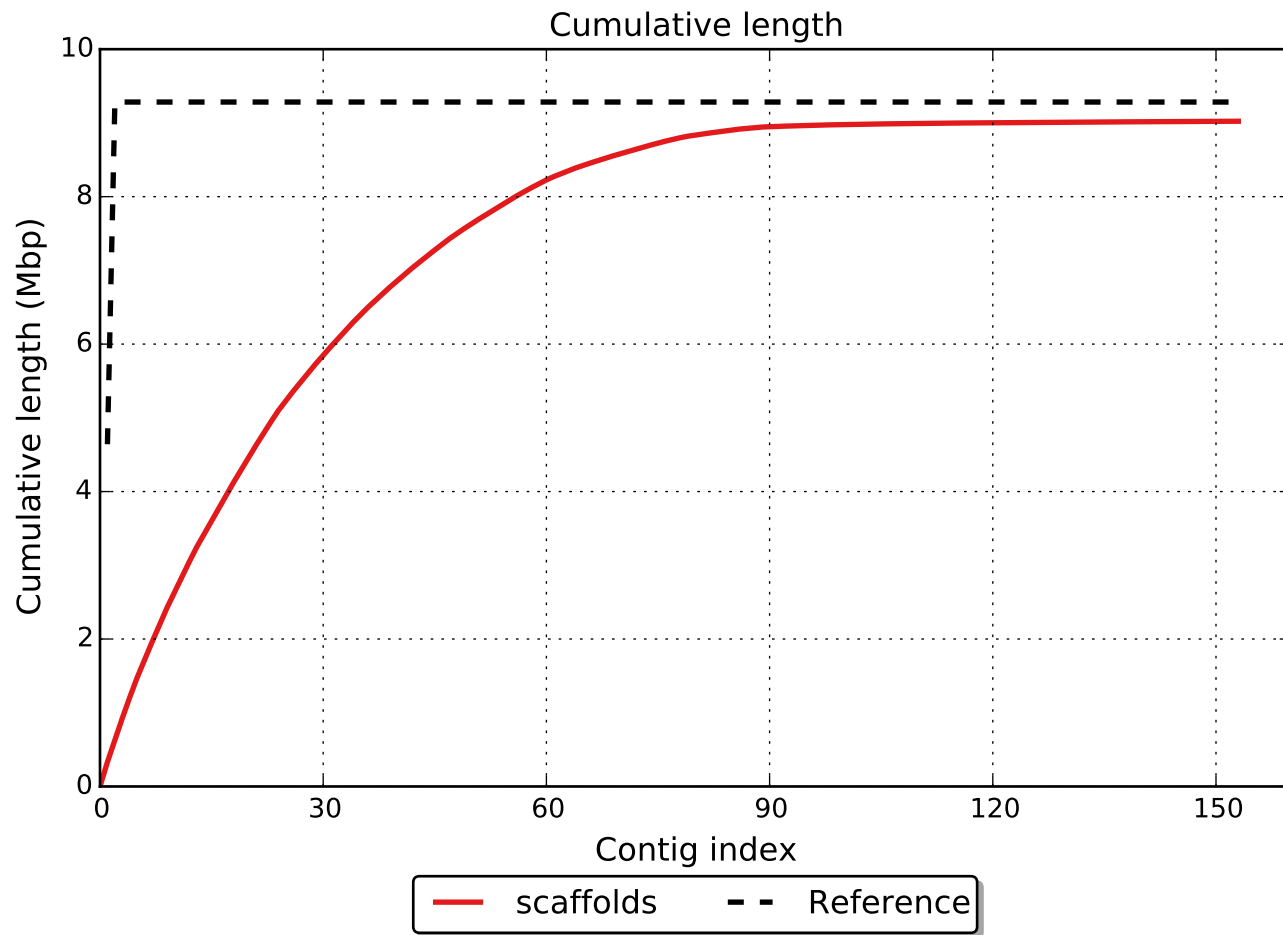
Unaligned report

	scaffolds
# fully unaligned contigs	16
Fully unaligned length	12501
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	447
# N's	0

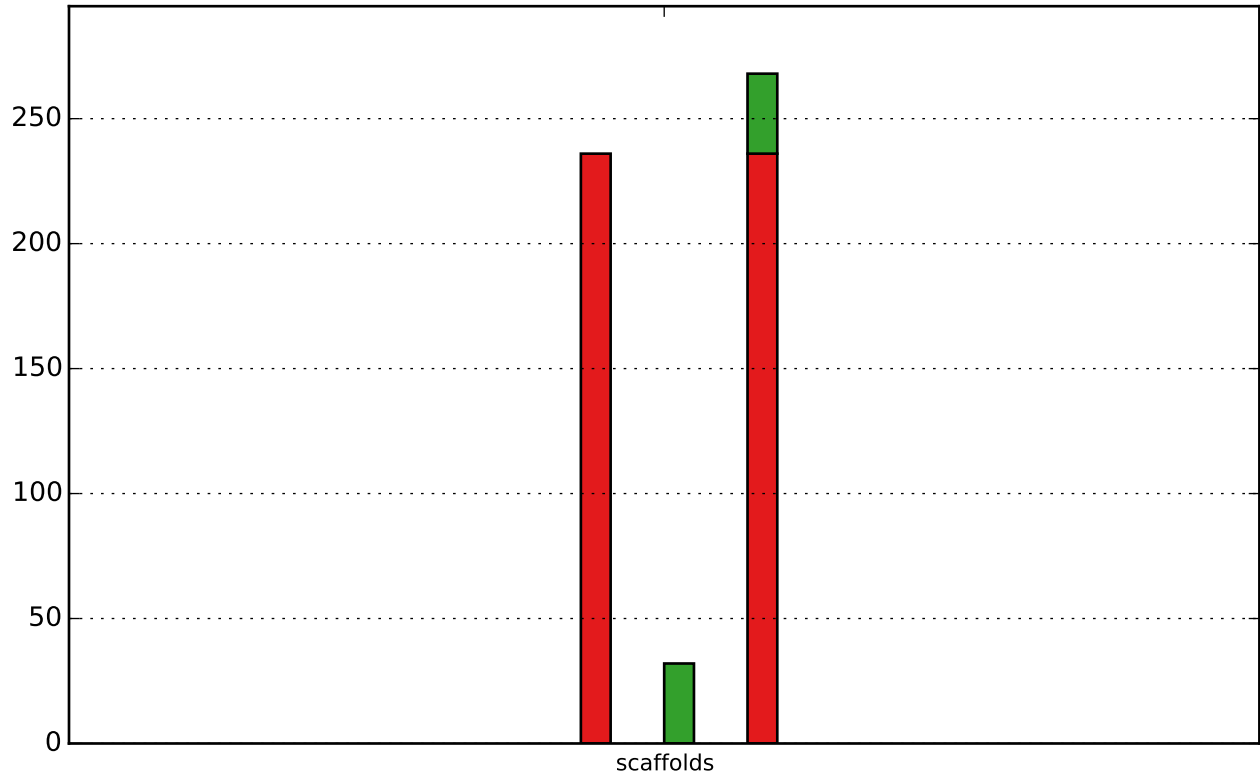
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

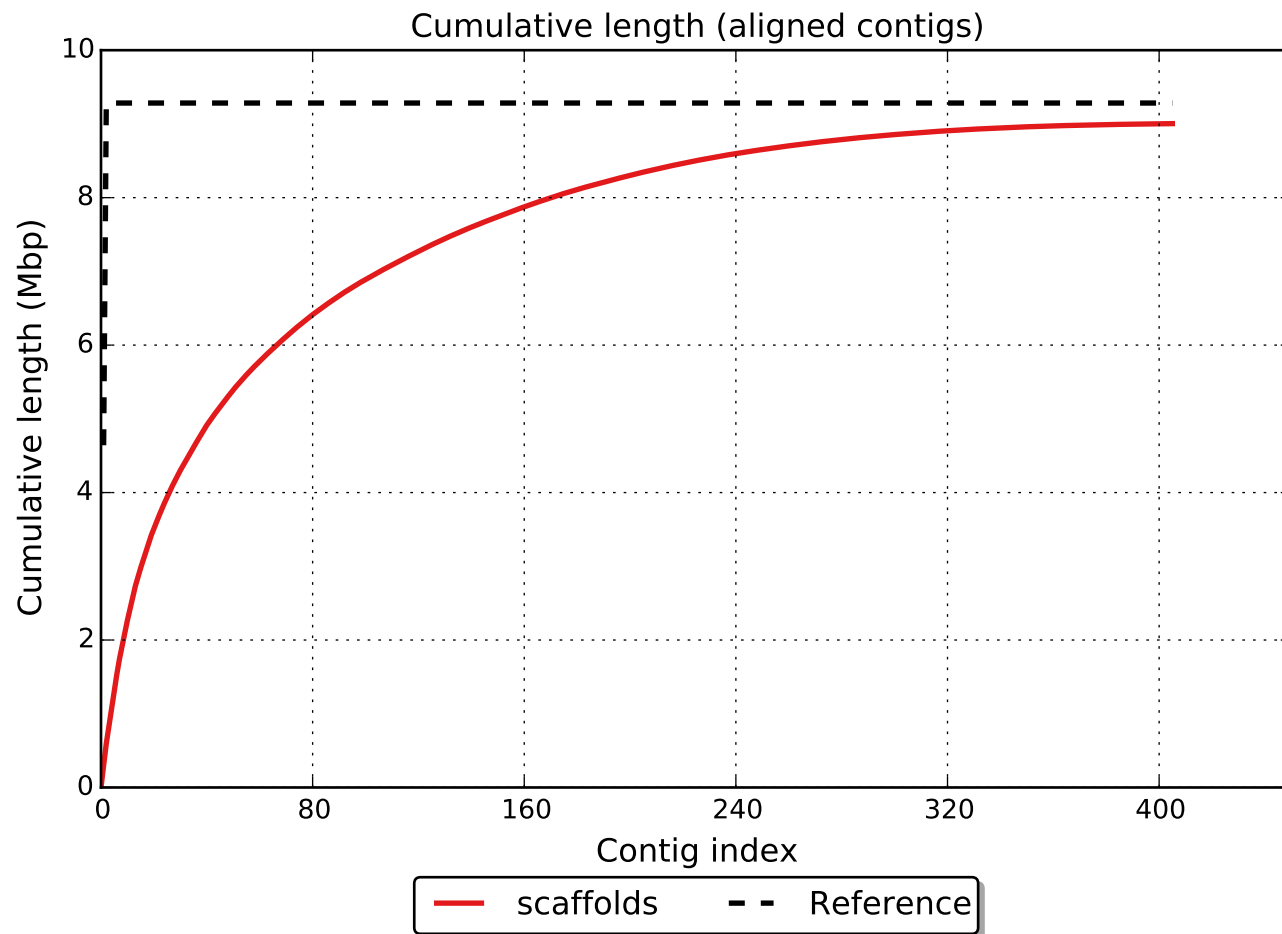
Nx





Misassemblies





NAx

