

## Report

	scaffolds
# contigs ( $\geq 0$ bp)	172
# contigs ( $\geq 1000$ bp)	92
# contigs ( $\geq 5000$ bp)	78
# contigs ( $\geq 10000$ bp)	74
# contigs ( $\geq 25000$ bp)	67
# contigs ( $\geq 50000$ bp)	48
Total length ( $\geq 0$ bp)	9124414
Total length ( $\geq 1000$ bp)	9091674
Total length ( $\geq 5000$ bp)	9067452
Total length ( $\geq 10000$ bp)	9037240
Total length ( $\geq 25000$ bp)	8933081
Total length ( $\geq 50000$ bp)	8257195
# contigs	115
Largest contig	472565
Total length	9108144
Reference length	9283304
N50	208897
N75	108452
L50	15
L75	30
# misassemblies	90
# misassembled contigs	20
Misassembled contigs length	2198687
# local misassemblies	6
# unaligned contigs	14 + 29 part
Unaligned length	1653389
Genome fraction (%)	49.679
Duplication ratio	1.616
# N's per 100 kbp	0.11
# mismatches per 100 kbp	592.97
# indels per 100 kbp	1.19
Largest alignment	472565
NA50	49429
NA75	2152
LA50	25
LA75	195

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	90
# relocations	85
# translocations	0
# inversions	4
# interspecies translocations	1
# possibly misassembled contigs	41
# misassembled contigs	20
Misassembled contigs length	2198687
# local misassemblies	6
# mismatches	27347
# indels	55
# short indels	55
# long indels	0
Indels length	57

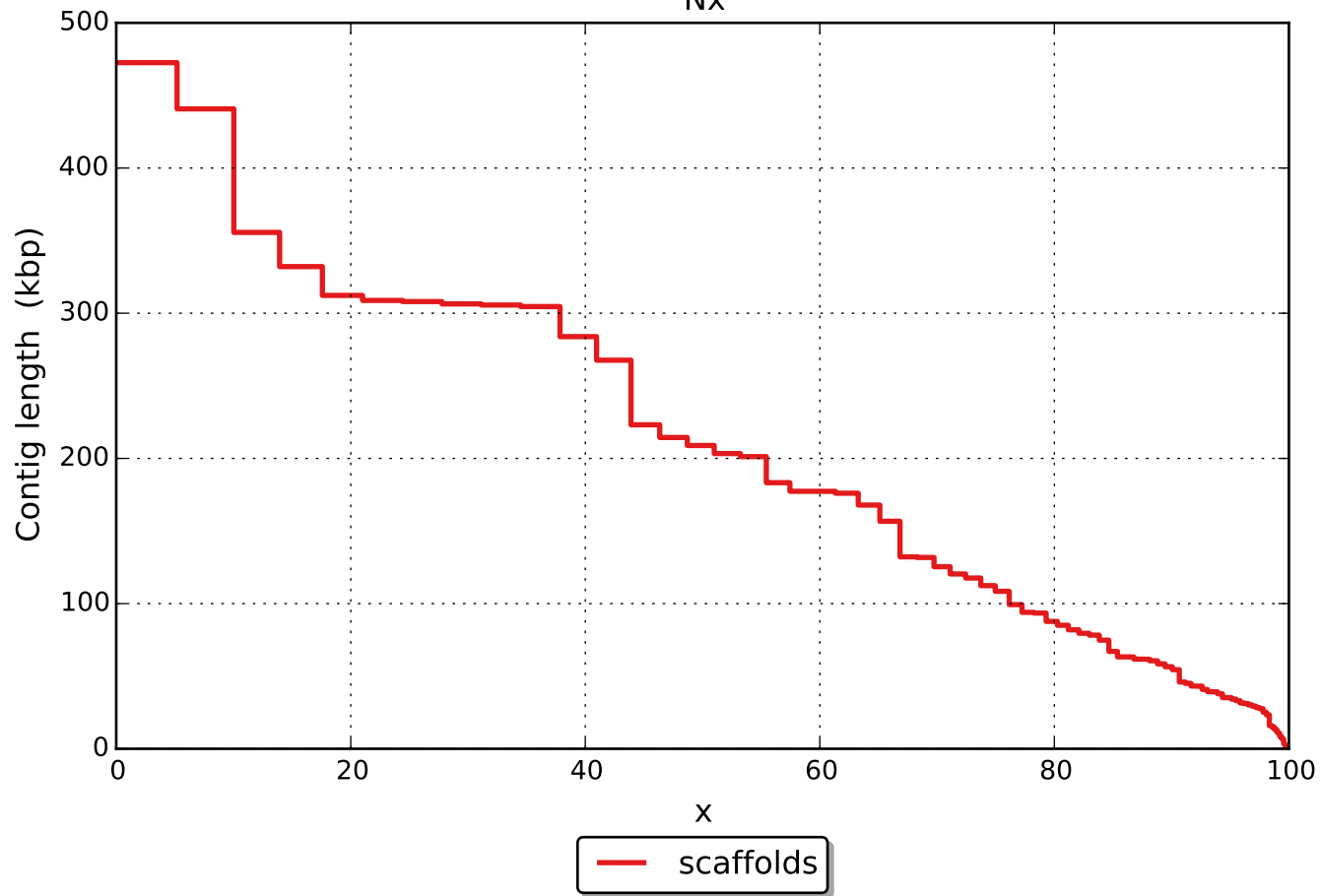
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

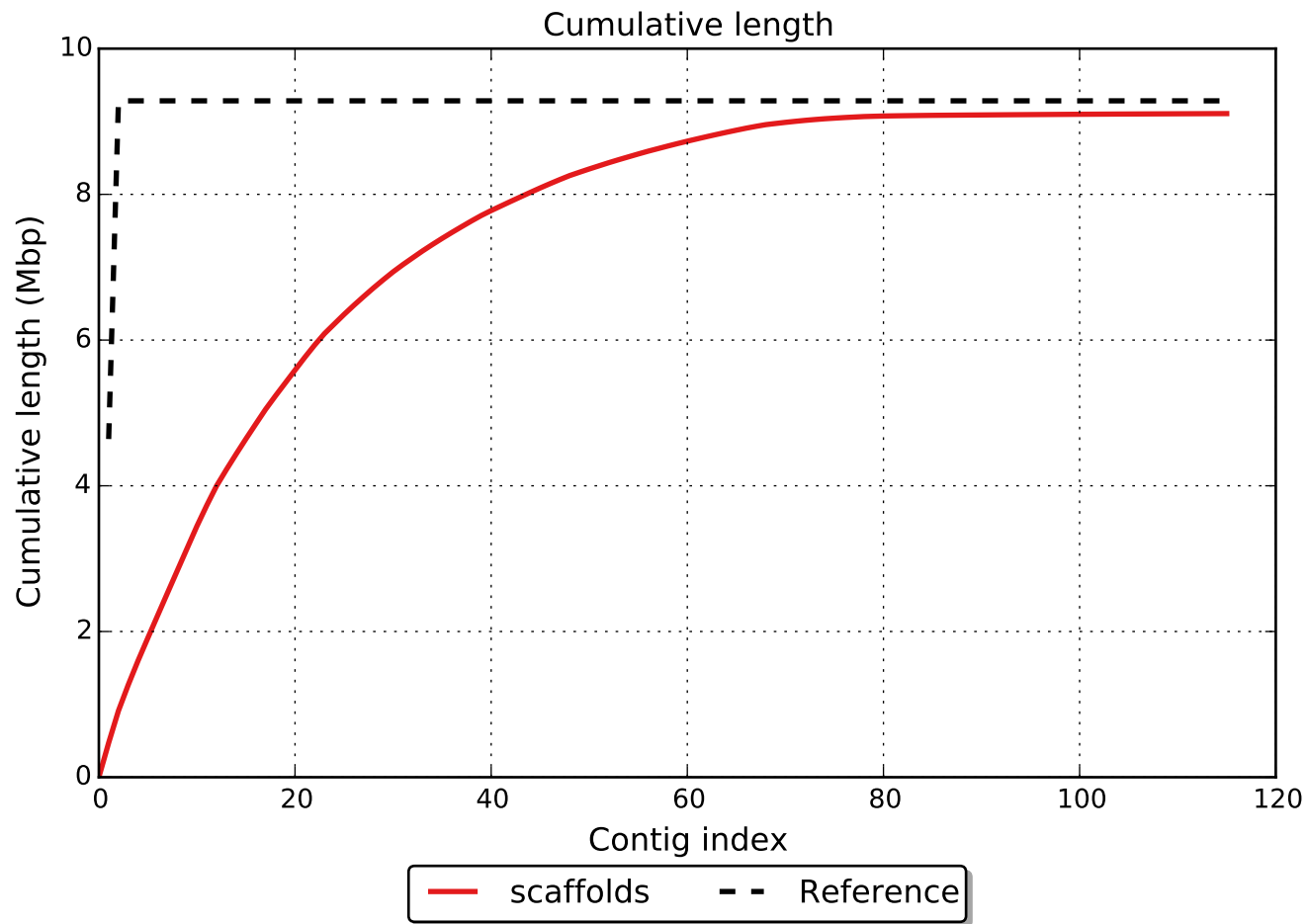
## Unaligned report

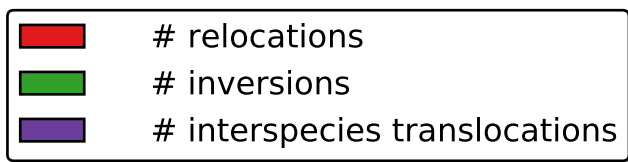
	scaffolds
# fully unaligned contigs	14
Fully unaligned length	130446
# partially unaligned contigs	29
# with misassembly	14
# both parts are significant	24
Partially unaligned length	1522943
# N's	10

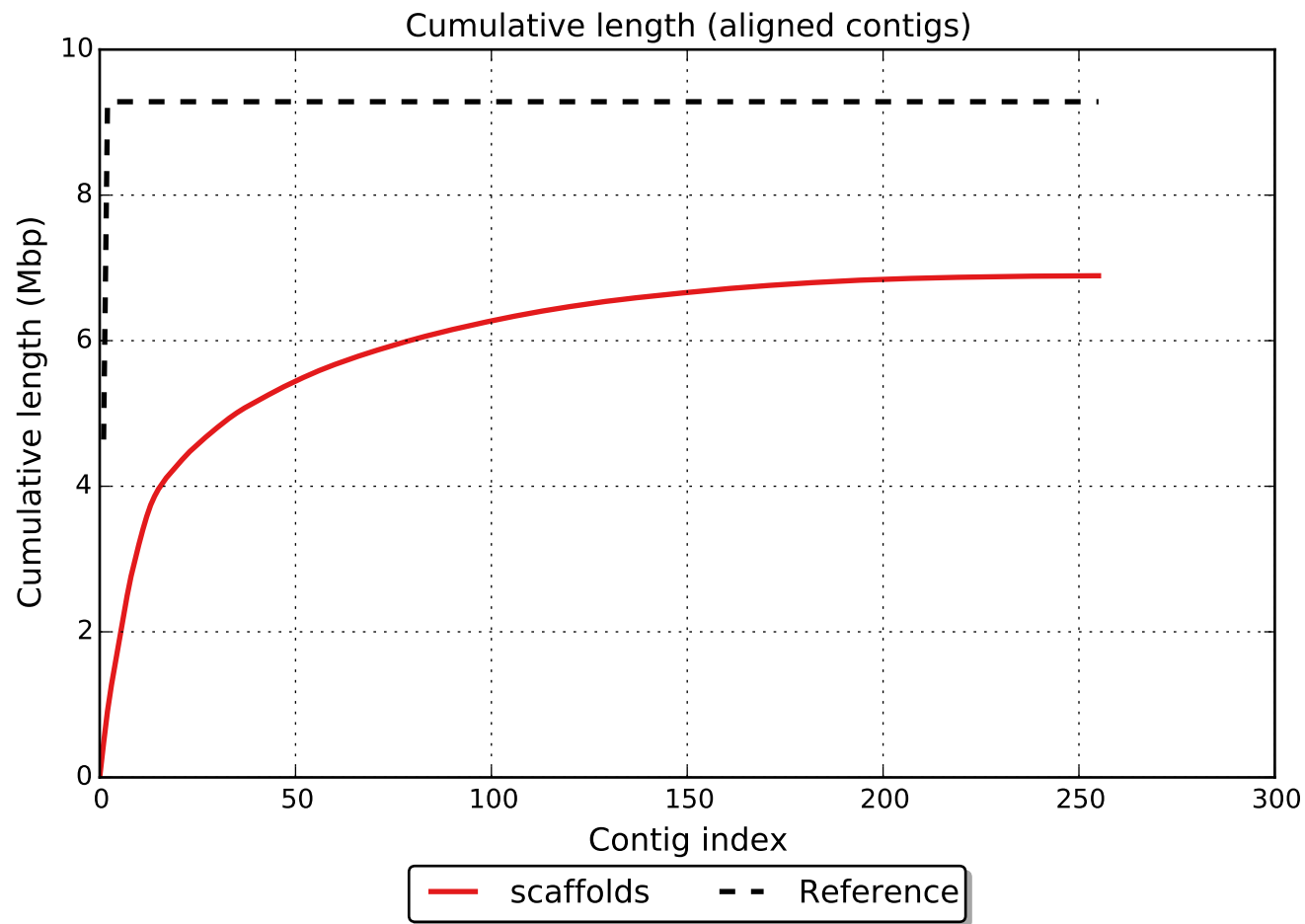
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Nx









NAx

