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TECESdb: A database of Transposable Elements in Cancer EST Sequences

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Transposable elements are the most abundant interspersed sequences in human genome. It has been estimated that approximately 45% of the human genome comprises of transposable elements. Recent studies have shown that transposable elements could affect coding sequences, splicing patterns, and transcriptional regulation of human genes. In the present study, we investigated the transposable elements in relation to human cancer. Our analysis pipeline adopted for screening methods of the cancer specific expression from human expressed sequences. We developed a database for understanding the mechanism of cancer development in relation to transposable elements. Totally, 999 genes were identified to be integrated in their mRNA sequences by transposable element. We believe that our work might help many scientists who interested in cancer research to gain the insight of transposable element for understanding the human cancer.

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Acquired Promoter of HERV-H LTR and Various Alternative Splicing of GSDML Gene

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Human endogenous retroviruses (HERVs) have been integrated in our common ancestor genome during primate evolution. Long terminal repeats (LTRs) of HERVs sometimes could affect transcription activity and could provide a transcription start site (TSS) of adjacent gene transcript. The GSDML (gasdermin-like protein) gene has been reported to acquire the novel promoter and TSS by the integration of antisense HERV-H LTR after the divergence of hominoid and Old World monkeys. Potential transcription factor binding sites of LTR promoter were identified by in silico analysis. Critical region for transcription activity were investigated by the construction of deletion mutants in LTR promoter region. Interestingly, deletion of 5′flanking region of LTR sequences showed maximum activity of transcription and deletion of U5 region showed low level transcription activity. To identify the original transcript, genbank database sequences (EST and mRNA) were mined and analyzed with bioinformatics tools. Totally, 10 different alternative splicing patterns were found and their structures were reconstructed. Our findings provide a good example of acquired LTR promoter for gene transcription and basis of expression and alternative splicing for further investigation of GSDML gene.