Unravelling the Role of Long Noncoding RNAs in the Context of Cell-growth and Regeneration

Long noncoding RNAs (lncRNAs) have proven biological roles in plethora cellular contexts. Nonetheless, only a handful have been clearly characterized, leaving thousands of newly discovered lncRNAs without an associated function, and sometimes considered as transcriptional by-products. To this end, this thesis work had focused on exploring lncRNA functionality in two scenarios. First, in order to discern between lncRNAs affecting cell-growth rate (lncRNA-hits) and lncRNA-not-hits, we built a tree-based classifier based on high-throughput CRISPRi functional screen data in seven human cell lines, as well as, cell-specific ENCODE transcription factor ChIP-seq data; finding that the genomic features used in our study showed small effects and tend to be transcript-specific. Our classifier outperformed previous algorithms, displayed balanced sensitivity and specificity values, and uncovered a lncRNA *(LINC00879)* involved in cell-growth. Additionally, we unveiled a list of 40 lncRNAs as candidates for experimental validation. Second, we characterized the lncRNA profile during regeneration, using *Drosophila* wing imaginal disc as a regeneration-model. We selected a candidate lncRNA *(CR40469)* and evaluated its role in regeneration at the early stage of cell-damage. Subsequently, using RNA-seq data, we observed significant transcriptomic alterations in consequence of the *CR40469* genetic deletion, suggesting its role in regeneration. In this study we have generated a list of lncRNAs whose possible biological role in cell-growth and in regeneration can be further studied.

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