

LTR Parser Results

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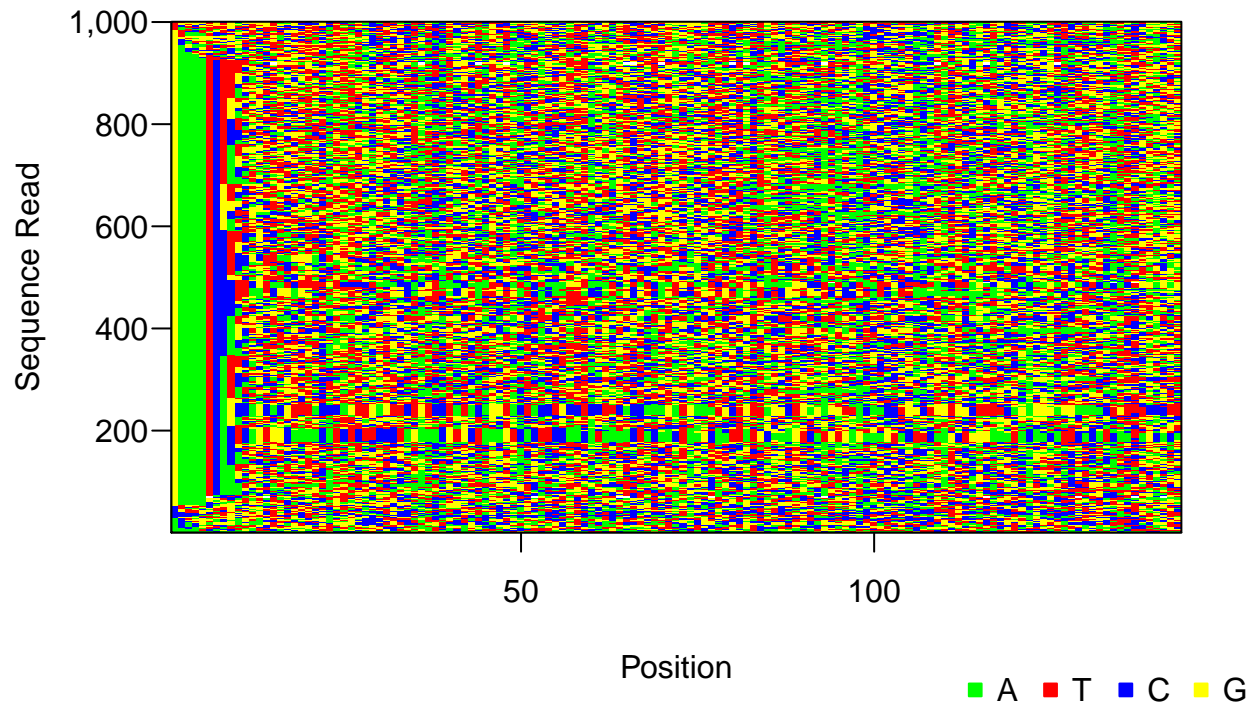
Overview

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

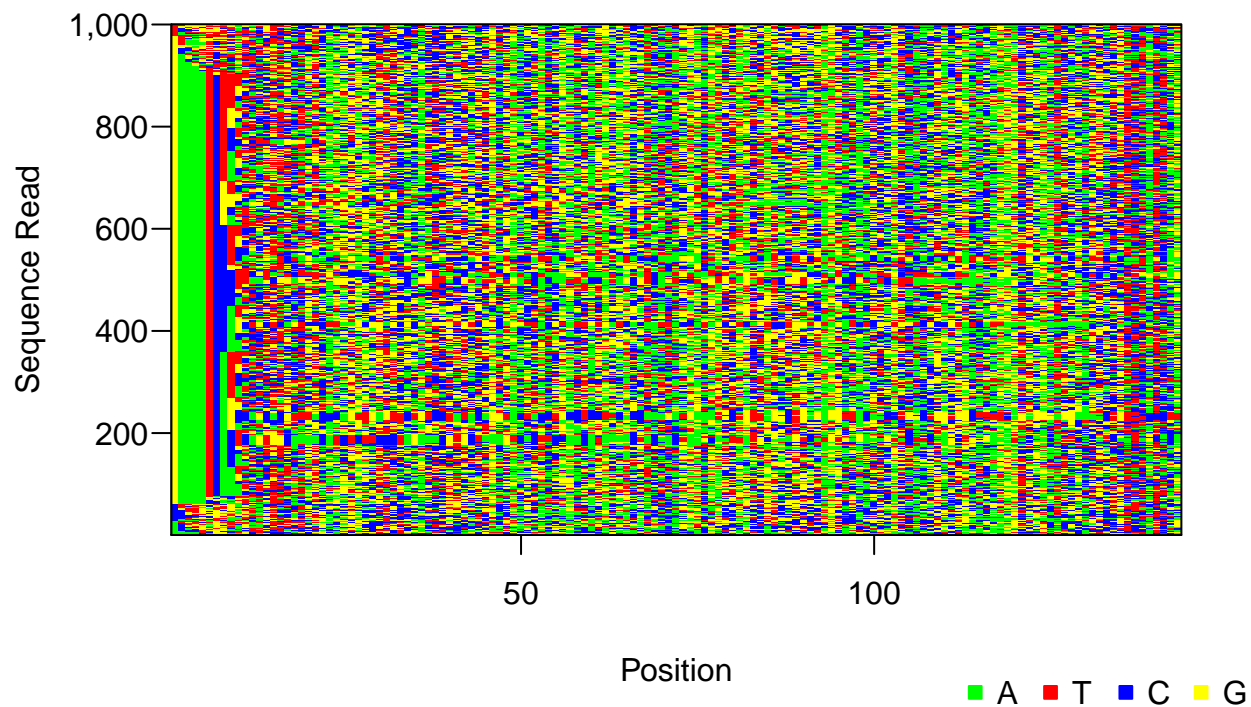
/home/kevin/dev/ltrparser/testdata/genetherapy/GTSP3585-2.R2.fastq.gz

| | |
|--------------------------------------|------|
| Total number of reads in sample | 1230 |
| Number of distinct reads in sample | 1144 |
| Number of copies of most common read | 20 |

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.