

Report

	scaffolds
# contigs (≥ 0 bp)	880
# contigs (≥ 1000 bp)	180
# contigs (≥ 5000 bp)	124
# contigs (≥ 10000 bp)	111
# contigs (≥ 25000 bp)	83
# contigs (≥ 50000 bp)	52
Total length (≥ 0 bp)	8453644
Total length (≥ 1000 bp)	8181545
Total length (≥ 5000 bp)	8046360
Total length (≥ 10000 bp)	7950075
Total length (≥ 25000 bp)	7476560
Total length (≥ 50000 bp)	6399646
# contigs	242
Largest contig	333495
Total length	8221188
Reference length	9283304
N50	96440
N75	63382
L50	23
L75	48
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	302873
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.878
Duplication ratio	1.025
# N's per 100 kbp	0.63
# mismatches per 100 kbp	1024.75
# indels per 100 kbp	0.91
Largest alignment	333495
NA50	96440
NA75	59112
LA50	23
LA75	49

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	1
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	302873
# local misassemblies	5
# mismatches	85502
# indels	76
# short indels	76
# long indels	0
Indels length	91

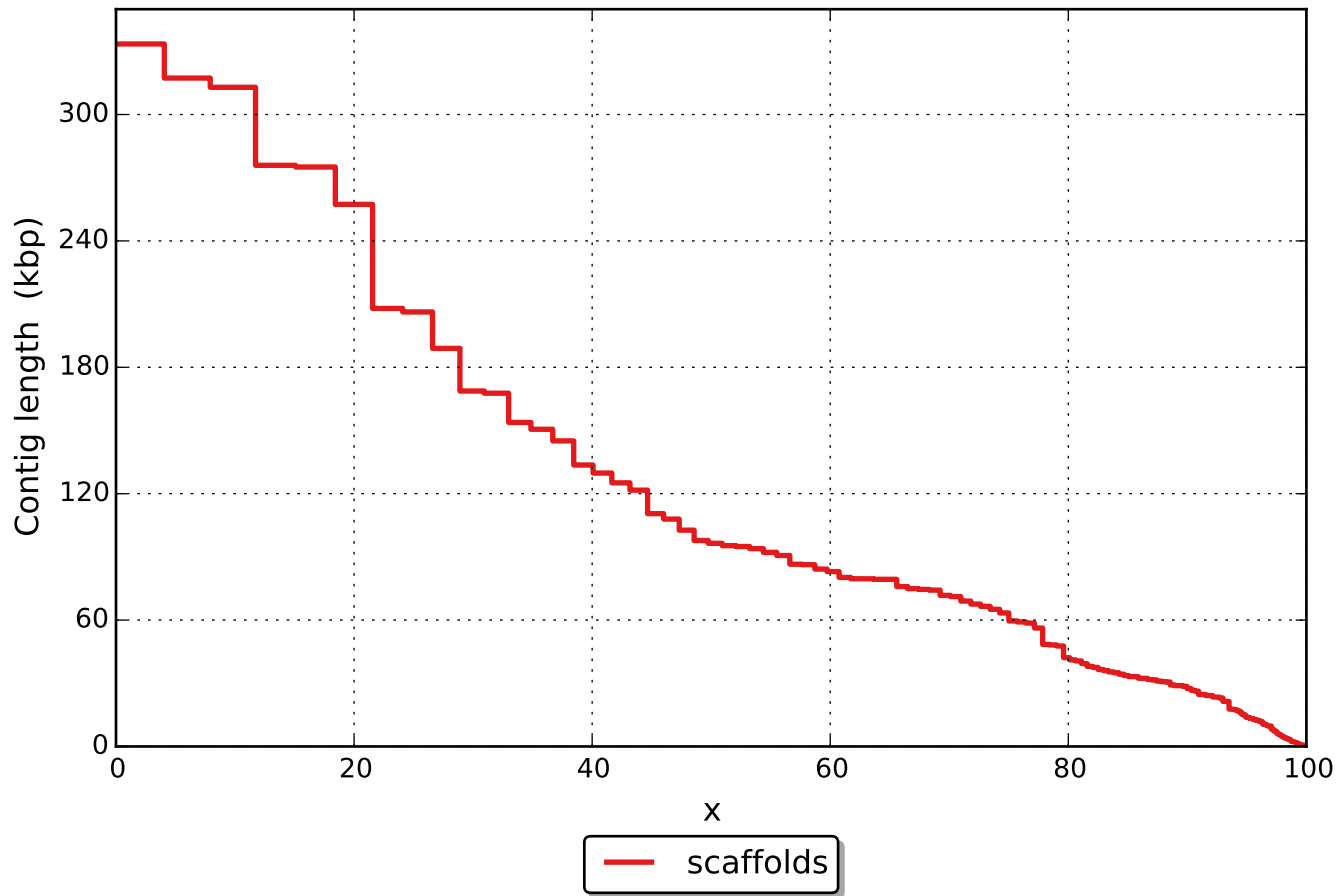
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

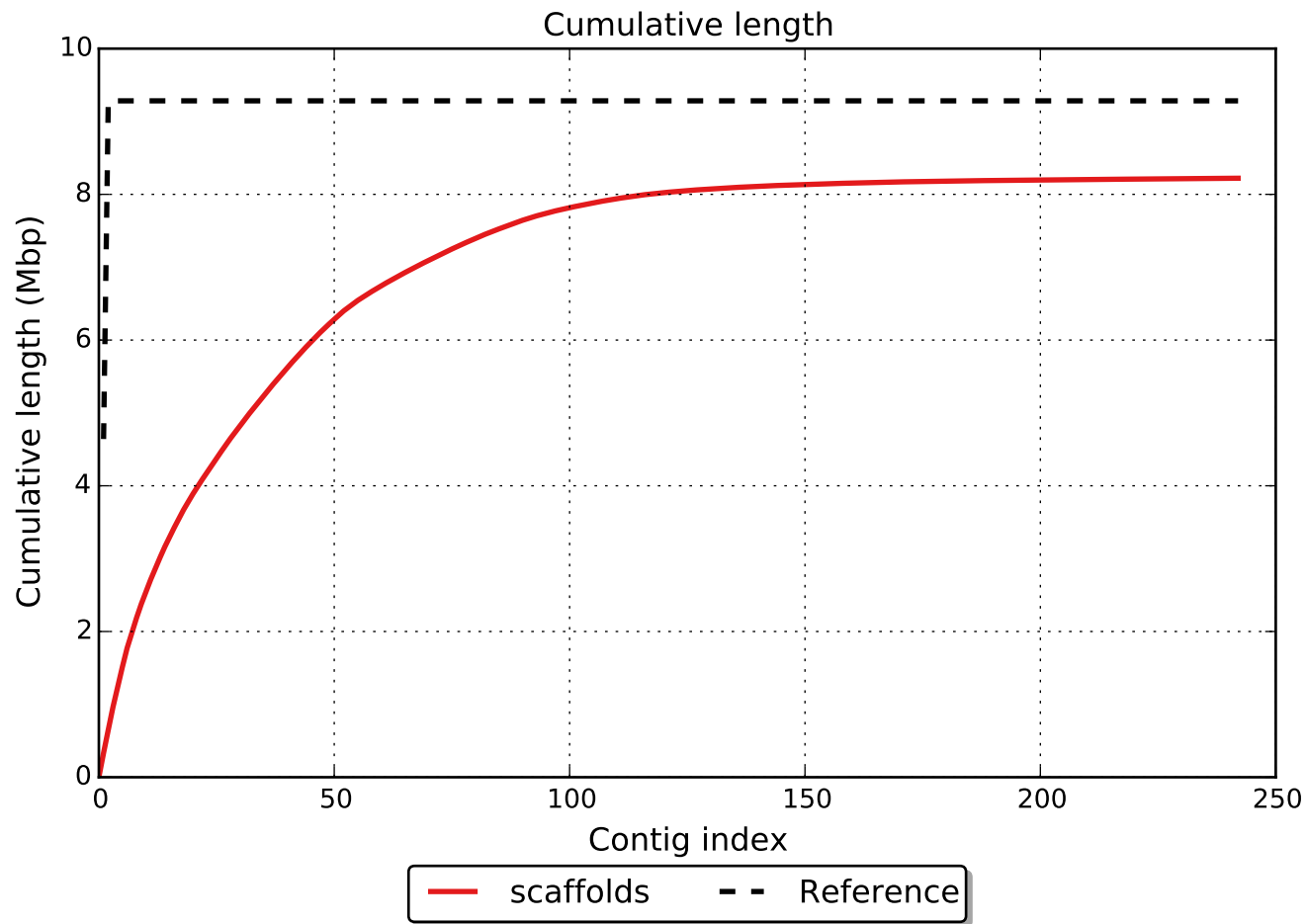
Unaligned report

	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	52

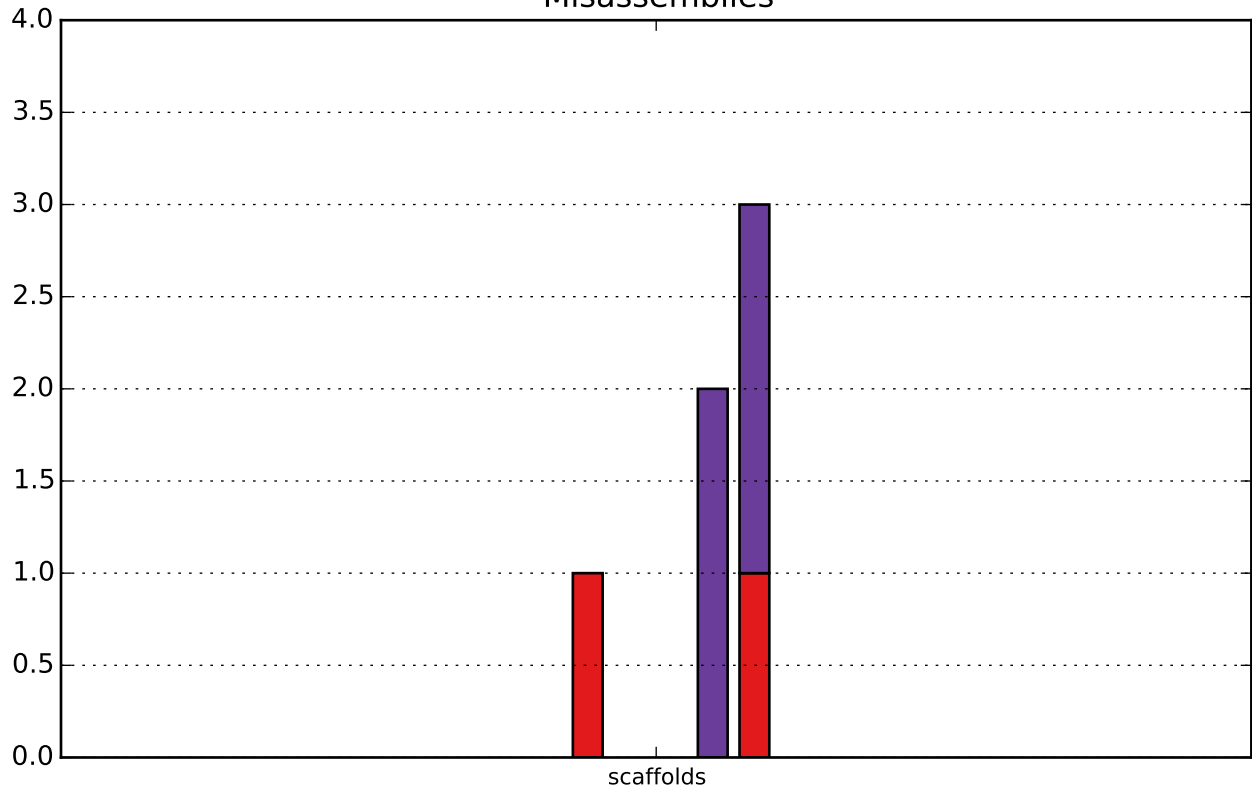
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

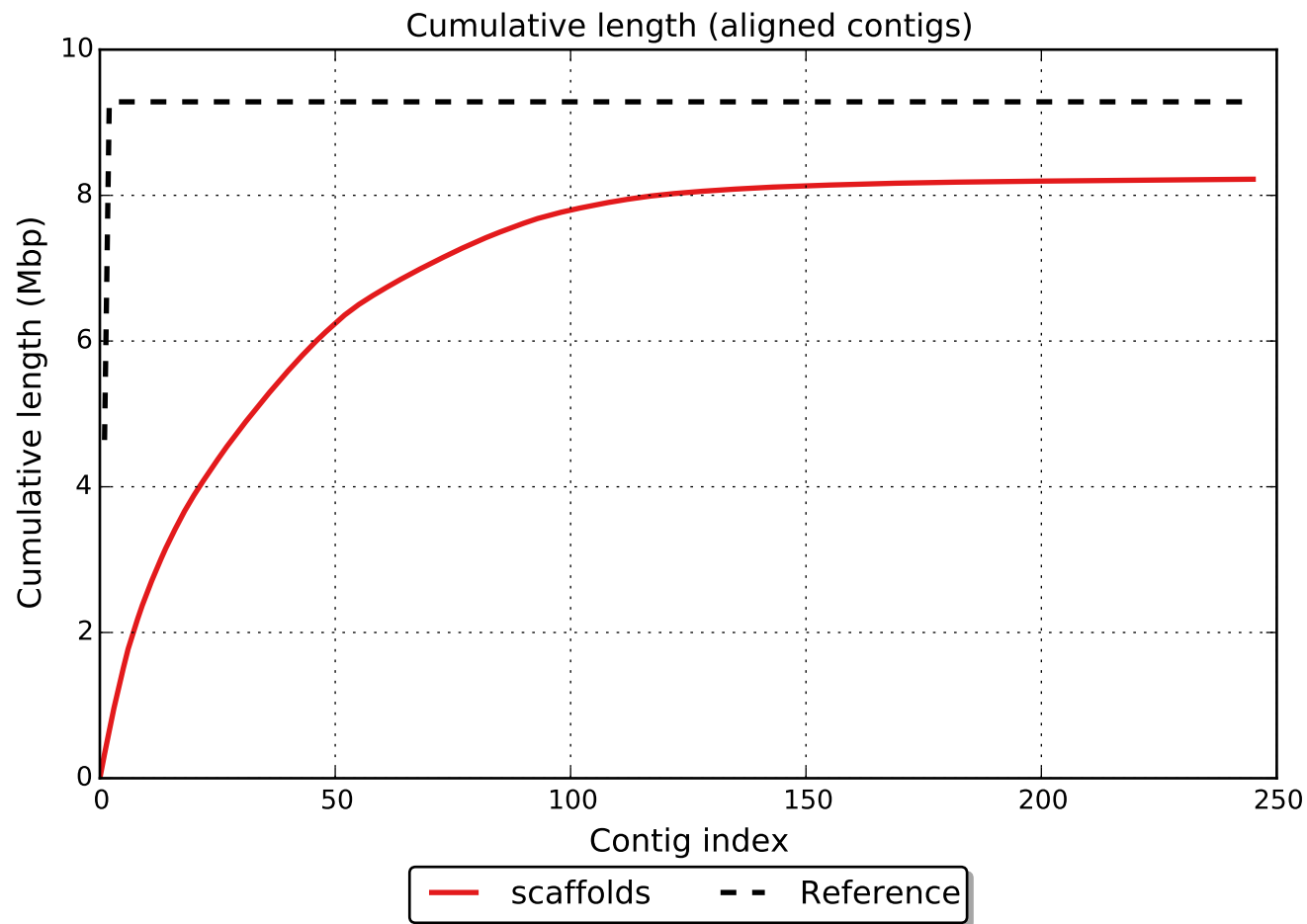
Nx





Misassemblies





NAx

