Platform for Single Cell Genomics and Epigenomics (PRECISE)

In the past 8 years single-cell RNA sequencing (scRNA-seq) has revolutionized the Genomics and Systems Biology fields. Until recently, transcriptomic studies were carried out in bulk samples of living organisms and human health, the results merely reflected an average contribution of each component of the systems or the interplay between them. The advent of the next generation of transcriptomics at single-cell resolution started with the combination of FACS and microfluidic devices for isolating single cells along with improvements in sequencing chemistry and a sharp reduction in library preparation and sequencing costs.

To further promote the introduction of single-cell technologies into the laboratory routine we launched PRECISE, a joint venture between the University of Bonn and the DZNE. A special focus is on developing and applying new single-cell high-throughput genomics technologies and making them available to internal as well as external cooperation partners.

Apart from bulk methods (stranded RNA-seq, ATAC-seq and ChIP-seq)

- **SMART-seq2**: SMART-seq2 (Picelli et al., Nature Methods, 2013, Picelli sequencing of the entire transcript and it entirely relies on off-the-shelf reagents. SMART-seq2 is, therefore, the best choice when it comes to the study of splice variants, SNPs or monoallelic gene expression. It also allows for combination of transcriptomics and proteomics data by means of index sorting (Paul SeqWell: The SeqWell method allows the sequencing of several thousand cells per experiment (Gierahn the 3´-end of each transcript and is most suitable in the initial (discovery) phase of an experiment due to its high throughput and significantly lower cost per cell as compared to Smart-seq2. It combines the benefits of performing reactions on a nanoliter scale with the compartmentalization of individual cells in microwells sealed with a semi-permeable membrane.

- **BD Rhapsody**: PRECISE is the only lab in Europe that was alpha-tester for this technology recently introduced on the market by BD Genomics. Rhapsody is based on the CytoSeq method (Fan et al., Science, 2015) and allows the 3´-end sequencing of gene panels but is also equipped with an imaging system for cell visualization and focuses on pre-determined gene panels. It is a suitable technology when tens of thousands of cells need to be reliably analyzed for a specific set of genes.