# LTR Parser Results

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Overview

This report contains the results of attempted primer & LTR identification in the following FASTQ file:

/home/kevin/dev/ltrparser/testdata/GTSP3518-1_u3.R2.fastq.gz

Total number of reads in sample	154596
Number of distinct reads in sample	58213
Number of copies of most common read	8310

Visualization of 1000 sequencing reads, selected randomly and arranged by nucleotide sequence:
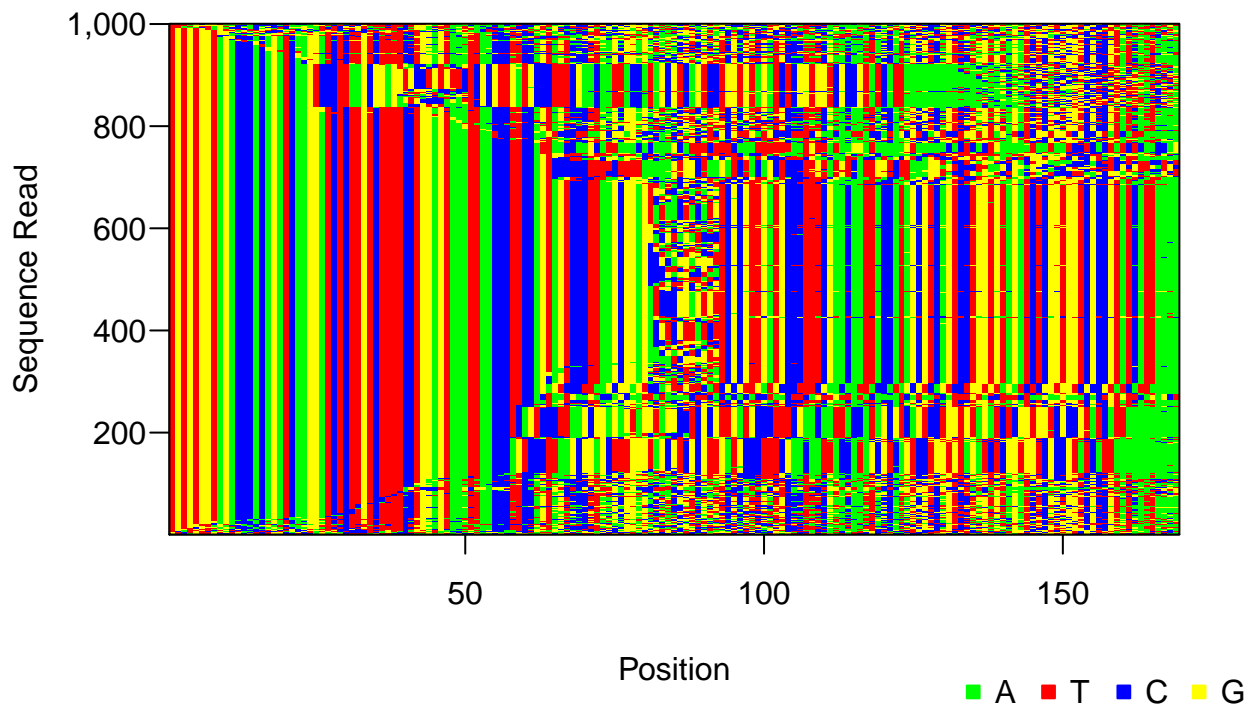
Visualization of 1000 distinct sequencing reads (after removing duplicates), selected randomly and arrangedy by nucleotide sequence:
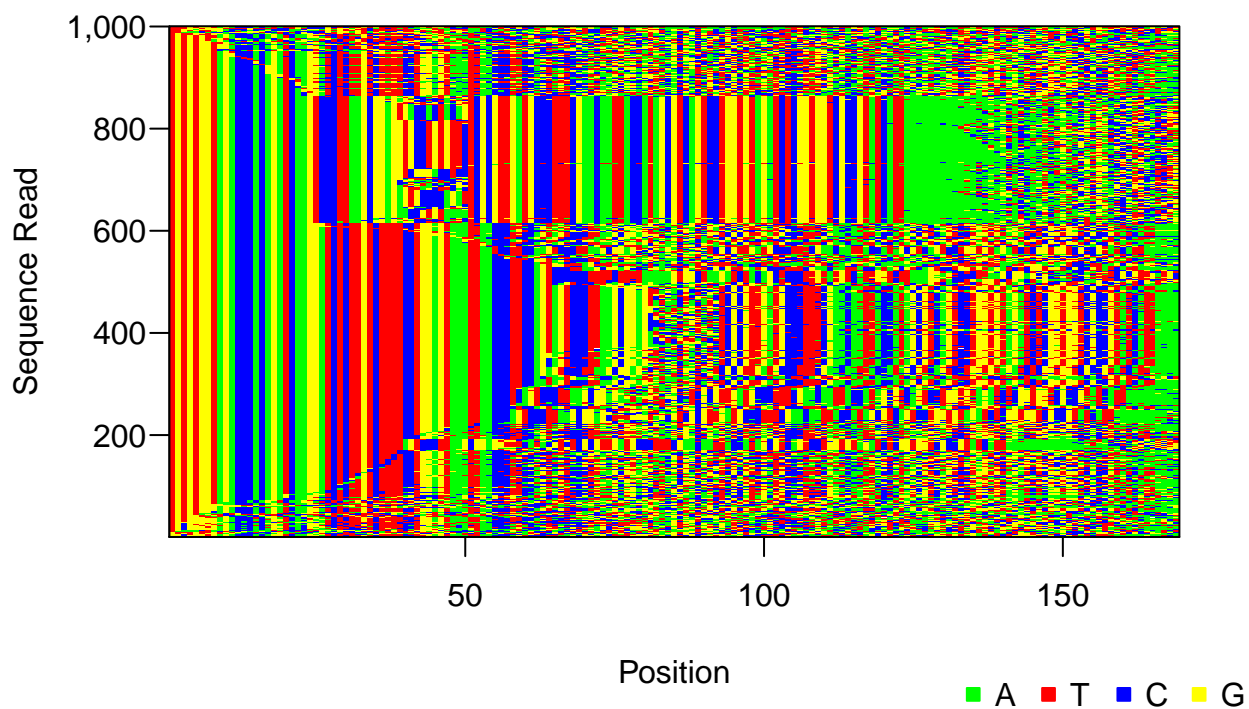
No primer LTR pairs appeared in more than 5% of total reads.