

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	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.102
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	550.25
# indels per 100 kbp	1.00
Largest alignment	600951
NA50	200817
NA75	110783
LA50	16
LA75	31

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	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	50112
# indels	91
# short indels	91
# long indels	0
Indels length	92

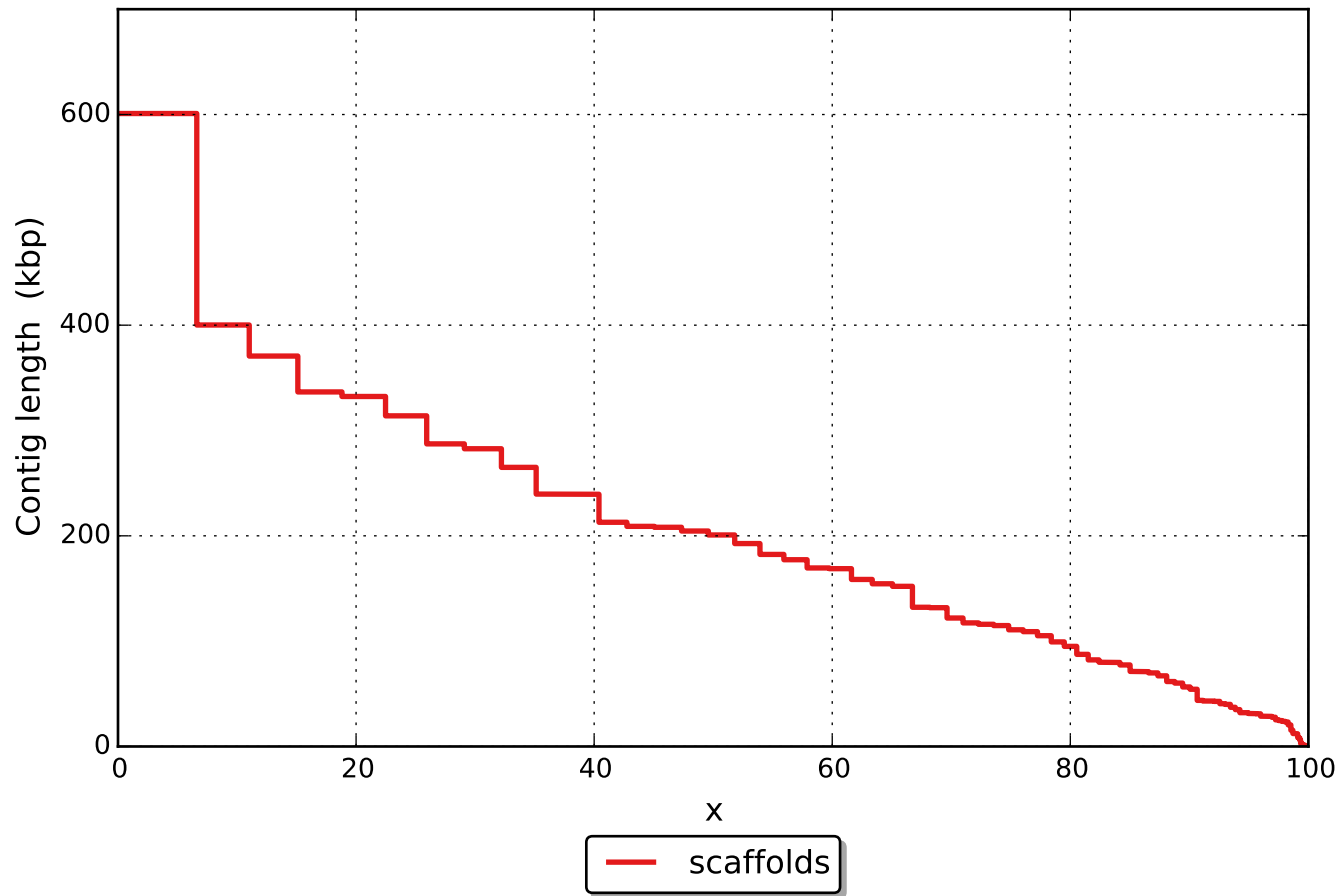
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

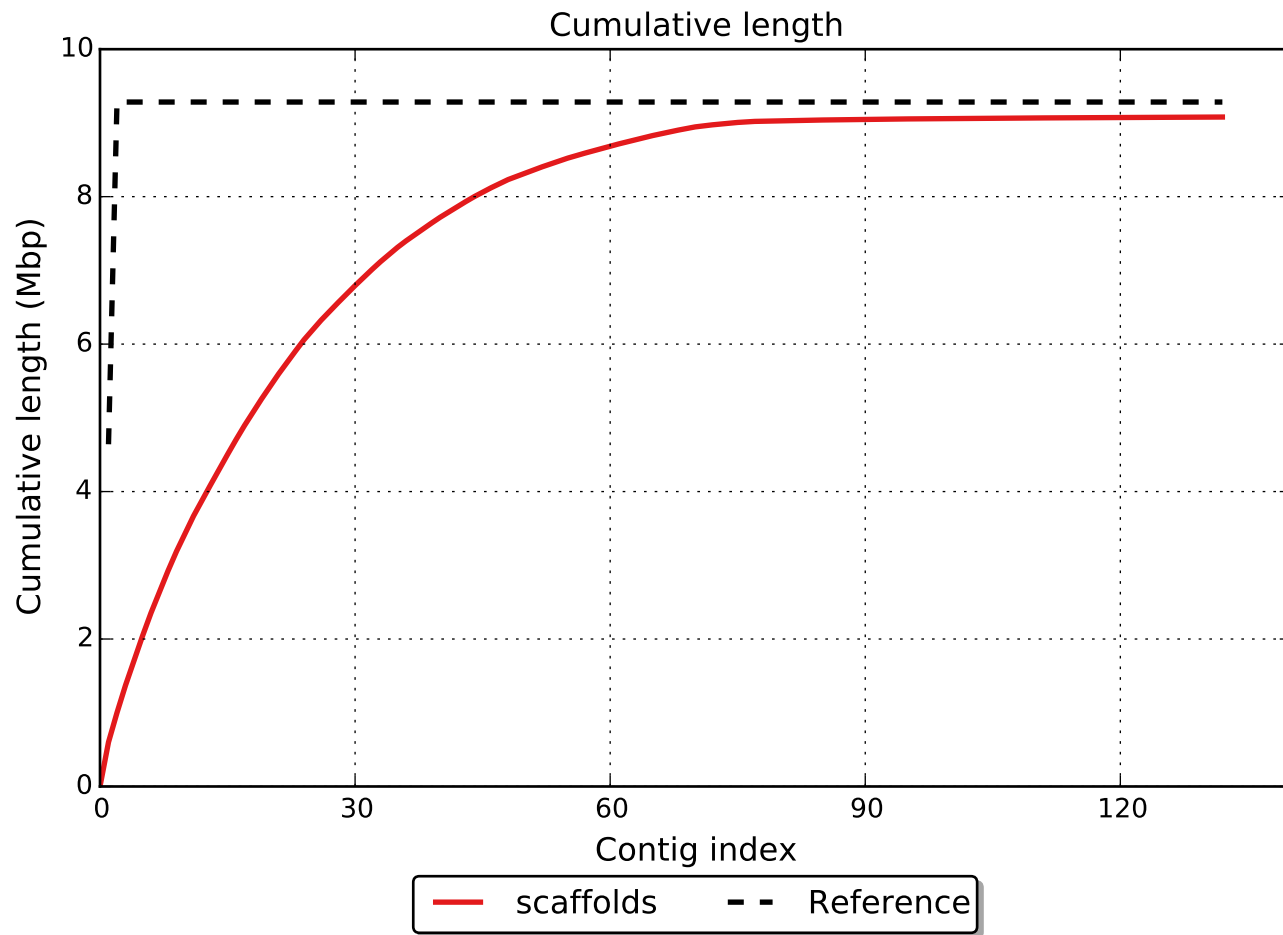
Unaligned report

	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

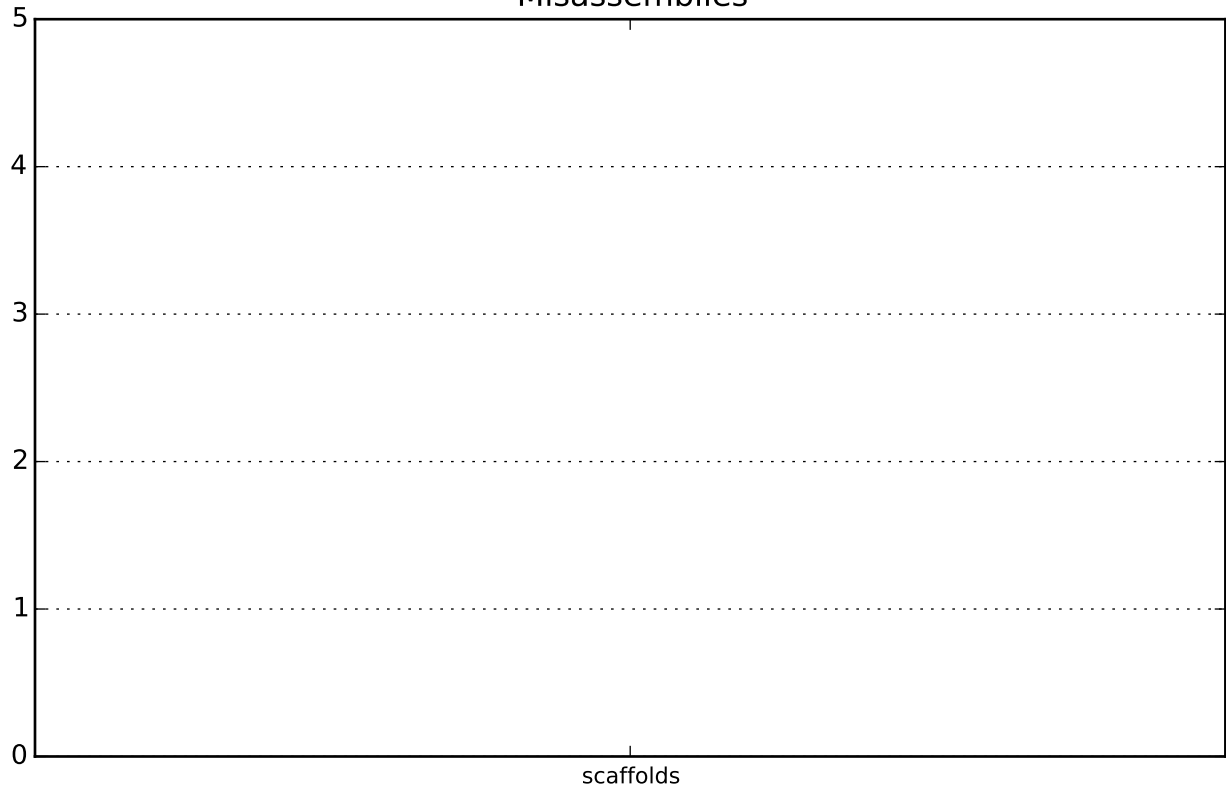
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

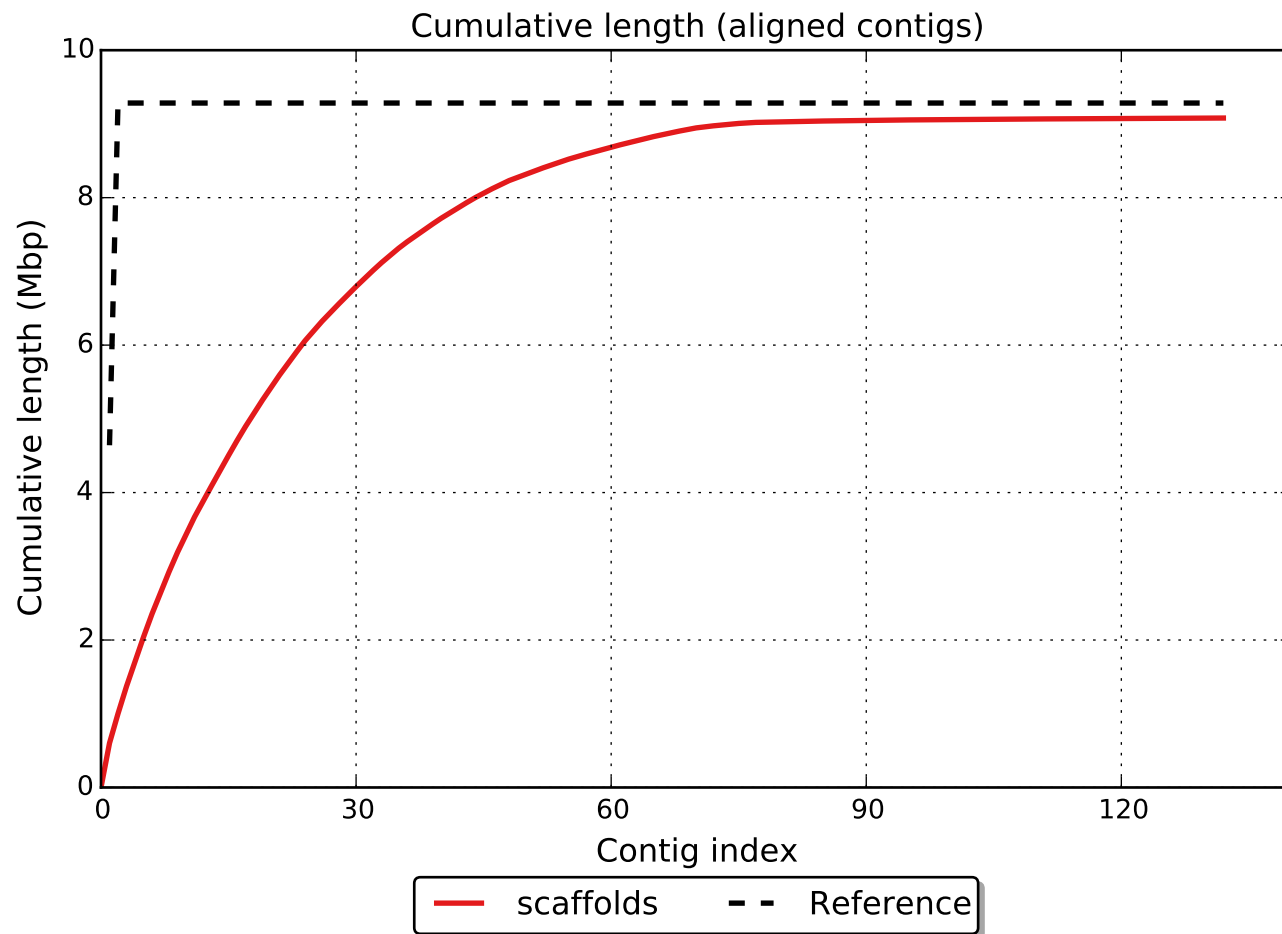
Nx





Misassemblies





NAx

