



Identification of tissue specific cancer driver gene interactors

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Cancer driver genes, when mutated, contribute to cancer development. Driver genes are usually identified by being frequently mutated in cancer samples. Some drivers are involved in many cancer types (generalist drivers), but most of them are associated with a restricted number of cancers (specific drivers). Recently we observed that specific drivers tend to have different interactions (protein physical interactions, signaling and regulatory interactions) in the tissues where they contribute to cancer development in comparison with other tissues. This observation suggests that these differential tissue specific interactors may play relevant roles in cancer development. This project aims to identify and characterize such tissue specific cancer driver interactors for multiple cancers using a comparative interactome analysis across tissues. The project consists in: 1 – collecting molecular interaction data to build a global interactome, 2- construction of tissue specific interactions through the analysis of tissue gene expression datasets (GTEx, Human Protein Atlas, TCGA), 3- development of quantitative scores to rank driver gene interactors according to their ability to preferentially interact with driver genes in the tissues where these drivers are (or are not) associated with cancer development, 4- identification, in each tissue, of tissue specific cancer driver gene interactors, 5- functional characterization of these driver interactors. We expect to find potential drug targets or biomarkers among these tissue specific driver interactors, contributing for the improvement of patient stratification and personalized medicine goals.