# 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/genetherapy/UninfectedControl-200313-2.R2.fastq.gz

Total number of reads in sample	14
Number of distinct reads in sample	14
Number of copies of most common read	1

Visualization of 14 sequencing reads, selected randomly and arranged by nucleotide sequence:
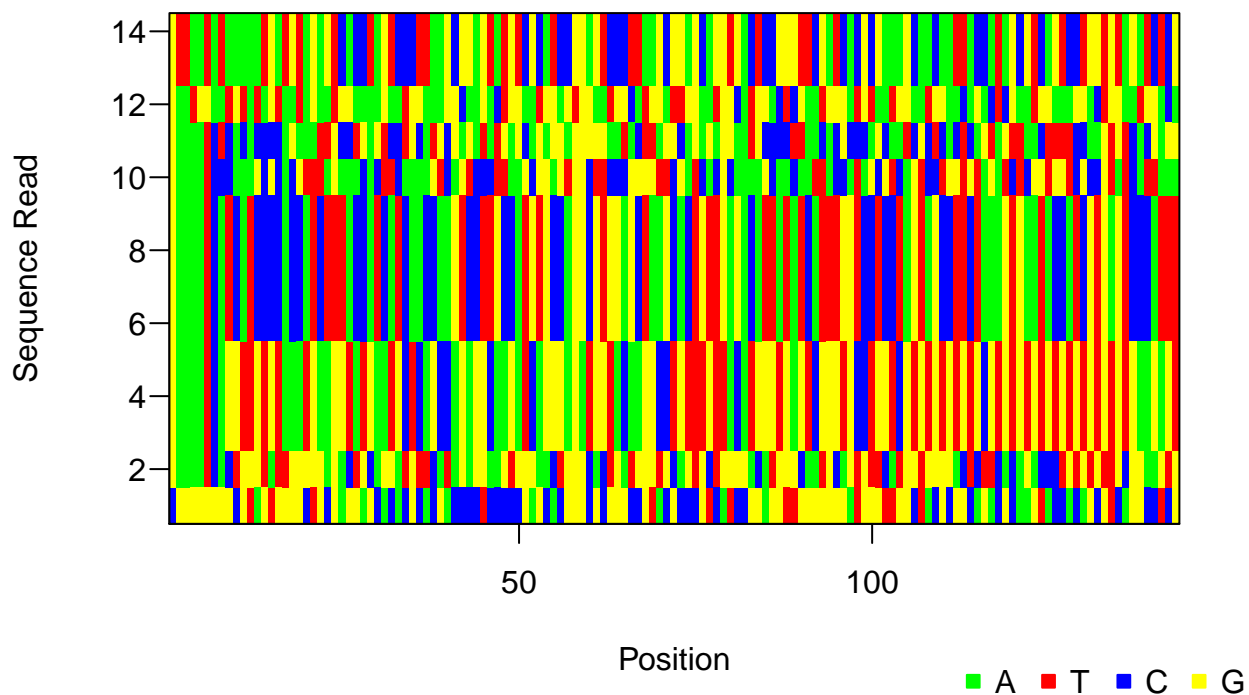
Visualization of 14 distinct sequencing reads (after removing duplicates), selected randomly and arrangedy by nucleotide sequence:
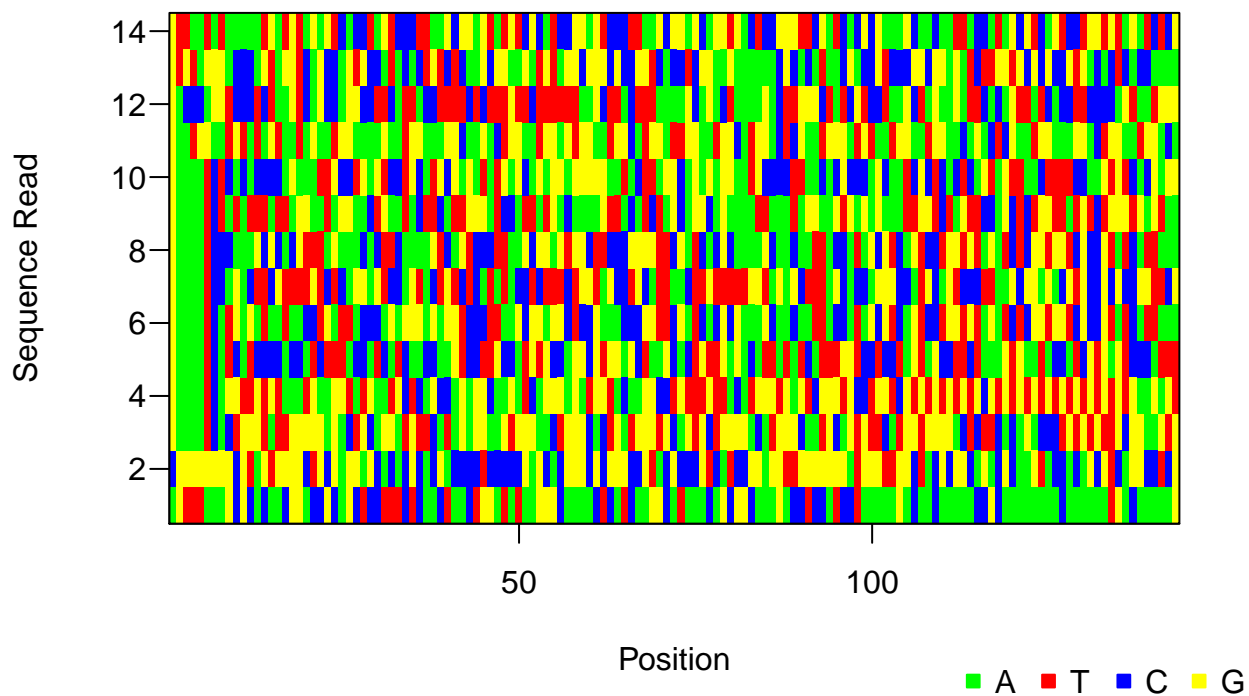
No primer LTR pairs appeared in more than 5% of total reads.