

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	5
# misassembled contigs	5
Misassembled contigs length	475557
# local misassemblies	5
# unaligned contigs	0 + 1 part
Unaligned length	55
Genome fraction (%)	49.911
Duplication ratio	1.002
# N's per 100 kbp	79.50
# mismatches per 100 kbp	712.48
# indels per 100 kbp	0.73
Largest alignment	122264
NA50	51643
NA75	29407
LA50	32
LA75	63

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	5
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	5
# possibly misassembled contigs	2
# misassembled contigs	5
Misassembled contigs length	475557
# local misassemblies	5
# mismatches	33012
# indels	34
# short indels	23
# long indels	11
Indels length	635

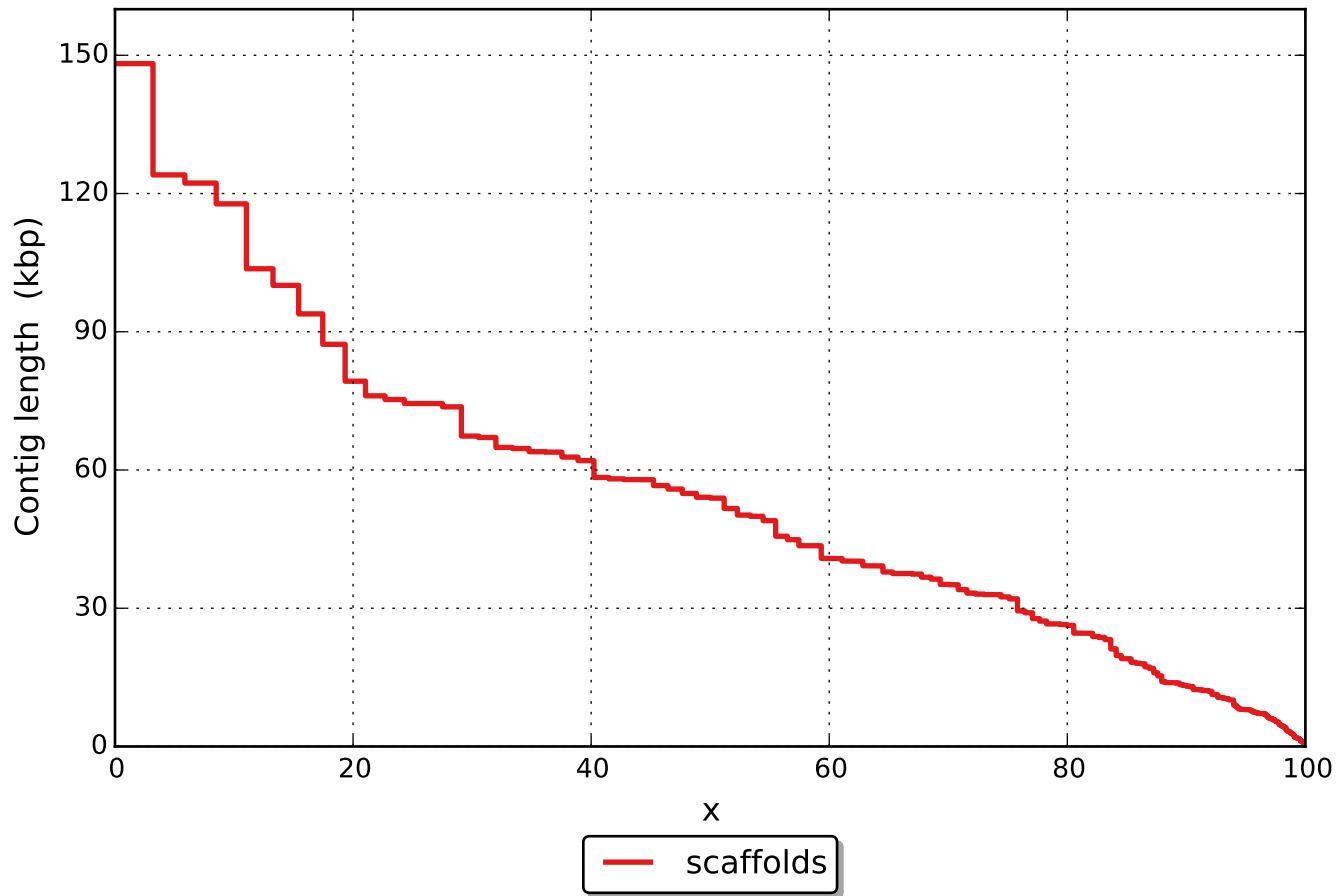
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

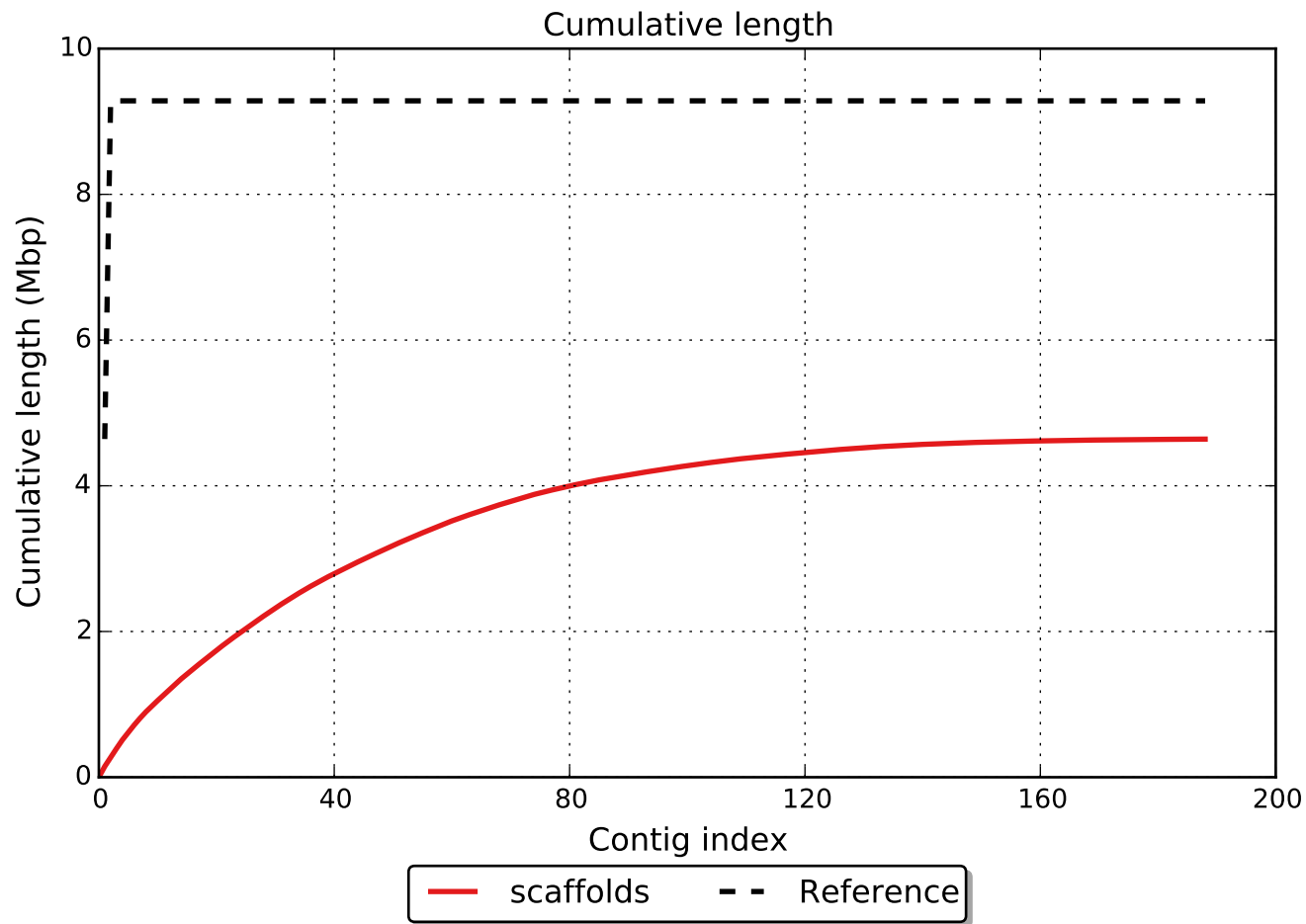
Unaligned report

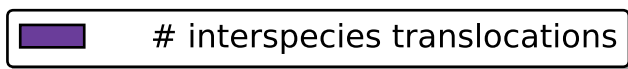
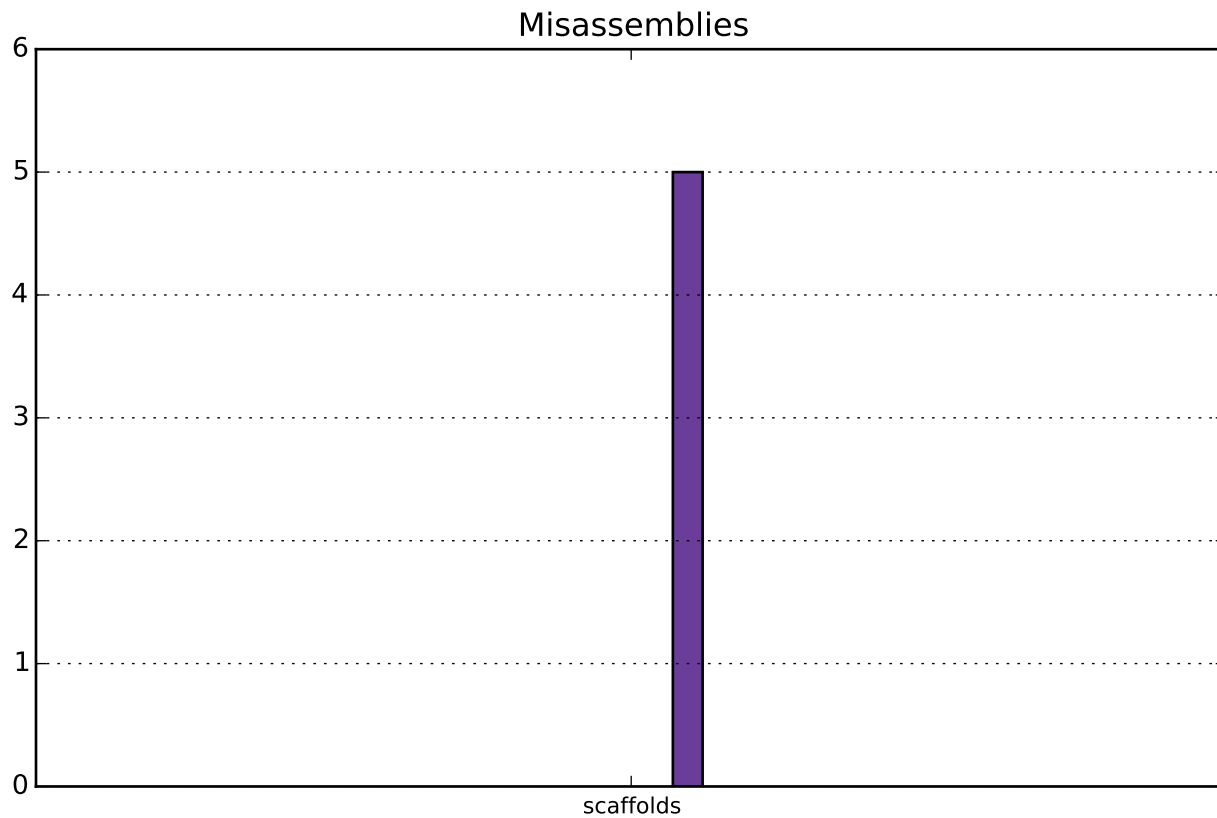
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	55
# N's	3689

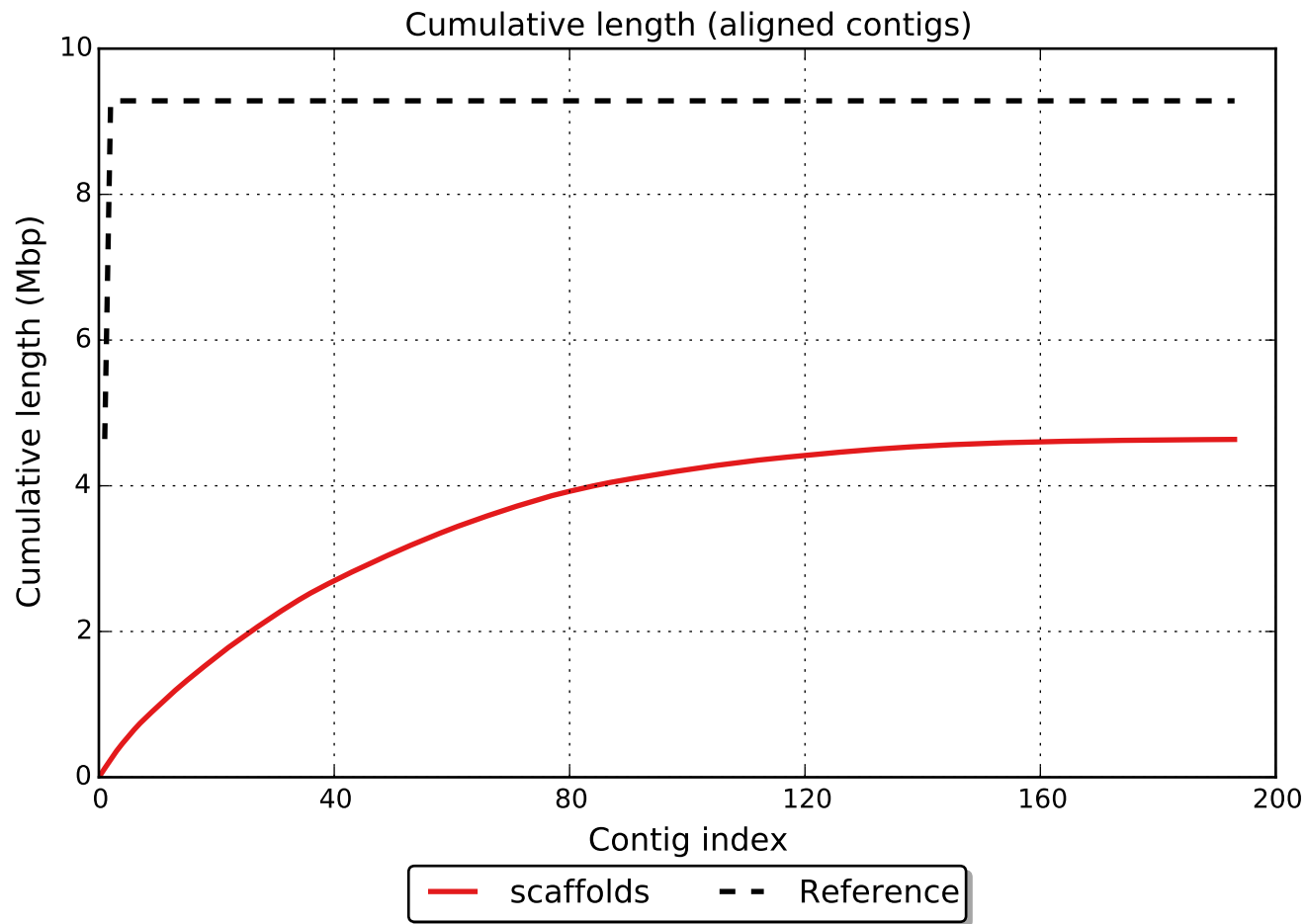
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

