

# LTR Parser Results

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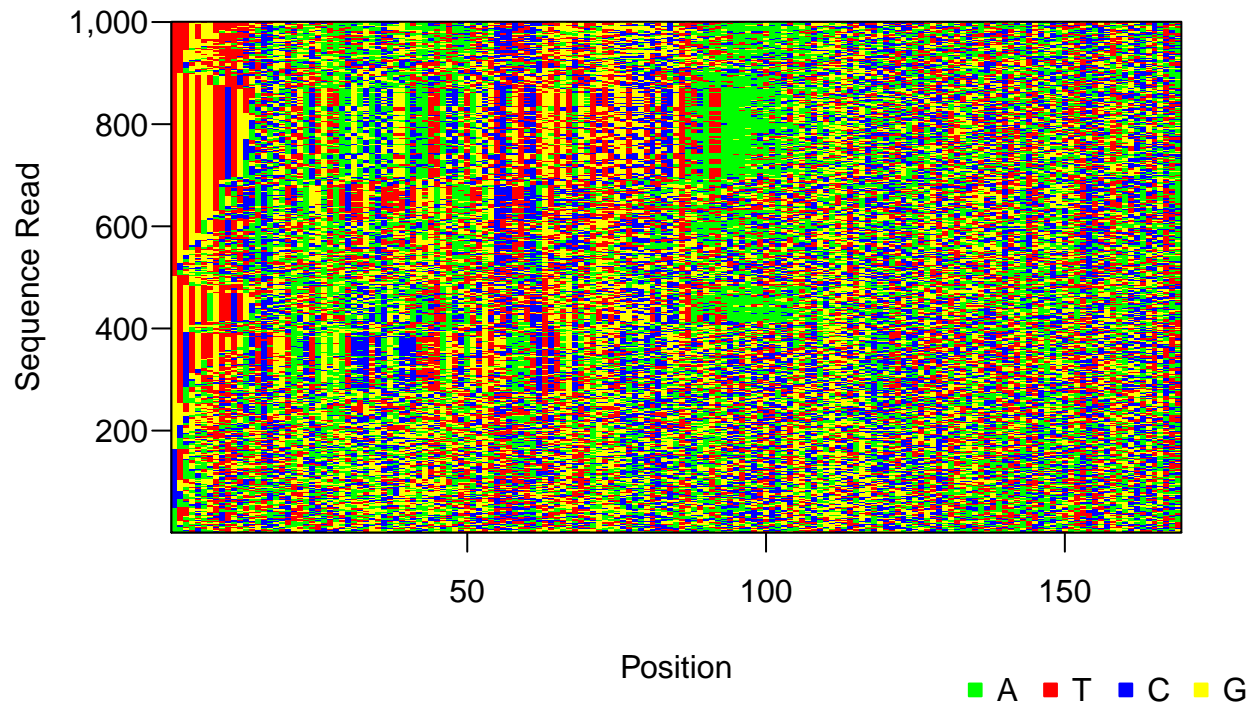
## Overview

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

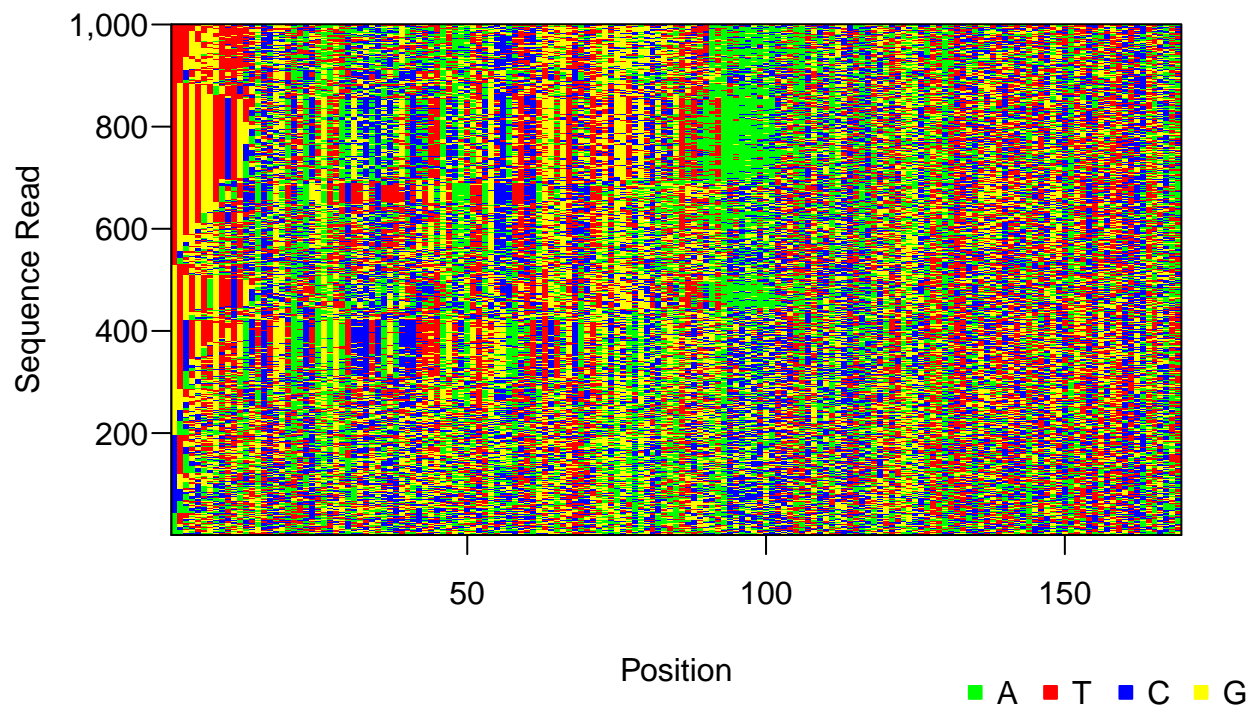
/home/kevin/dev/ltrparser/testdata/20200303H2OControl-1\_\_u3.R2.fastq.gz

|                                      |      |
|--------------------------------------|------|
| Total number of reads in sample      | 1133 |
| Number of distinct reads in sample   | 1133 |
| Number of copies of most common read | 1    |

Visualization of 1000 sequencing reads, selected randomly and arranged by nucleotide sequence:



Visualization of 1000 distinct sequencing reads (after removing duplicates), selected randomly and arranged by nucleotide sequence:



No primer LTR pairs appeared in more than 5% of total reads.