LTR Parser Results

Kevin McCormick

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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_u5.R2.fastq.gz

Vincent project, sample: H1-2 (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.
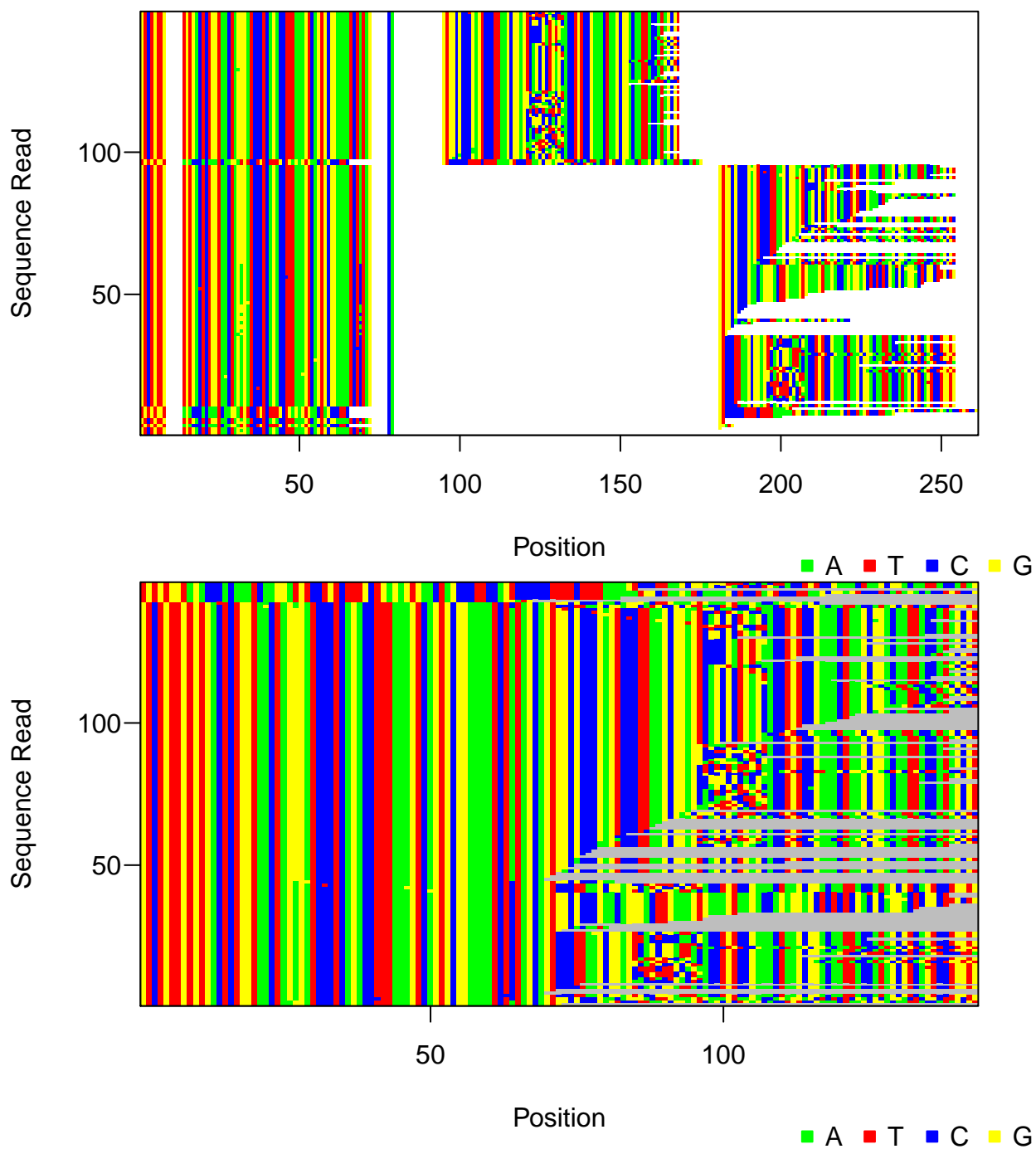
id	primer	LTR	expectedLTR	LANL
1	GTCTGTTG	TGTGACTCTGGTAACTAGAGATCCCTCAGACCTTTAAAGTCAGTGCGGAAAATCTCTAGCA	FALSE	TRUE

Variable	Total	1
Distinct	8882	142 (1.6%)
DistinctHuman	485	0 (0%)
DistinctLinker	1508	52 (3.4%)
Max	2130	99 (4.6%)
MaxHuman	77	0 (0%)
MaxLinker	2130	99 (4.6%)
Total	22474	321 (1.4%)
TotalHuman	723	0 (0%)
TotalLinker	5564	193 (3.5%)

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)

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logo        TGTGACTCTGGTAACTAGAGATCCCTCAGACCTTAAGTCAGTGCGGAAAATCTCTAGCA

1           TGTGACTCTGGTAACTAGAGATCCCTCAGACCTTTAAAGTCAGTGCGGAAAATCTCTAGCA   61
HXB2        TGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTAGTCAGTGTGGAAAATCTCTAGCA   61
consensus   !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!! !!  !!!!!!!! !!!!!!!!!!!!!!!
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X   non conserved
X   ≥ 50% conserved