

## Report

	contigs
# contigs ( $\geq 1000$ bp)	84
# contigs ( $\geq 5000$ bp)	55
# contigs ( $\geq 10000$ bp)	50
# contigs ( $\geq 25000$ bp)	41
# contigs ( $\geq 50000$ bp)	32
Total length ( $\geq 1000$ bp)	4498510
Total length ( $\geq 5000$ bp)	4434113
Total length ( $\geq 10000$ bp)	4397044
Total length ( $\geq 25000$ bp)	4241448
Total length ( $\geq 50000$ bp)	3927769
# contigs	112
Largest contig	431470
Total length	4516104
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.78
N50	105688
NG50	105224
N75	69056
NG75	63924
L50	10
LG50	11
L75	24
LG75	25
# misassemblies	7
# misassembled contigs	2
Misassembled contigs length	198850
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.899
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	953.16
# indels per 100 kbp	1.03
Largest alignment	431470
NA50	96103
NGA50	96103
NA75	63011
NGA75	60735
LA50	11
LGA50	11
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	7
# relocations	7
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	198850
# local misassemblies	5
# mismatches	41543
# indels	45
# short indels	44
# long indels	1
Indels length	54

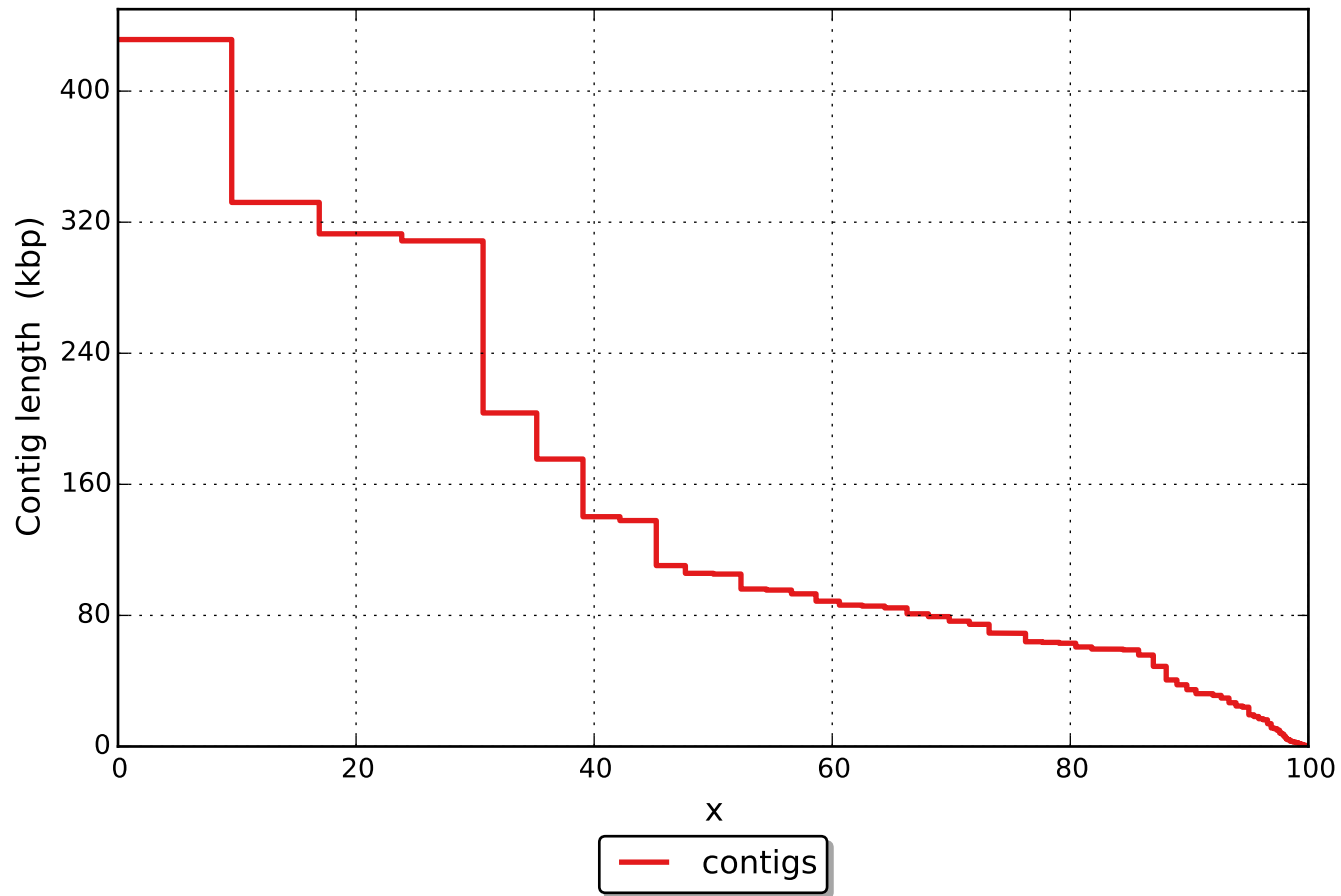
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

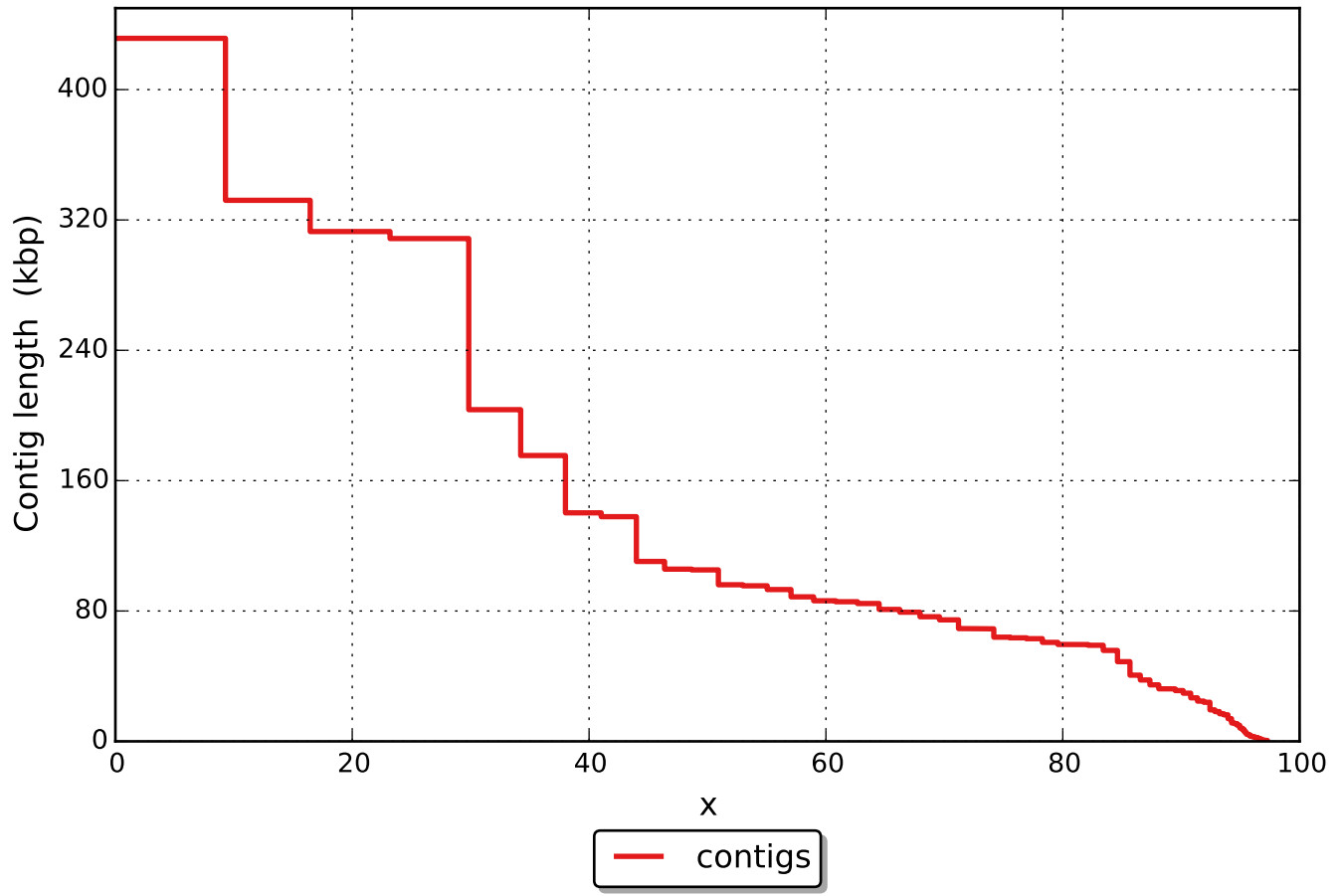
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

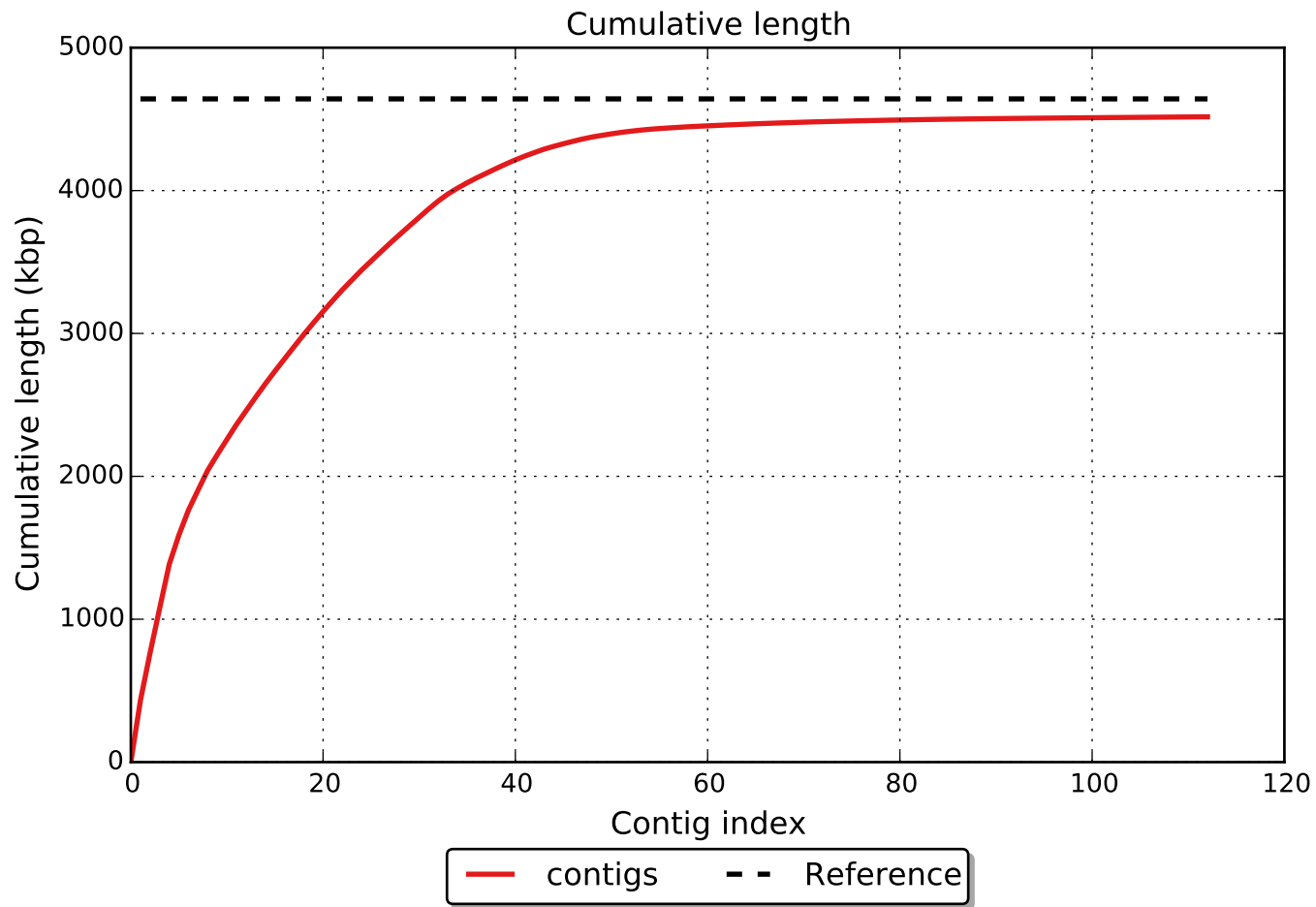
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

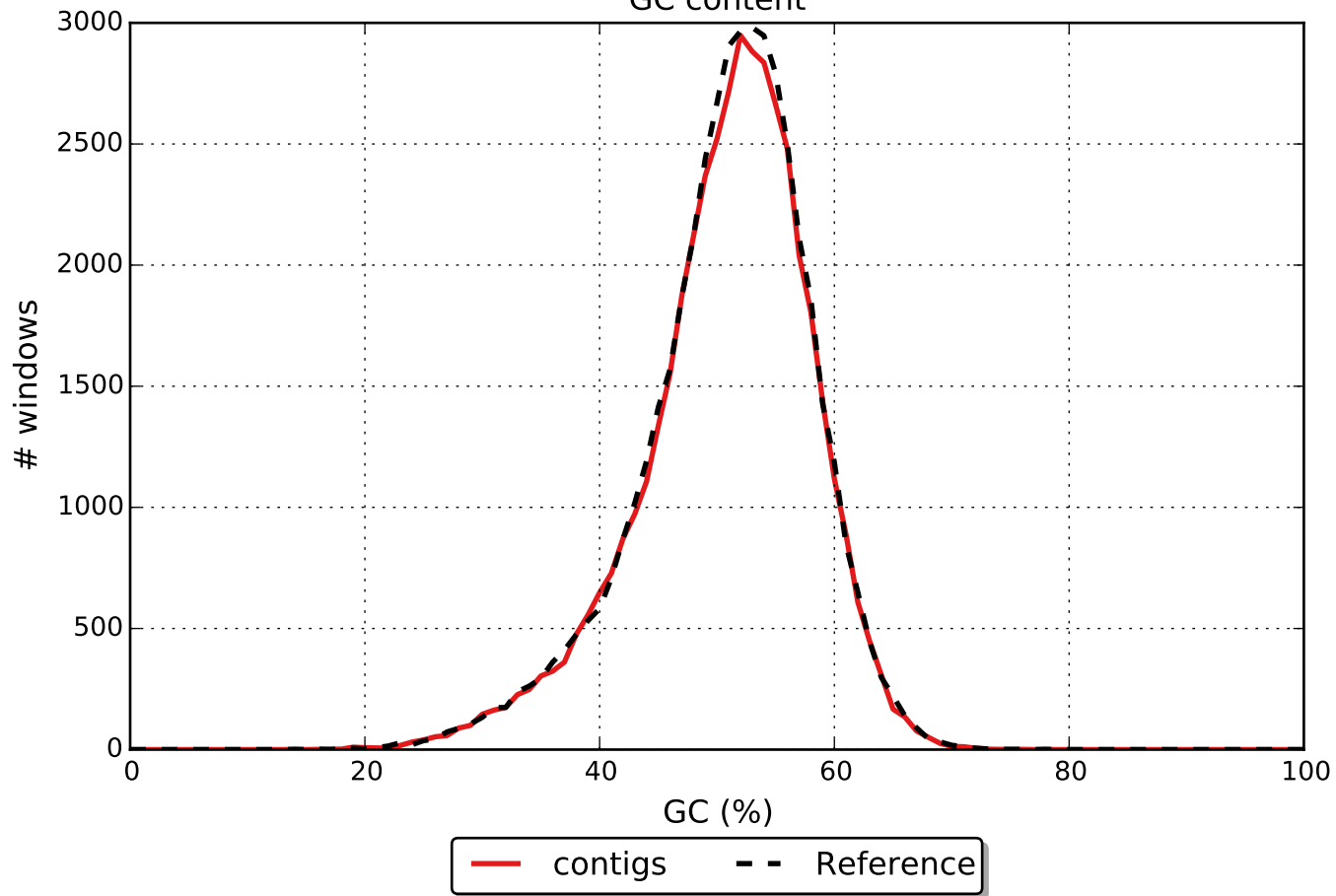


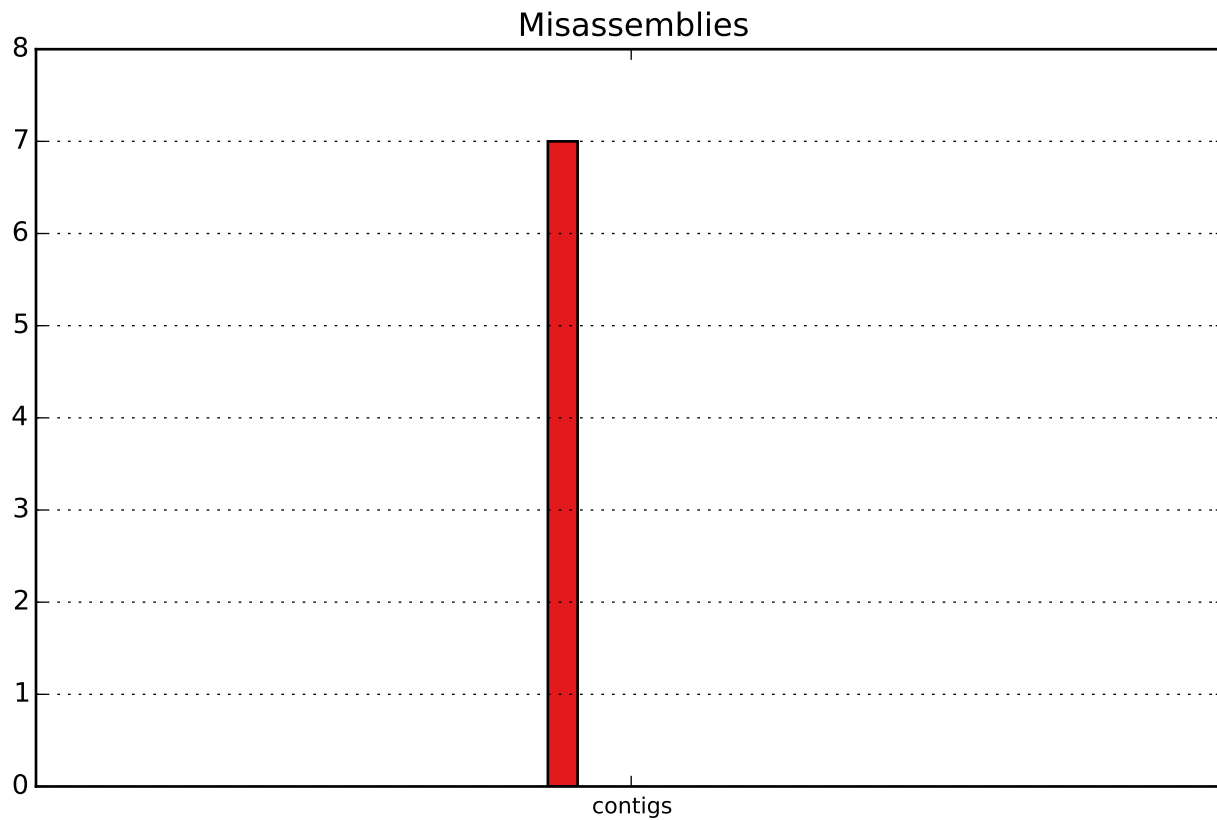
NGx





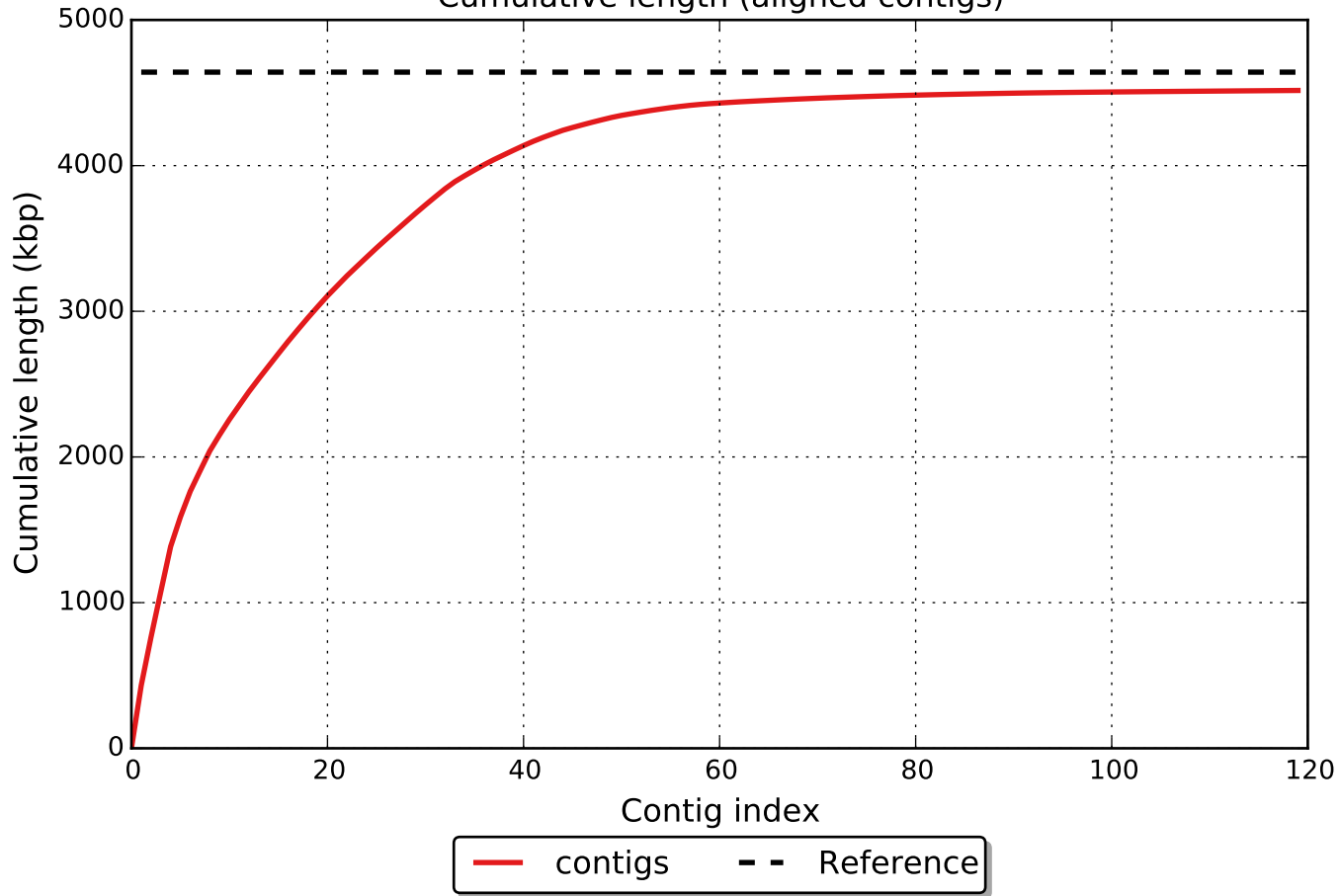
GC content



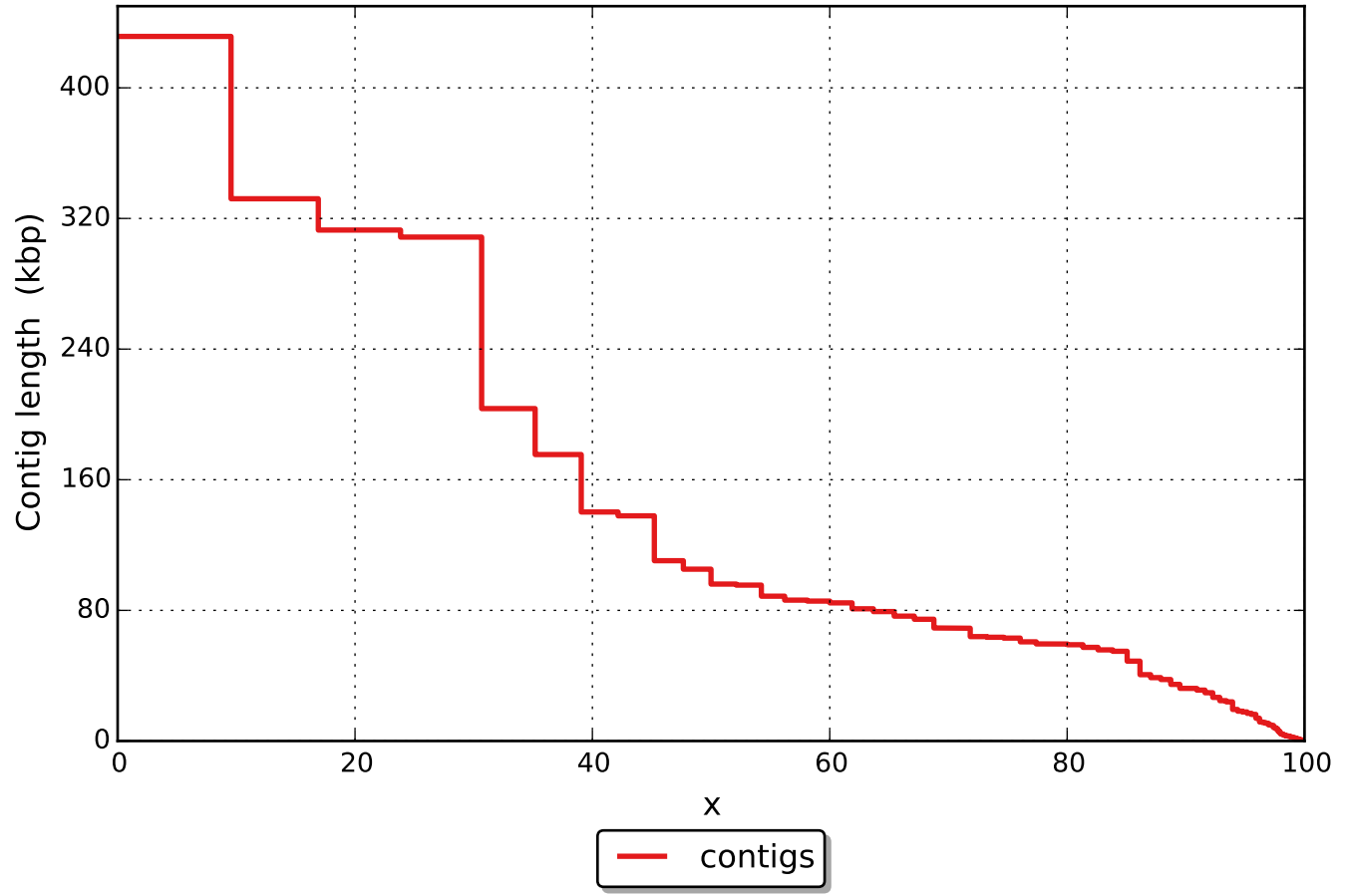




Cumulative length (aligned contigs)



NAx



# NGAx

