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Omics Evidence: Single Nucleotide Variants Transmissions on Chromosome 20 in Liver Cancer Cell Lines

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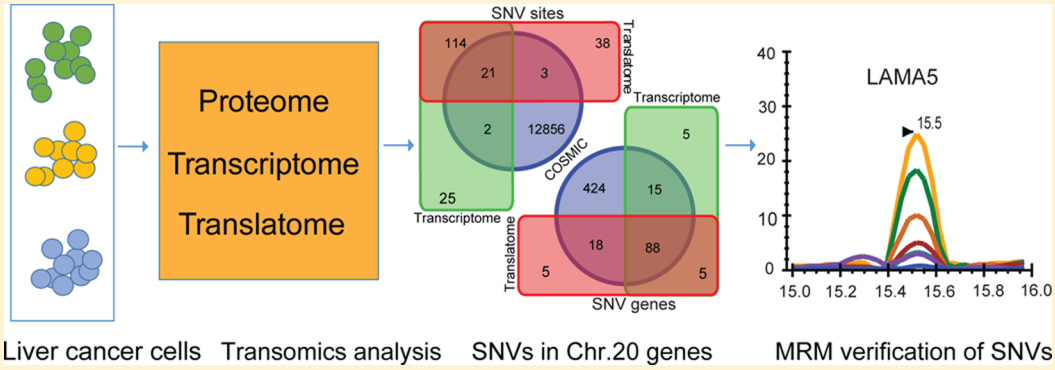
Supporting Information



ABSTRACT: Cancer genomics unveils many cancer-related mutations, including some chromosome 20 (Chr.20) genes. The mutated messages have been found in the corresponding mRNAs; however, whether they could be translated to proteins still requires more evidence. Herein, we proposed a transomics strategy to profile the expression status of human Chr.20 genes (555 in Ensembl v72). The data of transcriptome and translatome (the mRNAs bound with ribosome, translating mRNAs) revealed that ~80% of the coding genes on Chr.20 were detected with mRNA signals in three liver cancer cell lines, whereas of the proteome identified, only ~45% of the Chr.20 coding genes were detected. The high amount of overlapping of identified genes in mRNA and RNC-mRNA (ribosome nascent-chain complex-bound mRNAs, translating mRNAs) and the consistent distribution of the abundance averages of mRNA and RNC-mRNA along the Chr.20 subregions in three liver cancer cell lines indicate that the mRNA information is efficiently transmitted from transcriptional to translational stage, qualitatively and quantitatively. Of the 457 genes identified in mRNAs and RNC-mRNA, 136 were found to contain SNVs with 213 sites, and >40% of these SNVs existed only in metastatic cell lines, suggesting them as the metastasis-related SNVs. Proteomics analysis showed that 16 genes with 20 SNV sites were detected with reliable MS/MS signals, and some SNVs were further validated by the MRM approach. With the integration of the omics data at the three expression phases, therefore, we are able to achieve the overall view of the gene expression of Chr.20, which is constructive in understanding the potential trend of encoding genes in a cell line and exploration of a new type of markers related to cancers.

KEYWORDS: *Proteome, transcriptome, translatome, Chromosome, mutation*

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