Re-analysis of GSE160729 adipocyte snRNAseq

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1 Purpose

To reanalyse a single cell RNAseq study on adipocyte tissue.

2 Experimental Details

Savari et al used HFD-induced obesity and then did single nuclei isolation.

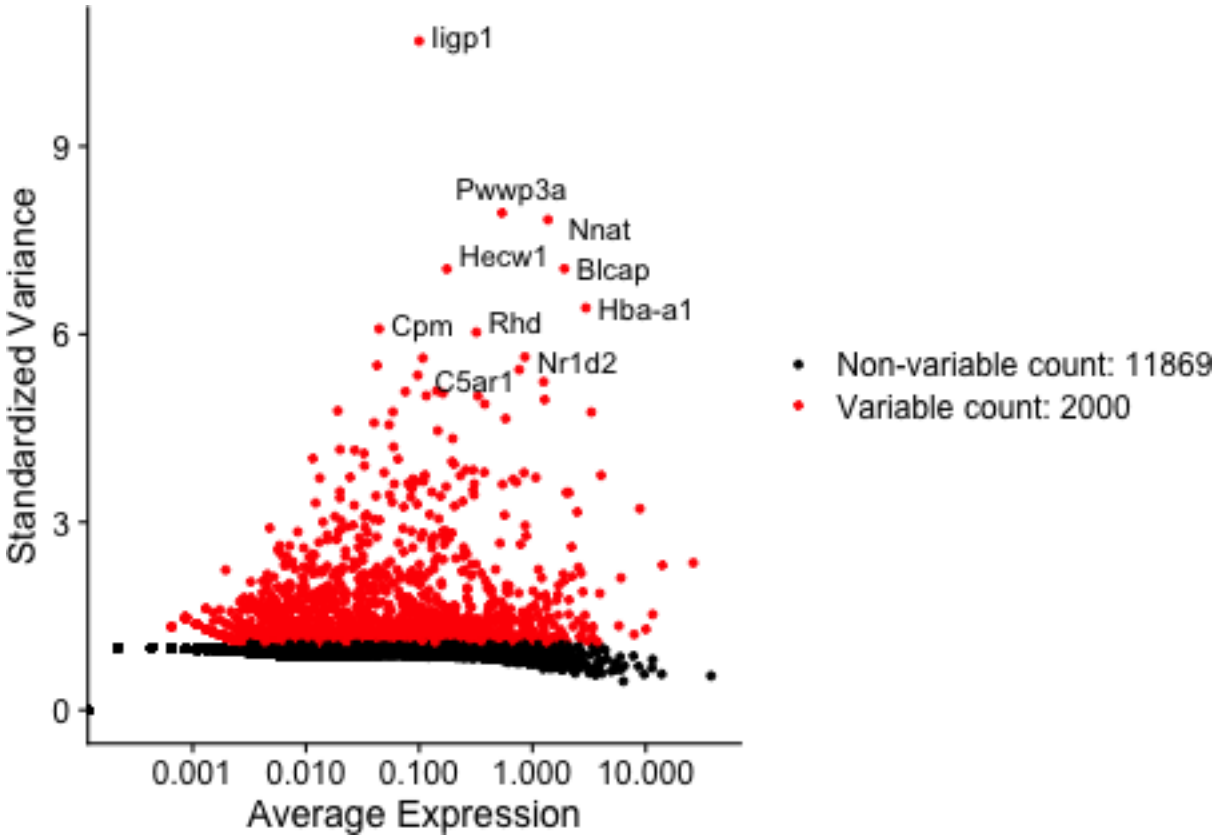
3 Raw Data

Savari et al shared code and Rds friles for annotated adipocytes at https://osf.io/tsjqc/ and https://github.com/JesperGrud/snRNAseq_eWAT

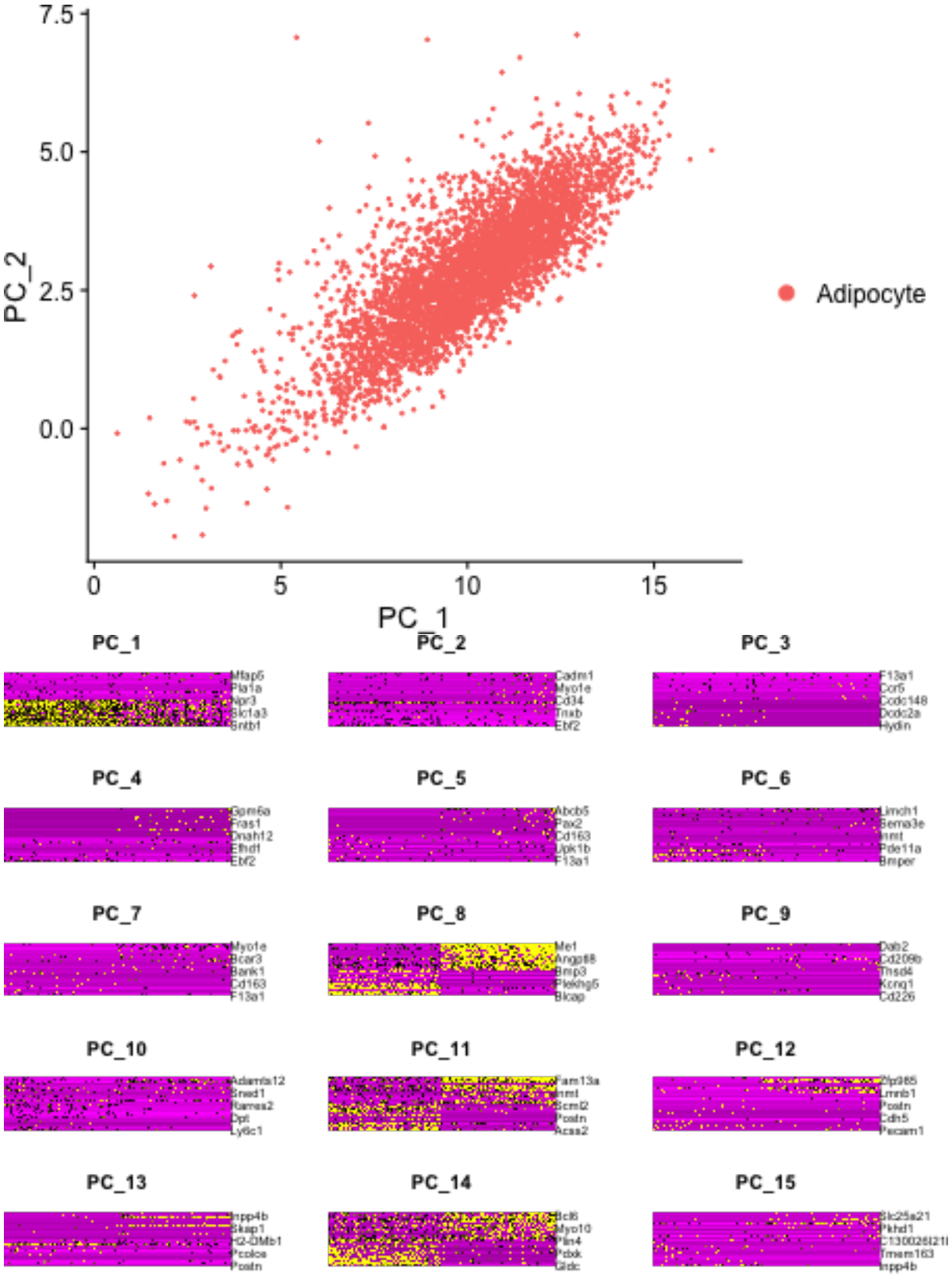
Loaded in the annotated Rds file from OSF, renamed as '`input.rds.adipocytes`

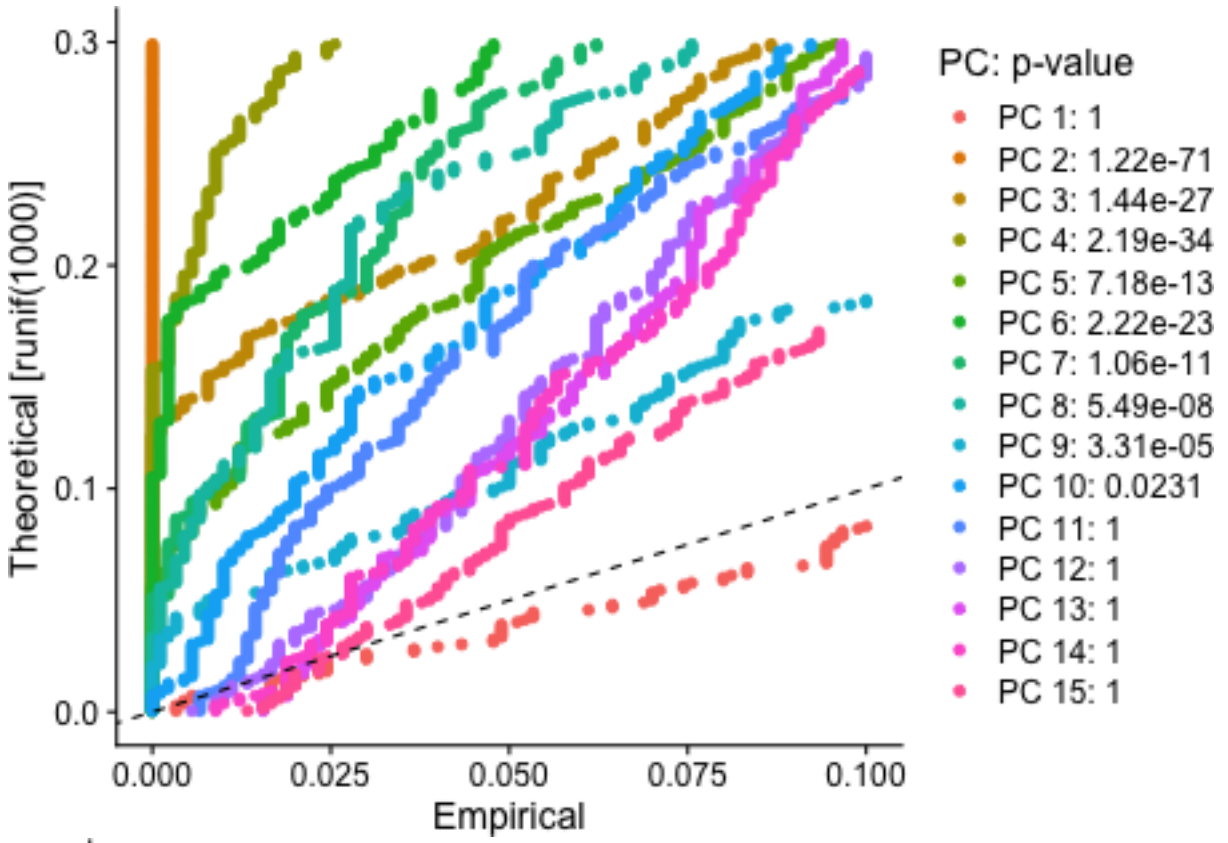
Followed the Seurat clustering protocol https://satijalab.org/seurat/articles/pbmc3k_tutorial.html

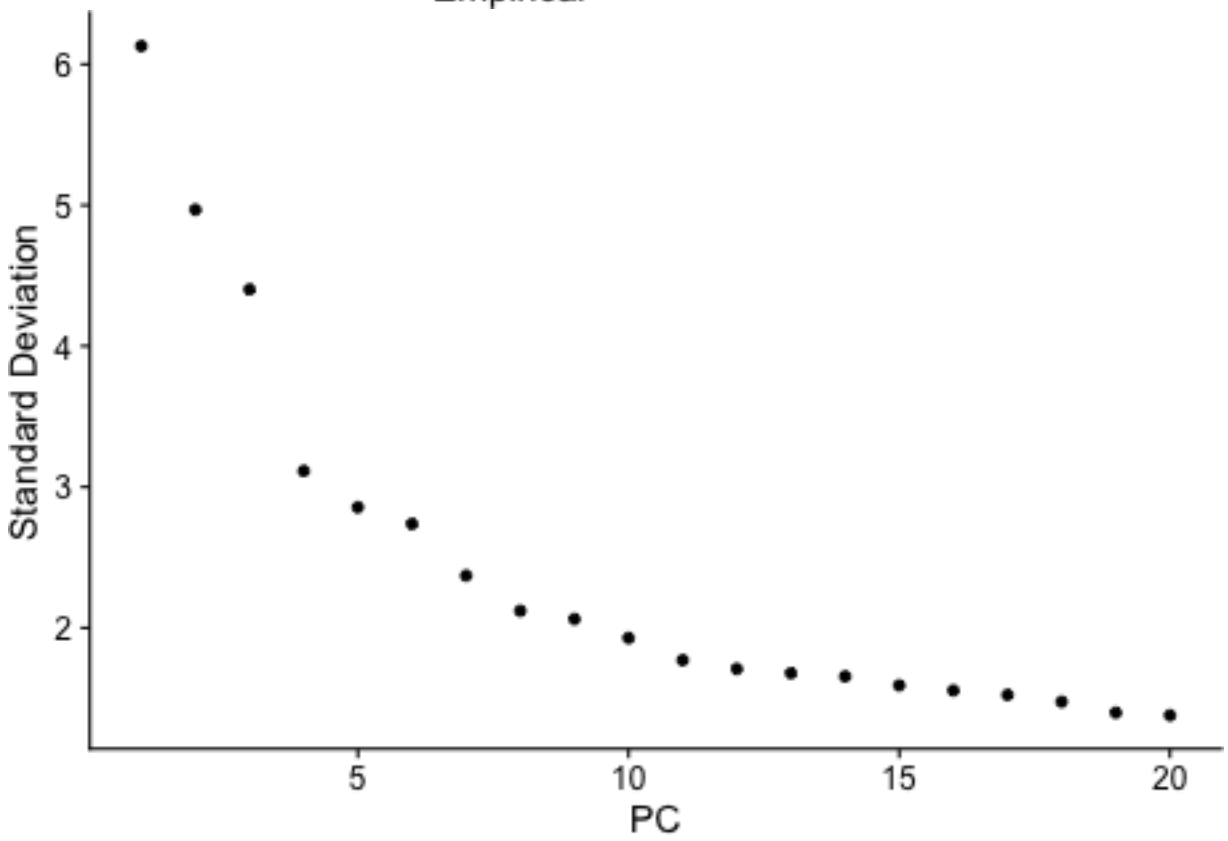
3.1 Highly Variable Features in Adipocytes



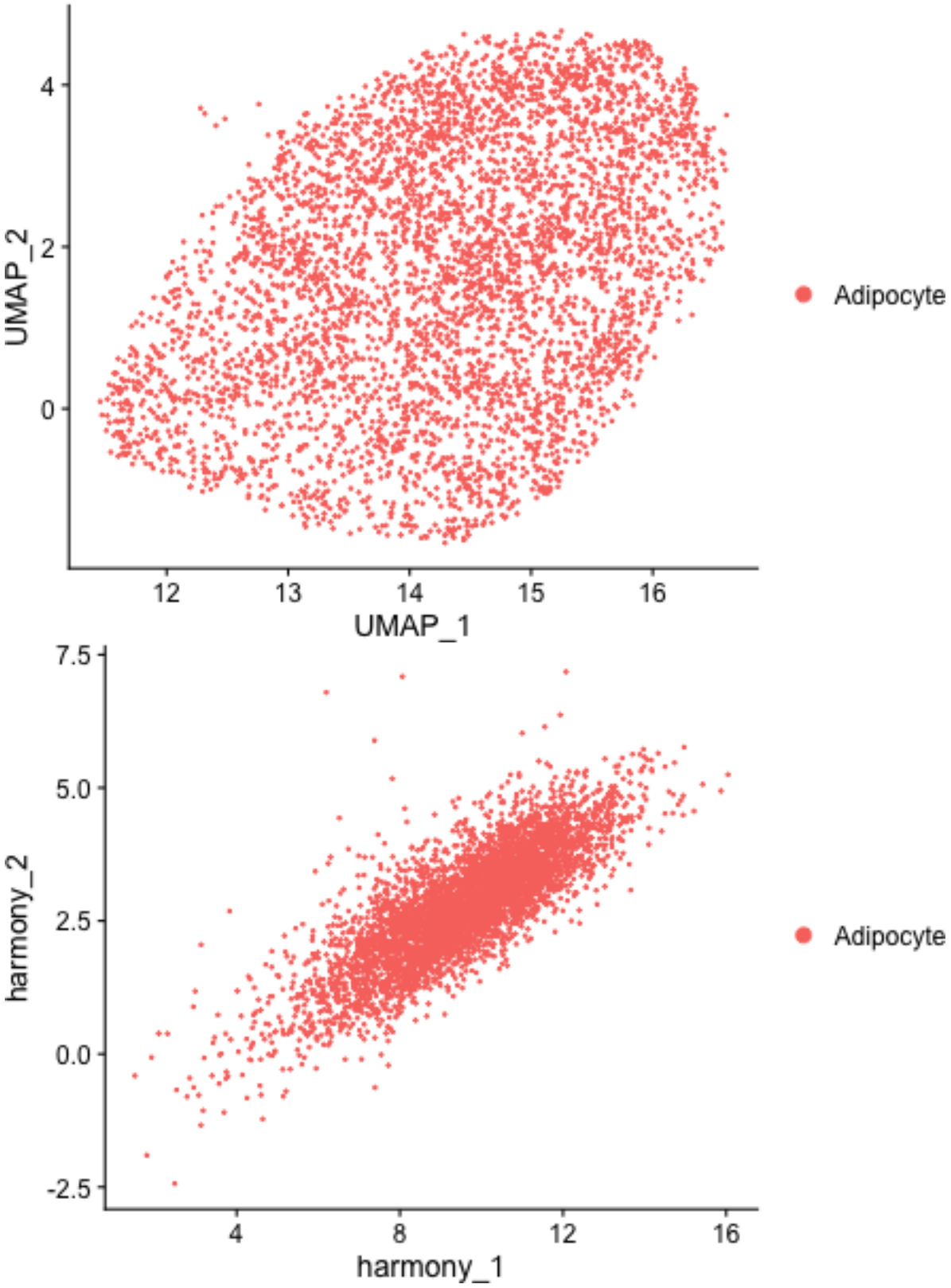
4 Scaling and Dimensional Reduction

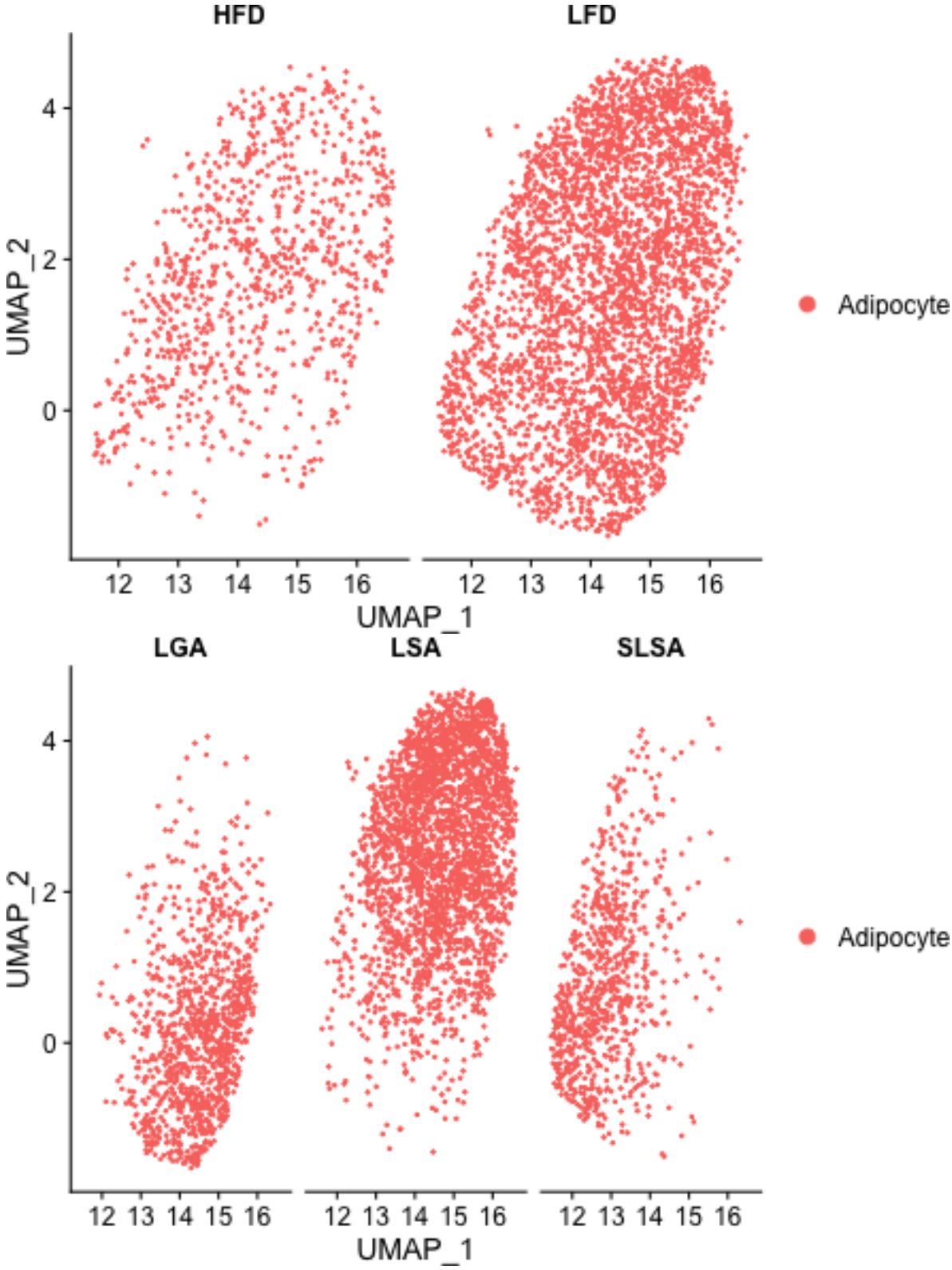



Theoretical [runif(1000)]
0.3
0.2
0.1
0.0
0.000
0.025
0.050
0.075
0.100
Empirical
PC: p-value
PC 1: 1
PC 2: 1.22e-71
PC 3: 1.44e-27
PC 4: 2.19e-34
PC 5: 7.18e-13
PC 6: 2.22e-23
PC 7: 1.06e-11
PC 8: 5.49e-08
PC 9: 3.31e-05
PC 10: 0.0231
PC 11: 1
PC 12: 1
PC 13: 1
PC 14: 1
PC 15: 1


Standard Deviation
6
5
4
3
2
5
10
15
20
PC

4.1 Cell Clustering




HFD
LFD
LGA
LSA
SLSA
UMAP_2
UMAP_1
4
2
0
12
13
14
15
16
Adipocyte

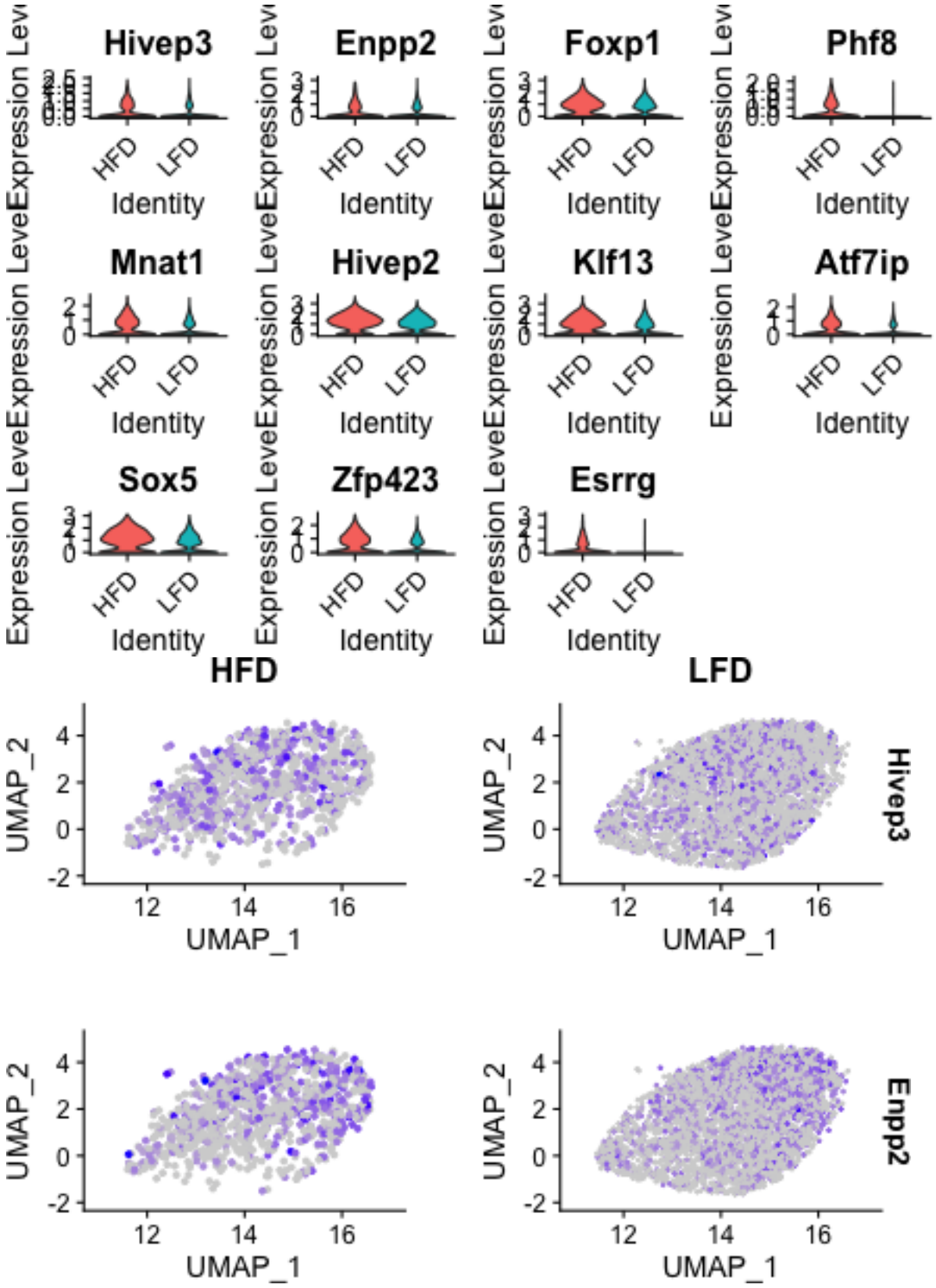
4.2 Cluster Biomarkers

5 Differential Expresion

```
##            p_val avg_log2FC pct.1 pct.2 p_val_adj
## Svs5   9.94e-189       7.32 0.576 0.010 1.38e-184
## Svs4   1.76e-189       6.05 0.576 0.006 2.44e-185
## Svs6   1.10e-189       4.45 0.576 0.005 1.52e-185
## Acaca   0.00e+00       3.75 0.964 0.517  0.00e+00
## Spinkl 3.60e-186       3.11 0.566 0.001 4.99e-182
## Thrsp  2.87e-289       2.99 0.842 0.185 3.98e-285
```

Table 1: HFD-Differentially Expressed Transcription Factors in Adipocytes

Gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj
Esrrg	0.000	-0.728	0.104	0.399	0.000
Zfp423	0.000	-0.520	0.452	0.637	0.000
Sox5	0.000	-0.511	0.625	0.768	0.000
Atf7ip	0.000	-0.481	0.294	0.509	0.000
Klf13	0.000	-0.446	0.565	0.734	0.000
Hivep2	0.000	-0.400	0.747	0.852	0.000
Mnat1	0.000	-0.381	0.408	0.570	0.000
Phf8	0.000	-0.376	0.221	0.410	0.000
Foxp1	0.000	-0.295	0.601	0.713	0.000
Enpp2	0.004	-0.262	0.364	0.405	1.000
Hivep3	0.000	-0.257	0.296	0.425	0.000
Ar	0.000	0.281	0.383	0.289	0.000
Nr3c1	0.000	0.325	0.366	0.207	0.000
Esr1	0.000	0.327	0.345	0.235	0.000
Ppargc1b	0.000	0.352	0.343	0.203	0.000
Tcf7l2	0.000	0.410	0.745	0.655	0.000
Bcl6	0.000	0.450	0.493	0.426	0.001
Nfib	0.000	0.453	0.915	0.847	0.000
Zfpm2	0.000	0.540	0.478	0.256	0.000
Sox6	0.000	0.561	0.662	0.461	0.000
Ebf2	0.000	0.738	0.524	0.239	0.000
Ank2	0.000	1.086	0.796	0.482	0.000
Pparg	0.000	1.254	0.963	0.839	0.000
Nfia	0.000	1.712	0.988	0.877	0.000
Thrsp	0.000	2.988	0.842	0.185	0.000


Hivep3
Enpp2
Foxp1
Phf8
Mnat1
Hivep2
Klf13
Atf7ip
Sox5
Zfp423
Esrrg
Expression Level
HFD
LFD
Identity
HFD
LFD
UMAP_2
UMAP_1
Hivep3
Enpp2

6 Session Information

```
sessionInfo()
```

```
## R version 4.0.2 (2020-06-22)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS  10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/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] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] ggplot2_3.3.3      rvest_1.0.0        SeuratObject_4.0.1 Seurat_4.0.2
## [5] umap_0.2.7.0       tibble_3.1.2       dplyr_1.0.6        tidyr_1.1.3
## [9] knitr_1.33
##
## loaded via a namespace (and not attached):
##   [1] Rtsne_0.15            colorspace_2.0-1      deldir_0.2-10
##   [4] ellipsis_0.3.2        ggridges_0.5.3        spatstat.data_2.1-0
##   [7] farver_2.1.0          leiden_0.3.7          listenv_0.8.0
##  [10] ggrepel_0.9.1         RSpectra_0.16-0       fansi_0.5.0
##  [13] xml2_1.3.2            codetools_0.2-18      splines_4.0.2
##  [16] polyclip_1.10-0       jsonlite_1.7.2        ica_1.0-2
##  [19] cluster_2.1.2         png_0.1-7             uwot_0.1.10
##  [22] shiny_1.6.0           sctransform_0.3.2     spatstat.sparse_2.0-0
##  [25] compiler_4.0.2        httr_1.4.2            assertthat_0.2.1
##  [28] Matrix_1.3-3          fastmap_1.1.0         lazyeval_0.2.2
##  [31] limma_3.46.0          later_1.2.0           htmltools_0.5.1.1
##  [34] tools_4.0.2           igraph_1.2.6          gtable_0.3.0
##  [37] glue_1.4.2            RANN_2.6.1            reshape2_1.4.4
##  [40] Rcpp_1.0.6            scattermore_0.7       vctrs_0.3.8
##  [43] nlme_3.1-152          lmtest_0.9-38         xfun_0.23
##  [46] stringr_1.4.0         globals_0.14.0        mime_0.10
##  [49] miniUI_0.1.1.1        lifecycle_1.0.0       irlba_2.3.3
##  [52] goftest_1.2-2         future_1.21.0         MASS_7.3-54
##  [55] zoo_1.8-9             scales_1.1.1          spatstat.core_2.1-2
##  [58] promises_1.2.0.1      spatstat.utils_2.1-0  parallel_4.0.2
##  [61] RColorBrewer_1.1-2    curl_4.3.1            yaml_2.2.1
##  [64] reticulate_1.20       pbapply_1.4-3         gridExtra_2.3
##  [67] rpart_4.1-15          stringi_1.6.2         highr_0.9
##  [70] rlang_0.4.11          pkgconfig_2.0.3       matrixStats_0.58.0
##  [73] evaluate_0.14         lattice_0.20-44       ROCR_1.0-11
##  [76] purrr_0.3.4           tensor_1.5            labeling_0.4.2
##  [79] patchwork_1.1.1       htmlwidgets_1.5.3     cowplot_1.1.1
##  [82] tidyselect_1.1.1      parallelly_1.25.0     RcppAnnoy_0.0.18
##  [85] plyr_1.8.6            magrittr_2.0.1        R6_2.5.0
```

```
##  [88] magick_2.7.2          generics_0.1.0        DBI_1.1.1
##  [91] withr_2.4.2           pillar_1.6.1          mgcv_1.8-35
##  [94] fitdistrplus_1.1-3    survival_3.2-11       abind_1.4-5
##  [97] future.apply_1.7.0    crayon_1.4.1          KernSmooth_2.23-20
## [100] utf8_1.2.1            spatstat.geom_2.1-0   plotly_4.9.3
## [103] rmarkdown_2.8         grid_4.0.2            data.table_1.14.0
## [106] digest_0.6.27         xtable_1.8-4          httpuv_1.6.1
## [109] openssl_1.4.4         munsell_0.5.0         viridisLite_0.4.0
## [112] askpass_1.1
```