

Report

	scaffolds
# contigs (≥ 0 bp)	125
# contigs (≥ 1000 bp)	77
# contigs (≥ 5000 bp)	64
# contigs (≥ 10000 bp)	61
# contigs (≥ 25000 bp)	54
# contigs (≥ 50000 bp)	41
Total length (≥ 0 bp)	9146130
Total length (≥ 1000 bp)	9129851
Total length (≥ 5000 bp)	9102772
Total length (≥ 10000 bp)	9077538
Total length (≥ 25000 bp)	8967925
Total length (≥ 50000 bp)	8536857
# contigs	86
Largest contig	663492
Total length	9137424
Reference length	9283304
N50	263950
N75	151678
L50	12
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.363
Duplication ratio	1.001
# N's per 100 kbp	0.51
# mismatches per 100 kbp	159.86
# indels per 100 kbp	0.50
Largest alignment	663492
NA50	263950
NA75	151676
LA50	12
LA75	25

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	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	478751
# local misassemblies	3
# mismatches	14597
# indels	46
# short indels	44
# long indels	2
Indels length	110

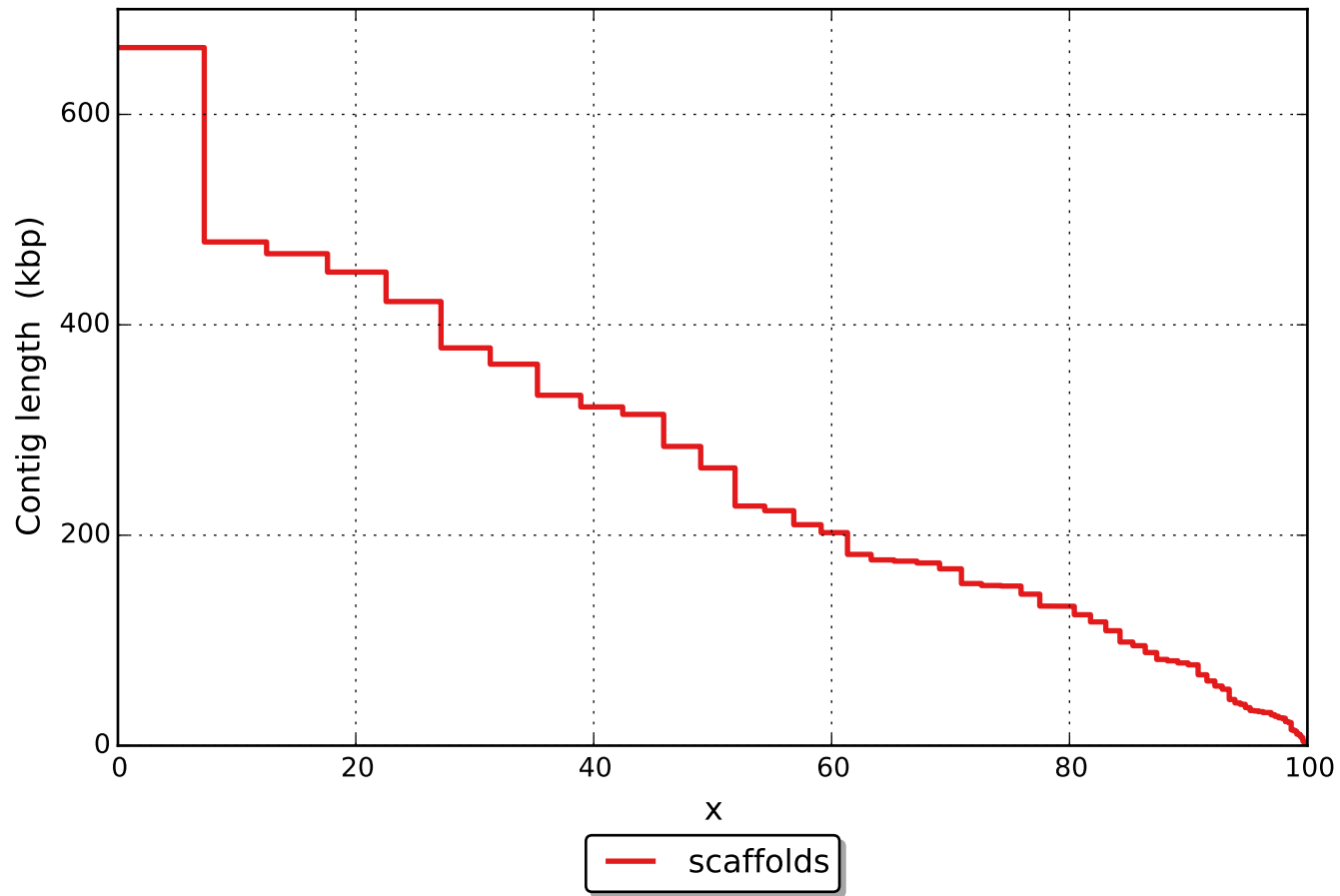
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

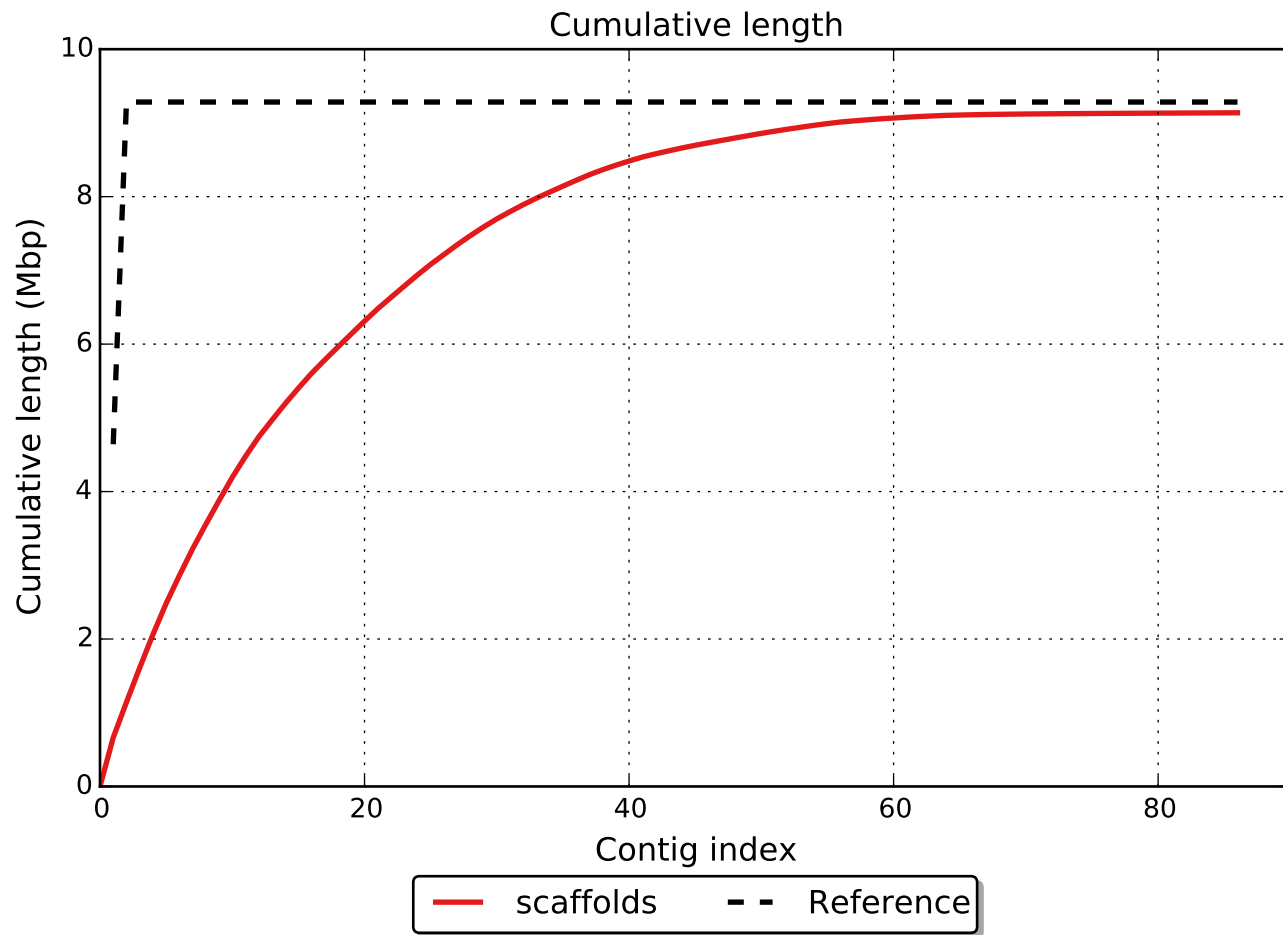
Unaligned report

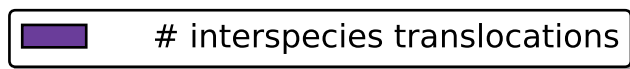
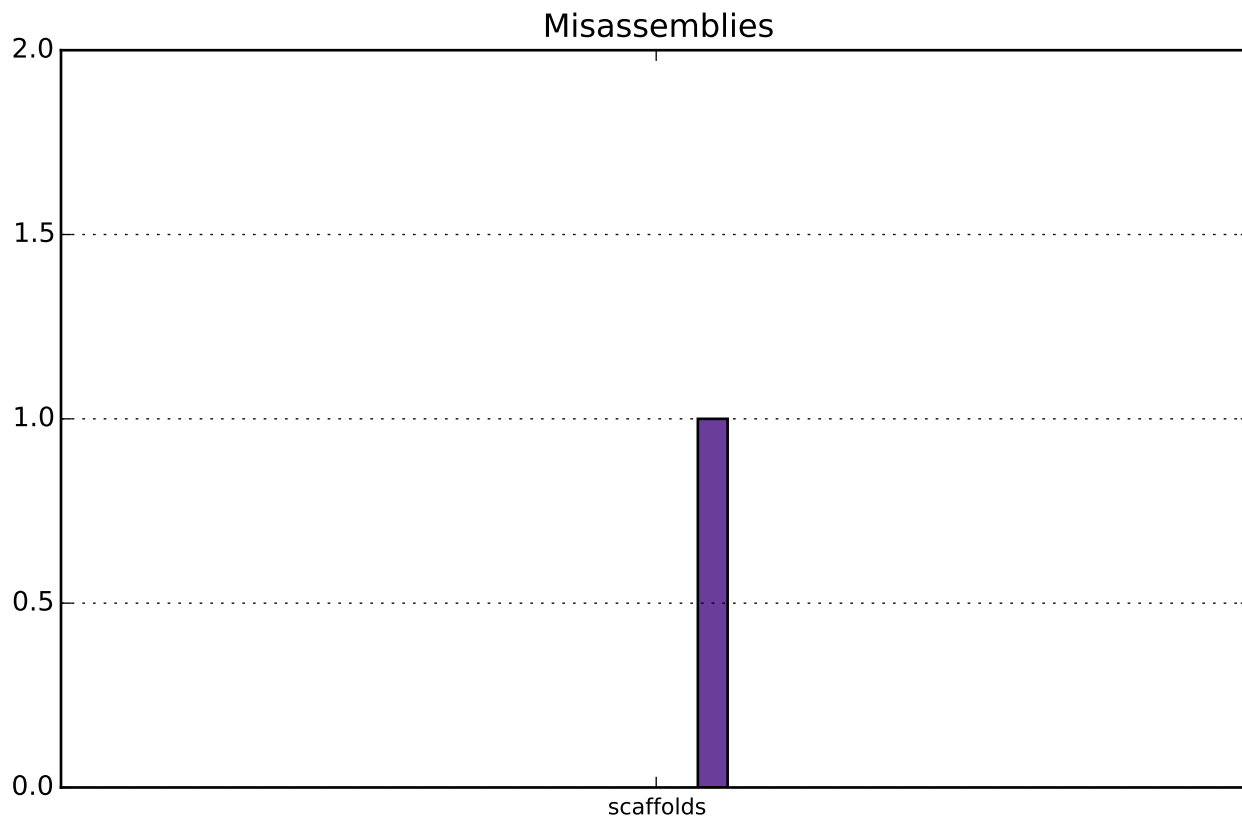
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	47

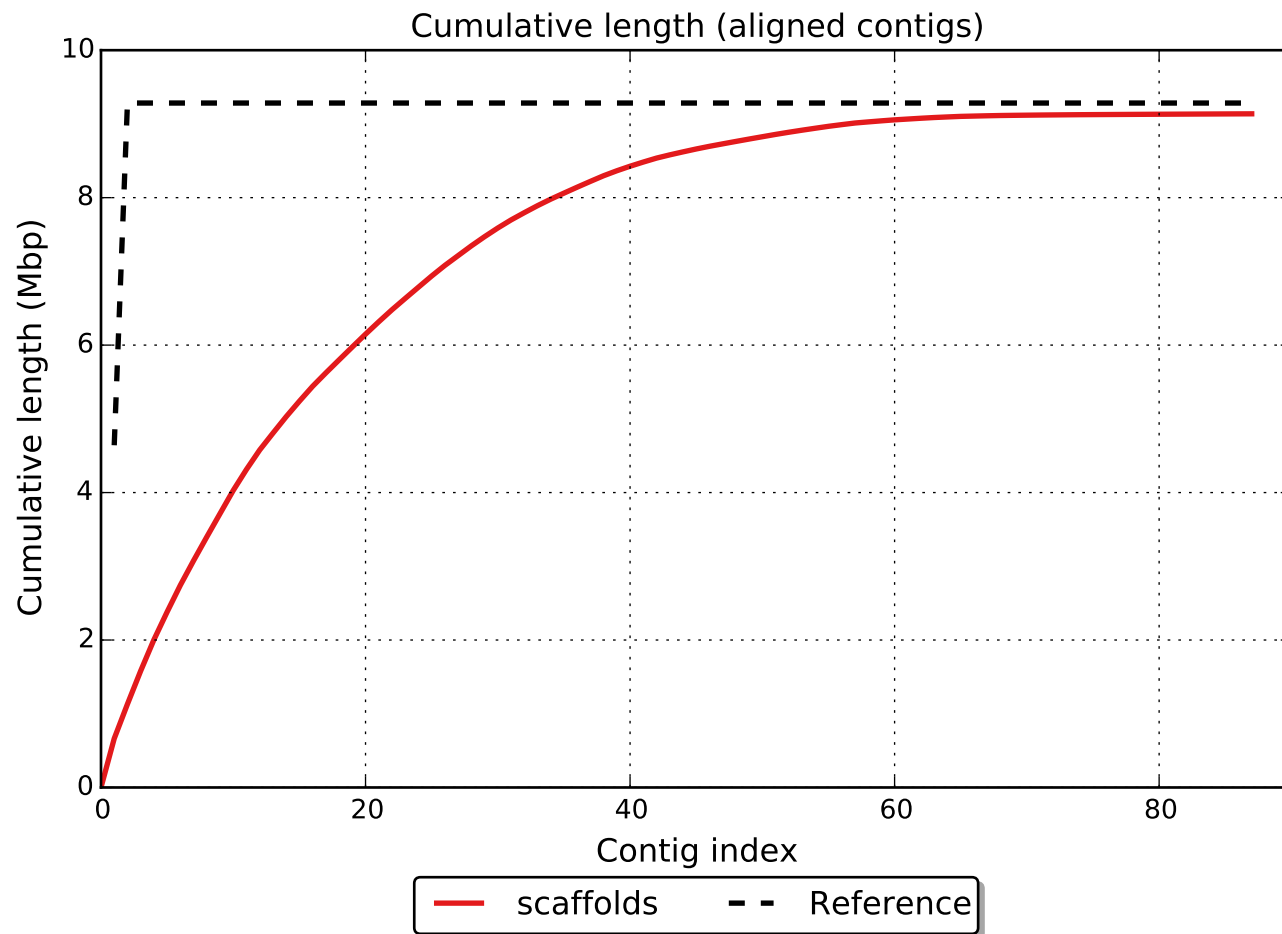
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx









NAx

