Microexons splicing regulation in differentiating cells and across tissues in human and mouse.
Haerty group

Nearly 95% of the genes in human undergo alternative splicing – the process by which multiple transcripts are produced from a single gene. Alternative splicing is a highly regulated process across tissues, and across development and lifespan within an individual.

The average length of a mammalian exon is about 140 nucleotides (nt) however, we previously identified a class of exon that are between 6 and 21nt, called **microexons**. These microexons show significant evidence of evolutionary conservation, and active regulation, especially in neurological tissues. We are interested to further understand the dynamics of regulation of these very small exons through the investigation of short and long read RNA-Seq data from cells undergoing differentiation as well as from multiple brain tissues in human.

This project is a great opportunity to develop bioinformatics skills, gain experience in manipulating and analysing large transcriptomic data sets, including some arising from single cell sequencing.