

Report

	scaffolds
# contigs (≥ 0 bp)	553
# contigs (≥ 1000 bp)	170
# contigs (≥ 5000 bp)	133
# contigs (≥ 10000 bp)	108
# contigs (≥ 25000 bp)	68
# contigs (≥ 50000 bp)	33
Total length (≥ 0 bp)	4742072
Total length (≥ 1000 bp)	4628660
Total length (≥ 5000 bp)	4538215
Total length (≥ 10000 bp)	4360771
Total length (≥ 25000 bp)	3737309
Total length (≥ 50000 bp)	2476487
# contigs	188
Largest contig	148188
Total length	4640522
Reference length	9283304
N50	54079
N75	32460
L50	30
L75	59
# misassemblies	21
# misassembled contigs	19
Misassembled contigs length	1112114
# local misassemblies	6
# unaligned contigs	4 + 5 part
Unaligned length	3311
Genome fraction (%)	49.035
Duplication ratio	1.019
# N's per 100 kbp	79.50
# mismatches per 100 kbp	742.94
# indels per 100 kbp	0.83
Largest alignment	122264
NA50	45250
NA75	28463
LA50	35
LA75	68

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	21
# relocations	17
# translocations	0
# inversions	4
# interspecies translocations	0
# possibly misassembled contigs	3
# misassembled contigs	19
Misassembled contigs length	1112114
# local misassemblies	6
# mismatches	33819
# indels	38
# short indels	27
# long indels	11
Indels length	639

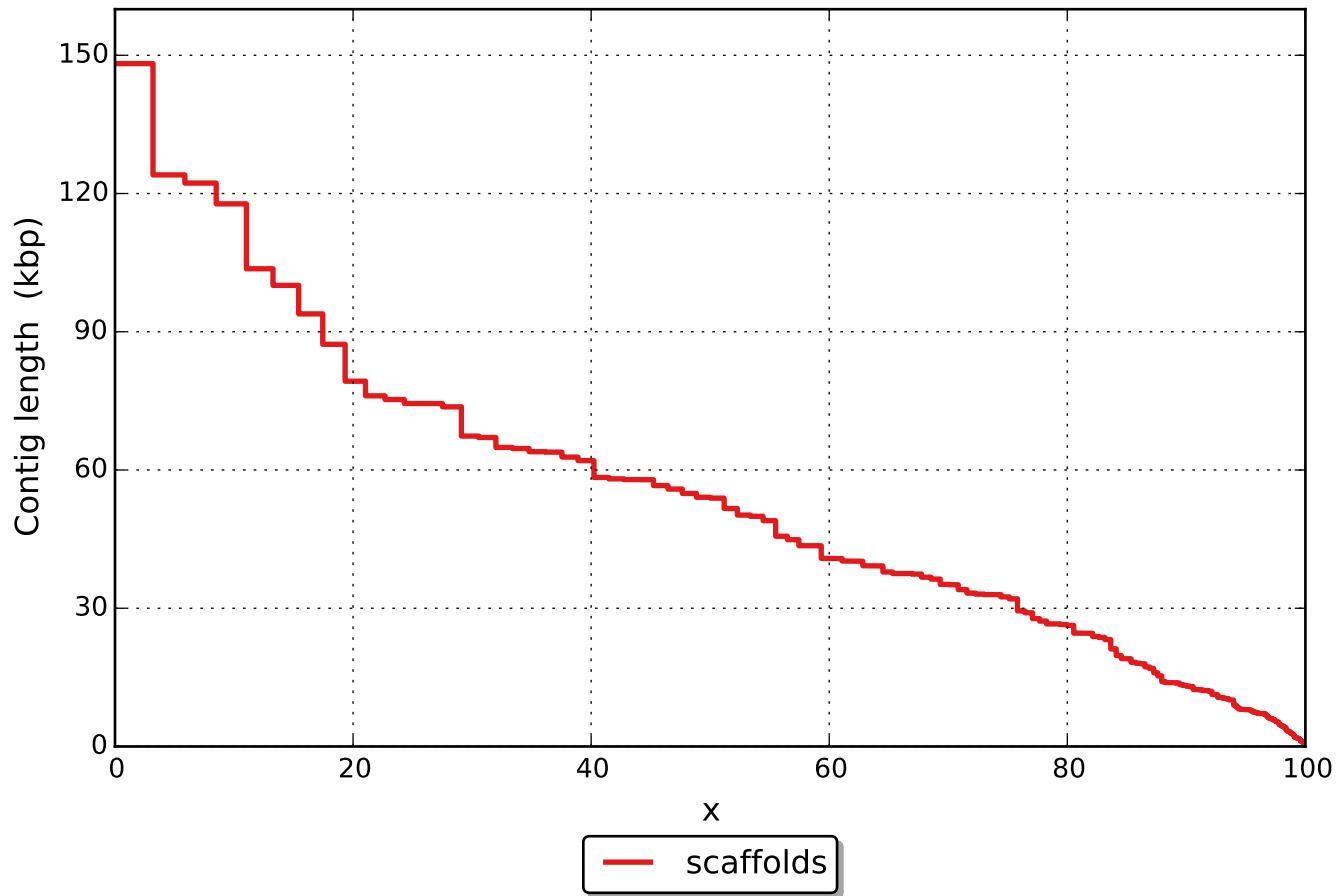
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

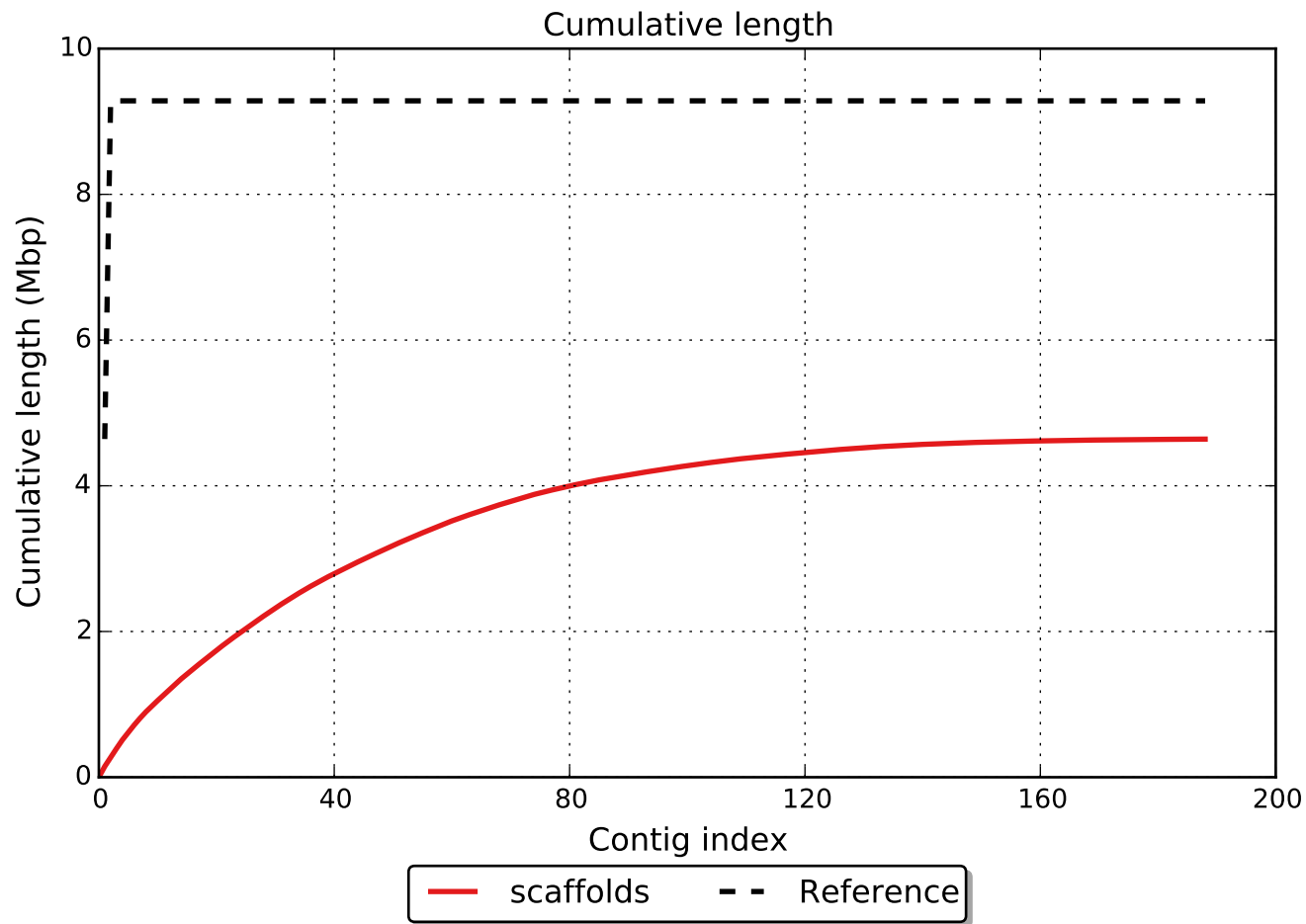
Unaligned report

	scaffolds
# fully unaligned contigs	4
Fully unaligned length	2222
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1089
# N's	3689

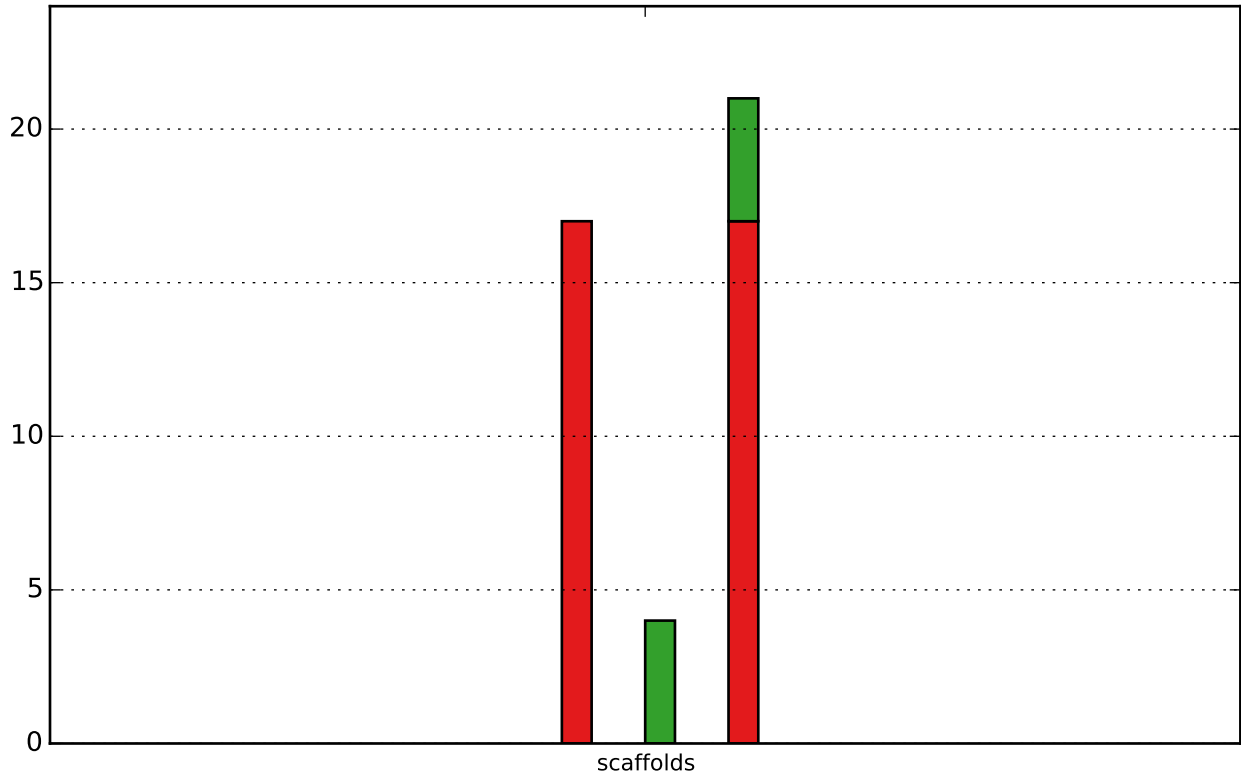
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

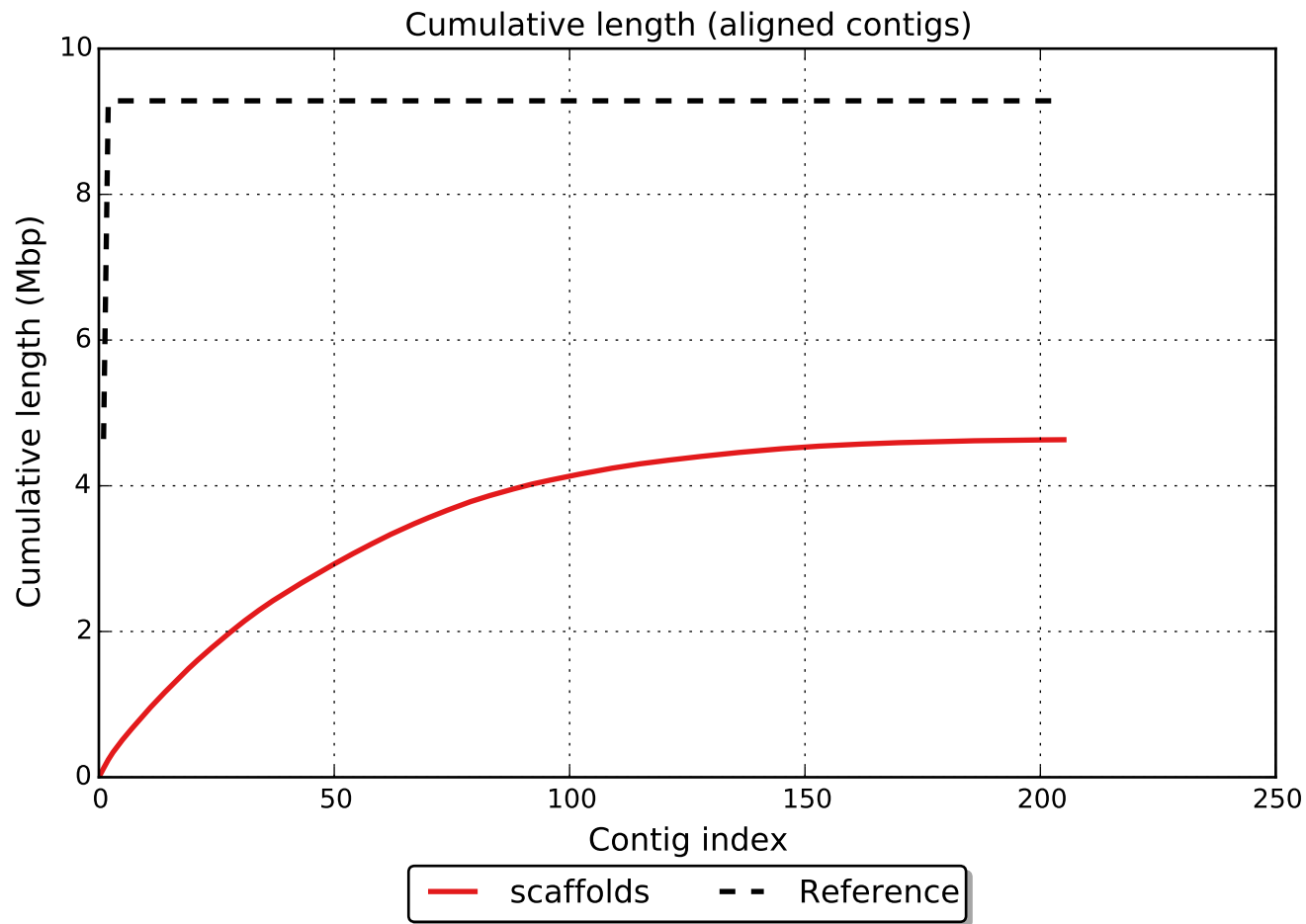
Nx





Misassemblies





NAx

