Evaluation of reverse phase protein array (RPPA)-based pathway-activation profiling in 84 non-small cell lung cancer (NSCLC) cell lines as platform for cancer proteomics and biomarker discovery.

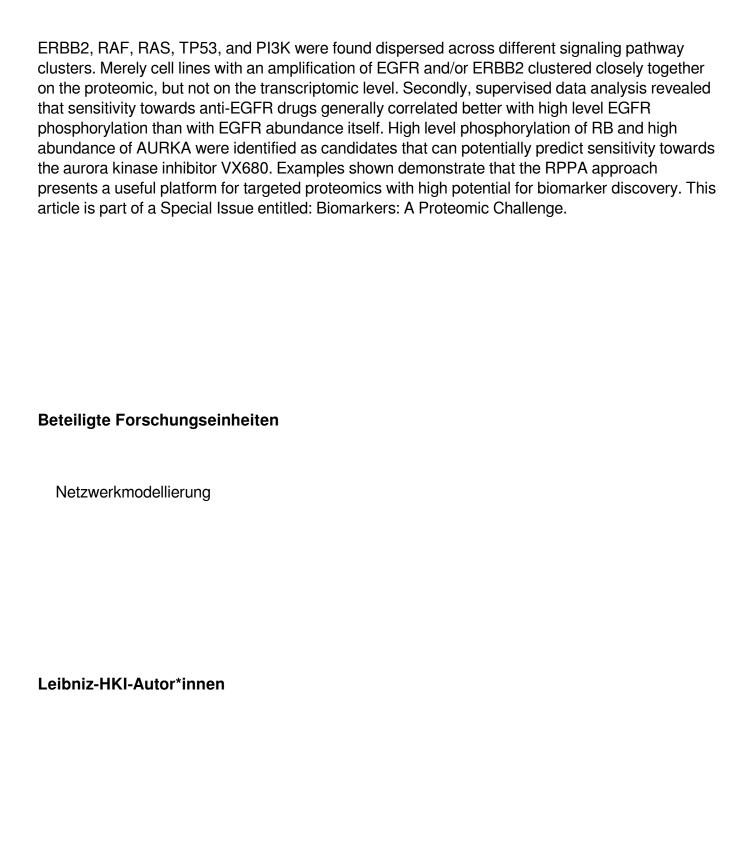
Ummanni R, Mannsperger HA, Sonntag J, Oswald M, Sharma AK, König R, Korf U (2014) Evaluation of reverse phase protein array (RPPA)-based pathway-activation profiling in 84 non-small cell lung cancer (NSCLC) cell lines as platform for cancer proteomics and biomarker discovery. *Biochim Biophys Acta* 1844(5), 950-959.

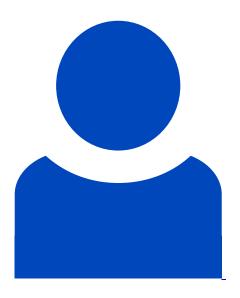
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Abstract

The reverse phase protein array (RPPA) approach was employed for a quantitative analysis of 71 cancer-relevant proteins and phosphoproteins in 84 non-small cell lung cancer (NSCLC) cell lines and by monitoring the activation state of selected receptor tyrosine kinases, PI3K/AKT and MEK/ERK1/2 signaling, cell cycle control, apoptosis, and DNA damage. Additional information on NSCLC cell lines such as that of transcriptomic data, genomic aberrations, and drug sensitivity was analyzed in the context of proteomic data using supervised and non-supervised approaches for data analysis. First, the unsupervised analysis of proteomic data indicated that proteins clustering closely together reflect well-known signaling modules, e.g. PI3K/AKT- and RAS/RAF/ERK-signaling, cell cycle regulation, and apoptosis. However, mutations of EGFR,





Rainer König

Details



Marcus Oswald

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