### **Title: Fabrication and characterization of a thick, viable bi-layered stem cell-derived surrogate for future myocardial tissue regeneration**

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# **Supplemental Materials and Methods**

# **Flow cytometry analysis**

Flow cytometry analysis was performed as described previously  $50-52$ . Briefly, cells were dissociated using 0.25 % trypsin and resuspended as single cells, permeabilized in 0.1 % Triton X-100 at 4 °C for 10 min, then incubated with primary and secondary antibodies for 30 min at 4 °C with 3 x 5 min wash in between. Finally, cells were resuspended in 2% fetal bovine serum/phosphate-buffered saline (FBS/PBS) containing 5 μL of propidium iodide (10 μg/mL) and evaluated with a FACS Aria instrument (BD Biosciences, USA). Antibodies used, along with dilutions, are listed Supplemental Table 1.

# **Cardiomyocyte proliferation assay**

Cardiomyocyte proliferation was tested using a proliferation assay from CyQUANT Direct Cell Proliferation Assay Kit (Invitrogen, Cat# C35011). Briefly, CM proliferation was determined via green fluorescent nucleic acid staining of the nucleus, after which the fluorescence intensity of the readout was obtained 120 min after reagent addition via microplate reader. Based on the results, there was no significant difference between the proliferation of 28-day-old and 42-day-old hiPSC-CMs (see Supplemental Figure 2). Student t-test was performed,  $p = 0.6565$  (n = 6).

Supplemental Table 1: Antibodies used for flow cytometry, FACS, and immunofluorescent staining.



## **Supplemental Figures**



Supplemental Figure 1: Characterization data confirming differentiation and purification for iECs (a) and iCMs (b) using immunofluorescent staining (1) and flow cytometry (2) analysis.



Supplemental Figure 2: Fluorescence-based cell proliferation assay showing the (a) standard curve and (b) the resulting measurements at Day 28 (12 hours) of hiPSC-CMs culture in 96 well plate (15,000 cells/well) as well as measurements at Day (14 days). p = 0.6565 (n = 6)



Supplemental Figure 3: Immunofluorescent staining showing presence of DAPI and phosphorylated MLKL (Ser358, pMLKL) after 4 weeks in culture.



Supplemental Figure 4: Immunofluorescent staining showing presence of DAPI, cTnT and CD31 after (a) 1 week in culture and (b) 4 weeks in culture. Quantification of expression intensity and subsequent expression ratios for all 4 weeks for (c) CD31/cTnT expression as well as (d) cTnT/DAPI. No statistically significant difference noted between groups for (c) or for  $(d)$ ,  $n = 3$ .



Supplemental Figure 5: Immunofluorescent staining showing connexin 43 (Cx43) gap junction presence after (a) 1 week in culture and (b) 2 weeks in culture, along with the (c) quantification of the ratio of Cx43/DAPI fluorescence expression. \*p < 0.05, with  $n = 4$ 



Supplemental Figure 6: Confocal micrograph of junctophilin (JP2) and ryanodine receptor (RyR) expression levels in cardiac tissue surrogates after (a) 7 days, and (b) 28 days in culture, respectively.

#### **Supplemental Matlab code: Generalized Maxwell model of order four**

%% Load datasets % Raw data sheets used in this file/program should only consist of numbers % Delete the graphs and the titles in all the columns or MatLab won't % recognize the file % convert the Excel file to a .csv if necessary % Ensure that all the files are in the same folder % Ensure the directory is set (left click the tab at the top to % set directory) %%

load('PDMS6edit.csv') % loads the Raw data file generated with Low Force Testbench into MatLab Do = 2.830\*10^-3; % Sample thickness - sample-dependent (meters) PlotOn = 1; %  $1 = plot$ ,  $0 = don't plot$ %FileName = 'DataSet02'; % creates a new destination to store results

#### %%

% Section converts the load obtained from instrument to Stress measurements,

% and identifies point were sample strain was introduced

Force = PDMS6edit(:,7); % Load value in gram-force

Force = Force/101.971621; %Gram-force to Newton

Area =  $4.165*10^{-1}5$ ; % Area of sample (in m2)

Stress = Force / Area; % Y-Values in Graph (Stress)

Time = PDMS6edit(:,2); % Elapsed Time (s) (temporarily uses entire Time column before selecting for the desired range)

%plot (Time, Stress)

 $Ep = 0.1$ ; % 10 percent sample strain

[StressVal, StressPos] = max(Stress(:)); %find max Y-value

%%

%create new matrix - only consider data points relevant to 10 percent %strain

NewMat = [Time, Stress]; %assign Time to column1 and Stress to column2 of NewMatrix  $k = 1$ :

for i = StressPos:size(NewMat, 1) maxT(k) = Time(i) - Time(StressPos);  $maxS(k) = \text{Stress}(i);$ 

 $k = k + 1$ ; end

max\_mat = [maxT', maxS']; %this is the new matrix containing only the experimental data relevant to the strain experiment

%plot (maxT, maxS)

#### $0/0/2$

opts = fitoptions( 'Method', 'NonlinearLeastSquares' ); ft = fittype( $a + b0*exp(-0)*x$ ) + b1\*exp(-c1\*x) + b2\*exp(-c2\*x) + b3\*exp(-c3\*x)', 'independent', 'x', 'dependent', 'y'); %model fitting

opts.DiffMaxChange = 100000; %how much the coefficients of each a, b0, c0 etc. changes with ongoing iterations

opts.DiffMinChange = 1e-10; opts.Display = 'Off'; opts.Lower = [0 0 0 0 0 0 0 0 0]; %lower limits of exponents should be zero at minimum opts.MaxFunEvals = 10000; opts.MaxIter = 100000; %number of iterations opts.Robust = 'LAR'; %LAR refers to least absolute residuals - ensures more robust fit of model opts.StartPoint = [36000 3500 4500 4500 1800 0.002 1e-04 1e-05 1e-06]; opts.Upper = [100000 10000 10000 10000 10000 10000 10000 10000 10000]; %ceiling of a, b0, c0 etc  $[fitresult, gof] = fit(maxT', maxS', ft, opts);$ % Plot fit with data. Name = 'Result %d'; %figure( 'Name', sprintf(Name));  $h = plot(fitresult, maxT', maxS')$ ; set(h,'LineWidth',2) legend( h, 'Data', 'Fit', 'Location', 'NorthEast' ); % Label axes xlabel Time ylabel Stress grid on %% This is using the fit parameters for  $i = 1 : 4$  $a(i)$  = fitresult.a;  $b0(i)$  = fitresult.b0;  $c0(i)$  = fitresult.c0;  $b1(i)$  = fitresult.b1;  $c1(i)$  = fitresult.c1;  $b2(i)$  = fitresult.b2;  $c2(i)$  = fitresult.c2;  $b3(i)$  = fitresult.b3;  $c3(i)$  = fitresult.c3; R2\_Value(i) = gof.rsquare; %gof -goodness of fit end for  $i = 1:4$  $E0(i) = a(i)/Ep;$  $E1(i) = b0(i)/Ep;$  $n1(i) = E1(i)/c0(i);$  $E2(i) = b1(i)/Ep;$  $n2(i) = E2(i)/c1(i);$  $E3(i) = b2(i)/Ep;$  $n3(i) = E3(i)/c2(i);$  $E4(i) = b3(i)/Ep;$  $n4(i) = E4(i)/c3(i);$ end

%%