

LTR Parser Results

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20 April, 2020

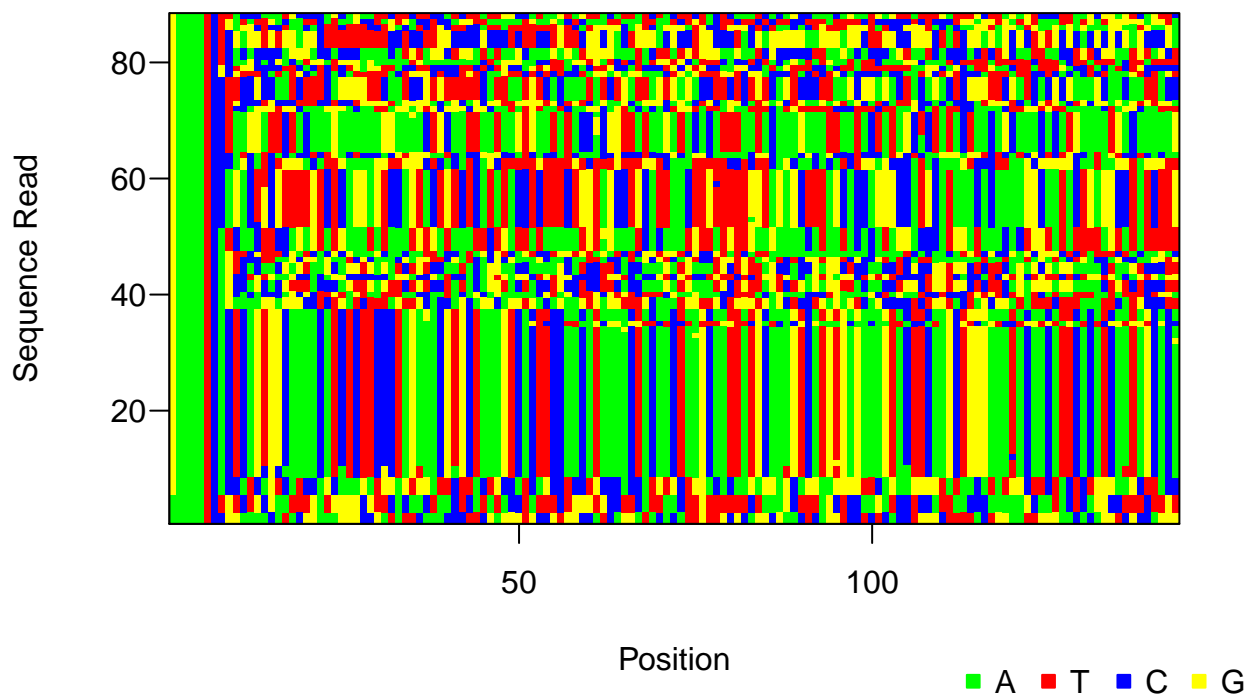
Overview

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

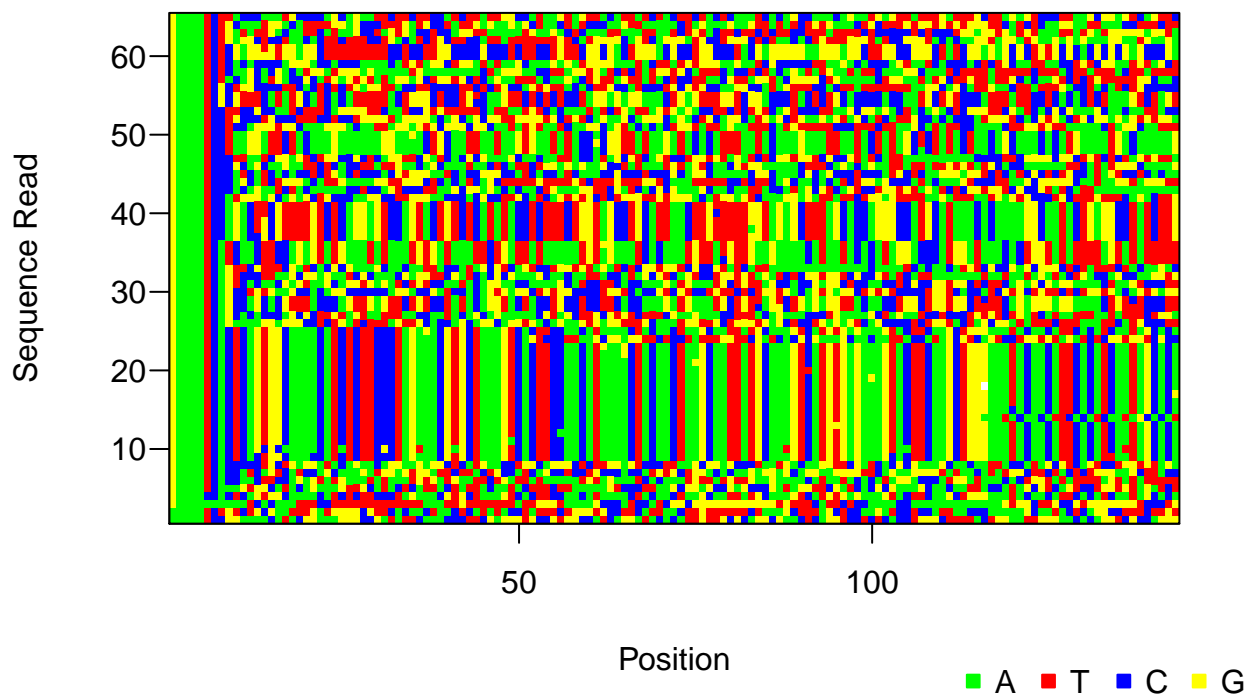
/home/kevin/dev/ltrparser/testdata/genetherapy/UninfectedControl-200313-4.R2.fastq.gz

Total number of reads in sample	88
Number of distinct reads in sample	65
Number of copies of most common read	17

Visualization of 88 sequencing reads, selected randomly and arranged by nucleotide sequence:



Visualization of 65 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.