

## Report

	contigs
# contigs ( $\geq 0$ bp)	6199
# contigs ( $\geq 1000$ bp)	312
# 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)	3040535
Total length ( $\geq 1000$ bp)	410767
Total length ( $\geq 5000$ bp)	6365
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	2136
Largest contig	6365
Total length	1647157
Reference length	4641652
GC (%)	50.70
Reference GC (%)	50.79
N50	765
N75	614
L50	791
L75	1393
# misassemblies	34
# misassembled contigs	34
Misassembled contigs length	49585
# local misassemblies	1
# unaligned contigs	5 + 11 part
Unaligned length	5103
Genome fraction (%)	35.258
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1443.09
# indels per 100 kbp	1.41
Largest alignment	6022
NA50	759
NGA50	-
NA75	607
LA50	804
LA75	1412

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	34
# relocations	34
# translocations	0
# inversions	0
# misassembled contigs	34
Misassembled contigs length	49585
# local misassemblies	1
# mismatches	23617
# indels	23
# short indels	22
# long indels	1
Indels length	29

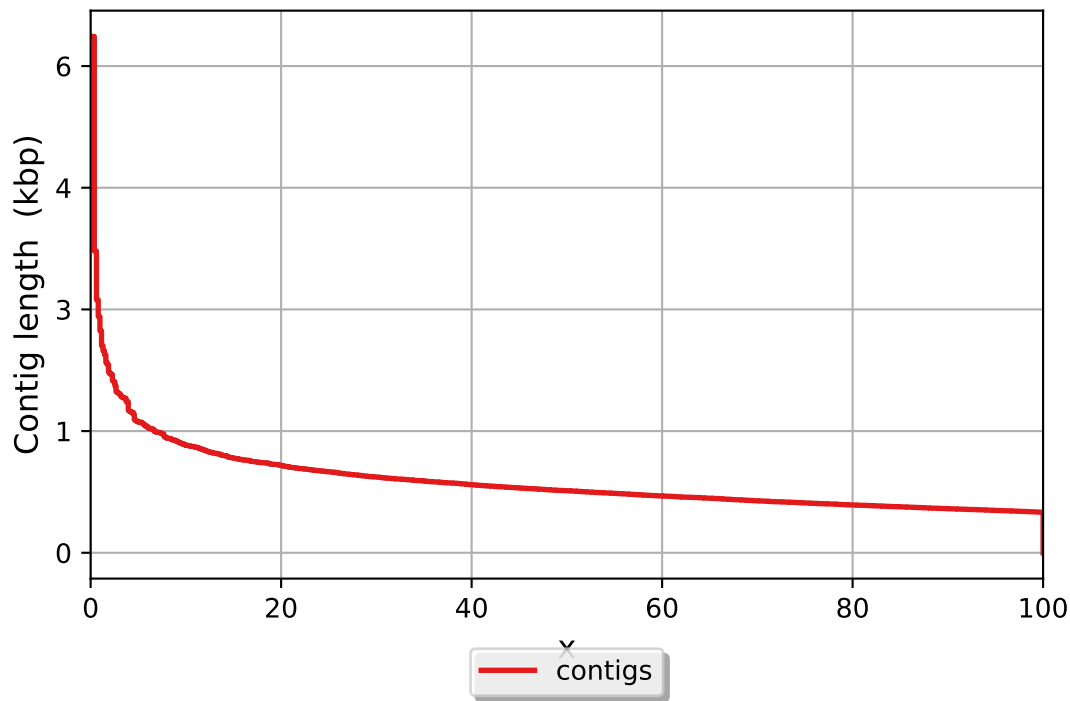
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

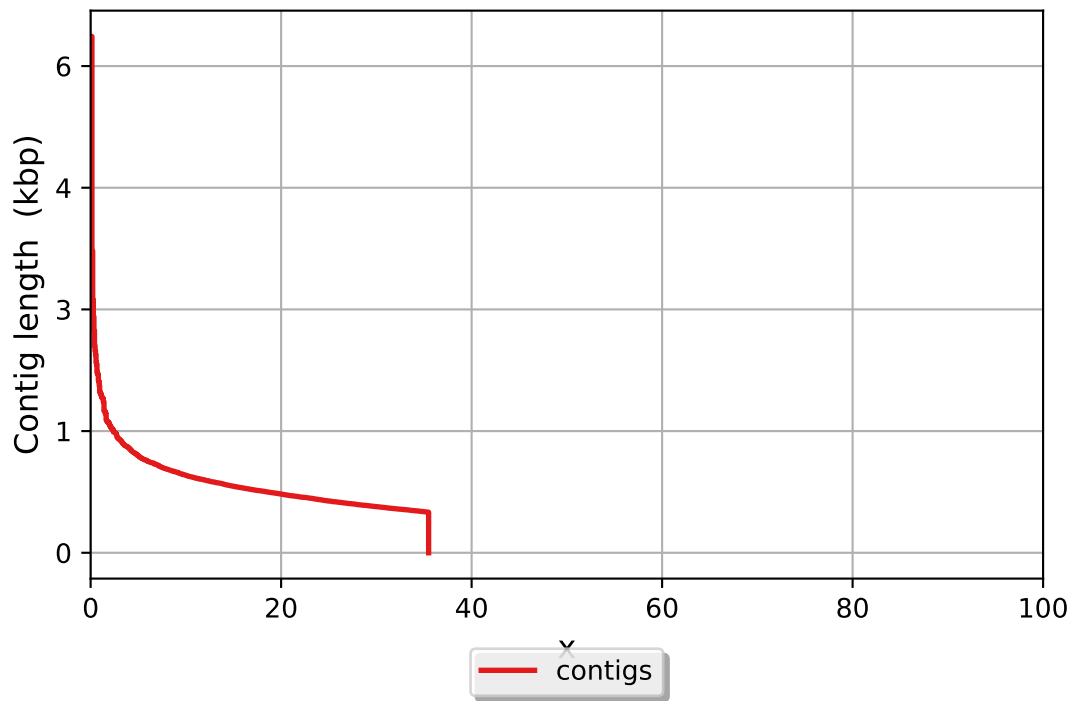
	contigs
# fully unaligned contigs	5
Fully unaligned length	3769
# partially unaligned contigs	11
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1334
# N's	0

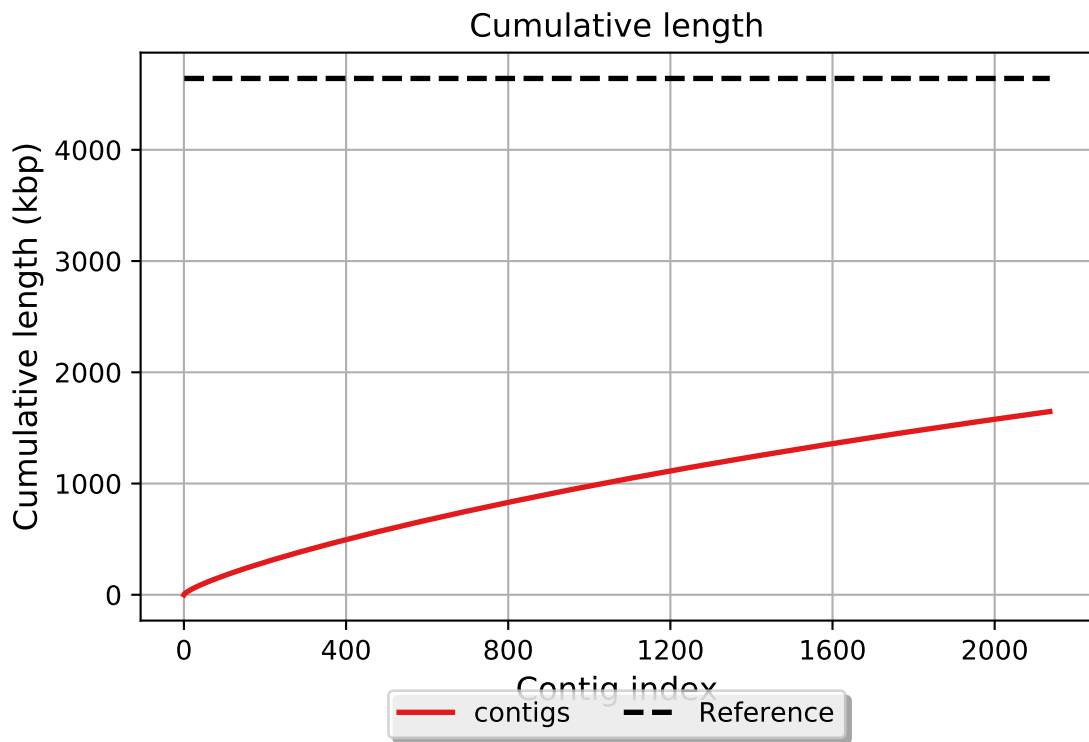
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

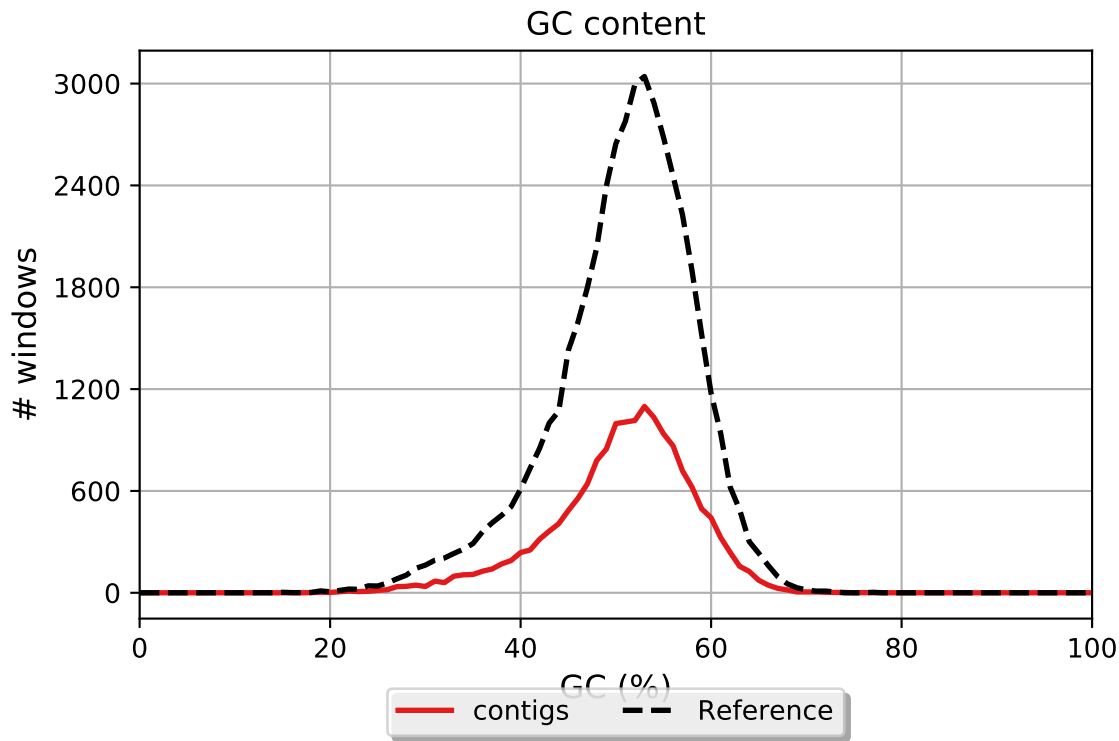
Nx



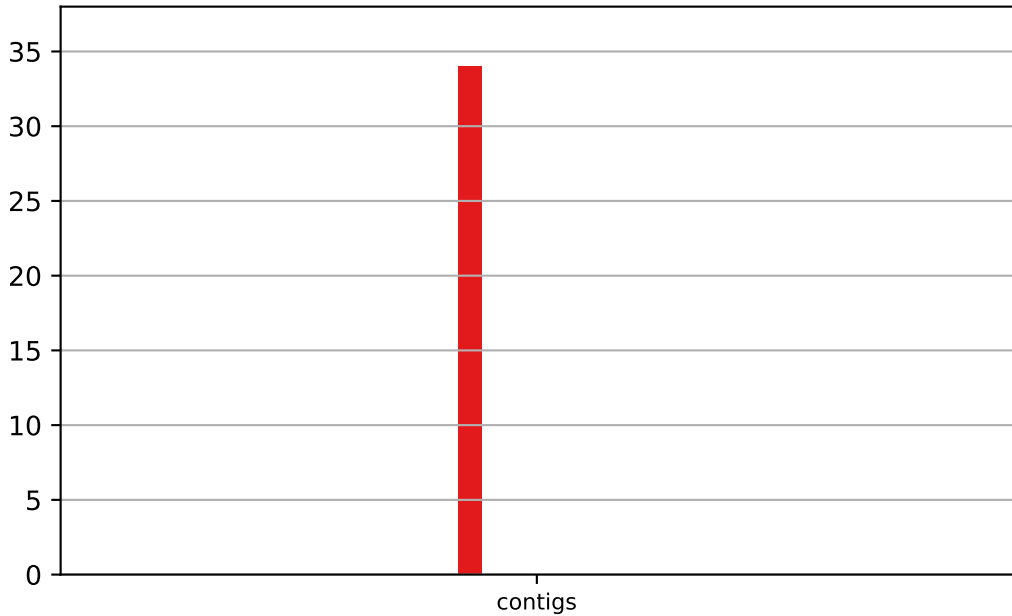
NGx





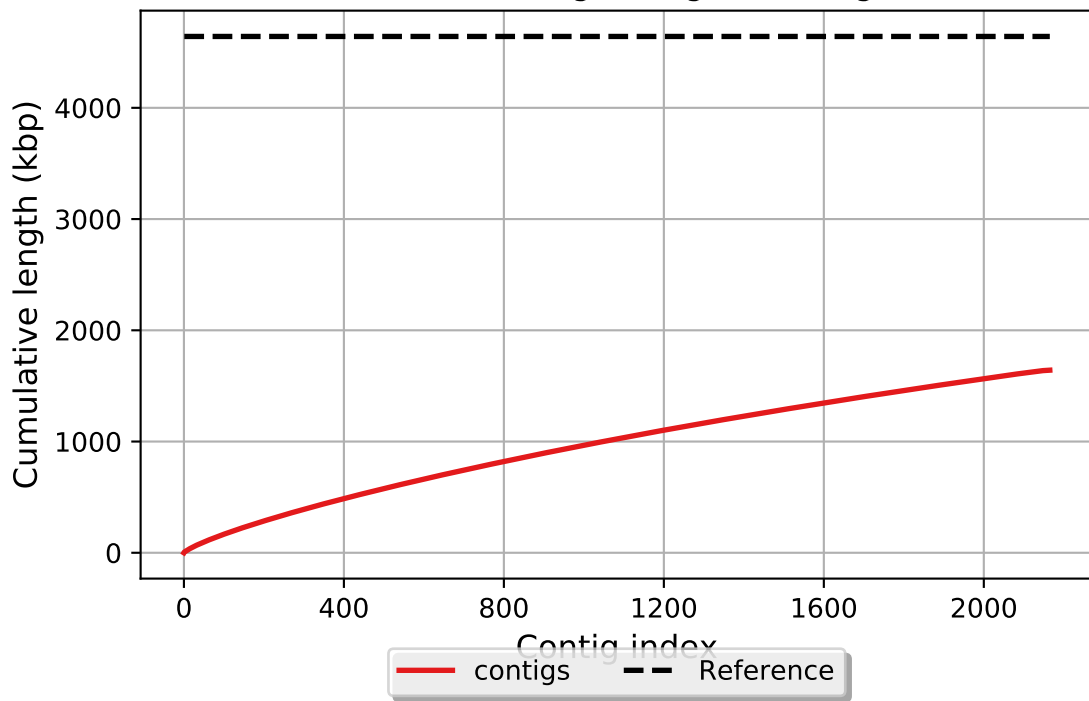


## Misassemblies

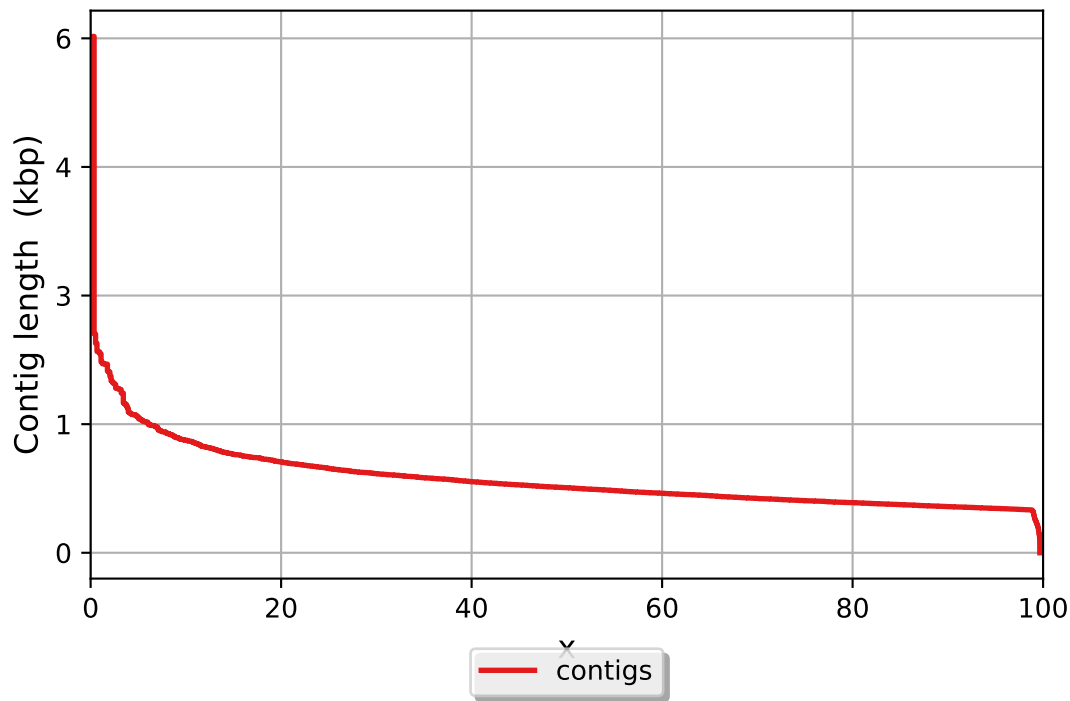




Cumulative length (aligned contigs)



NAx



NGAx

