

## Report

	contigs
# contigs ( $\geq 0$ bp)	603
# contigs ( $\geq 1000$ bp)	10
# contigs ( $\geq 5000$ bp)	1
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	183567
Total length ( $\geq 1000$ bp)	19018
Total length ( $\geq 5000$ bp)	5665
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	20
Largest contig	5665
Total length	25093
Reference length	4641652
GC (%)	52.25
Reference GC (%)	50.79
N50	1496
N75	1031
L50	5
L75	10
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	8595
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	164
Genome fraction (%)	0.537
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1143.48
# indels per 100 kbp	20.06
Largest alignment	5541
NA50	1394
NGA50	-
NA75	940
LA50	5
LA75	11

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	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	8595
# local misassemblies	0
# mismatches	285
# indels	5
# short indels	5
# long indels	0
Indels length	5

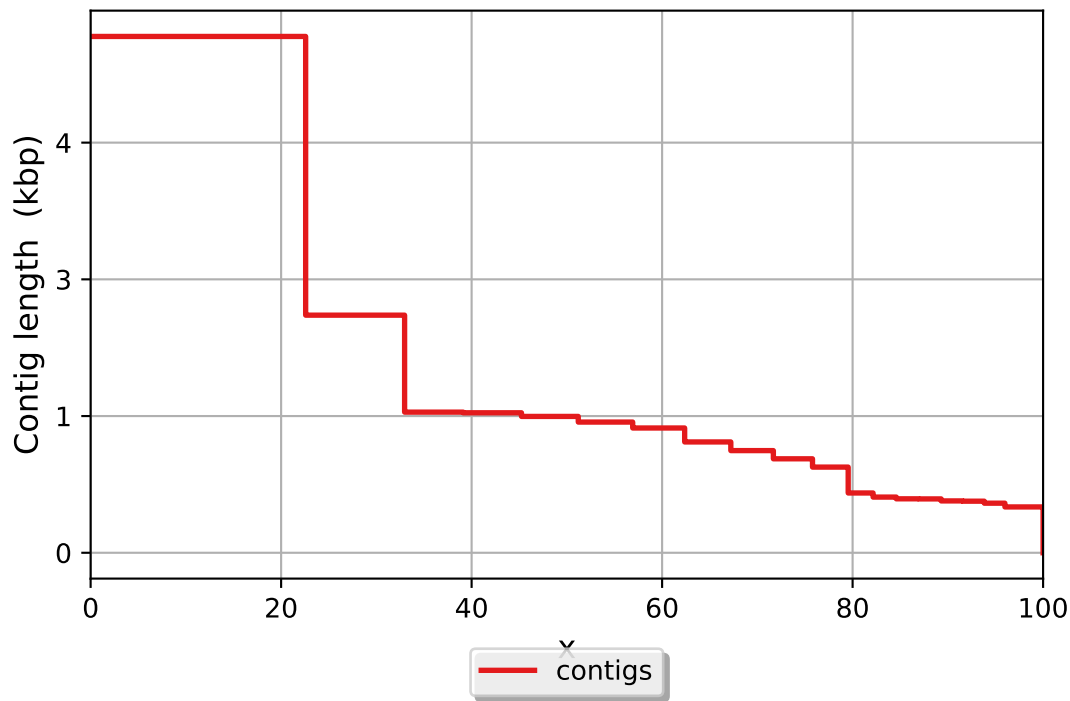
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

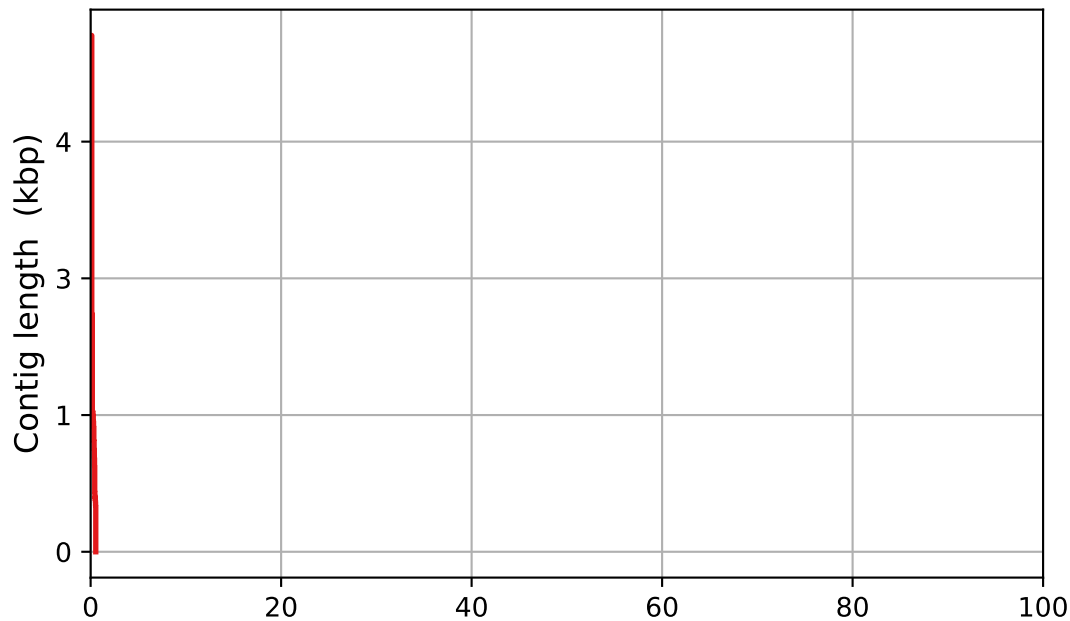
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	164
# N's	0

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).

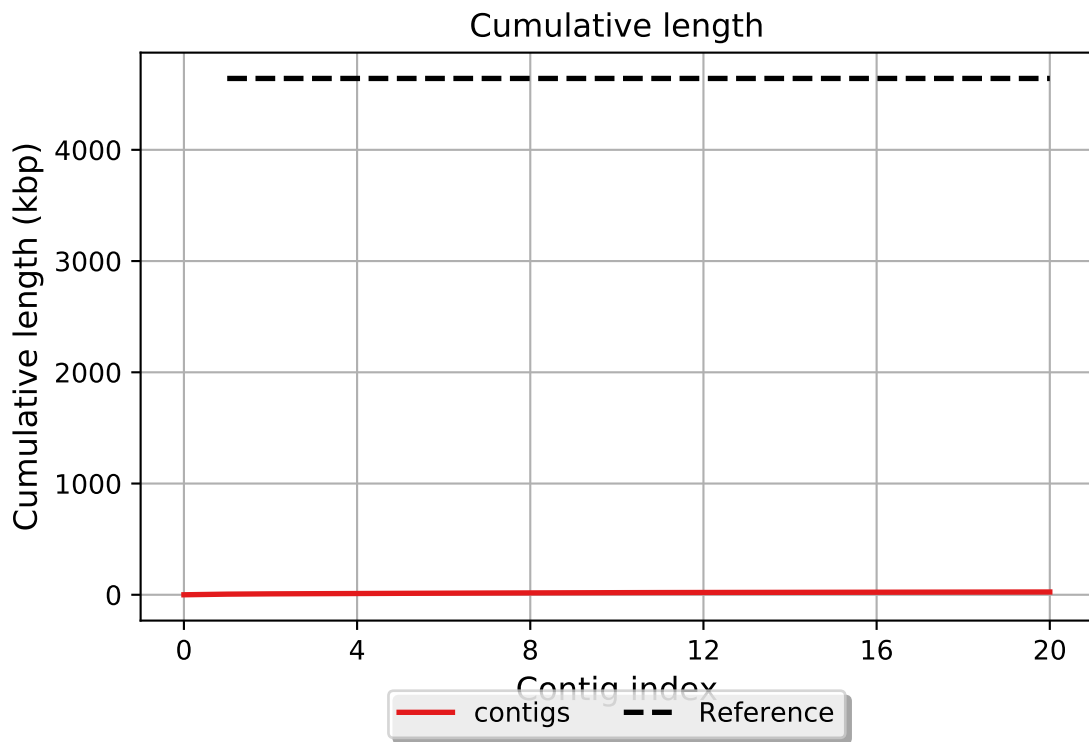
Nx

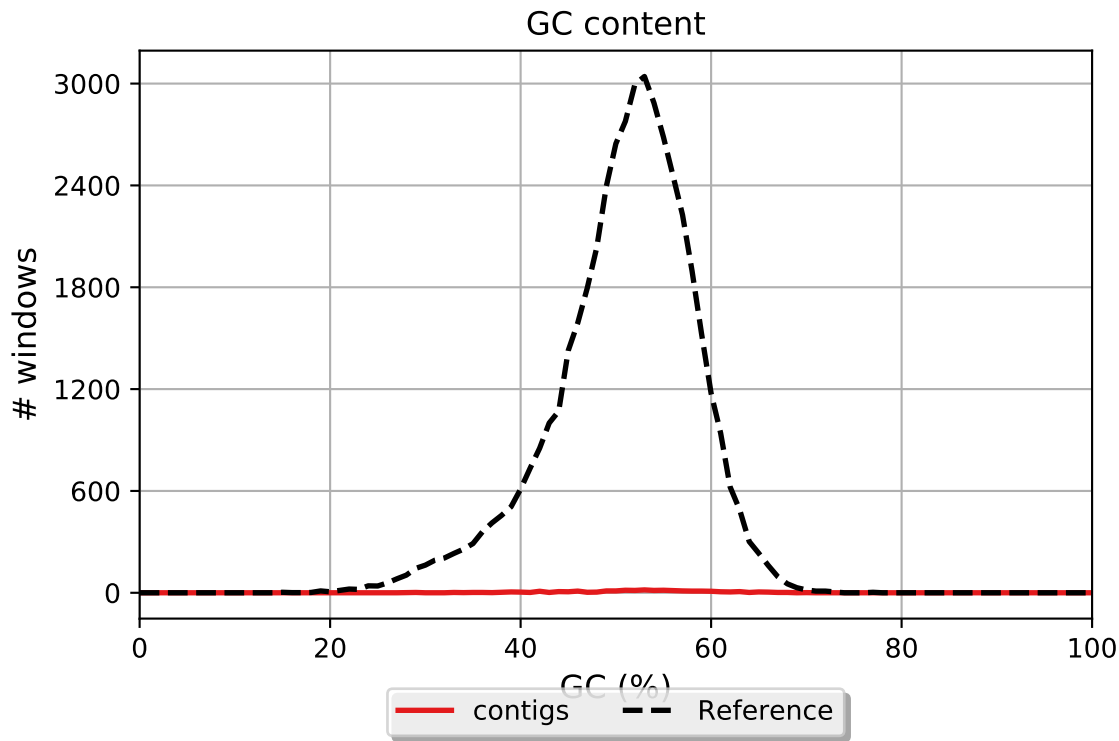


NGx

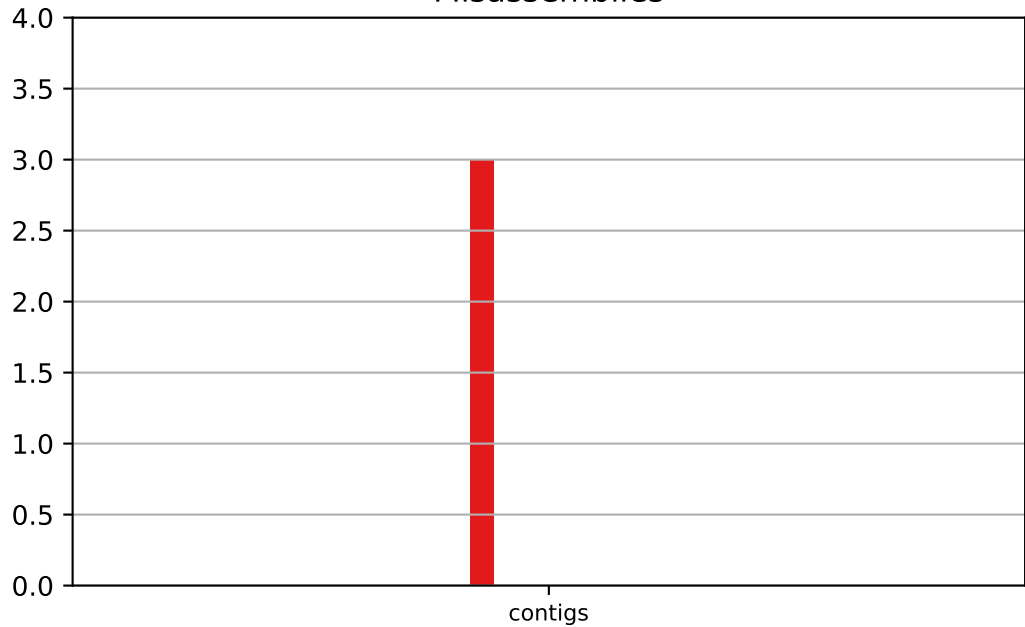


x  
contigs



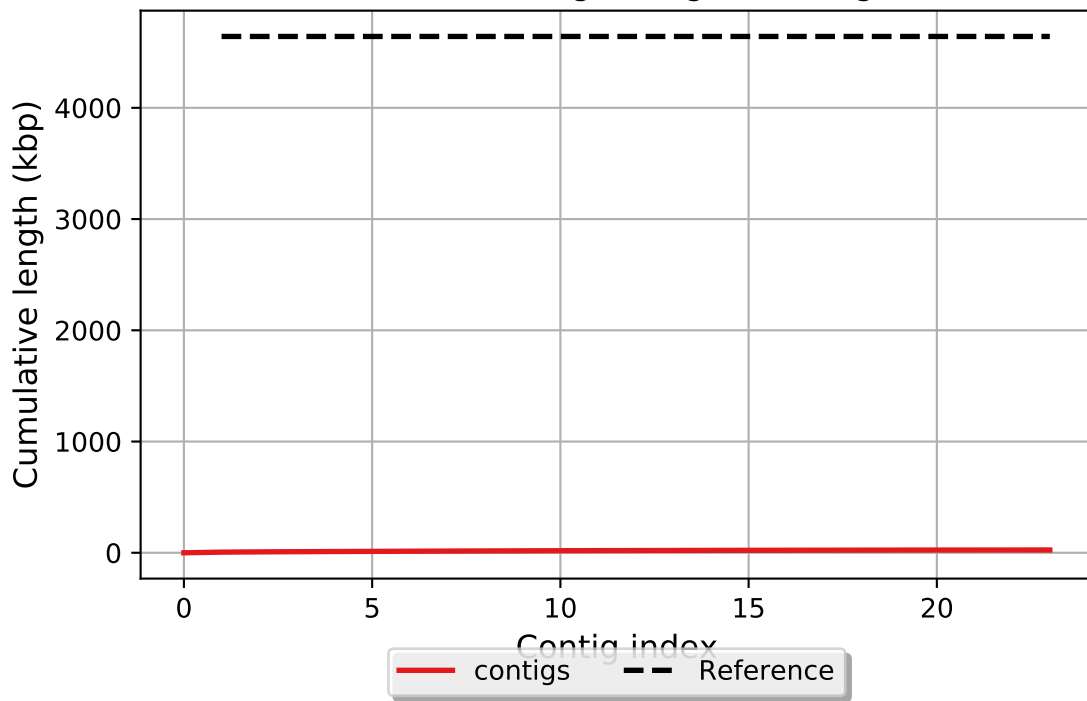


## Misassemblies

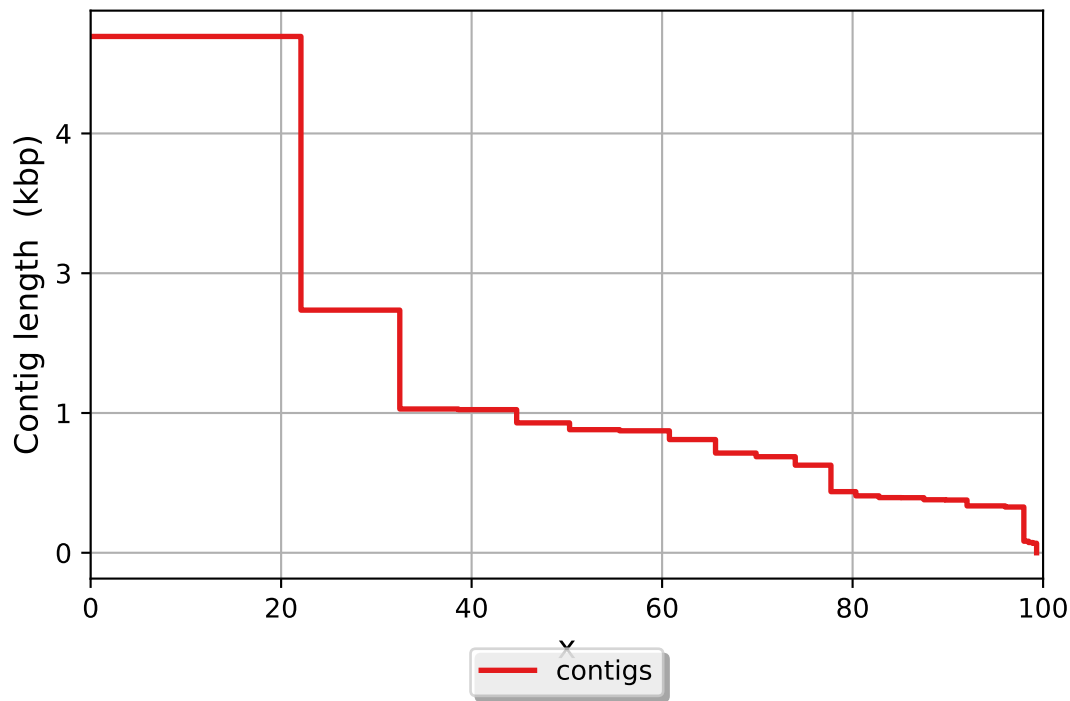




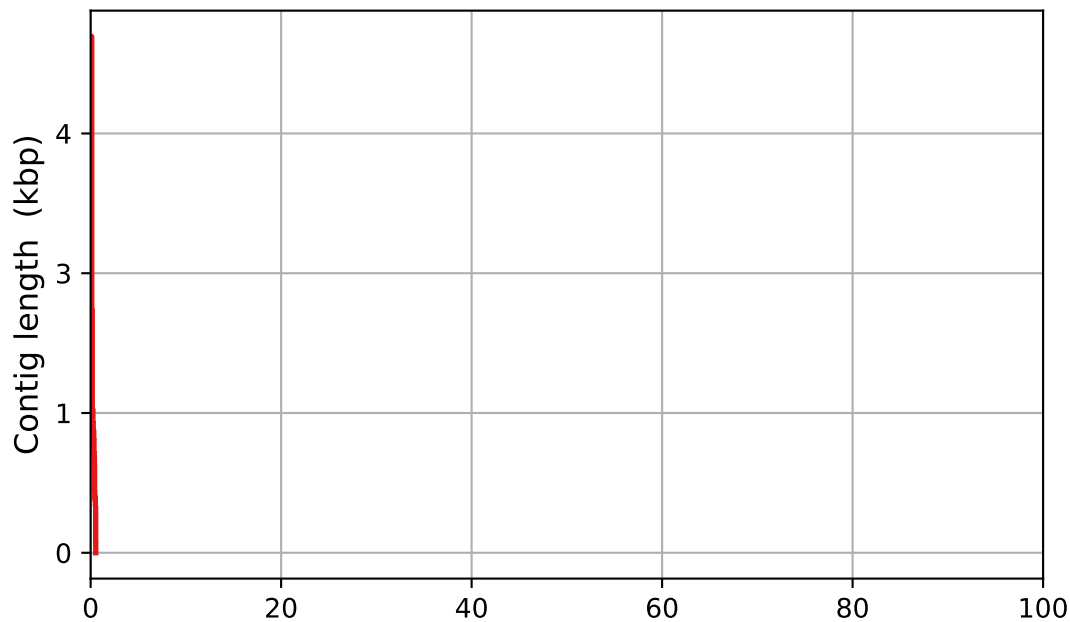
Cumulative length (aligned contigs)



NAx



NGAx



x  
contigs