

Report

	scaffolds
# contigs (≥ 0 bp)	129
# contigs (≥ 1000 bp)	81
# contigs (≥ 5000 bp)	65
# contigs (≥ 10000 bp)	62
# contigs (≥ 25000 bp)	55
# contigs (≥ 50000 bp)	42
Total length (≥ 0 bp)	9154890
Total length (≥ 1000 bp)	9138006
Total length (≥ 5000 bp)	9102733
Total length (≥ 10000 bp)	9079038
Total length (≥ 25000 bp)	8957964
Total length (≥ 50000 bp)	8511321
# contigs	92
Largest contig	1053360
Total length	9145425
Reference length	9283304
N50	224139
N75	132462
L50	11
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36005
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.532
Duplication ratio	1.000
# N's per 100 kbp	0.11
# mismatches per 100 kbp	147.27
# indels per 100 kbp	0.56
Largest alignment	1053360
NA50	224139
NA75	132462
LA50	11
LA75	24

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	36005
# local misassemblies	2
# mismatches	13471
# indels	51
# short indels	49
# long indels	2
Indels length	127

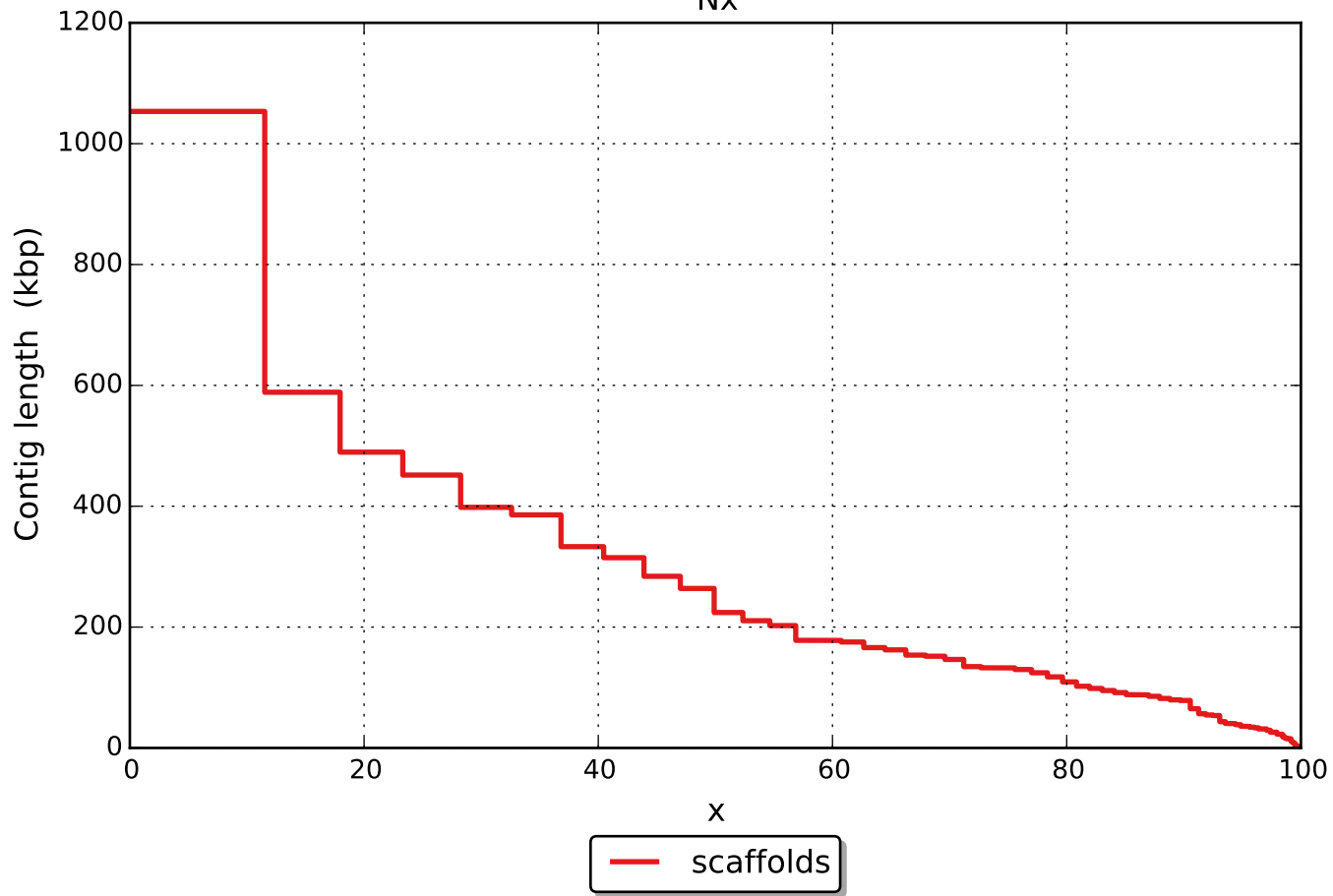
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

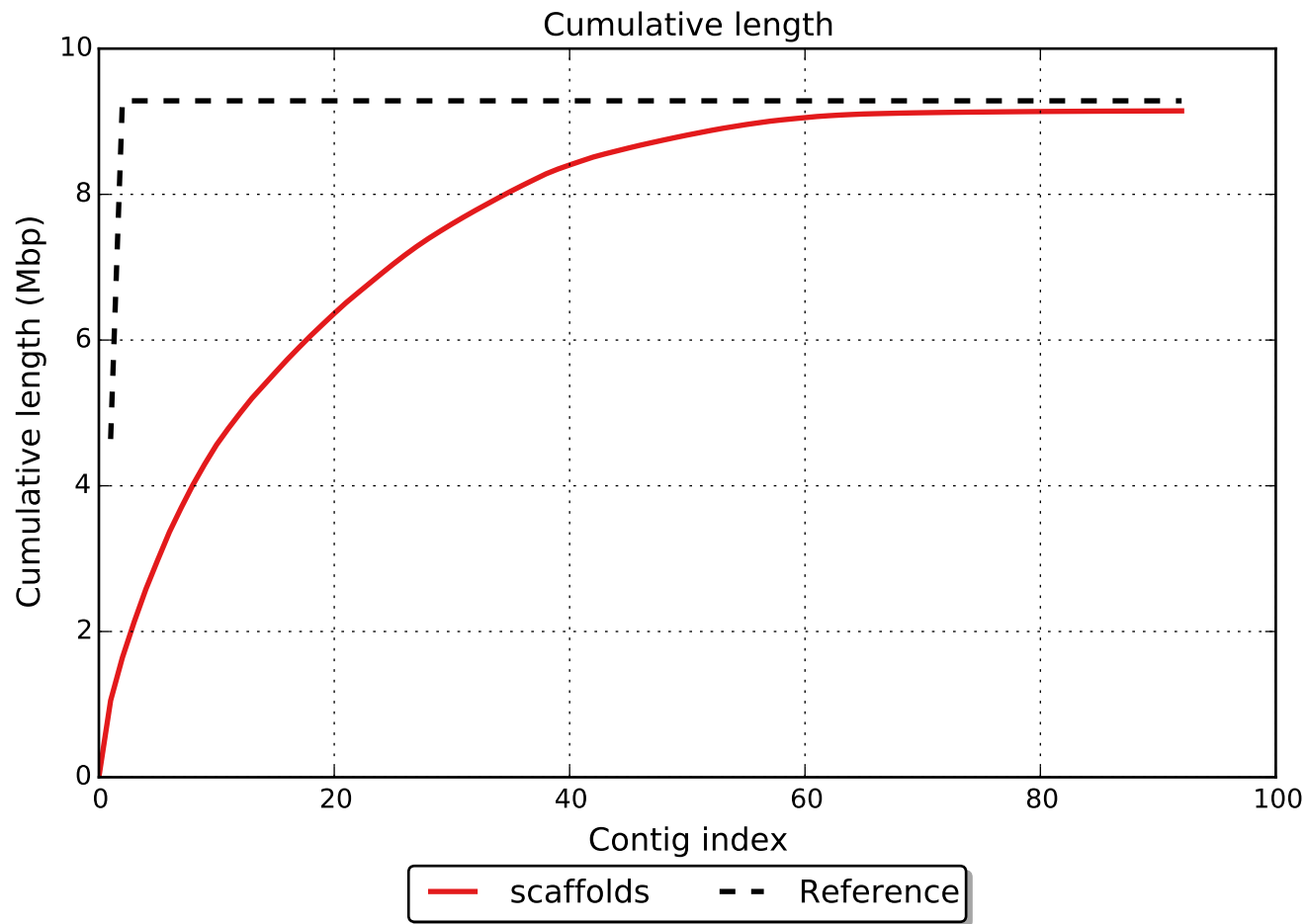
Unaligned report

	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	10

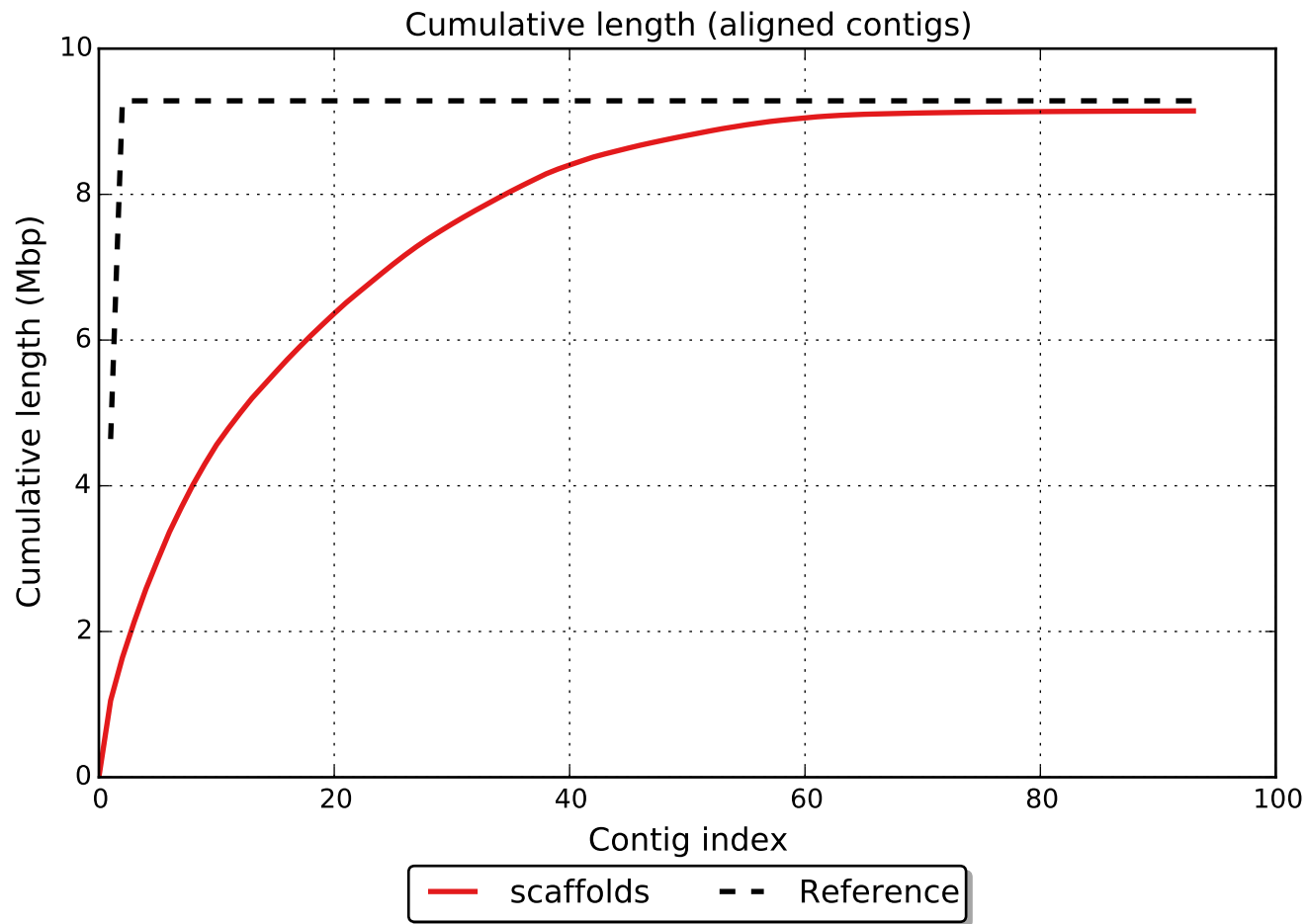
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

