

## Report

	contigs
# contigs ( $\geq 0$ bp)	141
# contigs ( $\geq 1000$ bp)	81
# contigs ( $\geq 5000$ bp)	58
# contigs ( $\geq 10000$ bp)	54
# contigs ( $\geq 25000$ bp)	46
# contigs ( $\geq 50000$ bp)	31
Total length ( $\geq 0$ bp)	4573711
Total length ( $\geq 1000$ bp)	4556118
Total length ( $\geq 5000$ bp)	4506269
Total length ( $\geq 10000$ bp)	4476610
Total length ( $\geq 25000$ bp)	4358183
Total length ( $\geq 50000$ bp)	3834902
# contigs	93
Largest contig	327173
Total length	4564644
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	132608
NG50	132608
N75	67374
NG75	66295
L50	13
LG50	13
L75	25
LG75	26
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.304
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.64
# indels per 100 kbp	0.02
Largest alignment	327173
NA50	132608
NGA50	132608
NA75	67374
NGA75	66295
LA50	13
LGA50	13
LA75	25
LGA75	26

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

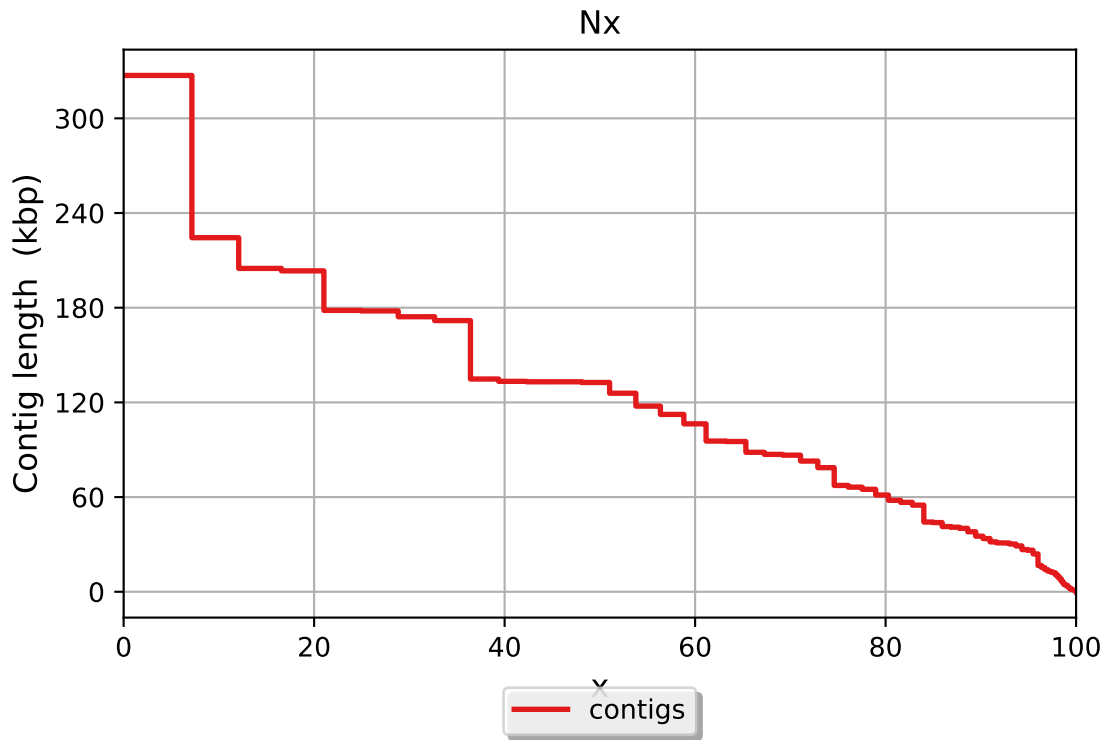
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	29
# indels	1
# short indels	1
# long indels	0
Indels length	1

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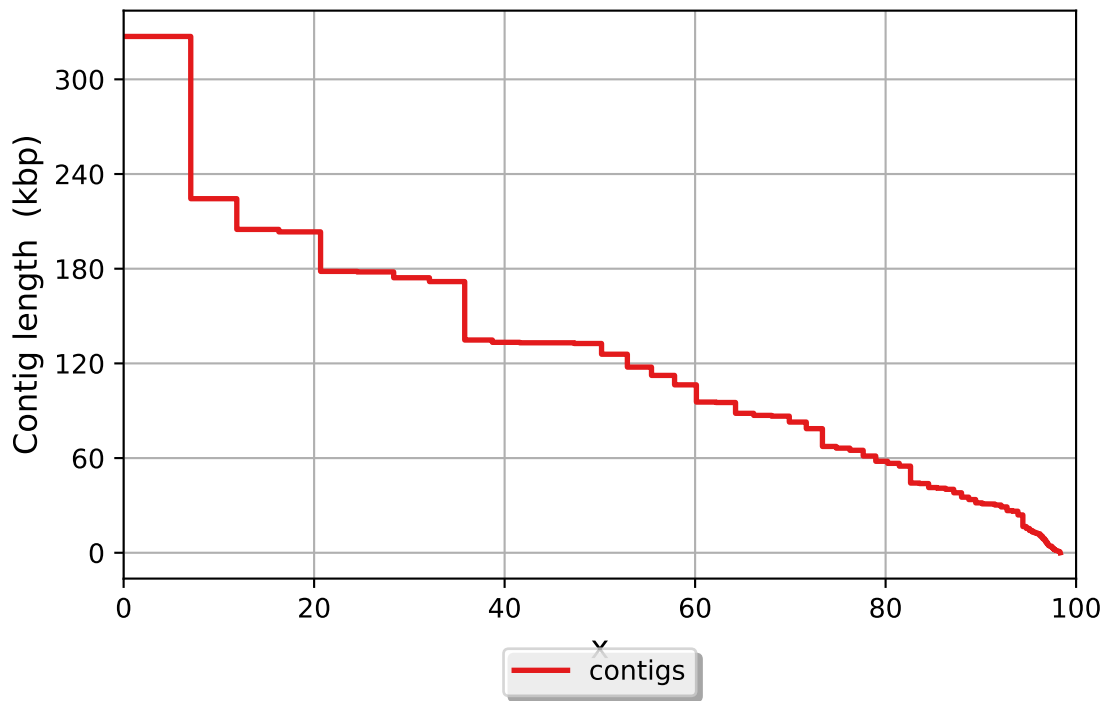
## Unaligned report

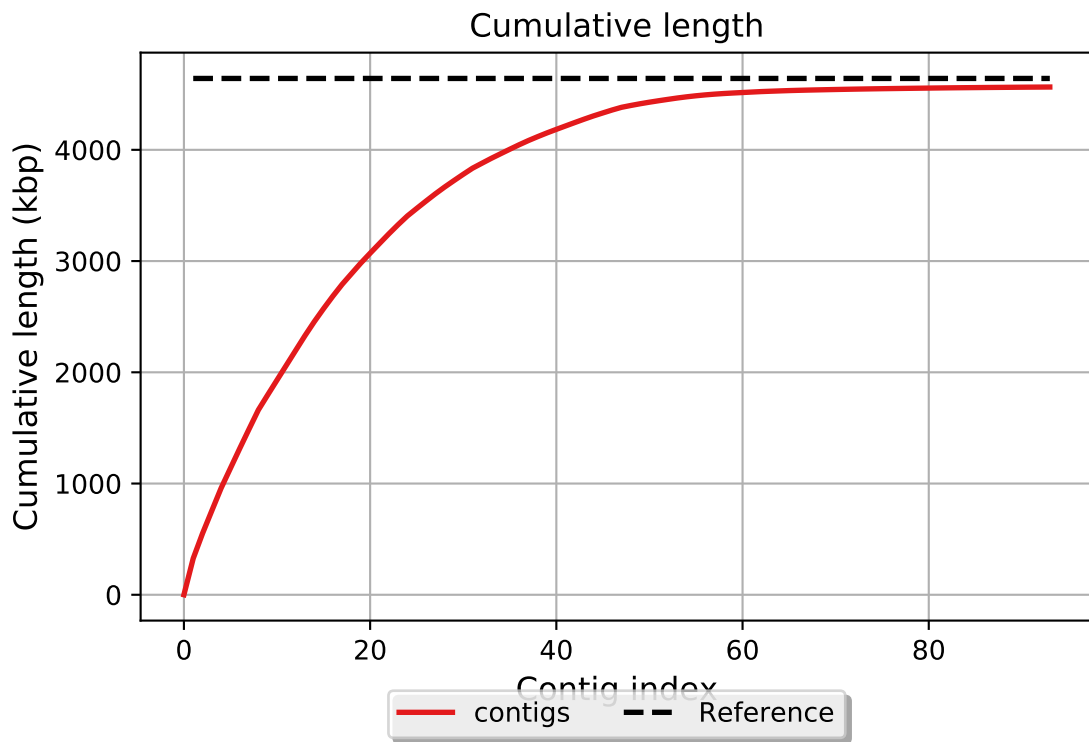
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

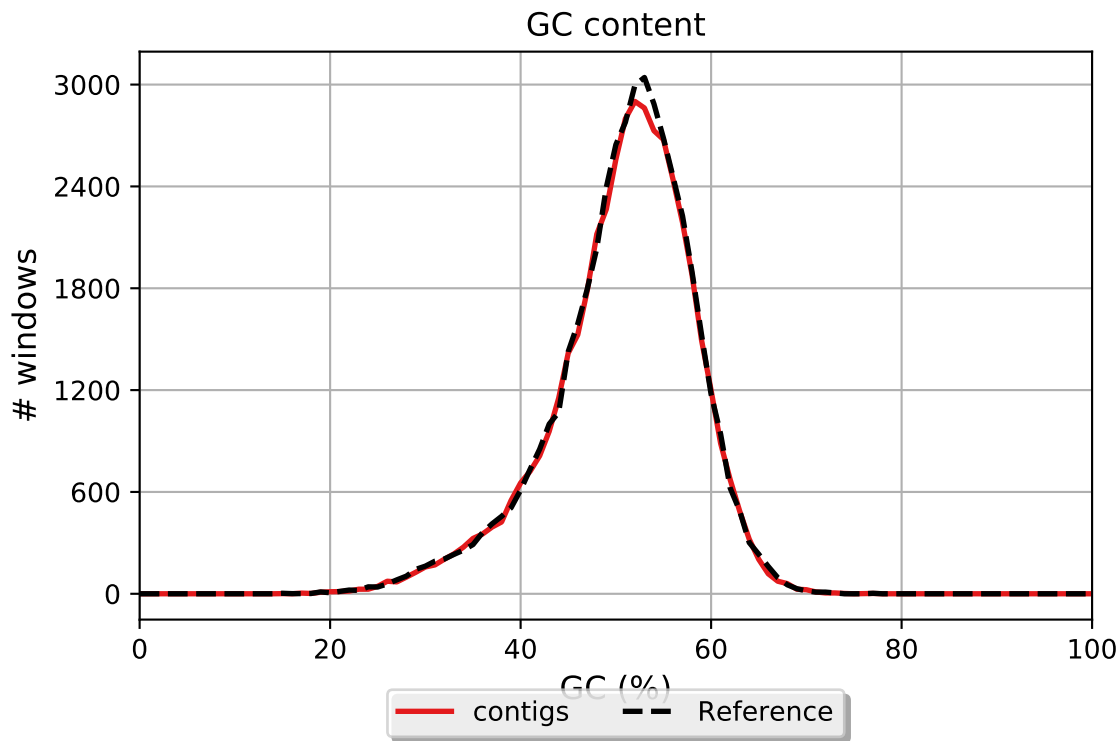
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



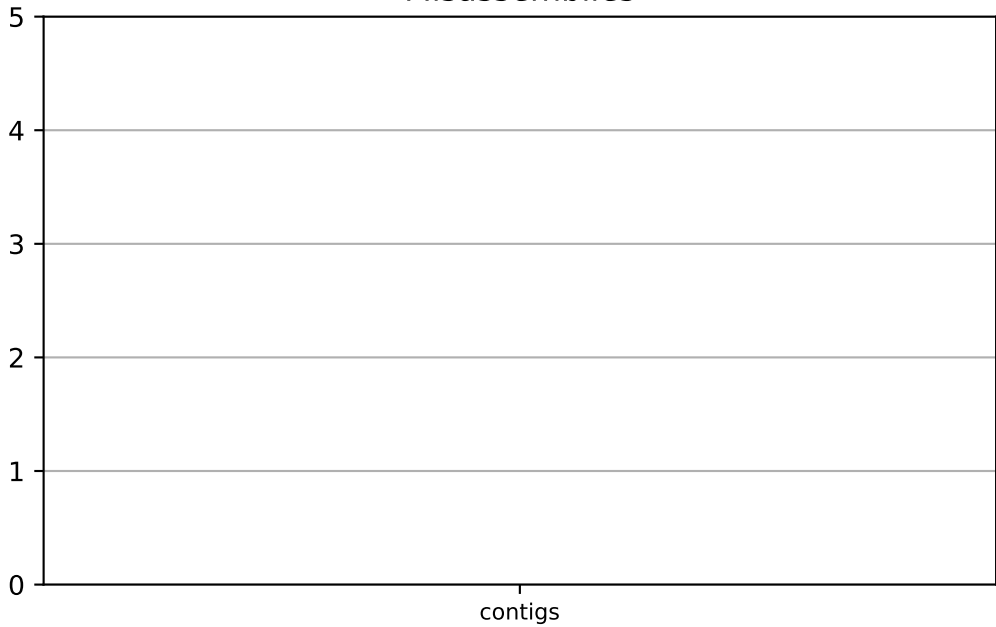
# NGx





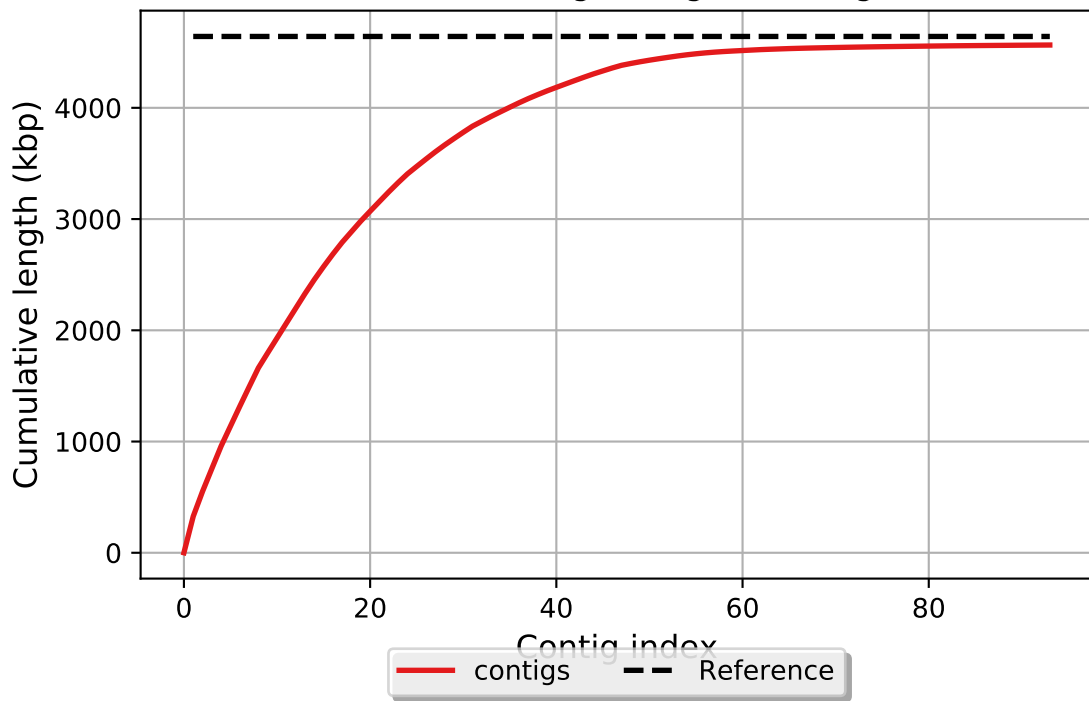


## Misassemblies

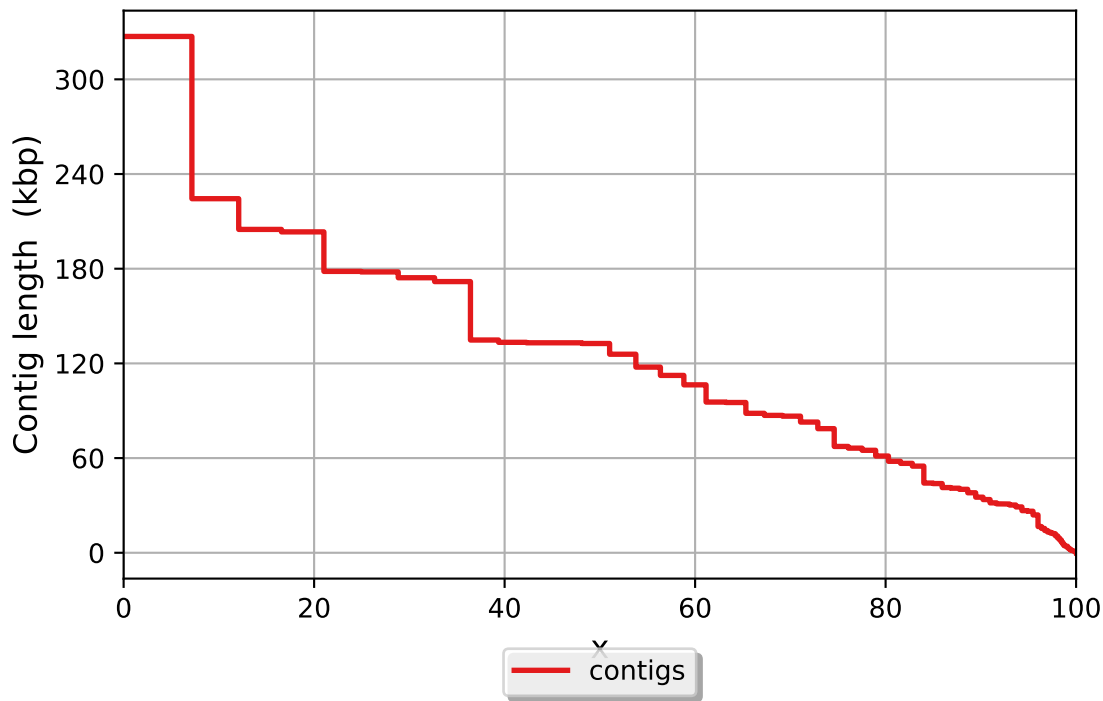




Cumulative length (aligned contigs)



NAx



# NGAx

