Neues Denken. Neue Materialien.

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"TARGETED PROTEOMICS IN PERSONALIZED ONCOLOGY"

Prof. Dr. Stefan Wiemann
Deutsches Krebsforschungszentrum, Heildelberg

Dienstag, 18.12.2018, 11.00 Uhr

INM, Leibniz-Saal, Campus D2 5
Gastgeber: Prof. Dr. Dr. h.c. Niels de Jonge

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The rising number of targeted cancer therapies call for sophisticated methods of patient stratification in order to apply targeted anti-cancer agents efficiently. Whilst genomic and transcriptomic data is easily accessible and is starting to be used in modern clinical practice, major activation stages and druggable targets are restricted to the proteomic level. We have applied a targeted proteomic approach using Reverse Phase Protein Array (RPPA) technology to explore the proteomic landscape of 134 tumor samples from 17 tumor entities that had previously undergone comprehensive genomic and transcriptomic profiling within NCT MASTER (Molecularly Aided Stratification for Tumor Eradication Research). Twenty-three antibodies for key proteins and posttranslational modifications (PTMs) mapping into the NCT MASTER therapeutic baskets were incubated, and signal intensities bioinformatically processed. Proteins reflecting activation of cancer signaling pathways were thus investigated to evaluate whether proteomic data would add relevant information towards shaping therapy recommendations. Results were compared with recommendations based on genomic data alone. Disparate results were found for many cases suggesting that targeted proteomics indeed adds an additional, clinically meaningful layer to treatment stratification. Implementation of a proteomic workflow into the NCT MASTER program is under way.

Wir laden 15 Minuten vor Beginn zu einem Get-together mit dem Referenten ein.