

## Report

	contigs
# contigs ( $\geq 0$ bp)	130
# contigs ( $\geq 1000$ bp)	73
# contigs ( $\geq 5000$ bp)	54
# contigs ( $\geq 10000$ bp)	50
# contigs ( $\geq 25000$ bp)	42
# contigs ( $\geq 50000$ bp)	28
Total length ( $\geq 0$ bp)	4574431
Total length ( $\geq 1000$ bp)	4557486
Total length ( $\geq 5000$ bp)	4518960
Total length ( $\geq 10000$ bp)	4489692
Total length ( $\geq 25000$ bp)	4370447
Total length ( $\geq 50000$ bp)	3868109
# contigs	84
Largest contig	327173
Total length	4565136
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133059
NG50	133059
N75	87059
NG75	78649
L50	11
LG50	11
L75	21
LG75	22
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.320
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.72
# indels per 100 kbp	0.02
Largest alignment	327173
NA50	133059
NGA50	133059
NA75	87059
NGA75	78649
LA50	11
LGA50	11
LA75	21
LGA75	22

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

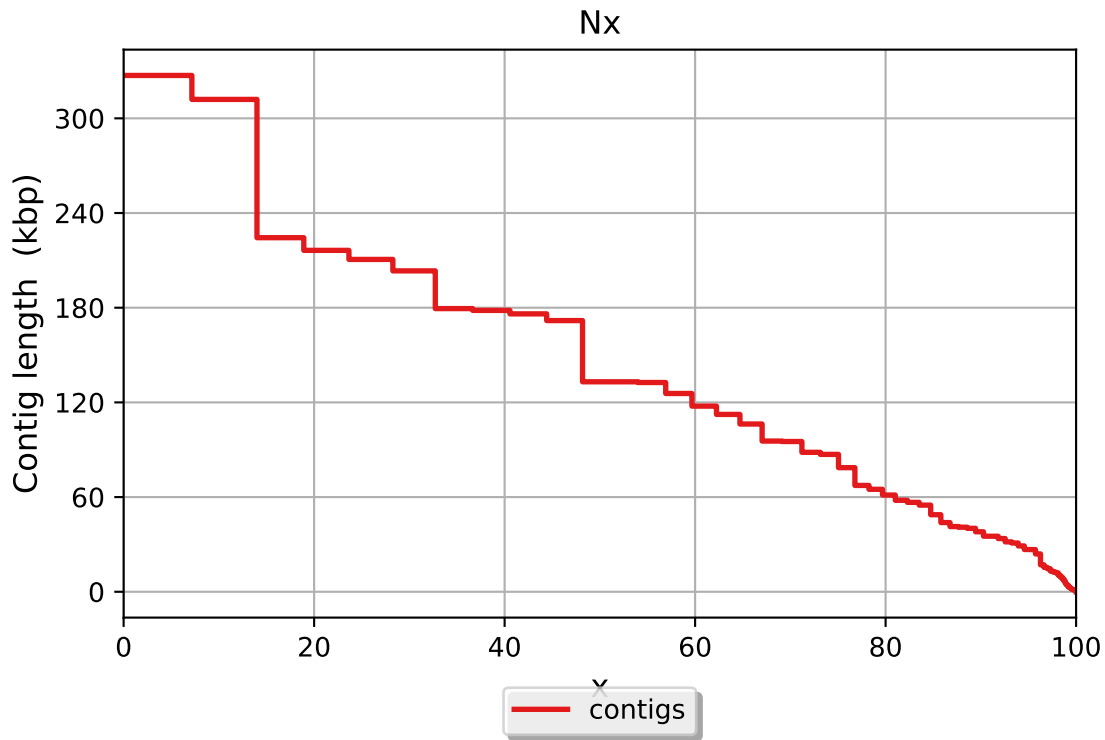
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	33
# indels	1
# short indels	1
# long indels	0
Indels length	1

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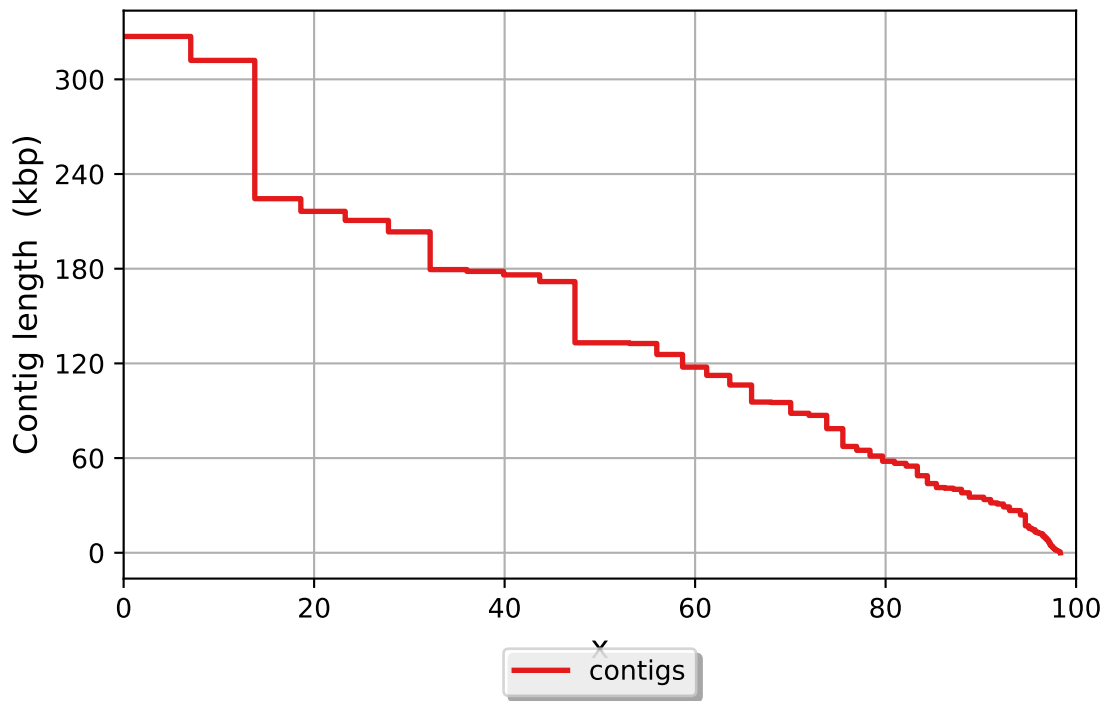
## Unaligned report

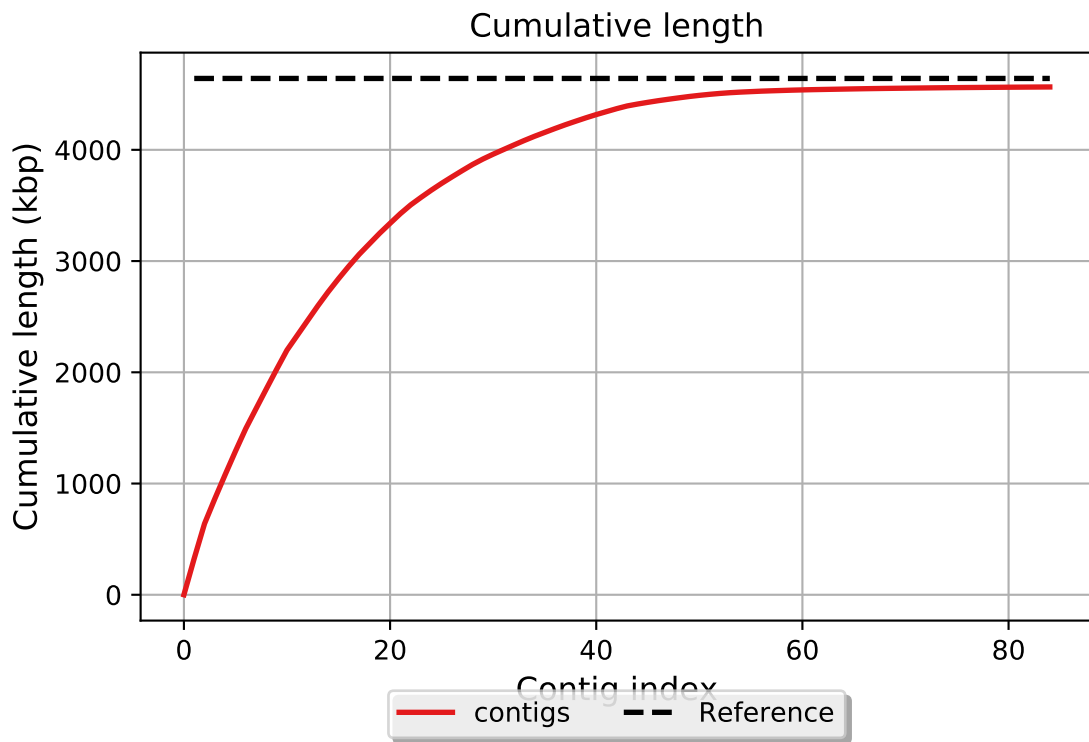
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

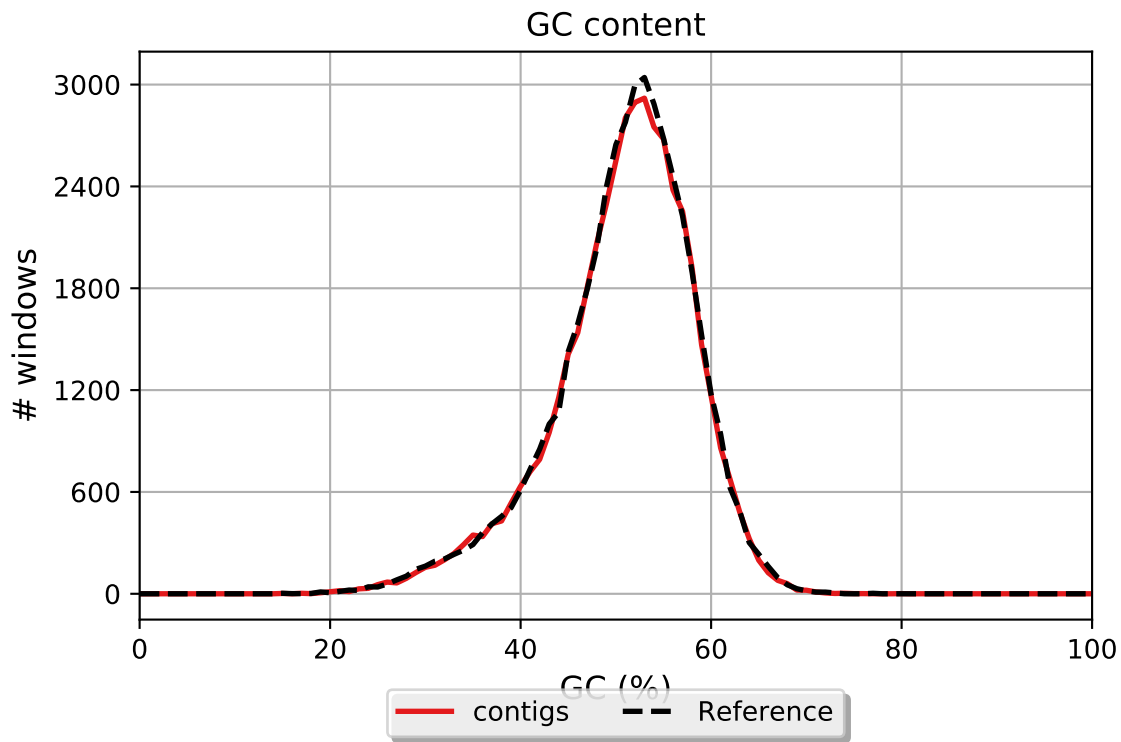
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



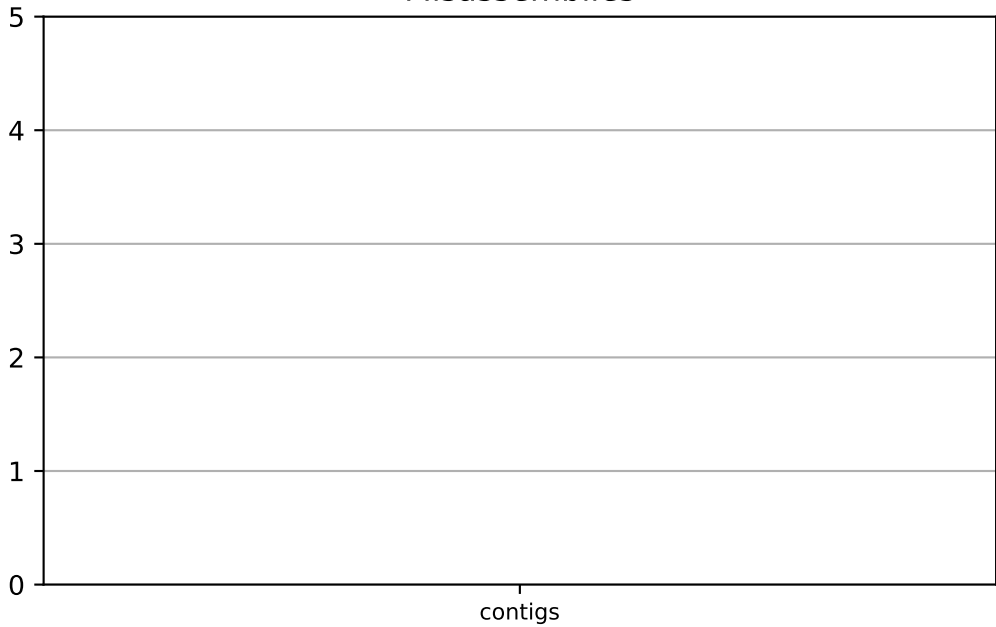
NGx





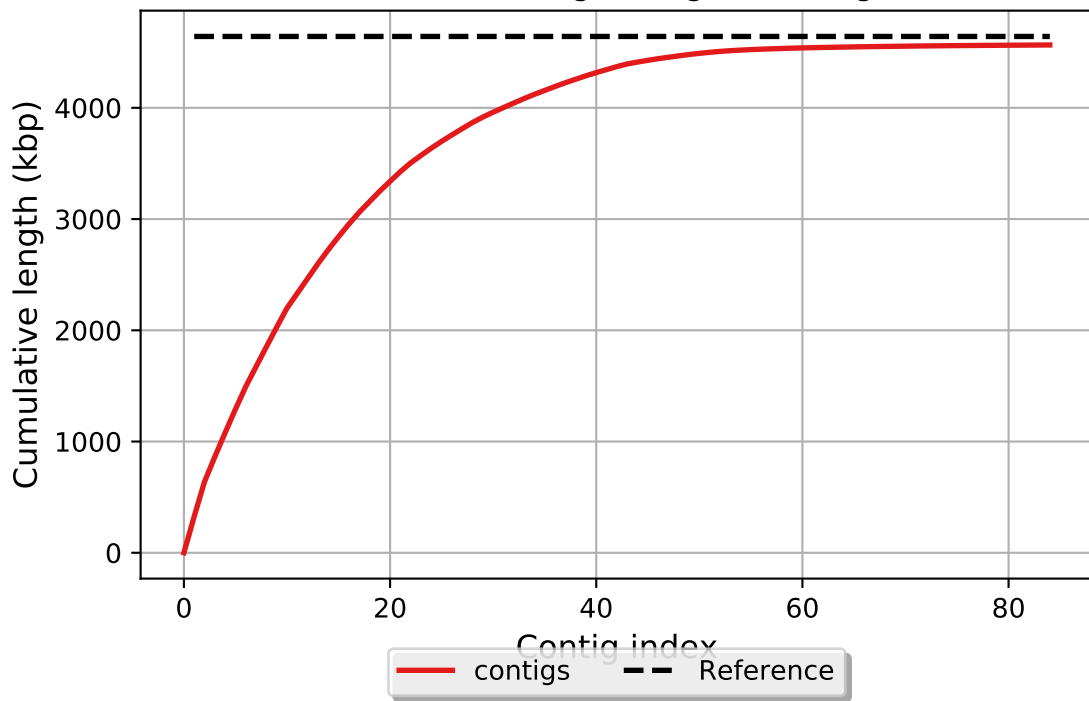


# Misassemblies

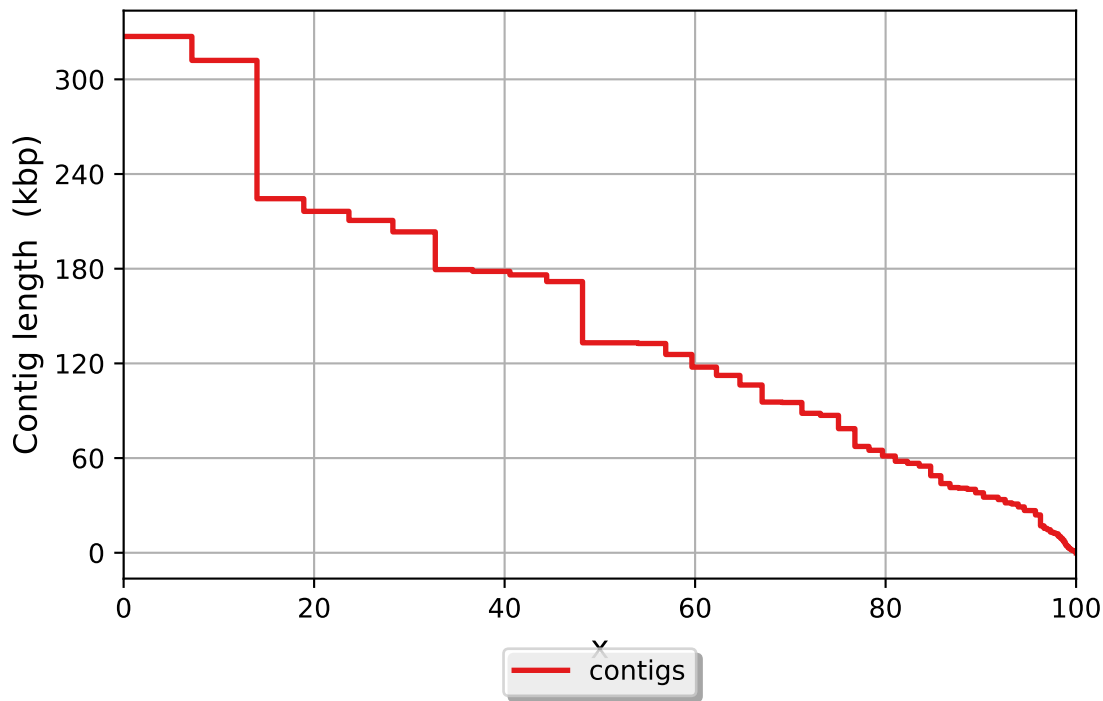




Cumulative length (aligned contigs)



NAx



# NGAx

