

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/hivTest7_u3.R2.fastq.gz

ODoherty project, sample: GTSP2314a (U3)

Analysis of common primer-LTR pairs

A total of 4 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.

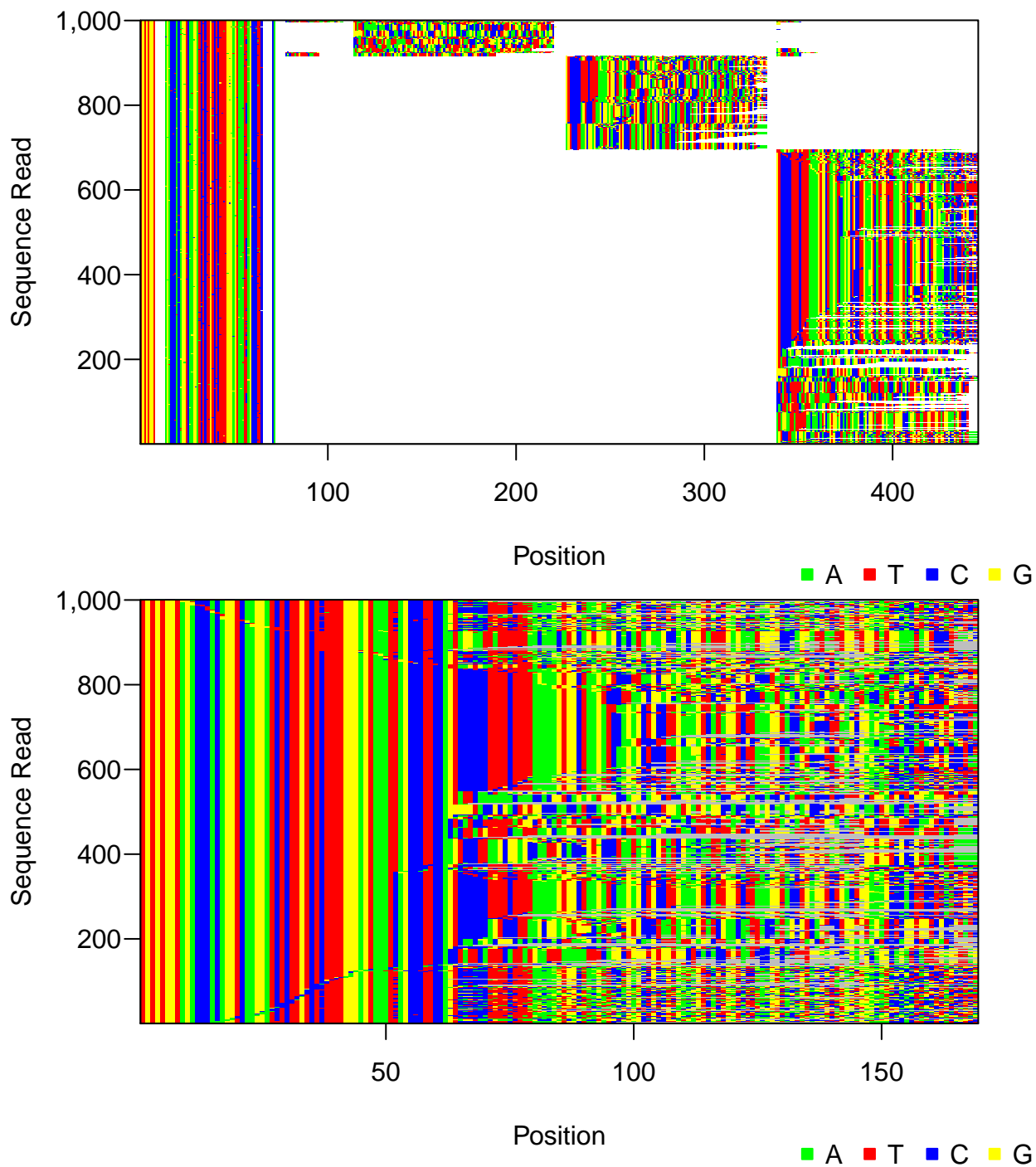
id	primer	LTR	expectedLTR	LANL
1	TGTGTGGT	AGACCCACAGGTCAAGGATCTCTTGTCCTTTTGGGAGTAAATTAGCCCTTCCA	FALSE	TRUE
2	TGTGTGGT	AGACCCACAGGTCAAGGATCTCTTGTCCTTTTGGGAGTAAATCAGCCCTTCCA	FALSE	TRUE
3	TGTGTGGT	AGACCCACAGGTCAAGGATCTCTTGTCCTTTTGGGAGTAAATTAGCCCTTCCA	FALSE	TRUE
4	TGTGTGGT	AGACCCACAGGTCAAGGATCTCTTGTCCTTTTGGGAGTAAATTAGCCCTTCCA	FALSE	TRUE

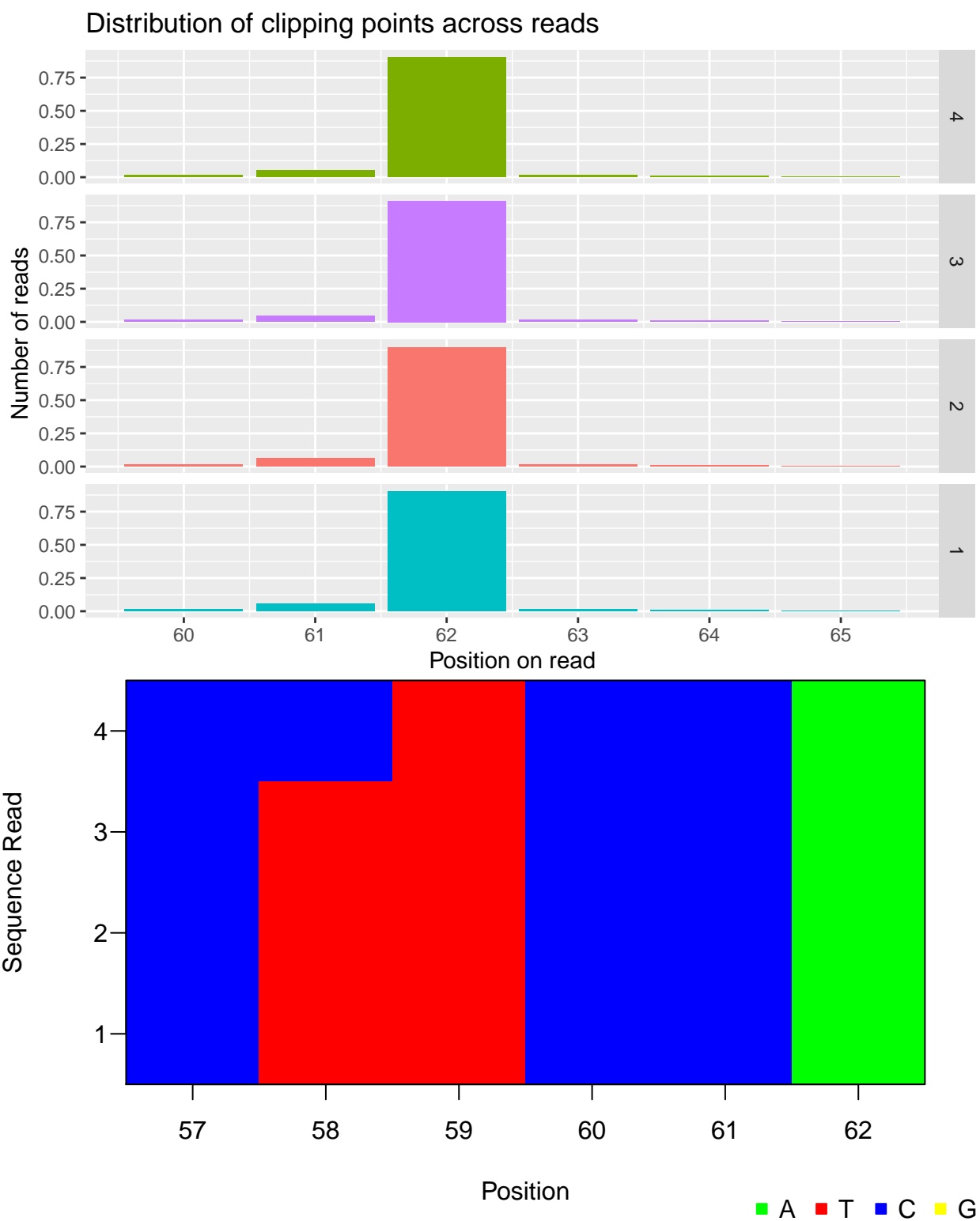
Variable	Total	1	2	3	4
Distinct	6968	4910 (70.5%)	4723 (67.8%)	4309 (61.8%)	4284 (61.5%)
DistinctHuman	476	391 (82.1%)	376 (79%)	346 (72.7%)	338 (71%)
DistinctLinker	1767	1052 (59.5%)	1007 (57%)	934 (52.9%)	944 (53.4%)
Max	1358	1358 (100%)	1358 (100%)	1358 (100%)	1358 (100%)
MaxHuman	415	415 (100%)	415 (100%)	415 (100%)	415 (100%)
MaxLinker	662	662 (100%)	662 (100%)	662 (100%)	662 (100%)
Total	23238	16230 (69.8%)	15817 (68.1%)	15241 (65.6%)	15210 (65.5%)
TotalHuman	1649	1521 (92.2%)	1507 (91.4%)	1463 (88.7%)	1455 (88.2%)
TotalLinker	5855	3713 (63.4%)	3650 (62.3%)	3568 (60.9%)	3579 (61.1%)

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