nanoparticle and incubated for one hour at 37 °C. The intensity of fluorescent nanoparticles was measured using flow cytometry. Lysosome and early endosome marker were used to study the intracellular fate of nanoparticles using confocal microscopy. Control and lipid-exchanged cells showed significant differences in nanoparticle uptake in serum-free medium. While SM (18:1) and some marker were used to study the intracellular fate of nanoparticles using flow cytometry experiments, while showing differences in intracellular localization of nanoparticles in control and lipid-exchanged cells. In conclusion, these results suggest that the outer leaflet lipid composition of the cell plasma membrane affects the internalization and localization of nanoparticles in A549 live cells.

746-Pos  
A Pipeline for High-Throughput Assessment of Electrophysiology and Protein Quantification in Small Samples of iPS-CM  
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Human induced pluripotent stem cell-derived cardiomyocytes (hiPSC-CMs) enable personalized cardiac electrophysiology studies and drugs cardiotoxic assays to be conducted in a high-throughput manner. Under 96-well plate culture format, electrophysiology properties of hiPSC-CMs in response to different perturbations could be studied from each individual sample. Considering the large-sample requirements to run traditional gel-based Western blots, protein quantification in such high-throughput format is not feasible. The desire for running precious samples in small, high-throughput format dictates the need for a pipeline that can allow both protein quantification and functional electrophysiological tests in the same samples. This study demonstrates the possibility of conducting both protein quantification and all-optical electrophysiological assessment on iPS-CM samples cultured under 96-well plate format. With 4uL of cell lysis, an automated capillary-based protein immunoassay could run up to 24 samples concurrently in 3 hours and yields reproducible quantitative data. The detection of both protein of interest and housekeeping protein is available by multiplexing in one sample to make normalization possible. The linear detection range of several multiplexed proteins has been tested with iPS-CMs lysis. Additionally, we optimized and validated a total protein assay method on the same platform as an alternative to protein normalization in human iPS-CMs. The linearity of the signals from serially-diluted samples provided confidence for total protein quantification. With the same amount of starting material, this method enables a reduction in the sample size (number of cells needed) by an order of magnitude to get comparable results. Our study leverages the high-throughput nature of the functional measurements by all-optical electrophysiology and extends the approach to protein quantification in the same format for more comprehensive sample characterization of human iPS-CMs.

747-Pos  
Fabrication of a Microfluidic Device to Study the Interactions between Human Chordoma UCH-1 and Human Adipose-Derived Stem Cells  
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According to the National Institute of Health, 80 percent of adults suffer low back pain at some point in their lifetime. The loss of intervertebral disc elements, such as the nucleus pulposus, leads to abnormal spine mechanics, inflammatory signaling and compression of neural structures that lead to pain. Recently, undifferentiated stem cells have been used to rescue specialized cells via transfer of mitochondria and growth factors. However, it is not known if this method could be used to aid in the regeneration of human nucleus pulposus. In this work, we used a microfluidic device to co-culture human adipose-derived stem cells (ADSCs) next to human chordoma UCH-1 cells. Human chordoma derived UCH-1 cells have the same genetic and morphological properties as nucleus pulposus cells and serve as a model for in vitro studies. We made a microfluidic device that consisted of two wells separated by a channel, each well allows for culture of a specific cell type. When the channel is opened, it mixes the media from each cell culture. The microfluidic device was fabricated using SLA resin 3D printing and polydimethylsiloxane (PDMS). On average we saw about a 50% increase in cell number when UCH-1 cells where cultured with ADSCs in such high-UCH1 cell density. These results indicate that even at a distance stem cells (ADSC) are able to influence the growth of UCH-1 cells. We observed ADSCs migrate towards the chamber with UCH-1 cells, suggesting that there is a chemotactic signal attracting ADSCs to the chordoma chamber. In the future, we want to check for the growth factors that affect cell proliferation and the maximum distance between cell groups at which effects can be seen.

748-Pos  
Engineering the Microenvironment for Heart Muscle Cell Mechanobiology  
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During development and disease, the heart undergoes biochemical changes. For example, after a heart attack, damaged myocardium regions change extracellular matrix (ECM) protein type composition. Cardiomyocytes (CMs) differentiated from human induced pluripotent stem cells (hiPSC-CMs) hold great potential as a model to expand our knowledge of human heart muscle cells and their interactions with the surrounding microenvironment. Polyaerylamide (PA) hydrogels are a common mechanobiology substrate with a tunable physical and mechanical stiffness that can be used for functional measurements such as traction force microscopy. By engineering microphysiological systems with tunable biochemical properties, our aim is to understand the hiPSC-CM mechanobiology of cell-ECM interactions. Our goal is to identify cell-substrate interfaces supporting maximal adhesion and force transfer from hiPSC-CMs. We use protein patterning techniques to obtain discrete ECM proteins to be able to pattern the surface of PA hydrogels. We focus on specific ECM protein types (e.g. Laminin-111, Collagen IV, Fibronectin and Collagen I) that are abundant in the myocardium during cardiac development or disease. We then analyze hiPSC-CM structure and function in response to these different ECM protein types. To further probe the role of hiPSC-CMs interactions with ECM on structure and function, we also profile the cell adhesion receptors available for in vitro cell-substrate interaction. Informed by available RNA-Seq data from stages of hiPSC-CMs differentiation and CM development literature, we focus on specific integrin subunits (e.g. a1, a2, a3, a4, a5, b1). We use integrin antibodies to obtain protein data using flow cytometry and compare this to gene expression data. The results of these studies enable tuning microenvironment properties and quantify cell-ECM interactions matched to cardiac development and in disease states.

749-Pos  
Phenotyping of Phagocytosing Neutrophil Populations using Deformability Cytometry  
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Deformability cytometry is a label free technique which utilizes non-uniform atomic force microscopy. In this study, we investigate the mechanical properties of neutrophils, the most abundant of white blood cells and essential components of the immune system that are among the first responders in defending against bacterial infections. Neutrophils mobilize to sites of infection, where they ingest bacteria through the process of phagocytosis. During phagocytosis, actin is polymerized and bacteria take up space in the neutrophil interior. Do these, or other effects change the mechanical properties of the cell in a way that affect deformability cytometry? Here, we use an undulating micro-fluidic channel for repeated measurements of deformability of HL-60 derived neutrophil populations which have phagocytosed bacteria and neutrophils which have not phagocytosed bacteria. We image deformations of neutrophils