

## Report

	contigs
# contigs ( $\geq 0$ bp)	607
# contigs ( $\geq 1000$ bp)	230
# contigs ( $\geq 5000$ bp)	168
# contigs ( $\geq 10000$ bp)	115
# contigs ( $\geq 25000$ bp)	59
# contigs ( $\geq 50000$ bp)	31
Total length ( $\geq 0$ bp)	4724465
Total length ( $\geq 1000$ bp)	4611108
Total length ( $\geq 5000$ bp)	4437305
Total length ( $\geq 10000$ bp)	4036697
Total length ( $\geq 25000$ bp)	3222986
Total length ( $\geq 50000$ bp)	2241364
# contigs	249
Largest contig	130415
Total length	4623710
Reference length	9283304
N50	42832
N75	17945
L50	33
L75	71
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	4
# unaligned contigs	0 + 1 part
Unaligned length	55
Genome fraction (%)	85.503
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	740.13
# indels per 100 kbp	0.45
Largest alignment	122264
NA50	40251
NA75	17675
LA50	35
LA75	75

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

	contigs
# misassemblies	4
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	4
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	4
# mismatches	58748
# indels	36
# short indels	36
# long indels	0
Indels length	43

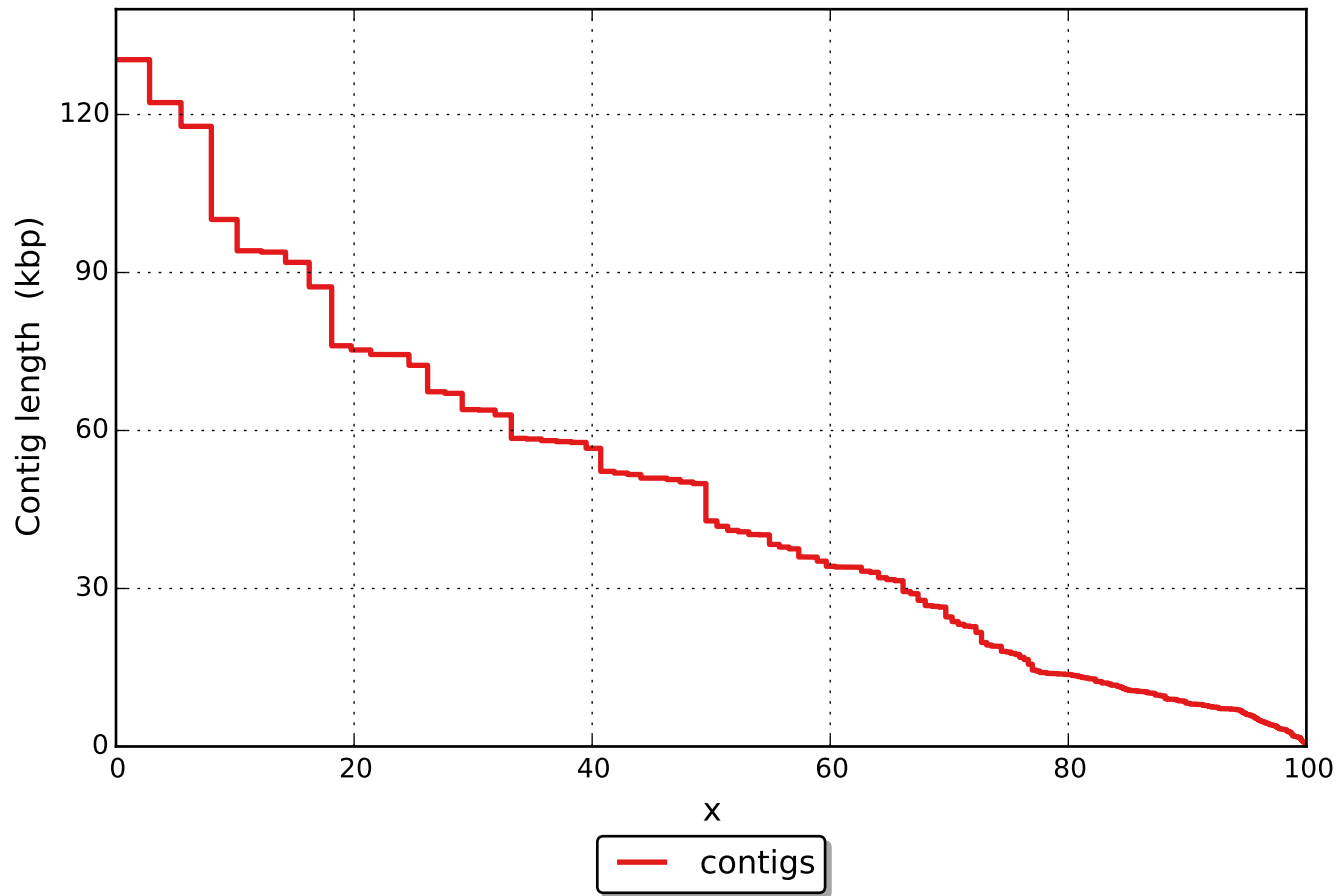
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

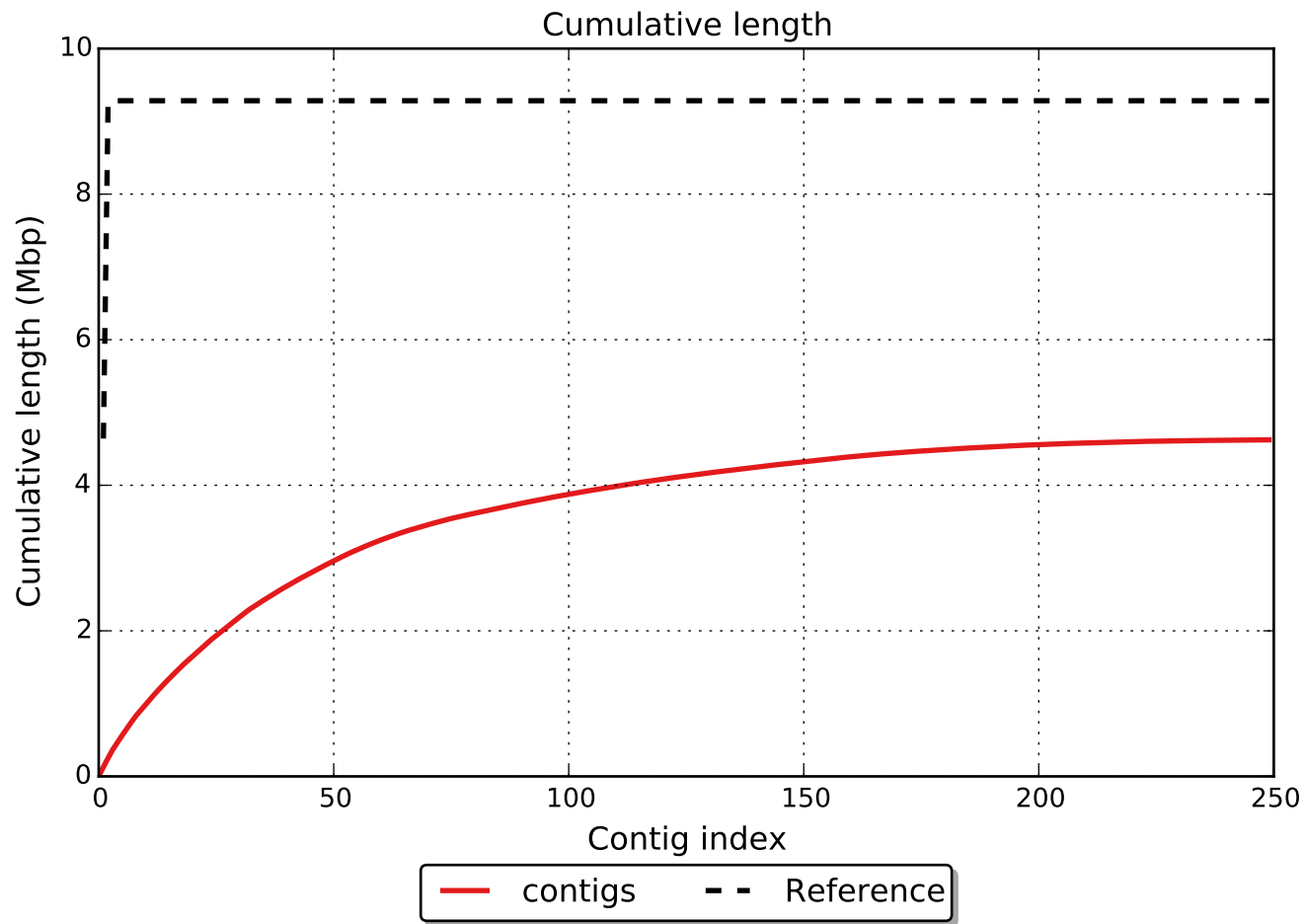
## Unaligned report

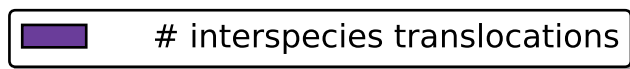
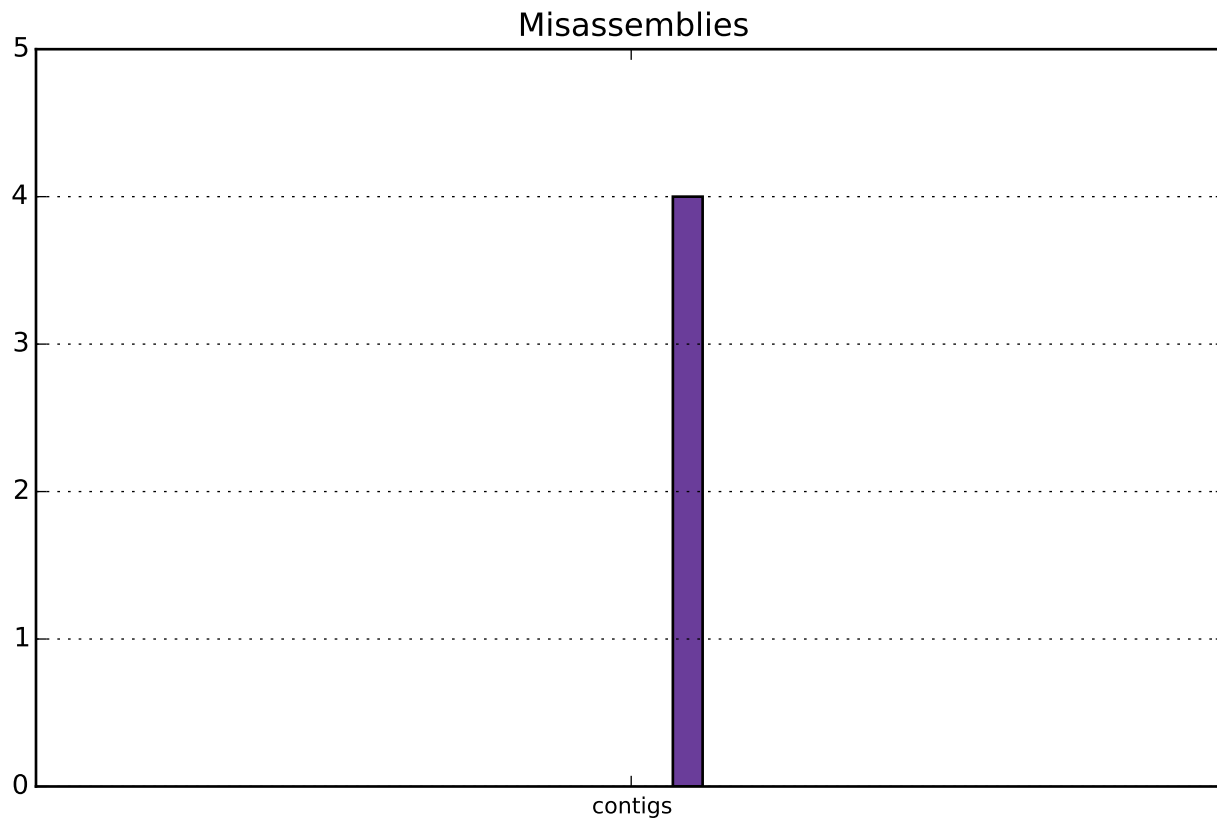
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	55
# N's	0

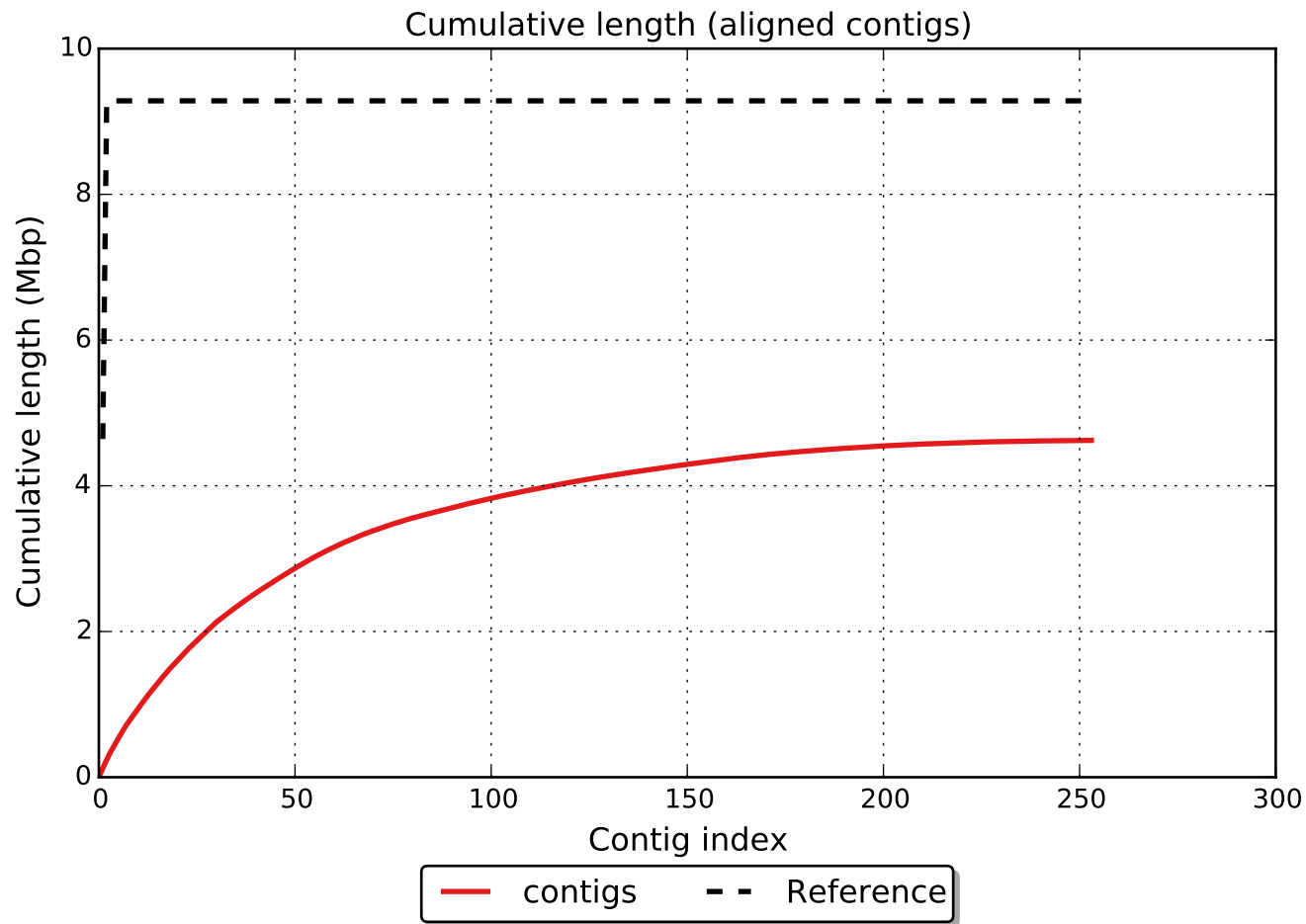
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Nx









NAx

