JDRF Sensitivity / Benchmark

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Benchmarking on pre-processing parameters:
1. Univariate cuttof at each assay (top_n)
2. clustering minimum correlation (h)

A. Setup

1. Load raw data sets and scale

```
data_task # mlr's task format. currently non-functional, so require sep
```

```
## Supervised task: mlr.Data
## Type: regr
## Target: cpep_model_decayrate
## Observations: 31
## Features:
##    numerics     factors     ordered functionals
##       76746           0           0           0
## Missings: TRUE
## Has weights: FALSE
## Has blocking: FALSE
## Has coordinates: FALSE
```

```
# pre-processing: Scaling
task_j<-data_task %>>% cpoScale()
```

2. mlr's learner setup

```
lrn.glmnet.1.orig<-makeLearner(cl= "regr.cvglmnet", par.vals = list(alpha=1, s='lambda.min') ) # s will

lrn_PreProcess_glmnet<-Fun_lrn_univ_Clusters_All_makePrep_MaG(lrn.glmnet.1.orig,
                                                              train_F   = F_PreProc_3_UnivClust_Train_Ma
                                                              Predict_F = F_PreProc13_BOTH_Predict_MaG,
                                                              param.Univ.filt.top.n.features = NA,
                                                              param.UnivClustRankTopN        = NA,
                                                              param.cluster_method_KH        = NA,
                                                              param.corrplot.n.clusters.k    = NA,
                                                              param.corrplot.n.clusters.h    = NA,
                                                              parame.gene.or.module          = NA,
                                                              param.LASSO.n.features.arbitrary=NA)
Assay.Analyte.sep<-'.ZZZ.'
is.numeric(param.impute.knn.k<-20)
```

```
## [1] TRUE
```

```
param.assay.type.vec<-c('Short', 'Long', 'Short', 'Short', rep('Long', 11))
lrn_PreProcess_glmnet$par.vals[['param.assay.type.vec']]<-param.assay.type.vec
lrn_PreProcess_glmnet$next.learner$properties %<>% c(., 'missings') # ok to add only because
lrn_PreProcess_glmnet
```

```
## Learner regr.cvglmnet.preproc from package glmnet
## Type: regr
## Name: ; Short name:
## Class: PreprocWrapper
## Properties: numerics,factors,missings,weights
## Predict-Type: response
## Hyperparameters: alpha=1,s=lambda.min
```

3. Benchmarking / sensitivity parameter setup

```
## 'gold standard'
param.corrplot.n.clusters.h<-0.3
param.Univ.filt.top.n.features<-30
```

3.1 pre-processing filtering h, top_n {fixed s=cv.glmnet 'lambda.min'}

```
param.LASSO.n.features.arbitrary<-6


## Primary(Univ + cluster_rank=1)
## Secondary(univariate only, without clustering).

h_seq<-c(seq.int(0, 20, by=1)/20)[-c(17:21)]; top_h_sqe<-seq.int(10,   60,  by = 5)
# h_seq<-c(0.1, 0.2, 0.25, 0.3, 0.35, 0.4, 0.5, 0.75); top_h_sqe<-c(5, 10, 20, 30, 40, 50)
# cs <- seq(0,0.75, 0.05); Ns <- seq(5, 60, 5)
# 1-h_seq


bmr_tib<-expand.grid(
  hclust_cutree_h = h_seq,
  Univ_top_n      = top_h_sqe) %>% as_tibble
# bmr_tib %<>% add_row(hclust_cutree_h = 0.3, Univ_top_n = 30, .before = 1)


## 0. setup
bmr_tib  %<>%
  mutate(args_vec_i = map2(Univ_top_n, hclust_cutree_h, ~list(.x, 1, 'method.h', 0,  .y, 'gene', param.
  mutate(lrd_ID_i = paste0('lrn_', 1:n())) %>%
  mutate(lrn_i = map2(args_vec_i, lrd_ID_i, ~Func_update_args_univ_clusters(lrn = lrn_PreProcess_glmnet
```

B. Run:

B.1: naive, manual loop (via appply-like / map), broken to pre-processed/baked -> s.control (cv.glmnet min) -> ML

```
##############################################################################
# bmr_tib_naive<-bmr_tib %>% mutate(whole_run = lrn_i %>% imap(~whole_run_function(task = task_j, lrn =
# save(bmr_tib_naive, file = 'data/bmr_tib_naive.rdata')
##############################################################################
# load(file = 'Z:/R_rhino/JDRFCAV/data/bmr_tib_naive.rdata') #
bmr_tib_naive
```

```
## # A tibble: 176 x 6
##    hclust_cutree_h Univ_top_n args_vec_i lrd_ID_i lrn_i           whole_run
##              <dbl>      <dbl> <list>     <chr>    <list>          <list>
##  1            0           10 <list [7]> lrn_1    <S3: PreprocWr~ <list [7~
##  2            0.05        10 <list [7]> lrn_2    <S3: PreprocWr~ <list [7~
##  3            0.1         10 <list [7]> lrn_3    <S3: PreprocWr~ <list [7~
##  4            0.15        10 <list [7]> lrn_4    <S3: PreprocWr~ <list [7~
##  5            0.2         10 <list [7]> lrn_5    <S3: PreprocWr~ <list [7~
##  6            0.25        10 <list [7]> lrn_6    <S3: PreprocWr~ <list [7~
##  7            0.3         10 <list [7]> lrn_7    <S3: PreprocWr~ <list [7~
##  8            0.35        10 <list [7]> lrn_8    <S3: PreprocWr~ <list [7~
##  9            0.4         10 <list [7]> lrn_9    <S3: PreprocWr~ <list [7~
## 10            0.45        10 <list [7]> lrn_10   <S3: PreprocWr~ <list [7~
## # ... with 166 more rows
```

C. Extract summary results: (single tib, pre-calculater fit + lambda_opt_list)

```
TargetName<-task_j %>% getTaskTargetNames

bmr_tib_naive_res<-bmr_tib_naive %>%
  mutate(fit_baked = whole_run %>% map('fit_baked')) %>%
  mutate(s =         whole_run %>% map('alt_lambda_list')) %>%
  mutate(Baked_x =   whole_run %>% map('Baked_x')) %>%
  mutate(Baked_y =   whole_run %>% map('Baked_y')) %>%
  mutate(UnivOnlyCoef = whole_run %>% map('UnivOnlyCoef')) %>%
  mutate(s_lambda.min = s %>% map_dbl('lambda.min')) %>%

  mutate(coef_s_min   = map2(fit_baked, s_lambda.min, ~coef(.x, s = .y) %>% tidy)) %>%
  mutate(predict_s_min = pmap(list(fit_baked, Baked_x, s_lambda.min), function(x,y,z)
      # x= bmr_tib_naive_res$fit_baked[[1]]; y=bmr_tib_naive_res$Baked_x; z=bmr_tib_naive_res$s_lambda.
     predict(object = x, newx = y, s = z) %>% data.frame %>% pull(X1) )) %>%
  mutate(rmse_s_min    = map2_dbl(predict_s_min, Baked_y, ~sqrt(mean((.x - .y) ^ 2)))) %>%
  mutate(n_coef_s_min  = coef_s_min %>% map_int(~nrow(.x)))


# bmr_tib_naive_res %>% filter(hclust_cutree_h == 0.3, Univ_top_n == 30) %>% t
```

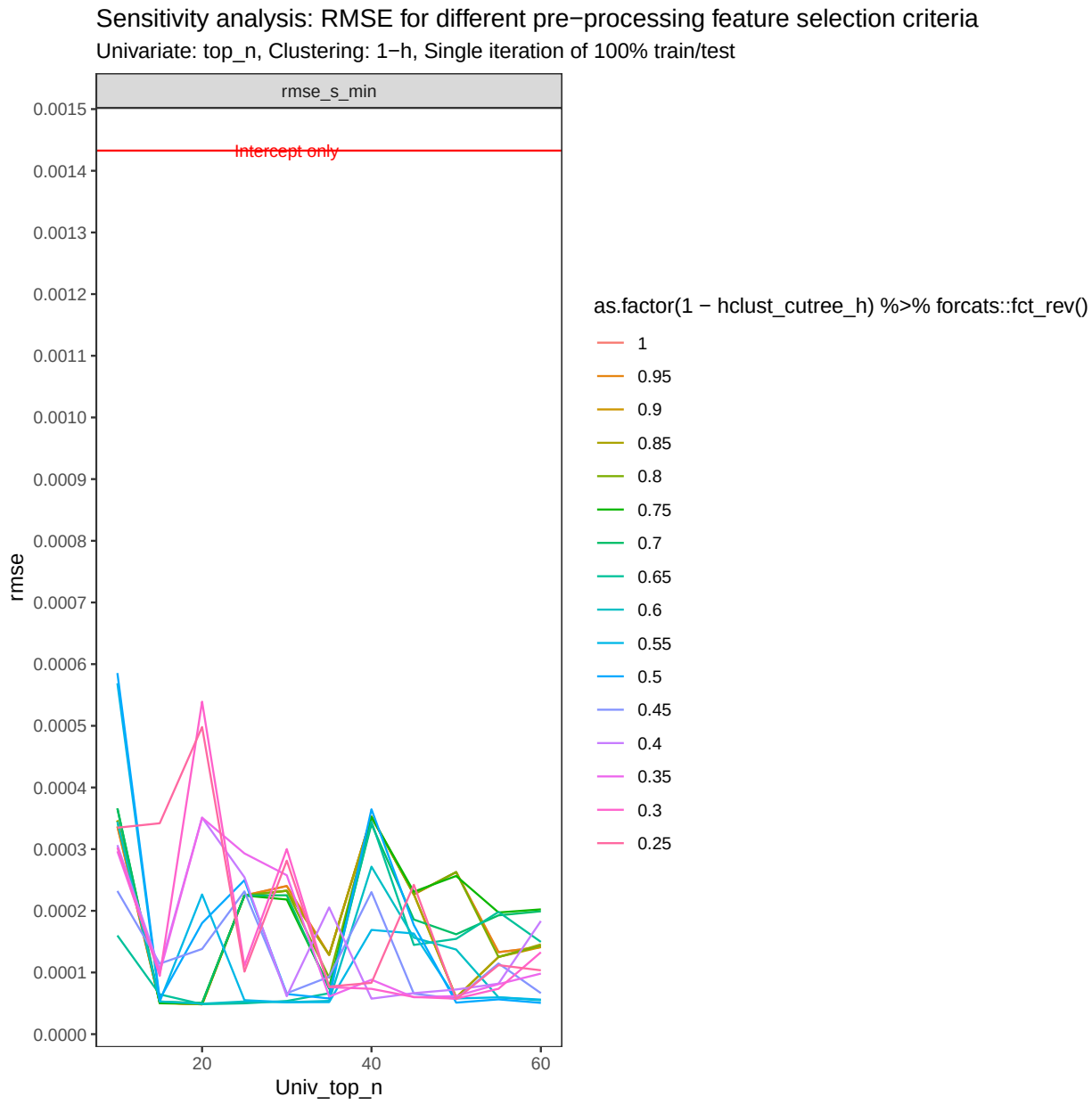
```
# bmr_tib_naive_res$n_coef_s_min
# bmr_tib_naive_res$n_coef_s_1se
# bmr_tib_naive_res$n_coef_s_pushed
```

plot #1: Benchmarking RMSE lines, by {h, top_n}

```
DF_rmse<-bmr_tib_naive_res %>%
  select(hclust_cutree_h, Univ_top_n, rmse_s_min) %>%
# select(hclust_cutree_h, Univ_top_n, rmse_s_min, rmse_s_1se, rmse_s_pushed) %>% gather('s_opt','rmse',
  gather('s_opt','rmse', 3)


## featureless / intercept only
y<-task_j %>% getTaskTargets
y_mean<-y %>% mean
rmse_null<-sqrt(mean((y - y_mean) ^ 2))

DF_rmse %>% filter(hclust_cutree_h == param.corrplot.n.clusters.h, Univ_top_n == param.Univ.filt.top.n.
```

```
## # A tibble: 1 x 4
##   hclust_cutree_h Univ_top_n s_opt          rmse
##             <dbl>      <dbl> <chr>         <dbl>
## 1             0.3         30 rmse_s_min 0.000225
```

```
  # filter(s_opt %in% c('rmse_s_1se','rmse_s_pushed')) %>%
  # filter(hclust_cutree_h %in% c(0.75)) %>%




DF_rmse %>%
  # filter(hclust_cutree_h == param.corrplot.n.clusters.h) %>%
  ggplot() +
  geom_line(aes(x = Univ_top_n, y = rmse, color = as.factor(1-hclust_cutree_h) %>% forcats::fct_rev() ))
facet_grid(.~s_opt) +
    annotate("text", label = "Intercept only", x = 30, y = rmse_null, size = 3, colour = "red")+
scale_y_continuous(breaks = pretty(c(rmse_null, DF_rmse$rmse), n = 10)) +
  theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank()) +
  labs(title = 'Sensitivity analysis: RMSE for different pre-processing feature selection criteria',
       subtitle = 'Univariate: top_n, Clustering: 1-h, Single iteration of 100% train/test')
```



plot #2: s_lambda

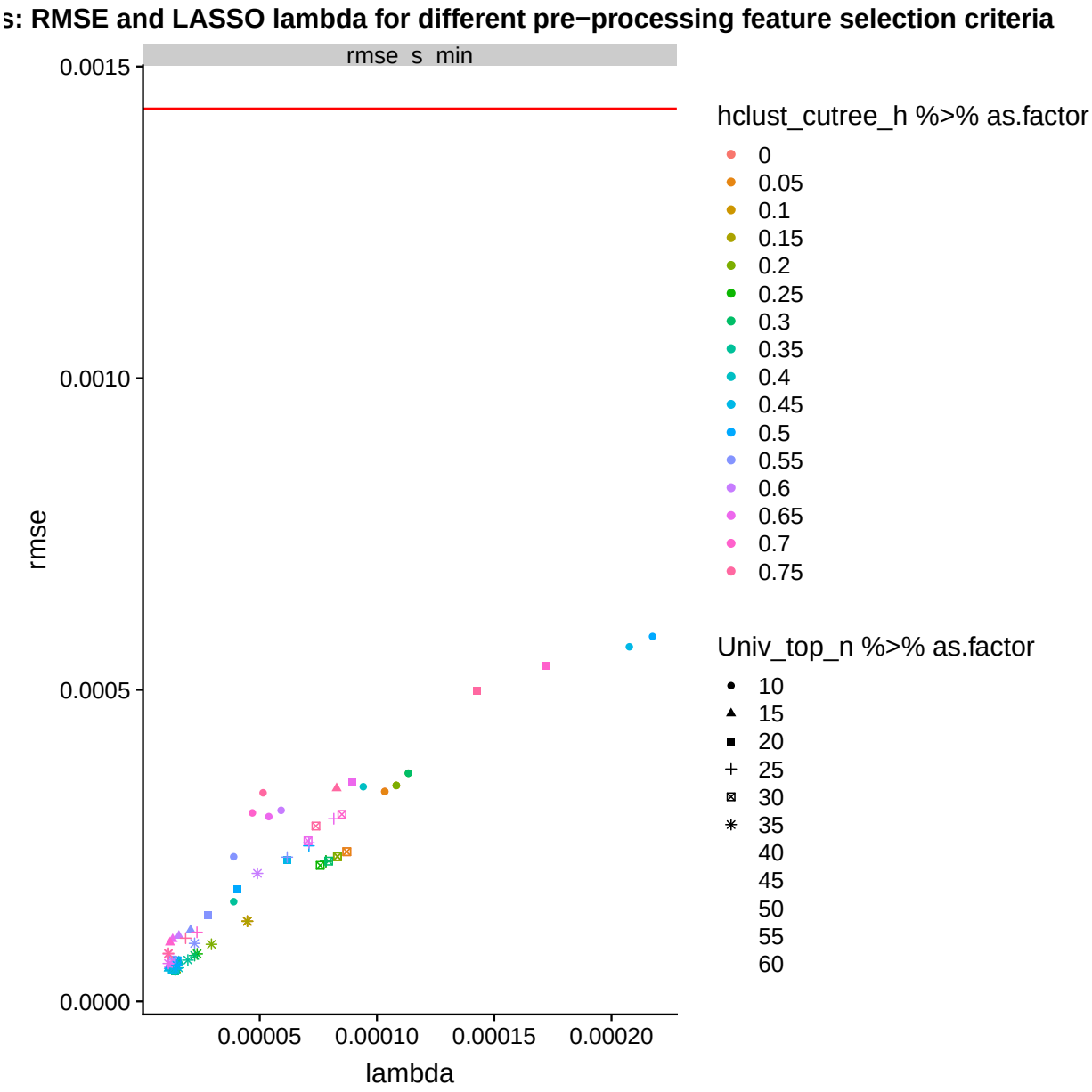
```
DF_s_lambda<-bmr_tib_naive_res %>%
  select(hclust_cutree_h, Univ_top_n,
#   s_lambda.min, s_lambda.1se, s_lambda.pushed) %>% gather('s_opt','lambda',3:5) %>%
   s_lambda.min) %>% gather('s_opt','lambda',3) %>%
  select(lambda)

DF_rmse_s_lambda<-cbind(DF_rmse, DF_s_lambda) %>% as_data_frame
```

```
## Warning: `as_data_frame()` is deprecated, use `as_tibble()` (but mind the new semantics).
## This warning is displayed once per session.
```

```
ggplot(DF_rmse_s_lambda) +
  geom_point(aes(x = lambda, y = rmse, col = hclust_cutree_h %>% as.factor, shape = Univ_top_n %>% as.fa
  geom_hline(yintercept = rmse_null, colour = "red") +
  facet_wrap(s_opt ~.) +
  labs(title = 'Sensitivity analysis: RMSE and LASSO lambda for different pre-processing feature selecti
```

```
## Warning: The shape palette can deal with a maximum of 6 discrete values
## because more than 6 becomes difficult to discriminate; you have
## 11. Consider specifying shapes manually if you must have them.
```

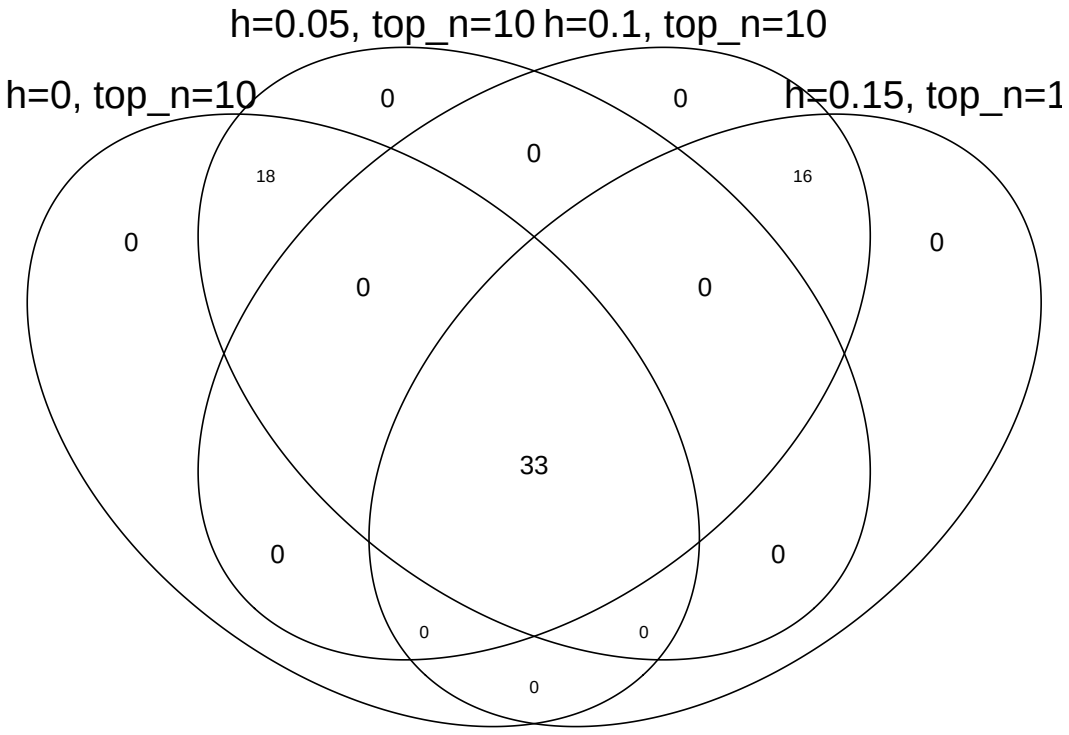
```
## Warning: Removed 80 rows containing missing values (geom_point).
```




```
# library(ggpubr)
# DF_rmse_s_lambda$hclust_cutree_h %<>% as.factor
# ggline(DF_rmse_s_lambda, x = "lambda", y = "rmse", add = c("mean_sd", "jitter"), color = "hclust_cutr
```

Features overlap accross first 4 runs

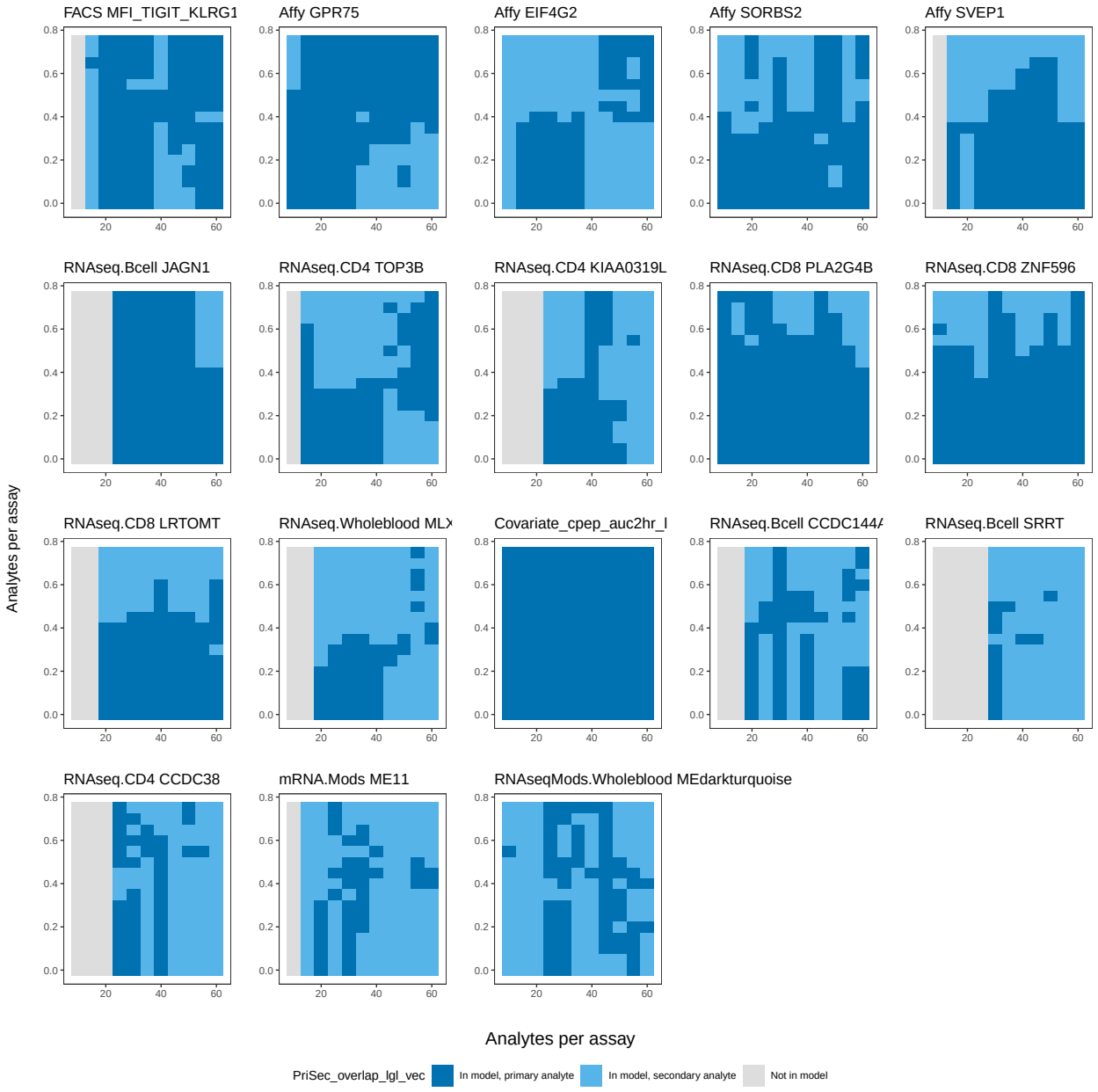
```
bmr_tib_naive_res$coef_s_min %>% setNames(str_c('h=', bmr_tib_naive_res$hclust_cutree_h, ', top_n=', bmr
  .[1:4] %>%
  gplots::venn()
```



Plot 3: Benchmark analytes comparison: overlap between each {top_n, h}i vs Gold-Standard {top_n = 30, h = 0.3}

```
bmr_all_comb<-bmr_tib_naive_res %>%
  select(hclust_cutree_h, Univ_top_n, coef_s_min, UnivOnlyCoef) %>%
  rename(secondary_analytes = UnivOnlyCoef) %>%
  mutate(primary_analytes   = coef_s_min %>% map(~.x$row[-1])) %>%
  mutate(check_overlap      = map2_lgl(primary_analytes, secondary_analytes, ~all(.x %in% .y))) ## Note
# bmr_all_comb$primary_analytes[[1]] %in% bmr_all_comb$secondary_analytes[[1]]
# bmr_all_comb_dim<-bmr_all_comb %>% select(hclust_cutree_h, Univ_top_n) %>% table %>% dim

GS_comb<-bmr_all_comb %>%
  filter(hclust_cutree_h == param.corrplot.n.clusters.h, Univ_top_n == param.Univ.filt.top.n.features) %


# REF: bmr_all_comb
GS_comb_primary_tib<-data.frame(GS_Primary_analyte = GS_comb$primary_analytes, stringsAsFactors = FALSE)

GS_comb_primary_tib %<>%
  mutate(bmr_all_comb_overlap_matrix_YN = GS_Primary_analyte %>% map(~{
    # .x = GS_comb_primary_tib$GS_Primary_analyte[[2]]
    # .x %in% bmr_all_comb$primary_analytes[[40]]

    bmr_all_comb %<>%
    ## Primary
     # .x %in% bmr_all_comb$secondary_analytes[[3]] %>% head
     # sec_list<-bmr_all_comb %>% pull(secondary_analytes)
     # sec_list %>% map(function(sec) .x %in% sec) %>% unlist

      mutate(primary_overlap_lgl_vec = primary_analytes %>%
               map_lgl(function(primary_comb_i) .x %in% primary_comb_i) %>%
               setNames(bmr_all_comb %>% unite('h_topN', c('hclust_cutree_h','Univ_top_n')) %>%
                          pull(h_topN) )) %>%

    ## Secondary
      mutate(secondary_overlap_lgl_vec = secondary_analytes %>%
               map_lgl(function(secondary_comb_i) .x %in% secondary_comb_i) %>%
               setNames(bmr_all_comb %>% unite('h_topN', c('hclust_cutree_h', 'Univ_top_n')) %>%
                          pull(h_topN) )) %>%

    ## Primary + Secondary (primary over secondary via any() )
      mutate(PriSec_overlap_lgl_vec = map2_chr(primary_overlap_lgl_vec, secondary_overlap_lgl_vec,
          ~ifelse(.y, ifelse(.x, 'In model, primary analyte', 'In model, secondary analyte'),
                  'Not in model' )))
    # end internal DF matrix for all {h,top_n} combinations
 }))

# bmr_all_comb$primary_overlap_lgl_vec %>% table
## Nested tibble with TRUE/FALSE values for (vector) overlap
# GS_comb_primary_tib$bmr_all_comb_overlap_matrix_YN[[1]] %>% select(primary_overlap_lgl_vec, secondary

# GS_comb_primary_tib %<>% mutate(overlap_matrix_YN = bmr_all_comb_overlap_matrix_YN %>% map(~.x$primar
```

```r
## coariates were forced to be at all models be definition. they are not part of the pre-processing, th
GS_comb_primary_tib[GS_comb_primary_tib$GS_Primary_analyte=='Covariate_cpep_auc2hr_log_baseline','bmr_al

## Rename analytes
# !!! FOR VISUALIZATION ONLY. NOT RELEVANT IF OTHER ANALYTES ARE SELECTED, OR IN DIFFERENT ORDER !!!
GS_comb_primary_tib$GS_Primary_analyte %<>% str_replace('.ZZZ.',' ')
GS_comb_primary_tib$GS_Primary_analyte[2:5]<-paste('Affy', c('GPR75','EIF4G2','SORBS2','SVEP1'), sep='

# library(RColorBrewer)
myColors <- c("#DDDDDD", "#56B4E9", "#0072B2")
names(myColors) <- c("Not in model", "In model, secondary analyte", "In model, primary analyte")
#names(myColors) <- c("TRUE", "FALSE", "NA")


GS_comb_primary_tib %<>%
  mutate(overlap_matrix_ggplot = map2(bmr_all_comb_overlap_matrix_YN, GS_Primary_analyte, ~
    # .x = GS_comb_primary_tib$bmr_all_comb_overlap_matrix_YN[[15]]; .y = GS_comb_primary_tib$GS_Primary
    # DF<-.x %>% select(hclust_cutree_h, Univ_top_n, PriSec_overlap_lgl_vec)
      #DF$hclust_cutree_h %>% table; DF$Univ_top_n %>% table
    .x %>%
      #select(hclust_cutree_h, Univ_top_n, PriSec_overlap_lgl_vec) %>%
      ggplot() + geom_tile(aes(x = Univ_top_n, y = hclust_cutree_h, fill = PriSec_overlap_lgl_vec)) +
        scale_fill_manual(values = myColors) +
        # labs(x = "Analytes per assay", y = "Min correlation in cluster", title = .y) +
        labs(x = "", y = "", title = .y) +
# scale_y_reverse() +
        theme(legend.position = "none", text = element_text(size=12),
              plot.title = element_text(size = 12)) +
        theme_bw(base_size = 10) + theme(panel.grid.major = element_blank(),
                                         panel.grid.minor = element_blank())

  ))
# GS_comb_primary_tib$overlap_matrix_ggplot[[15]] # MLXIP


## remove some analytes from plot
Exclude_analytes<-c(6, 8, 11, 16, 17)
GS_comb_primary_tib_ordered<-GS_comb_primary_tib[c(c(1:18)[-Exclude_analytes], Exclude_analytes),]

common_legend<-get_legend(GS_comb_primary_tib_ordered$overlap_matrix_ggplot[[1]] + theme(legend.positio
# plot_grid(NULL, common_legend, ncol=1)

Grid<-plot_grid(plotlist = GS_comb_primary_tib_ordered$overlap_matrix_ggplot %>% map(~.x + theme(legend
Grid_xlab<-ggdraw(add_sub(Grid, "Analytes per assay"))
#Grid_yx_shared<-ggdraw(add_sub(Grid_y_shared, "Min correlation in cluster"))
# Grid_no_axes_shared_legend<-plot_grid(Grid, common_legend, ncol = 1, rel_heights = c(1,.2))
ggpubr::annotate_figure(Grid_xlab, left = 'Analytes per assay', bottom = common_legend)
```



?. Session information

```
sessionInfo()
```

```
## R version 3.5.0 (2018-04-23)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 14393)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.1252
```

```
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] bindrcpp_0.2.2    knitr_1.21        JDRFCAV_0.1.0
##  [4] impute_1.54.0     limma_3.36.1      biobroom_1.12.0
##  [7] broom_0.5.0       glmnet_2.0-16     foreach_1.4.4
## [10] Matrix_1.2-14     mlrCPO_0.3.4      mlr_2.13.9000
## [13] ParamHelpers_1.12 cowplot_0.9.3     ggplot2_3.1.0
## [16] tibble_2.0.1      tidyr_0.8.2       stringr_1.3.1
## [19] purrr_0.2.5       magrittr_1.5      dplyr_0.7.8
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.0          lattice_0.20-35     gtools_3.8.1
##  [4] assertthat_0.2.0    digest_0.6.18       utf8_1.1.4
##  [7] R6_2.3.0            plyr_1.8.4          backports_1.1.3
## [10] evaluate_0.12       pillar_1.3.1        gplots_3.0.1
## [13] rlang_0.3.1         lazyeval_0.2.1      data.table_1.12.0
## [16] gdata_2.18.0        checkmate_1.9.1     rmarkdown_1.11
## [19] labeling_0.3        splines_3.5.0       munsell_0.5.0
## [22] compiler_3.5.0      xfun_0.4            pkgconfig_2.0.2
## [25] BiocGenerics_0.26.0 BBmisc_1.11         htmltools_0.3.6
## [28] tidyselect_0.2.5    gridExtra_2.3       codetools_0.2-15
## [31] XML_3.98-1.16       fansi_0.4.0         ggpubr_0.1.7
## [34] crayon_1.3.4        withr_2.1.2         bitops_1.0-6
## [37] grid_3.5.0          nlme_3.1-137        gtable_0.2.0
## [40] scales_1.0.0        KernSmooth_2.23-15  cli_1.0.1
## [43] stringi_1.2.4       reshape2_1.4.3      parallelMap_1.4
## [46] fastmatch_1.1-0     iterators_1.0.10    tools_3.5.0
## [49] forcats_0.3.0       Biobase_2.40.0      glue_1.3.0
## [52] parallel_3.5.0      survival_2.41-3     yaml_2.2.0
## [55] colorspace_1.4-0    caTools_1.17.1.1    bindr_0.1.1
```

```
bmr_tib_naive_res<-bmr_tib_naive %>%

  # s_lambda.1se
  mutate(s_lambda.1se = s %>% map_dbl('lambda.1se')) %>%
  mutate(coef_s_1se   = map2(fit_baked, s_lambda.1se, ~coef(.x, s = .y) %>% tidy)) %>%
  mutate(predict_s_1se = pmap(list(fit_baked, Baked_x, s_lambda.1se), function(x,y,z)
     predict(object = x, newx = y, s = z) %>% data.frame %>% pull(X1) )) %>%
  mutate(rmse_s_1se    = map2_dbl(predict_s_1se, Baked_y, ~sqrt(mean((.x - .y) ^ 2)))) %>%
  mutate(n_coef_s_1se  = coef_s_1se %>% map_int(~nrow(.x))) %>%

# s_lambda.pushed
  mutate(s_lambda.pushed = s %>% map_dbl('pushed_lambda')) %>%
  mutate(coef_s_pushed   = map2(fit_baked, s_lambda.pushed, ~coef(.x, s = .y) %>% tidy)) %>%
  mutate(predict_s_pushed = pmap(list(fit_baked, Baked_x, s_lambda.pushed), function(x,y,z)
     predict(object = x, newx = y, s = z) %>% data.frame %>% pull(X1) )) %>%
  mutate(rmse_s_pushed    = map2_dbl(predict_s_pushed, Baked_y, ~sqrt(mean((.x - .y) ^ 2)))) %>%
```

```
  mutate(n_coef_s_pushed  = coef_s_pushed %>% map_int(~nrow(.x)))
```

B.2: automatic via mlr::benchmark(). However, no manual control for s.

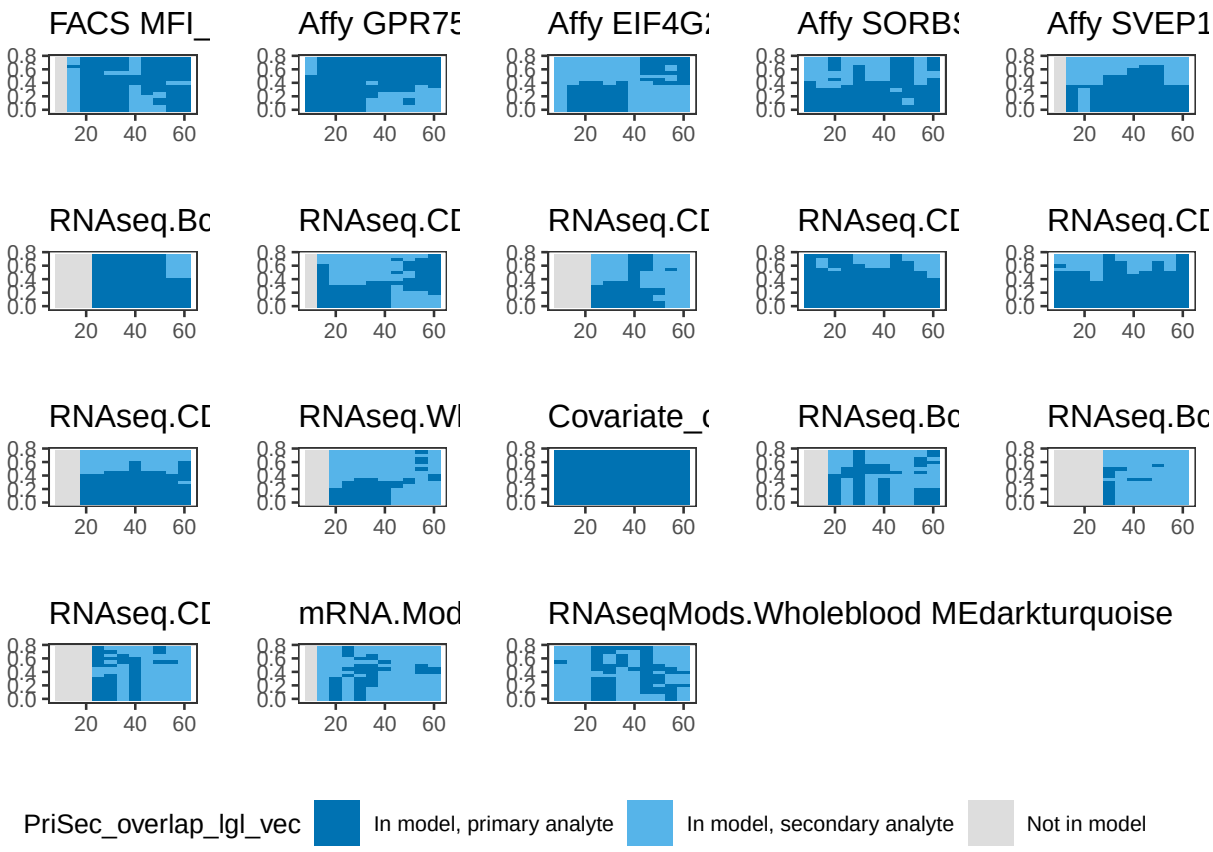
```
# benchmark's default require some additional nested resampling. here will force test to be the same 10

## test = 100% train
Task_j_N<-task_j %>% getTaskSize
Holdout_single_pair_AA<-makeFixedHoldoutInstance(train.inds = 1:Task_j_N, test.inds  = 1:Task_j_N, size
Holdout_single_pair_AA$desc$predict = 'both'

## prediction by default is done here with the learner's original s
bmr<-benchmark(bmr_tib$lrn_i, task_j, resamplings = Holdout_single_pair_AA, measures = list(rmse))
```

```
library(tidyverse)
```

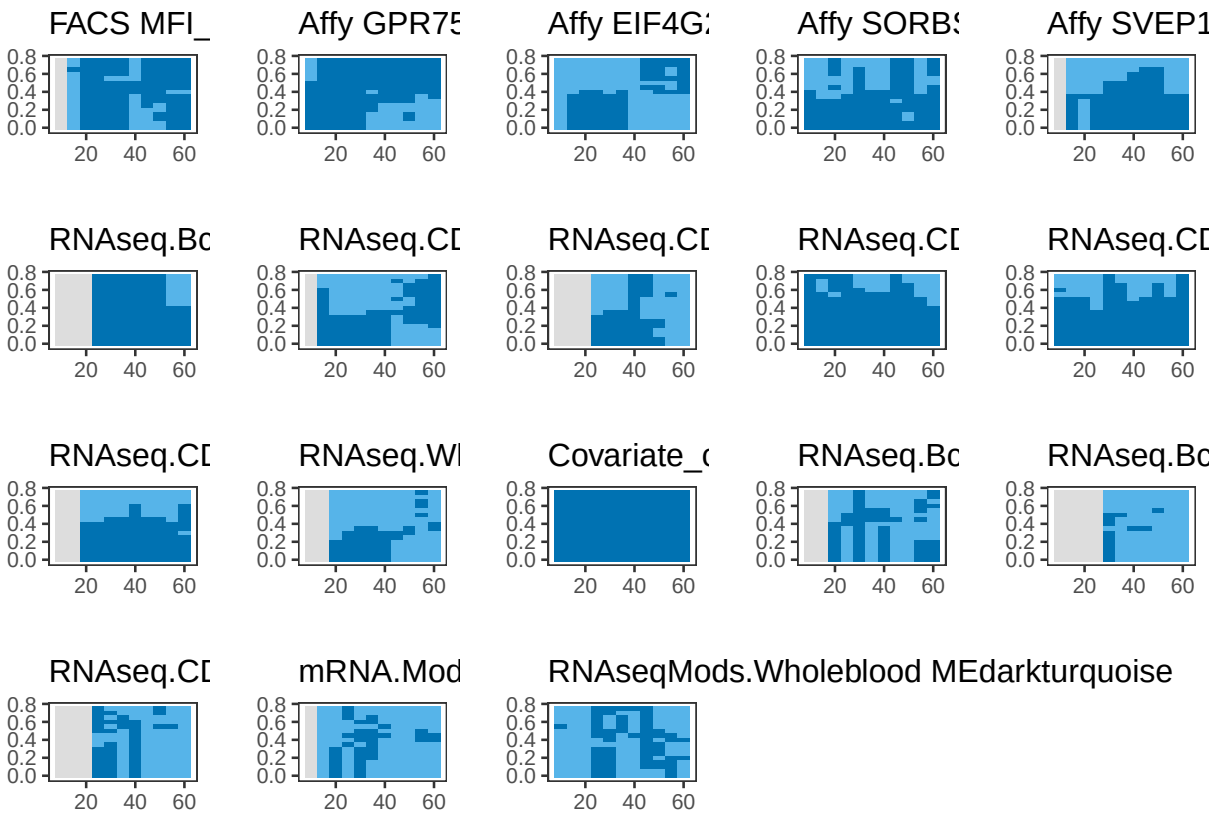
```
## -- Attaching packages ---------------------------------------------------------- tidyverse 1.2.1 --
## v readr   1.1.1     v forcats 0.3.0
## -- Conflicts ------------------------------------------------------------------ tidyverse_conflicts() --
## x foreach::accumulate() masks purrr::accumulate()
## x Matrix::expand()      masks tidyr::expand()
## x tidyr::extract()      masks magrittr::extract()
## x dplyr::filter()       masks stats::filter()
## x cowplot::ggsave()     masks ggplot2::ggsave()
## x dplyr::lag()          masks stats::lag()
## x purrr::set_names()    masks magrittr::set_names()
## x foreach::when()       masks purrr::when()
```

```
library(cowplot)

df <- data.frame(
  x = rep(c(2, 5, 7, 9, 12), 2),
  y = rep(c(1, 2), each = 5),
  z = factor(rep(1:5, each = 2)),
  w = rep(diff(c(0, 4, 6, 8, 10, 14)), 2)
)

myColors <- c("#DDDDDD", "#56B4E9", "#0072B2", "#56E4E9", "#0172B2")


gg_master<-df %>% ggplot() + geom_tile(aes(x = x, y = y, fill = z)) +
  scale_fill_manual(values = myColors) +
  labs(x = "Analytes per assay", y = "Min correlation in cluster") +
  # scale_y_reverse() +
  theme(legend.position = "none", text = element_text(size=12), plot.title = element_text(size = 12)) +
  theme_bw(base_size = 10) + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank

gg_1<-gg_master + labs(title = 'g1')
gg_2<-gg_master + labs(title = 'g2')
gg_3<-gg_master + labs(title = 'g3')
gg_4<-gg_master + labs(title = 'g4')
gg_5<-gg_master + labs(title = 'g5')
```

```
common_legend<-get_legend(GS_comb_primary_tib_ordered$overlap_matrix_ggplot[[1]] + theme(legend.positio

pg<-plot_grid(plotlist = GS_comb_primary_tib_ordered$overlap_matrix_ggplot %>% map(~.x + theme(legend.p

plot_grid(pg, common_legend, ncol = 1, rel_heights = c(1,.1))
```




```
pg
```


FACS MFI_
Affy GPR75
Affy EIF4G2
Affy SORBS
Affy SVEP1
RNAseq.Bc
RNAseq.CD
RNAseq.CD
RNAseq.CD
RNAseq.CD
RNAseq.CD
RNAseq.Wh
Covariate_c
RNAseq.Bc
RNAseq.Bc
RNAseq.CD
mRNA.Mod
RNAseqMods.Wholeblood MEdarkturquoise
0.0
0.2
0.4
0.6
0.8
20
40
60