

Report

	scaffolds
# contigs (≥ 0 bp)	117
# contigs (≥ 1000 bp)	100
# contigs (≥ 5000 bp)	81
# contigs (≥ 10000 bp)	67
# contigs (≥ 25000 bp)	49
# contigs (≥ 50000 bp)	30
Total length (≥ 0 bp)	4551826
Total length (≥ 1000 bp)	4546459
Total length (≥ 5000 bp)	4504936
Total length (≥ 10000 bp)	4403489
Total length (≥ 25000 bp)	4111791
Total length (≥ 50000 bp)	3453079
# contigs	103
Largest contig	327367
Total length	4548491
Reference length	4641652
N50	105658
N75	53520
L50	14
L75	30
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	624215
# local misassemblies	8
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.962
Duplication ratio	1.000
# N's per 100 kbp	27.77
# mismatches per 100 kbp	64.86
# indels per 100 kbp	9.65
Largest alignment	327367
NA50	95467
NA75	43798
LA50	14
LA75	32

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	10
# relocations	10
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	10
Misassembled contigs length	624215
# local misassemblies	8
# mismatches	2949
# indels	439
# short indels	409
# long indels	30
Indels length	1107

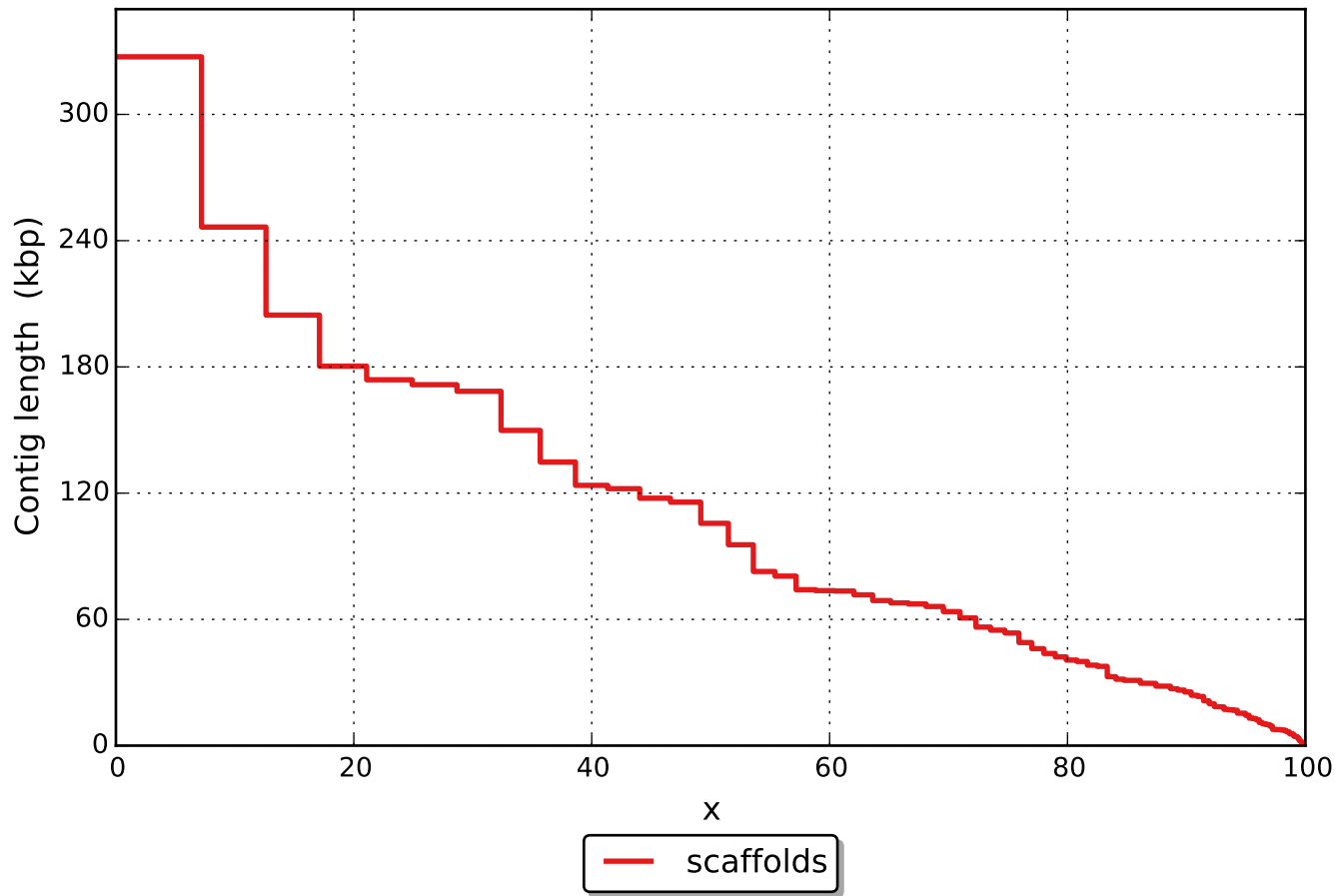
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

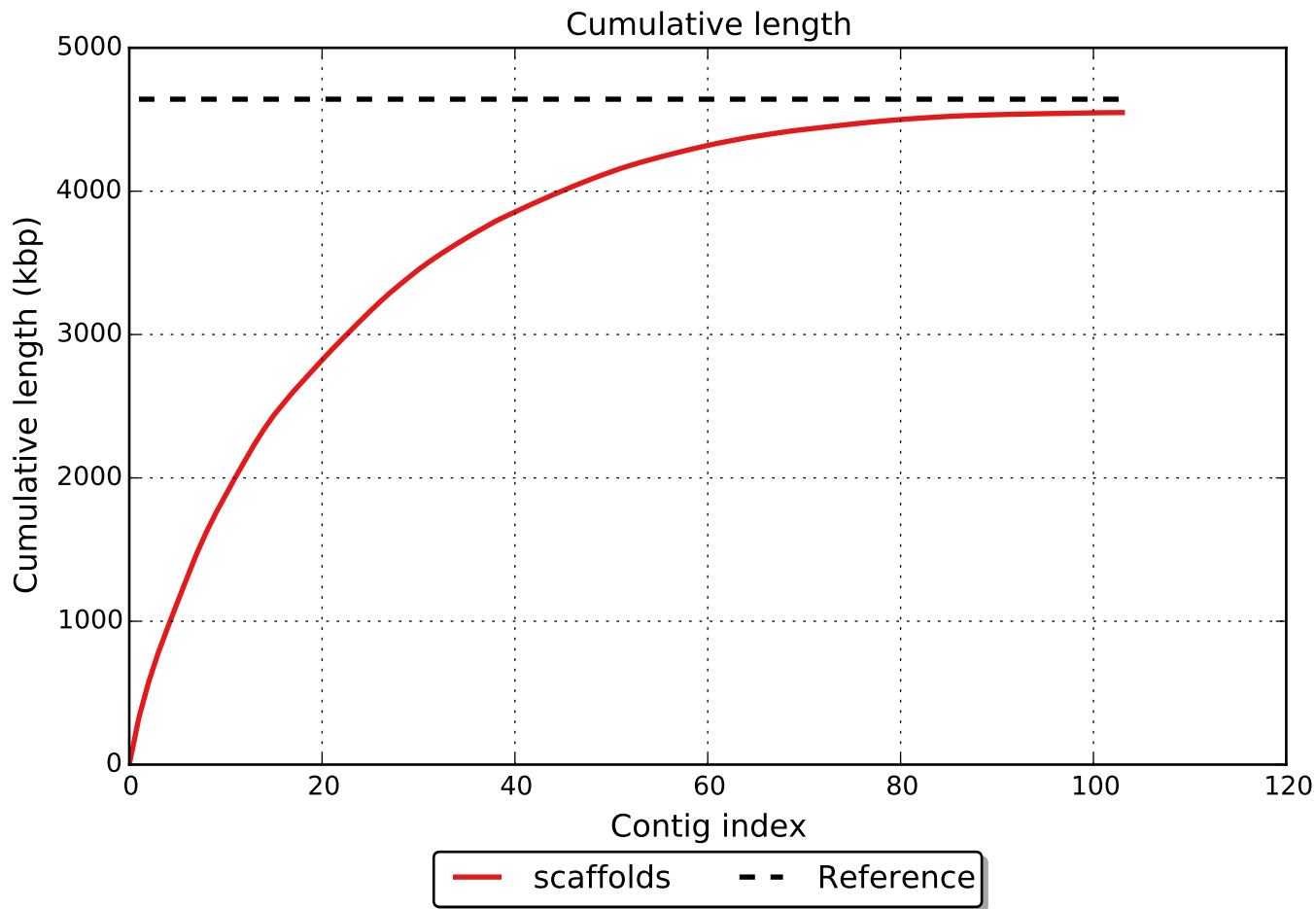
Unaligned report

	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	1263

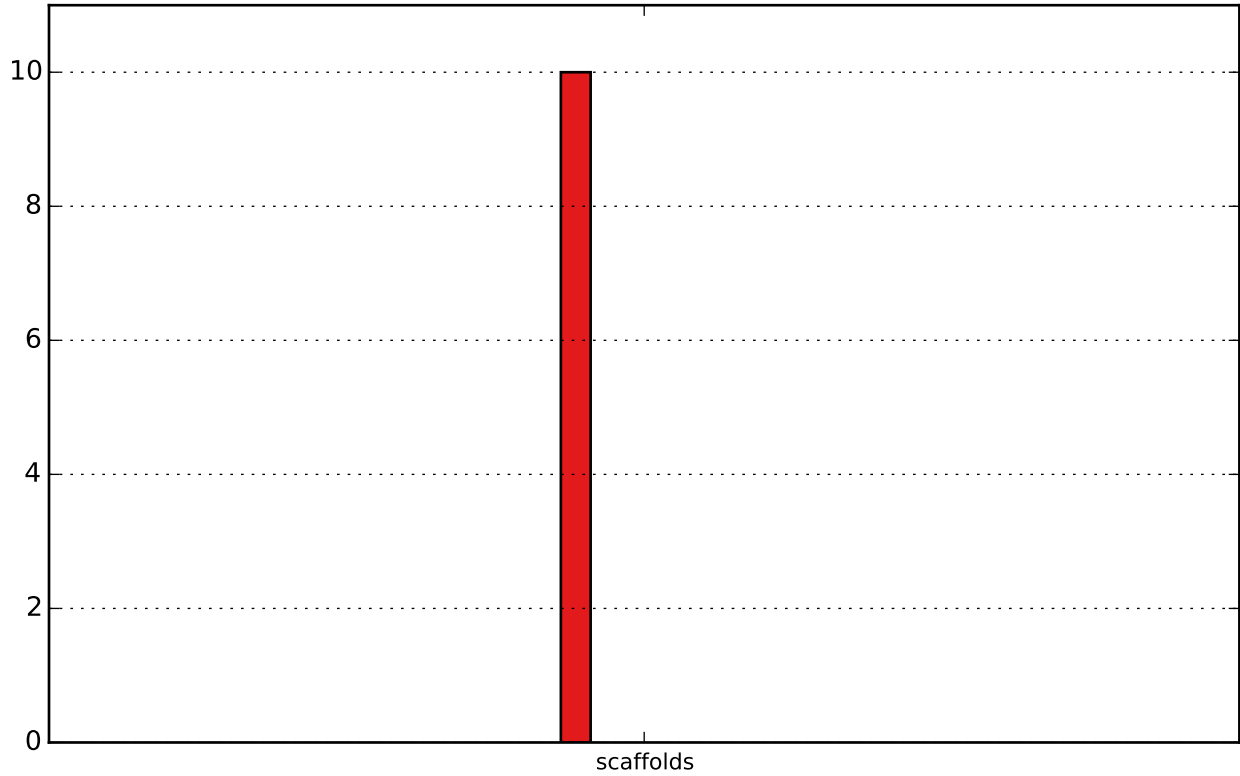
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

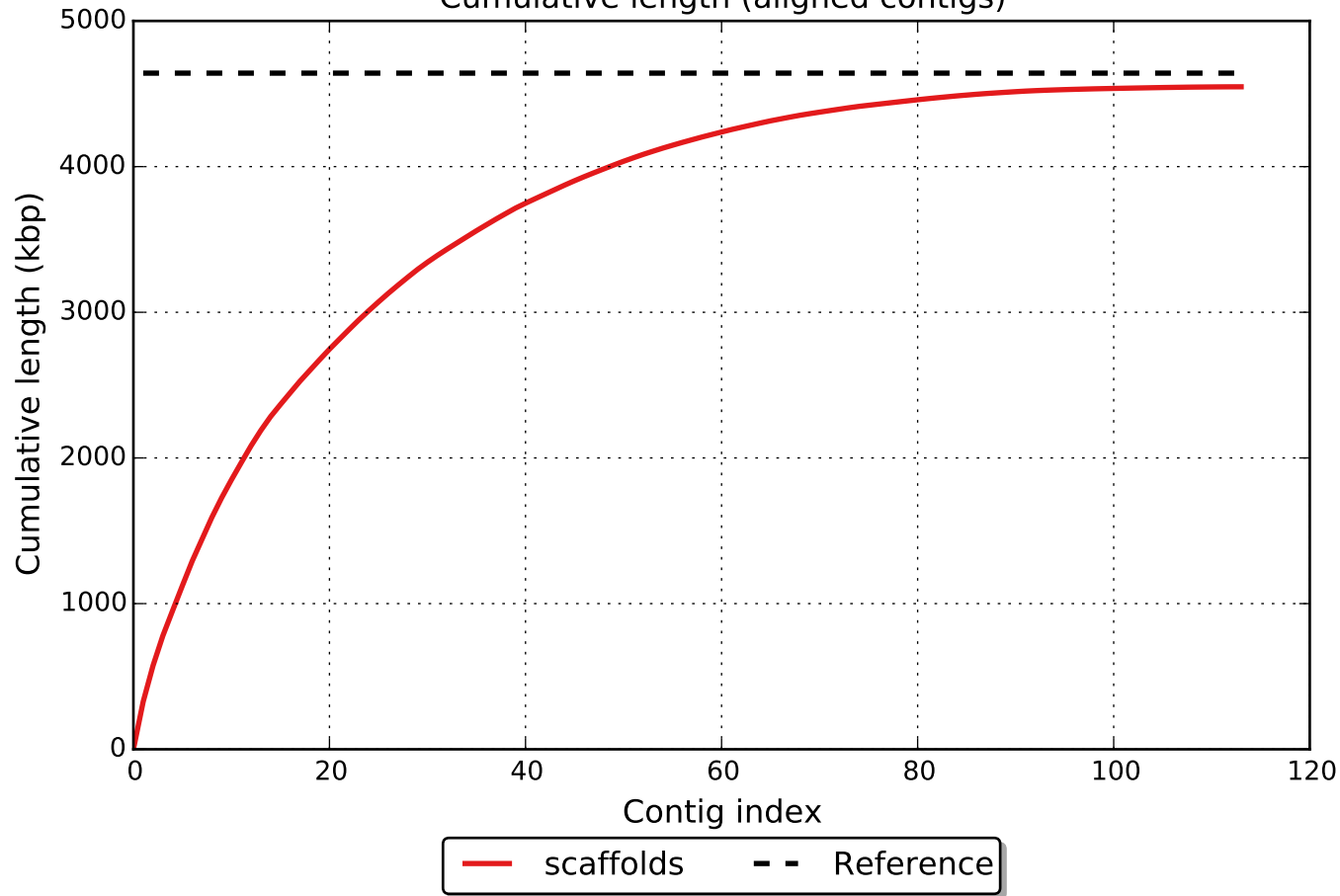




Misassemblies



Cumulative length (aligned contigs)



NAx

