

Report

	scaffolds
# contigs (≥ 0 bp)	302
# contigs (≥ 1000 bp)	121
# contigs (≥ 5000 bp)	92
# contigs (≥ 10000 bp)	87
# contigs (≥ 25000 bp)	75
# contigs (≥ 50000 bp)	58
Total length (≥ 0 bp)	9077926
Total length (≥ 1000 bp)	9011157
Total length (≥ 5000 bp)	8960493
Total length (≥ 10000 bp)	8921146
Total length (≥ 25000 bp)	8704633
Total length (≥ 50000 bp)	8130674
# contigs	154
Largest contig	527156
Total length	9033467
Reference length	9283304
N50	132337
N75	86976
L50	19
L75	39
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.444
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	648.97
# indels per 100 kbp	0.84
Largest alignment	527156
NA50	132337
NA75	86976
LA50	19
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	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# mismatches	58706
# indels	76
# short indels	76
# long indels	0
Indels length	82

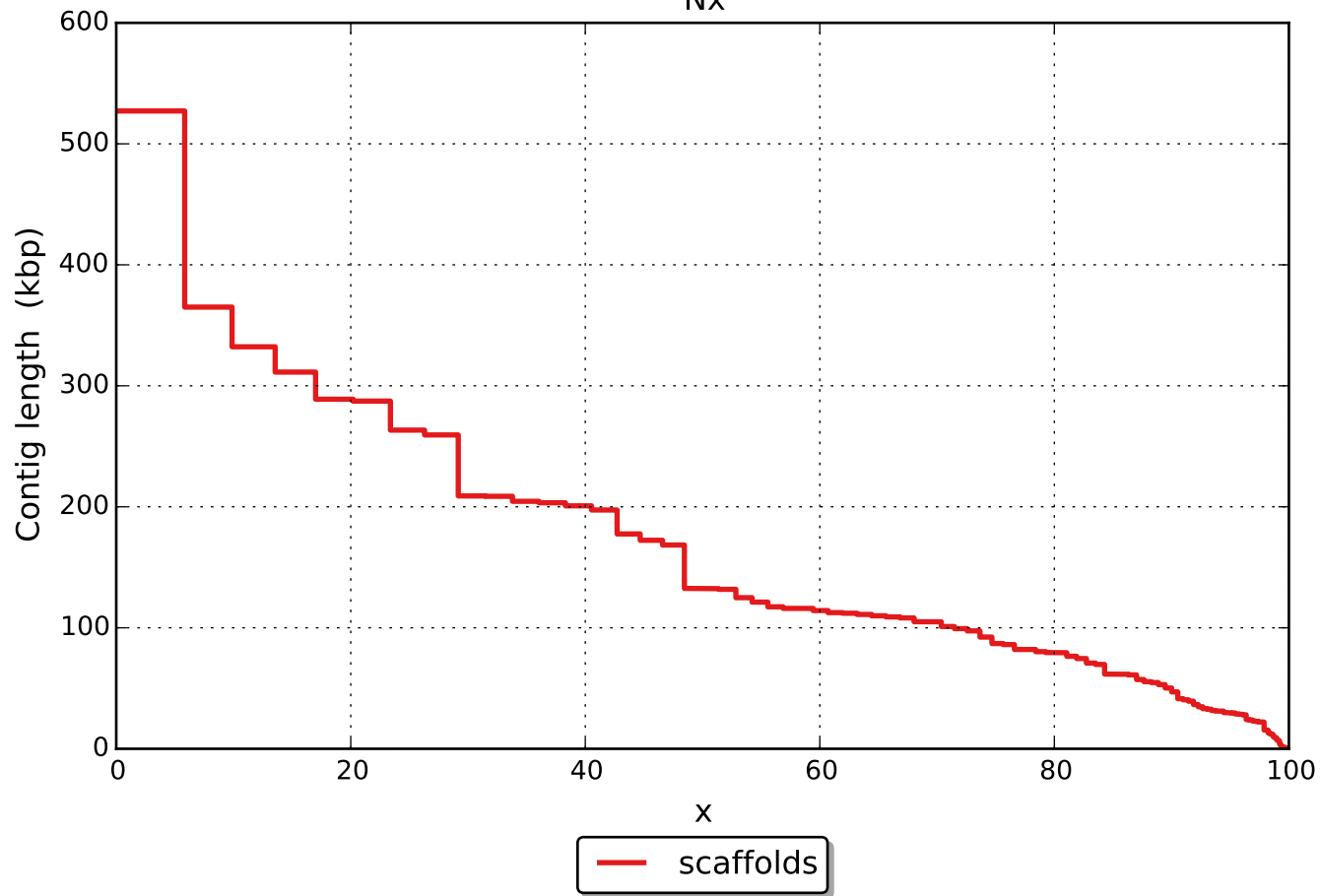
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

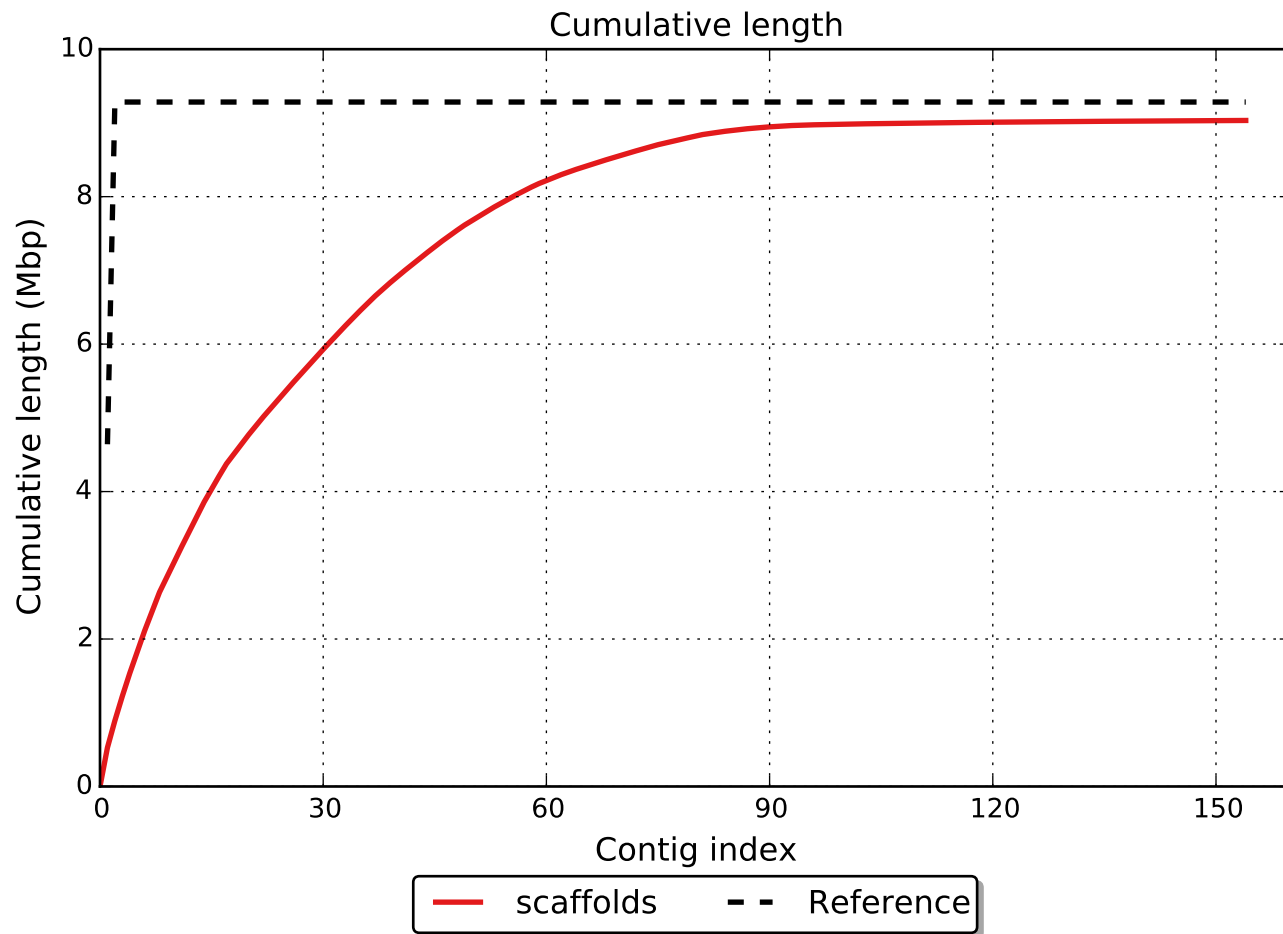
Unaligned report

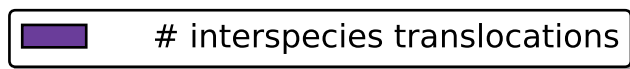
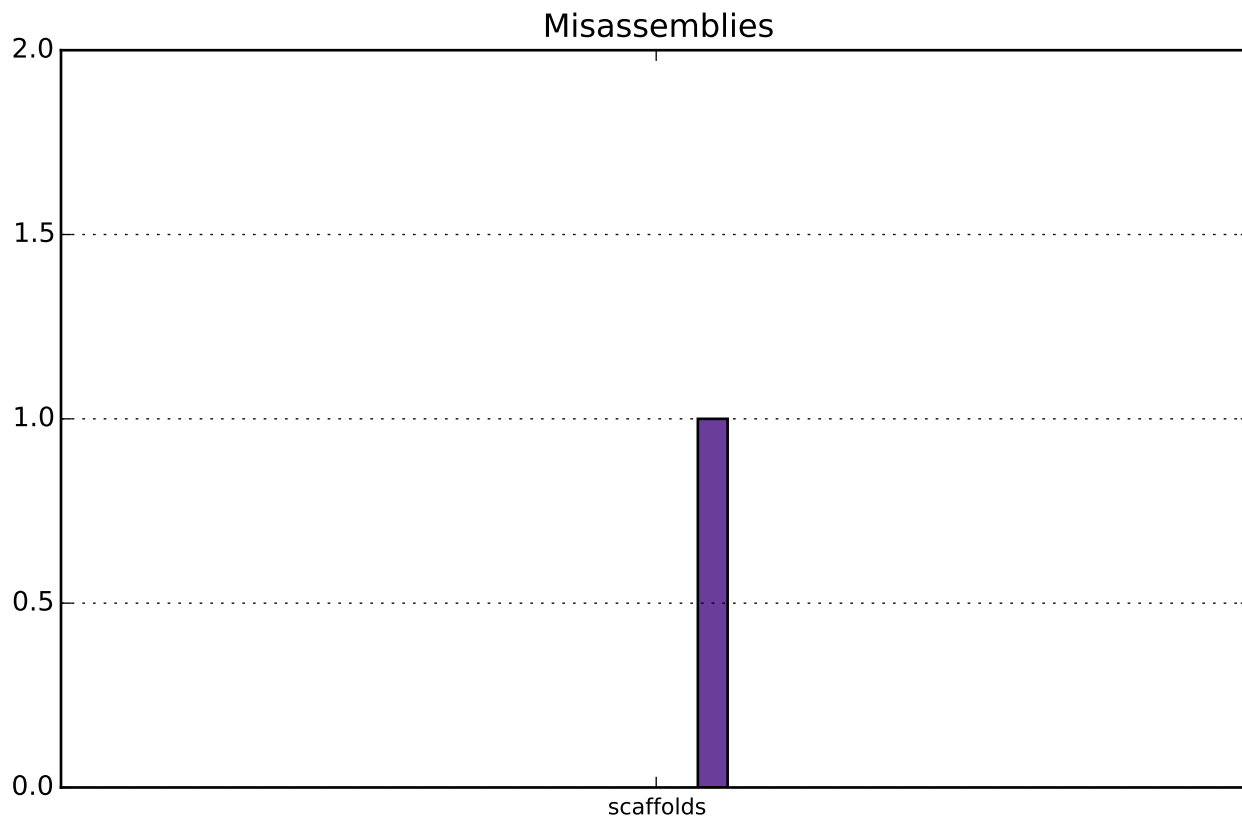
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

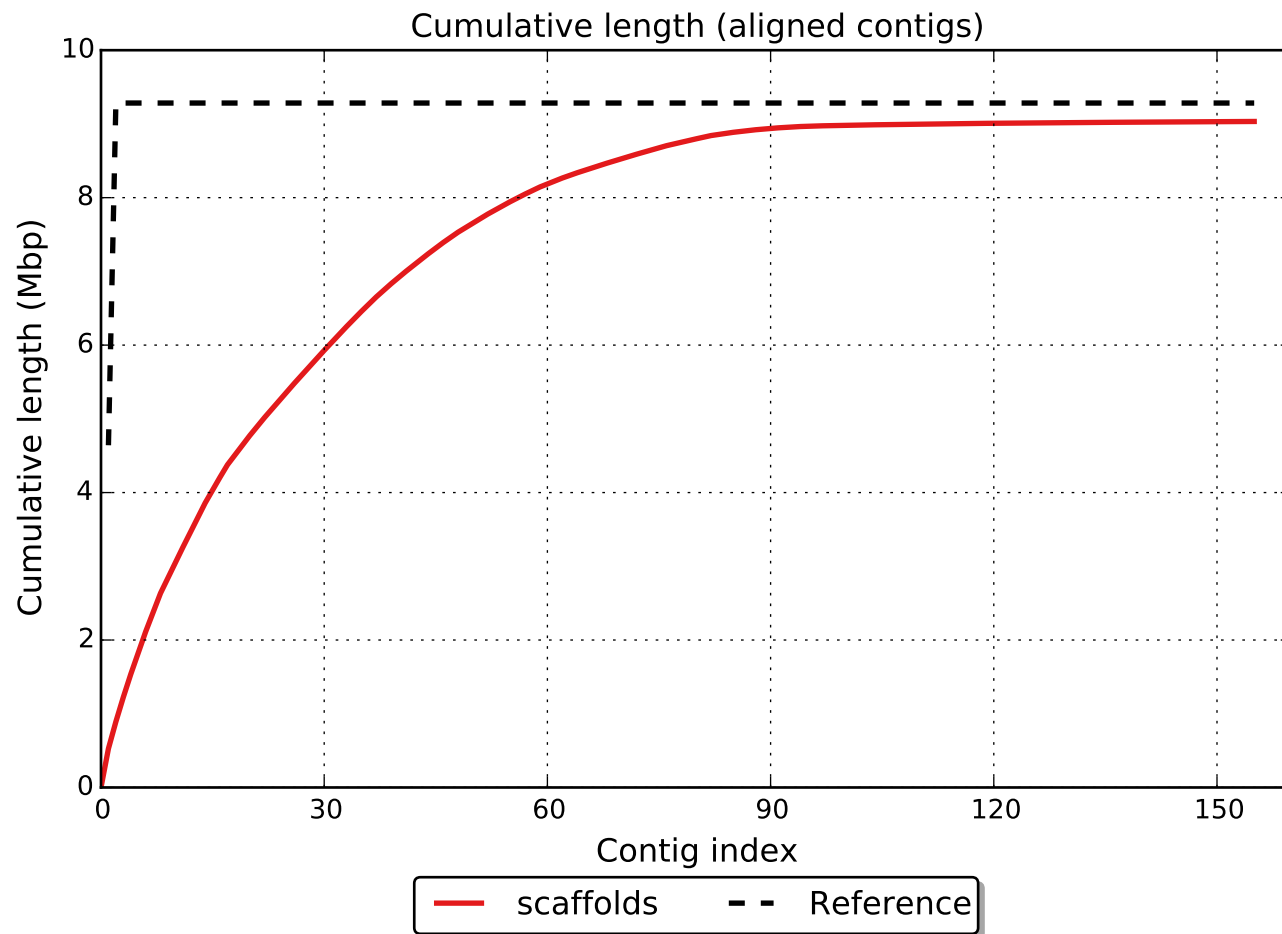
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

