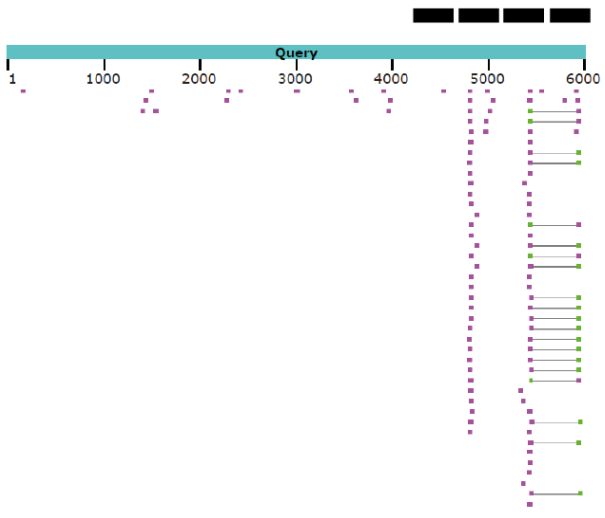
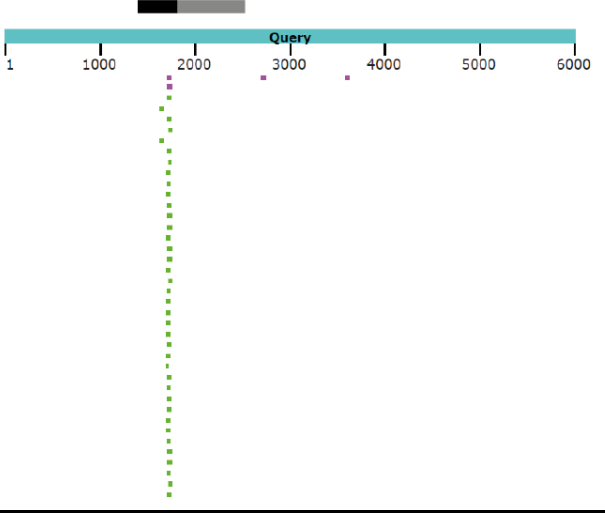
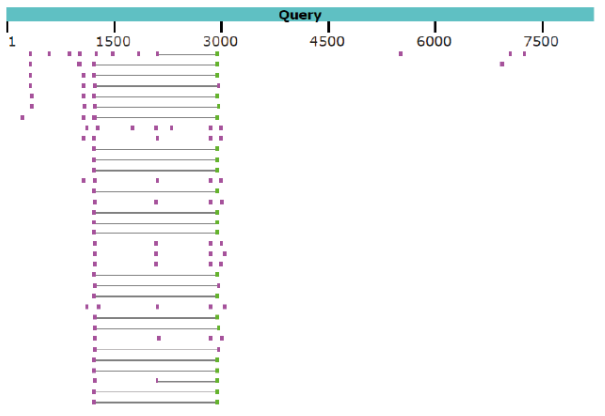
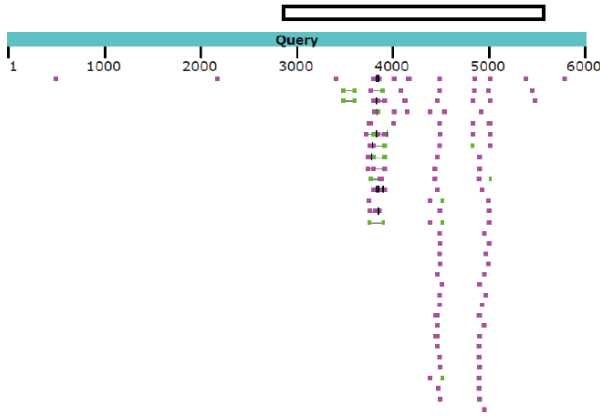
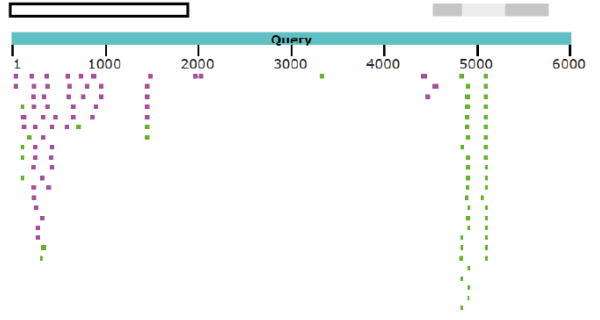
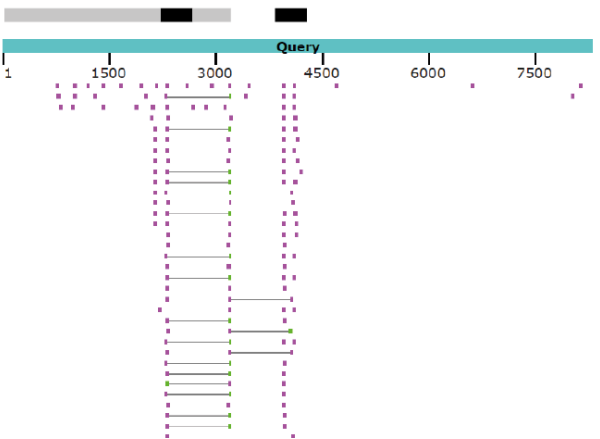


Table S1. Schematic illustration of the regions, alignment reads and genome repeats. The illustration shows alignment of Raji cell line RNA-Seq reads (SRX1981036) from Sequence Read Archive Nucleotide BLAST (NSBI). The positions of genome repeats were obtained from UCSC Genome Browser on Human (hg38) Assembly. The three areas that were selected are highlighted in green.

#	Coordinates of region (hg 38)	Alignment of reads and repeats position
1	11:68378000-68384000	<div> <div> <div>SINE</div> <div>SINE</div> <div>SINE</div> </div> </div>
2	11:68576671-68582671	<div> <div>LINE</div> <div>LINE</div> <div>SINE</div> </div>

5	14:105058665-105064665	<p>SINE SINE</p> 
6	14:105069641-105075641	<p>SINE LINE</p> 
7	14:105555400-105563600	<p>LTR SINE LTR SINE</p> 

8	14:105579331-105585331	<p>no repeats</p> 
9	14:105628900-105634900	<p>no repeats LTR DNA LTR</p> 
10	14:105674707-105683021	<p>LTR SINE LTR SINE</p> 

11	14:105744600-105750600	<p>no repeats no repeats LTR</p>
12	14:106398526-106404526	<p>SINE LTR SINE</p>
13	14:67458397-67464397	<p>SINE SINE SINE</p>

