

## Basic Statistics

Filename1: ulaz1.fastq

Filename2: ulaz2.fastq

Poor Quality Border: 28

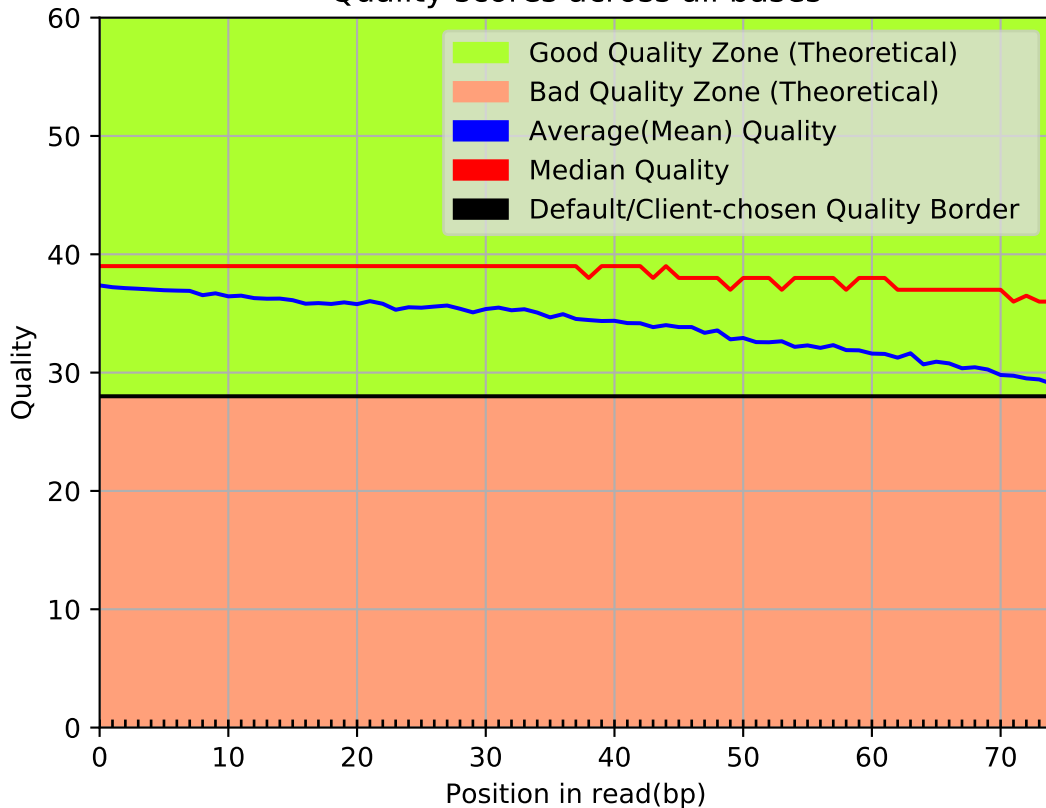
Total Sequences 344

Seq. Flaged as poor Quality: 58

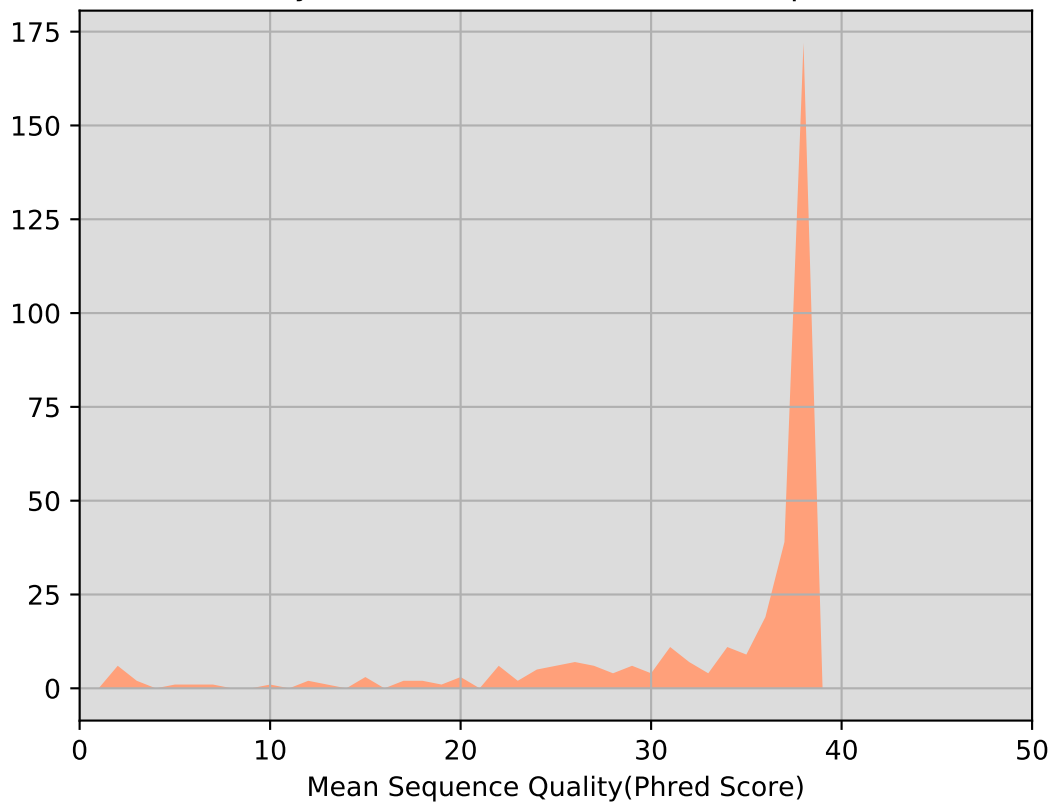
Sequence Length: 77

%GC: 38.2

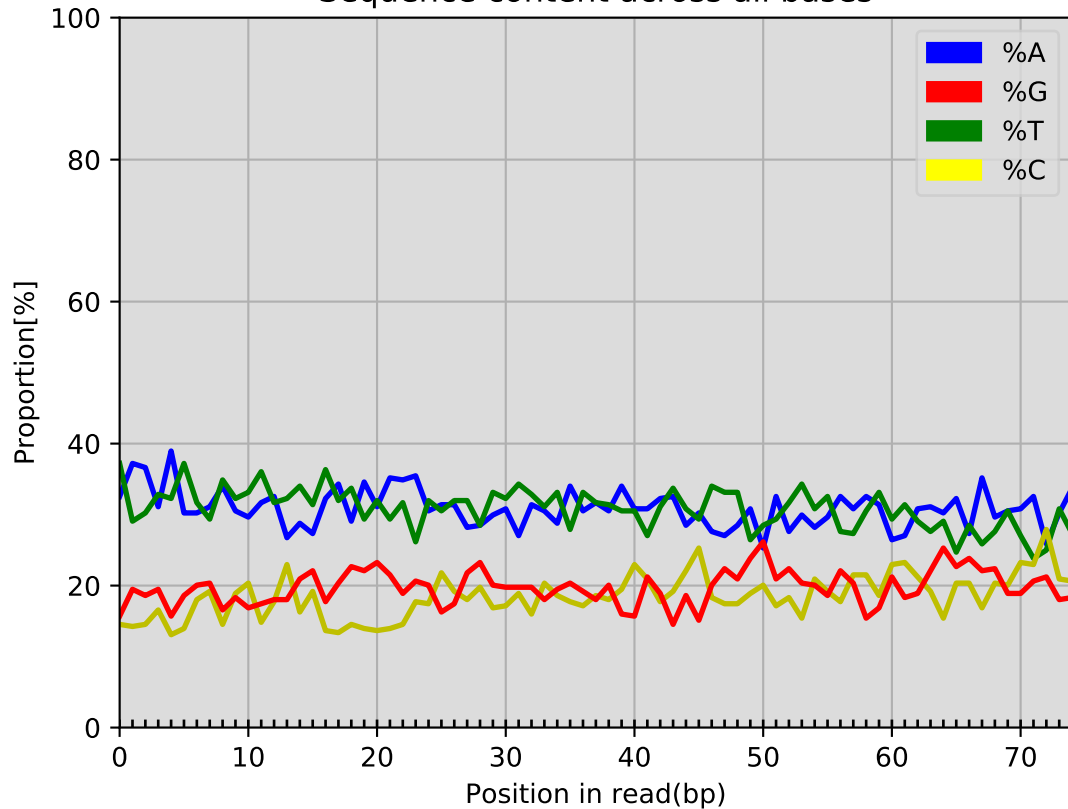
Quality scores across all bases



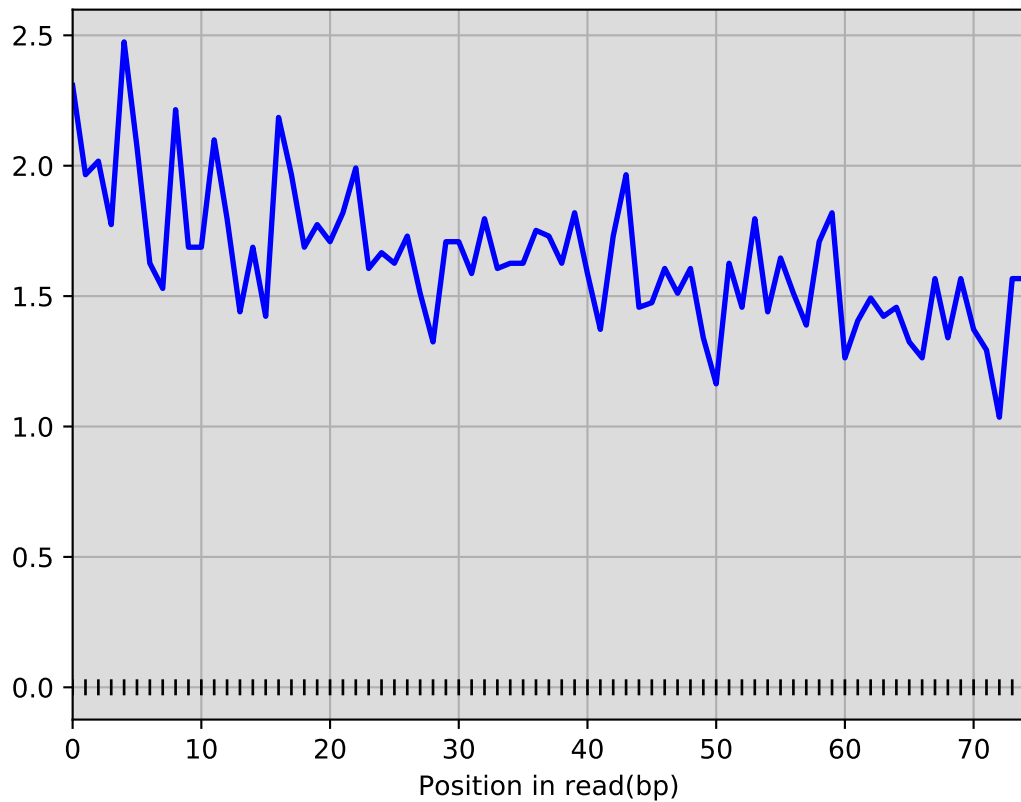
Quality score distribution over all sequences



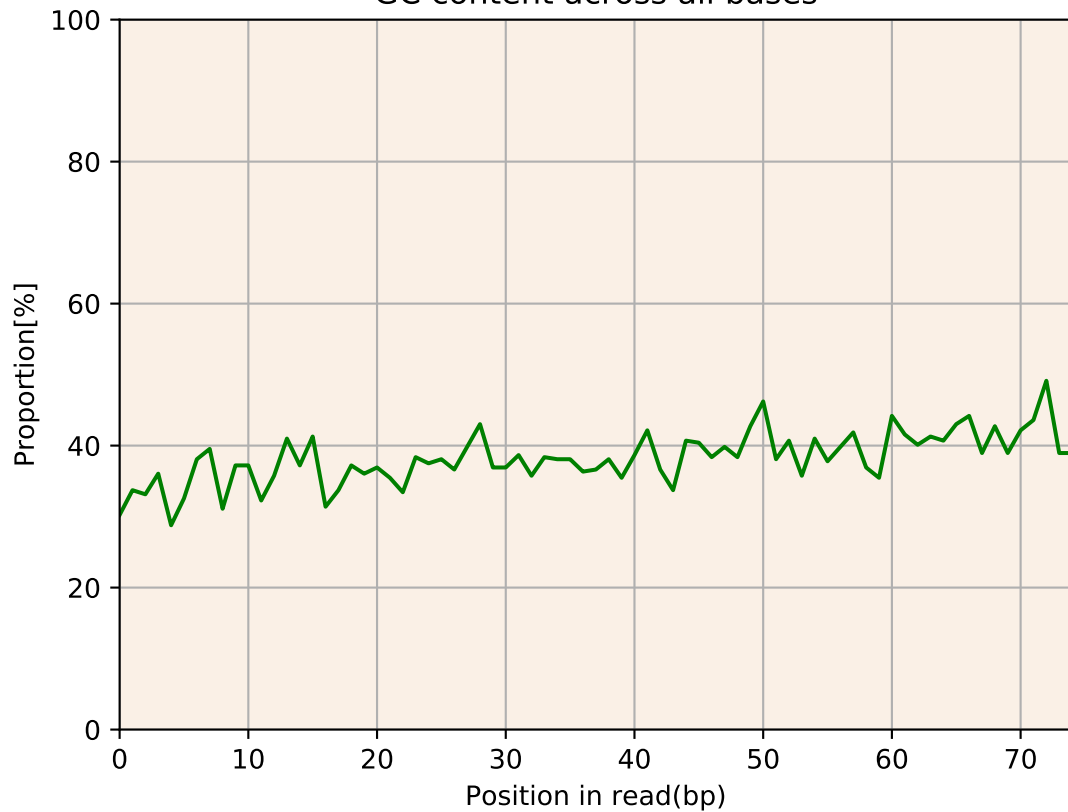
Sequence content across all bases



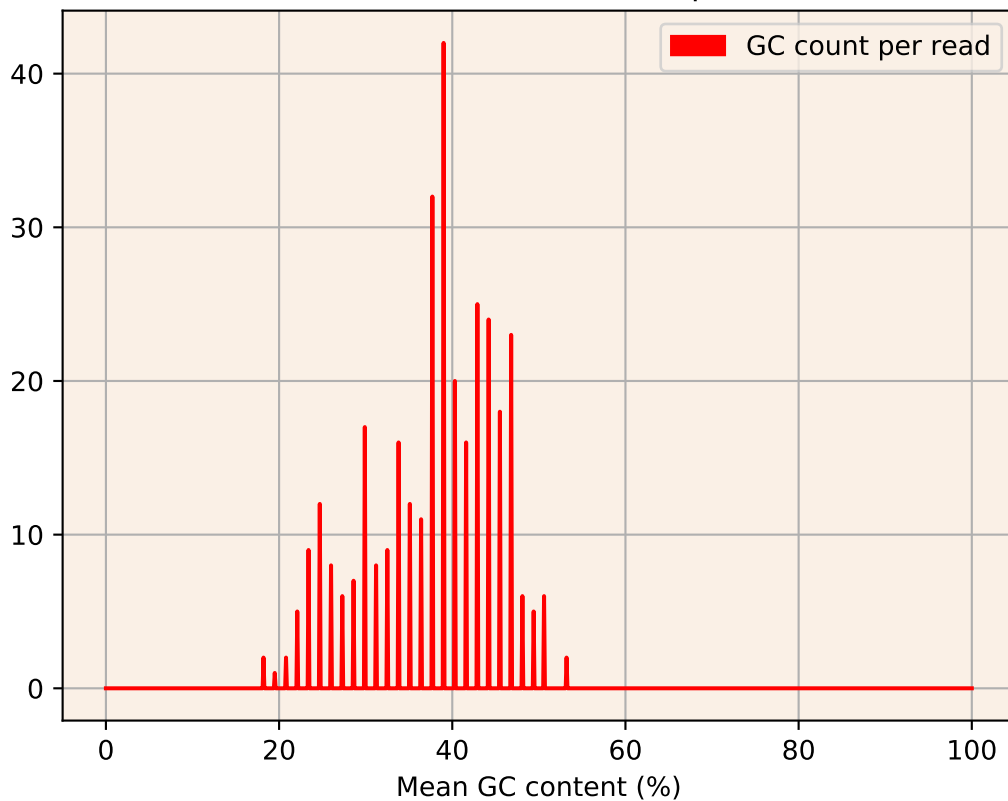
AT/GC ratio



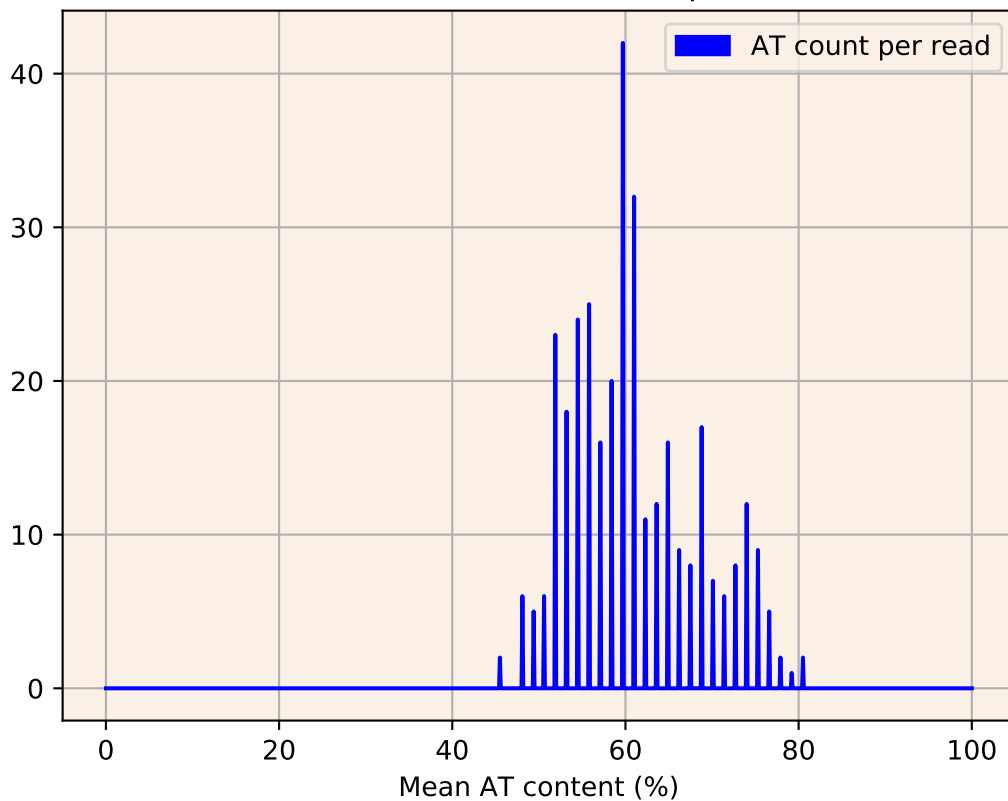
GC content across all bases



GC distribution over all sequences

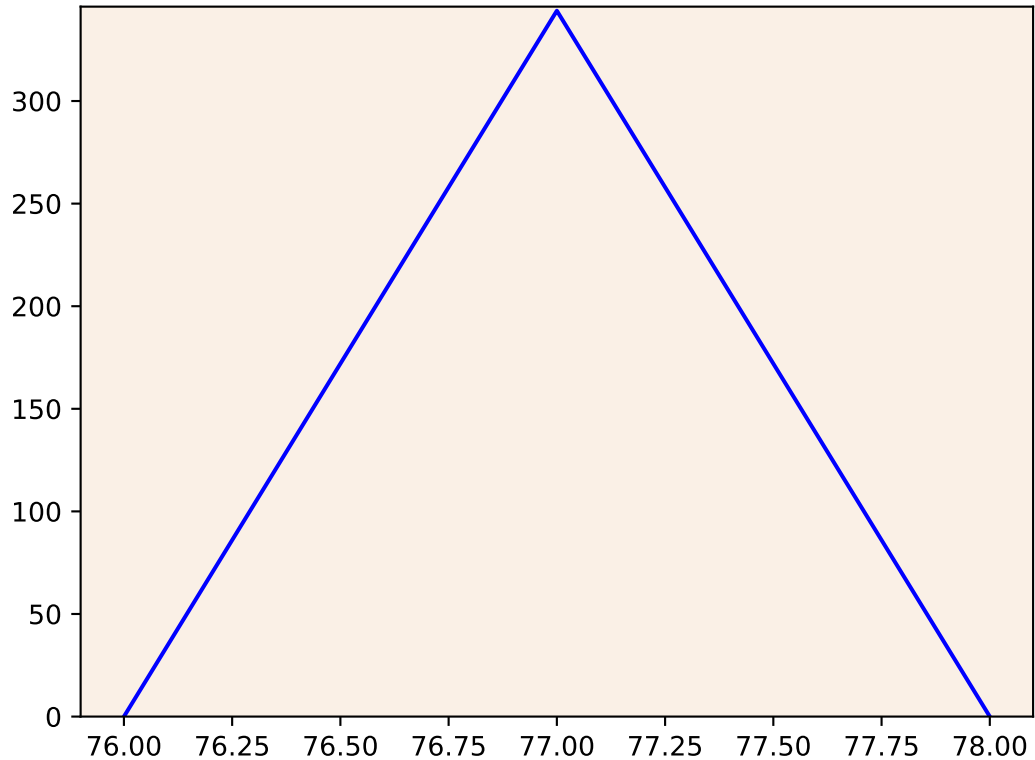


AT distribution over all sequences





Sequence Length Distribution



N content across all bases

