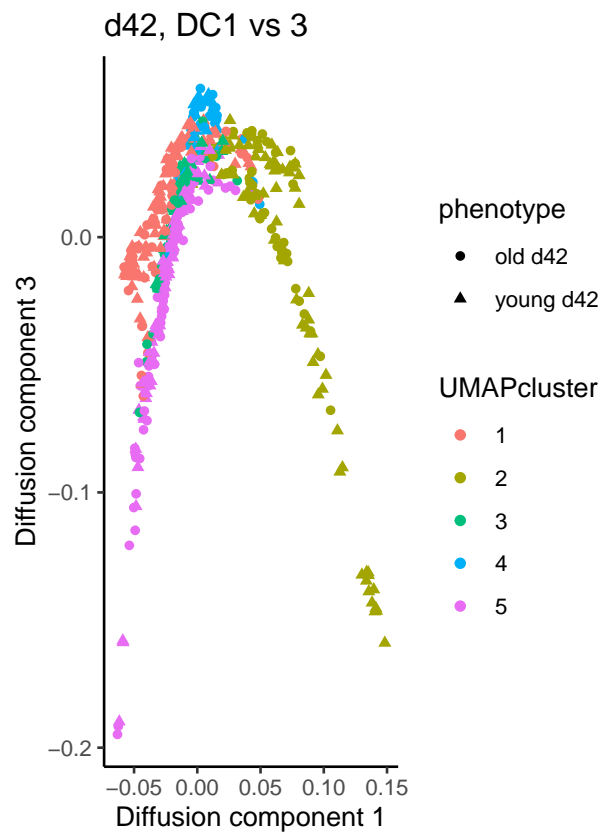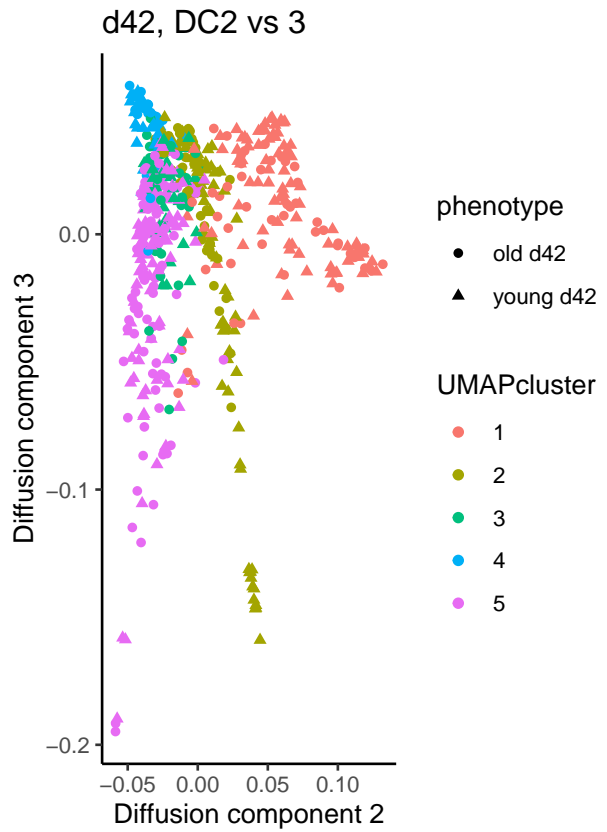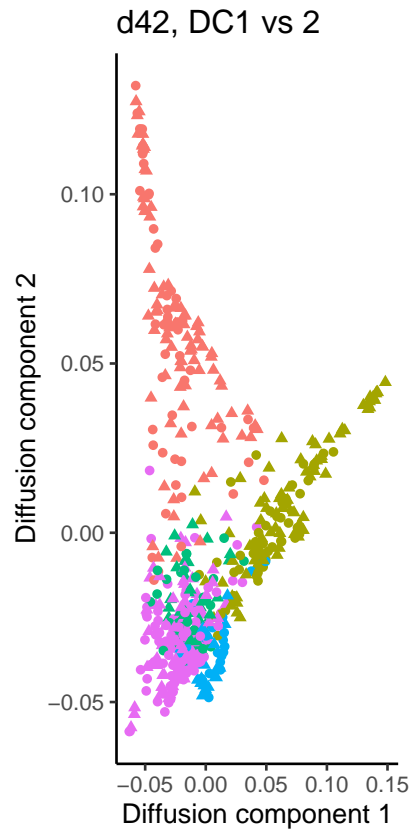Some brief plots here (see the main figure .Rmd for polished versions).

SessionInfo

```
## R version 3.6.1 (2019-07-05)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: CentOS Linux 7 (Core)
##
## Matrix products: default
## BLAS:    /bi/apps/R/3.6.1/lib64/R/lib/libRblas.so
## LAPACK: /bi/apps/R/3.6.1/lib64/R/lib/libRlapack.so
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C         LC_TIME=C
##  [4] LC_COLLATE=C         LC_MONETARY=C        LC_MESSAGES=C
##  [7] LC_PAPER=C           LC_NAME=C            LC_ADDRESS=C
## [10] LC_TELEPHONE=C       LC_MEASUREMENT=C     LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel  stats4    stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
##  [1] destiny_3.0.1               edgeR_3.28.0
##  [3] limma_3.42.0               org.Hs.eg.db_3.10.0
##  [5] ggpubr_0.2.4               magrittr_1.5
##  [7] rtracklayer_1.46.0         ensembldb_2.10.2
##  [9] AnnotationFilter_1.10.0    GenomicFeatures_1.38.0
## [11] AnnotationDbi_1.48.0       AnnotationHub_2.18.0
## [13] BiocFileCache_1.10.2       dbplyr_1.4.2
## [15] scran_1.14.5               scater_1.14.5
## [17] ggplot2_3.3.2              SingleCellExperiment_1.8.0
## [19] SummarizedExperiment_1.16.0 DelayedArray_0.12.0
## [21] BiocParallel_1.20.0        matrixStats_0.55.0
## [23] Biobase_2.46.0             GenomicRanges_1.38.0
## [25] GenomeInfoDb_1.22.0        IRanges_2.20.1
## [27] S4Vectors_0.24.1           BiocGenerics_0.32.0
## [29] dplyr_1.0.2
##
## loaded via a namespace (and not attached):
##  [1] tidyselect_1.1.0           RSQLite_2.1.4
##  [3] grid_3.6.1                 ranger_0.11.2
##  [5] munsell_0.5.0              codetools_0.2-16
##  [7] statmod_1.4.32             withr_2.1.2
##  [9] colorspace_1.4-1           knitr_1.26
## [11] robustbase_0.93-5          ggsignif_0.6.0
## [13] vcd_1.4-4                  VIM_4.8.0
## [15] TTR_0.23-6                 labeling_0.3
## [17] GenomeInfoDbData_1.2.2     bit64_0.9-7
## [19] farver_2.0.1               vctrs_0.3.6
## [21] generics_0.0.2             xfun_0.11
## [23] ggthemes_4.2.0             R6_2.4.1
## [25] ggbeeswarm_0.6.0           rsvd_1.0.2
## [27] RcppEigen_0.3.3.7.0        locfit_1.5-9.1
## [29] bitops_1.0-6               assertthat_0.2.1
## [31] promises_1.1.0             scales_1.1.0
```

```
##  [33] nnet_7.3-12                    beeswarm_0.2.3
##  [35] gtable_0.3.0                    rlang_0.4.10
##  [37] scatterplot3d_0.3-41           splines_3.6.1
##  [39] lazyeval_0.2.2                 hexbin_1.28.0
##  [41] BiocManager_1.30.10            yaml_2.2.0
##  [43] reshape2_1.4.3                 abind_1.4-5
##  [45] httpuv_1.5.2                   tools_3.6.1
##  [47] ellipsis_0.3.0                 proxy_0.4-23
##  [49] Rcpp_1.0.3                     plyr_1.8.5
##  [51] progress_1.2.2                 zlibbioc_1.32.0
##  [53] purrr_0.3.3                    RCurl_1.95-4.12
##  [55] prettyunits_1.0.2              openssl_1.4.1
##  [57] viridis_0.5.1                  cowplot_1.0.0
##  [59] zoo_1.8-8                      haven_2.2.0
##  [61] tinytex_0.18                   data.table_1.12.8
##  [63] RSpectra_0.16-0                openxlsx_4.1.4
##  [65] lmtest_0.9-37                  pcaMethods_1.78.0
##  [67] ProtGenerics_1.18.0            hms_0.5.2
##  [69] mime_0.7                       evaluate_0.14
##  [71] xtable_1.8-4                   smoother_1.1
##  [73] XML_3.98-1.20                  rio_0.5.16
##  [75] readxl_1.3.1                   gridExtra_2.3
##  [77] compiler_3.6.1                 biomaRt_2.42.0
##  [79] tibble_3.0.4                   crayon_1.3.4
##  [81] htmltools_0.4.0                later_1.0.0
##  [83] tidyr_1.0.0                    RcppParallel_4.4.4
##  [85] DBI_1.1.0                      formatR_1.7
##  [87] MASS_7.3-51.4                  rappdirs_0.3.1
##  [89] boot_1.3-23                    Matrix_1.2-17
##  [91] car_3.0-5                      igraph_1.2.4.2
##  [93] forcats_0.4.0                  pkgconfig_2.0.3
##  [95] GenomicAlignments_1.22.1       foreign_0.8-72
##  [97] laeken_0.5.0                   sp_1.3-2
##  [99] vipor_0.4.5                    dqrng_0.2.1
## [101] XVector_0.26.0                 stringr_1.4.0
## [103] digest_0.6.23                  Biostrings_2.54.0
## [105] rmarkdown_2.0                  cellranger_1.1.0
## [107] uwot_0.1.5                     DelayedMatrixStats_1.8.0
## [109] curl_4.3                       shiny_1.4.0
## [111] Rsamtools_2.2.1                ggplot.multistats_1.0.0
## [113] lifecycle_0.2.0                carData_3.0-3
## [115] BiocNeighbors_1.4.1            viridisLite_0.3.0
## [117] askpass_1.1                    BSgenome_1.54.0
## [119] pillar_1.4.7                   lattice_0.20-38
## [121] fastmap_1.0.1                  httr_1.4.1
## [123] DEoptimR_1.0-8                 interactiveDisplayBase_1.24.0
## [125] glue_1.4.2                     xts_0.12-0
## [127] zip_2.0.4                      BiocVersion_3.10.1
## [129] bit_1.1-14                     class_7.3-15
## [131] stringi_1.4.3                  blob_1.2.0
## [133] RcppHNSW_0.2.0                 BiocSingular_1.2.0
## [135] memoise_1.1.0                  irlba_2.3.3
## [137] knn.covertree_1.0              e1071_1.7-3
```