

FOCUS A -TUMOR INTRINSIC **MECHANISMS**

FOCUS B — TUMOR MICRO-**ENVIRONMENT**

FOCUS C -**TECHNOLOGICAL** INNOVATION

FOCUS D -UNITE CORES

D01 - UNITE INTEGRATED TISSUE AND PATIENT DERIVED MODEL CORE Andreas von Deimling, Daniel Hänggi & Christel Herold-Mende







SUMMARY

This central project aims at ensuring uniform availability and quality of tissue material and high-throughput data in costeffective and state-of-technology way to be used in UNITE subprojects (coined UNITE Core Collection). Our aim is to work with and provide material and data from newly diagnosed patients and matching recurrences, which has been stringently standardized, characterized and anaylzed reflecting the multilevel approach of the CRC.

TASK

Task 1 – Tumor Banking and clinical data management in Heidelberg and Mannheim

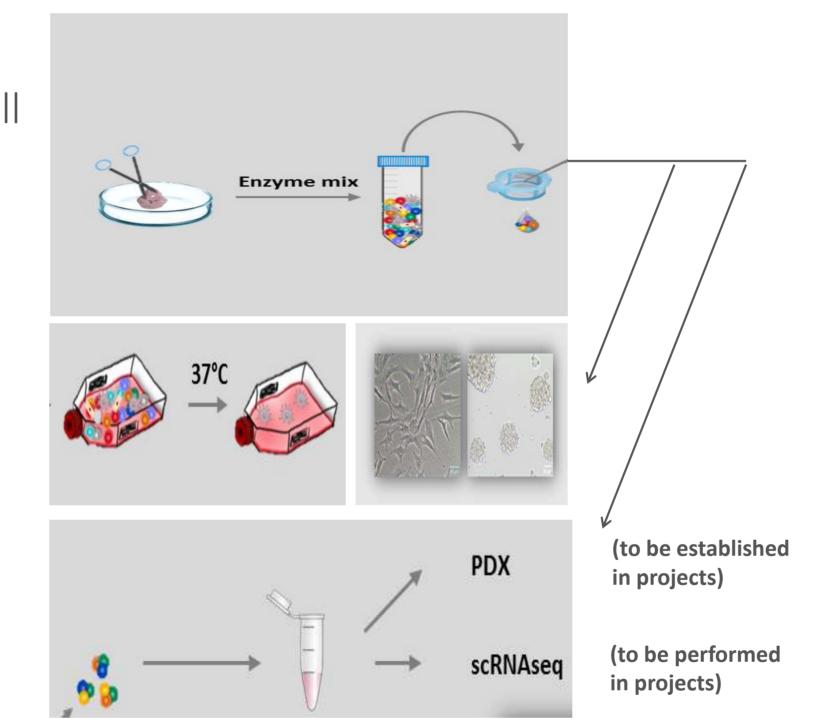
Cryo sections **HE-staining** Neuropathology Tumor cell content ≥ 60 %

VISUAL ABSTRACT

WORKFLOW

- Obtaining patient consent
- Archiving tumor tissue
- Quality control
- Preparing tumor sections, RNA, DNA and proteins
- Assessing clinical data

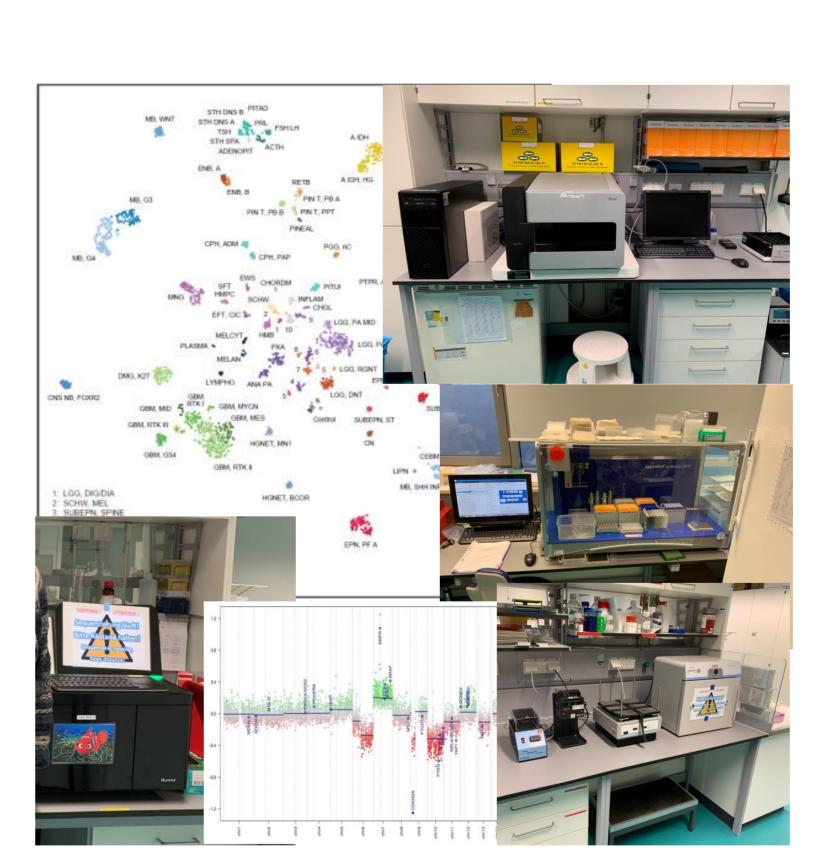
Task 2 – Preparation of cell isolates and primary cell cultures



- Preparing single cell suspensions from tumor tissues for functional analyses, PDX models, primary cultures and further sorting of distinct cell populations
- Establishing primary cultures

100 newly diagnosed

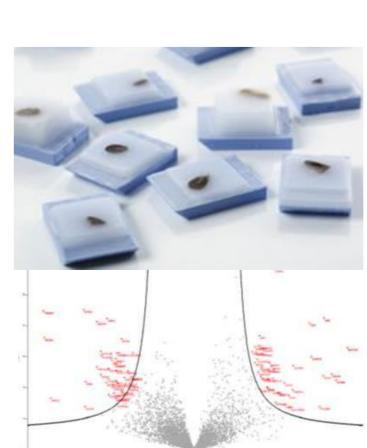
Task 3 – Molecular characterization of tumors and primary cell culture **UNITE** Core Collection



glioblastoma samples and 20 matching recurrences, for which we will establish an uniform data matrix (costs: 5.500€per sample), consisting of epigenome analysis, wholegenome sequencing, RNA sequencing, single cell sequencing, data on a set of currently relevant biomarkers, and metabolomics and proteomic profiling as well as fully characterized PDX of >30%

Task 4 – Proteomics





- Development and implementation of protocols for identification and quantification of proteins extracted from FFPE tissue
- Development and implementation of protocols for identification and quantification of protein modifications on fresh frozen tissue

