

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	25
# misassembled contigs	19
Misassembled contigs length	706576
# local misassemblies	4
# unaligned contigs	9 + 9 part
Unaligned length	6763
Genome fraction (%)	49.054
Duplication ratio	1.031
# N's per 100 kbp	25.88
# mismatches per 100 kbp	923.57
# indels per 100 kbp	0.68
Largest alignment	125463
NA50	29578
NA75	17458
LA50	53
LA75	103

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	25
# relocations	18
# translocations	0
# inversions	6
# interspecies translocations	1
# possibly misassembled contigs	1
# misassembled contigs	19
Misassembled contigs length	706576
# local misassemblies	4
# mismatches	42058
# indels	31
# short indels	27
# long indels	4
Indels length	254

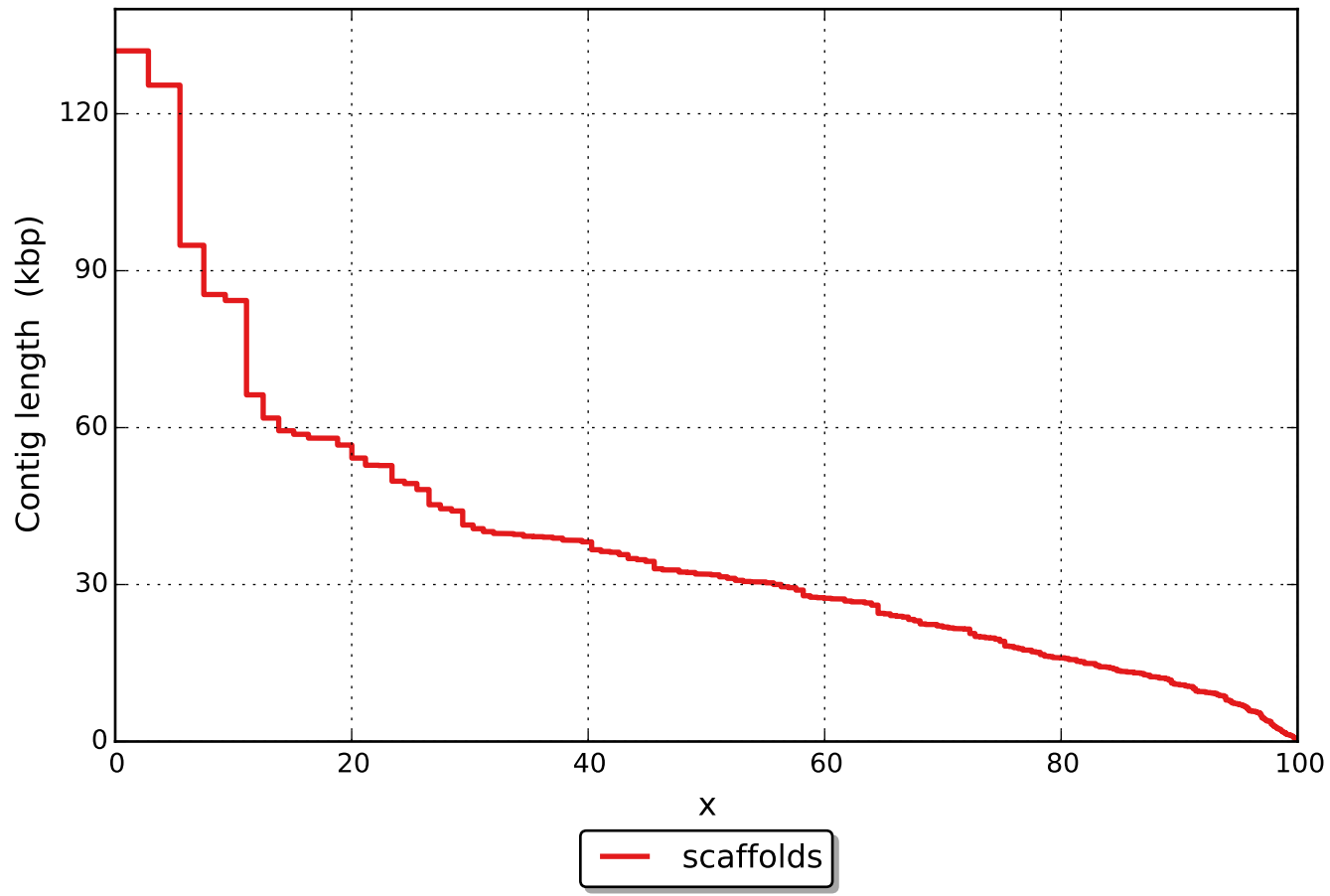
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

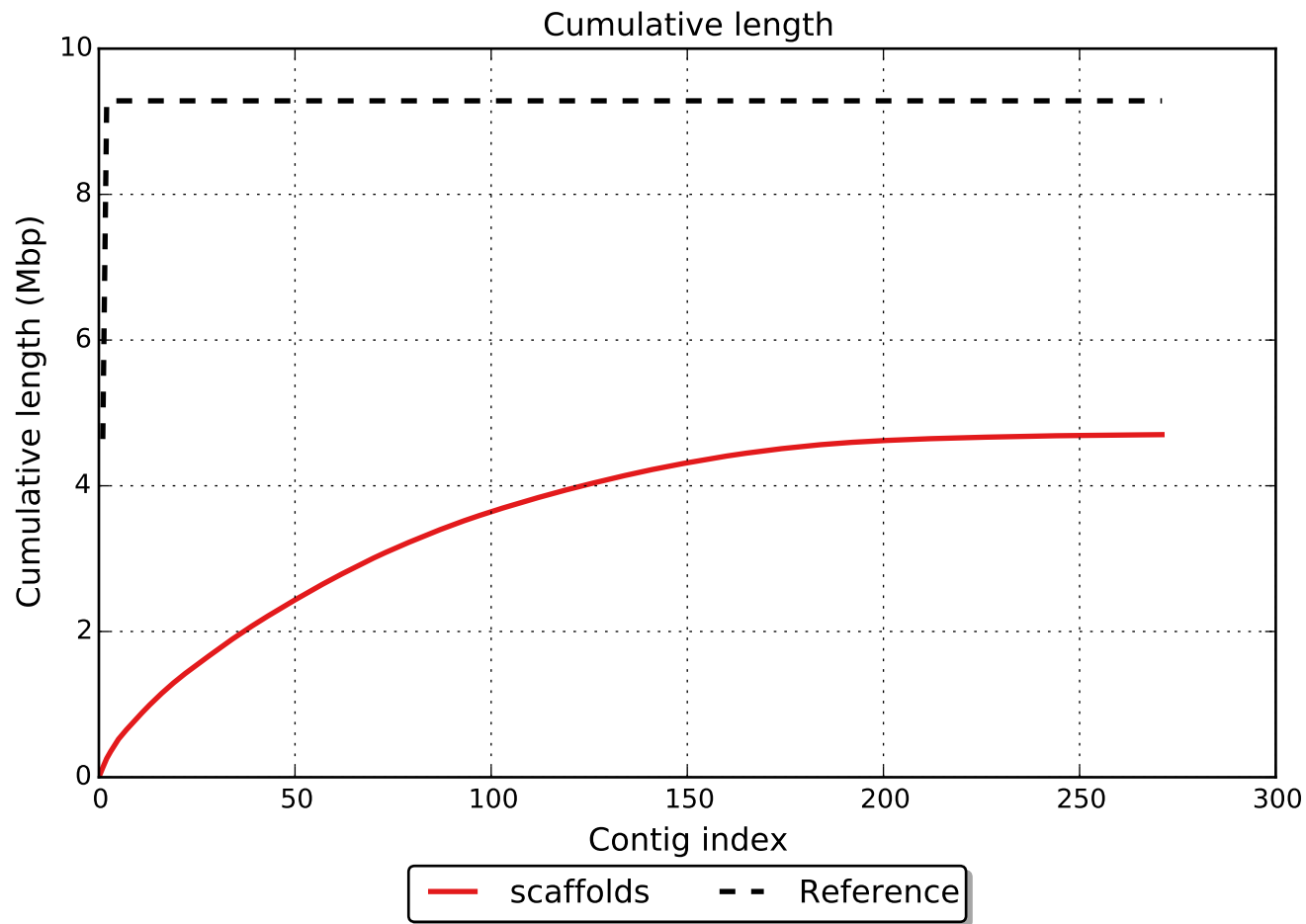
Unaligned report

	scaffolds
# fully unaligned contigs	9
Fully unaligned length	5129
# partially unaligned contigs	9
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1634
# N's	1217

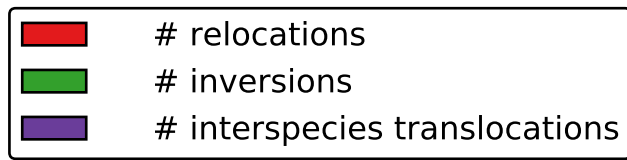
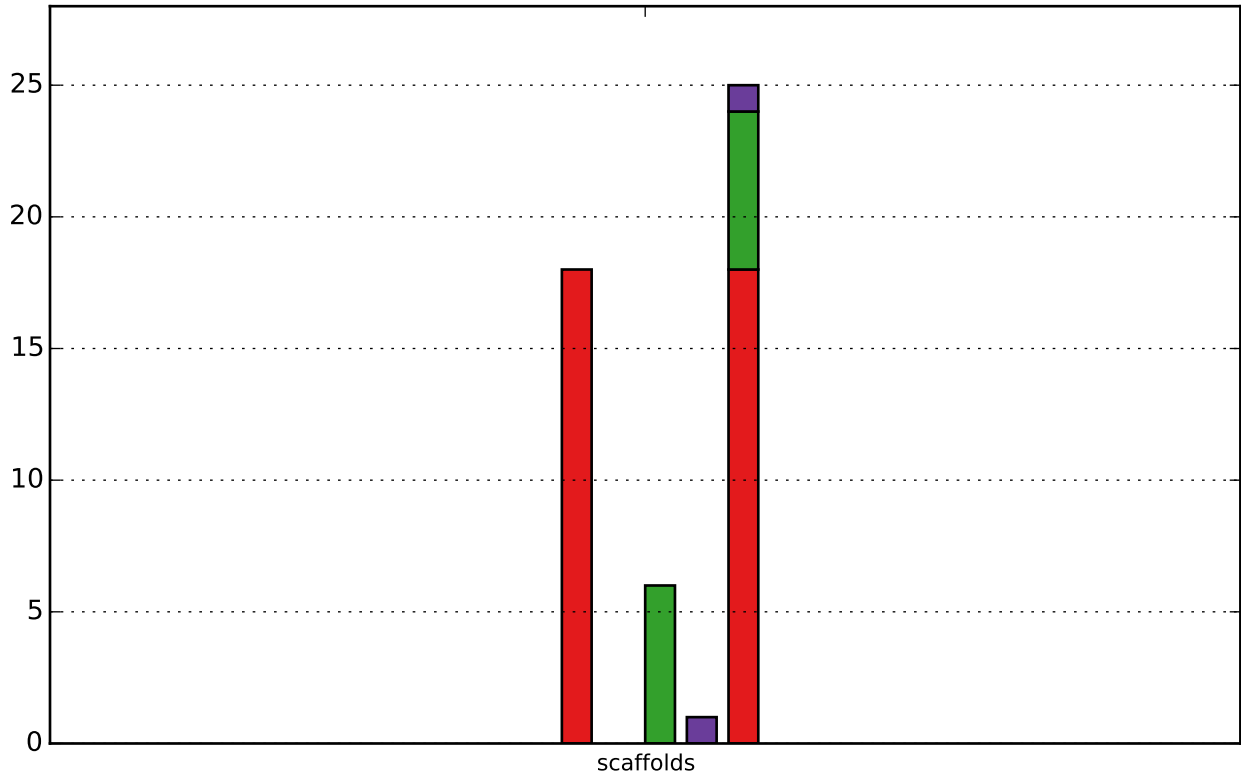
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

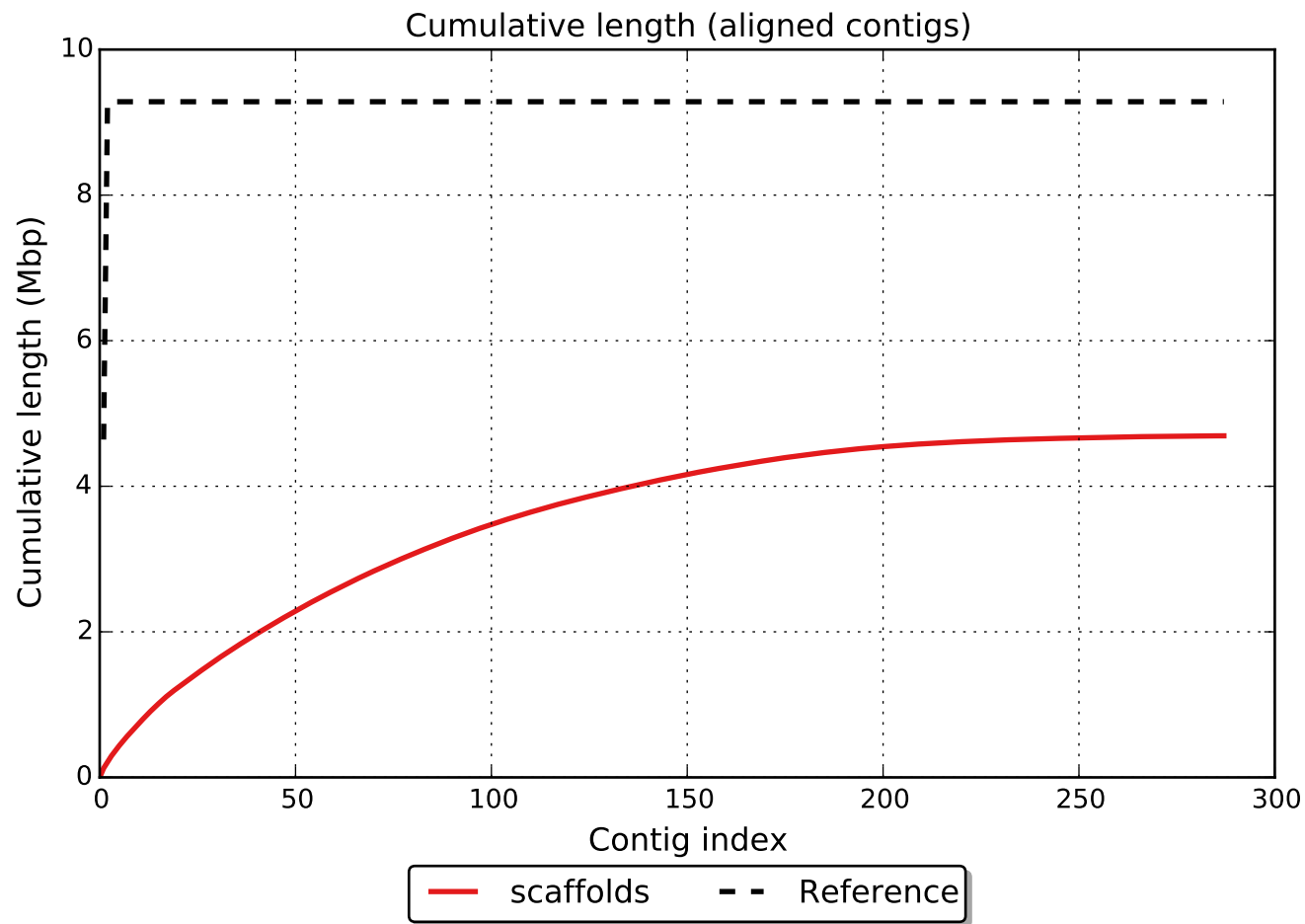
Nx





Misassemblies





NAx

