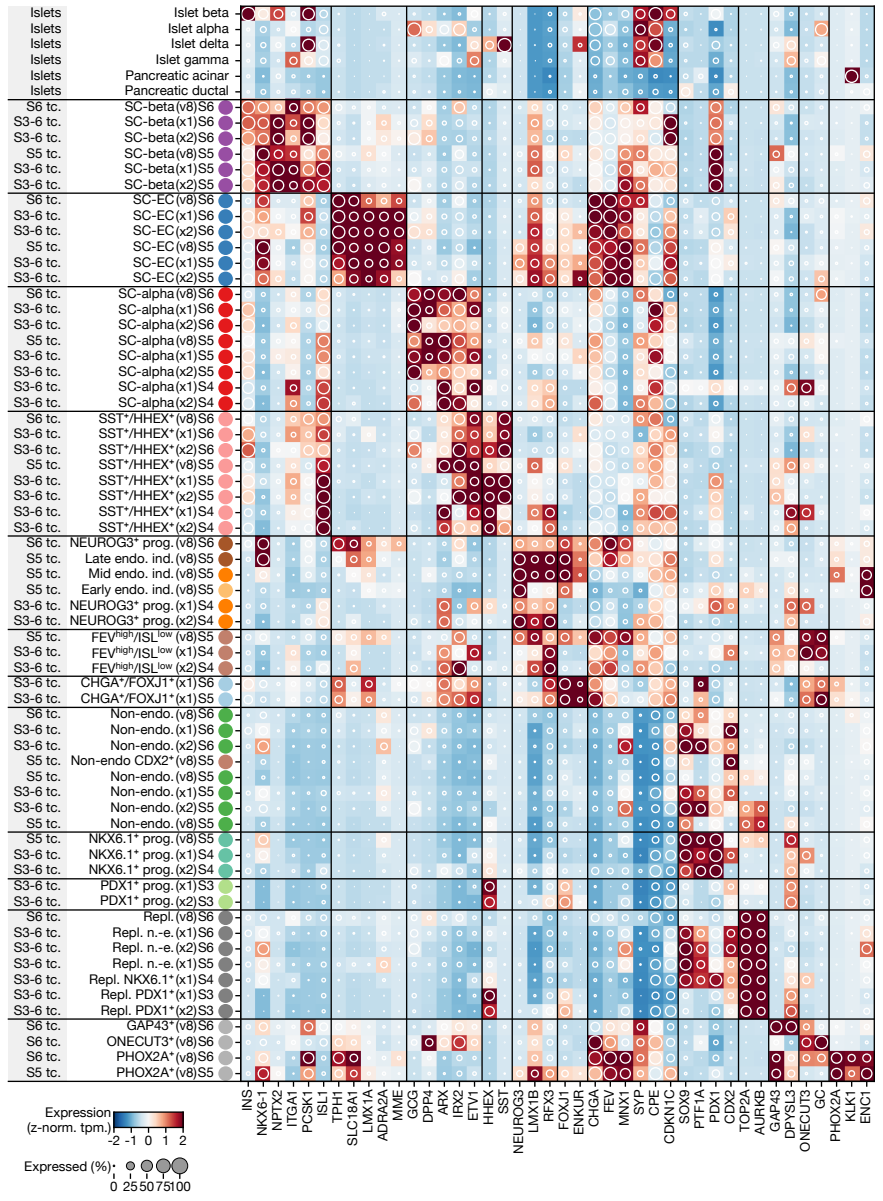
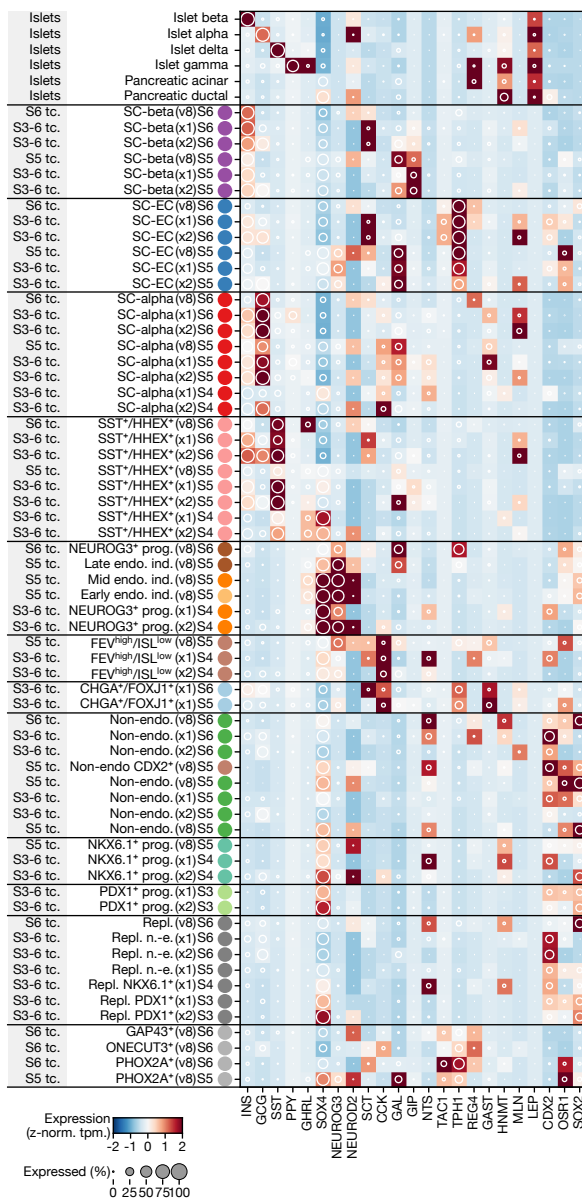


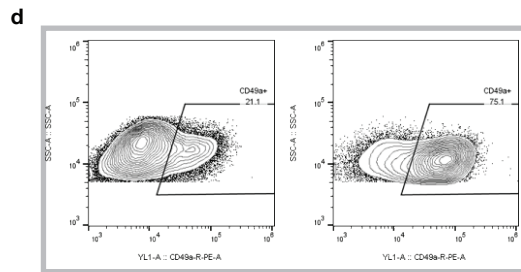
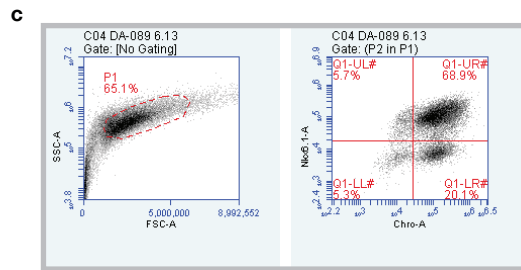
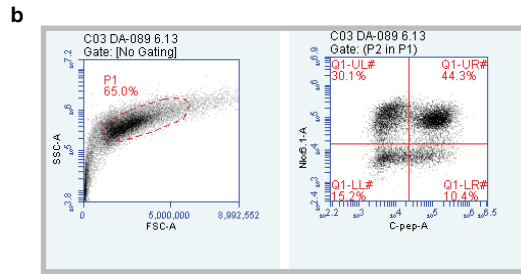
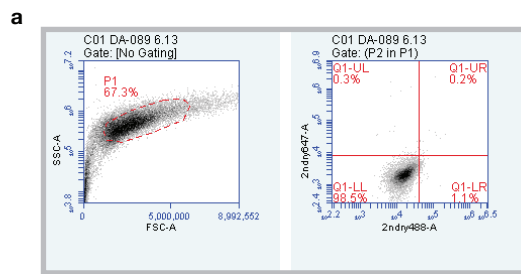
**Supplementary Figure 1**



# Supplementary Figure 2



# Supplementary Figure 3



# Supplementary Table 2

	Purpose	Cells used	Cells sequenced	Data presented in
<b>Stages 3-6 time course</b>	<ul style="list-style-type: none"> <li>Identify populations in each stage</li> <li>Compare two protocol variants</li> </ul>	2 differentiations  HUES8, protocol x1 HUES8, protocol x2	42,097 cells  from 16 libraries  inDrops v2 (Harvard Single Cell core)	Figure 1; Extended Data Figure 1
<b>Stage 6 weekly time course</b>	<ul style="list-style-type: none"> <li>Track long-term gene expression changes after differentiation</li> </ul>	3 differentiations  HUES8, protocol v8	38,494 cells  from 36 libraries  inDrops v2 (1Cell Bio)	Figures 2, 3, 4; Extended Data Figures 3,4,6;
<b>Stage 5 daily time course</b>	<ul style="list-style-type: none"> <li>Establish lineage map of endocrine induction during Stage 5</li> </ul>	2 differentiations  HUES8, protocol v8	51,274 cells  from 32 libraries  inDrops v2 (1Cell Bio)	Figure 5; Extended Data Figure 8
<b>hESC vs hiPSC comparison</b>	<ul style="list-style-type: none"> <li>Compare cell populations produced by different pluripotent stem cell lines</li> </ul>	3 differentiations  HUES8, protocol v4 HUES8, protocol x3 iPS1016/31, protocol v4	4,312 cells  from 6 libraries  inDrops v3 (Harvard Single Cell core)	Extended Data Figure 1
<b>Re-aggregation analysis</b>	<ul style="list-style-type: none"> <li>Identify which populations are retained by re-aggregation</li> </ul>	1 differentiation HUES8, protocol v4  processed into two conditions at the end of Stage 5: - native, in MCDB131 - RA, in MCBD131	5,636 cells  from 4 libraries  inDrops v3 (Harvard Single Cell core)	Extended Data Figure 7