

## Report

	contigs
# contigs ( $\geq 0$ bp)	5972
# contigs ( $\geq 1000$ bp)	800
# contigs ( $\geq 5000$ bp)	0
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	3621725
Total length ( $\geq 1000$ bp)	1131313
Total length ( $\geq 5000$ bp)	0
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	2840
Largest contig	4591
Total length	2555834
Reference length	4641652
GC (%)	50.87
Reference GC (%)	50.79
N50	932
NG50	567
N75	688
L50	952
LG50	2398
L75	1751
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	18057
# local misassemblies	3
# unaligned contigs	0 + 12 part
Unaligned length	564
Genome fraction (%)	54.985
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.14
# indels per 100 kbp	0.67
Largest alignment	4256
NA50	931
NGA50	565
NA75	687
LA50	956
LGA50	2404
LA75	1756

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	8
# relocations	8
# translocations	0
# inversions	0
# misassembled contigs	8
Misassembled contigs length	18057
# local misassemblies	3
# mismatches	361
# indels	17
# short indels	17
# long indels	0
Indels length	22

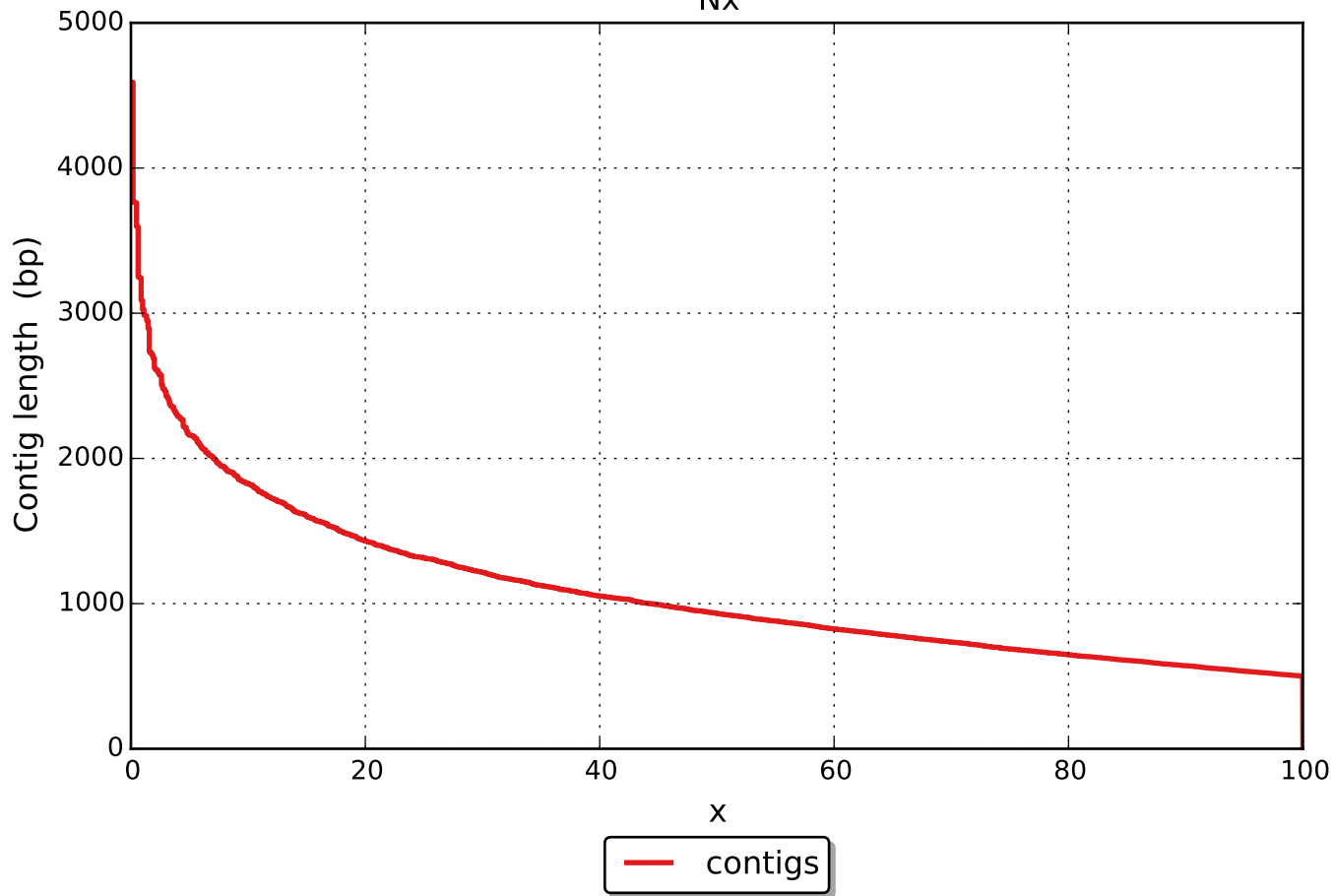
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

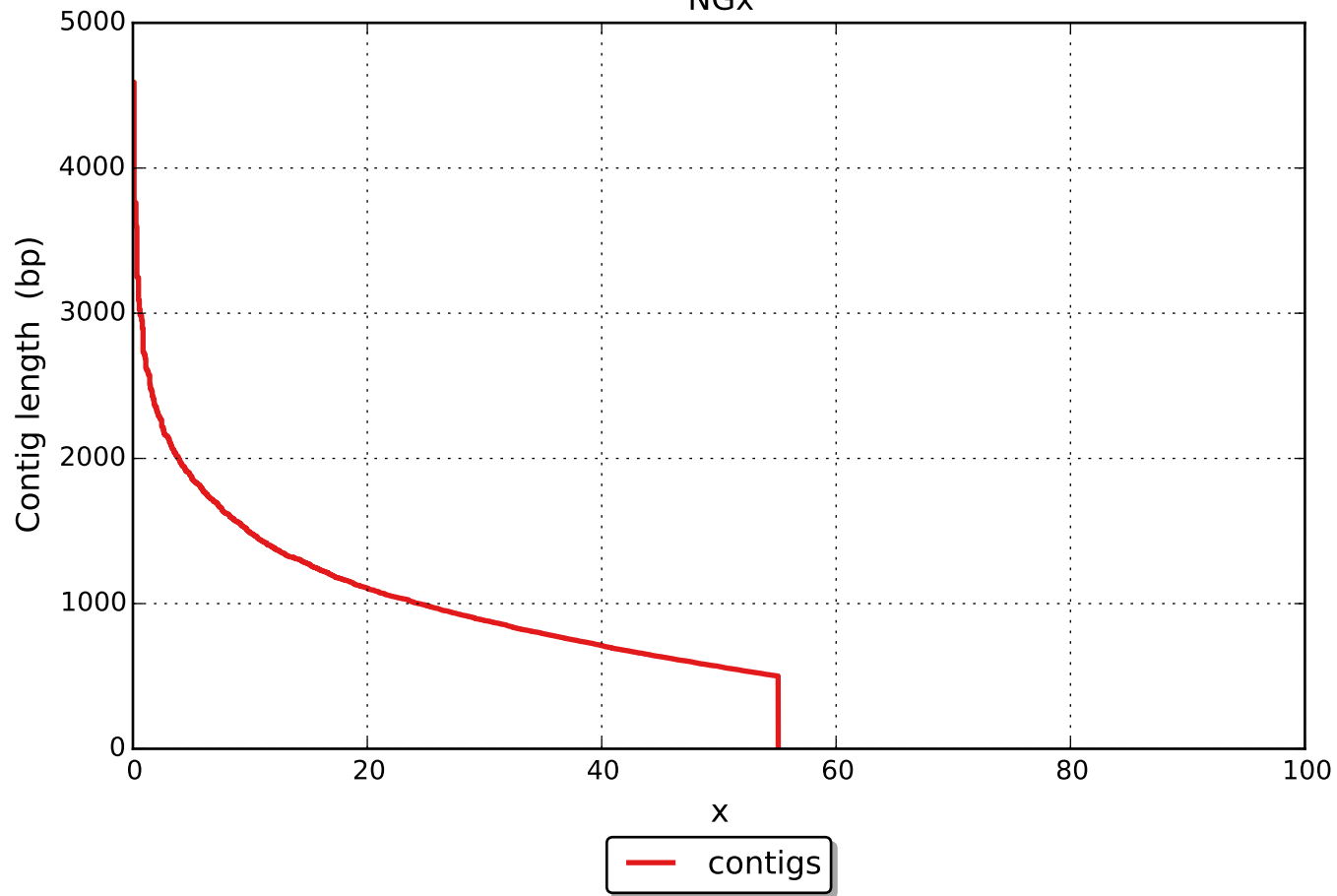
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	12
# with misassembly	0
# both parts are significant	0
Partially unaligned length	564
# N's	0

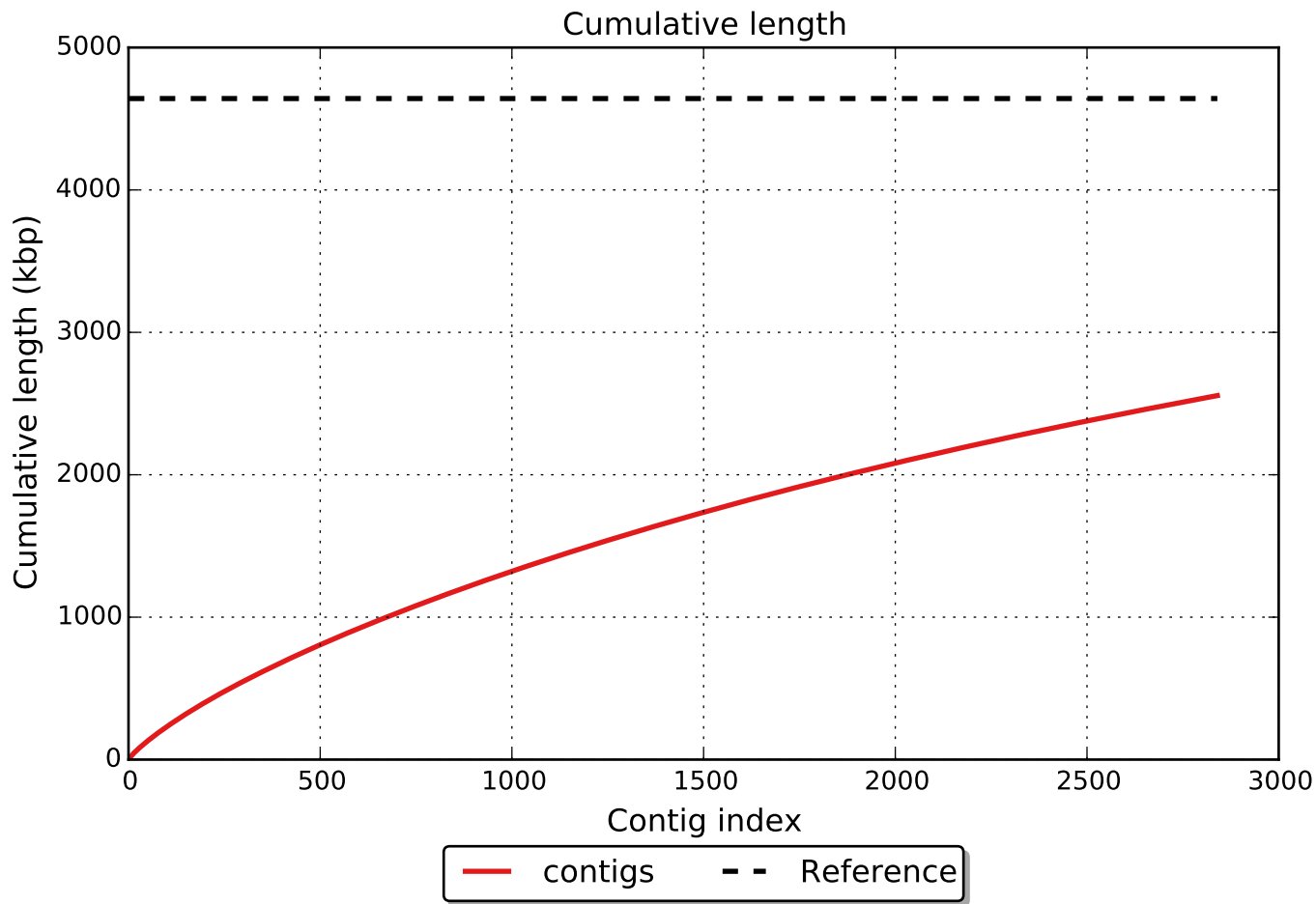
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

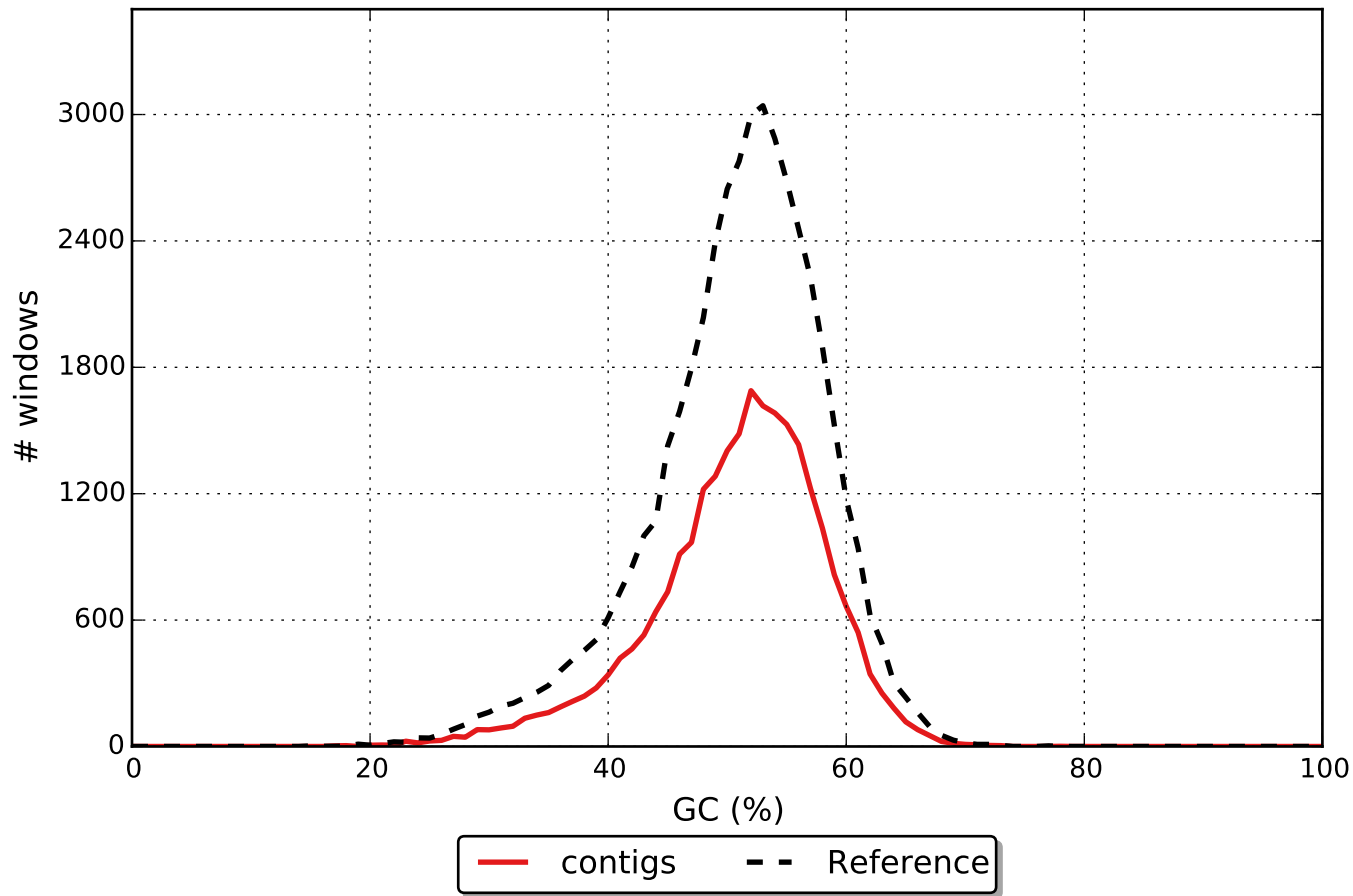


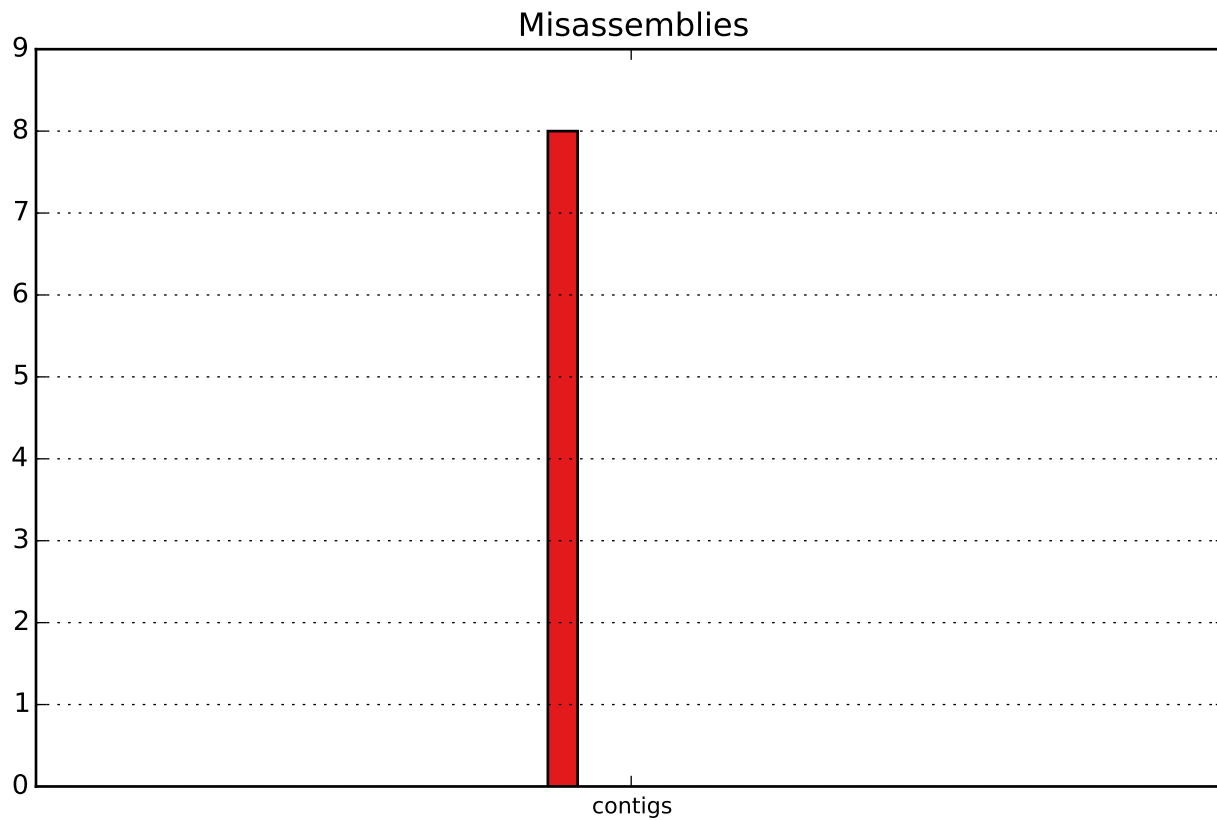
NGx





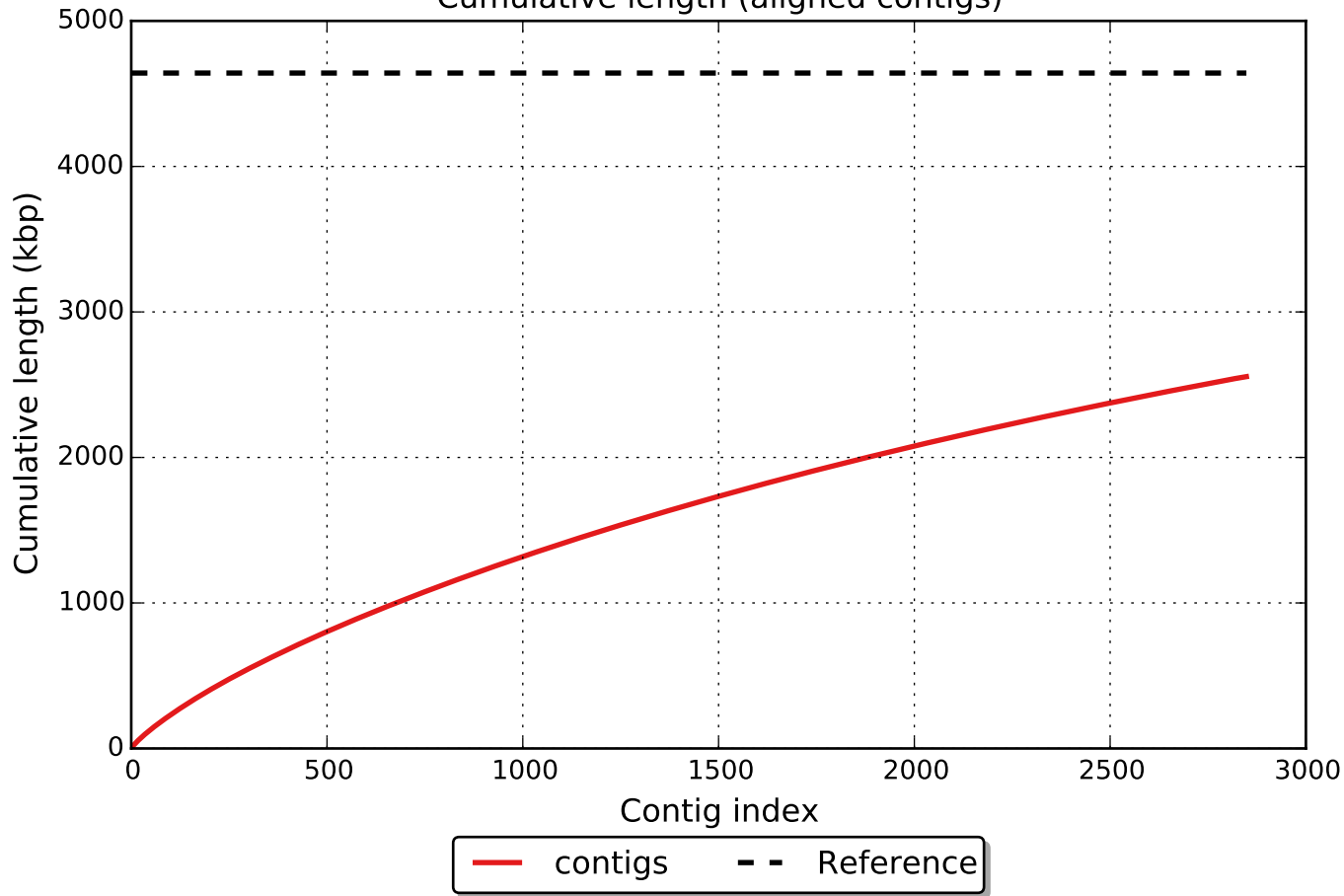
GC content



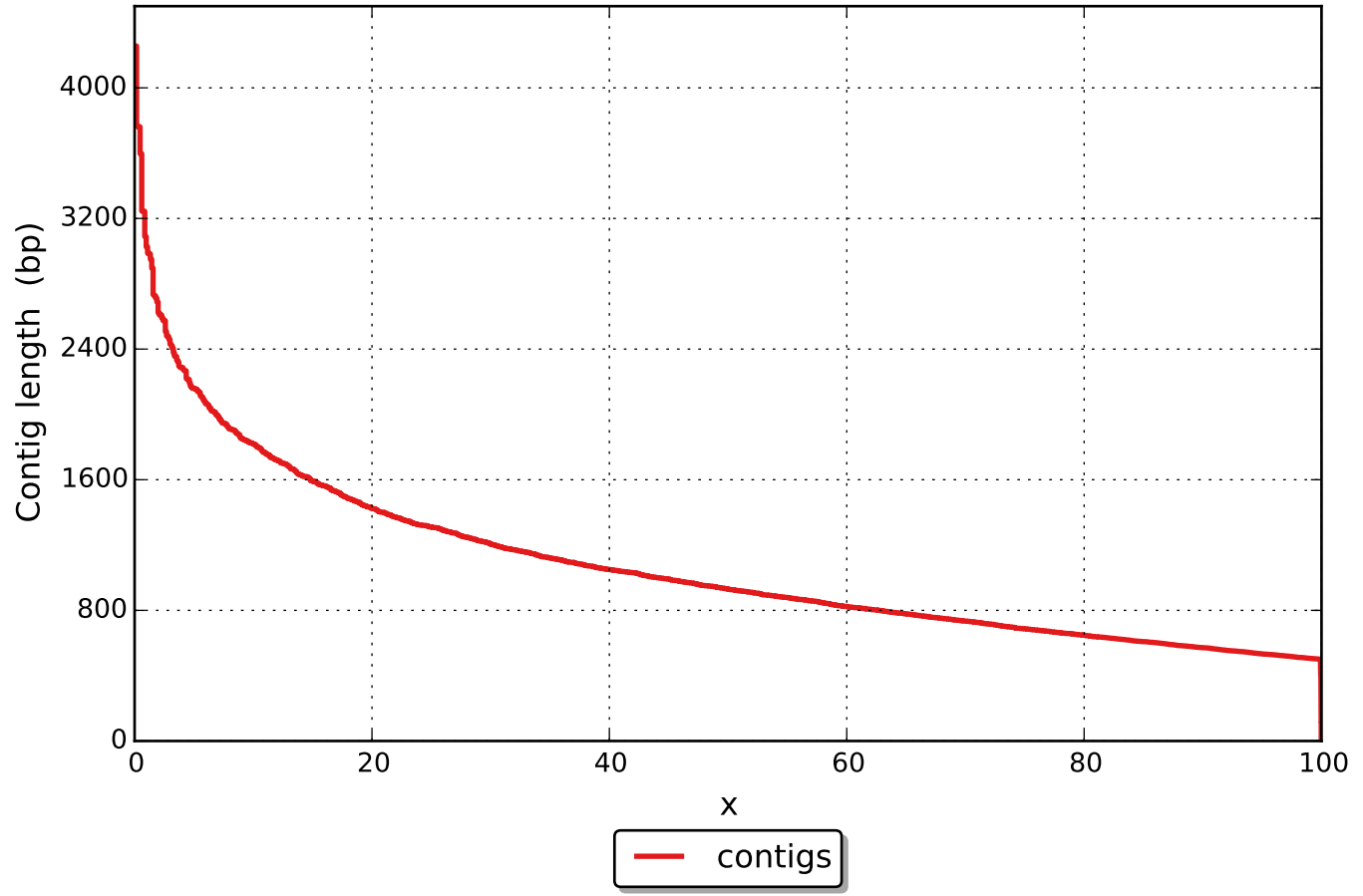




Cumulative length (aligned contigs)



NAx



NGAx

