

LTR Parser Results

Kevin McCormick

22 June, 2020

Overview

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

/home/kevin/dev/ltrparser/testdata/demo/fastq.gz/hivTest5_u5.R2.fastq.gz

Blankson project, sample: GTSP3503-2 (U5)

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.

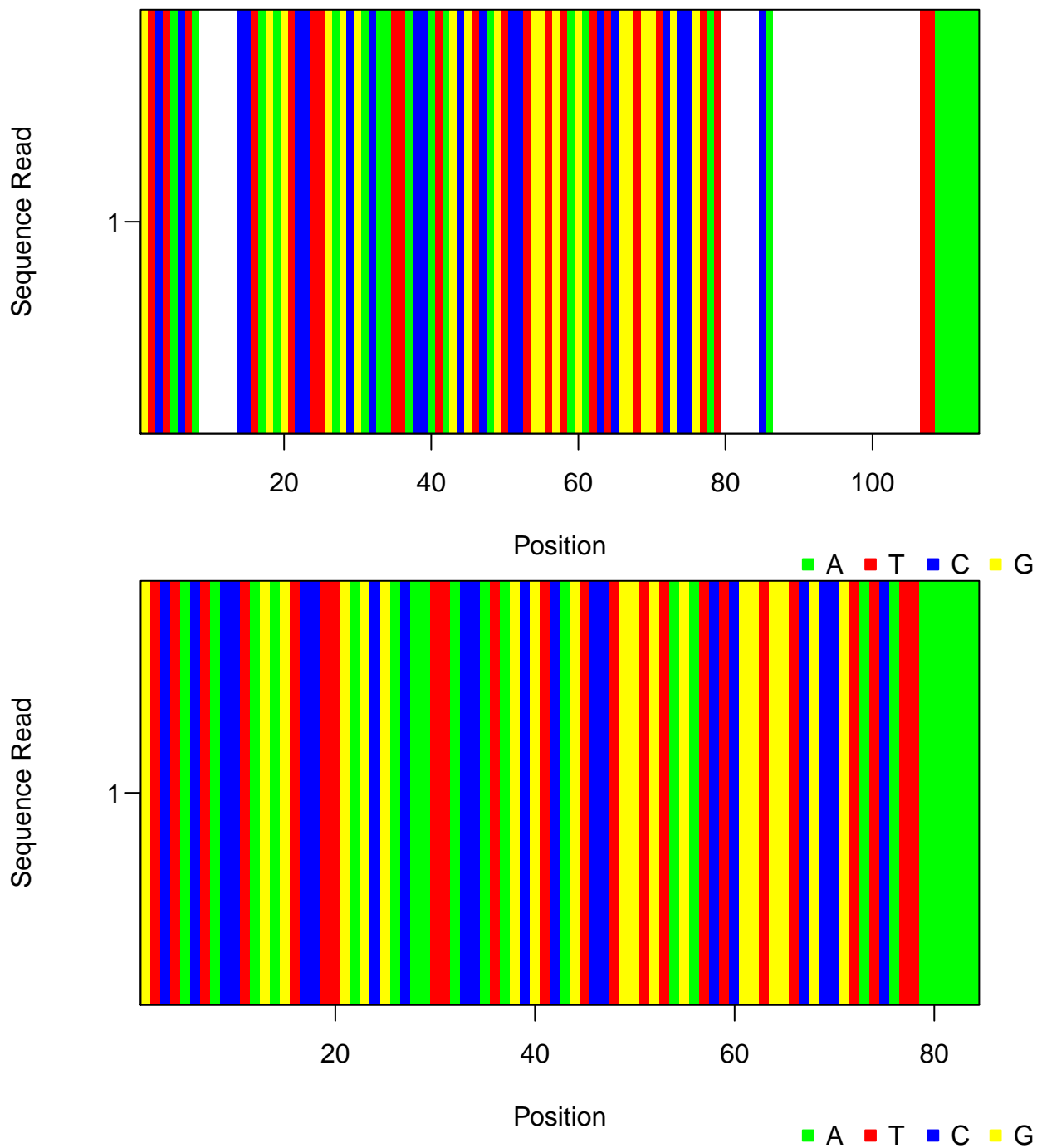
id	primer	LTR	expectedLTR	LANL
1	GTCTACTA	CCTAGAGTCCTTGAGCGACAATTACCATAGCGTCAGTCCTGGTGTAGATCTCGGTGGTCGCCGTATCA	FALSE	FALSE

Variable	Total	1
Distinct	5230	1 (0%)
DistinctHuman	205	0 (0%)
DistinctLinker	2773	0 (0%)
Max	3858	1 (0%)
MaxHuman	100	0 (0%)
MaxLinker	3858	0 (0%)
Total	24049	1 (0%)
TotalHuman	373	0 (0%)
TotalLinker	18257	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)





☐ non conserved
☒ $\geq 50\%$ conserved