

## Basic Statistics

Filename1: ulaz1.fastq

Filename2: ulaz2.fastq

Poor Quality Border: \*

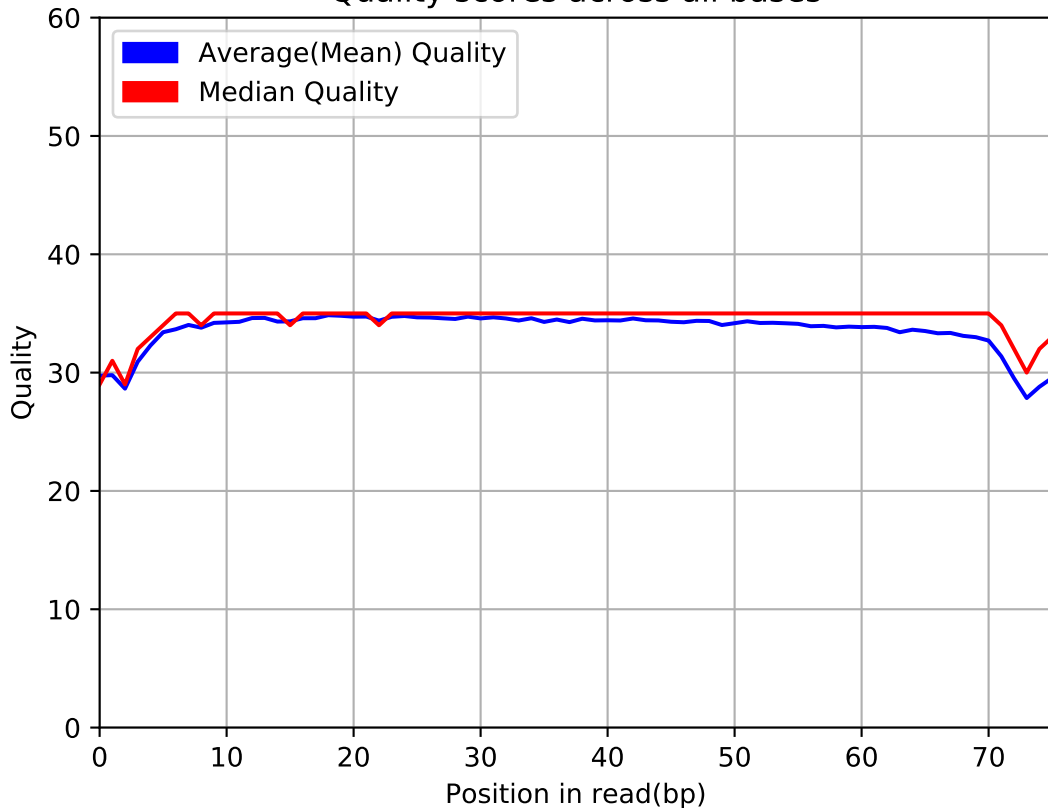
Total Sequences 1632890

Seq. Flaged as poor Quality: 14218

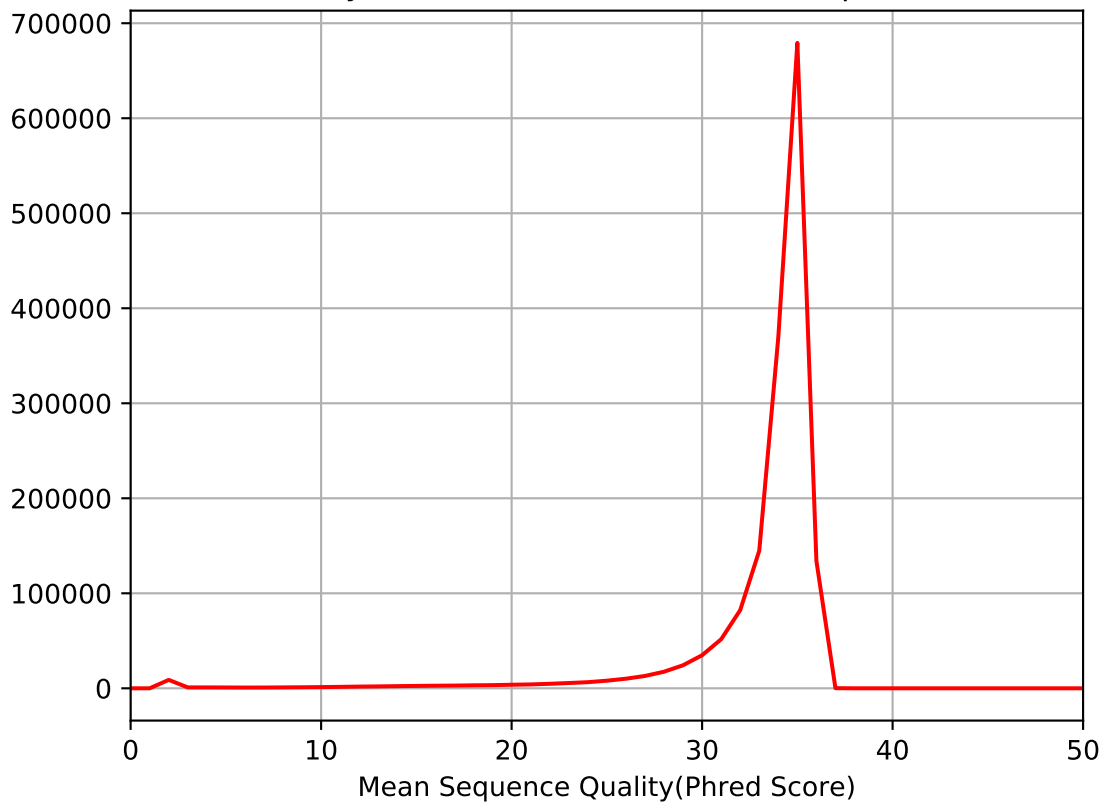
Sequence Length: 77

%GC: 52.4

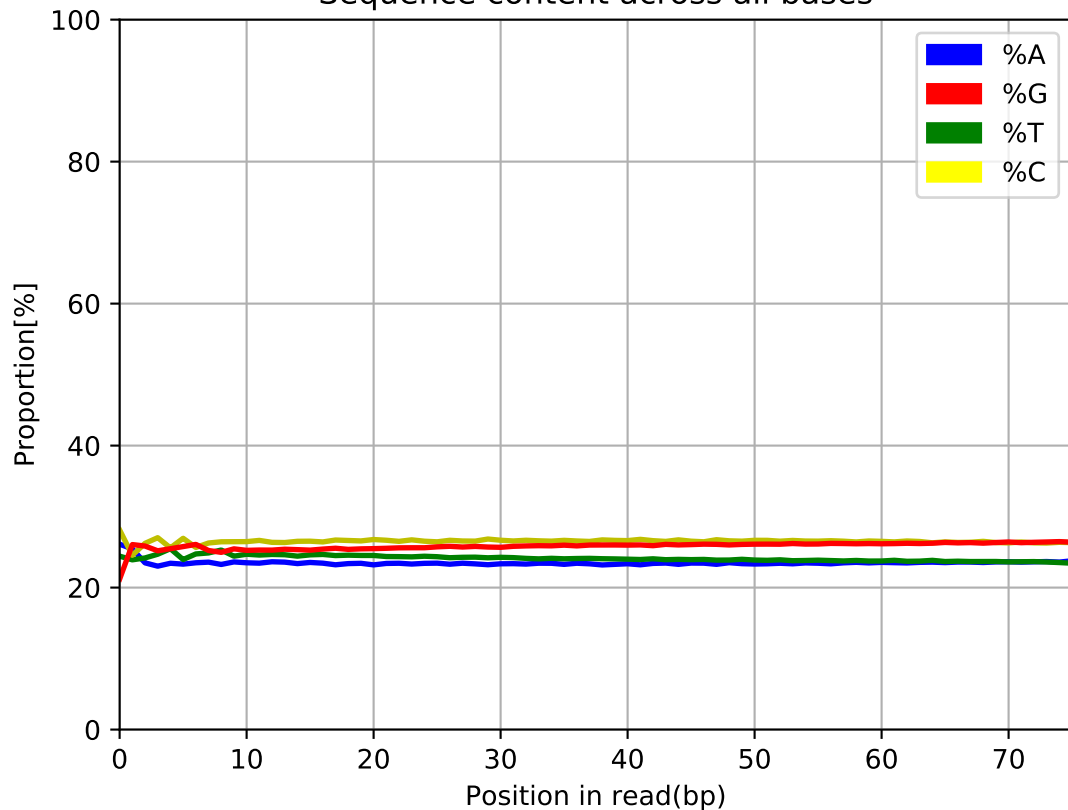
Quality scores across all bases



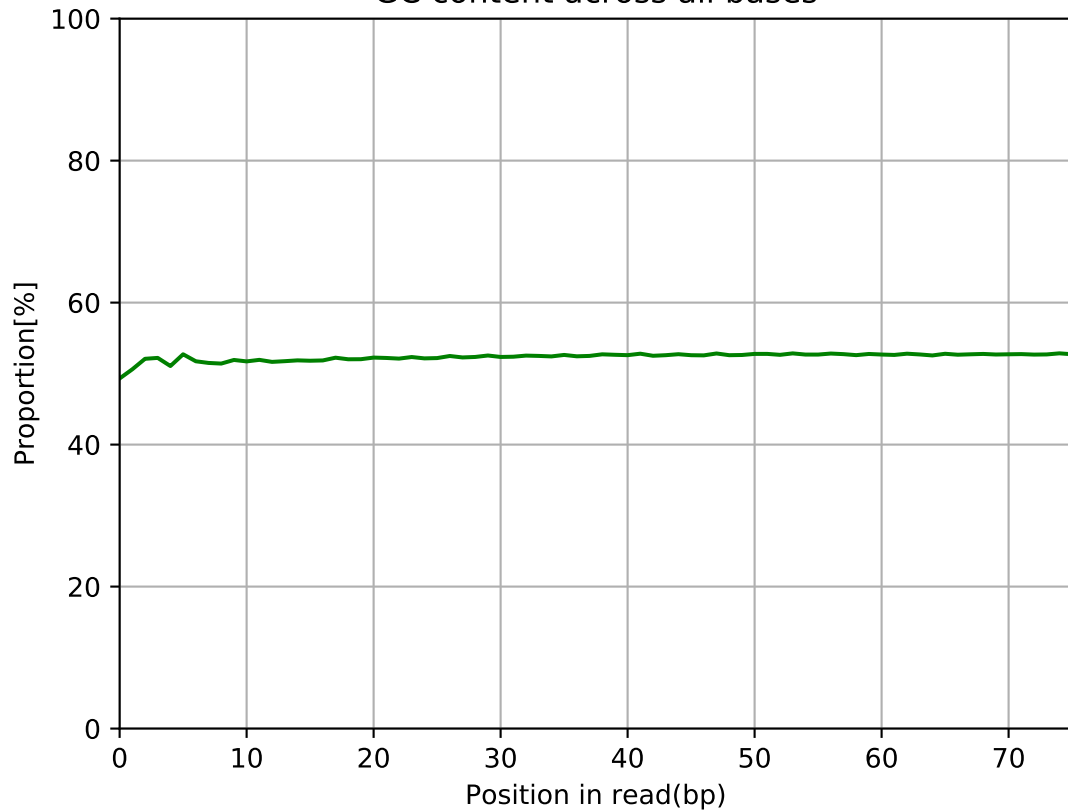
Quality score distribution over all sequences



Sequence content across all bases



GC content across all bases



GC distribution over all sequences

