# Postdoc position in **Single cell genomics for cancer evolution**

SFB 1243 Genetic and Epigenetic Evolution of Hematopoietic Neoplasms

Project A14, Wolfgang Enard, Chair Anthropology and Human Genomics
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The Challenge

While the evolutionary nature of cancer is well established, it is challenging to generate and analyze data to quantify the dynamics of this Darwinian process. In the clinic, this process manifests itself for example when therapy-resistant cancer cells regrow after an initially successful treatment. Hence, patients die because the tumor is able to evolve. Hematologic neoplasms such as leukemia and lymphoma are well suited to study this process, because live cells can be sampled and studied in detail over the course of the disease. To better understand and eventually influence this process, it is necessary to measure the amount of genetic and epigenetic heterogeneity. New technologies to characterize genetic and phenotypic heterogeneity at the single cell level render it possible to tackle this issue. This position is embedded in a newly established Collaborative Research Center (CRC) "Genetic and Epigenetic Evolution of Hematopoietic Neoplasms" combining over twenty labs from the clinic, computational biology, population genetics, genomics and biochemistry.
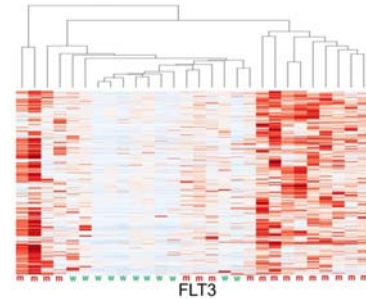
For further information please see www.sfb1243.bio.lmu.de and Enard lab.

Your Opportunities and Responsibilities

- Work on an exciting project that bridges genomics, evolutionary theory and oncology and will strengthen your profile in a field of great scientific and medical relevance
- Investigate heterogeneity of hematologic neoplasms on the single cell level.
- Optimize established transcriptional single cell technologies (Fluidigm C1, SCRB-seq, Drop-seq) and make them available to collaborations within the CRC. This includes the molecular techniques as well as first analyses.
- Improve and extend the existing single cell technologies to combine RNA-seq, DNA-seq and ATAC-seq.
- The CRC enables you to work in a highly multidisciplinary environment with cutting edge technologies in the field of genomics and cancer research.

Your Profile

- You should hold a PhD in biology, molecular biomedicine, biotechnology or a related subject.
- You should have a strong background in genomic wet-lab methods (e.g. RNA-seq), ideally in a cancer-related field
- You should be open to extend your statistical, bioinformatic and computational skills to analyze genomic data (R).
- You should enjoy working in collaborations.

Applications are now being accepted until **September 30, 2016**. Please apply to enard@bio.lmu.de.

The position should start 1st of January 2017 and is for a period of up to 3 years. The LMU is an equal opportunity employer. Preference will be given to suitably qualified female applicants or handicapped people, all other considerations being equal.