

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/hivTest3_u3.R2.fastq.gz

ODoherty project, sample: GTSP3456-1 (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.

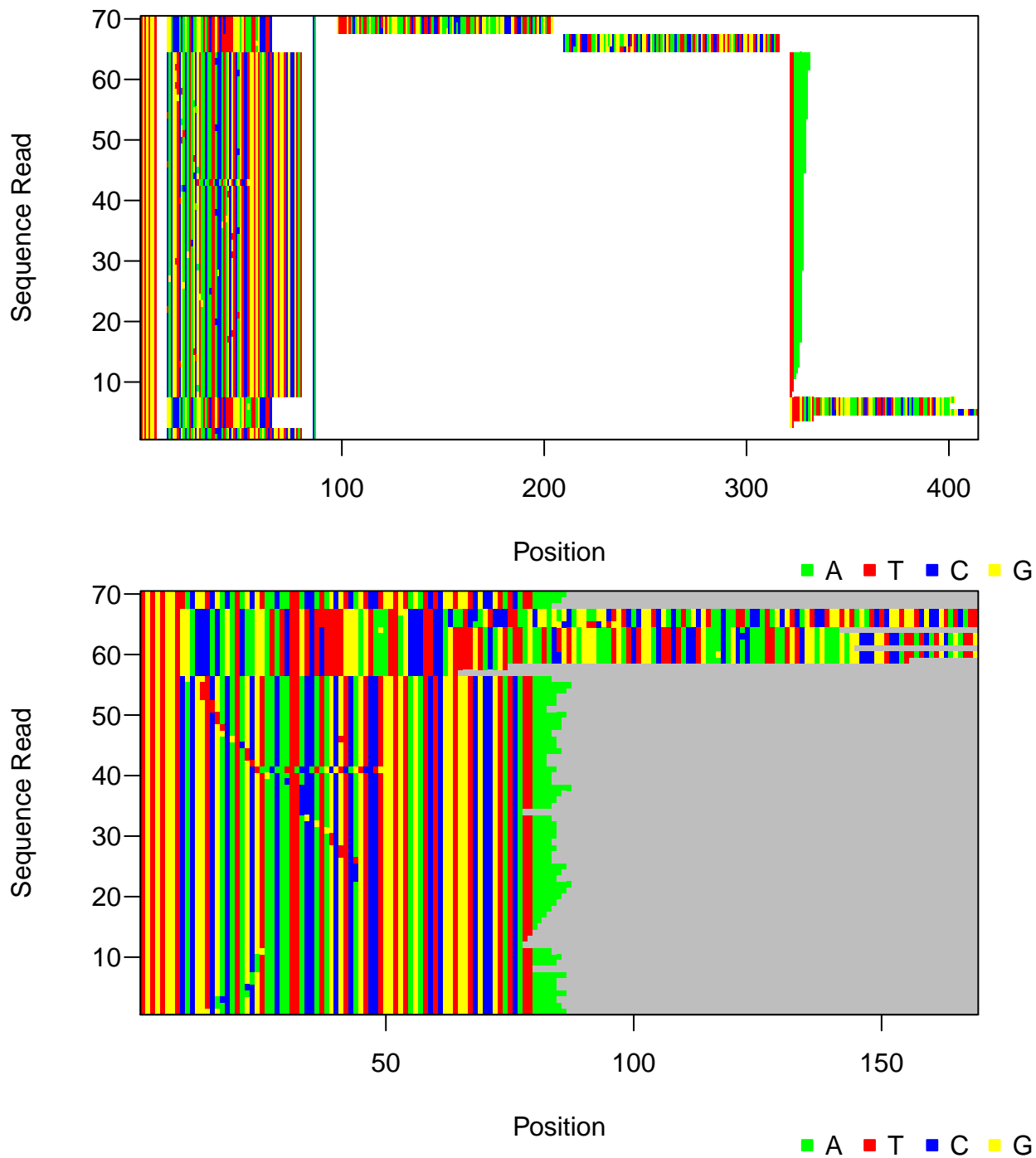
id	primer	LTR	expectedLTR	LANL
1	TGTGTGGT	CACGGTCGACATAGCGTAACAATTACCATAGCGTCAGTCCTGGTGTAGATCTCGGTGGTCGCCGTATCA	FALSE	FALSE

Variable	Total	1
Distinct	8894	59 (0.7%)
DistinctHuman	285	0 (0%)
DistinctLinker	597	0 (0%)
Max	866	316 (36.5%)
MaxHuman	4	0 (0%)
MaxLinker	8	0 (0%)
Total	19622	998 (5.1%)
TotalHuman	304	0 (0%)
TotalLinker	610	0 (0%)

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 $\geq 50\%$ conserved