Spatial transcriptomics of cardiomyocytes

Cardiovascular diseases are a major health burden; put it as a leading cause of death and morbidity. To better understand the human disease, we should have a clear picture of how normal molecular process work. The functional unit of heart is cardiomyocyte, which is large, elongated cells measure around 100 um in length and 20-30 um in diameter. For proper heart function, cardiomyocytes need to act as one unit with organized synchronized and timed contraction. Otherwise, this will lead to arrythmia which is a class of common heart disease where this normal pattern is disturbed. To do so; cardiomyocyte is connected thorough a specialized dynamic structure called intercalated discs which enable rapid transfer of electrolytes between cardiomyocytes. Many of proteins of ICDs have short half-lives and need to be synthesized continually. As the case in many cells, local translation of these protein maybe warranted. To achieve this cell; a well-known biological phenomenon called RNA-asymmetry where RNA distribution is not the same within the cells. Based on many lines of experimental and logical evidence; we are hypothesizing that there is an enrichment of specific RNA population at intercalated discs region. The rational for this; 1- The evidence for local translation at intercalated discs. 2- presence of rna binding proteins at intercalated discs. 3- Logically; it will be time and energetically unfavorable to replenish ICDs protein pool from distant site of their target region. Methods

`Intercalted discs isolation:`

Intercalted discs will be isolated using Laser capture microdissection microscope.

`RNA isolation`

RNA from dissected samples will beisolated using low inpur RNA isolation kit as Picopure toral RNA isolation kit.

`cDNA library prepartion`

Isolated RNA will be further used for cDNA library preparion usin low input Total RNA isolationv3 SMARTer kit by Takara.

`RNA sequenincg`

RNA will be sequenced using Nova-seq SP lane ; paired end sequeicnig at coverage $\sim$ 20 million read

`RNA-anlaysis`

RNA -seq analysis will be done using R language. The comparison of RNA-enrichment between ICDs and non ICDs region will be represented by volcano plot. We also make cluster analysis based on their functionality. Results

Preliminary data show enrichment of specifc mRNA related to transaltion and mitochodnria and some mebranous protein enriched at intercaled discs. I attahced a volcano plot of differntial expression profile.