

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	2
# misassembled contigs	1
Misassembled contigs length	210680
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.463
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	752.92
# indels per 100 kbp	0.88
Largest alignment	332068
NA50	164195
NA75	91954
LA50	21
LA75	39

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	2
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	210680
# local misassemblies	4
# mismatches	68123
# indels	80
# short indels	79
# long indels	1
Indels length	95

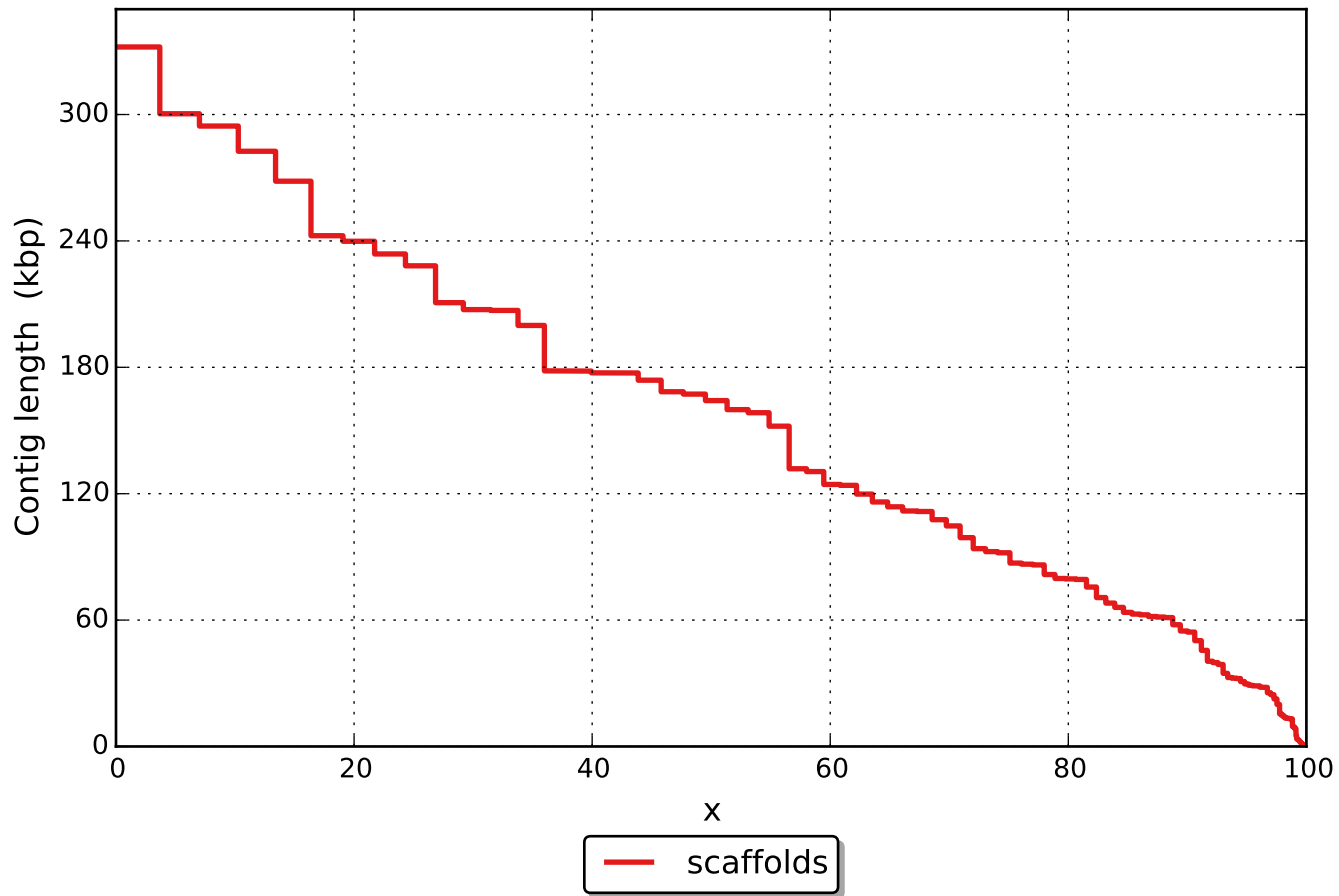
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

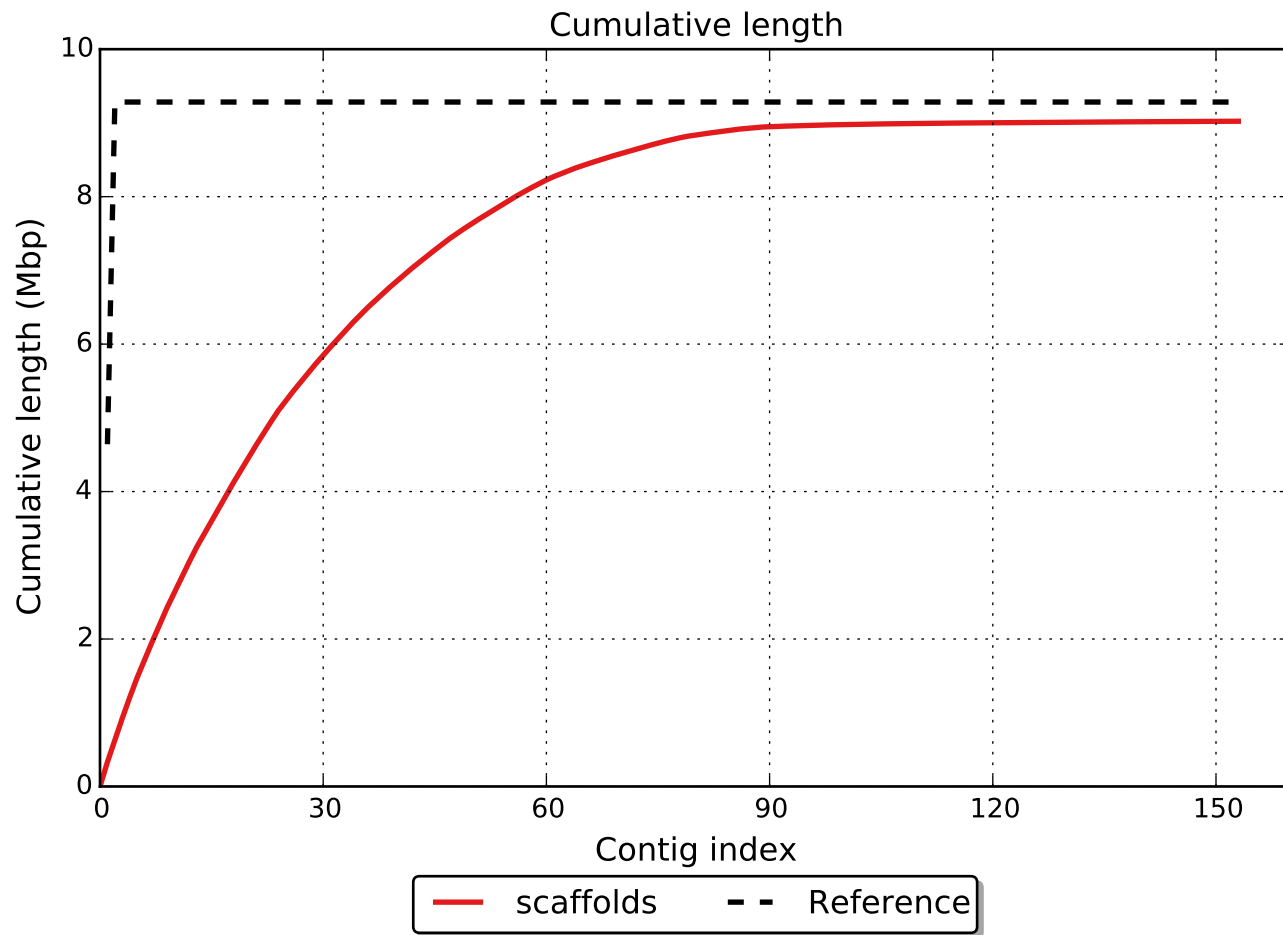
Unaligned report

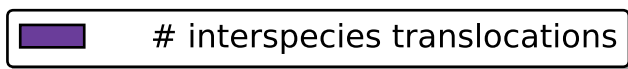
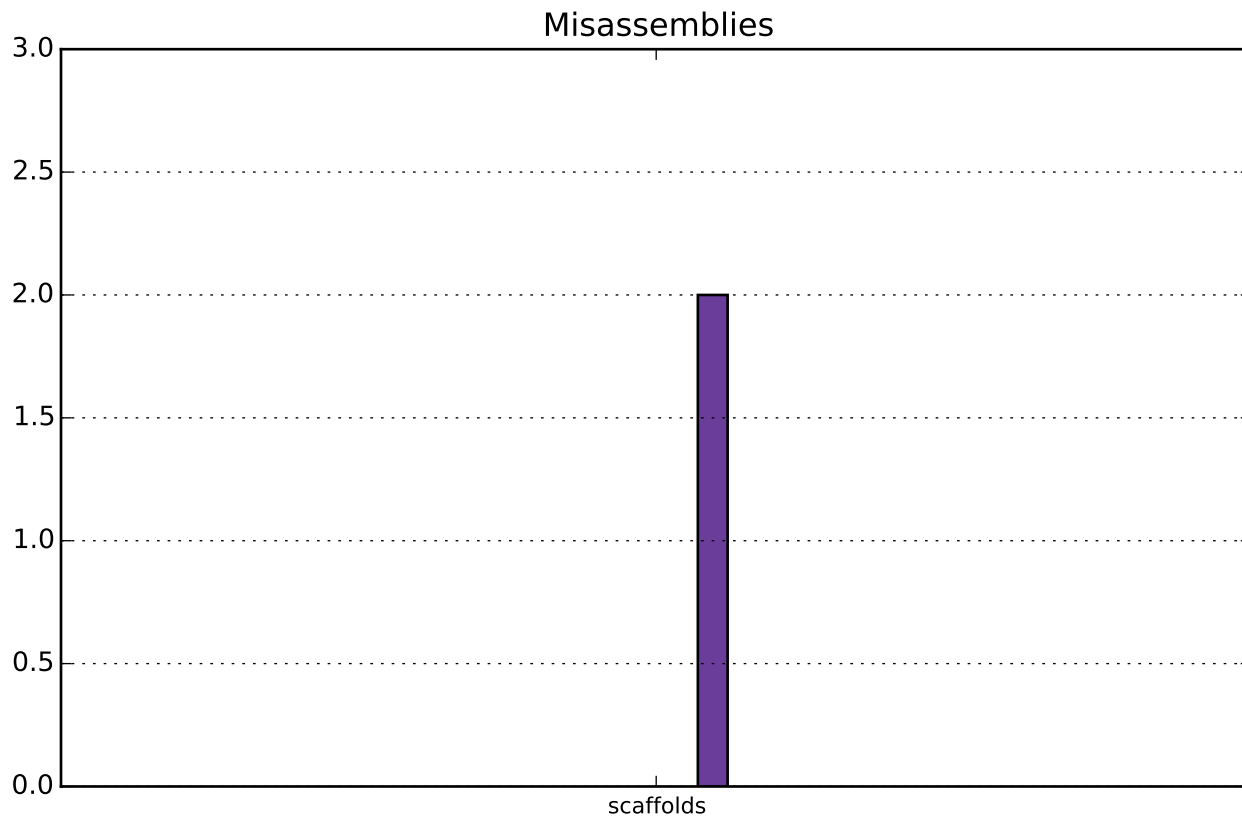
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

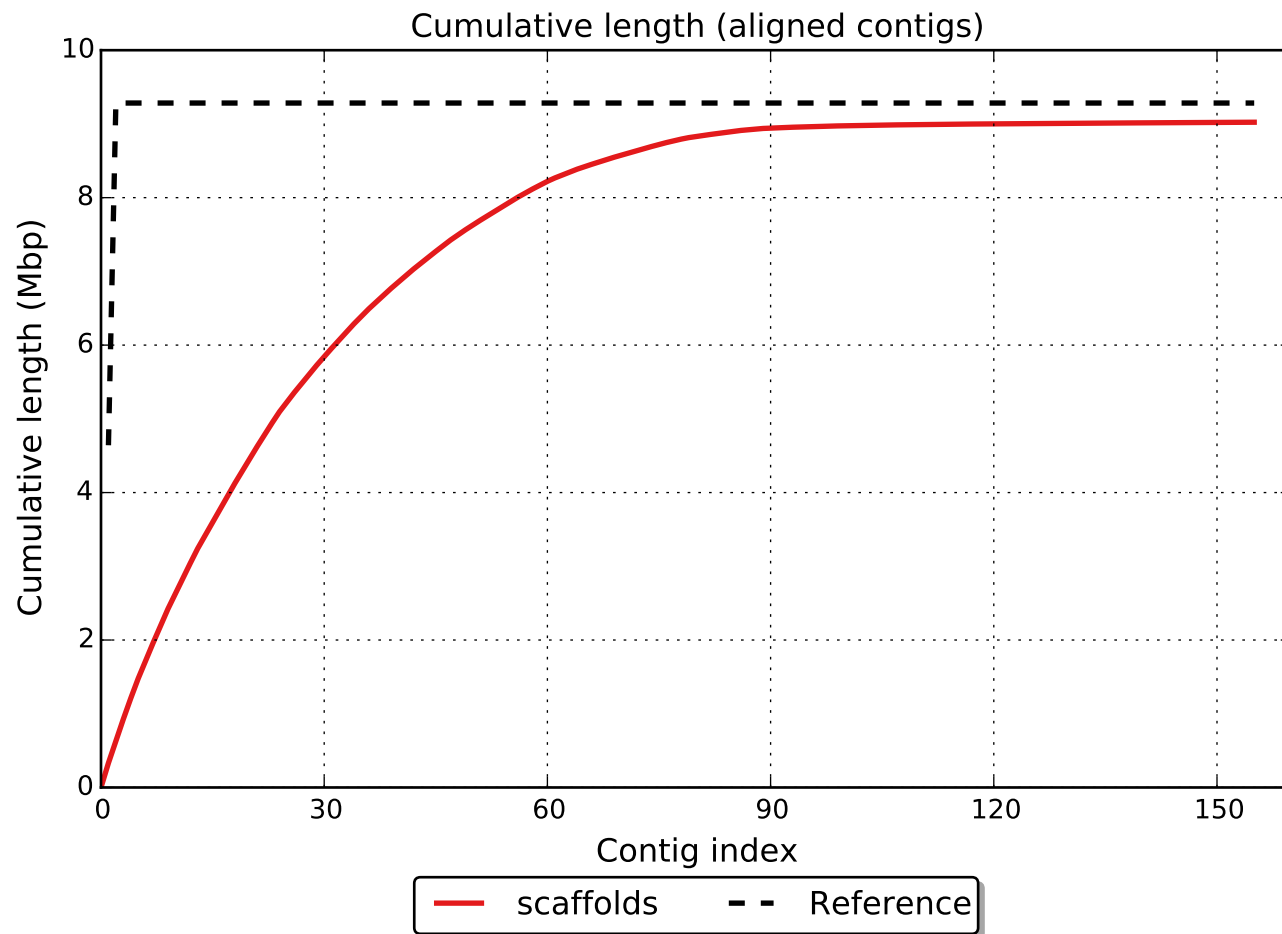
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

