

Report

	scaffolds
# contigs (≥ 0 bp)	172
# contigs (≥ 1000 bp)	92
# contigs (≥ 5000 bp)	78
# contigs (≥ 10000 bp)	74
# contigs (≥ 25000 bp)	67
# contigs (≥ 50000 bp)	48
Total length (≥ 0 bp)	9124414
Total length (≥ 1000 bp)	9091674
Total length (≥ 5000 bp)	9067452
Total length (≥ 10000 bp)	9037240
Total length (≥ 25000 bp)	8933081
Total length (≥ 50000 bp)	8257195
# contigs	115
Largest contig	472565
Total length	9108144
Reference length	9283304
N50	208897
N75	108452
L50	15
L75	30
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	405365
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	46
Genome fraction (%)	98.334
Duplication ratio	1.002
# N's per 100 kbp	0.11
# mismatches per 100 kbp	491.98
# indels per 100 kbp	1.11
Largest alignment	472565
NA50	203339
NA75	108452
LA50	16
LA75	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).

Misassemblies report

	scaffolds
# misassemblies	3
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	3
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	405365
# local misassemblies	2
# mismatches	44911
# indels	101
# short indels	96
# long indels	5
Indels length	186

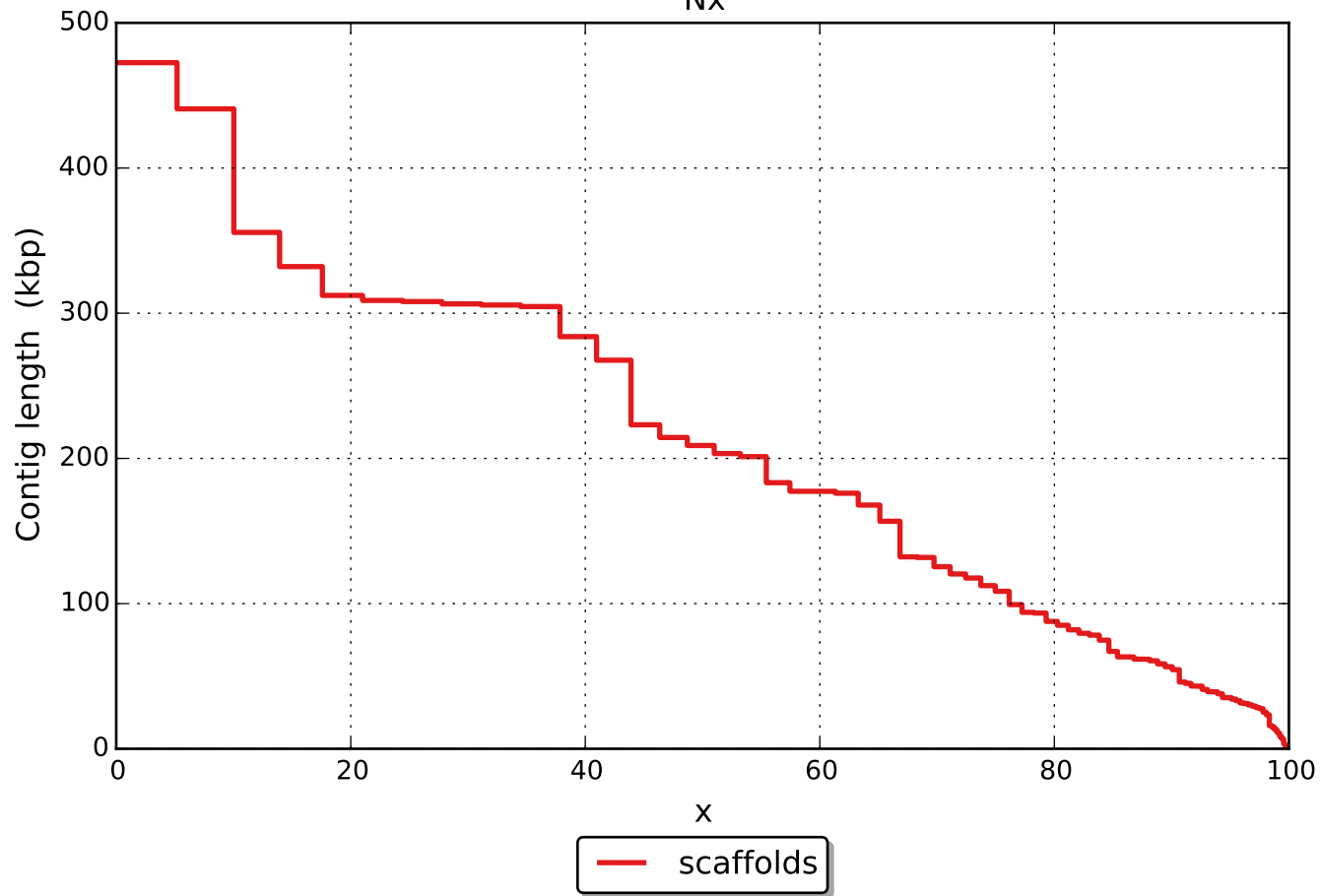
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

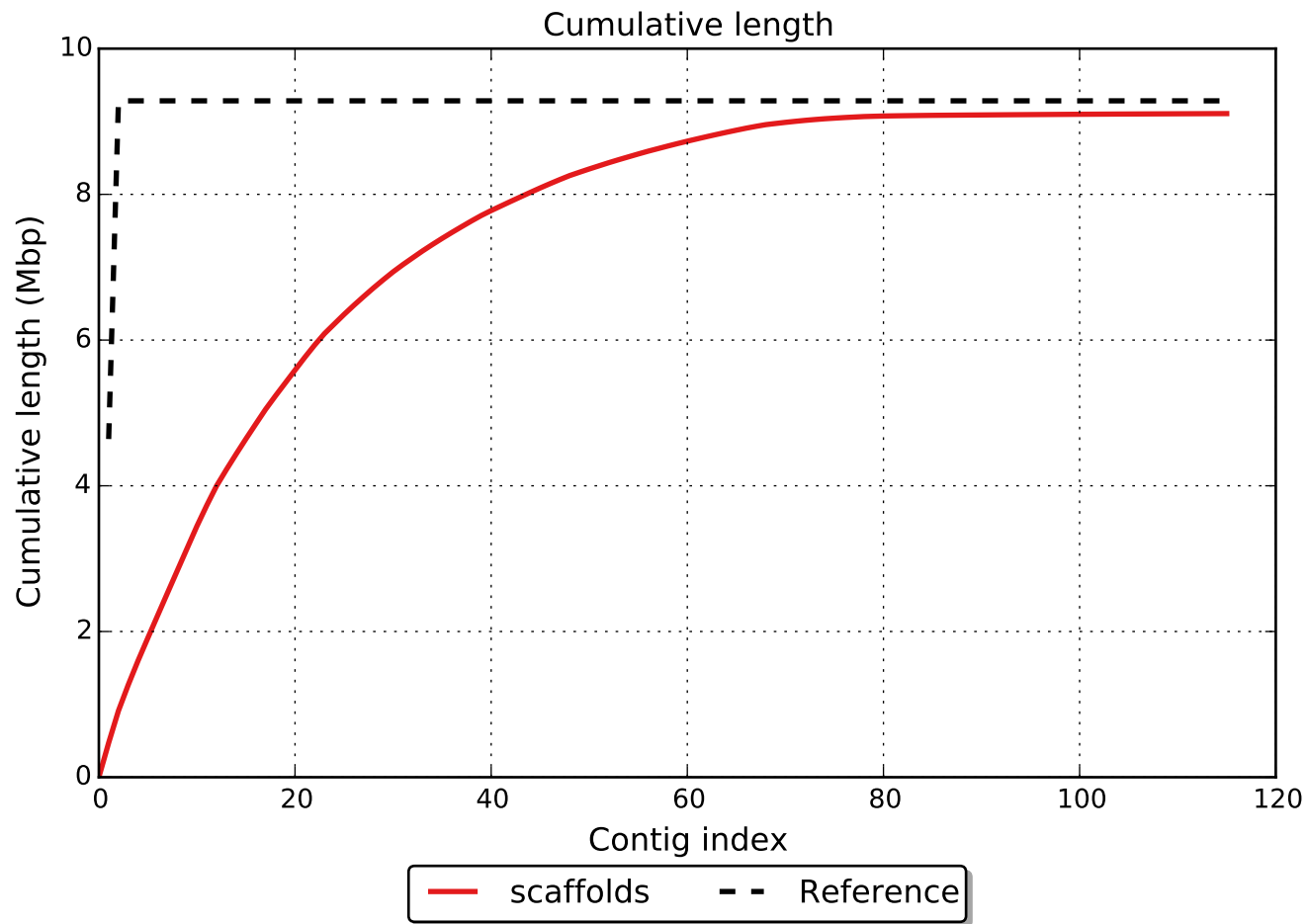
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	46
# N's	10

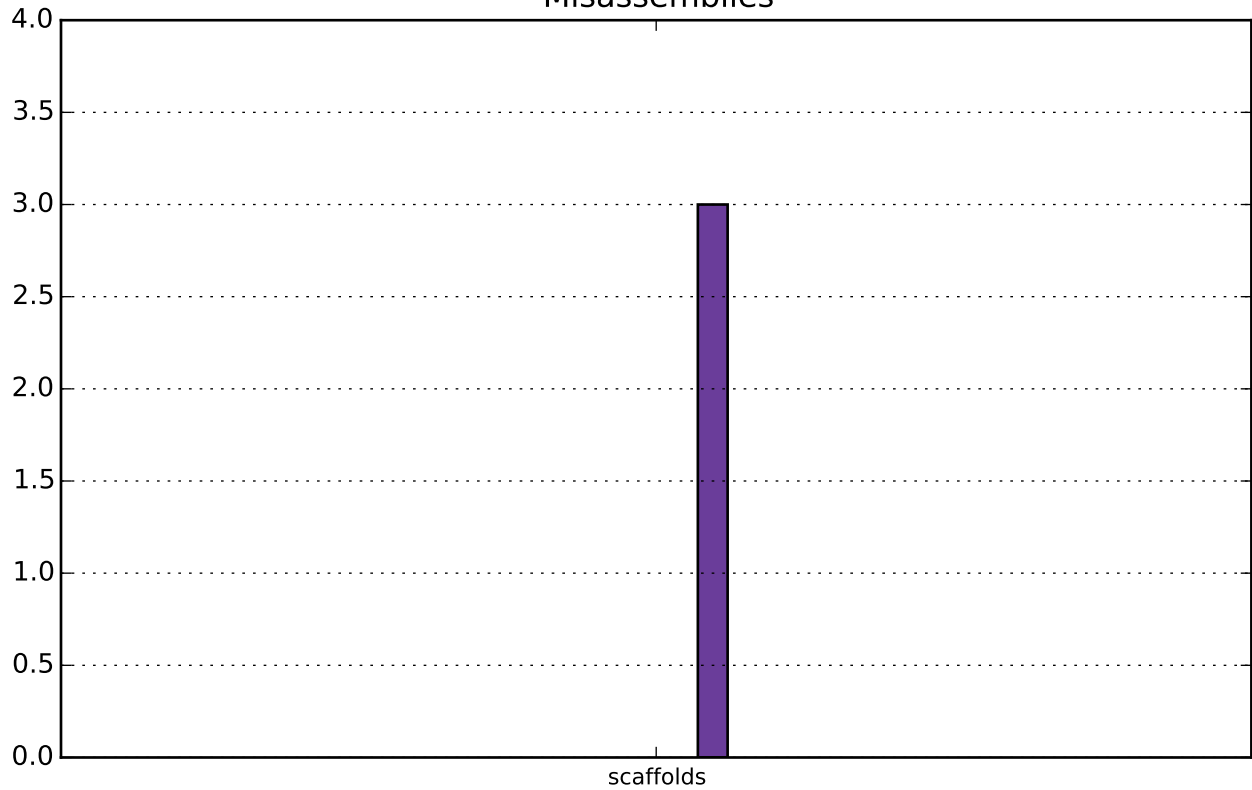
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

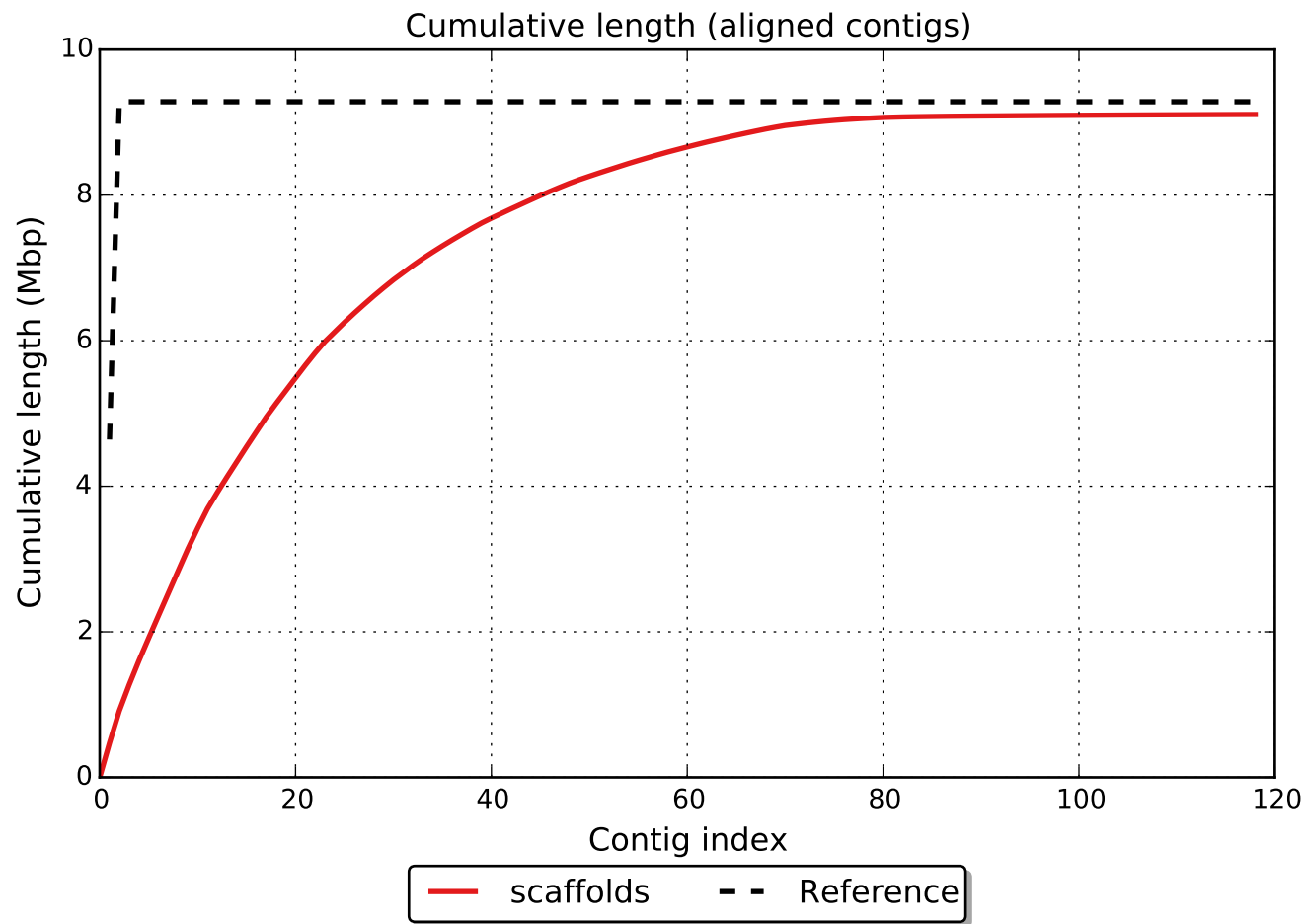




Misassemblies



 # interspecies translocations



NAx

