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Abstract:

Background RNA-binding proteins (RBPs) play important roles in cellular homeostasis by controlling gene expression at the post-transcriptional level. Results We explore the expression of more than 800 RBPs in sixteen healthy human tissues and their patterns of dysregulation in cancer genomes from The Cancer Genome Atlas project. We show that genes encoding RBPs are consistently and significantly highly expressed compared with other classes of genes, including those encoding regulatory components such as transcription factors, miRNAs and long non-coding RNAs. We also demonstrate that a set of RBPs, numbering approximately 30, are strongly upregulated (SUR) across at least two-thirds of the nine cancers profiled in this study. Analysis of the protein–protein interaction network properties for the SUR and non-SUR groups of RBPs suggests that path length distributions between SUR RBPs is significantly lower than those observed for non-SUR RBPs. We further find that the mean path lengths between SUR RBPs increases in proportion to their contribution to prognostic impact. We also note that RBPs exhibiting higher variability in the extent of dysregulation across breast cancer patients have a higher number of protein–protein interactions. We propose that fluctuating RBP levels might result in an increase in non-specific protein interactions, potentially leading to changes in the functional consequences of RBP binding. Finally, we show that the expression variation of a gene within a patient group is inversely correlated with prognostic impact. Conclusions Overall, our results provide a roadmap for understanding the impact of RBPs on cancer pathogenesis.

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