

# Report

	contigs
# contigs ( $\geq 1000$ bp)	66
# contigs ( $\geq 5000$ bp)	46
# contigs ( $\geq 10000$ bp)	36
# contigs ( $\geq 25000$ bp)	24
# contigs ( $\geq 50000$ bp)	14
Total length ( $\geq 1000$ bp)	1964897
Total length ( $\geq 5000$ bp)	1920590
Total length ( $\geq 10000$ bp)	1848374
Total length ( $\geq 25000$ bp)	1668715
Total length ( $\geq 50000$ bp)	1334363
# contigs	70
Largest contig	264572
Total length	1968103
Reference length	4641652
GC (%)	50.82
Reference GC (%)	50.79
N50	66357
N75	33667
L50	9
L75	18
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	307071
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	42.324
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	542.63
# indels per 100 kbp	0.87
Largest alignment	264572
NA50	64886
NGA50	-
NA75	32331
LA50	10
LA75	20

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	10660
# indels	17
# short indels	17
# long indels	0
Indels length	23

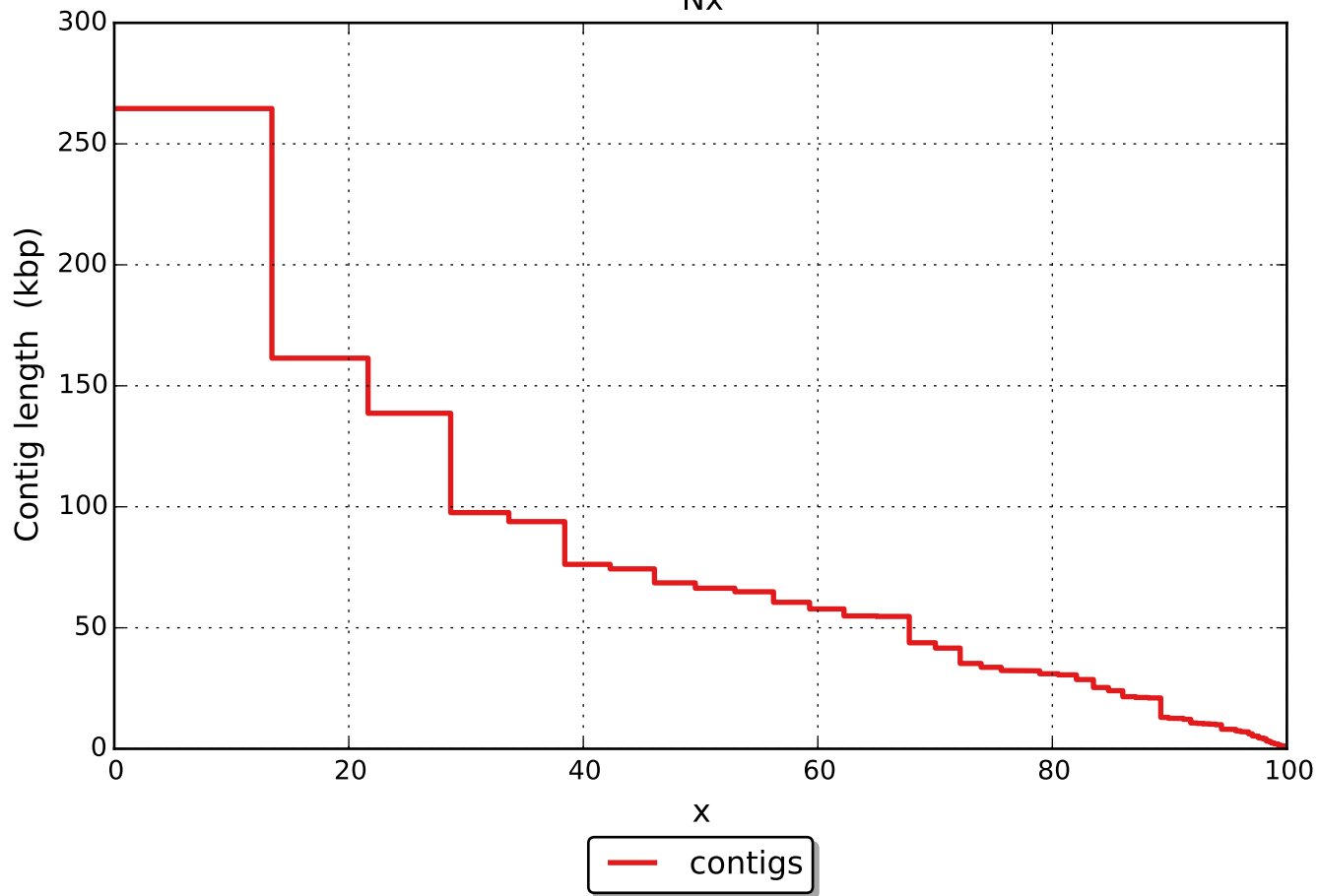
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

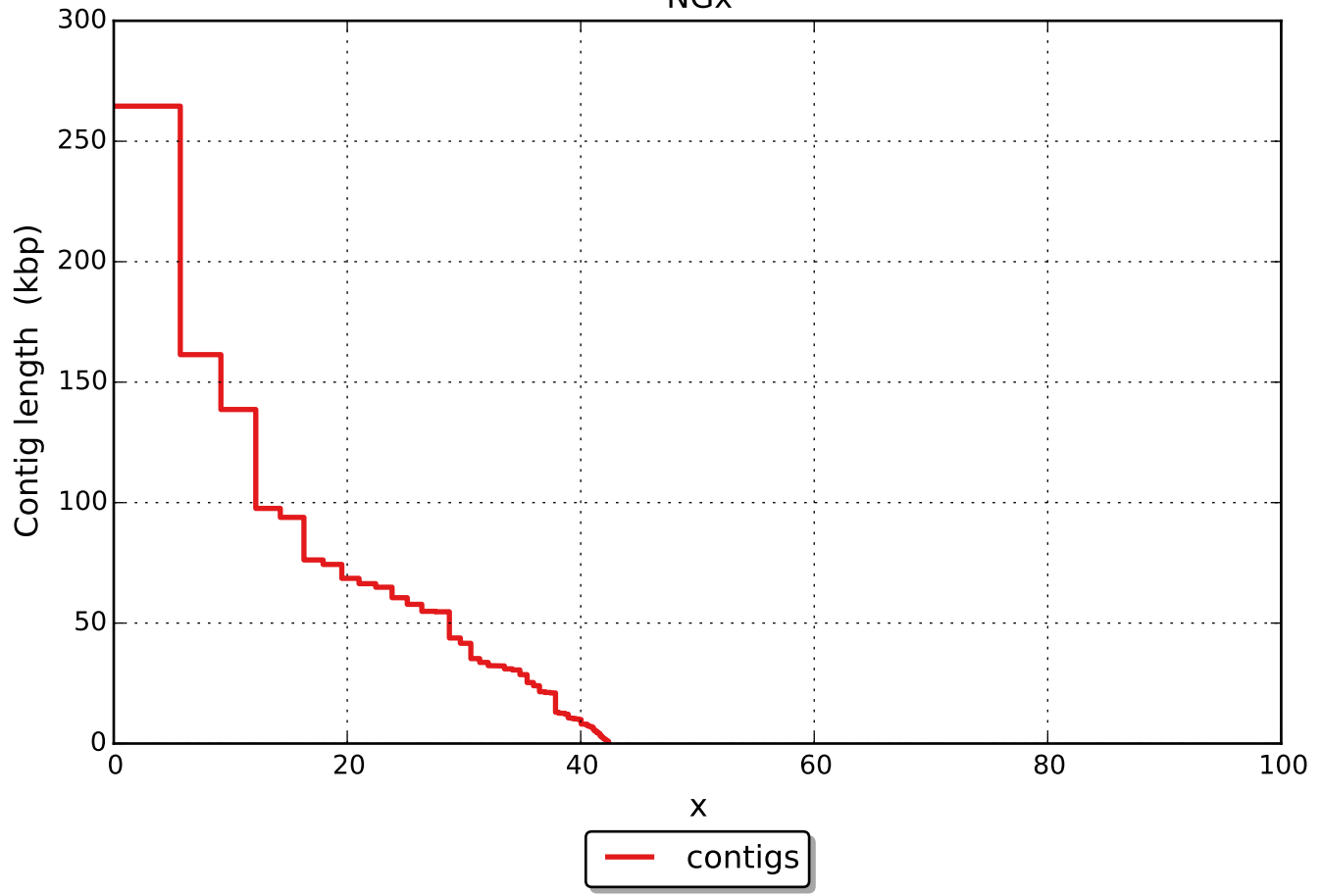
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

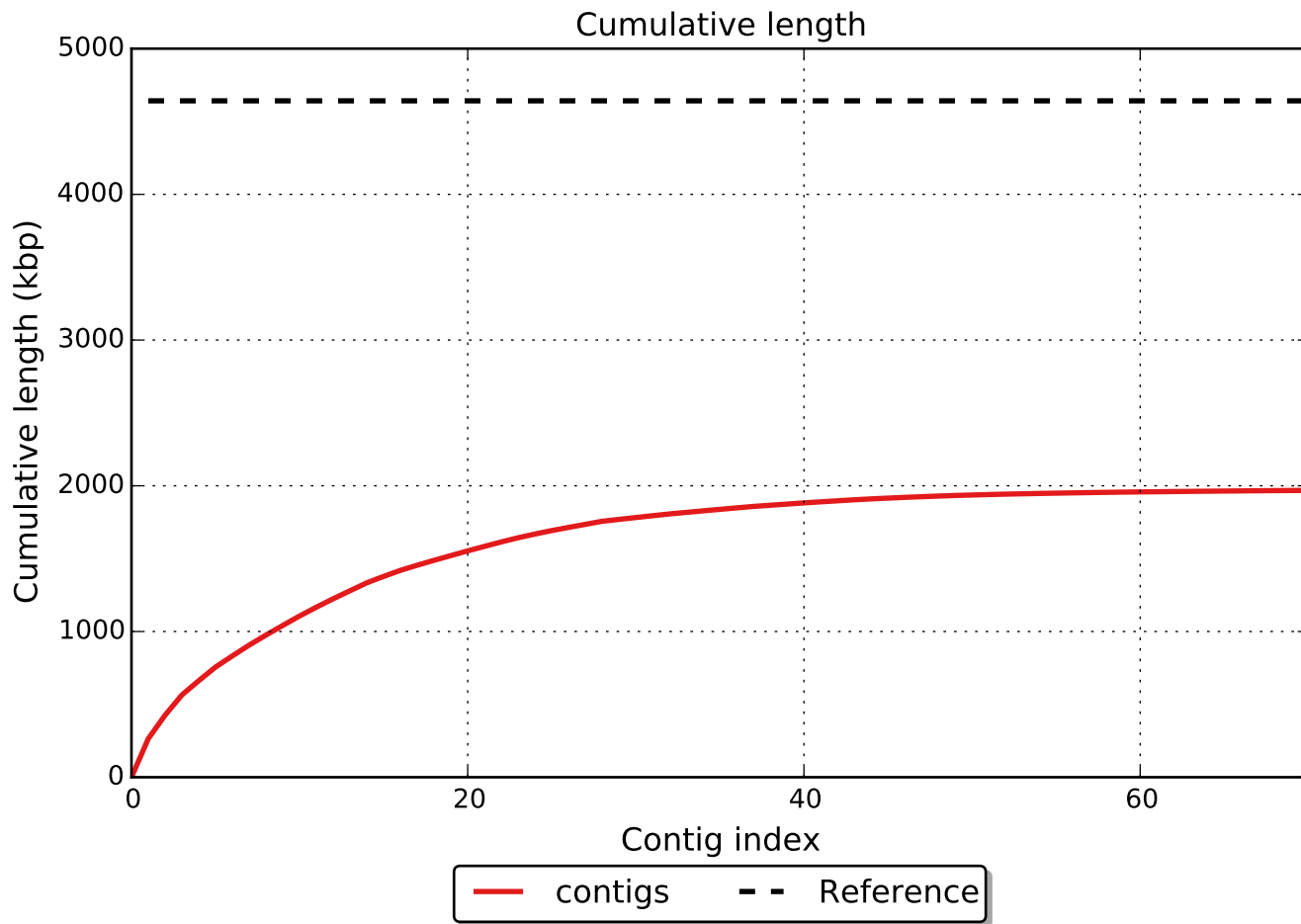
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

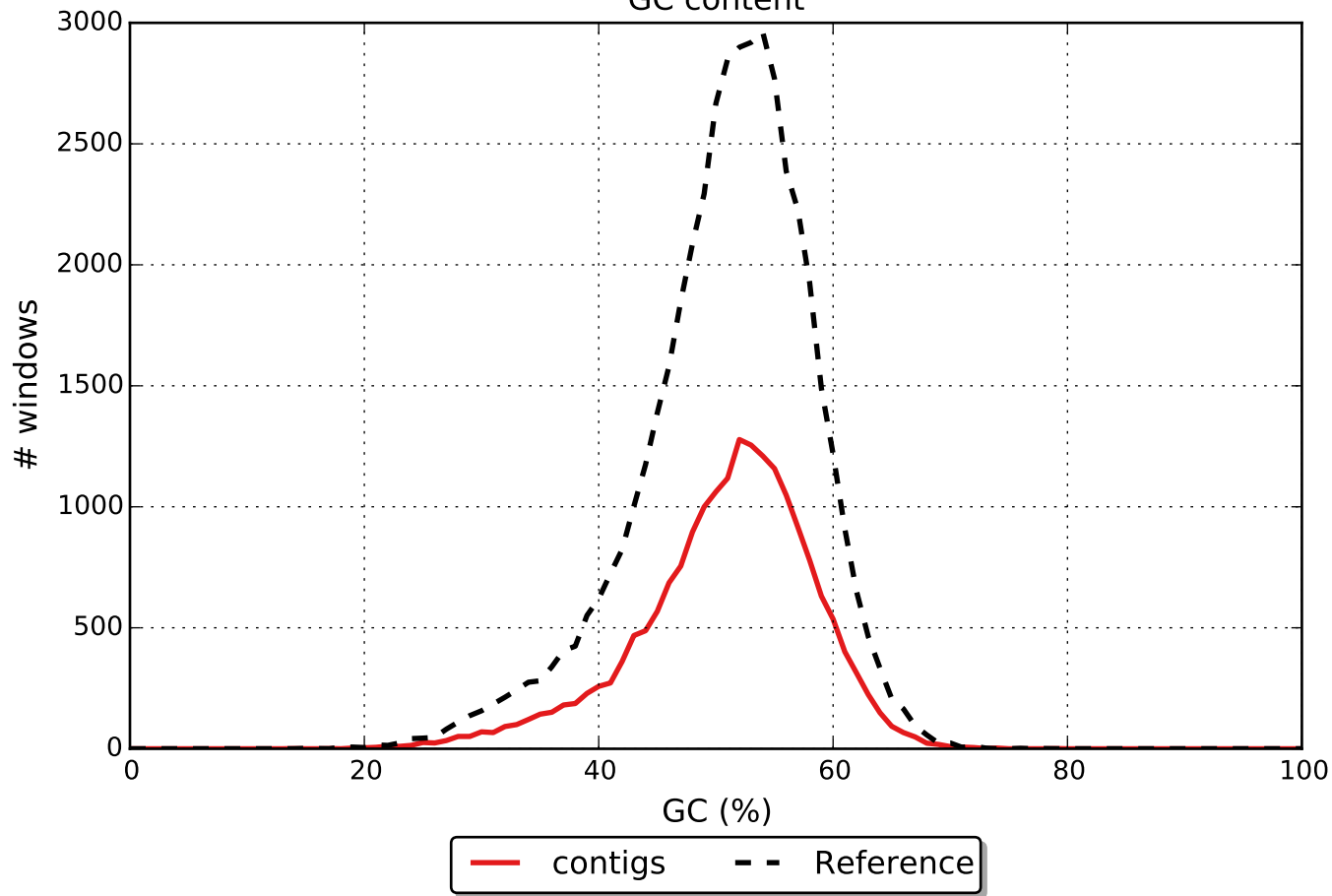


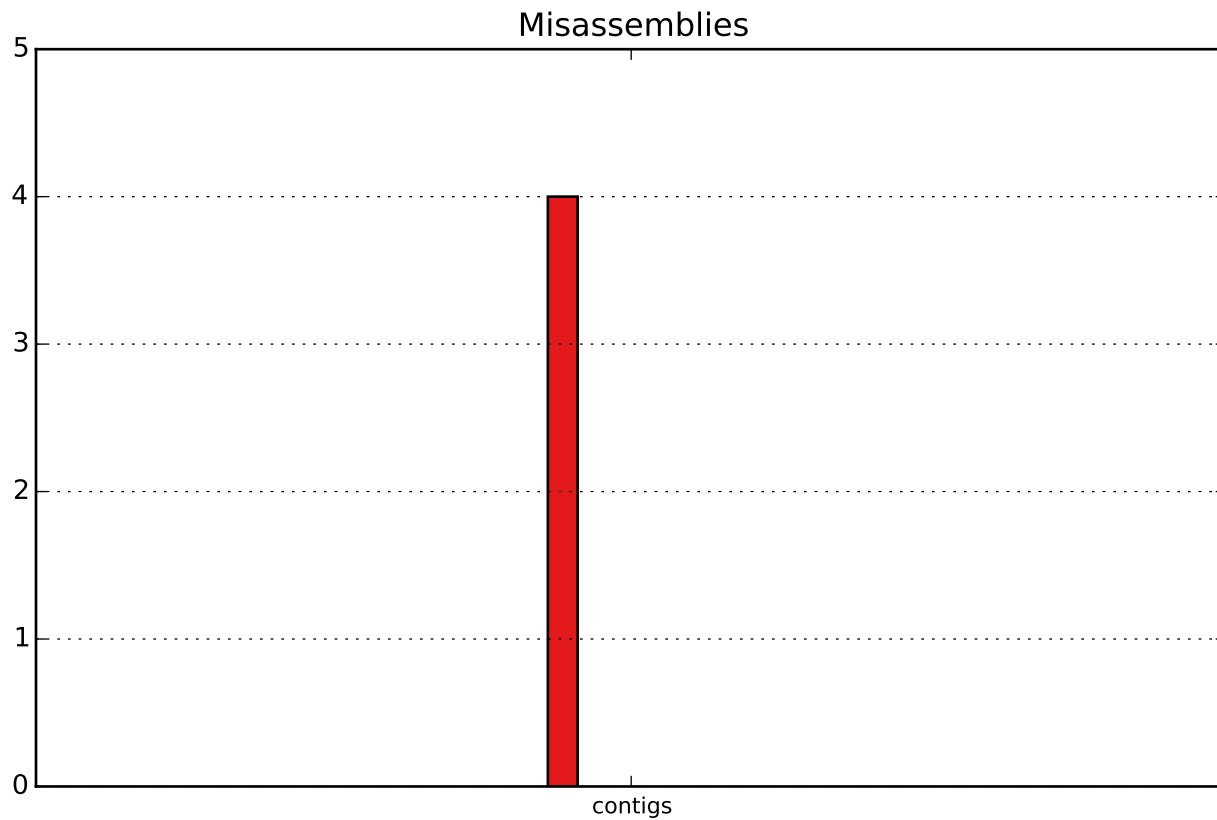
NGx





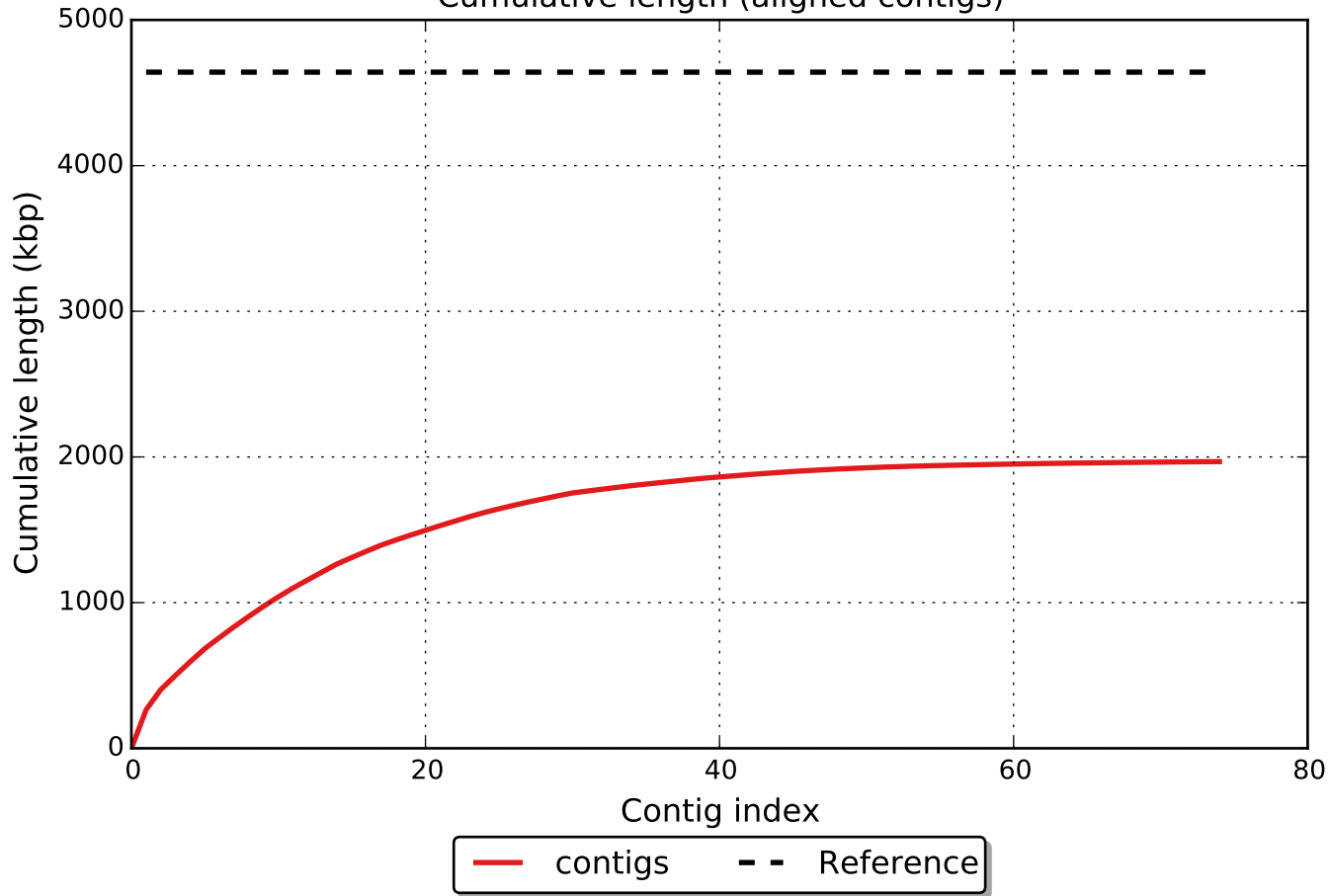
# GC content



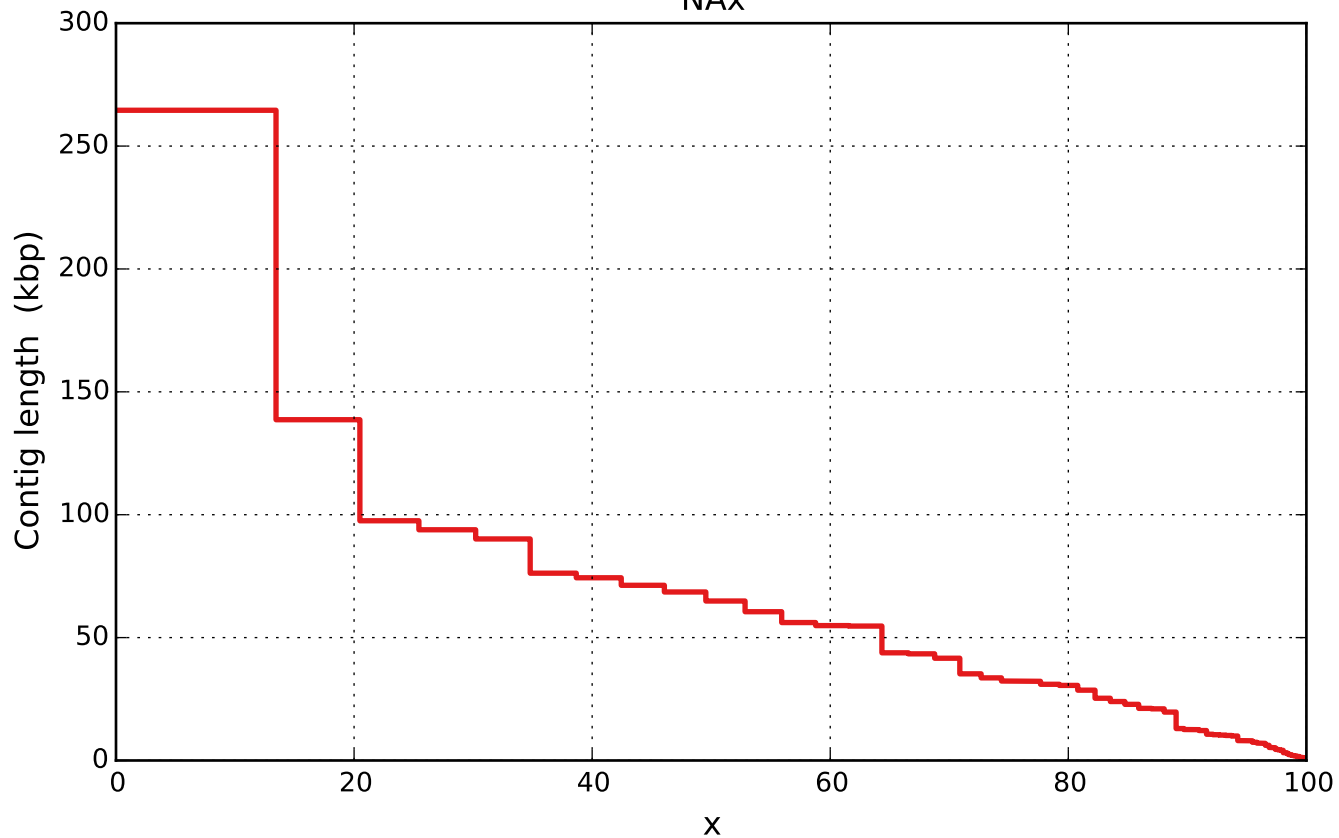




Cumulative length (aligned contigs)

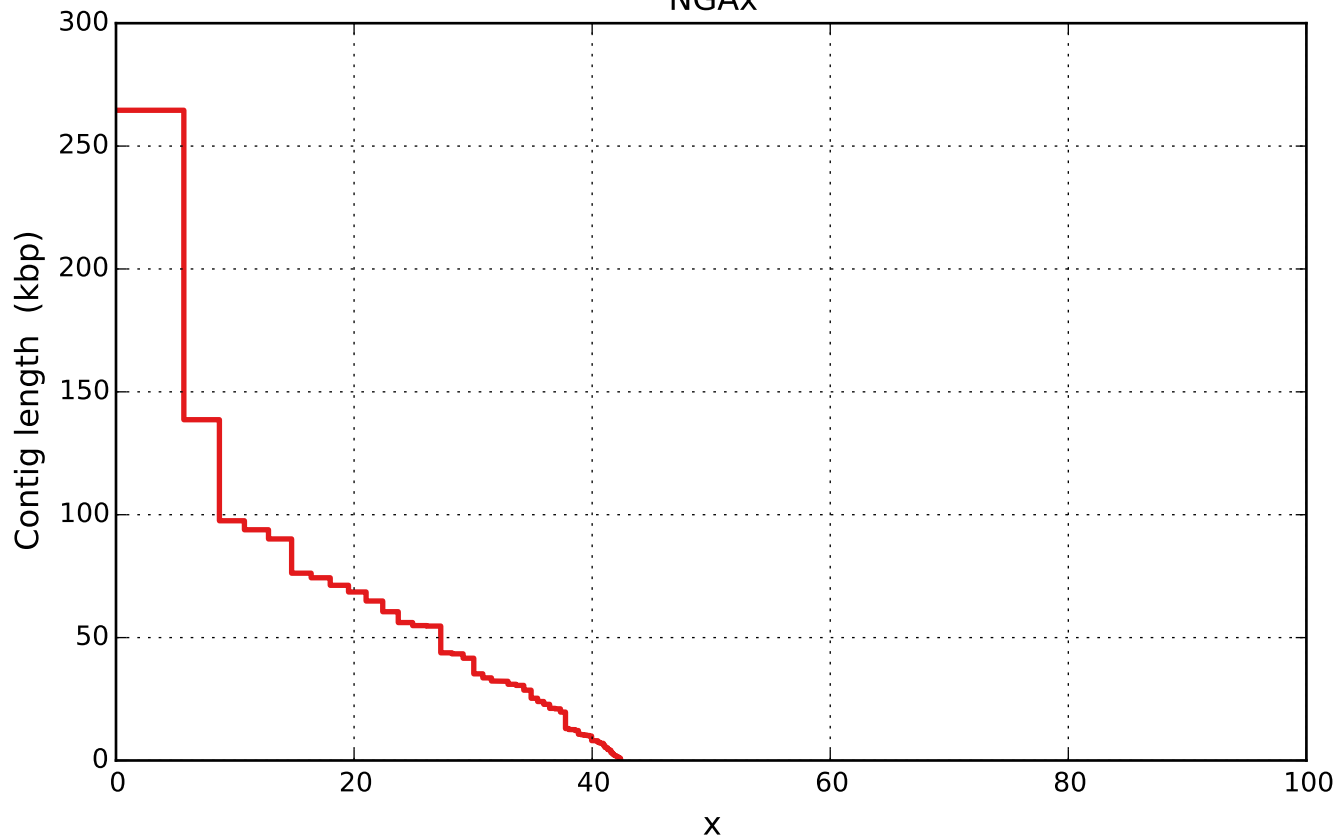


NAx



contigs

NGAx



contigs