

Figure S1. Generation and characterization of hiPSCs.

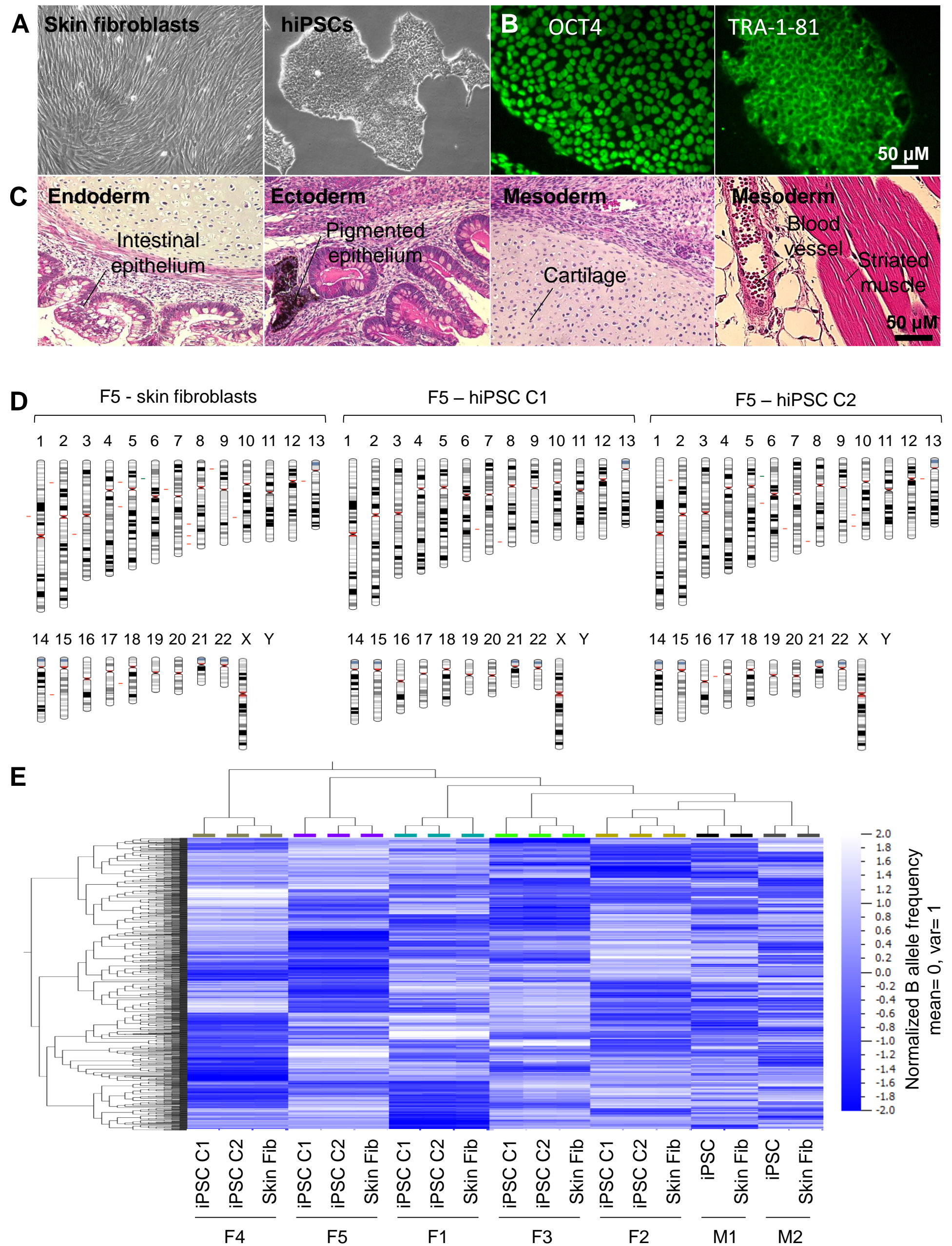
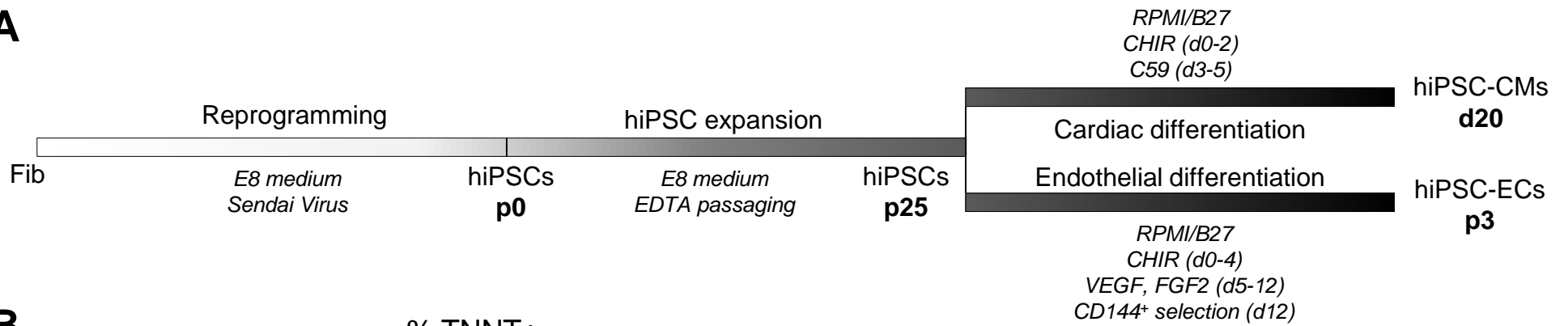
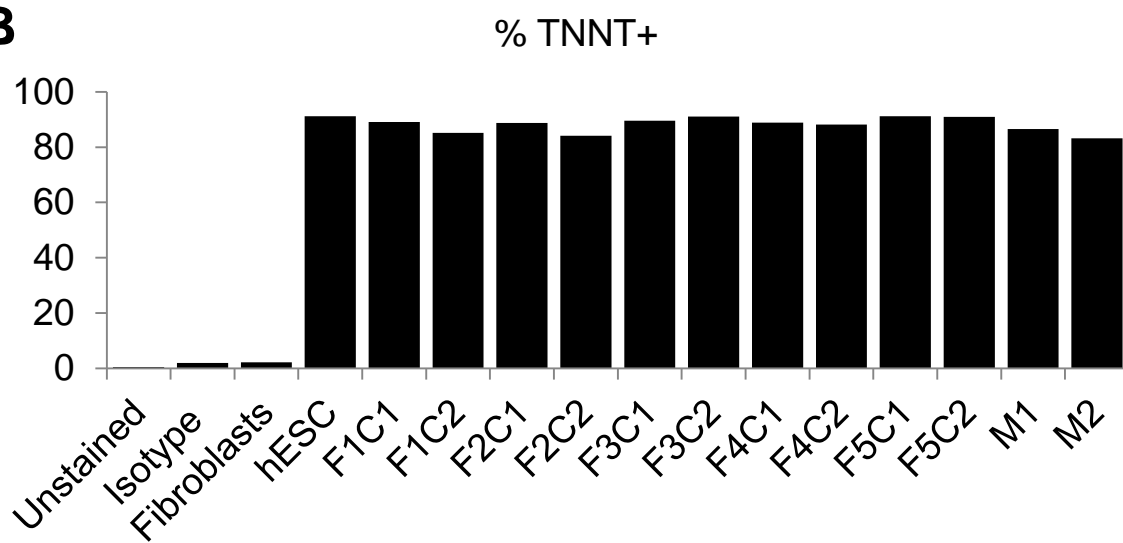


Figure S2. Generation and characterization of hiPSC-ECs and hiPSC-CMs.

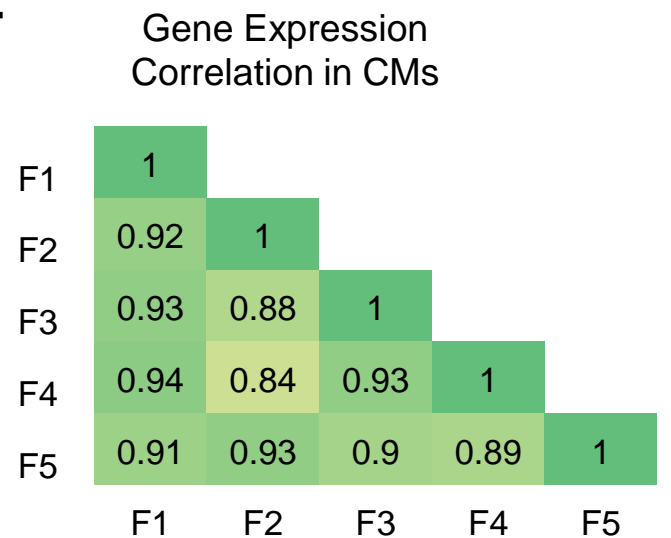
A



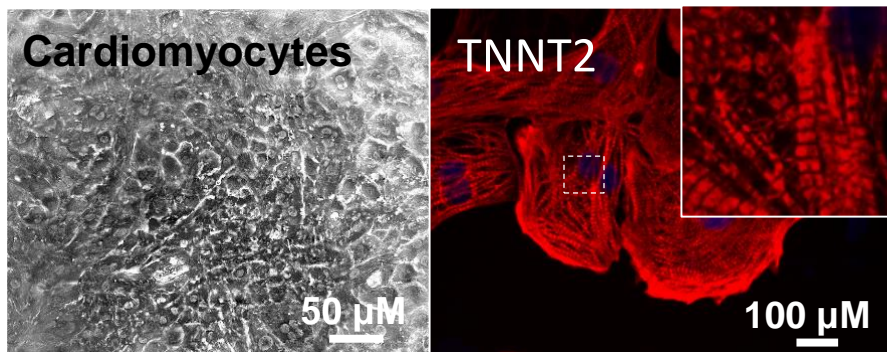
B



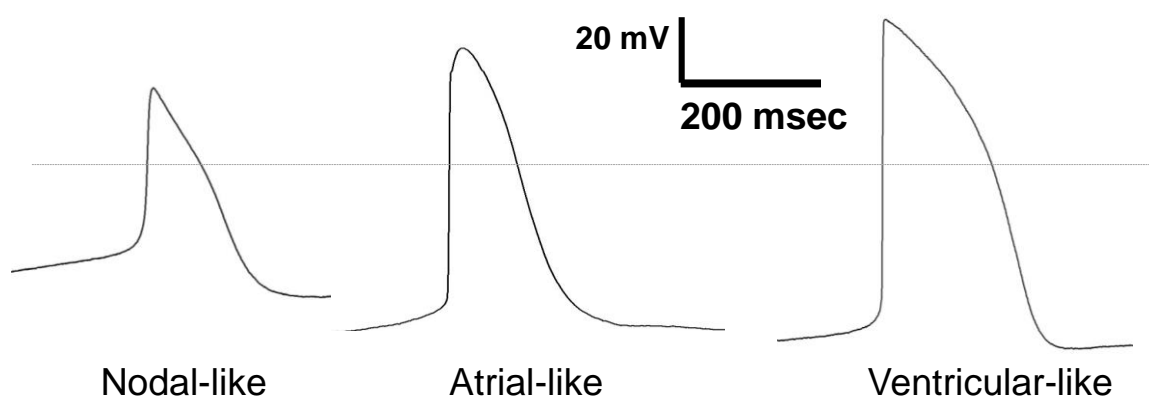
F



C

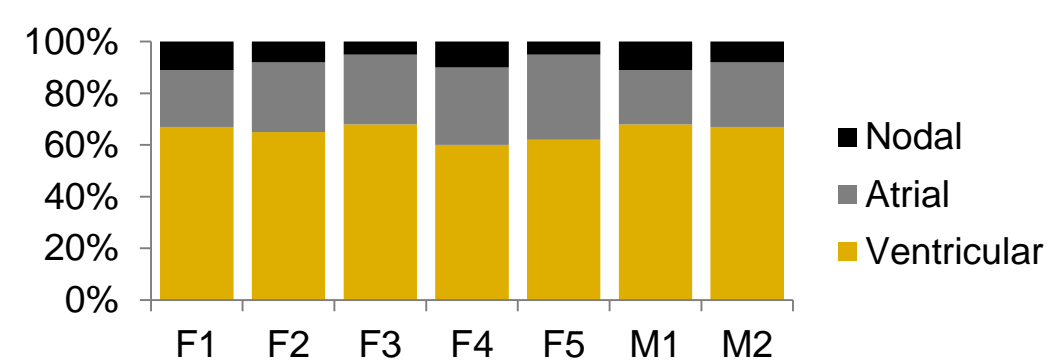


D

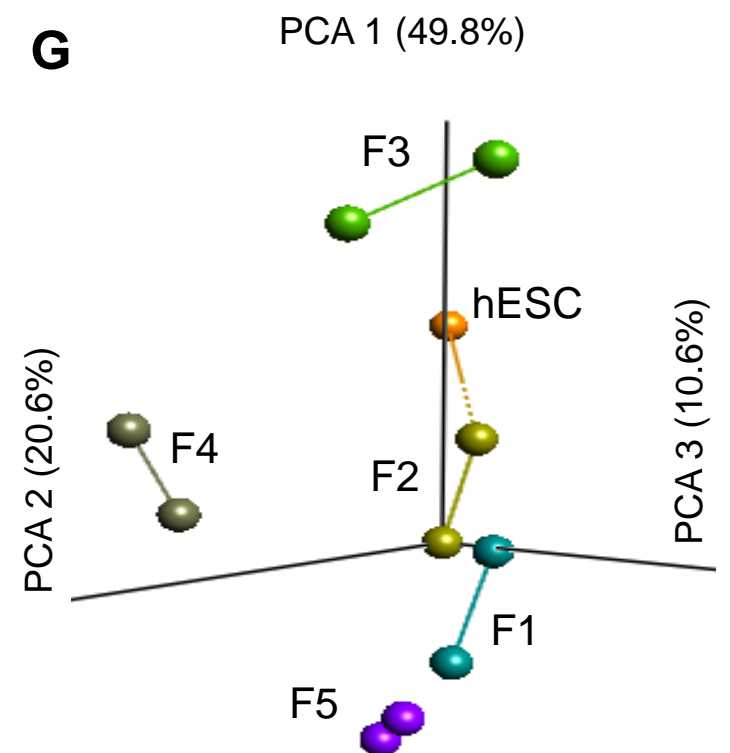


E

Cardiomyocyte sub-type identity



G



H

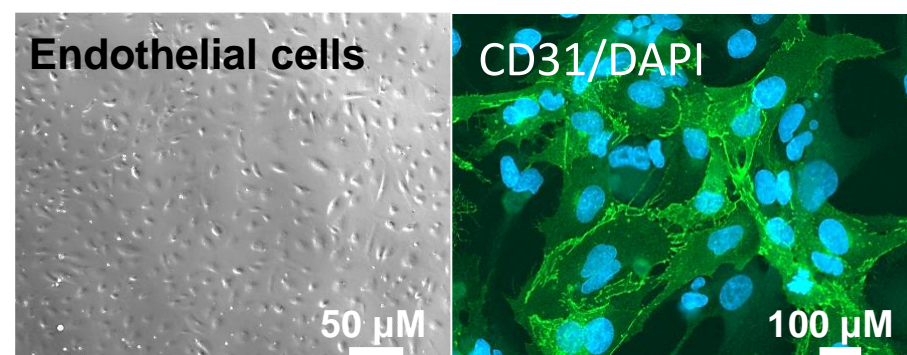


Figure S3. Transcriptomic comparison of isogenic LV tissue vs. hiPSC-CMs.

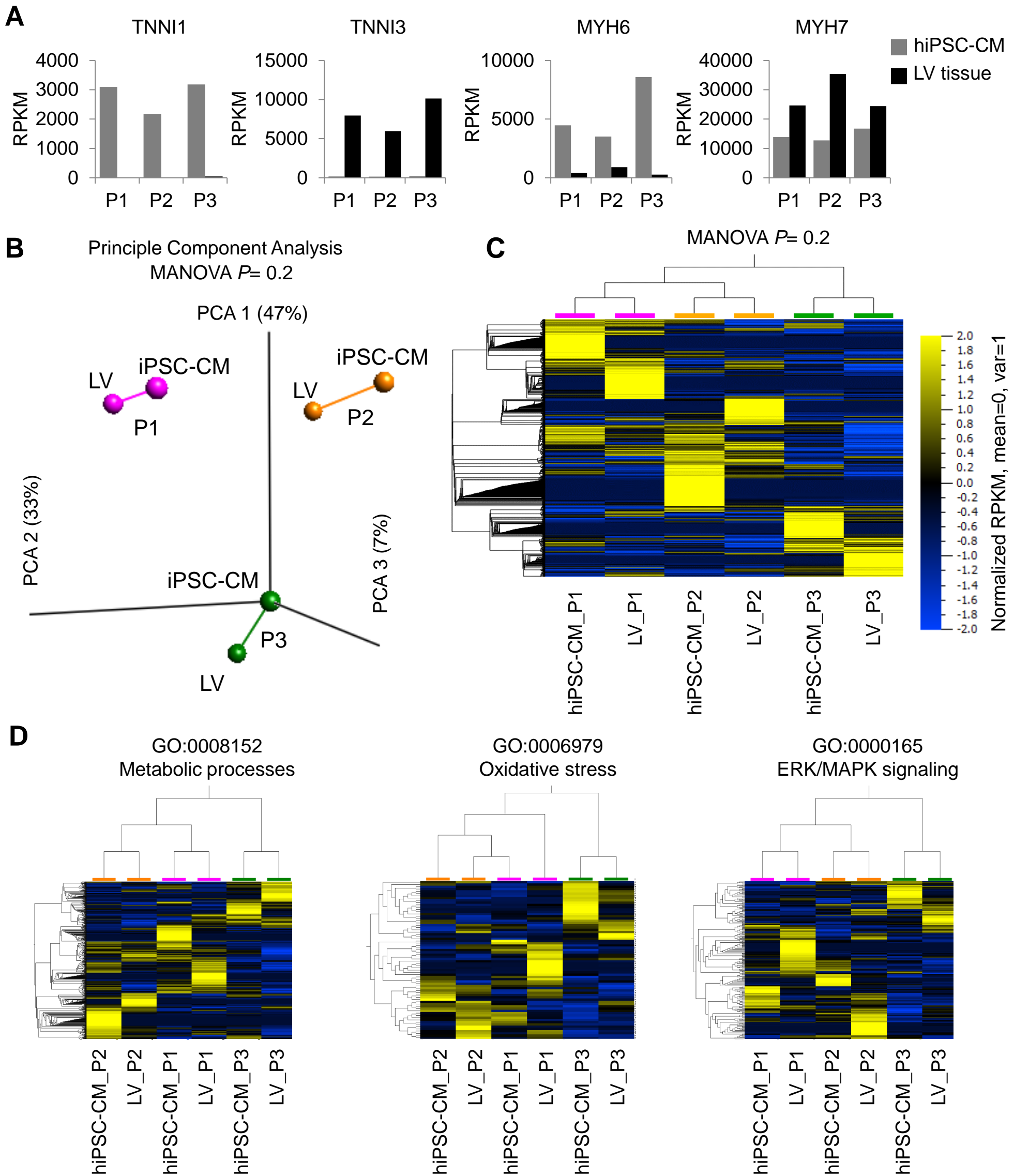


Figure S4. Live/dead staining for determination of optimal drug concentrations.

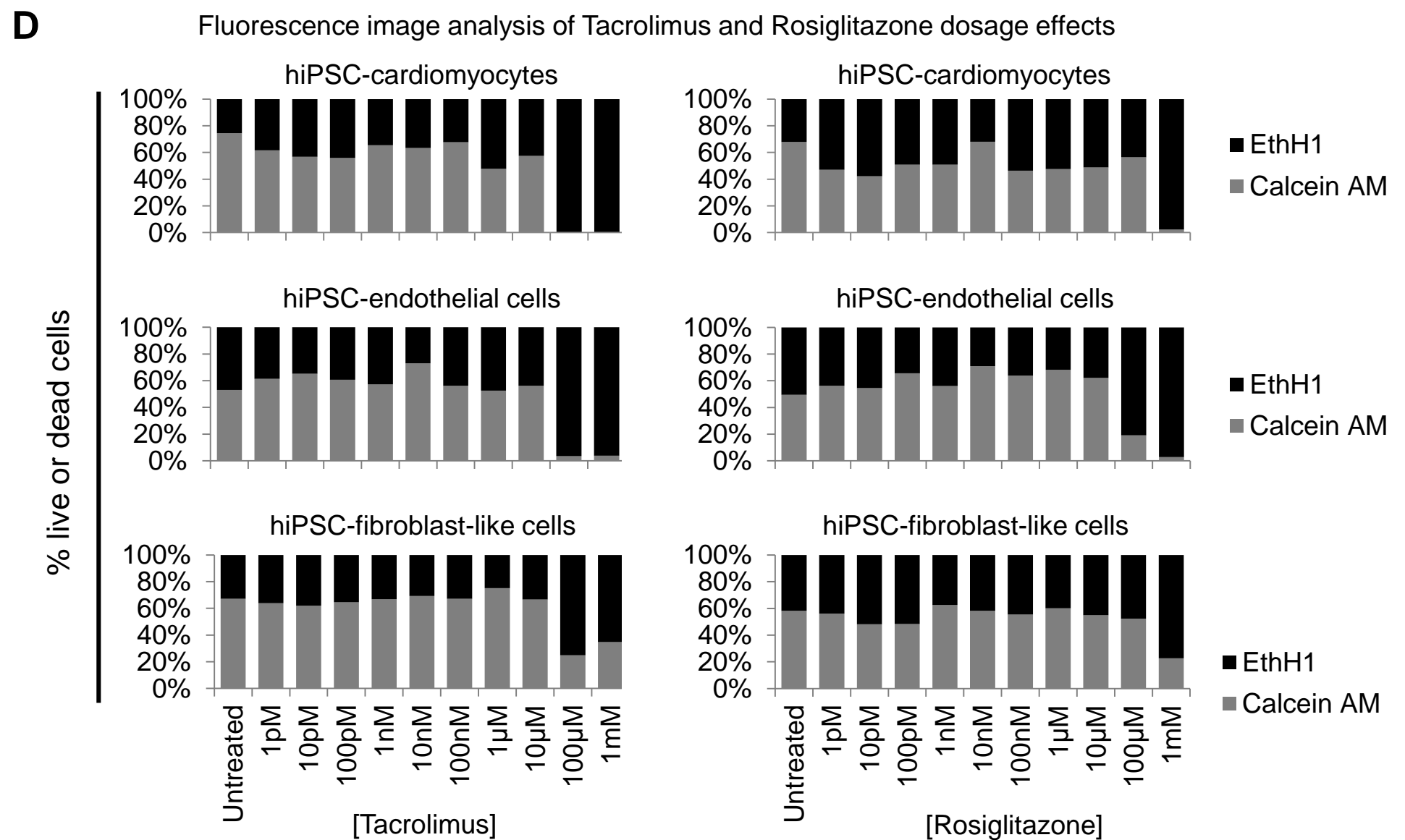
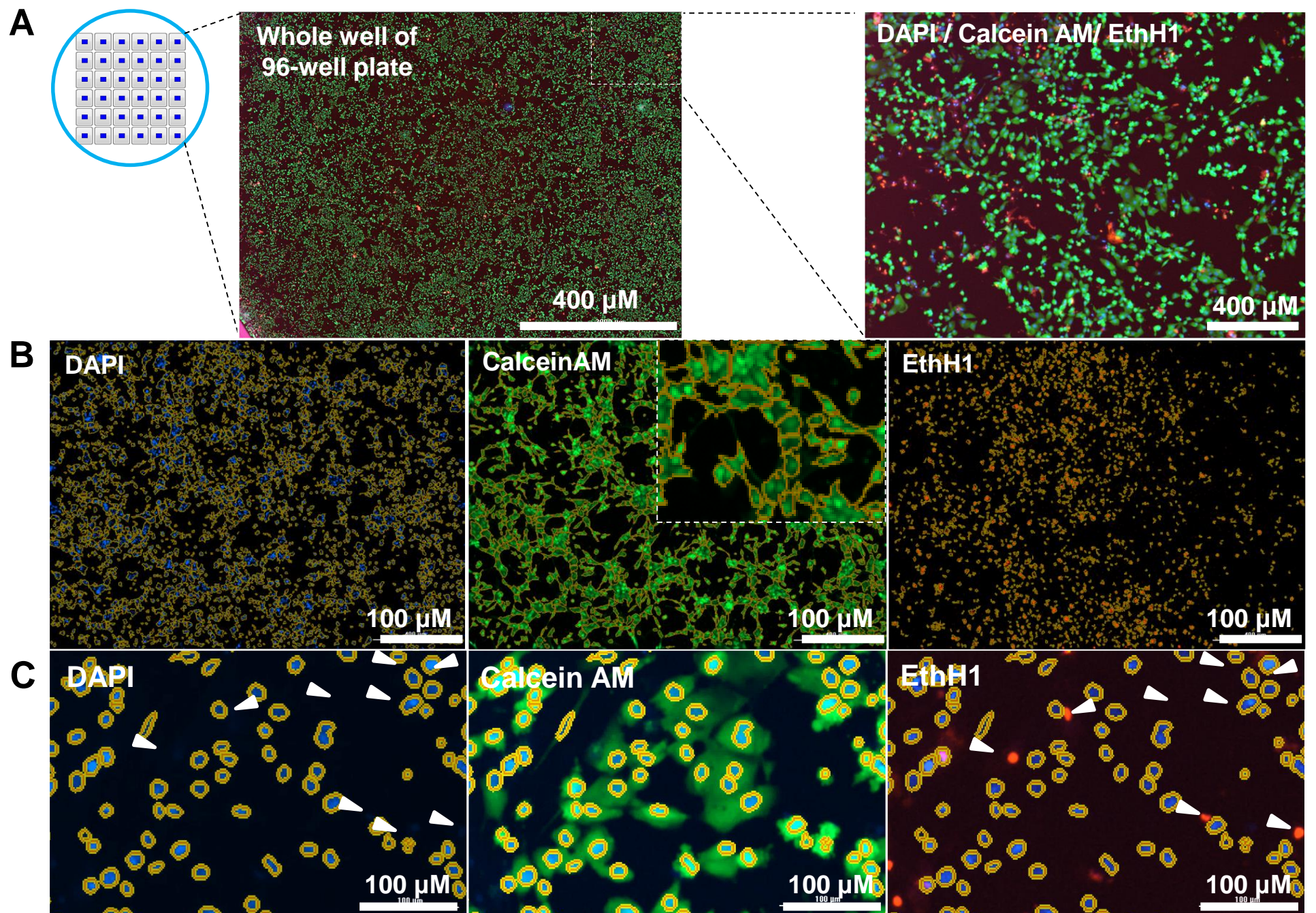
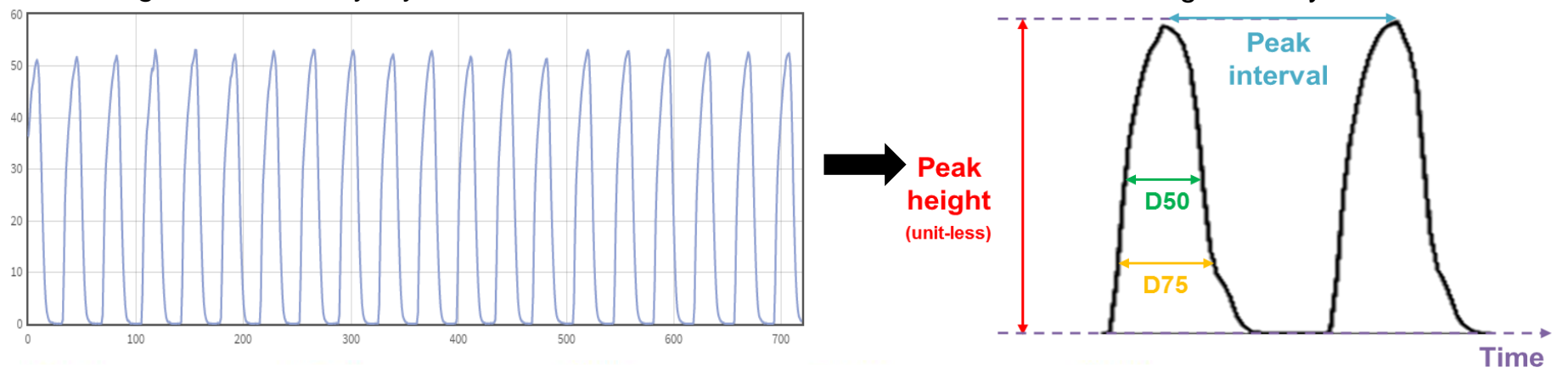
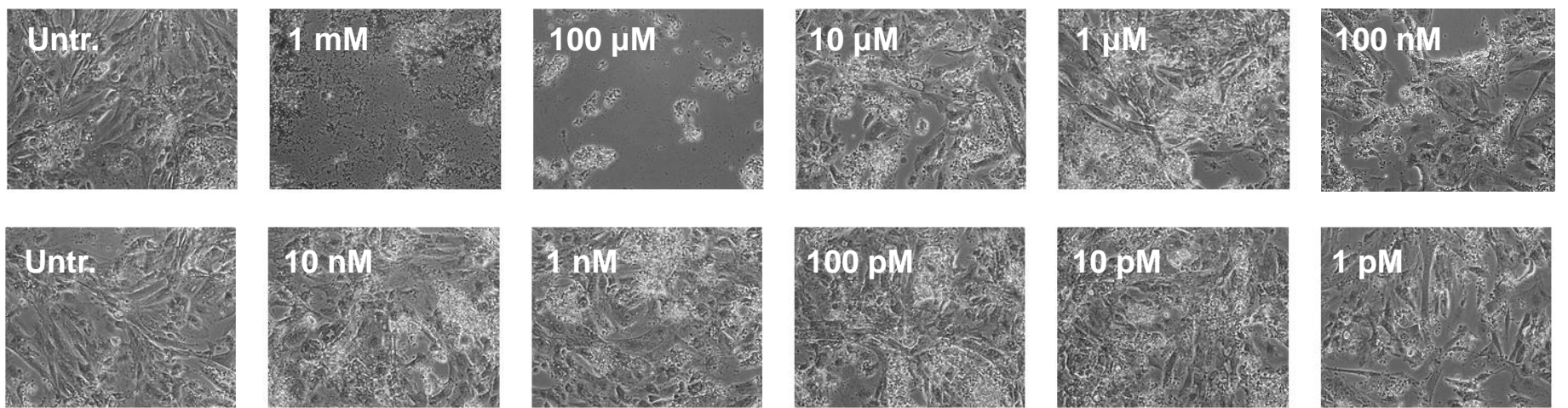


Figure S5. Contractility analysis for determination of optimal drug concentration

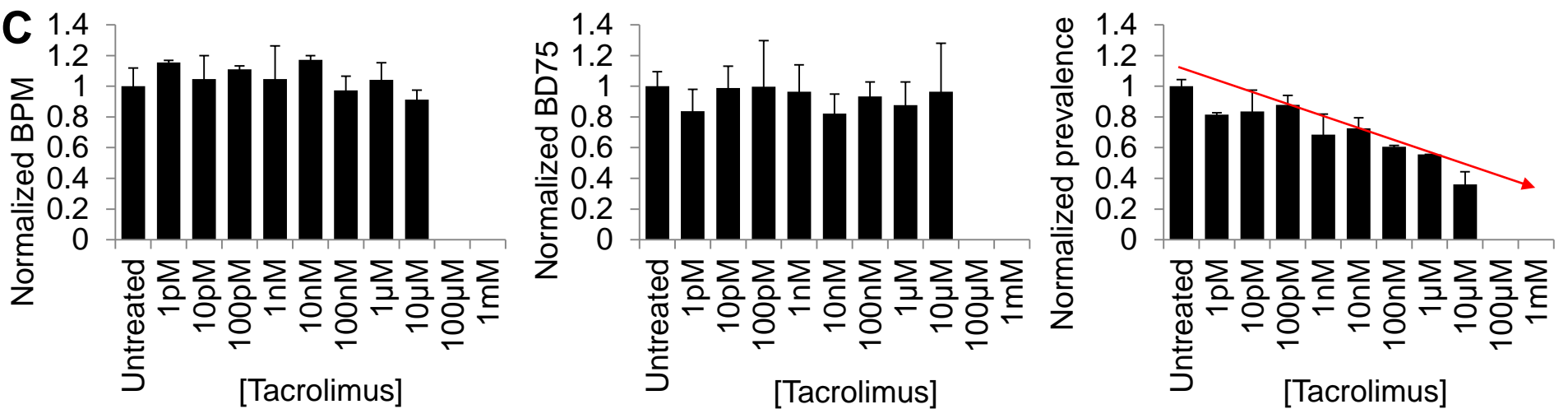
A Raw signal of cardiomyocyte contraction / relaxation



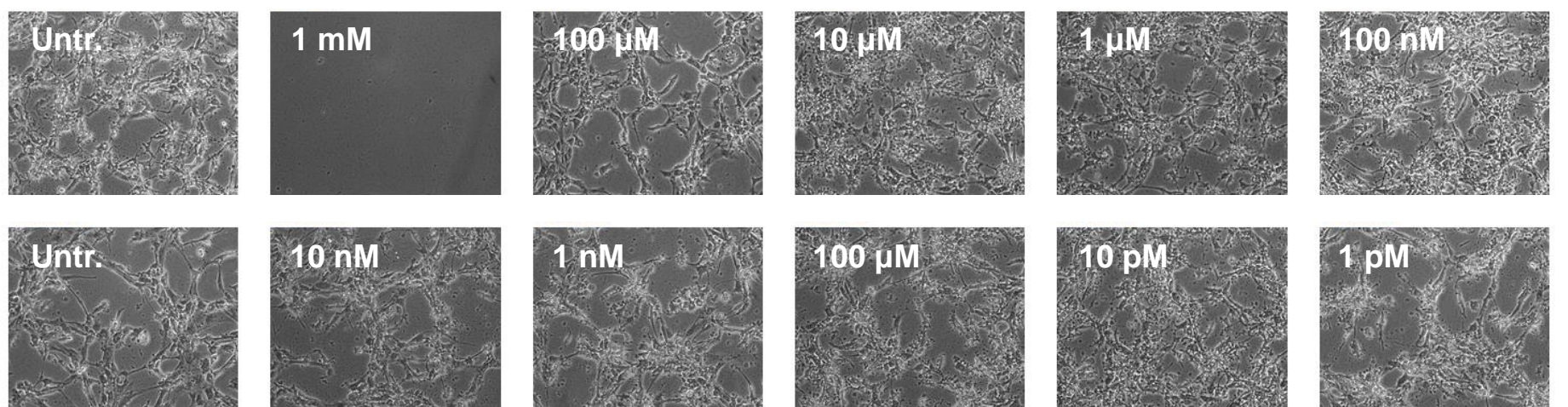
B



C



D



E

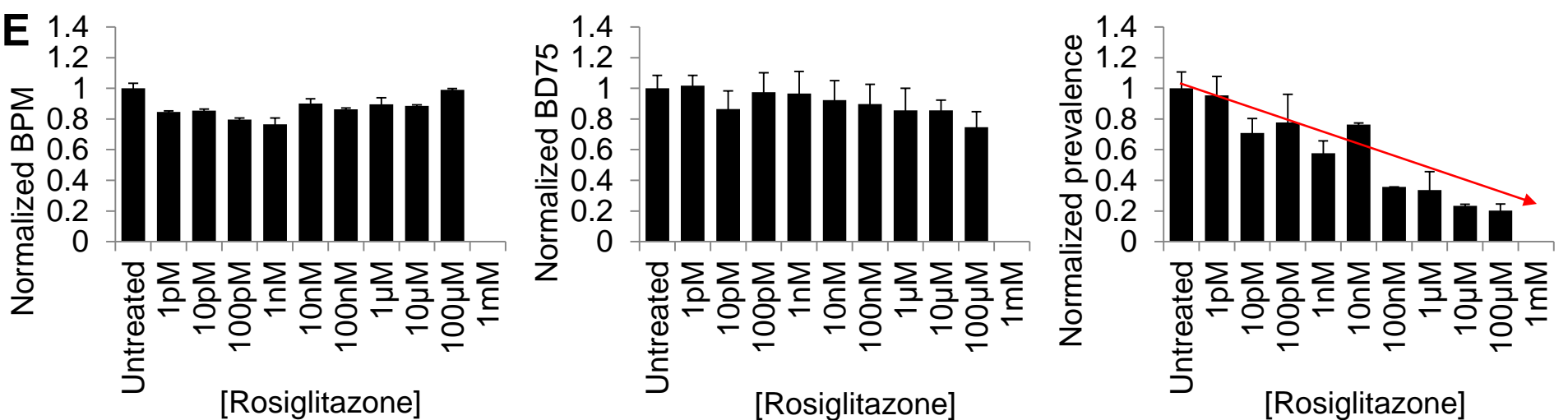
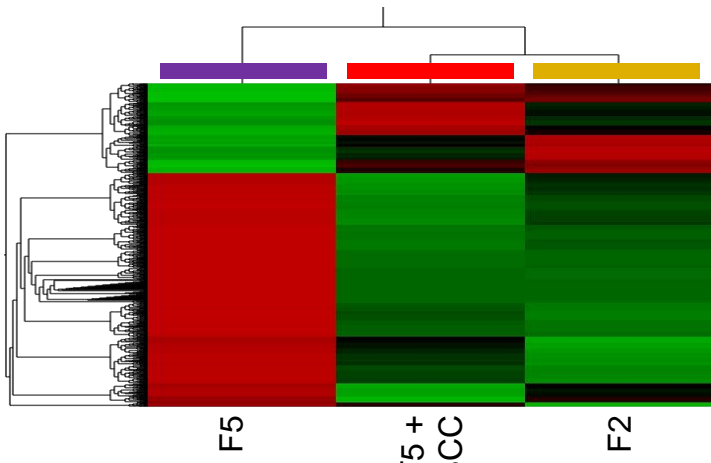


Figure S6. Fold change in gene expression with tacrolimus and rosiglitazone.

A

Two-way t-test $P=0.05$



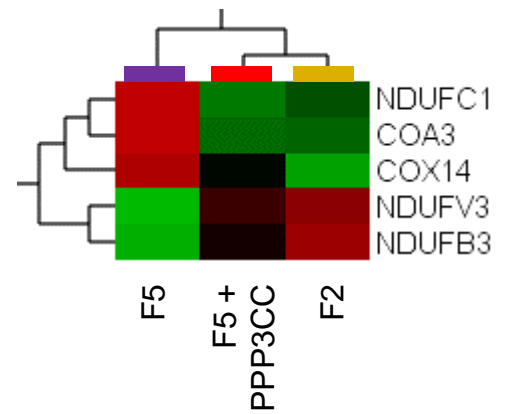
Fold change in RPKM in
tacrolimus-treated vs. untreated
samples per line, mean= 0, var= 1



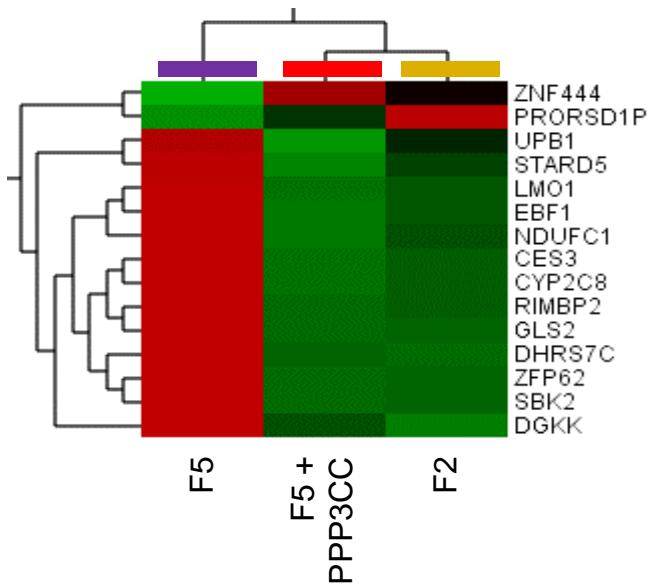
B

GO:xxx

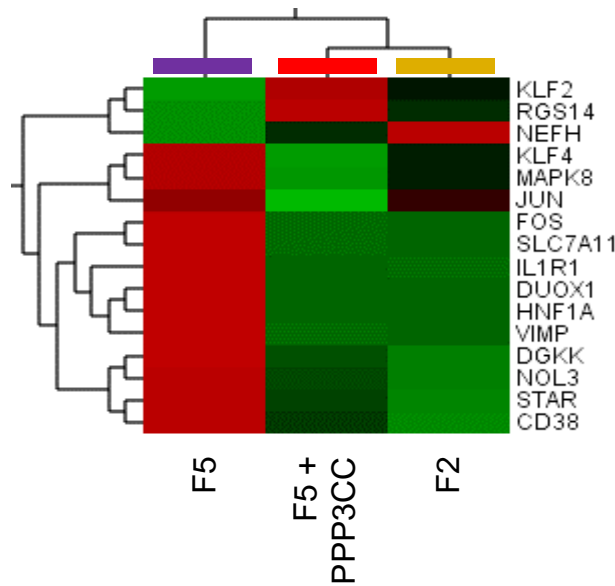
Respiratory chain



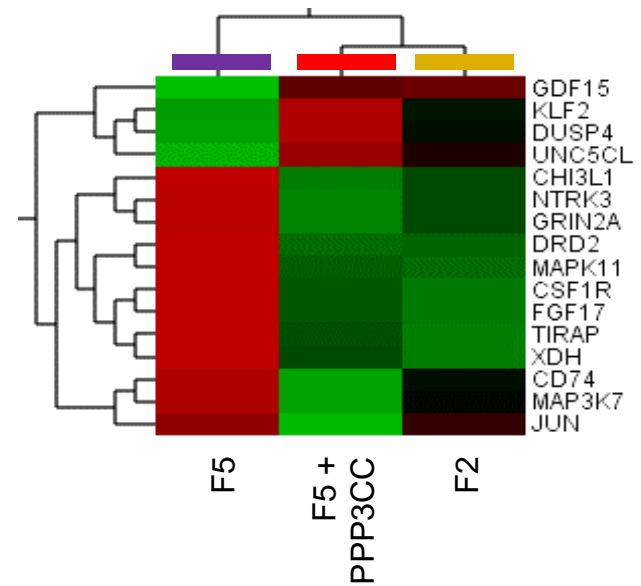
GO:0008152
Metabolic processes



GO:0006979
Oxidative stress

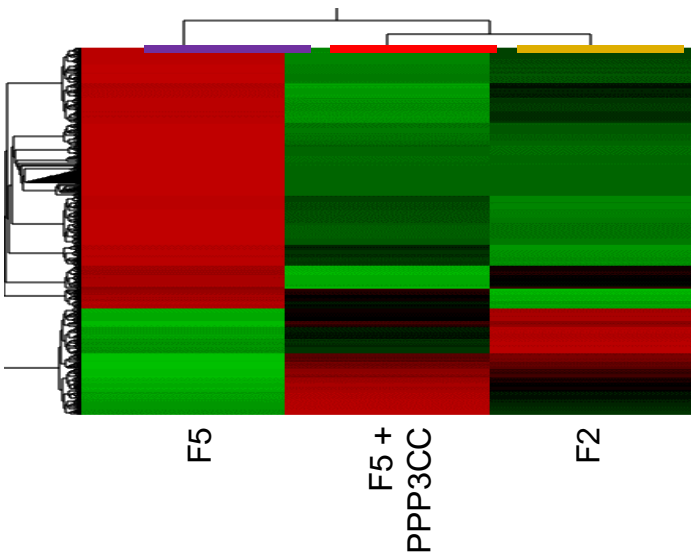


GO:0000165
ERK/MAPK signaling

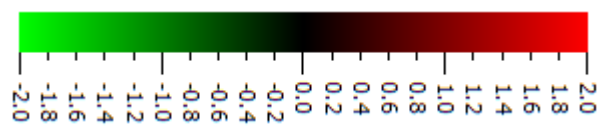


C

Two-way t-test $P=0.05$



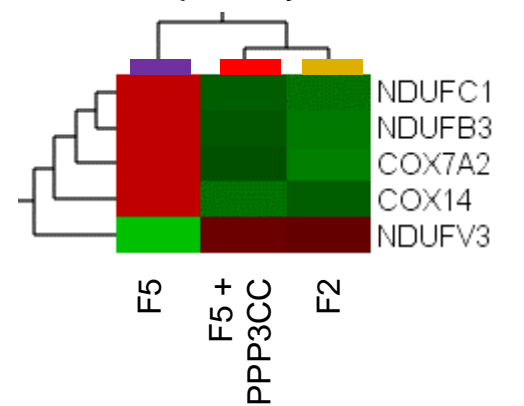
Fold change in RPKM in
rosiglitazone-treated vs. untreated
samples per line, mean= 0, var= 1



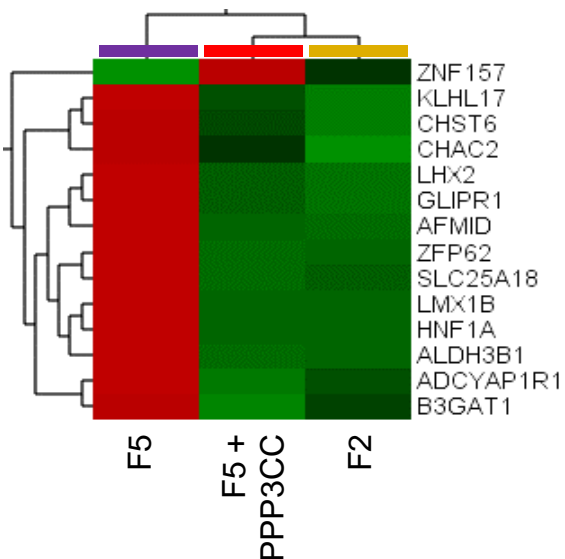
D

GO:xxx

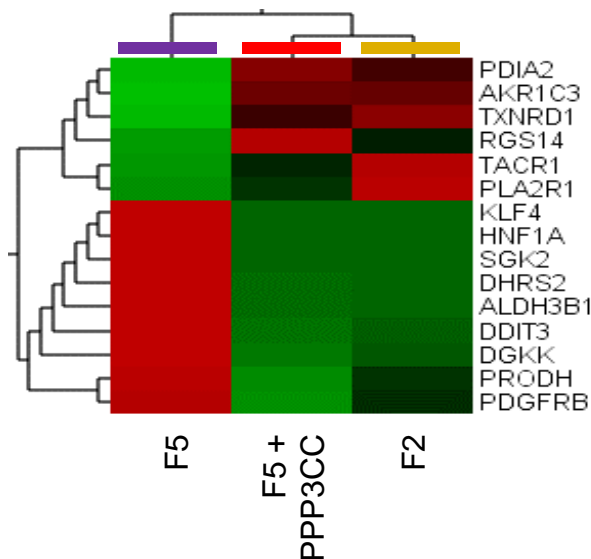
Respiratory chain



GO:0008152
Metabolic processes



GO:0006979
Oxidative stress



GO:0000165
ERK/MAPK signaling

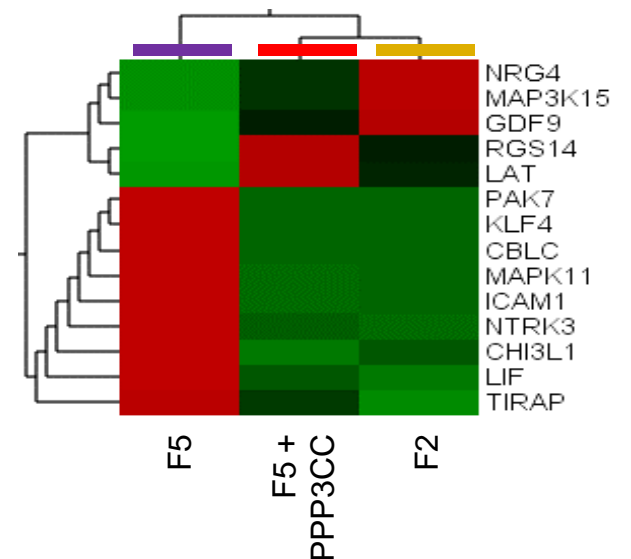


Figure S7. Effects of tacrolimus or rosiglitazone treatment in hiPSC-ECs.

