My project:

The development of multicellular organisms is tightly regulated and transcription factors (TFs) are fundamental actors in fine-tuning defined developmental processes. One class of highly conserved TFs, the Hox proteins are the master regulators of the body segment identities along the anterior-posterior body axis of animals. To elucidate the cell- and tissue-specific function of Hox proteins and to understand how they regulate their highly context-dependent outputs, I analyze tissue-specific Hox-DNA and Hox-cofactor interactions and chromatin modifications (**ChIP-Seq**) in combination with the corresponding transcriptomes (**RNA-Seq**). This multi-layered approach allows me to correlate Hox input requirements with cell-type specific outputs in a so far unprecedented manner and thus to answer the question of how Hox TFs gain their high *in vivo* tissue specificity.

Other techniques I use in my project are the **INTACT** procedure for purifying individual cell types, **bioinformatics** to analyse the ChIPseq and RNAseq data and the **CRISPR-Cas9** technology for modifying the *Drosophila* genome.

My CV:

I obtained my PhD from the Institute of Developmental Biology in Erlangen (Germany) in the Lab of Hanh T. Nguyen, where I got interested in the question of how the transcriptional machinery and a defined set of proteins can instruct the establishment of precise structures. This fundamental interest led me to study two genes (*abba, mib2*) and their role in maintaining the integrity of muscle structures in *Drosophila.* Since 2013 I work in Ingrid's group and use genomic approaches to understand how Hox TFs execute their specific functions during *Drosophila* development.