

# Report

	contigs
# contigs ( $\geq 0$ bp)	144
# contigs ( $\geq 1000$ bp)	83
# contigs ( $\geq 5000$ bp)	65
# contigs ( $\geq 10000$ bp)	62
# contigs ( $\geq 25000$ bp)	55
# contigs ( $\geq 50000$ bp)	42
Total length ( $\geq 0$ bp)	9167402
Total length ( $\geq 1000$ bp)	9143132
Total length ( $\geq 5000$ bp)	9102454
Total length ( $\geq 10000$ bp)	9078759
Total length ( $\geq 25000$ bp)	8957685
Total length ( $\geq 50000$ bp)	8511042
# contigs	102
Largest contig	1053360
Total length	9156263
Reference length	9283304
N50	224139
N75	132462
L50	11
L75	24
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36005
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.604
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	147.37
# indels per 100 kbp	0.55
Largest alignment	1053360
NA50	224139
NA75	132462
LA50	11
LA75	24

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36005
# local misassemblies	2
# mismatches	13490
# indels	50
# short indels	49
# long indels	1
Indels length	69

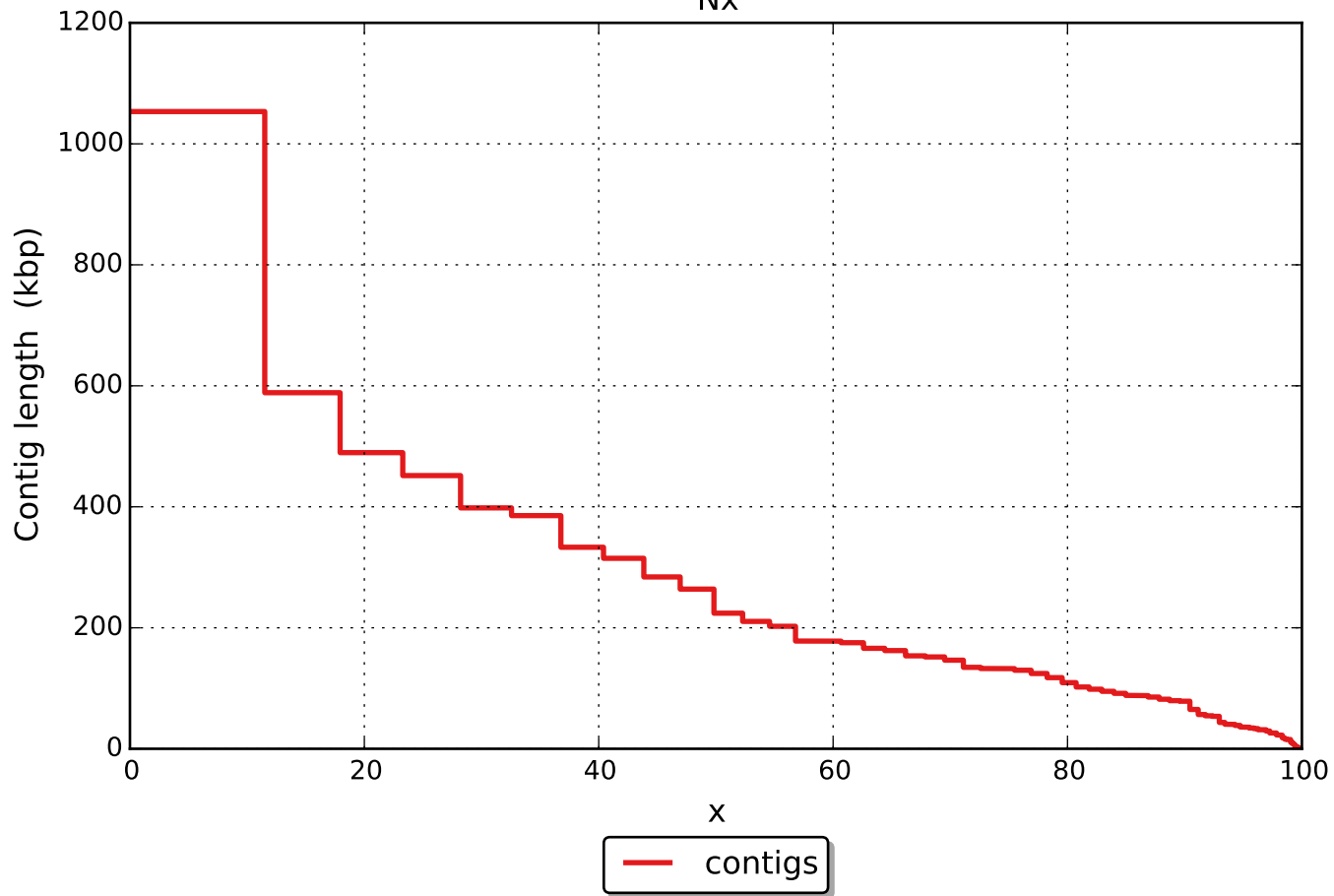
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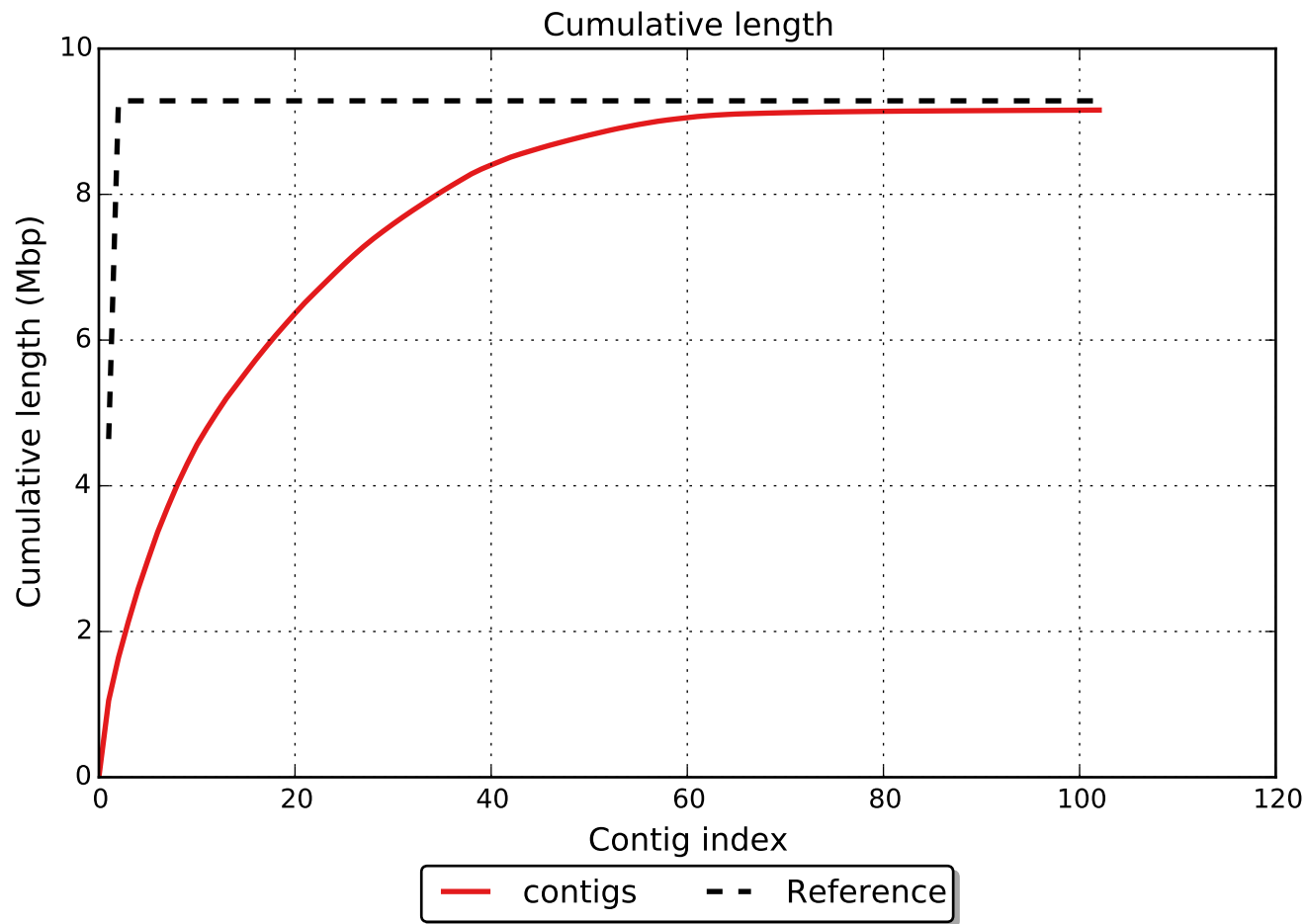
## Unaligned report

	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

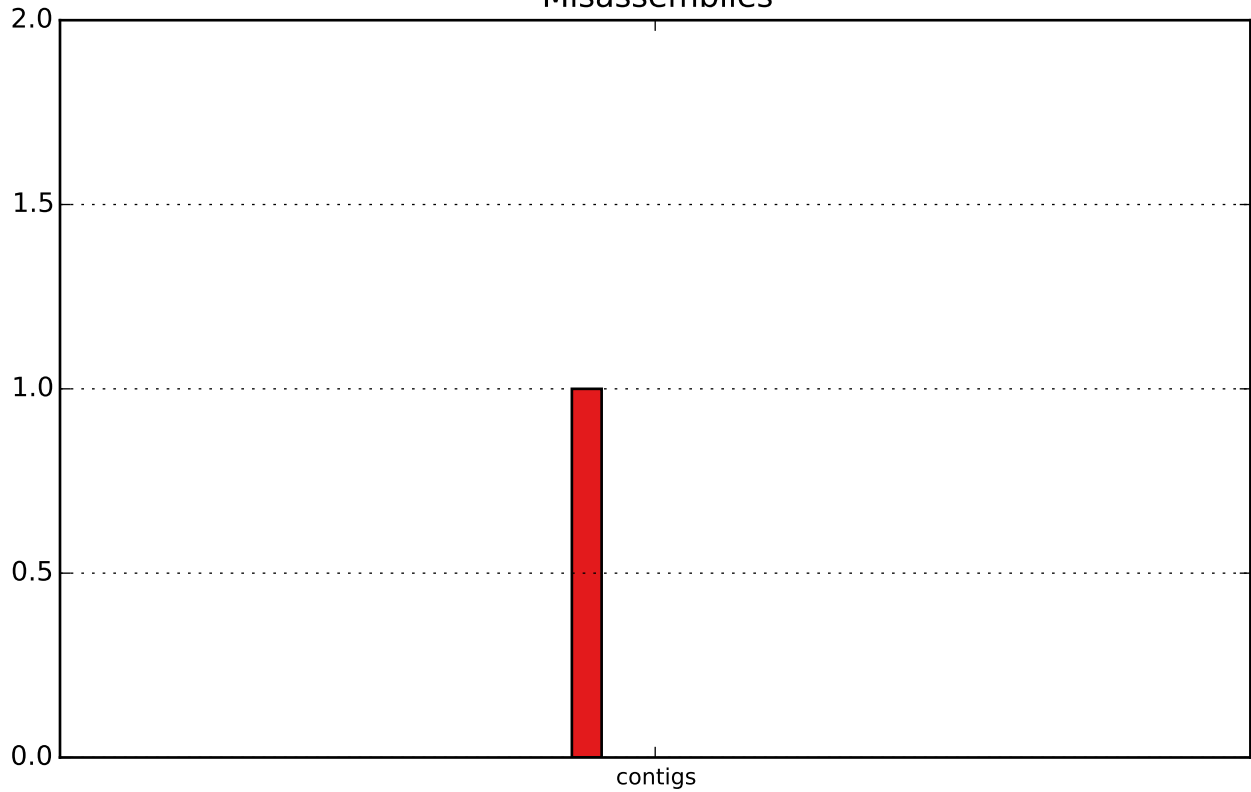
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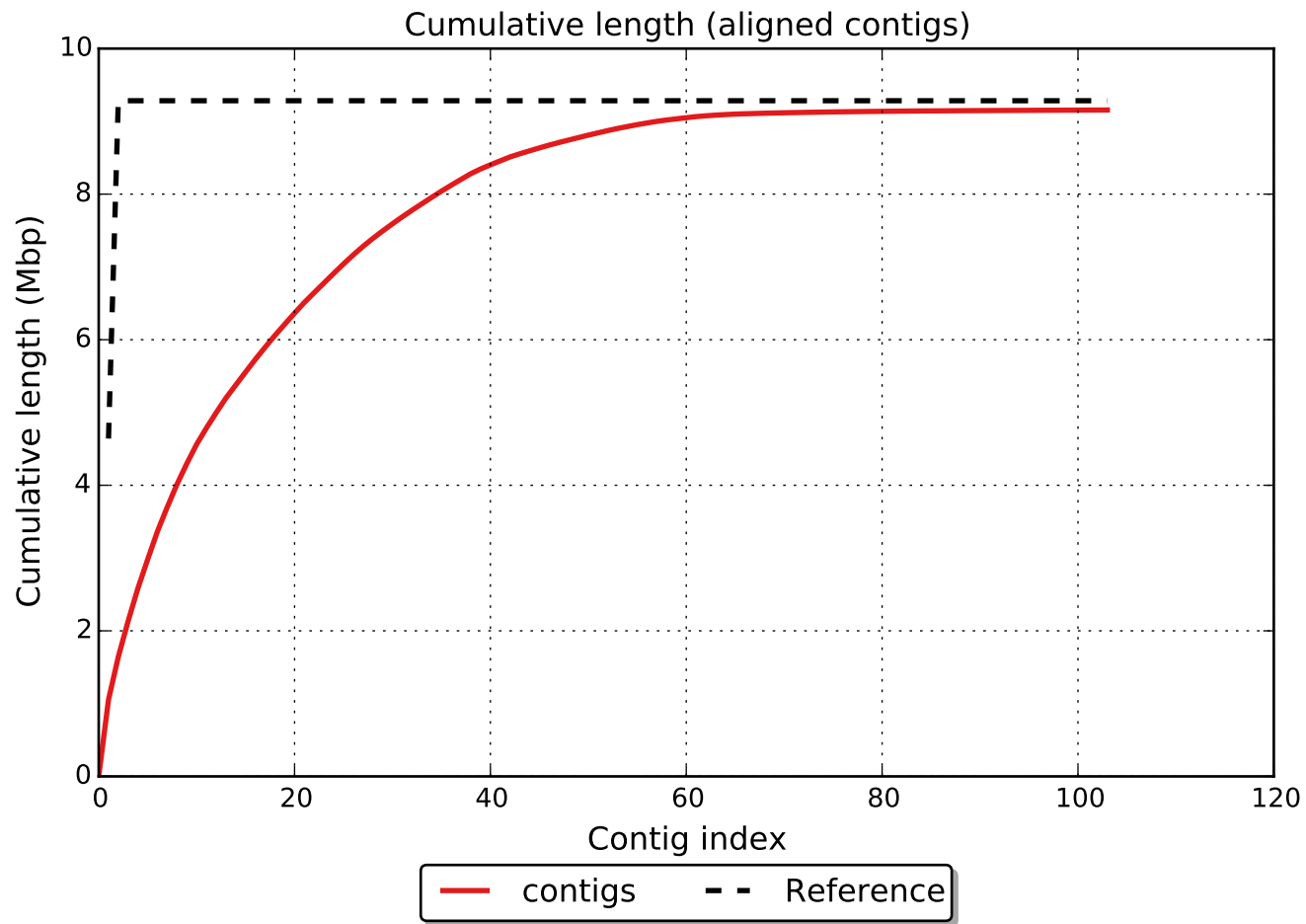
Nx





# Misassemblies





NAx

