

Report

	scaffolds
# contigs (≥ 0 bp)	408
# contigs (≥ 1000 bp)	142
# contigs (≥ 5000 bp)	94
# contigs (≥ 10000 bp)	90
# contigs (≥ 25000 bp)	77
# contigs (≥ 50000 bp)	54
Total length (≥ 0 bp)	9004717
Total length (≥ 1000 bp)	8899397
Total length (≥ 5000 bp)	8801812
Total length (≥ 10000 bp)	8773143
Total length (≥ 25000 bp)	8562938
Total length (≥ 50000 bp)	7768873
# contigs	203
Largest contig	475325
Total length	8939282
Reference length	9283304
N50	164261
N75	80872
L50	19
L75	39
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.783
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	838.68
# indels per 100 kbp	1.10
Largest alignment	475325
NA50	164261
NA75	80872
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	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	75353
# indels	99
# short indels	97
# long indels	2
Indels length	130

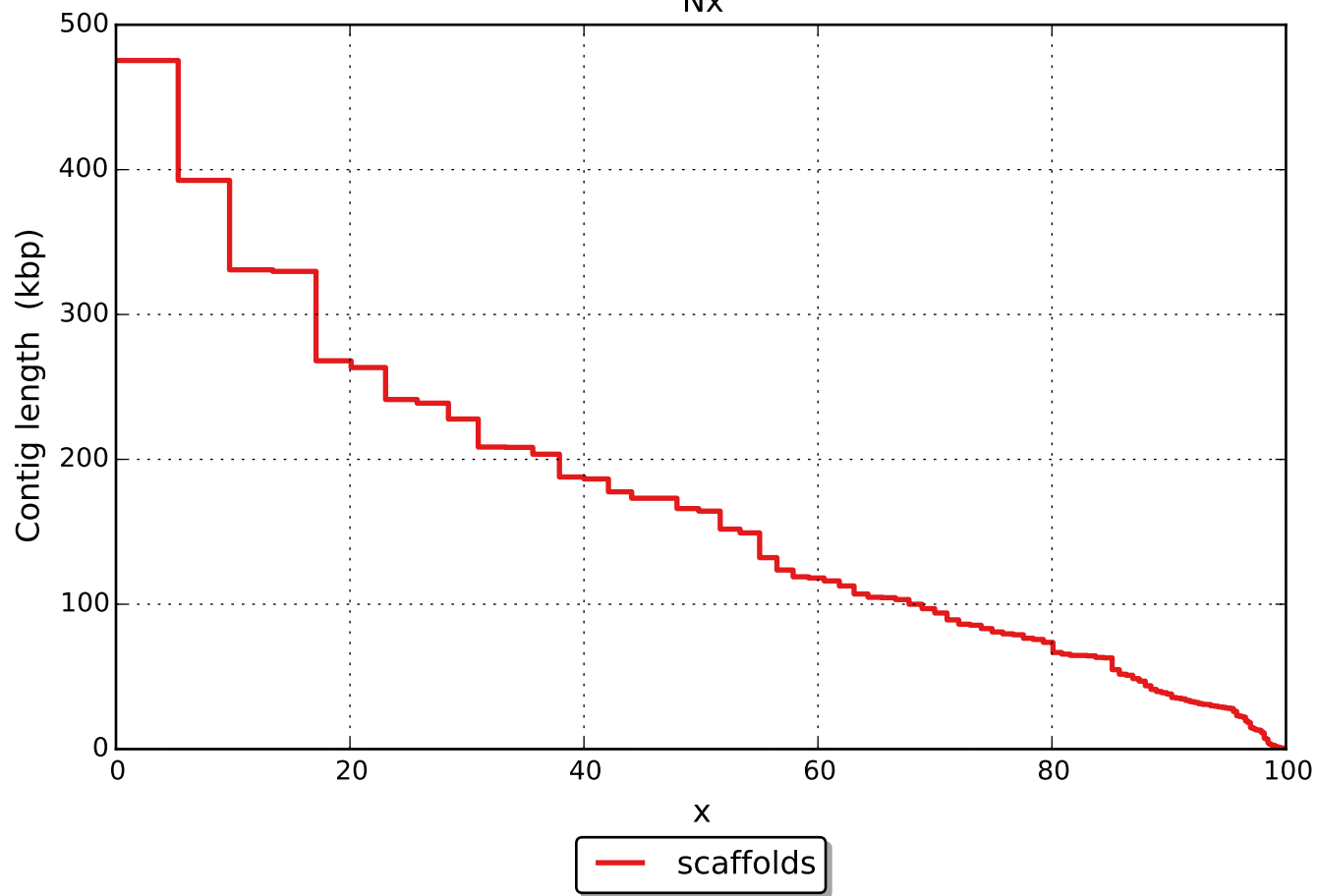
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

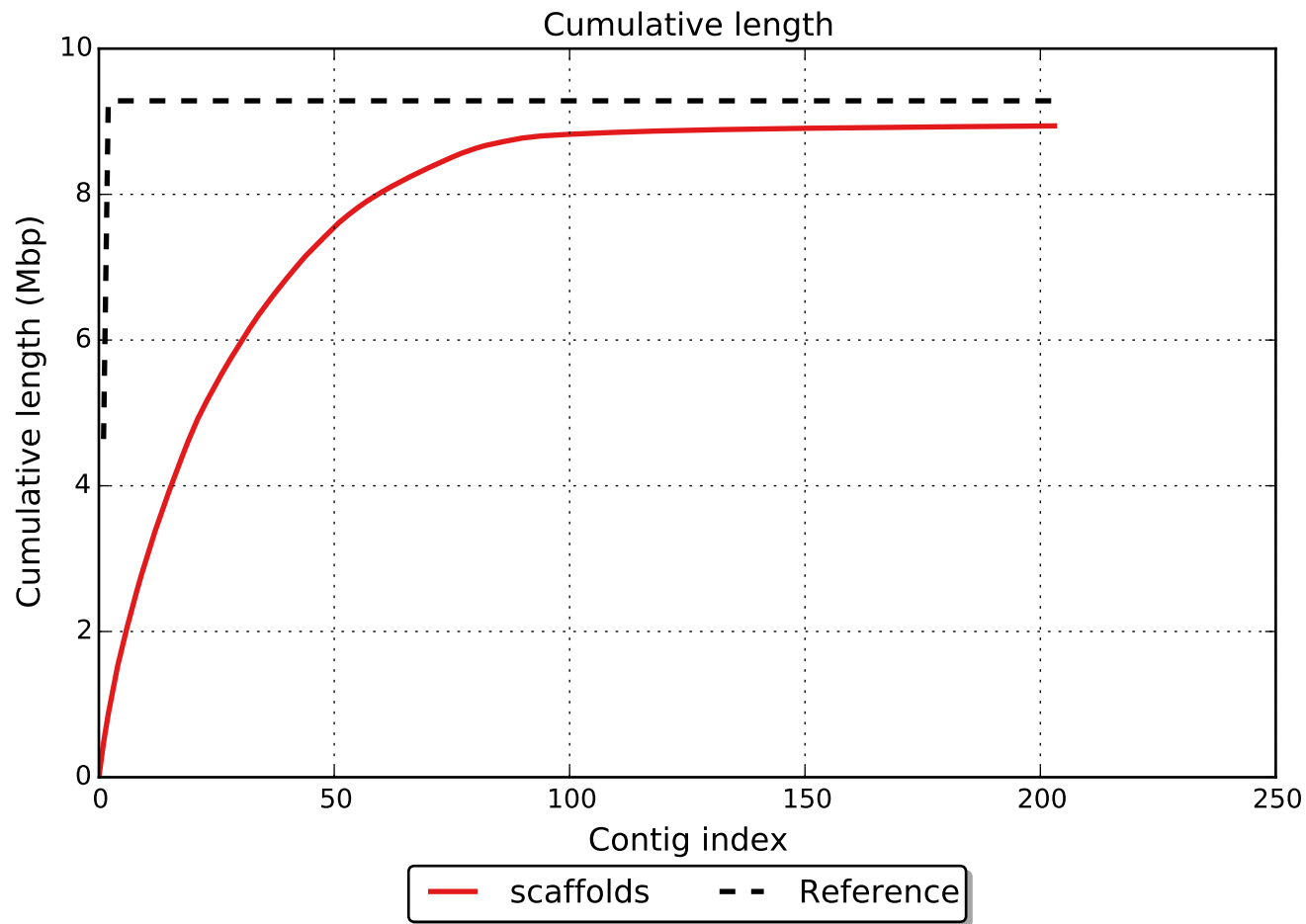
Unaligned report

	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

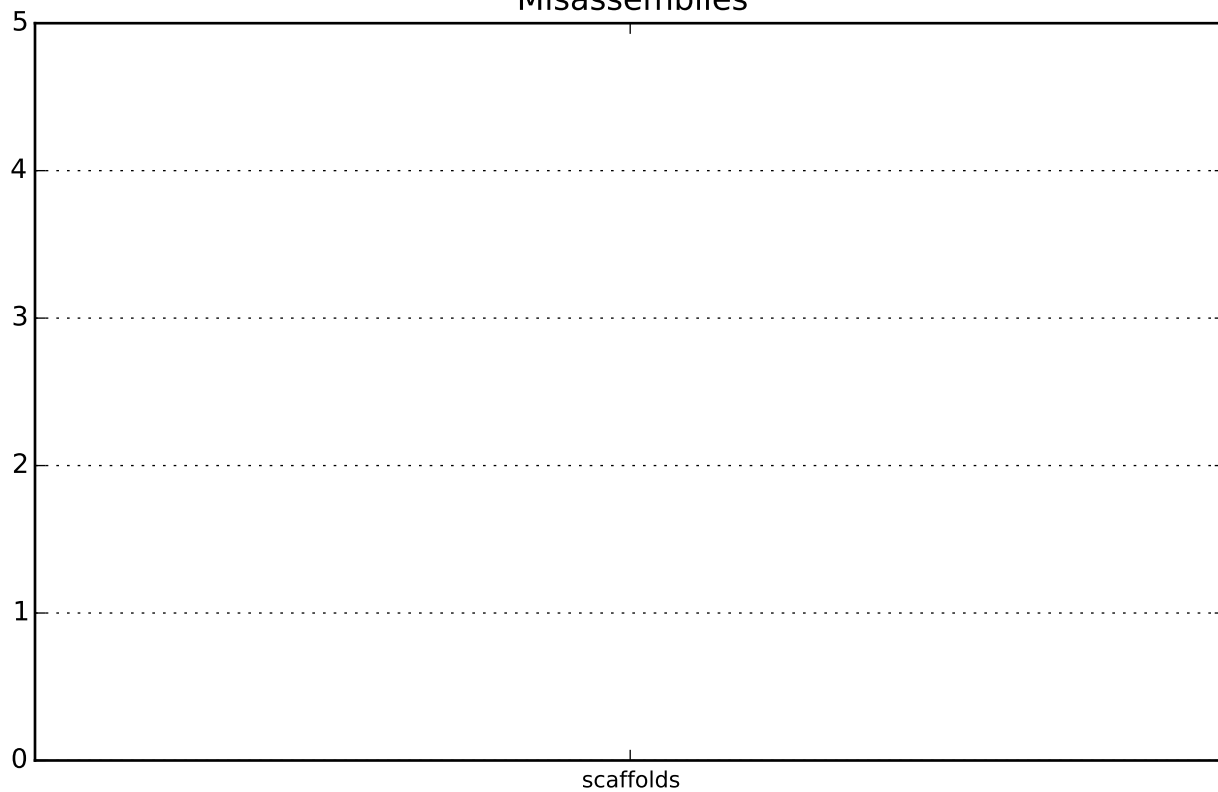
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

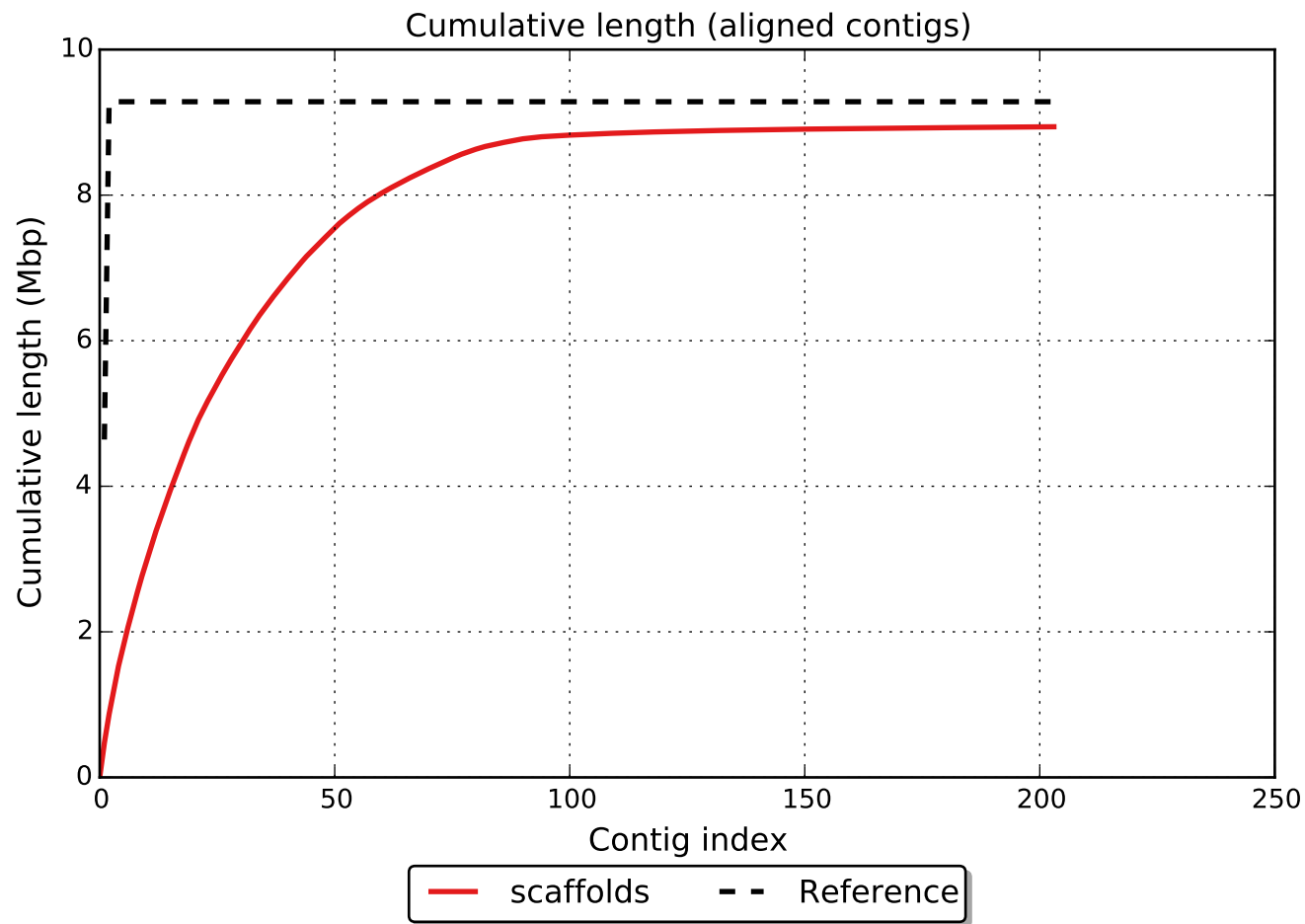
Nx





Misassemblies





NAx

