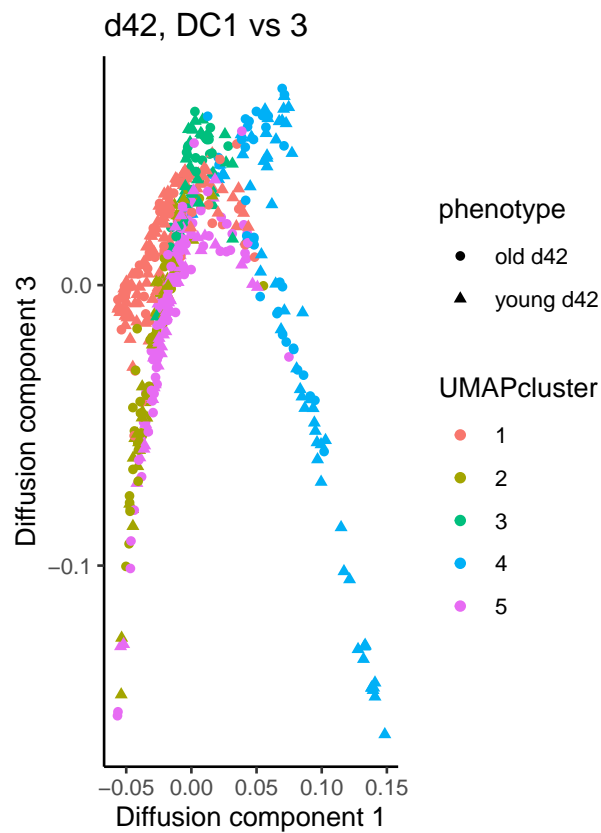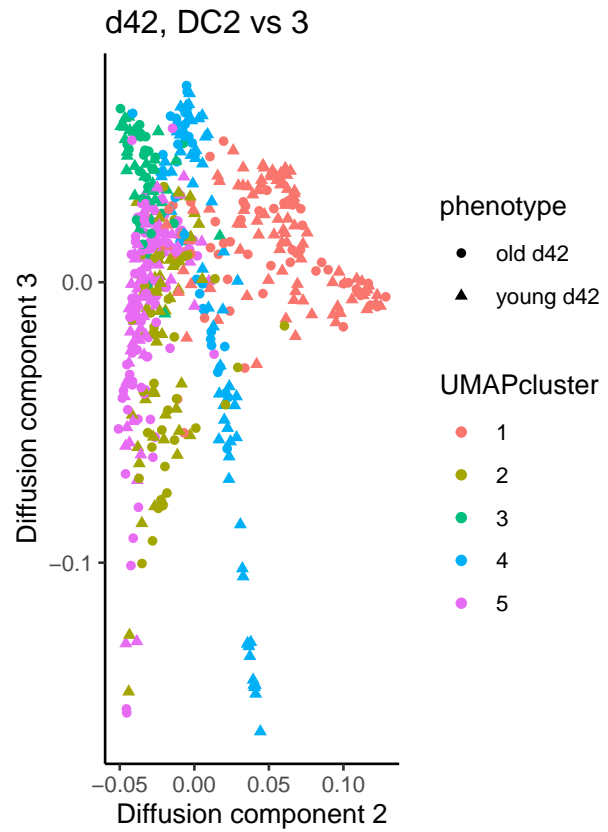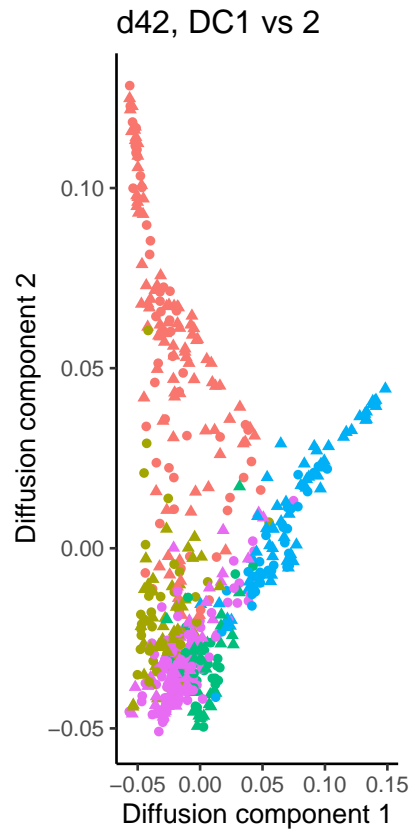Some brief plots here (see the main figure .Rmd for polished versions).

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_GB.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_GB.UTF-8        LC_COLLATE=en_GB.UTF-8
##  [5] LC_MONETARY=en_GB.UTF-8    LC_MESSAGES=en_GB.UTF-8
##  [7] LC_PAPER=en_GB.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_GB.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] grid      parallel  stats4    stats     graphics  grDevices utils
## [8] datasets  methods   base
##
## other attached packages:
##  [1] Seurat_3.2.2             gtable_0.3.0
##  [3] forcats_0.4.0            stringr_1.4.0
##  [5] purrr_0.3.3              readr_1.3.1
##  [7] tidyr_1.0.0              tibble_3.0.4
##  [9] tidyverse_1.3.0          SingleR_1.0.6
## [11] rstatix_0.6.0            ggcyto_1.18.0
## [13] flowWorkspace_3.34.1     ncdfFlow_2.32.0
## [15] BH_1.72.0-2              RcppArmadillo_0.10.1.2.0
## [17] flowCore_1.52.1          cowplot_1.0.0
## [19] pals_1.6                 MultiAssayExperiment_1.12.1
## [21] destiny_3.0.1            edgeR_3.28.0
## [23] limma_3.42.0             org.Hs.eg.db_3.10.0
## [25] AnnotationDbi_1.48.0     dplyr_1.0.2
## [27] ggpubr_0.2.4             magrittr_1.5
## [29] scater_1.14.5            ggplot2_3.3.2
## [31] scran_1.14.5             SingleCellExperiment_1.8.0
## [33] SummarizedExperiment_1.16.0 DelayedArray_0.12.0
## [35] BiocParallel_1.20.0      matrixStats_0.55.0
## [37] Biobase_2.46.0           GenomicRanges_1.38.0
## [39] GenomeInfoDb_1.22.0      IRanges_2.20.1
## [41] S4Vectors_0.24.1         BiocGenerics_0.32.0
##
## loaded via a namespace (and not attached):
##   [1] rappdirs_0.3.1           ggthemes_4.2.0
##   [3] bit64_0.9-7              knitr_1.26
##   [5] irlba_2.3.3              rpart_4.1-15
##   [7] data.table_1.12.8        RCurl_1.95-4.12
##   [9] generics_0.0.2           RSQLite_2.1.4
##  [11] RANN_2.6.1               proxy_0.4-23
##  [13] future_1.20.1            bit_1.1-14
##  [15] spatstat.data_1.4-3      xml2_1.2.2
```

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##  [17] lubridate_1.7.4             httpuv_1.5.2
##  [19] assertthat_0.2.1            viridis_0.5.1
##  [21] xfun_0.11                   hms_0.5.2
##  [23] evaluate_0.14               promises_1.1.0
##  [25] DEoptimR_1.0-8              fansi_0.4.0
##  [27] caTools_1.17.1.3            dbplyr_1.4.2
##  [29] readxl_1.3.1                htmlwidgets_1.5.1
##  [31] Rgraphviz_2.30.0            igraph_1.2.4.2
##  [33] DBI_1.1.0                   ellipsis_0.3.0
##  [35] RSpectra_0.16-0             backports_1.1.5
##  [37] markdown_1.1                deldir_0.1-23
##  [39] RcppParallel_4.4.4          vctrs_0.3.6
##  [41] TTR_0.23-6                  ROCR_1.0-7
##  [43] abind_1.4-5                 RcppEigen_0.3.3.7.0
##  [45] withr_2.1.2                 robustbase_0.93-5
##  [47] vcd_1.4-4                   sctransform_0.3.2.9000
##  [49] xts_0.12-0                  goftest_1.2-2
##  [51] cluster_2.1.0               ExperimentHub_1.12.0
##  [53] lazyeval_0.2.2              laeken_0.5.0
##  [55] crayon_1.3.4                pkgconfig_2.0.3
##  [57] labeling_0.3                nlme_3.1-141
##  [59] vipor_0.4.5                 nnet_7.3-12
##  [61] globals_0.13.1              rlang_0.4.10
##  [63] miniUI_0.1.1.1              lifecycle_0.2.0
##  [65] BiocFileCache_1.10.2        modelr_0.1.5
##  [67] rsvd_1.0.2                  AnnotationHub_2.18.0
##  [69] dichromat_2.0-0             polyclip_1.10-0
##  [71] cellranger_1.1.0            RcppHNSW_0.2.0
##  [73] lmtest_0.9-37               graph_1.64.0
##  [75] Matrix_1.2-17               carData_3.0-3
##  [77] boot_1.3-23                 zoo_1.8-8
##  [79] reprex_0.3.0                beeswarm_0.2.3
##  [81] ggridges_0.5.2              pheatmap_1.0.12
##  [83] png_0.1-7                   viridisLite_0.3.0
##  [85] knn.covertree_1.0           bitops_1.0-6
##  [87] KernSmooth_2.23-15          blob_1.2.0
##  [89] DelayedMatrixStats_1.8.0    parallelly_1.21.0
##  [91] ggsignif_0.6.0              scales_1.1.0
##  [93] ica_1.0-2                   memoise_1.1.0
##  [95] plyr_1.8.5                  hexbin_1.28.0
##  [97] gplots_3.0.1.1              gdata_2.18.0
##  [99] zlibbioc_1.32.0             compiler_3.6.1
## [101] dqrng_0.2.1                 tinytex_0.18
## [103] RColorBrewer_1.1-2          pcaMethods_1.78.0
## [105] rrcov_1.4-9                 fitdistrplus_1.1-1
## [107] cli_2.0.0                   XVector_0.26.0
## [109] listenv_0.8.0               pbapply_1.4-2
## [111] patchwork_1.0.0             formatR_1.7
## [113] mgcv_1.8-28                 ggplot.multistats_1.0.0
## [115] MASS_7.3-51.4               tidyselect_1.1.0
## [117] stringi_1.4.3               yaml_2.2.0
## [119] BiocSingular_1.2.0          locfit_1.5-9.1
## [121] ggrepel_0.8.1               latticeExtra_0.6-28
## [123] tools_3.6.1                 future.apply_1.6.0
```

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## [125] rio_0.5.16                       rstudioapi_0.10
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## [131] farver_2.0.1                     Rtsne_0.15
## [133] digest_0.6.23                    BiocManager_1.30.10
## [135] ggtext_0.1.1                     shiny_1.4.0
## [137] gridtext_0.1.4                   Rcpp_1.0.3
## [139] car_3.0-5                        broom_0.7.3
## [141] BiocVersion_3.10.1               later_1.0.0
## [143] RcppAnnoy_0.0.14                 httr_1.4.1
## [145] IDPmisc_1.1.20                   colorspace_1.4-1
## [147] tensor_1.5                       reticulate_1.14
## [149] rvest_0.3.5                      fs_1.3.1
## [151] ranger_0.11.2                    splines_3.6.1
## [153] uwot_0.1.5                       statmod_1.4.32
## [155] spatstat.utils_1.17-0            sp_1.3-2
## [157] mapproj_1.2.7                    plotly_4.9.1
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## [163] pillar_1.4.7                     htmltools_0.4.0
## [165] mime_0.7                         glue_1.4.2
## [167] fastmap_1.0.1                    VIM_4.8.0
## [169] BiocNeighbors_1.4.1              class_7.3-15
## [171] interactiveDisplayBase_1.24.0 codetools_0.2-16
## [173] maps_3.3.0                       pcaPP_1.9-73
## [175] mvtnorm_1.0-11                   lattice_0.20-38
## [177] flowViz_1.48.0                   curl_4.3
## [179] ggbeeswarm_0.6.0                 leiden_0.3.4
## [181] gtools_3.8.1                     zip_2.0.4
## [183] openxlsx_4.1.4                   survival_2.44-1.1
## [185] rmarkdown_2.0                    munsell_0.5.0
## [187] e1071_1.7-3                      GenomeInfoDbData_1.2.2
## [189] haven_2.2.0                      reshape2_1.4.3
```