catalysts

Modulation of Human Mesenchymal Stem Cells by Electrical Stimulation Using an Enzymatic Biofuel Cell

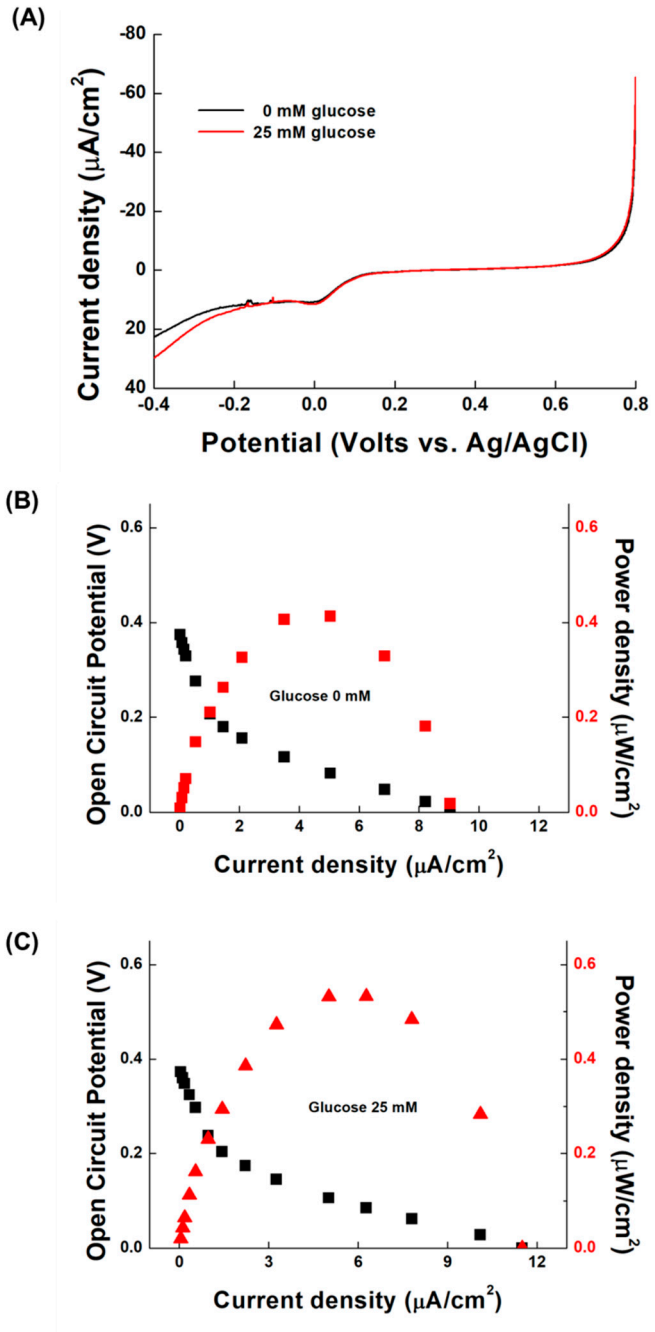


Figure S1. Linear sweep voltammogram (**A**) of cathode electrode with BOD and polarization curves with (**B**) 0mM and (**C**) 25 mM glucose.

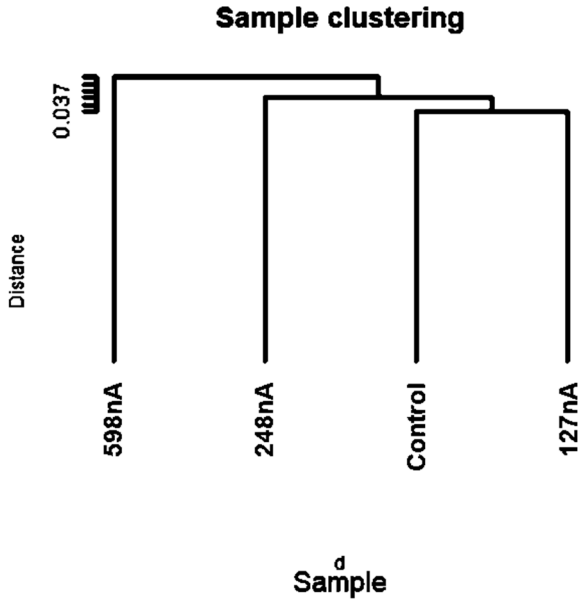
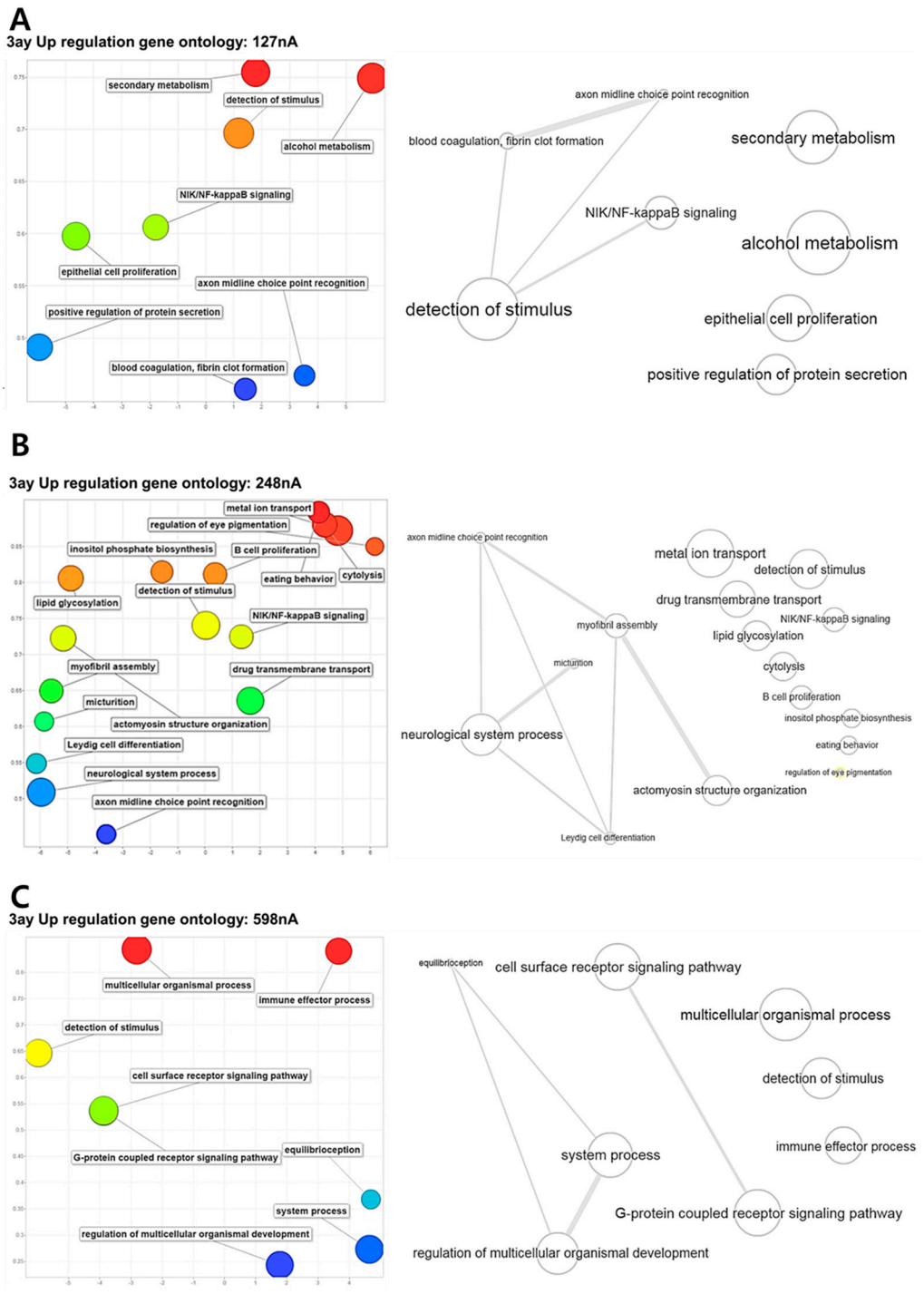


Figure S2 Hierarchical clustering of the differentially expressed genes (DEGs) identified by RNA sequencing. Dendrogram of hierarchical clustering indicates the correlation between electrically-stimulated hAC-MSCs. The ruler in left side denotes the average distance between the analyzed samples.


A
3ay Up regulation gene ontology: 127nA
secondary metabolism
detection of stimulus
alcohol metabolism
NIK/NF-kappaB signaling
epithelial cell proliferation
axon midline choice point recognition
positive regulation of protein secretion
blood coagulation, fibrin clot formation
axon midline choice point recognition
blood coagulation, fibrin clot formation
secondary metabolism
NIK/NF-kappaB signaling
alcohol metabolism
detection of stimulus
epithelial cell proliferation
positive regulation of protein secretion
B
3ay Up regulation gene ontology: 248nA
metal ion transport
regulation of eye pigmentation
inositol phosphate biosynthesis
B cell proliferation
eating behavior
cytolysis
lipid glycosylation
detection of stimulus
NIK/NF-kappaB signaling
myofibril assembly
drug transmembrane transport
micturition
actomyosin structure organization
Leydig cell differentiation
neurological system process
axon midline choice point recognition
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metal ion transport
detection of stimulus
drug transmembrane transport
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lipid glycosylation
micturition
cytolysis
B cell proliferation
inositol phosphate biosynthesis
neurological system process
eating behavior
regulation of eye pigmentation
actomyosin structure organization
Leydig cell differentiation
C
3ay Up regulation gene ontology: 598nA
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immune effector process
detection of stimulus
cell surface receptor signaling pathway
G-protein coupled receptor signaling pathway
equilibrioception
system process
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cell surface receptor signaling pathway
multicellular organismal process
detection of stimulus
immune effector process
system process
G-protein coupled receptor signaling pathway
regulation of multicellular organismal development

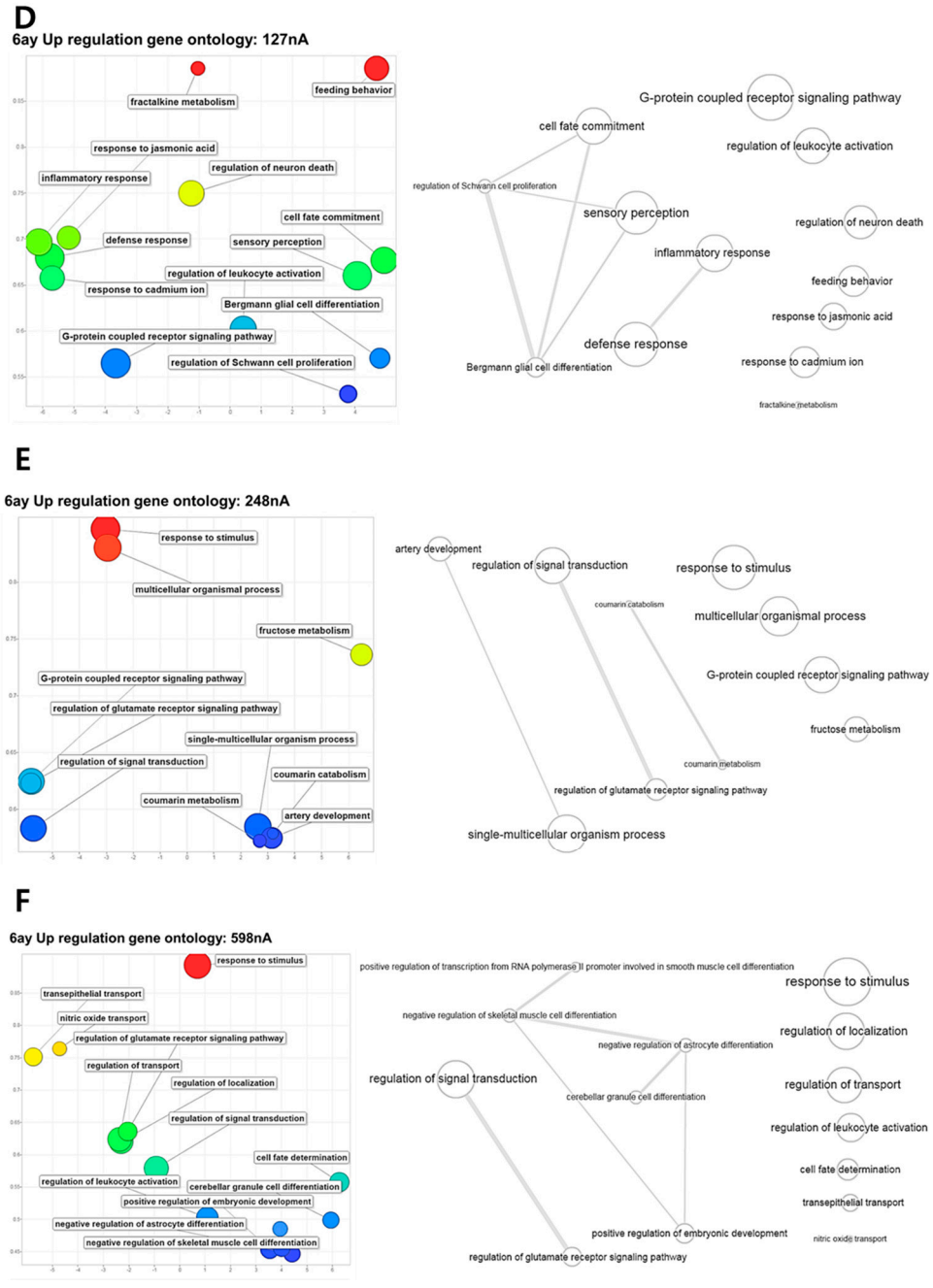

Figure S3 Interactive graph of GO functions for up-regulated DEGs in electrically-stimulated hAC-MSCs on day 3 (**A**) 127 nA, (**B**) 248 nA and (**C**) 598 nA; on day 6 (**D**) 127 nA, (**E**) 248 nA and (**F**)598 nA. The top 20 GO terms (sorted by p value) are shown. The identified GO terms and representative term subsets were converted into a network layout. A circular node represents each term, and its size is proportional to the number of input genes included in that term. The color represents the p-value of a given term, with darker color representing higher statistical significance. Terms with a similarity score > 0.3 are linked by an edge (the edge thickness represents the similarity score). Up- and down regulated genes in the top-ranking list are graphically represented depending on the culture day. Scatter plots with x and y coordinates assigned to each term reflect the close relationship between semantically-similar GO terms in the plot. In the left scatter plot, cycle color enriched GO data represent that red and orange cycles are GO terms with more significant log10 p-values than the green and blue cycles compare with control groups. In addition, each scatter plot clearly represents the unique changes in gene expression. Further, each plot correlates the cellular response to electrical current range. The right interactive graph also visualizes the co-relationship of each gene on the scatter plot. Bubble size indicates the GO term assignment frequency in the underlying biological signaling process. Highly-similar GO terms are linked by edges in the graph, where the line width indicates the degree of similarity.