

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
```

Results

Table 1: Pancreatic beta-cell gene expression³ and percentile rank⁴ of GNA12 and GNA13 genes across WT samples from studies GSE29674 and GSE16048.

EnsemblID	Gene name	Mean expression	Percentile rank	Study
ENSMUSG00000020611	gna13	5.298699	0.4688176	GSE29674
ENSMUSG00000000149	gna12	3.490793	0.3242475	GSE29674
ENSMUSG00000020611	gna13	8.245162	0.6560356	GSE16048
ENSMUSG00000000149	gna12	6.405584	0.4173311	GSE16048

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
```

¹Log2 RMA normalized expression signal

²Percentage of expression values in its frequency distribution that are less than a given gene expression value.

³Log2 RMA normalized expression signal

⁴Percentage of expression values in its frequency distribution that are less than a given gene expression value.

```
##
## 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
```