

Report

	scaffolds
# contigs (≥ 0 bp)	187
# contigs (≥ 1000 bp)	86
# contigs (≥ 5000 bp)	71
# contigs (≥ 10000 bp)	67
# contigs (≥ 25000 bp)	62
# contigs (≥ 50000 bp)	48
Total length (≥ 0 bp)	9140317
Total length (≥ 1000 bp)	9103206
Total length (≥ 5000 bp)	9082242
Total length (≥ 10000 bp)	9049457
Total length (≥ 25000 bp)	8968226
Total length (≥ 50000 bp)	8515864
# contigs	110
Largest contig	529642
Total length	9118481
Reference length	9283304
N50	210553
N75	117600
L50	14
L75	28
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	20404
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.196
Duplication ratio	1.000
# N's per 100 kbp	0.33
# mismatches per 100 kbp	402.39
# indels per 100 kbp	0.80
Largest alignment	529642
NA50	210553
NA75	117600
LA50	14
LA75	28

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	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	20404
# local misassemblies	0
# mismatches	36681
# indels	73
# short indels	73
# long indels	0
Indels length	76

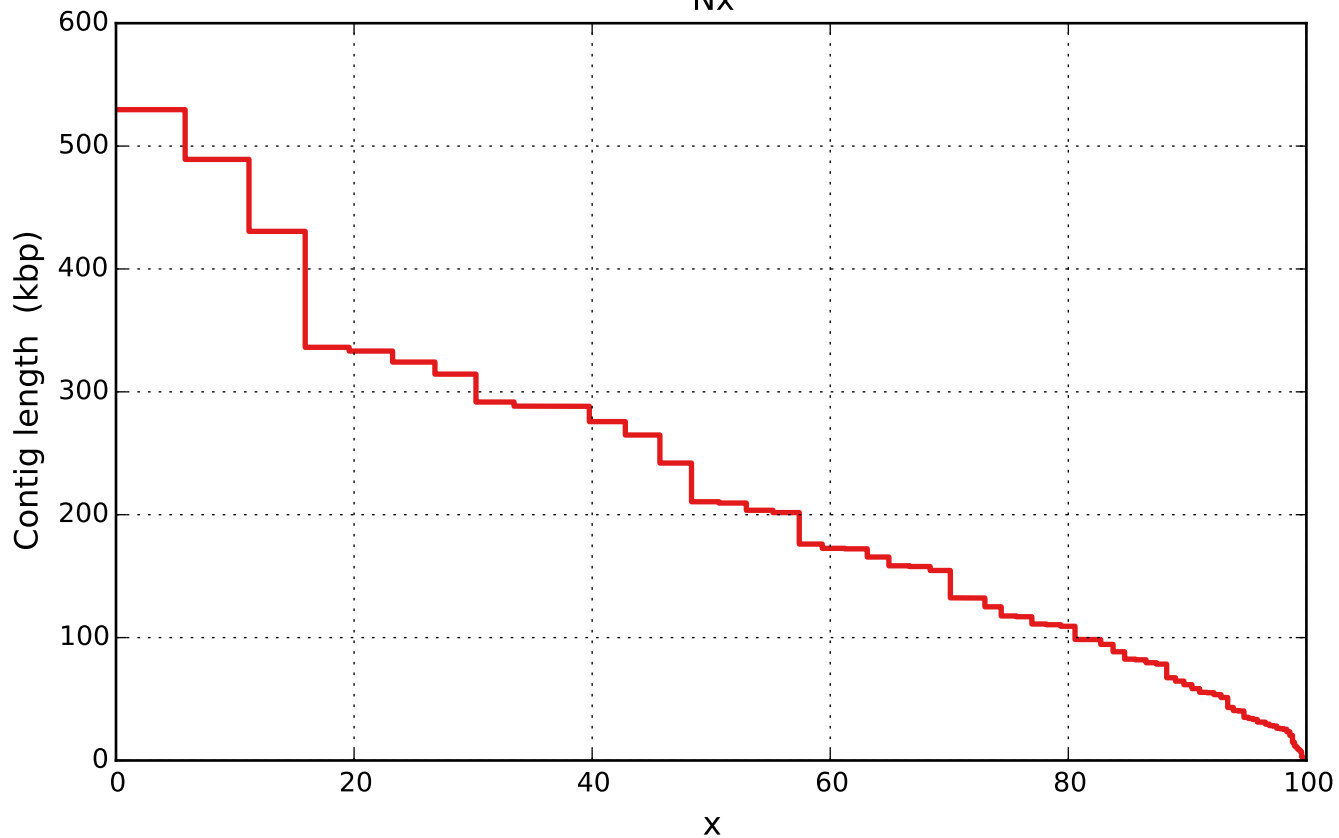
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

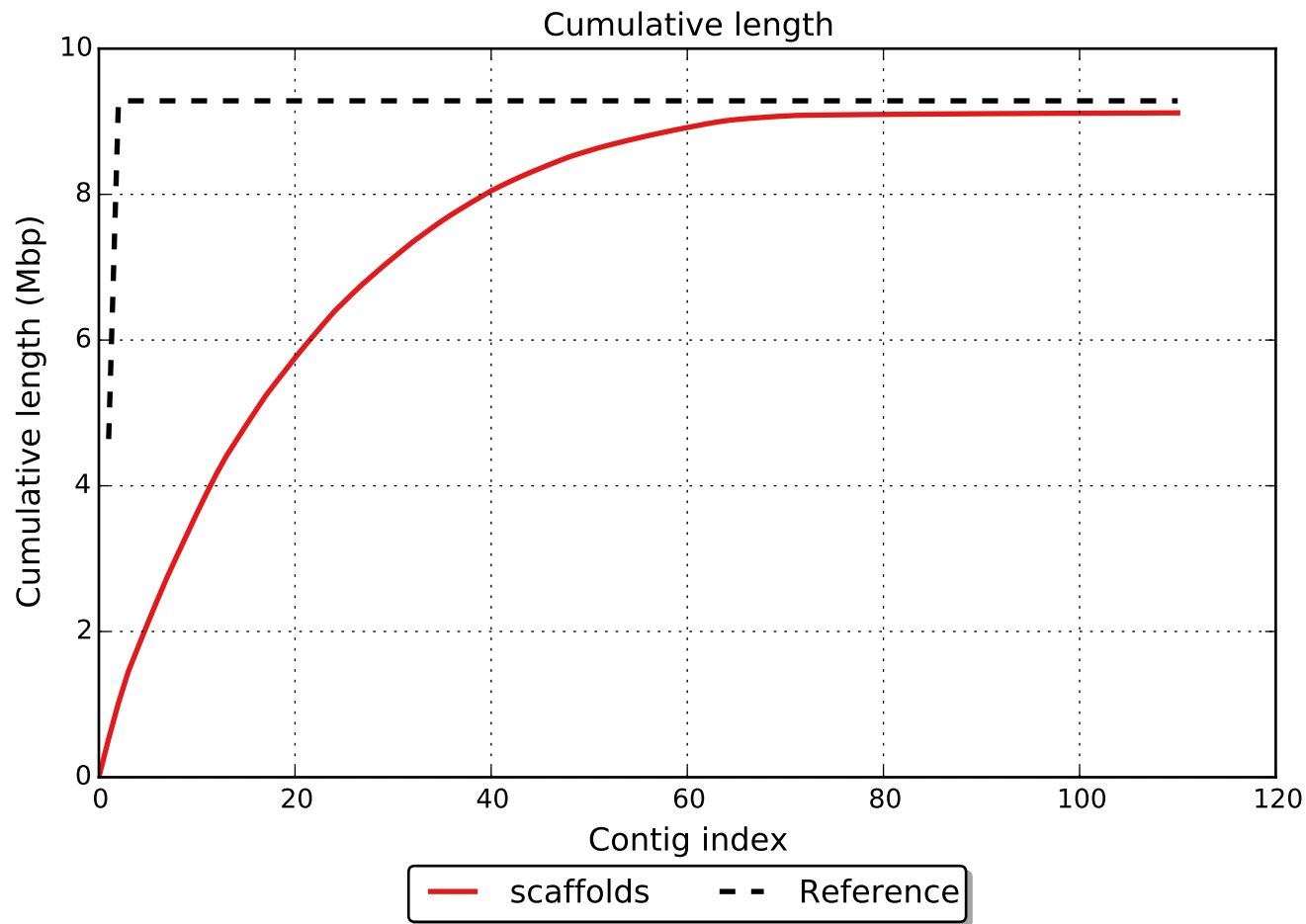
Unaligned report

	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	30

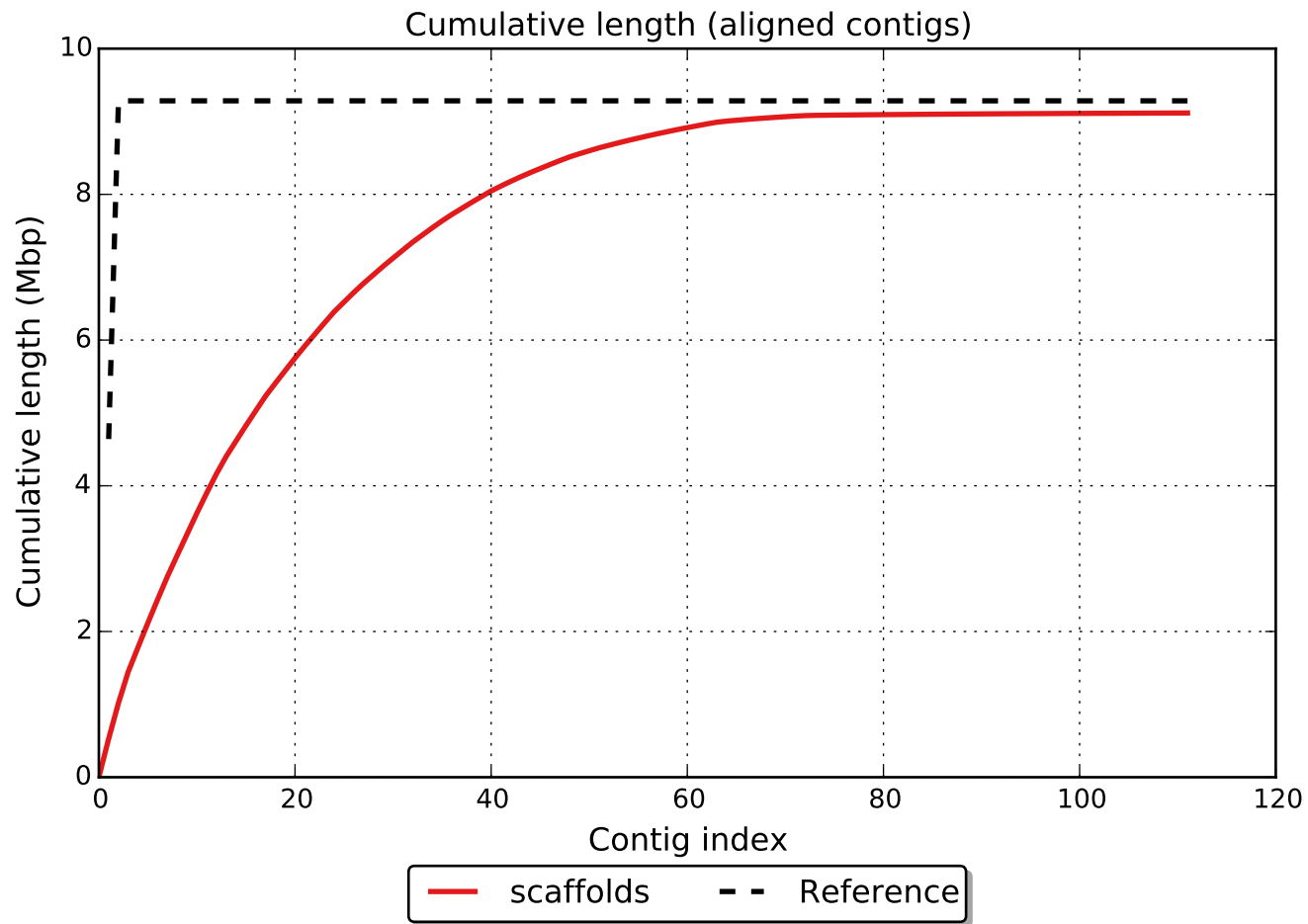
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

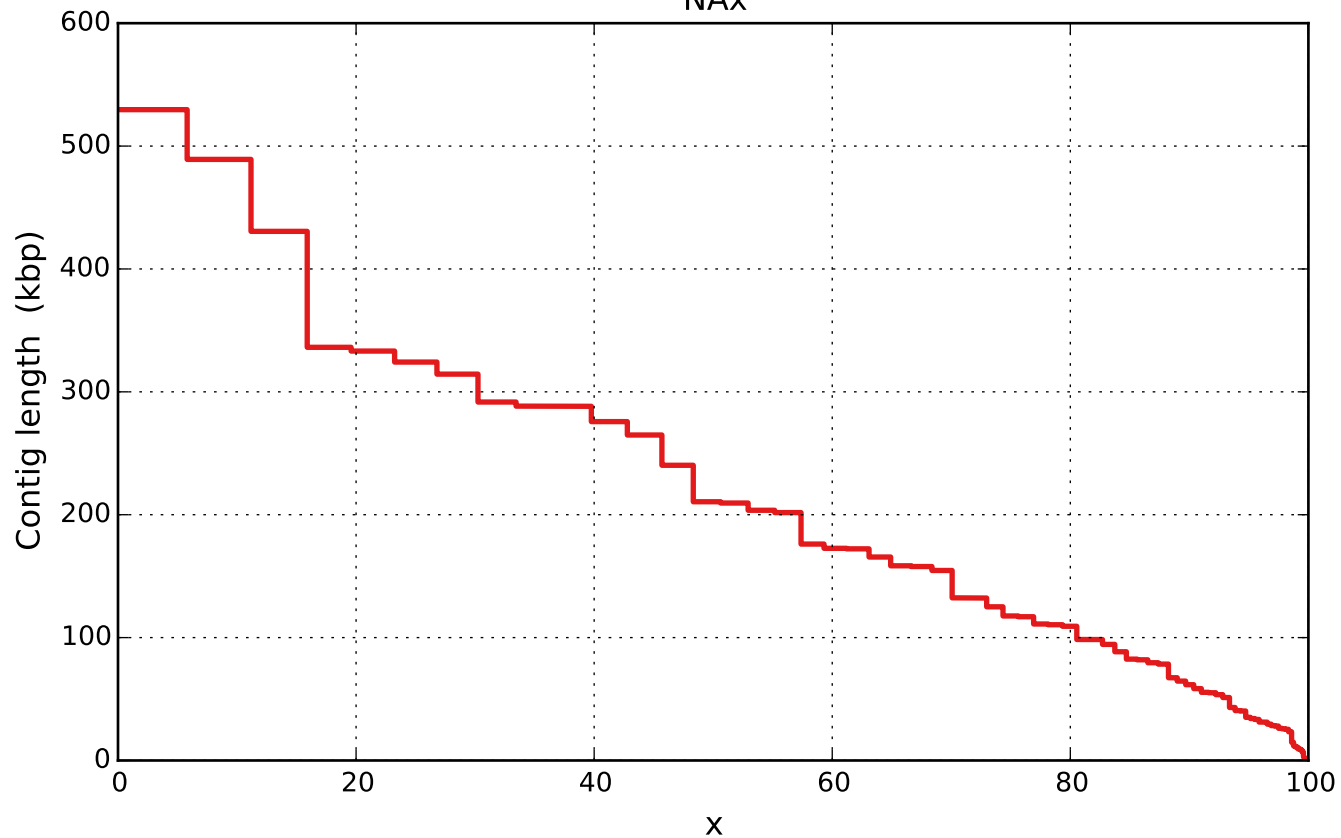








NAx



— scaffolds