

## Report

	final.contigs
# contigs (>= 0 bp)	318
# contigs (>= 1000 bp)	233
# contigs (>= 5000 bp)	184
# contigs (>= 10000 bp)	146
# contigs (>= 25000 bp)	61
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	4569350
Total length (>= 1000 bp)	4535541
Total length (>= 5000 bp)	4410087
Total length (>= 10000 bp)	4121602
Total length (>= 25000 bp)	2746097
Total length (>= 50000 bp)	1198644
# contigs	255
Largest contig	94996
Total length	4551272
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	30931
NG50	30566
N75	17611
NG75	16956
L50	45
LG50	46
L75	94
LG75	97
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.989
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.73
# indels per 100 kbp	0.09
Largest alignment	94996
NA50	30931
NGA50	30566
NA75	17611
NGA75	16956
LA50	45
LGA50	46
LA75	94
LGA75	97

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

## Misassemblies report

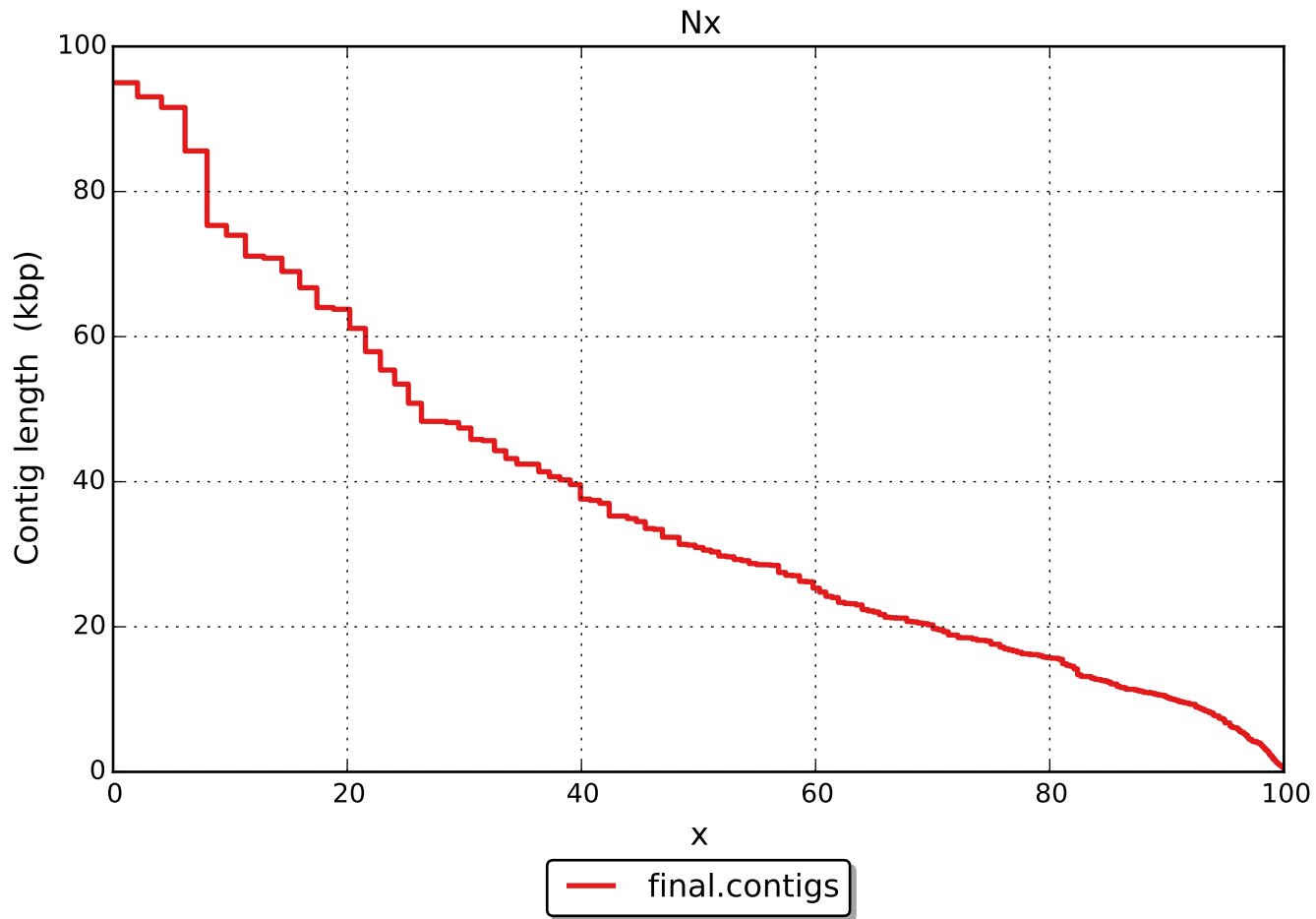
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	33
# indels	4
# short indels	3
# long indels	1
Indels length	88

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).

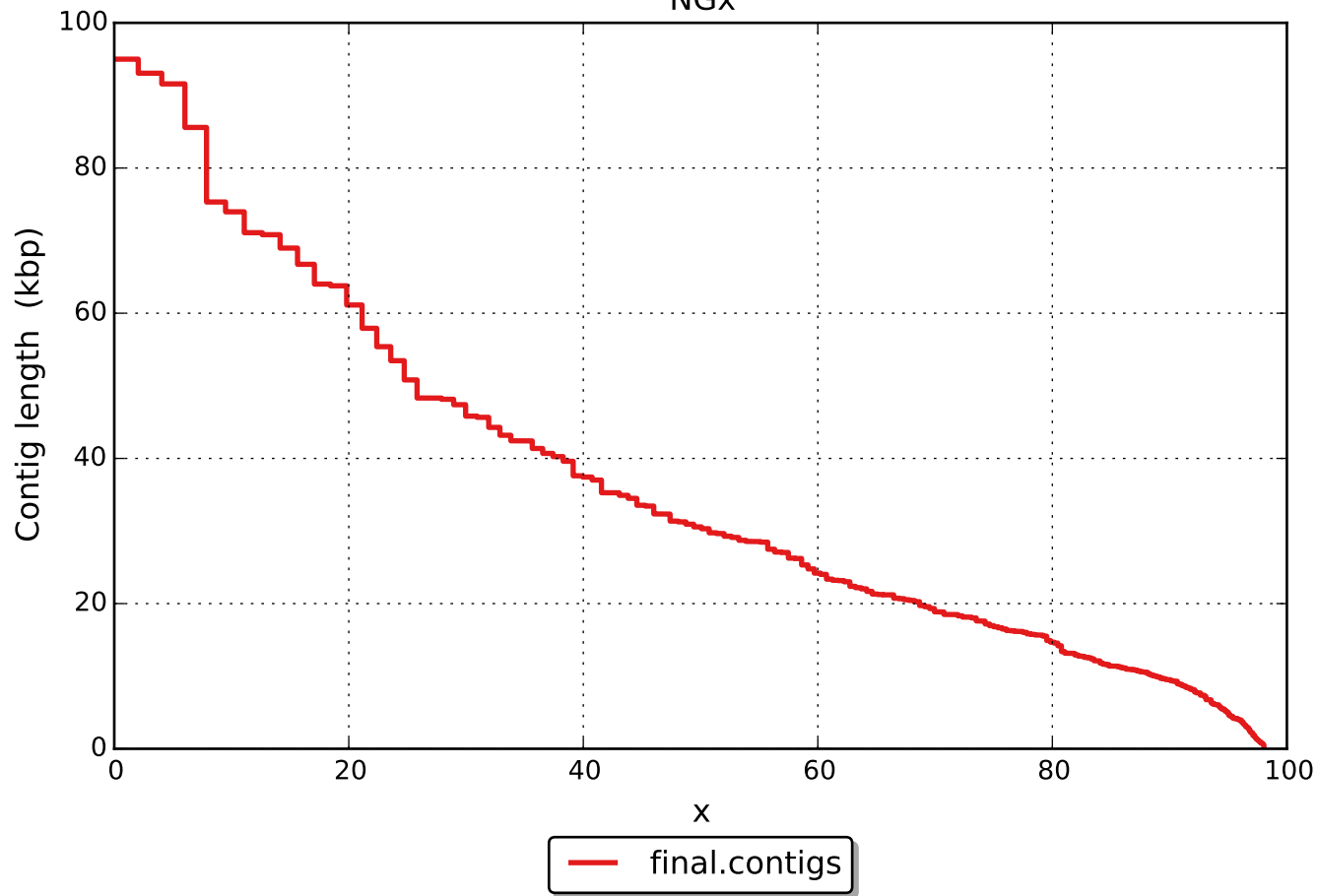
## Unaligned report

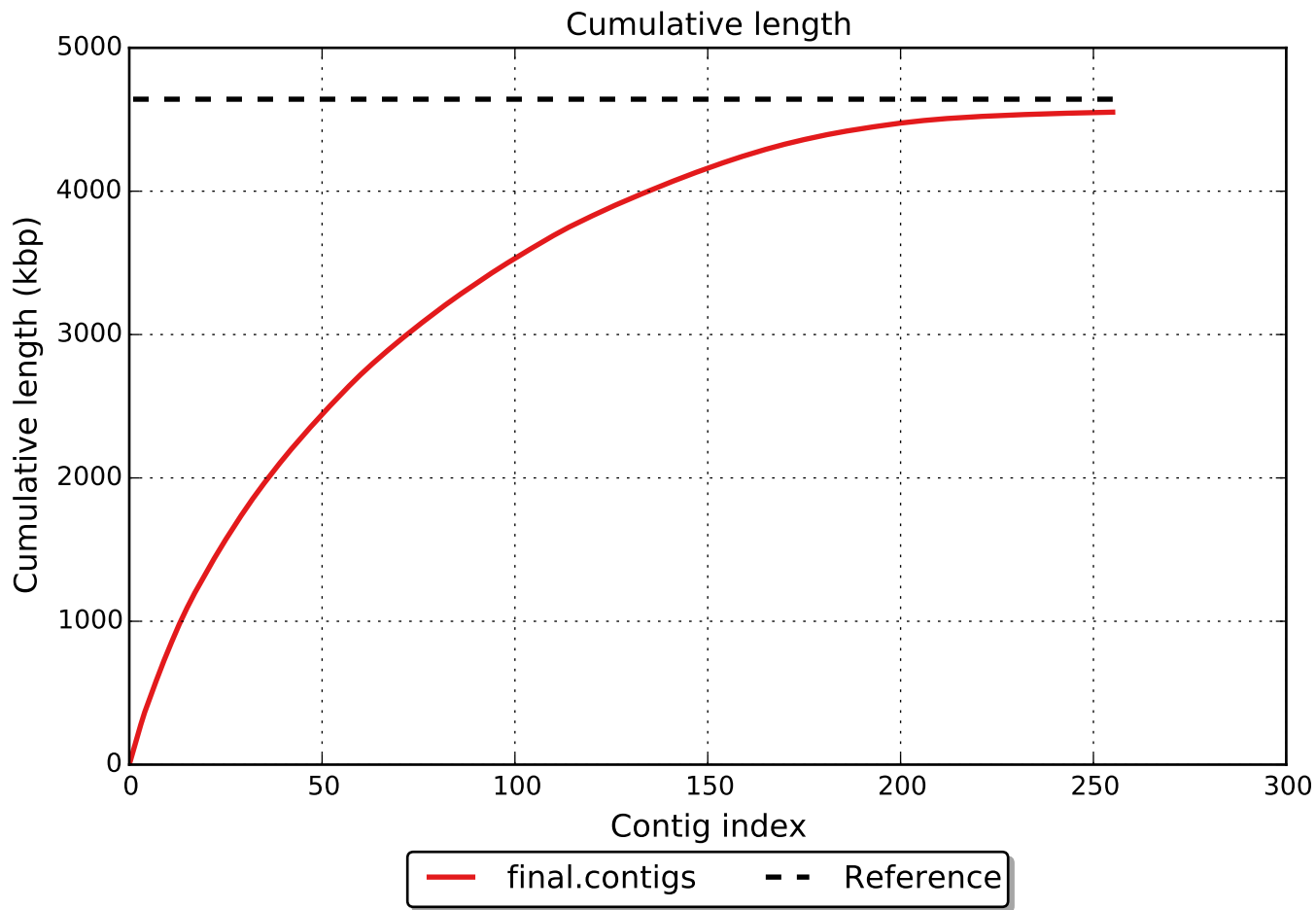
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

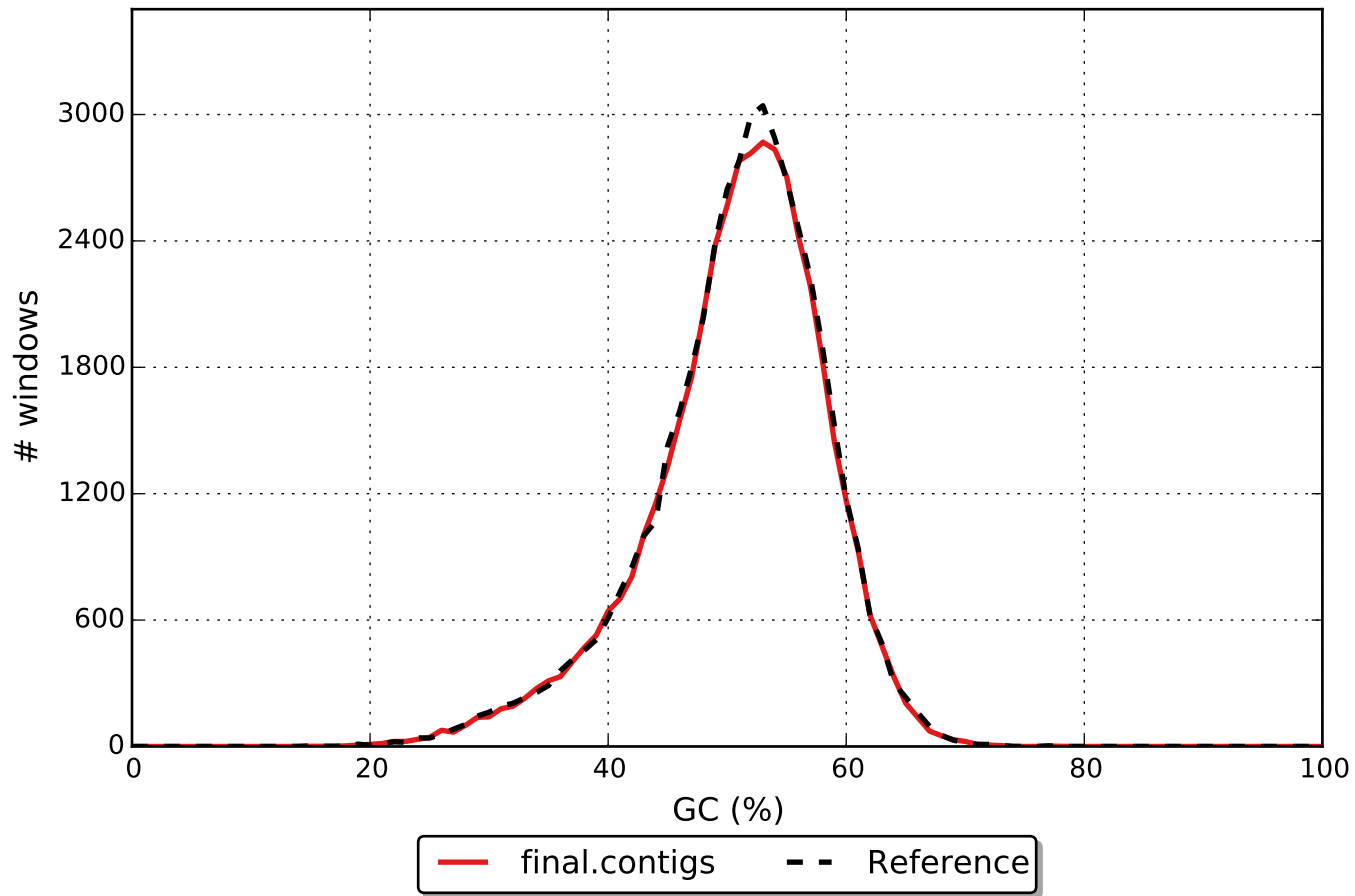


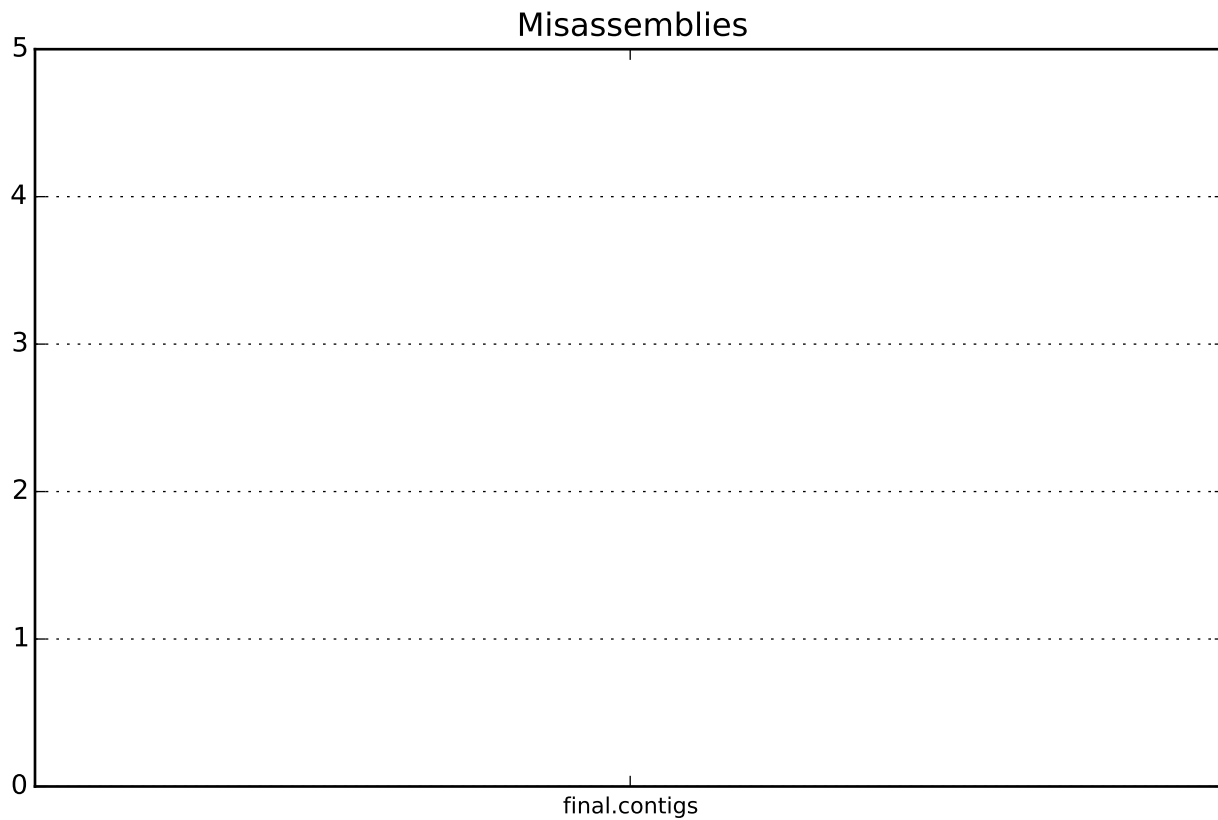
NGx





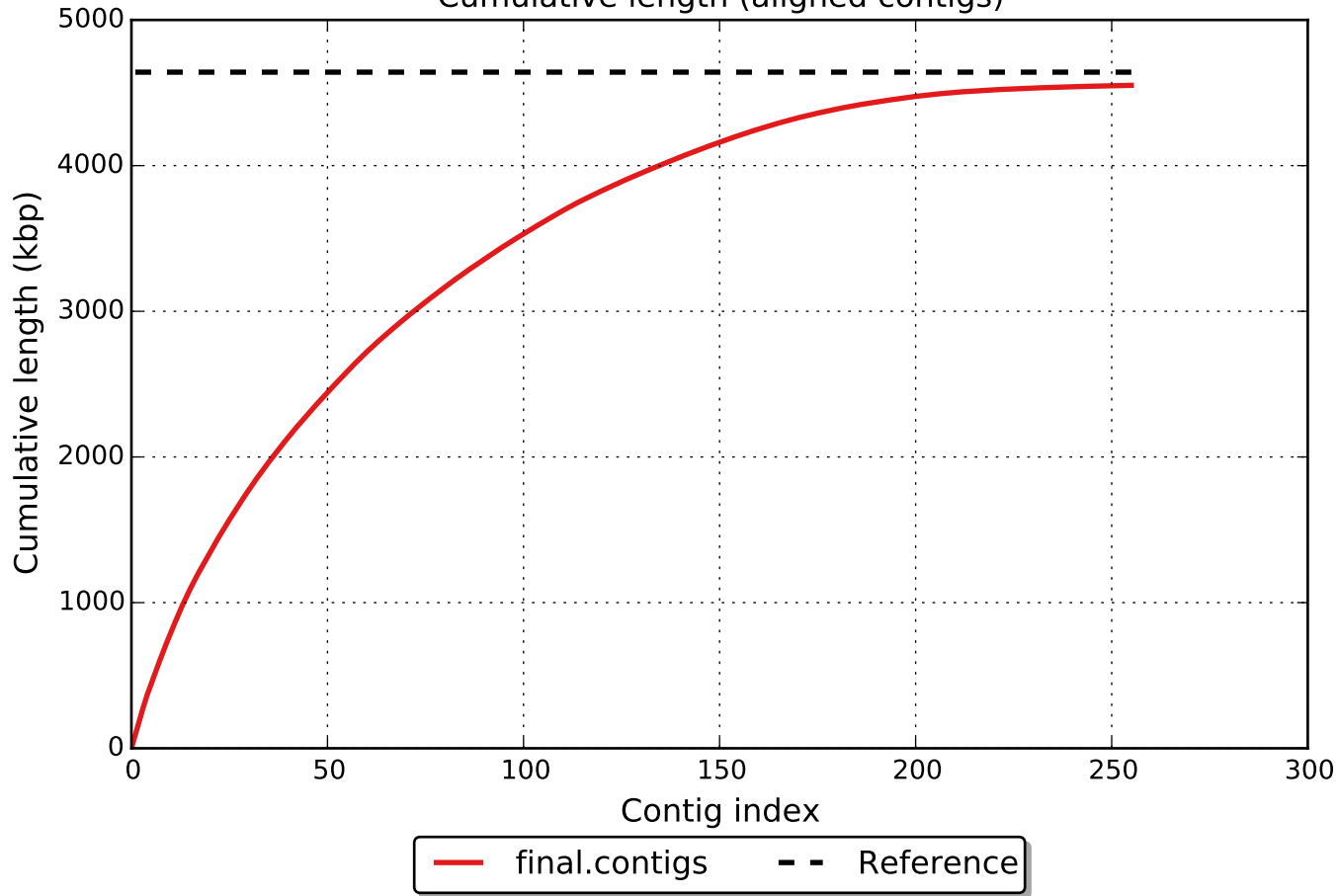
GC content



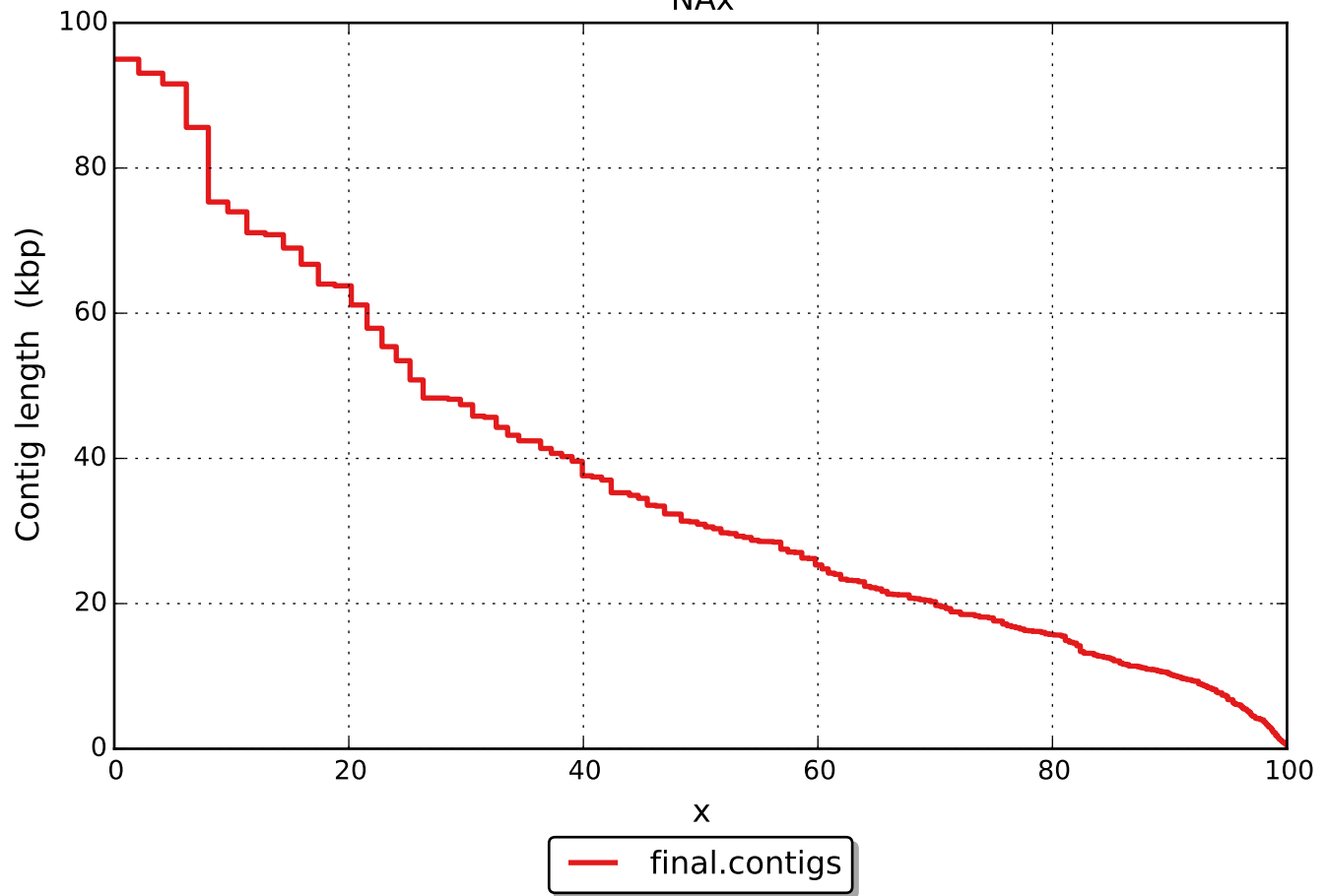




Cumulative length (aligned contigs)



NAx



NGAx

