

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	221
# misassembled contigs	44
Misassembled contigs length	4158295
# local misassemblies	11
# unaligned contigs	15 + 2 part
Unaligned length	9815
Genome fraction (%)	49.506
Duplication ratio	1.929
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1320.68
# indels per 100 kbp	1.50
Largest alignment	431470
NA50	58608
NA75	25158
LA50	40
LA75	100

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	221
# relocations	179
# translocations	0
# inversions	35
# interspecies translocations	7
# possibly misassembled contigs	1
# misassembled contigs	44
Misassembled contigs length	4158295
# local misassemblies	11
# mismatches	60696
# indels	69
# short indels	68
# long indels	1
Indels length	79

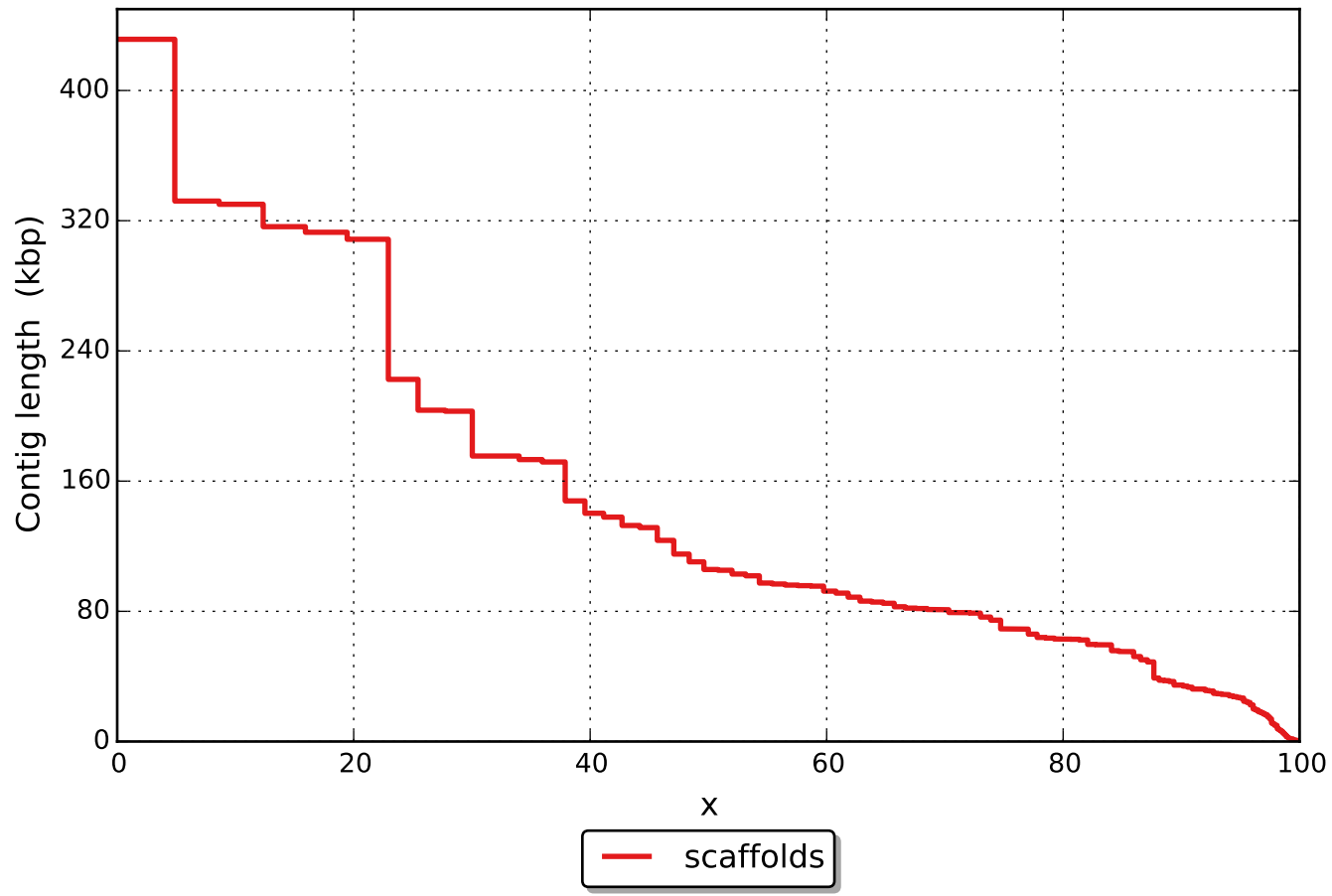
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

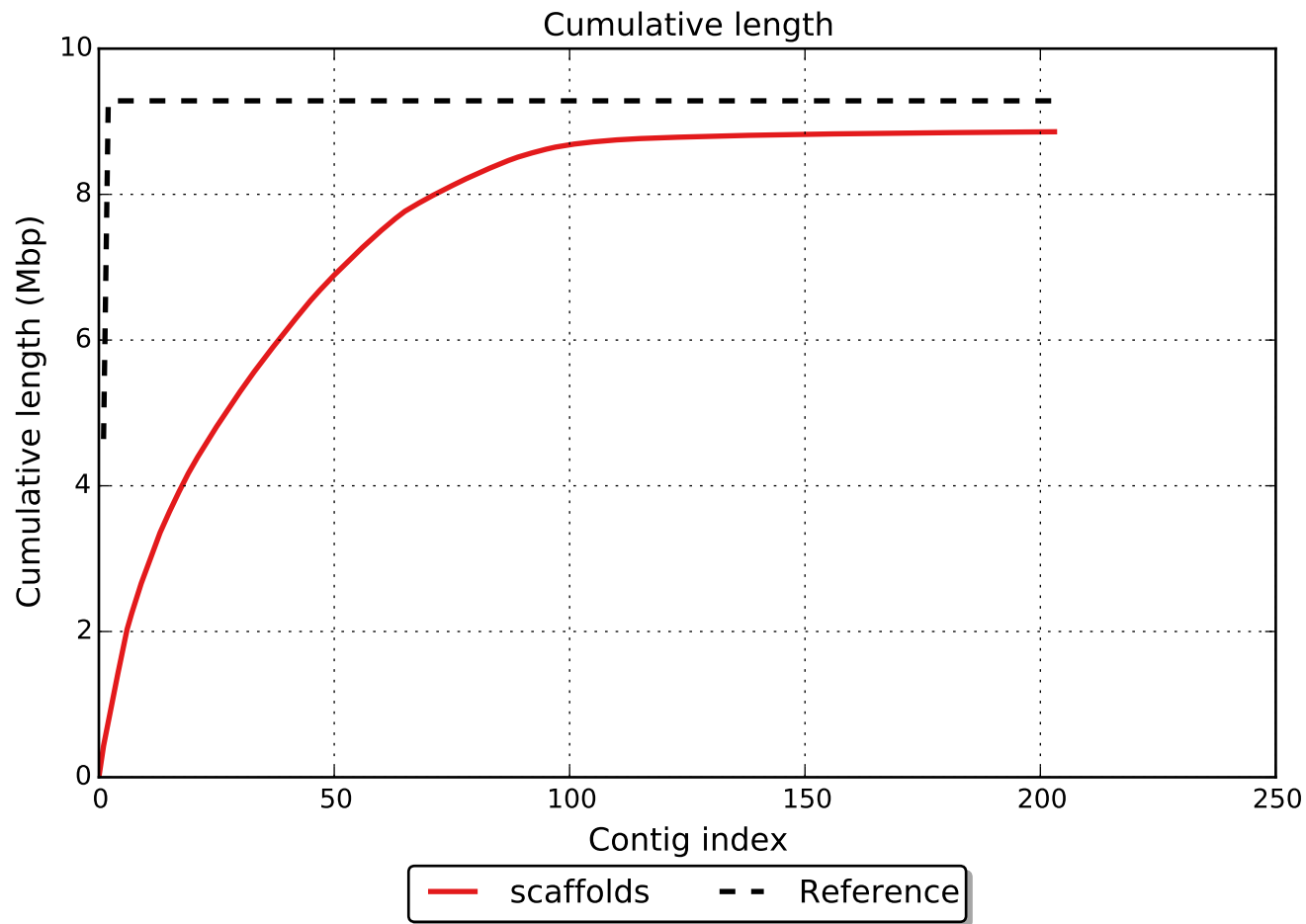
Unaligned report

	scaffolds
# fully unaligned contigs	15
Fully unaligned length	9425
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	390
# N's	0

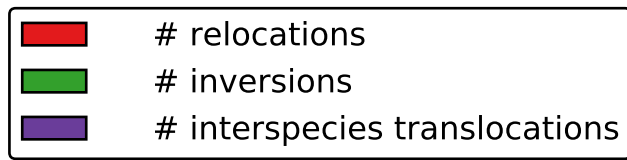
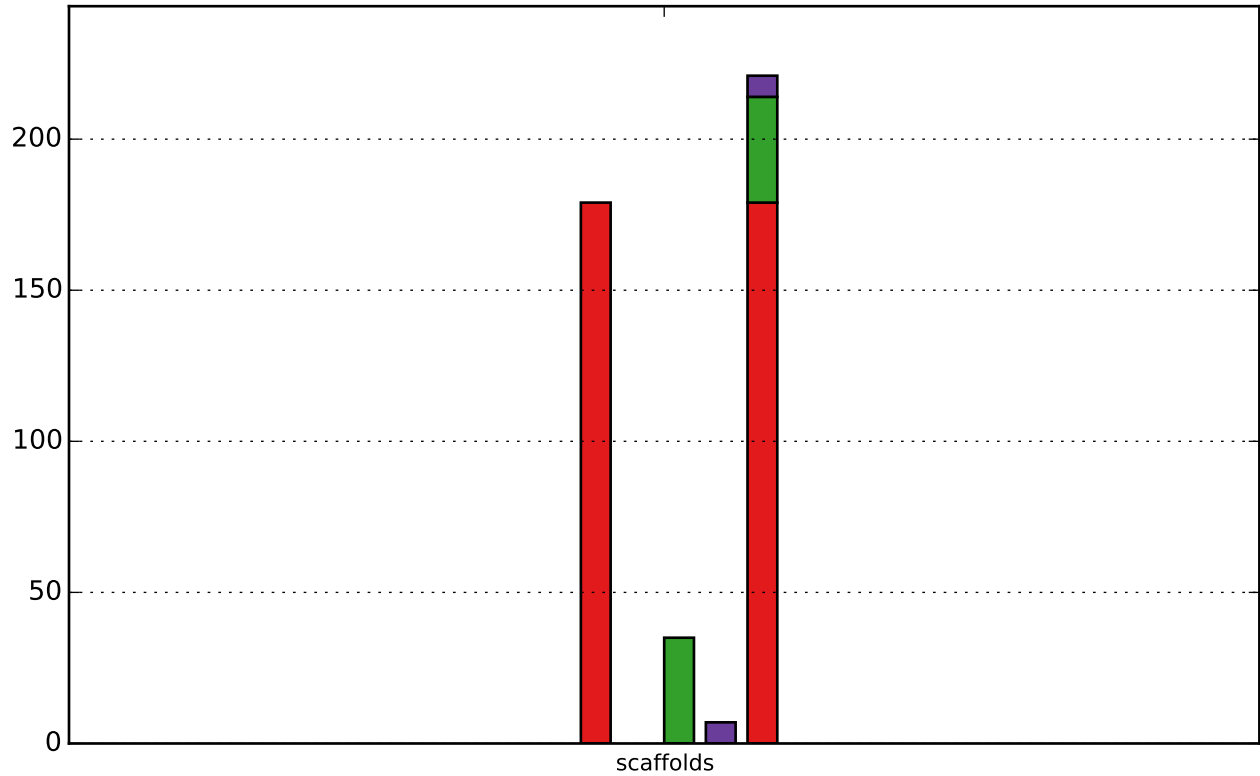
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

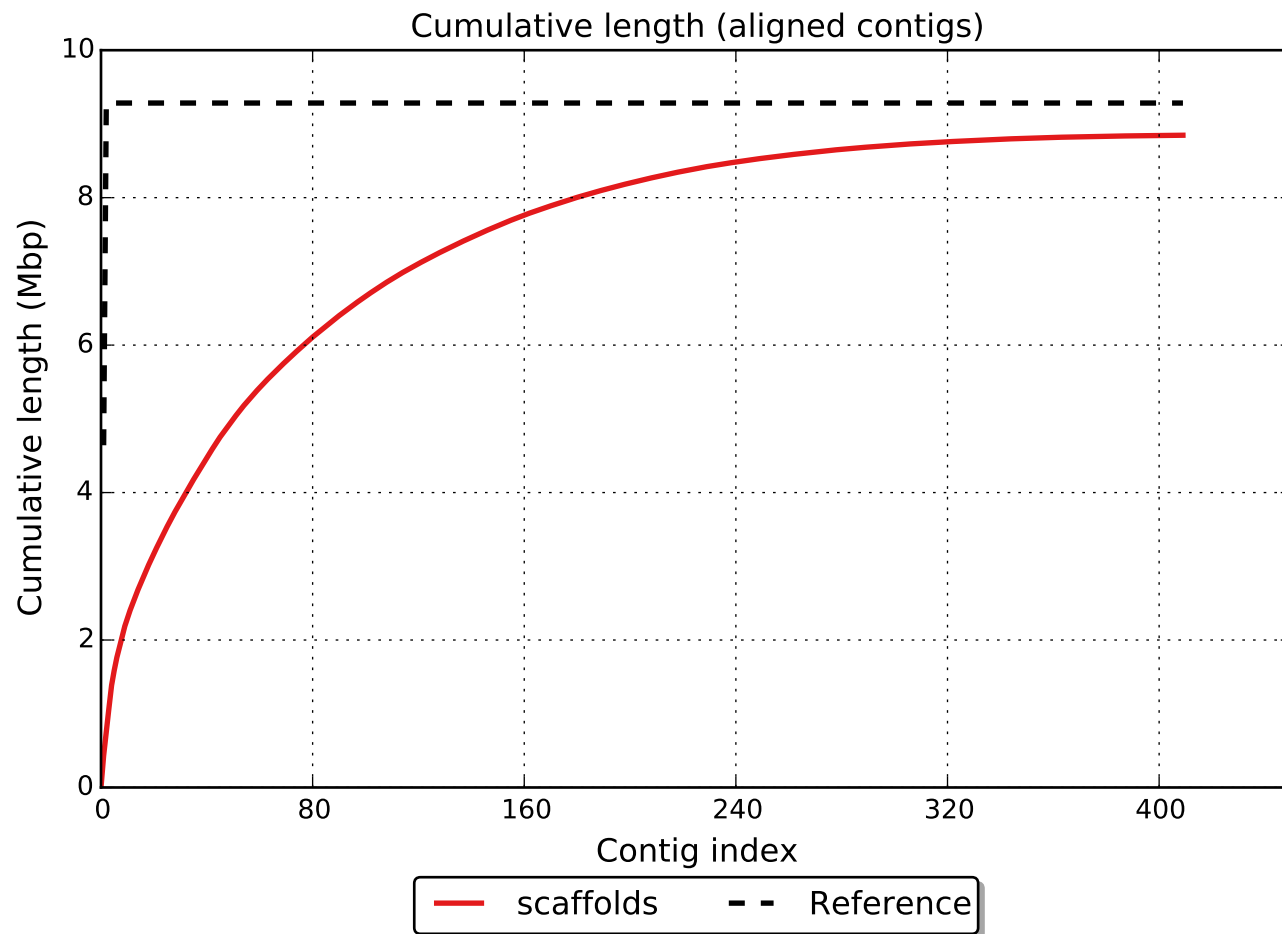
Nx





Misassemblies





NAx

