

## CONTEXT-SPECIFIC CELL SIGNALING ANALYSIS USING LOGIC FRAMEWORK

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The description of signaling networks in textbooks and online resources is usually not context specific, because it is typically based on evidence from multiple experiments, performed for different cell types growing under various conditions. Thus, any analysis of such networks alone will lack all context-specific information that originates from context dependent signaling. Here, we developed a logic-based novel method to perform context-based analysis using signaling networks and context-specific transcriptomics and proteomics data. To understand the interactions of NOTCH1 signaling system in different cancer types we integrated cancer cell line encyclopedia (CCLE; (Barretina et al, 2012) data into the system. In previous studies, MYC was found as expressed in each cancer and it is known to be a key player in many cancers. Additionally, to identify potential cancer biomarkers we integrated CCLE data once again into the atlas of cancer signaling that is large-scale curated signaling map up till now (Kuperstein et al, 2015). Subsequently, we identified many potential cancer biomarkers associated with apoptosis, cell proliferation, and cell survival. Biomarkers, such as FGF3, FGF4, and HIF1A were identified in each cancer types and they are known to be cancer biomarkers (<https://www.cancergenomeinterpreter.org/>).

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