

1

Create annotation for full-length intact L1s

2

Align uniquely paired end reads of whole genome of interest sequencing and input in IGV to assess mappability in any given genomic region

3

Harvest cytoplasmic RNA from sample of interest and sequence

Align uniquely paired end reads to hg19 genome

Separate top strand

Separate bottom strand

Identify reads for + L1

Identify reads for - L1

Identify reads for + L1

Identify reads for - L1

Input mapped reads in excel and IGV

Manually curate