Sleeping genes

Effects of insufficient sleep on gene expression by restriction on sleep time during working week.

Problem Statement

Background Rationale

- Restriction on sleep has many adverse effects on human physiology and health. It correlates directly with the cardiometabolic diseases.
- The SR studies on humans has also shown activation in immune defense during sleep restriction.
- The Experimental sleep restriction (SR) data has provided some insight on the increase in cardiometabolic diseases, BP, heart rate etc.

Links : Data Reference Paper

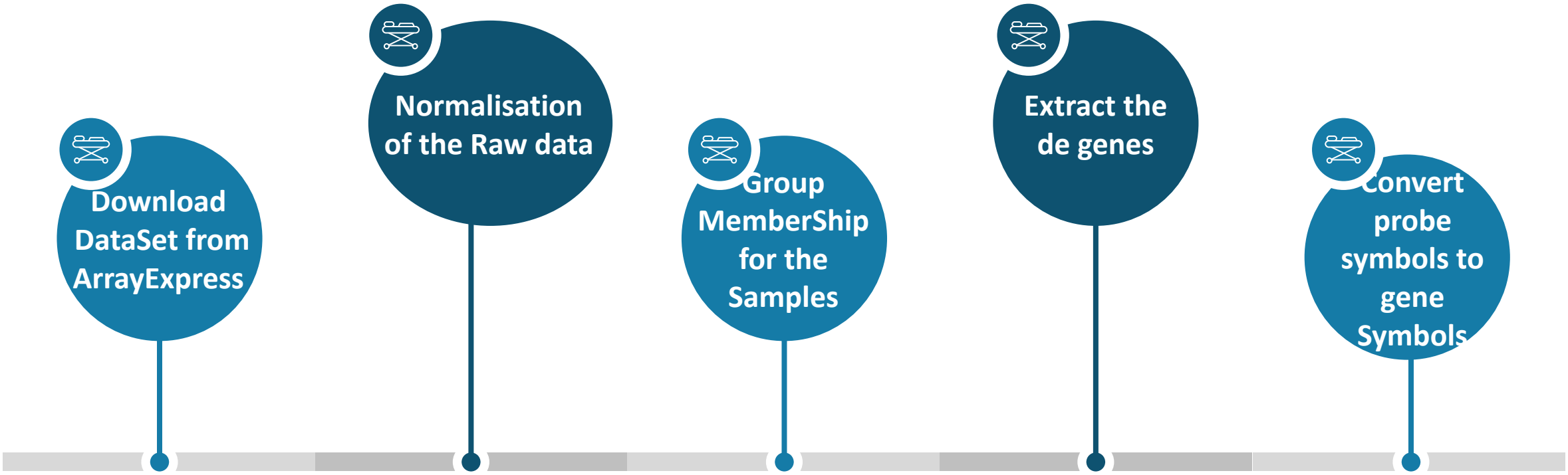
Code

```
library(ArrayExpress)
library("affy")
library("limma")
library(DataExplorer)


AEset1 = ArrayExpress("E-MEXP-3936")
AEsetnorm1 = rma(AEset1)
fac1 = grep("Factor.Value",colnames(pData(AEsetnorm1)), value=T)
if (suppressWarnings(require("arrayQualityMetrics", quietly=TRUE))) {
  qanorm = arrayQualityMetrics(AEsetnorm1,outdir = "QAnorm",intgroup = fac)}

express1 = exprs(AEsetnorm1)

qx <- as.numeric(quantile(express1,c(0.0,0.25,0.5,0.75,0.99,1.0),na.rm=T))
LogC <- (qx[5] > 100 || (qx[6] - qx[1] > 50 && qx[2] > 0))
if(LogC) { express1[which (express1<= 0)] <- NaN
exprs(AEsetnorm1) <- log2(express1)}    #Log transformation of exprs(gset) for DE
gene analysis


# group membership for all samples
gsms <- paste0("0X10X10X10X10X10X10X10X10X10X10X10X1")
#gsms <- paste0("X01X01X01X01X01X01X01X01X01X01X01X01")
sml <- strsplit(gsms, split="")[[1]]
```

Github Repository

https://github.com/krag-harsh/PB_group/edit/main/PBProject.R

Methodology



We downloaded the dataset from the arrayExpress database using the ArrayExpress library in R

rma normalisation of the data was done and then the quantile normalisation and log transformation were also done after

The samples were divided into groups to do the differential gene analysis.The analysis was only done on the baseline and the sleep restriction group

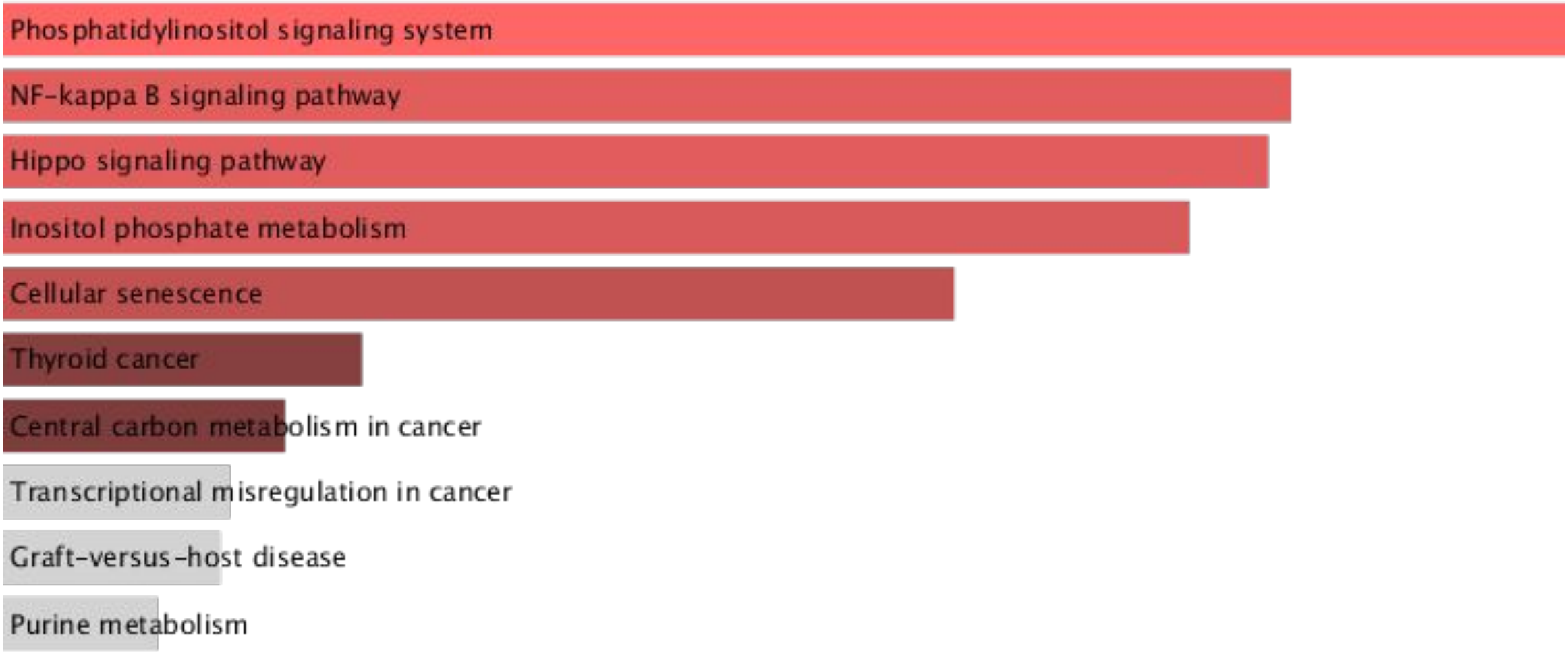
the differentially expressed genes were extracted from the above data which had logFC<1.2 and P Value<0.05 in the form of probe symbols

The probe symbols extracted from the program was then converted into their respective gene Symbols

OUTCOME

Affymetrix Probe Symbols	Gene Symbols	Pathway Analysis on EnrichR	Pathways affected found
• Gene Probe Symbols were found from the above R code	• A third party website(DAVID) was used to convert Affymetrix Probe Symbols to Gene symbols	• The gene Symbols now found were analysed on Enrich R to find the pathways Affected	• The affected pathways were found that can be observed to get an inference on what could be effects of sleep restriction at the gene level.

Affected Pathways



Sorted according to P value ranking

Affected Pathways With their respective score

Index	Name	P-value	Adjusted p-value	Odds Ratio	Combined score
1	Phosphatidylinositol signaling system	0.001612	0.2965	2.82	18.14
2	NF-kappa B signaling pathway	0.003329	0.2965	2.70	15.38
3	Hippo signaling pathway	0.003537	0.2965	2.22	12.54
4	Inositol phosphate metabolism	0.004360	0.2965	2.91	15.82
5	Cellular senescence	0.008140	0.4428	2.07	9.98
6	Thyroid cancer	0.03917	1.000	2.90	9.40
7	Central carbon metabolism in cancer	0.04804	1.000	2.24	6.81
8	Transcriptional misregulation in cancer	0.05556	1.000	1.63	4.72
9	Graft-versus-host disease	0.05708	1.000	2.58	7.38
10	Purine metabolism	0.06735	1.000	1.73	4.68