**Table S1. Summary of four single-cell RNA-seq datasets. Related to Figure 1.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Studies | | Enge | Segerstolpe | Wang\_C1 | Wang\_C1HT |
| Single cell platform | | Plate based Smart-seq2 | Plate based Smart-seq2 | Fluidigm C1 | Fluidigm C1HT |
| Median reads/cell | | 510,388 | 312,402 | 1,820,102 | 378,824 |
| Median genes/cell | | 3,244 | 6,186 | 6,102 | 4,127 |
| Number of cells | total | 2,504 | 2,470 | 1283 | 4917 |
| alpha | 1,016 | 1,038 | 369 | 1,718 |
| beta | 441 | 310 | 296 | 801 |
| delta | 71 | 101 | 35 | 151 |
| epsilon | 8 | 7 | 1 | 19 |
| pp | 20 | 201 | 33 | 32 |
| ductal | 418 | 436 | 244 | 736 |
| acinar | 405 | 208 | 139 | 681 |
| endothelial | 13 | 25 | 31 | 125 |
| fibroblast | 60 | 67 | 103 | 180 |
| immune | 1 | 19 | 12 | 23 |
| doublets | 51 | 58 | 28 | 451 |