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Single-cell mapping of microRNA expression during cardiac development

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The heart is an exceptionally complex tissue comprised of a variety of different cell types. Understanding physiological cardiac development and its relationship to the development of pathological cardiac diseases require the careful investigation of their related developmental pathways. A highly significant regulatory layer during cellular differentiation is the post-transcriptional regulation via non-coding RNAs and, more specifically, microRNAs (Liu *et al.*, 2010). Previous microRNA transcriptomic studies in the heart lacked in the identification of their differential expression per cell-type (Leptidis *et al.*, 2013). Since microRNAs can target many mRNAs, identifying their cell-type-specific expression is necessary to elucidate the intricate cellular interactions and regulatory pathways and the development of targeted therapeutic approaches.

This study uses data from single-cell small RNA sequencing (small-seq) (Faridani *et al.*, 2016) from early embryonic cardiac progenitor murine cells. We aim to identify the transcriptional profile of small RNAs, mainly microRNAs, during cardiac development. Unlike single-cell RNA sequencing (scRNAseq), there are no established cell-type markers nor data analysis methods in the case of small-seq. Thus, we develop a methodology for identifying cell-types using their microRNA profile, coupled to their predicted targets stemming from various miRNA target prediction algorithms. These data are then cross-referenced with preliminary scRNAseq data in the same tissue, with established cell-types. Deciphering the transcriptomic landscape of microRNAs during cardiac development, along with identifying cell-types based on the relationship between their RNA and microRNA fingerprint, enables the in-depth study of the intricate regulatory interactions between cells, cell-types and different embryonic days.

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