

Report

	scaffolds
# contigs (≥ 0 bp)	920
# contigs (≥ 1000 bp)	238
# contigs (≥ 5000 bp)	182
# contigs (≥ 10000 bp)	148
# contigs (≥ 25000 bp)	71
# contigs (≥ 50000 bp)	15
Total length (≥ 0 bp)	4912814
Total length (≥ 1000 bp)	4681396
Total length (≥ 5000 bp)	4554718
Total length (≥ 10000 bp)	4296558
Total length (≥ 25000 bp)	3033633
Total length (≥ 50000 bp)	1100704
# contigs	271
Largest contig	132022
Total length	4701919
Reference length	9283304
N50	31972
N75	19156
L50	48
L75	94
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	152553
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	82.896
Duplication ratio	1.021
# N's per 100 kbp	25.88
# mismatches per 100 kbp	908.19
# indels per 100 kbp	0.64
Largest alignment	132022
NA50	31853
NA75	18252
LA50	49
LA75	96

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	4
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	4
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	152553
# local misassemblies	4
# mismatches	69889
# indels	49
# short indels	45
# long indels	4
Indels length	278

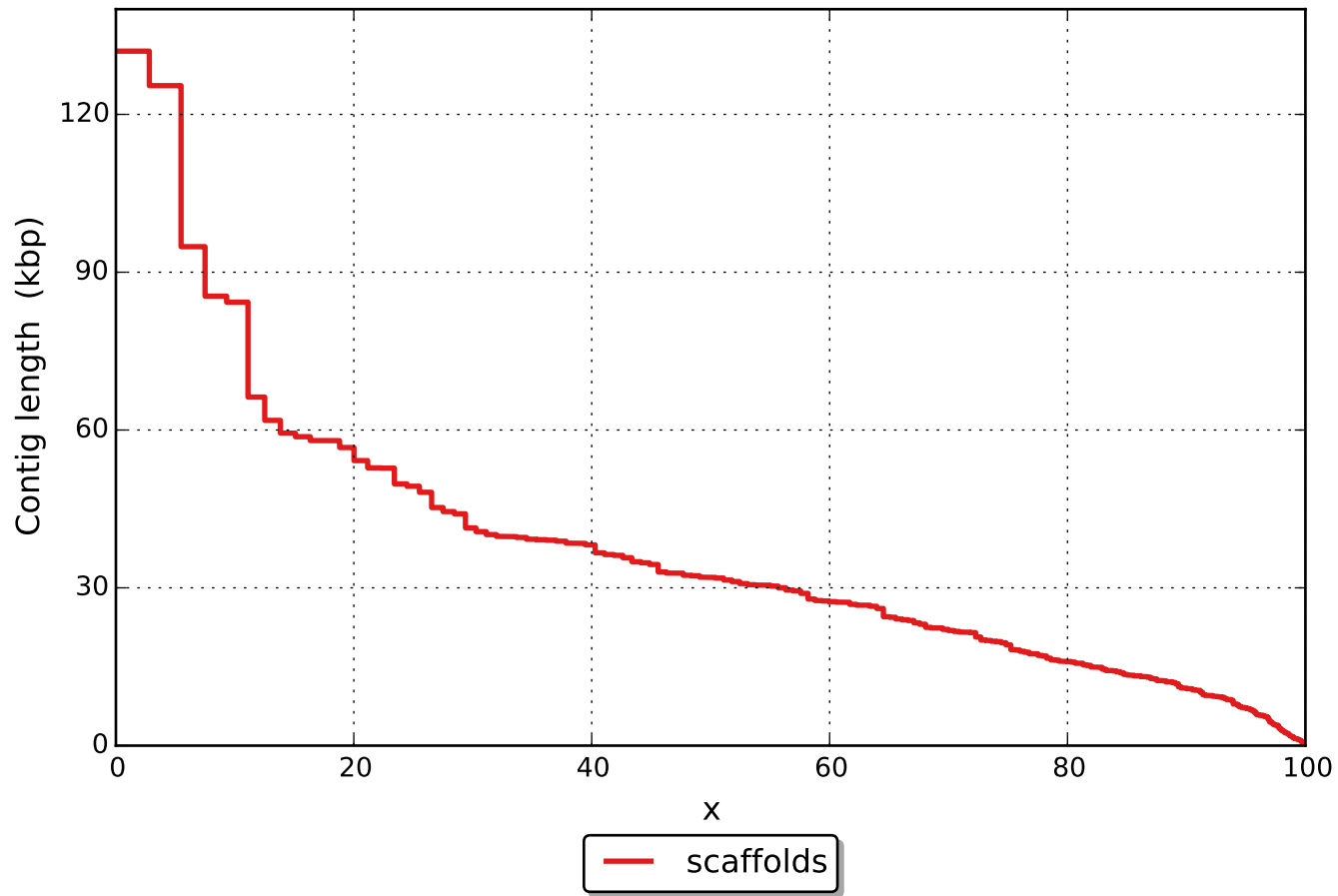
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

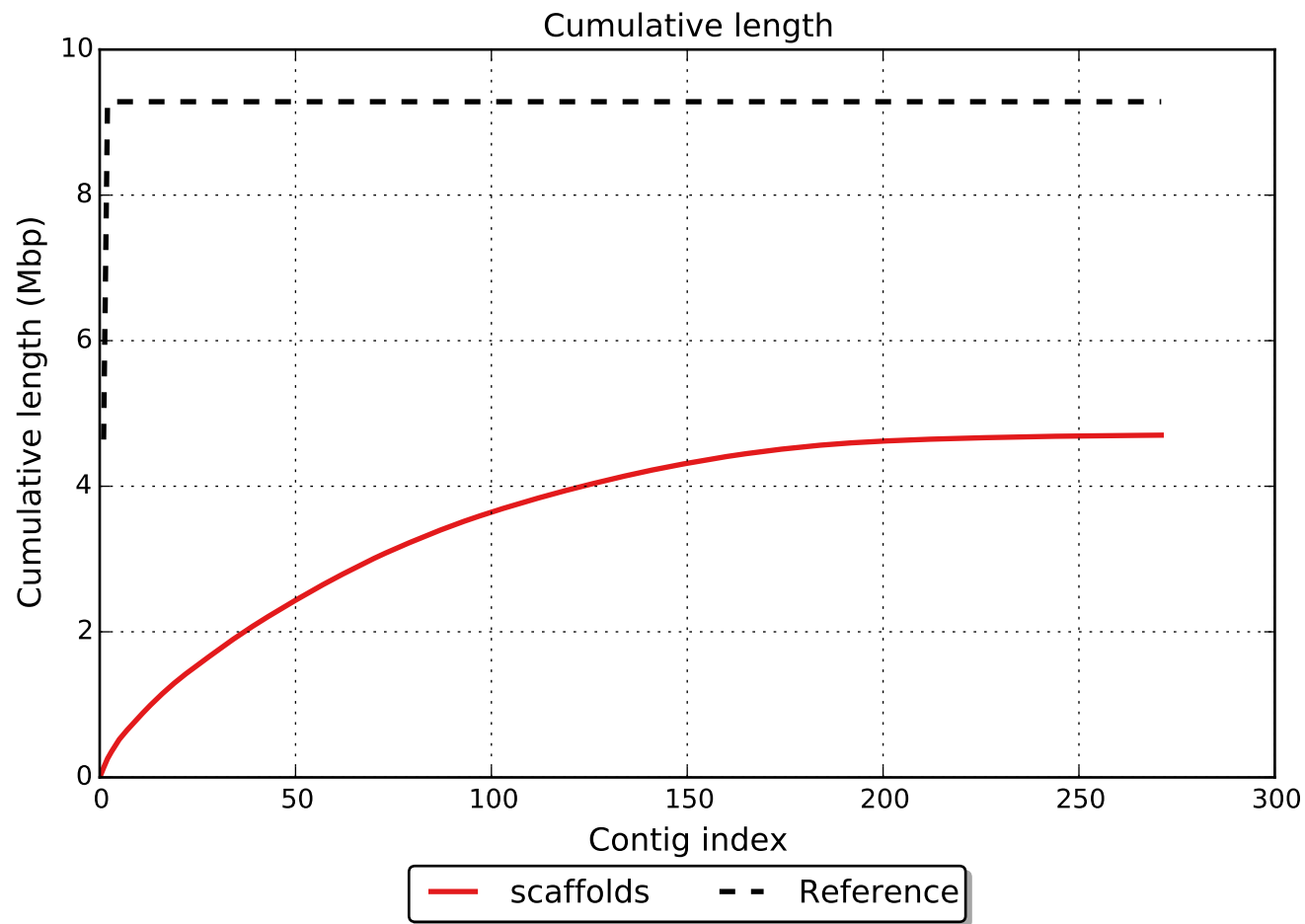
Unaligned report

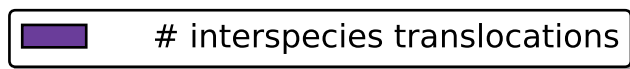
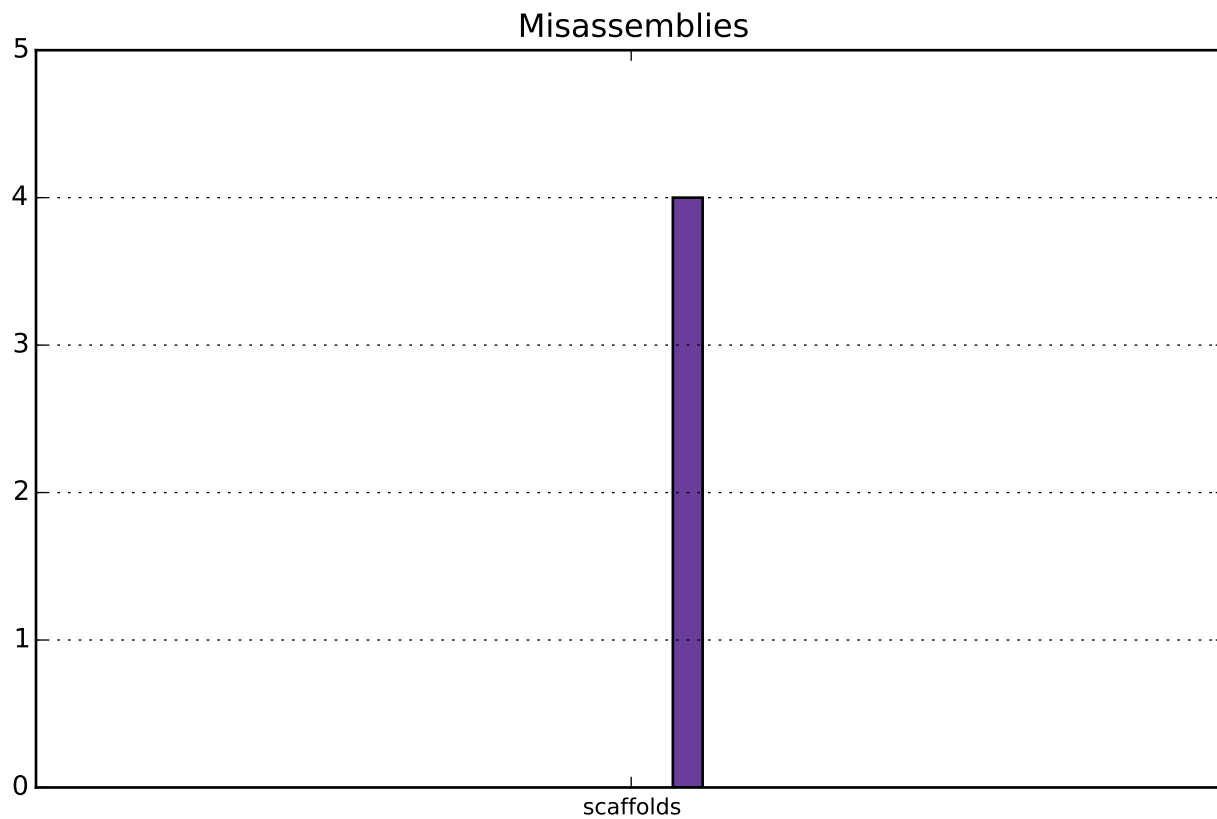
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	1217

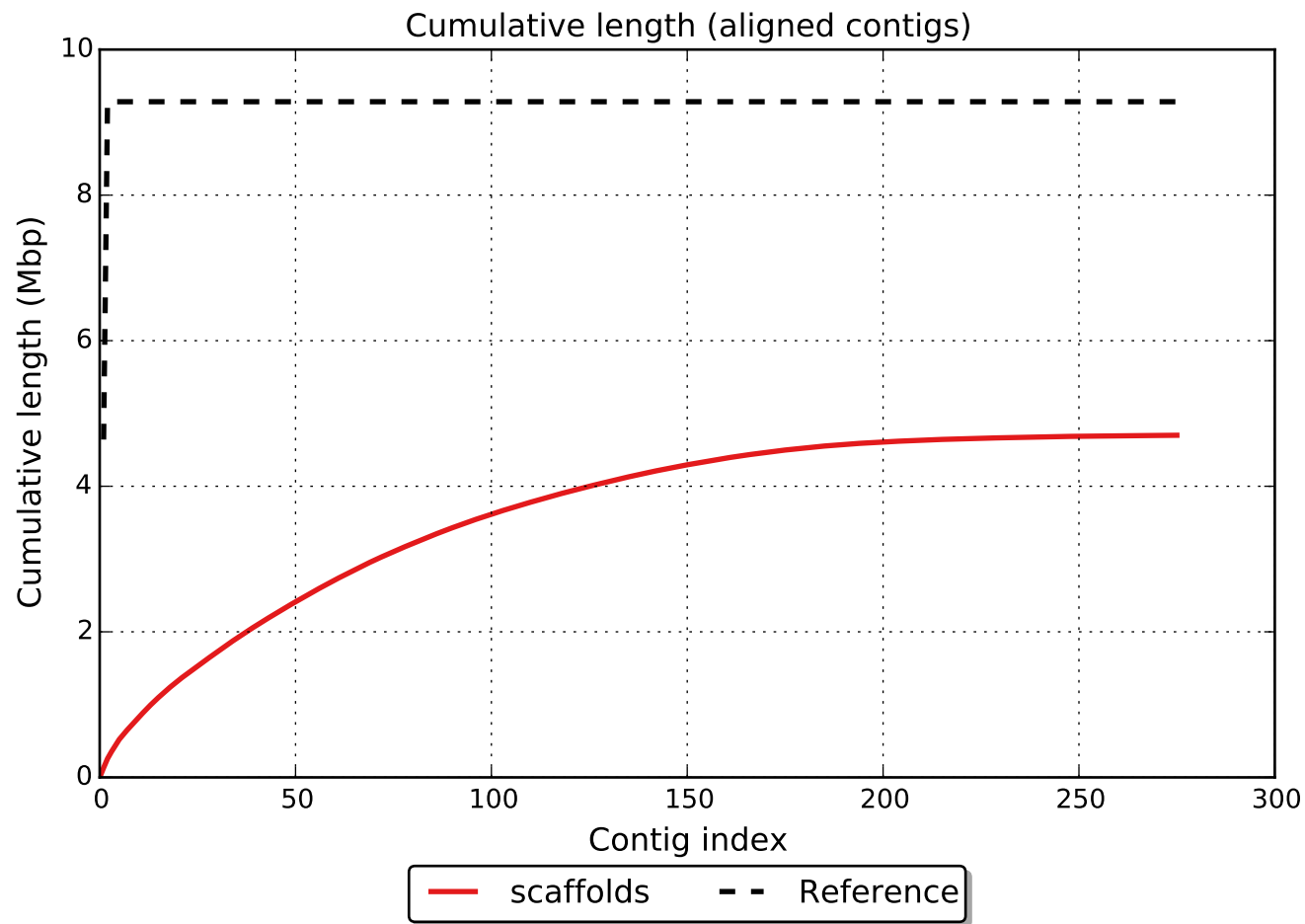
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

