

Transcriptome of failing human heart reveals atrial myocytes reprogramming

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Heart diseases are the leading cause of death worldwide, however genome regulation behind it remains barely studied in human. In the way to fulfil lacking information we created an atlas of transcribed promoters and enhancers in healthy and failing adult human hearts. Total RNA was extracted from atriums and ventricles, left and right sides, and submitted to cap analysis of gene expression (CAGE) libraries protocol. In total 109 samples from 31 donors were sequenced and analyzed. We observed to general expression patterns in our data representing atrial and ventricular types respectively. While all failing ventricle heart samples keep ventricular expression profiles and showed activation of immune system processes, on the contrary failing atrium samples loosen immune responses and activated sarcomere, myofibril, and oxidation associated processes. Interestingly, most of failing atrium samples had ventricular type expression profiles, which might be explained by atrial-ventricular transdifferentiation. To confirm our observation, we reanalyzed a relevant subset of heartcellatlas.org single cell data (left/right, ventricle/atrium), and use it for deconvolution of bulk CAGE libraries. In atrium samples with ventricular type expression atrial myocytes were replaced with ventricular myocytes. Expression profiles of known cardiomyocytes marker genes like MYL2 and MYL7 confirms such reorganization, but from another side reprogrammed atrium samples could be clearly distinguished from other ventricle samples by NPPA gene activity, which is significantly higher in atrial samples.

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