

## Report

	contigs
# contigs ( $\geq 1000$ bp)	126
# contigs ( $\geq 5000$ bp)	92
# contigs ( $\geq 10000$ bp)	66
# contigs ( $\geq 25000$ bp)	38
# contigs ( $\geq 50000$ bp)	22
Total length ( $\geq 1000$ bp)	2803196
Total length ( $\geq 5000$ bp)	2716375
Total length ( $\geq 10000$ bp)	2519417
Total length ( $\geq 25000$ bp)	2119186
Total length ( $\geq 50000$ bp)	1570029
# contigs	138
Largest contig	130415
Total length	2810883
Reference length	4641652
GC (%)	50.81
Reference GC (%)	50.79
N50	51643
NG50	14008
N75	26461
L50	19
LG50	49
L75	38
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	55
Genome fraction (%)	59.673
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	703.80
# indels per 100 kbp	0.36
Largest alignment	117700
NA50	50218
NGA50	14008
NA75	23279
LA50	20
LGA50	53
LA75	42

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

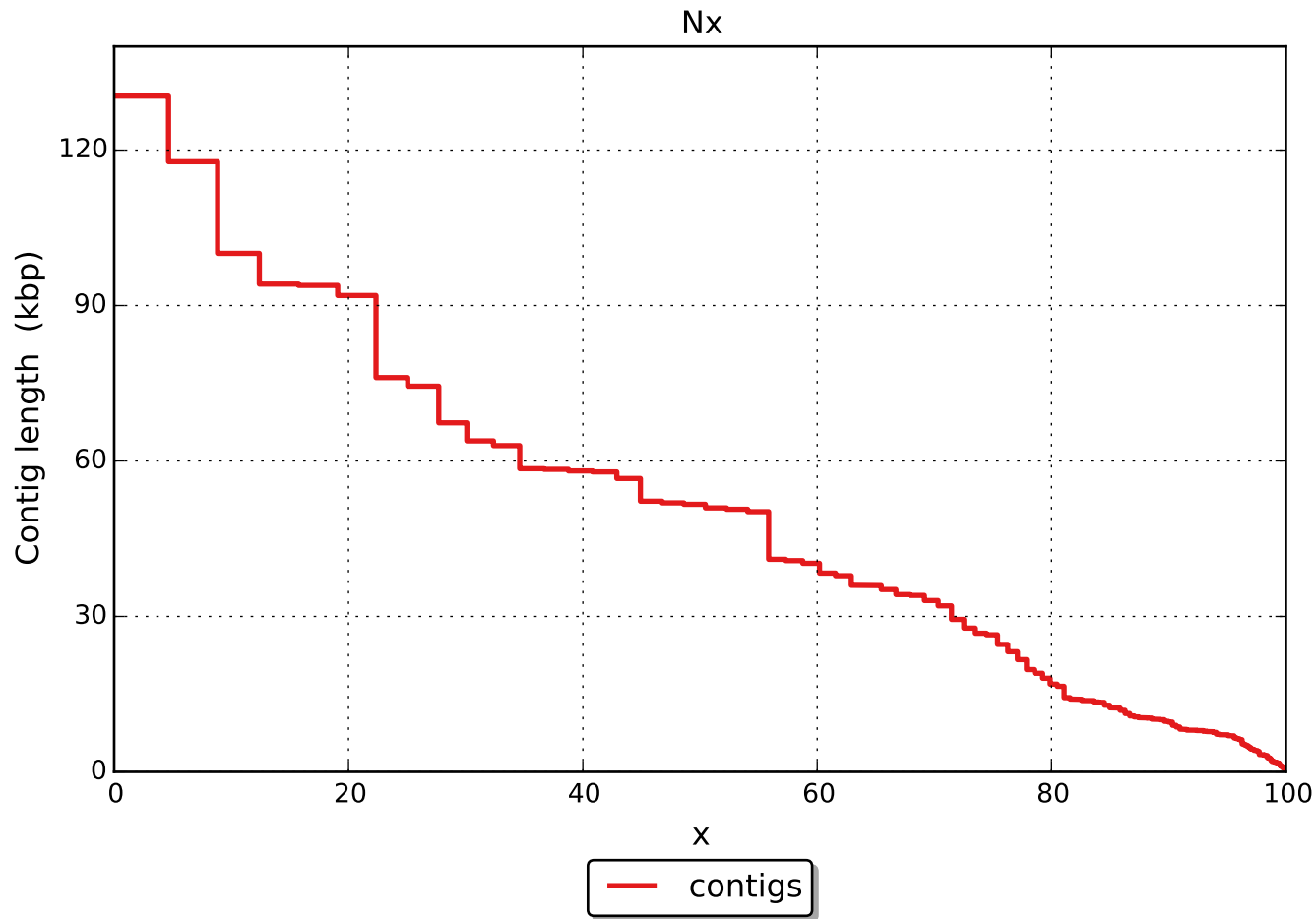
	contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	1
# mismatches	19494
# indels	10
# short indels	10
# long indels	0
Indels length	11

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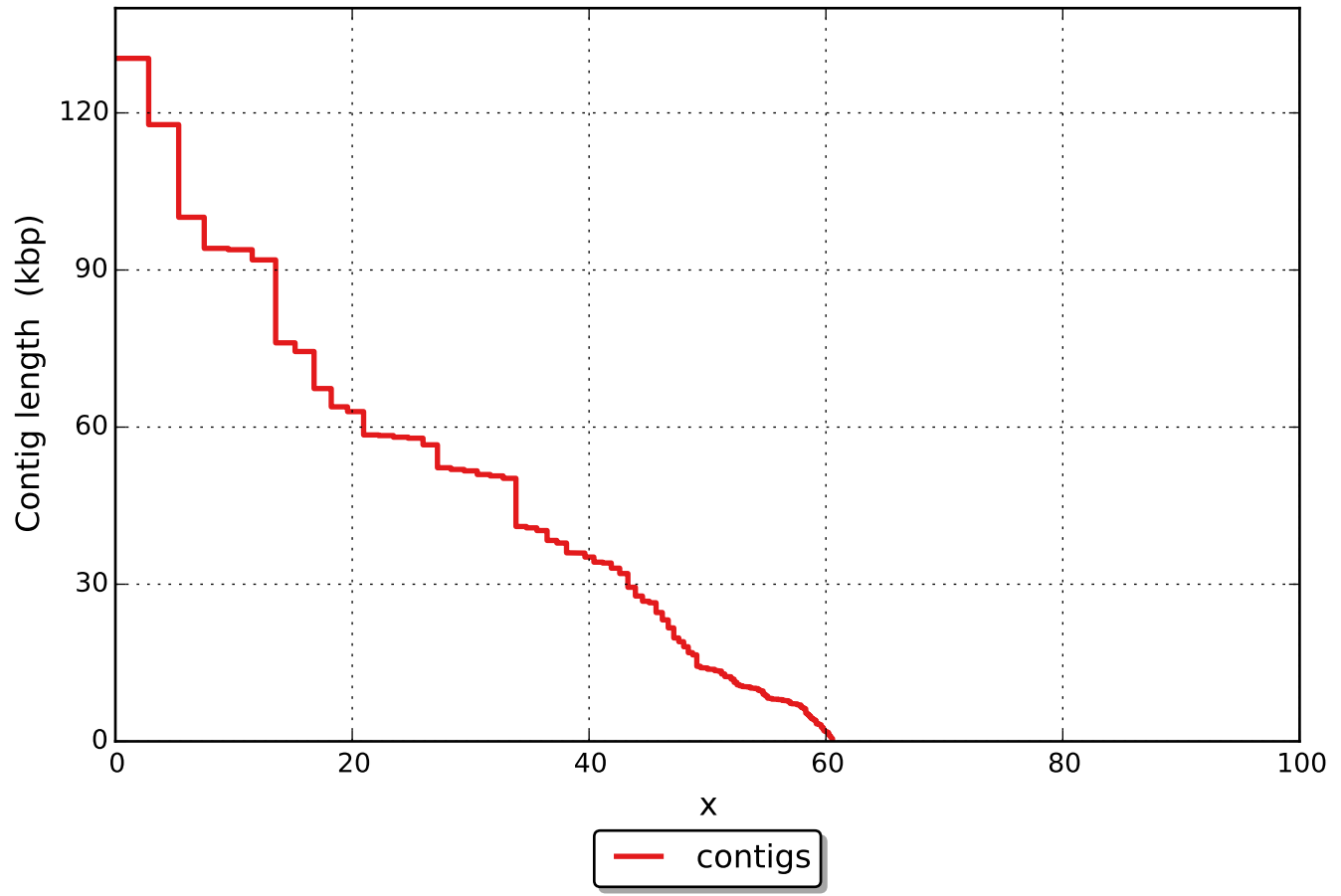
## Unaligned report

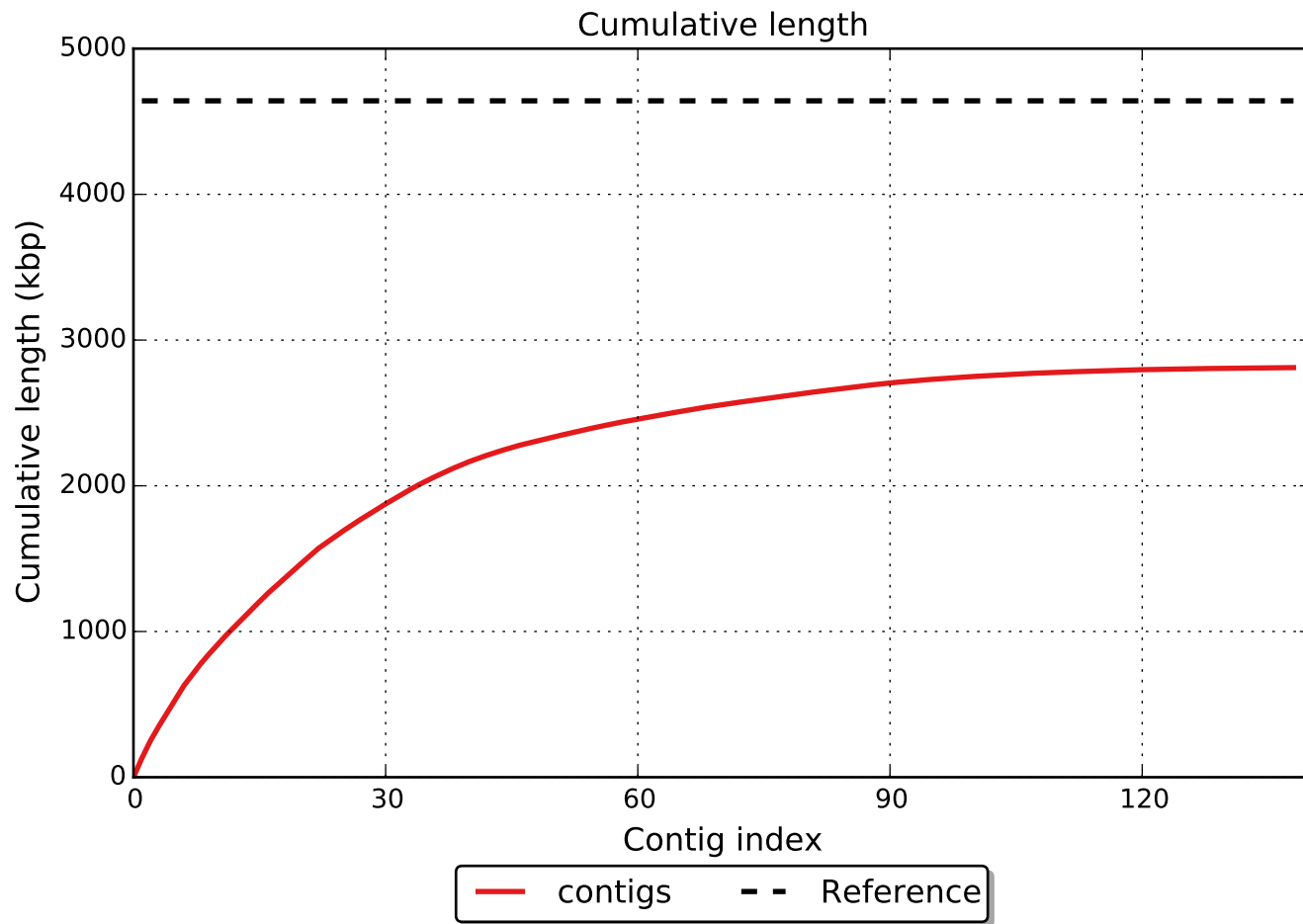
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	55
# N's	0

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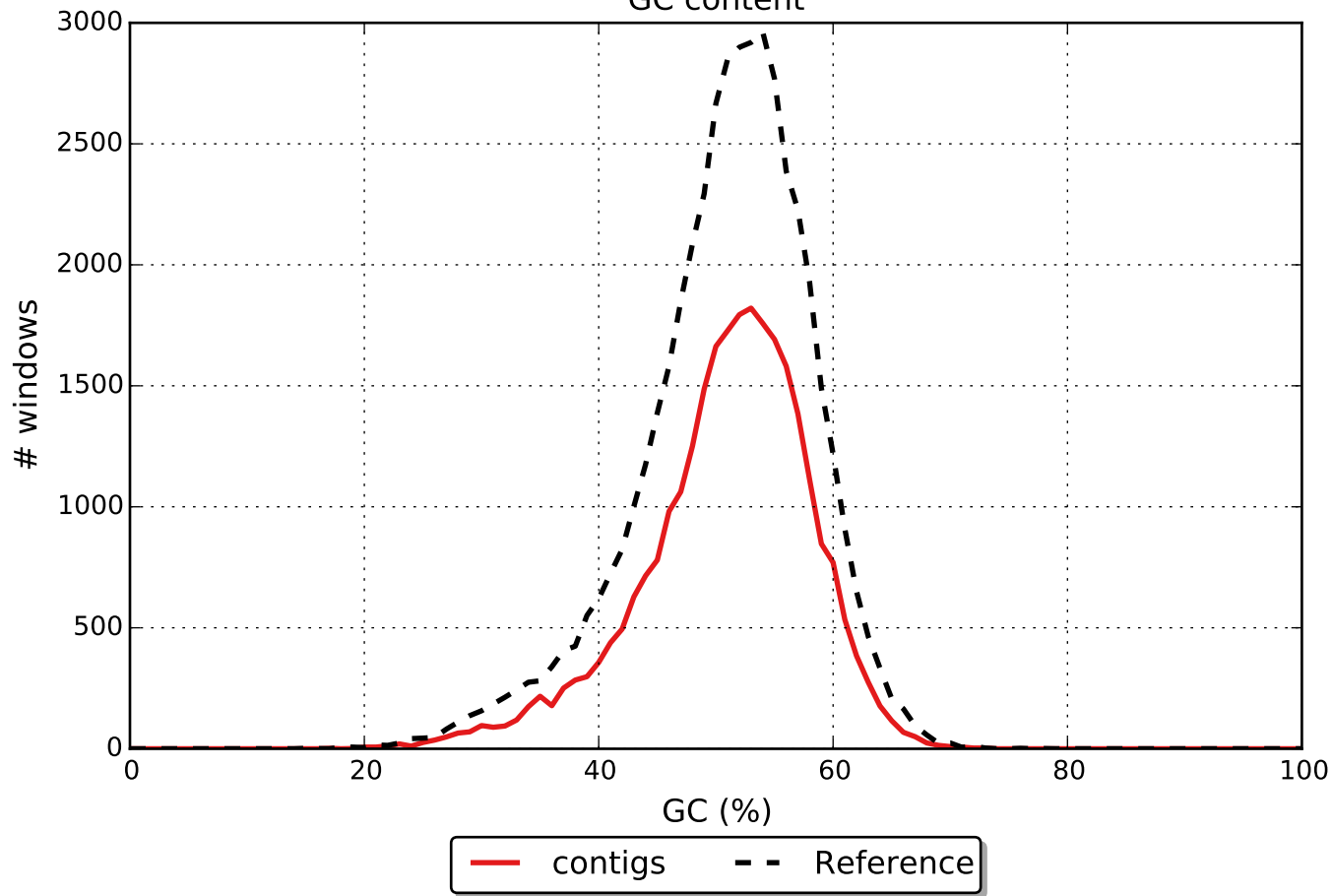


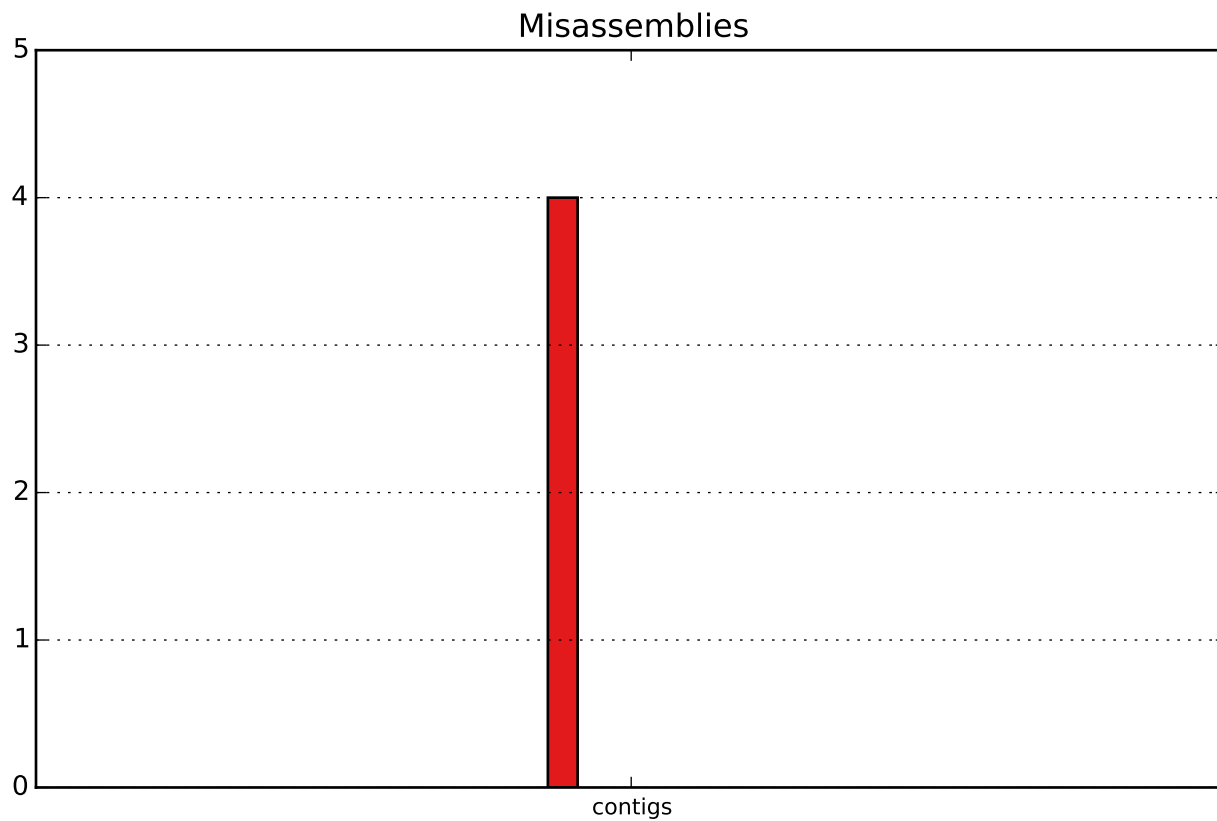
NGx





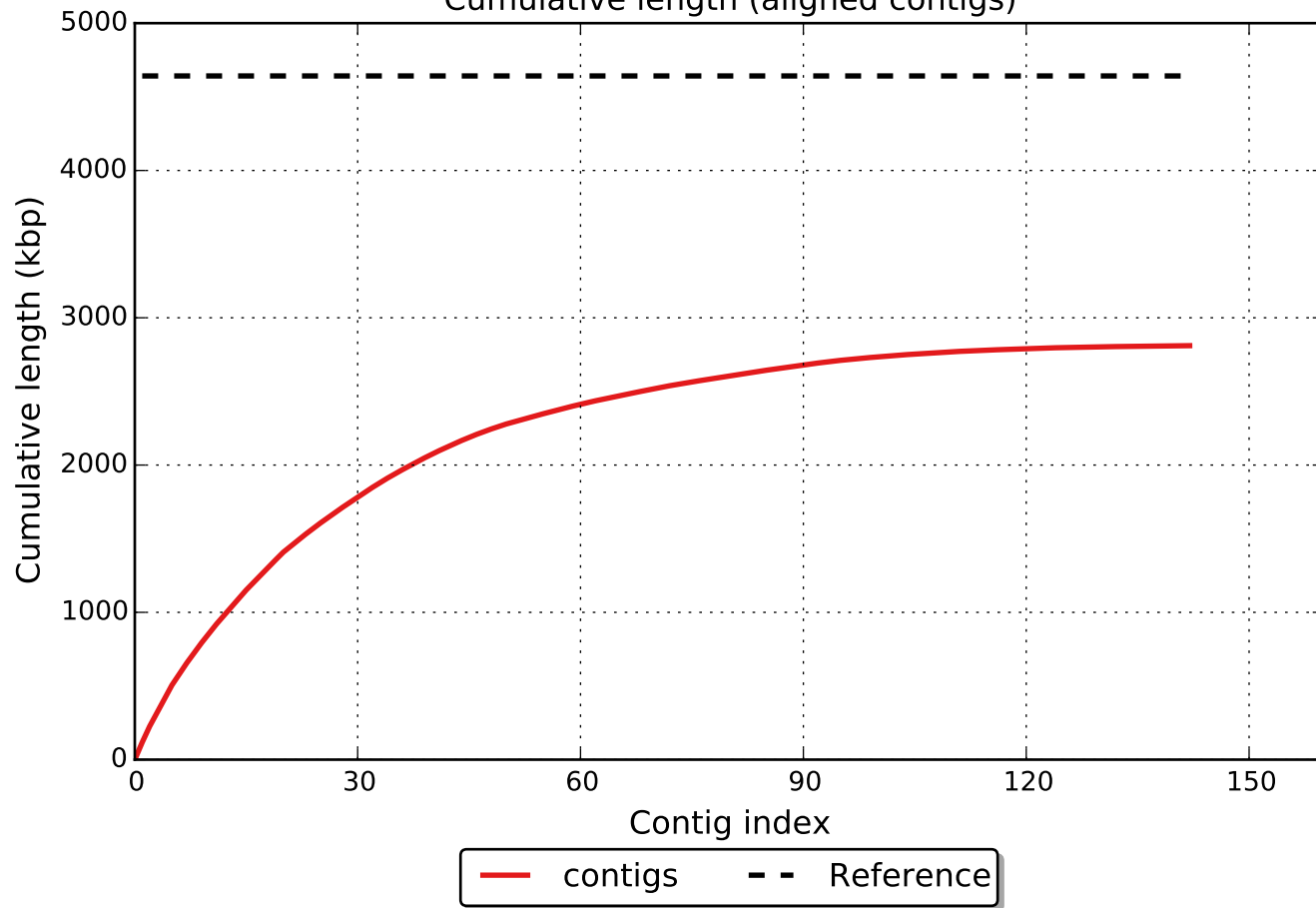
# GC content



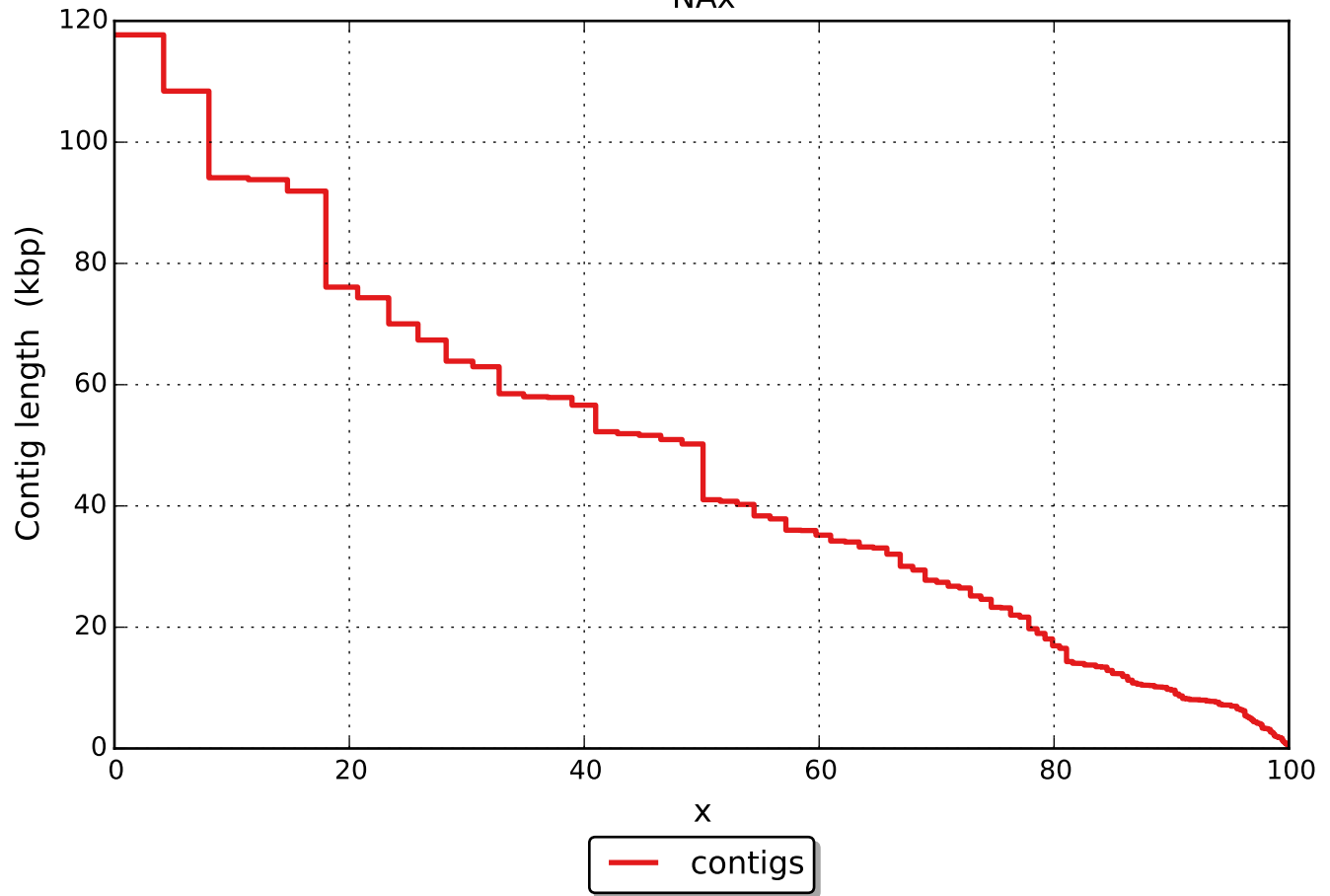




Cumulative length (aligned contigs)



NAx



NGAx

