

Figure 1

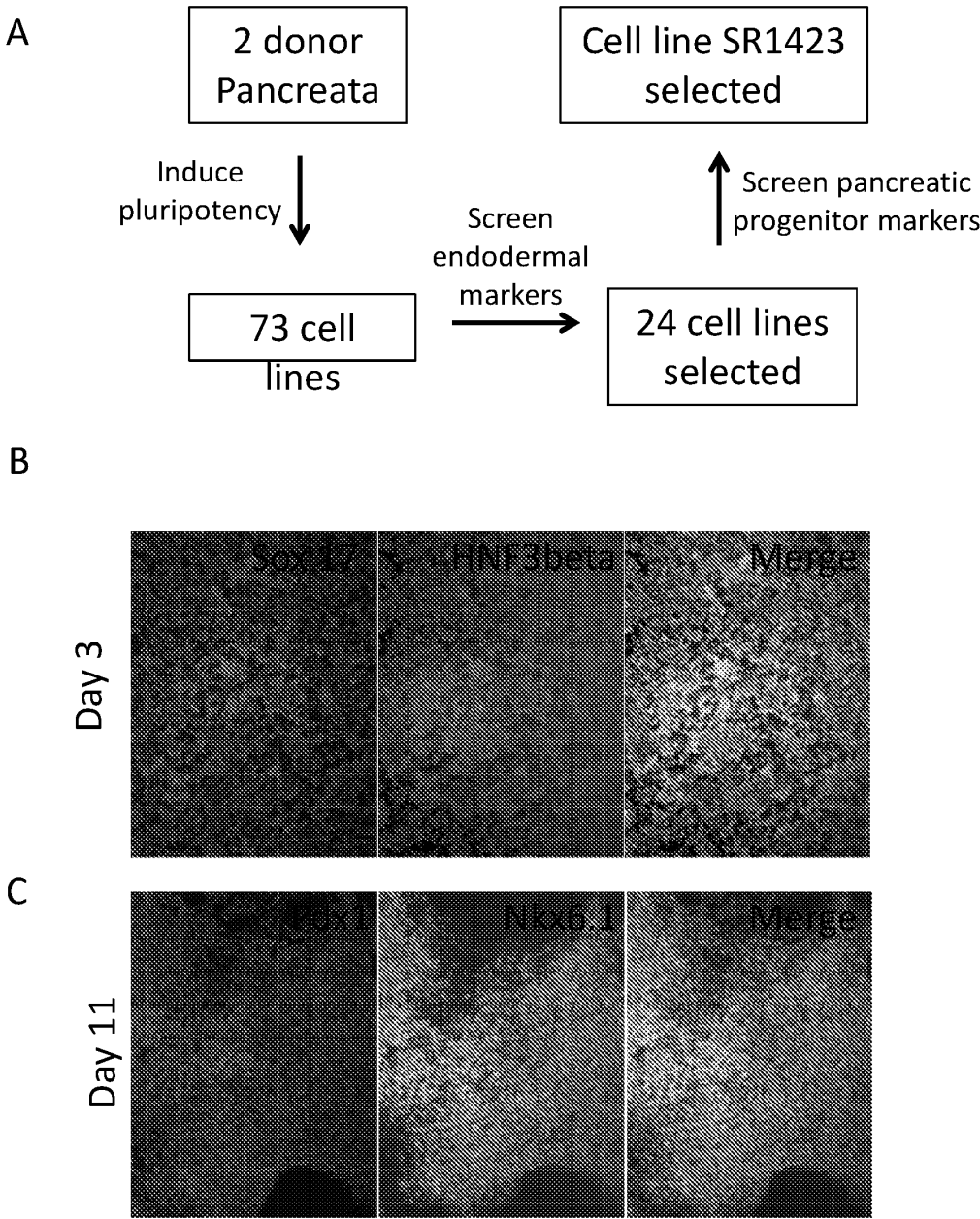


Figure 2

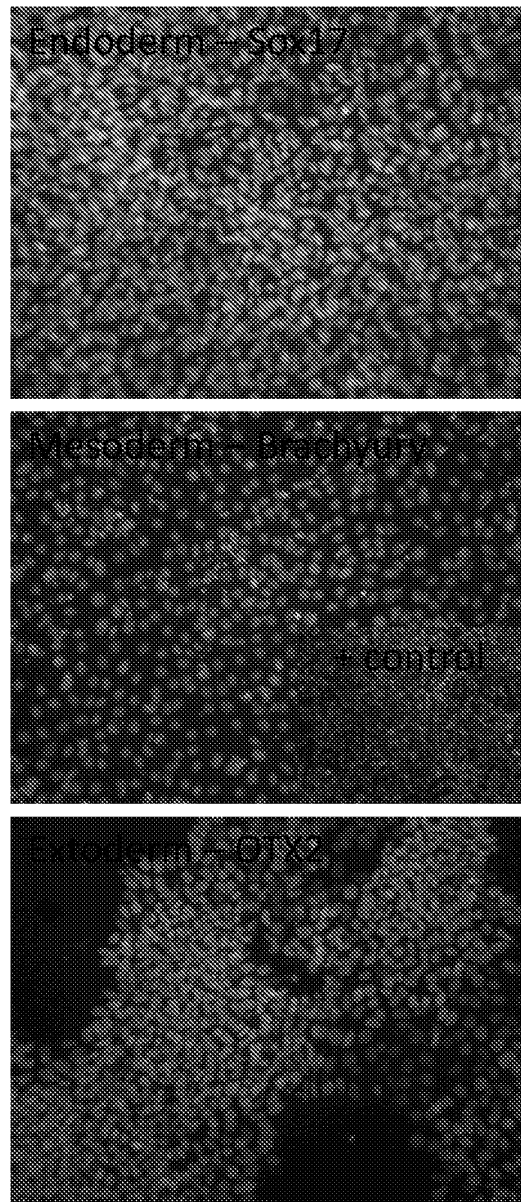
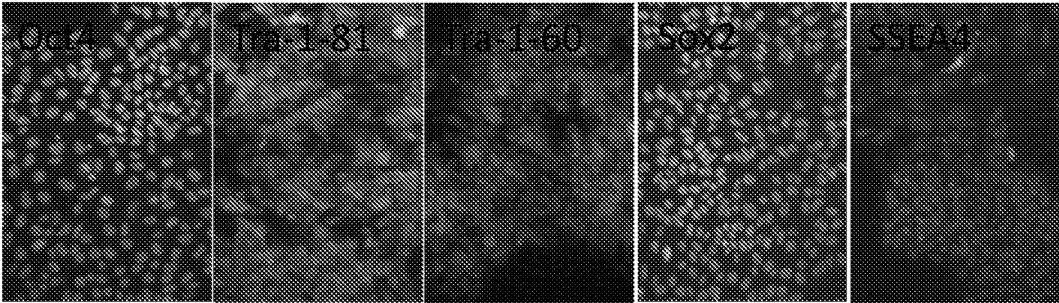
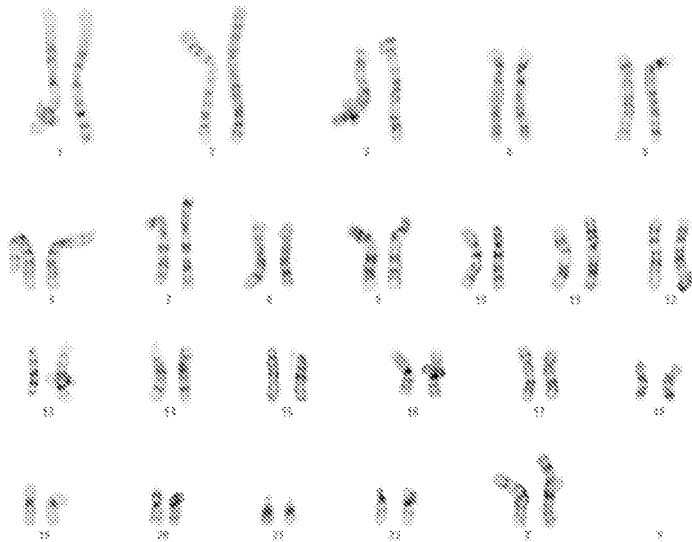


Figure 3

A.



B.



C.

DNA fingerprint					
Amelogenin	X	Y	D18S51	15	17
vWA Penta E	15	18	Penta E	7	15
D8S1179	13		D5S818	11	
TPOX	9	12	D13S317	12	13
FGA	22	25	D7S820	10	13
D3S1358	15	16	D16S539	9	12
TH01 C	6	7	SF1PO	10	12
D21S11	31		Penta	11	13

D.

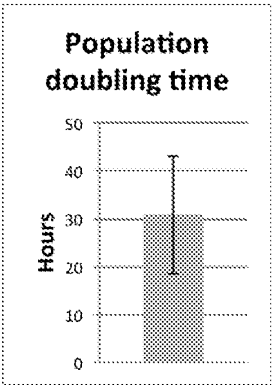
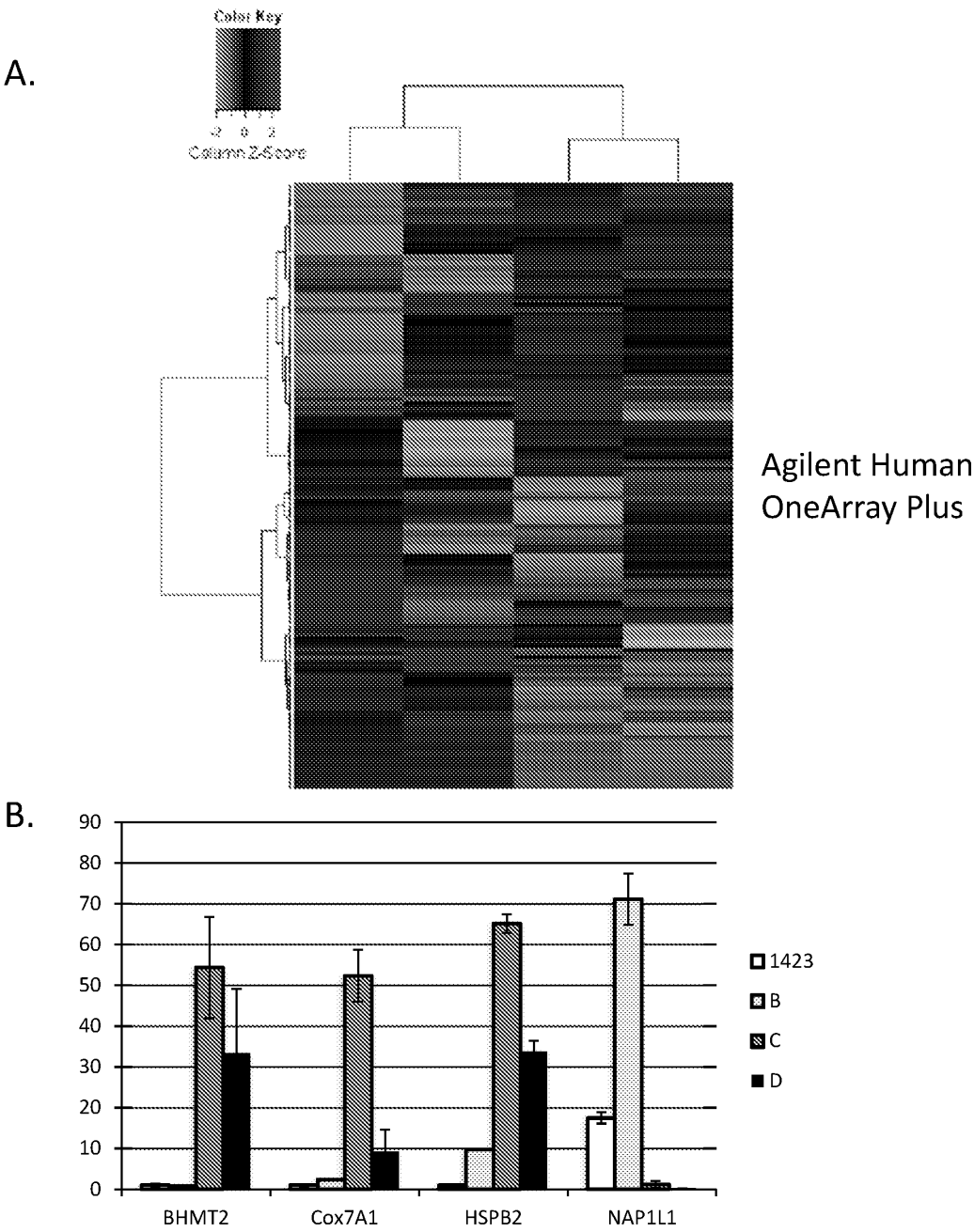


Figure 4



The correlation of expression profiles between samples and treatment conditions was demonstrated by unsupervised hierarchical clustering analysis. Clustering was performed to visualize the correlations among the replicates and the differences between sample conditions. Up- and down-regulated genes are represented in red and green colors, respectively. A subset of differentially expressed genes was selected for this clustering analysis based on an intensity filter that pulls out genes with large expression differences between conditions. The top 250 genes passing this filter are represented above.

Figure 5

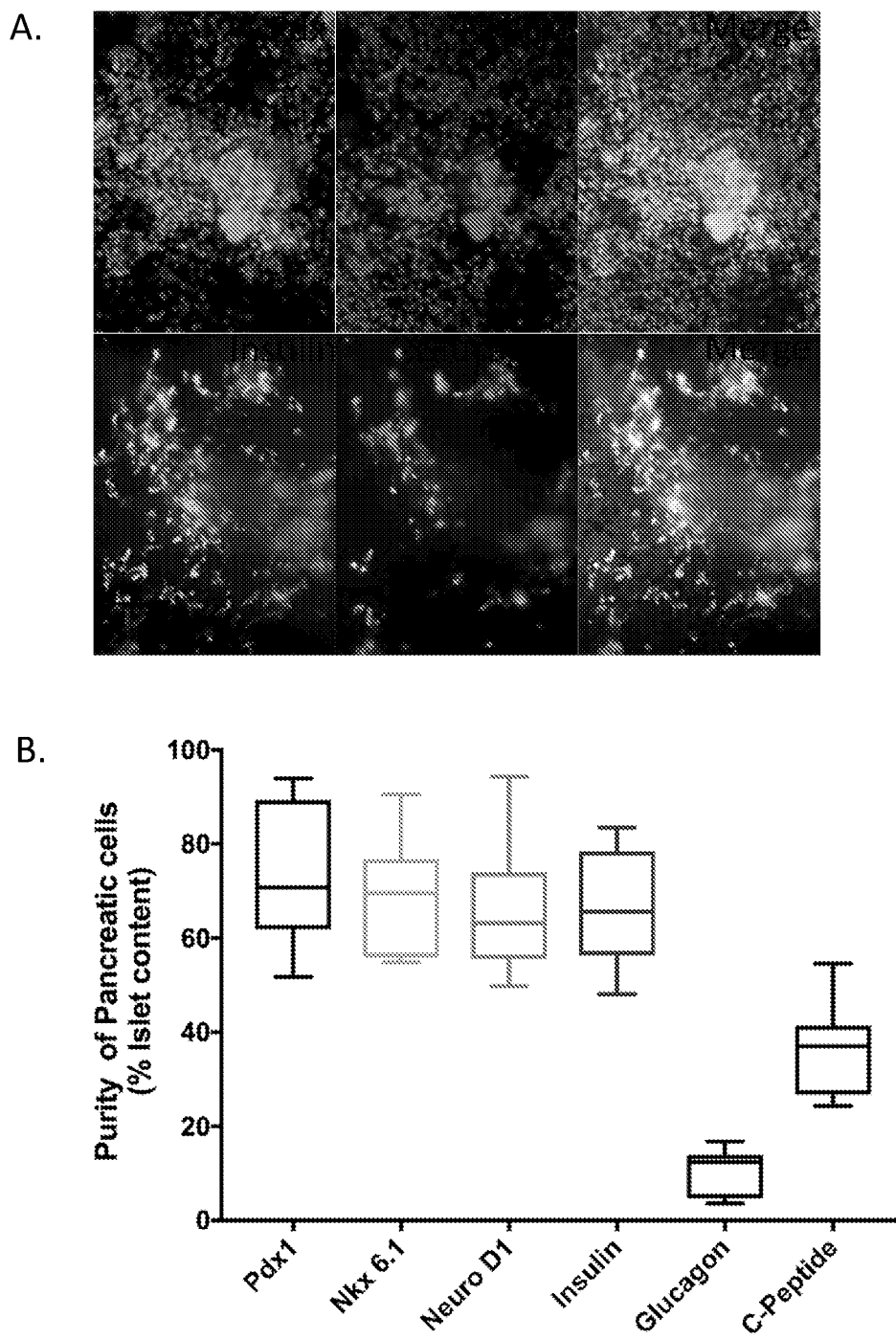


Figure 6
Merge

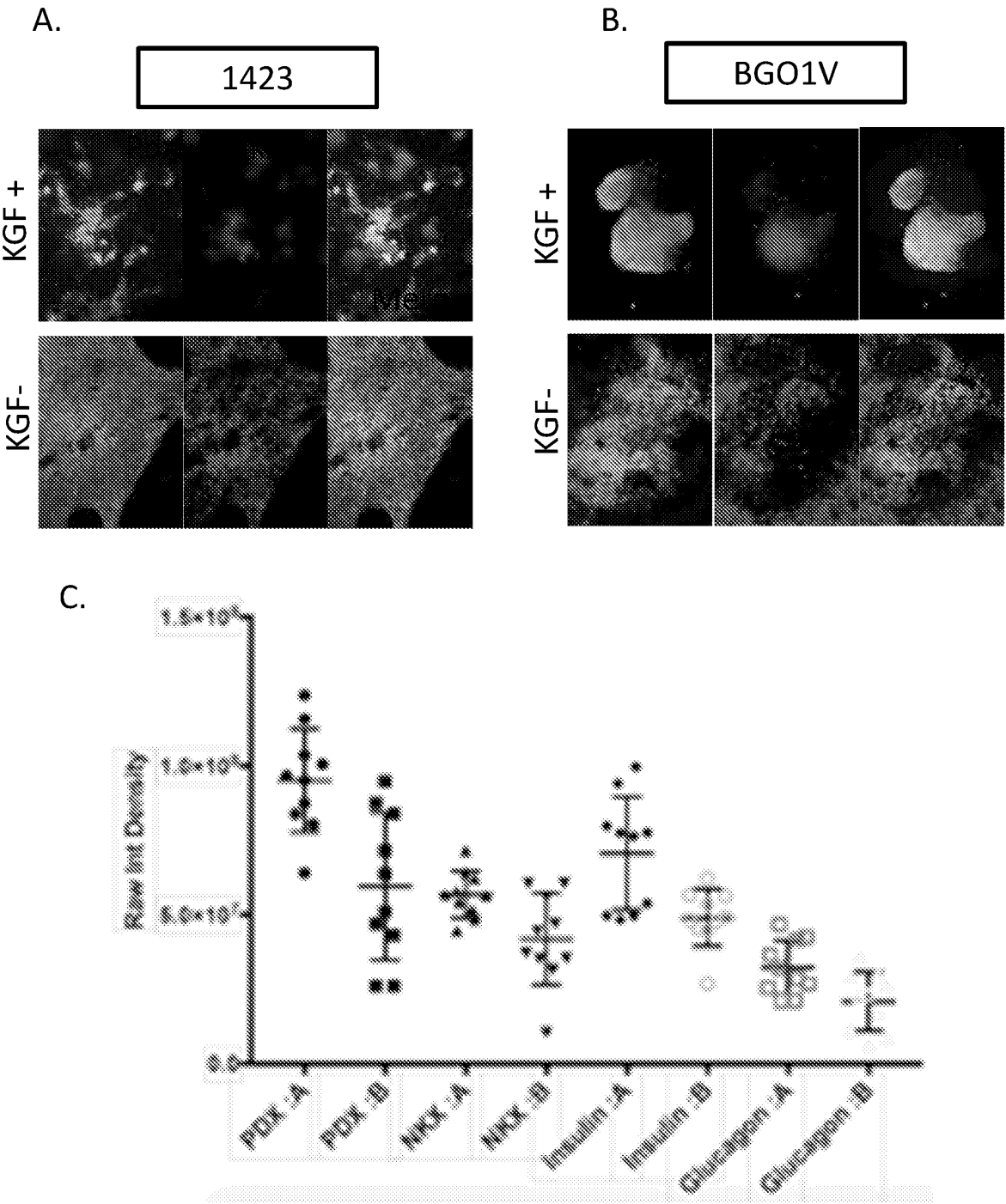


Figure 7

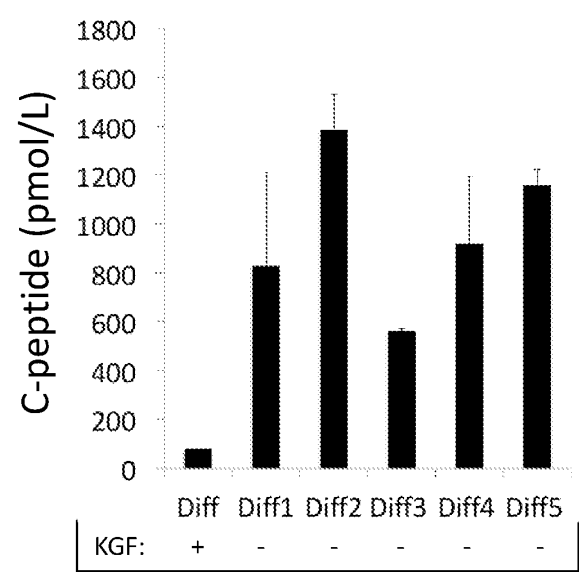


Figure 8

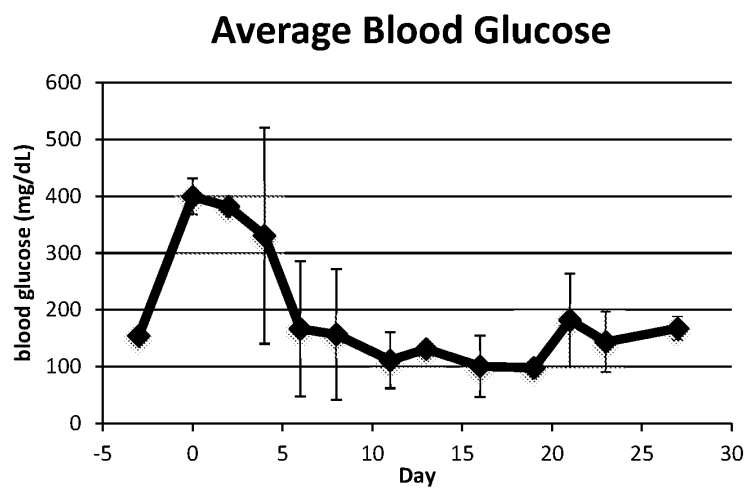


Figure 9

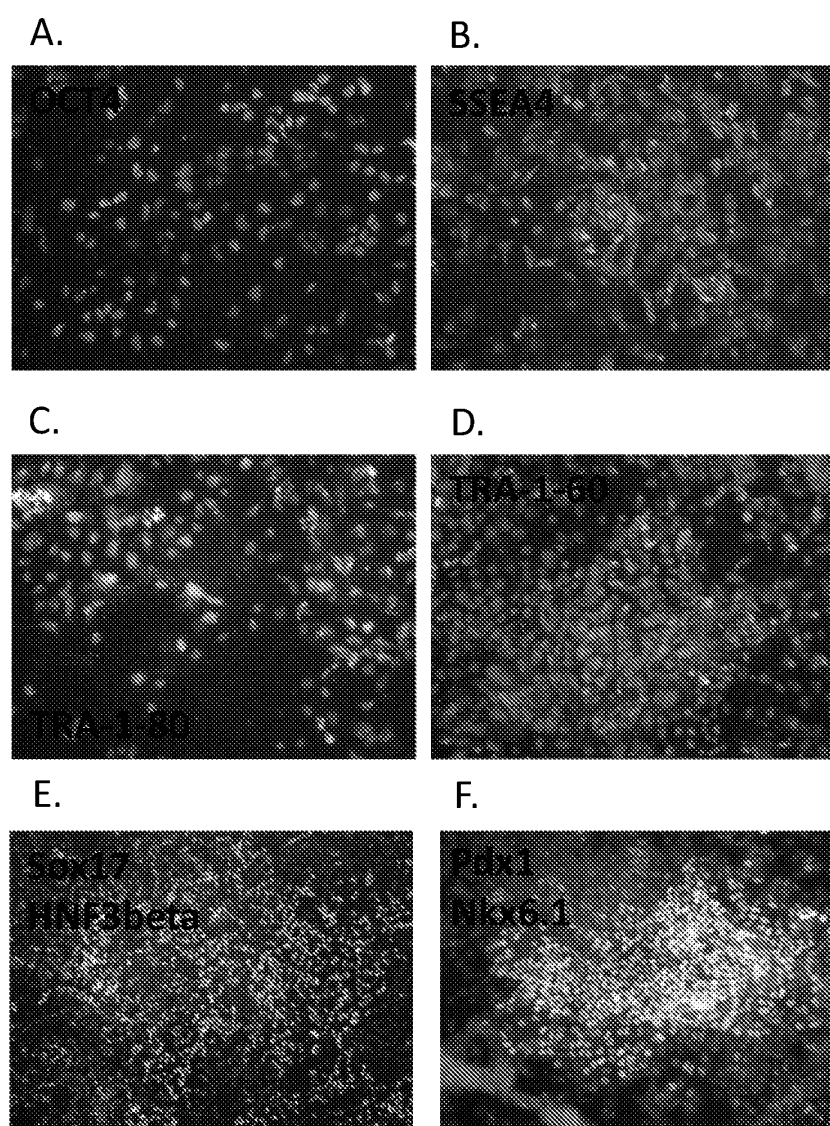


Figure 10.

