

TK_63: Expression of Gna12 and Gna13 genes in mouse pancreatic beta cells

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Summary: to find the murine G-proteins *GNA12* and *GNA13* expression levels in pancreatic beta cells.

Candidate projects with expression info for G12/G13 proteins in pancreatic beta cells are here. From these studies the analysis was run on WT samples from the following two datasets: GSE16048 and GSE29674.

For dataset GSE16048 islets were isolated and RNA prepared from 8-week-old (gender not specified). All the mice were bred on a mixed genetic background (SV 129/C57BL/6)

For dataset GSE29674 islets were isolated and RNA prepared from five 5-week-old female mice (C57/129 genetic background).

R code

Load libraries

```
library(tidyverse)
```

Load dataset GSE16048

```
# Load ensemblid2affyid file
ensembl2affy <- read_delim(file = "./data/ensemblid2affyid.txt", delim = "\t", col_names = c("EnsemblID", "AffyID"))

# Only load WT samples
# VALUES represent Log2 RMA normalized expression signal
for (sample in c("GSM401525", "GSM401526", "GSM401527")){
  assign(x = sample, value = read_delim(file = paste0("https://www.ebi.ac.uk/biostudies/files/E-GEOD-16048", sample, ".txt"), delim = "\t", col_names = c("EnsemblID", "AffyID")))
}

# Merge datasets
data.16048 <- tibble(Probe=GSM401525$ID_REF, GSM401525=GSM401525$VALUE, GSM401526=GSM401526$VALUE, GSM401527=GSM401527$VALUE)

# Add column with median expression value per probe
data.16048 <- data.16048 %>%
  rowwise() %>%
```

```

mutate(median=median(c(GSM401525,GSM401526,GSM401527)))

# Add column with mean expression value per probe
data.16048 <- data.16048 %>%
  rowwise() %>%
  mutate(mean=mean(c(GSM401525,GSM401526,GSM401527)))

data.16048_gene <- inner_join(x=data.16048, y=ensembl2affy, by=join_by(Probe == Affy_MOE430A_ID))

```

Load dataset GSE29674

```

# Only load WT samples
# VALUES represent Log2 RMA normalized expression signal
for (sample in c("GSM735944","GSM735945","GSM735946","GSM735947","GSM735948")){
  assign(x = sample, value = read_delim(file = paste0("https://www.ebi.ac.uk/biostudies/files/E-GEOD-29674/"),
  )

# Merge datasets
data.29674 <- tibble(Probe=GSM735944$ID_REF,
                     GSM735944=GSM735944$VALUE,
                     GSM735945=GSM735945$VALUE,
                     GSM735946=GSM735946$VALUE,
                     GSM735947=GSM735947$VALUE,
                     GSM735948=GSM735948$VALUE,)

# Add column with median expression value per probe
data.29674 <- data.29674 %>%
  rowwise() %>%
  mutate(median=median(c(GSM735944,GSM735946,GSM735946,GSM735947,GSM735948)))

# Add column with mean expression value per probe
data.29674 <- data.29674 %>%
  rowwise() %>%
  mutate(mean=mean(c(GSM735944,GSM735946,GSM735946,GSM735947,GSM735948)))

data.29674_gene <- inner_join(x=data.29674, y=ensembl2affy, by=join_by(Probe == Affy_MOE430A_ID))

```

Summarize mean expression by gene (dataset GSE16048)

```

mean_exp_per_gene.GSE16048 <- data.16048_gene %>% group_by(EnsemblID) %>% summarise(Mean_exp=mean(mean))

gna12 <- 'ENSMUSG00000000149'
gna13 <- 'ENSMUSG000000020611'

# Print percent rank for gna12 and gna13
print(filter(mean_exp_per_gene.GSE16048, EnsemblID %in% c(gna12, gna13)))

```

```

## # A tibble: 2 x 4
##   EnsemblID      Mean_exp Dataset Percent_rank

```

```
##   <chr>                <dbl> <chr>                <dbl>
## 1 ENSMUSG00000020611    8.25 GSE16048            0.656
## 2 ENSMUSG00000000149    6.41 GSE16048            0.417
```

Summarize mean expression by gene (dataset GSE29674)

```
mean_exp_per_gene.GSE29674 <- data.29674_gene %>% group_by(EnsemblID) %>% summarise(Mean_exp=mean(mean))

gna12 <- 'ENSMUSG00000000149'
gna13 <- 'ENSMUSG00000020611'

# Print percent rank for gna12 and gna13
print(filter(mean_exp_per_gene.GSE29674, EnsemblID %in% c(gna12, gna13)))
```

```
## # A tibble: 2 x 4
##   EnsemblID      Mean_exp Dataset  Percent_rank
##   <chr>          <dbl> <chr>          <dbl>
## 1 ENSMUSG00000020611    5.30 GSE29674        0.469
## 2 ENSMUSG00000000149    3.49 GSE29674        0.324
```

R session information

```
sessionInfo()
```

```
## R version 4.2.2 (2022-10-31)
## Platform: aarch64-apple-darwin20 (64-bit)
## Running under: macOS Ventura 13.2.1
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2-arm64/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] lubridate_1.9.2 forcats_1.0.0  stringr_1.5.0  dplyr_1.1.2
## [5] purrr_1.0.1     readr_2.1.4    tidyr_1.3.0    tibble_3.2.1
## [9] ggplot2_3.4.2    tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] pillar_1.9.0      compiler_4.2.2  tools_4.2.2     bit_4.0.5
## [5] digest_0.6.33     timechange_0.2.0 evaluate_0.21    lifecycle_1.0.3
## [9] gtable_0.3.3      pkgconfig_2.0.3 rlang_1.1.1     cli_3.6.1
## [13] rstudioapi_0.15.0 curl_5.0.1      parallel_4.2.2  yaml_2.3.7
## [17] xfun_0.39         fastmap_1.1.1   withr_2.5.0     knitr_1.43
## [21] generics_0.1.3    vctrs_0.6.3     hms_1.1.3       bit64_4.0.5
```

## [25]	grid_4.2.2	tidyselect_1.2.0	glue_1.6.2	R6_2.5.1
## [29]	fansi_1.0.4	vroom_1.6.3	rmarkdown_2.23	tzdb_0.4.0
## [33]	magrittr_2.0.3	scales_1.2.1	htmltools_0.5.5	colorspace_2.1-0
## [37]	utf8_1.2.3	stringi_1.7.12	munsell_0.5.0	crayon_1.5.2