

## Report

	scaffolds
# contigs ( $\geq 0$ bp)	229
# contigs ( $\geq 1000$ bp)	99
# contigs ( $\geq 5000$ bp)	77
# contigs ( $\geq 10000$ bp)	74
# contigs ( $\geq 25000$ bp)	66
# contigs ( $\geq 50000$ bp)	48
Total length ( $\geq 0$ bp)	9110170
Total length ( $\geq 1000$ bp)	9058514
Total length ( $\geq 5000$ bp)	9020683
Total length ( $\geq 10000$ bp)	8998158
Total length ( $\geq 25000$ bp)	8853949
Total length ( $\geq 50000$ bp)	8231677
# contigs	132
Largest contig	600951
Total length	9079929
Reference length	9283304
N50	200817
N75	110783
L50	16
L75	31
# misassemblies	261
# misassembled contigs	37
Misassembled contigs length	4271262
# local misassemblies	10
# unaligned contigs	22 + 5 part
Unaligned length	81336
Genome fraction (%)	49.550
Duplication ratio	1.958
# N's per 100 kbp	0.00
# mismatches per 100 kbp	760.30
# indels per 100 kbp	1.37
Largest alignment	600951
NA50	65859
NA75	18999
LA50	26
LA75	95

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

## Misassemblies report

	scaffolds
# misassemblies	261
# relocations	236
# translocations	0
# inversions	22
# interspecies translocations	3
# possibly misassembled contigs	27
# misassembled contigs	37
Misassembled contigs length	4271262
# local misassemblies	10
# mismatches	34973
# indels	63
# short indels	63
# long indels	0
Indels length	65

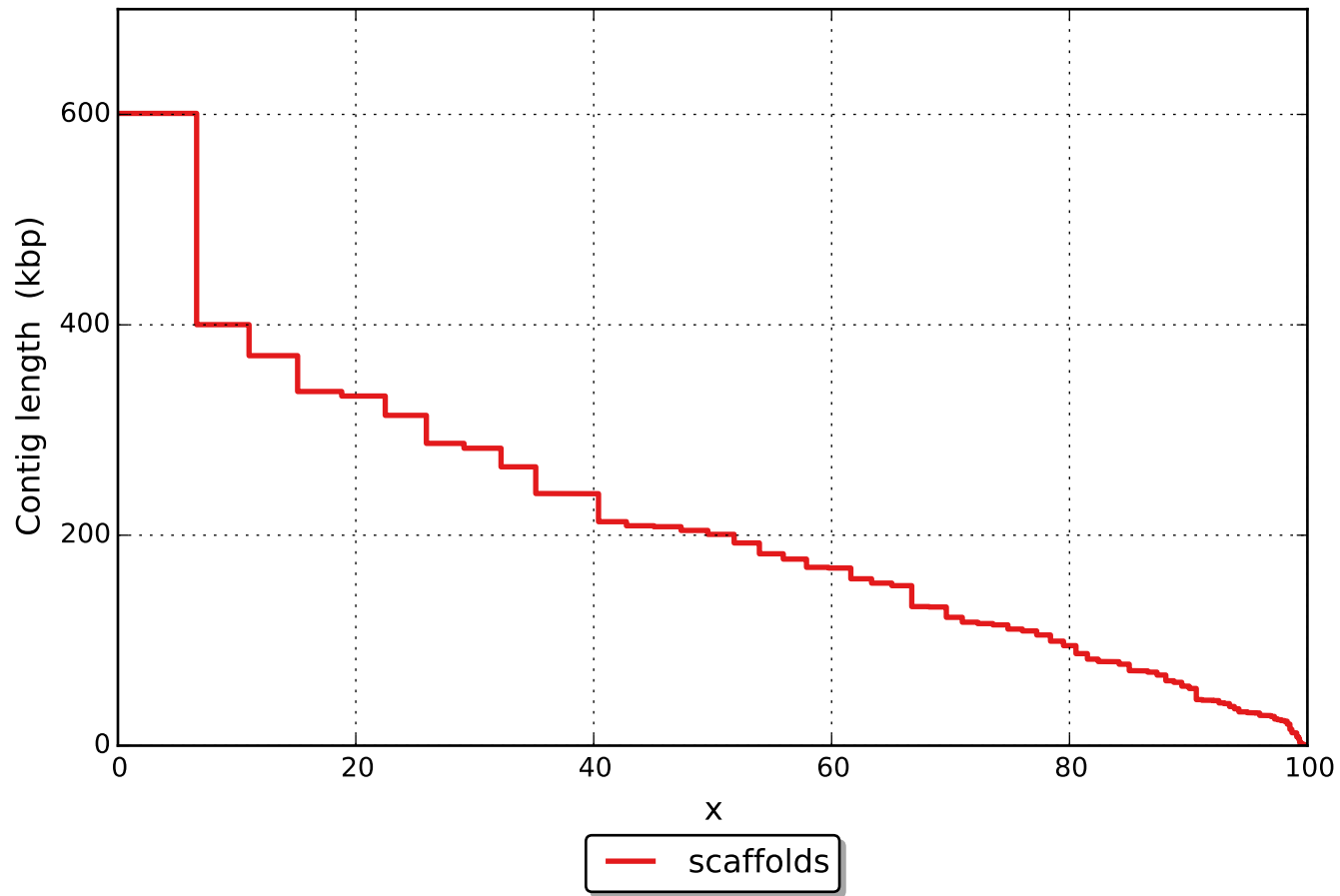
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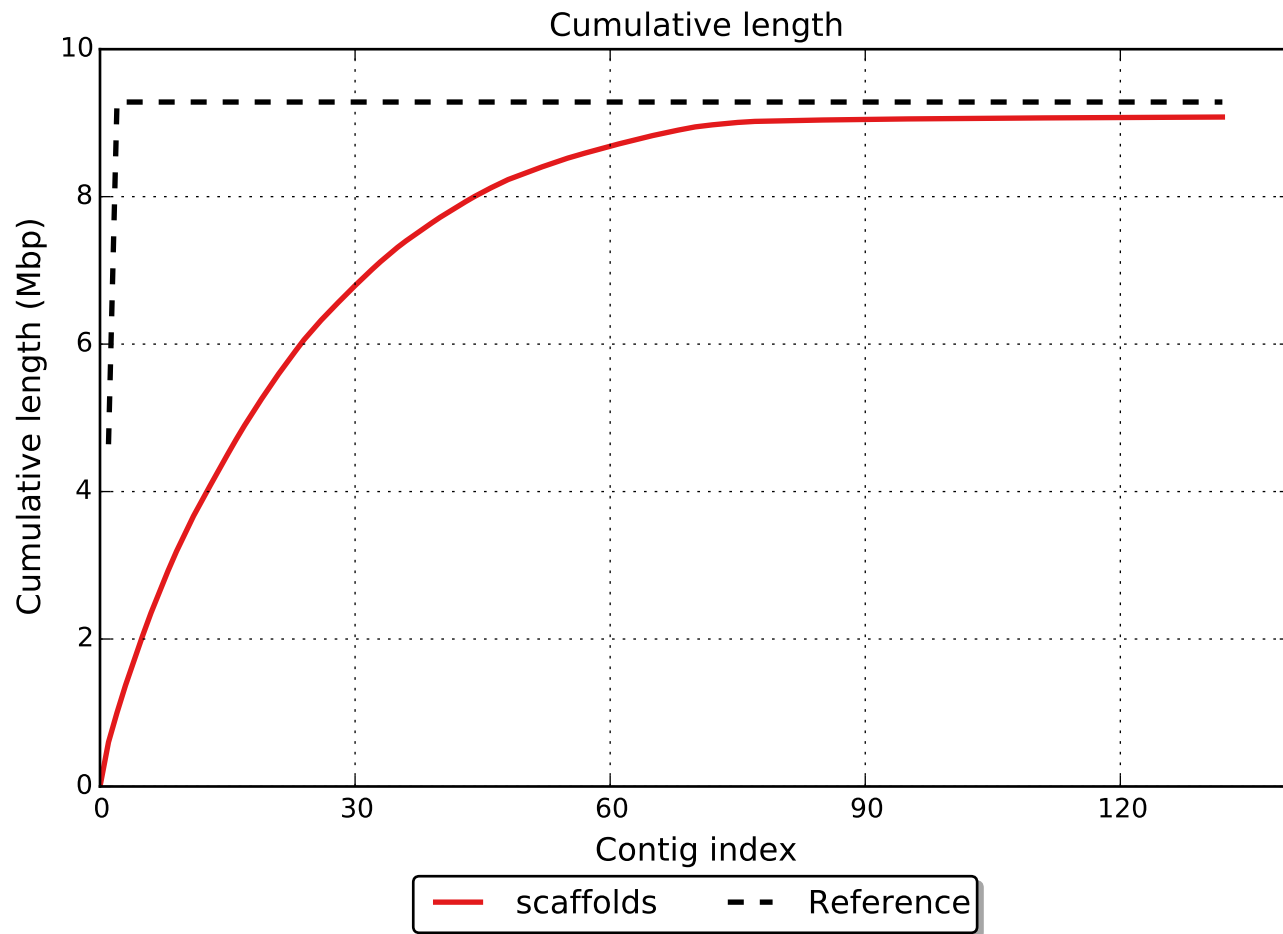
## Unaligned report

	scaffolds
# fully unaligned contigs	22
Fully unaligned length	20880
# partially unaligned contigs	5
# with misassembly	1
# both parts are significant	3
Partially unaligned length	60456
# N's	0

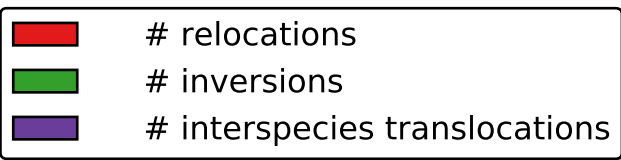
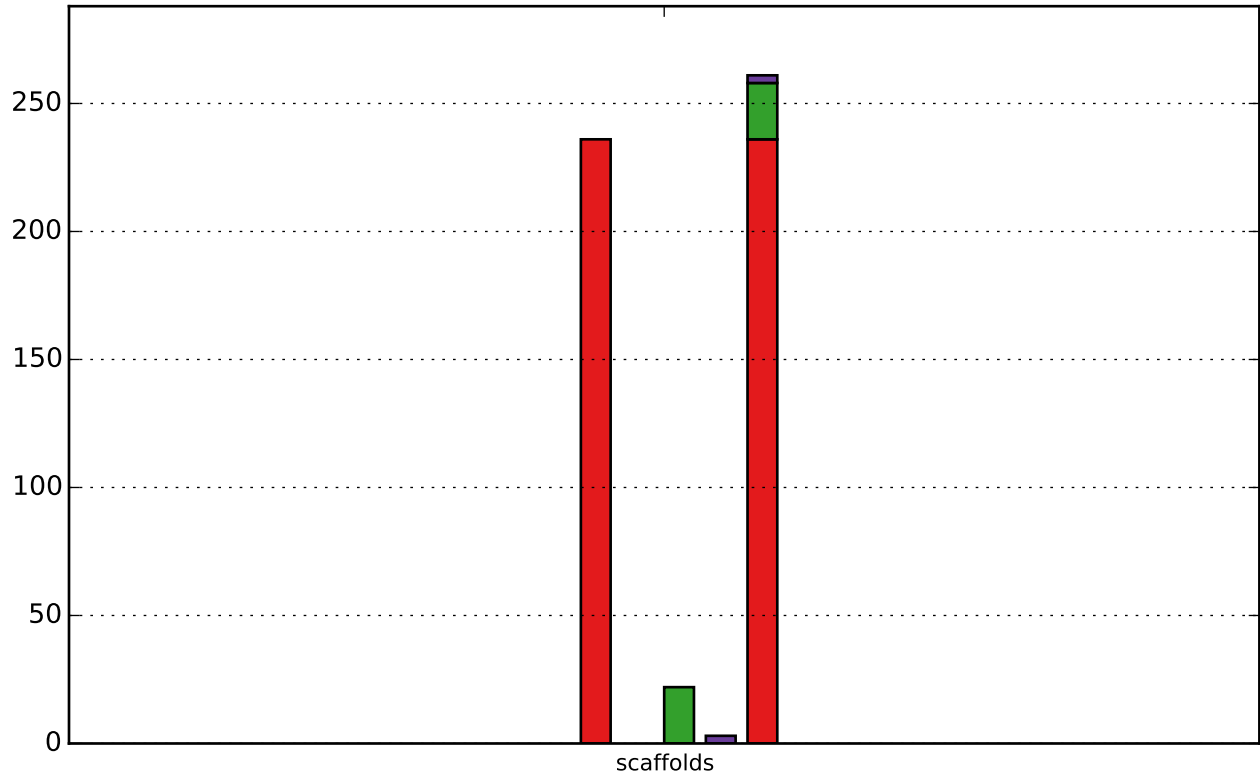
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

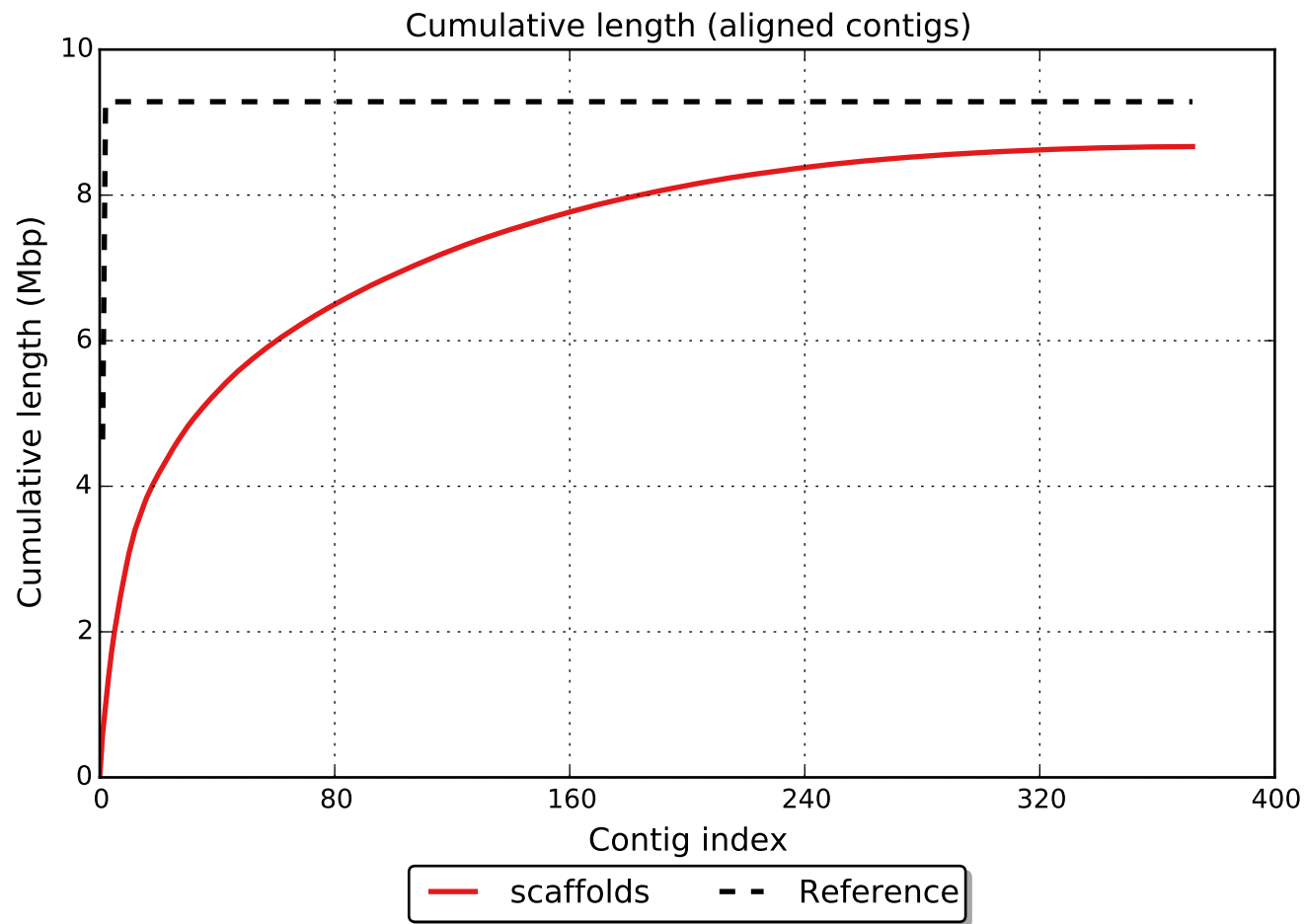
Nx





## Misassemblies





NAx

