

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/hivTest6_u3.R2.fastq.gz

Vincent project, sample: H1-2 (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.

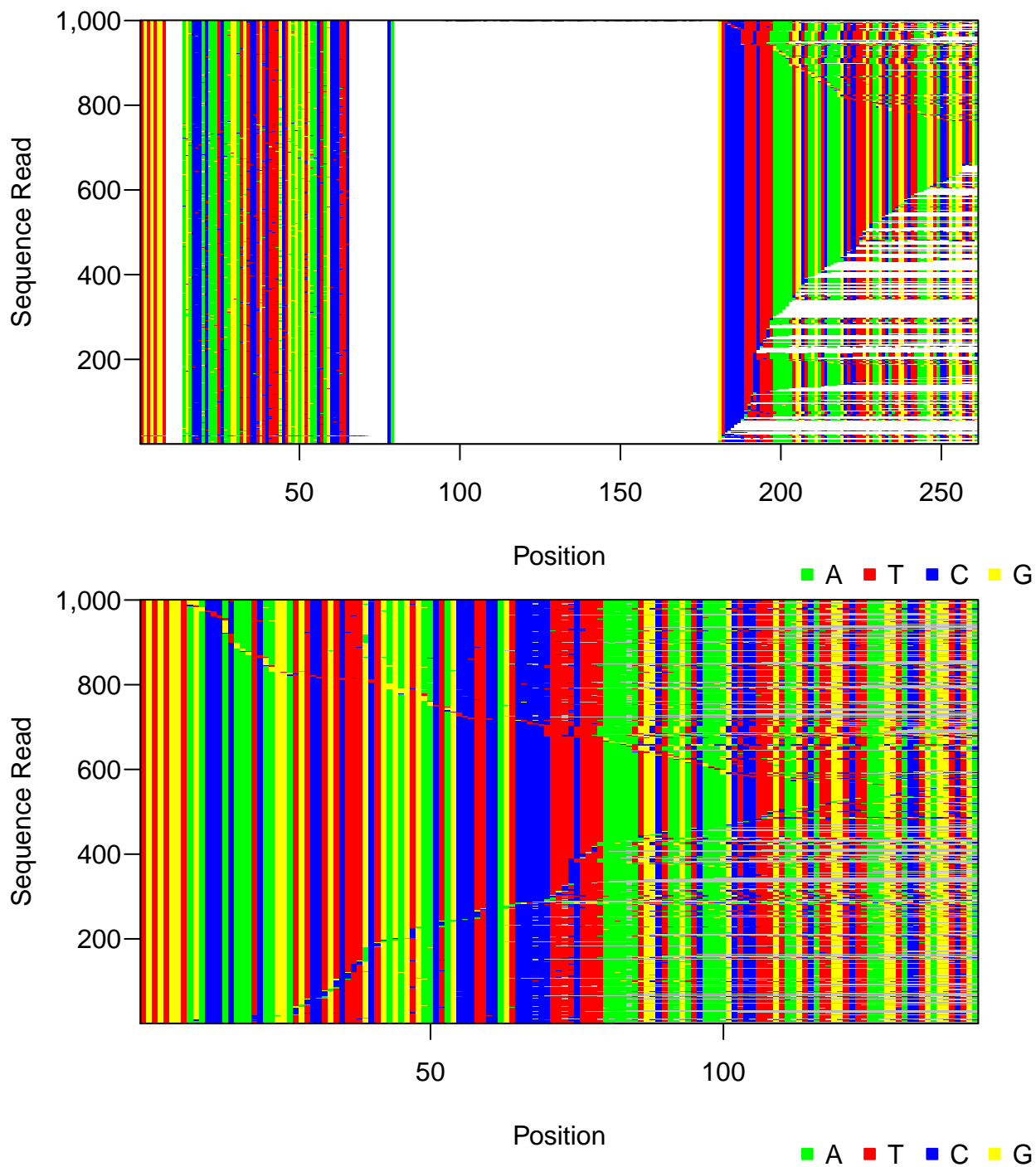
id	primer	LTR	expectedLTR	LANL
1	TGTGTGGT	AGACCCACAAATCAAGGATGTCCTGTCCTTTGCTGAGAGTGAAGTACGCCCTTCCA	FALSE	TRUE

Variable	Total	1
Distinct	3216	1622 (50.4%)
DistinctHuman	299	0 (0%)
DistinctLinker	177	2 (1.1%)
Max	3832	3832 (100%)
MaxHuman	38	0 (0%)
MaxLinker	12	1 (8.3%)
Total	18233	9528 (52.3%)
TotalHuman	413	0 (0%)
TotalLinker	198	2 (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