

## Report

	contigs
# contigs ( $\geq 1000$ bp)	60
# contigs ( $\geq 5000$ bp)	42
# contigs ( $\geq 10000$ bp)	41
# contigs ( $\geq 25000$ bp)	35
# contigs ( $\geq 50000$ bp)	30
Total length ( $\geq 1000$ bp)	4606478
Total length ( $\geq 5000$ bp)	4575859
Total length ( $\geq 10000$ bp)	4568658
Total length ( $\geq 25000$ bp)	4459806
Total length ( $\geq 50000$ bp)	4285593
# contigs	75
Largest contig	527156
Total length	4616403
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.78
N50	197358
NG50	197358
N75	101046
NG75	86132
L50	8
LG50	8
L75	18
LG75	19
# misassemblies	6
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.118
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	679.42
# indels per 100 kbp	0.94
Largest alignment	527156
NA50	197358
NGA50	197358
NA75	101046
NGA75	86132
LA50	8
LGA50	8
LA75	18
LGA75	19

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	6
# relocations	4
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	0
# mismatches	30943
# indels	43
# short indels	43
# long indels	0
Indels length	43

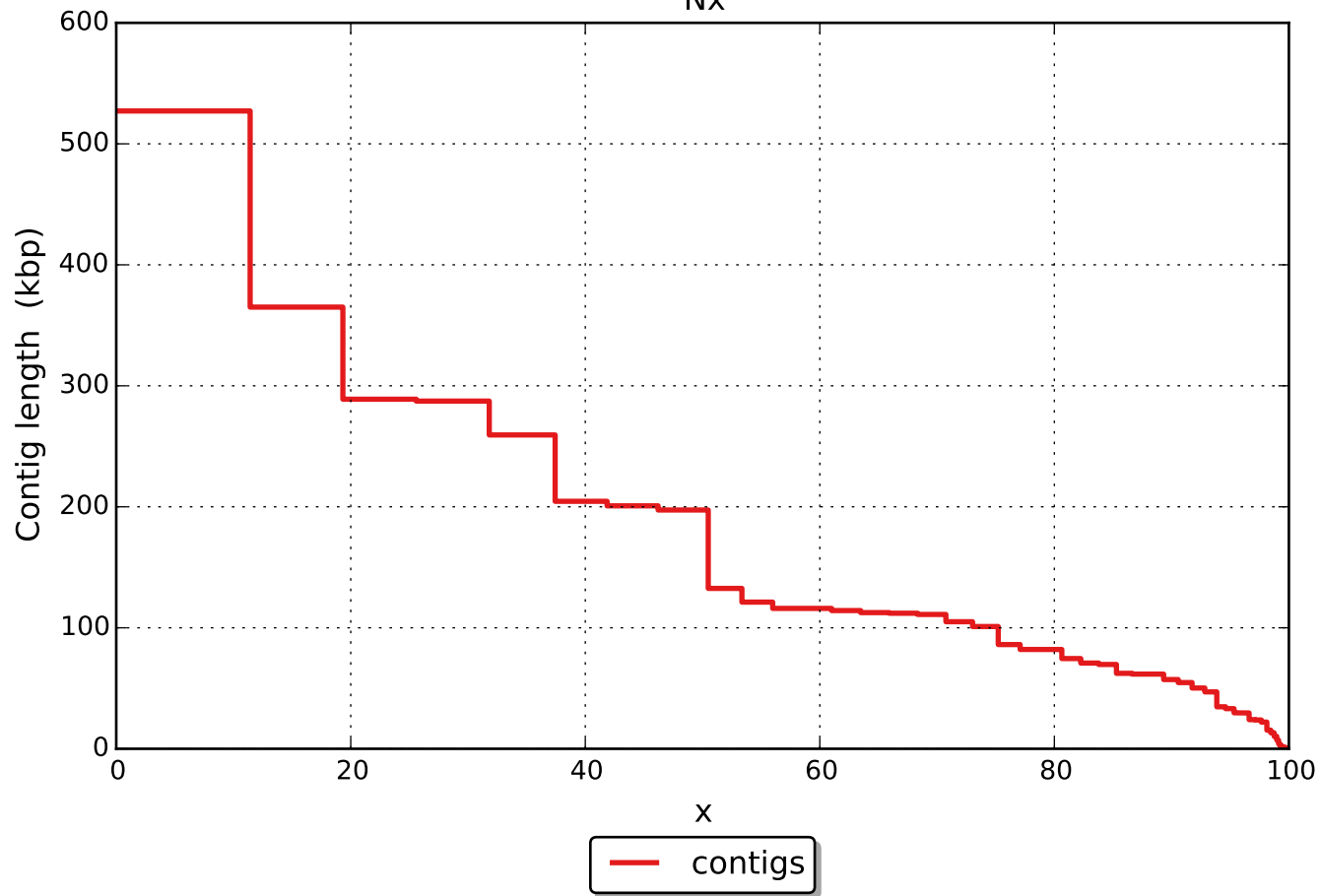
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

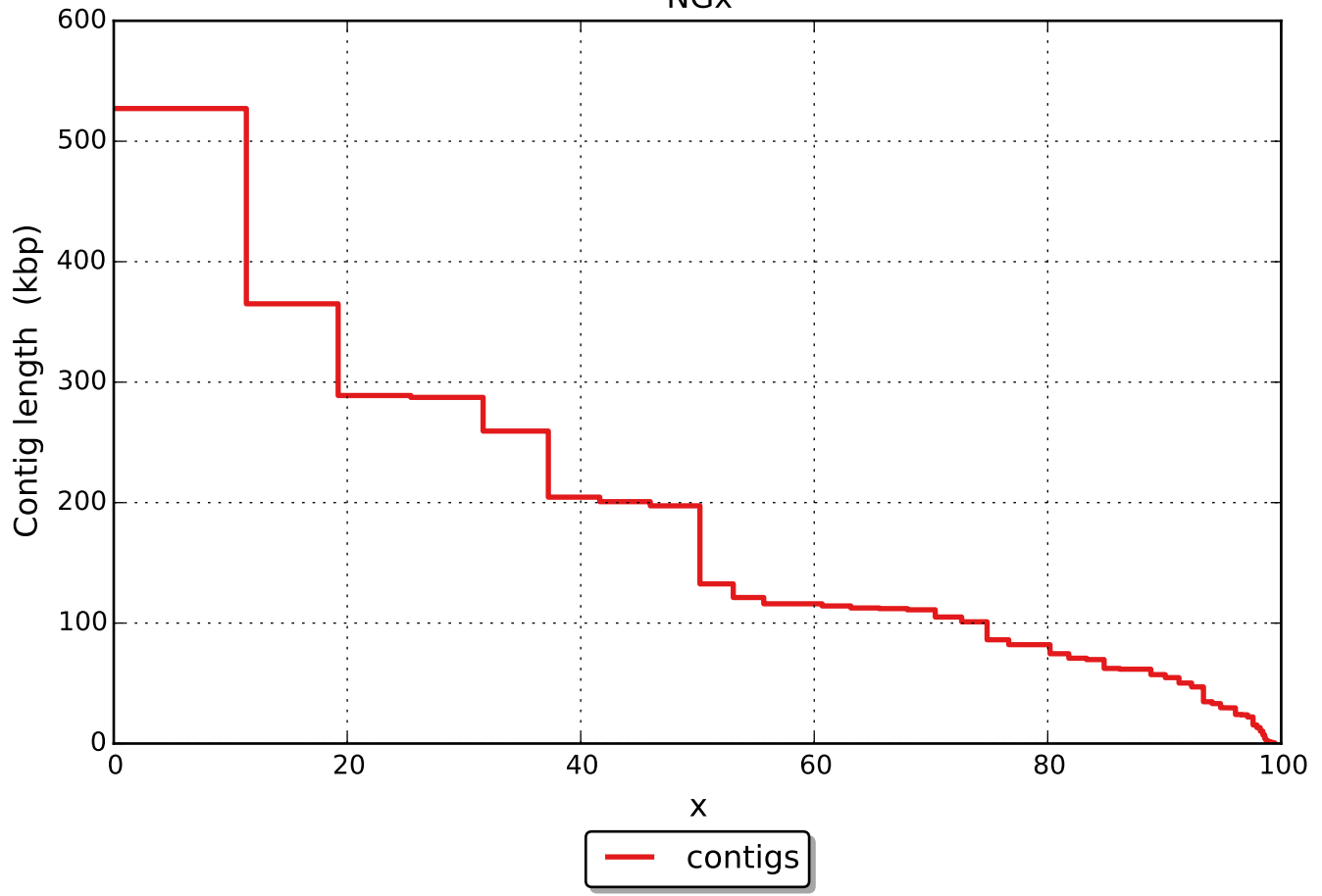
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

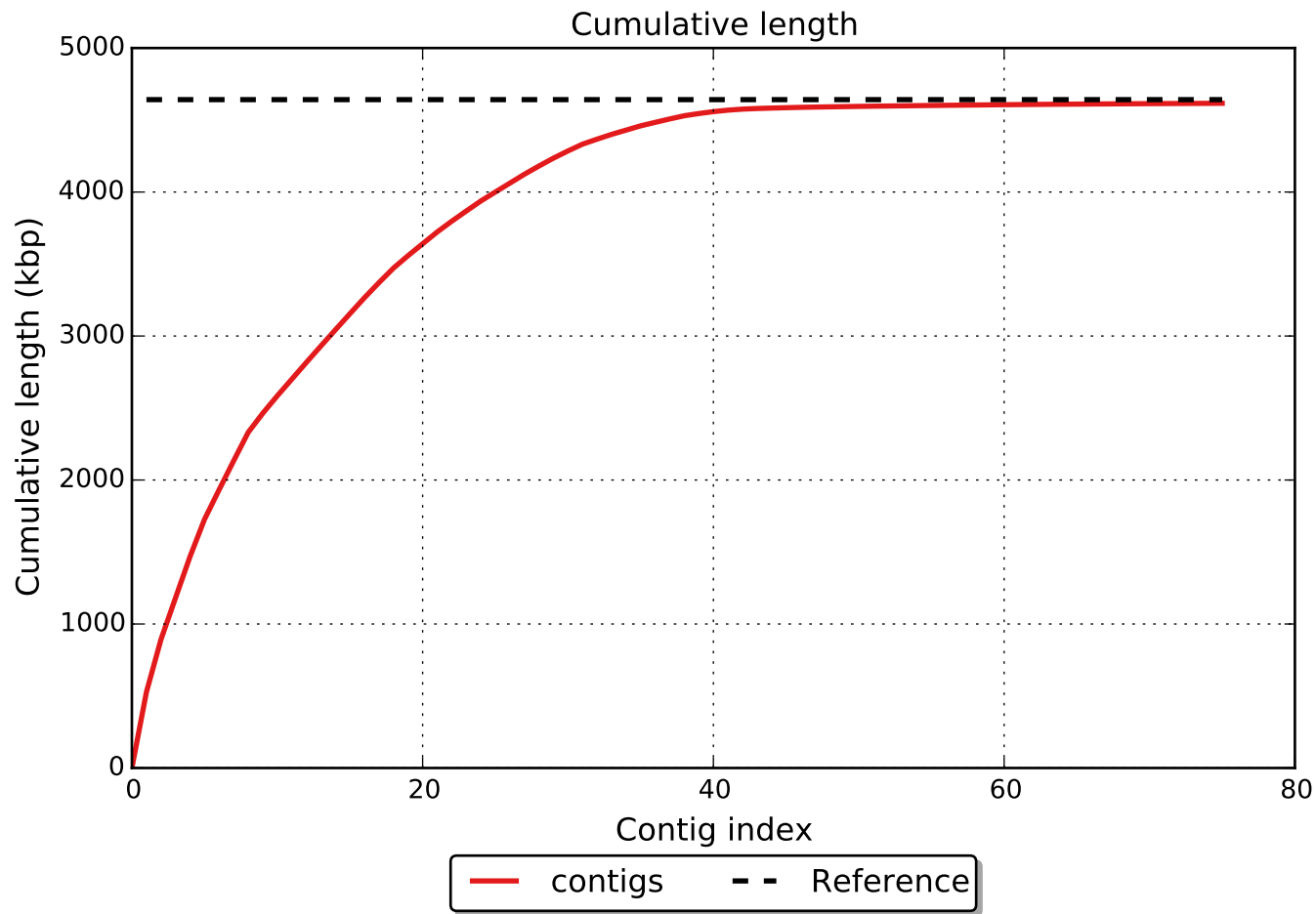
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

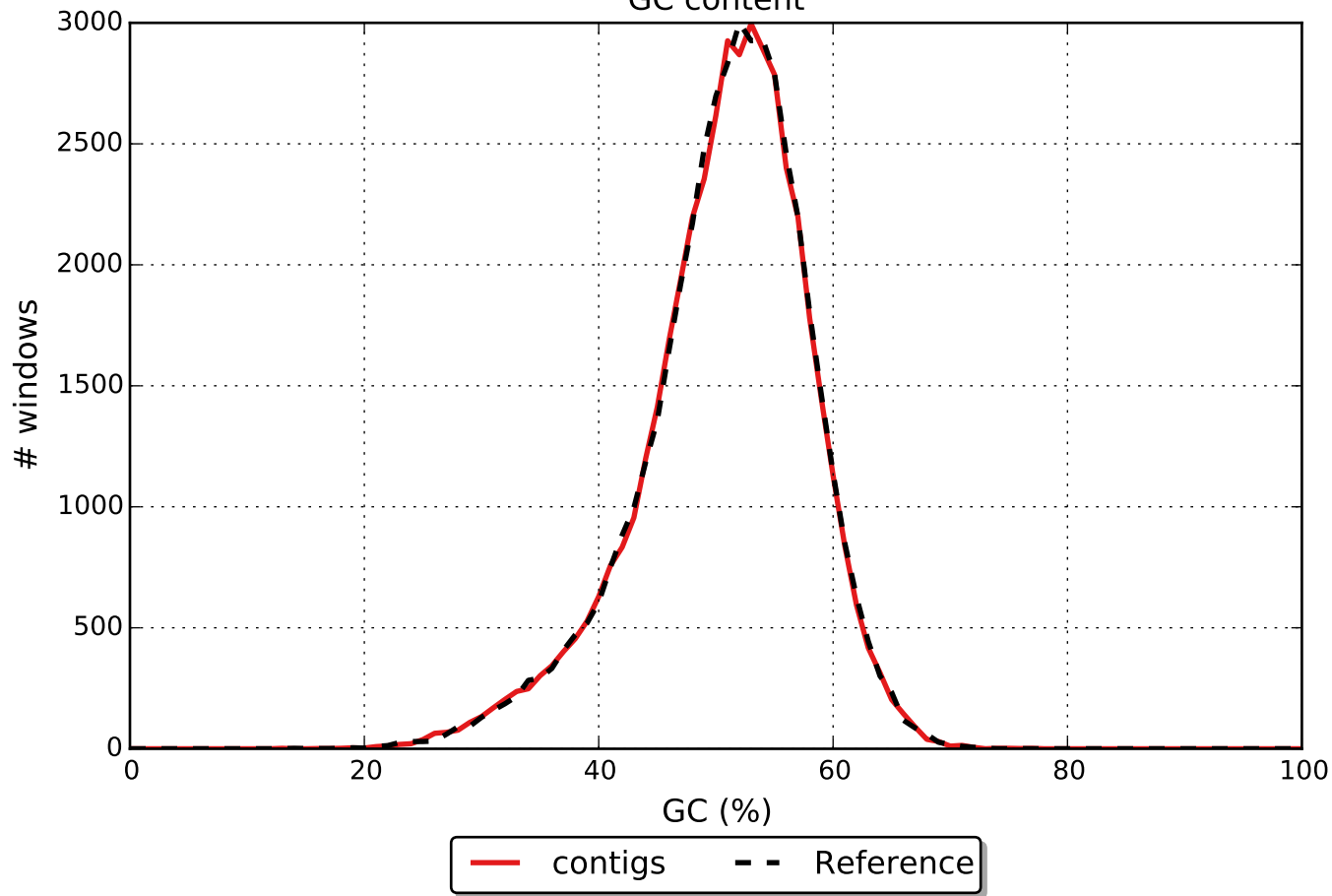


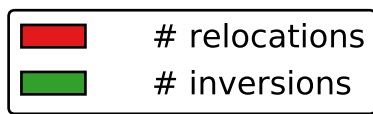
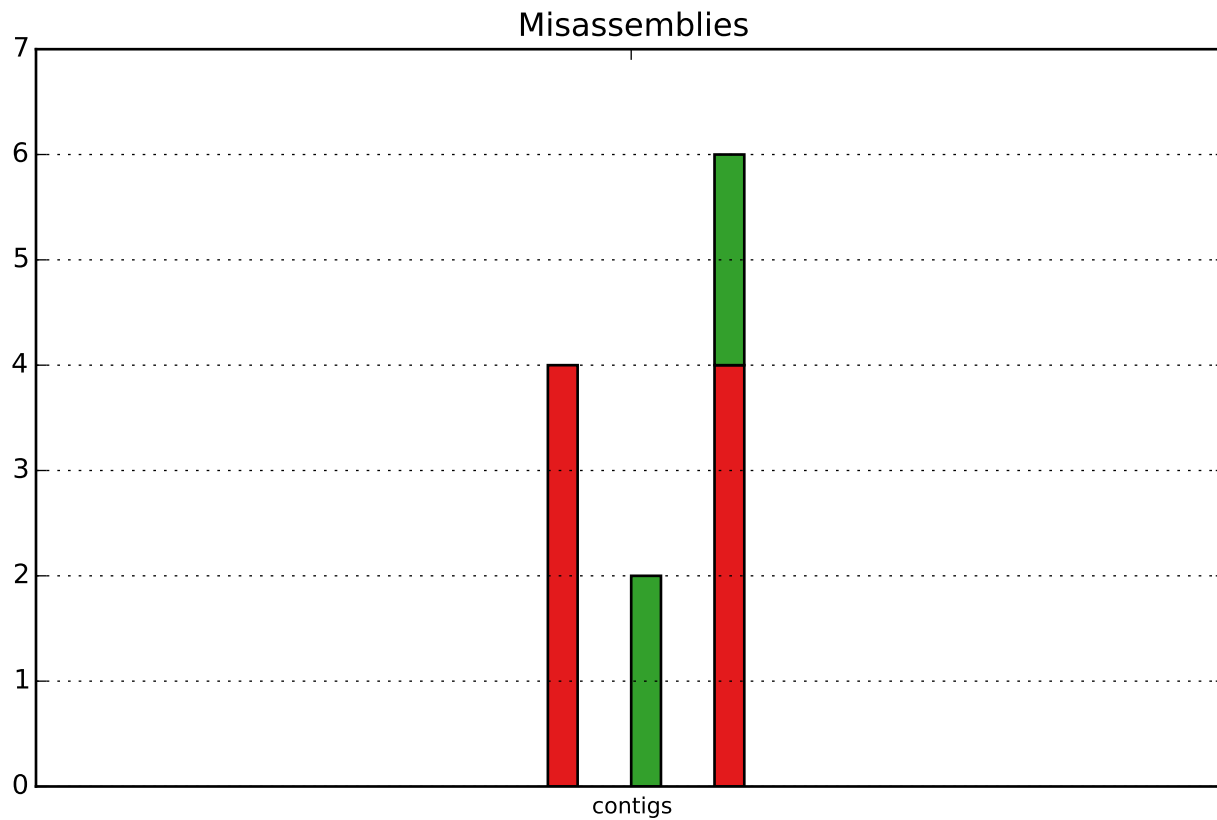
NGx





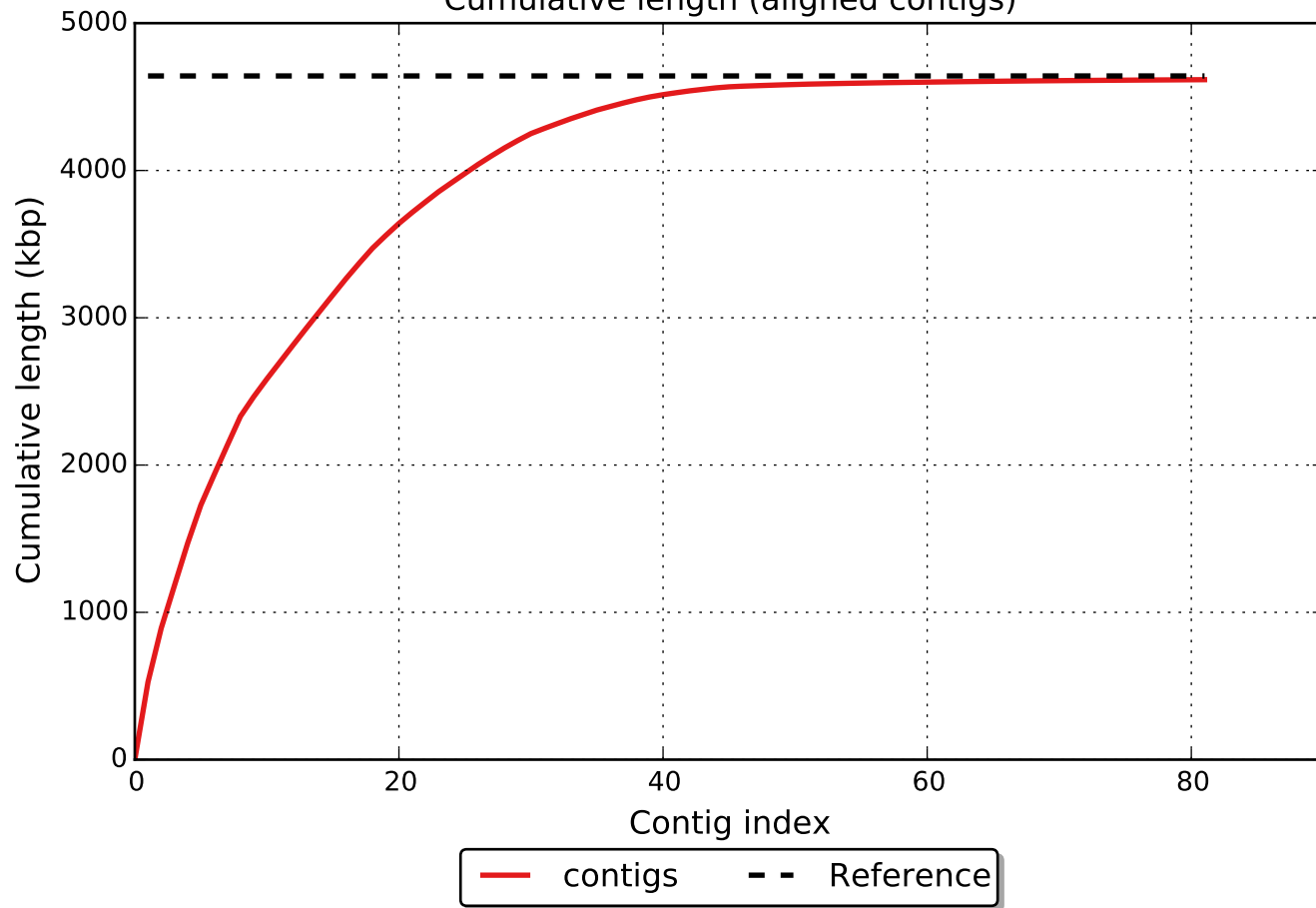
GC content



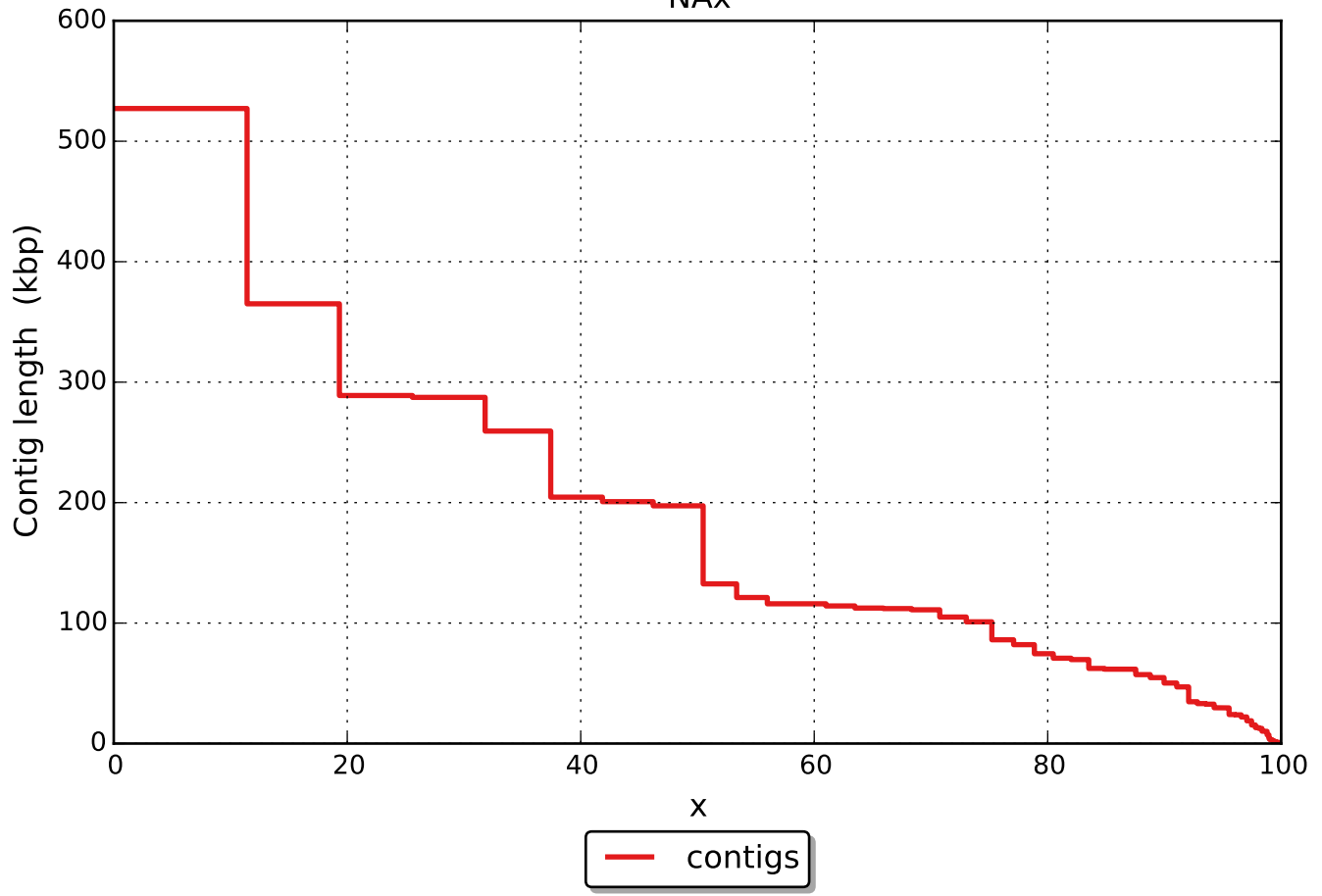




Cumulative length (aligned contigs)



NAx



# NGAx

