

Figures based on scRNA-seq data

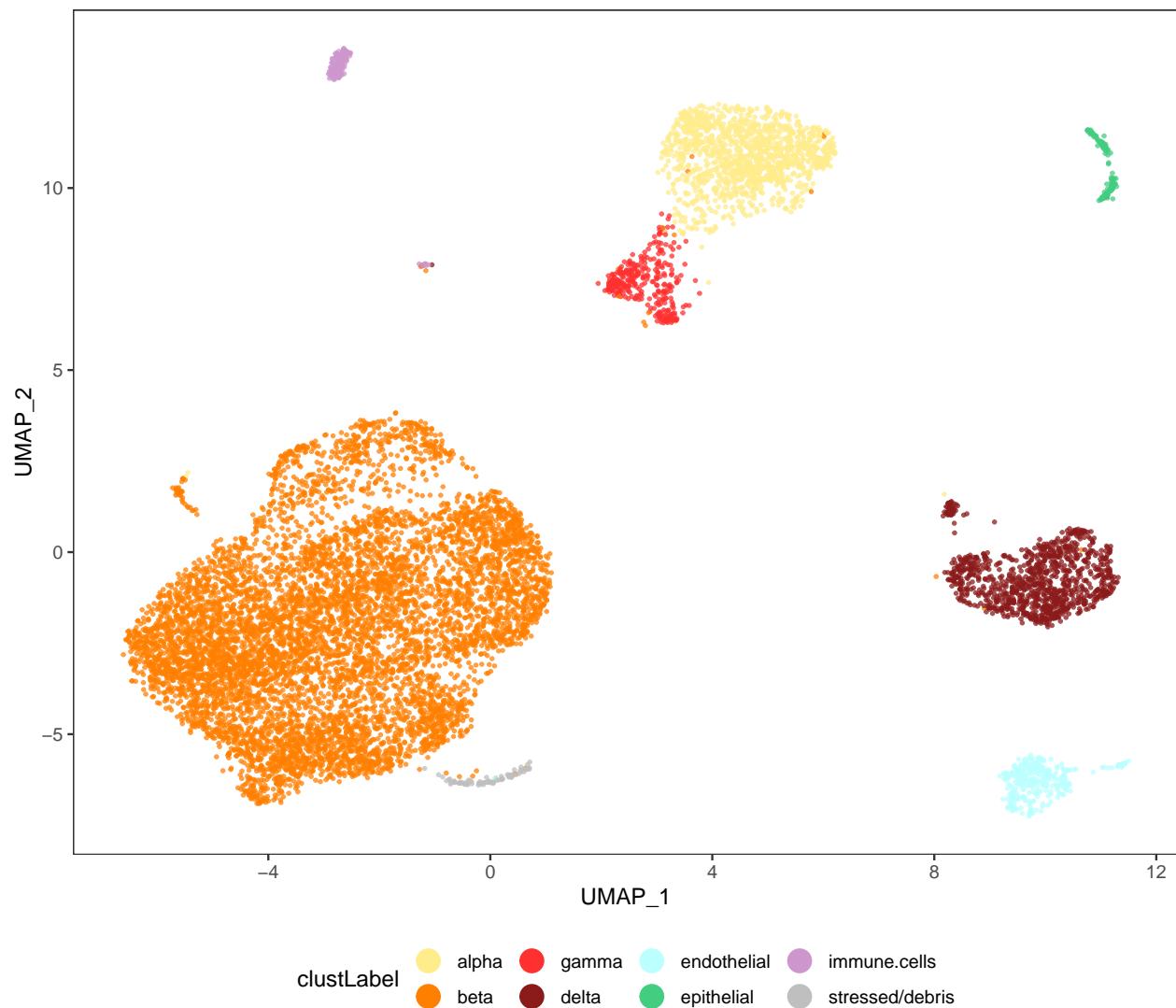
Friederike Dündar, Applied Bioinformatics Core, Weill Cornell Medicine

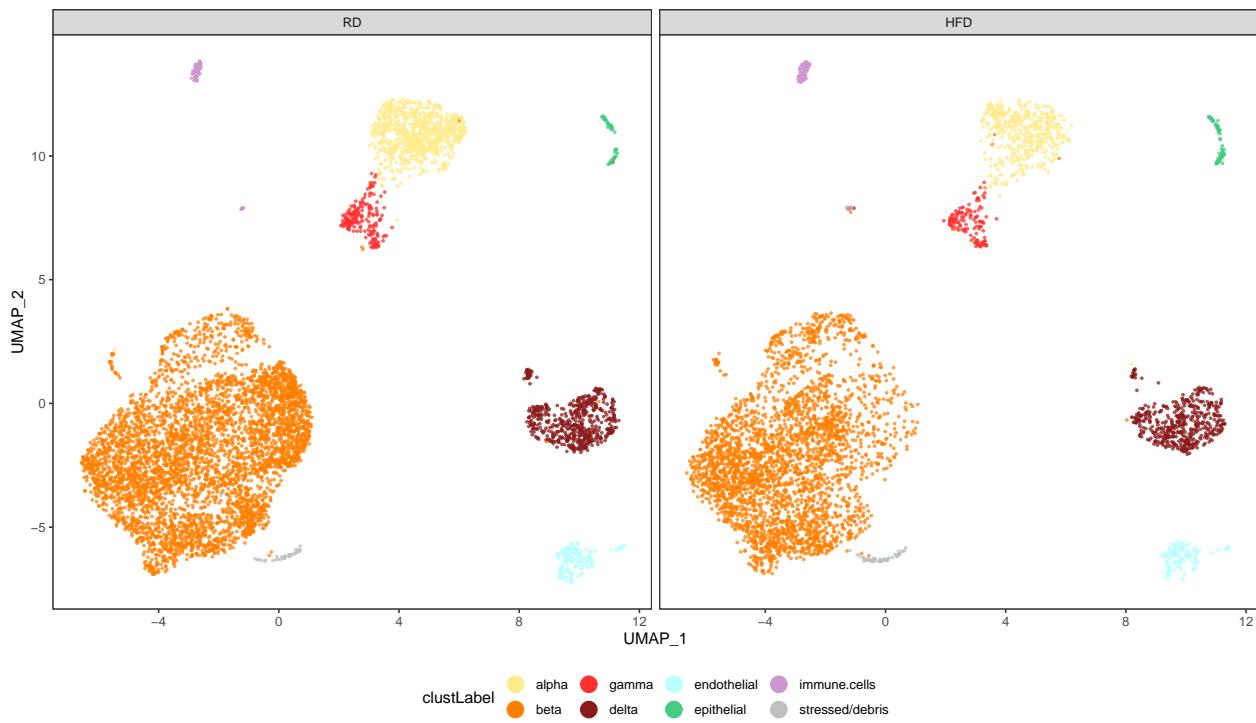
updated 2022-05-13

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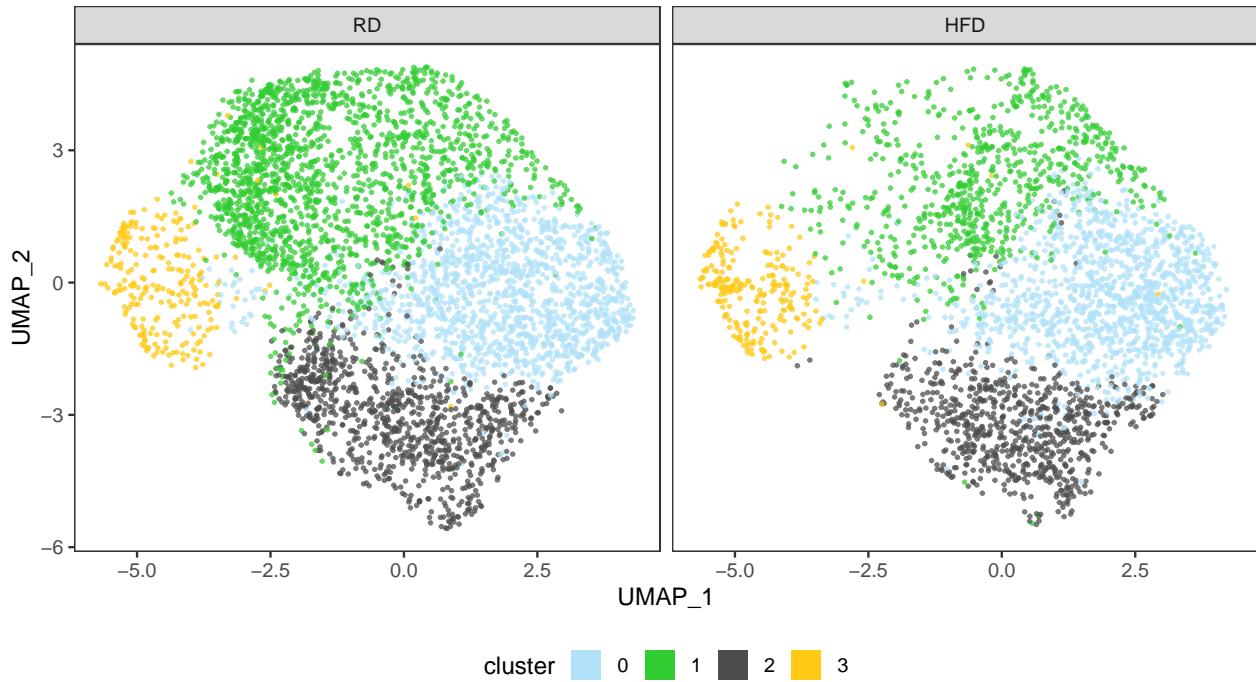
UMAP of pancreatic cell types





UMAP of beta cell clusters

```
## Cached data here: ~/Library/Caches/BiocFileCache/16a9ea59310a_ncr8szvwoeu1ip3uxtizwk3vsxzzczc6.rds
```



Number of cells per cluster per condition:

```
##
##      HFD    WT
##      0 1226 1389
```

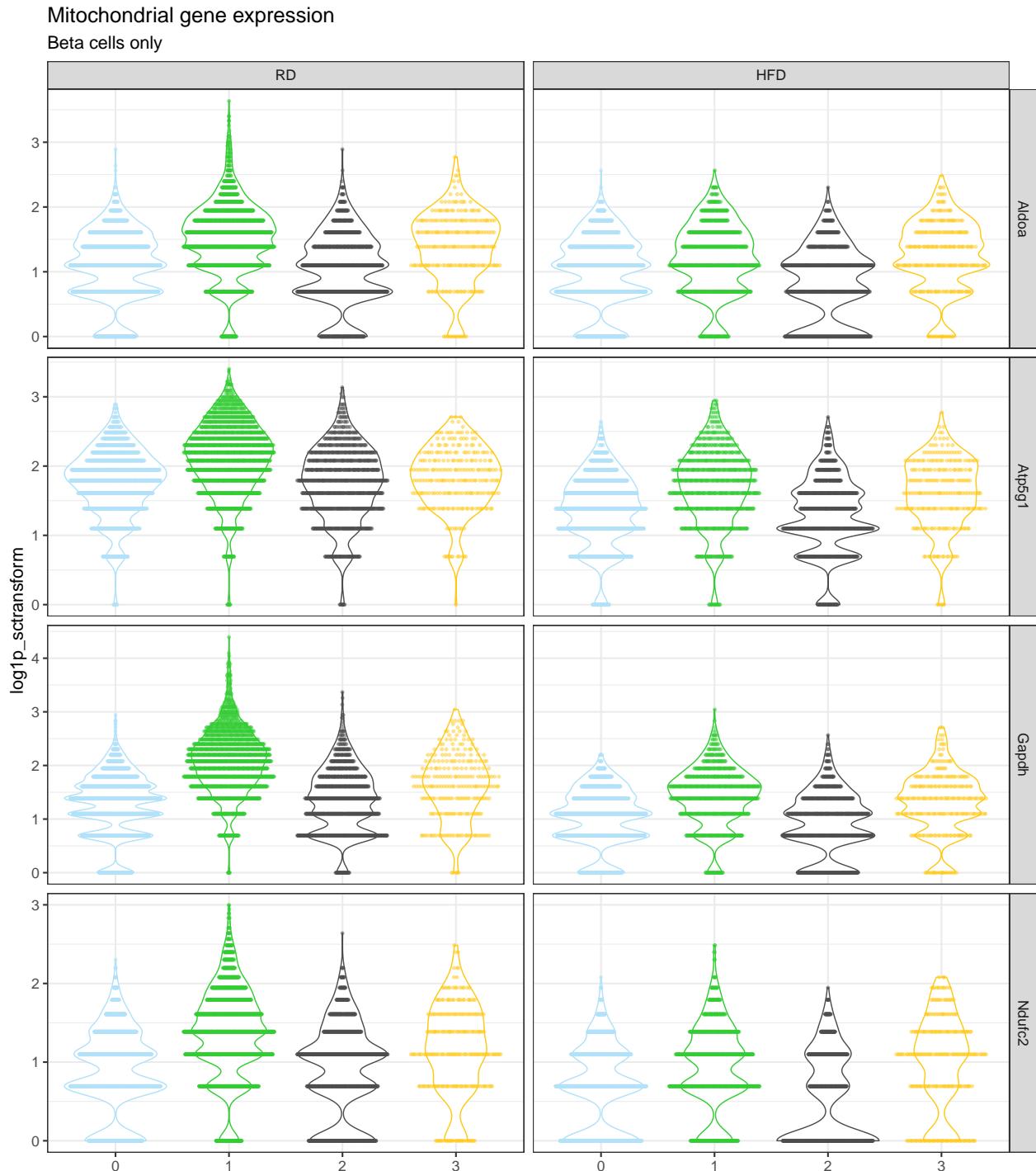
```

##   1 735 1813
##   2 749 946
##   3 237 240

```

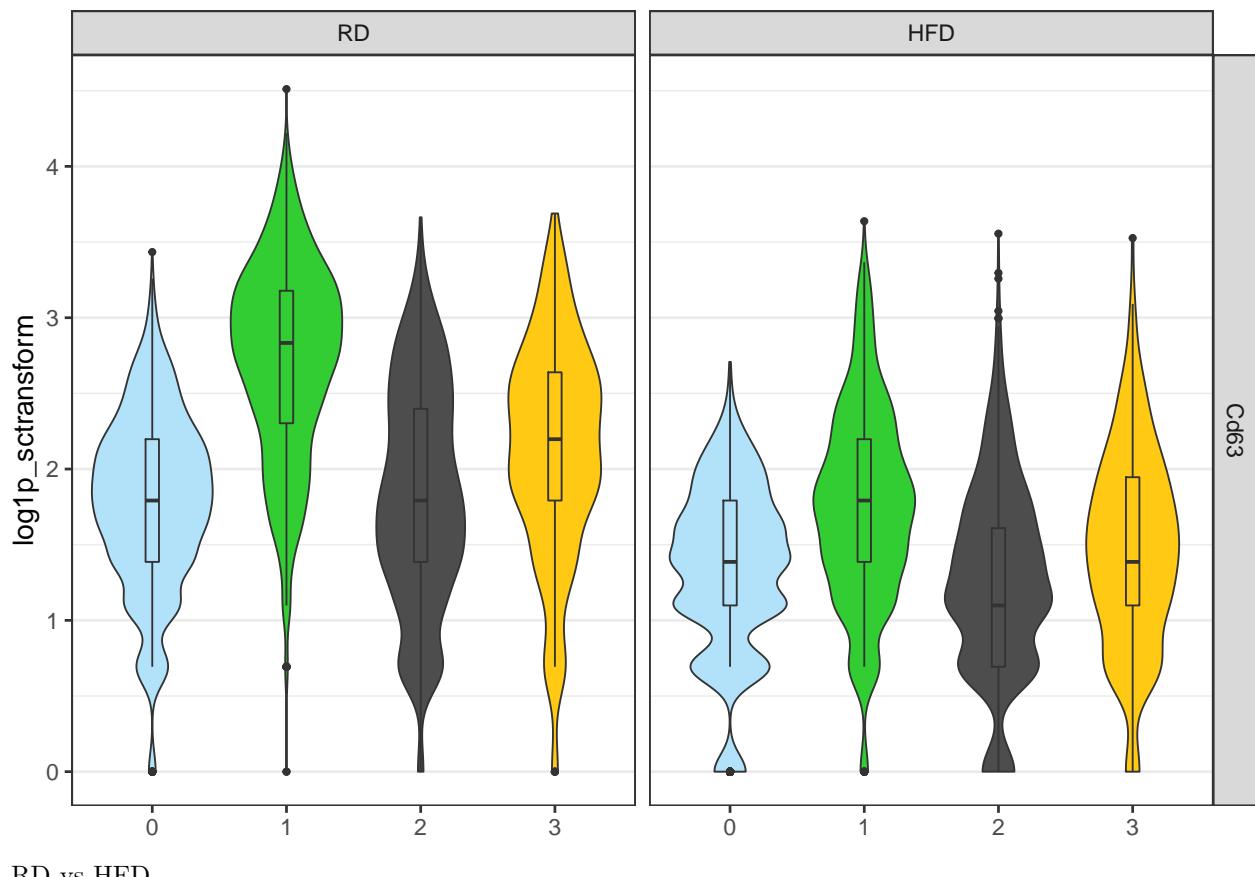
Expression of marker genes

The violin plots can easily be reproduced with `dittoSeq::dittoBoxPlots()` instead of our home-grown package.

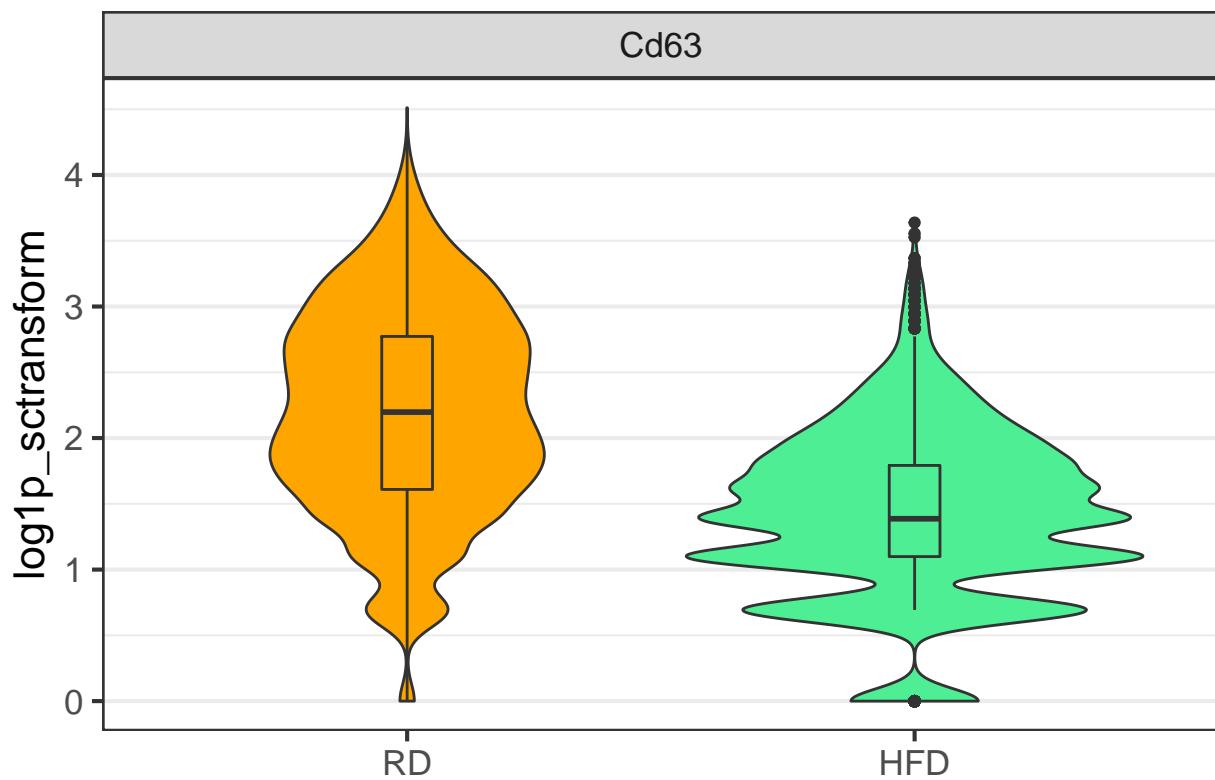


CD63 expression

Per cluster



RD vs HFD

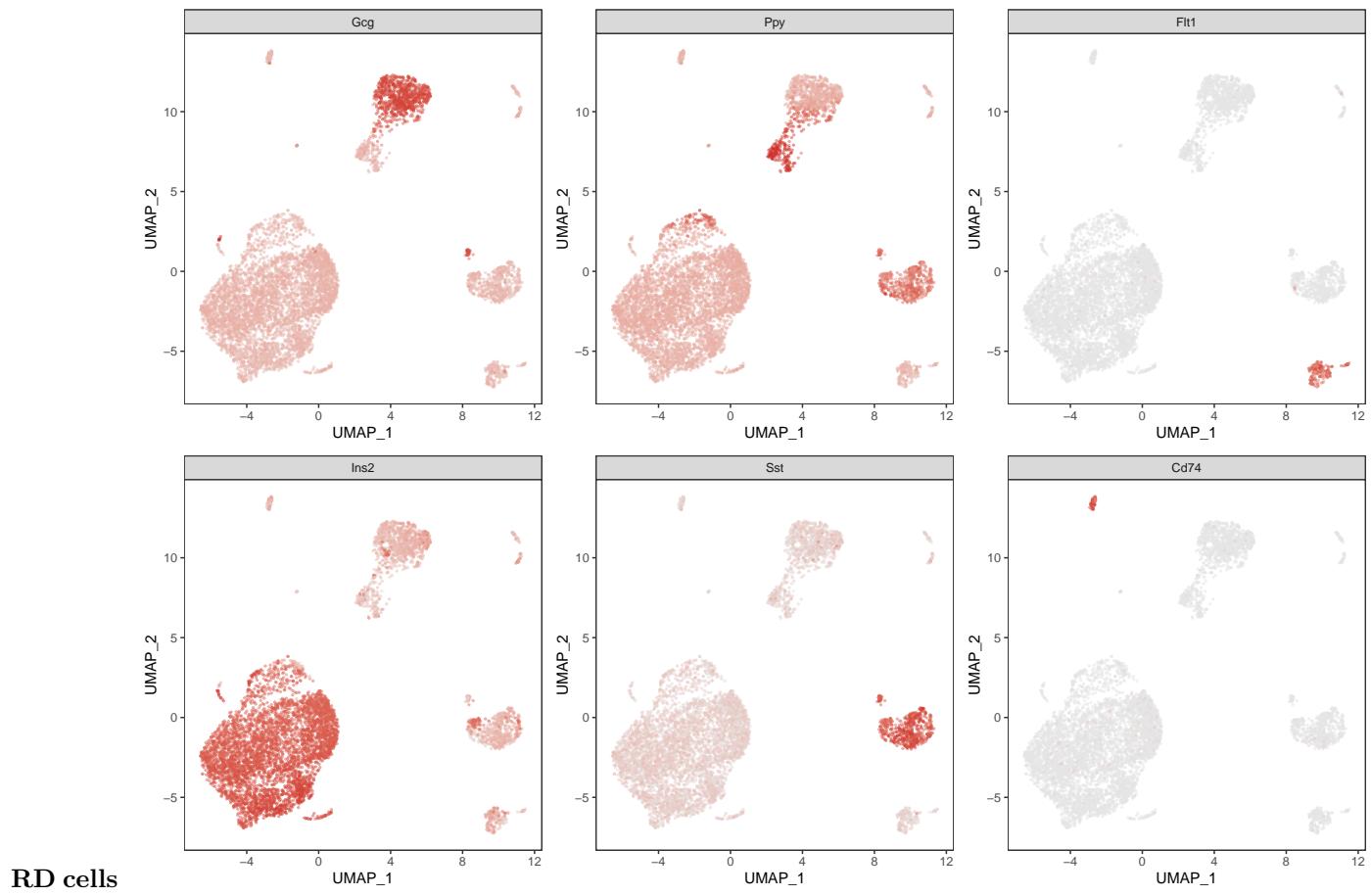


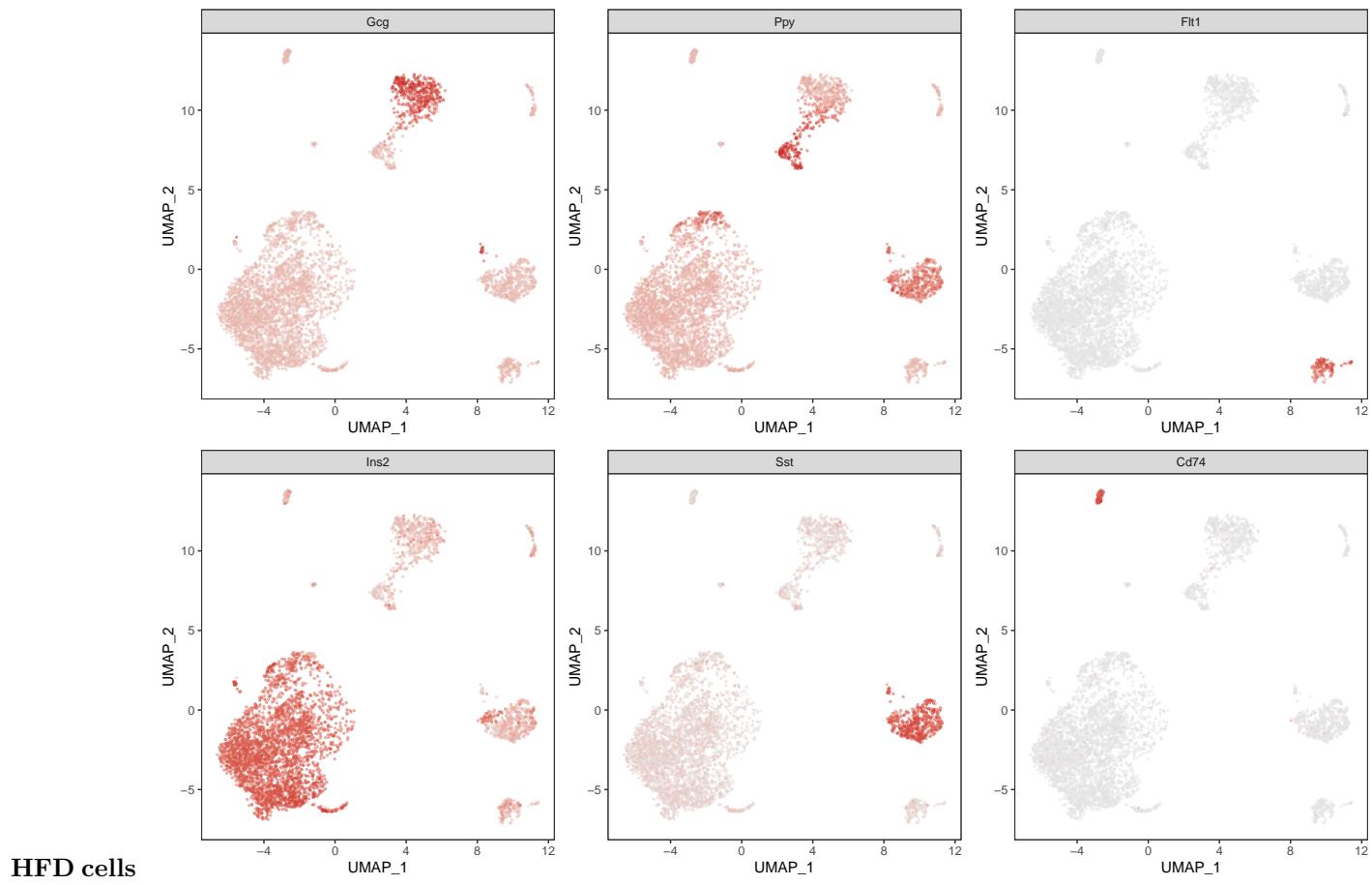
Extended Figures

Expression of pancreatic marker genes

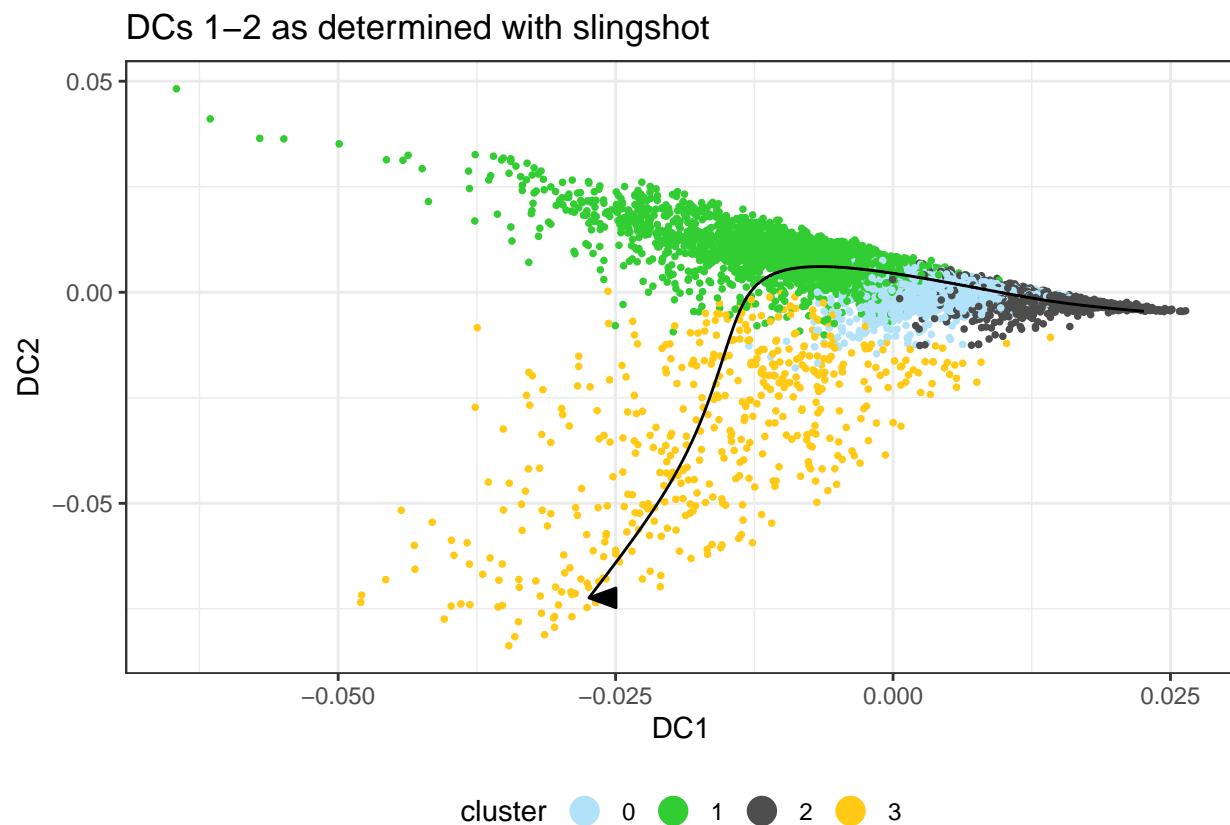
```
##
##      alpha beta gamma delta endothelial epithelial immune.cells
##    HFD    445  3108    130    492        140       79       95
##    WT     806  4578    192    572        196       60       69
##
##      stressed/debris
##    HFD            50
##    WT            36
```

- UMAP of marker gene expression: Ins2, Gcg, Ppy, Sst, Flt1, Cd74





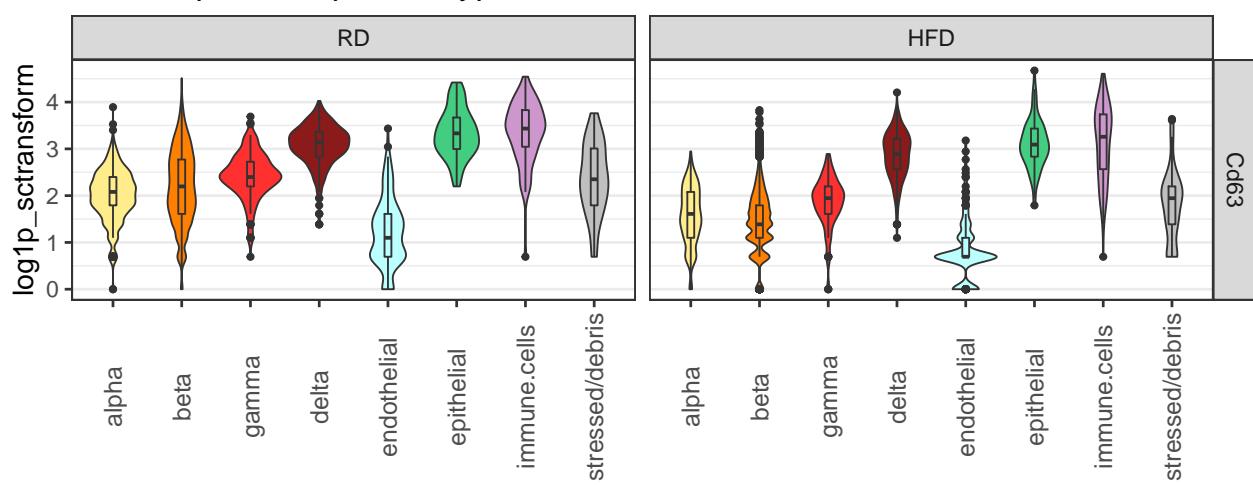
Diffusion map



Cd63 in different pancreatic cell types

- all cells, by condition and cell label

Cd63 expression per cell type



SessionInfo

```
## R version 3.6.2 (2019-12-12)
```

```

## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Catalina 10.15.4 ##
## Matrix products: default

## BLAS: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib ##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8 ##

## attached base packages:
## [1] stats4 parallel stats
## [8] methods   base
##
## other attached packages:
##  [1] ReactomePA_1.30.0          clusterProfiler_3.14.3
##  [3] destiny_3.0.1              dittoSeq_1.1.2
##  [5] slingshot_1.4.0            printrcurve_2.1.4
##  [7] patchwork_1.0.0            scater_1.14.6
##  [9] ggplot2_3.3.0              SingleCellExperiment_1.8.0
## [11] SummarizedExperiment_1.16.1 DelayedArray_0.12.3
## [13] BiocParallel_1.20.1        matrixStats_0.56.0
## [15] Biobase_2.46.0             GenomicRanges_1.38.0
## [17] GenomeInfoDb_1.22.1       IRanges_2.20.2
## [19] S4Vectors_0.24.4           BiocGenerics_0.32.0
## [21] data.table_1.12.8          magrittr_1.5
##
## loaded via a namespace (and not attached):
##  [1] rappdirs_0.3.1              ggthemes_4.2.0          tidyverse_1.0.2
##  [4] bit64_0.9-7                knitr_1.28              irlba_2.3.3
##  [7] RCurl_1.98-1.1             cowplot_1.0.0           RSQLite_2.2.0
##  [10] RANN_2.6.1                 europePMC_0.3           proxy_0.4-24
## [13] future_1.16.0              bit_1.1-15.2            enrichplot_1.6.1
## [16] webshot_0.5.2              xml2_1.3.1              assertthat_0.2.1
## [19] viridis_0.5.1              xfun_0.13               hms_0.5.3
## [22] evaluate_0.14              DEoptimR_1.0-8           fansi_0.4.1
## [25] progress_1.2.2             caTools_1.18.0           readxl_1.3.1
## [28] htmlwidgets_1.5.1           igraph_1.2.5            DBI_1.1.0
## [31] purrrr_0.3.3               ellipsis_0.3.0          RSpectra_0.16-0
## [34] dplyr_0.8.5                backports_1.1.6          vctrs_0.2.4
## [37] TTR_0.23-6                ROCR_1.0-7              abind_1.4-5
## [40] RcppEigen_0.3.3.7.0        withr_2.1.2              ggforce_0.3.1
## [43] triebeard_0.3.0            robustbase_0.93-6        checkmate_2.0.0
## [46] vcd_1.4-7                 sctransform_0.2.1        scran_1.14.6
## [49] xts_0.12-0                prettyunits_1.1.1        cluster_2.1.0
## [52] DOSE_3.12.0               lazyeval_0.2.2           ape_5.3
## [55] laeken_0.5.1              crayon_1.3.4             labeling_0.3
## [58] edgeR_3.28.1              pkgconfig_2.0.3          tweenr_1.0.1
## [61] nlme_3.1-147              viper_0.4.5              drat_0.1.5
## [64] nnet_7.3-13                rlang_0.4.5              globals_0.12.5
## [67] lifecycle_0.2.0             rsvd_1.0.3               cellranger_1.1.0
## [70] polyclip_1.10-0            RcppHNSW_0.2.0           lmtest_0.9-37
## [73] graph_1.64.0               Matrix_1.2-18            urltools_1.7.3
## [76] carData_3.0-4              boot_1.3-24              zoo_1.8-7
## [79] beeswarm_0.2.3             ggridges_0.5.2           pheatmap_1.0.12
## [82] png_0.1-7                  viridisLite_0.3.0        bitops_1.0-6

```

```

## [85] KernSmooth_2.23-16          blob_1.2.1           DelayedMatrixStats_1.8.0
## [88] stringr_1.4.0               qvalue_2.18.0        readr_1.3.1
## [91] gridGraphics_0.5-0          reactome.db_1.70.0   scales_1.1.0
## [94] memoise_1.1.0              graphite_1.32.0     plyr_1.8.6
## [97] hexbin_1.28.1              ica_1.0-2            gplots_3.0.3
## [100] gdata_2.18.0              zlibbioc_1.32.0    compiler_3.6.2
## [103] lsei_1.2-0                ABCUtilities_0.3.3  dqrng_0.2.1
## [106] kableExtra_1.1.0          RColorBrewer_1.1-2  pcaMethods_1.78.0
## [109] fitdistrplus_1.0-14       cli_2.0.2            XVector_0.26.0
## [112] listenv_0.8.0             pbapply_1.4-2        ggplot.multistats_1.0.0
## [115] MASS_7.3-51.5             tidyselect_1.0.0    stringi_1.4.6
## [118]forcats_0.5.0             highr_0.8            yaml_2.2.1
## [121] GOSemSim_2.12.1          BiocSingular_1.2.2  locfit_1.5-9.4
## [124] ggrepel_0.8.2             grid_3.6.2           fastmatch_1.1-0
## [127] tools_3.6.2              future.apply_1.5.0  rio_0.5.16
## [130] rstudioapi_0.11           foreign_0.8-76      gridExtra_2.3
## [133] smoother_1.1              scatterplot3d_0.3-41 farver_2.0.3
## [136] Rtsne_0.15                ggraph_2.0.2         digest_0.6.25
## [139] rvcheck_0.1.8             BiocManager_1.30.10 Rcpp_1.0.4
## [142] car_3.0-8                RcppAnnoy_0.0.16    httr_1.4.1
## [145] AnnotationDbi_1.48.0     npsurv_0.4-0         scABC2_0.3.1
## [148] colorspace_1.4-1          reticulate_1.15    rvest_0.3.5
## [151] ranger_0.12.1             splines_3.6.2        statmod_1.4.34
## [154] uwot_0.1.8                graphlayouts_0.6.0  sp_1.4-1
## [157] ggp盗窃ify_0.0.5          plotly_4.9.2.1      jsonlite_1.6.1
## [160] tidygraph_1.1.2            R6_2.4.1             pillar_1.4.3
## [163] htmltools_0.4.0           glue_1.4.0           VIM_5.1.1
## [166] BiocNeighbors_1.4.2       class_7.3-16         codetools_0.2-16
## [169] fgsea_1.12.0              tsne_0.1-3           lattice_0.20-41
## [172] tibble_3.0.0              curl_4.3             ggbeeswarm_0.6.0
## [175] leiden_0.3.3              gtools_3.8.2          zip_2.0.4
## [178] GO.db_3.10.0              openxlsx_4.1.4       survival_3.1-12
## [181] limma_3.42.2              rmarkdown_2.1         munsell_0.5.0
## [184] e1071_1.7-3               DO.db_2.9            GenomeInfoDbData_1.2.2
## [187] haven_2.2.0                reshape2_1.4.4        gtable_0.3.0
## [190] Seurat_3.1.5

```