

Report

	scaffolds
# contigs (≥ 0 bp)	425
# contigs (≥ 1000 bp)	150
# contigs (≥ 5000 bp)	109
# contigs (≥ 10000 bp)	99
# contigs (≥ 25000 bp)	86
# contigs (≥ 50000 bp)	64
Total length (≥ 0 bp)	8934170
Total length (≥ 1000 bp)	8823885
Total length (≥ 5000 bp)	8742657
Total length (≥ 10000 bp)	8670492
Total length (≥ 25000 bp)	8439598
Total length (≥ 50000 bp)	7717920
# contigs	203
Largest contig	431470
Total length	8858840
Reference length	9283304
N50	105688
N75	69219
L50	22
L75	47
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	196859
# local misassemblies	7
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.021
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	942.51
# indels per 100 kbp	1.11
Largest alignment	431470
NA50	105224
NA75	66896
LA50	22
LA75	48

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	2
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	196859
# local misassemblies	7
# mismatches	83140
# indels	98
# short indels	97
# long indels	1
Indels length	116

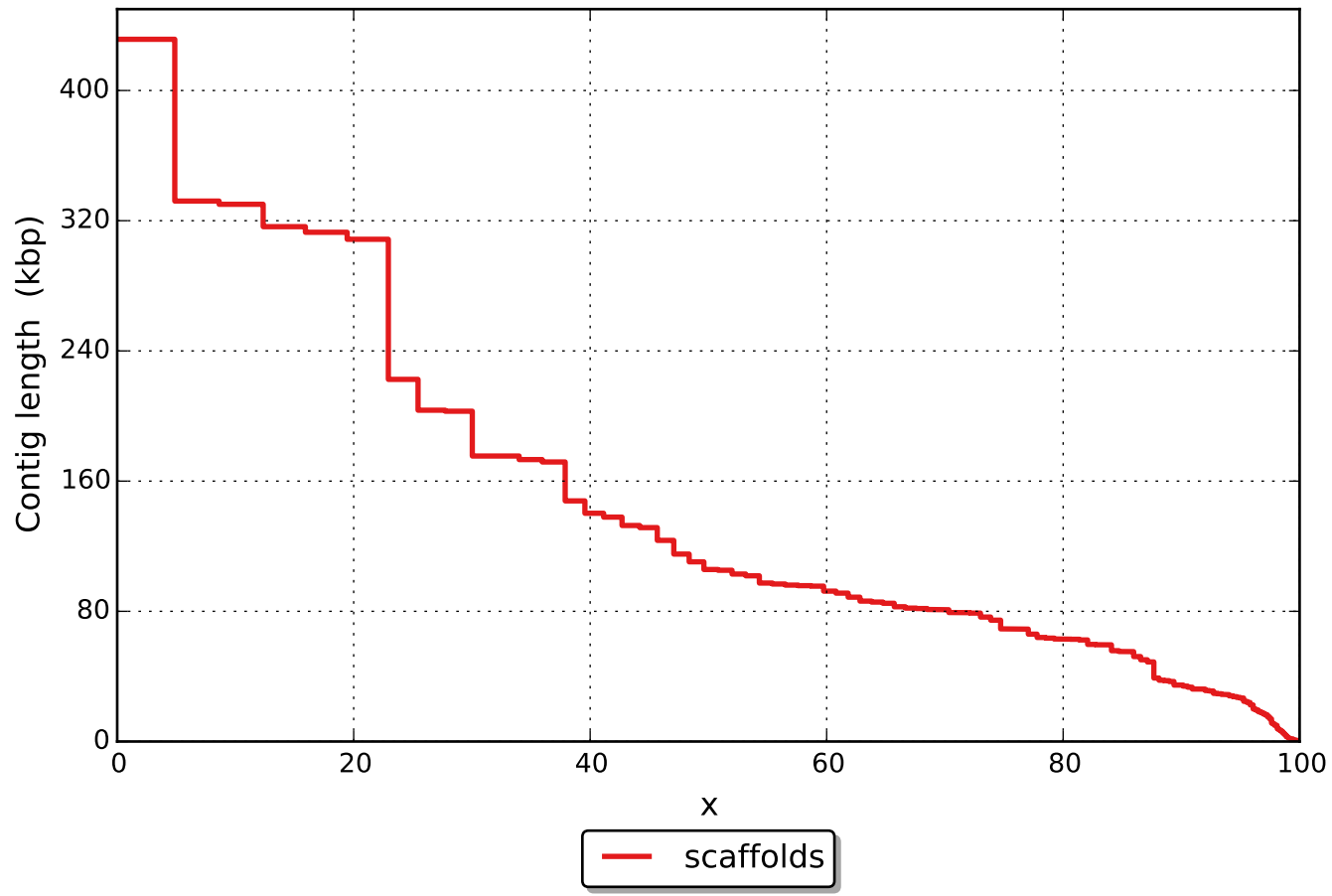
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

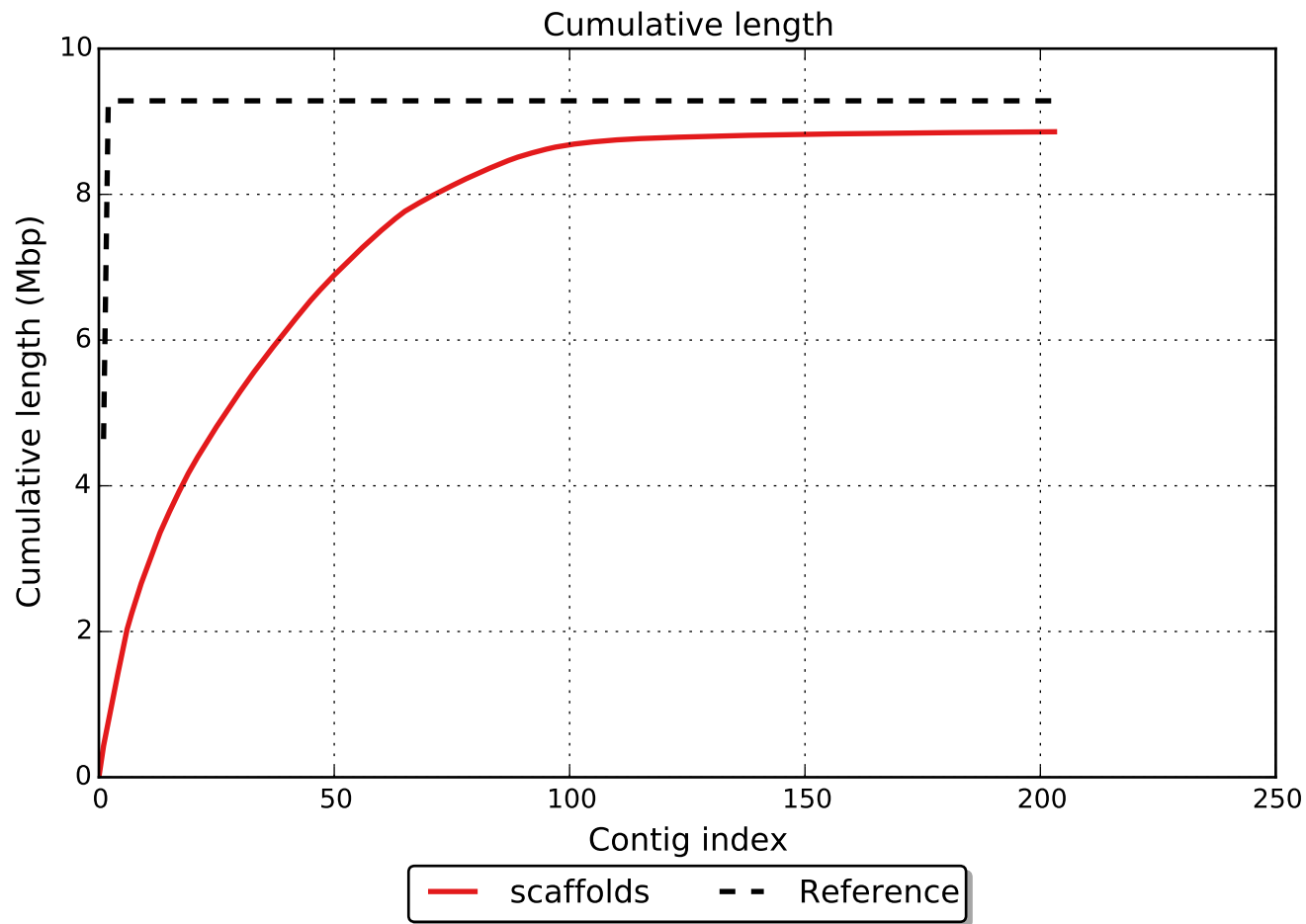
Unaligned report

	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

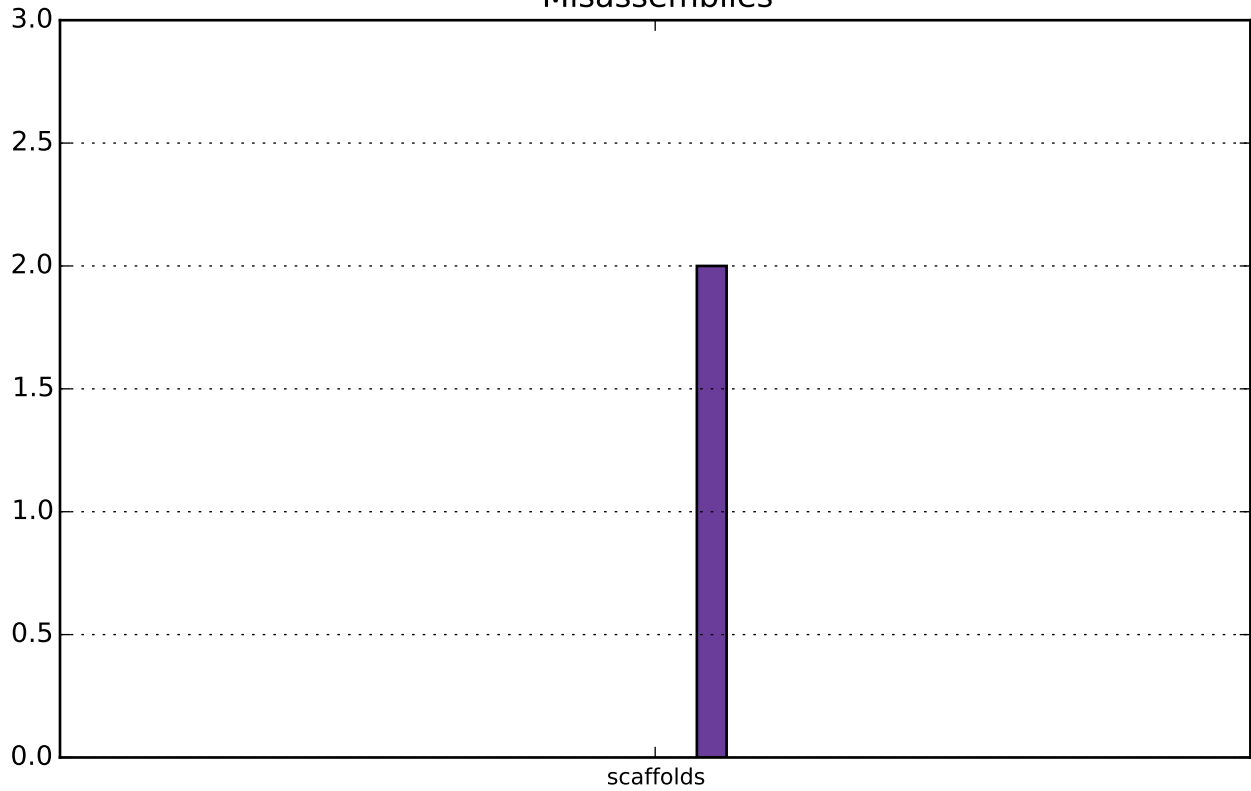
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).


Nx

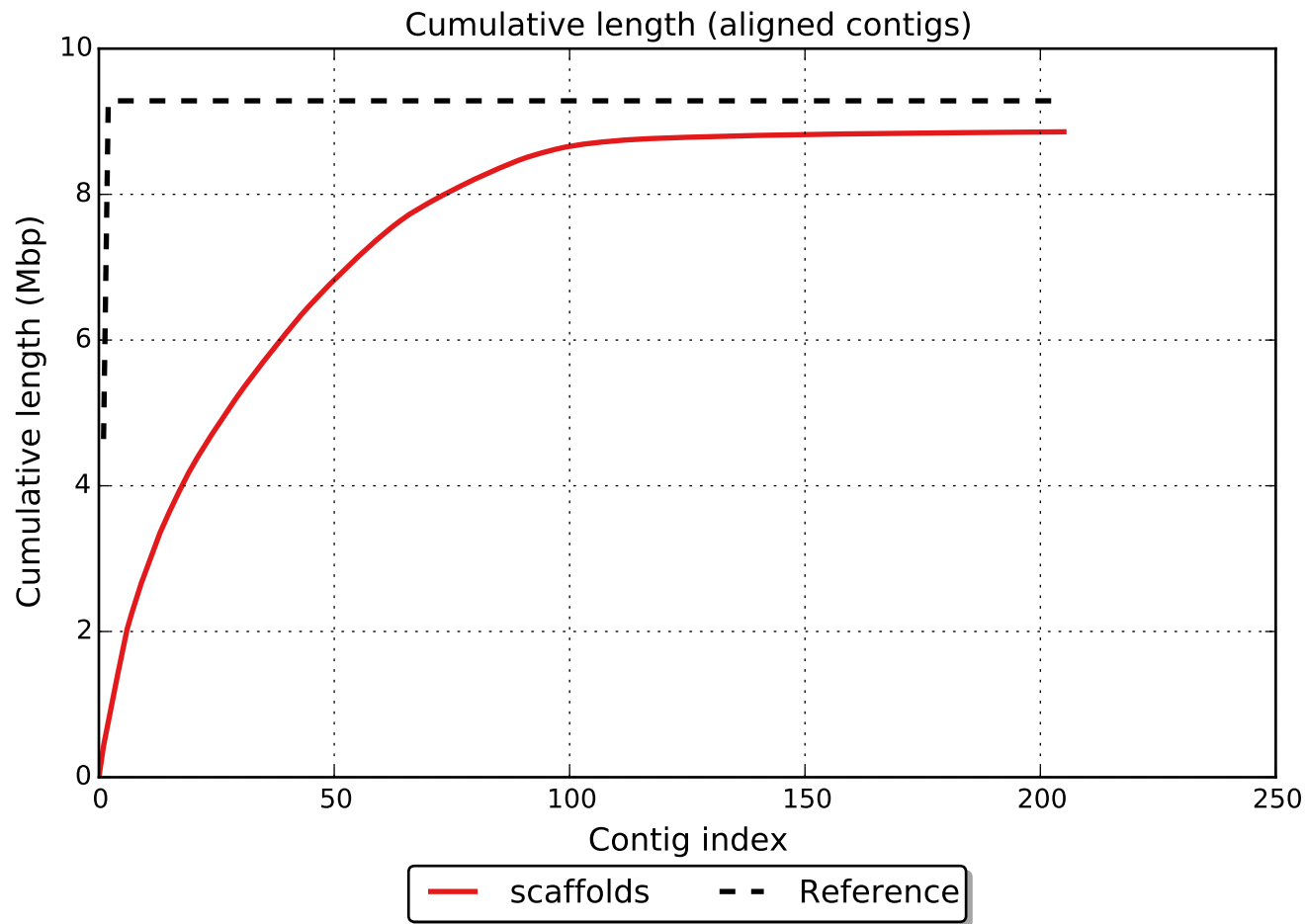




Misassemblies



 # interspecies translocations



NAx

