

LTR Parser Results

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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/hivTest2_u3.R2.fastq.gz

Jones project, sample: GTSP3588-1 (U3)

Analysis of common primer-LTR pairs

A total of 2 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.

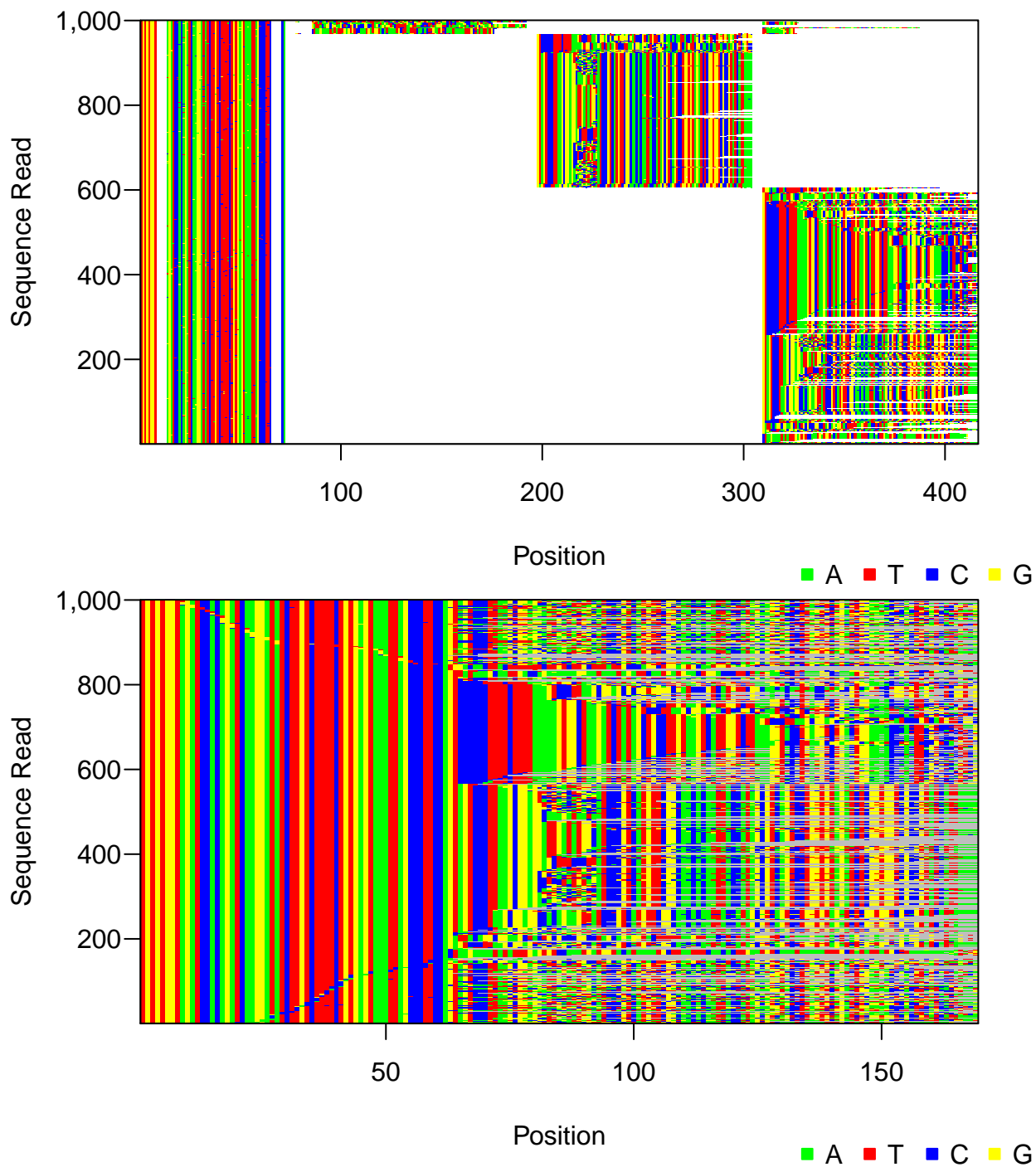
id	primer	LTR	expectedLTR	LANL
1	TGTGTGGT	AGATCCACAGATCAAGGATATCTTGTCTTTCTGTGAGTAAATTAGCCCTTCCA	FALSE	TRUE
2	TGTGTGGT	AGATCCACAGATCAAGGATATCTTGTCTTTCTGTGAGTAAATTAGCCCTCCA	FALSE	TRUE

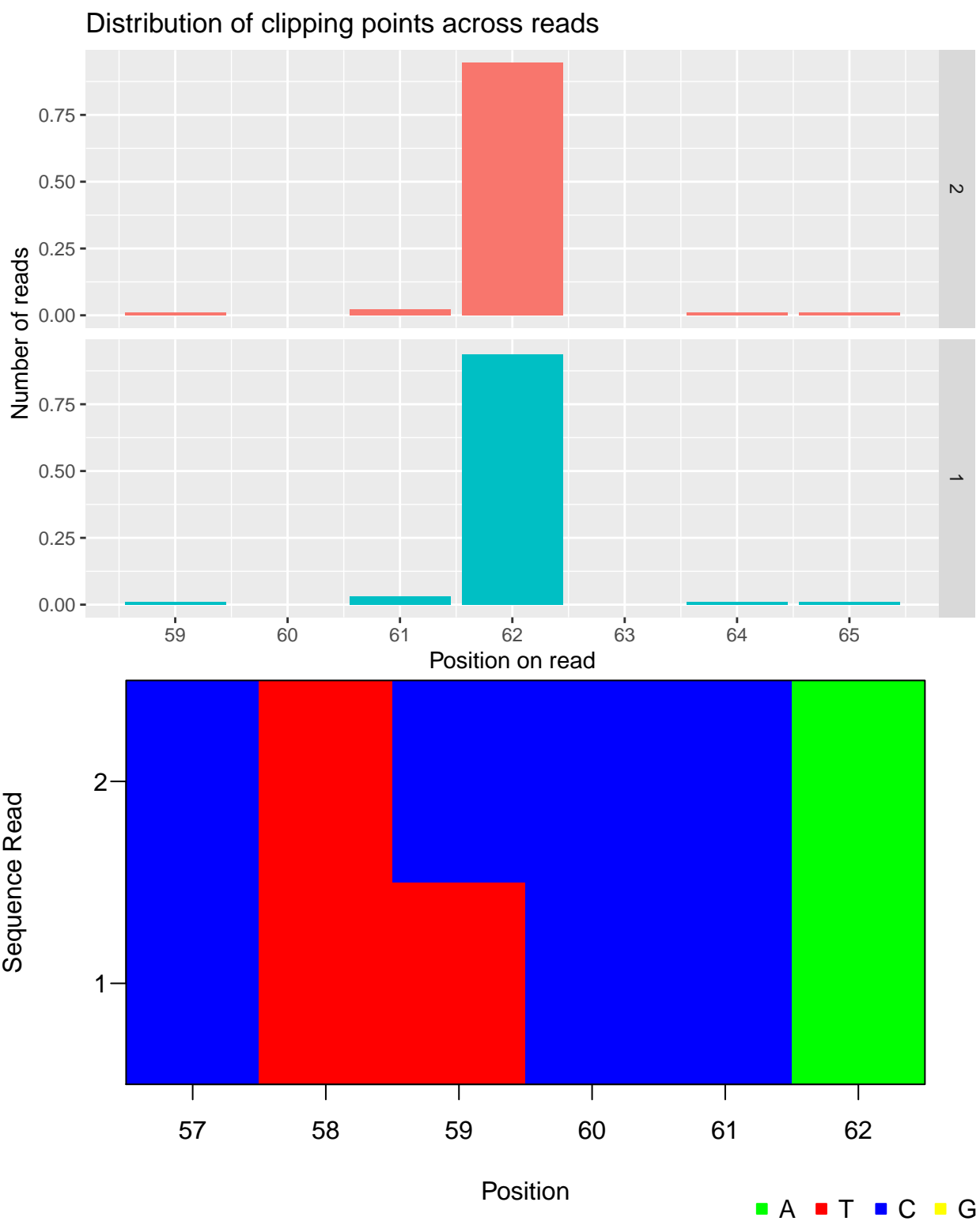
Variable	Total	1	2
Distinct	8116	2980 (36.7%)	2922 (36%)
DistinctHuman	106	96 (90.6%)	92 (86.8%)
DistinctLinker	2194	1068 (48.7%)	1046 (47.7%)
Max	1643	1643 (100%)	1643 (100%)
MaxHuman	96	96 (100%)	96 (100%)
MaxLinker	1643	1643 (100%)	1643 (100%)
Total	22551	10159 (45%)	10101 (44.8%)
TotalHuman	309	299 (96.8%)	295 (95.5%)
TotalLinker	7896	4758 (60.3%)	4736 (60%)

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