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/hivIntSite1.fastq.gz

Analysis of common primer-LTR pairs

A total of 6 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	AGACCCACAGATCAAGGATCTCTTGGCTTTTCCTGGAGTAAATTAACCCTTCCA	FALSE	TRUE
2	TGTGTGGT	AGACCCACAGATCAAGGATCTCTTGTCTTTTCCTGGAGTAAATTAACCCTCCCA	FALSE	TRUE
3	TGTGTGGT	AGACCCACAGATCAAGGATCTCTTGTCTTTTCCTGGAGTAAATTAACCCTTCCA	FALSE	TRUE
4	TGTGTGGT	AGACCCACAGATCAAGGATCTCTTGTCTTTTCCTGGAGTAAATTAGCCCTTCCA	FALSE	TRUE
5	TGTGTGGT	AGACCCACAGATCAAGGGTCTCTTGTCTTTTCCTGGAGTAAATTAACCCTTCCA	FALSE	TRUE
6	TGTGTGGT	AGACCCACAGATCACGGATCTCTTGTCTTTTCCTGGAGTACATTAACCCTTCCA	FALSE	TRUE

Variable	Total	1	2	3	4	5	6
Distinct	2374	1407 (59.3%)	1412 (59.5%)	1480 (62.3%)	1409 (59.4%)	1410 (59.4%)	951 (40.1%)
DistinctHuman	64	57 (89.1%)	57 (89.1%)	57 (89.1%)	57 (89.1%)	57 (89.1%)	39 (60.9%)
DistinctLinker	0	0 (NaN%)					
Max	206	206 (100%)	206 (100%)	206 (100%)	206 (100%)	206 (100%)	206 (100%)
MaxHuman	31	31 (100%)	31 (100%)	31 (100%)	31 (100%)	31 (100%)	31 (100%)
MaxLinker	0	0 (NaN%)					
Total	4807	2947 (61.3%)	2952 (61.4%)	3022 (62.9%)	2949 (61.3%)	2950 (61.4%)	2371 (49.3%)
TotalHuman	119	112 (94.1%)	112 (94.1%)	112 (94.1%)	112 (94.1%)	112 (94.1%)	94 (79%)
TotalLinker	0	0 (NaN%)					

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)

