

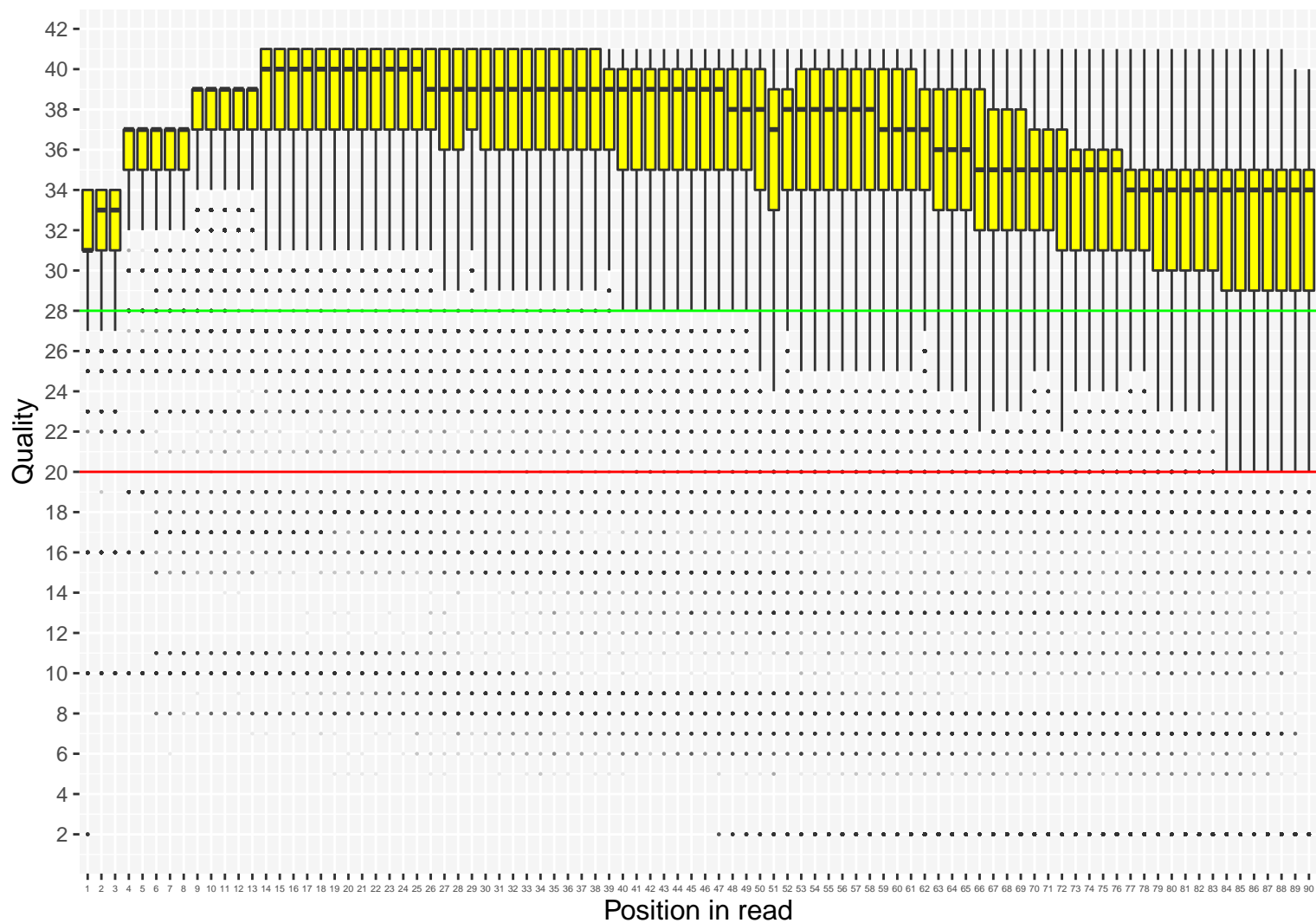
# fastQCer Report

R package: tinyfuncr  
Author: Yujie Liu

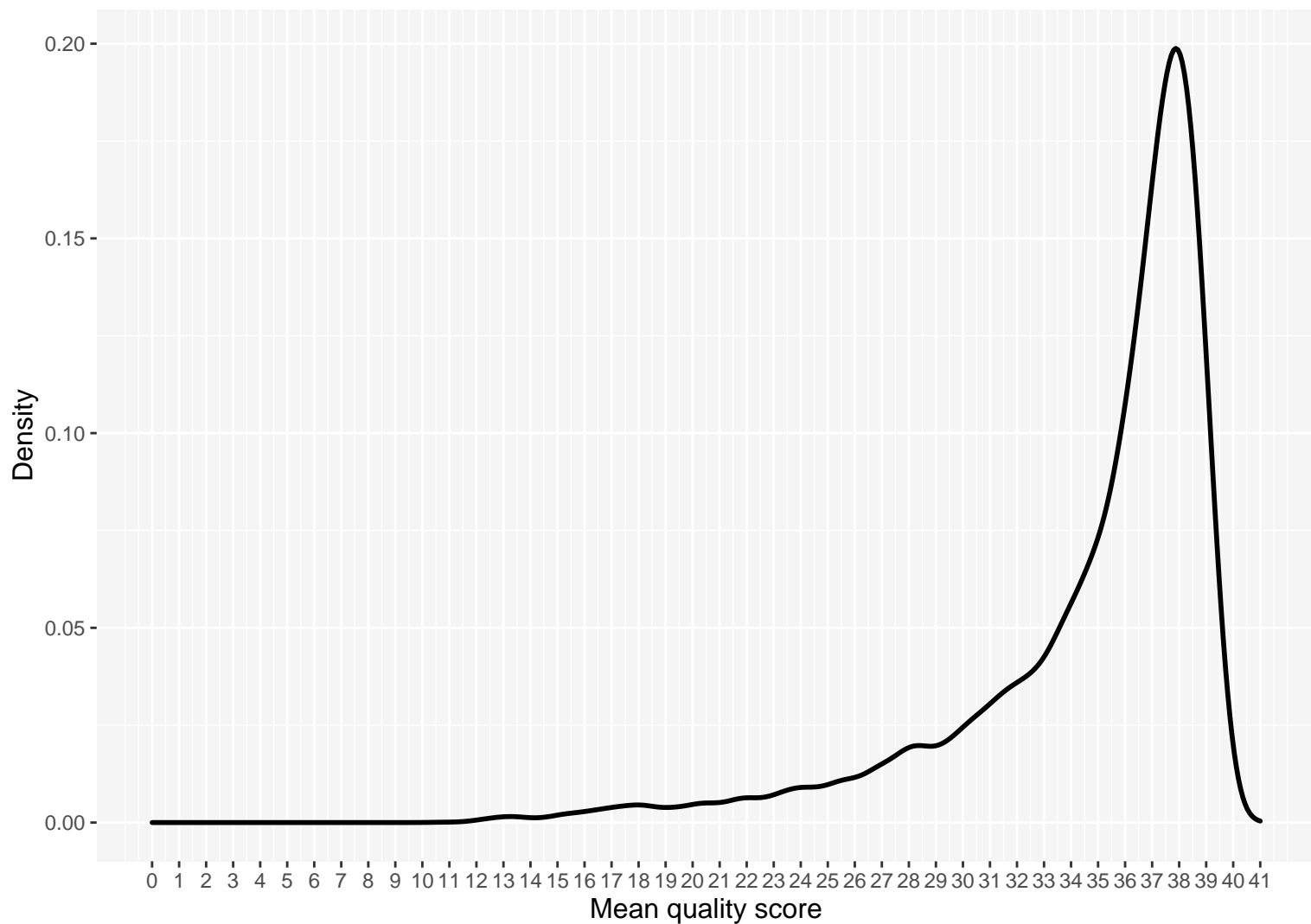
## Basic Statistics

Filename	test/2.fq
File Type	FASTQ
Encoding	Sanger / Illumina 1.8+
Total Sequences	10000
Used Sequences	10000
Sequence Length	90
Total GC content	43.35%

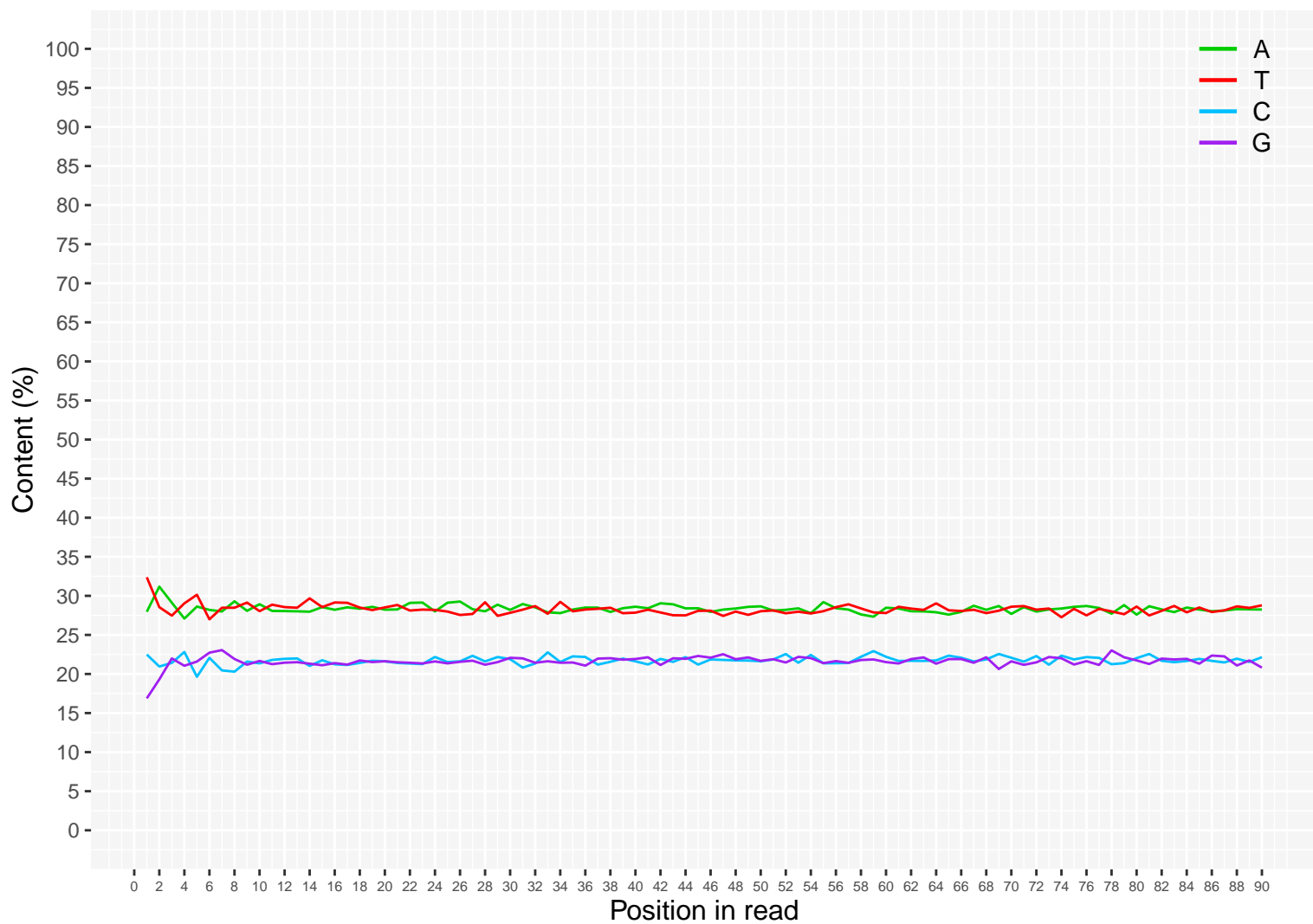
# Quality scores across all bases



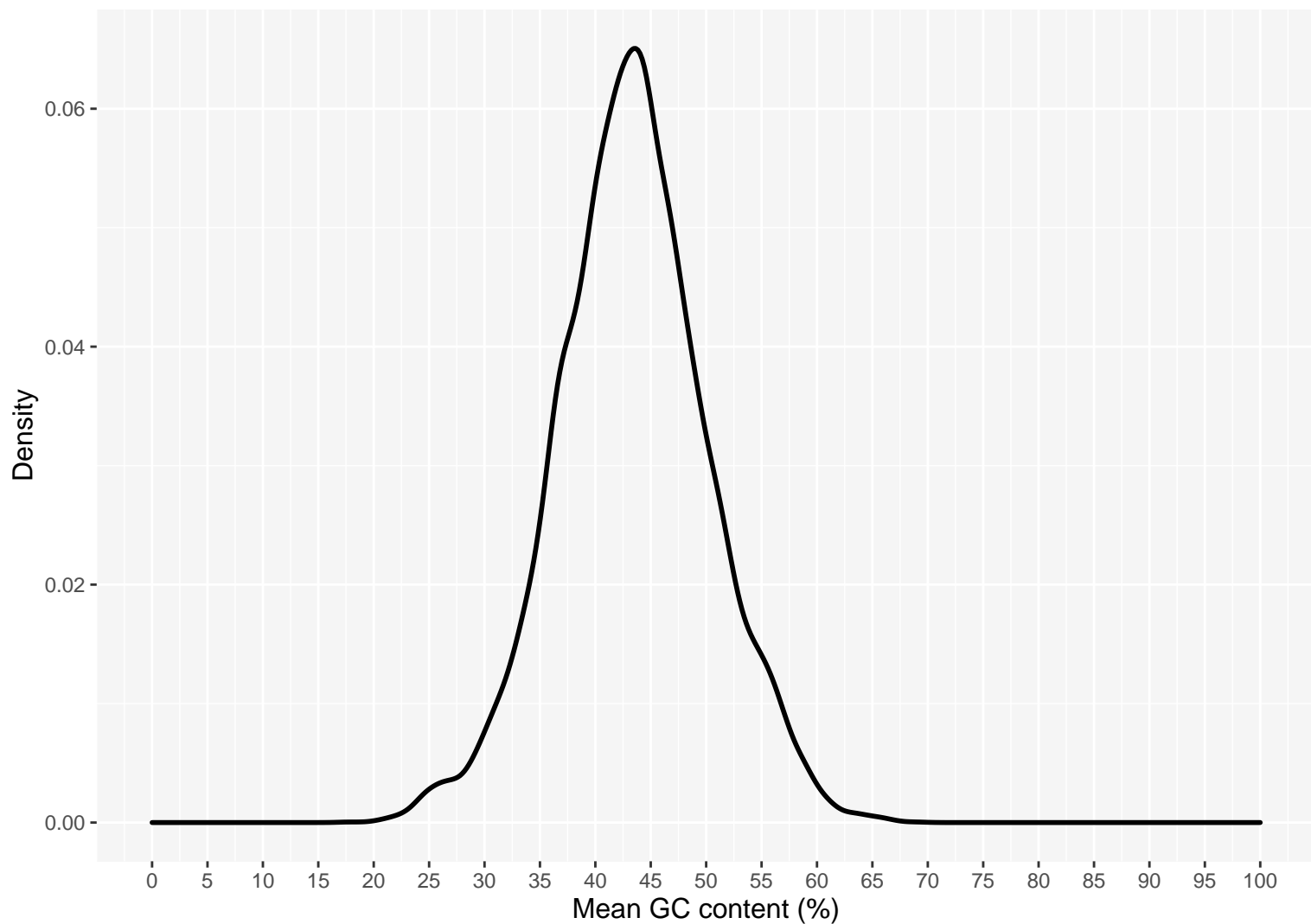
# Quality score over all reads



# Sequence content across all bases



# GC distribution over all reads



# N content across all bases

