

## Report

	contigs
# contigs ( $\geq 1000$ bp)	120
# contigs ( $\geq 5000$ bp)	90
# contigs ( $\geq 10000$ bp)	68
# contigs ( $\geq 25000$ bp)	42
# contigs ( $\geq 50000$ bp)	27
Total length ( $\geq 1000$ bp)	3469214
Total length ( $\geq 5000$ bp)	3390104
Total length ( $\geq 10000$ bp)	3229484
Total length ( $\geq 25000$ bp)	2833440
Total length ( $\geq 50000$ bp)	2336199
# contigs	126
Largest contig	264572
Total length	3473785
Reference length	4641652
GC (%)	50.84
Reference GC (%)	50.79
N50	66357
NG50	51851
N75	32212
L50	17
LG50	27
L75	35
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	307071
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	74.710
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	559.20
# indels per 100 kbp	0.49
Largest alignment	264572
NA50	64886
NGA50	43808
NA75	32212
LA50	18
LGA50	29
LA75	36

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	307071
# local misassemblies	1
# mismatches	19392
# indels	17
# short indels	17
# long indels	0
Indels length	23

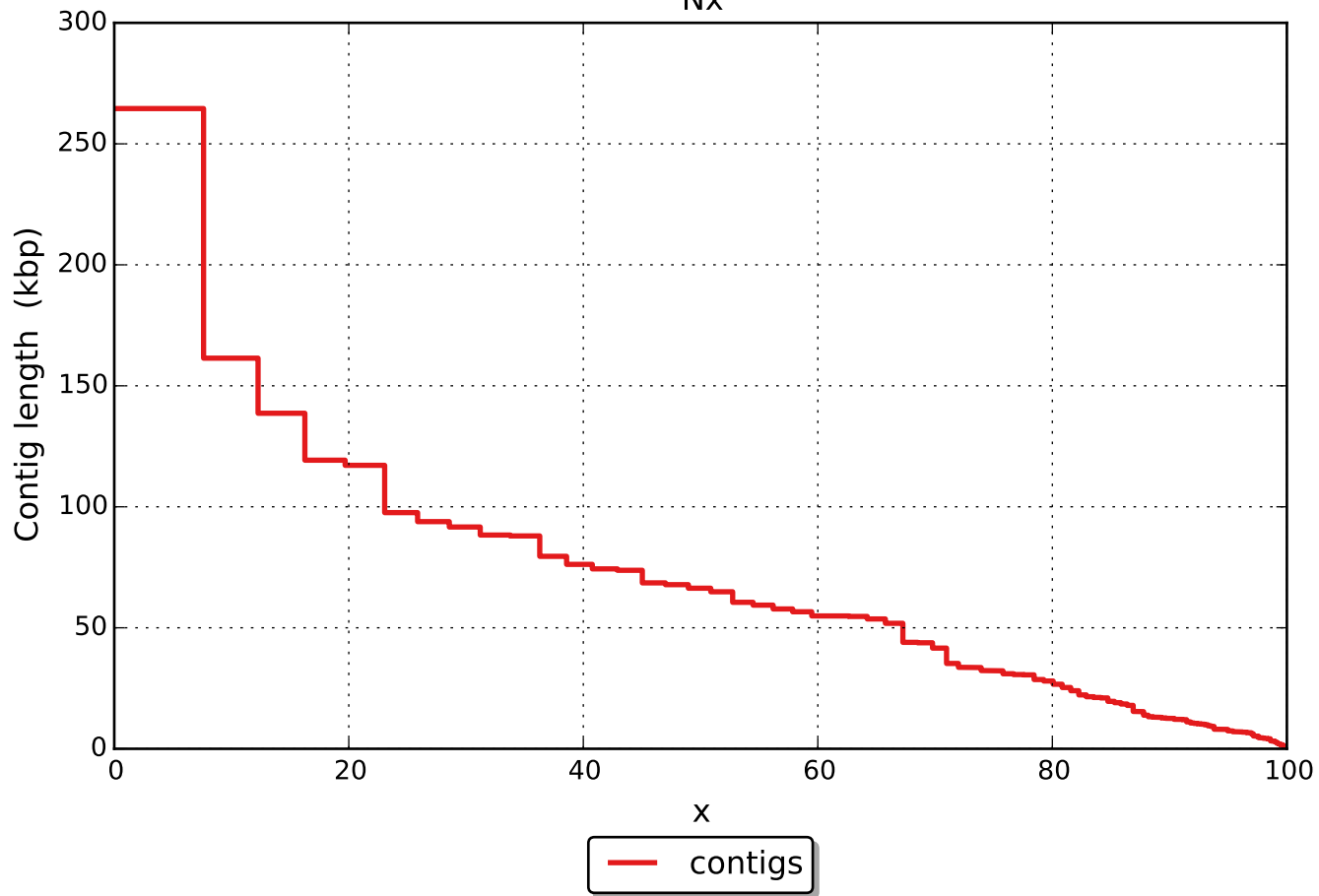
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

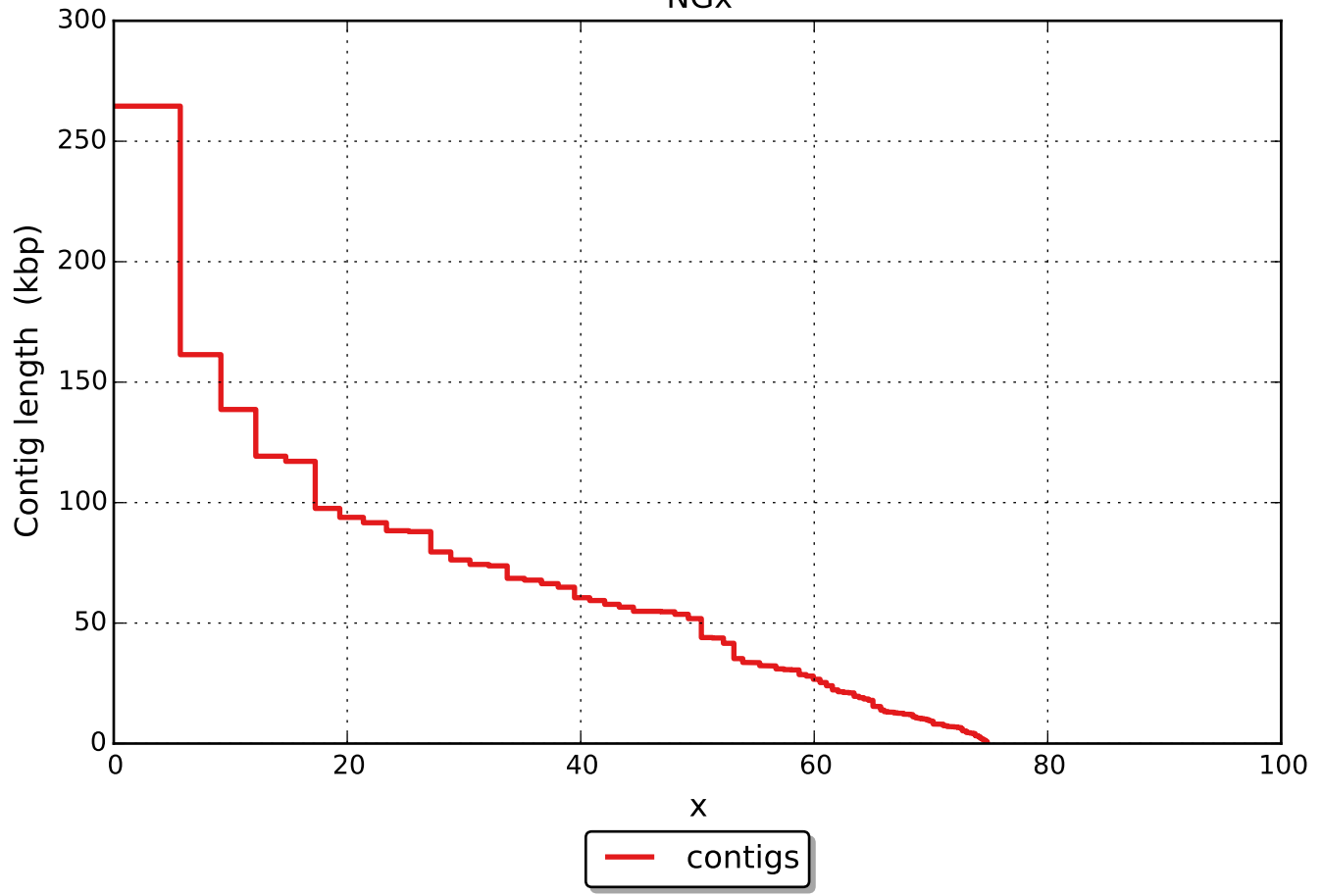
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

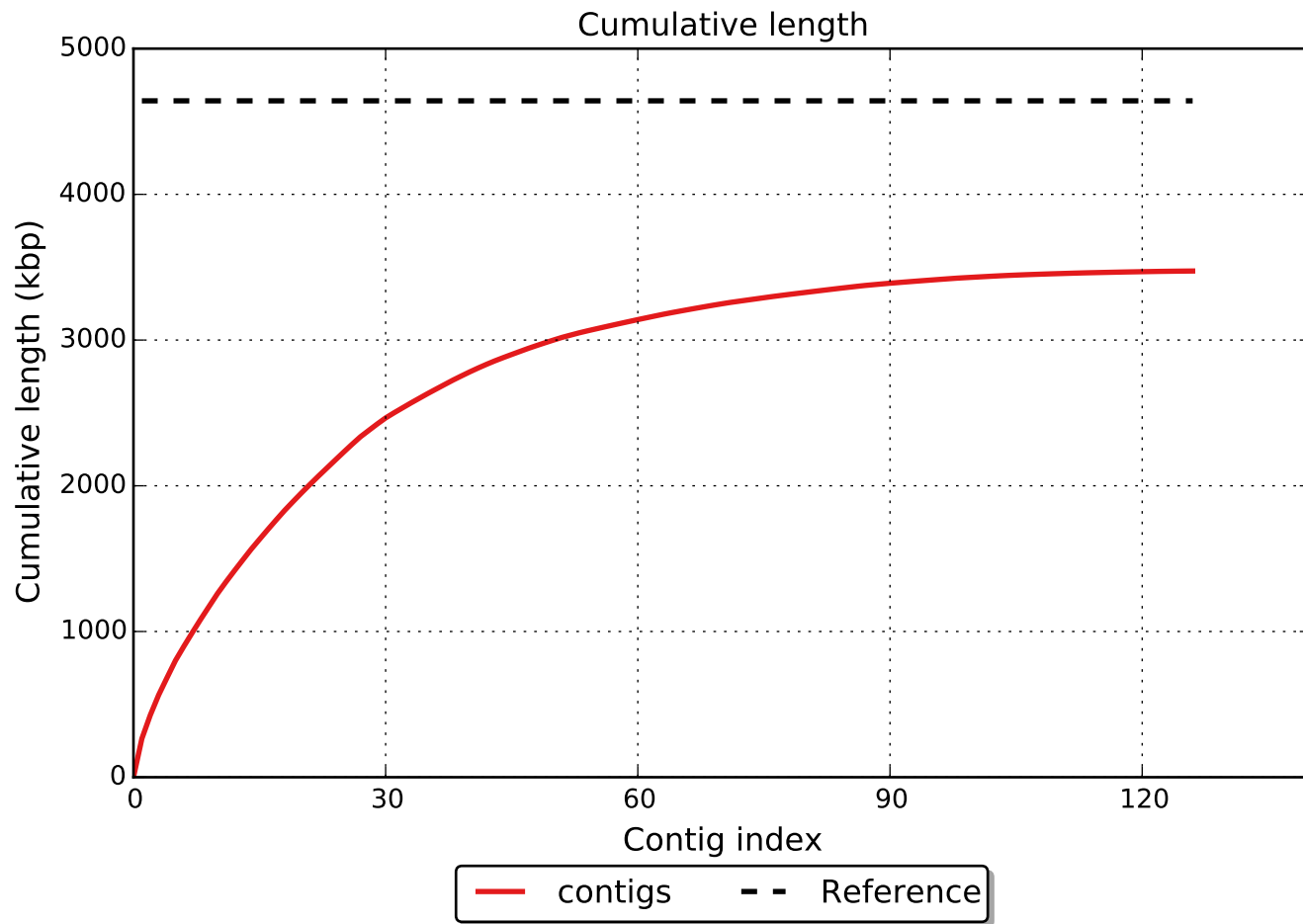
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

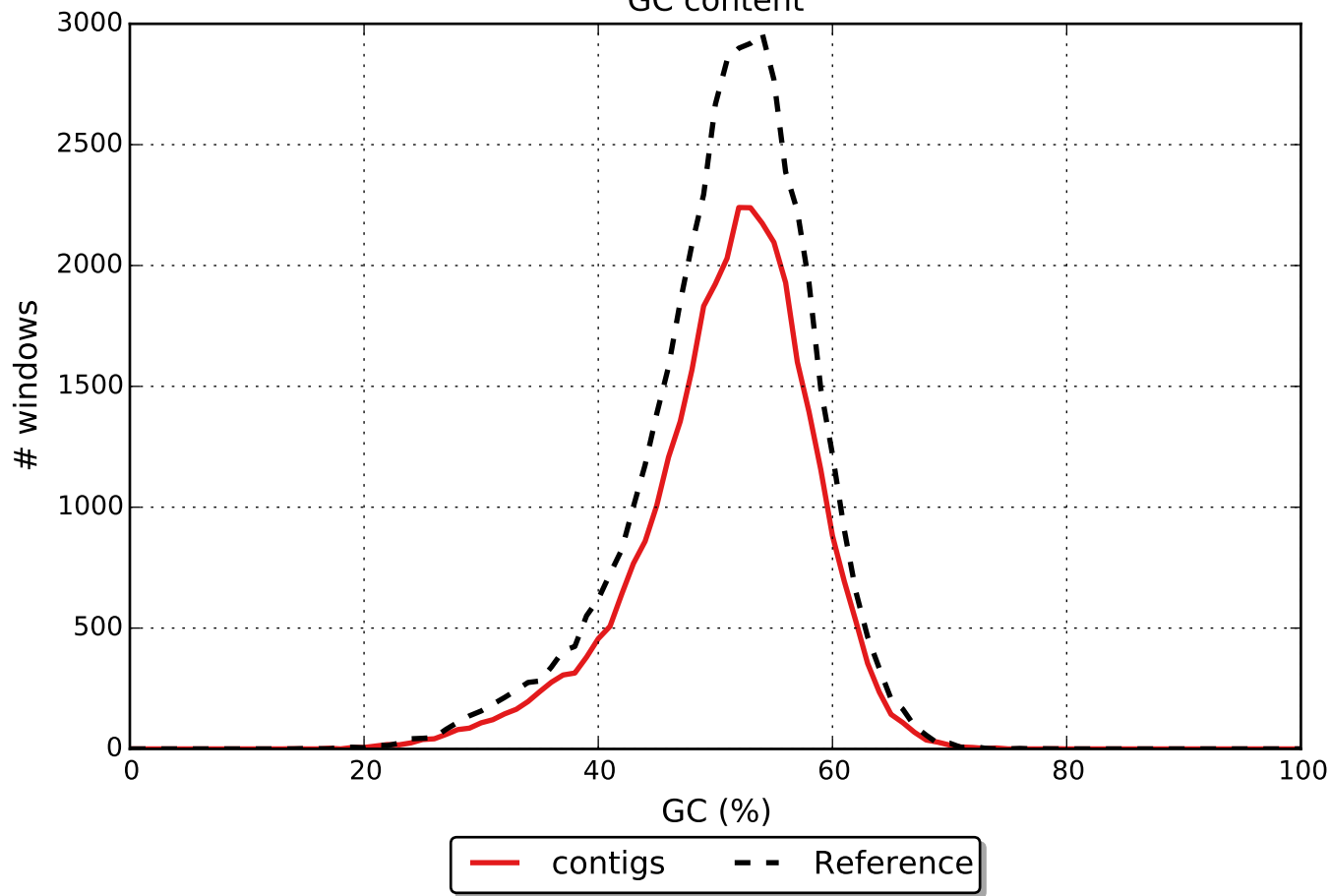


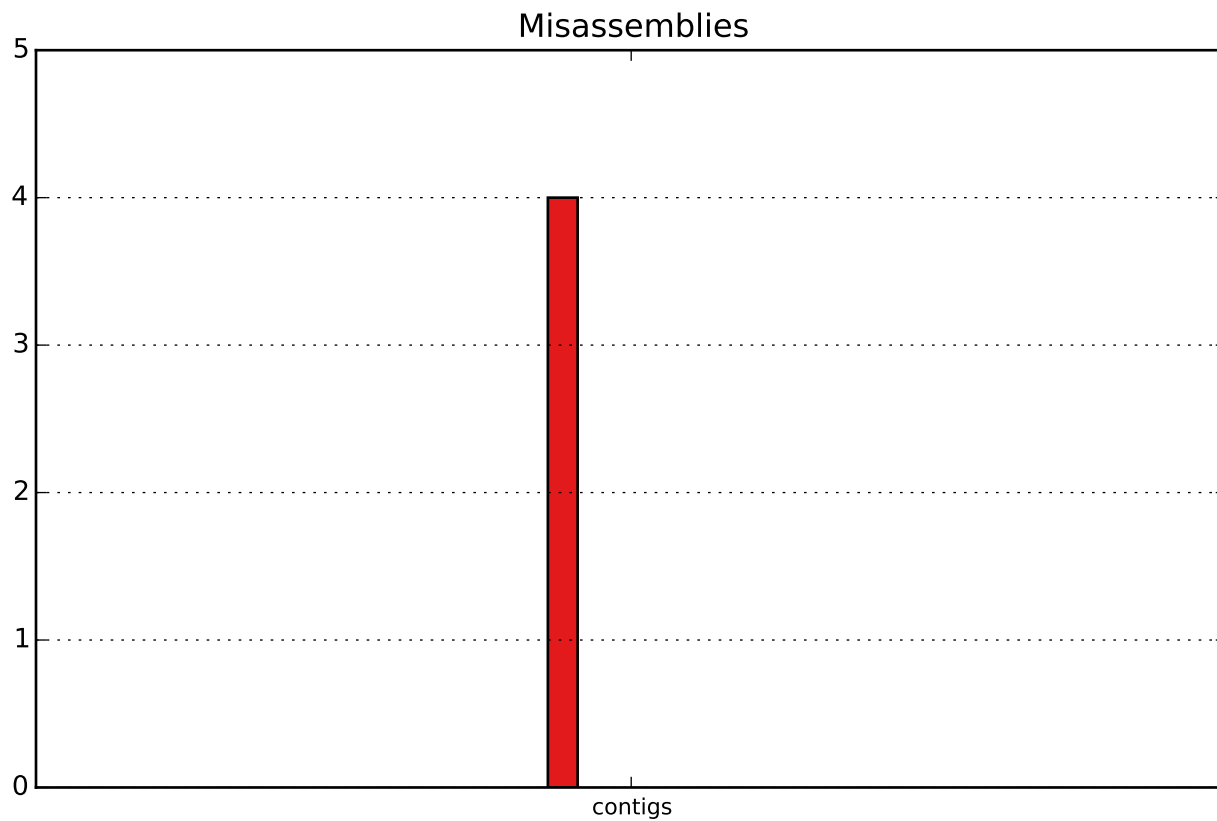
NGx





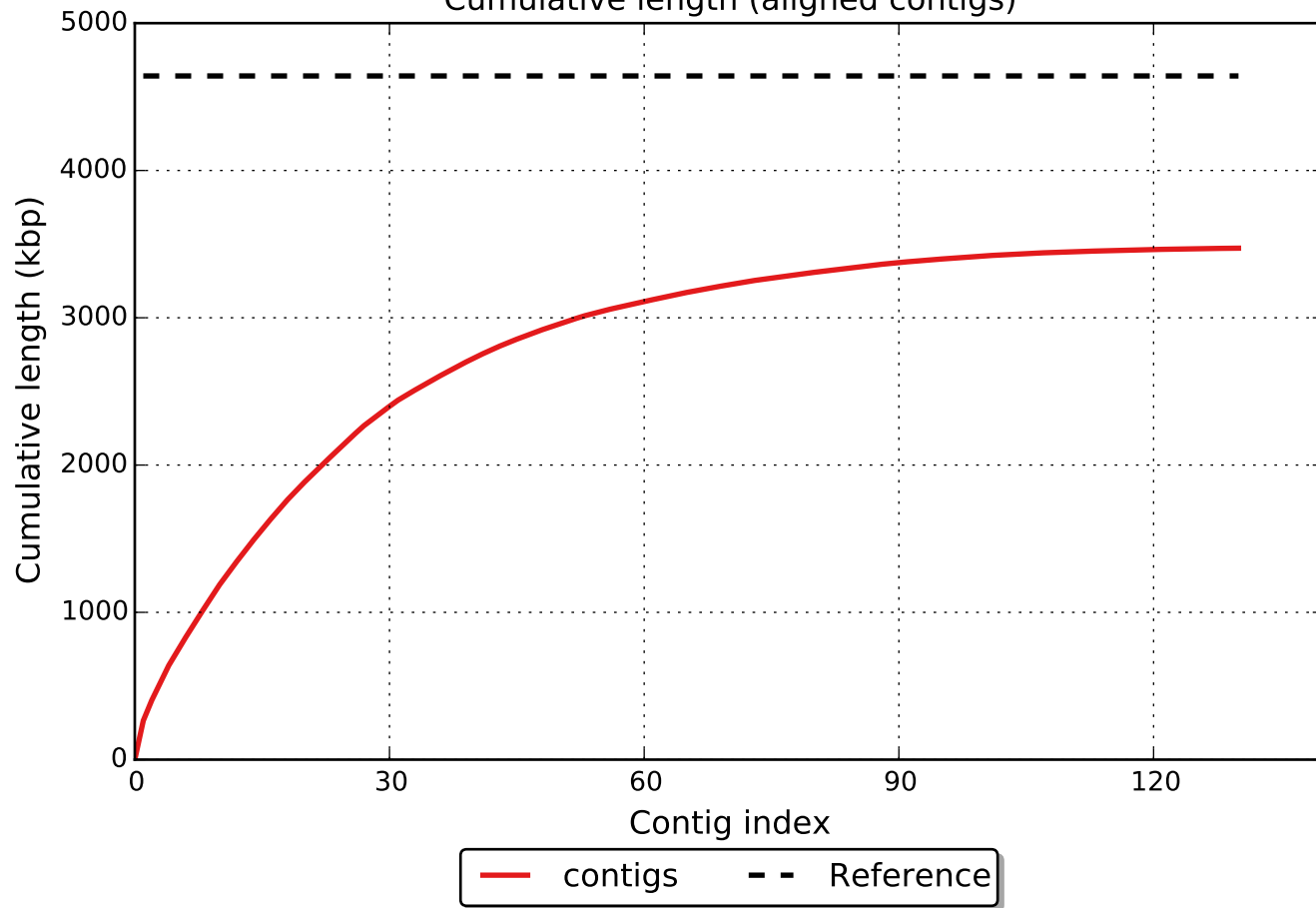
# GC content



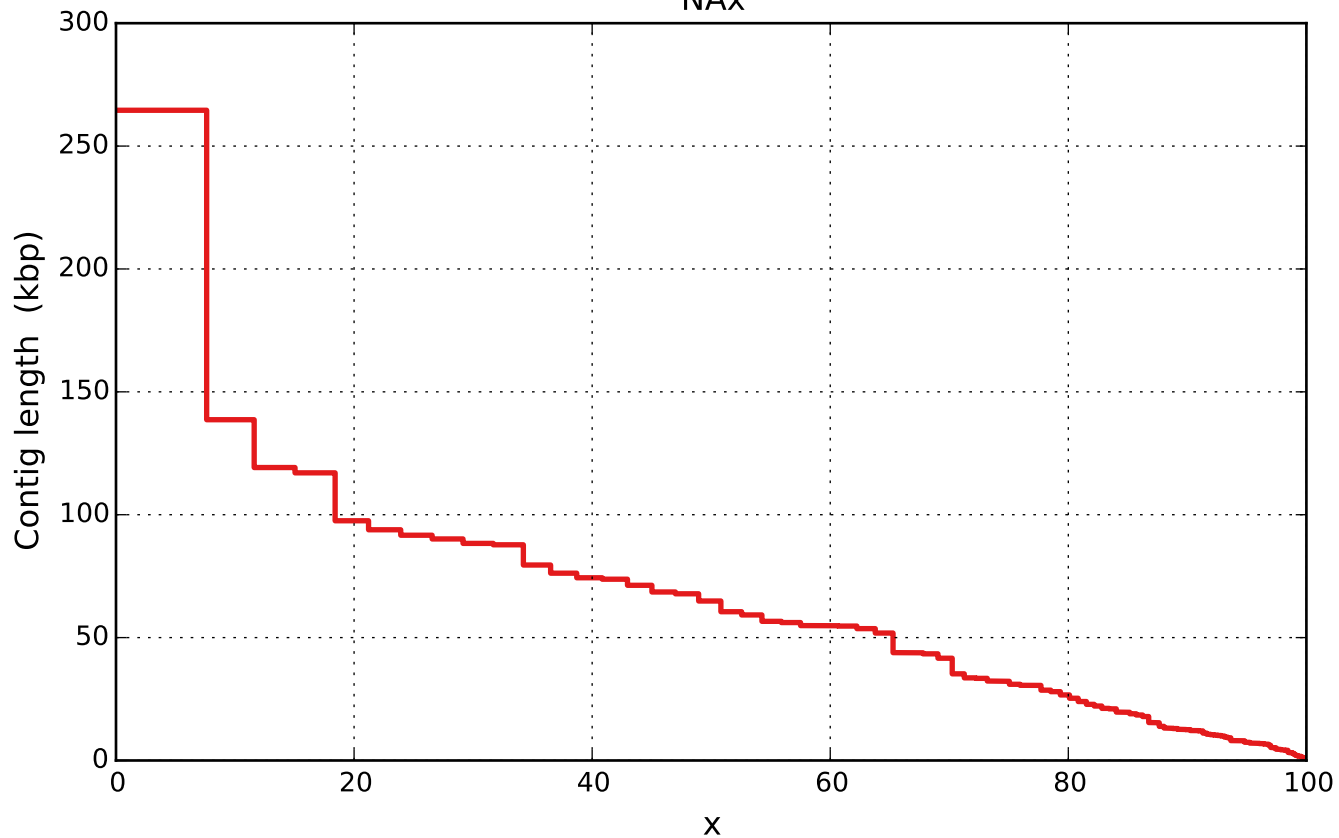




Cumulative length (aligned contigs)



NAx



contigs

NGAx

