# 01.2_Prepare-CredbileSet-T2D-Metabo-file.Rmd

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*March 15, 2017*

Setup libraries and directories

```r
"%&%" <- function(a,b) paste0(a,b)
library("dplyr")
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library("data.table")
```

```
## -------------------------------------------------------------------------
## data.table + dplyr code now lives in dtplyr.
## Please library(dtplyr)!
## -------------------------------------------------------------------------
##
## Attaching package: 'data.table'

## The following objects are masked from 'package:dplyr':
##
##     between, first, last
```

```r
library("ggplot2")
```

```
## Warning: package 'ggplot2' was built under R version 3.3.2
```

```r
serv.dir <- "/Users/jtorres/FUSE/"
rds.dir <- serv.dir %&% "projects/wtsa/enhancer_driven/probe_design/rds/"

fgwas.dir <- serv.dir %&% "projects/wtsa/enhancer_driven/probe_design/fgwas_output/"

fgwas.input.file <- serv.dir %&% "projects/t2d-integration/fgwas/" %&% "credsets_metabochip/fgwas_input,

cred.df <- fread(fgwas.input.file) %>% dplyr::select(one_of("SNPID","CHR","POS","SEGNUMBER","PPA","LOCUS

fgwas.outfile <- fgwas.dir  %&% "metabochip_gwasmod.bfs.gz"
fgwas.df <- fread("cat " %&% fgwas.outfile %&% " | zmore") %>% dplyr::select(one_of("id","PPA","chunk")
names(fgwas.df) <- c("SNPID","PPA.fgwas","SEGNUMBER")
fgwas.df$SEGNUMBER <- fgwas.df$SEGNUMBER + 1 # fgwas file is 0-based

cred.df <- inner_join(cred.df,fgwas.df,by="SNPID")
cred.df <- cred.df[(cred.df$SEGNUMBER.x == cred.df$SEGNUMBER.y),]
cred.df <- mutate(cred.df, change=PPA.fgwas-PPA) %>% arrange(desc(change))
```

```r
cred.df <- dplyr::select(cred.df, -SEGNUMBER.y)
names(cred.df)[which(names(cred.df)=="SEGNUMBER.x")] = "SEGNUMBER"

saveRDS(cred.df,file=rds.dir%&%"fgwas.cred.metab.df.RDS")
```