

# 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/demo/fastq.gz/hivTest4\_u3.R2.fastq.gz

Scott project, sample: GTSP3518-1 (U3)

## Analysis of common primer-LTR pairs

A total of 1 potential primer-LTR pairs were identified.

This table shows how the reads captured by each primer-LTR pair compare to each other and to the raw FASTQ file.

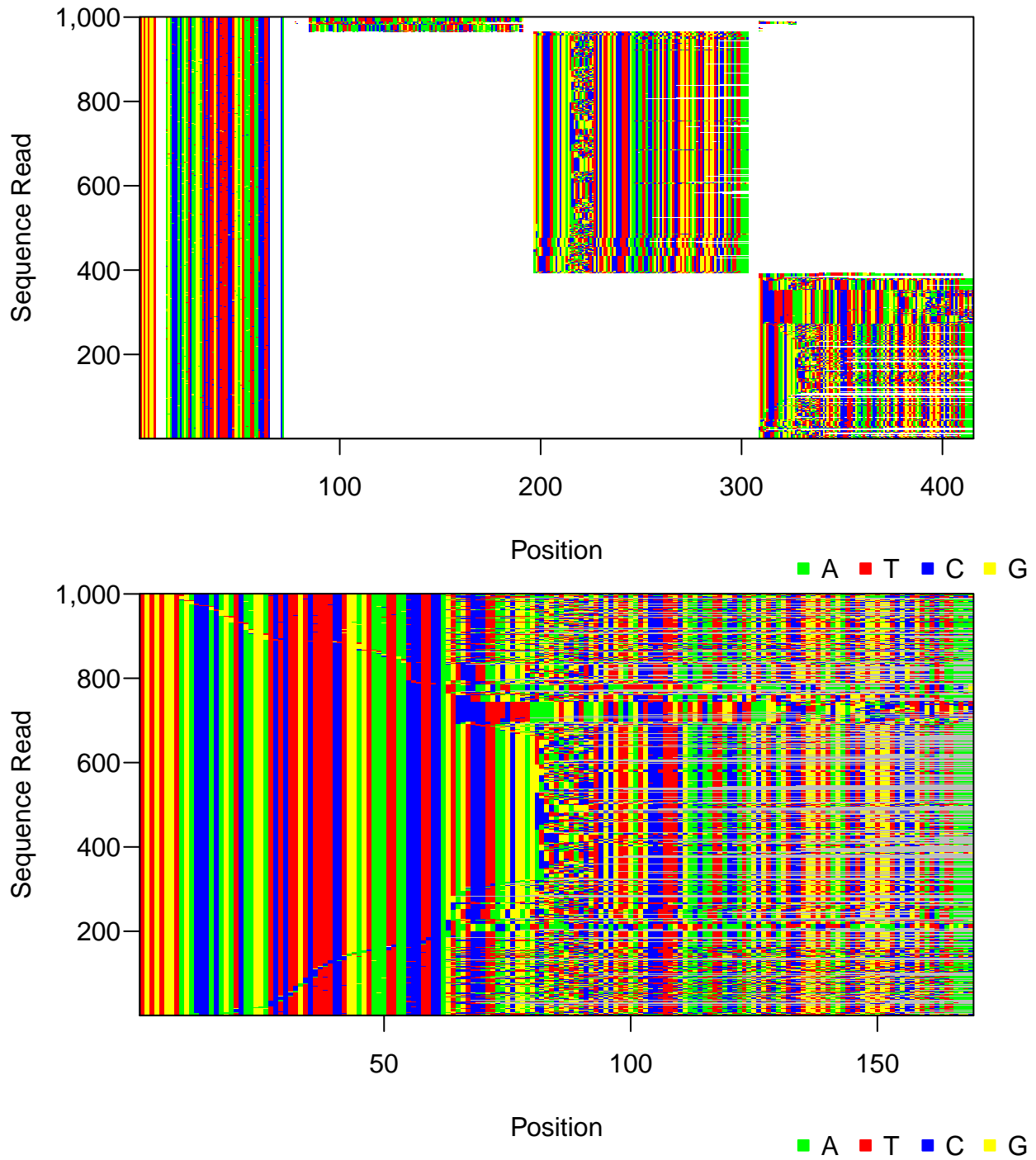
id	primer	LTR	expectedLTR	LANL
1	TGTGTGGT	AGACCCACAGATCAAGGATCTCTTGTCTTTTCCTGGAGTAAATTAACCCTTCCA	FALSE	TRUE

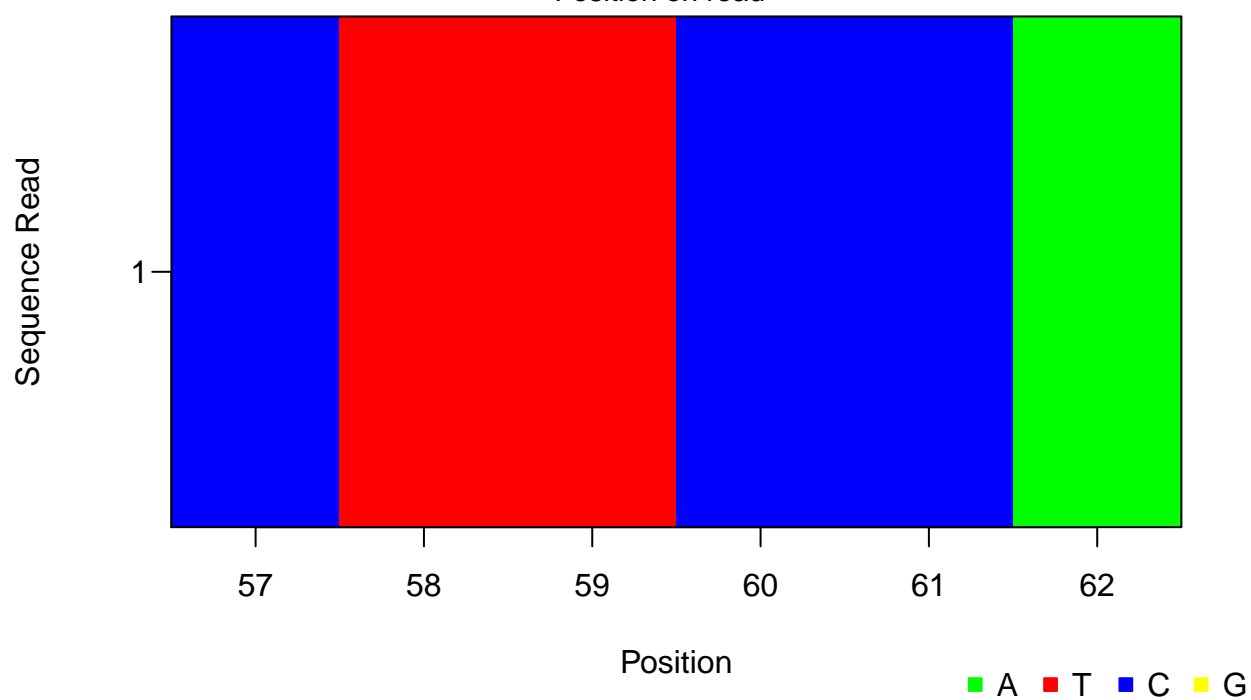
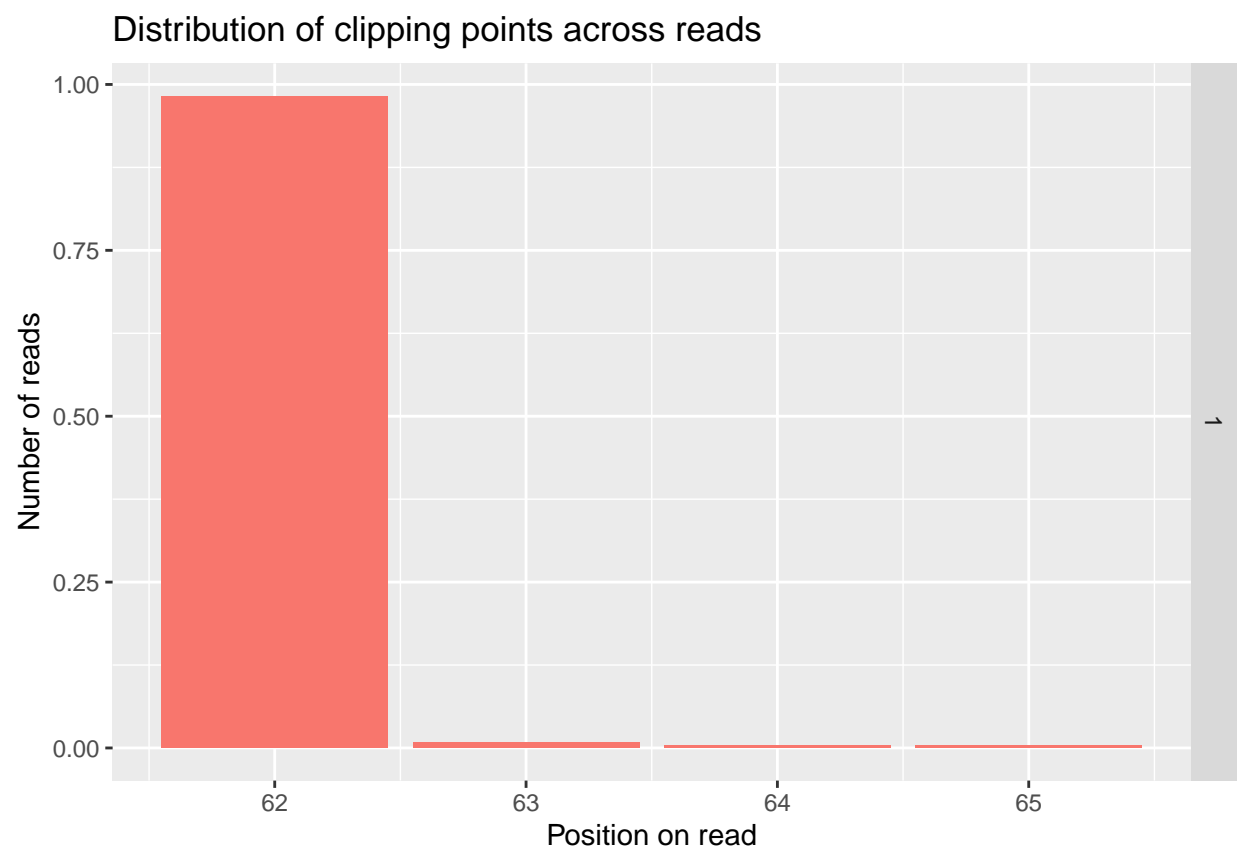
Variable	Total	1
Distinct	9257	5855 (63.2%)
DistinctHuman	268	231 (86.2%)
DistinctLinker	5470	3349 (61.2%)
Max	1109	1109 (100%)
MaxHuman	175	175 (100%)
MaxLinker	1109	1109 (100%)
Total	24065	14990 (62.3%)
TotalHuman	641	603 (94.1%)
TotalLinker	16253	10748 (66.1%)

## Visualization of reads

Reads are sectioned off into sections separated by white (nucleotide color legend is below the plot).

Primer /// LTR /// CA /// (unmatched) /// human-matching /// linker-matching /// (unmatched)







X non conserved  
X ≥ 50% conserved