

# Report

	scaffolds
# contigs ( $\geq 0$ bp)	920
# contigs ( $\geq 1000$ bp)	238
# contigs ( $\geq 5000$ bp)	182
# contigs ( $\geq 10000$ bp)	148
# contigs ( $\geq 25000$ bp)	71
# contigs ( $\geq 50000$ bp)	15
Total length ( $\geq 0$ bp)	4912814
Total length ( $\geq 1000$ bp)	4681396
Total length ( $\geq 5000$ bp)	4554718
Total length ( $\geq 10000$ bp)	4296558
Total length ( $\geq 25000$ bp)	3033633
Total length ( $\geq 50000$ 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 (%)	49.952
Duplication ratio	1.014
# N's per 100 kbp	25.88
# mismatches per 100 kbp	845.58
# indels per 100 kbp	0.41
Largest alignment	132022
NA50	31853
NA75	18252
LA50	49
LA75	96

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	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	39211
# indels	19
# short indels	15
# long indels	4
Indels length	243

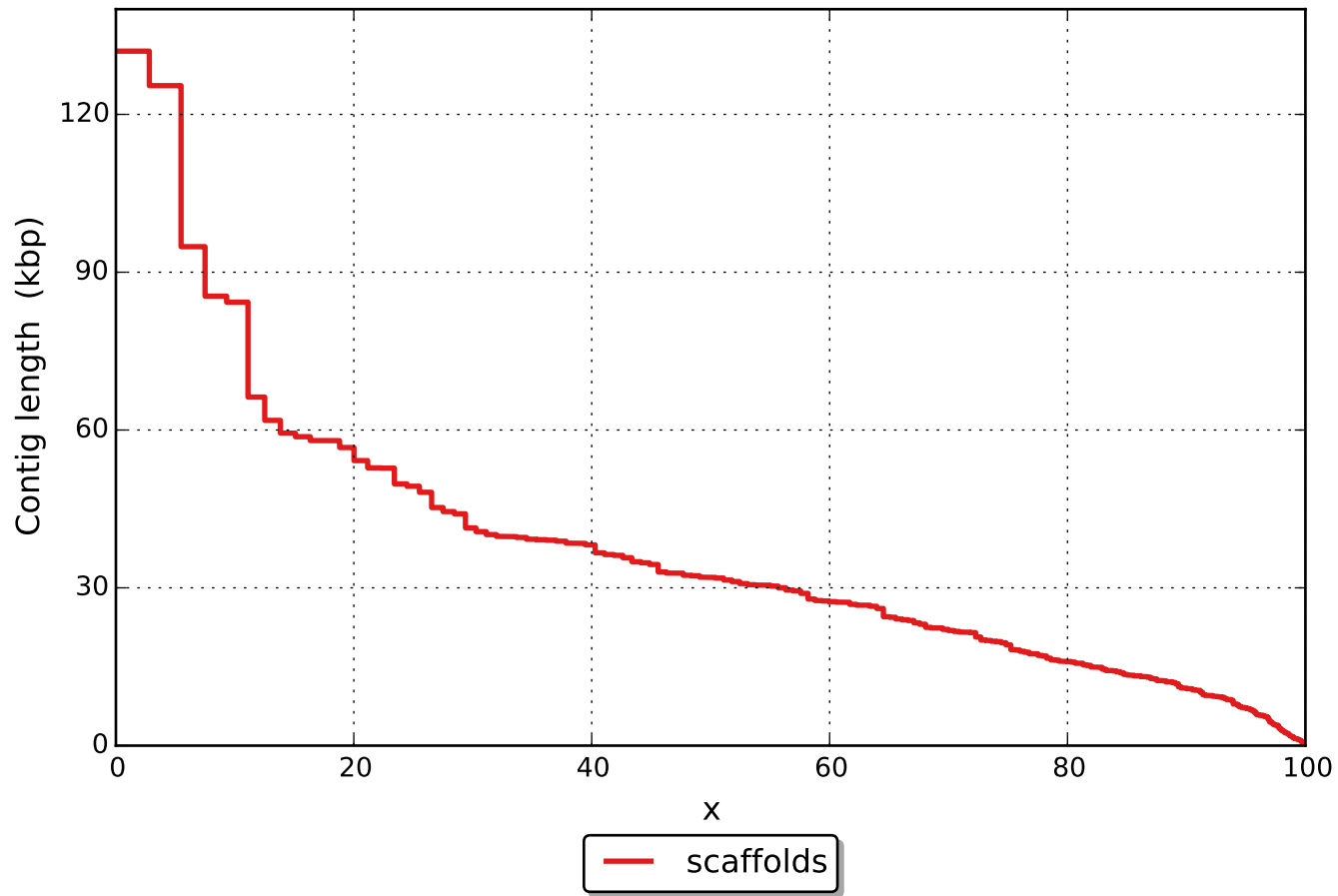
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

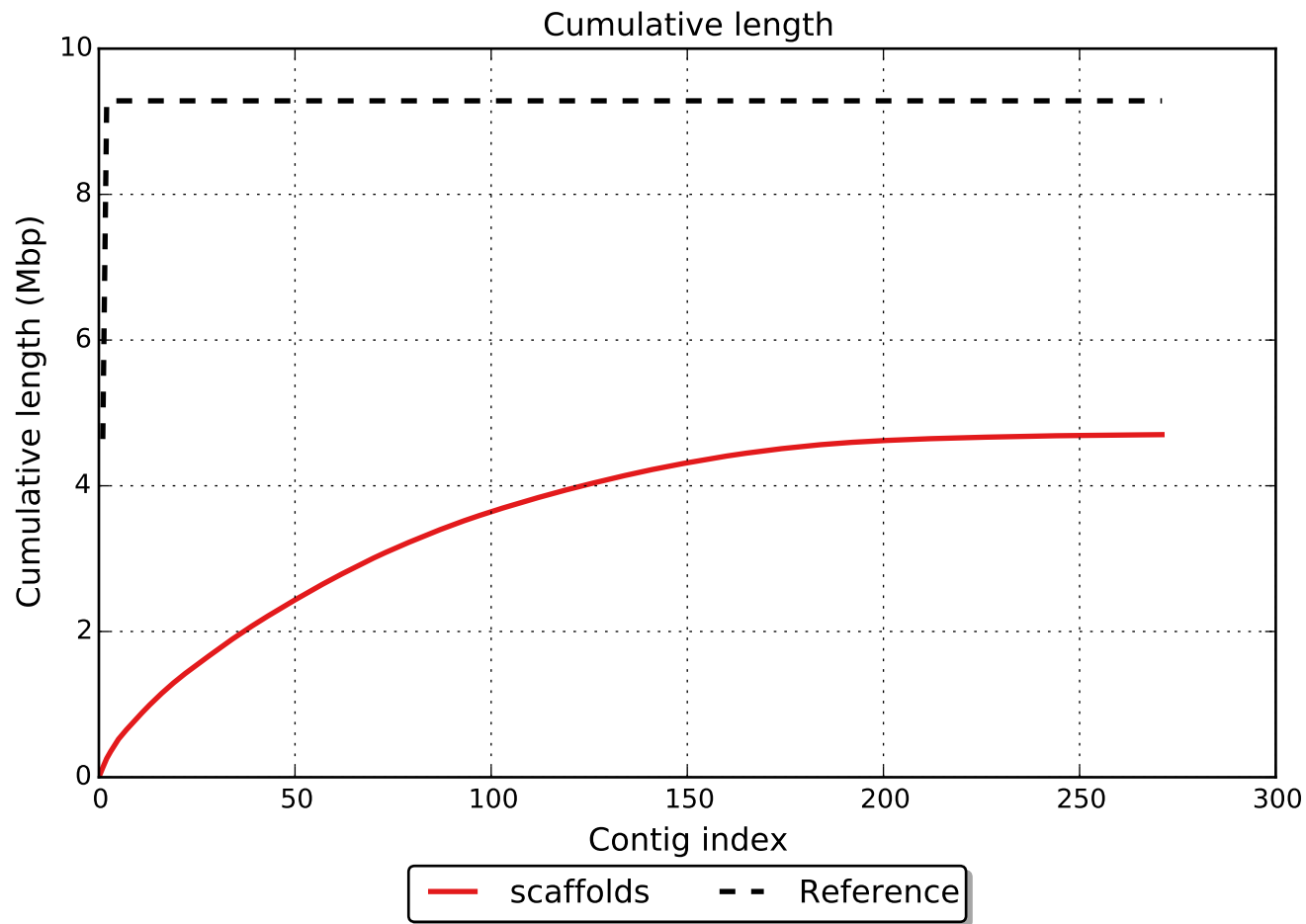
## Unaligned report

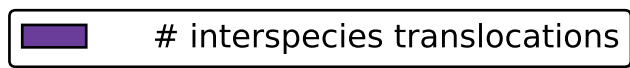
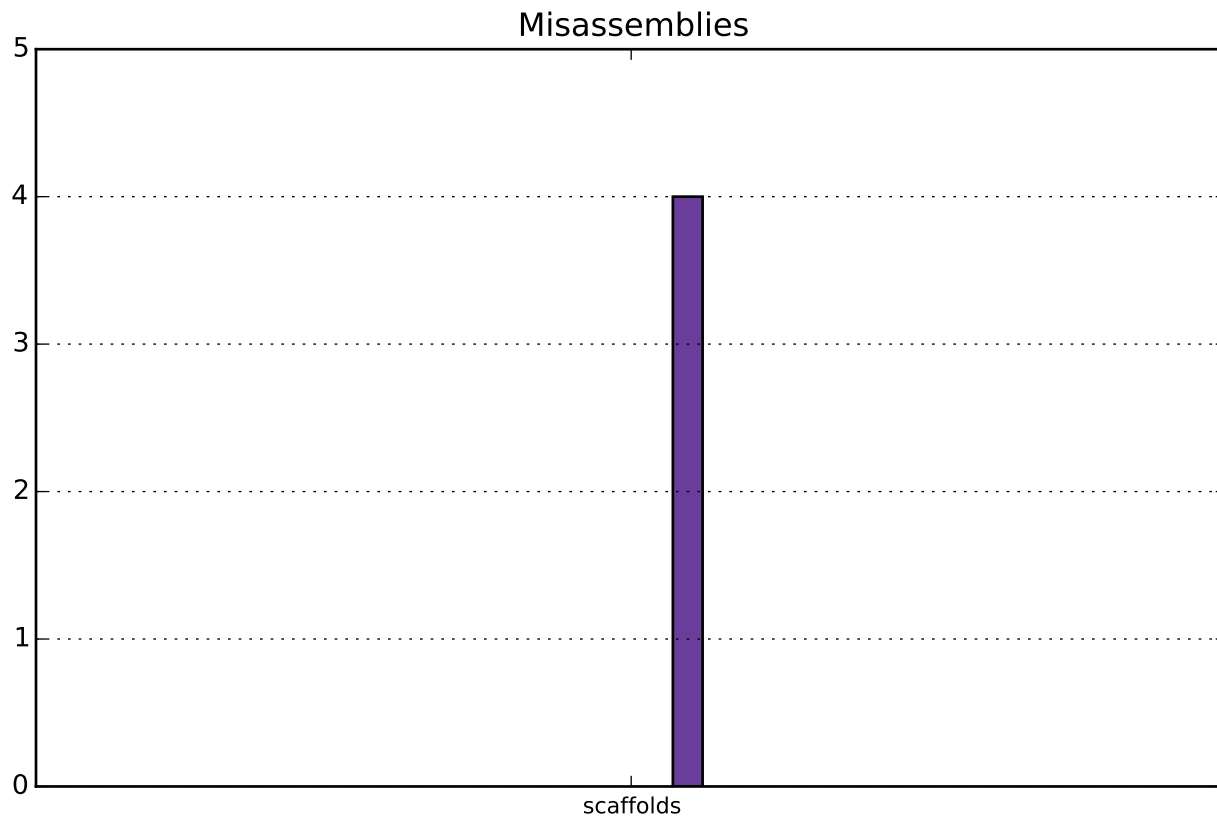
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	1217

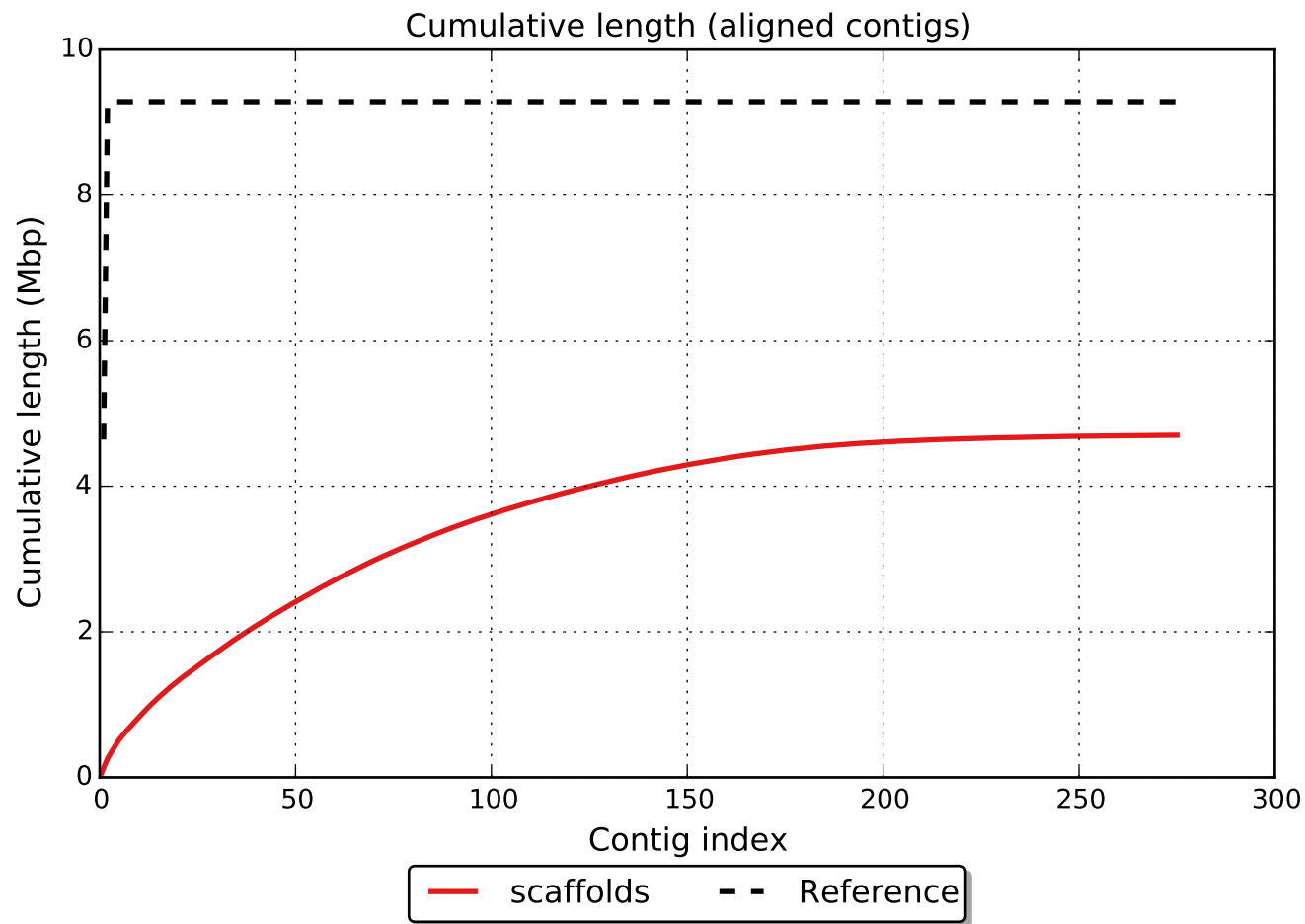
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Nx









NAx

