

## Report

	contigs
# contigs ( $\geq 0$ bp)	148
# contigs ( $\geq 1000$ bp)	75
# contigs ( $\geq 5000$ bp)	55
# contigs ( $\geq 10000$ bp)	51
# contigs ( $\geq 25000$ bp)	43
# contigs ( $\geq 50000$ bp)	28
Total length ( $\geq 0$ bp)	4575286
Total length ( $\geq 1000$ bp)	4554617
Total length ( $\geq 5000$ bp)	4512097
Total length ( $\geq 10000$ bp)	4482438
Total length ( $\geq 25000$ bp)	4364074
Total length ( $\geq 50000$ bp)	3818200
# contigs	86
Largest contig	327173
Total length	4562029
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133038
NG50	133036
N75	78649
NG75	67374
L50	11
LG50	12
L75	22
LG75	23
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.258
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.68
# indels per 100 kbp	0.09
Largest alignment	327173
NA50	133038
NGA50	133036
NA75	78649
NGA75	67374
LA50	11
LGA50	12
LA75	22
LGA75	23

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

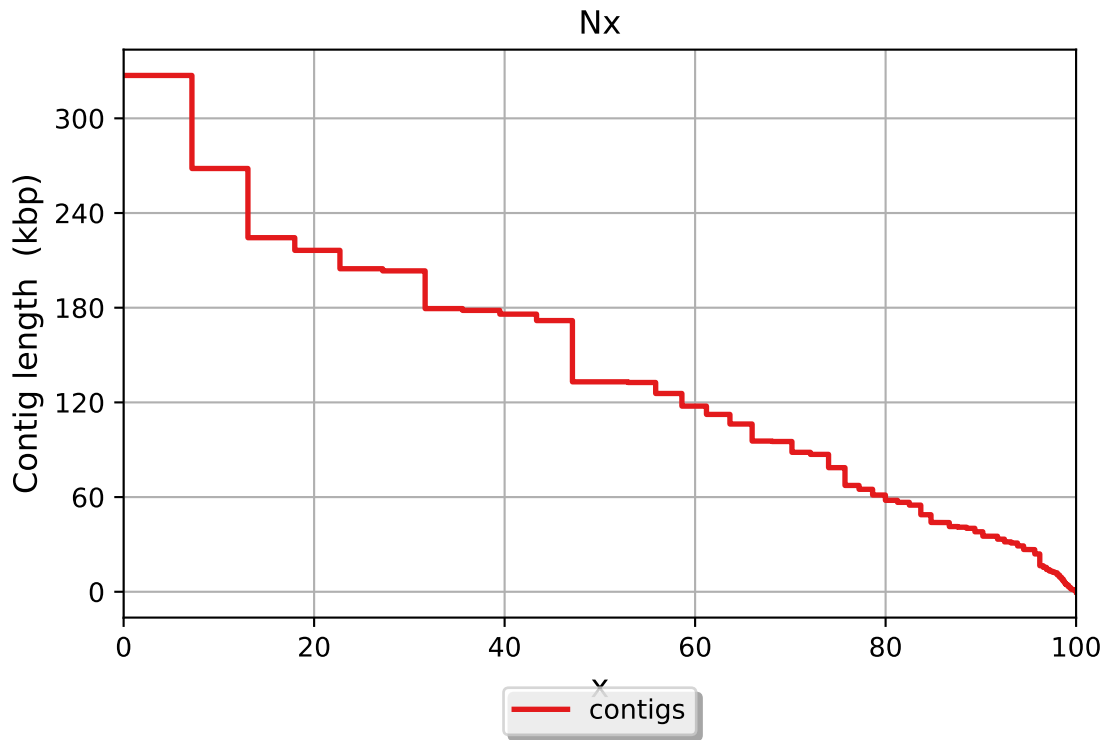
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	31
# indels	4
# short indels	4
# long indels	0
Indels length	5

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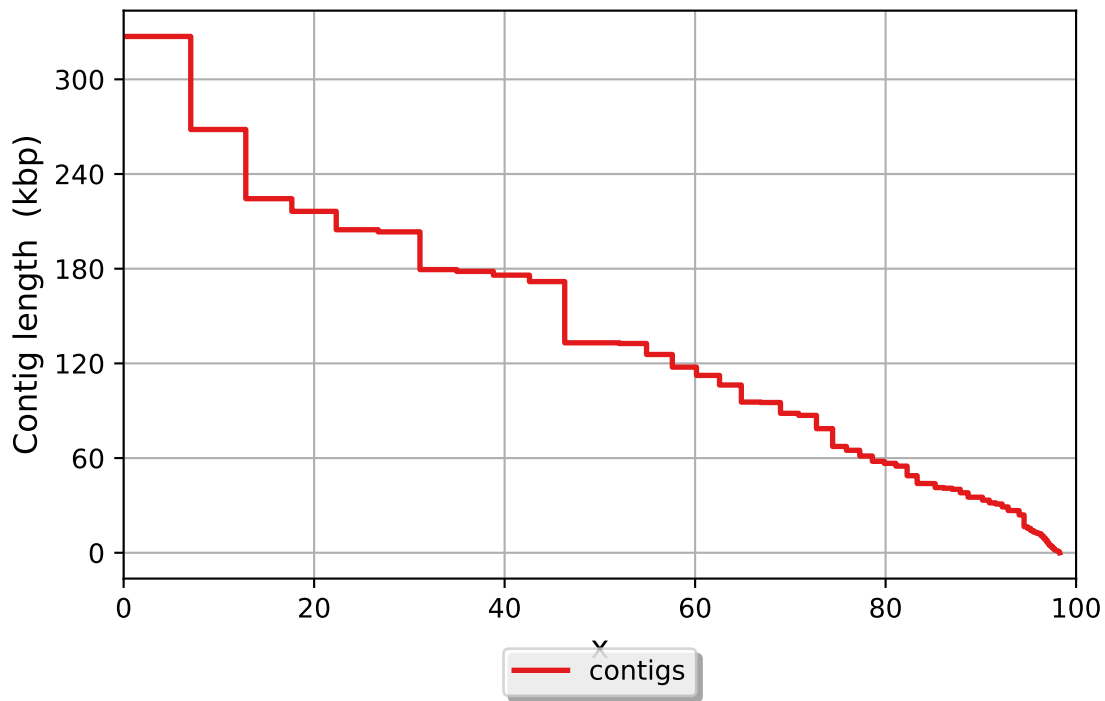
## Unaligned report

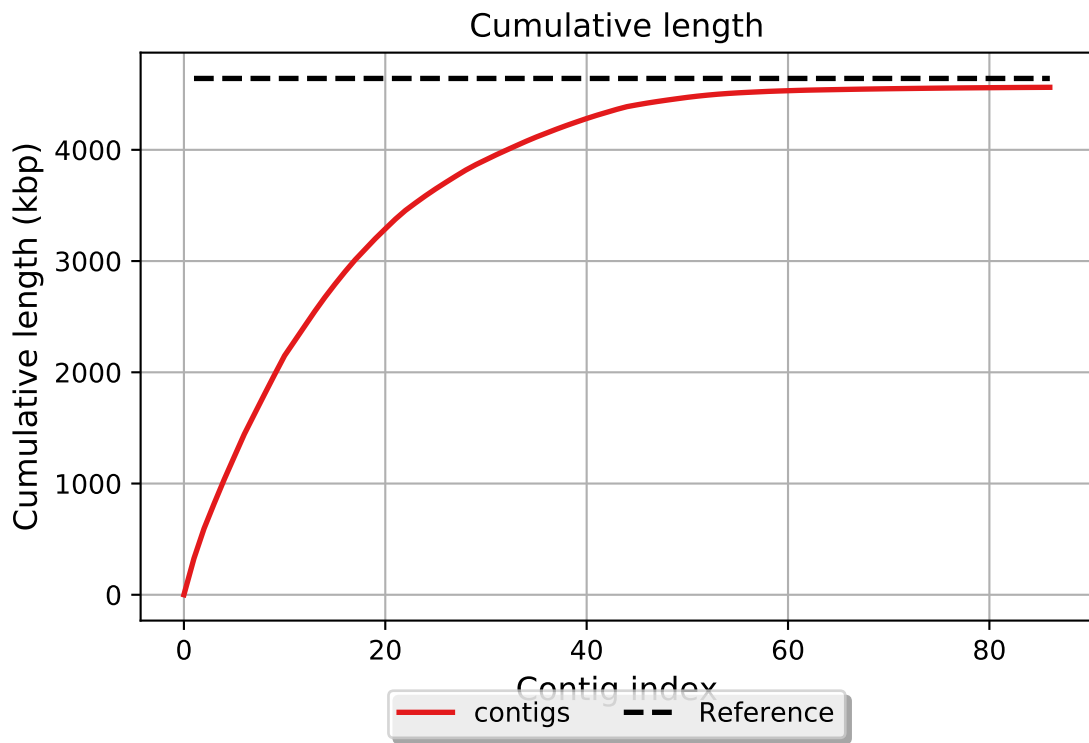
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

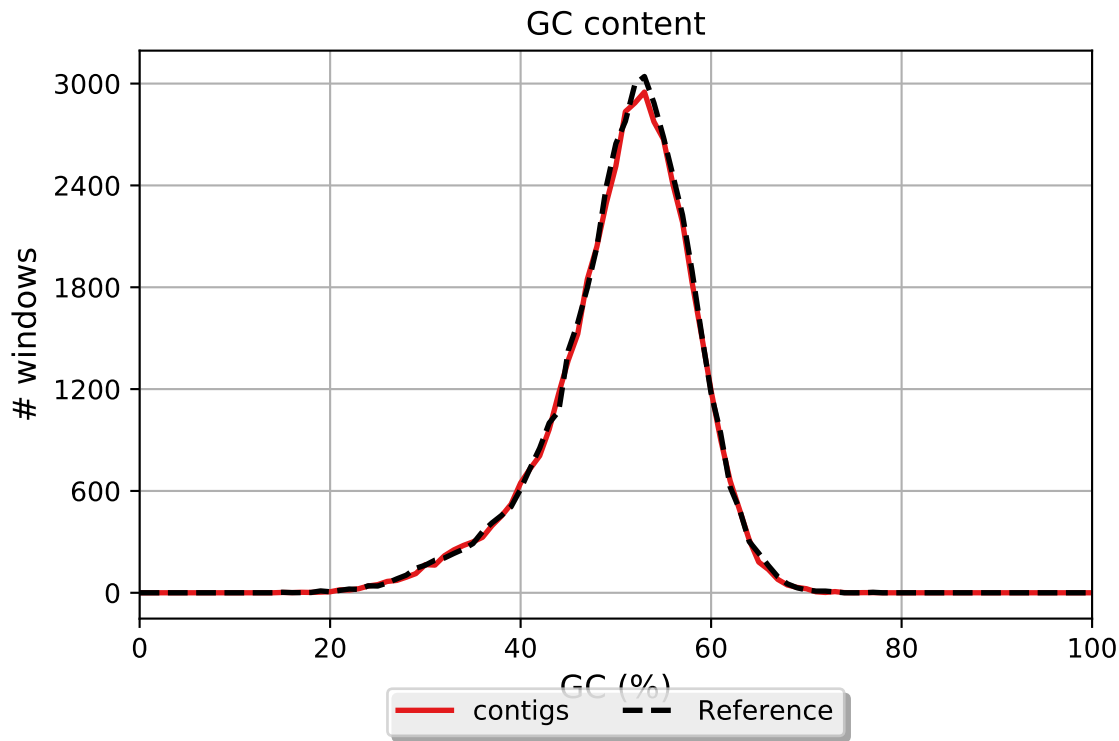
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



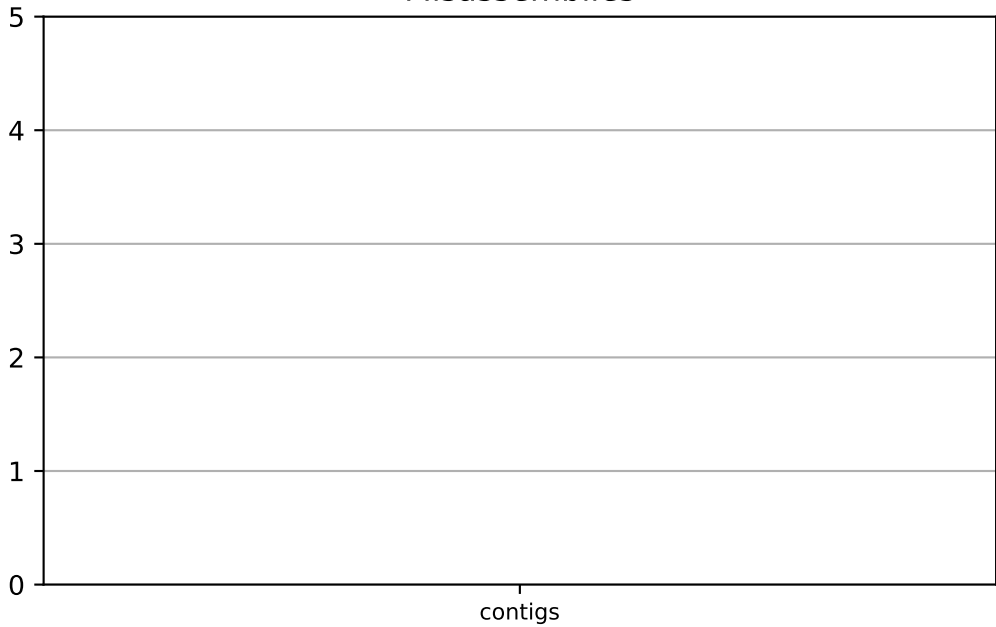
NGx





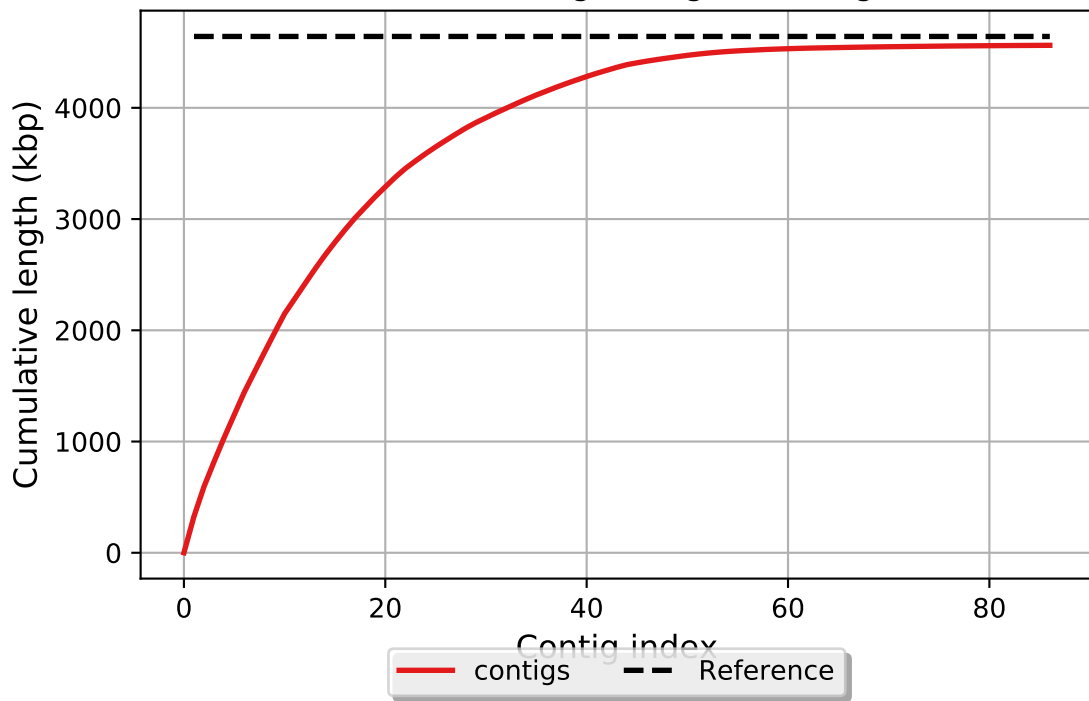


## Misassemblies

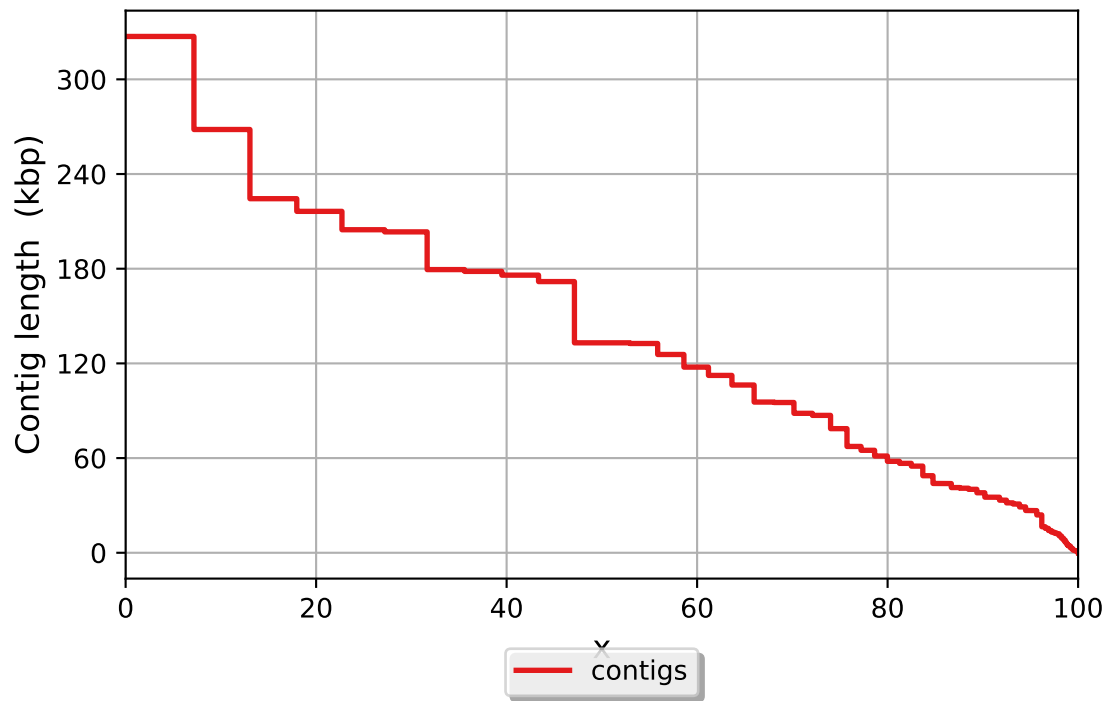




Cumulative length (aligned contigs)



NAx



# NGAx

