

Cell Line Screens Identify Biomarkers of Drug Sensitivity in GLIOMA Cancer

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Abstract : Clinical responses to anticancer therapies are often restricted to a subset of patients. In some cases, mutated cancer genes are potent biomarkers of response to targeted agents. There is an urgent need to identify biomarkers that predict which patients with are most likely to respond to treatment. Systematic efforts to correlate tumor mutational data with biologic dependencies may facilitate the translation of somatic mutation catalogs into meaningful biomarkers for patient stratification. To identify genomic features associated with drug sensitivity and uncover new biomarkers of sensitivity and resistance to cancer therapeutics, we have screened and integrated a panel of several hundred cancer cell lines from different databases, mutation, DNA copy number, and gene expression data for hundreds of cell lines with their responses to targeted and cytotoxic therapies with drugs under clinical and preclinical investigation. We found mutated cancer genes were associated with cellular response to most currently available Glioma cancer drugs and some frequently mutated genes were associated with sensitivity to a broad range of therapeutic agents. By linking drug activity to the functional complexity of cancer genomes, systematic pharmacogenomic profiling in cancer cell lines provides a powerful biomarker discovery platform to guide rational cancer therapeutic strategies.

Keywords : cancer, gene network, Lasso, penalized regression, P-values, unbiased estimator

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