

## Report

	contigs
# contigs ( $\geq 0$ bp)	188
# contigs ( $\geq 1000$ bp)	98
# 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)	9139063
Total length ( $\geq 1000$ bp)	9100406
Total length ( $\geq 5000$ bp)	9063769
Total length ( $\geq 10000$ bp)	9033557
Total length ( $\geq 25000$ bp)	8929398
Total length ( $\geq 50000$ bp)	8253512
# contigs	127
Largest contig	472565
Total length	9121224
Reference length	9283304
N50	208897
N75	108452
L50	15
L75	30
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	405365
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.736
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	492.44
# indels per 100 kbp	1.15
Largest alignment	472565
NA50	203339
NA75	99313
LA50	16
LA75	31

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	405365
# local misassemblies	3
# mismatches	45137
# indels	105
# short indels	100
# long indels	5
Indels length	188

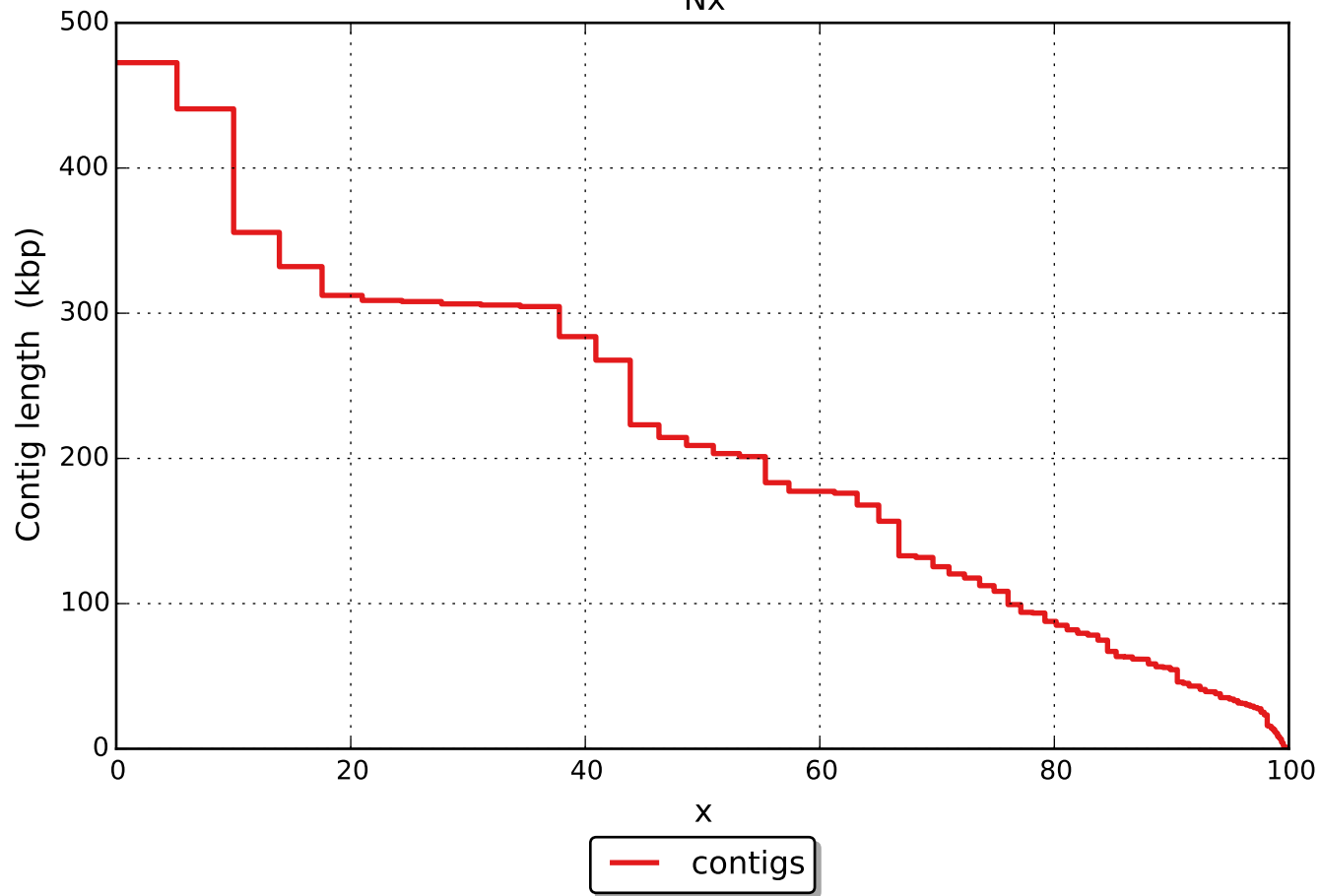
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

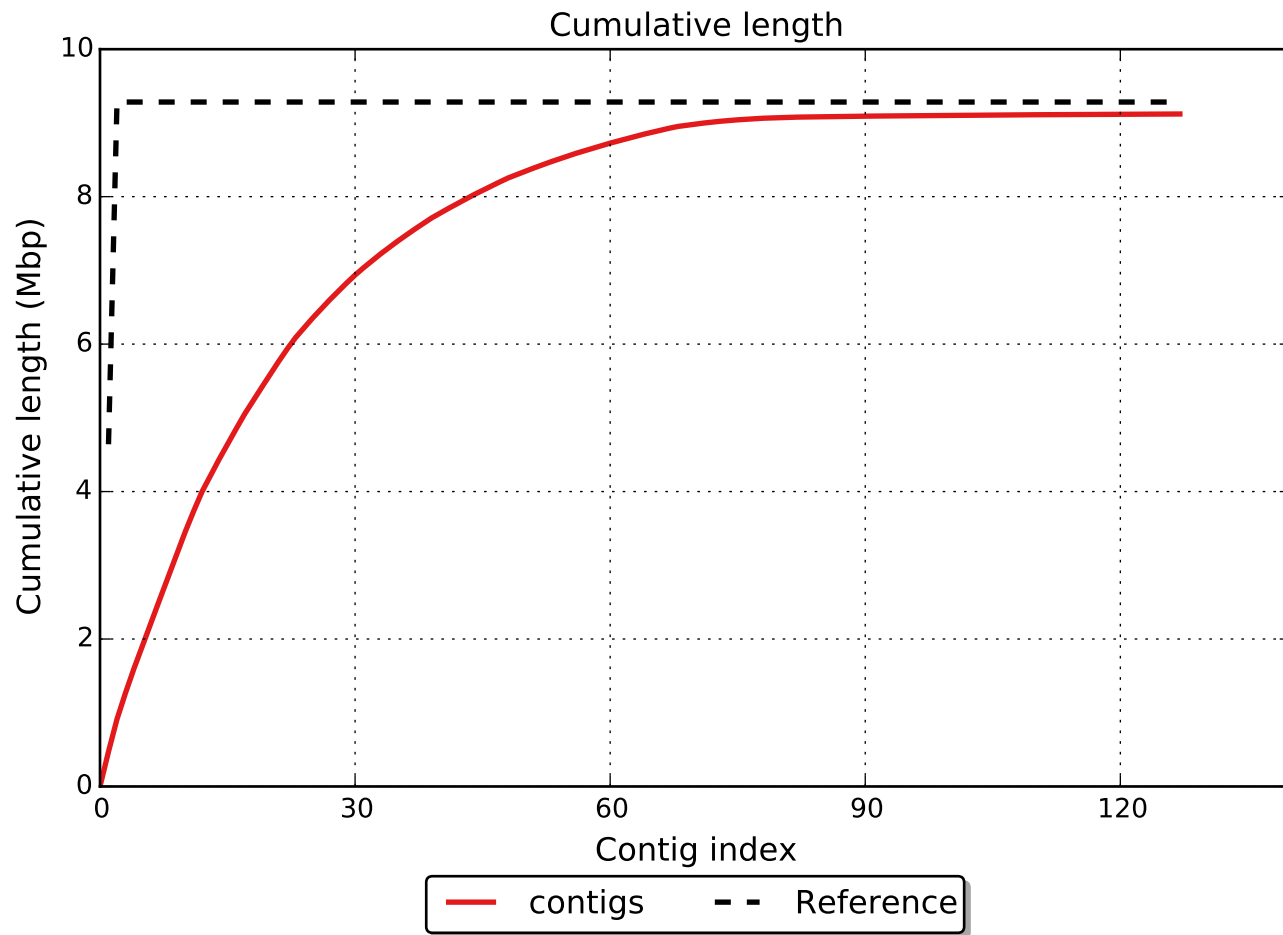
## Unaligned report

	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

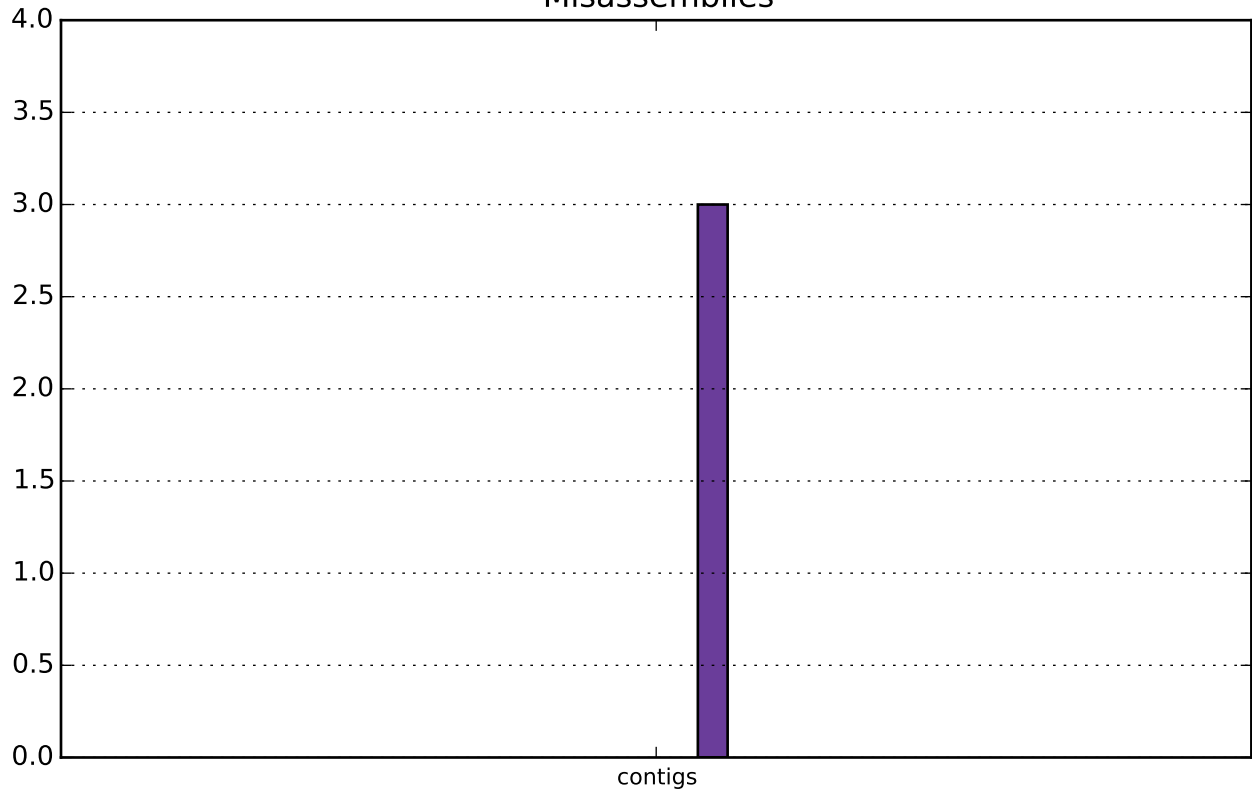
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

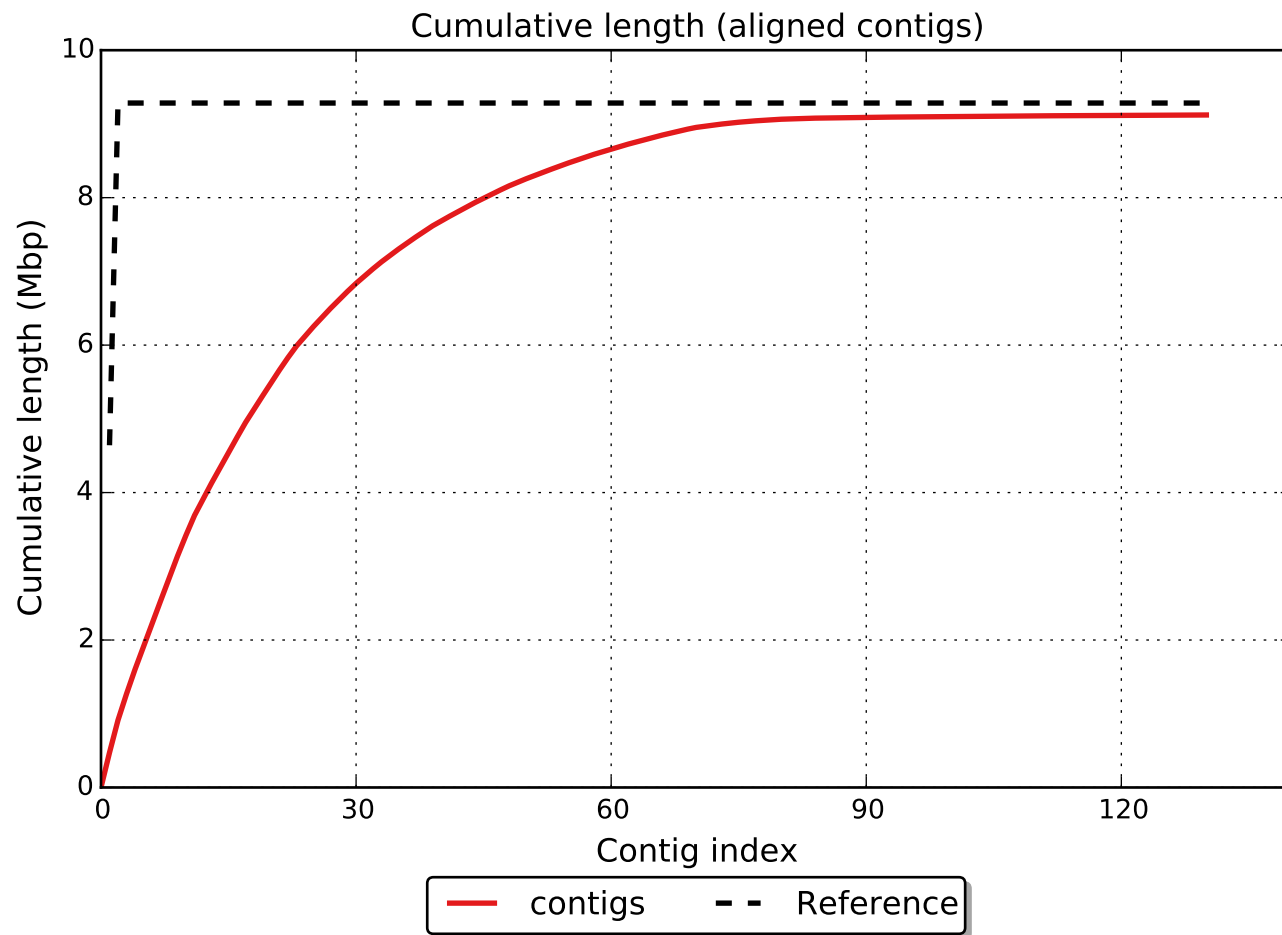




# Misassemblies



 # interspecies translocations



NAx

