

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/hivTest4_u5.R2.fastq.gz

Scott project, sample: GTSP3518-1 (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.

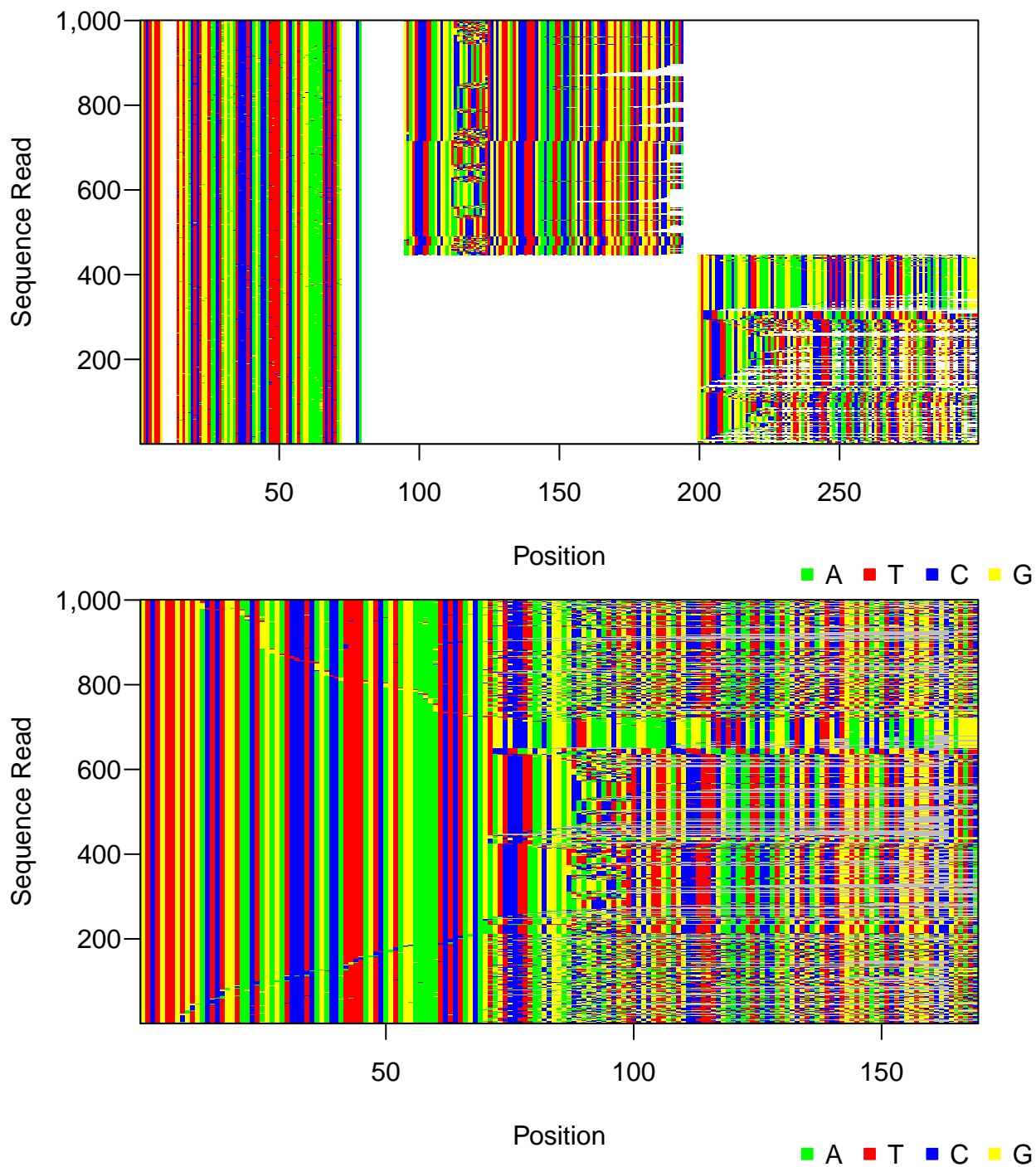
id	primer	LTR	expectedLTR	LANL
1	GTCTGTTG	TGTGACTCTGGTAACTAGAGATCCCTCAGACCATTTTAGTCAGTAGGAAAAATCTCTAGCA	FALSE	TRUE

Variable	Total	1
Distinct	7344	3213 (43.8%)
DistinctHuman	31	0 (0%)
DistinctLinker	4409	1767 (40.1%)
Max	1099	1099 (100%)
MaxHuman	2	0 (0%)
MaxLinker	1099	1099 (100%)
Total	24101	10328 (42.9%)
TotalHuman	32	0 (0%)
TotalLinker	17801	7297 (41%)


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

 ≥ 50% conserved