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Description

The Transcriptomics and Functional Genomics Lab, led by Marta Melé, is interested in understanding how the information encoded in our genome determines gene expression and splicing variation across individuals and tissues. To address this, we use a combination of cutting-edge computational analyses, next generation sequencing, and high-throughput functional assays.

Our goal is to perform integrative analyses of "-omics" data to ultimately understand how trasncriptomic changes in both coding and non-coding genes are associated with different human phenotypes and diseases. The group participates in different international consortia such as the Genotype-Tissue Expression Project (GTEx) and the single-cell eQTLGen Consortium (sc-eQTLGen).

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