

# Report

	contigs
# contigs ( $\geq 0$ bp)	1019
# contigs ( $\geq 1000$ bp)	349
# contigs ( $\geq 5000$ bp)	238
# contigs ( $\geq 10000$ bp)	157
# contigs ( $\geq 25000$ bp)	54
# contigs ( $\geq 50000$ bp)	12
Total length ( $\geq 0$ bp)	4980951
Total length ( $\geq 1000$ bp)	4750539
Total length ( $\geq 5000$ bp)	4446394
Total length ( $\geq 10000$ bp)	3855251
Total length ( $\geq 25000$ bp)	2302653
Total length ( $\geq 50000$ bp)	862603
# contigs	385
Largest contig	119434
Total length	4773660
Reference length	9283304
N50	23337
N75	11845
L50	58
L75	133
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	50.375
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	829.29
# indels per 100 kbp	0.36
Largest alignment	119434
NA50	23337
NA75	11803
LA50	58
LA75	134

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

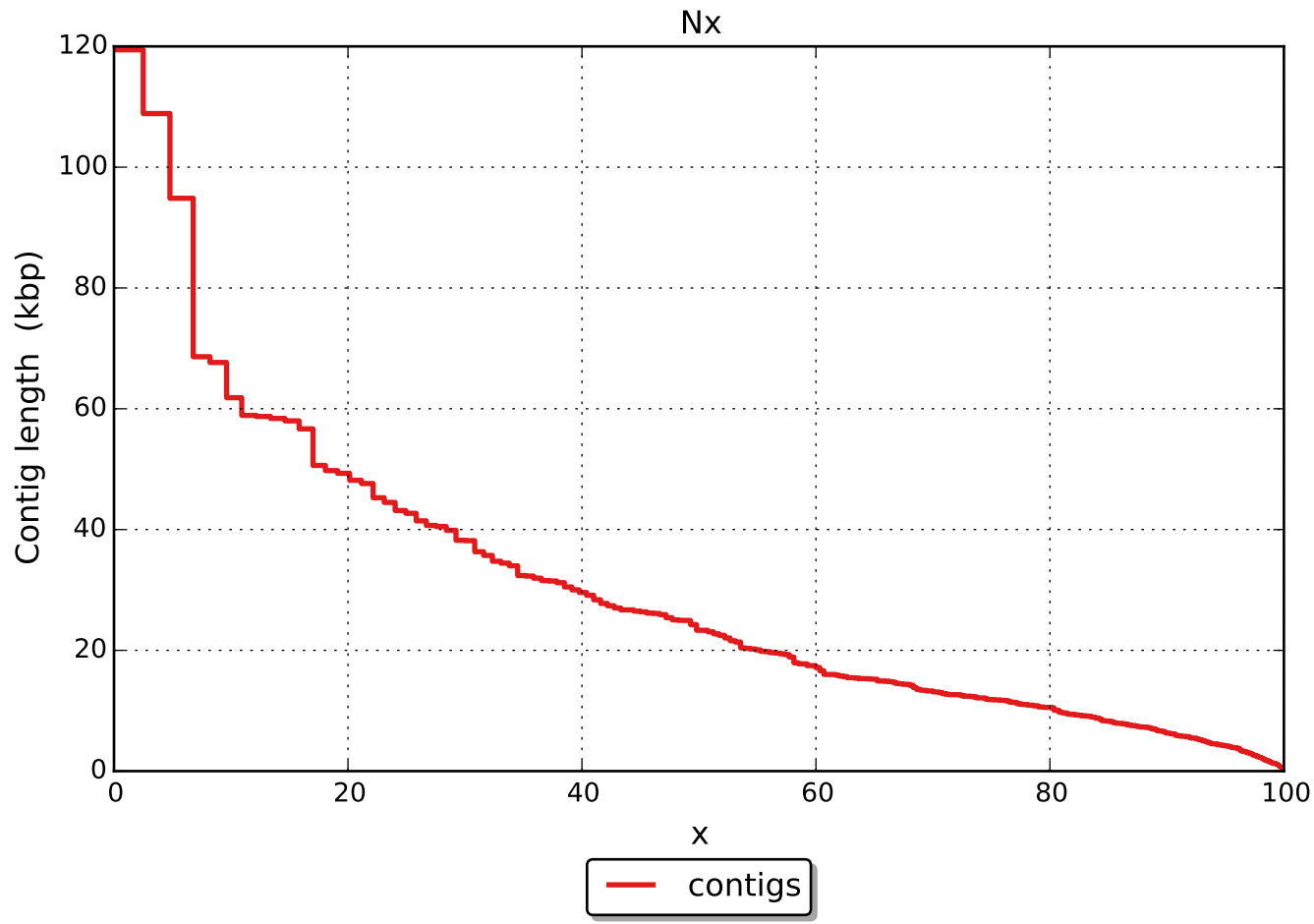
	contigs
# misassemblies	3
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	3
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	4
# mismatches	38781
# indels	17
# short indels	17
# long indels	0
Indels length	25

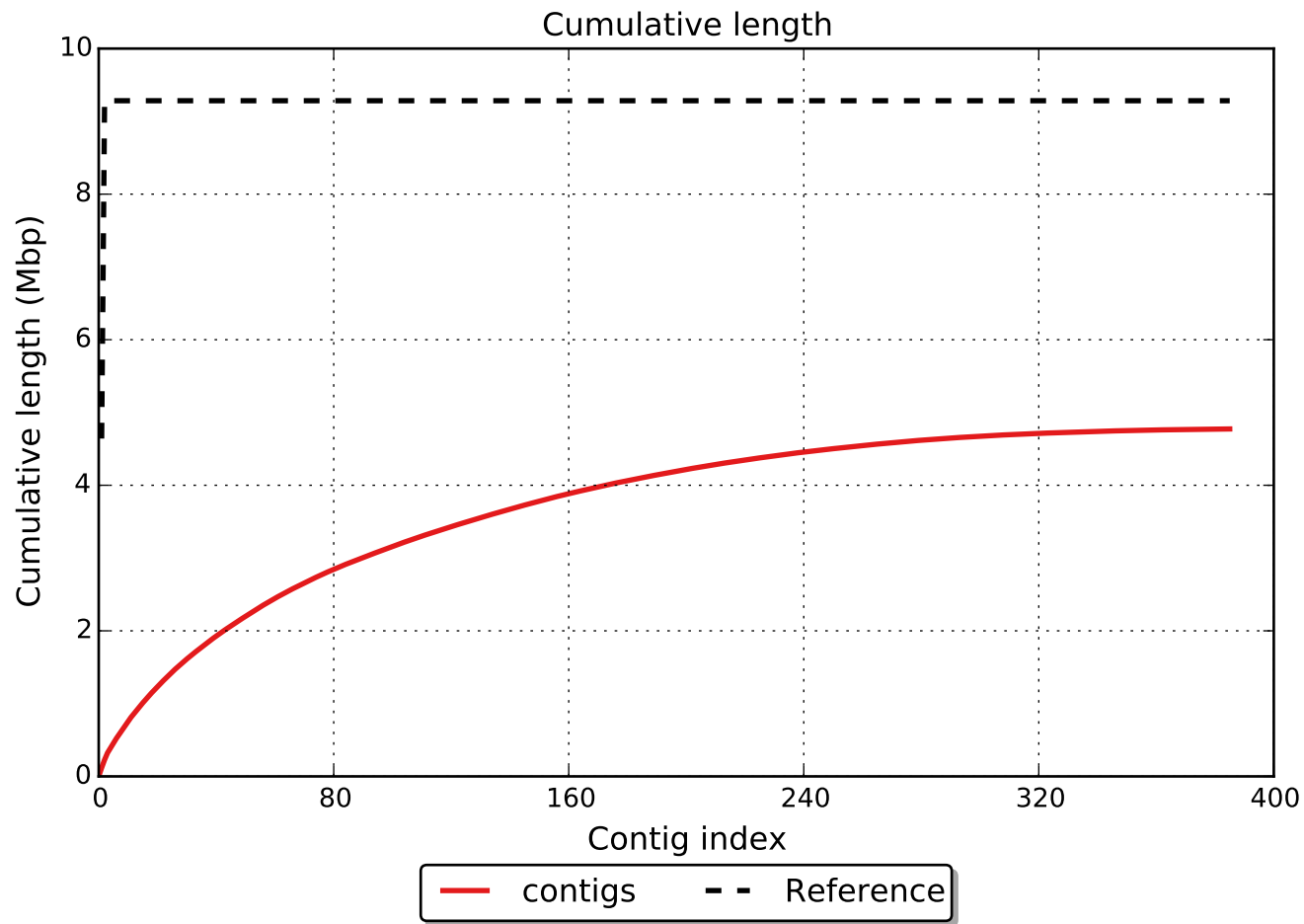
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

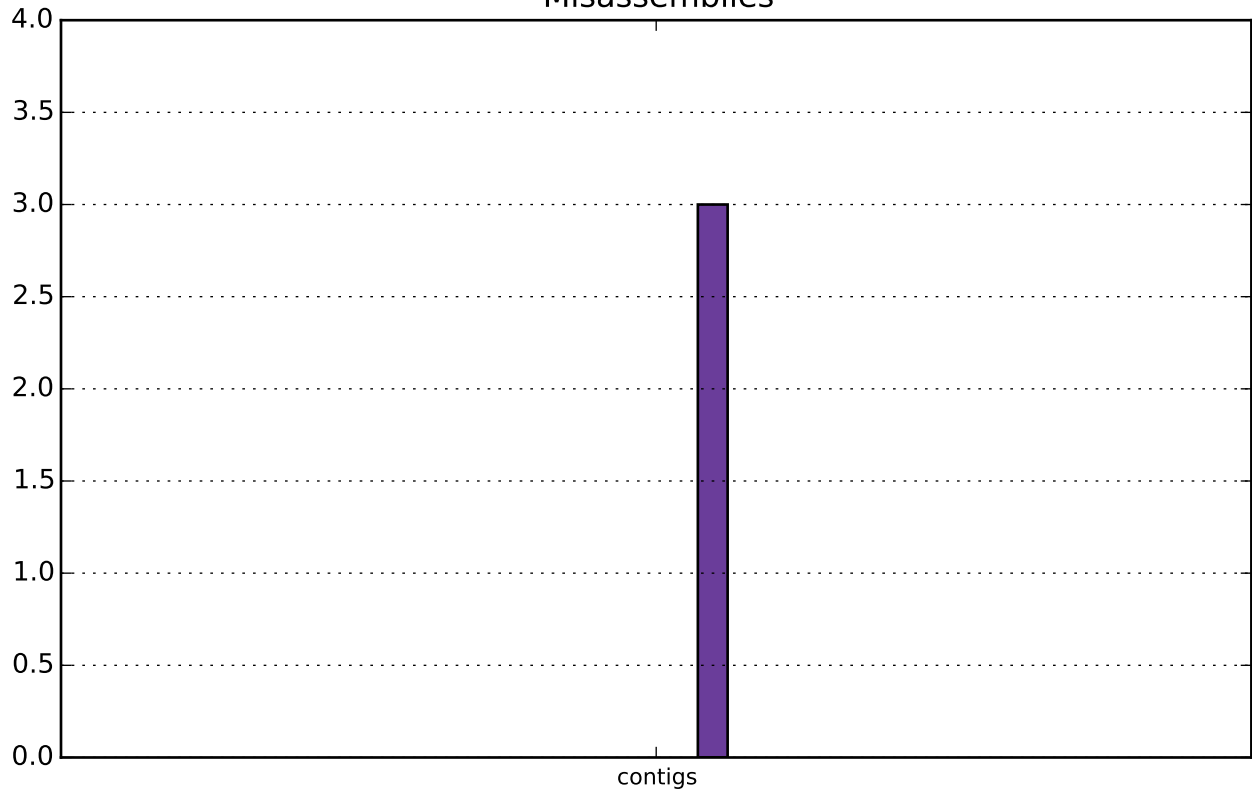
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0


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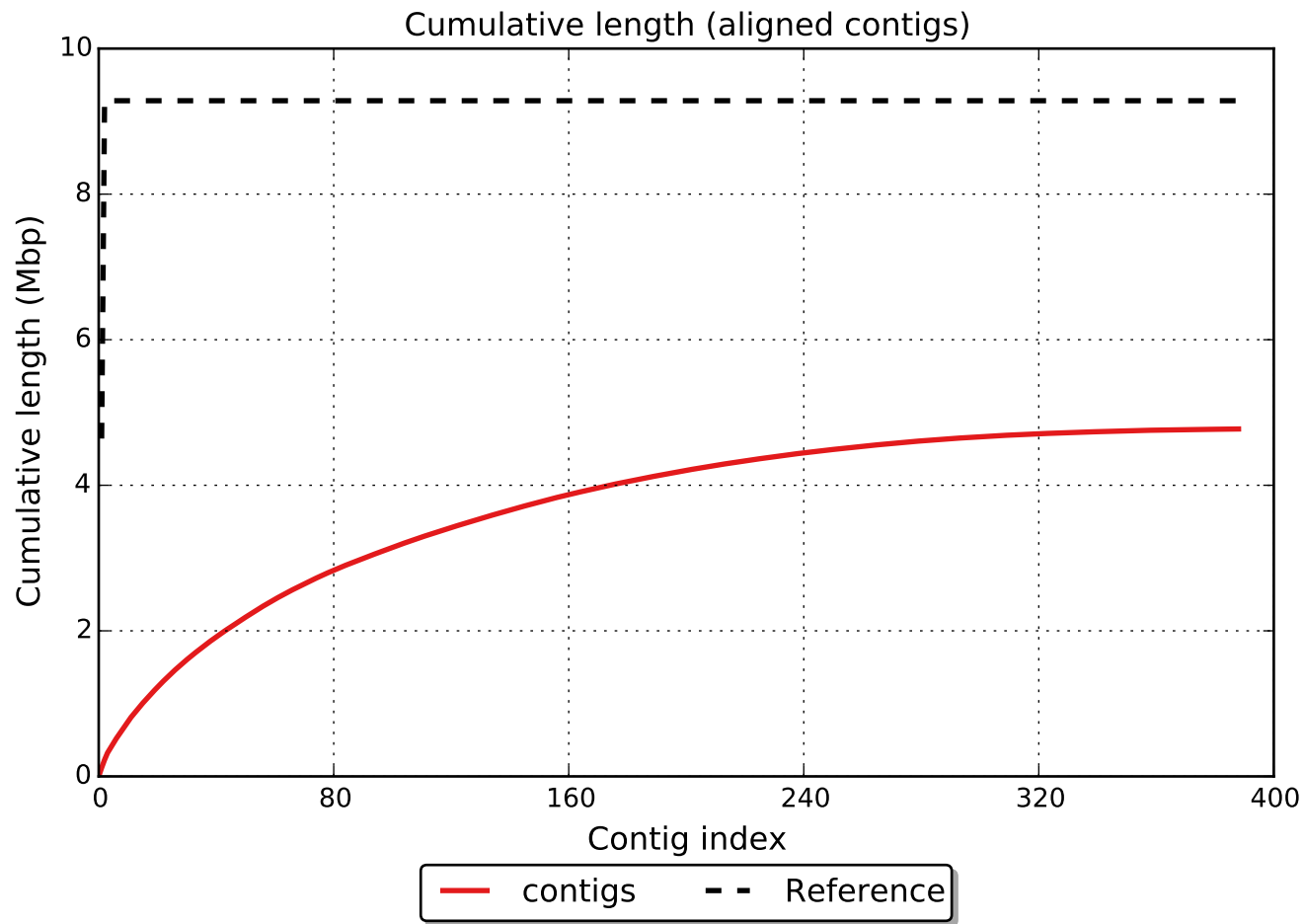




# Misassemblies



 # interspecies translocations



NAx

