Project abstract

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Group homepage: *Please visit our website for further information on our research and recent publications.*	**www.translational-cancer-epigenomics.de/** **https://pubmed.ncbi.nlm.nih.gov/?term=lipka+db&sort=date&size=200**

PROJECT PROPOSAL

We combine basic and translational research to discover and implement novel diagnostic and therapeutic approaches to malignant diseases. The main focus is on the analysis of epigenomic alterations occurring in pre-malignant and malignant cells as compared to their normal counterparts in order to understand how aberrant epigenetic programming impacts on tumor initiation and progression. We combine analyses of primary patient samples with innovative mouse and cell culture models using single-cell multi-omics approaches as well as cutting-edge third-generation sequencing technologies, e.g. nanopore sequencing, to assess the impact of epigenetic dysregulation on the malignant phenotype at the systems level. Findings are validated in pre-clinical models and patient samples provided by national and international collaboration partners.

In a current project, we aim at identifying the molecular determinants of treatment outcome in patients with oligo-metastatic colorectal cancer (CRC) using non-invasive analysis of circulating tumor cells (CTCs). CTCs provide a unique opportunity to comprehensively assess the molecular intra-tumor heterogeneity and enable time-resolved analyses using serial samples. We aim to understand how the acquisition of secondary mutations and epigenetic abnormalities shape the molecular landscape and the phenotype of the tumor cells. Results from these analyses will be validated in *ex vivo* and *in vivo* models (cell lines, organoids, patient-derived xenografts) and will be used to develop new monitoring and treatment strategies for CRC patients.

The project involves various cell and molecular biology methods (e.g. PCR, FACS, colony formation assays, CRISPR-Cas9 genome editing), the generation of single-cell multi-omics sequencing libraries, bioinformatic analysis and data interpretation. Project-related experience in oncology research and/or computational biology would be ideal but are not a prerequisite. The successful candidate should have excellent communication skills and should demonstrate commitment toward highly interdisciplinary research. This work will benefit from already established experimental workflows and analysis pipelines but will also involve the development of novel methods.

We provide excellent working conditions in a dynamic international group of scientists together with collaboration partners in the field of translational oncology (Prof. Loges, Prof. Fröhling, PD Dr. Köhler, PD Dr. Boch), bioinformatics (Prof. Stegle), and single-cell sequencing (scOpenLab, Dr. Mallm).