

Human genes with a greater number of transcript variants tend to have biologically important roles

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Alternative splicing is a process occurred in eukaryotic cells during gene expression that results in a multi-exon gene to produce multiple mRNA products. Although physiologically important, many aspects of genes with different number of transcript variants still remain to be characterized. Here, we suggest bioinformatic evidences that human genes with a greater number of transcript variants tend to play functionally important roles in cells. The genes with a greater transcript variants exhibited greater frequencies of acting as housekeeping and essential genes rather than tissue-selective and non-essential genes. These findings were confirmed by 60 cancer metabolic simulations. All these results indicate that human genes with a greater number of transcript variants play biologically more fundamental roles. [This work was supported by the Technology Development Program to Solve Climate Changes on Systems Metabolic Engineering for Biorefineries from the Ministry of Science, ICT and Future Planning (MSIP) through the National Research Foundation (NRF) of Korea (NRF-2012M1A2A2026556 and NRF-2012M1A2A2026557).]