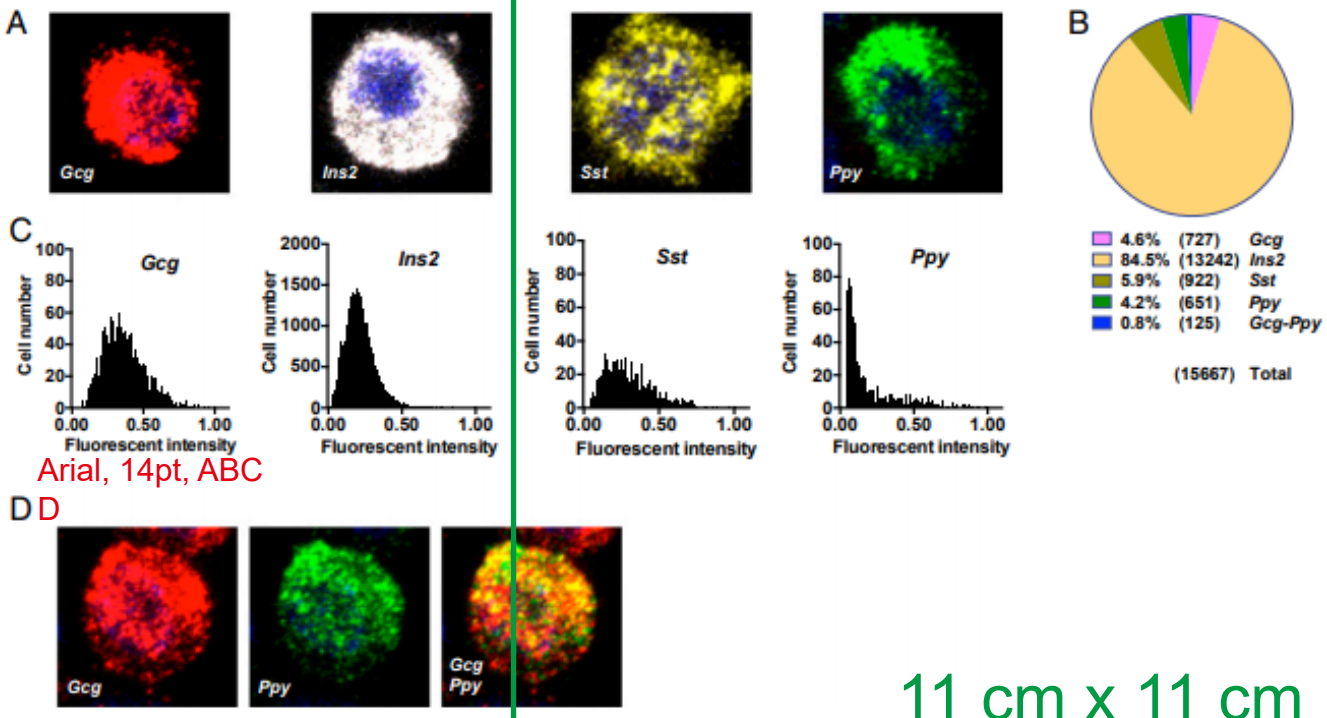

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Fig. 1. Mouse islet cells rarely express more than one hormone. (*A*) Representative RNA FISH images of single mouse islet cells expressing glucagon (*Gcg*), insulin (*Ins2*), somatostatin (*Sst*), or pancreatic polypeptide (*Ppy*). (*B*) Distribution of islet cells. (*C*) Intensity distribution histograms of Gcg^+, $Ins2^+$, Sst^+, or Ppy^+ cells. (*D*) Representative RNA FISH images of Gcg^+-Ppy^+ cells.

as the cell viability gene set (*Methods*). These genes account for >30% of total expression in RPKM. Fig. 2*B* shows that the median expression of the cell viability gene set is 12-fold higher ($P = 5.6e^{-23}$) in cluster 1 cells, whereas the expression of all other genes is 285-fold ($P = 6.0e^{-23}$) reduced. Fig. 2*C* shows the distribution of the sequenced cells according to their viability score (*Methods*). Cells with a score >0.3 are likely to be of low

mainly cluster between Gcg^+ and $Ins2^+$ cells (*SI Appendix*, Fig. S7). This, combined with the RNA FISH data of the input islet cell suspensions (cf. Fig. 1), suggests that nearly all multiple-hormone–expressing cells are artifacts that arise during the cell capture process due to damage or cell–cell fusion. Therefore, the cells that coexpress more than one hormone were excluded from subsequent analysis (*SI Appendix*, Fig. S2). Fig. 3*C* shows the dis-

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